



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:12 AM UTC

PDB ID : 3PGF / pdb_00003pgf
Title : Crystal structure of maltose bound MBP with a conformationally specific synthetic antigen binder (sAB)
Authors : Kossiakoff, A.A.; Duguid, E.M.; Sandstrom, A.
Deposited on : 2010-11-01
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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
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

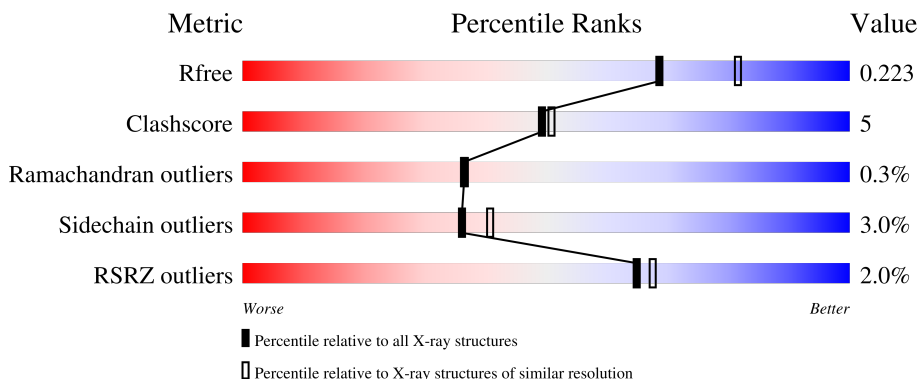
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

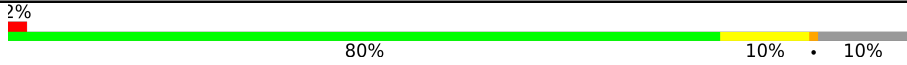


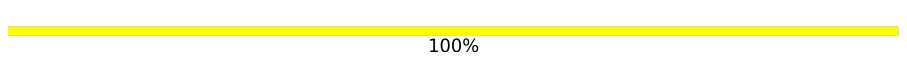
The reported resolution of this entry is 2.10 Å.

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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (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	398	 2% 80% 10% 10%
2	H	231	 3% 81% 14% . .
3	L	215	 % 80% 17% .
4	B	2	 100%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 6592 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 Maltose-binding periplasmic protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	358	2800	1806	455	533	6	0	4	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-30	MET	-	initiating methionine	UNP P0AEX9
A	-29	LYS	-	expression tag	UNP P0AEX9
A	-28	HIS	-	expression tag	UNP P0AEX9
A	-27	HIS	-	expression tag	UNP P0AEX9
A	-26	HIS	-	expression tag	UNP P0AEX9
A	-25	HIS	-	expression tag	UNP P0AEX9
A	-24	HIS	-	expression tag	UNP P0AEX9
A	-23	HIS	-	expression tag	UNP P0AEX9
A	-22	HIS	-	expression tag	UNP P0AEX9
A	-21	HIS	-	expression tag	UNP P0AEX9
A	-20	HIS	-	expression tag	UNP P0AEX9
A	-19	HIS	-	expression tag	UNP P0AEX9
A	-18	SER	-	expression tag	UNP P0AEX9
A	-17	SER	-	expression tag	UNP P0AEX9
A	-16	ASP	-	expression tag	UNP P0AEX9
A	-15	TYR	-	expression tag	UNP P0AEX9
A	-14	LYS	-	expression tag	UNP P0AEX9
A	-13	ASP	-	expression tag	UNP P0AEX9
A	-12	ASP	-	expression tag	UNP P0AEX9
A	-11	ASP	-	expression tag	UNP P0AEX9
A	-10	ASP	-	expression tag	UNP P0AEX9
A	-9	LYS	-	expression tag	UNP P0AEX9
A	-8	GLY	-	expression tag	UNP P0AEX9
A	-7	GLU	-	expression tag	UNP P0AEX9
A	-6	ASN	-	expression tag	UNP P0AEX9
A	-5	LEU	-	expression tag	UNP P0AEX9
A	-4	TYR	-	expression tag	UNP P0AEX9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	PHE	-	expression tag	UNP P0AEX9
A	-2	GLN	-	expression tag	UNP P0AEX9
A	-1	GLY	-	expression tag	UNP P0AEX9
A	0	SER	-	expression tag	UNP P0AEX9
A	367	ASN	ARG	conflict	UNP P0AEX9

- Molecule 2 is a protein called SAB Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	222	1688	1073	276	331	8	0	7	0

- Molecule 3 is a protein called SAB Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	L	214	1659	1036	274	342	7	0	8	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	123	SER	GLU	engineered mutation	UNP Q8TCD0

- Molecule 4 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
4	B	2	23	12	11	0	0	0

- Molecule 5 is IMIDAZOLE (CCD ID: IMD) (formula: C₃H₅N₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	N	0	0
			5	3	2		
5	A	1	Total	C	N	0	0
			5	3	2		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	H	1	Total	C	O	0	0
			6	3	3		
6	L	1	Total	C	O	0	0
			6	3	3		

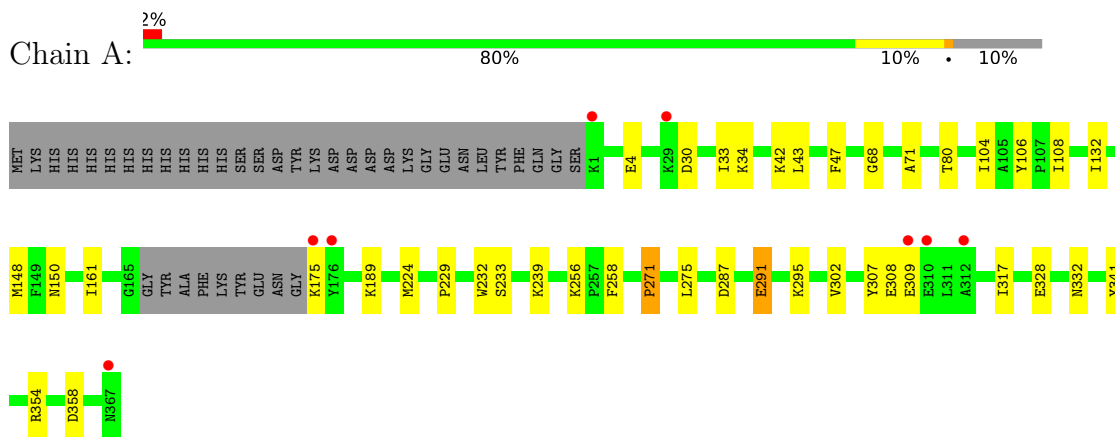
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	188	Total 188	O 188	0	0
7	H	81	Total 81	O 81	0	0
7	L	131	Total 131	O 131	0	0

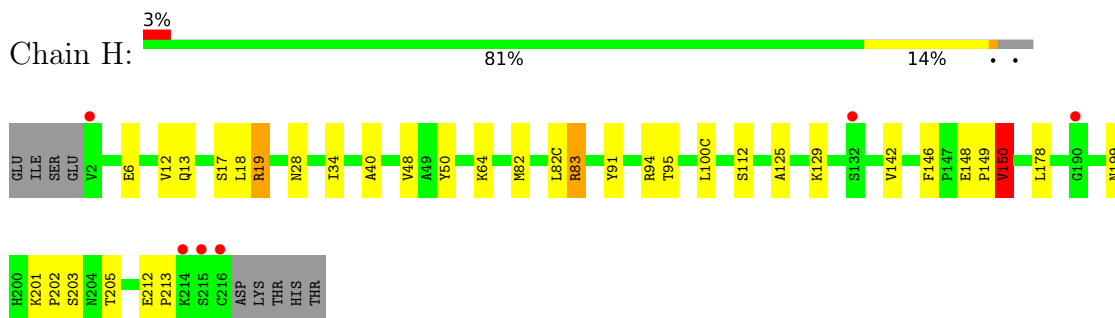
3 Residue-property plots [i](#)

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

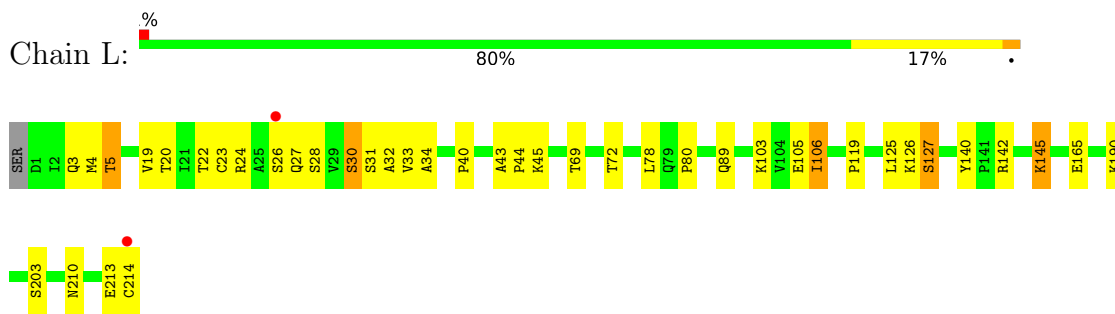
- Molecule 1: Maltose-binding periplasmic protein




- Molecule 2: SAB Heavy Chain



- Molecule 3: SAB Light Chain



- Molecule 4: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain B:  100%

GLC1
GLC2

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	63.87Å 228.46Å 135.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.07 – 2.10 38.07 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.0 (38.07-2.10) 97.0 (38.07-2.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.19 (at 2.10Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.177 , 0.227 0.174 , 0.223	Depositor DCC
R_{free} test set	2815 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	19.6	Xtrriage
Anisotropy	0.349	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 35.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6592	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.36% 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: GLC, GOL, IMD

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	1.42	10/2877 (0.3%)	1.19	6/3901 (0.2%)
2	H	1.31	3/1757 (0.2%)	1.11	5/2400 (0.2%)
3	L	1.38	4/1718 (0.2%)	1.18	4/2331 (0.2%)
All	All	1.38	17/6352 (0.3%)	1.17	15/8632 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	H	0	1

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	132	ILE	CA-CB	8.29	1.59	1.53
3	L	19	VAL	CA-CB	7.10	1.63	1.54
1	A	150	ASN	C-O	-5.89	1.17	1.24
1	A	132	ILE	CA-C	5.87	1.57	1.52
1	A	161	ILE	C-O	5.76	1.30	1.24
1	A	271	PRO	CA-C	5.57	1.57	1.52
2	H	150	VAL	CA-C	5.54	1.59	1.52
2	H	148	GLU	CA-C	5.42	1.59	1.52
1	A	106	TYR	C-O	-5.34	1.17	1.24
2	H	40	ALA	CA-CB	5.24	1.61	1.52
1	A	239	LYS	CA-C	5.24	1.59	1.52
3	L	119	PRO	CA-C	5.18	1.56	1.52
1	A	47	PHE	C-O	-5.13	1.17	1.24
1	A	224	MET	N-CA	5.12	1.52	1.45
1	A	317	ILE	CA-CB	5.06	1.60	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	140	TYR	CA-CB	5.03	1.61	1.54
3	L	34	ALA	CA-C	5.02	1.58	1.52

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	309	GLU	N-CA-C	-7.30	103.34	112.90
2	H	48	VAL	N-CA-C	7.28	120.24	112.96
3	L	30	SER	N-CA-C	-7.23	99.25	110.17
1	A	80	THR	CA-C-N	-6.48	113.28	119.76
1	A	80	THR	C-N-CA	-6.48	113.28	119.76
3	L	5	THR	CB-CA-C	-6.06	101.09	110.78
1	A	108	ILE	CB-CA-C	-5.68	106.05	111.44
3	L	28	SER	N-CA-C	5.47	117.15	108.67
1	A	30	ASP	N-CA-C	5.46	121.80	113.61
1	A	132	ILE	N-CA-CB	5.25	113.81	110.50
2	H	125	ALA	CA-C-N	5.24	125.49	119.83
2	H	125	ALA	C-N-CA	5.24	125.49	119.83
3	L	127	SER	N-CA-C	5.24	120.32	113.30
2	H	18	LEU	CA-C-N	-5.20	115.77	123.05
2	H	18	LEU	C-N-CA	-5.20	115.77	123.05

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	146	PHE	Peptide

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	2800	0	2807	19	0
2	H	1688	0	1640	16	0
3	L	1659	0	1630	32	0
4	B	23	0	21	0	0
5	A	10	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	H	6	0	8	0	0
6	L	6	0	8	0	0
7	A	188	0	0	5	0
7	H	81	0	0	3	0
7	L	131	0	0	8	0
All	All	6592	0	6124	66	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 5.

All (66) 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)
3:L:213:GLU:O	3:L:214:CYS:HB2	1.70	0.90
1:A:233:SER:HB3	7:A:380:HOH:O	1.74	0.87
2:H:83:ARG:HD3	7:H:274:HOH:O	1.82	0.78
1:A:341:TYR:HE1	7:A:489:HOH:O	1.69	0.76
3:L:190:LYS:HE3	3:L:210:ASN:HB3	1.68	0.75
3:L:4:MET:HE3	3:L:23:CYS:SG	2.30	0.71
3:L:45:LYS:HD2	7:L:382:HOH:O	1.89	0.70
3:L:40:PRO:HG3	3:L:165[A]:GLU:HG3	1.76	0.68
1:A:308:GLU:O	1:A:308:GLU:HG3	1.95	0.64
2:H:13:GLN:HG3	7:H:355:HOH:O	1.98	0.63
3:L:30:SER:C	3:L:32:ALA:H	2.06	0.63
3:L:30:SER:O	3:L:32:ALA:N	2.30	0.63
3:L:213:GLU:O	3:L:214:CYS:CB	2.47	0.62
2:H:199[B]:ASN:HD21	2:H:201:LYS:HG3	1.65	0.62
3:L:103:LYS:HE2	7:L:376:HOH:O	1.98	0.61
1:A:341:TYR:CE1	7:A:489:HOH:O	2.47	0.61
3:L:22:THR:HG23	7:L:275:HOH:O	2.00	0.60
3:L:142:ARG:NH1	7:L:297:HOH:O	2.37	0.57
1:A:308:GLU:O	1:A:308:GLU:CG	2.52	0.57
3:L:40:PRO:CG	3:L:165[A]:GLU:HG3	2.35	0.56
1:A:189[B]:LYS:HD2	1:A:358:ASP:OD1	2.07	0.55
2:H:12:VAL:HG11	2:H:82(C):LEU:HD13	1.88	0.54
2:H:64:LYS:HD3	7:H:381:HOH:O	2.07	0.53
3:L:40:PRO:HG3	3:L:165[A]:GLU:CG	2.39	0.52
3:L:20:THR:HG23	3:L:72:THR:HG23	1.92	0.52
1:A:33:ILE:HD13	1:A:275:LEU:CD2	2.40	0.51
3:L:145:LYS:HG3	7:L:301:HOH:O	2.09	0.51
3:L:40:PRO:HG2	3:L:165[B]:GLU:OE1	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:69:THR:HB	7:L:393:HOH:O	2.11	0.49
3:L:40:PRO:HA	7:L:389:HOH:O	2.12	0.49
1:A:42[A]:LYS:HD2	7:A:551:HOH:O	2.13	0.48
1:A:68:GLY:HA3	1:A:332:ASN:O	2.15	0.47
1:A:148:MET:HG2	7:A:559:HOH:O	2.14	0.47
1:A:4:GLU:HG3	1:A:271:PRO:HB2	1.97	0.47
2:H:142:VAL:HG11	2:H:150:VAL:HG11	1.97	0.47
3:L:203[B]:SER:HB3	7:L:276:HOH:O	2.15	0.47
1:A:328:GLU:CD	2:H:28:ASN:HD22	2.23	0.46
2:H:203:SER:OG	2:H:205:THR:OG1	2.26	0.45
3:L:125:LEU:O	3:L:127:SER:N	2.49	0.45
1:A:33:ILE:HD13	1:A:275:LEU:HD22	1.97	0.45
3:L:40:PRO:HG3	3:L:165[A]:GLU:CD	2.42	0.45
2:H:212:GLU:HB2	2:H:213:PRO:HD2	1.99	0.45
2:H:95:THR:HG23	2:H:100(C):LEU:HD23	2.00	0.44
3:L:33:VAL:HA	3:L:89:GLN:O	2.18	0.44
1:A:229:PRO:HA	1:A:232:TRP:CE2	2.53	0.44
3:L:20:THR:HG23	3:L:72:THR:CG2	2.47	0.44
1:A:291:GLU:O	1:A:295:LYS:HG2	2.18	0.44
1:A:71:ALA:HB2	1:A:104[B]:ILE:HD12	1.99	0.43
3:L:30:SER:C	3:L:32:ALA:N	2.73	0.43
2:H:34:ILE:O	2:H:50:TYR:HA	2.18	0.43
3:L:3:GLN:HB2	3:L:26:SER:HB3	2.01	0.43
1:A:287:ASP:O	1:A:291:GLU:HB2	2.19	0.42
2:H:19:ARG:HG2	2:H:19:ARG:HH11	1.85	0.42
1:A:256:LYS:HB3	1:A:256:LYS:HE3	1.58	0.42
2:H:201:LYS:N	2:H:202:PRO:CD	2.83	0.42
3:L:20:THR:CG2	3:L:72:THR:HG23	2.49	0.42
3:L:125:LEU:C	3:L:127:SER:N	2.76	0.42
3:L:43:ALA:HA	3:L:44:PRO:HD3	1.95	0.42
3:L:78:LEU:HD21	3:L:106:ILE:HD12	2.02	0.41
2:H:17[A]:SER:HA	2:H:82:MET:O	2.20	0.41
1:A:302:VAL:HG21	1:A:307:TYR:HD2	1.85	0.41
3:L:80:PRO:HA	3:L:106:ILE:HG13	2.03	0.41
3:L:145:LYS:HD2	3:L:145:LYS:C	2.46	0.41
2:H:6:GLU:OE2	2:H:91:TYR:HA	2.20	0.41
2:H:17[B]:SER:HA	2:H:82:MET:O	2.20	0.40
3:L:145:LYS:C	3:L:145:LYS:CD	2.94	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	358/398 (90%)	353 (99%)	5 (1%)	0	100	100
2	H	227/231 (98%)	222 (98%)	5 (2%)	0	100	100
3	L	220/215 (102%)	212 (96%)	6 (3%)	2 (1%)	14	10
All	All	805/844 (95%)	787 (98%)	16 (2%)	2 (0%)	36	44

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	L	31	SER
3	L	126	LYS

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	292/323 (90%)	286 (98%)	6 (2%)	47	54
2	H	192/194 (99%)	184 (96%)	8 (4%)	26	28
3	L	197/190 (104%)	191 (97%)	6 (3%)	36	41
All	All	681/707 (96%)	661 (97%)	20 (3%)	36	42

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	LYS

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Mol	Chain	Res	Type
1	A	43	LEU
1	A	175	LYS
1	A	258	PHE
1	A	291	GLU
1	A	354	ARG
2	H	19	ARG
2	H	83	ARG
2	H	94	ARG
2	H	112	SER
2	H	129	LYS
2	H	149	PRO
2	H	150	VAL
2	H	178	LEU
3	L	5	THR
3	L	24	ARG
3	L	27	GLN
3	L	105	GLU
3	L	106	ILE
3	L	145	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	ASN
1	A	100	ASN
1	A	201	ASN
1	A	218	ASN
1	A	365	GLN
2	H	28	ASN
2	H	76	ASN
3	L	37	GLN
3	L	199	GLN
3	L	210	ASN

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](#)

2 monosaccharides 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	GLC	B	1	4	12,12,12	0.52	0	17,17,17	2.28	6 (35%)
4	GLC	B	2	4	11,11,12	1.34	2 (18%)	15,15,17	1.47	3 (20%)

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	GLC	B	1	4	-	2/2/22/22	0/1/1/1
4	GLC	B	2	4	-	0/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	2	GLC	O5-C1	-3.15	1.38	1.43
4	B	2	GLC	C1-C2	2.46	1.58	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1	GLC	O1-C1-O5	-4.24	97.81	110.41
4	B	1	GLC	C1-O5-C5	3.99	121.36	113.65
4	B	1	GLC	O5-C5-C6	-3.76	97.12	106.44
4	B	2	GLC	C2-C3-C4	-3.70	104.36	110.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1	GLC	O2-C2-C3	-3.13	103.00	110.38
4	B	2	GLC	C1-O5-C5	2.80	115.94	112.19
4	B	1	GLC	O3-C3-C2	-2.59	104.26	110.38
4	B	1	GLC	C3-C4-C5	-2.56	105.58	110.23
4	B	2	GLC	O5-C5-C6	-2.14	103.49	107.66

There are no chirality outliers.

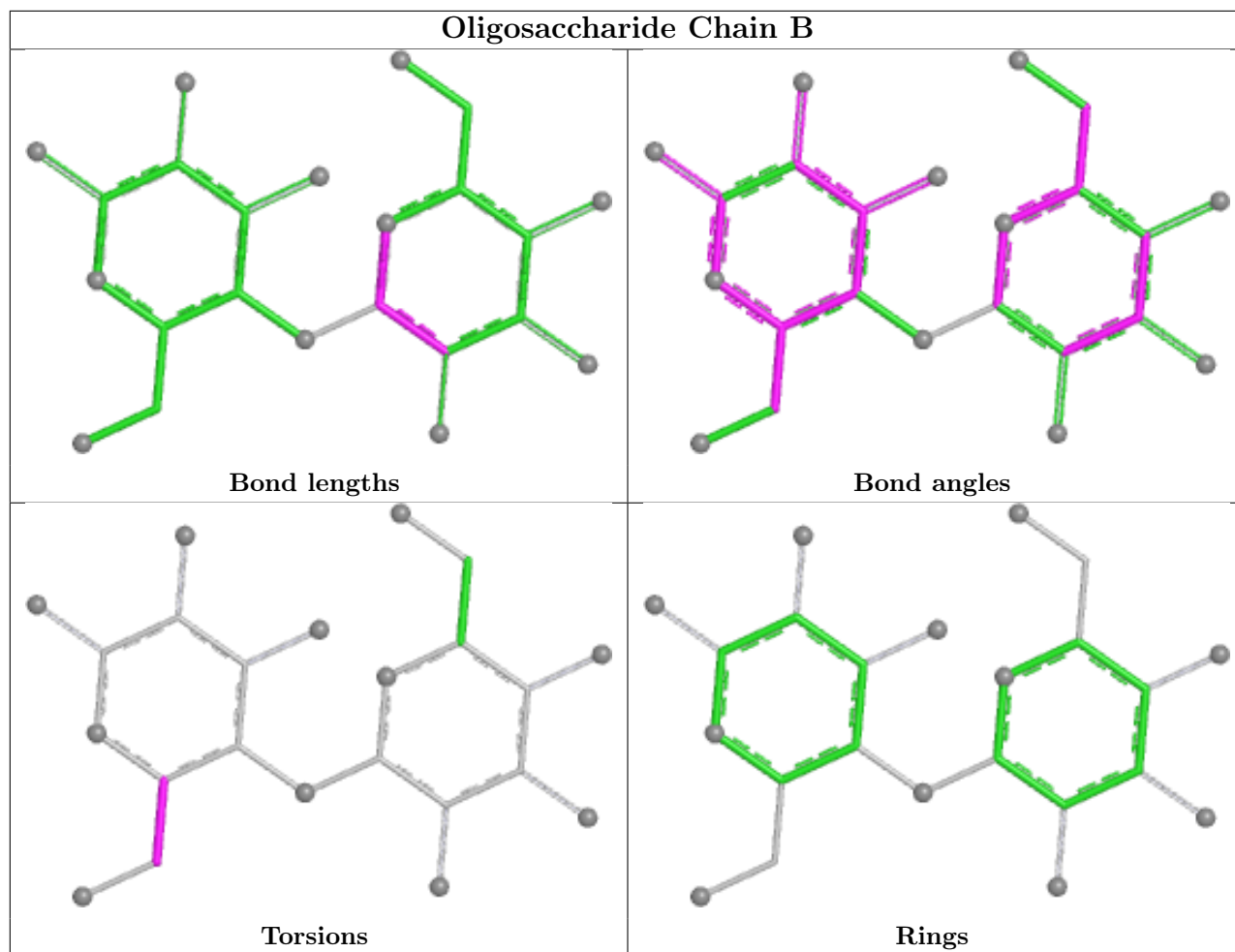
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1	GLC	O5-C5-C6-O6
4	B	1	GLC	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



5.6 Ligand geometry [i](#)

4 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	$\# Z > 2$
6	GOL	H	222	-	5,5,5	1.06	0	5,5,5	1.65	1 (20%)
6	GOL	L	215	-	5,5,5	0.35	0	5,5,5	0.87	0
5	IMD	A	368	-	5,5,5	1.44	1 (20%)	5,5,5	1.26	0
5	IMD	A	369	-	5,5,5	1.64	1 (20%)	5,5,5	0.81	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GOL	L	215	-	-	0/4/4/4	-
6	GOL	H	222	-	-	0/4/4/4	-
5	IMD	A	369	-	-	-	0/1/1/1
5	IMD	A	368	-	-	-	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	369	IMD	C5-C4	2.28	1.43	1.35
5	A	368	IMD	C2-N3	2.03	1.41	1.32

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	H	222	GOL	O1-C1-C2	-3.38	95.17	110.38

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	358/398 (89%)	-0.45	8 (2%) 62 65	10, 19, 40, 56	4 (1%)
2	H	222/231 (96%)	-0.16	6 (2%) 56 59	12, 27, 42, 111	7 (3%)
3	L	214/215 (99%)	-0.36	2 (0%) 81 83	9, 20, 45, 58	9 (4%)
All	All	794/844 (94%)	-0.35	16 (2%) 65 67	9, 22, 42, 111	20 (2%)

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	216	CYS	6.9
3	L	214	CYS	4.9
2	H	2	VAL	4.5
2	H	132	SER	3.6
1	A	309	GLU	3.4
2	H	214	LYS	3.4
1	A	310	GLU	3.3
1	A	367	ASN	2.8
1	A	176	TYR	2.6
1	A	1	LYS	2.5
2	H	190	GLY	2.4
1	A	175	LYS	2.3
3	L	26	SER	2.2
1	A	312	ALA	2.2
2	H	215	SER	2.2
1	A	29	LYS	2.1

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

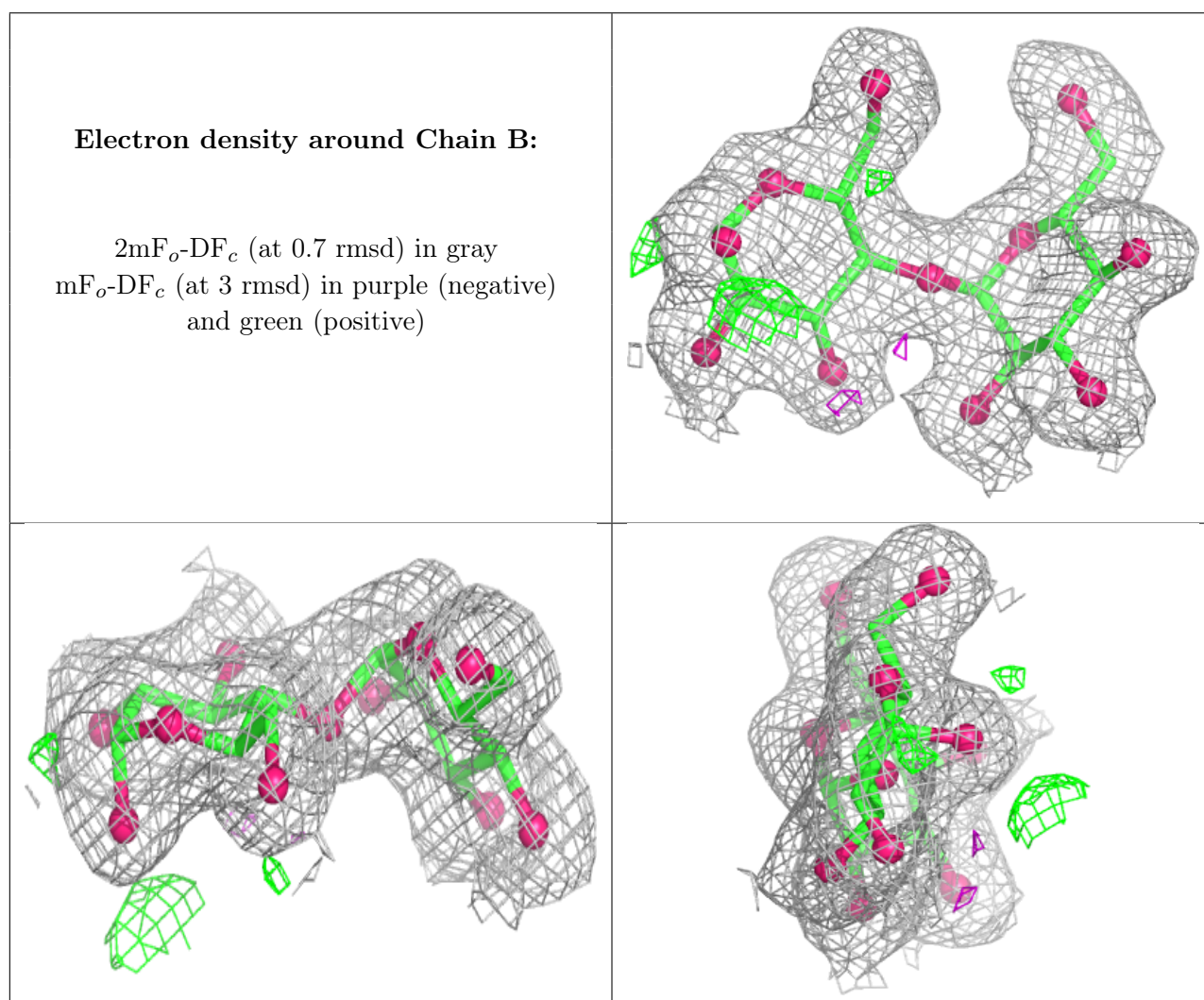
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

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	GLC	B	1	12/12	-	-	9,12,15,17	0
4	GLC	B	2	11/12	-	-	8,9,10,11	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	IMD	A	368	5/5	0.84	0.21	21,22,23,24	0
5	IMD	A	369	5/5	0.86	0.19	19,20,21,26	0
6	GOL	H	222	6/6	0.89	0.13	14,18,19,19	0
6	GOL	L	215	6/6	0.96	0.10	15,16,17,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.