Full wwPDB X-ray Structure Validation Report (i)

Jun 12, 2024 – 09:57 PM EDT

PDB ID	:	1LJY
Title	:	Crystal Structure of a Novel Regulatory 40 kDa Mammary Gland Protein (MGP-40) secreted during Involution
Authors	:	Mohanty, A.K.; Singh, G.; Paramasivam, M.; Saravanan, K.; Jabeen, T.; Sharma, S.; Yadav, S.; Kaur, P.; Kumar, P.; Srinivasan, A.; Singh, T.P.
Deposited on	:	2002-04-23
Resolution	:	2.90 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

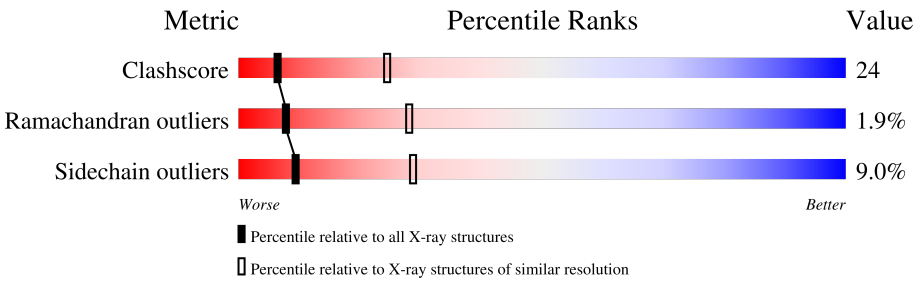
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	361	56% 37% 6% •
2	B	2	100%

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
2	NAG	B	1	-	-	X	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2942 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 MGP-40.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	361	2866	1828	504	525	9	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	VAL	ILE	conflict	GB 19526603
A	87	ALA	LYS	conflict	GB 19526603
A	131	ALA	GLY	conflict	GB 19526603
A	205	ASN	GLN	conflict	GB 19526603
A	206	SER	GLU	conflict	GB 19526603
A	208	GLY	ALA	conflict	GB 19526603
A	?	-	ASP	deletion	GB 19526603
A	253	GLY	VAL	conflict	GB 19526603

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	2	28	16	2	10	0	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	48	48	48	0	0

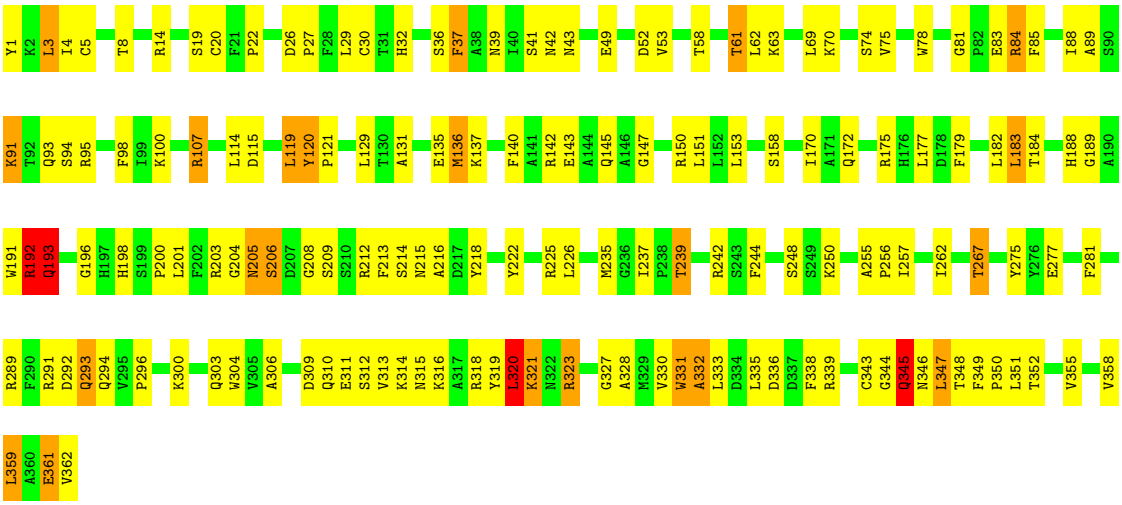
3 Residue-property plots (i)

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. 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: MGP-40

Chain A: 56% 37% 6%



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

Chain B: 100%

4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	62.95Å 65.89Å 107.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.73 – 2.90	Depositor
% Data completeness (in resolution range)	99.2 (19.73-2.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.181 , 0.234	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2942	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

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: NDG, NAG

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	0.50	3/2942 (0.1%)	0.90	13/3988 (0.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	344	GLY	C-N	8.72	1.54	1.34
1	A	343	CYS	C-N	-6.95	1.20	1.33
1	A	61	THR	CA-CB	5.40	1.67	1.53

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	344	GLY	O-C-N	20.35	155.25	122.70
1	A	344	GLY	CA-C-N	-15.67	82.73	117.20
1	A	343	CYS	O-C-N	-8.28	109.13	123.20
1	A	209	SER	N-CA-C	-7.31	91.26	111.00
1	A	192	ARG	N-CA-C	6.32	128.06	111.00
1	A	61	THR	N-CA-CB	6.29	122.25	110.30
1	A	208	GLY	N-CA-C	6.19	128.56	113.10
1	A	343	CYS	CA-C-N	6.14	128.48	116.20
1	A	193	GLN	N-CA-C	6.06	127.36	111.00
1	A	332	ALA	N-CA-C	5.89	126.92	111.00
1	A	331	TRP	N-CA-CB	5.67	120.81	110.60
1	A	119	LEU	CA-CB-CG	-5.27	103.18	115.30
1	A	320	LEU	CA-CB-CG	5.13	127.11	115.30

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	2866	0	2794	132	0
2	B	28	0	24	7	0
3	A	48	0	0	1	0
All	All	2942	0	2818	135	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 24.

All (135) 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:39:ASN:HD21	2:B:1:NAG:C1	1.25	1.47
2:B:1:NAG:C4	2:B:2:NDG:C1	2.30	1.08
1:A:330:VAL:HG12	1:A:331:TRP:O	1.65	0.97
1:A:239:THR:HG21	1:A:332:ALA:O	1.65	0.96
2:B:1:NAG:O4	2:B:2:NDG:O5	2.00	0.78
1:A:239:THR:CG2	1:A:335:LEU:HB2	2.14	0.76
1:A:84:ARG:O	1:A:88:ILE:HG12	1.85	0.76
1:A:39:ASN:ND2	2:B:1:NAG:O5	2.08	0.76
1:A:212:ARG:HD2	1:A:215:ASN:HD21	1.53	0.74
1:A:75:VAL:CG2	1:A:114:LEU:HD11	2.19	0.73
1:A:361:GLU:O	1:A:362:VAL:HG23	1.89	0.72
1:A:8:THR:HA	1:A:36:SER:HB2	1.72	0.71
1:A:39:ASN:ND2	2:B:1:NAG:C2	2.56	0.68
1:A:319:TYR:CZ	1:A:323:ARG:HD2	2.29	0.68
1:A:188:HIS:CD2	1:A:196:GLY:HA3	2.29	0.68
1:A:204:GLY:HA2	1:A:292:ASP:HB3	1.75	0.68
1:A:107:ARG:HD3	1:A:143:GLU:OE2	1.95	0.67
1:A:267:THR:HB	1:A:277:GLU:OE1	1.95	0.67
1:A:142:ARG:HA	1:A:145:GLN:NE2	2.12	0.65
1:A:1:TYR:CE2	1:A:321:LYS:HD3	2.33	0.64
1:A:200:PRO:HB3	1:A:293:GLN:HG2	1.78	0.64
1:A:27:PRO:HG3	1:A:62:LEU:HD22	1.80	0.64
1:A:205:ASN:C	1:A:205:ASN:HD22	2.01	0.63
1:A:1:TYR:CZ	1:A:321:LYS:HD3	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:ASP:HB3	1:A:29:LEU:HB2	1.83	0.60
1:A:213:PHE:CD1	1:A:213:PHE:N	2.69	0.60
1:A:39:ASN:CG	2:B:1:NAG:C1	2.69	0.60
1:A:91:LYS:HB3	1:A:93:GLN:HG2	1.84	0.60
1:A:205:ASN:HD22	1:A:206:SER:N	1.99	0.59
1:A:262:ILE:H	1:A:303:GLN:HE22	1.51	0.59
1:A:131:ALA:O	1:A:135:GLU:HG3	2.03	0.59
1:A:121:PRO:HG3	1:A:129:LEU:HD12	1.83	0.58
1:A:291:ARG:HG3	1:A:292:ASP:N	2.18	0.58
1:A:244:PHE:HB3	1:A:257:ILE:HD12	1.86	0.57
1:A:91:LYS:HB3	1:A:93:GLN:CG	2.34	0.57
1:A:191:TRP:CE3	1:A:192:ARG:HB2	2.40	0.56
1:A:262:ILE:H	1:A:303:GLN:NE2	2.02	0.56
1:A:78:TRP:CH2	1:A:331:TRP:CZ2	2.93	0.56
1:A:172:GLN:O	1:A:175:ARG:HG2	2.06	0.56
1:A:222:TYR:O	1:A:226:LEU:HD23	2.05	0.55
1:A:237:ILE:HG21	1:A:313:VAL:HG13	1.89	0.55
1:A:311:GLU:HG3	1:A:312:SER:N	2.22	0.55
1:A:78:TRP:CZ3	1:A:331:TRP:CZ2	2.95	0.54
1:A:212:ARG:O	1:A:215:ASN:ND2	2.40	0.54
1:A:294:GLN:NE2	1:A:315:ASN:OD1	2.41	0.53
1:A:93:GLN:HG3	1:A:94:SER:H	1.73	0.53
1:A:212:ARG:C	1:A:214:SER:H	2.12	0.53
1:A:43:ASN:O	1:A:98:PHE:HA	2.09	0.53
1:A:78:TRP:NE1	1:A:119:LEU:HD13	2.24	0.52
1:A:83:GLU:H	1:A:83:GLU:CD	2.12	0.52
1:A:222:TYR:CZ	1:A:226:LEU:HD21	2.45	0.52
1:A:37:PHE:HA	1:A:74:SER:O	2.09	0.52
1:A:93:GLN:HG3	1:A:94:SER:N	2.25	0.51
1:A:20:CYS:HB2	1:A:338:PHE:CZ	2.46	0.51
1:A:310:GLN:NE2	1:A:345:GLN:OE1	2.44	0.51
1:A:191:TRP:HE3	1:A:192:ARG:CG	2.24	0.50
2:B:1:NAG:H4	2:B:2:NDG:C1	2.34	0.50
1:A:4:ILE:HD12	1:A:4:ILE:N	2.27	0.50
1:A:239:THR:HG22	1:A:335:LEU:HB2	1.91	0.50
1:A:309:ASP:OD1	1:A:312:SER:HB3	2.12	0.49
1:A:5:CYS:HB3	1:A:333:LEU:HD21	1.94	0.49
1:A:349:PHE:N	1:A:350:PRO:HD3	2.28	0.49
1:A:140:PHE:CD2	1:A:151:LEU:HB2	2.46	0.49
1:A:37:PHE:HB2	3:A:368:HOH:O	2.12	0.48
1:A:3:LEU:HD22	1:A:5:CYS:SG	2.53	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:336:ASP:OD1	1:A:350:PRO:HD2	2.14	0.48
1:A:320:LEU:HD11	1:A:327:GLY:C	2.33	0.48
1:A:203:ARG:HB3	1:A:212:ARG:HH11	1.79	0.48
1:A:5:CYS:HB3	1:A:333:LEU:CG	2.44	0.48
1:A:49:GLU:HB2	1:A:52:ASP:OD1	2.14	0.47
1:A:4:ILE:HG12	1:A:179:PHE:CE2	2.50	0.47
1:A:212:ARG:C	1:A:214:SER:N	2.66	0.47
1:A:78:TRP:CD1	1:A:119:LEU:HD13	2.50	0.47
1:A:136:MET:HB3	1:A:153:LEU:HD22	1.97	0.47
1:A:213:PHE:HA	1:A:218:TYR:CD2	2.48	0.47
1:A:81:GLY:O	1:A:84:ARG:HG3	2.15	0.47
1:A:153:LEU:HG	1:A:177:LEU:HD23	1.97	0.46
1:A:182:LEU:HB3	1:A:184:THR:HG23	1.97	0.46
1:A:244:PHE:HB3	1:A:257:ILE:CD1	2.45	0.46
1:A:75:VAL:HG23	1:A:114:LEU:HD11	1.94	0.46
1:A:22:PRO:HB2	1:A:58:THR:HG22	1.97	0.46
1:A:275:TYR:CE2	1:A:351:LEU:HD13	2.50	0.46
1:A:81:GLY:HA3	1:A:83:GLU:OE1	2.16	0.46
1:A:191:TRP:HE3	1:A:192:ARG:HG3	1.81	0.45
1:A:212:ARG:O	1:A:214:SER:N	2.50	0.45
1:A:239:THR:O	1:A:275:TYR:HB2	2.16	0.45
1:A:348:THR:O	1:A:349:PHE:HB2	2.16	0.45
1:A:205:ASN:C	1:A:205:ASN:ND2	2.69	0.45
1:A:120:TYR:HA	1:A:121:PRO:HD2	1.89	0.45
1:A:347:LEU:HD23	1:A:348:THR:H	1.82	0.45
1:A:320:LEU:CD1	1:A:328:ALA:HB2	2.47	0.45
1:A:239:THR:O	1:A:239:THR:HG23	2.17	0.45
1:A:188:HIS:H	1:A:198:HIS:HA	1.83	0.44
1:A:304:TRP:CZ3	1:A:306:ALA:HB2	2.52	0.44
1:A:320:LEU:C	1:A:320:LEU:HD23	2.36	0.44
1:A:95:ARG:NE	1:A:135:GLU:OE1	2.48	0.44
1:A:145:GLN:C	1:A:147:GLY:H	2.21	0.43
1:A:293:GLN:HE21	1:A:293:GLN:N	2.15	0.43
1:A:314:LYS:O	1:A:318:ARG:HG3	2.17	0.43
1:A:63:LYS:HG3	1:A:69:LEU:HD12	2.01	0.43
1:A:137:LYS:HE3	1:A:150:ARG:CZ	2.49	0.43
1:A:292:ASP:HB2	1:A:293:GLN:HE21	1.83	0.43
1:A:313:VAL:CG1	1:A:355:VAL:CG2	2.97	0.43
1:A:32:HIS:HA	1:A:70:LYS:O	2.19	0.43
1:A:201:LEU:HD12	1:A:216:ALA:HB3	2.01	0.43
1:A:355:VAL:HG12	1:A:359:LEU:HD22	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:TRP:HH2	1:A:331:TRP:CZ2	2.35	0.42
1:A:321:LYS:HE3	1:A:358:VAL:O	2.19	0.42
1:A:345:GLN:O	1:A:347:LEU:N	2.53	0.42
1:A:74:SER:HA	1:A:115:ASP:O	2.19	0.42
1:A:222:TYR:CE2	1:A:226:LEU:HD21	2.54	0.42
1:A:5:CYS:HB3	1:A:333:LEU:HG	2.00	0.42
1:A:330:VAL:HG21	1:A:352:THR:HG23	2.01	0.42
1:A:235:MET:CE	1:A:316:LYS:HB3	2.50	0.42
1:A:345:GLN:C	1:A:347:LEU:H	2.23	0.42
1:A:347:LEU:HD23	1:A:348:THR:N	2.35	0.42
1:A:339:ARG:HH11	1:A:339:ARG:HG2	1.85	0.41
1:A:89:ALA:O	1:A:95:ARG:NH1	2.53	0.41
1:A:248:SER:C	1:A:250:LYS:H	2.23	0.41
1:A:192:ARG:CZ	1:A:193:GLN:HB3	2.50	0.41
1:A:309:ASP:H	1:A:312:SER:HB3	1.85	0.41
1:A:213:PHE:N	1:A:213:PHE:HD1	2.19	0.41
1:A:292:ASP:HB2	1:A:293:GLN:NE2	2.36	0.41
1:A:3:LEU:O	1:A:30:CYS:HB3	2.20	0.41
1:A:78:TRP:CZ3	1:A:331:TRP:HZ2	2.36	0.41
1:A:289:ARG:NH2	1:A:309:ASP:OD2	2.48	0.41
1:A:5:CYS:HB3	1:A:333:LEU:CD2	2.51	0.41
1:A:14:ARG:O	1:A:19:SER:HB2	2.21	0.40
1:A:41:SER:O	1:A:42:ASN:HB2	2.21	0.40
1:A:183:LEU:N	1:A:183:LEU:HD23	2.36	0.40
1:A:248:SER:C	1:A:250:LYS:N	2.75	0.40
1:A:120:TYR:CE1	1:A:158:SER:HB2	2.56	0.40
1:A:203:ARG:HB3	1:A:212:ARG:HD3	2.03	0.40
1:A:255:ALA:HA	1:A:256:PRO:HD3	1.83	0.40
1:A:281:PHE:O	1:A:300:LYS:HE3	2.22	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	359/361 (99%)	322 (90%)	30 (8%)	7 (2%)	8 28

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	193	GLN
1	A	346	ASN
1	A	189	GLY
1	A	345	GLN
1	A	37	PHE
1	A	120	TYR
1	A	170	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	300/300 (100%)	273 (91%)	27 (9%)	9 29

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	53	VAL
1	A	61	THR
1	A	84	ARG
1	A	85	PHE
1	A	91	LYS
1	A	100	LYS
1	A	107	ARG
1	A	136	MET
1	A	183	LEU
1	A	192	ARG
1	A	193	GLN
1	A	205	ASN
1	A	206	SER

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Mol	Chain	Res	Type
1	A	225	ARG
1	A	239	THR
1	A	242	ARG
1	A	267	THR
1	A	293	GLN
1	A	296	PRO
1	A	320	LEU
1	A	321	LYS
1	A	323	ARG
1	A	345	GLN
1	A	347	LEU
1	A	359	LEU
1	A	361	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	ASN
1	A	42	ASN
1	A	60	ASN
1	A	145	GLN
1	A	188	HIS
1	A	193	GLN
1	A	205	ASN
1	A	293	GLN
1	A	294	GLN
1	A	303	GLN
1	A	310	GLN
1	A	315	ASN
1	A	345	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

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	NAG	B	1	2,1	14,14,15	1.20	2 (14%)	17,19,21	2.76	7 (41%)
2	NDG	B	2	2	14,14,15	1.14	2 (14%)	17,19,21	2.00	4 (23%)

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	NAG	B	1	2,1	-	3/6/23/26	0/1/1/1
2	NDG	B	2	2	-	1/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	NAG	C3-C2	-2.63	1.46	1.52
2	B	1	NAG	O5-C5	-2.44	1.38	1.43
2	B	2	NDG	C1-C2	-2.25	1.49	1.52
2	B	2	NDG	O5-C1	2.05	1.47	1.43

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1	NAG	O4-C4-C3	-6.52	95.27	110.35
2	B	2	NDG	O5-C1-C2	6.48	121.52	111.29
2	B	1	NAG	C6-C5-C4	4.92	124.53	113.00
2	B	1	NAG	C3-C4-C5	4.21	117.76	110.24
2	B	1	NAG	C1-O5-C5	-4.16	106.56	112.19
2	B	2	NDG	C1-O5-C5	2.72	115.88	112.19
2	B	1	NAG	C4-C3-C2	2.72	115.00	111.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	2	NDG	C2-N2-C7	-2.35	119.56	122.90
2	B	1	NAG	O3-C3-C2	2.31	114.25	109.47
2	B	1	NAG	C1-C2-N2	-2.30	106.57	110.49
2	B	2	NDG	C4-C3-C2	2.01	113.96	111.02

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1	NAG	C4-C5-C6-O6
2	B	1	NAG	C1-C2-N2-C7
2	B	1	NAG	O5-C5-C6-O6
2	B	2	NDG	C4-C5-C6-O6

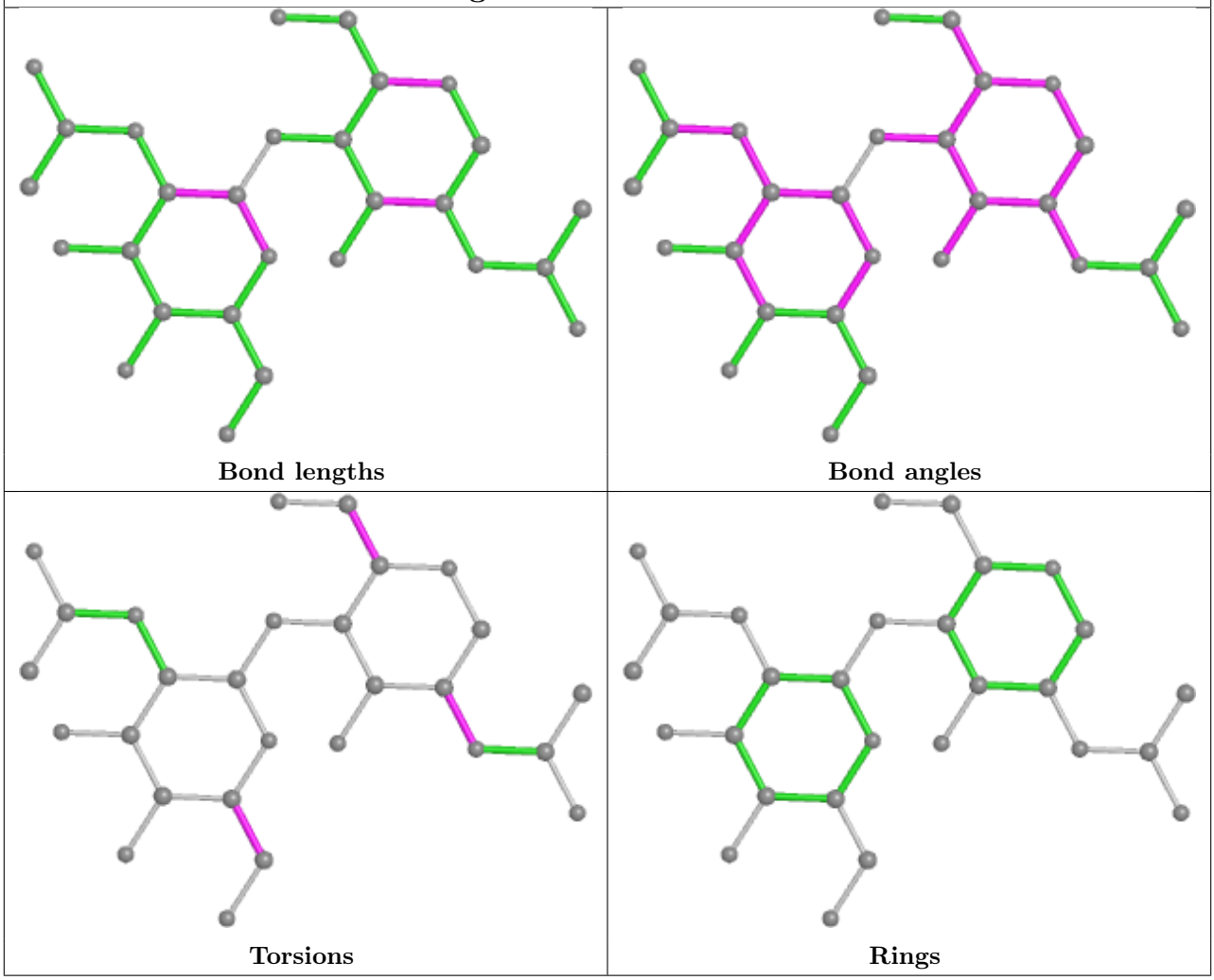
There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2	NDG	3	0
2	B	1	NAG	7	0

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

Oligosaccharide Chain B



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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.