



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 02:49 PM UTC

PDB ID : 7TTJ / pdb_00007ttj
Title : Stable-5-LOX elongated Ha2
Authors : Gilbert, N.C.; Newcomer, M.E.
Deposited on : 2022-02-01
Resolution : 2.10 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

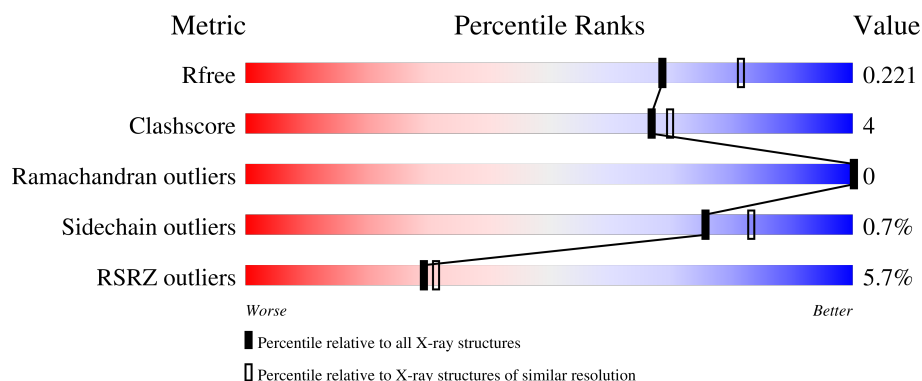
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	691	5% 84% 9% 7%
1	B	691	5% 79% 7% 15%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 20248 atoms, of which 9827 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 Arachidonate 5-lipoxygenase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	590	Total	C	H	N	O	S	0	1	0
			9516	3084	4704	818	890	20			
1	A	643	Total	C	H	N	O	S	0	0	0
			10371	3368	5123	887	970	23			

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	MET	-	initiating methionine	UNP P09917
B	-13	GLY	-	expression tag	UNP P09917
B	-12	SER	-	expression tag	UNP P09917
B	-11	SER	-	expression tag	UNP P09917
B	-10	HIS	-	expression tag	UNP P09917
B	-9	HIS	-	expression tag	UNP P09917
B	-8	HIS	-	expression tag	UNP P09917
B	-7	HIS	-	expression tag	UNP P09917
B	-6	HIS	-	expression tag	UNP P09917
B	-6A	HIS	-	expression tag	UNP P09917
B	-6B	SER	-	expression tag	UNP P09917
B	-6C	SER	-	expression tag	UNP P09917
B	-6D	GLY	-	expression tag	UNP P09917
B	-6E	LEU	-	expression tag	UNP P09917
B	-6F	VAL	-	expression tag	UNP P09917
B	-6G	PRO	-	expression tag	UNP P09917
B	-6H	ARG	-	expression tag	UNP P09917
B	-6I	GLY	-	expression tag	UNP P09917
B	-6J	SER	-	expression tag	UNP P09917
B	-6K	HIS	-	expression tag	UNP P09917
B	16	GLU	TRP	conflict	UNP P09917
B	17	HIS	PHE	conflict	UNP P09917
B	?	-	PRO	deletion	UNP P09917
B	?	-	PHE	deletion	UNP P09917
B	?	-	TYR	deletion	UNP P09917

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Chain	Residue	Modelled	Actual	Comment	Reference
B	43	GLY	ASN	conflict	UNP P09917
B	44	SER	ASP	conflict	UNP P09917
B	75	GLY	TRP	conflict	UNP P09917
B	76	SER	LEU	conflict	UNP P09917
B	240	ALA	CYS	conflict	UNP P09917
B	561	ALA	CYS	conflict	UNP P09917
B	653	GLU	LYS	conflict	UNP P09917
B	654	ASN	LYS	conflict	UNP P09917
B	655	LEU	LYS	conflict	UNP P09917
A	-17	MET	-	initiating methionine	UNP P09917
A	-16	GLY	-	expression tag	UNP P09917
A	-15	SER	-	expression tag	UNP P09917
A	-14	SER	-	expression tag	UNP P09917
A	-13	HIS	-	expression tag	UNP P09917
A	-12	HIS	-	expression tag	UNP P09917
A	-11	HIS	-	expression tag	UNP P09917
A	-10	HIS	-	expression tag	UNP P09917
A	-9	HIS	-	expression tag	UNP P09917
A	-8	HIS	-	expression tag	UNP P09917
A	-7	SER	-	expression tag	UNP P09917
A	-6	SER	-	expression tag	UNP P09917
A	-5	GLY	-	expression tag	UNP P09917
A	-4	LEU	-	expression tag	UNP P09917
A	-3	VAL	-	expression tag	UNP P09917
A	-2	PRO	-	expression tag	UNP P09917
A	-1	ARG	-	expression tag	UNP P09917
A	0	GLY	-	expression tag	UNP P09917
A	1	SER	-	expression tag	UNP P09917
A	2	HIS	-	expression tag	UNP P09917
A	16	GLU	TRP	conflict	UNP P09917
A	17	HIS	PHE	conflict	UNP P09917
A	?	-	PRO	deletion	UNP P09917
A	?	-	PHE	deletion	UNP P09917
A	?	-	TYR	deletion	UNP P09917
A	43	GLY	ASN	conflict	UNP P09917
A	44	SER	ASP	conflict	UNP P09917
A	75	GLY	TRP	conflict	UNP P09917
A	76	SER	LEU	conflict	UNP P09917
A	240	ALA	CYS	conflict	UNP P09917
A	561	ALA	CYS	conflict	UNP P09917
A	653	GLU	LYS	conflict	UNP P09917
A	654	ASN	LYS	conflict	UNP P09917

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Chain	Residue	Modelled	Actual	Comment	Reference
A	655	LEU	LYS	conflict	UNP P09917

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

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

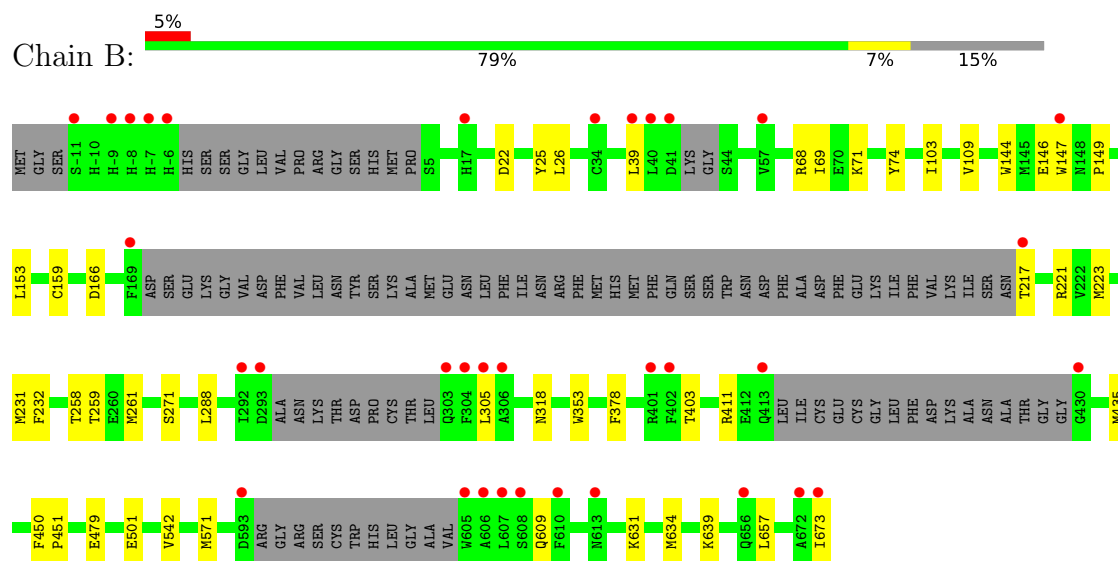
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	164	Total O 164 164	0	0
3	A	195	Total O 195 195	0	0

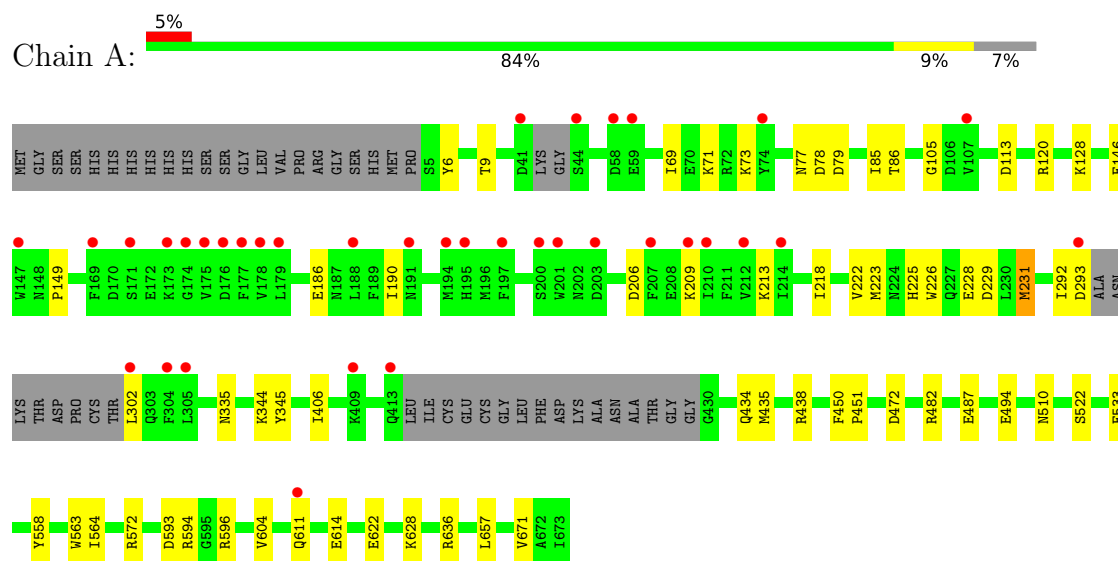
3 Residue-property plots

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: Arachidonate 5-lipoxygenase



• Molecule 1: Arachidonate 5-lipoxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	52.73Å 204.57Å 74.11Å 90.00° 107.65° 90.00°	Depositor
Resolution (Å)	50.25 – 2.10 50.25 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.5 (50.25-2.10) 99.7 (50.25-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.79 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.184 , 0.224 0.186 , 0.221	Depositor DCC
R_{free} test set	4090 reflections (4.68%)	wwPDB-VP
Wilson B-factor (Å ²)	38.8	Xtriage
Anisotropy	0.684	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 47.7	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	0.97	EDS
Total number of atoms	20248	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% 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: 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	0.55	0/5380	0.66	3/7297 (0.0%)
1	B	0.55	0/4935	0.64	0/6696
All	All	0.55	0/10315	0.65	3/13993 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	563	TRP	CA-C-N	6.82	124.53	120.24
1	A	563	TRP	C-N-CA	6.82	124.53	120.24
1	A	564	ILE	CB-CA-C	-5.44	108.59	114.35

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	5248	5123	5135	45	0
1	B	4812	4704	4706	29	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	195	0	0	13	0
3	B	164	0	0	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	10421	9827	9841	74	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 (74) 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:223:MET:SD	3:B:961:HOH:O	2.12	1.07
1:B:159:CYS:SG	3:B:933:HOH:O	2.19	1.01
1:A:229:ASP:OD2	3:A:801:HOH:O	1.93	0.86
1:A:594:ARG:NH1	3:A:804:HOH:O	2.10	0.84
1:A:622:GLU:OE1	3:A:803:HOH:O	2.06	0.74
1:A:522:SER:OG	3:A:802:HOH:O	2.05	0.74
1:A:406:ILE:HD11	1:A:671:VAL:HG12	1.72	0.71
1:A:472:ASP:OD1	3:A:805:HOH:O	2.11	0.69
1:A:213:LYS:HD2	1:A:223:MET:HE1	1.78	0.66
1:B:479:GLU:OE1	3:B:801:HOH:O	2.14	0.65
1:A:335:ASN:O	3:A:806:HOH:O	2.14	0.65
1:A:482:ARG:NH2	1:A:533:GLU:OE2	2.31	0.64
1:A:128:LYS:NZ	3:A:814:HOH:O	2.31	0.63
1:A:78:ASP:OD2	3:A:807:HOH:O	2.16	0.62
1:B:25:TYR:CE1	1:B:39:LEU:HD23	2.35	0.62
1:B:221:ARG:HD2	1:B:657:LEU:HD13	1.82	0.61
1:A:6:TYR:OH	3:A:808:HOH:O	2.16	0.59
1:A:120:ARG:NH2	1:A:494:GLU:OE1	2.36	0.57
1:A:71:LYS:O	1:A:73:LYS:NZ	2.39	0.56
1:B:25:TYR:CZ	1:B:39:LEU:HD23	2.43	0.54
1:A:450:PHE:HB3	1:A:451:PRO:HD3	1.89	0.54
1:A:206:ASP:HB3	1:A:594:ARG:HD3	1.89	0.54
1:A:510:ASN:OD1	3:A:809:HOH:O	2.19	0.53
1:A:487:GLU:OE2	1:A:636:ARG:NH2	2.41	0.53
1:A:218:ILE:HG12	1:A:657:LEU:HD22	1.91	0.52
1:B:103:ILE:HG12	1:B:109:VAL:HG21	1.91	0.52
1:B:144:TRP:HB3	1:B:153:LEU:HD23	1.91	0.52
1:A:69:ILE:HD11	1:A:85:ILE:CD1	2.39	0.52
1:B:403:THR:OG1	3:B:802:HOH:O	2.19	0.51
1:A:222:VAL:O	1:A:226:TRP:HB3	2.11	0.51
1:B:305:LEU:O	3:B:803:HOH:O	2.19	0.50
1:A:292:ILE:HG22	1:A:293:ASP:H	1.75	0.50
1:A:71:LYS:HE3	1:A:78:ASP:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:39:LEU:C	1:B:39:LEU:HD13	2.38	0.48
1:A:209:LYS:HZ2	1:A:594:ARG:HE	1.60	0.48
1:B:22:ASP:HA	1:B:74:TYR:HB3	1.96	0.47
1:A:105:GLY:HA2	3:A:899:HOH:O	2.15	0.47
1:B:68:ARG:NH2	3:B:820:HOH:O	2.48	0.47
1:B:450:PHE:HB3	1:B:451:PRO:HD3	1.96	0.47
1:A:558:TYR:HA	1:A:604:VAL:HG12	1.97	0.46
1:A:206:ASP:O	1:A:209:LYS:HB3	2.16	0.45
1:B:673:ILE:OXT	3:B:805:HOH:O	2.21	0.45
1:A:593:ASP:OD2	1:A:596:ARG:HG2	2.17	0.45
1:B:501:GLU:OE1	3:B:804:HOH:O	2.20	0.45
1:B:258:THR:H	1:B:261:MET:HE3	1.82	0.45
1:A:344:LYS:HG3	1:A:345:TYR:N	2.31	0.45
1:A:9:THR:HB	1:A:86:THR:OG1	2.16	0.45
1:B:609:GLN:O	1:B:673:ILE:HD13	2.17	0.44
1:A:79:ASP:O	3:A:807:HOH:O	2.20	0.44
1:B:166:ASP:HB3	3:B:814:HOH:O	2.17	0.44
1:A:73:LYS:HD2	1:A:77:ASN:HA	1.99	0.44
1:A:225:HIS:ND1	1:A:228:GLU:OE2	2.43	0.44
1:A:572:ARG:HD3	1:A:593:ASP:H	1.83	0.44
1:B:147:TRP:CD1	1:B:411:ARG:HD2	2.53	0.44
1:B:378:PHE:CG	1:B:542:VAL:HG22	2.54	0.43
1:A:69:ILE:HD11	1:A:85:ILE:HD12	2.00	0.43
1:B:232:PHE:O	3:B:806:HOH:O	2.21	0.42
1:A:186:GLU:O	1:A:190:ILE:HG13	2.19	0.42
1:A:302:LEU:HD23	1:A:302:LEU:N	2.34	0.42
1:A:113:ASP:OD1	1:A:113:ASP:C	2.62	0.42
1:B:631:LYS:HA	1:B:634:MET:HE3	2.01	0.42
1:A:292:ILE:HG22	1:A:293:ASP:N	2.34	0.42
1:A:611:GLN:HG2	1:A:614:GLU:OE2	2.20	0.42
1:B:146:GLU:OE1	1:B:149:PRO:HA	2.20	0.41
1:A:434:GLN:O	1:A:438:ARG:HG3	2.20	0.41
1:A:435:MET:HE2	1:A:435:MET:HB3	1.89	0.41
1:A:593:ASP:HA	3:A:821:HOH:O	2.20	0.41
1:A:146:GLU:OE2	1:A:149:PRO:HA	2.21	0.41
1:B:26:LEU:HD12	1:B:69:ILE:HD11	2.03	0.41
1:B:259:THR:HG21	1:B:271:SER:HA	2.02	0.41
1:B:435:MET:HE2	1:B:435:MET:HB3	1.82	0.41
1:B:353:TRP:CE2	1:B:571:MET:HE3	2.57	0.40
1:B:305:LEU:HD12	1:B:305:LEU:C	2.47	0.40
1:A:231:MET:HE3	1:A:231:MET:HB2	1.97	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	635/691 (92%)	620 (98%)	15 (2%)	0	100	100
1	B	577/691 (84%)	569 (99%)	8 (1%)	0	100	100
All	All	1212/1382 (88%)	1189 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	570/608 (94%)	568 (100%)	2 (0%)	84	89
1	B	523/608 (86%)	517 (99%)	6 (1%)	65	74
All	All	1093/1216 (90%)	1085 (99%)	8 (1%)	76	83

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	71	LYS
1	B	217	THR
1	B	231	MET
1	B	288	LEU
1	B	318	ASN

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Mol	Chain	Res	Type
1	B	639	LYS
1	A	231	MET
1	A	628	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	65	GLN
1	B	123	GLN
1	B	168	GLN
1	B	235	GLN
1	B	326	GLN
1	B	328	ASN
1	B	432	HIS
1	B	566	ASN
1	A	191	ASN
1	A	235	GLN
1	A	328	ASN
1	A	566	ASN
1	A	656	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 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

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	643/691 (93%)	0.30	36 (5%)	30 32	37, 56, 103, 148	0
1	B	590/691 (85%)	0.29	34 (5%)	29 30	38, 58, 96, 127	1 (0%)
All	All	1233/1382 (89%)	0.29	70 (5%)	29 31	37, 57, 99, 148	1 (0%)

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	41	ASP	6.8
1	A	41	ASP	5.5
1	B	-6	HIS	5.4
1	A	201	TRP	5.2
1	B	305	LEU	4.8
1	B	169	PHE	4.6
1	B	-7	HIS	4.6
1	A	302	LEU	4.4
1	B	304	PHE	4.3
1	A	305	LEU	4.1
1	A	210	ILE	4.1
1	B	606	ALA	4.1
1	A	169	PHE	3.8
1	B	673	ILE	3.8
1	A	179	LEU	3.8
1	B	605	TRP	3.5
1	A	195	HIS	3.5
1	A	177	PHE	3.3
1	A	147	TRP	3.3
1	A	212	VAL	3.3
1	A	107	VAL	3.2
1	B	303	GLN	3.2
1	A	194	MET	3.1
1	A	44	SER	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	147	TRP	3.0
1	B	607	LEU	3.0
1	A	175	VAL	3.0
1	B	292	ILE	3.0
1	A	59	GLU	2.9
1	A	413	GLN	2.9
1	B	293	ASP	2.9
1	A	74	TYR	2.9
1	A	207	PHE	2.9
1	B	401	ARG	2.8
1	B	40	LEU	2.8
1	B	613	ASN	2.8
1	B	57	VAL	2.8
1	B	-8	HIS	2.7
1	A	293	ASP	2.6
1	A	409	LYS	2.6
1	A	304	PHE	2.6
1	B	402	PHE	2.5
1	A	197	PHE	2.5
1	B	-9	HIS	2.5
1	A	178	VAL	2.5
1	B	413	GLN	2.4
1	A	200	SER	2.4
1	A	191	ASN	2.4
1	B	306	ALA	2.4
1	A	188	LEU	2.4
1	B	608	SER	2.4
1	B	430	GLY	2.3
1	A	173	LYS	2.3
1	A	176	ASP	2.3
1	B	34[A]	CYS	2.2
1	A	58	ASP	2.2
1	A	203	ASP	2.2
1	A	174	GLY	2.2
1	B	656	GLN	2.2
1	A	171	SER	2.2
1	A	214	ILE	2.1
1	A	611	GLN	2.1
1	A	209	LYS	2.1
1	B	672	ALA	2.1
1	B	610	PHE	2.1
1	B	217	THR	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	-11	SER	2.0
1	B	39	LEU	2.0
1	B	593	ASP	2.0
1	B	17	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

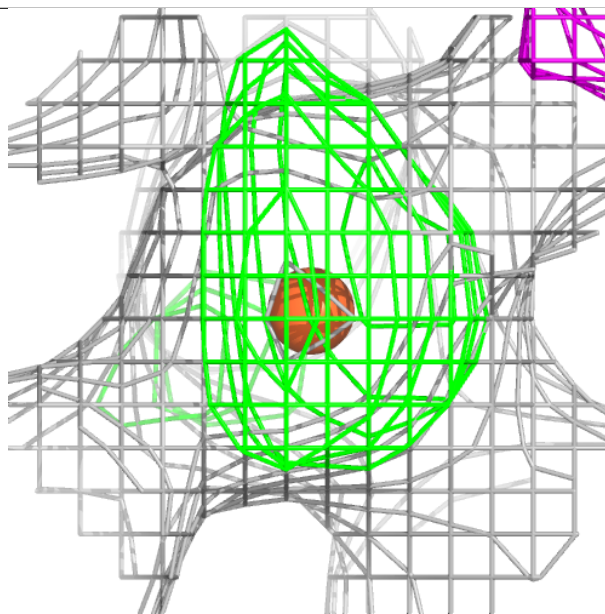
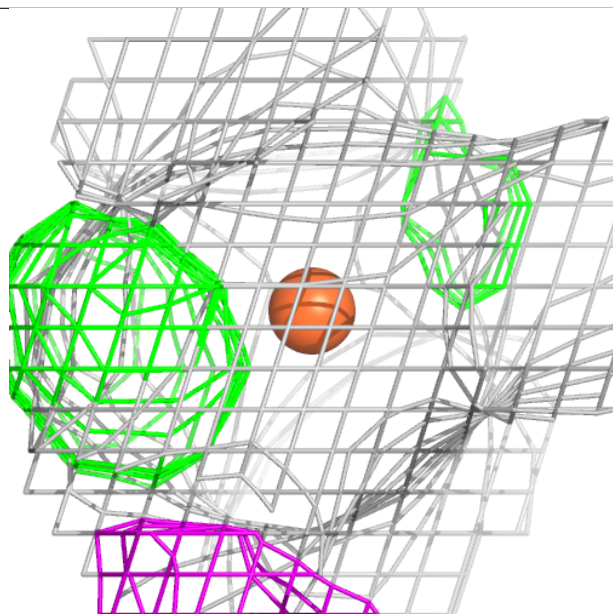
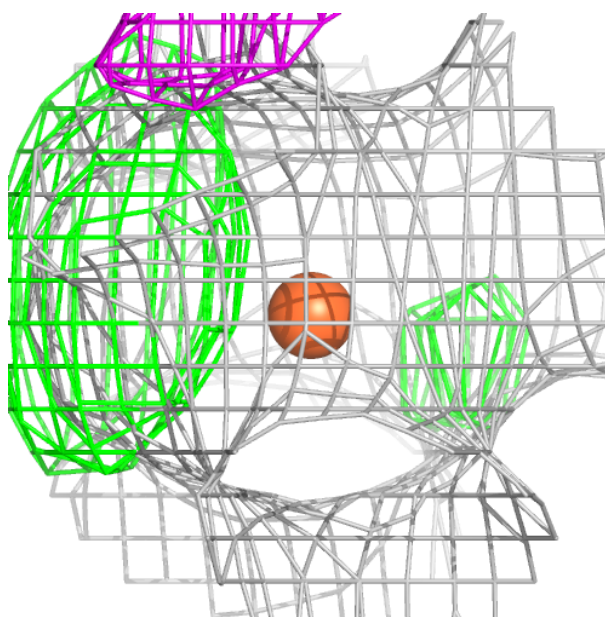
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	FE2	A	701	1/1	0.98	0.04	43,43,43,43	0
2	FE2	B	701	1/1	0.99	0.04	52,52,52,52	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.

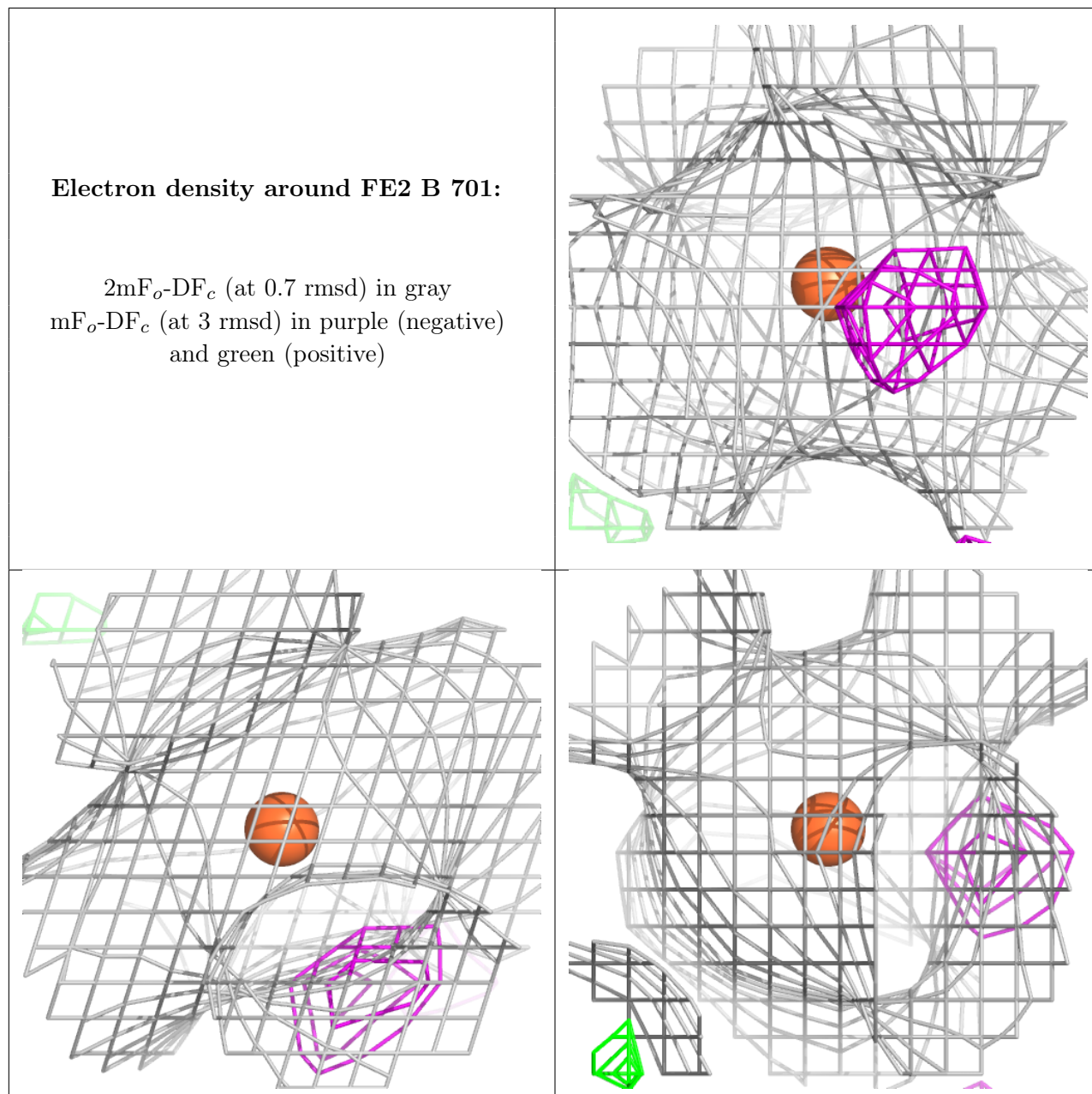
Electron density around FE2 A 701:

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



Electron density around FE2 B 701:

$2mF_o-DF_c$ (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.