



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 30, 2023 – 05:41 PM EDT

PDB ID : 8U6J
Title : Crystal Structure of HIV-1 Reverse Transcriptase in Complex with N-(2-(5-chloro-2-((2-cyanoindolizin-8-yl)oxy)phenoxy)ethyl)-N-methylacrylamide (JLJ746), a non-nucleoside inhibitor
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Deposited on : 2023-09-13
Resolution : 2.64 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

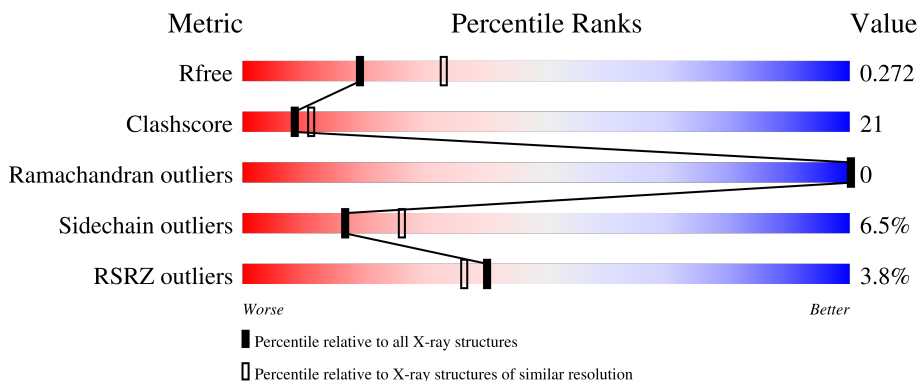
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


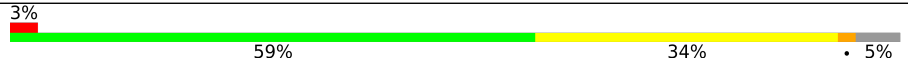
The reported resolution of this entry is 2.64 Å.

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}	130704	1426 (2.66-2.62)
Clashscore	141614	1472 (2.66-2.62)
Ramachandran outliers	138981	1446 (2.66-2.62)
Sidechain outliers	138945	1446 (2.66-2.62)
RSRZ outliers	127900	1408 (2.66-2.62)

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	 4% 61% 34% ••
2	B	428	 3% 59% 34% • 5%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7344 atoms, of which 18 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
			Total	C	N	O	S			
1	A	543	4124	2670	674	774	6	0	0	0

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

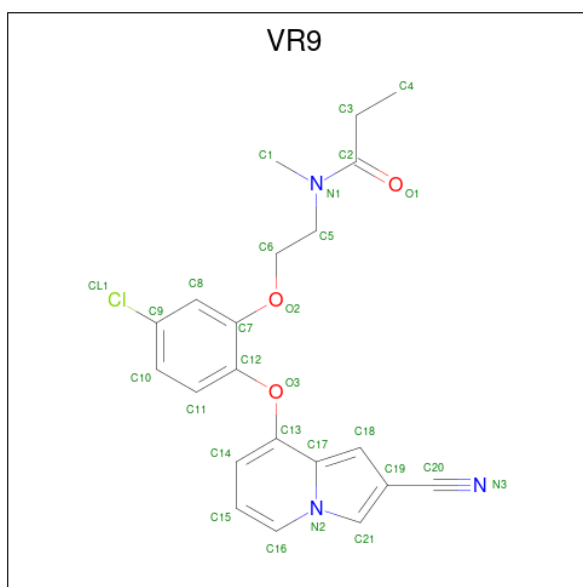
- Molecule 2 is a protein called p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	408	3162	2051	515	591	5	0	0	0

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-[2-(5-chloro-2-{{(4R)-2-cyanoindolizin-8-yl}oxy}phenoxy)ethyl]-N-methylpropanamide (three-letter code: VR9) (formula: C₂₁H₂₀ClN₃O₃) (labeled as "Ligand of Interest" by depositor).



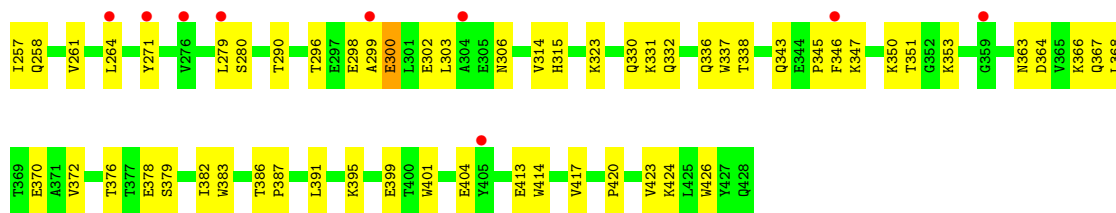
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	Cl	H	N			O
3	A	1	46	21	1	18	3	3	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total	O	0	0
			3	3		
5	B	8	Total	O	0	0
			8	8		



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	224.43Å 69.63Å 105.06Å 90.00° 105.89° 90.00°	Depositor
Resolution (Å)	43.26 – 2.64 43.26 – 2.64	Depositor EDS
% Data completeness (in resolution range)	96.8 (43.26-2.64) 96.8 (43.26-2.64)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 2.65Å)	Xtrriage
Refinement program	PHENIX (1.20.1_4487)	Depositor
R, R_{free}	0.239 , 0.274 0.241 , 0.272	Depositor DCC
R_{free} test set	1997 reflections (4.47%)	wwPDB-VP
Wilson B-factor (Å ²)	82.3	Xtrriage
Anisotropy	0.065	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 68.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7344	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtrriage'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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: VR9, MG

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	0.43	0/4236	0.59	0/5811
2	B	0.50	0/3254	0.59	0/4458
All	All	0.46	0/7490	0.59	0/10269

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	4124	0	3855	186	0
2	B	3162	0	2956	122	0
3	A	28	18	0	0	0
4	B	1	0	0	0	0
5	A	3	0	0	1	0
5	B	8	0	0	0	0
All	All	7326	18	6811	293	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 21.

All (293) 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:458:VAL:HG22	1:A:464:GLN:HG2	1.36	1.05
2:B:50:ILE:HD12	2:B:51:GLY:H	1.24	0.96
1:A:278:GLN:HG2	1:A:298:GLU:HB2	1.48	0.96
1:A:253:THR:HG23	1:A:256:ASP:H	1.39	0.87
2:B:180:ILE:HG12	2:B:189:VAL:HG12	1.57	0.86
1:A:91:GLN:HE21	2:B:137:ASN:HB3	1.42	0.83
1:A:411:ILE:O	1:A:411:ILE:HG23	1.80	0.81
1:A:532:TYR:CE2	1:A:534:ALA:HB2	2.16	0.80
2:B:50:ILE:HD12	2:B:51:GLY:N	1.96	0.79
1:A:324:ASP:O	1:A:343:GLN:HG2	1.84	0.78
1:A:91:GLN:NE2	2:B:137:ASN:HB3	2.00	0.76
2:B:50:ILE:CD1	2:B:51:GLY:H	1.99	0.74
2:B:132:ILE:HD12	2:B:132:ILE:N	2.05	0.72
1:A:134:SER:HB3	1:A:139:THR:OG1	1.89	0.72
2:B:253:THR:O	2:B:257:ILE:HG12	1.88	0.72
1:A:473:THR:HG23	1:A:476:LYS:CB	2.20	0.71
1:A:516:GLU:HA	1:A:519:ASN:HD22	1.55	0.71
1:A:88:TRP:CZ2	2:B:143:ARG:HD3	2.26	0.71
2:B:101:LYS:O	2:B:236:PRO:HB2	1.90	0.71
2:B:368:LEU:O	2:B:372:VAL:HG23	1.91	0.71
2:B:108:VAL:HG22	2:B:188:TYR:CD2	2.27	0.70
1:A:366:LYS:HE2	1:A:405:TYR:OH	1.91	0.70
1:A:246:LEU:HD22	1:A:260:LEU:CD1	2.22	0.69
1:A:105:SER:HB2	1:A:198:HIS:CE1	2.27	0.69
1:A:3:SER:HB3	1:A:5:ILE:HD12	1.74	0.69
2:B:350:LYS:HE3	2:B:378:GLU:OE1	1.93	0.69
1:A:240:THR:OG1	1:A:315:HIS:ND1	2.27	0.68
1:A:253:THR:HG22	1:A:256:ASP:CG	2.14	0.68
2:B:85:GLN:HA	2:B:88:TRP:NE1	2.09	0.67
1:A:164:MET:HE1	1:A:214:LEU:HD13	1.77	0.67
2:B:296:THR:HG22	2:B:298:GLU:N	2.10	0.67
1:A:503:LEU:HD22	1:A:535:TRP:HB2	1.76	0.66
2:B:10:VAL:HG22	2:B:87:PHE:CZ	2.30	0.65
1:A:58:THR:HG23	1:A:59:PRO:HD2	1.78	0.65
2:B:189:VAL:HG21	2:B:202:ILE:HD12	1.78	0.65
1:A:164:MET:HE2	1:A:164:MET:HA	1.80	0.64
2:B:10:VAL:HG22	2:B:87:PHE:CE2	2.32	0.64
2:B:189:VAL:HG21	2:B:202:ILE:CD1	2.27	0.64
2:B:401:TRP:HE3	2:B:404:GLU:HG3	1.63	0.64
1:A:489:SER:OG	1:A:528:LYS:HE3	1.98	0.64
1:A:39:THR:HG23	1:A:42:GLU:OE1	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:ILE:HD11	1:A:183:TYR:CE1	2.33	0.63
1:A:241:VAL:HG13	1:A:266:TRP:HE1	1.63	0.63
1:A:130:PHE:O	1:A:143:ARG:HD2	1.99	0.63
1:A:79:GLU:HG3	1:A:83:ARG:NH1	2.14	0.63
2:B:27:THR:OG1	2:B:30:LYS:HG3	1.99	0.63
2:B:103:LYS:HE2	2:B:179:VAL:HG23	1.81	0.62
2:B:246:LEU:HD11	2:B:264:LEU:HD21	1.81	0.62
2:B:332:GLN:HB2	2:B:336:GLN:O	1.99	0.62
2:B:302:GLU:O	2:B:306:ASN:ND2	2.33	0.61
1:A:439:THR:HG22	1:A:441:TYR:CE1	2.35	0.61
2:B:296:THR:HG22	2:B:299:ALA:H	1.65	0.61
1:A:254:VAL:HG13	1:A:283:LEU:HD21	1.83	0.60
1:A:3:SER:HB3	1:A:5:ILE:CD1	2.31	0.60
2:B:366:LYS:O	2:B:370:GLU:HG3	2.02	0.60
2:B:118:VAL:HG11	2:B:149:LEU:HD11	1.83	0.60
2:B:210:LEU:HD22	2:B:214:LEU:O	2.00	0.60
1:A:134:SER:O	1:A:136:ASN:N	2.34	0.60
1:A:324:ASP:N	1:A:324:ASP:OD1	2.33	0.60
1:A:115:TYR:CD2	1:A:156:SER:HB3	2.35	0.60
1:A:3:SER:OG	1:A:5:ILE:HG13	2.01	0.60
1:A:411:ILE:O	1:A:411:ILE:CG2	2.49	0.60
1:A:518:VAL:O	1:A:522:ILE:HG13	2.01	0.60
2:B:175:ASN:OD1	2:B:201:LYS:HE3	2.02	0.60
1:A:533:LEU:HD12	1:A:534:ALA:H	1.67	0.59
1:A:469:LEU:HB3	1:A:472:THR:HG21	1.84	0.59
1:A:84:THR:HG21	1:A:153:TRP:HE1	1.66	0.59
1:A:290:THR:O	1:A:290:THR:HG22	2.02	0.59
1:A:382:ILE:HG23	2:B:136:ASN:HD21	1.67	0.59
1:A:382:ILE:HG23	2:B:136:ASN:ND2	2.17	0.59
1:A:114:ALA:HB1	1:A:160:PHE:CE1	2.38	0.59
1:A:533:LEU:HD12	1:A:534:ALA:N	2.18	0.59
1:A:3:SER:OG	1:A:4:PRO:HD2	2.02	0.58
2:B:237:ASP:OD1	2:B:238:LYS:N	2.36	0.58
1:A:27:THR:HG22	1:A:29:GLU:N	2.18	0.58
2:B:27:THR:O	2:B:31:ILE:HD12	2.04	0.58
2:B:138:GLU:HG3	2:B:139:THR:HG23	1.85	0.58
1:A:105:SER:HB2	1:A:198:HIS:ND1	2.19	0.57
1:A:21:VAL:CG1	1:A:59:PRO:HD3	2.34	0.57
1:A:191:SER:OG	1:A:198:HIS:ND1	2.27	0.57
1:A:41:MET:HG3	1:A:47:ILE:HD11	1.85	0.57
1:A:38:CYS:O	1:A:47:ILE:HD11	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:LEU:CD2	1:A:209:LEU:HD11	2.35	0.56
1:A:435:VAL:CG1	2:B:290:THR:HG21	2.35	0.56
1:A:13:LYS:HE3	1:A:82:LYS:O	2.06	0.56
1:A:341:ILE:HG21	1:A:383:TRP:CH2	2.41	0.56
1:A:180:ILE:CG2	1:A:187:LEU:HD22	2.36	0.56
1:A:88:TRP:CE2	2:B:143:ARG:HD3	2.41	0.56
1:A:164:MET:HE1	1:A:214:LEU:CD1	2.35	0.56
1:A:233:GLU:N	1:A:240:THR:O	2.25	0.56
1:A:420:PRO:HA	1:A:422:LEU:N	2.21	0.56
1:A:492:GLU:HG2	1:A:530:LYS:HB2	1.87	0.56
1:A:27:THR:O	1:A:31:ILE:HG13	2.06	0.55
1:A:406:TRP:CD1	2:B:420:PRO:HB3	2.42	0.55
2:B:236:PRO:HA	2:B:239:TRP:CD2	2.42	0.55
1:A:194:GLU:CD	1:A:196:GLY:H	2.10	0.55
1:A:241:VAL:HG13	1:A:266:TRP:NE1	2.22	0.55
1:A:246:LEU:HD22	1:A:260:LEU:HD12	1.88	0.55
2:B:253:THR:H	2:B:256:ASP:HB2	1.72	0.55
1:A:408:ALA:HB2	2:B:337:TRP:HH2	1.72	0.54
2:B:105:SER:O	2:B:190:GLY:HA2	2.07	0.54
2:B:169:GLU:HA	2:B:169:GLU:OE1	2.08	0.54
2:B:132:ILE:N	2:B:132:ILE:CD1	2.71	0.54
1:A:427:TYR:CE2	1:A:525:LEU:HD13	2.43	0.54
2:B:118:VAL:HB	2:B:149:LEU:HD12	1.89	0.54
1:A:325:LEU:HD21	1:A:383:TRP:CE3	2.43	0.53
1:A:447:ASN:CG	1:A:450:THR:HG23	2.28	0.53
2:B:189:VAL:HG23	2:B:189:VAL:O	2.08	0.53
2:B:323:LYS:HB2	2:B:343:GLN:NE2	2.24	0.53
1:A:474:ASN:O	1:A:478:GLU:HG3	2.09	0.53
2:B:60:VAL:HG11	2:B:130:PHE:CD2	2.44	0.53
1:A:27:THR:HG22	1:A:29:GLU:H	1.74	0.53
2:B:205:LEU:O	2:B:209:LEU:HG	2.09	0.52
2:B:376:THR:HG23	2:B:386:THR:HG22	1.90	0.52
1:A:532:TYR:HE2	1:A:534:ALA:HB2	1.70	0.52
2:B:203:GLU:O	2:B:207:GLN:HG2	2.09	0.52
1:A:21:VAL:HG11	1:A:59:PRO:HD3	1.92	0.52
1:A:512:LYS:HG2	1:A:513:SER:H	1.75	0.52
2:B:279:LEU:N	2:B:279:LEU:HD23	2.25	0.52
2:B:296:THR:HB	2:B:299:ALA:HB3	1.92	0.51
1:A:439:THR:HG22	1:A:441:TYR:HE1	1.75	0.51
2:B:254:VAL:O	2:B:258:GLN:HG3	2.10	0.51
1:A:253:THR:CG2	1:A:256:ASP:H	2.18	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:326:ILE:HD12	1:A:342:TYR:O	2.11	0.51
2:B:279:LEU:HD22	2:B:299:ALA:HB1	1.92	0.51
2:B:332:GLN:HG3	2:B:338:THR:HG23	1.93	0.51
1:A:91:GLN:NE2	2:B:137:ASN:O	2.44	0.51
1:A:296:THR:HG22	1:A:299:ALA:CB	2.41	0.51
1:A:265:ASN:OD1	1:A:353:LYS:HE3	2.11	0.50
1:A:354:TYR:OH	1:A:370:GLU:OE1	2.28	0.50
1:A:240:THR:HG22	1:A:241:VAL:N	2.27	0.50
2:B:88:TRP:CH2	2:B:154:LYS:HD3	2.46	0.50
1:A:50:ILE:HD12	1:A:143:ARG:HB3	1.93	0.50
1:A:522:ILE:O	1:A:526:ILE:HG23	2.12	0.50
1:A:1:PRO:HA	1:A:46:LYS:HZ3	1.76	0.50
2:B:279:LEU:CD2	2:B:299:ALA:HB1	2.42	0.50
2:B:350:LYS:CE	2:B:378:GLU:OE1	2.59	0.50
1:A:458:VAL:HG22	1:A:464:GLN:CG	2.25	0.50
1:A:246:LEU:O	1:A:307:ARG:NH2	2.45	0.50
1:A:382:ILE:HA	2:B:136:ASN:HD22	1.77	0.50
1:A:429:LEU:HD21	1:A:506:ILE:HG22	1.94	0.50
2:B:208:HIS:O	2:B:212:TRP:HD1	1.95	0.49
2:B:191:SER:OG	2:B:198:HIS:ND1	2.26	0.49
2:B:138:GLU:CG	2:B:139:THR:HG23	2.42	0.49
1:A:47:ILE:HG22	1:A:145:GLN:O	2.12	0.49
1:A:400:THR:O	1:A:403:THR:HG22	2.12	0.49
1:A:515:SER:O	1:A:519:ASN:ND2	2.45	0.49
1:A:180:ILE:HG21	1:A:187:LEU:HD22	1.94	0.49
1:A:512:LYS:HD3	1:A:513:SER:N	2.28	0.49
1:A:97:PRO:HG2	1:A:232:TYR:CD1	2.48	0.48
1:A:233:GLU:O	1:A:239:TRP:HA	2.13	0.48
1:A:235:HIS:HB2	1:A:238:LYS:HG2	1.94	0.48
2:B:423:VAL:O	2:B:426:TRP:HB2	2.13	0.48
1:A:3:SER:CB	1:A:5:ILE:CD1	2.92	0.48
2:B:296:THR:CG2	2:B:299:ALA:H	2.26	0.48
2:B:257:ILE:O	2:B:261:VAL:HG22	2.13	0.48
1:A:298:GLU:H	1:A:298:GLU:CD	2.12	0.48
1:A:353:LYS:NZ	5:A:701:HOH:O	2.31	0.48
2:B:118:VAL:CG1	2:B:149:LEU:HD11	2.44	0.47
1:A:445:ALA:O	1:A:477:THR:HG21	2.14	0.47
1:A:153:TRP:CZ3	1:A:155:GLY:HA3	2.48	0.47
2:B:314:VAL:HG12	2:B:315:HIS:N	2.29	0.47
1:A:94:ILE:HD11	1:A:183:TYR:CZ	2.50	0.47
1:A:326:ILE:CD1	1:A:343:GLN:HA	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:406:TRP:CE2	2:B:420:PRO:HB3	2.49	0.47
2:B:85:GLN:HG3	2:B:88:TRP:CZ2	2.50	0.47
1:A:17:ASP:OD1	1:A:56:TYR:HE1	1.96	0.47
1:A:205:LEU:HD23	1:A:209:LEU:CD1	2.45	0.47
2:B:156:SER:N	2:B:157:PRO:HD2	2.29	0.47
1:A:91:GLN:OE1	2:B:140:PRO:HA	2.15	0.47
2:B:189:VAL:CG2	2:B:202:ILE:CD1	2.91	0.47
1:A:116:PHE:CE1	1:A:146:TYR:HE2	2.32	0.47
1:A:492:GLU:HA	1:A:530:LYS:O	2.15	0.47
2:B:247:PRO:O	2:B:252:TRP:HH2	1.98	0.47
1:A:126:LYS:HE3	1:A:127:TYR:CZ	2.50	0.46
1:A:523:GLU:O	1:A:526:ILE:HG13	2.15	0.46
1:A:5:ILE:CD1	1:A:167:ILE:HD11	2.46	0.46
1:A:303:LEU:O	1:A:307:ARG:HG3	2.15	0.46
1:A:296:THR:HG22	1:A:299:ALA:HB3	1.98	0.46
1:A:439:THR:CG2	1:A:441:TYR:HE1	2.28	0.46
1:A:485:ALA:O	1:A:489:SER:HB3	2.16	0.46
1:A:512:LYS:HG2	1:A:519:ASN:OD1	2.16	0.46
2:B:26:LEU:O	2:B:31:ILE:HD11	2.16	0.46
1:A:439:THR:CG2	1:A:441:TYR:CE1	2.98	0.46
1:A:276:VAL:O	1:A:280:SER:OG	2.31	0.46
1:A:377:THR:O	1:A:381:VAL:HG23	2.15	0.46
2:B:363:ASN:O	2:B:367:GLN:HG3	2.16	0.46
2:B:296:THR:HB	2:B:299:ALA:CB	2.46	0.46
1:A:80:LEU:O	1:A:84:THR:HG23	2.15	0.45
1:A:515:SER:OG	1:A:518:VAL:HG23	2.16	0.45
2:B:168:LEU:HD13	2:B:180:ILE:HG21	1.98	0.45
2:B:395:LYS:HE3	2:B:399:GLU:OE2	2.16	0.45
1:A:180:ILE:N	1:A:180:ILE:HD12	2.31	0.45
2:B:132:ILE:HD12	2:B:132:ILE:H	1.80	0.45
2:B:198:HIS:O	2:B:202:ILE:HG12	2.16	0.45
1:A:164:MET:SD	1:A:168:LEU:CD1	3.04	0.45
2:B:303:LEU:HD12	2:B:303:LEU:O	2.15	0.45
1:A:58:THR:CG2	1:A:59:PRO:HD2	2.45	0.45
2:B:88:TRP:CZ2	2:B:154:LYS:HD3	2.52	0.45
2:B:296:THR:O	2:B:300:GLU:HB2	2.17	0.45
1:A:31:ILE:CD1	1:A:133:PRO:HG2	2.46	0.45
2:B:206:ARG:NH1	2:B:216:THR:HG22	2.32	0.45
1:A:21:VAL:CG1	1:A:22:LYS:N	2.80	0.45
1:A:108:VAL:O	1:A:109:LEU:HD23	2.17	0.45
1:A:399:GLU:HA	1:A:402:TRP:CD1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:442:VAL:HB	1:A:481:ALA:HB1	1.99	0.45
2:B:331:LYS:NZ	2:B:364:ASP:OD2	2.41	0.45
1:A:94:ILE:HD11	1:A:183:TYR:OH	2.17	0.45
1:A:341:ILE:HD12	1:A:341:ILE:HG23	1.79	0.45
2:B:154:LYS:HE3	2:B:184:MET:HE1	1.98	0.45
2:B:201:LYS:NZ	2:B:204:GLU:OE1	2.46	0.45
1:A:235:HIS:HB2	1:A:238:LYS:CG	2.45	0.44
1:A:447:ASN:HB3	1:A:450:THR:OG1	2.17	0.44
1:A:183:TYR:CE2	1:A:184:MET:HG3	2.53	0.44
1:A:328:GLU:O	1:A:339:TYR:HA	2.16	0.44
2:B:7:THR:O	2:B:9:PRO:HD3	2.17	0.44
1:A:395:LYS:HA	1:A:414:TRP:HH2	1.83	0.44
2:B:53:GLU:OE1	2:B:53:GLU:N	2.49	0.44
1:A:362:THR:HG22	1:A:363:ASN:N	2.33	0.44
1:A:205:LEU:HD23	1:A:209:LEU:HG	2.00	0.44
1:A:404:GLU:HA	1:A:404:GLU:OE1	2.18	0.44
2:B:49:LYS:HA	2:B:143:ARG:O	2.18	0.44
2:B:60:VAL:HG13	2:B:130:PHE:HB2	1.99	0.44
2:B:116:PHE:CZ	2:B:151:GLN:HG3	2.53	0.44
2:B:391:LEU:O	2:B:417:VAL:HG12	2.17	0.44
2:B:345:PRO:HB2	2:B:346:PHE:CD2	2.53	0.44
2:B:28:GLU:HB2	2:B:135:ILE:HD11	2.00	0.43
2:B:194:GLU:O	2:B:195:ILE:C	2.56	0.43
1:A:395:LYS:HA	1:A:414:TRP:CH2	2.53	0.43
1:A:1:PRO:HD2	1:A:213:GLY:HA2	1.99	0.43
2:B:47:ILE:HG22	2:B:146:TYR:HA	2.00	0.43
2:B:75:VAL:HG11	2:B:77:PHE:CZ	2.54	0.43
1:A:442:VAL:HG12	1:A:457:TYR:HB3	2.01	0.43
2:B:163:SER:O	2:B:167:ILE:HG13	2.19	0.43
2:B:164:MET:HB2	2:B:164:MET:HE2	1.91	0.43
1:A:227:PHE:HB2	1:A:234:LEU:HB2	1.99	0.43
2:B:179:VAL:O	2:B:189:VAL:HA	2.17	0.43
1:A:164:MET:HE3	1:A:164:MET:HB2	1.78	0.43
1:A:484:LEU:HA	1:A:484:LEU:HD23	1.71	0.43
2:B:246:LEU:HD23	2:B:246:LEU:HA	1.68	0.43
1:A:115:TYR:O	1:A:149:LEU:HB2	2.19	0.43
1:A:184:MET:HB2	1:A:185:ASP:H	1.63	0.43
1:A:266:TRP:O	1:A:269:GLN:HG2	2.18	0.43
1:A:435:VAL:HG12	2:B:290:THR:HG21	2.00	0.43
2:B:92:LEU:O	2:B:161:GLN:NE2	2.52	0.43
2:B:379:SER:OG	2:B:387:PRO:HD3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:THR:HG22	1:A:340:GLN:NE2	2.34	0.42
2:B:21:VAL:HB	2:B:59:PRO:HD3	2.01	0.42
1:A:134:SER:HB3	1:A:139:THR:CB	2.48	0.42
1:A:425:LEU:HD23	1:A:425:LEU:HA	1.88	0.42
1:A:498:ASP:HB2	1:A:538:ALA:HB2	2.01	0.42
2:B:296:THR:HG22	2:B:298:GLU:H	1.84	0.42
1:A:258:GLN:CG	1:A:283:LEU:HD11	2.49	0.42
2:B:19:PRO:HG3	2:B:80:LEU:HB2	2.00	0.42
1:A:183:TYR:CD2	1:A:184:MET:HG3	2.55	0.42
1:A:512:LYS:CG	1:A:513:SER:H	2.31	0.42
1:A:53:GLU:OE1	1:A:53:GLU:N	2.38	0.42
1:A:116:PHE:HE1	1:A:146:TYR:HE2	1.66	0.42
1:A:235:HIS:HB2	1:A:238:LYS:O	2.20	0.42
1:A:136:ASN:C	1:A:138:GLU:H	2.23	0.42
1:A:79:GLU:OE2	1:A:83:ARG:NH1	2.52	0.42
1:A:327:ALA:HB2	1:A:341:ILE:CD1	2.50	0.42
2:B:382:ILE:HG22	2:B:383:TRP:CD2	2.55	0.42
1:A:416:PHE:CD1	1:A:417:VAL:N	2.88	0.41
2:B:315:HIS:O	2:B:347:LYS:NZ	2.52	0.41
1:A:420:PRO:HA	1:A:421:PRO:C	2.41	0.41
2:B:242:GLN:HG2	2:B:351:THR:O	2.20	0.41
2:B:97:PRO:HG3	2:B:181:TYR:HB2	2.02	0.41
1:A:303:LEU:HD12	1:A:303:LEU:HA	1.93	0.41
1:A:433:PRO:HD3	1:A:532:TYR:CZ	2.56	0.41
2:B:241:VAL:HG22	2:B:350:LYS:HA	2.03	0.41
1:A:164:MET:CE	1:A:214:LEU:HD13	2.49	0.41
1:A:235:HIS:N	1:A:238:LYS:O	2.53	0.41
2:B:34:LEU:HD23	2:B:34:LEU:HA	1.75	0.41
2:B:157:PRO:HG3	2:B:184:MET:HA	2.03	0.41
2:B:258:GLN:HA	2:B:261:VAL:HG22	2.02	0.41
2:B:330:GLN:OE1	2:B:338:THR:OG1	2.29	0.41
1:A:19:PRO:O	1:A:56:TYR:HB3	2.21	0.41
1:A:105:SER:O	1:A:190:GLY:HA2	2.21	0.41
1:A:115:TYR:N	1:A:115:TYR:CD1	2.89	0.41
1:A:164:MET:SD	1:A:187:LEU:HD11	2.61	0.41
1:A:491:LEU:H	1:A:491:LEU:HD22	1.86	0.41
2:B:132:ILE:CD1	2:B:132:ILE:H	2.33	0.41
1:A:50:ILE:CD1	1:A:143:ARG:HB3	2.50	0.40
1:A:171:PHE:HD1	1:A:171:PHE:O	2.03	0.40
1:A:246:LEU:HD22	1:A:260:LEU:HD13	2.02	0.40
1:A:457:TYR:O	1:A:458:VAL:HG23	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:LEU:HB3	1:A:197:GLN:HB2	2.03	0.40
1:A:205:LEU:HD23	1:A:209:LEU:HD11	2.03	0.40
1:A:225:PRO:HA	1:A:226:PRO:C	2.42	0.40
2:B:192:ASP:OD1	2:B:192:ASP:N	2.54	0.40
1:A:218:ASP:CB	1:A:221:HIS:CE1	3.04	0.40
1:A:435:VAL:HG13	2:B:290:THR:HG21	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	537/557 (96%)	504 (94%)	33 (6%)	0	100	100
2	B	402/428 (94%)	382 (95%)	20 (5%)	0	100	100
All	All	939/985 (95%)	886 (94%)	53 (6%)	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	408/495 (82%)	382 (94%)	26 (6%)	17	27
2	B	318/390 (82%)	297 (93%)	21 (7%)	16	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	726/885 (82%)	679 (94%)	47 (6%)	17	26

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	A	94	ILE
1	A	105	SER
1	A	134	SER
1	A	139	THR
1	A	171	PHE
1	A	177	ASP
1	A	178	ILE
1	A	184	MET
1	A	195	ILE
1	A	199	ARG
1	A	216	THR
1	A	221	HIS
1	A	248	GLU
1	A	255	ASN
1	A	296	THR
1	A	298	GLU
1	A	300	GLU
1	A	324	ASP
1	A	353	LYS
1	A	364	ASP
1	A	401	TRP
1	A	430	GLU
1	A	473	THR
1	A	512	LYS
1	A	533	LEU
2	B	32	LYS
2	B	40	GLU
2	B	50	ILE
2	B	113	ASP
2	B	132	ILE
2	B	136	ASN
2	B	138	GLU
2	B	169	GLU
2	B	192	ASP
2	B	200	THR
2	B	210	LEU

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Mol	Chain	Res	Type
2	B	234	LEU
2	B	240	THR
2	B	250	ASP
2	B	271	TYR
2	B	280	SER
2	B	300	GLU
2	B	353	LYS
2	B	413	GLU
2	B	414	TRP
2	B	424	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	519	ASN
2	B	136	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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
3	VR9	A	601	-	28,30,30	3.42	8 (28%)	31,41,41	2.83	7 (22%)

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	VR9	A	601	-	-	3/16/18/18	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	VR9	C2-N1	14.90	1.53	1.34
3	A	601	VR9	O1-C2	-4.84	1.12	1.23
3	A	601	VR9	C4-C3	-4.41	1.31	1.51
3	A	601	VR9	C19-C20	4.39	1.54	1.44
3	A	601	VR9	C21-C19	2.86	1.41	1.38
3	A	601	VR9	C18-C19	2.35	1.44	1.41
3	A	601	VR9	C9-CL1	2.16	1.79	1.74
3	A	601	VR9	C5-C6	2.10	1.57	1.50

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	VR9	C4-C3-C2	11.36	133.71	112.72
3	A	601	VR9	C3-C2-N1	7.45	129.78	117.94
3	A	601	VR9	O1-C2-C3	-4.28	112.30	121.42
3	A	601	VR9	O1-C2-N1	-3.24	117.43	122.12
3	A	601	VR9	C1-N1-C5	2.95	121.88	115.89
3	A	601	VR9	C1-N1-C2	-2.31	115.59	121.83
3	A	601	VR9	C10-C9-C8	-2.03	118.84	121.53

There are no chirality outliers.

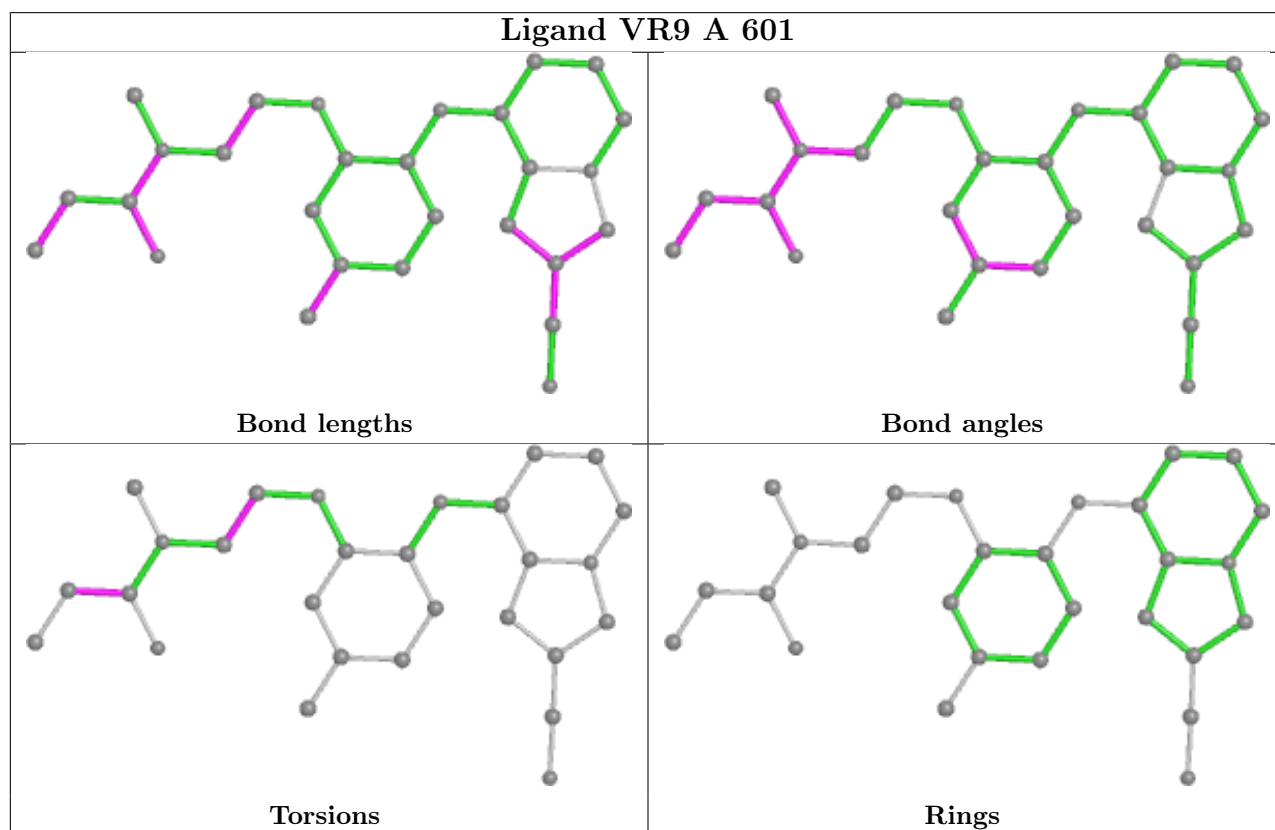
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	VR9	N1-C2-C3-C4
3	A	601	VR9	N1-C5-C6-O2
3	A	601	VR9	O1-C2-C3-C4

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	543/557 (97%)	0.12	23 (4%) 36 33	66, 97, 143, 194	0
2	B	408/428 (95%)	0.15	13 (3%) 47 44	65, 89, 153, 174	0
All	All	951/985 (96%)	0.14	36 (3%) 40 36	65, 95, 150, 194	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	60	VAL	4.6
2	B	276	VAL	4.3
2	B	359	GLY	4.3
1	A	247	PRO	4.2
2	B	299	ALA	4.0
1	A	59	PRO	3.9
2	B	252	TRP	3.7
2	B	232	TYR	3.4
1	A	133	PRO	3.4
1	A	246	LEU	3.4
1	A	61	PHE	3.2
2	B	264	LEU	3.2
1	A	132	ILE	3.0
2	B	279	LEU	2.9
1	A	549	ASP	2.7
1	A	130	PHE	2.6
1	A	260	LEU	2.5
1	A	482	ILE	2.5
1	A	71	TRP	2.5
1	A	279	LEU	2.4
2	B	100	LEU	2.4
1	A	541	GLY	2.4
2	B	116	PHE	2.4
2	B	304	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	362	THR	2.4
2	B	346	PHE	2.3
2	B	271	TYR	2.3
2	B	405	TYR	2.2
1	A	543	GLY	2.2
1	A	533	LEU	2.2
1	A	73	LYS	2.2
1	A	129	ALA	2.2
1	A	141	GLY	2.1
1	A	77	PHE	2.1
1	A	252	TRP	2.0
1	A	291	GLU	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](#)

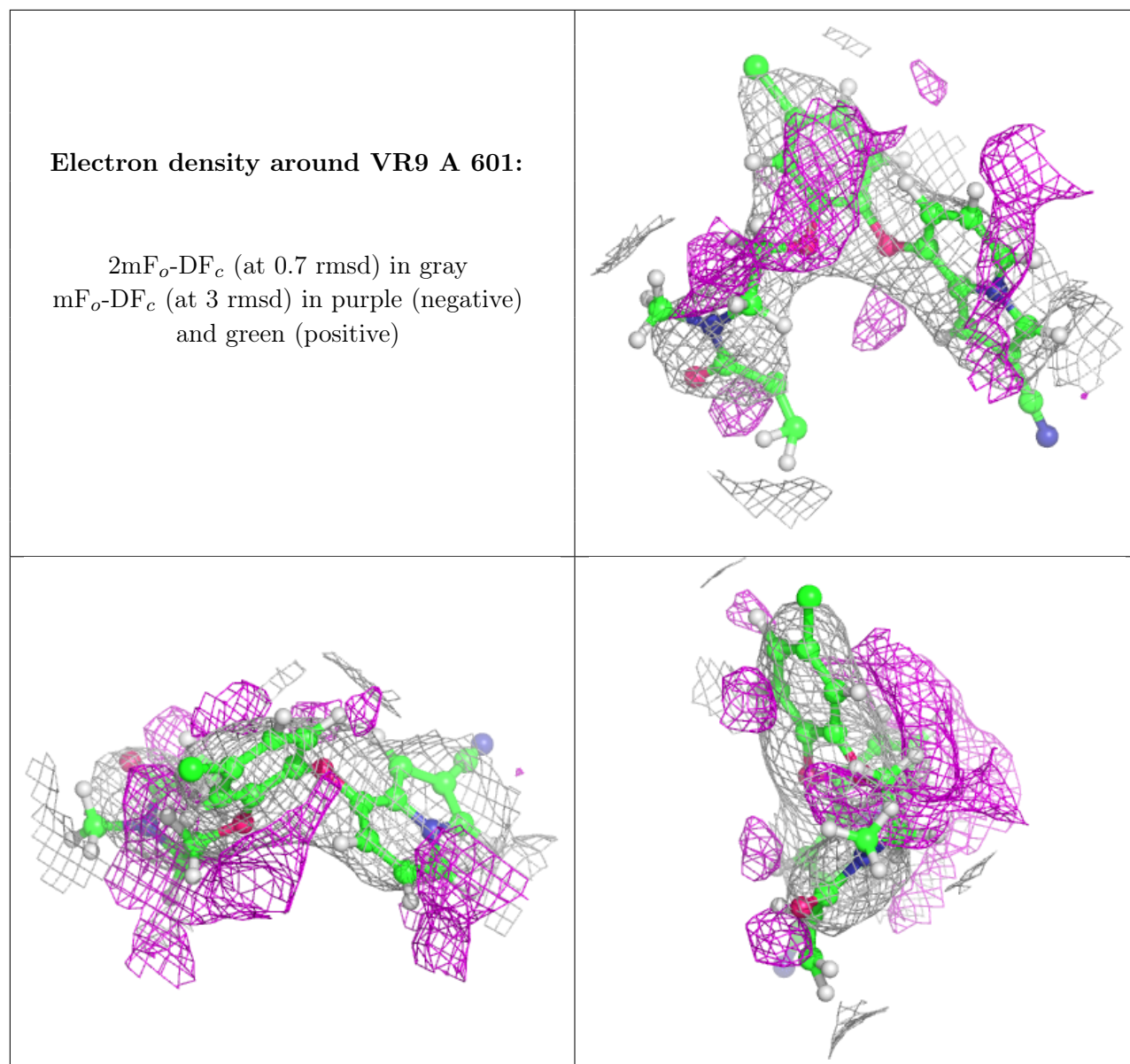
There are no monosaccharides in this entry.

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	MG	B	501	1/1	0.85	0.24	84,84,84,84	0
3	VR9	A	601	28/28	0.92	0.40	80,93,110,183	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.