



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 08:03 am BST

PDB ID : 5OBA
Title : Structure of a modified mouse H-chain ferritin with a lanthanide binding motif
Authors : Baiocco, P.; Trabuco, M.C.
Deposited on : 2017-06-26
Resolution : 2.85 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 ⓘ symbol.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

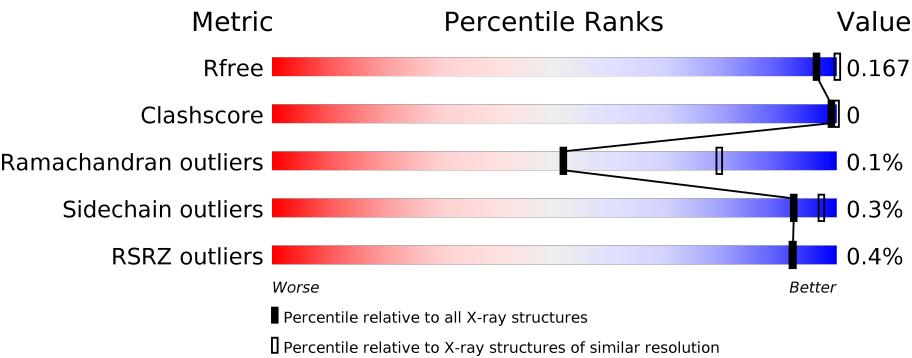
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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.




















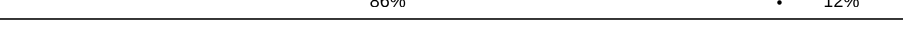
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	197	<div><div></div><div>87%12%</div></div>
1	B	197	<div><div>%</div><div>87%12%</div></div>
1	C	197	<div><div>%</div><div>87%12%</div></div>
1	D	197	<div><div>%</div><div>87%12%</div></div>
1	E	197	<div><div>%</div><div>87%12%</div></div>
1	F	197	<div><div></div><div>86%12%</div></div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	197	
1	H	197	
1	I	197	
1	J	197	
1	K	197	
1	L	197	
1	M	197	
1	N	197	
1	O	197	
1	P	197	
1	Q	197	
1	R	197	
1	S	197	
1	T	197	
1	U	197	
1	V	197	
1	W	197	
1	X	197	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 34060 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 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	173	Total	C	N	O	S	0	1	0
			1423	892	251	272	8			
1	B	173	Total	C	N	O	S	0	0	0
			1415	887	248	272	8			
1	C	173	Total	C	N	O	S	0	0	0
			1415	887	248	272	8			
1	D	173	Total	C	N	O	S	0	0	0
			1415	887	248	272	8			
1	E	173	Total	C	N	O	S	0	1	0
			1426	893	252	273	8			
1	F	174	Total	C	N	O	S	0	0	0
			1419	889	249	273	8			
1	G	174	Total	C	N	O	S	0	0	0
			1419	889	249	273	8			
1	H	173	Total	C	N	O	S	0	0	0
			1415	887	248	272	8			
1	I	173	Total	C	N	O	S	0	1	0
			1423	892	251	272	8			
1	J	171	Total	C	N	O	S	0	0	0
			1402	879	246	269	8			
1	K	173	Total	C	N	O	S	0	0	0
			1415	887	248	272	8			
1	L	174	Total	C	N	O	S	0	0	0
			1419	889	249	273	8			
1	M	173	Total	C	N	O	S	0	1	0
			1423	892	251	272	8			
1	N	171	Total	C	N	O	S	0	0	0
			1402	879	246	269	8			
1	O	173	Total	C	N	O	S	0	0	0
			1415	887	248	272	8			
1	P	173	Total	C	N	O	S	0	0	0
			1415	887	248	272	8			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	173	Total	C	N	O	S	0	1	0
			1426	893	252	273	8			
1	R	174	Total	C	N	O	S	0	0	0
			1419	889	249	273	8			
1	S	174	Total	C	N	O	S	0	0	0
			1419	889	249	273	8			
1	T	173	Total	C	N	O	S	0	0	0
			1415	887	248	272	8			
1	U	173	Total	C	N	O	S	0	1	0
			1423	892	251	272	8			
1	V	174	Total	C	N	O	S	0	0	0
			1419	889	249	273	8			
1	W	173	Total	C	N	O	S	0	0	0
			1415	887	248	272	8			
1	X	174	Total	C	N	O	S	0	0	0
			1419	889	249	273	8			

There are 480 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	177	GLY	-	expression tag	UNP P09528
A	178	SER	-	expression tag	UNP P09528
A	179	GLY	-	expression tag	UNP P09528
A	180	TYR	-	expression tag	UNP P09528
A	181	ILE	-	expression tag	UNP P09528
A	182	ASP	-	expression tag	UNP P09528
A	183	THR	-	expression tag	UNP P09528
A	184	ASN	-	expression tag	UNP P09528
A	185	ASN	-	expression tag	UNP P09528
A	186	ASP	-	expression tag	UNP P09528
A	187	GLY	-	expression tag	UNP P09528
A	188	TRP	-	expression tag	UNP P09528
A	189	ILE	-	expression tag	UNP P09528
A	190	GLU	-	expression tag	UNP P09528
A	191	GLY	-	expression tag	UNP P09528
A	192	ASP	-	expression tag	UNP P09528
A	193	GLU	-	expression tag	UNP P09528
A	194	LEU	-	expression tag	UNP P09528
A	195	LEU	-	expression tag	UNP P09528
A	196	ALA	-	expression tag	UNP P09528
B	177	GLY	-	expression tag	UNP P09528
B	178	SER	-	expression tag	UNP P09528
B	179	GLY	-	expression tag	UNP P09528

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	180	TYR	-	expression tag	UNP P09528
B	181	ILE	-	expression tag	UNP P09528
B	182	ASP	-	expression tag	UNP P09528
B	183	THR	-	expression tag	UNP P09528
B	184	ASN	-	expression tag	UNP P09528
B	185	ASN	-	expression tag	UNP P09528
B	186	ASP	-	expression tag	UNP P09528
B	187	GLY	-	expression tag	UNP P09528
B	188	TRP	-	expression tag	UNP P09528
B	189	ILE	-	expression tag	UNP P09528
B	190	GLU	-	expression tag	UNP P09528
B	191	GLY	-	expression tag	UNP P09528
B	192	ASP	-	expression tag	UNP P09528
B	193	GLU	-	expression tag	UNP P09528
B	194	LEU	-	expression tag	UNP P09528
B	195	LEU	-	expression tag	UNP P09528
B	196	ALA	-	expression tag	UNP P09528
C	177	GLY	-	expression tag	UNP P09528
C	178	SER	-	expression tag	UNP P09528
C	179	GLY	-	expression tag	UNP P09528
C	180	TYR	-	expression tag	UNP P09528
C	181	ILE	-	expression tag	UNP P09528
C	182	ASP	-	expression tag	UNP P09528
C	183	THR	-	expression tag	UNP P09528
C	184	ASN	-	expression tag	UNP P09528
C	185	ASN	-	expression tag	UNP P09528
C	186	ASP	-	expression tag	UNP P09528
C	187	GLY	-	expression tag	UNP P09528
C	188	TRP	-	expression tag	UNP P09528
C	189	ILE	-	expression tag	UNP P09528
C	190	GLU	-	expression tag	UNP P09528
C	191	GLY	-	expression tag	UNP P09528
C	192	ASP	-	expression tag	UNP P09528
C	193	GLU	-	expression tag	UNP P09528
C	194	LEU	-	expression tag	UNP P09528
C	195	LEU	-	expression tag	UNP P09528
C	196	ALA	-	expression tag	UNP P09528
D	177	GLY	-	expression tag	UNP P09528
D	178	SER	-	expression tag	UNP P09528
D	179	GLY	-	expression tag	UNP P09528
D	180	TYR	-	expression tag	UNP P09528
D	181	ILE	-	expression tag	UNP P09528

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	182	ASP	-	expression tag	UNP P09528
D	183	THR	-	expression tag	UNP P09528
D	184	ASN	-	expression tag	UNP P09528
D	185	ASN	-	expression tag	UNP P09528
D	186	ASP	-	expression tag	UNP P09528
D	187	GLY	-	expression tag	UNP P09528
D	188	TRP	-	expression tag	UNP P09528
D	189	ILE	-	expression tag	UNP P09528
D	190	GLU	-	expression tag	UNP P09528
D	191	GLY	-	expression tag	UNP P09528
D	192	ASP	-	expression tag	UNP P09528
D	193	GLU	-	expression tag	UNP P09528
D	194	LEU	-	expression tag	UNP P09528
D	195	LEU	-	expression tag	UNP P09528
D	196	ALA	-	expression tag	UNP P09528
E	177	GLY	-	expression tag	UNP P09528
E	178	SER	-	expression tag	UNP P09528
E	179	GLY	-	expression tag	UNP P09528
E	180	TYR	-	expression tag	UNP P09528
E	181	ILE	-	expression tag	UNP P09528
E	182	ASP	-	expression tag	UNP P09528
E	183	THR	-	expression tag	UNP P09528
E	184	ASN	-	expression tag	UNP P09528
E	185	ASN	-	expression tag	UNP P09528
E	186	ASP	-	expression tag	UNP P09528
E	187	GLY	-	expression tag	UNP P09528
E	188	TRP	-	expression tag	UNP P09528
E	189	ILE	-	expression tag	UNP P09528
E	190	GLU	-	expression tag	UNP P09528
E	191	GLY	-	expression tag	UNP P09528
E	192	ASP	-	expression tag	UNP P09528
E	193	GLU	-	expression tag	UNP P09528
E	194	LEU	-	expression tag	UNP P09528
E	195	LEU	-	expression tag	UNP P09528
E	196	ALA	-	expression tag	UNP P09528
F	177	GLY	-	expression tag	UNP P09528
F	178	SER	-	expression tag	UNP P09528
F	179	GLY	-	expression tag	UNP P09528
F	180	TYR	-	expression tag	UNP P09528
F	181	ILE	-	expression tag	UNP P09528
F	182	ASP	-	expression tag	UNP P09528
F	183	THR	-	expression tag	UNP P09528

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	184	ASN	-	expression tag	UNP P09528
F	185	ASN	-	expression tag	UNP P09528
F	186	ASP	-	expression tag	UNP P09528
F	187	GLY	-	expression tag	UNP P09528
F	188	TRP	-	expression tag	UNP P09528
F	189	ILE	-	expression tag	UNP P09528
F	190	GLU	-	expression tag	UNP P09528
F	191	GLY	-	expression tag	UNP P09528
F	192	ASP	-	expression tag	UNP P09528
F	193	GLU	-	expression tag	UNP P09528
F	194	LEU	-	expression tag	UNP P09528
F	195	LEU	-	expression tag	UNP P09528
F	196	ALA	-	expression tag	UNP P09528
G	177	GLY	-	expression tag	UNP P09528
G	178	SER	-	expression tag	UNP P09528
G	179	GLY	-	expression tag	UNP P09528
G	180	TYR	-	expression tag	UNP P09528
G	181	ILE	-	expression tag	UNP P09528
G	182	ASP	-	expression tag	UNP P09528
G	183	THR	-	expression tag	UNP P09528
G	184	ASN	-	expression tag	UNP P09528
G	185	ASN	-	expression tag	UNP P09528
G	186	ASP	-	expression tag	UNP P09528
G	187	GLY	-	expression tag	UNP P09528
G	188	TRP	-	expression tag	UNP P09528
G	189	ILE	-	expression tag	UNP P09528
G	190	GLU	-	expression tag	UNP P09528
G	191	GLY	-	expression tag	UNP P09528
G	192	ASP	-	expression tag	UNP P09528
G	193	GLU	-	expression tag	UNP P09528
G	194	LEU	-	expression tag	UNP P09528
G	195	LEU	-	expression tag	UNP P09528
G	196	ALA	-	expression tag	UNP P09528
H	177	GLY	-	expression tag	UNP P09528
H	178	SER	-	expression tag	UNP P09528
H	179	GLY	-	expression tag	UNP P09528
H	180	TYR	-	expression tag	UNP P09528
H	181	ILE	-	expression tag	UNP P09528
H	182	ASP	-	expression tag	UNP P09528
H	183	THR	-	expression tag	UNP P09528
H	184	ASN	-	expression tag	UNP P09528
H	185	ASN	-	expression tag	UNP P09528

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
H	186	ASP	-	expression tag	UNP P09528
H	187	GLY	-	expression tag	UNP P09528
H	188	TRP	-	expression tag	UNP P09528
H	189	ILE	-	expression tag	UNP P09528
H	190	GLU	-	expression tag	UNP P09528
H	191	GLY	-	expression tag	UNP P09528
H	192	ASP	-	expression tag	UNP P09528
H	193	GLU	-	expression tag	UNP P09528
H	194	LEU	-	expression tag	UNP P09528
H	195	LEU	-	expression tag	UNP P09528
H	196	ALA	-	expression tag	UNP P09528
I	177	GLY	-	expression tag	UNP P09528
I	178	SER	-	expression tag	UNP P09528
I	179	GLY	-	expression tag	UNP P09528
I	180	TYR	-	expression tag	UNP P09528
I	181	ILE	-	expression tag	UNP P09528
I	182	ASP	-	expression tag	UNP P09528
I	183	THR	-	expression tag	UNP P09528
I	184	ASN	-	expression tag	UNP P09528
I	185	ASN	-	expression tag	UNP P09528
I	186	ASP	-	expression tag	UNP P09528
I	187	GLY	-	expression tag	UNP P09528
I	188	TRP	-	expression tag	UNP P09528
I	189	ILE	-	expression tag	UNP P09528
I	190	GLU	-	expression tag	UNP P09528
I	191	GLY	-	expression tag	UNP P09528
I	192	ASP	-	expression tag	UNP P09528
I	193	GLU	-	expression tag	UNP P09528
I	194	LEU	-	expression tag	UNP P09528
I	195	LEU	-	expression tag	UNP P09528
I	196	ALA	-	expression tag	UNP P09528
J	177	GLY	-	expression tag	UNP P09528
J	178	SER	-	expression tag	UNP P09528
J	179	GLY	-	expression tag	UNP P09528
J	180	TYR	-	expression tag	UNP P09528
J	181	ILE	-	expression tag	UNP P09528
J	182	ASP	-	expression tag	UNP P09528
J	183	THR	-	expression tag	UNP P09528
J	184	ASN	-	expression tag	UNP P09528
J	185	ASN	-	expression tag	UNP P09528
J	186	ASP	-	expression tag	UNP P09528
J	187	GLY	-	expression tag	UNP P09528

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
J	188	TRP	-	expression tag	UNP P09528
J	189	ILE	-	expression tag	UNP P09528
J	190	GLU	-	expression tag	UNP P09528
J	191	GLY	-	expression tag	UNP P09528
J	192	ASP	-	expression tag	UNP P09528
J	193	GLU	-	expression tag	UNP P09528
J	194	LEU	-	expression tag	UNP P09528
J	195	LEU	-	expression tag	UNP P09528
J	196	ALA	-	expression tag	UNP P09528
K	177	GLY	-	expression tag	UNP P09528
K	178	SER	-	expression tag	UNP P09528
K	179	GLY	-	expression tag	UNP P09528
K	180	TYR	-	expression tag	UNP P09528
K	181	ILE	-	expression tag	UNP P09528
K	182	ASP	-	expression tag	UNP P09528
K	183	THR	-	expression tag	UNP P09528
K	184	ASN	-	expression tag	UNP P09528
K	185	ASN	-	expression tag	UNP P09528
K	186	ASP	-	expression tag	UNP P09528
K	187	GLY	-	expression tag	UNP P09528
K	188	TRP	-	expression tag	UNP P09528
K	189	ILE	-	expression tag	UNP P09528
K	190	GLU	-	expression tag	UNP P09528
K	191	GLY	-	expression tag	UNP P09528
K	192	ASP	-	expression tag	UNP P09528
K	193	GLU	-	expression tag	UNP P09528
K	194	LEU	-	expression tag	UNP P09528
K	195	LEU	-	expression tag	UNP P09528
K	196	ALA	-	expression tag	UNP P09528
L	177	GLY	-	expression tag	UNP P09528
L	178	SER	-	expression tag	UNP P09528
L	179	GLY	-	expression tag	UNP P09528
L	180	TYR	-	expression tag	UNP P09528
L	181	ILE	-	expression tag	UNP P09528
L	182	ASP	-	expression tag	UNP P09528
L	183	THR	-	expression tag	UNP P09528
L	184	ASN	-	expression tag	UNP P09528
L	185	ASN	-	expression tag	UNP P09528
L	186	ASP	-	expression tag	UNP P09528
L	187	GLY	-	expression tag	UNP P09528
L	188	TRP	-	expression tag	UNP P09528
L	189	ILE	-	expression tag	UNP P09528

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
L	190	GLU	-	expression tag	UNP P09528
L	191	GLY	-	expression tag	UNP P09528
L	192	ASP	-	expression tag	UNP P09528
L	193	GLU	-	expression tag	UNP P09528
L	194	LEU	-	expression tag	UNP P09528
L	195	LEU	-	expression tag	UNP P09528
L	196	ALA	-	expression tag	UNP P09528
M	177	GLY	-	expression tag	UNP P09528
M	178	SER	-	expression tag	UNP P09528
M	179	GLY	-	expression tag	UNP P09528
M	180	TYR	-	expression tag	UNP P09528
M	181	ILE	-	expression tag	UNP P09528
M	182	ASP	-	expression tag	UNP P09528
M	183	THR	-	expression tag	UNP P09528
M	184	ASN	-	expression tag	UNP P09528
M	185	ASN	-	expression tag	UNP P09528
M	186	ASP	-	expression tag	UNP P09528
M	187	GLY	-	expression tag	UNP P09528
M	188	TRP	-	expression tag	UNP P09528
M	189	ILE	-	expression tag	UNP P09528
M	190	GLU	-	expression tag	UNP P09528
M	191	GLY	-	expression tag	UNP P09528
M	192	ASP	-	expression tag	UNP P09528
M	193	GLU	-	expression tag	UNP P09528
M	194	LEU	-	expression tag	UNP P09528
M	195	LEU	-	expression tag	UNP P09528
M	196	ALA	-	expression tag	UNP P09528
N	177	GLY	-	expression tag	UNP P09528
N	178	SER	-	expression tag	UNP P09528
N	179	GLY	-	expression tag	UNP P09528
N	180	TYR	-	expression tag	UNP P09528
N	181	ILE	-	expression tag	UNP P09528
N	182	ASP	-	expression tag	UNP P09528
N	183	THR	-	expression tag	UNP P09528
N	184	ASN	-	expression tag	UNP P09528
N	185	ASN	-	expression tag	UNP P09528
N	186	ASP	-	expression tag	UNP P09528
N	187	GLY	-	expression tag	UNP P09528
N	188	TRP	-	expression tag	UNP P09528
N	189	ILE	-	expression tag	UNP P09528
N	190	GLU	-	expression tag	UNP P09528
N	191	GLY	-	expression tag	UNP P09528

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
N	192	ASP	-	expression tag	UNP P09528
N	193	GLU	-	expression tag	UNP P09528
N	194	LEU	-	expression tag	UNP P09528
N	195	LEU	-	expression tag	UNP P09528
N	196	ALA	-	expression tag	UNP P09528
O	177	GLY	-	expression tag	UNP P09528
O	178	SER	-	expression tag	UNP P09528
O	179	GLY	-	expression tag	UNP P09528
O	180	TYR	-	expression tag	UNP P09528
O	181	ILE	-	expression tag	UNP P09528
O	182	ASP	-	expression tag	UNP P09528
O	183	THR	-	expression tag	UNP P09528
O	184	ASN	-	expression tag	UNP P09528
O	185	ASN	-	expression tag	UNP P09528
O	186	ASP	-	expression tag	UNP P09528
O	187	GLY	-	expression tag	UNP P09528
O	188	TRP	-	expression tag	UNP P09528
O	189	ILE	-	expression tag	UNP P09528
O	190	GLU	-	expression tag	UNP P09528
O	191	GLY	-	expression tag	UNP P09528
O	192	ASP	-	expression tag	UNP P09528
O	193	GLU	-	expression tag	UNP P09528
O	194	LEU	-	expression tag	UNP P09528
O	195	LEU	-	expression tag	UNP P09528
O	196	ALA	-	expression tag	UNP P09528
P	177	GLY	-	expression tag	UNP P09528
P	178	SER	-	expression tag	UNP P09528
P	179	GLY	-	expression tag	UNP P09528
P	180	TYR	-	expression tag	UNP P09528
P	181	ILE	-	expression tag	UNP P09528
P	182	ASP	-	expression tag	UNP P09528
P	183	THR	-	expression tag	UNP P09528
P	184	ASN	-	expression tag	UNP P09528
P	185	ASN	-	expression tag	UNP P09528
P	186	ASP	-	expression tag	UNP P09528
P	187	GLY	-	expression tag	UNP P09528
P	188	TRP	-	expression tag	UNP P09528
P	189	ILE	-	expression tag	UNP P09528
P	190	GLU	-	expression tag	UNP P09528
P	191	GLY	-	expression tag	UNP P09528
P	192	ASP	-	expression tag	UNP P09528
P	193	GLU	-	expression tag	UNP P09528

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
P	194	LEU	-	expression tag	UNP P09528
P	195	LEU	-	expression tag	UNP P09528
P	196	ALA	-	expression tag	UNP P09528
Q	177	GLY	-	expression tag	UNP P09528
Q	178	SER	-	expression tag	UNP P09528
Q	179	GLY	-	expression tag	UNP P09528
Q	180	TYR	-	expression tag	UNP P09528
Q	181	ILE	-	expression tag	UNP P09528
Q	182	ASP	-	expression tag	UNP P09528
Q	183	THR	-	expression tag	UNP P09528
Q	184	ASN	-	expression tag	UNP P09528
Q	185	ASN	-	expression tag	UNP P09528
Q	186	ASP	-	expression tag	UNP P09528
Q	187	GLY	-	expression tag	UNP P09528
Q	188	TRP	-	expression tag	UNP P09528
Q	189	ILE	-	expression tag	UNP P09528
Q	190	GLU	-	expression tag	UNP P09528
Q	191	GLY	-	expression tag	UNP P09528
Q	192	ASP	-	expression tag	UNP P09528
Q	193	GLU	-	expression tag	UNP P09528
Q	194	LEU	-	expression tag	UNP P09528
Q	195	LEU	-	expression tag	UNP P09528
Q	196	ALA	-	expression tag	UNP P09528
R	177	GLY	-	expression tag	UNP P09528
R	178	SER	-	expression tag	UNP P09528
R	179	GLY	-	expression tag	UNP P09528
R	180	TYR	-	expression tag	UNP P09528
R	181	ILE	-	expression tag	UNP P09528
R	182	ASP	-	expression tag	UNP P09528
R	183	THR	-	expression tag	UNP P09528
R	184	ASN	-	expression tag	UNP P09528
R	185	ASN	-	expression tag	UNP P09528
R	186	ASP	-	expression tag	UNP P09528
R	187	GLY	-	expression tag	UNP P09528
R	188	TRP	-	expression tag	UNP P09528
R	189	ILE	-	expression tag	UNP P09528
R	190	GLU	-	expression tag	UNP P09528
R	191	GLY	-	expression tag	UNP P09528
R	192	ASP	-	expression tag	UNP P09528
R	193	GLU	-	expression tag	UNP P09528
R	194	LEU	-	expression tag	UNP P09528
R	195	LEU	-	expression tag	UNP P09528

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	196	ALA	-	expression tag	UNP P09528
S	177	GLY	-	expression tag	UNP P09528
S	178	SER	-	expression tag	UNP P09528
S	179	GLY	-	expression tag	UNP P09528
S	180	TYR	-	expression tag	UNP P09528
S	181	ILE	-	expression tag	UNP P09528
S	182	ASP	-	expression tag	UNP P09528
S	183	THR	-	expression tag	UNP P09528
S	184	ASN	-	expression tag	UNP P09528
S	185	ASN	-	expression tag	UNP P09528
S	186	ASP	-	expression tag	UNP P09528
S	187	GLY	-	expression tag	UNP P09528
S	188	TRP	-	expression tag	UNP P09528
S	189	ILE	-	expression tag	UNP P09528
S	190	GLU	-	expression tag	UNP P09528
S	191	GLY	-	expression tag	UNP P09528
S	192	ASP	-	expression tag	UNP P09528
S	193	GLU	-	expression tag	UNP P09528
S	194	LEU	-	expression tag	UNP P09528
S	195	LEU	-	expression tag	UNP P09528
S	196	ALA	-	expression tag	UNP P09528
T	177	GLY	-	expression tag	UNP P09528
T	178	SER	-	expression tag	UNP P09528
T	179	GLY	-	expression tag	UNP P09528
T	180	TYR	-	expression tag	UNP P09528
T	181	ILE	-	expression tag	UNP P09528
T	182	ASP	-	expression tag	UNP P09528
T	183	THR	-	expression tag	UNP P09528
T	184	ASN	-	expression tag	UNP P09528
T	185	ASN	-	expression tag	UNP P09528
T	186	ASP	-	expression tag	UNP P09528
T	187	GLY	-	expression tag	UNP P09528
T	188	TRP	-	expression tag	UNP P09528
T	189	ILE	-	expression tag	UNP P09528
T	190	GLU	-	expression tag	UNP P09528
T	191	GLY	-	expression tag	UNP P09528
T	192	ASP	-	expression tag	UNP P09528
T	193	GLU	-	expression tag	UNP P09528
T	194	LEU	-	expression tag	UNP P09528
T	195	LEU	-	expression tag	UNP P09528
T	196	ALA	-	expression tag	UNP P09528
U	177	GLY	-	expression tag	UNP P09528

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
U	178	SER	-	expression tag	UNP P09528
U	179	GLY	-	expression tag	UNP P09528
U	180	TYR	-	expression tag	UNP P09528
U	181	ILE	-	expression tag	UNP P09528
U	182	ASP	-	expression tag	UNP P09528
U	183	THR	-	expression tag	UNP P09528
U	184	ASN	-	expression tag	UNP P09528
U	185	ASN	-	expression tag	UNP P09528
U	186	ASP	-	expression tag	UNP P09528
U	187	GLY	-	expression tag	UNP P09528
U	188	TRP	-	expression tag	UNP P09528
U	189	ILE	-	expression tag	UNP P09528
U	190	GLU	-	expression tag	UNP P09528
U	191	GLY	-	expression tag	UNP P09528
U	192	ASP	-	expression tag	UNP P09528
U	193	GLU	-	expression tag	UNP P09528
U	194	LEU	-	expression tag	UNP P09528
U	195	LEU	-	expression tag	UNP P09528
U	196	ALA	-	expression tag	UNP P09528
V	177	GLY	-	expression tag	UNP P09528
V	178	SER	-	expression tag	UNP P09528
V	179	GLY	-	expression tag	UNP P09528
V	180	TYR	-	expression tag	UNP P09528
V	181	ILE	-	expression tag	UNP P09528
V	182	ASP	-	expression tag	UNP P09528
V	183	THR	-	expression tag	UNP P09528
V	184	ASN	-	expression tag	UNP P09528
V	185	ASN	-	expression tag	UNP P09528
V	186	ASP	-	expression tag	UNP P09528
V	187	GLY	-	expression tag	UNP P09528
V	188	TRP	-	expression tag	UNP P09528
V	189	ILE	-	expression tag	UNP P09528
V	190	GLU	-	expression tag	UNP P09528
V	191	GLY	-	expression tag	UNP P09528
V	192	ASP	-	expression tag	UNP P09528
V	193	GLU	-	expression tag	UNP P09528
V	194	LEU	-	expression tag	UNP P09528
V	195	LEU	-	expression tag	UNP P09528
V	196	ALA	-	expression tag	UNP P09528
W	177	GLY	-	expression tag	UNP P09528
W	178	SER	-	expression tag	UNP P09528
W	179	GLY	-	expression tag	UNP P09528

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
W	180	TYR	-	expression tag	UNP P09528
W	181	ILE	-	expression tag	UNP P09528
W	182	ASP	-	expression tag	UNP P09528
W	183	THR	-	expression tag	UNP P09528
W	184	ASN	-	expression tag	UNP P09528
W	185	ASN	-	expression tag	UNP P09528
W	186	ASP	-	expression tag	UNP P09528
W	187	GLY	-	expression tag	UNP P09528
W	188	TRP	-	expression tag	UNP P09528
W	189	ILE	-	expression tag	UNP P09528
W	190	GLU	-	expression tag	UNP P09528
W	191	GLY	-	expression tag	UNP P09528
W	192	ASP	-	expression tag	UNP P09528
W	193	GLU	-	expression tag	UNP P09528
W	194	LEU	-	expression tag	UNP P09528
W	195	LEU	-	expression tag	UNP P09528
W	196	ALA	-	expression tag	UNP P09528
X	177	GLY	-	expression tag	UNP P09528
X	178	SER	-	expression tag	UNP P09528
X	179	GLY	-	expression tag	UNP P09528
X	180	TYR	-	expression tag	UNP P09528
X	181	ILE	-	expression tag	UNP P09528
X	182	ASP	-	expression tag	UNP P09528
X	183	THR	-	expression tag	UNP P09528
X	184	ASN	-	expression tag	UNP P09528
X	185	ASN	-	expression tag	UNP P09528
X	186	ASP	-	expression tag	UNP P09528
X	187	GLY	-	expression tag	UNP P09528
X	188	TRP	-	expression tag	UNP P09528
X	189	ILE	-	expression tag	UNP P09528
X	190	GLU	-	expression tag	UNP P09528
X	191	GLY	-	expression tag	UNP P09528
X	192	ASP	-	expression tag	UNP P09528
X	193	GLU	-	expression tag	UNP P09528
X	194	LEU	-	expression tag	UNP P09528
X	195	LEU	-	expression tag	UNP P09528
X	196	ALA	-	expression tag	UNP P09528

- 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
-----	-------	----------	-------	---------	---------

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	P	2	Total Fe 2 2	0	0
2	K	2	Total Fe 2 2	0	0
2	B	1	Total Fe 1 1	0	0
2	W	1	Total Fe 1 1	0	0
2	N	1	Total Fe 1 1	0	0
2	X	1	Total Fe 1 1	0	0
2	S	1	Total Fe 1 1	0	0
2	J	1	Total Fe 1 1	0	0
2	E	2	Total Fe 2 2	0	0
2	V	2	Total Fe 2 2	0	0
2	A	2	Total Fe 2 2	0	0
2	R	1	Total Fe 1 1	0	0
2	M	2	Total Fe 2 2	0	0
2	D	1	Total Fe 1 1	0	0
2	I	1	Total Fe 1 1	0	0
2	U	1	Total Fe 1 1	0	0
2	L	1	Total Fe 1 1	0	0
2	G	2	Total Fe 2 2	0	0
2	Q	1	Total Fe 1 1	0	0
2	H	1	Total Fe 1 1	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	1	Total 1	Fe 1	0	0
2	T	2	Total 2	Fe 2	0	0
2	O	1	Total 1	Fe 1	0	0
2	F	1	Total 1	Fe 1	0	0

- Molecule 3 is water.

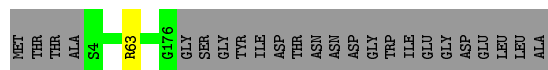
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	O 1	0	0
3	C	1	Total 1	O 1	0	0
3	D	1	Total 1	O 1	0	0
3	G	1	Total 1	O 1	0	0
3	H	2	Total 2	O 2	0	0
3	J	2	Total 2	O 2	0	0
3	M	1	Total 1	O 1	0	0
3	N	1	Total 1	O 1	0	0
3	O	1	Total 1	O 1	0	0
3	Q	1	Total 1	O 1	0	0

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 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.

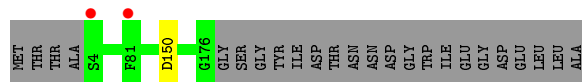
- Molecule 1: Ferritin heavy chain

Chain A: 




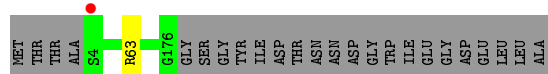
- Molecule 1: Ferritin heavy chain

Chain B: 




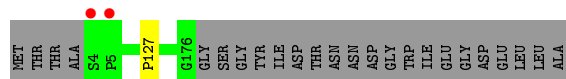
- Molecule 1: Ferritin heavy chain

Chain C: 




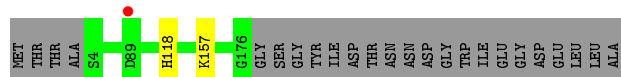
- Molecule 1: Ferritin heavy chain

Chain D: 




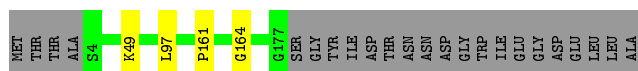
- Molecule 1: Ferritin heavy chain

Chain E: 




- Molecule 1: Ferritin heavy chain

Chain F:  86% 12%




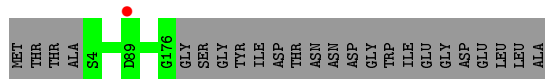
• Molecule 1: Ferritin heavy chain

Chain G:  86% 12%




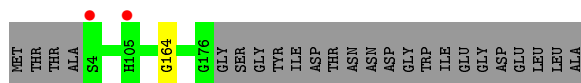
• Molecule 1: Ferritin heavy chain

Chain H:  88% 12%




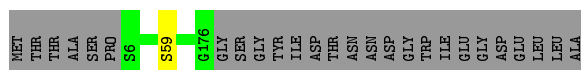
• Molecule 1: Ferritin heavy chain

Chain I:  87% 12%




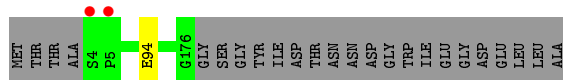
• Molecule 1: Ferritin heavy chain

Chain J:  86% 13%




• Molecule 1: Ferritin heavy chain

Chain K:  87% 12%




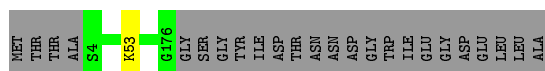
• Molecule 1: Ferritin heavy chain

Chain L:  88% 12%




• Molecule 1: Ferritin heavy chain

Chain M:  87% 12%




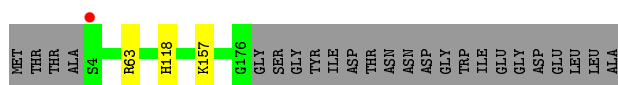
• Molecule 1: Ferritin heavy chain

Chain N:  84% 13%




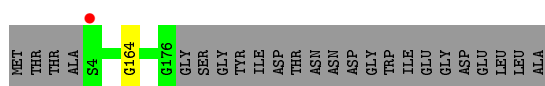
• Molecule 1: Ferritin heavy chain

Chain O:  86% 12%




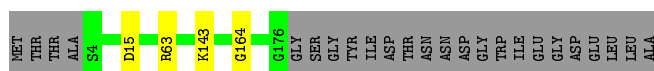
• Molecule 1: Ferritin heavy chain

Chain P:  87% 12%




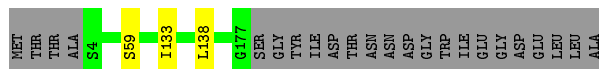
• Molecule 1: Ferritin heavy chain

Chain Q:  86% 12%




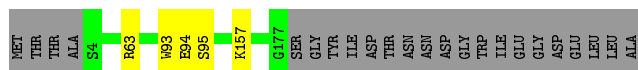
• Molecule 1: Ferritin heavy chain

Chain R:  87% 12%




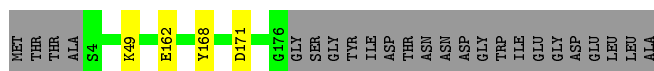
• Molecule 1: Ferritin heavy chain

Chain S:  86% 12%




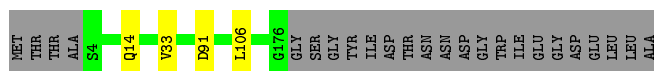
• Molecule 1: Ferritin heavy chain

Chain T:  86% 12%




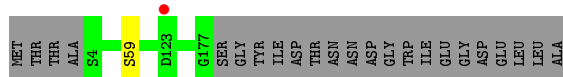
• Molecule 1: Ferritin heavy chain

Chain U:  86% 12%




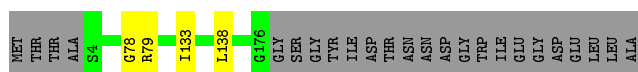
• Molecule 1: Ferritin heavy chain

Chain V:  88% 12%




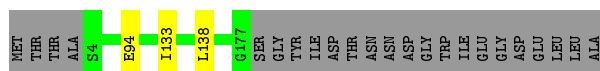
• Molecule 1: Ferritin heavy chain

Chain W:  86% 12%



• Molecule 1: Ferritin heavy chain

Chain X:  87% 12%



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	237.31Å 237.47Å 237.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.48 – 2.85 48.48 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.48-2.85) 99.8 (48.48-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.137 , 0.170 0.140 , 0.167	Depositor DCC
R_{free} test set	7872 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	49.6	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 31.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.007 for -h,-l,-k 0.007 for l,-k,h 0.006 for -k,-h,-l 0.001 for k,-l,-h 0.001 for -l,h,-k	Xtriage
Reported twinning fraction	0.362 for H, K, L 0.295 for K, -L, -H 0.343 for -L, -H, K	Depositor
Outliers	2 of 155560 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	34060	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.37% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: 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	0.27	0/1455	0.40	0/1957
1	B	0.27	0/1444	0.40	0/1943
1	C	0.27	0/1444	0.40	0/1943
1	D	0.27	0/1444	0.40	0/1943
1	E	0.26	0/1455	0.40	0/1957
1	F	0.27	0/1448	0.41	0/1948
1	G	0.27	0/1448	0.41	0/1948
1	H	0.27	0/1444	0.41	0/1943
1	I	0.27	0/1455	0.40	0/1957
1	J	0.26	0/1430	0.40	0/1923
1	K	0.27	0/1444	0.42	0/1943
1	L	0.27	0/1448	0.40	0/1948
1	M	0.27	0/1455	0.40	0/1957
1	N	0.27	0/1430	0.40	0/1923
1	O	0.27	0/1444	0.41	0/1943
1	P	0.27	0/1444	0.41	0/1943
1	Q	0.27	0/1455	0.38	0/1957
1	R	0.27	0/1448	0.41	0/1948
1	S	0.28	0/1448	0.41	0/1948
1	T	0.28	0/1444	0.42	0/1943
1	U	0.26	0/1455	0.40	0/1957
1	V	0.27	0/1448	0.41	0/1948
1	W	0.26	0/1444	0.40	0/1943
1	X	0.27	0/1448	0.39	0/1948
All	All	0.27	0/34722	0.40	0/46711

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1423	0	1377	1	0
1	B	1415	0	1364	0	0
1	C	1415	0	1364	1	0
1	D	1415	0	1364	1	0
1	E	1426	0	1376	2	0
1	F	1419	0	1367	2	0
1	G	1419	0	1367	2	0
1	H	1415	0	1364	0	0
1	I	1423	0	1377	1	0
1	J	1402	0	1352	1	0
1	K	1415	0	1364	0	0
1	L	1419	0	1367	0	0
1	M	1423	0	1377	0	0
1	N	1402	0	1352	3	0
1	O	1415	0	1364	3	0
1	P	1415	0	1364	1	0
1	Q	1426	0	1376	3	0
1	R	1419	0	1367	2	0
1	S	1419	0	1367	2	0
1	T	1415	0	1364	1	0
1	U	1423	0	1377	1	0
1	V	1419	0	1367	1	0
1	W	1415	0	1364	2	0
1	X	1419	0	1367	1	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	2	0	0	0	0
2	F	1	0	0	0	0
2	G	2	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	2	0	0	0	0
2	L	1	0	0	0	0
2	M	2	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	N	1	0	0	0	0
2	O	1	0	0	0	0
2	P	2	0	0	0	0
2	Q	1	0	0	0	0
2	R	1	0	0	0	0
2	S	1	0	0	0	0
2	T	2	0	0	0	0
2	U	1	0	0	0	0
2	V	2	0	0	0	0
2	W	1	0	0	0	0
2	X	1	0	0	0	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	G	1	0	0	0	0
3	H	2	0	0	0	0
3	J	2	0	0	0	0
3	M	1	0	0	0	0
3	N	1	0	0	0	0
3	O	1	0	0	0	0
3	Q	1	0	0	0	0
All	All	34060	0	32809	22	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 0.

All (22) 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:Q:63[B]:ARG:HG2	1:Q:63[B]:ARG:HH11	1.68	0.57
1:O:63:ARG:NH1	1:V:59:SER:OG	2.44	0.50
1:Q:63[B]:ARG:HG2	1:Q:63[B]:ARG:NH1	2.25	0.49
1:N:133:ILE:HG22	1:N:138:LEU:HG	1.94	0.49
1:P:164:GLY:HA3	1:S:157:LYS:O	2.12	0.48
1:C:63:ARG:NH1	1:J:59:SER:OG	2.45	0.48
1:E:157:LYS:O	1:I:164:GLY:HA3	2.13	0.48
1:G:78:GLY:O	1:G:79:ARG:NH1	2.47	0.48
1:G:133:ILE:HG22	1:G:138:LEU:HG	1.95	0.47
1:W:133:ILE:HG22	1:W:138:LEU:HG	1.95	0.47
1:F:97:LEU:HD23	1:F:161:PRO:HD3	1.99	0.44
1:U:33:VAL:HG11	1:U:106:LEU:HD22	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:127:PRO:HB3	1:E:118:HIS:CE1	2.52	0.44
1:W:78:GLY:O	1:W:79:ARG:NH1	2.51	0.44
1:F:164:GLY:HA3	1:N:157:LYS:O	2.18	0.43
1:O:157:LYS:O	1:Q:164:GLY:HA3	2.21	0.41
1:A:63[B]:ARG:NH2	1:R:59:SER:OG	2.53	0.41
1:S:93:TRP:O	1:S:95:SER:N	2.53	0.41
1:T:168:TYR:O	1:T:171:ASP:HB3	2.21	0.41
1:R:133:ILE:HG22	1:R:138:LEU:HG	2.03	0.40
1:X:133:ILE:HG22	1:X:138:LEU:HG	2.04	0.40
1:N:127:PRO:HB3	1:O:118:HIS:CE1	2.57	0.40

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	172/197 (87%)	169 (98%)	3 (2%)	0	100	100
1	B	171/197 (87%)	168 (98%)	3 (2%)	0	100	100
1	C	171/197 (87%)	169 (99%)	2 (1%)	0	100	100
1	D	171/197 (87%)	166 (97%)	5 (3%)	0	100	100
1	E	172/197 (87%)	170 (99%)	2 (1%)	0	100	100
1	F	172/197 (87%)	168 (98%)	4 (2%)	0	100	100
1	G	172/197 (87%)	167 (97%)	5 (3%)	0	100	100
1	H	171/197 (87%)	168 (98%)	3 (2%)	0	100	100
1	I	172/197 (87%)	168 (98%)	4 (2%)	0	100	100
1	J	169/197 (86%)	166 (98%)	3 (2%)	0	100	100
1	K	171/197 (87%)	169 (99%)	1 (1%)	1 (1%)	25	53
1	L	172/197 (87%)	168 (98%)	4 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	M	172/197 (87%)	167 (97%)	5 (3%)	0	100	100
1	N	169/197 (86%)	165 (98%)	3 (2%)	1 (1%)	25	53
1	O	171/197 (87%)	167 (98%)	4 (2%)	0	100	100
1	P	171/197 (87%)	167 (98%)	4 (2%)	0	100	100
1	Q	172/197 (87%)	166 (96%)	6 (4%)	0	100	100
1	R	172/197 (87%)	169 (98%)	3 (2%)	0	100	100
1	S	172/197 (87%)	168 (98%)	3 (2%)	1 (1%)	25	53
1	T	171/197 (87%)	168 (98%)	3 (2%)	0	100	100
1	U	172/197 (87%)	168 (98%)	4 (2%)	0	100	100
1	V	172/197 (87%)	168 (98%)	4 (2%)	0	100	100
1	W	171/197 (87%)	168 (98%)	3 (2%)	0	100	100
1	X	172/197 (87%)	166 (96%)	5 (3%)	1 (1%)	25	53
All	All	4113/4728 (87%)	4023 (98%)	86 (2%)	4 (0%)	51	79

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	S	94	GLU
1	K	94	GLU
1	N	94	GLU
1	X	94	GLU

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	154/171 (90%)	154 (100%)	0	100	100
1	B	153/171 (90%)	152 (99%)	1 (1%)	84	94
1	C	153/171 (90%)	153 (100%)	0	100	100
1	D	153/171 (90%)	153 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	154/171 (90%)	154 (100%)	0	100	100
1	F	153/171 (90%)	152 (99%)	1 (1%)	84	94
1	G	153/171 (90%)	152 (99%)	1 (1%)	84	94
1	H	153/171 (90%)	153 (100%)	0	100	100
1	I	154/171 (90%)	154 (100%)	0	100	100
1	J	151/171 (88%)	151 (100%)	0	100	100
1	K	153/171 (90%)	153 (100%)	0	100	100
1	L	153/171 (90%)	153 (100%)	0	100	100
1	M	154/171 (90%)	153 (99%)	1 (1%)	86	95
1	N	151/171 (88%)	151 (100%)	0	100	100
1	O	153/171 (90%)	153 (100%)	0	100	100
1	P	153/171 (90%)	153 (100%)	0	100	100
1	Q	154/171 (90%)	152 (99%)	2 (1%)	69	88
1	R	153/171 (90%)	153 (100%)	0	100	100
1	S	153/171 (90%)	152 (99%)	1 (1%)	84	94
1	T	153/171 (90%)	151 (99%)	2 (1%)	69	88
1	U	154/171 (90%)	152 (99%)	2 (1%)	69	88
1	V	153/171 (90%)	153 (100%)	0	100	100
1	W	153/171 (90%)	153 (100%)	0	100	100
1	X	153/171 (90%)	153 (100%)	0	100	100
All	All	3674/4104 (90%)	3663 (100%)	11 (0%)	92	97

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	150	ASP
1	F	49	LYS
1	G	63	ARG
1	M	53	LYS
1	Q	15	ASP
1	Q	143	LYS
1	S	63	ARG
1	T	49	LYS
1	T	162	GLU
1	U	14	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	U	91	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	83	GLN
1	H	10	GLN
1	I	21	ASN
1	I	23	GLN
1	N	112	GLN
1	R	83	GLN
1	T	10	GLN
1	T	83	GLN
1	U	21	ASN
1	U	23	GLN
1	U	83	GLN
1	U	112	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 32 ligands modelled in this entry, 32 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	173/197 (87%)	-0.39	0 100 100	44, 55, 66, 75	0
1	B	173/197 (87%)	-0.29	2 (1%) 79 78	51, 60, 76, 87	0
1	C	173/197 (87%)	-0.43	1 (0%) 89 89	44, 55, 66, 76	0
1	D	173/197 (87%)	-0.32	2 (1%) 79 78	48, 61, 72, 88	0
1	E	173/197 (87%)	-0.23	1 (0%) 89 89	51, 64, 76, 84	0
1	F	174/197 (88%)	-0.32	0 100 100	52, 63, 74, 84	0
1	G	174/197 (88%)	-0.35	0 100 100	44, 55, 66, 74	0
1	H	173/197 (87%)	-0.24	1 (0%) 89 89	47, 60, 70, 85	0
1	I	173/197 (87%)	-0.28	2 (1%) 79 78	48, 60, 73, 95	0
1	J	171/197 (86%)	-0.33	0 100 100	42, 54, 67, 78	0
1	K	173/197 (87%)	-0.37	2 (1%) 79 78	47, 59, 75, 93	0
1	L	174/197 (88%)	-0.37	1 (0%) 89 89	49, 60, 71, 76	0
1	M	173/197 (87%)	-0.21	0 100 100	45, 58, 69, 81	0
1	N	171/197 (86%)	-0.31	0 100 100	47, 60, 72, 82	0
1	O	173/197 (87%)	-0.48	1 (0%) 89 89	42, 55, 66, 75	0
1	P	173/197 (87%)	-0.36	1 (0%) 89 89	43, 57, 69, 77	0
1	Q	173/197 (87%)	-0.33	0 100 100	46, 59, 68, 79	0
1	R	174/197 (88%)	-0.33	0 100 100	45, 58, 73, 79	0
1	S	174/197 (88%)	-0.27	0 100 100	47, 58, 68, 75	0
1	T	173/197 (87%)	-0.38	0 100 100	50, 61, 73, 76	0
1	U	173/197 (87%)	-0.25	0 100 100	48, 60, 72, 78	0
1	V	174/197 (88%)	-0.31	1 (0%) 89 89	40, 53, 65, 72	0
1	W	173/197 (87%)	-0.36	0 100 100	45, 57, 68, 82	0
1	X	174/197 (88%)	-0.33	0 100 100	45, 56, 68, 77	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	4155/4728 (87%)	-0.33	15 (0%) 92 92	40, 58, 72, 95	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	4	SER	4.1
1	K	4	SER	3.7
1	P	4	SER	3.5
1	K	5	PRO	3.3
1	O	4	SER	3.0
1	D	5	PRO	2.8
1	H	89	ASP	2.8
1	L	4	SER	2.8
1	B	4	SER	2.7
1	I	4	SER	2.6
1	E	89	ASP	2.4
1	B	81	PHE	2.4
1	C	4	SER	2.3
1	I	105	HIS	2.3
1	V	123	ASP	2.2

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 carbohydrates 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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FE	P	202	1/1	0.85	0.08	90,90,90,90	1
2	FE	G	201	1/1	0.89	0.07	109,109,109,109	1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	FE	T	201	1/1	0.89	0.17	73,73,73,73	1
2	FE	M	202	1/1	0.92	0.08	91,91,91,91	1
2	FE	E	201	1/1	0.93	0.08	87,87,87,87	1
2	FE	K	202	1/1	0.94	0.09	101,101,101,101	1
2	FE	T	202	1/1	0.95	0.15	66,66,66,66	1
2	FE	V	202	1/1	0.95	0.06	102,102,102,102	0
2	FE	U	201	1/1	0.95	0.06	87,87,87,87	1
2	FE	S	201	1/1	0.97	0.08	83,83,83,83	1
2	FE	A	201	1/1	0.97	0.08	85,85,85,85	1
2	FE	B	201	1/1	0.97	0.09	80,80,80,80	1
2	FE	C	201	1/1	0.97	0.08	77,77,77,77	1
2	FE	K	201	1/1	0.98	0.14	79,79,79,79	1
2	FE	N	201	1/1	0.98	0.12	60,60,60,60	1
2	FE	I	201	1/1	0.98	0.07	72,72,72,72	1
2	FE	E	202	1/1	0.98	0.11	53,53,53,53	1
2	FE	D	201	1/1	0.98	0.06	94,94,94,94	0
2	FE	P	201	1/1	0.98	0.12	83,83,83,83	1
2	FE	Q	201	1/1	0.98	0.09	72,72,72,72	1
2	FE	O	201	1/1	0.99	0.11	89,89,89,89	0
2	FE	R	201	1/1	0.99	0.07	37,37,37,37	1
2	FE	M	201	1/1	0.99	0.08	74,74,74,74	1
2	FE	W	201	1/1	0.99	0.10	41,41,41,41	1
2	FE	L	201	1/1	0.99	0.07	37,37,37,37	1
2	FE	A	202	1/1	0.99	0.09	76,76,76,76	1
2	FE	G	202	1/1	0.99	0.08	93,93,93,93	1
2	FE	H	201	1/1	0.99	0.11	53,53,53,53	1
2	FE	V	201	1/1	0.99	0.07	79,79,79,79	1
2	FE	J	201	1/1	0.99	0.05	106,106,106,106	0
2	FE	X	201	1/1	0.99	0.08	83,83,83,83	0
2	FE	F	201	1/1	0.99	0.09	99,99,99,99	0

6.5 Other polymers ⓘ

There are no such residues in this entry.