



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 10:32 AM GMT

PDB ID : 3V83
Title : The 2.1 angstrom crystal structure of diferric human transferrin
Authors : Noinaj, N.; Steere, A.; Mason, A.B.; Buchanan, S.K.
Deposited on : 2011-12-22
Resolution : 2.10 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

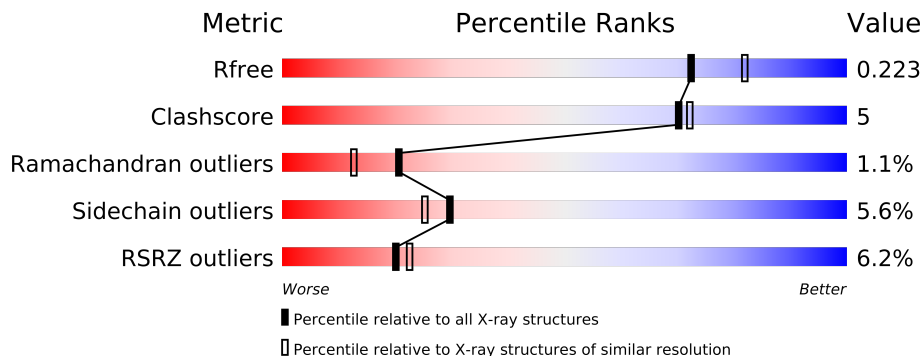
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.10 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}	66092	3012 (2.10-2.10)
Clashscore	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)
RSRZ outliers	66119	3013 (2.10-2.10)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	698	
1	B	698	
1	C	698	
1	D	698	
1	E	698	
1	F	698	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	BCT	D	702	-	X
2	BCT	E	702	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
2	BCT	F	702	-	X
3	FE	A	703	-	X
3	FE	B	704	-	X
3	FE	C	704	-	X
3	FE	D	703	-	X
3	FE	D	704	-	X
3	FE	E	703	-	X
3	FE	F	703	-	X
3	FE	F	704	-	X
4	SO4	A	705	-	X
4	SO4	A	706	-	X
4	SO4	A	707	-	X
4	SO4	A	708	-	X
4	SO4	B	711	-	X
4	SO4	C	705	-	X
4	SO4	C	711	-	X
4	SO4	D	712	-	X
4	SO4	E	706	-	X
4	SO4	E	711	-	X
4	SO4	F	706	-	X
4	SO4	F	709	-	X
5	P6G	A	710	-	X
5	P6G	A	711	-	X
5	P6G	B	714	-	X
5	P6G	B	715	-	X
5	P6G	C	712	-	X
5	P6G	D	714	-	X
5	P6G	D	715	-	X
5	P6G	E	714	-	X
5	P6G	E	715	-	X
5	P6G	F	710	-	X
5	P6G	F	711	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 33928 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

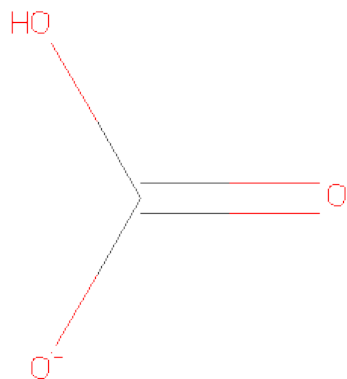
- Molecule 1 is a protein called Serotransferrin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	674	Total	C	N	O	S	0	0	0
			5160	3247	892	974	47			
1	B	677	Total	C	N	O	S	0	0	0
			5179	3260	898	974	47			
1	C	674	Total	C	N	O	S	0	0	0
			5124	3221	888	968	47			
1	D	675	Total	C	N	O	S	0	0	0
			5193	3263	897	986	47			
1	E	674	Total	C	N	O	S	0	0	0
			5202	3267	898	990	47			
1	F	676	Total	C	N	O	S	0	0	0
			5191	3263	900	981	47			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	429	VAL	ILE	VARIANT	UNP P02787
B	429	VAL	ILE	VARIANT	UNP P02787
C	429	VAL	ILE	VARIANT	UNP P02787
D	429	VAL	ILE	VARIANT	UNP P02787
E	429	VAL	ILE	VARIANT	UNP P02787
F	429	VAL	ILE	VARIANT	UNP P02787

- Molecule 2 is BICARBONATE ION (three-letter code: BCT) (formula: CHO_3).

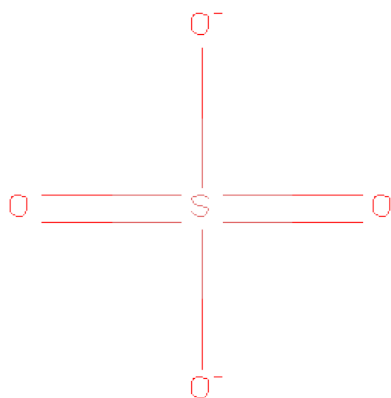


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	1	3		
2	A	1	Total	C	O	0	0
			4	1	3		
2	B	1	Total	C	O	0	0
			4	1	3		
2	B	1	Total	C	O	0	0
			4	1	3		
2	C	1	Total	C	O	0	0
			4	1	3		
2	C	1	Total	C	O	0	0
			4	1	3		
2	D	1	Total	C	O	0	0
			4	1	3		
2	D	1	Total	C	O	0	0
			4	1	3		
2	E	1	Total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

- Molecule 3 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	2	Total Fe 2 2	0	0
3	E	2	Total Fe 2 2	0	0
3	B	2	Total Fe 2 2	0	0
3	C	2	Total Fe 2 2	0	0
3	A	2	Total Fe 2 2	0	0
3	F	2	Total Fe 2 2	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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	A	1	Total O S 5 4 1	0	0
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

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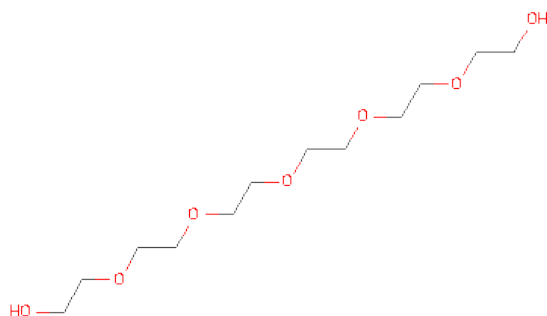
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	F	1	Total	O	S	0	0
			5	4	1		
4	F	1	Total	O	S	0	0
			5	4	1		
4	F	1	Total	O	S	0	0
			5	4	1		
4	F	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula: C₁₂H₂₆O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			19	12	7		
5	A	1	Total	C	O	0	0
			19	12	7		
5	A	1	Total	C	O	0	0
			19	12	7		
5	B	1	Total	C	O	0	0
			19	12	7		
5	B	1	Total	C	O	0	0
			19	12	7		
5	C	1	Total	C	O	0	0
			19	12	7		
5	C	1	Total	C	O	0	0
			19	12	7		
5	C	1	Total	C	O	0	0
			19	12	7		
5	D	1	Total	C	O	0	0
			19	12	7		
5	D	1	Total	C	O	0	0
			19	12	7		
5	E	1	Total	C	O	0	0
			19	12	7		
5	E	1	Total	C	O	0	0
			19	12	7		
5	F	1	Total	C	O	0	0
			19	12	7		
5	F	1	Total	C	O	0	0
			19	12	7		

- Molecule 6 is water.

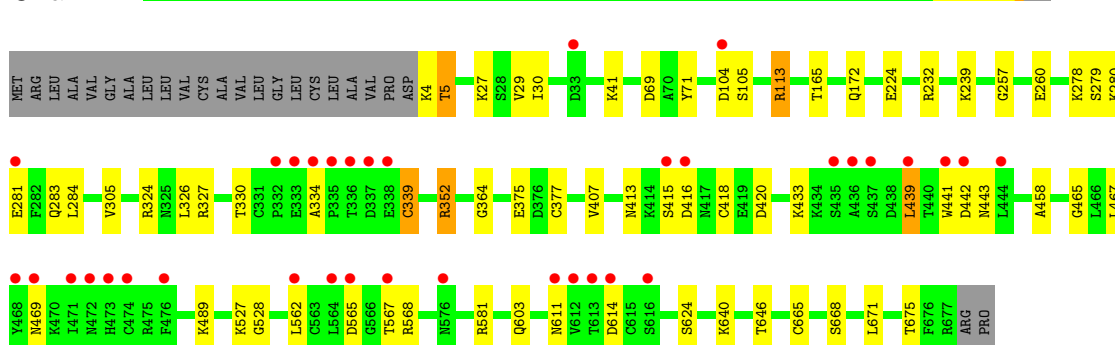
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	352	Total 352	O 352	0	0
6	B	454	Total 454	O 454	0	0
6	C	305	Total 305	O 305	0	0
6	D	398	Total 398	O 398	0	0
6	E	431	Total 431	O 431	0	0
6	F	393	Total 393	O 393	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

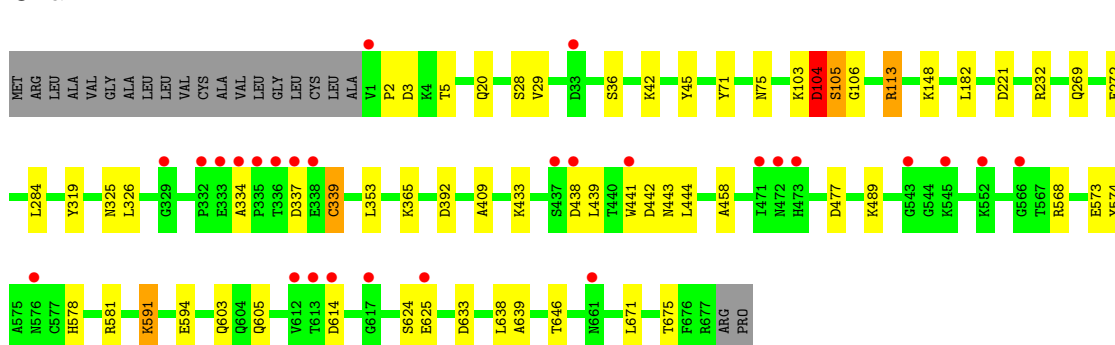
• Molecule 1: Serotransferrin

Chain A:



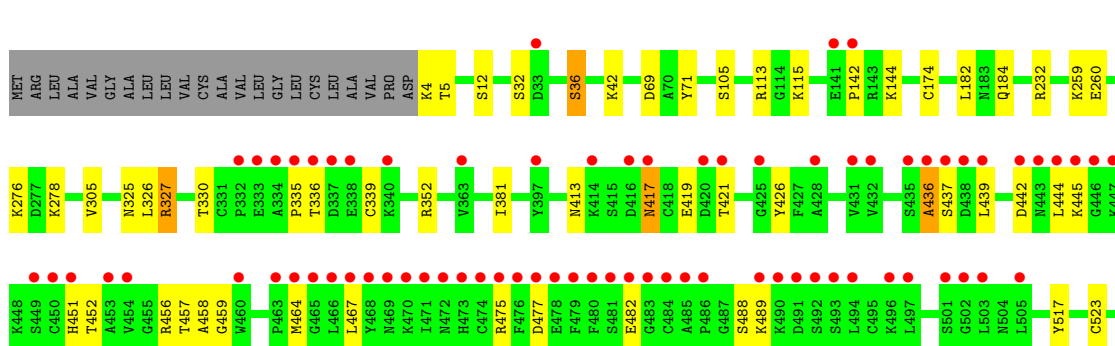
• Molecule 1: Serotransferrin

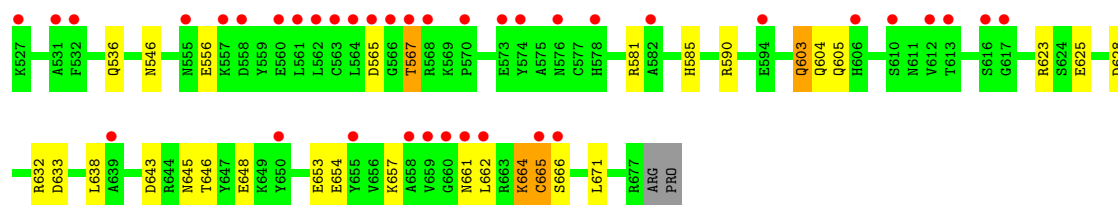
Chain B:



• Molecule 1: Serotransferrin

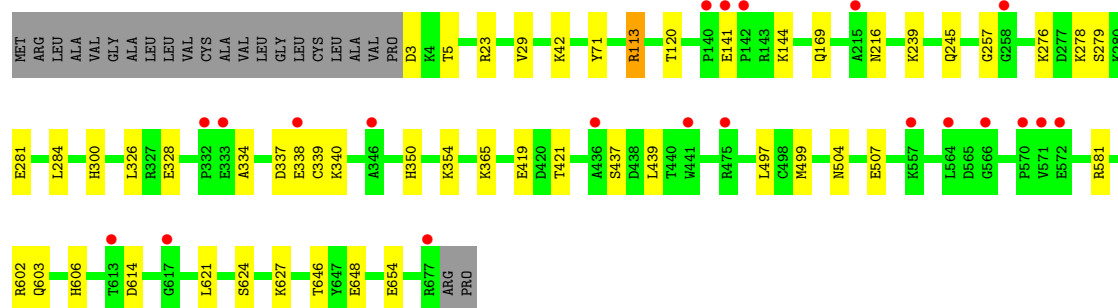
Chain C:





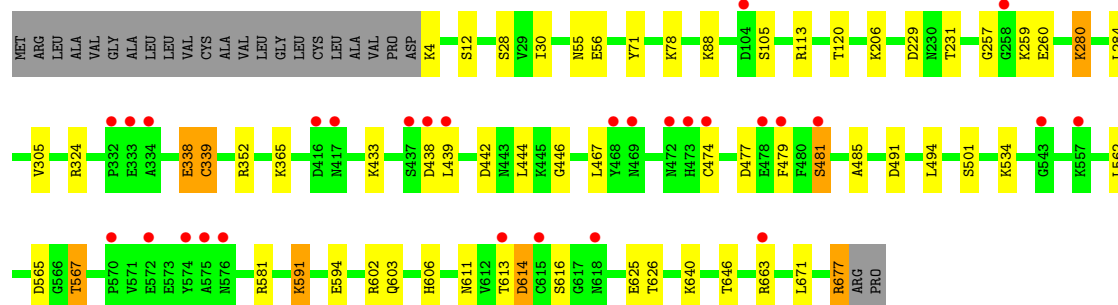
• Molecule 1: Serotransferrin

Chain D:



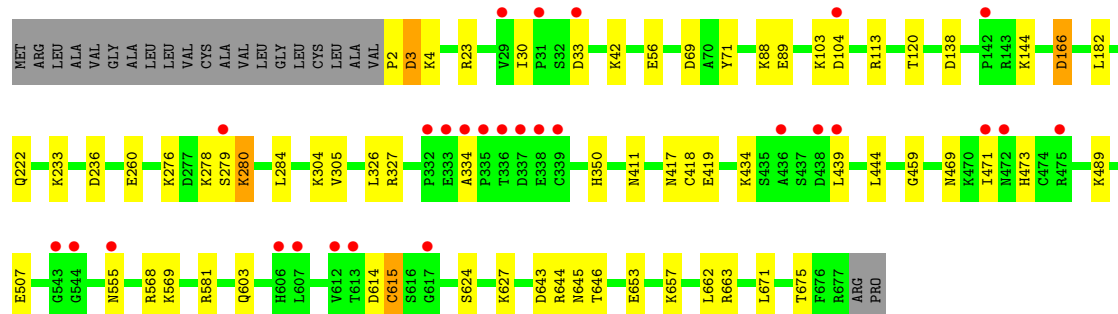
• Molecule 1: Serotransferrin

Chain E:



• Molecule 1: Serotransferrin

Chain F:



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	254.53Å 173.00Å 150.15Å 90.00° 123.26° 90.00°	Depositor
Resolution (Å)	29.95 – 2.10 49.25 – 2.10	Depositor EDS
% Data completeness (in resolution range)	94.4 (29.95-2.10) 94.4 (49.25-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 2.10Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.180 , 0.230 0.181 , 0.223	Depositor DCC
R_{free} test set	15028 reflections (5.06%)	DCC
Wilson B-factor (Å ²)	27.0	Xtriage
Anisotropy	0.250	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 46.2	EDS
Estimated twinning fraction	0.014 for -h-2*1,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 297219 reflections (0.000%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	33928	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.33% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BCT, FE, P6G, 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	0.38	0/5278	0.54	1/7144 (0.0%)
1	B	0.42	0/5298	0.57	2/7169 (0.0%)
1	C	0.39	0/5240	0.54	0/7097
1	D	0.41	0/5311	0.57	2/7184 (0.0%)
1	E	0.42	0/5320	0.57	2/7196 (0.0%)
1	F	0.40	0/5309	0.58	2/7183 (0.0%)
All	All	0.40	0/31756	0.56	9/42973 (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	D	0	2
1	E	0	2
All	All	0	4

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	113	ARG	NE-CZ-NH1	6.35	123.47	120.30
1	E	113	ARG	NE-CZ-NH1	6.23	123.41	120.30
1	D	113	ARG	NE-CZ-NH1	6.04	123.32	120.30
1	B	113	ARG	NE-CZ-NH2	-5.60	117.50	120.30
1	F	113	ARG	NE-CZ-NH2	-5.23	117.69	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	278	LYS	Peptide
1	D	279	SER	Peptide
1	E	613	THR	Peptide
1	E	614	ASP	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5160	0	144	21	0
1	B	5179	0	138	24	0
1	C	5124	0	144	38	0
1	D	5193	0	139	19	0
1	E	5202	0	144	21	0
1	F	5191	0	136	23	0
2	A	8	0	1	1	0
2	B	8	0	0	1	0
2	C	8	0	1	3	0
2	D	8	0	1	1	0
2	E	8	0	1	1	0
2	F	8	0	1	2	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
4	A	25	0	0	0	0
4	B	45	0	0	0	0
4	C	35	0	0	0	0
4	D	45	0	0	2	0
4	E	45	0	0	0	0
4	F	25	0	0	1	0
5	A	57	0	78	2	0
5	B	38	0	52	2	0
5	C	57	0	78	2	0
5	D	38	0	52	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	38	0	52	2	0
5	F	38	0	52	3	0
6	A	352	0	0	9	0
6	B	454	0	0	10	0
6	C	305	0	0	13	0
6	D	398	0	0	12	0
6	E	431	0	0	10	0
6	F	393	0	0	9	0
All	All	33928	0	1214	150	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

The worst 5 of 150 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:169:GLN:NE2	6:D:936:HOH:O	2.16	0.78
1:C:657:LYS:O	1:C:661:ASN:N	2.19	0.76
1:A:327:ARG:NH2	6:A:825:HOH:O	2.19	0.75
1:C:664:LYS:O	6:C:942:HOH:O	2.04	0.74
1:B:269:GLN:NE2	6:B:983:HOH:O	2.20	0.74

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	672/698 (96%)	621 (92%)	42 (6%)	9 (1%)	18 10
1	B	675/698 (97%)	630 (93%)	39 (6%)	6 (1%)	25 17
1	C	672/698 (96%)	617 (92%)	46 (7%)	9 (1%)	18 10
1	D	673/698 (96%)	630 (94%)	37 (6%)	6 (1%)	25 17
1	E	672/698 (96%)	632 (94%)	35 (5%)	5 (1%)	30 23
1	F	674/698 (97%)	623 (92%)	43 (6%)	8 (1%)	19 11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	4038/4188 (96%)	3753 (93%)	242 (6%)	43 (1%)	21	13

5 of 43 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	416	ASP
1	A	442	ASP
1	A	614	ASP
1	B	104	ASP
1	B	105	SER

5.3.2 Protein sidechains ⓘ

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	547/585 (94%)	514 (94%)	33 (6%)	27	22
1	B	547/585 (94%)	519 (95%)	28 (5%)	33	29
1	C	539/585 (92%)	503 (93%)	36 (7%)	23	18
1	D	555/585 (95%)	535 (96%)	20 (4%)	47	46
1	E	560/585 (96%)	525 (94%)	35 (6%)	25	21
1	F	553/585 (94%)	521 (94%)	32 (6%)	28	23
All	All	3301/3510 (94%)	3117 (94%)	184 (6%)	30	25

5 of 184 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	475	ARG
1	D	141	GLU
1	F	489	LYS
1	C	488	SER
1	C	646	THR

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

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 82 ligands modelled in this entry, 12 are monoatomic - leaving 70 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	BCT	A	701	3	0,3,3	0.00	-	0,3,3	0.00	-
2	BCT	A	702	3	0,3,3	0.00	-	0,3,3	0.00	-
4	SO4	A	705	-	4,4,4	0.17	0	6,6,6	0.10	0
4	SO4	A	706	-	4,4,4	0.07	0	6,6,6	0.22	0
4	SO4	A	707	-	4,4,4	0.17	0	6,6,6	0.18	0
4	SO4	A	708	-	4,4,4	0.25	0	6,6,6	0.10	0
4	SO4	A	709	-	4,4,4	0.20	0	6,6,6	0.10	0
5	P6G	A	710	-	18,18,18	0.70	0	17,17,17	1.45	0
5	P6G	A	711	-	18,18,18	0.65	0	17,17,17	1.50	0
5	P6G	A	712	-	18,18,18	0.70	0	17,17,17	1.43	0
2	BCT	B	701	3	0,3,3	0.00	-	0,3,3	0.00	-
2	BCT	B	702	3	0,3,3	0.00	-	0,3,3	0.00	-
4	SO4	B	705	-	4,4,4	0.26	0	6,6,6	0.28	0
4	SO4	B	706	-	4,4,4	0.18	0	6,6,6	0.16	0
4	SO4	B	707	-	4,4,4	0.20	0	6,6,6	0.09	0
4	SO4	B	708	-	4,4,4	0.09	0	6,6,6	0.24	0
4	SO4	B	709	-	4,4,4	0.21	0	6,6,6	0.21	0
4	SO4	B	710	-	4,4,4	0.16	0	6,6,6	0.16	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	B	711	-	4,4,4	0.23	0	6,6,6	0.10	0
4	SO4	B	712	-	4,4,4	0.14	0	6,6,6	0.06	0
4	SO4	B	713	-	4,4,4	0.18	0	6,6,6	0.14	0
5	P6G	B	714	-	18,18,18	0.73	0	17,17,17	1.25	1 (5%)
5	P6G	B	715	-	18,18,18	0.70	0	17,17,17	1.44	0
2	BCT	C	701	3	0,3,3	0.00	-	0,3,3	0.00	-
2	BCT	C	702	3	0,3,3	0.00	-	0,3,3	0.00	-
4	SO4	C	705	-	4,4,4	0.24	0	6,6,6	0.09	0
4	SO4	C	706	-	4,4,4	0.11	0	6,6,6	0.10	0
4	SO4	C	707	-	4,4,4	0.21	0	6,6,6	0.23	0
4	SO4	C	708	-	4,4,4	0.17	0	6,6,6	0.14	0
4	SO4	C	709	-	4,4,4	0.16	0	6,6,6	0.16	0
4	SO4	C	710	-	4,4,4	0.16	0	6,6,6	0.10	0
4	SO4	C	711	-	4,4,4	0.15	0	6,6,6	0.08	0
5	P6G	C	712	-	18,18,18	0.72	0	17,17,17	1.40	0
5	P6G	C	713	-	18,18,18	0.67	0	17,17,17	1.50	1 (5%)
5	P6G	C	714	-	18,18,18	0.65	0	17,17,17	1.50	0
2	BCT	D	701	3	0,3,3	0.00	-	0,3,3	0.00	-
2	BCT	D	702	3	0,3,3	0.00	-	0,3,3	0.00	-
4	SO4	D	705	-	4,4,4	0.13	0	6,6,6	0.11	0
4	SO4	D	706	-	4,4,4	0.21	0	6,6,6	0.10	0
4	SO4	D	707	-	4,4,4	0.16	0	6,6,6	0.22	0
4	SO4	D	708	-	4,4,4	0.19	0	6,6,6	0.12	0
4	SO4	D	709	-	4,4,4	0.22	0	6,6,6	0.15	0
4	SO4	D	710	-	4,4,4	0.16	0	6,6,6	0.17	0
4	SO4	D	711	-	4,4,4	0.20	0	6,6,6	0.09	0
4	SO4	D	712	-	4,4,4	0.17	0	6,6,6	0.14	0
4	SO4	D	713	-	4,4,4	0.22	0	6,6,6	0.07	0
5	P6G	D	714	-	18,18,18	0.68	0	17,17,17	1.52	0
5	P6G	D	715	-	18,18,18	0.61	0	17,17,17	1.72	3 (17%)
2	BCT	E	701	3	0,3,3	0.00	-	0,3,3	0.00	-
2	BCT	E	702	3	0,3,3	0.00	-	0,3,3	0.00	-
4	SO4	E	705	-	4,4,4	0.19	0	6,6,6	0.07	0
4	SO4	E	706	-	4,4,4	1.73	1 (25%)	6,6,6	1.21	1 (16%)
4	SO4	E	707	-	4,4,4	0.11	0	6,6,6	0.17	0
4	SO4	E	708	-	4,4,4	0.16	0	6,6,6	0.07	0
4	SO4	E	709	-	4,4,4	0.18	0	6,6,6	0.15	0
4	SO4	E	710	-	4,4,4	0.17	0	6,6,6	0.14	0
4	SO4	E	711	-	4,4,4	0.16	0	6,6,6	0.12	0
4	SO4	E	712	-	4,4,4	0.14	0	6,6,6	0.14	0
4	SO4	E	713	-	4,4,4	0.15	0	6,6,6	0.08	0
5	P6G	E	714	-	18,18,18	0.67	0	17,17,17	1.52	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	P6G	E	715	-	18,18,18	0.72	0	17,17,17	1.36	0
2	BCT	F	701	3	0,3,3	0.00	-	0,3,3	0.00	-
2	BCT	F	702	3	0,3,3	0.00	-	0,3,3	0.00	-
4	SO4	F	705	-	4,4,4	0.18	0	6,6,6	0.09	0
4	SO4	F	706	-	4,4,4	0.15	0	6,6,6	0.12	0
4	SO4	F	707	-	4,4,4	0.18	0	6,6,6	0.11	0
4	SO4	F	708	-	4,4,4	0.16	0	6,6,6	0.10	0
4	SO4	F	709	-	4,4,4	0.16	0	6,6,6	0.08	0
5	P6G	F	710	-	18,18,18	0.71	0	17,17,17	1.48	0
5	P6G	F	711	-	18,18,18	0.69	0	17,17,17	1.61	2 (11%)

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	BCT	A	701	3	-	0/0/0/0	0/0/0/0
2	BCT	A	702	3	-	0/0/0/0	0/0/0/0
4	SO4	A	705	-	-	0/0/0/0	0/0/0/0
4	SO4	A	706	-	-	0/0/0/0	0/0/0/0
4	SO4	A	707	-	-	0/0/0/0	0/0/0/0
4	SO4	A	708	-	-	0/0/0/0	0/0/0/0
4	SO4	A	709	-	-	0/0/0/0	0/0/0/0
5	P6G	A	710	-	-	0/16/16/16	0/0/0/0
5	P6G	A	711	-	-	0/16/16/16	0/0/0/0
5	P6G	A	712	-	-	0/16/16/16	0/0/0/0
2	BCT	B	701	3	-	0/0/0/0	0/0/0/0
2	BCT	B	702	3	-	0/0/0/0	0/0/0/0
4	SO4	B	705	-	-	0/0/0/0	0/0/0/0
4	SO4	B	706	-	-	0/0/0/0	0/0/0/0
4	SO4	B	707	-	-	0/0/0/0	0/0/0/0
4	SO4	B	708	-	-	0/0/0/0	0/0/0/0
4	SO4	B	709	-	-	0/0/0/0	0/0/0/0
4	SO4	B	710	-	-	0/0/0/0	0/0/0/0
4	SO4	B	711	-	-	0/0/0/0	0/0/0/0
4	SO4	B	712	-	-	0/0/0/0	0/0/0/0
4	SO4	B	713	-	-	0/0/0/0	0/0/0/0
5	P6G	B	714	-	-	0/16/16/16	0/0/0/0
5	P6G	B	715	-	-	0/16/16/16	0/0/0/0
2	BCT	C	701	3	-	0/0/0/0	0/0/0/0
2	BCT	C	702	3	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SO4	C	705	-	-	0/0/0/0	0/0/0/0
4	SO4	C	706	-	-	0/0/0/0	0/0/0/0
4	SO4	C	707	-	-	0/0/0/0	0/0/0/0
4	SO4	C	708	-	-	0/0/0/0	0/0/0/0
4	SO4	C	709	-	-	0/0/0/0	0/0/0/0
4	SO4	C	710	-	-	0/0/0/0	0/0/0/0
4	SO4	C	711	-	-	0/0/0/0	0/0/0/0
5	P6G	C	712	-	-	0/16/16/16	0/0/0/0
5	P6G	C	713	-	-	0/16/16/16	0/0/0/0
5	P6G	C	714	-	-	0/16/16/16	0/0/0/0
2	BCT	D	701	3	-	0/0/0/0	0/0/0/0
2	BCT	D	702	3	-	0/0/0/0	0/0/0/0
4	SO4	D	705	-	-	0/0/0/0	0/0/0/0
4	SO4	D	706	-	-	0/0/0/0	0/0/0/0
4	SO4	D	707	-	-	0/0/0/0	0/0/0/0
4	SO4	D	708	-	-	0/0/0/0	0/0/0/0
4	SO4	D	709	-	-	0/0/0/0	0/0/0/0
4	SO4	D	710	-	-	0/0/0/0	0/0/0/0
4	SO4	D	711	-	-	0/0/0/0	0/0/0/0
4	SO4	D	712	-	-	0/0/0/0	0/0/0/0
4	SO4	D	713	-	-	0/0/0/0	0/0/0/0
5	P6G	D	714	-	-	0/16/16/16	0/0/0/0
5	P6G	D	715	-	-	0/16/16/16	0/0/0/0
2	BCT	E	701	3	-	0/0/0/0	0/0/0/0
2	BCT	E	702	3	-	0/0/0/0	0/0/0/0
4	SO4	E	705	-	-	0/0/0/0	0/0/0/0
4	SO4	E	706	-	-	0/0/0/0	0/0/0/0
4	SO4	E	707	-	-	0/0/0/0	0/0/0/0
4	SO4	E	708	-	-	0/0/0/0	0/0/0/0
4	SO4	E	709	-	-	0/0/0/0	0/0/0/0
4	SO4	E	710	-	-	0/0/0/0	0/0/0/0
4	SO4	E	711	-	-	0/0/0/0	0/0/0/0
4	SO4	E	712	-	-	0/0/0/0	0/0/0/0
4	SO4	E	713	-	-	0/0/0/0	0/0/0/0
5	P6G	E	714	-	-	0/16/16/16	0/0/0/0
5	P6G	E	715	-	-	0/16/16/16	0/0/0/0
2	BCT	F	701	3	-	0/0/0/0	0/0/0/0
2	BCT	F	702	3	-	0/0/0/0	0/0/0/0
4	SO4	F	705	-	-	0/0/0/0	0/0/0/0
4	SO4	F	706	-	-	0/0/0/0	0/0/0/0
4	SO4	F	707	-	-	0/0/0/0	0/0/0/0
4	SO4	F	708	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SO4	F	709	-	-	0/0/0/0	0/0/0/0
5	P6G	F	710	-	-	0/16/16/16	0/0/0/0
5	P6G	F	711	-	-	0/16/16/16	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	706	SO4	O4-S	-2.31	1.39	1.47

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	706	SO4	O4-S-O3	-2.58	98.17	109.08
5	E	714	P6G	C14-O13-C12	2.42	124.04	113.38
5	F	711	P6G	O4-C5-C6	2.32	121.00	110.47
5	D	715	P6G	O7-C6-C5	2.20	120.46	110.47
5	F	711	P6G	C8-O7-C6	2.19	123.00	113.38

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	674/698 (96%)	0.01	36 (5%) 25 28	15, 39, 77, 97	0
1	B	677/698 (96%)	-0.10	27 (3%) 36 41	13, 33, 72, 97	0
1	C	674/698 (96%)	0.74	113 (16%) 2 2	13, 46, 117, 151	0
1	D	675/698 (96%)	-0.06	21 (3%) 47 52	16, 34, 66, 94	0
1	E	674/698 (96%)	-0.02	29 (4%) 34 38	13, 35, 73, 93	0
1	F	676/698 (96%)	-0.07	28 (4%) 35 40	13, 36, 70, 98	0
All	All	4050/4188 (96%)	0.08	254 (6%) 20 22	13, 36, 83, 151	0

The worst 5 of 254 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	479	PHE	13.6
1	C	474	CYS	12.8
1	C	478	GLU	12.1
1	C	564	LEU	11.1
1	C	445	LYS	10.8

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	SO4	E	706	5/5	0.44	14.87	111,112,113,113	5
4	SO4	B	711	5/5	0.19	12.69	63,68,74,77	0
5	P6G	F	710	19/19	0.16	9.18	37,48,68,71	0
3	FE	E	703	1/1	0.13	8.25	19,19,19,19	0
5	P6G	B	714	19/19	0.14	7.85	22,32,87,87	0
4	SO4	A	707	5/5	0.18	7.71	77,87,88,92	0
3	FE	A	703	1/1	0.15	7.53	19,19,19,19	0
5	P6G	E	714	19/19	0.20	7.06	28,45,83,84	0
4	SO4	E	711	5/5	0.17	6.82	73,77,84,87	0
5	P6G	A	711	19/19	0.17	6.08	46,66,84,85	0
4	SO4	C	711	5/5	0.19	5.78	106,109,109,110	0
3	FE	B	704	1/1	0.14	5.75	15,15,15,15	0
3	FE	F	703	1/1	0.13	5.71	16,16,16,16	0
3	FE	D	703	1/1	0.14	5.47	26,26,26,26	0
5	P6G	D	714	19/19	0.18	4.23	41,54,79,79	0
5	P6G	C	712	19/19	0.15	4.13	28,48,79,81	0
5	P6G	F	711	19/19	0.18	4.02	28,48,98,100	0
4	SO4	F	709	5/5	0.13	4.01	89,89,92,93	0
4	SO4	A	705	5/5	0.21	3.95	93,94,95,97	0
4	SO4	C	705	5/5	0.20	3.90	77,78,83,83	0
4	SO4	A	708	5/5	0.19	3.82	95,98,99,100	0
3	FE	D	704	1/1	0.14	3.62	20,20,20,20	0
3	FE	F	704	1/1	0.14	3.48	31,31,31,31	0
5	P6G	D	715	19/19	0.23	3.39	56,74,84,86	0
3	FE	C	704	1/1	0.13	3.32	16,16,16,16	0
2	BCT	F	702	4/4	0.13	3.04	19,20,21,24	0
2	BCT	D	702	4/4	0.12	2.98	23,26,29,32	0
4	SO4	D	712	5/5	0.18	2.86	95,95,99,100	0
4	SO4	F	706	5/5	0.15	2.84	89,92,95,98	0
5	P6G	E	715	19/19	0.16	2.78	44,56,71,71	0
5	P6G	A	710	19/19	0.15	2.50	37,48,77,77	0
5	P6G	B	715	19/19	0.16	2.32	32,46,94,95	0
2	BCT	E	702	4/4	0.13	2.15	26,28,29,30	0
4	SO4	A	706	5/5	0.15	2.04	51,66,69,77	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	BCT	E	701	4/4	0.10	1.95	14,17,17,18	0
3	FE	E	704	1/1	0.14	1.95	32,32,32,32	0
3	FE	B	703	1/1	0.11	1.90	29,29,29,29	0
5	P6G	C	713	19/19	0.16	1.74	43,57,83,83	0
3	FE	A	704	1/1	0.12	1.74	34,34,34,34	0
4	SO4	E	705	5/5	0.15	1.72	107,108,109,110	0
5	P6G	C	714	19/19	0.20	1.69	56,79,99,100	0
4	SO4	B	713	5/5	0.20	1.68	105,107,108,109	0
2	BCT	B	701	4/4	0.11	1.48	13,14,15,16	0
4	SO4	C	706	5/5	0.12	1.34	94,95,97,98	0
4	SO4	D	705	5/5	0.18	1.17	68,71,72,78	0
4	SO4	D	708	5/5	0.12	1.15	46,49,58,58	0
4	SO4	B	708	5/5	0.20	1.08	86,88,92,96	0
2	BCT	C	701	4/4	0.09	1.06	14,15,15,17	0
4	SO4	E	713	5/5	0.16	1.00	93,95,95,96	0
4	SO4	F	705	5/5	0.13	0.89	97,97,98,100	0
5	P6G	A	712	19/19	0.22	0.88	74,81,91,92	0
4	SO4	D	710	5/5	0.16	0.86	55,55,65,66	0
4	SO4	A	709	5/5	0.14	0.85	97,97,99,99	0
4	SO4	D	711	5/5	0.19	0.82	62,67,73,74	0
4	SO4	B	705	5/5	0.10	0.74	44,45,49,50	0
4	SO4	E	709	5/5	0.10	0.70	76,77,79,81	0
4	SO4	C	709	5/5	0.11	0.63	76,77,80,80	0
4	SO4	F	707	5/5	0.15	0.56	85,87,87,90	0
4	SO4	E	708	5/5	0.12	0.45	94,95,96,96	0
4	SO4	C	710	5/5	0.14	0.40	73,77,79,83	0
4	SO4	D	706	5/5	0.12	0.31	101,103,106,109	0
2	BCT	B	702	4/4	0.10	0.23	27,27,28,31	0
4	SO4	B	706	5/5	0.14	0.22	72,79,81,82	0
2	BCT	A	701	4/4	0.09	0.13	14,14,16,19	0
4	SO4	B	707	5/5	0.12	-0.01	85,87,90,92	0
2	BCT	D	701	4/4	0.10	-0.06	15,17,21,24	0
4	SO4	F	708	5/5	0.13	-0.18	80,85,87,90	0
4	SO4	C	707	5/5	0.10	-0.18	38,55,63,63	0
4	SO4	B	709	5/5	0.09	-0.31	66,67,68,73	0
4	SO4	D	709	5/5	0.10	-0.35	70,72,75,76	0
4	SO4	E	710	5/5	0.10	-0.44	73,73,75,79	0
2	BCT	A	702	4/4	0.10	-0.50	28,31,34,38	0
4	SO4	E	712	5/5	0.10	-0.53	44,48,49,50	0
4	SO4	C	708	5/5	0.09	-0.60	70,75,76,79	0
4	SO4	D	707	5/5	0.08	-0.81	57,58,59,65	0
4	SO4	D	713	5/5	0.11	-0.81	72,73,74,78	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	SO4	E	707	5/5	0.09	-0.83	41,55,61,63	0
4	SO4	B	710	5/5	0.09	-1.03	44,61,65,72	0
2	BCT	F	701	4/4	0.08	-1.04	8,9,10,11	0
2	BCT	C	702	4/4	0.14	-1.33	32,36,38,44	0
4	SO4	B	712	5/5	0.11	-1.58	77,80,83,84	0
3	FE	C	703	1/1	0.11	-2.83	38,38,38,38	0

6.5 Other polymers ⓘ

There are no such residues in this entry.