



wwPDB X-ray Structure Validation Summary Report i

Feb 27, 2014 – 11:51 PM GMT

PDB ID : 2Y3Q
Title : 1.55A STRUCTURE OF APO BACTERIOFERRITIN FROM E. COLI
Authors : Hough, M.A.; Antonyuk, S.V.
Deposited on : 2010-12-22
Resolution : 1.55 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>

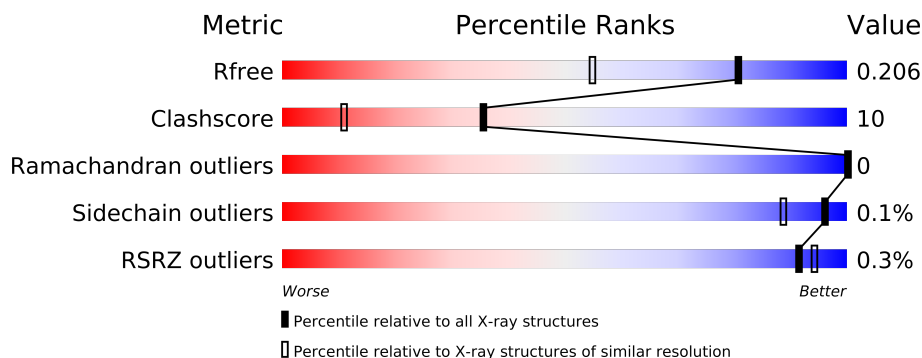
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.55 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	1117 (1.58-1.54)
Clashscore	79885	1249 (1.58-1.54)
Ramachandran outliers	78287	1212 (1.58-1.54)
Sidechain outliers	78261	1210 (1.58-1.54)
RSRZ outliers	66119	1117 (1.58-1.54)

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	158	
1	B	158	
1	C	158	
1	D	158	
1	E	158	
1	F	158	
1	G	158	
1	H	158	
1	I	158	
1	J	158	
1	K	158	
1	L	158	

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	HEM	A	200[A]	-	X
2	HEM	A	200[B]	-	X
2	HEM	B	200[A]	-	X
2	HEM	B	200[B]	-	X
2	HEM	C	200[A]	-	X
2	HEM	C	200[B]	-	X
2	HEM	D	200[A]	-	X
2	HEM	D	200[B]	-	X
2	HEM	E	200	-	X
2	HEM	F	200[A]	-	X
2	HEM	F	200[B]	-	X
2	HEM	G	200[A]	-	X
2	HEM	G	200[B]	-	X
2	HEM	H	200[A]	-	X
2	HEM	H	200[B]	-	X
2	HEM	I	200[A]	-	X
2	HEM	I	200[B]	-	X
2	HEM	J	200[A]	-	X
2	HEM	J	200[B]	-	X
2	HEM	K	200[A]	-	X
2	HEM	K	200[B]	-	X
2	HEM	L	200[A]	-	X
2	HEM	L	200[B]	-	X
3	SO4	A	1159	-	X
3	SO4	B	1159	-	X
3	SO4	B	1161	-	X
3	SO4	C	1159	-	X
3	SO4	C	1160	-	X
3	SO4	D	1159	-	X
3	SO4	E	1160	-	X
3	SO4	F	1159	-	X
3	SO4	G	1159	-	X
3	SO4	H	1160	-	X
3	SO4	I	1159	-	X
3	SO4	I	1161	-	X
3	SO4	J	1159	-	X
3	SO4	K	1159	-	X
3	SO4	L	1159	-	X
4	ACT	D	1160	-	X
4	ACT	F	1160	-	X
4	ACT	J	1160	-	X
4	ACT	K	1160	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
5	BTB	D	1161	-	X
5	BTB	I	1162	-	X
5	BTB	K	1161	-	X
5	BTB	L	1161	-	X

2 Entry composition

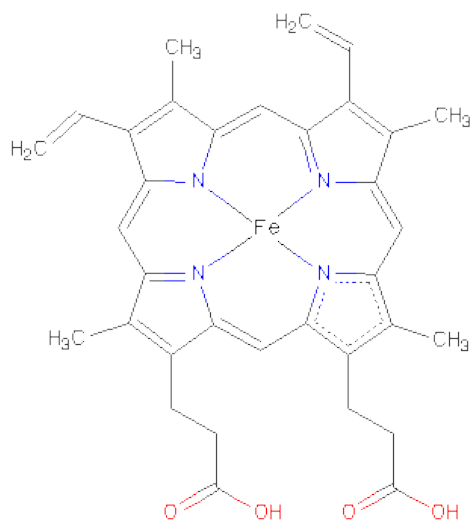
There are 6 unique types of molecules in this entry. The entry contains 20288 atoms, of which 0 are hydrogen and 0 are deuterium.

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 BACTERIOFERRITIN.

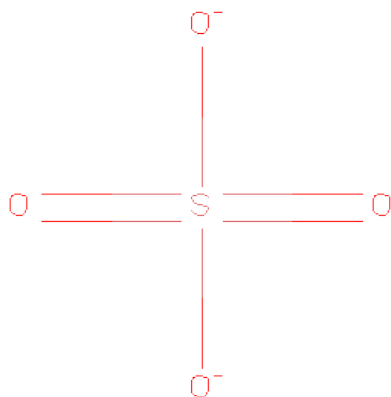
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	158	Total	C	N	O	S	0	15	1
			1394	879	231	277	7			
1	B	158	Total	C	N	O	S	0	17	1
			1403	887	234	275	7			
1	C	158	Total	C	N	O	S	0	15	1
			1383	876	229	271	7			
1	D	158	Total	C	N	O	S	0	13	1
			1371	868	230	266	7			
1	E	158	Total	C	N	O	S	0	14	1
			1381	874	229	271	7			
1	F	158	Total	C	N	O	S	0	16	1
			1400	883	236	274	7			
1	G	158	Total	C	N	O	S	0	16	1
			1393	881	233	272	7			
1	H	158	Total	C	N	O	S	0	13	1
			1379	868	232	272	7			
1	I	158	Total	C	N	O	S	0	16	1
			1388	877	232	272	7			
1	J	158	Total	C	N	O	S	0	12	1
			1365	863	227	268	7			
1	K	158	Total	C	N	O	S	0	14	1
			1373	868	228	270	7			
1	L	158	Total	C	N	O	S	0	11	1
			1361	860	228	266	7			

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	A	1	Total 45	C 36	Fe 1	N 4	O 4	0	1
2	B	1	Total 45	C 36	Fe 1	N 4	O 4	0	1
2	C	1	Total 45	C 36	Fe 1	N 4	O 4	0	1
2	D	1	Total 45	C 36	Fe 1	N 4	O 4	0	1
2	E	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	F	1	Total 45	C 36	Fe 1	N 4	O 4	0	1
2	G	1	Total 45	C 36	Fe 1	N 4	O 4	0	1
2	H	1	Total 45	C 36	Fe 1	N 4	O 4	0	1
2	I	1	Total 45	C 36	Fe 1	N 4	O 4	0	1
2	J	1	Total 45	C 36	Fe 1	N 4	O 4	0	1
2	K	1	Total 45	C 36	Fe 1	N 4	O 4	0	1
2	L	1	Total 45	C 36	Fe 1	N 4	O 4	0	1

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



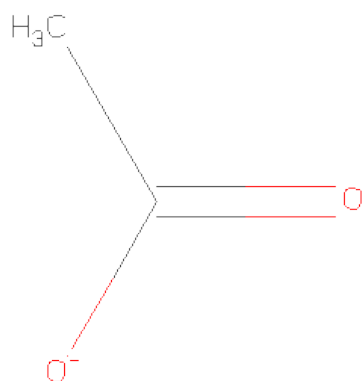
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total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

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

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



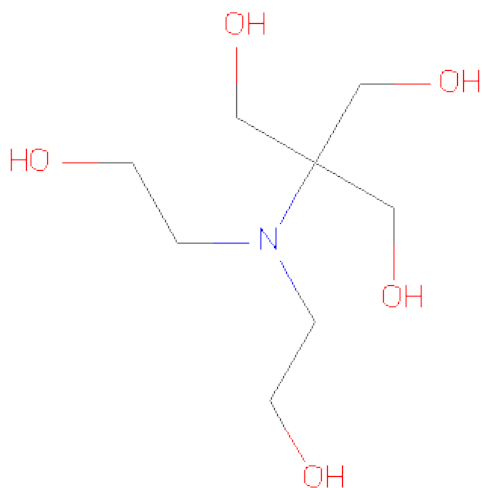
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	E	1	Total	C	O	0	0
			4	2	2		
4	F	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	G	1	Total	C	O	0	0
			4	2	2		
4	H	1	Total	C	O	0	0
			4	2	2		
4	I	1	Total	C	O	0	0
			4	2	2		
4	J	1	Total	C	O	0	0
			4	2	2		
4	K	1	Total	C	O	0	0
			4	2	2		
4	L	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (three-letter code: BTB) (formula: C₈H₁₉NO₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	D	1	Total	C	N	O	0	0
			8	4	1	3		
5	I	1	Total	C	N	O	0	0
			8	4	1	3		
5	K	1	Total	C	N	O	0	0
			8	4	1	3		
5	L	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	254	Total 256	O 256	0	2
6	B	235	Total 236	O 236	0	1
6	C	249	Total 251	O 251	0	2
6	D	247	Total 247	O 247	0	0
6	E	256	Total 257	O 257	0	1
6	F	243	Total 243	O 243	0	0
6	G	250	Total 250	O 250	0	0
6	H	245	Total 245	O 245	0	0
6	I	257	Total 257	O 257	0	0
6	J	254	Total 254	O 254	0	0
6	K	255	Total 255	O 255	0	0
6	L	233	Total 233	O 233	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: BACTERIOFERRITIN

Chain A: 



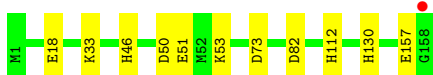
- Molecule 1: BACTERIOFERRITIN

Chain B: 



- Molecule 1: BACTERIOFERRITIN

Chain C: 



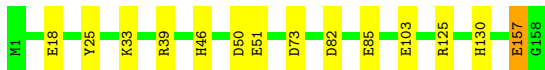
- Molecule 1: BACTERIOFERRITIN

Chain D: 



- Molecule 1: BACTERIOFERRITIN

Chain E: 



- Molecule 1: BACTERIOFERRITIN

Chain F: 



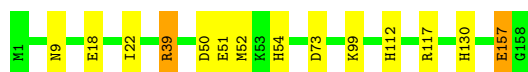
● Molecule 1: BACTERIOFERRITIN

Chain G: 

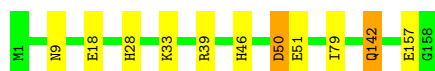
● Molecule 1: BACTERIOFERRITIN

Chain H: 

● Molecule 1: BACTERIOFERRITIN

Chain I: 

● Molecule 1: BACTERIOFERRITIN

Chain J: 

● Molecule 1: BACTERIOFERRITIN

Chain K: 

● Molecule 1: BACTERIOFERRITIN

Chain L: 

4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	208.00Å 208.00Å 142.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.23 – 1.55 43.23 – 1.55	Depositor EDS
% Data completeness (in resolution range)	100.0 (43.23-1.55) 98.4 (43.23-1.55)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.35 (at 1.55Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.165 , 0.200 0.175 , 0.206	Depositor DCC
R_{free} test set	21922 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	10.1	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 40.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	53 of 438427 reflections (0.012%)	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	20288	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 45.32 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.3450e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: HEM, ACT, SO4, BTB

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	0.69	1/1448 (0.1%)	0.78	0/1949
1	B	0.69	1/1464 (0.1%)	0.79	0/1970
1	C	0.73	1/1444 (0.1%)	0.80	0/1944
1	D	0.71	1/1427 (0.1%)	0.79	0/1921
1	E	0.72	1/1441 (0.1%)	0.80	1/1938 (0.1%)
1	F	0.71	1/1456 (0.1%)	0.78	0/1958
1	G	0.67	0/1448	0.80	1/1949 (0.1%)
1	H	0.72	0/1422	0.83	4/1915 (0.2%)
1	I	0.70	1/1449 (0.1%)	0.83	3/1952 (0.2%)
1	J	0.70	1/1418 (0.1%)	0.80	0/1908
1	K	0.72	1/1436 (0.1%)	0.81	0/1934
1	L	0.72	1/1409 (0.1%)	0.80	1/1896 (0.1%)
All	All	0.71	10/17262 (0.1%)	0.80	10/23234 (0.0%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	157	GLU	C-N	-6.14	1.22	1.33
1	F	157	GLU	C-N	-5.98	1.22	1.33
1	B	157	GLU	C-N	-5.98	1.22	1.33
1	L	157	GLU	C-N	-5.48	1.23	1.33
1	J	157	GLU	C-N	-5.47	1.23	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	125	ARG	NE-CZ-NH1	-7.44	116.58	120.30
1	I	117	ARG	NE-CZ-NH2	-5.90	117.35	120.30
1	H	117	ARG	NE-CZ-NH2	-5.78	117.41	120.30
1	E	125	ARG	NE-CZ-NH1	-5.75	117.43	120.30
1	H	132	ASP	CB-CG-OD1	5.59	123.33	118.30

There are no chirality outliers.

There are no planarity outliers.

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	1394	0	0	10	0
1	B	1403	0	0	15	0
1	C	1383	0	0	12	0
1	D	1371	0	0	14	0
1	E	1381	0	0	14	0
1	F	1400	0	0	15	0
1	G	1393	0	0	10	0
1	H	1379	0	0	13	0
1	I	1388	0	0	16	0
1	J	1365	0	0	9	0
1	K	1373	0	0	11	0
1	L	1361	0	0	11	1
2	A	45	0	0	1	0
2	B	45	0	0	4	0
2	C	45	0	0	1	0
2	D	45	0	0	4	0
2	E	43	0	0	2	0
2	F	45	0	0	1	0
2	G	45	0	0	1	0
2	H	45	0	0	1	0
2	I	45	0	0	1	0
2	J	45	0	0	1	0
2	K	45	0	0	4	0
2	L	45	0	0	1	0
3	A	5	0	0	0	0
3	B	15	0	0	1	0
3	C	15	0	0	1	0
3	D	5	0	0	1	0
3	E	10	0	0	1	0
3	F	5	0	0	1	0
3	G	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	10	0	0	1	0
3	I	10	0	0	0	0
3	J	5	0	0	0	0
3	K	5	0	0	1	0
3	L	5	0	0	1	0
4	A	4	0	0	0	0
4	B	4	0	0	0	0
4	C	4	0	0	0	0
4	D	4	0	0	0	0
4	E	4	0	0	0	0
4	F	4	0	0	0	0
4	G	4	0	0	0	0
4	H	4	0	0	0	0
4	I	4	0	0	0	0
4	J	4	0	0	0	0
4	K	4	0	0	0	0
4	L	4	0	0	0	0
5	D	8	0	0	1	0
5	I	8	0	0	0	0
5	K	8	0	0	0	0
5	L	8	0	0	0	0
6	A	256	0	0	5	1
6	B	236	0	0	13	0
6	C	251	0	0	6	1
6	D	247	0	0	12	0
6	E	257	0	0	10	0
6	F	243	0	0	13	2
6	G	250	0	0	8	2
6	H	245	0	0	11	0
6	I	257	0	0	9	0
6	J	254	0	0	6	0
6	K	255	0	0	8	1
6	L	233	0	0	8	2
All	All	20288	0	0	179	5

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 10.

The worst 5 of 179 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:46[B]:HIS:CE1	6:D:2105:HOH:O	1.82	1.30
1:E:46[A]:HIS:CD2	6:E:2103:HOH:O	1.67	1.26

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:46[A]:HIS:CE1	6:H:2103:HOH:O	1.65	1.26
1:D:46[B]:HIS:ND1	6:D:2105:HOH:O	1.61	1.26
1:C:46[A]:HIS:CD2	6:C:2102:HOH:O	1.86	1.25

All (5) 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	Distance(Å)	Clash(Å)
6:G:2230:HOH:O	6:L:2075:HOH:O[8_665]	1.52	0.68
6:C:2084:HOH:O	6:G:2200:HOH:O[8_665]	1.88	0.32
1:L:6:LYS:CE	6:F:2007:HOH:O[5_555]	1.96	0.24
6:F:2185:HOH:O	6:L:2170:HOH:O[5_545]	2.14	0.06
6:A:2190:HOH:O	6:K:2193:HOH:O[6_565]	2.16	0.04

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	172/158 (109%)	170 (99%)	2 (1%)	0	100	100
1	B	173/158 (110%)	169 (98%)	4 (2%)	0	100	100
1	C	171/158 (108%)	168 (98%)	3 (2%)	0	100	100
1	D	169/158 (107%)	166 (98%)	3 (2%)	0	100	100
1	E	170/158 (108%)	168 (99%)	2 (1%)	0	100	100
1	F	173/158 (110%)	172 (99%)	1 (1%)	0	100	100
1	G	172/158 (109%)	167 (97%)	5 (3%)	0	100	100
1	H	169/158 (107%)	166 (98%)	3 (2%)	0	100	100
1	I	172/158 (109%)	170 (99%)	2 (1%)	0	100	100
1	J	168/158 (106%)	166 (99%)	2 (1%)	0	100	100
1	K	170/158 (108%)	168 (99%)	2 (1%)	0	100	100
1	L	167/158 (106%)	166 (99%)	1 (1%)	0	100	100
All	All	2046/1896 (108%)	2016 (98%)	30 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	153/139 (110%)	153 (100%)	0	100	100
1	B	154/139 (111%)	154 (100%)	0	100	100
1	C	151/139 (109%)	151 (100%)	0	100	100
1	D	149/139 (107%)	149 (100%)	0	100	100
1	E	152/139 (109%)	152 (100%)	0	100	100
1	F	154/139 (111%)	154 (100%)	0	100	100
1	G	152/139 (109%)	152 (100%)	0	100	100
1	H	149/139 (107%)	149 (100%)	0	100	100
1	I	153/139 (110%)	153 (100%)	0	100	100
1	J	150/139 (108%)	147 (98%)	3 (2%)	68	35
1	K	151/139 (109%)	151 (100%)	0	100	100
1	L	149/139 (107%)	149 (100%)	0	100	100
All	All	1817/1668 (109%)	1814 (100%)	3 (0%)	96	88

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	50[A]	ASP
1	J	50[B]	ASP
1	J	142	GLN

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 ⓘ

58 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	A	1159	-	4,4,4	0.66	0	6,6,6	0.67	0
4	ACT	A	1160	-	1,3,3	1.39	0	0,3,3	0.00	-
2	HEM	A	200[A]	-	0,1,50	0.00	-	0,0,82	0.00	-
2	HEM	A	200[B]	-	0,1,50	0.00	-	0,0,82	0.00	-
3	SO4	B	1159	-	4,4,4	0.33	0	6,6,6	0.33	0
3	SO4	B	1160	-	4,4,4	0.36	0	6,6,6	0.25	0
3	SO4	B	1161	-	4,4,4	0.67	0	6,6,6	0.74	0
4	ACT	B	1162	-	1,3,3	1.10	0	0,3,3	0.00	-
2	HEM	B	200[A]	-	0,1,50	0.00	-	0,0,82	0.00	-
2	HEM	B	200[B]	-	0,1,50	0.00	-	0,0,82	0.00	-
3	SO4	C	1158	-	4,4,4	0.49	0	6,6,6	0.23	0
3	SO4	C	1159	-	4,4,4	0.58	0	6,6,6	0.63	0
3	SO4	C	1160	-	4,4,4	0.16	0	6,6,6	0.26	0
4	ACT	C	1161	-	1,3,3	1.88	0	0,3,3	0.00	-
2	HEM	C	200[A]	-	0,1,50	0.00	-	0,0,82	0.00	-
2	HEM	C	200[B]	-	0,1,50	0.00	-	0,0,82	0.00	-
3	SO4	D	1159	-	4,4,4	0.67	0	6,6,6	0.66	0
4	ACT	D	1160	-	1,3,3	1.66	0	0,3,3	0.00	-
5	BTB	D	1161	-	7,7,13	0.86	0	6,9,16	1.58	1 (16%)
2	HEM	D	200[A]	-	0,1,50	0.00	-	0,0,82	0.00	-
2	HEM	D	200[B]	-	0,1,50	0.00	-	0,0,82	0.00	-
3	SO4	E	1159	-	4,4,4	0.47	0	6,6,6	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	E	1160	-	4,4,4	0.49	0	6,6,6	0.63	0
4	ACT	E	1161	-	1,3,3	1.44	0	0,3,3	0.00	-
2	HEM	E	200	1	49,50,50	2.03	12 (24%)	46,82,82	2.24	10 (21%)
3	SO4	F	1159	-	4,4,4	0.68	0	6,6,6	0.77	0
4	ACT	F	1160	-	1,3,3	1.80	0	0,3,3	0.00	-
2	HEM	F	200[A]	-	0,1,50	0.00	-	0,0,82	0.00	-
2	HEM	F	200[B]	-	0,1,50	0.00	-	0,0,82	0.00	-
3	SO4	G	1159	-	4,4,4	0.69	0	6,6,6	0.93	1 (16%)
4	ACT	G	1160	-	1,3,3	1.71	0	0,3,3	0.00	-
2	HEM	G	200[A]	-	0,1,50	0.00	-	0,0,82	0.00	-
2	HEM	G	200[B]	-	0,1,50	0.00	-	0,0,82	0.00	-
3	SO4	H	1159	-	4,4,4	0.43	0	6,6,6	0.20	0
3	SO4	H	1160	-	4,4,4	0.72	0	6,6,6	0.50	0
4	ACT	H	1161	-	1,3,3	0.98	0	0,3,3	0.00	-
2	HEM	H	200[A]	-	0,1,50	0.00	-	0,0,82	0.00	-
2	HEM	H	200[B]	-	0,1,50	0.00	-	0,0,82	0.00	-
3	SO4	I	1159	-	4,4,4	0.65	0	6,6,6	0.55	0
4	ACT	I	1160	-	1,3,3	0.88	0	0,3,3	0.00	-
3	SO4	I	1161	-	4,4,4	0.46	0	6,6,6	0.62	0
5	BTB	I	1162	-	7,7,13	0.95	0	6,9,16	1.48	1 (16%)
2	HEM	I	200[A]	-	0,1,50	0.00	-	0,0,82	0.00	-
2	HEM	I	200[B]	-	0,1,50	0.00	-	0,0,82	0.00	-
3	SO4	J	1159	-	4,4,4	0.67	0	6,6,6	1.00	1 (16%)
4	ACT	J	1160	-	1,3,3	1.10	0	0,3,3	0.00	-
2	HEM	J	200[A]	-	0,1,50	0.00	-	0,0,82	0.00	-
2	HEM	J	200[B]	-	0,1,50	0.00	-	0,0,82	0.00	-
3	SO4	K	1159	-	4,4,4	0.67	0	6,6,6	0.86	0
4	ACT	K	1160	-	1,3,3	2.07	1 (100%)	0,3,3	0.00	-
5	BTB	K	1161	-	7,7,13	1.03	1 (14%)	6,9,16	1.91	2 (33%)
2	HEM	K	200[A]	-	0,1,50	0.00	-	0,0,82	0.00	-
2	HEM	K	200[B]	-	0,1,50	0.00	-	0,0,82	0.00	-
3	SO4	L	1159	-	4,4,4	0.73	0	6,6,6	0.32	0
4	ACT	L	1160	-	1,3,3	1.23	0	0,3,3	0.00	-
5	BTB	L	1161	-	7,7,13	0.82	0	6,9,16	1.32	1 (16%)
2	HEM	L	200[A]	-	0,1,50	0.00	-	0,0,82	0.00	-
2	HEM	L	200[B]	-	0,1,50	0.00	-	0,0,82	0.00	-

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	1159	-	-	0/0/0/0	0/0/0/0
4	ACT	A	1160	-	-	0/0/0/0	0/0/0/0
2	HEM	A	200[A]	-	-	0/0/0/114	0/0/0/8
2	HEM	A	200[B]	-	-	0/0/0/114	0/0/0/8
3	SO4	B	1159	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1160	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1161	-	-	0/0/0/0	0/0/0/0
4	ACT	B	1162	-	-	0/0/0/0	0/0/0/0
2	HEM	B	200[A]	-	-	0/0/0/114	0/0/0/8
2	HEM	B	200[B]	-	-	0/0/0/114	0/0/0/8
3	SO4	C	1158	-	-	0/0/0/0	0/0/0/0
3	SO4	C	1159	-	-	0/0/0/0	0/0/0/0
3	SO4	C	1160	-	-	0/0/0/0	0/0/0/0
4	ACT	C	1161	-	-	0/0/0/0	0/0/0/0
2	HEM	C	200[A]	-	-	0/0/0/114	0/0/0/8
2	HEM	C	200[B]	-	-	0/0/0/114	0/0/0/8
3	SO4	D	1159	-	-	0/0/0/0	0/0/0/0
4	ACT	D	1160	-	-	0/0/0/0	0/0/0/0
5	BTB	D	1161	-	-	0/9/9/21	0/0/0/0
2	HEM	D	200[A]	-	-	0/0/0/114	0/0/0/8
2	HEM	D	200[B]	-	-	0/0/0/114	0/0/0/8
3	SO4	E	1159	-	-	0/0/0/0	0/0/0/0
3	SO4	E	1160	-	-	0/0/0/0	0/0/0/0
4	ACT	E	1161	-	-	0/0/0/0	0/0/0/0
2	HEM	E	200	1	-	0/14/114/114	0/0/8/8
3	SO4	F	1159	-	-	0/0/0/0	0/0/0/0
4	ACT	F	1160	-	-	0/0/0/0	0/0/0/0
2	HEM	F	200[A]	-	-	0/0/0/114	0/0/0/8
2	HEM	F	200[B]	-	-	0/0/0/114	0/0/0/8
3	SO4	G	1159	-	-	0/0/0/0	0/0/0/0
4	ACT	G	1160	-	-	0/0/0/0	0/0/0/0
2	HEM	G	200[A]	-	-	0/0/0/114	0/0/0/8
2	HEM	G	200[B]	-	-	0/0/0/114	0/0/0/8
3	SO4	H	1159	-	-	0/0/0/0	0/0/0/0
3	SO4	H	1160	-	-	0/0/0/0	0/0/0/0
4	ACT	H	1161	-	-	0/0/0/0	0/0/0/0
2	HEM	H	200[A]	-	-	0/0/0/114	0/0/0/8
2	HEM	H	200[B]	-	-	0/0/0/114	0/0/0/8
3	SO4	I	1159	-	-	0/0/0/0	0/0/0/0
4	ACT	I	1160	-	-	0/0/0/0	0/0/0/0
3	SO4	I	1161	-	-	0/0/0/0	0/0/0/0
5	BTB	I	1162	-	-	0/9/9/21	0/0/0/0
2	HEM	I	200[A]	-	-	0/0/0/114	0/0/0/8

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	I	200[B]	-	-	0/0/0/114	0/0/0/8
3	SO4	J	1159	-	-	0/0/0/0	0/0/0/0
4	ACT	J	1160	-	-	0/0/0/0	0/0/0/0
2	HEM	J	200[A]	-	-	0/0/0/114	0/0/0/8
2	HEM	J	200[B]	-	-	0/0/0/114	0/0/0/8
3	SO4	K	1159	-	-	0/0/0/0	0/0/0/0
4	ACT	K	1160	-	-	0/0/0/0	0/0/0/0
5	BTB	K	1161	-	-	0/9/9/21	0/0/0/0
2	HEM	K	200[A]	-	-	0/0/0/114	0/0/0/8
2	HEM	K	200[B]	-	-	0/0/0/114	0/0/0/8
3	SO4	L	1159	-	-	0/0/0/0	0/0/0/0
4	ACT	L	1160	-	-	0/0/0/0	0/0/0/0
5	BTB	L	1161	-	-	0/9/9/21	0/0/0/0
2	HEM	L	200[A]	-	-	0/0/0/114	0/0/0/8
2	HEM	L	200[B]	-	-	0/0/0/114	0/0/0/8

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	200	HEM	C3B-C2B	-5.61	1.34	1.43
2	E	200	HEM	C3C-C2C	-5.37	1.34	1.43
2	E	200	HEM	C3D-C2D	5.34	1.53	1.43
2	E	200	HEM	C3C-CAC	4.43	1.54	1.40
2	E	200	HEM	C3B-CAB	4.21	1.53	1.40

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	200	HEM	C3B-C4B-NB	-8.02	108.26	114.00
2	E	200	HEM	C4D-ND-C1D	6.39	111.70	105.16
2	E	200	HEM	C2D-C1D-ND	-4.01	108.20	112.93
2	E	200	HEM	CHD-C1D-ND	3.87	127.80	124.58
2	E	200	HEM	CBD-CAD-C3D	-3.79	106.11	114.37

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	158/158 (100%)	-0.64	1 (0%) 86 90	5, 9, 14, 27	3 (1%)
1	B	158/158 (100%)	-0.66	0 100 100	6, 9, 15, 27	2 (1%)
1	C	158/158 (100%)	-0.64	1 (0%) 86 90	6, 9, 14, 29	2 (1%)
1	D	158/158 (100%)	-0.65	1 (0%) 86 90	6, 9, 14, 29	3 (1%)
1	E	158/158 (100%)	-0.66	0 100 100	5, 9, 14, 27	4 (2%)
1	F	158/158 (100%)	-0.62	0 100 100	6, 8, 14, 27	1 (0%)
1	G	158/158 (100%)	-0.64	0 100 100	5, 9, 15, 30	3 (1%)
1	H	158/158 (100%)	-0.64	1 (0%) 86 90	5, 9, 14, 29	0
1	I	158/158 (100%)	-0.64	0 100 100	5, 9, 14, 25	2 (1%)
1	J	158/158 (100%)	-0.64	0 100 100	5, 9, 15, 28	2 (1%)
1	K	158/158 (100%)	-0.65	1 (0%) 86 90	6, 9, 14, 30	3 (1%)
1	L	158/158 (100%)	-0.65	0 100 100	6, 9, 15, 28	5 (3%)
All	All	1896/1896 (100%)	-0.64	5 (0%) 91 94	5, 9, 15, 30	30 (1%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	158	GLY	4.3
1	K	158	GLY	3.3
1	A	158	GLY	2.6
1	D	158	GLY	2.5
1	H	158	GLY	2.5

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	SO4	D	1159	5/5	0.16	30.85	17,18,20,20	5
3	SO4	C	1159	5/5	0.12	22.30	19,20,23,23	5
2	HEM	B	200[A]	2/43	0.10	19.80	18,18,18,18	2
3	SO4	E	1160	5/5	0.12	16.36	21,22,25,26	5
3	SO4	B	1161	5/5	0.14	15.10	15,15,19,20	5
5	BTB	I	1162	8/14	0.20	14.24	30,32,34,35	1
3	SO4	F	1159	5/5	0.17	13.66	15,16,19,20	5
2	HEM	J	200[A]	2/43	0.10	13.46	16,16,16,17	2
3	SO4	K	1159	5/5	0.14	12.87	16,16,18,20	5
2	HEM	F	200[A]	2/43	0.11	12.74	14,14,14,16	2
2	HEM	L	200[A]	2/43	0.12	12.40	13,13,13,13	2
5	BTB	D	1161	8/14	0.15	11.89	24,32,32,34	0
3	SO4	I	1159	5/5	0.13	11.65	19,19,23,24	5
5	BTB	K	1161	8/14	0.18	11.55	20,31,32,32	0
2	HEM	D	200[B]	2/43	0.11	10.76	20,20,20,20	2
5	BTB	L	1161	8/14	0.19	10.07	30,32,32,32	0
3	SO4	G	1159	5/5	0.13	10.00	18,19,22,23	5
3	SO4	H	1160	5/5	0.13	9.94	15,15,19,20	5
3	SO4	J	1159	5/5	0.13	9.23	24,25,29,30	5
2	HEM	J	200[B]	2/43	0.10	9.19	14,14,14,14	2
2	HEM	C	200[B]	2/43	0.10	9.17	11,11,11,13	2
2	HEM	A	200[A]	2/43	0.10	9.15	14,14,14,15	2
2	HEM	K	200[B]	2/43	0.12	8.77	10,10,10,10	2
2	HEM	K	200[A]	2/43	0.12	8.49	12,12,12,13	2
2	HEM	L	200[B]	2/43	0.12	7.50	11,11,11,12	2
3	SO4	A	1159	5/5	0.13	6.76	25,26,27,29	5
2	HEM	D	200[A]	2/43	0.11	6.05	17,17,17,19	2
3	SO4	L	1159	5/5	0.09	5.92	23,25,28,30	5
3	SO4	C	1160	5/5	0.11	5.49	12,15,16,18	5

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	HEM	G	200[B]	2/43	0.10	5.46	18,18,18,19	2
2	HEM	G	200[A]	2/43	0.10	5.46	20,20,20,21	2
2	HEM	F	200[B]	2/43	0.11	5.27	8,8,8,11	2
2	HEM	H	200[B]	2/43	0.09	5.04	12,12,12,12	2
2	HEM	E	200	43/43	0.10	4.70	5,7,11,14	43
2	HEM	I	200[A]	2/43	0.11	4.48	17,17,17,18	2
2	HEM	C	200[A]	2/43	0.10	4.42	11,11,11,12	2
2	HEM	B	200[B]	2/43	0.10	4.35	16,16,16,17	2
2	HEM	A	200[B]	2/43	0.10	4.13	13,13,13,14	2
2	HEM	H	200[A]	2/43	0.09	4.12	12,12,12,13	2
2	HEM	I	200[B]	2/43	0.11	3.98	17,17,17,17	2
3	SO4	I	1161	5/5	0.12	3.56	11,13,16,17	5
4	ACT	K	1160	4/4	0.09	3.43	18,19,20,20	0
3	SO4	B	1159	5/5	0.11	3.12	14,15,18,20	5
4	ACT	D	1160	4/4	0.10	2.84	19,21,22,22	0
4	ACT	J	1160	4/4	0.11	2.39	16,19,19,21	0
4	ACT	F	1160	4/4	0.10	2.06	18,22,22,23	0
4	ACT	G	1160	4/4	0.11	1.92	19,21,21,22	0
4	ACT	L	1160	4/4	0.09	1.75	18,21,21,21	0
4	ACT	A	1160	4/4	0.10	1.32	17,20,20,21	0
4	ACT	I	1160	4/4	0.08	1.23	15,17,18,18	0
4	ACT	C	1161	4/4	0.07	0.87	17,19,19,20	0
4	ACT	E	1161	4/4	0.07	0.71	17,18,19,19	0
4	ACT	B	1162	4/4	0.06	-0.16	17,19,20,20	0
4	ACT	H	1161	4/4	0.05	-0.76	16,17,17,18	0
3	SO4	E	1159	5/5	0.03	-2.31	10,10,11,13	0
3	SO4	H	1159	5/5	0.03	-3.50	10,10,11,13	0
3	SO4	B	1160	5/5	0.02	-4.08	10,10,12,13	0
3	SO4	C	1158	5/5	0.03	-4.75	10,10,11,12	0

6.5 Other polymers ⓘ

There are no such residues in this entry.