Full wwPDB X-ray Structure Validation Report (i)

Feb 21, 2017 – 04:51 PM EST

PDB ID	:	5H41
Title	:	Crystal Structure of 1,2-beta-oligoglucan phosphorylase from Lachnoclostridium phytofermentans in complex with sophorose, isofagomine, sulfate ion
Authors	:	Nakajima, M.; Tanaka, N.; Furukawa, N.; Nihira, T.; Kodutsumi, Y.; Takahashi, Y.; Sugimoto, N.; Miyanaga, A.; Fushinobu, S.; Taguchi, H.; Nakai, H.
Deposited on	:	2016-10-28
Resolution	:	2.00 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

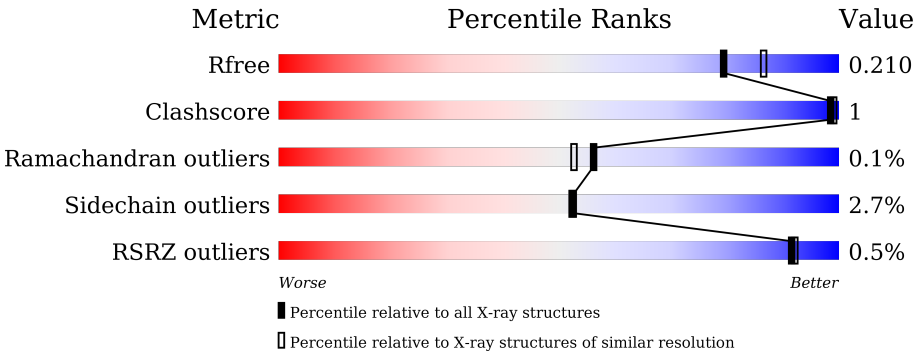
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20028442

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 2.00 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}	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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. 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	1122	% 93% 5%
1	B	1122	93% 6%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 18781 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.

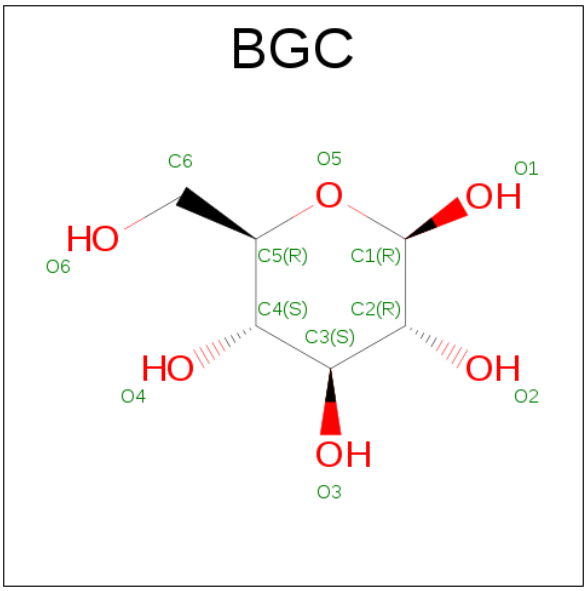
- Molecule 1 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1113	Total	C	N	O	S	0	1	0
			8928	5718	1486	1692	32			
1	B	1113	Total	C	N	O	S	0	1	0
			8928	5718	1486	1692	32			

There are 20 discrepancies between the modelled and reference sequences:

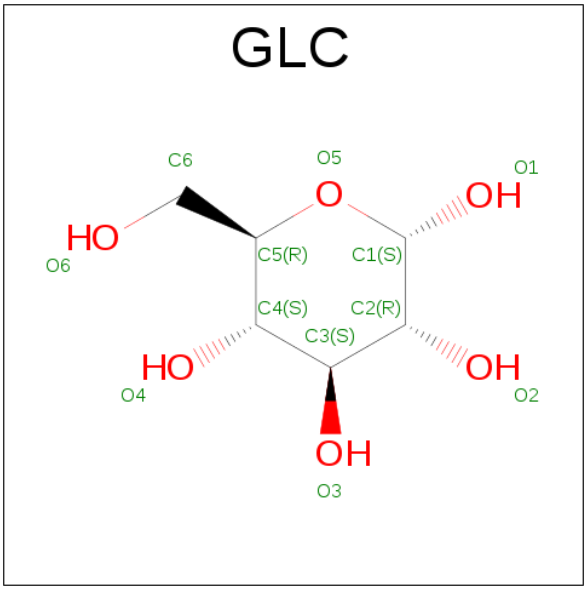
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP A9KJS6
A	1	GLY	-	expression tag	UNP A9KJS6
A	1114	LEU	-	expression tag	UNP A9KJS6
A	1115	GLU	-	expression tag	UNP A9KJS6
A	1116	HIS	-	expression tag	UNP A9KJS6
A	1117	HIS	-	expression tag	UNP A9KJS6
A	1118	HIS	-	expression tag	UNP A9KJS6
A	1119	HIS	-	expression tag	UNP A9KJS6
A	1120	HIS	-	expression tag	UNP A9KJS6
A	1121	HIS	-	expression tag	UNP A9KJS6
B	0	MET	-	expression tag	UNP A9KJS6
B	1	GLY	-	expression tag	UNP A9KJS6
B	1114	LEU	-	expression tag	UNP A9KJS6
B	1115	GLU	-	expression tag	UNP A9KJS6
B	1116	HIS	-	expression tag	UNP A9KJS6
B	1117	HIS	-	expression tag	UNP A9KJS6
B	1118	HIS	-	expression tag	UNP A9KJS6
B	1119	HIS	-	expression tag	UNP A9KJS6
B	1120	HIS	-	expression tag	UNP A9KJS6
B	1121	HIS	-	expression tag	UNP A9KJS6

- Molecule 2 is BETA-D-GLUCOSE (three-letter code: BGC) (formula: $C_6H_{12}O_6$).



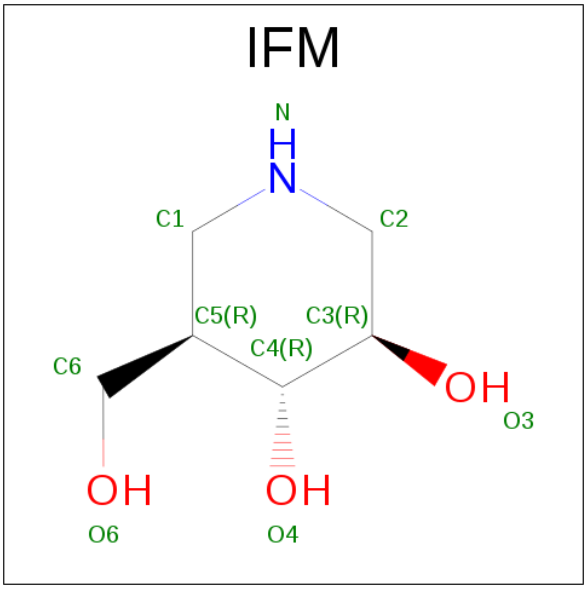
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 11 6 5	0	0
2	B	1	Total C O 11 6 5	0	0

- Molecule 3 is ALPHA-D-GLUCOSE (three-letter code: GLC) (formula: $C_6H_{12}O_6$).



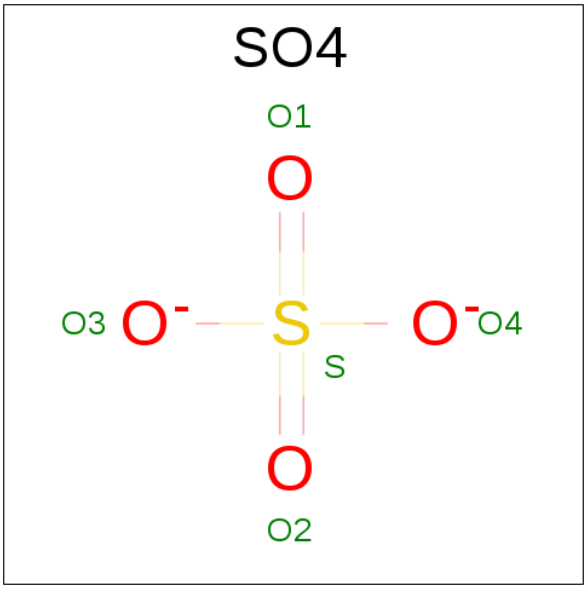
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 12 6 6	0	0
3	B	1	Total C O 12 6 6	0	0

- Molecule 4 is 5-HYDROXYMETHYL-3,4-DIHYDROXYPIPERIDINE (three-letter code: IFM) (formula: $C_6H_{13}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			10	6	1	3		
4	B	1	Total	C	N	O	0	0
			10	6	1	3		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 6 is water.

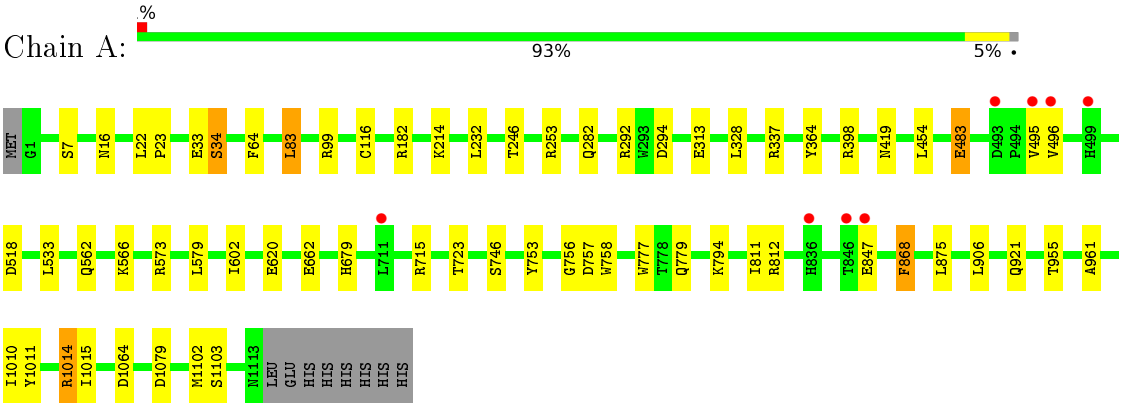
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	383	Total O 383 383	0	0
6	B	456	Total O 456 456	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

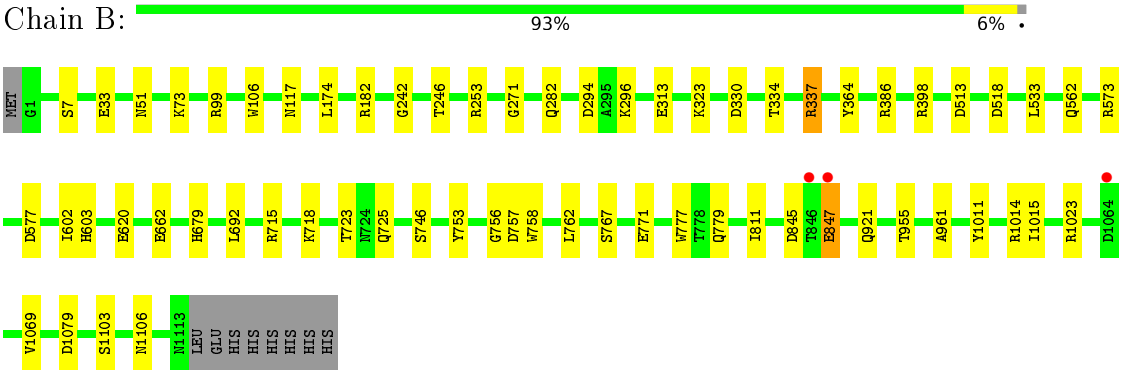
- Molecule 1: Uncharacterized protein

Chain A:



- Molecule 1: Uncharacterized protein

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	86.69Å 94.88Å 157.36Å 90.00° 100.81° 90.00°	Depositor
Resolution (Å)	48.27 – 2.00 47.44 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.27-2.00) 99.7 (47.44-2.00)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.79 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.168 , 0.204 0.176 , 0.210	Depositor DCC
R_{free} test set	8340 reflections (5.21%)	DCC
Wilson B-factor (Å^2)	24.5	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 50.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	18781	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GLC, IFM, BGC, 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	0.84	0/9154	0.88	16/12435 (0.1%)
1	B	0.86	1/9154 (0.0%)	0.88	11/12435 (0.1%)
All	All	0.85	1/18308 (0.0%)	0.88	27/24870 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	73	LYS	N-CA	6.25	1.58	1.46

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	182	ARG	NE-CZ-NH1	8.10	124.35	120.30
1	A	182	ARG	NE-CZ-NH1	7.48	124.04	120.30
1	B	182	ARG	NE-CZ-NH2	-7.39	116.60	120.30
1	B	398	ARG	NE-CZ-NH2	-6.87	116.86	120.30
1	B	294	ASP	CB-CG-OD1	6.50	124.15	118.30
1	A	294	ASP	CB-CG-OD1	6.46	124.11	118.30
1	B	757	ASP	CB-CG-OD2	-6.43	112.51	118.30
1	A	83	LEU	CA-CB-CG	6.40	130.01	115.30
1	B	253	ARG	NE-CZ-NH1	6.39	123.49	120.30
1	A	398	ARG	NE-CZ-NH2	-6.36	117.12	120.30
1	A	182	ARG	NE-CZ-NH2	-6.35	117.12	120.30
1	A	715	ARG	NE-CZ-NH1	6.22	123.41	120.30
1	A	292	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	B	1023	ARG	NE-CZ-NH1	5.78	123.19	120.30
1	B	99	ARG	NE-CZ-NH1	5.67	123.14	120.30
1	A	715	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	A	757	ASP	CB-CG-OD2	-5.40	113.44	118.30
1	B	715	ARG	NE-CZ-NH1	5.32	122.96	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	99	ARG	NE-CZ-NH1	5.31	122.96	120.30
1	B	386	ARG	NE-CZ-NH2	-5.29	117.66	120.30
1	A	812	ARG	NE-CZ-NH2	5.26	122.93	120.30
1	A	253	ARG	NE-CZ-NH1	5.23	122.92	120.30
1	A	1102	MET	CG-SD-CE	5.17	108.48	100.20
1	A	868	PHE	CB-CG-CD1	5.14	124.40	120.80
1	A	573	ARG	NE-CZ-NH1	5.11	122.85	120.30
1	B	337	ARG	NE-CZ-NH2	-5.05	117.77	120.30
1	A	757	ASP	CB-CG-OD1	5.02	122.82	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	8928	0	8681	14	0
1	B	8928	0	8681	16	0
2	A	11	0	10	1	0
2	B	11	0	10	0	0
3	A	12	0	11	0	0
3	B	12	0	10	0	0
4	A	10	0	13	1	0
4	B	10	0	13	0	0
5	A	10	0	0	0	0
5	B	10	0	0	0	0
6	A	383	0	0	0	0
6	B	456	0	0	0	0
All	All	18781	0	17429	31	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 1.

All (31) 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:483:GLU:HG2	1:A:483:GLU:O	1.97	0.65
1:B:518:ASP:HA	1:B:533:LEU:O	2.06	0.56
1:A:518:ASP:HA	1:A:533:LEU:O	2.08	0.53
1:B:753:TYR:CZ	1:B:756:GLY:HA2	2.44	0.53
1:B:662:GLU:OE2	1:B:725:GLN:NE2	2.43	0.52
1:B:33:GLU:HB2	1:B:246:THR:HG21	1.93	0.51
1:B:845:ASP:OD1	1:B:847:GLU:OE1	2.30	0.50
1:A:753:TYR:CZ	1:A:756:GLY:HA2	2.47	0.49
1:A:33:GLU:HB2	1:A:246:THR:HG21	1.94	0.49
1:A:662:GLU:HB2	1:A:723:THR:HG21	1.95	0.48
1:A:779:GLN:NE2	1:A:811:ILE:HG23	2.29	0.47
1:B:662:GLU:HB2	1:B:723:THR:HG21	1.97	0.47
1:A:955:THR:HG22	1:A:961:ALA:O	2.16	0.46
1:A:33:GLU:O	1:A:34:SER:CB	2.63	0.46
1:B:779:GLN:NE2	1:B:811:ILE:HG23	2.30	0.46
1:A:758:TRP:HB2	1:A:777:TRP:CH2	2.51	0.46
1:B:767:SER:O	1:B:771:GLU:HG3	2.15	0.45
1:B:758:TRP:HB2	1:B:777:TRP:CH2	2.52	0.45
1:B:955:THR:HG22	1:B:961:ALA:O	2.17	0.45
1:A:16:ASN:HB3	1:A:33:GLU:HG2	1.99	0.44
1:B:323:LYS:HB3	1:B:603[B]:HIS:CE1	2.53	0.44
1:B:573:ARG:NH2	1:B:577:ASP:OD2	2.50	0.43
1:B:330:ASP:O	1:B:334:THR:HG23	2.19	0.43
1:B:337:ARG:HD3	1:B:620:GLU:OE2	2.18	0.43
1:A:1011:TYR:CE2	1:A:1015:ILE:HD11	2.55	0.42
1:A:337:ARG:HD3	1:A:620:GLU:OE2	2.19	0.42
1:B:106:TRP:CZ2	1:B:242:GLY:HA3	2.55	0.41
2:A:1201:BGC:O2	4:A:1203:IFM:H1C2	2.21	0.41
1:A:22:LEU:HB3	1:A:23:PRO:HD2	2.02	0.41
1:B:1011:TYR:CE2	1:B:1015:ILE:HD11	2.56	0.40
1:A:1010:ILE:O	1:A:1014:ARG:HD2	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	1112/1122 (99%)	1063 (96%)	47 (4%)	2 (0%)	52	48
1	B	1112/1122 (99%)	1068 (96%)	43 (4%)	1 (0%)	56	53
All	All	2224/2244 (99%)	2131 (96%)	90 (4%)	3 (0%)	56	53

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	496	VAL
1	B	271	GLY
1	A	906	LEU

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	976/984 (99%)	946 (97%)	30 (3%)	47	46
1	B	976/984 (99%)	953 (98%)	23 (2%)	57	58
All	All	1952/1968 (99%)	1899 (97%)	53 (3%)	52	52

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	SER
1	A	34	SER
1	A	64	PHE
1	A	83	LEU
1	A	116	CYS
1	A	214	LYS
1	A	232	LEU
1	A	282	GLN
1	A	313	GLU
1	A	328	LEU

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Mol	Chain	Res	Type
1	A	364	TYR
1	A	419	ASN
1	A	454	LEU
1	A	483	GLU
1	A	495	VAL
1	A	562	GLN
1	A	566	LYS
1	A	579	LEU
1	A	602	ILE
1	A	679	HIS
1	A	746	SER
1	A	794	LYS
1	A	847	GLU
1	A	868	PHE
1	A	875	LEU
1	A	921	GLN
1	A	1014	ARG
1	A	1064	ASP
1	A	1079	ASP
1	A	1103	SER
1	B	7	SER
1	B	51	ASN
1	B	117	ASN
1	B	174	LEU
1	B	282	GLN
1	B	296	LYS
1	B	313	GLU
1	B	364	TYR
1	B	513	ASP
1	B	562	GLN
1	B	602	ILE
1	B	679	HIS
1	B	692	LEU
1	B	718	LYS
1	B	746	SER
1	B	762	LEU
1	B	847	GLU
1	B	921	GLN
1	B	1014	ARG
1	B	1069	VAL
1	B	1079	ASP
1	B	1103	SER

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Mol	Chain	Res	Type
1	B	1106	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	283	ASN

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

There are no carbohydrates in this entry.

5.6 Ligand geometry

10 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	$\#\|Z\|>2$
2	BGC	A	1201	3	11,11,12	1.19	2 (18%)	15,15,17	0.88	0
3	GLC	A	1202	2	12,12,12	2.37	4 (33%)	17,17,17	1.91	5 (29%)
4	IFM	A	1203	-	9,10,10	1.58	1 (11%)	9,13,13	1.24	1 (11%)
5	SO4	A	1204	-	4,4,4	1.50	1 (25%)	6,6,6	0.66	0
5	SO4	A	1205	-	4,4,4	1.05	0	6,6,6	0.26	0
2	BGC	B	1201	3	11,11,12	0.90	0	15,15,17	1.13	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	GLC	B	1202	2	12,12,12	2.04	3 (25%)	17,17,17	1.91	2 (11%)
4	IFM	B	1203	-	9,10,10	1.79	1 (11%)	9,13,13	1.62	2 (22%)
5	SO4	B	1204	-	4,4,4	1.44	0	6,6,6	0.42	0
5	SO4	B	1205	-	4,4,4	0.71	0	6,6,6	0.62	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BGC	A	1201	3	-	0/2/19/22	0/1/1/1
3	GLC	A	1202	2	-	0/2/22/22	0/1/1/1
4	IFM	A	1203	-	-	0/2/16/16	0/1/1/1
5	SO4	A	1204	-	-	0/0/0/0	0/0/0/0
5	SO4	A	1205	-	-	0/0/0/0	0/0/0/0
2	BGC	B	1201	3	-	0/2/19/22	0/1/1/1
3	GLC	B	1202	2	-	0/2/22/22	0/1/1/1
4	IFM	B	1203	-	-	0/2/16/16	0/1/1/1
5	SO4	B	1204	-	-	0/0/0/0	0/0/0/0
5	SO4	B	1205	-	-	0/0/0/0	0/0/0/0

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1202	GLC	O5-C1	-2.58	1.38	1.43
3	A	1202	GLC	O4-C4	-2.30	1.37	1.43
2	A	1201	BGC	O2-C2	-2.11	1.38	1.43
5	A	1204	SO4	O4-S	2.23	1.55	1.47
2	A	1201	BGC	C4-C5	2.37	1.58	1.53
3	A	1202	GLC	O5-C5	3.10	1.52	1.44
3	A	1202	GLC	O1-C1	3.17	1.50	1.39
3	B	1202	GLC	O3-C3	3.27	1.50	1.43
4	A	1203	IFM	C5-C4	3.71	1.57	1.53
4	B	1203	IFM	C5-C4	4.59	1.59	1.53
3	B	1202	GLC	O2-C2	4.82	1.54	1.43
3	A	1202	GLC	O2-C2	5.42	1.55	1.43

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1202	GLC	C1-O5-C5	-2.95	107.91	113.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1201	BGC	C1-O5-C5	-2.58	108.34	112.14
4	A	1203	IFM	O3-C3-C2	-2.53	104.70	109.60
4	B	1203	IFM	O3-C3-C2	-2.05	105.62	109.60
3	A	1202	GLC	O1-C1-O5	2.43	117.09	110.33
3	A	1202	GLC	O2-C2-C1	2.94	116.18	109.74
3	A	1202	GLC	O3-C3-C4	2.95	117.01	110.36
4	B	1203	IFM	C1-N-C2	3.32	115.44	111.88
3	B	1202	GLC	O2-C2-C3	4.76	121.09	110.36
3	A	1202	GLC	C1-C2-C3	4.81	118.57	110.68
3	B	1202	GLC	C1-C2-C3	5.44	119.60	110.68

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1201	BGC	1	0
4	A	1203	IFM	1	0

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

6.1 Protein, DNA and RNA chains

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, 95^{th} 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	1113/1122 (99%)	-0.40	8 (0%) 89 89	16, 26, 47, 77	0
1	B	1113/1122 (99%)	-0.48	3 (0%) 94 94	15, 24, 43, 72	0
All	All	2226/2244 (99%)	-0.44	11 (0%) 91 92	15, 25, 45, 77	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	495	VAL	6.5
1	A	846	THR	3.7
1	A	847	GLU	3.1
1	A	496	VAL	3.0
1	B	847	GLU	3.0
1	A	493	ASP	2.8
1	A	499	HIS	2.6
1	B	846	THR	2.5
1	B	1064	ASP	2.4
1	A	836	HIS	2.3
1	A	711	LEU	2.1

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
4	IFM	B	1203	10/10	0.96	0.11	0.65	20,23,24,25	0
3	GLC	A	1202	12/12	0.94	0.11	0.40	23,26,29,33	0
2	BGC	B	1201	11/12	0.97	0.11	0.27	25,25,26,27	0
3	GLC	B	1202	12/12	0.97	0.11	0.27	24,26,28,30	0
2	BGC	A	1201	11/12	0.96	0.11	-0.24	24,26,28,28	0
4	IFM	A	1203	10/10	0.97	0.09	-0.27	20,22,23,23	0
5	SO4	A	1204	5/5	0.99	0.07	-2.10	22,22,24,26	0
5	SO4	B	1204	5/5	0.99	0.05	-3.41	22,22,24,27	0
5	SO4	A	1205	5/5	0.99	0.06	-	27,27,30,31	0
5	SO4	B	1205	5/5	0.99	0.08	-	27,30,31,33	0

6.5 Other polymers

There are no such residues in this entry.