



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2016 – 11:13 AM GMT

PDB ID : 4YXD
Title : CRYSTAL STRUCTURE OF PORCINE HEART MITOCHONDRIAL COM-
PLEX II BOUND WITH flutolanil
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Inaoka, D.K.; Sakamoto, K.; Inoue, M.; Honma, T.; Kita, K.
Deposited on : 2015-03-23
Resolution : 3.00 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
<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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
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) : rb-20026982

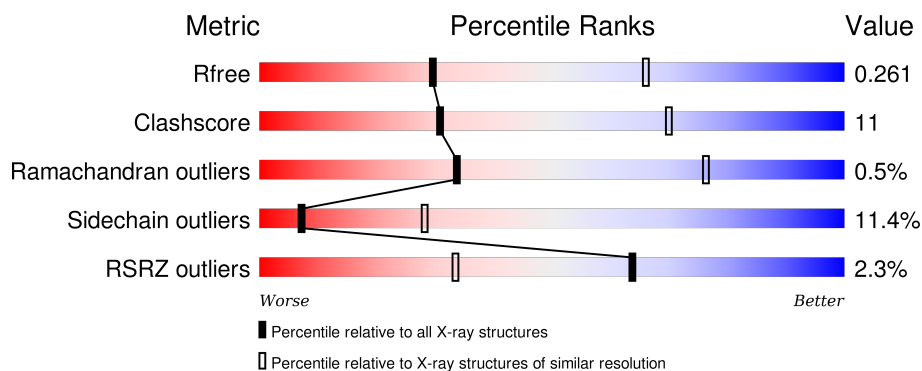
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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	664	<div> <div>3%</div> <div> <div></div> <div>66%</div> <div>23%</div> <div>8%</div> </div> </div>
2	B	280	<div> <div>61%</div> <div>20%</div> <div>15%</div> </div>
3	C	169	<div> <div>%</div> <div>60%</div> <div>19%</div> <div>18%</div> </div>
4	D	159	<div> <div>3%</div> <div>54%</div> <div>9%</div> <div>36%</div> </div>

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 8618 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 Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	613	Total	C	N	O	S	0	0	0
			4729	2954	848	895	32			

- Molecule 2 is a protein called Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	239	Total	C	N	O	S	0	0	0
			1922	1214	326	360	22			

- Molecule 3 is a protein called Succinate dehydrogenase cytochrome b560 subunit, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	138	Total	C	N	O	S	0	0	0
			1064	695	179	183	7			

- Molecule 4 is a protein called Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial.

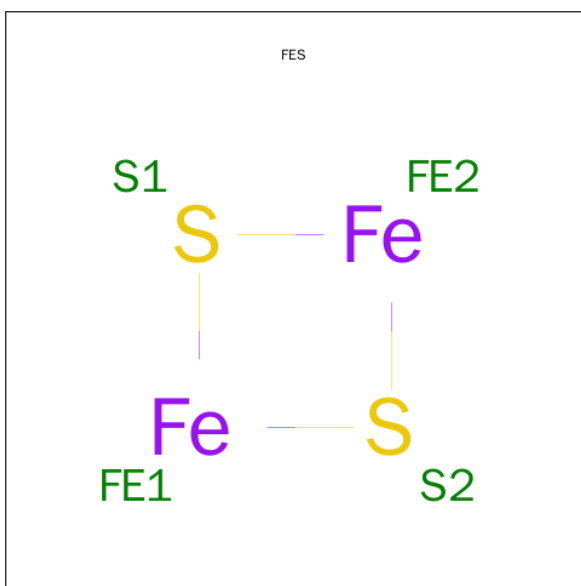
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	102	Total	C	N	O	S	0	0	0
			765	499	128	133	5			

- Molecule 5 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 6 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



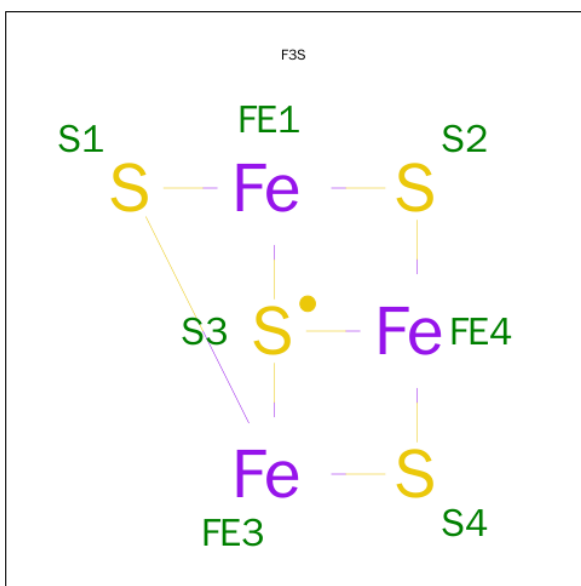
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 7 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



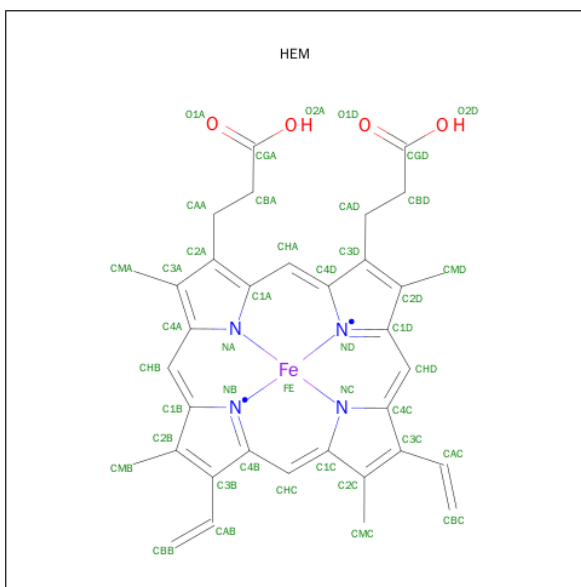
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 8 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe_3S_4).



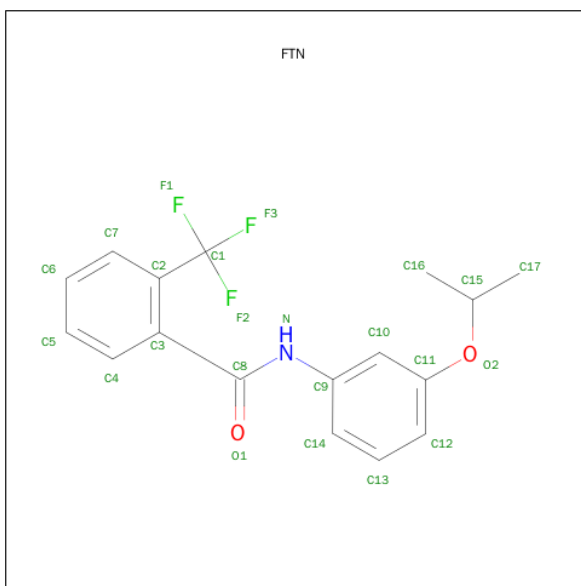
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	Fe	S	0	0
			7	3	4		

- Molecule 9 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $\text{C}_{34}\text{H}_{32}\text{FeN}_4\text{O}_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 10 is N-[3-(1-methylethoxy)phenyl]-2-(trifluoromethyl)benzamide (three-letter code: FTN) (formula: $C_{17}H_{16}F_3NO_2$).

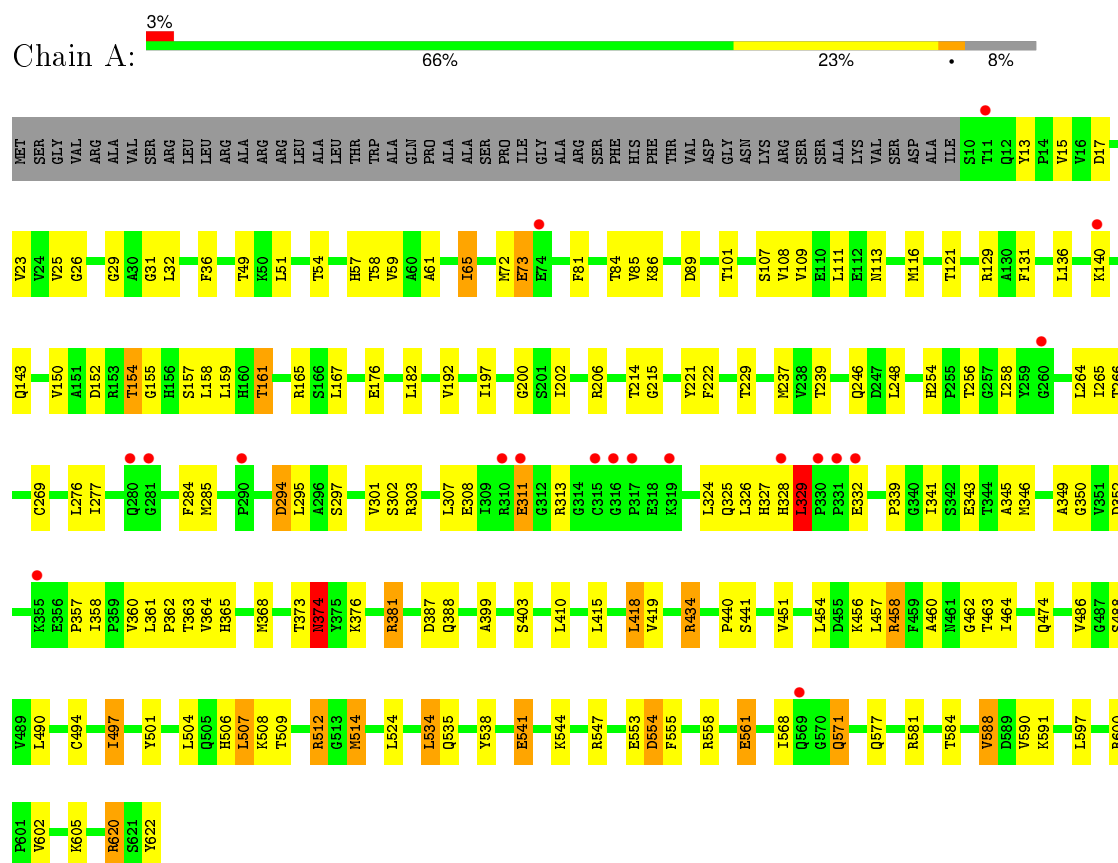


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	C	1	Total	C	F	N	O	0	0
			23	17	3	1	2		

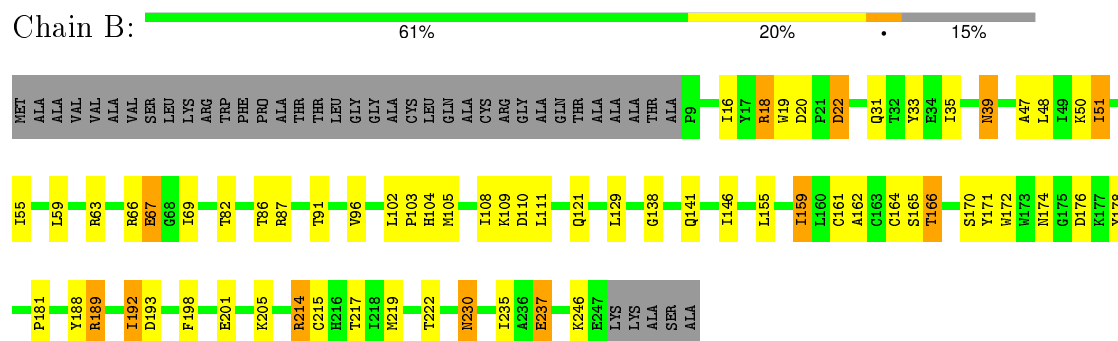
3 Residue-property plots

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.

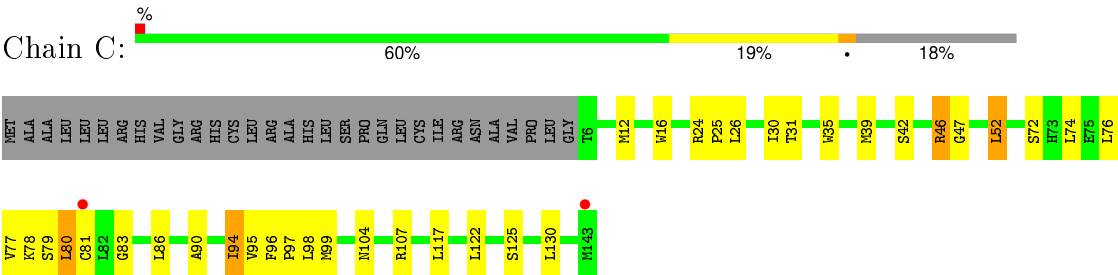
- Molecule 1: Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial



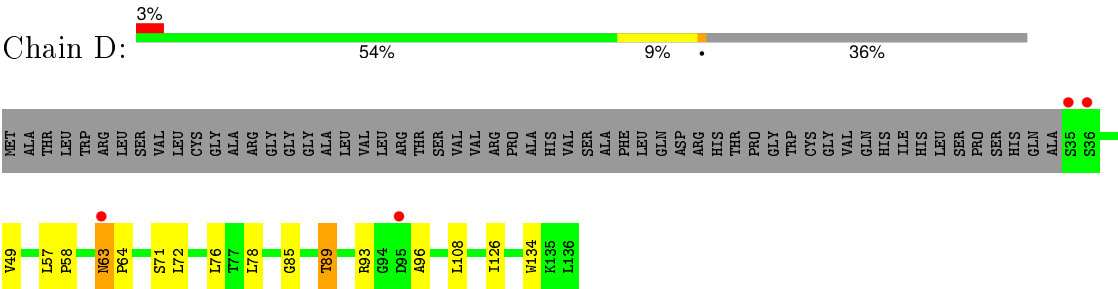
- Molecule 2: Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial



● Molecule 3: Succinate dehydrogenase cytochrome b560 subunit, mitochondrial



● Molecule 4: Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	70.37Å 83.75Å 292.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 19.95 – 3.00	Depositor EDS
% Data completeness (in resolution range)	97.5 (20.00-3.00) 97.6 (19.95-3.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.03 (at 2.98Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.206 , 0.258 0.206 , 0.261	Depositor DCC
R_{free} test set	1742 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	72.5	Xtriage
Anisotropy	0.100	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 34645 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8618	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.06% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, F3S, FES, HEM, FAD, FTN

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	0.40	0/4828	0.64	0/6531
2	B	0.41	0/1964	0.64	0/2648
3	C	0.40	0/1091	0.60	0/1483
4	D	0.40	0/784	0.59	0/1066
All	All	0.41	0/8667	0.63	0/11728

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	18	ARG	Sidechain

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	4729	0	4618	116	0
2	B	1922	0	1901	46	0
3	C	1064	0	1104	25	0
4	D	765	0	770	6	0
5	A	53	0	31	10	0
6	B	4	0	0	0	0
7	B	8	0	0	1	0
8	B	7	0	0	0	0
9	C	43	0	30	6	0
10	C	23	0	16	2	0
All	All	8618	0	8470	187	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 11.

All (187) 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)
2:B:18:ARG:NH1	2:B:59:LEU:HA	1.82	0.93
2:B:164:CYS:HG	7:B:302:SF4:FE1	0.61	0.87
2:B:111:LEU:N	2:B:111:LEU:HD23	1.93	0.83
1:A:157:SER:O	1:A:161:THR:HG23	1.79	0.81
3:C:77:VAL:HA	3:C:80:LEU:HD11	1.63	0.80
2:B:18:ARG:HH11	2:B:59:LEU:HA	1.50	0.77
2:B:215:CYS:SG	2:B:235:ILE:HG21	2.27	0.75
1:A:29:GLY:H	1:A:58:THR:HG21	1.53	0.74
1:A:116:MET:HA	1:A:161:THR:HG21	1.72	0.71
1:A:464:ILE:O	1:A:508:LYS:N	2.22	0.71
1:A:457:LEU:O	1:A:509:THR:HG21	1.90	0.71
1:A:86:LYS:O	1:A:620:ARG:NH1	2.23	0.70
1:A:264:LEU:HB3	5:A:700:FAD:HM73	1.75	0.69
1:A:258:ILE:HG13	1:A:265:ILE:HD11	1.75	0.68
1:A:202:ILE:HD13	1:A:451:VAL:HG22	1.75	0.67
9:C:301:HEM:HBC2	9:C:301:HEM:HMC2	1.77	0.66
1:A:113:ASN:HD22	2:B:138:GLY:H	1.45	0.65
1:A:311:GLU:N	1:A:311:GLU:OE1	2.30	0.65
1:A:265:ILE:HD13	1:A:360:VAL:HG12	1.79	0.64
3:C:77:VAL:O	3:C:80:LEU:HD21	1.99	0.62
1:A:58:THR:HG23	5:A:700:FAD:O1A	1.99	0.62
2:B:110:ASP:C	2:B:111:LEU:HD23	2.19	0.61
1:A:311:GLU:CA	1:A:311:GLU:OE1	2.48	0.61
1:A:57:HIS:NE2	5:A:700:FAD:C8M	2.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:69:ILE:O	2:B:159:ILE:HD11	2.01	0.61
1:A:58:THR:HG22	5:A:700:FAD:O4'	2.01	0.60
3:C:76:LEU:O	3:C:80:LEU:CD1	2.50	0.60
2:B:35:ILE:HD11	2:B:51:ILE:HG22	1.83	0.58
1:A:89:ASP:OD2	1:A:558:ARG:NH1	2.35	0.58
3:C:96:PHE:HB3	3:C:97:PRO:CD	2.34	0.58
1:A:158:LEU:HD23	1:A:415:LEU:HD22	1.85	0.58
1:A:51:LEU:HD11	1:A:229:THR:HG21	1.85	0.57
1:A:182:LEU:HD22	1:A:237:MET:HB3	1.86	0.57
1:A:328:HIS:O	1:A:329:LEU:O	2.23	0.57
1:A:434:ARG:HE	1:A:434:ARG:HA	1.70	0.57
1:A:215:GLY:N	1:A:399:ALA:HB2	2.20	0.57
2:B:165:SER:HA	2:B:181:PRO:HD2	1.85	0.57
1:A:54:THR:O	1:A:59:VAL:HG21	2.04	0.56
1:A:327:HIS:ND1	1:A:357:PRO:HD3	2.19	0.56
2:B:222:THR:OG1	2:B:230:ASN:ND2	2.38	0.56
2:B:108:ILE:HG23	3:C:24:ARG:NH2	2.19	0.56
1:A:326:LEU:HD12	1:A:358:ILE:CG1	2.35	0.56
1:A:61:ALA:HB3	1:A:155:GLY:HA3	1.86	0.56
3:C:90:ALA:O	3:C:94:ILE:HD13	2.06	0.56
1:A:462:GLY:HA3	1:A:506:HIS:O	2.05	0.56
1:A:311:GLU:HB2	1:A:313:ARG:HD2	1.88	0.55
1:A:264:LEU:HD21	1:A:266:THR:HA	1.89	0.55
2:B:18:ARG:HH11	2:B:59:LEU:HD12	1.70	0.55
1:A:345:ALA:O	1:A:349:ALA:HB3	2.05	0.55
2:B:18:ARG:HH12	2:B:59:LEU:HA	1.71	0.55
2:B:18:ARG:NH1	2:B:110:ASP:OD2	2.39	0.54
1:A:152:ASP:HB2	1:A:339:PRO:HD2	1.90	0.54
2:B:33:TYR:CD2	2:B:51:ILE:HD13	2.42	0.54
1:A:381:ARG:NH1	1:A:388:GLN:OE1	2.40	0.54
1:A:554:ASP:N	1:A:554:ASP:OD1	2.37	0.54
1:A:59:VAL:HG23	1:A:159:LEU:HD23	1.90	0.53
3:C:46:ARG:HG2	9:C:301:HEM:O2D	2.08	0.53
1:A:509:THR:HG23	1:A:512:ARG:HH12	1.73	0.53
1:A:361:LEU:HD12	1:A:362:PRO:HD2	1.89	0.53
1:A:58:THR:CG2	5:A:700:FAD:O1A	2.57	0.52
1:A:490:LEU:HD13	1:A:541:GLU:HA	1.89	0.52
3:C:99:MET:CE	3:C:99:MET:HA	2.40	0.52
2:B:82:THR:HG21	2:B:87:ARG:NH2	2.25	0.52
2:B:39:ASN:HD22	2:B:39:ASN:N	2.07	0.52
1:A:57:HIS:NE2	5:A:700:FAD:HM82	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:67:GLU:HB3	2:B:69:ILE:HG13	1.92	0.51
2:B:181:PRO:HA	2:B:235:ILE:HD11	1.92	0.51
1:A:547:ARG:NH1	1:A:558:ARG:HD3	2.25	0.51
1:A:326:LEU:HD12	1:A:358:ILE:HG12	1.91	0.51
3:C:80:LEU:HD13	3:C:80:LEU:N	2.26	0.51
2:B:162:ALA:O	2:B:166:THR:HG22	2.11	0.51
1:A:81:PHE:HA	1:A:101:THR:HG21	1.91	0.51
3:C:77:VAL:HG12	3:C:77:VAL:O	2.10	0.51
3:C:107:ARG:HD2	3:C:125:SER:HB2	1.93	0.50
9:C:301:HEM:HBB2	9:C:301:HEM:HMB2	1.94	0.50
2:B:47:ALA:O	2:B:51:ILE:HG23	2.12	0.50
1:A:547:ARG:NH1	1:A:558:ARG:CD	2.74	0.50
2:B:176:ASP:HB3	3:C:16:TRP:CZ2	2.46	0.50
1:A:57:HIS:NE2	5:A:700:FAD:HM81	2.26	0.50
1:A:13:TYR:OH	1:A:458:ARG:NH1	2.44	0.50
4:D:72:LEU:HB3	4:D:126:ILE:HD11	1.94	0.50
1:A:297:SER:O	1:A:301:VAL:HG23	2.11	0.49
1:A:269:CYS:HB3	1:A:326:LEU:HD21	1.93	0.49
2:B:155:LEU:HD12	2:B:192:ILE:HD11	1.95	0.49
1:A:239:THR:CG2	1:A:588:VAL:HG13	2.42	0.49
2:B:16:ILE:HD12	2:B:33:TYR:HD1	1.78	0.49
1:A:59:VAL:CG2	1:A:159:LEU:HD23	2.43	0.49
2:B:104:HIS:CE1	2:B:172:TRP:O	2.66	0.49
1:A:501:TYR:OH	1:A:590:VAL:O	2.20	0.48
4:D:85:GLY:O	4:D:89:THR:HG22	2.13	0.48
1:A:84:THR:HA	1:A:410:LEU:HD22	1.94	0.48
2:B:198:PHE:HD2	2:B:201:GLU:HG3	1.79	0.48
1:A:328:HIS:O	1:A:329:LEU:C	2.51	0.48
1:A:111:LEU:HD11	1:A:419:VAL:HG21	1.96	0.48
1:A:460:ALA:HB3	1:A:509:THR:HG22	1.96	0.47
1:A:54:THR:O	1:A:59:VAL:CG2	2.62	0.47
1:A:158:LEU:CD2	1:A:415:LEU:HD22	2.43	0.47
1:A:59:VAL:HG11	2:B:69:ILE:O	2.14	0.47
1:A:269:CYS:SG	1:A:341:ILE:HD13	2.55	0.47
3:C:80:LEU:H	3:C:80:LEU:HD22	1.79	0.47
2:B:159:ILE:HA	2:B:159:ILE:HD13	1.83	0.47
2:B:103:PRO:HD2	2:B:166:THR:HG23	1.97	0.47
1:A:454:LEU:CD2	1:A:524:LEU:HD11	2.44	0.47
9:C:301:HEM:HBC2	9:C:301:HEM:CMC	2.45	0.46
1:A:254:HIS:HB2	1:A:365:HIS:CB	2.46	0.46
1:A:246:GLN:HA	1:A:584:THR:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:PHE:HB2	1:A:308:GLU:OE2	2.16	0.45
3:C:96:PHE:HB3	3:C:97:PRO:HD3	1.99	0.45
1:A:346:MET:O	1:A:350:GLY:N	2.48	0.45
2:B:102:LEU:HB3	2:B:166:THR:HG21	1.99	0.45
1:A:73:GLU:HG3	1:A:136:LEU:HD21	1.99	0.45
1:A:150:VAL:H	1:A:154:THR:HB	1.80	0.45
1:A:374:ASN:HB3	1:A:376:LYS:H	1.80	0.45
1:A:454:LEU:HD22	1:A:524:LEU:HD11	1.99	0.45
1:A:116:MET:CA	1:A:161:THR:HG21	2.43	0.45
2:B:121:GLN:NE2	2:B:171:TYR:OH	2.48	0.45
1:A:256:THR:HG21	1:A:324:LEU:HD12	1.99	0.44
3:C:35:TRP:CD2	10:C:302:FTN:H17	2.51	0.44
1:A:568:ILE:O	1:A:571:GLN:HB2	2.17	0.44
2:B:35:ILE:HG23	2:B:50:LYS:HD3	2.00	0.44
1:A:65:ILE:HD12	1:A:108:VAL:HG22	1.98	0.44
1:A:89:ASP:HB3	1:A:547:ARG:HG3	2.00	0.44
1:A:264:LEU:HD13	1:A:365:HIS:CE1	2.53	0.43
2:B:161:CYS:O	2:B:162:ALA:HB3	2.18	0.43
2:B:174:ASN:HD22	4:D:93:ARG:NH1	2.16	0.43
1:A:254:HIS:HB2	1:A:365:HIS:CG	2.52	0.43
1:A:415:LEU:HA	1:A:418:LEU:HD22	1.99	0.43
1:A:25:VAL:CG2	1:A:192:VAL:HG11	2.47	0.43
1:A:89:ASP:O	1:A:547:ARG:CD	2.66	0.43
1:A:387:ASP:OD2	1:A:600:ARG:NH1	2.51	0.43
2:B:178:TYR:CD1	2:B:214:ARG:HB2	2.54	0.43
1:A:248:LEU:HD12	1:A:535:GLN:CB	2.49	0.43
3:C:98:LEU:HD13	3:C:99:MET:HE2	2.00	0.43
1:A:258:ILE:CG1	1:A:265:ILE:HD11	2.44	0.43
2:B:188:TYR:CE1	2:B:237:GLU:HB3	2.53	0.43
1:A:113:ASN:HD22	2:B:138:GLY:N	2.12	0.42
1:A:327:HIS:CD2	1:A:328:HIS:N	2.87	0.42
1:A:544:LYS:HG2	1:A:555:PHE:CZ	2.54	0.42
1:A:486:VAL:CG1	1:A:553:GLU:HB2	2.50	0.42
1:A:59:VAL:HG23	1:A:159:LEU:CD2	2.48	0.42
1:A:72:MET:CE	1:A:121:THR:HG21	2.50	0.42
5:A:700:FAD:O2'	5:A:700:FAD:O4'	2.38	0.42
1:A:302:SER:HB2	1:A:362:PRO:HB3	1.99	0.42
1:A:26:GLY:O	1:A:31:GLY:HA3	2.19	0.42
2:B:20:ASP:OD2	2:B:22:ASP:N	2.53	0.42
1:A:143:GLN:NE2	1:A:295:LEU:HD23	2.34	0.42
2:B:189:ARG:NH2	2:B:193:ASP:OD1	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:HIS:CE1	5:A:700:FAD:HM82	2.54	0.42
3:C:46:ARG:O	3:C:47:GLY:C	2.56	0.42
1:A:221:TYR:CG	1:A:364:VAL:HG21	2.54	0.42
2:B:16:ILE:HD12	2:B:33:TYR:CD1	2.54	0.42
1:A:497:ILE:HG23	1:A:534:LEU:HD12	2.02	0.42
2:B:19:TRP:CZ3	3:C:25:PRO:HD2	2.55	0.42
3:C:52:LEU:HB3	9:C:301:HEM:CBC	2.50	0.42
2:B:219:MET:CE	3:C:117:LEU:HD22	2.50	0.42
1:A:308:GLU:OE2	1:A:313:ARG:NH1	2.53	0.41
1:A:65:ILE:HD12	1:A:108:VAL:CG2	2.50	0.41
1:A:72:MET:HE3	1:A:121:THR:HG21	2.02	0.41
1:A:109:VAL:HG22	2:B:141:GLN:HB3	2.01	0.41
1:A:256:THR:HG22	1:A:360:VAL:HG21	2.03	0.41
3:C:35:TRP:CE2	10:C:302:FTN:H17	2.55	0.41
1:A:25:VAL:HG12	1:A:214:THR:HG22	2.02	0.41
4:D:63:ASN:N	4:D:64:PRO:HD3	2.35	0.41
1:A:504:LEU:O	1:A:507:LEU:HG	2.21	0.41
1:A:418:LEU:HD21	5:A:700:FAD:H4'	2.02	0.41
1:A:311:GLU:HA	1:A:311:GLU:OE1	2.20	0.41
1:A:361:LEU:HD12	1:A:362:PRO:CD	2.50	0.41
1:A:544:LYS:HG3	1:A:555:PHE:CE2	2.56	0.41
1:A:561:GLU:OE2	1:A:581:ARG:HD3	2.21	0.41
4:D:57:LEU:HB2	4:D:58:PRO:HD3	2.03	0.41
1:A:276:LEU:HB2	1:A:294:ASP:OD2	2.21	0.41
1:A:176:GLU:C	1:A:197:ILE:HD12	2.42	0.41
2:B:109:LYS:O	2:B:110:ASP:C	2.57	0.40
3:C:83:GLY:O	3:C:86:LEU:N	2.54	0.40
3:C:80:LEU:O	3:C:81:CYS:SG	2.70	0.40
1:A:265:ILE:HG23	1:A:341:ILE:HB	2.03	0.40
1:A:150:VAL:HB	1:A:154:THR:HA	2.02	0.40
1:A:373:THR:HG22	1:A:374:ASN:O	2.21	0.40
3:C:74:LEU:O	3:C:78:LYS:N	2.53	0.40
1:A:494:CYS:HB3	1:A:538:TYR:CE1	2.56	0.40
1:A:200:GLY:HA3	1:A:514:MET:HB3	2.04	0.40
1:A:15:VAL:HG23	1:A:15:VAL:O	2.22	0.40
3:C:52:LEU:HB3	9:C:301:HEM:CAC	2.51	0.40
1:A:222:PHE:HA	1:A:474:GLN:HE21	1.85	0.40
1:A:307:LEU:O	1:A:311:GLU:HG2	2.21	0.40
2:B:176:ASP:OD2	4:D:93:ARG:NH2	2.55	0.40
1:A:206:ARG:NH1	1:A:440:PRO:O	2.54	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	611/664 (92%)	556 (91%)	52 (8%)	3 (0%)	34	76
2	B	237/280 (85%)	219 (92%)	17 (7%)	1 (0%)	39	80
3	C	136/169 (80%)	121 (89%)	15 (11%)	0	100	100
4	D	100/159 (63%)	87 (87%)	12 (12%)	1 (1%)	19	61
All	All	1084/1272 (85%)	983 (91%)	96 (9%)	5 (0%)	34	76

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	374	ASN
4	D	96	ALA
1	A	441	SER
2	B	55	ILE
1	A	329	LEU

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	499/538 (93%)	445 (89%)	54 (11%)	8	30
2	B	214/239 (90%)	189 (88%)	25 (12%)	7	27
3	C	117/142 (82%)	101 (86%)	16 (14%)	4	20
4	D	76/122 (62%)	68 (90%)	8 (10%)	8	32
All	All	906/1041 (87%)	803 (89%)	103 (11%)	7	28

All (103) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ASP
1	A	23	VAL
1	A	32	LEU
1	A	36	PHE
1	A	49	THR
1	A	65	ILE
1	A	73	GLU
1	A	85	VAL
1	A	107	SER
1	A	129	ARG
1	A	131	PHE
1	A	140	LYS
1	A	154	THR
1	A	161	THR
1	A	165	ARG
1	A	167	LEU
1	A	277	ILE
1	A	285	MET
1	A	294	ASP
1	A	303	ARG
1	A	311	GLU
1	A	325	GLN
1	A	329	LEU
1	A	332	GLU
1	A	343	GLU
1	A	352	ASP
1	A	363	THR
1	A	368	MET
1	A	374	ASN
1	A	381	ARG
1	A	403	SER
1	A	418	LEU
1	A	434	ARG
1	A	456	LYS
1	A	458	ARG
1	A	463	THR
1	A	488	SER
1	A	497	ILE
1	A	507	LEU
1	A	512	ARG
1	A	514	MET
1	A	534	LEU

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Mol	Chain	Res	Type
1	A	541	GLU
1	A	554	ASP
1	A	561	GLU
1	A	571	GLN
1	A	577	GLN
1	A	588	VAL
1	A	591	LYS
1	A	597	LEU
1	A	602	VAL
1	A	605	LYS
1	A	620	ARG
1	A	622	TYR
2	B	22	ASP
2	B	31	GLN
2	B	39	ASN
2	B	48	LEU
2	B	51	ILE
2	B	63	ARG
2	B	66	ARG
2	B	67	GLU
2	B	86	THR
2	B	91	THR
2	B	96	VAL
2	B	105	MET
2	B	129	LEU
2	B	146	ILE
2	B	159	ILE
2	B	166	THR
2	B	170	SER
2	B	189	ARG
2	B	192	ILE
2	B	205	LYS
2	B	214	ARG
2	B	217	THR
2	B	230	ASN
2	B	237	GLU
2	B	246	LYS
3	C	12	MET
3	C	26	LEU
3	C	30	ILE
3	C	31	THR
3	C	39	MET

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Mol	Chain	Res	Type
3	C	42	SER
3	C	46	ARG
3	C	52	LEU
3	C	72	SER
3	C	79	SER
3	C	80	LEU
3	C	94	ILE
3	C	95	VAL
3	C	104	ASN
3	C	122	LEU
3	C	130	LEU
4	D	49	VAL
4	D	63	ASN
4	D	71	SER
4	D	76	LEU
4	D	78	LEU
4	D	89	THR
4	D	108	LEU
4	D	134	TRP

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

Mol	Chain	Res	Type
1	A	113	ASN
1	A	143	GLN
1	A	246	GLN
1	A	579	HIS
2	B	31	GLN
2	B	39	ASN
2	B	121	GLN
2	B	174	ASN
2	B	230	ASN
3	C	104	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
5	FAD	A	700	-	52,58,58	1.34	7 (13%)	52,89,89	2.25	11 (21%)
6	FES	B	301	2	0,4,4	0.00	-	0,4,4	0.00	-
7	SF4	B	302	2	0,12,12	0.00	-	0,24,24	0.00	-
8	F3S	B	303	2	0,9,9	0.00	-	0,15,15	0.00	-
9	HEM	C	301	3,4	24,50,50	0.88	1 (4%)	16,82,82	0.96	0
10	FTN	C	302	-	24,24,24	1.20	1 (4%)	33,34,34	1.04	2 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	FAD	A	700	-	-	0/30/50/50	0/6/6/6
6	FES	B	301	2	-	0/0/4/4	0/1/1/1
7	SF4	B	302	2	-	0/0/48/48	0/6/5/5
8	F3S	B	303	2	-	0/0/24/24	0/0/3/3
9	HEM	C	301	3,4	-	0/6/54/54	0/0/8/8
10	FTN	C	302	-	-	0/18/18/18	0/2/2/2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	C	301	HEM	C1B-NB	-2.60	1.33	1.36
5	A	700	FAD	C9A-N10	2.39	1.42	1.38
5	A	700	FAD	C10-N10	2.65	1.42	1.39
5	A	700	FAD	C8-C7	2.85	1.48	1.41
5	A	700	FAD	C5A-C4A	3.05	1.47	1.40
5	A	700	FAD	C4-C4X	3.19	1.47	1.41
5	A	700	FAD	C9A-C5X	3.58	1.50	1.42
5	A	700	FAD	C4X-C10	3.63	1.47	1.40
10	C	302	FTN	C3-C2	5.42	1.49	1.40

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	700	FAD	N3A-C2A-N1A	-8.16	122.46	128.87
5	A	700	FAD	C1B-N9A-C4A	-4.94	121.30	126.81
5	A	700	FAD	N3-C2-N1	-3.58	121.66	127.69
5	A	700	FAD	C4-C4X-C10	-3.43	117.75	119.94
5	A	700	FAD	C4X-C4-N3	-3.32	119.19	123.52
5	A	700	FAD	C8M-C8-C7	-2.31	115.77	120.73
10	C	302	FTN	F3-C1-C2	-2.25	108.85	112.67
5	A	700	FAD	C6-C5X-C9A	2.08	121.41	119.11
5	A	700	FAD	O4B-C1B-N9A	2.26	112.38	108.11
5	A	700	FAD	C4X-N5-C5X	3.40	120.73	116.72
5	A	700	FAD	C1'-N10-C9A	3.84	123.28	118.83
10	C	302	FTN	C11-O2-C15	3.86	124.29	119.41
5	A	700	FAD	C4-N3-C2	7.87	121.72	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	700	FAD	10	0
7	B	302	SF4	1	0
9	C	301	HEM	6	0
10	C	302	FTN	2	0

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	613/664 (92%)	-0.21	19 (3%) 52 24	53, 82, 144, 169	0
2	B	239/280 (85%)	-0.55	0 100 100	53, 71, 98, 109	0
3	C	138/169 (81%)	-0.47	2 (1%) 78 51	50, 77, 114, 155	0
4	D	102/159 (64%)	-0.42	4 (3%) 43 18	58, 78, 102, 132	0
All	All	1092/1272 (85%)	-0.34	25 (2%) 64 33	50, 79, 138, 169	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	35	SER	5.9
1	A	317	PRO	3.4
1	A	328	HIS	3.1
1	A	330	PRO	3.0
1	A	11	THR	2.9
3	C	143	MET	2.9
1	A	280	GLN	2.9
1	A	331	PRO	2.8
1	A	290	PRO	2.8
4	D	36	SER	2.8
3	C	81	CYS	2.6
1	A	74	GLU	2.6
1	A	311	GLU	2.5
1	A	569	GLN	2.5
1	A	310	ARG	2.5
1	A	319	LYS	2.4
1	A	316	GLY	2.4
4	D	95	ASP	2.4
1	A	332	GLU	2.3
1	A	315	CYS	2.2
1	A	281	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	140	LYS	2.2
1	A	355	LYS	2.1
4	D	63	ASN	2.0
1	A	260	GLY	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 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
9	HEM	C	301	43/43	0.97	0.18	1.75	55,75,83,95	0
8	F3S	B	303	7/7	0.99	0.17	0.89	54,64,69,69	0
10	FTN	C	302	23/23	0.93	0.18	0.29	66,75,115,116	0
5	FAD	A	700	53/53	0.96	0.15	-0.33	57,69,89,90	0
7	SF4	B	302	8/8	0.99	0.14	-0.50	59,67,76,76	0
6	FES	B	301	4/4	0.99	0.14	-1.13	56,56,60,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.