



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:25 PM UTC

PDB ID : 8U6F / pdb_00008u6f
Title : Crystal Structure of HIV-1 Reverse Transcriptase in Complex with N-(2-(5-chloro-2-(3-chloro-5-cyanophenoxy)phenoxy)ethyl)-N-methylacrylamide (JLJ742), a non-nucleoside inhibitor
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Deposited on : 2023-09-13
Resolution : 2.69 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

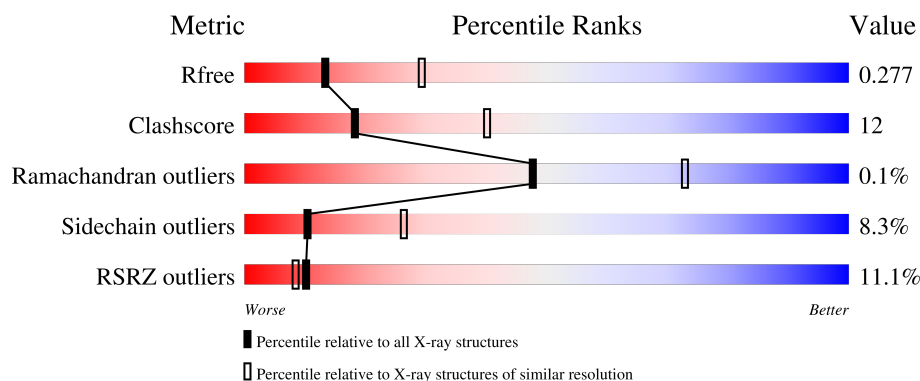
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.69 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	554	12% 71% 24% • •
2	B	428	9% 68% 26% • 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7356 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	546	Total	C	N	O	S	0	0	0
			4098	2632	689	769	8			

There are 5 discrepancies between the modelled and reference sequences:

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

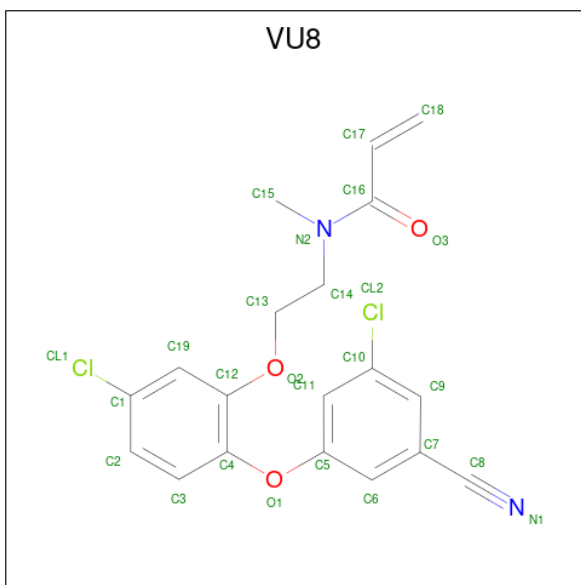
- Molecule 2 is a protein called p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	406	Total	C	N	O	S	0	1	0
			3215	2093	525	591	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-{2-[5-chloro-2-(3-chloro-5-cyanophenoxy)phenoxy]ethyl}-N-methylprop-2-enamide (CCD ID: VU8) (formula: C₁₉H₁₆Cl₂N₂O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	0	0
			26	19	2	2	3		

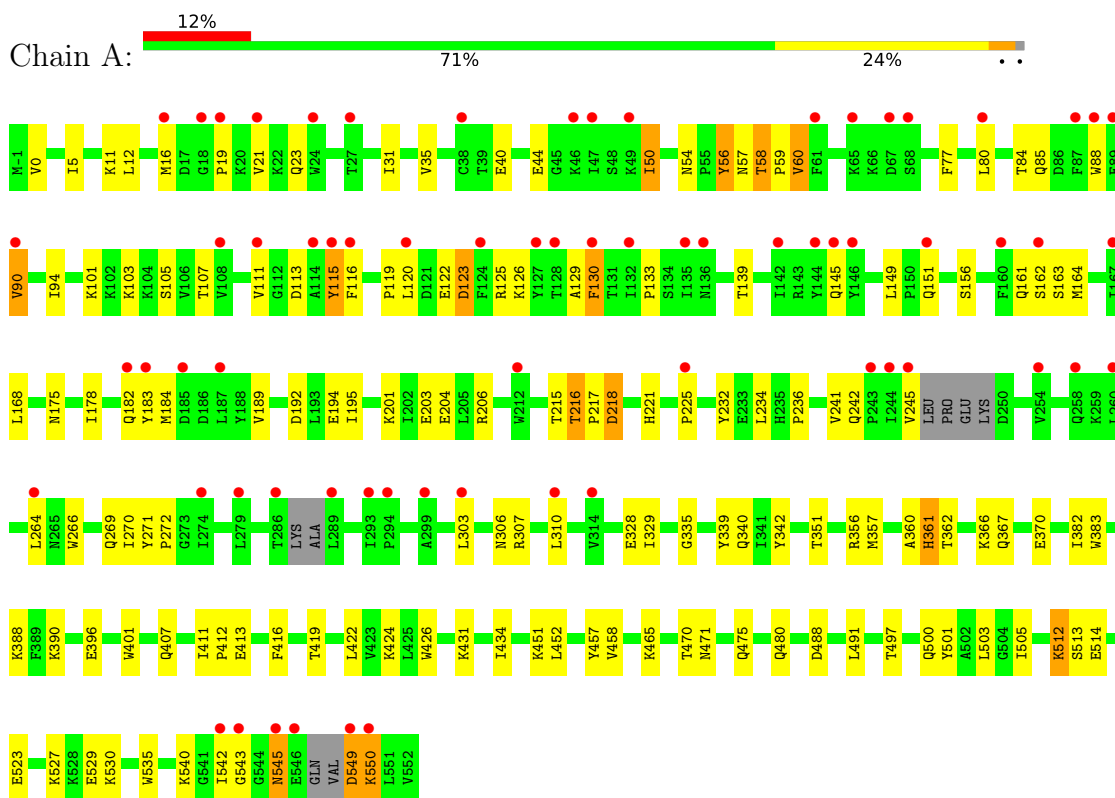
- Molecule 4 is water.

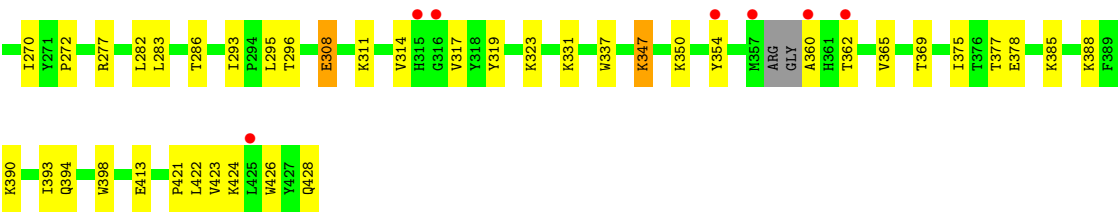
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	14	Total	O	0	0
			14	14		
4	B	3	Total	O	0	0
			3	3		

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





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	162.97Å 74.36Å 109.50Å 90.00° 99.89° 90.00°	Depositor
Resolution (Å)	35.96 – 2.69 35.96 – 2.69	Depositor EDS
% Data completeness (in resolution range)	99.6 (35.96-2.69) 99.6 (35.96-2.69)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 2.68Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487)	Depositor
R, R_{free}	0.235 , 0.284 0.244 , 0.277	Depositor DCC
R_{free} test set	1810 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	76.7	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 55.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7356	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.13% 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: VU8

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	0.51	0/4205	0.72	0/5756
2	B	0.47	0/3307	0.65	0/4516
All	All	0.49	0/7512	0.69	0/10272

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4098	0	3768	101	0
2	B	3215	0	3081	86	0
3	A	26	0	0	2	0
4	A	14	0	0	1	0
4	B	3	0	0	0	0
All	All	7356	0	6849	172	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 12.

All (172) 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:282:LEU:HD21	2:B:296:THR:HG23	1.35	1.06
1:A:182:GLN:HE21	2:B:140:PRO:HG3	1.23	0.97
1:A:182:GLN:NE2	2:B:140:PRO:HG3	1.89	0.86
2:B:308:GLU:HA	2:B:311:LYS:HE2	1.58	0.86
2:B:369:THR:HG22	2:B:398:TRP:CZ3	2.15	0.81
1:A:182:GLN:HE21	2:B:140:PRO:CG	1.94	0.79
2:B:277:ARG:H	2:B:277:ARG:HD2	1.48	0.79
2:B:388:LYS:HD2	2:B:413:GLU:HB2	1.69	0.75
1:A:542:ILE:HG23	2:B:283:LEU:HD13	1.69	0.75
2:B:282:LEU:HD21	2:B:296:THR:CG2	2.17	0.73
1:A:452:LEU:HD23	1:A:470:THR:HA	1.71	0.73
1:A:303:LEU:HA	1:A:306:ASN:HB2	1.73	0.71
1:A:122:GLU:HA	1:A:125:ARG:HG3	1.73	0.70
2:B:254:VAL:HG22	2:B:293:ILE:HD11	1.72	0.69
2:B:365:VAL:O	2:B:369:THR:HG23	1.95	0.67
2:B:23:GLN:HE21	2:B:133:PRO:HG3	1.60	0.67
2:B:39:THR:HG22	2:B:40:GLU:OE1	1.95	0.67
2:B:282:LEU:CD2	2:B:296:THR:HG23	2.19	0.66
1:A:458:VAL:HG22	2:B:286:THR:HG21	1.78	0.66
2:B:21:VAL:O	2:B:57:ASN:ND2	2.29	0.65
1:A:206:ARG:CZ	1:A:218:ASP:HB2	2.26	0.65
1:A:342:TYR:OH	1:A:390:LYS:NZ	2.25	0.65
1:A:113:ASP:OD2	1:A:215:THR:HB	1.97	0.64
1:A:88:TRP:HE1	1:A:90:VAL:HG23	1.62	0.63
2:B:180:ILE:HG12	2:B:189:VAL:HG12	1.81	0.62
1:A:12:LEU:HD23	1:A:84:THR:HA	1.80	0.62
1:A:90:VAL:HG11	2:B:140:PRO:HB3	1.80	0.61
2:B:79:GLU:HG3	2:B:83:ARG:HE	1.65	0.61
1:A:11:LYS:O	1:A:85:GLN:HB3	2.00	0.61
2:B:317:VAL:HG12	2:B:347:LYS:HB3	1.83	0.61
2:B:18:GLY:HA3	2:B:127:TYR:CD1	2.36	0.60
1:A:217:PRO:HB2	1:A:221:HIS:HB3	1.84	0.59
2:B:354[B]:TYR:HE2	2:B:375:ILE:HG13	1.68	0.59
1:A:366:LYS:O	1:A:370:GLU:HG3	2.03	0.58
1:A:503:LEU:HD22	1:A:535:TRP:HB2	1.84	0.58
2:B:47:ILE:HG22	2:B:146:TYR:HA	1.85	0.58
2:B:74:LEU:HD12	2:B:75:VAL:H	1.69	0.58
1:A:77:PHE:O	1:A:80:LEU:N	2.37	0.57
1:A:328:GLU:HG3	1:A:390:LYS:HB2	1.85	0.57
2:B:20:LYS:HE2	2:B:55:PRO:HB2	1.86	0.57
1:A:225:PRO:HB2	1:A:236:PRO:HD3	1.88	0.56
1:A:60:VAL:HG11	1:A:130:PHE:HD2	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:ILE:HG21	1:A:145:GLN:HG3	1.87	0.56
2:B:422:LEU:C	2:B:422:LEU:HD12	2.31	0.56
2:B:21:VAL:HB	2:B:59:PRO:HD3	1.88	0.55
2:B:393:ILE:HD13	2:B:398:TRP:HB2	1.88	0.55
1:A:543:GLY:HA2	2:B:283:LEU:O	2.06	0.55
2:B:163:SER:O	2:B:167:ILE:HG12	2.07	0.55
2:B:125:ARG:HB3	2:B:146:TYR:O	2.07	0.55
1:A:366:LYS:HE2	1:A:401:TRP:HH2	1.72	0.54
1:A:94:ILE:HG12	1:A:183:TYR:OH	2.07	0.54
1:A:58:THR:N	1:A:129:ALA:O	2.37	0.54
1:A:361:HIS:ND1	1:A:513:SER:OG	2.23	0.54
1:A:206:ARG:HD2	1:A:216:THR:OG1	2.07	0.54
1:A:21:VAL:O	1:A:57:ASN:ND2	2.31	0.54
2:B:182:GLN:HB2	2:B:187:LEU:HD12	1.89	0.54
1:A:103:LYS:H	3:A:601:VU8:C15	2.21	0.54
1:A:388:LYS:HE2	1:A:413:GLU:OE2	2.09	0.53
1:A:77:PHE:HB3	1:A:80:LEU:HB3	1.91	0.53
1:A:126:LYS:HA	1:A:145:GLN:OE1	2.09	0.52
1:A:491:LEU:HB3	1:A:529:GLU:HG3	1.92	0.52
1:A:120:LEU:HD12	1:A:149:LEU:HD23	1.90	0.52
1:A:175:ASN:O	1:A:178:ILE:HG12	2.10	0.52
2:B:40:GLU:OE1	2:B:40:GLU:N	2.43	0.52
1:A:360:ALA:O	1:A:514:GLU:HG2	2.10	0.51
2:B:232:TYR:HD1	2:B:233:GLU:N	2.08	0.51
2:B:120:LEU:H	2:B:125:ARG:HH21	1.58	0.51
1:A:126:LYS:HA	1:A:145:GLN:CD	2.36	0.50
2:B:232:TYR:HD1	2:B:233:GLU:H	1.58	0.50
2:B:44:GLU:OE1	2:B:46:LYS:HE3	2.11	0.50
1:A:21:VAL:HB	1:A:59:PRO:HD3	1.93	0.50
1:A:182:GLN:NE2	2:B:140:PRO:CG	2.65	0.50
1:A:201:LYS:HA	1:A:204:GLU:HG3	1.93	0.50
2:B:120:LEU:HD22	2:B:125:ARG:HG2	1.94	0.50
2:B:239:TRP:HB2	2:B:242:GLN:NE2	2.26	0.50
2:B:120:LEU:HD21	2:B:124:PHE:HB3	1.94	0.49
2:B:151:GLN:HB3	2:B:185:ASP:OD2	2.12	0.49
2:B:331:LYS:HB2	2:B:337:TRP:CZ3	2.47	0.49
1:A:340:GLN:HG3	1:A:351:THR:HG22	1.94	0.49
2:B:369:THR:HG22	2:B:398:TRP:HZ3	1.73	0.49
1:A:457:TYR:OH	1:A:488:ASP:OD2	2.26	0.49
2:B:150:PRO:HG2	2:B:153:TRP:HB2	1.93	0.49
1:A:266:TRP:O	1:A:269:GLN:HG2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:ILE:HG22	1:A:412:PRO:O	2.13	0.49
2:B:160:PHE:CD2	2:B:164:MET:HB2	2.48	0.49
1:A:5:ILE:O	1:A:119:PRO:HG2	2.13	0.48
1:A:120:LEU:HD23	1:A:125:ARG:HG2	1.95	0.48
1:A:480:GLN:NE2	4:A:701:HOH:O	2.46	0.48
2:B:107:THR:HA	2:B:232:TYR:O	2.13	0.48
1:A:40:GLU:O	1:A:44:GLU:HG3	2.14	0.48
2:B:106:VAL:HG22	2:B:190:GLY:HA3	1.96	0.47
1:A:543:GLY:H	2:B:283:LEU:HB3	1.79	0.47
2:B:319:TYR:OH	2:B:385:LYS:HE2	2.15	0.47
1:A:23:GLN:HG3	1:A:133:PRO:HG3	1.96	0.47
2:B:75:VAL:HB	2:B:77:PHE:CE2	2.50	0.47
1:A:162:SER:CB	2:B:52:PRO:HD3	2.44	0.47
1:A:424:LYS:HD3	1:A:426:TRP:CH2	2.50	0.47
1:A:116:PHE:CZ	1:A:151:GLN:HG3	2.50	0.47
1:A:549:ASP:HB3	1:A:550:LYS:HE3	1.97	0.47
1:A:103:LYS:HA	1:A:192:ASP:OD1	2.16	0.46
2:B:56:TYR:O	2:B:129:ALA:HB3	2.15	0.46
1:A:101:LYS:HE3	1:A:101:LYS:HB2	1.57	0.46
1:A:206:ARG:NH2	1:A:218:ASP:HB2	2.31	0.46
2:B:132:ILE:N	2:B:132:ILE:HD13	2.29	0.46
1:A:225:PRO:CB	1:A:236:PRO:HD3	2.46	0.46
2:B:112:GLY:HA3	2:B:185:ASP:HB3	1.97	0.46
1:A:232:TYR:C	1:A:242:GLN:HG3	2.41	0.46
1:A:451:LYS:O	1:A:471:ASN:N	2.49	0.46
1:A:183:TYR:CD2	1:A:184:MET:HG3	2.51	0.45
1:A:356:ARG:HG2	1:A:357:MET:O	2.16	0.45
1:A:269:GLN:HA	1:A:351:THR:O	2.16	0.45
1:A:512:LYS:HA	1:A:512:LYS:HD3	1.52	0.45
1:A:475:GLN:HG2	1:A:501:TYR:CD2	2.52	0.45
1:A:182:GLN:HG3	1:A:182:GLN:O	2.17	0.45
2:B:270:ILE:C	2:B:272:PRO:HD3	2.41	0.45
2:B:317:VAL:HG12	2:B:347:LYS:HD3	1.98	0.45
1:A:164:MET:O	1:A:168:LEU:HG	2.16	0.45
1:A:105:SER:OG	1:A:195:ILE:HD13	2.17	0.45
1:A:503:LEU:HA	1:A:503:LEU:HD12	1.73	0.45
2:B:57:ASN:HA	2:B:129:ALA:O	2.16	0.45
1:A:542:ILE:O	1:A:545:ASN:HB2	2.17	0.44
2:B:191:SER:HB2	2:B:193:LEU:HG	1.99	0.44
2:B:282:LEU:CD1	2:B:295:LEU:HD23	2.47	0.44
1:A:182:GLN:HE21	2:B:140:PRO:CD	2.30	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:360:ALA:C	2:B:362:THR:H	2.26	0.44
2:B:106:VAL:HA	2:B:190:GLY:HA2	1.99	0.44
2:B:421:PRO:HB2	2:B:423:VAL:HG22	1.99	0.44
1:A:422:LEU:HA	1:A:422:LEU:HD13	1.74	0.44
1:A:434:ILE:HD13	1:A:530:LYS:HB3	2.00	0.44
2:B:99:GLY:O	2:B:103:LYS:HG2	2.18	0.44
1:A:328:GLU:O	1:A:339:TYR:HA	2.17	0.44
1:A:120:LEU:H	1:A:125:ARG:HH21	1.66	0.44
2:B:354[B]:TYR:CE2	2:B:375:ILE:HG13	2.51	0.44
2:B:18:GLY:HA3	2:B:127:TYR:HD1	1.79	0.43
1:A:221:HIS:CD2	1:A:221:HIS:C	2.96	0.43
2:B:42:GLU:OE2	2:B:49:LYS:HG3	2.17	0.43
1:A:356:ARG:HD3	1:A:367:GLN:NE2	2.32	0.43
2:B:393:ILE:HG21	2:B:398:TRP:HB2	2.01	0.43
1:A:54:ASN:OD1	1:A:56:TYR:HD1	2.01	0.43
1:A:416:PHE:HE1	1:A:422:LEU:HD11	1.84	0.43
1:A:270:ILE:O	1:A:272:PRO:HD3	2.18	0.42
1:A:335:GLY:HA2	1:A:367:GLN:OE1	2.18	0.42
1:A:88:TRP:NE1	2:B:143:ARG:HD3	2.34	0.42
2:B:97:PRO:HG3	2:B:181:TYR:HB2	2.01	0.42
2:B:17:ASP:O	2:B:83:ARG:HD3	2.18	0.42
1:A:271:TYR:CE2	1:A:310:LEU:HD22	2.55	0.42
2:B:42:GLU:HA	2:B:47:ILE:O	2.20	0.42
1:A:542:ILE:O	1:A:543:GLY:C	2.63	0.42
2:B:17:ASP:OD1	2:B:56:TYR:OH	2.29	0.42
2:B:41:MET:HB3	2:B:47:ILE:HG12	2.01	0.41
1:A:303:LEU:HD11	1:A:307:ARG:CB	2.50	0.41
1:A:161:GLN:OE1	1:A:184:MET:HA	2.20	0.41
1:A:31:ILE:O	1:A:35:VAL:HG23	2.19	0.41
2:B:72:ARG:NH2	2:B:151:GLN:OE1	2.54	0.41
2:B:354[B]:TYR:OH	2:B:378:GLU:OE2	2.30	0.41
1:A:115:TYR:CE1	1:A:156:SER:HB3	2.56	0.41
2:B:74:LEU:HD12	2:B:75:VAL:N	2.35	0.41
1:A:236:PRO:HA	3:A:601:VU8:C17	2.51	0.41
1:A:382:ILE:HG22	1:A:383:TRP:CE2	2.55	0.41
2:B:423:VAL:HG12	2:B:426:TRP:CE3	2.56	0.41
1:A:123:ASP:OD2	1:A:123:ASP:N	2.53	0.41
1:A:540:LYS:HB2	1:A:542:ILE:HD12	2.03	0.41
2:B:422:LEU:CD1	2:B:426:TRP:CZ3	3.04	0.41
1:A:407:GLN:OE1	2:B:394:GLN:HG2	2.21	0.41
1:A:458:VAL:CG2	2:B:286:THR:HG21	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:500:GLN:OE1	2:B:422:LEU:HD21	2.20	0.41
2:B:16:MET:HE3	2:B:16:MET:HB2	1.79	0.40
1:A:203:GLU:O	1:A:204:GLU:C	2.64	0.40
1:A:50:ILE:HG21	1:A:145:GLN:CG	2.51	0.40
1:A:194:GLU:H	1:A:194:GLU:CD	2.26	0.40
1:A:264:LEU:HA	1:A:264:LEU:HD23	1.64	0.40
2:B:234:LEU:O	2:B:234:LEU:HD12	2.22	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	538/554 (97%)	500 (93%)	37 (7%)	1 (0%)	43	68
2	B	399/428 (93%)	378 (95%)	21 (5%)	0	100	100
All	All	937/982 (95%)	878 (94%)	58 (6%)	1 (0%)	48	73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	PRO

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	394/494 (80%)	359 (91%)	35 (9%)	9	23
2	B	331/390 (85%)	306 (92%)	25 (8%)	12	30
All	All	725/884 (82%)	665 (92%)	60 (8%)	10	26

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	VAL
1	A	16	MET
1	A	50	ILE
1	A	56	TYR
1	A	58	THR
1	A	60	VAL
1	A	90	VAL
1	A	107	THR
1	A	111	VAL
1	A	115	TYR
1	A	123	ASP
1	A	130	PHE
1	A	139	THR
1	A	163	SER
1	A	189	VAL
1	A	216	THR
1	A	218	ASP
1	A	234	LEU
1	A	241	VAL
1	A	245	VAL
1	A	329	ILE
1	A	361	HIS
1	A	362	THR
1	A	396	GLU
1	A	419	THR
1	A	431	LYS
1	A	465	LYS
1	A	497	THR
1	A	505	ILE
1	A	512	LYS
1	A	523	GLU
1	A	527	LYS
1	A	545	ASN
1	A	549	ASP
1	A	550	LYS

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Mol	Chain	Res	Type
2	B	7	THR
2	B	32	LYS
2	B	39	THR
2	B	42	GLU
2	B	60	VAL
2	B	63	ILE
2	B	64	LYS
2	B	82	LYS
2	B	94	ILE
2	B	101	LYS
2	B	118	VAL
2	B	131	THR
2	B	139	THR
2	B	154	LYS
2	B	163	SER
2	B	257	ILE
2	B	308	GLU
2	B	314	VAL
2	B	323	LYS
2	B	347	LYS
2	B	350	LYS
2	B	377	THR
2	B	390	LYS
2	B	424	LYS
2	B	428	GLN

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

Mol	Chain	Res	Type
1	A	137	ASN
1	A	182	GLN
1	A	336	GLN
1	A	545	ASN
2	B	175	ASN
2	B	182	GLN
2	B	208	HIS
2	B	258	GLN
2	B	361	HIS

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$
3	VU8	A	601	-	27,27,27	1.90	5 (18%)	36,36,36	1.52	4 (11%)

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	VU8	A	601	-	-	3/18/18/18	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	VU8	C16-N2	7.19	1.45	1.35
3	A	601	VU8	C7-C8	3.79	1.52	1.44
3	A	601	VU8	C10-CL2	2.26	1.79	1.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	VU8	C17-C16	2.12	1.55	1.49
3	A	601	VU8	C12-C4	-2.09	1.36	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	VU8	C17-C16-N2	4.17	126.15	117.94
3	A	601	VU8	O3-C16-N2	-3.06	114.44	121.57
3	A	601	VU8	C18-C17-C16	3.03	127.42	121.27
3	A	601	VU8	C13-C14-N2	-2.43	105.43	113.50

There are no chirality outliers.

All (3) torsion outliers are listed below:

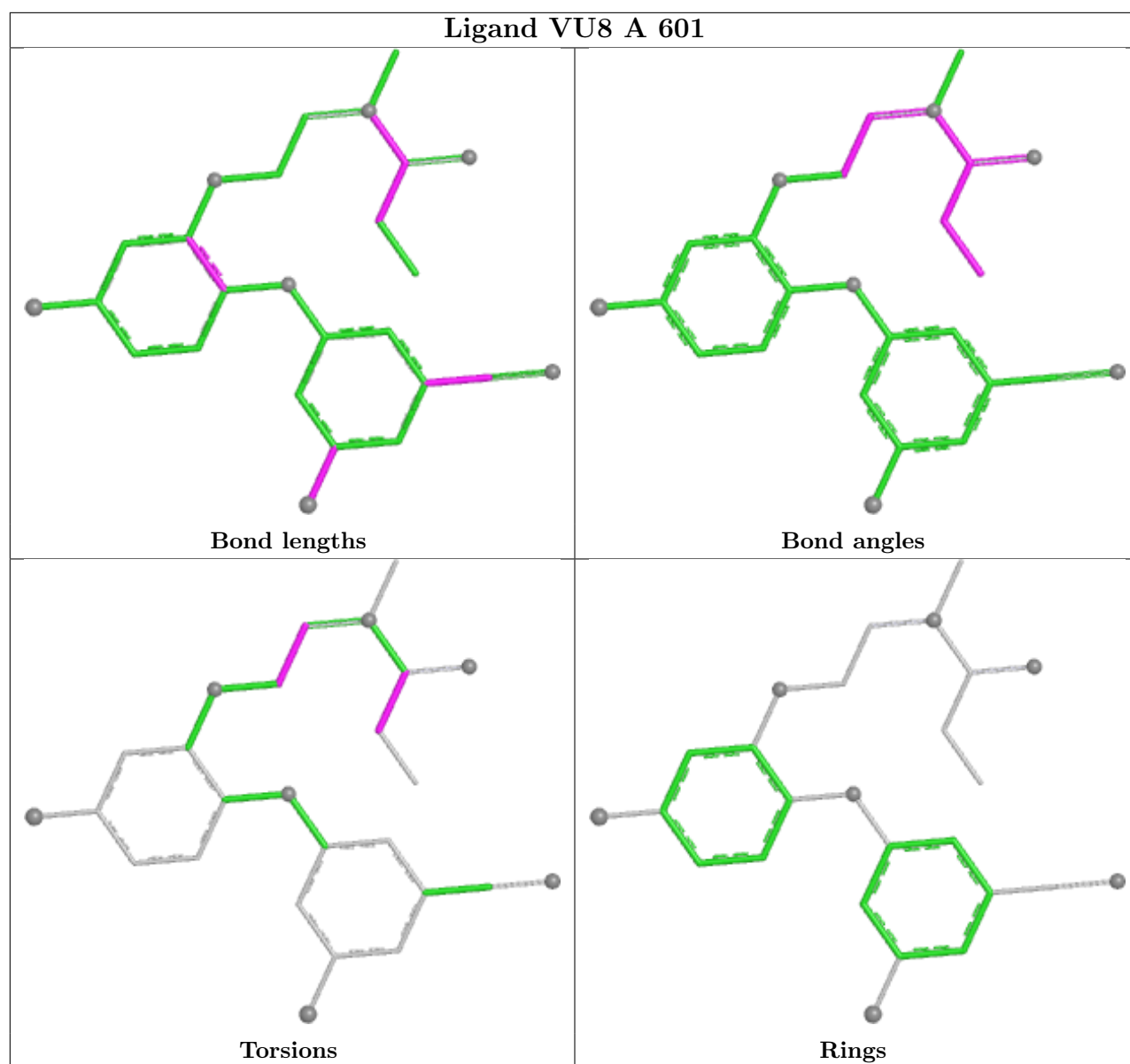
Mol	Chain	Res	Type	Atoms
3	A	601	VU8	N2-C16-C17-C18
3	A	601	VU8	O3-C16-C17-C18
3	A	601	VU8	O2-C13-C14-N2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	601	VU8	2	0

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	546/554 (98%)	0.77	69 (12%) 8 7	43, 92, 152, 162	0
2	B	406/428 (94%)	0.71	37 (9%) 15 12	37, 86, 143, 159	1 (0%)
All	All	952/982 (96%)	0.75	106 (11%) 10 8	37, 88, 147, 162	1 (0%)

All (106) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	232	TYR	5.1
2	B	150	PRO	5.0
1	A	146	TYR	4.8
2	B	362	THR	4.3
2	B	234	LEU	4.2
1	A	124	PHE	4.1
1	A	47	ILE	3.9
2	B	94	ILE	3.8
2	B	357	MET	3.7
1	A	142	ILE	3.6
2	B	124	PHE	3.6
2	B	149	LEU	3.5
2	B	354[A]	TYR	3.5
1	A	286	THR	3.4
1	A	289	LEU	3.4
1	A	160	PHE	3.4
1	A	128	THR	3.2
1	A	114	ALA	3.2
1	A	27	THR	3.1
2	B	128	THR	3.1
1	A	130	PHE	3.1
1	A	24	TRP	3.1
1	A	245	VAL	3.1
2	B	146	TYR	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	542	ILE	2.9
1	A	258	GLN	2.9
2	B	213	GLY	2.9
1	A	46	LYS	2.9
2	B	154	LYS	2.9
1	A	274	ILE	2.8
1	A	144	TYR	2.8
1	A	264	LEU	2.8
2	B	178	ILE	2.8
2	B	141	GLY	2.8
1	A	243	PRO	2.7
1	A	132	ILE	2.7
1	A	543	GLY	2.7
1	A	545	ASN	2.7
1	A	90	VAL	2.7
1	A	303	LEU	2.7
2	B	203	GLU	2.6
1	A	550	LYS	2.6
1	A	19	PRO	2.6
1	A	127	TYR	2.6
1	A	80	LEU	2.6
1	A	279	LEU	2.6
1	A	225	PRO	2.6
1	A	182	GLN	2.6
1	A	88	TRP	2.6
1	A	187	LEU	2.6
1	A	108	VAL	2.6
2	B	360	ALA	2.6
1	A	151	GLN	2.6
1	A	61	PHE	2.5
1	A	21	VAL	2.5
1	A	145	GLN	2.5
2	B	114	ALA	2.5
2	B	87	PHE	2.4
1	A	183	TYR	2.4
1	A	310	LEU	2.4
1	A	546	GLU	2.4
2	B	8	VAL	2.4
2	B	144	TYR	2.3
2	B	168	LEU	2.3
1	A	136	ASN	2.3
1	A	68	SER	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	229	TRP	2.3
1	A	115	TYR	2.3
2	B	248	GLU	2.3
2	B	425	LEU	2.3
1	A	299	ALA	2.3
1	A	185	ASP	2.3
2	B	68	SER	2.3
1	A	38	CYS	2.2
1	A	67	ASP	2.2
1	A	116	PHE	2.2
2	B	131	THR	2.2
1	A	260	LEU	2.2
1	A	254	VAL	2.2
1	A	16	MET	2.2
1	A	244	ILE	2.2
2	B	205	LEU	2.2
2	B	230	MET	2.2
1	A	293	ILE	2.2
2	B	198	HIS	2.2
1	A	49	LYS	2.2
1	A	65	LYS	2.2
2	B	316	GLY	2.2
1	A	135	ILE	2.2
1	A	167	ILE	2.2
1	A	162	SER	2.1
2	B	5	ILE	2.1
2	B	315	HIS	2.1
1	A	549	ASP	2.1
1	A	87	PHE	2.1
2	B	227	PHE	2.1
1	A	89	GLU	2.1
1	A	212	TRP	2.1
1	A	18	GLY	2.1
1	A	314	VAL	2.1
2	B	165	THR	2.0
2	B	171	PHE	2.0
1	A	294	PRO	2.0
1	A	120	LEU	2.0
2	B	210	LEU	2.0
1	A	111	VAL	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](#)

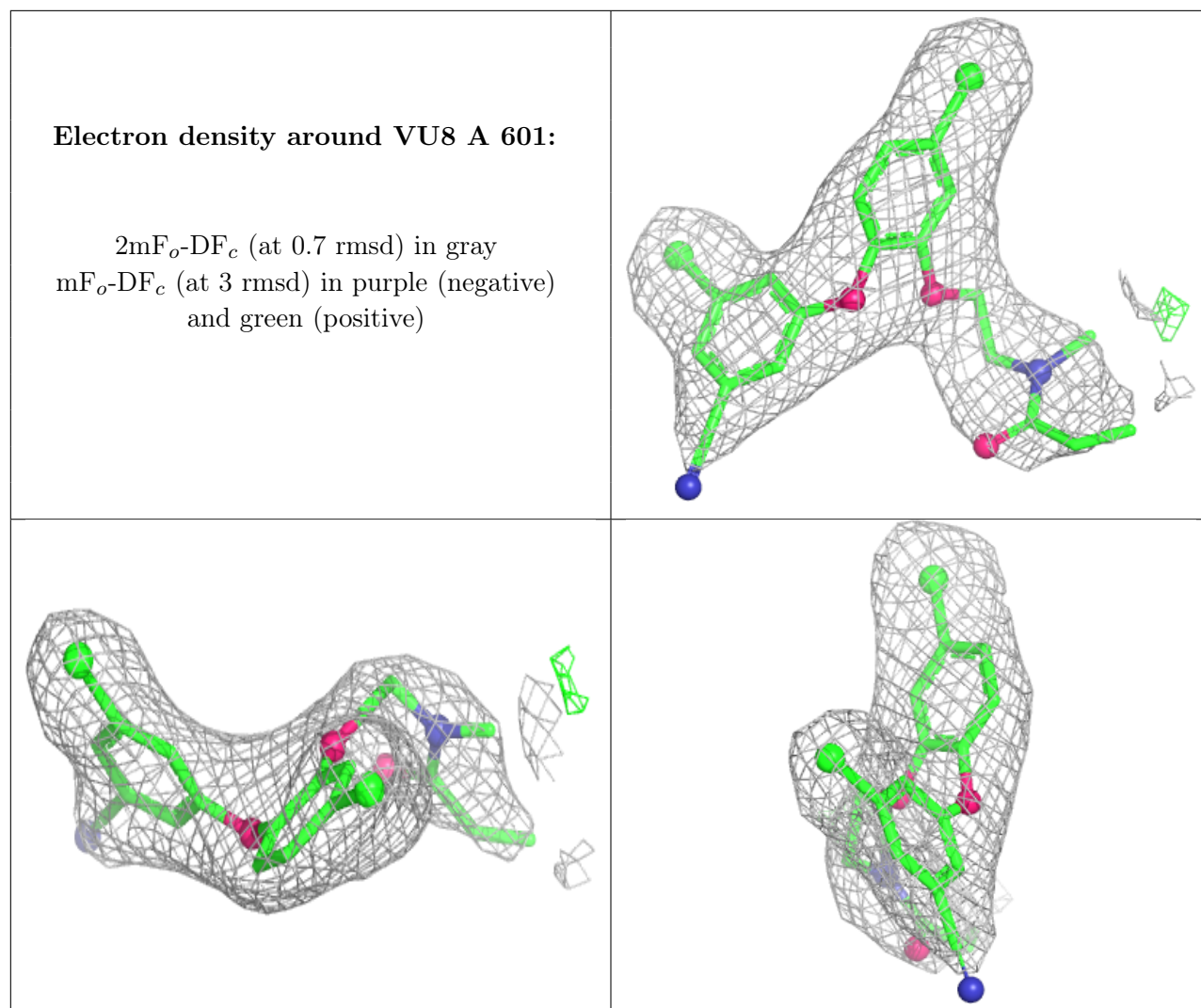
There are no oligosaccharides in this entry.

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
3	VU8	A	601	26/26	0.94	0.12	65,73,84,88	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.