Full wwPDB X-ray Structure Validation Report ⓘ

Oct 6, 2024 – 05:39 pm BST

PDB ID	:	5A8M
Title	:	Crystal structure of the selenomethionine derivative of beta-glucanase SdGluc5_26A from Saccharophagus degradans
Authors	:	Sulzenbacher, G.; Lafond, M.; Freyd, T.; Henrissat, B.; Coutinho, R.M.; Berrin, J.G.; Garron, M.L.
Deposited on	:	2015-07-16
Resolution	:	1.86 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 ⓘ 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 ⓘ) were used in the production of this report:

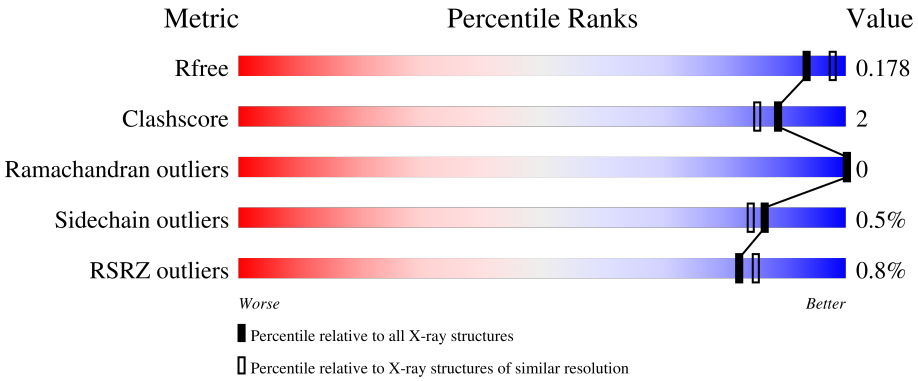
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 1.86 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}	164625	3097 (1.86-1.86)
Clashscore	180529	3359 (1.86-1.86)
Ramachandran outliers	177936	3335 (1.86-1.86)
Sidechain outliers	177891	3335 (1.86-1.86)
RSRZ outliers	164620	3097 (1.86-1.86)

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	365	88% · 8%
1	B	365	89% · 8%
1	C	365	90% · 8%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 9903 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 PUTATIVE RETAINING B-GLYCOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	337	Total	C	N	O	Se	0	14	0
			2855	1868	466	515	6			
1	B	337	Total	C	N	O	Se	0	9	0
			2839	1855	469	509	6			
1	C	337	Total	C	N	O	Se	0	9	0
			2829	1846	464	513	6			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	82	ARG	GLN	cloning artifact	UNP Q21KE5
A	176	GLN	LYS	cloning artifact	UNP Q21KE5
B	82	ARG	GLN	cloning artifact	UNP Q21KE5
B	176	GLN	LYS	cloning artifact	UNP Q21KE5
C	82	ARG	GLN	cloning artifact	UNP Q21KE5
C	176	GLN	LYS	cloning artifact	UNP Q21KE5

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Cl	0	0
			3	3		
2	B	3	Total	Cl	0	0
			3	3		
2	C	3	Total	Cl	0	0
			3	3		

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

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

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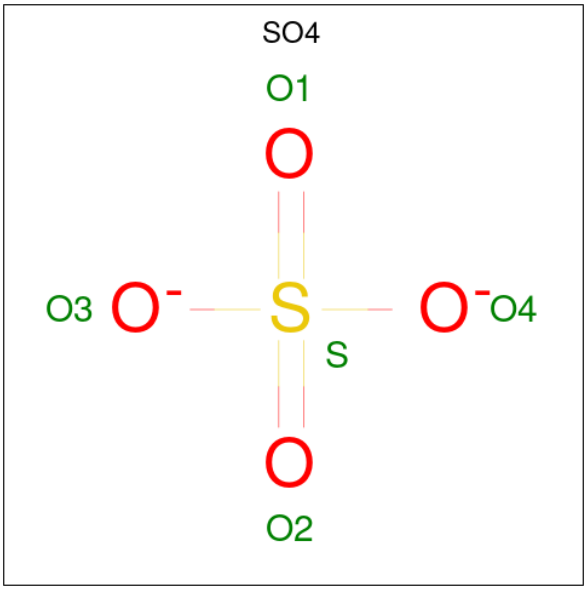
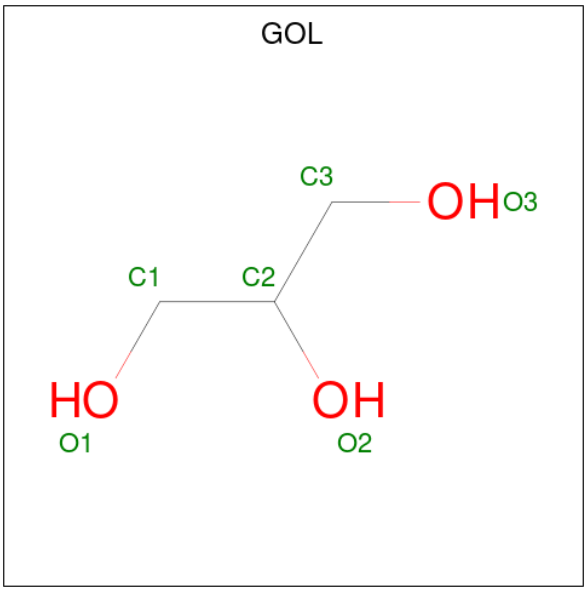
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



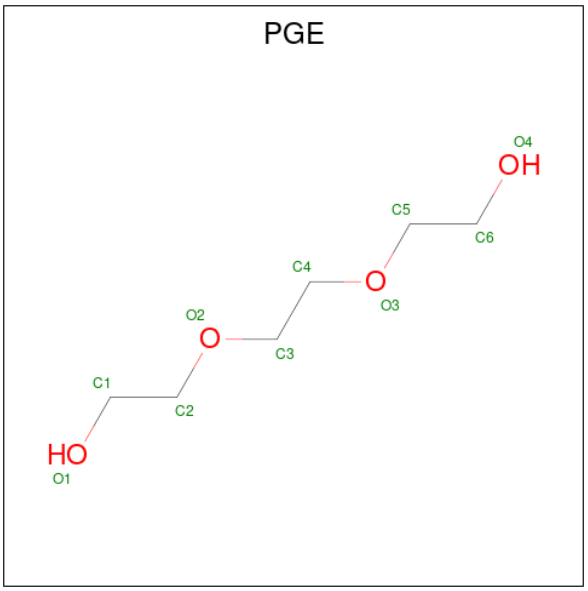
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	C	1	Total O S 5 4 1	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 6 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0

- Molecule 7 is water.

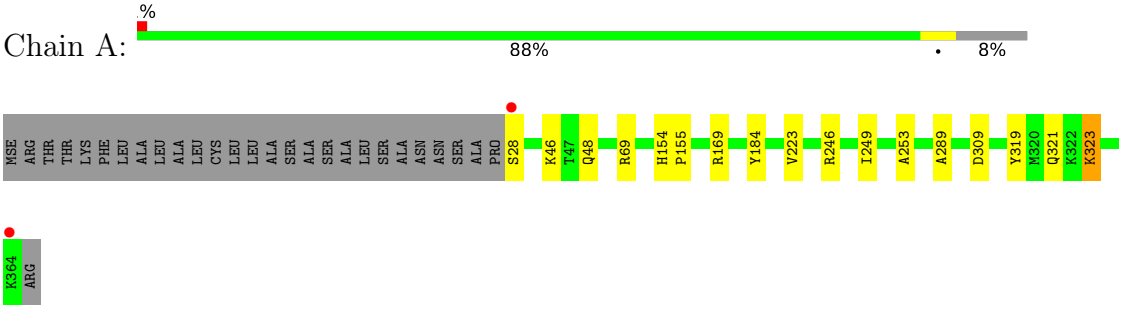
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	437	Total O 437 437	0	0
7	B	403	Total O 403 403	0	0
7	C	383	Total O 383 383	0	0

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.

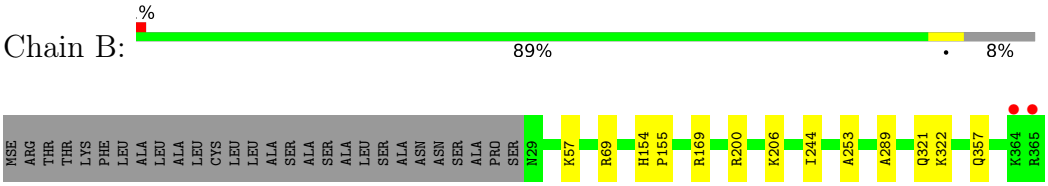
• Molecule 1: PUTATIVE RETAINING B-GLYCOSIDASE

Chain A:



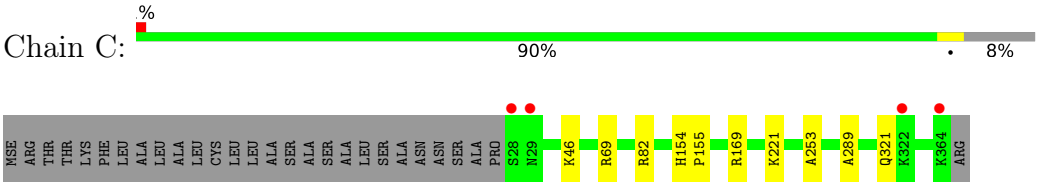
• Molecule 1: PUTATIVE RETAINING B-GLYCOSIDASE

Chain B:



• Molecule 1: PUTATIVE RETAINING B-GLYCOSIDASE

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	142.60Å 142.60Å 136.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.33 – 1.86 47.33 – 1.86	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.33-1.86) 99.2 (47.33-1.86)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.47 (at 1.86Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.143 , 0.165 0.161 , 0.178	Depositor DCC
R_{free} test set	5841 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	16.0	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 44.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	0.064 for -h,-l,-k 0.046 for l,-k,h	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	9903	wwPDB-VP
Average B, all atoms (Å^2)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.74% 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: CL, PGE, MG, GOL, 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	0.58	0/2986	0.70	1/4058 (0.0%)
1	B	0.58	0/2952	0.71	0/4011
1	C	0.59	0/2942	0.70	1/3999 (0.0%)
All	All	0.58	0/8880	0.71	2/12068 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	309	ASP	CB-CG-OD1	5.21	122.99	118.30
1	C	82	ARG	NE-CZ-NH1	5.01	122.81	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2855	0	2802	12	0
1	B	2839	0	2777	11	0
1	C	2829	0	2753	6	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
4	C	5	0	0	0	0
5	A	18	0	24	2	0
5	B	12	0	16	0	0
5	C	12	0	16	0	0
6	A	28	0	35	1	0
6	B	36	0	45	3	0
6	C	24	0	30	0	0
7	A	437	0	0	3	1
7	B	403	0	0	7	1
7	C	383	0	0	4	0
All	All	9903	0	8498	30	1

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 2.

All (30) 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:C:46[B]:LYS:NZ	7:C:2046:HOH:O	1.65	1.29
1:A:321[B]:GLN:HG3	7:A:2394:HOH:O	1.73	0.89
1:C:321:GLN:HG3	7:C:2345:HOH:O	1.83	0.77
1:B:57[B]:LYS:HE2	7:B:2060:HOH:O	1.85	0.75
1:B:321[A]:GLN:HG3	7:B:2358:HOH:O	1.87	0.73
1:B:200:ARG:HH22	6:B:1374:PGE:H1	1.59	0.67
6:B:1381:PGE:O2	7:B:2330:HOH:O	2.14	0.64
1:B:206:LYS:HG3	1:B:244:ILE:HD13	1.80	0.63
1:B:57[B]:LYS:CE	7:B:2060:HOH:O	2.48	0.59
1:A:246:ARG:HB2	1:A:249[B]:ILE:CD1	2.34	0.58
1:B:322:LYS:NZ	7:B:2333:HOH:O	2.37	0.56
1:A:48:GLN:O	5:A:1372:GOL:H12	2.11	0.50
1:A:184:TYR:CE2	1:A:223[A]:VAL:HG21	2.47	0.50
1:C:69[A]:ARG:HD2	7:C:2094:HOH:O	2.07	0.49
1:B:357[B]:GLN:NE2	7:B:2390:HOH:O	2.46	0.48
1:C:221:LYS:HE3	7:C:2267:HOH:O	2.15	0.47
1:A:69[B]:ARG:HD2	7:A:2105:HOH:O	2.14	0.47
1:A:184:TYR:CZ	1:A:223[A]:VAL:HG21	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:200:ARG:HH22	6:B:1374:PGE:C1	2.27	0.45
1:B:69[B]:ARG:HD2	7:B:2091:HOH:O	2.15	0.44
1:A:319:TYR:CZ	1:A:323:LYS:HD2	2.53	0.43
1:A:46:LYS:HA	6:A:1378:PGE:H22	2.01	0.43
1:B:253:ALA:O	1:B:289:ALA:HA	2.19	0.43
1:A:48:GLN:O	5:A:1372:GOL:C1	2.66	0.43
1:C:154:HIS:CG	1:C:155:PRO:HD2	2.55	0.42
1:A:154:HIS:CG	1:A:155:PRO:HD2	2.55	0.42
1:A:253:ALA:O	1:A:289:ALA:HA	2.20	0.42
1:B:154:HIS:CG	1:B:155:PRO:HD2	2.55	0.41
1:A:28:SER:O	7:A:2001:HOH:O	2.22	0.41
1:C:253:ALA:O	1:C:289:ALA:HA	2.21	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2207:HOH:O	7:B:2050:HOH:O[8_665]	2.18	0.02

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	349/365 (96%)	345 (99%)	4 (1%)	0	100	100
1	B	344/365 (94%)	338 (98%)	6 (2%)	0	100	100
1	C	344/365 (94%)	340 (99%)	4 (1%)	0	100	100
All	All	1037/1095 (95%)	1023 (99%)	14 (1%)	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	310/310 (100%)	308 (99%)	2 (1%)	84	81
1	B	305/310 (98%)	304 (100%)	1 (0%)	91	90
1	C	305/310 (98%)	304 (100%)	1 (0%)	91	90
All	All	920/930 (99%)	916 (100%)	4 (0%)	86	88

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	169	ARG
1	A	323	LYS
1	B	169	ARG
1	C	169	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 44 ligands modelled in this entry, 12 are monoatomic - leaving 32 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	$\#\|Z\| > 2$
6	PGE	B	1378	-	3,3,9	0.56	0	2,2,8	0.27	0
6	PGE	C	1374	-	3,3,9	0.38	0	2,2,8	0.31	0
4	SO4	B	1370	-	4,4,4	0.26	0	6,6,6	0.34	0
5	GOL	A	1371	-	5,5,5	0.49	0	5,5,5	0.56	0
5	GOL	B	1372	-	5,5,5	0.51	0	5,5,5	0.81	0
6	PGE	B	1373	-	3,3,9	0.45	0	2,2,8	0.38	0
6	PGE	C	1373	-	3,3,9	0.28	0	2,2,8	0.26	0
6	PGE	A	1373	-	3,3,9	0.50	0	2,2,8	0.45	0
5	GOL	A	1372	-	5,5,5	0.35	0	5,5,5	0.33	0
6	PGE	C	1375	-	3,3,9	0.54	0	2,2,8	0.79	0
5	GOL	C	1370	-	5,5,5	0.38	0	5,5,5	0.64	0
6	PGE	A	1376	-	3,3,9	0.67	0	2,2,8	0.41	0
6	PGE	B	1380	-	3,3,9	0.51	0	2,2,8	0.34	0
6	PGE	B	1375	-	3,3,9	0.47	0	2,2,8	0.50	0
6	PGE	C	1376	-	3,3,9	0.40	0	2,2,8	0.41	0
6	PGE	B	1377	-	3,3,9	0.30	0	2,2,8	0.71	0
6	PGE	C	1377	-	3,3,9	0.38	0	2,2,8	0.20	0
6	PGE	B	1376	-	3,3,9	0.60	0	2,2,8	0.68	0
4	SO4	C	1369	-	4,4,4	0.36	0	6,6,6	0.53	0
6	PGE	C	1372	-	3,3,9	0.44	0	2,2,8	0.14	0
5	GOL	A	1370	-	5,5,5	0.39	0	5,5,5	0.30	0
6	PGE	A	1379	-	3,3,9	0.54	0	2,2,8	0.46	0
6	PGE	B	1379	-	3,3,9	0.37	0	2,2,8	0.75	0
6	PGE	A	1374	-	3,3,9	0.31	0	2,2,8	0.37	0
5	GOL	B	1371	-	5,5,5	0.29	0	5,5,5	0.35	0
6	PGE	A	1375	-	3,3,9	0.34	0	2,2,8	0.25	0
4	SO4	A	1369	-	4,4,4	0.38	0	6,6,6	0.31	0
6	PGE	B	1381	-	3,3,9	0.38	0	2,2,8	0.41	0
5	GOL	C	1371	-	5,5,5	0.28	0	5,5,5	0.46	0
6	PGE	A	1378	-	3,3,9	0.37	0	2,2,8	0.54	0
6	PGE	A	1377	-	3,3,9	0.50	0	2,2,8	0.18	0
6	PGE	B	1374	-	3,3,9	0.31	0	2,2,8	0.12	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
6	PGE	B	1378	-	-	0/1/1/7	-
6	PGE	C	1374	-	-	1/1/1/7	-
5	GOL	A	1371	-	-	2/4/4/4	-
5	GOL	B	1372	-	-	2/4/4/4	-
6	PGE	B	1373	-	-	0/1/1/7	-
6	PGE	C	1373	-	-	1/1/1/7	-
6	PGE	A	1373	-	-	1/1/1/7	-
5	GOL	A	1372	-	-	1/4/4/4	-
6	PGE	C	1375	-	-	1/1/1/7	-
5	GOL	C	1370	-	-	0/4/4/4	-
6	PGE	A	1376	-	-	1/1/1/7	-
6	PGE	B	1380	-	-	1/1/1/7	-
6	PGE	B	1375	-	-	0/1/1/7	-
6	PGE	C	1376	-	-	0/1/1/7	-
6	PGE	B	1377	-	-	1/1/1/7	-
6	PGE	C	1377	-	-	1/1/1/7	-
6	PGE	B	1376	-	-	1/1/1/7	-
6	PGE	C	1372	-	-	0/1/1/7	-
5	GOL	A	1370	-	-	2/4/4/4	-
6	PGE	A	1379	-	-	0/1/1/7	-
6	PGE	B	1379	-	-	0/1/1/7	-
6	PGE	A	1374	-	-	0/1/1/7	-
5	GOL	B	1371	-	-	0/4/4/4	-
6	PGE	A	1375	-	-	1/1/1/7	-
6	PGE	B	1381	-	-	1/1/1/7	-
5	GOL	C	1371	-	-	2/4/4/4	-
6	PGE	A	1378	-	-	0/1/1/7	-
6	PGE	A	1377	-	-	1/1/1/7	-
6	PGE	B	1374	-	-	0/1/1/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1370	GOL	O1-C1-C2-C3
5	A	1371	GOL	O1-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
5	B	1372	GOL	O1-C1-C2-C3
5	C	1371	GOL	O1-C1-C2-C3
5	A	1370	GOL	O1-C1-C2-O2
6	A	1375	PGE	O1-C1-C2-O2
6	B	1380	PGE	O1-C1-C2-O2
6	C	1374	PGE	O1-C1-C2-O2
6	C	1377	PGE	O1-C1-C2-O2
5	A	1371	GOL	O1-C1-C2-O2
6	B	1381	PGE	O1-C1-C2-O2
5	B	1372	GOL	O1-C1-C2-O2
6	A	1377	PGE	O1-C1-C2-O2
6	C	1373	PGE	O1-C1-C2-O2
6	C	1375	PGE	O1-C1-C2-O2
5	C	1371	GOL	O1-C1-C2-O2
6	A	1373	PGE	O1-C1-C2-O2
5	A	1372	GOL	C1-C2-C3-O3
6	A	1376	PGE	O1-C1-C2-O2
6	B	1376	PGE	O1-C1-C2-O2
6	B	1377	PGE	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1372	GOL	2	0
6	B	1381	PGE	1	0
6	A	1378	PGE	1	0
6	B	1374	PGE	2	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	331/365 (90%)	-0.64	2 (0%)	85	88	7, 14, 27, 55	14 (4%)
1	B	331/365 (90%)	-0.58	2 (0%)	85	88	7, 15, 28, 72	9 (2%)
1	C	331/365 (90%)	-0.62	4 (1%)	76	79	7, 14, 29, 63	9 (2%)
All	All	993/1095 (90%)	-0.61	8 (0%)	82	85	7, 14, 28, 72	32 (3%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	28	SER	4.3
1	A	28	SER	3.4
1	B	365	ARG	2.7
1	C	29	ASN	2.6
1	C	322	LYS	2.2
1	C	364	LYS	2.2
1	B	364	LYS	2.1
1	A	364	LYS	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 monosaccharides 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. 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	B-factors(Å^2)	Q<0.9
6	PGE	B	1381	4/10	0.74	0.15	46,46,47,48	0
6	PGE	B	1377	4/10	0.75	0.17	40,42,42,45	0
6	PGE	B	1376	4/10	0.76	0.17	31,31,31,32	0
6	PGE	B	1379	4/10	0.79	0.15	32,34,36,43	0
6	PGE	A	1374	4/10	0.82	0.15	31,32,34,36	0
6	PGE	A	1376	4/10	0.83	0.15	31,33,34,35	0
6	PGE	B	1375	4/10	0.83	0.15	36,43,45,48	0
6	PGE	A	1375	4/10	0.83	0.16	33,34,36,37	0
6	PGE	B	1380	4/10	0.85	0.13	32,39,41,42	0
6	PGE	A	1377	4/10	0.85	0.13	37,40,41,43	0
6	PGE	C	1375	4/10	0.85	0.14	29,29,30,30	0
6	PGE	A	1378	4/10	0.87	0.18	37,37,38,38	0
2	CL	B	1368	1/1	0.87	0.13	49,49,49,49	0
5	GOL	A	1372	6/6	0.88	0.15	23,26,28,31	0
2	CL	A	1367	1/1	0.89	0.13	55,55,55,55	0
6	PGE	C	1373	4/10	0.89	0.13	27,29,32,36	0
6	PGE	B	1378	4/10	0.89	0.11	25,28,30,30	0
2	CL	B	1367	1/1	0.90	0.11	43,43,43,43	0
2	CL	C	1366	1/1	0.90	0.13	47,47,47,47	0
6	PGE	A	1379	4/10	0.90	0.10	29,34,35,38	0
6	PGE	C	1376	4/10	0.91	0.10	25,26,27,29	0
6	PGE	C	1377	4/10	0.91	0.12	35,36,36,38	0
5	GOL	B	1372	6/6	0.92	0.12	18,22,25,26	0
2	CL	C	1367	1/1	0.93	0.10	53,53,53,53	0
6	PGE	B	1374	4/10	0.93	0.10	32,33,36,39	0
6	PGE	C	1374	4/10	0.93	0.10	28,31,34,36	0
5	GOL	B	1371	6/6	0.94	0.09	16,21,24,29	0
6	PGE	B	1373	4/10	0.94	0.08	19,21,22,24	0
5	GOL	A	1371	6/6	0.94	0.13	18,22,22,23	0
5	GOL	C	1370	6/6	0.94	0.10	19,20,21,21	0
2	CL	A	1366	1/1	0.94	0.13	47,47,47,47	0
6	PGE	A	1373	4/10	0.96	0.07	18,20,20,22	0
5	GOL	A	1370	6/6	0.96	0.07	18,22,26,29	0
4	SO4	A	1369	5/5	0.96	0.11	25,29,32,33	0
4	SO4	C	1369	5/5	0.96	0.08	30,30,34,34	0
6	PGE	C	1372	4/10	0.96	0.09	21,22,23,25	0
5	GOL	C	1371	6/6	0.97	0.06	18,22,24,26	0
4	SO4	B	1370	5/5	0.98	0.08	24,30,31,33	0
3	MG	A	1368	1/1	0.99	0.02	16,16,16,16	0
3	MG	C	1368	1/1	0.99	0.05	18,18,18,18	0
2	CL	B	1366	1/1	1.00	0.02	15,15,15,15	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	CL	C	1365	1/1	1.00	0.02	13,13,13,13	0
3	MG	B	1369	1/1	1.00	0.03	15,15,15,15	0
2	CL	A	1365	1/1	1.00	0.02	15,15,15,15	0

6.5 Other polymers (i)

There are no such residues in this entry.