



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2014 – 02:31 AM GMT

PDB ID : 3AE3
Title : Crystal structure of porcine heart mitochondrial complex II bound with 2-Nitro-N-phenyl-benzamide
Authors : Harada, S.; Sasaki, T.; Shindo, M.; Kido, Y.; Inaoka, D.K.; Omori, J.; Osanai, A.; Sakamoto, K.; Mao, J.; Matsuoka, S.; Inoue, M.; Honma, T.; Tanaka, A.; Kita, K.
Deposited on : 2010-02-04
Resolution : 3.35 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

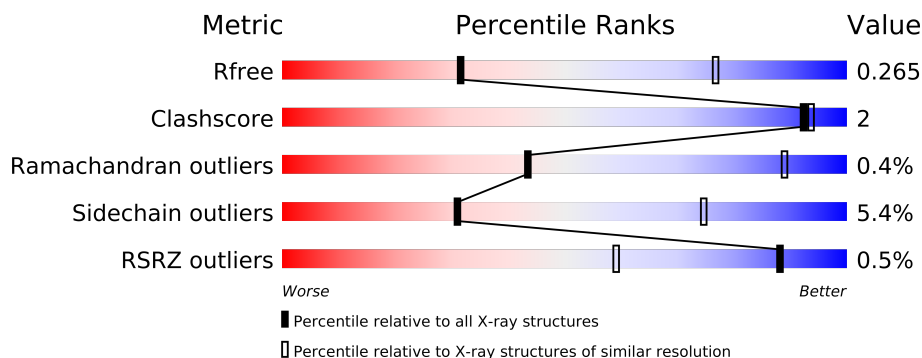
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.35 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}	66092	1141 (3.50-3.22)
Clashscore	79885	1030 (3.48-3.24)
Ramachandran outliers	78287	1008 (3.48-3.24)
Sidechain outliers	78261	1007 (3.48-3.24)
RSRZ outliers	66119	1141 (3.50-3.22)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	622	
2	B	252	
3	C	140	
4	D	103	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
10	EPH	D	1306	-	X
11	NBI	B	1201	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 8657 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

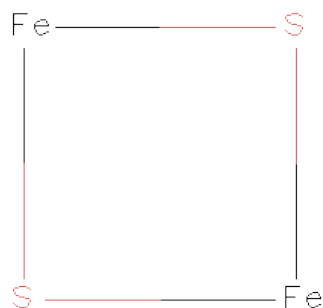
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	102	Total	C	N	O	S	0	0	0
			765	499	128	133	5			

- Molecule 5 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



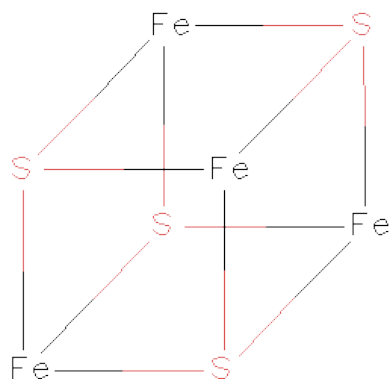
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 6 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



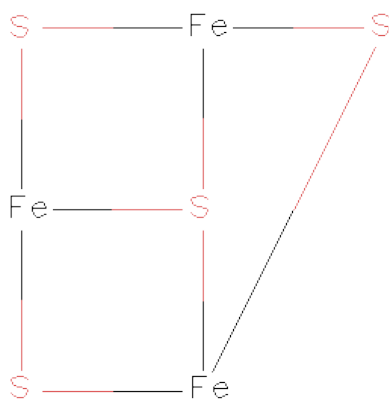
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 7 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



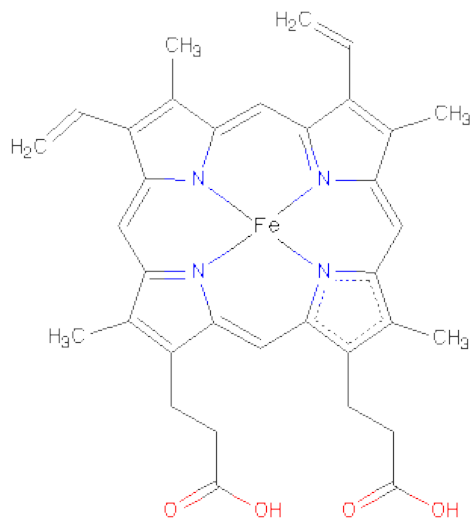
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	Fe	S	0	0
			8	4	4		

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



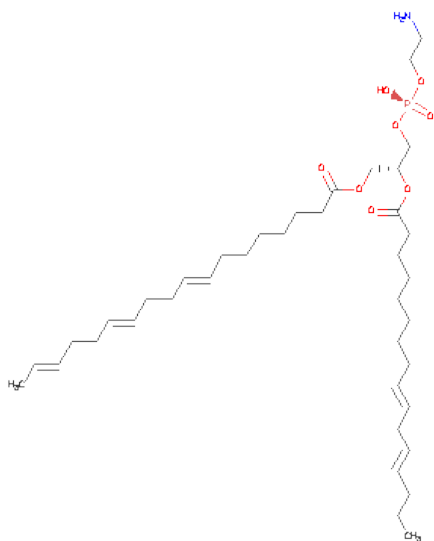
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	Fe	S	0	0
			7	3	4		

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



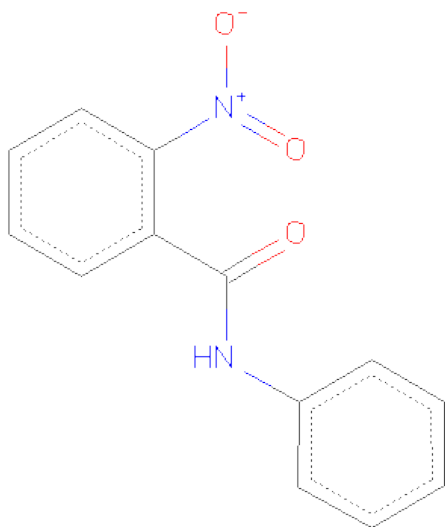
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	C	1	Total	C	Fe	N	O	
			43	34	1	4	4	

- Molecule 10 is L-ALPHA-PHOSPHATIDYL-BETA-OLEOYL-GAMMA-PALMITOYL-PHOSPHATIDYLETHANOLAMINE (three-letter code: EPH) (formula: $C_{39}H_{68}NO_8P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	D	1	Total	C	N	O	P	
			44	34	1	8	1	

- Molecule 11 is 2-NITRO-N-PHENYLBENZAMIDE (three-letter code: NBI) (formula: $C_{13}H_{10}N_2O_3$).

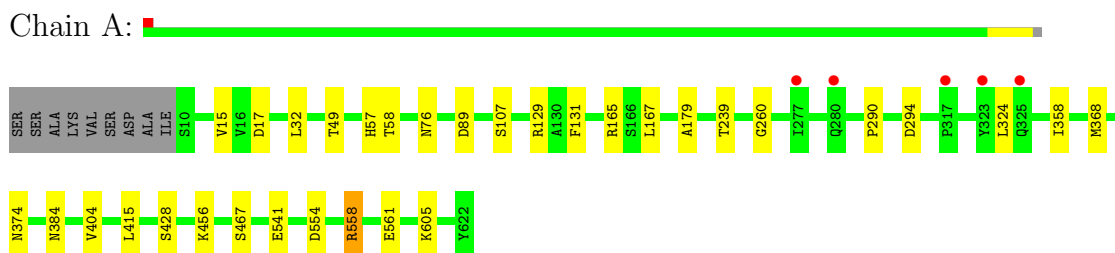


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
11	B	1	18	13	2	3	0	0

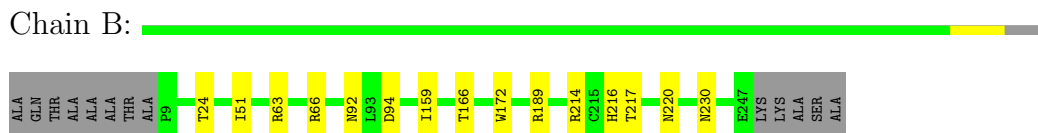
3 Residue-property plots

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

- Molecule 1: 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	71.51Å 84.50Å 295.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.44 – 3.35 48.44 – 3.35	Depositor EDS
% Data completeness (in resolution range)	85.1 (48.44-3.35) 85.1 (48.44-3.35)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 3.33Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.214 , 0.261 0.217 , 0.265	Depositor DCC
R_{free} test set	1144 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	78.7	Xtriage
Anisotropy	0.125	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 25.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 22687 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	8657	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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	0.32	0/4828	0.49	0/6531
2	B	0.31	0/1964	0.46	0/2648
3	C	0.33	0/1091	0.48	0/1483
4	D	0.30	0/784	0.45	0/1066
All	All	0.32	0/8667	0.48	0/11728

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4729	0	0	12	0
2	B	1922	0	0	2	0
3	C	1064	0	0	0	0
4	D	765	0	0	0	0
5	A	53	0	31	10	0
6	B	4	0	0	0	0
7	B	8	0	0	0	0
8	B	7	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	C	43	0	30	0	0
10	D	44	0	53	0	0
11	B	18	0	10	1	0
All	All	8657	0	124	15	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 2.

All (15) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:57:HIS:CE1	5:A:700:FAD:HM82	1.51	1.43
1:A:57:HIS:NE2	5:A:700:FAD:HM82	1.47	1.28
1:A:57:HIS:CE1	5:A:700:FAD:C8M	2.39	1.04
1:A:57:HIS:CD2	1:A:57:HIS:O	2.30	0.85
1:A:57:HIS:NE2	5:A:700:FAD:HM81	1.94	0.83
1:A:57:HIS:CG	1:A:57:HIS:O	2.45	0.70
1:A:57:HIS:NE2	5:A:700:FAD:C8	2.56	0.68
1:A:89:ASP:OD2	1:A:558:ARG:NH1	2.39	0.55
1:A:49:THR:OG1	5:A:700:FAD:O2B	2.26	0.49
1:A:179:ALA:N	5:A:700:FAD:N1A	2.63	0.47
1:A:58:THR:CG2	5:A:700:FAD:O4'	2.66	0.44
1:A:415:LEU:CG	5:A:700:FAD:C2	2.97	0.42
2:B:166:THR:O	2:B:172:TRP:NE1	2.54	0.41
5:A:700:FAD:H1'1	5:A:700:FAD:H9	1.81	0.41
2:B:216:HIS:CD2	11:B:1201:NBI:H6	2.56	0.41

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	611/622 (98%)	562 (92%)	46 (8%)	3 (0%)	38 85
2	B	237/252 (94%)	217 (92%)	19 (8%)	1 (0%)	43 89

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	136/140 (97%)	131 (96%)	5 (4%)	0	100	100
4	D	100/103 (97%)	97 (97%)	3 (3%)	0	100	100
All	All	1084/1117 (97%)	1007 (93%)	73 (7%)	4 (0%)	43	89

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	374	ASN
1	A	290	PRO
2	B	24	THR
1	A	260	GLY

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	499/506 (99%)	475 (95%)	24 (5%)	35	78
2	B	214/220 (97%)	203 (95%)	11 (5%)	33	76
3	C	117/118 (99%)	108 (92%)	9 (8%)	18	60
4	D	76/76 (100%)	71 (93%)	5 (7%)	24	68
All	All	906/920 (98%)	857 (95%)	49 (5%)	31	74

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	VAL
1	A	17	ASP
1	A	32	LEU
1	A	76	ASN
1	A	107	SER
1	A	129	ARG
1	A	131	PHE
1	A	165	ARG
1	A	167	LEU
1	A	239	THR

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Mol	Chain	Res	Type
1	A	294	ASP
1	A	324	LEU
1	A	358	ILE
1	A	368	MET
1	A	384	ASN
1	A	404	VAL
1	A	428	SER
1	A	456	LYS
1	A	467	SER
1	A	541	GLU
1	A	554	ASP
1	A	558	ARG
1	A	561	GLU
1	A	605	LYS
2	B	51	ILE
2	B	63	ARG
2	B	66	ARG
2	B	92	ASN
2	B	94	ASP
2	B	159	ILE
2	B	189	ARG
2	B	214	ARG
2	B	217	THR
2	B	220	ASN
2	B	230	ASN
3	C	23	ASN
3	C	30	ILE
3	C	64	LEU
3	C	80	LEU
3	C	85	THR
3	C	86	LEU
3	C	98	LEU
3	C	108	HIS
3	C	122	LEU
4	D	52	LEU
4	D	63	ASN
4	D	72	LEU
4	D	108	LEU
4	D	134	TRP

Some 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 chains 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 ⓘ

7 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	1	58,58,58	1.05	5 (8%)	85,89,89	1.95	14 (16%)
11	NBI	B	1201	-	19,19,19	1.56	3 (15%)	25,25,25	0.75	1 (4%)
6	FES	B	302	2	0,4,4	0.00	-	0,4,4	0.00	-
7	SF4	B	303	2	12,12,12	4.30	12 (100%)	0,24,24	0.00	-
8	F3S	B	304	2	3,9,9	18.81	3 (100%)	0,15,15	0.00	-
9	HEM	C	1305	3,4	49,50,50	2.31	14 (28%)	46,82,82	2.12	7 (15%)
10	EPH	D	1306	-	42,43,48	2.26	9 (21%)	46,48,53	2.04	9 (19%)

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	1	-	0/34/50/50	0/1/6/6
11	NBI	B	1201	-	-	0/12/12/12	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	FES	B	302	2	-	0/0/4/4	0/0/1/1
7	SF4	B	303	2	-	0/0/48/48	0/0/5/5
8	F3S	B	304	2	-	0/0/24/24	0/0/3/3
9	HEM	C	1305	3,4	-	0/14/114/114	0/0/8/8
10	EPH	D	1306	-	1/1/4/14	0/47/47/52	0/0/0/0

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	B	304	F3S	S3-FE3	-19.23	2.20	2.33
8	B	304	F3S	S3-FE1	-18.73	2.20	2.33
8	B	304	F3S	S3-FE4	-18.45	2.20	2.33
10	D	1306	EPH	C31-C30	-8.71	1.51	1.55
9	C	1305	HEM	C3D-C2D	5.88	1.54	1.43
7	B	303	SF4	S4-FE1	-5.43	2.29	2.33
10	D	1306	EPH	P1-O6	5.37	1.79	1.55
9	C	1305	HEM	C3B-C2B	-5.25	1.34	1.43
9	C	1305	HEM	C2B-C1B	5.22	1.45	1.44
9	C	1305	HEM	C3C-C2C	-5.21	1.34	1.43
7	B	303	SF4	S1-FE3	-4.65	2.30	2.33
9	C	1305	HEM	C3C-CAC	4.65	1.55	1.40
7	B	303	SF4	S3-FE2	-4.64	2.30	2.33
7	B	303	SF4	S4-FE3	-4.60	2.30	2.33
7	B	303	SF4	S2-FE4	-4.56	2.30	2.33
9	C	1305	HEM	C3B-CAB	4.51	1.54	1.40
9	C	1305	HEM	C4A-C3A	4.18	1.45	1.40
10	D	1306	EPH	C16-C15	4.15	1.53	1.30
7	B	303	SF4	S1-FE4	-4.15	2.30	2.33
10	D	1306	EPH	O2-C4	4.13	1.46	1.33
7	B	303	SF4	S3-FE4	-4.12	2.30	2.33
10	D	1306	EPH	O1-C3	4.10	1.46	1.34
7	B	303	SF4	S4-FE2	-4.08	2.30	2.33
7	B	303	SF4	S2-FE1	-4.02	2.30	2.33
7	B	303	SF4	S2-FE3	-4.01	2.30	2.33
11	B	1201	NBI	C1-N2	-3.96	1.40	1.46
10	D	1306	EPH	C13-C12	3.86	1.53	1.31
10	D	1306	EPH	C25-C24	3.84	1.52	1.31
10	D	1306	EPH	C29-C28	3.84	1.52	1.31
7	B	303	SF4	S3-FE1	-3.64	2.30	2.33
11	B	1201	NBI	C2-C1	3.55	1.49	1.41
9	C	1305	HEM	C2D-C1D	3.37	1.45	1.44
7	B	303	SF4	S1-FE2	-3.36	2.31	2.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	B	1201	NBI	C8-N1	-3.29	1.35	1.41
5	A	700	FAD	C2A-N3A	3.11	1.38	1.32
5	A	700	FAD	C1'-C2'	2.63	1.54	1.51
9	C	1305	HEM	FE-NA	2.58	2.03	1.92
9	C	1305	HEM	CMB-C2B	2.55	1.55	1.47
9	C	1305	HEM	CMC-C2C	2.50	1.55	1.47
9	C	1305	HEM	FE-ND	2.43	2.06	1.97
5	A	700	FAD	C1'-N10	2.38	1.50	1.48
9	C	1305	HEM	CMD-C2D	2.37	1.54	1.47
5	A	700	FAD	C2A-N1A	2.35	1.38	1.33
5	A	700	FAD	C5X-N5	2.28	1.38	1.35
10	D	1306	EPH	P1-O7	2.20	1.59	1.51
9	C	1305	HEM	FE-NB	2.07	2.05	1.97

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	700	FAD	N3A-C2A-N1A	-10.99	119.52	128.71
10	D	1306	EPH	C14-C15-C16	-10.17	111.16	126.73
9	C	1305	HEM	C3B-C4B-NB	-8.85	107.67	114.00
9	C	1305	HEM	C4D-ND-C1D	6.86	112.18	105.16
5	A	700	FAD	C2-N1-C10	6.41	121.44	114.98
5	A	700	FAD	C2'-C1'-N10	-4.24	106.82	112.45
10	D	1306	EPH	C30-C29-C28	-4.09	110.76	125.02
9	C	1305	HEM	C2D-C1D-ND	-3.92	108.30	112.93
10	D	1306	EPH	O1-C3-C5	3.67	119.59	111.56
5	A	700	FAD	N3A-C4A-N9A	3.57	131.88	125.43
5	A	700	FAD	C4X-C10-N1	-3.45	119.28	122.73
5	A	700	FAD	C4X-N5-C5X	3.40	120.51	116.69
5	A	700	FAD	O4B-C1B-N9A	3.15	111.37	108.44
5	A	700	FAD	C5X-C9A-N10	3.13	119.89	116.80
10	D	1306	EPH	O2-C4-C18	3.12	121.76	111.94
9	C	1305	HEM	C1B-NB-C4B	3.04	108.27	105.16
9	C	1305	HEM	C4C-NC-C1C	3.02	108.67	105.53
9	C	1305	HEM	C4A-CHB-C1B	-2.80	123.78	127.47
9	C	1305	HEM	CMA-C3A-C4A	-2.66	124.53	128.62
5	A	700	FAD	C4-N3-C2	-2.61	120.03	125.39
10	D	1306	EPH	C11-C12-C13	-2.55	110.98	125.43
10	D	1306	EPH	C26-C25-C24	-2.55	111.00	125.43
10	D	1306	EPH	C23-C24-C25	-2.48	111.35	125.43
10	D	1306	EPH	C27-C28-C29	-2.38	111.94	125.43
5	A	700	FAD	N7A-C8A-N9A	-2.20	108.13	114.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	700	FAD	P-O3P-PA	-2.20	125.24	131.68
10	D	1306	EPH	C14-C13-C12	-2.18	111.40	124.86
5	A	700	FAD	C2A-N3A-C4A	2.17	120.19	114.01
5	A	700	FAD	C5A-C4A-N3A	-2.17	120.98	125.70
11	B	1201	NBI	C6-C1-N2	2.16	119.73	116.61
5	A	700	FAD	C4A-C5A-N7A	-2.07	107.75	109.52

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
10	D	1306	EPH	C2

There are no torsion outliers.

There are no ring outliers.

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	613/622 (98%)	0.01	5 (0%) 83 47	57, 82, 137, 161	0
2	B	239/252 (94%)	-0.04	0 100 100	54, 75, 112, 136	0
3	C	138/140 (98%)	-0.10	0 100 100	67, 84, 140, 157	0
4	D	102/103 (99%)	-0.19	0 100 100	68, 86, 114, 128	0
All	All	1092/1117 (97%)	-0.03	5 (0%) 88 59	54, 81, 129, 161	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	323	TYR	3.3
1	A	277	ILE	3.1
1	A	280	GLN	2.2
1	A	325	GLN	2.1
1	A	317	PRO	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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
10	EPH	D	1306	44/49	0.58	5.24	105,110,116,116	0
11	NBI	B	1201	18/18	0.33	2.65	86,86,87,87	0
9	HEM	C	1305	43/43	0.24	1.52	74,75,77,78	0
5	FAD	A	700	53/53	0.33	0.56	64,66,70,70	0
6	FES	B	302	4/4	0.21	-0.84	58,58,58,59	0
7	SF4	B	303	8/8	0.17	-1.17	56,56,56,57	0
8	F3S	B	304	7/7	0.14	-1.33	61,61,62,62	0

6.5 Other polymers ⓘ

There are no such residues in this entry.