



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:31 PM UTC

PDB ID : 5VQY / pdb_00005vqy
Title : Crystal Structure of HIV-1 Reverse Transcriptase (K103N, 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
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Deposited on : 2017-05-09
Resolution : 2.35 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

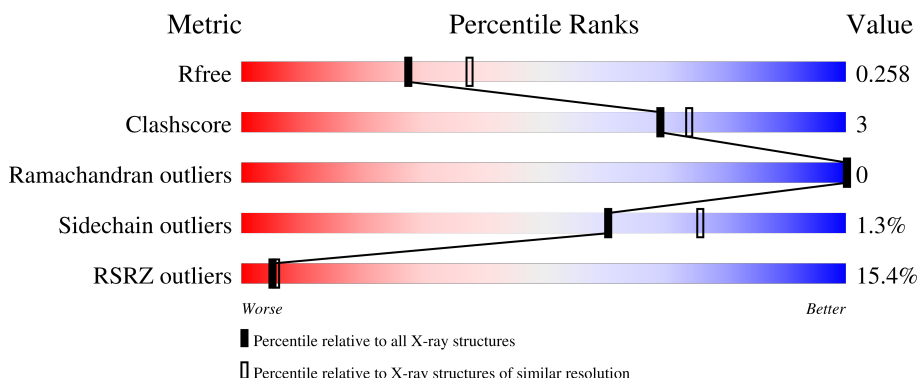
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	12% 87% 11% .
2	B	428	18% 82% 11% 6%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7972 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
			4412	2856	729	818	9			

There are 7 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	103	ASN	LYS	engineered mutation	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

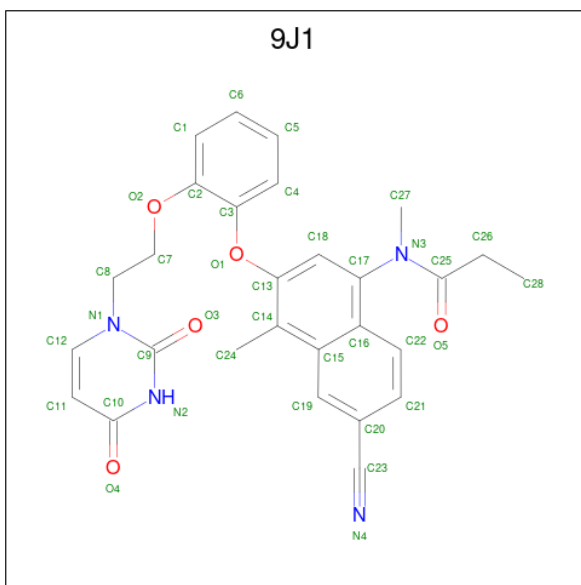
- Molecule 2 is a protein called p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	401	Total	C	N	O	S	0	0	0
			3323	2163	551	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		
4	A	1	Total	O	S	0	0
			5	4	1		

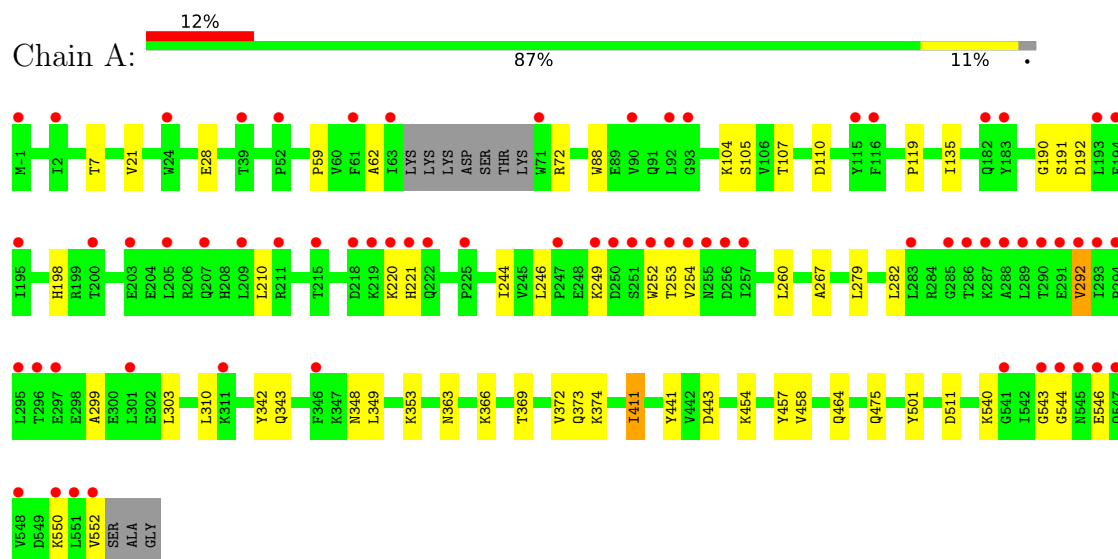
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	123	Total 123	O 123	0	0
5	B	67	Total 67	O 67	0	0

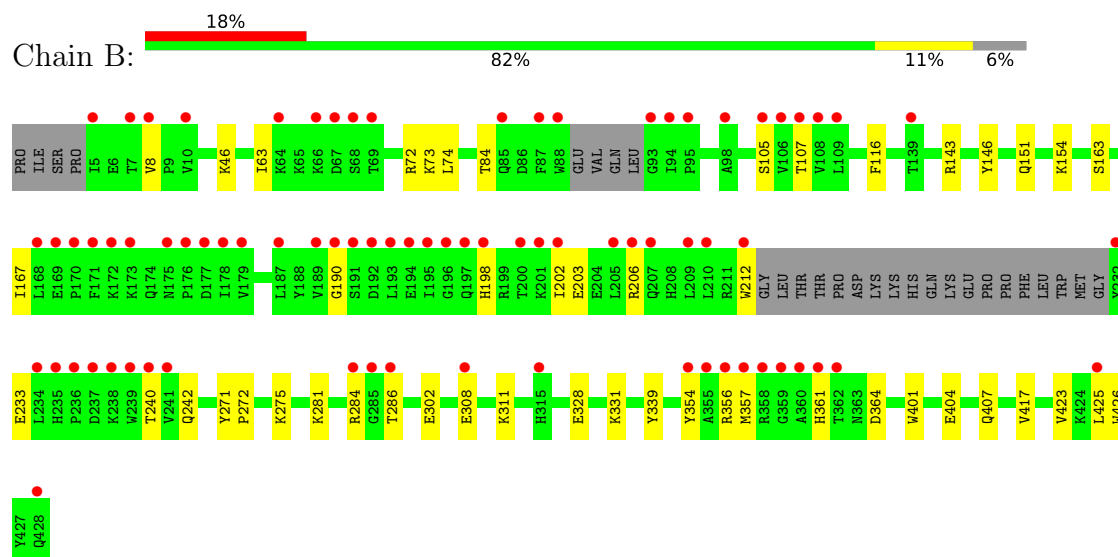
3 Residue-property plots [i](#)

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	163.26Å 73.70Å 108.85Å 90.00° 99.80° 90.00°	Depositor
Resolution (Å)	38.41 – 2.35 38.41 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.9 (38.41-2.35) 95.7 (38.41-2.35)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 2.34Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.226 , 0.256 0.228 , 0.258	Depositor DCC
R_{free} test set	2000 reflections (3.75%)	wwPDB-VP
Wilson B-factor (Å ²)	43.4	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 35.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7972	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.36% 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: SO4, 9J1

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	0.11	0/4528	0.31	0/6166
2	B	0.11	0/3417	0.29	0/4639
All	All	0.11	0/7945	0.30	0/10805

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	4412	0	4418	31	0
2	B	3323	0	3352	26	0
3	A	37	0	0	0	0
4	A	10	0	0	0	0
5	A	123	0	0	0	0
5	B	67	0	0	0	0
All	All	7972	0	7770	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 3.

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)
2:B:73:LYS:NZ	2:B:146:TYR:OH	2.25	0.68
1:A:443:ASP:HB3	1:A:550:LYS:HD3	1.78	0.66
1:A:110:ASP:HB2	1:A:221:HIS:HE2	1.61	0.65
1:A:544:GLY:HA2	2:B:286:THR:HG22	1.77	0.65
2:B:72:ARG:NH2	2:B:151:GLN:OE1	2.31	0.64
1:A:543:GLY:HA3	2:B:284:ARG:HA	1.80	0.62
1:A:372:VAL:HG11	1:A:411:ILE:HG13	1.83	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	1.84	0.58
2:B:203:GLU:HA	2:B:206:ARG:HG2	1.88	0.55
1:A:28:GLU:HG3	1:A:135:ILE:HD12	1.91	0.52
2:B:84:THR:HB	2:B:154:LYS:HE2	1.93	0.51
1:A:353:LYS:O	1:A:374:LYS:NZ	2.43	0.50
1:A:88:TRP:CD1	2:B:143:ARG:HD2	2.48	0.49
2:B:354:TYR:CE1	2:B:356:ARG:HB3	2.48	0.49
1:A:279:LEU:HD23	1:A:299:ALA:HB1	1.96	0.48
1:A:191:SER:OG	1:A:198:HIS:ND1	2.37	0.48
1:A:105:SER:O	1:A:190:GLY:HA2	2.14	0.47
1:A:21:VAL:HB	1:A:59:PRO:HD3	1.95	0.47
1:A:107:THR:OG1	1:A:198:HIS:NE2	2.38	0.46
1:A:454:LYS:HZ2	1:A:552:VAL:HB	1.81	0.46
2:B:46:LYS:HE2	2:B:116:PHE:HB3	1.98	0.46
1:A:363:ASN:ND2	1:A:366:LYS:HE3	2.31	0.45
1:A:363:ASN:HA	1:A:511:ASP:OD1	2.16	0.45
2:B:425:LEU:HD23	2:B:425:LEU:HA	1.87	0.45
1:A:260:LEU:HD21	1:A:303:LEU:HD13	1.98	0.45
2:B:105:SER:O	2:B:190:GLY:HA2	2.16	0.45
1:A:244:ILE:HG13	1:A:267:ALA:HB2	1.99	0.44
1:A:104:LYS:HB2	1:A:192:ASP:HA	1.99	0.44
2:B:167:ILE:HG12	2:B:212:TRP:CE3	2.51	0.44
1:A:475:GLN:HB3	1:A:501:TYR:CE2	2.53	0.44
2:B:331:LYS:NZ	2:B:364:ASP:OD2	2.50	0.44
1:A:458:VAL:HG12	1:A:464:GLN:HG2	2.00	0.44
2:B:281:LYS:HG2	2:B:284:ARG:NH1	2.33	0.43
1:A:62:ALA:HA	1:A:72:ARG:O	2.18	0.43
2:B:107:THR:OG1	2:B:198:HIS:NE2	2.40	0.43
1:A:246:LEU:HD11	1:A:310:LEU:HD12	2.00	0.43
1:A:342:TYR:HB3	1:A:348:ASN:HA	2.01	0.42
1:A:249:LYS:HB2	1:A:252:TRP:CE2	2.55	0.42
1:A:369:THR:O	1:A:373:GLN:HG2	2.19	0.42
2:B:63:ILE:HD12	2:B:407:GLN:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:423:VAL:HA	2:B:426:TRP:CE3	2.54	0.42
1:A:343:GLN:HG3	1:A:349:LEU:HD11	2.01	0.42
1:A:540:LYS:HD3	1:A:540:LYS:HA	1.90	0.41
1:A:7:THR:HG22	1:A:119:PRO:HG2	2.03	0.41
2:B:163:SER:O	2:B:167:ILE:HG13	2.19	0.41
2:B:275:LYS:HG2	2:B:302:GLU:OE2	2.20	0.41
1:A:441:TYR:O	1:A:457:TYR:HA	2.21	0.41
2:B:271:TYR:HA	2:B:272:PRO:HD3	1.94	0.41
2:B:401:TRP:HE3	2:B:404:GLU:HG3	1.86	0.40
2:B:328:GLU:O	2:B:339:TYR:HA	2.21	0.40
2:B:202:ILE:HD13	2:B:202:ILE:HA	1.90	0.40
2:B:240:THR:O	2:B:242:GLN:NE2	2.48	0.40
1:A:253:THR:HA	1:A:292:VAL:HA	2.03	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	543/557 (98%)	536 (99%)	7 (1%)	0	100	100
2	B	395/428 (92%)	387 (98%)	8 (2%)	0	100	100
All	All	938/985 (95%)	923 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	480/495 (97%)	473 (98%)	7 (2%)	57	72
2	B	365/390 (94%)	361 (99%)	4 (1%)	65	79
All	All	845/885 (96%)	834 (99%)	11 (1%)	61	76

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	210	LEU
1	A	220	LYS
1	A	254	VAL
1	A	282	LEU
1	A	292	VAL
1	A	411	ILE
1	A	546	GLU
2	B	8	VAL
2	B	74	LEU
2	B	233	GLU
2	B	417	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	182	GLN
1	A	197	GLN
2	B	175	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 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	$\# Z > 2$
3	9J1	A	601	1	40,40,40	1.01	2 (5%)	53,56,56	1.09	5 (9%)
4	SO4	A	602	-	4,4,4	0.25	0	6,6,6	0.10	0
4	SO4	A	603	-	4,4,4	0.25	0	6,6,6	0.07	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
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	2.65	1.41	1.37
3	A	601	9J1	C22-C21	2.09	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	4.51	123.16	119.07
3	A	601	9J1	C8-N1-C12	2.70	123.56	119.75
3	A	601	9J1	C13-O1-C3	2.38	123.76	118.09
3	A	601	9J1	C18-C13-C14	-2.24	119.83	122.39
3	A	601	9J1	N2-C9-N1	2.10	116.67	114.86

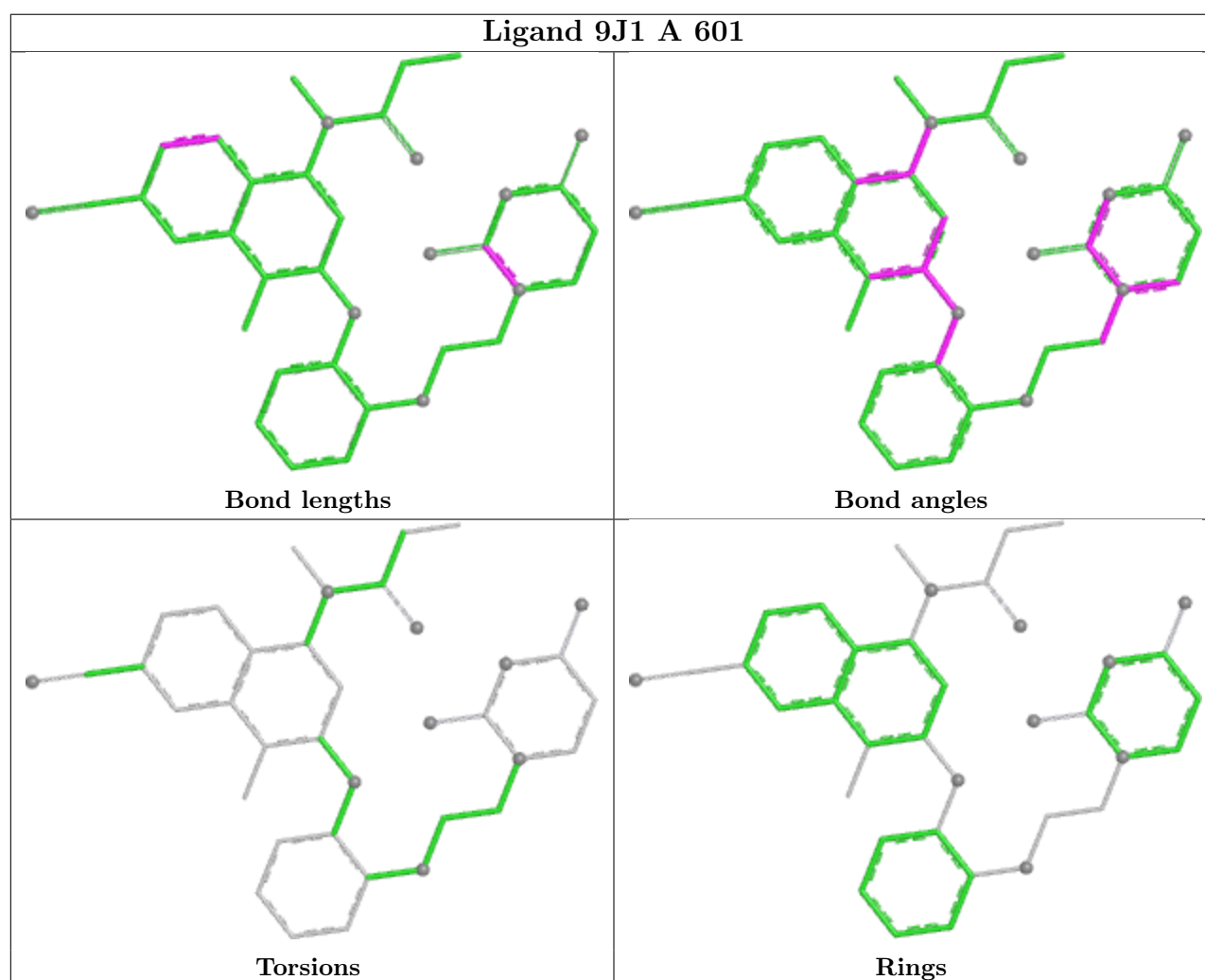
There are no chirality outliers.

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%)	0.71	68 (12%) 8 9	27, 47, 87, 125	0
2	B	401/428 (93%)	0.91	78 (19%) 3 3	28, 48, 104, 117	0
All	All	948/985 (96%)	0.79	146 (15%) 5 6	27, 48, 95, 125	0

All (146) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	241	VAL	9.4
2	B	193	LEU	7.1
1	A	225	PRO	5.4
2	B	240	THR	5.4
1	A	552	VAL	5.4
2	B	88	TRP	5.3
2	B	239	TRP	5.3
1	A	292	VAL	4.9
1	A	288	ALA	4.9
2	B	94	ILE	4.9
1	A	548	VAL	4.7
2	B	212	TRP	4.7
1	A	289	LEU	4.7
1	A	290	THR	4.6
2	B	200	THR	4.5
2	B	195	ILE	4.5
2	B	5	ILE	4.3
1	A	295	LEU	4.3
1	A	551	LEU	4.2
2	B	354	TYR	4.1
2	B	198	HIS	4.0
1	A	544	GLY	4.0
2	B	196	GLY	4.0
2	B	202	ILE	4.0

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Mol	Chain	Res	Type	RSRZ
2	B	358	ARG	3.9
2	B	425	LEU	3.9
2	B	168	LEU	3.9
2	B	232	TYR	3.8
1	A	221	HIS	3.8
1	A	63	ILE	3.8
2	B	8	VAL	3.6
1	A	293	ILE	3.5
1	A	550	LYS	3.5
2	B	69	THR	3.5
2	B	357	MET	3.5
2	B	171	PHE	3.5
2	B	205	LEU	3.4
1	A	195	ILE	3.4
2	B	360	ALA	3.4
1	A	24	TRP	3.4
1	A	543	GLY	3.4
1	A	283	LEU	3.3
2	B	95	PRO	3.3
2	B	236	PRO	3.3
2	B	355	ALA	3.3
1	A	218	ASP	3.3
1	A	115	TYR	3.2
1	A	291	GLU	3.2
2	B	315	HIS	3.2
1	A	116	PHE	3.2
1	A	194	GLU	3.1
1	A	285	GLY	3.1
1	A	90	VAL	3.1
1	A	92	LEU	3.1
2	B	210	LEU	3.1
1	A	257	ILE	3.1
2	B	238	LYS	3.0
2	B	93	GLY	3.0
2	B	98	ALA	3.0
2	B	209	LEU	3.0
2	B	178	ILE	3.0
2	B	234	LEU	2.9
1	A	220	LYS	2.9
2	B	191	SER	2.9
2	B	359	GLY	2.9
2	B	109	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
2	B	87	PHE	2.8
1	A	203	GLU	2.8
2	B	206	ARG	2.8
2	B	106	VAL	2.8
2	B	85	GLN	2.8
1	A	254	VAL	2.7
1	A	2	ILE	2.7
2	B	284	ARG	2.7
2	B	64	LYS	2.6
1	A	200	THR	2.6
1	A	209	LEU	2.6
1	A	222	GLN	2.6
1	A	211	ARG	2.6
2	B	170	PRO	2.6
2	B	67	ASP	2.5
2	B	428	GLN	2.5
1	A	252	TRP	2.5
2	B	105	SER	2.5
1	A	205	LEU	2.5
1	A	182	GLN	2.5
2	B	7	THR	2.5
1	A	219	LYS	2.5
1	A	547	GLN	2.5
2	B	108	VAL	2.4
2	B	189	VAL	2.4
1	A	545	ASN	2.4
2	B	176	PRO	2.4
1	A	93	GLY	2.4
1	A	286	THR	2.4
2	B	286	THR	2.4
2	B	356	ARG	2.4
2	B	192	ASP	2.3
1	A	249	LYS	2.3
2	B	172	LYS	2.3
1	A	253	THR	2.3
1	A	301	LEU	2.3
1	A	294	PRO	2.3
1	A	39	THR	2.3
2	B	173	LYS	2.3
1	A	247	PRO	2.3
2	B	190	GLY	2.3
1	A	71	TRP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	251	SER	2.3
1	A	297	GLU	2.3
1	A	346	PHE	2.2
2	B	237	ASP	2.2
1	A	193	LEU	2.2
2	B	179	VAL	2.2
1	A	541	GLY	2.2
2	B	66	LYS	2.2
2	B	197	GLN	2.2
1	A	207	GLN	2.2
2	B	187	LEU	2.2
1	A	61	PHE	2.2
1	A	255	ASN	2.2
2	B	169	GLU	2.2
1	A	-1	MET	2.1
2	B	194	GLU	2.1
2	B	285	GLY	2.1
1	A	296	THR	2.1
2	B	107	THR	2.1
2	B	139	THR	2.1
2	B	201	LYS	2.1
1	A	52	PRO	2.1
2	B	362	THR	2.1
1	A	311	LYS	2.1
2	B	235	HIS	2.1
2	B	175	ASN	2.1
2	B	177	ASP	2.1
2	B	361	HIS	2.1
1	A	183	TYR	2.1
2	B	10	VAL	2.1
1	A	215	THR	2.0
2	B	308	GLU	2.0
1	A	287	LYS	2.0
1	A	546	GLU	2.0
2	B	68	SER	2.0
2	B	207	GLN	2.0
1	A	250	ASP	2.0
1	A	256	ASP	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](#)

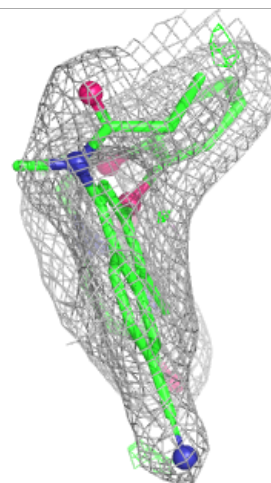
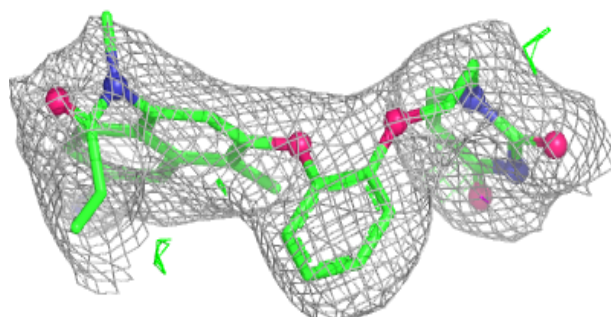
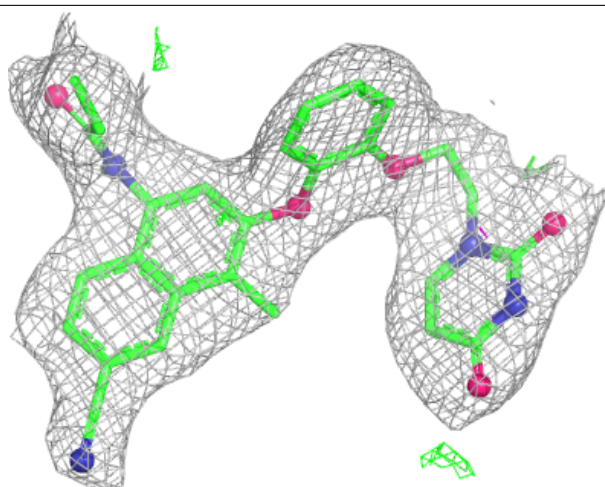
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
4	SO4	A	603	5/5	0.59	0.15	89,96,107,111	0
4	SO4	A	602	5/5	0.87	0.10	70,75,85,89	0
3	9J1	A	601	37/37	0.93	0.10	34,40,50,50	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 ⓘ

There are no such residues in this entry.