



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 06:54 AM EDT

PDB ID : 6FND
Title : Crystal structure of Toxoplasma gondii AKMT
Authors : Pivovarova, Y.; Dong, G.
Deposited on : 2018-02-02
Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.37.1
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

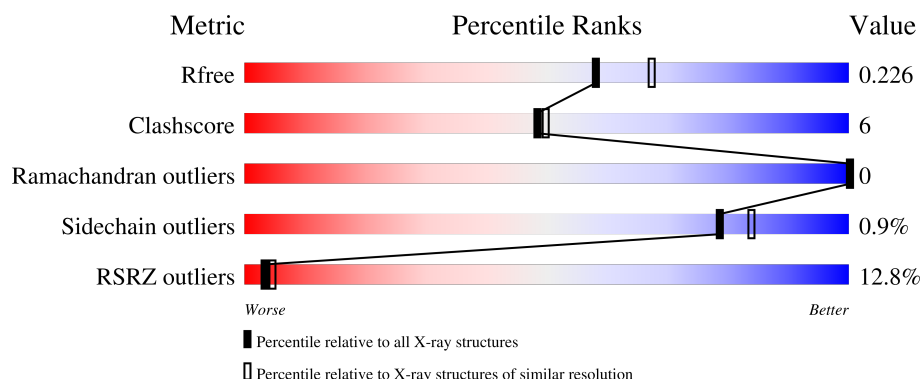
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	423	<div> <div>21%</div> <div>83%</div> <div>16%</div> <div>.</div> </div>
2	B	418	<div> <div>10%</div> <div>87%</div> <div>13%</div> <div>.</div> </div>
3	C	424	<div> <div>10%</div> <div>87%</div> <div>11%</div> <div>..</div> </div>
4	D	425	<div> <div>8%</div> <div>91%</div> <div>8%</div> <div>.</div> </div>

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
6	SO4	D	803	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 14140 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 Apical complex lysine methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	423	3390	2155	572	638	25	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	285	GLY	-	expression tag	UNP A0A151H4R7
A	286	SER	-	expression tag	UNP A0A151H4R7
A	287	HIS	-	expression tag	UNP A0A151H4R7
A	288	MET	-	expression tag	UNP A0A151H4R7

- Molecule 2 is a protein called Apical complex lysine methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	418	3377	2150	568	635	24	0	2	0

- Molecule 3 is a protein called Apical complex lysine methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	420	3378	2149	569	636	24	0	1	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	285	GLY	-	expression tag	UNP A0A151H4R7
C	286	SER	-	expression tag	UNP A0A151H4R7
C	287	HIS	-	expression tag	UNP A0A151H4R7
C	288	MET	-	expression tag	UNP A0A151H4R7

- Molecule 4 is a protein called Apical complex lysine methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	422	Total	C	N	O	S	0	0	0
			3389	2157	569	638	25			

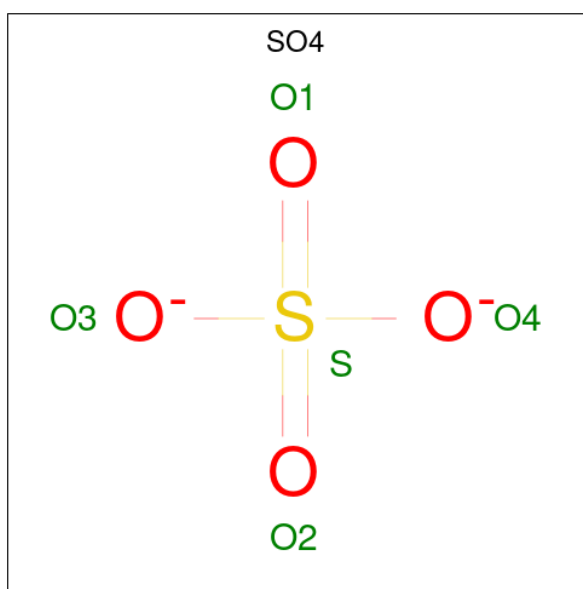
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	285	GLY	-	expression tag	UNP A0A151H4R7
D	286	SER	-	expression tag	UNP A0A151H4R7
D	287	HIS	-	expression tag	UNP A0A151H4R7
D	288	MET	-	expression tag	UNP A0A151H4R7

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

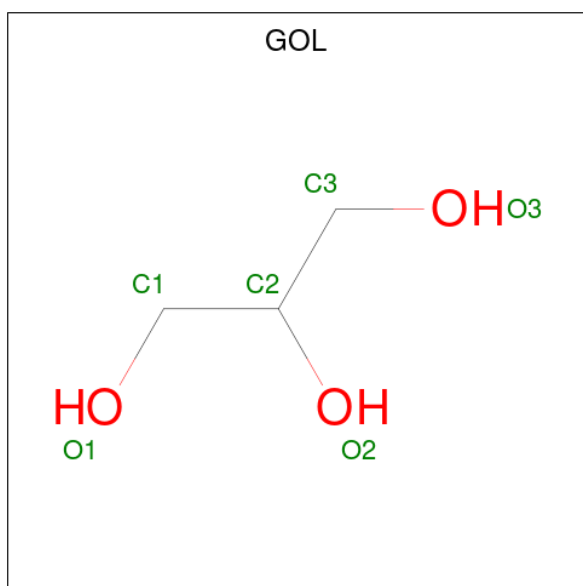
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Zn	0	2
			2	2		
5	B	2	Total	Zn	0	2
			2	2		
5	C	2	Total	Zn	0	2
			2	2		
5	D	2	Total	Zn	0	0
			2	2		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total O S 5 4 1	0	0
6	B	1	Total O S 5 4 1	0	0
6	B	1	Total O S 5 4 1	0	0
6	C	1	Total O S 5 4 1	0	0
6	D	1	Total O S 5 4 1	0	0

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



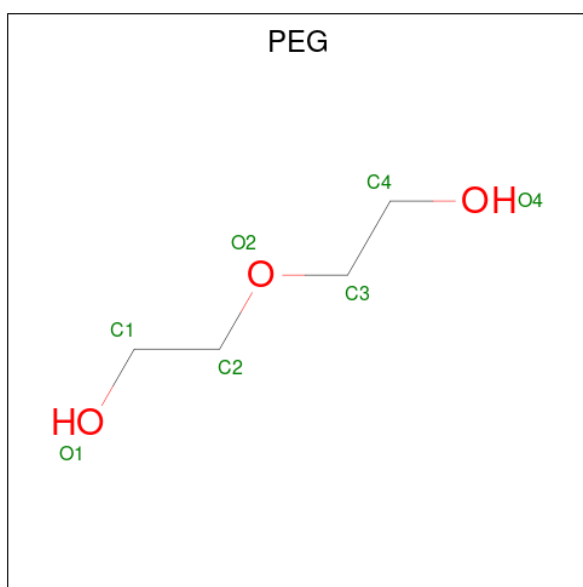
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			4	2	2		
8	A	1	Total	C	O	0	0
			4	2	2		
8	A	1	Total	C	O	0	0
			4	2	2		
8	A	1	Total	C	O	0	0
			4	2	2		
8	B	1	Total	C	O	0	0
			4	2	2		
8	B	1	Total	C	O	0	0
			4	2	2		
8	B	1	Total	C	O	0	0
			4	2	2		
8	B	1	Total	C	O	0	0
			4	2	2		
8	B	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			4	2	2		
8	C	1	Total	C	O	0	0
			4	2	2		
8	C	1	Total	C	O	0	0
			4	2	2		
8	C	1	Total	C	O	0	0
			4	2	2		
8	C	1	Total	C	O	0	0
			4	2	2		
8	C	1	Total	C	O	0	0
			4	2	2		
8	C	1	Total	C	O	0	0
			4	2	2		
8	D	1	Total	C	O	0	0
			4	2	2		
8	D	1	Total	C	O	0	0
			4	2	2		
8	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 9 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	O	0	0
			7	4	3		

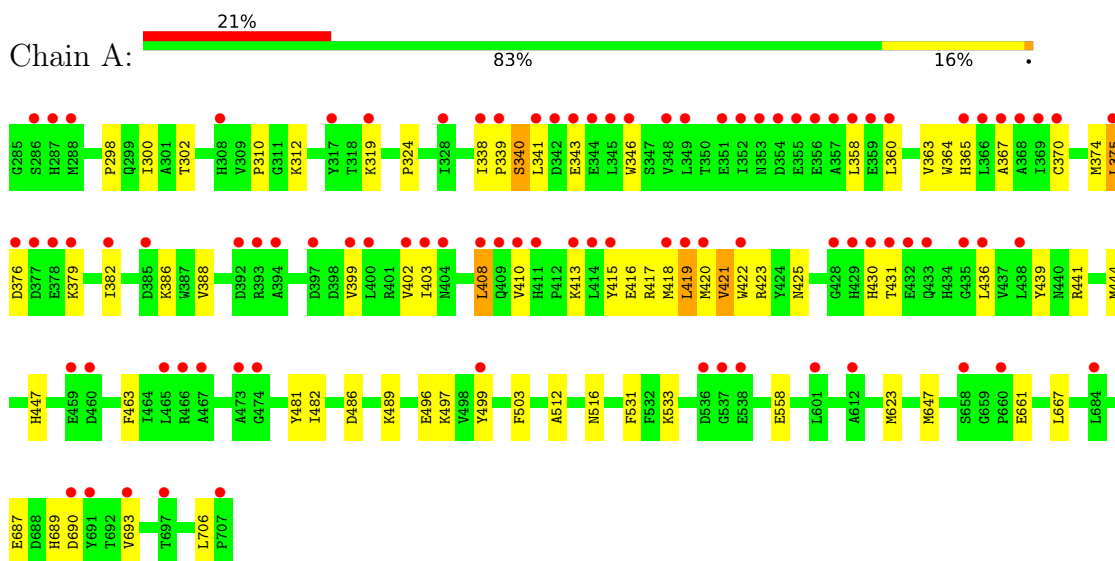
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	69	Total	O	0	0
			69	69		
10	B	117	Total	O	0	0
			117	117		
10	C	134	Total	O	0	0
			134	134		
10	D	114	Total	O	0	0
			114	114		

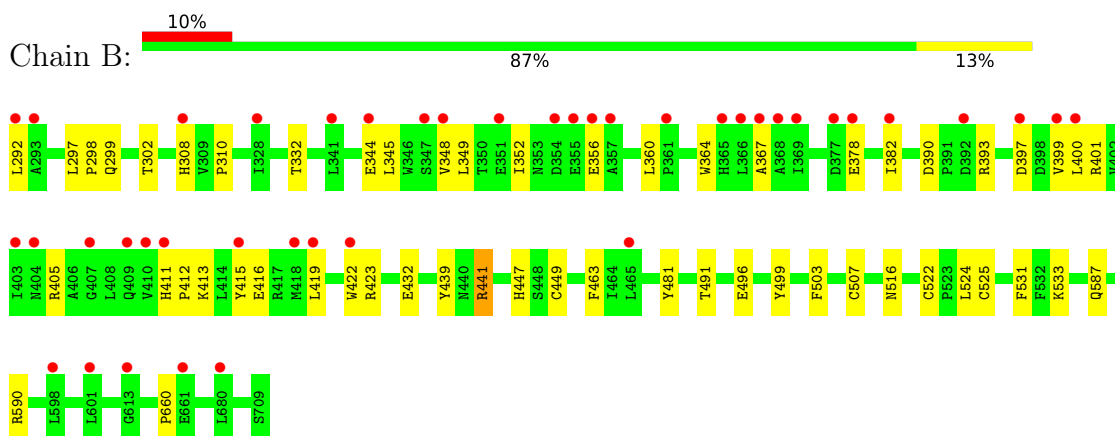
3 Residue-property plots [i](#)

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.

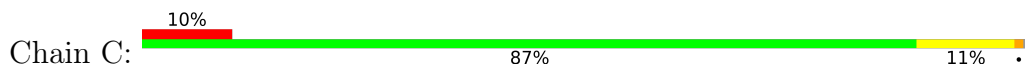
- Molecule 1: Apical complex lysine methyltransferase

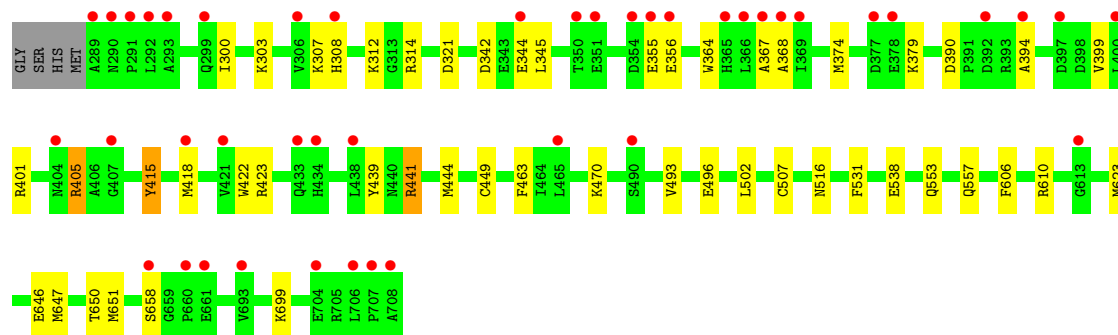


- Molecule 2: Apical complex lysine methyltransferase

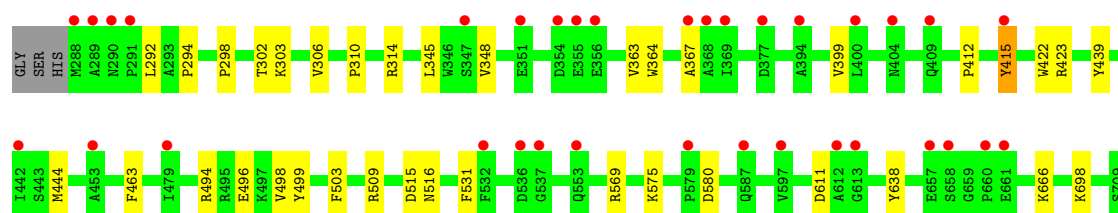
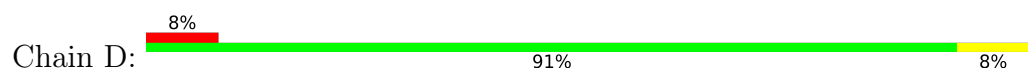


- Molecule 3: Apical complex lysine methyltransferase





● Molecule 4: Apical complex lysine methyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	61.94Å 89.37Å 91.72Å 108.69° 101.31° 103.41°	Depositor
Resolution (Å)	20.07 – 2.10 20.07 – 2.10	Depositor EDS
% Data completeness (in resolution range)	83.1 (20.07-2.10) 82.7 (20.07-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.44 (at 2.09Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.191 , 0.226 0.191 , 0.226	Depositor DCC
R_{free} test set	1943 reflections (2.33%)	wwPDB-VP
Wilson B-factor (Å ²)	40.4	Xtriage
Anisotropy	0.194	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 52.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.011 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14140	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.14% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MLY, PEG, ZN, EDO, GOL, MLZ, SO4

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	0.30	0/3376	0.52	2/4599 (0.0%)
2	B	0.27	0/3286	0.46	0/4470
3	C	0.27	0/3352	0.46	1/4569 (0.0%)
4	D	0.26	0/3319	0.45	0/4522
All	All	0.28	0/13333	0.47	3/18160 (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	419	LEU	CA-CB-CG	7.34	132.19	115.30
3	C	441	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	A	421	VAL	CG1-CB-CG2	5.04	118.97	110.90

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	3390	0	3278	59	0
2	B	3377	0	3272	46	0
3	C	3378	0	3271	36	0
4	D	3389	0	3281	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	2	0	0	0	0
5	B	2	0	0	0	0
5	C	2	0	0	0	0
5	D	2	0	0	0	0
6	A	5	0	0	0	0
6	B	10	0	0	0	0
6	C	5	0	0	0	0
6	D	5	0	0	3	0
7	A	24	0	32	0	0
7	C	12	0	16	0	0
7	D	12	0	16	1	0
8	A	16	0	24	0	0
8	B	28	0	42	0	0
8	C	28	0	42	1	0
8	D	12	0	18	0	0
9	B	7	0	10	1	0
10	A	69	0	0	5	0
10	B	117	0	0	5	0
10	C	134	0	0	7	0
10	D	114	0	0	7	0
All	All	14140	0	13302	162	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 6.

All (162) 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:496:GLU:OE1	10:A:901:HOH:O	1.86	0.93
1:A:512:ALA:O	1:A:533:LYS:NZ	2.07	0.88
2:B:348:VAL:HG12	2:B:352:ILE:HD11	1.59	0.84
4:D:292:LEU:O	10:D:901:HOH:O	1.99	0.78
2:B:352:ILE:HG22	2:B:401:ARG:HH21	1.50	0.77
1:A:388:VAL:HG11	1:A:417:ARG:HE	1.52	0.74
1:A:367:ALA:HB2	1:A:436:LEU:HD11	1.70	0.74
2:B:590:ARG:NH2	10:B:901:HOH:O	2.14	0.73
6:D:803:SO4:S	10:D:903:HOH:O	2.46	0.73
4:D:345:LEU:HA	4:D:348:VAL:HG12	1.73	0.71
3:C:394:ALA:O	10:C:901:HOH:O	2.10	0.70
1:A:338:ILE:HG13	1:A:340:SER:H	1.57	0.69
1:A:408:LEU:HD13	1:A:410:VAL:HG22	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:401:ARG:NH2	10:C:905:HOH:O	2.24	0.69
2:B:352:ILE:HG22	2:B:401:ARG:NH2	2.07	0.69
4:D:515:ASP:OD2	10:D:902:HOH:O	2.11	0.66
1:A:358:LEU:HD21	1:A:365:HIS:NE2	2.10	0.66
1:A:403:ILE:HG12	1:A:408:LEU:HD11	1.78	0.66
1:A:363:VAL:HG23	10:A:905:HOH:O	1.95	0.65
3:C:557:GLN:NE2	10:C:907:HOH:O	2.29	0.65
1:A:558:GLU:OE1	10:A:902:HOH:O	2.14	0.65
3:C:390:ASP:OD1	10:C:902:HOH:O	2.15	0.65
6:D:803:SO4:O2	10:D:903:HOH:O	2.13	0.65
2:B:352:ILE:HG12	2:B:405:ARG:HD3	1.80	0.63
3:C:307:LYS:HE2	3:C:502:LEU:O	1.98	0.63
2:B:348:VAL:O	2:B:352:ILE:HD12	1.99	0.62
6:D:803:SO4:O4	10:D:903:HOH:O	2.16	0.62
1:A:422:TRP:CE3	1:A:436:LEU:HD13	2.35	0.61
1:A:388:VAL:HG23	1:A:420:MET:HB2	1.82	0.59
1:A:687:GLU:O	10:A:903:HOH:O	2.16	0.59
1:A:375:LEU:HB2	1:A:379:LYS:HB2	1.84	0.58
2:B:352:ILE:CG1	2:B:405:ARG:HD3	2.34	0.58
1:A:343:GLU:OE1	1:A:346:TRP:HB3	2.05	0.56
2:B:522:CYS:HB3	2:B:525:CYS:SG	2.47	0.55
1:A:364:TRP:CZ3	1:A:423:ARG:HA	2.42	0.55
2:B:590:ARG:NH2	10:B:905:HOH:O	2.39	0.55
3:C:538:GLU:OE1	10:C:903:HOH:O	2.19	0.54
2:B:441:ARG:HH21	4:D:306:VAL:HG23	1.73	0.53
2:B:308:HIS:CD2	4:D:314:ARG:NH2	2.77	0.53
3:C:344:GLU:HG2	3:C:345:LEU:N	2.24	0.53
2:B:344:GLU:O	2:B:348:VAL:HG23	2.08	0.53
1:A:496:GLU:HA	1:A:499:TYR:CD2	2.44	0.53
1:A:421:VAL:O	1:A:425:ASN:HB2	2.10	0.52
2:B:299:GLN:O	2:B:302:THR:OG1	2.26	0.52
4:D:412:PRO:O	4:D:415:TYR:HB3	2.11	0.51
2:B:292:LEU:N	10:B:907:HOH:O	2.43	0.51
2:B:364:TRP:CZ3	2:B:423:ARG:HA	2.46	0.51
3:C:423:ARG:NH1	8:C:811:EDO:O2	2.44	0.51
3:C:312:MLY:HH12	10:C:985:HOH:O	2.11	0.51
3:C:516:ASN:HA	3:C:531:PHE:CD1	2.45	0.51
2:B:399:VAL:HG13	2:B:415:TYR:CD2	2.47	0.50
2:B:416:GLU:O	2:B:419:LEU:HB2	2.11	0.50
3:C:344:GLU:HG2	3:C:345:LEU:H	1.77	0.49
4:D:345:LEU:HA	4:D:348:VAL:CG1	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:ILE:HD12	1:A:339:PRO:HD2	1.95	0.49
1:A:376:ASP:HB3	1:A:379:LYS:HG3	1.94	0.49
2:B:516:ASN:HA	2:B:531:PHE:CD1	2.47	0.49
3:C:606:PHE:HE1	3:C:650:THR:HG21	1.77	0.49
4:D:364:TRP:CZ3	4:D:423:ARG:HA	2.47	0.49
1:A:441:ARG:HG3	3:C:300:ILE:HG21	1.95	0.48
2:B:356:GLU:O	2:B:401:ARG:NH2	2.42	0.48
4:D:298:PRO:O	4:D:302:THR:HG23	2.12	0.48
1:A:416:GLU:HA	1:A:419:LEU:HG	1.94	0.48
1:A:516:ASN:HA	1:A:531:PHE:CD1	2.48	0.48
3:C:364:TRP:CZ3	3:C:423:ARG:HA	2.47	0.48
2:B:356:GLU:HB3	2:B:401:ARG:NH2	2.27	0.48
1:A:399:VAL:HG13	1:A:415:TYR:CD2	2.49	0.48
3:C:355:GLU:OE2	3:C:405:ARG:NH2	2.47	0.48
1:A:367:ALA:CB	1:A:436:LEU:HD11	2.42	0.48
2:B:411:HIS:NE2	2:B:413:MLY:HB3	2.29	0.48
2:B:400:LEU:HD12	2:B:401:ARG:N	2.28	0.48
2:B:590:ARG:NH1	10:B:901:HOH:O	2.47	0.48
1:A:310:PRO:HB3	1:A:503:PHE:HB3	1.94	0.47
1:A:319:LYS:HG3	3:C:303:LYS:C	2.34	0.47
3:C:441:ARG:O	3:C:444:MET:HG2	2.14	0.47
4:D:509:ARG:HE	7:D:804:GOL:H2	1.79	0.47
1:A:416:GLU:OE2	1:A:419:LEU:HD11	2.15	0.47
2:B:367:ALA:HB1	2:B:422:TRP:CD2	2.50	0.47
3:C:321:ASP:HB3	3:C:470:MLY:HH11	1.97	0.47
4:D:363:VAL:N	10:D:904:HOH:O	2.13	0.47
2:B:447:HIS:HB2	2:B:481:TYR:CG	2.49	0.47
1:A:382:ILE:HG22	1:A:386:LYS:NZ	2.30	0.47
1:A:623:MET:HG2	1:A:647:MET:CE	2.44	0.47
1:A:346:TRP:HH2	1:A:363:VAL:HG22	1.79	0.46
4:D:516:ASN:HA	4:D:531:PHE:CD1	2.50	0.46
1:A:346:TRP:CH2	1:A:363:VAL:HG22	2.51	0.46
3:C:553:GLN:NE2	10:C:914:HOH:O	2.48	0.46
1:A:358:LEU:HD23	1:A:360:LEU:O	2.16	0.46
1:A:300:ILE:HG22	3:C:441:ARG:NH2	2.31	0.45
2:B:390:ASP:OD2	2:B:393:ARG:HB2	2.17	0.45
4:D:496:GLU:HA	4:D:499:TYR:CD2	2.51	0.45
1:A:430:HIS:ND1	1:A:431:THR:HG23	2.32	0.45
3:C:449:CYS:HB2	3:C:507:CYS:SG	2.55	0.45
3:C:342:ASP:OD1	3:C:344:GLU:HG2	2.16	0.45
4:D:310:PRO:HB3	4:D:503:PHE:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:370:CYS:O	1:A:374:MET:HB2	2.17	0.45
4:D:367:ALA:HB1	4:D:422:TRP:CD2	2.52	0.45
3:C:470:MLY:HH13	3:C:470:MLY:HD3	1.73	0.44
3:C:368:ALA:HA	3:C:418:MET:HG2	1.99	0.44
1:A:482:ILE:HD12	1:A:497:MLY:HB3	1.98	0.44
4:D:569:ARG:NH2	4:D:580:ASP:OD1	2.50	0.44
4:D:303:MLZ:HA	4:D:303:MLZ:HD3	1.80	0.44
1:A:379:LYS:O	1:A:382:ILE:HB	2.17	0.44
4:D:575:LYS:HE2	4:D:611:ASP:OD2	2.18	0.44
2:B:298:PRO:O	2:B:302:THR:HG23	2.18	0.43
2:B:356:GLU:HB3	2:B:401:ARG:CZ	2.48	0.43
4:D:666:MLZ:HD2	4:D:666:MLZ:HA	1.55	0.43
2:B:297:LEU:H	2:B:297:LEU:HD22	1.81	0.43
1:A:363:VAL:N	10:A:905:HOH:O	2.34	0.43
2:B:332:THR:HG23	4:D:294:PRO:HB3	2.00	0.43
3:C:493:VAL:O	3:C:496:GLU:HB2	2.18	0.43
3:C:356:GLU:HB3	3:C:401:ARG:NH1	2.32	0.43
2:B:348:VAL:HG12	2:B:352:ILE:CD1	2.38	0.43
3:C:399:VAL:HG13	3:C:415:TYR:CD2	2.54	0.43
1:A:324:PRO:HD2	2:B:524:LEU:HD21	2.00	0.43
2:B:378:GLU:O	2:B:382:ILE:HG13	2.19	0.42
1:A:661:GLU:H	1:A:661:GLU:HG2	1.66	0.42
3:C:367:ALA:HB1	3:C:422:TRP:CD2	2.54	0.42
1:A:319:LYS:HB3	1:A:319:LYS:HE2	1.85	0.42
1:A:417:ARG:O	1:A:421:VAL:HG13	2.19	0.42
4:D:494:ARG:O	4:D:498:VAL:HG22	2.19	0.42
4:D:439:TYR:CZ	4:D:463:PHE:HB2	2.54	0.42
2:B:447:HIS:HB2	2:B:481:TYR:CD1	2.55	0.42
4:D:638:TYR:OH	10:D:905:HOH:O	2.15	0.42
4:D:439:TYR:CE1	4:D:463:PHE:HB2	2.55	0.42
1:A:439:TYR:CE2	1:A:463:PHE:HB2	2.54	0.42
3:C:314:ARG:HG3	3:C:444:MET:HE3	2.00	0.42
3:C:651:MET:HE3	3:C:651:MET:HB3	1.88	0.42
2:B:412:PRO:O	2:B:415:TYR:HB3	2.19	0.42
3:C:610:ARG:NH1	3:C:646:GLU:OE2	2.52	0.42
1:A:418:MET:O	1:A:421:VAL:HG22	2.19	0.41
2:B:660:PRO:O	10:B:902:HOH:O	2.22	0.41
1:A:341:LEU:HG	1:A:374:MET:HE3	2.02	0.41
1:A:413:LYS:HD3	1:A:413:LYS:H	1.85	0.41
2:B:439:TYR:CE1	2:B:463:PHE:HB2	2.55	0.41
2:B:449:CYS:HB2	2:B:507:CYS:SG	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:623:MET:N	3:C:647:MET:HE1	2.36	0.41
3:C:439:TYR:CE1	3:C:463:PHE:HB2	2.55	0.41
3:C:646:GLU:O	3:C:650:THR:HG23	2.20	0.41
1:A:298:PRO:O	1:A:302:THR:HG23	2.19	0.41
1:A:312:MLY:HH22	1:A:312:MLY:HD3	1.81	0.41
2:B:310:PRO:HB3	2:B:503:PHE:HB3	2.02	0.41
2:B:345:LEU:O	2:B:349:LEU:HG	2.21	0.41
1:A:447:HIS:HB2	1:A:481:TYR:CG	2.56	0.41
2:B:496:GLU:HA	2:B:499:TYR:CD2	2.56	0.41
2:B:587:GLN:HG3	9:B:812:PEG:O4	2.20	0.41
3:C:374:MET:HE3	3:C:374:MET:HB3	1.94	0.41
1:A:346:TRP:CH2	1:A:363:VAL:HA	2.56	0.41
1:A:647:MET:HB2	1:A:647:MET:HE2	1.75	0.41
1:A:689:HIS:O	1:A:693:VAL:HG13	2.21	0.41
2:B:397:ASP:HA	2:B:400:LEU:HG	2.03	0.41
1:A:402:VAL:HG11	1:A:415:TYR:OH	2.21	0.41
1:A:486:ASP:OD1	1:A:489:MLY:HH23	2.21	0.41
3:C:307:LYS:HD2	3:C:308:HIS:N	2.36	0.41
4:D:399:VAL:HG13	4:D:415:TYR:CD2	2.56	0.40
1:A:363:VAL:HG12	1:A:436:LEU:HG	2.03	0.40
2:B:439:TYR:CZ	2:B:463:PHE:HB2	2.57	0.40
1:A:482:ILE:HD11	1:A:486:ASP:CB	2.52	0.40
1:A:690:ASP:HA	1:A:693:VAL:HG22	2.03	0.40
2:B:360:LEU:HD22	2:B:419:LEU:HD12	2.03	0.40
2:B:491:THR:HG21	2:B:533:MLZ:HCM1	2.03	0.40
1:A:667:LEU:HD12	1:A:706:LEU:HD23	2.04	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	412/423 (97%)	403 (98%)	9 (2%)	0	100	100
2	B	402/418 (96%)	386 (96%)	16 (4%)	0	100	100
3	C	409/424 (96%)	397 (97%)	12 (3%)	0	100	100
4	D	406/425 (96%)	393 (97%)	13 (3%)	0	100	100
All	All	1629/1690 (96%)	1579 (97%)	50 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	357/357 (100%)	353 (99%)	4 (1%)	73	79
2	B	348/348 (100%)	346 (99%)	2 (1%)	86	90
3	C	354/356 (99%)	350 (99%)	4 (1%)	73	79
4	D	351/353 (99%)	349 (99%)	2 (1%)	86	90
All	All	1410/1414 (100%)	1398 (99%)	12 (1%)	78	84

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	340	SER
1	A	375	LEU
1	A	408	LEU
1	A	444	MET
2	B	432	GLU
2	B	441	ARG
3	C	379	LYS
3	C	405	ARG
3	C	415	TYR
3	C	658	SER
4	D	415	TYR
4	D	444	MET

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

Mol	Chain	Res	Type
2	B	308	HIS
4	D	553	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

49 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	$\# Z > 2$
2	MLZ	B	379[B]	2	8,9,10	0.77	0	4,9,11	0.57	0
1	MLY	A	489	1	9,10,11	0.59	0	6,11,13	0.82	0
1	MLZ	A	380	1	8,9,10	0.76	0	4,9,11	0.61	0
2	MLZ	B	303	2	8,9,10	0.76	0	4,9,11	0.68	0
3	MLY	C	666	3	9,10,11	0.56	0	6,11,13	0.87	0
1	MLY	A	627	1	9,10,11	0.66	0	6,11,13	0.75	0
3	MLY	C	627	3	9,10,11	0.68	0	6,11,13	0.68	0
4	MLY	D	312	4	9,10,11	0.48	0	6,11,13	0.85	0
4	MLZ	D	533	4	8,9,10	0.77	0	4,9,11	0.73	0
2	MLZ	B	666	2	8,9,10	0.75	0	4,9,11	0.54	0
4	MLY	D	627	4	9,10,11	0.73	0	6,11,13	0.66	0
4	MLZ	D	303	4	8,9,10	0.78	0	4,9,11	0.55	0
4	MLZ	D	666	4	8,9,10	0.81	0	4,9,11	0.56	0
2	MLZ	B	319	2	8,9,10	0.76	0	4,9,11	0.67	0
2	MLY	B	489	2	9,10,11	0.56	0	6,11,13	0.62	0
2	MLZ	B	699[A]	2	8,9,10	0.81	0	4,9,11	0.58	0
3	MLY	C	575	3	9,10,11	0.48	0	6,11,13	0.83	0
2	MLZ	B	379[A]	2	8,9,10	0.79	0	4,9,11	0.62	0
2	MLZ	B	575	2	8,9,10	0.75	0	4,9,11	0.70	0
3	MLY	C	319	3	9,10,11	0.55	0	6,11,13	0.76	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLZ	A	470	1	8,9,10	0.77	0	4,9,11	0.68	0
3	MLZ	C	699	3	8,9,10	0.84	1 (12%)	4,9,11	0.64	0
4	MLZ	D	380	4	8,9,10	0.77	0	4,9,11	0.60	0
4	MLY	D	497	4	9,10,11	0.56	0	6,11,13	0.65	0
2	MLZ	B	497	2	8,9,10	0.75	0	4,9,11	0.67	0
1	MLY	A	666	1	9,10,11	0.54	0	6,11,13	0.85	0
2	MLY	B	627	2	9,10,11	0.77	0	6,11,13	0.99	0
2	MLY	B	312	2	9,10,11	0.53	0	6,11,13	0.84	0
3	MLZ	C	380	3	8,9,10	0.75	0	4,9,11	0.53	0
1	MLY	A	497	1	9,10,11	0.49	0	6,11,13	0.86	0
4	MLY	D	470	4	9,10,11	0.56	0	6,11,13	0.79	0
1	MLY	A	312	1	9,10,11	0.51	0	6,11,13	0.88	0
3	MLY	C	497	3	9,10,11	0.51	0	6,11,13	0.82	0
2	MLY	B	413	2	9,10,11	0.49	0	6,11,13	1.06	0
4	MLZ	D	698	4	8,9,10	0.83	1 (12%)	4,9,11	0.69	0
4	MLY	D	319	4	9,10,11	0.52	0	6,11,13	0.85	0
3	MLY	C	312	3	9,10,11	0.62	0	6,11,13	0.77	0
1	MLY	A	303	1	9,10,11	0.55	0	6,11,13	0.58	0
3	MLY	C	470	3	9,10,11	0.59	0	6,11,13	0.89	0
4	MLY	D	307	4	9,10,11	0.54	0	6,11,13	0.87	0
4	MLY	D	379	4	9,10,11	0.51	0	6,11,13	0.85	0
2	MLY	B	307	2	9,10,11	0.59	0	6,11,13	0.74	0
2	MLZ	B	654	2	8,9,10	0.77	0	4,9,11	0.63	0
1	MLY	A	307	1	9,10,11	0.62	0	6,11,13	0.89	0
4	MLY	D	489	4	9,10,11	0.52	0	6,11,13	0.66	0
4	MLY	D	413	4	9,10,11	0.59	0	6,11,13	0.78	0
2	MLZ	B	699[B]	2	8,9,10	0.80	0	4,9,11	0.60	0
2	MLZ	B	533	2	8,9,10	0.76	0	4,9,11	0.65	0
3	MLY	C	489	3	9,10,11	0.53	0	6,11,13	0.66	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
2	MLZ	B	379[B]	2	-	3/7/8/10	-
1	MLY	A	489	1	-	1/8/9/11	-
1	MLZ	A	380	1	-	1/7/8/10	-
2	MLZ	B	303	2	-	0/7/8/10	-
3	MLY	C	666	3	-	2/8/9/11	-
1	MLY	A	627	1	-	0/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MLY	C	627	3	-	1/8/9/11	-
4	MLY	D	312	4	-	1/8/9/11	-
4	MLZ	D	533	4	-	2/7/8/10	-
2	MLZ	B	666	2	-	1/7/8/10	-
4	MLY	D	627	4	-	1/8/9/11	-
4	MLZ	D	303	4	-	3/7/8/10	-
4	MLZ	D	666	4	-	4/7/8/10	-
2	MLZ	B	319	2	-	0/7/8/10	-
2	MLY	B	489	2	-	0/8/9/11	-
2	MLZ	B	699[A]	2	-	4/7/8/10	-
3	MLY	C	575	3	-	0/8/9/11	-
2	MLZ	B	379[A]	2	-	4/7/8/10	-
2	MLZ	B	575	2	-	0/7/8/10	-
3	MLY	C	319	3	-	0/8/9/11	-
1	MLZ	A	470	1	-	3/7/8/10	-
3	MLZ	C	699	3	-	3/7/8/10	-
4	MLZ	D	380	4	-	1/7/8/10	-
4	MLY	D	497	4	-	0/8/9/11	-
2	MLZ	B	497	2	-	0/7/8/10	-
1	MLY	A	666	1	-	3/8/9/11	-
2	MLY	B	627	2	-	0/8/9/11	-
2	MLY	B	312	2	-	0/8/9/11	-
3	MLZ	C	380	3	-	1/7/8/10	-
1	MLY	A	497	1	-	0/8/9/11	-
4	MLY	D	470	4	-	0/8/9/11	-
1	MLY	A	312	1	-	1/8/9/11	-
3	MLY	C	497	3	-	4/8/9/11	-
2	MLY	B	413	2	-	6/8/9/11	-
4	MLZ	D	698	4	-	0/7/8/10	-
4	MLY	D	319	4	-	0/8/9/11	-
3	MLY	C	312	3	-	3/8/9/11	-
1	MLY	A	303	1	-	0/8/9/11	-
3	MLY	C	470	3	-	3/8/9/11	-
4	MLY	D	307	4	-	0/8/9/11	-
4	MLY	D	379	4	-	2/8/9/11	-
2	MLY	B	307	2	-	1/8/9/11	-
2	MLZ	B	654	2	-	3/7/8/10	-
1	MLY	A	307	1	-	2/8/9/11	-
4	MLY	D	489	4	-	0/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MLY	D	413	4	-	2/8/9/11	-
2	MLZ	B	699[B]	2	-	3/7/8/10	-
2	MLZ	B	533	2	-	4/7/8/10	-
3	MLY	C	489	3	-	0/8/9/11	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	699	MLZ	O-C	2.05	1.28	1.19
4	D	698	MLZ	O-C	2.05	1.28	1.19

There are no bond angle outliers.

There are no chirality outliers.

All (73) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	312	MLY	O-C-CA-CB
1	A	380	MLZ	CD-CE-NZ-CM
2	B	379[A]	MLZ	C-CA-CB-CG
2	B	379[B]	MLZ	N-CA-CB-CG
2	B	379[B]	MLZ	C-CA-CB-CG
2	B	413	MLY	N-CA-CB-CG
2	B	413	MLY	C-CA-CB-CG
2	B	533	MLZ	C-CA-CB-CG
3	C	312	MLY	O-C-CA-CB
3	C	497	MLY	O-C-CA-CB
4	D	312	MLY	O-C-CA-CB
4	D	379	MLY	C-CA-CB-CG
4	D	533	MLZ	C-CA-CB-CG
2	B	654	MLZ	CG-CD-CE-NZ
2	B	699[A]	MLZ	CG-CD-CE-NZ
2	B	699[B]	MLZ	CG-CD-CE-NZ
1	A	666	MLY	CD-CE-NZ-CH1
1	A	666	MLY	CD-CE-NZ-CH2
3	C	312	MLY	CD-CE-NZ-CH1
4	D	666	MLZ	CA-CB-CG-CD
2	B	654	MLZ	CD-CE-NZ-CM
2	B	699[A]	MLZ	CD-CE-NZ-CM
2	B	533	MLZ	CG-CD-CE-NZ
4	D	533	MLZ	CG-CD-CE-NZ

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Mol	Chain	Res	Type	Atoms
1	A	307	MLY	CD-CE-NZ-CH2
1	A	489	MLY	CD-CE-NZ-CH2
2	B	413	MLY	CD-CE-NZ-CH1
2	B	413	MLY	CD-CE-NZ-CH2
1	A	307	MLY	CD-CE-NZ-CH1
3	C	312	MLY	CD-CE-NZ-CH2
3	C	666	MLY	CD-CE-NZ-CH2
3	C	497	MLY	CD-CE-NZ-CH2
4	D	413	MLY	CD-CE-NZ-CH2
2	B	413	MLY	CG-CD-CE-NZ
2	B	379[B]	MLZ	CA-CB-CG-CD
2	B	699[A]	MLZ	CA-CB-CG-CD
2	B	699[B]	MLZ	CE-CD-CG-CB
1	A	470	MLZ	CA-CB-CG-CD
2	B	699[B]	MLZ	CD-CE-NZ-CM
3	C	380	MLZ	CD-CE-NZ-CM
4	D	413	MLY	CE-CD-CG-CB
4	D	303	MLZ	CE-CD-CG-CB
3	C	627	MLY	CG-CD-CE-NZ
4	D	380	MLZ	CE-CD-CG-CB
4	D	627	MLY	CG-CD-CE-NZ
2	B	379[A]	MLZ	CA-CB-CG-CD
3	C	699	MLZ	CA-CB-CG-CD
1	A	470	MLZ	CG-CD-CE-NZ
3	C	666	MLY	CE-CD-CG-CB
2	B	699[A]	MLZ	CE-CD-CG-CB
4	D	666	MLZ	CE-CD-CG-CB
2	B	666	MLZ	CD-CE-NZ-CM
4	D	666	MLZ	CD-CE-NZ-CM
3	C	470	MLY	CG-CD-CE-NZ
4	D	303	MLZ	CA-CB-CG-CD
4	D	303	MLZ	CD-CE-NZ-CM
3	C	497	MLY	CA-CB-CG-CD
2	B	533	MLZ	N-CA-CB-CG
4	D	666	MLZ	N-CA-CB-CG
2	B	379[A]	MLZ	CG-CD-CE-NZ
3	C	470	MLY	CD-CE-NZ-CH1
3	C	699	MLZ	CD-CE-NZ-CM
2	B	533	MLZ	CE-CD-CG-CB
3	C	497	MLY	CD-CE-NZ-CH1
4	D	379	MLY	CG-CD-CE-NZ
3	C	699	MLZ	CE-CD-CG-CB

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Mol	Chain	Res	Type	Atoms
3	C	470	MLY	CE-CD-CG-CB
2	B	379[A]	MLZ	CD-CE-NZ-CM
2	B	307	MLY	CG-CD-CE-NZ
2	B	654	MLZ	CE-CD-CG-CB
2	B	413	MLY	CA-CB-CG-CD
1	A	470	MLZ	CD-CE-NZ-CM
1	A	666	MLY	CA-CB-CG-CD

There are no ring outliers.

9 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	489	MLY	1	0
4	D	303	MLZ	1	0
4	D	666	MLZ	1	0
1	A	497	MLY	1	0
1	A	312	MLY	1	0
2	B	413	MLY	1	0
3	C	312	MLY	1	0
3	C	470	MLY	2	0
2	B	533	MLZ	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 43 ligands modelled in this entry, 8 are monoatomic - leaving 35 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	$\# Z > 2$
9	PEG	B	812	-	6,6,6	0.49	0	5,5,5	0.35	0
8	EDO	B	809	-	3,3,3	0.46	0	2,2,2	0.28	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	EDO	B	811	-	3,3,3	0.46	0	2,2,2	0.36	0
8	EDO	C	807	-	3,3,3	0.46	0	2,2,2	0.34	0
8	EDO	B	805	-	3,3,3	0.44	0	2,2,2	0.34	0
6	SO4	D	803	-	4,4,4	0.14	0	6,6,6	0.05	0
8	EDO	A	810	-	3,3,3	0.46	0	2,2,2	0.29	0
6	SO4	C	803	-	4,4,4	0.14	0	6,6,6	0.05	0
8	EDO	B	806	-	3,3,3	0.45	0	2,2,2	0.35	0
8	EDO	C	809	-	3,3,3	0.45	0	2,2,2	0.37	0
8	EDO	C	811	-	3,3,3	0.45	0	2,2,2	0.30	0
7	GOL	A	806	-	5,5,5	0.34	0	5,5,5	0.42	0
7	GOL	D	805	-	5,5,5	0.37	0	5,5,5	0.32	0
8	EDO	A	809	-	3,3,3	0.46	0	2,2,2	0.26	0
7	GOL	C	805	-	5,5,5	0.37	0	5,5,5	0.21	0
6	SO4	B	803	-	4,4,4	0.14	0	6,6,6	0.04	0
7	GOL	C	804	-	5,5,5	0.37	0	5,5,5	0.27	0
8	EDO	A	811	-	3,3,3	0.41	0	2,2,2	0.43	0
8	EDO	B	807	-	3,3,3	0.46	0	2,2,2	0.36	0
8	EDO	C	808	-	3,3,3	0.45	0	2,2,2	0.40	0
8	EDO	A	808	-	3,3,3	0.46	0	2,2,2	0.29	0
8	EDO	C	812	-	3,3,3	0.46	0	2,2,2	0.30	0
8	EDO	C	806	-	3,3,3	0.46	0	2,2,2	0.31	0
6	SO4	A	803	-	4,4,4	0.14	0	6,6,6	0.07	0
8	EDO	D	807	-	3,3,3	0.45	0	2,2,2	0.29	0
6	SO4	B	804	-	4,4,4	0.15	0	6,6,6	0.05	0
7	GOL	A	807	-	5,5,5	0.38	0	5,5,5	0.26	0
8	EDO	D	808	-	3,3,3	0.46	0	2,2,2	0.32	0
8	EDO	B	808	-	3,3,3	0.45	0	2,2,2	0.36	0
8	EDO	C	810	-	3,3,3	0.43	0	2,2,2	0.40	0
7	GOL	D	804	-	5,5,5	0.38	0	5,5,5	0.10	0
8	EDO	D	806	-	3,3,3	0.45	0	2,2,2	0.35	0
7	GOL	A	805	-	5,5,5	0.38	0	5,5,5	0.26	0
8	EDO	B	810	-	3,3,3	0.45	0	2,2,2	0.37	0
7	GOL	A	804	-	5,5,5	0.38	0	5,5,5	0.29	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
9	PEG	B	812	-	-	1/4/4/4	-
8	EDO	B	809	-	-	1/1/1/1	-
8	EDO	B	811	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	EDO	C	807	-	-	0/1/1/1	-
8	EDO	B	805	-	-	0/1/1/1	-
8	EDO	A	810	-	-	1/1/1/1	-
8	EDO	B	806	-	-	0/1/1/1	-
8	EDO	C	809	-	-	1/1/1/1	-
8	EDO	C	811	-	-	0/1/1/1	-
7	GOL	A	806	-	-	3/4/4/4	-
7	GOL	D	805	-	-	2/4/4/4	-
8	EDO	A	809	-	-	1/1/1/1	-
7	GOL	C	805	-	-	2/4/4/4	-
7	GOL	C	804	-	-	0/4/4/4	-
8	EDO	A	811	-	-	1/1/1/1	-
8	EDO	B	807	-	-	1/1/1/1	-
8	EDO	C	808	-	-	0/1/1/1	-
8	EDO	A	808	-	-	0/1/1/1	-
8	EDO	C	812	-	-	0/1/1/1	-
8	EDO	C	806	-	-	0/1/1/1	-
8	EDO	D	807	-	-	0/1/1/1	-
7	GOL	A	807	-	-	2/4/4/4	-
8	EDO	D	808	-	-	0/1/1/1	-
8	EDO	B	808	-	-	1/1/1/1	-
8	EDO	C	810	-	-	0/1/1/1	-
7	GOL	D	804	-	-	3/4/4/4	-
8	EDO	D	806	-	-	0/1/1/1	-
7	GOL	A	805	-	-	2/4/4/4	-
8	EDO	B	810	-	-	0/1/1/1	-
7	GOL	A	804	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	807	GOL	C1-C2-C3-O3
7	C	805	GOL	O1-C1-C2-C3
7	D	804	GOL	C1-C2-C3-O3
7	C	805	GOL	O1-C1-C2-O2
7	D	804	GOL	O2-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
7	A	806	GOL	O1-C1-C2-C3
7	A	806	GOL	C1-C2-C3-O3
7	D	805	GOL	O1-C1-C2-C3
7	A	806	GOL	O2-C2-C3-O3
7	A	807	GOL	O2-C2-C3-O3
8	B	807	EDO	O1-C1-C2-O2
7	D	805	GOL	O1-C1-C2-O2
8	B	808	EDO	O1-C1-C2-O2
9	B	812	PEG	O1-C1-C2-O2
7	A	805	GOL	O1-C1-C2-C3
8	A	810	EDO	O1-C1-C2-O2
8	A	811	EDO	O1-C1-C2-O2
8	B	809	EDO	O1-C1-C2-O2
8	B	811	EDO	O1-C1-C2-O2
7	A	805	GOL	O1-C1-C2-O2
8	A	809	EDO	O1-C1-C2-O2
8	C	809	EDO	O1-C1-C2-O2
7	D	804	GOL	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	B	812	PEG	1	0
6	D	803	SO4	3	0
8	C	811	EDO	1	0
7	D	804	GOL	1	0

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	414/423 (97%)	1.07	90 (21%) 0 0	31, 61, 140, 170	0
2	B	404/418 (96%)	0.57	42 (10%) 6 8	32, 50, 100, 120	0
3	C	410/424 (96%)	0.48	43 (10%) 6 8	28, 46, 91, 123	0
4	D	408/425 (96%)	0.36	34 (8%) 11 14	29, 48, 84, 111	0
All	All	1636/1690 (96%)	0.62	209 (12%) 3 4	28, 51, 107, 170	0

All (209) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	431	THR	9.5
1	A	382	ILE	9.3
2	B	292	LEU	7.9
3	C	289	ALA	7.5
1	A	660	PRO	6.7
1	A	368	ALA	6.4
1	A	357	ALA	6.2
1	A	345	LEU	6.2
1	A	365	HIS	6.1
1	A	349	LEU	6.0
3	C	708	ALA	6.0
1	A	351	GLU	6.0
4	D	289	ALA	5.9
1	A	344	GLU	5.9
1	A	430	HIS	5.8
1	A	399	VAL	5.8
4	D	288	MET	5.8
1	A	404	ASN	5.6
1	A	377	ASP	5.5
3	C	290	ASN	5.3
2	B	293	ALA	5.3

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Mol	Chain	Res	Type	RSRZ
1	A	358	LEU	5.2
2	B	409	GLN	5.2
1	A	308	HIS	5.2
1	A	394	ALA	5.1
1	A	353	ASN	5.0
2	B	382	ILE	5.0
2	B	378	GLU	4.9
2	B	368	ALA	4.9
2	B	351	GLU	4.8
1	A	415	TYR	4.8
1	A	352	ILE	4.8
2	B	400	LEU	4.8
1	A	348	VAL	4.8
1	A	422	TRP	4.7
2	B	344	GLU	4.7
1	A	418	MET	4.7
3	C	707	PRO	4.6
2	B	355	GLU	4.6
1	A	419	LEU	4.6
1	A	413	LYS	4.5
2	B	356	GLU	4.5
3	C	706	LEU	4.4
1	A	366	LEU	4.4
1	A	428	GLY	4.4
3	C	660	PRO	4.3
3	C	366	LEU	4.3
3	C	661	GLU	4.2
4	D	355	GLU	4.2
1	A	697	THR	4.2
3	C	433	GLN	4.2
1	A	367	ALA	4.1
1	A	369	ILE	4.1
1	A	459	GLU	4.1
4	D	347	SER	4.1
3	C	291	PRO	4.0
1	A	403	ILE	4.0
2	B	377	ASP	4.0
3	C	368	ALA	4.0
1	A	338	ILE	4.0
4	D	356	GLU	4.0
1	A	537	GLY	3.9
2	B	404	ASN	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	410	VAL	3.9
1	A	465	LEU	3.9
3	C	404	ASN	3.9
4	D	354	ASP	3.8
1	A	402	VAL	3.8
4	D	377	ASP	3.8
2	B	354	ASP	3.8
1	A	359	GLU	3.8
2	B	365	HIS	3.7
1	A	354	ASP	3.7
2	B	348	VAL	3.7
3	C	355	GLU	3.7
2	B	410	VAL	3.7
1	A	658	SER	3.6
3	C	369	ILE	3.6
1	A	339	PRO	3.6
1	A	379	LYS	3.6
1	A	286	SER	3.6
2	B	367	ALA	3.6
2	B	369	ILE	3.6
2	B	366	LEU	3.6
1	A	409	GLN	3.5
4	D	657	GLU	3.5
2	B	598	LEU	3.5
1	A	397	ASP	3.4
1	A	288	MET	3.4
1	A	376	ASP	3.4
1	A	400	LEU	3.3
1	A	432	GLU	3.3
2	B	601	LEU	3.3
1	A	378	GLU	3.3
1	A	429	HIS	3.2
1	A	341	LEU	3.2
4	D	394	ALA	3.2
2	B	613	GLY	3.2
1	A	346	TRP	3.1
1	A	460	ASP	3.1
1	A	474	GLY	3.1
2	B	392	ASP	3.1
4	D	613	GLY	3.1
1	A	411	HIS	3.1
3	C	365	HIS	3.1

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Mol	Chain	Res	Type	RSRZ
3	C	292	LEU	3.1
2	B	357	ALA	3.0
3	C	418	MET	3.0
1	A	473	ALA	3.0
3	C	377	ASP	3.0
1	A	536	ASP	3.0
1	A	375	LEU	3.0
1	A	438	LEU	3.0
4	D	369	ILE	2.9
4	D	532	PHE	2.9
1	A	538	GLU	2.9
1	A	612	ALA	2.9
4	D	612	ALA	2.9
2	B	419	LEU	2.9
3	C	308	HIS	2.9
3	C	344	GLU	2.9
3	C	490	SER	2.9
3	C	306	VAL	2.9
3	C	367	ALA	2.9
2	B	411	HIS	2.8
2	B	661	GLU	2.8
1	A	392	ASP	2.8
2	B	407	GLY	2.8
4	D	415	TYR	2.8
3	C	394	ALA	2.8
1	A	343	GLU	2.8
4	D	368	ALA	2.7
4	D	453	ALA	2.7
2	B	415	TYR	2.7
3	C	351	GLU	2.7
1	A	393	ARG	2.7
4	D	536	ASP	2.7
3	C	378	GLU	2.7
4	D	367	ALA	2.7
1	A	433	GLN	2.7
3	C	704	GLU	2.6
1	A	356	GLU	2.6
3	C	356	GLU	2.6
1	A	328	ILE	2.6
1	A	360	LEU	2.6
4	D	290	ASN	2.6
1	A	499	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	342	ASP	2.6
4	D	553	GLN	2.6
2	B	403	ILE	2.5
4	D	404	ASN	2.5
2	B	680	LEU	2.5
4	D	537	GLY	2.5
2	B	399	VAL	2.5
4	D	351	GLU	2.5
3	C	354	ASP	2.5
3	C	407	GLY	2.5
2	B	341	LEU	2.4
1	A	317	TYR	2.4
2	B	328	ILE	2.4
1	A	414	LEU	2.4
1	A	436	LEU	2.4
1	A	601	LEU	2.4
4	D	442	ILE	2.4
3	C	434	HIS	2.4
1	A	684	LEU	2.4
3	C	658	SER	2.4
4	D	658	SER	2.4
3	C	392	ASP	2.4
1	A	408	LEU	2.4
3	C	400	LEU	2.4
1	A	691	TYR	2.4
1	A	385	ASP	2.4
4	D	661	GLU	2.3
1	A	693	VAL	2.3
2	B	418	MET	2.3
2	B	397	ASP	2.3
4	D	660	PRO	2.3
1	A	355	GLU	2.3
4	D	587	GLN	2.3
1	A	319	LYS	2.3
3	C	421	VAL	2.2
4	D	597	VAL	2.2
2	B	361	PRO	2.2
1	A	467	ALA	2.2
1	A	466	ARG	2.2
3	C	397	ASP	2.2
3	C	465	LEU	2.2
4	D	579	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
3	C	350	THR	2.2
1	A	370	CYS	2.2
1	A	435	GLY	2.2
2	B	465	LEU	2.1
2	B	308	HIS	2.1
3	C	613	GLY	2.1
4	D	409	GLN	2.1
2	B	422	TRP	2.1
3	C	299	GLN	2.1
2	B	347	SER	2.1
1	A	690	ASP	2.1
4	D	400	LEU	2.1
3	C	693	VAL	2.1
1	A	420	MET	2.0
1	A	707	PRO	2.0
3	C	438	LEU	2.0
1	A	287	HIS	2.0
3	C	293	ALA	2.0
4	D	291	PRO	2.0
4	D	479	ILE	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
4	MLY	D	413	11/12	0.74	0.34	62,68,82,83	0
2	MLY	B	413	11/12	0.76	0.30	79,84,91,92	0
1	MLZ	A	380	10/11	0.77	0.20	108,116,121,122	0
4	MLY	D	379	11/12	0.85	0.26	57,71,73,73	0
1	MLY	A	497	11/12	0.88	0.13	48,54,66,67	0
1	MLY	A	307	11/12	0.88	0.19	51,58,63,66	0
3	MLY	C	627	11/12	0.89	0.14	35,40,64,64	0
1	MLY	A	312	11/12	0.89	0.16	63,65,68,69	0
2	MLZ	B	666	10/11	0.89	0.18	46,50,64,65	0
4	MLY	D	627	11/12	0.89	0.14	35,42,58,59	0
1	MLY	A	666	11/12	0.90	0.17	52,56,62,62	0
4	MLZ	D	380	10/11	0.90	0.13	60,63,65,71	0
3	MLZ	C	380	10/11	0.90	0.15	61,63,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	MLY	D	497	11/12	0.90	0.16	35,44,60,62	0
2	MLZ	B	654	10/11	0.90	0.16	50,60,69,70	0
1	MLY	A	627	11/12	0.91	0.14	32,38,60,61	0
2	MLZ	B	533	10/11	0.91	0.20	50,60,68,70	0
2	MLZ	B	575	10/11	0.91	0.14	56,62,64,72	0
1	MLY	A	303	11/12	0.91	0.15	32,39,51,54	0
2	MLZ	B	379[A]	10/11	0.91	0.22	74,79,80,83	10
2	MLZ	B	379[B]	10/11	0.91	0.22	74,79,80,83	10
3	MLZ	C	699	10/11	0.92	0.14	50,55,63,65	0
4	MLY	D	312	11/12	0.92	0.17	33,39,44,46	0
1	MLZ	A	470	10/11	0.92	0.17	54,60,71,71	0
2	MLY	B	307	11/12	0.92	0.15	53,59,64,66	0
2	MLY	B	312	11/12	0.92	0.15	45,48,54,58	0
3	MLY	C	470	11/12	0.92	0.18	31,35,56,58	0
4	MLZ	D	533	10/11	0.92	0.19	39,49,63,64	0
1	MLY	A	489	11/12	0.92	0.15	34,40,49,49	0
4	MLY	D	307	11/12	0.93	0.17	50,60,65,66	0
2	MLZ	B	699[A]	10/11	0.93	0.16	38,42,44,45	10
2	MLZ	B	699[B]	10/11	0.93	0.16	38,42,44,45	10
2	MLZ	B	303	10/11	0.93	0.20	51,59,75,77	0
4	MLZ	D	666	10/11	0.93	0.15	41,48,64,65	0
3	MLY	C	666	11/12	0.94	0.16	54,57,67,70	0
3	MLY	C	497	11/12	0.94	0.11	34,45,59,59	0
4	MLZ	D	303	10/11	0.94	0.12	49,52,62,64	0
3	MLY	C	319	11/12	0.94	0.10	36,40,46,48	0
4	MLZ	D	698	10/11	0.94	0.11	44,53,57,58	0
2	MLZ	B	497	10/11	0.95	0.11	47,49,63,63	0
3	MLY	C	312	11/12	0.95	0.14	41,43,50,56	0
3	MLY	C	575	11/12	0.95	0.12	42,47,54,59	0
4	MLY	D	319	11/12	0.95	0.11	35,37,47,50	0
2	MLY	B	489	11/12	0.96	0.14	33,38,40,41	0
2	MLZ	B	319	10/11	0.96	0.09	43,49,52,54	0
3	MLY	C	489	11/12	0.96	0.15	32,35,41,45	0
4	MLY	D	470	11/12	0.96	0.12	35,43,48,49	0
4	MLY	D	489	11/12	0.96	0.15	31,36,44,46	0
2	MLY	B	627	11/12	0.97	0.11	29,33,58,60	0

6.3 Carbohydrates

There are no monosaccharides 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(Å ²)	Q<0.9
8	EDO	C	812	4/4	0.71	0.24	78,79,81,81	0
7	GOL	A	806	6/6	0.76	0.24	64,69,70,72	0
7	GOL	A	807	6/6	0.77	0.22	93,93,94,94	0
8	EDO	B	808	4/4	0.78	0.14	80,81,82,82	0
6	SO4	B	804	5/5	0.79	0.28	117,117,117,117	0
8	EDO	D	808	4/4	0.79	0.17	67,68,69,69	0
8	EDO	A	811	4/4	0.80	0.23	73,75,75,77	0
7	GOL	D	804	6/6	0.80	0.18	38,46,52,56	0
8	EDO	C	808	4/4	0.81	0.25	62,63,66,68	0
9	PEG	B	812	7/7	0.81	0.22	78,79,84,85	0
8	EDO	B	807	4/4	0.82	0.33	73,76,78,78	0
8	EDO	A	809	4/4	0.82	0.25	61,65,66,67	0
6	SO4	B	803	5/5	0.82	0.18	123,124,125,126	0
8	EDO	B	811	4/4	0.83	0.12	73,74,75,76	0
7	GOL	D	805	6/6	0.84	0.18	84,88,89,90	0
7	GOL	A	805	6/6	0.84	0.41	77,79,79,80	0
8	EDO	A	810	4/4	0.85	0.09	72,73,73,73	0
8	EDO	B	809	4/4	0.85	0.15	74,78,80,80	0
8	EDO	C	811	4/4	0.85	0.12	77,78,78,80	0
8	EDO	C	806	4/4	0.86	0.13	56,63,68,70	0
8	EDO	D	807	4/4	0.87	0.17	61,62,65,67	0
5	ZN	A	801[L]	1/1	0.88	0.10	42,42,42,42	1
8	EDO	C	807	4/4	0.89	0.29	71,71,73,73	0
6	SO4	C	803	5/5	0.89	0.14	103,104,105,106	0
8	EDO	C	809	4/4	0.89	0.28	63,66,67,68	0
8	EDO	A	808	4/4	0.89	0.10	73,74,74,77	0
8	EDO	C	810	4/4	0.90	0.33	75,76,76,77	0
8	EDO	B	810	4/4	0.90	0.18	79,80,80,83	0
5	ZN	B	802[L]	1/1	0.90	0.09	45,45,45,45	1
8	EDO	B	806	4/4	0.91	0.35	53,54,57,58	0
8	EDO	D	806	4/4	0.91	0.10	77,77,77,77	0
7	GOL	A	804	6/6	0.91	0.16	44,49,55,59	0
6	SO4	D	803	5/5	0.91	0.13	102,102,103,104	0
8	EDO	B	805	4/4	0.91	0.11	66,68,70,72	0
6	SO4	A	803	5/5	0.92	0.10	94,94,97,99	0
7	GOL	C	805	6/6	0.93	0.18	58,63,64,67	0
7	GOL	C	804	6/6	0.95	0.12	40,44,53,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	ZN	D	802	1/1	0.96	0.05	46,46,46,46	0
5	ZN	D	801	1/1	0.96	0.07	40,40,40,40	0
5	ZN	C	801[L]	1/1	0.97	0.09	36,36,36,36	1
5	ZN	B	801[L]	1/1	0.97	0.09	39,39,39,39	1
5	ZN	C	802[L]	1/1	0.98	0.06	37,37,37,37	1
5	ZN	A	802[L]	1/1	0.98	0.07	38,38,38,38	1

6.5 Other polymers [i](#)

There are no such residues in this entry.