



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 07:32 AM UTC

PDB ID : 4BFE / pdb_00004bfe
Title : Structure of the extracellular portion of mouse CD200RLa
Authors : Hatherley, D.; Lea, S.M.; Johnson, S.; Barclay, A.N.
Deposited on : 2013-03-18
Resolution : 2.50 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (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

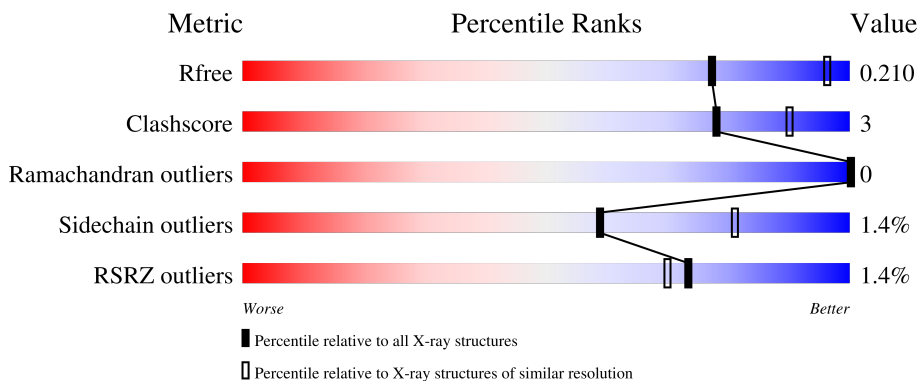
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	221	 76% 9% 15%
1	B	221	 80% 5% 15%
1	C	221	 76% 8% 15%

2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 5206 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 CELL SURFACE GLYCOPROTEIN CD200 RECEPTOR 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	188	1440	898	246	284	12	0	1	0
1	B	188	1435	893	246	284	12	0	0	0
1	C	187	1432	892	244	284	12	0	2	0

There are 24 discrepancies between the modelled and reference sequences:

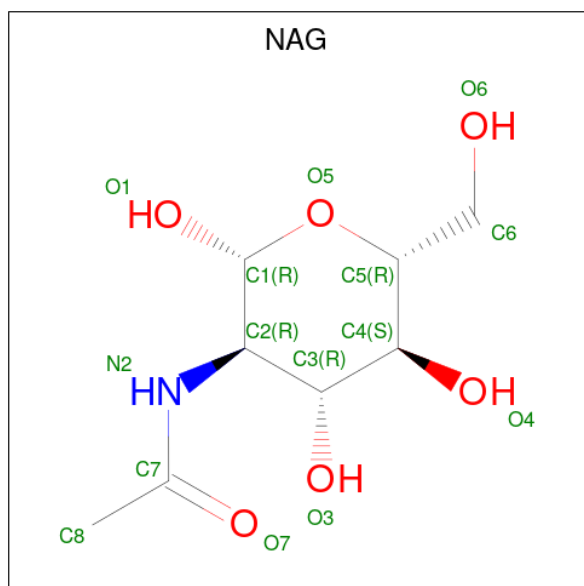
Chain	Residue	Modelled	Actual	Comment	Reference
A	215	THR	-	expression tag	UNP Q6XJV4
A	216	ARG	-	expression tag	UNP Q6XJV4
A	217	HIS	-	expression tag	UNP Q6XJV4
A	218	HIS	-	expression tag	UNP Q6XJV4
A	219	HIS	-	expression tag	UNP Q6XJV4
A	220	HIS	-	expression tag	UNP Q6XJV4
A	221	HIS	-	expression tag	UNP Q6XJV4
A	222	HIS	-	expression tag	UNP Q6XJV4
B	215	THR	-	expression tag	UNP Q6XJV4
B	216	ARG	-	expression tag	UNP Q6XJV4
B	217	HIS	-	expression tag	UNP Q6XJV4
B	218	HIS	-	expression tag	UNP Q6XJV4
B	219	HIS	-	expression tag	UNP Q6XJV4
B	220	HIS	-	expression tag	UNP Q6XJV4
B	221	HIS	-	expression tag	UNP Q6XJV4
B	222	HIS	-	expression tag	UNP Q6XJV4
C	215	THR	-	expression tag	UNP Q6XJV4
C	216	ARG	-	expression tag	UNP Q6XJV4
C	217	HIS	-	expression tag	UNP Q6XJV4
C	218	HIS	-	expression tag	UNP Q6XJV4
C	219	HIS	-	expression tag	UNP Q6XJV4
C	220	HIS	-	expression tag	UNP Q6XJV4
C	221	HIS	-	expression tag	UNP Q6XJV4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	222	HIS	-	expression tag	UNP Q6XJV4

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



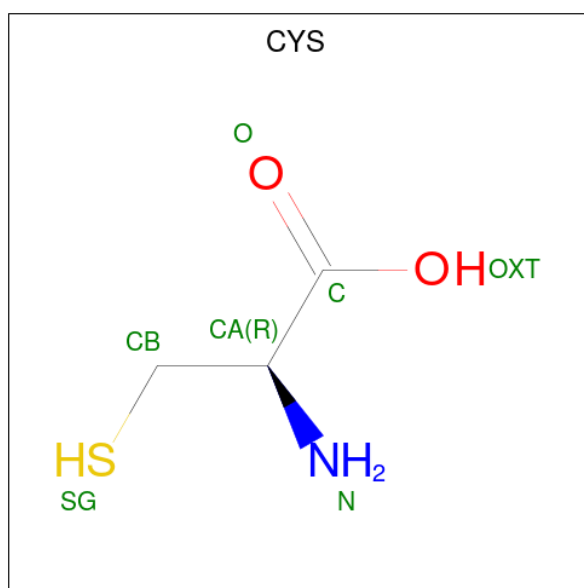
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is CYSTEINE (CCD ID: CYS) (formula: $C_3H_7NO_2S$).



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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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

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



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	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 water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	173	Total O 173 173	0	0
6	B	197	Total O 197 197	0	0
6	C	245	Total O 245 245	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	157.59Å 157.59Å 167.94Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	15.00 – 2.50 15.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.5 (15.00-2.50) 96.9 (15.00-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 2.51Å)	Xtrriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.171 , 0.205 0.176 , 0.210	Depositor DCC
R_{free} test set	2127 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	43.3	Xtrriage
Anisotropy	0.172	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 62.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5206	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.10% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, GOL, NAG

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	0.87	0/1473	1.11	2/2013 (0.1%)
1	B	0.85	0/1465	1.13	2/2002 (0.1%)
1	C	0.92	0/1468	1.15	5/2006 (0.2%)
All	All	0.88	0/4406	1.13	9/6021 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	65	ASP	CA-CB-CG	6.65	119.25	112.60
1	A	19	VAL	N-CA-CB	6.28	117.79	110.82
1	C	41	ILE	CA-C-N	-5.60	114.52	122.41
1	C	41	ILE	C-N-CA	-5.60	114.52	122.41
1	B	19	VAL	N-CA-CB	5.44	117.00	110.31
1	C	156	ASP	CA-CB-CG	5.20	117.80	112.60
1	C	131	PHE	N-CA-C	5.18	114.80	108.11
1	C	60	ILE	N-CA-CB	5.15	119.04	111.52
1	A	156	ASP	CA-CB-CG	5.02	117.62	112.60

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	1440	0	1410	11	0
1	B	1435	0	1399	6	0
1	C	1432	0	1401	7	0
2	A	70	0	65	0	0
2	B	70	0	65	0	0
2	C	70	0	65	0	0
3	A	7	0	3	1	0
3	B	7	0	3	0	0
3	C	7	0	3	2	0
4	A	10	0	0	0	0
4	B	15	0	0	1	0
4	C	10	0	0	0	0
5	C	18	0	24	1	0
6	A	173	0	0	1	0
6	B	197	0	0	0	0
6	C	245	0	0	1	0
All	All	5206	0	4438	25	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 3.

All (25) 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:76:ARG:HD2	6:A:2043:HOH:O	2.02	0.59
1:C:177:CYS:HB2	1:C:179:TRP:CH2	2.40	0.57
5:C:1209:GOL:H11	6:C:2223:HOH:O	2.07	0.53
1:C:35:CYS:HB3	1:C:88:PRO:HG2	1.91	0.52
1:A:177:CYS:HB2	1:A:179:TRP:CH2	2.45	0.52
1:A:153:TRP:CD1	1:A:177:CYS:SG	3.03	0.51
1:A:87:SER:HB3	3:A:1206:CYS:HB2	1.93	0.51
1:A:35:CYS:HB3	1:A:88:PRO:HG2	1.93	0.50
1:B:35:CYS:HB3	1:B:88:PRO:HG2	1.92	0.50
1:A:44:VAL:HG23	1:A:45[B]:LEU:HG	1.94	0.50
1:B:136:ARG:NH2	1:B:181:GLN:O	2.44	0.50
1:B:46:ILE:HD12	1:B:64:LEU:HD11	1.97	0.46
1:C:87:SER:HB3	3:C:1206:CYS:HB2	1.97	0.46
1:C:37:SER:HB2	3:C:1206:CYS:HB3	1.99	0.45
1:C:46:ILE:HD12	1:C:64:LEU:HD11	1.97	0.45
1:A:46:ILE:HD12	1:A:64:LEU:HD11	1.98	0.45
1:A:35:CYS:SG	1:A:107:ILE:HD11	2.58	0.44
1:A:153:TRP:NE1	1:A:177:CYS:SG	2.92	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:79:THR:HB	4:B:1208:SO4:O4	2.20	0.42
1:B:35:CYS:SG	1:B:107:ILE:HD11	2.60	0.41
1:A:62:TYR:CD2	1:A:69:ASN:HB3	2.56	0.41
1:B:46:ILE:HD13	1:B:88:PRO:HG3	2.02	0.41
1:C:50:ILE:HG12	1:C:103:TYR:CD2	2.56	0.40
1:C:35:CYS:SG	1:C:107:ILE:HD11	2.60	0.40
1:A:50:ILE:HG12	1:A:103:TYR:CD2	2.57	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	187/221 (85%)	183 (98%)	4 (2%)	0	100	100
1	B	186/221 (84%)	184 (99%)	2 (1%)	0	100	100
1	C	187/221 (85%)	183 (98%)	4 (2%)	0	100	100
All	All	560/663 (84%)	550 (98%)	10 (2%)	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	170/201 (85%)	169 (99%)	1 (1%)	78	91
1	B	169/201 (84%)	168 (99%)	1 (1%)	78	91
1	C	170/201 (85%)	167 (98%)	3 (2%)	51	77
All	All	509/603 (84%)	504 (99%)	5 (1%)	59	86

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

Mol	Chain	Res	Type
1	A	180	GLU
1	B	159	CYS
1	C	27	MET
1	C	165	SER
1	C	180	GLU

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	98	GLN
1	A	182	ASN
1	B	178	HIS
1	C	54	HIS
1	C	178	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](#)

28 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
5	GOL	C	1211	-	5,5,5	0.10	0	5,5,5	0.37	0
2	NAG	A	1970	1	14,14,15	0.31	0	17,19,21	0.64	0
4	SO4	B	1209	-	4,4,4	0.29	0	6,6,6	0.10	0
2	NAG	A	1680	1	14,14,15	0.31	0	17,19,21	0.94	1 (5%)
2	NAG	A	770	1	14,14,15	0.29	0	17,19,21	0.58	0
3	CYS	A	1206	1	5,6,6	0.99	0	3,7,7	0.65	0
2	NAG	B	1680	1	14,14,15	0.32	0	17,19,21	1.00	1 (5%)
2	NAG	C	770	1	14,14,15	0.48	0	17,19,21	1.32	2 (11%)
2	NAG	B	690	1	14,14,15	0.40	0	17,19,21	1.23	2 (11%)
2	NAG	A	2000	1	14,14,15	0.32	0	17,19,21	0.43	0
4	SO4	B	1208	-	4,4,4	0.55	0	6,6,6	0.37	0
3	CYS	C	1206	1	5,6,6	1.03	0	3,7,7	1.41	1 (33%)
4	SO4	B	1207	-	4,4,4	0.36	0	6,6,6	0.25	0
5	GOL	C	1209	-	5,5,5	0.06	0	5,5,5	0.13	0
2	NAG	B	1970	1	14,14,15	0.32	0	17,19,21	0.66	0
2	NAG	C	2000	1	14,14,15	0.30	0	17,19,21	0.46	0
5	GOL	C	1210	-	5,5,5	0.10	0	5,5,5	0.27	0
3	CYS	B	1206	1	5,6,6	0.95	0	3,7,7	0.83	0
2	NAG	B	770	1	14,14,15	0.32	0	17,19,21	0.73	1 (5%)
4	SO4	A	1208	-	4,4,4	0.23	0	6,6,6	0.13	0
2	NAG	A	690	1	14,14,15	0.40	0	17,19,21	1.13	2 (11%)
2	NAG	B	2000	1	14,14,15	0.30	0	17,19,21	0.48	0
4	SO4	C	1208	-	4,4,4	0.26	0	6,6,6	0.17	0
2	NAG	C	1680	1	14,14,15	0.42	0	17,19,21	0.70	1 (5%)
2	NAG	C	690	1	14,14,15	0.32	0	17,19,21	0.94	1 (5%)
4	SO4	A	1207	-	4,4,4	0.39	0	6,6,6	0.24	0
4	SO4	C	1207	-	4,4,4	0.51	0	6,6,6	0.39	0
2	NAG	C	1970	1	14,14,15	0.34	0	17,19,21	0.59	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
5	GOL	C	1211	-	-	1/4/4/4	-
2	NAG	A	1970	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1680	1	-	0/6/23/26	0/1/1/1
2	NAG	A	770	1	-	0/6/23/26	0/1/1/1
3	CYS	A	1206	1	-	2/6/6/6	-
2	NAG	B	1680	1	-	0/6/23/26	0/1/1/1
2	NAG	C	770	1	-	1/6/23/26	0/1/1/1
2	NAG	B	690	1	-	2/6/23/26	0/1/1/1
2	NAG	A	2000	1	-	0/6/23/26	0/1/1/1
3	CYS	C	1206	1	-	4/6/6/6	-
5	GOL	C	1209	-	-	0/4/4/4	-
2	NAG	B	1970	1	-	0/6/23/26	0/1/1/1
2	NAG	C	2000	1	-	0/6/23/26	0/1/1/1
5	GOL	C	1210	-	-	3/4/4/4	-
3	CYS	B	1206	1	-	4/6/6/6	-
2	NAG	B	770	1	-	1/6/23/26	0/1/1/1
2	NAG	A	690	1	-	2/6/23/26	0/1/1/1
2	NAG	B	2000	1	-	0/6/23/26	0/1/1/1
2	NAG	C	1680	1	-	0/6/23/26	0/1/1/1
2	NAG	C	690	1	-	0/6/23/26	0/1/1/1
2	NAG	C	1970	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	770	NAG	C1-C2-N2	4.20	117.04	110.43
2	B	690	NAG	C1-C2-N2	-3.35	105.15	110.43
2	B	1680	NAG	C1-C2-N2	-3.35	105.16	110.43
2	A	1680	NAG	C1-C2-N2	-3.11	105.53	110.43
2	A	690	NAG	O5-C1-C2	3.09	116.08	111.29
2	B	690	NAG	O5-C1-C2	3.00	115.93	111.29
2	C	770	NAG	C2-N2-C7	2.52	126.28	122.90
2	B	770	NAG	C1-O5-C5	2.47	115.49	112.19
2	A	690	NAG	C1-C2-N2	-2.34	106.75	110.43
3	C	1206	CYS	CB-CA-C	2.11	112.00	109.89
2	C	1680	NAG	C1-C2-N2	-2.10	107.13	110.43
2	C	690	NAG	C1-O5-C5	2.02	114.90	112.19

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	770	NAG	C1-C2-N2-C7
3	A	1206	CYS	N-CA-CB-SG
3	A	1206	CYS	C-CA-CB-SG
3	B	1206	CYS	N-CA-CB-SG
3	B	1206	CYS	C-CA-CB-SG
3	C	1206	CYS	O-C-CA-N
3	C	1206	CYS	N-CA-CB-SG
3	C	1206	CYS	C-CA-CB-SG
5	C	1210	GOL	O1-C1-C2-C3
3	B	1206	CYS	OXT-C-CA-N
3	C	1206	CYS	OXT-C-CA-N
5	C	1210	GOL	O1-C1-C2-O2
5	C	1210	GOL	O2-C2-C3-O3
2	B	690	NAG	C4-C5-C6-O6
3	B	1206	CYS	O-C-CA-N
2	A	690	NAG	C4-C5-C6-O6
2	B	690	NAG	O5-C5-C6-O6
2	A	690	NAG	O5-C5-C6-O6
5	C	1211	GOL	C1-C2-C3-O3
2	B	770	NAG	O5-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1206	CYS	1	0
4	B	1208	SO4	1	0
3	C	1206	CYS	2	0
5	C	1209	GOL	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	188/221 (85%)	-0.38	3 (1%) 70 67	23, 43, 71, 106	1 (0%)
1	B	188/221 (85%)	-0.36	3 (1%) 70 67	27, 44, 74, 108	0
1	C	187/221 (84%)	-0.62	2 (1%) 78 75	19, 35, 69, 103	2 (1%)
All	All	563/663 (84%)	-0.45	8 (1%) 73 70	19, 41, 72, 108	3 (0%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	19	VAL	3.0
1	A	19	VAL	2.6
1	C	181	GLN	2.6
1	A	205	SER	2.5
1	B	18	GLN	2.3
1	A	86	HIS	2.3
1	C	42	ASN	2.1
1	B	86	HIS	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 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(Å ²)	Q<0.9
4	SO4	A	1208	5/5	0.59	0.18	144,145,145,146	0
4	SO4	C	1208	5/5	0.65	0.18	134,134,134,135	0
4	SO4	B	1209	5/5	0.66	0.16	165,165,165,166	0
2	NAG	B	690	14/15	0.71	0.21	97,106,109,110	0
2	NAG	A	2000	14/15	0.71	0.15	96,101,104,105	0
2	NAG	B	1970	14/15	0.72	0.14	65,75,80,82	0
2	NAG	A	770	14/15	0.72	0.17	103,108,110,111	0
2	NAG	C	770	14/15	0.73	0.20	77,84,90,91	0
2	NAG	A	690	14/15	0.73	0.15	72,92,95,96	0
5	GOL	C	1210	6/6	0.73	0.26	82,88,90,93	0
4	SO4	B	1208	5/5	0.76	0.27	125,127,128,129	0
2	NAG	A	1970	14/15	0.76	0.14	63,77,81,83	0
5	GOL	C	1209	6/6	0.77	0.23	74,80,83,84	0
2	NAG	B	2000	14/15	0.77	0.13	95,103,109,109	0
2	NAG	C	2000	14/15	0.79	0.13	112,114,116,117	0
2	NAG	B	770	14/15	0.82	0.14	90,95,101,102	0
4	SO4	B	1207	5/5	0.83	0.14	101,102,102,105	0
2	NAG	C	1970	14/15	0.83	0.10	62,74,87,89	0
5	GOL	C	1211	6/6	0.83	0.15	69,71,75,81	0
2	NAG	C	690	14/15	0.86	0.12	72,77,83,88	0
2	NAG	A	1680	14/15	0.87	0.12	50,55,65,70	0
3	CYS	C	1206	7/7	0.90	0.16	50,53,99,115	0
2	NAG	B	1680	14/15	0.91	0.10	48,54,63,65	0
4	SO4	A	1207	5/5	0.92	0.11	84,85,88,90	0
4	SO4	C	1207	5/5	0.92	0.17	72,81,84,87	0
3	CYS	A	1206	7/7	0.92	0.13	50,53,86,106	0
3	CYS	B	1206	7/7	0.93	0.12	57,59,89,115	0
2	NAG	C	1680	14/15	0.98	0.05	21,25,29,32	0

6.5 Other polymers

There are no such residues in this entry.