



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 19, 2026 – 01:43 AM UTC

PDB ID : 5VQV / pdb_00005vqv
Title : Crystal Structure of HIV-1 Reverse Transcriptase (Y181C) Variant in Complex with N-(6-cyano-3-(2-(2-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)ethoxy)phenoxy)-4-methylnaphthalen-1-yl)-N-methylacrylamide (JLJ684), a Non-nucleoside Inhibitor
Authors : Chan, A.H.; Anderson, K.S.
Deposited on : 2017-05-09
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

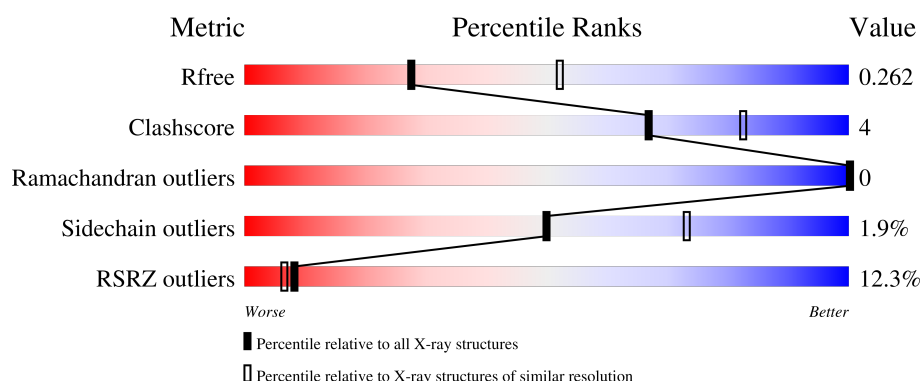
1 Overall quality at a glance

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	557	10% 86% 12% ..
2	B	428	14% 84% 10% 6%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7862 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	547	Total	C	N	O	S	0	0	0
			4407	2855	726	817	9			

There are 6 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	181	CYS	TYR	engineered mutation	UNP P03366
A	280	SER	CYS	engineered mutation	UNP P03366

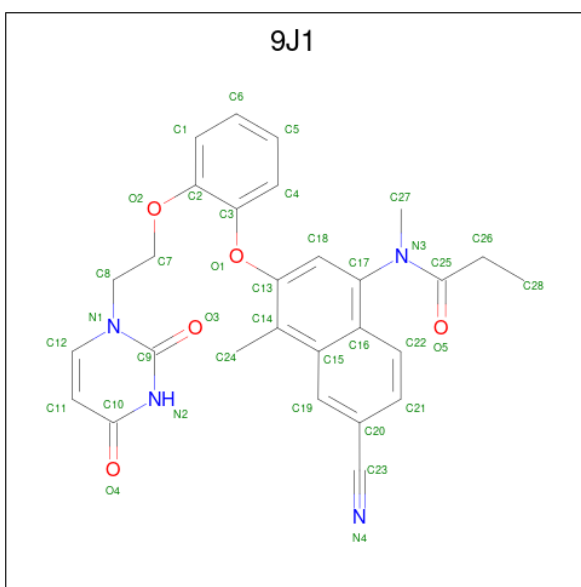
- Molecule 2 is a protein called p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	401	Total	C	N	O	S	0	0	0
			3319	2160	550	603	6			

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 N-(6-cyano-3-{2-[2-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)ethoxy]phenoxy}-4-methylnaphthalen-1-yl)-N-methylpropanamide (CCD ID: 9J1) (formula: C₂₈H₂₆N₄O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			37	28	4	5		

- 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		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	57	Total 57	O 57	0	0
5	B	37	Total 37	O 37	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	162.51Å 73.54Å 109.23Å 90.00° 99.42° 90.00°	Depositor
Resolution (Å)	43.23 – 2.58 43.23 – 2.58	Depositor EDS
% Data completeness (in resolution range)	99.7 (43.23-2.58) 93.4 (43.23-2.58)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.58Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.225 , 0.258 0.227 , 0.262	Depositor DCC
R_{free} test set	2000 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	49.2	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 32.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7862	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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: 9J1, SO4

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	0.13	0/4523	0.31	0/6159
2	B	0.11	0/3413	0.29	0/4635
All	All	0.12	0/7936	0.30	0/10794

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 [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	4407	0	4414	40	0
2	B	3319	0	3341	21	0
3	A	37	0	0	0	0
4	A	5	0	0	0	0
5	A	57	0	0	0	0
5	B	37	0	0	0	0
All	All	7862	0	7755	58	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 (58) 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:544:GLY:HA2	2:B:286:THR:HG22	1.74	0.69
2:B:73:LYS:NZ	2:B:146:TYR:OH	2.28	0.66
1:A:253:THR:HG22	1:A:292:VAL:HG22	1.78	0.65
1:A:543:GLY:HA3	2:B:284:ARG:HA	1.78	0.65
2:B:72:ARG:NH2	2:B:151:GLN:OE1	2.32	0.62
1:A:443:ASP:HB3	1:A:550:LYS:HD3	1.83	0.61
1:A:28:GLU:HG3	1:A:135:ILE:HD12	1.82	0.59
2:B:308:GLU:HA	2:B:311:LYS:HE2	1.86	0.58
2:B:357:MET:HE3	2:B:361:HIS:HB2	1.87	0.55
2:B:203:GLU:HA	2:B:206:ARG:HG2	1.89	0.54
1:A:372:VAL:HG11	1:A:411:ILE:HG13	1.90	0.52
1:A:454:LYS:HZ2	1:A:552:VAL:HB	1.75	0.52
1:A:249:LYS:HB2	1:A:252:TRP:CE2	2.46	0.51
1:A:252:TRP:HD1	1:A:295:LEU:HD21	1.74	0.51
1:A:46:LYS:HE2	1:A:116:PHE:CD2	2.44	0.51
2:B:28:GLU:HG2	2:B:32:LYS:HD2	1.93	0.50
2:B:354:TYR:CE1	2:B:356:ARG:HB3	2.47	0.50
1:A:258:GLN:HA	1:A:261:VAL:HG12	1.93	0.50
1:A:88:TRP:CD1	2:B:143:ARG:HD2	2.46	0.49
1:A:252:TRP:HB2	1:A:295:LEU:HD11	1.95	0.49
1:A:224:GLU:HB2	1:A:225:PRO:HD2	1.96	0.47
1:A:252:TRP:CD1	1:A:295:LEU:HD21	2.49	0.47
1:A:490:GLY:O	1:A:528:LYS:NZ	2.42	0.47
2:B:74:LEU:HD21	2:B:409:THR:HA	1.96	0.47
1:A:253:THR:OG1	1:A:255:ASN:OD1	2.33	0.47
1:A:343:GLN:HG3	1:A:349:LEU:HD11	1.97	0.46
1:A:363:ASN:HD21	1:A:366:LYS:HE3	1.81	0.46
1:A:369:THR:O	1:A:373:GLN:HG2	2.15	0.46
1:A:62:ALA:HA	1:A:72:ARG:O	2.15	0.46
2:B:328:GLU:O	2:B:339:TYR:HA	2.16	0.46
1:A:246:LEU:HD11	1:A:310:LEU:HD12	1.97	0.46
2:B:167:ILE:HG12	2:B:212:TRP:CE3	2.51	0.45
1:A:399:GLU:HA	1:A:402:TRP:CD1	2.51	0.44
1:A:342:TYR:HB3	1:A:348:ASN:HA	1.99	0.44
2:B:84:THR:HB	2:B:154:LYS:HE2	1.99	0.44
2:B:270:ILE:HG12	2:B:346:PHE:HB3	1.99	0.44
1:A:38:CYS:SG	1:A:132:ILE:HD11	2.58	0.43
1:A:475:GLN:HB3	1:A:501:TYR:CE2	2.53	0.43
1:A:363:ASN:HA	1:A:511:ASP:OD1	2.18	0.43
1:A:469:LEU:HD12	1:A:477:THR:HG22	2.00	0.43
2:B:393:ILE:HD13	2:B:398:TRP:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:SER:OG	1:A:139:THR:OG1	2.30	0.43
1:A:369:THR:HA	1:A:411:ILE:HD11	2.01	0.42
2:B:38:CYS:SG	2:B:132:ILE:HD11	2.59	0.42
1:A:540:LYS:HD3	1:A:540:LYS:HA	1.88	0.42
1:A:503:LEU:HD22	1:A:535:TRP:HB2	2.00	0.42
1:A:110:ASP:HB2	1:A:221:HIS:CD2	2.54	0.42
2:B:240:THR:O	2:B:242:GLN:NE2	2.48	0.42
1:A:363:ASN:ND2	1:A:366:LYS:HE3	2.34	0.42
2:B:105:SER:O	2:B:190:GLY:HA2	2.19	0.42
1:A:366:LYS:HE2	1:A:405:TYR:OH	2.19	0.42
2:B:425:LEU:HD23	2:B:425:LEU:HA	1.89	0.42
1:A:24:TRP:CE3	1:A:61:PHE:HE2	2.39	0.41
1:A:244:ILE:HG13	1:A:267:ALA:HB2	2.03	0.41
2:B:168:LEU:HD13	2:B:180:ILE:HG21	2.02	0.41
1:A:104:LYS:HB2	1:A:192:ASP:HA	2.01	0.41
1:A:179:VAL:O	1:A:189:VAL:HA	2.21	0.41
1:A:546:GLU:HB3	1:A:549:ASP:HB2	2.03	0.41

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	543/557 (98%)	533 (98%)	10 (2%)	0	100	100
2	B	395/428 (92%)	386 (98%)	9 (2%)	0	100	100
All	All	938/985 (95%)	919 (98%)	19 (2%)	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	479/495 (97%)	469 (98%)	10 (2%)	47	71
2	B	364/390 (93%)	358 (98%)	6 (2%)	55	77
All	All	843/885 (95%)	827 (98%)	16 (2%)	50	73

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

Mol	Chain	Res	Type
1	A	74	LEU
1	A	105	SER
1	A	215	THR
1	A	220	LYS
1	A	249	LYS
1	A	295	LEU
1	A	301	LEU
1	A	347	LYS
1	A	411	ILE
1	A	546	GLU
2	B	8	VAL
2	B	69	THR
2	B	74	LEU
2	B	185	ASP
2	B	233	GLU
2	B	417	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	182	GLN
1	A	197	GLN
2	B	175	ASN
2	B	255	ASN
2	B	278	GLN

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	$\# Z > 2$
4	SO4	A	602	-	4,4,4	0.24	0	6,6,6	0.09	0
3	9J1	A	601	1	40,40,40	1.04	2 (5%)	53,56,56	1.04	5 (9%)

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
3	9J1	A	601	1	-	0/22/22/22	0/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	9J1	C9-N1	2.81	1.41	1.37
3	A	601	9J1	C22-C21	2.13	1.41	1.36

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	9J1	C16-C17-N3	4.38	123.05	119.07
3	A	601	9J1	C8-N1-C12	2.37	123.09	119.75
3	A	601	9J1	C18-C13-C14	-2.28	119.78	122.39
3	A	601	9J1	C13-O1-C3	2.20	123.33	118.09
3	A	601	9J1	N2-C9-N1	2.06	116.63	114.86

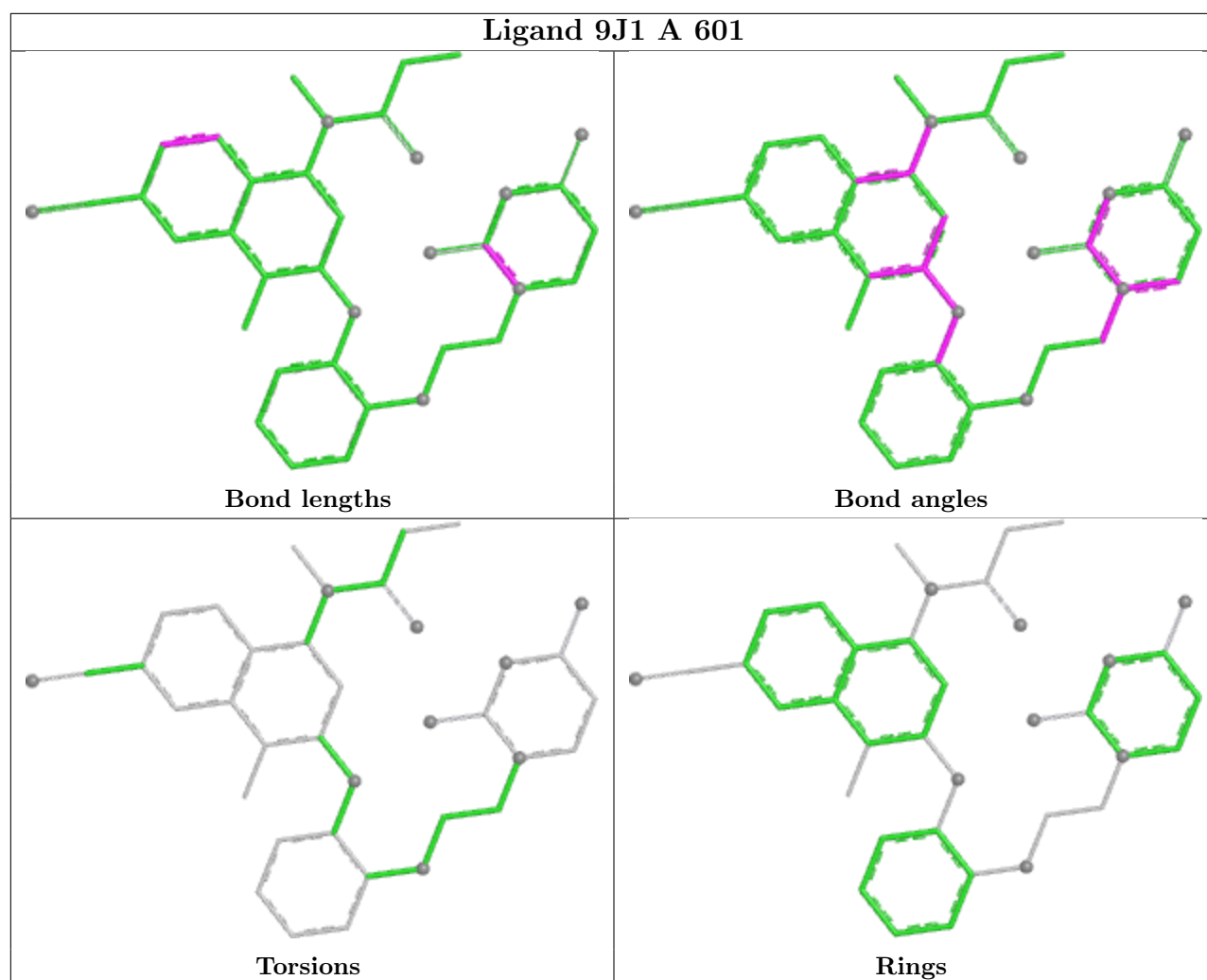
There are no chirality outliers.

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	547/557 (98%)	0.72	58 (10%) 11 9	34, 56, 100, 138	0
2	B	401/428 (93%)	0.77	59 (14%) 6 5	35, 56, 111, 124	0
All	All	948/985 (96%)	0.74	117 (12%) 8 6	34, 56, 106, 138	0

All (117) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	241	VAL	7.2
1	A	548	VAL	7.1
2	B	193	LEU	5.6
2	B	88	TRP	5.1
2	B	94	ILE	5.1
1	A	116	PHE	4.8
1	A	552	VAL	4.6
1	A	295	LEU	4.5
1	A	63	ILE	4.4
2	B	239	TRP	4.4
2	B	5	ILE	4.3
1	A	288	ALA	4.3
1	A	290	THR	4.2
2	B	240	THR	4.1
2	B	212	TRP	4.0
1	A	292	VAL	3.8
2	B	87	PHE	3.7
1	A	289	LEU	3.7
1	A	551	LEU	3.7
1	A	293	ILE	3.7
1	A	256	ASP	3.6
2	B	95	PRO	3.6
2	B	358	ARG	3.6
1	A	225	PRO	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	115	TYR	3.5
1	A	283	LEU	3.5
1	A	550	LYS	3.5
1	A	279	LEU	3.5
1	A	247	PRO	3.5
1	A	221	HIS	3.5
2	B	168	LEU	3.4
2	B	232	TYR	3.4
2	B	93	GLY	3.4
2	B	195	ILE	3.4
1	A	544	GLY	3.3
2	B	425	LEU	3.3
1	A	280	SER	3.2
2	B	355	ALA	3.2
2	B	171	PHE	3.1
1	A	24	TRP	3.1
2	B	210	LEU	3.1
1	A	195	ILE	3.1
2	B	202	ILE	3.1
1	A	282	LEU	3.1
2	B	191	SER	3.0
2	B	200	THR	3.0
2	B	357	MET	3.0
2	B	428	GLN	2.9
1	A	218	ASP	2.9
2	B	85	GLN	2.9
1	A	291	GLU	2.9
1	A	2	ILE	2.9
2	B	198	HIS	2.9
2	B	209	LEU	2.9
1	A	543	GLY	2.8
2	B	359	GLY	2.8
2	B	238	LYS	2.8
1	A	257	ILE	2.7
2	B	196	GLY	2.7
2	B	315	HIS	2.7
1	A	541	GLY	2.7
1	A	287	LYS	2.7
1	A	-1	MET	2.6
1	A	545	ASN	2.6
2	B	69	THR	2.6
2	B	67	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
2	B	354	TYR	2.6
2	B	236	PRO	2.6
1	A	193	LEU	2.5
2	B	205	LEU	2.5
1	A	222	GLN	2.5
1	A	285	GLY	2.5
2	B	360	ALA	2.5
1	A	252	TRP	2.5
2	B	109	LEU	2.5
2	B	105	SER	2.5
1	A	346	PHE	2.4
1	A	261	VAL	2.4
1	A	20	LYS	2.4
1	A	135	ILE	2.4
2	B	362	THR	2.4
1	A	251	SER	2.4
1	A	209	LEU	2.4
2	B	356	ARG	2.4
2	B	178	ILE	2.4
1	A	294	PRO	2.3
2	B	106	VAL	2.3
2	B	108	VAL	2.3
2	B	285	GLY	2.3
1	A	244	ILE	2.3
1	A	254	VAL	2.3
1	A	253	THR	2.2
1	A	542	ILE	2.2
2	B	192	ASP	2.2
2	B	233	GLU	2.2
2	B	8	VAL	2.2
1	A	296	THR	2.2
1	A	74	LEU	2.2
2	B	68	SER	2.2
2	B	272	PRO	2.2
1	A	245	VAL	2.2
2	B	237	ASP	2.2
2	B	7	THR	2.1
1	A	297	GLU	2.1
1	A	71	TRP	2.1
1	A	546	GLU	2.1
2	B	284	ARG	2.1
1	A	237	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	140	PRO	2.1
2	B	207	GLN	2.1
2	B	177	ASP	2.1
1	A	301	LEU	2.0
1	A	25	PRO	2.0
2	B	208	HIS	2.0
1	A	199	ARG	2.0
2	B	308	GLU	2.0
2	B	176	PRO	2.0

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](#)

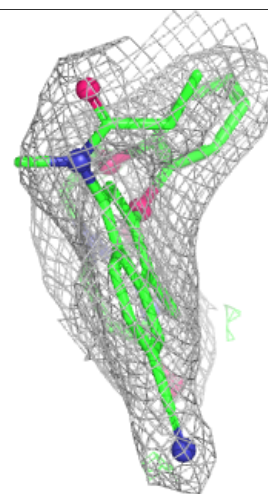
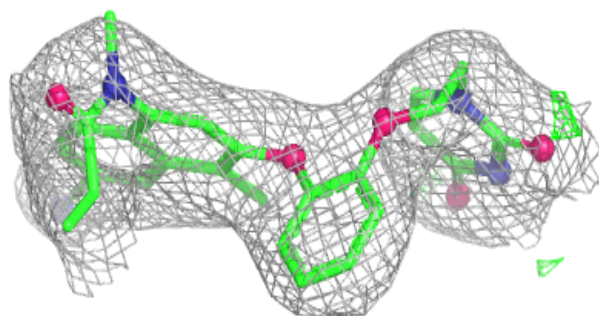
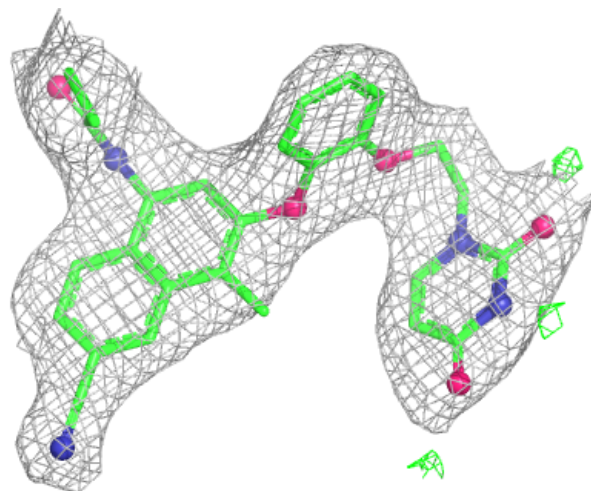
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
4	SO4	A	602	5/5	0.85	0.11	69,84,91,91	0
3	9J1	A	601	37/37	0.94	0.10	41,48,55,56	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 9J1 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.