wwPDB X-ray Structure Validation Summary Report (i)

Jun 23, 2024 – 06:08 AM EDT

PDB ID	:	6I60
Title	:	Structure of alpha-L-rhamnosidase from Dictyoglumus thermophilum
Authors	:	Lafite, P.; Daniellou, R.
Deposited on	:	2018-11-15
Resolution	:	2.74 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (1)) were used in the production of this report:

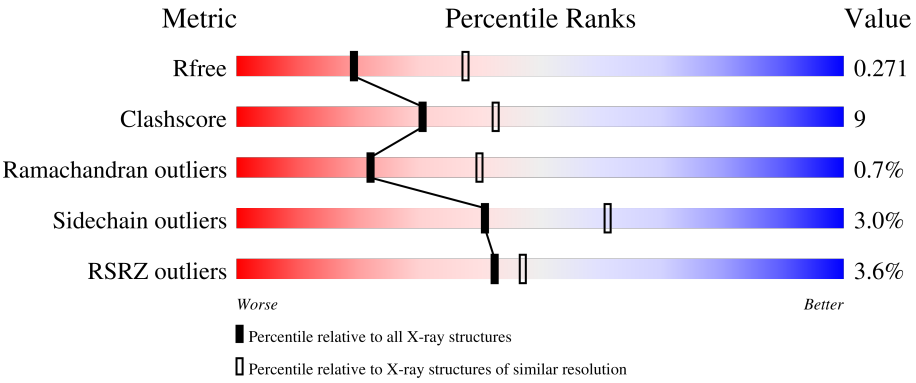
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.74 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	1271 (2.76-2.72)
Clashscore	141614	1322 (2.76-2.72)
Ramachandran outliers	138981	1297 (2.76-2.72)
Sidechain outliers	138945	1298 (2.76-2.72)
RSRZ outliers	127900	1243 (2.76-2.72)

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	944	3% 75% 18% • 6%
1	B	944	3% 73% 20% • 6%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PGE	A	1001	-	-	X	-
2	PGE	A	1007	-	-	X	-
2	PGE	A	1010	-	-	X	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 14789 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 Alpha-rhamnosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	883	Total	C	N	O	S	0	0	0
			7237	4694	1169	1356	18			
1	B	886	Total	C	N	O	S	0	0	0
			7251	4705	1174	1354	18			

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP B5YC64
A	2	GLY	-	expression tag	UNP B5YC64
A	3	SER	-	expression tag	UNP B5YC64
A	4	SER	-	expression tag	UNP B5YC64
A	5	HIS	-	expression tag	UNP B5YC64
A	6	HIS	-	expression tag	UNP B5YC64
A	7	HIS	-	expression tag	UNP B5YC64
A	8	HIS	-	expression tag	UNP B5YC64
A	9	HIS	-	expression tag	UNP B5YC64
A	10	HIS	-	expression tag	UNP B5YC64
A	11	SER	-	expression tag	UNP B5YC64
A	12	SER	-	expression tag	UNP B5YC64
A	13	GLY	-	expression tag	UNP B5YC64
A	14	LEU	-	expression tag	UNP B5YC64
A	15	VAL	-	expression tag	UNP B5YC64
A	16	PRO	-	expression tag	UNP B5YC64
A	17	ARG	-	expression tag	UNP B5YC64
A	18	GLY	-	expression tag	UNP B5YC64
A	19	SER	-	expression tag	UNP B5YC64
A	20	HIS	-	expression tag	UNP B5YC64
A	21	MET	-	expression tag	UNP B5YC64
A	22	ALA	-	expression tag	UNP B5YC64
A	23	SER	-	expression tag	UNP B5YC64
B	1	MET	-	initiating methionine	UNP B5YC64
B	2	GLY	-	expression tag	UNP B5YC64

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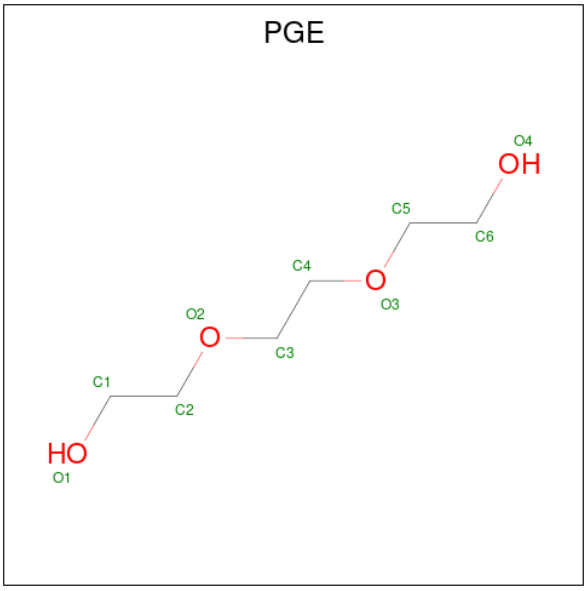
Chain	Residue	Modelled	Actual	Comment	Reference
B	3	SER	-	expression tag	UNP B5YC64
B	4	SER	-	expression tag	UNP B5YC64
B	5	HIS	-	expression tag	UNP B5YC64
B	6	HIS	-	expression tag	UNP B5YC64
B	7	HIS	-	expression tag	UNP B5YC64
B	8	HIS	-	expression tag	UNP B5YC64
B	9	HIS	-	expression tag	UNP B5YC64
B	10	HIS	-	expression tag	UNP B5YC64
B	11	SER	-	expression tag	UNP B5YC64
B	12	SER	-	expression tag	UNP B5YC64
B	13	GLY	-	expression tag	UNP B5YC64
B	14	LEU	-	expression tag	UNP B5YC64
B	15	VAL	-	expression tag	UNP B5YC64
B	16	PRO	-	expression tag	UNP B5YC64
B	17	ARG	-	expression tag	UNP B5YC64
B	18	GLY	-	expression tag	UNP B5YC64
B	19	SER	-	expression tag	UNP B5YC64
B	20	HIS	-	expression tag	UNP B5YC64
B	21	MET	-	expression tag	UNP B5YC64
B	22	ALA	-	expression tag	UNP B5YC64
B	23	SER	-	expression tag	UNP B5YC64

- Molecule 2 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	6	4		

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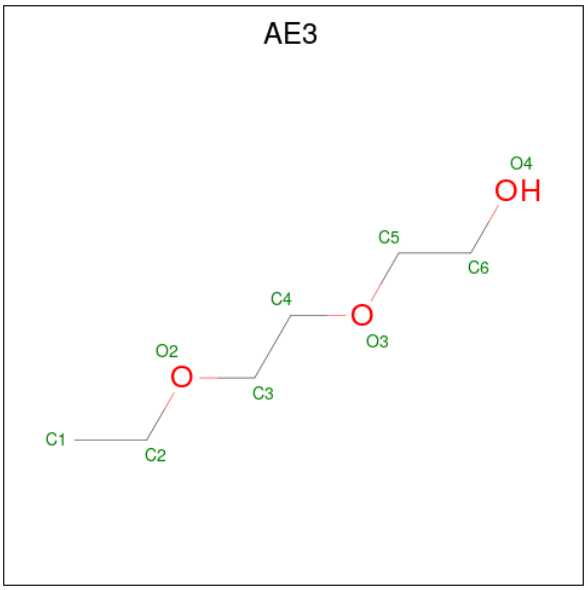
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 10 6 4	0	0
2	A	1	Total C O 10 6 4	0	0
2	A	1	Total C O 10 6 4	0	0
2	A	1	Total C O 10 6 4	0	0
2	A	1	Total C O 10 6 4	0	0
2	A	1	Total C O 10 6 4	0	0
2	A	1	Total C O 10 6 4	0	0
2	B	1	Total C O 10 6 4	0	0
2	B	1	Total C O 10 6 4	0	0
2	B	1	Total C O 10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

- Molecule 3 is 2-(2-ETHOXYETHOXY)ETHANOL (three-letter code: AE3) (formula: $C_6H_{14}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 9 6 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 8 5 3	0	0
3	B	1	Total C O 9 6 3	0	0
3	B	1	Total C O 8 5 3	0	0
3	B	1	Total C O 6 4 2	0	0

- Molecule 4 is water.

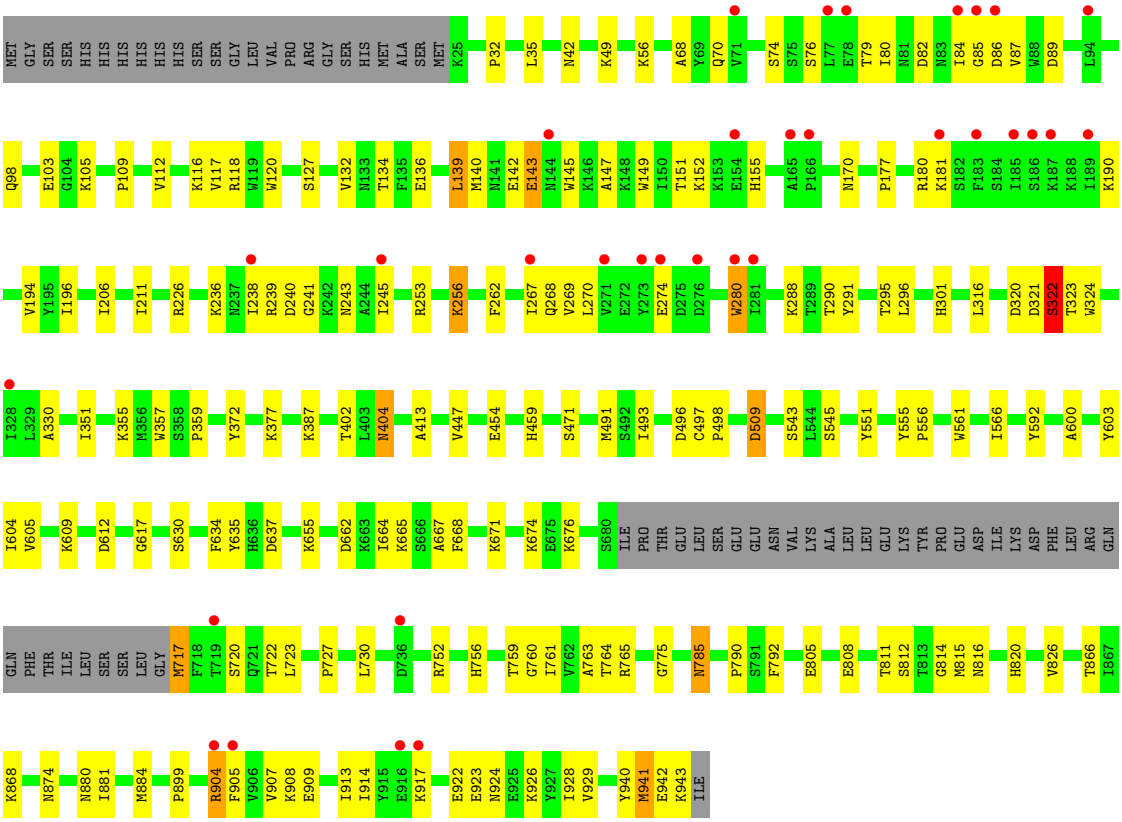
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	81	Total O 81 81	0	0
4	B	70	Total O 70 70	0	0

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.

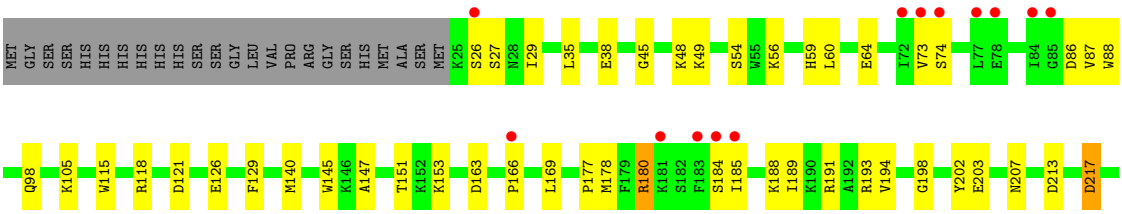
• Molecule 1: Alpha-rhamnosidase

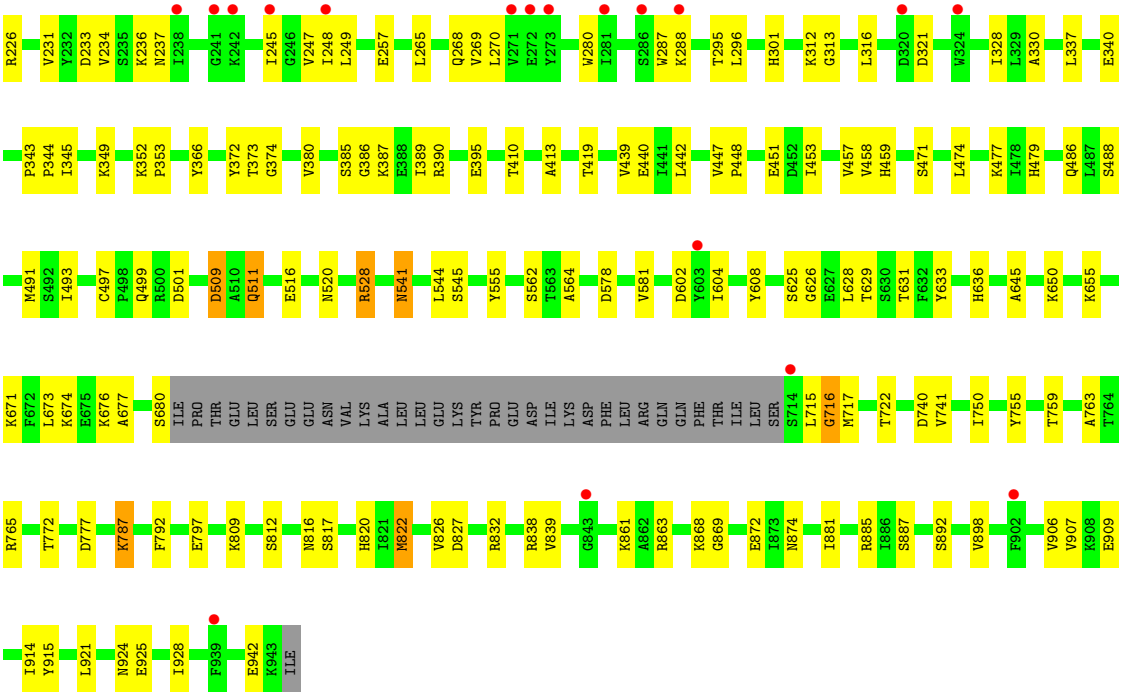
Chain A:



• Molecule 1: Alpha-rhamnosidase

Chain B:




R226 V231 Y232 D233 V234 S235 K236 N237 I238 G241 K242 I245 G246 V247 I248 L249 E257 L265 Q268 V269 L270 V271 E272 Y273 W280 I281 S286 W287 K288 T295 L296 H301 K312 G313 L316 D320 D321 W324 I328 L329 A330 L337 E340
P343 P344 I345 K349 K352 P353 Y366 Y372 T373 G374 V380 S385 G386 K387 E388 I389 R390 E395 T410 A413 T419 V439 E440 I441 L442 V447 P448 E451 D452 I453 V457 V458 H459 S471 L474 K477 I478 H479 Q486 L487 S488
M491 S492 I493 C497 P498 Q499 R500 D501 D509 A510 Q511 E516 N520 R528 N541 L544 S545 Y555 S562 T563 A564 D578 V581 D602 Y603 I604 Y608 S625 G626 E627 L628 T629 S630 T631 P632 Y633 H636 A645 K650 K655
K671 F672 L673 K674 E675 K676 A677 S680 ILE PRO THR GLU LEU SER GLU GLU ASN VAL LYS ALA LEU LEU GLU LYS TYR PRO GLU ASP ILE LYS ASP PHE LEU ARG GLN GLN PHE THR ILE LEU SER S714 L715 G716 M717 T722 D740 V741 I750 Y755 T759 A763 T764
R765 T772 D777 K787 F792 E797 K809 S812 N816 S817 H820 I821 M822 V826 D827 R832 R838 V839 G843 K861 A862 R863 K868 G869 E872 I873 N874 I881 R885 I886 S887 S892 V898 F902 V906 V907 K908 E909
I914 Y915 L921 N924 E925 I928 F939 E942 K943 ILE

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	173.22Å 161.53Å 124.38Å 90.00° 132.14° 90.00°	Depositor
Resolution (Å)	43.28 – 2.74 49.21 – 2.75	Depositor EDS
% Data completeness (in resolution range)	96.9 (43.28-2.74) 97.1 (49.21-2.75)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.94 (at 2.73Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.226 , 0.270 0.230 , 0.271	Depositor DCC
R_{free} test set	3203 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	60.8	Xtriage
Anisotropy	0.149	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 56.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.042 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	14789	wwPDB-VP
Average B, all atoms (Å^2)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% 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: AE3, PGE

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	0.36	0/7442	0.44	0/10098
1	B	0.28	0/7456	0.42	0/10115
All	All	0.32	0/14898	0.43	0/20213

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

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	7237	0	7030	135	0
1	B	7251	0	7059	131	0
2	A	80	0	112	30	0
2	B	30	0	42	6	0
3	A	17	0	23	1	0
3	B	23	0	32	4	0
4	A	81	0	0	2	0
4	B	70	0	0	2	0
All	All	14789	0	14298	267	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 9.

The worst 5 of 267 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:256:LYS:CE	2:A:1007:PGE:H42	1.79	1.11
1:A:355:LYS:HE2	2:A:1001:PGE:C6	1.81	1.10
1:A:256:LYS:HE3	2:A:1007:PGE:C4	1.83	1.08
1:B:787:LYS:HE3	3:B:1001:AE3:H1C2	1.40	1.04
1:B:27:SER:O	1:B:29:ILE:HD12	1.55	1.04

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	879/944 (93%)	818 (93%)	54 (6%)	7 (1%)	19	36
1	B	882/944 (93%)	814 (92%)	63 (7%)	5 (1%)	25	44
All	All	1761/1888 (93%)	1632 (93%)	117 (7%)	12 (1%)	22	40

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	323	THR
1	A	241	GLY
1	A	322	SER
1	A	815	MET
1	B	716	GLY

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	777/840 (92%)	755 (97%)	22 (3%)	43	63
1	B	778/840 (93%)	754 (97%)	24 (3%)	40	60
All	All	1555/1680 (93%)	1509 (97%)	46 (3%)	41	61

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	217	ASP
1	B	655	LYS
1	B	471	SER
1	B	528	ARG
1	B	740	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	404	ASN
1	A	499	GLN
1	A	731	ASN
1	B	268	GLN
1	B	541	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

16 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	PGE	B	1003	-	9,9,9	0.32	0	8,8,8	0.25	0
3	AE3	B	1006	-	5,5,8	0.37	0	4,4,7	0.29	0
2	PGE	B	1005	-	9,9,9	0.32	0	8,8,8	0.29	0
2	PGE	A	1004	-	9,9,9	0.31	0	8,8,8	0.30	0
2	PGE	A	1010	-	9,9,9	0.51	0	8,8,8	0.79	0
2	PGE	A	1007	-	9,9,9	0.28	0	8,8,8	0.63	0
3	AE3	A	1006	-	7,7,8	0.31	0	6,6,7	0.27	0
2	PGE	A	1009	-	9,9,9	0.32	0	8,8,8	0.32	0
3	AE3	B	1001	-	8,8,8	0.37	0	7,7,7	0.28	0
2	PGE	A	1002	-	9,9,9	0.32	0	8,8,8	0.28	0
2	PGE	A	1008	-	9,9,9	0.32	0	8,8,8	0.26	0
2	PGE	A	1003	-	9,9,9	0.32	0	8,8,8	0.29	0
3	AE3	A	1005	-	8,8,8	0.38	0	7,7,7	0.55	0
2	PGE	A	1001	-	9,9,9	0.33	0	8,8,8	0.30	0
2	PGE	B	1004	-	9,9,9	0.32	0	8,8,8	0.29	0
3	AE3	B	1002	-	7,7,8	0.32	0	6,6,7	0.24	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	PGE	B	1003	-	-	1/7/7/7	-
3	AE3	B	1006	-	-	1/3/3/6	-
2	PGE	B	1005	-	-	5/7/7/7	-
2	PGE	A	1004	-	-	3/7/7/7	-
2	PGE	A	1010	-	-	4/7/7/7	-
2	PGE	A	1007	-	-	6/7/7/7	-
3	AE3	A	1006	-	-	0/5/5/6	-
2	PGE	A	1009	-	-	0/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AE3	B	1001	-	-	2/6/6/6	-
2	PGE	A	1002	-	-	2/7/7/7	-
2	PGE	A	1008	-	-	2/7/7/7	-
2	PGE	A	1003	-	-	0/7/7/7	-
3	AE3	A	1005	-	-	4/6/6/6	-
2	PGE	A	1001	-	-	1/7/7/7	-
2	PGE	B	1004	-	-	6/7/7/7	-
3	AE3	B	1002	-	-	2/5/5/6	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1010	PGE	C4-C3-O2-C2
3	A	1005	AE3	C3-C4-O3-C5
3	A	1005	AE3	O2-C3-C4-O3
2	B	1005	PGE	O2-C3-C4-O3
2	A	1004	PGE	O2-C3-C4-O3

There are no ring outliers.

10 monomers are involved in 41 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1005	PGE	1	0
2	A	1004	PGE	1	0
2	A	1010	PGE	6	0
2	A	1007	PGE	12	0
3	B	1001	AE3	4	0
2	A	1002	PGE	1	0
2	A	1008	PGE	2	0
3	A	1005	AE3	1	0
2	A	1001	PGE	8	0
2	B	1004	PGE	5	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	883/944 (93%)	0.36	33 (3%)	41	46	42, 58, 81, 102	0
1	B	886/944 (93%)	0.31	31 (3%)	44	49	42, 60, 83, 97	0
All	All	1769/1888 (93%)	0.34	64 (3%)	42	47	42, 59, 82, 102	0

The worst 5 of 64 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	271	VAL	4.5
1	A	281	ILE	4.3
1	A	189	ILE	4.1
1	A	238	ILE	4.0
1	B	184	SER	3.8

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
3	AE3	B	1001	9/9	0.55	0.33	60,78,100,105	0
2	PGE	A	1004	10/10	0.69	0.30	64,77,83,84	0
3	AE3	A	1005	9/9	0.70	0.26	76,108,124,125	0
2	PGE	A	1007	10/10	0.71	0.36	79,82,87,88	0
3	AE3	B	1006	6/9	0.73	0.22	65,68,82,86	0
2	PGE	B	1004	10/10	0.76	0.24	64,71,78,80	0
3	AE3	B	1002	8/9	0.81	0.26	59,65,67,69	0
2	PGE	A	1010	10/10	0.85	0.29	20,20,20,20	0
2	PGE	A	1008	10/10	0.87	0.27	55,62,67,69	0
2	PGE	A	1002	10/10	0.87	0.23	62,66,74,75	0
2	PGE	A	1003	10/10	0.87	0.30	53,62,85,92	0
2	PGE	B	1005	10/10	0.87	0.26	55,62,67,67	0
2	PGE	A	1009	10/10	0.88	0.26	57,63,67,71	0
2	PGE	B	1003	10/10	0.88	0.21	66,73,86,87	0
3	AE3	A	1006	8/9	0.89	0.23	67,75,77,80	0
2	PGE	A	1001	10/10	0.89	0.19	61,67,72,73	0

6.5 Other polymers (i)

There are no such residues in this entry.