Full wwPDB X-ray Structure Validation Report (i)

Aug 15, 2023 – 04:15 PM EDT

PDB ID	:	1SR0
Title	:	Crystal structure of signalling protein from sheep(SPS-40) at 3.0A resolution using crystal grown in the presence of polysaccharides
Authors	:	Srivastava, D.B.; Ethayathulla, A.S.; Singh, N.; Kumar, J.; Sharma, S.; Singh, T.P.
Deposited on	:	2004-03-22
Resolution	:	3.05 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:

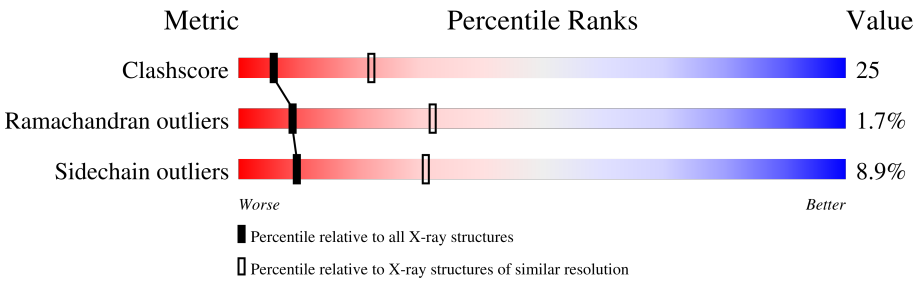
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 3.05 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	1864 (3.10-3.02)
Ramachandran outliers	138981	1794 (3.10-3.02)
Sidechain outliers	138945	1793 (3.10-3.02)

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	54% 38% 7% •
2	B	5	20% 80%

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	NDG	B	2	-	-	X	-

2 Entry composition (i)

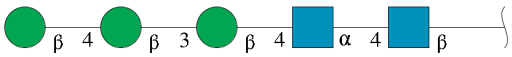
There are 3 unique types of molecules in this entry. The entry contains 3007 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 signal processing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	361	2868	1832	499	528	9	0	0	0

- Molecule 2 is an oligosaccharide called beta-D-mannopyranose-(1-4)-beta-D-mannopyranose -(1-3)-beta-D-mannopyranose-(1-4)-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	5	61	34	2	25	0	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	78	78	78	0	0

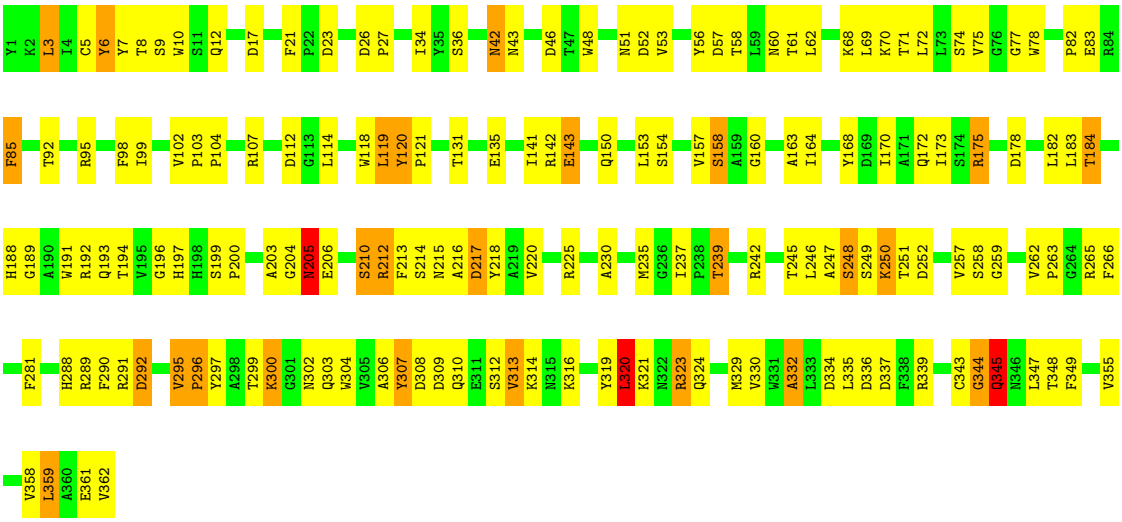
3 Residue-property plots (i)

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: signal processing protein

Chain A: 54% 38% 7% •



• Molecule 2: beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B: 20% 80%

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	62.79Å 66.39Å 107.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.00 – 3.05	Depositor
% Data completeness (in resolution range)	80.0 (56.00-3.05)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.172 , 0.205	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3007	wwPDB-VP
Average B, all atoms (Å^2)	29.0	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: NAG, NDG, BMA

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	1.15	4/2944 (0.1%)	1.10	13/3995 (0.3%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	330	VAL	CA-CB	-5.93	1.42	1.54
1	A	332	ALA	CA-CB	-5.65	1.40	1.52
1	A	6	TYR	CE2-CZ	-5.25	1.31	1.38
1	A	307	TYR	CE2-CZ	-5.04	1.31	1.38

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	217	ASP	CB-CG-OD2	8.48	125.93	118.30
1	A	336	ASP	CB-CG-OD2	8.40	125.86	118.30
1	A	300	LYS	CG-CD-CE	7.18	133.46	111.90
1	A	309	ASP	CB-CG-OD2	7.17	124.75	118.30
1	A	178	ASP	CB-CG-OD2	6.74	124.36	118.30
1	A	320	LEU	CA-CB-CG	6.72	130.76	115.30
1	A	337	ASP	CB-CG-OD2	6.48	124.13	118.30
1	A	46	ASP	CB-CG-OD2	6.44	124.09	118.30
1	A	112	ASP	CB-CG-OD2	6.21	123.89	118.30
1	A	210	SER	C-N-CA	-5.72	107.40	121.70
1	A	308	ASP	CB-CG-OD2	5.29	123.06	118.30
1	A	119	LEU	CA-CB-CG	-5.07	103.65	115.30
1	A	334	ASP	CB-CG-OD2	5.01	122.81	118.30

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	2868	0	2794	137	0
2	B	61	0	51	12	0
3	A	78	0	0	5	0
All	All	3007	0	2845	146	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 25.

All (146) 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)
2:B:1:NAG:H61	2:B:2:NDG:C2	1.85	1.07
2:B:1:NAG:C6	2:B:2:NDG:HA	1.69	1.03
1:A:203:ALA:HB2	1:A:212:ARG:HD2	1.43	0.99
2:B:1:NAG:H61	2:B:2:NDG:N2	1.78	0.98
2:B:1:NAG:H61	2:B:2:NDG:C1	1.97	0.94
2:B:1:NAG:H62	2:B:2:NDG:HA	1.34	0.93
1:A:57:ASP:O	1:A:61:THR:HG23	1.71	0.90
1:A:48:TRP:O	2:B:1:NAG:H81	1.77	0.84
1:A:48:TRP:CD1	2:B:1:NAG:H82	2.13	0.84
2:B:1:NAG:C6	2:B:2:NDG:N2	2.38	0.83
1:A:323:ARG:HH11	1:A:323:ARG:HG2	1.45	0.80
1:A:323:ARG:HG2	1:A:323:ARG:NH1	1.99	0.77
1:A:239:THR:HG23	1:A:239:THR:O	1.84	0.76
2:B:1:NAG:H61	2:B:2:NDG:HA	1.38	0.74
1:A:205:ASN:C	1:A:205:ASN:HD22	1.91	0.73
1:A:8:THR:HA	1:A:36:SER:HB2	1.71	0.73
1:A:216:ALA:O	1:A:220:VAL:HG23	1.89	0.72
1:A:205:ASN:HD22	1:A:206:GLU:N	1.87	0.72
1:A:347:LEU:HD23	1:A:348:THR:N	2.06	0.70
1:A:27:PRO:HG3	1:A:62:LEU:HD22	1.72	0.70
1:A:192:ARG:O	1:A:194:THR:N	2.25	0.70
1:A:95:ARG:CZ	1:A:131:THR:HG21	2.22	0.69
1:A:43:ASN:O	1:A:98:PHE:HA	1.91	0.69
1:A:310:GLN:O	1:A:314:LYS:HG3	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:332:ALA:CB	1:A:335:LEU:HD12	2.23	0.69
1:A:78:TRP:CD1	1:A:119:LEU:HD13	2.28	0.68
1:A:320:LEU:HD21	1:A:359:LEU:HD11	1.75	0.68
1:A:313:VAL:HG13	1:A:355:VAL:CG2	2.23	0.68
1:A:83:GLU:H	1:A:83:GLU:CD	1.99	0.66
1:A:120:TYR:CE2	1:A:158:SER:HB2	2.31	0.66
1:A:323:ARG:HH11	1:A:323:ARG:CG	2.08	0.66
1:A:213:PHE:HD1	1:A:218:TYR:CZ	2.13	0.66
1:A:164:ILE:HA	1:A:168:TYR:HD2	1.62	0.64
1:A:82:PRO:HD2	1:A:83:GLU:OE2	1.99	0.63
1:A:313:VAL:HG13	1:A:355:VAL:HG23	1.81	0.62
2:B:1:NAG:C6	2:B:2:NDG:C1	2.73	0.62
1:A:189:GLY:HA3	1:A:191:TRP:NE1	2.14	0.62
1:A:332:ALA:HB3	1:A:335:LEU:HD12	1.82	0.61
1:A:95:ARG:O	1:A:99:ILE:HG13	2.01	0.61
1:A:313:VAL:CG1	1:A:355:VAL:HG23	2.32	0.60
1:A:188:HIS:CD2	1:A:196:GLY:HA3	2.37	0.59
1:A:203:ALA:CB	1:A:212:ARG:HD2	2.26	0.59
1:A:172:GLN:O	1:A:175:ARG:HG2	2.04	0.58
1:A:3:LEU:HD22	1:A:5:CYS:SG	2.44	0.58
1:A:69:LEU:HD13	1:A:70:LYS:N	2.19	0.57
1:A:197:HIS:NE2	1:A:295:VAL:HB	2.19	0.57
1:A:205:ASN:ND2	1:A:292:ASP:OD2	2.37	0.57
1:A:213:PHE:CD1	1:A:218:TYR:CZ	2.92	0.56
1:A:248:SER:OG	1:A:250:LYS:HB2	2.07	0.55
1:A:242:ARG:HG3	1:A:242:ARG:HH11	1.72	0.55
1:A:304:TRP:CZ3	1:A:306:ALA:HB2	2.41	0.55
1:A:102:VAL:HB	1:A:103:PRO:HD3	1.89	0.54
1:A:77:GLY:C	1:A:119:LEU:HD12	2.28	0.54
1:A:7:TYR:O	1:A:36:SER:N	2.42	0.53
1:A:26:ASP:OD1	1:A:26:ASP:C	2.42	0.53
1:A:257:VAL:HG12	1:A:259:GLY:N	2.23	0.53
1:A:237:ILE:N	1:A:329:MET:O	2.38	0.52
1:A:319:TYR:CZ	1:A:323:ARG:HD2	2.44	0.52
1:A:197:HIS:HB2	1:A:290:PHE:HE2	1.75	0.51
1:A:135:GLU:HB3	3:A:403:HOH:O	2.09	0.51
1:A:205:ASN:ND2	1:A:206:GLU:HG2	2.26	0.51
1:A:299:THR:HA	1:A:303:GLN:O	2.11	0.51
1:A:239:THR:CG2	1:A:335:LEU:HB2	2.41	0.50
1:A:131:THR:O	1:A:135:GLU:HG3	2.12	0.50
1:A:6:TYR:HD2	1:A:36:SER:OG	1.95	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:GLU:CG	3:A:399:HOH:O	2.60	0.50
1:A:205:ASN:HA	3:A:440:HOH:O	2.12	0.49
1:A:7:TYR:O	1:A:36:SER:HB2	2.12	0.49
1:A:141:ILE:HA	1:A:150:GLN:NE2	2.27	0.49
1:A:257:VAL:HG12	1:A:259:GLY:H	1.77	0.49
1:A:230:ALA:HB1	1:A:324:GLN:O	2.12	0.49
1:A:75:VAL:CG2	1:A:114:LEU:HD11	2.43	0.48
1:A:48:TRP:O	2:B:1:NAG:C8	2.54	0.48
1:A:142:ARG:HB2	1:A:142:ARG:NH1	2.29	0.48
1:A:262:VAL:H	1:A:303:GLN:HE22	1.61	0.48
1:A:170:ILE:HD13	1:A:173:ILE:HD11	1.96	0.48
1:A:203:ALA:HB2	1:A:212:ARG:CD	2.30	0.48
1:A:197:HIS:HB2	1:A:290:PHE:CE2	2.49	0.47
1:A:8:THR:HB	1:A:10:TRP:CZ3	2.49	0.47
1:A:205:ASN:C	1:A:205:ASN:ND2	2.62	0.47
1:A:21:PHE:C	1:A:23:ASP:N	2.64	0.47
1:A:34:ILE:HG12	1:A:72:LEU:HB2	1.97	0.47
1:A:42:ASN:N	1:A:42:ASN:ND2	2.60	0.47
1:A:288:HIS:HB2	1:A:297:TYR:CE1	2.50	0.47
1:A:358:VAL:O	1:A:361:GLU:HB2	2.15	0.47
1:A:68:LYS:HA	1:A:68:LYS:HD2	1.56	0.46
1:A:78:TRP:NE1	1:A:119:LEU:HD13	2.29	0.46
1:A:153:LEU:HD12	1:A:154:SER:N	2.30	0.46
1:A:9:SER:O	1:A:12:GLN:HG2	2.15	0.46
1:A:242:ARG:HG3	1:A:242:ARG:NH1	2.29	0.46
2:B:4:BMA:C6	2:B:5:BMA:O5	2.64	0.46
1:A:239:THR:HG22	1:A:335:LEU:HB2	1.97	0.46
1:A:312:SER:O	1:A:316:LYS:HG3	2.15	0.46
1:A:51:ASN:N	1:A:51:ASN:OD1	2.49	0.46
1:A:281:PHE:O	1:A:300:LYS:HE3	2.16	0.45
1:A:343:CYS:O	1:A:344:GLY:C	2.54	0.45
1:A:8:THR:HG22	1:A:36:SER:CB	2.47	0.45
1:A:58:THR:O	1:A:61:THR:OG1	2.35	0.45
1:A:119:LEU:HA	1:A:119:LEU:HD23	1.64	0.45
1:A:52:ASP:O	1:A:53:VAL:C	2.53	0.45
1:A:203:ALA:HA	1:A:215:ASN:ND2	2.31	0.45
1:A:313:VAL:HG13	1:A:355:VAL:HG22	1.98	0.45
1:A:316:LYS:O	1:A:319:TYR:HB3	2.16	0.45
1:A:85:PHE:CE2	1:A:118:TRP:HA	2.52	0.45
1:A:188:HIS:ND1	1:A:189:GLY:N	2.65	0.45
1:A:345:GLN:HE21	1:A:345:GLN:HB3	1.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:SER:HB3	1:A:214:SER:OG	2.17	0.45
1:A:157:VAL:O	1:A:183:LEU:HG	2.17	0.44
1:A:199:SER:N	1:A:200:PRO:CD	2.81	0.44
1:A:235:MET:CE	1:A:316:LYS:HB3	2.48	0.44
1:A:184:THR:CG2	1:A:216:ALA:HA	2.48	0.44
1:A:217:ASP:OD1	1:A:217:ASP:C	2.55	0.44
1:A:247:ALA:HB2	1:A:258:SER:HB3	1.99	0.44
1:A:321:LYS:NZ	1:A:362:VAL:C	2.71	0.44
1:A:60:ASN:ND2	1:A:71:THR:OG1	2.51	0.43
1:A:120:TYR:HA	1:A:121:PRO:HD2	1.87	0.43
1:A:213:PHE:HD1	1:A:218:TYR:CE1	2.36	0.43
1:A:307:TYR:HB2	3:A:414:HOH:O	2.18	0.43
1:A:257:VAL:CG1	1:A:259:GLY:H	2.31	0.43
1:A:265:ARG:HB2	1:A:266:PHE:CD1	2.54	0.43
1:A:288:HIS:HB2	1:A:297:TYR:CZ	2.54	0.43
1:A:245:THR:HA	1:A:302:ASN:O	2.19	0.43
1:A:348:THR:O	1:A:349:PHE:C	2.57	0.43
1:A:212:ARG:O	1:A:212:ARG:HG3	2.16	0.42
1:A:118:TRP:C	1:A:118:TRP:CD1	2.92	0.42
1:A:213:PHE:HA	1:A:218:TYR:CG	2.55	0.42
1:A:344:GLY:O	1:A:345:GLN:C	2.58	0.42
1:A:17:ASP:HB3	1:A:339:ARG:HE	1.85	0.42
1:A:92:THR:HG22	1:A:95:ARG:NH2	2.36	0.41
1:A:120:TYR:CD2	1:A:120:TYR:N	2.86	0.41
1:A:220:VAL:HG23	1:A:220:VAL:H	1.67	0.41
1:A:182:LEU:HA	1:A:182:LEU:HD23	1.81	0.41
1:A:359:LEU:HD12	1:A:359:LEU:HA	1.82	0.41
1:A:265:ARG:HA	3:A:417:HOH:O	2.21	0.41
1:A:321:LYS:HZ2	1:A:362:VAL:C	2.23	0.41
1:A:213:PHE:HA	1:A:218:TYR:CD2	2.56	0.41
1:A:95:ARG:NH2	1:A:131:THR:HG21	2.36	0.41
1:A:103:PRO:N	1:A:104:PRO:HD2	2.36	0.41
1:A:262:VAL:HA	1:A:263:PRO:HD3	1.87	0.41
1:A:266:PHE:CD1	1:A:266:PHE:N	2.88	0.41
1:A:246:LEU:HD21	1:A:304:TRP:HB2	2.03	0.41
1:A:52:ASP:HB3	1:A:56:TYR:CE1	2.56	0.40
1:A:192:ARG:C	1:A:194:THR:H	2.25	0.40
1:A:160:GLY:O	1:A:163:ALA:HB3	2.21	0.40
1:A:289:ARG:HA	1:A:296:PRO:HA	2.02	0.40
1:A:157:VAL:HG12	1:A:158:SER:N	2.37	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%)	317 (88%)	36 (10%)	6 (2%)	9 32

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	193	GLN
1	A	205	ASN
1	A	344	GLY
1	A	345	GLN
1	A	120	TYR
1	A	204	GLY

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	302/302 (100%)	275 (91%)	27 (9%)	9 31

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

Mol	Chain	Res	Type
1	A	3	LEU
1	A	42	ASN
1	A	74	SER
1	A	85	PHE
1	A	107	ARG

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Mol	Chain	Res	Type
1	A	143	GLU
1	A	158	SER
1	A	175	ARG
1	A	184	THR
1	A	205	ASN
1	A	212	ARG
1	A	225	ARG
1	A	239	THR
1	A	248	SER
1	A	249	SER
1	A	250	LYS
1	A	251	THR
1	A	252	ASP
1	A	291	ARG
1	A	292	ASP
1	A	295	VAL
1	A	296	PRO
1	A	313	VAL
1	A	320	LEU
1	A	323	ARG
1	A	345	GLN
1	A	359	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	ASN
1	A	60	ASN
1	A	145	GLN
1	A	150	GLN
1	A	193	GLN
1	A	198	HIS
1	A	205	ASN
1	A	288	HIS
1	A	303	GLN
1	A	310	GLN
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)

5 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	1.33	2 (14%)	17,19,21	2.63	8 (47%)
2	NDG	B	2	2	14,14,15	1.22	1 (7%)	17,19,21	3.80	9 (52%)
2	BMA	B	3	2	11,11,12	0.68	0	15,15,17	2.10	6 (40%)
2	BMA	B	4	2	11,11,12	0.92	0	15,15,17	3.28	6 (40%)
2	BMA	B	5	2	11,11,12	0.77	0	15,15,17	3.48	5 (33%)

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	-	4/6/23/26	0/1/1/1
2	NDG	B	2	2	-	2/6/23/26	0/1/1/1
2	BMA	B	3	2	-	0/2/19/22	0/1/1/1
2	BMA	B	4	2	-	1/2/19/22	0/1/1/1
2	BMA	B	5	2	-	2/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	NDG	C1-C2	4.12	1.58	1.52
2	B	1	NAG	O5-C5	-3.03	1.37	1.43
2	B	1	NAG	O5-C1	-2.94	1.39	1.43

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	5	BMA	O5-C1-C2	11.51	128.53	110.77
2	B	4	BMA	O5-C1-C2	10.69	127.27	110.77
2	B	2	NDG	C1-C2-N2	10.61	128.61	110.49
2	B	2	NDG	O5-C5-C6	8.10	119.90	107.20
2	B	1	NAG	C1-C2-N2	5.01	119.05	110.49
2	B	1	NAG	O7-C7-C8	-4.99	112.79	122.06
2	B	1	NAG	C1-O5-C5	-4.56	106.01	112.19
2	B	2	NDG	C4-C3-C2	-4.49	104.43	111.02
2	B	5	BMA	C3-C4-C5	4.20	117.73	110.24
2	B	3	BMA	O5-C1-C2	3.94	116.84	110.77
2	B	5	BMA	O5-C5-C4	3.37	119.03	110.83
2	B	1	NAG	C8-C7-N2	3.34	121.75	116.10
2	B	2	NDG	C3-C4-C5	-3.24	104.46	110.24
2	B	4	BMA	O4-C4-C5	-3.11	101.58	109.30
2	B	3	BMA	C3-C4-C5	3.01	115.61	110.24
2	B	3	BMA	C1-O5-C5	3.01	116.27	112.19
2	B	1	NAG	C2-N2-C7	-3.00	118.64	122.90
2	B	4	BMA	O4-C4-C3	-2.94	103.55	110.35
2	B	4	BMA	O5-C5-C4	2.74	117.49	110.83
2	B	3	BMA	C1-C2-C3	-2.63	106.44	109.67
2	B	4	BMA	C3-C4-C5	2.60	114.88	110.24
2	B	2	NDG	O3-C3-C4	2.59	116.34	110.35
2	B	3	BMA	O5-C5-C6	2.47	111.08	107.20
2	B	3	BMA	C2-C3-C4	-2.34	106.84	110.89
2	B	5	BMA	C1-C2-C3	2.32	112.52	109.67
2	B	1	NAG	O3-C3-C2	-2.30	104.72	109.47
2	B	5	BMA	C1-O5-C5	2.29	115.30	112.19
2	B	2	NDG	C6-C5-C4	-2.26	107.72	113.00
2	B	2	NDG	C8-C7-N2	2.24	119.89	116.10
2	B	1	NAG	O4-C4-C5	-2.20	103.84	109.30
2	B	1	NAG	O5-C5-C6	-2.19	103.77	107.20
2	B	4	BMA	C1-O5-C5	2.18	115.15	112.19
2	B	2	NDG	O7-C7-C8	-2.15	118.06	122.06
2	B	2	NDG	O4-C4-C5	-2.13	104.01	109.30

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	NDG	O7-C7-N2-C2
2	B	2	NDG	C8-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
2	B	5	BMA	O5-C5-C6-O6
2	B	4	BMA	O5-C5-C6-O6
2	B	5	BMA	C4-C5-C6-O6
2	B	1	NAG	C4-C5-C6-O6
2	B	1	NAG	O5-C5-C6-O6
2	B	1	NAG	C8-C7-N2-C2
2	B	1	NAG	O7-C7-N2-C2

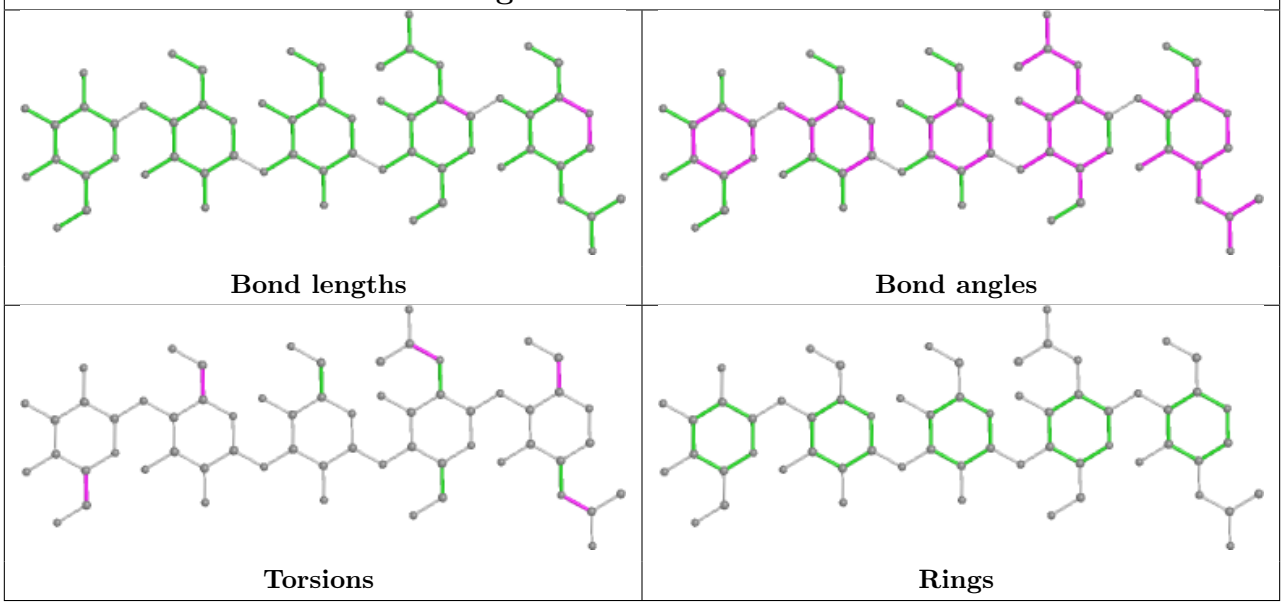
There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	NAG	11	0
2	B	2	NDG	8	0
2	B	4	BMA	1	0
2	B	5	BMA	1	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.