



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 10, 2020 – 02:22 AM BST

PDB ID : 1ANF
Title : MALTODEXTRIN BINDING PROTEIN WITH BOUND MALTOSE
Authors : Spurlino, J.C.; Quioco, F.A.
Deposited on : 1997-06-25
Resolution : 1.67 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 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

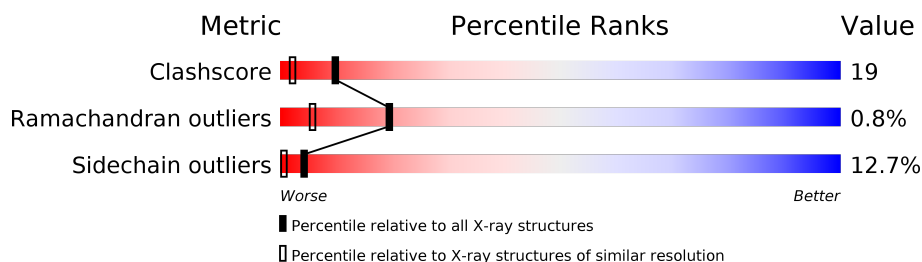
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.67 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))
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)

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 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	370	
2	B	2	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2987 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 MALTODEXTRIN-BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	370	Total	C	N	O	S	0	0	0
			2860	1843	468	543	6			

- Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



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

- Molecule 3 is water.

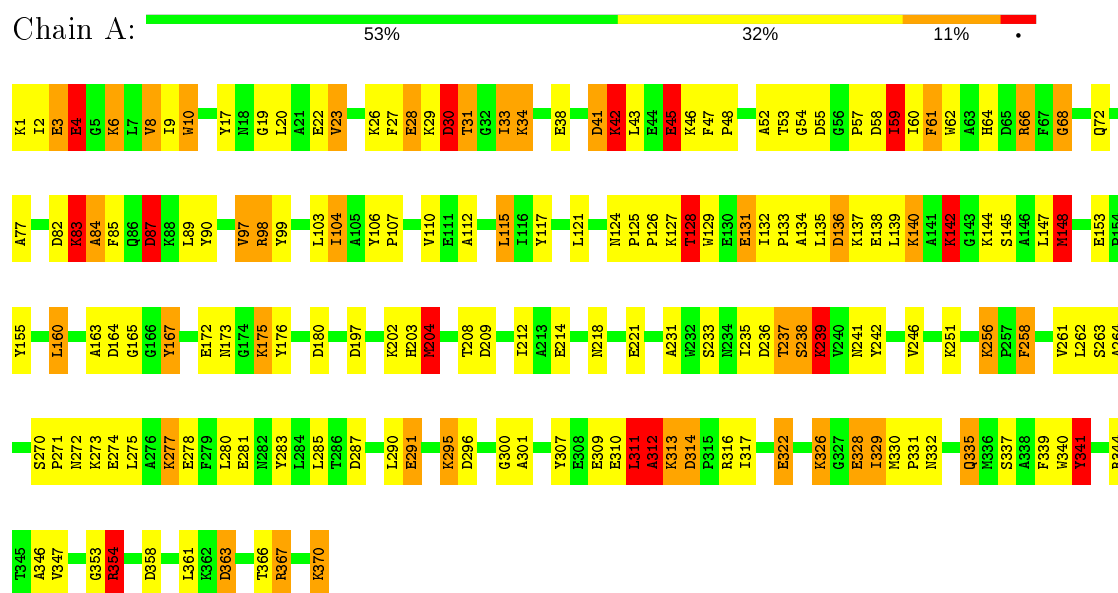
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	104	Total	O	0	0
			104	104		

3 Residue-property plots

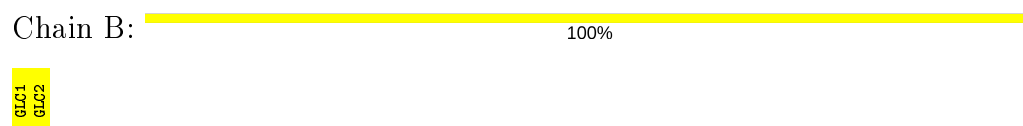
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: MALTODEXTRIN-BINDING PROTEIN



• Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	105.88Å 68.44Å 57.94Å 90.00° 112.54° 90.00°	Depositor
Resolution (Å)	10.00 – 1.67	Depositor
% Data completeness (in resolution range)	80.0 (10.00-1.67)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.10	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.182 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2987	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GLC

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	1.47	9/2929 (0.3%)	2.43	146/3978 (3.7%)

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
1	A	0	2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	238	SER	CB-OG	7.16	1.51	1.42
1	A	28	GLU	CD-OE2	-5.99	1.19	1.25
1	A	214	GLU	CD-OE1	-5.68	1.19	1.25
1	A	117	TYR	CG-CD2	5.55	1.46	1.39
1	A	138	GLU	C-O	5.46	1.33	1.23
1	A	22	GLU	CD-OE2	5.39	1.31	1.25
1	A	300	GLY	CA-C	5.22	1.60	1.51
1	A	155	TYR	CE2-CZ	5.07	1.45	1.38
1	A	66	ARG	CZ-NH1	5.02	1.39	1.33

All (146) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	354	ARG	NE-CZ-NH1	40.46	140.53	120.30
1	A	312	ALA	C-N-CA	19.76	171.09	121.70
1	A	341	TYR	CB-CG-CD2	-15.25	111.85	121.00
1	A	341	TYR	CB-CG-CD1	15.13	130.08	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	45	GLU	OE1-CD-OE2	14.94	141.22	123.30
1	A	354	ARG	NE-CZ-NH2	-14.26	113.17	120.30
1	A	316	ARG	NE-CZ-NH1	13.97	127.28	120.30
1	A	291	GLU	OE1-CD-OE2	13.43	139.41	123.30
1	A	354	ARG	NH1-CZ-NH2	-12.64	105.50	119.40
1	A	137	LYS	CA-CB-CG	12.46	140.80	113.40
1	A	287	ASP	CB-CG-OD1	11.96	129.06	118.30
1	A	30	ASP	CB-CG-OD2	11.07	128.26	118.30
1	A	311	LEU	C-N-CA	-10.73	94.87	121.70
1	A	341	TYR	CA-CB-CG	10.71	133.76	113.40
1	A	312	ALA	O-C-N	10.27	139.14	122.70
1	A	4	GLU	C-N-CA	9.89	143.08	122.30
1	A	30	ASP	CA-CB-CG	9.84	135.04	113.40
1	A	316	ARG	CD-NE-CZ	9.82	137.35	123.60
1	A	236	ASP	CB-CG-OD2	-9.71	109.56	118.30
1	A	367	ARG	NE-CZ-NH2	9.69	125.14	120.30
1	A	84	ALA	N-CA-CB	9.68	123.65	110.10
1	A	117	TYR	CB-CG-CD1	9.47	126.69	121.00
1	A	41	ASP	CB-CG-OD1	9.26	126.64	118.30
1	A	59	ILE	CA-CB-CG2	9.11	129.12	110.90
1	A	41	ASP	CB-CG-OD2	-9.10	110.11	118.30
1	A	197	ASP	CB-CG-OD2	-9.09	110.12	118.30
1	A	103	LEU	CB-CG-CD1	-8.85	95.95	111.00
1	A	197	ASP	CB-CG-OD1	8.80	126.22	118.30
1	A	17	TYR	CB-CG-CD2	8.43	126.06	121.00
1	A	322	GLU	OE1-CD-OE2	8.34	133.31	123.30
1	A	314	ASP	CB-CG-OD1	8.34	125.80	118.30
1	A	87	ASP	CB-CG-OD2	-8.19	110.93	118.30
1	A	99	TYR	CB-CG-CD2	-8.11	116.13	121.00
1	A	239	LYS	CB-CG-CD	8.09	132.65	111.60
1	A	17	TYR	CB-CG-CD1	-8.07	116.16	121.00
1	A	61	PHE	CB-CG-CD2	-8.02	115.18	120.80
1	A	58	ASP	CB-CG-OD2	-8.01	111.09	118.30
1	A	98	ARG	NE-CZ-NH1	7.96	124.28	120.30
1	A	153	GLU	OE1-CD-OE2	-7.91	113.81	123.30
1	A	278	GLU	CA-CB-CG	7.66	130.26	113.40
1	A	328	GLU	CA-CB-CG	7.62	130.17	113.40
1	A	121	LEU	CB-CG-CD2	-7.30	98.59	111.00
1	A	164	ASP	CB-CG-OD2	-7.24	111.79	118.30
1	A	358	ASP	CB-CG-OD2	7.14	124.72	118.30
1	A	176	TYR	CB-CG-CD2	-7.12	116.73	121.00
1	A	239	LYS	CD-CE-NZ	7.08	127.98	111.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	99	TYR	CB-CG-CD1	7.02	125.21	121.00
1	A	136	ASP	O-C-N	7.02	133.93	122.70
1	A	236	ASP	O-C-N	7.02	133.93	122.70
1	A	328	GLU	OE1-CD-OE2	7.01	131.71	123.30
1	A	272	ASN	CA-C-N	6.95	132.50	117.20
1	A	142	LYS	CA-CB-CG	6.91	128.61	113.40
1	A	131	GLU	CG-CD-OE1	6.91	132.12	118.30
1	A	209	ASP	CB-CG-OD2	6.85	124.47	118.30
1	A	148	MET	CG-SD-CE	-6.83	89.27	100.20
1	A	344	ARG	NE-CZ-NH2	6.81	123.70	120.30
1	A	291	GLU	CG-CD-OE2	-6.79	104.72	118.30
1	A	55	ASP	CB-CA-C	6.79	123.98	110.40
1	A	180	ASP	CB-CG-OD2	6.69	124.32	118.30
1	A	45	GLU	N-CA-CB	-6.51	98.87	110.60
1	A	358	ASP	OD1-CG-OD2	-6.50	110.94	123.30
1	A	358	ASP	CB-CG-OD1	6.50	124.15	118.30
1	A	326	LYS	CD-CE-NZ	-6.50	96.75	111.70
1	A	124	ASN	CA-CB-CG	6.48	127.65	113.40
1	A	10	TRP	CB-CG-CD2	-6.47	118.19	126.60
1	A	233	SER	CA-CB-OG	-6.47	93.73	111.20
1	A	38	GLU	O-C-N	6.45	133.01	122.70
1	A	316	ARG	NH1-CZ-NH2	-6.38	112.38	119.40
1	A	128	THR	N-CA-CB	-6.29	98.35	110.30
1	A	167	TYR	CB-CG-CD1	-6.25	117.25	121.00
1	A	363	ASP	CB-CG-OD2	-6.25	112.67	118.30
1	A	98	ARG	NE-CZ-NH2	-6.20	117.20	120.30
1	A	236	ASP	CB-CG-OD1	6.20	123.88	118.30
1	A	175	LYS	CB-CA-C	6.19	122.78	110.40
1	A	3	GLU	CB-CA-C	6.17	122.73	110.40
1	A	30	ASP	CB-CA-C	6.17	122.74	110.40
1	A	165	GLY	CA-C-O	-6.15	109.53	120.60
1	A	354	ARG	N-CA-CB	6.12	121.62	110.60
1	A	29	LYS	CA-CB-CG	6.06	126.74	113.40
1	A	28	GLU	CG-CD-OE1	-6.06	106.18	118.30
1	A	231	ALA	N-CA-CB	-6.06	101.62	110.10
1	A	172	GLU	CG-CD-OE2	-6.03	106.24	118.30
1	A	28	GLU	CG-CD-OE2	6.03	130.36	118.30
1	A	239	LYS	CG-CD-CE	5.99	129.87	111.90
1	A	136	ASP	CB-CG-OD2	5.97	123.68	118.30
1	A	331	PRO	O-C-N	-5.93	113.21	122.70
1	A	354	ARG	CA-CB-CG	5.88	126.34	113.40
1	A	341	TYR	CB-CA-C	5.87	122.13	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	23	VAL	CG1-CB-CG2	5.79	120.17	110.90
1	A	264	ALA	N-CA-CB	5.75	118.14	110.10
1	A	251	LYS	CG-CD-CE	5.74	129.13	111.90
1	A	347	VAL	O-C-N	5.73	131.86	122.70
1	A	256	LYS	CA-CB-CG	5.68	125.89	113.40
1	A	272	ASN	CB-CG-ND2	5.66	130.29	116.70
1	A	97	VAL	O-C-N	5.64	131.73	122.70
1	A	53	THR	CA-CB-CG2	5.63	120.28	112.40
1	A	61	PHE	CB-CG-CD1	5.61	124.72	120.80
1	A	134	ALA	CA-C-O	5.60	131.86	120.10
1	A	262	LEU	O-C-N	5.59	131.65	122.70
1	A	310	GLU	CG-CD-OE1	5.57	129.44	118.30
1	A	165	GLY	CA-C-N	5.54	127.28	116.20
1	A	301	ALA	CA-C-N	5.54	129.38	117.20
1	A	115	LEU	CA-CB-CG	5.53	128.02	115.30
1	A	277	LYS	CB-CG-CD	5.52	125.95	111.60
1	A	128	THR	OG1-CB-CG2	5.50	122.65	110.00
1	A	42	LYS	CB-CA-C	-5.49	99.41	110.40
1	A	353	GLY	CA-C-O	-5.49	110.71	120.60
1	A	285	LEU	O-C-N	-5.49	113.92	122.70
1	A	312	ALA	CB-CA-C	5.49	118.33	110.10
1	A	204	MET	N-CA-CB	-5.48	100.74	110.60
1	A	145	SER	N-CA-CB	5.45	118.68	110.50
1	A	361	LEU	O-C-N	5.44	131.40	122.70
1	A	307	TYR	CB-CG-CD1	-5.38	117.77	121.00
1	A	84	ALA	O-C-N	5.37	131.28	122.70
1	A	208	THR	O-C-N	5.36	131.27	122.70
1	A	33	ILE	O-C-N	5.35	131.26	122.70
1	A	242	TYR	CB-CG-CD2	5.32	124.19	121.00
1	A	160	LEU	CA-CB-CG	5.32	127.53	115.30
1	A	110	VAL	CG1-CB-CG2	5.31	119.39	110.90
1	A	135	LEU	CB-CA-C	5.31	120.28	110.20
1	A	335	GLN	CG-CD-NE2	5.28	129.38	116.70
1	A	55	ASP	CB-CG-OD1	5.27	123.04	118.30
1	A	237	THR	CA-CB-CG2	-5.27	105.02	112.40
1	A	103	LEU	CB-CA-C	5.21	120.09	110.20
1	A	353	GLY	O-C-N	5.20	131.02	122.70
1	A	322	GLU	CG-CD-OE1	-5.19	107.92	118.30
1	A	311	LEU	CB-CG-CD2	-5.19	102.18	111.00
1	A	155	TYR	CD1-CE1-CZ	5.18	124.46	119.80
1	A	312	ALA	CA-C-N	-5.18	105.80	117.20
1	A	90	TYR	CB-CG-CD1	-5.18	117.89	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	339	PHE	CB-CG-CD2	-5.18	117.17	120.80
1	A	246	VAL	CA-CB-CG2	-5.16	103.15	110.90
1	A	272	ASN	CA-C-O	-5.16	109.26	120.10
1	A	68	GLY	O-C-N	-5.16	114.43	123.20
1	A	10	TRP	CB-CG-CD1	5.16	133.70	127.00
1	A	307	TYR	CB-CG-CD2	5.14	124.08	121.00
1	A	346	ALA	O-C-N	-5.12	114.50	122.70
1	A	339	PHE	CG-CD2-CE2	-5.11	115.18	120.80
1	A	104	ILE	O-C-N	5.11	130.88	122.70
1	A	117	TYR	O-C-N	5.09	130.85	122.70
1	A	367	ARG	CD-NE-CZ	-5.07	116.50	123.60
1	A	112	ALA	N-CA-CB	5.04	117.16	110.10
1	A	129	TRP	CH2-CZ2-CE2	-5.04	112.36	117.40
1	A	8	VAL	CB-CA-C	5.02	120.94	111.40
1	A	340	TRP	CD1-NE1-CE2	5.02	113.52	109.00
1	A	167	TYR	CG-CD1-CE1	-5.01	117.29	121.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	312	ALA	Peptide
1	A	354	ARG	Sidechain

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	2860	0	2826	110	3
2	B	23	0	20	0	0
3	A	104	0	0	5	1
All	All	2987	0	2846	110	4

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 19.

All (110) 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:239:LYS:O	1:A:239:LYS:HE3	1.39	1.19
1:A:311:LEU:O	1:A:312:ALA:HB2	1.34	1.14
1:A:31:THR:HG23	1:A:33:ILE:H	1.09	1.07
1:A:239:LYS:O	1:A:239:LYS:CE	2.07	1.02
1:A:311:LEU:O	1:A:312:ALA:CB	1.98	0.99
1:A:31:THR:CG2	1:A:33:ILE:H	1.75	0.99
1:A:312:ALA:HB3	1:A:317:ILE:CG2	1.92	0.98
1:A:239:LYS:O	1:A:239:LYS:CD	2.14	0.95
1:A:312:ALA:CB	1:A:317:ILE:CG2	2.45	0.93
1:A:204:MET:CE	3:A:499:HOH:O	2.19	0.91
1:A:1:LYS:HA	1:A:54:GLY:O	1.72	0.90
1:A:204:MET:HE3	3:A:499:HOH:O	1.70	0.88
1:A:312:ALA:CB	1:A:317:ILE:HB	2.04	0.88
1:A:309:GLU:O	1:A:313:LYS:HE3	1.74	0.88
1:A:31:THR:HG23	1:A:33:ILE:N	1.91	0.85
1:A:312:ALA:HB3	1:A:317:ILE:HG21	1.61	0.82
1:A:239:LYS:O	1:A:239:LYS:CG	2.27	0.79
1:A:33:ILE:HG12	1:A:275:LEU:HD13	1.63	0.79
1:A:6:LYS:HA	1:A:33:ILE:HG23	1.65	0.79
1:A:312:ALA:HB3	1:A:317:ILE:HG22	1.66	0.77
1:A:31:THR:HG23	1:A:33:ILE:HD12	1.67	0.76
1:A:64:HIS:HD2	1:A:261:VAL:H	1.34	0.76
1:A:295:LYS:C	1:A:295:LYS:HD3	2.06	0.75
1:A:28:GLU:HA	1:A:31:THR:HG22	1.68	0.75
1:A:312:ALA:HA	1:A:314:ASP:H	1.51	0.74
1:A:312:ALA:CB	1:A:317:ILE:HG21	2.15	0.74
1:A:136:ASP:OD2	1:A:203:HIS:HD2	1.69	0.73
1:A:341:TYR:CD1	1:A:367:ARG:NH2	2.57	0.73
1:A:312:ALA:CB	1:A:317:ILE:CB	2.66	0.73
1:A:27:PHE:O	1:A:31:THR:HB	1.89	0.72
1:A:341:TYR:HD1	1:A:367:ARG:NH2	1.88	0.71
1:A:312:ALA:HB1	1:A:317:ILE:HB	1.72	0.71
1:A:64:HIS:HE1	1:A:330:MET:O	1.73	0.70
1:A:68:GLY:HA3	1:A:332:ASN:O	1.92	0.69
1:A:43:LEU:CD1	1:A:60:ILE:HD11	2.24	0.67
1:A:312:ALA:HB2	1:A:317:ILE:HB	1.77	0.67
1:A:83:LYS:O	1:A:87:ASP:HB2	1.96	0.66
1:A:59:ILE:HD12	1:A:280:LEU:HD11	1.75	0.66
1:A:237:THR:O	1:A:237:THR:HG22	1.96	0.64
1:A:59:ILE:CD1	1:A:280:LEU:HD21	2.28	0.64
1:A:43:LEU:HD13	1:A:60:ILE:HD11	1.79	0.63
1:A:48:PRO:O	1:A:52:ALA:HB2	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:309:GLU:O	1:A:313:LYS:CE	2.47	0.60
1:A:45:GLU:O	1:A:48:PRO:HD2	2.01	0.60
1:A:136:ASP:O	1:A:140:LYS:HB2	2.02	0.59
1:A:128:THR:HG21	3:A:412:HOH:O	2.03	0.59
1:A:64:HIS:CD2	1:A:261:VAL:H	2.19	0.58
1:A:1:LYS:CA	1:A:54:GLY:O	2.48	0.57
1:A:128:THR:HG22	1:A:131:GLU:H	1.69	0.57
1:A:295:LYS:HD3	1:A:296:ASP:N	2.19	0.56
1:A:3:GLU:O	1:A:4:GLU:CB	2.51	0.56
1:A:30:ASP:OD1	1:A:283:TYR:OH	2.24	0.56
1:A:329:ILE:O	1:A:329:ILE:HG23	2.06	0.55
1:A:136:ASP:OD2	1:A:203:HIS:CD2	2.56	0.54
1:A:140:LYS:HD2	1:A:144:LYS:O	2.07	0.54
1:A:19:GLY:O	1:A:23:VAL:HG23	2.08	0.53
1:A:202:LYS:HE2	1:A:202:LYS:HA	1.91	0.53
1:A:34:LYS:O	1:A:34:LYS:HG2	2.09	0.53
1:A:132:ILE:N	1:A:133:PRO:CD	2.71	0.53
1:A:204:MET:HE2	3:A:499:HOH:O	1.94	0.52
1:A:335:GLN:NE2	1:A:335:GLN:H	2.08	0.52
1:A:136:ASP:OD2	1:A:140:LYS:NZ	2.35	0.51
1:A:82:ASP:O	1:A:85:PHE:N	2.43	0.51
1:A:363:ASP:O	1:A:367:ARG:HG3	2.11	0.51
1:A:9:ILE:HG21	1:A:20:LEU:HD21	1.92	0.51
1:A:167:TYR:HE2	3:A:504:HOH:O	1.94	0.50
1:A:322:GLU:O	1:A:326:LYS:HG3	2.10	0.50
1:A:239:LYS:NZ	1:A:241:ASN:HB2	2.27	0.49
1:A:312:ALA:HB2	1:A:317:ILE:CB	2.39	0.49
1:A:64:HIS:CE1	1:A:330:MET:O	2.62	0.49
1:A:61:PHE:HA	1:A:263:SER:O	2.13	0.48
1:A:277:LYS:O	1:A:281:GLU:HG3	2.13	0.48
1:A:212:ILE:HD13	1:A:212:ILE:N	2.27	0.48
1:A:147:LEU:O	1:A:148:MET:HG2	2.13	0.48
1:A:136:ASP:HB3	1:A:203:HIS:CD2	2.48	0.48
1:A:237:THR:O	1:A:237:THR:CG2	2.60	0.47
1:A:62:TRP:CD1	1:A:66:ARG:HG3	2.50	0.46
1:A:144:LYS:HE2	1:A:221:GLU:HA	1.98	0.46
1:A:270:SER:HA	1:A:271:PRO:HD3	1.74	0.45
1:A:366:THR:O	1:A:370:LYS:HG3	2.15	0.45
1:A:85:PHE:C	1:A:85:PHE:CD1	2.89	0.45
1:A:312:ALA:CB	1:A:317:ILE:HG22	2.32	0.45
1:A:41:ASP:O	1:A:42:LYS:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:LYS:HZ1	1:A:241:ASN:HB2	1.80	0.44
1:A:97:VAL:O	1:A:104:ILE:HG12	2.17	0.44
1:A:6:LYS:HD2	1:A:8:VAL:HG23	1.99	0.44
1:A:139:LEU:HA	1:A:142:LYS:HE3	2.00	0.44
1:A:125:PRO:HA	1:A:126:PRO:HD3	1.82	0.43
1:A:132:ILE:N	1:A:133:PRO:HD3	2.33	0.43
1:A:59:ILE:HD11	1:A:280:LEU:HD21	2.00	0.43
1:A:31:THR:HG23	1:A:33:ILE:CD1	2.42	0.43
1:A:6:LYS:HA	1:A:33:ILE:CG2	2.41	0.42
1:A:106:TYR:HA	1:A:107:PRO:HD3	1.86	0.42
1:A:31:THR:CG2	1:A:33:ILE:N	2.60	0.42
1:A:31:THR:CG2	1:A:33:ILE:HD12	2.43	0.41
1:A:312:ALA:HB2	1:A:317:ILE:CG2	2.45	0.41
1:A:59:ILE:HD13	1:A:59:ILE:HG21	1.70	0.41
1:A:82:ASP:C	1:A:84:ALA:N	2.73	0.41
1:A:128:THR:CG2	1:A:131:GLU:H	2.31	0.41
1:A:42:LYS:HD2	1:A:42:LYS:N	2.35	0.41
1:A:10:TRP:CD1	1:A:57:PRO:HB3	2.55	0.41
1:A:290:LEU:HA	1:A:290:LEU:HD23	1.73	0.41
1:A:163:ALA:HA	1:A:256:LYS:HD3	2.02	0.41
1:A:77:ALA:HB2	1:A:273:LYS:HE2	2.01	0.41
1:A:41:ASP:O	1:A:42:LYS:CB	2.69	0.41
1:A:31:THR:CG2	1:A:33:ILE:CD1	2.99	0.41
1:A:47:PHE:HB3	1:A:48:PRO:HD3	2.03	0.41
1:A:72:GLN:O	1:A:72:GLN:HG2	2.20	0.41
1:A:218:ASN:HD21	1:A:235:ILE:HG12	1.87	0.40
1:A:258:PHE:CG	1:A:330:MET:HG2	2.57	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:ALA:CA	1:A:341:TYR:OH[4_547]	1.59	0.61
3:A:502:HOH:O	3:A:504:HOH:O[2_657]	2.00	0.20
1:A:84:ALA:CB	1:A:341:TYR:OH[4_547]	2.04	0.16
1:A:84:ALA:N	1:A:341:TYR:OH[4_547]	2.08	0.12

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	368/370 (100%)	349 (95%)	16 (4%)	3 (1%)	19 6

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	GLU
1	A	83	LYS
1	A	2	ILE

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	292/297 (98%)	255 (87%)	37 (13%)	4 1

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

Mol	Chain	Res	Type
1	A	6	LYS
1	A	26	LYS
1	A	30	ASP
1	A	31	THR
1	A	34	LYS
1	A	42	LYS
1	A	45	GLU
1	A	46	LYS

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Mol	Chain	Res	Type
1	A	59	ILE
1	A	83	LYS
1	A	87	ASP
1	A	89	LEU
1	A	98	ARG
1	A	115	LEU
1	A	127	LYS
1	A	128	THR
1	A	140	LYS
1	A	142	LYS
1	A	148	MET
1	A	160	LEU
1	A	173	ASN
1	A	175	LYS
1	A	204	MET
1	A	238	SER
1	A	239	LYS
1	A	258	PHE
1	A	274	GLU
1	A	291	GLU
1	A	295	LYS
1	A	311	LEU
1	A	313	LYS
1	A	328	GLU
1	A	329	ILE
1	A	337	SER
1	A	341	TYR
1	A	354	ARG
1	A	370	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	ASN
1	A	49	GLN
1	A	64	HIS
1	A	203	HIS
1	A	218	ASN
1	A	335	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

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$
2	GLC	B	1	2	12,12,12	1.20	1 (8%)	17,17,17	2.26	5 (29%)
2	GLC	B	2	2	11,11,12	1.58	1 (9%)	15,15,17	1.48	1 (6%)

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	GLC	B	1	2	-	0/2/22/22	0/1/1/1
2	GLC	B	2	2	-	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)
2	B	2	GLC	O5-C1	-4.12	1.37	1.43
2	B	1	GLC	O5-C1	-2.24	1.37	1.42

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	GLC	C1-O5-C5	6.20	125.37	113.66
2	B	2	GLC	C1-O5-C5	4.17	117.84	112.19
2	B	1	GLC	O1-C1-O5	-3.89	98.71	110.38
2	B	1	GLC	O5-C1-C2	3.66	116.82	110.28
2	B	1	GLC	O6-C6-C5	-2.55	102.56	111.29
2	B	1	GLC	O4-C4-C5	-2.16	103.94	109.30

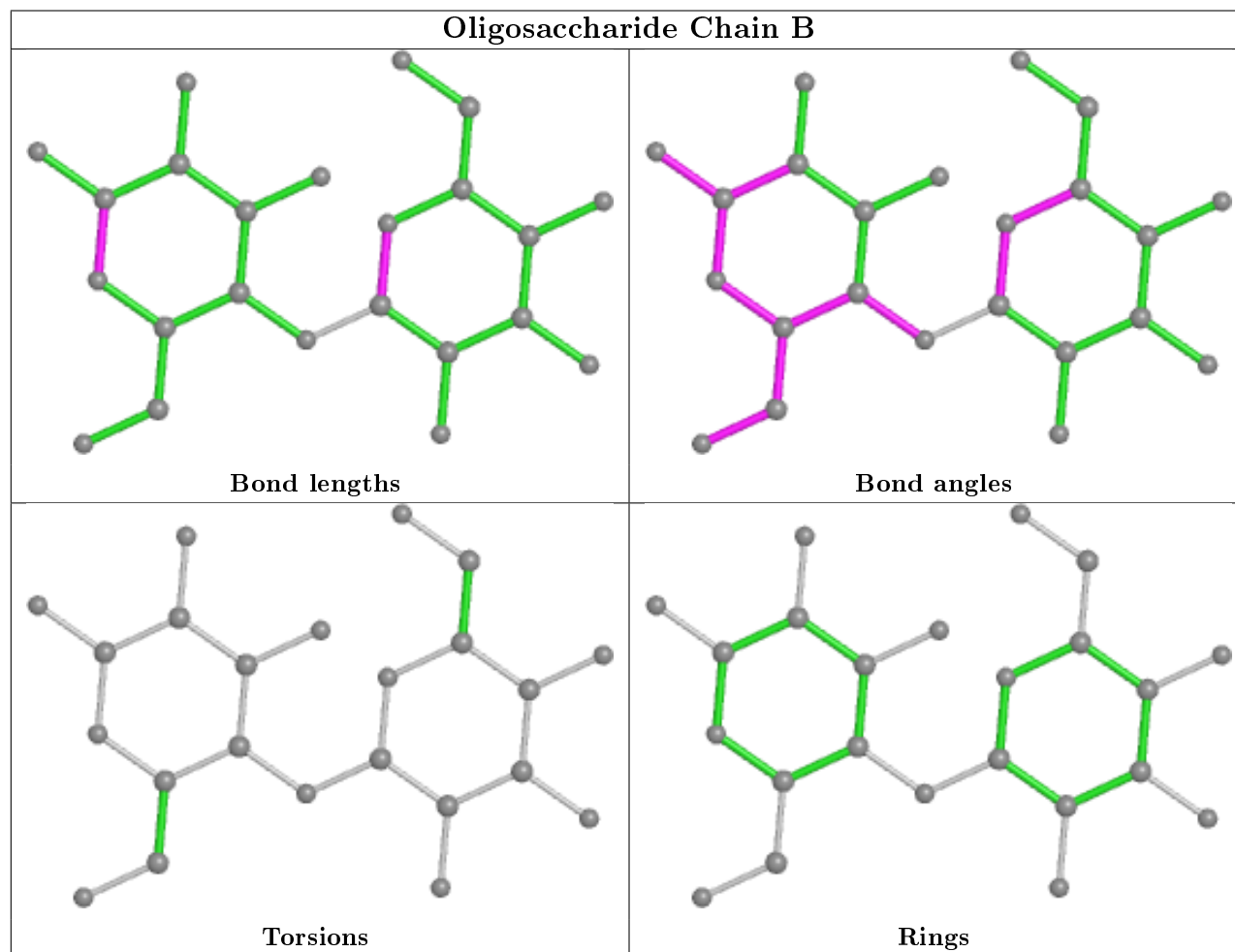
There are no chirality outliers.

There are no torsion outliers.

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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.