



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:54 PM UTC

PDB ID : 6AJJ / pdb_00006ajj
Title : Crystal structure of mycolic acid transporter MmpL3 from Mycobacterium smegmatis complexed with ICA38
Authors : Zhang, B.; Li, J.; Yang, X.L.; Wu, L.J.; Yang, H.T.; Rao, Z.H.
Deposited on : 2018-08-27
Resolution : 2.79 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

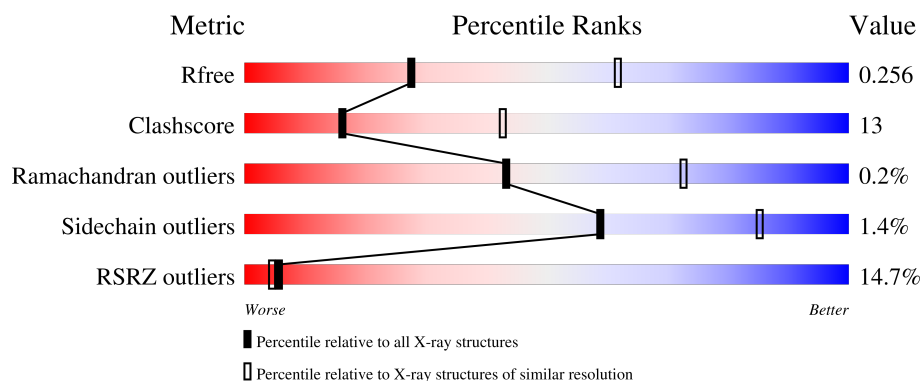
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.79 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	943	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MHA	A	1002	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7181 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 Drug exporters of the RND superfamily-like protein, Endolysin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	901	6955	4484	1182	1257	32	0	0	0

There are 37 discrepancies between the modelled and reference sequences:

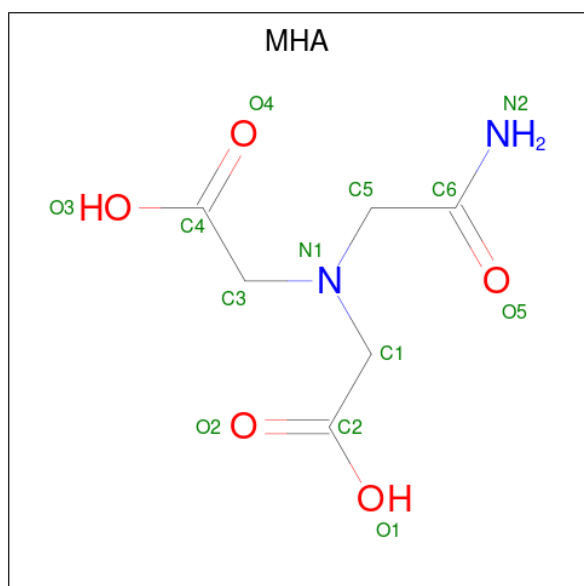
Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	MET	-	expression tag	UNP I7G2R2
A	-11	PRO	-	expression tag	UNP I7G2R2
A	-10	GLU	-	expression tag	UNP I7G2R2
A	-9	VAL	-	expression tag	UNP I7G2R2
A	-8	VAL	-	expression tag	UNP I7G2R2
A	-7	GLY	-	expression tag	UNP I7G2R2
A	-6	SER	-	expression tag	UNP I7G2R2
A	-5	TYR	-	expression tag	UNP I7G2R2
A	-4	PHE	-	expression tag	UNP I7G2R2
A	-3	GLN	-	expression tag	UNP I7G2R2
A	-2	SER	-	expression tag	UNP I7G2R2
A	-1	ASN	-	expression tag	UNP I7G2R2
A	0	ALA	-	expression tag	UNP I7G2R2
A	749	GLU	-	linker	UNP I7G2R2
A	750	PHE	-	linker	UNP I7G2R2
A	803	THR	CYS	engineered mutation	UNP D9IEF7
A	846	ALA	CYS	engineered mutation	UNP D9IEF7
A	911	GLU	-	expression tag	UNP D9IEF7
A	912	PHE	-	expression tag	UNP D9IEF7
A	913	HIS	-	expression tag	UNP D9IEF7
A	914	LEU	-	expression tag	UNP D9IEF7
A	915	GLY	-	expression tag	UNP D9IEF7
A	916	GLY	-	expression tag	UNP D9IEF7
A	917	ILE	-	expression tag	UNP D9IEF7
A	918	LYS	-	expression tag	UNP D9IEF7
A	919	ALA	-	expression tag	UNP D9IEF7
A	920	PHE	-	expression tag	UNP D9IEF7

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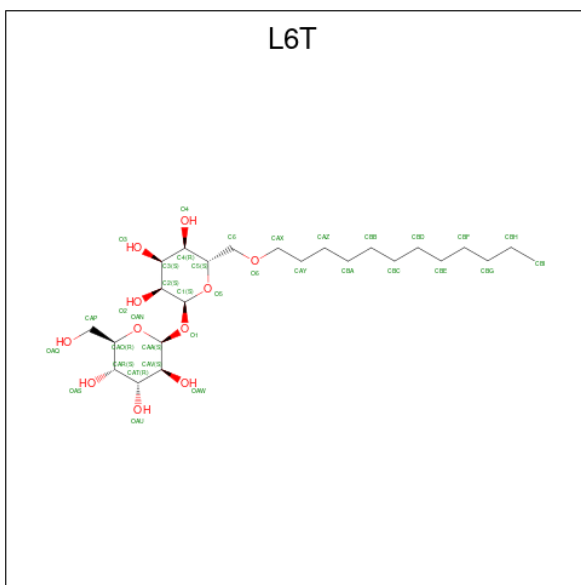
Chain	Residue	Modelled	Actual	Comment	Reference
A	921	HIS	-	expression tag	UNP D9IEF7
A	922	HIS	-	expression tag	UNP D9IEF7
A	923	HIS	-	expression tag	UNP D9IEF7
A	924	HIS	-	expression tag	UNP D9IEF7
A	925	HIS	-	expression tag	UNP D9IEF7
A	926	HIS	-	expression tag	UNP D9IEF7
A	927	HIS	-	expression tag	UNP D9IEF7
A	928	HIS	-	expression tag	UNP D9IEF7
A	929	HIS	-	expression tag	UNP D9IEF7
A	930	HIS	-	expression tag	UNP D9IEF7

- Molecule 2 is (CARBAMOYLMETHYL-CARBOXYMETHYL-AMINO)-ACETIC ACID (CCD ID: MHA) (formula: $C_6H_{10}N_2O_5$).



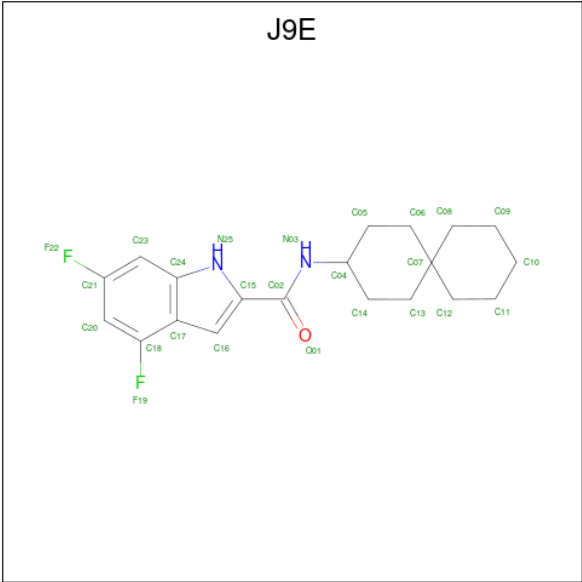
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			13	6	2	5		
2	A	1	Total	C	N	O	0	0
			13	6	2	5		

- Molecule 3 is alpha-D-glucopyranosyl 6-O-dodecyl-alpha-D-glucopyranoside (CCD ID: L6T) (formula: $C_{24}H_{46}O_{11}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 35	C 24	O 11	0	0
3	A	1	Total 35	C 24	O 11	0	0
3	A	1	Total 35	C 24	O 11	0	0
3	A	1	Total 35	C 24	O 11	0	0
3	A	1	Total 35	C 24	O 11	0	0

- Molecule 4 is 4,6-difluoro-N-(spiro[5.5]undecan-3-yl)-1H-indole-2-carboxamide (CCD ID: J9E) (formula: $\text{C}_{20}\text{H}_{24}\text{F}_2\text{N}_2\text{O}$).

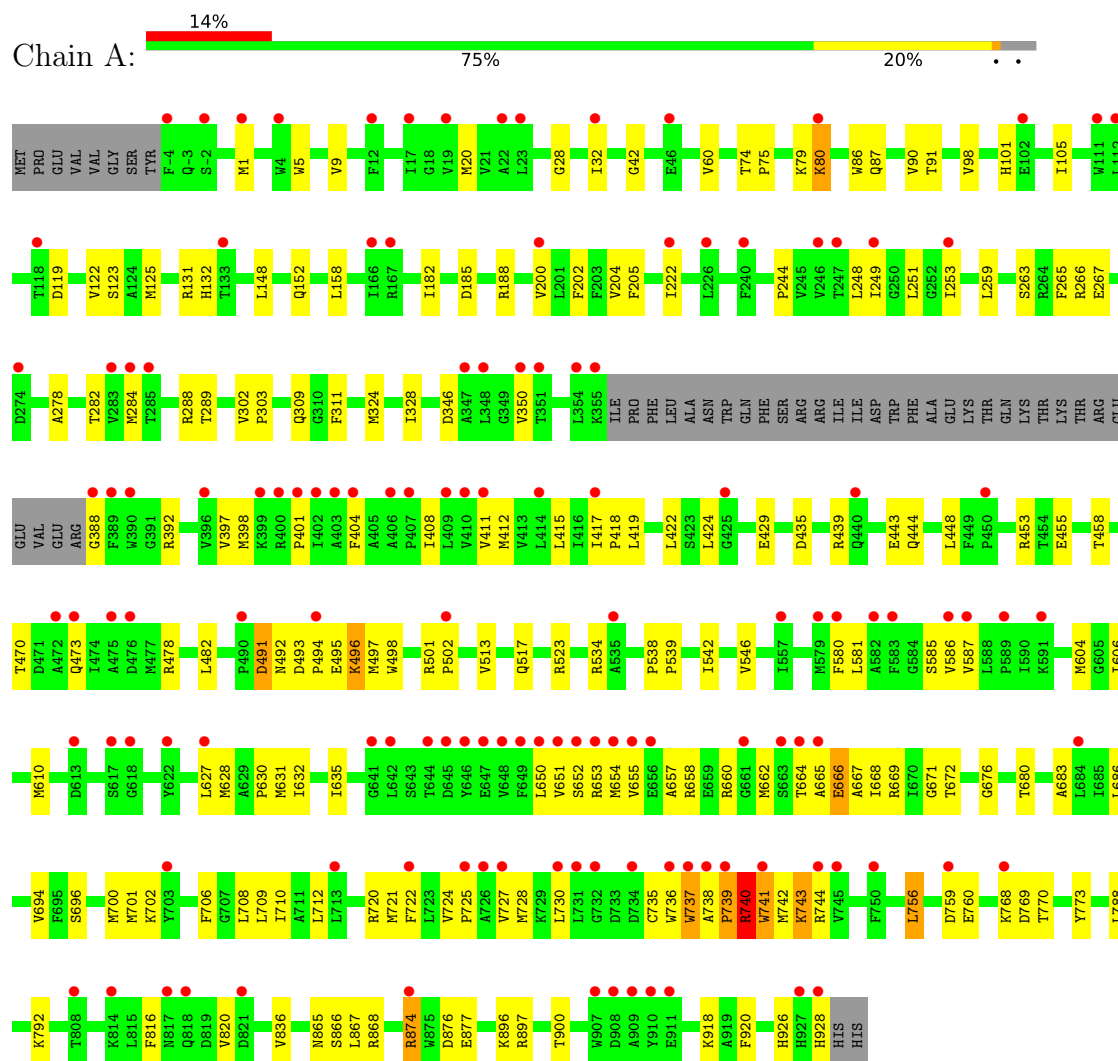


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	F	N	O	0	0
			25	20	2	2	1		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Drug exporters of the RND superfamily-like protein, Endolysin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.39Å 139.73Å 140.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.47 – 2.79 44.47 – 2.79	Depositor EDS
% Data completeness (in resolution range)	99.4 (44.47-2.79) 93.9 (44.47-2.79)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.218 , 0.253 0.225 , 0.256	Depositor DCC
R_{free} test set	2004 reflections (4.64%)	wwPDB-VP
Wilson B-factor (Å ²)	73.3	Xtriage
Anisotropy	0.455	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 29.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.014 for -h,l,k	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7181	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 3.25% 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: L6T, MHA, J9E

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	0.32	0/7099	0.54	3/9643 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	740	ARG	N-CA-C	7.94	122.74	112.41
1	A	80	LYS	CB-CG-CD	5.88	124.82	111.30
1	A	741	TRP	CB-CA-C	-5.36	110.37	116.54

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	6955	0	7120	183	0
2	A	26	0	16	8	0
3	A	175	0	0	14	0
4	A	25	0	0	1	0
All	All	7181	0	7136	187	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 13.

All (187) 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:740:ARG:CD	1:A:743:LYS:HG2	1.53	1.38
1:A:738:ALA:HB3	1:A:739:PRO:HD3	1.22	1.12
1:A:874:ARG:HH22	1:A:876:ASP:HB3	1.18	1.07
1:A:740:ARG:HD2	1:A:743:LYS:CG	1.84	1.06
1:A:740:ARG:HD2	1:A:743:LYS:HG2	0.99	0.99
1:A:740:ARG:HD3	1:A:743:LYS:HG2	1.48	0.96
1:A:740:ARG:CD	1:A:743:LYS:CG	2.41	0.95
1:A:738:ALA:CB	1:A:739:PRO:HD3	2.02	0.89
1:A:658:ARG:HG3	1:A:737:TRP:CZ2	2.09	0.87
1:A:866:SER:OG	2:A:1002:MHA:N2	2.08	0.85
1:A:122:VAL:HG22	3:A:1005:L6T:O4	1.77	0.84
1:A:493:ASP:OD1	1:A:494:PRO:HD2	1.82	0.80
1:A:651:VAL:HA	1:A:654:MET:HE2	1.65	0.78
1:A:655:VAL:HG12	1:A:736:TRP:CZ3	2.19	0.77
1:A:628:MET:HG3	1:A:630:PRO:HD2	1.67	0.76
1:A:289:THR:HB	3:A:1007:L6T:OAS	1.86	0.76
1:A:866:SER:CB	2:A:1002:MHA:N2	2.51	0.74
1:A:278:ALA:O	1:A:282:THR:HG23	1.88	0.73
1:A:655:VAL:HG12	1:A:736:TRP:HZ3	1.53	0.73
1:A:721:MET:HE3	1:A:722:PHE:HE1	1.55	0.71
1:A:680:THR:HG22	1:A:720:ARG:HH22	1.56	0.71
1:A:654:MET:HE1	1:A:728:MET:HE1	1.72	0.70
1:A:631:MET:HE3	1:A:700:MET:HB3	1.74	0.69
1:A:874:ARG:NH2	1:A:876:ASP:HB3	2.02	0.69
1:A:266:ARG:NH1	1:A:346:ASP:OD1	2.25	0.69
1:A:205:PHE:CZ	1:A:259:LEU:HD12	2.30	0.67
1:A:397:VAL:HG12	1:A:404:PHE:HD2	1.59	0.66
1:A:455:GLU:OE1	1:A:523:ARG:NE	2.28	0.66
1:A:60:VAL:HG21	1:A:513:VAL:HG11	1.77	0.66
1:A:586:VAL:HG22	1:A:739:PRO:HD2	1.76	0.66
1:A:652:SER:HB2	1:A:653:ARG:HH11	1.59	0.66
1:A:866:SER:H	2:A:1002:MHA:HN21	1.44	0.65
1:A:188:ARG:HD3	3:A:1004:L6T:O4	1.96	0.65
1:A:122:VAL:CG2	3:A:1005:L6T:O4	2.45	0.65
1:A:586:VAL:HG21	1:A:739:PRO:HG2	1.79	0.65
1:A:493:ASP:HB3	1:A:496:LYS:HB2	1.78	0.64
1:A:204:VAL:HG11	1:A:259:LEU:HD11	1.80	0.64
1:A:740:ARG:HD3	1:A:743:LYS:CG	2.21	0.64
1:A:439:ARG:O	1:A:443:GLU:HG3	1.99	0.63
1:A:740:ARG:O	1:A:741:TRP:C	2.40	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:478:ARG:NH1	1:A:498:TRP:O	2.30	0.62
1:A:288:ARG:CZ	3:A:1007:L6T:CAP	2.79	0.60
1:A:1:MET:SD	1:A:1:MET:N	2.69	0.60
1:A:538:PRO:HB2	1:A:542:ILE:HD11	1.83	0.59
1:A:75:PRO:HB2	1:A:79:LYS:O	2.03	0.59
1:A:289:THR:CA	3:A:1007:L6T:OAS	2.51	0.59
1:A:417:ILE:HG23	1:A:418:PRO:HD3	1.83	0.59
1:A:686:LEU:HD23	1:A:712:LEU:HD22	1.84	0.59
1:A:253:ILE:HD11	4:A:1008:J9E:N25	2.18	0.58
1:A:87:GLN:O	1:A:91:THR:HG23	2.02	0.58
1:A:470:THR:HG23	1:A:473:GLN:H	1.68	0.58
1:A:896:LYS:O	1:A:900:THR:HG23	2.02	0.58
1:A:668:ILE:O	1:A:672:THR:HG23	2.03	0.58
1:A:738:ALA:HB3	1:A:739:PRO:CD	2.15	0.58
1:A:676:GLY:O	1:A:680:THR:HG23	2.04	0.57
1:A:866:SER:CB	2:A:1002:MHA:HN22	2.16	0.57
1:A:538:PRO:HB2	1:A:542:ILE:CD1	2.35	0.57
1:A:122:VAL:HG13	1:A:125:MET:HE3	1.87	0.57
1:A:737:TRP:CD1	1:A:737:TRP:N	2.73	0.56
1:A:491:ASP:N	1:A:491:ASP:OD1	2.37	0.56
1:A:289:THR:CB	3:A:1007:L6T:OAS	2.53	0.56
1:A:632:ILE:HA	1:A:635:ILE:HG22	1.88	0.56
3:A:1006:L6T:CAY	3:A:1006:L6T:C5	2.84	0.55
1:A:586:VAL:CG2	1:A:739:PRO:HD2	2.36	0.55
1:A:119:ASP:O	1:A:123:SER:OG	2.21	0.55
1:A:388:GLY:O	1:A:392:ARG:NH1	2.40	0.55
1:A:482:LEU:HD22	1:A:497:MET:HE3	1.88	0.55
1:A:836:VAL:HG11	1:A:867:LEU:HD22	1.88	0.55
1:A:866:SER:N	2:A:1002:MHA:HN21	2.04	0.55
1:A:580:PHE:HD1	1:A:585:SER:O	1.89	0.55
3:A:1006:L6T:CBB	3:A:1006:L6T:CAX	2.85	0.55
1:A:60:VAL:HG11	1:A:513:VAL:HG13	1.88	0.54
1:A:654:MET:HG3	1:A:671:GLY:HA3	1.87	0.54
1:A:80:LYS:HD2	1:A:131:ARG:HG2	1.91	0.53
1:A:148:LEU:O	1:A:152:GLN:HG3	2.08	0.53
1:A:185:ASP:OD1	1:A:188:ARG:NH1	2.42	0.53
1:A:658:ARG:HG3	1:A:737:TRP:HZ2	1.69	0.53
1:A:248:LEU:HD22	1:A:701:MET:HE1	1.91	0.53
1:A:657:ALA:HB1	1:A:660:ARG:HH11	1.72	0.53
1:A:422:LEU:HD13	1:A:424:LEU:HD11	1.92	0.52
1:A:444:GLN:HG3	1:A:448:LEU:HD22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:738:ALA:CB	1:A:739:PRO:CD	2.82	0.52
1:A:302:VAL:HG23	1:A:303:PRO:HD3	1.92	0.51
1:A:86:TRP:O	1:A:90:VAL:HG22	2.11	0.51
1:A:865:ASN:HB2	2:A:1002:MHA:HC51	1.93	0.51
1:A:288:ARG:NH1	3:A:1007:L6T:CAP	2.73	0.51
1:A:662:MET:HE2	1:A:666:GLU:OE2	2.10	0.51
1:A:743:LYS:O	1:A:743:LYS:HE2	2.10	0.51
1:A:289:THR:HA	3:A:1007:L6T:OAS	2.10	0.51
1:A:222:ILE:HD11	1:A:251:LEU:HB2	1.93	0.51
1:A:658:ARG:HG3	1:A:737:TRP:CH2	2.46	0.51
1:A:683:ALA:O	1:A:712:LEU:HD21	2.11	0.51
1:A:265:PHE:HA	1:A:282:THR:HG21	1.92	0.50
1:A:664:THR:HG22	1:A:665:ALA:N	2.26	0.50
1:A:865:ASN:CG	1:A:868:ARG:HH21	2.18	0.50
1:A:756:LEU:HD23	1:A:760:GLU:HG3	1.94	0.50
1:A:417:ILE:CG2	1:A:418:PRO:HD3	2.42	0.50
1:A:652:SER:HB2	1:A:653:ARG:NH1	2.27	0.49
1:A:866:SER:HB2	2:A:1002:MHA:N2	2.24	0.49
1:A:311:PHE:HZ	1:A:631:MET:HE2	1.78	0.49
1:A:289:THR:CB	1:A:653:ARG:HH22	2.27	0.48
1:A:706:PHE:O	1:A:710:ILE:HG12	2.14	0.48
1:A:926:HIS:ND1	1:A:928:HIS:HE1	2.12	0.48
1:A:655:VAL:HG12	1:A:736:TRP:CE3	2.48	0.48
1:A:324:MET:O	1:A:328:ILE:HG12	2.14	0.48
1:A:655:VAL:HA	1:A:736:TRP:CZ3	2.49	0.48
1:A:657:ALA:HA	1:A:660:ARG:HB3	1.95	0.48
1:A:874:ARG:HH11	1:A:874:ARG:HA	1.78	0.47
1:A:874:ARG:HH12	1:A:876:ASP:H	1.62	0.47
1:A:496:LYS:HD3	1:A:496:LYS:HA	1.55	0.47
1:A:627:LEU:HD12	1:A:628:MET:H	1.79	0.47
1:A:182:ILE:HG23	1:A:244:PRO:HD3	1.95	0.47
1:A:606:ILE:O	1:A:610:MET:HG3	2.14	0.47
1:A:874:ARG:NH2	1:A:877:GLU:HG3	2.29	0.47
1:A:101:HIS:HB2	1:A:105:ILE:HD12	1.97	0.47
1:A:587:VAL:HG11	1:A:735:CYS:HA	1.97	0.47
1:A:727:VAL:O	1:A:730:LEU:HB2	2.14	0.47
1:A:918:LYS:H	2:A:1001:MHA:HN22	1.63	0.47
1:A:586:VAL:CG2	1:A:739:PRO:HG2	2.45	0.47
1:A:284:MET:O	1:A:288:ARG:HG3	2.15	0.47
1:A:580:PHE:HZ	1:A:740:ARG:HD2	1.79	0.47
1:A:586:VAL:CG2	1:A:739:PRO:CD	2.93	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:666:GLU:HB2	1:A:669:ARG:NH2	2.30	0.47
1:A:119:ASP:HB3	1:A:122:VAL:HB	1.97	0.46
1:A:662:MET:HE2	1:A:666:GLU:CD	2.40	0.46
1:A:662:MET:HB3	1:A:666:GLU:CD	2.40	0.46
1:A:759:ASP:OD1	1:A:897:ARG:NH1	2.48	0.46
1:A:249:ILE:O	1:A:253:ILE:HG12	2.16	0.46
1:A:415:LEU:O	1:A:418:PRO:HD2	2.16	0.46
1:A:458:THR:O	1:A:546:VAL:HA	2.15	0.46
1:A:724:VAL:O	1:A:728:MET:HE2	2.17	0.45
1:A:5:TRP:O	1:A:9:VAL:HG22	2.17	0.45
1:A:429:GLU:CD	1:A:453:ARG:HH12	2.24	0.45
1:A:493:ASP:HB3	1:A:496:LYS:HG2	1.98	0.45
1:A:694:VAL:O	1:A:702:LYS:HE3	2.17	0.45
1:A:188:ARG:NH1	1:A:696:SER:HA	2.32	0.45
1:A:654:MET:CG	1:A:671:GLY:HA3	2.47	0.45
1:A:664:THR:HG22	1:A:665:ALA:H	1.82	0.45
1:A:419:LEU:HD21	1:A:604:MET:HE2	1.99	0.44
1:A:495:GLU:CD	1:A:495:GLU:N	2.75	0.44
1:A:708:LEU:HD23	1:A:708:LEU:HA	1.84	0.44
1:A:5:TRP:CE2	1:A:9:VAL:HG13	2.51	0.44
1:A:42:GLY:O	1:A:309:GLN:HB3	2.16	0.44
1:A:263:SER:O	1:A:267:GLU:HG2	2.18	0.44
1:A:741:TRP:HB3	1:A:742:MET:H	1.65	0.44
1:A:539:PRO:HD2	1:A:542:ILE:HD11	2.00	0.44
1:A:654:MET:HG2	1:A:668:ILE:HA	2.00	0.43
1:A:74:THR:OG1	1:A:132:HIS:ND1	2.40	0.43
1:A:408:ILE:O	1:A:412:MET:HG3	2.17	0.43
3:A:1005:L6T:CAV	3:A:1005:L6T:CAP	2.91	0.43
1:A:289:THR:HB	1:A:653:ARG:HH22	1.83	0.43
1:A:650:LEU:HD22	1:A:720:ARG:HG3	1.99	0.43
1:A:724:VAL:O	1:A:728:MET:HB3	2.19	0.43
1:A:580:PHE:HZ	1:A:740:ARG:CD	2.31	0.43
1:A:721:MET:HB2	1:A:722:PHE:CD1	2.53	0.43
1:A:501:ARG:HB2	1:A:517:GLN:OE1	2.19	0.43
1:A:398:MET:HE1	1:A:665:ALA:O	2.19	0.43
1:A:654:MET:O	1:A:667:ALA:HB1	2.18	0.42
1:A:788:LEU:HD21	1:A:792:LYS:HE2	2.01	0.42
1:A:653:ARG:N	1:A:653:ARG:HD2	2.34	0.42
1:A:816:PHE:O	1:A:820:VAL:HG13	2.20	0.42
1:A:200:VAL:O	1:A:204:VAL:HG23	2.19	0.42
1:A:709:LEU:HD23	1:A:709:LEU:HA	1.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:724:VAL:HG12	1:A:725:PRO:HD3	2.02	0.42
1:A:770:THR:HG23	1:A:920:PHE:O	2.19	0.42
1:A:20:MET:HE3	1:A:20:MET:HB3	1.93	0.42
1:A:79:LYS:O	1:A:131:ARG:NH2	2.52	0.42
1:A:604:MET:HE2	1:A:604:MET:HB3	1.92	0.42
1:A:651:VAL:O	1:A:655:VAL:HG13	2.20	0.42
1:A:28:GLY:O	1:A:32:ILE:HG13	2.20	0.42
1:A:628:MET:O	1:A:631:MET:HB2	2.20	0.42
1:A:534:ARG:HG3	1:A:546:VAL:HG11	2.02	0.41
1:A:158:LEU:HD12	1:A:158:LEU:HA	1.91	0.41
1:A:202:PHE:HZ	1:A:350:VAL:HA	1.85	0.41
1:A:769:ASP:HB2	1:A:920:PHE:O	2.20	0.41
1:A:501:ARG:HG3	1:A:502:PRO:HD2	2.03	0.41
1:A:60:VAL:HG21	1:A:513:VAL:CG1	2.48	0.41
1:A:435:ASP:OD1	1:A:435:ASP:N	2.49	0.41
1:A:492:ASN:OD1	1:A:492:ASN:N	2.53	0.41
1:A:655:VAL:CG1	1:A:736:TRP:HZ3	2.28	0.41
1:A:289:THR:HB	3:A:1007:L6T:CAR	2.50	0.41
1:A:411:VAL:O	1:A:415:LEU:HG	2.20	0.41
1:A:493:ASP:HB3	1:A:496:LYS:CB	2.49	0.40
1:A:768:LYS:HA	1:A:773:TYR:O	2.22	0.40
1:A:98:VAL:HG22	1:A:105:ILE:HG21	2.02	0.40
3:A:1004:L6T:OAQ	3:A:1004:L6T:CAA	2.69	0.40
1:A:740:ARG:HD3	1:A:743:LYS:CB	2.52	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	897/943 (95%)	864 (96%)	31 (4%)	2 (0%)	43 72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	739	PRO
1	A	401	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	738/777 (95%)	728 (99%)	10 (1%)	59 85

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	491	ASP
1	A	496	LYS
1	A	581	LEU
1	A	666	GLU
1	A	737	TRP
1	A	740	ARG
1	A	743	LYS
1	A	744	ARG
1	A	756	LEU
1	A	874	ARG

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

Mol	Chain	Res	Type
1	A	172	ASN
1	A	554	GLN
1	A	802	ASN
1	A	928	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	L6T	A	1003	-	36,36,36	1.73	8 (22%)	47,47,47	1.33	7 (14%)
2	MHA	A	1001	-	12,12,12	1.33	1 (8%)	15,15,15	1.45	3 (20%)
3	L6T	A	1007	-	36,36,36	1.37	5 (13%)	47,47,47	1.63	11 (23%)
3	L6T	A	1006	-	36,36,36	1.40	5 (13%)	47,47,47	1.30	9 (19%)
2	MHA	A	1002	-	12,12,12	1.32	1 (8%)	15,15,15	1.14	1 (6%)
3	L6T	A	1005	-	36,36,36	1.26	3 (8%)	47,47,47	1.87	11 (23%)
4	J9E	A	1008	-	28,28,28	2.19	4 (14%)	39,41,41	3.32	16 (41%)
3	L6T	A	1004	-	36,36,36	1.46	6 (16%)	47,47,47	1.82	14 (29%)

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	L6T	A	1003	-	-	5/20/60/60	0/2/2/2
2	MHA	A	1001	-	-	8/12/12/12	-
3	L6T	A	1007	-	-	13/20/60/60	0/2/2/2
3	L6T	A	1006	-	-	9/20/60/60	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MHA	A	1002	-	-	5/12/12/12	-
3	L6T	A	1005	-	-	11/20/60/60	0/2/2/2
4	J9E	A	1008	-	-	0/8/30/30	0/4/4/4
3	L6T	A	1004	-	-	13/20/60/60	0/2/2/2

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1008	J9E	C17-C24	-7.30	1.34	1.41
4	A	1008	J9E	C15-N25	-5.22	1.31	1.38
4	A	1008	J9E	C02-N03	4.85	1.44	1.34
3	A	1006	L6T	OAN-CAO	4.23	1.54	1.44
3	A	1003	L6T	CAP-CAO	-4.03	1.38	1.51
3	A	1003	L6T	CAV-CAT	-3.85	1.42	1.52
3	A	1003	L6T	CAT-CAR	-3.63	1.42	1.52
3	A	1003	L6T	CAA-CAV	-3.49	1.42	1.52
3	A	1003	L6T	C3-C2	-3.40	1.43	1.52
3	A	1004	L6T	CAP-CAO	-3.39	1.40	1.51
4	A	1008	J9E	O01-C02	-3.38	1.17	1.23
3	A	1004	L6T	CAV-CAT	-3.33	1.43	1.52
3	A	1007	L6T	CAP-CAO	-3.33	1.40	1.51
3	A	1003	L6T	C4-C3	-3.32	1.43	1.52
2	A	1001	MHA	C6-N2	3.20	1.43	1.32
2	A	1002	MHA	C6-N2	3.19	1.43	1.32
3	A	1007	L6T	CAV-CAT	-3.11	1.44	1.52
3	A	1005	L6T	OAN-CAO	3.10	1.52	1.44
3	A	1007	L6T	C3-C2	-3.10	1.44	1.52
3	A	1005	L6T	CAP-CAO	-3.04	1.41	1.51
3	A	1004	L6T	C4-C3	-3.04	1.44	1.52
3	A	1004	L6T	C3-C2	-2.94	1.44	1.52
3	A	1004	L6T	OAN-CAO	2.92	1.51	1.44
3	A	1006	L6T	CAP-CAO	-2.77	1.42	1.51
3	A	1007	L6T	OAN-CAO	2.65	1.50	1.44
3	A	1006	L6T	O5-C1	2.57	1.48	1.41
3	A	1003	L6T	OAN-CAO	2.52	1.50	1.44
3	A	1003	L6T	C4-C5	-2.52	1.47	1.53
3	A	1005	L6T	O5-C1	2.44	1.48	1.41
3	A	1004	L6T	CAA-CAV	-2.43	1.45	1.52
3	A	1007	L6T	CAT-CAR	-2.39	1.46	1.52
3	A	1006	L6T	OAN-CAA	2.18	1.47	1.41
3	A	1006	L6T	OAW-CAV	2.09	1.48	1.43

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1008	J9E	C12-C07-C06	-14.59	86.52	110.47
4	A	1008	J9E	C05-C06-C07	-5.32	105.65	113.04
3	A	1004	L6T	O5-C5-C4	5.32	119.28	109.70
4	A	1008	J9E	C04-N03-C02	-5.19	114.42	123.09
3	A	1005	L6T	OAN-CAO-CAR	-5.08	100.55	109.70
4	A	1008	J9E	C13-C07-C12	4.76	118.28	110.47
3	A	1004	L6T	OAN-CAO-CAR	-4.71	101.21	109.70
3	A	1005	L6T	CAV-CAT-CAR	4.67	119.03	110.83
3	A	1005	L6T	CAA-CAV-CAT	4.43	119.33	110.01
3	A	1007	L6T	O5-C5-C4	4.39	117.61	109.70
3	A	1004	L6T	CAA-OAN-CAO	-4.39	105.15	113.72
4	A	1008	J9E	C11-C12-C07	-4.26	106.59	113.62
3	A	1005	L6T	C3-C4-C5	4.26	117.95	110.23
3	A	1006	L6T	O5-C5-C6	4.17	114.96	106.69
3	A	1007	L6T	C3-C4-C5	4.05	117.58	110.23
4	A	1008	J9E	C17-C24-N25	3.65	109.84	107.46
4	A	1008	J9E	C09-C08-C07	-3.43	107.97	113.62
4	A	1008	J9E	C24-C17-C16	-3.16	105.37	106.90
4	A	1008	J9E	C13-C14-C04	3.14	115.39	110.72
3	A	1007	L6T	CAT-CAR-CAO	3.05	115.76	110.23
4	A	1008	J9E	C13-C07-C06	3.05	113.99	108.34
3	A	1005	L6T	O5-C5-C6	3.01	112.66	106.69
4	A	1008	J9E	C06-C05-C04	-2.99	106.27	110.72
3	A	1007	L6T	OAU-CAT-CAR	-2.91	103.53	110.38
4	A	1008	J9E	F19-C18-C17	2.87	122.55	118.09
3	A	1004	L6T	C4-C3-C2	-2.84	105.85	110.83
4	A	1008	J9E	C13-C07-C08	2.81	115.08	110.47
3	A	1004	L6T	OAW-CAV-CAT	-2.77	103.84	110.38
3	A	1005	L6T	C6-C5-C4	-2.74	106.32	112.07
3	A	1004	L6T	CAP-CAO-CAR	-2.68	106.45	113.02
3	A	1005	L6T	C4-C3-C2	2.67	115.52	110.83
2	A	1001	MHA	C5-C6-N2	2.66	120.97	115.61
3	A	1003	L6T	C6-C5-C4	-2.63	106.55	112.07
3	A	1003	L6T	OAW-CAV-CAT	-2.62	104.19	110.38
3	A	1003	L6T	CAT-CAR-CAO	-2.61	105.50	110.23
3	A	1006	L6T	C1-C2-C3	2.55	115.38	110.01
3	A	1005	L6T	O1-CAA-CAV	2.54	114.34	108.09
3	A	1007	L6T	CAA-OAN-CAO	-2.54	108.77	113.72
3	A	1005	L6T	O1-C1-C2	2.53	114.31	108.09
3	A	1004	L6T	OAN-CAO-CAP	2.53	112.70	106.44
4	A	1008	J9E	C15-C02-N03	2.52	120.22	116.86
4	A	1008	J9E	C14-C04-C05	2.47	115.07	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1004	L6T	O4-C4-C3	-2.45	104.61	110.38
3	A	1006	L6T	O6-C6-C5	-2.44	103.53	109.24
3	A	1007	L6T	O1-CAA-OAN	-2.43	104.30	110.69
3	A	1004	L6T	C6-C5-C4	-2.40	107.02	112.07
2	A	1001	MHA	C6-C5-N1	-2.40	110.02	114.42
3	A	1007	L6T	O1-C1-C2	2.38	113.95	108.09
3	A	1004	L6T	C1-O5-C5	2.38	118.36	113.72
3	A	1005	L6T	O4-C4-C5	-2.34	103.55	109.32
3	A	1003	L6T	OAN-CAO-CAP	2.34	112.24	106.44
3	A	1003	L6T	CAP-CAO-CAR	-2.32	107.33	113.02
3	A	1004	L6T	O1-C1-C2	-2.32	102.39	108.09
3	A	1006	L6T	C1-O5-C5	-2.29	109.25	113.72
3	A	1006	L6T	O5-C5-C4	2.26	113.77	109.70
3	A	1006	L6T	C3-C4-C5	-2.25	106.15	110.23
3	A	1004	L6T	CAT-CAR-CAO	2.20	114.21	110.23
3	A	1003	L6T	OAN-CAO-CAR	-2.17	105.80	109.70
2	A	1002	MHA	C5-C6-N2	2.15	119.95	115.61
3	A	1006	L6T	CAA-O1-C1	-2.14	110.49	114.33
3	A	1005	L6T	O1-CAA-OAN	-2.14	105.06	110.69
3	A	1003	L6T	CAA-O1-C1	-2.12	110.52	114.33
3	A	1007	L6T	O1-CAA-CAV	2.09	113.23	108.09
3	A	1007	L6T	OAN-CAO-CAP	2.09	111.61	106.44
3	A	1007	L6T	O1-C1-O5	-2.08	105.23	110.69
3	A	1004	L6T	CAA-O1-C1	2.08	118.06	114.33
4	A	1008	J9E	C14-C13-C07	2.06	115.91	113.04
3	A	1006	L6T	OAN-CAO-CAP	2.03	111.48	106.44
3	A	1006	L6T	OAN-CAO-CAR	-2.03	106.04	109.70
2	A	1001	MHA	O1-C2-C1	2.02	121.36	113.38
3	A	1007	L6T	O3-C3-C2	-2.00	105.65	110.38
3	A	1004	L6T	O5-C5-C6	2.00	110.67	106.69

There are no chirality outliers.

All (64) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	MHA	N1-C1-C2-O2
2	A	1001	MHA	N1-C3-C4-O3
2	A	1001	MHA	N1-C3-C4-O4
2	A	1001	MHA	N1-C5-C6-O5
2	A	1001	MHA	N1-C5-C6-N2
2	A	1002	MHA	N1-C1-C2-O1
2	A	1002	MHA	N1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
2	A	1002	MHA	N1-C3-C4-O3
3	A	1004	L6T	OAN-CAA-O1-C1
3	A	1005	L6T	C2-C1-O1-CAA
3	A	1005	L6T	O5-C1-O1-CAA
3	A	1007	L6T	C2-C1-O1-CAA
3	A	1004	L6T	CAX-CAY-CAZ-CBA
3	A	1006	L6T	OAN-CAO-CAP-OAQ
2	A	1001	MHA	N1-C1-C2-O1
2	A	1002	MHA	N1-C3-C4-O4
3	A	1004	L6T	CAY-CAX-O6-C6
3	A	1007	L6T	CAZ-CBA-CBB-CBC
3	A	1006	L6T	CAY-CAZ-CBA-CBB
2	A	1001	MHA	C2-C1-N1-C5
2	A	1002	MHA	C2-C1-N1-C3
3	A	1007	L6T	C4-C5-C6-O6
3	A	1005	L6T	OAN-CAA-O1-C1
3	A	1007	L6T	O5-C1-O1-CAA
3	A	1006	L6T	CAR-CAO-CAP-OAQ
3	A	1007	L6T	O5-C5-C6-O6
3	A	1006	L6T	O5-C5-C6-O6
3	A	1005	L6T	CAV-CAA-O1-C1
3	A	1005	L6T	O6-CAX-CAY-CAZ
3	A	1004	L6T	CAR-CAO-CAP-OAQ
3	A	1007	L6T	CAX-CAY-CAZ-CBA
3	A	1005	L6T	C4-C5-C6-O6
3	A	1007	L6T	CBC-CBD-CBE-CBF
3	A	1007	L6T	CBE-CBF-CBG-CBH
3	A	1007	L6T	O6-CAX-CAY-CAZ
2	A	1001	MHA	C4-C3-N1-C1
3	A	1006	L6T	O6-CAX-CAY-CAZ
3	A	1004	L6T	OAN-CAO-CAP-OAQ
3	A	1003	L6T	CBB-CBC-CBD-CBE
3	A	1004	L6T	CBF-CBG-CBH-CBI
3	A	1005	L6T	O5-C5-C6-O6
3	A	1003	L6T	O6-CAX-CAY-CAZ
3	A	1003	L6T	CBC-CBD-CBE-CBF
3	A	1007	L6T	CBD-CBE-CBF-CBG
3	A	1005	L6T	CBC-CBD-CBE-CBF
3	A	1006	L6T	C4-C5-C6-O6
3	A	1003	L6T	CBD-CBE-CBF-CBG
3	A	1004	L6T	O6-CAX-CAY-CAZ
3	A	1007	L6T	CAY-CAX-O6-C6

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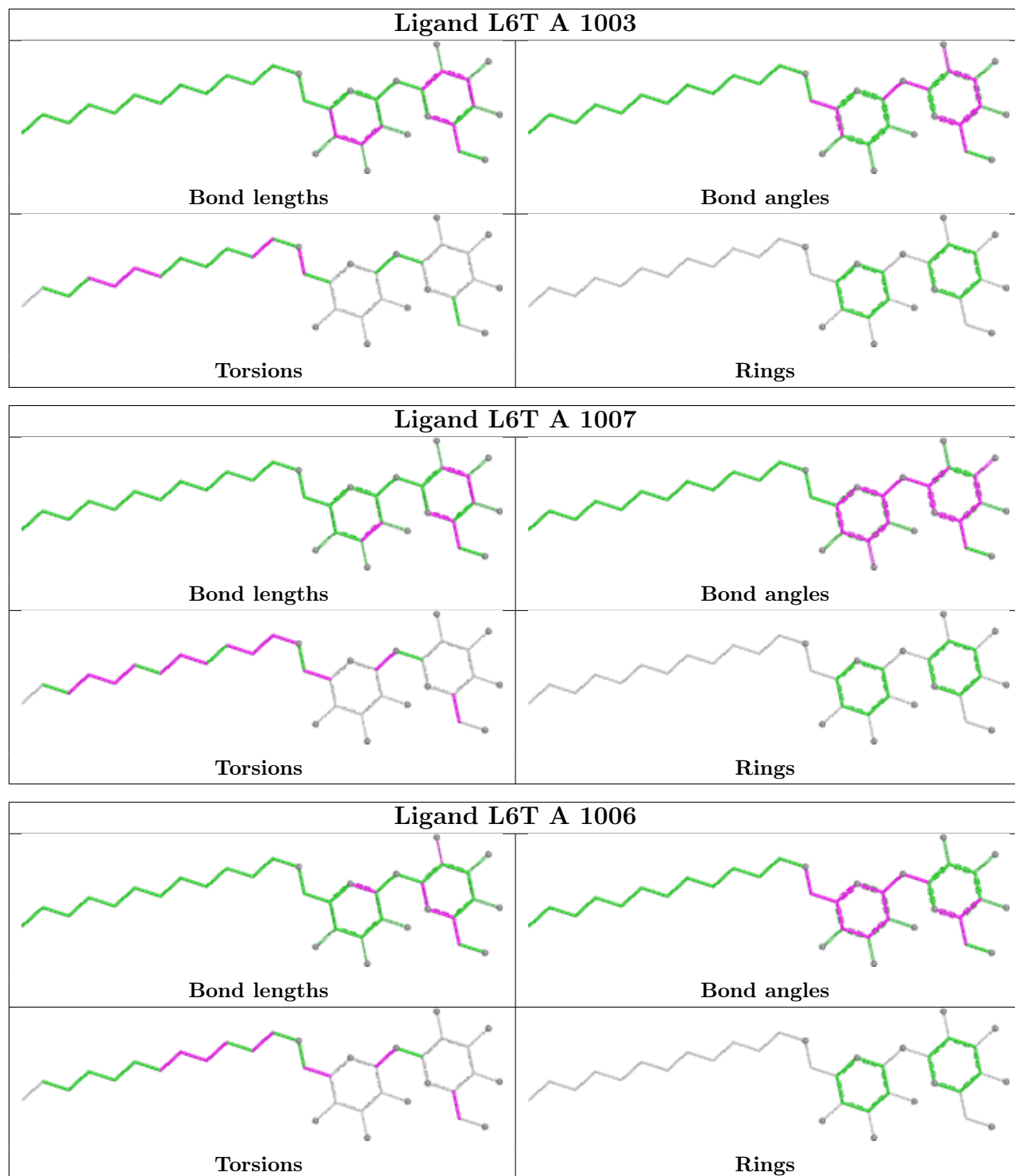
Mol	Chain	Res	Type	Atoms
3	A	1006	L6T	CBA-CBB-CBC-CBD
3	A	1007	L6T	CBA-CBB-CBC-CBD
3	A	1004	L6T	CBA-CBB-CBC-CBD
3	A	1007	L6T	CAR-CAO-CAP-OAQ
3	A	1003	L6T	C5-C6-O6-CAX
3	A	1005	L6T	CAY-CAX-O6-C6
3	A	1005	L6T	CAR-CAO-CAP-OAQ
3	A	1004	L6T	C4-C5-C6-O6
3	A	1005	L6T	CAX-CAY-CAZ-CBA
3	A	1006	L6T	CAZ-CBA-CBB-CBC
3	A	1004	L6T	CAZ-CBA-CBB-CBC
3	A	1004	L6T	O5-C1-O1-CAA
3	A	1006	L6T	O5-C1-O1-CAA
3	A	1004	L6T	CBB-CBC-CBD-CBE
3	A	1004	L6T	CAV-CAA-O1-C1

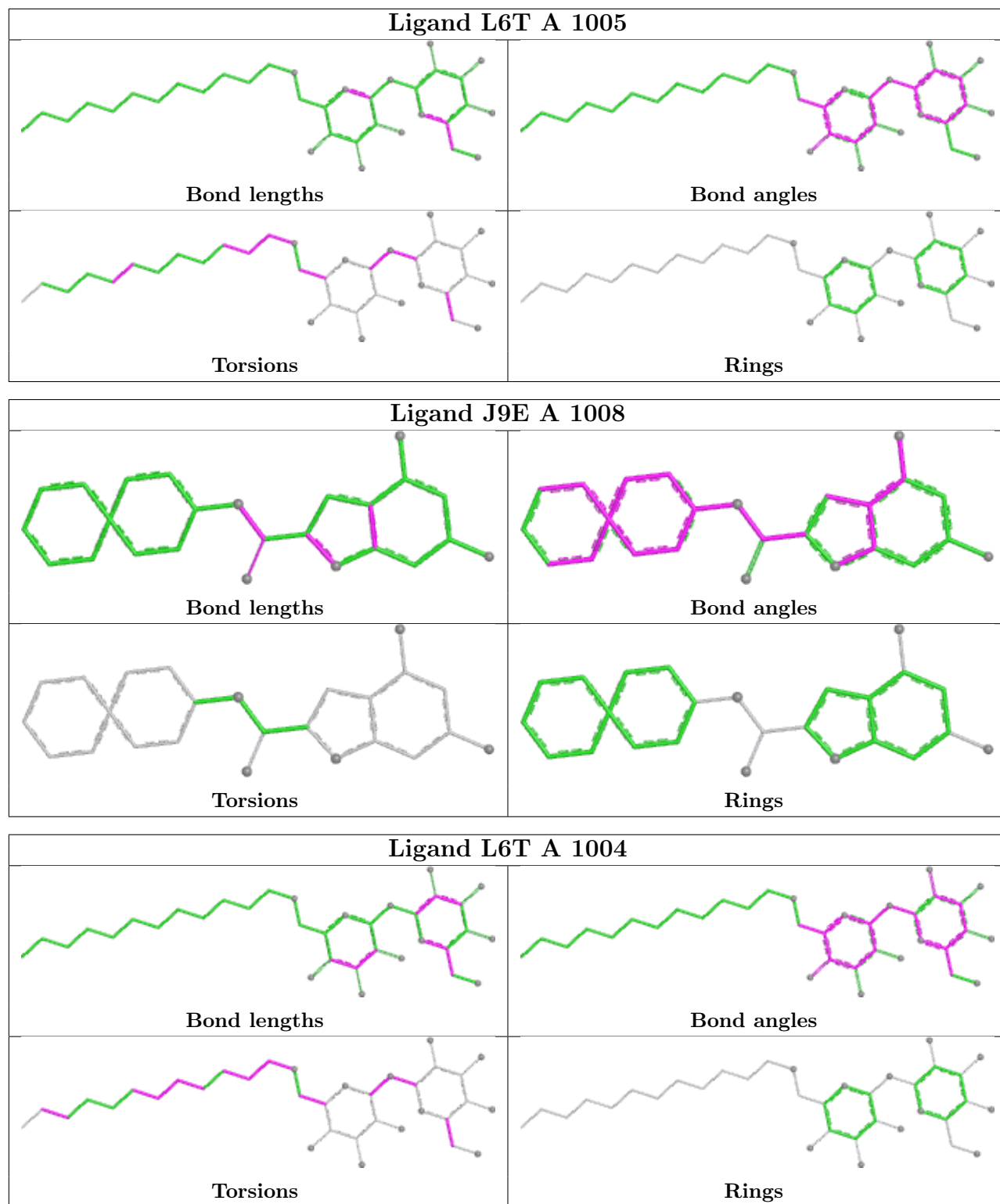
There are no ring outliers.

7 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	MHA	1	0
3	A	1007	L6T	7	0
3	A	1006	L6T	2	0
2	A	1002	MHA	7	0
3	A	1005	L6T	3	0
4	A	1008	J9E	1	0
3	A	1004	L6T	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 ⓘ

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 ⓘ

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	901/943 (95%)	0.88	132 (14%) 6 4	49, 80, 155, 242	0

All (132) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	652	SER	8.3
1	A	655	VAL	7.8
1	A	910	TYR	7.4
1	A	651	VAL	7.1
1	A	739	PRO	7.1
1	A	647	GLU	6.9
1	A	909	ALA	6.3
1	A	347	ALA	6.0
1	A	583	PHE	5.6
1	A	737	TRP	5.6
1	A	476	ASP	5.2
1	A	648	VAL	4.9
1	A	734	ASP	4.8
1	A	649	PHE	4.8
1	A	738	ALA	4.8
1	A	354	LEU	4.7
1	A	494	PRO	4.7
1	A	586	VAL	4.5
1	A	579	MET	4.4
1	A	406	ALA	4.4
1	A	731	LEU	4.2
1	A	726	ALA	4.1
1	A	821	ASP	4.1
1	A	665	ALA	4.1
1	A	646	TYR	4.0
1	A	410	VAL	4.0
1	A	654	MET	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	817	ASN	3.9
1	A	-2	SER	3.9
1	A	399	LYS	3.8
1	A	627	LEU	3.8
1	A	-4	PHE	3.8
1	A	645	ASP	3.8
1	A	32	ILE	3.7
1	A	249	ILE	3.7
1	A	390	TRP	3.7
1	A	618	GLY	3.7
1	A	727	VAL	3.7
1	A	351	THR	3.6
1	A	745	VAL	3.6
1	A	703	TYR	3.6
1	A	118	THR	3.5
1	A	102	GLU	3.5
1	A	744	ARG	3.5
1	A	284	MET	3.4
1	A	732	GLY	3.4
1	A	750	PHE	3.4
1	A	12	PHE	3.4
1	A	348	LEU	3.3
1	A	587	VAL	3.3
1	A	23	LEU	3.3
1	A	591	LYS	3.3
1	A	167	ARG	3.3
1	A	46	GLU	3.3
1	A	741	TRP	3.2
1	A	653	ARG	3.2
1	A	641	GLY	3.2
1	A	355	LYS	3.1
1	A	656	GLU	3.1
1	A	684	LEU	3.1
1	A	133	THR	3.1
1	A	22	ALA	3.1
1	A	736	TRP	3.1
1	A	663	SER	3.1
1	A	557	ILE	3.0
1	A	388	GLY	3.0
1	A	650	LEU	3.0
1	A	814	LYS	3.0
1	A	247	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	613	ASP	2.9
1	A	274	ASP	2.9
1	A	908	ASP	2.9
1	A	768	LYS	2.9
1	A	725	PRO	2.9
1	A	246	VAL	2.9
1	A	389	PHE	2.9
1	A	580	PHE	2.8
1	A	622	TYR	2.8
1	A	713	LEU	2.8
1	A	617	SER	2.8
1	A	19	VAL	2.8
1	A	409	LEU	2.7
1	A	403	ALA	2.7
1	A	285	THR	2.7
1	A	722	PHE	2.7
1	A	425	GLY	2.7
1	A	226	LEU	2.6
1	A	112	LEU	2.6
1	A	907	TRP	2.5
1	A	402	ILE	2.5
1	A	730	LEU	2.5
1	A	911	GLU	2.5
1	A	350	VAL	2.5
1	A	490	PRO	2.4
1	A	582	ALA	2.4
1	A	222	ILE	2.4
1	A	417	ILE	2.4
1	A	642	LEU	2.4
1	A	111	TRP	2.4
1	A	407	PRO	2.4
1	A	818	GLN	2.4
1	A	475	ALA	2.4
1	A	808	THR	2.3
1	A	927	HIS	2.3
1	A	400	ARG	2.3
1	A	473	GLN	2.3
1	A	535	ALA	2.2
1	A	759	ASP	2.2
1	A	4	TRP	2.2
1	A	396	VAL	2.2
1	A	440	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	166	ILE	2.2
1	A	661	GLY	2.2
1	A	200	VAL	2.2
1	A	17	ILE	2.2
1	A	283	VAL	2.2
1	A	664	THR	2.1
1	A	502	PRO	2.1
1	A	928	HIS	2.1
1	A	240	PHE	2.1
1	A	80	LYS	2.1
1	A	411	VAL	2.1
1	A	874	ARG	2.1
1	A	644	THR	2.1
1	A	450	PRO	2.1
1	A	1	MET	2.1
1	A	404	PHE	2.1
1	A	401	PRO	2.1
1	A	414	LEU	2.1
1	A	589	PRO	2.0
1	A	472	ALA	2.0
1	A	253	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	L6T	A	1006	35/35	0.63	0.19	79,147,177,178	0
3	L6T	A	1004	35/35	0.76	0.16	76,105,130,135	0

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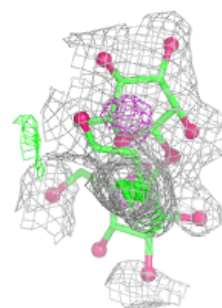
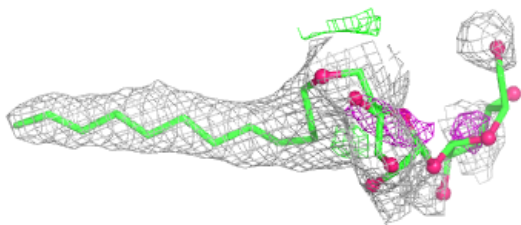
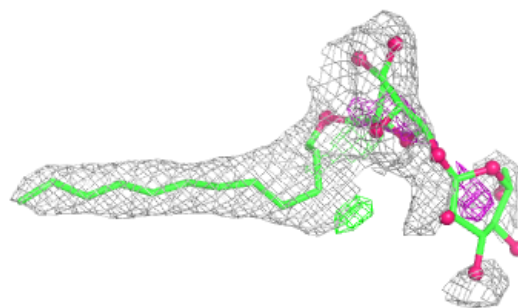
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	L6T	A	1005	35/35	0.77	0.18	55,142,179,180	0
3	L6T	A	1007	35/35	0.80	0.19	103,116,130,132	0
2	MHA	A	1001	13/13	0.85	0.14	62,75,90,97	0
2	MHA	A	1002	13/13	0.86	0.12	77,89,99,101	0
3	L6T	A	1003	35/35	0.93	0.10	47,61,68,71	0
4	J9E	A	1008	25/25	0.94	0.12	68,82,103,116	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

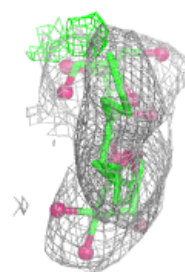
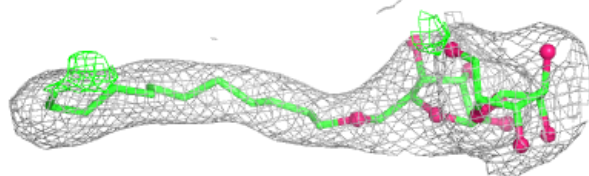
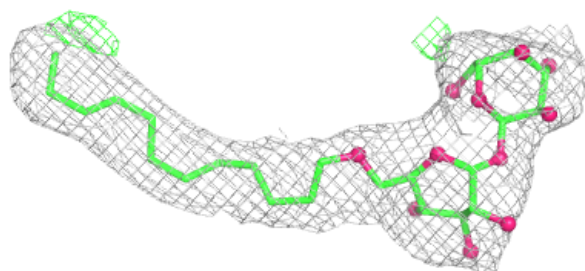
Electron density around L6T A 1006:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

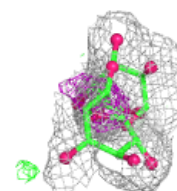
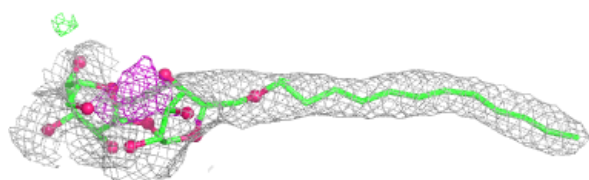
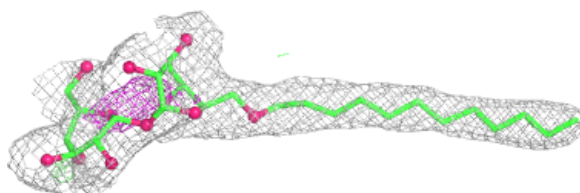


Electron density around L6T A 1004:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

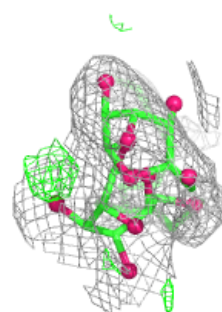
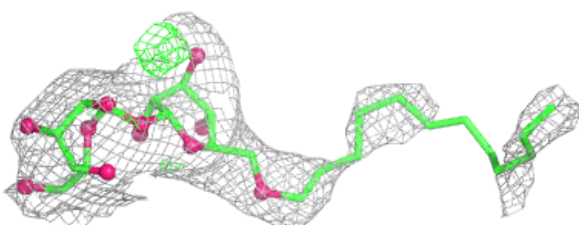
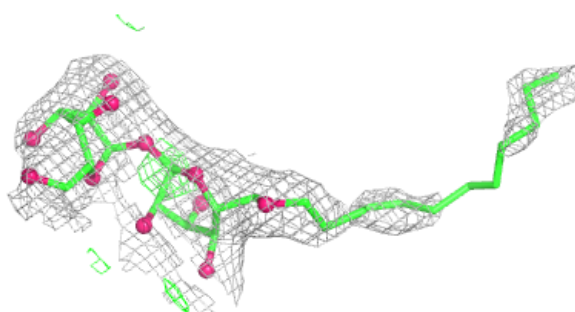
**Electron density around L6T A 1005:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

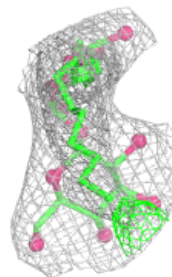
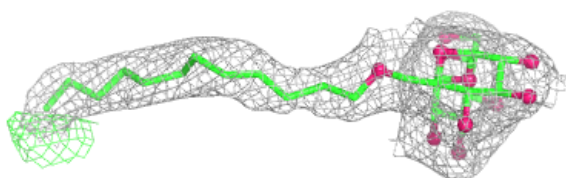
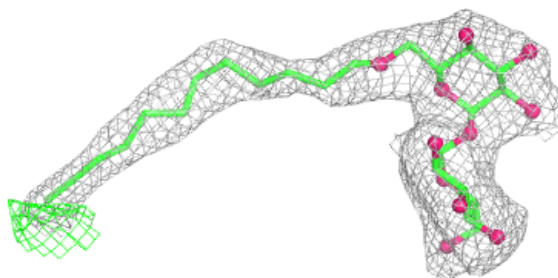


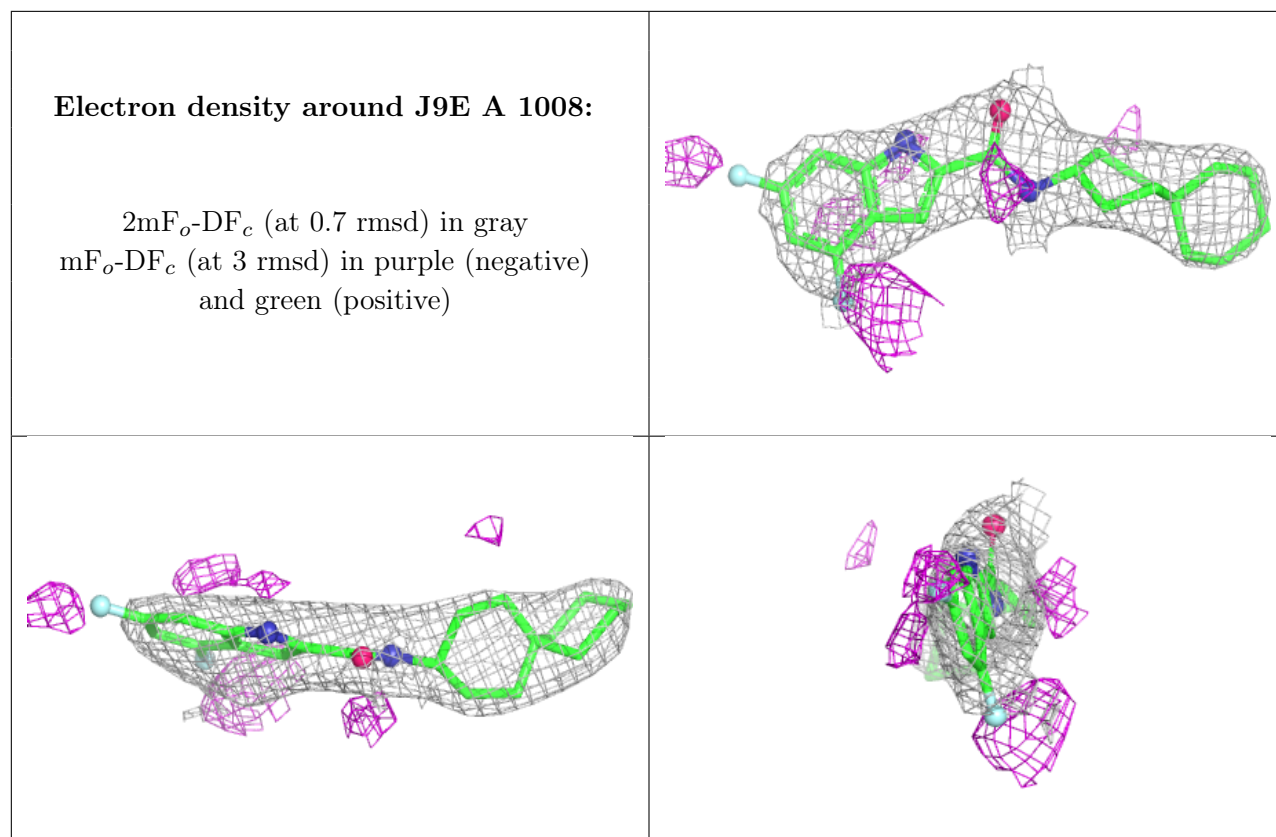
Electron density around L6T A 1007:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around L6T A 1003:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.