



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 4, 2025 – 04:06 PM EDT

PDB ID : 9MXB / pdb_00009mxb
Title : Crystal Structure of WT HIV-1 Reverse Transcriptase in Complex with 5-{2-[2-(2-oxo-4-sulfanylidene-3,4-dihydropyrimidin-1(2H)-yl)ethoxy] phenoxy}na phthalene-2-carbonitrile (JLJ648), a non-nucleoside inhibitor
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Deposited on : 2025-01-17
Resolution : 2.37 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)	:	2.45.1

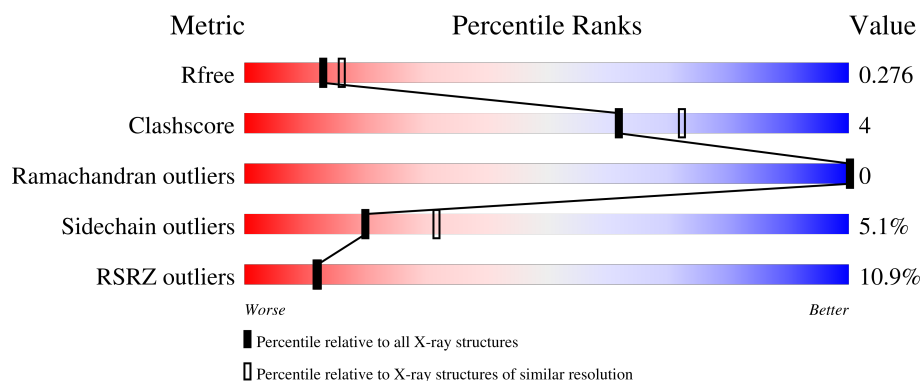
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.37 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	6699 (2.40-2.36)
Clashscore	180529	7414 (2.40-2.36)
Ramachandran outliers	177936	7337 (2.40-2.36)
Sidechain outliers	177891	7338 (2.40-2.36)
RSRZ outliers	164620	6699 (2.40-2.36)

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	557	<div> <div>11%</div> <div>84%</div> <div>13%</div> <div>..</div> </div>
2	B	428	<div> <div>11%</div> <div>83%</div> <div>12%</div> <div>..</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7646 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 Reverse transcriptase/ribonuclease H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	550	Total	C	N	O	S	0	1	0
			4338	2804	722	806	6			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP P03366
A	0	VAL	-	expression tag	UNP P03366
A	172	ALA	LYS	engineered mutation	UNP P03366
A	173	ALA	LYS	engineered mutation	UNP P03366
A	280	SER	CYS	engineered mutation	UNP P03366

- Molecule 2 is a protein called p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	410	Total	C	N	O	P S	0	1	0
			3244	2113	530	595	1 5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	280	SER	CYS	engineered mutation	UNP P03366

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

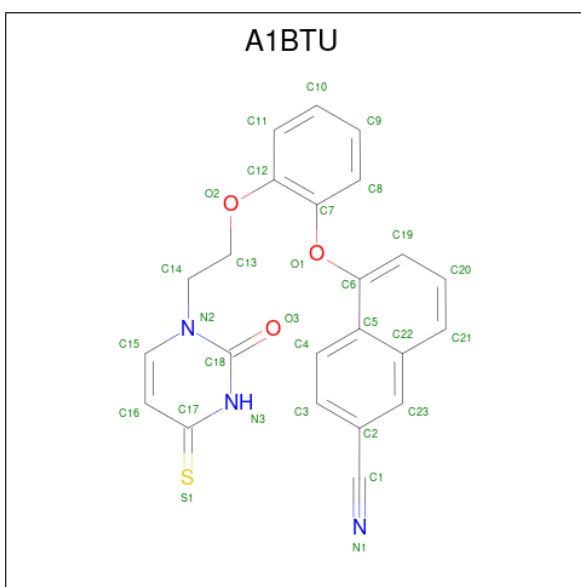
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Cl	0	0
			2	2		
3	B	1	Total	Cl	0	0
			1	1		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is 5-{2-[2-(2-oxo-4-sulfanylidene-3,4-dihydropyrimidin-1(2H)-yl)ethoxy]phenoxy} naphthalene-2-carbonitrile (CCD ID: A1BTU) (formula: C₂₃H₁₇N₃O₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			30	23	3	3	1		

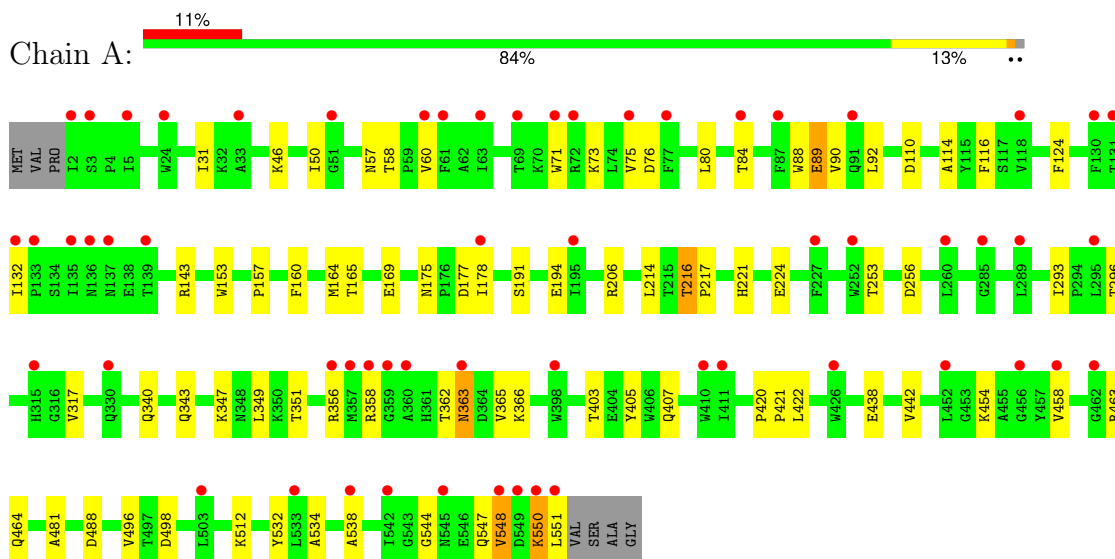
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	6	Total 6	O 6	0	0
6	B	15	Total 15	O 15	0	0

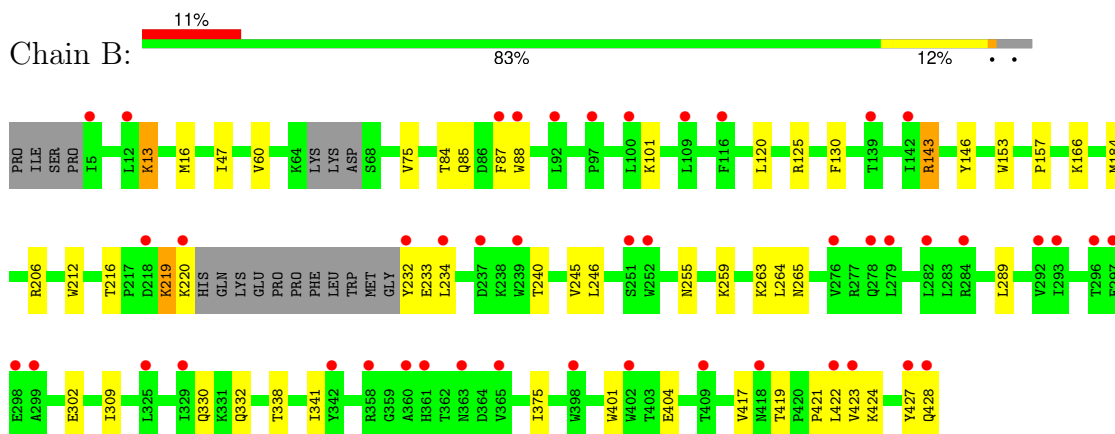
3 Residue-property plots [i](#)

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: Reverse transcriptase/ribonuclease H



- Molecule 2: p51 RT



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	224.07Å 69.57Å 104.95Å 90.00° 106.08° 90.00°	Depositor
Resolution (Å)	33.63 – 2.37 33.63 – 2.37	Depositor EDS
% Data completeness (in resolution range)	99.3 (33.63-2.37) 99.3 (33.63-2.37)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.21 (at 2.36Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.253 , 0.275 0.253 , 0.276	Depositor DCC
R_{free} test set	3135 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	75.6	Xtriage
Anisotropy	0.156	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 55.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7646	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.11% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, CL, TPO, A1BTU

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	0.18	0/4459	0.33	0/6088
2	B	0.22	0/3329	0.40	0/4549
All	All	0.20	0/7788	0.36	0/10637

There are no bond length outliers.

There are no bond angle outliers.

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	4338	0	4200	34	0
2	B	3244	0	3103	27	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
5	A	30	0	0	0	0
6	A	6	0	0	0	0
6	B	15	0	0	0	0
All	All	7646	0	7303	59	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 (59) 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)
2:B:246:LEU:HD11	2:B:264:LEU:HD21	1.79	0.64
1:A:363:ASN:HD21	1:A:365:VAL:HB	1.62	0.64
2:B:427:TYR:O	2:B:428:GLN:C	2.42	0.62
2:B:219:LYS:O	2:B:220:LYS:C	2.43	0.62
1:A:84:THR:HG22	1:A:124:PHE:HZ	1.65	0.62
1:A:206:ARG:HD2	1:A:216:THR:HG22	1.82	0.61
1:A:84:THR:HG21	1:A:153:TRP:HE1	1.69	0.57
1:A:498:ASP:HB2	1:A:538:ALA:HB2	1.88	0.56
2:B:341:ILE:HD11	2:B:375:ILE:HG23	1.88	0.55
2:B:206:ARG:NH2	2:B:219:LYS:HD2	2.22	0.55
2:B:166:LYS:HE2	2:B:212:TRP:HZ3	1.73	0.54
2:B:157:PRO:HG3	2:B:184:MET:HA	1.88	0.54
2:B:84:THR:HG22	2:B:87:PHE:HB3	1.91	0.53
1:A:50:ILE:HG13	1:A:143:ARG:HB3	1.92	0.52
1:A:46:LYS:HD3	1:A:116:PHE:HB3	1.90	0.52
1:A:80:LEU:O	1:A:84:THR:HG23	2.09	0.52
2:B:60:VAL:HG12	2:B:75:VAL:HG22	1.91	0.51
1:A:458:VAL:HG22	1:A:464:GLN:HG2	1.92	0.50
1:A:405:TYR:CE2	1:A:407:GLN:HB2	2.46	0.50
2:B:85:GLN:HA	2:B:88:TRP:CE2	2.47	0.50
1:A:356:ARG:NH1	1:A:362:THR:HG21	2.27	0.50
2:B:421:PRO:O	2:B:422:LEU:HB2	2.12	0.49
1:A:114:ALA:HB1	1:A:160:PHE:CE1	2.48	0.49
1:A:363:ASN:ND2	1:A:366:LYS:H	2.11	0.49
1:A:164:MET:HE1	1:A:214:LEU:HD13	1.95	0.48
2:B:332:GLN:HG3	2:B:338:THR:HG23	1.94	0.48
1:A:216:THR:HG23	1:A:217:PRO:HD2	1.95	0.48
1:A:89:GLU:HG2	1:A:92:LEU:HD21	1.96	0.47
1:A:442:VAL:HB	1:A:481:ALA:HB1	1.95	0.47
1:A:512:LYS:HD2	1:A:512:LYS:HA	1.66	0.47
2:B:219:LYS:HE2	2:B:219:LYS:HB3	1.71	0.46
1:A:496:VAL:HG21	2:B:289:LEU:HD21	1.95	0.46
2:B:84:THR:HG21	2:B:153:TRP:HZ2	1.79	0.46
1:A:420:PRO:HA	1:A:421:PRO:C	2.40	0.46
1:A:438:GLU:OE1	1:A:463:ARG:NH2	2.49	0.46
2:B:232:TYR:CD2	2:B:234:LEU:HD11	2.51	0.45
2:B:206:ARG:NH1	2:B:216:THR:OG1	2.49	0.45
1:A:90:VAL:HG21	1:A:157:PRO:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:120:LEU:HD23	2:B:125:ARG:HG2	2.00	0.44
1:A:544:GLY:O	1:A:548:VAL:HG23	2.17	0.43
1:A:31:ILE:HG23	1:A:132:ILE:HG22	2.00	0.43
1:A:343:GLN:HG3	1:A:349:LEU:HD11	2.01	0.43
2:B:245:VAL:O	2:B:263:LYS:NZ	2.52	0.43
2:B:13:LYS:H	2:B:13:LYS:HG2	1.50	0.42
2:B:255:ASN:O	2:B:259:LYS:HG2	2.19	0.42
1:A:356:ARG:NH1	1:A:356:ARG:HB3	2.35	0.42
2:B:47:ILE:HG22	2:B:146:TYR:HA	2.01	0.42
1:A:547:GLN:O	1:A:550:LYS:HD3	2.19	0.42
2:B:85:GLN:HG3	2:B:88:TRP:CH2	2.55	0.42
1:A:88:TRP:CE2	2:B:143:ARG:HD2	2.54	0.42
1:A:340:GLN:HG3	1:A:351:THR:HG22	2.02	0.42
2:B:401:TRP:HE3	2:B:404:GLU:HG3	1.85	0.41
1:A:253:THR:HG23	1:A:256:ASP:H	1.84	0.41
1:A:175:ASN:O	1:A:178:ILE:HG22	2.21	0.41
1:A:165:THR:O	1:A:169:GLU:HG3	2.20	0.41
2:B:60:VAL:HG11	2:B:130:PHE:CD2	2.56	0.41
1:A:57:ASN:OD1	1:A:58:THR:N	2.53	0.40
1:A:532:TYR:CE2	1:A:534:ALA:HB2	2.57	0.40
2:B:206:ARG:HH22	2:B:219:LYS:HD2	1.86	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	549/557 (99%)	543 (99%)	6 (1%)	0	100	100
2	B	404/428 (94%)	398 (98%)	6 (2%)	0	100	100
All	All	953/985 (97%)	941 (99%)	12 (1%)	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	449/495 (91%)	423 (94%)	26 (6%)	17	26
2	B	331/389 (85%)	317 (96%)	14 (4%)	25	40
All	All	780/884 (88%)	740 (95%)	40 (5%)	20	32

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	VAL
1	A	71	TRP
1	A	73	LYS
1	A	75	VAL
1	A	76	ASP
1	A	89	GLU
1	A	110	ASP
1	A	177	ASP
1	A	191	SER
1	A	194	GLU
1	A	216	THR
1	A	221	HIS
1	A	224	GLU
1	A	293	ILE
1	A	296	THR
1	A	317	VAL
1	A	347	LYS
1	A	358	ARG
1	A	363	ASN
1	A	403	THR
1	A	422	LEU
1	A	454	LYS
1	A	488	ASP
1	A	548	VAL
1	A	550	LYS

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Mol	Chain	Res	Type
1	A	551	LEU
2	B	13	LYS
2	B	16	MET
2	B	101	LYS
2	B	143	ARG
2	B	219	LYS
2	B	233	GLU
2	B	265	ASN
2	B	302	GLU
2	B	309	ILE
2	B	330	GLN
2	B	417	VAL
2	B	419	THR
2	B	423	VAL
2	B	424	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	235	HIS
1	A	330	GLN
1	A	334	GLN
1	A	336	GLN
1	A	340	GLN
1	A	361	HIS
1	A	363	ASN
1	A	507	GLN
1	A	520	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	$\# Z > 2$
2	TPO	B	240	2	8,10,11	2.58	1 (12%)	10,14,16	1.31	1 (10%)

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	TPO	B	240	2	-	5/9/11/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	240	TPO	P-OG1	7.12	1.72	1.59

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	240	TPO	OG1-P-O1P	-2.04	102.08	109.33

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	240	TPO	N-CA-CB-CG2
2	B	240	TPO	N-CA-CB-OG1
2	B	240	TPO	C-CA-CB-CG2
2	B	240	TPO	CB-OG1-P-O1P
2	B	240	TPO	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 for Mogul analysis.

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	$\# Z > 2$
4	SO4	A	603	-	4,4,4	0.72	0	6,6,6	0.12	0
4	SO4	B	502	-	4,4,4	0.73	0	6,6,6	0.09	0
5	A1BTU	A	604	-	33,33,33	0.57	0	45,45,45	1.11	3 (6%)

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
5	A1BTU	A	604	-	-	0/12/12/12	0/4/4/4

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	604	A1BTU	C17-N3-C18	-4.17	123.31	127.31
5	A	604	A1BTU	N3-C18-N2	3.80	118.12	114.86
5	A	604	A1BTU	C16-C17-N3	2.44	117.02	114.75

There are no chirality outliers.

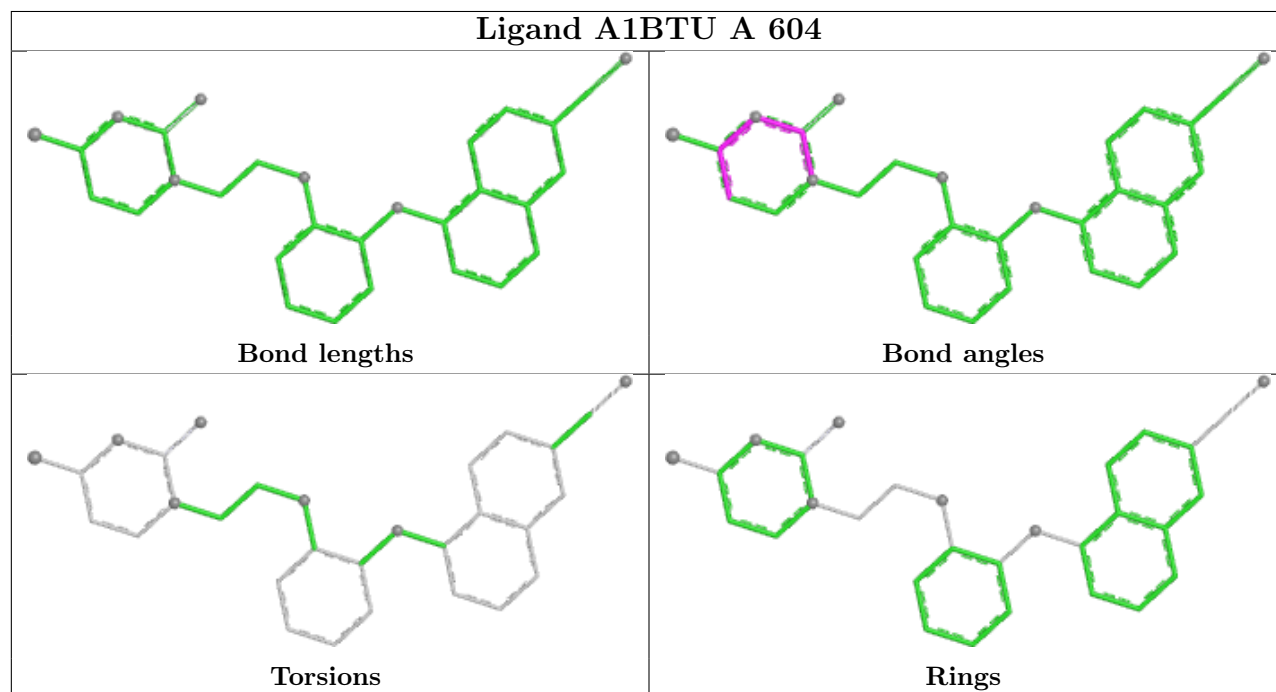
There are no torsion outliers.

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	550/557 (98%)	0.87	59 (10%)	12 12	52, 95, 136, 160	1 (0%)
2	B	409/428 (95%)	0.77	46 (11%)	11 11	61, 88, 132, 146	2 (0%)
All	All	959/985 (97%)	0.82	105 (10%)	12 12	52, 93, 134, 160	3 (0%)

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	232	TYR	4.8
2	B	423	VAL	4.6
1	A	533	LEU	3.9
1	A	542	ILE	3.9
2	B	299	ALA	3.8
1	A	135	ILE	3.7
1	A	137	ASN	3.7
1	A	178	ILE	3.6
1	A	130	PHE	3.6
2	B	365	VAL	3.5
2	B	427	TYR	3.4
1	A	91	GLN	3.4
1	A	132	ILE	3.3
1	A	411	ILE	3.3
1	A	77	PHE	3.3
1	A	359	GLY	3.3
2	B	220	LYS	3.3
2	B	422	LEU	3.3
2	B	298	GLU	3.3
1	A	315[A]	HIS	3.2
1	A	136	ASN	3.1
1	A	549	ASP	3.1
1	A	131	THR	3.1
1	A	295	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
2	B	360	ALA	3.1
1	A	503	LEU	3.0
2	B	282	LEU	3.0
1	A	2	ILE	3.0
1	A	75	VAL	3.0
1	A	538	ALA	2.9
2	B	293	ILE	2.9
1	A	548	VAL	2.9
1	A	252	TRP	2.8
1	A	426	TRP	2.8
1	A	60	VAL	2.8
2	B	361	HIS	2.8
2	B	418	ASN	2.8
1	A	360	ALA	2.7
1	A	410	TRP	2.7
1	A	61	PHE	2.7
2	B	239[A]	TRP	2.6
2	B	398	TRP	2.6
2	B	218	ASP	2.6
1	A	357	MET	2.6
1	A	71	TRP	2.6
1	A	133	PRO	2.6
1	A	84	THR	2.6
2	B	296	THR	2.5
1	A	398	TRP	2.5
1	A	452	LEU	2.5
1	A	551	LEU	2.5
1	A	545	ASN	2.5
1	A	550	LYS	2.5
2	B	279	LEU	2.5
1	A	69	THR	2.5
1	A	24	TRP	2.5
2	B	234	LEU	2.5
2	B	297	GLU	2.4
1	A	462	GLY	2.4
1	A	139	THR	2.4
1	A	356	ARG	2.4
1	A	3	SER	2.4
2	B	237	ASP	2.4
2	B	88	TRP	2.4
2	B	100	LEU	2.4
2	B	428	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	330	GLN	2.4
1	A	260	LEU	2.4
1	A	458	VAL	2.4
2	B	87	PHE	2.4
2	B	5	ILE	2.3
2	B	92	LEU	2.3
1	A	118	VAL	2.3
1	A	227	PHE	2.3
2	B	116	PHE	2.3
1	A	63	ILE	2.3
2	B	97	PRO	2.3
2	B	409	THR	2.3
1	A	285	GLY	2.3
1	A	456	GLY	2.3
2	B	12	LEU	2.3
2	B	252	TRP	2.3
2	B	342	TYR	2.2
1	A	289	LEU	2.2
2	B	325	LEU	2.2
1	A	5	ILE	2.2
2	B	402	TRP	2.2
1	A	51	GLY	2.2
1	A	363	ASN	2.2
2	B	278	GLN	2.2
1	A	72	ARG	2.2
1	A	358	ARG	2.2
2	B	363	ASN	2.2
2	B	329	ILE	2.2
2	B	284	ARG	2.2
2	B	139	THR	2.2
1	A	33	ALA	2.1
1	A	195	ILE	2.1
2	B	142	ILE	2.1
2	B	358	ARG	2.1
2	B	251	SER	2.1
1	A	87	PHE	2.0
2	B	109	LEU	2.0
2	B	276	VAL	2.0
2	B	292	VAL	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
2	TPO	B	240	11/12	0.62	0.17	115,124,140,149	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

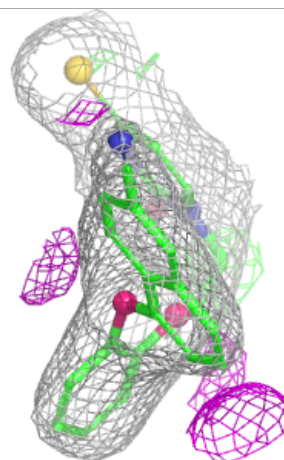
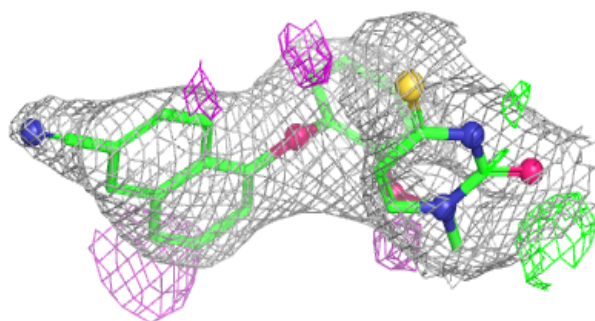
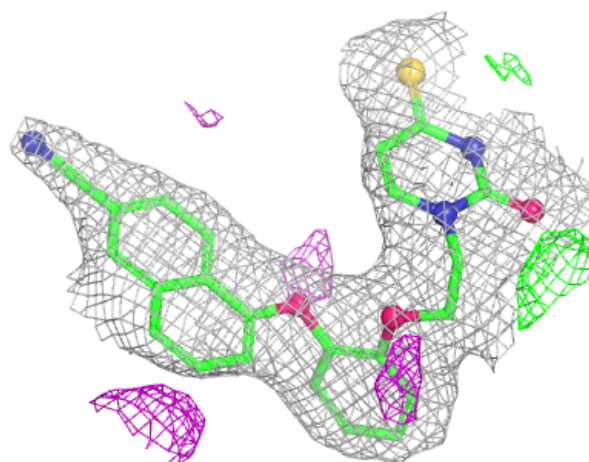
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	SO4	A	603	5/5	0.49	0.11	141,141,149,150	0
4	SO4	B	502	5/5	0.64	0.12	109,113,126,130	0
3	CL	A	601	1/1	0.82	0.10	103,103,103,103	0
3	CL	B	501	1/1	0.87	0.10	120,120,120,120	0
5	A1BTU	A	604	30/30	0.91	0.10	72,79,86,87	0
3	CL	A	602	1/1	0.94	0.10	111,111,111,111	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 A1BTU A 604:

$2mF_o-DF_c$ (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.