



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 14, 2017 – 12:18 AM EDT

PDB ID : 5VUY
Title : Structure of human neuronal nitric oxide synthase heme domain in complex with 7-(((4-(Dimethylamino)phenethyl)amino)methyl)quinolin-2-amine
Authors : Li, H.; Poulos, T.L.
Deposited on : unknown
Resolution : 2.15 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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-20029824

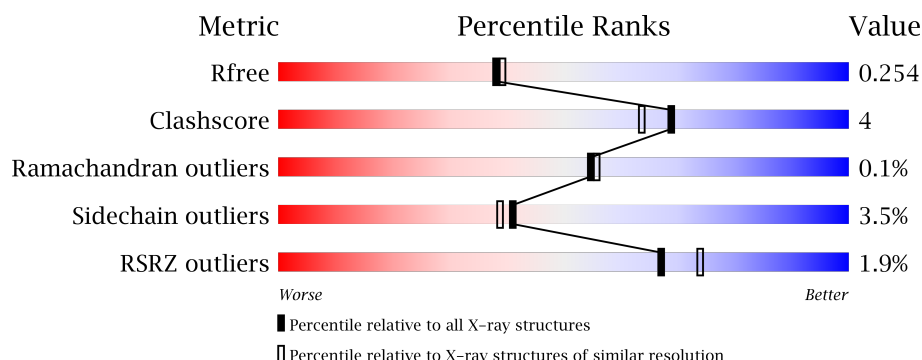
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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}	100719	1170 (2.16-2.16)
Clashscore	112137	1278 (2.16-2.16)
Ramachandran outliers	110173	1256 (2.16-2.16)
Sidechain outliers	110143	1255 (2.16-2.16)
RSRZ outliers	101464	1175 (2.16-2.16)

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	421	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%;"></div> <div style="position: absolute; bottom: 0; left: 0; width: 100%; height: 10px;"> <div style="width: 3%; height: 10px; background-color: red;"></div> <div style="width: 85%; height: 10px; background-color: green;"></div> <div style="width: 13%; height: 10px; background-color: yellow;"></div> <div style="width: 1%; height: 10px; background-color: grey;"></div> </div> </div> <div> <div style="width: 3%;"></div> <div style="width: 85%;"></div> <div style="width: 13%;"></div> <div style="width: 1%;"></div> </div> </div>
1	B	421	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%;"></div> <div style="position: absolute; bottom: 0; left: 0; width: 100%; height: 10px;"> <div style="width: 3%; height: 10px; background-color: red;"></div> <div style="width: 85%; height: 10px; background-color: green;"></div> <div style="width: 11%; height: 10px; background-color: yellow;"></div> <div style="width: 1%; height: 10px; background-color: grey;"></div> </div> </div> <div> <div style="width: 3%;"></div> <div style="width: 85%;"></div> <div style="width: 11%;"></div> <div style="width: 1%;"></div> </div> </div>

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.

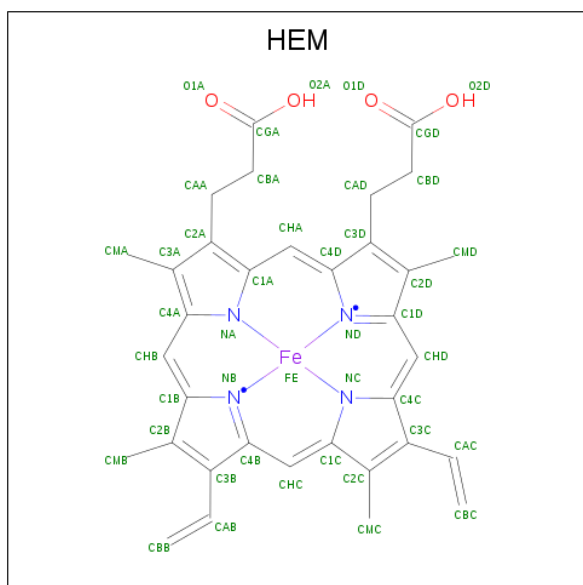
- Molecule 1 is a protein called Nitric oxide synthase, brain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	413	Total 3371	C 2159	N 574	O 616	S 22	0	2	0
1	B	408	Total 3341	C 2141	N 571	O 608	S 21	0	3	0

There are 4 discrepancies between the modelled and reference sequences:

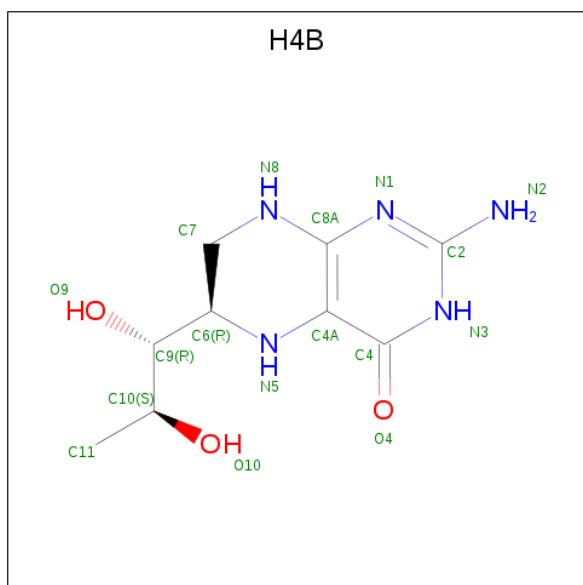
Chain	Residue	Modelled	Actual	Comment	Reference
A	354	ALA	ARG	engineered mutation	UNP P29475
A	357	ASP	GLY	engineered mutation	UNP P29475
B	354	ALA	ARG	engineered mutation	UNP P29475
B	357	ASP	GLY	engineered mutation	UNP P29475

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



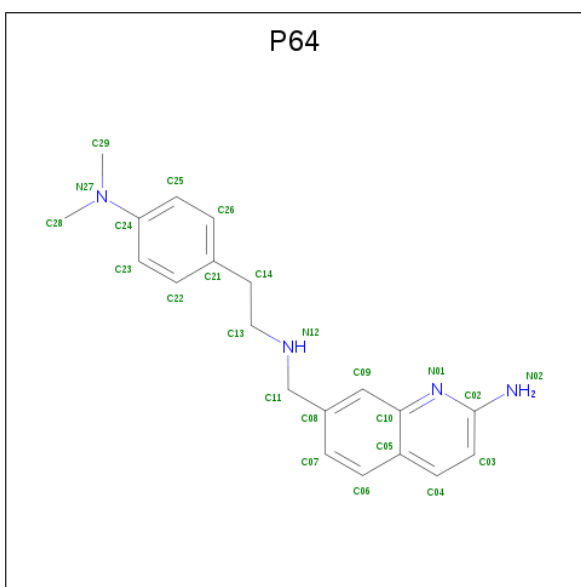
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	
			43	34	1	4	4	
2	B	1	Total	C	Fe	N	O	
			43	34	1	4	4	

- Molecule 3 is 5,6,7,8-TETRAHYDROBIOPTERIN (three-letter code: H4B) (formula: $C_9H_{15}N_5O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O		
			17	9	5	3		
3	B	1	Total	C	N	O		
			17	9	5	3		

- Molecule 4 is 7-[(2-[4-(dimethylamino)phenyl]ethyl)amino)methyl]quinolin-2-amine (three-letter code: P64) (formula: $C_{20}H_{24}N_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	0
			24	20	4		
4	B	1	Total	C	N	0	0
			24	20	4		

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Zn	0	0
			1	1		

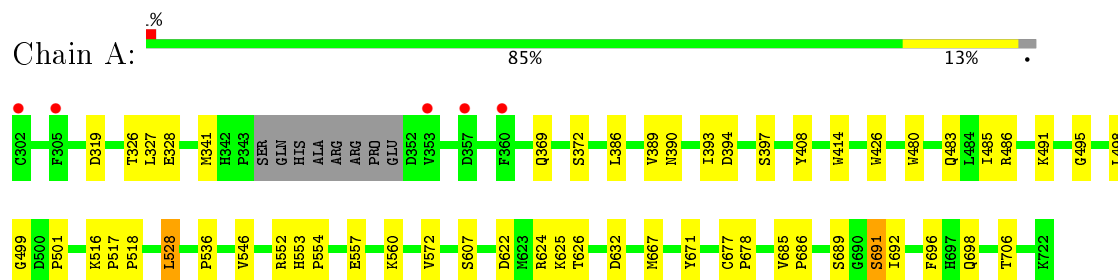
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	131	Total	O	0	0
			131	131		
6	B	113	Total	O	0	0
			113	113		

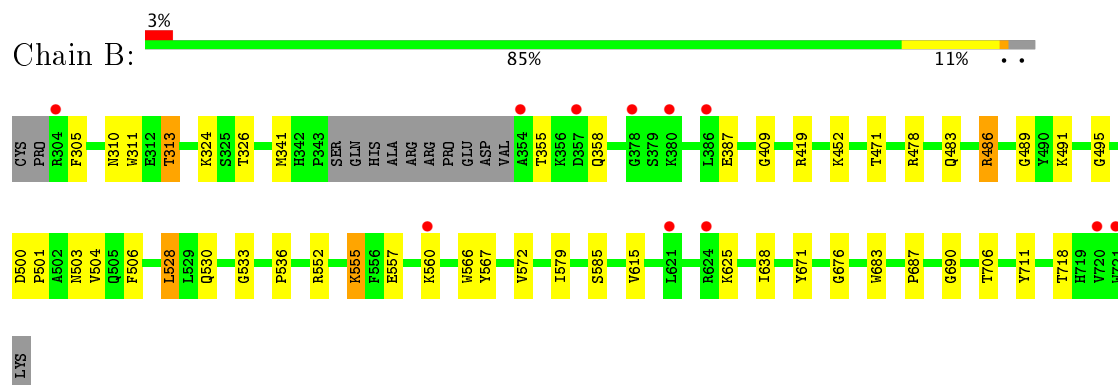
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Nitric oxide synthase, brain



- Molecule 1: Nitric oxide synthase, brain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.23Å 122.40Å 165.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.22 – 2.15 49.22 – 2.15	Depositor EDS
% Data completeness (in resolution range)	90.5 (49.22-2.15) 90.6 (49.22-2.15)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.23 (at 2.16Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.192 , 0.256 0.189 , 0.254	Depositor DCC
R_{free} test set	2572 reflections (4.86%)	DCC
Wilson B-factor (Å ²)	39.1	Xtriage
Anisotropy	1.152	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7125	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.47% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, ZN, H4B, P64

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	0.37	0/3473	0.54	0/4712
1	B	0.36	0/3445	0.51	0/4674
All	All	0.37	0/6918	0.52	0/9386

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

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	3371	0	3282	28	0
1	B	3341	0	3257	29	0
2	A	43	0	30	1	0
2	B	43	0	30	3	0
3	A	17	0	15	0	0
3	B	17	0	15	0	0
4	A	24	0	0	1	0
4	B	24	0	0	1	0
5	A	1	0	0	0	0
6	A	131	0	0	1	0
6	B	113	0	0	4	0
All	All	7125	0	6629	58	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 (58) 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:528:LEU:HD22	1:A:536:PRO:HB2	1.55	0.88
1:A:390:ASN:ND2	6:A:901:HOH:O	2.18	0.73
1:A:667:MET:HE1	1:A:698:GLN:HG2	1.69	0.72
1:B:486[B]:ARG:NH2	6:B:901:HOH:O	2.21	0.71
1:A:483:GLN:HB2	1:A:486:ARG:HG3	1.72	0.70
1:A:691:SER:HB3	1:B:687:PRO:HB2	1.74	0.69
1:B:572:VAL:HG21	4:B:803:P64:C07	2.24	0.68
1:A:480:TRP:HB2	1:A:528:LEU:HB3	1.77	0.66
1:A:485:ILE:HD13	1:A:546:VAL:HG13	1.77	0.65
1:B:491:LYS:HG2	1:B:504:VAL:HG11	1.79	0.65
1:A:557:GLU:OE2	1:A:560:LYS:NZ	2.32	0.63
1:A:572:VAL:HG21	4:A:803:P64:C07	2.30	0.62
1:B:528:LEU:HD22	1:B:536:PRO:HB2	1.81	0.61
2:A:801:HEM:HHC	2:A:801:HEM:HBB2	1.85	0.58
1:A:319:ASP:HB2	1:A:671:TYR:HE2	1.67	0.58
1:A:326:THR:HG21	1:A:706:THR:HG22	1.85	0.58
1:B:486[A]:ARG:HH11	1:B:503:ASN:HD21	1.53	0.57
2:B:801:HEM:HBB2	2:B:801:HEM:HHC	1.85	0.56
1:B:486[A]:ARG:HD2	1:B:503:ASN:HD21	1.71	0.56
1:A:414:TRP:CE3	1:A:426:TRP:HA	2.41	0.56
1:A:483:GLN:HB2	1:A:486:ARG:CG	2.36	0.55
1:A:622:ASP:OD1	1:A:624:ARG:NH2	2.40	0.54
1:A:341:MET:HG3	1:B:311:TRP:NE1	2.23	0.54
1:B:555:LYS:NZ	6:B:905:HOH:O	2.41	0.52
1:B:491:LYS:NZ	1:B:495:GLY:O	2.40	0.52
1:A:498:LEU:HD12	1:A:499:GLY:H	1.76	0.51
1:B:711:TYR:OH	2:B:801:HEM:O1D	2.22	0.51
1:B:625:LYS:HD3	6:B:948:HOH:O	2.12	0.48
1:B:486[B]:ARG:NH1	1:B:567:TYR:OH	2.47	0.48
1:A:689:SER:HB3	1:A:692:ILE:HG12	1.94	0.48
1:A:691:SER:HA	1:A:696:PHE:CG	2.49	0.47
1:B:478:ARG:HD3	1:B:585:SER:HB2	1.97	0.47
1:B:409:GLY:HA3	1:B:579:ILE:HD13	1.97	0.46
1:B:483:GLN:HB2	1:B:486[B]:ARG:HD3	1.98	0.46
1:B:557:GLU:O	1:B:560:LYS:NZ	2.49	0.45
1:B:310:ASN:OD1	1:B:313:THR:HG23	2.17	0.45
1:B:501:PRO:O	1:B:504:VAL:HG23	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:671:TYR:CE2	1:B:676:GLY:HA2	2.52	0.44
1:A:553:HIS:CG	1:A:554:PRO:HD2	2.54	0.43
1:A:517:PRO:HA	1:A:518:PRO:HD3	1.95	0.42
1:B:483:GLN:HB2	1:B:486[A]:ARG:HG3	2.01	0.42
1:B:486[B]:ARG:HH12	1:B:566:TRP:HZ2	1.66	0.42
1:B:355:THR:N	1:B:358:GLN:OE1	2.52	0.42
2:B:801:HEM:HBB2	2:B:801:HEM:CHC	2.50	0.41
1:A:491:LYS:HE3	1:A:495:GLY:O	2.21	0.41
1:B:530:GLN:HE21	1:B:533:GLY:HA2	1.86	0.41
1:A:501:PRO:HB2	1:A:607:SER:O	2.21	0.41
1:A:369:GLN:HG2	1:A:408:TYR:OH	2.21	0.41
1:A:498:LEU:HD12	1:A:499:GLY:N	2.35	0.41
1:A:685:VAL:HA	1:A:686:PRO:HD3	1.94	0.41
1:B:506:PHE:CE1	1:B:528:LEU:HD12	2.56	0.41
1:A:677:CYS:HA	1:A:678:PRO:HD2	1.93	0.41
1:B:419:ARG:HD3	1:B:683:TRP:CD2	2.57	0.40
1:B:615:VAL:HG21	1:B:638:ILE:HD11	2.04	0.40
1:B:489:GLY:HA3	1:B:500:ASP:O	2.22	0.40
1:A:389:VAL:O	1:A:393:ILE:HG13	2.21	0.40
1:A:491:LYS:HD2	1:A:491:LYS:HA	1.96	0.40
1:B:452:LYS:NZ	6:B:906:HOH:O	2.45	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	411/421 (98%)	398 (97%)	13 (3%)	0	100	100
1	B	407/421 (97%)	396 (97%)	10 (2%)	1 (0%)	51	50
All	All	818/842 (97%)	794 (97%)	23 (3%)	1 (0%)	55	56

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	690	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	371/376 (99%)	358 (96%)	13 (4%)	41	39
1	B	367/376 (98%)	353 (96%)	14 (4%)	38	35
All	All	738/752 (98%)	711 (96%)	27 (4%)	41	36

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

Mol	Chain	Res	Type
1	A	327	LEU
1	A	328	GLU
1	A	372	SER
1	A	386	LEU
1	A	394	ASP
1	A	397	SER
1	A	516	LYS
1	A	528	LEU
1	A	552	ARG
1	A	625	LYS
1	A	626	THR
1	A	632	ASP
1	A	691	SER
1	B	305	PHE
1	B	313	THR
1	B	324	LYS
1	B	326	THR
1	B	341	MET
1	B	387	GLU
1	B	471	THR
1	B	486[A]	ARG
1	B	486[B]	ARG

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Mol	Chain	Res	Type
1	B	528	LEU
1	B	552	ARG
1	B	555	LYS
1	B	706	THR
1	B	718	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	503	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 ⓘ

Of 7 ligands modelled in this entry, 1 is monoatomic - leaving 6 for Mogul analysis.

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	801	1	28,50,50	2.16	6 (21%)	17,82,82	2.00	8 (47%)
3	H4B	A	802	-	14,18,18	0.78	0	12,26,26	2.06	4 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	P64	A	803	-	26,26,26	1.25	2 (7%)	33,35,35	1.20	2 (6%)
2	HEM	B	801	1	28,50,50	2.20	6 (21%)	17,82,82	1.85	5 (29%)
3	H4B	B	802	-	14,18,18	0.84	0	12,26,26	2.42	6 (50%)
4	P64	B	803	-	26,26,26	1.27	2 (7%)	33,35,35	1.44	5 (15%)

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	801	1	-	0/6/54/54	0/0/8/8
3	H4B	A	802	-	-	0/8/17/17	0/2/2/2
4	P64	A	803	-	-	0/11/11/11	0/3/3/3
2	HEM	B	801	1	-	0/6/54/54	0/0/8/8
3	H4B	B	802	-	-	0/8/17/17	0/2/2/2
4	P64	B	803	-	-	0/11/11/11	0/3/3/3

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEM	C3B-C2B	-5.06	1.33	1.40
2	B	801	HEM	C3B-C2B	-4.97	1.33	1.40
2	A	801	HEM	C3C-C2C	-3.96	1.35	1.40
2	B	801	HEM	C3C-C2C	-3.77	1.35	1.40
4	A	803	P64	C09-C10	-2.70	1.37	1.41
4	B	803	P64	C02-N01	2.08	1.35	1.33
2	A	801	HEM	C4D-ND	2.72	1.40	1.36
2	B	801	HEM	C4D-ND	3.17	1.40	1.36
2	B	801	HEM	C3B-CAB	3.39	1.54	1.47
2	A	801	HEM	C3C-CAC	3.51	1.54	1.47
2	A	801	HEM	C3B-CAB	3.55	1.54	1.47
2	B	801	HEM	C3C-CAC	3.78	1.55	1.47
4	A	803	P64	C05-C10	4.07	1.48	1.42
4	B	803	P64	C05-C10	4.62	1.49	1.42
2	B	801	HEM	C3D-C2D	5.21	1.53	1.37
2	A	801	HEM	C3D-C2D	5.22	1.53	1.37

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	HEM	CBD-CAD-C3D	-3.81	105.20	112.47
4	A	803	P64	C11-C08-C09	-3.46	116.34	121.69
2	B	801	HEM	CBD-CAD-C3D	-3.45	105.88	112.47
2	A	801	HEM	CBA-CAA-C2A	-3.24	106.30	112.48
4	B	803	P64	C13-C14-C21	-3.23	106.05	112.81
3	B	802	H4B	N3-C2-N1	-3.11	120.41	125.45
3	A	802	H4B	N3-C2-N1	-3.00	120.59	125.45
2	A	801	HEM	CMA-C3A-C4A	-2.90	124.00	128.46
2	B	801	HEM	C1D-C2D-C3D	-2.87	105.00	107.00
3	B	802	H4B	C6-C7-N8	-2.65	106.81	111.01
2	B	801	HEM	CBA-CAA-C2A	-2.63	107.46	112.48
2	A	801	HEM	C1D-C2D-C3D	-2.60	105.19	107.00
2	B	801	HEM	CMA-C3A-C4A	-2.41	124.76	128.46
4	B	803	P64	C03-C04-C05	-2.38	117.13	120.83
4	B	803	P64	C11-C08-C09	-2.33	118.08	121.69
2	A	801	HEM	CAA-CBA-CGA	-2.33	108.67	112.66
2	B	801	HEM	CAD-CBD-CGD	-2.29	108.75	112.66
3	B	802	H4B	C4A-N5-C6	-2.15	115.31	121.16
2	A	801	HEM	CAD-CBD-CGD	-2.01	109.22	112.66
2	A	801	HEM	CMB-C2B-C3B	2.05	128.69	124.89
4	A	803	P64	C04-C03-C02	2.26	121.56	119.49
2	A	801	HEM	CMA-C3A-C2A	2.30	129.28	124.94
4	B	803	P64	N02-C02-N01	2.54	119.63	118.06
3	B	802	H4B	C2-N1-C8A	2.70	120.58	114.51
3	A	802	H4B	C2-N1-C8A	2.70	120.60	114.51
3	A	802	H4B	C4-N3-C2	3.03	120.42	116.06
3	B	802	H4B	C4-N3-C2	3.28	120.78	116.06
3	A	802	H4B	C4-C4A-C8A	4.00	118.19	114.56
4	B	803	P64	C04-C03-C02	4.03	123.18	119.49
3	B	802	H4B	C4-C4A-C8A	4.86	118.96	114.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	HEM	1	0
4	A	803	P64	1	0
2	B	801	HEM	3	0
4	B	803	P64	1	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	413/421 (98%)	0.26	5 (1%) 79 83	30, 50, 82, 102	0
1	B	408/421 (96%)	0.27	11 (2%) 55 63	29, 57, 95, 119	0
All	All	821/842 (97%)	0.27	16 (1%) 67 74	29, 53, 91, 119	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	380	LYS	3.8
1	A	353	VAL	3.7
1	B	721	TRP	3.3
1	B	624	ARG	3.3
1	B	304	ARG	2.8
1	B	378	GLY	2.6
1	B	354	ALA	2.5
1	A	360	PHE	2.4
1	B	621	LEU	2.4
1	B	386	LEU	2.3
1	A	302	CYS	2.3
1	B	720	VAL	2.2
1	B	357	ASP	2.2
1	A	305	PHE	2.2
1	A	357	ASP	2.2
1	B	560	LYS	2.1

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(\AA^2)	Q<0.9
2	HEM	B	801	43/43	0.98	0.15	1.31	31,43,49,57	0
5	ZN	A	804	1/1	1.00	0.16	1.15	49,49,49,49	0
4	P64	A	803	24/24	0.95	0.16	0.95	35,43,67,70	0
2	HEM	A	801	43/43	0.97	0.15	0.72	23,37,47,58	0
4	P64	B	803	24/24	0.94	0.14	0.70	25,55,74,76	0
3	H4B	A	802	17/17	0.97	0.15	0.32	37,39,43,45	0
3	H4B	B	802	17/17	0.98	0.10	-2.17	27,36,51,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.