wwPDB X-ray Structure Validation Summary Report (i)

Nov 15, 2023 – 06:07 PM JST

PDB ID	:	6JPS
Title	:	Human H chain ferritin mutant-MBP
Authors	:	Wang, Y.; Zang, J.; Chen, H.
Deposited on	:	2019-03-27
Resolution	:	3.50 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 (i)) were used in the production of this report:

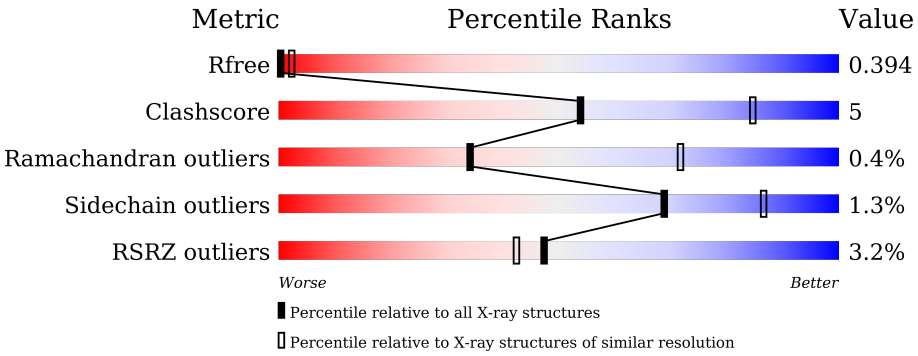
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 3.50 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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	189	4% 74% 17% 9%
1	B	189	2% 73% 18% 9%
1	C	189	3% 76% 14% 9%
1	D	189	2% 78% 13% 9%
1	E	189	2% 72% 18% 9%
1	F	189	3% 77% 13% 9%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	189	3% 76% 15% 9%
1	H	189	3% 75% 16% 9%
1	I	189	3% 74% 16% 9%
1	J	189	3% 80% 11% 9%
1	K	189	2% 74% 17% 9%
1	L	189	4% 77% 14% 9%
1	M	189	3% 77% 14% 9%
1	N	189	2% 80% 10% 9%
1	O	189	3% 77% 13% 9%
1	P	189	5% 76% 14% 9%
1	Q	189	2% 76% 15% 9%
1	R	189	2% 72% 19% 9%
1	S	189	3% 78% 13% 9%
1	T	189	4% 80% 11% 9%
1	U	189	3% 77% 14% 9%
1	V	189	3% 79% 12% 9%
1	W	189	3% 77% 14% 9%
1	X	189	6% 77% 13% 9%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 33912 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 Ferritin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	B	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	C	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	D	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	E	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	F	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	G	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	H	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	I	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	J	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	K	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	L	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	M	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	N	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	O	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	P	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	R	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	S	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	T	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	U	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	V	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	W	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			
1	X	172	Total	C	N	O	S	0	0	0
			1413	885	248	273	7			

There are 192 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	GLY	-	expression tag	UNP Q6NS36
A	-5	MET	-	expression tag	UNP Q6NS36
A	-4	THR	-	expression tag	UNP Q6NS36
A	-3	CYS	-	expression tag	UNP Q6NS36
A	-2	ALA	-	expression tag	UNP Q6NS36
A	-1	ALA	-	expression tag	UNP Q6NS36
A	0	CYS	-	expression tag	UNP Q6NS36
A	86	GLN	LYS	engineered mutation	UNP Q6NS36
B	-6	GLY	-	expression tag	UNP Q6NS36
B	-5	MET	-	expression tag	UNP Q6NS36
B	-4	THR	-	expression tag	UNP Q6NS36
B	-3	CYS	-	expression tag	UNP Q6NS36
B	-2	ALA	-	expression tag	UNP Q6NS36
B	-1	ALA	-	expression tag	UNP Q6NS36
B	0	CYS	-	expression tag	UNP Q6NS36
B	86	GLN	LYS	engineered mutation	UNP Q6NS36
C	-6	GLY	-	expression tag	UNP Q6NS36
C	-5	MET	-	expression tag	UNP Q6NS36
C	-4	THR	-	expression tag	UNP Q6NS36
C	-3	CYS	-	expression tag	UNP Q6NS36
C	-2	ALA	-	expression tag	UNP Q6NS36
C	-1	ALA	-	expression tag	UNP Q6NS36
C	0	CYS	-	expression tag	UNP Q6NS36

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	86	GLN	LYS	engineered mutation	UNP Q6NS36
D	-6	GLY	-	expression tag	UNP Q6NS36
D	-5	MET	-	expression tag	UNP Q6NS36
D	-4	THR	-	expression tag	UNP Q6NS36
D	-3	CYS	-	expression tag	UNP Q6NS36
D	-2	ALA	-	expression tag	UNP Q6NS36
D	-1	ALA	-	expression tag	UNP Q6NS36
D	0	CYS	-	expression tag	UNP Q6NS36
D	86	GLN	LYS	engineered mutation	UNP Q6NS36
E	-6	GLY	-	expression tag	UNP Q6NS36
E	-5	MET	-	expression tag	UNP Q6NS36
E	-4	THR	-	expression tag	UNP Q6NS36
E	-3	CYS	-	expression tag	UNP Q6NS36
E	-2	ALA	-	expression tag	UNP Q6NS36
E	-1	ALA	-	expression tag	UNP Q6NS36
E	0	CYS	-	expression tag	UNP Q6NS36
E	86	GLN	LYS	engineered mutation	UNP Q6NS36
F	-6	GLY	-	expression tag	UNP Q6NS36
F	-5	MET	-	expression tag	UNP Q6NS36
F	-4	THR	-	expression tag	UNP Q6NS36
F	-3	CYS	-	expression tag	UNP Q6NS36
F	-2	ALA	-	expression tag	UNP Q6NS36
F	-1	ALA	-	expression tag	UNP Q6NS36
F	0	CYS	-	expression tag	UNP Q6NS36
F	86	GLN	LYS	engineered mutation	UNP Q6NS36
G	-6	GLY	-	expression tag	UNP Q6NS36
G	-5	MET	-	expression tag	UNP Q6NS36
G	-4	THR	-	expression tag	UNP Q6NS36
G	-3	CYS	-	expression tag	UNP Q6NS36
G	-2	ALA	-	expression tag	UNP Q6NS36
G	-1	ALA	-	expression tag	UNP Q6NS36
G	0	CYS	-	expression tag	UNP Q6NS36
G	86	GLN	LYS	engineered mutation	UNP Q6NS36
H	-6	GLY	-	expression tag	UNP Q6NS36
H	-5	MET	-	expression tag	UNP Q6NS36
H	-4	THR	-	expression tag	UNP Q6NS36
H	-3	CYS	-	expression tag	UNP Q6NS36
H	-2	ALA	-	expression tag	UNP Q6NS36
H	-1	ALA	-	expression tag	UNP Q6NS36
H	0	CYS	-	expression tag	UNP Q6NS36
H	86	GLN	LYS	engineered mutation	UNP Q6NS36
I	-6	GLY	-	expression tag	UNP Q6NS36

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
I	-5	MET	-	expression tag	UNP Q6NS36
I	-4	THR	-	expression tag	UNP Q6NS36
I	-3	CYS	-	expression tag	UNP Q6NS36
I	-2	ALA	-	expression tag	UNP Q6NS36
I	-1	ALA	-	expression tag	UNP Q6NS36
I	0	CYS	-	expression tag	UNP Q6NS36
I	86	GLN	LYS	engineered mutation	UNP Q6NS36
J	-6	GLY	-	expression tag	UNP Q6NS36
J	-5	MET	-	expression tag	UNP Q6NS36
J	-4	THR	-	expression tag	UNP Q6NS36
J	-3	CYS	-	expression tag	UNP Q6NS36
J	-2	ALA	-	expression tag	UNP Q6NS36
J	-1	ALA	-	expression tag	UNP Q6NS36
J	0	CYS	-	expression tag	UNP Q6NS36
J	86	GLN	LYS	engineered mutation	UNP Q6NS36
K	-6	GLY	-	expression tag	UNP Q6NS36
K	-5	MET	-	expression tag	UNP Q6NS36
K	-4	THR	-	expression tag	UNP Q6NS36
K	-3	CYS	-	expression tag	UNP Q6NS36
K	-2	ALA	-	expression tag	UNP Q6NS36
K	-1	ALA	-	expression tag	UNP Q6NS36
K	0	CYS	-	expression tag	UNP Q6NS36
K	86	GLN	LYS	engineered mutation	UNP Q6NS36
L	-6	GLY	-	expression tag	UNP Q6NS36
L	-5	MET	-	expression tag	UNP Q6NS36
L	-4	THR	-	expression tag	UNP Q6NS36
L	-3	CYS	-	expression tag	UNP Q6NS36
L	-2	ALA	-	expression tag	UNP Q6NS36
L	-1	ALA	-	expression tag	UNP Q6NS36
L	0	CYS	-	expression tag	UNP Q6NS36
L	86	GLN	LYS	engineered mutation	UNP Q6NS36
M	-6	GLY	-	expression tag	UNP Q6NS36
M	-5	MET	-	expression tag	UNP Q6NS36
M	-4	THR	-	expression tag	UNP Q6NS36
M	-3	CYS	-	expression tag	UNP Q6NS36
M	-2	ALA	-	expression tag	UNP Q6NS36
M	-1	ALA	-	expression tag	UNP Q6NS36
M	0	CYS	-	expression tag	UNP Q6NS36
M	86	GLN	LYS	engineered mutation	UNP Q6NS36
N	-6	GLY	-	expression tag	UNP Q6NS36
N	-5	MET	-	expression tag	UNP Q6NS36
N	-4	THR	-	expression tag	UNP Q6NS36

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
N	-3	CYS	-	expression tag	UNP Q6NS36
N	-2	ALA	-	expression tag	UNP Q6NS36
N	-1	ALA	-	expression tag	UNP Q6NS36
N	0	CYS	-	expression tag	UNP Q6NS36
N	86	GLN	LYS	engineered mutation	UNP Q6NS36
O	-6	GLY	-	expression tag	UNP Q6NS36
O	-5	MET	-	expression tag	UNP Q6NS36
O	-4	THR	-	expression tag	UNP Q6NS36
O	-3	CYS	-	expression tag	UNP Q6NS36
O	-2	ALA	-	expression tag	UNP Q6NS36
O	-1	ALA	-	expression tag	UNP Q6NS36
O	0	CYS	-	expression tag	UNP Q6NS36
O	86	GLN	LYS	engineered mutation	UNP Q6NS36
P	-6	GLY	-	expression tag	UNP Q6NS36
P	-5	MET	-	expression tag	UNP Q6NS36
P	-4	THR	-	expression tag	UNP Q6NS36
P	-3	CYS	-	expression tag	UNP Q6NS36
P	-2	ALA	-	expression tag	UNP Q6NS36
P	-1	ALA	-	expression tag	UNP Q6NS36
P	0	CYS	-	expression tag	UNP Q6NS36
P	86	GLN	LYS	engineered mutation	UNP Q6NS36
Q	-6	GLY	-	expression tag	UNP Q6NS36
Q	-5	MET	-	expression tag	UNP Q6NS36
Q	-4	THR	-	expression tag	UNP Q6NS36
Q	-3	CYS	-	expression tag	UNP Q6NS36
Q	-2	ALA	-	expression tag	UNP Q6NS36
Q	-1	ALA	-	expression tag	UNP Q6NS36
Q	0	CYS	-	expression tag	UNP Q6NS36
Q	86	GLN	LYS	engineered mutation	UNP Q6NS36
R	-6	GLY	-	expression tag	UNP Q6NS36
R	-5	MET	-	expression tag	UNP Q6NS36
R	-4	THR	-	expression tag	UNP Q6NS36
R	-3	CYS	-	expression tag	UNP Q6NS36
R	-2	ALA	-	expression tag	UNP Q6NS36
R	-1	ALA	-	expression tag	UNP Q6NS36
R	0	CYS	-	expression tag	UNP Q6NS36
R	86	GLN	LYS	engineered mutation	UNP Q6NS36
S	-6	GLY	-	expression tag	UNP Q6NS36
S	-5	MET	-	expression tag	UNP Q6NS36
S	-4	THR	-	expression tag	UNP Q6NS36
S	-3	CYS	-	expression tag	UNP Q6NS36
S	-2	ALA	-	expression tag	UNP Q6NS36

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
S	-1	ALA	-	expression tag	UNP Q6NS36
S	0	CYS	-	expression tag	UNP Q6NS36
S	86	GLN	LYS	engineered mutation	UNP Q6NS36
T	-6	GLY	-	expression tag	UNP Q6NS36
T	-5	MET	-	expression tag	UNP Q6NS36
T	-4	THR	-	expression tag	UNP Q6NS36
T	-3	CYS	-	expression tag	UNP Q6NS36
T	-2	ALA	-	expression tag	UNP Q6NS36
T	-1	ALA	-	expression tag	UNP Q6NS36
T	0	CYS	-	expression tag	UNP Q6NS36
T	86	GLN	LYS	engineered mutation	UNP Q6NS36
U	-6	GLY	-	expression tag	UNP Q6NS36
U	-5	MET	-	expression tag	UNP Q6NS36
U	-4	THR	-	expression tag	UNP Q6NS36
U	-3	CYS	-	expression tag	UNP Q6NS36
U	-2	ALA	-	expression tag	UNP Q6NS36
U	-1	ALA	-	expression tag	UNP Q6NS36
U	0	CYS	-	expression tag	UNP Q6NS36
U	86	GLN	LYS	engineered mutation	UNP Q6NS36
V	-6	GLY	-	expression tag	UNP Q6NS36
V	-5	MET	-	expression tag	UNP Q6NS36
V	-4	THR	-	expression tag	UNP Q6NS36
V	-3	CYS	-	expression tag	UNP Q6NS36
V	-2	ALA	-	expression tag	UNP Q6NS36
V	-1	ALA	-	expression tag	UNP Q6NS36
V	0	CYS	-	expression tag	UNP Q6NS36
V	86	GLN	LYS	engineered mutation	UNP Q6NS36
W	-6	GLY	-	expression tag	UNP Q6NS36
W	-5	MET	-	expression tag	UNP Q6NS36
W	-4	THR	-	expression tag	UNP Q6NS36
W	-3	CYS	-	expression tag	UNP Q6NS36
W	-2	ALA	-	expression tag	UNP Q6NS36
W	-1	ALA	-	expression tag	UNP Q6NS36
W	0	CYS	-	expression tag	UNP Q6NS36
W	86	GLN	LYS	engineered mutation	UNP Q6NS36
X	-6	GLY	-	expression tag	UNP Q6NS36
X	-5	MET	-	expression tag	UNP Q6NS36
X	-4	THR	-	expression tag	UNP Q6NS36
X	-3	CYS	-	expression tag	UNP Q6NS36
X	-2	ALA	-	expression tag	UNP Q6NS36
X	-1	ALA	-	expression tag	UNP Q6NS36
X	0	CYS	-	expression tag	UNP Q6NS36

Continued on next page...

Continued from previous page...

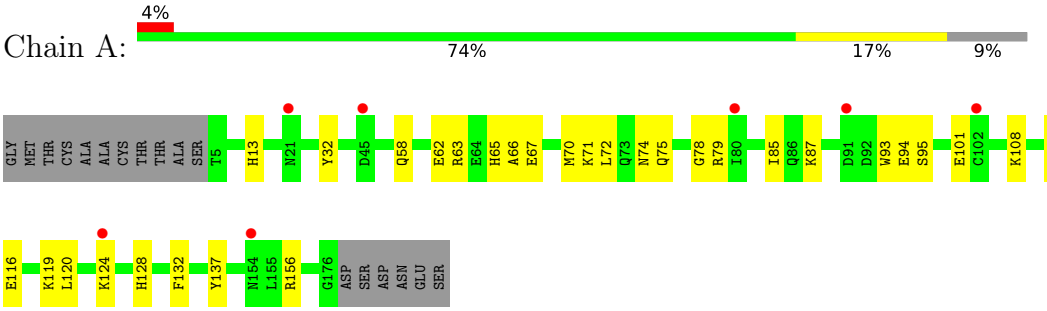
Chain	Residue	Modelled	Actual	Comment	Reference
X	86	GLN	LYS	engineered mutation	UNP Q6NS36

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.

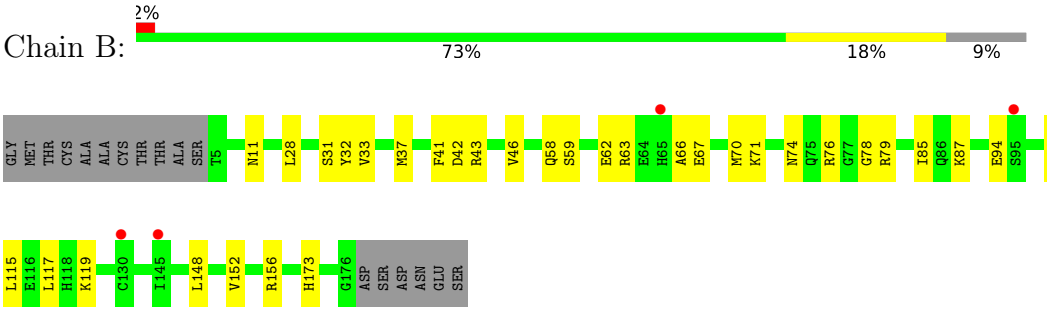
• Molecule 1: Ferritin

Chain A:



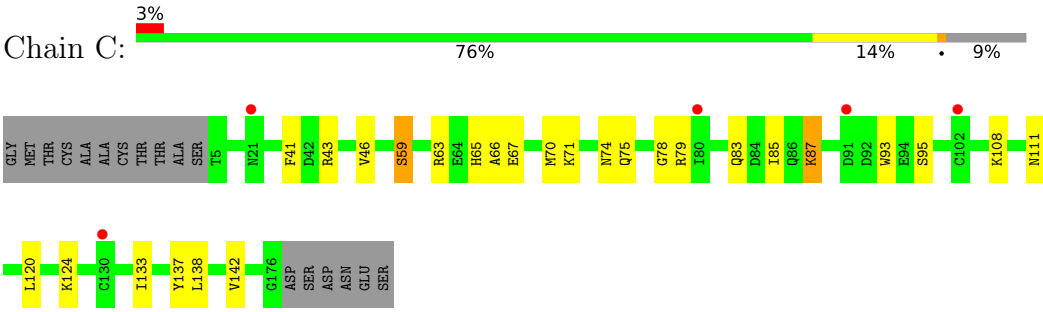
• Molecule 1: Ferritin

Chain B:



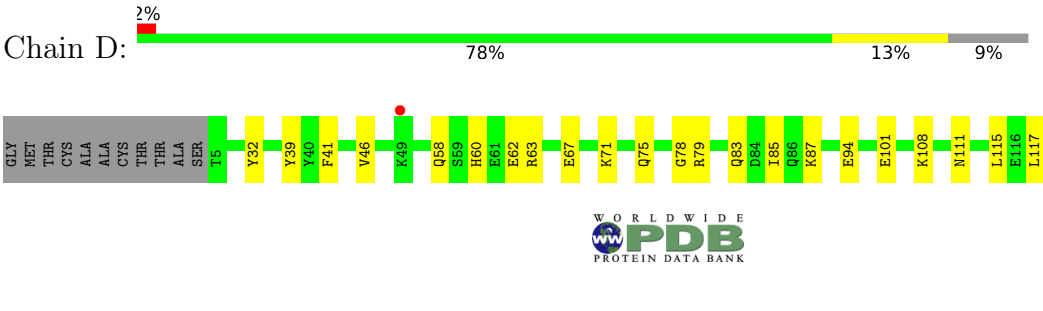
• Molecule 1: Ferritin

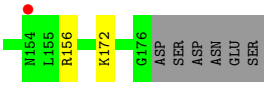
Chain C:



• Molecule 1: Ferritin

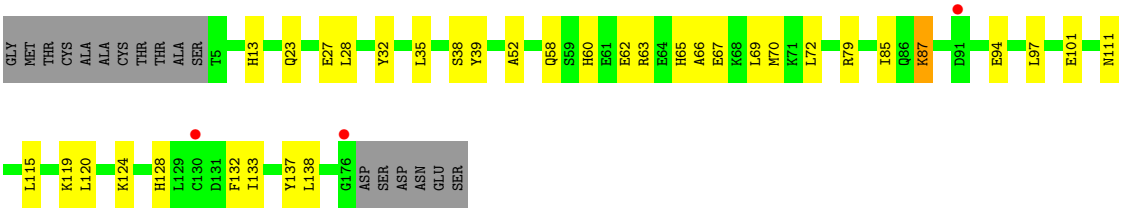
Chain D:





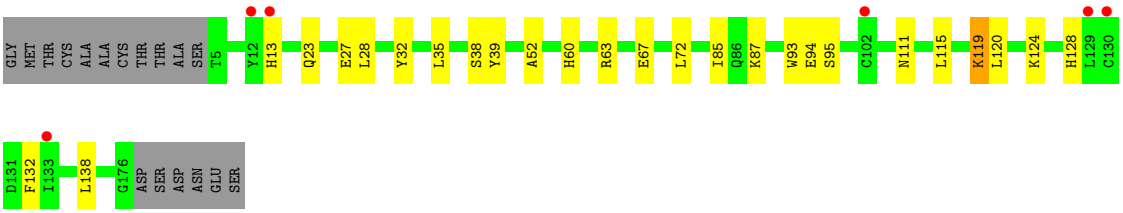
• Molecule 1: Ferritin

Chain E:



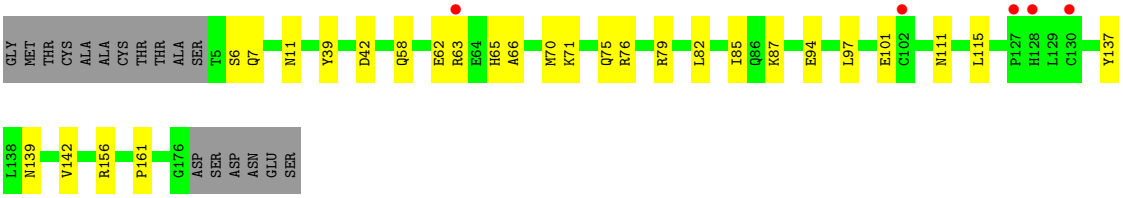
• Molecule 1: Ferritin

Chain F:



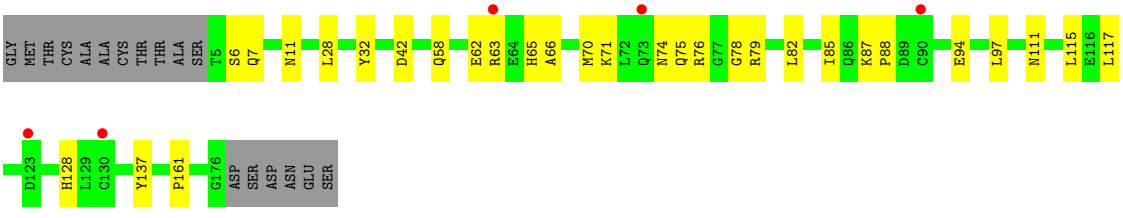
• Molecule 1: Ferritin

Chain G:



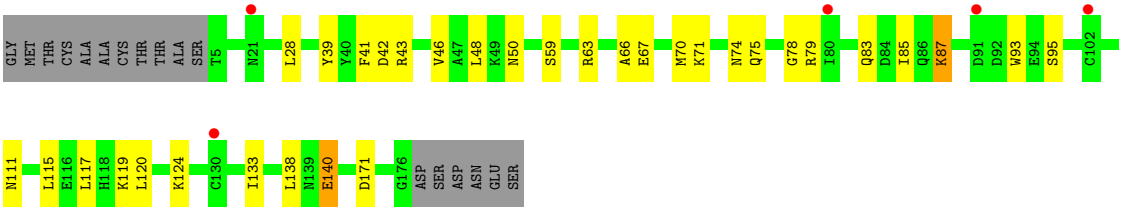
• Molecule 1: Ferritin

Chain H:



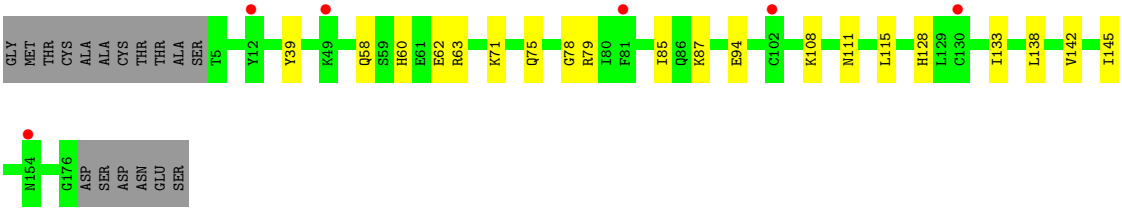
• Molecule 1: Ferritin

Chain I:



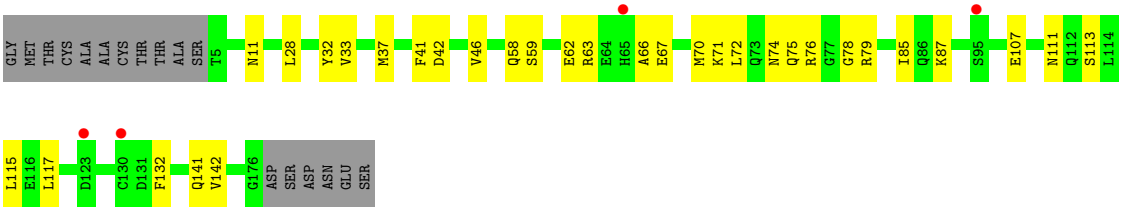
• Molecule 1: Ferritin

Chain J:



• Molecule 1: Ferritin

Chain K:

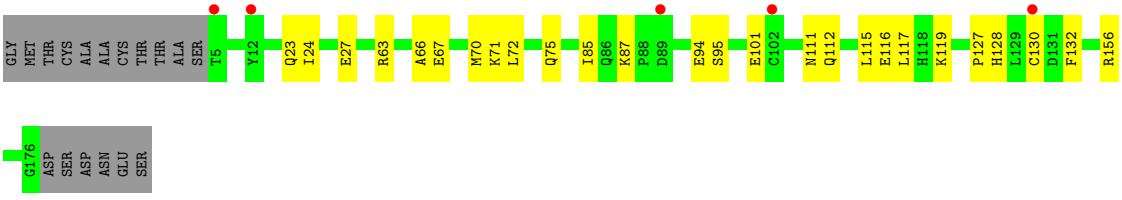


• Molecule 1: Ferritin

Chain L:

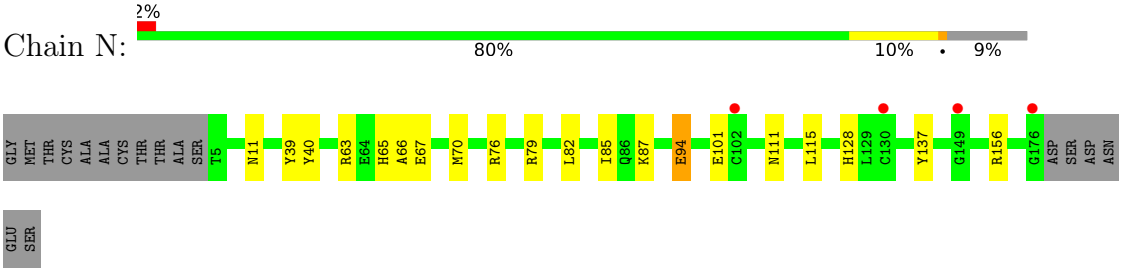
• Molecule 1: Ferritin

Chain M:



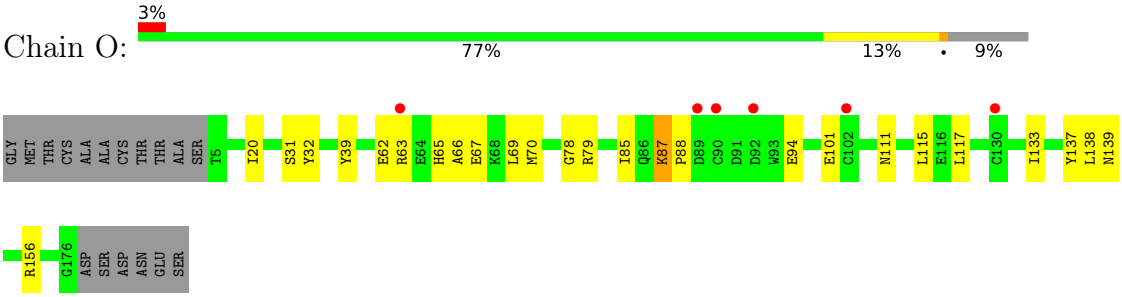
• Molecule 1: Ferritin

Chain N:



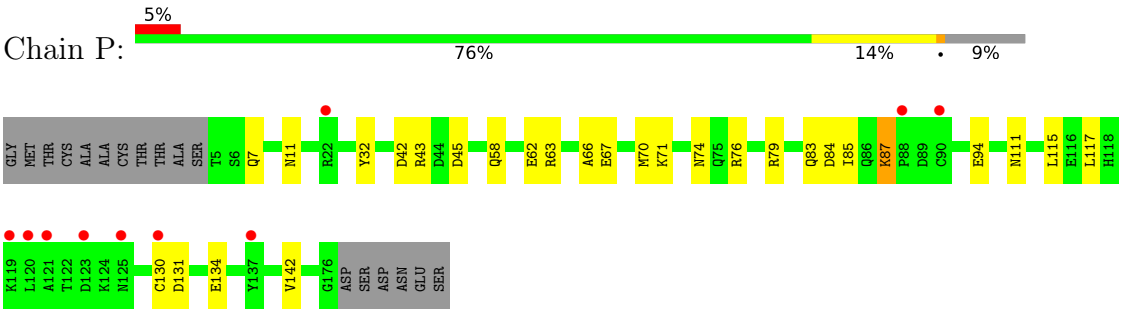
• Molecule 1: Ferritin

Chain O:



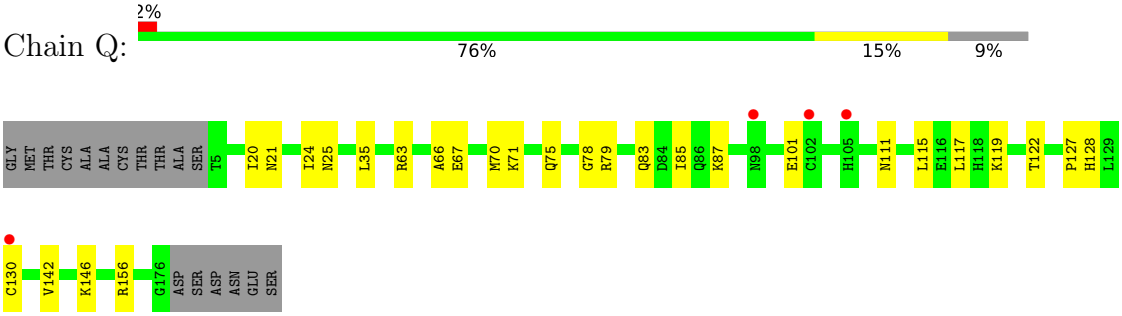
• Molecule 1: Ferritin

Chain P:



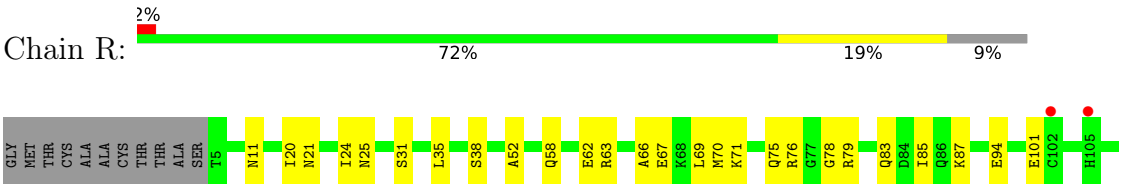
• Molecule 1: Ferritin

Chain Q:



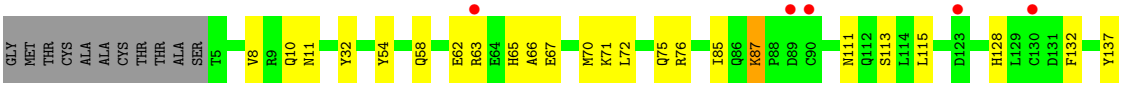
• Molecule 1: Ferritin

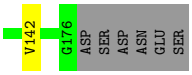
Chain R:



• Molecule 1: Ferritin

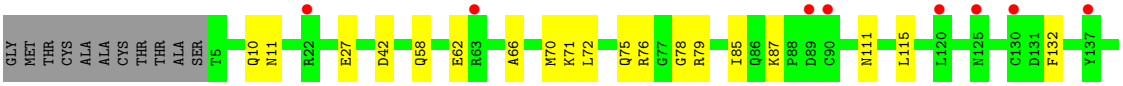
Chain S:

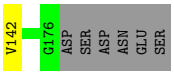




• Molecule 1: Ferritin

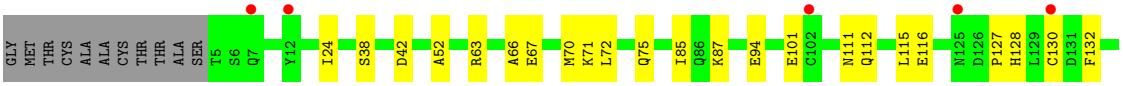
Chain T:

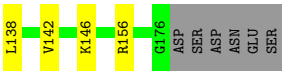




• Molecule 1: Ferritin

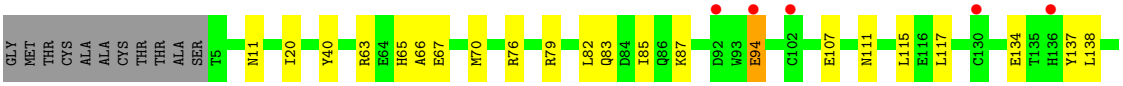
Chain U:

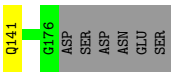




• Molecule 1: Ferritin

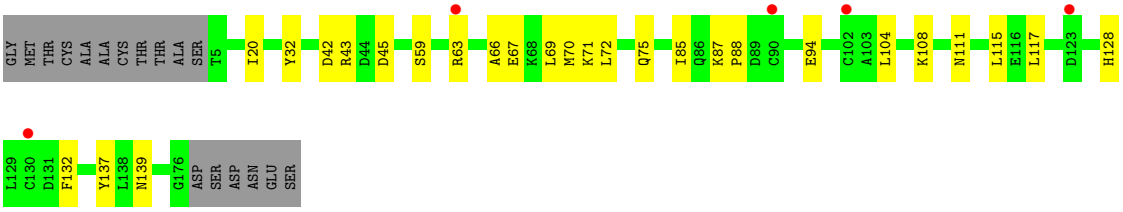
Chain V:



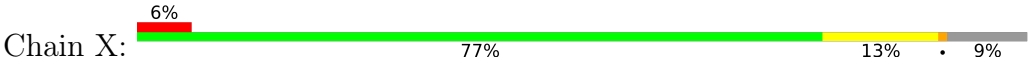


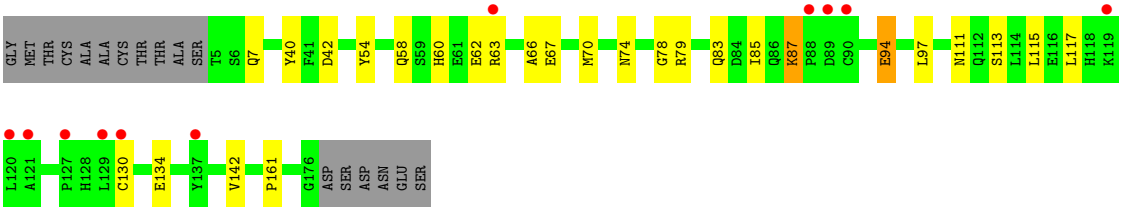
• Molecule 1: Ferritin

Chain W:



• Molecule 1: Ferritin





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 42	Depositor
Cell constants a, b, c, α, β, γ	217.52Å 217.52Å 146.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.75 – 3.50 49.65 – 3.50	Depositor EDS
% Data completeness (in resolution range)	98.3 (47.75-3.50) 98.3 (49.65-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.67 (at 3.48Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.339 , 0.399 0.338 , 0.394	Depositor DCC
R_{free} test set	1997 reflections (2.36%)	wwPDB-VP
Wilson B-factor (Å^2)	46.2	Xtriage
Anisotropy	0.119	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , -12.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.38$, $< L^2 > = 0.21$	Xtriage
Estimated twinning fraction	0.369 for h,-k,-l	Xtriage
F_o,F_c correlation	0.86	EDS
Total number of atoms	33912	wwPDB-VP
Average B, all atoms (Å^2)	34.0	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 47.06 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.0472e-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

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	0.24	0/1442	0.39	0/1943
1	B	0.24	0/1442	0.38	0/1943
1	C	0.25	0/1442	0.39	0/1943
1	D	0.25	0/1442	0.38	0/1943
1	E	0.26	0/1442	0.39	0/1943
1	F	0.31	1/1442 (0.1%)	0.39	0/1943
1	G	0.24	0/1442	0.38	0/1943
1	H	0.25	0/1442	0.38	0/1943
1	I	0.35	1/1442 (0.1%)	0.39	0/1943
1	J	0.25	0/1442	0.38	0/1943
1	K	0.25	0/1442	0.38	0/1943
1	L	0.25	0/1442	0.39	0/1943
1	M	0.32	1/1442 (0.1%)	0.39	0/1943
1	N	0.24	0/1442	0.39	0/1943
1	O	0.25	0/1442	0.38	0/1943
1	P	0.25	0/1442	0.38	0/1943
1	Q	0.24	0/1442	0.38	0/1943
1	R	0.24	0/1442	0.39	0/1943
1	S	0.24	0/1442	0.38	0/1943
1	T	0.25	0/1442	0.38	0/1943
1	U	0.24	0/1442	0.39	0/1943
1	V	0.25	0/1442	0.39	0/1943
1	W	0.24	0/1442	0.37	0/1943
1	X	0.25	0/1442	0.39	0/1943
All	All	0.26	3/34608 (0.0%)	0.38	0/46632

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	119	LYS	CD-CE	-7.12	1.33	1.51
1	I	140	GLU	CD-OE1	-6.90	1.18	1.25
1	F	119	LYS	CD-CE	-6.62	1.34	1.51

There are no bond angle outliers.

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	1413	0	1352	20	0
1	B	1413	0	1352	21	0
1	C	1413	0	1352	20	0
1	D	1413	0	1352	15	0
1	E	1413	0	1352	24	0
1	F	1413	0	1352	18	0
1	G	1413	0	1352	20	0
1	H	1413	0	1352	20	0
1	I	1413	0	1352	26	0
1	J	1413	0	1352	15	0
1	K	1413	0	1352	21	0
1	L	1413	0	1352	17	0
1	M	1413	0	1352	14	0
1	N	1413	0	1352	15	0
1	O	1413	0	1352	16	0
1	P	1413	0	1352	23	0
1	Q	1413	0	1352	18	0
1	R	1413	0	1352	23	0
1	S	1413	0	1352	15	0
1	T	1413	0	1352	12	0
1	U	1413	0	1352	18	0
1	V	1413	0	1352	15	0
1	W	1413	0	1352	16	0
1	X	1413	0	1352	20	0
All	All	33912	0	32448	353	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 5.

The worst 5 of 353 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:B:85:ILE:HB	1:H:85:ILE:HB	1.55	0.88
1:I:85:ILE:HB	1:P:85:ILE:HB	1.57	0.85
1:G:85:ILE:HB	1:K:85:ILE:HB	1.56	0.85
1:C:85:ILE:HB	1:X:85:ILE:HB	1.63	0.79
1:M:85:ILE:HB	1:Q:85:ILE:HB	1.67	0.77

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	170/189 (90%)	168 (99%)	1 (1%)	1 (1%)	25	64
1	B	170/189 (90%)	166 (98%)	3 (2%)	1 (1%)	25	64
1	C	170/189 (90%)	166 (98%)	4 (2%)	0	100	100
1	D	170/189 (90%)	167 (98%)	2 (1%)	1 (1%)	25	64
1	E	170/189 (90%)	166 (98%)	3 (2%)	1 (1%)	25	64
1	F	170/189 (90%)	165 (97%)	4 (2%)	1 (1%)	25	64
1	G	170/189 (90%)	167 (98%)	2 (1%)	1 (1%)	25	64
1	H	170/189 (90%)	165 (97%)	4 (2%)	1 (1%)	25	64
1	I	170/189 (90%)	164 (96%)	6 (4%)	0	100	100
1	J	170/189 (90%)	166 (98%)	3 (2%)	1 (1%)	25	64
1	K	170/189 (90%)	165 (97%)	5 (3%)	0	100	100
1	L	170/189 (90%)	168 (99%)	1 (1%)	1 (1%)	25	64
1	M	170/189 (90%)	165 (97%)	4 (2%)	1 (1%)	25	64
1	N	170/189 (90%)	166 (98%)	3 (2%)	1 (1%)	25	64
1	O	170/189 (90%)	165 (97%)	4 (2%)	1 (1%)	25	64
1	P	170/189 (90%)	167 (98%)	2 (1%)	1 (1%)	25	64

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	170/189 (90%)	165 (97%)	5 (3%)	0	100	100
1	R	170/189 (90%)	166 (98%)	3 (2%)	1 (1%)	25	64
1	S	170/189 (90%)	166 (98%)	4 (2%)	0	100	100
1	T	170/189 (90%)	167 (98%)	3 (2%)	0	100	100
1	U	170/189 (90%)	166 (98%)	3 (2%)	1 (1%)	25	64
1	V	170/189 (90%)	165 (97%)	4 (2%)	1 (1%)	25	64
1	W	170/189 (90%)	166 (98%)	3 (2%)	1 (1%)	25	64
1	X	170/189 (90%)	166 (98%)	3 (2%)	1 (1%)	25	64
All	All	4080/4536 (90%)	3983 (98%)	79 (2%)	18 (0%)	34	72

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	94	GLU
1	G	94	GLU
1	H	94	GLU
1	N	94	GLU
1	O	94	GLU

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	153/166 (92%)	151 (99%)	2 (1%)	69	86
1	B	153/166 (92%)	150 (98%)	3 (2%)	55	79
1	C	153/166 (92%)	150 (98%)	3 (2%)	55	79
1	D	153/166 (92%)	150 (98%)	3 (2%)	55	79
1	E	153/166 (92%)	152 (99%)	1 (1%)	84	93
1	F	153/166 (92%)	152 (99%)	1 (1%)	84	93
1	G	153/166 (92%)	152 (99%)	1 (1%)	84	93
1	H	153/166 (92%)	150 (98%)	3 (2%)	55	79

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	I	153/166 (92%)	150 (98%)	3 (2%)	55 79
1	J	153/166 (92%)	152 (99%)	1 (1%)	84 93
1	K	153/166 (92%)	150 (98%)	3 (2%)	55 79
1	L	153/166 (92%)	151 (99%)	2 (1%)	69 86
1	M	153/166 (92%)	150 (98%)	3 (2%)	55 79
1	N	153/166 (92%)	152 (99%)	1 (1%)	84 93
1	O	153/166 (92%)	152 (99%)	1 (1%)	84 93
1	P	153/166 (92%)	150 (98%)	3 (2%)	55 79
1	Q	153/166 (92%)	152 (99%)	1 (1%)	84 93
1	R	153/166 (92%)	152 (99%)	1 (1%)	84 93
1	S	153/166 (92%)	150 (98%)	3 (2%)	55 79
1	T	153/166 (92%)	152 (99%)	1 (1%)	84 93
1	U	153/166 (92%)	152 (99%)	1 (1%)	84 93
1	V	153/166 (92%)	152 (99%)	1 (1%)	84 93
1	W	153/166 (92%)	151 (99%)	2 (1%)	69 86
1	X	153/166 (92%)	150 (98%)	3 (2%)	55 79
All	All	3672/3984 (92%)	3625 (99%)	47 (1%)	69 86

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	M	117	LEU
1	R	87	LYS
1	N	87	LYS
1	P	87	LYS
1	S	87	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	W	139	ASN
1	T	11	ASN
1	I	25	ASN
1	G	139	ASN
1	P	74	ASN

5.3.3 RNA

There are no RNA molecules 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 monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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, 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	172/189 (91%)	0.41	7 (4%)	37	33	10, 31, 63, 83	0
1	B	172/189 (91%)	0.41	4 (2%)	60	54	9, 28, 62, 82	0
1	C	172/189 (91%)	0.40	5 (2%)	51	45	12, 32, 63, 83	0
1	D	172/189 (91%)	0.40	4 (2%)	60	54	11, 28, 64, 82	0
1	E	172/189 (91%)	0.39	3 (1%)	70	64	11, 30, 63, 83	0
1	F	172/189 (91%)	0.41	6 (3%)	44	39	12, 29, 62, 81	0
1	G	172/189 (91%)	0.40	5 (2%)	51	45	9, 28, 62, 80	0
1	H	172/189 (91%)	0.41	5 (2%)	51	45	9, 28, 62, 81	0
1	I	172/189 (91%)	0.43	5 (2%)	51	45	11, 32, 65, 85	0
1	J	172/189 (91%)	0.42	6 (3%)	44	39	12, 30, 66, 82	0
1	K	172/189 (91%)	0.42	4 (2%)	60	54	9, 29, 66, 83	0
1	L	172/189 (91%)	0.44	7 (4%)	37	33	11, 31, 65, 83	0
1	M	172/189 (91%)	0.45	5 (2%)	51	45	12, 30, 62, 83	0
1	N	172/189 (91%)	0.46	4 (2%)	60	54	10, 29, 64, 80	0
1	O	172/189 (91%)	0.37	6 (3%)	44	39	11, 30, 65, 84	0
1	P	172/189 (91%)	0.44	10 (5%)	23	20	9, 28, 64, 80	0
1	Q	172/189 (91%)	0.48	4 (2%)	60	54	10, 30, 64, 83	0
1	R	172/189 (91%)	0.50	3 (1%)	70	64	9, 30, 64, 85	0
1	S	172/189 (91%)	0.36	5 (2%)	51	45	10, 29, 66, 83	0
1	T	172/189 (91%)	0.46	8 (4%)	31	28	9, 31, 66, 84	0
1	U	172/189 (91%)	0.48	5 (2%)	51	45	12, 30, 62, 83	0
1	V	172/189 (91%)	0.45	5 (2%)	51	45	9, 29, 62, 80	0
1	W	172/189 (91%)	0.41	5 (2%)	51	45	11, 29, 64, 83	0
1	X	172/189 (91%)	0.46	11 (6%)	19	18	9, 29, 64, 81	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
All	All	4128/4536 (91%)	0.43	132 (3%)	47	42	9, 30, 64, 85	0

The worst 5 of 132 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	T	90	CYS	4.7
1	K	130	CYS	4.4
1	S	90	CYS	4.3
1	B	65	HIS	4.2
1	A	102	CYS	3.9

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

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.