



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 03:15 AM UTC

PDB ID : 4JAM / pdb_00004jam
Title : Crystal structure of broadly neutralizing anti-hiv-1 antibody ch103
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Deposited on : 2013-02-18
Resolution : 1.65 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 ⓘ 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

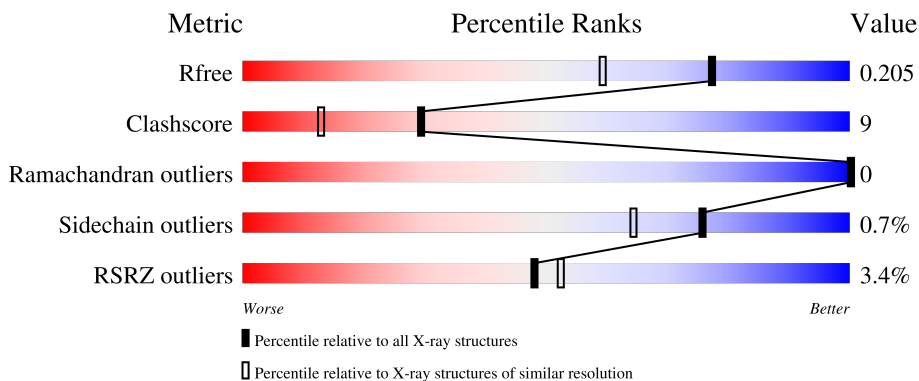
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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}	180053	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

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	226	 6% 82% 14% .
1	H	226	 6% 86% 12% ..
2	B	209	 89% 10% .
2	L	209	 86% 12% .

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 13687 atoms, of which 6390 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.

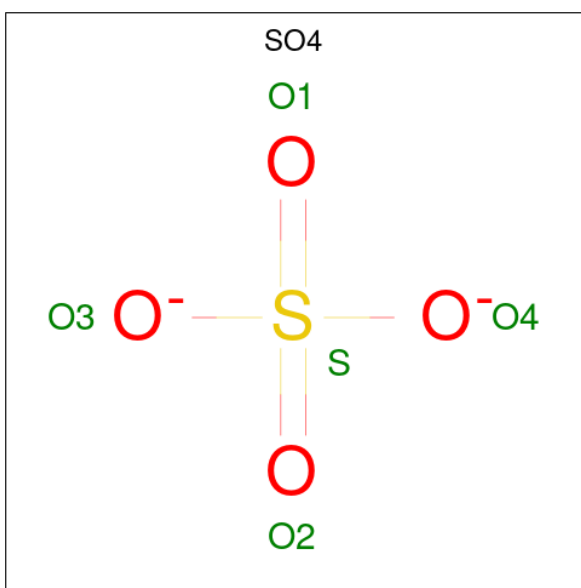
- Molecule 1 is a protein called ANTIGEN BINDING FRAGMENT OF HEAVY CHAIN of CH103.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	H	223	Total 3313	C 1051	H 1649	N 282	O 326	S 5	0	1	0
1	A	219	Total 3260	C 1035	H 1624	N 278	O 319	S 4	0	1	0

- Molecule 2 is a protein called ANTIGEN BINDING FRAGMENT OF LIGHT CHAIN of CH103.

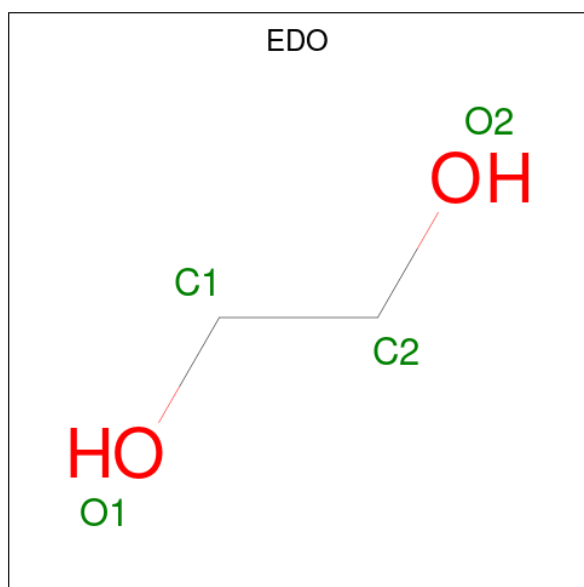
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
2	L	206	Total 3074	C 983	H 1511	N 258	O 317	S 5	0	0	0
2	B	205	Total 3100	C 989	H 1526	N 260	O 319	S 6	0	5	0

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	H	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	181	Total	O	0	0
			181	181		
6	L	153	Total	O	0	0
			153	153		
6	A	162	Total	O	0	0
			162	162		
6	B	230	Total	O	0	0
			230	230		

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	43.03Å 146.38Å 66.32Å 90.00° 97.71° 90.00°	Depositor
Resolution (Å)	38.19 – 1.65 38.19 – 1.65	Depositor EDS
% Data completeness (in resolution range)	98.0 (38.19-1.65) 98.1 (38.19-1.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 1.65Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.169 , 0.197 (Not available) , 0.205	Depositor DCC
R_{free} test set	4774 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	22.3	Xtrriage
Anisotropy	0.132	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 47.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	13687	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.87% 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: GOL, SO4, EDO

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	0.43	0/1678	0.77	1/2287 (0.0%)
1	H	0.45	0/1708	0.73	0/2329
2	B	0.48	0/1629	0.71	0/2230
2	L	0.42	0/1604	0.69	0/2196
All	All	0.44	0/6619	0.73	1/9042 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	102	ASN	N-CA-C	6.32	118.20	109.54

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	1636	1624	1622	31	0
1	H	1664	1649	1647	37	0
2	B	1574	1526	1534	19	0
2	L	1563	1511	1509	25	1
3	A	15	0	0	2	0
3	B	30	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	30	0	0	2	0
3	L	5	0	0	1	0
4	A	16	24	24	3	0
4	B	8	12	12	0	0
4	H	20	30	30	5	0
4	L	4	6	6	0	0
5	H	6	8	8	0	0
6	A	162	0	0	14	2
6	B	230	0	0	10	4
6	H	181	0	0	12	5
6	L	153	0	0	10	0
All	All	7297	6390	6392	112	6

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 112 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:82(A):ARG:NH1	6:A:510:HOH:O	1.67	1.25
1:A:148:GLU:OE2	6:A:423:HOH:O	1.73	1.07
2:L:12:SER:OG	2:L:110:LYS:NZ	1.96	0.98
2:L:156:LYS:NZ	6:L:501:HOH:O	2.00	0.93
2:B:4:LEU:O	6:B:628:HOH:O	1.90	0.90

The worst 5 of 6 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)
6:H:560:HOH:O	6:A:525:HOH:O[1_454]	1.96	0.24
6:H:514:HOH:O	6:B:618:HOH:O[2_546]	1.97	0.23
6:H:514:HOH:O	6:B:627:HOH:O[2_546]	1.98	0.22
2:L:123:GLU:OE2	6:A:410:HOH:O[1_454]	2.09	0.11
6:H:578:HOH:O	6:B:624:HOH:O[2_546]	2.15	0.05

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	216/226 (96%)	211 (98%)	5 (2%)	0	100	100
1	H	222/226 (98%)	217 (98%)	5 (2%)	0	100	100
2	B	208/209 (100%)	201 (97%)	7 (3%)	0	100	100
2	L	204/209 (98%)	199 (98%)	5 (2%)	0	100	100
All	All	850/870 (98%)	828 (97%)	22 (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	186/192 (97%)	183 (98%)	3 (2%)	55	34
1	H	190/192 (99%)	188 (99%)	2 (1%)	65	48
2	B	183/182 (100%)	183 (100%)	0	100	100
2	L	179/182 (98%)	179 (100%)	0	100	100
All	All	738/748 (99%)	733 (99%)	5 (1%)	76	64

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	14	SER
1	H	43	LYS

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Mol	Chain	Res	Type
1	A	66	ARG
1	A	110	SER
1	A	128	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	L	112	ASN
2	L	167	GLN
1	A	164	HIS

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](#)

29 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	$\# Z > 2$
3	SO4	H	302	-	4,4,4	0.24	0	6,6,6	0.17	0
3	SO4	L	301	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	H	304	-	4,4,4	0.22	0	6,6,6	0.14	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	A	307	-	3,3,3	0.42	0	2,2,2	0.29	0
3	SO4	A	302	-	4,4,4	0.24	0	6,6,6	0.12	0
4	EDO	H	308	-	3,3,3	0.40	0	2,2,2	0.40	0
4	EDO	H	310	-	3,3,3	0.40	0	2,2,2	0.33	0
4	EDO	B	308	-	3,3,3	0.43	0	2,2,2	0.33	0
4	EDO	H	311	-	3,3,3	0.44	0	2,2,2	0.32	0
3	SO4	A	301	-	4,4,4	0.25	0	6,6,6	0.22	0
4	EDO	A	305	-	3,3,3	0.36	0	2,2,2	0.53	0
3	SO4	H	305	-	4,4,4	0.23	0	6,6,6	0.12	0
4	EDO	H	307	-	3,3,3	0.40	0	2,2,2	0.49	0
5	GOL	H	312	-	5,5,5	0.43	0	5,5,5	0.45	0
3	SO4	H	303	-	4,4,4	0.24	0	6,6,6	0.16	0
3	SO4	A	303	-	4,4,4	0.29	0	6,6,6	0.11	0
3	SO4	B	305	-	4,4,4	0.22	0	6,6,6	0.10	0
4	EDO	A	306	-	3,3,3	0.43	0	2,2,2	0.42	0
3	SO4	B	306	-	4,4,4	0.25	0	6,6,6	0.09	0
4	EDO	H	309	-	3,3,3	0.41	0	2,2,2	0.37	0
3	SO4	B	303	-	4,4,4	0.23	0	6,6,6	0.07	0
3	SO4	B	304	-	4,4,4	0.32	0	6,6,6	0.29	0
3	SO4	B	301	-	4,4,4	0.25	0	6,6,6	0.07	0
4	EDO	B	307	-	3,3,3	0.43	0	2,2,2	0.30	0
4	EDO	L	302	-	3,3,3	0.40	0	2,2,2	0.41	0
3	SO4	B	302	-	4,4,4	0.25	0	6,6,6	0.10	0
4	EDO	A	304	-	3,3,3	0.44	0	2,2,2	0.42	0
3	SO4	H	306	-	4,4,4	0.23	0	6,6,6	0.11	0
3	SO4	H	301	-	4,4,4	0.22	0	6,6,6	0.10	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
4	EDO	B	308	-	-	0/1/1/1	-
4	EDO	H	309	-	-	1/1/1/1	-
4	EDO	A	305	-	-	0/1/1/1	-
4	EDO	H	307	-	-	0/1/1/1	-
5	GOL	H	312	-	-	0/4/4/4	-
4	EDO	B	307	-	-	1/1/1/1	-
4	EDO	L	302	-	-	0/1/1/1	-
4	EDO	A	307	-	-	0/1/1/1	-
4	EDO	A	306	-	-	0/1/1/1	-
4	EDO	A	304	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	H	308	-	-	1/1/1/1	-
4	EDO	H	310	-	-	0/1/1/1	-
4	EDO	H	311	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	309	EDO	O1-C1-C2-O2
4	B	307	EDO	O1-C1-C2-O2
4	H	308	EDO	O1-C1-C2-O2
4	A	304	EDO	O1-C1-C2-O2

There are no ring outliers.

12 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	302	SO4	1	0
3	L	301	SO4	1	0
4	A	307	EDO	1	0
3	A	302	SO4	1	0
4	H	311	EDO	2	0
3	A	301	SO4	1	0
4	A	305	EDO	1	0
4	H	307	EDO	2	0
3	H	303	SO4	1	0
4	A	306	EDO	1	0
4	H	309	EDO	1	0
3	B	301	SO4	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	219/226 (96%)	0.31	13 (5%) 28 32	11, 30, 61, 76	1 (0%)
1	H	223/226 (98%)	0.06	13 (5%) 29 32	11, 26, 56, 77	1 (0%)
2	B	205/209 (98%)	-0.40	1 (0%) 87 91	8, 19, 36, 65	5 (2%)
2	L	206/209 (98%)	-0.21	2 (0%) 79 84	13, 25, 44, 69	0
All	All	853/870 (98%)	-0.05	29 (3%) 48 52	8, 25, 55, 77	7 (0%)

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	190	GLY	5.1
1	A	27	GLY	4.4
1	A	113	ALA	3.7
1	A	112	THR	3.2
2	B	209	THR	3.1

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 oligosaccharides 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(\AA^2)	Q<0.9
4	EDO	B	307	4/4	0.70	0.19	41,49,58,59	0
4	EDO	H	309	4/4	0.76	0.15	47,56,63,63	0
3	SO4	B	306	5/5	0.78	0.12	67,69,73,77	0
4	EDO	A	306	4/4	0.79	0.13	35,43,45,51	0
4	EDO	A	307	4/4	0.81	0.12	42,51,56,56	0
3	SO4	H	306	5/5	0.81	0.11	59,66,71,71	0
3	SO4	H	301	5/5	0.82	0.11	52,59,63,67	0
4	EDO	B	308	4/4	0.85	0.12	34,41,56,66	0
3	SO4	B	303	5/5	0.86	0.10	50,66,68,77	0
4	EDO	H	307	4/4	0.87	0.13	25,30,33,34	0
3	SO4	B	305	5/5	0.87	0.10	57,64,72,74	0
3	SO4	A	303	5/5	0.87	0.09	31,52,59,61	0
3	SO4	H	305	5/5	0.88	0.10	54,58,62,66	0
4	EDO	H	310	4/4	0.89	0.12	24,38,45,45	0
4	EDO	L	302	4/4	0.89	0.13	27,33,54,64	0
4	EDO	H	308	4/4	0.90	0.11	39,47,51,56	0
3	SO4	L	301	5/5	0.91	0.07	71,76,78,80	0
3	SO4	B	302	5/5	0.92	0.10	43,45,51,52	0
3	SO4	A	302	5/5	0.92	0.07	39,44,48,56	0
4	EDO	H	311	4/4	0.92	0.07	25,30,34,34	0
3	SO4	H	304	5/5	0.92	0.11	47,51,53,57	0
5	GOL	H	312	6/6	0.92	0.14	16,25,36,36	0
4	EDO	A	304	4/4	0.94	0.06	24,31,39,41	0
3	SO4	A	301	5/5	0.94	0.08	33,33,40,50	0
3	SO4	H	303	5/5	0.95	0.07	35,36,44,49	0
3	SO4	H	302	5/5	0.95	0.07	33,33,34,45	0
3	SO4	B	304	5/5	0.95	0.10	21,23,26,29	0
3	SO4	B	301	5/5	0.95	0.08	31,33,35,38	0
4	EDO	A	305	4/4	0.95	0.06	18,22,27,33	0

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

There are no such residues in this entry.