



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 12:44 PM GMT

PDB ID : 3RGD
Title : Iron loaded frog M ferritin. Short soaking time
Authors : Bertini, I.; Lalli, D.; Mangani, S.; Pozzi, C.; Rosa, C.; Theil, E.C.; Turano, P.
Deposited on : 2011-04-08
Resolution : 2.89 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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

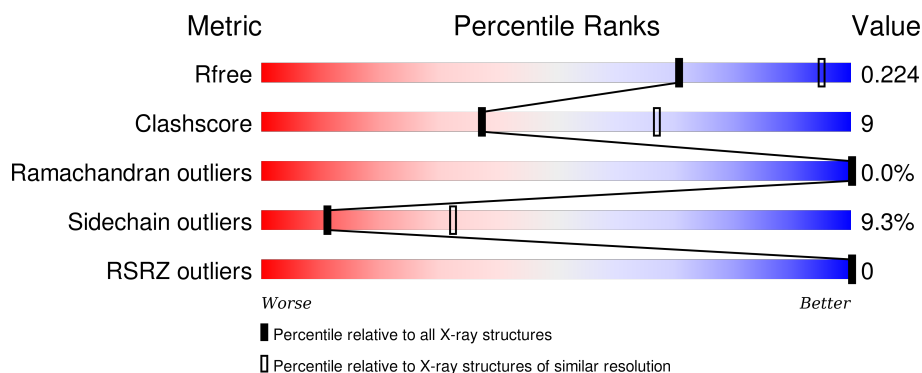
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.89 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.
















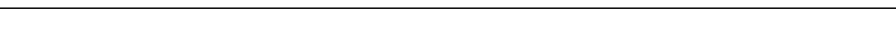





Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

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. 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	176	
1	B	176	
1	C	176	
1	D	176	
1	E	176	

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Mol	Chain	Length	Quality of chain
1	F	176	 77% 18% . .
1	G	176	 77% 17% . .
1	H	176	 76% 16% 5% .
1	I	176	 69% 23% 5% .
1	J	176	 71% 23% . .
1	K	176	 68% 24% 6% .
1	L	176	 70% 25% . .
1	M	176	 76% 20% . .
1	N	176	 73% 21% . .
1	O	176	 75% 19% . .
1	P	176	 71% 24% . .
1	Q	176	 66% 26% 6% .
1	R	176	 74% 21% . .
1	S	176	 73% 21% . .
1	T	176	 74% 20% . .
1	U	176	 78% 17% . .
1	V	176	 72% 24% . .
1	W	176	 75% 20% . .
1	X	176	 77% 18% . .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FE	B	180	-	-	-	X
2	FE	C	180	-	-	-	X
2	FE	C	181	-	-	-	X
2	FE	C	184	-	-	-	X
2	FE	D	181	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FE	F	181	-	-	-	X
2	FE	G	180	-	-	-	X
2	FE	H	181	-	-	-	X
2	FE	J	181	-	-	-	X
2	FE	L	181	-	-	-	X
2	FE	N	180	-	-	-	X
2	FE	N	181	-	-	-	X
2	FE	O	181	-	-	-	X
2	FE	P	180	-	-	-	X
2	FE	Q	181	-	-	-	X
2	FE	R	180	-	-	-	X
2	FE	T	181	-	-	-	X
2	FE	X	181	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 34941 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, middle subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	172	Total	C	N	O	S	0	0	0
			1418	892	247	272	7			
1	B	173	Total	C	N	O	S	0	0	0
			1427	897	248	275	7			
1	C	172	Total	C	N	O	S	0	0	0
			1418	892	247	272	7			
1	D	172	Total	C	N	O	S	0	0	0
			1418	892	247	272	7			
1	E	172	Total	C	N	O	S	0	0	0
			1418	892	247	272	7			
1	F	171	Total	C	N	O	S	0	0	0
			1409	886	245	271	7			
1	G	171	Total	C	N	O	S	0	0	0
			1409	886	245	271	7			
1	H	171	Total	C	N	O	S	0	0	0
			1409	886	245	271	7			
1	I	171	Total	C	N	O	S	0	0	0
			1409	886	245	271	7			
1	J	172	Total	C	N	O	S	0	0	0
			1418	892	247	272	7			
1	K	172	Total	C	N	O	S	0	0	0
			1418	892	247	272	7			
1	L	172	Total	C	N	O	S	0	0	0
			1418	892	247	272	7			
1	M	172	Total	C	N	O	S	0	0	0
			1418	892	247	272	7			
1	N	171	Total	C	N	O	S	0	0	0
			1409	886	245	271	7			
1	O	172	Total	C	N	O	S	0	0	0
			1418	892	247	272	7			
1	P	172	Total	C	N	O	S	0	0	0
			1418	892	247	272	7			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	172	Total	C	N	O	S	0	0	0
			1418	892	247	272	7			
1	R	171	Total	C	N	O	S	0	0	0
			1409	886	245	271	7			
1	S	171	Total	C	N	O	S	0	0	0
			1409	886	245	271	7			
1	T	171	Total	C	N	O	S	0	0	0
			1409	886	245	271	7			
1	U	172	Total	C	N	O	S	0	0	0
			1418	892	247	272	7			
1	V	172	Total	C	N	O	S	0	0	0
			1418	892	247	272	7			
1	W	172	Total	C	N	O	S	0	0	0
			1418	892	247	272	7			
1	X	171	Total	C	N	O	S	0	0	0
			1409	886	245	271	7			

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

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

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	36	Total 36	O 36	0	0
3	B	50	Total 50	O 50	0	0
3	C	32	Total 32	O 32	0	0
3	D	54	Total 54	O 54	0	0
3	E	46	Total 46	O 46	0	0
3	F	32	Total 32	O 32	0	0

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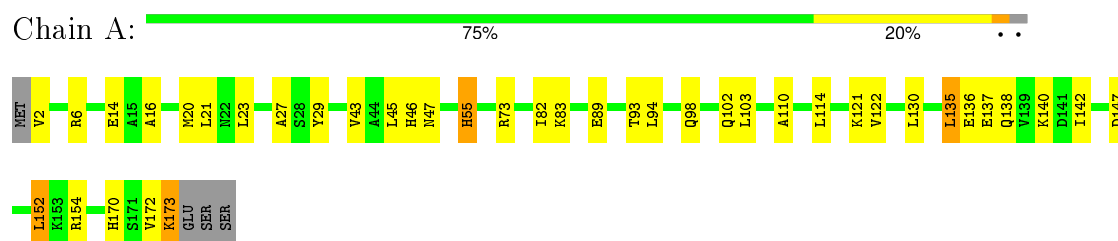
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	29	Total 29	O 29	0	0
3	H	43	Total 43	O 43	0	0
3	I	46	Total 46	O 46	0	0
3	J	36	Total 36	O 36	0	0
3	K	45	Total 45	O 45	0	0
3	L	49	Total 49	O 49	0	0
3	M	30	Total 30	O 30	0	0
3	N	22	Total 22	O 22	0	0
3	O	34	Total 34	O 34	0	0
3	P	48	Total 48	O 48	0	0
3	Q	24	Total 24	O 24	0	0
3	R	36	Total 36	O 36	0	0
3	S	30	Total 30	O 30	0	0
3	T	35	Total 35	O 35	0	0
3	U	32	Total 32	O 32	0	0
3	V	43	Total 43	O 43	0	0
3	W	48	Total 48	O 48	0	0
3	X	39	Total 39	O 39	0	0

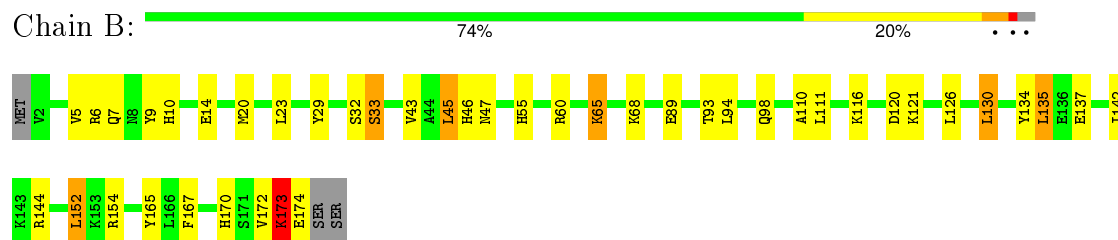
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

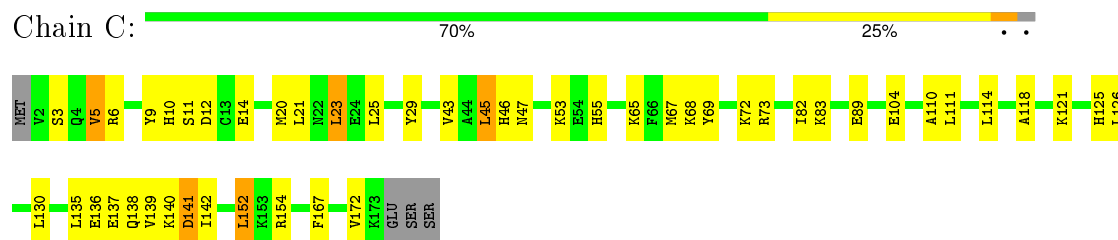
- Molecule 1: Ferritin, middle subunit



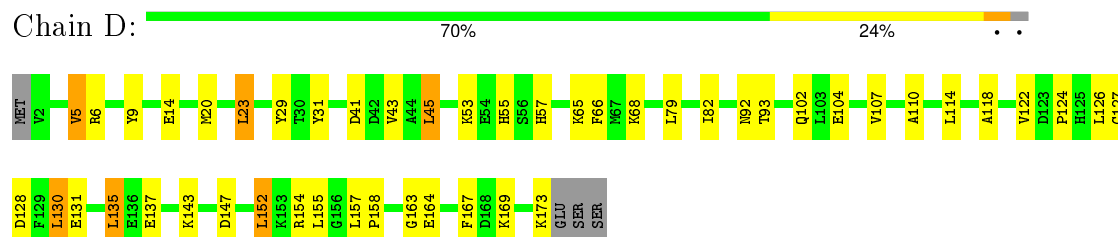
- Molecule 1: Ferritin, middle subunit



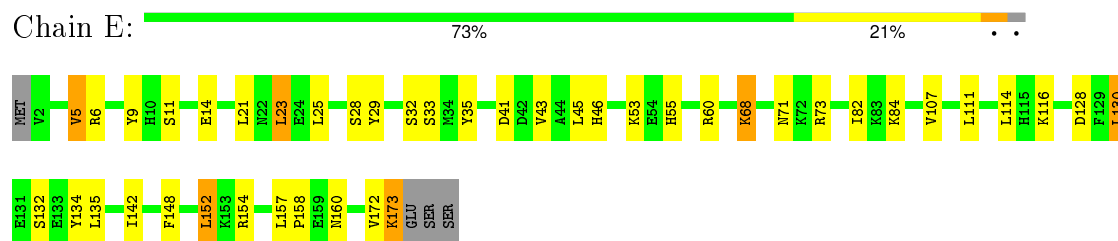
- Molecule 1: Ferritin, middle subunit



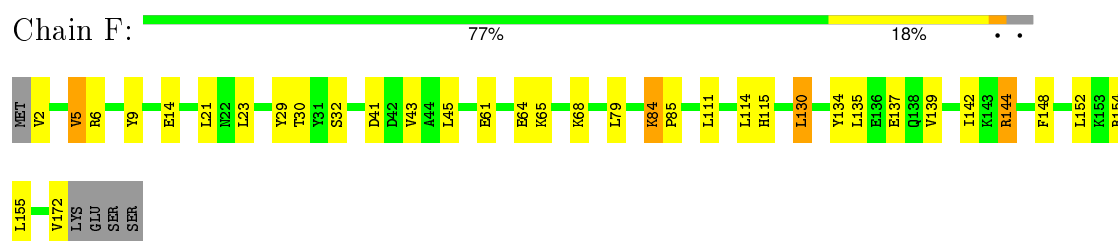
- Molecule 1: Ferritin, middle subunit



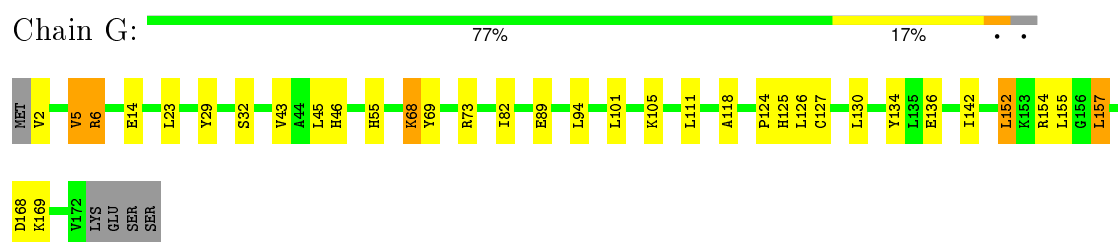
- Molecule 1: Ferritin, middle subunit



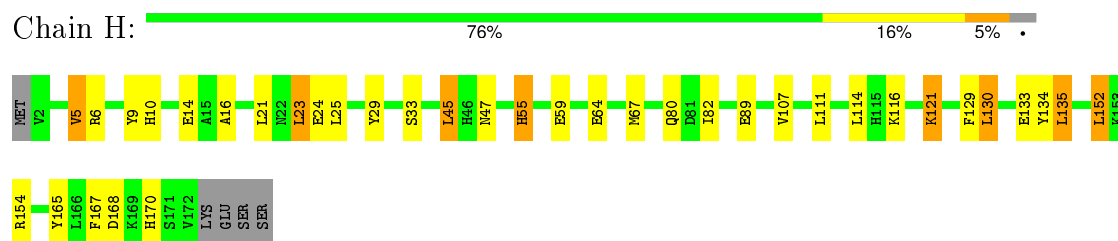
- Molecule 1: Ferritin, middle subunit



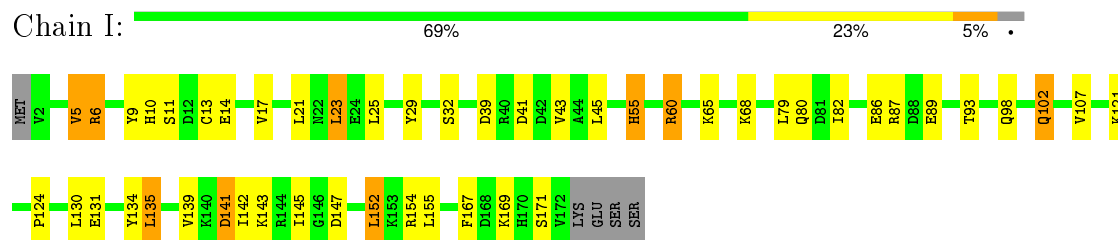
- Molecule 1: Ferritin, middle subunit



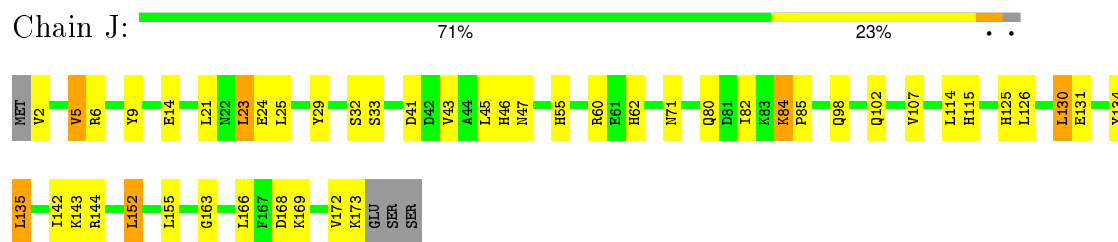
- Molecule 1: Ferritin, middle subunit



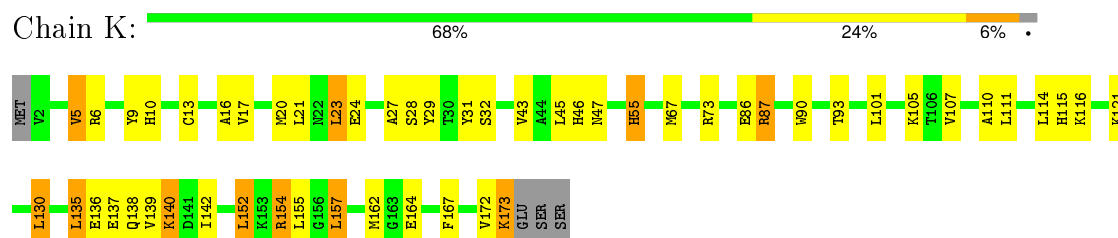
- Molecule 1: Ferritin, middle subunit



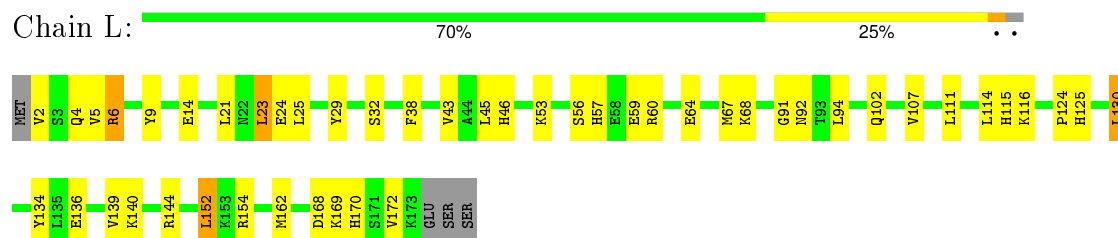
- Molecule 1: Ferritin, middle subunit



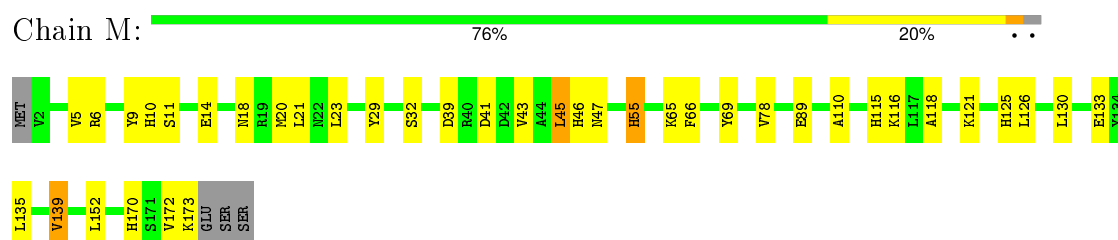
- Molecule 1: Ferritin, middle subunit



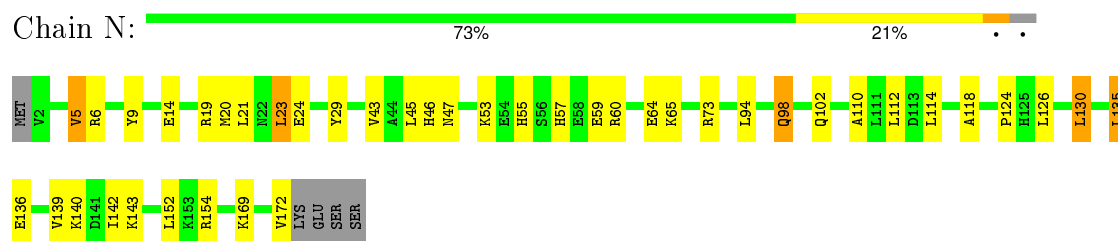
- Molecule 1: Ferritin, middle subunit



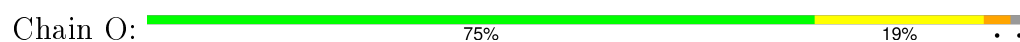
- Molecule 1: Ferritin, middle subunit

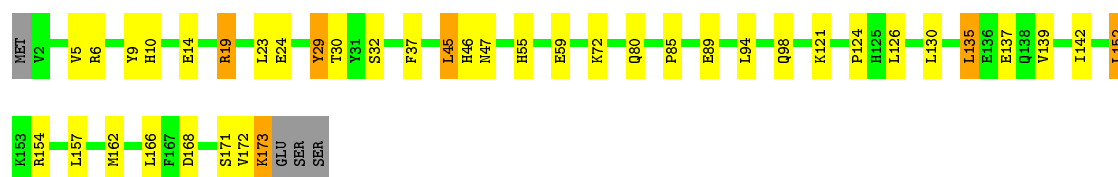


- Molecule 1: Ferritin, middle subunit



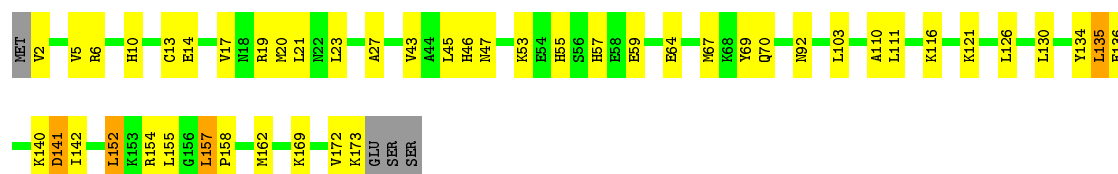
- Molecule 1: Ferritin, middle subunit





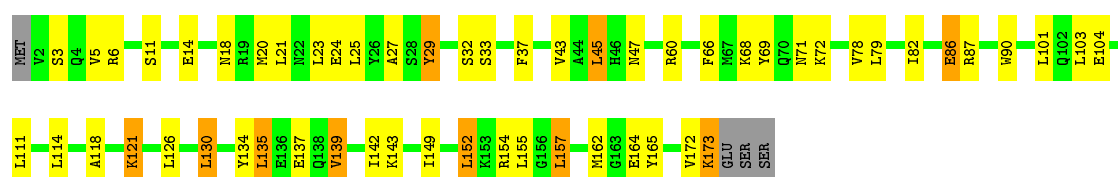
- Molecule 1: Ferritin, middle subunit

Chain P: 71% 24%



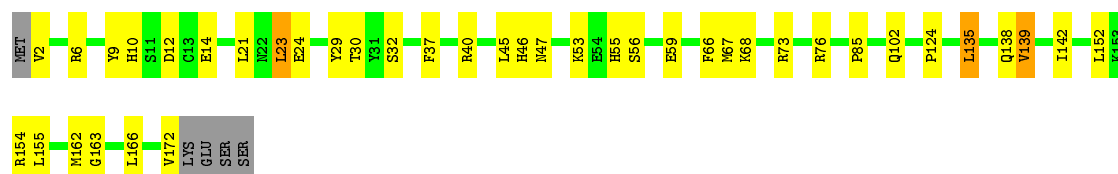
- Molecule 1: Ferritin, middle subunit

Chain Q: 66% 26% 6%



- Molecule 1: Ferritin, middle subunit

Chain R: 74% 21%



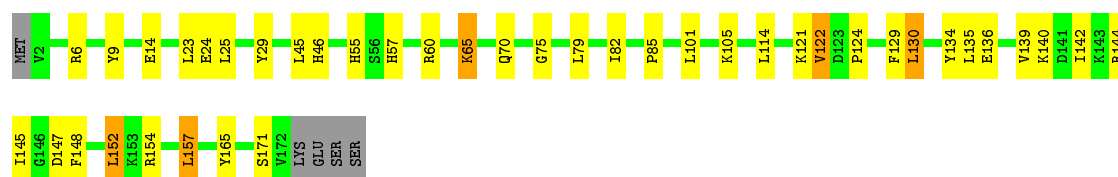
- Molecule 1: Ferritin, middle subunit

Chain S: 73% 21%



- Molecule 1: Ferritin, middle subunit

Chain T: 74% 20%



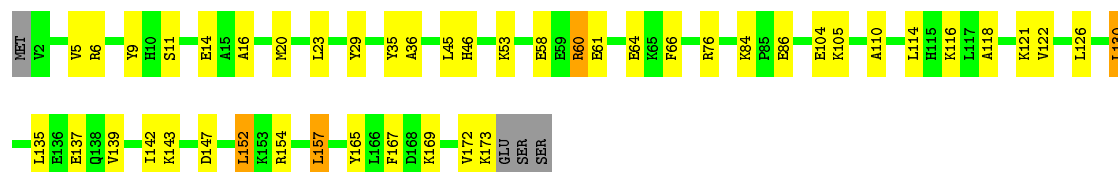
- Molecule 1: Ferritin, middle subunit

Chain U: 78% 17%



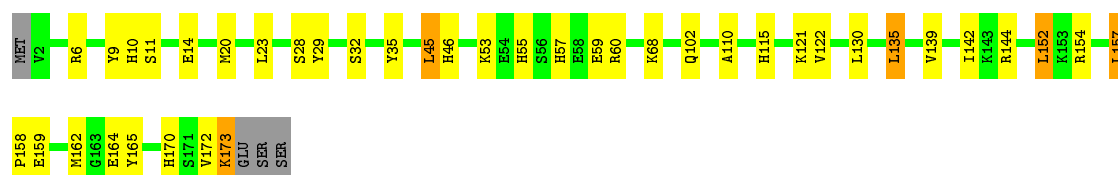
- Molecule 1: Ferritin, middle subunit

Chain V: 72% 24%



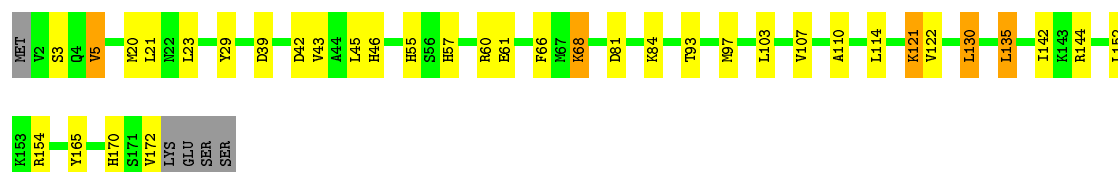
- Molecule 1: Ferritin, middle subunit

Chain W: 75% 20%



- Molecule 1: Ferritin, middle subunit

Chain X: 77% 18%



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	210.74Å 210.74Å 322.04Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.54 – 2.89 48.54 – 2.89	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.54-2.89) 99.7 (48.54-2.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.45 (at 2.91Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.172 , 0.229 0.165 , 0.224	Depositor DCC
R_{free} test set	9239 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	33.2	Xtriage
Anisotropy	0.104	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.5	EDS
Estimated twinning fraction	0.046 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	0 of 184090 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	34941	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.44	0/1446	0.57	0/1944
1	B	0.46	0/1455	0.56	0/1956
1	C	0.42	0/1446	0.56	0/1944
1	D	0.46	0/1446	0.57	0/1944
1	E	0.51	0/1446	0.57	0/1944
1	F	0.44	0/1437	0.54	0/1933
1	G	0.45	0/1437	0.58	0/1933
1	H	0.47	0/1437	0.55	0/1933
1	I	0.45	0/1437	0.60	0/1933
1	J	0.42	0/1446	0.54	0/1944
1	K	0.44	0/1446	0.56	0/1944
1	L	0.54	0/1446	0.60	0/1944
1	M	0.41	0/1446	0.52	0/1944
1	N	0.44	0/1437	0.53	0/1933
1	O	0.46	0/1446	0.59	0/1944
1	P	0.46	0/1446	0.55	0/1944
1	Q	0.44	0/1446	0.53	0/1944
1	R	0.43	0/1437	0.54	0/1933
1	S	0.42	0/1437	0.55	0/1933
1	T	0.46	0/1437	0.55	0/1933
1	U	0.46	0/1446	0.55	0/1944
1	V	0.47	0/1446	0.59	0/1944
1	W	0.45	0/1446	0.57	0/1944
1	X	0.60	0/1437	0.58	0/1933
All	All	0.46	0/34632	0.56	0/46569

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	1418	0	1370	28	0
1	B	1427	0	1376	28	0
1	C	1418	0	1370	31	0
1	D	1418	0	1370	36	0
1	E	1418	0	1370	29	0
1	F	1409	0	1357	25	0
1	G	1409	0	1357	20	0
1	H	1409	0	1357	30	0
1	I	1409	0	1357	31	0
1	J	1418	0	1370	41	0
1	K	1418	0	1370	39	0
1	L	1418	0	1370	30	0
1	M	1418	0	1370	30	0
1	N	1409	0	1357	34	0
1	O	1418	0	1370	24	0
1	P	1418	0	1370	31	0
1	Q	1418	0	1370	45	0
1	R	1409	0	1357	24	0
1	S	1409	0	1357	27	0
1	T	1409	0	1357	29	0
1	U	1418	0	1370	24	0
1	V	1418	0	1370	35	0
1	W	1418	0	1370	30	0
1	X	1409	0	1357	37	0
2	A	2	0	0	0	0
2	B	3	0	0	0	0
2	C	4	0	0	0	0
2	D	4	0	0	0	0
2	E	3	0	0	0	0
2	F	3	0	0	0	0
2	G	2	0	0	0	0
2	H	3	0	0	0	0
2	I	3	0	0	0	0
2	J	3	0	0	0	0
2	K	3	0	0	0	0
2	L	2	0	0	0	0
2	M	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	N	3	0	0	0	0
2	O	3	0	0	0	0
2	P	2	0	0	0	0
2	Q	2	0	0	0	0
2	R	2	0	0	0	0
2	S	2	0	0	0	0
2	T	3	0	0	0	0
2	U	2	0	0	0	0
2	V	2	0	0	0	0
2	W	2	0	0	0	0
2	X	2	0	0	0	0
3	A	36	0	0	4	0
3	B	50	0	0	3	0
3	C	32	0	0	1	0
3	D	54	0	0	5	0
3	E	46	0	0	3	0
3	F	32	0	0	1	0
3	G	29	0	0	1	0
3	H	43	0	0	1	0
3	I	46	0	0	1	0
3	J	36	0	0	6	0
3	K	45	0	0	2	0
3	L	49	0	0	2	0
3	M	30	0	0	3	0
3	N	22	0	0	2	0
3	O	34	0	0	2	0
3	P	48	0	0	1	0
3	Q	24	0	0	1	0
3	R	36	0	0	2	0
3	S	30	0	0	4	0
3	T	35	0	0	3	0
3	U	32	0	0	1	0
3	V	43	0	0	1	0
3	W	48	0	0	4	0
3	X	39	0	0	5	0
All	All	34941	0	32769	624	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 9.

The worst 5 of 624 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:A:142:ILE:HG22	1:X:5:VAL:HG22	1.44	1.00
1:B:5:VAL:HG22	1:V:142:ILE:HG22	1.39	0.99
1:C:142:ILE:HG22	1:S:5:VAL:HG22	1.40	0.99
1:F:144:ARG:HH21	1:F:144:ARG:HG2	1.25	0.97
1:E:142:ILE:HG22	1:V:5:VAL:HG22	1.47	0.95

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	170/176 (97%)	167 (98%)	3 (2%)	0	100	100
1	B	171/176 (97%)	166 (97%)	4 (2%)	1 (1%)	30	67
1	C	170/176 (97%)	165 (97%)	5 (3%)	0	100	100
1	D	170/176 (97%)	165 (97%)	5 (3%)	0	100	100
1	E	170/176 (97%)	166 (98%)	4 (2%)	0	100	100
1	F	169/176 (96%)	163 (96%)	6 (4%)	0	100	100
1	G	169/176 (96%)	162 (96%)	7 (4%)	0	100	100
1	H	169/176 (96%)	166 (98%)	3 (2%)	0	100	100
1	I	169/176 (96%)	162 (96%)	7 (4%)	0	100	100
1	J	170/176 (97%)	166 (98%)	4 (2%)	0	100	100
1	K	170/176 (97%)	164 (96%)	6 (4%)	0	100	100
1	L	170/176 (97%)	164 (96%)	6 (4%)	0	100	100
1	M	170/176 (97%)	162 (95%)	8 (5%)	0	100	100
1	N	169/176 (96%)	163 (96%)	6 (4%)	0	100	100
1	O	170/176 (97%)	161 (95%)	9 (5%)	0	100	100
1	P	170/176 (97%)	161 (95%)	9 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	170/176 (97%)	160 (94%)	10 (6%)	0	100	100
1	R	169/176 (96%)	163 (96%)	6 (4%)	0	100	100
1	S	169/176 (96%)	162 (96%)	7 (4%)	0	100	100
1	T	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	U	170/176 (97%)	164 (96%)	6 (4%)	0	100	100
1	V	170/176 (97%)	166 (98%)	4 (2%)	0	100	100
1	W	170/176 (97%)	165 (97%)	5 (3%)	0	100	100
1	X	169/176 (96%)	164 (97%)	5 (3%)	0	100	100
All	All	4072/4224 (96%)	3932 (97%)	139 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	173	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	153/157 (98%)	139 (91%)	14 (9%)	11	33
1	B	154/157 (98%)	140 (91%)	14 (9%)	12	34
1	C	153/157 (98%)	137 (90%)	16 (10%)	8	25
1	D	153/157 (98%)	139 (91%)	14 (9%)	11	33
1	E	153/157 (98%)	138 (90%)	15 (10%)	10	30
1	F	152/157 (97%)	135 (89%)	17 (11%)	7	22
1	G	152/157 (97%)	137 (90%)	15 (10%)	10	29
1	H	152/157 (97%)	142 (93%)	10 (7%)	21	51
1	I	152/157 (97%)	132 (87%)	20 (13%)	5	14
1	J	153/157 (98%)	138 (90%)	15 (10%)	10	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	153/157 (98%)	136 (89%)	17 (11%)	8	22
1	L	153/157 (98%)	138 (90%)	15 (10%)	10	30
1	M	153/157 (98%)	141 (92%)	12 (8%)	16	41
1	N	152/157 (97%)	140 (92%)	12 (8%)	15	41
1	O	153/157 (98%)	140 (92%)	13 (8%)	13	37
1	P	153/157 (98%)	142 (93%)	11 (7%)	18	46
1	Q	153/157 (98%)	140 (92%)	13 (8%)	13	37
1	R	152/157 (97%)	140 (92%)	12 (8%)	15	41
1	S	152/157 (97%)	137 (90%)	15 (10%)	10	29
1	T	152/157 (97%)	140 (92%)	12 (8%)	15	41
1	U	153/157 (98%)	141 (92%)	12 (8%)	16	41
1	V	153/157 (98%)	135 (88%)	18 (12%)	6	19
1	W	153/157 (98%)	139 (91%)	14 (9%)	11	33
1	X	152/157 (97%)	138 (91%)	14 (9%)	11	33
All	All	3664/3768 (97%)	3324 (91%)	340 (9%)	11	32

5 of 340 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	32	SER
1	M	130	LEU
1	W	29	TYR
1	K	116	LYS
1	L	45	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	80	GLN
1	N	57	HIS
1	W	80	GLN
1	K	115	HIS
1	L	98	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 62 ligands modelled in this entry, 62 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 [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	172/176 (97%)	-0.70	0 100 100	19, 27, 40, 52	0
1	B	173/176 (98%)	-0.63	0 100 100	20, 26, 40, 62	0
1	C	172/176 (97%)	-0.64	0 100 100	24, 31, 42, 54	0
1	D	172/176 (97%)	-0.75	0 100 100	17, 25, 39, 46	0
1	E	172/176 (97%)	-0.69	0 100 100	19, 25, 37, 44	0
1	F	171/176 (97%)	-0.67	0 100 100	20, 27, 39, 47	0
1	G	171/176 (97%)	-0.77	0 100 100	19, 25, 37, 47	0
1	H	171/176 (97%)	-0.72	0 100 100	19, 25, 35, 46	0
1	I	171/176 (97%)	-0.70	0 100 100	18, 24, 35, 46	0
1	J	172/176 (97%)	-0.58	0 100 100	24, 32, 47, 54	0
1	K	172/176 (97%)	-0.70	0 100 100	18, 26, 40, 50	0
1	L	172/176 (97%)	-0.69	0 100 100	16, 25, 39, 47	0
1	M	172/176 (97%)	-0.60	0 100 100	24, 30, 43, 53	0
1	N	171/176 (97%)	-0.63	0 100 100	24, 31, 43, 53	0
1	O	172/176 (97%)	-0.55	0 100 100	22, 29, 43, 55	0
1	P	172/176 (97%)	-0.77	0 100 100	19, 24, 38, 50	0
1	Q	172/176 (97%)	-0.67	0 100 100	22, 30, 42, 49	0
1	R	171/176 (97%)	-0.64	0 100 100	26, 32, 44, 53	0
1	S	171/176 (97%)	-0.61	0 100 100	23, 32, 44, 54	0
1	T	171/176 (97%)	-0.71	0 100 100	17, 26, 40, 43	0
1	U	172/176 (97%)	-0.54	0 100 100	20, 28, 40, 51	0
1	V	172/176 (97%)	-0.73	0 100 100	17, 25, 40, 47	0
1	W	172/176 (97%)	-0.69	0 100 100	19, 26, 39, 48	0
1	X	171/176 (97%)	-0.59	0 100 100	23, 29, 42, 51	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	4120/4224 (97%)	-0.66	0 100 100	16, 28, 41, 62	0

There are no RSRZ outliers to report.

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	FE	P	180	1/1	0.96	0.20	65.28	50,50,50,50	0
2	FE	G	180	1/1	0.96	0.23	9.50	52,52,52,52	0
2	FE	B	180	1/1	0.96	0.18	8.67	56,56,56,56	0
2	FE	C	181	1/1	0.98	0.28	8.45	56,56,56,56	0
2	FE	D	181	1/1	0.89	0.30	5.55	63,63,63,63	0
2	FE	N	181	1/1	0.95	0.22	3.85	73,73,73,73	0
2	FE	R	180	1/1	0.96	0.17	3.67	49,49,49,49	0
2	FE	H	181	1/1	0.93	0.20	3.35	56,56,56,56	0
2	FE	L	181	1/1	0.96	0.21	3.30	59,59,59,59	0
2	FE	N	180	1/1	0.97	0.18	3.06	60,60,60,60	0
2	FE	J	181	1/1	0.91	0.18	3.04	67,67,67,67	0
2	FE	F	181	1/1	0.82	0.20	2.60	59,59,59,59	0
2	FE	O	181	1/1	0.89	0.21	2.45	72,72,72,72	0
2	FE	Q	181	1/1	0.81	0.19	2.43	69,69,69,69	0
2	FE	C	180	1/1	0.96	0.18	2.20	54,54,54,54	0
2	FE	C	184	1/1	0.96	0.18	2.07	50,50,50,50	0
2	FE	X	181	1/1	0.95	0.17	2.07	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	FE	T	181	1/1	0.97	0.17	2.04	59,59,59,59	0
2	FE	W	180	1/1	0.97	0.15	1.92	40,40,40,40	0
2	FE	U	181	1/1	0.82	0.19	1.82	61,61,61,61	0
2	FE	A	180	1/1	0.97	0.17	1.81	43,43,43,43	0
2	FE	P	181	1/1	0.86	0.17	1.53	68,68,68,68	0
2	FE	O	184	1/1	0.99	0.17	1.51	46,46,46,46	0
2	FE	X	180	1/1	0.96	0.17	1.32	51,51,51,51	0
2	FE	K	180	1/1	0.98	0.15	1.31	48,48,48,48	0
2	FE	I	181	1/1	0.91	0.16	0.96	49,49,49,49	0
2	FE	K	181	1/1	0.94	0.17	0.90	53,53,53,53	0
2	FE	I	180	1/1	0.97	0.16	0.83	42,42,42,42	0
2	FE	E	181	1/1	0.93	0.15	0.82	60,60,60,60	0
2	FE	M	181	1/1	0.94	0.19	0.79	66,66,66,66	0
2	FE	U	180	1/1	0.97	0.15	0.62	52,52,52,52	0
2	FE	F	180	1/1	0.97	0.17	0.57	48,48,48,48	0
2	FE	G	181	1/1	0.87	0.16	0.43	64,64,64,64	0
2	FE	I	184	1/1	0.99	0.14	0.27	39,39,39,39	0
2	FE	V	180	1/1	0.99	0.13	0.13	49,49,49,49	0
2	FE	A	181	1/1	0.95	0.15	-0.13	56,56,56,56	0
2	FE	R	181	1/1	0.86	0.13	-0.20	71,71,71,71	0
2	FE	Q	180	1/1	0.97	0.12	-0.22	47,47,47,47	0
2	FE	E	180	1/1	0.97	0.12	-0.39	38,38,38,38	0
2	FE	B	181	1/1	0.95	0.12	-0.42	62,62,62,62	0
2	FE	M	180	1/1	0.96	0.13	-0.56	48,48,48,48	0
2	FE	V	181	1/1	0.94	0.13	-0.64	62,62,62,62	0
2	FE	D	180	1/1	0.99	0.12	-0.67	37,37,37,37	0
2	FE	L	180	1/1	0.99	0.11	-0.87	35,35,35,35	0
2	FE	D	184	1/1	0.98	0.11	-1.25	44,44,44,44	0
2	FE	H	180	1/1	0.97	0.11	-1.37	40,40,40,40	0
2	FE	W	181	1/1	0.94	0.11	-1.41	55,55,55,55	0
2	FE	S	180	1/1	0.95	0.09	-1.64	53,53,53,53	0
2	FE	O	180	1/1	0.96	0.11	-1.86	47,47,47,47	0
2	FE	S	181	1/1	0.95	0.09	-1.98	64,64,64,64	0
2	FE	N	184	1/1	0.98	0.11	-2.16	42,42,42,42	0
2	FE	T	180	1/1	0.94	0.10	-3.06	39,39,39,39	0
2	FE	E	184	1/1	0.98	0.11	-4.07	41,41,41,41	0
2	FE	T	183	1/1	0.92	0.19	-	56,56,56,56	0
2	FE	J	180	1/1	0.99	0.15	-	54,54,54,54	0
2	FE	B	183	1/1	0.80	0.14	-	59,59,59,59	0
2	FE	F	183	1/1	0.86	0.17	-	52,52,52,52	0
2	FE	C	183	1/1	0.88	0.20	-	61,61,61,61	0
2	FE	D	183	1/1	0.57	0.15	-	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	FE	H	183	1/1	0.92	0.14	-	56,56,56,56	0
2	FE	J	183	1/1	0.86	0.13	-	60,60,60,60	0
2	FE	K	183	1/1	0.70	0.12	-	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.