Full wwPDB X-ray Structure Validation Report (i)

Oct 30, 2023 – 09:02 PM JST

PDB ID	:	4ZOD
Title	:	Crystal Structure of beta-glucosidase from Listeria innocua in complex with glucose
Authors	:	Nakajima, M.; Yoshida, R.; Miyanaga, A.; Abe, K.; Takahashi, Y.; Sugimoto, N.; Toyoizumi, H.; Nakai, H.; Kitaoka, M.; Taguchi, H.
Deposited on	:	2015-05-06
Resolution	:	2.10 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:

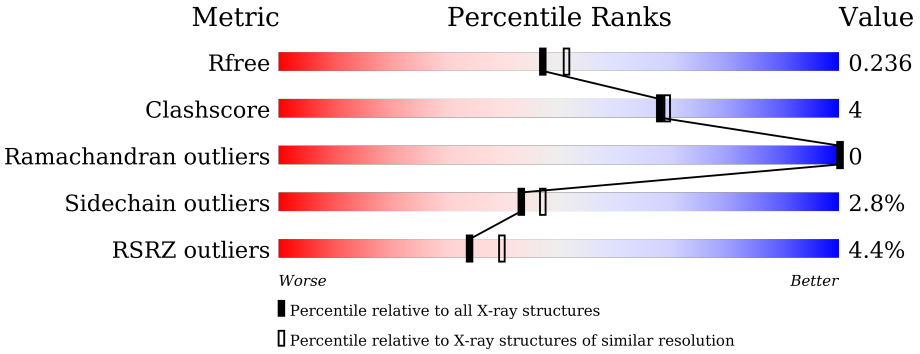
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	731	4% 88% 10% • •
1	B	731	5% 89% 9% • •

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 11754 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.

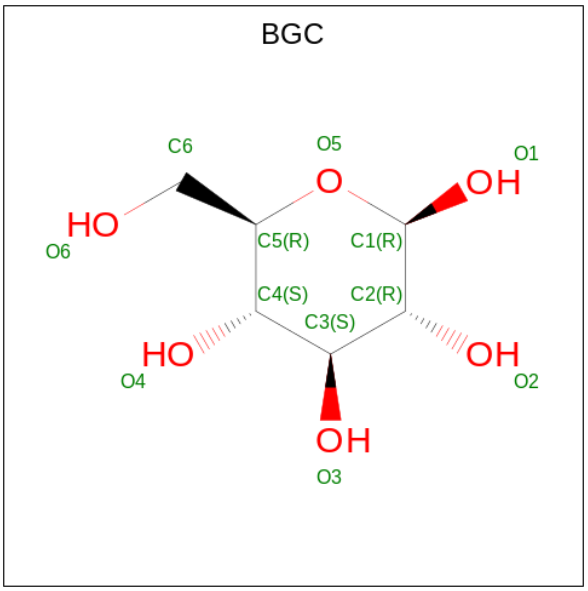
- Molecule 1 is a protein called Lin1840 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	720	5578	3533	923	1097	25	0	2	0
1	B	721	5578	3531	923	1099	25	0	1	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	GLU	LYS	engineered mutation	UNP Q92AS9
A	724	LEU	-	expression tag	UNP Q92AS9
A	725	GLU	-	expression tag	UNP Q92AS9
A	726	HIS	-	expression tag	UNP Q92AS9
A	727	HIS	-	expression tag	UNP Q92AS9
A	728	HIS	-	expression tag	UNP Q92AS9
A	729	HIS	-	expression tag	UNP Q92AS9
A	730	HIS	-	expression tag	UNP Q92AS9
A	731	HIS	-	expression tag	UNP Q92AS9
B	2	GLU	LYS	engineered mutation	UNP Q92AS9
B	724	LEU	-	expression tag	UNP Q92AS9
B	725	GLU	-	expression tag	UNP Q92AS9
B	726	HIS	-	expression tag	UNP Q92AS9
B	727	HIS	-	expression tag	UNP Q92AS9
B	728	HIS	-	expression tag	UNP Q92AS9
B	729	HIS	-	expression tag	UNP Q92AS9
B	730	HIS	-	expression tag	UNP Q92AS9
B	731	HIS	-	expression tag	UNP Q92AS9

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

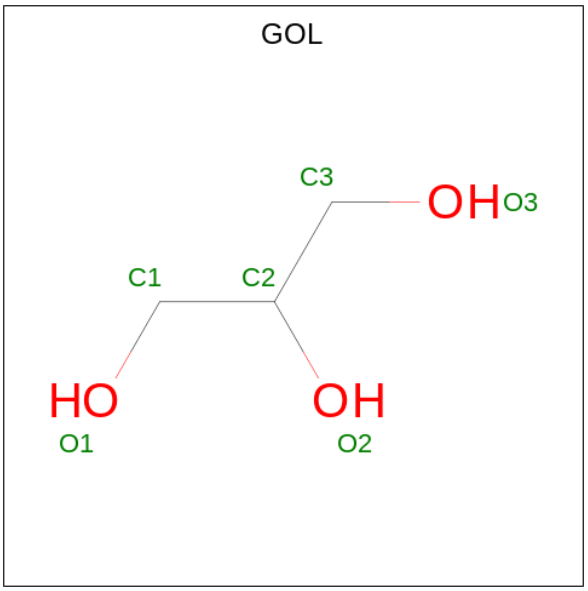


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	12	6	6	0	0
			Total	C	O		
2	B	1	12	6	6	0	0
			Total	C	O		
2	B	1	12	6	6	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

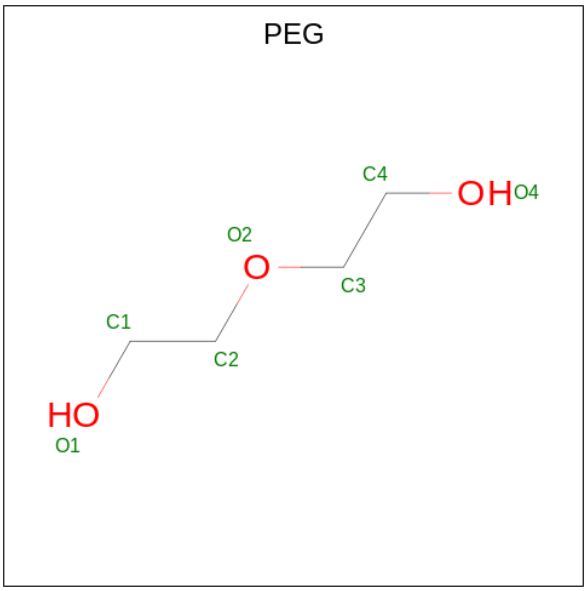
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	A	1	1	1	0	0
			Total	Mg		
3	B	1	1	1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



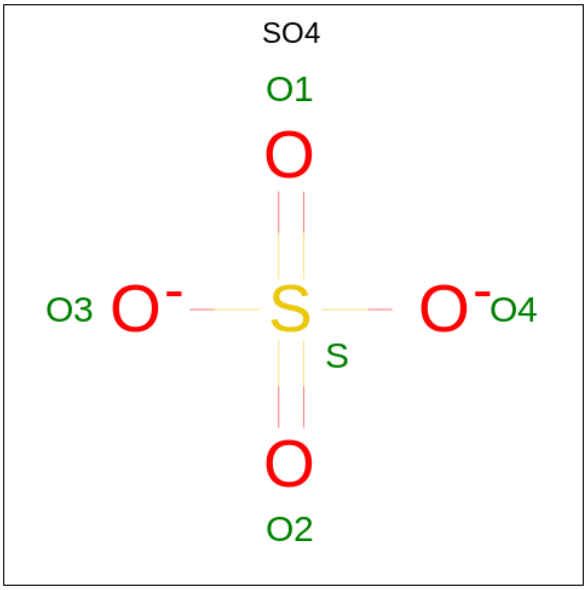
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	12	6	6	0	1
			Total	C	O		
4	A	1	12	6	6	0	1
			Total	C	O		
4	A	1	6	3	3	0	0
			Total	C	O		
4	A	1	12	6	6	0	1
			Total	C	O		
4	B	1	12	6	6	0	1
			Total	C	O		
4	B	1	6	3	3	0	0
			Total	C	O		
4	B	1	6	3	3	0	0

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	7	4	3	0	0
			Total	C	O		
5	B	1	7	4	3	0	0

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 7 is water.

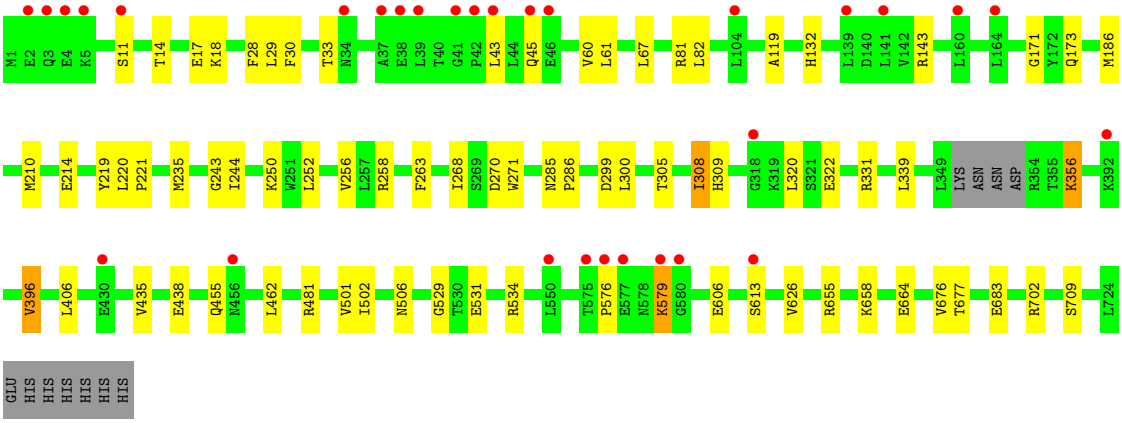
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	242	242	242	0	0
			Total	O		
7	B	233	233	233	0	0

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.

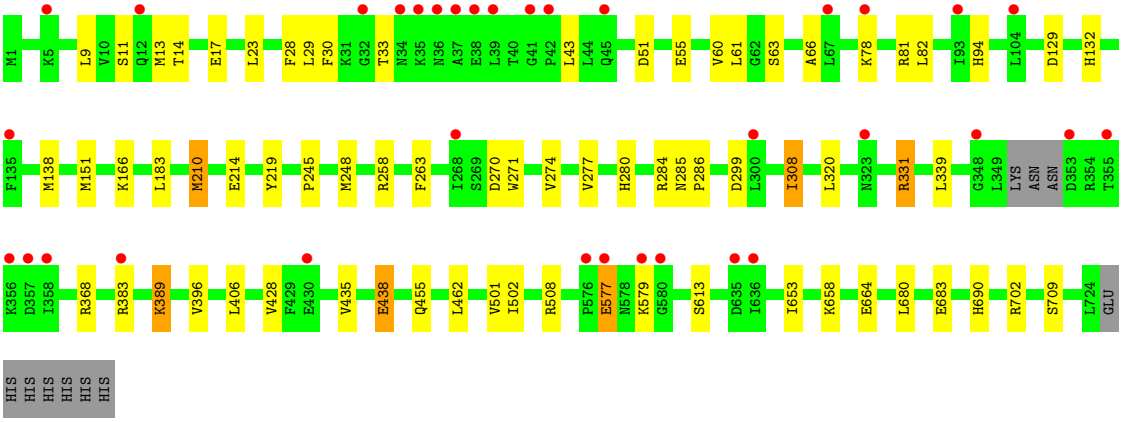
• Molecule 1: Lin1840 protein

Chain A:



• Molecule 1: Lin1840 protein

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	89.79Å 95.41Å 213.23Å 90.00° 97.27° 90.00°	Depositor
Resolution (Å)	37.10 – 2.10 37.11 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.5 (37.10-2.10) 97.6 (37.11-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.10 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.167 , 0.233 0.177 , 0.236	Depositor DCC
R_{free} test set	5084 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	25.0	Xtriage
Anisotropy	0.062	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 53.2	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	0.96	EDS
Total number of atoms	11754	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.18% 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: SO4, MG, PEG, BGC, GOL

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	0.85	0/5679	0.92	3/7696 (0.0%)
1	B	0.82	0/5679	0.91	8/7695 (0.1%)
All	All	0.84	0/11358	0.91	11/15391 (0.1%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	702	ARG	NE-CZ-NH1	7.54	124.07	120.30
1	A	702	ARG	NE-CZ-NH1	7.41	124.00	120.30
1	B	368	ARG	NE-CZ-NH1	-6.76	116.92	120.30
1	B	210[A]	MET	CG-SD-CE	-6.62	89.61	100.20
1	B	210[B]	MET	CG-SD-CE	-6.62	89.61	100.20
1	B	331	ARG	NE-CZ-NH1	5.76	123.18	120.30
1	B	501	VAL	CB-CA-C	-5.74	100.49	111.40
1	A	501	VAL	CB-CA-C	-5.59	100.78	111.40
1	B	284	ARG	NE-CZ-NH1	5.57	123.09	120.30
1	A	655	ARG	NE-CZ-NH1	5.29	122.95	120.30
1	B	508	ARG	NE-CZ-NH1	5.08	122.84	120.30

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	5578	0	5534	46	0
1	B	5578	0	5527	41	0
2	A	12	0	12	1	0
2	B	24	0	24	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	42	0	56	5	0
4	B	24	0	32	2	0
5	A	7	0	10	1	0
5	B	7	0	10	1	0
6	A	5	0	0	0	0
7	A	242	0	0	2	0
7	B	233	0	0	3	0
All	All	11754	0	11205	86	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 4.

All (86) 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:B:299:ASP:OD1	1:B:331:ARG:NH1	2.08	0.86
1:A:244[A]:ILE:HD11	1:B:653:ILE:HD13	1.66	0.75
1:A:299:ASP:OD1	1:A:331:ARG:NH1	2.20	0.74
1:A:270:ASP:OD1	2:A:801:BGC:H1	1.91	0.71
1:A:210[A]:MET:HE1	1:A:219:TYR:CD1	2.29	0.67
1:B:331:ARG:NH2	7:B:901:HOH:O	2.28	0.66
1:A:244[A]:ILE:HD11	1:B:653:ILE:CD1	2.27	0.65
4:A:804[A]:GOL:H12	7:A:1008:HOH:O	1.99	0.62
1:A:28:PHE:HA	1:A:33:THR:HG21	1.81	0.62
1:B:23:LEU:HD22	1:B:308:ILE:HG13	1.81	0.61
1:B:166:LYS:HD3	7:B:1078:HOH:O	1.99	0.61
1:B:28:PHE:HA	1:B:33:THR:HG21	1.83	0.60
1:B:299:ASP:CG	1:B:331:ARG:HH11	2.04	0.59
1:A:210[A]:MET:CE	1:A:214:GLU:HB3	2.33	0.58
1:A:308:ILE:HD12	1:A:309:HIS:CE1	2.39	0.58
1:B:270:ASP:OD1	2:B:802:BGC:H1	2.05	0.56
4:A:804[A]:GOL:C1	7:A:1008:HOH:O	2.54	0.56
1:A:258:ARG:HG2	1:A:263:PHE:O	2.05	0.56
1:B:210[A]:MET:HE1	1:B:219:TYR:CD1	2.40	0.55
1:A:30:PHE:CE2	1:A:60:VAL:HG22	2.43	0.54
1:A:271:TRP:CD2	4:A:803[B]:GOL:H32	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:577:GLU:H	1:B:577:GLU:CD	2.10	0.53
1:A:285:ASN:HB2	1:A:286:PRO:CD	2.39	0.53
1:B:51:ASP:O	1:B:55:GLU:HB2	2.10	0.52
1:B:577:GLU:OE2	1:B:577:GLU:N	2.39	0.51
1:B:214:GLU:OE2	4:B:805[B]:GOL:O2	2.27	0.51
1:A:210[A]:MET:CE	1:A:219:TYR:CD1	2.93	0.51
1:B:258:ARG:HG2	1:B:263:PHE:O	2.11	0.51
1:B:30:PHE:CE2	1:B:60:VAL:HG22	2.47	0.50
1:A:143:ARG:HH22	4:A:804[A]:GOL:H32	1.76	0.50
1:B:210[A]:MET:CE	1:B:219:TYR:CD1	2.94	0.50
1:A:243:GLY:C	1:A:244[A]:ILE:HD13	2.32	0.50
1:A:18:LYS:NZ	1:A:322:GLU:OE2	2.40	0.50
1:A:14:THR:OG1	1:A:17:GLU:HG3	2.12	0.50
1:A:285:ASN:HB2	1:A:286:PRO:HD2	1.93	0.50
1:B:658:LYS:HE2	1:B:709:SER:O	2.12	0.50
1:A:210[A]:MET:HE2	1:A:214:GLU:CB	2.42	0.49
1:A:210[A]:MET:HE2	1:A:214:GLU:HB3	1.94	0.49
1:B:285:ASN:HB2	1:B:286:PRO:HD2	1.95	0.48
1:B:9:LEU:O	1:B:13:MET:HG3	2.13	0.48
1:A:305:THR:CG2	1:A:308:ILE:HD11	2.44	0.48
1:A:119:ALA:HB3	1:A:171:GLY:HA3	1.96	0.47
1:B:285:ASN:HB2	1:B:286:PRO:CD	2.44	0.47
1:A:81:ARG:HH21	1:A:82:LEU:HD21	1.80	0.47
1:A:356:LYS:N	1:A:356:LYS:CD	2.78	0.47
1:B:183:LEU:HD23	1:B:183:LEU:N	2.28	0.47
1:B:690:HIS:HB2	5:B:801:PEG:H41	1.96	0.47
1:A:438:GLU:HB3	4:A:805:GOL:H32	1.95	0.47
1:B:462:LEU:O	1:B:502:ILE:HA	2.13	0.47
1:A:132:HIS:HB3	1:A:339:LEU:HD13	1.97	0.46
1:B:132:HIS:HB3	1:B:339:LEU:HD13	1.97	0.46
1:A:299:ASP:CG	1:A:331:ARG:HH11	2.18	0.46
1:A:271:TRP:C	1:A:271:TRP:CD1	2.90	0.45
1:A:576:PRO:O	1:A:579:LYS:HG2	2.17	0.45
1:A:235:MET:HA	1:A:268:ILE:O	2.17	0.45
1:B:274:VAL:O	1:B:277:VAL:HG22	2.16	0.45
1:A:396:VAL:HA	1:A:435:VAL:O	2.17	0.45
1:A:81:ARG:NH2	1:A:82:LEU:HD21	2.32	0.45
1:B:81:ARG:HH21	1:B:82:LEU:HD21	1.82	0.45
1:B:438:GLU:HG3	7:B:904:HOH:O	2.17	0.45
1:A:462:LEU:O	1:A:502:ILE:HA	2.17	0.44
1:A:220:LEU:N	1:A:221:PRO:CD	2.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244[A]:ILE:CD1	1:B:653:ILE:HD13	2.44	0.44
1:A:305:THR:HG22	1:A:308:ILE:HD11	2.00	0.44
1:A:173:GLN:HG2	1:A:186:MET:O	2.18	0.43
1:B:577:GLU:CD	1:B:577:GLU:N	2.71	0.43
1:B:29:LEU:HD21	1:B:43:LEU:HD23	2.01	0.43
1:B:210[B]:MET:HE3	1:B:210[B]:MET:HB3	1.89	0.42
1:A:29:LEU:HD21	1:A:43:LEU:HD23	2.00	0.42
1:A:626:VAL:O	1:A:677:THR:HA	2.19	0.42
1:B:66:ALA:N	1:B:129:ASP:OD1	2.46	0.42
1:A:268:ILE:HD12	1:A:300:LEU:HD23	2.00	0.42
1:B:94:HIS:HE1	1:B:406:LEU:O	2.02	0.42
1:B:245:PRO:HG3	1:B:280:HIS:CG	2.55	0.41
1:A:406:LEU:HA	1:A:529:GLY:HA2	2.03	0.41
1:B:438:GLU:HB3	4:B:807:GOL:H11	2.02	0.41
1:A:658:LYS:HE2	1:A:709:SER:O	2.19	0.41
1:B:14:THR:OG1	1:B:17:GLU:HG3	2.21	0.41
1:B:389:LYS:HG2	1:B:428:VAL:O	2.19	0.41
1:B:271:TRP:CD1	1:B:271:TRP:C	2.93	0.41
1:A:531:GLU:OE1	1:A:534:ARG:HD2	2.21	0.41
1:B:396:VAL:HA	1:B:435:VAL:O	2.21	0.41
1:A:481:ARG:O	5:A:806:PEG:H12	2.21	0.40
1:A:506:ASN:OD1	1:A:506:ASN:N	2.54	0.40
1:A:252:LEU:O	1:A:256:VAL:HB	2.20	0.40
1:B:248:MET:HG2	1:B:277:VAL:HG11	2.03	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	718/731 (98%)	696 (97%)	22 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	718/731 (98%)	694 (97%)	24 (3%)	0	100	100
All	All	1436/1462 (98%)	1390 (97%)	46 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	603/612 (98%)	587 (97%)	16 (3%)	44	48
1	B	603/612 (98%)	585 (97%)	18 (3%)	41	44
All	All	1206/1224 (98%)	1172 (97%)	34 (3%)	43	47

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	SER
1	A	45	GLN
1	A	61	LEU
1	A	67	LEU
1	A	250	LYS
1	A	308	ILE
1	A	320	LEU
1	A	356	LYS
1	A	396	VAL
1	A	455	GLN
1	A	579	LYS
1	A	606	GLU
1	A	613	SER
1	A	664	GLU
1	A	676	VAL
1	A	683	GLU
1	B	11	SER
1	B	61	LEU

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Mol	Chain	Res	Type
1	B	63	SER
1	B	78	LYS
1	B	138	MET
1	B	151	MET
1	B	308	ILE
1	B	320	LEU
1	B	383	ARG
1	B	389	LYS
1	B	438	GLU
1	B	455	GLN
1	B	577	GLU
1	B	579	LYS
1	B	613	SER
1	B	664	GLU
1	B	680	LEU
1	B	683	GLU

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

Mol	Chain	Res	Type
1	A	185	GLN
1	B	182	ASN
1	B	185	GLN
1	B	625	HIS
1	B	690	HIS
1	B	691	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)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 19 ligands modelled in this entry, 2 are monoatomic - leaving 17 for Mogul analysis.

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	$\#\|Z\| > 2$
4	GOL	A	804[B]	-	5,5,5	0.38	0	5,5,5	0.33	0
4	GOL	B	806	-	5,5,5	0.23	0	5,5,5	0.65	0
2	BGC	A	801	-	12,12,12	0.96	1 (8%)	17,17,17	1.55	3 (17%)
2	BGC	B	802	-	12,12,12	0.70	0	17,17,17	1.40	3 (17%)
4	GOL	A	808[A]	-	5,5,5	0.45	0	5,5,5	1.30	1 (20%)
4	GOL	A	803[A]	-	5,5,5	0.72	0	5,5,5	1.37	0
4	GOL	A	804[A]	-	5,5,5	0.69	0	5,5,5	0.72	0
6	SO4	A	807	-	4,4,4	0.29	0	6,6,6	0.30	0
4	GOL	B	805[B]	-	5,5,5	0.48	0	5,5,5	0.64	0
4	GOL	B	807	-	5,5,5	0.49	0	5,5,5	1.22	1 (20%)
4	GOL	A	808[B]	-	5,5,5	0.53	0	5,5,5	0.83	0
4	GOL	A	805	-	5,5,5	0.45	0	5,5,5	0.80	0
5	PEG	B	801	-	6,6,6	0.65	0	5,5,5	0.24	0
4	GOL	A	803[B]	-	5,5,5	0.75	0	5,5,5	0.90	0
4	GOL	B	805[A]	-	5,5,5	0.50	0	5,5,5	0.52	0
5	PEG	A	806	-	6,6,6	0.47	0	5,5,5	1.28	1 (20%)
2	BGC	B	803	-	12,12,12	0.99	0	17,17,17	2.72	8 (47%)

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
4	GOL	A	804[B]	-	-	0/4/4/4	-
4	GOL	B	806	-	-	0/4/4/4	-
2	BGC	A	801	-	-	0/2/22/22	0/1/1/1
2	BGC	B	802	-	-	0/2/22/22	0/1/1/1
4	GOL	A	808[A]	-	-	4/4/4/4	-
4	GOL	A	803[A]	-	-	3/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	A	804[A]	-	-	2/4/4/4	-
4	GOL	B	805[B]	-	-	2/4/4/4	-
4	GOL	B	807	-	-	2/4/4/4	-
4	GOL	A	808[B]	-	-	4/4/4/4	-
4	GOL	A	805	-	-	2/4/4/4	-
5	PEG	B	801	-	-	2/4/4/4	-
4	GOL	A	803[B]	-	-	0/4/4/4	-
4	GOL	B	805[A]	-	-	2/4/4/4	-
5	PEG	A	806	-	-	2/4/4/4	-
2	BGC	B	803	-	-	2/2/22/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	BGC	C4-C3	2.02	1.57	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	803	BGC	C6-C5-C4	5.58	126.08	113.00
2	B	803	BGC	O1-C1-C2	4.01	120.33	109.03
2	A	801	BGC	O5-C5-C4	-3.99	102.45	109.69
2	B	803	BGC	C3-C4-C5	-3.86	103.36	110.24
2	B	803	BGC	O2-C2-C3	-3.49	102.28	110.35
2	B	803	BGC	O3-C3-C4	3.30	117.98	110.35
2	B	802	BGC	C6-C5-C4	3.17	120.44	113.00
2	B	803	BGC	O2-C2-C1	3.03	116.18	109.16
2	B	803	BGC	O1-C1-O5	-2.87	101.78	110.38
2	B	802	BGC	O5-C5-C4	-2.77	104.67	109.69
2	B	803	BGC	O6-C6-C5	-2.71	101.98	111.29
2	B	802	BGC	O3-C3-C4	2.69	116.57	110.35
5	A	806	PEG	O2-C3-C4	-2.49	99.11	110.07
4	B	807	GOL	O2-C2-C1	-2.28	99.08	109.12
2	A	801	BGC	C6-C5-C4	2.20	118.16	113.00
4	A	808[A]	GOL	C3-C2-C1	-2.19	103.18	111.70
2	A	801	BGC	O3-C3-C2	2.03	115.03	110.35

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	804[A]	GOL	O1-C1-C2-C3
4	A	808[A]	GOL	C1-C2-C3-O3
4	A	808[B]	GOL	C1-C2-C3-O3
4	B	805[B]	GOL	C1-C2-C3-O3
2	B	803	BGC	C4-C5-C6-O6
4	A	808[A]	GOL	O2-C2-C3-O3
4	B	807	GOL	O2-C2-C3-O3
5	B	801	PEG	O1-C1-C2-O2
2	B	803	BGC	O5-C5-C6-O6
4	A	803[A]	GOL	O1-C1-C2-C3
4	A	803[A]	GOL	C1-C2-C3-O3
4	A	805	GOL	O1-C1-C2-C3
4	A	808[A]	GOL	O1-C1-C2-C3
4	A	808[B]	GOL	O1-C1-C2-C3
4	B	807	GOL	C1-C2-C3-O3
4	A	804[A]	GOL	O1-C1-C2-O2
4	A	805	GOL	O1-C1-C2-O2
4	A	808[A]	GOL	O1-C1-C2-O2
4	A	808[B]	GOL	O2-C2-C3-O3
4	B	805[B]	GOL	O2-C2-C3-O3
5	A	806	PEG	O2-C3-C4-O4
4	A	808[B]	GOL	O1-C1-C2-O2
4	A	803[A]	GOL	O1-C1-C2-O2
4	B	805[A]	GOL	C1-C2-C3-O3
5	B	801	PEG	O2-C3-C4-O4
4	B	805[A]	GOL	O1-C1-C2-O2
5	A	806	PEG	C4-C3-O2-C2

There are no ring outliers.

9 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	BGC	1	0
2	B	802	BGC	1	0
4	A	804[A]	GOL	3	0
4	B	805[B]	GOL	1	0
4	B	807	GOL	1	0
4	A	805	GOL	1	0
5	B	801	PEG	1	0
4	A	803[B]	GOL	1	0
5	A	806	PEG	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 (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	720/731 (98%)	0.09	30 (4%)	36	42	12, 26, 50, 73	0
1	B	721/731 (98%)	0.11	34 (4%)	31	37	12, 27, 50, 70	0
All	All	1441/1462 (98%)	0.10	64 (4%)	34	40	12, 27, 50, 73	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	579	LYS	5.9
1	B	579	LYS	5.2
1	A	39	LEU	4.7
1	A	576	PRO	4.2
1	B	34	ASN	4.1
1	B	67	LEU	3.9
1	A	42	PRO	3.8
1	B	37	ALA	3.8
1	B	580	GLY	3.8
1	B	356	LYS	3.5
1	B	353	ASP	3.5
1	A	318	GLY	3.5
1	B	576	PRO	3.4
1	A	38	GLU	3.2
1	B	383	ARG	3.1
1	A	430	GLU	3.0
1	A	41	GLY	3.0
1	B	38	GLU	3.0
1	B	355	THR	3.0
1	B	577	GLU	3.0
1	A	392	LYS	2.9
1	A	580	GLY	2.7
1	B	39	LEU	2.7
1	B	348	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	575	THR	2.6
1	B	12	GLN	2.6
1	B	268	ILE	2.6
1	A	577	GLU	2.6
1	B	41	GLY	2.6
1	B	300	LEU	2.5
1	A	4	GLU	2.5
1	B	430	GLU	2.5
1	A	456	ASN	2.5
1	B	636	ILE	2.5
1	B	357	ASP	2.4
1	A	34	ASN	2.4
1	A	43	LEU	2.4
1	B	323	ASN	2.4
1	A	104	LEU	2.4
1	B	36	ASN	2.3
1	A	5	LYS	2.3
1	B	45	GLN	2.3
1	A	550	LEU	2.3
1	B	135	PHE	2.3
1	A	2	GLU	2.3
1	B	78	LYS	2.2
1	B	42	PRO	2.2
1	B	35	LYS	2.2
1	A	164	LEU	2.1
1	A	139	LEU	2.1
1	A	37	ALA	2.1
1	B	93	ILE	2.1
1	B	358	ILE	2.1
1	A	613	SER	2.1
1	A	45	GLN	2.1
1	B	104	LEU	2.1
1	A	11	SER	2.0
1	A	141	LEU	2.0
1	A	46	GLU	2.0
1	B	635	ASP	2.0
1	B	5	LYS	2.0
1	A	160	LEU	2.0
1	A	3	GLN	2.0
1	B	32	GLY	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)

There are no monosaccharides in this entry.

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
4	GOL	A	803[A]	6/6	0.90	0.17	18,23,24,25	6
4	GOL	A	803[B]	6/6	0.90	0.17	19,20,21,22	6
2	BGC	B	803	12/12	0.92	0.21	33,41,55,57	0
4	GOL	A	808[A]	6/6	0.92	0.18	9,18,23,25	6
4	GOL	A	808[B]	6/6	0.92	0.18	22,23,24,26	6
5	PEG	B	801	7/7	0.92	0.10	39,44,50,53	0
4	GOL	A	805	6/6	0.93	0.26	39,44,47,50	0
4	GOL	A	804[A]	6/6	0.94	0.19	10,14,14,17	6
4	GOL	B	807	6/6	0.94	0.13	32,39,44,48	0
5	PEG	A	806	7/7	0.94	0.12	32,36,39,43	0
4	GOL	A	804[B]	6/6	0.94	0.19	18,26,28,36	6
4	GOL	B	806	6/6	0.96	0.14	40,47,50,50	0
3	MG	A	802	1/1	0.96	0.05	24,24,24,24	0
4	GOL	B	805[A]	6/6	0.96	0.21	22,23,23,23	6
4	GOL	B	805[B]	6/6	0.96	0.21	17,22,24,26	6
2	BGC	B	802	12/12	0.97	0.14	20,24,26,28	0
2	BGC	A	801	12/12	0.97	0.13	15,19,20,22	0
6	SO4	A	807	5/5	0.97	0.20	16,17,18,18	5
3	MG	B	804	1/1	0.99	0.03	24,24,24,24	0

6.5 Other polymers (i)

There are no such residues in this entry.