



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 11:45 PM UTC

PDB ID : 7SLS / pdb_00007sls
Title : HIV Reverse Transcriptase with compound Pyr02
Authors : Klein, D.J.; Zebisch, M.; Gu, M.
Deposited on : 2021-10-24
Resolution : 2.08 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 Phenix2.0
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

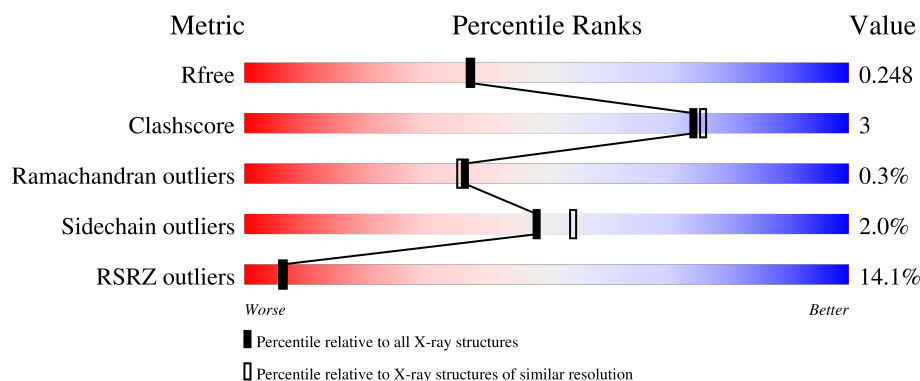
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.08 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	8172 (2.10-2.06)
Clashscore	190562	8714 (2.10-2.06)
Ramachandran outliers	187476	8641 (2.10-2.06)
Sidechain outliers	187428	8642 (2.10-2.06)
RSRZ outliers	180081	8177 (2.10-2.06)

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	561	
1	B	561	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	9PJ	A	601	X	-	-	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8148 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.

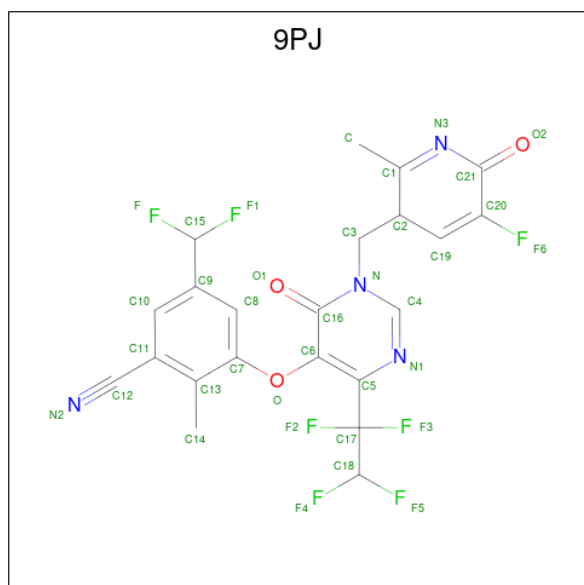
- Molecule 1 is a protein called Reverse transcriptase/ribonuclease H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	539	Total	C	N	O	S	0	3	0
			4430	2870	736	815	9			
1	B	405	Total	C	N	O	S	0	1	0
			3360	2189	554	610	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP P04585
B	0	MET	-	initiating methionine	UNP P04585

- Molecule 2 is 5-(difluoromethyl)-3-{[1-{{[(3S)-5-fluoro-2-methyl-6-oxo-3,6-dihydropyridin-3-yl]methyl}-6-oxo-4-(1,1,2,2-tetrafluoroethyl)-1,6-dihydropyrimidin-5-yl]oxy}-2-methylbenzonitrile (CCD ID: 9PJ) (formula: C₂₂H₁₅F₇N₄O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			36	22	7	4	3		

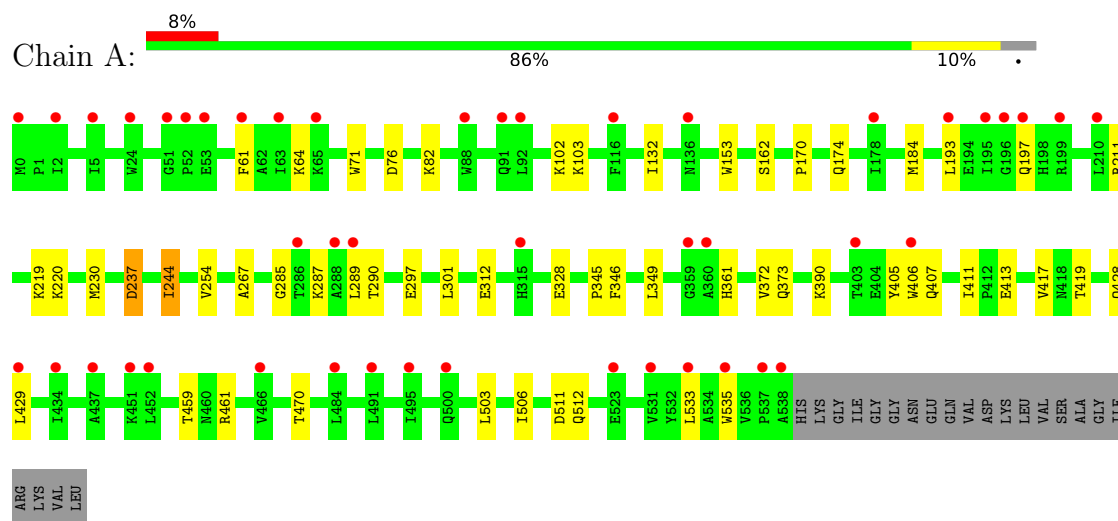
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	200	Total	O	0	0
			200	200		
3	B	122	Total	O	0	0
			122	122		

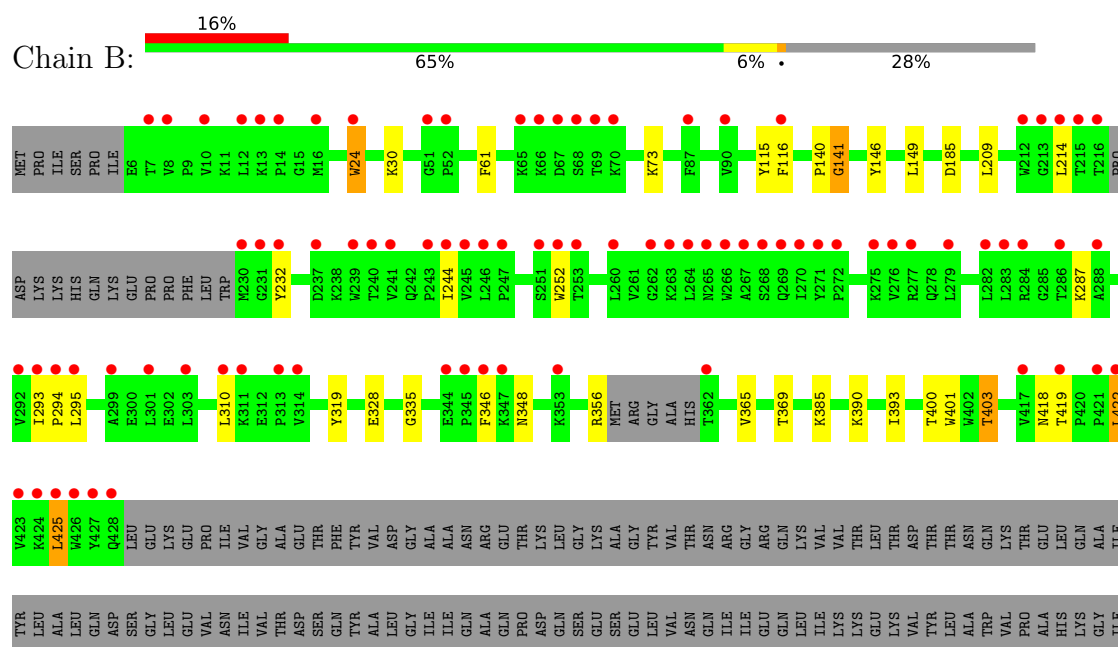
3 Residue-property plots

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 1: Reverse transcriptase/ribonuclease H



GLY
GLY
ASN
GLU
GLN
VAL
ASP
LYS
LEU
VAL
SER
ALA
GLY
ILE
ARG
LYS
VAL
LEU

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	117.73Å 154.25Å 155.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	93.58 – 2.08 93.58 – 2.08	Depositor EDS
% Data completeness (in resolution range)	82.2 (93.58-2.08) 82.2 (93.58-2.08)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 2.08Å)	Xtriage
Refinement program	BUSTER 2.11.8 (10-DEC-2020)	Depositor
R, R_{free}	0.227 , 0.259 0.221 , 0.248	Depositor DCC
R_{free} test set	3468 reflections (4.07%)	wwPDB-VP
Wilson B-factor (Å ²)	54.0	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 48.6	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	8148	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% 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: 9PJ

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	0.75	1/4554 (0.0%)	1.05	5/6190 (0.1%)
1	B	0.72	0/3458	1.07	5/4700 (0.1%)
All	All	0.74	1/8012 (0.0%)	1.06	10/10890 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	184	MET	CA-C	5.33	1.57	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	132	ILE	N-CA-C	-7.48	100.76	107.56
1	B	116	PHE	CA-CB-CG	7.38	121.19	113.80
1	A	153	TRP	CA-C-N	7.07	130.06	120.38
1	A	153	TRP	C-N-CA	7.07	130.06	120.38
1	A	349	LEU	N-CA-C	-6.60	103.35	111.40
1	A	361	HIS	N-CA-C	-6.39	98.12	108.41
1	B	232	TYR	N-CA-C	-5.96	104.41	111.03
1	B	401	TRP	N-CA-C	5.27	119.98	113.50
1	B	348	ASN	N-CA-C	5.21	117.73	109.96
1	B	185	ASP	CA-CB-CG	5.02	117.62	112.60

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	4430	0	4479	28	0
1	B	3360	0	3388	29	0
2	A	36	0	0	0	0
3	A	200	0	0	0	0
3	B	122	0	0	1	0
All	All	8148	0	7867	49	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 (49) 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:B:252:TRP:CD1	1:B:295:LEU:HD11	2.03	0.92
1:B:252:TRP:HD1	1:B:295:LEU:HD11	1.48	0.79
1:B:422:LEU:HA	1:B:425:LEU:HB2	1.70	0.73
1:A:535:TRP:CD2	1:B:422:LEU:HD13	2.29	0.67
1:A:193:LEU:HB3	1:A:197:GLN:HG3	1.76	0.67
1:A:406:TRP:CH2	1:B:418:ASN:HA	2.31	0.66
1:A:328:GLU:HG2	1:A:390:LYS:HB2	1.78	0.65
1:B:287:LYS:HD2	1:B:293:ILE:HD11	1.82	0.61
1:A:61[B]:PHE:HE2	1:A:76:ASP:HB2	1.65	0.61
1:B:209:LEU:HD22	1:B:214:LEU:HD22	1.84	0.60
1:A:373:GLN:NE2	1:B:400:THR:OG1	2.37	0.57
1:B:422:LEU:HD23	1:B:425:LEU:HD13	1.88	0.55
1:A:102:LYS:HE2	1:A:237:ASP:HB3	1.89	0.55
1:A:535:TRP:CG	1:B:422:LEU:HD11	2.43	0.54
1:B:115:TYR:HB3	1:B:149:LEU:HB2	1.90	0.53
1:B:209:LEU:HB3	1:B:214:LEU:HB2	1.89	0.53
1:A:170:PRO:O	1:A:174:GLN:HG2	2.09	0.53
1:A:405:TYR:CE2	1:A:407:GLN:HB3	2.46	0.51
1:B:244:ILE:HB	1:B:310:LEU:HD22	1.92	0.51
1:B:365:VAL:O	1:B:369:THR:HG23	2.12	0.49
1:B:328:GLU:HG3	1:B:390:LYS:HD3	1.96	0.48
1:A:535:TRP:CD2	1:B:422:LEU:CD1	2.98	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:ILE:HD12	1:A:267:ALA:HB2	1.97	0.47
1:A:285:GLY:HA3	1:A:287:LYS:HE2	1.96	0.46
1:A:407:GLN:CG	1:B:393:ILE:HA	2.45	0.46
1:A:254:VAL:HG21	1:A:287:LYS:HB2	1.97	0.46
1:B:24[B]:TRP:CD1	1:B:24[B]:TRP:H	2.33	0.45
1:B:140:PRO:O	1:B:141:GLY:O	2.33	0.45
1:A:503:LEU:HD12	1:A:533:LEU:HD23	1.98	0.45
1:A:417:VAL:HG22	1:A:419:THR:HG23	1.98	0.45
1:A:372:VAL:HG11	1:A:411:ILE:HG23	1.97	0.44
1:A:297:GLU:O	1:A:301:LEU:HG	2.17	0.44
1:A:345:PRO:HA	1:A:346:PHE:HA	1.73	0.44
1:A:82:LYS:HE3	1:A:82:LYS:HB2	1.85	0.44
1:A:289:LEU:HG	1:A:290:THR:HG23	2.00	0.43
1:A:535:TRP:CG	1:B:422:LEU:CD1	3.01	0.43
1:B:346:PHE:N	1:B:346:PHE:CD1	2.84	0.43
1:A:407:GLN:HG3	1:B:393:ILE:HA	2.01	0.42
1:A:429:LEU:HD11	1:A:506:ILE:HG22	2.00	0.42
1:B:319:TYR:OH	1:B:385:LYS:HD3	2.18	0.42
1:A:503:LEU:HD22	1:A:535:TRP:HB2	2.00	0.42
1:A:511:ASP:OD1	1:A:512:GLN:NE2	2.52	0.42
1:B:61:PHE:CD1	1:B:403:THR:HG21	2.54	0.42
1:B:293:ILE:HA	1:B:294:PRO:HD3	1.96	0.42
1:B:335:GLY:HA3	1:B:356:ARG:HG2	2.02	0.41
1:B:30:LYS:HD3	3:B:669:HOH:O	2.21	0.41
1:B:73:LYS:NZ	1:B:146:TYR:OH	2.54	0.41
1:A:64:LYS:HB2	1:A:71:TRP:CD2	2.57	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	540/561 (96%)	530 (98%)	9 (2%)	1 (0%)	43	44
1	B	400/561 (71%)	387 (97%)	11 (3%)	2 (0%)	24	21
All	All	940/1122 (84%)	917 (98%)	20 (2%)	3 (0%)	36	36

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	141	GLY
1	A	413	GLU
1	B	419	THR

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	487/501 (97%)	474 (97%)	13 (3%)	39	43
1	B	370/501 (74%)	365 (99%)	5 (1%)	59	66
All	All	857/1002 (86%)	839 (98%)	18 (2%)	48	52

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	103	LYS
1	A	162	SER
1	A	211	ARG
1	A	219	LYS
1	A	220	LYS
1	A	230	MET
1	A	237	ASP
1	A	244	ILE
1	A	312	GLU
1	A	428	GLN
1	A	459	THR
1	A	461	ARG
1	A	470	THR

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Mol	Chain	Res	Type
1	B	24[A]	TRP
1	B	24[B]	TRP
1	B	403	THR
1	B	422	LEU
1	B	425	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	222	GLN
1	A	255	ASN
1	A	258	GLN
1	A	330	GLN
1	A	336	GLN
1	A	340	GLN
1	A	373	GLN
1	A	447	ASN
1	A	480	GLN
1	A	507	GLN
1	B	91	GLN
1	B	137	ASN
1	B	147	ASN
1	B	197	GLN
1	B	258	GLN
1	B	265	ASN

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

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	9PJ	A	601	-	32,38,38	2.17	3 (9%)	38,57,57	2.28	4 (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	9PJ	A	601	-	1/1/7/8	3/24/42/42	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	9PJ	C2-C1	-11.28	1.35	1.51
2	A	601	9PJ	C2-C19	-3.79	1.43	1.50
2	A	601	9PJ	C17-C18	2.06	1.57	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	9PJ	C3-C2-C1	10.18	122.02	109.86
2	A	601	9PJ	C19-C2-C1	5.95	118.99	104.83
2	A	601	9PJ	C20-C21-N3	-4.70	112.83	118.42
2	A	601	9PJ	C-C1-N3	-4.51	113.25	119.71

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	601	9PJ	C2

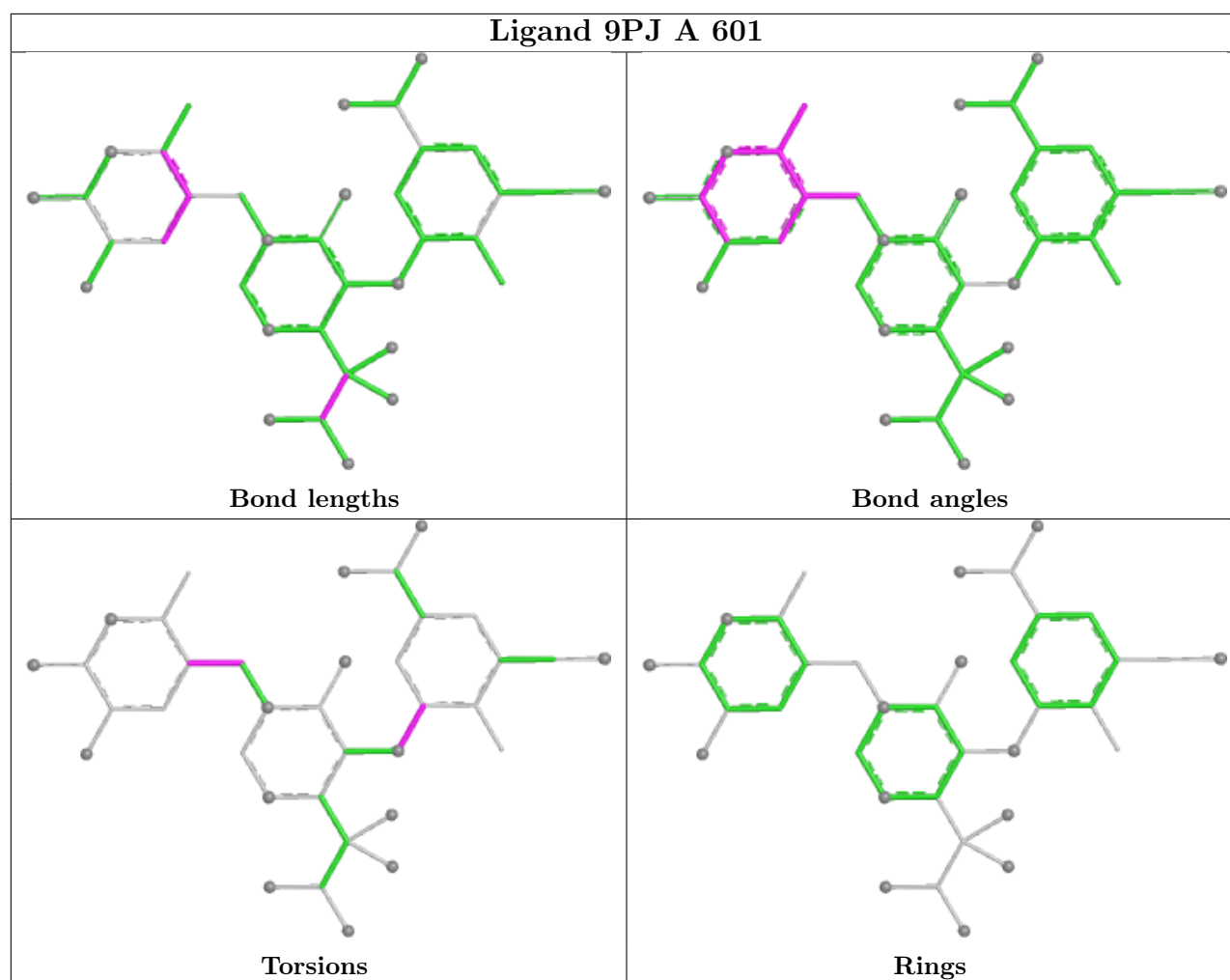
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	9PJ	C19-C2-C3-N
2	A	601	9PJ	C8-C7-O-C6
2	A	601	9PJ	C13-C7-O-C6

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	539/561 (96%)	0.79	46 (8%)	16 17	24, 55, 74, 95	3 (0%)
1	B	405/561 (72%)	1.12	87 (21%)	2 2	30, 57, 92, 110	1 (0%)
All	All	944/1122 (84%)	0.93	133 (14%)	6 6	24, 56, 89, 110	4 (0%)

All (133) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	422	LEU	7.6
1	B	266	TRP	7.1
1	B	426	TRP	7.0
1	B	270	ILE	5.8
1	B	346	PHE	5.4
1	B	282	LEU	4.8
1	B	241	VAL	4.8
1	B	423	VAL	4.7
1	B	216	THR	4.7
1	A	286	THR	4.5
1	B	425	LEU	4.4
1	B	295	LEU	4.2
1	B	362	THR	4.1
1	B	272	PRO	4.1
1	B	303	LEU	4.0
1	A	2	ILE	4.0
1	B	24[A]	TRP	3.9
1	B	232	TYR	3.9
1	B	66	LYS	3.8
1	B	421	PRO	3.8
1	A	91[A]	GLN	3.7
1	B	293	ILE	3.7
1	B	68	SER	3.6
1	A	495	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	244	ILE	3.5
1	B	276	VAL	3.4
1	B	262	GLY	3.4
1	B	215	THR	3.4
1	B	279	LEU	3.4
1	B	283	LEU	3.4
1	A	52	PRO	3.3
1	A	484	LEU	3.3
1	B	231	GLY	3.3
1	B	240	THR	3.2
1	B	247	PRO	3.2
1	A	406	TRP	3.2
1	B	230	MET	3.2
1	B	419	THR	3.2
1	B	301	LEU	3.1
1	B	69	THR	3.1
1	B	67	ASP	3.1
1	A	434	ILE	3.1
1	B	345	PRO	3.1
1	B	292	VAL	3.1
1	A	359	GLY	3.0
1	A	315[A]	HIS	3.0
1	B	8	VAL	2.9
1	B	116	PHE	2.9
1	A	88	TRP	2.9
1	A	197	GLN	2.9
1	A	193	LEU	2.8
1	B	214	LEU	2.8
1	B	10	VAL	2.8
1	A	491	LEU	2.8
1	B	314	VAL	2.8
1	B	428	GLN	2.7
1	A	116	PHE	2.7
1	B	65	LYS	2.7
1	A	360	ALA	2.7
1	B	288	ALA	2.7
1	B	271	TYR	2.7
1	B	16	MET	2.7
1	B	275	LYS	2.7
1	B	213	GLY	2.7
1	B	424	LYS	2.7
1	A	537	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	14	PRO	2.6
1	B	13	LYS	2.6
1	A	195	ILE	2.6
1	A	210	LEU	2.6
1	B	52	PRO	2.6
1	B	277	ARG	2.6
1	B	243	PRO	2.6
1	B	12	LEU	2.5
1	B	310	LEU	2.5
1	A	51	GLY	2.5
1	A	288	ALA	2.5
1	A	0	MET	2.5
1	A	65	LYS	2.5
1	B	427	TYR	2.4
1	B	313	PRO	2.4
1	B	87	PHE	2.4
1	A	24	TRP	2.4
1	B	212	TRP	2.4
1	B	267	ALA	2.4
1	B	344	GLU	2.4
1	A	61[A]	PHE	2.4
1	B	252	TRP	2.4
1	B	264	LEU	2.3
1	B	265	ASN	2.3
1	B	347	LYS	2.3
1	B	51	GLY	2.3
1	A	466	VAL	2.3
1	B	245	VAL	2.3
1	B	263	LYS	2.3
1	B	311	LYS	2.3
1	A	63	ILE	2.3
1	B	269	GLN	2.3
1	B	90	VAL	2.3
1	B	253	THR	2.3
1	A	429	LEU	2.3
1	A	5	ILE	2.2
1	A	178	ILE	2.2
1	A	531	VAL	2.2
1	B	237	ASP	2.2
1	A	535	TRP	2.2
1	B	417	VAL	2.2
1	A	437	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	289	LEU	2.2
1	B	268	SER	2.2
1	B	286	THR	2.2
1	B	284	ARG	2.2
1	B	70	LYS	2.2
1	A	136	ASN	2.2
1	A	403	THR	2.2
1	A	533	LEU	2.1
1	B	294	PRO	2.1
1	B	239	TRP	2.1
1	A	500	GLN	2.1
1	A	196	GLY	2.1
1	A	199	ARG	2.1
1	A	538	ALA	2.1
1	A	92	LEU	2.1
1	B	246	LEU	2.1
1	B	251	SER	2.1
1	B	260	LEU	2.1
1	A	53	GLU	2.1
1	B	7	THR	2.1
1	A	451	LYS	2.1
1	A	523	GLU	2.0
1	B	353	LYS	2.0
1	B	299	ALA	2.0
1	A	452	LEU	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 ⓘ

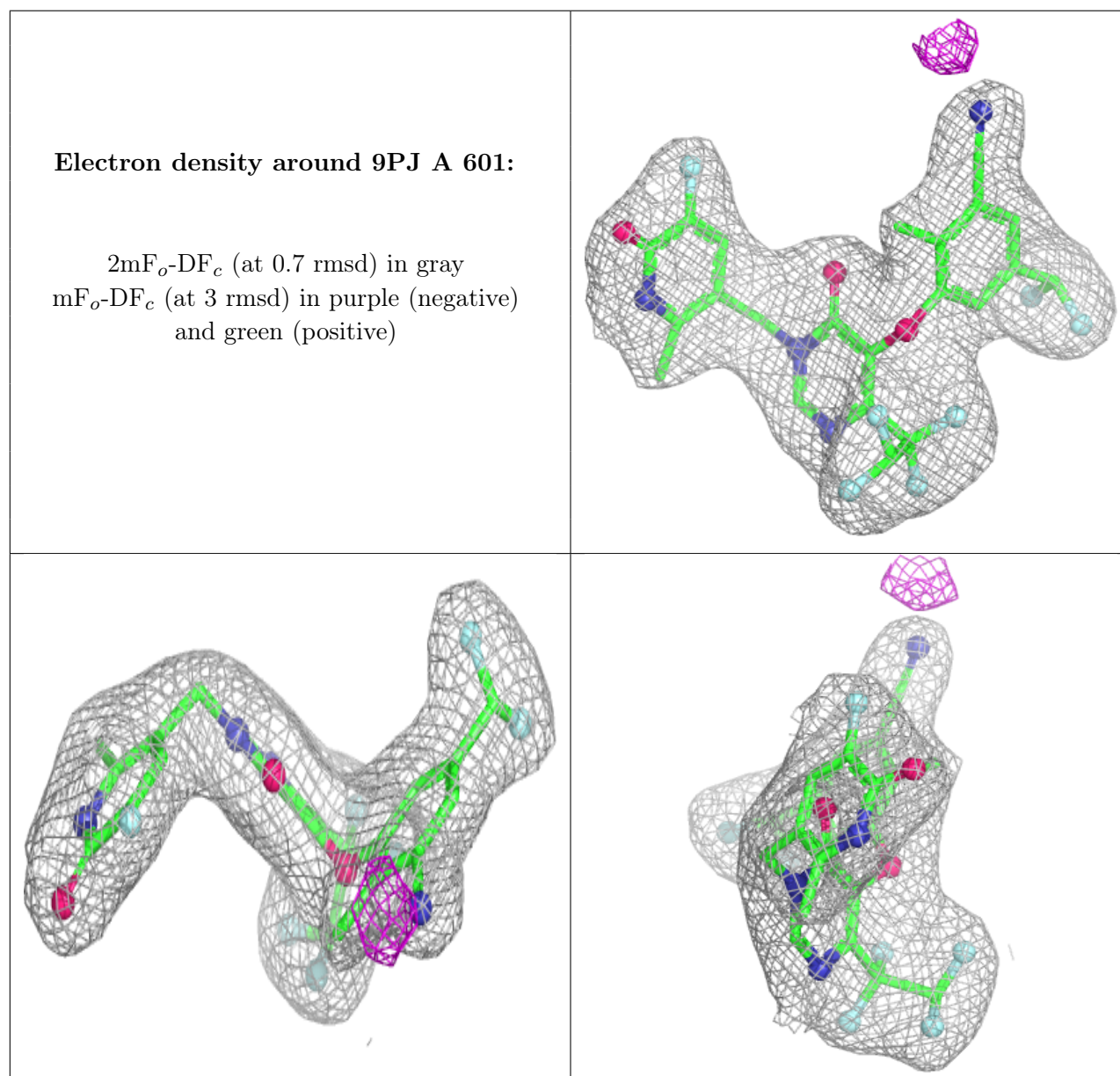
There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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	9PJ	A	601	36/36	0.95	0.08	45,48,55,57	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 ⓘ

There are no such residues in this entry.