



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 17, 2022 – 04:18 pm BST

PDB ID : 6I8F
Title : STRUCTURE OF ESTER-HYDROLASE EH1AB1 FROM THE METAGENOME OF LAKE ARREO
Authors : Cea-Rama, I.; Sanz-Aparicio, J.
Deposited on : 2018-11-20
Resolution : 2.11 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 : 2.31.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

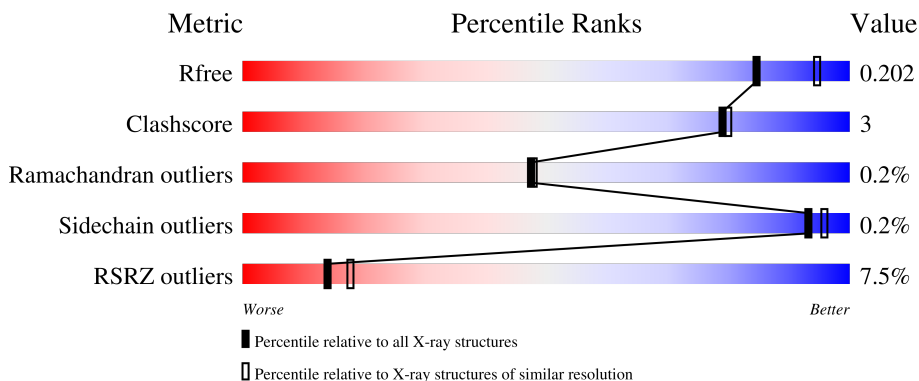
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.11 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	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705 (2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)
RSRZ outliers	127900	6112 (2.14-2.10)

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 $\leq 5\%$. 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	329	
1	B	329	

2 Entry composition [i](#)

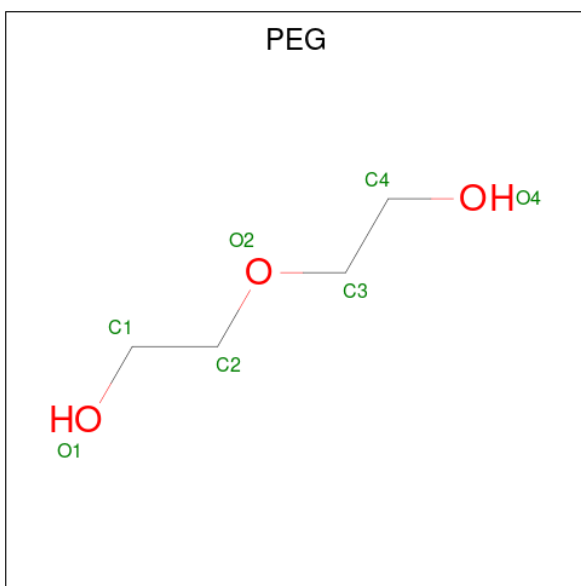
There are 5 unique types of molecules in this entry. The entry contains 5244 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 EH1AB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	315	Total 2385	C 1500	N 419	O 455	S 11	0	0	0
1	B	315	Total 2385	C 1500	N 419	O 455	S 11	0	0	0

- Molecule 2 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



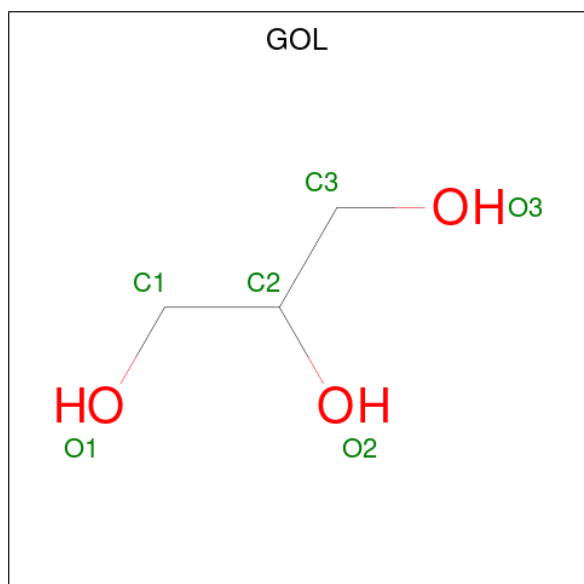
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	Total 7	C 4	O 3	0	0
2	A	1	Total 7	C 4	O 3	0	0
2	A	1	Total 7	C 4	O 3	0	0
2	A	1	Total 7	C 4	O 3	0	0

Continued on next page...

Continued from previous page...

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

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

Continued on next page...

Continued from previous page...

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

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

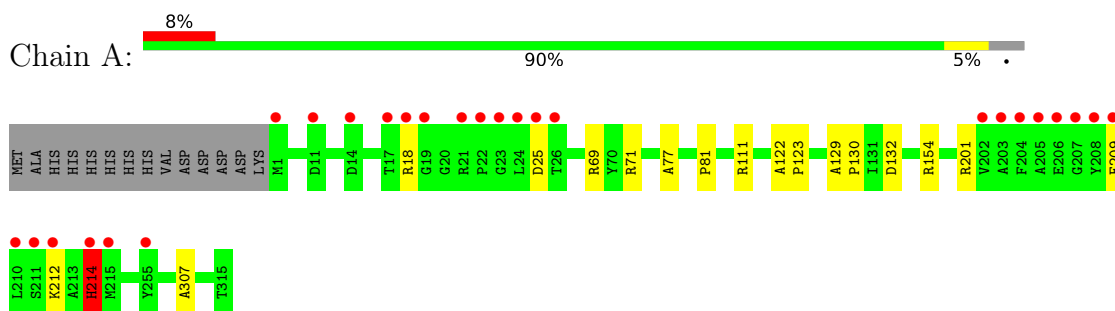
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	170	Total O 170 170	0	0
5	B	172	Total O 172 172	0	0

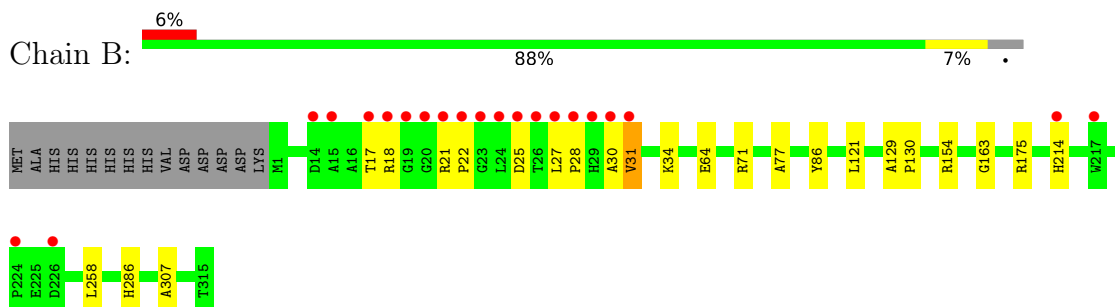
3 Residue-property plots [i](#)

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: EH1AB1



- Molecule 1: EH1AB1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	82.23Å 86.05Å 98.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.02 – 2.11 43.02 – 2.11	Depositor EDS
% Data completeness (in resolution range)	99.8 (43.02-2.11) 99.8 (43.02-2.11)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 2.10Å)	Xtrriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.160 , 0.198 0.171 , 0.202	Depositor DCC
R_{free} test set	2081 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	23.3	Xtrriage
Anisotropy	0.269	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.018 for k,h,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5244	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.81% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: PEG, MG, 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	0.42	0/2443	0.63	2/3318 (0.1%)
1	B	0.43	0/2443	0.61	0/3318
All	All	0.43	0/4886	0.62	2/6636 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
1	B	0	1
All	All	0	6

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	214	HIS	CB-CA-C	6.25	122.90	110.40
1	A	214	HIS	CA-CB-CG	-5.78	103.77	113.60

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	111	ARG	Sidechain
1	A	18	ARG	Sidechain
1	A	201	ARG	Sidechain
1	A	214	HIS	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	A	69	ARG	Sidechain
1	B	18	ARG	Sidechain

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	2385	0	2298	13	0
1	B	2385	0	2298	14	1
2	A	35	0	50	1	0
2	B	35	0	50	1	0
3	A	36	0	48	3	0
3	B	24	0	32	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	170	0	0	3	1
5	B	172	0	0	1	1
All	All	5244	0	4776	27	2

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 3.

All (27) 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:71:ARG:NH2	1:B:77:ALA:O	2.11	0.83
1:B:154:ARG:HH12	3:B:408:GOL:H11	1.43	0.82
1:A:307:ALA:HB1	1:B:307:ALA:HB1	1.60	0.81
1:B:17:THR:HG21	1:B:22:PRO:HG3	1.63	0.81
1:A:154:ARG:HH22	3:A:409:GOL:H11	1.44	0.80
1:A:209:PHE:CE1	5:A:659:HOH:O	2.36	0.77
1:A:209:PHE:HE1	5:A:659:HOH:O	1.69	0.74
1:B:27:LEU:N	1:B:28:PRO:HD3	2.14	0.62
1:A:154:ARG:NH2	3:A:409:GOL:H11	2.16	0.61
1:A:81:PRO:HG3	1:A:154:ARG:CZ	2.30	0.61
1:B:121:LEU:HB2	2:B:404:PEG:H41	1.86	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:30:ALA:O	1:B:34:LYS:HG2	2.06	0.56
1:A:71:ARG:NH2	1:A:77:ALA:O	2.29	0.51
1:B:64:GLU:HG3	5:B:621:HOH:O	2.12	0.50
1:B:25:ASP:OD2	1:B:214:HIS:HB3	2.13	0.49
1:A:25:ASP:HB3	1:A:214:HIS:CG	2.49	0.48
2:A:401:PEG:H41	5:A:612:HOH:O	2.14	0.47
1:A:129:ALA:HB3	1:A:130:PRO:HD3	1.97	0.46
1:A:132:ASP:OD2	3:A:408:GOL:H31	2.15	0.46
1:B:129:ALA:HB3	1:B:130:PRO:HD3	1.99	0.45
1:B:258:LEU:HD12	1:B:286:HIS:CE1	2.54	0.42
1:A:81:PRO:HG3	1:A:154:ARG:NH1	2.34	0.42
1:B:21:ARG:N	1:B:22:PRO:HD3	2.35	0.41
1:A:122:ALA:HB1	1:A:123:PRO:HA	2.03	0.41
1:B:25:ASP:OD1	1:B:214:HIS:HB3	2.20	0.41
1:B:86:TYR:O	1:B:163:GLY:HA3	2.21	0.41
1:A:81:PRO:HB3	1:A:154:ARG:HB3	2.02	0.40

All (2) 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)
1:B:31:VAL:CG2	1:B:175:ARG:O[4_445]	2.02	0.18
5:A:503:HOH:O	5:B:625:HOH:O[3_454]	2.16	0.04

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	313/329 (95%)	299 (96%)	13 (4%)	1 (0%)	41	40
1	B	313/329 (95%)	292 (93%)	21 (7%)	0	100	100
All	All	626/658 (95%)	591 (94%)	34 (5%)	1 (0%)	47	48

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	212	LYS

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	238/251 (95%)	238 (100%)	0	100	100
1	B	238/251 (95%)	237 (100%)	1 (0%)	91	94
All	All	476/502 (95%)	475 (100%)	1 (0%)	93	96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	31	VAL

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 22 ligands modelled in this entry, 2 are monoatomic - leaving 20 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
2	PEG	B	404	-	6,6,6	0.47	0	5,5,5	0.44	0
3	GOL	A	407	-	5,5,5	0.31	0	5,5,5	0.78	0
3	GOL	B	406	-	5,5,5	0.39	0	5,5,5	0.55	0
2	PEG	A	404	-	6,6,6	0.53	0	5,5,5	0.22	0
3	GOL	A	411	-	5,5,5	0.28	0	5,5,5	0.25	0
3	GOL	B	408	-	5,5,5	0.16	0	5,5,5	0.22	0
3	GOL	A	408	-	5,5,5	0.23	0	5,5,5	0.37	0
2	PEG	B	402	-	6,6,6	0.42	0	5,5,5	0.66	0
2	PEG	A	402	-	6,6,6	0.52	0	5,5,5	0.21	0
2	PEG	B	401	-	6,6,6	0.53	0	5,5,5	0.26	0
3	GOL	A	410	-	5,5,5	0.30	0	5,5,5	0.42	0
2	PEG	B	405	-	6,6,6	0.54	0	5,5,5	0.36	0
2	PEG	A	403	-	6,6,6	0.44	0	5,5,5	0.24	0
2	PEG	A	405	-	6,6,6	0.38	0	5,5,5	0.32	0
3	GOL	A	406	-	5,5,5	0.38	0	5,5,5	0.96	0
3	GOL	A	409	-	5,5,5	0.37	0	5,5,5	0.42	0
3	GOL	B	407	-	5,5,5	0.28	0	5,5,5	0.74	0
3	GOL	B	409	-	5,5,5	0.32	0	5,5,5	0.40	0
2	PEG	B	403	-	6,6,6	0.52	0	5,5,5	0.15	0
2	PEG	A	401	-	6,6,6	0.34	0	5,5,5	0.41	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PEG	B	404	-	-	1/4/4/4	-
3	GOL	A	407	-	-	4/4/4/4	-
3	GOL	B	406	-	-	2/4/4/4	-
2	PEG	A	404	-	-	1/4/4/4	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	411	-	-	0/4/4/4	-
3	GOL	B	408	-	-	0/4/4/4	-
3	GOL	A	408	-	-	0/4/4/4	-
2	PEG	B	402	-	-	4/4/4/4	-
2	PEG	A	402	-	-	3/4/4/4	-
2	PEG	B	401	-	-	2/4/4/4	-
3	GOL	A	410	-	-	0/4/4/4	-
2	PEG	B	405	-	-	3/4/4/4	-
2	PEG	A	403	-	-	2/4/4/4	-
2	PEG	A	405	-	-	1/4/4/4	-
3	GOL	A	406	-	-	3/4/4/4	-
3	GOL	A	409	-	-	2/4/4/4	-
3	GOL	B	407	-	-	0/4/4/4	-
3	GOL	B	409	-	-	2/4/4/4	-
2	PEG	B	403	-	-	1/4/4/4	-
2	PEG	A	401	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (33) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	406	GOL	O1-C1-C2-O2
3	A	407	GOL	C1-C2-C3-O3
3	A	409	GOL	O1-C1-C2-C3
3	B	406	GOL	C1-C2-C3-O3
3	B	406	GOL	O2-C2-C3-O3
3	B	409	GOL	O1-C1-C2-C3
3	A	409	GOL	O1-C1-C2-O2
3	B	409	GOL	O1-C1-C2-O2
2	A	401	PEG	O1-C1-C2-O2
2	A	404	PEG	O2-C3-C4-O4
2	B	402	PEG	O1-C1-C2-O2
2	B	403	PEG	O1-C1-C2-O2
3	A	406	GOL	O1-C1-C2-C3
2	B	402	PEG	O2-C3-C4-O4
3	A	407	GOL	O2-C2-C3-O3
2	B	401	PEG	O2-C3-C4-O4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	A	402	PEG	O1-C1-C2-O2
2	B	405	PEG	O1-C1-C2-O2
2	B	405	PEG	O2-C3-C4-O4
2	A	401	PEG	O2-C3-C4-O4
2	B	405	PEG	C1-C2-O2-C3
2	B	402	PEG	C4-C3-O2-C2
3	A	407	GOL	O1-C1-C2-C3
2	A	403	PEG	O2-C3-C4-O4
2	B	404	PEG	C4-C3-O2-C2
2	A	403	PEG	C1-C2-O2-C3
2	B	402	PEG	C1-C2-O2-C3
2	A	402	PEG	C1-C2-O2-C3
2	B	401	PEG	O1-C1-C2-O2
2	A	405	PEG	O1-C1-C2-O2
3	A	406	GOL	O2-C2-C3-O3
2	A	402	PEG	O2-C3-C4-O4
3	A	407	GOL	O1-C1-C2-O2

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	404	PEG	1	0
3	B	408	GOL	1	0
3	A	408	GOL	1	0
3	A	409	GOL	2	0
2	A	401	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

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, 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	315/329 (95%)	0.00	26 (8%) 11 14	15, 23, 64, 142	0
1	B	315/329 (95%)	0.18	21 (6%) 17 22	14, 23, 68, 143	0
All	All	630/658 (95%)	0.09	47 (7%) 14 18	14, 23, 66, 143	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	209	PHE	16.3
1	B	31	VAL	15.2
1	B	20	GLY	12.5
1	A	210	LEU	11.5
1	B	29	HIS	11.3
1	A	208	TYR	10.9
1	B	22	PRO	10.7
1	B	30	ALA	10.2
1	B	24	LEU	9.4
1	B	27	LEU	9.4
1	B	19	GLY	8.8
1	B	26	THR	8.6
1	B	25	ASP	8.4
1	B	17	THR	7.9
1	A	207	GLY	6.7
1	B	23	GLY	6.6
1	B	21	ARG	6.6
1	B	18	ARG	6.2
1	A	212	LYS	5.7
1	A	211	SER	5.7
1	A	22	PRO	5.7
1	B	28	PRO	5.0
1	A	215	MET	5.0
1	A	205	ALA	4.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	206	GLU	4.1
1	B	15	ALA	4.0
1	A	214	HIS	3.9
1	A	204	PHE	3.6
1	A	17	THR	3.5
1	A	1	MET	3.5
1	A	21	ARG	3.4
1	A	25	ASP	3.2
1	A	203	ALA	2.9
1	A	202	VAL	2.9
1	B	226	ASP	2.9
1	A	14	ASP	2.8
1	A	19	GLY	2.8
1	B	214	HIS	2.6
1	B	217	TRP	2.5
1	B	224	PRO	2.4
1	A	18	ARG	2.3
1	B	14	ASP	2.3
1	A	23	GLY	2.3
1	A	255	TYR	2.2
1	A	11	ASP	2.1
1	A	26	THR	2.1
1	A	24	LEU	2.1

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.

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	PEG	B	405	7/7	0.73	0.24	50,54,60,61	0
2	PEG	A	402	7/7	0.74	0.21	53,58,64,64	0
2	PEG	B	404	7/7	0.75	0.18	44,47,52,52	0
2	PEG	A	404	7/7	0.75	0.17	50,55,56,60	0
3	GOL	A	410	6/6	0.78	0.15	60,64,66,68	0
3	GOL	B	406	6/6	0.79	0.26	31,36,41,42	0
3	GOL	A	407	6/6	0.81	0.20	52,53,56,64	0
2	PEG	B	403	7/7	0.82	0.17	56,58,63,64	0
2	PEG	A	405	7/7	0.82	0.17	52,53,55,55	0
2	PEG	B	401	7/7	0.82	0.17	59,59,60,60	0
3	GOL	A	411	6/6	0.83	0.20	58,61,65,67	0
2	PEG	B	402	7/7	0.83	0.23	39,40,42,42	0
3	GOL	B	409	6/6	0.84	0.15	53,60,61,66	0
3	GOL	A	408	6/6	0.86	0.15	48,56,56,61	0
3	GOL	A	409	6/6	0.86	0.17	49,55,57,59	0
2	PEG	A	403	7/7	0.87	0.12	52,53,59,60	0
3	GOL	B	408	6/6	0.90	0.26	53,56,58,62	0
3	GOL	A	406	6/6	0.90	0.19	28,33,35,43	0
3	GOL	B	407	6/6	0.91	0.17	32,37,41,48	0
2	PEG	A	401	7/7	0.94	0.14	41,41,47,50	0
4	MG	B	410	1/1	0.94	0.09	20,20,20,20	0
4	MG	A	412	1/1	0.95	0.12	21,21,21,21	0

6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.