



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 29, 2025 – 07:51 AM EDT

PDB ID : 2H8H / pdb_00002h8h
Title : Src kinase in complex with a quinazoline inhibitor
Authors : Otterbein, L.R.; Norman, R.; Pauptit, R.A.; Rowsell, S.; Breed, J.
Deposited on : 2006-06-07
Resolution : 2.20 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 Phenix2.0rc1
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

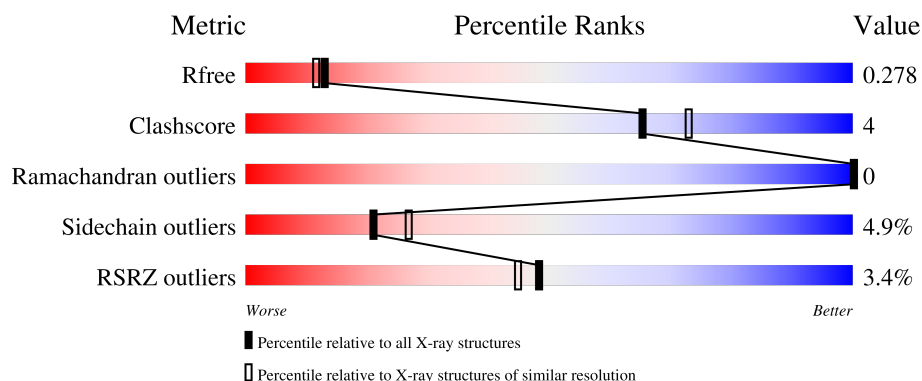
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	164625	5791 (2.20-2.20)
Clashscore	180529	6634 (2.20-2.20)
Ramachandran outliers	177936	6560 (2.20-2.20)
Sidechain outliers	177891	6561 (2.20-2.20)
RSRZ outliers	164620	5791 (2.20-2.20)

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	535	

2 Entry composition [i](#)

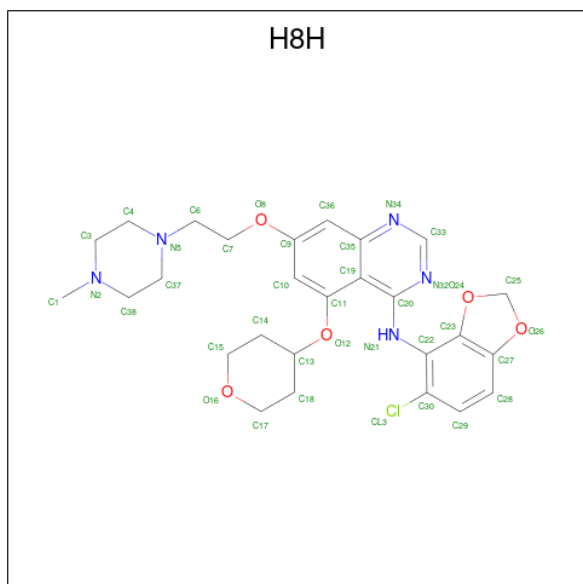
There are 3 unique types of molecules in this entry. The entry contains 3862 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Proto-oncogene tyrosine-protein kinase Src.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	445	3603	2292	611	679	1	20	0	3	0

- Molecule 2 is N-(5-CHLORO-1,3-BENZODIOXOL-4-YL)-7-[2-(4-METHYLPYPERAZIN-1-YL)ETHOXY]-5-(TETRAHYDRO-2H-PYRAN-4-YLOXY)QUINAZOLIN-4-AMINE (CCD ID: H8H) (formula: C₂₇H₃₂ClN₅O₅).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	N	O		
2	A	1	38	27	1	5	5	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	221	Total	O	0	0
			221	221		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	49.81Å 72.47Å 171.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.67 – 2.20 47.67 – 2.20	Depositor EDS
% Data completeness (in resolution range)	95.5 (47.67-2.20) 95.5 (47.67-2.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.204 , 0.272 0.216 , 0.278	Depositor DCC
R_{free} test set	1566 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	32.7	Xtriage
Anisotropy	0.049	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 31.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3862	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.54% 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: PTR, H8H

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	0.80	0/3677	0.89	2/4980 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	407	LEU	N-CA-C	5.80	117.68	111.36
1	A	342	SER	N-CA-C	5.44	117.96	111.71

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	208	ASP	Peptide

5.2 Too-close contacts [i](#)

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	3603	0	3535	27	0
2	A	38	0	32	2	0
3	A	221	0	0	2	0
All	All	3862	0	3567	27	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 4.

All (27) 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:A:527:PTR:C	1:A:528:GLN:HG2	2.27	0.63
1:A:114:THR:N	1:A:115[B]:GLU:OE1	2.37	0.58
1:A:304:PRO:HB3	1:A:330:SER:O	2.09	0.53
1:A:469:ARG:HG2	3:A:648:HOH:O	2.09	0.52
1:A:113:ASN:C	1:A:115[B]:GLU:OE1	2.55	0.49
1:A:155:ARG:HB3	1:A:175:ARG:NH2	2.27	0.49
1:A:341:MET:O	2:A:534:H8H:H72	2.13	0.49
1:A:329:VAL:HB	1:A:335:TYR:HB2	1.96	0.48
1:A:200:LYS:CG	1:A:528:GLN:HE22	2.27	0.47
1:A:317:LEU:HD21	1:A:382[B]:TYR:CD1	2.50	0.47
1:A:384:HIS:O	1:A:385:ARG:HB2	2.15	0.46
1:A:224:GLN:HE21	1:A:224:GLN:H	1.64	0.46
1:A:359:ARG:HB2	1:A:362:GLN:NE2	2.31	0.46
1:A:338:THR:OG1	2:A:534:H8H:H252	2.16	0.45
1:A:207:LEU:N	1:A:211:GLY:O	2.49	0.45
1:A:186:LEU:HD21	1:A:241:LEU:HD21	1.99	0.45
1:A:117:ASP:HB3	1:A:253:GLN:HB3	2.00	0.44
1:A:90:TYR:CZ	1:A:250:PRO:HD3	2.52	0.44
1:A:359:ARG:HB3	1:A:361:PRO:HD2	1.99	0.44
1:A:85:THR:HG22	1:A:124:LEU:HD11	2.00	0.42
1:A:467:VAL:HG22	1:A:470:GLU:HG3	2.01	0.42
1:A:251:GLN:NE2	1:A:326:TYR:OH	2.53	0.41
1:A:458:LYS:N	3:A:589:HOH:O	2.33	0.41
1:A:206:LYS:HA	1:A:211:GLY:O	2.21	0.41
1:A:279:GLY:HA3	1:A:296:THR:O	2.19	0.41
1:A:109:GLN:HB2	1:A:124:LEU:HD21	2.03	0.40
1:A:114:THR:C	1:A:115[B]:GLU:OE1	2.65	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	445/535 (83%)	428 (96%)	17 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	388/447 (87%)	369 (95%)	19 (5%)	21	27

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	152	LYS
1	A	207	LEU
1	A	218	THR
1	A	224	GLN
1	A	225	GLN
1	A	243	THR
1	A	261	GLU
1	A	269	LEU
1	A	308	LEU
1	A	318	ARG
1	A	359	ARG
1	A	396	GLU
1	A	460	ARG

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Mol	Chain	Res	Type
1	A	469	ARG
1	A	472	LEU
1	A	476	GLU
1	A	490	SER
1	A	523	THR
1	A	524	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	109	GLN
1	A	122	HIS
1	A	164	ASN
1	A	221	ASN
1	A	224	GLN
1	A	251	GLN
1	A	253	GLN
1	A	324	GLN
1	A	362	GLN
1	A	414	ASN
1	A	420	GLN
1	A	528	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
1	PTR	A	527	1	15,16,17	0.74	0	17,22,24	0.96	0

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
1	PTR	A	527	1	-	1/10/11/13	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	527	PTR	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	527	PTR	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	H8H	A	534	-	43,43,43	0.87	2 (4%)	54,60,60	2.22	17 (31%)

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	H8H	A	534	-	-	5/14/38/38	0/6/6/6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	534	H8H	C20-N21	2.76	1.40	1.36
2	A	534	H8H	C35-N34	-2.09	1.33	1.37

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	534	H8H	C33-N32-C20	6.80	121.88	116.60
2	A	534	H8H	O26-C25-O24	-5.34	99.71	108.09
2	A	534	H8H	C33-N34-C35	5.23	121.37	115.43
2	A	534	H8H	C11-C19-C20	-4.44	122.99	126.31
2	A	534	H8H	N34-C33-N32	-4.31	122.82	128.67
2	A	534	H8H	C11-O12-C13	-3.77	113.18	119.11
2	A	534	H8H	C7-O8-C9	-3.58	108.63	117.93
2	A	534	H8H	C19-C35-N34	-3.21	118.41	122.23
2	A	534	H8H	O24-C23-C27	-2.98	106.50	109.82
2	A	534	H8H	C36-C35-N34	2.88	121.32	118.01
2	A	534	H8H	O26-C27-C23	-2.68	106.90	109.62
2	A	534	H8H	C6-N5-C4	-2.59	104.35	111.24
2	A	534	H8H	O26-C27-C28	2.56	132.66	127.72
2	A	534	H8H	C15-C14-C13	2.40	112.87	109.89
2	A	534	H8H	C20-C19-C35	2.39	117.61	115.34
2	A	534	H8H	C6-N5-C37	-2.34	104.99	111.24
2	A	534	H8H	C17-O16-C15	2.04	116.48	109.88

There are no chirality outliers.

All (5) torsion outliers are listed below:

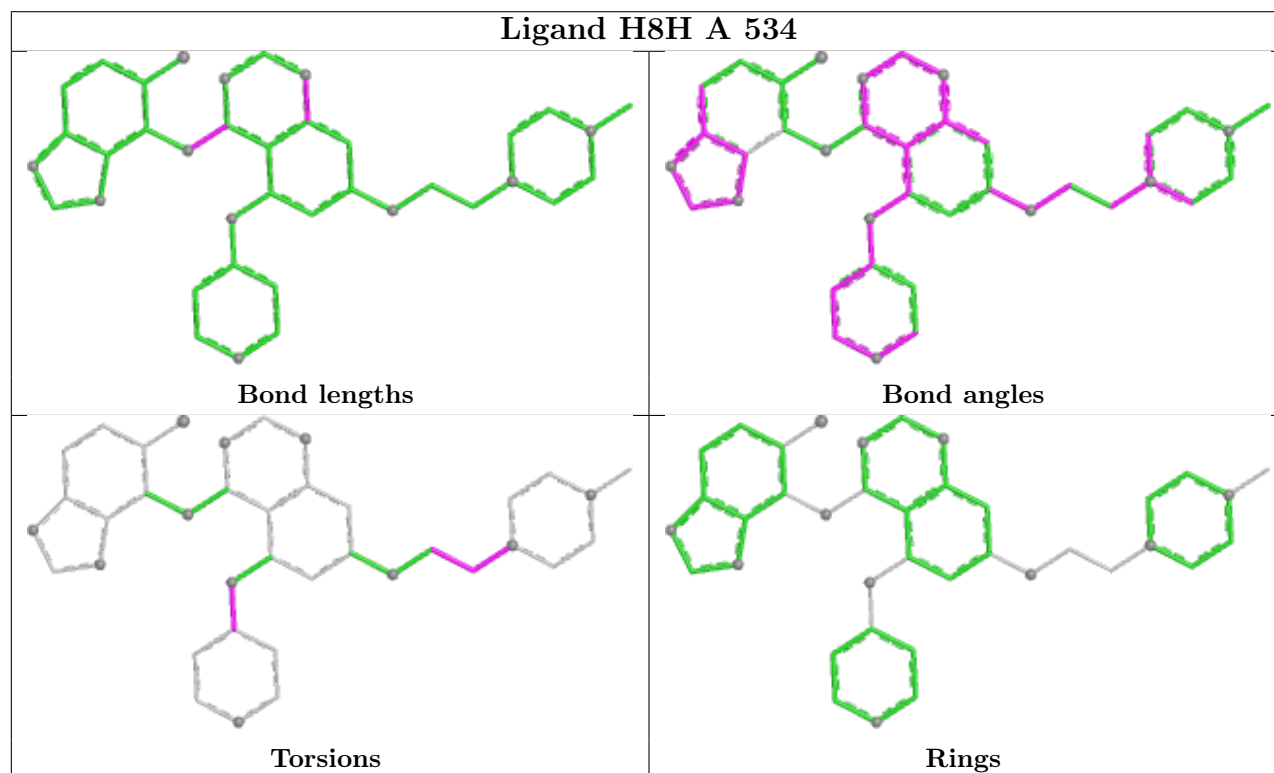
Mol	Chain	Res	Type	Atoms
2	A	534	H8H	N5-C6-C7-O8
2	A	534	H8H	C7-C6-N5-C4
2	A	534	H8H	C7-C6-N5-C37
2	A	534	H8H	C14-C13-O12-C11
2	A	534	H8H	C18-C13-O12-C11

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	534	H8H	2	0

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	444/535 (82%)	0.19	15 (3%)	48 45	23, 36, 53, 64	3 (0%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	115[A]	GLU	4.3
1	A	523	THR	4.1
1	A	529	PRO	3.6
1	A	521	THR	3.2
1	A	524	GLU	3.1
1	A	405	PHE	3.1
1	A	116	GLY	2.9
1	A	522	SER	2.8
1	A	417	THR	2.7
1	A	211	GLY	2.6
1	A	210	GLY	2.5
1	A	418	ALA	2.4
1	A	141	ASP	2.3
1	A	208	ASP	2.1
1	A	253	GLN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	PTR	A	527	16/17	0.95	0.10	42,49,55,56	0

6.3 Carbohydrates [i](#)

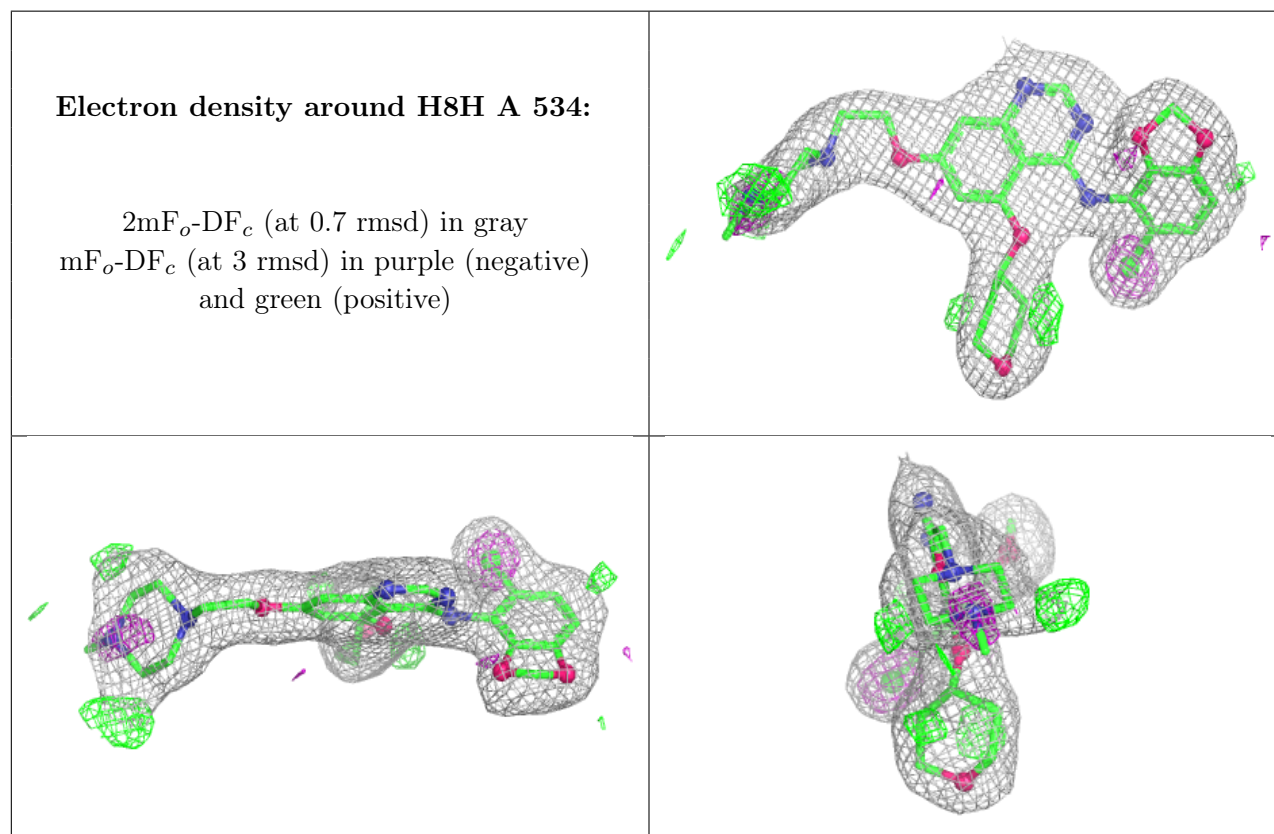
There are no monosaccharides in this entry.

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(\AA^2)	Q<0.9
2	H8H	A	534	38/38	0.93	0.10	27,32,49,54	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.