wwPDB X-ray Structure Validation Summary Report (i)

Mar 13, 2024 – 03:39 PM JST

PDB ID	:	5C6F
Title	:	Crystal structures of ferritin mutants reveal side-on binding to diiron and end-on cleavage of oxygen
Authors	:	Kim, S.; Kim, K.H.; Seok, J.H.; Park, Y.H.; Jung, S.W.; Chung, Y.B.; Lee, D.B.; Lee, J.H.; Han, K.R.; Cho, A.E.; Lee, C.; Chung, M.S.
Deposited on	:	2015-06-23
Resolution	:	2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

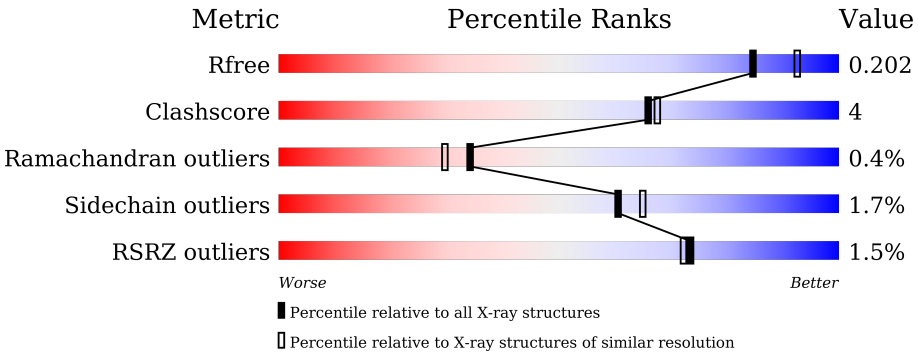
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	173	91% 8%
1	B	173	91% 9%
1	C	173	92% 7%
1	D	173	92% 7%
1	E	173	92% 8%
1	F	173	88% 10%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	173	2% 88% 12%
1	H	173	% 87% 12%
1	I	173	2% 84% 14%
1	J	173	2% 94% 5%
1	K	173	% 88% 11%
1	L	173	2% 90% 9%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 19666 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Bacterial non-heme ferritin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	172	Total	C	N	O	S	0	6	0
			1452	923	242	282	5			
1	B	172	Total	C	N	O	S	0	3	0
			1431	912	240	274	5			
1	C	172	Total	C	N	O	S	0	5	0
			1446	920	242	279	5			
1	D	172	Total	C	N	O	S	0	1	0
			1414	901	237	271	5			
1	E	172	Total	C	N	O	S	0	3	0
			1430	911	240	274	5			
1	F	172	Total	C	N	O	S	0	3	0
			1431	910	241	275	5			
1	G	172	Total	C	N	O	S	0	1	0
			1414	901	237	271	5			
1	H	172	Total	C	N	O	S	0	4	0
			1437	915	240	277	5			
1	I	172	Total	C	N	O	S	0	2	0
			1422	907	238	272	5			
1	J	172	Total	C	N	O	S	0	1	0
			1414	901	237	271	5			
1	K	172	Total	C	N	O	S	0	2	0
			1424	907	240	272	5			
1	L	172	Total	C	N	O	S	0	1	0
			1414	901	237	271	5			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	expression tag	UNP Q9ZLI1
A	-4	HIS	-	expression tag	UNP Q9ZLI1
A	-3	SER	-	expression tag	UNP Q9ZLI1
A	-2	GLN	-	expression tag	UNP Q9ZLI1
A	-1	ASP	-	expression tag	UNP Q9ZLI1

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	PRO	-	expression tag	UNP Q9ZLI1
A	93	LEU	HIS	engineered mutation	UNP Q9ZLI1
B	-5	HIS	-	expression tag	UNP Q9ZLI1
B	-4	HIS	-	expression tag	UNP Q9ZLI1
B	-3	SER	-	expression tag	UNP Q9ZLI1
B	-2	GLN	-	expression tag	UNP Q9ZLI1
B	-1	ASP	-	expression tag	UNP Q9ZLI1
B	0	PRO	-	expression tag	UNP Q9ZLI1
B	93	LEU	HIS	engineered mutation	UNP Q9ZLI1
C	-5	HIS	-	expression tag	UNP Q9ZLI1
C	-4	HIS	-	expression tag	UNP Q9ZLI1
C	-3	SER	-	expression tag	UNP Q9ZLI1
C	-2	GLN	-	expression tag	UNP Q9ZLI1
C	-1	ASP	-	expression tag	UNP Q9ZLI1
C	0	PRO	-	expression tag	UNP Q9ZLI1
C	93	LEU	HIS	engineered mutation	UNP Q9ZLI1
D	-5	HIS	-	expression tag	UNP Q9ZLI1
D	-4	HIS	-	expression tag	UNP Q9ZLI1
D	-3	SER	-	expression tag	UNP Q9ZLI1
D	-2	GLN	-	expression tag	UNP Q9ZLI1
D	-1	ASP	-	expression tag	UNP Q9ZLI1
D	0	PRO	-	expression tag	UNP Q9ZLI1
D	93	LEU	HIS	engineered mutation	UNP Q9ZLI1
E	-5	HIS	-	expression tag	UNP Q9ZLI1
E	-4	HIS	-	expression tag	UNP Q9ZLI1
E	-3	SER	-	expression tag	UNP Q9ZLI1
E	-2	GLN	-	expression tag	UNP Q9ZLI1
E	-1	ASP	-	expression tag	UNP Q9ZLI1
E	0	PRO	-	expression tag	UNP Q9ZLI1
E	93	LEU	HIS	engineered mutation	UNP Q9ZLI1
F	-5	HIS	-	expression tag	UNP Q9ZLI1
F	-4	HIS	-	expression tag	UNP Q9ZLI1
F	-3	SER	-	expression tag	UNP Q9ZLI1
F	-2	GLN	-	expression tag	UNP Q9ZLI1
F	-1	ASP	-	expression tag	UNP Q9ZLI1
F	0	PRO	-	expression tag	UNP Q9ZLI1
F	93	LEU	HIS	engineered mutation	UNP Q9ZLI1
G	-5	HIS	-	expression tag	UNP Q9ZLI1
G	-4	HIS	-	expression tag	UNP Q9ZLI1
G	-3	SER	-	expression tag	UNP Q9ZLI1
G	-2	GLN	-	expression tag	UNP Q9ZLI1
G	-1	ASP	-	expression tag	UNP Q9ZLI1

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	0	PRO	-	expression tag	UNP Q9ZLI1
G	93	LEU	HIS	engineered mutation	UNP Q9ZLI1
H	-5	HIS	-	expression tag	UNP Q9ZLI1
H	-4	HIS	-	expression tag	UNP Q9ZLI1
H	-3	SER	-	expression tag	UNP Q9ZLI1
H	-2	GLN	-	expression tag	UNP Q9ZLI1
H	-1	ASP	-	expression tag	UNP Q9ZLI1
H	0	PRO	-	expression tag	UNP Q9ZLI1
H	93	LEU	HIS	engineered mutation	UNP Q9ZLI1
I	-5	HIS	-	expression tag	UNP Q9ZLI1
I	-4	HIS	-	expression tag	UNP Q9ZLI1
I	-3	SER	-	expression tag	UNP Q9ZLI1
I	-2	GLN	-	expression tag	UNP Q9ZLI1
I	-1	ASP	-	expression tag	UNP Q9ZLI1
I	0	PRO	-	expression tag	UNP Q9ZLI1
I	93	LEU	HIS	engineered mutation	UNP Q9ZLI1
J	-5	HIS	-	expression tag	UNP Q9ZLI1
J	-4	HIS	-	expression tag	UNP Q9ZLI1
J	-3	SER	-	expression tag	UNP Q9ZLI1
J	-2	GLN	-	expression tag	UNP Q9ZLI1
J	-1	ASP	-	expression tag	UNP Q9ZLI1
J	0	PRO	-	expression tag	UNP Q9ZLI1
J	93	LEU	HIS	engineered mutation	UNP Q9ZLI1
K	-5	HIS	-	expression tag	UNP Q9ZLI1
K	-4	HIS	-	expression tag	UNP Q9ZLI1
K	-3	SER	-	expression tag	UNP Q9ZLI1
K	-2	GLN	-	expression tag	UNP Q9ZLI1
K	-1	ASP	-	expression tag	UNP Q9ZLI1
K	0	PRO	-	expression tag	UNP Q9ZLI1
K	93	LEU	HIS	engineered mutation	UNP Q9ZLI1
L	-5	HIS	-	expression tag	UNP Q9ZLI1
L	-4	HIS	-	expression tag	UNP Q9ZLI1
L	-3	SER	-	expression tag	UNP Q9ZLI1
L	-2	GLN	-	expression tag	UNP Q9ZLI1
L	-1	ASP	-	expression tag	UNP Q9ZLI1
L	0	PRO	-	expression tag	UNP Q9ZLI1
L	93	LEU	HIS	engineered mutation	UNP Q9ZLI1

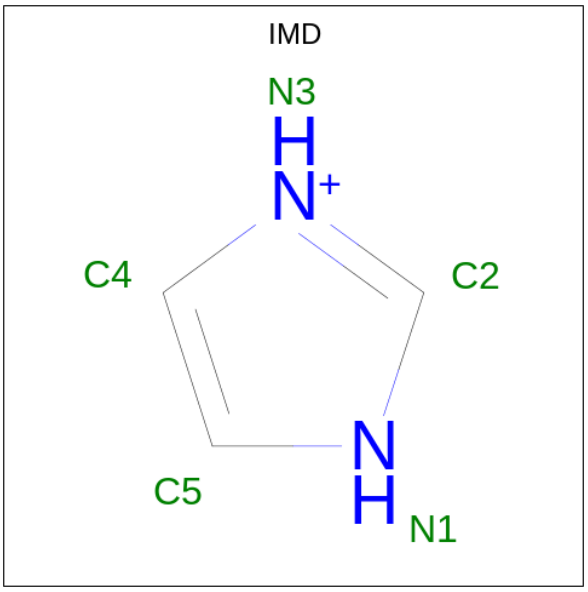
- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	3	Total Fe 3 3	0	0
2	B	1	Total Fe 1 1	0	0
2	F	1	Total Fe 1 1	0	0
2	G	1	Total Fe 1 1	0	0
2	I	1	Total Fe 1 1	0	0
2	J	1	Total Fe 1 1	0	0
2	K	1	Total Fe 1 1	0	0

- Molecule 3 is IMIDAZOLE (three-letter code: IMD) (formula: $C_3H_5N_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N 5 3 2	0	0
3	B	1	Total C N 5 3 2	0	0
3	C	1	Total C N 5 3 2	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total C N 5 3 2	0	0
3	E	1	Total C N 5 3 2	0	0
3	G	1	Total C N 5 3 2	0	0
3	H	1	Total C N 5 3 2	0	0
3	I	1	Total C N 5 3 2	0	0
3	J	1	Total C N 5 3 2	0	0
3	K	1	Total C N 5 3 2	0	0
3	L	1	Total C N 5 3 2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	198	Total O 198 198	0	0
4	B	180	Total O 180 180	0	0
4	C	180	Total O 180 180	0	0
4	D	163	Total O 163 163	0	0
4	E	194	Total O 194 194	0	0
4	F	211	Total O 211 211	0	0
4	G	217	Total O 217 217	0	0
4	H	225	Total O 225 225	0	0
4	I	229	Total O 229 229	0	0
4	J	242	Total O 242 242	0	0
4	K	203	Total O 203 203	0	0

Continued on next page...

Continued from previous page...

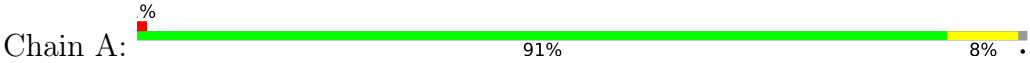
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	231	Total	O	0	0
			231	231		

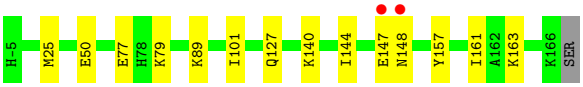
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: Bacterial non-heme ferritin

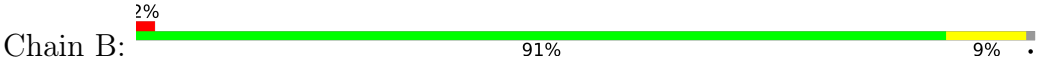
Chain A:





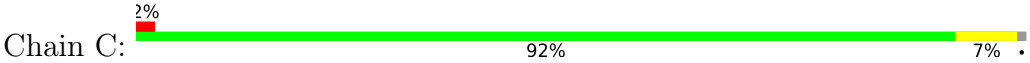
• Molecule 1: Bacterial non-heme ferritin

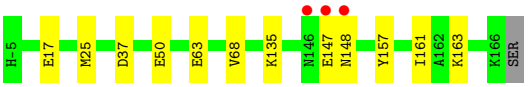
Chain B:



• Molecule 1: Bacterial non-heme ferritin

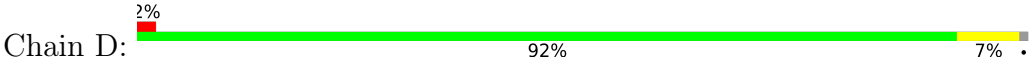
Chain C:

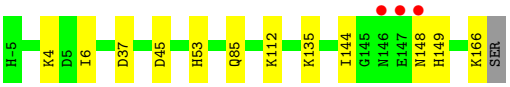




• Molecule 1: Bacterial non-heme ferritin

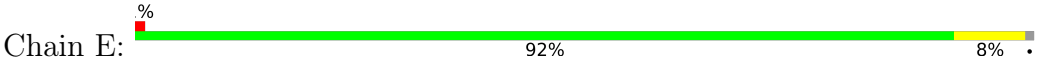
Chain D:

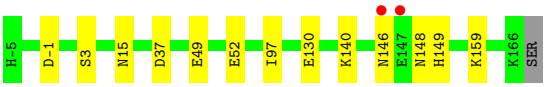




• Molecule 1: Bacterial non-heme ferritin

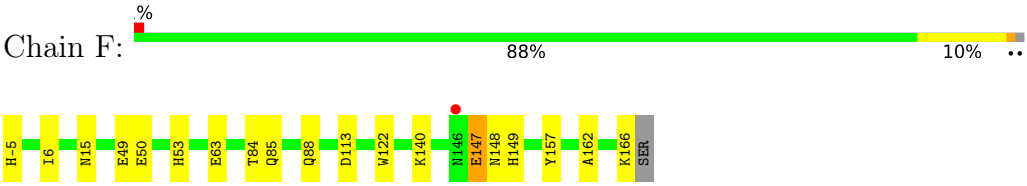
Chain E:





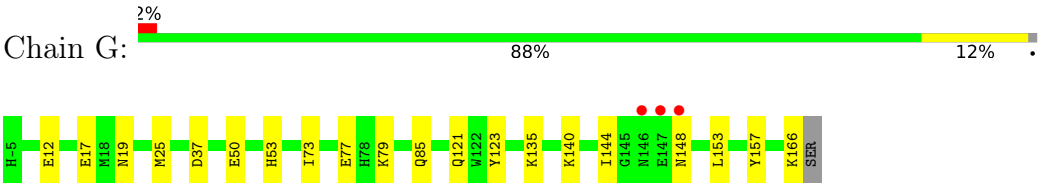
• Molecule 1: Bacterial non-heme ferritin

Chain F:



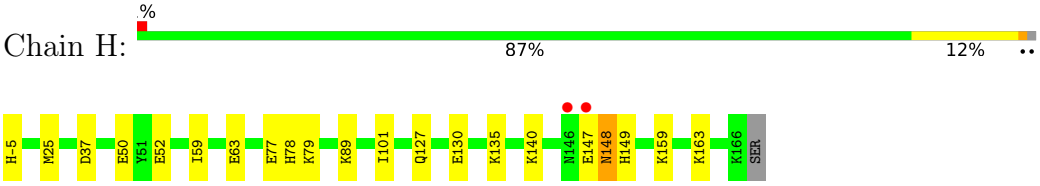
• Molecule 1: Bacterial non-heme ferritin

Chain G:



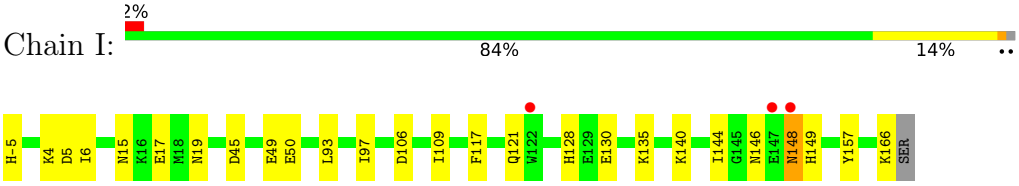
• Molecule 1: Bacterial non-heme ferritin

Chain H:



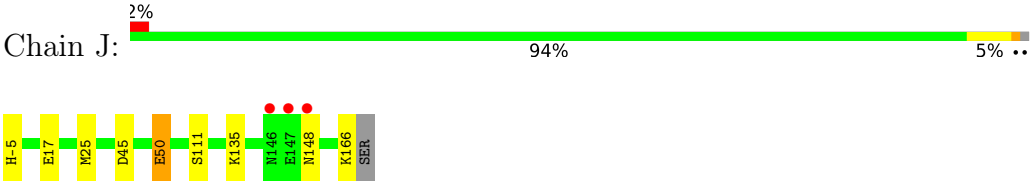
• Molecule 1: Bacterial non-heme ferritin

Chain I:



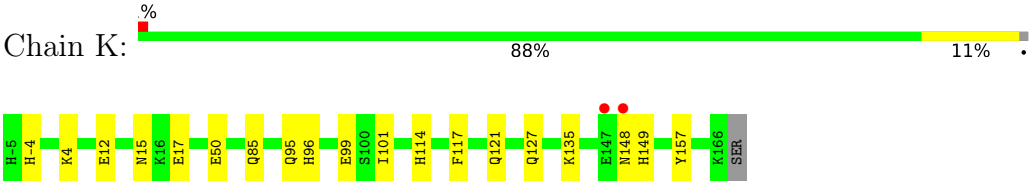
• Molecule 1: Bacterial non-heme ferritin

Chain J:



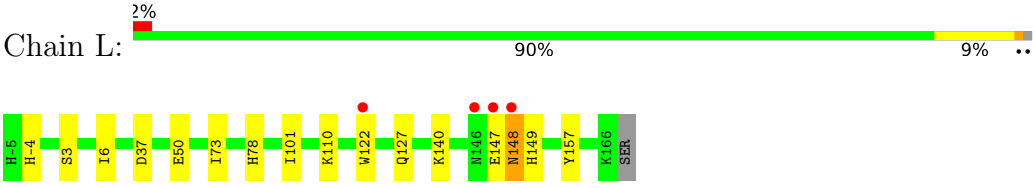
• Molecule 1: Bacterial non-heme ferritin

Chain K:



• Molecule 1: Bacterial non-heme ferritin

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 4	Depositor
Cell constants a, b, c, α, β, γ	128.05Å 128.05Å 165.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.00 47.05 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (50.00-2.00) 100.0 (47.05-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.24 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.149 , 0.195 0.159 , 0.202	Depositor DCC
R_{free} test set	8947 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	20.1	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 62.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	19666	wwPDB-VP
Average B, all atoms (Å^2)	25.0	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 41.77 % 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 2.2504e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: IMD, FE

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	0.88	1/1485 (0.1%)	0.83	1/2004 (0.0%)
1	B	0.95	3/1464 (0.2%)	0.86	0/1976
1	C	0.87	0/1479	0.85	3/1996 (0.2%)
1	D	0.87	0/1447	0.83	1/1953 (0.1%)
1	E	0.94	1/1463 (0.1%)	0.84	2/1975 (0.1%)
1	F	0.92	2/1464 (0.1%)	0.84	1/1976 (0.1%)
1	G	0.94	1/1447 (0.1%)	0.85	3/1953 (0.2%)
1	H	1.02	1/1470 (0.1%)	0.89	2/1984 (0.1%)
1	I	1.01	1/1455 (0.1%)	0.90	1/1964 (0.1%)
1	J	1.02	1/1447 (0.1%)	0.90	2/1953 (0.1%)
1	K	0.99	0/1458	0.90	1/1968 (0.1%)
1	L	0.98	1/1447 (0.1%)	0.84	1/1953 (0.1%)
All	All	0.95	12/17526 (0.1%)	0.86	18/23655 (0.1%)

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	50	GLU	CD-OE2	-7.47	1.17	1.25
1	J	50	GLU	CD-OE1	7.42	1.33	1.25
1	L	122	TRP	CB-CG	7.11	1.63	1.50
1	B	51	TYR	CZ-OH	6.50	1.49	1.37
1	G	50	GLU	CD-OE2	-5.88	1.19	1.25

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	-1	ASP	CB-CG-OD2	-6.42	112.53	118.30
1	E	37	ASP	CB-CG-OD1	6.39	124.05	118.30
1	J	25	MET	CG-SD-CE	-6.32	90.09	100.20
1	G	25	MET	CG-SD-CE	-6.30	90.13	100.20
1	C	37	ASP	CB-CG-OD1	5.79	123.52	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1452	0	1393	12	0
1	B	1431	0	1382	8	0
1	C	1446	0	1391	5	0
1	D	1414	0	1365	11	0
1	E	1430	0	1380	10	0
1	F	1431	0	1378	15	0
1	G	1414	0	1365	14	0
1	H	1437	0	1384	17	0
1	I	1422	0	1375	22	0
1	J	1414	0	1365	4	0
1	K	1424	0	1371	14	0
1	L	1414	0	1365	15	0
2	A	3	0	0	0	0
2	B	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
3	A	5	0	5	0	0
3	B	5	0	5	0	0
3	C	5	0	5	0	0
3	D	5	0	5	1	0
3	E	5	0	5	0	0
3	G	5	0	5	2	0
3	H	5	0	5	0	0
3	I	5	0	5	0	0
3	J	5	0	5	0	0
3	K	5	0	5	1	0
3	L	5	0	5	0	0
4	A	198	0	0	4	0
4	B	180	0	0	3	0
4	C	180	0	0	3	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	163	0	0	1	0
4	E	194	0	0	9	0
4	F	211	0	0	10	0
4	G	217	0	0	8	0
4	H	225	0	0	9	0
4	I	229	0	0	11	0
4	J	242	0	0	2	0
4	K	203	0	0	7	0
4	L	231	0	0	9	0
All	All	19666	0	16569	134	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 134 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:149[B]:HIS:HE1	4:E:435:HOH:O	1.26	1.16
1:L:149[B]:HIS:HE1	4:L:442:HOH:O	1.31	1.11
1:L:73:ILE:CD1	4:L:305:HOH:O	2.13	0.95
1:L:73:ILE:HD11	4:L:305:HOH:O	1.67	0.94
1:H:149[B]:HIS:HE1	4:H:402:HOH:O	1.51	0.92

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	176/173 (102%)	174 (99%)	1 (1%)	1 (1%)	25	19
1	B	173/173 (100%)	171 (99%)	1 (1%)	1 (1%)	25	19

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	175/173 (101%)	173 (99%)	2 (1%)	0	100	100
1	D	171/173 (99%)	169 (99%)	1 (1%)	1 (1%)	25	19
1	E	173/173 (100%)	170 (98%)	2 (1%)	1 (1%)	25	19
1	F	173/173 (100%)	170 (98%)	3 (2%)	0	100	100
1	G	171/173 (99%)	169 (99%)	1 (1%)	1 (1%)	25	19
1	H	174/173 (101%)	171 (98%)	2 (1%)	1 (1%)	25	19
1	I	172/173 (99%)	168 (98%)	4 (2%)	0	100	100
1	J	171/173 (99%)	169 (99%)	1 (1%)	1 (1%)	25	19
1	K	172/173 (99%)	170 (99%)	1 (1%)	1 (1%)	25	19
1	L	171/173 (99%)	169 (99%)	1 (1%)	1 (1%)	25	19
All	All	2072/2076 (100%)	2043 (99%)	20 (1%)	9 (0%)	34	30

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	148	ASN
1	D	148	ASN
1	E	148	ASN
1	G	148	ASN
1	H	148	ASN

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	161/156 (103%)	160 (99%)	1 (1%)	86	90
1	B	158/156 (101%)	153 (97%)	5 (3%)	39	38
1	C	160/156 (103%)	157 (98%)	3 (2%)	57	61
1	D	156/156 (100%)	153 (98%)	3 (2%)	57	61
1	E	158/156 (101%)	157 (99%)	1 (1%)	86	90
1	F	158/156 (101%)	156 (99%)	2 (1%)	69	74

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	G	156/156 (100%)	153 (98%)	3 (2%)	57 61
1	H	159/156 (102%)	155 (98%)	4 (2%)	47 49
1	I	157/156 (101%)	153 (98%)	4 (2%)	47 49
1	J	156/156 (100%)	155 (99%)	1 (1%)	86 90
1	K	157/156 (101%)	155 (99%)	2 (1%)	69 74
1	L	156/156 (100%)	154 (99%)	2 (1%)	69 74
All	All	1892/1872 (101%)	1861 (98%)	31 (2%)	60 67

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	147	GLU
1	K	4	LYS
1	G	135	LYS
1	L	6	ILE
1	I	135	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	15	ASN
1	I	128	HIS
1	J	-4	HIS
1	E	15	ASN
1	C	148	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 20 ligands modelled in this entry, 9 are monoatomic - leaving 11 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	IMD	D	201	-	3,5,5	0.21	0	4,5,5	0.94	0
3	IMD	E	201	-	3,5,5	0.53	0	4,5,5	0.54	0
3	IMD	B	202	-	3,5,5	0.63	0	4,5,5	0.38	0
3	IMD	G	202	-	3,5,5	0.77	0	4,5,5	0.74	0
3	IMD	H	201	-	3,5,5	0.63	0	4,5,5	0.75	0
3	IMD	K	202	-	3,5,5	0.44	0	4,5,5	0.58	0
3	IMD	L	201	-	3,5,5	0.53	0	4,5,5	0.77	0
3	IMD	C	201	-	3,5,5	0.24	0	4,5,5	0.93	0
3	IMD	A	204	-	3,5,5	0.37	0	4,5,5	0.62	0
3	IMD	J	202	-	3,5,5	0.54	0	4,5,5	0.78	0
3	IMD	I	202	-	3,5,5	0.53	0	4,5,5	0.44	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	IMD	D	201	-	-	-	0/1/1/1
3	IMD	E	201	-	-	-	0/1/1/1
3	IMD	B	202	-	-	-	0/1/1/1
3	IMD	G	202	-	-	-	0/1/1/1
3	IMD	H	201	-	-	-	0/1/1/1
3	IMD	K	202	-	-	-	0/1/1/1
3	IMD	L	201	-	-	-	0/1/1/1
3	IMD	C	201	-	-	-	0/1/1/1
3	IMD	A	204	-	-	-	0/1/1/1
3	IMD	J	202	-	-	-	0/1/1/1
3	IMD	I	202	-	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	201	IMD	1	0
3	G	202	IMD	2	0
3	K	202	IMD	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

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, 95^{th} 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	172/173 (99%)	-0.70	2 (1%)	79	78	14, 22, 40, 91	0
1	B	172/173 (99%)	-0.56	3 (1%)	70	68	16, 23, 44, 85	0
1	C	172/173 (99%)	-0.60	3 (1%)	70	68	17, 24, 43, 85	0
1	D	172/173 (99%)	-0.54	3 (1%)	70	68	17, 27, 48, 75	0
1	E	172/173 (99%)	-0.63	2 (1%)	79	78	14, 22, 42, 80	0
1	F	172/173 (99%)	-0.71	1 (0%)	89	88	14, 20, 36, 71	0
1	G	172/173 (99%)	-0.75	3 (1%)	70	68	12, 19, 37, 81	0
1	H	172/173 (99%)	-0.67	2 (1%)	79	78	12, 19, 39, 79	0
1	I	172/173 (99%)	-0.64	3 (1%)	70	68	12, 22, 42, 77	0
1	J	172/173 (99%)	-0.75	3 (1%)	70	68	13, 19, 37, 73	0
1	K	172/173 (99%)	-0.58	2 (1%)	79	78	12, 20, 40, 76	0
1	L	172/173 (99%)	-0.67	4 (2%)	60	59	11, 18, 35, 73	0
All	All	2064/2076 (99%)	-0.65	31 (1%)	73	72	11, 21, 42, 91	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	148	ASN	4.7
1	D	148	ASN	4.6
1	C	147	GLU	4.5
1	I	147	GLU	4.4
1	E	146	ASN	4.2

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 (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	IMD	C	201	5/5	0.94	0.11	26,27,28,32	0
3	IMD	D	201	5/5	0.94	0.10	28,29,34,35	0
3	IMD	I	202	5/5	0.94	0.08	25,27,28,30	0
2	FE	F	201	1/1	0.96	0.09	59,59,59,59	1
3	IMD	E	201	5/5	0.96	0.08	25,26,27,29	0
3	IMD	G	202	5/5	0.96	0.09	16,16,20,21	0
2	FE	A	202	1/1	0.96	0.07	53,53,53,53	1
3	IMD	K	202	5/5	0.96	0.08	28,28,33,35	0
3	IMD	L	201	5/5	0.96	0.08	25,26,27,30	0
3	IMD	J	202	5/5	0.97	0.07	21,22,23,25	0
3	IMD	H	201	5/5	0.97	0.07	19,20,20,21	0
2	FE	I	201	1/1	0.97	0.08	41,41,41,41	1
2	FE	A	201	1/1	0.98	0.04	41,41,41,41	1
3	IMD	A	204	5/5	0.98	0.07	23,23,25,25	0
3	IMD	B	202	5/5	0.98	0.09	23,25,30,30	0
2	FE	G	201	1/1	0.99	0.05	36,36,36,36	1
2	FE	B	201	1/1	0.99	0.04	18,18,18,18	1
2	FE	J	201	1/1	0.99	0.07	19,19,19,19	1
2	FE	K	201	1/1	0.99	0.09	18,18,18,18	1
2	FE	A	203	1/1	0.99	0.05	22,22,22,22	1

6.5 Other polymers (i)

There are no such residues in this entry.