



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 09:08 PM GMT

PDB ID : 1NFV
Title : X-ray structure of Desulfovibrio desulfuricans bacterioferritin: the diiron centre in different catalytic states (as-isolated structure)
Authors : Macedo, S.; Romao, C.V.; Mitchell, E.; Matias, P.M.; Liu, M.Y.; Xavier, A.V.; LeGall, J.; Teixeira, M.; Lindley, P.; Carrondo, M.A.
Deposited on : 2002-12-16
Resolution : 1.95 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

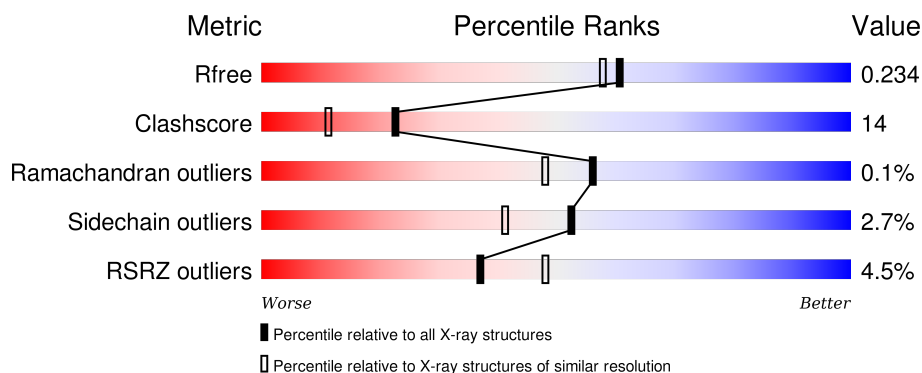
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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}	91344	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (1.96-1.96)

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. 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	179	
1	B	179	
1	C	179	
1	D	179	
1	E	179	

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Mol	Chain	Length	Quality of chain
1	F	179	
1	G	179	
1	H	179	
1	I	179	
1	J	179	
1	K	179	
1	L	179	
1	M	179	
1	N	179	
1	O	179	
1	P	179	

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
3	SO4	A	1105	-	-	X	X
3	SO4	B	1005	-	-	-	X
3	SO4	E	1401	-	-	-	X
3	SO4	F	1502	-	-	X	-
3	SO4	G	1607	-	-	-	X
3	SO4	I	1802	-	-	X	-
3	SO4	J	1906	-	-	X	-
3	SO4	K	2001	-	-	-	X
3	SO4	L	2102	-	-	X	-
3	SO4	L	2107	-	-	-	X
3	SO4	M	2206	-	-	X	-
3	SO4	O	2409	-	-	-	X
4	3PY	D	1310	-	X	-	-
6	GOL	A	1010	-	X	-	-
6	GOL	B	1011	-	X	-	-
6	GOL	B	1110	-	X	-	X
6	GOL	C	1210	-	X	-	X
6	GOL	D	1211	-	X	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	GOL	E	1410	-	X	X	X
6	GOL	E	1411	-	X	-	-
6	GOL	F	1510	-	X	-	-
6	GOL	F	1512	-	X	-	-
6	GOL	G	1610	-	X	-	X
6	GOL	G	1611	-	X	-	-
6	GOL	H	1710	-	X	-	X
6	GOL	H	1814	-	X	-	-
6	GOL	I	1713	-	X	-	-
6	GOL	I	1810	-	X	X	X
6	GOL	J	1811	-	X	-	X
6	GOL	J	1910	-	X	X	X
6	GOL	K	2011	-	X	-	-
6	GOL	M	2210	-	X	X	X
6	GOL	M	2211	-	X	-	-
6	GOL	N	2310	-	X	-	-
6	GOL	O	2410	-	X	-	-
6	GOL	O	2411	-	X	-	-
6	GOL	P	2510	-	X	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 25080 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 bacterioferritin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	169	Total	C	N	O	S	0	4	0
			1365	848	239	272	6			
1	B	170	Total	C	N	O	S	0	5	0
			1378	856	242	274	6			
1	C	170	Total	C	N	O	S	0	4	0
			1361	845	236	274	6			
1	D	170	Total	C	N	O	S	0	6	0
			1383	858	243	276	6			
1	E	170	Total	C	N	O	S	0	5	0
			1374	852	240	276	6			
1	F	170	Total	C	N	O	S	0	4	0
			1365	848	240	271	6			
1	G	169	Total	C	N	O	S	0	6	0
			1380	856	243	275	6			
1	H	170	Total	C	N	O	S	0	5	0
			1374	853	241	274	6			
1	I	170	Total	C	N	O	S	0	5	0
			1382	858	242	276	6			
1	J	170	Total	C	N	O	S	0	4	0
			1369	851	241	271	6			
1	K	170	Total	C	N	O	S	0	5	0
			1378	855	241	276	6			
1	L	170	Total	C	N	O	S	0	5	0
			1374	853	242	273	6			
1	M	170	Total	C	N	O	S	0	4	0
			1373	853	241	273	6			
1	N	170	Total	C	N	O	S	0	4	0
			1369	850	240	273	6			
1	O	169	Total	C	N	O	S	0	5	0
			1366	847	239	274	6			
1	P	170	Total	C	N	O	S	0	5	0
			1378	855	241	276	6			

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	P	2	Total 2	Fe 2	0	0
2	G	2	Total 2	Fe 2	0	0
2	J	2	Total 2	Fe 2	0	0
2	D	2	Total 2	Fe 2	0	0
2	K	2	Total 2	Fe 2	0	0
2	E	2	Total 2	Fe 2	0	0
2	H	2	Total 2	Fe 2	0	0
2	B	2	Total 2	Fe 2	0	0
2	I	2	Total 2	Fe 2	0	0
2	C	2	Total 2	Fe 2	0	0
2	A	2	Total 2	Fe 2	0	0
2	N	2	Total 2	Fe 2	0	0
2	O	2	Total 2	Fe 2	0	0
2	L	2	Total 2	Fe 2	0	0
2	F	2	Total 2	Fe 2	0	0
2	M	2	Total 2	Fe 2	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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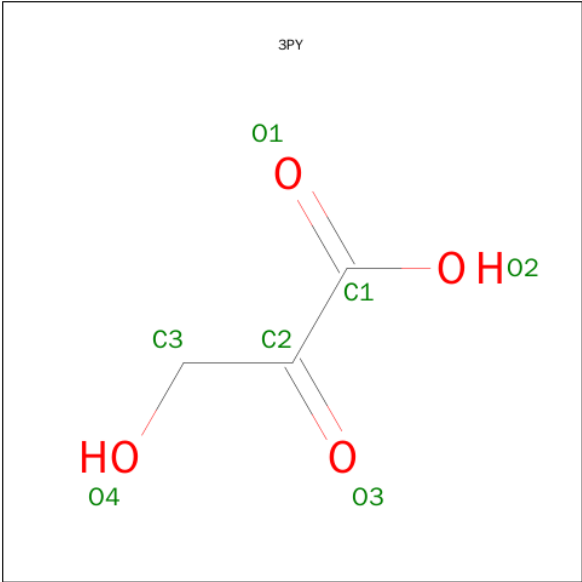
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	K	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	I	1	Total	O	S	0	0
			5	4	1		
3	I	1	Total	O	S	0	0
			5	4	1		
3	I	1	Total	O	S	0	0
			5	4	1		
3	I	1	Total	O	S	0	0
			5	4	1		
3	J	1	Total	O	S	0	0
			5	4	1		
3	J	1	Total	O	S	0	0
			5	4	1		
3	J	1	Total	O	S	0	0
			5	4	1		
3	K	1	Total	O	S	0	0
			5	4	1		

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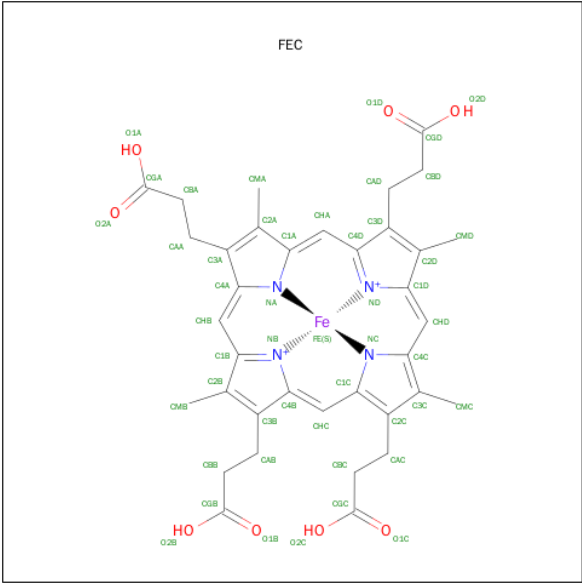
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	K	1	Total	O	S	0	0
			5	4	1		
3	K	1	Total	O	S	0	0
			5	4	1		
3	L	1	Total	O	S	0	0
			5	4	1		
3	L	1	Total	O	S	0	0
			5	4	1		
3	L	1	Total	O	S	0	0
			5	4	1		
3	L	1	Total	O	S	0	0
			5	4	1		
3	M	1	Total	O	S	0	0
			5	4	1		
3	M	1	Total	O	S	0	0
			5	4	1		
3	N	1	Total	O	S	0	0
			5	4	1		
3	N	1	Total	O	S	0	0
			5	4	1		
3	N	1	Total	O	S	0	0
			5	4	1		
3	O	1	Total	O	S	0	0
			5	4	1		
3	O	1	Total	O	S	0	0
			5	4	1		
3	P	1	Total	O	S	0	0
			5	4	1		
3	P	1	Total	O	S	0	0
			5	4	1		
3	P	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is 3-HYDROXYPYRUVIC ACID (three-letter code: 3PY) (formula: C₃H₄O₄).



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

- Molecule 5 is 1,3,5,8-TETRAMETHYL-PORPHINE-2,4,6,7-TETRAPROPIONIC ACID FERROUS COMPLEX (three-letter code: FEC) (formula: C₃₆H₃₆FeN₄O₈).



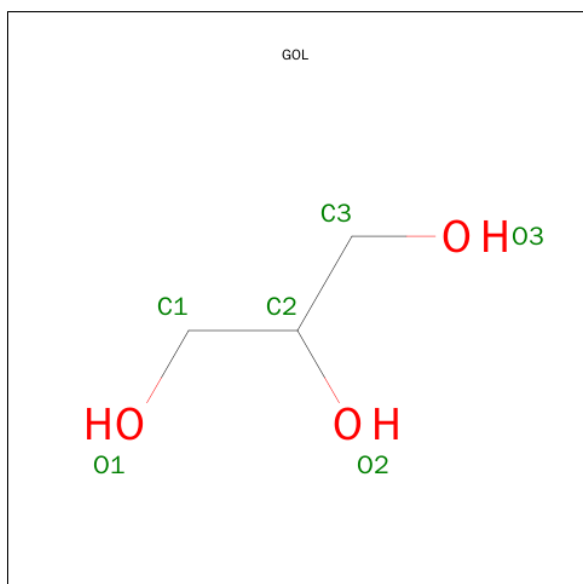
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	Fe	N	O	0	1
			98	72	2	8	16		
5	D	1	Total	C	Fe	N	O	0	1
			98	72	2	8	16		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	F	1	Total	C	Fe	N	O	0	1
			98	72	2	8	16		
5	G	1	Total	C	Fe	N	O	0	1
			98	72	2	8	16		
5	I	1	Total	C	Fe	N	O	0	1
			98	72	2	8	16		
5	L	1	Total	C	Fe	N	O	0	1
			98	72	2	8	16		
5	M	1	Total	C	Fe	N	O	0	1
			98	72	2	8	16		
5	P	1	Total	C	Fe	N	O	0	1
			98	72	2	8	16		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	E	1	Total	C	O	0	0
			6	3	3		
6	E	1	Total	C	O	0	0
			6	3	3		
6	F	1	Total	C	O	0	0
			6	3	3		
6	F	1	Total	C	O	0	0
			6	3	3		
6	G	1	Total	C	O	0	0
			6	3	3		
6	G	1	Total	C	O	0	0
			6	3	3		
6	H	1	Total	C	O	0	0
			6	3	3		
6	I	1	Total	C	O	0	0
			6	3	3		
6	I	1	Total	C	O	0	0
			6	3	3		
6	J	1	Total	C	O	0	0
			6	3	3		
6	H	1	Total	C	O	0	0
			6	3	3		
6	J	1	Total	C	O	0	0
			6	3	3		
6	K	1	Total	C	O	0	0
			6	3	3		
6	M	1	Total	C	O	0	0
			6	3	3		
6	M	1	Total	C	O	0	0
			6	3	3		
6	N	1	Total	C	O	0	0
			6	3	3		
6	O	1	Total	C	O	0	0
			6	3	3		
6	O	1	Total	C	O	0	0
			6	3	3		
6	P	1	Total	C	O	0	0
			6	3	3		

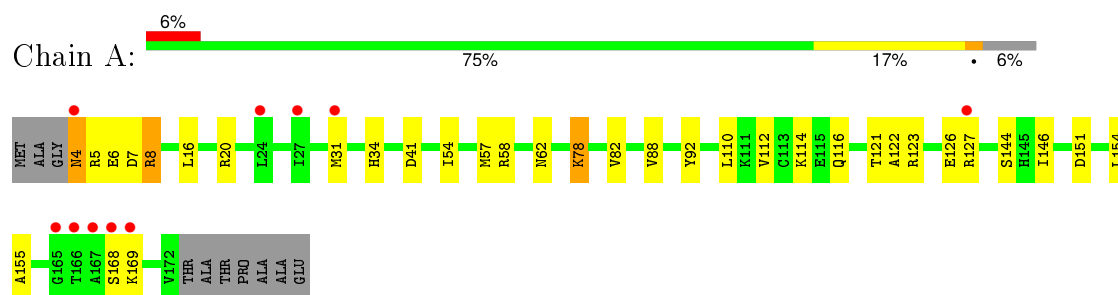
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	131	Total 131	O 131	0	0
7	B	142	Total 142	O 142	0	0
7	C	117	Total 117	O 117	0	0
7	D	99	Total 99	O 99	0	0
7	E	101	Total 101	O 101	0	0
7	F	103	Total 103	O 103	0	0
7	G	146	Total 146	O 146	0	0
7	H	91	Total 91	O 91	0	0
7	I	131	Total 131	O 131	0	0
7	J	99	Total 99	O 99	0	0
7	K	130	Total 130	O 130	0	0
7	L	134	Total 134	O 134	0	0
7	M	122	Total 122	O 122	0	0
7	N	124	Total 124	O 124	0	0
7	O	105	Total 105	O 105	0	0
7	P	115	Total 115	O 115	0	0

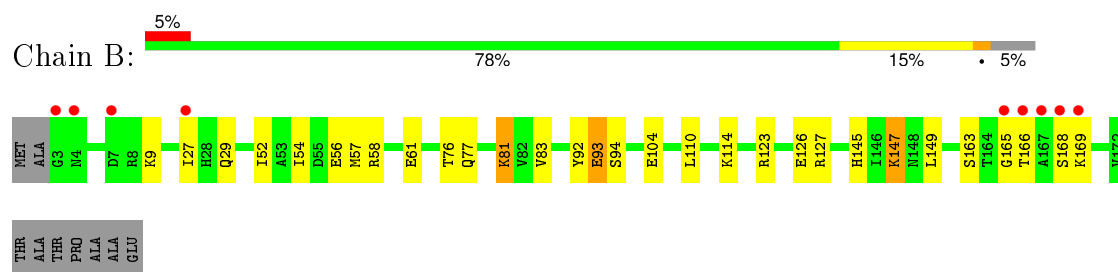
3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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.

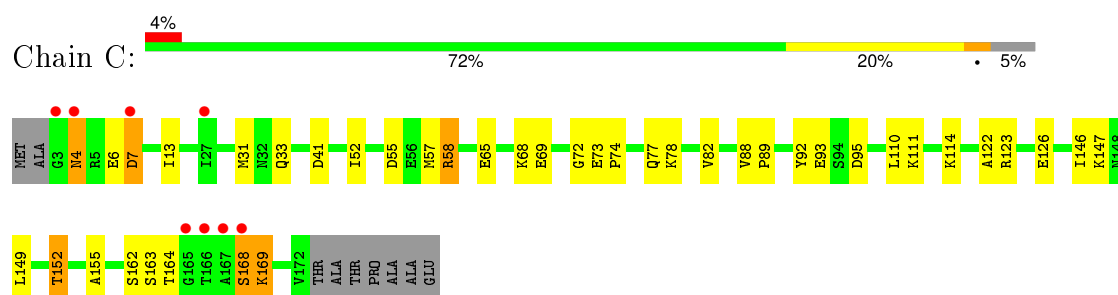
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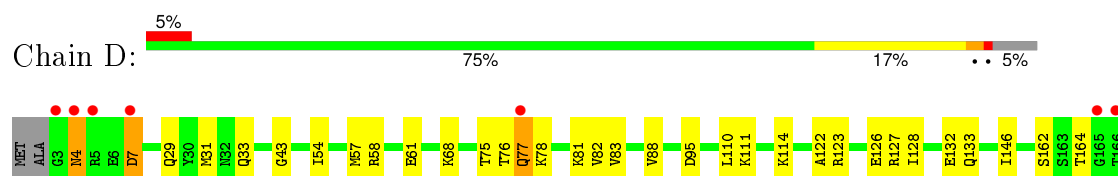
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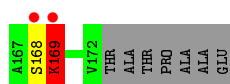


- Molecule 1: bacterioferritin

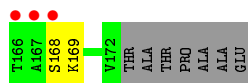
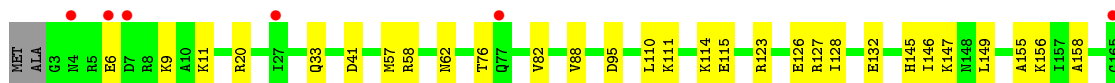
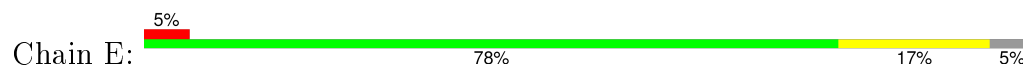


- Molecule 1: bacterioferritin

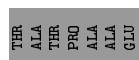
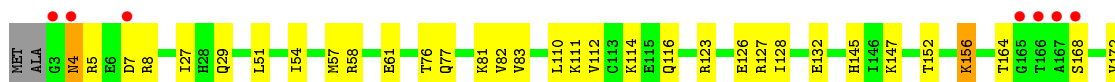




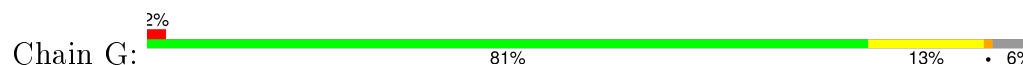
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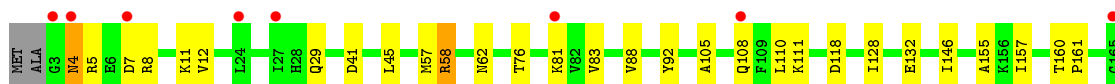
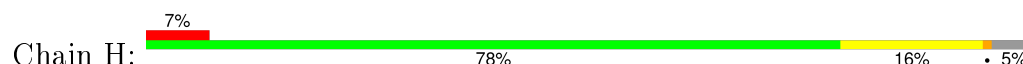
- Molecule 1: bacterioferritin



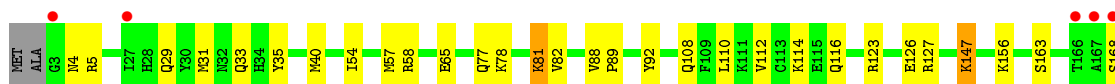
- Molecule 1: bacterioferritin



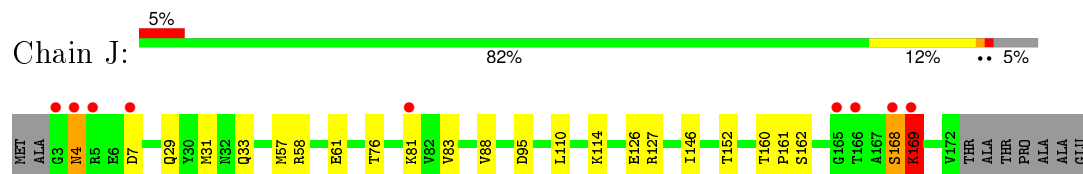
- Molecule 1: bacterioferritin



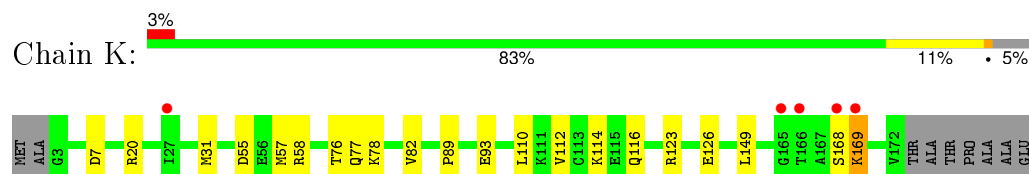
- Molecule 1: bacterioferritin



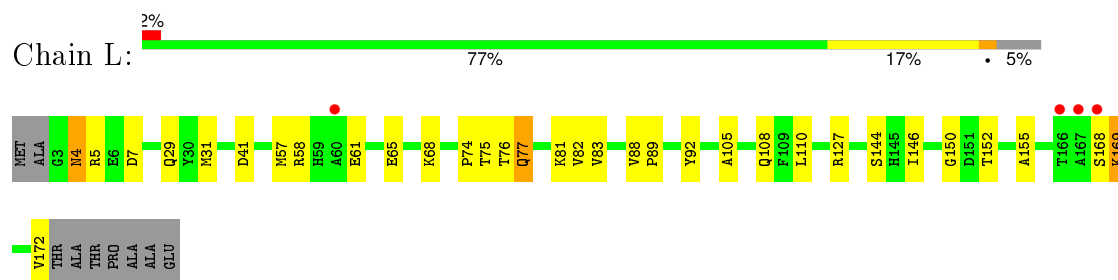
- Molecule 1: bacterioferritin



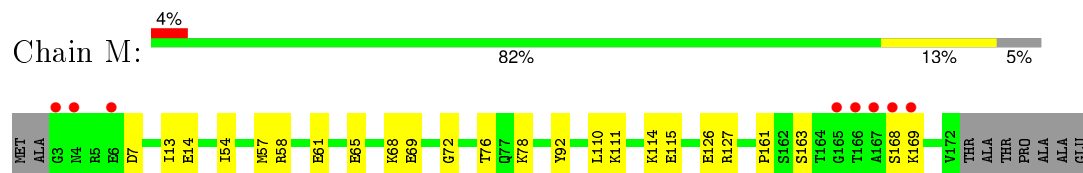
- Molecule 1: bacterioferritin



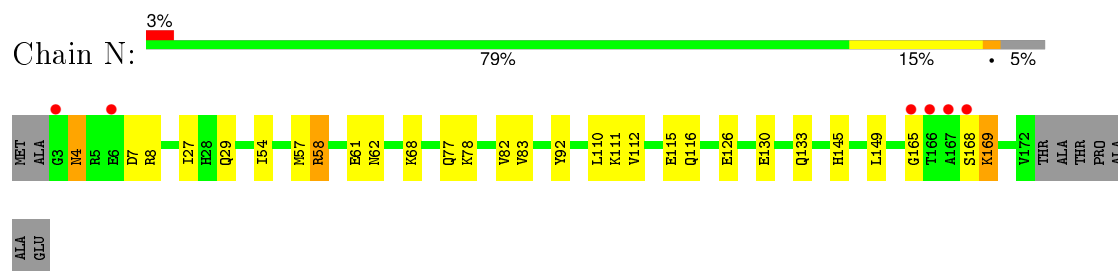
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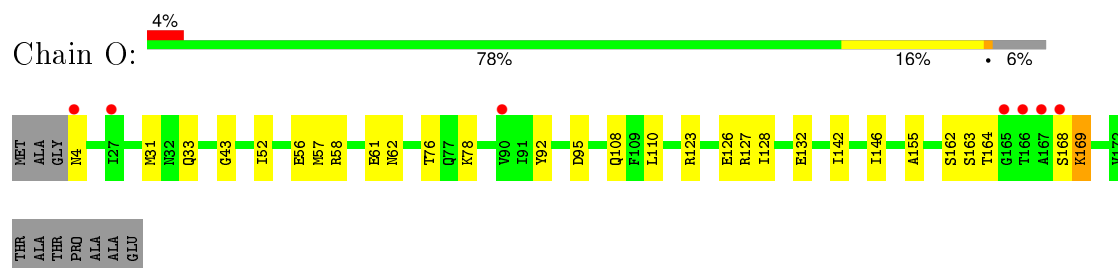
- Molecule 1: bacterioferritin



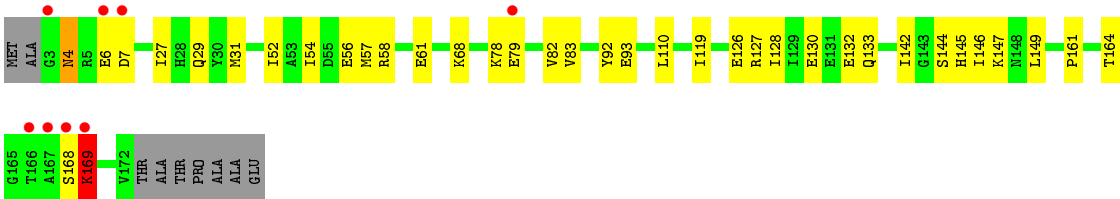
- Molecule 1: bacterioferritin



- Molecule 1: bacterioferritin



● Molecule 1: bacterioferritin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	225.30 Å 225.30 Å 225.30 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.95 29.84 – 1.95	Depositor EDS
% Data completeness (in resolution range)	98.9 (30.00-1.95) 99.2 (29.84-1.95)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.66 (at 1.95 Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.214 , 0.254 0.185 , 0.234	Depositor DCC
R_{free} test set	5260 reflections (1.98%)	DCC
Wilson B-factor (Å ²)	26.5	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 60.2	EDS
Estimated twinning fraction	0.018 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 271079 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	25080	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.36% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: 3PY, SO4, FE, FEC, 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	0.31	0/1385	0.93	3/1864 (0.2%)
1	B	0.31	0/1398	0.84	1/1880 (0.1%)
1	C	0.32	0/1381	0.89	3/1861 (0.2%)
1	D	0.51	2/1407 (0.1%)	0.86	0/1892
1	E	0.31	0/1398	0.84	1/1881 (0.1%)
1	F	0.31	0/1389	0.83	0/1868
1	G	0.44	2/1405 (0.1%)	0.91	1/1890 (0.1%)
1	H	0.32	0/1394	0.85	1/1876 (0.1%)
1	I	0.31	0/1402	0.86	1/1885 (0.1%)
1	J	0.34	0/1389	0.86	2/1868 (0.1%)
1	K	0.32	0/1398	0.88	3/1881 (0.2%)
1	L	1.07	2/1398 (0.1%)	0.90	3/1880 (0.2%)
1	M	0.31	0/1393	0.84	1/1873 (0.1%)
1	N	0.30	0/1389	0.80	1/1869 (0.1%)
1	O	0.77	2/1390 (0.1%)	0.92	3/1872 (0.2%)
1	P	0.60	2/1402 (0.1%)	0.85	3/1885 (0.2%)
All	All	0.48	10/22318 (0.0%)	0.87	27/30025 (0.1%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	169[A]	LYS	CB-CG	27.00	2.25	1.52
1	L	169[B]	LYS	CB-CG	27.00	2.25	1.52
1	O	169[A]	LYS	CB-CG	18.20	2.01	1.52
1	O	169[B]	LYS	CB-CG	18.20	2.01	1.52
1	P	169[A]	LYS	CB-CG	13.45	1.88	1.52

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	169[A]	LYS	CA-CB-CG	-9.37	92.78	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	169[B]	LYS	CA-CB-CG	-9.37	92.78	113.40
1	O	169[A]	LYS	CA-CB-CG	-7.31	97.32	113.40
1	O	169[B]	LYS	CA-CB-CG	-7.31	97.32	113.40
1	C	58[A]	ARG	NE-CZ-NH2	-6.23	117.18	120.30

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	1365	0	1325	44	0
1	B	1378	0	1343	43	0
1	C	1361	0	1312	51	0
1	D	1383	0	1341	55	0
1	E	1374	0	1326	37	0
1	F	1365	0	1328	37	0
1	G	1380	0	1340	43	0
1	H	1374	0	1332	35	0
1	I	1382	0	1348	53	0
1	J	1369	0	1335	34	0
1	K	1378	0	1335	32	0
1	L	1374	0	1335	35	0
1	M	1373	0	1341	54	0
1	N	1369	0	1329	56	0
1	O	1366	0	1312	46	0
1	P	1378	0	1338	47	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
2	M	2	0	0	0	0
2	N	2	0	0	0	0
2	O	2	0	0	0	0
2	P	2	0	0	0	0
3	A	25	0	0	3	0
3	B	20	0	0	3	0
3	C	15	0	0	2	0
3	D	10	0	0	0	0
3	E	15	0	0	1	0
3	F	15	0	0	3	0
3	G	15	0	0	1	0
3	H	15	0	0	0	0
3	I	20	0	0	2	7
3	J	15	0	0	4	0
3	K	20	0	0	1	0
3	L	20	0	0	3	7
3	M	10	0	0	2	0
3	N	15	0	0	0	0
3	O	10	0	0	2	0
3	P	15	0	0	2	0
4	D	6	0	1	1	0
5	B	98	0	64	17	0
5	D	98	0	64	22	0
5	F	98	0	64	17	0
5	G	98	0	64	15	0
5	I	98	0	64	18	0
5	L	98	0	64	23	0
5	M	98	0	64	18	0
5	P	98	0	64	21	0
6	A	6	0	4	1	0
6	B	12	0	8	3	0
6	C	6	0	5	0	0
6	D	6	0	4	5	0
6	E	12	0	8	6	0
6	F	12	0	8	3	0
6	G	12	0	9	3	0
6	H	12	0	8	1	0
6	I	12	0	8	16	0
6	J	12	0	8	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	K	6	0	4	1	0
6	M	12	0	8	8	0
6	N	6	0	4	1	0
6	O	12	0	8	4	0
6	P	6	0	4	2	0
7	A	131	0	0	6	0
7	B	142	0	0	5	0
7	C	117	0	0	0	0
7	D	99	0	0	9	0
7	E	101	0	0	2	0
7	F	103	0	0	2	0
7	G	146	0	0	5	0
7	H	91	0	0	0	0
7	I	131	0	0	5	0
7	J	99	0	0	5	0
7	K	130	0	0	4	0
7	L	134	0	0	5	0
7	M	122	0	0	3	0
7	N	124	0	0	1	0
7	O	105	0	0	5	0
7	P	115	0	0	5	0
All	All	25080	0	21931	603	7

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 14.

The worst 5 of 603 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:M:168[A]:SER:CB	1:N:58[A]:ARG:HH22	1.00	1.53
1:G:168[A]:SER:CB	1:H:58[A]:ARG:HH22	1.23	1.49
1:O:58[B]:ARG:NH2	1:P:168[B]:SER:H	1.15	1.44
1:M:168[A]:SER:HB2	1:N:58[A]:ARG:NH2	1.32	1.44
1:G:168[A]:SER:HB2	1:H:58[A]:ARG:NH2	1.12	1.41

The worst 5 of 7 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)
3:I:1802:SO4:S	3:L:2102:SO4:S[9_465]	0.16	2.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:1802:SO4:O1	3:L:2102:SO4:O3[9_465]	0.22	1.98
3:I:1802:SO4:O4	3:L:2102:SO4:O2[9_465]	0.35	1.85
3:I:1802:SO4:O2	3:L:2102:SO4:O4[9_465]	0.37	1.83
3:I:1802:SO4:O3	3:L:2102:SO4:O1[9_465]	0.49	1.71

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	171/179 (96%)	170 (99%)	1 (1%)	0	100	100
1	B	173/179 (97%)	170 (98%)	3 (2%)	0	100	100
1	C	172/179 (96%)	169 (98%)	3 (2%)	0	100	100
1	D	174/179 (97%)	173 (99%)	1 (1%)	0	100	100
1	E	173/179 (97%)	170 (98%)	3 (2%)	0	100	100
1	F	172/179 (96%)	170 (99%)	2 (1%)	0	100	100
1	G	173/179 (97%)	171 (99%)	2 (1%)	0	100	100
1	H	173/179 (97%)	171 (99%)	0	2 (1%)	16	5
1	I	173/179 (97%)	168 (97%)	5 (3%)	0	100	100
1	J	172/179 (96%)	169 (98%)	1 (1%)	2 (1%)	16	5
1	K	173/179 (97%)	169 (98%)	4 (2%)	0	100	100
1	L	173/179 (97%)	168 (97%)	5 (3%)	0	100	100
1	M	172/179 (96%)	170 (99%)	2 (1%)	0	100	100
1	N	172/179 (96%)	169 (98%)	1 (1%)	2 (1%)	16	5
1	O	172/179 (96%)	170 (99%)	2 (1%)	0	100	100
1	P	173/179 (97%)	168 (97%)	3 (2%)	2 (1%)	16	5
All	All	2761/2864 (96%)	2715 (98%)	38 (1%)	8 (0%)	56	35

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	169[A]	LYS
1	H	169[B]	LYS
1	J	168[A]	SER
1	J	168[B]	SER
1	N	169[A]	LYS

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	143/145 (99%)	140 (98%)	3 (2%)	61	53
1	B	144/145 (99%)	138 (96%)	6 (4%)	36	21
1	C	142/145 (98%)	130 (92%)	12 (8%)	13	4
1	D	145/145 (100%)	138 (95%)	7 (5%)	31	15
1	E	144/145 (99%)	143 (99%)	1 (1%)	88	88
1	F	143/145 (99%)	137 (96%)	6 (4%)	36	21
1	G	145/145 (100%)	144 (99%)	1 (1%)	88	88
1	H	143/145 (99%)	136 (95%)	7 (5%)	31	15
1	I	145/145 (100%)	141 (97%)	4 (3%)	51	39
1	J	143/145 (99%)	137 (96%)	6 (4%)	36	21
1	K	144/145 (99%)	140 (97%)	4 (3%)	51	39
1	L	144/145 (99%)	139 (96%)	5 (4%)	43	29
1	M	144/145 (99%)	143 (99%)	1 (1%)	88	88
1	N	143/145 (99%)	139 (97%)	4 (3%)	51	39
1	O	143/145 (99%)	142 (99%)	1 (1%)	88	88
1	P	145/145 (100%)	140 (97%)	5 (3%)	44	30
All	All	2300/2320 (99%)	2227 (97%)	73 (3%)	52	33

5 of 73 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	147	LYS

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Mol	Chain	Res	Type
1	H	81	LYS
1	O	163	SER
1	H	11	LYS
1	H	111	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	133	GLN
1	J	133	GLN
1	P	62	ASN
1	I	32	ASN
1	J	4	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 124 ligands modelled in this entry, 32 are monoatomic - leaving 92 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
3	SO4	A	1001	-	4,4,4	3.04	2 (50%)	6,6,6	1.02	0
3	SO4	A	1004	-	4,4,4	3.09	2 (50%)	6,6,6	0.93	0
3	SO4	A	1006	-	4,4,4	0.54	0	6,6,6	0.86	0
3	SO4	A	1008	-	4,4,4	1.03	0	6,6,6	1.82	2 (33%)
6	GOL	A	1010	-	5,5,5	4.91	5 (100%)	5,5,5	5.76	3 (60%)
3	SO4	A	1105	-	4,4,4	1.03	0	6,6,6	1.83	2 (33%)
3	SO4	B	1005	-	4,4,4	1.03	0	6,6,6	1.83	2 (33%)
6	GOL	B	1011	-	5,5,5	4.87	5 (100%)	5,5,5	3.94	3 (60%)
3	SO4	B	1101	-	4,4,4	3.09	2 (50%)	6,6,6	0.93	0
3	SO4	B	1104	-	4,4,4	3.32	2 (50%)	6,6,6	1.02	0
3	SO4	B	1106	-	4,4,4	0.45	0	6,6,6	1.41	1 (16%)
5	FEC	B	1107[A]	1	34,56,56	1.04	0	43,90,90	1.77	10 (23%)
5	FEC	B	1107[B]	1	34,56,56	1.04	1 (2%)	43,90,90	1.85	6 (13%)
6	GOL	B	1110	-	5,5,5	4.76	5 (100%)	5,5,5	4.41	3 (60%)
3	SO4	C	1201	-	4,4,4	3.14	2 (50%)	6,6,6	0.96	0
3	SO4	C	1203	-	4,4,4	0.44	0	6,6,6	1.62	1 (16%)
3	SO4	C	1206	-	4,4,4	0.73	0	6,6,6	0.37	0
6	GOL	C	1210	-	5,5,5	4.64	5 (100%)	5,5,5	4.90	3 (60%)
6	GOL	D	1211	-	5,5,5	4.76	5 (100%)	5,5,5	4.60	3 (60%)
3	SO4	D	1301	-	4,4,4	3.28	2 (50%)	6,6,6	0.94	0
3	SO4	D	1303	-	4,4,4	0.43	0	6,6,6	0.52	0
4	3PY	D	1310	1	5,5,6	12.89	5 (100%)	4,5,7	9.11	4 (100%)
5	FEC	D	1311[A]	1	34,56,56	1.06	0	43,90,90	1.75	8 (18%)
5	FEC	D	1311[B]	1	34,56,56	1.07	0	43,90,90	1.45	5 (11%)
3	SO4	E	1304	1	4,4,4	3.13	2 (50%)	6,6,6	0.95	0
3	SO4	E	1401	-	4,4,4	3.15	2 (50%)	6,6,6	1.02	0
3	SO4	E	1406	-	4,4,4	0.45	0	6,6,6	0.93	0
6	GOL	E	1410	-	5,5,5	4.79	5 (100%)	5,5,5	4.28	3 (60%)
6	GOL	E	1411	-	5,5,5	4.69	5 (100%)	5,5,5	4.12	3 (60%)
3	SO4	F	1501	-	4,4,4	3.33	2 (50%)	6,6,6	0.90	0
3	SO4	F	1502	-	4,4,4	3.18	2 (50%)	6,6,6	1.04	0
3	SO4	F	1506	-	4,4,4	0.48	0	6,6,6	1.64	1 (16%)
5	FEC	F	1507[A]	1	34,56,56	1.09	0	43,90,90	1.61	9 (20%)
5	FEC	F	1507[B]	1	34,56,56	1.05	0	43,90,90	1.64	7 (16%)
6	GOL	F	1510	-	5,5,5	4.69	5 (100%)	5,5,5	4.70	3 (60%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	GOL	F	1512	-	5,5,5	4.79	5 (100%)	5,5,5	3.67	3 (60%)
3	SO4	G	1603	-	4,4,4	3.31	2 (50%)	6,6,6	1.02	0
3	SO4	G	1606	-	4,4,4	0.40	0	6,6,6	0.67	0
3	SO4	G	1607	-	4,4,4	0.30	0	6,6,6	0.50	0
5	FEC	G	1608[A]	1	34,56,56	1.04	0	43,90,90	1.63	9 (20%)
5	FEC	G	1608[B]	1	34,56,56	1.08	0	43,90,90	1.61	9 (20%)
6	GOL	G	1610	-	5,5,5	4.80	5 (100%)	5,5,5	5.59	3 (60%)
6	GOL	G	1611	-	5,5,5	4.63	5 (100%)	5,5,5	4.32	2 (40%)
3	SO4	H	1701	-	4,4,4	3.05	2 (50%)	6,6,6	0.94	0
3	SO4	H	1703	-	4,4,4	0.62	0	6,6,6	0.54	0
3	SO4	H	1706	-	4,4,4	0.69	0	6,6,6	0.49	0
6	GOL	H	1710	-	5,5,5	4.79	5 (100%)	5,5,5	5.56	3 (60%)
6	GOL	H	1814	-	5,5,5	4.89	5 (100%)	5,5,5	4.67	3 (60%)
6	GOL	I	1713	-	5,5,5	4.74	5 (100%)	5,5,5	5.52	3 (60%)
3	SO4	I	1801	-	4,4,4	3.23	2 (50%)	6,6,6	1.00	0
3	SO4	I	1802	3	4,4,4	3.37	2 (50%)	6,6,6	0.97	0
3	SO4	I	1803	-	4,4,4	0.29	0	6,6,6	0.50	0
3	SO4	I	1806	-	4,4,4	0.62	0	6,6,6	0.52	0
5	FEC	I	1807[A]	1	34,56,56	1.03	0	43,90,90	1.67	6 (13%)
5	FEC	I	1807[B]	1	34,56,56	1.03	0	43,90,90	1.80	10 (23%)
6	GOL	I	1810	1	5,5,5	4.62	5 (100%)	5,5,5	3.83	3 (60%)
6	GOL	J	1811	-	5,5,5	4.78	5 (100%)	5,5,5	5.32	3 (60%)
3	SO4	J	1901	-	4,4,4	3.07	2 (50%)	6,6,6	0.94	0
3	SO4	J	1904	-	4,4,4	3.23	2 (50%)	6,6,6	0.99	0
3	SO4	J	1906	-	4,4,4	0.35	0	6,6,6	0.60	0
6	GOL	J	1910	-	5,5,5	4.81	5 (100%)	5,5,5	4.81	3 (60%)
3	SO4	K	1504	-	4,4,4	3.18	2 (50%)	6,6,6	0.94	0
3	SO4	K	2001	-	4,4,4	3.22	2 (50%)	6,6,6	1.05	0
3	SO4	K	2003	-	4,4,4	3.16	2 (50%)	6,6,6	1.04	0
3	SO4	K	2006	-	4,4,4	0.51	0	6,6,6	1.05	1 (16%)
6	GOL	K	2011	-	5,5,5	4.69	5 (100%)	5,5,5	4.74	3 (60%)
3	SO4	L	2101	-	4,4,4	3.16	2 (50%)	6,6,6	0.92	0
3	SO4	L	2102	3	4,4,4	3.20	2 (50%)	6,6,6	0.95	0
3	SO4	L	2103	1	4,4,4	3.18	2 (50%)	6,6,6	0.94	0
3	SO4	L	2107	-	4,4,4	3.17	2 (50%)	6,6,6	0.94	0
5	FEC	L	2108[A]	1	34,56,56	1.10	0	43,90,90	1.62	7 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	FEC	L	2108[B]	1	34,56,56	1.09	1 (2%)	43,90,90	1.54	5 (11%)
3	SO4	M	2201	-	4,4,4	3.16	2 (50%)	6,6,6	0.96	0
3	SO4	M	2206	-	4,4,4	0.60	0	6,6,6	0.32	0
5	FEC	M	2207[A]	1	34,56,56	1.08	1 (2%)	43,90,90	1.59	8 (18%)
5	FEC	M	2207[B]	1	34,56,56	1.08	1 (2%)	43,90,90	1.39	5 (11%)
6	GOL	M	2210	1	5,5,5	4.76	5 (100%)	5,5,5	4.32	2 (40%)
6	GOL	M	2211	-	5,5,5	4.77	5 (100%)	5,5,5	4.50	3 (60%)
3	SO4	N	2301	-	4,4,4	3.20	2 (50%)	6,6,6	0.92	0
3	SO4	N	2303	-	4,4,4	0.21	0	6,6,6	0.78	0
3	SO4	N	2306	-	4,4,4	0.51	0	6,6,6	0.67	0
6	GOL	N	2310	-	5,5,5	4.77	5 (100%)	5,5,5	5.42	3 (60%)
3	SO4	O	2406	-	4,4,4	0.59	0	6,6,6	1.54	1 (16%)
3	SO4	O	2409	-	4,4,4	0.81	0	6,6,6	0.33	0
6	GOL	O	2410	-	5,5,5	4.66	5 (100%)	5,5,5	4.74	3 (60%)
6	GOL	O	2411	-	5,5,5	4.66	5 (100%)	5,5,5	3.86	3 (60%)
3	SO4	P	2501	-	4,4,4	3.16	2 (50%)	6,6,6	0.99	0
3	SO4	P	2503	-	4,4,4	0.51	0	6,6,6	0.71	0
3	SO4	P	2506	-	4,4,4	0.79	0	6,6,6	0.34	0
5	FEC	P	2507[A]	1	34,56,56	1.02	0	43,90,90	1.73	9 (20%)
5	FEC	P	2507[B]	1	34,56,56	1.00	0	43,90,90	1.89	7 (16%)
6	GOL	P	2510	-	5,5,5	4.72	5 (100%)	5,5,5	4.61	3 (60%)

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
3	SO4	A	1001	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1004	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1006	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1008	-	-	0/0/0/0	0/0/0/0
6	GOL	A	1010	-	-	0/4/4/4	0/0/0/0
3	SO4	A	1105	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1005	-	-	0/0/0/0	0/0/0/0
6	GOL	B	1011	-	-	0/4/4/4	0/0/0/0
3	SO4	B	1101	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1104	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1106	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	FEC	B	1107[A]	1	-	0/12/100/100	0/0/8/8
5	FEC	B	1107[B]	1	-	0/12/100/100	0/0/8/8
6	GOL	B	1110	-	-	0/4/4/4	0/0/0/0
3	SO4	C	1201	-	-	0/0/0/0	0/0/0/0
3	SO4	C	1203	-	-	0/0/0/0	0/0/0/0
3	SO4	C	1206	-	-	0/0/0/0	0/0/0/0
6	GOL	C	1210	-	-	0/4/4/4	0/0/0/0
6	GOL	D	1211	-	-	0/4/4/4	0/0/0/0
3	SO4	D	1301	-	-	0/0/0/0	0/0/0/0
3	SO4	D	1303	-	-	0/0/0/0	0/0/0/0
4	3PY	D	1310	1	-	0/1/4/6	0/0/0/0
5	FEC	D	1311[A]	1	-	1/12/100/100	0/0/8/8
5	FEC	D	1311[B]	1	-	0/12/100/100	0/0/8/8
3	SO4	E	1304	1	-	0/0/0/0	0/0/0/0
3	SO4	E	1401	-	-	0/0/0/0	0/0/0/0
3	SO4	E	1406	-	-	0/0/0/0	0/0/0/0
6	GOL	E	1410	-	-	0/4/4/4	0/0/0/0
6	GOL	E	1411	-	-	0/4/4/4	0/0/0/0
3	SO4	F	1501	-	-	0/0/0/0	0/0/0/0
3	SO4	F	1502	-	-	0/0/0/0	0/0/0/0
3	SO4	F	1506	-	-	0/0/0/0	0/0/0/0
5	FEC	F	1507[A]	1	-	0/12/100/100	0/0/8/8
5	FEC	F	1507[B]	1	-	0/12/100/100	0/0/8/8
6	GOL	F	1510	-	-	0/4/4/4	0/0/0/0
6	GOL	F	1512	-	-	0/4/4/4	0/0/0/0
3	SO4	G	1603	-	-	0/0/0/0	0/0/0/0
3	SO4	G	1606	-	-	0/0/0/0	0/0/0/0
3	SO4	G	1607	-	-	0/0/0/0	0/0/0/0
5	FEC	G	1608[A]	1	-	0/12/100/100	0/0/8/8
5	FEC	G	1608[B]	1	-	0/12/100/100	0/0/8/8
6	GOL	G	1610	-	-	0/4/4/4	0/0/0/0
6	GOL	G	1611	-	-	0/4/4/4	0/0/0/0
3	SO4	H	1701	-	-	0/0/0/0	0/0/0/0
3	SO4	H	1703	-	-	0/0/0/0	0/0/0/0
3	SO4	H	1706	-	-	0/0/0/0	0/0/0/0
6	GOL	H	1710	-	-	0/4/4/4	0/0/0/0
6	GOL	H	1814	-	-	0/4/4/4	0/0/0/0
6	GOL	I	1713	-	-	0/4/4/4	0/0/0/0
3	SO4	I	1801	-	-	0/0/0/0	0/0/0/0
3	SO4	I	1802	3	-	0/0/0/0	0/0/0/0
3	SO4	I	1803	-	-	0/0/0/0	0/0/0/0
3	SO4	I	1806	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	FEC	I	1807[A]	1	-	0/12/100/100	0/0/8/8
5	FEC	I	1807[B]	1	-	0/12/100/100	0/0/8/8
6	GOL	I	1810	1	-	0/4/4/4	0/0/0/0
6	GOL	J	1811	-	-	0/4/4/4	0/0/0/0
3	SO4	J	1901	-	-	0/0/0/0	0/0/0/0
3	SO4	J	1904	-	-	0/0/0/0	0/0/0/0
3	SO4	J	1906	-	-	0/0/0/0	0/0/0/0
6	GOL	J	1910	-	-	0/4/4/4	0/0/0/0
3	SO4	K	1504	-	-	0/0/0/0	0/0/0/0
3	SO4	K	2001	-	-	0/0/0/0	0/0/0/0
3	SO4	K	2003	-	-	0/0/0/0	0/0/0/0
3	SO4	K	2006	-	-	0/0/0/0	0/0/0/0
6	GOL	K	2011	-	-	0/4/4/4	0/0/0/0
3	SO4	L	2101	-	-	0/0/0/0	0/0/0/0
3	SO4	L	2102	3	-	0/0/0/0	0/0/0/0
3	SO4	L	2103	1	-	0/0/0/0	0/0/0/0
3	SO4	L	2107	-	-	0/0/0/0	0/0/0/0
5	FEC	L	2108[A]	1	-	0/12/100/100	0/0/8/8
5	FEC	L	2108[B]	1	-	0/12/100/100	0/0/8/8
3	SO4	M	2201	-	-	0/0/0/0	0/0/0/0
3	SO4	M	2206	-	-	0/0/0/0	0/0/0/0
5	FEC	M	2207[A]	1	-	0/12/100/100	0/0/8/8
5	FEC	M	2207[B]	1	-	0/12/100/100	0/0/8/8
6	GOL	M	2210	1	-	0/4/4/4	0/0/0/0
6	GOL	M	2211	-	-	0/4/4/4	0/0/0/0
3	SO4	N	2301	-	-	0/0/0/0	0/0/0/0
3	SO4	N	2303	-	-	0/0/0/0	0/0/0/0
3	SO4	N	2306	-	-	0/0/0/0	0/0/0/0
6	GOL	N	2310	-	-	0/4/4/4	0/0/0/0
3	SO4	O	2406	-	-	0/0/0/0	0/0/0/0
3	SO4	O	2409	-	-	0/0/0/0	0/0/0/0
6	GOL	O	2410	-	-	0/4/4/4	0/0/0/0
6	GOL	O	2411	-	-	0/4/4/4	0/0/0/0
3	SO4	P	2501	-	-	0/0/0/0	0/0/0/0
3	SO4	P	2503	-	-	0/0/0/0	0/0/0/0
3	SO4	P	2506	-	-	0/0/0/0	0/0/0/0
5	FEC	P	2507[A]	1	-	0/12/100/100	0/0/8/8
5	FEC	P	2507[B]	1	-	0/12/100/100	0/0/8/8
6	GOL	P	2510	-	-	0/4/4/4	0/0/0/0

The worst 5 of 181 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1310	3PY	C3-C2	-20.13	1.21	1.51
6	A	1010	GOL	C3-C2	-8.36	1.20	1.52
6	H	1710	GOL	C3-C2	-8.16	1.21	1.52
6	J	1811	GOL	C3-C2	-8.10	1.21	1.52
6	G	1610	GOL	C3-C2	-8.08	1.21	1.52

The worst 5 of 205 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1310	3PY	O3-C2-C1	-8.53	108.23	123.22
5	P	2507[B]	FEC	CAA-C3A-C4A	-5.66	120.86	127.01
5	F	1507[B]	FEC	CAA-C3A-C4A	-4.73	121.87	127.01
5	B	1107[B]	FEC	CAA-C3A-C4A	-4.56	122.06	127.01
5	D	1311[A]	FEC	CAA-C3A-C4A	-4.50	122.12	127.01

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	1311[A]	FEC	C3C-C2C-CAC-CBC

There are no ring outliers.

59 monomers are involved in 247 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1010	GOL	1	0
3	A	1105	SO4	3	0
3	B	1005	SO4	1	0
3	B	1104	SO4	1	0
3	B	1106	SO4	1	0
5	B	1107[A]	FEC	10	0
5	B	1107[B]	FEC	7	0
6	B	1110	GOL	3	0
3	C	1203	SO4	1	0
3	C	1206	SO4	1	0
6	D	1211	GOL	5	0
4	D	1310	3PY	1	0
5	D	1311[A]	FEC	8	0
5	D	1311[B]	FEC	14	0
3	E	1304	SO4	1	0
6	E	1410	GOL	6	0
3	F	1501	SO4	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	1502	SO4	2	0
5	F	1507[A]	FEC	4	0
5	F	1507[B]	FEC	13	0
6	F	1510	GOL	3	0
3	G	1606	SO4	1	0
5	G	1608[A]	FEC	9	0
5	G	1608[B]	FEC	6	0
6	G	1610	GOL	2	0
6	G	1611	GOL	1	0
6	H	1710	GOL	1	0
6	I	1713	GOL	1	0
3	I	1802	SO4	1	7
3	I	1803	SO4	1	0
5	I	1807[A]	FEC	9	0
5	I	1807[B]	FEC	9	0
6	I	1810	GOL	15	0
6	J	1811	GOL	1	0
3	J	1904	SO4	1	0
3	J	1906	SO4	3	0
6	J	1910	GOL	4	0
3	K	1504	SO4	1	0
6	K	2011	GOL	1	0
3	L	2102	SO4	1	7
3	L	2103	SO4	1	0
3	L	2107	SO4	1	0
5	L	2108[A]	FEC	11	0
5	L	2108[B]	FEC	12	0
3	M	2206	SO4	2	0
5	M	2207[A]	FEC	10	0
5	M	2207[B]	FEC	8	0
6	M	2210	GOL	5	0
6	M	2211	GOL	3	0
6	N	2310	GOL	1	0
3	O	2406	SO4	1	0
3	O	2409	SO4	1	0
6	O	2410	GOL	2	0
6	O	2411	GOL	2	0
3	P	2501	SO4	1	0
3	P	2506	SO4	1	0
5	P	2507[A]	FEC	8	0
5	P	2507[B]	FEC	13	0
6	P	2510	GOL	2	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	169/179 (94%)	0.15	10 (5%) 26 36	16, 24, 43, 65	0
1	B	170/179 (94%)	0.01	9 (5%) 30 41	15, 24, 45, 65	0
1	C	170/179 (94%)	-0.02	8 (4%) 35 46	16, 25, 45, 65	0
1	D	170/179 (94%)	0.05	9 (5%) 30 41	16, 25, 44, 65	1 (0%)
1	E	170/179 (94%)	0.08	9 (5%) 30 41	17, 25, 47, 65	1 (0%)
1	F	170/179 (94%)	0.00	7 (4%) 41 52	16, 25, 46, 68	1 (0%)
1	G	169/179 (94%)	-0.05	4 (2%) 62 72	15, 24, 43, 65	0
1	H	170/179 (94%)	0.05	12 (7%) 19 29	16, 25, 44, 65	0
1	I	170/179 (94%)	0.04	7 (4%) 41 52	16, 24, 43, 65	0
1	J	170/179 (94%)	0.02	9 (5%) 30 41	17, 25, 47, 65	0
1	K	170/179 (94%)	-0.02	5 (2%) 55 65	16, 24, 46, 68	0
1	L	170/179 (94%)	0.02	4 (2%) 62 72	16, 24, 43, 65	1 (0%)
1	M	170/179 (94%)	-0.01	8 (4%) 35 46	15, 24, 47, 65	0
1	N	170/179 (94%)	-0.00	6 (3%) 48 58	16, 24, 43, 65	0
1	O	169/179 (94%)	0.14	7 (4%) 41 52	16, 25, 44, 68	1 (0%)
1	P	170/179 (94%)	-0.05	8 (4%) 35 46	17, 25, 48, 65	0
All	All	2717/2864 (94%)	0.03	122 (4%) 37 48	15, 25, 46, 68	5 (0%)

The worst 5 of 122 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	166	THR	7.3
1	C	166	THR	7.3
1	E	168[A]	SER	6.9
1	N	166	THR	6.7
1	I	166	THR	6.5

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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	SO4	G	1607	5/5	0.60	0.39	15.39	67,67,70,70	0
3	SO4	A	1105	5/5	0.89	0.48	13.85	51,53,55,61	0
3	SO4	O	2409	5/5	0.75	0.41	6.98	57,63,66,67	0
6	GOL	P	2510	6/6	0.86	0.28	5.08	32,51,74,105	0
6	GOL	J	1910	6/6	0.78	0.30	4.46	46,52,80,104	0
3	SO4	L	2107	5/5	0.91	0.19	3.87	78,78,78,79	0
6	GOL	H	1710	6/6	0.83	0.26	3.56	50,52,61,94	0
6	GOL	I	1810	6/6	0.81	0.30	3.38	27,42,66,76	0
6	GOL	C	1210	6/6	0.87	0.28	3.13	32,43,67,71	0
3	SO4	B	1005	5/5	0.93	0.29	3.12	51,53,55,61	0
6	GOL	E	1410	6/6	0.93	0.23	2.81	39,50,75,155	0
3	SO4	K	2001	5/5	0.81	0.27	2.74	51,53,53,54	0
6	GOL	G	1610	6/6	0.86	0.21	2.66	44,46,56,106	0
3	SO4	E	1401	5/5	0.83	0.28	2.23	67,68,68,68	0
6	GOL	B	1110	6/6	0.82	0.20	2.20	40,46,69,84	0
6	GOL	M	2210	6/6	0.90	0.26	2.03	34,50,95,99	0
6	GOL	J	1811	6/6	0.88	0.23	2.01	40,57,107,154	0
6	GOL	A	1010	6/6	0.81	0.29	1.58	42,68,89,111	0
3	SO4	H	1701	5/5	0.90	0.20	1.52	54,54,55,56	0
6	GOL	I	1713	6/6	0.79	0.22	1.51	52,57,84,157	0
3	SO4	D	1301	5/5	0.87	0.24	1.40	58,59,60,60	0
6	GOL	F	1510	6/6	0.88	0.21	1.36	52,62,92,104	0
6	GOL	F	1512	6/6	0.95	0.13	1.36	22,37,47,49	0
6	GOL	H	1814	6/6	0.83	0.16	1.33	38,49,55,61	0
3	SO4	J	1901	5/5	0.73	0.29	1.19	66,67,67,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	GOL	O	2410	6/6	0.86	0.21	1.06	47,53,59,61	0
3	SO4	A	1001	5/5	0.89	0.22	1.04	53,54,54,55	0
6	GOL	G	1611	6/6	0.83	0.19	0.97	31,53,70,78	0
6	GOL	N	2310	6/6	0.87	0.18	0.77	38,48,69,155	0
3	SO4	P	2501	5/5	0.84	0.18	0.76	62,62,63,63	0
3	SO4	M	2201	5/5	0.91	0.19	0.75	51,51,52,53	0
4	3PY	D	1310	6/7	0.87	0.19	0.64	50,63,70,78	0
3	SO4	L	2101	5/5	0.83	0.20	0.54	64,64,65,65	0
3	SO4	C	1201	5/5	0.84	0.18	0.53	65,65,67,67	0
6	GOL	E	1411	6/6	0.76	0.19	0.51	34,56,92,108	0
3	SO4	N	2301	5/5	0.91	0.21	0.50	62,63,63,63	0
6	GOL	B	1011	6/6	0.90	0.17	0.46	24,48,57,79	0
6	GOL	M	2211	6/6	0.86	0.16	0.45	40,61,98,143	0
6	GOL	K	2011	6/6	0.91	0.14	0.24	46,57,59,146	0
2	FE	L	201	1/1	0.79	0.11	0.24	42,42,42,42	0
3	SO4	B	1101	5/5	0.88	0.17	0.15	66,66,67,67	0
2	FE	A	201	1/1	0.87	0.12	0.15	44,44,44,44	0
5	FEC	D	1311[A]	49/49	0.95	0.19	0.14	15,19,28,37	49
3	SO4	I	1801	5/5	0.94	0.17	0.08	61,61,62,63	0
5	FEC	D	1311[B]	49/49	0.95	0.19	0.06	10,19,28,46	49
5	FEC	G	1608[A]	49/49	0.96	0.19	0.03	15,18,28,37	49
2	FE	M	201	1/1	0.87	0.10	0.03	40,40,40,40	0
5	FEC	P	2507[A]	49/49	0.96	0.17	0.02	15,18,28,37	49
5	FEC	B	1107[A]	49/49	0.96	0.20	0.01	15,18,28,37	49
5	FEC	G	1608[B]	49/49	0.96	0.19	0.01	10,17,29,38	49
5	FEC	L	2108[B]	49/49	0.97	0.19	-0.01	13,18,28,39	49
5	FEC	M	2207[B]	49/49	0.97	0.18	-0.04	13,18,27,39	49
5	FEC	I	1807[A]	49/49	0.97	0.18	-0.05	15,19,28,37	49
5	FEC	M	2207[A]	49/49	0.97	0.18	-0.06	14,18,28,37	49
5	FEC	B	1107[B]	49/49	0.96	0.20	-0.07	15,18,27,38	49
5	FEC	L	2108[A]	49/49	0.97	0.19	-0.07	15,18,28,37	49
3	SO4	F	1501	5/5	0.91	0.16	-0.07	66,66,67,67	0
2	FE	D	201	1/1	0.88	0.09	-0.11	46,46,46,46	0
5	FEC	I	1807[B]	49/49	0.97	0.18	-0.15	14,19,27,38	49
5	FEC	F	1507[A]	49/49	0.96	0.17	-0.16	15,19,29,36	49
5	FEC	P	2507[B]	49/49	0.96	0.17	-0.17	16,18,28,33	49
5	FEC	F	1507[B]	49/49	0.96	0.17	-0.20	16,19,31,38	49
2	FE	C	201	1/1	0.93	0.09	-0.24	46,46,46,46	0
3	SO4	I	1802	5/5	0.95	0.15	-0.38	36,37,38,38	0
3	SO4	L	2102	5/5	0.96	0.16	-0.46	78,78,78,79	5
2	FE	B	201	1/1	0.78	0.09	-0.48	44,44,44,44	0
2	FE	O	201	1/1	0.96	0.09	-0.51	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	FE	H	201	1/1	0.92	0.09	-0.51	43,43,43,43	0
2	FE	N	201	1/1	0.93	0.09	-0.56	43,43,43,43	0
6	GOL	D	1211	6/6	0.90	0.12	-0.60	45,49,55,68	0
2	FE	G	201	1/1	0.92	0.08	-0.69	43,43,43,43	0
2	FE	I	201	1/1	0.93	0.09	-0.82	43,43,43,43	0
2	FE	O	200	1/1	0.99	0.06	-1.02	29,29,29,29	0
2	FE	L	200	1/1	0.99	0.07	-1.11	26,26,26,26	0
2	FE	B	200	1/1	1.00	0.07	-1.40	25,25,25,25	0
2	FE	M	200	1/1	0.99	0.06	-1.55	26,26,26,26	0
2	FE	E	201	1/1	0.95	0.07	-1.64	44,44,44,44	0
2	FE	E	200	1/1	0.99	0.08	-1.69	29,29,29,29	0
2	FE	A	200	1/1	0.98	0.07	-1.83	27,27,27,27	0
2	FE	F	201	1/1	0.89	0.06	-1.95	46,46,46,46	0
2	FE	F	200	1/1	0.99	0.06	-2.03	29,29,29,29	0
2	FE	D	200	1/1	1.00	0.06	-2.03	29,29,29,29	0
2	FE	N	200	1/1	0.99	0.05	-2.04	25,25,25,25	0
2	FE	K	200	1/1	0.99	0.06	-2.14	28,28,28,28	0
2	FE	P	201	1/1	0.95	0.05	-2.29	45,45,45,45	0
2	FE	G	200	1/1	0.99	0.06	-2.62	26,26,26,26	0
2	FE	P	200	1/1	0.99	0.05	-3.22	28,28,28,28	0
2	FE	C	200	1/1	0.99	0.04	-3.38	28,28,28,28	0
2	FE	I	200	1/1	0.99	0.06	-3.70	27,27,27,27	0
2	FE	H	200	1/1	0.99	0.04	-3.77	26,26,26,26	0
2	FE	J	200	1/1	0.99	0.04	-3.94	30,30,30,30	0
3	SO4	H	1706	5/5	0.88	0.33	-	47,55,58,60	0
2	FE	J	201	1/1	0.93	0.07	-	46,46,46,46	0
3	SO4	E	1304	5/5	0.75	0.40	-	65,65,67,67	0
3	SO4	B	1104	5/5	0.90	0.15	-	73,73,74,75	0
3	SO4	J	1906	5/5	0.85	0.35	-	50,51,59,59	0
3	SO4	J	1904	5/5	0.93	0.22	-	61,61,62,63	5
3	SO4	K	1504	5/5	0.73	0.23	-	78,78,78,79	0
3	SO4	O	2406	5/5	0.88	0.21	-	41,44,46,47	5
3	SO4	P	2503	5/5	0.79	0.28	-	42,43,47,49	5
3	SO4	H	1703	5/5	0.79	0.49	-	40,43,48,48	0
3	SO4	G	1603	5/5	0.79	0.41	-	73,73,74,75	0
3	SO4	N	2306	5/5	0.90	0.23	-	60,65,69,71	0
3	SO4	E	1406	5/5	0.94	0.22	-	62,67,67,70	0
3	SO4	G	1606	5/5	0.85	0.26	-	58,65,67,73	0
3	SO4	A	1008	5/5	0.91	0.42	-	51,53,55,61	0
3	SO4	C	1206	5/5	0.87	0.36	-	46,46,47,49	0
3	SO4	F	1502	5/5	0.81	0.43	-	69,69,69,71	0
3	SO4	M	2206	5/5	0.85	0.31	-	58,60,67,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	SO4	L	2103	5/5	0.79	0.36	-	78,78,78,79	0
3	SO4	K	2003	5/5	0.93	0.29	-	69,69,69,71	0
3	SO4	D	1303	5/5	0.79	0.23	-	39,44,45,50	5
3	SO4	N	2303	5/5	0.90	0.50	-	64,68,70,72	0
3	SO4	B	1106	5/5	0.88	0.33	-	64,66,74,75	0
3	SO4	I	1803	5/5	0.86	0.36	-	67,67,70,70	0
2	FE	K	201	1/1	0.91	0.09	-	43,43,43,43	0
3	SO4	K	2006	5/5	0.95	0.23	-	52,55,60,61	0
3	SO4	A	1004	5/5	0.42	0.51	-	66,66,67,67	5
6	GOL	O	2411	6/6	0.92	0.11	-	26,52,74,76	0
3	SO4	C	1203	5/5	0.89	0.34	-	56,58,62,64	0
3	SO4	F	1506	5/5	0.91	0.25	-	65,67,68,69	0
3	SO4	P	2506	5/5	0.95	0.24	-	57,63,66,67	0
3	SO4	A	1006	5/5	0.89	0.36	-	56,67,69,74	0
3	SO4	I	1806	5/5	0.91	0.31	-	62,65,67,69	0

6.5 Other polymers [i](#)

There are no such residues in this entry.