



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:47 AM UTC

PDB ID : 6AJI / pdb_00006aji
Title : Crystal structure of mycolic acid transporter MmpL3 from Mycobacterium smegmatis complexed with Rimonabant
Authors : Zhang, B.; Li, J.; Yang, X.L.; Wu, L.J.; Yang, H.T.; Rao, Z.H.
Deposited on : 2018-08-27
Resolution : 2.90 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

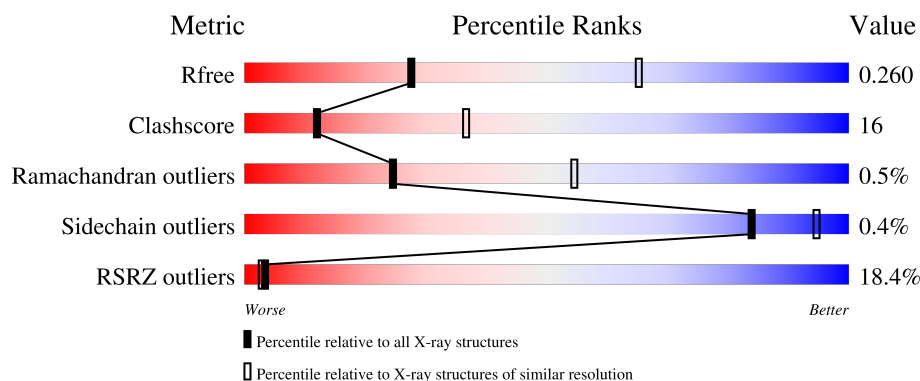
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	17% 67% 25% 7%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6874 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
1	A	873	Total	C	N	O	S	0	0	0
			6713	4324	1137	1222	30			

There are 37 discrepancies between the modelled and reference sequences:

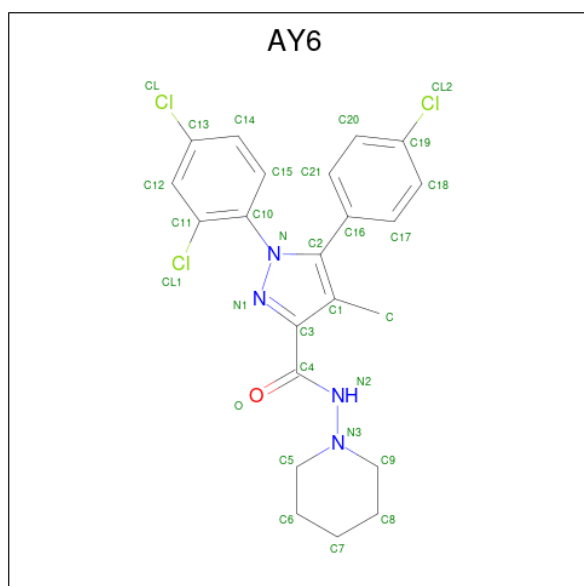
Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	MET	-	expression tag	UNP I7G2R2
A	-11	PRO	-	expression tag	UNP I7G2R2
A	-10	GLU	-	expression tag	UNP I7G2R2
A	-9	VAL	-	expression tag	UNP I7G2R2
A	-8	VAL	-	expression tag	UNP I7G2R2
A	-7	GLY	-	expression tag	UNP I7G2R2
A	-6	SER	-	expression tag	UNP 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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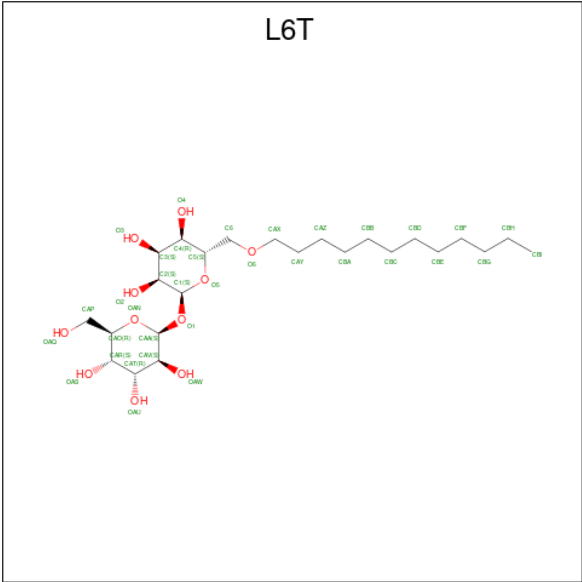
Chain	Residue	Modelled	Actual	Comment	Reference
A	921	HIS	-	expression tag	UNP D9IEF7
A	922	HIS	-	expression tag	UNP D9IEF7
A	923	HIS	-	expression tag	UNP D9IEF7
A	924	HIS	-	expression tag	UNP D9IEF7
A	925	HIS	-	expression tag	UNP D9IEF7
A	926	HIS	-	expression tag	UNP D9IEF7
A	927	HIS	-	expression tag	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 5-(4-chlorophenyl)-1-(2,4-dichlorophenyl)-4-methyl-N-(piperidin-1-yl)-1H-pyrazole-3-carboxamide (CCD ID: AY6) (formula: C₂₂H₂₁Cl₃N₄O).



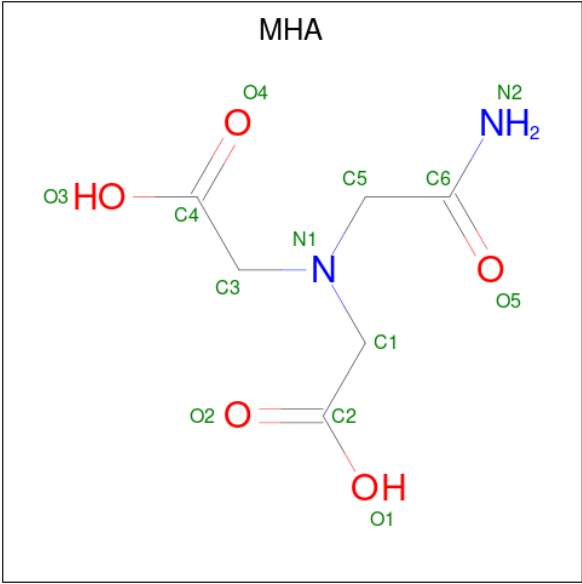
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	N	O		
2	A	1	30	22	3	4	1	0	0

- Molecule 3 is alpha-D-glucopyranosyl 6-O-dodecyl-alpha-D-glucopyranoside (CCD ID: L6T) (formula: C₂₄H₄₆O₁₁).

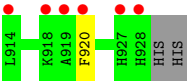


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			35	24	11		
3	A	1	Total	C	O	0	0
			35	24	11		
3	A	1	Total	C	O	0	0
			35	24	11		

- Molecule 4 is (CARBAMOYLMETHYL-CARBOXYMETHYL-AMINO)-ACETIC ACID (CCD ID: MHA) (formula: C₆H₁₀N₂O₅).



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.70Å 140.60Å 141.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.81 – 2.90 44.81 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.8 (44.81-2.90) 99.0 (44.81-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.42 (at 2.90Å)	Xtriage
Refinement program	PHENIX 1.12 _2829	Depositor
R, R_{free}	0.230 , 0.254 0.238 , 0.260	Depositor DCC
R_{free} test set	2009 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	91.0	Xtriage
Anisotropy	0.520	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 40.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.010 for -h,l,k	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	6874	wwPDB-VP
Average B, all atoms (Å ²)	102.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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, AY6, MHA

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	0.31	0/6850	0.55	3/9306 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	418	PRO	N-CA-C	-8.08	103.33	113.84
1	A	417	ILE	N-CA-C	6.86	123.70	108.88
1	A	662	MET	O-C-N	5.99	129.39	123.46

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	6713	0	6860	216	0
2	A	30	0	0	3	0
3	A	105	0	0	4	0
4	A	26	0	16	0	0
All	All	6874	0	6876	216	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 16.

All (216) 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:662:MET:HE3	1:A:663:SER:HB3	1.13	1.12
1:A:662:MET:HE3	1:A:663:SER:CB	1.82	1.08
1:A:588:LEU:HA	1:A:591:LYS:NZ	1.71	1.05
1:A:662:MET:CE	1:A:663:SER:HB3	1.89	1.02
1:A:588:LEU:HA	1:A:591:LYS:HZ2	0.85	1.01
1:A:588:LEU:CA	1:A:591:LYS:HZ2	1.75	0.98
1:A:542:ILE:HD12	1:A:542:ILE:O	1.69	0.90
1:A:755:MET:HE2	1:A:850:ASN:HD22	1.36	0.90
1:A:542:ILE:HD12	1:A:542:ILE:C	2.01	0.86
1:A:463:ARG:HB3	1:A:542:ILE:HG22	1.61	0.82
1:A:415:LEU:O	1:A:418:PRO:HD2	1.78	0.81
1:A:668:ILE:HD13	1:A:728:MET:HB3	1.62	0.79
1:A:60:VAL:HG21	1:A:513:VAL:HG11	1.64	0.79
1:A:266:ARG:NH1	1:A:346:ASP:OD1	2.17	0.78
1:A:537:GLN:N	1:A:537:GLN:OE1	2.18	0.76
1:A:595:MET:HE2	1:A:723:LEU:HD22	1.66	0.76
1:A:453:ARG:HD3	3:A:1003:L6T:CBE	2.20	0.72
1:A:650:LEU:HD12	1:A:675:THR:OG1	1.90	0.71
1:A:424:LEU:HD22	1:A:629:ALA:HA	1.72	0.70
1:A:453:ARG:NE	3:A:1003:L6T:CBG	2.55	0.69
1:A:765:LYS:HB2	1:A:806:VAL:HG22	1.74	0.69
1:A:538:PRO:CB	1:A:542:ILE:HD11	2.23	0.69
1:A:516:ILE:O	1:A:516:ILE:HD12	1.94	0.68
1:A:534:ARG:HG2	1:A:546:VAL:HG21	1.76	0.68
1:A:1:MET:N	1:A:1:MET:SD	2.67	0.67
1:A:664:THR:OG1	1:A:665:ALA:N	2.28	0.67
1:A:662:MET:HE3	1:A:663:SER:CA	2.24	0.67
1:A:662:MET:HG3	1:A:663:SER:O	1.96	0.66
1:A:666:GLU:HA	1:A:669:ARG:HD2	1.77	0.66
1:A:459:LEU:HB2	1:A:516:ILE:HD11	1.76	0.66
1:A:155:GLU:HG3	1:A:156:PRO:HD3	1.78	0.65
1:A:634:LEU:O	1:A:638:VAL:HG12	1.97	0.65
1:A:542:ILE:C	1:A:542:ILE:CD1	2.70	0.65
1:A:98:VAL:HG22	1:A:105:ILE:HG21	1.79	0.65
1:A:588:LEU:HG	1:A:591:LYS:HZ3	1.62	0.64
1:A:663:SER:OG	1:A:664:THR:N	2.26	0.64
1:A:101:HIS:HB3	1:A:104:GLN:HG2	1.80	0.64
1:A:459:LEU:HB2	1:A:516:ILE:CD1	2.28	0.64
1:A:119:ASP:HB3	1:A:122:VAL:HB	1.81	0.63
1:A:606:ILE:O	1:A:610:MET:HG3	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:ILE:C	1:A:419:LEU:N	2.55	0.62
1:A:873:LYS:HG3	1:A:875:TRP:CZ2	2.35	0.62
1:A:1:MET:HE3	1:A:1:MET:H	1.64	0.62
1:A:417:ILE:HD12	1:A:417:ILE:O	2.01	0.61
1:A:101:HIS:HA	1:A:104:GLN:HE21	1.65	0.60
1:A:1:MET:H	1:A:1:MET:CE	2.13	0.60
1:A:759:ASP:OD1	1:A:897:ARG:NH1	2.32	0.60
1:A:87:GLN:O	1:A:91:THR:HG23	2.01	0.60
1:A:482:LEU:HD23	1:A:497:MET:HE3	1.83	0.60
1:A:331:ILE:HD12	1:A:332:THR:HG23	1.84	0.59
1:A:538:PRO:HB2	1:A:542:ILE:CD1	2.33	0.59
1:A:101:HIS:CA	1:A:104:GLN:HE21	2.16	0.58
1:A:727:VAL:O	1:A:731:LEU:HD23	2.02	0.58
1:A:538:PRO:HB2	1:A:542:ILE:HD11	1.84	0.58
1:A:529:LYS:O	1:A:533:LEU:HD12	2.04	0.58
1:A:851:MET:HB2	1:A:860:VAL:HG11	1.84	0.58
1:A:572:ILE:HG22	1:A:640:TRP:CZ2	2.39	0.57
1:A:854:GLN:HB2	1:A:894:ARG:NH2	2.19	0.57
1:A:277:ALA:O	1:A:281:ARG:HG3	2.04	0.57
1:A:680:THR:HG22	1:A:720:ARG:HH12	1.70	0.57
1:A:453:ARG:CD	3:A:1003:L6T:CBG	2.82	0.57
1:A:571:LEU:HD21	1:A:640:TRP:CD1	2.39	0.57
1:A:453:ARG:HE	3:A:1003:L6T:CBG	2.17	0.57
1:A:538:PRO:CB	1:A:542:ILE:CD1	2.82	0.57
1:A:724:VAL:HG22	1:A:728:MET:HG2	1.87	0.57
1:A:60:VAL:HG11	1:A:513:VAL:HG13	1.88	0.56
1:A:733:ASP:HA	1:A:736:TRP:HZ3	1.70	0.56
1:A:571:LEU:HD21	1:A:640:TRP:CG	2.40	0.56
1:A:49:GLN:HB3	1:A:534:ARG:NH1	2.21	0.56
1:A:482:LEU:CD2	1:A:497:MET:HE3	2.35	0.56
1:A:666:GLU:HA	1:A:669:ARG:CD	2.36	0.56
1:A:416:ILE:O	1:A:419:LEU:HG	2.05	0.55
1:A:658:ARG:HD3	1:A:736:TRP:CE2	2.41	0.55
1:A:417:ILE:HD12	1:A:419:LEU:O	2.05	0.55
1:A:412:MET:CB	1:A:598:LEU:HD21	2.36	0.55
1:A:463:ARG:NH1	1:A:465:ASP:OD1	2.40	0.55
1:A:498:TRP:H	1:A:518:ASN:HD22	1.54	0.55
1:A:595:MET:O	1:A:599:THR:HG22	2.07	0.54
1:A:723:LEU:O	1:A:726:ALA:HB3	2.07	0.54
1:A:19:VAL:HG23	1:A:20:MET:HG2	1.90	0.54
1:A:71:ALA:HB1	1:A:166:ILE:HD11	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:GLY:O	1:A:32:ILE:HG12	2.07	0.54
1:A:658:ARG:HD3	1:A:736:TRP:NE1	2.24	0.53
1:A:654:MET:HB3	1:A:671:GLY:HA3	1.90	0.53
1:A:417:ILE:O	1:A:419:LEU:O	2.26	0.53
1:A:263:SER:O	1:A:267:GLU:HG3	2.09	0.53
1:A:429:GLU:OE1	1:A:429:GLU:N	2.32	0.53
1:A:480:LYS:O	1:A:483:THR:HB	2.09	0.53
1:A:794:GLU:O	1:A:797:LYS:HG3	2.09	0.53
1:A:676:GLY:O	1:A:680:THR:HG23	2.09	0.52
1:A:412:MET:HB3	1:A:598:LEU:HD21	1.92	0.52
1:A:588:LEU:HD23	1:A:591:LYS:HD2	1.90	0.52
1:A:848:LEU:HA	1:A:851:MET:HG3	1.92	0.52
1:A:86:TRP:O	1:A:90:VAL:HG22	2.09	0.52
1:A:148:LEU:O	1:A:152:GLN:HG3	2.11	0.51
1:A:836:VAL:O	1:A:840:LEU:HD22	2.10	0.51
1:A:455:GLU:HB3	1:A:550:PRO:HD3	1.91	0.51
1:A:292:PHE:CE2	1:A:296:ILE:HD11	2.46	0.51
1:A:579:MET:HE3	1:A:648:VAL:HG12	1.92	0.51
1:A:588:LEU:CA	1:A:591:LYS:NZ	2.51	0.51
1:A:410:VAL:HG23	1:A:411:VAL:HG13	1.92	0.51
1:A:439:ARG:O	1:A:443:GLU:HG3	2.11	0.51
1:A:770:THR:HG23	1:A:920:PHE:O	2.12	0.50
1:A:249:ILE:HD13	1:A:323:VAL:HG23	1.93	0.50
1:A:575:THR:O	1:A:579:MET:HG3	2.10	0.50
1:A:570:ILE:O	1:A:574:THR:HG23	2.12	0.50
1:A:588:LEU:HD12	1:A:735:CYS:O	2.10	0.50
1:A:42:GLY:O	1:A:309:GLN:HB3	2.12	0.49
1:A:494:PRO:HA	1:A:497:MET:HG3	1.94	0.49
1:A:268:GLU:OE2	1:A:281:ARG:NH2	2.46	0.49
1:A:456:PRO:HA	1:A:519:GLY:HA2	1.95	0.49
1:A:101:HIS:HA	1:A:104:GLN:NE2	2.27	0.49
1:A:297:ILE:HG21	1:A:323:VAL:HG21	1.95	0.49
1:A:654:MET:SD	1:A:728:MET:HE2	2.53	0.49
1:A:685:ILE:O	1:A:689:VAL:HG23	2.12	0.49
1:A:739:PRO:HB2	1:A:740:ARG:HD3	1.95	0.48
1:A:755:MET:HE3	1:A:910:TYR:CZ	2.48	0.48
1:A:689:VAL:HB	2:A:1001:AY6:CL	2.50	0.48
1:A:709:LEU:HA	1:A:712:LEU:CD2	2.43	0.48
1:A:727:VAL:HA	1:A:730:LEU:HB3	1.94	0.48
1:A:860:VAL:HA	1:A:863:PHE:CD1	2.48	0.48
1:A:4:TRP:O	1:A:8:THR:HG23	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:670:ILE:O	1:A:674:THR:HG22	2.13	0.48
1:A:538:PRO:HB3	1:A:542:ILE:CD1	2.44	0.48
1:A:482:LEU:HD23	1:A:497:MET:CE	2.43	0.48
1:A:222:ILE:HG13	1:A:250:GLY:HA3	1.96	0.48
1:A:860:VAL:HA	1:A:863:PHE:HD1	1.79	0.48
1:A:105:ILE:HD11	1:A:154:VAL:HG11	1.95	0.48
1:A:174:LEU:O	1:A:178:LEU:HD12	2.14	0.48
1:A:833:LEU:HD21	1:A:860:VAL:HG23	1.96	0.47
1:A:587:VAL:HG23	1:A:591:LYS:NZ	2.29	0.47
1:A:651:VAL:HA	1:A:654:MET:HG2	1.97	0.47
1:A:292:PHE:HZ	1:A:578:LEU:C	2.21	0.47
1:A:662:MET:HG3	1:A:663:SER:N	2.28	0.47
1:A:419:LEU:HD21	1:A:604:MET:C	2.39	0.47
1:A:588:LEU:HG	1:A:591:LYS:NZ	2.30	0.47
1:A:101:HIS:C	1:A:104:GLN:HE21	2.22	0.47
1:A:459:LEU:HD21	1:A:533:LEU:HB3	1.96	0.47
1:A:347:ALA:HB3	1:A:348:LEU:HD12	1.96	0.47
1:A:691:GLY:O	1:A:694:VAL:HG22	2.14	0.47
1:A:15:ILE:O	1:A:19:VAL:HG13	2.16	0.46
1:A:406:ALA:O	1:A:410:VAL:HG13	2.16	0.46
1:A:759:ASP:HB3	1:A:894:ARG:HD2	1.96	0.46
1:A:292:PHE:CZ	1:A:578:LEU:HB3	2.50	0.46
1:A:320:ILE:O	1:A:324:MET:HG2	2.16	0.46
1:A:279:VAL:HG21	1:A:339:ALA:HB2	1.97	0.46
1:A:662:MET:HE3	1:A:663:SER:N	2.30	0.46
1:A:579:MET:HB2	1:A:589:PRO:HG3	1.98	0.46
1:A:111:TRP:NE1	1:A:126:LYS:HZ1	2.14	0.46
1:A:549:THR:OG1	1:A:550:PRO:HD3	2.16	0.46
1:A:408:ILE:O	1:A:412:MET:HG3	2.16	0.45
1:A:662:MET:CG	1:A:663:SER:N	2.78	0.45
1:A:830:ASN:OD1	1:A:832:LYS:N	2.44	0.45
1:A:516:ILE:HD12	1:A:516:ILE:C	2.40	0.45
1:A:476:ASP:OD1	1:A:480:LYS:NZ	2.36	0.45
1:A:458:THR:HG23	1:A:515:VAL:HG13	1.98	0.45
1:A:344:ARG:HB3	1:A:344:ARG:NH2	2.32	0.45
1:A:412:MET:HB2	1:A:598:LEU:HD21	1.97	0.45
1:A:458:THR:O	1:A:546:VAL:HA	2.16	0.45
1:A:538:PRO:HB3	1:A:542:ILE:HD11	1.97	0.45
1:A:523:ARG:HD2	1:A:550:PRO:HG3	1.99	0.45
1:A:461:MET:SD	1:A:477:MET:HG2	2.57	0.45
1:A:681:GLY:O	1:A:685:ILE:HG13	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:ILE:N	1:A:418:PRO:CD	2.79	0.45
1:A:736:TRP:CD2	1:A:736:TRP:N	2.85	0.45
1:A:435:ASP:HA	1:A:440:GLN:HE21	1.81	0.44
1:A:662:MET:SD	1:A:666:GLU:HB3	2.58	0.44
1:A:10:TYR:CZ	1:A:276:GLU:HB3	2.52	0.44
1:A:836:VAL:O	1:A:839:SER:HB3	2.18	0.44
1:A:865:ASN:O	1:A:869:MET:HG3	2.18	0.43
1:A:666:GLU:CD	1:A:669:ARG:HD3	2.43	0.43
1:A:301:SER:OG	1:A:319:ILE:HG21	2.18	0.43
1:A:528:LYS:O	1:A:532:GLU:HG3	2.18	0.43
1:A:854:GLN:NE2	1:A:887:TRP:HE1	2.16	0.43
1:A:585:SER:CB	1:A:588:LEU:HD12	2.49	0.43
1:A:226:LEU:HD23	1:A:226:LEU:HA	1.85	0.43
1:A:341:LEU:O	1:A:344:ARG:HG2	2.19	0.43
1:A:421:GLN:N	1:A:421:GLN:OE1	2.52	0.43
1:A:107:GLY:O	1:A:138:PRO:HD2	2.19	0.43
1:A:804:ASN:O	1:A:804:ASN:ND2	2.48	0.42
1:A:653:ARG:HD2	1:A:653:ARG:HA	1.85	0.42
1:A:97:VAL:HG11	1:A:158:LEU:HD13	1.99	0.42
1:A:453:ARG:HG3	1:A:453:ARG:HH11	1.84	0.42
1:A:230:ARG:NH1	1:A:234:GLU:OE1	2.53	0.42
1:A:598:LEU:C	1:A:598:LEU:HD23	2.45	0.42
1:A:755:MET:HE2	1:A:850:ASN:ND2	2.18	0.42
1:A:112:LEU:HD12	1:A:112:LEU:HA	1.80	0.42
1:A:417:ILE:C	1:A:419:LEU:H	2.26	0.42
1:A:572:ILE:HD12	1:A:573:VAL:N	2.34	0.42
1:A:253:ILE:HD11	2:A:1001:AY6:C3	2.49	0.41
1:A:841:ASP:O	1:A:845:ARG:HG3	2.20	0.41
1:A:854:GLN:HE22	1:A:887:TRP:HE1	1.68	0.41
1:A:174:LEU:C	1:A:178:LEU:HD12	2.46	0.41
1:A:248:LEU:CD2	2:A:1001:AY6:CL	3.05	0.41
1:A:530:ILE:O	1:A:534:ARG:HG3	2.21	0.41
1:A:620:MET:SD	1:A:706:PHE:HZ	2.43	0.41
1:A:329:LEU:HD23	1:A:329:LEU:HA	1.93	0.41
1:A:627:LEU:HD12	1:A:627:LEU:N	2.35	0.41
1:A:79:LYS:C	1:A:80:LYS:HD3	2.45	0.41
1:A:327:ALA:O	1:A:331:ILE:HG13	2.20	0.41
1:A:23:LEU:O	1:A:27:GLY:N	2.38	0.41
1:A:432:LEU:O	1:A:439:ARG:NH2	2.52	0.41
1:A:281:ARG:HH21	1:A:281:ARG:HD3	1.74	0.41
1:A:412:MET:HB3	1:A:412:MET:HE2	1.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:453:ARG:HH11	1:A:453:ARG:CG	2.33	0.41
1:A:194:ILE:HB	1:A:195:PRO:HD3	2.02	0.41
1:A:735:CYS:HB2	1:A:736:TRP:CE3	2.56	0.41
1:A:694:VAL:O	1:A:702:LYS:NZ	2.46	0.40
1:A:69:VAL:HG23	1:A:139:LEU:HD11	2.03	0.40
1:A:406:ALA:C	1:A:408:ILE:H	2.29	0.40
1:A:84:LYS:HD3	1:A:84:LYS:HA	1.88	0.40
1:A:520:LEU:HD12	1:A:520:LEU:HA	1.91	0.40
1:A:1:MET:HA	1:A:4:TRP:HB3	2.03	0.40
1:A:470:THR:OG1	1:A:471:ASP:N	2.54	0.40
1:A:528:LYS:HD2	1:A:528:LYS:HA	1.86	0.40
1:A:530:ILE:HD13	1:A:551:ALA:HA	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	867/943 (92%)	832 (96%)	31 (4%)	4 (0%)	24 54

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	539	PRO
1	A	665	ALA
1	A	417	ILE
1	A	766	ILE

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	712/777 (92%)	709 (100%)	3 (0%)	84 94

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	417	ILE
1	A	418	PRO
1	A	840	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	GLN
1	A	104	GLN
1	A	243	GLN
1	A	518	ASN
1	A	621	ASN
1	A	802	ASN
1	A	854	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](#)

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

6 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
4	MHA	A	1006	-	12,12,12	1.31	1 (8%)	15,15,15	1.36	2 (13%)
3	L6T	A	1003	-	36,36,36	1.48	6 (16%)	47,47,47	1.33	5 (10%)
4	MHA	A	1005	-	12,12,12	1.38	1 (8%)	15,15,15	1.39	1 (6%)
3	L6T	A	1004	-	36,36,36	1.34	4 (11%)	47,47,47	1.55	7 (14%)
3	L6T	A	1002	-	36,36,36	1.44	6 (16%)	47,47,47	1.35	8 (17%)
2	AY6	A	1001	-	33,33,33	3.84	11 (33%)	45,47,47	1.77	7 (15%)

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
4	MHA	A	1006	-	-	8/12/12/12	-
3	L6T	A	1003	-	-	7/20/60/60	0/2/2/2
4	MHA	A	1005	-	-	2/12/12/12	-
3	L6T	A	1004	-	-	14/20/60/60	0/2/2/2
3	L6T	A	1002	-	-	9/20/60/60	0/2/2/2
2	AY6	A	1001	-	-	0/16/24/24	0/4/4/4

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	AY6	N2-N3	-18.06	1.20	1.41
2	A	1001	AY6	C2-N	-6.34	1.30	1.36
2	A	1001	AY6	C4-N2	6.23	1.46	1.35
3	A	1002	L6T	OAN-CAO	4.14	1.54	1.44
3	A	1003	L6T	OAN-CAO	4.04	1.54	1.44
2	A	1001	AY6	C3-C4	4.00	1.56	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	AY6	C2-C1	3.79	1.48	1.39
3	A	1004	L6T	OAN-CAO	3.57	1.53	1.44
4	A	1006	MHA	C6-N2	3.15	1.43	1.32
3	A	1002	L6T	CAP-CAO	-3.15	1.41	1.51
3	A	1003	L6T	CAP-CAO	-3.09	1.41	1.51
4	A	1005	MHA	C6-N2	3.08	1.42	1.32
3	A	1004	L6T	CAP-CAO	-3.02	1.41	1.51
2	A	1001	AY6	C5-N3	-2.90	1.41	1.46
3	A	1003	L6T	O5-C1	2.79	1.49	1.41
2	A	1001	AY6	C7-C6	-2.65	1.42	1.51
2	A	1001	AY6	C16-C2	2.58	1.52	1.48
2	A	1001	AY6	C18-C19	2.53	1.42	1.38
3	A	1003	L6T	CAV-CAT	-2.43	1.46	1.52
3	A	1002	L6T	O5-C1	2.41	1.48	1.41
3	A	1002	L6T	CAV-CAT	-2.33	1.46	1.52
3	A	1004	L6T	O5-C1	2.31	1.47	1.41
2	A	1001	AY6	C8-C7	-2.26	1.43	1.51
2	A	1001	AY6	N-N1	-2.22	1.34	1.39
3	A	1002	L6T	OAN-CAA	2.21	1.47	1.41
3	A	1002	L6T	OAW-CAV	2.09	1.48	1.43
3	A	1003	L6T	OAN-CAA	2.08	1.47	1.41
3	A	1004	L6T	CAV-CAT	-2.05	1.47	1.52
3	A	1003	L6T	OAW-CAV	2.03	1.48	1.43

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	AY6	C3-N1-N	6.61	111.42	104.81
2	A	1001	AY6	C1-C3-N1	-5.55	107.73	112.02
3	A	1004	L6T	CAT-CAR-CAO	4.35	118.12	110.23
3	A	1003	L6T	CAT-CAR-CAO	4.20	117.86	110.23
3	A	1004	L6T	CAA-CAV-CAT	4.12	118.67	110.01
3	A	1004	L6T	CAV-CAT-CAR	4.05	117.93	110.83
3	A	1002	L6T	O5-C5-C4	3.86	116.66	109.70
3	A	1003	L6T	O5-C1-C2	3.75	118.08	110.37
3	A	1003	L6T	C1-C2-C3	3.71	117.81	110.01
3	A	1004	L6T	O5-C5-C4	3.39	115.81	109.70
2	A	1001	AY6	C5-N3-N2	-3.17	105.93	110.33
3	A	1002	L6T	CAA-O1-C1	-3.10	108.76	114.33
3	A	1002	L6T	OAN-CAA-CAV	2.99	116.51	110.37
2	A	1001	AY6	C10-N-N1	2.91	123.21	118.74
3	A	1004	L6T	C1-C2-C3	2.83	115.97	110.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1002	L6T	C3-C4-C5	2.68	115.09	110.23
3	A	1002	L6T	O5-C1-C2	2.62	115.75	110.37
2	A	1001	AY6	C6-C5-N3	2.57	113.69	110.29
3	A	1002	L6T	O1-C1-O5	-2.50	104.11	110.69
4	A	1005	MHA	C6-C5-N1	-2.49	109.86	114.42
4	A	1006	MHA	C6-C5-N1	-2.38	110.07	114.42
3	A	1004	L6T	CAA-OAN-CAO	-2.34	109.15	113.72
3	A	1003	L6T	O5-C5-C4	2.34	113.91	109.70
2	A	1001	AY6	C2-N-N1	-2.25	110.24	112.32
3	A	1004	L6T	OAN-CAO-CAR	-2.18	105.76	109.70
4	A	1006	MHA	C5-C6-N2	2.13	119.92	115.61
3	A	1003	L6T	CAA-O1-C1	-2.10	110.57	114.33
2	A	1001	AY6	C4-N2-N3	2.08	124.48	120.12
3	A	1002	L6T	O1-CAA-OAN	-2.05	105.29	110.69
3	A	1002	L6T	OAN-CAO-CAP	2.01	111.41	106.44

There are no chirality outliers.

All (40) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1006	MHA	N1-C1-C2-O1
4	A	1006	MHA	N1-C1-C2-O2
3	A	1004	L6T	OAN-CAO-CAP-OAQ
3	A	1003	L6T	OAN-CAO-CAP-OAQ
3	A	1004	L6T	CAY-CAZ-CBA-CBB
3	A	1004	L6T	CBE-CBF-CBG-CBH
3	A	1004	L6T	CAR-CAO-CAP-OAQ
3	A	1004	L6T	CAY-CAX-O6-C6
3	A	1003	L6T	O5-C5-C6-O6
3	A	1002	L6T	O6-CAX-CAY-CAZ
3	A	1004	L6T	C2-C1-O1-CAA
3	A	1003	L6T	C4-C5-C6-O6
3	A	1004	L6T	O5-C1-O1-CAA
3	A	1004	L6T	O5-C5-C6-O6
3	A	1004	L6T	CAZ-CBA-CBB-CBC
3	A	1002	L6T	CBA-CBB-CBC-CBD
3	A	1002	L6T	CBC-CBD-CBE-CBF
3	A	1004	L6T	CBA-CBB-CBC-CBD
3	A	1002	L6T	CBD-CBE-CBF-CBG
3	A	1004	L6T	CBC-CBD-CBE-CBF
3	A	1003	L6T	CBC-CBD-CBE-CBF
3	A	1002	L6T	CBE-CBF-CBG-CBH

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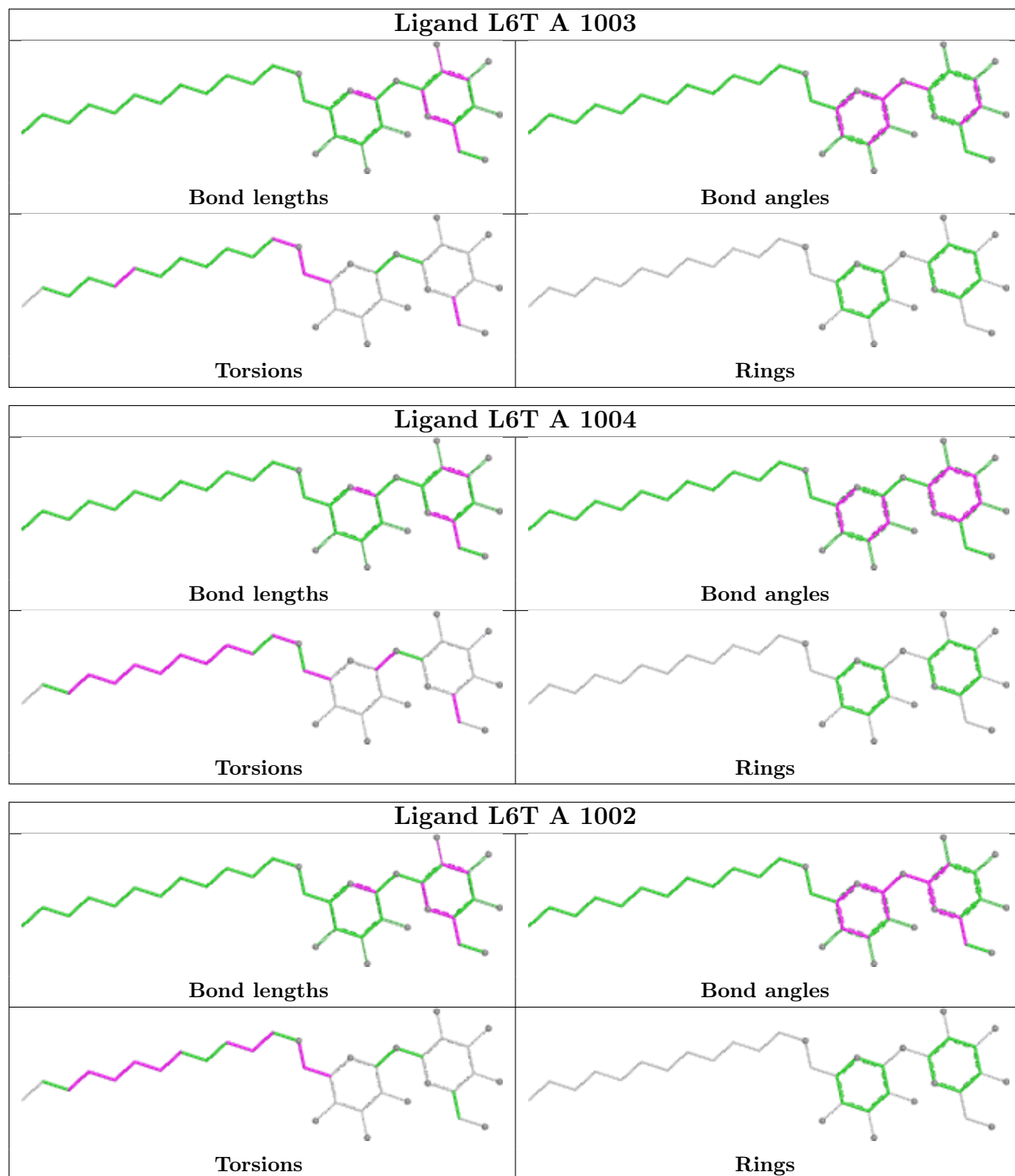
Mol	Chain	Res	Type	Atoms
4	A	1006	MHA	C2-C1-N1-C5
3	A	1004	L6T	CAX-CAY-CAZ-CBA
3	A	1003	L6T	CAR-CAO-CAP-OAQ
3	A	1002	L6T	CBB-CBC-CBD-CBE
3	A	1002	L6T	O5-C5-C6-O6
3	A	1003	L6T	CAY-CAX-O6-C6
4	A	1006	MHA	C2-C1-N1-C3
4	A	1006	MHA	N1-C5-C6-N2
3	A	1002	L6T	CAX-CAY-CAZ-CBA
4	A	1006	MHA	C4-C3-N1-C1
4	A	1006	MHA	N1-C5-C6-O5
4	A	1005	MHA	C6-C5-N1-C1
3	A	1004	L6T	CBD-CBE-CBF-CBG
3	A	1003	L6T	C5-C6-O6-CAX
3	A	1004	L6T	CBB-CBC-CBD-CBE
4	A	1005	MHA	N1-C5-C6-N2
4	A	1006	MHA	C4-C3-N1-C5
3	A	1002	L6T	C5-C6-O6-CAX

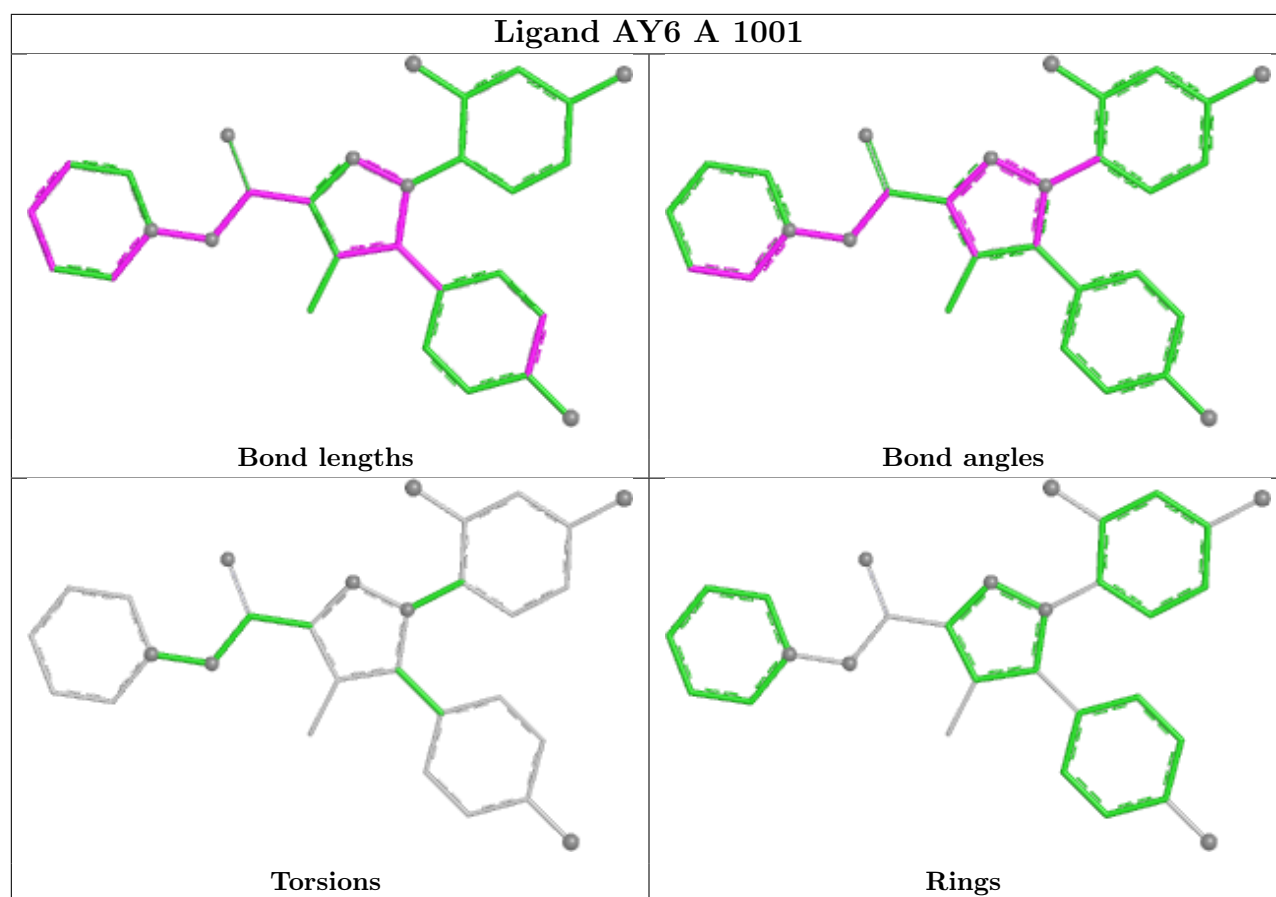
There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1003	L6T	4	0
2	A	1001	AY6	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 [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	873/943 (92%)	1.00	161 (18%) 3 3	63, 95, 150, 198	0

All (161) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	660	ARG	16.4
1	A	349	GLY	8.7
1	A	425	GLY	7.3
1	A	268	GLU	7.3
1	A	426	GLY	7.0
1	A	842	ALA	7.0
1	A	424	LEU	6.5
1	A	522	ASN	6.1
1	A	271	GLU	5.6
1	A	789	ASN	5.2
1	A	281	ARG	5.2
1	A	540	HIS	5.0
1	A	772	GLY	5.0
1	A	69	VAL	5.0
1	A	768	LYS	5.0
1	A	770	THR	4.9
1	A	172	ASN	4.6
1	A	499	LYS	4.5
1	A	175	ALA	4.4
1	A	583	PHE	4.3
1	A	845	ARG	4.2
1	A	264	ARG	4.2
1	A	427	ILE	4.2
1	A	401	PRO	4.2
1	A	771	GLU	4.1
1	A	137	ILE	4.1
1	A	656	GLU	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	523	ARG	4.1
1	A	405	ALA	4.1
1	A	54	SER	4.1
1	A	661	GLY	4.0
1	A	444	GLN	4.0
1	A	708	LEU	3.9
1	A	81	VAL	3.9
1	A	344	ARG	3.9
1	A	74	THR	3.8
1	A	584	GLY	3.8
1	A	133	THR	3.8
1	A	96	GLN	3.8
1	A	82	THR	3.7
1	A	503	ALA	3.7
1	A	524	ASN	3.7
1	A	132	HIS	3.7
1	A	402	ILE	3.6
1	A	43	PHE	3.6
1	A	525	ASP	3.6
1	A	334	LEU	3.5
1	A	490	PRO	3.5
1	A	260	PHE	3.4
1	A	267	GLU	3.4
1	A	138	PRO	3.4
1	A	235	PHE	3.4
1	A	736	TRP	3.4
1	A	415	LEU	3.4
1	A	837	TYR	3.4
1	A	464	GLU	3.3
1	A	500	GLU	3.3
1	A	173	PRO	3.3
1	A	748	LYS	3.3
1	A	184	GLU	3.3
1	A	177	GLU	3.3
1	A	588	LEU	3.3
1	A	641	GLY	3.3
1	A	139	LEU	3.2
1	A	646	TYR	3.2
1	A	72	ILE	3.2
1	A	126	LYS	3.2
1	A	633	GLY	3.2
1	A	206	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	920	PHE	3.2
1	A	448	LEU	3.1
1	A	821	ASP	3.1
1	A	155	GLU	3.1
1	A	130	LEU	3.1
1	A	414	LEU	3.1
1	A	635	ILE	3.1
1	A	639	ILE	3.1
1	A	168	LEU	3.1
1	A	843	VAL	3.1
1	A	94	LEU	3.1
1	A	158	LEU	3.1
1	A	273	TYR	3.1
1	A	151	TYR	3.0
1	A	324	MET	3.0
1	A	510	ASP	3.0
1	A	282	THR	3.0
1	A	404	PHE	3.0
1	A	928	HIS	2.9
1	A	159	GLN	2.9
1	A	160	GLN	2.9
1	A	628	MET	2.9
1	A	804	ASN	2.9
1	A	674	THR	2.9
1	A	203	PHE	2.8
1	A	841	ASP	2.8
1	A	68	HIS	2.8
1	A	202	PHE	2.8
1	A	-2	SER	2.8
1	A	585	SER	2.8
1	A	637	ALA	2.8
1	A	76	PRO	2.7
1	A	411	VAL	2.7
1	A	927	HIS	2.7
1	A	672	THR	2.7
1	A	707	GLY	2.7
1	A	536	LEU	2.7
1	A	832	LYS	2.6
1	A	831	ALA	2.6
1	A	417	ILE	2.6
1	A	906	THR	2.6
1	A	78	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	55	LEU	2.6
1	A	171	LEU	2.6
1	A	284	MET	2.5
1	A	629	ALA	2.5
1	A	769	ASP	2.5
1	A	165	ASP	2.4
1	A	632	ILE	2.4
1	A	111	TRP	2.4
1	A	615	HIS	2.4
1	A	521	GLU	2.4
1	A	549	THR	2.4
1	A	1	MET	2.4
1	A	92	GLU	2.4
1	A	477	MET	2.4
1	A	537	GLN	2.3
1	A	115	PRO	2.3
1	A	481	ALA	2.3
1	A	918	LYS	2.3
1	A	502	PRO	2.3
1	A	548	GLY	2.3
1	A	609	TRP	2.3
1	A	679	ILE	2.3
1	A	213	LEU	2.3
1	A	914	LEU	2.2
1	A	864	THR	2.2
1	A	919	ALA	2.2
1	A	594	LEU	2.2
1	A	40	GLN	2.2
1	A	740	ARG	2.2
1	A	109	VAL	2.2
1	A	70	VAL	2.2
1	A	546	VAL	2.2
1	A	136	SER	2.2
1	A	564	LEU	2.2
1	A	453	ARG	2.1
1	A	886	ARG	2.1
1	A	83	ASP	2.1
1	A	179	THR	2.1
1	A	483	THR	2.1
1	A	552	LEU	2.1
1	A	108	TRP	2.1
1	A	114	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	416	ILE	2.1
1	A	557	ILE	2.1
1	A	544	VAL	2.1
1	A	580	PHE	2.0
1	A	649	PHE	2.0
1	A	217	ILE	2.0
1	A	729	LYS	2.0
1	A	725	PRO	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](#)

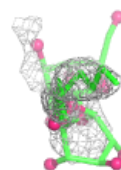
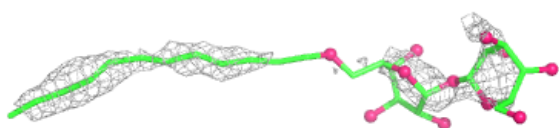
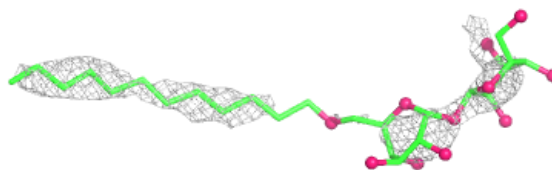
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	L6T	A	1003	35/35	0.74	0.20	59,171,183,186	0
3	L6T	A	1004	35/35	0.87	0.15	109,150,180,183	0
4	MHA	A	1006	13/13	0.88	0.10	103,117,120,120	0
4	MHA	A	1005	13/13	0.93	0.07	81,88,100,107	0
3	L6T	A	1002	35/35	0.94	0.15	61,73,94,105	0
2	AY6	A	1001	30/30	0.95	0.12	104,116,157,175	0

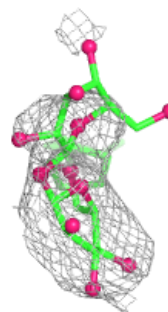
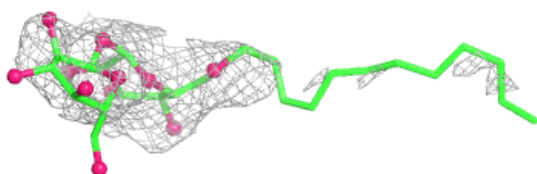
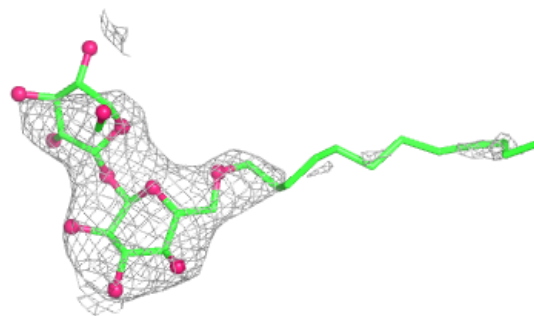
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around L6T A 1003:

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

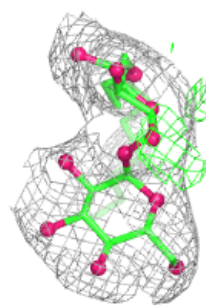
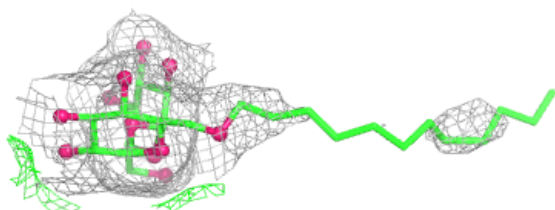
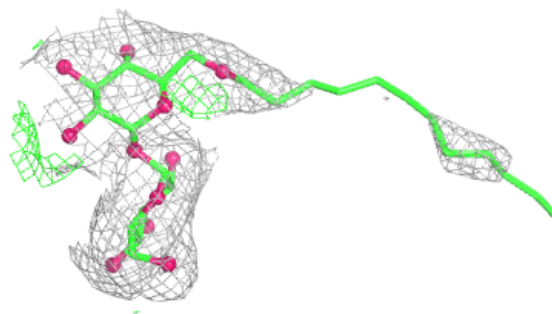
**Electron density around L6T A 1004:**

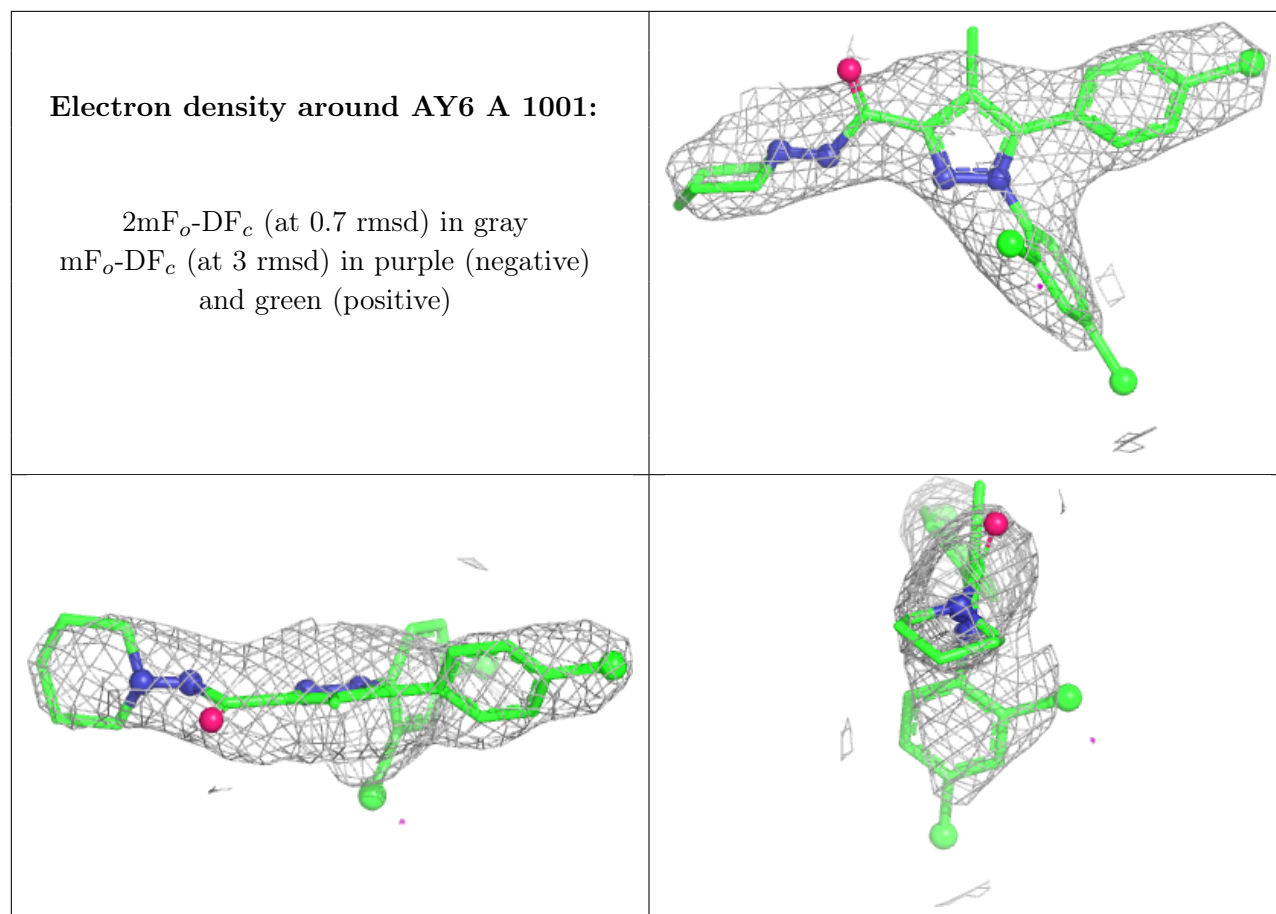
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around L6T A 1002:

$2mF_o-DF_c$ (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.