



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 09:36 AM GMT

PDB ID : 3IS8
Title : Structure of mineralized Bfrb soaked with FeSO₄ from *Pseudomonas aeruginosa* to 2.25Å Resolution
Authors : Lovell, S.; Weeratunga, S.K.; Battaile, K.P.; Rivera, M.
Deposited on : 2009-08-25
Resolution : 2.25 Å(reported)

This is a full wwPDB validation 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>

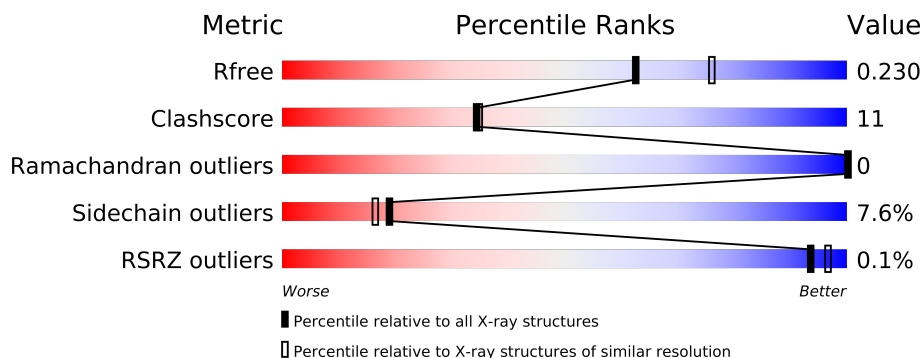
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.25 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.









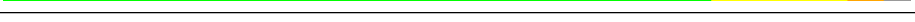

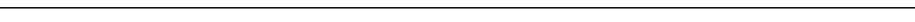

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1108 (2.28-2.24)
Clashscore	79885	1326 (2.28-2.24)
Ramachandran outliers	78287	1291 (2.28-2.24)
Sidechain outliers	78261	1291 (2.28-2.24)
RSRZ outliers	66119	1110 (2.28-2.24)

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	
1	M	158	
1	N	158	

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Mol	Chain	Length	Quality of chain
1	O	158	
1	P	158	
1	Q	158	
1	R	158	
1	S	158	
1	T	158	
1	U	158	
1	V	158	
1	W	158	
1	X	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
4	HEM	P	163	-	X
5	SO4	B	165	-	X
5	SO4	D	163	-	X
5	SO4	F	164	-	X
5	SO4	I	164	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 32963 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	155	Total	C	N	O	S	0	2	0
			1289	816	224	243	6			
1	B	155	Total	C	N	O	S	0	2	0
			1287	815	223	243	6			
1	C	155	Total	C	N	O	S	0	2	0
			1288	816	223	243	6			
1	D	154	Total	C	N	O	S	0	2	0
			1280	810	222	242	6			
1	E	155	Total	C	N	O	S	0	2	0
			1286	814	223	243	6			
1	F	155	Total	C	N	O	S	0	2	0
			1285	813	223	243	6			
1	G	155	Total	C	N	O	S	0	2	0
			1286	814	223	243	6			
1	H	154	Total	C	N	O	S	0	2	0
			1280	810	222	242	6			
1	I	154	Total	C	N	O	S	0	2	0
			1280	810	222	242	6			
1	J	155	Total	C	N	O	S	0	2	0
			1286	814	223	243	6			
1	K	155	Total	C	N	O	S	0	2	0
			1289	816	224	243	6			
1	L	155	Total	C	N	O	S	0	2	0
			1286	814	223	243	6			
1	M	155	Total	C	N	O	S	0	2	0
			1280	810	221	243	6			
1	N	155	Total	C	N	O	S	0	2	0
			1280	810	221	243	6			
1	O	155	Total	C	N	O	S	0	2	0
			1285	814	222	243	6			
1	P	155	Total	C	N	O	S	0	2	0
			1282	811	222	243	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	155	Total	C	N	O	S	0	2	0
			1289	816	224	243	6			
1	R	155	Total	C	N	O	S	0	2	0
			1284	813	222	243	6			
1	S	155	Total	C	N	O	S	0	2	0
			1284	813	222	243	6			
1	T	155	Total	C	N	O	S	0	2	0
			1281	811	221	243	6			
1	U	154	Total	C	N	O	S	0	2	0
			1276	808	220	242	6			
1	V	155	Total	C	N	O	S	0	2	0
			1281	811	221	243	6			
1	W	155	Total	C	N	O	S	0	2	0
			1279	809	221	243	6			
1	X	155	Total	C	N	O	S	0	2	0
			1282	811	222	243	6			

- Molecule 2 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	P	4	Total	Fe	0	0
			4	4		
2	K	4	Total	Fe	0	0
			4	4		
2	B	5	Total	Fe	0	0
			5	5		
2	W	3	Total	Fe	0	0
			3	3		
2	N	5	Total	Fe	0	0
			5	5		
2	X	3	Total	Fe	0	0
			3	3		
2	S	4	Total	Fe	0	0
			4	4		
2	J	4	Total	Fe	0	0
			4	4		
2	E	5	Total	Fe	0	0
			5	5		
2	V	3	Total	Fe	0	0
			3	3		
2	A	5	Total	Fe	0	0
			5	5		

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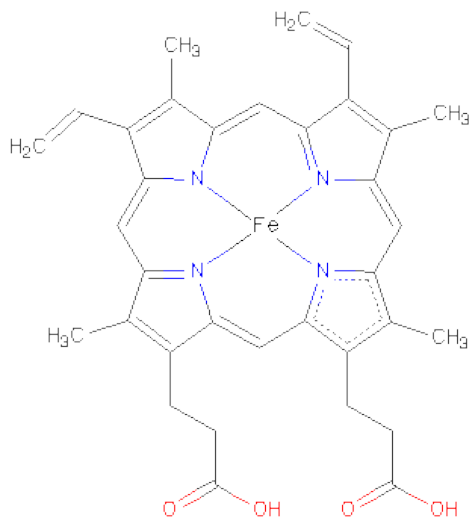
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	R	4	Total 4	Fe 4	0	0
2	M	4	Total 4	Fe 4	0	0
2	D	4	Total 4	Fe 4	0	0
2	I	4	Total 4	Fe 4	0	0
2	U	3	Total 3	Fe 3	0	0
2	L	4	Total 4	Fe 4	0	0
2	G	5	Total 5	Fe 5	0	0
2	Q	4	Total 4	Fe 4	0	0
2	H	3	Total 3	Fe 3	0	0
2	C	5	Total 5	Fe 5	0	0
2	T	3	Total 3	Fe 3	0	0
2	O	4	Total 4	Fe 4	0	0
2	F	4	Total 4	Fe 4	0	0

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

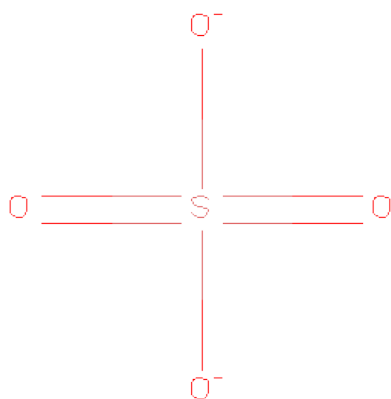
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	1	Total 1	K 1	0	0
3	E	1	Total 1	K 1	0	0
3	B	1	Total 1	K 1	0	0
3	C	1	Total 1	K 1	0	0
3	A	1	Total 1	K 1	0	0
3	N	1	Total 1	K 1	0	0

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	F	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	H	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	I	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	L	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	N	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	P	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	Q	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	S	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	U	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	X	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	F	1	Total	O	S	0	0
			5	4	1		
5	I	1	Total	O	S	0	0
			5	4	1		
5	M	1	Total	O	S	0	0
			5	4	1		
5	O	1	Total	O	S	0	0
			5	4	1		
5	R	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	61	Total	O	0	0
			61	61		
6	B	56	Total	O	0	0
			56	56		
6	C	65	Total	O	0	0
			65	65		

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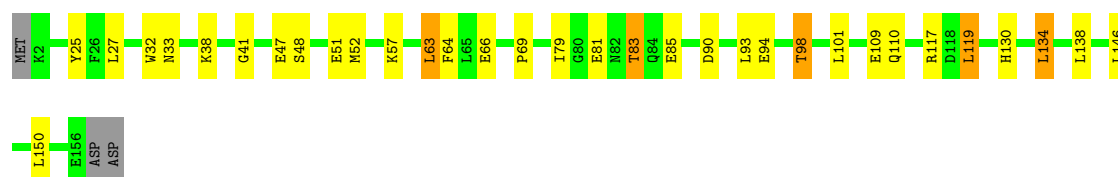
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	62	Total 62	O 62	0	0
6	E	69	Total 69	O 69	0	0
6	F	62	Total 62	O 62	0	0
6	G	70	Total 70	O 70	0	0
6	H	73	Total 73	O 73	0	0
6	I	61	Total 61	O 61	0	0
6	J	58	Total 58	O 58	0	0
6	K	67	Total 67	O 67	0	0
6	L	59	Total 59	O 59	0	0
6	M	57	Total 57	O 57	0	0
6	N	51	Total 51	O 51	0	0
6	O	68	Total 68	O 68	0	0
6	P	52	Total 52	O 52	0	0
6	Q	70	Total 70	O 70	0	0
6	R	72	Total 72	O 72	0	0
6	S	64	Total 64	O 64	0	0
6	T	51	Total 51	O 51	0	0
6	U	69	Total 69	O 69	0	0
6	V	68	Total 68	O 68	0	0
6	W	65	Total 65	O 65	0	0
6	X	50	Total 50	O 50	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 ($RSRZ > 2$). 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.

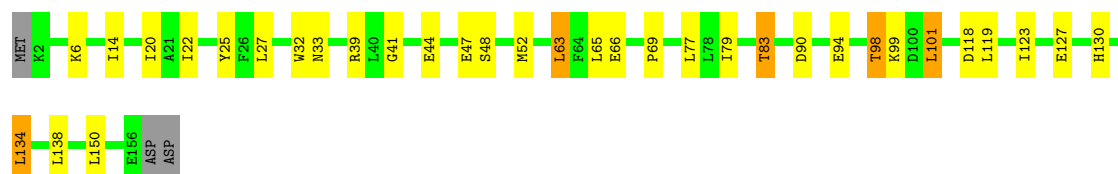
- Molecule 1: Bacterioferritin

Chain A: 



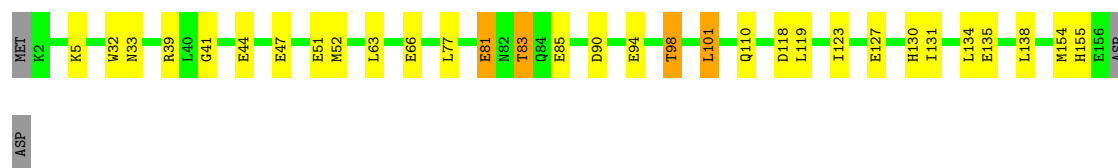
- Molecule 1: Bacterioferritin

Chain B: 



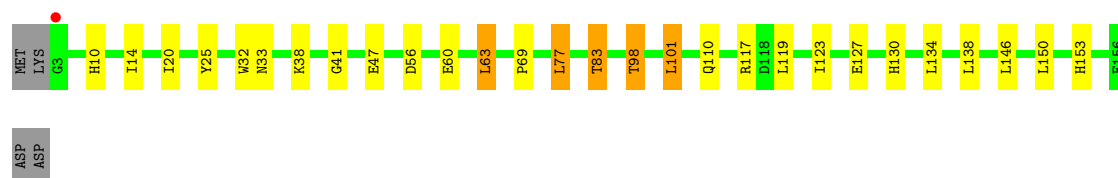
- Molecule 1: Bacterioferritin

Chain C: 



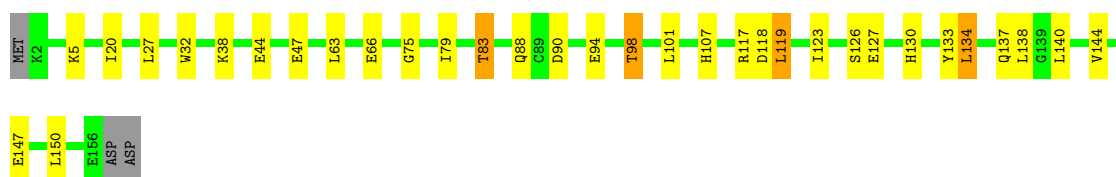
- Molecule 1: Bacterioferritin

Chain D: 



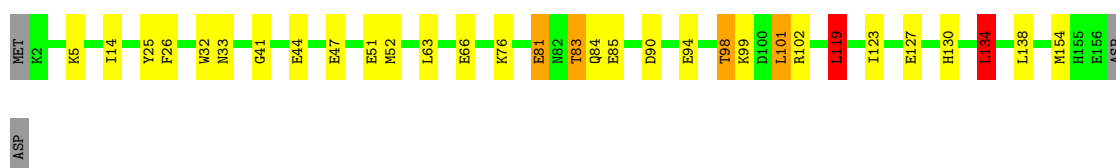
- Molecule 1: Bacterioferritin

Chain E: 



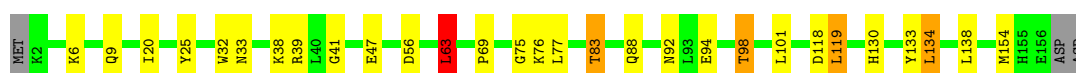
- Molecule 1: Bacterioferritin

Chain F:



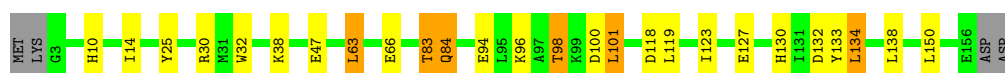
- Molecule 1: Bacterioferritin

Chain G:



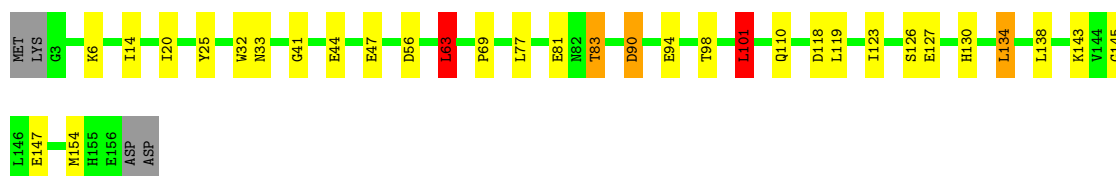
- Molecule 1: Bacterioferritin

Chain H:



- Molecule 1: Bacterioferritin

Chain I:



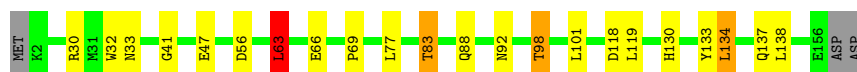
- Molecule 1: Bacterioferritin

Chain J:



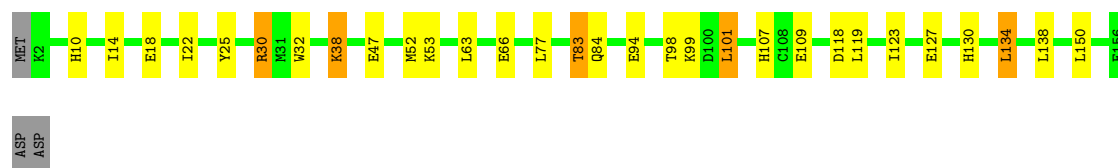
- Molecule 1: Bacterioferritin

Chain K:



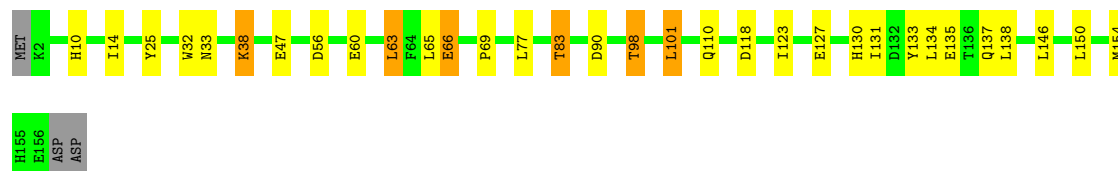
- Molecule 1: Bacterioferritin

Chain L:



- Molecule 1: Bacterioferritin

Chain M:



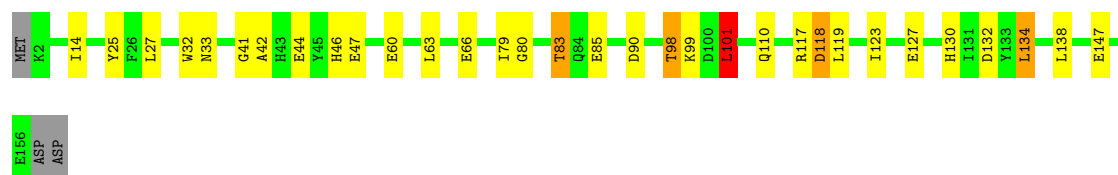
- Molecule 1: Bacterioferritin

Chain N:



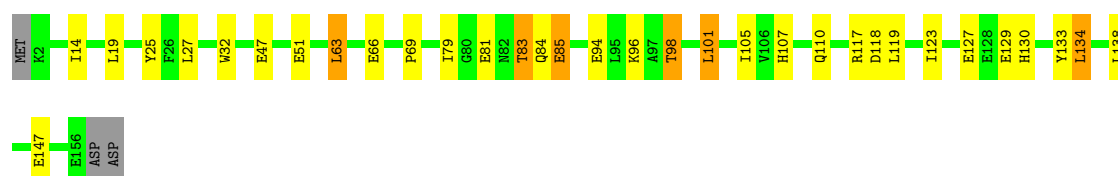
- Molecule 1: Bacterioferritin

Chain O:



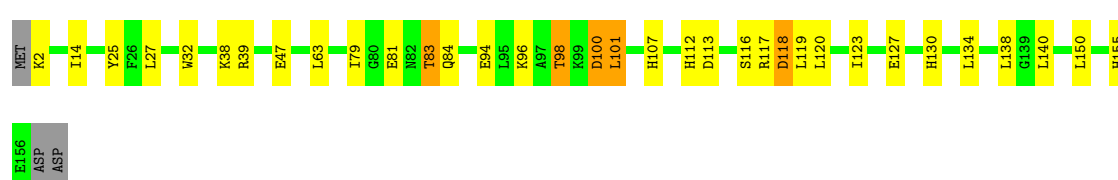
- Molecule 1: Bacterioferritin

Chain P:



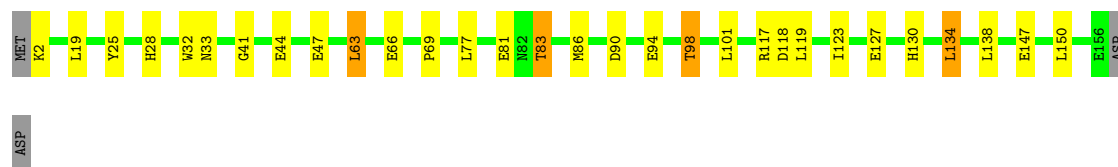
- Molecule 1: Bacterioferritin

Chain Q:



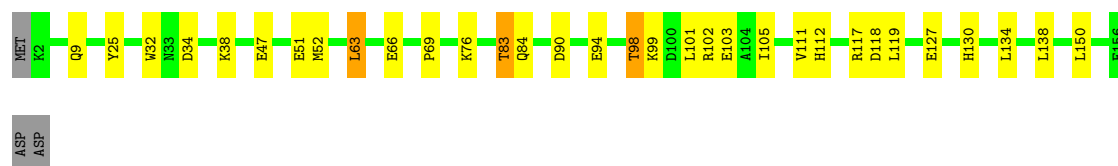
- Molecule 1: Bacterioferritin

Chain R:



- Molecule 1: Bacterioferritin

Chain S:



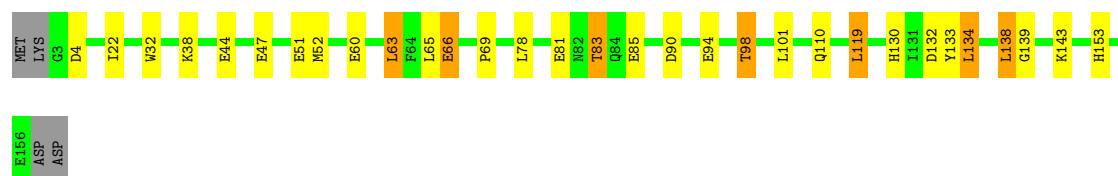
- Molecule 1: Bacterioferritin

Chain T:



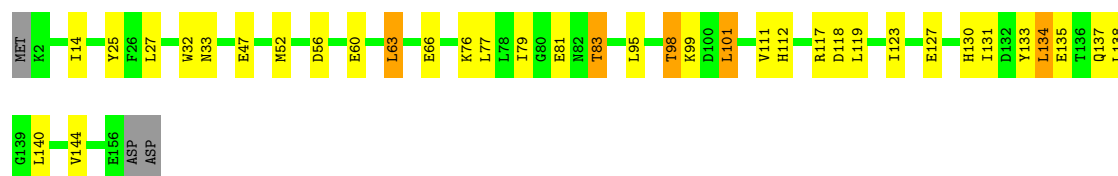
- Molecule 1: Bacterioferritin

Chain U:



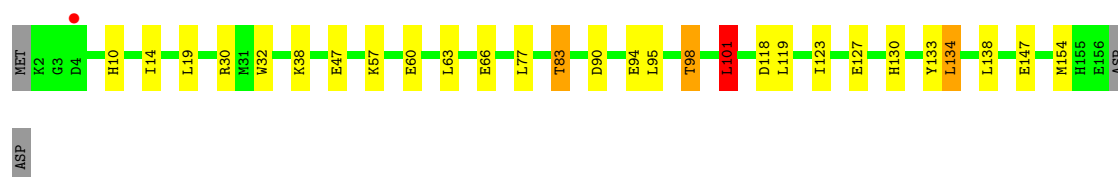
- Molecule 1: Bacterioferritin

Chain V:



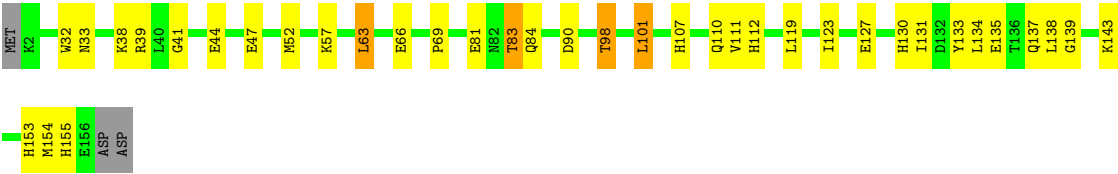
- Molecule 1: Bacterioferritin

Chain W:



● Molecule 1: Bacterioferritin

Chain X: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	125.72Å 203.28Å 207.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.25 49.36 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.00-2.25) 99.7 (49.36-2.25)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 2.25Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.177 , 0.226 0.185 , 0.230	Depositor DCC
R_{free} test set	12585 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	24.4	Xtriage
Anisotropy	0.024	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 24.1	EDS
Estimated twinning fraction	0.005 for -h,l,k	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 250555 reflections (0.000%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	32963	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.04% 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: HEM, K, FE2, 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	0.97	2/1318 (0.2%)	0.83	0/1774
1	B	0.92	0/1316	0.82	1/1772 (0.1%)
1	C	0.90	1/1317 (0.1%)	0.81	1/1773 (0.1%)
1	D	0.94	0/1309	0.84	0/1763
1	E	0.87	0/1315	0.82	1/1771 (0.1%)
1	F	0.92	2/1314 (0.2%)	0.82	2/1770 (0.1%)
1	G	0.89	0/1315	0.87	5/1771 (0.3%)
1	H	0.90	0/1309	0.86	2/1763 (0.1%)
1	I	0.88	1/1309 (0.1%)	0.90	6/1763 (0.3%)
1	J	0.92	1/1315 (0.1%)	0.85	1/1771 (0.1%)
1	K	0.87	0/1318	0.86	4/1774 (0.2%)
1	L	0.89	1/1315 (0.1%)	0.84	1/1771 (0.1%)
1	M	0.86	0/1309	0.80	1/1765 (0.1%)
1	N	0.82	0/1309	0.79	1/1765 (0.1%)
1	O	0.87	1/1314 (0.1%)	0.80	2/1770 (0.1%)
1	P	0.88	2/1311 (0.2%)	0.83	0/1767
1	Q	0.91	0/1318	0.88	4/1774 (0.2%)
1	R	0.87	0/1313	0.81	0/1769
1	S	0.90	0/1313	0.84	2/1769 (0.1%)
1	T	0.86	0/1310	0.83	0/1766
1	U	0.93	1/1305 (0.1%)	0.87	2/1759 (0.1%)
1	V	0.91	0/1310	0.86	2/1766 (0.1%)
1	W	0.90	2/1308 (0.2%)	0.83	3/1764 (0.2%)
1	X	0.86	0/1311	0.79	1/1767 (0.1%)
All	All	0.89	14/31501 (0.0%)	0.84	42/42437 (0.1%)

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	66	GLU	CB-CG	7.83	1.67	1.52
1	F	66	GLU	CB-CG	7.68	1.66	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	66	GLU	CG-CD	6.27	1.61	1.51
1	L	99	LYS	CD-CE	5.96	1.66	1.51
1	U	60	GLU	CG-CD	5.75	1.60	1.51
1	W	66	GLU	CG-CD	5.75	1.60	1.51
1	C	81	GLU	CG-CD	5.73	1.60	1.51
1	P	85	GLU	CG-CD	5.56	1.60	1.51
1	J	60	GLU	CG-CD	5.45	1.60	1.51
1	P	129	GLU	CG-CD	5.29	1.59	1.51
1	O	60	GLU	CG-CD	5.29	1.59	1.51
1	I	81	GLU	CG-CD	5.26	1.59	1.51
1	W	66	GLU	CB-CG	5.24	1.62	1.52
1	F	66	GLU	CG-CD	5.18	1.59	1.51

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	56	ASP	CB-CG-OD1	7.74	125.27	118.30
1	Q	101	LEU	CA-CB-CG	7.72	133.07	115.30
1	Q	118	ASP	CB-CG-OD1	-7.02	111.99	118.30
1	C	101	LEU	CA-CB-CG	7.00	131.41	115.30
1	I	90	ASP	CB-CG-OD1	6.79	124.41	118.30
1	W	90	ASP	CB-CG-OD1	6.72	124.35	118.30
1	V	63	LEU	CA-CB-CG	6.62	130.52	115.30
1	G	56	ASP	CB-CG-OD1	6.46	124.11	118.30
1	E	134	LEU	CA-CB-CG	6.21	129.59	115.30
1	K	30	ARG	NE-CZ-NH2	-6.14	117.23	120.30
1	H	63	LEU	CA-CB-CG	5.85	128.75	115.30
1	J	101	LEU	CA-CB-CG	5.79	128.63	115.30
1	Q	100	ASP	CB-CG-OD1	-5.65	113.22	118.30
1	N	101	LEU	CA-CB-CG	5.64	128.26	115.30
1	G	63	LEU	CA-CB-CG	5.62	128.21	115.30
1	G	39	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	K	56	ASP	CB-CG-OD1	5.56	123.30	118.30
1	S	90	ASP	CB-CG-OD1	5.51	123.26	118.30
1	B	39	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	V	63	LEU	CB-CG-CD1	5.49	120.34	111.00
1	U	138	LEU	CB-CG-CD1	5.48	120.32	111.00
1	M	90	ASP	CB-CG-OD1	5.47	123.22	118.30
1	K	30	ARG	NE-CZ-NH1	5.45	123.02	120.30
1	I	56	ASP	CB-CG-OD2	-5.44	113.40	118.30
1	U	78	LEU	CB-CG-CD2	-5.41	101.81	111.00
1	S	102	ARG	NE-CZ-NH1	5.39	122.99	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	63	LEU	CB-CG-CD1	5.36	120.11	111.00
1	W	101	LEU	CA-CB-CG	5.36	127.63	115.30
1	I	134	LEU	CA-CB-CG	5.32	127.53	115.30
1	H	30	ARG	NE-CZ-NH1	5.31	122.95	120.30
1	G	63	LEU	CB-CG-CD1	5.29	119.98	111.00
1	F	119	LEU	CB-CG-CD2	-5.28	102.03	111.00
1	Q	100	ASP	CB-CG-OD2	5.24	123.02	118.30
1	W	90	ASP	CB-CG-OD2	-5.21	113.61	118.30
1	I	101	LEU	CA-CB-CG	5.20	127.26	115.30
1	F	134	LEU	CA-CB-CG	5.18	127.20	115.30
1	G	56	ASP	CB-CG-OD2	-5.13	113.68	118.30
1	O	101	LEU	CA-CB-CG	5.13	127.11	115.30
1	K	63	LEU	CA-CB-CG	5.10	127.03	115.30
1	O	134	LEU	CB-CG-CD1	5.09	119.65	111.00
1	L	30	ARG	NE-CZ-NH2	-5.07	117.76	120.30
1	X	101	LEU	CA-CB-CG	5.06	126.93	115.30

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	1289	0	1275	31	0
1	B	1287	0	1268	29	0
1	C	1288	0	1270	25	0
1	D	1280	0	1262	25	0
1	E	1286	0	1266	26	0
1	F	1285	0	1264	32	0
1	G	1286	0	1266	24	0
1	H	1280	0	1262	23	0
1	I	1280	0	1262	20	0
1	J	1286	0	1266	23	0
1	K	1289	0	1275	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L	1286	0	1266	23	0
1	M	1280	0	1248	25	0
1	N	1280	0	1248	19	0
1	O	1285	0	1261	22	0
1	P	1282	0	1255	26	0
1	Q	1289	0	1275	22	0
1	R	1284	0	1259	22	0
1	S	1284	0	1259	25	0
1	T	1281	0	1250	25	0
1	U	1276	0	1248	29	0
1	V	1281	0	1250	30	0
1	W	1279	0	1246	25	0
1	X	1282	0	1255	31	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	4	0	0	0	0
2	E	5	0	0	0	0
2	F	4	0	0	0	0
2	G	5	0	0	0	0
2	H	3	0	0	0	0
2	I	4	0	0	0	0
2	J	4	0	0	0	0
2	K	4	0	0	0	0
2	L	4	0	0	0	0
2	M	4	0	0	0	0
2	N	5	0	0	0	0
2	O	4	0	0	0	0
2	P	4	0	0	0	0
2	Q	4	0	0	0	0
2	R	4	0	0	0	0
2	S	4	0	0	0	0
2	T	3	0	0	0	0
2	U	3	0	0	0	0
2	V	3	0	0	0	0
2	W	3	0	0	0	0
2	X	3	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	N	1	0	0	0	0
4	A	43	0	30	7	0
4	C	43	0	30	6	0
4	F	43	0	30	11	0
4	H	43	0	30	9	0
4	I	43	0	30	7	0
4	L	43	0	30	6	0
4	N	43	0	30	8	0
4	P	43	0	30	6	0
4	Q	43	0	30	0	0
4	S	43	0	30	7	0
4	U	43	0	30	9	0
4	X	43	0	30	13	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
5	D	5	0	0	2	0
5	F	5	0	0	0	0
5	I	5	0	0	1	0
5	M	5	0	0	1	0
5	O	5	0	0	2	0
5	R	5	0	0	1	0
6	A	61	0	0	6	0
6	B	56	0	0	9	0
6	C	65	0	0	5	0
6	D	62	0	0	5	0
6	E	69	0	0	8	0
6	F	62	0	0	5	0
6	G	70	0	0	6	0
6	H	73	0	0	8	0
6	I	61	0	0	6	0
6	J	58	0	0	5	0
6	K	67	0	0	7	0
6	L	59	0	0	8	0
6	M	57	0	0	6	0
6	N	51	0	0	5	0
6	O	68	0	0	8	0
6	P	52	0	0	5	0
6	Q	70	0	0	4	0
6	R	72	0	0	6	0
6	S	64	0	0	8	0
6	T	51	0	0	5	0
6	U	69	0	0	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	V	68	0	0	7	0
6	W	65	0	0	10	0
6	X	50	0	0	10	0
All	All	32963	0	30616	669	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 11.

All (669) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:47:GLU:OE1	1:E:130[B]:HIS:CD2	1.81	1.32
1:P:47:GLU:OE1	1:P:130[B]:HIS:CD2	1.83	1.30
1:P:96:LYS:HD2	6:P:854:HOH:O	1.34	1.22
1:L:47:GLU:OE1	1:L:130[B]:HIS:CD2	1.93	1.21
1:O:98:THR:HG21	6:O:1032:HOH:O	1.40	1.18
4:X:162:HEM:HBB2	4:X:162:HEM:CMB	1.66	1.17
4:X:162:HEM:HBC2	4:X:162:HEM:CMC	1.62	1.16
4:N:165:HEM:CMC	4:N:165:HEM:HBC2	1.72	1.14
1:A:47:GLU:OE2	1:A:130[B]:HIS:CD2	2.00	1.14
1:A:98:THR:HG21	6:A:638:HOH:O	1.46	1.12
4:P:163:HEM:HBB2	4:P:163:HEM:HMB2	1.32	1.09
1:Q:38:LYS:HD3	6:Q:522:HOH:O	1.53	1.09
4:X:162:HEM:HMB2	4:X:162:HEM:HBB2	1.09	1.07
1:V:83:THR:HG23	6:V:166:HOH:O	1.53	1.05
1:R:98:THR:HG21	6:R:616:HOH:O	1.55	1.05
1:G:47:GLU:OE1	1:G:130[B]:HIS:CD2	2.11	1.04
4:X:162:HEM:HMC1	4:X:162:HEM:CBC	1.85	1.02
4:U:162:HEM:HBB2	4:U:162:HEM:HMB1	1.41	1.02
1:H:98:THR:HG21	6:H:517:HOH:O	1.62	1.00
4:U:162:HEM:CMB	4:U:162:HEM:HBB2	1.88	0.99
1:G:38:LYS:HD2	6:W:323:HOH:O	1.62	0.99
1:F:119:LEU:HD23	1:F:119:LEU:C	1.83	0.99
1:B:98:THR:HG21	6:B:254:HOH:O	1.61	0.98
1:F:83:THR:HG23	6:F:427:HOH:O	1.63	0.98
1:T:98:THR:HG21	6:T:164:HOH:O	1.65	0.96
4:P:163:HEM:CMB	4:P:163:HEM:HBB2	1.92	0.96
4:S:163:HEM:HBB2	4:S:163:HEM:HHC	1.49	0.95
4:S:163:HEM:HBC2	4:S:163:HEM:HHD	1.47	0.95
1:X:83:THR:HG23	6:X:367:HOH:O	1.67	0.95
1:I:32:TRP:HE1	1:I:83:THR:HB	1.31	0.94
1:E:27:LEU:HD23	1:E:79:ILE:HD12	1.49	0.94
1:E:147:GLU:HG3	6:E:430:HOH:O	1.65	0.94

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:F:163:HEM:HBC2	4:F:163:HEM:HHD	1.50	0.94
4:X:162:HEM:HMB2	4:X:162:HEM:CBB	1.94	0.93
1:O:83:THR:HG23	6:O:248:HOH:O	1.67	0.93
1:M:98:THR:HG21	6:M:960:HOH:O	1.67	0.93
1:S:98:THR:HG21	6:S:734:HOH:O	1.68	0.92
1:C:98:THR:HG21	6:C:545:HOH:O	1.70	0.91
1:L:83:THR:CG2	6:L:756:HOH:O	2.18	0.90
4:N:165:HEM:CMC	4:N:165:HEM:CBC	2.50	0.90
1:D:83:THR:HG23	6:D:184:HOH:O	1.70	0.90
1:V:98:THR:HG21	6:V:567:HOH:O	1.69	0.90
1:C:32:TRP:HE1	1:C:83:THR:HB	1.34	0.90
1:H:83:THR:HG23	6:H:167:HOH:O	1.71	0.90
4:A:165:HEM:CMB	4:A:165:HEM:HBB2	2.01	0.89
1:E:98:THR:HG21	6:E:368:HOH:O	1.72	0.89
1:N:47:GLU:OE1	1:N:130[B]:HIS:CD2	2.25	0.89
4:N:165:HEM:HBC2	4:N:165:HEM:HMC2	1.52	0.89
1:T:32:TRP:HE1	1:T:83:THR:HB	1.37	0.88
1:X:98:THR:HG21	6:X:1336:HOH:O	1.72	0.88
1:M:32:TRP:HE1	1:M:83:THR:HB	1.37	0.88
4:F:163:HEM:HBB2	4:F:163:HEM:CMB	2.03	0.88
4:X:162:HEM:HMC1	4:X:162:HEM:HBC2	0.89	0.87
1:B:32:TRP:HE1	1:B:83:THR:HB	1.39	0.87
1:K:130[B]:HIS:CE1	6:K:257:HOH:O	2.26	0.87
1:H:25:TYR:CE2	1:H:130[B]:HIS:HE1	1.93	0.87
1:V:47:GLU:OE1	1:V:130[B]:HIS:CD2	2.28	0.87
1:N:83:THR:HG23	6:N:166:HOH:O	1.74	0.87
1:J:83:THR:HG23	6:J:165:HOH:O	1.73	0.86
1:A:25:TYR:CE2	1:A:130[B]:HIS:HE1	1.93	0.86
1:F:119:LEU:O	1:F:119:LEU:HD23	1.73	0.86
1:U:130[B]:HIS:CE1	6:U:166:HOH:O	2.29	0.86
1:S:32:TRP:HE1	1:S:83:THR:HB	1.40	0.86
1:C:81:GLU:HG2	1:C:85:GLU:OE2	1.76	0.85
1:T:14:ILE:HD12	1:T:101:LEU:HD13	1.59	0.85
1:W:130[B]:HIS:CE1	6:W:164:HOH:O	2.28	0.84
4:I:163:HEM:HHD	4:I:163:HEM:HBC2	1.59	0.84
4:N:165:HEM:HMC2	4:N:165:HEM:CBC	2.06	0.84
1:A:98:THR:CG2	6:A:638:HOH:O	2.13	0.84
1:S:83:THR:HG22	6:S:166:HOH:O	1.77	0.84
1:A:47:GLU:OE2	1:A:130[B]:HIS:NE2	2.09	0.83
1:T:94:GLU:OE2	1:T:130[B]:HIS:ND1	2.10	0.83
4:N:165:HEM:HMC3	4:N:165:HEM:HBC2	1.61	0.83
1:G:47:GLU:OE1	1:G:130[B]:HIS:NE2	2.11	0.83

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:U:162:HEM:CBB	4:U:162:HEM:HMB1	2.09	0.83
1:G:98:THR:HG21	6:G:445:HOH:O	1.78	0.82
4:L:163:HEM:HBB2	4:L:163:HEM:CMB	2.09	0.82
1:C:47:GLU:OE2	1:C:130[B]:HIS:CD2	2.33	0.82
1:A:32:TRP:HE1	1:A:83:THR:HB	1.43	0.82
1:W:98:THR:HG21	6:W:513:HOH:O	1.79	0.82
1:K:32:TRP:HE1	1:K:83:THR:HB	1.42	0.81
1:S:83:THR:CG2	6:S:166:HOH:O	2.27	0.81
1:A:83:THR:HG23	6:A:173:HOH:O	1.81	0.80
1:F:119:LEU:CD2	1:F:119:LEU:C	2.49	0.80
1:K:83:THR:HG23	6:K:337:HOH:O	1.82	0.80
1:L:83:THR:HG23	6:L:756:HOH:O	1.79	0.79
1:U:81:GLU:HG2	1:U:85:GLU:OE2	1.83	0.79
1:P:47:GLU:OE1	1:P:130[B]:HIS:NE2	2.15	0.79
1:U:83:THR:HG23	6:U:165:HOH:O	1.82	0.79
1:X:32:TRP:HE1	1:X:83:THR:HB	1.47	0.78
1:R:130[B]:HIS:CD2	1:R:134:LEU:HD22	2.19	0.78
4:H:162:HEM:HBC2	4:H:162:HEM:CMC	2.13	0.78
4:C:165:HEM:CMB	4:C:165:HEM:HBB2	2.13	0.78
1:P:47:GLU:OE1	1:P:130[B]:HIS:CG	2.36	0.78
1:N:94:GLU:OE2	1:N:130[B]:HIS:ND1	2.15	0.78
1:K:47:GLU:OE2	1:K:130[B]:HIS:CD2	2.36	0.78
1:G:32:TRP:HE1	1:G:83:THR:HB	1.48	0.77
1:F:47:GLU:OE1	1:F:130[B]:HIS:CD2	2.36	0.77
1:C:83:THR:CG2	6:C:170:HOH:O	2.33	0.77
1:H:130[B]:HIS:CE1	6:H:164:HOH:O	2.38	0.76
1:Q:32:TRP:HE1	1:Q:83:THR:HB	1.51	0.76
1:S:98:THR:CG2	6:S:734:HOH:O	2.30	0.76
1:H:130[B]:HIS:NE2	6:H:164:HOH:O	2.19	0.76
1:L:47:GLU:OE1	1:L:130[B]:HIS:CG	2.40	0.75
1:L:32:TRP:HE1	1:L:83:THR:HB	1.51	0.75
4:C:165:HEM:HMB1	4:C:165:HEM:HBB2	1.69	0.74
4:P:163:HEM:CBB	4:P:163:HEM:HMB2	2.13	0.74
1:S:84:GLN:NE2	6:S:894:HOH:O	2.21	0.74
1:C:83:THR:HG23	6:C:170:HOH:O	1.86	0.74
1:J:25:TYR:CE2	1:J:130[B]:HIS:HE1	2.05	0.74
4:F:163:HEM:HBB2	4:F:163:HEM:HMB1	1.70	0.74
1:D:98:THR:HG21	6:D:750:HOH:O	1.87	0.74
1:H:47:GLU:OE1	1:H:47:GLU:HA	1.87	0.74
1:F:32:TRP:HE1	1:F:83:THR:HB	1.51	0.73
1:F:83:THR:CG2	6:F:427:HOH:O	2.26	0.73
1:Q:84:GLN:NE2	6:Q:165:HOH:O	2.22	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:83:THR:HG22	6:L:756:HOH:O	1.84	0.72
4:I:163:HEM:CMB	4:I:163:HEM:HBB2	2.19	0.72
1:R:32:TRP:HE1	1:R:83:THR:HB	1.54	0.72
6:S:1361:HOH:O	1:T:76:LYS:HE2	1.90	0.72
4:A:165:HEM:HMB1	4:A:165:HEM:HBB2	1.71	0.71
1:H:25:TYR:CE2	1:H:130[B]:HIS:CE1	2.79	0.71
1:R:83:THR:HG23	6:R:187:HOH:O	1.88	0.71
1:O:27:LEU:HD23	1:O:79:ILE:HD12	1.72	0.71
1:B:27:LEU:HD23	1:B:79:ILE:HD12	1.73	0.71
1:W:32:TRP:HE1	1:W:83:THR:HB	1.54	0.71
1:K:130[B]:HIS:HE1	6:K:257:HOH:O	1.70	0.71
1:R:47:GLU:OE1	1:R:130[A]:HIS:CD2	2.44	0.70
1:I:47:GLU:OE1	1:I:130[A]:HIS:CD2	2.44	0.70
1:H:94:GLU:OE2	1:H:130[B]:HIS:ND1	2.25	0.70
1:S:47:GLU:CD	1:S:130[B]:HIS:CD2	2.65	0.70
1:E:47:GLU:OE1	1:E:130[B]:HIS:NE2	2.25	0.70
1:B:83:THR:HG22	6:B:173:HOH:O	1.91	0.70
4:P:163:HEM:HBC2	4:P:163:HEM:HHD	1.73	0.69
1:E:83:THR:HG23	6:E:172:HOH:O	1.92	0.69
1:B:118:ASP:OD2	6:B:902:HOH:O	2.09	0.69
1:B:83:THR:CG2	6:B:173:HOH:O	2.40	0.69
1:D:32:TRP:HE1	1:D:83:THR:HB	1.57	0.69
1:S:99:LYS:NZ	1:S:103:GLU:OE1	2.26	0.69
1:X:38:LYS:HD2	6:X:312:HOH:O	1.94	0.68
1:R:147:GLU:HG3	6:R:166:HOH:O	1.94	0.68
4:X:162:HEM:CBC	4:X:162:HEM:CMC	2.49	0.68
1:T:14:ILE:CD1	1:T:101:LEU:HD13	2.23	0.68
1:W:19:LEU:CD2	4:X:162:HEM:HBB1	2.24	0.68
4:A:165:HEM:HMB1	4:A:165:HEM:CBB	2.24	0.68
1:W:123:ILE:O	1:W:127:GLU:HG2	1.94	0.68
4:I:163:HEM:HBC2	4:I:163:HEM:CHD	2.23	0.67
4:A:165:HEM:CMB	4:A:165:HEM:CBB	2.72	0.67
1:C:47:GLU:CD	1:C:130[B]:HIS:CD2	2.68	0.67
1:I:83:THR:CG2	6:I:279:HOH:O	2.42	0.67
1:O:83:THR:CG2	6:O:248:HOH:O	2.33	0.67
1:H:83:THR:CG2	6:H:167:HOH:O	2.33	0.67
1:B:47:GLU:OE2	1:B:130[B]:HIS:CD2	2.47	0.67
1:O:147:GLU:HG3	6:O:164:HOH:O	1.94	0.67
4:H:162:HEM:HBB2	4:H:162:HEM:CMB	2.24	0.67
1:T:25:TYR:CE2	1:T:130[B]:HIS:HE1	2.13	0.67
1:P:32:TRP:HE1	1:P:83:THR:HB	1.59	0.67
1:Q:14:ILE:HD13	1:Q:120:LEU:HD22	1.77	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:T:60:GLU:OE1	6:T:1157:HOH:O	2.12	0.67
1:I:32:TRP:NE1	1:I:83:THR:HB	2.07	0.67
1:O:32:TRP:HE1	1:O:83:THR:HB	1.60	0.66
1:M:98:THR:CG2	6:M:960:HOH:O	2.35	0.66
1:P:81:GLU:HG2	1:P:85:GLU:OE2	1.96	0.66
1:Q:47:GLU:OE1	1:Q:130[A]:HIS:CD2	2.49	0.66
1:C:32:TRP:NE1	1:C:83:THR:HB	2.09	0.66
1:V:32:TRP:HE1	1:V:83:THR:HB	1.61	0.66
1:C:81:GLU:HG2	1:C:85:GLU:CD	2.16	0.66
1:G:83:THR:HG23	6:G:229:HOH:O	1.95	0.66
1:O:132:ASP:OD2	6:O:319:HOH:O	2.12	0.66
1:T:32:TRP:NE1	1:T:83:THR:HB	2.10	0.66
1:X:47:GLU:OE1	1:X:130[A]:HIS:CD2	2.49	0.66
1:D:153:HIS:HE1	1:F:154:MET:HE1	1.60	0.65
1:A:25:TYR:CE2	1:A:130[B]:HIS:CE1	2.82	0.65
1:X:83:THR:CG2	6:X:367:HOH:O	2.35	0.65
1:V:47:GLU:OE1	1:V:130[B]:HIS:NE2	2.29	0.65
1:K:32:TRP:NE1	1:K:83:THR:HB	2.11	0.65
1:U:130[B]:HIS:NE2	6:U:166:HOH:O	2.30	0.64
1:M:56:ASP:O	1:M:60:GLU:HG3	1.97	0.64
1:U:119:LEU:C	1:U:119:LEU:HD22	2.17	0.64
1:L:47:GLU:OE1	1:L:130[B]:HIS:NE2	2.31	0.64
1:I:44:GLU:OE2	1:I:90:ASP:OD2	2.16	0.64
1:M:47:GLU:OE1	1:M:130[A]:HIS:CD2	2.50	0.64
1:E:27:LEU:HD23	1:E:79:ILE:CD1	2.26	0.64
4:N:165:HEM:CMB	4:N:165:HEM:HBB2	2.28	0.64
1:G:47:GLU:OE1	1:G:130[B]:HIS:CG	2.50	0.64
1:R:83:THR:CG2	6:R:187:HOH:O	2.46	0.64
4:F:163:HEM:CBB	4:F:163:HEM:CMB	2.76	0.64
1:S:47:GLU:OE1	1:S:130[A]:HIS:CD2	2.51	0.64
1:G:47:GLU:OE1	1:G:130[B]:HIS:CE1	2.50	0.63
1:P:147:GLU:HG3	6:P:288:HOH:O	1.97	0.63
1:E:32:TRP:HE1	1:E:83:THR:HB	1.63	0.63
1:J:147:GLU:HG3	6:J:166:HOH:O	1.98	0.63
1:W:47:GLU:OE1	1:W:47:GLU:HA	2.00	0.62
4:F:163:HEM:HMB1	4:F:163:HEM:CBB	2.27	0.62
1:W:60:GLU:OE1	6:W:1016:HOH:O	2.15	0.62
1:E:83:THR:CG2	6:E:172:HOH:O	2.46	0.62
1:U:119:LEU:C	1:U:119:LEU:CD2	2.67	0.62
4:L:163:HEM:HBB2	4:L:163:HEM:HMB1	1.81	0.61
1:J:94:GLU:OE2	1:J:130[B]:HIS:ND1	2.33	0.61
1:G:83:THR:CG2	6:G:229:HOH:O	2.47	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:10:HIS:O	1:D:14:ILE:HG12	2.00	0.61
1:E:47:GLU:OE1	1:E:130[B]:HIS:CG	2.49	0.61
1:U:32:TRP:HE1	1:U:83:THR:HB	1.65	0.61
1:I:83:THR:HG23	6:I:279:HOH:O	1.99	0.61
4:I:163:HEM:CMB	4:I:163:HEM:CBB	2.78	0.61
1:Q:27:LEU:HD23	1:Q:79:ILE:HD12	1.82	0.61
1:R:63:LEU:HD13	1:R:69:PRO:HD3	1.83	0.60
4:L:163:HEM:CBB	4:L:163:HEM:CMB	2.80	0.60
1:D:14:ILE:HD12	1:D:101:LEU:HD13	1.83	0.60
1:E:88:GLN:OE1	6:E:1159:HOH:O	2.15	0.60
1:N:44:GLU:OE2	1:N:90:ASP:OD2	2.20	0.60
1:P:32:TRP:HE1	1:P:83:THR:CG2	2.14	0.60
4:I:163:HEM:HHH	4:I:163:HEM:CBC	2.32	0.59
1:G:98:THR:CG2	6:G:445:HOH:O	2.40	0.59
1:F:26:PHE:CE1	4:F:163:HEM:HBC1	2.37	0.59
1:T:14:ILE:HD12	1:T:101:LEU:CD1	2.31	0.59
1:M:154:MET:HE1	1:X:153:HIS:HE1	1.67	0.59
1:F:14:ILE:HD13	1:F:101:LEU:CD1	2.32	0.59
1:F:130[B]:HIS:CD2	1:F:134:LEU:HD22	2.38	0.59
5:M:163:SO4:O2	1:T:117:ARG:NH2	2.34	0.59
1:W:19:LEU:HD21	4:X:162:HEM:HBB1	1.83	0.59
1:N:47:GLU:OE1	1:N:130[B]:HIS:CG	2.55	0.59
1:S:32:TRP:NE1	1:S:83:THR:HB	2.15	0.59
1:X:32:TRP:NE1	1:X:83:THR:HB	2.16	0.59
1:D:123:ILE:O	1:D:127:GLU:HG2	2.03	0.59
1:L:109:GLU:OE1	6:L:1051:HOH:O	2.17	0.59
1:E:94:GLU:OE2	1:E:130[B]:HIS:ND1	2.32	0.59
1:U:32:TRP:HE1	1:U:83:THR:CG2	2.16	0.59
1:X:107:HIS:HB2	6:X:1021:HOH:O	2.02	0.59
1:O:117:ARG:NE	5:O:163:SO4:O2	2.35	0.59
1:F:98:THR:HG22	6:F:167:HOH:O	2.01	0.58
1:B:130[B]:HIS:NE2	6:B:171:HOH:O	2.32	0.58
1:H:14:ILE:HD12	1:H:101:LEU:HD13	1.85	0.58
1:V:77:LEU:HD23	1:V:79:ILE:HD11	1.85	0.58
4:U:162:HEM:HBC2	4:U:162:HEM:HHH	1.83	0.58
1:E:98:THR:CG2	6:E:368:HOH:O	2.40	0.58
4:H:162:HEM:CMC	4:H:162:HEM:CBC	2.79	0.58
1:P:105:ILE:HG23	1:P:117:ARG:HG3	1.85	0.58
1:B:20:ILE:HG23	1:B:77:LEU:HD12	1.86	0.58
1:N:84:GLN:HB2	6:N:404:HOH:O	2.04	0.58
1:A:32:TRP:NE1	1:A:83:THR:HB	2.18	0.58
6:N:890:HOH:O	1:O:118:ASP:HB3	2.03	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:56:ASP:O	1:D:60:GLU:HG3	2.04	0.58
1:B:44:GLU:OE2	1:B:90:ASP:OD2	2.22	0.57
1:M:47:GLU:HG3	1:M:130[B]:HIS:NE2	2.19	0.57
1:K:32:TRP:HE1	1:K:83:THR:CB	2.14	0.57
1:D:98:THR:CG2	6:D:750:HOH:O	2.48	0.57
1:D:33:ASN:ND2	1:D:41:GLY:HA3	2.20	0.57
1:X:32:TRP:HE1	1:X:83:THR:CB	2.16	0.57
1:C:47:GLU:OE1	1:C:130[A]:HIS:CD2	2.58	0.57
4:H:162:HEM:CBC	4:H:162:HEM:HMC1	2.35	0.57
1:F:98:THR:CG2	6:F:167:HOH:O	2.52	0.57
1:M:33:ASN:O	1:M:38:LYS:NZ	2.37	0.57
1:E:119:LEU:O	1:E:119:LEU:HD22	2.03	0.57
1:J:38:LYS:HD2	6:J:345:HOH:O	2.03	0.57
1:R:94:GLU:OE2	1:R:130[B]:HIS:ND1	2.38	0.57
1:F:123:ILE:O	1:F:127:GLU:HG2	2.05	0.57
1:V:47:GLU:OE1	1:V:130[B]:HIS:CE1	2.58	0.56
1:N:32:TRP:HE1	1:N:83:THR:HB	1.69	0.56
4:L:163:HEM:CBB	4:L:163:HEM:HMB1	2.34	0.56
1:F:25:TYR:CE2	1:F:130[B]:HIS:HE1	2.23	0.56
1:D:47:GLU:OE1	1:D:130[A]:HIS:CD2	2.58	0.56
1:F:26:PHE:CE1	4:F:163:HEM:CBC	2.88	0.56
1:M:32:TRP:NE1	1:M:83:THR:HB	2.15	0.56
1:V:47:GLU:OE1	1:V:130[B]:HIS:CG	2.58	0.56
1:W:32:TRP:NE1	1:W:83:THR:HB	2.20	0.56
1:K:98:THR:HG22	6:K:426:HOH:O	2.04	0.56
4:I:163:HEM:HMB1	4:I:163:HEM:CBB	2.36	0.56
1:X:38:LYS:HE2	6:X:312:HOH:O	2.06	0.56
1:Q:94:GLU:OE2	1:Q:130[B]:HIS:ND1	2.37	0.56
1:N:47:GLU:CD	1:N:130[B]:HIS:CD2	2.79	0.56
1:W:147:GLU:HG3	6:W:163:HOH:O	2.06	0.56
1:L:98:THR:HG21	6:L:659:HOH:O	2.06	0.56
1:E:123:ILE:O	1:E:127:GLU:HG2	2.06	0.56
1:B:32:TRP:NE1	1:B:83:THR:HB	2.15	0.56
4:H:162:HEM:HBC2	4:H:162:HEM:HMC1	1.88	0.55
5:D:163:SO4:O3	1:E:117:ARG:NE	2.38	0.55
1:N:65:LEU:O	1:N:66:GLU:CB	2.54	0.55
4:A:165:HEM:HMB3	4:A:165:HEM:HBB2	1.86	0.55
1:X:63:LEU:HD13	1:X:69:PRO:HD3	1.87	0.55
1:V:117:ARG:HG2	6:V:954:HOH:O	2.06	0.55
1:L:123:ILE:O	1:L:127:GLU:HG2	2.06	0.55
1:B:83:THR:HG21	1:B:150:LEU:CD2	2.36	0.55
1:M:146:LEU:O	1:M:150:LEU:HG	2.07	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:H:162:HEM:CBB	4:H:162:HEM:CMB	2.82	0.55
1:F:81:GLU:HG2	1:F:85:GLU:OE2	2.07	0.55
1:I:83:THR:HG22	6:I:279:HOH:O	2.07	0.55
1:G:32:TRP:NE1	1:G:83:THR:HB	2.19	0.55
1:P:98:THR:HG22	6:P:292:HOH:O	2.07	0.55
1:H:98:THR:HG22	6:H:541:HOH:O	2.06	0.54
1:L:38:LYS:HG3	6:L:1406:HOH:O	2.07	0.54
1:V:14:ILE:HD12	1:V:101:LEU:HD13	1.89	0.54
1:H:32:TRP:HE1	1:H:83:THR:HB	1.72	0.54
1:S:47:GLU:OE2	1:S:130[B]:HIS:CD2	2.59	0.54
4:C:165:HEM:HBC2	4:C:165:HEM:HHD	1.88	0.54
1:T:77:LEU:CD1	1:T:77:LEU:N	2.70	0.54
1:M:131:ILE:O	1:M:135:GLU:HG3	2.08	0.54
1:O:33:ASN:ND2	1:O:41:GLY:HA3	2.23	0.54
1:R:19:LEU:HD13	6:R:585:HOH:O	2.07	0.54
1:I:14:ILE:HD12	1:I:101:LEU:HD13	1.89	0.54
1:A:48:SER:O	1:A:52:MET:HG3	2.08	0.54
1:J:81:GLU:HG2	1:J:85:GLU:OE2	2.08	0.53
1:P:19:LEU:CD2	4:P:163:HEM:HBB1	2.38	0.53
1:G:25:TYR:CE2	1:G:130[B]:HIS:HE1	2.26	0.53
1:L:107:HIS:CE1	6:L:1184:HOH:O	2.61	0.53
1:P:25:TYR:CE2	1:P:130[B]:HIS:HE1	2.27	0.53
1:P:94:GLU:OE2	1:P:130[B]:HIS:ND1	2.40	0.53
1:A:32:TRP:HE1	1:A:83:THR:CB	2.17	0.53
1:F:26:PHE:CZ	4:F:163:HEM:CBC	2.91	0.53
1:M:98:THR:HG23	6:M:572:HOH:O	2.07	0.53
1:W:47:GLU:OE1	1:W:130[A]:HIS:CD2	2.62	0.53
1:P:123:ILE:O	1:P:127:GLU:HG2	2.07	0.53
1:H:84:GLN:HB2	6:H:201:HOH:O	2.07	0.53
1:K:119:LEU:O	1:K:119:LEU:HD23	2.09	0.53
1:S:52:MET:HB3	4:S:163:HEM:CHD	2.39	0.52
1:Q:94:GLU:O	1:Q:98:THR:HB	2.09	0.52
1:A:130[B]:HIS:CD2	1:A:134:LEU:HD22	2.44	0.52
4:U:162:HEM:HBC2	4:U:162:HEM:CHD	2.38	0.52
1:P:32:TRP:HE1	1:P:83:THR:CB	2.21	0.52
1:T:147:GLU:HG3	6:T:432:HOH:O	2.09	0.52
4:X:162:HEM:HMB3	4:X:162:HEM:HBB2	1.81	0.52
4:U:162:HEM:HMB3	4:U:162:HEM:HBB2	1.87	0.52
1:W:47:GLU:HG3	1:W:130[B]:HIS:NE2	2.25	0.52
1:Q:32:TRP:NE1	1:Q:83:THR:HB	2.22	0.52
1:M:10:HIS:ND1	6:M:521:HOH:O	2.32	0.52
1:T:98:THR:CG2	6:T:164:HOH:O	2.39	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:83:THR:HG22	6:C:170:HOH:O	2.06	0.52
4:U:162:HEM:HHD	4:U:162:HEM:CBC	2.39	0.52
1:A:27:LEU:HD23	1:A:79:ILE:HD12	1.91	0.52
1:V:98:THR:CG2	6:V:567:HOH:O	2.38	0.51
1:B:83:THR:HG21	1:B:150:LEU:HD21	1.91	0.51
1:X:139:GLY:O	1:X:143:LYS:HG3	2.09	0.51
1:M:47:GLU:CD	1:M:130[B]:HIS:CD2	2.84	0.51
1:V:123:ILE:O	1:V:127:GLU:HG2	2.09	0.51
1:K:33:ASN:ND2	1:K:41:GLY:HA3	2.25	0.51
1:S:47:GLU:HG3	1:S:130[B]:HIS:NE2	2.25	0.51
1:J:44:GLU:OE2	1:J:90:ASP:OD2	2.27	0.51
1:X:130[A]:HIS:HD2	6:X:554:HOH:O	1.93	0.51
1:F:33:ASN:ND2	1:F:41:GLY:HA3	2.26	0.51
1:L:130[B]:HIS:CD2	1:L:134:LEU:HD22	2.46	0.51
1:S:83:THR:HG21	1:S:150:LEU:CD2	2.41	0.51
1:P:32:TRP:HE1	1:P:83:THR:HG22	1.76	0.51
1:C:154:MET:HE1	1:U:153:HIS:HE1	1.75	0.51
1:F:32:TRP:NE1	1:F:83:THR:HB	2.24	0.51
1:R:117:ARG:NE	5:R:163:SO4:O3	2.44	0.51
1:Q:38:LYS:CD	6:Q:522:HOH:O	2.29	0.50
1:D:32:TRP:HE1	1:D:83:THR:CB	2.24	0.50
1:F:94:GLU:OE2	1:F:130[B]:HIS:ND1	2.44	0.50
1:P:27:LEU:HD23	1:P:79:ILE:HD12	1.93	0.50
1:K:130[A]:HIS:HD2	6:K:1099:HOH:O	1.93	0.50
1:W:98:THR:CG2	6:W:513:HOH:O	2.49	0.50
1:H:10:HIS:O	1:H:14:ILE:HG12	2.11	0.50
1:N:112:HIS:HE1	6:N:917:HOH:O	1.93	0.50
1:U:32:TRP:HE1	1:U:83:THR:HG22	1.77	0.50
4:N:165:HEM:CMB	4:N:165:HEM:CBB	2.88	0.50
1:J:47:GLU:OE1	1:J:130[A]:HIS:CD2	2.64	0.50
1:V:111:VAL:O	1:V:112:HIS:HB2	2.11	0.50
1:A:83:THR:CG2	6:A:173:HOH:O	2.47	0.49
1:O:14:ILE:HG12	1:O:101:LEU:HD13	1.93	0.49
1:F:84:GLN:HB2	6:F:320:HOH:O	2.11	0.49
1:H:123:ILE:O	1:H:127:GLU:HG2	2.12	0.49
1:V:130[B]:HIS:CD2	1:V:134:LEU:HD13	2.47	0.49
1:U:47:GLU:HA	1:U:47:GLU:OE1	2.12	0.49
1:L:52:MET:HB3	4:L:163:HEM:CHB	2.43	0.49
1:B:130[B]:HIS:CD2	1:B:134:LEU:HD22	2.47	0.49
1:F:52:MET:HB3	4:F:163:HEM:CHB	2.43	0.49
1:N:47:GLU:OE1	1:N:130[A]:HIS:CD2	2.66	0.49
1:K:83:THR:CG2	6:K:337:HOH:O	2.48	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:V:27:LEU:HD23	1:V:79:ILE:HD12	1.94	0.49
1:K:119:LEU:HD23	1:K:119:LEU:C	2.33	0.49
1:J:32:TRP:HE1	1:J:83:THR:CG2	2.26	0.49
1:R:25:TYR:CE2	1:R:130[B]:HIS:HE1	2.30	0.49
1:E:133:TYR:O	1:E:137:GLN:HG2	2.13	0.49
1:L:25:TYR:CE2	1:L:130[B]:HIS:HE1	2.31	0.49
1:V:133:TYR:HD2	1:V:134:LEU:HD13	1.78	0.49
1:I:94:GLU:OE2	1:I:130[B]:HIS:ND1	2.44	0.49
1:Q:47:GLU:OE1	1:Q:130[A]:HIS:NE2	2.45	0.49
1:P:84:GLN:HB2	6:P:482:HOH:O	2.12	0.49
1:E:20:ILE:HD11	1:E:75:GLY:HA3	1.94	0.49
1:P:47:GLU:O	1:P:51:GLU:HG2	2.13	0.49
5:I:164:SO4:O4	1:Q:117:ARG:NE	2.40	0.49
1:X:131:ILE:O	1:X:135:GLU:HG3	2.12	0.49
1:M:123:ILE:O	1:M:127:GLU:HG2	2.12	0.49
1:J:14:ILE:HD13	1:J:101:LEU:HD13	1.93	0.49
1:W:130[B]:HIS:NE2	6:W:164:HOH:O	2.34	0.48
4:H:162:HEM:CBB	4:H:162:HEM:HMB1	2.42	0.48
1:G:20:ILE:HD11	1:G:75:GLY:HA3	1.96	0.48
1:B:25:TYR:CE2	1:B:130[B]:HIS:HE1	2.31	0.48
1:V:56:ASP:O	1:V:60:GLU:HG3	2.13	0.48
1:X:98:THR:HG23	6:X:239:HOH:O	2.12	0.48
1:K:32:TRP:HE1	1:K:83:THR:CG2	2.25	0.48
1:R:98:THR:HG22	6:R:1163:HOH:O	2.13	0.48
1:N:32:TRP:HE1	1:N:83:THR:CG2	2.27	0.48
1:P:32:TRP:NE1	1:P:83:THR:HB	2.26	0.48
1:X:33:ASN:ND2	1:X:41:GLY:HA3	2.29	0.48
1:S:105:ILE:HG23	1:S:117:ARG:HG3	1.96	0.48
1:R:83:THR:HG21	1:R:150:LEU:HD21	1.94	0.48
1:B:130[B]:HIS:CE1	6:B:171:HOH:O	2.65	0.48
1:T:77:LEU:N	1:T:77:LEU:HD12	2.29	0.48
1:A:119:LEU:C	1:A:119:LEU:CD2	2.81	0.48
1:B:33:ASN:ND2	1:B:41:GLY:HA3	2.28	0.48
1:L:25:TYR:N	1:L:25:TYR:CD1	2.79	0.48
1:D:83:THR:CG2	6:D:184:HOH:O	2.45	0.48
4:I:163:HEM:HMB3	4:I:163:HEM:HBB2	1.94	0.48
1:C:47:GLU:HG3	1:C:130[B]:HIS:NE2	2.27	0.48
1:W:57:LYS:NZ	6:W:713:HOH:O	2.41	0.48
1:M:110:GLN:NE2	6:M:1415:HOH:O	2.38	0.48
1:Q:25:TYR:CE2	1:Q:130[B]:HIS:HE1	2.32	0.48
4:S:163:HEM:HHH	4:S:163:HEM:CBC	2.33	0.47
1:J:25:TYR:CE2	1:J:130[B]:HIS:CE1	2.93	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:64:PHE:CE1	1:H:132:ASP:HB2	2.49	0.47
1:P:14:ILE:HD13	1:P:101:LEU:HD13	1.96	0.47
1:D:32:TRP:HE1	1:D:83:THR:CG2	2.27	0.47
1:S:47:GLU:OE2	1:S:130[B]:HIS:HD2	1.97	0.47
1:G:119:LEU:HD22	1:G:119:LEU:O	2.13	0.47
1:C:47:GLU:O	1:C:51:GLU:HG2	2.15	0.47
1:E:119:LEU:C	1:E:119:LEU:HD22	2.34	0.47
1:I:33:ASN:ND2	1:I:41:GLY:HA3	2.28	0.47
1:Q:2:LYS:HA	1:Q:2:LYS:HE3	1.97	0.47
1:W:14:ILE:HD12	1:W:101:LEU:HD13	1.97	0.47
1:J:32:TRP:HE1	1:J:83:THR:HB	1.77	0.47
1:B:33:ASN:ND2	6:B:454:HOH:O	2.42	0.47
1:G:33:ASN:ND2	1:G:41:GLY:HA3	2.30	0.47
1:J:25:TYR:CZ	1:J:130[B]:HIS:HE1	2.32	0.47
1:W:10:HIS:O	1:W:14:ILE:HG12	2.14	0.47
1:B:14:ILE:HD12	1:B:101:LEU:HD13	1.96	0.47
1:I:147:GLU:HG3	6:I:170:HOH:O	2.14	0.47
1:A:94:GLU:OE2	1:A:130[B]:HIS:ND1	2.48	0.47
1:T:19:LEU:HD13	6:T:188:HOH:O	2.14	0.47
1:C:52:MET:HB3	4:C:165:HEM:CHD	2.45	0.47
1:H:96:LYS:NZ	1:H:100:ASP:OD2	2.48	0.47
1:S:127:GLU:OE1	1:S:127:GLU:HA	2.14	0.47
1:L:32:TRP:NE1	1:L:83:THR:HB	2.25	0.46
1:T:32:TRP:HE1	1:T:83:THR:CB	2.17	0.46
1:J:14:ILE:HD13	1:J:101:LEU:CD1	2.45	0.46
1:A:146:LEU:O	1:A:150:LEU:HG	2.15	0.46
1:P:25:TYR:CE2	1:P:130[B]:HIS:CE1	3.03	0.46
1:Q:83:THR:HG21	1:Q:150:LEU:CD2	2.46	0.46
4:A:165:HEM:HMC1	4:A:165:HEM:HBC2	1.98	0.46
1:T:94:GLU:OE2	1:T:130[B]:HIS:CE1	2.68	0.46
1:C:33:ASN:ND2	1:C:41:GLY:HA3	2.31	0.46
1:Q:113:ASP:CG	1:Q:116:SER:HB2	2.36	0.46
1:M:14:ILE:HD12	1:M:101:LEU:HD13	1.96	0.46
1:C:47:GLU:OE2	1:C:130[B]:HIS:HD2	1.93	0.46
1:R:32:TRP:NE1	1:R:83:THR:HB	2.26	0.46
1:E:118:ASP:OD2	6:E:1372:HOH:O	2.21	0.46
1:E:140:LEU:O	1:E:144:VAL:HG22	2.16	0.46
1:J:83:THR:CG2	6:J:165:HOH:O	2.48	0.46
1:R:33:ASN:ND2	1:R:41:GLY:HA3	2.31	0.46
1:U:133:TYR:CD2	1:U:134:LEU:HD13	2.51	0.46
1:B:65:LEU:O	1:B:66:GLU:HB2	2.15	0.46
1:A:81:GLU:HG2	1:A:85:GLU:OE2	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:123:ILE:O	1:I:127:GLU:HG2	2.15	0.46
1:V:95:LEU:O	1:V:98:THR:HG22	2.16	0.46
1:B:83:THR:HG23	6:B:173:HOH:O	2.13	0.46
1:U:47:GLU:OE2	1:U:130[B]:HIS:CD2	2.69	0.46
1:W:47:GLU:CD	1:W:130[B]:HIS:CD2	2.89	0.46
1:Q:123:ILE:O	1:Q:127:GLU:HG2	2.16	0.46
1:A:110:GLN:HB2	6:A:1143:HOH:O	2.16	0.46
1:B:48:SER:O	1:B:52:MET:HG3	2.16	0.46
1:I:20:ILE:HG23	1:I:77:LEU:HD12	1.98	0.46
1:G:6:LYS:NZ	1:G:9:GLN:OE1	2.42	0.45
1:O:44:GLU:OE2	1:O:90:ASP:OD2	2.34	0.45
1:G:130[B]:HIS:CD2	1:G:134:LEU:HD22	2.51	0.45
1:W:95:LEU:O	1:W:98:THR:HG22	2.17	0.45
1:V:117:ARG:CG	6:V:954:HOH:O	2.61	0.45
1:I:145:GLY:HA3	6:I:450:HOH:O	2.15	0.45
1:A:57:LYS:HE3	6:A:351:HOH:O	2.16	0.45
1:O:42:ALA:O	1:O:46[B]:HIS:HD2	1.98	0.45
1:L:94:GLU:OE2	1:L:130[B]:HIS:ND1	2.48	0.45
4:X:162:HEM:CBB	4:X:162:HEM:CMB	2.52	0.45
1:D:47:GLU:OE1	1:D:130[A]:HIS:NE2	2.49	0.45
1:J:133:TYR:HD2	1:J:134:LEU:HD13	1.81	0.45
1:X:133:TYR:O	1:X:137:GLN:HG2	2.16	0.45
1:H:133:TYR:CD2	1:H:134:LEU:HD13	2.51	0.45
1:G:33:ASN:ND2	6:G:1033:HOH:O	2.47	0.45
1:R:123:ILE:O	1:R:127:GLU:HG2	2.17	0.45
1:V:83:THR:CG2	6:V:166:HOH:O	2.31	0.45
1:B:98:THR:CG2	6:B:254:HOH:O	2.38	0.45
1:V:130[B]:HIS:CD2	1:V:134:LEU:HD22	2.52	0.45
1:I:63:LEU:HD13	1:I:69:PRO:HD3	1.98	0.45
1:Q:112:HIS:HE1	6:Q:457:HOH:O	1.99	0.45
1:A:33:ASN:ND2	1:A:41:GLY:HA3	2.31	0.45
1:F:25:TYR:CE2	1:F:130[B]:HIS:CE1	3.04	0.45
1:K:133:TYR:O	1:K:137:GLN:HG2	2.17	0.45
1:H:83:THR:HG21	1:H:150:LEU:HD21	1.98	0.45
4:C:165:HEM:CMB	4:C:165:HEM:CBB	2.92	0.45
1:L:53:LYS:HB2	6:L:317:HOH:O	2.15	0.45
1:N:42:ALA:O	1:N:46[B]:HIS:CD2	2.70	0.45
1:Q:39:ARG:HD2	1:Q:155:HIS:O	2.16	0.45
1:H:130[B]:HIS:CD2	1:H:134:LEU:HD22	2.52	0.45
1:E:32:TRP:NE1	1:E:83:THR:HB	2.30	0.45
1:U:132:ASP:OD2	6:U:598:HOH:O	2.20	0.45
1:U:98:THR:HG22	6:U:1134:HOH:O	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:143:LYS:HE2	6:O:505:HOH:O	2.16	0.45
1:J:47:GLU:OE1	1:J:47:GLU:HA	2.17	0.45
1:M:154:MET:CE	1:X:153:HIS:HE1	2.29	0.45
1:U:94:GLU:O	1:U:98:THR:HB	2.17	0.45
4:H:162:HEM:HMC3	4:H:162:HEM:HBC2	1.96	0.44
1:C:98:THR:CG2	6:C:545:HOH:O	2.45	0.44
1:V:33:ASN:ND2	6:V:939:HOH:O	2.51	0.44
1:U:44:GLU:OE2	1:U:90:ASP:OD2	2.35	0.44
1:F:102:ARG:HG2	1:F:102:ARG:HH11	1.82	0.44
1:F:14:ILE:HD13	1:F:101:LEU:HD13	1.99	0.44
1:H:83:THR:HG21	1:H:150:LEU:CD2	2.47	0.44
4:F:163:HEM:HBB2	4:F:163:HEM:HMB3	1.93	0.44
1:N:25:TYR:CE2	1:N:130[B]:HIS:HE1	2.36	0.44
4:H:162:HEM:HBB2	4:H:162:HEM:HMB3	1.98	0.44
1:W:133:TYR:HD2	1:W:134:LEU:HD13	1.82	0.44
1:A:63:LEU:HD13	1:A:69:PRO:CG	2.47	0.44
1:S:130[A]:HIS:HD2	6:S:1255:HOH:O	1.99	0.44
1:A:47:GLU:O	1:A:51:GLU:HG2	2.17	0.44
1:G:130[A]:HIS:CD2	6:G:523:HOH:O	2.70	0.44
1:U:32:TRP:NE1	1:U:83:THR:HB	2.32	0.44
1:Q:140:LEU:HD23	1:Q:140:LEU:HA	1.86	0.44
1:U:139:GLY:O	1:U:143:LYS:HG3	2.18	0.44
1:R:28:HIS:CD2	1:R:86:MET:HG2	2.53	0.44
1:L:10:HIS:O	1:L:14:ILE:HG12	2.17	0.44
1:V:32:TRP:HE1	1:V:83:THR:CG2	2.31	0.44
4:A:165:HEM:CMC	4:A:165:HEM:HBC2	2.48	0.44
1:T:97:ALA:O	1:T:101:LEU:HD22	2.17	0.44
1:E:83:THR:HG21	1:E:150:LEU:HD21	1.99	0.44
1:P:81:GLU:HG2	1:P:85:GLU:CD	2.37	0.44
1:D:47:GLU:OE2	1:D:130[B]:HIS:CD2	2.71	0.44
1:O:80:GLY:CA	1:O:85:GLU:HG2	2.48	0.44
1:P:63:LEU:HD13	1:P:69:PRO:HD3	2.00	0.44
1:H:98:THR:CG2	6:H:541:HOH:O	2.64	0.43
1:D:32:TRP:NE1	1:D:83:THR:HB	2.27	0.43
1:B:123:ILE:O	1:B:127:GLU:HG2	2.17	0.43
1:O:123:ILE:O	1:O:127:GLU:HG2	2.18	0.43
1:N:10:HIS:CE1	6:N:1330:HOH:O	2.71	0.43
1:U:65:LEU:O	1:U:66:GLU:HB2	2.18	0.43
1:G:88:GLN:NE2	1:G:92:ASN:OD1	2.44	0.43
1:E:44:GLU:OE2	1:E:90:ASP:OD2	2.36	0.43
1:X:52:MET:HE1	4:X:162:HEM:C4A	2.54	0.43
4:C:165:HEM:HMB1	4:C:165:HEM:CBB	2.42	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:47:GLU:CD	1:D:130[B]:HIS:CD2	2.91	0.43
1:D:117:ARG:HD3	6:D:893:HOH:O	2.17	0.43
1:U:65:LEU:O	1:U:66:GLU:CB	2.65	0.43
1:K:63:LEU:HD13	1:K:69:PRO:HD3	2.01	0.43
1:D:25:TYR:N	1:D:25:TYR:CD1	2.85	0.43
1:A:25:TYR:CZ	1:A:130[B]:HIS:HE1	2.34	0.43
1:O:25:TYR:CE2	1:O:130[B]:HIS:HE1	2.36	0.43
1:V:32:TRP:HE1	1:V:83:THR:CB	2.29	0.43
1:G:133:TYR:CD2	1:G:134:LEU:HD13	2.54	0.43
1:R:83:THR:HG21	1:R:150:LEU:CD2	2.48	0.43
1:X:47:GLU:OE1	1:X:130[A]:HIS:NE2	2.52	0.43
1:F:44:GLU:OE2	1:F:90:ASP:OD2	2.37	0.43
1:M:63:LEU:HD13	1:M:69:PRO:CD	2.49	0.43
1:S:94:GLU:O	1:S:98:THR:HB	2.19	0.43
1:T:25:TYR:CE2	1:T:130[B]:HIS:CE1	3.01	0.43
1:O:42:ALA:O	1:O:46[B]:HIS:CD2	2.71	0.43
1:K:88:GLN:NE2	1:K:92:ASN:OD1	2.51	0.43
1:S:111:VAL:O	1:S:112:HIS:HB2	2.19	0.43
1:M:33:ASN:ND2	6:M:1291:HOH:O	2.51	0.43
1:L:14:ILE:HD12	1:L:101:LEU:HD13	2.00	0.43
1:B:63:LEU:HD13	1:B:69:PRO:HD3	2.00	0.43
4:F:163:HEM:CHD	4:F:163:HEM:HBC2	2.25	0.43
1:S:83:THR:HG23	6:S:166:HOH:O	2.03	0.43
1:R:44:GLU:OE2	1:R:90:ASP:OD2	2.37	0.43
1:V:131:ILE:O	1:V:135:GLU:HG3	2.19	0.43
1:M:65:LEU:O	1:M:66:GLU:CB	2.66	0.43
4:L:163:HEM:HBB2	4:L:163:HEM:HMB3	1.95	0.43
1:D:20:ILE:HG23	1:D:77:LEU:HD12	2.01	0.43
1:X:84:GLN:NE2	6:X:634:HOH:O	2.51	0.43
1:V:130[B]:HIS:HD2	1:V:134:LEU:HD13	1.84	0.42
1:B:25:TYR:CD1	1:B:25:TYR:N	2.86	0.42
1:X:39:ARG:HD2	1:X:155:HIS:O	2.19	0.42
1:O:98:THR:CG2	6:O:1032:HOH:O	2.25	0.42
1:N:47:GLU:OE1	1:N:130[B]:HIS:NE2	2.51	0.42
1:X:47:GLU:OE2	1:X:130[B]:HIS:CD2	2.72	0.42
1:J:133:TYR:CD2	1:J:134:LEU:HD13	2.53	0.42
1:Q:96:LYS:NZ	1:Q:100:ASP:OD2	2.44	0.42
4:U:162:HEM:CHB	1:V:52:MET:HB3	2.50	0.42
1:I:25:TYR:CE2	1:I:130[B]:HIS:HE1	2.37	0.42
1:O:47:GLU:OE1	1:O:130[A]:HIS:CD2	2.73	0.42
1:J:98:THR:HG22	6:J:315:HOH:O	2.18	0.42
1:C:44:GLU:OE2	1:C:90:ASP:OD2	2.37	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:X:123:ILE:O	1:X:127:GLU:HG2	2.19	0.42
1:J:25:TYR:N	1:J:25:TYR:CD1	2.83	0.42
1:X:47:GLU:CD	1:X:130[B]:HIS:CD2	2.92	0.42
1:S:25:TYR:N	1:S:25:TYR:CD1	2.86	0.42
1:G:94:GLU:OE2	1:G:130[B]:HIS:ND1	2.53	0.42
1:V:133:TYR:O	1:V:137:GLN:HG2	2.19	0.42
1:N:117:ARG:NE	5:O:163:SO4:O1	2.52	0.42
1:D:117:ARG:NE	5:D:163:SO4:O4	2.52	0.42
1:W:38:LYS:HG3	6:W:1088:HOH:O	2.20	0.42
1:M:133:TYR:O	1:M:137:GLN:HG2	2.20	0.42
1:I:130[B]:HIS:CE1	6:I:166:HOH:O	2.72	0.42
1:S:83:THR:HG21	1:S:150:LEU:HD21	2.00	0.42
1:B:22:ILE:HD11	1:B:52:MET:HA	2.02	0.42
1:E:44:GLU:HB2	6:E:1137:HOH:O	2.19	0.42
1:C:123:ILE:O	1:C:127:GLU:HG2	2.19	0.42
1:V:140:LEU:O	1:V:144:VAL:HG22	2.20	0.42
4:N:165:HEM:HMB1	4:N:165:HEM:CBB	2.49	0.42
1:X:32:TRP:HE1	1:X:83:THR:CG2	2.33	0.42
1:W:32:TRP:HE1	1:W:83:THR:CB	2.29	0.42
1:W:133:TYR:CD2	1:W:134:LEU:HD13	2.53	0.42
1:X:44:GLU:OE2	1:X:90:ASP:OD2	2.37	0.42
1:M:25:TYR:N	1:M:25:TYR:CD1	2.84	0.42
1:L:83:THR:HG21	1:L:150:LEU:CD2	2.50	0.42
1:V:25:TYR:CE2	1:V:130[B]:HIS:HE1	2.37	0.42
1:T:47:GLU:OE1	1:T:130[A]:HIS:CD2	2.73	0.42
1:J:140:LEU:O	1:J:144:VAL:HG22	2.20	0.42
1:H:25:TYR:CZ	1:H:130[B]:HIS:HE1	2.35	0.41
1:K:33:ASN:ND2	6:K:207:HOH:O	2.48	0.41
1:C:154:MET:HE1	1:U:153:HIS:CE1	2.54	0.41
1:D:146:LEU:O	1:D:150:LEU:HG	2.20	0.41
1:G:25:TYR:CE2	1:G:130[B]:HIS:CE1	3.08	0.41
1:U:47:GLU:OE1	1:U:130[A]:HIS:CD2	2.73	0.41
1:I:143:LYS:CE	6:O:505:HOH:O	2.67	0.41
1:A:32:TRP:HE1	1:A:83:THR:CG2	2.33	0.41
1:U:32:TRP:HE1	1:U:83:THR:CB	2.31	0.41
1:F:47:GLU:OE1	1:F:130[B]:HIS:CG	2.74	0.41
1:B:94:GLU:OE2	1:B:130[B]:HIS:ND1	2.53	0.41
1:E:119:LEU:CD2	1:E:119:LEU:C	2.88	0.41
4:P:163:HEM:CHD	4:P:163:HEM:HBC2	2.43	0.41
4:S:163:HEM:HBC2	4:S:163:HEM:CHD	2.24	0.41
1:Q:83:THR:HG21	1:Q:150:LEU:HD22	2.02	0.41
1:M:65:LEU:O	1:M:66:GLU:HB2	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:T:25:TYR:CZ	1:T:130[B]:HIS:HE1	2.38	0.41
1:R:130[B]:HIS:CD2	1:R:134:LEU:CD2	2.96	0.41
1:I:47:GLU:OE2	1:I:130[B]:HIS:CD2	2.73	0.41
1:X:52:MET:CE	4:X:162:HEM:NB	2.83	0.41
1:A:51:GLU:OE1	1:A:51:GLU:HA	2.20	0.41
1:W:94:GLU:CD	1:W:130[B]:HIS:HD1	2.24	0.41
1:C:127:GLU:HA	1:C:127:GLU:OE1	2.20	0.41
1:F:5:LYS:HE3	1:F:5:LYS:HB3	1.91	0.41
1:O:32:TRP:NE1	1:O:83:THR:HB	2.30	0.41
1:C:131:ILE:O	1:C:135:GLU:HG3	2.21	0.41
1:T:33:ASN:ND2	1:T:41:GLY:HA3	2.36	0.41
1:O:99:LYS:HE3	1:O:99:LYS:HB2	1.66	0.41
1:L:18:GLU:O	1:L:22:ILE:HG13	2.20	0.41
4:S:163:HEM:CBC	1:T:26:PHE:CE1	3.03	0.41
1:W:130[B]:HIS:HE1	6:W:164:HOH:O	1.85	0.41
1:U:83:THR:CG2	6:U:165:HOH:O	2.56	0.41
1:X:111:VAL:O	1:X:112:HIS:HB2	2.21	0.41
1:D:38:LYS:HG2	1:D:38:LYS:HZ2	1.72	0.41
1:N:123:ILE:O	1:N:127:GLU:HG2	2.20	0.41
1:A:25:TYR:CD1	1:A:25:TYR:N	2.87	0.41
1:B:127:GLU:OE1	1:B:127:GLU:HA	2.21	0.41
1:C:39:ARG:HD2	1:C:155:HIS:O	2.21	0.41
1:A:109:GLU:HB2	1:A:117:ARG:HH11	1.85	0.41
1:A:90:ASP:HB3	1:A:134:LEU:HD21	2.03	0.40
1:K:130[B]:HIS:CD2	1:K:134:LEU:HD22	2.55	0.40
1:F:76:LYS:HD2	1:F:76:LYS:HA	1.81	0.40
4:S:163:HEM:CHB	1:T:52:MET:HB3	2.51	0.40
1:R:47:GLU:OE1	1:R:130[A]:HIS:NE2	2.53	0.40
1:S:47:GLU:O	1:S:51:GLU:HG2	2.21	0.40
1:F:154:MET:HE3	1:F:154:MET:HB3	1.91	0.40
1:O:127:GLU:HA	1:O:127:GLU:OE1	2.20	0.40
1:A:93:LEU:HD12	1:A:93:LEU:HA	1.90	0.40
1:M:77:LEU:CD1	1:M:77:LEU:N	2.84	0.40
1:U:63:LEU:HD13	1:U:69:PRO:HD3	2.03	0.40
1:U:52:MET:CE	4:U:162:HEM:NB	2.83	0.40
1:K:63:LEU:HD13	1:K:69:PRO:CD	2.52	0.40
1:C:94:GLU:O	1:C:98:THR:HB	2.22	0.40
1:U:130[B]:HIS:HE1	6:U:166:HOH:O	1.87	0.40
1:X:38:LYS:CE	6:X:312:HOH:O	2.67	0.40
1:P:133:TYR:CD2	1:P:134:LEU:HD13	2.57	0.40
1:S:63:LEU:HD13	1:S:69:PRO:CG	2.52	0.40
1:G:63:LEU:HD13	1:G:69:PRO:CD	2.52	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:N:47:GLU:OE1	1:N:130[A]:HIS:CG	2.74	0.40
1:J:32:TRP:HE1	1:J:83:THR:HG22	1.86	0.40
1:F:47:GLU:O	1:F:51:GLU:HG2	2.22	0.40
1:D:63:LEU:HD13	1:D:69:PRO:HD3	2.03	0.40
1:U:22:ILE:HG13	1:U:51:GLU:HB2	2.03	0.40
1:P:107:HIS:CE1	6:P:338:HOH:O	2.74	0.40
1:J:109:GLU:HB2	1:J:117:ARG:HH11	1.87	0.40

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	155/158 (98%)	155 (100%)	0	0	100	100
1	B	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
1	C	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
1	D	154/158 (98%)	150 (97%)	4 (3%)	0	100	100
1	E	155/158 (98%)	155 (100%)	0	0	100	100
1	F	155/158 (98%)	155 (100%)	0	0	100	100
1	G	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
1	H	154/158 (98%)	153 (99%)	1 (1%)	0	100	100
1	I	154/158 (98%)	154 (100%)	0	0	100	100
1	J	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
1	K	155/158 (98%)	153 (99%)	2 (1%)	0	100	100
1	L	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
1	M	155/158 (98%)	153 (99%)	2 (1%)	0	100	100
1	N	155/158 (98%)	152 (98%)	3 (2%)	0	100	100
1	O	155/158 (98%)	153 (99%)	2 (1%)	0	100	100
1	P	155/158 (98%)	153 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	155/158 (98%)	153 (99%)	2 (1%)	0	100	100
1	R	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
1	S	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
1	T	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
1	U	154/158 (98%)	153 (99%)	1 (1%)	0	100	100
1	V	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
1	W	155/158 (98%)	155 (100%)	0	0	100	100
1	X	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
All	All	3716/3792 (98%)	3687 (99%)	29 (1%)	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	142/144 (99%)	134 (94%)	8 (6%)	30	30
1	B	141/144 (98%)	132 (94%)	9 (6%)	25	23
1	C	141/144 (98%)	129 (92%)	12 (8%)	15	13
1	D	141/144 (98%)	132 (94%)	9 (6%)	25	23
1	E	141/144 (98%)	129 (92%)	12 (8%)	15	13
1	F	141/144 (98%)	132 (94%)	9 (6%)	25	23
1	G	141/144 (98%)	130 (92%)	11 (8%)	18	15
1	H	141/144 (98%)	130 (92%)	11 (8%)	18	15
1	I	141/144 (98%)	129 (92%)	12 (8%)	15	13
1	J	141/144 (98%)	131 (93%)	10 (7%)	21	19
1	K	142/144 (99%)	133 (94%)	9 (6%)	25	24
1	L	141/144 (98%)	129 (92%)	12 (8%)	15	13
1	M	139/144 (96%)	130 (94%)	9 (6%)	24	23
1	N	139/144 (96%)	129 (93%)	10 (7%)	21	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	O	140/144 (97%)	130 (93%)	10 (7%)	21	19
1	P	140/144 (97%)	130 (93%)	10 (7%)	21	19
1	Q	142/144 (99%)	132 (93%)	10 (7%)	21	19
1	R	140/144 (97%)	128 (91%)	12 (9%)	15	12
1	S	140/144 (97%)	127 (91%)	13 (9%)	13	9
1	T	139/144 (96%)	129 (93%)	10 (7%)	21	18
1	U	139/144 (96%)	128 (92%)	11 (8%)	18	15
1	V	139/144 (96%)	127 (91%)	12 (9%)	15	12
1	W	139/144 (96%)	128 (92%)	11 (8%)	18	15
1	X	140/144 (97%)	128 (91%)	12 (9%)	15	12
All	All	3370/3456 (98%)	3116 (92%)	254 (8%)	19	17

All (254) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	LYS
1	A	63	LEU
1	A	83	THR
1	A	98	THR
1	A	101	LEU
1	A	119	LEU
1	A	134	LEU
1	A	138	LEU
1	B	6	LYS
1	B	63	LEU
1	B	83	THR
1	B	98	THR
1	B	99	LYS
1	B	101	LEU
1	B	119	LEU
1	B	134	LEU
1	B	138	LEU
1	C	5	LYS
1	C	63	LEU
1	C	66	GLU
1	C	77	LEU
1	C	83	THR
1	C	98	THR

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Mol	Chain	Res	Type
1	C	101	LEU
1	C	110	GLN
1	C	118	ASP
1	C	119	LEU
1	C	134	LEU
1	C	138	LEU
1	D	63	LEU
1	D	77	LEU
1	D	83	THR
1	D	98	THR
1	D	101	LEU
1	D	110	GLN
1	D	119	LEU
1	D	134	LEU
1	D	138	LEU
1	E	5	LYS
1	E	38	LYS
1	E	63	LEU
1	E	66	GLU
1	E	83	THR
1	E	98	THR
1	E	101	LEU
1	E	107	HIS
1	E	119	LEU
1	E	126	SER
1	E	134	LEU
1	E	138	LEU
1	F	63	LEU
1	F	81	GLU
1	F	83	THR
1	F	98	THR
1	F	99	LYS
1	F	101	LEU
1	F	119	LEU
1	F	134	LEU
1	F	138	LEU
1	G	63	LEU
1	G	76	LYS
1	G	77	LEU
1	G	83	THR
1	G	98	THR
1	G	101	LEU

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Mol	Chain	Res	Type
1	G	118	ASP
1	G	119	LEU
1	G	134	LEU
1	G	138	LEU
1	G	154	MET
1	H	38	LYS
1	H	63	LEU
1	H	66	GLU
1	H	83	THR
1	H	84	GLN
1	H	98	THR
1	H	101	LEU
1	H	118	ASP
1	H	119	LEU
1	H	134	LEU
1	H	138	LEU
1	I	6	LYS
1	I	63	LEU
1	I	83	THR
1	I	98	THR
1	I	101	LEU
1	I	110	GLN
1	I	118	ASP
1	I	119	LEU
1	I	126	SER
1	I	134	LEU
1	I	138	LEU
1	I	154	MET
1	J	63	LEU
1	J	76	LYS
1	J	83	THR
1	J	98	THR
1	J	99	LYS
1	J	101	LEU
1	J	118	ASP
1	J	119	LEU
1	J	134	LEU
1	J	138	LEU
1	K	63	LEU
1	K	66	GLU
1	K	77	LEU
1	K	83	THR

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Mol	Chain	Res	Type
1	K	98	THR
1	K	101	LEU
1	K	118	ASP
1	K	134	LEU
1	K	138	LEU
1	L	30	ARG
1	L	38	LYS
1	L	63	LEU
1	L	66	GLU
1	L	77	LEU
1	L	83	THR
1	L	84	GLN
1	L	101	LEU
1	L	118	ASP
1	L	119	LEU
1	L	134	LEU
1	L	138	LEU
1	M	38	LYS
1	M	63	LEU
1	M	66	GLU
1	M	83	THR
1	M	98	THR
1	M	101	LEU
1	M	118	ASP
1	M	134	LEU
1	M	138	LEU
1	N	38	LYS
1	N	63	LEU
1	N	66	GLU
1	N	76	LYS
1	N	83	THR
1	N	101	LEU
1	N	118	ASP
1	N	119	LEU
1	N	134	LEU
1	N	138	LEU
1	O	63	LEU
1	O	66	GLU
1	O	83	THR
1	O	98	THR
1	O	101	LEU
1	O	110	GLN

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Mol	Chain	Res	Type
1	O	118	ASP
1	O	119	LEU
1	O	134	LEU
1	O	138	LEU
1	P	63	LEU
1	P	66	GLU
1	P	83	THR
1	P	98	THR
1	P	101	LEU
1	P	110	GLN
1	P	118	ASP
1	P	119	LEU
1	P	134	LEU
1	P	138	LEU
1	Q	63	LEU
1	Q	81	GLU
1	Q	83	THR
1	Q	98	THR
1	Q	101	LEU
1	Q	107	HIS
1	Q	118	ASP
1	Q	119	LEU
1	Q	134	LEU
1	Q	138	LEU
1	R	2	LYS
1	R	63	LEU
1	R	66	GLU
1	R	77	LEU
1	R	81	GLU
1	R	83	THR
1	R	98	THR
1	R	101	LEU
1	R	118	ASP
1	R	119	LEU
1	R	134	LEU
1	R	138	LEU
1	S	9	GLN
1	S	34	ASP
1	S	38	LYS
1	S	63	LEU
1	S	66	GLU
1	S	76	LYS

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Mol	Chain	Res	Type
1	S	83	THR
1	S	98	THR
1	S	101	LEU
1	S	118	ASP
1	S	119	LEU
1	S	134	LEU
1	S	138	LEU
1	T	14	ILE
1	T	63	LEU
1	T	66	GLU
1	T	83	THR
1	T	98	THR
1	T	101	LEU
1	T	118	ASP
1	T	119	LEU
1	T	134	LEU
1	T	138	LEU
1	U	4	ASP
1	U	38	LYS
1	U	63	LEU
1	U	66	GLU
1	U	83	THR
1	U	98	THR
1	U	101	LEU
1	U	110	GLN
1	U	119	LEU
1	U	134	LEU
1	U	138	LEU
1	V	63	LEU
1	V	66	GLU
1	V	76	LYS
1	V	81	GLU
1	V	83	THR
1	V	98	THR
1	V	99	LYS
1	V	101	LEU
1	V	118	ASP
1	V	119	LEU
1	V	134	LEU
1	V	138	LEU
1	W	30	ARG
1	W	63	LEU

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Mol	Chain	Res	Type
1	W	77	LEU
1	W	83	THR
1	W	98	THR
1	W	101	LEU
1	W	118	ASP
1	W	119	LEU
1	W	134	LEU
1	W	138	LEU
1	W	154	MET
1	X	57	LYS
1	X	63	LEU
1	X	66	GLU
1	X	81	GLU
1	X	83	THR
1	X	98	THR
1	X	101	LEU
1	X	110	GLN
1	X	119	LEU
1	X	134	LEU
1	X	138	LEU
1	X	154	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (78) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	ASN
1	A	33	ASN
1	B	17	ASN
1	B	33	ASN
1	B	110	GLN
1	B	137	GLN
1	C	17	ASN
1	C	33	ASN
1	C	84	GLN
1	D	9	GLN
1	D	17	ASN
1	D	33	ASN
1	D	137	GLN
1	E	17	ASN
1	E	33	ASN
1	E	88	GLN
1	E	110	GLN

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Mol	Chain	Res	Type
1	E	137	GLN
1	F	17	ASN
1	F	33	ASN
1	G	17	ASN
1	G	33	ASN
1	H	17	ASN
1	H	33	ASN
1	H	110	GLN
1	H	137	GLN
1	I	17	ASN
1	I	33	ASN
1	I	110	GLN
1	I	137	GLN
1	J	17	ASN
1	J	33	ASN
1	J	137	GLN
1	K	17	ASN
1	K	33	ASN
1	K	110	GLN
1	L	17	ASN
1	L	33	ASN
1	L	137	GLN
1	M	17	ASN
1	M	33	ASN
1	M	43	HIS
1	N	17	ASN
1	N	33	ASN
1	O	17	ASN
1	O	33	ASN
1	O	84	GLN
1	O	110	GLN
1	O	137	GLN
1	O	142	GLN
1	P	17	ASN
1	P	33	ASN
1	P	137	GLN
1	Q	17	ASN
1	Q	33	ASN
1	Q	137	GLN
1	R	17	ASN
1	R	33	ASN
1	R	137	GLN

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Mol	Chain	Res	Type
1	S	17	ASN
1	S	33	ASN
1	T	17	ASN
1	T	33	ASN
1	T	43	HIS
1	T	84	GLN
1	T	137	GLN
1	U	17	ASN
1	U	33	ASN
1	U	84	GLN
1	V	17	ASN
1	V	33	ASN
1	V	137	GLN
1	W	17	ASN
1	W	33	ASN
1	W	137	GLN
1	X	17	ASN
1	X	33	ASN
1	X	84	GLN

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 122 ligands modelled in this entry, 102 are monoatomic - leaving 20 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	$\# Z > 2$
4	HEM	A	165	1	49,50,50	3.38	15 (30%)	46,82,82	2.21	9 (19%)
5	SO4	A	166	-	4,4,4	0.45	0	6,6,6	0.21	0
5	SO4	B	165	-	4,4,4	0.24	0	6,6,6	0.33	0
4	HEM	C	165	1	49,50,50	2.43	16 (32%)	46,82,82	2.39	11 (23%)
5	SO4	D	163	-	4,4,4	0.25	0	6,6,6	0.39	0
4	HEM	F	163	1	49,50,50	3.61	14 (28%)	46,82,82	2.18	9 (19%)
5	SO4	F	164	-	4,4,4	0.56	0	6,6,6	0.25	0
4	HEM	H	162	1	49,50,50	2.56	17 (34%)	46,82,82	2.37	14 (30%)
4	HEM	I	163	1	49,50,50	2.40	15 (30%)	46,82,82	2.54	13 (28%)
5	SO4	I	164	-	4,4,4	0.26	0	6,6,6	0.51	0
4	HEM	L	163	1	49,50,50	2.50	14 (28%)	46,82,82	2.51	10 (21%)
5	SO4	M	163	-	4,4,4	0.51	0	6,6,6	0.21	0
4	HEM	N	165	1	49,50,50	2.45	13 (26%)	46,82,82	2.56	15 (32%)
5	SO4	O	163	-	4,4,4	0.16	0	6,6,6	0.29	0
4	HEM	P	163	1	49,50,50	3.13	17 (34%)	46,82,82	2.48	13 (28%)
4	HEM	Q	163	1	49,50,50	2.46	16 (32%)	46,82,82	2.40	13 (28%)
5	SO4	R	163	-	4,4,4	0.29	0	6,6,6	0.45	0
4	HEM	S	163	1	49,50,50	2.65	15 (30%)	46,82,82	2.46	12 (26%)
4	HEM	U	162	1	49,50,50	2.59	15 (30%)	46,82,82	2.47	12 (26%)
4	HEM	X	162	1	49,50,50	2.15	14 (28%)	46,82,82	2.38	11 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	HEM	A	165	1	-	0/14/114/114	0/0/8/8
5	SO4	A	166	-	-	0/0/0/0	0/0/0/0
5	SO4	B	165	-	-	0/0/0/0	0/0/0/0
4	HEM	C	165	1	-	0/14/114/114	0/0/8/8
5	SO4	D	163	-	-	0/0/0/0	0/0/0/0
4	HEM	F	163	1	-	0/14/114/114	0/0/8/8
5	SO4	F	164	-	-	0/0/0/0	0/0/0/0
4	HEM	H	162	1	-	0/14/114/114	0/0/8/8
4	HEM	I	163	1	-	0/14/114/114	0/0/8/8
5	SO4	I	164	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	HEM	L	163	1	-	0/14/114/114	0/0/8/8
5	SO4	M	163	-	-	0/0/0/0	0/0/0/0
4	HEM	N	165	1	-	0/14/114/114	0/0/8/8
5	SO4	O	163	-	-	0/0/0/0	0/0/0/0
4	HEM	P	163	1	-	0/14/114/114	0/0/8/8
4	HEM	Q	163	1	-	0/14/114/114	0/0/8/8
5	SO4	R	163	-	-	0/0/0/0	0/0/0/0
4	HEM	S	163	1	-	0/14/114/114	0/0/8/8
4	HEM	U	162	1	-	0/14/114/114	0/0/8/8
4	HEM	X	162	1	-	0/14/114/114	0/0/8/8

All (181) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	163	HEM	C2B-C1B	15.04	1.48	1.44
4	A	165	HEM	C3D-C4D	12.96	1.47	1.44
4	F	163	HEM	C2D-C1D	12.61	1.47	1.44
4	A	165	HEM	C2B-C1B	10.98	1.47	1.44
4	P	163	HEM	C3D-C4D	9.63	1.47	1.44
4	S	163	HEM	C2D-C1D	8.97	1.46	1.44
4	U	162	HEM	C2B-C1B	8.55	1.46	1.44
4	U	162	HEM	C3C-C2C	-7.52	1.30	1.43
4	F	163	HEM	C3C-C2C	-7.17	1.31	1.43
4	S	163	HEM	C3B-C2B	-7.01	1.31	1.43
4	H	162	HEM	C3C-C2C	-7.00	1.31	1.43
4	P	163	HEM	C2D-C1D	6.98	1.46	1.44
4	P	163	HEM	C3B-C2B	-6.91	1.31	1.43
4	F	163	HEM	C3B-C2B	-6.91	1.31	1.43
4	N	165	HEM	C2D-C1D	6.88	1.46	1.44
4	H	162	HEM	C3B-C2B	-6.87	1.31	1.43
4	C	165	HEM	C3C-C2C	-6.85	1.31	1.43
4	L	163	HEM	C3C-C2C	-6.85	1.31	1.43
4	H	162	HEM	C2B-C1B	6.83	1.46	1.44
4	Q	163	HEM	C3D-C4D	6.82	1.46	1.44
4	X	162	HEM	C3C-C2C	-6.80	1.31	1.43
4	I	163	HEM	C3B-C2B	-6.79	1.31	1.43
4	X	162	HEM	C3B-C2B	-6.79	1.31	1.43
4	Q	163	HEM	C3C-C2C	-6.76	1.31	1.43
4	P	163	HEM	C2B-C1B	6.70	1.46	1.44
4	U	162	HEM	C3B-C2B	-6.68	1.32	1.43
4	N	165	HEM	C3C-C2C	-6.68	1.32	1.43
4	I	163	HEM	C3C-C2C	-6.65	1.32	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	S	163	HEM	C3C-C2C	-6.62	1.32	1.43
4	Q	163	HEM	C3B-C2B	-6.60	1.32	1.43
4	A	165	HEM	C3B-C2B	-6.49	1.32	1.43
4	P	163	HEM	C3C-C2C	-6.44	1.32	1.43
4	A	165	HEM	C3C-C2C	-6.29	1.32	1.43
4	L	163	HEM	C3D-C4D	-6.18	1.43	1.44
4	L	163	HEM	C3B-C2B	-6.13	1.33	1.43
4	P	163	HEM	C3D-C2D	6.04	1.54	1.43
4	C	165	HEM	C3B-C2B	-5.76	1.33	1.43
4	I	163	HEM	C3D-C2D	5.75	1.53	1.43
4	N	165	HEM	C3B-C2B	-5.68	1.33	1.43
4	A	165	HEM	C2D-C1D	5.36	1.45	1.44
4	N	165	HEM	C3D-C4D	-5.31	1.43	1.44
4	C	165	HEM	FE-NB	5.30	2.17	1.97
4	N	165	HEM	FE-ND	5.20	2.16	1.97
4	L	163	HEM	C2B-C1B	5.12	1.45	1.44
4	C	165	HEM	C4A-C3A	5.10	1.46	1.40
4	Q	163	HEM	C3D-C2D	5.08	1.52	1.43
4	A	165	HEM	C3D-C2D	5.06	1.52	1.43
4	H	162	HEM	FE-NA	5.04	2.14	1.92
4	C	165	HEM	C3D-C4D	5.04	1.45	1.44
4	P	163	HEM	FE-NA	4.86	2.13	1.92
4	F	163	HEM	C4A-C3A	4.85	1.46	1.40
4	P	163	HEM	C4A-C3A	4.84	1.46	1.40
4	F	163	HEM	C3D-C4D	-4.83	1.43	1.44
4	A	165	HEM	C3C-CAC	4.81	1.55	1.40
4	L	163	HEM	C3D-C2D	4.79	1.52	1.43
4	S	163	HEM	C3D-C2D	4.70	1.52	1.43
4	A	165	HEM	C4A-C3A	4.66	1.46	1.40
4	Q	163	HEM	C4A-C3A	4.58	1.45	1.40
4	S	163	HEM	C3D-C4D	-4.57	1.43	1.44
4	U	162	HEM	C3D-C2D	4.51	1.51	1.43
4	H	162	HEM	C3D-C2D	4.46	1.51	1.43
4	N	165	HEM	C3D-C2D	4.45	1.51	1.43
4	L	163	HEM	C4A-C3A	4.37	1.45	1.40
4	H	162	HEM	C4A-C3A	4.36	1.45	1.40
4	I	163	HEM	C3D-C4D	4.36	1.45	1.44
4	L	163	HEM	C2D-C1D	4.33	1.45	1.44
4	A	165	HEM	C3B-CAB	4.27	1.53	1.40
4	H	162	HEM	C2D-C1D	-4.21	1.43	1.44
4	X	162	HEM	FE-ND	4.21	2.13	1.97
4	C	165	HEM	C3D-C2D	4.16	1.51	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	165	HEM	C3B-CAB	4.10	1.53	1.40
4	I	163	HEM	FE-NC	4.09	2.13	1.97
4	S	163	HEM	C3B-CAB	4.08	1.53	1.40
4	F	163	HEM	C3D-C2D	4.06	1.50	1.43
4	C	165	HEM	C3C-CAC	4.05	1.53	1.40
4	U	162	HEM	C3B-CAB	4.04	1.53	1.40
4	P	163	HEM	FE-NB	3.99	2.12	1.97
4	X	162	HEM	C3D-C2D	3.99	1.50	1.43
4	L	163	HEM	C3B-CAB	3.98	1.52	1.40
4	N	165	HEM	C3B-CAB	3.97	1.52	1.40
4	P	163	HEM	C3C-CAC	3.93	1.52	1.40
4	S	163	HEM	C3C-CAC	3.87	1.52	1.40
4	I	163	HEM	C3C-CAC	3.87	1.52	1.40
4	I	163	HEM	CHA-C4D	3.82	1.41	1.35
4	Q	163	HEM	C3B-CAB	3.80	1.52	1.40
4	P	163	HEM	C3B-CAB	3.75	1.52	1.40
4	S	163	HEM	C4A-C3A	3.75	1.44	1.40
4	H	162	HEM	C3B-CAB	3.73	1.52	1.40
4	I	163	HEM	C2B-C1B	3.72	1.45	1.44
4	N	165	HEM	C3C-CAC	3.72	1.52	1.40
4	N	165	HEM	C4A-C3A	3.71	1.44	1.40
4	U	162	HEM	FE-ND	3.65	2.11	1.97
4	F	163	HEM	C3C-CAC	3.64	1.51	1.40
4	X	162	HEM	C3B-CAB	3.62	1.51	1.40
4	F	163	HEM	C3B-CAB	3.58	1.51	1.40
4	L	163	HEM	C3C-CAC	3.56	1.51	1.40
4	A	165	HEM	FE-NA	3.54	2.07	1.92
4	S	163	HEM	FE-ND	3.50	2.10	1.97
4	P	163	HEM	CHB-C1B	3.49	1.40	1.35
4	U	162	HEM	C4A-C3A	3.49	1.44	1.40
4	U	162	HEM	C3D-C4D	-3.45	1.43	1.44
4	P	163	HEM	FE-NC	3.44	2.10	1.97
4	Q	163	HEM	C3C-CAC	3.41	1.51	1.40
4	X	162	HEM	C3C-CAC	3.33	1.50	1.40
4	U	162	HEM	C3C-CAC	3.33	1.50	1.40
4	I	163	HEM	C3B-CAB	3.32	1.50	1.40
4	X	162	HEM	C4A-C3A	3.29	1.44	1.40
4	H	162	HEM	C3C-CAC	3.26	1.50	1.40
4	L	163	HEM	FE-NA	3.23	2.06	1.92
4	S	163	HEM	FE-NA	3.20	2.06	1.92
4	C	165	HEM	FE-ND	3.18	2.09	1.97
4	U	162	HEM	C2D-C1D	-3.15	1.43	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	I	163	HEM	FE-NA	3.04	2.05	1.92
4	X	162	HEM	CHA-C4D	2.94	1.40	1.35
4	Q	163	HEM	C2B-C1B	2.93	1.45	1.44
4	U	162	HEM	FE-NA	2.88	2.04	1.92
4	Q	163	HEM	FE-NA	2.88	2.04	1.92
4	A	165	HEM	CMC-C2C	2.85	1.56	1.47
4	H	162	HEM	C4C-NC	-2.75	1.34	1.38
4	P	163	HEM	CMB-C2B	2.73	1.55	1.47
4	Q	163	HEM	CMD-C2D	2.70	1.55	1.47
4	F	163	HEM	CMB-C2B	2.69	1.55	1.47
4	C	165	HEM	C3B-C4B	-2.67	1.41	1.44
4	X	162	HEM	CMC-C2C	2.68	1.55	1.47
4	H	162	HEM	C3D-C4D	2.67	1.45	1.44
4	L	163	HEM	CMC-C2C	2.62	1.55	1.47
4	F	163	HEM	FE-ND	2.61	2.07	1.97
4	X	162	HEM	C2B-C1B	2.61	1.45	1.44
4	Q	163	HEM	CHA-C4D	2.60	1.39	1.35
4	L	163	HEM	FE-NC	2.60	2.07	1.97
4	I	163	HEM	CMD-C2D	2.58	1.55	1.47
4	I	163	HEM	FE-NB	2.58	2.07	1.97
4	F	163	HEM	CMC-C2C	2.57	1.55	1.47
4	Q	163	HEM	FE-ND	2.57	2.07	1.97
4	I	163	HEM	C4A-C3A	2.57	1.43	1.40
4	S	163	HEM	CMB-C2B	2.53	1.55	1.47
4	S	163	HEM	FE-NC	2.51	2.07	1.97
4	Q	163	HEM	CMB-C2B	2.51	1.55	1.47
4	P	163	HEM	CMC-C2C	2.46	1.55	1.47
4	S	163	HEM	CMC-C2C	2.44	1.55	1.47
4	U	162	HEM	CMD-C2D	2.42	1.54	1.47
4	P	163	HEM	CMD-C2D	2.41	1.54	1.47
4	U	162	HEM	CMC-C2C	2.39	1.54	1.47
4	C	165	HEM	CMD-C2D	2.39	1.54	1.47
4	N	165	HEM	CMC-C2C	2.36	1.54	1.47
4	S	163	HEM	FE-NB	2.35	2.06	1.97
4	H	162	HEM	CHA-C4D	2.35	1.39	1.35
4	H	162	HEM	FE-ND	2.32	2.06	1.97
4	N	165	HEM	CMD-C2D	2.31	1.54	1.47
4	A	165	HEM	CMD-C2D	2.31	1.54	1.47
4	H	162	HEM	CMD-C2D	2.30	1.54	1.47
4	Q	163	HEM	CMC-C2C	2.30	1.54	1.47
4	Q	163	HEM	C2D-C1D	2.30	1.45	1.44
4	X	162	HEM	CAA-C2A	2.28	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	162	HEM	CMB-C2B	2.28	1.54	1.47
4	U	162	HEM	CMB-C2B	2.28	1.54	1.47
4	I	163	HEM	CMC-C2C	2.26	1.54	1.47
4	A	165	HEM	CMB-C2B	2.26	1.54	1.47
4	L	163	HEM	FE-ND	2.25	2.06	1.97
4	I	163	HEM	CMB-C2B	2.25	1.54	1.47
4	C	165	HEM	C2B-C1B	2.22	1.45	1.44
4	X	162	HEM	CMB-C2B	2.22	1.54	1.47
4	F	163	HEM	FE-NC	2.21	2.06	1.97
4	L	163	HEM	CMB-C2B	2.20	1.54	1.47
4	N	165	HEM	CHD-C4C	2.18	1.40	1.36
4	X	162	HEM	FE-NC	2.17	2.06	1.97
4	H	162	HEM	CMA-C3A	2.17	1.56	1.51
4	X	162	HEM	CMD-C2D	2.15	1.54	1.47
4	N	165	HEM	FE-NA	2.14	2.01	1.92
4	A	165	HEM	FE-NB	2.14	2.05	1.97
4	P	163	HEM	CHA-C4D	2.11	1.38	1.35
4	H	162	HEM	CHB-C1B	2.10	1.38	1.35
4	C	165	HEM	C1C-NC	2.10	1.41	1.38
4	A	165	HEM	C4C-NC	-2.09	1.35	1.38
4	S	163	HEM	C2B-C1B	2.09	1.45	1.44
4	C	165	HEM	CMB-C2B	2.08	1.53	1.47
4	F	163	HEM	CMD-C2D	2.07	1.53	1.47
4	Q	163	HEM	FE-NC	2.05	2.05	1.97
4	C	165	HEM	CHA-C4D	2.04	1.38	1.35
4	C	165	HEM	C2D-C1D	2.03	1.45	1.44
4	U	162	HEM	CMA-C3A	2.02	1.55	1.51

All (142) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	X	162	HEM	C3B-C4B-NB	-9.97	106.87	114.00
4	S	163	HEM	C3B-C4B-NB	-9.75	107.03	114.00
4	N	165	HEM	C3B-C4B-NB	-9.45	107.24	114.00
4	H	162	HEM	C3B-C4B-NB	-9.15	107.45	114.00
4	L	163	HEM	C3B-C4B-NB	-8.78	107.72	114.00
4	Q	163	HEM	C3B-C4B-NB	-8.60	107.85	114.00
4	I	163	HEM	C3B-C4B-NB	-8.56	107.88	114.00
4	P	163	HEM	C3B-C4B-NB	-7.98	108.29	114.00
4	A	165	HEM	C3B-C4B-NB	-7.85	108.38	114.00
4	C	165	HEM	C3B-C4B-NB	-7.79	108.43	114.00
4	U	162	HEM	C4D-ND-C1D	7.75	113.09	105.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	163	HEM	C4D-ND-C1D	7.37	112.70	105.16
4	C	165	HEM	CHC-C1C-NC	7.23	131.02	124.73
4	L	163	HEM	CHC-C4B-NB	7.07	130.46	124.58
4	L	163	HEM	C4D-ND-C1D	6.91	112.23	105.16
4	P	163	HEM	C4D-ND-C1D	6.86	112.18	105.16
4	N	165	HEM	C4D-ND-C1D	6.71	112.03	105.16
4	S	163	HEM	C4D-ND-C1D	6.61	111.92	105.16
4	U	162	HEM	C3B-C4B-NB	-6.59	109.28	114.00
4	A	165	HEM	CHC-C4B-NB	6.51	130.00	124.58
4	F	163	HEM	C3B-C4B-NB	-6.34	109.46	114.00
4	F	163	HEM	C4D-ND-C1D	6.28	111.59	105.16
4	Q	163	HEM	C4D-ND-C1D	6.22	111.52	105.16
4	U	162	HEM	CBA-CAA-C2A	-6.20	101.76	112.69
4	Q	163	HEM	CHC-C4B-NB	6.20	129.74	124.58
4	U	162	HEM	CHC-C4B-NB	5.92	129.50	124.58
4	F	163	HEM	CHC-C4B-NB	5.73	129.35	124.58
4	H	162	HEM	CBA-CAA-C2A	-5.66	102.73	112.69
4	C	165	HEM	C4D-ND-C1D	5.46	110.75	105.16
4	H	162	HEM	C4D-ND-C1D	5.43	110.72	105.16
4	I	163	HEM	CHC-C4B-NB	5.36	129.04	124.58
4	X	162	HEM	CBD-CAD-C3D	-5.30	102.79	114.37
4	P	163	HEM	CHC-C4B-NB	5.24	128.94	124.58
4	C	165	HEM	CBD-CAD-C3D	-5.14	103.15	114.37
4	A	165	HEM	C4D-ND-C1D	5.13	110.41	105.16
4	P	163	HEM	CBA-CAA-C2A	-5.09	103.73	112.69
4	X	162	HEM	C4D-ND-C1D	4.79	110.06	105.16
4	I	163	HEM	CBA-CAA-C2A	-4.76	104.31	112.69
4	L	163	HEM	C2D-C1D-ND	-4.72	107.35	112.93
4	X	162	HEM	CHC-C4B-NB	4.63	128.44	124.58
4	A	165	HEM	CBD-CAD-C3D	-4.56	104.41	114.37
4	H	162	HEM	CHC-C4B-NB	4.53	128.35	124.58
4	N	165	HEM	CHC-C1C-NC	4.48	128.62	124.73
4	L	163	HEM	CBD-CAD-C3D	-4.48	104.60	114.37
4	Q	163	HEM	CBA-CAA-C2A	-4.47	104.81	112.69
4	U	162	HEM	CBD-CAD-C3D	-4.37	104.84	114.37
4	F	163	HEM	CBD-CAD-C3D	-4.35	104.89	114.37
4	S	163	HEM	C2D-C1D-ND	-4.32	107.83	112.93
4	F	163	HEM	C2D-C1D-ND	-4.29	107.86	112.93
4	Q	163	HEM	CBD-CAD-C3D	-4.18	105.24	114.37
4	S	163	HEM	C4C-NC-C1C	4.15	109.85	105.53
4	N	165	HEM	CBD-CAD-C3D	-4.15	105.32	114.37
4	N	165	HEM	C2D-C1D-ND	-4.07	108.12	112.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	162	HEM	CBD-CAD-C3D	-4.06	105.51	114.37
4	C	165	HEM	CBA-CAA-C2A	-4.02	105.61	112.69
4	I	163	HEM	C2D-C1D-ND	-3.99	108.22	112.93
4	N	165	HEM	CHD-C4C-NC	3.95	128.16	124.73
4	I	163	HEM	C4A-CHB-C1B	-3.93	122.30	127.47
4	S	163	HEM	CBD-CAD-C3D	-3.92	105.83	114.37
4	F	163	HEM	CBA-CAA-C2A	-3.86	105.89	112.69
4	P	163	HEM	C2D-C1D-ND	-3.84	108.39	112.93
4	X	162	HEM	CHD-C4C-NC	3.83	128.06	124.73
4	U	162	HEM	C2D-C1D-ND	-3.83	108.41	112.93
4	S	163	HEM	CBA-CAA-C2A	-3.79	106.01	112.69
4	N	165	HEM	CHC-C4B-NB	3.68	127.64	124.58
4	I	163	HEM	CBD-CAD-C3D	-3.57	106.58	114.37
4	N	165	HEM	CBA-CAA-C2A	-3.55	106.44	112.69
4	P	163	HEM	CHC-C1C-NC	3.51	127.78	124.73
4	L	163	HEM	CBA-CAA-C2A	-3.33	106.83	112.69
4	C	165	HEM	C1B-NB-C4B	3.32	108.56	105.16
4	P	163	HEM	C3A-C4A-NA	-3.32	106.91	109.41
4	P	163	HEM	CHA-C4D-ND	3.31	128.85	124.31
4	L	163	HEM	C4A-CHB-C1B	-3.27	123.17	127.47
4	A	165	HEM	C4A-CHB-C1B	-3.25	123.19	127.47
4	U	162	HEM	C4A-CHB-C1B	-3.24	123.20	127.47
4	X	162	HEM	CBA-CAA-C2A	-3.16	107.12	112.69
4	L	163	HEM	CHA-C4D-ND	3.16	128.65	124.31
4	N	165	HEM	CHD-C1D-ND	-2.97	122.11	124.58
4	I	163	HEM	C1A-C2A-C3A	2.92	109.94	106.92
4	H	162	HEM	CHD-C4C-NC	2.91	127.26	124.73
4	Q	163	HEM	CHC-C1C-NC	2.89	127.24	124.73
4	I	163	HEM	CHA-C4D-ND	2.88	128.26	124.31
4	S	163	HEM	CHC-C1C-NC	2.85	127.21	124.73
4	X	162	HEM	CMA-C3A-C4A	-2.81	124.29	128.62
4	N	165	HEM	C4C-NC-C1C	2.81	108.46	105.53
4	Q	163	HEM	C2D-C1D-ND	-2.72	109.72	112.93
4	H	162	HEM	C1B-NB-C4B	2.70	107.92	105.16
4	N	165	HEM	C1B-NB-C4B	2.70	107.92	105.16
4	C	165	HEM	C2D-C1D-ND	-2.66	109.78	112.93
4	U	162	HEM	CHA-C1A-NA	2.65	129.01	124.58
4	S	163	HEM	C1B-NB-C4B	2.65	107.87	105.16
4	P	163	HEM	CHD-C1D-ND	2.64	126.78	124.58
4	P	163	HEM	CBD-CAD-C3D	-2.61	108.67	114.37
4	Q	163	HEM	C1A-C2A-C3A	2.61	109.62	106.92
4	I	163	HEM	C2A-C1A-NA	-2.60	106.12	109.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	162	HEM	C3A-C4A-NA	-2.58	107.46	109.41
4	A	165	HEM	C3A-C4A-NA	-2.56	107.48	109.41
4	A	165	HEM	CHA-C1A-NA	2.53	128.81	124.58
4	F	163	HEM	CHA-C4D-ND	2.52	127.77	124.31
4	P	163	HEM	C4C-NC-C1C	2.46	108.09	105.53
4	S	163	HEM	C1A-C2A-C3A	2.42	109.42	106.92
4	L	163	HEM	CHD-C1D-ND	2.40	126.58	124.58
4	N	165	HEM	CHA-C4D-ND	2.39	127.59	124.31
4	U	162	HEM	O2D-CGD-CBD	2.37	122.60	114.22
4	H	162	HEM	CHA-C4D-ND	2.37	127.56	124.31
4	C	165	HEM	CHA-C1A-NA	2.34	128.48	124.58
4	U	162	HEM	O1D-CGD-CBD	-2.33	115.00	123.03
4	N	165	HEM	CMA-C3A-C4A	-2.33	125.04	128.62
4	S	163	HEM	C2A-C1A-NA	-2.32	106.52	109.73
4	I	163	HEM	O1A-CGA-CBA	-2.30	115.10	123.03
4	I	163	HEM	C4C-NC-C1C	2.29	107.91	105.53
4	A	165	HEM	CBA-CAA-C2A	-2.29	108.66	112.69
4	X	162	HEM	CHA-C4D-ND	2.28	127.44	124.31
4	F	163	HEM	O1A-CGA-CBA	-2.28	115.19	123.03
4	L	163	HEM	C1B-NB-C4B	2.24	107.46	105.16
4	I	163	HEM	CMA-C3A-C4A	-2.23	125.20	128.62
4	U	162	HEM	CHD-C4C-NC	2.21	126.66	124.73
4	X	162	HEM	CAD-C3D-C4D	2.21	128.50	124.53
4	P	163	HEM	C4A-CHB-C1B	-2.20	124.58	127.47
4	X	162	HEM	C1B-NB-C4B	2.19	107.41	105.16
4	C	165	HEM	CHA-C4D-ND	2.18	127.31	124.31
4	U	162	HEM	CHA-C4D-ND	2.16	127.27	124.31
4	F	163	HEM	C1A-CHA-C4D	-2.15	124.65	127.47
4	C	165	HEM	O2A-CGA-CBA	2.13	121.76	114.22
4	A	165	HEM	CAD-C3D-C4D	2.11	128.32	124.53
4	P	163	HEM	O2A-CGA-CBA	2.11	121.68	114.22
4	Q	163	HEM	C2A-C1A-NA	-2.10	106.82	109.73
4	Q	163	HEM	CHA-C4D-ND	2.09	127.18	124.31
4	N	165	HEM	CMA-C3A-C2A	2.09	128.88	124.94
4	Q	163	HEM	CMA-C3A-C4A	-2.08	125.42	128.62
4	Q	163	HEM	CAD-C3D-C4D	2.06	128.24	124.53
4	S	163	HEM	CAA-CBA-CGA	-2.05	106.87	113.47
4	N	165	HEM	C4A-CHB-C1B	-2.04	124.78	127.47
4	S	163	HEM	CHD-C4C-NC	2.04	126.51	124.73
4	H	162	HEM	CAD-CBD-CGD	-2.03	107.14	113.48
4	X	162	HEM	CHC-C1C-NC	2.03	126.49	124.73
4	C	165	HEM	O1D-CGD-CBD	-2.02	116.07	123.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	162	HEM	C2D-C1D-ND	-2.01	110.55	112.93
4	H	162	HEM	CHC-C1C-NC	2.01	126.48	124.73
4	H	162	HEM	C2A-C1A-NA	-2.01	106.95	109.73
4	Q	163	HEM	C1B-NB-C4B	2.01	107.21	105.16
4	H	162	HEM	C4A-NA-C1A	2.00	109.40	106.76

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(Å²)	Q<0.9
1	A	155/158 (98%)	-0.53	0	100	100	18, 24, 33, 46	0
1	B	155/158 (98%)	-0.46	0	100	100	17, 23, 35, 46	0
1	C	155/158 (98%)	-0.47	0	100	100	16, 22, 33, 49	0
1	D	154/158 (97%)	-0.44	1 (0%)	86	91	16, 23, 32, 50	0
1	E	155/158 (98%)	-0.53	0	100	100	15, 22, 34, 50	0
1	F	155/158 (98%)	-0.54	0	100	100	16, 22, 32, 43	0
1	G	155/158 (98%)	-0.55	0	100	100	15, 22, 34, 44	0
1	H	154/158 (97%)	-0.46	0	100	100	17, 23, 35, 42	0
1	I	154/158 (97%)	-0.45	0	100	100	17, 23, 33, 42	0
1	J	155/158 (98%)	-0.54	0	100	100	17, 22, 32, 44	0
1	K	155/158 (98%)	-0.49	0	100	100	16, 23, 34, 49	0
1	L	155/158 (98%)	-0.47	0	100	100	16, 23, 34, 44	0
1	M	155/158 (98%)	-0.44	0	100	100	19, 25, 35, 47	0
1	N	155/158 (98%)	-0.39	0	100	100	20, 27, 38, 51	0
1	O	155/158 (98%)	-0.46	0	100	100	20, 27, 37, 50	0
1	P	155/158 (98%)	-0.49	0	100	100	20, 25, 36, 47	0
1	Q	155/158 (98%)	-0.49	0	100	100	16, 23, 32, 47	0
1	R	155/158 (98%)	-0.47	0	100	100	16, 23, 33, 48	0
1	S	155/158 (98%)	-0.53	0	100	100	15, 22, 32, 45	0
1	T	155/158 (98%)	-0.50	0	100	100	17, 24, 34, 44	0
1	U	154/158 (97%)	-0.46	0	100	100	15, 21, 30, 38	0
1	V	155/158 (98%)	-0.52	0	100	100	16, 22, 32, 41	0
1	W	155/158 (98%)	-0.41	1 (0%)	86	91	17, 24, 35, 48	0
1	X	155/158 (98%)	-0.39	0	100	100	19, 27, 37, 50	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	3716/3792 (97%)	-0.48	2 (0%) 93 96	15, 24, 34, 51	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	3	GLY	3.2
1	W	4	ASP	3.2

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
5	SO4	D	163	5/5	0.20	3.26	51,53,53,56	0
4	HEM	P	163	43/43	0.14	2.56	25,31,37,44	0
5	SO4	B	165	5/5	0.19	2.26	51,52,55,55	0
5	SO4	I	164	5/5	0.19	2.09	55,55,57,58	0
5	SO4	F	164	5/5	0.15	2.02	48,50,52,52	0
4	HEM	C	165	43/43	0.12	1.82	20,24,34,39	0
4	HEM	L	163	43/43	0.13	1.74	21,26,34,40	0
4	HEM	I	163	43/43	0.13	1.58	21,27,34,38	0
4	HEM	N	165	43/43	0.13	1.57	25,30,37,40	0
4	HEM	U	162	43/43	0.13	1.57	21,24,35,37	0
4	HEM	X	162	43/43	0.12	1.25	25,28,38,44	0
4	HEM	A	165	43/43	0.13	1.21	22,27,34,37	0
4	HEM	S	163	43/43	0.12	1.15	23,27,34,38	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	HEM	F	163	43/43	0.12	1.10	21,27,37,41	0
4	HEM	H	162	43/43	0.11	1.05	21,25,35,38	0
5	SO4	O	163	5/5	0.15	0.91	56,58,58,59	0
4	HEM	Q	163	43/43	0.13	0.90	23,27,36,39	0
5	SO4	A	166	5/5	0.15	0.75	49,49,51,51	0
5	SO4	R	163	5/5	0.12	0.45	47,48,50,50	0
2	FE2	D	159	1/1	0.10	0.40	26,26,26,26	0
5	SO4	M	163	5/5	0.15	0.33	55,55,57,58	0
2	FE2	S	160	1/1	0.09	-0.79	25,25,25,25	0
2	FE2	A	161	1/1	0.08	-1.05	24,24,24,24	0
2	FE2	L	160	1/1	0.10	-1.12	26,26,26,26	0
2	FE2	F	160	1/1	0.08	-1.16	26,26,26,26	0
2	FE2	D	160	1/1	0.08	-1.21	24,24,24,24	0
2	FE2	S	159	1/1	0.08	-1.22	22,22,22,22	0
2	FE2	L	159	1/1	0.09	-1.31	24,24,24,24	0
2	FE2	G	161	1/1	0.07	-1.31	22,22,22,22	0
2	FE2	G	160	1/1	0.09	-1.32	24,24,24,24	0
2	FE2	R	160	1/1	0.08	-1.32	23,23,23,23	0
2	FE2	H	159	1/1	0.08	-1.36	27,27,27,27	0
2	FE2	B	161	1/1	0.07	-1.48	25,25,25,25	0
2	FE2	D	161	1/1	0.06	-1.56	37,37,37,37	0
2	FE2	W	159	1/1	0.07	-1.57	26,26,26,26	0
2	FE2	X	159	1/1	0.08	-1.58	28,28,28,28	0
2	FE2	Q	161	1/1	0.08	-1.77	25,25,25,25	0
2	FE2	N	160	1/1	0.07	-1.78	27,27,27,27	0
2	FE2	N	161	1/1	0.05	-1.81	28,28,28,28	0
2	FE2	E	163	1/1	0.04	-1.81	36,36,36,36	0
2	FE2	H	161	1/1	0.05	-1.89	39,39,39,39	0
2	FE2	N	159	1/1	0.06	-1.90	29,29,29,29	0
2	FE2	U	161	1/1	0.05	-1.91	35,35,35,35	0
2	FE2	K	159	1/1	0.07	-1.96	24,24,24,24	0
2	FE2	V	161	1/1	0.04	-1.96	32,32,32,32	0
2	FE2	U	159	1/1	0.07	-1.97	25,25,25,25	0
2	FE2	J	160	1/1	0.08	-2.00	24,24,24,24	0
2	FE2	I	160	1/1	0.05	-2.00	25,25,25,25	0
2	FE2	G	162	1/1	0.07	-2.00	35,35,35,35	0
2	FE2	G	163	1/1	0.06	-2.01	37,37,37,37	0
2	FE2	C	159	1/1	0.09	-2.02	19,19,19,19	0
2	FE2	K	161	1/1	0.04	-2.04	31,31,31,31	0
2	FE2	C	161	1/1	0.07	-2.04	23,23,23,23	0
2	FE2	E	160	1/1	0.08	-2.04	24,24,24,24	0
2	FE2	T	160	1/1	0.04	-2.05	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	FE2	Q	159	1/1	0.05	-2.08	24,24,24,24	0
2	FE2	V	159	1/1	0.07	-2.09	23,23,23,23	0
2	FE2	P	162	1/1	0.03	-2.16	40,40,40,40	0
2	FE2	W	161	1/1	0.05	-2.19	33,33,33,33	0
2	FE2	M	159	1/1	0.06	-2.20	28,28,28,28	0
2	FE2	I	159	1/1	0.08	-2.26	27,27,27,27	0
2	FE2	N	162	1/1	0.05	-2.32	39,39,39,39	0
2	FE2	P	159	1/1	0.07	-2.36	29,29,29,29	0
2	FE2	X	160	1/1	0.04	-2.37	38,38,38,38	0
2	FE2	Q	160	1/1	0.07	-2.37	21,21,21,21	0
2	FE2	U	160	1/1	0.03	-2.40	32,32,32,32	0
2	FE2	K	160	1/1	0.07	-2.43	24,24,24,24	0
2	FE2	E	159	1/1	0.06	-2.49	21,21,21,21	0
2	FE2	J	161	1/1	0.08	-2.50	43,43,43,43	0
2	FE2	B	163	1/1	0.04	-2.51	33,33,33,33	0
2	FE2	A	162	1/1	0.05	-2.52	26,26,26,26	0
2	FE2	J	162	1/1	0.04	-2.53	36,36,36,36	0
2	FE2	X	161	1/1	0.04	-2.60	42,42,42,42	0
2	FE2	D	162	1/1	0.04	-2.62	35,35,35,35	0
2	FE2	B	162	1/1	0.03	-2.63	35,35,35,35	0
2	FE2	I	162	1/1	0.04	-2.64	37,37,37,37	0
2	FE2	M	161	1/1	0.04	-2.71	34,34,34,34	0
2	FE2	R	162	1/1	0.04	-2.72	32,32,32,32	0
2	FE2	A	163	1/1	0.04	-2.76	37,37,37,37	0
3	K	C	164	1/1	0.06	-2.83	24,24,24,24	0
2	FE2	T	159	1/1	0.07	-2.90	23,23,23,23	0
2	FE2	L	161	1/1	0.04	-2.90	34,34,34,34	0
2	FE2	W	160	1/1	0.03	-2.98	35,35,35,35	0
2	FE2	N	163	1/1	0.04	-3.04	39,39,39,39	0
2	FE2	H	160	1/1	0.05	-3.06	36,36,36,36	0
3	K	B	164	1/1	0.04	-3.11	27,27,27,27	0
2	FE2	F	159	1/1	0.07	-3.13	24,24,24,24	0
2	FE2	Q	162	1/1	0.04	-3.13	31,31,31,31	0
2	FE2	R	159	1/1	0.08	-3.20	25,25,25,25	0
2	FE2	S	161	1/1	0.03	-3.25	33,33,33,33	0
2	FE2	O	159	1/1	0.05	-3.51	23,23,23,23	0
2	FE2	O	160	1/1	0.06	-3.53	30,30,30,30	0
2	FE2	V	160	1/1	0.04	-3.58	34,34,34,34	0
2	FE2	B	160	1/1	0.06	-3.61	25,25,25,25	0
2	FE2	C	163	1/1	0.04	-3.65	32,32,32,32	0
3	K	A	164	1/1	0.06	-3.67	32,32,32,32	0
2	FE2	C	162	1/1	0.04	-3.72	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	FE2	F	161	1/1	0.03	-3.86	32,32,32,32	0
2	FE2	L	162	1/1	0.04	-3.92	32,32,32,32	0
2	FE2	O	161	1/1	0.03	-3.98	39,39,39,39	0
2	FE2	T	161	1/1	0.03	-4.01	33,33,33,33	0
3	K	N	164	1/1	0.04	-4.02	31,31,31,31	0
2	FE2	C	160	1/1	0.08	-4.04	21,21,21,21	0
2	FE2	E	162	1/1	0.03	-4.12	35,35,35,35	0
2	FE2	G	159	1/1	0.06	-4.22	24,24,24,24	0
3	K	G	164	1/1	0.05	-4.22	33,33,33,33	0
2	FE2	B	159	1/1	0.06	-4.35	25,25,25,25	0
2	FE2	P	160	1/1	0.06	-4.39	28,28,28,28	0
2	FE2	M	160	1/1	0.08	-4.40	27,27,27,27	0
2	FE2	O	162	1/1	0.04	-4.49	45,45,45,45	0
2	FE2	M	162	1/1	0.04	-4.53	42,42,42,42	0
2	FE2	K	162	1/1	0.03	-4.58	31,31,31,31	0
2	FE2	I	161	1/1	0.04	-4.68	35,35,35,35	0
2	FE2	P	161	1/1	0.02	-4.93	35,35,35,35	0
3	K	E	164	1/1	0.04	-5.01	26,26,26,26	0
2	FE2	R	161	1/1	0.03	-5.41	29,29,29,29	0
2	FE2	E	161	1/1	0.05	-6.33	21,21,21,21	0
2	FE2	F	162	1/1	0.04	-8.20	31,31,31,31	0
2	FE2	A	160	1/1	0.06	-10.07	24,24,24,24	0
2	FE2	J	159	1/1	0.06	-10.66	24,24,24,24	0
2	FE2	S	162	1/1	0.03	-11.62	32,32,32,32	0
2	FE2	A	159	1/1	0.05	-12.06	25,25,25,25	0

6.5 Other polymers ⓘ

There are no such residues in this entry.