



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 1, 2025 – 12:19 PM JST

PDB ID : 8WIE
Title : Peptide 10-1/FTH1-1 Complex
Authors : Fu, D.; Wang, M.; Guo, Y.
Deposited on : 2023-09-24
Resolution : 2.30 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.2

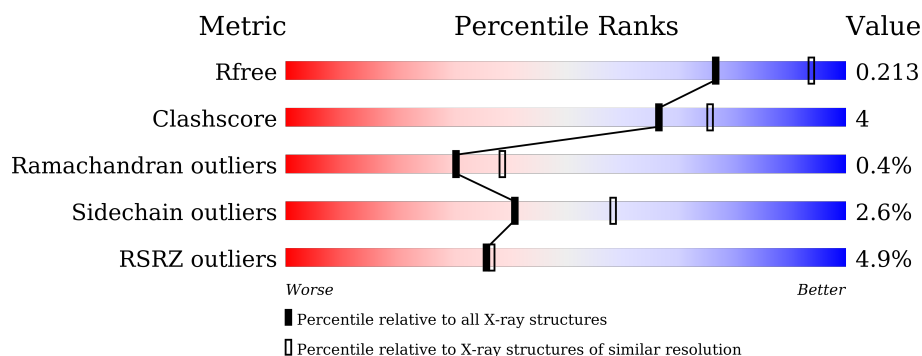
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	164625	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

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 $\leq 5\%$. 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	200	<div> <div>6%</div> <div> <div></div> <div>86%</div> <div>8%</div> <div>5%</div> </div> </div>
1	B	200	<div> <div>5%</div> <div> <div></div> <div>86%</div> <div>7%</div> <div>6%</div> </div> </div>
1	C	200	<div> <div>4%</div> <div> <div></div> <div>86%</div> <div>8%</div> <div>5%</div> </div> </div>
1	D	200	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>10%</div> <div>6%</div> </div> </div>
1	E	200	<div> <div>4%</div> <div> <div></div> <div>82%</div> <div>11%</div> <div>6%</div> </div> </div>
1	F	200	<div> <div>4%</div> <div> <div></div> <div>83%</div> <div>10%</div> <div>6%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9759 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 Peptide 10-1,Ferritin heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	190	Total	C	N	O	S	0	0	0
			1554	978	271	298	7			
1	D	189	Total	C	N	O	S	0	0	0
			1550	976	270	297	7			
1	E	188	Total	C	N	O	S	0	0	0
			1546	974	269	296	7			
1	F	187	Total	C	N	O	S	0	0	0
			1537	968	267	295	7			
1	A	190	Total	C	N	O	S	0	0	0
			1554	978	271	298	7			
1	B	188	Total	C	N	O	S	0	0	0
			1546	974	269	296	7			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	15	ARG	GLN	engineered mutation	UNP P02794
C	23	LYS	ARG	engineered mutation	UNP P02794
C	26	THR	ASN	engineered mutation	UNP P02794
C	87	GLN	LYS	engineered mutation	UNP P02794
C	110	GLU	ASN	engineered mutation	UNP P02794
C	114	GLU	SER	engineered mutation	UNP P02794
C	117	ASN	GLU	engineered mutation	UNP P02794
D	15	ARG	GLN	engineered mutation	UNP P02794
D	23	LYS	ARG	engineered mutation	UNP P02794
D	26	THR	ASN	engineered mutation	UNP P02794
D	87	GLN	LYS	engineered mutation	UNP P02794
D	110	GLU	ASN	engineered mutation	UNP P02794
D	114	GLU	SER	engineered mutation	UNP P02794
D	117	ASN	GLU	engineered mutation	UNP P02794
E	15	ARG	GLN	engineered mutation	UNP P02794
E	23	LYS	ARG	engineered mutation	UNP P02794
E	26	THR	ASN	engineered mutation	UNP P02794

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Chain	Residue	Modelled	Actual	Comment	Reference
E	87	GLN	LYS	engineered mutation	UNP P02794
E	110	GLU	ASN	engineered mutation	UNP P02794
E	114	GLU	SER	engineered mutation	UNP P02794
E	117	ASN	GLU	engineered mutation	UNP P02794
F	15	ARG	GLN	engineered mutation	UNP P02794
F	23	LYS	ARG	engineered mutation	UNP P02794
F	26	THR	ASN	engineered mutation	UNP P02794
F	87	GLN	LYS	engineered mutation	UNP P02794
F	110	GLU	ASN	engineered mutation	UNP P02794
F	114	GLU	SER	engineered mutation	UNP P02794
F	117	ASN	GLU	engineered mutation	UNP P02794
A	15	ARG	GLN	engineered mutation	UNP P02794
A	23	LYS	ARG	engineered mutation	UNP P02794
A	26	THR	ASN	engineered mutation	UNP P02794
A	87	GLN	LYS	engineered mutation	UNP P02794
A	110	GLU	ASN	engineered mutation	UNP P02794
A	114	GLU	SER	engineered mutation	UNP P02794
A	117	ASN	GLU	engineered mutation	UNP P02794
B	15	ARG	GLN	engineered mutation	UNP P02794
B	23	LYS	ARG	engineered mutation	UNP P02794
B	26	THR	ASN	engineered mutation	UNP P02794
B	87	GLN	LYS	engineered mutation	UNP P02794
B	110	GLU	ASN	engineered mutation	UNP P02794
B	114	GLU	SER	engineered mutation	UNP P02794
B	117	ASN	GLU	engineered mutation	UNP P02794

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total Fe 1 1	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total Ca 1 1	0	0


- Molecule 4 is water.

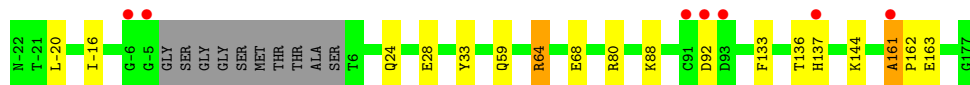
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	82	Total 82	O 82	0	0
4	D	70	Total 70	O 70	0	0
4	E	73	Total 73	O 73	0	0
4	F	69	Total 69	O 69	0	0
4	A	87	Total 87	O 87	0	0
4	B	89	Total 89	O 89	0	0

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.

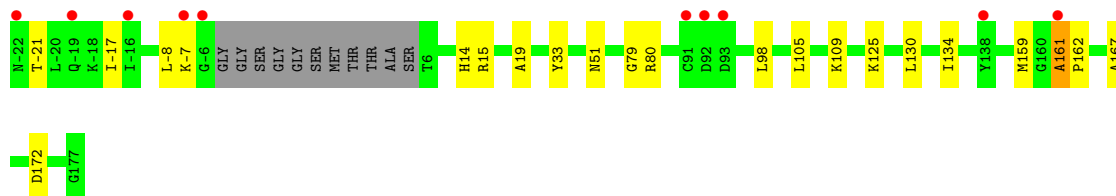
- Molecule 1: Peptide 10-1,Ferritin heavy chain

Chain C: 




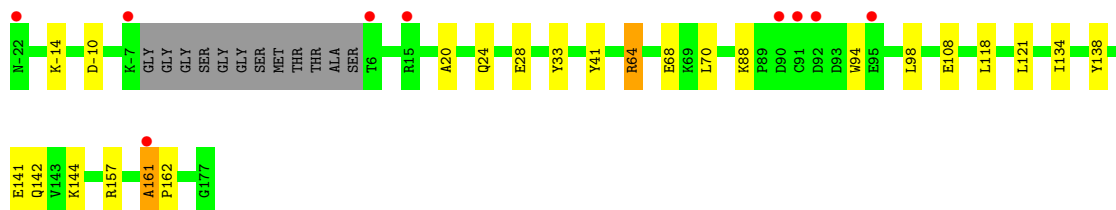
- Molecule 1: Peptide 10-1,Ferritin heavy chain

Chain D: 




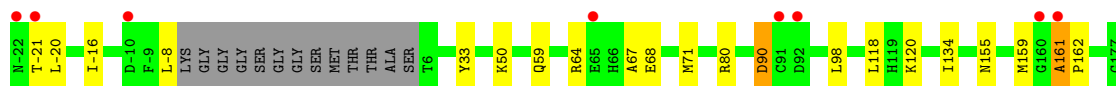
- Molecule 1: Peptide 10-1,Ferritin heavy chain

Chain E: 



- Molecule 1: Peptide 10-1,Ferritin heavy chain

Chain F: 



- Molecule 1: Peptide 10-1,Ferritin heavy chain

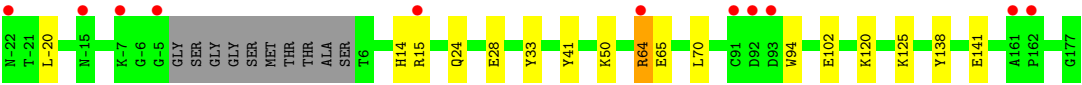
Chain A:

6%

86%

8%

5%



● Molecule 1: Peptide 10-1,Ferritin heavy chain

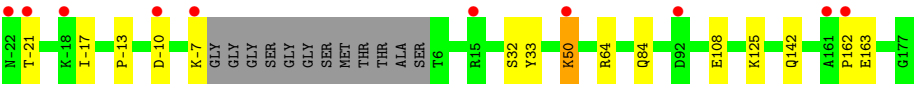
Chain B:

5%

86%

7%

6%



4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	142.83Å 142.83Å 183.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.67 – 2.30 33.67 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.6 (33.67-2.30) 99.6 (33.67-2.30)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.13 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.194 , 0.212 0.196 , 0.213	Depositor DCC
R_{free} test set	79525 reflections (2.45%)	wwPDB-VP
Wilson B-factor (Å ²)	31.0	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 39.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	0.005 for -h,k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9759	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.93% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, 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	0/1584	0.46	0/2131
1	B	0.25	0/1576	0.43	0/2121
1	C	0.28	0/1584	0.49	0/2131
1	D	0.25	0/1580	0.43	0/2126
1	E	0.25	0/1576	0.45	0/2121
1	F	0.25	0/1567	0.43	0/2110
All	All	0.26	0/9467	0.45	0/12740

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 [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	1554	0	1513	9	0
1	B	1546	0	1507	7	0
1	C	1554	0	1513	10	0
1	D	1550	0	1510	14	0
1	E	1546	0	1507	16	0
1	F	1537	0	1494	13	0
2	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	1	0	0	0	0
4	A	87	0	0	1	0
4	B	89	0	0	0	0
4	C	82	0	0	0	0
4	D	70	0	0	2	0
4	E	73	0	0	0	0
4	F	69	0	0	0	0
All	All	9759	0	9044	65	0

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

All (65) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:98:LEU:HD23	1:E:162:PRO:HD3	1.69	0.74
1:D:98:LEU:HD23	1:D:162:PRO:HD3	1.71	0.72
1:F:98:LEU:HD23	1:F:162:PRO:HD3	1.71	0.72
1:E:161:ALA:HB1	1:E:162:PRO:HD2	1.73	0.71
1:C:64:ARG:NH1	1:C:68:GLU:OE2	2.20	0.70
1:D:161:ALA:HB1	1:D:162:PRO:HD2	1.75	0.69
1:E:64:ARG:HD2	1:F:64:ARG:HH21	1.59	0.68
1:E:118:LEU:HG	1:E:134:ILE:HD11	1.78	0.66
1:B:50:LYS:HD2	1:B:50:LYS:H	1.60	0.66
1:F:161:ALA:HB1	1:F:162:PRO:HD2	1.82	0.62
1:D:-8:LEU:HG	1:D:19:ALA:HB2	1.85	0.58
1:E:-14:LYS:NZ	1:E:-10:ASP:OD2	2.40	0.54
1:A:102:GLU:HG2	4:A:285:HOH:O	2.07	0.54
1:B:162:PRO:HG2	1:B:163:GLU:OE2	2.08	0.53
1:D:125:LYS:NZ	4:D:301:HOH:O	2.33	0.52
1:C:136:THR:OG1	1:C:137:HIS:CD2	2.63	0.52
1:C:133:PHE:O	1:C:137:HIS:HB2	2.10	0.51
1:F:155:ASN:O	1:F:159:MET:HG3	2.12	0.50
1:C:161:ALA:HB1	1:C:162:PRO:HD3	1.93	0.50
1:B:-13:PRO:HD2	1:B:-10:ASP:OD2	2.12	0.49
1:D:105:LEU:O	1:D:109:LYS:HG2	2.12	0.49
1:B:108:GLU:HG3	1:B:142:GLN:NE2	2.28	0.48
1:D:14:HIS:CD2	1:D:125:LYS:HD2	2.49	0.48
1:F:67:ALA:O	1:F:71:MET:HG3	2.13	0.48
1:D:-7:LYS:HE3	4:D:362:HOH:O	2.13	0.48
1:F:-21:THR:HG23	1:F:90:ASP:OD2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:80:ARG:HA	1:D:80:ARG:HD3	1.63	0.47
1:E:108:GLU:OE1	1:E:142:GLN:NE2	2.46	0.47
1:F:80:ARG:HD3	1:F:80:ARG:HA	1.58	0.47
1:E:141:GLU:OE2	1:E:144:LYS:NZ	2.46	0.47
1:E:41:TYR:CZ	1:E:94:TRP:O	2.68	0.46
1:B:-21:THR:O	1:B:-17:ILE:HG13	2.14	0.46
1:D:79:GLY:O	1:D:80:ARG:NH1	2.49	0.46
1:F:-20:LEU:O	1:F:-16:ILE:HG13	2.16	0.46
1:D:161:ALA:HB1	1:D:162:PRO:CD	2.45	0.46
1:C:161:ALA:HB1	1:C:162:PRO:CD	2.46	0.46
1:C:144:LYS:HB2	1:C:144:LYS:HE3	1.73	0.45
1:E:98:LEU:HD21	1:E:157:ARG:HG2	1.99	0.45
1:F:161:ALA:HB1	1:F:162:PRO:CD	2.46	0.44
1:C:-20:LEU:O	1:C:-16:ILE:HG13	2.18	0.44
1:E:64:ARG:NH1	1:E:68:GLU:OE2	2.51	0.44
1:D:-21:THR:O	1:D:-17:ILE:HG13	2.18	0.43
1:C:24:GLN:O	1:C:28:GLU:HG2	2.17	0.43
1:A:15:ARG:HA	1:A:15:ARG:HD3	1.79	0.43
1:A:70:LEU:HG	1:A:138:TYR:OH	2.18	0.43
1:E:70:LEU:HG	1:E:138:TYR:OH	2.19	0.43
1:F:118:LEU:HG	1:F:134:ILE:HD11	2.01	0.43
1:E:161:ALA:HB1	1:E:162:PRO:CD	2.46	0.42
1:A:24:GLN:O	1:A:28:GLU:HG2	2.19	0.42
1:A:64:ARG:NH2	1:B:32:SER:OG	2.45	0.42
1:C:80:ARG:HA	1:C:80:ARG:HE	1.84	0.42
1:A:41:TYR:CZ	1:A:94:TRP:O	2.73	0.42
1:E:20:ALA:HB1	1:E:118:LEU:HD13	2.01	0.42
1:E:24:GLN:O	1:E:28:GLU:HG2	2.20	0.42
1:E:64:ARG:HD2	1:F:64:ARG:NH2	2.32	0.41
1:D:51:ASN:HB2	1:D:172:ASP:OD2	2.19	0.41
1:A:64:ARG:HG2	1:B:64:ARG:NH1	2.35	0.41
1:A:141:GLU:OE1	1:A:141:GLU:N	2.51	0.41
1:A:14:HIS:CD2	1:A:125:LYS:HE3	2.55	0.41
1:C:88:LYS:HE3	1:C:88:LYS:HB2	1.71	0.41
1:F:64:ARG:HD3	1:F:68:GLU:OE2	2.21	0.41
1:D:130:LEU:O	1:D:134:ILE:HG13	2.20	0.40
1:D:159:MET:HB3	1:D:167:ALA:HB1	2.02	0.40
1:F:-8:LEU:HD23	1:F:-8:LEU:HA	1.88	0.40
1:E:88:LYS:HE3	1:E:88:LYS:HB2	1.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	186/200 (93%)	184 (99%)	2 (1%)	0	100	100
1	B	184/200 (92%)	181 (98%)	3 (2%)	0	100	100
1	C	186/200 (93%)	182 (98%)	3 (2%)	1 (0%)	25	32
1	D	185/200 (92%)	180 (97%)	4 (2%)	1 (0%)	25	32
1	E	184/200 (92%)	180 (98%)	3 (2%)	1 (0%)	25	32
1	F	183/200 (92%)	178 (97%)	4 (2%)	1 (0%)	25	32
All	All	1108/1200 (92%)	1085 (98%)	19 (2%)	4 (0%)	30	39

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	161	ALA
1	D	161	ALA
1	E	161	ALA
1	F	161	ALA

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	169/175 (97%)	163 (96%)	6 (4%)	30	44
1	B	169/175 (97%)	164 (97%)	5 (3%)	36	52
1	C	169/175 (97%)	164 (97%)	5 (3%)	36	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	169/175 (97%)	167 (99%)	2 (1%)	67	81
1	E	169/175 (97%)	166 (98%)	3 (2%)	54	71
1	F	168/175 (96%)	163 (97%)	5 (3%)	36	52
All	All	1013/1050 (96%)	987 (97%)	26 (3%)	41	58

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	33	TYR
1	C	59	GLN
1	C	64	ARG
1	C	92	ASP
1	C	163	GLU
1	D	15	ARG
1	D	33	TYR
1	E	33	TYR
1	E	64	ARG
1	E	121	LEU
1	F	33	TYR
1	F	50	LYS
1	F	59	GLN
1	F	90	ASP
1	F	120	LYS
1	A	-20	LEU
1	A	33	TYR
1	A	50	LYS
1	A	64	ARG
1	A	65	GLU
1	A	120	LYS
1	B	-7	LYS
1	B	33	TYR
1	B	50	LYS
1	B	84	GLN
1	B	125	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	137	HIS
1	D	-19	GLN

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Mol	Chain	Res	Type
1	D	-15	ASN
1	D	140	ASN
1	E	84	GLN
1	A	-15	ASN
1	A	84	GLN
1	B	74	GLN
1	B	87	GLN
1	B	137	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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 ⓘ

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	190/200 (95%)	0.19	11 (5%) 30 32	21, 30, 50, 69	0
1	B	188/200 (94%)	0.09	10 (5%) 33 34	20, 29, 50, 61	0
1	C	190/200 (95%)	0.22	7 (3%) 45 47	24, 31, 51, 63	0
1	D	189/200 (94%)	0.23	10 (5%) 33 34	24, 33, 54, 67	0
1	E	188/200 (94%)	0.28	9 (4%) 36 37	24, 33, 54, 64	0
1	F	187/200 (93%)	0.11	8 (4%) 40 41	24, 32, 52, 65	0
All	All	1132/1200 (94%)	0.18	55 (4%) 36 37	20, 31, 52, 69	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	161	ALA	6.3
1	A	161	ALA	5.6
1	D	161	ALA	5.6
1	F	161	ALA	5.5
1	C	161	ALA	5.3
1	E	161	ALA	5.1
1	B	162	PRO	5.1
1	B	92	ASP	4.3
1	A	92	ASP	4.2
1	D	-7	LYS	4.0
1	C	91	CYS	4.0
1	A	162	PRO	3.7
1	C	92	ASP	3.7
1	D	-6	GLY	3.6
1	E	92	ASP	3.4
1	A	91	CYS	3.3
1	C	-5	GLY	3.3
1	E	-22	ASN	3.3
1	B	-7	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
1	F	92	ASP	3.2
1	A	-22	ASN	3.2
1	B	-21	THR	3.1
1	E	-7	LYS	3.1
1	F	-22	ASN	3.0
1	C	93	ASP	2.9
1	D	-19	GLN	2.8
1	E	6	THR	2.8
1	D	-22	ASN	2.8
1	E	95	GLU	2.7
1	F	91	CYS	2.6
1	A	64	ARG	2.5
1	B	-18	LYS	2.5
1	D	93	ASP	2.5
1	A	15	ARG	2.4
1	A	-15	ASN	2.4
1	F	65	GLU	2.3
1	C	137	HIS	2.3
1	E	91	CYS	2.3
1	C	-6	GLY	2.3
1	D	91	CYS	2.3
1	B	15	ARG	2.3
1	B	-10	ASP	2.2
1	F	-10	ASP	2.2
1	E	90	ASP	2.2
1	B	-22	ASN	2.1
1	D	-16	ILE	2.1
1	D	138	TYR	2.1
1	D	92	ASP	2.1
1	A	-5	GLY	2.1
1	A	-7	LYS	2.1
1	B	50	LYS	2.1
1	A	93	ASP	2.1
1	F	-21	THR	2.1
1	E	15	ARG	2.0
1	F	160	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

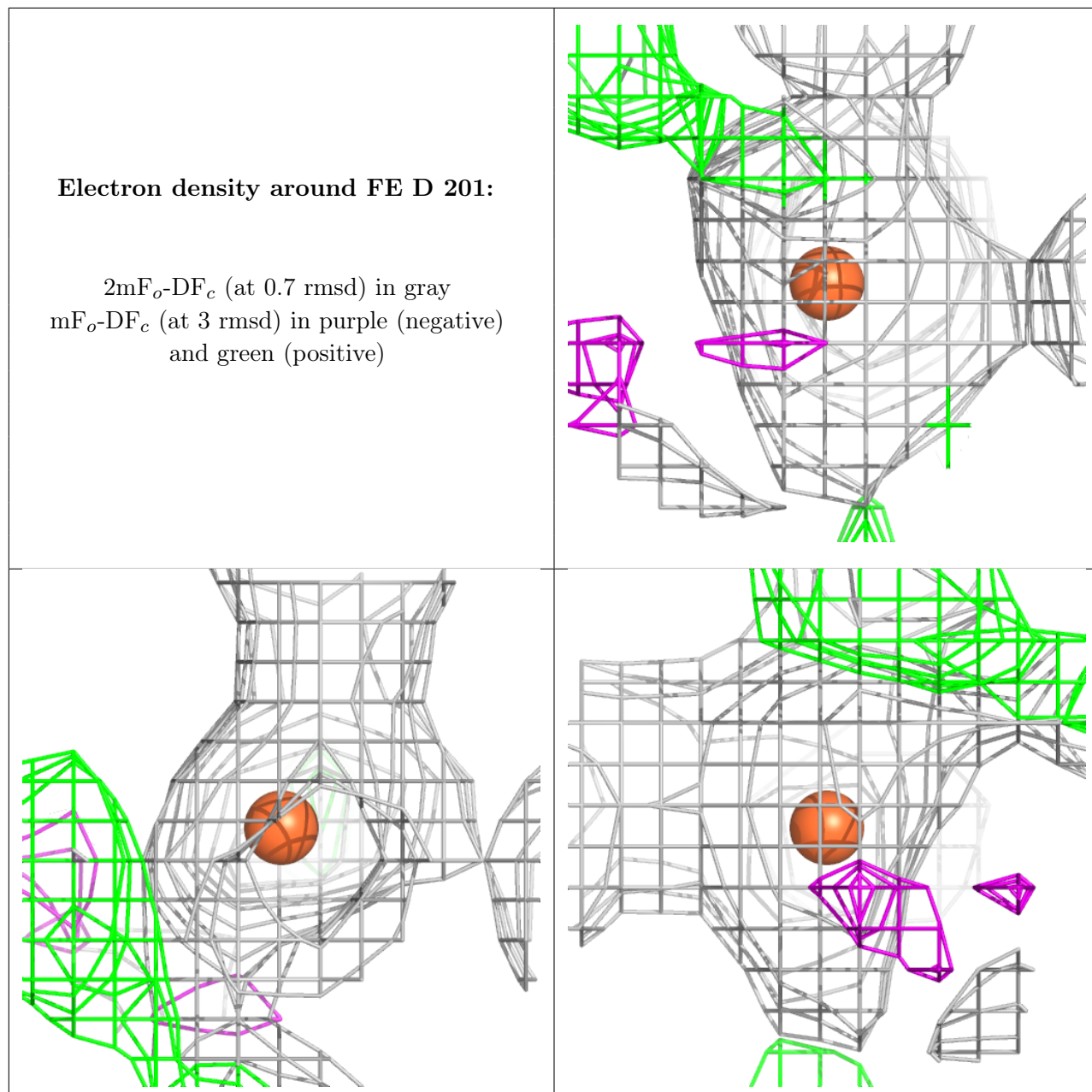
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	FE	D	201	1/1	0.73	0.20	110,110,110,110	0
3	CA	D	202	1/1	0.97	0.07	40,40,40,40	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

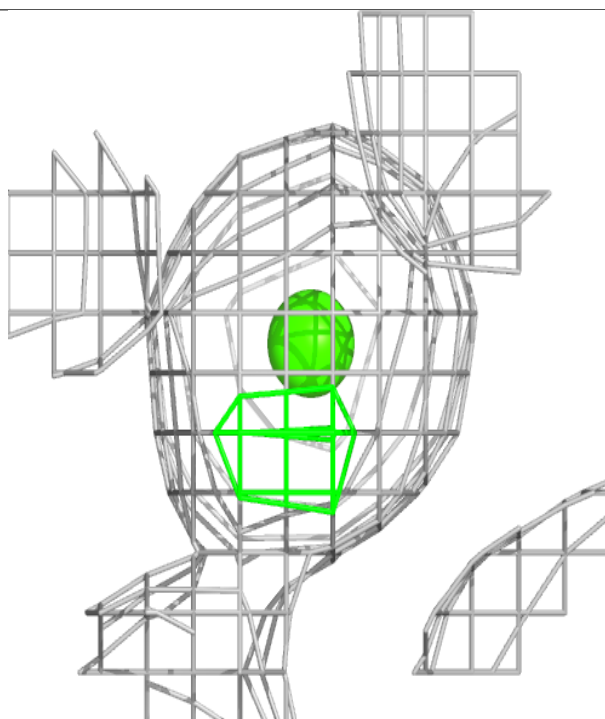
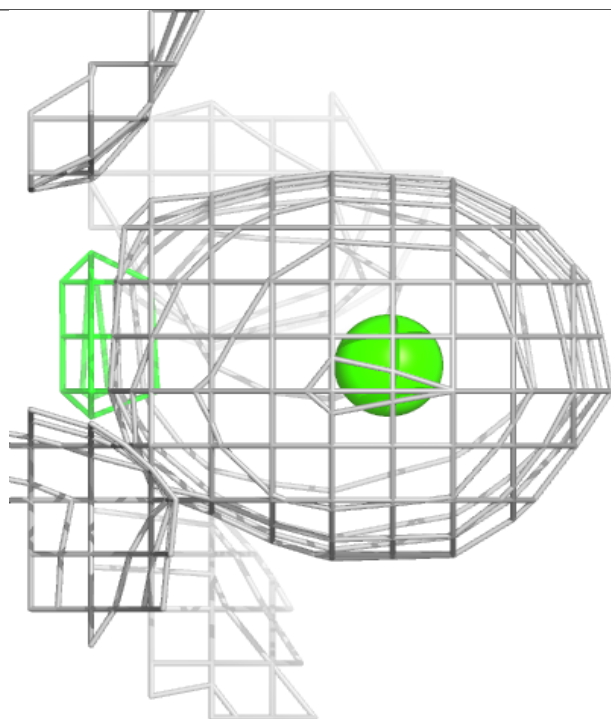
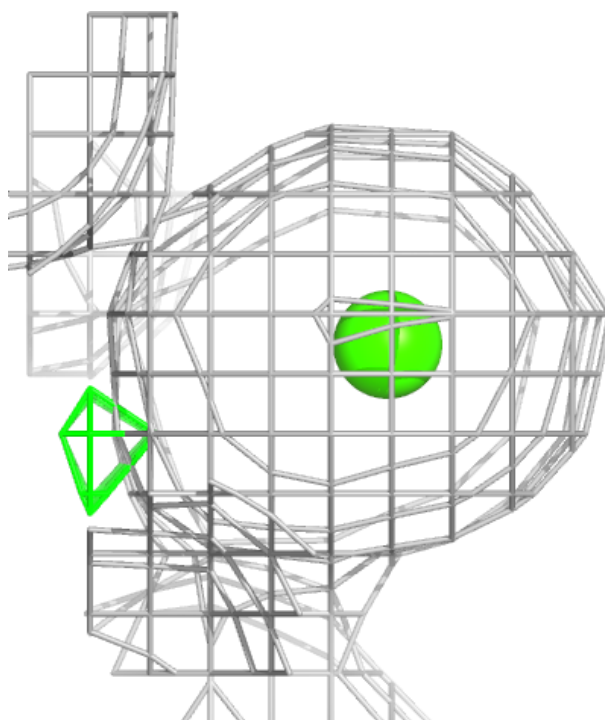
Electron density around FE D 201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around CA D 202:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers ⓘ

There are no such residues in this entry.