CRYSTAL ENGINEERING WITH THIOUREAS: A STRUCTURE-BASED INQUIRY

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DISSERTATION ABSTRACT

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Structural trends applicable to crystal engineering were studied in three classes of thiourea-based compounds. The aim of the study was to identify, predict, and ultimately design reliable single-molecule structural features, which could then be used to engineer crystals with desirable properties. In one class of compounds, this goal was achieved: Nalkyl and N-aryl derivatives of N,N'-bis(3-thioureidopropyl)piperazine adopted an identical conformation in the solid state, which resulted in near-identical crystal packing. A second class of closely related compounds, N-substituted tris(2-thioureidoethyl)amines, showed no such reliability in the solid state, likely because the parent structure lacked hydrogen-bonding functionalities sufficient to control intramolecular structure. In the third class of compounds that we studied, 1-benzoyl-3-(2-pyridyl)thioureas, substitution patterns were often predictive of molecular conformation; however, these intramolecular trends did not lead to recognizable crystal packing motifs. Nevertheless, certain physical properties observed in this last class of compounds—color, solubility, and often crystallinity—were conformer-specific, interestingly without any apparent relevance to crystal lattice structure. Solution-state and solid-state conformational trends in these 1benzoyl-3-(2-pyridyl)thioureas have been documented, and speculations as to the source of color in one of the two observed conformations have been noted.

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To my family, without whom none of this work would have been possible.

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CHAPTER I

INTRODUCTION

Due to the often inexorable link between a solid substance's desirable physical or chemical properties and its supramolecular structure, gaining a predictive understanding of the factors that determine solid-state organization is very valuable to materials science research. The study of solid-state organization, crystal engineering, has applications in areas as diverse as catalysis, thin films, thin films, fliquid crystals, and drug discovery, the pigments, metal-organic frameworks, flequency of non-linear optical and ferroelectronic materials, flequency and the development of new technology for information storage. Because crystal engineering is a relatively new field, few predictive models for supramolecular organization are currently available; flew predictive models for supramolecular organization are currently available; consequently, most work still depends heavily on *a posteriori* structure analysis, rather than any theoretical or computational method. See

Despite nearly 40 years of research directed at the prediction of solid-state behavior, structural similarity—even among highly similar classes of compounds—often appears to be the exception, rather than the rule. The prevalence of structural diveristy periodically evokes lamentations that true predictivity will remain elusive, due to the "mysticism"²⁷ inherent in crystal structure formation.^{28,29} Nevertheless, many examples of

predictable solid-state behavior can be found in the chemical literature, and it can only be surmised that the irregularity observed among other classes of compounds correlates more with observational shortcomings than with some inherent exception to the predictable ordering of the natural world.

Although it is entirely possible that the forces governing crystal formation are sufficiently intricate to surpass human cerebral processing power, it is also quite likely that, given a sufficient quantity of data, an algorithm may someday elucidate the more arcane aspects of solid-state organization, yielding a means of engineering complex solid-state architectures. In the past decade, crystal structure predicition (CSP) software has improved dramatically, and it is now common to find naturally-occurring polymorphs among the 10-100 structures within about 10 kJ/mol of the global minimum.³⁰ In one recent study, the three lowest-energy DFT(d) optimized crystal structures of a small organic molecule corresponded to the three known polymorphs of that molecule.³¹

Nevertheless, the scope of CSP is still quite limited, as its "success depends to a large extent on finding the right combination of model accuracy and computational cost," and its current incarnation serves only to complement—rather than replace—traditional polymorphic screening.³³

Despite both its recent progress and its forseeable potential, CSP still has relatively little impact on the intentional design of solid-state materials, the fundamental goal of crystal engineering. The distinction³⁴ between CSP and crystal engineering can best be characterized as one of different approaches to a similar problem, with different idealized outcomes. CSP aims to successfully model (and predict) molecular mechanics

within a crystal lattice, whereas crystal engineering is very much a materials-based discipline. At best, CSP can predict likely polymorphs of a known (or theoretical) compound, but it cannot determine the molecular structure most apt to form a desirable crystal lattice, and it cannot link structural characteristics with useful physical properties. For this reason, *a posteriori* studies are still the best approach to developing crystal engineering strategies, and the need for crystallographic data is only growing.

While early crystal engineering efforts tended to focus on establishing common crystal packing motifs within certain classes of compounds, 35,36 current research in crystal engineering tends to favor a supramolecular,²⁹ or network,⁸ approach. In this author's humble opinion, the distinction between these methodologies is largely pedantic: both rely on identifying common intermolecular interactions, and thereby developing building blocks by which complex solids may be intentionally designed. For example, in 1989, Desiraju and Gavezzotti described the earlier approach as "statistical in nature, [one which] generalizes from a large amount of crystallographic data and extrapolates from common geometrical motifs therein to derive new structures."³⁷ Over a decade later, Sharma described the network approach as one which advocates "simplify[ing] complex crystalline structural features into easily identifiable network topologies based on chemical and structural information of the constituent molecular building blocks."8 These "molecular building blocks" can then be linked into a "network topology" by a series of intermolecular interactions, also known as supramolecular synthons. ¹⁷ As far as this author can tell, the primary—and (vide infra) most important—difference between

[§] Not formally quantified by peer-reviewed methodology

these two methodologies is that the latter approach recognizes the need for a reliable subunit, around which complex crystal packing interactions can be designed.

The network approach—and crystal engineering, in general—tends to function most smoothly in inorganic^{38,39} and organometallic^{17 18} compounds, most likely due to the predictable and relatively rigid coordination geometry around the metal center.⁴⁰ In strictly organic compounds, however, crystal engineering—of any variety—is considerably more challenging, as organic compounds tend to exhibit greater conformational flexibility, compared to their metal-centered brethren. (**Figure 1.1**).^{43,44}

Figure 1.1. Crystal engineering with organometallics vs. "pure" organics. Crystals of the ruthenium complex (left) can grow in five different morphologies, depending on solvent choice—but all crystals share an identical unit cell.⁴¹ Comparatively, the red, orange, and yellow hues of its six polymorphic forms have earned the organic carbonitrile (right) the moniker of "ROY."⁴²

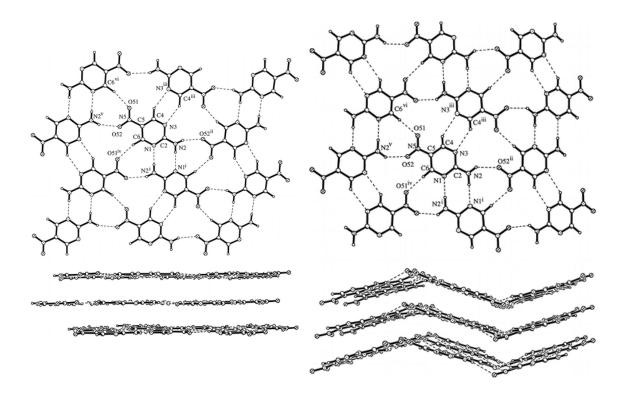
Computational studies performed on various organic molecules have shown that the multiple (local) energetic minima found for a single compound may differ in energy by as little as 10-25 J/mol.¹¹ Even translated into the crystal lattice, this energy difference tends

to be relatively insignficant: the energies of most polymorphs fall within a range of 1-3 kJ/mol. ^{11,45,46}

Much of this small variability in crystal lattice energy likely originates in the multitude of weak "hydrogen-bonding" interactions such as CH...X and CH... π , ⁴⁷ which, in all but the simplest compounds, are liable to overwhelm stronger intermolecular interactions between heteroatomic donor/acceptor pairs. The overall effect of these weak interactions is such that at least one author has referred to a compound's hydrocarbon backbone as a "solid-state functional group," to be considered alongside functional groups more common to crystal engineering studies, such as amides, carboxylic acids, ureas, and alcohols. ⁴⁸ For example, Forms I and II of 2-amino-5-nitropyrimidine form hydrogen bonds between the same four donor-acceptor pairs, yet have significantly different crystal packing arrangements (**Figure 1.2**). ⁴⁹ Given the very small difference between many molecules' global and local conformational energetic minima, the energy that can be gained through even very weak, van der Waals-type interactions is likely sufficient to direct crystal lattice formation—in ways that are difficult to predict via "traditional," functional group-based methodologies.

Adding an additional layer of complexity to organic structure prediction, many functional groups are capable of forming more than one supramolecular synthon, thereby reducing the predictability with which "molecular building blocks" may be knit together. ⁴⁸ Carboxylic acids, for example, commonly form either chains (b) or dimers (a) (**Figure 1.3**) in the solid state; ⁵⁰ however, in molecules with at least one additional hydrogen-bonding functional group, one of these two homosynthons forms only 34% of

Figure 1.2. Hydrogen bonding patterns and crystal packing in Forms I (left) and II (right) of 2-amino-5-nitropyrimidine.



the time.⁵¹ Comprising the remaining 66% of intermolecular interactions observed among carboxylic acids in the CSD, heterosynthons, or interactions between two different functional groups, were found to be similarly preferential in other classes of compounds, as well. Taken from the same study, the data shown in **Table 1.1** indicate the overall preference for heterosynthon formation when carboxylic acids are present alongside other hydrogen-bonding functional groups. Compounded by the conformational flexibility of organic compounds, this relative lack of predictability in synthon formation clearly incorporates a new degree of difficulty into crystal engineering efforts.

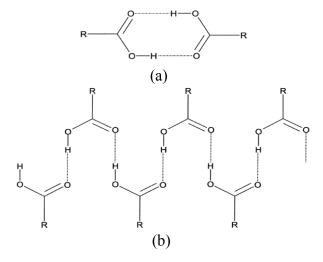


Figure 1.3. Carboxylic acid homosynthons. The two most common intermolecular interactions between COOH groups, (a) dimers and (b) chains, form in 31% and 3%, respectively, of all CSD structures containing at least one COOH unit.

Table 1.1. Supramolecular synthon formation in carboxylic acids containing at least one other hydrogen-bonding functional group.⁵¹ "Refined" structures are those in which the CSD search was limited to molecules containing COOH and the specified functional group, with no additional hydrogen-bonding moieties. The sum of homosynthons and heterosynthons may not be equal to the total number of structures, as both may occur concurrently within one structure, and both may be entirely absent from another.

Functional Group	Cl-	ОН	$CONH_2$	Aromatic N	C=O
# CSD Structures	267	1176	177	607	597
# Homosynthons ^a	3 (1%)	235 (20%)	$8 (5\%)^b$	45 (7%)	167 (28%)
# Heterosynthons	172 (64%)	540 (46%)	101 (57%)	468 (77%)	235 (20%)
# Refined CSD Structures	51	276	19	126	178
# Refined Homosynthons	0 (0%)	82 (30%)	2 (5%) ^c	9 (7%)	111 (62%)
# Refined Heterosynthons	51 (100%)	191 (69%)	16 (84%)	123 (98%)	85 (48%)

^aCOOH...COOH interactions, both cyclic dimers and chains

^b52 structures (29% of total) have CONH₂...CONH₂ homosynthon

^c2 structures (11% of total) have CONH₂...CONH₂ homosynthon

Considering all of these factors, it appears that the best approach to crystal engineering is probably one which avoids the pedantic distinction between earlier and more contemporary methodologies. Functional group interactions are still quite relevant to supramolecular design, as certain synthons—such as the COOH...N_{arom} interaction shown in **Table 1.1**—can be highly dependable in well-defined circumstances. These interactions are particularly relevant when attempting to incorporate flexible organic molecules into network-based synthetic strategies, as reliable *intra*molecular interactions can add a significant degree of predictability to monomeric molecular shape, thereby facilitating complex supramolecular schemes. By discovering functional group interactions that possess the ability to define molecular shape, and incorporating these rigid structural features into new-material design, it will be possible to successfully apply the principles of network-based crystal engineering to flexible organic molecules—and, more than likely, this research will uncover compounds that violate all predetermined principles, but remain quite fascinating, nonetheless.

Incorporating the principles of this "reformatted" approach to crystal engineering, this work deals with the solid-state structural features of a diverse series of thioureas, a class of compounds in which solid-state trends have been repeatedly characterized as difficult to predict.⁵² Particularly when compared to the isostructural ureas, which are well-known for the reliability with which they form certain supramolecular synthons, ⁵³⁻⁵⁵ thioureas' propensity for structural variability is at times utterly confounding, and must be at least partially responsible for the relative dearth of solid-state studies in the chemical

literature. Otherwise, given both medicinal chemists' burgeoning interest in thioureacontaining compounds⁵⁶⁻⁶⁰ and the importance of polymorphism in drug discovery, ^{1,2,11,12,61} it seems unlikely that the crystalline organization of thioureas would have garnered so little apparent interest.

Perfectly in tune with both the promises and the pitfalls of crystal engineering, this work contributes both one of the most reliable crystal packing motifs to be found in the chemical literature (**Chapter III**), and a set of structures (**Chapter II**) that, despite being produced from a series of similar and similarly-related compounds, appear to offer little in the way of predictability. Perhaps also in tune with the highly serendipitous nature of science, on the whole, this work also introduces a series of thioureas (**Chapters IV-VI**) which, although offering very little in terms of crystal lattice prediction, present a fascinating example of the effect that solid-state structure—even on a monomeric level—can have on a compound's physical characteristics. This latter class of thioureas also offers a insight into certain hydrogen-bonding interactions, providing the first experimental backing for a 20-year-old theoretical postulate.

Therefore, despite lacking a unified theory of thiourea crystal structure prediction,§ this work contributes a great deal to the study of solid-state thioureas—and also to the study of the hydrogen bonding itself. Ultimately, it may be that with thiourea crystal engineering—as with many other facets of existence—the sage advice of this author's father will again prove apt, and comforting:

[§] The vicissitudes of crystal lattice formation have thoroughly dashed any delusions of grandeur that this author may once have possessed!

If you get a hit one out of every three times you step up to the plate, you're going to the Hall of Fame. That means that the best of the best still fail two-thirds of the time. Ted Williams, who was at least partially immortal, failed almost 60% of the time in 1941, and he was the last person to crack .400. So don't ever let failure get to you, because failure is part of success. If you got it right every time, there'd be no reason to keep trying...

CHAPTER II

TRIS(N-ALKYLTHIOUREIDO)AMINES:

AN EXERCISE IN STRUCTURAL DIVERSITY

Introduction

In contrast to ureas, which, with relatively few exceptions, prefer a *trans-trans* conformation (**Figure 2.1**) in the solid state,⁶² thioureas tend to exhibit a significant degree of conformational flexibility: both the *trans-trans* and *trans-cis* conformations are well represented within the chemical literature.²⁶ While solution-state studies indicate that the *trans-cis* conformer is the predominant solvated species,⁶³ the approximate ratio of

trans-trans to trans-cis conformers in the solid state appears to coincide with the calculated energy difference between the two species, which, for N,N'-disubstituted thioureas, is approximately 1-2 kcal/mol, in favor of the trans-cis conformation. ²⁶ Because the trans position is higher in energy for monoalkylated

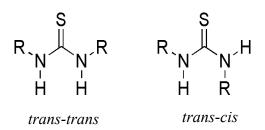


Figure 2.1. Stable conformations of N,N'-disubstituted thioureas.

thioureas, by approximately 0.5-1 kcal/mol,⁶⁴ it may be that the greater double bond character of the thiourea C=N bonds leads to increased steric repulsion between two

trans substituents, creating the small observed (and calculated) preference for the *trans-cis* conformation.

Custalcean, *et al*, propose that, at least in the solid state, conformational preferences are closely related to the potential for hydrogen bond formation.⁵² Because the energetic difference between the *trans-trans* and *trans-cis* conformations is so small, the energetic benefit of hydrogen bonding may outweigh any destabilization consequent to steric crowding. In relatively simple N,N'-homodisubstituted thioureas⁶ and N,N'-disubstituted bis(thioureas),⁶⁵ bulky substituents were found to favor the *trans-trans* conformation, likely because steric repulsion in the *cis* position (*i.e.* anti-periplanar to the thiocarbonyl moiety) inhibited hydrogen bond formation. In a related series of bis(thioureas), however, N-substitution appeared to have little impact on the preferred conformation of the thiourea moiety, and hydrogen bonding trends were most closely associated with packing effects originating in other parts of the molecule.⁶⁶

This discrepancy is representative of the difficulties inherent to crystal engineering: patterns of solid state behavior may remain static within a narrowly-defined class of compounds, but do not necessarily translate to similar systems. Rather than representing an inherent limitation of crystal engineering itself, this discrepancy merely reflects our relatively modest understanding of the factors that determine solid-state structure, and emphasizes the need for an increased body of crystallographic data, from which solid-state predictions may be more thoroughly refined. Both the irregularity with which highly similar molecules precipitate from solution, and the potential for solid-state

predictions found in the consistencies that exist even within a diverse body of structures, are exemplified by compounds **1-5** (**Figure 2.2**), the subject of this chapter.

Figure 2.2. General structure of compounds 1-5.

Results

Thioureas 1-5 were prepared from alkyl isothiocyanates and tris(2-aminoethyl)amine, in 60-90% yield. In our initial synthesis, the reaction mixture was stirred at room temperature for 1-3 days, then filtered through a silica plug and washed quickly with ethanol. The resultant product, obtained in somewhat low yield, was sufficiently clean for both spectral analysis and successful crystallization, and we made no attempt to further optimize the reaction.

While resynthesizing thioureas **3** and **5** to obtain full characterization data for these compounds, we used a different synthetic procedure. Instead of stirring the reaction mixture at room temperature for a few days, we refluxed it gently overnight. We also omitted the silica plug, and instead simply removed the reaction solvent (THF) and

recrystallized the solid residue from acetone/hexanes. This procedure increased the product yield from 60-65% to 85-90%, and is certainly the methodology that we would recommend for future synthetic attempts.

Single crystals for X-ray crystallography were grown from either binary or ternary solvent systems, using hexanes as a counter-solvent. We were able to obtain only a single polymorph of each of compounds 2-5, although we observed more than one crystal morphology in both 2 and 4. We obtained a second polymorph of 1 from ethanol/water—which, interestingly enough, had the same prismatic morphology as the polymorph grown from ethanol/hexanes, albeit a different unit cell—but it was too disordered for further structure elucidation. Consequently, we propose that morphology is not indicative of crystal structure, at least in the case of compounds 1-5. Selected crystallographic data can be found in Table 2.1.

Discussion

Highlighting the conformational flexibility of solid-state thioureas, both *trans-trans* and *trans-cis* conformers are present in all crystal structures that we obtained for compounds **1-5**. Two *trans-trans* conformers are present in all compounds except **3**, which has only one *trans-trans* moiety. At first glance, the presence of both thiourea conformations appears to be one of the only common features of these structures—apart from their near-identical atomic composition—as both hydrogen bonding interactions and macroscale crystal packing are otherwise quite disparate. The two *trans-trans* thiourea moieties in compound **1** (R = ethyl) engage in characteristic head-to-tail hydrogen bonding, both intramolecularly and intermolecularly, forming infinite chains of inversely-

Table 2.1. Selected crystallographic data for 1-5.

Compound	1	2	3	4	5
Substituent	ethyl	<i>n</i> -propyl	isopropyl	tert-butyl	phenyl
Formula	$C_{15}H_{33}N_{7}S_{3} \\$	$C_{18}H_{39}N_{7}S_{3} \\$	$C_{18}H_{39}N_{7}S_{3} \\$	$C_{21}H_{45}N_{7}S_{3} \\$	$C_{27}H_{33}N_{7}S_{3} \\$
Crystallization Solvents	ethanol hexanes	ethanol hexanes	dichloroethane hexanes	acetonitrile xylenes hexanes	Dichloroethane hexanes
Crystal Morphology	prisms	prisms	prisms	cubes	needles
Crystal system	monoclinic	triclinic	monoclinic	monoclinic	monoclinic
Space Group	$P2_1/c$	P1	$P2_1/c$	$P2_1/c$	C2/c
Cell volume (ų)	2163.4(3)	1207.17(10)	2612.4(3)	2868.8(3)	5445.0(9)
$\rho_{calc}~(g/cm^3)$	1.252	1.237	1.143	1.139	1.346
R-Factor (%)	6.22	5.26	5.05	4.54	4.54
trans-cis : trans-trans	2:1	2:1	1:2	2:1	2:1
intramolecular head-to-tail H- bonds ^a	1	1			2
intermolecular head-to-tail H- bonds ^{a,b}	2		2	4	
# R ² ₂ (8) cyclic dimers ^{b,c}		1	2	1	1
# additional intramolecular H-bonds	1	2	1	1	1
# additional intermolecular H-bonds ^c		2	4	2	
Total # of H- bonds ^{c,d}	7	8	13	13	7

^a Each head-to-tail bond set (two N-H donors and one C=S acceptor) counted as a single unit

^b Counted as the number of bond sets *per monomer*, including both donor and acceptor moieties

^c Each cyclic dimer (two N-H donors and two C=S acceptors) counted as a single unit

^d Each donor-acceptor interaction counted individually, e.g. 1 head-to-tail interaction = 2 H-bonds

oriented monomers, stacked on top of each other via weak van der Waals interactions (**Figure 2.3**). The third thiourea moiety, which adopts the *trans-cis* conformation, forms only a single, intramolecular hydrogen bond—with the central, tertiary nitrogen—and displays no intermolecular hydrogen bonding. apart from very weak S...H(CH₂) contacts $(d_{S...H} = 2.912, 2.944 \text{ Å})$ with molecules in neighboring chains. Conversely, compound 5 (R = phenyl), which also contains two *trans-trans* thiourea moieties, forms its crystal lattice from stacked cyclic dimers, comprised of $R_2^2(8)$ interactions between the single trans-cis thiourea moiety on two neighboring molecules. While the trans-trans thioureas in compound 5 do engage in the expected head-to-tail hydrogen bonding, this occurs only intramolecularly. Other significant crystal packing factors in this compound may include π -stacking ($d_{Ph...Ph} = 3.502 \text{ Å}$) and $\pi...H(CH)$ interactions (2.683 Å). The hydrogenbonding patterns observed in compound 2 (R = n-propyl) are, interestingly enough, much closer to those found in compound 5 than they are to those found in compound 1. As in compound 5, the single trans-cis moiety in 2 forms an $R^2(8)$ cyclic dimer with the transcis moiety in a neighboring molecule, and the trans-trans moieties are involved in intramolecular, head-to-tail hydrogen bonding. Unlike 5, however, compound 2 does not form two complete intramolecular head-to-tail interactions; instead of interacting with the nearest thiourea sulfur, one *cis* hydrogen interacts with the central amino nitrogen, forming the S(5) intramolecular interaction observed in all thioureas 1-5.

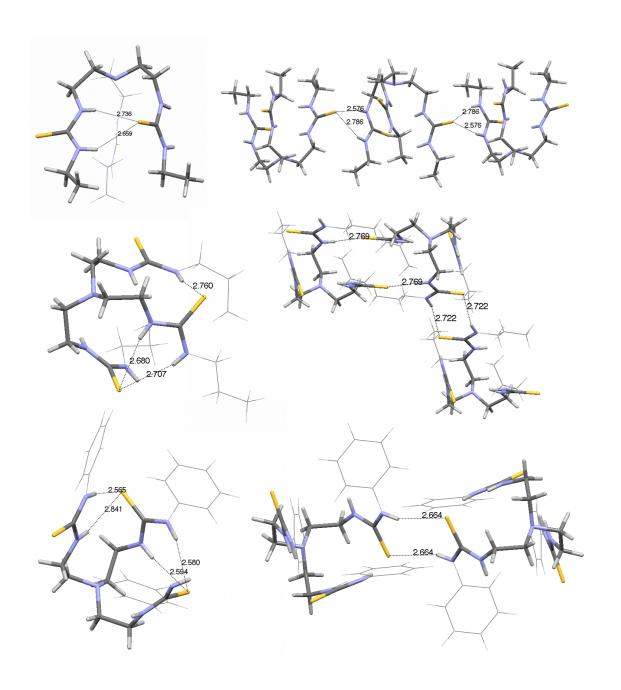


Figure 2.3. Intra- and intermolecular hydrogen bonding patterns in (from top to bottom) compounds **1**, **2**, and **5**. Intramolecular interactions between thiourea moieties are displayed on the left-hand side; for clarity, the N...H(N) interaction between the amino nitrogen and the thiourea hydrogen has been omitted. Intermoleculear hydrogen-bonding interactions for each monomer are shown on the right-hand side.

Also in contrast with **5**, compound **2** forms an additional R²₂(20) "pseudo-dimer," linking the *cis* hydrogen of the *trans-cis* thiourea moiety on one molecule with the sulfur of the S(5) N...H(N) donor thiourea moiety on another, and *vice versa*.§ In combination, these dimer-type intermolecular interactions produce zig-zag infinite chains within the crystal lattice; the angle formed through the centroids of the three molecules that form a single, repeating unit of this chain (**Figure 2.3**) is 108.25°.

Compounds 3 (R = isopropyl) and 4 (R = *tert*-butyl) present a significant deviation from the comparable-yet-distinct hydrogen bonding trends observed in 1, 2, and 5. Likely due to the increased steric bulk of their substituents, the thiourea-containing "arms" in 3 and 4 (Figure 2.4) are splayed out, rather than concentrated on a single face of the central amino nitrogen, as in 1, 2, and 5. In correlation with this structural change, neither 3 nor 4 form intramolecular hydrogen bonds between thiourea moieties: the sole intramolecular interaction is the S(5) N...H(N) pseudocyle observed in all compounds 1-5.

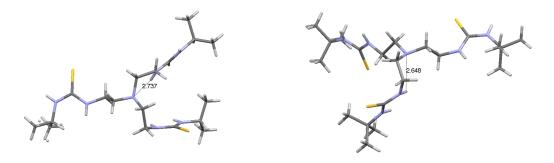


Figure 2.4. Monomeric units of **3** (left) and **4** (right), showing splayed molecular conformation and labeled S(5) N...H(N) intramolecular hydrogen bond.

While difficult to describe in words, this interaction is clearly shown in Figure 2.3 (bond length = 2.769 Å vs. 2.722 Å for the $R^2(8)$ cyclic dimer.)

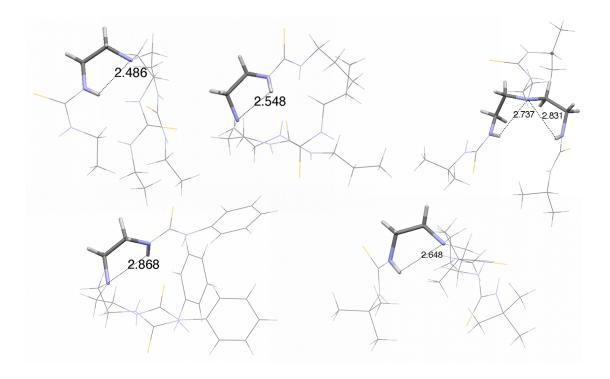


Figure 2.5. Intramolecular S(5) N...H(N) interaction in (clockwise from top left) **1**, **2**, **3**, **4**, and **5**. For clarity, the fragments involved in this interaction are emphasized. In **3**, there are two intramolecular N...H(N) interactions, differing in length by less than 0.1 Å.

As evidenced by the data presented in **Table 2.1**, however, compounds **3** and **4** do not exhibit reduced hydrogen bonding ability as a result of their splayed molecular conformation. Instead, the absence of intramolecular hydrogen bonding appears to correlate with an increase in the total number of hydrogen bonding interactions: 10 in **3** and 13 in **4**, as compared with 7 in **1** and **5**, and 8 in **4**. Additionally, while **1**, **2**, and **5** interact with 2, 3, and 1 molecules/monomer, respectively, each monomer of **3** and **4** forms hydrogen bonds with 5 other molecules, leading to an intricately interwoven

crystal lattice.§ It is likely that, in compounds **3** and **4**, steric bulk inhibits intramolecular hydrogen bonding, leading to a conformation that better promotes intermolecular interaction.

Regardless of the disparities found among their respective hydrogen-bonding patterns, compounds **1-5** do display certain structural similarities. In a foreshadowing of things to come (*vide infra*), each monomer features an S(5) intramolecular hydrogen bond between one thiourea hydrogen and the central, tertiary amino nitrogen (**Figure 2.5**). Bilton, *et al*, calculate the probability of formation (P_s)[‡] for this type of interaction to be 17.5,⁶⁷ so its consistent occurrence in **1-5** is certainly remarkable. Because the bond lengths (**Table 2.2**) in these interactions are longer than 2.30 Å, the commonly-accepted limit for significant N...H(N) electrostatic interactions,^{68,69} it is unlikely that they represent a driving force behind the solid-state organization in **1-5**.

Table 2.2. Bond lengths, bond angles, and conformations observed in the S(5) N...H(N) interactions in thioureas 1-5.

Compound	1	2	3 (1)	3 (2)	4	5
$d_{NH(N)}$ (Å)	2.486	2.548	2.831	2.737	2.648	2.868
$d_{NN}\left(\mathring{A}\right)$	2.819	2.870	2.909	3.005	2.874	3.029
donor conformation	trans-cis	trans-trans	trans-trans	trans-cis	trans-trans	trans-trans
> NH(N) (°)	108.33	106.84	88.01	100.91	97.44	92.69

[§] For this reason, intermolecular interactions in 4 and 5 are not depicted in two-dimensional format; instead, they can be viewed in the attached crystallographic files.

P_s is defined as the percentage of structures in the CSD that form a particular intramolecular contact, relative to the total number of structures that are theoretically capable of forming that contact. In the case of the S(5) N...H(N) interaction, Bilton, *et al.*, found 372 structures in the CSD with a NH--(CH₂)₂--NR₂ fragment; of these, 65, or 17.5%, exhibited the intramolecular hydrogen bond observed in **1-5**.

In addition to the intramolecular N...H(N) interaction, thioureas **1-5** exhibit similarities in other structural trends, albeit unrelated to supramolecular architecture or crystal engineering. As was previously observed in unrelated thioureas, ⁷⁰ elongation of the C=S bond in **1-5** correlates well with hydrogen bonding occurrence. When uncoordinated, the average C=S bond length in **1-5** is 1.680 Å, close to the mean C=S bond length (1.681 Å) reported by Allen, *et al*, and corresponding to approximately 50% double-bond character. When the S is coordinated to 1, 2, or 3 thiourea hydrogens, the average C=S bond length increases to 1.695, 1.704, and 1.713 Å, respectively, indicating a correlation between hydrogen bonding and decreased double-bond character. A corresponding trend of (S=)C—N bond truncation was also observed, presumably due to resonance support for the elongated C=S bond.

Conclusion

Despite similarity in chemical structure, compounds **1-5** exhibit significant diversity in their solid state conformational preferences. Certain consistencies do exist, such as the S(5) N...H(N) intramolecular interaction observed in each structure, but these tris(2-thioureidoethyl)amine derivatives are more exemplary of the unpredictability of solid-state structure than of a set of predictable crystal engineering synthons.

Nevertheless, both the S(5) N...H(N) intramolecular interaction and the changes in bond length consequent to hydrogen bonding that we observed in **1-5** foreshadow structural features found among more consistent classes of compounds (*vide infra*), and may offer an (albeit shaky) starting point for more reliable solid-state thiourea synthons.

CHAPTER III

THE SPIRAL GALAXY:

A ROBUST THIOUREA SYNTHON FOR CRYSTAL ENGINEERING

Introduction

While the solid-state behavior of the ureas is well-understood, and often exploited for a variety of chemical applications, ^{55,72} crystalline organization in the isostructural thioureas remains somewhat more obscure. ²⁶ As a likely consequence of the increased conformational flexibility of thioureas over ureas, ⁶⁴ observed solid-state trends of the former are more tenuous than those of the latter, and few reliable synthons have been established in the chemical literature. ²⁶ Nevertheless, the strong hydrogen-bonding ability of thioureas has shown utility in areas ranging from anion complexation ⁷³ and organic synthesis ^{74,75} to non-linear optics, ⁷⁶ and we believe that improving our understanding of and control over their solid-state behavior will lend greater utility to this very promising functional group.

In order to establish control over the crystalline structure of substituted thioureas, it is necessary to identify reliable, solid-state motifs, which can be both utilized as such, and built upon, in the development of new materials. We noticed, in an unpublished survey of tris(N-substitutedthiourea) derivatives of tris(2-aminoethyl)amine, that,

although these compounds exhibit the structural diversity characteristic of crystalline thioureas, one reliable, solid-state feature can still be found: an intramolecular contact between each central, tertiary nitrogen atom and a hydrogen atom from one of its thiourea "arms," resulting in a five-membered ring. While this motif appeared to contribute little to the organization to these compounds, we found its invariable presence, amid the overwhelming inconsistencies of these compounds, to be of interest.

Focusing on the potential for interaction between attached thiourea moieties and central, tertiary nitrogens, we selected N,N'-bis(3-aminopropyl)piperazine as a candidate for further solid-state investigation. Although we initially believed that the flexibility of the piperazine ring might allow these molecules to form dimeric structures similar to

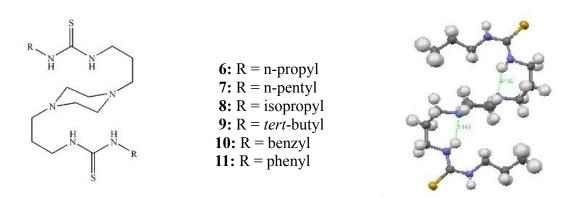


Figure 3.1. The Spiral Galaxy Motif. General structure of thioureas **6-11** (left) and representative crystal structure (right, thiourea **6**)

those reported in a previous work, ^{10,66} we instead discovered, quite serendipitously, that these compounds presented a heretofore unreported thiourea synthon: the "spiral galaxy," shown in **Figure 3.1**. Named after the appearance of the solid-state structure of thioureas **6-11**, this intramolecular motif forms quite reliably, when a monosubstitued thiourea

moiety is separated from a tertiary nitrogen atom by a 3-carbon, alkyl chain, and may exert signficant control over crystal packing in the compounds that contain it. In this work, we have explored the ubiquitousness of this motif, both in the thiourea derivatives of N,N'-bis(3-aminopropyl)piperazine, and in other molecules with appropriate structural characteristics. Due to the current dearth of reliable thiourea synthons, we believe that this "spiral galaxy" motif will provide significant assistance to the efforts of all those engaged in crystal engineering with these intriguing and useful molecules.

Results and Discussion

Despite the propensity of thioureas to display significant conformational flexibility, five of six N,N'-bis(3-aminopropyl)piperazine derivatives, thioureas 6-11, form identical intramolecular hydrogen bonds, illustrated by the representative molecular structures of 6 and 7 (Figure 3.2). These intramolecular contacts result in the formation of a six-membered ring, with a chair-like conformation, on each face of the molecule. In 10, this intramolecular contact forms between the piperazine nitrogen and the far thiourea hydrogen, resulting in an 8-membered ring; however, this difference does not appear to result in additional structural changes. The torsion angle found between the carbon-carbon bond in the piperazine ring, and the intramolecular hydrogen bond formed between the adjacent nitrogen atom and the relevant thiourea hydrogen, is approximately 90 degrees, placing the covalently-bound ring and the hydrogen-bound ring in a near-perpendicular arrangement. With the exception of 11, which will be discussed in greater detail below, the length of this intramolecular contact increases, from 2.141 A to 2.316 Å,

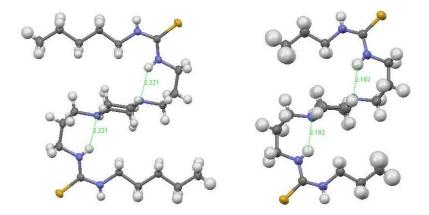


Figure 3.2. Molecular structures of **6** (right) and **7** (left), showing intramolecular hydrogen bonds

in proportion to the relative size of the substituent (**Table 3.1**). Interestingly, even the *tert*-butyl-substituted thiourea **9** forms this intramolecular contact, although its length is significantly extended. This can be contrasted to the observations of Custalcean *et al*, ⁵² who reported that the solid-state conformation of certain N,N'-dialkylthioureas could be controlled by the bulkiness of the two alkyl substituents. In that work, an N-*tert*-butyl-N'-

Table 3.1. Intramolecular hydrogen bonding in thioureas 6-11.

Thiourea	Substituent	NH(N) (Å)	NN(H) (Å)
6	n-propyl	2.182	2.912
7	n-pentyl	2.221	2.929
8	isopropyl	2.218	2.936
9	<i>tert</i> -butyl	2.316	3.009
10	benzyl	2.141	2.946
11	phenyl	2.493	3.011

ethylthiourea adopted the *trans-trans* conformation--as did all other N-*tert*-butyl thioureas, if the N' substituent was bulkier than a simple methyl group--and not the *trans-cis* conformation found in thiourea 9.

Table 3.2. Intermolecular hydrogen bonding in thioureas 6-10

Thiourea	Substituent	SH(N) (Å)	SN(H) (Å)	Space Group
6	<i>n</i> -propyl	2.647	3.452	P-1
7	<i>n</i> -pentyl	2.700	3.473	P-1
8	isopropyl	2.631; 2.607	3.460; 3.379	$P2_1/n$
9	<i>tert</i> -butyl	2.729	3.519	P-1
10	benzyl	2.651	3.436	P-1

Similarly independent of significant substituent effects, the intermolecular contacts of thioureas **6-10** are also surprisingly identical. Because the formation of the "spiral galaxy" motif forces both thiourea moieties into the *trans-cis* conformation, the sulfur atom and the adjacent thiourea hydrogen atom are ideally located to form an eightmembered cyclic dimer, one of the two most prevalent solid-state thiourea structural motifs, with a neighboring molecule. In thioureas **6-10**, the formation of this cyclic dimer on each face of the molecule results in long chains of identically-configured molecules, which stack in a staggered arrangement (**Figure 3.3**) in the crystal structure. The length of the S...H(N) contact in these structures ranges from 2.607 Å to 2.729 Å, and demonstrates no apparent correlation with substituent size (**Table 3.2**).

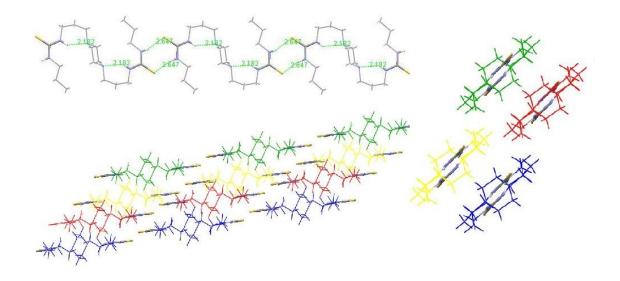


Figure 3.3. Crystal packing in spiral galaxy thioureas **6-10**. Clockwise from upper left: (a) Infinite chain of cyclic dimers; (b) side view of infinite chains (shaded for clarity; thiourea units retain standard coloration); (c) rows of infinite chains

With the exception of **8**, which crystallizes in space group P2₁/n, these thioureas also crystallize in the same space group, P-1. The variance seen in **8** is likely due to asymmetry in the three-dimensional environment around the isopropyl substituent, evidenced by non-equivalent S...H(N) bond lengths in the cyclic dimer; the intramolecular contacts and intermolecular contacts remain identical to those of compounds **6**, **7**, **9**, and **10**.

Apart from the definitional differences seen in the space group classification of compound **8**, and the difference in intramolecular ring size seen in **10**, only compound **11**, the bis(N"-phenylthioureido) derivative of N,N'-bis(3-aminopropyl)piperazine, presents a

real deviation from the trends in inter- and intramolecular hydrogen bonding seen in this class of molecules. Crystallizing in space group P2₁/c, thiourea 11 forms the predictable, six-membered intramolecular contact, yet its intermolecular contacts, shown in Figure 3.4, differ from those present in thioureas 6-10. Instead of forming a cyclic dimer with a neighboring thiourea molecule, the available hydrogen and sulfur atoms on each "arm" of 11 instead form an eight-membered cyclic dimer with a molecule of DMSO, one of the two crystallization solvents. The bond between the thiourea hydrogen atom and the DMSO oxygen atom is 2.006 Å, and the bond between the thiourea sulfur atom and the α-proton on the DMSO molecule is 2.986 Å; both of these bond lengths fall within range for hydrogen bonding with the specified heteroatom.^{77,78} In addition to this cyclic dimer, each DMSO oxygen atom also interacts with the mildly acidic⁷⁹ aromatic hydrogen α to the thiourea moiety on a neighboring molecule of 11, serving as a "bridge" between the two thiourea-containing molecules. This type of hydrogen bonding has been observed in proteins, as well as smaller organic molecules. 80-82 As each molecule of 11 also bonds to two different DMSO molecules, the solvent serves only as a "spacer" between thioureas, an extra linkage in the long chains—albeit with different three-dimensional organization--also seen as a supramolecular motif in compounds 6-10.

Table 3.3. Crystal morphology, crystallization solvent(s), and space group assignment for thioureas **6-11**

Thiourea	Morphology	Space Group	Crystallization Solvent(s)
6	clear plates	P-1	ethanol/water
7	clear plates	P-1	ethanol/hexanes
8	clear needles	$P2_1/n$	ethanol/hexanes
9	clear prisms	P-1	acetonitrile/water
9	clear needles	P-1	$DMSO-d_6$
10	clear prisms	P-1	ethanol/water
11	clear needles	$P2_1/c$	DMSO/ethyl acetate

Because the presence of DMSO in 11 appears to mostly augment, rather than interrupt, the supramolecular trends seen in 6-10, we believe that the presence of DMSO in the crystal structure of 11 is probably a consequence of the compound's idiosyncratic solubility, rather than an indictment of the "spiral galaxy" model, itself. Thioureas 6-10 have remarkably similar solubility profiles, and can be reliably crystallized from a variety of different solvents (detailed in Table 3.3) but thiourea 11 did not share these solubility trends. Dissolving a non-negligible amount of 11, even upon sonication-preceded boiling,

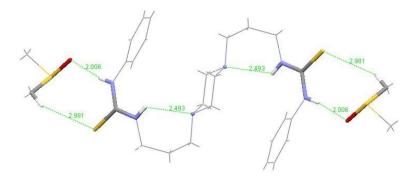


Figure 3.4. Hydrogen bonding in 11.

was accomplished only in strongly dipolar solvents, such as DMSO, DMF, and N-methylpyrrolidinone, and at high temperatures. It is therefore probable that the same intermolecular contacts seen in **6-10** exist in compound **11**, in its non-solvated form, and that the conditions required to obtain an analytical crystal are responsible for its asynchronous, solvated crystal structure.

Because the "spiral galaxy" motif was so overwhelmingly consistent among the bis(N"-substituted thioureido) derivatives of N,N'-bis(3-aminopropyl) piperazine, we explored the versatility of this synthon in other, structurally appropriate compounds. To form the six-membered, intramolecular contact observed in **6-11**, the target molecule must contain a tertiary amine, ¹⁷ separated from the thiourea by a three-carbon alkyl chain.

Figure 3.5. Thioureas 12 (left) and 13 (right)

Two compounds, **12** and **13**, shown in **Figure 3.5**, were synthesized, to test the applicability of the "spiral galaxy" motif in other systems: both crystal structures featured the expected intramolecular contact.

Compound 12, synthesized from N-(3-aminopropyl)morpholine and phenyl isothiocyanate, crystallized in the P2₁/n space group, and, in addition to the sixmembered, intramolecular contact, also formed the eight-membered, cyclic dimer seen in compounds 6-10. The intramolecular hydrogen bond length in 12 was 2.271 Å, which was significantly shorter than that observed in 11, 2.493 Å, despite the similar structure of these compounds. Interestingly, and possibly suggestive of an explanation for the differing bond lengths, the phenyl substituent in 12 is twisted away from the face of the morpholine ring, whereas, in 11, the phenyl substituent is almost perfectly parallel to the face of the piperazine ring, with a torsion angle of 0.01 degrees; apparently, sharing the same thiourea substituent as 11 did not cause 12 to deviate dramatically from the trends in solubility and observed intermolecular contacts seen in 6-10. Because the morpholine ring possessed only one thiourea-containing "arm," these dimers did not form the chains seen in the N,N'-bis(3-aminopropyl)piperazine-derived thioureas; however, weak contacts, with bond lengths of 2.669 Å and 2.544 Å, were observed between the morpholine oxygen atom and two alkyl hydrogen atoms on a neighboring molecule.

In contrast to compound 12, the intermolecular trends seen in compound 13 were remarkably similar to those observed in compounds 6-10. Crystallizing in the $P2_{1/c}$ space group, and featuring the "spiral galaxy" -type intramolecular motif, between one of its thiourea "arms," and its central, tertiary nitrogen atom, compound 13 also formed infinite

chains of cyclic dimers, as each thiourea "arm" formed two hydrogen bonds with a single, neighboring molecules. The length of the intramolecular hydrogen bond is 2.083 Å, which correlates well with the trend in bond length vs. substituent size observed in **6-10**; the intermolecular hydrogen bond lengths are 2.514 Å and 2.436 Å, respectively. In addition to these five hydrogen bonds, the crystal structure of **13** also features an intramolecular interaction between one aryl proton and the π -cloud of the other aromatic ring, with the former located 2.763 Å from the mean plane of the latter, which is consistent with known values for this type of interaction. 82,84

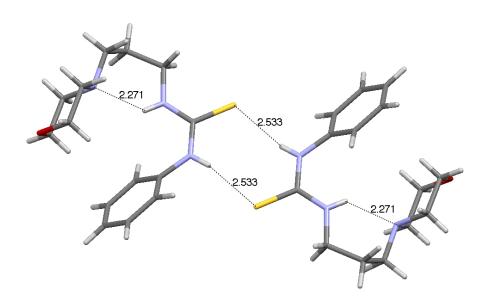


Figure 3.6. Hydrogen bonding in thiourea 12

Conclusion

We have discovered a new, solid-state structural motif, the "spiral galaxy," common among all reported derivatives of N,N'-bis[3-(N"-substitutedthioureido)-propyl]piperazine. We have also demonstrated that the robustness of this synthon extends to other thioureas, which possess the requisite structural characteristics: a three-carbon chain, separating an N-substituted thiourea moiety and a tertiary amine. The "spiral galaxy" motif also appears to direct intermolecular hydrogen bonding, at least in the N,N'-bis[3-(N"-substitutedthioureido)propyl]piperazine compounds examined in this paper. More work is needed in this area, to determine the consistency of the "spiral galaxy" motif in directing intermolecular hydrogen bonding--and, consequently, crystal packing--in a diverse array of thioureas, to explore its use as a synthetic building block in solid-state design.

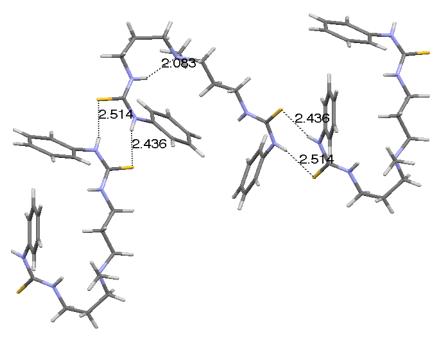


Figure 3.7: Hydrogen bonding in thiourea 13

CHAPTER IV

A RESONANT COMPETITOR:

INTRAMOLECULAR SUPERNOVA OBLITERATES THE SPIRAL GALAXY IN N,N'-DISUBSTITUTED THIOUREAS

Introduction

The robustness of the "spiral galaxy" synthon prompted us to subject it to competitive interaction from other functional groups. The structural motif displayed in

Figure 4.1 is well-documented in the chemical literature, among both carbonyl-⁸³⁻⁸⁹ and pyridyl-subsituted^{84,90-98} thioureas; this reliability led us to believe that it would pose a significant challenge to the robustness of the "spiral galaxy" interaction. Because, as was mentioned in **Chapter I**, the presence of a competitive functional group tends to decrease the prevalence of a supramolecular homosynthon,⁵¹ we believed it likely that this trend could extend to intramolecular

X = O, N--R''

Figure 4.1. Intramolecular interaction(s) selected for competition with the "spiral galaxy" synthon

interactions, as well. On the basis of estimated $\Delta p K_a$ values, which have been used to predict hydrogen bonding affinity in a wide variety of molecular complexes, ⁹⁹ we hypothesized that the "spiral galaxy" motif would predominate, in both cases.

Results and Discussion

The 2-pyridylthioureido derivative of N,N'-bis(3-aminopropyl)piperazine was initially selected for further investigation, to explore the relative hydrogen-bonding strength of the pyridyl nitrogen and the piperazine nitrogen. As shown in **Figure 4.2**, these two acceptor atoms would be forced to compete for the same thiourea proton, thereby testing the strength of the spiral galaxy motif in compounds with potentially competitive functionalities. The synthesis and isolation of this compound proved difficult; however, a related compound, N-[3-(2-pyridylthioureido)propyl]morpholine, **14** (**Figure 4.3**), was successfully prepared. Because the spiral galaxy motif had been previously observed in **12**, the N-phenyl analog of **14**, we believed that this compound would serve the same purpose as the desired piperazine derivative. On the basis of

Figure 4.2. Two possible intramolecular hydrogen bonds in N,N'-bis[3-(2-pyridylthioureido)propyl]piperazine

reported pK_a values for the protonated species (7.01-8.69 for N-alkyl morpholines^{100,101} and 3.33-6.68 for various related pyridines¹⁰²), we hypothesized that the morpholine nitrogen would form the intramolecular hydrogen bond, due to both its greater basicity and its increased proton affinity.

Both the ¹H NMR spectrum (**Figure 4.4**) and the crystal structure of compound **14** clearly indicated that this was not the case. In compounds **6-11**, the thiourea protons were observed as very broad singlets around 6 ppm; however, in the CDCl₃ ¹H NMR spectrum of compound **14**, the thiourea protons were observed as a triplet at 11.9 ppm, and a singlet 8.8 ppm. While somewhat broadened in comparison with more-upfield aromatic protons, these signals were nevertheless far sharper than a "typical" heteroatomic proton resonance, indicating a low rate of exchange. Far-downfield signals in the ¹H NMR have been associated with intramolecular hydrogen bonding in N-(2-pyridyl) thioureas, ¹⁰³ and the splitting of the signal at 11.9 ppm correlates with the presence of two α-hydrogens on the N-propylmorpholine substituent.

Figure 4.3. Two possible intramolecular hydrogen bonds in N-[3-(2-pyridylthioureido)propyl]morpholine

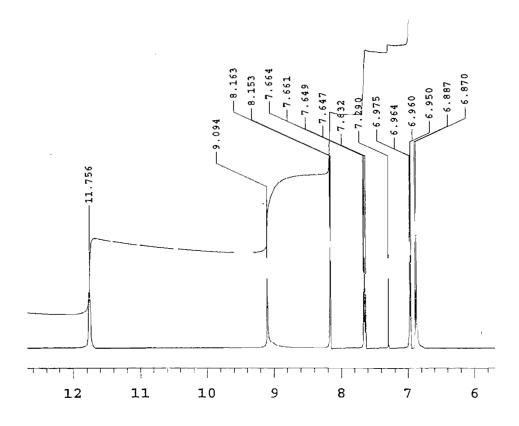


Figure 4.4. Aromatic region of ¹H NMR spectrum of **14**. Pyridyl-bound proton can be observed as a broad triplet at 11.756 ppm.

Corroborating the 1 H NMR evidence, the crystal structure of **14** shows an intramolecular, six-membered ring, formed between the pyridyl nitrogen and the "contested" thiourea hydrogen. Having adopted the *trans-cis* conformation in order to effect this intramolecular contact, the compound is well-suited to form cyclic thiourea dimers, and a centrosymmetric $R_2^2(8)$ intermolecular interaction ($d_8..._{H(N)} = 2.587$ Å) was indeed observed. Interestingly, despite the non-spiral galaxy-type intramolecular interaction, crystal packing in **14** closely resembled that observed in **6-11**.

Complementing the aforementioned $R_2^2(8)$ interaction, a weak interaction was also observed between the morpholine O and the proton α to the pyridyl nitrogen, forming a centrosymmetric $R_2^2(28)$ dimer. This second dimer served as a proxy for the second $R_2^2(8)$ interaction observed in **6-11**, creating nearly-identical chains of opposite-oriented monomers, which also packed in a staggered arrangement, with no observed π - π interactions (**Figure 4.5**).

Because the intramolecular hydrogen bond observed in 14 did not match our initial prediction—which had been based on literature values for pK_as found for the pyridyl and morpholyl functionalities in related compounds—the pK_as of the diprotic salt of 14 were determined. A sample of 14 was dissolved in acetone, and concentrated HCl (aq) was added dropwise, until the pH of the solution was pink to indicator paper (pH \approx 1) and a colorless solid precipitated. This solid was washed with water, acetone, and ether; air-dried to constant weight; and confirmed by ¹H-NMR to be the diprotic salt of 14. It was then titrated with 0.05 M NaOH in three separate trials (sample titration curve shown in Figure 4.6). In each trial, two equivalence points were observed, corresponding

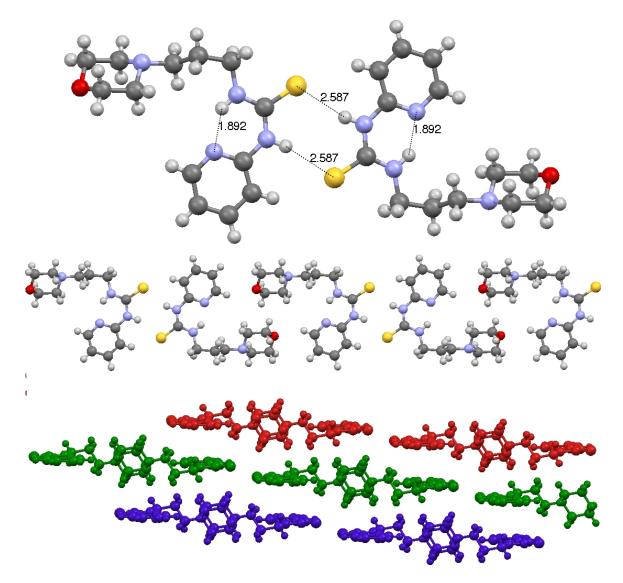


Figure 4.5. Intra- and intermolecular hydrogen bonding and crystal packing in **14**. At top, centrosymmetric $R_2^2(8)$ cyclic thiourea dimer; in the middle, infinite chains formed from $R_2^2(28)$ and $R_2^2(8)$ dimers; at bottom, stacks of infinite chains, colored for clarity.

to pK_as of 3.15 ± 0.05 and 7.3 ± 0.3 , which we assigned to the pyridinium and morpholinium ions, respectively. While the latter pK_a value (*i.e.* for the morpholinium proton) falls within the anticipated range, the former is somewhat lower than previous

studies have predicted;¹⁰² this discrepancy can likely be attributed to the solution-state hydrogen bond that forms upon deprotonation.¹⁰⁴

Because these relative pK_a values did not predict the preferred hydrogen bond acceptor in **14**, we searched the literature for another explanation. Resonance-Assisted Hydrogen Bonding (RAHB) has been described as "the interplay between hydrogen bond and heterodienes (or more generally heteroconjugated systems) [that] can strengthen remarkably the hydrogen bond itself."¹⁰⁵ DFT calculations have shown that, in general, RAHBs (which will be discussed at greater length in **Chapter V**) are approximately twice as strong as ordinary hydrogen bonds, ¹⁰⁶ which correlates well with the short d_{N---H(N)} (1.892 Å) observed in **14**.

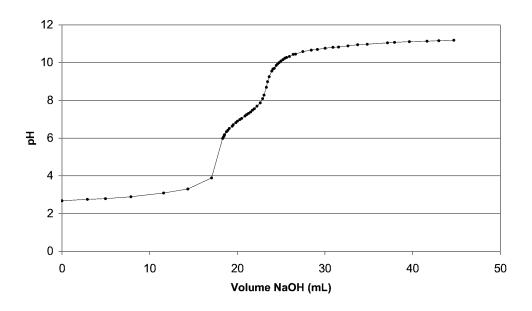


Figure 4.6. Titration of diprotic HCl salt of 14.

RAHB has also been observed in enolones, enaminones, enaminoimines, enolimines, β -diketones, β -keto-esters, amide-amidine coupling, amide dimers, thymine-adenine coupling, and guanine-cytosine coupling, and we synthesized compound **15**, N,N'-bis[3-(N"-benzoylthioureido)propyl]piperazine to test the plausibilty of RAHB as an explanation for the non-pK_a-based competitive behavior observed in **14**. Because the pK_a of the protonated carbonyl moiety should be less than zero, there is no way that, on the basis pK_a values alone, it could be expected to compete with the piperazinyl nitrogen.

Shown in **Figure 4.7**, the crystal structure of bis(thiourea) **15** suggests that RAHB out-competes the spiral galaxy as an intramolecular hydrogen-bonding motif. As in **14**, the observed intramolecular interaction is between the thiourea proton and the unsaturated substituent attached to the opposing nitrogen (2 per molecule); the tertiary amino nitrogens do not participate in hydrogen bonding. Interestingly, the *trans-cis* thiourea moieties do not form the anticipated $R_2^2(8)$ dimers observed in **6-11**. Instead, monomers are linked by two, single S...H(N) interactions (2.856 Å), one on each "arm" of the piperazine moiety, forming infinite $C(4)^{\ddagger}$ chains of identically-oriented molecules. These chains are linked by phenyl-RAHB π - π stacking (*vide infra*) between opposite-oriented monomers, resulting in a fully cross-linked supramolecular network structure.

[‡] Technically, as each monomer forms two S...H(N) H-bonds with each neighboring molecule (1 as a donor and 1 as an acceptor), this should be categorized as an R₂²(30) interaction; however, the C(4) interaction is far easier to visualize and understand.

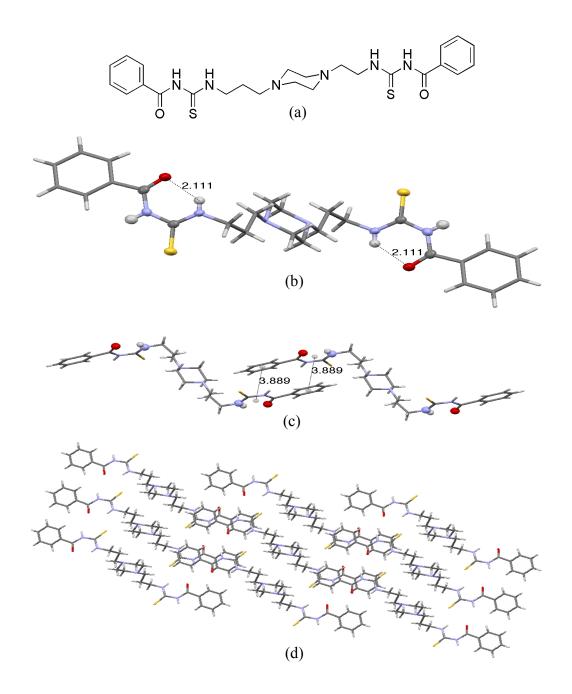


Figure 4.7. Hydrogen bonding and crystal packing in **15**. (a) Chemical diagram of **15**; (b) intramolecular (C=)O...H(N) RAHBs in the single-crystal structure; (c) RAHB-phenyl π - π stacking (centroid-centroid distance = 3.889 Å); (d) crosslinked crystal network. C(4) interactions are apparent on either end of (d); overlapping phenyl rings and RAHB pseudo-rings are also shown.

CHAPTER V

RESONANCE-ASSISTED HYDROGEN BONDING:

A TALE OF TWO CONFORMERS

Introduction

Believed to possess a variety of interesting-yet-underutilized optical and electronic properties, 83 N-aroyl thioureas have shown promise as anion receptors, 108-111 metal chelators, 112-114 antibacterial and antifungal agents, 115,116 building blocks for liquid crystals, ¹¹⁷ plant-growth regulators, ¹¹⁸ and materials useful for molecular recognition^{2,75} and non-linear optics. 76,83,119 These compounds reliably assume a well-known conformation, both in solution^{83,89} and in the solid state; ^{84,85} depicted in **Figure 5.1**, this conformation features an S(6) intramolecular hydrogen bond between the carbonyl oxygen and the γ-thiourea proton. Heterocyclic nitrogen acceptors, such as pyridyl, 84,92 pyrimidyl, 10,98 and thiazolyl, 94,120 are known to form a similar S(6) interaction in thioureas; these compounds are well-known NNRTIs, 96,121,122 with high **Figure 5.1**. S(6) binding affinity and anti-HIV microbicidal IC₅₀'s reported as intramolecular RAHB in N-

low as 3.8 nM.¹²³

 $NR''(CH)_{n}R'); R' = CH, N, S)$ Despite formal cross-conjugation across the thiourea thioureas moiety, the type of intramolecular hydrogen bond observed in both N-aroyl and Nheterocyclic thioureas can be classified as a form of Resonance-Assisted Hydrogen

aroyl (X = O; R' = Ph) and N-

heterocyclic (X =

Bond[ing] (RAHB), due to the electron delocalization made possible by unsaturated

donor and acceptor groups.¹²⁴ Since first proposed in 1989,¹⁰⁵ Resonance-Assisted Hydrogen Bonding (RAHB) has received considerable attention given its crucial role in biological transformations,^{125,126} as well as its relevance to the pursuit of a unified theory of hydrogen bonding.¹²⁷ Recently, RAHB has been identified as a significant factor in many biological processes, including membrane permeability^{128,129} and ligand-receptor binding;^{130,131} consequently, RAHB plays an increasingly important role in medicinal chemistry, especially in small-molecule drug design.^{132,133} RAHB has also been used as a structural element in the design of new organic syntheses,^{134,135} and as a reliable structural motif in crystal engineering.¹³⁶

Despite its importance to these diverse fields, the origin of RAHB has yet to be fully elucidated. Initially ascribed to π -electron delocalization within the pseudo-ring that forms from the donor-acceptor hydrogen bonding interaction, RAHB has also been attributed to charge rearrangement in the electronic σ -framework; recent computational studies have been published on both sides of this debate. A notable complication in the study of RAHB is the difficulty of quantifying its effect on molecular structure, as compounds capable of forming such strong hydrogen bonds will, as a rule, form them. While the "open" and "closed" conformations of RAHB systems have been examined by semi-empirical methods, 139,140 there are, to the best of our knowledge, no comparative empirical studies in the chemical literature.

Representing the first structurally characterized example of "open" and "closed" RAHB systems, 1-(3-nitrobenzoyl)-3-(6-methyl-2-pyridyl)-thiourea (16) has the capacity to form one of two dramatically different conformations (160 and 16N, Figure 5.2), both

in the solid state and in solution. Both conformations are characterized by the presence of a strong, RAHB-type intramolecular hydrogen bond, formed at the expense of the alternative intramolecular hydrogen bond; thus, **160** represents the "open" conformation of **16N**, and *vice versa*. The experimental data that we have obtained for this compound-x-ray crystal structures of both **16O** and **16N**, as well as solution-state energetic parameters—is corroborated by electronic calculation at the B3LYP/6-311++G(2d,p) level, providing intriguing support for many principles of RAHB theory.

Compound **16** was prepared by treatment of *m*-nitrobenzoylisothiocyanate (prepared from the acid chloride and KSCN) with 2-amino-6-methylpyridine. Crystallization from a mixture of ethyl acetate and hexanes afforded pale-yellow **16O**, while crystallization from acetonitrile afforded bright-yellow **16N**, each of which was characterized by single-crystal x-ray diffraction.

The RAHB-type intramolecular interactions observed in **16O** and **16N** are individually well-documented in the chemical literature, in thioureas which bear either acyl⁸³⁻⁸⁹ or N-heterocyclic substituents, such as pyridine, ^{84,91-98,120,141} pyrimidine, ^{92,98} or thiazole. ^{94,120} When, as in the case of compound **16**, the thiourea bears both types of substituents (and therefore potentially has two low-energy conformations, **16O** and **16N**), RAHB theory predicts ^{142,143} that the homonuclear N···H(N) interaction should be stronger than the heteronuclear O···H(N) interaction. However, all literature examples of such bifunctional thioureas – with one exception hond, both in the solid state and in solution. ¹⁴⁵ While **16N** this initially appears to refute RAHB theory, our experiment of computational data for

16O and **16N** – thus far the only reported example of such a bifunctional thiourea for which *both* conformers have been isolated and crystallographically characterized – provide a satisfying explanation for this apparent inconsistency, as well as a model for the structural changes effected by RAHB.

Results and Discussion

Structural data for **16O** and **16N** provide a quantitative description of the structural effects of both intramolecular RAHBs, as significant changes in bond length are observed as a result of both interactions. Selected bond lengths are reported in **Table 5.1**. Whereas bonds between atoms not involved in either RAHB differ in length between

Figure 5.2. Line drawing and single crystal structural drawing of 16O and 16N

16O and **16N** by an average of \pm 0.008 Å, roughly within experimental error, RAHB-involved bonds vary by as much as \pm 0.033 Å. Perhaps most notably, amide-type delocalization²¹² is significantly lower in **16N**, as bond *b* (**Figure 5.2**) lengthens from 1.374 Å to 1.394 Å, and bond *a* correspondingly shortens, from 1.222 Å to 1.207 Å. These changes in bond length likely reflect the changes in electron density that correlate with the coordination status of the carbonyl moiety.

Table 5.1. Selected experimentally- and computationally*-derived bond lengths for conformers **16O** and **16N** of 1-(3-nitro-benzoyl)-3-(6-methyl-2-pyridyl)-thiourea. Bond identifiers correspond to those displayed in **Figure 5.2**.

Bond	16O (Å)		16N (Å)		$\Delta (\mathring{\mathbf{A}})^a$	
	Exp.b	Calc.c	Exp.	Calc.	Exp.	Calc.
а	1.222(4)	1.233	1.207(2)	1.217	0.015	0.016
b	1.374(5)	1.383	1.394(2)	1.396	-0.020	-0.013
С	1.405(4)	1.408	1.372(2)	1.377	0.033	0.031
d	1.341(4)	1.345	1.357(2)	1.361	-0.016	-0.016
e	1.418(4)	1.417	1.411(2)	1.413	0.007	0.004
f	1.335(4)	1.345	1.335(2)	1.337	0.000	0.008

^{*}Computational results provided by Prof. Tonglei Li, at the University of Kentucky.

While of lesser magnitude, the change in the length of bond e (1.418 Å in **16O** vs. 1.411 Å in **16N**), corroborated by the change in hybridization calculated via NBO analysis (sp^{2.70} vs. sp^{2.60}), also reflects the structural changes resulting from the shifts in electron density produced by RAHB. Recent literature¹³⁷ indicates that such changes are

^a Change in bond length, defined as difference between **16O** and **16N**

^b From X-ray crystal structure

^c From gas-phase structures, optimized at the B3LYP/6-311++G(2d,p) level

largely produced by electronic rearrangement in the σ -skeleton, a conclusion that is corroborated by our data. Despite formal "cross-conjugation" across the thiourea moiety, the structural effects of RAHB are observed in both of its substituents. Additionally, the fragments of **16O** and **16N** that remain uninvolved in either RAHB do not display significant structural changes resulting from conformational change, as might be expected in conjugated systems undergoing significant π -rearrangement. Computational data also supported this hypothesis, as the interaction between the antibond of the N-H donor and the lone pair(s) of electrons from the hydrogen-bonding acceptor (O in **16O** and N in **16N**) possesses primarily σ -character.

Despite these apparently non-conjugative structural changes, the equalization of bond length predicted by Gilli, *et al.*, ^{105,146} is unambiguously demonstrated by the structural data for **16O** and **16N**. The Q-value of 0.088 for the heteronuclear RAHB in **16O** is, contrary to prediction, slightly lower than the Q-value for the homonuclear RAHB in **16N**, 0.091. Nevertheless, the standard deviation for the lengths of the four bonds (to non-hydrogen atoms) involved in the RAHB is ± 0.08 in **16O** and ± 0.03 in **16N**, indicating that bond-length equalization is, in accordance with prediction, significantly greater in **16N**. Due to the different types of bonds (as well as the different donor-acceptor pairs) involved in the two RAHB systems, it is likely that the Q-value is not a useful rubric for determining relative RAHB strength in this particular case. NBO donor-acceptor stabilization energy, calculated at the B3LYP/6-311++g(2d,p) level with Gaussian 03 software, proved to be more useful in achieving this goal. Although **16O** was determined to be the low-energy conformer (in the gas phase) by 4.72 kcal/mol

(**Table 5.2**), **16N** possesses greater donor-acceptor stabilization energy for the intramolecular RAHB (-18.46 kcal/mol, vs. -16.84 kcal/mol for **16O**),[‡] in accordance with the predictions of RAHB theory. ^{105,143}

Table 5.2. Selected properties of **16O** and **16N**.

	E _{optimized} ^a (Ha)	E _{lattice} ^b (kcal/mol)	E _{RAHB} ^b (kcal/mol)	$\partial X \cdots \mathbf{H}(N)^c$ (ppm)	m.p. ^d (°C)	p ^a (Debye)
160	-1382.13556	-127.92	-16.84	12.77	155.6	4.49
16N	-1382.12804	-131.81	-18.46	15.45	160.7	12.44
Δ (O-N)	-4.72 ^e	3.89	1.62			

^a Computationally determined at the B3LYP/6-311++G(2d,p) level (single molecule, gasphase).

Qualitative methods of determining polymorphic stability¹¹ led us to conclude that **16N** was the preferred solid-state conformer, given its higher melting point, lower solubility in all tested solvents, slower nucleation, and non-reversible precipitation from a slurry of **16O**. With lattice energy calculations (**Table 5.2**) confirming this qualitative assessment, we suggest that the conformational preference of compound **16** may be determined by factors other than relative RAHB strength. This is corroborated by the

^b Computationally determined for solid-state structure, using Crystal 06¹⁴⁷ and the B3LYP/6-21G(d,p) basis set.

^c In CDCl₃.

^d Determined by differential scanning calorimetry.

^e In kcal/mol.

[‡] Three intramolecular interactions contribute to the total bond strength of the RAHB in **16O**: lone pair on pyridyl $N \cdots H(N)$: 0.60 kcal/mol; lone pair #1 on $O \cdots H(N)$: 4.21 kcal/mol; lone pair #2 on $O \cdots H(N)$: 12.03 kcal/mol. In **16N**, the lone pair on the pyridyl $N \cdots H(N)$ is the sole contributor to the RAHB.

strong correlation between the results of our NBO analysis and solution-state data collected for compound **16**.

In contrast to prior literature reports of related 1-acyl-3-(2-pyridyl) thioureas, which suggested the presence of only the $O \cdots (N)$ conformer in solution, both 160 and 16N are present in all tested solvents.[‡] In agreement with gas-phase calculations, 16O is always the dominant species, albeit to a lesser extent – its relative population ranges from 50:1 in toluene-d₈ to 4:1 in DMSO-d₆, corresponding to energy differences (at 25°C) of -2.3 kcal/mol and -0.82 kcal/mol, respectively. Variable-temperature NMR studies demonstrate that the predominance of 160 depends on entropic factors, as 16N is significantly lower in enthalpy (**Table 5.3**). In CDCl₃, ΔH for the conversion of **16O** to **16N** was determined to be -2.01 kcal/mol, while ΔS was -10.1 eu. These data correlate well with the significantly smaller dipole moment (p) of 160 (Table 5.2), which would likely lead to decreased solvent ordering about that conformer and a concomitant solution-state conformational preference that is not tied to the relative strength of either intramolecular RAHB. Chemical shift data also lend credence to this hypothesis – at 15.45 ppm, the coordinated proton in 16N is nearly 3 ppm downfield from that in 16O (12.77 ppm), consistent with the increased strength of the $N \cdots (N)$ contact predicted by RAHB theory. 105,143

[‡] Discussed at greater length in Chapter VII.

Table 5.3. Thermodynamic parameters (kcal/mol) for the $16O \rightarrow 16N$ conformational transformation, in the gas phase (calculated) and in various solvents (experimentally-determined)

AG	$\Delta G_{25^{\circ}\mathrm{C}}$	$\Delta G_{25^{\circ}\mathrm{C}}$	$\Delta G_{25^{\circ}\mathrm{C}}$	$\Delta G_{25^{\circ}\mathrm{C}}$
$\Delta G_{ m gas\ phase}$	(CDCl ₃)	(DMSO-d ₆)	(toluene-d ₈)	(CD_3CN)
4.72	0.97	0.82	2.31	0.96

Conclusion

The equilibrium between **16O** and **16N** represents the first empirical example of "open" and "closed" RAHB, and offers support for many of its principles. Interestingly, computational and experimental data both appear to indicate that conformational stability lacks an inexorable link to relative RAHB strength, as other factors – which may or may not result from the electronic effects of the RAHB – also play a significant role in determining the dominant conformation.

CHAPTER VI

CONFORMATIONAL EXCHANGE IN

1-BENZOYL-3-(2-PYRIDYL) THIOUREAS:

THE SOLID STATE

Introduction

The ability to form two different RAHBs imbues 1-aroyl-3-(2-pyridyl) thioureas with a peculiar blend of both structural flexibility and structural rigidity, creating the basis for a fascinating case study of structure-property relationships and crystal structure predictions. Perhaps the most intriguing feature of this class of compounds is that their solid-state physical properties correlate most closely with their respective preferred conformation, rather than their respective substitution pattern. Because it is well-known that altering aromatic substitution patterns often provokes dramatically different physical properties in otherwise identical molecules, ¹⁴⁸ especially in relation to color and/or absorption spectra, ¹⁴⁹ the conformation-specific physical characteristics of BzPTUs **16-46** suggest the influence of electronic factors unrelated to simple molecular connectivity or chemical composition.

In this chapter, we will explore X-ray crystallographic data from 30 different compounds, describing the general structural characteristics of both conformers, both on

a monomeric level and in terms of crystal packing. We will also describe the influence of substituents on a BzPTU's preferred solid-state conformation, and discuss potential factors contributing to these compounds' conformationally-dependent physical characteristics. Our unusually large sample size of highly similar compounds allows us to explore many structural features from a statistically significant standpoint, and we believe that our work represents not only the solid-state trends in BzPTU structure, but also, in a larger sense, both the pitfalls and the promise of crystal engineering research.

Results

BzPTUs **16-46** were prepared by addition of the corresponding benzoyl isothiocyanate and an aminopyridine, using the procedure outlined in **Scheme 6.1**. Aroyl isothiocyanates were prepared in accordance with the literature procedure for the parent compound, benzoyl isothiocyanate (R = H in **Scheme 6.1**);¹⁵⁰ because these reaction conditions yielded satisfactory results, further optimization was not explored. When the parent benzoyl chloride was not commercially available, it was prepared from the corresponding benzoic acid.¹⁵¹ We made no attempt to isolate the intermediate isothiocyanates or acid chlorides, as we found that satisfactory yields (65-80%, calculated from the initial amount of either the acid chloride or the isothiocyanate) of BzPTUs could be obtained without additional purification steps. Direct isolation of the BzPTU from the reaction mixture could be achieved by the addition of deionized water, upon completion of the reaction; the precipitated material, after drying, was satisfactorily pure by ¹H NMR.[‡] Complete synthetic and characterization data can be found in **Appendix A**.

[‡] While yield could be increased by removing the reaction solvent and chromatographing the BzPTU

Scheme 6.1. Synthesis of 16-46^a

^aReagents and conditions: (a) SOCl₂, catalytic DMF, reflux, 5-15 min; (b) KSCN, MeCN, rt, 1-16 h; (c) 2-aminopyridine (R' = H) / 2-amino-6-picoline (R' = 6-CH₃) / 2-amino-5-picoline (R' = 5-CH₃) / 2-amino-3-picoline (R' = 3-CH₃), THF, rt, 2-16 h; (d) H₂O, rt, 1 h.

Single crystals suitable for X-ray crystallography were grown at room temperature, from a diverse selection of solvents. Crystals from the same vial as those selected for X-ray crystallography were used for both spectral characterization and elemental analysis. **Table 6.1** contains the experimental conditions under which we obtained single crystals of BzPTUs **16-46**, as well as their relevant physical and spectroscopic properties, and **Table 6.2** contains selected crystallographic data for these

product, we did not believe this improvement sufficient to justify either the time or the significant increase in solvent usage and chromatographic support that it entailed.

same structures. Bonds for which length appears to be conformer-specific, as described previously, are labeled in **Figure 6.1**, and their lengths in BzPTUs **16-22**, **24**, **26-41**, and **43-46**, as determined via X-ray crystallography, are recorded in **Table 6.3**. Full crystallographic data files can be found in **Appendix B**.

Table 6.1: Crystallization solvents, crystal morphologies, and physical and spectroscopic properties related to conformer identification (vide infra) in BzPTUs **16-46**. Melting points reported as a temperature range recorded on MelTemp apparatus; melting points reported as a single integer recorded via DSC.

CMPD	R	R'	Solvent(s)	Morphology	Color	v _{C=0} (cm ⁻¹)	m.p. (°C)	O/N
16N	3-NO ₂	6-CH ₃	MeCN	Dodecahedral	Yellow	1716	161	N
160	3-NO ₂	6-CH ₃	EtOAc / hexanes	Columnar	Pale yellow	1672	156	О
17N	Н	6-CH ₃	CHCl₃	Cubic	Yellow	1709	140-145 (dec.)	N^a
17N	Н	6-CH ₃	MeCN	Cubic	yellow	1709	150	N^b
170	Н	6-CH ₃	THF (wet)	Prisms	colorless	1680	116; 150°	O^a
18	4-NO ₂	6-CH ₃	Acetone / H ₂ O	Columnar	Yellow- orange	1715	185-186	N
19	2- OCH ₃	6-CH ₃	Toluene / EtOH	columnar	colorless	1660	136-138	О
20	4- OCH ₃	6-CH ₃	DMF (wet)	Hexagonal	Yellow	1707	171-173	N
21	3-C1	6-CH ₃	МеОН	Needles	colorless	1678	161-162	O^a
22	4-C1	6-CH ₃	Acetone	Prisms	Yellow	1717	166-167	N
23	3-CN	6-CH ₃	many	amorphous	Pale yellow	1676, 1717	147-148 (dec.)	O, N ^{b,d}
24	4-CN	6-CH ₃	MeCN	Cubic	Yellow	1720	172-173 (dec.)	N
25	3,4-C1	6-CH ₃	CH₃COOH	Prisms	colorless	1681	167-168	O^b
26	3,5-Cl	6-CH ₃	DCE	prisms	Deep Yellow	1700	175-176 (dec.)	N

Table 6.1. (continued).

CMPD	R	R'	Solvent(s)	Morphology	Color	v _{C=0} (cm ⁻¹)	m.p. (°C)	O/N
27	4-Br	6-CH ₃	DCM	prisms	yellow	1718	166-168 (dec.)	N
28	2-Br	6-CH ₃	EtOH / hexanes	columnar	colorless	1667	146-148	О
29	Н	Н	EtOH	Columnar	Off-white	1674	143-144	О
30O	3-NO ₂	Н	МеОН	Needles	Pale yellow	1671	176	О
30N	3-NO ₂	Н	MeCN	powder	Deep yellow- orange	1705	173	N^b
31	4-NO ₂	Н	МеОН	Needles	Yellow- orange	1703	178-180	N
32	2- OCH ₃	Н	DCE / hexanes	Glassy; amorphous	colorless	1660	186-188	О
33	4- OCH ₃	Н	EtOAc / hexanes	columnar	colorless	1666	155-156	О
34	3-C1	Н	EtOH / hexanes	Columnar	colorless	1673	148-150	О
35	4-C1	Н	THF (wet)	Columnar	colorless	1676	140-142	O^a
36	3-CN	Н	DMF (wet)	Needles	colorless	1675	149-151 (dec.)	\mathbf{O}^a
37a	4-CN	Н	DCM	Plates	off-white	1676	177-180 (dec.)	O^a
37b	4-CN	Н	IPA / acetone	Cubic	Pale yellow			O^a
37c	4-CN	Н	CHCl ₃	Needles	off-white	1677	181-185 (dec.)	O^a
38	3,4-Cl	Н	DCM / acetone	needles	colorless	1674	194-195	О
39	3,5-C1	Н	MeCN; acetone ^e	Columnar; octahedral ^e	Yellow	1704	180-183 (dec.)	N
40	4-Br	Н	EtOH	Striated prisms	colorless	1667	160-161	О
41	2-Br	Н	EtOH / hexanes	cubic	colorless	1683	104-106	О
42	4-CF ₃	Н	MeCN	Foliated plates	Yellow- orange	1701	158-160	N
43	3,5-Cl	5-CH ₃	DCE	Pentagonal dodecahedron	Yellow	1699	191	N
43	3,5-C1	5-CH ₃	Toluene	Fibrous needles	Colorless	1674	195	O^b

Table 6.1. (continued).

CMPD	R	R'	Solvent(s)	Morphology	Color	v _{C=0} (cm ⁻¹)	m.p. (°C)	O/N
44	Н	3-CH ₃	EtOH / hexanes	Prisms	colorless	1670	131-133	О
45	4-NO ₂	3-CH ₃	MeCN	Prisms	Pale yellow	1673		О
46	2-Br	3-CH ₃	EtOH / hexanes	Needles	colorless	1675		О

^aSolvate

Table 6.2. Selected crystallographic data for BzPTUs **16-22**, **24**, **26-41**, and **43-46**. Full crystallographic data files can be found in **Appendix B**.

CMPD	Space Group	Formula	a, b, c (Å)	α, β, γ (deg)	V (ų)	Z	d _{calc} (g/cm ³)	R- Factor (%)	C ^a
16N	P2 ₁ /n	$C_{14}H_{12}N_4O_3S$	7.9095(18), 9.972(2), 17.615(4)	90.00, 92.752(4), 90.00	1387.75	4	1.514	3.8	0.76
160	P1	$C_{14}H_{12}N_4O_3S$	3.888(2), 11.984(7), 15.455(10)	98.299(10), 92.188(11), 98.434(10)	703.563	2	1.493	5.9	0.75
17N	P2 ₁ /c	C ₁₅ H ₁₄ N ₃ OSCl ₃	8.239(2), 19.570(5), 10.609(3)	90.00, 95.5090(4), 90.00	1702.66	4	1.524	3.32	0.66
170	I2/a	$C_{14}H_{14}N_3O_{1.5}S$	22.125(2), 5.5825(5), 23.134(2)	90.00, 112.6390(10), 90.00	2637.18	8	1.412	3.21	0.77
18	P1	$C_{14}H_{12}N_4O_3S$	8.108(3), 9.351(4), 9.484(4)	90.913(7), 107.255(7), 90.624(7)	686.516	2	1.530	4.02	0.77

^bNo X-ray quality crystals were produced, but the conformer present in the amorphous material was confirmed by IR

 $^{^{\}circ}$ Endotherm (*vide infra*) observed at 116.2 $^{\circ}$ C; a second endotherm, presumed to be the melting point, occurs at 150.5 $^{\circ}$ C

^dA mixture of both conformers, in approximately equal proportions, precipitated from all tested solvents.

^eDistinct morphologies obtained from different solvents; both have same unit cell

Table 6.2. (continued).

CMPD	Space Group	Formula	a, b, c (Å)	α, β, γ (deg)	V (Å ³)	Z	d _{calc} (g/cm ³)	R- Factor (%)	C ^a
19	P2 ₁ /c	$C_{15}H_{15}N_3O_2S$	7.9072(8), 20.077(2), 9.8693(10)	90.00, 110.242(2), 90.00	1470.01	4	1.362	3.65	0.72
20	P1	$C_{15}H_{15}N_3O_2S$	7.6729(13), 8.8309(15), 11.1319(19)	90.702(3), 94.510(3), 113.241(2)	690.157	2	1.450	3.62	0.77
21	P1	$C_{15}H_{16}N_3O_2SC1$	9.341(2), 9.771(1), 10.285(2)	71.226(3), 75.821(3), 62.355(2)	782.18	2	1.434	3.07	0.74
22	P1	C ₁₄ H ₁₂ N ₃ OSCl	8.2738(11), 9.0380(12), 9.9752(13)	80.899(2), 66.546(2), 87.438(2)	675.551	2	1.503	3.16	0.76
24	P1	$C_{15}H_{12}N_4OS$	8.0301(10), 12.3036(15), 14.6822(18)	74.324(2), 81.402(2), 81.197(2)	1371.24	4	1.435	5.52	0.75
26	P2 ₁ /c	$C_{14}H_{12}N_3OSCl_2$	9.2966(16), 10.2930(18), 15.738(3)	90.00, 106.729(3), 90.00	1442.23	4	1.567	3.66	0.74
27	P1	$C_{14}H_{12}N_3OSBr$	8.4483(12), 9.0131(13), 9.9963(15)	80.951(2), 66.510(2), 85.899(2)	689.372	2	1.687	2.79	0.75
28	P2 ₁ /c	$C_{14}H_{12}N_3OSBr$	11.3779(7), 14.0996(9), 9.3236(6)	90.00, 98.2030, 90.00	1480.42	4	1.571	2.98	0.70
29	P2 ₁ /n	$C_{13}H_{11}N_3OS$	5.2724(7), 20.335(3), 11.7435(16)	90.00, 90.372(2), 90.00	1259.04	4	1.357	4.2	0.71
30	P2 ₁ /n	$C_{13}H_{10}N_{4}O_{3}S \\$	3.8902(12), 14.372(4), 22.813(7)	90.00, 91.211(5), 90.00	1275.19	4	1.575	4.57	0.77
31	P2 ₁ /n	$C_{13}H_{10}N_4O_3S$	4.9793(6), 13.2760(16), 19.753(2)	90.00, 94.136(2), 90.00	1302.38	4	1.542	4.74	0.76
32	P2 ₁ /c	$C_{14}H_{13}N_3O_2S$	8.9570(9), 15.7256(16), 10.3383(11)	90.00, 111.8080(10) , 90.00	1351.98	4	1.412	3.31	0.74
33	P2 ₁ /c	$C_{14}H_{13}N_3O_2S$	12.064(2), 15.599(3), 7.2365(12)	90.00, 90.612(3), 90.00	1361.73	4	1.401	3.47	0.77
34	P2 ₁ /n	C ₁₃ H ₁₀ N ₃ OSCl	3.9319(6), 14.423(2), 22.706(4)	90.00, 92.806(3), 90.00	1286.11	4	1.507	4.95	0.74

Table 6.2. (continued).

CMPD	Space Group	Formula	a, b, c (Å)	α, β, γ (deg)	V (Å ³)	Z	d _{calc} (g/cm ³)	R- Factor (%)	C ^a
35	C2/c	C ₁₃ H ₁₁ N ₃ O _{1.5} SCl	28.847(6), 3.8548(7), 24.769(5)	90.00, 105.929(3), 90.00	2648.54	8	1.509	3.59	0.76
36	P2 ₁ /n	$C_{17}H_{17}N_5O_2S$	4.0338(3), 15.7779(10), 26.9519(18)	90.00, 90.1090(10), 90.00	1715.35	4	1.376	4.26	0.72
37a	C2/c	C _{14.5} H ₁₁ N ₄ OSCl	33.415(4), 3.8956(5), 23.215(3)	90.00, 106.891(2), 90.00	2891.56	8	1.492	4.41	0.78
37b	P1	C _{14.8} H _{11.5} N ₄ O _{1.2} S	9.4152(6), 12.2161(8), 12.6685(8)	79.9620(10), 81.9860(10), 79.1500(10)	1400.55	4	1.408	3.87	0.87
37c	P1	C _{14.2} H _{10.2} Cl _{0.8} N ₄ OS	9.476(4), 12.217(5), 12.643(5)	80.248(6), 82.254(6), 78.770(6)	1407.02	4	1.474	5.1	0.8
38	P2 ₁ /c	C ₁₃ H ₉ N ₃ OSCl ₂	12.142(3), 3.8366(10), 28.817(7)	90.00, 98.822(5), 90.00	1326.53	4	1.633	3.91	0.75
39	P2 ₁ /n	C ₁₃ H ₉ N ₃ OSCl ₂	10.9182(17), 8.5112(13), 15.526(2)	90.00, 105.631(2), 90.00	1389.43	4	1.559	3.02	0.72
40	P2 ₁ /c	C ₁₃ H ₁₀ N ₃ OSBr	4.1131(5), 20.410(3), 15.5094(19)	90.00, 94.927(2), 90.00	1297.18	4	1.722	2.94	0.74
41	Pbca	C ₁₃ H ₁₀ N ₃ OSBr	14.2904(10), 9.2601(6), 20.4694(14)	90.00, 90.00, 90.00	2708.73	8	1.649	2.42	0.71
43	P2 ₁ /n	C ₁₄ H ₁₂ N ₃ OSCl ₂	10.7954(12), 8.3644(9), 16.6231(19)	90.00, 101.726(2), 90.000	1467.7	4	1.538	2.85	0.72
44	C2/c	$C_{14}H_{13}N_3OS$	24.295(2), 7.8990(8), 14.0166(14)	90.00, 93.537(2), 90.00	2684.75	8	1.343	4.45	0.71
45	P2 ₁ /n	$C_{14}H_{12}N_4O_3S$	11.1286(19), 11.1776(19), 11.963(2)	90.00, 110.005 (2), 90.00	1398.3	4	1.503	3	0.75
46	P1	C ₁₄ H ₁₂ N ₃ OSBr	6.4016(13), 10.803(2), 16.578(3)	71.448(3), 82.704(3), 88.942(3)	1077.81	3	1.619	3.33	0.72

^a Kitaigorodskii packing coefficient¹⁷ = (Molecular Volume¹⁵² x Z) / Unit Cell Volume

Figure 6.1. Conformers O (left) and N (right) with labeled bonds. Bond labels are the same for both conformers.

Table 6.3. Lengths of labeled bonds from **Figure 6.1**. For the sake of brevity, uncertainty in bond length has been omitted; however, these values can be found in **Appendix B**.

CMPD	O/N	OH(N) or NH(N) ^a (Å)	ON or NN ^a (Å)	NH(N) or SO ^b (Å)	a (Å)	b (Å)	c (Å)	d (Å)	e (Å)	f (Å)	g (Å)	h (Å)
16N	N	1.927	2.671	2.996	1.207	1.394	1.372	1.671	1.357	1.411	1.335	1.359
160	О	1.892	2.615	2.263	1.223	1.374	1.405	1.659	1.341	1.417	1.336	1.345
17N	N	1.940	2.667	2.986	1.211	1.397	1.366	1.672	1.357	1.412	1.332	1.354
170	О	1.978	2.651	2.464	1.224	1.386	1.386	1.681	1.334	1.426	1.329	1.343
18	N	1.918	2.658	2.971	1.205	1.393	1.375	1.668	1.357	1.414	1.335	1.354
19	О	1.899	2.632	2.327	1.228	1.374	1.393	1.660	1.340	1.410	1.334	1.343
20	N	1.945	2.697	2.918	1.207	1.404	1.365	1.674	1.363	1.408	1.337	1.350
21	О	1.916	2.634	2.307	1.226	1.378	1.399	1.658	1.345	1.413	1.343	1.340
22	N	2.004	2.661	3.013	1.209	1.393	1.370	1.671	1.359	1.410	1.335	1.354
24°	N	1.840	2.625	3.057	1.202	1.401	1.369	1.667	1.364	1.407	1.337	1.341
24 ^c	N	1.940	2.644	3.012	1.200	1.401	1.369	1.667	1.362	1.405	1.334	1.348
26	N	1.958	2.701	2.959	1.217	1.373	1.382	1.656	1.360	1.403	1.335	1.358
27	N	1.981	2.659	3.014	1.208	1.389	1.370	1.674	1.356	1.411	1.338	1.355
28	О	1.934	2.631	2.248	1.229	1.366	1.406	1.661	1.335	1.415	1.340	1.339
29	О	1.852	2.592	2.254	1.225	1.385	1.392	1.665	1.336	1.406	1.330	1.333
30	О	1.925	2.604	2.262	1.224	1.375	1.397	1.660	1.336	1.408	1.330	1.332

Table 6.3. (continued).

CMPD	O/N	OH(N) or NH(N) ^a (Å)	ON or NN ^a (Å)	NH(N) or SO ^b (Å)	a (Å)	b (Å)	c (Å)	d (Å)	e (Å)	f (Å)	g (Å)	h (Å)
31	N	1.905	2.664	3.018	1.209	1.386	1.376	1.654	1.367	1.405	1.332	1.349
32	О	1.896	2.644	2.292	1.227	1.374	1.399	1.656	1.344	1.408	1.340	1.339
33	О	1.888	2.632	2.277	1.232	1.388	1.390	1.667	1.339	1.410	1.336	1.339
34	О	1.926	2.620	2.279	1.218	1.389	1.396	1.663	1.339	1.412	1.335	1.331
35	О	1.886	2.594	2.256	1.220	1.388	1.396	1.664	1.338	1.414	1.338	1.335
36	О	1.893	2.608	2.251	1.231	1.371	1.399	1.648	1.347	1.401	1.335	1.332
37a	О	1.886	2.617	2.262	1.226	1.371	1.409	1.661	1.335	1.415	1.336	1.341
37b ^c	О	1.809	2.608	2.290	1.224	1.378	1.402	1.662	1.337	1.419	1.338	1.338
37b ^c	О	1.815	2.603	2.329	1.221	1.382	1.401	1.666	1.335	1.418	1.335	1.342
37c ^c	О	1.869	2.595	2.315	1.224	1.382	1.403	1.667	1.331	1.417	1.328	1.340
37c ^c	О	1,874	2.612	2.249	1.222	1.379	1.398	1.658	1.339	1.412	1.342	1.337
38	О	1.816	2.600	2.270	1.228	1.374	1.407	1.661	1.340	1.411	1.338	1.340
39	N	1.912	2.637	3.051	1.215	1.377	1.377	1.660	1.361	1.402	1.334	1.347
40	О	1.995	2.645	2.260	1.222	1.373	1.401	1.658	1.340	1.409	1.338	1.337
41	О	1.994	2.657	2.590	1.219	1.370	1.391	1.666	1.334	1.425	1.330	1.346
43	N	1.881	2.654	3.055	1.215	1.376	1.382	1.660	1.361	1.402	1.334	1.346
44	О	1.920	2.629	2.564	1.229	1.372	1.391	1.663	1.335	1.438	1.325	1.344
45	О	1.966	2.664	2.515	1.222	1.380	1.398	1.665	1.340	1.434	1.330	1.345
46°	О	2.004	2.656	2.614	1.227	1.371	1.393	1.669	1.329	1.439	1.329	1.340
46 ^c	О	1.963	2.640	2.584	1.215	1.370	1.398	1.661	1.323	1.424	1.332	1.331
46 ^c	О	1.994	2.651	2.442	1.209	1.383	1.394	1.654	1.335	1.432	1.337	1.339

^a Bond lengths listed are for donor-acceptor separation, both D...H(A) and D...A. In conformer **O**, these values are for O...H(N) and O...N, respectively; in conformer **N**, these values are for N...H(N) and N...N.

^b Bond lengths refer to the secondary, N...H(N) IMHB in conformer **O**, or the short (*i.e.* less than the sum of their van der Waals radii, 3.2 Å) O...S separation in conformer **N**.

^c When at least two non-equivalent molecules are present in the unit cell, bond lengths are listed for each molecule.

Because BzPTUs **16-46** invariably form either conformer **O** or conformer **N** in the solid state, very little potential for structural variability—at least on the monomeric level —exists in these compounds. Nevertheless, this conformational rigidity appears to lack an overarching influence on supramolecular architecture, as both intermolecular hydrogen bonding and π -stacking—the two most significant crystal packing forces observed in BzPTUs **16-46**—exhibit dramatic variance across this series of compounds. Although crystal engineering studies of thioureas tend to focus on trends in intermolecular hydrogen bonding,²⁶ we found it most useful to characterize crystal packing patterns using Desiraju's and Gavezzotti's polynuclear aromatic hydrocarbon structure types,³⁷ with a few modifications that made them more suited to trends observed in our BzPTUS.

Table 6.4 provides a summary of the dominant intermolecular interactions observed in BzPTUs **16-22**, **24**, and **26-46**, and **Figure 6.2**, which immediately precedes it, provides graphical depictions of these interactions, including both Desiraju's and Gavezzotti's original structure types and our modifications.

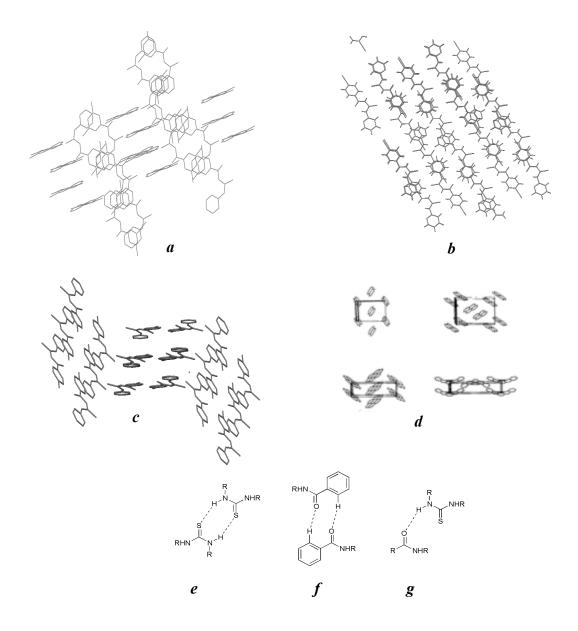


Figure 6.2. Common crystal packing motifs and intermolecular hydrogen bonds observed in BzPTUs **16-46**. (*a*) Basketweave, with brick-type π -stacking; (*b*) generalized brick-type π -stacking; (*c*) doubled γ ; (*d*) Desiraju's structures (clockwise from top left): herringbone, sandwich herringbone, β, γ ; (*e*) R²₂(8) cyclic thiourea dimer; (*f*) R²₂(10) aroyl cyclic dimer; (*g*) C(6) or D(6) (C=)O...H(N) interaction.

Table 6.4. Intermolecular hydrogen bonding and crystal packing interactions in BzPTUs **16-22**, **24**, **26-41**, and **43-46**.

CMPD	O/N	Length SH(N)	Length OH(Ar)	Length OH(N)		π	-stacki	ng (Å)		Structure
CIVIT D		R ² ₂ (8) (Å)	R ² ₂ (10) (Å)	C/D(6) (Å)	Ph- Ph	Ph- Pyr	Pyr- Pyr	RAHB- Ph	RAHB- Pyr	Туре
16N	N	2.609	2.372							β
160	О	2.717	2.453		3.4		3.5			Doubled γ
17N	N	2.645			3.6	3.8				γ
170	О		2.530							Doubled herringbone
18	N	2.599	2.433			3.5				Sandwich β
19	О		2.523					3.4		Sandwich herringbone
20	N	2.566	2.520		3.4				3.4	Brick γ
21	О				3.4	3.4	3.4			Brick γ
22	N	2.674	2.563			3.6				γ
24	N	2.642, 2.543			3.9				3.3, 3.5	Brick γ
26	N			2.134		3.6			3.3	Basketweave
27	N	2.668	2.565			3.6				γ
28	О			2.003	3.6		3.4			Basketweave
29	О	2.736	2.488					3.9	3.7	Sandwich herringbone
30	О	2.602	2.606		3.4		3.4			γ
31	N			2.337						β
32	О		2.527						3.3	Sandwich herringbone
33	О	2.707	2.571		3.5				3.7	Doubled brick γ
34	О	2.635			3.4		3.5			γ
35	О	2.456			3.4		3.4			Doubled γ
36	О				3.5		3.6			γ
37a	О		2.458		3.5		3.5			Doubled γ
$37b^c$	О	2.774, 2.775	2.507, 2.609		3.6	3.5	3.5			Doubled brick γ
37c ^c	О	2.712, 2.822	2.526, 2.494		3.6	3.5	3.5			Doubled brick γ
38	О	2.847	2.368		3.5		3.5			γ

Table 6.4. (continued).

CMPD	O/N	Length SH(N)	Length OH(Ar)		π-stacking (Å)					H(N) Stacking (1)		Structure
		R ² ₂ (8) (Å)	$\begin{array}{c c} R^2_2(10) \\ (\mathring{A}) \end{array}$			Ph- Pyr	Pyr- Pyr	RAHB- Ph	RAHB- Pyr	Туре		
39	N			2.123	3.4	3.6	3.3			Basketweave		
40	О		2.418		3.3		3.3			Doubled γ		
41	О									Herringbone		
43	N			2.119	3.4	3.2	3.4			Basketweave		
44	О	2.755					3.7, 3.5			Basketweave		
45	О	2.722		2.600						Herringbone		
46	О	2.549	2.110							β		

Although we did not observe any predictive correlation between single-molecule conformation and crystal packing interactions, there were nevertheless certain trends that could be observed in preferred packing arrangements. Conformer **N** was more likely to engage in brick-type π -stacking (**Figure 6.2b**), as part of either a γ -type (**Figure 6.2d**) or basketweave-type (**Figure 6.2a**) packing motif. The apparent prevalence of the basketweave motif among conformer **N** structures may actually be related to the packing similarities among 3,5-dichloro BzPTUs **26**, **39**, and **43**, all of which crystallized as conformer **N**, and all of which packed in the basketweave motif. In the absence of aromatic stacking, conformer **N** was also more likely to form "graphite-like" β -sheets (**Figure 6.2d**), in contrast to the herringbone architecture observed exclusively among non- π -stacking, conformer **O** crystal structures. As displayed in **Figure 6.3**, however, these trends could also be related to phenyl substitution patterns, as *para*-substituted BzPTUs showed a distinct preference for the γ -type packing motifs.

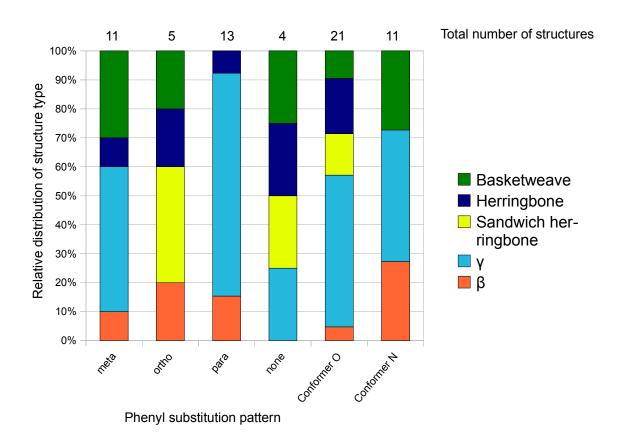
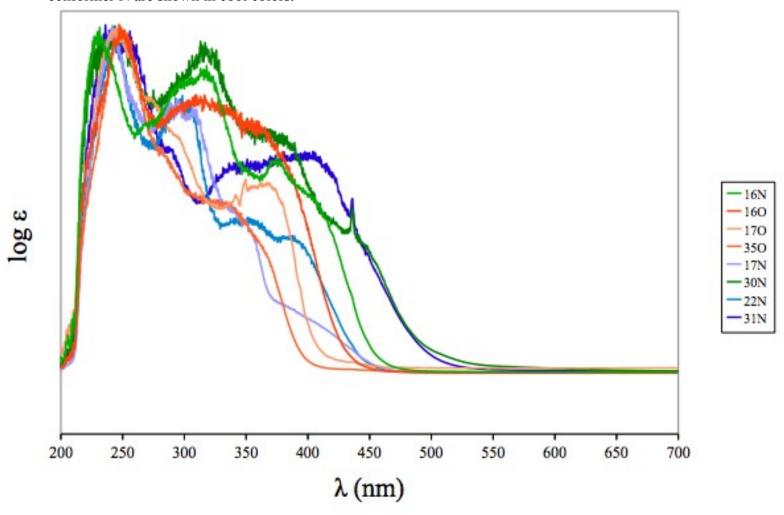


Figure 6.3. Distribution of crystal packing motifs in BzPTUs **16-46**, relative to both phenyl substitution (*ortho*, *meta*, *para*, none [i.e. R = H] and solid-state conformation (conformer **O** / conformer **N**). Variations on a certain packing motif (*e.g.* doubled γ , brick γ , etc.) have been combined into a single structure type (*e.g.* γ). Compound **38** was not included, due to its irregular 3,4-dichlorophenyl substituent (see footnote on page 73 for a more extensive discussion).

In an effort to identify the source of the yellow color in conformer N, diffuse reflectance UV-vis spectra were collected for BzPTUs 16O, 16N, 17O, 17N, 22, 30, 31, and 35. All conformer N compounds displayed absorbance in the visible region ($\lambda > 400$ nm), and, of the conformer O compounds, only 16O displayed significant absorbance above 410 nm (terminating at 440 nm), most likely due to the nitro substituent on its phenyl ring. Visible-light absorbance in 17N and 35 extended to approximately 450 nm, and, in 16N, it was detected as high as 475 nm. In 30 and 31(R = $3-NO_2/4--NO_2$; R' = H), statistically significant absorbance was detected above 500 nm, extending to nearly 550 nm in 30, and correlating well with the orange hues observed in both of these compounds. Figure 6.4 contains a stacked plot of all the UV-vis spectra that we collected, and Figure 6.5 contains comparative plots of selected UV-vis spectra, which we find far easier to interpret. Table 6.5 contains absorbance maxima and the corresponding band gaps for each data set. Band gaps were calculated from the slope of the best-fit line through each absorbance maximum. 153

Figure 6.4. Diffuse reflectance UV-vis spectra for BzPTUs 16O/N, 17O/N, 22, 30, 31, and 35. Compounds identified as conformer O are shown in warm colors, and compounds identified as conformer N are shown in cool colors.



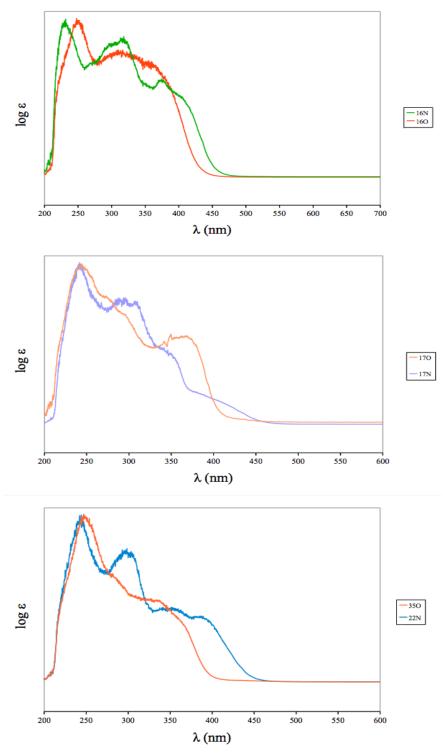


Figure 6.5. Diffuse reflectance UV-vis spectra for 16O/N (top), 17O/N (middle), and 22/25 (bottom). Dotted line indicates the beginning of the visible region.

Table 6.5. Calculated band gaps and their corresponding wavelengths, as derived from the diffuse reflectance UV-vis spectra of selected BzPTUs.

Compound	Band Gap	λ
	(eV)	(nm)
	4.44	279
16N	3.41	364
	2.78	446
160	4.22	294
100	2.88	430
	4.29	289
17N	3.62	342
1/1	3.15	393
	2.82	440
	4.15	299
170	3.64	340
	3.1	400
	4.45	278
22N	3.71	334
	2.80	443
	4.13	300
30N	3.25	381
JUN	2.86	433
	2.56	484
	4.32	287
31N	4.16	298
3111	3.75	331
	2.66	466
	4.29	289
350	3.67	338
	3.19	388

Differential scanning calorimetry was employed to precisely determine the melting point and the enthalpy of crystallization of conformers **N** and **O**, in the four compounds (16, 17, 30, and 43) for which we were able to isolate reasonably pure samples of both conformers. Interestingly, the melting point of conformer **N** was higher than that of conformer **O** only in compound 16. Melting point is not necessarily an indication of polymorphic stability, however, 46 and in all but 30, the enthalpy of crystallization is higher in conformer **N** than in conformer **O** (**Table 6.6**).

Table 6.6. Melting point and enthalpy of crystallization in both conformers of BzPTUs **16**, **17**, **30**, and **43**, as determined by differential scanning calorimetry

CMPD	16N	160	17N	170	30N	30O	43N	430
m.p. (°C)	161	156	150	150	173	176	191	195
ΔH (kJ/mol)	38.0	33.8	33.0	32.4	41.5	50.9	44.8	42.7

Both the melting point and the enthalpy of crystallization were found to be essentially identical in 17N and 17O; however, a broad, endothermic phase transition was observed at 116°C in 17O, prior to the melting point transition at 150°C (Figure 6.6). The heat of the transition at 116°C was found to be 22 kJ/mol, or approximately half the heat of vaporization of water, 41 kJ/mol. Because we observed that 17O could be readily converted to 17N by leaving an unsealed vial of 17O on top of an oven overnight (T ~

80°C), and our solved crystal structure of **17O** contains 0.5 equivalents of H₂O per unit cell, we believe it highly likely that the first transition corresponds a the loss of water from **17O** (and the concomitant phase transition to **17N**).

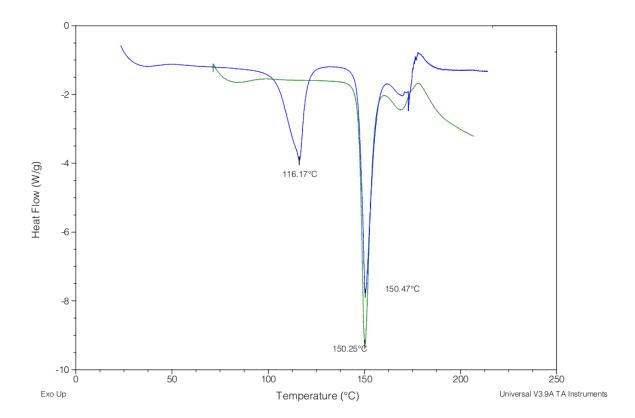


Figure 6.6. Differential scanning calorimetry plot obtained for **17N** (green) and **17O** (blue). The dashed vertical line drawn on the graph illustrates that the beginning of the first endotherm in **17O** approximately corresponds to the vaporization temperature of water. The decomposition that occurs upon melting can be observed in the small peak immediately to the left of the melting endotherm.

Discussion

All BzPTUs 16-46 occupy one of two possible low-energy conformations, conformers **O** and **N**. As was previously discussed, calculations performed for 16 found that conformer **O** was the low-energy conformer in both the gas phase and the solution phase; however, conformer **N** was determined to be the thermodynamically-preferred solid phase conformer, a finding that was in agreement with our empirical observations. In general, the relative solubilities of polymorphs are roughly predictive of their relatively stabilities—especially on a kinetic timeline, as the rate at which a crystal dissolves should be proportionate to the energy it gains (or loses) by forming the intermolecular bonds that allow it to precipitate from solution. Both solubility and rate of dissolution—as far as we have qualitatively observed—are far greater in conformer **O** than in conformer **N**, regardless of solvent choice, and regardless of BzPTU selection; that is, any conformer **N** solid sample has a lower solubility and rate of dissolution than any conformer **O** sample, even if their substitution patterns are completely unrelated to each other.

Given the extent to which conformation influences the solubility of BzPTUs 16-46, it is perhaps unsurprising that the solid-state conformational preferences of these compounds are largely independent of solvent choice. Most BzPTUs crystallize exclusively as either conformer O or conformer N, regardless of the chosen crystallization solvent; our reasonably exhaustive solvent studies on representative

The one exception to these two trends is **38**, which crystallizes as conformer **O**, yet has both low solubility in most solvents and the highest melting point recorded for any BzPTU that we examined (194-195°C). Chains of Cl...Cl intermolecular contacts (3.394 Å), which are also observed in 3,5-dichloro BzPTUs **26** and **39**, may account for the enhanced stability of **38**'s crystal lattice.

compounds can be found in **Table 6.7**. Although we were not able to obtain crystals suitable for X-ray analysis from all—or even from most—tested solvents, we found that conformation could be confirmed efficiently via IR spectroscopy, as the carbonyl stretching frequency in conformer **O** (~1670 cm⁻¹) is consistently lower in energy than in it is in conformer **N** (~1710 cm⁻¹), as would be expected from the RAHB that it forms in the former compound. Interestingly, two aspects of intermolecular hydrogen bonding also correlated well with C=O stretch in the IR spectra: the C(6) or D(6) (C=)O...H(N) interaction observed in many conformer **N** species led to a lower-frequency C=O stretch (1700-1705 cm⁻¹, as compared to 1707-1717 cm⁻¹ in conformer **N** structures that lacked this interaction), and marginally higher-frequency absorbance (1678-1680 cm⁻¹) was observed in **17O** and **21O**, presumably due to solvent coordination.

Table 6.7. Solvent-structure relationships in BzPTUs **16**, **17**, **21**, **31**, and **33**. For each solvent, the C=O stretching frequencies (cm⁻¹) and corresponding conformations are reported.

CMPD	MeCN	MeNO ₂	МеОН	СН₃СООН	EtOAc	(CH ₃) ₂ CO	THF	CHCl ₃
16	1716; N ^a	1716; N ^a	1680; O ^b	1678; O ^b	1672; O ^c	1716; N ^a	1672; O	1672; O
	1672; O ^a	1672; O ^a			1716; N ^c	1672; O ^a		
17	1709; N	1710; N	1709; N	1710; N	1709; N	1709; N	1680; O ^d	1709; N
							1709; N ^d	
21	1674; O	1674; O	1678; O ^b	1678; O ^b	1673; O	1674; O	1678; O ^b	1674; O
								1074, 0
31	1703; N	1702; N	1703; N	1703; N				
								1705, 1
33	1707; N	1707; N	1706; N	1707; N	1707; N	1707; N	1707; N	1707; N
								1668; O ^e

^a Conformer **O** precipitates first; complete conversion to conformer **N** occurs in 3-10 days.

Although our large library of BzPTU crystal structures--and the high consistency in their conformer-specific C=O stretching frequencies—likely contribute a significant amount of accuracy to our IR-based conformational assignments, we nevertheless wanted more experimental evidence to support our assumptions. As in BzPTUs 16-46, compound 47, bis(benzoyl)thiourea, has the potential to form one of two competing—albeit chemically indistinguishable—intramolecular (C=)O...H(N) RAHBs, both identical to that found in conformer **O**. Because only one RAHB can form intramolecularly, however, the two C=O moieties in 47 occupy different chemical environments—confirmed by X-

^b Solvent coordination to O(=C) is likely

^c Conformer **O** precipitates first; however, conversion to conformer **N** is still incomplete after 48 days.

^d Both conformers precipitate, in reproducibly attainable quantities (90% **O**; 10% **N**), from the evaporation of a wet THF solution—of any concentration—under ambient conditions.

^eAllowing a solution of **33** to evaporate rapidly on a salt plate resulted in a mixture of conformers **O** and **N**; however, our many attempts at recrystallization yielded only conformer **N**.

ray data—and therefore show two different stretching frequencies in the IR—one "conformer **O**-like," at 1661 cm⁻¹, and one "conformer **N**-like," at 1716 cm⁻¹ (**Figure 6.7**).

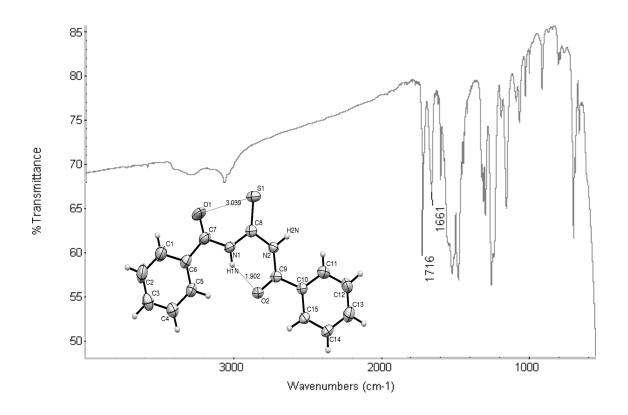


Figure 6.7. IR spectrum and ORTEP diagram (inset) of **47**, showing "conformer N-like" and "conformer **O**-like" carbonyl moieties, with their distinct stretching frequencies.

Returning to the data presented in **Table 6.6**, it is evident that solvent effects have only limited influence in determining the conformation of BzPTUs **16-46**. Of the five compounds for which we performed formal solvent studies, only **16** displays any significant degree of solvent-specific conformational flexibility—and we believe it likely that this flexibility correlates more with the higher solubility of **160** in more-polar solvents, rather than any intrinsic solvent properties that stabilize one conformer over

another. As discussed in **Chapter V**, the relative free energies of **16O** and **16N** are essentially identical in acetonitrile and in chloroform, yet only **16O** precipitates from chloroform, while a mixture of both conformers, leading inexorably to **16N**, precipitates from acetonitrile; therefore, it is unlikely that the proportion of conformer **N** in solution has significant relevance to its formation in the solid state. Further exemplifying this disconnect between solution-state conformation, and crystal structure, **20O** and **20N** exist in an approximately 50:1 ratio in chloroform, at 25°C, yet we have been unable to isolate **20O** in the solid state, under any conditions—and, in the 18 months required to obtain X-ray quality crystals of this compound, we subjected it to over 30 different solvents! **17N** has a similarly small solution-state population (~3%), yet **17O** forms only under a single set of conditions (*i.e.* the slow evaporation of wet THF), and reverts to **17N** upon the slow loss of water at 60°C; conversely, **26**, which is 12% conformer **N** (in chloroform, at 25°C) has never—to the best of our knowledge—precipitated from solution as anything other than conformer **O**.

Because conformer **N** is more stable in the solid state than conformer **O** in all of the BzPTUs for which we have observed its formation, we can extrapolate that it is the thermodynamically-preferred polymorph in all BzPTU—even those for which we have only observed the formation of conformer **O**. Regardless of its thermodynamic stability, however, the appearance of a particular polymorph is largely determined by its kinetic accessibility, *i.e.* the barrier to nucleation.¹⁵⁴ If the nucleation of conformer **N** is kinetically disfavored in certain BzPTUs, for whatever reason, we will observe only conformer **O** in the solid state—regardless of the solution-state population of either

conformer, and regardless of the relative thermodynamic stability of either crystalline solid.

Interestingly, despite its negligible impact on solubility, rate of dissolution, and melting point, aromatic substitution appears inexorably—if not always explicably—linked to the kinetic accessibility of conformer **N**, and, therefore, to the observed solid-state conformation. While we have by no means arrived at any method of quantitative prediction, we have observed certain trends in conformational preference that appear to be quite reliable, within this selection of BzPTUs:

- 1. Highly electron-withdrawing (-NO₂, -CF₃, etc.) R-groups *para* to the carbonyl moiety usually crystallize as conformer N, even when R'= H. Compounds **26** and **39**, which also crystallize in this conformation, provide evidence to suggest that electron density *para* to the carbonyl moiety—and not necessarily *para*-substitution—is responsible for this effect.
- 2. When R'= H, all but the most electronegative R-groups crystallize as conformer **O**.
- When R'= 6-CH₃, para-substituted (4-R) compounds crystallize as conformer
 N, without exception.
- 4. *Ortho*-substitution on either the phenyl ring (2-R) or the pyridyl ring (3-R') favors conformer **O**.
- 5. Moderately electron-withdrawing *meta*-substituents (3-R) crystallize as conformer **O** even when R'= 6-CH₃; highly electronegative *meta*-substituents

result in a high degree of conformational flexibility, regardless of pyridyl substitution.

In only four of the 30 BzPTUs that we studied were we able to isolate both conformers in the solid state, although all (except 19 and 32, vide infra) displayed at least some degree of conformational equilibrium in solution, where [conformer N] $\propto 1/T$. Three of these compounds (16, 30, and 43) have *meta*-substituents on the phenyl ring (3-NO₂, 3-NO₂, and 3,5-Cl, respectively), although, as we noted above, 43's symmetrical phenyl-substitution pattern tends to fit trends observed in *para*-substituted BzPTUs (4-R), rather than their *meta*-substituted counterparts. It may be that the 5-methyl substituent on the pyridyl ring does not favor the nucleation of conformer N as strongly as the 6-methyl substituent; the published, non-solvate structure of 1-aroyl-3-(4-methyl-2-pyridyl) thiourea¹⁵⁵ (R' = 4-CH₃) is that of conformer \mathbf{O} ; to the best of our knowledge, the corresponding 5-methyl structure has not been reported. By contrast, 17 (R' = 6-CH₃) forms conformer **O** (as an H₂O solvate) only under a single set of conditions (**Table 6.7**), and otherwise crystallizes preferentially as conformer N. It is therefore likely that the kinetics of nucleation are affected by both phenyl and pyridyl substitution patterns, and, were we to explore pyridyl substitution patterns in greater depth, we would probably discover that certain substituents evoked the same polymorphic accessibility observed among BzPTUs with electronegative *meta*-substituents.

While we were disappointed that we were unable to obtain more than two sets of polymorphic crystal structures in BzPTUs 16-46, 16O/N and 17O/N nevertheless served to confirm our suspicion that solid-state conformation, rather than a similar substitution

pattern, was responsible for the different structural trends observed in conformers **O** and **N**. Because **Chapter V** covered the structural changes associated with RAHB in conformers **O** and **N**, we will not readdress those topics here: as was previously mentioned, the structural features of these compounds tend to be conformer-specific, and the description of both conformers found in **Chapter V** is generally applicable to all BzPTUs **16-46**. A summary of crystallographically-determined, conformer-specific structural characteristics in BzPTUs **16-46** can be found in **Table 6.8**. For convenience, **Figure 6.1** has been reproduced on the following page, as well.

Unsurprisingly, the lengths of bonds involved in RAHB in either conformer \mathbf{O} or conformer \mathbf{N} tend to be highly conformationally-specific, although certain fluctuations relating to pyridyl substitution are also apparent in our data. The partial double-bond character of amide bonds a and b is lower, on average, in conformer \mathbf{N} ; however, this difference is most pronounced when R' = 6-CH₃, and is actually somewhat negligible when R' = H. The partial double-bond character of thioureido bond \mathbf{c} is similarly less pronounced in conformer \mathbf{N} when R = H, although it is still significantly greater than that observed in conformer \mathbf{O} , regardless of the latter's pyridyl substitution status. It may be that the absence of the 6-CH₃ substituent on the pyridine ring, and the consequent decrease in steric strain, allows a greater contribution of electron density from the pyridyl nitrogen to the pseudo-heterocyclic RAHB, thereby supporting greater conjugation in the otherwise isolated amide bonds. The shorter \mathbf{N} ... $\mathbf{H}(\mathbf{N})$ bond length ($\Delta = 0.030$ Å) when $\mathbf{R} = \mathbf{H}$ in conformer \mathbf{N} may be evidence of this stronger interaction.

Table 6.8. Average lengths of selected bonds in **16-47**, as determined by X-ray crystallography.

Average bond length (Å)	OH(N) or NH(N) ^a	ON or NN ^a	a	b	c	d	e	f	g	h
Conformer O, all	1.912	2.625	1.224	1.377	1.398	1.662	1.337	1.417	1.335	1.339
Conformer O, R' = 6- CH ₃	1.923	2.633	1.226	1.376	1.399	1.663	1.338	1.416	1.338	1.341
Conformer O, R' = H	1.888	2.615	1.224	1.379	1.399	1.662	1.340	1.413	1.335	1.337
Conformer N, all	1.934	2.662	1.208	1.392	1.372	1.667	1.360	1.408	1.335	1.352
Conformer N, R' = 6- CH ₃	1.939	2.665	1.208	1.394	1.371	1.669	1.359	1.409	1.335	1.353
Conformer N, R' = H	1.909	2.651	1.212	1.382	1.377	1.657	1.364	1.404	1.333	1.348
47 "O-like" ^b	1.902	2.608	1.233	1.375	1.415	1.629				
47 " N-like" ^b			1.203	1.399	1.367	1.629				

 $[^]aD...H(A) = N...H(N)$ in conformer **N** and O...H(N) in conformer **O**. D...A = N...N in conformer **N** and O...N in conformer **O**.

b"O-" and "N-like" refer to the coordination status of the carbonyl moiety, where the (C=)O engaged in RAHB is "O-like" and the free (C=)O is "N-like." Labeled bonds correspond with those in the appropriate conformer.

Interestingly, the lengths of the two sets of amide bonds *a* and *b* in **47** mirror those observed in BzPTUs **16-46**, in the corresponding conformers. In the "**O**-like" (*i.e.* RAHB-involved) carbonyl moiety, the C=O bond is elongated (1.233 Å), and the (O=)C—N bond is shortened (1.375 Å), relative to those in the "**N**-like" carbonyl moiety (1.203 Å and 1.399 Å, respectively). The corresponding bond lengths in conformer **O** (1.224 Å and 1.377 Å) and conformer **N** (1.208 Å and 1.392 Å) are similar enough those in **47** that we believe these structural changes are evoked entirely by intramolecular RAHB, rather than some conformation-dependent peculiarity in the BzPTUs' molecular structure.

Apart from differences in bond length, one of the more striking—and, quite frankly, most fascinating—differences between conformers **O** and **N** is their coloration (or, in the case of conformer **O**, the lack thereof). The distinctive yellow color of conformer **N** is present both in the solid state and in solution, whereas—with the exception of R-NO₂ BzPTUs **16** and **30**—conformer **O** is essentially colorless.[‡] Because such a great level of diversity in crystal packing exists in solid-state BzPTUs **16-47**, even among those crystallizing as the same conformer, we concluded that lattice forces likely contribute very little to conformer **N**'s consistently yellow hue. Similarities observed in the single-molecule structures of **16-18**, **20**, **22**, **24**, **26**, **27**, **31**, **39**, **42**, and **43**—all of which crystallize as conformer **N**—led us to propose three potential sources of this lowenergy, visible light absorption:

Due to the presence of both conformers in the mother liquor, small amounts of conformer **N** are almost impossible to remove from samples of conformer **O**, as the former's much lower solubility complicates sample washing. Therefore, many conformer **O** crystals appeared "off-white," or very slightly yellow, due to the residual presence of conformer **N** on the crystal surface. This small amount of conformer **N**, identified from its C=O stretch, was detectable in the IR spectra of these compounds, but did not affect either single crystal X-ray data collection or elemental analysis.

- 1. Charge-transfer behavior across the RAHB, due to facile proton transfer
- 2. Increased conjugation between the phenyl ring and the carbonyl moiety, due to the greater planarity between these two groups observed in conformer N
- 3. Syn-periplanar orientation (and assumed interaction) of the carbonyl and thiocarbonyl moieties, where $d_{\text{S...O}} = 2.918 3.057 \text{ Å}$ (*i.e.* less than the sum of van der Waals radii, 3.32 Å)

The vibrant yellow color observed in 47 quickly eliminated charge-transfer across the RAHB as a viable option for the coloration observed in conformer N, as 47, bis(benzoyl)thiourea, lacks the requisite N...H(N) intramolecular interaction. This compound also lacks obvious visible light chromophores, due to cross-conjugation across the thiocarbonyl moiety, so it is unlikely that the color observed in 47 originates from a different source than that observed in conformer N. Increased conjugation between the phenyl and carbonyl moieties in conformer N remained a plausible explanation, as the average coplanarity of the phenyl ring and the carbonyl moiety, calculated as the torsion angle between bond n and the aromatic n0 conformer n0 (average torsion = 27.95°). Even when *ortho*-substituents were not included in the average, the average torsion angle in conformer n0, 19.1°, was still significantly smaller than that found in conformer n0.

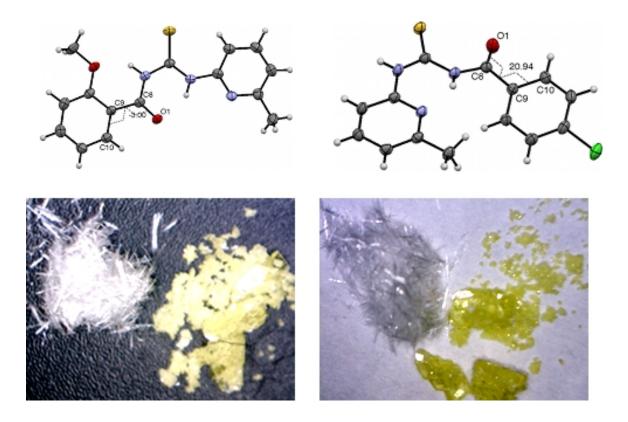


Figure 6.8. ORTEP diagrams (top) and photographs (bottom) of **19** and **22**. Atoms used to calculate torsion angle are labeled at top. Photographs at approximately 10X magnification were captured using a Celestron digital microscope and the Mac OS X image capture program, Photo Booth. To best illustrate the coloration of **19** (fine, colorless, columnar crystals, at left in both images) and **22** (yellow prisms, at right in both images), images were collected on both a black and a white background.

Nevertheless, we were somewhat skeptical of increased phenyl-carbonyl conjugation as the origin of the yellow color in conformer **N**. Despite the lower average torsion angle in conformer **N**, many exceptions exist among BzPTUs **16-46**, with no accompanying change in coloration. BzPTU **19**, for example, shown on the left in **Figure 6.7**, has a phenyl-carbonyl torsion angle of 3.00°, and is completely colorless; conversely, in BzPTU **22**, shown on the right in **Figure 6.8**, this angle is 20.94°--yet its

color is quite unequivocally yellow. It is also unlikely that different substitution patterns have any real effect on the extent to which coplanarity is required for electron delocalization—at least in terms of lowering the energy of the BzPTU sufficiently for a visible-wavelength electronic transition—as the phenyl-carbonyl torsion angle in colorless 35, the R' = H analog of yellow-hued 22, is only 14.00°. These inconsistencies observed in phenyl-carbonyl torsion angles appeared incongruous with the uniformity of the yellow color observed in all conformer N crystals, and we believed that increased conjugation was likely an oversimplified explanation for the presence of color in conformer N.

The final explanation that we considered, an S...O intramolecular interaction related to the syn-periplanar orientation of the carbonyl and thiocarbonyl moieties in all conformer $\bf N$ structures, seemed the most likely of the three. This S...O interaction was present both in all conformer $\bf N$ structures and in 47, where it formed between the non-coordinated, "N-like" carbonyl oxygen and the thiocarbonyl sulfur, and was absent from all conformer $\bf O$ structures, in which the carbonyl and thiocarbonyl moieties were antiperiplanar as a consequence of the intramolecular RAHB. Interestingly, in a survey of published crystal structures of N-benzoyl-N',N'-disubstituted thioureas, ¹⁵⁶⁻¹⁶⁰ which lack the capacity to form an S(6) intramolecular RAHB, we found that the carbonyl and thiocarbonyl moieties adopted a more anti-periplanar conformation (torsion angle \sim 100°), and therefore lacked the S...O close contact observed in conformer $\bf N$. Because the S...O close contact does not appear to be commonplace among benzoyl thioureas, yet is consistent throughout all of our conformer $\bf N$ structures, we believed that it was likely to

have some structural significance, quite possibly relating to the yellow color observed, also consistently, in these compounds.

Close contacts (*i.e.* less than the sum of van der Waals radii, 3.32 Å) between oxygen and sulfur have been well-documented in the literature, ^{161,162} are implicated in a number of biological transformations, ¹⁶³ and have even been employed as rigidifying structural components of polymeric electrooptic materials ¹⁶⁴ and stereochemical directors in asymmetric reactions. ^{165,166} Despite its relevance to both biochemistry and organic structural and synthetic chemistry, the electronic nature of the S...O interaction has not been definitively characterized. In the literature, this contact has been described, varyingly, as electrostatic, ¹⁶⁷ electrostatic-covalent, ¹⁶² hypervalent, ¹⁶⁸ "prematurely" hypervalent, ¹⁶² and, more simply—and perhaps in an effort to circumvent any nomenclatural controversy—non-bonded. ¹⁶⁵

Among reports characterizing the S...O interaction as anything other than purely electrostatic, the general consensus is that this interaction consists of some form of electron donation from oxygen to sulfur, although opinions differ as to the precise nature of this electron donation. Most reports characterize it as an $n_{(0)}$ to $\sigma^*_{(S)}$ interaction, ¹⁶⁹ while others believe that, at least in proteins, the donor orbital is actually $\pi_{(HOMO)}$ of the carbonyl bond. ¹⁷⁰ Ángyan ¹⁶² and Pandya ¹⁶⁸ both implicate some measure of d-orbital participation, inferring that the S...O interaction possesses partial covalent character (Ángyan quantifies this covalent character as 10-30% of the total bond composition); however, the relatively low energy estimated for the S...O interaction (3-8 kcal/mol, depending on the computational methodology) indicates that "covalent character" is more

a qualifier of electronic composition than a statement on bond order or atomic connectivity. Nevertheless, even a relatively weak $n_{(O)} \rightarrow \sigma^*_{(S)}$ interaction—especially one with lower energy, d-orbital participation—can result in visible light absorption sufficient to produce empirically observable coloration,¹⁷¹ and we therefore believe that this is the most plausible explanation for the yellow color in conformer N BzPTUs (and 47).[‡]

Conclusion

BzPTUs 16-46 crystallize in one of two conformers, both of which feature an S(6) intramolecular RAHB. For most of these BzPTUs, we have found that only one conformer is kinetically accessible in the solid phase; however, we managed to isolate solid samples of both conformers in four of these BzPTUs, and we obtained single crystal X-ray data for two conformer pairs. By observing structure-based conformational preferences in these BzPTUs, we also developed a qualitative sense of the factors that favor conformers **O** and **N**, concluding that methyl substitution at the 6-position on the pyridine ring and electronegative *para*-substitution are the best predictors of conformer **N** in the solid phase. Because crystal packing forces did not correlate well with conformational preference, however, we were unable to use this handle on single-molecule conformational preference to intentionally engineer supramolecular structure.

Nevertheless, we found that single-molecule conformational preference did have a significant impact on the observed physical properties of solid-phase BzPTUs **16-46**, in a

[‡] The reality is that we are probably completely off-base, in terms of our suspicions as to where the color originates; however, it is far more entertaining to be wrong about a hypothesis than it is to have no hypothesis at all.

way that was apparently independent of supramolecular architecture. All conformer N solids were significantly less soluble—both thermodynamically and kinetically—than their conformer O counterparts, and all were also bright, "sulfur yellow," a color which persisted even in solution. Based on similarities between the conformer N crystal structures, we concluded that the yellow color most likely originates in the $n_{(O)} \rightarrow \sigma^*_{(S)}$ interaction between the coplanar carbonyl and thiocarbonyl moieties.

Overall, our work with BzPTUs 16-46 exemplifies both the problems and the potential of organic crystal engineering. These compounds exhibit an extraordinary correlation between molecular conformation and certain observed physical properties, yet also display a somewhat mind-boggling incongruousness between these same physical properties and supramolecular structure / crystal packing. While crystal packing must certainly play some role in determining macroscopic properties, its correlation with the physical characterisitics observed in BzPTUs 16-46 remains nebulous, and, in predicting the physical properties of these fascinating compounds, we are better served by considering single-molecule conformation, rather than any trends in supramolecular organization.

CHAPTER VII

CONFORMATIONAL EXCHANGE IN

1-BENZOYL-3-(2-PYRIDYL) THIOUREAS:

THE SOLUTION STATE

Introduction

As discussed in Chapters **V** and **VI**, compound **16**, 1-(3-nitrobenzoyl)-3-(6-methyl-2-pyridyl)thiourea is—to the best of our knowledge—the first experimental example of a "switchable" RAHB-containing system. This compound has the capacity to form two different RAHBs, and the two resultant conformations, **O** and **N** in **Figure 7.1**, are both reproducibly isolable in the solid state, and readily discernable in both ¹H- and ¹³C-NMR. RAHB theory predicts that the homonuclear N...H(N) intramolecular

than the heteronuclear O...H(N)

contact, and this preference is

reflected in the enhanced crystalline

stability of 16N, the

thermodynamically-preferred solidstate conformation. Nevertheless, we

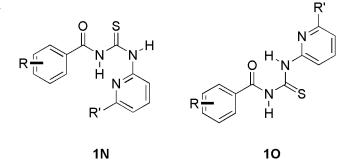


Figure 7.1. General structure of both possible conformers of BzPTUs **16-46**.

found that **16O** is significantly more stable than **16N** both in solution and as determined by our gas-phase calculations, and we concluded it unlikely that the relative strength of the intramolecular RAHB represents the driving force behind phase-specific conformational preference. Because **16N** and **16O** have vastly different electronic characteristics—perhaps best demonstrated by their calculated dipole moments, 12.4 D and 4.5 D, respectively—it is more likely that phase-specific conformational preference is determined by external factors, such as the energetic contributions of substrate-substrate and substrate-solvent interactions.

To further explore the conformational preferences of this intriguing class of compounds, we synthesized a series of 1-benzoyl-3-(2-pyridyl) thioureas (BzPTUs), compounds **16-46**. The enhanced solution-state stability of conformer **O** is ubiquitous among all of these compounds, and all but two display "switchable" behavior in solution, resulting in a dynamic equilibrium between conformers **O** and **N**. To the best of our knowledge, the presence of conformer **N** in solution has never been reported in any such disubstituted BzPTUs, although its appearance in the solid state has been reported in **17**. In many BzPTUs, the proportion of conformer **N** is relatively small, and we believe this omission is likely related to peak overlap (*vide infra*) and the signal-to-noise common in diagnostic HNMR scans. As in the solid state, which will be discussed separately, substituent effects play a significant—and relatively predictable—role in determining the extent to which conformer **O** is favored in solution, with conformational free energy differences that are inversely proportional (in terms of absolute magnitude) to Hammett substituent constants. Because few BzPTUs with electron-withdrawing

substituents have been reported, it is entirely possible that the presence of conformer N was previously overlooked.

Results and Discussion

Synthesis of Bifunctional Thioureas

BzPTUs **16-46** were prepared from addition of the corresponding benzoyl isothiocyanate and either 2-aminopyridine or 2-amino-6-picoline, using the procedure outlined in **Scheme 6.1**. Aroyl isothiocyanates were prepared in accordance with the literature procedure for the parent compound, benzoyl isothiocyanate (R = H in **Scheme 6.1**);¹⁵⁰ because these reaction conditions yielded satisfactory results, further optimization was not explored. When the parent benzoyl chloride was not commercially available, ‡ it was prepared from the corresponding benzoic acid. ¹⁵¹ We made no attempt to isolate the intermediate isothiocyanates or acid chlorides, as we found that satisfactory yields (65-80%, calculated from the initial amount of either the acid chloride or the isothiocyanate) of BzPTUs could be obtained without additional purification steps. Direct isolation of the BzPTU from the reaction mixture could be achieved by the addition of deionized water, upon completion of the reaction; the precipitated material, after drying, was satisfactorily pure by ¹H NMR.§

In an effort to reduce solvent waste, we attempted to synthesize the BzPTUs in a quasi-one-pot reaction, adding the aminopyridine directly to the filtrate from Step **b**,

[‡] In some cases, the parent benzoyl chloride was commercially available, but we chose to prepare it from the corresponding benzoic acid, which could be obtained, free of charge, from our Reuse Chemical Facility.

While yield could be increased by removing the reaction solvent and chromatographing the BzPTU product, we did not believe this improvement sufficient to justify either the time or the significant increase in solvent usage that it entailed.

Scheme 6.1. In BzPTUs that preferred to crystallize as conformer O, this process was highly effective; however, BzPTUs that preferred to crystallize as conformer N tended to precipitate from the reaction mixture as highly intractable powders, negligibly soluble in all but the most polar solvents (e.g. DMSO, DMF, etc.) and effectively useless for both the growth of single crystals and solution-state spectral analysis. Replacing acetonitrile with acetone produced similar results, and THF—by far the best solvent for all BzPTUs 16-46—could not be used for the synthesis of isothiocyanates, due to its inability to dissolve a sufficient quantity of KSCN. Solvents such as dichlormethane, ethyl acetate, and diethyl ether were similarly ineffective in the synthesis of isothiocyanates, and were also incompatible with the final purification step (i.e. the addition of water) of the BzPTU synthesis, so we concluded that the two-pot reaction sequence described in Scheme 6.1 was the most efficient route to BzPTUs.

Conformer Identification

In RAHBs, strong donor-acceptor interactions tend to result in significant deshielding of the coordinated proton. Pecause the homonuclear N...H(N) intramolecular interaction (conformer N) should be stronger than the heteronuclear O...H(N) interaction (conformer O), as a result of better orbital overlap, and in all cases the farthest-downfield signal in the major conformer was > 2 ppm upfield from the farthest-downfield signal in the minor conformer, we hypothesized that the major conformer in all BzPTUs 16-46 was conformer O.

Additional 1D spectral evidence corroborated this hypothesis. Amide-type

deshielding of coplanar γ-protons is well-known in thioureas.⁸⁹ and should be observed in the pyridyl proton *ortho* to the thiourea moiety (proton F in **Figure 7.2**) only in conformer O. A secondary interaction between the RAHB-involved thiourea proton and the pyridyl nitrogen restricts rotation of the pyridyl ring, enforcing the coplanar arrangement of the *ortho*-pyridyl proton and the C=S bond. In accord with these structure-based predictions, this proton displays a downfield shift of ~2 ppm in the major conformer, at a frequency (8.3 ppm) consistent with amide-type deshielding. This large change in chemical shift was observed in all BzPTUs 16-46, and it was by far the largest chemical shift change observed among C—H protons; only heteroatomic protons A and B displayed such a similarly drastic change in chemical environment, between conformers O and N. Furthermore, ¹H NMR spectra of BzPTUs 19 and 32 show only the F₀ frequency, at 8.97 ppm and 8.66 ppm, respectively. Because these compounds do not display dynamic equilibrium between conformers O and N, likely due to a "locked" conformation produced by a second intramolecular RAHB, which forms between the ortho-methoxy substituent and thiourea proton B₀. This conformation appears in the crystal structures that we obtained for both of these compounds (Figure 7.3), and, given

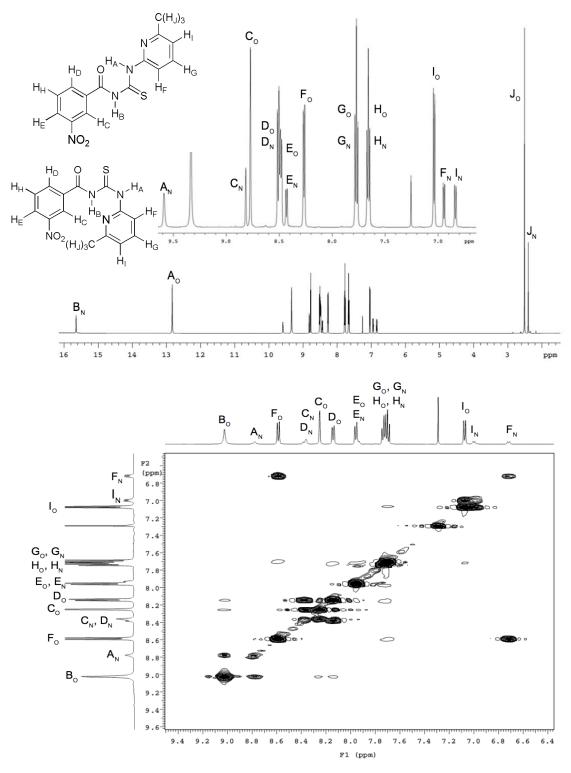


Figure 7.2. Clockwise from top left: **16O** with labeled protons; ¹H-NMR spectrum of **16** (inset: zoomed-in view of aromatic region); 2D NOESY spectrum of **23**, where peak assignments are identical to those in **16O/N**; **16N** with labeled protons.

the downfield resonance of proton B_0 (11.16 ppm in **32** and 11.11 ppm in **19**), is evidently present in the solution state, as well.

2D NOESY data confirmed proton assignments from the 1D spectra, and provided further confirmation that conformer **O** was indeed the preferred solution-state conformation. Cross-peaks from chemical (e.g. conformational) exchange are of the same phase as the peaks along the diagonal, and are therefore easy to distinguish from NOEderived cross-peaks, which are inverse-phase. The chemical exchange cross-peak between protons F_0 and F_N is clearly evident in **Figure 7.2**, confirming the identity of this proton, as assigned from the 1D spectrum. The predominance of conformer **O** in solution is confirmed by the opposite-phase (i.e. NOE) cross-peaks B_0 / C_0 and B_0 / D_0 ; only in conformer **O** are the *ortho*-protons on the phenyl ring sufficiently close to the amide proton to display NOEs, and the far-upfield resonance of B₀ (9.01 ppm vs. 12.76 ppm for A₀) indicates that it is not the major conformer's RAHB-involved N—H proton. Additionally, the strong NOE expected between J⁴ protons A_N and F_N, which are coplanar in conformer N and separated by no more than 2.38 Å in any of our conformer N crystal structures, is not observed at this resolution, as would be anticipated if conformer N were the predominant solution-state entity.

Variable-Temperature ¹H-NMR – Thermodynamic Measurements

Within the range of concentration (0.01 - 0.05 M) that proved optimal for our variable-temperature NMR measurements, we found that conformational equilibrium did

not vary with sample concentration, outside of reasonable estimations of error inherent in NMR peak integration.^{172,173} Because both the solubility and rate of dissolution of conformer **N** are significantly lower and slower, respectively, than those of conformer **O**, sample concentration was primarily determined by expediency, *i.e.* one which afforded quick data collection, yet could be achieved in an acceptable period of time, instead of after 8 hours on the sonicator.

Samples were prepared by dissolving 10-20 mg of BzPTUs **16-46** in 0.5 mL CDCl₃. For solvent studies performed on **16**, 5-10 mg were dissolved in 0.5 mL of the chosen solvent. Spectra were collected at intervals of 5 – 10°C, between -15 and 45°C; specific temperature ranges are reported in **Table 7.1**. In all cases, data were collected at a minimum of five temperatures, over a minimum of 30°C. For most samples, the low boundary of the temperature range was determined by the lowest temperature that the spectrometer could achieve without external cooling, and the high boundary was determined by the temperature at which peak broadening interfered with integration. In the case of DMSO-d₆, the low boundary of the temperature range was set at 20°C, 2°C above the solvent's melting point.

Thermodynamic Measurements – CDCl₃

In all BzPTUs **16-46**, conformer **O** was thermodynamically favored in CDCl₃. Values of ΔG for the formation of conformer **O** (at 25°C) ranged from -0.84 kcal/mol (**26**) to -3.3 kcal/mol (**33**); in general, BzPTUS with electron-withdrawing *meta*-substituents on the phenyl ring and/or a 6-CH₃ substituent on the pyridyl ring had the smallest (least

negative) free energy differences between conformers. The magnitude of the stabilization offered by both substitution trends can easily quantified by comparing $\Delta\Delta G_{25^{\circ}C}$ values from related BzPTUs. When identical R' substituents were present on the pyridyl ring, moving an R group from the *para* position to the *meta* position—for example, as in compounds **16** and **18**—lowered the free energy difference between conformers **O** and **N** by 0.2 ± 0.2 kcal/mol, on average, with a maximum *meta*-stabilization of 0.5 kcal/mol. This trend was not perfectly consistent, however, as conformer **N** in compound **21** (R = m-Cl) was actually 0.1 kcal/mol higher in energy, relative to conformer **O**, than in **22** (R = p-Cl)

Both improved consistency and greater stabilization of conformer **N** were observed in BzPTUs with a 6-CH₃ pyridyl substituent. Incorporating this methyl group

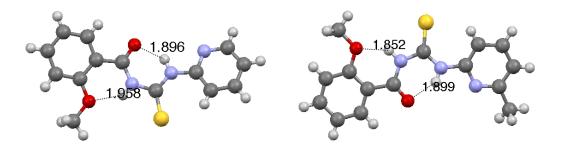


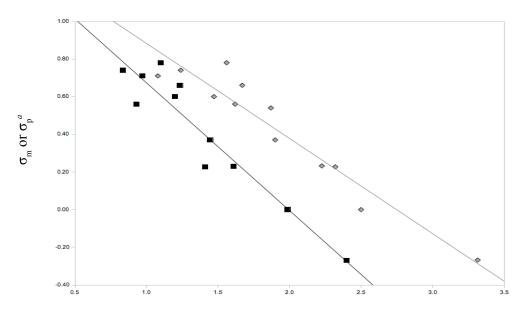
Figure 7.3. X-ray crystal structures of **32** (left) and **19** (right). Dashed lines indicate intramolecular hydrogen bonds; bond lengths are in Å.

stabilized conformer **N** by 0.5 ± 0.3 kcal/mol, relative to 6-H BzPTUs with identical R groups; $\Delta\Delta G_{25^{\circ}C}$ ranged from 0.9 kcal/mol (BzPTUs **22** and **35**) to 0.1 kcal/mol (BzPTUs **16** and **30**), and in no case was conformer **N** more favored in BzPTUs with a 6-H pyridyl substituent. After accounting for the stabilizing effect of the 6-CH₃ substituent, Hammett

substituent constants¹⁷⁴ were roughly predictive of relative $\Delta G_{25^{\circ}C}$, where larger values of σ_m and σ_p were associated with the increased stability of conformer **N** (**Figure 7.4**). Because we observed no correlation between Hammett constants and either entropy or enthalpy, we believe that electronegative phenyl substituents serve primarily to weaken the (C=)O...H(N) intramolecular interaction, thereby destabilizing conformer **O** in relation to conformer **N**.

Table 7.1. Thermodynamic parameters for the formation of conformer O in chloroform, in BzPTUs 16-46. Compounds are listed in ascending order, relative to the absolute magnitude of $\Delta G_{25^{\circ}C}$. Because BzPTUs 19 and 32 do not undergo conformational interconversion, they are not included in this table.

CMDD	D	Di	$\Delta \mathbf{G}_{25^{\circ}\mathrm{C}}$	ΔΗ	ΔS	T range
CMPD	R	R'	(kcal/mol)	(kcal/mol)	(e.u.)	(°C)
26	3,5-Cl	6-CH ₃	-0.84	3.0	13.0	-15 – 25
23	3-CN	6-CH ₃	-0.93	2.7	12.1	-15 – 30
16	$3-NO_2$	6-CH ₃	-0.97	2.0	10.1	-10 - 45
30	3-NO ₂	Н	-1.1	1.8	9.7	-10 - 30
18	4-NO ₂	6-CH ₃	-1.1	1.8	9.7	-15 - 25
25	3,4-Cl	6-CH ₃	-1.2	2.8	13.3	-20 - 25
24	4-CN	6-CH ₃	-1.2	2.2	11.7	-15 – 35
39	3,5-Cl	Н	-1.2	2.4	12.1	5 - 35
22	4-C1	6-CH ₃	-1.4	1.7	10.5	-15 – 25
21	3-C1	6-CH ₃	-1.5	2.7	14.0	-10 - 25
38	3,4-C1	Н	-1.5	2.0	11.2	-10 – 20
31	4-NO ₂	Н	-1.6	1.9	11.7	-10 - 25
36	3-CN	Н	-1.6	1.4	9.9	-20 - 20
37	4-CN	Н	-1.7	1.4	10.4	-15 – 25
34	3-C1	Н	-1.9	2.4	14.5	5 - 30
17	Н	6-CH ₃	-2.0	3.2	17.4	-10 - 25
41	2-Br	Н	-2.2	4.1	21.1	- 9 - 30
40	4-Br	Н	-2.2	3.8	20.2	-10 - 30
35	4-C1	Н	-2.3	2.4	15.8	-15 – 25
20	4-OCH ₃	6-CH ₃	-2.4	3.1	17.6	-10 - 30
29	Н	Н	-2.5	3.1	18.8	-10 - 25
33	4-OCH ₃	Н	-3.3	5.0	26.5	-10 - 20



 $\Delta G_{25^{\circ}C}$ (kcal/mol) for the formation of conformer N

^aRef. 174

Figure 7.4. Correlation between Hammett substituent constant and conformer **O** / conformer **N** free energy difference in BzPTUs **16-28** (gray) and **29-46** (black)

Despite performing calculations with a variety of basis sets, we were unable to computationally reproduce the solution-state equilibrium between conformers \mathbf{O} and \mathbf{N} . The gas-phase energy difference between $\mathbf{16O}$ and $\mathbf{16N}$, -4.72 kcal/mol, calculated at the B3LYP/6-31G++(d,p) level of theory, was four times larger (in terms of absolute magnitude) than the experimentally-determined value of $\Delta G_{25^{\circ}C}$ for the formation of \mathbf{O} , -1.0 kcal/mol. This discrepancy is far outside the range of error anticipated for this type of calculation, ¹⁷⁵ and is unlikely to result from solvation: additional computational studies, performed at the RB3LYP/6-31G(D) level in Spartan 08, indicated that, in

chloroform, $\Delta G_{N\to 0}$ was 4.89 kcal/mol—even greater than that determined in the gas phase, albeit at a different level of theory. Although we have not observed molecular aggregation in our 2D studies, it may be that dimerization and/or other intermolecular interactions lead to solution-state energy changes that single-molecule computational studies cannot easily reproduce. Lattice energy calculations for 16N/O indicate that 16N is the preferred solid-state conformer, by 3.89 kcal/mol, so it may be that some of the intermolecular interactions favoring 16N are present in solution, thereby lowering the N/O free energy difference.

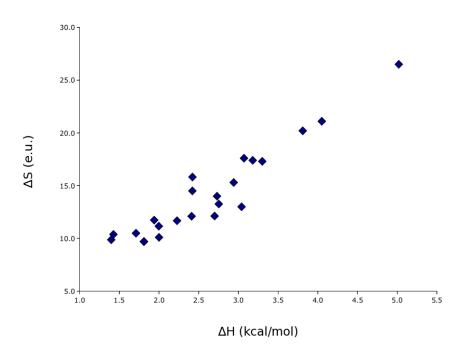


Figure 7.5. Linear correlation between entropy and enthalpy in BzPTUs 16-46.

[‡] It may also simply be that there are no protons within 5-6 Å of the thiourea moiety that would only show NOESY correlations in either the dimerized species or the monomer, but not in both.

Entropic and enthalpic values obtained for the $N \rightarrow O$ transformation in BzPTUs 16-46 lend some credence to this hypothesis. In all cases, the formation of conformer O is associated with an increase in entropy ($\Delta S > 0$), yet enthalpic factors unilaterally favor conformer N, by 1.81 to 5.02 kcal/mol. Our computational studies of 16 indicate that the gas-phase dipole moment in 16N is nearly three times greater than that in 16O, which is in agreement with both the higher disorder associated with the formation of 16O and the higher aggregation postulated for 16N, as an increase in polarity should correlate with stronger intermolecular interactions. Perhaps unsurprisingly, given the consistency in the direction (i.e. mathematical sign) of entropy, enthalpy, and free energy among all BzPTUs 16-46, we observed a near-linear correlation between entropy and enthalpy (Figure 7.5; $R^2 = 0.9$) in these compounds, which may also be consistent with increased intermolecular aggregation in conformer N.

These entropic and enthalpic data also appear to provide some rationale behind the quite divergent, phase-specific stabilities of conformers \mathbf{O} and \mathbf{N} . If one imagines the solid state to represent the condition wherein $\Delta S \to 0$, the free energy difference between \mathbf{O} and \mathbf{N} will approach ΔH , thereby favoring conformer \mathbf{N} . Conversely, if one imagines the gas phase as a situation where $\Delta S \to \infty$, it is clear that enthalpic contributions to ΔG will be quite small, and \mathbf{O} should be the low-energy conformer. Given that this is exactly what our calculations predict—and, in the case of solid-phase conformers, what our empirical data confirms—we believe that the solution-phase behavior of these BzPTUs can be interpreted (at least qualitatively) as a "transition phase" between each conformer's sphere of dominance.

Thermodynamic Measurements – Solvent Studies

Thermodynamic parameters obtained for **16** in DMSO-d₆, CD₃CN, toluene-d₈, and CD₃OD (**Table 7.2**) indicated that both intermolecular aggregation and solvent polarity play a significant role in stabilizing conformer **N**.

Solvent	$\Delta G_{25^{\circ}C}$	ΔΗ	ΔS	Dielectric Constant ¹⁷⁶
CDCl ₃	-0.97	2.0	10.1	4.81
DMSO-d ₆	-0.82	6.1	23.3	47.0
CD ₃ CN	-0.99	1.10	7.2	37.5
toluene-d ₈	-2.3	2.6	16.5	2.38

Table 7.2. Thermodynamic parameters for the dynamic equilibrium between **16O** and **16N**, in various solvents. All values are defined for the **16N** \rightarrow **16O** transition, *i.e.* the formation of **15O**.

As might be expected, conformer N is more stable in DMSO-d₆ than in CDCl₃, consistent with the greater polarity of DMSO-d₆. In CD₃CN, however, the free energy difference between conformers N and O is approximately equal to that observed in CDCl₃, so polarity alone cannot account for the relative stabilities of O and N in various solvents. Therefore, molecular aggregation must also play some role in determining the conformational free energy difference, at least in certain solvents. Both $\Delta H_{N\to O}$ and $\Delta S_{N\to O}$ are much smaller (*i.e.* less negative) in CD₃CN than in CDCl₃, so it may be that molecular aggregation is responsible for the increased stability of conformer N in CDCl₃, relative to what might be expected purely on the basis of solvent polarity. Because both $\Delta H_{N\to O}$ and $\Delta S_{N\to O}$ are even larger in toluene-d₈ than they are in CDCl₃, it is unlikely that solvent

ordering and solvent-solute interactions account entirely for these parameters; solutesolute interactions must also play a role in stabilizing conformer **N**.

Variable-Temperature ¹H-NMR – Kinetic Measurements

Samples were prepared as for thermodynamic measurements; in the case of kinetic parameters obtained via peak coalescence, the same samples (and spectra) were used for both. From the peak separation in the 1D spectra of BzPTUs 16-46 (Figure 7.2), which could be as high as 6 ppm, it was evident that exchange at room temperature, and in CDCl₃, was either very fast or very slow on the NMR timescale. Because the solubility of conformer N in CDCl₃ was significantly lower than that of conformer O, yet conformer O predominated in solution, we believed that the barrier to interconversion was likely quite high; however, because fast exchange—and a low barrier to interconversion—was theoretically possible, we wanted to determine the free energy of activation for these BzPTUs.

The compounds for which we obtained kinetic data were largely self-selecting: in most cases, 1D ¹H-NMR peaks from BzPTUs **16-46** did not coalesce within the sampling range of CDCl₃ (i.e. below 55°C). DMSO-d₆ appeared to accelerate the room-temperature exchange rate—and decrease the coalescence temperature—but its high melting point made it impossible to obtain slow-exchange values for peak separation (Δν), so we were unable to use it for kinetic calculations. Most BzPTUs **16-46** had very low solubility in in CD₃CN, acetone-d₆, and/or toluene-d₈, making it difficult to obtain useful signal-to-noise ratios within reasonable limits for instrument time. Therefore, while we would have

preferred to obtain ΔG^{\ddagger} for all BzPTUs **16-46**, practical considerations limited our sample pool.

When coalescence was observed, the free energy of activation at that temperature was calculated using Shanan-Atidi's and Bar-Eli's modification of the Erying equation. Because we found that literature reports of these calculations showed significant variance in terms of the actual formula used to calculated ΔG^{\ddagger} , and our own experimentation with these various formulas led us to conclude that only the original (*i.e.* from the Shanan-Atidi and Bar-Eli paper) actually produced values of ΔG^{\ddagger} that agreed with the thermodynamic energy difference between the two conformers, we have outlined our calculations below.

In kcal/mol, the activation energies for the $N \to O$ and $O \to N$ transitions can be found from the following equations:

$$\Delta G_{0 \to N}^{\ddagger} = 0.00457 T_c \{ 10.62 + \log \left[X / 2\pi (1 - \Delta n) \right] + \log (T_c / \Delta \nu) \} \quad (1)^{177}$$

$$\Delta G_{N\to 0}^{\ddagger} = 0.00457 T_c \{ 10.62 + \log \left[X / 2\pi (1 + \Delta n) \right] + \log (T_c / \Delta v) \} \quad (2)^{177}$$

where T_c is the coalescence temperature, Δn is the difference between the mole fractions of \mathbf{O} and \mathbf{N} at coalescence ($n_0 - n_N$ at T_c), and Δv is the low-temperature (*i.e.* slow-exchange, or maximum) peak separation, in Hertz, between the coalescing peaks. The variable X is defined as $2\pi\Delta v \tau_{avg}$, where τ_{avg} is the *weighted* average of the lifetimes of the coalescing peaks, during slow exchange. In unequally-populated systems, τ_{avg} can be found by simplifying the following equation:

$$\Delta n = [(X^2 - 2) / 3]^{3/2} \cdot (1 / X) \tag{3}^{177}$$

After accounting for all constants, and replacing X with $2\pi\Delta\nu\tau_{avg}$, Equation (3) can be reduced to a cubic equation:

$$248.1(\Delta v)^3 (\tau_{\text{avg}})^3 - 32.65 \Delta v \tau_{\text{avg}} - 2.83 = 0$$
 (4)

which, when solved, will yield τ_{avg} as its positively-signed root.

In some reports, $_{\text{avg}}^{178}$ τ_{avg} for unequally-populated sites has been erroneously calculated from the average rate constant, k_{avg} , which may be used to calculate the average lifetime of peaks in equally-populated systems, where the forward and backward rates are equal.

$$k_{\text{avg}} = 2.22\Delta v = 1/2\tau_{\text{avg}}$$
 (5)¹⁷⁸

This method of finding τ_{avg} cannot, however, be used in unequally-populated systems, as it does not produce a *weighted* average, and therefore does not account for the unequal contributions of the two conformer populations.

Another error that we have noticed in the literature relates to a misprinting of Shanan-Atidi and Bar-Eli's formula, where Equation (3) has been replaced by

$$\Delta n = (X^2 - 2 / 3)^{3/2} \cdot (1 / X) \tag{5}^{179}$$

Using either Equation (5) or $k_{\rm avg}$ to calculate $\tau_{\rm avg}$ for an unequally-populated system will result in a calculated transition state free energy difference that does not correspond to the thermodynamic free energy difference between the two conformers ($\Delta\Delta G^{\ddagger} \neq \Delta G_{TC}^{\ddagger}$). Because the principle of microscopic reversibility prohibits this kind of discrepancy, and only Shanan-Atidi and Bar-Eli's modification of the Eyring equation produces values for $\Delta\Delta G^{\ddagger}$ that correspond with our empirical data for the thermodynamic free energy difference between $\bf O$ and $\bf N$, we believe that this is the most reliable method for determining activation energy from coalescence temperature, in unequally-populated systems.

In the BzPTUs for which we observed coalescence in CDCl₃, ΔG^{\ddagger} for the $\mathbf{O} \rightarrow \mathbf{N}$ transition ranged from 16.8 to 18.8 kcal/mol, and from 14.9 and 16.0 kcal/mol in the opposite direction (**Table 7.3**). $\Delta\Delta G^{\ddagger}$ was in all cases comparable (or equivalent) to ΔG at the coalescence temperature; the primary source of error is likely to be found in peak integration.

[‡] TC = Coalescence Temperature

Table 7.3. Free energy of activation for selected BzPTUs, at their respective coalescence temperatures

BzPTU	R	X	T _C ^a (°C)	Proton	Δν (Hz)	$\begin{array}{c} \Delta G_{O\rightarrow} \\ N^{\sharp b} \\ \text{(kcal/m} \\ \text{ol)} \end{array}$	$\Delta G_{ m N ightarrow o}^{\dagger b}$ (kcal/m ol)	ΔΔG [‡] (kcal/m ol)	ΔG_{TC}^{c} (kcal/m ol)
40	4-Br	Н	25.0	F	30.4	17.3	14.9	2.5	2.2
27	4-Br	CH ₃	45.0	F	56.2	17.5	15.5	1.9	1.9
35	4-C1	Н	25.0	F	27.2	17.2	14.9	2.2	2.3
22	4-CN	CH ₃	45.0	F	41.1	17.2	15.7	1.5	1.6
23	3-CN	CH ₃	35.0	J	12.0	17.1	16.0	1.2	1.2
21	3-C1	CH ₃	55.0	F	55.9	18.6	16.0	2.5	2.5
17	Н	CH ₃	50.0	F	66.5	18.8	15.7	3.1	3.1
43	4-CF ₃	Н	40.0	F	34.4	18.4	15.6	2.8	2.8
37	4-CN	Н	25.0	F	25.0	16.8	15.0	1.8	1.8
25	3,4-C1	CH ₃	25.0	J	6.0	17.0	15.9	1.2	1.2

^a Coalescence temperature

Because it has been noted that inaccuracies inherent in data collection can lead to grossly inaccurate values of ΔG^{\ddagger} , the free energy of activation for the conformational exchange in **23** was also determined via 2D-EXSY spectroscopy, ¹⁸⁰⁻¹⁸² as a means of comparison. 2D-EXSY is identical, in terms of pulse sequence, to 2D-NOESY; dynamic conformational exchange produces cross-peaks of significant intensity, and of the same phase as the peaks found along the diagonal of the spectrum. At very short mixing times $(t_m < 100 \text{ ms})$, the intensities of these cross-peaks (I_{ij}) are related to the rate of chemical exchange (k_{ji}) and the initial equilibrium magnetization vector (M_{ji}) by the equation (M_{ij})

^b Free energy of activation at the coalescence temperature.

^c Absolute value; calculated from non-coalesced peaks in the 1D spectrum, at the coalescence temperature of the peaks used to calculate ΔG^{\ddagger} .

$$I_{ij}(t_{\rm m}) \approx k_{ji}t_{\rm m}M_i^{\,0} \tag{8}$$

The rate constant can then be found as the slope of the best-fit line through a plot of I_{ij}/M_j^0 vs. t_m . M_j^0 is approximated by I_{ij} at $t_m = 0$ ms. To reduce the margin of error inherent in peak integration, the arithmetic mean of all values of I_{ij}/M_j^0 at each t_m was used in creating the rate constant plot. Once the rate constant is known, the Eyring equation can be used to calculate the free energy of activation. A sample plot of I_{ij}/M_j^0 vs. t_m for 23 is shown in **Figure 7.6**.

At 25°C, we found that the free energy of activation for the conformational exchange between 23N and 23O was comparable to that determined for the same compound at 35°C, the coalescence temperature for protons J_O and J_N . ΔG^{\ddagger} for the $N \rightarrow O$ transformation was found to be 17.6 kcal/mol, 1.6 kcal/mol higher than the value of ΔG^{\ddagger} found at 35°C; for the $O \rightarrow N$ transition, this parameter was found to be 18.9 kcal/mol, 1.8 kcal/mol higher than at 35°C. The free energy of activation calculated from 2D EXSY was less precise than that calculated from the coalescence temperature: $\Delta\Delta G_{25^{\circ}C}^{\ddagger}$ was 0.4 kcal/mol higher than $\Delta G_{25^{\circ}C}(1.3 \text{ kcal/mol vs. 0.9 kcal/mol)}$, whereas $\Delta\Delta G_{35^{\circ}C}^{\ddagger}$ and $\Delta G_{35^{\circ}C}^{\ast}$ were found to be of the same magnitude (1.2 kcal/mol). Nevertheless, both methods of calculating the free energy of activation produced values which were believable, given the observed peak separation (or lack thereof), and confirmed our suspicion that conformational interconversion was slow on the NMR timescale.

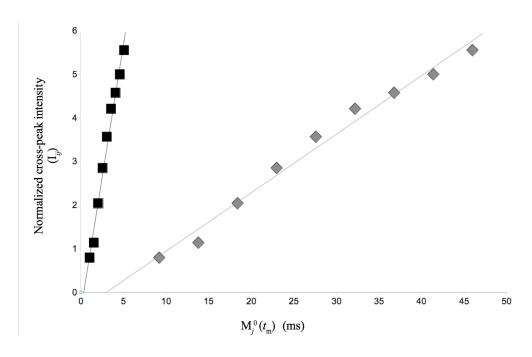


Figure 7.6. 2D EXSY rate constant plot for **23** at 25°C, for both the formation of **N** (black squares) and the formation of **O** (gray diamonds).

Conclusion

In the absence of a secondary, intramolecular hydrogen bond acceptor, BzPTUs display solution-state conformational equilibrium between conformers **O** and **N**. In all cases, conformer **O** is favored in solution; free energy differences range from 0.9 to 3.3 kcal/mol. After accounting for pyridyl substitution, Hammett substituent constants are roughly predictive of the free energy difference between conformers **O** and **N**, where larger Hammett constants are associated with a greater proportion of conformer **N** in solution. Entropy is likely to be the driving force in determining conformational

equilibrium at room temperature: although enthalpic factors favor conformer **N** by 1.4 to 5.0 kcal/mol, entropy increases (by 9.7 to 27 e.u.) upon the formation of conformer **O**. This solution-state equilibrium can be envisioned as a representative "transition phase" between the gas phase, where entropic considerations would dominate the free-energy equation, and the solid phase, where enthalpic factors would carry greater weight. Unfortunately, as none of these thermodynamic parameters accurately predict the preferred solid-state conformation of BzPTUs **16-46**, it is clear that factors other than solution-state equilibrium play a role in determining solid-state polymorphic preference.

CHAPTER VIII

ALL GOOD THINGS MUST COME TO AN END:

THE DECOMPOSITION OF 1-BENZOYL-3-(2-PYRIDYL)THIOUREAS

Introduction

Alkyl and aryl thioureas are well-known to be stable to both ambient and aqueous conditions. Surprisingly, N-benzoyl thioureas also exhibit low reactivity under similar conditions, most likely as a result of the stabilizing effect of a characteristic, pseudoheterocyclic resonance-assisted hydrogen bond (Figure 8.1). This stability has been recognized to enhance thioureas' catalytic utility in many synthetic procedures, including the asymmetric reduction of carbonyl compounds, 183,184 the asymmetric hydroformylation of styrene¹⁸⁵ and hydrogenation of

Nevertheless, thioureas do exhibit predictable reactivity under certain conditions; this behavior

enamides, 186 and the Heck reaction of aryl halides. 187

Figure 8.1. Intramolecular hydrogen bonding in Nbenzovl thioureas with at least one N' hydrogen atom

enhances their utility as a synthetic material. Thioureas are notably used in the production of thiazoles, a heterocycle found in many natural products, 188 as well as in pharmaceuticals, ¹⁸⁹ fungicides, ¹⁹⁰ and dyes. ^{191,192} Methods for converting thioureas into

thiazoles include condensation with an α -halo ketone, ¹⁹³ domino alkylation-cyclization with a propargyl bromide under microwave radiation, ¹⁹⁴ and reaction with 1*H*-1-(1'-alkynyl)-5-methyl-1,2,3-benziodoxathiole 3,3-dioxides under basic conditions. ¹⁹⁵

Thiourea anions have also enjoyed recent utility as nucleophilic coupling reagents in the production of aryl sulfides (**Scheme 8.1**). In this reaction, the sulfur nucleophile condenses with a *o*-amide aryl radical species, producing a thiolate anion intermediate, which liberates [NCN]•– and is then quenched with MeI to yield the desired methyl sulfide product. A radical mechanism was also proposed for the formation of Sphenylisothiouronium derivatives from phenylazotriphenylmethane and thiourea;

$$Ph-N=N-C(Ph)_{3} \xrightarrow{h_{0}} Ph \cdot + S$$

$$Ph-S-C(NH_{2})_{2} \xrightarrow{R^{\bullet}} Ph-S$$

$$NH_{2}$$

$$Ph-S-C(NH_{2})_{2} \xrightarrow{Ph-S-C(NH_{2})_{2}} Ph \cdot S$$

$$Ph-S-C(NH_{2})_{2} \xrightarrow{Ph-S-C(NH_{2})_{2}} Ph \cdot S$$

Scheme 8.1. Proposed mechanisms for aryl sulfide formation via coupling between an aryl radical and anionic/radical thiourea. In the bottom reaction, ¹⁵ pathways 1 and 2 indicate the two possible thiourea radical intermediates proposed by the study's authors.

although Ph• clearly plays some role in the radical transformation, the authors of this study speculate that a radical sulfur species, produced by abstraction of the thiourea N—H, may in fact be the active coupling agent.¹⁹⁷

In the absence of a radical inititator, sulfur arylation is believed to occur via an S_NAr_i transformation. In a methoxide ion-catalyzed process, 1,3-benzothiazoles are produced in high yield from the self-condensation of 1-benzoyl-3-(2-halophenyl) thioureas (**Scheme 8.2**). Upon deprotonation of the thiourea N—H, the resultant anionic sulfur nucleophile displaces the *ortho*-halogen substituent, yielding the cyclized, heterocyclic product. While this reaction bears many similarities to both of the aforementioned radical transformations, the authors report no indication of a radical intermediate, either in the isolated side products or the reaction kinetics. When $R = CH_3$, methoxide-catalyzed solvolysis at the carbonyl moiety, rather than intramolecular ring formation, was found to be the rate-limiting step; however, when $R = C_6H_5$, these two

$$O_{2}N \xrightarrow{X} S \xrightarrow{O} O_{2}N \xrightarrow{X} S \xrightarrow{O} OMe \xrightarrow{-RC(=O)OMe} O_{2}N \xrightarrow{X} S \xrightarrow{N} OMe \xrightarrow{-RC(=O)OMe} O_{2}N \xrightarrow{N} NH_{2}$$

$$O_{2}N \xrightarrow{X} S \xrightarrow{N} OMe \xrightarrow{-RC(=O)OMe} O_{2}N \xrightarrow{N} NH_{2}$$

$$O_{2}N \xrightarrow{N} NH_{2} O_{2}N \xrightarrow{N} NH_{2}$$

$$O_{2}N \xrightarrow{N} NH_{2} O_{2}N \xrightarrow{N} NH_{2}$$

Scheme 8.2. Proposed mechanism of S_NAr_i benzothiazole formation from 1-benzoyl-3-(2-halophenyl) thiourea.

steps are believed to occur in parallel to each other. Interestingly, when $R = C_6H_5$, cyclization sometimes occurs independently, and the benzodithiazole product retains the N-benzoyl substituent found in the parent thiourea.

Otherwise isostructural with the benzothiazole product formed from the reaction

shown in **Scheme 8.2**, the 1-aroylimido-[1,2,4]thiadiazolo-[2,3-a]pyridines (**48-53**, **Figure 8.2**) formed from intramolecular cyclization of 1-aroyl-3-(2-pyridyl) thioureas retain the N-aroyl moiety in the final product. A number of heterocyclic thiadiazoles have been reported from the interaction of N,N'-disubstituted thioureas with CuCl₂, ¹¹⁶ PCl₅/

Figure 8.2. Thiadiazoles **48-53**. **48**, R, R' = H; **49**, R = H, R' = 3,5-NO₂; **50**, R = 6-CH₃, R' = 4-OCH₃; **51**, R = H, R' = 4-CF₃; **52**, R = 3-CH₃, R' = H; **53**, R = H, R' = 2-Br

POCl₃, ¹⁹⁹ Ni(II) or Zn(II), ²⁰⁰ and Br₂, ²⁰¹ but, to the best of our knowledge, no mechanistic studies have been performed.

Li, *et al*, speculate that cyclization in the presence of CuCl₂ likely proceeds through an organometallic intermediate.¹¹⁶ In their recent work, **48** (R, R' = H) was produced by dropping a dilute solution of BzPTU **29** into a large excess of CuCl₂. Although isolated as part of a Cu coordination complex (**Figure 8.3**), an uncoordinated sample of **48** did not appear to coordinate with CuCl₂ under the previously optimized conditions, and Li, *et al*, concluded that the coordination complex likely represented the final stage of a Cu-promoted oxidative cyclization. Under the different experimental conditions of their work, Sridevi, *et al*, theorized that S—N bond formation might proceed by nucleophilic attack of the heterocyclic nitrogen on the thiourea sulfur—which presumably had been rendered somewhat electron-deficient by coordination to PCl₅—but presented no evidence to support this idea.¹⁹⁹ Although reaction with Br₂ is the oldest

reported method of [1,2,4]thiadiazolo-[2,3-a]pyridine synthesis, to the best of our knowledge, the literature lacks even the most speculative or mechanistic reports on this topic. Suffice it to say, the mechanism of [1,2,4]thiadiazolo-[2,3-a]pyridine formation is not well-understood, and certainly merits further study.

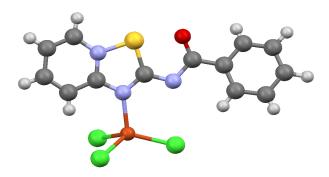


Figure 8.3. X-ray crystal structure of Cu-coordinated **48**. ¹⁷

All studies of the oxidative cyclization of BzPTUs report that at least one equivalent—and usually a large excess—of the reaction-promoting reagent (*e.g.* CuCl₂, Br₂, etc.) is required for the transformation. Li, *et al*, reported that, in the absence of a large excess of CuCl₂, coordination of BzPTU **29** to the metal center occurred without any evidence of oxidative cyclization, and we have yet to find any reports of this transformation occurring by a catalytic process. ¹¹⁶ We were therefore surprised to isolate five 1-benzoylimido-[1,2,4]dithiazolo-[2,3-a]pyridines (**49-53**) from crystallization vials originally containing their parent BzPTUs—all of which had been set up under normal crystallization conditions, and in the absence of any cyclization-promoting reagent. Close analysis of experimental conditions and molecular structure allow us to conjecture that

the formation of thiadiazoles **49-53** proceeds via the self-catalyzed, heterolytic oxidation of their parent BzPTUs, with a mechanistic pathway similar to that shown for the methoxide-catalyzed process in **Scheme 8.2**.

Additionally, four of these dithiazoles were obtained as single crystals, which are, to the best of our knowledge, the first non-coordinated 1-benzoylimido-[1,2,4]thiadiazolo -[2,3-a]pyridines studied by X-ray diffraction. These polyheterocyclic structures provide a fascinating study of 3-center-4-electron bond formation across three different heteroatoms, and represent some of the scarce known examples of polarized (weak) hypervalent²⁰² O—S—N bonding.

Results and Discussion

The thiourea precursors (**20**, **40**, **42**, and **44**) for compounds **49-53** were synthesized as previously described; **54** was synthesized using the same methodology (see Experimental Section for details). No evidence of the cyclized product was observed in either the crude ¹H-NMR or IR spectra, which were both collected immediately following product isolation.

The conditions under which cyclization occurred varied from compound to compound. Decomposition of **42** and **54** occurred rapidly, most likely as a consequence of heating during the crystallization process, and thiadiazoles **49** and **51** precipitated--as single crystals--from their respective mother liquors in less than 24 hours. Conversely, we found that **20** and **40** were stable, under similar conditions, for well over a year. The thiadiazoles obtained from oxidative cyclization of these thioureas, **50** and **53**, were harvested from the mother liquor found in crystallization vials that had spent 16 and 22 months, respectively, on the shelf. **44** fell in between these two groups, in terms of stability, decomposing to thidiazole **52** in four months.

Solvent effects are unlikely to account for these different decomposition rates. As

shown in **Table 8.1**, most of thiadiazoles **49-53** formed in different solvent systems, and the only real consistency was that each sample was heated to boiling, then cooled to room temperature. Furthermore, extensive solvent studies were performed on **20**, and oxidative cyclization was not observed in any of the resultant samples, although some of them remained on the shelf for over six months. X-ray quality crystals of **20** were obtained from wet DMF—the same solvent system from which **49** precipitated in 24 hours—after approximately three months in a crystallization vial. Similarly, while acetonitrile apparently facilitated cyclization in **42**, it had no such effect in **20**; recrystallization proceeded normally with this latter sample, and we found no evidence of thiadiazole formation in either the precipitate or the mother liquor.

Table 8.1. Details of crystal growth and selected crystallographic data in thiadiazoles **49-53**. Single crystal data was not obtained for **53**; therefore, only crystal growth data is reported for this compound.

Compound		49	50	51	52	53
Thiourea precursor		54	20	42	44	40
R		Н	6-CH ₃	Н	3-CH ₃	Н
R'		3,5-NO ₂	4-OCH ₃	4-CF ₃	Н	2-Br
Empirical	formula	$C_{13}H_7N_5O_5S$	$C_{13}H_7N_5O_5S$	$C_{13}H_7N_5O_5S$	C ₁₄ H ₁₁ N ₃ OS	
Hammett o	value ¹⁷⁴	1.42 ^a	-0.268	0.54 0.0		n/a
Solvent(s)		DMF/H ₂ O	acetone/ hexanes	MeCN acetone/hexanes		ethanol/ hexanes
Time	e ^b	24 h	16 m ^c	24 h 4 m ^c		22 m ^c
Crystal system		orthorhombic	Orthorhombic	triclinic monoclinic		
Space group		Pbca	Pbca	P-1 P2 ₁ /n		
	a (Å)	12.998(3)	7.1771(11)	7.1910(10)	7.1743(7)	
	b (Å)	9.6376(19)	14.384(2)	7.5060(10)	17.6933(17)	
Unit cell	c (Å)	22.538(4)	26.594(4)	13.2866(18)	9.6301(9)	
dimensions	α (deg.)	90	90	98.390(2)	90	
	β (deg.)	90	90	97.769(2)	96.128(2)	
	γ (deg.)	90	90	113.467(2)	90	
Cell volur	ne (ų)	2823.3(10)	2745.4(7)	635.86(15) 1215.4(2)		
Z		8	8 2		4	
Density (calc., g/cm³)		1.625	1.448	1.689	1.472	
# of independent reflections		3092	2990	2762	2646	
R (%)		4.24	3.09	5.69	3.09	

^aCalculated as the sum of both m-NO₂ substituents, each with a σ value of 0.710.

^bAll time designations are approximate, defined as the amount of time that elapsed between the initial crystallization attempt and the realization that decomposition had occurred—and which may, in the case of slowly-decomposing BzPTUs, comprise a significant amount of error.

^cMonths

While we initially hypothesized that oxidative cyclization may have proceeded via a radical pathway, presumably initiated by the oxygen present under ambient conditions, we currently believe it more likely that both hydrogens cleave in a self-catalyzed, heterolytic process, for which a possible mechanism is shown in **Scheme 8.3**. This process is similar to that shown in **Scheme 8.2**; however, the absence of a nucleophile—and the inherent acid/base functionalities of BzPTUs—led us to conclude that oxidative cyclization was more likely to occur in a base-catalyzed process. The parent BzPTUs of thiadiazoles **49-53** possess both a strongly acidic, N-acyl thioureido proton and a non-nucleophilic, moderately basic pyridyl nitrogen. While precise pK_a values for **49-53** have not been determined, the pK_a of an N-benzoyl-N'-aryl thiourea was found to be 13.06 ± 0.04 in a buffered methanolic solution. In the strong likely that the pK_a of the N-acyl thioureido proton in BzPTUs—especially those with electronegative substituents—is reasonably accessible to even the thioureido-substituted nitrogen, which should have slightly lower proton affinity than unsubstituted pyridine, due to the presence of the electron-withdrawing substituent.

The relative rates of decomposition observed—qualitatively—in BzPTUs 20, 40, 42, 44, and 55 also support the heterolytic, base-catalyzed mechanistic process schown in Scheme 8.3. BzPTUs 42 and 54, which underwent cyclization—or at least partial cyclization—literally overnight, both have strongly electron-withdrawing phenyl substituents. Conversely, BzPTU 20, with its electron-releasing p-OCH3 phenyl substituent, was stable to many solvent conditions and cyclized only after 16 months in a crystallization vial. While we isolated thiadiazole 53 22 months after obtaining single crystals of 40 from the same vial, it is entirely possible that cyclization occurred well before that, as the vial had been undisturbed—at the back of a shelf—for over a year

Scheme 8.3. Proposed mechanistic pathway for the self-catalyzed decomposition / oxidative cyclization of BzPTUs 20, 40, 42, 44, and 54. The base represented as "B:" is most likely the pyridyl nitrogen of a second BzPTU molecule.

before the tiny brown needles of 53 were first observed. As it has been established that

the pK_a values of substituted benzamides correlate linearly with Hammett σ constants, ²⁰⁴ these roughly-established reaction rates appear to support a heterolytic, base-catalyzed cyclization process. Loss of molecular hydrogen in the final step of the cyclization process is supported by the evolution of gas observed upon heating 20 past its melting point, which results in partial conversion to 50, as determined by ¹H-NMR spectroscopy.

All of the thiadiazoles for which we obtained single crystal X-ray data (49-52)

Figure 8.4. Hypervalent O—S—N bond in a spiro- λ^4 -sulfane.

featured a 3-center-4-electron bond, formed between the nearly colinear O, S, and N atoms. This type of interaction has previously been described as the sum total of a covalent S—N bond and a highly polarized, hypervalent²⁰² O—S bond, and the bond lengths that we observed in 49-52 (Table 8.2) fit well with this description. The N—S bonds ranged in length from 1.755 Å (49) to 1.785 Å (50), which is slightly longer than the sum of covalent radii (1.74 Å).²⁰⁵ These bond lengths were within the range of lengths reported for N—S bonds in spiro- λ^4 -sulfanes (1.724 Å²⁰⁶ to 1.804 Å,²⁰² **Figure 8.4**), the class of compounds in which this type of N—S—O interaction has been most thoroughly examined; however, they are considerably shorter than the bond lengths (1.889 Å to 1.962 Å) observed in the analogous N $-S(R_2)$ -N hypervalent interaction. 202,207,208 Conversely, the O—S bond lengths observed in **49-52** (2.077 Å to 2.215 Å) are considerably longer than in the symmetrical $O-S(R_2)-O$ interaction $(1.84 \text{ Å})^{202}$ although both hypervalent interactions are significantly longer than the sum of the S, O covalent radii, 1.66 Å.²⁰⁵ Taken together, this variation in the S—O and S—N bonds, relative to the lengths observed in symmetrical, otherwise isostructural compounds, appears consistent with the polarized, hypervalent bond type proposed for this interaction.

$$R' = \begin{bmatrix} 0 - \frac{a}{1} - S & \frac{n}{N} & \frac{i}{1} \\ 0 & \frac{a}{1} & \frac{i}{N} \\ 0 & \frac{a}{1} & \frac{i}{N} \\ 0 & \frac{i}{N} & \frac{i}{N} \\$$

Figure 8.5. Labled bonds in thiadiazoles 49-53 and BzPTUs 16-46

Table 8.2. Selected bond lengths and angles in **49-52** and BzPTUs **16-46** (italicized). Bonds are identified in **Figure 8.5**. All values are in Å, unless otherwise noted.

Compound	49	50	20	51	52	44	16-46 (avg.)
a	2.215	2.142	2.918	2.077	2.098		
b	1.258	1.268	1.207	1.276	1.274	1.229	1.219
c	1.340	1.346	1.404	1.333	1.341	1.372	1.382
d	1.340	1.334	1.365	1.347	1.342	1.391	1.390
e	1.770	1.774	1.674	1.773	1.772	1.663	1.662
f	1.319	1.322	1.363	1.285	1.323	1.335	1.347
g	1.357	1.351	1.408	1.376	1.358	1.438	1.415
h	1.359	1.362	1.337	1.359	1.361	1.325	1.335
i	1.365	1.373	1.350	1.369	1.363	1.344	1.342
j	1.357	1.372	1.391	1.358	1.358	1.373	1.382
k	1.402	1.402	1.384	1.393	1.405	1.365	1.380
1	1.366	1.369	1.376	1.377	1.375	1.397	1.383
m	1.407	1.408	1.396	1.399	1.415	1.390	1.389
n	1.755	1.785		1.770	1.770		
Torsion O=CC=S (deg.)	2.20	0.89	1.25	0.27	0.41	179.33	1.27 ^a ; 172.8 ^b
Torsion O=CPh (deg.)	7.86	9.92	12.59	4.11	3.62	36.09	12.33 ^a ; 24.24 ^b
∠ NSO (deg.)	165.37	165.95		166.96	166.85		

^aConformer N

 $[^]b$ Conformer **O**

The aromatic character of polyheterocyclic thiadiazoles **49-52** is illustrated both by the planarity observed in the newly formed, 5-membered rings (**Figure 8.6**) and in the delocalization of π-electrons inferred from bond lengths—especially when considered in relation to the corresponding bonds in the parent thioureas. The three amide / thioamide C=N bonds (**c**, **d**, and **f** in **Figure 8.5**) are significantly shorter in **49-52** than in BzPTUs **16-46**, decreasing from 1.382 Å, 1.390 Å, and 1.347 Å, respectively, in **16-46**, to 1.340 Å, 1.341 Å, and 1.312 Å, also respectively, in the cyclized decomposition products. In **51**, bond **f** very nearly approaches the sum of covalent radii in a formal C=N bond, 1.27 Å, ²⁰⁵ although its length in **49**, **50**, and **52** (~1.32 Å) more closely approximates that of an aromatic C=N bond (1.34 Å in pyridines²⁰⁹), which is also observed in bonds **c** and **d**.

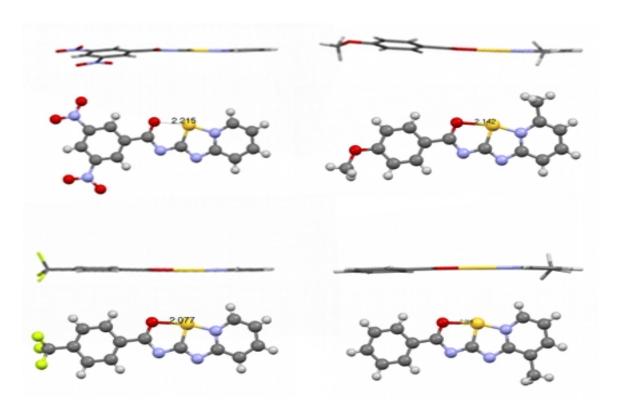


Figure 8.6. Single-molecule structures of (clockwise from upper left) **49**, **50**, **52**, **51**. Planarity of thiadiazole moiety is shown in the side view.

Changes in bond length, presumably related to enhanced electron delocalization, are also evident in both the carbonyl and thiocarbonyl moieties. In BzPTUs **16-46**, the average length of the C=S bond is 1.662 Å, which, although demonstrative of the conjugative effects expected from the two C—N bonds in thioureas, is nevertheless comparable to the sum of covalent radii, 1.61 Å.²⁰⁵ In **49-52**, however, the length of bond **e** increases to 1.772 Å, approximating the sum of covalent radii in a C—S [single] bond, 1.76 Å.²⁰⁵ The C=O bond exhibits similar—albeit less drastic—elongation in the BzPTU decomposition products, increasing from an average of 1.219 Å (1.208 Å in the somewhat more isoelectronic conformer **N** BzPTUs) in **16-46** to 1.269 Å in **49-53**. For comparison, the sum of covalent radii in C, O single and double bonds have been calculated as 1.33 Å and 1.24 Å, respectively—although it has been noted that polar covalent bonds tend to be shorter than the sum of calculated radii, and crystallographic data from related compounds—such as BzPTUs **16-46**—tend to be a more useful means of comparison.²¹⁰

Also reflecting the altered aromatization in the polyheterocyclic decomposition products **49-52**, bond **g** and pyridyl bonds **h-m** display significant changes in length, relative to their BzPTU precursors. Bond **g**, which at an average of 1.415 Å shows only minor conjugative effects in BzPTUs **16-46**, shortens to an average of 1.361 Å in **49-52**. reflecting the aromaticity of the 5-membered dithiazole moiety. While longer than the aforementioned C=N bonds **c**, **d**, and **f**, bond **g** is nevertheless within range of C=N bonds reported in 5-membered nitrogen heterocycles, such as pyrrole or imidazole (~1.37 Å), or indole (~1.36 Å).²⁰⁹ This elongation may also reflect structural effects relating to the the longer C—S and S—N bonds. Pyridyl bonds **h** and **i** are similar in average length (1.360 Å and 1.368 Å, respectively) to bond **g** in **49-52**, although this change represents an elongation—rather than a truncation—from the corresponding bonds in BzPTUs **16-46** (1.335 Å and 1.342 Å, respectively). Interestingly, bonds **j-m** display a pattern of

alternating lengths in **49-52**, corresponding to what may be a significant contribution of traditional diene character, rather than complete aromaticity. At an average of 1.361 Å and 1.372 Å, respectively, bonds **j** and **l** are far closer in length to the sum of covalent radii in C=C bonds (1.34 Å) than in Csp²—Csp² bonds (1.46 Å); while the average lengths of bonds **k** (1.401 Å) and **m** (1.407 Å) clearly indicate at least some degree of conjugation, the difference is nevertheless noticeable. For comparison, the average lengths of bonds **j-m** in BzPTUs differ by a maximum 0.009 Å, ranging from 1.380 Å to 1.389 Å—although, as in **49-52**, more variation can be found in each individual compound, often relating to substituent effects.

Crystal packing in **49-52** is both diverse and reasonably straightforward. All of these thiadiazoles lack hydrogen bond donors, and, as might be expected, aromatic π -stacking appears to be the foremost crystal packing force—at least in **50-52**. While there is a π - π interaction (**Figure 8.7a**) between neighboring thiadiazole moieties in **49**, contributing to its sandwich herringbone structure type (**Figure 8.7b**),³⁷ its nitro substituents also form infinite chains of N...O contacts (**Figure 8.7c**), with one donor group and one acceptor group on each phenyl ring. This type of dipolar, intermolecular interaction has been observed in mononitroarenes,²¹¹ although, by necessity, the donor O and acceptor N are part of the same nitro group, leading to a C(2) chain, instead of the C(6) chain present in **49**. In our structure, d_{O...N} is 2.770 Å, far less than the sum of van der Waals radii (3.07 Å), and appears to be an interaction between the O lone pair and the partially empty p-orbital on the N: the angle between the donor O and the N—C(Ar) (angle O2-N5-C12) bond is 90.03°.

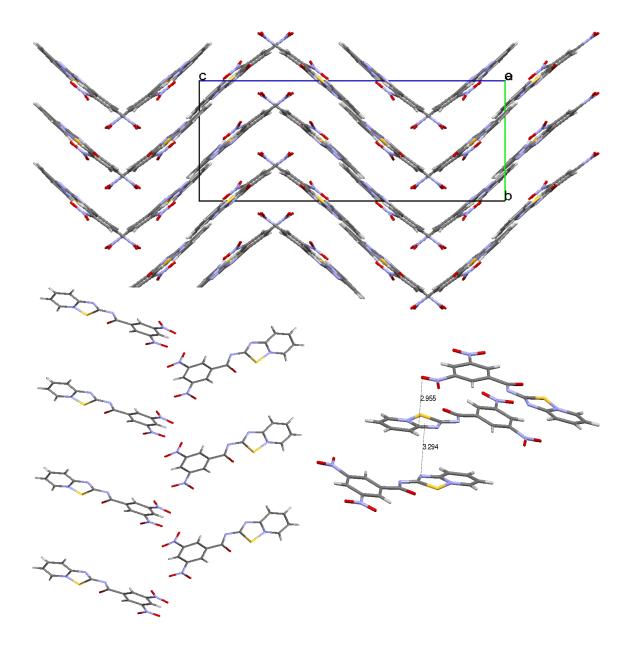


Figure 8.7. Crystal packing interactions in **49**. Clockwise from top: (a) sandwich herringbone structure type (more closely resembles herringbone, but π - π interaction technically classifies it as "sandwich"); (b) π - π interaction between thiadiazole rings (3.924 Å) and π ...O(N) contact (2.955 Å); (c) Chain formed by N...O dipolar contact (dO...N = 2.770 Å; \angle O-N-C(Ar) = 90.03°)

Thiadiazoles 50-52, which lack functional groups with strong donor-acceptor capabilities, display crystal packing patterns typical³⁷ for aromatic systems. Shown as (a) in Figures 8.8 and 8.9, alternately-oriented monomers form the backbone of 50's y structure type, where π - π stacking (d = ~3.5 Å) occurs between pyridine rings, and a weak, dimer-like (OCH₂)H... π interaction (2.635 Å) links the π -stacks together. Similar packing behavior is observed in 51 (Figure 8.8b), which also crystallizes in the γ structure type. In 51, however, the alternately-oriented monomers stack more completely on top of each other, leading to phenyl-pyridyl interactions (~3.6 Å) and what appears to be π - π stacking between the planar, hypervalently fused "[1,2,4]-oxathiazole" rings (3.5) Å - 3.6 Å), lending credence to the proposed aromatic character of this 5-membered heterocycle (**Figure 8.9b**). A π - π interaction is also observed between the "oxathiazole" rings in 52 (Figure 8.9c). In this compound, two "sandwiched" monomers engage in π stacking very similar to that observed in 51 ($d_{Ph...Pvr} = 3.461 \text{ Å}$); a second π - π interaction between pyridine rings on neighboring "sandwiches" (3.350 Å) leads to a brick-type[‡] packing pattern for this compound. Weak H_{Pyr} Ph interactions hold the brick-type π stacks nearly perpendicular to each other (78.10°), resulting in the basketweave crystal packing structure* assigned to 52.

[!] Chapter VI.

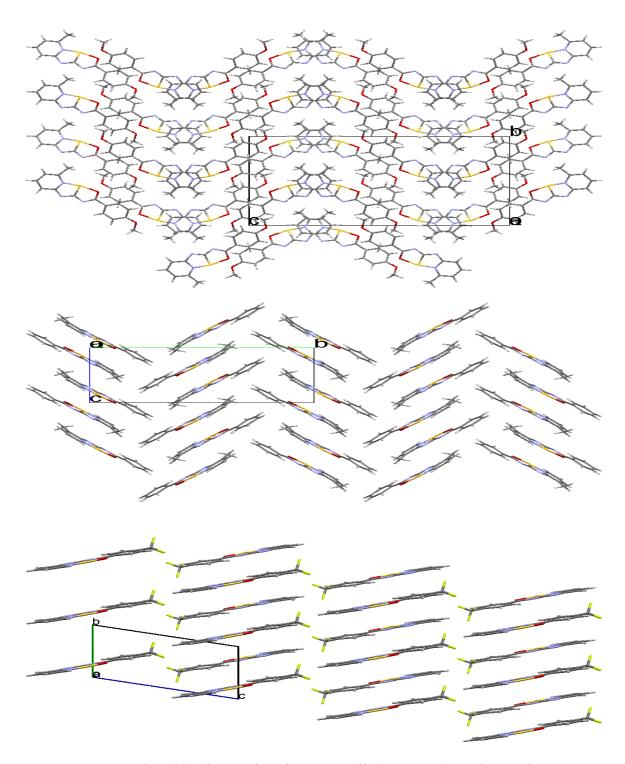


Figure 8.8. Crystal packing interactions in **50-52**. All views are along the *a*-axis. From top to bottom: (a) Top-down view of γ -type π -stacking in **50** (dashed line indicates row of stacks); (b) Side-on view of γ -type π -stacking in **51**; (c) basketweave-type crystal packing in **52**.

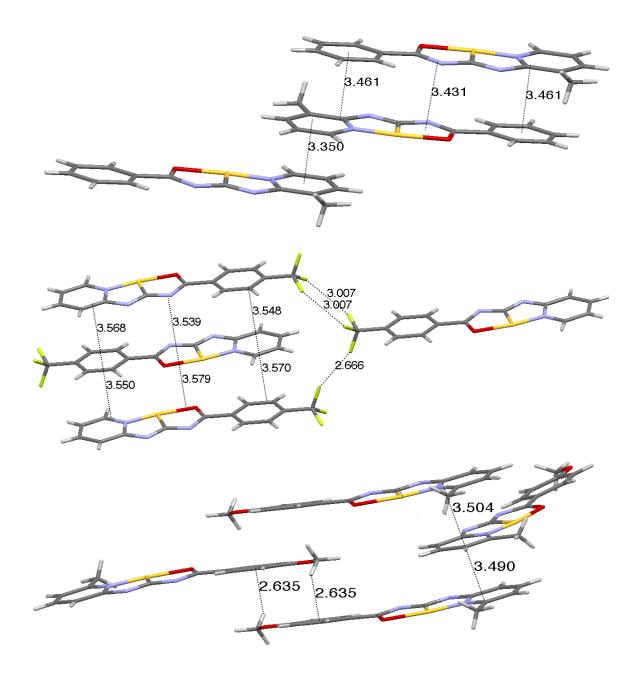


Figure 8.9. Major intermolecular interactions in **50-52**. Top to bottom: (a) in **50,** π - π interaction between pyridine rings in (3.504, 3.490 Å) and weak (OCH₂)H... π contact between methoxyphenyl groups (2.635 Å); (b) in **51**, π - π interaction between proposed oxathiazole rings (3.539, 3.579 Å), and also between alternating phenyl and pyridyl rings (3.568, 3.550 Å). An F...F contact (2.666 Å) provides link between γ -stacks; the other F...F interactions (3.007 Å) are outside the sum of van der Waals radii. (c) In **52**, pyridyl-pyridyl interactions (3.350 Å) form the link between alternately-oriented monomers, "sandwiched" together by phenyl-pyridyl interactions (3.461 Å, 2 contacts per "sandwich"), and additional π -stacking between oxathiazoles (3.431 Å).

Conclusion

Although remarkably stable under both ambient and aqueous conditions, BzPTUs will, under certain circumstances, undergo oxidative cyclization, most likely via a self-catalyzed, heterolytic process. The resultant 1-benzoylimido-[1,2,4]thiadiazolo-[2,3-a]pyridine also features a close S—O contact; the very short interatomic distance (≥ 2.2 Å), coupled with the planarity of the interacting groups, electron delocalization inferred from bond lengths in the crystal structures, and apparent π - π interactions in the crystal lattice, may indicate that the five-membered ring formed from this interaction should best be treated as a formally fused [1,2,4]oxathiazole, rather than a weak, intramolecular, van der Waals interaction.

APPENDIX A

EXPERIMENTAL RESULTS

Chapter II

Tris[(N-ethylthioureido)ethyl]amine (1)

2 mL tris(2-aminoethyl)amine (13 mmol) were dissolved in 20 mL THF. Dry nitrogen was bubbled into the flask for 10 minutes, with stirring, and the flask was cooled to 0° C in an ice-water bath. 3.4 mL (3.4 g, 39 mmol) ethyl isothiocyanate were added by syringe, and the reaction was allowed to return to room temperature, then stirred for two days (40 h). The reaction mixture was then filtered through a 5 cm x 7 cm column of silica gel (100-200 mesh) and washed with 2 x 10 mL EtOH. The solvent was removed on the rotovap, yielding a brittle, orange-yellow solid, which weighed 3.45 g (65%). **IR** (KBr, cm⁻¹) 3237, 3065, 3008, 2968, 2822, **1562**, 1383, 1337, 1299, 1214, 1150, 1090, 1004, 678, 642; ¹**H NMR** (300 MHz, CDCl₃) ∂ 6.68 (bs, 6H), 3.70 (d, J = 4 Hz, 6H), 3.51 (bs, 6H), 2.66 (t, J = 5 Hz, 6H), 1.21 (t, J = 4 Hz, 9H). ¹³C **NMR** (151 MHz, CDCl₃) ∂ 181.6, 53.3, 42.8, 39.5, 14.6; **MP** 120-121°C.

Tris[(N-n-propylthioureido)ethyl]amine (2)

2 mL (1.97 g, 19.5 mmol) *n*-propylisothiocyanate were added to 1 mL tris(2-aminoethyl) amine (6.5 mmol) in 10 mL dry THF, at 0 °C. The reaction was stirred for 6 hours, the solvent was removed on the rotatory evaporator, and the semisolid reside was recrystallized from ethanol/hexanes (1:4). ¹**H NMR** (600 MHz, CDCl₃) ∂ 6.85 (bs, 3H), 6.71 (bs, 3H), 3.69 (bs, 6H), 3.44 (bs, 6H), 2.65 (t, J = 5 Hz, 6H), 1.61 (m, 6H), 0.95 (t, 9H). ¹³**C NMR** (75 MHz, CDCl₃) ∂ 181.8, 53.3, 46.5, 42.8, 22.6, 11.5; **MP** 111.5-113 °C.

133Tris[(N-isopropylthioureido)ethyl]amine (3)

1 mL tris(2-aminoethyl)amine was added, dropwise, to 2.1 mL isopropylisothiocyanate (1.97 g, 19.5 mmol) in 15 mL THF, at 0 °C. The reaction was stirred overnight (16 h) and the solvent was then removed on the rotovap. The residue was dissolved in hot ethanol, and hexanes were added until the solution became cloudy. Cubic crystals weighing 1.81 g (61%) were recovered from the flask. ¹H NMR (300 MHz, CDCl₃) ∂ 6.68 (bs, 6H), 3.44 (bs, 6H), 2.65 (t, 6H), 1.60 (m, 6H), 0.95 (t, 18H). ¹³C NMR (75 MHz, CDCl₃) ∂ 181.8, 53.3, 46.5, 42.8, 22.6, 11.5; MP 151.5-153°C.

Tris[(N-*tert***-butylthioureido)ethyl]amine (4)** 1 mL tris(2-aminoethylamine) was added dropwise to 2.5 mL (2.25 g, 19.5 mmol) in 15 mL dry THF, at 0 °C. Heat evolved, and the solution foamed slightly. The reaction was stirred for 16 h, and the solvent was removed on the rotovap. A fluffy, slightly sticky, colorless solid remained on the walls of the flask; this was recrystallized from hot acetone/hexanes, yielding 2.72 g of a white, crystalline solid (85%). Crystals suitable for X-ray analysis were grown from acetonitrile/hexanes, with a quantity of xylenes sufficient to induce mixing between the two layers. **IR** (KBr, cm⁻¹) 3331, 3229, 3068, 3029, 2959, 2804, **1531**, 1354, 1281, 1202, 1055, 690, 671; ¹**H NMR** (300 MHz, CDCl₃) ∂ 6.41 (bs, 3H), 6.33 (bs, 3H), 3.64 (q, J = 5.5 Hz, 6H), 2.69 (t, J = 5.5 Hz, 6H), 1.46 (s, 27H). ¹³**C NMR** (151 MHz, CDCl₃) ∂ 181.0, 53.6, 53.3, 43.1, 29.5; **MP** 160-164 °C (dec.)

Tris[(N-phenylthioureido)ethyl]amine (5)

0.5 mL (0.48 g, 3.3 mmol) tris(2-aminoethyl)amine was dissolved in 20 mL THF, and 1.2 mL (1.35 g, 10 mmol) phenylisothiocyanate was added drop-wise. The reaction mixture was stirred for 4 h, then refluxed gently overnight, and the solvent was removed on the rotatory evaporator. The residue was recrystallized from acetone/hexanes and washed with toluene, yielding 1.64 g (90%) of a colorless, crystalline solid. Colorless needles suitable for X-ray analysis were grown from a dilute solution of isopropanol/hexanes. **IR** (KBr, cm⁻¹) 3358, 3239, 3100, 2922, 2813, 1558, 1508, 1492, 1347, 1313, 1252, 1155,

1093, 758, 696; ¹**H NMR** (300 MHz, CDCl₃) ∂ 8.37 (s, 3H), 7.25 (d, 6H), 7.18 (d, 6H), 7.13 (t, 3H), 6.81 (s, 3H), 3.71 (bq, 6H), 2.67 (t, 6H); ¹³**C NMR** (75 MHz, CDCl₃) ∂ 180.7, 137.1, 129.7, 126.5, 124.8, 53.1, 43.1; **MP** 143-144°C.

Chapter III

General procedure for the preparation of thioureas 6-13.

In a cool water bath, the appropriate isothiocyanate (2 eq.) was added to N,N'-bis(3-aminopropyl)piperazine (1 eq.), N,N-bis(3-aminopropyl)-N-methylamine (1 eq.), or N-(3-aminopropyl)morpholine (2 eq.), in dry THF (1.5-2 mL/mmol), and stirred overnight (16-20 hours). The solvent was removed, and the white, powdery solid was shown, by ¹H NMR, to contain neither starting material nor side product, and was used directly for crystallization.

N,N'-bis[3-(N-propylthioureido)propyl|piperazine (6)

Thiourea 6 was prepared as described above, using n-propyl isothiocyanate and N, N'-bis(3-aminopropyl)pipearzine (100%). Colorless prisms, suitable for X-ray spectroscopy, were grown from ethanol/water, and crystallized in the monoclinic P-1 space group. At a later time, colorless needles precipitated from DMSO- d 6, and were determined to have the same unit cell. An analytical sample was prepared by triturating a small amount of the compound with methylene chloride, in which it has only limited solubility, filtering the precipitated solid, and further drying the thiourea on a vacuum line, for approximately 96 hours, in order to remove the last traces of solvent. **IR v**_{max} (KBr/cm⁻¹) 1558.10 (C=S); ¹**H NMR** (CDCl₃, 300 MHz) ∂ 7.18 (bs, 2H, NH), 3.52 (bs, 4H), 3.35 (bs, 4H), 2.50 (m, 12H), 1.76 (m, 4H), 1.65 (m, 4H), 0.98 (t, 6H); ¹³**C NMR** (DMSO-d₆, 75 MHz) ∂ 181.6 (C=S), 55.4 (N-CH₂), 52.8 (N-CH₂), 45.2 (N-CH₂), 42.1 (N-CH₂), 25.9 (CH₂), 22.0 (CH₂), 11.4 (CH₃); **MP** 176-178°C.

N,N'-bis[3-(N-pentylthioureido)propyl|piperazine (7)

Thiourea 7 was prepared as described above, using n-pentyl isothiocyanate and N, N'-bis(3-aminopropyl)pipearzine (100%). Fine, colorless prisms, suitable for X-ray spectroscopy, were grown from ethanol/hexanes, and crystallized in the monoclinic P-1 space group. An analytical sample was prepared by triturating a small amount of the compound with methylene chloride, in which it has only limited solubility, filtering the

precipitated solid, and further drying the thiourea on a vacuum line, for approximately 96 hours, in order to remove the last traces of solvent. **IR** (cm⁻¹) ¹**H NMR** (CDCl₃, 300 MHz) ∂ 7.24 (bs, 2H, NH), 6.59 (bs, 2H, NH), 3.46 (bs, 4H), 3.34 (bs, 4H), 2.43 (bt, 11H), 1.71 (m, 4H), 1.57 (m, 4H), 1.30 (m, 9H), 0.86 (t, 6H); ¹³**C-NMR** (DMSO-d₆, 75 MHz) ∂ 181.6 (C=S), 55.4 (N-CH₂), 52.8 (N-CH₂), 43.5 (N-CH₂), 41.9 (N-CH₂), 28.6 (CH₂), 28.5 (CH₂), 25.9 (CH₂), 21.9 (CH₂), 13.9 (CH₃); **EA** Calc. C, 57.60; H, 10.11; N, 18.32; S, 13.98; Found C, 58.35; H, 9.89; N, 17.92; **MP** 127.5-129°C.

N,N'-bis[3-(N-isopropylthioureido)propyl[piperazine (8)

Thiourea **8** was prepared as described above, using isopropyl isothiocyanate and N, N'-bis(3-aminopropyl)pipearzine (100%). Colorless needles, suitable for X-ray spectroscopy, were grown from ethanol/hexanes, and crystallized in the P2 1/n space group. An analytical sample was prepared by triturating a small amount of the compound with methylene chloride, in which it has only limited solubility, filtering the precipitated solid, and further drying the thiourea on a vacuum line, for approximately 96 hours, in order to remove the last traces of solvent. **IR** v_{max} (KBr/cm⁻¹) 3223.7 (NH); ¹**H NMR** (DMSO-d₆, 300 MHz) ∂ 7.38 (bs, 2H, NH), 7.29 (d, 2H, NH), 4.35 (bs, 2H), 3.47 (bs, 4H), 2.46 (m, 12H), 1.75 (m, 4H), 1.24 (d, 12H); ¹³**C NMR** (DMSO-d₆, 75 MHz) ∂ 180.8 (C=S), 55.4 (N-CH₂), 52.7 (N-CH₂), 44.8 (N-CH₂), 41.8 (N-CH₂), 25.9 (CH), 22.3 (CH3); **EA** Calc. C, 53.69; H, 9.51; N, 20.87; S, 15.93; Found: C, 53.79; H, 9.19; N, 20.68; **MP** 151-153°C.

N,N'-bis[3-(N-tert-butylthioureido)propyl]piperazine (9) Thiourea 9 was prepared as described above, using *tert*-butyl isothiocyanate and N, N'- bis(3-aminopropyl)pipearzine (100%). Fine, colorless plates, suitable for X-ray spectroscopy, were grown from acetonitrile/water, and crystallized in the monoclinic P-1 space group. An analytical sample was prepared by triturating a small amount of the compound with methylene chloride, in which it has only limited solubility, filtering the precipitated solid, and further drying the thiourea on a vacuum line, for approximately 96 hours, in order to remove the last traces of solvent. **IR** \mathbf{v}_{max} (KBr/cm⁻¹) 1525.85 (C=S); ¹H NMR (DMSO-d₆, 300 MHz)

∂ 6.65 (bs, 2H, NH), 5.92 (bs, 2H, NH), 3.64 (bq, 4H), 2.51 (m, 12H), 1.81 (m, 4H), 1.45 (s, 18H); ¹³C NMR (DMSO-d₆, 75 MHz) ∂ 181.2 (C=S), 55.5 (N-CH₂), 52.8 (N-CH₂), 52.0 (N-CH₂), 41.4 (N-CH₂), 27.0 (C), 26.0 (CH3); **EA** Calc. C, 55.77; H, 9.83; N, 19.51; S, 14.89; Found C, 55.78; H, 9.58; N, 19.32; S, 14.47; MP 169-170°C (boils).

N,N'-bis[3-(N-benzylthioureido)propyl]piperazine (10)

Thiourea **10** was prepared as described above, using benzyl isothiocyanate and N, N'-bis(3-aminopropyl)pipearzine (100%). Fine, colorless plates, suitable for X-ray spectroscopy, were grown from ethanol/water, and crystallized in the monoclinic P-1 space group. An analytical sample was prepared by triturating a small amount of the compound with methylene chloride, in which it has only limited solubility, filtering the precipitated solid, and further drying the thiourea on a vacuum line, for approximately 96 hours, in order to remove the last traces of solvent. **IR v**_{max} (KBr/cm⁻¹) 3237.51 (NH); ¹**H NMR** (DMSO-d₆, 300 MHz) ∂ 7.85 (bs, 2H, NH), 7.48 (bs, 2H, NH), 7.29 (m, 10H), 4.65 (bs, 4H), 3.35 (bs, 4H), 2.25 (m, 12H), 1.61 (m, 4H); ¹³**C NMR** (DMSO-d₆, 75 MHz) ∂ 183.0 (C=S), 140.2 (C), 128.9 (CH), 127.9 (CH), 127.5 (CH), 55.9 (N-CH₂), 53.4 (N-CH₂), 47.7 (N-CH₂), 42.6 (N-CH₂), 26.7 (CH₂); **EA** Calc. C, 62.61; H, 7.68; N, 16.85; S, 12.86; Found C, 62.77; H, 7.65; N, 16.82; **MP** 147-148°C.

N,N'-bis[3-(N-phenylthioureido)propyl]piperazine (11)

Thiourea 11 was prepared as described above, using phenyl isothiocyanate and N, N'-bis(3-aminopropyl)pipearzine. Due to its poor solubility in most organic solvents, its purity was assured by trituration with boiling DMSO; a white, crystalline solid was collected by vacuum filtration, after cooling to room temperature (65%). Colorless needles, suitable for X-ray spectroscopy, were grown from DMSO/ethyl acetate, and crystallized, as a 1:1 DMSO solvate, in the P2₁/c space group. An analytical sample was prepared by triturating a small amount of the compound with methylene chloride, in which it has only limited solubility, filtering the precipitated solid, and further drying the thiourea on a vacuum line, for approximately 96 hours, in order to remove the last traces of solvent. IR v_{max} (KBr/cm⁻¹) 1523.33 (C=S); ¹H NMR (DMSO-d₆, 300 MHz) ∂ 9.43

(bs, 2H, NH), 7.71 (bs, 2H, NH), 7.30 (m, 8H), 7.06 (t, 2H), 3.44 (bs, 4H), 2.22 (bt, 12H), 1.62 (m, 4H); ¹³C NMR (DMSO-d₆, 75 MHz) ∂ 180.1 (C=S), 128.7 (CH), 124.1 (CH), 123.0 (CH), 55.6 (N-CH₂), 52.6 (N-CH₂), 42.8 (N-CH₂), 25.5 (CH₂); MP (DMSO solvate) 197-198°C.

N-[3-(N-phenylthioureido)propyl|morpholine (12)

Thiourea 12 was prepared as described above, using phenyl isothiocyanate and N-(3-aminopropyl)morpholine (100%). Colorless crystals, suitable for X-ray analysis, were grown from acetonitrile/water, and crystallized in the P2₁/n space group. An analytical sample was prepared by crystallization from hot THF, which yielded colorless, octahedral crystals, with an average diameter of 2.5-5 mm, which were washed with acetone and airdried; a single crystal was submitted for elemental analysis. These crystals were also examined by X-ray spectroscopy, and were found to have the same unit cell as those grown from acetonitrile/water. IR \mathbf{v}_{max} (KBr/cm⁻¹) 1529.45 (C=S); ¹H NMR (CDCl₃, 300 MHz) ∂ 7.62 (bs, 1H, NH), 7.44 (t, 2H, CH), 7.30 (t, 1H, CH), 7.23 (d, 2H, CH), 3.81 (bs, 2H), 3.24 (bs, 4H), 2.39 (m, 2H), 2.27 (bs, 4H), 1.75 (m, 2H) ¹³C NMR (CDCl₃, 300 MHz) ∂ 180.7 (C=S), 137.5 (CH), 130.6 (CH), 127.3 (CH), 125.3 (CH), 66.8 (O-CH₂), 59.8 (N-CH₂), 54.2 (N-CH₂), 46.6 (N-CH₂), 24.9 (CH₂). EA Calc. C, 60.18; H, 7.58; N, 15.04; O, 5.73; S, 11.48; Found: C, 60.35; H, 7.46; N, 15.02; S, 11.28; MP 126-127°C.

N,N'-bis[3-(N-phenylthioureido)propyl]-N"-methylamine (13)

Thiourea **13** was prepared as described above, using phenyl isothiocyanate and N, N'-bis(3-aminopropyl)methylamine (100%). Colorless, cubic crystals, suitable for X-ray spectroscopy, were grown from dichloroethane/hexanes, and crystallized in the monoclinic P2₁/c space group. An analytical sample was prepared by recrystallization from acetone; the powdery white solid was washed with acetone over an aspirator, and allowed to air dry overnight. **IR v**_{max} (KBr/cm⁻¹) 1533.85 (C=S); ¹**H NMR** (CDCl₃, 300 MHz) ∂ 8.10 (bs, 2H, NH), 7.38 (t, 4H), 7.21 (m, 8H), 3.55 (q, 4H), 2.18 (t, 4H), 1.44 (m, 4H); ¹³**C NMR** (CDCl₃, 300 MHz) ∂ 180.2 (C=S), 136.7 (CH), 130.0 (CH), 126.9 (CH), 125.4 (CH), 56.3 (N-CH₂), 45.5 (N-CH₂), 41.9 (N-CH₃), 25.4 (CH₂). **EA** Calc. 60.69; H,

7.03; N, 16.85; S, 15.43; Found: C, 60.56; H, 6.84; N, 16.67; S, 15.15; **MP** 138-140°C.

Chapter IV

N-(3-isothiocyanatopropyl)morpholine (14a)

[Not isolated] Isothiocyanate 14a was prepared in accordance with a modified literature procedure. 213 A stirred solution of 1 mL N-(3-aminopropyl)morpholine (7.1 mmol) and 1.7 g 50% (w/w) NaOH (21.3 mmol) in 10 mL THF was cooled in an ice-water bath, and 1.3 mL carbon disulfide (21.3 mmol) were added drop-wise. A white precipitate formed almost immediately, and a yellow liquid was evident at the bottom of the flask. To facilitate stirring, 10 mL water were added; the mixture turned bright orange, and was stirred for 1 hour, until the starting material had disappeared completely (determined by TLC: silica/acetone/I₂ vapor development). Additional ice was added to the cooling bath, and 1.7 mL "30%" H₂O₂ (21.3 mmol) was added slowly, with care taken to ensure that the temperature of the reaction did not exceed 40°C. [It is important to add the H_2O_2 in small portions, and wait for a few minutes between additions, as temperature spikes generally do not occur immediately upon addition.] Upon the addition of H₂O₂, the color of the reaction mixture faded to a cloudy yellow. The reaction was stirred for 0.5 h, and additional H₂O₂(0.4-1.0 mL) was added, as necessary, until the reaction reached completion. 10 mL water were added, and the reaction mixture was quickly extracted with 4 x 15 mL Et₂O and dried over Na₂SO₄. The crude yield of **14a** ranged from 65-85%. ¹H NMR (300 MHz, CDCl₃) ∂ 3.64 (t, J = 4.8 Hz, 4H); 3.56 (t, J = 6.3 Hz, 2H); 2.39 (m, 6H); 1.80 (m, J = 6.3 Hz, 2H); $\mathbf{R}_f 0.55$ (acetone/silica).

N-[3-(N'-2-pyridylthioureido)propyl|morpholine (14)

1.1 g (12 mmol) 2-aminopyridine were added to 0.561 g CaH₂ (13 mmol) in 10 mL dry THF (4 Å molecular sieves), under an Ar balloon. The mixture was stirred until bubbling ceased; 2.26 g **14a** (12 mmol) were added, and the reaction was stirred under Ar, overnight and at room temperature. The reaction mixture was filtered over a vacuum, and the solvent was removed on the rotatory evaporator. The residue was then recrystallized from iPrOH, yielding 0.93 g (28%) of an iridescent, colorless, flaky solid. Single crystals suitable for X-ray analysis were grown from layered methanol/hexanes. ¹H NMR (500

MHz, CDCl₃) ∂ 11.76 (bt, 1H); 9.09 (bs, 1H); 8.16 (d, J = 5 Hz, 1H); 7.65 (m, 1H), 6.96 (dd, 1H, J = 5Hz, 7.5Hz); 6.88 (d, J = 8.5H, 1H); 3.83 (q, J = 6.9Hz, 2H); 3.73 (t, J = 4.8Hz, 4H); 2.49 (m, 6H); 1.93 (m, 2H); ¹³C **NMR** (125 MHz, CDCl₃) ∂ 181.4, 149.0, 137.0, 123.8, 121.8, 66.7, 66.6, 53.6, 53.5, 36.7, 24.6; **MP** 126-127°C.

N,N'-bis[3-(N"-benzoylthioureido)propyl]piperazine (15)

To a stirred solution of 1.35 mL N,N'-bis(3-aminopropyl)piperazine (6.55 mmol) in 20 mL THF were added 2.17 g benzoyl isothiocyanate, which had been prepared in accordance with a literature procedure. The reaction mixture was stirred overnight, and the solvent was removed on the rotatory evaporator. The crude orange solid weighed 3.8 g, and consisted of approximately a 1:1 mixture of the desired thiourea and what was believed to be a bis(benzamide) side product. The thiourea was liberated as a pale brown, crystalline solid via recrystallization with DMSO/H₂O (1.24 g, 36%), and single crystals suitable for X-ray (and other spectral) analysis were obtained from DMSO/MeOH. IR (KBr, cm⁻¹) 3228 (br), 2947, 2813, 1674, 1559, 1528, 1174, 1141, 1073; ¹H NMR (500 MHz, CDCl₃) ∂ 11.28 (bs, 2H); 10.99 (t, J=5.5, 2H); 7.98 (d, J=7.0Hz, 4H); 7.68 (t, J=7.0Hz, 7.5Hz, 2H); 7.58 (t, J=7.0Hz, 7.5 Hz, 4H); 3.71 (q, J=6.0Hz, 7.0Hz, 4H); 2.6-2.3 (m, J=6.0 Hz, 7.0Hz, 12H), 1.84 (m, 4H); ¹³C NMR (125 MHz, CDCl₃) ∂ 181.4, 141, 149.0, 137.0, 123.8, 121.8, 66.7, 66.6, 53.6, 53.5, 36.7, 24.6; MP 126-127 °C.

Chapter V

3-Nitrobenzoylisothiocyanate (16a)

[Not isolated] 0.972 g (10 mmol) KSCN were dissolved in 20 mL MeCN, at room temperature. 1.86 g 3-nitrobenzoyl chloride (14.9 mmol) were added; the reaction mixture instantly became cloudy. After five minutes of stirring, a yellow color appeared, along with copious quantities of white precipitate (KCl). The reaction was stirred for 2 hours, during which time the color deepened to a chalky, brownish-peach hue, then filtered through a Celite column (7 cm x 7 cm). The solvent was removed on the rotatory evaporator, yielding 2.0 g of a peach-colored solid, which was used without additional purification. **IR** (NaCl, cm⁻¹) 2943, 2839, **1977**, 1675, 1599, 1578, 1486, 1293, 1216, 860, 751; 1 **H NMR** (300 MHz, CDCl₃) ∂ 8.90 (t, J = 2.1 Hz, 1H), 8.53 (m, 1H), 8.41 (dt, J = 8.0, 1.0 Hz, 1H), 7.74 (t, J = 8.0 Hz, 1H).

1-(3-Nitrobenzoyl)-3-(6-methyl-2-pyridyl)thiourea (16)

The crude isothiocyanate **16a** was added to a stirred solution of 2-amino-6-methylpyridine (1.08 g, 10 mmol) in 15 mL dry THF. The reaction was stirred overnight, at room temperature, and \sim 10 mL DI water were added, until permanent cloudiness was achieved. The reaction continued to stir for 1 hr, at which point the fluffy, pale yellow precipitate was filtered over a Buchner funnel, washed with water (2 x 10 mL), and allowed to air-dry (2.31 g, 73% yield from the acid chloride). In order to expedite drying, the product could be transferred to a watch glass, and placed on top of a hot oven (ambient temperature \sim 100°C) with no apparent decrease in either yield or purity. As isolated, the product consisted primarily of **160**, as determined by IR (KBr).

160

Pale-yellow needles suitable for x-ray diffraction were grown from ethyl acetate/hexanes. This conformer could also be reproducibly prepared via trituration of the initial product with methanol, ethanol, isopropanol, acetone/water, chloroform, or acetic acid. Trituration with nitromethane, acetonitrile, acetone, or acetone/hexanes also affords **16O**,

but prolonged contact with these solvents leads to the precipitation of **16N** (1-7 days, depending on the solvent/solution concentration). **IR** (KBr, cm⁻¹): 3224 (N-H), 1672 (C=O), 1526 (C=S); ¹**H NMR** (CDCl₃, 300 MHz): ∂ 12.79 (bs, 1H), 9.06 (bs, 1H), 8.78 (t, 1H, J=1.5 Hz), 8.58 (d, 1H, J=8.4 Hz), 8.52 (m, 1H), 8.26 (d, 1H, J=7.8 Hz), 7.80 (t, 1H, J=8.1 Hz), 7.69 (t, 1H, J=7.8 Hz), 7.06 (d, 1H, J = 7.2 Hz), 2.55 (s, 3H). ¹³**C NMR** (CDCl₃, 500 MHz): ∂ 176.2 (C=S), 164.3 (C=O),158.1 (C-NO₂), 150.4, 140.4, 138.2, 134.7, 133.4, 130.7, 128.2, 123.0, 121.6, 113.1, 24.3; **MP** (DSC) 155.6 °C (dec.).

16N

Bright-yellow crystals suitable for X-ray diffraction were grown from acetonitrile. (**160** precipitates initially, but disappears as **16N** crystallizes from the resulting slurry.) Trituration of the initial product with nitromethane also provides this conformer. Dissolution of the initial product or of **160** in acetone or acetone/hexanes yields variable amounts of **16N**; however, the conversion from **160** is generally incomplete over the the observed period of time (1-30 days). **IR** (KBr, cm⁻¹): 3183 (N-H), 1716 (C=O), 1559 (C=S) cm⁻¹; ¹**H-NMR** (CDCl₃, 300 MHz): ∂ 15.45 (bs, 1H), 8.84 (s, 1H), 8.70 (bs, 1H), 8.53 (d, 1H), 8.45 (d, 1H, J = 7.8 Hz), 7.80 (t, 1H), 7.69 (t, 1H), 6.96 (d, 1H, J = 7.5 Hz), 6.80 (d, 1H, J = 8.7 Hz), 2.44 (s, 3H). ¹³**C-NMR** (CDCl₃, 125 MHz): ∂ 177.7 (C=S), 163.6 (C=O), 155.8 (C-NO₂), 151.6, 140.4, 136.4, 133.4, 130.2, 127.5, 122.6, 119.1, 110.0, 109.7, 23.8; **EA** Calc. C, 53.16; H, 3.82; N, 17.71; O, 15.17; S, 10.14; found C, 53.33; H, 3.60; N, 17.73; S, 9.97; **MP** (DSC) 160.7°C (dec.)

Chapter VI

General Preparation of Isothiocyanates 17a-13a and 27a.

0.972 g (10 mmol) KSCN were dissolved in 20 mL MeCN. 10 mmol of the appropriate acid chloride were added to the stirred reaction mixture. The reaction mixture instantly grew cloudy, and within a few minutes, copious quantities of white solids were observed to have precipitated. The reaction was monitored by TLC (CH₂Cl₂/silica); the R_f value of the isothiocyanate product was invariably larger than that of the acid chloride. When TLC indicated that the reaction had gone to completion, ~10 mL Et₂O were added to the reaction mixture, precipitating most of the KCl which had remained in solution. The reaction mixture was then filtered through a 7 cm x 7 cm column of Celite. The filter cake was washed once with Et₂O, and the filtrate was liberated of solvent on the rotatory evaporator. The complete disappearance of acid chloride was confirmed by ¹H NMR, and the presence of isothiocyanate was confirmed by IR, wherein it displayed a characteristic broad absorption around 1970 cm⁻¹.

General Preparation of BzPTUs 17-46.

The crude isothiocyanate was dissolved in 15 mL THF, and 10 mmol of either 2-aminopyridine or 2-amino-6-picoline were added to the reaction flask. This mixture was stirred at room temperature for 1-16 hours, or overnight, until the isothiocyanate was completely consumed. Water was added until the solution clouded, and then 5 mL more were added to ensure complete precipitation of the product. The reaction was stirred for another hour, and then the precipitate was filtered over a vacuum, washed with 10 mL water, and air dried, yielding a white, yellow, or orange powder that was found, by ¹H NMR, to be free of both starting materials and organic side products. Occasionally, a small amount of KCl could be found in the final product; however, this was readily removed by either additional water washes or dissolving the product in chloroform, then filtering off the salt.

1-Benzoyl-3-(2-pyridyl)thiourea (17)

To a stirred solution of 2-aminopyridine (941 mg, 10 mmol) in 15 mL dry THF (4 Å molecular sieves) was added 1.63 g (10 mmol) benzoyl isothiocyanate, which had been prepared according to a literature procedure. The reaction was stirred overnight, at room temperature, and ~10 mL water were added, until permanent cloudiness was achieved. The reaction continued to stir for 1 hr, at which point the pale yellow, cotton candy-like precipitate was filtered over a Buchner funnel, washed with water (2 x 10 mL), and allowed to air-dry (2.64 g, 90%). In order to expedite drying, the product could be transferred to a watch glass, and placed on top of a hot oven (ambient temperature ~ 100°C) with no apparent decrease in either yield or purity.

17N

Sulfur-yellow, cubic crystals suitable for X-ray analysis were grown from CHCl 3. High-quality crystals could also be reliably produced from acetonitrile, acetone, DCM, and even acetic acid. **IR** (KBr, cm⁻¹) 3200 (br), 3122 (br), 2985, 1714, 1612, 1558, 1528, 1446, 1337, **1247**, 1213, 1197, 1161, 798, 749, 701; ¹**H NMR** (300 MHz, CDCl₃, -9 °C) ∂ 15.30 (bs, 1H), 9.23 (bs, 1H), 8.08 (d, 2H), 7.89 (m, 1H), 7.65 (m, 2H), 7.53 (m, 1H), 7.53 (m, 1H), 6.92 (d, 1H), 6.74 (d, 1H), 2.47 (s, 3H); ¹³**C NMR** [not recorded, due to small population of **17N** in solution]; **MP** (DSC) 150.3 °C (dec).

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Slender, colorless prisms suitable for X-ray analysis were grown by slow evaporation of a THF solution. Upon prolonged heating above 80-90 ℃, these crystals lose water and convert into **17N**. **IR** (KBr, cm⁻¹) 3441 (br), 3126 (br), 3069, 1680, 1600, **1525**m 1452m 1320, 1256, 1172, 755, 714, 673; ¹**H-NMR** (CDCl₃, 300 MHz): ∂ 13.00 (bs, 1H), 9.04 (bs, 1H), 8.61 (d, 1H), 7.92 (d, 2H), 7.69 (m, 2H), 7.56 (t, 2H), 7.04 (d, 1H), 2.54 (s, 3H); ¹³**C-NMR** (CDCl₃, 125 MHz): ∂ 176.6, 166.1, 157.6, 150.2, 137.7, 133.5, 131.4, 129.0, 127.3, 120.9, 112.9, 23.8; **MP** (DSC) 116 ℂ [phase transition], 150.5 ℂ (dec).

4-nitrobenzoylisothiocyanate (18a)

[Not Isolated] To a well-stirred solution of 0.972 g (10 mmol) KSCN in 20 mL MeCN

were added 1.86 g (10 mmol) 4-nitrobenzoyl chloride; large quantities of KCl precipitated immediately. The reaction was monitored by TLC (20% EtOAc in hexanes), which indicated that the acid chloride had been completely consumed in 2 hrs. The orange reaction mixture was filtered through Celite (7 cm x 7 cm), and the filter cake was washed with Et₂O (2 x 10 mL). The solvents were then removed on the rotatory evaporator, yielding 2.0 g of a peach-colored solid, which was used without further purification. **IR** (NaCl, cm⁻¹) 3105, 1958, 1689, 1600, **1529**, 1346, 1244, 1103, 876, 839, 709; ¹**H NMR** (300 MHz, CDCl₃) ∂ 8.36 (dt, J = 9.3, 1.8 Hz, 2H), 8.26 (dt, J = 9.3, 1.8 Hz, 2H).

1-(4-nitrobenzoyl)-3-(6-methyl-2-pyridyl)thiourea (18) To a well-stirred solution of 1.06 g (5.1 mmol) **18a** in 15 mL dry THF were added 0.55 g 6-methyl-2-picoline (5.1 mmol). The reaction was stirred overnight (16h), and ~2 mL water were added to the sulfur-yellow suspension, to ensure full precipitation of the product. The reaction mixture was filtered over a Buchner funnel, washed with water (2 x 10 mL), and dried on top of the oven ($T \sim 100 \,^{\circ}$ C). 1.28 g of the yellow, powdery product were recovered, and a single crystal suitable for X-ray analysis was grown from methanol/acetone. 79% yield; **IR** (KBr, cm⁻¹) 3184 (br), 3109, 3017, 1715, 1612, 1560, **1520**, 1456, 1441, 1348, 1242, 1156, 867, 796, 712; ¹**H-NMR** (300 MHz, CDCl₃) ∂ 12.77 (bs, 1H), 9.01 (bs, 1H), 8.60 (d, 1H, J=8.1 Hz), 8.43 (d, 2H, J=9 Hz), 8.12 (d, 2H, J=9.3 Hz), 7.70 (t, 1H, J=7.5 Hz, 8 Hz), 7.08 (d, 1H, J=7.5 Hz); ¹³C-NMR (151 MHz, DMSO- d6) ∂ 177.3, 165.7, 154.2, 149.8, 146.9, 144.1, 136.4, 130.6, 123.6, 111.6, 109.9, 23.5; **EA** Calc. C, 53.16; H, 3.82; N, 17.71; Found C, 52.89; H, 3.64; N, 17.49; **MP** 185-186 °C.

2-methoxybenzoylisothiocyanate (19a)

[Not Isolated] 1.44 g (14.9 mmol) KSCN were dissolved in 20 mL MeCN, at room temperature. 2.0 mL 2-methoxybenzoyl chloride (14.9 mmol) were added via syringe; the reaction mixture instantly became cloudy. After five minutes of stirring, a yellow color appeared, along with copious quantities of white precipitate (KCl). The reaction was stirred overnight (16h), during which time the color deepened to a chalky orange hue,

then filtered through a Celite column (7cm x 7cm). The solvent was removed on the rotatory evaporator, yielding 2.98 g of a red-orange oil, which contained visible KCl particles. After a second filtration, through a 20 μ m membrane, 2.60 g of the oil were collected, and used without additional purification. **IR** (NaCl, cm⁻¹) 2943, 2839, **1977**, 1675 (d), 1599, 1578, 1486, 1293, 1216, 860, 751; ¹**H-NMR** (300 MHz, CDCl₃) ∂ 7.74 (dd, J = 7.8, 1.8 Hz, 1H), 7.06 (td, J = 8.7, 1.8 Hz, 1H), 6.62 (td, J = 7.7 Hz, 1H), 6.34 (d, J = 8.7 Hz, 1H), 3.26 (s, 3H).

1-(2-methoxybenzoyl)-3-(6-methyl-2-pyridyl)thiourea (19)

To a stirred solution of 2-aminopicoline (564 mg, 5.2 mmol) in 15 mL dry THF (4 Å molecular sieves) was added 1.00 g (5.2 mmol) **19a**. The reaction was stirred overnight, at room temperature, and ~10 mL water were added, until permanent cloudiness was achieved. The reaction continued to stir for 1 hr, at which point the colorless, crystalline precipitate was filtered over a Buchner funnel, washed with water (2 x 5 mL), and allowed to air-dry (1.35 g, 86%, 2 steps). Slender prisms suitable for analysis were grown from ethanol/toluene. **IR** (KBr, cm⁻¹) 3289, 1660, 1595. 1535, 1483, **1456**, 1335, 1185, 1084, 1015, 763; ¹**H NMR** (300 MHz, CDCl₃) ∂ 13.19 (bs, 1H), 11.11 (bs, 1H), 8.66 (d, 1H), 8.22 (dd, 1H), 7.64 (t, 1H), 7.57 (dt, 1H), 7.13 (t, 1H), 7.04 (d, 1H), 7.00 (d, 1H), 4.00 (s, 3H), 2.45 (s, 3H); ¹³**C NMR** (75 MHz, CDCl₃) ∂ 177.3, 164.5, 158.0, 157.8, 150.9, 137.9, 135.5, 132.9, 122.0, 120.9, 118.9, 113.1, 111.9, 56.6, 24.3; **MP** 186-188 ℃.

4-methoxybenzoylisothiocyanate (20a)

[Not Isolated] To a stirred solution of 0.97 g KSCN (10 mmol) in 20 mL MeCN were added 1.72 g p-methoxybenzoyl chloride (10 mmol). Upon addition, copious quantities of white precipitate formed (KCl); the reaction was stirred at room temperature for four hours, and monitored by TLC ($R_f = 0.73 / CH_2Cl_2$). The reaction mixture was then filtered through a Celite plug (d = 7 cm; h = 7cm), and the solvent was removed on the rotovap. The resultant yellow solid weighed 1.858 g (crude yield = 96%), and was used without further purification. **IR** (NaCl, cm⁻¹) 1977, 1685, 1603, 1508, **1249**, 1163, 1081, 1025, 862, 843, 786, 750; ¹**H NMR** (300 MHz, CDCl₃) ∂ 8.02 (d, J = 9 Hz, 2H), 6.96 (d, J = 9

1-(4-methoxybenzoyl)-3-(6-methyl-2-pyridyl)thiourea (20)

To a stirred solution of **20a** (0.89 g, 4.6 mmol) in 15 mL THF were added 0.43 g (4.6 mmol) 2-amino-6-methylpyridine; the reaction was stirred for 16 hours (i.e. overnight) at room temperature, and ca. 8 mL water were added to precipitate the product. After the addition of water, the reaction was stirred for an additional hour, and the sulfur-yellow solids were filtered over a Buchner funnel, washed with water, and air-dried to constant weight, 0.89 g (65%, 2 steps). As prepared, the product was suitable for spectral analysis; sulfur-yellow hexagonal crystals suitable for X-ray diffraction were grown from DMF. **IR** (KBr, cm⁻¹) 3178, 3016, 1707, 1610, 1532, 1509, 1446, 1343, **1235**, 1182, 1077, 1024, 789; ¹**H NMR** (CDCl₃, 300 MHz) # 13.08 (bs, 1H), 8.96 (bs, 1H), 8.60 (d, 1H), 8.89 (dt, 2H), 7.67 (t, 1H), 7.02 (m, 3H), 3.91 (s, 3H), 2.51 (s, 3H); ¹³**C NMR** (CDCl₃, 300 MHz) ∂ 177.2 (C=S), 165.9 (C=O),164.2 (C-OCH 3), 158.0, 150.7, 138.0, 129.9, 123.7, 121.1, 114.6, 113.2, 55.8, 24.3; **EA** Calc. C, 59.78; H, 5.02; N, 13.94; Found C, 59.55; H, 4.99; N, 13.95; **MP** 171-173°C.

3-chlorobenzoylisothiocyanate (21a)

[Not Isolated] To a stirred solution of 0.97 g KSCN (10 mmol) in 20 mL MeCN were added 1.3 mL 3-chlorobenzoyl chloride (1.78 g, 10 mmol). Upon addition, copious quantities of white precipitate formed (KCl); the reaction was stirred at room temperature for four hours, and monitored by TLC ($R_f = 0.84 / CH_2Cl_2$). When the reaction was complete, 10 mL Et₂O were added, and the reaction mixture was then filtered through a Celite plug (d = 7 cm; h = 7cm), washed with 10 mL Et₂O, and stripped of solvent on the rotovap. The resultant brown liquid weighed 2.1 g, and was used without further purification. **IR** (NaCl, cm⁻¹) **1959** (br), 1702, 1593, 1574, 1473, 1425, 1279, 1241, 1117. 1071, 885, 765, 723, 646; ¹**H NMR** (300 MHz, CDCl₃) ∂ 8.05 (t, J=1.8Hz, 1H); 7.96 (d, J=8Hz, 1H); 7.64 (m, 1H); 7.46 (t, 8Hz, 1H).

1-(3-chlorobenzoyl)-3-(6-methyl-2-pyridyl)thiourea (21) To a stirred solution of crude

21a in 15 mL THF were added 1.08 g (10 mmol) 2-amino- 6-methylpyridine; the reaction was stirred for 16 hours (i.e. overnight) at room temperature, and ca. 10 mL water were added to precipitate the product. After the addition of water, the reaction was stirred for an additional hour, and the fluffy white solids were filtered over a Buchner funnel, washed with water, and air-dried to constant weight, 2.35 g (77%, 2 steps). As prepared, the product was suitable for spectral analysis; colorless, cubic crystals were grown from methanol. **IR** (KBr, cm⁻¹) 3229 (br), 3050, 1678, 1558, **1528**, 1458, 1341, 1250, 1151, 785, 733; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 12.85 (bs, 1H); 8.98 (bs, 1H), 8.58 (d, 1H), 7.91 (t, 1H, J=1.8Hz), 7.78 (d, 1H), 7.66 (m, 2H), 7.49 (t, 1H), 7.04 (d, 1H), 2.54 (s, 3H); ¹³**C NMR** (CDCl₃, 300 MHz) ∂ 176.6, 165.1, 158.0, 150.5, 138.1, 135.8, 133.9, 133.7, 130.7, 128.1, 125.6, 121.4, 113.3, 24.3; **MP** 161-162°C.

4-chlorobenzoylisothiocyanate (22a)

[Not Isolated] To a stirred solution of 0.97 g KSCN (10 mmol) in 20 mL MeCN were added 1.75 g (10 mmol) 4-chlorobenzoyl chloride. Upon addition, copious quantities of white precipitate formed (KCl); the reaction was stirred at room temperature for four hours, and monitored by TLC. When the reaction was complete, 10 mL Et₂O were added, and the reaction mixture was then filtered through a Celite plug (d = 7 cm; h = 7cm), washed with 10 mL Et₂O, and stripped of solvent on the rotovap. The resultant yellow oil was used without further purification. **IR** (NaCl, cm⁻¹) 3090, 1989 (br), **1684**, 1593, 1485, 1401, 1255, 1902, 864, 840, 738, 667; ¹**H NMR** (300 MHz, CDCl₃) ∂ 8.01 (d, J=8.4Hz, 2H), 7.49 (d, J=8.4Hz, 2H).

1-(4-chlorobenzoyl)-3-(6-methyl-2-pyridyl)thiourea (22)

To a stirred solution of crude **22a** in 15 mL THF were added 1.08 g (10 mmol) 2-amino-6-methylpyridine; the reaction was stirred for 16 hours (i.e. overnight) at room temperature, and ca. 10 mL water were added to precipitate the product. After the addition of water, the reaction was stirred for an additional hour, and the chalky yellow solid was filtered over a Buchner funnel, washed with water, and air-dried to constant weight, 2.991 g (98%, 2 steps). As prepared, the product was suitable for spectral

analysis; yellow prisms were grown from the slow evaporation of an acetone solution . **IR** (KBr, cm⁻¹) 3189, 3019, 1716, 1611, 1562, 1533, 1443, 1334, **1244**, 1156, 1093, 792, 749; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 12.94 (bs, 1H); 9.00 (bs, 1H), 8.60 (d, 1H), 7.88 (d, 2H), 7.69 (t, 1H), 7.56 (d, 2H), 7.06 (d, 1H), 2.55 (s, 3H); ¹³**C NMR** (CDCl₃, 300 MHz) ∂ 176.6, 165.3, 157.9, 150.4, 140.3, 137.9, 130.1, 129.6, 129.0, 121.2, 113.1, 24.1; **EA** Calc. C, 54.99; H, 3.96; N, 13.74; Found, C, 54.85; H, 4.02; N, 13.69; **MP** 166-167°C.

3-cyanobenzoylisothiocyanate (23a)

[Not Isolated] 1.98 g (12 mmol) 3-cyanobenzoyl chloride were prepared from 3-cyanobenzoic acid, using a literature procedure. This amount of the acid chloride was added to a stirred solution of 1.17 g KSCN (12 mmol) in 20 mL MeCN. Upon addition, copious quantities of white precipitate formed (KCl); the reaction was stirred at room temperature for 2 hours, and monitored by TLC (R_f = 0.71, CH_2Cl_2 /silica). When the reaction was complete, 10 mL Et_2O were added, and the reaction mixture was then filtered through a silica plug (d = 7 cm; h = 7cm), washed with 10 mL Et_2O , and stripped of solvent on the rotovap. The resultant yellow solid weighed 2.258 g (97%), and was used without further purification. **IR** (NaCl, cm⁻¹) 3071, 2230, 1973 (br), **1685**, 1431, 1166, 909, 727; ¹**H NMR** (300 MHz, $CDCl_3$) ∂ 8.34 (s, 1H); 8.29 (d, 7.8 Hz, 1H), 7.93 (d, J=7.8 Hz, 1H), 7.66 (t, J=7.8Hz, 1H).

1-(3-cyanobenzoyl)-3-(6-methyl-2-pyridyl)thiourea (23)

To a stirred solution of crude **23a** in 15 mL THF were added 1.3 g (12 mmol) 2-amino-6-methylpyridine; the reaction was stirred for 16 hours (i.e. overnight) at room temperature, and ca. 10 mL water were added to precipitate the product. After the addition of water, the reaction was stirred for an additional hour, and the pale yellow solid was filtered over a Buchner funnel, washed with water, and air-dried to constant weight, 2.25 g (76%, 3 steps). As prepared, the product was suitable for spectral analysis . **IR** (KBr, cm-1) 3254 (br), 2923, 2234, 1676, 1601, **1529**, 1456, 1343, 1262, 1143, 790, 740, 679 (NaCl); ¹**H NMR** (CDCl₃, 300 MHz) ∂ 12.76 (bs, 1H), 9.01 (bs, 1H), 8.57 (d, 1H), 8.24 (s, 1H), 8.12 (d, 1H), 7.94 (d, 1H), 7.70 (m, 2H), 7.06 (d, 1H), 2.54 (s, 3H); ¹³**C NMR** (CDCl₃, 75

MHz) ∂ 176.1, 164.2, 158.0, 150.2, 148.5, 138.0, 133.5, 133.2, 130.6, 128.0, 122.8, 121.4, 113.1, 24.1; **MP** 147-148 C.

4-cyanobenzoylisothiocyanate (24a)

[Not Isolated] 0.825 g (5 mmol) 3-cyanobenzoyl chloride were prepared from 3-cyanobenzoic acid, using a literature procedure. This amount of the acid chloride was added to a stirred solution of 486 mg KSCN (5 mmol) in 10 mL MeCN. Upon addition, the reaction mixture turned cloudy organge. The reaction was stirred at room temperature for 2 hours, and monitored by TLC ($R_f = 0.73$, $CH_2Cl_2/silica$). When the reaction was complete, 10 mL Et2O were added, and the reaction mixture was then filtered through a silica plug (d = 7 cm; h = 7cm), washed with 10 mL Et₂O, and stripped of solvent on the rotovap. The resultant solid was pale yellow and crystalline, and was used without further purification. **IR** (NaCl, cm⁻¹) 2231, 1967, **1918**, 1695, 1261, 1177, 1095, 860, 750, 674; **1H NMR** (300 MHz, CDCl₃) ∂ 8.24 (d, J=8.4Hz, 2H), 7.84 (d, J=8.4Hz, 2H).

1-(4-cyanobenzoyl)-3-(6-methyl-2-pyridyl)thiourea (24)

To a stirred solution of crude **24a** in 10 mL MeCN were added 0.54 g (5 mmol) 2-amino-6-methylpyridine. The deep pink solution turned orange upon addition of the amine; after stirring overnight, the solution was clear and pale yellow. Water was added (10 mL) and the reaction mixture was stirred for an additional hour, at which point 1.04 g of a pale yellow solid (70%, 3 steps) were removed via vacuum filtration. Single crystals suitable for X-ray analysis were grown from acetonitrile. **IR** (KBr, cm⁻¹) 3189 (br), 3040, 2227, 1720, 1677, 1602, 1565, **1533**, 1459, 1350, 1263, 1177, 1152, 854, 793, 749, 532; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 12.75 (bs, 1H), 9.03 (bs, 1H), 8.58 (d, 1H), 8.41 (d, 2H), 8.11 (d, 2H), 7.69 (t, 1H), 7.07 (d, 1H), 2.55 (s, 3H); ¹³**C NMR** (CDCl₃, 75 MHz) ∂ 176.3, 164.8, 150.4, 150.0, 138.2, 135.8, 133.2, 128.4, 121.6, 117.4, 113.2, 24.3; **MP** 172-173 °C.

3,4-dichlorobenzoylisothiocyanate (25a)

[Not Isolated] 1.98 g (12 mmol) 3,4-dichlorobenzoyl chloride were prepared from 3-cyanobenzoic acid, using known literature procudures.²¹⁴ This amount of the acid chloride

was added to a stirred solution of 1.17 g KSCN (12 mmol) in 20 mL MeCN. Upon addition, copious quantities of white precipitate formed (KCl); the reaction was stirred at room temperature for 2 hours, and monitored by TLC ($R_f = 0.71$, $CH_2Cl_2/silica$). When the reaction was complete, 10 mL Et_2O were added, and the reaction mixture was then filtered through a silica plug (d = 7 cm; h = 7cm), washed with 10 mL Et_2O , and stripped of solvent on the rotovap. The resultant yellow solid weighed 2.258 g (97%), and was used without further purification. **IR** (NaCl, cm⁻¹) 1949 (br), 1696, 1585, 1546, 1382, 1268, 1227, **1095**, 1032, 893; ¹**H NMR** (300 MHz, CDCl₃) ∂ 8.34 (s, 1H); 8.29 (d, 7.8 Hz, 1H), 7.93 (d, J=7.8 Hz, 1H), 7.66 (t, J=7.8Hz, 1H).

1-(3,4-dichlorobenzoy)-3-(6-methyl-2-pyridyl)thiourea (25)

To a stirred solution of 2.32 g (10 mmol) **25a** in 15 mL THF were added 1.08 g (10 mmol) 2-amino-6-methylpyridine; the reaction was stirred for 16 hours (i.e. overnight) at room temperature, and ca. 10 mL water were added to precipitate the product. After the addition of water, the reaction was stirred for an additional hour, and the white solid was filtered over a Buchner funnel, washed with water, and air-dried to constant weight, 2.7 g (79%, 2 steps). As prepared, the product was suitable for spectral analysis; long, colorless prisms were grown from acetic acid . **IR** (KBr, cm⁻¹) 3163, 2986, 1681, 1542, **1518**, 1437, 1340, 1299, 1284, 1162, 1172, 755, 745; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 12.80 (bs, 1H), 8.92 (bs, 1H), 8.57 (d, 1H, *J*=8.1Hz), 8.02 (d, 1H, *J*=2.1Hz), 7.68 (m, 3H), 7.05 (d, 1H, *J*=7.5Hz), 2.54 (s, 3H); ¹³**C NMR** (CDCl₃, 75 MHz) ∂ 176.3, 164.1, 158.0, 150.3, 138.6, 138.0, 134.1, 131.5, 131.3, 129.8, 126.4, 121.3, 113.1, 24.1; **MP** 167-168 °C.

3,5-dichlorobenzoylisothiocyanate (26a)

2.09 g (10 mmol) 3,5-dichlorobenzoyl chloride were added to a stirred solution of 0.97 g KSCN (10 mmol) in 20 mL MeCN. Upon addition, copious quantities of white precipitate formed (KCl); the reaction was stirred overnight (16 h). The chunky orange suspension was diluted with 10 mL MeCN and filtered through a column of silica gel (200 mesh; d = 7 cm; h = 1 cm), washed with 5 mL acetone, and stripped of solvent on the rotovap. The resultant orange solid weighed 2.046 g, and was used without further

purification. ¹**H NMR** (300 MHz, CDCl₃) ∂ 7.93 (d, J=1.8, 2H); 7.64 (t, J=1.8, 1H); $\mathbf{R_f}$ 0.84 (CH₂Cl₂/silica).

1-(3,5-dichlorobenzoyl)-3-(6-methyl-2-pyridyl)thiourea (24)

To a stirred solution of crude **10a** (ca. 10 mmol) in 15 mL THF were added 1.08 g (10 mmol) 2-amino-6-methylpyridine; the reaction was stirred for 16 hours (i.e. overnight) at room temperature, and ca. 15 mL water were added to precipitate the product. After the addition of water, the reaction was stirred for an additional hour, and the bright yellow solid was filtered over a Buchner funnel, washed with water, and air-dried to constant weight, 2.116 g (62%, 2 steps). As prepared, the product was suitable for spectral analysis; small yellow prisms were grown from dichloroethane . **IR** (KBr, cm⁻¹) 3274, 2917, 1700, 1610, 1558, 1533, 1457, 1340, **1260**, 1237, 1158, 797, 752; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 12.73 (bs, 1H), 8.94 (bs, 1H), 8.56 (d, 1H), 7.77 (d, 1H), 7.68 (m, 3H), 7.06 (d, 1H); ¹³**C NMR** (CDCl₃, 125 MHz) ∂ 176.3, 163.9, 158.2, 150.4, 138.2, 136.5, 133.7, 126.8, 126.2, 121.5, 113.3, 24.3; **MP** 174-176°C (dec.)

4-bromobenzoylisothiocyanate (27a)

4.132 g (20 mmol) 4-bromobenzoyl chloride were added to a stirred solution of 1.944 g KSCN (20 mmol) in 30 mL MeCN. Upon addition, copious quantities of white precipitate formed (KCl); the reaction was stirred overnight (16 h), then filtered through a column of silica gel (100-200 mesh; d = 7 cm; h = 7 cm), washed with 5 mL Et₂O, and stripped of solvent on the rotovap. The pale brown oil weighed 4.01 g, and was used without further purification. **IR** (NaCl, cm⁻¹) 2045, 1983, **1685**, 1588, 1397, 1254, 1067, 837, 734, 666; ¹**H-NMR** (300 MHz, CDCl₃) ∂ 7.93 (dt, 2H), 6.66 (dt, 2H). **R**_f = 0.78 (CH₂Cl₂/silica).

1-(4-bromobenzoyl)-3-(6-methyl-2-pyridyl)thiourea (27)

To a stirred solution of 2.0 g **27a** (8.6 mmol) in 15 mL THF were added 0.93 g (8.6 mmol) 2-amino-6-methylpyridine; the reaction was stirred for 72 hours (*i.e.* over the weekend) at room temperature. 25 mL water were added to precipitate the product, and

the reaction was stirred for an additional hour, then filtered over a Buchner funnel, washed with water (2 x 15 mL) and ethanol (2 x 5 mL), and air-dried to constant weight, 2.005 g (57%, 2 steps). As prepared, the lemon-yellow product was suitable for spectral analysis; yellow cubic crystals were grown from acetonitrile . **IR** (KBr, cm⁻¹) 3189 (br), 3123, 3083, 3019, 1718, 1611, **1560**, 1534, 1443, 1334, 1246, 1201, 1156, 1069, 1011, 898, 791, 744, 524; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 12.93 (bs, 1H), 9.04 (bs, 1H), 8.54 (d, 1H), 7.77 (d, 2H), 7.65 (m, 3H), 7.03 (d, 1H), 2.51 (s, 3H); ¹³C-NMR (CDCl₃, 75 MHz) ∂ 176.5, 165.4, 157.9, 150.4, 137.9, 132.6, 130.6, 129.1, 129.0, 121.2, 113.1, 24.1; **MP** 166-168°C (dec.)

2-bromobenzoylisothiocyanate (28a)

2.2 g (1.3 mL, 10 mmol) 2-bromobenzoyl chloride were added to a stirred solution of 0.972 g KSCN (10 mmol) in 20 mL MeCN. Upon addition, copious quantities of white precipitate formed (KCl); the reaction was stirred overnight (16 h), then filtered through a column of Celite (d = 7 cm; h = 7 cm), washed with 5 mL Et₂O, and stripped of solvent on the rotovap. The pale yellow oil weighed 2.25 g, and was used without further purification. **IR** (NaCl, cm⁻¹) **1959**, 1703, 1585, 1565, 1466, 1433, 1273, 1228, 1132, 1092, 1031, 858, 733; ¹**H NMR** (300 MHz, CDCl₃) ∂ 7.95 (m, 1H), 7.72 (m, 1H), 7.42 (m, 2H). **R**_f = 0.65 (CH₂Cl₂/silica).

1-(2-bromobenzoyl)-3-(6-methyl-2-pyridyl)thiourea (28)

To a stirred solution of 1.0 g (4.1 mmol) **28a** in 15 mL THF were added 0.379 g (4.1 mmol) 2-amino-6-methylpyridine; the reaction was stirred for 16 hours (*i.e.* overnight) at room temperature. The solvent was removed on the rotovap, and the residual solids were recrystallized from isopropanol, yielding 1.0 g (70%) of pale yellow needles. **IR** (KBr, cm⁻¹) 3155 (br), 1667, 1600, **1526**, 1455, 1347, 1168, 1147, 1087, 743; ¹**H-NMR** (CDCl₃, 300 MHz) ∂ 12.69 (bs, 1H), 9.43 (bs, 1H), 8.54 (d, 1H), 7.63 (m, 3H), 7.40 (m, 2H), 7.01 (d, 1H), 2.50 (s, 3H); ¹³**C-NMR** (CDCl₃, 75 MHz) ∂ 176.6, 167.1, 158.0, 150.6, 138.2, 135.1, 134.2, 133.3, 130.2, 128.2, 121.4, 113.5, 24.4; **MP** 146-148°C.

1-(3-nitrobenzoyl)-3-(2-pyridyl)thiourea (30)

2.937 g crude **16a** were added to a stirred solution of 2-aminopyridine (0.941 g, 10 mmol) in 15 mL dry THF. The reaction was stirred overnight, at room temperature, and then ca. 10 mL water were added, until permanent cloudiness was achieved. The reaction continued to stir for 1 hr, at which point the pumpkin-orange precipitate (R_f = 0.41; CH_2Cl_2 /silica) was filtered over a Buchner funnel, washed with water (2 x 10 mL), and allowed to air-dry (2.42 g, 81% yield from the acid chloride). After drying, the color of the precipitate was deep ochre-yellow.

300

Pale yellow needles suitable for X-ray analysis were grown from methanol. **IR** (KBr, cm⁻¹) 3473 (br), 3224, 3093, 1672, 1602, 1558, **1526**, 1457, 1349, 1252, 1150, 1111, 790, 713; ¹**H NMR** (600 MHz, CDCl₃) ∂ 12.84 (bs, 1H), 9.10 (bs, 1H), 8.81 (d, 1H), 8.77 (s, 1H), 8.51 (d, 1H), 8.48 (d, 1H), 8.26 (d, 1H), 7.79 (m, 2H), 7.20 (t, 1H); ¹³**C NMR** (75 MHz, CDCl₃) ∂ 176.3, 164.1, 151.0, 148.7, 137.9, 133.5, 133.2, 130.6, 128.1, 122.7, 121.8, 116.1, 110.0; **MP** (DSC) 175.8°C.

30N

Deep yellow crystalline solids could be reproducibly prepared from a variety of solvents, including MeCN, NO2Me, and acetone. **IR** (KBr, cm⁻¹) 3318, 3060, 1701, 1603, 1559 **1525**, 1479, 1426, 1347, 1322, 1266, 1247, 1153, 784, 713; ¹**H NMR** (300 MHz, CDCl₃ / 0.05 M DMSO-d₆) ∂ 15.69 (s, 1H), 11.05 (s, 1H), 8.81 (s, 1H), 8.26 (m, 3H), 7.59 (m, 2H), 7.13 (d, 1H), 6.98 (m, 1H); **MP** (DSC) 173.0°C.

1-(4-nitrobenzoyl)-3-(2-pyridyl)thiourea (31)

2.0 g crude **18a** was added to a stirred solution of 2-aminopyridine (0.941 g, 10 mmol) in 15 mL dry THF. The reaction was stirred for 1.5 h, at room temperature, and \sim 5 mL water were added, until permanent cloudiness was achieved. The reaction continued to stir for 1 hr, at which point the pumpkin-orange precipitate was filtered over a Buchner funnel, washed with water (2 x 10 mL), and allowed to air-dry (2.30 g, 76% yield from the acid

chloride). An analytical sample was prepared by recrystallization from acetonitrile. **IR** (KBr, cm⁻¹) 3456 (br), 3318, 1703, **1604**, 1559, 1518, 1481, 1345, 1324, 1247; ¹**H NMR** (300 MHz, CDCl₃, conformer **O**) ∂ 12.90 (bs, 1H), 9.03 (bs, 1H), 8.83 (d, 1H), 8.50 (dd, 1H), 8.42 (dt, 2H), 8.11 (d, 2H), 7.82 (td, 1H), 7.21 (dd, 1H); ¹³**C NMR** (75 MHz, DMSO-d₆) ∂ 178.3, 167.8, 151.9, 150.5, 149.2, 138.9, 130.9, 124.1, 122.3, 116.3; **MP** 178-180°C.

1-(2-methoxybenzoyl)-3-(2-pyridyl)thiourea (32)

To a stirred solution of 2-aminopyridine (490 mg, 5.2 mmol) in 15 mL dry THF (4 Å molecular sieves) was added 1.00 g (5.2 mmol) **19a**. The reaction was stirred overnight, at room temperature, and ~10 mL water were added, until permanent cloudiness was achieved. The reaction continued to stir for 1 hr, at which point the colorless, needle-like precipitate was filtered over a Buchner funnel, washed with water (2 x 10 mL), and allowed to air-dry (1.19 g, 80%). In order to expedite drying, the product could be transferred to a watch glass, and placed on top of a hot oven (ambient temperature ~ 100 °C) with no apparent decrease in either yield or purity. A glassy, amorphous solid suitable for X-ray analysis was grown via slow evaporation from dichloroethane/hexanes. **IR** (KBr, cm⁻¹) 3294, 3024 (br), 1660, 1578, **1540**, 1480, 1439, 1339, 1148, 1005, 753, 476; **¹H NMR** (CDCl₃, 300 MHz) ∂ 13.35 (bs, 1H), 11.15 (bs, 1H), 8.89 (d, J = 8.7 Hz, 1H), 8.49 (m, 1H), 8.24 (dd, J = 7.8, 1.8 Hz, 1H), 7.74 (td, J = 7.2, 1.8 Hz, 1H), 7.59 (m, 1H), 7.15 (m, 2H), 7.06 (d, J = 8.7 Hz, 1H), 4.10 (s, 3H); ¹³C **NMR** (CDCl₃,75 MHz) ∂ 177.6, 164.7, 158.0, 151.7, 148.8, 137.8, 135.6, 133.1, 122.1, 121.6, 119.0, 116.2, 112.0, 56.7; **MP** 136-138°C.

1-(4-methoxybenzoyl)-3-(2-pyridyl)thiourea (33)

To a stirred solution of **20a** (0.97 g, 5 mmol) in 20 mL THF was added 0.47 g (5 mmol) 2-aminopyridine; the reaction was stirred for 16 hours (*i.e.* overnight) at room temperature, and ca. 15 mL water were added to precipitate the product. After the addition of water, the reaction was stirred for an additional hour, and the fluffy, white, crystalline needles were filtered over a Buchner funnel, washed with water, and air-dried

to constant weight, 1.198 g (77%, 2 steps). As prepared, the product was suitable for spectral analysis; colorless prisms suitable for X-ray diffraction were grown from ethyl acetate / hexanes. **IR** (KBr, cm⁻¹) 3276 (br), 3010, 2848, 1666, 1603, 1577, **1534**, 1504, 1438, 1336, 1252, 1171, 1164, 1032, 840, 616; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 13.20 (bs,1H), 9.02 (bs, 1H), 8.82 (d, 1H), 8.44 (d, 1H), 7.88 (d, 2H), 7.77 (m, 1H), 7.16 (dd, 1H), 7.01 (dt, 2H), 3.89 (s, 3H); ¹³**C NMR** (CDCl₃, 75 MHz) ∂ 177.5 (C=S), 166.1 (C=O),164.3 (C-OCH₃), 151.6, 148.9, 137.9, 130.0, 123.7, 121.7, 116.3, 114.7, 55.9; **EA** Calc. C, 58.52; H, 4.56; N, 14.62; Found C, 58.37; H, 4.66; N, 14.67; **MP** 155-156 °C; **R**_f = 0.58 (CH₂Cl₂/silica).

1-(3-chlorobenzoyl)-3-(2-pyridyl)thiourea (34)

To 2.1 g crude **21a** in 20 mL THF was added 0.941 g (10 mmol) 2-aminopyridine; the reaction was stirred for 16 hours (*i.e.* overnight) at room temperature, and ca. 15 mL water were added to precipitate the product. After the addition of water, the reaction was stirred for an additional hour, and the fluffy, white needles were filtered over a Buchner funnel, washed with water, and air-dried to constant weight, 2.24 g (77%, 2 steps). As prepared, the product was suitable for spectral analysis; colorless needles were grown from ethanol/hexanes. **IR** (KBr, cm⁻¹) 3224 (br), 3023, 1673, 1552, **1533**, 1440, 1341, 1251, 1167, 771, 784, 738; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 113.02 (bs, 1H), 9.53 (bs, 1H), 8.75 (d, 1H), 8.42 (d, 1H), 7.93 (s, 1H), 7.78 (m, 2H), 7.57 (dq, 1H), 7.44 (t, 1H), 7.16 (dd, 1H); ¹³**C NMR** (CDCl₃, 75 MHz) ∂ 176.8, 165.3, 151.2, 148.8, 135.7, 133.9, 133.6, 130.6, 128.1, 125.6, 121.8, 116.2; **MP** 148-150°C; **R**_f 0.15 (CH₂Cl₂/silica).

1-(4-chlorobenzoyl)-3-(2-pyridyl)thiourea (35)

To 1.432 g crude **22a** in 20 mL THF was added 0.941 g (10 mmol) 2-aminopyridine; the reaction was stirred for 16 hours (*i.e.* overnight) at room temperature, and ca. 15 mL water were added to precipitate the product. After the addition of water, the reaction was stirred for an additional hour, and the fluffy, pale yellow product was filtered over a Buchner funnel, washed with water, and air-dried to constant weight, 1.832 g (63%, 2 steps). As prepared, the product was suitable for spectral analysis; colorless, columnar

crystals were grown from the slow evaporation of a chloroform solution. **IR** (KBr, cm⁻¹) 3355, 3256, 3032, 1676, **1523**, 1438, 1335, 1162, 1120, 1094, 762, 745; ¹**H NMR** (CDCl₃, 600 MHz) ∂ 13.08 (bs, 1H), 9.02 (bs, 1H), 8.81 (d, 1H), 8.45 (d, 1H), 7.86 (d, 2H), 7.80 (t, 1H), 7.52 (d, 2H), 7.19 (dd, 1H); ¹³**C NMR** (CDCl₃, 75 MHz) ∂ 176.8, 165.4, 151.2, 148.6, 140.3, 137.7, 130.0, 129.5, 129.0, 121.6, 116.1; **MP** 140-142°C (dec.)

1-(3-cyanobenzoyl)-3-(2-pyridyl)thiourea (36)

To 1.0 g (5.2 mmol) crude **23a** in 10 mL THF was added 0.49 g (5.2 mmol) 2-aminopyridine; the reaction was stirred for 16 hours (*i.e.* overnight) at room temperature, and ca. 15 mL water were added to precipitate the product. After the addition of water, the reaction was stirred for an additional hour, and the fluffy, pale yellow product was filtered over a Buchner funnel, washed with water, and air-dried to constant weight, 1.1 g (75%, 3 steps). As prepared, the product was suitable for spectral analysis; colorless needles were grown from DMF. **IR** (KBr, cm⁻¹) 3217 (br), 3064, 3032, 2236, 1675, **1534**, 1444, 1349, 1282, 1261, 1191, 1156, 1147, 898, 776, 742, 687; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 12.92 (bs, 1H), 9.18 (bs, 1H), 8.81 (d, 1H), 8.47 (d, 1H), 8.26 (s, 1H), 8.16 (d, 1H), 7.94 (d, 1H), 7.81 (t, 1H), 7.71 (t, 1H), 7.21 (t, 1H); ¹³C **NMR** (CDCl₃, 75 MHz) ∂ 176.5, 164.5, 151.0, 148.7, 137.9, 136.6, 133.1, 131.7, 131.4, 130.2, 127.8, 117.3, 116.2, 113.9; **MP** 149-151°C (dec.)

1-(4-cyanobenzoyl)-3-(2-pyridyl)thiourea (37)

To a stirred solution of crude **24a** in 10 mL MeCN were added 0.54 g (5 mmol) 2-amino-6-methylpyridine. Upon addition, the reaction mixture turned dark red, and, ca. 10 minutes later, an orange solid suddenly precipitated. Additional MeCN was added to loosen the stir bar (10 mL), and the reaction was stirred for 2 hours at room temperature. The solvent was removed on the rotatory evaporator, yielding 1.493 g of a pale yellow solid (70%, 3 steps), which crystallized in the NMR tube. Single crystals suitable for X-ray analysis were grown from CH₂Cl₂ (**37a**), IPA/acetone (**37b**), and CDCl₃ (**37c**). **IR** (KBr, cm-1) 3352, 2231, 1672, 1556, **1532**, 1156, 1123, 755; ¹**H NMR** (CDCl₃, 300

MHz) ∂ 12.91 (bs, 1H), 9.04 (bs, 1H), 8.81 (d, 1H), 8.47 (d, 1H), 8.04 (d, 2H), 7.86 (dd, 2H), 7.81 (td, 1H), 7.21 (dd, 1H); ¹³C NMR (CDCl₃, 75 MHz) ∂ 176.3, 164.6, 151.1, 148.8, 148.6, 137.8, 135.6, 132.9, 128.2, 121.9, 121.6, 117.3, 116.1, 116.0; MP 181-185°C (37c; dec.)

1-(3,4-dichlorobenzoy)-3-(2-pyridyl)thiourea (38)

To 1.3 g (5.6 mmol) **25a** in 10 mL THF was added 0.53 g (5.6 mmol) 2-aminopyridine; the reaction was stirred for 16 hours (*i.e.* overnight) at room temperature, and ca. 10 mL water were added to precipitate the product. After the addition of water, the reaction was stirred for an additional hour, and the white solids were collected via vacuum filtration, washed with water, and air-dried to constant weight, 1.62 g (89%, 2 steps). As prepared, the product was suitable for spectral analysis; colorless needles were grown from CH₂Cl₂/acetone. **IR** (KBr, cm⁻¹) 3324, 3011, 1674, 1580, **1526**, 1455, 1440, 1384, 1345, 1253, 1171, 1149, 1140, 1031, 746; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 12.91 (bs, 1H), 8.90 (bs, 1H), 8.81 (d, 1H), 8.45 (d, 1H), 8.02 (d, 1H); 7.79 (td, 1H), 7.73 (dd, 1H), 7.64 (d, 1H), 7.19 (dd, 1H); ¹³**C NMR** (DMSO-d₆, 151 MHz) ∂ 178.1, 166.7, 151.6, 148.8, 138.6, 136.5, 136.3, 133.1, 131.8, 131.2, 129.3, 122.0, 116.1; **MP** 194-195°C (dec.)

1-(3,5-dichlorobenzoyl)-3-(2-pyridyl)thiourea (39)

To 2.05 g crude **26a** in 15 mL THF was added 0.94 g (10 mmol) 2-aminopyridine; the reaction was stirred for 18 hours (*i.e.* overnight) at room temperature, and the solvent was removed on the rotovap. The yellow residue was dissolved in 20 mL acetone, then 10 mL water were added, and the chunky yellow precipitate was filtered over a vacuum, and dried to constant weight. 1.957 g (62%, 2 steps) of a bright yellow solid were isolated; as prepared, the product was suitable for spectral analysis. Slender yellow prisims were grown from acetonitrile. **IR** (KBr, cm⁻¹) 3243 (br), 3067, 1702, 1606, 1565, 1530, 1478, 1427, 1324, 1269, 1237, 1204, 872, 774, 748; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 12.85 (bs,1H); 8.91 (bs, 1H), 8.82 (d, 1H), 8.47 (d, 1H), 7.81 (m, 3H), 7.65 (t, 1H), 7.21 (t, 1H); ¹³**C NMR** (CDCl₃, 75 MHz) ∂ 177.0, 165.2, 151.2, 148.5, 137.6, 135.4, 132.8, 127.0, 126.5, 121.4, 116.2; **EA** Calc. C, 47.87; H, 2.78; N, 12.88; S, 9.83; Found C, 47.95; H,

1-(4-bromobenzoyl)-3-(2-pyridyl)thiourea (40)

To 2.0 g (8.6 mmol) crude **27a** in 15 mL THF was added 0.844 g (8.6 mmol) 2-aminopyridine; the reaction was stirred for 72 hours (*i.e.* over the weekend) at room temperature, then 25 mL water were added, and the mixture was stirred for 0.5 h. The precipitate was collected over a Buchner funnel, washed with water (2 x 15 mL) and ethanol (3 x 5 mL), and dried over a vacuum to yield 1.82 g (54%, 2 steps) of a pale yellow solid; as prepared, the product was suitable for spectral analysis. Slender, colorless columns were grown from acetonitrile. **IR** (KBr, cm⁻¹) 3438, 3049, 1675, 1585, **1551**, 1512, 1483, 1436, 1154, 1121, 1008, 743, 579; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 13.03 (bs, 1H), 8.96 (bs, 1H), 8.83 (d, 1H), 8.50 (d, 1H), 7.81 (m, 3H), 7.71 (d, 2H), 7.19 (dd, 1H); ¹³**C NMR** (CDCl₃, 75 MHz) ∂ 176.9, 165.7, 151.3, 148.8, 137.9, 132.7, 130.6, 129.3, 129.2, 121.8, 116.3; **EA** Calc. C, 46.44; H, 3.00; N, 12.50; O, 4.76; S, 9.54; Br, 23.77; Found C, 46.30; H, 2.90; N, 12.47; **MP** 160-161°C (dec.)

1-(2-bromobenzoyl)-3-(2-pyridyl)thiourea (41) To 1.21 g (5 mmol) **28a** in 15 mL THF was added 0.486 g (5 mmol) 2-aminopyridine; the reaction was stirred for 16 hours (*i.e.* overnight) at room temperature, then the solvent was removed on the rotovap, yielding 1.6 g of a pale yellow solid, which likely contained a residual amount of KCl. This solid was triturated with isopropanol, yielding 1.1 g of colorless needles (65%, 2 steps). The addition of water as the final step in the reaction sequence produced a biphasic solution, from which no solids could be precipitated, in both **28** and **41**, and it was therefore necessary to remove the reaction solvent, and recrystallize the crude product, in both cases. **IR** (KBr, cm⁻¹) 3243 (br), 3067, 1702, 1606, 1565, 1530, 1478, 1427, 1324, 1269, 1237, 1204, 872, 774, 748; ¹H NMR (CDCl₃, 300 MHz) ∂ 12.83 (bs, 1H), 9.09 (bs, 1H), 8.82 (d, 1H), 8.50 (d, 1H), 7.80 (dt, 1H), 7.78 (td, 2H), 7.45 (m, 2H), 7.19 (dd, 1H); ¹³C NMR (CDCl₃, 75 MHz) ∂ 176.4, 166.7, 151.1, 148.5, 137.7, 134.7, 133.9, 133.1, 130.1, 127.9, 121.6, 119.4, 116.2; MP 104-106°C.

4-Trifluoromethylbenzoylisothiocyanate (42a)

[Not Isolated] To 1.9 g (9.1 mmol) trifluoromethylbenzoyl chloride in 15 mL MeCN was added 0.89 g KSCN. The reaction mixture was stirred for 1 hr; 10 mL Et₂O were added, and the reaction mixture was filtered through 4 cm x 4 cm Celite. The solvent was removed on the rotatory evaporator, yielding 1.948 g of an orange solid. ¹H NMR (CDCl₃, 300 MHz) ∂ 8.12 (d, J=8.4, 2H), 7.79 (d, J=8.4, 2H).

1-(4-trifluoromethylbenzoyl)-3-(2-pyridyl)thiourea (42)

To crude **42a** in 15 mL THF was added 0.856 g (9.1 mmol) 2-aminopyridine; the reaction was stirred for 16 hours (*i.e.* overnight) at room temperature. 10 mL water were added, and the mixture was left to sit over the weekend (72h). The precipitate was collected over a Buchner funnel, washed with water (2 x 15 mL), and dried over a vacuum to yield 2.358 g (80%, 2 steps) of a bright yellow solid; as prepared, the product was suitable for spectral analysis. Bright orange-yellow plates were grown from acetonitrile; while visually resembling analytical crystals, X-ray spectroscopy determined that these plates were mica-like, and could not be analyzed. **IR** (KBr, cm⁻¹) 3260, 1701, 1607, 1559, 1422, **1333**, 1272, 1248, 1114, 1069, 1017, 770, 766, 717, 693; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 12.97 (bs, 1H), 9.05 (bs, 1H), 8.82 (d, 1H), 8.47 (d, 1H), 8.04 (d, 1H), 7.81 (m, 3H), 7.20 (dd, 1H); ¹³**C NMR** (CDCl₃, 151 MHz) ∂ 176.7, 165.3, 151.3, 148.9, 138.0, 135.5, 135.2, 128.3, 126.5, 124.4, 121.9, 116.2; **MP** 158-160°C.

1-(3,5-Dichlorobenzoyl)-3-(5-methyl-2-pyridyl)thiourea (43)

3,5-dichlorobenzoylisothiocyanate was prepared from 2.09 g (10 mmol) of the acid chloride, as described for **26a**. The solvent was not removed from the isothiocyanate; instead, 1.08 g (10 mmol) 2-amino-5-methyl-pyridine were added directly to the MeCN / Et₂O / isothiocyanate filtrate. The mixture was stirred overnight, and then ca. 20 mL water were added to precipitate the product, which was a fluffy, pale-yellow solid, weighing 2.736 g (80%, 2 steps).

43N

A single crystal suitable for X-ray analysis was grown from MeOH. Single crystals were also grown from chloroform; however, these re-dissolved into solution before X-ray data could be collected. **IR** (KBr, cm⁻¹) 3438 (br), 3245, 3066, 2861, 1699, 1598, 1568, 1492, 1380, 1314, **1273**, 1240, 1199, 872, 811, 749; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 15.39 (bs, 1H), 8.66 (bs, 1H), 8.16 (s, 1H), 7.98 (d, 2H), 6.80 (d, J = 7.8 Hz, 2H), 2.35 (s, 3H); **MP** (DSC) 190.6 °C.

430

Clusters of fiberous needles were prepared from a toluene solution. **IR** (KBr, cm⁻¹) 3425, 3223, 1674, **1536**, 1432, 1389, 1357, 1255, 1164, 1122, 873, 825, 731, 699; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 12.76 (bs, 1H), 8.92 (bs, 1H), 8.64 (d, J=8.1 Hz, 1H), 8.28 (d, J=2.1 Hz, 1H), 7.76 (d, J=1.8 Hz, 2H), 7.63 (m, 2H), 2.37 (s, 3H); **MP** (DSC) 194.9 °C

1-Benzoyl-3-(3-methyl-2-pyridyl)thiourea (44)

To 1.55 g (8.4 mmol) crude benzoyl isothiocyanate in 15 mL THFwere added 0.84 mL (8.4 mmol) 2-amino-3-picoline. Upon addition of the amine, the reaction turned bright orange, and a significant amount of heat is evolved. The reaction was stirred overnight, water was added, and 2.03 g (89%) of a colorless solid were removed by vacuum filtration. Single crystals suitable for X-ray analysis were grown from ethanol / hexanes. **IR** (KBr, cm⁻¹) 3196 (br), 1670, 1599, 1577, **1521**, 1330, 1253, 1155, 777, 715, 672; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 12.97 (bs, 1H), 9.05 (bs, 1H), 8.82 (d, 1H), 8.47 (d, 1H), 8.04 (d, 1H), 7.81 (m, 3H), 7.20 (dd, 1H); ¹³**C NMR** (CDCl₃, 75 MHz) ∂ 180.0, 167.3, 149.9, 147.1, 140.1, 134.0, 131.8, 130.7, 129.4, 127.9, 123.8, 17.9; **MP** 131-133°C.

1-(4-Nitrobenzoyl)-3-(3-methyl-2-pyridyl)thiourea (45)

To 1.05 g (5 mmol) crude **18a** in 15 mL THFwere added 0.5 mL (5 mmol) 2-amino-3-picoline. Upon addition of the amine, the reaction turned bright orange, and a significant amount of heat is evolved. The cloudy orange reaction mixture was stirred overnight, water was added, and 1.392 g (88%) of a colorless solid were removed by vacuum filtration. Pale yellow prisms suitable for X-ray analysis were grown from acetonitrile. **IR**

(KBr, cm⁻¹) 3424 (br), 3223, 3068, 1673, 1605, **1527**, 1451, 1349, 1163, 1027, 1008, 872, 780, 723, 701; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 12.17 (bs, 1H), 9.74 (bs, 1H), 8.38 (d, 3H), 8.15 (m, 3H), 7.66 (d, 1H), 2.40 (s, 3H); ¹³**C NMR** (CDCl₃, 75 MHz) ∂ 179.9, 166.6, 150.2, 149.8, 146.3, 139.6, 138.1, 130.3, 123.4, 17.2. **MP** 178-180°C.

1-(2-Bromobenzoyl)-3-(3-methyl-2-pyridyl)thiourea (46)

To 1.44 g crude **28a** in 10 mL THF was added 0.6 mL (6 mmol) 2-amino-3-picoline. The reaction was stirred overnight, until TLC indicated that the starting material had completely disappeared. The solvent was removed on the rotatory evaporator, yielding 1.95 g of a light yellow powder (93%). Colorless needles suitable for X-ray analysis were grown from ethanol / hexanes. **IR** (KBr, cm⁻¹) 3160 (br), 1675, **1521**, 1452, 1339, 1246, 1160, 1028, 775, 745, 686, 651; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 12.07 (bs, 1H), 9.26 (bs, 1H), 8.42 (d, 1H), 7.66 (m, 3H), 7.42 (m, 2H), 7.25 (t, 1H), 2.41 (s, 3H); ¹³**C NMR** (CDCl₃, 75 MHz) ∂ 179.9, 166.6, 150.2, 149.8, 146.3, 139.6, 138.1, 130.3, 123.4, 17.2. **MP** 104-106°C.

N,N'-Bis(benzoyl)thiourea (47)

[Synthesis adapted from a literature procedure.²¹⁵] To a well-stirred solution of 0.76 g (10 mmol) thiourea and 0.28 mL (20 mmol) triethylamine in 20 mL acetonitrile, which had previously been dried over 4 Å molecular sieves, 2.3 mL benzoyl chloride (20 mmol) were added drop-wise. The mixture was heated to a gentle reflux, and after a few hours of stirring, the colorless thiourea-benzoyl chloride suspension became bright yellow. In the morning, the deep red-orange reaction mixture was homogeneous; however, TLC (CDCl₃ / silica) showed that the reaction had not gone to completion, and an additional equilvalent of triethylamine was added, in 10 mL MeCN. The reaction was stirred for 10 minutes, at which point TLC indicated that all of the benzoyl chloride had been consumed. The solvent was removed on the rotatory evaporator, and slender orange needles suitable for X-ray analysis were grown from iPrOH/H₂O (52%). IR (NaCl, cm⁻¹) 3064, 1716, 1661, 1600, 1521, 1479, 1296, 1257, 1155, 1066, 914, 700, 663; ¹H NMR (CDCl₃, 300 MHz) ∂ 11.78 (bs, 2H), 8.01 (d, 4H), 7.68 (t, 2H), 7.58 (t, 4H); ¹³C NMR

(CDCl₃, 75 MHz) ∂ 177.3, 165.8, 134.1, 132.1, 129.5, 128.0. **EA** Calc. C, 63.36; H, 4.25; N, 9.85; O, 11.25; S, 11.28; Found C, 63.38; H, 4.14; N, 9.97; **MP** 167-169 °C.

Chapter VIII

General Notes: Because thiadiazoles 49-53 were obtained as decomposition products, and never synthesized directly, synthetic data is not available. Characterization data, however, is detailed below.

1-(3,5-Dinitrobenzoyl)imido-[1,2,4]dithiazolo-[2,3-a]pyridine (49)

Long, slender, brown, columnar crystals suitable for X-ray analysis were obtained from DMF/H₂O. **IR** (NaCl, cm⁻¹) 3101, 1625, 1602, 1538, 1497, 1433, **1321**, 1266, 1155, 1087, 786, 752, 731, 719; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 9.55 (d, J = 1.8 Hz, 2H), 9.21 (t, J = 1.8 Hz, 1H), 8.58 (d, J = 6.3 Hz, 1H), 7.99 (m, 1H), 7.89 (d, 1H), 7.30 (m, 1H); **MP** 298°C.

1-(4-Methoxybenzoyl)imido-[1,2,4]dithiazolo-5-methyl-[2,3-a]pyridine (50)

Pale brown cubic crystals suitable for X-ray analysis were obtained from ethanol. **IR** (KBr, cm⁻¹) 1604, 1582, 1523, 1491, 1418, 1394, 1375, **1328**, 1258, 1162, 1025, 903, 776; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 8.37 (d, 2H), 8.05 (d, 1H), 7.78 (m, 1H), 6.98 (d, 2H), 6.92 (d, 1H), 3.85 (s, 3H), 2.80 (s, 3H); ¹³**C NMR** (CDCl₃, 75 MHz) ∂ 177.6, 175.8, 163.2, 156.4, 145.0, 137.5, 131.4, 131.3, 126.0, 116.7, 115.8, 113.7, 55.4, 20.6; **MP** 240-241°C.

1-(4-Trifluoromethylbenzoyl)imido-[1,2,4]dithiazolo-[2,3-a]pyridine (51)

Pale brown cubic crystals suitable for X-ray analysis were obtained from acetonitrile. Because this compound was obtained as a "lucky crystal," and we were not successful in reproducing it, limited spectral data is available. **IR** (KBr, cm⁻¹) 1607, 1559, **1333**, 1248, 1115.

1-Benzoylimido-[1,2,4]dithiazolo-8-methyl-[2,3-a]pyridine (52)

Yellow columnar crystals suitable for X-ray analysis were obtained from acetone / hexanes. **IR** (KBr, cm⁻¹) 1604, 1582, 1523, 1491, 1418, 1394, 1375, **1328**, 1258, 1162,

1025, 903, 776; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 8.44 (dt, 2H), 8.31 (d, 1H), 7.64 (dt, 1H), 7.50 (m, 3H), 7.05 (t, 1H), 6.92 (d, 1H), 2.69 (s, 3H); ¹³**C NMR** (CDCl₃, 75 MHz) ∂ 178.4, 171.2, 164.4, 156.3, 137.0, 133.4, 132.7, 130.3, 130.1, 129.8, 129.6, 128.5, 116.1, 17.7; **MP** 193-194°C.

1-(2-Bromobenzoyl)imido-[1,2,4]dithiazolo-[2,3-a]pyridine (53)

Clusters of fine brown prisms were obtained from ethanol / hexanes. **IR** (KBr, cm⁻¹) 3065, 3028, 1624, 1568, 1529, 1487, 1436, 1379, **1325**, 1264, 1205, 1022, 924, 777, 757; ¹**H NMR** (CDCl₃, 300 MHz) ∂ 8.47 (dt, 1H), 7.88 (ddd, 1H), 7.79 (dt, 1H), 7.71 (d, 1H), 7.43 (td, 1H), 7.33 (td, 1H), 7.18 (td, 1H); ¹³**C NMR** (CDCl₃, 75 MHz) ∂ 178.4, 171.2, 164.4, 156.3, 137.0, 133.4, 132.7, 130.3, 130.1, 129.8, 129.6, 128.5, 116.1, 17.7.

1-(3,5-dinitrobenzoyl)-3-(2-pyridyl)thiourea (54)

[Not Isolated]. Prepared on 10 mmol scale from the acid chloride, as described in the general procedure for BzPTU preparation in **Chapter VI**. Solvent was removed on the rotovap; crude spectral data is made available, as the product decomposed upon recrystallization. **IR** (KBr, cm-1) 3430, 3268, 3100,1704, 1606, 1540, 1480, 1422, **1344**, 1318, 1280, 1239, 1077, 786, 729, 706; ¹**H NMR** (DMSO-d₆, 300 MHz) ∂ 12.93 (bs, 1H), 12.47 (bs, 1H), 9.10 (d, 3H), 9.04 (s, 1H), 8.46 (d, 1H), 7.95 (t, 1H), 7.32 (t, 1H).

APPENDIX B

CRYSTALLOGRAPHIC DATA

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F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
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C7\ 0.0339(17)\ 0.0402(18)\ 0.043(2)\ 0.0074(16)\ 0.0145(17)\ 0.0052(14)
C8 0.0306(16) 0.0431(18) 0.0294(17) 0.0016(14) 0.0081(14) 0.0004(13)
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C10 0.078(3) 0.077(3) 0.066(3) -0.015(3) 0.035(3) -0.023(3)
C11\ 0.0369(18)\ 0.0371(19)\ 0.052(2)\ -0.0033(16)\ 0.0134(17)\ -0.0026(14)
C12 0.0337(18) 0.0380(18) 0.057(3) 0.0008(16) 0.0184(18) -0.0028(14)
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C14\ 0.044(2)\ 0.044(2)\ 0.060(3)\ -0.0036(18)\ 0.020(2)\ 0.0016(16)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
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H12B H -0.186(4) 0.536(4) 0.222(3) 0.068(10) Uiso 1 1 d . . .
H12C H -0.080(4) 0.594(4) 0.159(3) 0.069(10) Uiso 1 1 d . . .
H13A H 0.420(3) 0.383(3) 0.544(2) 0.033(6) Uiso 1 1 d . . .
H13B H 0.315(3) 0.351(3) 0.618(2) 0.038(7) Uiso 1 1 d . . .
H14A H 0.261(3) 0.553(3) 0.588(2) 0.035(6) Uiso 1 1 d . . .
H14B H 0.142(3) 0.442(3) 0.528(2) 0.034(6) Uiso 1 1 d . . .
H16A H 0.365(4) 0.782(4) 0.325(3) 0.065(10) Uiso 1 1 d . . .
H16B H 0.211(3) 0.731(3) 0.267(2) 0.047(8) Uiso 1 1 d . . .
H17A H 0.379(4) 0.747(4) 0.143(3) 0.082(12) Uiso 1 1 d . . .
H17B H 0.466(4) 0.625(4) 0.162(3) 0.076(11) Uiso 1 1 d . . .
H18A H 0.320(4) 0.534(5) -0.009(4) 0.097(14) Uiso 1 1 d . . .
H18B H 0.268(4) 0.461(4) 0.076(3) 0.077(11) Uiso 1 1 d . . .
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are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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refine special details
Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F<sup>2</sup>, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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S2 S -0.01248(5) 0.20786(4) -0.26049(3) 0.04179(15) Uani 1 1 d . . .
S3 S 0.47325(5) -0.33935(4) 0.00274(3) 0.04267(15) Uani 1 1 d . . .
N1 N 0.27683(17) -0.03391(11) -0.13424(8) 0.0390(4) Uani 1 1 d . . .
N2 N 0.2249(2) 0.07948(14) -0.01218(10) 0.0493(5) Uani 1 1 d . . .
N3 N 0.2466(2) 0.22520(16) 0.04973(11) 0.0536(5) Uani 1 1 d . . .
N4 N 0.0084(2) 0.02239(14) -0.21026(10) 0.0471(4) Uani 1 1 d . . .
N5 N -0.1207(2) 0.1272(2) -0.16156(13) 0.0680(7) Uani 1 1 d . . .
N6 N 0.2794(2) -0.31056(13) -0.10711(10) 0.0486(5) Uani 1 1 d . . .
N7 N 0.3656(2) -0.46891(13) -0.09247(10) 0.0495(5) Uani 1 1 d . . .
C1 C 0.3793(3) 0.01502(17) -0.08218(13) 0.0508(5) Uani 1 1 d . . .
C2 C 0.3250(3) 0.10723(17) -0.05190(13) 0.0493(5) Uani 1 1 d . . .
C3 C 0.1864(2) 0.13668(17) 0.03520(11) 0.0473(5) Uani 1 1 d . . .
C4 C 0.2204(3) 0.2953(2) 0.10264(14) 0.0611(6) Uani 1 1 d . . .
C5 C 0.3383(4) 0.2939(3) 0.16170(15) 0.0810(9) Uani 1 1 d . . .
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H5A H 0.3504 0.2258 0.1805 0.122 Uiso 1 1 calc R . .
H5B H 0.3203 0.3402 0.1968 0.122 Uiso 1 1 calc R . .
H5C H 0.4216 0.3146 0.1464 0.122 Uiso 1 1 calc R . .
C6 C 0.1968(6) 0.4001(3) 0.0715(2) 0.1147(16) Uani 1 1 d . . .
H6A H 0.1193 0.3982 0.0330 0.172 Uiso 1 1 calc R . .
H6B H 0.2789 0.4220 0.0556 0.172 Uiso 1 1 calc R . .
H6C H 0.1771 0.4472 0.1059 0.172 Uiso 1 1 calc R . .
C7 C 0.2572(2) 0.01982(16) -0.19927(11) 0.0447(5) Uani 1 1 d . . .
C8 C 0.1197(3) -0.00324(17) -0.24342(11) 0.0492(5) Uani 1 1 d . . .
C9 C -0.0427(2) 0.11528(16) -0.20713(10) 0.0414(4) Uani 1 1 d . . .
C10 C -0.1940(3) 0.2169(3) -0.14897(18) 0.0793(10) Uani 1 1 d . . .
C11 C -0.1228(4) 0.2702(3) -0.0862(3) 0.1103(14) Uani 1 1 d . . .
H11A H -0.0315 0.2909 -0.0920 0.165 Uiso 1 1 calc R . .
H11B H -0.1146 0.2250 -0.0470 0.165 Uiso 1 1 calc R . .
H11C H -0.1757 0.3296 -0.0785 0.165 Uiso 1 1 calc R . .
C12 C -0.3365(5) 0.1870(5) -0.1408(4) 0.192(3) Uani 1 1 d . . .
H12A H -0.3833 0.1525 -0.1820 0.288 Uiso 1 1 calc R . .
H12B H -0.3881 0.2473 -0.1334 0.288 Uiso 1 1 calc R . .
H12C H -0.3303 0.1421 -0.1016 0.288 Uiso 1 1 calc R . .
C13 C 0.3133(2) -0.13925(15) -0.14248(11) 0.0424(5) Uani 1 1 d . . .
C14 C 0.2626(3) -0.20562(15) -0.09174(12) 0.0474(5) Uani 1 1 d . . .
C15 C 0.3649(2) -0.37487(14) -0.07061(10) 0.0369(4) Uani 1 1 d . A .
C16 C 0.2798(2) -0.51346(15) -0.15280(11) 0.0490(5) Uani 0.473(6) 1 d P A 1
H16A H 0.2416 -0.4593 -0.1856 0.059 Uiso 0.473(6) 1 calc PR A 1
C17 C 0.3599(9) -0.5868(7) -0.1869(4) 0.099(3) Uani 0.473(6) 1 d P A 1
H17A H 0.4196 -0.5498 -0.2117 0.148 Uiso 0.473(6) 1 calc PR A 1
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H17C H 0.4156 -0.6295 -0.1524 0.148 Uiso 0.473(6) 1 calc PR A 1
C18 C 0.1658(7) -0.5636(6) -0.1258(3) 0.077(2) Uani 0.473(6) 1 d P A 1
H18A H 0.1037 -0.5123 -0.1142 0.116 Uiso 0.473(6) 1 calc PR A 1
H18B H 0.2042 -0.6024 -0.0850 0.116 Uiso 0.473(6) 1 calc PR A 1
H18C H 0.1153 -0.6085 -0.1606 0.116 Uiso 0.473(6) 1 calc PR A 1
C16A C 0.2798(2) -0.51346(15) -0.15280(11) 0.0490(5) Uani 0.527(6) 1 d P A 2
H16B H 0.1909 -0.4766 -0.1637 0.059 Uiso 0.527(6) 1 calc PR A 2
C17A C 0.3562(6) -0.5000(5) -0.2109(3) 0.0671(17) Uani 0.527(6) 1 d P A 2
H17D H 0.3725 -0.4283 -0.2172 0.101 Uiso 0.527(6) 1 calc PR A 2
H17E H 0.3015 -0.5276 -0.2529 0.101 Uiso 0.527(6) 1 calc PR A 2
H17F H 0.4439 -0.5353 -0.2001 0.101 Uiso 0.527(6) 1 calc PR A 2
C18A C 0.2527(7) -0.6243(4) -0.1422(3) 0.073(2) Uani 0.527(6) 1 d P A 2
H18D H 0.1841 -0.6309 -0.1135 0.110 Uiso 0.527(6) 1 calc PR A 2
H18E H 0.3376 -0.6570 -0.1198 0.110 Uiso 0.527(6) 1 calc PR A 2
H18F H 0.2188 -0.6562 -0.1863 0.110 Uiso 0.527(6) 1 calc PR A 2
H2N H 0.173(3) 0.032(2) -0.0254(15) 0.069(9) Uiso 1 1 d . . .
H3N H 0.314(3) 0.2410(19) 0.0279(13) 0.051(7) Uiso 1 1 d . . .
H4N H -0.008(3) -0.013(2) -0.1821(14) 0.052(7) Uiso 1 1 d . . .
H5N H -0.124(3) 0.083(2) -0.1386(14) 0.051(7) Uiso 1 1 d . . .
H6N H 0.229(3) -0.3294(19) -0.1398(14) 0.052(7) Uiso 1 1 d . . .
H7N H 0.414(3) -0.5066(19) -0.0695(13) 0.048(7) Uiso 1 1 d . . .
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H2B H 0.399(3) 0.138(2) -0.0229(14) 0.064(8) Uiso 1 1 d . . .
H4 H 0.145(3) 0.266(3) 0.1203(17) 0.085(10) Uiso 1 1 d . . .
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H7B H 0.260(2) 0.0885(18) -0.1897(11) 0.042(6) Uiso 1 1 d . . .
H8A H 0.114(2) -0.074(2) -0.2542(12) 0.052(7) Uiso 1 1 d . . .
H8B H 0.109(2) 0.0358(19) -0.2851(13) 0.055(7) Uiso 1 1 d . . .
H10 H -0.221(4) 0.248(3) -0.1877(19) 0.096(12) Uiso 1 1 d . . .
H13A H 0.407(3) -0.1478(18) -0.1391(12) 0.049(6) Uiso 1 1 d . . .
H13B H 0.274(3) -0.1591(19) -0.1846(13) 0.050(7) Uiso 1 1 d . . .
H14A H 0.165(3) -0.1928(19) -0.0947(13) 0.053(7) Uiso 1 1 d . . .
H14B H 0.313(3) -0.1922(19) -0.0465(14) 0.057(7) Uiso 1 1 d . . .
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C1\ 0.0508(13)\ 0.0367(11)\ 0.0586(14)\ -0.0088(10)\ -0.0048(11)\ -0.0042(9)
C2\ 0.0586(14)\ 0.0346(11)\ 0.0524(12)\ -0.0081(9)\ 0.0050(10)\ -0.0096(10)
C3 0.0485(12) 0.0435(11) 0.0467(11) 0.0103(9) 0.0017(9) -0.0019(9)
C4 0.0670(16) 0.0617(15) 0.0596(15) -0.0106(12) 0.0248(13) 0.0033(13)
C5 0.090(2) 0.096(2) 0.0594(16) -0.0269(16) 0.0205(15) 0.0086(18)
C6 0.193(5) 0.074(2) 0.089(2) -0.0002(19) 0.056(3) 0.055(3)
C7\ 0.0570(13)\ 0.0297(10)\ 0.0474(12)\ 0.0045(8)\ 0.0102(10)\ 0.0027(9)
C8\ 0.0710(15)\ 0.0363(11)\ 0.0366(11)\ 0.0036(9)\ 0.0017(10)\ 0.0060(10)
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C12 0.069(3) 0.267(8) 0.244(7) -0.136(6) 0.042(4) 0.007(4)
C13 0.0493(12) 0.0297(9) 0.0434(11) -0.0032(8) -0.0027(9) 0.0042(8)
C14\ 0.0635(15)\ 0.0289(10)\ 0.0447(12)\ 0.0014(8)\ -0.0024(10)\ 0.0066(9)
C15 0.0408(10) 0.0283(9) 0.0374(9) 0.0027(7) -0.0022(8) -0.0034(7)
C16\ 0.0591(13)\ 0.0316(10)\ 0.0446(11)\ -0.0021(8)\ -0.0186(10)\ 0.0011(9)
C17 0.117(6) 0.099(7) 0.069(4) -0.040(4) -0.008(4) 0.028(5)
C18 0.068(4) 0.077(5) 0.070(4) -0.002(3) -0.025(3) -0.021(3)
C16A \ 0.0591(13) \ 0.0316(10) \ 0.0446(11) \ -0.0021(8) \ -0.0186(10) \ 0.0011(9)
C17A 0.078(3) 0.065(4) 0.052(3) -0.012(2) -0.004(2) 0.002(3)
C18A 0.092(5) 0.040(3) 0.069(3) -0.004(2) -0.031(3) -0.022(3)
_geom_special_details
All esds (except the esd in the dihedral angle between two l.s. planes)
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are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds involving l.s. planes.

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C11 H11C 0.9800.?
C12 H12A 0.9800 . ?
C12 H12B 0.9800 . ?
C12 H12C 0.9800 . ?
C13 C14 1.508(3) . ?
C13 H13A 0.93(3) . ?
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C3 N2 C2 125.11(19) . . ?
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C2 N2 H2N 118(2) . . ?
C3 N3 C4 125.7(2) . . ?
C3 N3 H3N 116.8(17) . . ?
C4 N3 H3N 117.3(17) . . ?
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C9 N4 H4N 113.0(19) . . ?
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H8A C8 H8B 110(2) . . ? N5 C9 N4 115.1(2) . . ? N5 C9 S2 123.36(18) . . ? N4 C9 S2 121.54(17) . . ? N5 C10 C11 111.4(3) . . ? N5 C10 C12 108.7(4) . . ? C11 C10 C12 109.5(3) . . ? N5 C10 H10 109(2) . . ? C11 C10 H10 122(3) . . ? C12 C10 H10 95(2) . . ? C10 C11 H11A 109.5 . . ? C10 C11 H11B 109.5 . . ? H11A C11 H11B 109.5 . . ? C10 C11 H11C 109.5 . . ? H11A C11 H11C 109.5 . . ? H11B C11 H11C 109.5 . . ? C10 C12 H12A 109.5 . . ? C10 C12 H12B 109.5 . . ? H12A C12 H12B 109.5 . . ? C10 C12 H12C 109.5 . . ? H12A C12 H12C 109.5 . . ? H12B C12 H12C 109.5 . . ? N1 C13 C14 111.18(18) . . ? N1 C13 H13A 112.1(15) . . ? C14 C13 H13A 110.1(15) . . ? N1 C13 H13B 108.4(16) . . ? C14 C13 H13B 108.5(16) . . ? H13A C13 H13B 106(2) . . ? N6 C14 C13 110.7(2) . . ? N6 C14 H14A 108.1(15) . . ? C13 C14 H14A 108.5(15) . . ? N6 C14 H14B 108.5(15) . . ? C13 C14 H14B 110.1(15) . . ? H14A C14 H14B 111(2) . . ? N6 C15 N7 118.19(18) . . ? N6 C15 S3 121.75(15) . . ? N7 C15 S3 120.06(14) . . ? N7 C16 C17 111.1(3) . . ? N7 C16 C18 104.1(3) . . ? C17 C16 C18 112.4(5) . . ? N7 C16 H16A 109.7 . . ? C17 C16 H16A 109.7 . . ? C18 C16 H16A 109.7 . . ? C16 C17 H17A 109.5 . . ? C16 C17 H17B 109.5 . . ? H17A C17 H17B 109.5 . . ? C16 C17 H17C 109.5 . . ? H17A C17 H17C 109.5 . . ? H17B C17 H17C 109.5 . . ? C16 C18 H18A 109.5 . . ? C16 C18 H18B 109.5 . . ? H18A C18 H18B 109.5 . . ? C16 C18 H18C 109.5 . . ?

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N4 H4N S1 0.78(3) 2.56(3) 3.325(2) 167(2) 3
N5 H5N S1 0.75(3) 2.72(3) 3.435(3) 159(3) 3
N6 H6N S2 0.79(3) 2.68(3) 3.3812(19) 149(2) 2 544
N7 H7N S3 0.78(3) 2.58(3) 3.3477(19) 167(2) 3 645
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Refinement of F^2^ against ALL reflections. The weighted R-factor wR and goodness of fit S are based on F^2^, conventional R-factors R are based on F, with F set to zero for negative F^2^. The threshold expression of $F^2^- > 2 \operatorname{sigma}(F^2^-)$ is used only for calculating R-factors(gt) etc. and is not relevant to the choice of reflections for refinement. R-factors based on F^2^ are statistically about twice as large as those based on F, and R-

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- C3 N3 C4 129.73(17) . . ?
- C3 N3 H3N 113.7(15) . . ?

- C4 N3 H3N 115.6(14) . . ?
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- N2 C3 S1 120.78(14) . . ?
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- H9A C9 H9B 111.4(16) . . ?
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- N5 C11 C12 104.86(18) . . ?
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- C11 C12 H12B 107.8(15) . . ?
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- C11 C12 H12C 110.7(18) . . ?
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- C11 C14 H14C 109.0(15) . . ?
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- N7 C17 S3 119.37(14) . . ?

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H19A C19 H19B 104.3(19) . . ?

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C18 C21 H21C 111.3(14) . . ?

H21A C21 H21C 112(2) . . ?

H21B C21 H21C 106.4(19) . . ?

loop_

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C18 N7 C17 N6 5.2(3) . . . . ?
C18 N7 C17 S3 -175.68(17) . . . . ?
C17 N7 C18 C19 -69.6(3) . . . . ?
C17 N7 C18 C20 172.6(2) . . . . ?
C17 N7 C18 C21 54.9(3) . . . . ?
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_geom_hbond_angle_DHA
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N2 H2N S3 0.82(2) 2.99(2) 3.7561(17) 155.6(19) 3 666
N7 H7N S3 0.80(2) 2.60(2) 3.3847(17) 167.9(18) 3_676
N5 H5N S1 0.76(2) 2.78(2) 3.530(2) 169.0(2) 3_566
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cell length c
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reflns number total
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reflns threshold expression
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computing cell refinement
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                                'Bruker SAINT'
computing data reduction
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computing molecular graphics
                                   'Bruker SHELXTL'
_computing_publication_material 'Bruker SHELXTL'
refine special details
Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F<sup>2</sup>, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
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_refine_ls_weighting_scheme
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refine ls weighting details
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atom sites solution secondary
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atom sites solution hydrogens
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_atom_site_fract_y
_atom_site_fract z
atom site U iso or equiv
atom site adp type
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_atom_site_calc flag
atom site refinement flags
atom site disorder assembly
 atom site disorder group
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S2 S 0.08103(4) 0.17491(4) 0.70095(2) 0.03370(15) Uani 1 1 d . . .
S3 S -0.02035(5) 0.56788(5) 0.67694(3) 0.0542(2) Uani 1 1 d . . .
N1 N 0.32165(11) 0.39721(12) 0.70112(6) 0.0256(4) Uani 1 1 d . . .
N2 N 0.33446(14) 0.42886(15) 0.59491(6) 0.0313(4) Uani 1 1 d . . .
N3 N 0.21692(13) 0.37256(14) 0.53640(6) 0.0312(4) Uani 1 1 d . . .
N4 N 0.25502(13) 0.20528(13) 0.67494(7) 0.0323(4) Uani 1 1 d . . .
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C12 C 0.16100(15) 0.18742(14) 0.66092(7) 0.0271(5) Uani 1 1 d . . .
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C18 C -0.04220(17) 0.17523(18) 0.59220(9) 0.0381(6) Uani 1 1 d . . .
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C24 C -0.30515(19) 0.4167(2) 0.62044(9) 0.0449(7) Uani 1 1 d . . .
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into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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                               0.71073
_diffrn_radiation_type
                            MoK\a
diffrn radiation source
                             'fine-focus sealed tube'
diffrn radiation monochromator graphite
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diffrn measurement device type 'CCD area detector Bruker Apex'
diffrn measurement method
                                 'phi and omega scans'
_diffrn_detector_area_resol_mean ?
diffrn standards number
diffrn standards interval count ?
diffrn standards interval time?
 diffrn standards decay %
_diffrn_reflns_number
                             5522
_diffrn_reflns_av_R_equivalents 0.0198
diffrn reflns av sigmaI/netI
                              0.0281
diffrn reflns limit h min
                              -9
diffrn reflns limit h max
                              9
diffrn reflns limit k min
                              -10
diffrn reflns limit k max
                              10
diffrn reflns limit 1 min
                             -11
diffrn reflns limit 1 max
                              11
diffrn reflns theta min
                             2.33
diffrn reflns theta max
                             25.00
_reflns_number total
                            2000
_reflns_number gt
                            1597
_reflns_threshold_expression
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computing data collection
                               'Bruker SMART'
_computing_cell_refinement
                               'Bruker SMART'
_computing data reduction
                               'Bruker SAINT'
_computing_structure_solution
                                'Bruker SHELXTL'
computing structure refinement 'Bruker SHELXTL'
computing molecular graphics
                                  'Bruker SHELXTL'
computing publication material
                                 'Bruker SHELXTL'
_refine_special_details
Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2sigma(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
_refine_ls_structure_factor_coef_Fsqd
_refine_ls_matrix_type
refine ls weighting scheme
                                calc
refine ls weighting details
'calc w=1/[\s^2(Fo^2)+(0.0803P)^2+0.2634P] where P=(Fo^2+2Fc^2)/3'
_atom_sites_solution primary
                                direct
_atom_sites_solution_secondary
                                difmap
atom sites solution hydrogens
                                 geom
refine ls hydrogen treatment
                                mixed
_refine_ls_extinction_method
                               none
_refine_ls_extinction coef
refine ls number reflns
                              2000
```

```
refine ls number parameters
refine ls number restraints
_refine_ls_R_factor_all
                             0.0702
refine ls R factor gt
                             0.0557
refine ls wR factor ref
                               0.1571
refine ls wR factor gt
                              0.1442
refine ls goodness of fit ref 1.066
_refine_ls_restrained S all
                              1.066
_refine_ls_shift/su_max
                             0.000
refine ls shift/su mean
                              0.000
loop
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_atom_site_type symbol
_atom_site_fract_x
atom site fract y
atom site fract z
_atom_site_U_iso_or_equiv
_atom_site_adp_type
_atom_site_occupancy
_atom_site_symmetry_multiplicity
atom site calc flag
atom site refinement flags
atom site disorder assembly
 atom site disorder group
S1 S 0.45883(11) 0.00646(10) 0.23449(8) 0.0522(3) Uani 1 1 d . . .
N1 N 0.8447(3) 0.4522(3) 0.1267(3) 0.0462(6) Uani 1 1 d . . .
N2 N 0.6594(4) 0.2073(3) 0.1808(3) 0.0515(7) Uani 1 1 d . . .
N3 N 0.7064(3) 0.1080(3) -0.0213(3) 0.0472(6) Uani 1 1 d . . .
C1 C 0.9575(4) 0.6115(4) -0.1338(3) 0.0550(8) Uani 1 1 d . . .
H1A H 0.9393 0.5370 -0.1777 0.066 Uiso 1 1 calc R . .
H1B H 0.9334 0.7259 -0.2020 0.066 Uiso 1 1 calc R . .
C2 C 0.8152(4) 0.6193(4) 0.0216(4) 0.0570(8) Uani 1 1 d . . .
H2A H 0.8290 0.6982 0.0634 0.068 Uiso 1 1 calc R . .
H2B H 0.6829 0.6633 0.0125 0.068 Uiso 1 1 calc R . .
C3 C 0.7054(5) 0.4662(4) 0.2787(3) 0.0617(9) Uani 1 1 d . . .
H3A H 0.5799 0.5470 0.2650 0.074 Uiso 1 1 calc R . .
H3B H 0.7502 0.5135 0.3305 0.074 Uiso 1 1 calc R . .
C4 C 0.6768(6) 0.3050(5) 0.3786(4) 0.0706(10) Uani 1 1 d . . .
H4A H 0.6079 0.3212 0.4839 0.085 Uiso 1 1 calc R . .
H4B H 0.8048 0.2201 0.3797 0.085 Uiso 1 1 calc R . .
C5 C 0.5665(5) 0.2328(5) 0.3360(3) 0.0599(9) Uani 1 1 d . . .
H5A H 0.5593 0.1236 0.4085 0.072 Uiso 1 1 calc R . .
H5B H 0.4336 0.3111 0.3442 0.072 Uiso 1 1 calc R . .
C6 C 0.6161(4) 0.1147(3) 0.1255(3) 0.0404(6) Uani 1 1 d . . .
C7 C 0.8386(4) 0.1998(4) -0.1276(3) 0.0500(7) Uani 1 1 d . . .
H7A H 0.9471 0.1697 -0.0869 0.060 Uiso 1 1 calc R . .
H7B H 0.7713 0.3227 -0.1383 0.060 Uiso 1 1 calc R . .
C8 C 0.9154(5) 0.1587(5) -0.2818(3) 0.0644(9) Uani 1 1 d . . .
H8A H 0.9793 0.0353 -0.2697 0.077 Uiso 1 1 calc R . .
H8B H 0.8062 0.1902 -0.3220 0.077 Uiso 1 1 calc R . .
C9 C 1.0548(6) 0.2472(6) -0.3951(4) 0.0857(13) Uani 1 1 d . . .
H9A H 1.1002 0.2146 -0.4924 0.129 Uiso 1 1 calc R . .
```

```
H9B H 1.1644 0.2155 -0.3569 0.129 Uiso 1 1 calc R . .
H9C H 0.9913 0.3696 -0.4105 0.129 Uiso 1 1 calc R . .
H2N H 0.731(5) 0.271(4) 0.121(4) 0.063(10) Uiso 1 1 d . . .
H3N H 0.660(4) 0.064(4) -0.054(3) 0.049(8) Uiso 1 1 d . . .
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atom site aniso label
_atom_site_aniso U 11
_atom_site_aniso_U_22
atom site aniso U 33
atom site aniso U 23
atom site aniso U 13
 atom site aniso U 12
$1 0.0646(5) 0.0674(5) 0.0402(4) -0.0071(3) -0.0104(3) -0.0446(4)
N1 0.0478(14) 0.0497(14) 0.0440(13) -0.0145(11) -0.0034(11) -0.0243(11)
N2 0.0669(17) 0.0682(17) 0.0345(13) -0.0120(12) -0.0027(11) -0.0467(15)
N3 0.0547(15) 0.0661(16) 0.0372(13) -0.0149(11) -0.0072(11) -0.0378(13)
C1\ 0.0597(19)\ 0.0556(18)\ 0.0514(17)\ -0.0044(14)\ -0.0175(15)\ -0.0251(15)
C2\ 0.0452(17)\ 0.0520(18)\ 0.064(2)\ -0.0108(15)\ -0.0074(15)\ -0.0159(14)
C3 0.070(2) 0.072(2) 0.0518(18) -0.0274(16) 0.0044(16) -0.0404(18)
C4 0.096(3) 0.092(3) 0.0418(17) -0.0238(17) 0.0004(17) -0.059(2)
C5\ 0.076(2)\ 0.084(2)\ 0.0362(15)\ -0.0205(15)\ 0.0038(14)\ -0.0546(19)
C6 0.0441(15) 0.0486(15) 0.0349(14) -0.0069(11) -0.0123(11) -0.0223(12)
C7\ 0.0567(18)\ 0.0670(19)\ 0.0370(15)\ -0.0121(14)\ -0.0065(13)\ -0.0361(15)
C8 0.072(2) 0.094(3) 0.0449(17) -0.0240(17) -0.0037(16) -0.049(2)
C9 0.096(3) 0.125(4) 0.050(2) -0.022(2) 0.0060(19) -0.072(3)
_geom_special details
All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
loop
_geom_bond_atom_site_label 1
geom bond atom site label 2
_geom_bond_distance
_geom_bond_site_symmetry 2
 geom bond publ flag
S1 C6 1.692(3) . ?
N1 C1 1.461(4) 2 765 ?
N1 C2 1.467(4).?
N1 C3 1.477(4) . ?
N2 C6 1.340(3) . ?
N2 C5 1.460(4) . ?
N2 H2N 0.87(3) . ?
N3 C6 1.340(3) . ?
N3 C7 1.454(3) . ?
N3 H3N 0.83(3) . ?
```

```
C1 N1 1.461(4) 2_765 ?
C1 C2 1.503(4).?
C1 H1A 0.9900.?
C1 H1B 0.9900.?
C2 H2A 0.9900 . ?
C2 H2B 0.9900 . ?
C3 C4 1.476(4).?
C3 H3A 0.9900.?
C3 H3B 0.9900 . ?
C4 C5 1.519(4) . ?
C4 H4A 0.9900 . ?
C4 H4B 0.9900.?
C5 H5A 0.9900 . ?
C5 H5B 0.9900.?
C7 C8 1.506(4) . ?
C7 H7A 0.9900 . ?
C7 H7B 0.9900 . ?
C8 C9 1.491(4) . ?
C8 H8A 0.9900 . ?
C8 H8B 0.9900 . ?
C9 H9A 0.9800.?
C9 H9B 0.9800 . ?
C9 H9C 0.9800.?
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_geom_angle_site_symmetry 1
_geom_angle_site_symmetry_3
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C1 N1 C2 108.1(2) 2 765.?
C1 N1 C3 111.3(2) 2 765.?
C2 N1 C3 109.5(2) ...?
C6 N2 C5 123.3(2) . . ?
C6 N2 H2N 122(2) . . ?
C5 N2 H2N 114(2) . . ?
C6 N3 C7 125.6(2) . . ?
C6 N3 H3N 113(2) . . ?
C7 N3 H3N 120(2) . . ?
N1 C1 C2 111.5(3) 2_765 . ?
N1 C1 H1A 109.3 2 765 . ?
C2 C1 H1A 109.3 . . ?
N1 C1 H1B 109.3 2_765 . ?
C2 C1 H1B 109.3 . . ?
H1A C1 H1B 108.0 . . ?
N1 C2 C1 111.3(2) . . ?
N1 C2 H2A 109.4 . . ?
C1 C2 H2A 109.4 . . ?
N1 C2 H2B 109.4 . . ?
C1 C2 H2B 109.4 . . ?
H2A C2 H2B 108.0 . . ?
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```
N1 C3 C4 114.3(3) . . ?
N1 C3 H3A 108.7 . . ?
C4 C3 H3A 108.7 . . ?
N1 C3 H3B 108.7 . . ?
C4 C3 H3B 108.7 . . ?
H3A C3 H3B 107.6 . . ?
C3 C4 C5 116.3(3) . . ?
C3 C4 H4A 108.2 . . ?
C5 C4 H4A 108.2 . . ?
C3 C4 H4B 108.2 . . ?
C5 C4 H4B 108.2 . . ?
H4A C4 H4B 107.4 . . ?
N2 C5 C4 111.1(2) . . ?
N2 C5 H5A 109.4 . . ?
C4 C5 H5A 109.4 . . ?
N2 C5 H5B 109.4 . . ?
C4 C5 H5B 109.4 . . ?
H5A C5 H5B 108.0 . . ?
N3 C6 N2 117.0(2) . . ?
N3 C6 S1 120.5(2) . . ?
N2 C6 S1 122.4(2) . . ?
N3 C7 C8 110.9(2) . . ?
N3 C7 H7A 109.5 . . ?
C8 C7 H7A 109.5 . . ?
N3 C7 H7B 109.5 . . ?
C8 C7 H7B 109.5 . . ?
H7A C7 H7B 108.0 . . ?
C9 C8 C7 113.3(3) . . ?
C9 C8 H8A 108.9 . . ?
C7 C8 H8A 108.9 . . ?
C9 C8 H8B 108.9 . . ?
C7 C8 H8B 108.9 . . ?
H8A C8 H8B 107.7 . . ?
C8 C9 H9A 109.5 . . ?
C8 C9 H9B 109.5 . . ?
H9A C9 H9B 109.5 . . ?
C8 C9 H9C 109.5 . . ?
H9A C9 H9C 109.5 . . ?
H9B C9 H9C 109.5 . . ?
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_geom_torsion_site_symmetry 1
_geom_torsion_site_symmetry_2
_geom_torsion_site_symmetry_3
_geom_torsion_site_symmetry_4
 geom_torsion_publ_flag
C1 N1 C2 C1 57.2(4) 2 765 . . . ?
C3 N1 C2 C1 178.6(3) . . . . ?
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N1 C1 C2 N1 -59.2(4) 2_765 . . . ?
C1 N1 C3 C4 -79.6(4) 2 765 . . . ?
C2 N1 C3 C4 161.0(3) . . . . ?
N1 C3 C4 C5 -71.7(4) . . . . ?
C6 N2 C5 C4 166.0(3) . . . . ?
C3 C4 C5 N2 57.4(4) . . . . ?
C7 N3 C6 N2 -3.7(4) . . . . ?
C7 N3 C6 S1 177.6(2) . . . . ?
C5 N2 C6 N3 177.1(3) . . . . ?
C5 N2 C6 S1 -4.2(4) . . . . ?
C6 N3 C7 C8 178.9(3) . . . . ?
N3 C7 C8 C9 -179.0(3) . . . . ?
loop
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_geom_hbond_atom_site label H
_geom_hbond_atom_site_label_A
_geom_hbond_distance_DH
_geom_hbond_distance HA
_geom_hbond_distance_DA
_geom_hbond_angle_DHA
 geom hbond site symmetry A
N3 H3N S1 0.83(3) 2.65(3) 3.452(2) 163(3) 2 655
N2 H2N N1 0.87(3) 2.18(3) 2.911(3) 142(3).
_diffrn_measured_fraction_theta_max 0.998
diffrn reflns theta full
                              25.00
diffrn measured fraction theta full 0.998
_refine_diff_density_max 0.698
_refine_diff_density_min -0.247
_refine_diff_density_rms 0.052
#===END
data 7
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_chemical_name_systematic
?
                                ?
_chemical_name_common
                             ?
chemical melting point
                               ?
chemical formula moiety
chemical formula sum
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_chemical_formula_weight
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_atom_type_symbol
_atom_type_description
_atom_type_scat_dispersion_real
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_atom_type_scat_dispersion_imag
 atom type scat source
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'International Tables Vol C Tables 4.2.6.8 and 6.1.1.4'
'H' 'H' 0.0000 0.0000
'International Tables Vol C Tables 4.2.6.8 and 6.1.1.4'
'N' 'N' 0.0061 0.0033
'International Tables Vol C Tables 4.2.6.8 and 6.1.1.4'
'S' 'S' 0.1246 0.1234
'International Tables Vol C Tables 4.2.6.8 and 6.1.1.4'
_symmetry_cell_setting
                             Triclinic
_symmetry_space_group_name H-M P-1
loop
symmetry equiv pos as xyz
'x, y, z'
'-x, -y, -z'
_cell_length_a
                         7.5087(9)
_cell_length_b
                         9.4482(12)
cell length c
                         9.4581(12)
cell angle alpha
                           85.891(2)
_cell_angle_beta
                          76.883(2)
_cell_angle_gamma
                            82.603(2)
_cell_volume
                         647.42(14)
cell formula units Z
                             1
cell measurement temperature
                                 173(2)
_cell_measurement_reflns_used
                                2220
_cell_measurement_theta_min
                                2.18
_cell_measurement_theta_max
                                 27.43
_exptl_crystal_description
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exptl crystal colour
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exptl crystal size max
                             0.28
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                             0.23
_exptl_crystal_size_min
                             0.08
exptl crystal density meas
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exptl absorpt process details SADABS
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?
diffrn ambient temperature
                               173(2)
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```
diffrn radiation wavelength
                                0.71073
diffrn radiation type
                             MoK\a
_diffrn_radiation_source
                             'fine-focus sealed tube'
diffrn radiation monochromator graphite
diffrn measurement device type 'CCD area detector Bruker Apex'
diffrn measurement method
                                 'phi and omega scans'
 diffrn detector area resol mean?
_diffrn_standards number
_diffrn_standards_interval_count ?
diffrn standards interval time ?
diffrn standards decay %
diffrn reflns number
                             7305
diffrn reflns av R equivalents 0.0230
diffrn reflns av sigmaI/netI
                               0.0287
                               -9
diffrn reflns limit h min
diffrn reflns limit h max
                               9
diffrn reflns limit k min
                               -12
_diffrn_reflns_limit_k_max
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_diffrn_reflns_limit 1 min
                              -12
_diffrn_reflns_limit_l_max
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                              2.18
_diffrn_reflns_theta_min
diffrn reflns theta max
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reflns number total
                             2800
_reflns_number_gt
                            2351
reflns threshold expression
                               >2sigma(I)
                                'Bruker SMART'
computing data collection
computing cell refinement
                                'Bruker SMART'
                                'Bruker SAINT'
computing data reduction
_computing_structure_solution
                                 'Bruker SHELXTL'
_computing_structure_refinement 'Bruker SHELXTL'
computing molecular graphics
                                  'Bruker SHELXTL'
_computing_publication_material 'Bruker SHELXTL'
refine special details
Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
_refine_ls_matrix type
_refine_ls_weighting_scheme
                                 calc
refine ls weighting details
'calc w=1/[\s^2^(Fo^2^)+(0.0536P)^2^+0.1235P] where P=(Fo^2^+2Fc^2^-)/3
_atom_sites_solution_primary
                                 direct
atom sites solution secondary
                                 difmap
atom sites solution hydrogens
```

```
refine ls hydrogen treatment
                                refall
refine ls extinction method
                                none
_refine_ls extinction coef
refine ls number reflns
                               2800
refine ls number parameters
                                 228
refine ls number restraints
refine ls R factor all
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_refine_ls_R_factor_gt
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_refine_ls_wR_factor_ref
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refine ls wR factor gt
                              0.0964
refine ls goodness of fit ref 1.046
_refine_ls_restrained S all
                              1.046
_refine_ls_shift/su_max
                              0.001
refine ls shift/su mean
                              0.000
atom site label
_atom_site_type_symbol
_atom_site_fract x
_atom_site_fract_y
_atom_site_fract_z
atom site U iso or equiv
atom site adp type
_atom_site_occupancy
_atom_site_symmetry multiplicity
_atom_site_calc flag
atom site refinement flags
atom site disorder assembly
 atom site disorder group
S1 S 0.19140(6) 0.56239(4) 0.29176(4) 0.03720(15) Uani 1 1 d . . .
N1 N 0.13615(16) 0.09888(13) -0.01088(12) 0.0269(3) Uani 1 1 d . . .
N2 N 0.12567(18) 0.37221(14) 0.12038(14) 0.0315(3) Uani 1 1 d . . .
N3 N -0.08475(18) 0.40433(14) 0.33429(15) 0.0327(3) Uani 1 1 d . . .
C1 C -0.1552(2) 0.04375(17) -0.05910(17) 0.0307(3) Uani 1 1 d . . .
C2 C 0.0306(2) 0.09390(17) -0.12345(16) 0.0303(3) Uani 1 1 d . . .
C3 C 0.3196(2) 0.14434(18) -0.07466(18) 0.0341(4) Uani 1 1 d . . .
C4 C 0.3153(2) 0.30339(18) -0.11601(17) 0.0357(4) Uani 1 1 d . . .
C5 C 0.2941(2) 0.39593(18) 0.01334(17) 0.0346(4) Uani 1 1 d . . .
C6 C 0.0715(2) 0.43834(15) 0.24626(16) 0.0287(3) Uani 1 1 d . . .
C7 C -0.1987(2) 0.30277(17) 0.30236(17) 0.0308(3) Uani 1 1 d . . .
C8 C -0.3793(2) 0.30532(19) 0.41329(19) 0.0347(4) Uani 1 1 d . . .
C9 C -0.5038(2) 0.20519(18) 0.37778(17) 0.0320(3) Uani 1 1 d . . .
C10 C -0.6816(2) 0.2003(2) 0.49173(19) 0.0374(4) Uani 1 1 d . . .
C11 C -0.8081(3) 0.1026(2) 0.4550(2) 0.0451(4) Uani 1 1 d . . .
H2N H 0.079(2) 0.2996(19) 0.1085(18) 0.036(5) Uiso 1 1 d . . .
H3N H -0.107(2) 0.4304(18) 0.416(2) 0.034(5) Uiso 1 1 d . . .
H1A H -0.223(2) 0.0399(16) -0.1344(17) 0.028(4) Uiso 1 1 d . . .
H1B H -0.230(2) 0.1154(17) 0.0126(18) 0.031(4) Uiso 1 1 d . . .
H2A H 0.013(2) 0.1832(18) -0.1678(17) 0.029(4) Uiso 1 1 d . . .
H2B H 0.100(2) 0.0286(17) -0.1987(17) 0.028(4) Uiso 1 1 d . . .
H3A H 0.392(2) 0.1220(17) -0.0010(18) 0.032(4) Uiso 1 1 d . . .
H3B H 0.376(2) 0.0847(18) -0.158(2) 0.041(5) Uiso 1 1 d . . .
H4A H 0.424(3) 0.3198(18) -0.1802(19) 0.036(4) Uiso 1 1 d . . .
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H5B H 0.402(2) 0.3713(18) 0.0604(18) 0.037(4) Uiso 1 1 d . . .
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H7B H -0.223(2) 0.3261(18) 0.2069(19) 0.039(5) Uiso 1 1 d . . .
H8A H -0.349(3) 0.2779(19) 0.509(2) 0.045(5) Uiso 1 1 d . . .
H8B H -0.440(3) 0.397(2) 0.419(2) 0.051(5) Uiso 1 1 d . . .
H9A H -0.443(2) 0.1055(18) 0.3691(17) 0.033(4) Uiso 1 1 d . . .
H9B H -0.534(2) 0.2324(18) 0.2801(19) 0.040(5) Uiso 1 1 d . . .
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H10B H -0.651(3) 0.1666(19) 0.588(2) 0.047(5) Uiso 1 1 d . . .
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H11B H -0.745(3) 0.002(2) 0.444(2) 0.052(6) Uiso 1 1 d . . .
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F<sup>2</sup>, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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H11A H 0.3886(14) 0.9963(12) 0.2376(11) 0.040(4) Uiso 1 1 d . . .
H11B H 0.3852(16) 0.8921(12) 0.2011(13) 0.047(4) Uiso 1 1 d . . .
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H12A H 0.3774(14) 0.6317(12) 0.2780(11) 0.038(4) Uiso 1 1 d . . .
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into account individually in the estimation of esds in distances, angles
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goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2^2 > 2 \operatorname{sigma}(F^2^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
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N2 N 0.32742(16) 0.79707(17) 0.21947(16) 0.0213(3) Uani 1 1 d . . .
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atom site aniso U 22
atom site aniso U 33
atom site aniso U 23
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 atom site aniso U 12
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C4 0.0158(8) 0.0348(9) 0.0306(9) -0.0180(8) 0.0042(6) -0.0046(7)
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C9 0.0279(10) 0.0383(11) 0.0273(9) -0.0128(8) -0.0012(7) -0.0032(8)
C10\ 0.0184(8)\ 0.0340(10)\ 0.0430(11)\ -0.0226(9)\ 0.0015(7)\ -0.0027(7)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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C1 H1B 0.999(18) . ?
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C2 H2B 0.981(18) . ?
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C3 H3B 1.016(17) . ?
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N1 C1 C2 112.19(14) 2_676 . ?
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refine special details
Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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265

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C4 C 0.2243(2) 0.7071(2) 0.70655(15) 0.0305(3) Uani 1 1 d . . .
C5 C 0.3085(2) 0.58911(18) 0.61446(14) 0.0276(3) Uani 1 1 d . . .
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C7 C 0.3029(2) 0.88962(17) 0.20854(14) 0.0264(3) Uani 1 1 d . . .
C8 C 0.46963(19) 0.80663(16) 0.11929(13) 0.0245(3) Uani 1 1 d . . .
C9 C 0.6459(2) 0.80378(18) 0.12495(15) 0.0292(3) Uani 1 1 d . . .
C10 C 0.7992(2) 0.7260(2) 0.04439(16) 0.0332(3) Uani 1 1 d . . .
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H1A H 0.790(2) 0.8650(19) 0.5634(15) 0.024(4) Uiso 1 1 d . . .
H1B H 0.721(2) 0.838(2) 0.4475(16) 0.026(4) Uiso 1 1 d . . .
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H2B H 0.494(2) 0.918(2) 0.6868(17) 0.031(4) Uiso 1 1 d . . .
H3A H 0.098(2) 0.930(2) 0.5857(18) 0.033(4) Uiso 1 1 d . . .
H3B H 0.158(2) 0.955(2) 0.7046(17) 0.031(4) Uiso 1 1 d . . .
H4A H 0.105(3) 0.695(2) 0.7530(19) 0.044(5) Uiso 1 1 d . . .
H4B H 0.308(2) 0.668(2) 0.7733(18) 0.037(5) Uiso 1 1 d . . .
H5A H 0.335(2) 0.475(2) 0.6710(18) 0.034(4) Uiso 1 1 d . . .
H5B H 0.426(2) 0.6056(19) 0.5612(16) 0.024(4) Uiso 1 1 d . . .
H7A H 0.311(2) 0.996(2) 0.2128(16) 0.029(4) Uiso 1 1 d . . .
H7B H 0.193(2) 0.915(2) 0.1721(16) 0.026(4) Uiso 1 1 d . . .
H9 H 0.662(2) 0.855(2) 0.1835(19) 0.041(5) Uiso 1 1 d . . .
H10 H 0.921(3) 0.728(2) 0.0510(19) 0.042(5) Uiso 1 1 d . . .
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H12 H 0.588(3) 0.602(2) -0.1096(19) 0.041(5) Uiso 1 1 d . . .
H13 H 0.331(3) 0.730(2) 0.0258(18) 0.038(5) Uiso 1 1 d . . .
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C2 0.0256(7) 0.0243(7) 0.0257(7) -0.0045(5) -0.0071(5) -0.0095(5)
C3 0.0236(7) 0.0359(8) 0.0285(7) -0.0124(6) 0.0017(6) -0.0127(6)
C4 0.0316(8) 0.0394(8) 0.0235(7) -0.0047(6) 0.0004(6) -0.0200(7)
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C9 0.0342(8) 0.0297(7) 0.0267(7) -0.0036(6) -0.0071(6) -0.0145(6)
C10 0.0289(8) 0.0359(8) 0.0334(8) -0.0014(6) -0.0051(6) -0.0142(6)
C11 0.0331(8) 0.0319(8) 0.0262(7) -0.0029(6) 0.0014(6) -0.0110(6)
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C13 0.0307(8) 0.0320(8) 0.0249(7) -0.0039(6) -0.0057(6) -0.0140(6)
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All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles

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and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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N2 C5 1.4596(19).?
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- N2 C5 C4 115.31(13) . . ?
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- N2 C6 S1 119.45(10) . . ?
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Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
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on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
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H2B H -0.031(3) 0.5514(8) 0.623(2) 0.022(5) Uiso 1 1 d . . .
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H12 H 0.053(3) 0.6514(7) 0.410(2) 0.021(5) Uiso 1 1 d . . .
H1SA H 0.627(4) 0.2739(10) 1.018(3) 0.049(7) Uiso 1 1 d . . .
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H2SA H 0.080(4) 0.2299(11) 0.816(3) 0.052(8) Uiso 1 1 d . . .
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C3 0.0228(10) 0.0285(12) 0.0213(10) -0.0002(9) 0.0048(8) -0.0064(9)
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C12 0.0188(9) 0.0211(10) 0.0232(10) 0.0005(8) 0.0056(8) -0.0014(8)
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C1S 0.0426(14) 0.0305(13) 0.0442(15) 0.0088(12) 0.0119(12) 0.0045(11)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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refine special details
Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
refine ls matrix type
refine ls weighting scheme
                                 calc
refine ls weighting details
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C4 C 0.0854(3) -0.25957(12) -0.04777(19) 0.0518(5) Uani 1 1 d . . .
C5 C 0.3105(2) -0.05951(13) 0.0459(2) 0.0481(4) Uani 1 1 d . . .
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C7 C 0.36481(18) -0.03331(11) 0.29677(19) 0.0356(4) Uani 1 1 d . . .
C8 C 0.15253(15) -0.04837(8) 0.37486(14) 0.0251(3) Uani 1 1 d . . .
C9 C -0.04422(16) -0.15864(9) 0.28724(14) 0.0266(3) Uani 1 1 d . . .
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C2\ 0.0602(12)\ 0.0411(10)\ 0.0427(10)\ 0.0064(8)\ 0.0141(9)\ 0.0144(9)
C3 0.0500(10) 0.0498(11) 0.0294(8) 0.0016(7) 0.0087(8) 0.0186(8)
C4 0.0757(14) 0.0363(10) 0.0331(9) 0.0008(7) 0.0066(9) 0.0070(9)
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C7\ 0.0282(8)\ 0.0356(9)\ 0.0471(10)\ -0.0079(7)\ 0.0184(7)\ -0.0046(6)
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C9 0.0304(7) 0.0280(7) 0.0243(6) -0.0056(5) 0.0133(6) -0.0058(6)
C10\ 0.0423(9)\ 0.0305(8)\ 0.0367(8)\ -0.0034(6)\ 0.0154(7)\ 0.0008(7)
C11 0.0749(14) 0.0295(9) 0.0563(11) -0.0106(8) 0.0375(10) -0.0049(9)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
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H21B H 0.948(3) 0.3066(14) 0.2720(12) 0.065(7) Uiso 1 1 d . . .
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H21C H 0.825(2) 0.3564(11) 0.2129(11) 0.040(5) Uiso 1 1 d . . .

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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F^2. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
refine ls matrix type
refine ls weighting scheme
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C6 C 0.26432(13) 0.89522(13) 0.37644(13) 0.0247(2) Uani 1 1 d . . .
C7 C 0.43704(15) 0.74949(16) 0.20446(15) 0.0326(3) Uani 1 1 d . . .
C8 C 0.57630(14) 0.62740(15) 0.20949(15) 0.0306(3) Uani 1 1 d . . .
C9 C 0.73177(14) 0.69703(14) 0.16486(15) 0.0299(3) Uani 1 1 d . . .
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C13 C 1.01584(15) 0.65021(16) 0.09945(15) 0.0342(3) Uani 1 1 d . . .
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H3N H 0.4502(19) 0.7731(18) 0.3980(19) 0.039(4) Uiso 1 1 d . . .
H1 H 0.640(2) 0.7024(19) 0.6431(19) 0.045(4) Uiso 1 1 d . . .
H2 H 0.5568(19) 0.7753(18) 0.8667(19) 0.038(4) Uiso 1 1 d . . .
H3 H 0.311(2) 0.9214(19) 0.9273(19) 0.046(4) Uiso 1 1 d . . .
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H7A H 0.4695(18) 0.8387(18) 0.1082(19) 0.036(4) Uiso 1 1 d . . .
H7B H 0.3471(19) 0.7075(18) 0.2138(18) 0.038(4) Uiso 1 1 d . . .
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H9B H 0.7153(17) 0.7678(17) 0.2208(17) 0.034(4) Uiso 1 1 d . . .
H10A H 0.8434(19) 0.6021(19) 0.3878(19) 0.041(4) Uiso 1 1 d . . .
H10B H 0.751(2) 0.466(2) 0.409(2) 0.046(4) Uiso 1 1 d . . .
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H11B H 0.992(2) 0.312(2) 0.337(2) 0.050(5) Uiso 1 1 d . . .
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are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2^2 > 2 \operatorname{sigma}(F^2^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
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C6 C 0.0662(5) 0.0516(4) 0.18486(18) 0.0269(6) Uani 1 1 d . . .
C7 C -0.1074(5) 0.2115(4) 0.04308(18) 0.0295(6) Uani 1 1 d . . .
C8 C -0.0468(5) 0.3066(4) -0.04797(18) 0.0284(6) Uani 1 1 d . . .
C9 C 0.1761(5) 0.2891(4) -0.08688(19) 0.0329(6) Uani 1 1 d . . .
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H1B H -0.452(6) 0.731(4) 0.449(2) 0.044(9) Uiso 1 1 d . . .
H2A H -0.604(7) 0.567(5) 0.360(3) 0.063(11) Uiso 1 1 d . . .
H2B H -0.733(5) 0.479(4) 0.439(2) 0.028(8) Uiso 1 1 d . . .
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H4B H -0.052(5) 0.120(3) 0.3797(17) 0.016(6) Uiso 1 1 d . . .
H5A H -0.291(5) -0.111(4) 0.3210(18) 0.025(7) Uiso 1 1 d . . .
H5B H -0.028(5) -0.161(4) 0.3248(19) 0.026(7) Uiso 1 1 d . . .
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H12 H -0.305(7) 0.589(5) -0.211(3) 0.061(11) Uiso 1 1 d . . .
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N1 0.0356(13) 0.0350(13) 0.0204(11) -0.0024(9) -0.0044(9) -0.0021(10)
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N3 0.0242(13) 0.0371(13) 0.0287(13) -0.0026(10) 0.0007(10) -0.0074(10)
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geom special details
All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F<sup>2</sup>, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2^2 > 2 \operatorname{sigma}(F^2^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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H3N H 0.478(3) 0.599(2) 0.0952(11) 0.027(5) Uiso 1 1 d . . .
H4 H 0.078(3) 1.049(2) 0.0784(11) 0.032(5) Uiso 1 1 d . . .
H5 H 0.006(3) 0.8211(19) 0.0561(11) 0.030(5) Uiso 1 1 d . . .
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N2 0.0145(8) 0.0180(7) 0.0352(9) -0.0013(6) -0.0077(6) -0.0002(5)
N3 0.0178(7) 0.0144(7) 0.0312(9) -0.0016(6) -0.0061(6) -0.0011(5)
N4 0.0226(8) 0.0338(9) 0.0314(9) -0.0017(7) -0.0041(7) 0.0061(7)
C1 0.0248(10) 0.0233(9) 0.0358(11) 0.0002(8) -0.0023(8) -0.0058(7)
C2\ 0.0248(9)\ 0.0199(8)\ 0.0219(9)\ 0.0007(7)\ -0.0024(7)\ -0.0025(7)
C3 0.0312(10) 0.0174(8) 0.0290(10) -0.0004(7) -0.0055(8) -0.0015(7)
C4 0.0288(10) 0.0216(9) 0.0337(11) -0.0028(8) -0.0075(8) 0.0064(7)
C5 0.0198(9) 0.0220(8) 0.0347(10) -0.0012(7) -0.0067(8) 0.0011(7)
C6 0.0223(9) 0.0181(8) 0.0231(9) 0.0003(7) -0.0037(7) 0.0008(6)
C7\ 0.0164(8)\ 0.0196(8)\ 0.0227(9)\ 0.0002(7)\ -0.0019(7)\ 0.0001(6)
C8 0.0183(9) 0.0190(8) 0.0293(10) 0.0004(7) -0.0030(7) -0.0002(6)
C9 0.0182(9) 0.0191(8) 0.0243(9) 0.0002(7) -0.0022(7) -0.0014(6)
C10\ 0.0203(9)\ 0.0198(8)\ 0.0255(9)\ -0.0008(7)\ -0.0015(7)\ 0.0017(7)
C11 0.0171(8) 0.0274(9) 0.0240(9) 0.0015(7) -0.0006(7) 0.0045(7)
C12\ 0.0197(9)\ 0.0307(9)\ 0.0252(9)\ 0.0004(8)\ -0.0047(7)\ -0.0035(7)
C13\ 0.0255(10)\ 0.0234(9)\ 0.0339(11)\ -0.0023(8)\ -0.0065(8)\ -0.0039(7)
C14\ 0.0212(9)\ 0.0205(8)\ 0.0332(10)\ -0.0009(7)\ -0.0063(7)\ 0.0024(7)
_geom_special_details
All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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O2 N4 1.231(2) . ?
O3 N4 1.222(2) . ?
N1 C6 1.335(2) . ?
N1 C2 1.359(2) . ?
N2 C7 1.357(2) . ?
N2 C6 1.411(2) . ?
N2 H2N 0.84(2) . ?
N3 C7 1.372(2) . ?
N3 C8 1.394(2) . ?
N3 H3N 0.84(2) . ?
N4 C11 1.477(2) . ?
C1 C2 1.499(3) . ?
C1 H1A 0.95(2) . ?
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C1 H1C 1.00(2) . ?
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C3 C4 1.386(3) . ?
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C3 H3 0.95(2) . ?
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C4 H4 0.95(2) . ?
C5 C6 1.395(2).?
C5 H5 0.93(2) . ?
C8 C9 1.499(2) . ?
C9 C10 1.393(2) . ?
C9 C14 1.397(2) . ?
C10 C11 1.376(2) . ?
C10 H10 0.93(2) . ?
C11 C12 1.383(2).?
C12 C13 1.385(3).?
C12 H12 0.94(2) . ?
C13 C14 1.387(3) . ?
C13 H13 0.97(2) . ?
C14 H14 0.90(2) . ?
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geom angle publ flag
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C7 N2 C6 131.34(15) . . ?
C7 N2 H2N 115.6(13) . . ?
C6 N2 H2N 112.9(13) . . ?
C7 N3 C8 128.06(14) . . ?
C7 N3 H3N 111.5(14) . . ?
C8 N3 H3N 120.4(14) . . ?
O3 N4 O2 124.03(16) . . ?
O3 N4 C11 118.28(15) . . ?
O2 N4 C11 117.67(15) . . ?
C2 C1 H1A 113.3(14) . . ?
C2 C1 H1B 109.8(15) . . ?
H1A C1 H1B 110(2) . . ?
C2 C1 H1C 109.8(13) . . ?
H1A C1 H1C 107.3(19) . . ?
H1B C1 H1C 106.8(19) . . ?
N1 C2 C3 121.65(16) . . ?
N1 C2 C1 116.46(15) . . ?
C3 C2 C1 121.88(16) . . ?
C4 C3 C2 119.01(16) . . ?
C4 C3 H3 120.5(13) . . ?
C2 C3 H3 120.5(13) . . ?
C5 C4 C3 119.89(17) . . ?
C5 C4 H4 120.6(12) . . ?
C3 C4 H4 119.5(12) . . ?
C4 C5 C6 117.71(17) . . ?
C4 C5 H5 122.9(12) . . ?
C6 C5 H5 119.4(12) . . ?
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N1 C6 C5 123.37(16) . . ?
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C5 C6 N2 117.68(16) . . ?
N2 C7 N3 114.66(14) . . ?
N2 C7 S1 119.19(13) . . ?
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O1 C8 C9 121.38(15) . . ?
N3 C8 C9 114.40(14) . . ?
C10 C9 C14 118.87(16) . . ?
C10 C9 C8 116.29(15) . . ?
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C11 C10 H10 119.5(13) . . ?
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C10 C11 C12 123.16(16) . . ?
C10 C11 N4 118.55(15) . . ?
C12 C11 N4 118.29(16) . . ?
C13 C12 C11 117.81(17) . . ?
C13 C12 H12 121.5(13) . . ?
C11 C12 H12 120.7(13) . . ?
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C12 C13 H13 119.6(12) . . ?
C14 C13 H13 120.1(12) . . ?
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C6 N1 C2 C1 -177.81(16) . . . . ?
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C8 N3 C7 N2 171.78(16) . . . . ?
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C7 N3 C8 O1 5.4(3) . . . . ?
C7 N3 C8 C9 -174.95(16) . . . . ?
O1 C8 C9 C10 8.4(3) . . . . ?
N3 C8 C9 C10 -171.27(15) . . . . ?
O1 C8 C9 C14 -171.82(18) . . . . ?
N3 C8 C9 C14 8.5(3) . . . . ?
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C8 C9 C10 C11 178.10(16) . . . . ?
C9 C10 C11 C12 -0.8(3) . . . . ?
C9 C10 C11 N4 178.50(15) . . . . ?
O3 N4 C11 C10 168.50(17) . . . . ?
O2 N4 C11 C10 -12.6(2) . . . . ?
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O2 N4 C11 C12 166.77(17) . . . . ?
C10 C11 C12 C13 2.7(3) . . . . ?
N4 C11 C12 C13 -176.62(16) . . . . ?
C11 C12 C13 C14 -2.0(3) . . . . ?
C12 C13 C14 C9 -0.4(3) . . . . ?
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C8 C9 C14 C13 -177.50(17) . . . . ?
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_geom_hbond_distance_DA
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geom hbond site symmetry A
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'-x, -y, -z'
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cell length c
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diffrn reflns theta max
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computing cell refinement
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computing molecular graphics
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_refine_special_details
Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
```

```
on F^2^ are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
refine Is matrix type
_refine_ls_weighting_scheme
                                calc
_refine_ls_weighting_details
'calc w=1/[\s^2^(Fo^2^)+(0.1079P)^2^+0.1797P] where P=(Fo^2^+2Fc^2^)/3'
atom sites solution primary
                                direct
atom sites solution secondary
                                difmap
atom sites solution hydrogens geom
_refine_ls_hydrogen treatment
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refine ls extinction method
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_refine_ls_extinction coef
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 atom site disorder group
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O1 O 0.5733(8) 0.8644(2) 0.45784(16) 0.0413(7) Uani 1 1 d . . .
O2 O 0.4179(9) 0.6743(3) 0.81125(18) 0.0578(9) Uani 1 1 d . . .
O3 O 0.7991(9) 0.7903(3) 0.89686(18) 0.0639(10) Uani 1 1 d . . .
N1 N 0.2750(7) 0.7626(2) 0.21137(18) 0.0264(7) Uani 1 1 d . . .
N2 N 0.2559(8) 0.6971(3) 0.34156(19) 0.0293(7) Uani 1 1 d . . .
N3 N 0.4431(8) 0.6801(3) 0.48173(19) 0.0265(7) Uani 1 1 d . . .
N4 N 0.6523(9) 0.7550(3) 0.8250(2) 0.0361(8) Uani 1 1 d . . .
C1 C 0.3473(10) 0.8527(3) 0.0814(2) 0.0361(9) Uani 1 1 d . . .
H1A H 0.4865 0.9110 0.1250 0.054 Uiso 1 1 calc R . .
H1B H 0.1580 0.8853 0.0556 0.054 Uiso 1 1 calc R . .
H1C H 0.4956 0.8263 0.0353 0.054 Uiso 1 1 calc R . .
```

```
C2 C 0.1967(9) 0.7539(3) 0.1249(2) 0.0283(8) Uani 1 1 d . . .
C3 C -0.0123(10) 0.6586(3) 0.0782(2) 0.0328(9) Uani 1 1 d . . .
C4 C -0.1466(11) 0.5707(4) 0.1219(3) 0.0348(9) Uani 1 1 d . . .
C5 C -0.0691(10) 0.5787(3) 0.2106(2) 0.0321(9) Uani 1 1 d . . .
C6 C 0.1463(9) 0.6753(3) 0.2514(2) 0.0260(8) Uani 1 1 d . . .
C7 C 0.2923(9) 0.6258(3) 0.3995(2) 0.0254(8) Uani 1 1 d . . .
C8 C 0.5719(9) 0.7936(3) 0.5075(2) 0.0282(8) Uani 1 1 d . . .
C9 C 0.7138(9) 0.8298(3) 0.6004(2) 0.0256(8) Uani 1 1 d . . .
C10 C 0.6172(9) 0.7704(3) 0.6683(2) 0.0244(8) Uani 1 1 d . . .
C11 C 0.7567(9) 0.8159(3) 0.7519(2) 0.0268(8) Uani 1 1 d . . .
C12 C 0.9862(10) 0.9173(3) 0.7701(2) 0.0291(8) Uani 1 1 d . . .
C13 C 1.0754(10) 0.9759(3) 0.7029(2) 0.0303(9) Uani 1 1 d . . .
C14 C 0.9411(10) 0.9336(3) 0.6183(2) 0.0300(9) Uani 1 1 d . . .
H2N H 0.346(10) 0.768(3) 0.358(2) 0.035(11) Uiso 1 1 d . . .
H3N H 0.472(11) 0.637(4) 0.517(3) 0.050(14) Uiso 1 1 d . . .
H3 H -0.050(9) 0.654(3) 0.019(2) 0.033(10) Uiso 1 1 d . . .
H4 H -0.249(12) 0.507(4) 0.091(3) 0.060(15) Uiso 1 1 d . . .
H5 H -0.152(9) 0.524(3) 0.237(2) 0.027(10) Uiso 1 1 d . . .
H10 H 0.458(10) 0.707(3) 0.664(3) 0.039(11) Uiso 1 1 d . . .
H12 H 1.085(9) 0.943(3) 0.834(2) 0.033(10) Uiso 1 1 d . . .
H13 H 1.208(10) 1.038(4) 0.708(3) 0.038(12) Uiso 1 1 d . . .
H14 H 1.006(9) 0.973(3) 0.570(2) 0.036(11) Uiso 1 1 d . . .
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atom site aniso U 22
atom site aniso U 33
atom site aniso U 23
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 atom site aniso U 12
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O1 0.065(2) 0.0274(15) 0.0288(14) 0.0064(12) -0.0100(13) -0.0009(13)
O2 0.082(2) 0.0427(19) 0.0387(17) 0.0075(14) -0.0005(16) -0.0221(18)
O3 0.076(2) 0.081(3) 0.0258(16) 0.0094(15) -0.0119(16) -0.0157(19)
N1 0.0261(16) 0.0270(17) 0.0264(16) 0.0021(12) -0.0014(13) 0.0075(13)
N2 0.0386(19) 0.0233(18) 0.0236(16) 0.0017(13) -0.0059(14) 0.0010(14)
N3 0.0340(17) 0.0210(17) 0.0231(16) 0.0027(13) -0.0044(13) 0.0022(13)
N4 0.044(2) 0.036(2) 0.0279(18) 0.0016(14) 0.0016(15) 0.0066(16)
C1\ 0.036(2)\ 0.040(2)\ 0.032(2)\ 0.0052(17)\ -0.0012(17)\ 0.0053(18)
C2\ 0.0269(19)\ 0.034(2)\ 0.0248(18)\ 0.0014(15)\ -0.0009(15)\ 0.0126(16)
C3 0.037(2) 0.036(2) 0.024(2) 0.0012(16) -0.0044(17) 0.0103(17)
C4 0.036(2) 0.032(2) 0.033(2) -0.0029(18) -0.0090(18) 0.0064(18)
C5 0.037(2) 0.026(2) 0.033(2) 0.0052(17) -0.0028(17) 0.0041(17)
C6 0.0264(18) 0.026(2) 0.0258(18) 0.0022(15) -0.0034(15) 0.0071(15)
C7\ 0.0197(17)\ 0.031(2)\ 0.0259(18)\ 0.0019(15)\ 0.0025(15)\ 0.0075(15)
C8 0.0295(19) 0.027(2) 0.0274(19) 0.0025(16) 0.0013(16) 0.0023(16)
C9 0.0291(19) 0.0222(19) 0.0258(18) 0.0006(14) -0.0022(15) 0.0088(15)
C10\ 0.0230(18)\ 0.0202(19)\ 0.0294(19)\ -0.0006(15)\ 0.0009(15)\ 0.0058(15)
C11\ 0.031(2)\ 0.027(2)\ 0.0240(18)\ 0.0023(15)\ 0.0004(15)\ 0.0099(16)
C12\ 0.0293(19)\ 0.029(2)\ 0.0263(19)\ -0.0049(15)\ -0.0045(16)\ 0.0077(16)
C13\ 0.028(2)\ 0.025(2)\ 0.035(2)\ 0.0000(16)\ 0.0002(17)\ 0.0021(17)
C14\ 0.034(2)\ 0.026(2)\ 0.030(2)\ 0.0022(16)\ 0.0020(17)\ 0.0042(16)
```

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_geom_special_details
All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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N1 C2 1.346(4).?
N2 C7 1.341(4).?
N2 C6 1.418(4).?
N2 H2N 0.87(4).?
N3 C8 1.374(5) . ?
N3 C7 1.405(4) . ?
N3 H3N 0.82(4) . ?
N4 C11 1.470(5).?
C1 C2 1.500(5).?
C1 H1A 0.9800.?
C1 H1B 0.9800 . ?
C1 H1C 0.9800 . ?
C2 C3 1.390(5) . ?
C3 C4 1.382(6) . ?
C3 H3 0.92(4) . ?
C4 C5 1.379(5) . ?
C4 H4 0.87(4) . ?
C5 C6 1.379(5).?
C5 H5 0.85(4) . ?
C8 C9 1.499(5).?
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C9 C14 1.401(5) . ?
C10 C11 1.384(5).?
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C11 C12 1.385(5) . ?
C12 C13 1.364(5) . ?
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C7 N2 C6 131.1(3) . . ?
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C8 N3 C7 128.4(3) . . ?
C8 N3 H3N 117(3) . . ?
C7 N3 H3N 114(3) . . ?
O3 N4 O2 123.4(3) . . ?
O3 N4 C11 118.0(3) . . ?
O2 N4 C11 118.5(3) . . ?
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C2 C1 H1B 109.5 . . ?
H1A C1 H1B 109.5 . . ?
C2 C1 H1C 109.5 . . ?
H1A C1 H1C 109.5 . . ?
H1B C1 H1C 109.5 . . ?
N1 C2 C3 121.8(3) . . ?
N1 C2 C1 116.4(3) . . ?
C3 C2 C1 121.7(3) . . ?
C4 C3 C2 119.1(4) . . ?
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C2 C3 H3 119(2) . . ?
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C5 C4 H4 121(3) . . ?
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C4 C5 C6 117.4(4) . . ?
C4 C5 H5 119(2) . . ?
C6 C5 H5 123(2) . . ?
N1 C6 C5 124.5(3) . . ?
N1 C6 N2 110.5(3) . . ?
C5 C6 N2 125.0(3) . . ?
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N3 C7 S1 118.6(3) . . ?
O1 C8 N3 122.6(3) . . ?
O1 C8 C9 119.8(3) . . ?
N3 C8 C9 117.6(3) . . ?
C10 C9 C14 119.6(3) . . ?
C10 C9 C8 123.8(3) . . ?
C14 C9 C8 116.5(3) . . ?
C11 C10 C9 117.9(3) . . ?
C11 C10 H10 116(3) . . ?
C9 C10 H10 125(3) . . ?
C10 C11 C12 123.0(3) . . ?
C10 C11 N4 118.7(3) . . ?
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C13 C12 H12 124(2) . . ?
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C12 C13 C14 120.4(4) . . ?
C12 C13 H13 125(3) . . ?
C14 C13 H13 115(3) . . ?
C13 C14 C9 120.6(3) . . ?
C13 C14 H14 121(2) . . ?
C9 C14 H14 118(2) . . ?
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_geom_torsion_site_symmetry_3
_geom_torsion_site_symmetry_4
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C7 N2 C6 C5 26.0(6) . . . . ?
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C8 N3 C7 N2 -3.9(5) . . . . ?
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O1 C8 C9 C14 -20.2(5) . . . . ?
N3 C8 C9 C14 159.9(3) . . . . ?
C14 C9 C10 C11 -1.2(5) . . . . ?
C8 C9 C10 C11 -177.2(3) . . . . ?
C9 C10 C11 C12 0.1(5) . . . . ?
C9 C10 C11 N4 179.0(3) . . . . ?
O3 N4 C11 C10 173.8(3) . . . . ?
O2 N4 C11 C10 -8.3(5) . . . . ?
O3 N4 C11 C12 -7.3(5) . . . . ?
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C10 C11 C12 C13 0.9(5) . . . . ?
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C11 C12 C13 C14 -0.7(5) . . . . ?
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refine diff density rms 0.125
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#
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                             monoclinic
symmetry space group name H-M 'P 21/c'
symmetry Int Tables number
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_symmetry_equiv_pos_as_xyz
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3 - x, -y, -z
4 \text{ x}, 1/2 - \text{y}, 1/2 + \text{z}
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cell length c
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atom site type symbol
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_atom_site_fract v
atom site fract z
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N3 N 0.17931(16) 0.51391(7) 0.17820(12)
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C5 C 0.06297(19) 0.32496(8) 0.07739(15)
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H3 H -0.170(3) 0.2473(11) 0.2610(19)
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#===END
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data 170
symmetry cell setting
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symmetry equiv pos as xyz
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4 - x, 1/2 + y, 1/2 - z
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atom site fract y
atom site fract z
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N1 N 0.52757(5) 0.2242(2) 0.15298(5)
N2 N 0.43544(6) 0.1194(2) 0.06708(5)
N3 N 0.35631(6) -0.1374(2) 0.00223(5)
C1 C 0.63022(8) 0.3008(3) 0.23902(8)
C2 C 0.56117(7) 0.3735(3) 0.19990(6)
C3 C 0.53387(7) 0.5835(3) 0.21147(7)
C4 C 0.47043(7) 0.6418(3) 0.17296(7)
C5 C 0.43515(7) 0.4896(3) 0.12476(7)
C6 C 0.46631(6) 0.2829(2) 0.11719(6)
C7 C 0.37622(6) 0.0224(2) 0.05191(6)
C8 C 0.39415(6) -0.2414(2) -0.02676(6)
C9 C 0.36042(6) -0.4242(2) -0.07530(6)
C10 C 0.39849(7) -0.6088(3) -0.08405(6)
C11 C 0.36993(7) -0.7871(3) -0.12754(7)
C12 C 0.30314(7) -0.7813(3) -0.16301(7)
C13 C 0.26499(7) -0.5955(3) -0.15534(7)
C14 C 0.29322(7) -0.4169(3) -0.11166(6)
H2N H 0.4587(9) 0.064(3) 0.0492(9)
H3N H 0.3203(9) -0.200(3) -0.0045(8)
H1A H 0.6316(11) 0.140(5) 0.2523(11)
H1B H 0.6596(10) 0.316(4) 0.2159(10)
H1C H 0.6469(11) 0.381(4) 0.2757(12)
H3 H 0.5588(9) 0.682(4) 0.2453(9)
H4 H 0.4514(8) 0.790(3) 0.1791(8)
H5 H 0.3904(8) 0.522(3) 0.0969(8)
H10 H 0.4433(8) -0.608(3) -0.0590(8)
H11 H 0.3942(8) -0.908(3) -0.1333(8)
H12 H 0.2827(9) -0.905(3) -0.1932(9)
H13 H 0.2173(9) -0.591(3) -0.1802(9)
H14 H 0.2672(8) -0.289(3) -0.1061(7)
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H1S H 0.2667(11) 0.435(4) 0.0311(10)
H1S H 0.2333(11) 0.435(4) -0.0311(10)
S1 S 0.174470(17) 0.07044(6) -0.089343(16)
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- O1 O 0.04800(4) -0.19130(18) 0.01226(5)
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- N2 N 0.06456(6) 0.1194(2) -0.06708(5)
- N3 N 0.14369(6) -0.1374(2) -0.00223(5)
- C1 C -0.13022(8) 0.3008(3) -0.23902(8)
- C2 C -0.06117(7) 0.3735(3) -0.19990(6)
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- C7 C 0.12378(6) 0.0224(2) -0.05191(6)
- C8 C 0.10585(6) -0.2414(2) 0.02676(6)
- C9 C 0.13958(6) -0.4242(2) 0.07530(6)
- C10 C 0.10151(7) -0.6088(3) 0.08405(6)
- C11 C 0.13007(7) -0.7871(3) 0.12754(7)
- C12 C 0.19686(7) -0.7813(3) 0.16301(7)
- C13 C 0.23501(7) -0.5955(3) 0.15534(7)
- C14 C 0.20678(7) -0.4169(3) 0.11166(6)
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- H1A H -0.1316(11) 0.140(5) -0.2523(11)
- H1B H -0.1596(10) 0.316(4) -0.2159(10)
- H1C H -0.1469(11) 0.381(4) -0.2757(12)
- H3 H -0.0588(9) 0.682(4) -0.2453(9)
- H4 H 0.0486(8) 0.790(3) -0.1791(8)
- H5 H 0.1096(8) 0.522(3) -0.0969(8)
- H10 H 0.0567(8) -0.608(3) 0.0590(8)
- H11 H 0.1058(8) -0.908(3) 0.1333(8)
- H12 H 0.2173(9) -0.905(3) 0.1932(9)
- H13 H 0.2827(9) -0.591(3) 0.1802(9)
- H14 H 0.2328(8) -0.289(3) 0.1061(7)
- O1S O 0.2500 -0.4694(3) 0.0000
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- H1S H 0.2333(11) -0.565(4) -0.0311(10)
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- C3 C 0.46613(7) -0.5835(3) -0.21147(7)
- C4 C 0.52957(7) -0.6418(3) -0.17296(7) C5 C 0.56485(7) -0.4896(3) -0.12476(7)
- C6 C 0.53369(6) -0.2829(2) -0.11719(6)
- C7 C 0.62378(6) -0.0224(2) -0.05191(6)
- C8 C 0.60585(6) 0.2414(2) 0.02676(6)
- C9 C 0.63958(6) 0.4242(2) 0.07530(6)
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- C11 C 0.63007(7) 0.7871(3) 0.12754(7)
- C12 C 0.69686(7) 0.7813(3) 0.16301(7)
- C13 C 0.73501(7) 0.5955(3) 0.15534(7)
- C14 C 0.70678(7) 0.4169(3) 0.11166(6)

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H3N H 0.6797(9) 0.200(3) 0.0045(8)
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H1C H 0.3531(11) -0.381(4) -0.2757(12)
H3 H 0.4412(9) -0.682(4) -0.2453(9)
H4 H 0.5486(8) -0.790(3) -0.1791(8)
H5 H 0.6096(8) -0.522(3) -0.0969(8)
H10 H 0.5567(8) 0.608(3) 0.0590(8)
H11 H 0.6058(8) 0.908(3) 0.1333(8)
H12 H 0.7173(9) 0.905(3) 0.1932(9)
H13 H 0.7827(9) 0.591(3) 0.1802(9)
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_cell_angle alpha
                          90.913(7)
_cell_angle_beta
                          107.255(7)
cell angle gamma
                            90.624(7)
                         686.5(5)
cell volume
_cell_formula_units Z
\_cell\_measurement\_temperature
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_exptl_crystal_size_mid
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_exptl_crystal_density_method
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_exptl_crystal_F_000
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exptl absorpt coefficient mu
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_exptl_absorpt_correction_T_min 0.9003
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exptl absorpt process details SADABS
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\_reflns\_number\_gt
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computing data reduction
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computing molecular graphics
                                   'Bruker SHELXTL'
computing_publication_material
                                  'Bruker SHELXTL'
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Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2^2 > 2 \operatorname{sigma}(F^2^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
_refine_ls_structure_factor_coef Fsqd
_refine_ls_matrix_type
_refine_ls_weighting_scheme
                                 calc
refine ls weighting details
'calc w=1/[\s^2^(Fo^2^)+(0.0616P)^2^+0.0968P] where P=(Fo^2^+2Fc^2^)/3'
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_atom_sites_solution_secondary
                                 difmap
                                  difmap
atom sites solution hydrogens
refine ls hydrogen treatment
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refine ls number restraints
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                             0.0402
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_refine_ls_wR_factor_gt
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refine ls restrained S all
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refine ls shift/su mean
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atom site symmetry multiplicity
atom site calc flag
atom site refinement flags
atom site disorder assembly
 atom site disorder group
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O1 O 0.39049(17) 0.57267(14) 0.66815(14) 0.0378(3) Uani 1 1 d . . .
O2 O 0.76107(19) -0.07526(15) 0.61082(15) 0.0462(4) Uani 1 1 d . . .
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C1 C 1.0184(3) 0.4131(2) 1.2360(2) 0.0326(4) Uani 1 1 d . . .
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C9 C 0.5875(2) 0.38898(18) 0.76665(18) 0.0235(4) Uani 1 1 d . . .
C10 C 0.5360(2) 0.31132(19) 0.63365(19) 0.0277(4) Uani 1 1 d . . .
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C14 C 0.7043(2) 0.32920(19) 0.88914(19) 0.0263(4) Uani 1 1 d . . .
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H3N H 0.679(2) 0.583(2) 0.958(2) 0.026(5) Uiso 1 1 d . . .
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H1B H 1.044(3) 0.411(2) 1.139(3) 0.051(6) Uiso 1 1 d . . .
H1C H 0.927(3) 0.342(2) 1.236(2) 0.043(6) Uiso 1 1 d . . .
H3 H 1.125(3) 0.599(2) 1.466(2) 0.032(5) Uiso 1 1 d . . .
H4 H 1.030(2) 0.826(2) 1.504(2) 0.033(5) Uiso 1 1 d . . .
H5 H 0.810(3) 0.921(2) 1.308(2) 0.036(5) Uiso 1 1 d . . .
H10 H 0.461(3) 0.349(2) 0.552(2) 0.032(5) Uiso 1 1 d . . .
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H13 H 0.846(3) 0.157(2) 0.959(2) 0.036(5) Uiso 1 1 d . . .
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O2 0.0524(9) 0.0422(9) 0.0395(8) -0.0133(6) 0.0067(7) 0.0133(7)
O3 0.0519(9) 0.0350(8) 0.0435(9) 0.0008(6) -0.0021(7) 0.0188(7)
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N3 0.0226(7) 0.0258(8) 0.0216(7) 0.0030(6) -0.0004(6) 0.0079(6)
N4 0.0273(8) 0.0288(8) 0.0359(9) -0.0023(7) 0.0041(7) 0.0044(6)
C1\ 0.0288(10)\ 0.0306(10)\ 0.0335(11)\ 0.0075(8)\ 0.0010(8)\ 0.0107(8)
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C3 0.0209(8) 0.0332(10) 0.0244(9) 0.0088(7) 0.0012(7) 0.0034(7)
C4 0.0279(9) 0.0341(10) 0.0230(9) 0.0006(7) 0.0009(7) 0.0013(7)
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C6 0.0188(8) 0.0269(9) 0.0229(8) 0.0052(7) 0.0040(7) 0.0038(6)
C7\ 0.0234(8)\ 0.0227(8)\ 0.0221(8)\ 0.0038(6)\ 0.0054(7)\ 0.0041(6)
C8 0.0227(8) 0.0270(9) 0.0221(8) 0.0030(7) 0.0042(7) 0.0034(7)
C9 0.0200(8) 0.0262(9) 0.0238(8) 0.0045(7) 0.0052(7) 0.0011(6)
C10\ 0.0247(9)\ 0.0311(10)\ 0.0227(9)\ 0.0035(7)\ -0.0003(7)\ 0.0025(7)
C11\ 0.0288(9)\ 0.0317(10)\ 0.0258(9)\ -0.0033(7)\ 0.0040(7)\ -0.0004(7)
C12\ 0.0245(8)\ 0.0238(9)\ 0.0314(9)\ 0.0001(7)\ 0.0080(7)\ 0.0020(7)
C13 0.0257(9) 0.0290(9) 0.0238(9) 0.0044(7) 0.0015(7) 0.0048(7)
C14\ 0.0277(9)\ 0.0258(9)\ 0.0225(9)\ 0.0000(7)\ 0.0030(7)\ 0.0045(7)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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N1 C2 1.355(2) . ?
N2 C7 1.357(2) . ?
N2 C6 1.413(2) . ?
N2 H2N 0.83(2) . ?
N3 C7 1.375(2) . ?
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C7 N3 H3N 114.5(12) . . ?
C8 N3 H3N 117.6(12) . . ?
O2 N4 O3 123.73(16) . . ?
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C2 C1 H1B 107.8(13) . . ?
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C2 C1 H1C 111.5(12) . . ?
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N1 C2 C1 116.63(16) . . ?
C3 C2 C1 121.69(16) . . ?
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C2 C3 C4 C5 -1.0(3) . . . . ?
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O3 N4 C12 C11 -172.82(16) . . . . ?
O2 N4 C12 C13 -171.87(16) . . . . ?
O3 N4 C12 C13 8.5(2) . . . . ?
C11 C12 C13 C14 -0.6(3) . . . . ?
N4 C12 C13 C14 177.97(15) . . . . ?
C12 C13 C14 C9 0.8(3) . . . . ?
C10 C9 C14 C13 0.4(3) . . . . ?
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loop_

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'-x, -y, -z'

'x, -y-1/2, z-1/2'

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cell length b 20.077(2)

_cell_length_c 9.8693(10)

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_cell_angle_gamma 90.00

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cell formula units Z 4

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27.19

cell measurement theta max

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Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2 sigma(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
_refine_ls_structure_factor_coef Fsqd
_refine_ls_matrix_type
                             full
refine ls weighting scheme
                                calc
refine ls weighting details
'calc w=1/[\s^2^(Fo^2^)+(0.0596P)^2^+0.3108P] where P=(Fo^2^+2Fc^2^)/3'
atom sites solution primary
                                direct
_atom_sites_solution_secondary
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C7 C 0.51777(19) 0.41176(7) 0.07928(15) 0.0281(3) Uani 1 1 d . . .
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C2 0.0323(8) 0.0354(8) 0.0281(7) -0.0002(6) 0.0079(6) -0.0036(6)
C3 0.0416(9) 0.0394(8) 0.0287(7) -0.0060(6) 0.0120(7) -0.0079(7)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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computing publication material 'Bruker SHELXTL'
refine special details
Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F<sup>2</sup>, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2sigma(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls_structure_factor_coef Fsqd
refine ls matrix type
_refine_ls_weighting scheme
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atom sites solution hydrogens
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refine ls hydrogen treatment
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O1 O 0.3370(2) 0.92420(14) 0.87100(12) 0.0557(4) Uani 1 1 d . . .
O2 O 0.29937(14) 0.29542(13) 1.14630(9) 0.0312(2) Uani 1 1 d . . .
N1 N -0.16581(15) 0.47485(13) 0.61371(9) 0.0223(2) Uani 1 1 d . . .
N2 N -0.06790(16) 0.75623(14) 0.56842(10) 0.0245(2) Uani 1 1 d . . .
N3 N 0.09755(15) 0.73419(14) 0.74535(9) 0.0228(2) Uani 1 1 d . . .
C1 C -0.2568(2) 0.18868(18) 0.66759(14) 0.0320(3) Uani 1 1 d . . .
C2 C -0.27193(18) 0.31451(16) 0.58250(12) 0.0238(3) Uani 1 1 d . . .
C3 C -0.3904(2) 0.26607(18) 0.47559(12) 0.0282(3) Uani 1 1 d . . .
C4 C -0.3978(2) 0.38501(18) 0.39791(12) 0.0283(3) Uani 1 1 d . . .
C5 C -0.2889(2) 0.54877(17) 0.42816(12) 0.0256(3) Uani 1 1 d . . .
C6 C -0.17578(17) 0.58798(16) 0.53783(11) 0.0214(3) Uani 1 1 d . . .
C7 C 0.06752(18) 0.83388(16) 0.66068(11) 0.0227(3) Uani 1 1 d . . .
C8 C 0.2339(2) 0.78189(17) 0.84546(12) 0.0272(3) Uani 1 1 d . . .
C9 C 0.24151(18) 0.64471(16) 0.91893(11) 0.0227(3) Uani 1 1 d . . .
C10 C 0.34537(19) 0.68853(17) 1.03236(12) 0.0253(3) Uani 1 1 d . . .
C11 C 0.36019(19) 0.56883(18) 1.10551(12) 0.0257(3) Uani 1 1 d . . .
C12 C 0.27448(18) 0.40309(17) 1.06702(11) 0.0237(3) Uani 1 1 d . . .
C13 C 0.17301(19) 0.35750(17) 0.95392(12) 0.0265(3) Uani 1 1 d . . .
C14 C 0.15751(19) 0.47936(17) 0.88136(12) 0.0248(3) Uani 1 1 d . . .
C15 C 0.2168(2) 0.12356(19) 1.11033(16) 0.0368(4) Uani 1 1 d . . .
H1A H -0.195(4) 0.126(3) 0.636(2) 0.085(8) Uiso 1 1 d . . .
H1B H -0.197(3) 0.233(3) 0.743(2) 0.075(7) Uiso 1 1 d . . .
H1C H -0.386(4) 0.113(3) 0.687(2) 0.073(7) Uiso 1 1 d . . .
H2N H -0.086(3) 0.818(2) 0.5167(16) 0.037(5) Uiso 1 1 d . . .
```

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H3 H -0.469(2) 0.151(2) 0.4544(15) 0.039(5) Uiso 1 1 d . . .
H3N H 0.023(2) 0.629(2) 0.7319(14) 0.031(4) Uiso 1 1 d . . .
H4 H -0.479(2) 0.357(2) 0.3229(16) 0.035(4) Uiso 1 1 d . . .
H5 H -0.291(2) 0.630(2) 0.3837(15) 0.034(4) Uiso 1 1 d . . .
H10 H 0.408(2) 0.799(2) 1.0590(14) 0.030(4) Uiso 1 1 d . . .
H11 H 0.434(2) 0.599(2) 1.1853(15) 0.033(4) Uiso 1 1 d . . .
H13 H 0.124(3) 0.249(2) 0.9255(16) 0.041(5) Uiso 1 1 d . . .
H14 H 0.091(2) 0.450(2) 0.8023(16) 0.036(4) Uiso 1 1 d . . .
H15A H 0.268(3) 0.078(3) 1.176(2) 0.064(6) Uiso 1 1 d . . .
H15B H 0.075(3) 0.082(2) 1.1011(15) 0.038(4) Uiso 1 1 d . . .
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O1 0.0733(9) 0.0199(6) 0.0508(7) 0.0009(5) -0.0364(6) 0.0017(5)
O2 0.0341(5) 0.0293(5) 0.0282(5) 0.0071(4) -0.0063(4) 0.0120(4)
N1 0.0243(5) 0.0200(5) 0.0213(5) 0.0023(4) -0.0004(4) 0.0079(4)
N2 0.0279(6) 0.0187(5) 0.0239(5) 0.0044(4) -0.0042(4) 0.0070(4)
N3 0.0251(5) 0.0179(5) 0.0216(5) 0.0021(4) -0.0040(4) 0.0056(4)
C1\ 0.0402(8)\ 0.0217(7)\ 0.0301(7)\ 0.0031(6)\ -0.0047(6)\ 0.0094(6)
C2 0.0257(6) 0.0209(6) 0.0235(6) 0.0006(5) 0.0000(5) 0.0084(5)
C3 0.0301(7) 0.0215(7) 0.0285(7) -0.0026(5) -0.0028(5) 0.0065(5)
C4 0.0302(7) 0.0297(7) 0.0228(6) -0.0026(5) -0.0055(5) 0.0112(6)
C5 0.0294(7) 0.0256(7) 0.0223(6) 0.0036(5) -0.0016(5) 0.0119(5)
C6 0.0221(6) 0.0205(6) 0.0209(6) 0.0013(5) 0.0010(5) 0.0080(5)
C7\ 0.0235(6)\ 0.0198(6)\ 0.0233(6)\ 0.0026(5)\ -0.0007(5)\ 0.0075(5)
C8 0.0315(7) 0.0213(6) 0.0244(6) 0.0001(5) -0.0057(5) 0.0074(5)
C9 0.0220(6) 0.0239(6) 0.0207(6) 0.0020(5) -0.0005(5) 0.0079(5)
C10\ 0.0265(6)\ 0.0230(7)\ 0.0224(6)\ -0.0020(5)\ -0.0029(5)\ 0.0068(5)
C11 0.0253(6) 0.0310(7) 0.0194(6) 0.0002(5) -0.0033(5) 0.0105(5)
C12 0.0214(6) 0.0278(7) 0.0221(6) 0.0061(5) 0.0010(5) 0.0102(5)
C13 0.0278(7) 0.0215(7) 0.0267(7) 0.0005(5) -0.0040(5) 0.0073(5)
C14 0.0262(6) 0.0241(7) 0.0205(6) 0.0007(5) -0.0055(5) 0.0077(5)
C15\ 0.0437(9)\ 0.0274(8)\ 0.0386(9)\ 0.0087(6)\ -0.0034(7)\ 0.0145(7)
geom special details
All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
loop
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O2 C15 1.4323(19) . ?
N1 C6 1.3374(16) . ?
N1 C2 1.3499(17) . ?
N2 C7 1.3628(16) . ?
N2 C6 1.4076(17) . ?
N2 H2N 0.84(2) . ?
N3 C7 1.3648(16) . ?
N3 C8 1.4040(16) . ?
N3 H3N 0.882(18) . ?
C1 C2 1.5020(19) . ?
C1 H1A 0.94(3) . ?
C1 H1B 0.92(2) . ?
C1 H1C 0.99(3) . ?
C2 C3 1.3914(18) . ?
C3 C4 1.384(2) . ?
C3 H3 0.972(18) . ?
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C4 H4 0.969(17) . ?
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C6 N1 C2 117.98(11) . . ?
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C6 N2 H2N 112.6(13) . . ?
C7 N3 C8 127.07(11) . . ?
C7 N3 H3N 114.0(11) . . ?
C8 N3 H3N 118.9(11) . . ?
C2 C1 H1A 112.4(17) . . ?
C2 C1 H1B 113.9(16) . . ?
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N1 C2 C1 117.40(12) . . ?
C3 C2 C1 120.77(12) . . ?
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O2 C12 C11 115.42(11) . . ?
C13 C12 C11 120.03(12) . . ?
C14 C13 C12 119.04(12)..?
C14 C13 H13 120.6(11) . . ?
C12 C13 H13 120.3(11) . . ?
C9 C14 C13 121.45(12) . . ?
C9 C14 H14 118.5(11) . . ?
C13 C14 H14 120.1(11) . . ?
O2 C15 H15A 101.0(14) . . ?
O2 C15 H15B 110.8(10) . . ?
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N1 C2 C3 C4 1.0(2) . . . . ?
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C6 N2 C7 N3 -5.5(2) . . . . ?
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C8 N3 C7 S1 -2.5(2) . . . . ?
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C14 C9 C10 C11 -1.17(19) . . . . ?
C8 C9 C10 C11 -179.61(12) . . . . ?
C9 C10 C11 C12 0.9(2) . . . . ?
C15 O2 C12 C13 0.6(2) . . . . ?
C15 O2 C12 C11 -178.96(12) . . . . ?
C10 C11 C12 O2 179.58(12) . . . ?
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O2 C12 C13 C14 179.85(12) . . . . ?
C11 C12 C13 C14 -0.6(2) . . . . ?
C10 C9 C14 C13 0.6(2) . . . . ?
C8 C9 C14 C13 178.86(12) . . . . ?
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 geom hbond site symmetry A
N2 H2N S1 0.84(2) 2.56(2) 3.3954(12) 170.0(17) 2 576
N3 H3N N1 0.882(18) 1.945(17) 2.6973(16) 142.2(15) .
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diffrn reflns theta full
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'-x, -y, -z'
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cell length c
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_cell_angle_gamma
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diffrn reflns limit k max
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computing publication material 'Bruker SHELXTL'
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Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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atom sites solution secondary
                                 difmap
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atom site fract z
atom site U iso or equiv
atom site adp type
atom site occupancy
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atom site refinement flags
atom site disorder assembly
 atom site disorder group
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S1 S 0.20421(4) 0.37914(4) 0.75400(4) 0.03211(11) Uani 1 1 d . . .
N1 N 0.44353(12) 0.65239(12) 0.83835(11) 0.0218(2) Uani 1 1 d . . .
N2 N 0.44146(13) 0.46127(13) 0.75961(11) 0.0226(2) Uani 1 1 d . . .
N3 N 0.49487(13) 0.30198(13) 0.61456(11) 0.0223(2) Uani 1 1 d . . .
O1 O 0.72572(11) 0.32596(12) 0.62081(10) 0.0287(2) Uani 1 1 d . . .
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C7 C 0.38516(15) 0.38409(14) 0.71238(13) 0.0214(2) Uani 1 1 d . . .
C8 C 0.65672(15) 0.27222(14) 0.57691(13) 0.0206(2) Uani 1 1 d . . .
C9 C 0.74462(14) 0.16876(14) 0.47740(12) 0.0202(2) Uani 1 1 d . . .
C10 C 0.87902(15) 0.18774(14) 0.39250(13) 0.0216(2) Uani 1 1 d . . .
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H6B H 0.557(3) 0.803(3) 0.961(3) 0.086(8) Uiso 1 1 d . . .
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C3 0.0245(6) 0.0373(7) 0.0240(6) -0.0116(6) 0.0055(5) -0.0119(6)
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C5 0.0194(6) 0.0236(6) 0.0197(6) -0.0082(5) -0.0012(5) -0.0073(5)
C6 0.0369(8) 0.0398(8) 0.0400(9) -0.0213(7) 0.0034(7) -0.0215(7)
C7\ 0.0200(6)\ 0.0218(6)\ 0.0219(6)\ -0.0071(5)\ -0.0003(5)\ -0.0080(5)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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symmetry cell setting

Monoclinic

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'-x, -y, -z'
'x, -y, z-1/2'
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diffrn measurement method

'phi and omega scans'

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Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
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on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2^2 > 2 \operatorname{sigma}(F^2^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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C3\ 0.0268(11)\ 0.0292(11)\ 0.0309(12)\ -0.0014(9)\ 0.0033(9)\ 0.0081(9)
C4 0.0289(11) 0.0283(11) 0.0227(11) 0.0012(9) 0.0083(9) 0.0035(8)
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C6 0.0207(9) 0.0189(9) 0.0219(10) -0.0017(7) 0.0058(8) -0.0010(7)
C7 0.0224(10) 0.0256(10) 0.0210(10) 0.0026(8) 0.0051(8) 0.0000(8)
C8 0.0184(9) 0.0232(10) 0.0191(10) -0.0001(7) 0.0032(8) -0.0003(7)
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C11 0.0172(9) 0.0239(10) 0.0266(10) -0.0038(8) 0.0037(8) 0.0003(8)
C12\ 0.0251(10)\ 0.0274(11)\ 0.0206(10)\ 0.0020(8)\ 0.0031(8)\ 0.0024(8)
C13\ 0.0234(10)\ 0.0295(11)\ 0.0206(10)\ 0.0019(8)\ 0.0076(8)\ -0.0009(8)
O1S 0.0223(11) 0.0387(13) 0.0268(11) 0.000 0.0073(9) 0.000
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles: correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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N2 C5 1.414(2) . ?
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Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F<sup>2</sup>, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2^2 > 2 \operatorname{sigma}(F^2^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
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refine ls matrix type
                             full
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C3 C 0.4924(3) 1.30330(18) 0.09364(15) 0.0280(4) Uani 1 1 d . . .
C4 C 0.3543(3) 1.24555(16) 0.13314(15) 0.0249(4) Uani 1 1 d . . .
C5 C 0.3741(2) 1.12856(16) 0.14172(13) 0.0202(4) Uani 1 1 d . . .
C6 C 0.2168(2) 0.95615(15) 0.20348(13) 0.0191(4) Uani 1 1 d . . .
C7 C 0.3669(2) 0.77542(16) 0.17275(13) 0.0196(4) Uani 1 1 d . . .
C8 C 0.5454(2) 0.72032(15) 0.15795(13) 0.0189(4) Uani 1 1 d . . .
C9 C 0.5645(2) 0.61635(16) 0.13383(15) 0.0237(4) Uani 1 1 d . . .
C10 C 0.7248(3) 0.56056(17) 0.11788(15) 0.0255(4) Uani 1 1 d . . .
C11 C 0.8664(2) 0.60827(16) 0.12633(13) 0.0215(4) Uani 1 1 d . . .
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C14 C 1.0347(2) 0.55215(16) 0.10742(14) 0.0245(4) Uani 1 1 d . . .
C15 C 0.8113(3) 1.0619(2) 0.04102(17) 0.0321(5) Uani 1 1 d . . .
S1' S 0.91676(6) 0.26863(4) 0.24391(4) 0.02572(16) Uani 1 1 d . . .
O1' O 0.70998(17) 0.43732(13) 0.34877(12) 0.0334(4) Uani 1 1 d . . .
N1' N 0.43230(19) 0.10476(13) 0.38183(11) 0.0197(3) Uani 1 1 d . . .
N2' N 0.7142(2) 0.11003(13) 0.30908(12) 0.0208(3) Uani 1 1 d . . .
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C1' C 0.3020(2) 0.04616(16) 0.42495(13) 0.0205(4) Uani 1 1 d . . .
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C8' C 0.4101(2) 0.45112(15) 0.35849(13) 0.0185(4) Uani 1 1 d . . .
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C12' C 0.1095(2) 0.47296(16) 0.34692(14) 0.0226(4) Uani 1 1 d . . .
C13' C 0.2708(2) 0.41595(16) 0.33391(14) 0.0219(4) Uani 1 1 d . . .
C14' C -0.0782(2) 0.62687(16) 0.39883(14) 0.0232(4) Uani 1 1 d . . .
C15' C 0.1461(3) 0.11306(19) 0.46136(17) 0.0289(5) Uani 1 1 d . . .
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H2N' H 0.801(3) 0.075(2) 0.2901(17) 0.027(6) Uiso 1 1 d . . .
H3 H 0.472(3) 1.388(2) 0.0871(19) 0.046(7) Uiso 1 1 d . . .
H3' H 0.479(3) -0.212(2) 0.4048(16) 0.029(6) Uiso 1 1 d . . .
H3N H 0.443(3) 0.9220(19) 0.1491(16) 0.023(6) Uiso 1 1 d . . .
H3N' H 0.503(3) 0.247(2) 0.3497(17) 0.034(6) Uiso 1 1 d . . .
H4 H 0.250(3) 1.284(2) 0.1485(17) 0.033(6) Uiso 1 1 d . . .
H4' H 0.694(3) -0.1041(19) 0.3378(16) 0.025(6) Uiso 1 1 d . . .
H9 H 0.464(3) 0.581(2) 0.1337(17) 0.034(6) Uiso 1 1 d . . .
H9' H 0.487(3) 0.569(2) 0.4113(17) 0.036(6) Uiso 1 1 d . . .
H10 H 0.743(3) 0.487(2) 0.0989(17) 0.035(6) Uiso 1 1 d . . .
H10' H 0.213(3) 0.668(2) 0.4365(17) 0.033(6) Uiso 1 1 d . . .
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H12' H 0.013(3) 0.4503(18) 0.3270(15) 0.022(5) Uiso 1 1 d . . .
H13 H 0.676(3) 0.832(2) 0.1899(18) 0.041(7) Uiso 1 1 d . . .
H13' H 0.290(3) 0.354(2) 0.3054(18) 0.039(7) Uiso 1 1 d . . .
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H15B H 0.872(4) 1.106(3) -0.015(2) 0.057(8) Uiso 1 1 d . . .
H15C H 0.774(4) 0.993(3) 0.022(2) 0.064(9) Uiso 1 1 d . . .
H15D H 0.070(4) 0.132(2) 0.419(2) 0.048(8) Uiso 1 1 d . . .
H15E H 0.090(4) 0.069(2) 0.525(2) 0.053(8) Uiso 1 1 d . . .
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O1 0.0170(7) 0.0242(7) 0.0440(9) -0.0133(6) 0.0003(6) -0.0023(6)
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N4 0.0223(9) 0.0298(9) 0.0456(11) -0.0137(8) 0.0012(8) 0.0056(7)
C1\ 0.0174(9)\ 0.0269(10)\ 0.0207(9)\ -0.0016(7)\ -0.0008(7)\ -0.0012(8)
C2 0.0188(9) 0.0281(10) 0.0298(11) -0.0021(8) 0.0000(8) -0.0056(8)
C3 0.0271(10) 0.0224(10) 0.0334(11) -0.0059(8) -0.0009(8) -0.0041(8)
C4 0.0196(9) 0.0203(9) 0.0340(11) -0.0098(8) 0.0019(8) 0.0003(8)
C5\ 0.0163(9)\ 0.0211(9)\ 0.0224(9)\ -0.0056(7)\ -0.0002(7)\ -0.0011(7)
C6 0.0139(8) 0.0200(9) 0.0230(9) -0.0065(7) -0.0016(7) 0.0009(7)
C7\ 0.0155(9)\ 0.0202(9)\ 0.0224(9)\ -0.0069(7)\ -0.0019(7)\ 0.0027(7)
C8 0.0169(9) 0.0180(9) 0.0201(9) -0.0041(7) -0.0026(7) 0.0025(7)
C9 0.0186(9) 0.0202(9) 0.0325(11) -0.0078(8) -0.0018(8) -0.0016(8)
C10 0.0227(10) 0.0186(9) 0.0347(11) -0.0088(8) -0.0022(8) 0.0016(8)
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C12 0.0158(9) 0.0260(10) 0.0377(11) -0.0135(8) -0.0029(8) 0.0006(8)
C13\ 0.0191(9)\ 0.0226(10)\ 0.0349(11)\ -0.0138(8)\ -0.0041(8)\ 0.0022(8)
C14\ 0.0211(10)\ 0.0206(9)\ 0.0301(10)\ -0.0062(8)\ -0.0001(8)\ -0.0006(8)
C15\ 0.0177(10)\ 0.0347(12)\ 0.0343(12)\ -0.0001(10)\ 0.0041(8)\ 0.0032(9)
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O1'0.0153(7)0.0339(8)0.0580(10)-0.0249(7)-0.0022(6)-0.0022(6)
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C14' \ 0.0220(10) \ 0.0182(9) \ 0.0267(10) \ -0.0035(7) \ -0.0005(8) \ -0.0006(8)
C15' \ 0.0146(9) \ 0.0298(11) \ 0.0397(12) \ -0.0102(9) \ 0.0042(8) \ 0.0012(8)
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All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles

and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds involving l.s. planes.

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N3 C6 1.369(2) . ?
N3 C7 1.401(2) . ?
N3 H3N 0.84(2) . ?
N4 C14 1.146(3) . ?
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C3 H3 1.01(3).?
C4 C5 1.397(3).?
C4 H4 0.93(2) . ?
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C13 H13 0.95(3) . ?
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C15 H15B 0.96(3) . ?
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C4' C5' 1.387(3) . ?
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                             MoK\a
_diffrn_radiation_source
                             'fine-focus sealed tube'
diffrn radiation monochromator graphite
diffrn measurement device type 'CCD area detector Bruker apex'
diffrn measurement method
                                 'phi and omega scans'
 diffrn detector area resol mean?
_diffrn_standards number
_diffrn_standards_interval_count ?
diffrn standards interval time ?
diffrn standards decay %
diffrn reflns number
                             16281
diffrn reflns av R equivalents 0.0219
_diffrn_reflns_av_sigmaI/netI
                               0.0157
diffrn reflns limit h min
                               -14
diffrn reflns limit h max
                               14
diffrn reflns limit k min
                               -18
_diffrn_reflns_limit_k max
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_diffrn_reflns_limit 1 min
                              -11
_diffrn_reflns_limit_l_max
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_diffrn_reflns_theta_min
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diffrn reflns theta max
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reflns number total
                             3220
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reflns threshold expression
                               >2sigma(I)
                                'Bruker SMART'
computing data collection
computing cell refinement
                                'Bruker SMART'
                                'Bruker SAINT'
computing data reduction
_computing_structure_solution
                                 'Bruker SHELXTL'
_computing_structure_refinement 'Bruker SHELXTL'
computing molecular graphics
                                  'Bruker SHELXTL'
_computing_publication_material 'Bruker SHELXTL'
refine special details
Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
_refine_ls_matrix type
_refine_ls_weighting_scheme
                                 calc
refine ls weighting details
'calc w=1/[\s^2^(Fo^2^)+(0.0329P)^2^+1.2938P] where P=(Fo^2^+2Fc^2^)/3'
_atom_sites_solution_primary
                                 direct
atom sites solution secondary
                                 difmap
atom sites solution hydrogens
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refine ls hydrogen treatment
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refine Is extinction method
                                none
_refine_ls extinction coef
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refine ls number parameters
                                 229
refine ls number restraints
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_refine_ls_R_factor_gt
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_refine_ls_wR_factor_ref
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refine ls wR factor gt
                              0.0714
refine ls goodness of fit ref 1.024
refine ls restrained S all
                              1.024
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                             0.002
refine ls shift/su mean
                              0.000
atom site label
_atom_site_type_symbol
_atom_site_fract x
_atom_site_fract_y
_atom_site_fract_z
atom site U iso or equiv
atom site adp type
_atom_site_occupancy
_atom_site_symmetry multiplicity
_atom_site_calc flag
atom site refinement flags
atom site disorder assembly
 atom site disorder group
Br1 Br 0.60452(2) 0.723935(19) 1.01272(3) 0.05102(10) Uani 1 1 d . . .
S1 S 0.14580(5) 0.59299(4) 0.55433(5) 0.03145(13) Uani 1 1 d . . .
O1 O 0.32503(14) 0.70557(10) 0.98876(14) 0.0301(3) Uani 1 1 d . . .
N1 N 0.15919(14) 0.46672(12) 1.01416(18) 0.0276(3) Uani 1 1 d . . .
N2 N 0.19436(15) 0.57322(12) 0.84501(18) 0.0266(3) Uani 1 1 d . . .
N3 N 0.27746(14) 0.70074(11) 0.74281(17) 0.0228(3) Uani 1 1 d . . .
C1 C 0.10872(18) 0.38914(14) 1.0615(2) 0.0321(4) Uani 1 1 d . . .
C2 C 0.0325(2) 0.33203(15) 0.9683(3) 0.0366(5) Uani 1 1 d . . .
C3 C 0.0093(2) 0.35592(15) 0.8241(3) 0.0362(5) Uani 1 1 d . . .
C4 C 0.06132(19) 0.43555(15) 0.7720(2) 0.0322(4) Uani 1 1 d . . .
C5 C 0.13518(17) 0.48842(13) 0.8731(2) 0.0261(4) Uani 1 1 d . . .
C6 C 0.20448(16) 0.61997(13) 0.72285(19) 0.0229(4) Uani 1 1 d . . .
C7 C 0.33422(17) 0.73857(13) 0.86890(19) 0.0228(4) Uani 1 1 d . . .
C8 C 0.40829(17) 0.82401(13) 0.85015(19) 0.0237(4) Uani 1 1 d . . .
C9 C 0.52738(18) 0.82855(15) 0.9108(2) 0.0310(4) Uani 1 1 d . . .
C10 C 0.5943(2) 0.90881(18) 0.8943(3) 0.0428(5) Uani 1 1 d . . .
C11 C 0.5414(2) 0.98491(18) 0.8171(3) 0.0463(6) Uani 1 1 d . . .
C12 C 0.4237(2) 0.98158(16) 0.7551(3) 0.0388(5) Uani 1 1 d . . .
C13 C 0.35723(19) 0.90113(14) 0.7715(2) 0.0283(4) Uani 1 1 d . . .
C14 C 0.1389(3) 0.3671(2) 1.2198(3) 0.0441(6) Uani 1 1 d . . .
H2N H 0.233(2) 0.5958(17) 0.917(3) 0.033(6) Uiso 1 1 d . . .
H3N H 0.290(2) 0.7271(16) 0.667(3) 0.028(6) Uiso 1 1 d . . .
H2 H -0.001(3) 0.2779(19) 1.011(3) 0.050(8) Uiso 1 1 d . . .
H3 H -0.041(2) 0.3184(19) 0.762(3) 0.042(7) Uiso 1 1 d . . .
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H4 H 0.046(2) 0.4523(17) 0.677(3) 0.038(6) Uiso 1 1 d . . .
H10 H 0.672(3) 0.9109(19) 0.934(3) 0.049(8) Uiso 1 1 d . . .
H11 H 0.587(3) 1.039(2) 0.808(3) 0.063(9) Uiso 1 1 d . . .
H12 H 0.390(2) 1.0305(19) 0.704(3) 0.041(7) Uiso 1 1 d . . .
H13 H 0.273(2) 0.8981(16) 0.727(2) 0.030(6) Uiso 1 1 d . . .
H14A H 0.069(4) 0.351(3) 1.265(4) 0.099(13) Uiso 1 1 d . . .
H14B H 0.192(3) 0.318(3) 1.230(4) 0.085(12) Uiso 1 1 d . . .
H14C H 0.178(3) 0.416(3) 1.278(4) 0.088(12) Uiso 1 1 d . . .
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atom site aniso label
atom site aniso U 11
atom site aniso U 22
atom site aniso U 33
atom site aniso U 23
atom site aniso U 13
atom site aniso U 12
Br1 0.03944(15) 0.05160(17) 0.05690(18) 0.00686(12) -0.01068(11) 0.00676(11)
$1 0.0340(3) 0.0360(3) 0.0221(2) -0.00314(19) -0.00379(19) -0.0058(2)
O1 0.0448(8) 0.0283(7) 0.0173(6) -0.0013(5) 0.0053(6) -0.0081(6)
N1 0.0267(8) 0.0254(8) 0.0308(8) 0.0027(7) 0.0045(7) -0.0007(6)
N2 0.0314(9) 0.0253(8) 0.0219(8) -0.0015(6) 0.0003(7) -0.0073(7)
N3 0.0284(8) 0.0240(8) 0.0157(7) 0.0001(6) 0.0026(6) -0.0027(6)
C1\ 0.0299(10)\ 0.0275(10)\ 0.0400(11)\ 0.0054(9)\ 0.0091(9)\ 0.0018(8)
C2\ 0.0347(11)\ 0.0254(10)\ 0.0515(13)\ 0.0021(9)\ 0.0120(10)\ -0.0051(8)
C3\ 0.0342(11)\ 0.0268(10)\ 0.0474(13)\ -0.0091(9)\ 0.0054(10)\ -0.0066(9)
C4 0.0333(11) 0.0300(10) 0.0325(11) -0.0045(9) 0.0026(9) -0.0042(8)
C5\ 0.0249(9)\ 0.0229(9)\ 0.0306(9)\ -0.0018(7)\ 0.0046(7)\ -0.0007(7)
C6 0.0219(8) 0.0238(9) 0.0228(9) -0.0031(7) 0.0027(7) 0.0019(7)
C7\ 0.0262(9)\ 0.0221(9)\ 0.0200(9)\ -0.0023(7)\ 0.0038(7)\ 0.0007(7)
C8 0.0272(9) 0.0257(9) 0.0189(8) -0.0043(7) 0.0057(7) -0.0033(7)
C9 0.0304(10) 0.0333(10) 0.0289(10) -0.0039(8) 0.0033(8) -0.0010(8)
C10\ 0.0303(12)\ 0.0481(14)\ 0.0501(14)\ -0.0071(11)\ 0.0062(10)\ -0.0116(10)
C11\ 0.0436(13)\ 0.0392(13)\ 0.0578(15)\ -0.0005(11)\ 0.0136(11)\ -0.0192(11)
C12\ 0.0459(13)\ 0.0289(11)\ 0.0427(12)\ 0.0051(10)\ 0.0100(10)\ -0.0054(10)
C13\ 0.0320(11)\ 0.0270(10)\ 0.0265(9)\ -0.0017(8)\ 0.0066(8)\ -0.0024(8)
C14\ 0.0474(14)\ 0.0415(13)\ 0.0436(14)\ 0.0147(11)\ 0.0069(11)\ -0.0064(12)
_geom_special details
All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
loop
geom bond atom site label 1
geom bond atom site label 2
geom bond distance
geom bond site symmetry 2
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geom bond publ flag
Br1 C9 1.900(2) . ?
S1 C6 1.6613(18).?
O1 C7 1.229(2).?
N1 C1 1.339(3) . ?
N1 C5 1.340(3) . ?
N2 C6 1.335(2) . ?
N2 C5 1.415(2) . ?
N2 H2N 0.81(3) . ?
N3 C7 1.366(2) . ?
N3 C6 1.406(2) . ?
N3 H3N 0.83(2).?
C1 C2 1.393(3).?
C1 C14 1.500(3) . ?
C2 C3 1.375(3).?
C2 H2 0.96(3) . ?
C3 C4 1.389(3).?
C3 H3 0.92(3) . ?
C4 C5 1.387(3).?
C4 H4 0.91(3) . ?
C7 C8 1.495(3) . ?
C8 C13 1.391(3) . ?
C8 C9 1.393(3) . ?
C9 C10 1.385(3) . ?
C10 C11 1.381(4).?
C10 H10 0.91(3) . ?
C11 C12 1.382(4) . ?
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C12 C13 1.383(3) . ?
C12 H12 0.89(3).?
C13 H13 0.98(2) . ?
C14 H14A 0.98(4) . ?
C14 H14B 0.91(4) . ?
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C6 N2 C5 132.56(17) . . ?
C6 N2 H2N 113.9(17) . . ?
C5 N2 H2N 113.4(17) . . ?
C7 N3 C6 128.89(16) . . ?
C7 N3 H3N 116.4(16) . . ?
C6 N3 H3N 114.6(16) . . ?
N1 C1 C2 121.7(2) . . ?
N1 C1 C14 116.4(2) . . ?
C2 C1 C14 121.9(2) . . ?
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C3 C2 C1 118.9(2) . . ?
C3 C2 H2 124.4(17) . . ?
C1 C2 H2 116.6(17) . . ?
C2 C3 C4 120.6(2) . . ?
C2 C3 H3 119.4(16) . . ?
C4 C3 H3 120.0(16) . . ?
C5 C4 C3 116.4(2) . . ?
C5 C4 H4 122.2(16) . . ?
C3 C4 H4 121.5(16) . . ?
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N1 C5 N2 109.81(16) . . ?
C4 C5 N2 125.91(18) . . ?
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N3 C6 S1 117.44(13) . . ?
O1 C7 N3 122.93(17) . . ?
O1 C7 C8 122.29(17) . . ?
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C10 C9 Br1 117.92(17) . . ?
C8 C9 Br1 121.36(15) . . ?
C11 C10 C9 119.2(2) . . ?
C11 C10 H10 120.9(18) . . ?
C9 C10 H10 119.9(18) . . ?
C10 C11 C12 121.0(2) . . ?
C10 C11 H11 118.3(19) . . ?
C12 C11 H11 120.6(19) . . ?
C11 C12 C13 119.6(2) . . ?
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C12 C13 C8 120.4(2) . . ?
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C8 C13 H13 119.6(13) . . ?
C1 C14 H14A 113(2) . . ?
C1 C14 H14B 109(2) . . ?
H14A C14 H14B 110(3) . . ?
C1 C14 H14C 116(2) . . ?
H14A C14 H14C 106(3) . . ?
H14B C14 H14C 104(3) . . ?
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_geom_torsion_site_symmetry_3
_geom_torsion_site_symmetry_4
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geom torsion publ flag
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N1 C1 C2 C3 0.4(3) . . . . ?
C14 C1 C2 C3 -179.5(2) . . . . ?
C1 C2 C3 C4 0.2(3) . . . . ?
C2 C3 C4 C5 -0.7(3) . . . . ?
C1 N1 C5 C4 -0.1(3) . . . . ?
C1 N1 C5 N2 178.79(17) . . . . ?
C3 C4 C5 N1 0.7(3) . . . . ?
C3 C4 C5 N2 -178.10(19) . . . . ?
C6 N2 C5 N1 175.2(2) . . . . ?
C6 N2 C5 C4 -5.9(3) . . . . ?
C5 N2 C6 N3 -177.10(18) . . . . ?
C5 N2 C6 S1 1.0(3) . . . . ?
C7 N3 C6 N2 -2.8(3) . . . . ?
C7 N3 C6 S1 178.91(16) . . . . ?
C6 N3 C7 O1 -2.1(3) . . . . ?
C6 N3 C7 C8 178.20(17) . . . . ?
O1 C7 C8 C13 -125.7(2) . . . . ?
N3 C7 C8 C13 54.0(2) . . . . ?
O1 C7 C8 C9 53.8(3) . . . . ?
N3 C7 C8 C9 -126.58(19) . . . . ?
C13 C8 C9 C10 0.4(3) . . . . ?
C7 C8 C9 C10 -179.02(19) . . . . ?
C13 C8 C9 Br1 -177.38(14) . . . . ?
C7 C8 C9 Br1 3.2(3) . . . . ?
C8 C9 C10 C11 0.3(3) . . . . ?
Br1 C9 C10 C11 178.13(19) . . . . ?
C9 C10 C11 C12 -0.7(4) . . . . ?
C10 C11 C12 C13 0.5(4) . . . . ?
C11 C12 C13 C8 0.2(3) . . . . ?
C9 C8 C13 C12 -0.6(3) . . . . ?
C7 C8 C13 C12 178.82(18) . . . . ?
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geom hbond atom site label H
_geom_hbond_atom_site_label A
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_geom_hbond_distance_HA
_geom_hbond_distance_DA
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geom hbond site symmetry A
N2 H2N O1 0.81(3) 1.93(2) 2.631(2) 143(2).
N3 H3N O1 0.83(2) 2.00(3) 2.831(2) 177(2) 4 575
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atom type scat dispersion imag
 atom type scat source
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'International Tables Vol C Tables 4.2.6.8 and 6.1.1.4'
'H' 'H' 0.0000 0.0000
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'N' 'N' 0.0061 0.0033
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'O' 'O' 0.0106 0.0060
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'S' 'S' 0.1246 0.1234
'International Tables Vol C Tables 4.2.6.8 and 6.1.1.4'
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'x, y, z'
'-x+1/2, y+1/2, -z+1/2'
'-x, -y, -z'
'x-1/2, -y-1/2, z-1/2'
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5.2724(7)

20.335(3)

90.00

11.7435(16)

90.372(2)

1259.1(3)

4

90.00

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_cell_length b

_cell_length_c

_cell_angle_alpha

_cell_angle_beta

_cell_volume

_cell_angle_gamma

_cell_formula_units_Z

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cell measurement theta max
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_exptl_crystal_size_mid
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exptl crystal size min
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exptl crystal density meas
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diffrn radiation wavelength
diffrn radiation type
                            MoK\a
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diffrn radiation source
_diffrn_radiation_monochromator graphite
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diffrn standards number
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diffrn reflns av R equivalents 0.0345
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diffrn reflns av sigmaI/netI
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_diffrn_reflns_limit_h_max
                              6
                              -25
diffrn reflns limit k min
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diffrn reflns limit k max
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computing data collection
                               'Bruker SMART'
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computing cell refinement
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computing data reduction
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_computing_structure_solution
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computing structure refinement
                                  'Bruker SHELXTL'
computing molecular graphics
                                  'Bruker SHELXTL'
_computing_publication_material
                                  'Bruker SHELXTL'
_refine_special_details
Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F<sup>2</sup>, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
_refine_ls_matrix_type
_refine_ls_weighting_scheme
                                calc
refine Is weighting details
'calc w=1/[\s^2^(Fo^2^)+(0.0735P)^2^+0.2907P] where P=(Fo^2^+2Fc^2^)/3'
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refine ls shift/su mean
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O1 O 0.5632(2) 0.06586(7) 0.63316(10) 0.0465(3) Uani 1 1 d . . .
N1 N 0.0789(3) 0.20415(8) 0.67727(13) 0.0526(4) Uani 1 1 d . . .
N2 N 0.2952(3) 0.12989(7) 0.78058(11) 0.0348(3) Uani 1 1 d . . .
N3 N 0.5760(3) 0.04738(6) 0.82481(11) 0.0311(3) Uani 1 1 d . . .
C1 C -0.0943(5) 0.25123(11) 0.66322(18) 0.0630(6) Uani 1 1 d . . .
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C3 C -0.2140(4) 0.24757(10) 0.85570(19) 0.0530(5) Uani 1 1 d . . .
C4 C -0.0363(4) 0.19877(10) 0.87347(17) 0.0445(4) Uani 1 1 d . . .
C5 C 0.1059(3) 0.17861(8) 0.78089(14) 0.0340(4) Uani 1 1 d . . .
C6 C 0.3923(3) 0.09143(7) 0.86210(13) 0.0309(3) Uani 1 1 d . . .
C7 C 0.6504(3) 0.03498(8) 0.71398(13) 0.0324(3) Uani 1 1 d . . .
C8 C 0.8400(3) -0.01810(7) 0.69713(13) 0.0305(3) Uani 1 1 d . . .
C9 C 1.0211(3) -0.03535(8) 0.77843(15) 0.0355(4) Uani 1 1 d . . .
C10 C 1.2016(3) -0.08271(9) 0.75274(18) 0.0433(4) Uani 1 1 d . . .
C11 C 1.2007(3) -0.11267(9) 0.64714(17) 0.0445(4) Uani 1 1 d . . .
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C13 C 0.8401(3) -0.04909(8) 0.59092(14) 0.0367(4) Uani 1 1 d . . .
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H3N H 0.626(3) 0.0217(10) 0.8751(17) 0.039(5) Uiso 1 1 d . . .
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H10 H 1.323(4) -0.0945(10) 0.805(2) 0.056(6) Uiso 1 1 d . . .
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H12 H 1.016(4) -0.1185(11) 0.494(2) 0.055(6) Uiso 1 1 d . . .
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O1 0.0584(8) 0.0572(8) 0.0241(6) 0.0115(5) 0.0089(5) 0.0208(6)
N1 0.0761(11) 0.0519(9) 0.0297(8) 0.0009(7) 0.0001(7) 0.0279(8)
N2 0.0454(8) 0.0363(7) 0.0229(7) 0.0019(5) 0.0043(5) 0.0064(6)
N3 0.0421(7) 0.0308(7) 0.0205(6) 0.0021(5) -0.0013(5) 0.0028(5)
C1\ 0.0907(16)\ 0.0601(13)\ 0.0382(11)\ 0.0036(9)\ -0.0040(10)\ 0.0356(12)
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C5 0.0409(8) 0.0308(8) 0.0304(8) -0.0005(6) -0.0002(6) 0.0006(6)
C6 0.0420(8) 0.0276(7) 0.0229(7) -0.0026(5) -0.0018(6) -0.0029(6)
C7\ 0.0364(8)\ 0.0362(8)\ 0.0246(8)\ 0.0028(6)\ 0.0041(6)\ -0.0011(6)
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C9 0.0318(8) 0.0381(8) 0.0365(9) 0.0012(7) -0.0005(6) -0.0080(7)
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C12\ 0.0475(10)\ 0.0404(9)\ 0.0378(10)\ 0.0003(7)\ 0.0139(8)\ -0.0007(7)
C13 0.0410(9) 0.0421(9) 0.0270(8) 0.0038(6) 0.0055(6) 0.0006(7)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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N2 H2N 0.86(2) . ?
N3 C7 1.3849(19) . ?
N3 C6 1.392(2) . ?
N3 H3N 0.83(2).?
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C5 N2 H2N 113.4(14) . . ?
C7 N3 C6 127.91(14) . . ?
C7 N3 H3N 117.6(13) . . ?
C6 N3 H3N 113.5(13) . . ?
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O1 C7 C8 121.24(14) . . ?
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C7 N3 C6 N2 -6.5(2) . . . . ?
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O1 C7 C8 C13 -25.0(2) . . . . ?
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'x-1/2, -y-1/2, z-1/2'
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Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F<sup>2</sup>, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
refine ls matrix type
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atom site disorder assembly
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O1 O 0.0654(6) 0.40185(14) 0.81583(9) 0.0346(6) Uani 1 1 d . . .
O2 O 0.2362(7) 0.81007(16) 0.89720(10) 0.0452(7) Uani 1 1 d . . .
O3 O -0.0406(7) 0.88453(15) 0.82940(11) 0.0484(7) Uani 1 1 d . . .
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N2 N 0.3385(7) 0.30839(16) 0.90278(11) 0.0242(6) Uani 1 1 d . . .
N3 N 0.1225(6) 0.45665(16) 0.90921(10) 0.0215(5) Uani 1 1 d . . .
N4 N 0.0483(7) 0.81242(17) 0.85357(10) 0.0293(6) Uani 1 1 d . . .
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C2 C 0.6487(8) 0.0378(2) 0.92509(13) 0.0268(7) Uani 1 1 d . . .
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C5 C 0.4545(7) 0.21746(18) 0.91499(11) 0.0201(6) Uani 1 1 d . . .
C6 C 0.2547(7) 0.37843(18) 0.93820(12) 0.0204(6) Uani 1 1 d . . .
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C9 C 0.0240(7) 0.64203(19) 0.85595(12) 0.0214(6) Uani 1 1 d . . .
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C12 C -0.3598(8) 0.6437(2) 0.75097(12) 0.0253(6) Uani 1 1 d . . .
C13 C -0.2679(7) 0.5605(2) 0.77661(12) 0.0240(6) Uani 1 1 d . . .
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H11 H -0.322(8) 0.784(2) 0.7613(14) 0.031(8) Uiso 1 1 d . . .
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O2\ 0.0787(18)\ 0.0296(12)\ 0.0262(12)\ -0.0017(10)\ -0.0228(12)\ -0.0062(12)
O3 0.0836(19) 0.0209(12) 0.0398(15) 0.0029(10) -0.0167(13) 0.0054(12)
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C2\ 0.0363(17)\ 0.0184(15)\ 0.0256(16)\ -0.0010(12)\ -0.0024(12)\ 0.0057(12)
C3 0.0327(16) 0.0264(15) 0.0204(15) 0.0011(12) -0.0065(12) 0.0050(13)
C4 0.0301(15) 0.0234(15) 0.0154(14) -0.0029(12) -0.0063(11) 0.0015(12)
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C7\ 0.0318(15)\ 0.0223(15)\ 0.0146(14)\ -0.0005(11)\ -0.0037(11)\ 0.0006(12)
C8 0.0284(14) 0.0222(15) 0.0120(13) 0.0001(11) -0.0014(11) 0.0025(11)
C9 0.0280(15) 0.0259(15) 0.0100(13) 0.0012(11) -0.0027(11) 0.0027(12)
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C12\ 0.0307(15)\ 0.0301(16)\ 0.0148(14)\ 0.0015(12)\ -0.0056(12)\ 0.0032(12)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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N2 C5 1.409(4) . ?
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N3 C6 1.397(3) . ?
N3 H3N 0.83(3).?
N4 C10 1.469(4) . ?
C1 C2 1.377(4) . ?
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C3 C4 1.371(4) . ?
C3 H3 0.95(3).?
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C4 C5 1.387(4) . ?
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C2 C3 H3 118.8(19) . . ?
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C9 C10 N4 118.6(2) . . ?
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C1 N1 C5 N2 179.9(3) . . . . ?
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N4 C10 C11 C12 177.5(3) . . . . ?
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Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
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goodness of fit S are based on F^2^, conventional R-factors R are based

on F, with F set to zero for negative F^2^. The threshold expression of

 $F^2 > 2 \operatorname{sigma}(F^2)$ is used only for calculating R-factors(gt) etc. and is

427

on F² are statistically about twice as large as those based on F, and Rfactors based on ALL data will be even larger. _refine_ls_structure_factor_coef Fsqd refine ls matrix type full _refine_ls_weighting_scheme calc _refine_ls_weighting_details 'calc w=1/[\s^2^(Fo^2^)+(0.0523P)^2^+0.1644P] where P=(Fo^2^+2Fc^2^)/3' _atom_sites_solution_primary direct atom sites solution secondary difmap atom sites solution hydrogens difmap _refine_ls_hydrogen_treatment refall _refine_ls_extinction_method none _refine_ls_extinction_coef _refine_ls_number_reflns 2855 refine ls number parameters 230 refine ls number restraints 0 _refine_ls_R_factor_all 0.0776 _refine_ls_R_factor_gt 0.0474 _refine_ls_wR_factor_ref 0.1172 _refine_ls_wR_factor_gt 0.1007

refine ls goodness of fit ref 1.042

1.042

0.000

0.000

refine ls restrained S all

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_refine_ls_shift/su_mean

not relevant to the choice of reflections for refinement. R-factors based

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O1 O -0.0947(3) -0.04278(11) 0.26825(8) 0.0322(4) Uani 1 1 d . . .
O2 O 0.9176(3) -0.29376(12) 0.45361(9) 0.0430(5) Uani 1 1 d . . .
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C6 C -0.1403(4) 0.17585(16) 0.28439(11) 0.0250(5) Uani 1 1 d . . .
C7 C 0.0543(4) 0.00559(16) 0.30682(12) 0.0245(5) Uani 1 1 d . . .
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C9 C 0.4606(5) 0.00649(18) 0.39460(12) 0.0283(5) Uani 1 1 d . . .
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C11 C 0.6792(4) -0.14822(16) 0.42343(11) 0.0251(5) Uani 1 1 d . . .
C12 C 0.5054(5) -0.20060(18) 0.37909(13) 0.0295(6) Uani 1 1 d . . .
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H2N H -0.192(5) 0.3176(18) 0.2837(12) 0.031(7) Uiso 1 1 d . . .
H3N H 0.157(5) 0.1390(19) 0.3413(13) 0.040(8) Uiso 1 1 d . . .
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H2 H 0.632(5) 0.4413(19) 0.4558(14) 0.052(8) Uiso 1 1 d . . .
H3 H 0.314(5) 0.541(2) 0.3948(14) 0.051(8) Uiso 1 1 d . . .
H4 H -0.027(5) 0.4595(18) 0.3233(13) 0.040(7) Uiso 1 1 d . . .
H9 H 0.443(5) 0.0746(18) 0.4012(12) 0.034(7) Uiso 1 1 d . . .
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H12 H 0.527(5) -0.2709(18) 0.3733(12) 0.033(7) Uiso 1 1 d . . .
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O2 0.0464(11) 0.0278(10) 0.0528(12) 0.0030(9) -0.0090(9) 0.0136(8)
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N2 0.0241(10) 0.0202(10) 0.0363(12) 0.0024(9) -0.0093(9) 0.0012(8)
N3 0.0222(10) 0.0214(10) 0.0365(12) 0.0003(9) -0.0082(9) 0.0001(8)
N4 0.0272(10) 0.0327(12) 0.0341(12) 0.0055(10) -0.0046(9) 0.0041(9)
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C2 0.0321(13) 0.0387(15) 0.0381(16) -0.0073(12) -0.0085(12) -0.0046(11)
C3\ 0.0446(16)\ 0.0243(13)\ 0.0479(17)\ -0.0014(12)\ -0.0093(13)\ -0.0057(11)
C4 0.0367(14) 0.0233(13) 0.0387(16) 0.0021(11) -0.0107(12) -0.0014(10)
C5 0.0226(11) 0.0262(12) 0.0287(13) -0.0007(10) -0.0021(10) -0.0007(9)
C6\ 0.0211(11)\ 0.0222(11)\ 0.0310(13)\ 0.0046(10)\ -0.0024(10)\ 0.0018(8)
C7\ 0.0202(11)\ 0.0227(11)\ 0.0302(13)\ 0.0023(10)\ -0.0015(10)\ -0.0014(9)
C8 0.0201(11) 0.0235(11) 0.0262(13) 0.0004(10) -0.0018(9) 0.0003(9)
C9 0.0288(12) 0.0204(12) 0.0343(14) -0.0014(10) -0.0061(10) 0.0004(10)
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C11\ 0.0202(11)\ 0.0265(12)\ 0.0281(13)\ 0.0025(10)\ -0.0015(9)\ 0.0050(9)
C12\ 0.0274(12)\ 0.0219(12)\ 0.0387(15)\ -0.0005(11)\ -0.0015(11)\ 0.0028(10)
C13\ 0.0244(11)\ 0.0241(12)\ 0.0384(15)\ -0.0019(11)\ -0.0058(10)\ -0.0018(10)
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All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds involving l.s. planes.

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- C3 H3 0.94(3).?
- C4 C5 1.393(3) . ?
- C4 H4 0.93(2) . ?
- C7 C8 1.510(3) . ?
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- C8 C9 1.395(3) . ?
- C9 C10 1.381(3).?
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- C10 H10 0.93(2) . ?
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Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic)

treatment of cell esds is used for estimating esds involving l.s. planes.

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- C2 C3 H3 120.4(10) . . ?
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- N1 C5 N2 110.76(11) . . ?
- C4 C5 N2 125.63(12) . . ?
- N2 C6 N3 113.98(11) . . ?
- N2 C6 S1 128.96(10) . . ?
- N3 C6 S1 117.06(9) . . ?
- O1 C7 N3 122.30(11) . . ?

- O1 C7 C8 120.99(11) . . ?
- N3 C7 C8 116.68(11) . . ?
- C9 C8 C13 118.29(11) . . ?
- C9 C8 C7 115.53(11) . . ?
- C13 C8 C7 126.18(11) . . ?
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- C8 C9 H9 117.0(10) . . ?
- C11 C10 C9 118.90(13) . . ?
- C11 C10 H10 119.9(10) . . ?
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- O2 C13 C12 122.66(11) . . ?
- O2 C13 C8 117.42(11) . . ?
- C12 C13 C8 119.91(12) . . ?
- O2 C14 H14A 104.9(11) . . ?
- O2 C14 H14B 111.0(11) . . ?
- H14A C14 H14B 108.3(15) . . ?
- O2 C14 H14C 109.7(10) . . ?
- H14A C14 H14C 108.9(15) . . ?
- H14B C14 H14C 113.7(15) . . ?

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C5 N2 C6 N3 177.75(12) . . . . ?
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C7 N3 C6 N2 -1.90(19) . . . . ?
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C13 C8 C9 C10 -0.47(19) . . . . ?
C7 C8 C9 C10 179.71(12) . . . . ?
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C9 C10 C11 C12 0.7(2) . . . . ?
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C14 O2 C13 C12 -4.81(18) . . . . ?
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diffrn reflns theta full
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diffrn measured fraction theta full 1.000
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'-x, -y, -z'
'x, -y-1/2, z-1/2'
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                         15.599(3)
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 diffrn reflns av sigmaI/netI
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_diffrn_reflns_limit_h_max
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                               -19
diffrn reflns limit k max
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                              9
diffrn reflns limit 1 max
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                              27.00
diffrn reflns theta max
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reflns number gt
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                                  'Bruker SHELXTL'
computing publication material 'Bruker SHELXTL'
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Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
refine ls matrix type
_refine_ls_weighting_scheme
                                calc
_refine_ls_weighting_details
'calc w=1/[\s^2^(Fo^2^)+(0.0568P)^2^+0.2968P] where P=(Fo^2^+2Fc^2^)/3'
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                                direct
atom sites solution secondary
                                 difmap
atom sites solution hydrogens
                                 difmap
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refine ls R factor all
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refine ls shift/su mean
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atom site type symbol
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atom site fract y
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atom site occupancy
atom site symmetry multiplicity
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atom site disorder assembly
 atom site disorder group
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O2 O 0.15303(9) 0.85182(6) 0.13355(14) 0.0461(3) Uani 1 1 d . . .
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C5 C 0.30473(11) 0.23399(8) 0.13365(17) 0.0363(3) Uani 1 1 d . . .
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H3N H 0.3790(13) 0.5084(11) 0.094(2) 0.044(4) Uiso 1 1 d . . .
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 atom site aniso U 12
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O2 0.0507(6) 0.0372(5) 0.0505(6) -0.0048(4) 0.0030(4) 0.0083(4)
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N3 0.0243(5) 0.0333(5) 0.0434(6) 0.0032(4) 0.0016(4) -0.0008(4)
C1\ 0.0558(9)\ 0.0419(8)\ 0.0599(9)\ 0.0095(7)\ -0.0074(7)\ -0.0097(7)
C2 0.0699(10) 0.0347(7) 0.0539(8) 0.0046(6) -0.0167(7) -0.0036(7)
C3 0.0599(10) 0.0417(8) 0.0588(9) -0.0054(7) -0.0088(7) 0.0093(7)
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C7\ 0.0252(6)\ 0.0401(6)\ 0.0347(6)\ 0.0012(5)\ 0.0018(4)\ -0.0002(5)
C8 0.0257(5) 0.0375(6) 0.0321(6) -0.0014(5) 0.0035(4) 0.0010(5)
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C10\ 0.0284(6)\ 0.0445(7)\ 0.0383(6)\ 0.0004(5)\ 0.0019(5)\ 0.0056(5)
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C14\ 0.0608(10)\ 0.0472(9)\ 0.0603(10)\ -0.0038(7)\ -0.0029(8)\ 0.0202(8)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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O2 C14 1.429(2) . ?
N1 C5 1.3360(17).?
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N2 C5 1.4103(17) . ?
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N3 C6 1.3898(16) . ?
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C8 C9 1.3968(17) . ?
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O1 C7 C8 122.70(11) . . ?
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C8 C13 H13 121.3(9) . . ?
O2 C14 H14A 108.0(15) . . ?
O2 C14 H14B 108.6(11) . . ?
H14A C14 H14B 113.5(17) . . ?
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H14B C14 H14C 111.0(16) . . ?
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N1 C1 C2 C3 0.2(2) . . . . ?
C1 C2 C3 C4 -0.2(2) . . . . ?
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Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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refine ls matrix type
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_refine_ls_weighting details
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N2 N 0.3327(6) 0.68961(16) 0.90021(11) 0.0262(6) Uani 1 1 d . . .
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N2 0.0404(15) 0.0207(13) 0.0171(14) 0.0019(10) -0.0035(10) -0.0056(10)
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C1\ 0.0392(18)\ 0.0248(16)\ 0.0254(17)\ 0.0052(13)\ 0.0036(13)\ -0.0005(13)
C2 0.0317(16) 0.0203(15) 0.0331(17) -0.0015(13) 0.0008(13) -0.0058(13)
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C5 0.0250(14) 0.0228(15) 0.0207(15) -0.0008(11) 0.0011(11) -0.0009(11)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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symmetry space group name H-M C2/c
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-x, y, -z+1/2
'x+1/2, y+1/2, z'
-x+1/2, y+1/2, -z+1/2
```

```
'-x, -y, -z'
'x, -y, z-1/2'
'-x+1/2, -y+1/2, -z'
'x+1/2, -y+1/2, z-1/2'
cell length a
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                         3.8548(7)
_cell_length c
                         24.769(5)
_cell_angle_alpha
                          90.00
cell angle beta
                          105.929(3)
cell angle gamma
                            90.00
_cell_volume
                         2648.5(9)
_cell_formula_units Z
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_cell_measurement_temperature
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                                 2930
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_cell_measurement theta min
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_cell_measurement_theta_max
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_exptl_crystal_size mid
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exptl absorpt coefficient mu
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_exptl_special_details
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diffrn reflns limit h max
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_diffrn_reflns_limit k max
                                4
                               -31
diffrn reflns limit 1 min
_diffrn_reflns_limit_l_max
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_computing_publication_material 'Bruker SHELXTL'
_refine_special_details
Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F<sup>2</sup>, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
refine Is matrix type
refine ls weighting scheme
                                 calc
refine ls weighting details
'calc w=1/[\s^2^(Fo^2^)+(0.0591P)^2^+0.7089P] where P=(Fo^2^+2Fc^2^)/3'
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                                 direct
atom sites solution secondary
                                  difmap
atom sites solution hydrogens
                                  difmap
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\_refine\_ls\_extinction\_method
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refine ls number parameters
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refine ls number restraints
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                               0.0930
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refine ls goodness of fit ref 1.145
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_atom_site_fract_y
atom site fract z
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atom site symmetry multiplicity
atom site calc flag
atom site refinement flags
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atom site disorder group
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N1 N 0.16128(6) 0.3754(4) 0.09590(7) 0.0257(4) Uani 1 1 d . . .
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N3 N 0.03299(6) 0.5989(4) 0.15821(7) 0.0223(4) Uani 1 1 d . . .
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C6 C 0.07925(7) 0.4616(5) 0.17917(8) 0.0205(4) Uani 1 1 d . . .
C7 C 0.00981(7) 0.6954(5) 0.10346(8) 0.0232(4) Uani 1 1 d . . .
C8 C -0.04070(7) 0.8190(5) 0.09233(8) 0.0206(4) Uani 1 1 d . . .
C9 C -0.06939(7) 0.7627(5) 0.12872(8) 0.0227(4) Uani 1 1 d . . .
C10 C -0.11673(7) 0.8738(5) 0.11455(9) 0.0245(4) Uani 1 1 d . . .
C11 C -0.13523(7) 1.0390(5) 0.06367(8) 0.0230(4) Uani 1 1 d . . .
C12 C -0.10791(7) 1.0983(5) 0.02655(8) 0.0250(4) Uani 1 1 d . . .
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H2 H 0.2688(8) 0.066(6) 0.1303(10) 0.037(6) Uiso 1 1 d . . .
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H3 H 0.2474(8) -0.097(6) 0.2141(9) 0.030(6) Uiso 1 1 d . . .
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H4 H 0.1730(7) 0.070(6) 0.2187(9) 0.022(5) Uiso 1 1 d . . .
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H1S H 0.0234(9) 0.071(7) 0.2535(12) 0.055(9) Uiso 1 1 d . . .
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atom site aniso label
atom site aniso U 11
atom site aniso U 22
atom site aniso U 33
atom site aniso U 23
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atom site aniso U 13
 atom site aniso U 12
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N1 0.0246(9) 0.0308(9) 0.0222(9) -0.0004(7) 0.0075(7) 0.0007(7)
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O1 0.0255(8) 0.0597(11) 0.0225(8) 0.0101(7) 0.0102(6) 0.0121(7)
C1\ 0.0270(11)\ 0.0369(12)\ 0.0298(12)\ -0.0036(9)\ 0.0139(9)\ -0.0002(9)
C2\ 0.0245(11)\ 0.0343(12)\ 0.0369(12)\ -0.0060(9)\ 0.0116(10)\ 0.0041(9)
C3 0.0268(11) 0.0292(11) 0.0309(12) -0.0014(9) 0.0033(9) 0.0081(9)
C4 0.0289(11) 0.0283(11) 0.0227(11) 0.0012(9) 0.0083(9) 0.0035(8)
C5 0.0202(10) 0.0222(10) 0.0245(10) -0.0039(8) 0.0058(8) -0.0006(8)
C6\ 0.0207(9)\ 0.0189(9)\ 0.0219(10)\ -0.0017(7)\ 0.0058(8)\ -0.0010(7)
C7\ 0.0224(10)\ 0.0256(10)\ 0.0210(10)\ 0.0026(8)\ 0.0051(8)\ 0.0000(8)
C8 0.0184(9) 0.0232(10) 0.0191(10) -0.0001(7) 0.0032(8) -0.0003(7)
C9 0.0232(10) 0.0257(10) 0.0187(10) 0.0022(8) 0.0048(8) -0.0022(8)
C10\ 0.0215(10)\ 0.0308(11)\ 0.0231(10)\ -0.0026(8)\ 0.0092(8)\ -0.0035(8)
C11 0.0172(9) 0.0239(10) 0.0266(10) -0.0038(8) 0.0037(8) 0.0003(8)
C12\ 0.0251(10)\ 0.0274(11)\ 0.0206(10)\ 0.0020(8)\ 0.0031(8)\ 0.0024(8)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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N2 C5 1.414(2) . ?
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N3 C7 1.388(2) . ?
N3 C6 1.396(2) . ?
N3 H3N 0.81(2) . ?
O1 C7 1.220(2) . ?
C1 C2 1.378(3) . ?
C1 H1 0.93(2) . ?
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C2 C3 1.377(3).?

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C8 C9 1.398(3).?
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C7 N3 H3N 115.8(16) . . ?
C6 N3 H3N 115.2(16) . . ?
N1 C1 C2 123.5(2) . . ?
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C2 C3 C4 C5 -0.3(3) . . . . ?
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C5 N2 C6 N3 177.39(19) . . . . ?
C5 N2 C6 S1 -3.0(3) . . . . ?
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C7 N3 C6 S1 179.50(16) . . . . ?
C6 N3 C7 O1 -2.4(3) . . . . ?
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O1 C7 C8 C13 -14.0(3) . . . . ?
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O1 C7 C8 C9 162.86(19) . . . . ?
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Cl1 Cl1 Cl2 Cl3 -179.69(15) . . . . ?
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'x-1/2, -y-1/2, z-1/2'
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cell length b
                         15.7779(10)
cell length c
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_cell_angle_gamma
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diffrn radiation monochromator graphite
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computing publication material 'Bruker SHELXTL'
_refine_special_details
Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F<sup>2</sup>, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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_refine_ls_matrix type
refine ls weighting scheme
                                calc
refine ls weighting details
'calc w=1/[\s^2^(Fo^2^)+(0.0579P)^2^+0.0000P] where P=(Fo^2^+2Fc^2^)/3'
atom sites solution primary
atom sites solution secondary
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atom sites solution hydrogens difmap
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_refine_ls_extinction method
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refine ls extinction coef
refine ls number reflns
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refine ls number parameters
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_refine_ls_number restraints
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_refine_ls_R_factor_all
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_refine_ls_R_factor_gt
                             0.0426
refine ls wR factor ref
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refine ls wR factor gt
                              0.0998
refine ls goodness of fit ref 1.015
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refine ls shift/su max
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refine ls shift/su mean
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_atom_site_fract_x
_atom_site_fract_y
atom site fract z
atom site U iso or equiv
_atom_site_adp_type
_atom_site occupancy
_atom_site_symmetry multiplicity
atom site calc flag
atom site refinement flags
atom site disorder assembly
 atom site disorder group
S1 S 0.13443(14) 0.26425(3) 0.204716(19) 0.04095(18) Uani 1 1 d . . .
O1 O 0.6396(4) 0.51220(8) 0.24178(5) 0.0402(4) Uani 1 1 d . . .
O2 O 0.8699(3) 0.30339(9) 0.32621(5) 0.0403(4) Uani 1 1 d . . .
N1 N 0.6485(4) 0.45463(10) 0.10165(6) 0.0376(4) Uani 1 1 d . . .
N2 N 0.4490(4) 0.40487(10) 0.17387(6) 0.0308(4) Uani 1 1 d . . .
N3 N 0.3161(4) 0.39644(9) 0.25688(6) 0.0281(4) Uani 1 1 d . . .
N4 N 0.0327(5) 0.38152(12) 0.47643(6) 0.0505(5) Uani 1 1 d . . .
N5 N 0.5527(4) 0.19253(10) 0.35094(6) 0.0348(4) Uani 1 1 d . . .
C1 C 0.7126(6) 0.44797(15) 0.05336(8) 0.0457(6) Uani 1 1 d . . .
C2 C 0.6372(6) 0.37811(14) 0.02524(8) 0.0449(6) Uani 1 1 d . . .
C3 C 0.4862(6) 0.31121(14) 0.04812(8) 0.0444(6) Uani 1 1 d . . .
C4 C 0.4141(6) 0.31562(13) 0.09802(8) 0.0382(5) Uani 1 1 d . . .
C5 C 0.5003(5) 0.38870(11) 0.12337(7) 0.0294(4) Uani 1 1 d . . .
C6 C 0.3091(4) 0.35821(11) 0.21006(6) 0.0278(4) Uani 1 1 d . . .
C7 C 0.4809(5) 0.46842(11) 0.27116(7) 0.0286(4) Uani 1 1 d . . .
C8 C 0.4647(4) 0.49404(11) 0.32453(6) 0.0271(4) Uani 1 1 d . . .
C9 C 0.3190(5) 0.44511(12) 0.36113(7) 0.0298(4) Uani 1 1 d . . .
C10 C 0.3114(5) 0.47504(12) 0.40982(7) 0.0309(4) Uani 1 1 d . . .
C11 C 0.4496(5) 0.55268(13) 0.42223(7) 0.0364(5) Uani 1 1 d . . .
C12 C 0.5980(6) 0.60022(13) 0.38539(8) 0.0377(5) Uani 1 1 d . . .
C13 C 0.6064(5) 0.57141(12) 0.33701(7) 0.0328(4) Uani 1 1 d . . .
C14 C 0.1564(5) 0.42319(13) 0.44741(7) 0.0367(5) Uani 1 1 d . . .
C15 C 0.7099(5) 0.23889(12) 0.31722(8) 0.0332(5) Uani 1 1 d . . .
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C16 C 0.5599(8) 0.21586(19) 0.40279(9) 0.0522(6) Uani 1 1 d . . .
C17 C 0.3800(6) 0.11523(14) 0.33748(11) 0.0451(6) Uani 1 1 d . . .
H1 H 0.815(6) 0.4966(14) 0.0404(8) 0.054(7) Uiso 1 1 d . . .
H2 H 0.684(5) 0.3769(13) -0.0104(9) 0.057(7) Uiso 1 1 d . . .
H2N H 0.526(5) 0.4529(14) 0.1831(7) 0.045(6) Uiso 1 1 d . . .
H3 H 0.424(5) 0.2616(13) 0.0306(8) 0.042(6) Uiso 1 1 d . . .
H3N H 0.208(5) 0.3675(12) 0.2788(7) 0.037(6) Uiso 1 1 d . . .
H4 H 0.310(5) 0.2737(12) 0.1138(7) 0.038(6) Uiso 1 1 d . . .
H9 H 0.226(5) 0.3925(12) 0.3535(7) 0.037(5) Uiso 1 1 d . . .
H11 H 0.447(4) 0.5699(12) 0.4560(7) 0.032(5) Uiso 1 1 d . . .
H12 H 0.700(5) 0.6504(14) 0.3927(8) 0.049(6) Uiso 1 1 d . . .
H13 H 0.714(5) 0.6032(12) 0.3108(7) 0.040(6) Uiso 1 1 d . . .
H15 H 0.695(5) 0.2167(12) 0.2837(8) 0.044(6) Uiso 1 1 d . . .
H16A H 0.664(7) 0.1698(18) 0.4205(10) 0.083(9) Uiso 1 1 d . . .
H16B H 0.337(7) 0.2277(16) 0.4136(10) 0.071(8) Uiso 1 1 d . . .
H16C H 0.692(6) 0.2662(16) 0.4054(9) 0.069(8) Uiso 1 1 d . . .
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H17B H 0.497(5) 0.0641(14) 0.3533(7) 0.047(6) Uiso 1 1 d . . .
H17C H 0.372(5) 0.1092(14) 0.3023(9) 0.056(7) Uiso 1 1 d . . .
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atom site aniso U 22
atom site aniso U 33
atom site aniso U 23
atom site aniso U 13
 atom site aniso U 12
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O1 0.0553(9) 0.0343(7) 0.0310(8) -0.0005(6) 0.0092(7) -0.0124(7)
O2 0.0429(9) 0.0359(8) 0.0421(8) 0.0025(6) 0.0034(7) -0.0089(7)
N1 0.0472(11) 0.0383(9) 0.0273(9) -0.0013(7) 0.0095(7) -0.0048(8)
N2 0.0438(10) 0.0247(8) 0.0240(8) 0.0005(7) 0.0054(7) -0.0023(7)
N3 0.0325(9) 0.0267(8) 0.0250(8) 0.0021(6) 0.0029(7) -0.0019(7)
N4 0.0679(14) 0.0520(11) 0.0316(10) 0.0026(9) 0.0075(9) -0.0035(10)
N5 0.0309(9) 0.0331(9) 0.0403(10) 0.0061(7) 0.0065(7) 0.0010(7)
C1 0.0578(15) 0.0476(13) 0.0318(12) 0.0027(10) 0.0156(10) -0.0048(12)
C2\ 0.0515(14)\ 0.0558(14)\ 0.0274(11)\ -0.0041(10)\ 0.0110(10)\ 0.0027(11)
C3\ 0.0542(15)\ 0.0420(13)\ 0.0370(12)\ -0.0134(10)\ 0.0000(10)\ 0.0056(11)
C4 0.0488(14) 0.0325(11) 0.0332(11) -0.0033(9) 0.0045(10) -0.0009(10)
C5 0.0321(11) 0.0302(10) 0.0259(9) -0.0016(7) 0.0023(8) 0.0041(8)
C6 0.0286(10) 0.0300(10) 0.0249(9) 0.0006(7) 0.0000(8) 0.0023(8)
C7 0.0337(11) 0.0238(9) 0.0283(10) 0.0008(7) 0.0017(8) 0.0038(8)
C8 0.0294(10) 0.0243(9) 0.0276(10) 0.0008(7) -0.0007(8) 0.0044(8)
C9 0.0344(11) 0.0274(10) 0.0275(10) -0.0013(8) -0.0015(8) 0.0010(9)
C10\ 0.0348(11)\ 0.0323(10)\ 0.0256(10)\ 0.0005(8)\ 0.0006(8)\ 0.0049(8)
C11\ 0.0468(13)\ 0.0363(11)\ 0.0260(11)\ -0.0054(9)\ -0.0030(9)\ 0.0066(9)
C12\ 0.0460(13)\ 0.0260(10)\ 0.0411(12)\ -0.0033(9)\ -0.0044(10)\ -0.0005(9)
C13 0.0379(12) 0.0270(10) 0.0334(11) 0.0017(8) 0.0015(9) 0.0036(9)
C14\ 0.0456(13)\ 0.0401(12)\ 0.0246(10)\ -0.0048(9)\ -0.0011(9)\ 0.0013(10)
C15\ 0.0333(11)\ 0.0310(11)\ 0.0351(12)\ 0.0032(9)\ 0.0001(9)\ 0.0013(9)
C16\ 0.0514(16)\ 0.0617(17)\ 0.0434(14)\ 0.0073(12)\ 0.0114(12)\ -0.0010(14)
C17\ 0.0381(14)\ 0.0313(12)\ 0.0660(17)\ 0.0038(11)\ 0.0105(12)\ -0.0032(10)
```

```
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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N1 C5 1.335(2).?
N2 C6 1.347(2) . ?
N2 C5 1.400(2) . ?
N2 H2N 0.86(2).?
N3 C7 1.371(2) . ?
N3 C6 1.399(2) . ?
N3 H3N 0.865(19) . ?
N4 C14 1.138(2) . ?
N5 C15 1.329(2) . ?
N5 C16 1.445(3) . ?
N5 C17 1.450(3).?
C1 C2 1.371(3) . ?
C1 H1 0.94(2) . ?
C2 C3 1.366(3).?
C2 H2 0.98(2) . ?
C3 C4 1.378(3).?
C3 H3 0.95(2) . ?
C4 C5 1.384(3).?
C4 H4 0.89(2) . ?
C7 C8 1.496(2) . ?
C8 C9 1.385(2).?
C8 C13 1.389(3).?
C9 C10 1.395(2) . ?
C9 H9 0.934(19) . ?
C10 C11 1.386(3).?
C10 C14 1.445(3) . ?
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C13 H13 0.97(2) . ?
C15 H15 0.97(2) . ?
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C16 H16A 0.97(3) . ?
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C17 H17A 0.95(2) . ?
C17 H17B 1.03(2) . ?
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C6 N2 H2N 115.2(14) . . ?
C5 N2 H2N 112.9(14) . . ?
C7 N3 C6 128.28(16) . . ?
C7 N3 H3N 119.3(13) . . ?
C6 N3 H3N 112.3(13) . . ?
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C16 N5 C17 117.69(19) . . ?
N1 C1 C2 124.1(2) . . ?
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C2 C1 H1 123.3(13) . . ?
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C3 C2 H2 120.9(13) . . ?
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C2 C3 H3 122.0(13) . . ?
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C3 C4 C5 118.1(2) . . ?
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C4 C5 N2 126.43(17) . . ?
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N2 C6 S1 127.46(14) . . ?
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O1 C7 N3 122.45(17) . . ?
O1 C7 C8 119.38(16) . . ?
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C11 C10 C9 121.10(18) . . ?
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C12 C13 C8 120.46(19) . . ?
C12 C13 H13 122.0(11) . . ?
C8 C13 H13 117.6(11) . . ?
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O2 C15 H15 120.8(12) . . ?
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C5 N2 C6 S1 -2.7(3) . . . . ?
C7 N3 C6 N2 -9.1(3) . . . . ?
C7 N3 C6 S1 171.36(15) . . . . ?
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O1 C7 C8 C13 6.0(3) . . . . ?
N3 C7 C8 C13 -173.91(17) . . . . ?
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C7 C8 C9 C10 -178.97(16) . . . . ?
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C8 C9 C10 C14 179.66(18) . . . . ?
C9 C10 C11 C12 -0.4(3) . . . . ?
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C11 C12 C13 C8 0.1(3) . . . . ?
C9 C8 C13 C12 -1.0(3) . . . . ?
C7 C8 C13 C12 179.12(17) . . . . ?
C11 C10 C14 N4 172(100) . . . . ?
C9 C10 C14 N4 -8(13) . . . . ?
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C17 N5 C15 O2 -177.49(19) . . . . ?
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_geom_hbond_site_symmetry_A
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N3 H3N O2 0.865(19) 2.13(2) 2.983(2) 170.2(18) 1_455
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'x+1/2, -y+1/2, z-1/2'
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diffrn reflns theta max
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refine special details
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Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F<sup>2</sup>, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2^2 > 2 \operatorname{sigma}(F^2^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
refine ls matrix type
_refine_ls_weighting scheme
                                 calc
refine ls weighting details
'calc w=1/[\s^2^(Fo^2^)+(0.0557P)^2^+4.7068P] where P=(Fo^2^+2Fc^2^)/3'
atom sites solution primary
                                 direct
atom sites solution secondary
                                 difmap
_atom_sites_solution_hydrogens geom
_refine_ls_hydrogen treatment
_refine_ls_extinction method
                                none
_refine_ls_extinction_coef
refine ls number reflns
                               3122
refine ls number parameters
                                 239
_refine_ls_number_restraints
_refine_ls_R_factor_all
                             0.0529
_refine_ls_R_factor_gt
                             0.0441
refine ls wR factor ref
                               0.1191
refine ls wR factor gt
                               0.1118
refine ls goodness of fit ref 1.100
_refine_ls_restrained_S_all
                               1.106
_refine_ls_shift/su_max
                              0.000
                              0.000
refine ls shift/su mean
loop
atom site label
_atom_site_type symbol
_atom_site_fract_x
atom site fract y
atom site fract z
atom site U iso or equiv
_atom_site_adp_type
_atom_site_occupancy
atom site symmetry multiplicity
atom site calc flag
_atom_site refinement flags
atom site disorder assembly
 atom site disorder group
S1 S 0.187877(16) 0.34672(14) 0.22009(2) 0.02468(16) Uani 1 1 d . . .
O1 O 0.22722(5) -0.0750(5) 0.06231(7) 0.0324(4) Uani 1 1 d . . .
N1 N 0.10964(5) -0.2028(5) 0.04709(8) 0.0283(4) Uani 1 1 d . . .
N2 N 0.16711(5) 0.0303(5) 0.11161(8) 0.0232(4) Uani 1 1 d . . .
N3 N 0.23560(5) 0.1985(5) 0.15158(8) 0.0228(4) Uani 1 1 d . . .
N4 N 0.45170(6) 0.4029(7) 0.10654(10) 0.0470(6) Uani 1 1 d . . .
```

```
C1 C 0.06889(7) -0.2835(7) 0.02904(10) 0.0325(5) Uani 1 1 d . . .
C2 C 0.04164(7) -0.2071(6) 0.06177(10) 0.0311(5) Uani 1 1 d . . .
C3 C 0.05716(7) -0.0390(7) 0.11605(11) 0.0323(5) Uani 1 1 d . . .
C4 C 0.09928(7) 0.0453(6) 0.13651(10) 0.0290(5) Uani 1 1 d . . .
C5 C 0.12394(6) -0.0402(5) 0.09976(9) 0.0225(4) Uani 1 1 d . . .
C6 C 0.19501(6) 0.1794(5) 0.15800(9) 0.0205(4) Uani 1 1 d . . .
C7 C 0.24981(6) 0.0819(5) 0.10535(9) 0.0213(4) Uani 1 1 d . . .
C8 C 0.29436(6) 0.1578(5) 0.10875(9) 0.0199(4) Uani 1 1 d . . .
C9 C 0.30727(7) 0.0621(6) 0.05905(9) 0.0245(4) Uani 1 1 d . . .
C10 C 0.34776(7) 0.1228(6) 0.05801(10) 0.0268(5) Uani 1 1 d . . .
C11 C 0.37565(6) 0.2822(6) 0.10731(10) 0.0249(4) Uani 1 1 d . . .
C12 C 0.36317(7) 0.3783(6) 0.15721(10) 0.0251(4) Uani 1 1 d . . .
C13 C 0.32242(6) 0.3162(5) 0.15774(9) 0.0219(4) Uani 1 1 d . . .
C14 C 0.41811(7) 0.3492(7) 0.10685(10) 0.0326(5) Uani 1 1 d . . .
C11S C1 0.45627(3) 0.9717(2) 0.25202(4) 0.0594(2) Uani 1 1 d D . .
C1S C 0.5027(3) 0.785(2) 0.2712(5) 0.112(5) Uani 0.50 1 d PD . 1
H2N H 0.1772(8) -0.038(7) 0.0840(12) 0.034(7) Uiso 1 1 d . . .
H3N H 0.2533(8) 0.277(8) 0.1825(13) 0.039(8) Uiso 1 1 d . . .
H1 H 0.0576(8) -0.395(7) -0.0102(11) 0.029(6) Uiso 1 1 d . . .
H2 H 0.0133(8) -0.261(7) 0.0447(11) 0.032(6) Uiso 1 1 d . . .
H3 H 0.0383(8) 0.010(7) 0.1383(12) 0.038(7) Uiso 1 1 d . . .
H4 H 0.1097(8) 0.166(7) 0.1709(12) 0.034(7) Uiso 1 1 d . . .
H9 H 0.2893(9) -0.052(8) 0.0269(13) 0.041(7) Uiso 1 1 d . . .
H10 H 0.3551(8) 0.059(7) 0.0249(12) 0.031(6) Uiso 1 1 d . . .
H12 H 0.3813(8) 0.493(7) 0.1887(12) 0.032(7) Uiso 1 1 d . . .
H13 H 0.3157(8) 0.381(6) 0.1906(12) 0.031(7) Uiso 1 1 d . . .
loop
atom site aniso label
_atom_site_aniso_U 11
atom site aniso U 22
atom site aniso U 33
atom site aniso U 23
atom site aniso U 13
 atom site aniso U 12
S1 0.0253(3) 0.0304(3) 0.0208(3) -0.0048(2) 0.0106(2) -0.0025(2)
O1 0.0222(7) 0.0486(10) 0.0280(8) -0.0147(7) 0.0097(6) -0.0079(7)
N1 0.0233(9) 0.0378(11) 0.0245(9) -0.0049(8) 0.0082(7) -0.0052(8)
N2 0.0196(8) 0.0336(10) 0.0182(8) -0.0029(7) 0.0080(7) -0.0019(7)
N3 0.0188(8) 0.0319(10) 0.0181(8) -0.0035(7) 0.0060(7) -0.0020(7)
N4 0.0255(10) 0.0736(17) 0.0456(13) -0.0056(12) 0.0161(9) -0.0097(11)
C1\ 0.0251(11)\ 0.0432(14)\ 0.0289(12)\ -0.0061(10)\ 0.0076(9)\ -0.0082(10)
C2\ 0.0199(10)\ 0.0390(13)\ 0.0343(12)\ -0.0004(10)\ 0.0075(9)\ -0.0055(9)
C3 0.0240(11) 0.0415(14) 0.0358(12) -0.0028(10) 0.0155(9) -0.0007(10)
C4 0.0232(10) 0.0390(13) 0.0268(11) -0.0051(10) 0.0102(9) -0.0021(9)
C5 0.0196(9) 0.0261(11) 0.0224(10) 0.0016(8) 0.0069(8) -0.0012(8)
C6 0.0203(9) 0.0222(10) 0.0198(9) 0.0030(8) 0.0070(7) 0.0010(8)
C7\ 0.0203(9)\ 0.0251(10)\ 0.0187(9)\ 0.0003(8)\ 0.0061(7)\ 0.0006(8)
C8 0.0193(9) 0.0212(10) 0.0203(9) 0.0011(8) 0.0076(7) 0.0009(8)
C9 0.0239(10) 0.0303(11) 0.0197(10) -0.0029(8) 0.0070(8) -0.0017(9)
C10\ 0.0275(11)\ 0.0337(12)\ 0.0221(10)\ -0.0020(9)\ 0.0118(8)\ 0.0008(9)
C11 0.0210(10) 0.0283(11) 0.0269(10) 0.0022(9) 0.0093(8) -0.0006(8)
C12\ 0.0234(10)\ 0.0274(11)\ 0.0239(10)\ -0.0034(9)\ 0.0059(8)\ -0.0029(9)
```

```
C13 0.0223(10) 0.0259(11) 0.0193(10) -0.0015(8) 0.0092(8) -0.0002(8)
C14\ 0.0296(12)\ 0.0431(14)\ 0.0269(11)\ -0.0017(10)\ 0.0113(9)\ -0.0026(10)
C11S 0.0598(5) 0.0575(5) 0.0694(5) 0.0079(4) 0.0321(4) 0.0020(4)
C1S 0.027(3) 0.111(6) 0.185(14) 0.106(8) 0.013(7) 0.002(5)
_geom_special_details
All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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_geom_bond_atom_site_label 2
_geom_bond_distance
_geom_bond_site_symmetry_2
 geom_bond_publ_flag
S1 C6 1.661(2) . ?
O1 C7 1.226(2) . ?
N1 C5 1.336(3).?
N1 C1 1.341(3).?
N2 C6 1.335(3) . ?
N2 C5 1.415(3) . ?
N2 H2N 0.85(3).?
N3 C7 1.371(3) . ?
N3 C6 1.409(2) . ?
N3 H3N 0.84(3).?
N4 C14 1.144(3) . ?
C1 C2 1.377(3) . ?
C1 H1 0.98(3).?
C2 C3 1.381(3) . ?
C2 H2 0.94(3) . ?
C3 C4 1.388(3).?
C3 H3 0.94(3).?
C4 C5 1.388(3) . ?
C4 H4 0.90(3) . ?
C7 C8 1.497(3) . ?
C8 C13 1.390(3).?
C8 C9 1.395(3) . ?
C9 C10 1.381(3) . ?
C9 H9 0.93(3).?
C10 C11 1.394(3).?
C10 H10 0.91(3) . ?
C11 C12 1.392(3) . ?
C11 C14 1.446(3).?
C12 C13 1.387(3) . ?
C12 H12 0.92(3) . ?
C13 H13 0.89(3) . ?
Cl1S C1S 1.654(9) . ?
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_geom_angle_atom_site_label 2
_geom_angle_atom_site_label_3
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geom angle site symmetry 1
geom angle site symmetry 3
 geom angle publ flag
C5 N1 C1 117.24(18) . . ?
C6 N2 C5 132.43(18) . . ?
C6 N2 H2N 114.1(18) . . ?
C5 N2 H2N 113.5(18) . . ?
C7 N3 C6 128.92(18) . . ?
C7 N3 H3N 118.0(18) . . ?
C6 N3 H3N 112.8(18) . . ?
N1 C1 C2 123.5(2) . . ?
N1 C1 H1 118.4(15)..?
C2 C1 H1 118.1(15) . . ?
C1 C2 C3 118.2(2) . . ?
C1 C2 H2 117.8(15) . . ?
C3 C2 H2 123.9(16) . . ?
C2 C3 C4 120.0(2) . . ?
C2 C3 H3 117.5(16) . . ?
C4 C3 H3 122.5(16) . . ?
C5 C4 C3 117.2(2) . . ?
C5 C4 H4 121.5(16) . . ?
C3 C4 H4 121.1(16) . . ?
N1 C5 C4 123.92(19) . . ?
N1 C5 N2 110.07(17) . . ?
C4 C5 N2 126.01(19) . . ?
N2 C6 N3 113.93(17) . . ?
N2 C6 S1 128.92(15) . . ?
N3 C6 S1 117.15(15) . . ?
O1 C7 N3 122.12(18) . . ?
O1 C7 C8 120.59(18) . . ?
N3 C7 C8 117.28(17) . . ?
C13 C8 C9 119.87(18) . . ?
C13 C8 C7 123.69(17) . . ?
C9 C8 C7 116.44(18) . . ?
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C10 C9 H9 118.6(17) . . ?
C8 C9 H9 120.7(17) . . ?
C9 C10 C11 119.11(19) . . ?
C9 C10 H10 118.4(16) . . ?
C11 C10 H10 122.5(16) . . ?
C12 C11 C10 120.84(19) . . ?
C12 C11 C14 119.31(19) . . ?
C10 C11 C14 119.85(19) . . ?
C13 C12 C11 119.53(19) . . ?
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Cl1S C1S 1.769(10) 2_655 ? C1S C1S 0.95(2) 2_655 ?

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C13 C12 H12 120.0(16) . . ?
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C12 C13 C8 120.05(19) . . ?
C12 C13 H13 116.7(16) . . ?
C8 C13 H13 123.3(16) . . ?
N4 C14 C11 179.8(3) . . ?
C1S C11S C1S 31.9(7) . 2 655 ?
C1S C1S C11S 80.7(10) 2 655.?
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CIIS CIS CIIS 119.1(4) . 2 655 ?
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geom torsion atom site label 4
geom torsion
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_geom_torsion_site_symmetry 2
_geom_torsion_site_symmetry_3
_geom_torsion_site_symmetry_4
 geom torsion publ flag
C5 N1 C1 C2 0.1(4) . . . . ?
N1 C1 C2 C3 -0.1(4) . . . . ?
C1 C2 C3 C4 -0.6(4) . . . . ?
C2 C3 C4 C5 1.3(4) . . . . ?
C1 N1 C5 C4 0.7(3) . . . . ?
C1 N1 C5 N2 -179.1(2) . . . . ?
C3 C4 C5 N1 -1.3(4) . . . . ?
C3 C4 C5 N2 178.4(2) . . . . ?
C6 N2 C5 N1 -178.6(2) . . . . ?
C6 N2 C5 C4 1.6(4) . . . . ?
C5 N2 C6 N3 180.0(2) . . . . ?
C5 N2 C6 S1 -1.2(4) . . . . ?
C7 N3 C6 N2 -1.0(3) . . . . ?
C7 N3 C6 S1 179.98(18) . . . . ?
C6 N3 C7 O1 -3.0(4) . . . . ?
C6 N3 C7 C8 176.21(19) . . . . ?
O1 C7 C8 C13 -176.0(2) . . . . ?
N3 C7 C8 C13 4.8(3) . . . . ?
O1 C7 C8 C9 4.3(3) . . . . ?
N3 C7 C8 C9 -174.92(19) . . . . ?
C13 C8 C9 C10 0.1(3) . . . . ?
C7 C8 C9 C10 179.8(2) . . . . ?
C8 C9 C10 C11 -0.2(3) . . . . ?
C9 C10 C11 C12 0.3(3) . . . . ?
C9 C10 C11 C14 -179.7(2) . . . . ?
C10 C11 C12 C13 -0.3(3) . . . . ?
C14 C11 C12 C13 179.7(2) . . . . ?
C11 C12 C13 C8 0.2(3) . . . . ?
C9 C8 C13 C12 -0.1(3) . . . . ?
C7 C8 C13 C12 -179.77(19) . . . . ?
C12 C11 C14 N4 -40(100) . . . . ?
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_geom_hbond_atom_site_label_H
_geom_hbond_atom_site_label A
\_geom\_hbond\_distance\_DH
_geom_hbond_distance_HA
geom hbond distance DA
geom hbond angle DHA
geom hbond site symmetry A
N3 H3N S1 0.84(3) 3.03(3) 3.5868(19) 125(2) 4 545
N2 H2N O1 0.85(3) 1.89(3) 2.617(2) 143(2).
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diffrn reflns theta full
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_refine_diff_density_min -0.612
_refine_diff_density_rms 0.065
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data 37b
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                               ?
_chemical_name_common
chemical melting point
                              ?
chemical formula moiety
chemical formula sum
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                              296.84
chemical formula weight
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atom type scat dispersion imag
 atom type scat source
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'H' 'H' 0.0000 0.0000
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'N' 'N' 0.0061 0.0033
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'O' 'O' 0.0106 0.0060
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                             Triclinic
symmetry space group name H-M P-1
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'-x, -y, -z'
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_cell_length b
                         12.2161(8)
_cell_length_c
                         12.6685(8)
_cell_angle_alpha
                          79.9620(10)
_cell_angle beta
                          81.9860(10)
cell angle gamma
                            79.1500(10)
_cell_volume
                         1400.55(16)
_cell_formula_units Z
_cell_measurement_temperature
                                 173(2)
_cell_measurement_reflns_used
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cell measurement theta min
                                2.19
cell measurement theta max
                                 28.25
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_exptl_crystal_colour
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exptl crystal size mid
                            0.18
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\_exptl\_crystal\_density\_diffrn
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_exptl_crystal_density_method
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exptl absorpt process details SADABS
_exptl_special_details
?
diffrn ambient temperature
                               173(2)
                               0.71073
diffrn radiation wavelength
_diffrn_radiation_type
                           MoK\a
_diffrn_radiation_source
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diffrn radiation monochromator graphite
_diffrn_measurement_device_type 'CCD area detector Bruker Apex'
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diffrn standards number
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diffrn standards interval count ?
diffrn standards interval time?
_diffrn_standards_decay %
diffrn reflns number
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diffrn reflns av R equivalents 0.0172
_diffrn_reflns_av_sigmaI/netI
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diffrn reflns limit h min
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_diffrn_reflns_limit_h_max
                               12
_diffrn_reflns_limit_k_min
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diffrn reflns limit k max
                               15
diffrn reflns limit 1 min
                              -16
diffrn reflns limit 1 max
                               16
diffrn reflns theta min
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diffrn reflns theta max
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                             6057
reflns number total
reflns number gt
                            5460
reflns threshold expression
                               >2sigma(I)
_computing_data_collection
                                'Bruker SMART'
_computing_cell_refinement
                                'Bruker SAINT'
                                'Bruker SAINT'
_computing_data_reduction
computing structure solution
                                 'Bruker SHELXTL'
computing structure refinement 'Bruker SHELXTL'
_computing_molecular_graphics
                                  'Bruker SHELXTL'
computing publication material 'Bruker SHELXTL'
_refine_special_details
Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F<sup>2</sup>, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
refine ls matrix type
_refine_ls_weighting_scheme
                                 calc
_refine_ls_weighting_ details
'calc w=1/[\s^2^(Fo^2^)+(0.0660P)^2^+0.4177P] where P=(Fo^2^+2Fc^2^)/3'
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atom sites solution secondary
                                 difmap
atom sites solution hydrogens
                                 difmap
refine ls hydrogen treatment
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_refine_ls_extinction_coef
refine ls number reflns
                               6057
refine ls number parameters
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                               2
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_refine_ls_R_factor_all
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refine ls R factor gt
                             0.0387
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refine ls wR factor gt
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refine ls shift/su max
                              0.001
refine ls shift/su mean
                              0.000
loop
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atom site type symbol
atom site fract x
atom site fract y
_atom_site_fract z
_atom_site_U_iso or equiv
_atom_site_adp_type
atom site occupancy
atom site symmetry multiplicity
atom site calc flag
_atom_site_refinement flags
atom site disorder assembly
 atom site disorder group
S1 S 0.46234(4) 0.06120(3) 0.26503(3) 0.03339(12) Uani 1 1 d . . .
O1 O 0.48195(12) 0.38818(8) 0.38294(8) 0.0336(2) Uani 1 1 d . . .
N1 N 0.28615(14) 0.41826(10) 0.12405(10) 0.0314(3) Uani 1 1 d . . .
N2 N 0.37501(13) 0.28479(10) 0.25718(9) 0.0246(2) Uani 1 1 d . . .
N3 N 0.53095(13) 0.19782(10) 0.38288(9) 0.0241(2) Uani 1 1 d . . .
N4 N 0.98326(19) 0.26769(14) 0.81492(13) 0.0504(4) Uani 1 1 d . . .
C1 C 0.21265(18) 0.45406(14) 0.03760(13) 0.0367(3) Uani 1 1 d . . .
C2 C 0.14548(17) 0.38481(14) -0.00710(12) 0.0340(3) Uani 1 1 d . . .
C3 C 0.15153(16) 0.27442(13) 0.04060(12) 0.0323(3) Uani 1 1 d . . .
C4 C 0.22648(16) 0.23452(12) 0.13044(12) 0.0287(3) Uani 1 1 d . . .
C5 C 0.29382(14) 0.30983(11) 0.16723(10) 0.0236(3) Uani 1 1 d . . .
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C7 C 0.54400(15) 0.29517(11) 0.41966(10) 0.0235(3) Uani 1 1 d . . .
C8 C 0.63931(14) 0.28211(11) 0.50782(10) 0.0221(3) Uani 1 1 d . . .
C9 C 0.67463(15) 0.18148(11) 0.57705(11) 0.0243(3) Uani 1 1 d . . .
C10 C 0.76377(16) 0.17667(12) 0.65682(11) 0.0271(3) Uani 1 1 d . . .
C11 C 0.81697(15) 0.27293(12) 0.66694(11) 0.0266(3) Uani 1 1 d . . .
C12 C 0.78106(16) 0.37456(12) 0.59819(11) 0.0280(3) Uani 1 1 d . . .
C13 C 0.69136(15) 0.37857(11) 0.51956(11) 0.0256(3) Uani 1 1 d . . .
C14 C 0.90958(18) 0.26943(13) 0.74964(13) 0.0346(3) Uani 1 1 d . . .
S1' S 0.81923(5) 0.96531(3) 0.43669(3) 0.03656(12) Uani 1 1 d . . .
O1' O 0.72968(12) 0.62916(8) 0.38013(8) 0.0319(2) Uani 1 1 d . . .
N1' N 0.94889(13) 0.60776(10) 0.62205(9) 0.0270(2) Uani 1 1 d . . .
N2' N 0.84390(13) 0.73998(10) 0.49547(9) 0.0256(2) Uani 1 1 d . . .
N3' N 0.70833(13) 0.82082(10) 0.35542(9) 0.0240(2) Uani 1 1 d . . .
N4' N 0.30785(18) 0.72593(14) -0.09640(12) 0.0491(4) Uani 1 1 d . . .
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C2' C 1.10783(16) 0.64183(13) 0.74073(11) 0.0301(3) Uani 1 1 d . . .
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C4' C 1.00004(16) 0.79510(12) 0.61499(11) 0.0275(3) Uani 1 1 d . . .
C5' C 0.93426(14) 0.71715(12) 0.58014(10) 0.0236(3) Uani 1 1 d . . .
C6' C 0.79288(14) 0.83535(11) 0.43308(10) 0.0230(3) Uani 1 1 d . . .
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C9' C 0.58624(16) 0.82340(12) 0.15489(11) 0.0264(3) Uani 1 1 d . . .
C10' C 0.50822(17) 0.82392(13) 0.06959(12) 0.0299(3) Uani 1 1 d . . .
C11' C 0.44887(15) 0.72928(12) 0.06422(11) 0.0281(3) Uani 1 1 d . . .
C12' C 0.46687(16) 0.63411(13) 0.14293(12) 0.0302(3) Uani 1 1 d . . .
C13' C 0.54454(16) 0.63447(12) 0.22760(11) 0.0276(3) Uani 1 1 d . . .
C14' C 0.36947(18) 0.72810(14) -0.02548(13) 0.0352(3) Uani 1 1 d . . .
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C1S C 0.0859(5) 0.9920(3) 0.0130(6) 0.0737(15) Uani 0.50 1 d PD . .
C2S C -0.0644(4) 1.0178(3) 0.0921(3) 0.1018(10) Uani 1 1 d D . .
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geom special details
All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles: correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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C9 C10 C11 C14 179.87(13) . . . . ?
C10 C11 C12 C13 0.1(2) . . . . ?
C14 C11 C12 C13 -179.41(13) . . . . ?
C11 C12 C13 C8 -1.0(2) . . . . ?
C9 C8 C13 C12 1.5(2) . . . . ?
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C7 C8 C13 C12 -179.49(12) . . . . ?
C10 C11 C14 N4 176(100) . . . . ?
C12 C11 C14 N4 -4(18) . . . . ?
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C5' N2' C6' N3' 178.40(13) . . . . ?
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O1' C7' C8' C9' -160.95(14) . . . . ?
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O1' C7' C8' C13' 17.59(19) . . . . ?
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C9' C10' C11' C12' -0.1(2) . . . . ?
C9' C10' C11' C14' -178.88(14) . . . . ?
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C9' C8' C13' C12' -1.2(2) . . . . ?
C7' C8' C13' C12' -179.77(13) . . . . ?
C10' C11' C14' N4' 129(13) . . . . ?
C12' C11' C14' N4' -49(13) . . . . ?
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N2 H2N O1 0.91(2) 1.81(2) 2.6027(15) 143.1(17).
N3' H3N' S1 0.83(2) 2.71(2) 3.5079(12) 161.7(17) 1 565
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Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
In the crystal structure there are chloroform, CHC13, solvent molecule
disordered around an inversion center. It was treated by SQUEEZE
[Van der Sluis, P. & Spek, A.L. (1990) Acta Cryst., Sect.A, A46, 194-201.].
Corrections of the X-ray data by SQUEEZE (63 electron/cell) was close to
the required values (58 electron/cell) for one CHCl3 molecule per
the unit cell.
refine ls structure factor coef Fsqd
refine ls matrix type
refine ls weighting scheme
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C1 C 0.2157(3) 0.9550(2) 0.0383(2) 0.0364(6) Uani 1 1 d . . .
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C8 C 0.6408(2) 0.78274(17) 0.50880(16) 0.0220(5) Uani 1 1 d . . .
C9 C 0.6780(3) 0.68252(18) 0.57773(17) 0.0248(5) Uani 1 1 d . . .
C10 C 0.7672(3) 0.6776(2) 0.65723(18) 0.0271(5) Uani 1 1 d . . .
C11 C 0.8193(2) 0.77396(19) 0.66669(17) 0.0267(5) Uani 1 1 d . . .
C12 C 0.7826(3) 0.8748(2) 0.59840(18) 0.0286(5) Uani 1 1 d . . .
C13 C 0.6930(3) 0.87920(19) 0.51980(18) 0.0258(5) Uani 1 1 d . . .
C14 C 0.9117(3) 0.7714(2) 0.7500(2) 0.0347(6) Uani 1 1 d . . .
S1' S 0.17897(7) 0.53492(5) 0.56213(5) 0.03705(19) Uani 1 1 d . . .
O1' O 0.27138(18) 0.87088(13) 0.61621(13) 0.0329(4) Uani 1 1 d . . .
N1' N 0.0487(2) 0.89213(15) 0.37679(14) 0.0282(4) Uani 1 1 d . . .
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C5' C 0.0640(2) 0.78235(19) 0.41834(17) 0.0240(5) Uani 1 1 d . . .
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C7' C 0.3128(2) 0.77932(18) 0.66871(17) 0.0245(5) Uani 1 1 d . . .
C8' C 0.3939(2) 0.77169(18) 0.76386(16) 0.0221(5) Uani 1 1 d . . .
C9' C 0.4066(3) 0.67984(19) 0.84536(18) 0.0275(5) Uani 1 1 d . . .
C10' C 0.4819(3) 0.6798(2) 0.93103(18) 0.0298(5) Uani 1 1 d . . .
C11' C 0.5449(2) 0.77198(19) 0.93580(17) 0.0266(5) Uani 1 1 d . . .
C12' C 0.5306(3) 0.8656(2) 0.85514(19) 0.0301(5) Uani 1 1 d . . .
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C13' C 0.4546(3) 0.8648(2) 0.77032(19) 0.0272(5) Uani 1 1 d . . .
C14' C 0.6240(3) 0.7730(2) 1.02529(19) 0.0323(6) Uani 1 1 d . . .
H1 H 0.209(3) 1.037(3) 0.014(2) 0.062(9) Uiso 1 1 d . . .
H1' H -0.042(3) 1.008(2) 0.2688(19) 0.041(7) Uiso 1 1 d . . .
H2 H 0.100(3) 0.914(2) -0.066(2) 0.057(9) Uiso 1 1 d . . .
H2' H -0.173(2) 0.8875(18) 0.2018(17) 0.022(6) Uiso 1 1 d . . .
H2N H 0.393(3) 0.841(2) 0.2821(19) 0.036(7) Uiso 1 1 d . . .
H2N' H 0.180(3) 0.820(2) 0.516(2) 0.044(8) Uiso 1 1 d . . .
H3 H 0.100(3) 0.733(2) 0.022(2) 0.044(8) Uiso 1 1 d . . .
H3' H -0.140(3) 0.699(2) 0.271(2) 0.055(9) Uiso 1 1 d . . .
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H3N' H 0.328(3) 0.623(2) 0.676(2) 0.042(8) Uiso 1 1 d . . .
H4 H 0.229(3) 0.668(2) 0.1715(18) 0.035(7) Uiso 1 1 d . . .
H4' H 0.016(2) 0.626(2) 0.4154(18) 0.032(6) Uiso 1 1 d . . .
H9 H 0.642(2) 0.6179(19) 0.5745(16) 0.021(6) Uiso 1 1 d . . .
H9' H 0.364(2) 0.623(2) 0.8444(17) 0.027(6) Uiso 1 1 d . . .
H10 H 0.795(3) 0.613(2) 0.7013(19) 0.034(7) Uiso 1 1 d . . .
H10' H 0.496(2) 0.618(2) 0.9875(18) 0.029(6) Uiso 1 1 d . . .
H12 H 0.818(3) 0.944(2) 0.6069(19) 0.041(7) Uiso 1 1 d . . .
H12' H 0.570(3) 0.929(2) 0.8598(19) 0.040(7) Uiso 1 1 d . . .
H13 H 0.660(3) 0.945(2) 0.474(2) 0.045(7) Uiso 1 1 d . . .
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N3 0.0314(11) 0.0176(10) 0.0265(10) -0.0019(8) -0.0133(8) -0.0009(8)
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C2\ 0.0360(15)\ 0.0400(15)\ 0.0290(13)\ -0.0003(11)\ -0.0165(11)\ -0.0026(12)
C3\ 0.0367(15)\ 0.0329(14)\ 0.0417(15)\ -0.0100(12)\ -0.0157(12)\ -0.0066(12)
C4 0.0337(14) 0.0262(13) 0.0294(13) -0.0019(10) -0.0095(10) -0.0061(10)
C5 0.0258(12) 0.0229(11) 0.0231(11) -0.0044(9) -0.0067(9) -0.0030(9)
C6\ 0.0232(12)\ 0.0212(11)\ 0.0242(11)\ -0.0015(9)\ -0.0051(9)\ -0.0053(9)
C7\ 0.0316(13)\ 0.0168(11)\ 0.0257(12)\ -0.0040(9)\ -0.0046(10)\ -0.0045(9)
C8 0.0260(12) 0.0206(11) 0.0206(11) -0.0029(9) -0.0044(9) -0.0054(9)
C9 0.0334(13) 0.0170(11) 0.0248(12) -0.0017(9) -0.0039(10) -0.0066(10)
C10\ 0.0328(14)\ 0.0226(12)\ 0.0250(12)\ 0.0005(10)\ -0.0080(10)\ -0.0026(10)
C11\ 0.0272(13)\ 0.0306(13)\ 0.0240(12)\ -0.0045(10)\ -0.0080(10)\ -0.0057(10)
C12\ 0.0366(14)\ 0.0235(12)\ 0.0292(13)\ -0.0043(10)\ -0.0078(10)\ -0.0103(10)
C13\ 0.0328(13)\ 0.0187(11)\ 0.0267(12)\ -0.0016(9)\ -0.0078(10)\ -0.0048(10)
C14\ 0.0388(15)\ 0.0331(14)\ 0.0335(14)\ 0.0012(11)\ -0.0122(12)\ -0.0088(11)
S1' 0.0466(4) 0.0190(3) 0.0514(4) -0.0052(3) -0.0268(3) -0.0051(3)
O1' 0.0479(11) 0.0183(8) 0.0367(9) -0.0001(7) -0.0201(8) -0.0085(7)
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N3' 0.0307(11) 0.0184(10) 0.0271(10) -0.0022(8) -0.0114(8) -0.0045(8)
N4' 0.0554(16) 0.0485(14) 0.0423(13) -0.0030(11) -0.0232(12) -0.0146(12)
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C3' \ 0.0324(14) \ 0.0371(14) \ 0.0275(13) \ -0.0066(11) \ -0.0085(10) \ -0.0108(11)
C4' 0.0320(13) 0.0252(13) 0.0300(13) -0.0023(10) -0.0089(10) -0.0084(10)
C5' \ 0.0253(12) \ 0.0273(12) \ 0.0200(11) \ -0.0020(9) \ -0.0050(9) \ -0.0055(9)
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C7' \ 0.0278(12) \ 0.0229(12) \ 0.0243(12) \ -0.0034(9) \ -0.0046(9) \ -0.0069(9)
C8' 0.0257(12) 0.0224(11) 0.0201(11) -0.0054(9) -0.0034(9) -0.0058(9)
C9' 0.0346(14) 0.0231(12) 0.0281(12) -0.0042(10) -0.0043(10) -0.0120(10)
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C11' \ 0.0265(12) \ 0.0337(13) \ 0.0230(11) \ -0.0080(10) \ -0.0070(9) \ -0.0076(10)
C12' \ 0.0354(14) \ 0.0291(13) \ 0.0308(13) \ -0.0078(10) \ -0.0069(10) \ -0.0130(11)
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C14' \ 0.0353(14) \ 0.0323(14) \ 0.0318(13) \ -0.0023(11) \ -0.0079(11) \ -0.0110(11)
_geom_special details
All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles: correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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geom bond site symmetry 2
 geom bond publ flag
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N1 C5 1.328(3).?
N1 C1 1.340(3) . ?
N2 C6 1.331(3) . ?
N2 C5 1.417(3).?
N2 H2N 0.83(2) . ?
N3 C7 1.382(3) . ?
N3 C6 1.403(3) . ?
N3 H3N 0.82(2) . ?
N4 C14 1.142(3) . ?
C1 C2 1.378(3) . ?
C1 H1 0.98(3).?
C2 C3 1.366(4).?
C2 H2 0.91(3) . ?
C3 C4 1.385(3) . ?
C3 H3 0.89(3).?
C4 C5 1.379(3).?
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C4 H4 0.90(2) . ?
C7 C8 1.489(3).?
C8 C9 1.391(3).?
C8 C13 1.398(3).?
C9 C10 1.385(3) . ?
C9 H9 0.93(2) . ?
C10 C11 1.390(3).?
C10 H10 0.90(2) . ?
C11 C12 1.392(3) . ?
C11 C14 1.450(3).?
C12 C13 1.379(3).?
C12 H12 1.00(3).?
C13 H13 0.94(3) . ?
S1' C6' 1.658(2) . ?
O1' C7' 1.222(2) . ?
N1' C1' 1.337(3) . ?
N1' C5' 1.342(3) . ?
N2' C6' 1.339(3) . ?
N2' C5' 1.411(3) . ?
N2' H2N' 0.87(3) . ?
N3' C7' 1.379(3) . ?
N3' C6' 1.399(3) . ?
N3' H3N' 0.79(3) . ?
N4' C14' 1.138(3) . ?
C1' C2' 1.376(3) . ?
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C3' H3' 0.95(3) . ?
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C4' H4' 0.98(2) . ?
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C11' C12' 1.396(3) . ?
C11' C14' 1.442(3) . ?
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N1 C1 H1 111.9(17) . . ?
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C3 C2 H2 121.3(18) . . ?
C1 C2 H2 120.7(18) . . ?
C2 C3 C4 120.0(2) . . ?
C2 C3 H3 120.8(17) . . ?
C4 C3 H3 119.1(17) . . ?
C5 C4 C3 117.4(2) . . ?
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N3 C6 S1 118.61(16) . . ?
O1 C7 N3 122.0(2) . . ?
O1 C7 C8 120.52(19) . . ?
N3 C7 C8 117.47(19) . . ?
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C9 C8 C7 123.87(19) . . ?
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C11 C10 H10 119.2(15) . . ?
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C12 C11 C14 118.6(2) . . ?
C13 C12 C11 119.4(2) . . ?
C13 C12 H12 119.7(14) . . ?
C11 C12 H12 120.9(14) . . ?
C12 C13 C8 120.0(2) . . ?
C12 C13 H13 123.7(15) . . ?
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C7' N3' H3N' 116.6(19) . . ?
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C9' C10' H10' 123.2(14) . . ?
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C7 N3 C6 S1 175.56(19) . . . . ?
C6 N3 C7 O1 1.5(4) . . . . ?
C6 N3 C7 C8 -178.46(19) . . . . ?
O1 C7 C8 C9 159.1(2) . . . . ?
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O1 C7 C8 C13 -20.9(3) . . . . ?
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C12 C11 C14 N4 11(12) . . . . ?
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C6' N3' C7' C8' 172.9(2) . . . . ?
O1' C7' C8' C9' 159.8(2) . . . . ?
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C13' C8' C9' C10' -1.5(3) . . . . ?
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C9' C10' C11' C14' 179.9(2) . . . . ?
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N2' H2N' O1' 0.87(3) 1.87(2) 2.612(2) 142(2) .
N3 H3N S1' 0.82(2) 2.79(3) 3.594(2) 169(2) 2 666
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'-x, -y, -z'
'x, -y-1/2, z-1/2'
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cell length b
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diffrn detector area resol mean?
diffrn standards number
diffrn standards interval count?
diffrn standards interval time?
diffrn standards decay %
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diffrn reflns limit k max
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reflns threshold expression
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                                'Bruker SAINT'
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_computing_structure_solution
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computing publication material
                                  'Bruker SHELXTL'
_refine_special_details
Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F<sup>2</sup>, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2sigma(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
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refine ls matrix type
                             full
refine ls weighting scheme
                                calc
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                                direct
atom sites solution secondary
                                 difmap
atom sites solution hydrogens
                                 difmap
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_atom_site_fract_x
atom site fract y
atom site fract z
atom site U iso or equiv
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atom site symmetry multiplicity
atom site calc flag
atom site refinement flags
atom site disorder assembly
 atom site disorder group
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Cl2 Cl 0.03954(6) -0.31632(18) 0.29827(2) 0.02814(19) Uani 1 1 d . . .
S1 S 0.51838(5) 0.29183(17) 0.56322(2) 0.02149(18) Uani 1 1 d . . .
O1 O 0.14386(15) 0.2721(6) 0.51719(7) 0.0339(5) Uani 1 1 d . . .
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N2 N 0.31145(18) 0.4507(6) 0.58002(7) 0.0222(5) Uani 1 1 d . . .
N3 N 0.32595(19) 0.2030(6) 0.50840(8) 0.0217(5) Uani 1 1 d . . .
C1 C 0.2367(2) 0.7696(8) 0.68461(10) 0.0305(7) Uani 1 1 d . . .
C2 C 0.3340(2) 0.8653(7) 0.71262(10) 0.0272(6) Uani 1 1 d . . .
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C4 C 0.4322(2) 0.6809(7) 0.65134(9) 0.0235(6) Uani 1 1 d . . .
C5 C 0.3302(2) 0.5914(6) 0.62581(8) 0.0196(5) Uani 1 1 d . . .
C6 C 0.3804(2) 0.3231(6) 0.55208(9) 0.0190(5) Uani 1 1 d . . .
C7 C 0.2134(2) 0.1844(7) 0.49266(9) 0.0221(5) Uani 1 1 d . . .
C8 C 0.1769(2) 0.0547(7) 0.44407(9) 0.0206(5) Uani 1 1 d . . .
C9 C 0.2396(2) 0.0965(6) 0.40782(9) 0.0188(5) Uani 1 1 d . . .
C10 C 0.1978(2) -0.0164(6) 0.36314(9) 0.0197(5) Uani 1 1 d . . .
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C11 C 0.0928(2) -0.1713(6) 0.35409(9) 0.0211(5) Uani 1 1 d . . .
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C13 C 0.0716(2) -0.0993(7) 0.43451(9) 0.0245(6) Uani 1 1 d . . .
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H2 H 0.332(3) 0.958(8) 0.7393(12) 0.039(9) Uiso 1 1 d . . .
H3 H 0.505(2) 0.884(7) 0.7153(9) 0.023(7) Uiso 1 1 d . . .
H4 H 0.493(3) 0.646(8) 0.6405(10) 0.030(8) Uiso 1 1 d . . .
H9 H 0.302(2) 0.195(7) 0.4113(9) 0.013(7) Uiso 1 1 d . . .
H12 H -0.041(2) -0.325(7) 0.3814(9) 0.025(7) Uiso 1 1 d . . .
H13 H 0.029(2) -0.129(7) 0.4592(9) 0.020(7) Uiso 1 1 d . . .
H2N H 0.238(2) 0.429(7) 0.5680(10) 0.026(8) Uiso 1 1 d . . .
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C13\ 0.0197(13)\ 0.0335(14)\ 0.0212(14)\ -0.0012(12)\ 0.0056(11)\ -0.0028(11)
_geom_special details
All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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N2 C6 1.340(3).?
N2 C5 1.409(3) . ?
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Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2^2 > 2 \operatorname{sigma}(F^2^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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atom site disorder assembly
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C4 0.0249(8) 0.0223(8) 0.0304(8) -0.0025(7) -0.0032(6) 0.0007(6)
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C13 0.0267(8) 0.0265(8) 0.0315(9) 0.0013(7) 0.0028(7) 0.0002(7)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles: correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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C1 C2 1.380(2) . ?
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C1 C2 C3 118.69(14) . . ?
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O1 C7 C8 121.15(14) . . ?
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C1 C2 C3 C4 1.7(3) . . . . ?
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Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
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on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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refine ls matrix type
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C4 C 0.93563(12) 0.70926(16) 0.45953(8) 0.0233(3) Uani 1 1 d . . .
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H10 H 0.3675(16) 0.086(2) 0.3029(11) 0.029(4) Uiso 1 1 d . . .
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Cl2 0.0398(2) 0.0383(2) 0.02022(17) 0.00329(13) 0.01187(13) 0.00860(14)
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O1 0.0257(4) 0.0305(5) 0.0192(4) -0.0053(4) 0.0051(3) -0.0018(4)
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N2 0.0244(5) 0.0239(5) 0.0174(5) 0.0014(4) 0.0073(4) -0.0040(4)
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C4 0.0217(6) 0.0261(6) 0.0222(6) 0.0019(5) 0.0050(5) -0.0017(5)
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C8 0.0211(6) 0.0194(6) 0.0202(6) -0.0011(4) 0.0061(5) 0.0028(4)
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C13 0.0267(6) 0.0244(6) 0.0214(6) 0.0035(5) 0.0094(5) 0.0074(5)
C14 0.0232(6) 0.0213(6) 0.0224(6) 0.0006(5) 0.0074(5) 0.0010(5)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
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and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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C8 C9 C14 C13 -178.78(11) . . . . ?
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Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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'calc w=1/[\s^2^(Fo^2^)+(0.0505P)^2^+3.6505P] where P=(Fo^2^+2Fc^2^)/3'
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'Bruker SMART'

computing data collection

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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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- N1 C5 1.325(3).?
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- N2 C5 1.438(2).?
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- N3 C8 1.372(3).?
- N3 C7 1.391(2) . ?
- N3 H3N 0.76(2) . ?
- C1 C2 1.373(4).?
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- C2 C3 1.365(4).?
- C2 H2 0.93(3) . ?
- C3 C4 1.397(3).?
- C3 H3 0.93(3).?
- C4 C5 1.390(3).?
- C4 C6 1.497(3) . ?
- C6 H6C 0.89(4) . ?
- C6 H6B 0.91(5) . ?
- C6 H6A 0.89(5) . ?
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- O1 C8 N3 122.95(17)..?
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diffrn radiation monochromator graphite
diffrn measurement device type 'Bruker Apex CCD area detector'
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diffrn standards decay %
diffrn reflns number
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_diffrn_reflns_av R equivalents 0.0215
                              0.0145
diffrn reflns av sigmaI/netI
diffrn reflns limit h min
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diffrn reflns limit h max
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diffrn reflns limit k min
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_diffrn_reflns_limit_l_min
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computing molecular graphics
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_computing_publication_material 'Bruker SHELXTL'
_refine_special_details
Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
refine ls matrix type
_refine_ls_weighting_scheme
                                calc
_refine_ls_weighting details
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atom sites solution secondary
                                 difmap
atom sites solution hydrogens difmap
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refine ls number reflns
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atom site calc flag
atom site refinement flags
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O3 O 0.28956(10) 0.09002(10) -0.57085(9) 0.0365(2) Uani 1 1 d . . .
N1 N 0.55959(10) 0.19844(10) 0.39850(10) 0.0260(2) Uani 1 1 d . . .
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N3 N 0.42076(10) 0.31782(10) 0.02257(9) 0.0208(2) Uani 1 1 d . . .
N4 N 0.23611(11) 0.16533(10) -0.53010(9) 0.0266(2) Uani 1 1 d . . .
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C2 C 0.55432(13) 0.28100(13) 0.58157(11) 0.0278(3) Uani 1 1 d . . .
C3 C 0.46056(13) 0.36098(12) 0.51905(11) 0.0244(3) Uani 1 1 d . . .
C4 C 0.41368(12) 0.36045(11) 0.39478(11) 0.0215(2) Uani 1 1 d . . .
C5 C 0.47223(11) 0.27895(11) 0.34124(10) 0.0213(2) Uani 1 1 d . . .
C6 C 0.30362(13) 0.43840(12) 0.32635(12) 0.0262(3) Uani 1 1 d . . .
C7 C 0.45753(11) 0.35032(11) 0.14244(10) 0.0199(2) Uani 1 1 d . . .
C8 C 0.38918(12) 0.20496(11) -0.02524(11) 0.0223(2) Uani 1 1 d . . .
C9 C 0.35089(11) 0.19850(11) -0.15778(10) 0.0209(2) Uani 1 1 d . . .
C10 C 0.27520(11) 0.28684(11) -0.23022(11) 0.0220(2) Uani 1 1 d . . .
C11 C 0.23587(12) 0.27567(11) -0.35310(11) 0.0230(3) Uani 1 1 d . . .
C12 C 0.27579(12) 0.17605(11) -0.39952(10) 0.0220(2) Uani 1 1 d . . .
C13 C 0.35285(12) 0.08770(11) -0.32982(11) 0.0243(3) Uani 1 1 d . . .
C14 C 0.38896(12) 0.09868(11) -0.20714(11) 0.0238(3) Uani 1 1 d . . .
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H2 H 0.5855(15) 0.2801(14) 0.6671(15) 0.030(4) Uiso 1 1 d . . .
H2N H 0.4144(17) 0.1995(17) 0.1847(16) 0.036(4) Uiso 1 1 d . . .
H3 H 0.4231(14) 0.4185(14) 0.5600(13) 0.026(4) Uiso 1 1 d . . .
H3N H 0.4307(15) 0.3695(15) -0.0217(14) 0.025(4) Uiso 1 1 d . . .
H6A H 0.2369(19) 0.3901(17) 0.2739(17) 0.047(5) Uiso 1 1 d . . .
H6B H 0.2669(18) 0.4783(17) 0.3778(18) 0.046(5) Uiso 1 1 d . . .
H6C H 0.3287(17) 0.4952(17) 0.2791(16) 0.042(5) Uiso 1 1 d . . .
H10 H 0.2461(15) 0.3540(14) -0.1989(13) 0.026(4) Uiso 1 1 d . . .
H11 H 0.1836(15) 0.3360(15) -0.4018(14) 0.027(4) Uiso 1 1 d . . .
H13 H 0.3804(15) 0.0231(15) -0.3625(14) 0.029(4) Uiso 1 1 d . . .
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 atom site aniso U 12
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O1 0.0503(6) 0.0219(5) 0.0214(4) 0.0008(4) 0.0126(4) -0.0025(4)
O2 0.0364(5) 0.0394(6) 0.0207(4) 0.0027(4) 0.0030(4) -0.0048(4)
O3 0.0452(6) 0.0412(6) 0.0246(5) -0.0118(4) 0.0138(4) -0.0045(5)
N1 0.0281(5) 0.0292(6) 0.0221(5) 0.0033(4) 0.0104(4) 0.0020(4)
N2 0.0308(5) 0.0205(5) 0.0167(5) -0.0015(4) 0.0092(4) -0.0027(4)
N3 0.0277(5) 0.0204(5) 0.0149(5) 0.0008(4) 0.0080(4) -0.0015(4)
N4 0.0295(6) 0.0299(6) 0.0201(5) -0.0046(4) 0.0081(4) -0.0110(4)
C1 0.0277(6) 0.0337(7) 0.0222(6) 0.0064(5) 0.0063(5) 0.0016(5)
C2 0.0324(7) 0.0328(7) 0.0167(6) 0.0016(5) 0.0064(5) -0.0072(5)
C3 0.0312(6) 0.0239(6) 0.0202(6) -0.0026(5) 0.0114(5) -0.0071(5)
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O1 O 0.39192(10) 0.11562(8) 0.03443(8) 0.0311(2) Uani 1 1 d . . .

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C4 0.0252(6) 0.0204(6) 0.0197(6) 0.0007(4) 0.0090(5) -0.0037(5)
C5 0.0248(6) 0.0230(6) 0.0167(5) 0.0003(4) 0.0080(5) -0.0039(5)
C6 0.0305(7) 0.0264(6) 0.0227(6) 0.0009(5) 0.0103(5) 0.0022(5)
C7 0.0209(5) 0.0223(6) 0.0170(5) -0.0004(4) 0.0070(4) 0.0022(4)
C8 0.0256(6) 0.0228(6) 0.0193(6) -0.0011(5) 0.0086(5) 0.0001(5)
C9 0.0236(6) 0.0214(6) 0.0182(6) -0.0019(4) 0.0076(4) -0.0038(4)
C10\ 0.0230(6)\ 0.0215(6)\ 0.0223(6)\ -0.0029(5)\ 0.0090(5)\ -0.0019(5)
C11 0.0219(6) 0.0241(6) 0.0218(6) 0.0015(5) 0.0058(5) -0.0019(5)
C12\ 0.0238(6)\ 0.0259(6)\ 0.0164(5)\ -0.0034(5)\ 0.0071(5)\ -0.0081(5)
C13 0.0294(6) 0.0215(6) 0.0243(6) -0.0050(5) 0.0122(5) -0.0034(5)
C14\ 0.0286(6)\ 0.0201(6)\ 0.0221(6)\ 0.0000(5)\ 0.0078(5)\ 0.0003(5)
_geom_special_details
All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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geom bond publ flag
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O1 C8 1.2218(15) . ?
O2 N4 1.2274(16) . ?
O3 N4 1.2241(15) . ?
N1 C5 1.3298(16) . ?
N1 C1 1.3448(17) . ?
N2 C7 1.3401(16) . ?
N2 C5 1.4337(15) . ?
N2 H2N 0.848(18) . ?
N3 C8 1.3801(16) . ?
N3 C7 1.3979(15) . ?
N3 H3N 0.816(17) . ?
N4 C12 1.4756(15) . ?
C1 C2 1.383(2).?
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C2 C3 1.3832(19) . ?
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C4 C6 1.4978(18) . ?
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C6 H6C 0.95(2).?
C8 C9 1.4961(16) . ?
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C9 C10 1.3915(17) . ?
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C10 H10 0.944(16) . ?
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C12 C13 1.3844(19) . ?
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C7 N2 C5 124.95(10) . . ?
C7 N2 H2N 115.5(12) . . ?
C5 N2 H2N 117.1(12) . . ?
C8 N3 C7 127.32(11) . . ?
C8 N3 H3N 116.8(11) . . ?
C7 N3 H3N 115.1(11) . . ?
O3 N4 O2 124.14(11) . . ?
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N1 C1 C2 122.89(12) . . ?
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C1 C2 H2 120.7(10) . . ?
C3 C2 H2 120.9(10) . . ?
C2 C3 C4 120.71(12) . . ?
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C5 C4 C3 115.33(11) . . ?
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N1 C5 N2 113.14(11) . . ?
C4 C5 N2 121.31(11) . . ?
C4 C6 H6A 109.6(12) . . ?
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H6A C6 H6C 107.8(16) . . ?
H6B C6 H6C 110.3(16) . . ?
N2 C7 N3 115.41(11) . . ?
N2 C7 S1 125.42(9) . . ?
N3 C7 S1 119.17(9) . . ?
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O1 C8 C9 121.39(11) . . ?
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C12 C13 H13 122.1(10) . . ?
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N1 C1 C2 C3 3.1(2) . . . . ?
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C2 C3 C4 C6 174.05(12) . . . . ?
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O3 N4 C12 C11 166.92(11) . . . . ?
O2 N4 C12 C11 -12.40(16) . . . . ?
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computing data collection
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computing publication material
                                  'Bruker SHELXTL'
_refine_special_details
Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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Flack H D (1983), Acta Cryst. A39, 876-881'
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S1A S 0.79379(15) 0.50684(8) 0.75461(6) 0.0267(2) Uani 1 1 d . . .
O1A O 0.8466(4) 0.9085(2) 0.55419(15) 0.0304(6) Uani 1 1 d . . .
N1A N 0.8449(4) 0.5199(3) 0.51706(18) 0.0251(7) Uani 1 1 d . . .
N2A N 0.9132(5) 0.6554(3) 0.59454(19) 0.0222(7) Uani 1 1 d . . .
N3A N 0.7712(5) 0.7631(3) 0.68783(19) 0.0216(6) Uani 1 1 d . . .
C1A C 0.9023(6) 0.4260(4) 0.4833(2) 0.0291(8) Uani 1 1 d . . .
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C6A C 1.3079(7) 0.5269(5) 0.6367(3) 0.0327(10) Uani 1 1 d . . .
C7A C 0.8307(5) 0.6458(3) 0.6737(2) 0.0198(7) Uani 1 1 d . . .
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C8A C 0.7734(5) 0.8855(3) 0.6289(2) 0.0210(7) Uani 1 1 d . . .
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C10A C 0.8240(7) 1.0927(4) 0.6572(2) 0.0313(9) Uani 1 1 d . . .
C11A C 0.7557(7) 1.1931(4) 0.6884(3) 0.0356(10) Uani 1 1 d . . .
C12A C 0.5489(8) 1.1916(4) 0.7252(3) 0.0389(10) Uani 1 1 d . . .
C13A C 0.4104(7) 1.0930(4) 0.7300(3) 0.0345(9) Uani 1 1 d . . .
C14A C 0.4804(6) 0.9911(3) 0.6994(2) 0.0266(8) Uani 1 1 d . . .
Br1B Br 1.22045(5) 0.45282(4) 0.91283(3) 0.04392(12) Uani 1 1 d . . .
S1B S 0.65851(17) 0.79871(9) 0.88022(6) 0.0311(2) Uani 1 1 d . . .
O1B O 0.7016(4) 0.4038(2) 1.08429(15) 0.0315(6) Uani 1 1 d . . .
N1B N 0.6167(5) 0.7937(3) 1.11794(19) 0.0258(7) Uani 1 1 d . . .
N2B N 0.5751(5) 0.6491(3) 1.04299(18) 0.0217(6) Uani 1 1 d . . .
N3B N 0.7218(5) 0.5458(3) 0.9477(2) 0.0225(6) Uani 1 1 d . . .
C1B C 0.5453(6) 0.8886(4) 1.1494(2) 0.0314(9) Uani 1 1 d . . .
C2B C 0.3558(6) 0.9468(4) 1.1352(2) 0.0293(8) Uani 1 1 d . . .
C3B C 0.2300(6) 0.9032(4) 1.0869(2) 0.0298(8) Uani 1 1 d . . .
C4B C 0.2965(5) 0.8056(3) 1.0533(2) 0.0256(8) Uani 1 1 d . . .
C5B C 0.4944(5) 0.7564(3) 1.0704(2) 0.0202(7) Uani 1 1 d . . .
C6B C 0.1579(7) 0.7540(5) 1.0040(3) 0.0388(10) Uani 1 1 d . . .
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C8B C 0.7446(5) 0.4258(3) 1.0067(2) 0.0224(7) Uani 1 1 d . . .
C9B C 0.8196(6) 0.3209(3) 0.9704(2) 0.0233(7) Uani 1 1 d . . .
C10B C 0.6781(7) 0.2167(4) 0.9820(3) 0.0334(9) Uani 1 1 d . . .
C11B C 0.7381(8) 0.1160(4) 0.9502(3) 0.0388(10) Uani 1 1 d . . .
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C14B C 1.0195(6) 0.3179(4) 0.9287(2) 0.0285(8) Uani 1 1 d . . .
Br1C Br 0.92033(5) -0.27519(3) 0.28495(2) 0.03058(9) Uani 1 1 d . . .
S1C S 0.53580(13) 0.18403(9) 0.44635(5) 0.02665(19) Uani 1 1 d . . .
O1C O 0.8855(3) 0.0231(2) 0.24682(14) 0.0242(5) Uani 1 1 d . . .
N1C N 0.3118(5) 0.2193(3) 0.21469(18) 0.0278(7) Uani 1 1 d . . .
N2C N 0.6110(4) 0.1911(3) 0.28228(19) 0.0217(6) Uani 1 1 d . . .
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C3C C 0.2582(6) 0.4714(4) 0.2208(2) 0.0299(8) Uani 1 1 d . . .
C4C C 0.4261(5) 0.4008(3) 0.2560(2) 0.0222(7) Uani 1 1 d . . .
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H10A H 0.960(6) 1.104(3) 0.629(2) 0.024(10) Uiso 1 1 d . . .
H11A H 0.854(6) 1.267(4) 0.684(2) 0.034(11) Uiso 1 1 d . . .
H12A H 0.495(6) 1.252(4) 0.748(3) 0.046(12) Uiso 1 1 d . . .
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H6AC H 1.431(7) 0.501(4) 0.628(2) 0.029(11) Uiso 1 1 d . . .
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H6BA H 0.162(6) 0.659(4) 1.021(3) 0.046(13) Uiso 1 1 d . . .
H6BB H 0.014(6) 0.778(4) 1.016(2) 0.026(11) Uiso 1 1 d . . .
H6BC H 0.201(6) 0.797(4) 0.944(2) 0.024(10) Uiso 1 1 d . . .
H1C H 0.048(6) 0.238(4) 0.157(2) 0.038(11) Uiso 1 1 d . . .
H2C H 0.013(7) 0.460(4) 0.158(3) 0.036(11) Uiso 1 1 d . . .
H3C H 0.225(5) 0.571(3) 0.2232(19) 0.011(7) Uiso 1 1 d . . .
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H13C H 1.268(5) -0.370(3) 0.3718(19) 0.006(8) Uiso 1 1 d . . .
H6CA H 0.593(7) 0.565(5) 0.261(3) 0.056(13) Uiso 1 1 d . . .
H6CB H 0.531(8) 0.454(5) 0.358(3) 0.077(16) Uiso 1 1 d . . .
H6CC H 0.711(6) 0.422(3) 0.286(2) 0.022(9) Uiso 1 1 d . . .
H2NA H 0.909(5) 0.730(4) 0.554(2) 0.019(9) Uiso 1 1 d . . .
H3NA H 0.728(5) 0.755(3) 0.737(2) 0.022(10) Uiso 1 1 d . . .
H2NB H 0.580(6) 0.577(4) 1.082(3) 0.031(11) Uiso 1 1 d . . .
H3NB H 0.740(6) 0.549(4) 0.900(2) 0.029(11) Uiso 1 1 d . . .
H2NC H 0.663(5) 0.153(3) 0.252(2) 0.018(9) Uiso 1 1 d . . .
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C2A 0.040(2) 0.025(2) 0.032(2) -0.0172(17) 0.0005(17) 0.0033(17)
C3A 0.027(2) 0.025(2) 0.033(2) -0.0080(16) -0.0013(16) 0.0094(16)
C4A 0.0286(19) 0.0193(17) 0.0229(18) -0.0082(14) 0.0003(15) 0.0035(15)
C5A \ 0.0233(18) \ 0.0200(18) \ 0.0199(17) \ -0.0068(14) \ -0.0012(14) \ 0.0036(14)
C6A 0.028(2) 0.040(3) 0.034(2) -0.017(2) -0.0077(19) 0.010(2)
C7A 0.0176(16) 0.0197(17) 0.0253(17) -0.0116(14) -0.0040(13) 0.0031(13)
C8A 0.0191(17) 0.0208(18) 0.0224(18) -0.0050(14) -0.0052(14) 0.0054(14)
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C14A 0.0282(19) 0.0261(19) 0.0279(19) -0.0106(16) -0.0070(15) 0.0055(15)
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S1B 0.0513(6) 0.0207(5) 0.0207(5) -0.0075(4) -0.0011(4) 0.0046(4)
O1B 0.0462(16) 0.0261(14) 0.0203(13) -0.0072(11) 0.0000(11) 0.0108(12)
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N2B 0.0296(16) 0.0193(16) 0.0165(14) -0.0064(13) -0.0023(12) 0.0026(13)
N3B 0.0290(17) 0.0219(16) 0.0185(16) -0.0104(13) -0.0005(13) 0.0031(12)
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C2B 0.044(2) 0.0195(19) 0.0259(19) -0.0114(16) 0.0011(17) 0.0041(16)
C3B 0.027(2) 0.033(2) 0.030(2) -0.0127(17) 0.0009(16) 0.0065(17)
C4B 0.0219(18) 0.0257(19) 0.0267(18) -0.0050(15) -0.0021(14) -0.0014(14)
C5B 0.0251(18) 0.0218(18) 0.0147(16) -0.0084(14) 0.0001(13) 0.0010(14)
C6B 0.030(2) 0.043(3) 0.051(3) -0.023(2) -0.013(2) 0.003(2)
C7B 0.0214(17) 0.0231(18) 0.0221(17) -0.0102(15) -0.0029(14) -0.0004(14)
C8B 0.0218(17) 0.0236(19) 0.0224(18) -0.0083(15) -0.0030(14) 0.0025(14)
C9B 0.0272(19) 0.0221(18) 0.0202(17) -0.0049(14) -0.0066(14) 0.0051(15)
C10B 0.044(3) 0.022(2) 0.033(2) -0.0086(17) 0.0015(18) -0.0026(17)
C11B 0.056(3) 0.023(2) 0.038(2) -0.0114(18) -0.004(2) -0.002(2)
C12B 0.065(3) 0.028(2) 0.032(2) -0.0127(19) -0.001(2) 0.014(2)
C13B 0.038(3) 0.041(3) 0.035(2) -0.017(2) 0.004(2) 0.010(2)
C14B 0.033(2) 0.029(2) 0.0281(19) -0.0145(16) -0.0070(16) 0.0077(16)
Br1C 0.0324(2) 0.02525(19) 0.0400(2) -0.01745(16) -0.00816(16) 0.00336(15)
S1C 0.0307(5) 0.0279(5) 0.0252(4) -0.0144(4) -0.0031(4) 0.0086(4)
O1C 0.0276(13) 0.0245(13) 0.0244(13) -0.0121(10) -0.0079(10) 0.0077(10)
N1C 0.0285(16) 0.0231(16) 0.0313(16) -0.0056(13) -0.0096(13) 0.0003(13)
N2C 0.0232(15) 0.0225(16) 0.0242(15) -0.0136(13) -0.0050(12) 0.0078(12)
N3C 0.0256(16) 0.0209(16) 0.0200(15) -0.0088(13) -0.0072(13) 0.0058(13)
C1C 0.028(2) 0.036(2) 0.032(2) -0.0022(17) -0.0108(16) -0.0019(17)
C2C 0.023(2) 0.035(2) 0.033(2) -0.0051(18) -0.0069(17) 0.0070(17)
C3C 0.030(2) 0.028(2) 0.0275(19) -0.0046(16) -0.0013(16) 0.0103(16)
C4C 0.0244(19) 0.0216(18) 0.0186(16) -0.0056(14) 0.0015(14) 0.0050(15)
C5C 0.0222(17) 0.0237(18) 0.0184(16) -0.0039(13) -0.0033(13) 0.0034(14)
C6C 0.039(2) 0.019(2) 0.043(2) -0.0144(18) -0.0130(19) 0.0080(17)
C7C\ 0.0226(17)\ 0.0175(17)\ 0.0244(17)\ -0.0083(14)\ -0.0045(14)\ -0.0010(13)
C8C 0.0183(16) 0.0199(17) 0.0207(17) -0.0064(14) 0.0001(13) -0.0018(13)
C9C 0.0221(18) 0.0178(17) 0.0211(17) -0.0064(14) -0.0007(14) 0.0015(14)
C10C\ 0.0241(18)\ 0.027(2)\ 0.0259(18)\ -0.0083(15)\ -0.0032(14)\ -0.0002(15)
C11C 0.0223(19) 0.036(2) 0.028(2) -0.0050(17) -0.0036(16) -0.0027(16)
C12C 0.024(2) 0.035(2) 0.034(2) 0.0005(18) -0.0038(17) 0.0056(17)
C13C\ 0.035(2)\ 0.022(2)\ 0.028(2)\ -0.0074(17)\ -0.0009(16)\ 0.0071(16)
C14C 0.0227(17) 0.0212(17) 0.0249(18) -0.0084(14) -0.0017(14) 0.0005(14)
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All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only

used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds involving l.s. planes.

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Br1B C14B 1.894(4) . ?
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                               >2sigma(I)
_computing_data_collection
                               'Bruker SMART'
_computing_cell_refinement
                                'Bruker SAINT'
_computing_data_reduction
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_computing_structure_solution
                                'Bruker SHELXTL'
computing structure refinement
                                 'Bruker SHELXTL'
computing molecular graphics
                                  'Bruker SHELXTL'
computing publication material 'Bruker SHELXTL'
_refine_special_details
Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F<sup>2</sup>, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
```

not relevant to the choice of reflections for refinement. R-factors based on F² are statistically about twice as large as those based on F, and Rfactors based on ALL data will be even larger. refine ls structure factor coef Fsqd _refine_ls_matrix_type _refine_ls_weighting scheme calc _refine_ls_weighting_details 'calc w=1/[\s^2^(Fo^2^)+(0.0408P)^2^+0.0000P] where P=(Fo^2^+2Fc^2^)/3' atom sites solution primary atom sites solution secondary difmap atom sites solution hydrogens difmap refine ls hydrogen treatment _refine_ls_extinction_method none refine ls extinction coef refine ls abs structure details 'Flack H D (1983), Acta Cryst. A39, 876-881' _refine_ls_abs_structure_Flack 0.03(10) _refine_ls_number reflns 2952 _refine_ls_number_parameters 229 refine ls number restraints _refine_ls_R_factor_all 0.0756 _refine_ls_R_factor_gt 0.0479 _refine_ls_wR factor ref 0.0979 _refine_ls_wR_factor_gt 0.0861 refine ls goodness of fit ref 1.048 refine ls restrained S all 1.048 _refine_ls_shift/su_max 0.001 _refine_ls_shift/su_mean 0.000 loop _atom_site_label atom site type symbol atom site fract x _atom_site_fract_v _atom_site_fract_z atom site U iso or equiv atom site adp type atom site occupancy atom site symmetry multiplicity _atom_site_calc flag _atom_site_refinement flags

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O2 O 0.8891(4) 0.45704(15) 0.39660(8) 0.0451(5) Uani 1 1 d . . .
N1 N 0.5081(5) 0.3932(2) 0.32539(11) 0.0407(6) Uani 1 1 d . . .
N2 N 0.7488(4) 0.55707(18) 0.31552(9) 0.0341(5) Uani 1 1 d . . .
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C2 C 0.0565(8) 0.0740(3) 0.41014(19) 0.0720(12) Uani 1 1 d . . .
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C11 C 1.1350(7) 0.7289(2) 0.34832(14) 0.0483(8) Uani 1 1 d . . .
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C3\ 0.059(2)\ 0.0482(17)\ 0.052(2)\ 0.0008(17)\ 0.0201(17)\ -0.0049(16)
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are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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N1 C7 1.399(3).?
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N2 C9 1.375(3) . ?
N2 C8 1.415(3) . ?
N2 H2N 0.90(2) . ?
C1 C6 1.374(4) . ?
C1 C2 1.386(5).?
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loop

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'-x, -y, -z'

'x-1/2, y, -z-1/2'

'x, -y-1/2, z-1/2'

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computing data reduction
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_computing_structure_refinement 'Bruker SHELXTL'
_computing_molecular_graphics
                                  'Bruker SHELXTL'
_computing_publication_material 'Bruker SHELXTL'
refine special details
Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
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factors based on ALL data will be even larger.

590

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_atom_site_occupancy
_atom_site_symmetry_multiplicity
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_atom_site_disorder_assembly
atom site disorder group
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O1 O 0.94202(12) 0.12749(18) 0.33323(7) 0.0444(4) Uani 1 1 d . . .
O2 O 0.73032(19) 0.3936(3) 0.19480(10) 0.0901(9) Uani 1 1 d . . .
O3 O 0.56515(17) 0.3968(3) 0.20442(11) 0.0834(8) Uani 1 1 d . . .
O4 O 0.40258(11) 0.15597(16) 0.36404(8) 0.0395(4) Uani 1 1 d . . .
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All esds (except the esd in the dihedral angle between two l.s. planes)

are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds involving l.s. planes.

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F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
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H1B H -0.111(3) 0.3753(14) 0.1711(8) 0.053(5) Uiso 1 1 d . . .
H1C H 0.097(3) 0.3435(13) 0.1776(7) 0.050(5) Uiso 1 1 d . . .
H3 H -0.027(2) 0.3653(13) 0.2961(6) 0.037(4) Uiso 1 1 d . . .
H4 H 0.029(2) 0.4943(12) 0.3527(6) 0.034(4) Uiso 1 1 d . . .
H5 H 0.105(2) 0.6364(12) 0.3173(6) 0.032(4) Uiso 1 1 d . . .
H10 H 0.020(2) 0.7001(11) -0.0055(6) 0.026(4) Uiso 1 1 d . . .
H11 H 0.052(2) 0.8097(11) -0.0693(6) 0.028(4) Uiso 1 1 d . . .
H13 H 0.265(2) 0.9932(11) 0.0308(6) 0.027(4) Uiso 1 1 d . . .
H14 H 0.236(2) 0.8840(10) 0.0943(6) 0.027(4) Uiso 1 1 d . . .
H15A H 0.251(2) 1.0909(11) -0.0888(7) 0.037(4) Uiso 1 1 d . . .
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O1 0.0343(5) 0.0194(4) 0.0235(4) -0.0001(3) -0.0004(4) -0.0018(4)
O2 0.0306(5) 0.0233(4) 0.0228(4) 0.0032(3) -0.0005(4) -0.0023(4)
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N2 0.0368(6) 0.0242(5) 0.0225(5) -0.0007(4) -0.0009(5) 0.0001(5)
N3 0.0335(6) 0.0202(5) 0.0224(5) -0.0002(4) 0.0000(4) -0.0016(4)
C1 0.0421(8) 0.0243(7) 0.0295(7) 0.0042(6) 0.0027(6) -0.0016(6)
C2 0.0232(6) 0.0242(6) 0.0286(7) 0.0044(5) 0.0011(5) 0.0030(5)
C3 0.0286(7) 0.0321(7) 0.0283(7) 0.0082(6) 0.0020(5) 0.0030(6)
C4 0.0305(7) 0.0404(8) 0.0222(6) 0.0060(6) -0.0003(5) 0.0066(6)
C5 0.0341(7) 0.0340(7) 0.0227(6) -0.0018(5) -0.0020(5) 0.0036(6)
C6 0.0254(6) 0.0262(6) 0.0239(6) -0.0009(5) -0.0006(5) 0.0025(5)
C7 0.0254(6) 0.0198(6) 0.0264(6) -0.0033(5) -0.0009(5) 0.0003(5)
C8 0.0205(6) 0.0209(6) 0.0239(6) -0.0003(5) 0.0009(5) 0.0010(5)
C9 0.0200(5) 0.0201(6) 0.0221(6) 0.0001(4) 0.0016(4) 0.0015(4)
C10\ 0.0218(6)\ 0.0199(6)\ 0.0255(6)\ -0.0031(5)\ 0.0002(5)\ -0.0007(5)
C11 0.0253(6) 0.0246(6) 0.0198(6) -0.0032(5) -0.0018(5) -0.0002(5)
C12 0.0193(5) 0.0218(6) 0.0227(6) 0.0015(5) 0.0018(4) 0.0024(5)
C13 0.0224(6) 0.0185(5) 0.0245(6) -0.0026(5) 0.0001(5) -0.0005(5)
C14\ 0.0235(6)\ 0.0220(6)\ 0.0210(6)\ -0.0020(4)\ -0.0009(5)\ 0.0014(5)
C15\ 0.0299(7)\ 0.0233(6)\ 0.0303(7)\ 0.0036(5)\ 0.0034(6)\ -0.0026(5)
geom special details
All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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S1 O1 2.1419(10) . ?
O1 C8 1.2680(15) . ?
O2 C12 1.3570(15) . ?
O2 C15 1.4298(16) . ?
N1 C6 1.3622(17) . ?
N1 C2 1.3728(16) . ?
N2 C7 1.3220(17) . ?
N2 C6 1.3512(17) . ?
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N3 C8 1.3457(16) . ?
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C1 H1A 0.94(2) . ?
C1 H1B 0.97(2).?
C1 H1C 0.98(2).?
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#
          Cambridge Crystallographic Data Centre
#
                  CCDC
#
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computing cell refinement
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refine special details
Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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refine ls matrix type
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are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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- N3 C7 1.3420(17).?
- C1 C2 1.358(2).?
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on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
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N2 N 0.97825(13) 0.12945(12) -0.09007(7) 0.0320(3) Uani 1 1 d . . .
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C4 C 0.23072(19) 0.10255(18) -0.32007(10) 0.0444(4) Uani 1 1 d . . .
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C7 C 0.56062(15) 0.01032(14) -0.15385(8) 0.0305(3) Uani 1 1 d . . .
C8 C 0.52563(17) -0.08443(15) -0.09474(9) 0.0348(3) Uani 1 1 d . . .
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H3 H 0.016(2) 0.0094(19) -0.3199(11) 0.054(5) Uiso 1 1 d . . .
H4 H 0.200(2) 0.157(2) -0.3656(12) 0.058(5) Uiso 1 1 d . . .
H5 H 0.4577(19) 0.1731(18) -0.3021(10) 0.041(4) Uiso 1 1 d . . .
H8 H 0.5858(18) -0.1170(18) -0.0485(10) 0.038(4) Uiso 1 1 d . . .
H9A H 0.748(2) 0.076(2) -0.2122(11) 0.052(5) Uiso 1 1 d . . .
H9B H 0.6942(18) 0.1925(18) -0.1539(10) 0.038(4) Uiso 1 1 d . . .
H10A H 0.8718(17) -0.0584(19) -0.1012(9) 0.041(4) Uiso 1 1 d . . .
H10B H 0.8024(16) 0.0475(16) -0.0377(9) 0.030(4) Uiso 1 1 d . . .
H12A H 1.285(2) 0.189(2) -0.0935(11) 0.049(5) Uiso 1 1 d . . .
H12B H 1.2020(18) 0.2899(17) -0.1613(10) 0.036(4) Uiso 1 1 d . . .
H13A H 1.429(3) 0.386(3) -0.0344(15) 0.083(7) Uiso 1 1 d . . .
H13B H 1.463(3) 0.368(3) -0.1332(14) 0.083(7) Uiso 1 1 d . . .
H13C H 1.346(2) 0.489(3) -0.1114(13) 0.073(6) Uiso 1 1 d . . .
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N1 0.0397(7) 0.0359(6) 0.0384(6) 0.0002(5) 0.0130(5) -0.0112(5)
N2 0.0288(6) 0.0275(5) 0.0405(6) -0.0078(5) 0.0076(5) -0.0026(4)
N3 0.0319(6) 0.0256(6) 0.0349(6) -0.0064(5) 0.0105(5) -0.0050(4)
C1 0.0342(7) 0.0297(6) 0.0344(7) -0.0098(5) 0.0115(5) -0.0046(5)
C2 0.0327(7) 0.0395(8) 0.0487(8) -0.0161(7) 0.0115(6) -0.0077(6)
C3 0.0347(8) 0.0528(9) 0.0480(9) -0.0179(7) -0.0004(6) 0.0012(7)
C4 0.0472(9) 0.0495(9) 0.0356(8) -0.0032(7) 0.0010(7) 0.0072(7)
C5 0.0387(7) 0.0380(7) 0.0332(7) -0.0022(6) 0.0086(6) 0.0002(6)
C6 0.0304(6) 0.0297(6) 0.0303(6) -0.0070(5) 0.0090(5) -0.0027(5)
C7\ 0.0313(7)\ 0.0297(6)\ 0.0314(6)\ -0.0027(5)\ 0.0078(5)\ -0.0042(5)
C8 0.0376(7) 0.0336(7) 0.0336(7) 0.0001(5) 0.0055(6) -0.0066(6)
C9 0.0333(7) 0.0362(8) 0.0360(7) 0.0027(6) 0.0074(6) -0.0080(6)
C10\ 0.0319(7)\ 0.0244(6)\ 0.0418(7)\ -0.0034(5)\ 0.0045(6)\ -0.0039(5)
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C11 0.0306(6) 0.0250(6) 0.0298(6) 0.0007(5) 0.0044(5) -0.0016(5)
C12 0.0309(7) 0.0370(7) 0.0400(8) -0.0069(6) 0.0103(6) -0.0015(6)
C13\ 0.0453(10)\ 0.0493(10)\ 0.0887(15)\ -0.0171(10)\ 0.0319(10)\ -0.0137(8)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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N1 H1N 0.86(2).?
N2 C11 1.3383(17).?
N2 C10 1.4588(17) . ?
N2 H2N 0.880(17) . ?
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N3 C12 1.4544(17) . ?
N3 H3N 0.826(18) . ?
C1 C2 1.400(2) . ?
C1 C6 1.4136(18) . ?
C2 C3 1.377(2) . ?
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C4 H4 0.91(2) . ?
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C5 H5 0.974(17) . ?
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C7 C8 1.3632(19) . ?
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C11 N2 H2N 118.9(11) . . ?
C10 N2 H2N 116.6(11) . . ?
C11 N3 C12 125.06(12) . . ?
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C12 N3 H3N 116.9(11) . . ?
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N1 C1 C6 107.52(12) . . ?
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C2 C3 H3 119.8(11) . . ?
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C1 C6 C7 C9 -179.12(12) . . . . ?
C6 C7 C8 N1 1.03(15) . . . . ?
C9 C7 C8 N1 179.58(13) . . . . ?
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C12 N3 C11 N2 5.2(2) . . . . ?
C12 N3 C11 S1 -176.22(11) . . . . ?
C10 N2 C11 N3 -178.16(12) . . . . ?
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C11 N3 C12 C13 -178.68(15) . . . . ?
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N3 H3N S1 0.826(18) 2.558(19) 3.3594(12) 163.9(15) 3_765
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computing publication material
                                 'Bruker SHELXTL'
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Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2sigma(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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                                calc
refine ls weighting details
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atom site calc flag
atom site refinement flags
atom site disorder assembly
 atom site disorder group
S1 S 0.03863(4) 0.10584(5) 0.11754(6) 0.0322(2) Uani 1 1 d . . .
N1 N 0.14799(16) 0.02341(18) 0.8157(2) 0.0332(5) Uani 1 1 d . . .
N2 N 0.11411(14) 0.20465(18) 0.3769(2) 0.0303(5) Uani 1 1 d . . .
N3 N -0.02428(14) 0.2749(2) 0.2583(2) 0.0372(6) Uani 1 1 d . . .
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C3 C 0.3577(2) 0.0407(3) 1.1207(3) 0.0494(8) Uani 1 1 d . . .
C4 C 0.4126(2) 0.0877(3) 1.0357(3) 0.0493(8) Uani 1 1 d . . .
C5 C 0.37834(18) 0.1112(2) 0.8863(3) 0.0403(7) Uani 1 1 d . . .
C6 C 0.28701(16) 0.08738(19) 0.8193(3) 0.0295(5) Uani 1 1 d . . .
C7 C 0.23055(15) 0.10122(19) 0.6695(2) 0.0277(5) Uani 1 1 d . . .
C8 C 0.14714(18) 0.0606(2) 0.6729(3) 0.0303(6) Uani 1 1 d . . .
C9 C 0.26184(17) 0.1513(2) 0.5420(3) 0.0324(6) Uani 1 1 d . . .
C10 C 0.19688(17) 0.1388(2) 0.3885(3) 0.0321(6) Uani 1 1 d . . .
C11 C 0.04325(16) 0.20206(19) 0.2583(2) 0.0274(5) Uani 1 1 d . . .
C12 C -0.10312(18) 0.2973(3) 0.1341(3) 0.0432(7) Uani 1 1 d . . .
C13 C -0.19167(18) 0.2794(3) 0.1750(3) 0.0393(7) Uani 1 1 d . . .
C14 C -0.27314(19) 0.3120(3) 0.0483(4) 0.0467(7) Uani 1 1 d . . .
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H2 H 0.2288(17) -0.013(2) 1.111(3) 0.044(8) Uiso 1 1 d . . .
H3 H 0.3835(19) 0.022(2) 1.225(4) 0.065(9) Uiso 1 1 d . . .
H4 H 0.4736(19) 0.101(2) 1.080(3) 0.048(8) Uiso 1 1 d . . .
H5 H 0.4159(19) 0.142(2) 0.829(3) 0.048(8) Uiso 1 1 d . . .
H8 H 0.0922(16) 0.056(2) 0.597(3) 0.029(6) Uiso 1 1 d . . .
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H10A H 0.2293(16) 0.165(2) 0.314(3) 0.040(7) Uiso 1 1 d . . .
H10B H 0.1790(15) 0.064(2) 0.371(2) 0.030(6) Uiso 1 1 d . . .
H12A H -0.099(2) 0.380(3) 0.106(3) 0.065(10) Uiso 1 1 d . . .
H12B H -0.0994(19) 0.244(3) 0.059(4) 0.065(9) Uiso 1 1 d . . .
H13A H -0.1985(19) 0.201(3) 0.203(3) 0.066(10) Uiso 1 1 d . . .
H13B H -0.1917(18) 0.329(3) 0.263(3) 0.059(9) Uiso 1 1 d . . .
H14A H -0.276(2) 0.267(3) -0.045(4) 0.088(12) Uiso 1 1 d . . .
H14B H -0.278(2) 0.394(3) 0.020(4) 0.075(10) Uiso 1 1 d . . .
H15A H -0.372(2) 0.202(3) 0.093(4) 0.100(13) Uiso 1 1 d . . .
H15B H -0.364(2) 0.323(3) 0.189(4) 0.082(11) Uiso 1 1 d . . .
H16A H -0.436(3) 0.420(4) -0.062(5) 0.124(18) Uiso 1 1 d . . .
H16B H -0.450(3) 0.300(4) -0.133(5) 0.115(16) Uiso 1 1 d . . .
H16C H -0.505(3) 0.328(3) -0.008(4) 0.088(12) Uiso 1 1 d . . .
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
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treatment of cell esds is used for estimating esds involving l.s. planes.

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on F, with F set to zero for negative F². The threshold expression of $F^2^2 > 2 \operatorname{sigma}(F^2^2)$ is used only for calculating R-factors(gt) etc. and is not relevant to the choice of reflections for refinement. R-factors based on F² are statistically about twice as large as those based on F, and Rfactors based on ALL data will be even larger. refine ls structure factor coef Fsqd refine ls matrix type refine ls weighting scheme calc refine ls weighting details 'calc w=1/[\s^2^(Fo^2^)+(0.0456P)^2^+0.4270P] where P=(Fo^2^+2Fc^2^)/3' _atom_sites_solution_primary direct atom sites solution secondary difmap atom sites solution hydrogens difmap _refine_ls_hydrogen_treatment refall _refine_ls_extinction method none _refine_ls_extinction coef _refine_ls_number_reflns 5082 refine ls number parameters 378 refine ls number restraints 0 _refine_ls_R_factor_all 0.0420 _refine_ls_R_factor_gt 0.0342 _refine_ls_wR_factor_ref 0.0912 refine ls wR factor gt 0.0845 refine ls goodness of fit ref 1.021 _refine_ls_restrained_S_all 1.021 _refine_ls_shift/su_max 0.001 refine ls shift/su mean 0.000 loop atom site label atom site type symbol _atom_site_fract_x _atom_site_fract_y atom site fract z atom site U iso or equiv atom site adp type atom site occupancy _atom_site_symmetry_multiplicity _atom_site_calc flag atom site refinement flags _atom_site_disorder_assembly atom site disorder group C11 C1 0.28319(5) -0.11525(4) -0.57556(4) 0.03473(12) Uani 1 1 d . . . Cl2 Cl 0.66436(6) 0.45378(5) 0.70274(5) 0.04702(15) Uani 1 1 d . . . S1 S 0.75615(5) -0.20602(4) -0.11224(4) 0.03433(12) Uani 1 1 d . . . S2 S 0.01787(6) 0.90363(5) 0.21368(4) 0.04386(14) Uani 1 1 d . . . O1 O 0.66837(14) 0.19740(11) 0.08330(11) 0.0353(3) Uani 1 1 d . . . O2 O 0.81239(15) 0.70439(12) 0.48044(12) 0.0403(3) Uani 1 1 d . . . N1 N 0.43662(17) 0.02872(13) -0.23684(13) 0.0304(3) Uani 1 1 d . . .

Refinement of F² against ALL reflections. The weighted R-factor wR and goodness of fit S are based on F², conventional R-factors R are based

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N2 N 0.62731(17) 0.00172(14) -0.11377(13) 0.0285(3) Uani 1 1 d . . .
N3 N 0.78898(17) 0.01834(13) 0.04978(13) 0.0281(3) Uani 1 1 d . . .
N4 N 0.34162(17) 0.53933(14) 0.90482(13) 0.0295(3) Uani 1 1 d . . .
N5 N 0.1830(2) 0.43361(19) 0.98025(16) 0.0402(4) Uani 1 1 d . . .
N6 N 0.1541(2) 0.70203(18) 0.0680(2) 0.0608(6) Uani 1 1 d . . .
C1 C 0.3589(2) 0.00318(17) -0.34264(16) 0.0311(4) Uani 1 1 d . . .
C2 C 0.39283(19) -0.08907(16) -0.44256(15) 0.0278(4) Uani 1 1 d . . .
C3 C 0.5140(2) -0.15795(16) -0.43458(16) 0.0289(4) Uani 1 1 d . . .
C4 C 0.5960(2) -0.13327(16) -0.32550(15) 0.0284(4) Uani 1 1 d . . .
C5 C 0.55157(19) -0.03893(15) -0.22867(14) 0.0258(3) Uani 1 1 d . . .
C6 C 0.71971(19) -0.05640(15) -0.06027(15) 0.0263(3) Uani 1 1 d . . .
C7 C 0.76562(19) 0.13984(15) 0.11490(15) 0.0277(4) Uani 1 1 d . . .
C8 C 0.8697(2) 0.19330(16) 0.22798(18) 0.0344(4) Uani 1 1 d . . .
C9 C 0.85632(19) 0.33008(16) 0.29349(15) 0.0293(4) Uani 1 1 d . . .
C10 C 0.7491(2) 0.37005(18) 0.36980(18) 0.0377(4) Uani 1 1 d . . .
C11 C 0.7368(2) 0.49545(18) 0.43046(18) 0.0377(4) Uani 1 1 d . . .
C12 C 0.8333(2) 0.58296(16) 0.41606(15) 0.0295(4) Uani 1 1 d . . .
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C14 C 0.9507(2) 0.41916(17) 0.27947(17) 0.0334(4) Uani 1 1 d . . .
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C17 C 0.5239(2) 0.44447(16) 0.78601(15) 0.0310(4) Uani 1 1 d . . .
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C19 C 0.3668(2) 0.32437(16) 0.85951(16) 0.0317(4) Uani 1 1 d . . .
C20 C 0.29401(19) 0.43230(16) 0.91650(15) 0.0290(4) Uani 1 1 d . . .
C21 C 0.0978(2) 0.78563(18) 0.12796(18) 0.0362(4) Uani 1 1 d . . .
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H5NA H 0.153(3) 0.504(3) 1.019(2) 0.059(7) Uiso 1 1 d . . .
H5NB H 0.157(3) 0.369(2) 0.991(2) 0.051(7) Uiso 1 1 d . . .
H8A H 0.850(2) 0.148(2) 0.2770(19) 0.043(6) Uiso 1 1 d . . .
H8B H 0.966(3) 0.178(2) 0.2088(19) 0.043(6) Uiso 1 1 d . . .
H10 H 0.685(3) 0.313(2) 0.385(2) 0.052(6) Uiso 1 1 d . . .
H11 H 0.665(2) 0.525(2) 0.483(2) 0.047(6) Uiso 1 1 d . . .
H13 H 1.006(2) 0.6008(19) 0.3286(17) 0.035(5) Uiso 1 1 d . . .
H14 H 1.021(3) 0.397(2) 0.233(2) 0.047(6) Uiso 1 1 d . . .
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H15B H 0.923(2) 0.802(2) 0.401(2) 0.052(7) Uiso 1 1 d . . .
H15C H 0.894(2) 0.869(2) 0.535(2) 0.045(6) Uiso 1 1 d . . .
H16 H 0.479(2) 0.6266(19) 0.8408(17) 0.035(5) Uiso 1 1 d . . .
H18 H 0.534(2) 0.2617(19) 0.7606(18) 0.036(5) Uiso 1 1 d . . .
H19 H 0.336(2) 0.255(2) 0.8724(19) 0.045(6) Uiso 1 1 d . . .
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atom site aniso U 11
atom site aniso U 22
atom site aniso U 33
atom site aniso U 23
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atom site aniso U 13
 atom site aniso U 12
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C21\ 0.0348(10)\ 0.0333(10)\ 0.0431(11)\ 0.0158(9)\ 0.0080(8)\ 0.0027(8)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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O2 C12 C11 115.47(16) . . ?
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C12 C13 H13 122.2(13) . . ?
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C9 C14 C13 121.80(17) . . ?
C9 C14 H14 120.4(15) . . ?
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refine special details
Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F^2^, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2^2 > 2 \operatorname{sigma}(F^2^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
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atom site U iso or equiv
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O1 O 0.11217(15) 0.33930(10) 0.19926(9) 0.0277(2) Uani 1 1 d . . .
O2 O 0.77010(15) 0.88659(11) 0.03020(10) 0.0316(2) Uani 1 1 d . . .
N1 N 0.27614(16) -0.03336(12) 0.44044(11) 0.0248(2) Uani 1 1 d . . .
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N3 N 0.08547(16) 0.41381(12) 0.36116(10) 0.0222(2) Uani 1 1 d . . .
C1 C 0.3299(2) -0.16721(15) 0.49936(14) 0.0277(3) Uani 1 1 d . . .
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into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
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C13 C 0.41564(11) 0.58334(18) 0.89061(9) 0.0279(4) Uani 1 1 d . . .
C14 C 0.38139(11) 0.68416(18) 0.93270(8) 0.0242(3) Uani 1 1 d . . .
H1N H 0.2503(12) 0.763(3) 1.0019(8) 0.026(5) Uiso 1 1 d . . .
H3 H 0.1834(14) 0.939(2) 1.1685(10) 0.040(6) Uiso 1 1 d . . .
H5 H 0.0371(13) 0.572(2) 1.2013(10) 0.035(6) Uiso 1 1 d . . .
H7 H 0.1162(12) 0.665(2) 1.0277(9) 0.023(5) Uiso 1 1 d . . .
H10 H 0.2937(14) 0.910(2) 0.8314(10) 0.037(6) Uiso 1 1 d . . .
H12 H 0.4297(14) 0.533(3) 0.7988(11) 0.040(6) Uiso 1 1 d . . .
H14 H 0.3898(13) 0.668(2) 0.9753(9) 0.027(5) Uiso 1 1 d . . .
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C12\ 0.0466(3)\ 0.0240(2)\ 0.0432(3)\ -0.00013(18)\ 0.0015(2)\ -0.01439(19)
Cl3 0.0784(4) 0.0583(4) 0.0257(3) -0.0042(2) 0.0008(2) 0.0171(3)
Cl4 0.0520(3) 0.0232(2) 0.0531(3) 0.00193(19) 0.0065(2) 0.0148(2)
O1 0.0329(6) 0.0159(6) 0.0301(6) -0.0015(5) 0.0064(5) -0.0025(4)
O2 0.0311(6) 0.0161(6) 0.0301(6) 0.0022(5) 0.0054(5) 0.0016(4)
N1 0.0303(7) 0.0113(7) 0.0298(8) 0.0000(5) 0.0070(6) 0.0003(5)
C1\ 0.0217(7)\ 0.0176(7)\ 0.0248(8)\ 0.0009(6)\ 0.0001(6)\ -0.0001(6)
C2 0.0225(8) 0.0172(7) 0.0253(8) 0.0024(6) 0.0016(6) 0.0012(6)
C3\ 0.0313(9)\ 0.0211(8)\ 0.0266(8)\ -0.0010(7)\ 0.0008(7)\ -0.0017(7)
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C4 0.0371(9) 0.0303(9) 0.0227(8) 0.0010(7) 0.0036(7) -0.0008(8)
C5 0.0327(9) 0.0264(9) 0.0281(8) 0.0075(7) 0.0049(7) -0.0023(7)
C6 0.0250(8) 0.0172(7) 0.0327(9) 0.0017(6) -0.0007(7) -0.0020(6)
C7 0.0259(8) 0.0182(8) 0.0245(8) 0.0005(6) 0.0017(6) 0.0010(6)
C8 0.0204(7) 0.0179(7) 0.0251(8) 0.0001(6) 0.0005(6) 0.0005(6)
C9 0.0216(7) 0.0164(7) 0.0287(8) -0.0018(6) 0.0039(6) -0.0016(6)
C10 0.0284(8) 0.0240(8) 0.0287(8) 0.0019(7) 0.0018(7) 0.0008(7)
C11\ 0.0380(9)\ 0.0336(10)\ 0.0255(9)\ -0.0026(7)\ 0.0024(7)\ 0.0006(8)
C12\ 0.0399(10)\ 0.0267(9)\ 0.0346(9)\ -0.0081(8)\ 0.0088(8)\ 0.0031(8)
C13 0.0283(8) 0.0169(8) 0.0384(9) -0.0001(7) 0.0049(7) 0.0025(6)
C14\ 0.0270(8)\ 0.0180(8)\ 0.0275(9)\ 0.0003(6)\ 0.0038(7)\ -0.0003(6)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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Cl4 C13 1.7352(17) . ?
O1 C1 1.2119(19) . ?
O2 C8 1.2123(19) . ?
N1 C8 1.386(2) . ?
N1 C1 1.388(2) . ?
N1 H1N 0.76(3).?
C1 C2 1.497(2) . ?
C2 C3 1.389(2) . ?
C2 C7 1.390(2) . ?
C3 C4 1.385(2) . ?
C3 H3 0.95(2) . ?
C4 C5 1.386(3) . ?
C5 C6 1.380(2) . ?
C5 H5 0.94(2) . ?
C6 C7 1.386(2).?
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C10 H10 0.94(2) . ?
C11 C12 1.391(3).?
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C1 N1 H1N 118.2(14) . . ?
O1 C1 N1 123.82(15) . . ?
O1 C1 C2 121.97(15) . . ?
N1 C1 C2 114.20(14) . . ?
C3 C2 C7 120.92(15) . . ?
C3 C2 C1 117.32(15) . . ?
C7 C2 C1 121.75(15) . . ?
C4 C3 C2 118.58(16) . . ?
C4 C3 H3 121.2(13) . . ?
C2 C3 H3 120.1(13) . . ?
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C3 C4 Cl1 119.25(14) . . ?
C5 C4 Cl1 118.94(14) . . ?
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C6 C5 H5 121.6(13) . . ?
C4 C5 H5 120.2(13) . . ?
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O2 C8 N1 124.23(15) . . ?
O2 C8 C9 122.26(15) . . ?
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O1 C1 C2 C7 145.82(17) . . . . ?
N1 C1 C2 C7 -35.5(2) . . . . ?
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C1 N1 C8 C9 178.64(15) . . . . ?
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C9 C10 C11 C12 -0.8(3) . . . . ?
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Cl3 Cl1 Cl2 Cl3 178.41(14) . . . . ?
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C11 C12 C13 C14 -179.79(14) . . . . ?
C12 C13 C14 C9 0.2(3) . . . . ?
Cl4 Cl3 Cl4 C9 -178.61(13) . . . . ?
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N1 H1N O2 0.76(3) 2.39(2) 3.0317(19) 143.5(18) 8 655
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'x-1/2, -y-1/2, z-1/2'
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computing publication material 'Bruker SHELXTL'
_refine_special_details
Refinement of F<sup>2</sup> against ALL reflections. The weighted R-factor wR and
goodness of fit S are based on F<sup>2</sup>, conventional R-factors R are based
on F, with F set to zero for negative F^2^. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
factors based on ALL data will be even larger.
refine ls structure factor coef Fsqd
refine Is matrix type
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_refine_ls_weighting_ details
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                                 direct
atom sites solution secondary
                                 difmap
atom sites solution hydrogens
                                 difmap
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atom site disorder assembly
 atom site disorder group
S1 S 0.67817(3) 0.11444(4) 0.075135(19) 0.02683(12) Uani 1 1 d . . .
O1 O 0.32020(9) 0.19181(13) 0.12478(5) 0.0302(2) Uani 1 1 d . . .
N1 N 0.50848(10) 0.62846(13) 0.12725(6) 0.0215(2) Uani 1 1 d . . .
N2 N 0.59194(10) 0.34449(13) 0.16751(6) 0.0209(2) Uani 1 1 d . . .
N3 N 0.44406(10) 0.29492(13) 0.04182(6) 0.0197(2) Uani 1 1 d . . .
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C3 C 0.39328(13) 0.65523(19) 0.25739(8) 0.0287(3) Uani 1 1 d . . .
C4 C 0.45915(13) 0.50218(17) 0.24470(7) 0.0261(3) Uani 1 1 d . . .
C5 C 0.51520(11) 0.49638(15) 0.17917(7) 0.0197(2) Uani 1 1 d . . .
C6 C 0.56965(11) 0.25745(15) 0.09695(7) 0.0197(2) Uani 1 1 d . . .
C7 C 0.32319(12) 0.25471(15) 0.06007(7) 0.0207(2) Uani 1 1 d . . .
C8 C 0.19616(12) 0.29652(15) -0.00313(7) 0.0210(2) Uani 1 1 d . . .
C9 C 0.19247(14) 0.4221(2) -0.06159(10) 0.0367(3) Uani 1 1 d . . .
C10 C 0.06935(16) 0.4681(2) -0.11453(11) 0.0460(4) Uani 1 1 d . . .
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C12 C -0.04665(15) 0.2623(2) -0.05241(10) 0.0415(4) Uani 1 1 d . . .
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H1 H 0.4422(16) 0.868(2) 0.1033(10) 0.028(4) Uiso 1 1 d . . .
H2 H 0.3417(17) 0.902(2) 0.2110(10) 0.033(4) Uiso 1 1 d . . .
H3 H 0.3553(17) 0.664(2) 0.3033(11) 0.038(4) Uiso 1 1 d . . .
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H4 H 0.4669(16) 0.403(2) 0.2789(10) 0.028(4) Uiso 1 1 d . . .
H9 H 0.272(2) 0.481(3) -0.0628(12) 0.062(6) Uiso 1 1 d . . .
H10 H 0.067(2) 0.559(3) -0.1526(14) 0.071(7) Uiso 1 1 d . . .
H11 H -0.131(2) 0.423(3) -0.1460(12) 0.053(5) Uiso 1 1 d . . .
H12 H -0.131(2) 0.210(3) -0.0498(13) 0.062(6) Uiso 1 1 d . . .
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H14B H 0.6853(19) 0.168(3) 0.2489(12) 0.048(5) Uiso 1 1 d . . .
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atom site aniso U 22
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atom site aniso U 23
atom site aniso U 13
 atom site aniso U 12
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N1 0.0204(5) 0.0228(5) 0.0207(5) 0.0001(4) 0.0041(4) 0.0007(4)
N2 0.0203(5) 0.0210(5) 0.0196(5) 0.0005(4) 0.0022(4) 0.0018(4)
N3 0.0182(5) 0.0234(5) 0.0173(5) -0.0005(4) 0.0042(4) 0.0003(4)
C1 0.0240(6) 0.0229(6) 0.0254(6) -0.0005(5) 0.0026(5) 0.0019(5)
C2 0.0216(6) 0.0277(6) 0.0305(6) -0.0084(5) 0.0035(5) 0.0023(5)
C3\ 0.0258(6)\ 0.0369(7)\ 0.0254(6)\ -0.0076(5)\ 0.0100(5)\ -0.0028(5)
C4 0.0284(6) 0.0287(6) 0.0220(6) -0.0003(5) 0.0078(5) -0.0032(5)
C5 0.0169(5) 0.0215(5) 0.0191(5) -0.0020(4) 0.0019(4) -0.0014(4)
C6 0.0186(5) 0.0190(5) 0.0217(5) 0.0015(4) 0.0052(4) -0.0012(4)
C7 0.0211(6) 0.0180(5) 0.0233(6) -0.0026(4) 0.0064(4) -0.0020(4)
C8 0.0192(5) 0.0211(5) 0.0229(5) -0.0035(4) 0.0058(4) 0.0000(4)
C9 0.0210(6) 0.0415(8) 0.0466(8) 0.0179(7) 0.0067(6) 0.0010(6)
C10\ 0.0297(7)\ 0.0526(10)\ 0.0521(9)\ 0.0259(8)\ 0.0041(7)\ 0.0066(7)
C11 0.0220(6) 0.0432(8) 0.0353(7) -0.0035(6) -0.0002(5) 0.0065(5)
C12 0.0212(7) 0.0569(10) 0.0428(8) 0.0017(7) 0.0014(6) -0.0118(6)
C13 0.0264(7) 0.0460(8) 0.0348(7) 0.0088(6) 0.0032(5) -0.0104(6)
C14 0.0289(7) 0.0309(7) 0.0237(6) 0.0005(5) -0.0033(5) 0.0065(5)
_geom_special_details
All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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C6 N3 H3N 117.3(10) . . ?
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on F, with F set to zero for negative F². The threshold expression of $F^2 > 2 \operatorname{sigma}(F^2)$ is used only for calculating R-factors(gt) etc. and is not relevant to the choice of reflections for refinement. R-factors based on F² are statistically about twice as large as those based on F, and Rfactors based on ALL data will be even larger. refine ls structure factor coef Fsqd refine ls matrix type refine ls weighting scheme calc refine Is weighting details 'calc w=1/[\s^2^(Fo^2^)+(0.0556P)^2^+0.5237P] where P=(Fo^2^+2Fc^2^)/3' _atom_sites_solution_primary atom sites solution secondary difmap atom sites solution hydrogens difmap _refine_ls_hydrogen_treatment refall _refine_ls_extinction method none _refine_ls_extinction coef _refine_ls_number_reflns 2374 refine ls number parameters 186 refine ls number restraints 0 _refine_ls_R_factor_all 0.0370 refine ls R factor gt 0.0342 _refine_ls_wR_factor_ref 0.0962 refine ls wR factor gt 0.0930 refine ls goodness of fit ref 1.039 _refine_ls_restrained_S_all 1.039 _refine_ls_shift/su_max 0.002 refine ls shift/su mean 0.000 loop atom site label _atom_site_type_symbol _atom_site_fract_x _atom_site_fract_y atom site fract z atom site U iso or equiv atom site adp type atom site occupancy _atom_site_symmetry multiplicity _atom_site_calc flag atom site refinement flags atom site disorder assembly atom site disorder group S1 S 1.02015(3) -0.10376(8) 0.330113(19) 0.02771(14) Uani 1 1 d . . . O1 O 0.83440(11) 0.6743(3) 0.47306(6) 0.0403(3) Uani 1 1 d . . . O2 O 0.71426(10) 0.6723(2) 0.37138(5) 0.0294(3) Uani 1 1 d . . . N1 N 0.80184(11) -0.0574(3) 0.22925(6) 0.0250(3) Uani 1 1 d . . . N2 N 0.83303(11) 0.2351(3) 0.32684(6) 0.0240(3) Uani 1 1 d . . . N3 N 0.97565(13) 0.2746(3) 0.41876(7) 0.0324(3) Uani 1 1 d . . . C1 C 0.73673(14) -0.1463(3) 0.16939(8) 0.0306(3) Uani 1 1 d . . .

Refinement of F² against ALL reflections. The weighted R-factor wR and goodness of fit S are based on F², conventional R-factors R are based

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C2 C 0.62971(15) -0.0357(4) 0.14696(8) 0.0339(4) Uani 1 1 d . . .
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C5 C 0.76547(12) 0.1418(3) 0.26799(7) 0.0228(3) Uani 1 1 d . . .
C6 C 0.94043(13) 0.1453(3) 0.36011(7) 0.0236(3) Uani 1 1 d . . .
C7 C 0.74574(13) 0.7400(3) 0.43331(8) 0.0251(3) Uani 1 1 d . . .
C8 C 0.65695(14) 0.9224(3) 0.46423(8) 0.0290(3) Uani 1 1 d . . .
F1 F 0.69883(11) 1.0304(3) 0.52533(6) 0.0539(3) Uani 1 1 d . . .
F2 F 0.61689(11) 1.1208(2) 0.42132(6) 0.0467(3) Uani 1 1 d . . .
F3 F 0.56260(10) 0.7764(3) 0.47525(6) 0.0480(3) Uani 1 1 d . . .
H1 H 0.7734(17) -0.282(4) 0.1465(10) 0.033(5) Uiso 1 1 d . . .
H1N H 0.876(2) -0.121(4) 0.2440(11) 0.046(6) Uiso 1 1 d . . .
H2 H 0.5820(19) -0.095(4) 0.1071(11) 0.040(5) Uiso 1 1 d . . .
H2N H 0.8016(17) 0.371(4) 0.3446(10) 0.033(5) Uiso 1 1 d . . .
H3 H 0.5154(18) 0.252(4) 0.1732(10) 0.035(5) Uiso 1 1 d . . .
H3NA H 0.9316(19) 0.410(5) 0.4316(11) 0.042(6) Uiso 1 1 d . . .
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O1 0.0304(6) 0.0524(8) 0.0343(6) -0.0123(6) -0.0095(5) 0.0135(6)
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N2 0.0221(6) 0.0264(6) 0.0227(6) -0.0043(5) -0.0002(5) 0.0030(5)
N3 0.0282(7) 0.0371(8) 0.0286(7) -0.0090(6) -0.0080(6) 0.0087(6)
C1 0.0302(8) 0.0344(8) 0.0262(7) -0.0067(6) -0.0004(6) -0.0021(7)
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C4 0.0245(7) 0.0323(8) 0.0270(7) -0.0027(6) 0.0012(6) 0.0025(6)
C5 0.0217(7) 0.0257(7) 0.0209(6) 0.0005(5) 0.0019(5) -0.0035(5)
C6 0.0213(7) 0.0252(7) 0.0233(7) 0.0003(6) 0.0001(5) -0.0014(5)
C7\ 0.0234(7)\ 0.0264(7)\ 0.0251(7)\ -0.0014(6)\ 0.0015(5)\ -0.0003(6)
C8 0.0299(8) 0.0341(8) 0.0222(7) -0.0014(6) 0.0006(6) 0.0047(6)
F1 0.0554(7) 0.0657(8) 0.0373(6) -0.0248(6) -0.0057(5) 0.0162(6)
F2 0.0557(7) 0.0421(6) 0.0441(6) 0.0121(5) 0.0133(5) 0.0232(5)
F3 0.0390(6) 0.0543(7) 0.0549(7) -0.0013(5) 0.0220(5) -0.0009(5)
_geom_special details
All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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O2 C7 C8 114.17(13) . . ?
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C1 N1 C5 C4 1.4(2) . . . . ?
C6 N2 C5 N1 -4.4(2) . . . . ?
C6 N2 C5 C4 176.19(15) . . . . ?
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C3 C4 C5 N2 178.57(15) . . . . ?
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O1 C7 C8 F1 13.3(2) . . . . ?
O2 C7 C8 F1 -169.20(14) . . . . ?
O1 C7 C8 F2 136.55(16) . . . . ?
O2 C7 C8 F2 -45.90(19) . . . . ?
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N1 H1N S1 0.92(2) 2.18(2) 2.9622(13) 142.9(18).
N3 H3NB O1 0.87(2) 2.06(2) 2.8149(18) 145(2) 3 766
N3 H3NA O1 0.90(2) 1.96(2) 2.8485(19) 171(2).
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Refinement of F^2^ against ALL reflections. The weighted R-factor wR and
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goodness of fit S are based on F^2^, conventional R-factors R are based on F, with F set to zero for negative F^2^. The threshold expression of $F^2^- > 2 \operatorname{sigma}(F^2^-)$ is used only for calculating R-factors(gt) etc. and is

on F² are statistically about twice as large as those based on F, and Rfactors based on ALL data will be even larger. _refine_ls_structure_factor_coef Fsqd refine ls matrix type full _refine_ls_weighting_scheme calc _refine_ls_weighting_details 'calc w=1/[\s^2^(Fo^2^)+(0.0412P)^2^+2.8360P] where P=(Fo^2^+2Fc^2^)/3' _atom_sites_solution_primary direct atom sites solution secondary difmap atom sites solution hydrogens difmap _refine_ls_hydrogen_treatment refall _refine_ls_extinction_method none _refine_ls_extinction_coef _refine_ls_number_reflns 4938 refine ls number parameters 395 refine ls number restraints 0 _refine_ls_R_factor_all 0.0581 _refine_ls_R_factor_gt 0.0475_refine_ls_wR_factor_ref 0.1128_refine_ls_wR_factor_gt 0.1040

refine ls goodness of fit ref 1.231

1.231

0.001

0.000

refine ls restrained S all

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_refine_ls_shift/su_mean

not relevant to the choice of reflections for refinement. R-factors based

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S2 S 0.59704(4) -0.08413(7) 0.158849(14) 0.02813(15) Uani 1 1 d . . .
N1 N 0.51548(12) 0.0785(2) 0.08621(4) 0.0223(4) Uani 1 1 d . . .
N2 N 0.36104(12) 0.1449(2) 0.07808(4) 0.0223(4) Uani 1 1 d . . .
N3 N 0.65794(12) 0.1991(2) 0.12983(4) 0.0214(4) Uani 1 1 d . . .
N4 N 0.61917(13) 0.2173(2) 0.18652(5) 0.0238(4) Uani 1 1 d . . .
O1 O 0.37538(10) 0.0011(2) 0.12746(4) 0.0296(4) Uani 1 1 d . . .
O2 O 0.19143(10) 0.2242(2) 0.06003(4) 0.0318(4) Uani 1 1 d . . .
O3 O 0.66247(12) 0.4755(2) 0.16693(4) 0.0312(4) Uani 1 1 d . . .
O4 O 0.58554(11) 0.2053(2) 0.25253(4) 0.0300(4) Uani 1 1 d . . .
C1 C 0.61064(14) 0.0601(3) 0.07699(5) 0.0213(4) Uani 1 1 d . . .
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C3 C 0.72726(17) -0.0380(3) 0.03861(6) 0.0306(5) Uani 1 1 d . . .
C4 C 0.79605(17) 0.0205(3) 0.05989(6) 0.0308(5) Uani 1 1 d . . .
C5 C 0.77210(15) 0.0966(3) 0.09018(6) 0.0262(5) Uani 1 1 d . . .
C6 C 0.67977(14) 0.1153(3) 0.09898(5) 0.0207(4) Uani 1 1 d . . .
C7 C 0.45215(14) 0.1553(3) 0.06699(5) 0.0211(4) Uani 1 1 d . . .
C8 C 0.32543(14) 0.0654(3) 0.10608(5) 0.0212(4) Uani 1 1 d . . .
C9 C 0.22234(14) 0.0596(3) 0.10904(5) 0.0206(4) Uani 1 1 d . . .
C10 C 0.18766(16) -0.0343(3) 0.13621(6) 0.0251(5) Uani 1 1 d . . .
C11 C 0.09417(16) -0.0553(3) 0.14130(6) 0.0284(5) Uani 1 1 d . . .
C12 C 0.03229(16) 0.0204(3) 0.11940(6) 0.0304(5) Uani 1 1 d . . .
C13 C 0.06378(15) 0.1138(3) 0.09225(6) 0.0286(5) Uani 1 1 d . . .
C14 C 0.15814(14) 0.1324(3) 0.08667(5) 0.0230(4) Uani 1 1 d . . .
C15 C 0.13001(18) 0.2566(3) 0.03216(6) 0.0320(5) Uani 1 1 d . . .
C16 C 0.62663(14) 0.1192(3) 0.15723(5) 0.0219(4) Uani 1 1 d . . .
C17 C 0.64167(14) 0.3851(3) 0.19081(5) 0.0227(4) Uani 1 1 d . . .
C18 C 0.64042(14) 0.4553(3) 0.22596(5) 0.0235(4) Uani 1 1 d . . .
C19 C 0.66912(15) 0.6233(3) 0.22867(6) 0.0286(5) Uani 1 1 d . . .
C20 C 0.67428(17) 0.7035(3) 0.25959(7) 0.0340(5) Uani 1 1 d . . .
C21 C 0.65031(18) 0.6153(4) 0.28859(7) 0.0369(6) Uani 1 1 d . . .
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H2N H 0.3236(17) 0.189(3) 0.0644(7) 0.030(7) Uiso 1 1 d . . .
H3N H 0.6740(18) 0.298(4) 0.1330(7) 0.036(8) Uiso 1 1 d . . .
H4N H 0.6054(19) 0.161(4) 0.2035(7) 0.041(8) Uiso 1 1 d . . .
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H3 H 0.7406(19) -0.092(3) 0.0182(6) 0.035(7) Uiso 1 1 d . . .
H4 H 0.860(2) 0.005(3) 0.0534(7) 0.043(8) Uiso 1 1 d . . .
H5 H 0.8171(18) 0.141(3) 0.1038(7) 0.035(7) Uiso 1 1 d . . .
H10 H 0.2302(17) -0.085(3) 0.1501(6) 0.030(7) Uiso 1 1 d . . .
H11 H 0.0695(19) -0.128(4) 0.1583(7) 0.040(7) Uiso 1 1 d . . .
H12 H -0.0319(18) 0.008(3) 0.1225(6) 0.034(7) Uiso 1 1 d . . .
H13 H 0.0199(17) 0.168(3) 0.0765(6) 0.032(7) Uiso 1 1 d . . .
H15A H 0.1684(17) 0.311(3) 0.0142(6) 0.032(7) Uiso 1 1 d . . .
H15B H 0.0827(18) 0.337(3) 0.0386(6) 0.036(7) Uiso 1 1 d . . .
H15C H 0.1019(18) 0.148(4) 0.0233(7) 0.042(8) Uiso 1 1 d . . .
H19 H 0.6852(18) 0.677(3) 0.2082(7) 0.036(7) Uiso 1 1 d . . .
H20 H 0.6955(17) 0.818(4) 0.2608(6) 0.036(7) Uiso 1 1 d . . .
H21 H 0.6558(17) 0.665(3) 0.3104(7) 0.035(7) Uiso 1 1 d . . .
H22 H 0.6025(18) 0.396(3) 0.3061(7) 0.037(7) Uiso 1 1 d . . .
H24A H 0.5603(18) -0.002(4) 0.2751(6) 0.032(7) Uiso 1 1 d . . .
H24B H 0.634(2) 0.108(4) 0.2955(7) 0.045(8) Uiso 1 1 d . . .
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atom site aniso U 12

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C17 0.0199(10) 0.0270(11) 0.0212(10) 0.0013(9) -0.0014(8) 0.0035(8)
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C19 0.0235(11) 0.0309(12) 0.0312(12) -0.0013(10) 0.0020(9) 0.0008(9)
C20\ 0.0289(12)\ 0.0321(13)\ 0.0410(14)\ -0.0120(11)\ 0.0027(10)\ -0.0027(10)
C21\ 0.0333(13)\ 0.0459(15)\ 0.0315(13)\ -0.0152(12)\ 0.0019(10)\ -0.0003(11)
C22 0.0285(12) 0.0423(14) 0.0243(12) -0.0052(10) 0.0032(10) 0.0011(10)
C23 0.0198(10) 0.0309(11) 0.0240(11) -0.0026(9) -0.0010(8) 0.0011(9)
C24\ 0.0348(14)\ 0.0387(14)\ 0.0226(12)\ 0.0055(10)\ 0.0027(10)\ -0.0049(11)
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All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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- N1 C1 1.431(3) . ?
- N1 H1N 0.85(3).?
- N2 C8 1.375(3) . ?
- N2 C7 1.391(3) . ?
- N2 H2N 0.84(3).?
- N3 C16 1.334(3) . ?
- N3 C6 1.425(3) . ?
- N3 H3N 0.83(3).?
- N4 C17 1.376(3) . ?
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- N4 H4N 0.83(3).?
- O1 C8 1.223(2) . ?
- O2 C14 1.368(3) . ?
- O2 C15 1.440(3) . ?
- O3 C17 1.223(3) . ?
- O4 C23 1.368(3).?
- O4 C24 1.437(3) . ?
- C1 C2 1.385(3) . ?
- C1 C6 1.396(3) . ?
- C2 C3 1.383(3).?
- C2 H2 0.95(2) . ?
- C3 C4 1.383(4) . ?
- C3 H3 0.93(3) . ?
- C4 C5 1.386(3).?
- C4 H4 0.97(3) . ?

- C5 C6 1.388(3).?
- C5 H5 0.92(3).?
- C8 C9 1.496(3) . ?
- C9 C10 1.400(3) . ?
- C9 C14 1.406(3) . ?
- C10 C11 1.377(3).?
- C10 H10 0.92(3) . ?
- C11 C12 1.382(3) . ?
- C11 H11 0.96(3).?
- C12 C13 1.381(3).?
- C12 H12 0.94(3).?
- C13 C14 1.390(3) . ?
- C13 H13 0.99(3) . ?
- C15 H15A 1.00(3) . ?
- C15 H15B 0.97(3) . ?
- C15 H15C 1.01(3).?
- C17 C18 1.499(3) . ?
- C18 C19 1.395(3) . ?
- C18 C23 1.406(3) . ?
- C19 C20 1.380(3) . ?
- C19 H19 0.94(3) . ?
- C20 C21 1.387(4) . ?
- C20 H20 0.95(3) . ?
- C21 C22 1.372(4) . ?
- C21 H21 0.95(3) . ?
- C22 C23 1.394(3).?

- C22 H22 0.92(3) . ?
- C24 H24A 0.96(3) . ?
- C24 H24B 0.99(3).?
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- C8 N2 C7 129.52(19) . . ?
- C8 N2 H2N 117.9(17) . . ?
- C7 N2 H2N 112.5(17) . . ?
- C16 N3 C6 123.52(19) . . ?
- C16 N3 H3N 114.8(19) . . ?
- C6 N3 H3N 120.6(19) . . ?
- C17 N4 C16 128.16(19) . . ?
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on F, with F set to zero for negative F<sup>2</sup>. The threshold expression of
F^2 > 2 \operatorname{sigma}(F^2) is used only for calculating R-factors(gt) etc. and is
not relevant to the choice of reflections for refinement. R-factors based
on F<sup>2</sup> are statistically about twice as large as those based on F, and R-
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C3 0.0230(7) 0.0306(7) 0.0331(7) -0.0135(6) 0.0018(6) -0.0002(5)
C4 0.0273(7) 0.0387(8) 0.0237(7) -0.0088(6) -0.0028(5) 0.0070(6)
C5 0.0280(7) 0.0275(7) 0.0240(6) -0.0024(5) 0.0026(5) 0.0054(5)
C6 0.0200(6) 0.0233(6) 0.0224(6) -0.0058(5) 0.0037(5) 0.0014(5)
C7\ 0.0319(7)\ 0.0243(7)\ 0.0243(6)\ -0.0015(5)\ 0.0035(5)\ -0.0015(5)
C8 0.0438(9) 0.0259(7) 0.0260(7) 0.0000(6) -0.0034(6) 0.0009(6)
C9 0.0344(8) 0.0295(7) 0.0229(7) 0.0001(5) 0.0002(6) 0.0001(6)
C10\ 0.0468(9)\ 0.0304(8)\ 0.0298(8)\ -0.0015(6)\ -0.0025(7)\ 0.0033(7)
C11 0.0557(11) 0.0382(9) 0.0315(8) -0.0084(7) -0.0016(7) 0.0003(8)
C12\ 0.0592(11)\ 0.0502(10)\ 0.0239(8)\ -0.0035(7)\ -0.0052(7)\ 0.0005(8)
C13 0.0530(10) 0.0418(9) 0.0252(7) 0.0057(7) -0.0022(7) 0.0036(8)
C14 0.0374(8) 0.0302(7) 0.0257(7) 0.0030(6) 0.0035(6) 0.0010(6)
C15\ 0.0642(13)\ 0.0317(9)\ 0.0378(9)\ 0.0112(7)\ 0.0042(9)\ 0.0108(8)
C16\ 0.0239(6)\ 0.0207(6)\ 0.0177(6)\ -0.0004(5)\ 0.0012(5)\ 0.0023(5)
C17 0.0256(6) 0.0215(6) 0.0224(6) -0.0017(5) 0.0041(5) 0.0001(5)
C18 0.0245(6) 0.0175(6) 0.0249(6) -0.0012(5) 0.0014(5) 0.0022(5)
C19\ 0.0274(7)\ 0.0237(6)\ 0.0295(7)\ -0.0015(5)\ 0.0055(5)\ 0.0018(5)
C20 0.0264(7) 0.0288(7) 0.0420(8) -0.0042(6) 0.0052(6) -0.0033(6)
C21 0.0310(8) 0.0274(7) 0.0378(8) -0.0089(6) -0.0020(6) -0.0031(6)
C22 0.0335(7) 0.0252(7) 0.0268(7) -0.0053(5) 0.0025(6) 0.0010(6)
C23 0.0255(7) 0.0187(6) 0.0257(6) -0.0004(5) 0.0028(5) 0.0021(5)
C24 0.0383(9) 0.0518(11) 0.0329(8) -0.0144(8) 0.0137(7) -0.0053(8)
_geom_special details
All esds (except the esd in the dihedral angle between two l.s. planes)
are estimated using the full covariance matrix. The cell esds are taken
into account individually in the estimation of esds in distances, angles
and torsion angles; correlations between esds in cell parameters are only
used when they are defined by crystal symmetry. An approximate (isotropic)
treatment of cell esds is used for estimating esds involving l.s. planes.
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O4 C24 1.4303(18) . ?
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N2 C7 1.4016(18) . ?
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C11 H11 0.94(2) . ?
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O2 C15 H15C 103.4(12) . . ?
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H15B C15 H15C 112.3(17) . . ?
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N3 H3N O3 0.855(18) 1.974(18) 2.6438(15) 134.4(16) .
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REFERENCES CITED

- 1. Price, S. L., Acc. Chem. Res., 2009, 42 (1), 117-126.
- 2. McCrone, W. C. In *Physics and Chemistry of the Organic Solid State*, Vol. 2, Fox, D.; Labes, M. M.; Weissberger, A., Eds.; Wiley Interscience: New York, 2003; pp. 725-767.
- 3. Yamada, Y. M. A. Chem. Pharm. Bull. 2005, 53, pp. 723-739.
- 4. Yoon, J. H.; Park, Y. J.; Lee, J. H.; Yoo, J.; Jun, C. H. *Org. Lett.* **2005**, *7*, pp. 2889-2892.
- 5. Yang, J.; Ding, S. J.; Radosz, M.; Shen, Y. Q. *Macromolecules* **2004**, *37*, pp. 1728-1734.
- 6. Ding, S. J.; Yang, J.; Radosz, M.; Shen, Y. Q. J. *Polym. Sci., Part A: Polym. Chem.* **2004**, *42*, pp. 22-30.
- 7. Jahromi, S.; Moosheimer, U. *Macromolecules* **2000**, *33*, 7582–7587.
- 8. Sharma, C. V. K. *Cryst. Growth Des.*, **2002**, *2* (6), pp. 465-474.
- 9. Suarez, M.; Lehn, J.-M.; Zimmerman, S. C.; Skoulios, A.; Heinrich, B. *J. Am. Chem. Soc.* **1998**, *120*, 9526–9532.
- 10. Barbera, J.; Iglesias, R.; Serrano, J. L.; Sierra, T.; de La Fuente, M. R.; Palacios, B.; Perez-Jubindo, M. A.; Vazquez, J. T. *J. Am. Chem. Soc.* **1998**, *120*, 2908–2918.
- 11. Bernstein, Joel. *Polymorphism in Molecular Crystals*. New York: Oxford University Press, 2002.
- 12. Alleso, M.; van den Berg, F.; Cornett, C.; Jorgensen, F. S.; Halling-Sorensen, B.; Lopez de Diego, H.; Hovgaard, L.; Aaltonen, J.; Rantanen, J.; *J. Pharm. Sci.* **2008**, *97* (6), pp. 2145-2159.

- 13. Wang, F.; Wachter, J. A.; Antosz, F. J.; Berglund, K. A. *Org. Proc. Res. Dev.*, **2000**, *4*(5), pp. 391-395.
- 14. Datta, S.; Grant, D. J. W. *Nature Rev. Drug Discov.*, **2004**, *3*, pp. 42-57.
- 15. Garti, N.; Xour, H.. J. Cryst. Growth, 1997, 172, pp. 486-498.
- 16. Biradha, K.; Hongo, Y; Fujita, M. Angew. Chem. Int. Ed., 2000, 39, pp. 3843-3845.
- 17. Hollingsworth, M. D. Science, 2002, 295 (5564), pp. 2410-2413.
- 18. Eddaoudi, M.; Kim, J.; Rosi, N.; Vodak, D.; Wachter, J.; O'Keefe, M.; Yaghi, O. M. *Science*, **2002**, *295* (5554), pp. 469-472.
- 19. Irie, M.; Kobatake, S.; Horichi, M. *Science*, **2001**, *291* (5509), pp. 1769-1772.
- 20. Brown, M. E.; Hollingsworth, M. D. *Nature*, **2002**, *376*, pp. 323-327.
- 21. Feng, M.; Gao, L.; Du, S. X.; Deng, Z. T.; Cheng, Z. H.; Ji, W.; Zhang, D. Q.; Guo, X. F.; Lin, X.; Chi, L. F.; Zhu, D. B.; Fuchs, H.; Gao, H. J. *Adv. Funct. Mater.* **2007**, *17*, pp. 770-76.
- 22. Kroutvar, M.; Ducommun, Y.; Heiss, D.; Bichler, M.; Schuh, D.; Abstreiter, G.; Finley, J. J. *Nature*, **2004**, *432*, pp. 8-23.
- 23. Diederich, F. Pure Appl. Chem. 2005, 77, pp. 1851-863.
- 24. Rancatore, B. J.; Mauldin, C. E.; Tung, S.-H.; Wang, C.; Hexemer, A.; Strzalka, J.; Fréchet, J. M. J.; Xu, T. *ACS Nano*, **2010**, *4* (5), pp. 2721-2729.
- 25. Aakeröy, C. B.; Champness, N. R.; Janiak, C. CrystEngComm, 2010, 12, pp. 22-43.
- 26. Miller, J. S. *CrystEngComm*, **2005**, 7, pp. 458-461.
- 27. Miller, J. S. *CrystEngComm*, **2005**, 7, pp. 458-461.
- 28. Lommerse, J.-P. M.; Motherwell, W. D. S.; Ammon, H. L.; Dunitz, J. D.; Gavezzotti, A.; Hofmann, D. W. M.; Leusen, F. J. J.; Mooji, W. T. M.; Price, S. L.; Schweizer, B.; Schmidt, M. U.; van Eijck, B. P.; Verwer, P.; Williams, D. E. *Acta Cryst.* **2000**, *B56*, 697–714.
- 29. Sarma, J. A. R. P.; Desiraju, G. R. Cryst. Growth Des., 2002, 2 (2), pp. 93-100.

- 30. Salager, E.; Day, G. M.; Stein, R. S.; Pickard, C. J.; Elena, B.; Emsley, L. *J. Am. Chem. Soc.*, **2010**, *132* (8), pp. 2564-2566.
- 31. Chan, H. C. S.; Kendrick, J.; Leusen, F. J. J. *Angew. Chem. Int. Ed.*, **2011**, *50* (13), pp. 2979-2981.
- 32. Kazantsev, A. V.; Karamertzanis, P. G.; Adijman, C. S.; Pantelides, C. C.; Price, S. L.; Galek, P. T. A.; Day, G. M.; Cruz-Cabeza, A. J. *Int. J. Pharmaceutics*, **2011**, DOI:10.1016/j.ijpharm.2011.03.058.
- 33. Braun, D. E.; Karamertzanis, P. G.; Arlin, J. B.; Florence, A. J.; Kahlenberg, V.; Tocher, D. A.; Griesser, U. J.; Price, S. L. *Cryst. Growth Des.*, **2011**, *11* (1), pp. 210-220.
- 34. Woodley, S. M.; Catlow, R. *Nature Materials*, **2008**, 7, pp. 937-946.
- 35. Hagler, A.; Leiserowitz, L. Proc. R. Soc. London Ser. A., 1983, 388, pp. 133-175.
- 36. Sarma, J. A. R. P.; Desiraju, G. R. Acc. Chem. Res., 1986, 19, pp. 222-228.
- 37. Desiraju, G. R.; Gavezzotti, A. Acta Cryst., 1989, B45, pp. 473-482.
- 38. Cotton, F. A.; Lin, C.; Murillo, C. A. *Inorg. Chem.*, **2001**, 40 (3), pp. 575-577.
- 39. Li, J.-R.; Yakovenko, A. A.; Lu, W.; Timmons, D. J.; Zhuang, W.; Yuan, D.; Zhou, H.-C. *J. Am. Chem. Soc.*, **2010**, *132* (49), pp. 17499-17610.
- 40. Gispert, J. R. *Coordination Chemistry*; Wiley-VCH Verlag GmbH & Co.: New York, **2008**, p. 522.
- 41. Bacchi, A.; Cantoni, G. Angew. Chem. Int. Ed., 2011, 50 (11), pp. 3198-3201.
- 42. Yu, L. Acc. Chem. Res., **2010**, 43 (9), pp. 1257-1266.
- 43. Desiraju, G. R. *Nature*, **2001**, *412*, pp. 397-400.
- 44. MacDonald, J. C.; Whitesides, G. M. Chem. Rev., 1994, 94 (8), pp. 2383-2420.
- 45. Dunitz, J. D. and Bernstein, J.; Acc. Chem. Res. 1995, 28(4), pp. 193-200.
- 46. Yu, L.; Stephenson, G. A.; Mitchell, C. A.; Bunnell, C. A.; Snorek, S. V.; Bowyer, J. J.; Borchardt, T. B.; Stowell, J. G.; Byrn, S. R. *J. Am. Chem. Soc.*, **2000**, *122* (4), pp. 585-591.

- 47. Moulton, B.; Zaworotko, M. J. Chem. Rev., 2001, 101 (6), pp. 1629-1658.
- 48. Desiraju, G. R. Angew. Chem. Int. Ed., 2007, 46 (44), pp. 8342-8356.
- 49. Aakeröy, C. B.; Nieuwenhuyzen, M.; Price, S. L. *J. Am. Chem. Soc.*, **1998**, *120* (35), pp. 8986-8993.
- 50. Frankenbach, G. M.; Etter, M. C. Chem. Mater., 1992, 4, pp. 272-278.
- 51. Shattock, T. R.; Arora, K. K.; Vishweshar, P.; Zaworotko, M. J. *Cryst. Growth Des.*, **2008**, *8* (12), pp. 4533-4545.
- 52. Custalcean, R.; Gorbunova, M. G.; Bonnesen, P. V. *Chem.-10ur. J.*, **2005**, *11* (5), pp. 1459-1466.
- 53. Zhao, X.; Chang, Y. L.; Fowler, F. W.; Lauher, J. W. J. Am. Chem. Soc., **1990**, 112 (18), pp. 6627-6634.
- 54. Hollingsworth, M. D.; Brown, M. E.; Santarsiero, B. D.; Huffman, J. C.; Goss, C. R. *Chem. Mater.*, **1994**, *6* (8), pp. 1227-1244.
- 55. Kane, J. J.; Liao, R.-F.; Lauher, J. W.; Fowler, F. W. J. Am. Chem. Soc., **1995**, 117 (48), pp. 12003-12004.
- 56. D'Cruz, O. J.; Uckun, F. M. Mol. Hum. Reprod., 2005, 11 (10), pp. 767-777.
- 57. Maruyama, T.; Seki, N.; Onda, K.; Kawazoe, S.; Hayakawa, M.; Matsui, T.; Takasu, T.; Ohta, M. *Bioorg. Med. Chem.*, **2009**, *17* (15), pp. 5510-5519.
- 58. Chern, J.-H.; Hsu, P.-C.; Wang, L.-W.; Tsay, H.-J.; Kang, I.-J.; Shie, F.-S. *Chem.-Biol. Interact.*, **2010**, *188* (1), pp. 228-236.
- 59. Buchholz, M.; Heiser, U.; Schilling, S.; Neistroj, A. J.; Zunkel, K.; Demuth, H.-U. *J. Med. Chem.*, **2006**, *49*, (2), pp. 664-677.
- 60. Saeed, S.; Rashid, N.; Jones, P. G.; Ali, M.; Hussain, R. Eur. J. Med. Chem., 2010, 45 (4), pp. 1323-1331.
- 61. Bauer, J.; Spanton, S.; Henry, R.; Quick, J.; Dziki, W.; Porter, W.; Morris, J. *Pharm. Res.* **2001**, *18*, pp. 859-866.
- 62. Semetey, V., Hemmerlin, C., Didierjean, C., Schaffner, A. P., Giner, A. G., Aubry, A., Briand, J. P., Marraud, M., Guichard, G., *Org. Lett.*, 3(24), **2001**, 3843-3846.

- 63. Gonzalez, G. and Yutronic, N., Spectrochimica Acta, 46A(12), 1729-1736, 1990.
- 64. Bryantsev, V. S.; Hay, B. P. J. Phys. Chem. A, **2006**, 110 (14), pp. 4678-4688.
- 65. Custalcean, R.; Engle, N. L.; Bonnesen, P. V. CrystEngComm, 2007, 9, pp. 452-455.
- 66. Succaw, G. L.; Weakley, T. J. R.; Han, F.; Doxsee, K. M. *Cryst. Growth Des.*, **2005**, *5* (6), pp. 2288-2298.
- 67. Bilton, C.; Allen, F. H.; Shields, G. P.; Howard, J. A. K. *Acta Crystallogr. B*, **2000**, *56* (5), pp. 849-856.
- 68. Steiner, T. Angew. Chem. Int. Ed., 2002, 41 (1), pp. 48-76.
- 69. Allen, F. H.; Motherwell, S.; Raithby, P. R.; Shields, G. P.; Taylor, R. *New J. Chem.*, **1999**, *23* (1), pp. 25-34.
- 70. Allen, F. H.; Bird, C. M.; Rowland, S.; Raithby, P. R. *Acta Crystallogr. B.*, **1997**, *53*, pp. 680-695.
- 71. Abrahams, S. C. *Q. Rev. Chem. Soc.*, **1956**, *10*, pp. 407-436.
- 72. George, S.; Nangia, A.; Lam, C.-K.; Mak, T. C. W.; Nicoud, J.-F. *Chem. Commun.*, **2004**, pp. 1202-1206.
- 73. Wittkopp, A.; Schreiner, P. R. *Chem.-10ur. J.*, **2003**, 9 (2), pp. 407-414.
- 74. Fuerst, D. E.; Jacobsen, E. N.; J. Am. Chem. Soc., 2005, 127 (25), pp. 8964-8965.
- 75. Takemoto, Y., Org. Biomol. Chem., 2005, 3, pp. 4299-4306.
- 76. Jin, Z.-M.; Zhao, B.; Zhou, W.; Jin, Z.; *Powder Diffrac.* **1997**, *12*(1), pp. 47-48.
- 77. Li, W.-K.; Zhou, G.-D.; Mak, T. C. W.; *Advanced Strutcural Inorganic Chemistry*, Oxford University Press: New York, **2008**, p. 404.
- 78. Ohba, S.; Miyamoto, H.; Fujioka, A.; Ikeuchi, T.; Lehn, J.-M.; *Acta Cryst.* **2005**, *E61*, pp. o182-o184.
- 79. Jeffrey, G. A.; Crystallog. Rev. 2003, 9 (2), pp. 135-176.
- 80. Nanda, V.; Schmiedekamp, A.; *Prot. Struct. Funct. Bioinform.* **2007**, *70* (2), pp. 489-497.

- 81. Desiraju, G. R.; Steiner, T.; *The Weak Hydrogen Bond in Structural Chemistry and Biology*, Oxford University Press, Oxford, **1999**, pp. 175-185.
- 82. Madhavi, N. N. L.; Bilton, C.; Howard, J. A. K.; Allen, F. H.; Nangia, A.; Desiraju, G. R.; *New J. Chem.* **2000**, *24*, pp. 1-4.
- 83. Aly, A. A.; Ahmed, E. K.; El-Mokadem, K. M.; Hegazy, M. E.-A. F. *J. Sulfur Chem.*, **2007**, *28*(1), pp. 73-93.
- 84. West, D. X.; Hermetet, A. K.; Ackerman, L. J.; Valdez-Martinez, J.; Hernandez-Ortega, S. *Acta Crystallogr.*, **1999**, *C55*, pp. 811-813.
- 85. Raj, S. S.; Puviarasan, K.; Velmurugan, D.; Jayanthi, G.; Fun, H.-K. *Acta Crystallogr.* **1999**, *C55*, pp. 1318-1320.
- 86. Zhang, O.-C.; Zhang, Y.-Q.; Cao, Y.; Zha, O.-B. *Acta Crystallogr.*, **1996**, *C52*, pp. 1716-1718.
- 87. Cao, Y.; Zha, O.-B.; Zhang, Y.-Q.; Zhang, O.-C. *Acta Crystallogr.*, **1996**, *C52*, pp. 1772-1774.
- 88. Li, Q.-J.; Yang, C.-L. J. Chem. Crystallogr., 2008, 38(12), pp. 927-930.
- 89. Kascheres, A.; Ueno, M. J. Heterocyclic Chem., 1991, 28, pp. 2057-2058.
- 90. Angelova, O.; Kossev, K.; Atanasov, V. Acta Cryst. 1999, C55, 220-222.
- 91. Valdés-Martínez, J.; Hernández-Ortega, S.; West, D. X.; Ackerman, L. J.; Swearingen, J. K.; Hermetet, A. K. *J. Mol. Struct.*, **1998**, 478 (1-3), pp. 219-226.
- 92. Saxena, A.; Pike, R. D. J. Chem. Crystallogr., 2007, 37, pp. 755-764.
- 93. Kaminsky, W.; Goldberg, K. I.; West, D. X. J. Mol. Struct., 2002, 605, p. 9.
- 94. Venkatachalam, T. Sudbeck, E.; Uckun, F. M. J. Mol. Struct., 2004, 687 (1-3), 45-56.
- 95. Ahgren, C.; Backro, K.; Bell, F. W.; Cantrell, A. S.; Clemens, M.; Colacino, J. M.; Deeter, J. B.; Engelhardt, J. A.; Hogberg, M.; Jaskunas, S. R.; Johansson, N. G.; Jordan, C. L.; Kasher, J. S.; Kinnick, M. D.; Lind, P.; Lopez, C.; Morin, Jr., J. M.; Muesing, M. A.; Noreen, R., et al. Antimicrob. Agents Chemo., 1995, 39 (6), 1329-1335.

- 96. Mao, C.; Vig, R.; Venkatachalam, T. K.; Sudbeck, E. A.; Uckun, F. M. *Bioorg. Med. Chem. Lett.*, **1998**, *8*(16), 2213-2218.
- 97. Glesen, J. M.; Claborn, K. A.; Goldberg, K. I.; Kaminsky, W.; West, D. X. *J. Mol. Struct.*, **2002**, *613* (1-3), 223-233.
- 98. Saxena, A.; Dugan, E. C.; Liaw, J.; Dembo, M. D.; Pike, R. D. *Polyhedron*, **2009**, *28*(18), 4017-4031.
- 99. Sobczyk, L. Chem. Rev., 2005, 105 (10), 3513–3560.
- 100. Xu, S., Otto, F. D., and Mather, A. E., Can. J. Chem. 71, 1993, 1048-1051.
- 101. Hall, H.K., Jr. J. A.m. Chem. Soc., 79, 1957, 5441.
- 102. "pKa data compiled by R. Williams." [Online]. Available: http://research.chem.psu.edu/brpgroup/pKa compilation.pdf . (December 3, **2008**).
- 103. Sudha, L. V. and Sathyanarayana, D. N., Spectrochem. Acta, 40A (8), 1984, 751.
- 104. Pine, S.H.; Hendrickson, J.B.; Cram, D.J.; Hammond, G.S., *Organic chemistry*, Section 6.2, McGraw-Hill, **1980**.
- 105. Gilli, G., Bellucci, F., Ferretti, V., Bertolasi, V., J. Am. Chem. Soc., 1989, 111 (3), 1023.
- 106. Chin, J., Kim, D. C., Kim, H., Panosyan, F. B., Kim, K. M., Org. Lett., 2004, 6 (15), 2591.
- 107. Mock, W. L.; Chua, D. C. Y. J. Chem. Soc. Perkin Trans. 2, **1995**, 11, pp. 2069-2074.
- 108. Wei, T.-B.; Wei, W.; Cao, C.; Zhang, Y.-M. Ind. J. Chem., 2007, 46B, pp. 1028-1032.
- 109. Beer, P. D.; Gale, P. A. Angew. Chem. Int. Ed., 2001, 40, pp. 486-516.
- 110. Schmidtchen, F. P.; Berger, M. Chem. Rev., 1997, 97, pp. 1609-1646.
- 111. Gomez, D. E.; Fabbrizzi, L.; Licchelli, M.; Monzani, E. *Org. Biomol. Chem.*, **2005**, *3*, pp. 1495-1500.
- 112. Shoukrey, M. M.; Mahgoub, A. E. S.; Elnagdi, M. H. *J. Inorg. Nuc. Chem.*, **1979**, *42*, pp. 1171-1176.

- 113. Shome, S. C.; Mazumdar, M.; Haldar, P. K. *J. Ind. Chem. Soc.*, **1980**, *57*, pp. 139-141.
- 114. Mohamadou, A.; Dechamps-Olivier, I.; Barbier, I. P. Polyhedron, 1994, 13, p. 3277.
- 115. Anthline, W.; Taketa, F. J. Inorg. Biochem. 1982, 16, pp. 145-154.
- 116. Li, G.; Che, D.-J.; Li, Z.-F.; Zhu, Y.; Zou, D.-P. New. J. Chem. **2002**, 26, p. 1629.
- 117. Seshadri, T.; Haupt, H.-J. *J. Mater. Chem.* **1998**, *8*, pp. 1345-1350.
- 118. Zhang, Y-M.; Wei. T.-B.; Gao, L.M., Synth. Commun. 2001, 31(20), pp. 3099-3105.
- 119. Zhou, W.; Zhang, Z.; Jin, Z.; Jin, Z.-M. Powder Diffraction 2002, 17(3), pp.238-240.
- 120. Rudd, M. D.; Lindeman, S. V.; Husebye, S. *Phosphorous Sulfur Silicon Relat. Elem.* **1997**, *123*(1), 313-327.
- 121. Cantrell, A. S.; Engelhardt, P.; Hoberg, M.; Jaskunas, S. R.; Johansson, N. G.; Jordan, C.; Kangasmetsa, J.; Kinnick, M. D.; Lind, P.; Morin; Muesing, M. A.; Noreen, R.; Oberg, B.; Pranc, P.; Sahlberg, C.; Ternansky, R. J.; Vasileff, R. T.; Vrang, L.; West, S. J.; Zhang, H. *J. Med. Chem.*, **1996**, *39* (21), pp. 4261-4274.
- 122. Ravichandran, V.; Agrawal, R. K. *Bioorg. Med. Chem. Lett.*, **2007**, *17* (8), pp. 2197-2202.
- 123. Hunter, R.; Younis, Y.; Muhanji, C. I.; Curtin, T.-I.; Naidoo, K. J.; Petersen, M.; Bailey, C. M.; Basavapathruni, A.; Anderson, K. S. *Bioorg. Med. Chem.*, **2008** *16* (24), pp. 10270-10280.
- 124. Caminiti, R.; Pieretti, A.; Bencivenni, L. J. Phys. Chem., 1996, 100 (26), pp. 10928-10935.
- 125. Perrin, C. L.; Nielson, J. B. Ann. Rev. Phys. Chem. 1997, 48, 511-544.
- 126. Gerlt, J. A.; Kreevoy, M. M.; Cleland, W. W.; Frey, P. A. *Chem. Biol.* **1997**, *4*, 259-267.
- 127. Gilli, G.; Gilli, P. J. Mol. Struct. **2000**, 552, 1-15.
- 128. Goodwin, J. T.; Conradi, R. A.; Ho, N. F. H.; Burton, P. S. *J. Med. Chem.*, **2001**, *44* (22), pp. 3721-3729.

- 129. Rezai, T.; Bock, J. E.; Zhou, M. V.; Kalyanaraman, C.; Lokey, R. S.; Jacobson, M. P. *J. Am. Chem. Soc.* **2006**, *128* (43), pp. 14073–14080.
- 130. Kuhn, B.; Mohr, P.; Stahl, M. J. Med. Chem., 2010, 53 (6), pp. 2601-2611.
- 131. Ashwood, V. A.; Field, M. J.; Horwell, D. C.; Julien-Larose, C.; Lewthwaite, R. A.; McCleary, S.; Pritchard, M. C.; Raphy, J.; Singh, L. *J. Med. Chem.*, **2001**, *44* (14), pp. 2276-2285.
- 132. Lord, A.-M.; Mahon, M. F.; Lloyd, M. D.; Threadgill, M. D. *J. Med. Chem.*, **2009**, *52*, (3), pp. 868-877.
- 133. Sasaki, S.; Cho, N.; Nara, Y.; Harada, M.; Endo, S.; Suzuki, N.; Furuya, S.; Fujino, M. *J. Med. Chem.*, **2003**, *46* (1), pp. 113-124.
- 134. Park, H.; Kim, K. M.; Lee, A.; Ham, S.; Nam, W.; Chin, J. J. Am. Chem. Soc., 2007, 129 (6). [[/ 1518-1519.
- 135. Chin, J.; Mancin, F.; Thavarajah, N.; Lee, D.; Lough, A.; Chung, D. S. *J. Am. Chem. Soc.*, **2003**, *125* (50), pp. 15276-15277.
- 136. Bertolasi, V.; Gilli, P.; Ferretti, V.; Gilli, G. Chem.-Eur. J., 2006, 2 (8), pp. 925-934.
- 137. Kurzcab, R.; Mitoraj, M. P.; Michalak, A.; Ziegler, T. *J. Phys. Chem. A*, **2010**, *114* (13), pp. 8581-8590.
- 138. Zubatyuk, R. I.; Shishkin, O. V.; Gorb, L.; Leszyzynski, J. J. Phys. Chem. A., **2009**, 113 (12), pp. 2943-2952.
- 139. Jablonski, M.; Kaczmarek, A.; Sadlej, A. J.; *J. Phys. Chem. A.* **2006**, *110*, 10890-10898.
- 140. Grabowski, S. J. J. Phys. Org. Chem. **2003**, 16, 797-802.
- 141. Sarkis, G. Y.; Faisal, E. D. J. Heterocycl. Chem., 1985, 22, pp. 137-140.
- 142. Gilli, P.; Bertolasi, V.; Ferretti, V.; Gilli, G. J. Am. Chem. Soc. 1994, 116, 909-915.
- 143. Perrin, C. L. Science **1994**, 266, 1665-1668.
- 144. Yusof, M. S. M.; Soh, S. K. C.; Ngah, N.; Yamin, B. M. *Acta Cryst.* **2006**, *E62*, o1446-o1448.

- 145. Otazo-Sánchez, E.; Ortiz-del-Toro, P.; Estévez-Hernández, O.; Pérez-Marín, L.; Goicoecha, I.; Cerón-Beltran, A.; Villagómez-Ibarra, J. R. *Spectrochim. Acta Part A: Mol. Biomol. Spectroscopy* **2002**, *58*(10), 2281-2290.
- 146. Sethukumar, A.; Arul Prakasam, B. *J. Mol. Struct.* **2010**, *963*, 250-257.
- 147. Dovesi, R.; Saunders, V. R.; Roetti, R.; Orlando, R.; Zicovich-Wilson, C. M.; Pascale, F.; Civalleri, B.; Doll, K.; Harrison, N. M.; Bush, I. J.; D'Arco, P.; Llunell, M.; *CRYSTAL06 User's Manual*. University of Torino: Torino, **2006**.
- 148. Foye, William O. H.; Lemke, T. L. *Foye's Principles of Medicinal Chemistry, 6th Ed.* Lemke, T. L., Ed.; Williams, D. A., Ed.; Roche, V. F., Ed.; Zito, S. W., Ed. Lippincott Williams & Williams: Baltimore, **2008**.
- 149. Zollinger, H. *Color Chemistry: Synthesis, Properties, and Applications of Organic Dyes and Pigments, 3rd Ed.* Zurich: Verlag Helvetica Chimica Acta, **2003**.
- 150. Mo, B. L.; Li, J.; Liang, S. P. Anal. Biochem. 1997, 252, pp. 169-176.
- 151. Vogel, A. I. *Practical Organic Chemistry, Fifth Ed.*; Longman Scientific & Technical: Essex, U.K., **1989**, p. 692.
- 152. Calculated using Molinspiration online cheminformatics software (www.molinspiration.com)
- 153. Sanchez, E.; Lopez, T. *Mat. Lett.*, **1995**, *25*, pp. 271-275.
- 154. Desiraju, G. Crystal Engineering: The Design of Organic Solids; Elsevier: New York, **1989**.
- 155. Yesilkaynak, T.; Florke, U.; Kulcu, N.; Arslan, H. *Acta Cryst.*, **2006**, *E62* (9), pp. o3934-o3935.
- 156. Kavak, G.; Özbey, S.; Binzet, G.; Külcü, N. Turkish J. Chem., 2009, 33 (6), pp. 857-868.
- 157. Binzet, G.; Emen, F. M. *Acta Cryst.*, **2009**, *E65*, pp. o81-o82.
- 158. Binzet, G.; Flörke, U.; Külcü, N.; Arslan, H. Acta Cryst., 2009, E65, pp. 0427-0428.
- 159. Dillen, J.; Woldu, M. G.; Koch, K. R. Acta Cryst., **2006**, E62, pp. o5225-o5227.
- 160. Gunaskaran, N.; Karvembu, R.; Ng, S. W.; Tiekink, E. R. T. *Acta Cryst.*, **2010**, *E66*, pp. o2113-o2114.

- 161. Burling, F. T.; Goldstein, B. M. Acta Cryst. B, 1993, 49 (4), pp. 738-744.
- 162. Angyan, J. G.; Poirier, R. A.; Kucsman, A.; Czizmadia, I. G. *J. Am. Chem. Soc.*, **1987**, *109* (8), pp. 2237-2245.
- 163. Wu, S.; Greer, A. J. Org. Chem., 2000, 65 (16), pp. 4883-4887.
- 164. Raimundo, J.-M.; Blanchard, P.; Gallego-Planas, N.; Mercier, N.; Ledoux-Rak, I.; Hierle, R.; Roncali, J. *J. Org. Chem.*, **2002**, *67* (1), pp. 205-218.
- 165. Nagao, Y.; Miyamoto, S.; Miyamoto, M.; Takeshige, H.; Hayashi, K.; Sano, S.; Shiro, M.; Yamguchi, K.; Sei, Y. *J. Am. Chem. Soc.*, **2006**, *128* (30), pp. 9722-9729.
- 166. González, F. V.; Jain, A.; Rodríguez, S.; Sáez, J. A.; Vicent, C.; Peris, G. *J. Org. Chem.*, **2010**, *75* (17), pp. 5888-5894.
- 167. Destro, R.; Soave, R.; Barzaghi, M.; Lo Presti, L. *Chem.-Eur. J.*, **2005**, *11*, pp. 4621-4634.
- 168. Pandya, N.; Basile, A. J.; Gupta, A. K.; Hand, P.; MacLaurin, C. L.; Mohammad, T.; Ratemi, E. S.; Gibson, M. S.; Richardson, M. F. *Can. J. Chem.*, **1993**, *71* (4), pp. 561-571.
- 169. Wu, S.; Greer, A. J. Org. Chem., 2000, 65 (16), pp. 4883-4887.
- 170. Iwaoka, M.; Takemoto, S.; Okada, M.; Tomoda, S. *Chem. Lett.*, **2001**, *30* (2), pp. 132-133.
- 171. Nassau, K. "The Physics and Chemistry of Color: the 15 Mechanisms," *The Science of Color, 2nd Ed.* Steven K. Shevell, Ed. Oxford: Elsevier Science, **2003**.
- 172. Bauer, M.; Bertario, A.; Boccardi, G.; Fontaine, X.; Rao, R.; Verrier, D. *J. Pharm. Biomed. Anal.* **1998**, *17*(3), pp. 419-425.
- 173. Gören, A. C.; Çıkrıkçı, S.; Çergel, M.; Bisel, G. Food Chem. **2009**, 113(4), pp. 1239-1242.
- 174. McDaniel, D. H. and Brown, H. C. J. Org. Chem., 1958, 23 (3), pp. 420-427.
- 175. Schwabe, T.; Grimme, S. Acc. Chem. Res., 2008, 41 (4), pp. 569-579.
- 176. Dean, J. A., *Ed. Lange's Handbook of Chemistry*, 13th ed.; McGraw-Hill: New York, **1987**.

- 177. Shanan-Atidi, H. and Bar-Eli, K. H. J. Phys. Chem., 1970, 74, p. 961.
- 178. Muruganantham, R. and Namboorthiri, I. N. N. J. Org. Chem., **2010**, 75 (7), pp. 2197-2205.
- 179. Zhang, P. C.; Wang, Y. H.; Liu, X.; Yi, X.; Chen, R. Y.; Yu, D. Q. *Chinese Chem. Lett.*, **2002**, *13* (7), pp. 645-648.
- 180. Perrin, C. L.; Gipe, R. K. J. Am. Chem. Soc., **1984**, 106, 4036.
- 181. Aguirre, G.; Somanathan, R.; Hellberg, L. H.; Dwyer, T. J.; North, R. *Magn. Reson. Chem.*, **2003**, *41*, pp. 131-134.
- 182. Kesanli, B.; Charles, S.; Lam, Y.-F.; Bott, S. G.; Fettinger, J.; Eichhorn, B. *J. Am. Chem. Soc.*, **2000**, *122* (45), pp. 11101-11107.
- 183. Touchard, F.; Fache, F.; Lemaire, M. *Tetrahed. Asym.*, **1997**, 8 (19), pp. 3319-3326.
- 184. Touchard, F.; Bernard, M.; Fache, F.; Lemaire, M. J. Mol. Catalysis A: Chem., 1999, 140 (1), pp. 1-11.
- 185. Breuzard, J. A. J.; Tommasino, M. L.; Touchard, F.; Lemaire, M.; Bonnet, M. C. *J. Mol. Catalysis A: Chem.*, **2000**, *156* (1-2), pp. 223-232.
- 186. Tommasino, M. L.; Casalta, M.; Breuzard, J. A. J.; Lemaire, M. *Tetrahed. Asym.*, **2000**, *11* (24), pp. 4835-4841.
- 187. Yang, D.; Chen, Y.-C.; Zhu, N.-Y. *Org. Lett.*, **2004**, 6 (10), pp. 1577-1580.
- 188. Bowers, A. A.; Acker, M. G.; Koglin, A.; Walsh, C. T. J. Am. Chem. Soc., **2010**, 132 (21), pp. 7519-7527.
- 189. Lu, Y.; Li, C. M.; Wang, Z.; Ross, C. R. 2nd; Chen, J.; Dalton, J. T.; Li, W.; Miller, D. D. *J. Med. Chem.*, **2009**, *52* (6), pp. 1701-1711.
- 190. Siddiqui, N.; Arshad, M. F.; Ashan, W.; Alam, M. S. *Int. J. Pharm. Sci. Drug Res.*, **2009**, *1* (3), pp. 136-143.
- 191. Li, H.; Xia, Y.; Pu, S.; Cui, S. Adv. Mat. Res., 2011, 156-157, pp. 650-654.
- 192. Yamgar, B. A.; Sawant, V. A.; Bharate, B. G.; Chavan, S. S. Spectrochim. Acta A: Mol. Biomol. Spectroscopy, 2011, 78A (1), pp. 102-106.
- 193. Alajarín, M.; Cabrera, J.; Pastor, A.; Sánchez-Andrada, P.; Bautista, D. *J. Org. Chem.*, **2006**, *71* (14), pp. 5328-5339.

- 194. Castagnolo, D.; Pagano, M.; Bernadini, M.; Botta, M. Synlett, 2009, pp. 2093-2096.
- 195. Ishiwata, Y.; Togo, H. Synlett, **2008**, pp. 2637-2641.
- 196. Rey, V.; Pierini, A. B.; Peñéñory, A. B. J. Org. Chem., 2009, 74, pp. 1223-1230.
- 197. Kandror, I. I., Kopylova, B. V.; Freidlina, R. K. *Tet. Lett.*, **1978**, *34*, pp. 3087-3088.
- 198. Sedlák, M.; Hanusek, J.; Holčapek, M.; Štěrba, V. *J. Phys. Org. Chem.*, **2001**, *14*, pp. 187-195.
- 199. Sridevi, G.; Rao, P. J.; Reddy, K. K. Ind. J. Chem., 1988, 27B, pp. 997-1000.
- 200. Iliopoulos, P.; Murray, K. S. J. Chem. Soc., Dalton Trans., 1988, 2, pp. 433-443.
- 201. Johanson, F. E.; Hamilton, C. S. J. Am. Chem. Soc., 1949, 71 (1), pp. 74-76.
- 202. Szabó, D.; Kuti, M.; Kapovits, I.; Rábal, J.; Kucsman, Á.; Argay, G.; Czugler, M.; Kálmán, A.; Párkányi, L. *J. Mol. Struct.*, **1997**, *415* (1-2), pp. 1-16.
- 203. Jones, R. A.; Katritzky, A. R. J. Chem. Soc., 1959, pp. 1317-1323.
- 204. Ankem, R. V.; Murphy, J. L.; Nagorski, R. W. Tet. Lett., 2008, 49 (46), pp. 6547-6549.
- 205. Pyykkö, P.; Atsumi, M. *Chem.-Eur. J.*, **2009**, *15*, pp. 186–197.
- 206. Morel, G.; Marchand, E.; Sinbandhit, S.; Toupet, L. *Heteroatom Chem.*, **2003**, *14* (1), pp. 95-105.
- 207. Adzima, L. J.; Chiang, C. C.; Paul, I. C.; Martin, J. C. J. Am. Chem. Soc., 1978, 100, pp. 953-
- 208. Huang, R.-B.; Lu, X.; Zheng, N.-F.; Zou, Y.-S.; Deng, S.-L.; Zhong, H.-P.; Xie, S.-Y.; Long, L.-S.; Zheng, L.-S. *J. Mol. Struct.*, **2002**, *610* (1-3), pp. 265-270.
- 209. CRC Handbook of Chemistry and Physics; Lide, D. R., Ed. Boca Raton: CRC Press LCC, 1972.
- 210. Allen, F. H.; Kennard, O.; Watson, D. G.; Brammer, L.; Orpen, A. G.; Taylor, R. *J. Chem. Soc., Perkin Trans.*, **1987**, *2*, pp. S1–S19.
- 211. Garden, S. J.; Wardell, J. L.; Low, J. N.; Skakle, J. M. S.; Glidewell, C. *Acta Cryst.*, **2006**, *E62*, pp. o3762-o3764.

- 212. Mujika, J. I.; Matxain, J. M.; Eriksson, L. A.; Lopez, X. *Chem. Eur. J.* **2006**, *12*, 7215-7224.
- 213. Li, G.; Tajima, H.; Ohtani, T. J. Org. Chem., 1997, 62 (13), pp. 4539-4540.
- 214. Vogel, A. I. *Vogel's Textbook of Practical Organic Chemistry*, 5th ed.; Furniss, B. S., Ed; Longman Group UK Limited and John Wiley & Sons, Inc.: New York, 1989, p. 692.
- 215. Jhaumeer-Laulloo, B. S. *Ind. J. Heterocycl. Chem.*, 9 (3), pp. 193-196.