



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:14 PM GMT

PDB ID : 1JFB
Title : X-ray structure of nitric oxide reductase (cytochrome P450nor) in the ferric resting state at atomic resolution
Authors : Shimizu, H.; Adachi, S.; Park, S.Y.; Shiro, Y.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2001-06-20
Resolution : 1.00 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

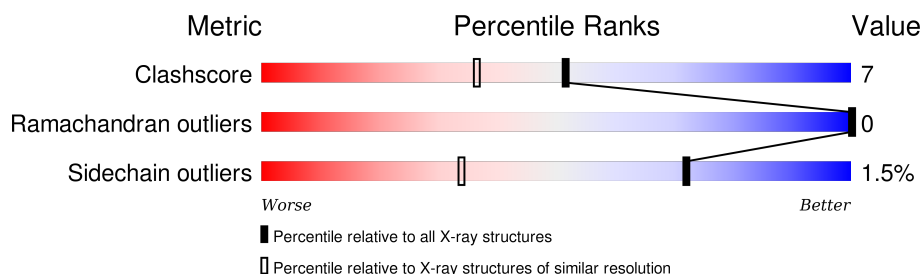
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.00 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))
Clashscore	102246	1333 (1.10-0.90)
Ramachandran outliers	100387	1247 (1.10-0.90)
Sidechain outliers	100360	1246 (1.10-0.90)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	404	 83% 15% ..

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 nitric-oxide reductase cytochrome P450 55A1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	399	Total	C	H	N	O	S	0	41	0
			6701	2129	3362	566	628	16			

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Fe	H	N	O	0	1
			146	68	2	60	8	8		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $\text{C}_3\text{H}_8\text{O}_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

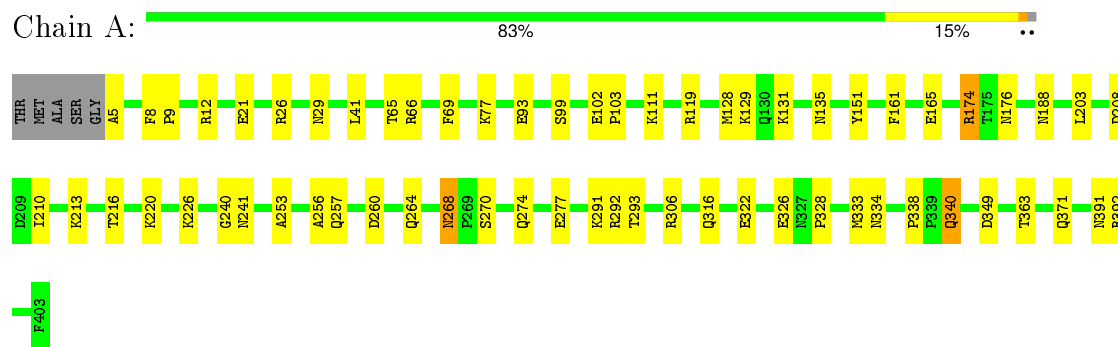
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1044	Total	O	0	88
			1044	1044		

3 Residue-property plots [i](#)

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.

Note EDS was not executed.

- Molecule 1: nitric-oxide reductase cytochrome P450 55A1



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.66 Å 82.13 Å 85.84 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.00	Depositor
% Data completeness (in resolution range)	98.0 (10.00-1.00)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.102 , 0.139	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7897	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, HEM

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	0.80	1/3512 (0.0%)	1.21	33/4769 (0.7%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	21	GLU	CD-OE1	-5.12	1.20	1.25

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	293[A]	THR	N-CA-CB	8.63	126.70	110.30
1	A	293[B]	THR	N-CA-CB	8.63	126.70	110.30
1	A	306[A]	ARG	NE-CZ-NH1	8.16	124.38	120.30
1	A	306[B]	ARG	NE-CZ-NH1	8.16	124.38	120.30
1	A	161	PHE	CB-CG-CD1	-7.87	115.29	120.80
1	A	119	ARG	CD-NE-CZ	7.57	134.20	123.60
1	A	208[A]	ASP	CB-CG-OD2	-6.61	112.35	118.30
1	A	208[B]	ASP	CB-CG-OD2	-6.61	112.35	118.30
1	A	208[A]	ASP	CB-CG-OD1	6.50	124.15	118.30
1	A	208[B]	ASP	CB-CG-OD1	6.50	124.15	118.30
1	A	161	PHE	CG-CD1-CE1	-6.42	113.73	120.80
1	A	69	PHE	CG-CD1-CE1	-6.32	113.85	120.80
1	A	12	ARG	NE-CZ-NH2	-6.09	117.25	120.30
1	A	151	TYR	CB-CG-CD1	6.09	124.65	121.00
1	A	41[A]	LEU	O-C-N	5.96	132.24	122.70
1	A	41[B]	LEU	O-C-N	5.96	132.24	122.70
1	A	128[A]	MET	CA-C-N	5.95	130.30	117.20
1	A	128[B]	MET	CA-C-N	5.95	130.30	117.20
1	A	174[A]	ARG	CD-NE-CZ	5.82	131.75	123.60
1	A	174[B]	ARG	CD-NE-CZ	5.82	131.75	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	161	PHE	CD1-CG-CD2	5.81	125.85	118.30
1	A	174[A]	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	A	174[B]	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	A	69	PHE	CD1-CE1-CZ	5.66	126.89	120.10
1	A	93	GLU	OE1-CD-OE2	-5.46	116.75	123.30
1	A	326	GLU	OE1-CD-OE2	5.45	129.84	123.30
1	A	392[A]	ARG	CD-NE-CZ	5.40	131.16	123.60
1	A	392[B]	ARG	CD-NE-CZ	5.40	131.16	123.60
1	A	208[A]	ASP	CA-C-N	-5.37	105.39	117.20
1	A	208[B]	ASP	CA-C-N	-5.37	105.39	117.20
1	A	292	ARG	NE-CZ-NH1	5.25	122.92	120.30
1	A	161	PHE	CZ-CE2-CD2	-5.08	114.00	120.10
1	A	66	ARG	NE-CZ-NH1	-5.02	117.79	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	3339	3362	3379	46	0
2	A	86	60	60	3	0
3	A	6	0	8	0	0
4	A	1044	0	0	32	0
All	All	4475	3422	3447	47	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 7.

All (47) 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:A:77:LYS:HE3	4:A:1485:HOH:O	1.68	0.93
1:A:131:LYS:HD3	4:A:963:HOH:O	1.70	0.91
1:A:371[B]:GLN:HG2	4:A:1481:HOH:O	1.79	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363[B]:THR:HG21	4:A:1566[B]:HOH:O	1.85	0.75
1:A:216[B]:THR:HG22	4:A:977:HOH:O	1.85	0.75
1:A:174[B]:ARG:HE	1:A:188:ASN:HD22	1.34	0.73
1:A:102[A]:GLU:HG2	4:A:1029:HOH:O	1.89	0.72
1:A:349:ASP:OD2	4:A:856:HOH:O	2.13	0.66
1:A:103:PRO:HB2	4:A:1601:HOH:O	1.96	0.64
1:A:322:GLU:HG3	1:A:328:PRO:HG3	1.80	0.62
1:A:264:GLN:HE22	1:A:334:ASN:HD21	1.48	0.62
1:A:220:LYS:HE2	4:A:1396:HOH:O	1.99	0.60
1:A:268:ASN:HD21	1:A:270:SER:HB2	1.67	0.60
1:A:213:LYS:HD3	4:A:1571[A]:HOH:O	2.00	0.59
1:A:213:LYS:HB3	4:A:1571[A]:HOH:O	2.03	0.58
1:A:9[B]:PRO:HG2	4:A:1366:HOH:O	2.04	0.57
1:A:5:ALA:N	4:A:1569:HOH:O	2.39	0.56
1:A:203[B]:LEU:HD12	1:A:220:LYS:HE3	1.89	0.55
1:A:129:LYS:HD2	4:A:1482:HOH:O	2.06	0.54
1:A:291:LYS:HE2	4:A:1628:HOH:O	2.09	0.53
1:A:135:ASN:ND2	4:A:1094:HOH:O	2.40	0.53
1:A:260:ASP:HB2	4:A:1574[B]:HOH:O	2.09	0.52
1:A:277[A]:GLU:HG2	4:A:1267:HOH:O	2.11	0.50
1:A:210:ILE:HG13	4:A:1598[B]:HOH:O	2.13	0.48
1:A:8:PHE:CG	1:A:9[A]:PRO:HA	2.49	0.47
1:A:338:PRO:HB2	1:A:340[A]:GLN:NE2	2.29	0.47
1:A:274[A]:GLN:HG3	4:A:685:HOH:O	2.14	0.47
1:A:203[A]:LEU:HD11	1:A:226:LYS:HG2	1.97	0.47
1:A:240:GLY:HA3	2:A:501[B]:HEM:C4B	2.50	0.47
1:A:77:LYS:HE2	4:A:1608:HOH:O	2.16	0.46
1:A:99[A]:SER:HB2	4:A:1614:HOH:O	2.15	0.46
1:A:253:ALA:O	1:A:257[B]:GLN:HG2	2.17	0.45
1:A:240:GLY:HA3	2:A:501[A]:HEM:C1C	2.52	0.45
1:A:8:PHE:CG	1:A:9[B]:PRO:HA	2.52	0.45
1:A:316:GLN:NE2	4:A:1596:HOH:O	2.49	0.44
1:A:9[A]:PRO:HB2	4:A:1366:HOH:O	2.18	0.44
1:A:111[A]:LYS:NZ	4:A:932:HOH:O	2.35	0.43
2:A:501[B]:HEM:HBC1	4:A:605:HOH:O	2.18	0.43
1:A:256:ALA:HA	4:A:1634:HOH:O	2.19	0.43
1:A:26:ARG:NH2	4:A:1134:HOH:O	2.52	0.42
1:A:65[A]:THR:HG23	4:A:1163:HOH:O	2.19	0.42
1:A:241:ASN:HB3	4:A:1595:HOH:O	2.18	0.42
1:A:165[B]:GLU:HG3	4:A:1641:HOH:O	2.18	0.41
1:A:176:ASN:ND2	4:A:1165:HOH:O	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203[B]:LEU:HD11	1:A:220:LYS:HG3	2.04	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	439/404 (109%)	430 (98%)	9 (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	382/343 (111%)	374 (98%)	8 (2%)	61 21

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

Mol	Chain	Res	Type
1	A	29[A]	ASN
1	A	29[B]	ASN
1	A	268	ASN
1	A	333[A]	MET
1	A	333[B]	MET

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Mol	Chain	Res	Type
1	A	340[A]	GLN
1	A	340[B]	GLN
1	A	391	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	GLN
1	A	135	ASN
1	A	176	ASN
1	A	188	ASN
1	A	201	GLN
1	A	264	GLN
1	A	268	ASN
1	A	391	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

3 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
2	HEM	A	501[A]	1,4	30,50,50	1.97	6 (20%)	24,82,82	2.35	7 (29%)
2	HEM	A	501[B]	1	30,50,50	2.23	7 (23%)	24,82,82	2.16	7 (29%)
3	GOL	A	502	-	5,5,5	1.83	2 (40%)	5,5,5	0.60	0

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
2	HEM	A	501[A]	1,4	-	0/10/54/54	0/0/8/8
2	HEM	A	501[B]	1	-	0/10/54/54	0/0/8/8
3	GOL	A	502	-	-	0/4/4/4	0/0/0/0

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501[A]	HEM	C2D-C3D	-6.74	1.34	1.54
2	A	501[B]	HEM	C2D-C3D	-5.88	1.36	1.54
2	A	501[B]	HEM	C3B-C4B	-4.49	1.47	1.51
2	A	501[B]	HEM	C2C-C1C	-4.38	1.44	1.52
2	A	501[A]	HEM	C3B-C4B	-4.32	1.48	1.51
2	A	501[B]	HEM	C3D-C4D	-4.25	1.46	1.51
2	A	501[B]	HEM	CAD-C3D	-2.91	1.48	1.54
2	A	501[A]	HEM	CAA-C2A	-2.66	1.47	1.52
2	A	501[A]	HEM	CAD-C3D	-2.28	1.49	1.54
2	A	501[A]	HEM	C2C-C1C	-2.24	1.48	1.52
2	A	501[A]	HEM	C2D-C1D	-2.11	1.45	1.51
3	A	502	GOL	C1-C2	2.36	1.61	1.52
2	A	501[B]	HEM	C1C-NC	2.52	1.39	1.36
3	A	502	GOL	O3-C3	2.95	1.55	1.42
2	A	501[B]	HEM	C4C-NC	3.49	1.40	1.36

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501[B]	HEM	C3C-CAC-CBC	2.21	127.85	124.46
2	A	501[A]	HEM	C2D-C3D-C4D	2.37	105.51	101.50
2	A	501[A]	HEM	CMD-C2D-C3D	2.86	127.01	114.35
2	A	501[B]	HEM	C2D-C3D-C4D	2.98	106.55	101.50
2	A	501[B]	HEM	CMD-C2D-C3D	3.01	127.66	114.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501[A]	HEM	C3C-CAC-CBC	3.23	129.41	124.46
2	A	501[A]	HEM	CAD-C3D-C4D	3.37	124.35	112.47
2	A	501[B]	HEM	CAD-C3D-C4D	3.67	125.43	112.47
2	A	501[B]	HEM	CMB-C2B-C3B	4.25	127.13	116.53
2	A	501[B]	HEM	CMC-C2C-C3C	4.64	128.10	116.53
2	A	501[A]	HEM	CMC-C2C-C3C	4.87	128.68	116.53
2	A	501[B]	HEM	CAD-C3D-C2D	5.13	127.96	113.22
2	A	501[A]	HEM	CMB-C2B-C3B	5.31	129.79	116.53
2	A	501[A]	HEM	CAD-C3D-C2D	5.88	130.13	113.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501[A]	HEM	1	0
2	A	501[B]	HEM	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.