



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 10, 2024 – 10:11 AM JST

PDB ID : 8X21
Title : HIV-1 reverse transcriptase mutant Q151M/Y115F/F116Y/L74V:DNA:ETV
-TP ternary complex
Authors : Yasutake, Y.; Hattori, S.I.; Mitsuya, H.
Deposited on : 2023-11-09
Resolution : 2.33 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)
Xtrriage (Phenix) : 1.13
EDS : 2.37.1
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) : 2.37.1

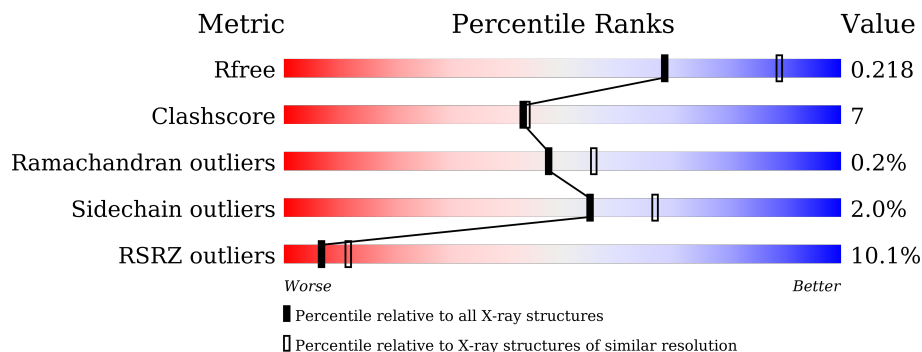
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.33 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	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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	 7% 83% 16% ..
1	C	557	 13% 82% 16% ..
2	B	444	 13% 74% 16% • 9%
2	D	444	 6% 78% 12% • 9%
3	E	38	 61% 24% 8% 8%
3	F	38	 3% 71% 24% 5%

2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 17751 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 Pol protein (Fragment).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	553	Total	C	N	O	S	0	0	0
			4497	2910	750	829	8			
1	C	553	Total	C	N	O	S	0	1	0
			4505	2915	751	830	9			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	initiating methionine	UNP D3XFN5
A	0	VAL	-	expression tag	UNP D3XFN5
A	74	VAL	LEU	engineered mutation	UNP D3XFN5
A	115	PHE	TYR	engineered mutation	UNP D3XFN5
A	116	TYR	PHE	engineered mutation	UNP D3XFN5
A	151	MET	GLN	engineered mutation	UNP D3XFN5
A	162	SER	CYS	engineered mutation	UNP D3XFN5
A	280	SER	CYS	engineered mutation	UNP D3XFN5
C	-1	MET	-	initiating methionine	UNP D3XFN5
C	0	VAL	-	expression tag	UNP D3XFN5
C	74	VAL	LEU	engineered mutation	UNP D3XFN5
C	115	PHE	TYR	engineered mutation	UNP D3XFN5
C	116	TYR	PHE	engineered mutation	UNP D3XFN5
C	151	MET	GLN	engineered mutation	UNP D3XFN5
C	162	SER	CYS	engineered mutation	UNP D3XFN5
C	280	SER	CYS	engineered mutation	UNP D3XFN5

- Molecule 2 is a protein called HIV-1 RT p51 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	406	Total	C	N	O	S	0	0	0
			3347	2178	557	606	6			
2	D	406	Total	C	N	O	S	0	0	0
			3347	2178	557	606	6			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	MET	-	expression tag	UNP P12497
B	-14	ALA	-	expression tag	UNP P12497
B	-13	HIS	-	expression tag	UNP P12497
B	-12	HIS	-	expression tag	UNP P12497
B	-11	HIS	-	expression tag	UNP P12497
B	-10	HIS	-	expression tag	UNP P12497
B	-9	HIS	-	expression tag	UNP P12497
B	-8	HIS	-	expression tag	UNP P12497
B	-7	ALA	-	expression tag	UNP P12497
B	-6	LEU	-	expression tag	UNP P12497
B	-5	GLU	-	expression tag	UNP P12497
B	-4	VAL	-	expression tag	UNP P12497
B	-3	LEU	-	expression tag	UNP P12497
B	-2	PHE	-	expression tag	UNP P12497
B	-1	GLN	-	expression tag	UNP P12497
B	0	GLY	-	expression tag	UNP P12497
B	162	SER	CYS	engineered mutation	UNP P12497
B	280	SER	CYS	engineered mutation	UNP P12497
D	-15	MET	-	expression tag	UNP P12497
D	-14	ALA	-	expression tag	UNP P12497
D	-13	HIS	-	expression tag	UNP P12497
D	-12	HIS	-	expression tag	UNP P12497
D	-11	HIS	-	expression tag	UNP P12497
D	-10	HIS	-	expression tag	UNP P12497
D	-9	HIS	-	expression tag	UNP P12497
D	-8	HIS	-	expression tag	UNP P12497
D	-7	ALA	-	expression tag	UNP P12497
D	-6	LEU	-	expression tag	UNP P12497
D	-5	GLU	-	expression tag	UNP P12497
D	-4	VAL	-	expression tag	UNP P12497
D	-3	LEU	-	expression tag	UNP P12497
D	-2	PHE	-	expression tag	UNP P12497
D	-1	GLN	-	expression tag	UNP P12497
D	0	GLY	-	expression tag	UNP P12497
D	162	SER	CYS	engineered mutation	UNP P12497
D	280	SER	CYS	engineered mutation	UNP P12497

- Molecule 3 is a DNA chain called DNA/RNA (38-MER).

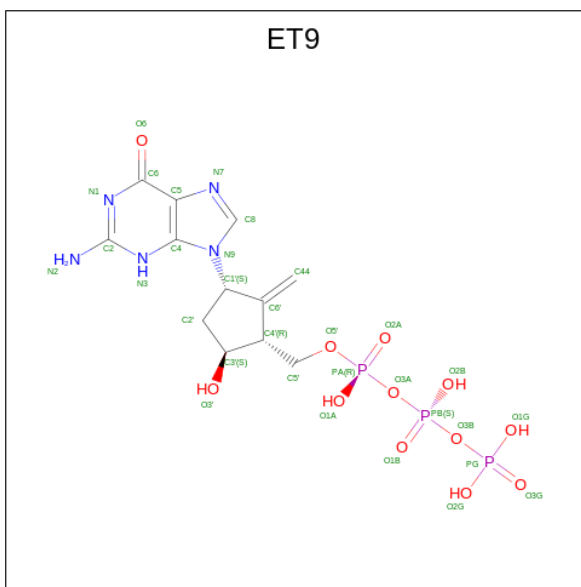
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	E	35	718	339	128	216	35	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	F	38	777	369	140	231	37	0	0	0

- Molecule 4 is [[(1R,3S,5S)-3-(2-azanyl-6-oxidanylidene-3H-purin-9-yl)-2-methylidene-5-oxidanyl-cyclopentyl]methoxy-oxidanyl-phosphoryl] phosphono hydrogen phosphate (three-letter code: ET9) (formula: C₁₂H₁₈N₅O₁₂P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	A	1	32	12	5	12	3	0	0
4	C	1	32	12	5	12	3	0	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
5	A	1	1	1	0	0
5	C	1	1	1	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 6 3 3	0	0
6	B	1	Total C O 6 3 3	0	0
6	E	1	Total C O 6 3 3	0	0
6	D	1	Total C O 6 3 3	0	0
6	D	1	Total C O 6 3 3	0	0
6	D	1	Total C O 6 3 3	0	0

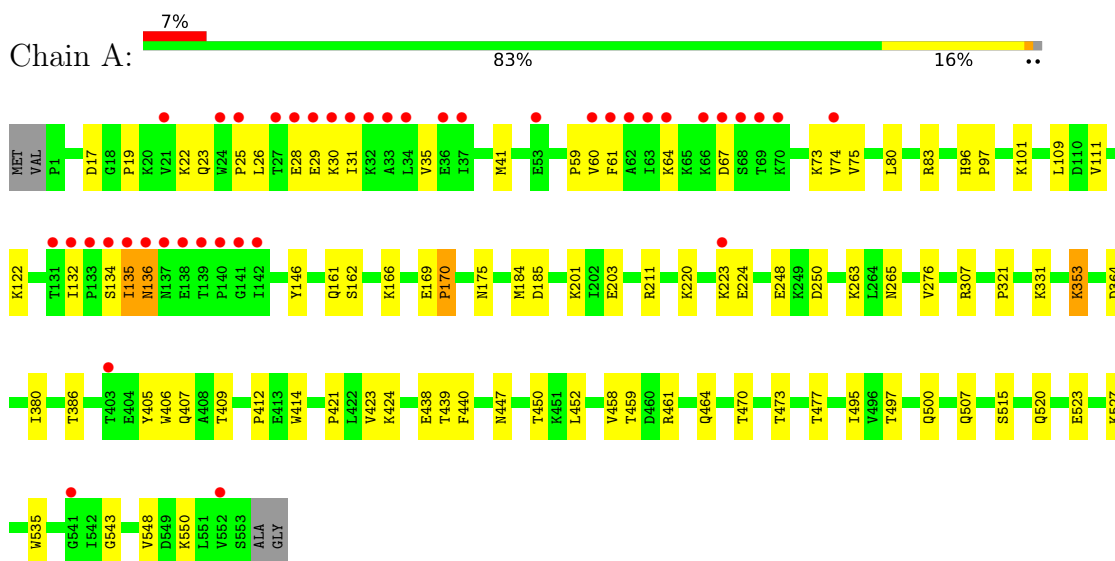
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	122	Total O 122 122	0	0
7	B	58	Total O 58 58	0	0
7	E	43	Total O 43 43	0	0
7	C	111	Total O 111 111	0	0
7	D	92	Total O 92 92	0	0
7	F	32	Total O 32 32	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.

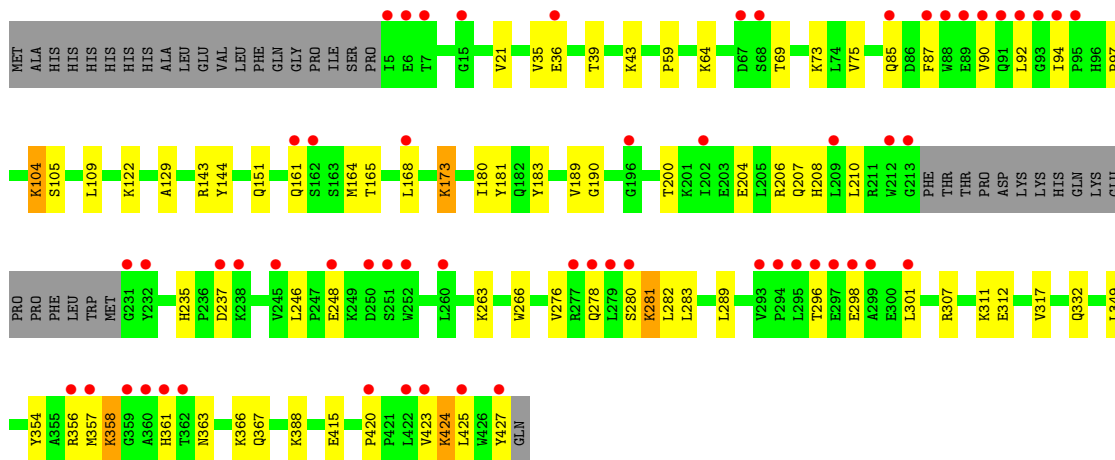
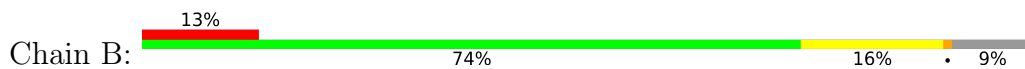
- Molecule 1: Pol protein (Fragment)



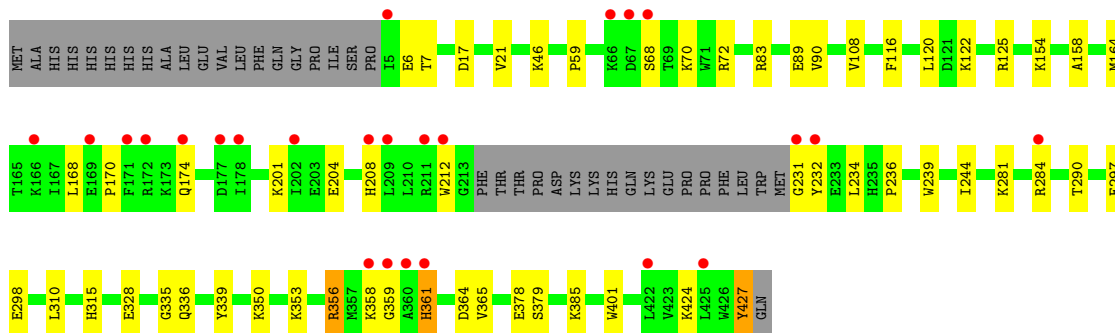
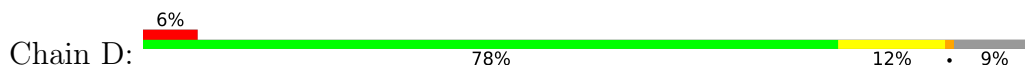
- Molecule 1: Pol protein (Fragment)



- Molecule 2: HIV-1 RT p51 subunit



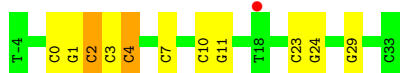
• Molecule 2: HIV-1 RT p51 subunit



• Molecule 3: DNA/RNA (38-MER)



• Molecule 3: DNA/RNA (38-MER)



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	284.45Å 284.45Å 95.73Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.67 – 2.33 48.67 – 2.33	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.67-2.33) 100.0 (48.67-2.33)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.34Å)	Xtrriage
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, R_{free}	0.175 , 0.218 0.175 , 0.218	Depositor DCC
R_{free} test set	6262 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	49.3	Xtrriage
Anisotropy	0.133	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 49.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.015 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	17751	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.19% 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: MG, OMC, ET9, GOL

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	0.62	2/4615 (0.0%)	0.64	2/6267 (0.0%)
1	C	0.57	1/4623 (0.0%)	0.64	1/6277 (0.0%)
2	B	0.54	1/3441 (0.0%)	0.64	1/4673 (0.0%)
2	D	0.58	0/3441	0.63	0/4673
3	E	1.36	6/756 (0.8%)	1.14	1/1165 (0.1%)
3	F	1.14	0/823	1.06	1/1269 (0.1%)
All	All	0.67	10/17699 (0.1%)	0.70	6/24324 (0.0%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	170	PRO	N-CA	12.35	1.68	1.47
1	C	139	THR	C-N	8.57	1.50	1.34
3	E	8	DT	C5-C7	6.92	1.54	1.50
3	E	5	DC	N1-C6	6.55	1.41	1.37
2	B	183	TYR	CD2-CE2	5.34	1.47	1.39
3	E	5	DC	C4-C5	5.33	1.47	1.43
3	E	3	DC	C3'-O3'	-5.19	1.37	1.44
1	A	169	GLU	C-N	5.17	1.44	1.34
3	E	5	DC	C3'-O3'	-5.13	1.37	1.44
3	E	27	DG	C3'-O3'	-5.00	1.37	1.44

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	133	PRO	N-CA-C	7.94	132.74	112.10
2	B	36	GLU	CA-CB-CG	-7.71	96.45	113.40
1	A	170	PRO	CA-N-CD	-6.12	102.93	111.50
1	A	170	PRO	N-CA-C	-5.58	97.58	112.10
3	F	7	DC	O5'-P-OP1	5.22	116.97	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	27	DG	O4'-C4'-C3'	-5.05	102.48	104.50

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	4497	0	4551	72	0
1	C	4505	0	4559	63	0
2	B	3347	0	3379	59	0
2	D	3347	0	3379	36	0
3	E	718	0	397	8	0
3	F	777	0	432	7	0
4	A	32	0	0	0	0
4	C	32	0	0	0	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
6	A	6	0	8	3	0
6	B	6	0	7	0	0
6	D	18	0	24	1	0
6	E	6	0	7	0	0
7	A	122	0	0	3	0
7	B	58	0	0	0	0
7	C	111	0	0	0	0
7	D	92	0	0	1	0
7	E	43	0	0	0	0
7	F	32	0	0	0	0
All	All	17751	0	16743	231	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 7.

All (231) 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:170:PRO:N	1:A:170:PRO:CA	1.68	1.35
1:C:26:LEU:HD11	1:C:31:ILE:HD12	1.12	1.11
2:B:248:GLU:HG2	2:B:307:ARG:NH2	1.75	1.00
1:A:439:THR:CG2	2:B:289:LEU:HD13	1.94	0.97
1:A:439:THR:HG21	2:B:289:LEU:HD13	1.47	0.93
1:C:26:LEU:HD11	1:C:31:ILE:CD1	2.00	0.91
1:A:31:ILE:HG21	1:A:134:SER:HA	1.53	0.88
1:C:67:ASP:OD1	1:C:70:LYS:HD2	1.73	0.88
1:C:26:LEU:CD1	1:C:31:ILE:HD12	2.01	0.86
2:B:248:GLU:HG2	2:B:307:ARG:HH22	1.35	0.85
1:A:439:THR:HG21	2:B:289:LEU:CD1	2.06	0.84
1:A:459:THR:HG22	1:A:461:ARG:H	1.39	0.84
1:C:31:ILE:HD11	1:C:133:PRO:HG2	1.59	0.84
1:C:60:VAL:HG12	1:C:75:VAL:HG22	1.60	0.83
2:B:87:PHE:HB3	2:B:92:LEU:HB2	1.61	0.82
6:A:603:GOL:H11	7:A:752:HOH:O	1.81	0.79
1:A:31:ILE:HD13	1:A:135:ILE:H	1.49	0.78
1:A:26:LEU:HD22	1:A:30:LYS:HE2	1.66	0.77
2:B:311:LYS:HG2	2:B:312:GLU:HG2	1.66	0.76
1:A:135:ILE:HG22	1:A:135:ILE:O	1.86	0.74
1:A:170:PRO:N	1:A:170:PRO:C	2.42	0.73
1:A:35:VAL:HG23	1:A:132:ILE:HD11	1.74	0.70
1:C:136:ASN:O	1:C:138:GLU:N	2.25	0.69
1:A:459:THR:CG2	1:A:461:ARG:H	2.06	0.69
2:B:388:LYS:NZ	2:B:415:GLU:OE1	2.26	0.69
2:B:85:GLN:O	2:B:85:GLN:HG3	1.92	0.68
1:A:459:THR:HG22	1:A:461:ARG:N	2.07	0.67
2:D:90:VAL:HG21	2:D:158:ALA:HA	1.77	0.67
1:A:439:THR:HG23	2:B:289:LEU:HD13	1.75	0.67
1:C:438:GLU:OE1	1:C:463:ARG:HD3	1.94	0.67
1:A:331:LYS:NZ	1:A:364:ASP:OD2	2.24	0.66
1:A:447:ASN:HB3	1:A:450:THR:HB	1.78	0.66
2:B:35:VAL:O	2:B:39:THR:HG23	1.94	0.66
1:A:26:LEU:HD22	1:A:30:LYS:CE	2.26	0.66
1:A:438:GLU:OE2	1:A:459:THR:HG21	1.95	0.66
1:A:31:ILE:CG2	1:A:134:SER:HA	2.24	0.65
1:A:161:GLN:NE2	1:A:184:MET:SD	2.69	0.64
1:C:343:GLN:HG3	1:C:349:LEU:HD11	1.79	0.64
2:B:298:GLU:CD	2:B:298:GLU:H	2.01	0.63
1:A:135:ILE:O	1:A:135:ILE:CG2	2.47	0.63
1:C:203:GLU:O	1:C:207:GLN:HG2	1.98	0.63
2:B:358:LYS:HZ1	2:B:367:GLN:HG3	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:VAL:HG11	3:E:0:DC:C2	2.34	0.62
1:A:439:THR:CG2	2:B:289:LEU:CD1	2.73	0.61
2:B:278:GLN:HE21	2:B:298:GLU:CB	2.13	0.61
3:F:3:DC:H2'	3:F:4:OMC:C6	2.36	0.61
2:D:232:TYR:CE1	2:D:234:LEU:HD21	2.37	0.60
1:A:223:LYS:HG3	1:A:224:GLU:HG2	1.84	0.59
1:C:208:HIS:HA	1:C:211:ARG:CZ	2.31	0.59
2:D:108:VAL:HG21	2:D:232:TYR:CZ	2.38	0.59
2:B:207:GLN:HA	2:B:210:LEU:HD12	1.85	0.58
1:C:31:ILE:CD1	1:C:133:PRO:HG2	2.32	0.58
3:F:1:DG:H2'	3:F:2:OMC:C6	2.39	0.58
2:B:85:GLN:HE22	2:B:90:VAL:HG21	1.67	0.58
1:A:184:MET:HG3	3:E:33:DC:H1'	1.86	0.57
3:E:23:DC:H2''	3:E:24:DG:C8	2.39	0.57
1:C:339:TYR:CZ	1:C:352:GLY:HA3	2.40	0.57
2:D:122:LYS:HG2	2:D:125:ARG:CZ	2.34	0.57
1:A:28:GLU:HG2	1:A:29:GLU:N	2.20	0.57
2:D:170:PRO:O	2:D:174:GLN:HG3	2.04	0.57
1:A:35:VAL:HG23	1:A:132:ILE:CD1	2.35	0.57
1:C:50:ILE:HD11	1:C:145:GLN:HB3	1.86	0.56
2:B:64:LYS:NZ	2:B:69:THR:HG22	2.19	0.56
1:C:331:LYS:NZ	1:C:364:ASP:OD1	2.32	0.56
1:A:405:TYR:CE2	1:A:407:GLN:HB2	2.41	0.56
2:B:278:GLN:HE21	2:B:298:GLU:HB2	1.71	0.55
1:A:543:GLY:HA3	2:B:283:LEU:O	2.06	0.55
1:A:458:VAL:HG22	1:A:548:VAL:HB	1.88	0.55
1:C:3:SER:HB2	1:C:212:TRP:O	2.07	0.55
2:B:424:LYS:HA	2:B:424:LYS:CE	2.37	0.55
1:C:435:ILE:HG13	2:D:290:THR:HG21	1.88	0.55
1:A:23:GLN:HA	1:A:59:PRO:HB3	1.89	0.54
1:C:417:VAL:HG22	1:C:419:THR:HG23	1.90	0.54
1:A:22:LYS:HD2	1:A:23:GLN:H	1.72	0.54
2:B:90:VAL:HG12	2:B:90:VAL:O	2.08	0.54
1:C:110:ASP:HB3	1:C:220:LYS:HD3	1.89	0.54
1:C:34:LEU:HD21	1:C:62:ALA:HB2	1.91	0.53
2:D:356:ARG:NH1	2:D:361:HIS:HB2	2.23	0.53
1:A:41:MET:HE1	1:A:73:LYS:HD2	1.91	0.53
2:B:332:GLN:OE1	2:B:424:LYS:HD2	2.08	0.53
1:C:396:GLU:CD	1:C:396:GLU:H	2.12	0.53
1:C:139:THR:O	1:C:139:THR:OG1	2.27	0.53
1:A:248:GLU:HG2	1:A:307:ARG:HH22	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:68:SER:OG	2:D:70:LYS:N	2.26	0.52
1:C:447:ASN:HB3	1:C:450:THR:HG22	1.92	0.52
1:C:30:LYS:HE3	1:C:62:ALA:H	1.74	0.52
1:A:31:ILE:CD1	1:A:135:ILE:H	2.21	0.52
1:A:17:ASP:O	1:A:83:ARG:HD3	2.09	0.51
1:A:440:PHE:HB2	1:A:495:ILE:CD1	2.40	0.51
6:D:503:GOL:H32	7:D:610:HOH:O	2.10	0.51
2:B:85:GLN:NE2	2:B:90:VAL:HG21	2.26	0.51
1:C:451:LYS:HD3	1:C:471:ASP:HA	1.93	0.51
3:E:1:DG:H2'	3:E:2:OMC:C6	2.45	0.51
1:A:364:ASP:HB3	1:A:423:VAL:HG13	1.92	0.50
1:A:111:VAL:HB	1:A:185:ASP:HB2	1.94	0.50
2:B:143:ARG:HG2	2:B:143:ARG:HH11	1.75	0.50
2:B:87:PHE:HD2	2:B:92:LEU:HD12	1.77	0.50
2:B:423:VAL:HB	2:B:425:LEU:CD2	2.42	0.50
2:B:94:ILE:HG12	2:B:161:GLN:NE2	2.26	0.50
2:D:358:LYS:HG2	2:D:359:GLY:N	2.27	0.50
1:A:73:LYS:HE2	1:A:146:TYR:OH	2.12	0.50
1:A:26:LEU:HD11	1:A:61:PHE:HA	1.93	0.50
1:C:30:LYS:NZ	1:C:61:PHE:HB2	2.27	0.49
1:C:450:THR:HG23	1:C:452:LEU:H	1.77	0.49
1:A:162:SER:O	1:A:166:LYS:HG3	2.12	0.49
1:C:78:ARG:HE	3:F:0:DC:H5''	1.78	0.49
1:A:19:PRO:HG3	1:A:80:LEU:HB2	1.94	0.49
1:C:379:SER:OG	1:C:387:PRO:HD3	2.13	0.49
2:D:365:VAL:HG11	2:D:401:TRP:HB2	1.95	0.49
1:C:65:LYS:HD3	1:C:72:ARG:CZ	2.43	0.48
1:A:25:PRO:HA	1:A:136:ASN:OD1	2.13	0.48
2:D:46:LYS:HE3	2:D:116:PHE:CD2	2.48	0.48
1:C:320:ASP:OD2	1:C:322:SER:HB3	2.13	0.48
3:F:10:DC:H2''	3:F:11:DG:C8	2.49	0.48
2:B:73:LYS:HE2	2:B:75:VAL:HG23	1.95	0.48
2:D:244:ILE:HB	2:D:310:LEU:HD13	1.94	0.48
2:D:350:LYS:NZ	2:D:378:GLU:OE2	2.39	0.48
1:C:237:ASP:OD1	1:C:237:ASP:N	2.45	0.48
2:D:201:LYS:HA	2:D:204:GLU:HG3	1.95	0.48
1:A:380:ILE:HD11	1:A:386:THR:HG23	1.96	0.48
2:D:236:PRO:HA	2:D:239:TRP:CD2	2.49	0.48
1:A:23:GLN:OE1	1:A:60:VAL:HG12	2.14	0.47
1:C:181:TYR:HB2	1:C:188:TYR:HB3	1.97	0.47
2:B:180:ILE:HG12	2:B:189:VAL:HG22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:23:GLN:OE1	1:C:60:VAL:HG22	2.14	0.47
2:D:297:GLU:HG2	2:D:298:GLU:OE1	2.14	0.47
3:F:23:DC:H2"	3:F:24:DG:C8	2.50	0.47
2:B:317:VAL:HG12	2:B:349:LEU:HD23	1.95	0.47
2:B:237:ASP:OD1	2:B:237:ASP:O	2.32	0.47
1:A:23:GLN:OE1	1:A:59:PRO:HA	2.15	0.47
1:A:263:LYS:NZ	7:A:706:HOH:O	2.47	0.47
2:D:108:VAL:O	2:D:231:GLY:HA3	2.15	0.47
6:A:603:GOL:C1	7:A:752:HOH:O	2.52	0.46
1:C:448:ARG:NH2	1:C:474:ASN:HD21	2.14	0.46
2:B:280:SER:HB2	2:B:281:LYS:HE2	1.97	0.46
2:B:363:ASN:HB3	2:B:366:LYS:HB3	1.96	0.46
2:D:68:SER:OG	2:D:70:LYS:HB3	2.16	0.46
1:A:276:VAL:HG22	1:A:353:LYS:HE2	1.98	0.46
1:C:35:VAL:HG22	1:C:132:ILE:HG21	1.97	0.46
1:C:412:PRO:O	1:C:414:TRP:HD1	1.98	0.46
1:C:244:ILE:HD13	1:C:267:ALA:HB2	1.97	0.46
1:A:452:LEU:HD23	1:A:470:THR:HA	1.97	0.46
2:B:282:LEU:HD21	2:B:296:THR:HG23	1.97	0.46
1:C:473:THR:O	1:C:477:THR:HG23	2.15	0.46
1:C:78:ARG:O	1:C:82:LYS:HG3	2.16	0.46
2:D:68:SER:HG	2:D:70:LYS:H	1.60	0.46
2:D:164:MET:HE3	2:D:168:LEU:HG	1.97	0.46
1:A:31:ILE:HG12	1:A:134:SER:H	1.81	0.45
1:A:500:GLN:CD	1:A:500:GLN:H	2.19	0.45
1:A:67:ASP:OD2	1:A:220:LYS:HE2	2.16	0.45
1:A:248:GLU:HG2	1:A:307:ARG:NH2	2.31	0.45
1:A:458:VAL:HG12	1:A:464:GLN:HG2	1.99	0.45
2:B:266:TRP:CE3	2:B:425:LEU:HG	2.51	0.45
2:D:6:GLU:HG2	2:D:7:THR:N	2.31	0.45
1:C:76:ASP:OD1	1:C:78:ARG:HG3	2.16	0.45
2:D:281:LYS:HG2	2:D:284:ARG:HH21	1.83	0.44
1:C:96:HIS:CG	1:C:97:PRO:HD2	2.52	0.44
2:D:361:HIS:CD2	2:D:361:HIS:H	2.35	0.44
2:B:424:LYS:HA	2:B:424:LYS:HE2	1.99	0.44
2:D:17:ASP:O	2:D:83:ARG:HD3	2.18	0.44
2:D:232:TYR:CD1	2:D:234:LEU:HD21	2.51	0.44
1:A:175:ASN:HD21	1:A:201:LYS:NZ	2.16	0.44
2:B:423:VAL:HB	2:B:425:LEU:HD22	2.00	0.44
1:A:523:GLU:O	1:A:527:LYS:HG3	2.18	0.44
1:C:442:VAL:HB	1:C:481:ALA:HB1	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:129:ALA:HA	2:B:144:TYR:O	2.18	0.43
2:B:161:GLN:O	2:B:165:THR:HG23	2.18	0.43
2:D:120:LEU:HD23	2:D:125:ARG:HG2	1.99	0.43
1:A:497:THR:O	1:A:535:TRP:HA	2.18	0.43
2:B:64:LYS:CE	2:B:69:THR:HG22	2.48	0.43
2:B:276:VAL:O	2:B:280:SER:OG	2.35	0.43
1:A:64:LYS:HB3	1:A:64:LYS:HE2	1.71	0.43
2:B:200:THR:O	2:B:204:GLU:HG3	2.17	0.43
1:C:26:LEU:CD1	1:C:31:ILE:CD1	2.80	0.43
2:B:354:TYR:OH	2:B:356:ARG:HD2	2.17	0.43
2:B:357:MET:SD	2:B:361:HIS:CE1	3.11	0.43
1:C:475:GLN:HB3	1:C:501:TYR:CE2	2.53	0.43
1:A:96:HIS:CG	1:A:97:PRO:HD2	2.54	0.43
1:A:101:LYS:HE2	1:A:321:PRO:HG3	2.00	0.43
1:A:412:PRO:O	1:A:414:TRP:HD1	2.01	0.43
2:B:151:GLN:HE21	2:B:151:GLN:HB2	1.61	0.43
1:A:265:ASN:OD1	1:A:353:LYS:HE3	2.19	0.42
1:C:450:THR:O	1:C:452:LEU:HD12	2.19	0.42
2:D:336:GLN:HG3	2:D:427:TYR:OH	2.19	0.42
2:D:379:SER:HB3	2:D:385:LYS:O	2.18	0.42
1:A:406:TRP:CZ2	2:B:420:PRO:HG3	2.54	0.42
2:B:280:SER:HB2	2:B:281:LYS:NZ	2.33	0.42
2:B:263:LYS:HB2	2:B:423:VAL:HG11	2.01	0.42
2:D:208:HIS:CE1	2:D:212:TRP:HE1	2.36	0.42
2:B:105:SER:O	2:B:190:GLY:HA2	2.18	0.42
2:D:336:GLN:OE1	2:D:353:LYS:HE3	2.19	0.42
1:A:409:THR:OG1	6:A:603:GOL:H31	2.20	0.42
3:E:3:DC:H2'	3:E:4:OMC:C6	2.54	0.42
1:C:28:GLU:N	1:C:28:GLU:OE1	2.52	0.42
1:A:61:PHE:HZ	3:E:0:DC:C6	2.36	0.42
2:B:21:VAL:HB	2:B:59:PRO:HD3	2.00	0.42
2:B:109:LEU:HD22	2:B:206:ARG:HE	1.84	0.42
1:C:125:ARG:HE	1:C:147:ASN:HA	1.83	0.42
2:D:335:GLY:HA3	2:D:356:ARG:HG2	2.01	0.42
3:F:4:OMC:HM23	3:F:4:OMC:H1'	1.82	0.42
1:C:172:ARG:NH2	1:C:180:ILE:HB	2.34	0.42
2:B:73:LYS:HE2	2:B:75:VAL:CG2	2.50	0.42
1:C:308:GLU:O	1:C:311:LYS:HG2	2.20	0.42
1:A:60:VAL:HB	1:A:75:VAL:HG22	2.02	0.42
1:A:74:VAL:HG11	3:E:0:DC:N1	2.35	0.42
2:B:246:LEU:HD12	2:B:307:ARG:HG2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:207:GLN:O	1:C:211:ARG:HG3	2.20	0.42
1:C:497:THR:O	1:C:535:TRP:HA	2.20	0.41
1:A:473:THR:O	1:A:477:THR:HG23	2.20	0.41
1:A:520:GLN:O	1:A:523:GLU:HG3	2.19	0.41
1:C:405:TYR:CE2	1:C:407:GLN:HB2	2.54	0.41
1:C:30:LYS:HB3	1:C:30:LYS:HE2	1.78	0.41
1:C:402:TRP:HE1	2:D:364:ASP:CG	2.23	0.41
2:B:97:PRO:HD3	2:B:181:TYR:CD1	2.55	0.41
1:C:110:ASP:HB3	1:C:220:LYS:HB3	2.02	0.41
1:C:454:LYS:HG3	1:C:552:VAL:HG13	2.02	0.41
1:A:353:LYS:NZ	3:E:7:DC:OP1	2.53	0.41
2:B:173:LYS:HA	2:B:173:LYS:HD3	1.79	0.41
2:B:104:LYS:O	2:B:235:HIS:ND1	2.36	0.41
1:C:169:GLU:N	1:C:170:PRO:HD2	2.36	0.41
1:A:421:PRO:HG2	1:C:301:LEU:HD23	2.02	0.41
2:B:39:THR:O	2:B:43:LYS:HG3	2.21	0.41
1:C:259:LYS:HG2	3:F:29:DG:O3'	2.21	0.41
1:C:31:ILE:HD11	1:C:133:PRO:CG	2.41	0.41
2:B:164:MET:O	2:B:168:LEU:HG	2.21	0.40
2:D:21:VAL:HB	2:D:59:PRO:HD3	2.02	0.40
1:C:281:LYS:HB3	1:C:281:LYS:HE3	1.92	0.40
2:D:424:LYS:HG2	2:D:424:LYS:O	2.21	0.40
1:C:215:THR:HG23	1:C:217:PRO:HD3	2.04	0.40
2:D:232:TYR:HE1	2:D:234:LEU:HD21	1.81	0.40
2:D:328:GLU:O	2:D:339:TYR:HA	2.21	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	551/557 (99%)	533 (97%)	16 (3%)	2 (0%)	34 38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	552/557 (99%)	528 (96%)	23 (4%)	1 (0%)	47	55
2	B	402/444 (90%)	386 (96%)	16 (4%)	0	100	100
2	D	402/444 (90%)	387 (96%)	15 (4%)	0	100	100
All	All	1907/2002 (95%)	1834 (96%)	70 (4%)	3 (0%)	47	55

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	137	ASN
1	A	135	ILE
1	A	136	ASN

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	492/494 (100%)	482 (98%)	10 (2%)	55	66
1	C	493/494 (100%)	485 (98%)	8 (2%)	62	74
2	B	365/400 (91%)	356 (98%)	9 (2%)	47	58
2	D	365/400 (91%)	358 (98%)	7 (2%)	57	68
All	All	1715/1788 (96%)	1681 (98%)	34 (2%)	55	66

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	109	LEU
1	A	122	LYS
1	A	203	GLU
1	A	211	ARG
1	A	250	ASP
1	A	353	LYS
1	A	424	LYS
1	A	507	GLN

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Mol	Chain	Res	Type
1	A	515	SER
1	A	550	LYS
2	B	104	LYS
2	B	122	LYS
2	B	173	LYS
2	B	208	HIS
2	B	281	LYS
2	B	301	LEU
2	B	358	LYS
2	B	424	LYS
2	B	427	TYR
1	C	31	ILE
1	C	32	LYS
1	C	66	LYS
1	C	184	MET
1	C	185	ASP
1	C	448	ARG
1	C	451	LYS
1	C	454	LYS
2	D	72	ARG
2	D	89	GLU
2	D	154	LYS
2	D	315	HIS
2	D	356	ARG
2	D	361	HIS
2	D	427	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	174	GLN
1	A	175	ASN
1	A	221	HIS
1	A	373	GLN
1	A	464	GLN
2	B	151	GLN
2	B	161	GLN
2	B	182	GLN
2	B	278	GLN
1	C	174	GLN
1	C	221	HIS
1	C	330	GLN

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Mol	Chain	Res	Type
1	C	340	GLN
1	C	407	GLN
2	D	137	ASN
2	D	182	GLN
2	D	197	GLN
2	D	394	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

4 non-standard protein/DNA/RNA residues 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	OMC	E	2	3	19,22,23	2.47	8 (42%)	26,31,34	0.79	0
3	OMC	F	2	3	19,22,23	2.73	8 (42%)	26,31,34	1.07	1 (3%)
3	OMC	E	4	3	19,22,23	2.58	8 (42%)	26,31,34	0.94	1 (3%)
3	OMC	F	4	3	19,22,23	2.49	7 (36%)	26,31,34	0.64	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	OMC	E	2	3	-	1/9/27/28	0/2/2/2
3	OMC	F	2	3	-	0/9/27/28	0/2/2/2
3	OMC	E	4	3	-	0/9/27/28	0/2/2/2
3	OMC	F	4	3	-	0/9/27/28	0/2/2/2

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	2	OMC	C6-C5	6.28	1.49	1.35
3	F	4	OMC	C6-C5	5.85	1.48	1.35
3	E	4	OMC	C2-N3	5.43	1.47	1.36
3	E	4	OMC	C6-C5	5.11	1.46	1.35
3	F	2	OMC	C2-N3	5.02	1.46	1.36
3	E	2	OMC	C6-C5	4.81	1.46	1.35
3	F	4	OMC	C2-N3	4.78	1.46	1.36
3	F	2	OMC	C2-N1	4.66	1.50	1.40
3	E	2	OMC	C4-N3	4.56	1.43	1.34
3	E	4	OMC	C2-N1	4.33	1.49	1.40
3	F	2	OMC	C4-N3	4.26	1.43	1.34
3	E	2	OMC	C2-N1	4.20	1.49	1.40
3	E	2	OMC	C2-N3	3.98	1.44	1.36
3	F	4	OMC	C2-N1	3.92	1.48	1.40
3	F	4	OMC	C4-N3	3.74	1.42	1.34
3	E	4	OMC	C4-N3	3.56	1.41	1.34
3	E	4	OMC	C4-N4	3.48	1.42	1.33
3	F	4	OMC	C6-N1	3.46	1.46	1.38
3	E	4	OMC	C6-N1	3.33	1.46	1.38
3	E	2	OMC	C5-C4	3.29	1.50	1.42
3	F	2	OMC	C4-N4	3.26	1.41	1.33
3	F	2	OMC	C6-N1	3.20	1.45	1.38
3	E	2	OMC	C6-N1	3.09	1.45	1.38
3	E	2	OMC	C4-N4	2.92	1.40	1.33
3	F	2	OMC	O2-C2	-2.90	1.18	1.23
3	E	2	OMC	O2-C2	-2.74	1.18	1.23
3	F	2	OMC	C5-C4	2.59	1.48	1.42
3	E	4	OMC	C5-C4	2.56	1.48	1.42
3	F	4	OMC	O2-C2	-2.53	1.19	1.23
3	F	4	OMC	C5-C4	2.34	1.48	1.42
3	E	4	OMC	O2-C2	-2.33	1.19	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	2	OMC	O2-C2-N3	-2.66	118.00	122.33
3	E	4	OMC	C6-C5-C4	2.42	121.41	117.50

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	2	OMC	C1'-C2'-O2'-CM2

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	2	OMC	1	0
3	F	2	OMC	1	0
3	E	4	OMC	1	0
3	F	4	OMC	2	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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
6	GOL	B	501	-	5,5,5	1.71	2 (40%)	5,5,5	0.71	0
6	GOL	D	503	-	5,5,5	1.39	0	5,5,5	0.95	0
4	ET9	A	601	5	25,34,34	1.17	2 (8%)	28,54,54	1.87	6 (21%)
6	GOL	D	502	-	5,5,5	1.45	1 (20%)	5,5,5	1.32	1 (20%)
6	GOL	E	101	-	5,5,5	0.98	0	5,5,5	1.22	1 (20%)
6	GOL	D	501	-	5,5,5	0.93	0	5,5,5	0.94	0
4	ET9	C	601	5	25,34,34	1.02	2 (8%)	28,54,54	1.80	7 (25%)
6	GOL	A	603	-	5,5,5	0.14	0	5,5,5	0.69	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
6	GOL	B	501	-	-	2/4/4/4	-
6	GOL	D	503	-	-	3/4/4/4	-
4	ET9	A	601	5	-	6/18/38/38	0/3/3/3
6	GOL	D	502	-	-	3/4/4/4	-
6	GOL	E	101	-	-	4/4/4/4	-
6	GOL	D	501	-	-	0/4/4/4	-
4	ET9	C	601	5	-	3/18/38/38	0/3/3/3
6	GOL	A	603	-	-	2/4/4/4	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	601	ET9	C6-N1	-2.57	1.33	1.39
6	B	501	GOL	O2-C2	-2.55	1.35	1.43
4	A	601	ET9	C4'-C6'	-2.54	1.48	1.51
4	C	601	ET9	C6-N1	-2.48	1.33	1.39
6	D	502	GOL	C1-C2	2.29	1.61	1.51
6	B	501	GOL	C1-C2	2.17	1.60	1.51
4	C	601	ET9	C2'-C1'	-2.03	1.52	1.54

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	601	ET9	C2'-C1'-N9	-5.72	105.05	114.73
4	A	601	ET9	C2'-C1'-N9	-5.49	105.44	114.73
4	A	601	ET9	PB-O3B-PG	-3.95	119.26	132.83
4	A	601	ET9	C4'-C6'-C44	-3.70	121.30	127.72
4	A	601	ET9	C4'-C6'-C1'	3.46	115.32	105.76
4	C	601	ET9	C4'-C6'-C44	-3.37	121.89	127.72
4	C	601	ET9	PB-O3B-PG	-3.33	121.40	132.83
4	C	601	ET9	C4'-C6'-C1'	3.13	114.41	105.76
4	C	601	ET9	PB-O3A-PA	-2.44	124.46	132.83
6	D	502	GOL	C3-C2-C1	-2.41	102.33	111.70
4	C	601	ET9	C8-N7-C5	2.41	107.58	102.99
6	E	101	GOL	C3-C2-C1	-2.35	102.57	111.70
4	A	601	ET9	C8-N7-C5	2.29	107.35	102.99
4	A	601	ET9	C4-C5-C6	-2.18	116.34	121.16
4	C	601	ET9	C4-C5-C6	-2.04	116.63	121.16

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	601	ET9	C3'-C4'-C5'-O5'
4	A	601	ET9	C6'-C4'-C5'-O5'
4	A	601	ET9	C5'-O5'-PA-O1A
4	A	601	ET9	C5'-O5'-PA-O2A
6	A	603	GOL	C1-C2-C3-O3
6	D	503	GOL	O1-C1-C2-C3
6	B	501	GOL	O1-C1-C2-C3
6	E	101	GOL	O1-C1-C2-C3
6	E	101	GOL	C1-C2-C3-O3
6	D	502	GOL	O1-C1-C2-C3
6	E	101	GOL	O1-C1-C2-O2
6	A	603	GOL	O2-C2-C3-O3
6	D	503	GOL	O1-C1-C2-O2
6	D	502	GOL	O1-C1-C2-O2
6	D	503	GOL	O2-C2-C3-O3
4	C	601	ET9	C5'-O5'-PA-O3A
6	E	101	GOL	O2-C2-C3-O3
4	C	601	ET9	C5'-O5'-PA-O2A
4	A	601	ET9	PA-O3A-PB-O2B
4	C	601	ET9	PA-O3A-PB-O2B
6	D	502	GOL	C1-C2-C3-O3
4	A	601	ET9	C5'-O5'-PA-O3A
6	B	501	GOL	O1-C1-C2-O2

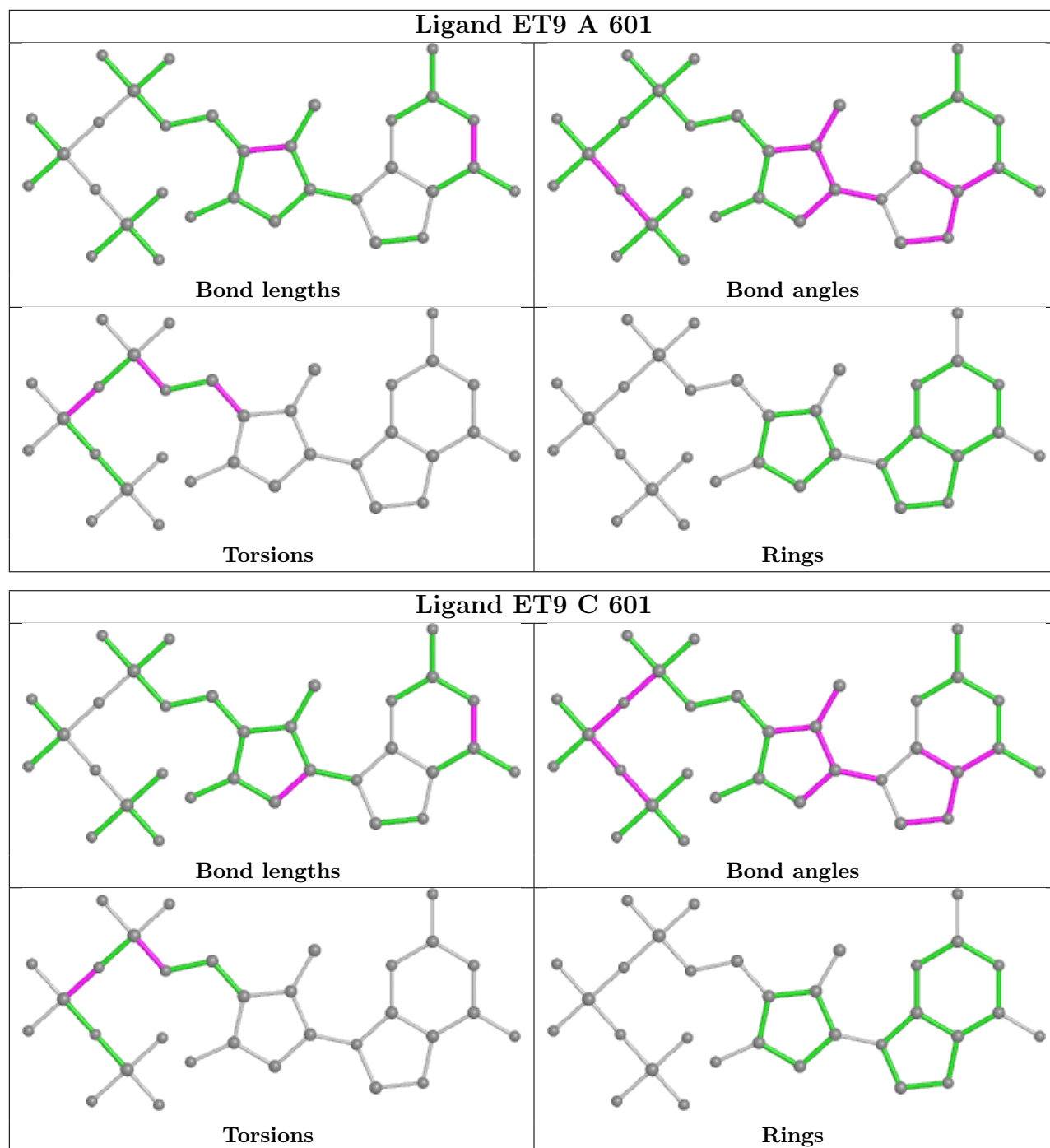
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	503	GOL	1	0
6	A	603	GOL	3	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

There are no chain breaks in this entry.

6 Fit of model and data i

6.1 Protein, DNA and RNA chains i

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	553/557 (99%)	0.51	41 (7%) 14 21	32, 55, 101, 170	0
1	C	553/557 (99%)	0.81	75 (13%) 3 4	33, 60, 127, 181	0
2	B	406/444 (91%)	0.88	58 (14%) 2 4	35, 68, 128, 174	0
2	D	406/444 (91%)	0.45	25 (6%) 20 28	34, 55, 99, 163	0
3	E	33/38 (86%)	-0.12	0 100 100	35, 52, 85, 140	0
3	F	36/38 (94%)	0.05	1 (2%) 53 63	38, 65, 113, 168	0
All	All	1987/2078 (95%)	0.64	200 (10%) 7 11	32, 59, 118, 181	0

All (200) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	69	THR	11.5
2	B	360	ALA	11.2
1	C	133	PRO	10.9
2	B	88	TRP	10.2
1	A	133	PRO	10.2
1	A	140	PRO	10.1
1	C	67	ASP	9.3
2	B	301	LEU	9.2
1	C	140	PRO	9.0
1	C	132	ILE	8.9
1	C	135	ILE	8.7
1	A	137	ASN	8.6
2	D	360	ALA	8.2
2	B	90	VAL	8.2
1	C	26	LEU	8.2
1	A	66	LYS	7.7
1	A	68	SER	7.7
1	C	141	GLY	7.7
1	C	68	SER	7.6

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Mol	Chain	Res	Type	RSRZ
1	C	62	ALA	7.5
2	B	92	LEU	7.4
1	C	69	THR	7.4
1	A	132	ILE	7.4
2	B	91	GLN	7.3
2	B	93	GLY	7.2
1	A	33	ALA	7.2
2	B	357	MET	7.2
1	C	35	VAL	7.1
1	C	142	ILE	7.0
1	C	34	LEU	6.8
2	D	67	ASP	6.7
1	A	27	THR	6.7
2	D	231	GLY	6.7
1	C	50	ILE	6.7
2	B	212	TRP	6.6
1	C	134	SER	6.4
2	B	359	GLY	6.3
1	A	138	GLU	6.1
1	C	137	ASN	6.1
2	D	359	GLY	6.0
2	D	212	TRP	5.9
1	A	28	GLU	5.9
2	B	361	HIS	5.9
1	C	138	GLU	5.7
2	D	232	TYR	5.6
2	B	94	ILE	5.5
1	A	134	SER	5.5
1	C	70	LYS	5.4
1	A	139	THR	5.4
1	C	136	ASN	5.4
2	B	5	ILE	5.3
1	C	52	PRO	5.3
2	B	168	LEU	5.2
1	C	448	ARG	5.1
1	A	67	ASP	5.1
2	D	358	LYS	5.1
1	C	71	TRP	5.1
2	B	362	THR	5.1
1	C	553	SER	5.0
1	C	63	ILE	5.0
2	B	295	LEU	4.9

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Mol	Chain	Res	Type	RSRZ
1	C	139	THR	4.9
2	B	297	GLU	4.9
2	B	67	ASP	4.8
1	A	135	ILE	4.8
1	C	552	VAL	4.8
2	B	89	GLU	4.8
2	D	425	LEU	4.8
1	A	61	PHE	4.7
1	C	131	THR	4.6
1	A	25	PRO	4.6
1	A	34	LEU	4.6
1	C	32	LYS	4.6
2	D	5	ILE	4.5
2	D	68	SER	4.4
1	C	452	LEU	4.3
2	D	361	HIS	4.3
1	C	28	GLU	4.3
1	C	457	TYR	4.3
1	A	24	TRP	4.3
1	A	141	GLY	4.3
1	A	136	ASN	4.2
2	B	245	VAL	4.2
1	A	70	LYS	4.2
2	D	166	LYS	4.2
1	C	59	PRO	4.2
1	C	469	LEU	4.1
1	C	449	GLU	4.1
1	A	32	LYS	4.1
1	C	64	LYS	4.0
1	A	36	GLU	4.0
1	C	39	THR	4.0
1	A	142	ILE	3.9
1	A	62	ALA	3.9
1	C	25	PRO	3.9
1	C	550	LYS	3.8
1	C	37	ILE	3.8
2	B	6	GLU	3.8
2	B	68	SER	3.8
1	C	33	ALA	3.8
2	D	211	ARG	3.7
2	B	252	TRP	3.7
2	B	95	PRO	3.7

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Mol	Chain	Res	Type	RSRZ
1	C	27	THR	3.7
1	C	36	GLU	3.6
1	C	450	THR	3.6
1	C	51	GLY	3.6
2	B	296	THR	3.6
2	B	196	GLY	3.5
2	B	213	GLY	3.4
2	B	248	GLU	3.4
1	C	143	ARG	3.3
1	C	144	TYR	3.2
2	B	427	TYR	3.2
2	B	161	GLN	3.2
1	A	60	VAL	3.2
3	F	18	DT	3.2
1	C	24	TRP	3.1
1	C	49	LYS	3.1
2	B	298	GLU	3.1
1	C	74	VAL	3.0
2	B	278	GLN	3.0
2	B	279	LEU	3.0
1	C	54	ASN	2.9
1	C	55	PRO	2.9
2	D	66	LYS	2.9
2	B	232	TYR	2.9
1	C	61	PHE	2.9
1	C	30	LYS	2.9
1	A	63	ILE	2.8
2	B	251	SER	2.8
2	B	299	ALA	2.8
1	C	31	ILE	2.8
1	C	357[A]	MET	2.8
2	B	238	LYS	2.8
2	B	280	SER	2.8
2	B	250	ASP	2.8
1	C	60	VAL	2.8
1	C	15	GLY	2.7
2	D	174	GLN	2.7
2	D	172	ARG	2.7
1	C	451	LYS	2.7
1	C	29	GLU	2.7
1	A	21	VAL	2.7
2	B	356	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	29	GLU	2.6
1	C	65	LYS	2.6
1	C	130	PHE	2.6
2	B	87	PHE	2.6
1	C	56	TYR	2.6
1	C	75	VAL	2.6
1	C	17	ASP	2.6
1	C	53	GLU	2.5
1	A	37	ILE	2.5
1	C	551	LEU	2.5
1	A	131	THR	2.5
1	C	195	ILE	2.5
2	B	209	LEU	2.5
2	D	209	LEU	2.5
1	C	58	THR	2.5
1	C	41	MET	2.5
2	B	237	ASP	2.4
2	B	162	SER	2.4
1	A	64	LYS	2.4
2	D	208	HIS	2.4
1	A	31	ILE	2.4
2	B	202	ILE	2.4
1	C	447	ASN	2.4
1	C	116	TYR	2.4
2	B	422	LEU	2.4
1	A	403	THR	2.4
2	B	277	ARG	2.3
1	C	470	THR	2.3
2	B	85	GLN	2.3
1	C	66	LYS	2.3
2	B	260	LEU	2.3
2	B	7	THR	2.3
2	D	177	ASP	2.3
2	B	36	GLU	2.3
2	D	202	ILE	2.3
2	B	15	GLY	2.3
2	B	423	VAL	2.3
2	B	294	PRO	2.3
2	B	420	PRO	2.3
1	A	541	GLY	2.2
2	B	231	GLY	2.2
2	B	425	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	293	VAL	2.2
1	A	223	LYS	2.2
2	D	169	GLU	2.2
1	A	552	VAL	2.2
1	A	30	LYS	2.2
1	C	128	THR	2.1
2	D	422	LEU	2.1
1	A	53	GLU	2.1
2	D	171	PHE	2.1
1	A	74	VAL	2.1
2	D	284	ARG	2.0
2	D	178	ILE	2.0
1	C	104	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
3	OMC	E	2	21/22	0.97	0.19	33,39,42,48	0
3	OMC	F	2	21/22	0.97	0.16	48,53,58,61	0
3	OMC	E	4	21/22	0.98	0.20	28,35,42,46	0
3	OMC	F	4	21/22	0.98	0.19	32,40,45,50	0

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.

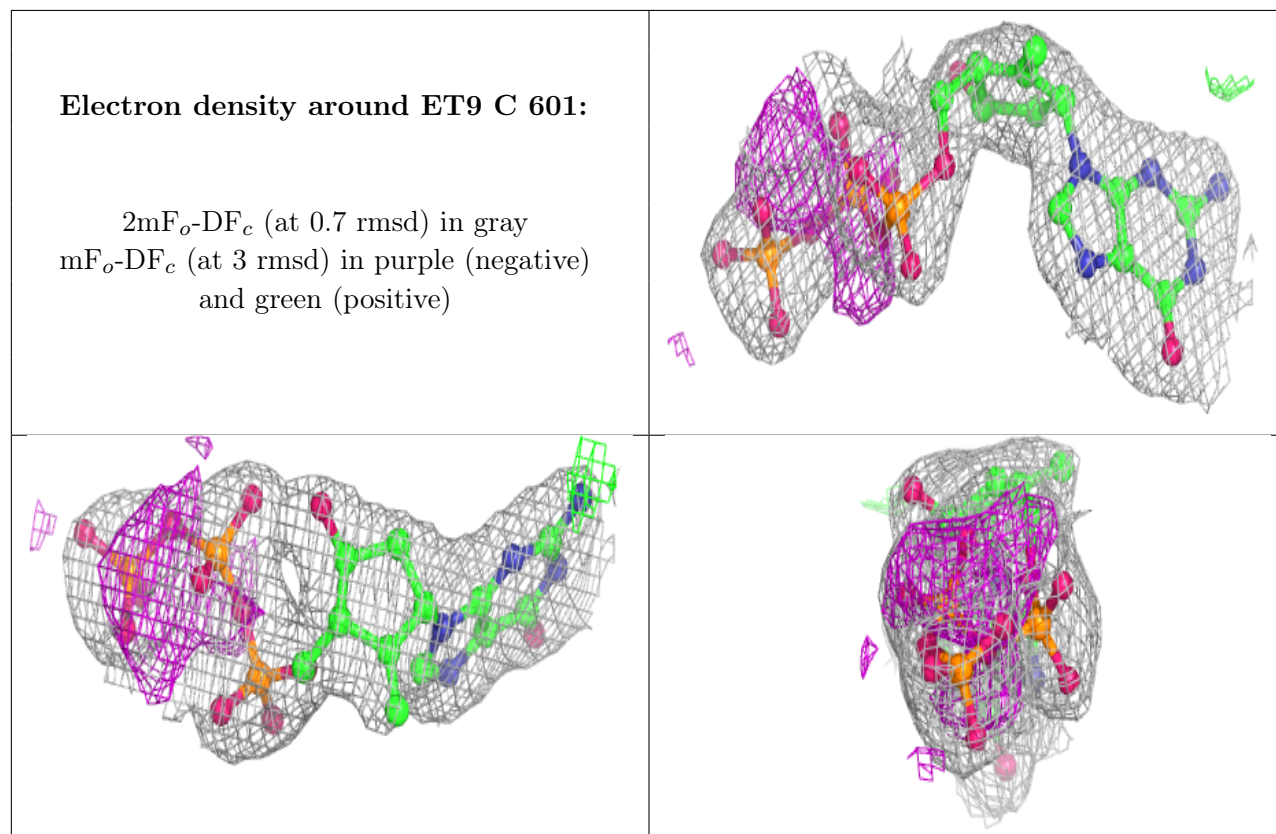
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	MG	C	602	1/1	0.64	0.26	65,65,65,65	0

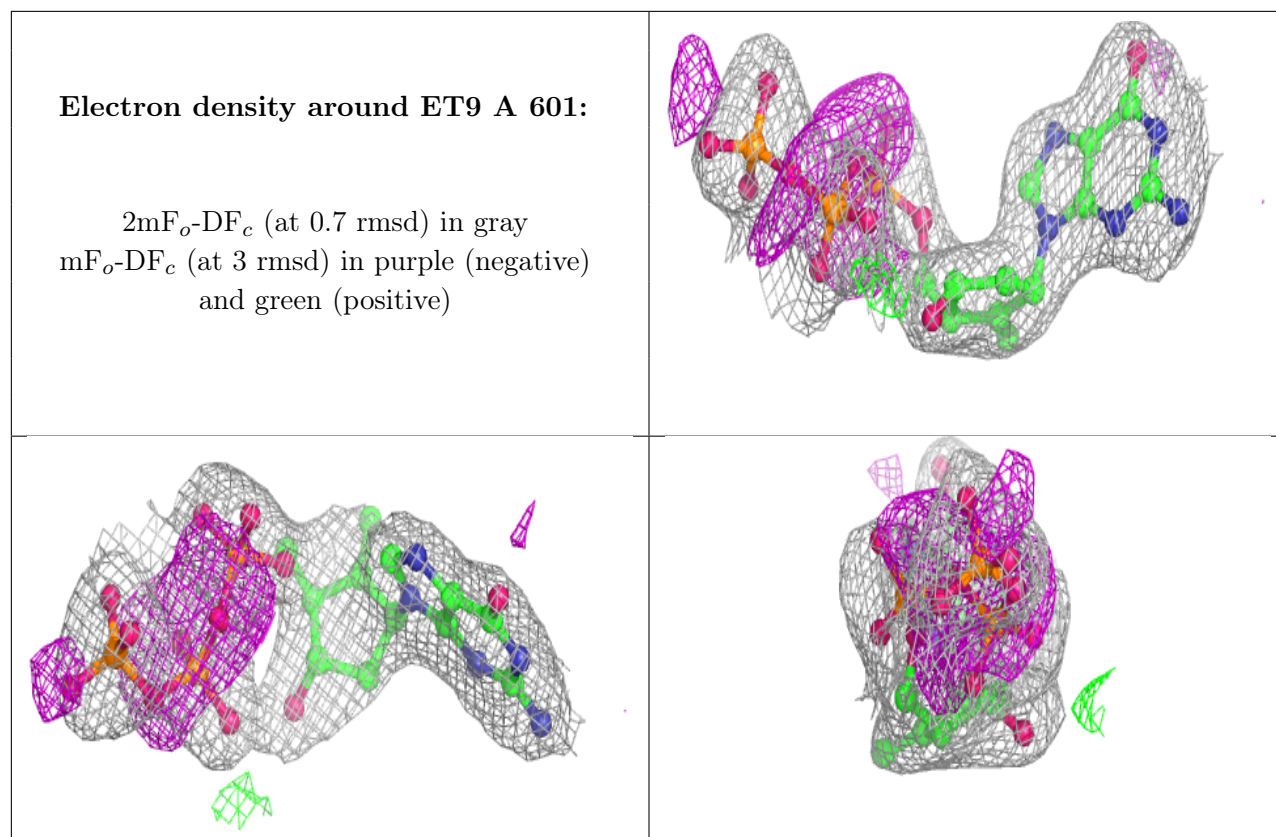
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	GOL	A	603	6/6	0.81	0.22	52,65,69,70	0
5	MG	A	602	1/1	0.82	0.07	61,61,61,61	0
4	ET9	C	601	32/32	0.86	0.16	66,73,93,96	0
4	ET9	A	601	32/32	0.86	0.16	47,63,87,94	0
6	GOL	E	101	6/6	0.92	0.30	59,67,68,70	0
6	GOL	D	503	6/6	0.93	0.19	50,59,61,64	0
6	GOL	D	501	6/6	0.95	0.20	39,43,47,48	0
6	GOL	D	502	6/6	0.95	0.19	49,52,54,55	0
6	GOL	B	501	6/6	0.95	0.26	44,46,51,53	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.