



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:07 PM GMT

PDB ID : 1IV8
Title : Crystal Structure of Maltooligosyl trehalose synthase
Authors : Kobayashi, M.; Kubota, M.; Matsuura, Y.
Deposited on : 2002-03-15
Resolution : 1.90 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

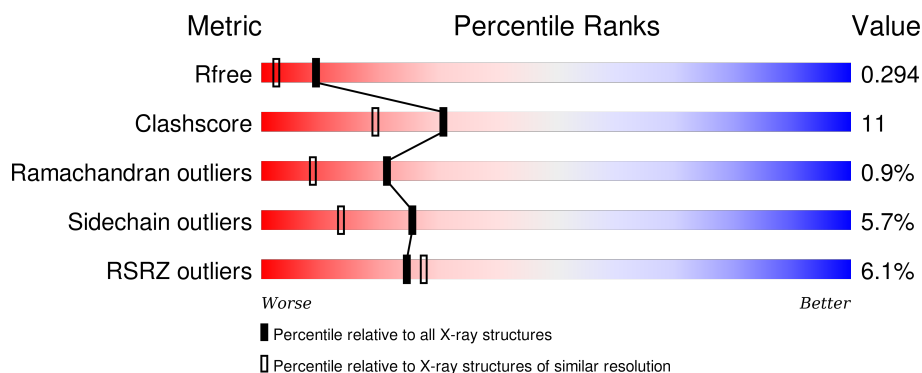
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	720	<div> <div>6%</div> <div>78%</div> <div>19%</div> <div>.</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6379 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 MALTOOLIGOSYL TREHALOSE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	720	Total	C	N	O	S	0	0	0
			6013	3879	991	1122	21			

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	MLZ	LYS	MODIFIED RESIDUE	UNP Q53688
A	105	MLZ	LYS	MODIFIED RESIDUE	UNP Q53688
A	108	MLZ	LYS	MODIFIED RESIDUE	UNP Q53688
A	109	MLY	LYS	MODIFIED RESIDUE	UNP Q53688
A	111	MLY	LYS	MODIFIED RESIDUE	UNP Q53688
A	206	MLY	LYS	MODIFIED RESIDUE	UNP Q53688
A	216	MLY	LYS	MODIFIED RESIDUE	UNP Q53688
A	250	MLY	LYS	MODIFIED RESIDUE	UNP Q53688
A	310	MLZ	LYS	MODIFIED RESIDUE	UNP Q53688
A	326	MLZ	LYS	MODIFIED RESIDUE	UNP Q53688
A	390	MLY	LYS	MODIFIED RESIDUE	UNP Q53688
A	467	MLZ	LYS	MODIFIED RESIDUE	UNP Q53688
A	504	MLY	LYS	MODIFIED RESIDUE	UNP Q53688
A	508	MLZ	LYS	MODIFIED RESIDUE	UNP Q53688
A	513	MLZ	LYS	MODIFIED RESIDUE	UNP Q53688
A	519	MLZ	LYS	MODIFIED RESIDUE	UNP Q53688
A	558	MLY	LYS	MODIFIED RESIDUE	UNP Q53688
A	616	MLY	LYS	MODIFIED RESIDUE	UNP Q53688
A	638	MLZ	LYS	MODIFIED RESIDUE	UNP Q53688

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	366	Total	O	0	0
			366	366		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: MALTOOLIGOSYL TREHALOSE SYNTHASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.50Å 68.50Å 93.77Å 90.00° 101.46° 90.00°	Depositor
Resolution (Å)	8.00 – 1.90 29.39 – 1.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-1.90) 93.3 (29.39-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.66 (at 1.91Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.197 , 0.256 0.260 , 0.294	Depositor DCC
R_{free} test set	3611 reflections (7.61%)	DCC
Wilson B-factor (Å ²)	19.2	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 51.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 51748 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6379	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.26% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MLZ, MLY

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	0.38	0/5930	0.65	4/7992 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	258	LEU	CA-CB-CG	6.19	129.54	115.30
1	A	273	GLY	N-CA-C	5.27	126.27	113.10
1	A	277	LEU	CA-CB-CG	5.12	127.07	115.30
1	A	7	ARG	NE-CZ-NH1	5.05	122.83	120.30

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	6013	0	6024	131	0
2	A	366	0	0	20	0
All	All	6379	0	6024	131	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 11.

All (131) 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:621:ASN:HD21	1:A:630:ARG:HH22	1.08	1.01
1:A:94:ASN:HD22	1:A:96:LEU:H	1.10	0.94
1:A:359:GLU:OE2	2:A:902:HOH:O	1.92	0.86
1:A:362:LYS:HE2	1:A:364:ASN:HD21	1.38	0.86
1:A:94:ASN:ND2	1:A:96:LEU:H	1.75	0.85
1:A:164:THR:H	1:A:177:GLN:HE22	1.23	0.83
1:A:362:LYS:HG2	1:A:364:ASN:ND2	1.94	0.82
1:A:11:ASN:HD22	1:A:13:ASN:H	1.30	0.80
1:A:623:LEU:HD11	1:A:713:LEU:HD21	1.71	0.73
1:A:621:ASN:ND2	1:A:630:ARG:HH22	1.87	0.72
1:A:150:ASP:O	1:A:151:GLU:HB2	1.91	0.71
1:A:68:TYR:HE2	1:A:220:LEU:HD13	1.54	0.71
1:A:545:ASN:HD22	1:A:548:PHE:H	1.40	0.69
1:A:68:TYR:CE2	1:A:220:LEU:HD13	2.27	0.68
1:A:362:LYS:HG2	1:A:364:ASN:HD21	1.59	0.68
1:A:475:ILE:O	1:A:477:PRO:HD3	1.94	0.67
1:A:496:TYR:O	1:A:497:GLU:HB2	1.95	0.67
1:A:467:MLZ:HE2	1:A:555:PHE:HB2	1.77	0.67
1:A:442:HIS:HD2	2:A:749:HOH:O	1.77	0.67
1:A:172:ASP:CG	2:A:1068:HOH:O	2.36	0.64
1:A:65:GLU:OE2	1:A:216:MLY:HH22	1.98	0.64
1:A:385:PRO:HB2	2:A:835:HOH:O	1.97	0.64
1:A:1:MET:SD	1:A:33:HIS:CE1	2.91	0.63
1:A:170:ILE:H	1:A:170:ILE:HD13	1.64	0.63
1:A:1:MET:HB2	1:A:251:ILE:HG13	1.80	0.62
1:A:390:MLY:HE3	2:A:1079:HOH:O	2.00	0.62
1:A:404:ILE:H	1:A:489:GLN:HE22	1.46	0.62
1:A:94:ASN:HD22	1:A:96:LEU:N	1.91	0.61
1:A:137:VAL:HG13	1:A:142:LEU:HB2	1.84	0.60
1:A:302:LYS:N	1:A:302:LYS:HD2	2.16	0.60
1:A:364:ASN:HD22	1:A:364:ASN:H	1.50	0.60
1:A:172:ASP:OD1	2:A:1068:HOH:O	2.16	0.59
1:A:1:MET:SD	1:A:33:HIS:HE1	2.25	0.59
1:A:11:ASN:ND2	1:A:13:ASN:H	1.98	0.58
1:A:407:ASN:N	1:A:407:ASN:HD22	2.01	0.58
1:A:28:ASP:OD2	1:A:616:MLY:HH13	2.03	0.58
1:A:362:LYS:HE2	1:A:364:ASN:ND2	2.15	0.57
1:A:519:MLZ:HD3	2:A:930:HOH:O	2.02	0.57
1:A:320:LEU:HD21	2:A:1079:HOH:O	2.03	0.57
1:A:289:GLU:H	1:A:289:GLU:CD	2.08	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:442:HIS:H	1:A:442:HIS:CD2	2.21	0.56
1:A:55:HIS:HD2	1:A:115:TYR:OH	1.88	0.56
1:A:158:LYS:HB2	1:A:158:LYS:NZ	2.20	0.56
1:A:569:SER:HB3	1:A:677:ILE:HG23	1.88	0.56
1:A:430:ARG:HG2	1:A:430:ARG:HH11	1.70	0.55
1:A:436:LEU:HD22	1:A:436:LEU:N	2.21	0.55
1:A:206:MLY:HE3	2:A:1046:HOH:O	2.06	0.55
1:A:154:LEU:HG	1:A:163:LEU:HD21	1.87	0.55
1:A:106:MET:HB2	1:A:110:SER:HB2	1.89	0.55
1:A:362:LYS:CE	1:A:364:ASN:HD21	2.16	0.54
1:A:15:ASN:HB2	1:A:62:LEU:O	2.08	0.54
1:A:298:PHE:O	1:A:481:ARG:HD2	2.08	0.53
1:A:364:ASN:HD22	1:A:364:ASN:N	2.05	0.53
1:A:229:HIS:HB2	2:A:977:HOH:O	2.09	0.52
1:A:143:LEU:HD22	1:A:154:LEU:HD22	1.92	0.52
1:A:2:ILE:HG22	1:A:3:SER:N	2.24	0.52
1:A:621:ASN:HD21	1:A:630:ARG:NH2	1.91	0.52
1:A:359:GLU:H	1:A:359:GLU:CD	2.13	0.51
1:A:1:MET:HB3	1:A:33:HIS:CE1	2.45	0.51
1:A:364:ASN:CG	1:A:365:GLU:H	2.14	0.51
1:A:513:MLZ:HG2	1:A:524:TRP:HZ2	1.76	0.51
1:A:296:GLU:O	1:A:300:ALA:HA	2.11	0.50
1:A:496:TYR:O	1:A:496:TYR:CD2	2.65	0.50
1:A:362:LYS:HD3	1:A:362:LYS:N	2.27	0.50
1:A:430:ARG:HD2	2:A:978:HOH:O	2.12	0.49
1:A:296:GLU:HB3	1:A:302:LYS:HE3	1.94	0.49
1:A:218:LEU:HD22	1:A:247:ILE:HD13	1.94	0.49
1:A:126:ARG:HA	1:A:180:THR:HG23	1.94	0.49
1:A:32:SER:OG	1:A:33:HIS:HD2	1.95	0.49
1:A:550:LYS:O	1:A:554:LYS:HG2	2.13	0.48
1:A:361:ASP:O	1:A:363:THR:N	2.46	0.48
1:A:361:ASP:C	1:A:362:LYS:HD3	2.33	0.48
1:A:271:THR:O	1:A:436:LEU:HD23	2.14	0.48
1:A:545:ASN:ND2	1:A:548:PHE:H	2.08	0.48
1:A:170:ILE:O	1:A:174:LEU:HG	2.12	0.48
1:A:404:ILE:H	1:A:489:GLN:NE2	2.12	0.48
1:A:617:LYS:HD3	2:A:1039:HOH:O	2.13	0.47
1:A:644:LYS:HG3	1:A:645:GLN:N	2.28	0.47
1:A:567:SER:O	1:A:571:VAL:HG23	2.13	0.47
1:A:225:TYR:CE1	1:A:247:ILE:HG12	2.50	0.47
1:A:55:HIS:HE1	2:A:734:HOH:O	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:GLY:C	1:A:151:GLU:H	2.15	0.46
1:A:164:THR:N	1:A:177:GLN:HE22	2.04	0.46
1:A:430:ARG:NH1	1:A:430:ARG:HG2	2.30	0.46
1:A:634:TYR:CZ	1:A:638:MLZ:HG2	2.51	0.46
1:A:7:ARG:HG3	2:A:749:HOH:O	2.14	0.46
1:A:214:HIS:HE1	1:A:239:TYR:OH	2.00	0.45
1:A:41:MET:HG2	1:A:53:ILE:HG13	1.98	0.45
1:A:649:ASP:O	1:A:653:GLY:HA3	2.17	0.45
1:A:621:ASN:HD22	1:A:630:ARG:HH12	1.65	0.45
1:A:621:ASN:ND2	1:A:630:ARG:HH12	2.15	0.45
1:A:407:ASN:H	1:A:407:ASN:HD22	1.63	0.45
1:A:508:MLZ:HG2	1:A:539:VAL:HG11	1.99	0.44
1:A:638:MLZ:HCM3	2:A:846:HOH:O	2.17	0.44
1:A:313:LYS:HD3	2:A:797:HOH:O	2.18	0.44
1:A:160:LYS:HE3	2:A:1018:HOH:O	2.18	0.44
1:A:152:TYR:HB3	1:A:163:LEU:HD12	2.00	0.43
1:A:1:MET:HG2	1:A:2:ILE:HG12	2.00	0.43
1:A:615:SER:O	1:A:634:TYR:HD1	2.01	0.43
1:A:505:GLU:O	1:A:509:GLN:HG2	2.19	0.43
1:A:404:ILE:HA	1:A:407:ASN:ND2	2.33	0.43
1:A:361:ASP:CG	1:A:361:ASP:O	2.56	0.43
1:A:253:ILE:HD13	1:A:436:LEU:HD21	1.99	0.43
1:A:308:SER:O	1:A:312:ILE:HG13	2.17	0.43
1:A:316:ILE:HA	1:A:316:ILE:HD13	1.91	0.43
1:A:623:LEU:HD21	1:A:713:LEU:CD2	2.49	0.43
1:A:55:HIS:CD2	1:A:115:TYR:OH	2.72	0.43
1:A:170:ILE:N	1:A:170:ILE:HD13	2.30	0.43
1:A:510:HIS:HD2	2:A:753:HOH:O	2.02	0.43
1:A:605:PHE:O	1:A:609:HIS:CD2	2.72	0.42
1:A:367:GLU:O	1:A:371:LYS:HG3	2.19	0.42
1:A:116:PHE:HB2	1:A:118:PHE:CE1	2.54	0.42
1:A:266:LEU:HD23	2:A:890:HOH:O	2.18	0.42
1:A:407:ASN:ND2	1:A:407:ASN:N	2.66	0.42
1:A:639:LEU:HD21	1:A:716:ILE:HG13	2.02	0.42
1:A:500:SER:HB2	2:A:840:HOH:O	2.20	0.42
1:A:248:LYS:HB3	1:A:249:ASN:H	1.54	0.42
1:A:433:LYS:HA	1:A:433:LYS:HE3	2.02	0.42
1:A:495:PHE:O	1:A:496:TYR:C	2.59	0.41
1:A:170:ILE:H	1:A:170:ILE:CD1	2.33	0.41
1:A:356:ILE:HG13	1:A:367:GLU:HG2	2.01	0.41
1:A:533:ASN:O	1:A:537:GLU:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:LYS:HD3	1:A:379:LYS:HA	1.87	0.41
1:A:384:MET:N	1:A:385:PRO:HD2	2.36	0.41
1:A:170:ILE:HG12	1:A:171:TYR:N	2.35	0.41
1:A:143:LEU:HA	1:A:143:LEU:HD23	1.93	0.41
1:A:620:LYS:C	1:A:620:LYS:HD2	2.42	0.41
1:A:403:LEU:HA	1:A:403:LEU:HD12	1.93	0.40
1:A:329:ALA:HB2	1:A:339:LEU:HD12	2.03	0.40
1:A:323:TYR:O	1:A:327:ARG:HG3	2.21	0.40
1:A:97:ASN:C	1:A:97:ASN:HD22	2.24	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	699/720 (97%)	663 (95%)	30 (4%)	6 (1%)	21 9

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	151	GLU
1	A	362	LYS
1	A	496	TYR
1	A	2	ILE
1	A	497	GLU
1	A	403	LEU

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	647/647 (100%)	610 (94%)	37 (6%)	25	13

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ARG
1	A	11	ASN
1	A	29	LEU
1	A	47	ASN
1	A	71	LEU
1	A	94	ASN
1	A	97	ASN
1	A	133	ASP
1	A	151	GLU
1	A	170	ILE
1	A	175	GLN
1	A	180	THR
1	A	247	ILE
1	A	263	GLU
1	A	268	SER
1	A	277	LEU
1	A	289	GLU
1	A	303	ILE
1	A	307	GLU
1	A	328	LEU
1	A	339	LEU
1	A	362	LYS
1	A	364	ASN
1	A	407	ASN
1	A	428	GLN
1	A	430	ARG
1	A	433	LYS
1	A	478	LYS
1	A	491	LEU
1	A	526	ASN
1	A	545	ASN
1	A	568	LEU
1	A	620	LYS
1	A	621	ASN

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Mol	Chain	Res	Type
1	A	656	LYS
1	A	674	LEU
1	A	717	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	ASN
1	A	22	ASN
1	A	33	HIS
1	A	55	HIS
1	A	84	GLN
1	A	94	ASN
1	A	97	ASN
1	A	177	GLN
1	A	214	HIS
1	A	249	ASN
1	A	285	ASN
1	A	287	ASN
1	A	297	ASN
1	A	315	GLN
1	A	331	GLN
1	A	364	ASN
1	A	407	ASN
1	A	442	HIS
1	A	472	HIS
1	A	489	GLN
1	A	510	HIS
1	A	526	ASN
1	A	527	GLN
1	A	545	ASN
1	A	621	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

19 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	$\# Z > 2$
1	MLZ	A	105	1	8,9,10	0.36	0	7,9,11	0.92	0
1	MLZ	A	108	1	8,9,10	0.48	0	7,9,11	0.94	1 (14%)
1	MLY	A	109	1	9,10,11	0.39	0	9,11,13	0.84	0
1	MLY	A	111	1	9,10,11	0.58	0	9,11,13	0.84	0
1	MLY	A	206	1	9,10,11	0.41	0	9,11,13	0.85	0
1	MLY	A	216	1	9,10,11	0.49	0	9,11,13	0.99	0
1	MLY	A	250	1	9,10,11	0.48	0	9,11,13	0.76	0
1	MLZ	A	27	1	8,9,10	0.34	0	7,9,11	1.05	0
1	MLZ	A	310	1	8,9,10	0.32	0	7,9,11	0.97	0
1	MLZ	A	326	1	8,9,10	0.34	0	7,9,11	1.02	1 (14%)
1	MLY	A	390	1	9,10,11	0.46	0	9,11,13	0.85	0
1	MLZ	A	467	1	8,9,10	0.32	0	7,9,11	0.98	0
1	MLY	A	504	1	9,10,11	0.44	0	9,11,13	0.94	0
1	MLZ	A	508	1	8,9,10	0.33	0	7,9,11	0.91	0
1	MLZ	A	513	1	8,9,10	0.44	0	7,9,11	0.95	1 (14%)
1	MLZ	A	519	1	8,9,10	0.37	0	7,9,11	0.96	0
1	MLY	A	558	1	9,10,11	0.49	0	9,11,13	0.83	0
1	MLY	A	616	1	9,10,11	0.43	0	9,11,13	0.94	0
1	MLZ	A	638	1	8,9,10	0.36	0	7,9,11	0.93	1 (14%)

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
1	MLZ	A	105	1	-	0/6/8/10	0/0/0/0
1	MLZ	A	108	1	-	0/6/8/10	0/0/0/0
1	MLY	A	109	1	-	0/7/9/11	0/0/0/0
1	MLY	A	111	1	-	0/7/9/11	0/0/0/0
1	MLY	A	206	1	-	0/7/9/11	0/0/0/0
1	MLY	A	216	1	-	0/7/9/11	0/0/0/0
1	MLY	A	250	1	-	0/7/9/11	0/0/0/0
1	MLZ	A	27	1	-	0/6/8/10	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLZ	A	310	1	-	0/6/8/10	0/0/0/0
1	MLZ	A	326	1	-	0/6/8/10	0/0/0/0
1	MLY	A	390	1	-	0/7/9/11	0/0/0/0
1	MLZ	A	467	1	-	0/6/8/10	0/0/0/0
1	MLY	A	504	1	-	0/7/9/11	0/0/0/0
1	MLZ	A	508	1	-	0/6/8/10	0/0/0/0
1	MLZ	A	513	1	-	0/6/8/10	0/0/0/0
1	MLZ	A	519	1	-	0/6/8/10	0/0/0/0
1	MLY	A	558	1	-	0/7/9/11	0/0/0/0
1	MLY	A	616	1	-	0/7/9/11	0/0/0/0
1	MLZ	A	638	1	-	0/6/8/10	0/0/0/0

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	326	MLZ	O-C-CA	-2.18	119.81	125.49
1	A	108	MLZ	O-C-CA	-2.05	120.15	125.49
1	A	638	MLZ	O-C-CA	-2.02	120.22	125.49
1	A	513	MLZ	O-C-CA	-2.00	120.28	125.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	206	MLY	1	0
1	A	216	MLY	1	0
1	A	390	MLY	1	0
1	A	467	MLZ	1	0
1	A	508	MLZ	1	0
1	A	513	MLZ	1	0
1	A	519	MLZ	1	0
1	A	616	MLY	1	0
1	A	638	MLZ	2	0

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	701/720 (97%)	0.77	43 (6%)	25 27	5, 17, 40, 70	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	363	THR	9.0
1	A	1	MET	8.3
1	A	149	GLY	6.9
1	A	150	ASP	4.5
1	A	157	PHE	3.5
1	A	496	TYR	3.4
1	A	338	ILE	3.1
1	A	300	ALA	3.0
1	A	260	PHE	2.8
1	A	2	ILE	2.7
1	A	475	ILE	2.7
1	A	113	TYR	2.7
1	A	164	THR	2.7
1	A	153	PHE	2.7
1	A	168	ASN	2.6
1	A	362	LYS	2.6
1	A	719	ARG	2.5
1	A	103	VAL	2.4
1	A	333	GLY	2.4
1	A	170	ILE	2.4
1	A	261	GLN	2.4
1	A	204	VAL	2.4
1	A	241	ASN	2.3
1	A	377	TYR	2.3
1	A	706	LYS	2.3
1	A	356	ILE	2.3
1	A	720	MET	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	652	LYS	2.2
1	A	236	PRO	2.2
1	A	361	ASP	2.2
1	A	133	ASP	2.2
1	A	689	LEU	2.2
1	A	691	GLU	2.2
1	A	339	LEU	2.2
1	A	705	LYS	2.2
1	A	369	ALA	2.1
1	A	259	GLY	2.1
1	A	146	VAL	2.0
1	A	240	ILE	2.0
1	A	112	TYR	2.0
1	A	342	TYR	2.0
1	A	148	ASP	2.0
1	A	188	PRO	2.0

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
1	MLZ	A	326	10/11	0.86	0.19	-	17,19,31,34	0
1	MLZ	A	508	10/11	0.93	0.12	-	9,13,31,33	0
1	MLZ	A	310	10/11	0.86	0.24	-	18,27,50,51	0
1	MLY	A	111	11/12	0.80	0.21	-	14,16,32,35	0
1	MLZ	A	638	10/11	0.88	0.18	-	14,22,37,39	0
1	MLY	A	109	11/12	0.75	0.19	-	15,18,22,24	0
1	MLZ	A	467	10/11	0.92	0.13	-	12,16,28,28	0
1	MLY	A	558	11/12	0.84	0.17	-	18,22,33,34	0
1	MLZ	A	105	10/11	0.84	0.23	-	16,22,51,52	0
1	MLY	A	390	11/12	0.93	0.14	-	6,9,33,33	0
1	MLZ	A	519	10/11	0.89	0.17	-	11,21,45,46	0
1	MLY	A	206	11/12	0.87	0.17	-	10,15,30,30	0
1	MLZ	A	108	10/11	0.79	0.19	-	13,23,37,37	0
1	MLY	A	250	11/12	0.80	0.20	-	14,17,33,34	0
1	MLY	A	504	11/12	0.92	0.12	-	9,12,20,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
1	MLY	A	216	11/12	0.82	0.18	-	12,15,26,29	0
1	MLZ	A	27	10/11	0.91	0.14	-	14,17,30,31	0
1	MLZ	A	513	10/11	0.91	0.13	-	10,17,37,41	0
1	MLY	A	616	11/12	0.84	0.17	-	25,33,40,41	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.