



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 07:13 AM UTC

PDB ID : 6TND / pdb_00006tnd
Title : X-RAY STRUCTURE OF MPS1 IN COMPLEX WITH COMPOUND 79
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Deposited on : 2019-12-06
Resolution : 2.58 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](#) ①) 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

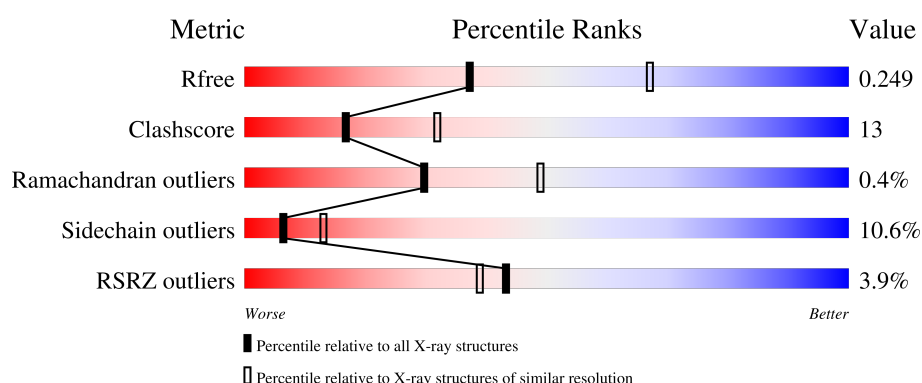
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.58 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	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (2.60-2.56)

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	294	3% 58% 23% 5% 14%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2166 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.

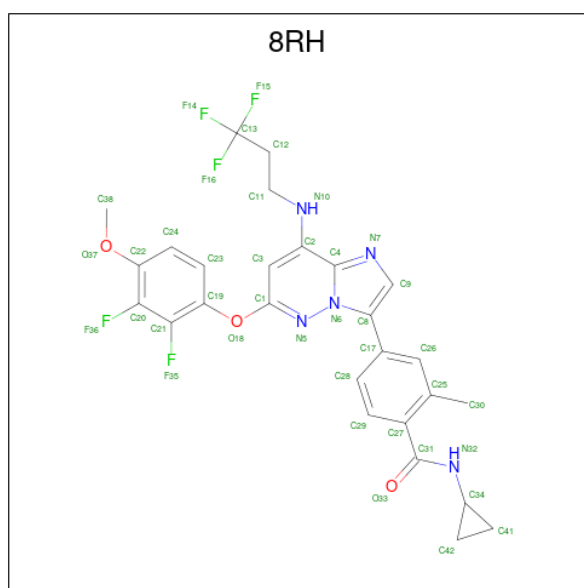
- Molecule 1 is a protein called Dual specificity protein kinase TTK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	254	2087	1345	346	383	13	0	1	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	513	GLY	-	expression tag	UNP P33981
A	514	SER	-	expression tag	UNP P33981

- Molecule 2 is BAY 1217389 (CCD ID: 8RH) (formula: $C_{27}H_{24}F_5N_5O_3$) (labeled as "Ligand of Interest" by depositor).

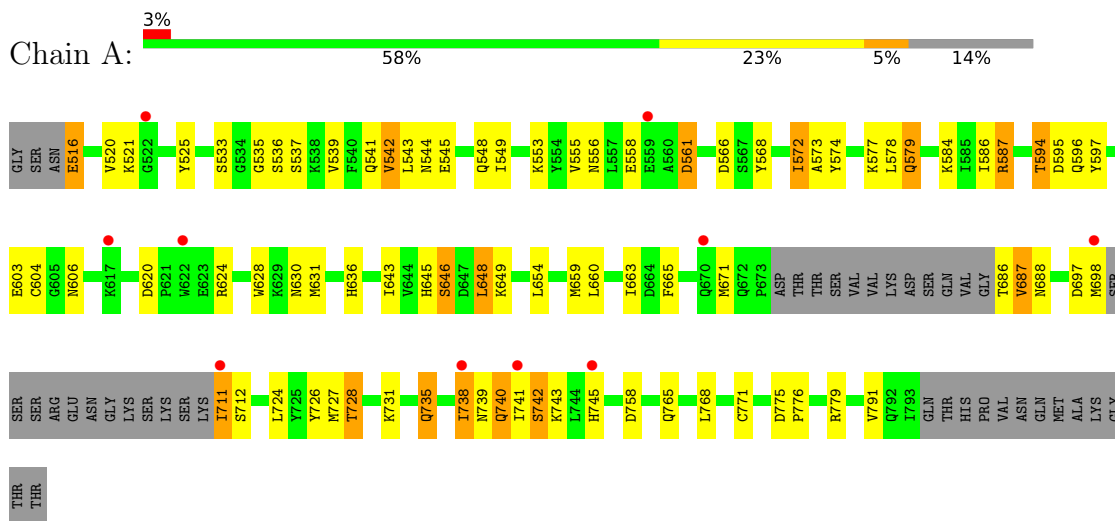


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	O		
2	A	1	40	27	5	5	3	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	39	Total 39	O 39	0	0

- Molecule 1: Dual specificity protein kinase TTK



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	71.13Å 107.80Å 112.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.91 – 2.58 40.91 – 2.58	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.91-2.58) 99.9 (40.91-2.58)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 2.58Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.186 , 0.249 0.195 , 0.249	Depositor DCC
R_{free} test set	702 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	56.8	Xtriage
Anisotropy	0.323	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 40.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.019 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2166	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.58% 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: 8RH

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	1.12	1/2133 (0.0%)	1.53	11/2882 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	636	HIS	C-O	5.76	1.30	1.24

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	697	ASP	CA-CB-CG	6.43	119.03	112.60
1	A	579	GLN	CB-CA-C	-6.38	100.87	110.88
1	A	595	ASP	N-CA-C	-5.71	105.19	111.82
1	A	566	ASP	CA-CB-CG	-5.53	107.07	112.60
1	A	735	GLN	CA-C-N	5.33	127.85	120.29
1	A	735	GLN	C-N-CA	5.33	127.85	120.29
1	A	604	CYS	CA-C-N	-5.21	116.22	122.16
1	A	604	CYS	C-N-CA	-5.21	116.22	122.16
1	A	568	TYR	CB-CA-C	5.15	119.60	110.85
1	A	521	LYS	CB-CA-C	5.14	119.66	111.95
1	A	620	ASP	CA-CB-CG	5.01	117.61	112.60

There are no chirality outliers.

There are no planarity outliers.

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	2087	0	2107	53	0
2	A	40	0	0	5	0
3	A	39	0	0	1	0
All	All	2166	0	2107	54	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 13.

All (54) 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:654:LEU:HD13	1:A:663[A]:ILE:HD11	1.60	0.82
1:A:516:GLU:O	1:A:516:GLU:HG2	1.84	0.76
1:A:645:HIS:CG	1:A:648:LEU:HD13	2.26	0.70
1:A:544:ASN:HD21	1:A:548:GLN:HE21	1.41	0.67
1:A:556:ASN:OD1	1:A:558:GLU:HG3	1.95	0.66
1:A:561:ASP:OD1	1:A:561:ASP:N	2.27	0.66
1:A:711:ILE:HA	3:A:1035:HOH:O	1.95	0.65
1:A:628:TRP:HA	1:A:631:MET:HE3	1.80	0.64
1:A:724:LEU:O	1:A:728:THR:HG23	1.97	0.63
1:A:594:THR:HG22	1:A:596:GLN:H	1.64	0.62
1:A:686:THR:HG21	1:A:688:ASN:HD22	1.66	0.59
1:A:771:CYS:O	1:A:779:ARG:HD2	2.02	0.59
1:A:630:ASN:HD22	1:A:660:LEU:H	1.52	0.58
1:A:741:ILE:O	1:A:745:HIS:CD2	2.57	0.58
1:A:541:GLN:HE21	1:A:549:ILE:HD11	1.69	0.56
1:A:624:ARG:HG3	1:A:727:MET:HE2	1.86	0.56
1:A:686:THR:CG2	1:A:688:ASN:HD22	2.18	0.56
1:A:525:TYR:HB3	1:A:542:VAL:HG13	1.88	0.54
1:A:579:GLN:HE22	1:A:587:ARG:HG3	1.73	0.54
1:A:594:THR:HG22	1:A:597:TYR:H	1.73	0.54
1:A:724:LEU:HG	1:A:768:LEU:HD21	1.91	0.52
1:A:586:ILE:CD1	1:A:654:LEU:HD23	2.42	0.50
1:A:594:THR:HG22	1:A:596:GLN:N	2.27	0.50
1:A:739:ASN:ND2	1:A:742:SER:HB2	2.28	0.49
1:A:574:TYR:CD1	1:A:643:ILE:HD11	2.48	0.48
1:A:594:THR:CG2	1:A:596:GLN:H	2.24	0.48
1:A:584:LYS:HE3	1:A:659:MET:SD	2.54	0.48
1:A:525:TYR:HA	1:A:543:LEU:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:578:LEU:HD12	1:A:665:PHE:CE1	2.50	0.47
1:A:541:GLN:NE2	1:A:549:ILE:HD11	2.29	0.47
1:A:553:LYS:CE	2:A:901:8RH:O33	2.63	0.47
1:A:536:SER:HB2	1:A:556:ASN:O	2.15	0.47
1:A:740:GLN:NE2	1:A:740:GLN:CA	2.79	0.46
1:A:630:ASN:ND2	1:A:660:LEU:H	2.12	0.46
1:A:758:ASP:HA	1:A:765:GLN:HE22	1.81	0.45
1:A:740:GLN:HE21	1:A:740:GLN:N	2.14	0.45
1:A:539:VAL:HG23	1:A:671:MET:HE2	1.99	0.45
2:A:901:8RH:C26	2:A:901:8RH:N5	2.80	0.44
1:A:537:SER:HB3	1:A:555:VAL:HG22	2.00	0.43
1:A:572:ILE:HG13	1:A:573:ALA:N	2.33	0.43
1:A:724:LEU:O	1:A:728:THR:CG2	2.67	0.43
1:A:726:TYR:HA	1:A:731:LYS:O	2.19	0.42
1:A:586:ILE:HD13	1:A:654:LEU:CD2	2.48	0.42
1:A:738:ILE:H	1:A:738:ILE:HD12	1.83	0.42
1:A:553:LYS:HE2	2:A:901:8RH:O33	2.18	0.42
1:A:775:ASP:HA	1:A:776:PRO:HD2	1.92	0.41
1:A:539:VAL:HG22	1:A:553:LYS:HG3	2.02	0.41
1:A:645:HIS:O	1:A:646:SER:HB2	2.21	0.41
1:A:586:ILE:CD1	1:A:654:LEU:CD2	2.99	0.41
1:A:663[A]:ILE:O	2:A:901:8RH:N32	2.53	0.41
1:A:738:ILE:HD12	1:A:738:ILE:N	2.36	0.41
1:A:686:THR:CG2	1:A:688:ASN:ND2	2.83	0.40
1:A:654:LEU:HD11	2:A:901:8RH:C4	2.50	0.40
1:A:687:VAL:HG12	1:A:743:LYS:HD2	2.01	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	249/294 (85%)	236 (95%)	12 (5%)	1 (0%)	30	49

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	535	GLY

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	236/270 (87%)	211 (89%)	25 (11%)	6	13

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	516	GLU
1	A	520	VAL
1	A	533	SER
1	A	542	VAL
1	A	545	GLU
1	A	561	ASP
1	A	572	ILE
1	A	577	LYS
1	A	587	ARG
1	A	594	THR
1	A	603	GLU
1	A	606	ASN
1	A	646	SER
1	A	648	LEU
1	A	649	LYS
1	A	687	VAL
1	A	698	MET
1	A	711	ILE
1	A	712	SER
1	A	728	THR

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Mol	Chain	Res	Type
1	A	735	GLN
1	A	738	ILE
1	A	740	GLN
1	A	742	SER
1	A	791	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	530	GLN
1	A	541	GLN
1	A	548	GLN
1	A	579	GLN
1	A	630	ASN
1	A	735	GLN
1	A	739	ASN
1	A	740	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

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	8RH	A	901	-	43,44,44	1.94	12 (27%)	55,65,65	2.46	19 (34%)

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	8RH	A	901	-	-	7/24/27/27	0/5/5/5

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	901	8RH	C1-N5	5.43	1.35	1.29
2	A	901	8RH	N6-N5	-5.16	1.25	1.38
2	A	901	8RH	C17-C8	-3.85	1.42	1.48
2	A	901	8RH	O18-C19	-3.57	1.34	1.41
2	A	901	8RH	C8-N6	3.34	1.43	1.38
2	A	901	8RH	C11-N10	-2.89	1.39	1.46
2	A	901	8RH	C9-C8	-2.76	1.34	1.37
2	A	901	8RH	C2-N10	-2.58	1.29	1.34
2	A	901	8RH	C41-C34	2.46	1.54	1.48
2	A	901	8RH	C26-C25	-2.45	1.36	1.39
2	A	901	8RH	C27-C31	2.16	1.54	1.50
2	A	901	8RH	C42-C34	2.09	1.53	1.48

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	8RH	C3-C2-N10	-7.71	112.56	124.86
2	A	901	8RH	C12-C11-N10	-6.68	97.78	111.62
2	A	901	8RH	C42-C34-N32	-4.94	112.05	118.52
2	A	901	8RH	C11-C12-C13	-4.87	103.69	112.98
2	A	901	8RH	O37-C22-C20	4.83	119.94	116.28
2	A	901	8RH	C3-C1-N5	-4.48	119.90	125.16
2	A	901	8RH	F15-C13-C12	-4.20	98.16	112.86
2	A	901	8RH	F14-C13-F15	4.04	120.68	106.44
2	A	901	8RH	C9-N7-C4	3.63	109.62	105.13
2	A	901	8RH	C8-N6-C4	-3.41	104.70	108.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	8RH	C8-C9-N7	-3.00	109.14	112.37
2	A	901	8RH	C25-C27-C31	-2.93	117.93	120.52
2	A	901	8RH	C17-C8-N6	-2.60	120.72	125.75
2	A	901	8RH	F14-C13-C12	-2.32	104.74	112.86
2	A	901	8RH	C41-C34-N32	-2.29	115.51	118.52
2	A	901	8RH	C23-C19-C21	2.19	121.46	117.88
2	A	901	8RH	O37-C22-C24	-2.16	120.66	124.30
2	A	901	8RH	C4-N6-N5	-2.12	121.98	126.18
2	A	901	8RH	O18-C1-C3	-2.06	112.95	116.22

There are no chirality outliers.

All (7) torsion outliers are listed below:

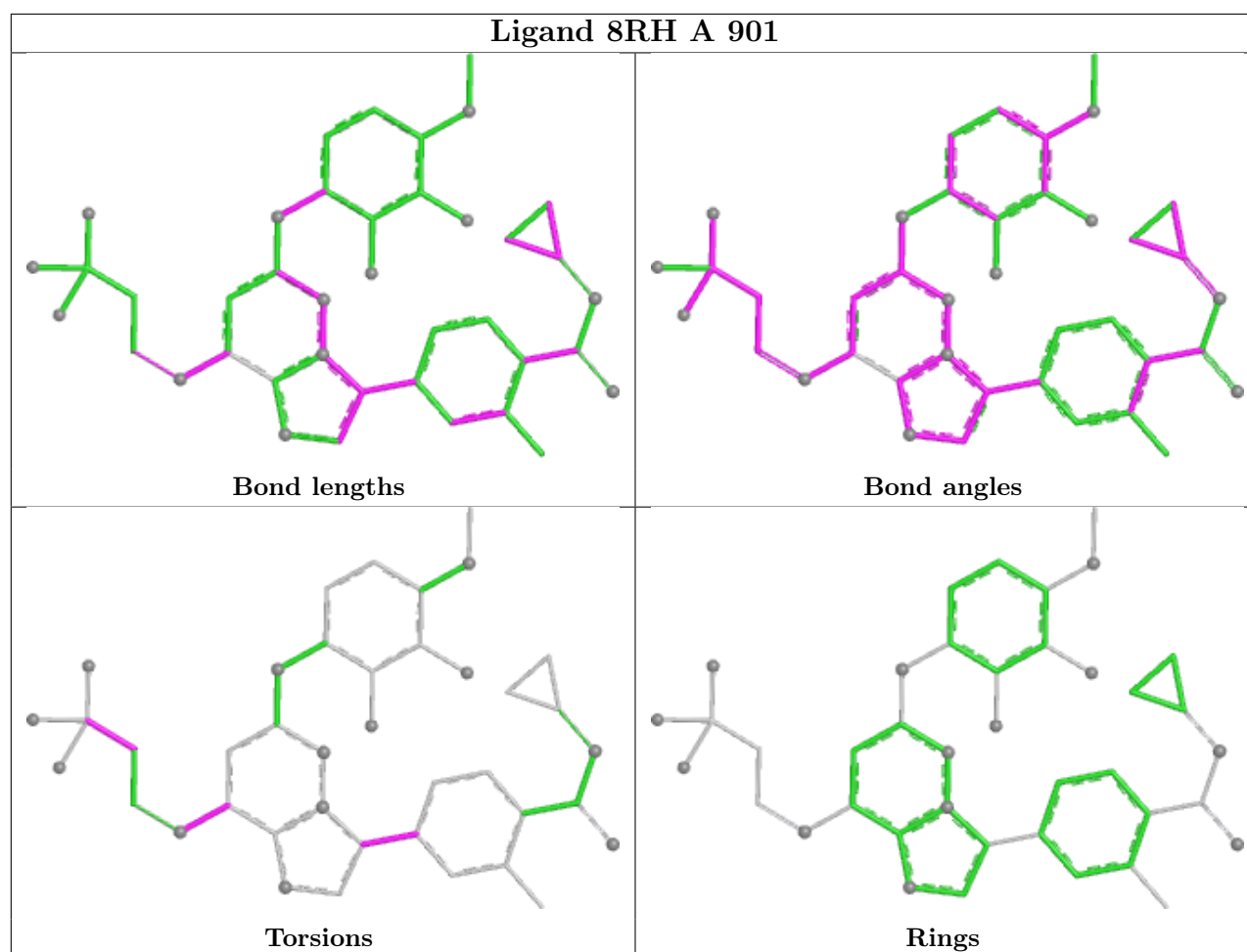
Mol	Chain	Res	Type	Atoms
2	A	901	8RH	C3-C2-N10-C11
2	A	901	8RH	C4-C2-N10-C11
2	A	901	8RH	C11-C12-C13-F16
2	A	901	8RH	C11-C12-C13-F15
2	A	901	8RH	C11-C12-C13-F14
2	A	901	8RH	C26-C17-C8-N6
2	A	901	8RH	C26-C17-C8-C9

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	8RH	5	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 [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 [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	254/294 (86%)	0.14	10 (3%) 43 39	20, 60, 103, 133	1 (0%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	698	MET	4.5
1	A	738	ILE	3.8
1	A	622	TRP	3.7
1	A	711	ILE	2.8
1	A	745	HIS	2.7
1	A	617	LYS	2.4
1	A	741	ILE	2.3
1	A	670	GLN	2.3
1	A	559	GLU	2.2
1	A	522	GLY	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

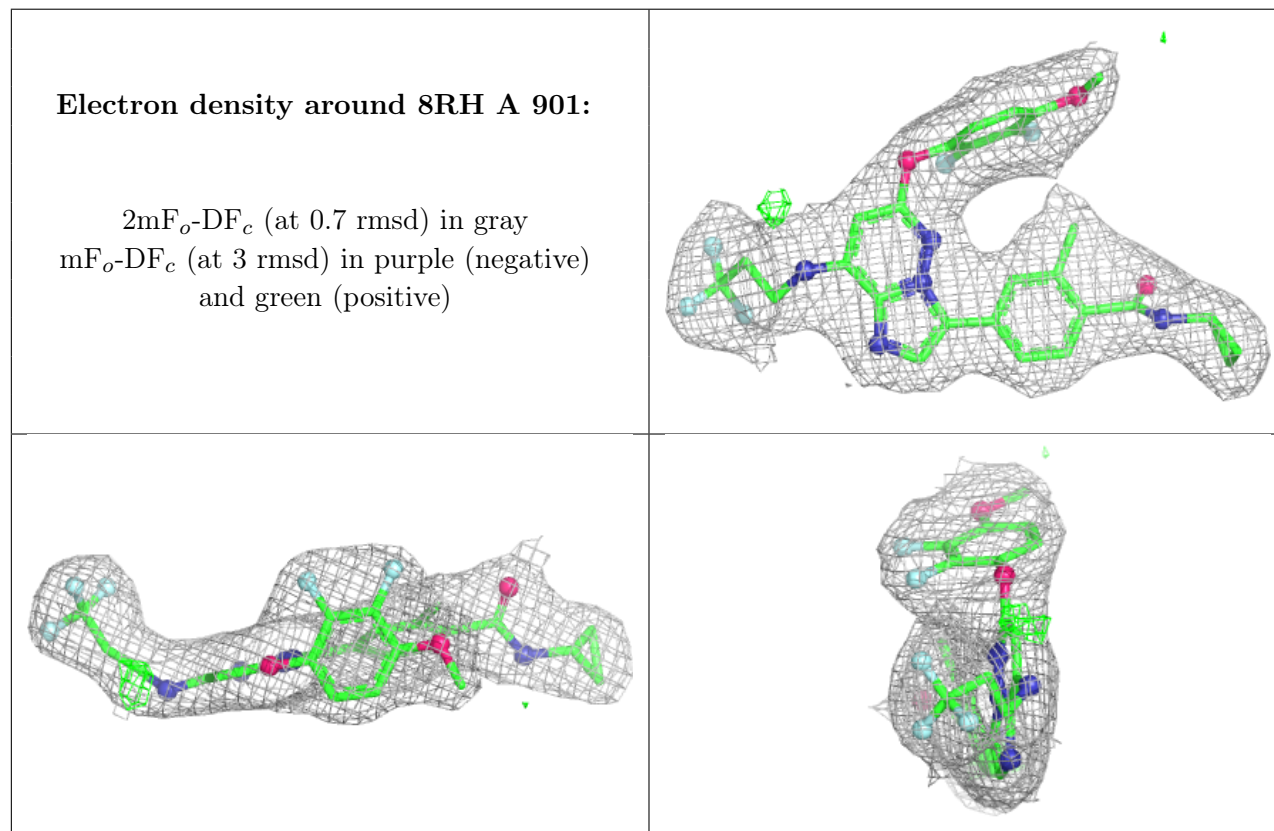
There are no oligosaccharides in this entry.

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	8RH	A	901	40/40	0.95	0.08	45,55,71,72	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.