Full wwPDB X-ray Structure Validation Report (i)

Aug 6, 2023 – 06:40 PM EDT

PDB ID	:	1LF9
Title	:	CRYSTAL STRUCTURE OF BACTERIAL GLUCOAMYLASE COMPLEXED WITH ACARBOSE
Authors	:	Aleshin, A.E.; Feng, P.-H.; Honzatko, R.B.; Reilly, P.J.
Deposited on	:	2002-04-10
Resolution	:	2.20 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:

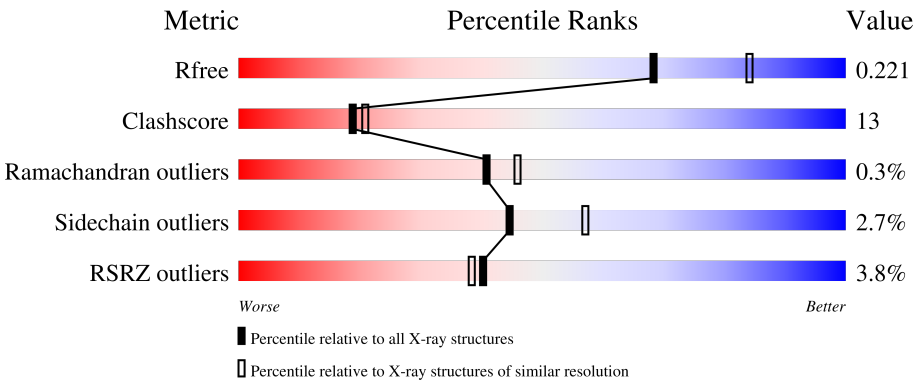
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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% 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	684	5% 73% 24% • •
1	B	684	2% 74% 23% • •
2	C	3	67% 33%
2	D	3	67% 33%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 11438 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 GLUCOAMYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	674	5333	3385	881	1052	15	0	0	0
1	B	674	5333	3385	881	1052	15	0	0	0

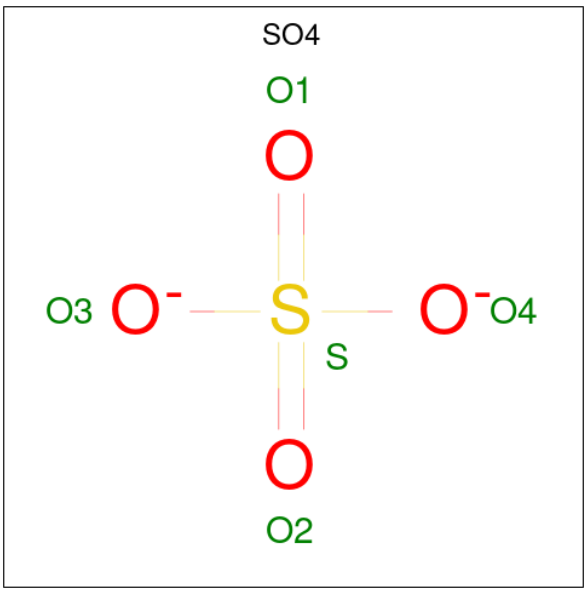
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	125	PHE	-	SEE REMARK 999	GB 3243238
A	252	GLN	GLY	conflict	GB 3243238
A	680	LYS	-	SEE REMARK 999	GB 3243238
A	681	ARG	-	SEE REMARK 999	GB 3243238
A	682	TYR	-	SEE REMARK 999	GB 3243238
A	683	VAL	-	SEE REMARK 999	GB 3243238
A	684	ALA	-	SEE REMARK 999	GB 3243238
B	125	PHE	-	SEE REMARK 999	GB 3243238
B	252	GLN	GLY	conflict	GB 3243238
B	680	LYS	-	SEE REMARK 999	GB 3243238
B	681	ARG	-	SEE REMARK 999	GB 3243238
B	682	TYR	-	SEE REMARK 999	GB 3243238
B	683	VAL	-	SEE REMARK 999	GB 3243238
B	684	ALA	-	SEE REMARK 999	GB 3243238

- Molecule 2 is an oligosaccharide called 4,6-dideoxy-4-{[(1S,4R,5S,6S)-4,5,6-trihydroxy-3-(hydroxymethyl)cyclohex-2-en-1-yl]amino}-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	3	44	25	1	18	0	0	0
2	D	3	44	25	1	18	0	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0

- Molecule 4 is water.

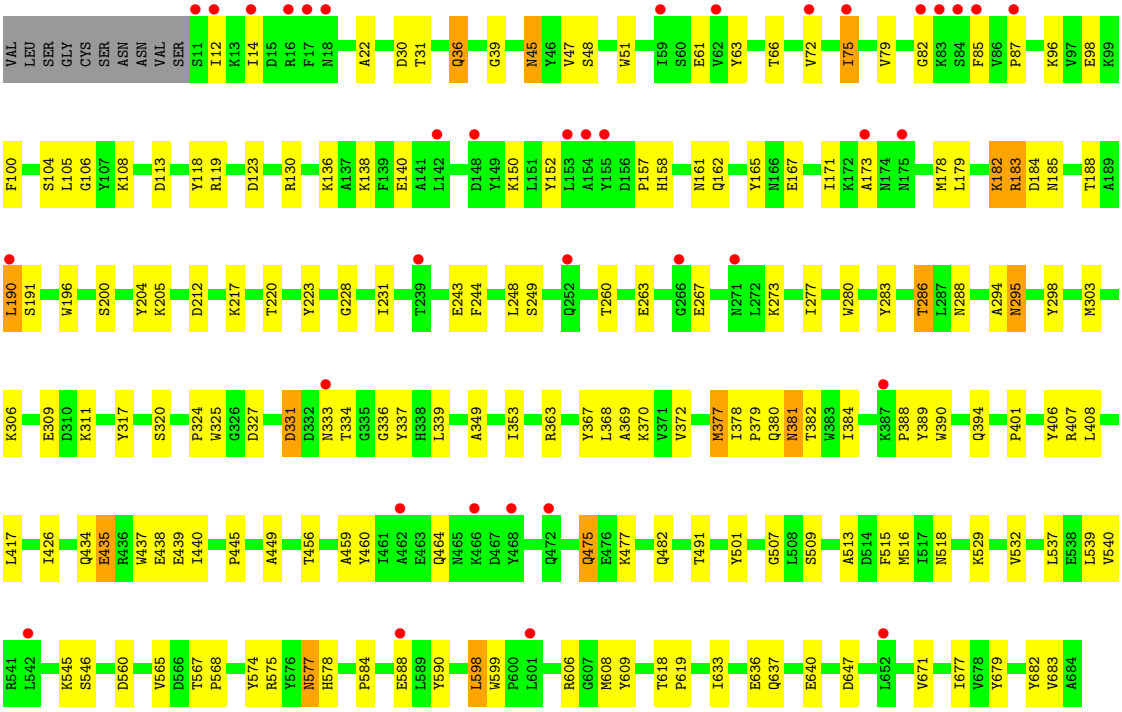
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	284	Total O 284 284	0	0
4	B	390	Total O 390 390	0	0

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.

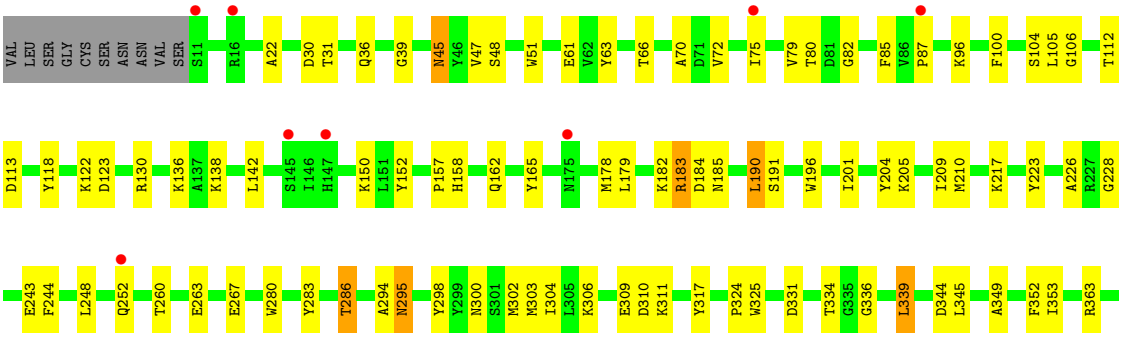
• Molecule 1: GLUCOAMYLASE

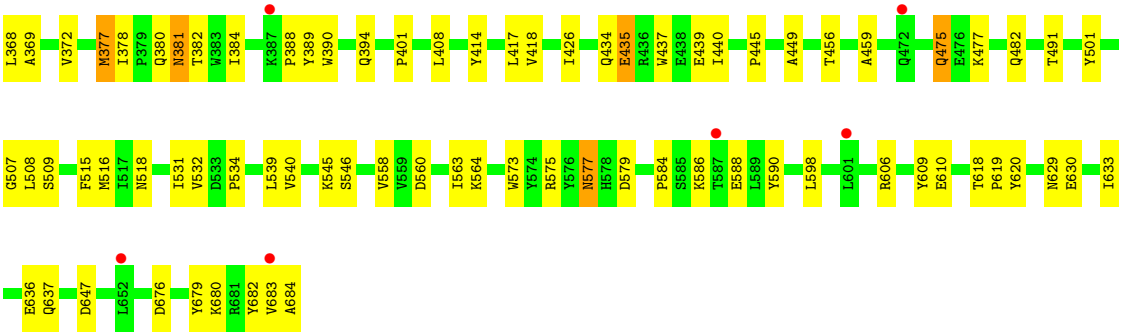
Chain A:



• Molecule 1: GLUCOAMYLASE

Chain B:



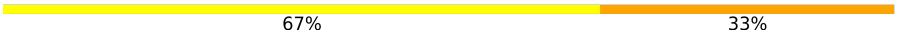


• Molecule 2: 4,6-dideoxy-4-{[(1S,4R,5S,6S)-4,5,6-trihydroxy-3-(hydroxymethyl)cyclohex-2-en-1-yl]amino}-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain C:

• Molecule 2: 4,6-dideoxy-4-{[(1S,4R,5S,6S)-4,5,6-trihydroxy-3-(hydroxymethyl)cyclohex-2-en-1-yl]amino}-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	80.49Å 102.93Å 164.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.86 – 2.20 29.86 – 2.19	Depositor EDS
% Data completeness (in resolution range)	92.4 (29.86-2.20) 91.9 (29.86-2.19)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.93 (at 2.20Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.191 , 0.227 0.185 , 0.221	Depositor DCC
R_{free} test set	4621 reflections (7.11%)	wwPDB-VP
Wilson B-factor (Å^2)	32.4	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 43.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	11438	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.09% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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, AC1, SO4

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	0.32	0/5453	0.56	0/7391
1	B	0.34	0/5453	0.57	0/7391
All	All	0.33	0/10906	0.56	0/14782

There are no bond length outliers.

There are no bond angle outliers.

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	5333	0	5172	143	0
1	B	5333	0	5172	139	0
2	C	44	0	30	1	0
2	D	44	0	30	1	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	284	0	0	9	0
4	B	390	0	0	5	0
All	All	11438	0	10404	278	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 13.

All (278) 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:516:MET:H	1:B:518:ASN:HD21	1.12	0.89
1:A:288:ASN:HB3	4:A:973:HOH:O	1.74	0.86
1:B:334:THR:HG22	1:B:336:GLY:H	1.39	0.86
1:A:334:THR:HG22	1:A:336:GLY:H	1.41	0.84
1:A:518:ASN:HD21	1:B:516:MET:H	1.23	0.82
1:A:45:ASN:HD21	1:A:48:SER:H	1.27	0.79
1:B:79:VAL:O	1:B:87:PRO:HD2	1.82	0.78
1:B:45:ASN:HD21	1:B:48:SER:H	1.31	0.77
1:A:79:VAL:O	1:A:87:PRO:HD2	1.85	0.76
1:A:309:GLU:HB2	1:A:317:TYR:CE1	2.19	0.76
1:A:280:TRP:HB3	1:A:303:MET:HE3	1.68	0.75
1:A:575:ARG:HD3	1:A:599:TRP:CZ2	2.25	0.72
1:A:368:LEU:HD13	1:A:401:PRO:HB3	1.73	0.71
1:A:157:PRO:O	1:A:158:HIS:HD2	1.74	0.71
1:A:426:ILE:HG23	1:A:477:LYS:HE3	1.72	0.70
1:B:309:GLU:HB2	1:B:317:TYR:CE1	2.27	0.70
1:A:540:VAL:HG21	1:A:609:TYR:HD2	1.56	0.70
1:A:105:LEU:N	1:A:303:MET:HE1	2.07	0.69
1:A:353:ILE:HD11	1:A:408:LEU:HD21	1.73	0.69
1:B:283:TYR:CZ	1:B:306:LYS:HG3	2.27	0.69
1:B:575:ARG:HD3	1:B:579:ASP:OD2	1.92	0.69
1:B:280:TRP:HB3	1:B:303:MET:HE3	1.75	0.69
1:A:516:MET:H	1:B:518:ASN:ND2	1.89	0.69
1:B:353:ILE:HD11	1:B:408:LEU:HD21	1.75	0.69
1:B:157:PRO:O	1:B:158:HIS:HD2	1.75	0.68
1:A:45:ASN:ND2	1:A:48:SER:H	1.92	0.68
1:B:79:VAL:HG13	1:B:87:PRO:HG2	1.75	0.67
1:B:113:ASP:HB2	1:B:118:TYR:CE1	2.30	0.66
1:A:381:ASN:HD21	1:A:390:TRP:H	1.41	0.66
1:B:381:ASN:HD21	1:B:390:TRP:H	1.44	0.66
1:A:546:SER:HA	1:A:683:VAL:HG13	1.76	0.66
1:B:368:LEU:HD13	1:B:401:PRO:HB3	1.76	0.66
1:B:381:ASN:ND2	1:B:390:TRP:H	1.93	0.66
1:A:66:THR:HB	1:A:384:ILE:CD1	2.26	0.65
1:B:456:THR:HG23	1:B:475:GLN:OE1	1.96	0.65
1:B:31:THR:O	1:B:158:HIS:HE1	1.80	0.65
1:A:381:ASN:ND2	1:A:390:TRP:H	1.93	0.65
1:A:66:THR:HB	1:A:384:ILE:HD11	1.78	0.65
1:B:546:SER:HA	1:B:683:VAL:HG13	1.78	0.65
1:A:36:GLN:HA	1:A:36:GLN:HE21	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:306:LYS:HD3	4:B:806:HOH:O	1.98	0.63
1:A:79:VAL:HG13	1:A:87:PRO:HG2	1.80	0.62
1:A:45:ASN:HD22	1:A:47:VAL:H	1.45	0.62
1:B:540:VAL:HG21	1:B:609:TYR:HD2	1.65	0.62
1:A:75:ILE:HD11	1:A:248:LEU:HD22	1.82	0.61
1:A:82:GLY:HA2	1:A:217:LYS:O	2.00	0.61
1:A:377:MET:HG2	1:A:378:ILE:N	2.15	0.61
1:B:283:TYR:O	1:B:286:THR:HG22	2.00	0.61
1:A:309:GLU:OE2	1:A:363:ARG:HD2	2.00	0.61
1:A:456:THR:HG23	1:A:475:GLN:OE1	1.99	0.61
1:A:104:SER:HA	1:A:303:MET:HE3	1.82	0.60
1:B:309:GLU:OE2	1:B:363:ARG:HD2	2.00	0.60
1:A:283:TYR:O	1:A:286:THR:HG22	2.01	0.60
1:B:445:PRO:HG2	4:B:948:HOH:O	2.02	0.60
1:B:532:VAL:HG22	1:B:577:ASN:HD21	1.67	0.59
1:A:434:GLN:HA	1:A:440:ILE:O	2.02	0.59
1:B:45:ASN:HD22	1:B:47:VAL:H	1.50	0.59
1:A:575:ARG:HD3	1:A:599:TRP:CE2	2.36	0.59
1:B:105:LEU:N	1:B:303:MET:HE1	2.17	0.59
1:A:136:LYS:HE2	1:A:243:GLU:OE1	2.02	0.59
1:A:51:TRP:CZ2	1:A:311:LYS:HG3	2.39	0.58
1:A:113:ASP:HB2	1:A:118:TYR:CE1	2.38	0.58
1:B:434:GLN:HA	1:B:440:ILE:O	2.04	0.58
1:A:369:ALA:HA	1:A:417:LEU:HD13	1.86	0.58
1:A:12:ILE:HD12	1:A:173:ALA:HB1	1.85	0.57
1:B:45:ASN:ND2	1:B:48:SER:H	2.00	0.57
1:B:66:THR:HB	1:B:384:ILE:CD1	2.34	0.57
1:B:82:GLY:HA2	1:B:217:LYS:O	2.04	0.57
1:A:130:ARG:NE	1:A:263:GLU:HB3	2.20	0.57
1:B:104:SER:HA	1:B:303:MET:HE3	1.87	0.57
1:B:449:ALA:HB2	1:B:539:LEU:HD23	1.86	0.56
1:A:382:THR:HG22	1:A:388:PRO:HA	1.88	0.56
1:B:283:TYR:CE1	1:B:306:LYS:HG3	2.40	0.56
1:B:377:MET:HG2	1:B:378:ILE:N	2.21	0.56
1:B:437:TRP:O	1:B:439:GLU:HG3	2.05	0.56
1:A:162:GLN:HG2	1:A:183:ARG:NH2	2.20	0.55
1:A:560:ASP:OD1	1:A:606:ARG:NH1	2.40	0.55
1:B:30:ASP:HB3	1:B:331:ASP:OD2	2.06	0.55
1:A:45:ASN:HD22	1:A:47:VAL:N	2.04	0.55
1:A:283:TYR:CE1	1:A:306:LYS:HG3	2.41	0.55
1:A:406:TYR:OH	1:A:677:ILE:HG12	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:295:ASN:ND2	1:A:298:TYR:H	2.05	0.55
1:B:66:THR:HB	1:B:384:ILE:HD11	1.88	0.54
1:A:130:ARG:HB3	1:A:260:THR:HG23	1.89	0.54
1:A:283:TYR:CZ	1:A:306:LYS:HG3	2.42	0.54
1:B:380:GLN:HG3	1:B:394:GLN:NE2	2.22	0.54
1:B:75:ILE:HD11	1:B:248:LEU:HD22	1.89	0.53
1:B:138:LYS:HB3	1:B:243:GLU:HG3	1.91	0.53
1:B:162:GLN:HG2	1:B:183:ARG:NH2	2.24	0.53
1:A:513:ALA:O	1:A:529:LYS:HE3	2.08	0.53
1:A:584:PRO:HG2	1:A:588:GLU:HB2	1.90	0.53
1:A:190:LEU:HD22	1:A:196:TRP:CZ2	2.44	0.52
1:A:39:GLY:HA2	1:A:633:ILE:HD11	1.92	0.52
1:B:85:PHE:HD1	1:B:87:PRO:HD3	1.74	0.52
1:B:294:ALA:HB1	1:B:298:TYR:CD2	2.45	0.52
1:B:560:ASP:OD1	1:B:606:ARG:NH1	2.43	0.52
1:A:204:TYR:CZ	1:A:205:LYS:HE3	2.44	0.51
1:A:334:THR:HG22	1:A:336:GLY:N	2.20	0.51
1:A:150:LYS:HD2	4:A:878:HOH:O	2.10	0.51
1:A:532:VAL:HG22	1:A:577:ASN:HD21	1.76	0.51
1:A:546:SER:OG	1:A:683:VAL:HG13	2.09	0.51
1:B:629:ASN:HB2	4:B:926:HOH:O	2.11	0.51
1:B:426:ILE:HG23	1:B:477:LYS:HE3	1.92	0.51
1:B:130:ARG:NE	1:B:263:GLU:HB3	2.26	0.50
1:B:369:ALA:HA	1:B:417:LEU:HD13	1.93	0.50
1:A:30:ASP:HB3	1:A:331:ASP:OD2	2.12	0.50
1:B:381:ASN:HD21	1:B:390:TRP:N	2.08	0.50
1:B:45:ASN:HD22	1:B:47:VAL:N	2.09	0.50
1:A:22:ALA:HA	1:A:223:TYR:CD1	2.46	0.50
1:A:309:GLU:HB2	1:A:317:TYR:CZ	2.47	0.49
1:A:560:ASP:CG	1:A:606:ARG:HH12	2.14	0.49
1:B:459:ALA:CB	1:B:475:GLN:HG2	2.42	0.49
1:B:546:SER:OG	1:B:683:VAL:HG13	2.11	0.49
1:A:100:PHE:CD1	1:A:106:GLY:HA3	2.47	0.49
1:A:96:LYS:HD3	4:A:935:HOH:O	2.11	0.49
1:A:482:GLN:HG3	1:A:682:TYR:CD1	2.47	0.49
1:A:349:ALA:O	1:A:353:ILE:HG12	2.12	0.49
1:B:349:ALA:O	1:B:353:ILE:HG12	2.12	0.49
1:A:647:ASP:HB2	4:A:979:HOH:O	2.12	0.49
1:B:136:LYS:HE2	1:B:243:GLU:OE1	2.13	0.49
1:B:309:GLU:HG2	1:B:310:ASP:O	2.12	0.49
1:A:61:GLU:HA	1:A:72:VAL:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:353:ILE:CD1	1:A:408:LEU:HD21	2.40	0.49
1:A:437:TRP:O	1:A:439:GLU:HG3	2.13	0.49
1:B:394:GLN:HG3	1:B:434:GLN:HG3	1.96	0.48
1:B:618:THR:N	1:B:619:PRO:HD2	2.29	0.48
1:A:178:MET:HG2	1:A:191:SER:HB3	1.94	0.48
1:B:507:GLY:HA3	1:B:515:PHE:CE1	2.49	0.48
1:B:244:PHE:CD1	1:B:244:PHE:N	2.81	0.48
1:B:325:TRP:HA	1:B:647:ASP:OD2	2.14	0.48
1:A:150:LYS:HB3	1:A:152:TYR:CE1	2.49	0.48
1:B:280:TRP:CE3	1:B:303:MET:HE2	2.49	0.48
1:A:244:PHE:CD1	1:A:244:PHE:N	2.82	0.47
1:B:295:ASN:ND2	1:B:298:TYR:H	2.12	0.47
1:B:534:PRO:HD2	1:B:575:ARG:O	2.14	0.47
1:A:407:ARG:HD3	4:A:1065:HOH:O	2.14	0.47
1:A:491:THR:HG22	1:A:501:TYR:O	2.14	0.47
1:A:104:SER:C	1:A:303:MET:HE1	2.35	0.47
1:B:295:ASN:C	1:B:295:ASN:HD22	2.18	0.47
1:B:100:PHE:CD1	1:B:106:GLY:HA3	2.50	0.47
1:A:546:SER:HA	1:A:683:VAL:CG1	2.44	0.47
1:A:325:TRP:CD2	1:A:590:TYR:HB3	2.50	0.47
1:B:190:LEU:HD22	1:B:196:TRP:CZ2	2.50	0.47
1:B:501:TYR:CD1	1:B:558:VAL:HG21	2.50	0.47
1:B:534:PRO:HD3	1:B:563:ILE:CD1	2.45	0.47
1:B:546:SER:HA	1:B:683:VAL:CG1	2.45	0.47
1:A:85:PHE:HD1	1:A:87:PRO:HD3	1.79	0.46
1:A:273:LYS:O	1:A:277:ILE:HG13	2.15	0.46
1:B:105:LEU:HG	1:B:303:MET:HE1	1.96	0.46
1:B:204:TYR:CZ	1:B:205:LYS:HE3	2.50	0.46
1:A:545:LYS:C	1:A:683:VAL:HG22	2.36	0.46
1:B:584:PRO:HG2	1:B:588:GLU:HB2	1.97	0.46
1:A:79:VAL:HG11	1:A:118:TYR:CE1	2.51	0.46
1:A:104:SER:HA	1:A:303:MET:CE	2.44	0.46
1:B:394:GLN:CG	1:B:434:GLN:HG3	2.46	0.46
1:A:165:TYR:HA	1:A:228:GLY:HA2	1.97	0.46
1:B:39:GLY:HA2	1:B:633:ILE:HD11	1.98	0.46
1:A:295:ASN:C	1:A:295:ASN:HD22	2.19	0.46
1:B:491:THR:HG22	1:B:501:TYR:O	2.15	0.46
1:A:380:GLN:HG3	1:A:394:GLN:NE2	2.31	0.46
1:B:372:VAL:HG21	1:B:417:LEU:HD12	1.98	0.46
1:A:98:GLU:OE1	1:A:108:LYS:HD3	2.16	0.45
1:B:575:ARG:NH1	2:D:3:AC1:O3	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:309:GLU:HB2	1:B:317:TYR:CZ	2.51	0.45
1:A:381:ASN:HD22	1:A:381:ASN:N	2.14	0.45
1:A:546:SER:CA	1:A:683:VAL:HG13	2.42	0.45
1:A:320:SER:HB3	1:A:337:TYR:HB3	1.97	0.45
1:B:165:TYR:HA	1:B:228:GLY:HA2	1.97	0.45
1:A:204:TYR:OH	1:A:205:LYS:HE3	2.17	0.45
1:A:36:GLN:HA	1:A:36:GLN:NE2	2.31	0.45
1:A:367:TYR:O	1:A:370:LYS:HB3	2.17	0.45
1:A:518:ASN:ND2	1:B:516:MET:H	2.02	0.45
1:A:537:LEU:O	1:A:540:VAL:HG22	2.17	0.45
1:B:45:ASN:HD22	1:B:45:ASN:C	2.19	0.45
1:B:150:LYS:HB3	1:B:152:TYR:CE1	2.51	0.45
1:B:339:LEU:HD21	1:B:389:TYR:CD2	2.52	0.45
1:A:31:THR:O	1:A:158:HIS:HE1	2.00	0.45
1:B:381:ASN:N	1:B:381:ASN:HD22	2.14	0.45
1:B:546:SER:CA	1:B:683:VAL:HG13	2.46	0.45
1:B:300:ASN:O	1:B:304:ILE:HG13	2.17	0.45
1:A:679:TYR:CD1	1:A:683:VAL:HB	2.52	0.45
1:B:130:ARG:HB3	1:B:260:THR:HG23	1.98	0.45
1:B:586:LYS:HE2	4:B:1078:HOH:O	2.16	0.45
1:A:51:TRP:HB2	1:A:63:TYR:HB2	1.99	0.44
1:A:327:ASP:OD1	1:A:327:ASP:N	2.50	0.44
1:B:130:ARG:HE	1:B:263:GLU:HB3	1.82	0.44
1:A:119:ARG:HD2	1:A:140:GLU:OE2	2.17	0.44
1:A:167:GLU:HB3	1:A:182:LYS:HG3	2.00	0.44
1:A:379:PRO:HG2	1:A:382:THR:CG2	2.47	0.44
1:B:105:LEU:HG	1:B:303:MET:CE	2.47	0.44
1:B:112:THR:HG23	1:B:142:LEU:HD11	2.00	0.44
1:B:325:TRP:CD2	1:B:590:TYR:HB3	2.53	0.44
1:B:353:ILE:CD1	1:B:408:LEU:HD21	2.47	0.44
1:A:14:ILE:HG23	1:A:171:ILE:HD12	2.00	0.44
1:B:162:GLN:HA	1:B:331:ASP:O	2.17	0.44
1:A:475:GLN:CA	1:A:475:GLN:HE21	2.29	0.43
1:A:540:VAL:HG21	1:A:609:TYR:CD2	2.45	0.43
1:B:482:GLN:HG3	1:B:682:TYR:CD1	2.53	0.43
1:A:130:ARG:HE	1:A:263:GLU:HB3	1.83	0.43
1:A:567:THR:HB	1:A:568:PRO:HD2	2.01	0.43
1:B:680:LYS:HA	1:B:684:ALA:CB	2.48	0.43
1:B:63:TYR:CE1	1:B:70:ALA:HB2	2.53	0.43
1:B:475:GLN:CA	1:B:475:GLN:HE21	2.31	0.43
1:B:532:VAL:HG22	1:B:577:ASN:ND2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:PRO:O	1:A:158:HIS:CD2	2.63	0.43
1:A:507:GLY:HA3	1:A:515:PHE:CE1	2.53	0.43
1:B:680:LYS:HA	1:B:684:ALA:HB2	2.01	0.43
1:A:123:ASP:HB2	1:A:136:LYS:HB3	1.99	0.43
1:B:414:TYR:HA	1:B:418:VAL:HB	2.01	0.43
1:A:306:LYS:HD3	4:A:925:HOH:O	2.17	0.43
1:A:379:PRO:O	1:A:380:GLN:C	2.57	0.43
1:B:209:ILE:HG23	1:B:210:MET:N	2.33	0.43
1:B:382:THR:HG22	1:B:388:PRO:HA	2.00	0.43
1:B:435:GLU:OE2	1:B:437:TRP:HB2	2.18	0.43
1:A:200:SER:HA	1:A:223:TYR:O	2.19	0.43
1:A:460:TYR:O	1:A:464:GLN:HG2	2.19	0.43
1:B:123:ASP:HB2	1:B:136:LYS:HB3	2.01	0.43
1:B:184:ASP:HB3	1:B:185:ASN:H	1.60	0.43
1:B:22:ALA:HA	1:B:223:TYR:CD1	2.53	0.42
1:B:252:GLN:HB2	4:B:1017:HOH:O	2.18	0.42
1:A:577:ASN:O	1:A:578:HIS:HB2	2.19	0.42
1:B:381:ASN:ND2	1:B:389:TYR:HB3	2.33	0.42
1:A:113:ASP:HB2	1:A:118:TYR:CD1	2.55	0.42
1:A:372:VAL:HG21	1:A:417:LEU:HD12	2.00	0.42
1:A:565:VAL:HB	1:A:598:LEU:HD21	2.00	0.42
1:A:179:LEU:N	1:A:179:LEU:HD12	2.35	0.42
1:A:449:ALA:HB2	1:A:539:LEU:HD23	2.02	0.42
1:B:79:VAL:CG1	1:B:87:PRO:HG2	2.45	0.42
1:B:302:MET:HE1	1:B:352:PHE:HA	2.01	0.42
1:A:381:ASN:ND2	1:A:389:TYR:HB3	2.34	0.42
1:B:545:LYS:C	1:B:683:VAL:HG22	2.39	0.42
1:A:363:ARG:NH2	4:A:842:HOH:O	2.43	0.42
1:B:51:TRP:CZ2	1:B:311:LYS:HG3	2.54	0.42
1:B:178:MET:HG2	1:B:191:SER:HB3	2.01	0.42
1:B:324:PRO:HB2	1:B:325:TRP:CE3	2.55	0.42
1:B:679:TYR:CD1	1:B:683:VAL:HB	2.55	0.42
1:B:345:LEU:C	1:B:345:LEU:HD23	2.40	0.42
1:A:445:PRO:HG2	4:A:825:HOH:O	2.19	0.42
1:A:459:ALA:CB	1:A:475:GLN:HG2	2.50	0.42
1:B:79:VAL:HG11	1:B:118:TYR:CE1	2.54	0.42
1:A:138:LYS:HB3	1:A:243:GLU:HG3	2.02	0.42
1:A:574:TYR:OH	1:A:640:GLU:HG2	2.20	0.41
1:B:113:ASP:HB2	1:B:118:TYR:CD1	2.55	0.41
1:B:560:ASP:CG	1:B:606:ARG:HH12	2.24	0.41
1:A:325:TRP:HA	1:A:647:ASP:OD2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:435:GLU:OE2	1:A:437:TRP:HB2	2.20	0.41
1:A:618:THR:N	1:A:619:PRO:HD2	2.35	0.41
1:A:636:GLU:HG2	1:A:637:GLN:HG3	2.02	0.41
1:B:45:ASN:ND2	1:B:45:ASN:C	2.73	0.41
1:B:113:ASP:HB2	1:B:118:TYR:CZ	2.54	0.41
1:B:96:LYS:HA	1:B:630:GLU:OE2	2.20	0.41
1:A:438:GLU:OE1	2:C:3:AC1:N4A	2.53	0.41
1:B:79:VAL:HG11	1:B:118:TYR:CZ	2.56	0.41
1:A:79:VAL:HG11	1:A:118:TYR:CZ	2.55	0.41
1:A:379:PRO:HA	4:A:869:HOH:O	2.21	0.41
1:B:201:ILE:HG22	1:B:226:ALA:HB3	2.03	0.41
1:B:676:ASP:HB2	1:B:680:LYS:HE2	2.02	0.41
1:A:184:ASP:HB3	1:A:185:ASN:H	1.53	0.41
1:A:212:ASP:OD2	1:A:220:THR:HB	2.21	0.41
1:A:294:ALA:HB1	1:A:298:TYR:CD2	2.55	0.41
1:B:61:GLU:HA	1:B:72:VAL:O	2.20	0.41
1:B:122:LYS:HA	1:B:136:LYS:O	2.20	0.41
1:B:179:LEU:N	1:B:179:LEU:HD12	2.36	0.41
1:B:636:GLU:HG2	1:B:637:GLN:HG3	2.02	0.41
1:A:324:PRO:HB2	1:A:325:TRP:CE3	2.55	0.41
1:B:80:THR:HG22	1:B:152:TYR:HE1	1.85	0.41
1:B:534:PRO:HD3	1:B:563:ILE:HD12	2.03	0.41
1:B:564:LYS:HB2	1:B:573:TRP:NE1	2.36	0.41
1:A:161:ASN:O	1:A:333:ASN:HA	2.21	0.40
1:A:204:TYR:CD1	1:A:231:ILE:HD11	2.55	0.40
1:A:598:LEU:O	1:A:637:GLN:HA	2.20	0.40
1:A:608:MET:HE3	1:A:671:VAL:HG13	2.03	0.40
1:A:381:ASN:HD21	1:A:390:TRP:N	2.13	0.40
1:B:36:GLN:HA	1:B:36:GLN:HE21	1.86	0.40
1:B:334:THR:HG22	1:B:336:GLY:N	2.20	0.40
1:B:531:ILE:HA	1:B:577:ASN:OD1	2.22	0.40
1:A:188:THR:HA	1:A:249:SER:O	2.22	0.40
1:B:610:GLU:HG3	1:B:620:TYR:CE2	2.57	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	672/684 (98%)	635 (94%)	34 (5%)	3 (0%)	34	37
1	B	672/684 (98%)	637 (95%)	34 (5%)	1 (0%)	51	60
All	All	1344/1368 (98%)	1272 (95%)	68 (5%)	4 (0%)	41	46

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	331	ASP
1	A	509	SER
1	B	509	SER
1	A	75	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	566/575 (98%)	551 (97%)	15 (3%)	44	57
1	B	566/575 (98%)	550 (97%)	16 (3%)	43	56
All	All	1132/1150 (98%)	1101 (97%)	31 (3%)	44	57

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	GLN
1	A	45	ASN

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Mol	Chain	Res	Type
1	A	182	LYS
1	A	183	ARG
1	A	190	LEU
1	A	267	GLU
1	A	286	THR
1	A	295	ASN
1	A	339	LEU
1	A	377	MET
1	A	381	ASN
1	A	435	GLU
1	A	475	GLN
1	A	577	ASN
1	A	598	LEU
1	B	45	ASN
1	B	182	LYS
1	B	183	ARG
1	B	190	LEU
1	B	267	GLU
1	B	286	THR
1	B	295	ASN
1	B	339	LEU
1	B	344	ASP
1	B	377	MET
1	B	381	ASN
1	B	435	GLU
1	B	475	GLN
1	B	508	LEU
1	B	577	ASN
1	B	598	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	ASN
1	A	45	ASN
1	A	56	ASN
1	A	158	HIS
1	A	218	GLN
1	A	275	ASN
1	A	295	ASN
1	A	300	ASN
1	A	381	ASN

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Mol	Chain	Res	Type
1	A	464	GLN
1	A	493	ASN
1	A	518	ASN
1	A	554	ASN
1	A	666	ASN
1	B	19	ASN
1	B	45	ASN
1	B	56	ASN
1	B	158	HIS
1	B	218	GLN
1	B	275	ASN
1	B	295	ASN
1	B	381	ASN
1	B	464	GLN
1	B	493	ASN
1	B	518	ASN
1	B	554	ASN
1	B	666	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)

6 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	C	1	2	12,12,12	1.55	3 (25%)	17,17,17	0.56	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	GLC	C	2	2	11,11,12	1.81	5 (45%)	15,15,17	1.30	2 (13%)
2	AC1	C	3	2	21,22,23	2.82	8 (38%)	22,32,34	1.03	2 (9%)
2	GLC	D	1	2	12,12,12	1.50	2 (16%)	17,17,17	0.58	0
2	GLC	D	2	2	11,11,12	1.58	4 (36%)	15,15,17	1.29	2 (13%)
2	AC1	D	3	2	21,22,23	2.96	10 (47%)	22,32,34	0.95	1 (4%)

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	C	1	2	-	0/2/22/22	0/1/1/1
2	GLC	C	2	2	-	0/2/19/22	0/1/1/1
2	AC1	C	3	2	-	4/6/43/46	0/2/2/2
2	GLC	D	1	2	-	0/2/22/22	0/1/1/1
2	GLC	D	2	2	-	0/2/19/22	0/1/1/1
2	AC1	D	3	2	-	3/6/43/46	0/2/2/2

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	3	AC1	C4A-C5B	7.13	1.57	1.51
2	D	3	AC1	C4A-C5B	7.03	1.57	1.51
2	D	3	AC1	C7B-C5B	6.39	1.41	1.32
2	C	3	AC1	C7B-C5B	5.89	1.41	1.32
2	D	3	AC1	C3B-C4A	5.45	1.61	1.53
2	C	3	AC1	C3B-C4A	5.35	1.60	1.53
2	D	3	AC1	C2B-C1B	3.74	1.57	1.52
2	D	3	AC1	O5-C5	3.58	1.51	1.43
2	C	3	AC1	O5-C5	3.17	1.50	1.43
2	C	3	AC1	C1B-C7B	3.14	1.54	1.50
2	C	2	GLC	C2-C3	3.00	1.56	1.52
2	D	3	AC1	C1B-C7B	2.99	1.54	1.50
2	D	1	GLC	O5-C1	2.95	1.50	1.42
2	C	3	AC1	C2B-C1B	2.84	1.56	1.52
2	D	3	AC1	C4-N4A	2.79	1.52	1.47
2	C	1	GLC	O5-C1	2.77	1.49	1.42
2	D	1	GLC	O5-C5	2.73	1.51	1.44
2	C	2	GLC	O5-C5	2.68	1.48	1.43
2	D	3	AC1	C2-C3	2.65	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	3	AC1	C2-C3	2.63	1.56	1.52
2	C	2	GLC	C4-C3	2.52	1.58	1.52
2	C	1	GLC	O5-C5	2.50	1.50	1.44
2	D	2	GLC	C4-C3	2.50	1.58	1.52
2	D	2	GLC	C2-C3	2.43	1.56	1.52
2	D	2	GLC	O5-C5	2.37	1.48	1.43
2	C	3	AC1	O5-C1	2.20	1.47	1.43
2	C	1	GLC	O4-C4	2.19	1.48	1.43
2	D	2	GLC	C1-C2	2.17	1.57	1.52
2	C	2	GLC	C1-C2	2.15	1.57	1.52
2	D	3	AC1	C1B-N4A	2.14	1.51	1.47
2	C	2	GLC	O4-C4	2.03	1.47	1.43
2	D	3	AC1	O5-C1	2.01	1.46	1.43

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	3	AC1	C2-C3-C4	-2.55	108.38	110.63
2	D	3	AC1	O4-C4A-C3B	-2.25	105.88	110.53
2	C	2	GLC	C1-O5-C5	2.22	115.20	112.19
2	C	3	AC1	O4-C4A-C3B	-2.17	106.05	110.53
2	D	2	GLC	C1-O5-C5	2.09	115.03	112.19
2	C	2	GLC	C1-C2-C3	-2.03	107.17	109.67
2	D	2	GLC	C1-C2-C3	-2.03	107.17	109.67

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	3	AC1	C5-C4-N4A-C1B
2	C	3	AC1	C4A-C5B-C6B-O6B
2	C	3	AC1	C7B-C5B-C6B-O6B
2	D	3	AC1	C5-C4-N4A-C1B
2	D	3	AC1	C4A-C5B-C6B-O6B
2	C	3	AC1	C3-C4-N4A-C1B
2	D	3	AC1	C7B-C5B-C6B-O6B

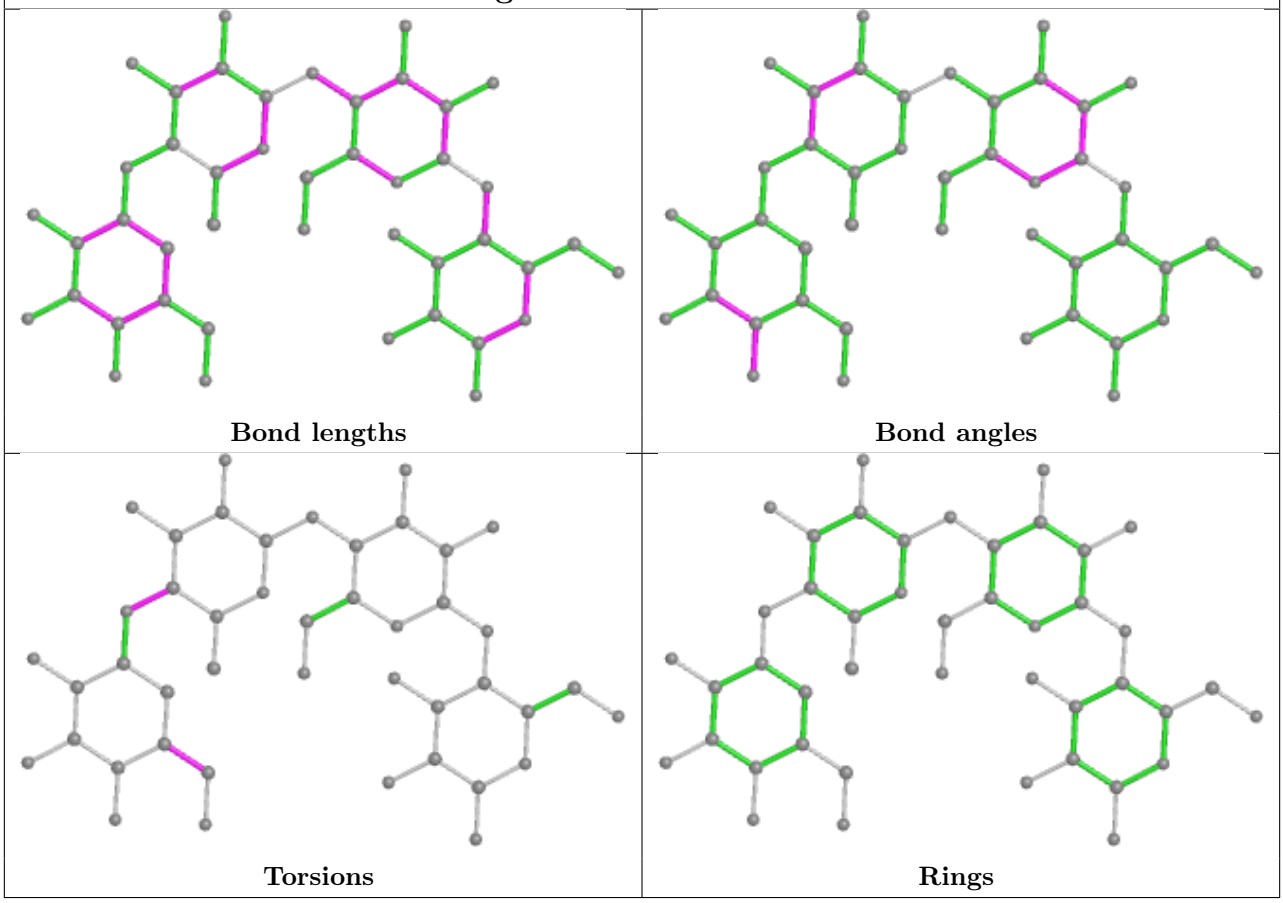
There are no ring outliers.

2 monomers are involved in 2 short contacts:

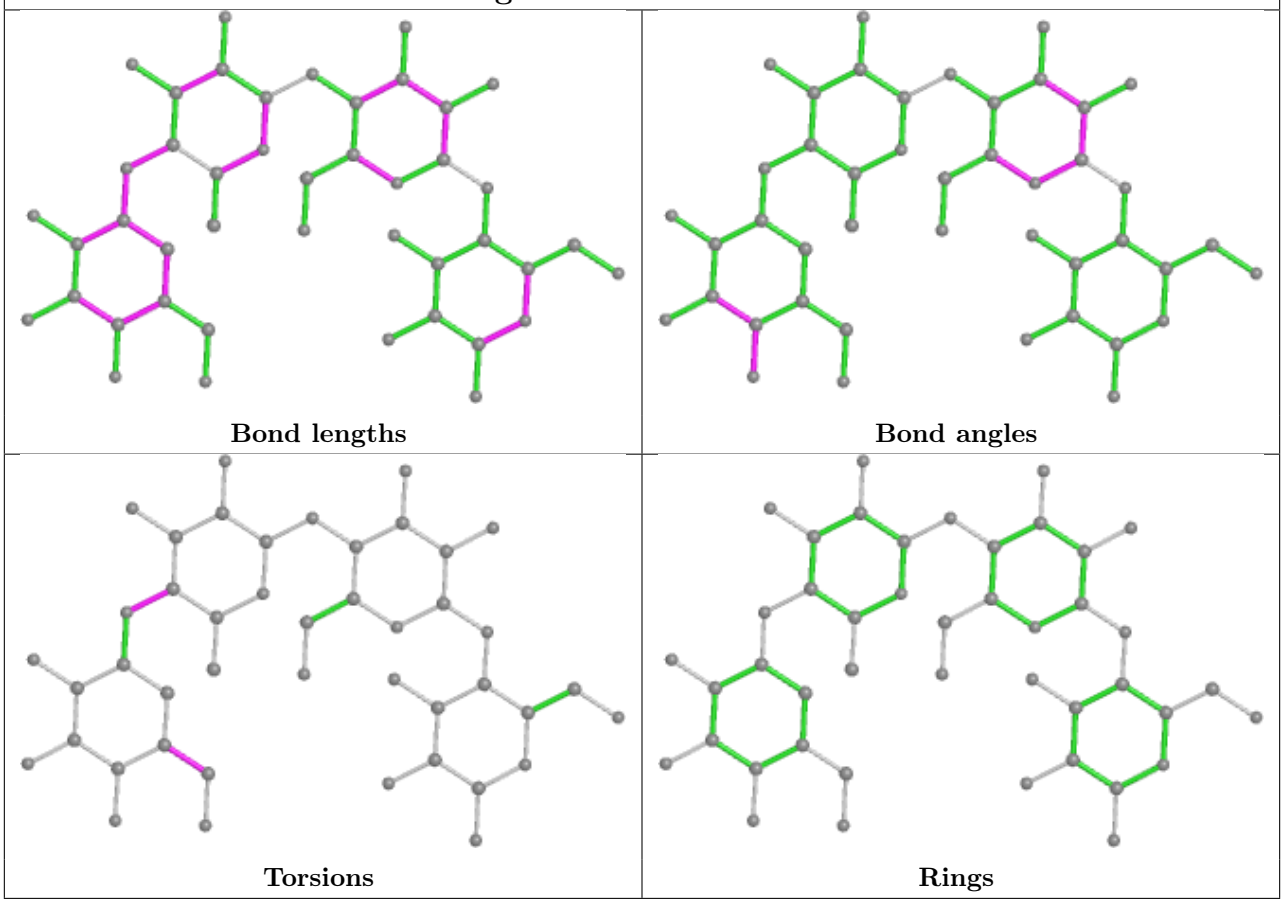
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	3	AC1	1	0
2	C	3	AC1	1	0

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 C



Oligosaccharide Chain D



5.6 Ligand geometry (i)

2 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	$\#\|Z\| > 2$
3	SO4	B	800	-	4,4,4	0.29	0	6,6,6	0.13	0
3	SO4	A	801	-	4,4,4	0.25	0	6,6,6	0.09	0

There are no bond length outliers.

There are no bond angle outliers.

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	674/684 (98%)	0.06	37 (5%)	25	24	19, 37, 59, 80	0
1	B	674/684 (98%)	-0.18	14 (2%)	63	61	17, 31, 51, 71	0
All	All	1348/1368 (98%)	-0.06	51 (3%)	40	38	17, 34, 56, 80	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	12	ILE	6.5
1	A	11	SER	6.0
1	A	84	SER	4.6
1	A	252	GLN	4.2
1	A	142	LEU	4.0
1	A	85	PHE	3.8
1	A	17	PHE	3.6
1	A	175	ASN	3.6
1	A	18	ASN	3.5
1	B	252	GLN	3.4
1	B	683	VAL	3.2
1	A	72	VAL	3.1
1	A	14	ILE	3.1
1	A	266	GLY	3.0
1	A	154	ALA	3.0
1	A	333	ASN	2.9
1	A	472	GLN	2.9
1	A	468	TYR	2.9
1	A	82	GLY	2.8
1	B	11	SER	2.8
1	B	147	HIS	2.8
1	A	75	ILE	2.5
1	A	239	THR	2.4
1	A	387	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	173	ALA	2.4
1	A	62	VAL	2.4
1	B	75	ILE	2.4
1	A	87	PRO	2.4
1	B	601	LEU	2.3
1	A	466	LYS	2.3
1	A	83	LYS	2.3
1	A	153	LEU	2.3
1	B	16	ARG	2.3
1	A	190	LEU	2.3
1	B	87	PRO	2.3
1	A	601	LEU	2.2
1	A	148	ASP	2.2
1	A	16	ARG	2.2
1	B	387	LYS	2.2
1	B	145	SER	2.2
1	B	652	LEU	2.2
1	A	271	ASN	2.1
1	A	462	ALA	2.1
1	B	472	GLN	2.1
1	A	59	ILE	2.1
1	A	588	GLU	2.1
1	B	175	ASN	2.1
1	A	155	TYR	2.0
1	A	652	LEU	2.0
1	B	587	THR	2.0
1	A	542	LEU	2.0

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
2	GLC	D	1	12/12	0.77	0.24	46,58,60,62	0

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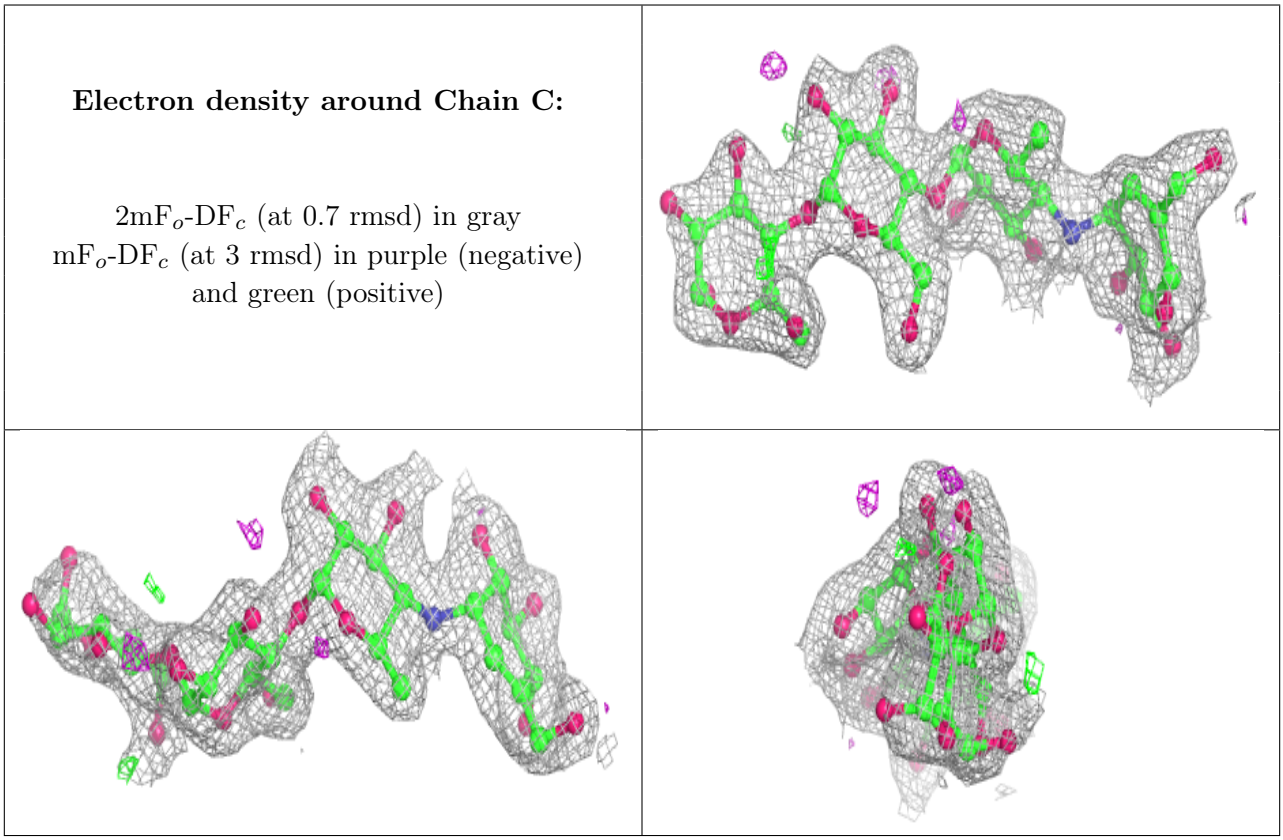
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	GLC	C	1	12/12	0.83	0.26	48,57,60,61	0
2	GLC	D	2	11/12	0.92	0.10	25,31,37,38	0
2	GLC	C	2	11/12	0.93	0.09	30,34,42,42	0
2	AC1	C	3	21/22	0.94	0.14	24,25,27,29	0
2	AC1	D	3	21/22	0.95	0.17	18,23,27,29	0

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.

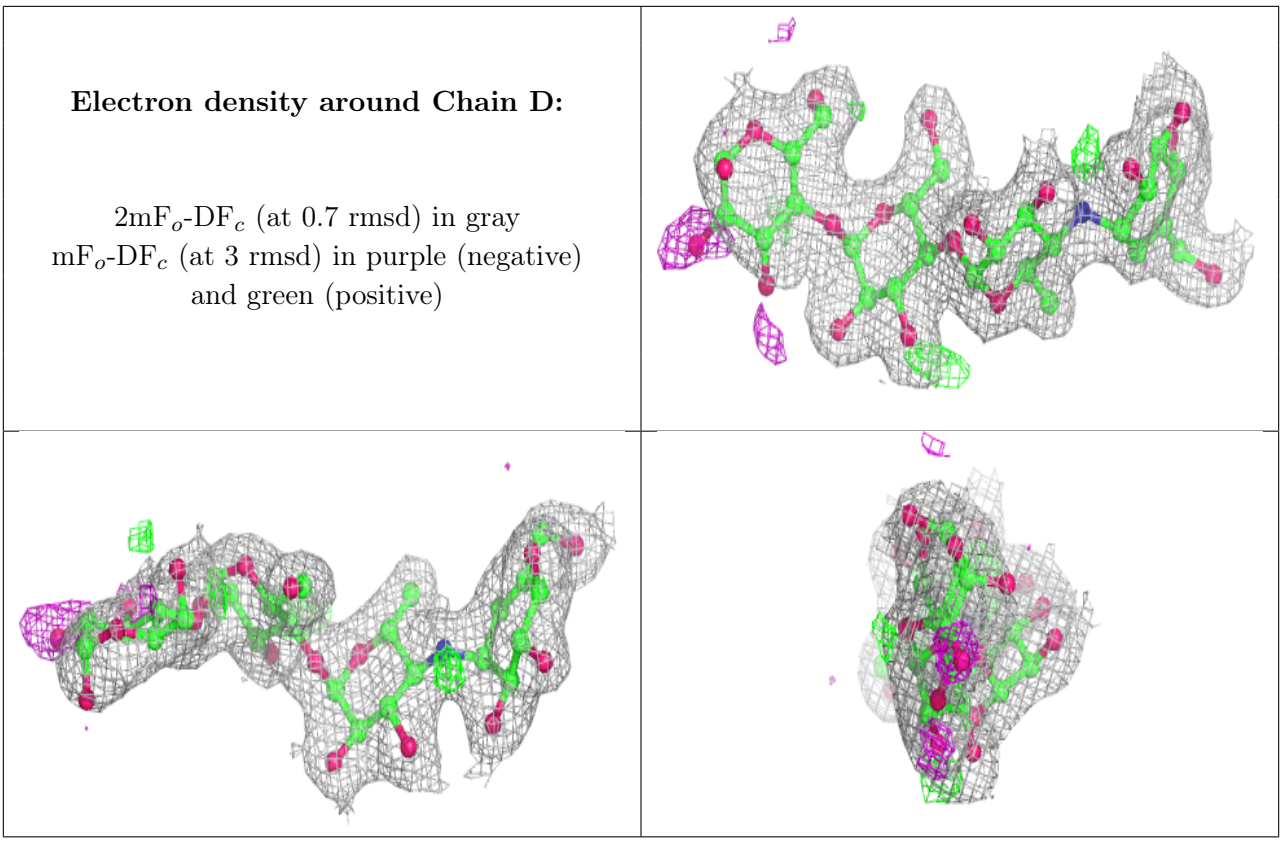
Electron density around Chain C:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)



Electron density around Chain D:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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
3	SO4	A	801	5/5	0.94	0.19	66,67,68,69	0
3	SO4	B	800	5/5	0.94	0.22	64,64,64,64	0

6.5 Other polymers (i)

There are no such residues in this entry.