



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 12:09 PM UTC

PDB ID : 8S0Q / pdb_00008s0q
Title : A fragment-based inhibitor of SHP2
Authors : Cleasby, A.; Price, A.
Deposited on : 2024-02-14
Resolution : 1.87 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

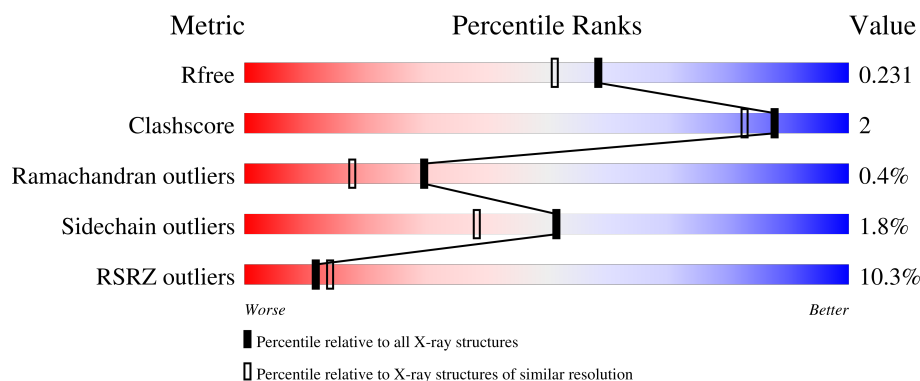
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.87 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1220 (1.88-1.88)
Clashscore	190562	1234 (1.88-1.88)
Ramachandran outliers	187476	1222 (1.88-1.88)
Sidechain outliers	187428	1222 (1.88-1.88)
RSRZ outliers	180081	1220 (1.88-1.88)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	537	 9% 85% 8% • 7%
1	B	537	 10% 84% 9% • 6%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	A1H4T	B	601	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9077 atoms, of which 42 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

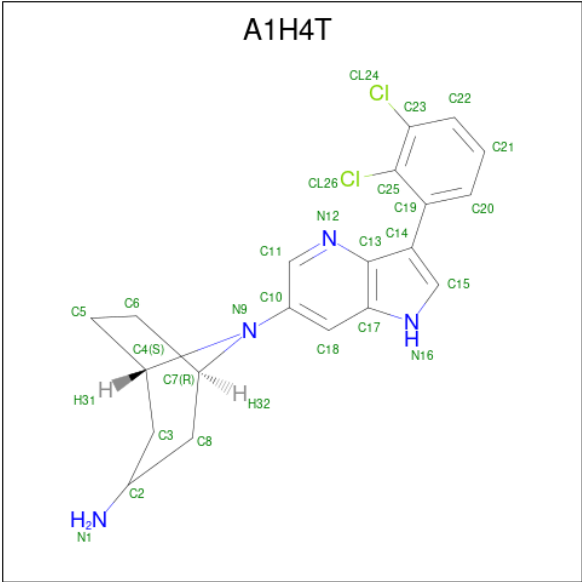
- Molecule 1 is a protein called Tyrosine-protein phosphatase non-receptor type 11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	502	Total	C	N	O	S	0	1	0
			4076	2563	729	766	18			
1	B	504	Total	C	N	O	S	0	0	0
			4085	2566	734	767	18			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	HIS	-	expression tag	UNP Q06124
A	529	LEU	-	expression tag	UNP Q06124
A	530	GLU	-	expression tag	UNP Q06124
A	531	HIS	-	expression tag	UNP Q06124
A	532	HIS	-	expression tag	UNP Q06124
A	533	HIS	-	expression tag	UNP Q06124
A	534	HIS	-	expression tag	UNP Q06124
A	535	HIS	-	expression tag	UNP Q06124
A	536	HIS	-	expression tag	UNP Q06124
B	0	HIS	-	expression tag	UNP Q06124
B	529	LEU	-	expression tag	UNP Q06124
B	530	GLU	-	expression tag	UNP Q06124
B	531	HIS	-	expression tag	UNP Q06124
B	532	HIS	-	expression tag	UNP Q06124
B	533	HIS	-	expression tag	UNP Q06124
B	534	HIS	-	expression tag	UNP Q06124
B	535	HIS	-	expression tag	UNP Q06124
B	536	HIS	-	expression tag	UNP Q06124

- Molecule 2 is (1S,5R)-8-[3-[2,3-bis(chloranyl)phenyl]-1H-pyrrolo[3,2-b]pyridin-6-yl]-8-azabicyclo[3.2.1]octan-3-amine (CCD ID: A1H4T) (formula: C₂₀H₂₀Cl₂N₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 47	C 20	Cl 2	H 21	N 4	0	0
2	B	1	Total 47	C 20	Cl 2	H 21	N 4	0	0

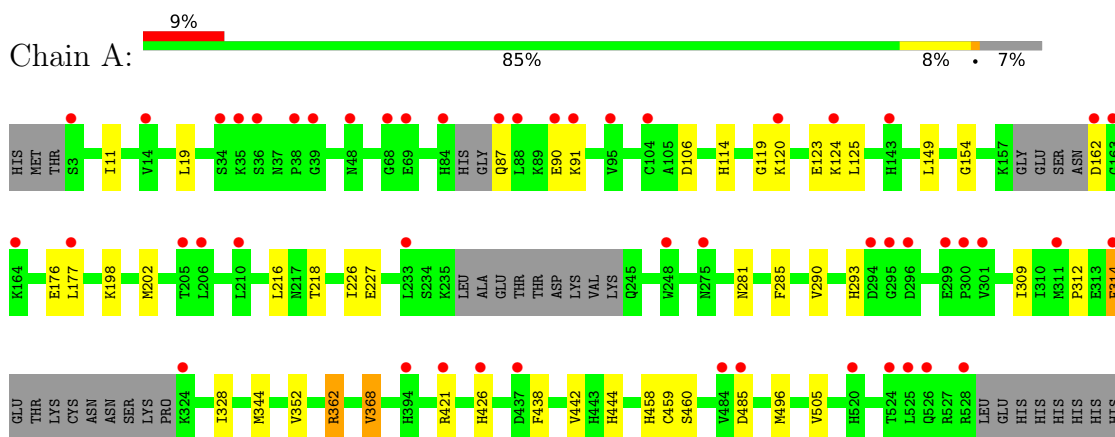
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	409	Total	O	0	0
			409	409		
3	B	413	Total	O	0	0
			413	413		

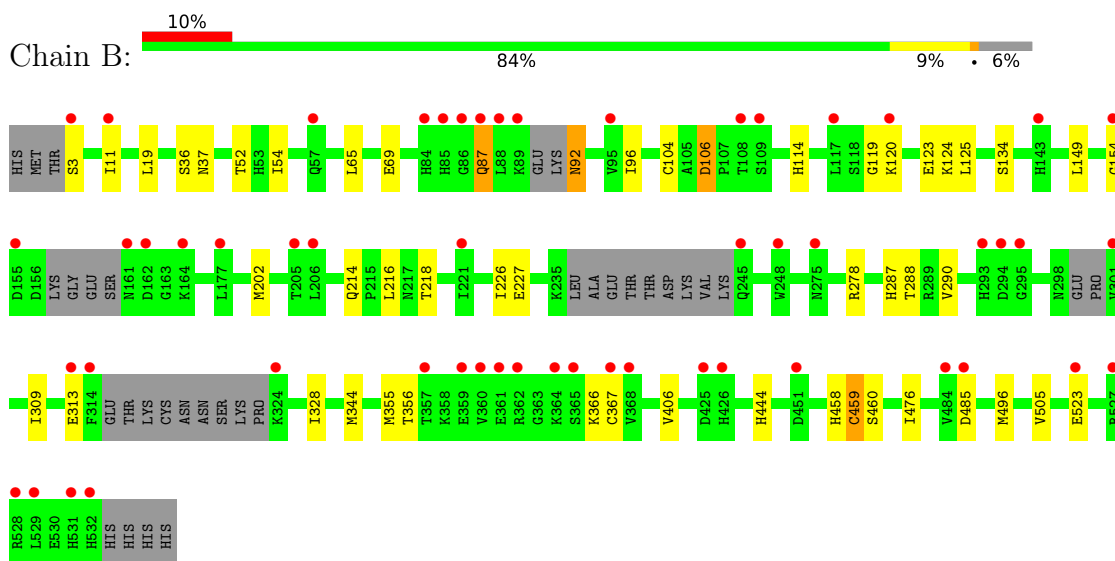
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Tyrosine-protein phosphatase non-receptor type 11



- Molecule 1: Tyrosine-protein phosphatase non-receptor type 11



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	45.74Å 214.34Å 55.77Å 90.00° 97.09° 90.00°	Depositor
Resolution (Å)	55.34 – 1.87 55.34 – 1.87	Depositor EDS
% Data completeness (in resolution range)	99.0 (55.34-1.87) 98.9 (55.34-1.87)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 1.87Å)	Xtriage
Refinement program	BUSTER	Depositor
R, R_{free}	0.193 , 0.236 0.195 , 0.231	Depositor DCC
R_{free} test set	4365 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	28.3	Xtriage
Anisotropy	0.288	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9077	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.45% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: A1H4T

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	1.02	3/4163 (0.1%)	1.03	15/5612 (0.3%)
1	B	1.05	6/4169 (0.1%)	1.04	6/5620 (0.1%)
All	All	1.03	9/8332 (0.1%)	1.04	21/11232 (0.2%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	476	ILE	CG1-CD1	-7.98	1.20	1.51
1	A	460	SER	CA-C	6.90	1.59	1.53
1	A	496	MET	SD-CE	6.26	1.95	1.79
1	B	459	CYS	N-CA	5.58	1.52	1.46
1	B	496	MET	SD-CE	5.21	1.92	1.79
1	B	496	MET	CA-C	5.21	1.59	1.52
1	B	355	MET	SD-CE	-5.18	1.66	1.79
1	A	368	VAL	CA-CB	5.08	1.59	1.54
1	B	406	VAL	CA-C	5.01	1.58	1.52

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	458	HIS	CA-CB-CG	7.17	120.97	113.80
1	A	458	HIS	CA-C-N	6.48	133.93	121.54
1	A	458	HIS	C-N-CA	6.48	133.93	121.54
1	A	314	PHE	CA-CB-CG	6.16	119.96	113.80
1	A	312	PRO	CA-C-N	6.14	131.54	122.82
1	A	312	PRO	C-N-CA	6.14	131.54	122.82
1	A	106	ASP	CA-CB-CG	5.98	118.58	112.60
1	B	444	HIS	CA-CB-CG	-5.90	107.90	113.80
1	A	438	PHE	CA-CB-CG	5.90	119.70	113.80
1	B	485	ASP	CA-CB-CG	5.88	118.48	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	154	GLY	N-CA-C	5.85	117.87	110.38
1	A	485	ASP	CA-CB-CG	5.56	118.16	112.60
1	A	281	ASN	CA-CB-CG	-5.49	107.11	112.60
1	B	106	ASP	CA-CB-CG	5.41	118.01	112.60
1	B	92	ASN	CA-CB-CG	5.39	117.99	112.60
1	A	444	HIS	CA-CB-CG	-5.37	108.43	113.80
1	B	154	GLY	N-CA-C	5.28	117.32	110.45
1	A	285	PHE	CA-CB-CG	5.25	119.05	113.80
1	A	421	ARG	CB-CG-CD	5.13	123.09	111.30
1	A	293	HIS	CA-CB-CG	-5.12	108.68	113.80
1	A	458	HIS	CA-CB-CG	5.08	118.88	113.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4076	0	4006	13	0
1	B	4085	0	4002	19	0
2	A	26	21	0	0	0
2	B	26	21	0	0	0
3	A	409	0	0	0	0
3	B	413	0	0	1	0
All	All	9035	42	8008	32	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (32) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:356:THR:OG1	1:B:459:CYS:HB3	1.54	1.06
1:B:356:THR:OG1	1:B:459:CYS:CB	2.19	0.90
1:A:362:ARG:NH2	1:A:426[A]:HIS:CD2	2.77	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:356:THR:OG1	1:B:459:CYS:HB2	2.08	0.52
1:B:287:HIS:CD2	1:B:288:THR:HG23	2.45	0.51
1:A:120:LYS:O	1:A:124:LYS:HG2	2.12	0.50
1:B:120:LYS:O	1:B:124:LYS:HG2	2.12	0.49
1:A:309:ILE:HD13	1:A:328:ILE:HG12	1.93	0.49
1:B:309:ILE:HD13	1:B:328:ILE:HG12	1.96	0.47
1:A:176:GLU:O	1:A:177:LEU:HB2	2.14	0.47
1:A:90:GLU:HG3	1:A:91:LYS:N	2.30	0.46
1:B:65:LEU:C	1:B:65:LEU:HD23	2.41	0.45
1:B:104:CYS:SG	1:B:106:ASP:HB3	2.57	0.45
1:B:290:VAL:HG11	1:B:344:MET:HG3	2.00	0.44
1:A:149:LEU:HD23	1:A:202:MET:HE1	2.00	0.44
1:A:352:VAL:HG11	1:A:442:VAL:HG13	1.99	0.44
1:B:149:LEU:HD23	1:B:202:MET:HE1	2.00	0.43
1:B:226:ILE:HG23	1:B:227:GLU:N	2.34	0.43
1:B:114:HIS:CE1	1:B:218:THR:HG21	2.54	0.43
1:A:114:HIS:CE1	1:A:218:THR:HG21	2.54	0.43
1:A:290:VAL:HG11	1:A:344:MET:HG3	2.01	0.43
1:A:226:ILE:HG23	1:A:227:GLU:N	2.34	0.42
1:A:11:ILE:CD1	1:A:19:LEU:HD12	2.49	0.42
1:B:11:ILE:CD1	1:B:19:LEU:HD12	2.49	0.42
1:A:119:GLY:O	1:A:123:GLU:HG3	2.20	0.42
1:B:119:GLY:O	1:B:123:GLU:HG3	2.20	0.41
1:B:54:ILE:HD11	1:B:96:ILE:HD13	2.02	0.41
1:B:134:SER:HA	1:B:214:GLN:O	2.20	0.41
1:B:278:ARG:NH2	3:B:718:HOH:O	2.54	0.41
1:A:125:LEU:HB3	1:A:216:LEU:HD21	2.03	0.41
1:B:69:GLU:OE1	1:B:87:GLN:OE1	2.39	0.40
1:B:125:LEU:HB3	1:B:216:LEU:HD21	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	493/537 (92%)	482 (98%)	9 (2%)	2 (0%)	30	18
1	B	492/537 (92%)	474 (96%)	16 (3%)	2 (0%)	30	18
All	All	985/1074 (92%)	956 (97%)	25 (2%)	4 (0%)	30	18

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	459	CYS
1	B	460	SER
1	A	505	VAL
1	B	505	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	448/479 (94%)	442 (99%)	6 (1%)	61	50
1	B	448/479 (94%)	438 (98%)	10 (2%)	45	30
All	All	896/958 (94%)	880 (98%)	16 (2%)	51	38

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	87	GLN
1	A	162	ASP
1	A	198	LYS
1	A	314	PHE
1	A	362	ARG
1	A	368	VAL
1	B	3	SER
1	B	36	SER
1	B	37	ASN
1	B	52	THR
1	B	87	GLN
1	B	92	ASN

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Mol	Chain	Res	Type
1	B	313	GLU
1	B	366	LYS
1	B	367	CYS
1	B	523	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	87	GLN
1	A	114	HIS
1	A	141	GLN
1	A	196	HIS
1	A	200	ASN
1	A	293	HIS
1	A	298	ASN
1	B	10	ASN
1	B	87	GLN
1	B	92	ASN
1	B	114	HIS
1	B	141	GLN
1	B	196	HIS
1	B	200	ASN
1	B	245	GLN
1	B	256	GLN
1	B	339	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	A1H4T	A	601	-	29,30,30	0.68	1 (3%)	38,45,45	0.93	2 (5%)
2	A1H4T	B	601	-	29,30,30	0.82	1 (3%)	38,45,45	1.00	2 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	A1H4T	A	601	-	-	2/8/29/29	0/6/5/5
2	A1H4T	B	601	-	3/3/4/4	0/8/29/29	0/6/5/5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	A1H4T	C13-C14	-3.13	1.40	1.47
2	A	601	A1H4T	C13-C14	-2.03	1.42	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	A1H4T	C14-C15-N16	-3.96	107.90	110.46
2	A	601	A1H4T	C14-C15-N16	-2.60	108.78	110.46
2	B	601	A1H4T	C13-C14-C15	2.30	107.22	105.60
2	A	601	A1H4T	C10-N9-C4	2.21	123.55	121.18

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	601	A1H4T	C4

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Mol	Chain	Res	Type	Atom
2	B	601	A1H4T	C2
2	B	601	A1H4T	C7

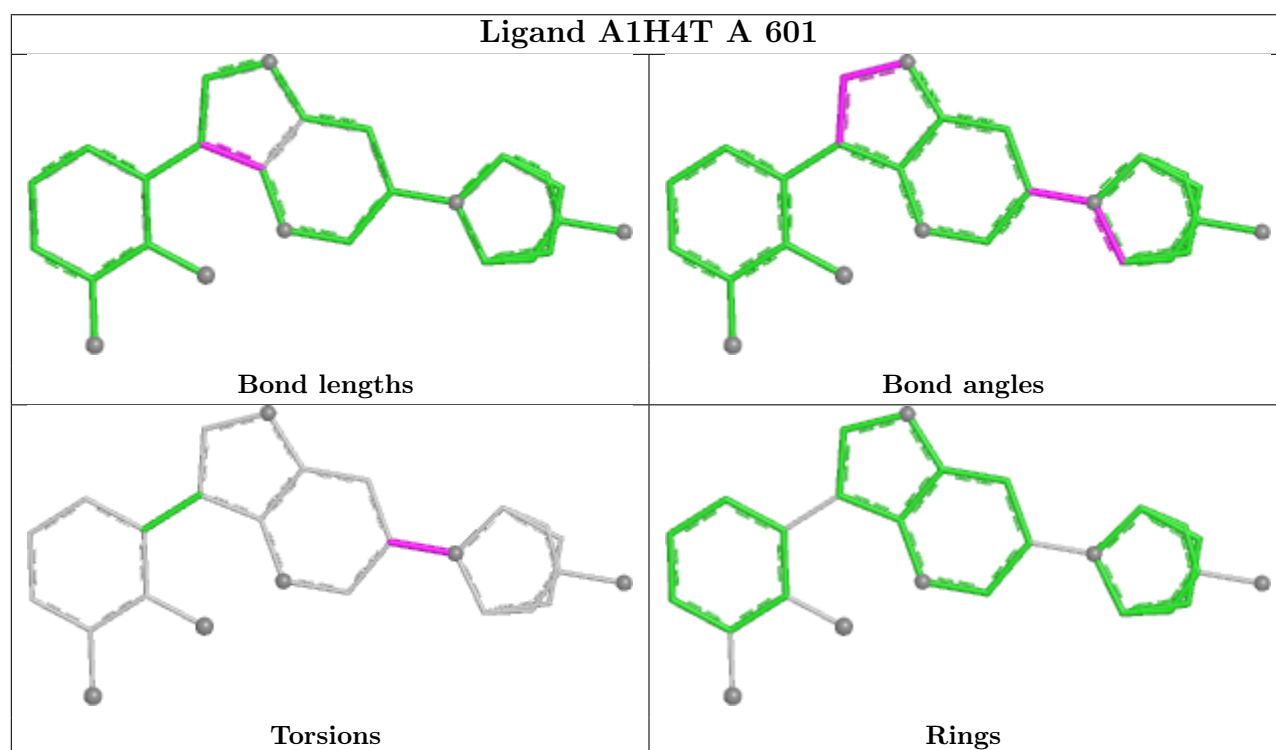
All (2) torsion outliers are listed below:

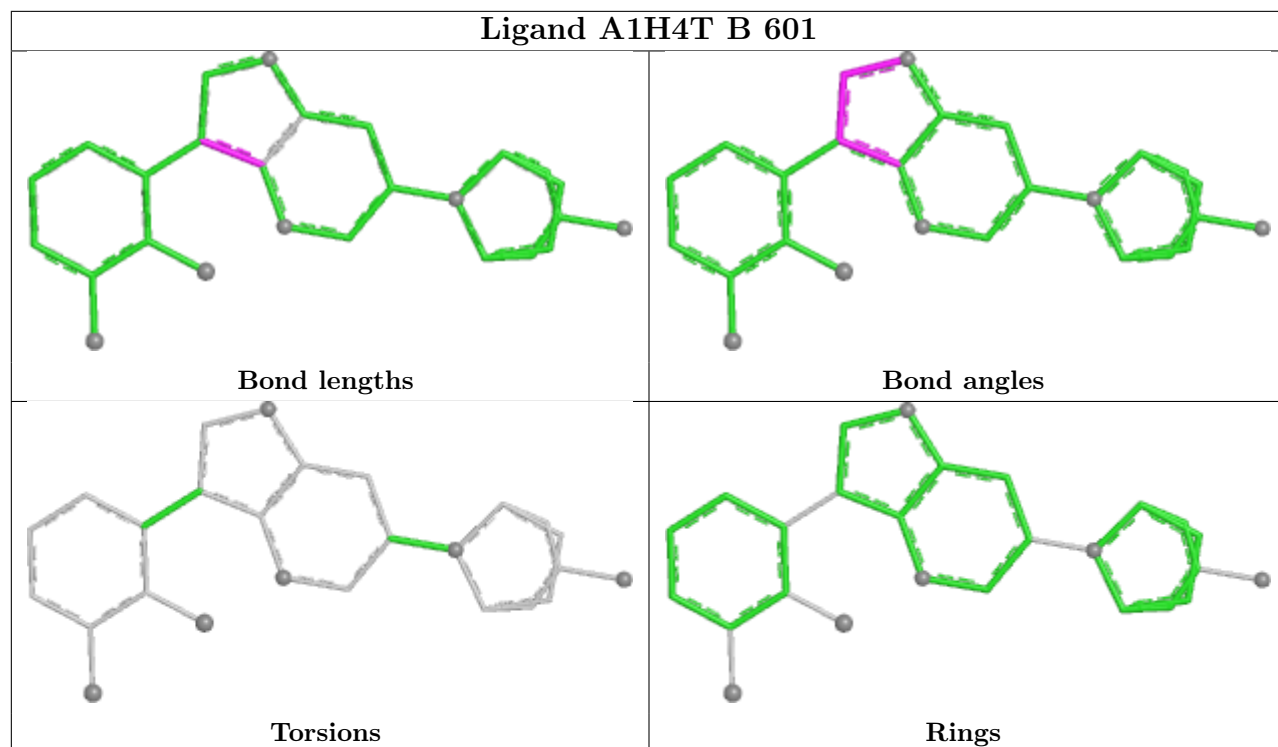
Mol	Chain	Res	Type	Atoms
2	A	601	A1H4T	C18-C10-N9-C7
2	A	601	A1H4T	C11-C10-N9-C7

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	502/537 (93%)	0.51	50 (9%)	12 14	17, 37, 67, 93	1 (0%)
1	B	504/537 (93%)	0.62	54 (10%)	11 13	18, 39, 68, 84	0
All	All	1006/1074 (93%)	0.56	104 (10%)	12 14	17, 38, 68, 93	1 (0%)

All (104) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	368	VAL	5.6
1	A	38	PRO	5.0
1	A	314	PHE	4.8
1	B	86	GLY	4.6
1	B	367	CYS	4.4
1	A	525	LEU	4.3
1	B	532	HIS	4.1
1	A	294	ASP	4.0
1	B	177	LEU	3.9
1	B	362	ARG	3.9
1	A	205	THR	3.8
1	B	484	VAL	3.7
1	A	248	TRP	3.7
1	A	301	VAL	3.7
1	B	301	VAL	3.6
1	B	293	HIS	3.5
1	A	484	VAL	3.3
1	B	426	HIS	3.3
1	A	84	HIS	3.2
1	B	87	GLN	3.2
1	A	177	LEU	3.2
1	B	275	ASN	3.2
1	B	154	GLY	3.2
1	B	84	HIS	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	35	LYS	3.2
1	A	295	GLY	3.2
1	B	324	LYS	3.1
1	A	206	LEU	3.1
1	A	162	ASP	3.0
1	B	294	ASP	3.0
1	B	360	VAL	3.0
1	B	361	GLU	3.0
1	A	300	PRO	2.9
1	A	426[A]	HIS	2.9
1	A	296	ASP	2.9
1	B	206	LEU	2.9
1	B	529	LEU	2.9
1	B	248	TRP	2.9
1	B	365	SER	2.9
1	B	357	THR	2.8
1	A	526	GLN	2.8
1	B	221	ILE	2.8
1	A	95	VAL	2.8
1	A	120	LYS	2.8
1	B	89	LYS	2.7
1	B	85	HIS	2.7
1	B	314	PHE	2.7
1	A	163	GLY	2.7
1	A	485	ASP	2.7
1	B	205	THR	2.7
1	A	299	GLU	2.7
1	A	39	GLY	2.6
1	B	164	LYS	2.6
1	B	109	SER	2.6
1	A	524	THR	2.6
1	A	311	MET	2.5
1	B	11	ILE	2.5
1	B	523	GLU	2.5
1	B	364	LYS	2.5
1	B	88	LEU	2.5
1	B	117	LEU	2.5
1	B	95	VAL	2.5
1	B	425	ASP	2.5
1	A	528	ARG	2.4
1	A	421	ARG	2.4
1	B	527	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	531	HIS	2.4
1	A	69	GLU	2.4
1	A	124	LYS	2.4
1	A	87	GLN	2.3
1	B	245	GLN	2.3
1	A	48	ASN	2.3
1	A	164	LYS	2.3
1	A	324	LYS	2.3
1	A	143	HIS	2.3
1	A	91	LYS	2.3
1	B	359	GLU	2.3
1	B	120	LYS	2.3
1	A	34	SER	2.3
1	B	155	ASP	2.3
1	B	143	HIS	2.3
1	A	104	CYS	2.2
1	A	520	HIS	2.2
1	A	14	VAL	2.2
1	B	162	ASP	2.2
1	B	485	ASP	2.2
1	A	3	SER	2.2
1	A	68	GLY	2.2
1	B	528	ARG	2.2
1	B	3	SER	2.1
1	A	88	LEU	2.1
1	A	233	LEU	2.1
1	A	90	GLU	2.1
1	B	451	ASP	2.1
1	A	210	LEU	2.1
1	A	36	SER	2.1
1	A	275	ASN	2.1
1	B	161	ASN	2.1
1	B	57	GLN	2.1
1	B	313	GLU	2.0
1	B	108	THR	2.0
1	A	394	HIS	2.0
1	A	437	ASP	2.0
1	B	295	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

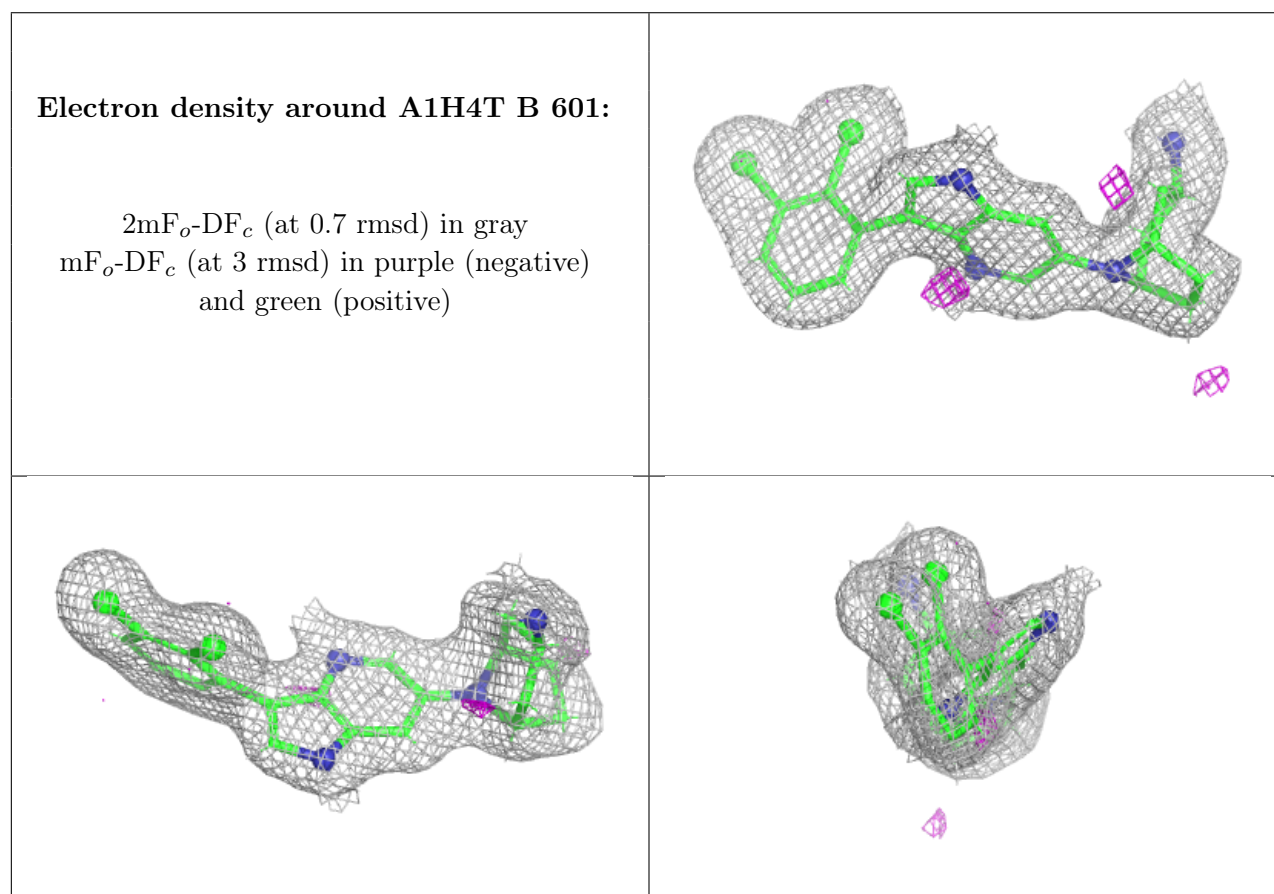
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

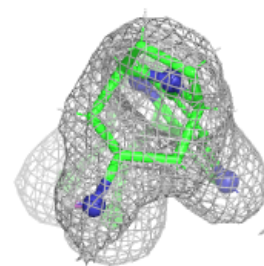
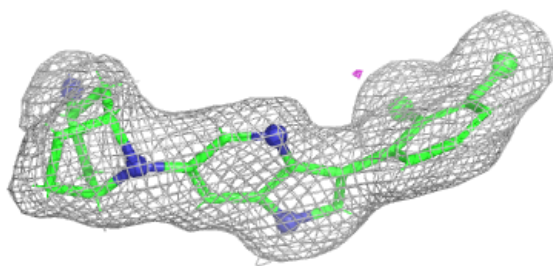
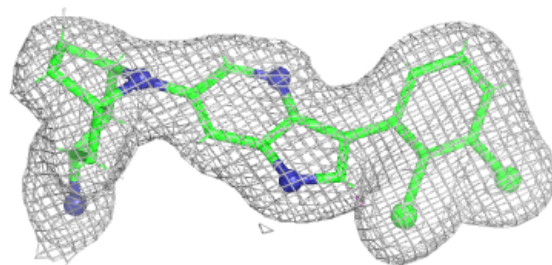
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	A1H4T	B	601	26/26	0.95	0.07	33,34,36,38	0
2	A1H4T	A	601	26/26	0.96	0.07	33,34,35,37	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around A1H4T A 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.