



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 12, 2022 – 02:21 PM JST

PDB ID : 7EYR
Title : Fe(II)/(alpha)ketoglutarate-dependent dioxygenase SptF apo
Authors : Tao, H.; Mori, T.; Abe, I.
Deposited on : 2021-06-01
Resolution : 2.12 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 : 2.27
buster-report : 1.1.7 (2018)
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) : 2.27

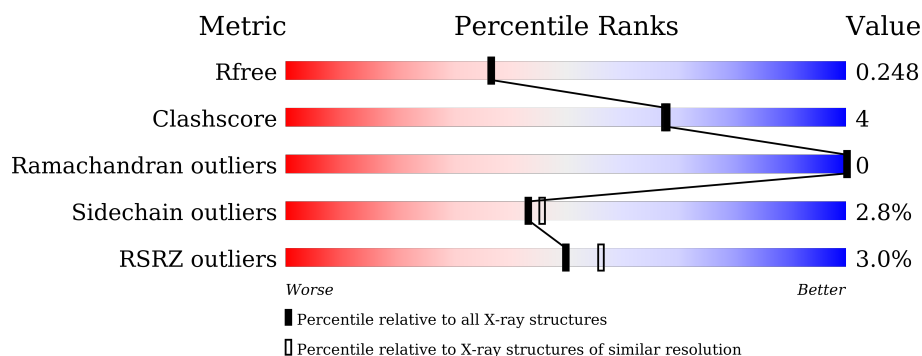
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION





The reported resolution of this entry is 2.12 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	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705 (2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)
RSRZ outliers	127900	6112 (2.14-2.10)

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	296	
1	B	296	
1	C	296	
1	D	296	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9264 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 2-oxoglutarate/Fe(II)-dependent dioxygenase SptF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	279	Total	C	N	O	S	0	1	0
			2237	1417	400	405	15			
1	A	279	Total	C	N	O	S	0	0	0
			2246	1419	398	414	15			
1	B	279	Total	C	N	O	S	0	0	0
			2211	1400	387	409	15			
1	D	262	Total	C	N	O	S	0	0	0
			2075	1316	359	385	15			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	3	MET	-	initiating methionine	UNP A0A6J4CX17
C	286	LYS	-	expression tag	UNP A0A6J4CX17
C	287	LEU	-	expression tag	UNP A0A6J4CX17
C	288	ALA	-	expression tag	UNP A0A6J4CX17
C	289	ALA	-	expression tag	UNP A0A6J4CX17
C	290	ALA	-	expression tag	UNP A0A6J4CX17
C	291	LEU	-	expression tag	UNP A0A6J4CX17
C	292	GLU	-	expression tag	UNP A0A6J4CX17
C	293	HIS	-	expression tag	UNP A0A6J4CX17
C	294	HIS	-	expression tag	UNP A0A6J4CX17
C	295	HIS	-	expression tag	UNP A0A6J4CX17
C	296	HIS	-	expression tag	UNP A0A6J4CX17
C	297	HIS	-	expression tag	UNP A0A6J4CX17
C	298	HIS	-	expression tag	UNP A0A6J4CX17
A	3	MET	-	initiating methionine	UNP A0A6J4CX17
A	286	LYS	-	expression tag	UNP A0A6J4CX17
A	287	LEU	-	expression tag	UNP A0A6J4CX17
A	288	ALA	-	expression tag	UNP A0A6J4CX17
A	289	ALA	-	expression tag	UNP A0A6J4CX17
A	290	ALA	-	expression tag	UNP A0A6J4CX17
A	291	LEU	-	expression tag	UNP A0A6J4CX17

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Chain	Residue	Modelled	Actual	Comment	Reference
A	292	GLU	-	expression tag	UNP A0A6J4CX17
A	293	HIS	-	expression tag	UNP A0A6J4CX17
A	294	HIS	-	expression tag	UNP A0A6J4CX17
A	295	HIS	-	expression tag	UNP A0A6J4CX17
A	296	HIS	-	expression tag	UNP A0A6J4CX17
A	297	HIS	-	expression tag	UNP A0A6J4CX17
A	298	HIS	-	expression tag	UNP A0A6J4CX17
B	3	MET	-	initiating methionine	UNP A0A6J4CX17
B	286	LYS	-	expression tag	UNP A0A6J4CX17
B	287	LEU	-	expression tag	UNP A0A6J4CX17
B	288	ALA	-	expression tag	UNP A0A6J4CX17
B	289	ALA	-	expression tag	UNP A0A6J4CX17
B	290	ALA	-	expression tag	UNP A0A6J4CX17
B	291	LEU	-	expression tag	UNP A0A6J4CX17
B	292	GLU	-	expression tag	UNP A0A6J4CX17
B	293	HIS	-	expression tag	UNP A0A6J4CX17
B	294	HIS	-	expression tag	UNP A0A6J4CX17
B	295	HIS	-	expression tag	UNP A0A6J4CX17
B	296	HIS	-	expression tag	UNP A0A6J4CX17
B	297	HIS	-	expression tag	UNP A0A6J4CX17
B	298	HIS	-	expression tag	UNP A0A6J4CX17
D	3	MET	-	initiating methionine	UNP A0A6J4CX17
D	280F	LYS	-	expression tag	UNP A0A6J4CX17
D	286	LEU	-	expression tag	UNP A0A6J4CX17
D	287	ALA	-	expression tag	UNP A0A6J4CX17
D	288	ALA	-	expression tag	UNP A0A6J4CX17
D	289	ALA	-	expression tag	UNP A0A6J4CX17
D	290	LEU	-	expression tag	UNP A0A6J4CX17
D	291	GLU	-	expression tag	UNP A0A6J4CX17
D	292	HIS	-	expression tag	UNP A0A6J4CX17
D	293	HIS	-	expression tag	UNP A0A6J4CX17
D	294	HIS	-	expression tag	UNP A0A6J4CX17
D	295	HIS	-	expression tag	UNP A0A6J4CX17
D	296	HIS	-	expression tag	UNP A0A6J4CX17
D	297	HIS	-	expression tag	UNP A0A6J4CX17

- Molecule 2 is FE (II) ION (three-letter code: FE2) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

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

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

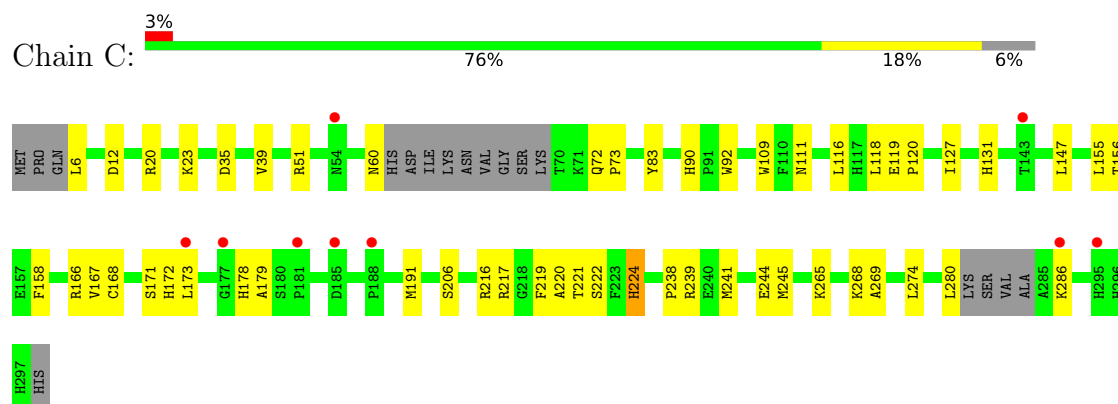
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	104	Total 104	O 104	0	0
3	A	169	Total 169	O 169	0	0
3	B	126	Total 126	O 126	0	0
3	D	92	Total 92	O 92	0	0

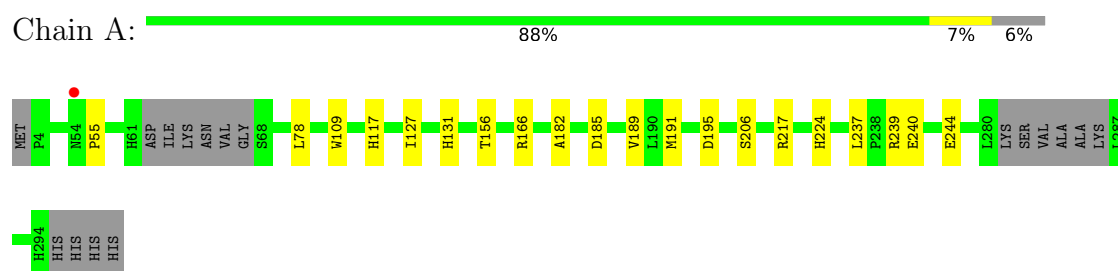
3 Residue-property plots [i](#)

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.

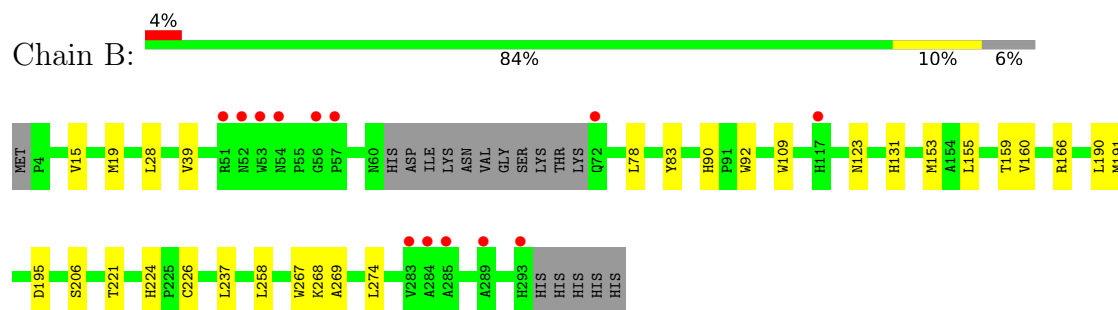
- Molecule 1: 2-oxoglutarate/Fe(II)-dependent dioxygenase SptF



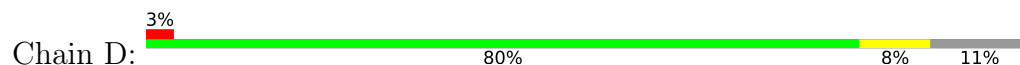
- Molecule 1: 2-oxoglutarate/Fe(II)-dependent dioxygenase SptF

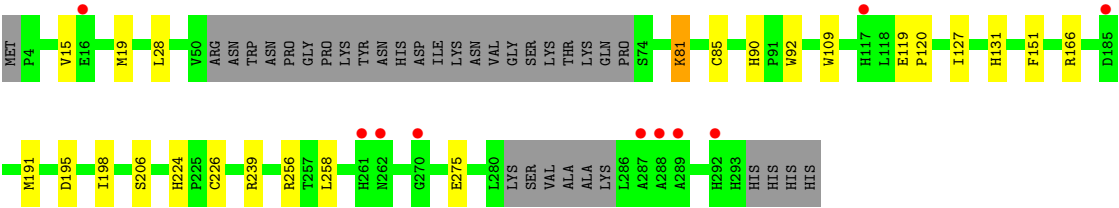


- Molecule 1: 2-oxoglutarate/Fe(II)-dependent dioxygenase SptF



- Molecule 1: 2-oxoglutarate/Fe(II)-dependent dioxygenase SptF





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	49.57Å 72.70Å 78.98Å 82.08° 84.95° 70.13°	Depositor
Resolution (Å)	46.57 – 2.12 48.57 – 2.12	Depositor EDS
% Data completeness (in resolution range)	97.5 (46.57-2.12) 97.7 (48.57-2.12)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.56 (at 2.12Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.196 , 0.251 0.194 , 0.248	Depositor DCC
R_{free} test set	2000 reflections (3.52%)	wwPDB-VP
Wilson B-factor (Å ²)	20.6	Xtriage
Anisotropy	0.666	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 49.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9264	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 55.93 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.9449e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: FE2

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	0.25	0/2315	0.48	0/3150
1	B	0.25	0/2279	0.48	0/3108
1	C	0.25	0/2307	0.48	0/3142
1	D	0.25	0/2137	0.47	0/2911
All	All	0.25	0/9038	0.48	0/12311

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	2246	0	2134	10	0
1	B	2211	0	2086	13	0
1	C	2237	0	2118	33	0
1	D	2075	0	1954	10	0
2	A	1	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
3	A	169	0	0	0	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	126	0	0	2	1
3	C	104	0	0	0	0
3	D	92	0	0	0	0
All	All	9264	0	8292	64	1

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:78:LEU:HD23	1:B:237:LEU:HG	1.73	0.70
1:C:156:THR:HG23	1:C:217:ARG:HB2	1.75	0.69
1:C:72:GLN:HG3	1:C:73:PRO:HD2	1.76	0.67
1:C:158:PHE:HB2	1:C:191:MET:HB2	1.78	0.65
1:B:39:VAL:HG13	1:B:155:LEU:HD23	1.80	0.64
1:D:226:CYS:HB2	1:D:258:LEU:HD13	1.81	0.61
1:C:127:ILE:HA	1:C:206:SER:HB3	1.83	0.60
1:A:156:THR:HG23	1:A:217:ARG:HB2	1.83	0.60
1:D:119:GLU:HG3	1:D:120:PRO:HD2	1.83	0.59
1:C:118:LEU:HB2	1:C:216:ARG:HB3	1.85	0.57
1:C:178:HIS:HD1	1:C:179:ALA:N	2.03	0.56
1:D:81:LYS:HD3	1:D:85:CYS:SG	2.47	0.54
1:D:191:MET:HB3	1:D:195:ASP:HB2	1.89	0.54
1:A:182:ALA:N	1:A:185:ASP:OD2	2.42	0.53
1:B:191:MET:HB3	1:B:195:ASP:HB2	1.91	0.52
1:C:90:HIS:CE1	1:C:92:TRP:HB2	2.44	0.52
1:C:286:LYS:HE2	1:C:286:LYS:HA	1.90	0.52
1:A:127:ILE:HA	1:A:206:SER:HB3	1.91	0.52
1:C:119:GLU:HG2	1:C:120:PRO:HD2	1.92	0.51
1:D:28:LEU:C	1:D:28:LEU:HD12	2.30	0.51
1:B:123:ASN:ND2	3:B:413:HOH:O	2.43	0.51
1:C:39[A]:VAL:HG23	1:C:219:PHE:CE2	2.46	0.50
1:B:160:VAL:HG23	1:B:190:LEU:HD21	1.94	0.50
1:C:168:CYS:O	1:C:171:SER:OG	2.26	0.50
1:A:78:LEU:HD12	1:A:237:LEU:HG	1.94	0.49
1:C:39[B]:VAL:HG12	1:C:155:LEU:HD13	1.94	0.49
1:B:268:LYS:NZ	3:B:406:HOH:O	2.38	0.49
1:B:90:HIS:CE1	1:B:92:TRP:HB2	2.48	0.49
1:D:127:ILE:HA	1:D:206:SER:HB3	1.94	0.49
1:B:159:THR:HA	1:B:190:LEU:HD22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:90:HIS:CE1	1:D:92:TRP:HB2	2.49	0.48
1:C:39[B]:VAL:HG13	1:C:219:PHE:CE2	2.50	0.47
1:A:191:MET:HB3	1:A:195:ASP:HB2	1.97	0.46
1:A:239:ARG:HG2	1:A:239:ARG:HH11	1.80	0.46
1:B:15:VAL:O	1:B:19:MET:HG2	2.16	0.46
1:C:20:ARG:HH11	1:C:20:ARG:HG2	1.80	0.46
1:C:241:MET:O	1:C:244:GLU:HG2	2.15	0.45
1:D:256:ARG:HG2	1:D:275:GLU:HB3	1.98	0.44
1:C:12:ASP:HA	1:A:55:PRO:HG2	2.00	0.44
1:A:240:GLU:O	1:A:244:GLU:HG3	2.18	0.43
1:C:6:LEU:HD13	1:C:167:VAL:HG21	1.99	0.43
1:C:92:TRP:CZ2	1:A:55:PRO:HG3	2.53	0.43
1:B:39:VAL:HG13	1:B:155:LEU:CD2	2.47	0.43
1:C:280:LEU:HD23	1:C:280:LEU:HA	1.86	0.43
1:C:269:ALA:HB2	1:C:274:LEU:HA	2.01	0.43
1:C:83:TYR:OH	1:C:221:THR:HG22	2.19	0.42
1:A:189:VAL:HG12	1:A:191:MET:HG3	2.00	0.42
1:C:178:HIS:HD1	1:C:178:HIS:C	2.23	0.42
1:C:241:MET:O	1:C:245:MET:HG3	2.20	0.42
1:B:269:ALA:HB2	1:B:274:LEU:HA	2.02	0.42
1:C:39[A]:VAL:HG22	1:C:155:LEU:HD13	2.01	0.42
1:B:83:TYR:OH	1:B:221:THR:HG22	2.20	0.42
1:D:15:VAL:O	1:D:19:MET:HG2	2.20	0.42
1:C:35:ASP:OD1	1:C:35:ASP:N	2.53	0.41
1:C:265:LYS:HB2	1:C:268:LYS:HD3	2.01	0.41
1:C:111:ASN:HB3	1:C:222:SER:OG	2.19	0.41
1:C:116:LEU:HD11	1:C:220:ALA:HB2	2.03	0.41
1:D:151:PHE:CD2	1:D:198:ILE:HD12	2.55	0.41
1:C:147:LEU:O	1:C:224:HIS:HB2	2.21	0.41
1:C:172:HIS:CE1	1:C:173:LEU:HG	2.56	0.41
1:C:118:LEU:HD23	1:C:118:LEU:HA	1.92	0.40
1:C:238:PRO:HD2	1:C:241:MET:SD	2.61	0.40
1:C:178:HIS:ND1	1:C:179:ALA:N	2.69	0.40
1:B:226:CYS:HB2	1:B:258:LEU:HD13	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:511:HOH:O	3:B:438:HOH:O[1_645]	2.15	0.05

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	273/296 (92%)	268 (98%)	5 (2%)	0	100	100
1	B	275/296 (93%)	270 (98%)	5 (2%)	0	100	100
1	C	274/296 (93%)	269 (98%)	5 (2%)	0	100	100
1	D	256/296 (86%)	253 (99%)	3 (1%)	0	100	100
All	All	1078/1184 (91%)	1060 (98%)	18 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	247/261 (95%)	242 (98%)	5 (2%)	55	59
1	B	239/261 (92%)	231 (97%)	8 (3%)	38	39
1	C	242/261 (93%)	234 (97%)	8 (3%)	38	39
1	D	225/261 (86%)	219 (97%)	6 (3%)	44	47
All	All	953/1044 (91%)	926 (97%)	27 (3%)	43	46

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	23	LYS
1	C	51	ARG

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Mol	Chain	Res	Type
1	C	60	ASN
1	C	109	TRP
1	C	131	HIS
1	C	166	ARG
1	C	224	HIS
1	C	239	ARG
1	A	109	TRP
1	A	117	HIS
1	A	131	HIS
1	A	166	ARG
1	A	224	HIS
1	B	28	LEU
1	B	109	TRP
1	B	131	HIS
1	B	153	MET
1	B	166	ARG
1	B	206	SER
1	B	224	HIS
1	B	267	TRP
1	D	81	LYS
1	D	109	TRP
1	D	131	HIS
1	D	166	ARG
1	D	224	HIS
1	D	239	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 4 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	279/296 (94%)	0.13	1 (0%) 92 93	10, 21, 36, 50	0
1	B	279/296 (94%)	0.24	13 (4%) 31 36	10, 24, 43, 50	0
1	C	279/296 (94%)	0.31	9 (3%) 47 54	12, 27, 43, 53	0
1	D	262/296 (88%)	0.16	10 (3%) 40 46	11, 26, 41, 50	0
All	All	1099/1184 (92%)	0.21	33 (3%) 50 56	10, 25, 42, 53	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	283	VAL	5.7
1	B	285	ALA	4.4
1	B	284	ALA	4.2
1	B	52	ASN	3.7
1	D	288	ALA	3.7
1	B	54	ASN	3.4
1	B	56	GLY	3.3
1	D	292	HIS	3.0
1	C	143	THR	2.9
1	B	51	ARG	2.8
1	C	185	ASP	2.8
1	C	188	PRO	2.7
1	D	185	ASP	2.6
1	C	54	ASN	2.6
1	B	53	TRP	2.6
1	B	289	ALA	2.6
1	C	177	GLY	2.5
1	D	289	ALA	2.4
1	D	270	GLY	2.4
1	D	287	ALA	2.3
1	B	293	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	57	PRO	2.3
1	A	54	ASN	2.2
1	D	262	ASN	2.2
1	C	181	PRO	2.2
1	C	286	LYS	2.2
1	B	72	GLN	2.1
1	D	117	HIS	2.1
1	C	173	LEU	2.1
1	C	295	HIS	2.1
1	D	16	GLU	2.0
1	D	261	HIS	2.0
1	B	117	HIS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

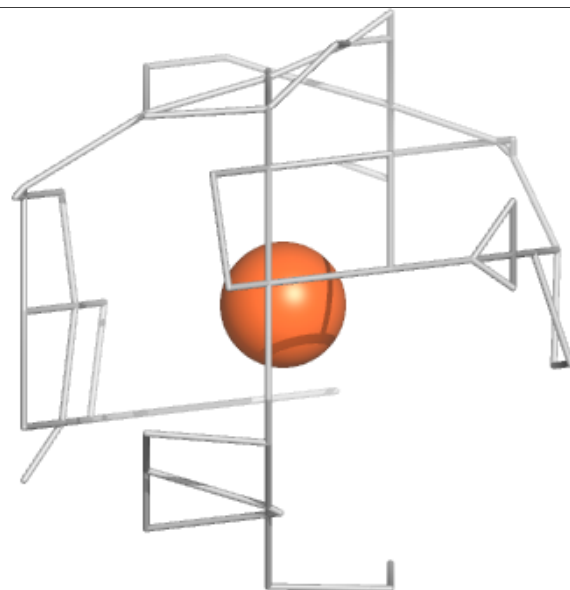
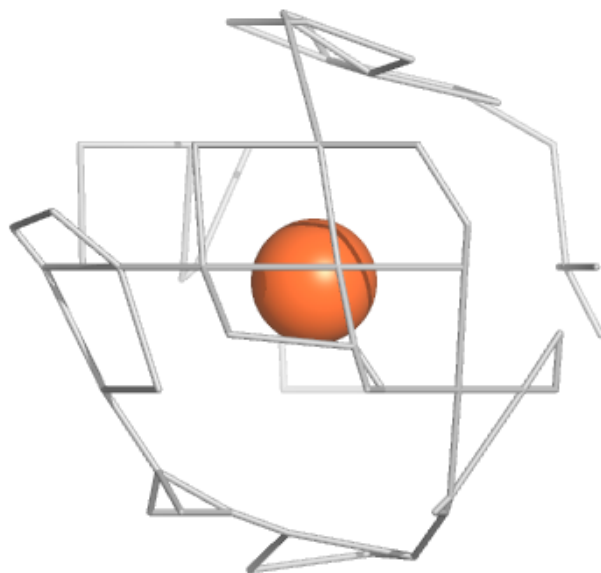
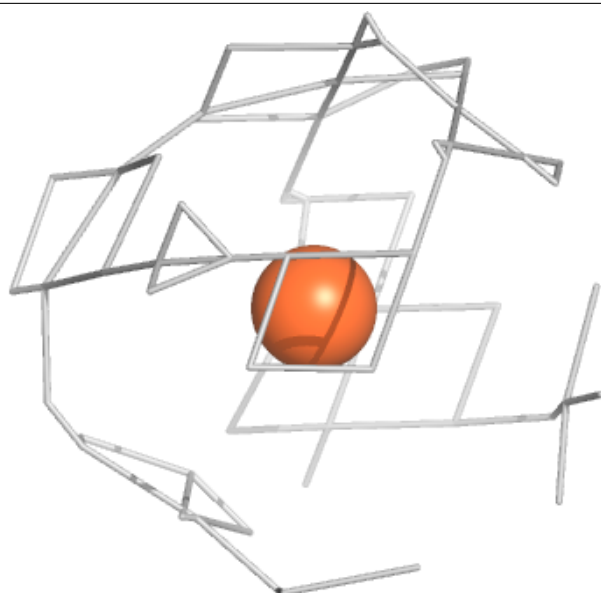
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	FE2	C	301	1/1	0.92	0.15	51,51,51,51	0
2	FE2	B	301	1/1	0.95	0.15	47,47,47,47	0
2	FE2	D	301	1/1	0.98	0.18	45,45,45,45	0
2	FE2	A	301	1/1	0.99	0.10	44,44,44,44	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.

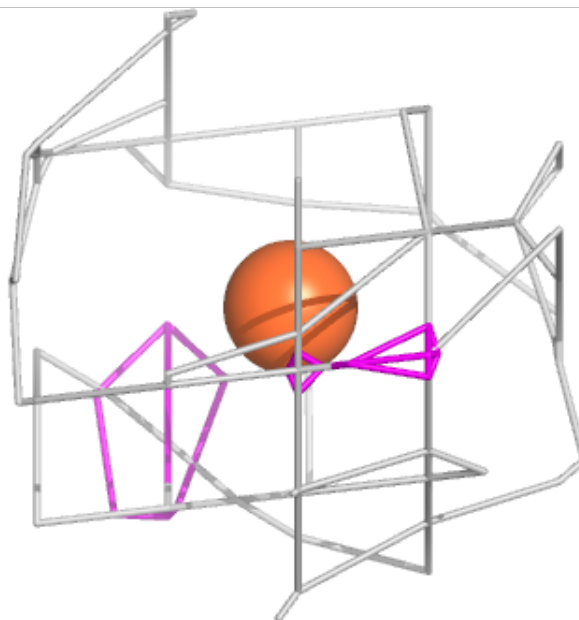
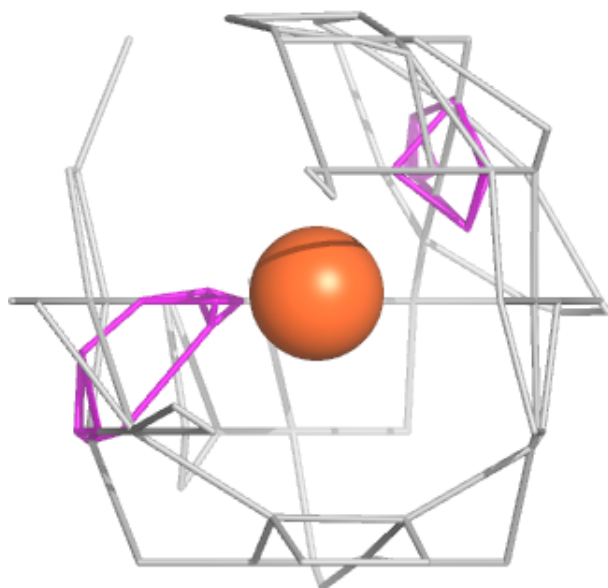
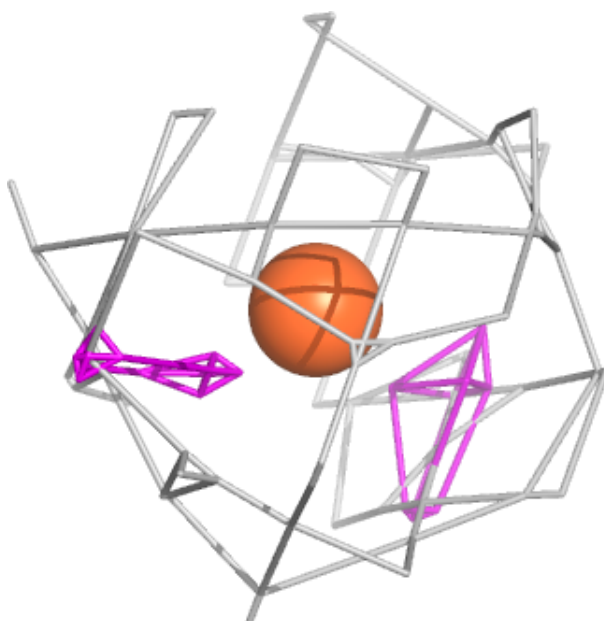
Electron density around FE2 C 301:

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



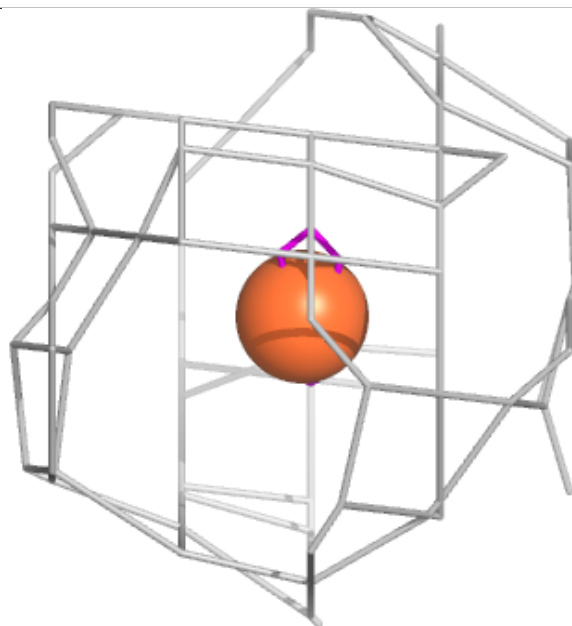
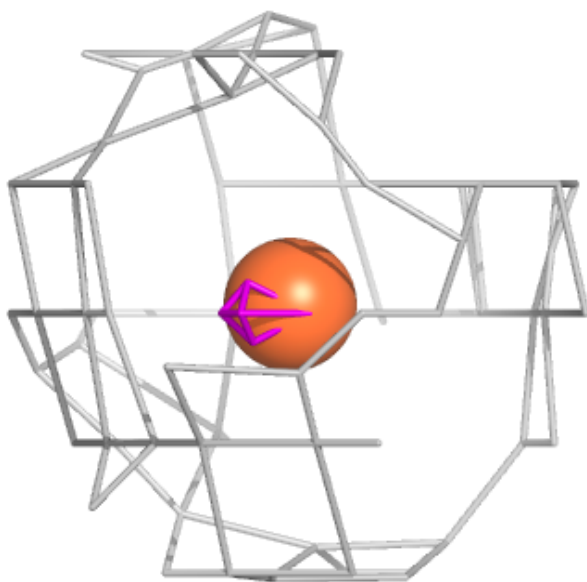
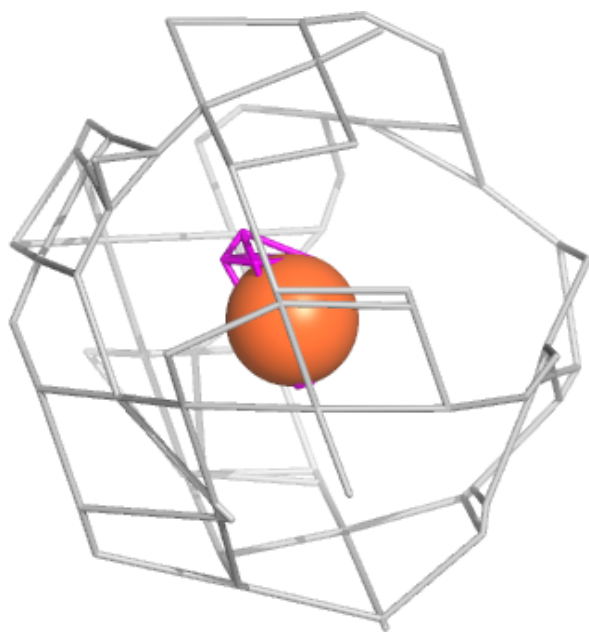
Electron density around FE2 B 301:

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



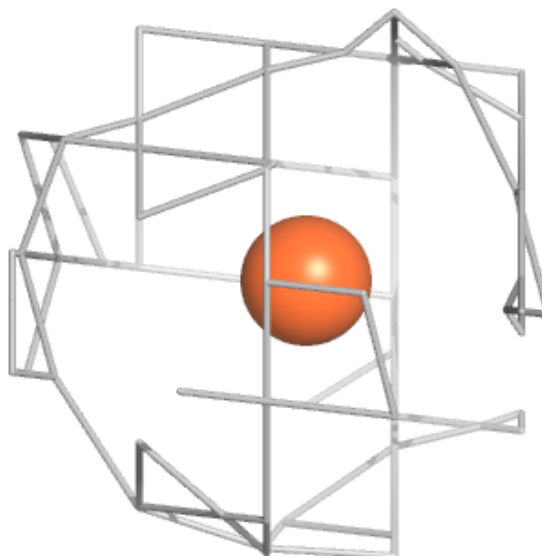
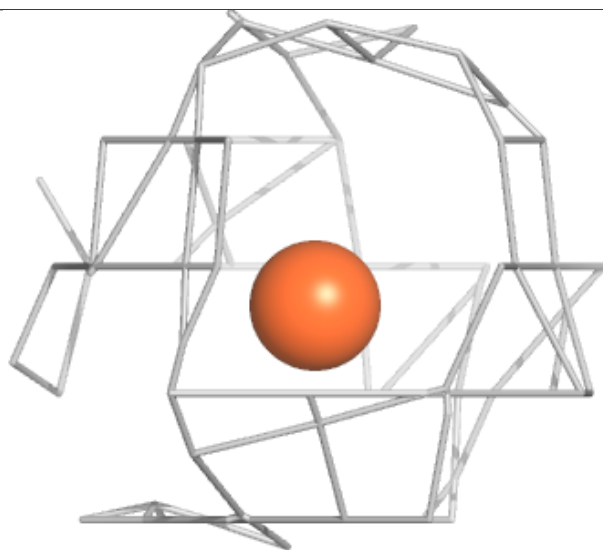
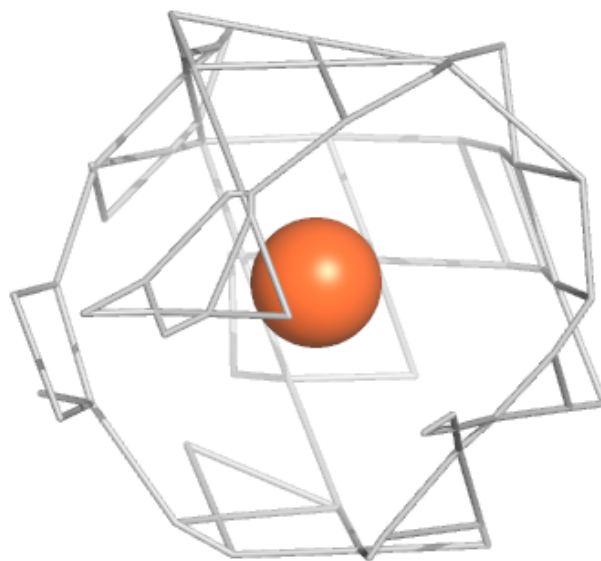
Electron density around FE2 D 301:

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



Electron density around FE2 A 301:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.