



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 05:22 am GMT

PDB ID : 5AD6
Title : Structure of rat neuronal nitric oxide synthase heme domain in complex with
7-((3-(Dimethylamino)methyl)phenoxy)methyl)quinolin-2- amine
Authors : Li, H.; Poulos, T.L.
Deposited on : 2015-08-20
Resolution : 2.00 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
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) : recalc28949

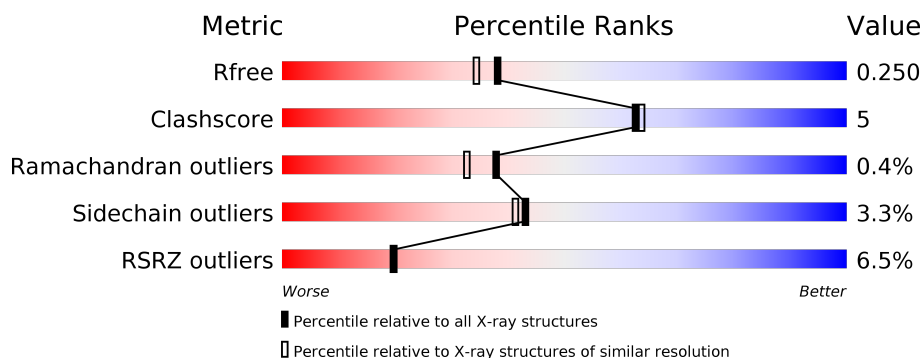
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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.

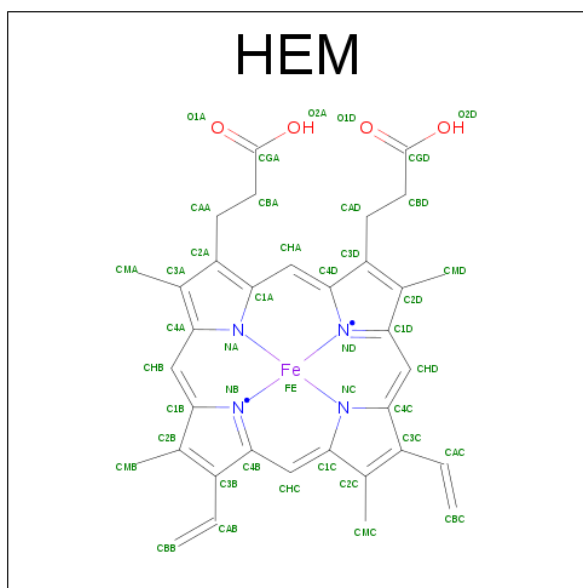
Mol	Chain	Length	Quality of chain
1	A	422	<div> <div>10%</div> <div> <div></div> <div>81%</div> <div>15%</div> <div>••</div> </div> </div>
1	B	422	<div> <div>3%</div> <div> <div></div> <div>85%</div> <div>12%</div> <div>•</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	HEM	B	750	-	-	-	X
4	7M3	A	800	-	-	-	X
4	7M3	B	800	-	-	-	X
5	ACT	B	860	-	-	-	X

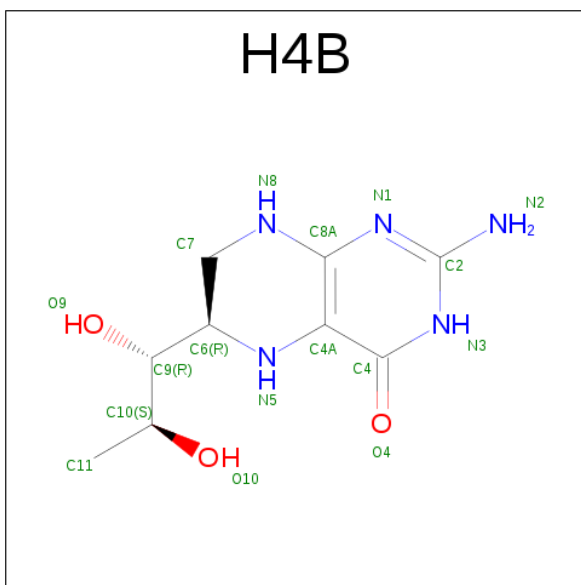
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

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



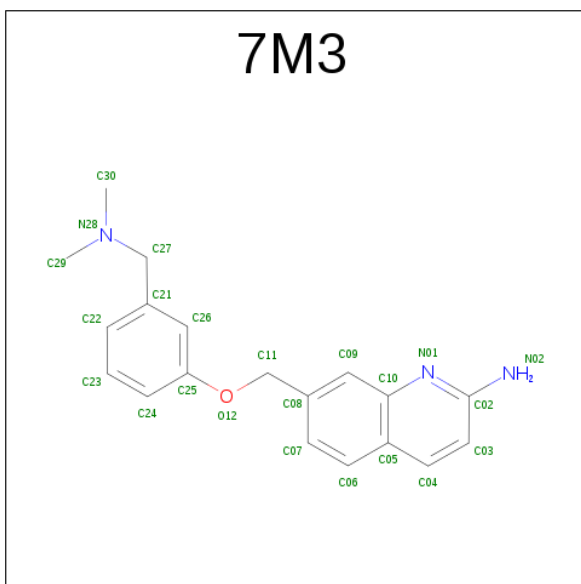
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is 5,6,7,8-TETRAHYDROBIOPTERIN (three-letter code: H4B) (formula: $\text{C}_9\text{H}_{15}\text{N}_5\text{O}_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			17	9	5	3		
3	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 4 is 7-[[3-[(DIMETHYLAMINO)METHYL]PHENOXY]METHYL]QUINOLIN-2-AMINE (three-letter code: 7M3) (formula: C₁₉H₂₁N₃O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			23	19	3	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			23	19	3	1		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Zn	0	0
			1	1		

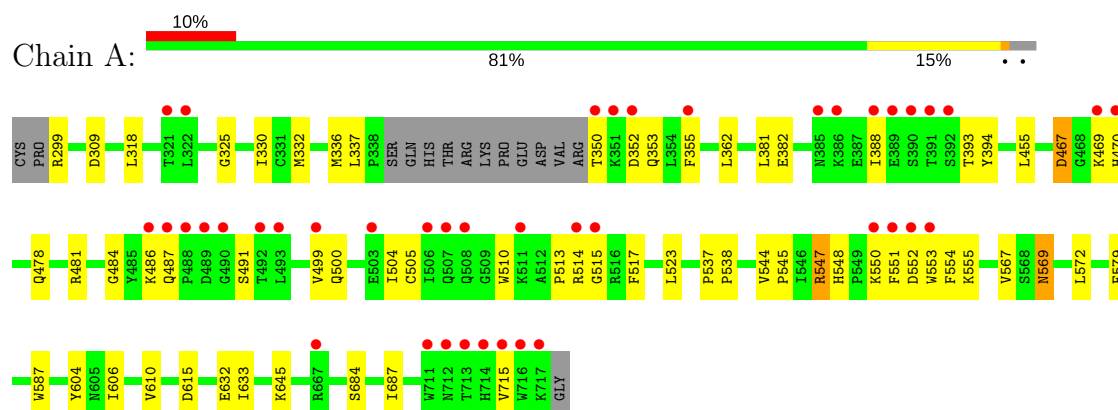
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	199	Total	O	0	0
			199	199		
7	B	235	Total	O	0	0
			235	235		

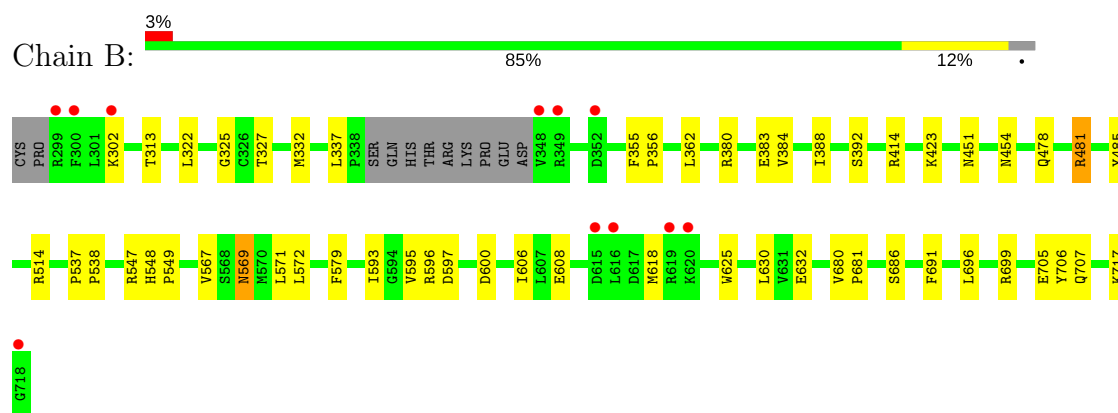
3 Residue-property plots [i](#)

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	51.76Å 111.67Å 164.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.16 – 2.00 39.16 – 2.00	Depositor EDS
% Data completeness (in resolution range)	78.3 (39.16-2.00) 78.3 (39.16-2.00)	Depositor EDS
R_{merge}	0.26	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.03 (at 2.00Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.192 , 0.251 0.191 , 0.250	Depositor DCC
R_{free} test set	2485 reflections (4.88%)	DCC
Wilson B-factor (Å ²)	26.2	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 57.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7286	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.47% 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: 7M3, HEM, ZN, H4B, ACT

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	0.39	0/3422	0.55	0/4643
1	B	0.43	0/3453	0.56	0/4681
All	All	0.41	0/6875	0.55	0/9324

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	3323	0	3232	31	0
1	B	3354	0	3270	32	0
2	A	43	0	30	2	0
2	B	43	0	30	4	0
3	A	17	0	15	0	0
3	B	17	0	15	0	0
4	A	23	0	21	1	0
4	B	23	0	21	5	0
5	A	4	0	3	0	0
5	B	4	0	3	0	0
6	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	199	0	0	0	0
7	B	235	0	0	2	0
All	All	7286	0	6640	68	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 5.

All (68) 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:A:750:HEM:HBB2	2:A:750:HEM:HHC	1.67	0.76
1:A:330:ILE:HD11	1:B:696:LEU:HD22	1.71	0.72
2:B:750:HEM:HHC	2:B:750:HEM:HBB2	1.73	0.70
1:B:699:ARG:NH2	1:B:705:GLU:OE1	2.28	0.66
2:A:750:HEM:HMC2	2:A:750:HEM:HBC2	1.79	0.65
4:B:800:7M3:H07	4:B:800:7M3:H24	1.80	0.64
2:B:750:HEM:HBC2	2:B:750:HEM:HMC2	1.83	0.61
1:B:478:GLN:HB2	1:B:481:ARG:HG3	1.83	0.60
1:A:567:VAL:HG21	4:A:800:7M3:C07	2.32	0.60
1:B:593:ILE:HA	1:B:597:ASP:HB2	1.86	0.58
1:A:569:ASN:H	1:A:569:ASN:HD22	1.51	0.56
1:A:478:GLN:HB2	1:A:481:ARG:HG3	1.88	0.56
1:A:355:PHE:HD1	1:A:388:ILE:HD12	1.75	0.52
1:A:545:PRO:HG2	1:A:547:ARG:NH1	2.25	0.52
1:B:569:ASN:H	1:B:569:ASN:HD22	1.58	0.52
1:A:486:LYS:HE2	1:A:499:VAL:HG11	1.93	0.51
1:B:325:GLY:O	1:B:332:MET:HG3	2.12	0.50
1:B:322:LEU:HB2	1:B:699:ARG:HB2	1.95	0.49
1:B:388:ILE:O	1:B:392:SER:N	2.42	0.49
1:B:485:TYR:CZ	1:B:514:ARG:HA	2.49	0.48
1:A:455:LEU:HD12	1:A:587:TRP:HB3	1.96	0.48
1:A:606:ILE:O	1:A:610:VAL:HG23	2.14	0.47
1:A:325:GLY:O	1:A:332:MET:HG3	2.13	0.47
1:A:500:GLN:O	1:A:504:ILE:HG13	2.14	0.47
1:B:380:ARG:NH1	1:B:383:GLU:OE1	2.41	0.47
1:A:572:LEU:HB3	1:A:579:PHE:HB2	1.97	0.47
1:B:706:TYR:OH	2:B:750:HEM:O1D	2.29	0.46
1:A:469:LYS:HE3	1:A:470:HIS:HE1	1.80	0.46
1:A:393:THR:OG1	1:A:394:TYR:N	2.48	0.46
1:B:686:SER:HA	1:B:691:PHE:CG	2.51	0.46
1:B:606:ILE:HA	7:B:2203:HOH:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:548:HIS:NE2	1:B:632:GLU:OE1	2.49	0.46
1:B:572:LEU:HB3	1:B:579:PHE:HB2	1.97	0.45
1:B:548:HIS:CG	1:B:549:PRO:HD2	2.51	0.45
1:B:596:ARG:O	1:B:600:ASP:HB2	2.16	0.45
1:A:505:CYS:O	1:A:510:TRP:N	2.43	0.45
1:A:299:ARG:HG2	1:A:318:LEU:HD11	1.99	0.45
1:B:414:ARG:NH1	1:B:706:TYR:OH	2.49	0.45
1:A:517:PHE:HE1	1:A:604:TYR:CZ	2.36	0.44
1:B:302:LYS:HE3	1:B:302:LYS:HB2	1.42	0.44
1:B:567:VAL:HG21	4:B:800:7M3:C07	2.47	0.44
1:A:484:GLY:O	1:A:499:VAL:HA	2.18	0.44
1:A:469:LYS:HE3	1:A:470:HIS:CE1	2.52	0.44
1:A:610:VAL:HG21	1:A:633:ILE:HD11	1.98	0.44
1:A:513:PRO:O	1:A:515:GLY:N	2.50	0.44
1:A:548:HIS:NE2	1:A:632:GLU:OE1	2.47	0.44
1:B:595:VAL:HG13	1:B:630:LEU:HD11	2.00	0.43
1:B:680:VAL:HA	1:B:681:PRO:HD3	1.89	0.43
1:B:355:PHE:N	1:B:356:PRO:HD2	2.33	0.43
1:A:350:THR:N	1:A:353:GLN:OE1	2.52	0.43
1:A:569:ASN:HD22	1:A:569:ASN:N	2.14	0.43
1:B:618:MET:HA	1:B:625:TRP:CD1	2.53	0.43
1:A:548:HIS:HB2	1:A:554:PHE:CG	2.54	0.43
1:B:537:PRO:HA	1:B:538:PRO:HD3	1.88	0.43
1:B:569:ASN:HD21	4:B:800:7M3:C22	2.31	0.42
1:B:569:ASN:HD21	4:B:800:7M3:C23	2.32	0.42
1:A:362:LEU:HA	1:A:362:LEU:HD23	1.85	0.42
1:A:684:SER:HB3	1:A:687:ILE:HD11	2.02	0.42
1:B:608:GLU:HB2	7:B:2202:HOH:O	2.20	0.42
1:B:569:ASN:N	1:B:569:ASN:HD22	2.18	0.41
1:A:537:PRO:HA	1:A:538:PRO:HD3	1.86	0.41
1:B:571:LEU:HD12	1:B:707:GLN:OE1	2.19	0.41
1:A:467:ASP:OD1	1:A:467:ASP:N	2.54	0.41
1:B:362:LEU:HD11	1:B:384:VAL:HG21	2.02	0.41
1:B:451:ASN:HB3	1:B:454:ASN:O	2.21	0.40
1:A:544:VAL:HA	1:A:545:PRO:HD2	1.89	0.40
1:A:551:PHE:HB3	1:A:553:TRP:CE2	2.57	0.40
2:B:750:HEM:HBA2	4:B:800:7M3:H111	2.04	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	406/422 (96%)	382 (94%)	21 (5%)	3 (1%)	25	18
1	B	409/422 (97%)	395 (97%)	14 (3%)	0	100	100
All	All	815/844 (97%)	777 (95%)	35 (4%)	3 (0%)	38	33

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	514	ARG
1	A	491	SER
1	A	309	ASP

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	365/377 (97%)	349 (96%)	16 (4%)	33	28
1	B	368/377 (98%)	360 (98%)	8 (2%)	57	60
All	All	733/754 (97%)	709 (97%)	24 (3%)	43	41

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	336	MET
1	A	337	LEU
1	A	352	ASP

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Mol	Chain	Res	Type
1	A	381	LEU
1	A	382	GLU
1	A	467	ASP
1	A	487	GLN
1	A	523	LEU
1	A	547	ARG
1	A	550	LYS
1	A	552	ASP
1	A	555	LYS
1	A	569	ASN
1	A	615	ASP
1	A	645	LYS
1	A	715	VAL
1	B	313	THR
1	B	327	THR
1	B	337	LEU
1	B	423	LYS
1	B	481	ARG
1	B	547	ARG
1	B	569	ASN
1	B	717	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	407	HIS
1	A	500	GLN
1	A	569	ASN
1	B	508	GLN
1	B	569	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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 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	750	1	28,50,50	2.21	6 (21%)	17,82,82	1.81	5 (29%)
3	H4B	A	760	-	14,18,18	0.89	0	12,26,26	2.40	4 (33%)
4	7M3	A	800	-	25,25,25	1.04	3 (12%)	33,34,34	1.02	2 (6%)
5	ACT	A	860	-	1,3,3	1.60	0	0,3,3	0.00	-
2	HEM	B	750	1	28,50,50	2.29	7 (25%)	17,82,82	2.01	5 (29%)
3	H4B	B	760	-	14,18,18	1.04	1 (7%)	12,26,26	2.47	5 (41%)
4	7M3	B	800	-	25,25,25	0.96	2 (8%)	33,34,34	1.14	2 (6%)
5	ACT	B	860	-	1,3,3	0.95	0	0,3,3	0.00	-

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	750	1	-	0/6/54/54	0/0/8/8
3	H4B	A	760	-	-	0/8/17/17	0/2/2/2
4	7M3	A	800	-	-	0/9/9/9	0/3/3/3
5	ACT	A	860	-	-	0/0/0/0	0/0/0/0
2	HEM	B	750	1	-	0/6/54/54	0/0/8/8
3	H4B	B	760	-	-	0/8/17/17	0/2/2/2
4	7M3	B	800	-	-	0/9/9/9	0/3/3/3
5	ACT	B	860	-	-	0/0/0/0	0/0/0/0

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	750	HEM	C3B-C2B	-5.18	1.33	1.40
2	B	750	HEM	C3B-C2B	-4.86	1.33	1.40
2	B	750	HEM	C3C-C2C	-4.67	1.34	1.40
2	A	750	HEM	C3C-C2C	-3.98	1.35	1.40
3	B	760	H4B	C4-C4A	-2.11	1.38	1.41
4	A	800	7M3	C04-C03	2.03	1.40	1.36
4	B	800	7M3	C06-C07	2.12	1.41	1.36
4	B	800	7M3	C02-N01	2.13	1.35	1.33
4	A	800	7M3	C02-N01	2.18	1.35	1.33
2	A	750	HEM	C4D-ND	2.27	1.39	1.36
2	B	750	HEM	C1B-NB	2.32	1.39	1.36
4	A	800	7M3	C06-C07	2.36	1.41	1.36
2	B	750	HEM	C4D-ND	2.79	1.40	1.36
2	B	750	HEM	C3B-CAB	3.22	1.54	1.47
2	A	750	HEM	C3B-CAB	3.59	1.55	1.47
2	A	750	HEM	C3C-CAC	3.64	1.55	1.47
2	B	750	HEM	C3C-CAC	4.12	1.55	1.47
2	B	750	HEM	C3D-C2D	5.31	1.53	1.37
2	A	750	HEM	C3D-C2D	5.39	1.53	1.37

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	750	HEM	CBA-CAA-C2A	-4.34	104.19	112.48
2	B	750	HEM	C1D-C2D-C3D	-4.07	104.16	107.00
3	B	760	H4B	N3-C2-N1	-3.57	119.65	125.45
2	B	750	HEM	CAD-CBD-CGD	-3.51	106.67	112.66
2	A	750	HEM	C1D-C2D-C3D	-3.48	104.58	107.00
3	A	760	H4B	N3-C2-N1	-3.45	119.85	125.45
2	A	750	HEM	CAD-CBD-CGD	-3.02	107.50	112.66
2	A	750	HEM	CBD-CAD-C3D	-2.97	106.81	112.47
4	A	800	7M3	C03-C02-N01	-2.80	119.39	122.25
4	B	800	7M3	C21-C27-N28	-2.66	108.30	113.07
4	B	800	7M3	C03-C02-N01	-2.60	119.60	122.25
2	B	750	HEM	CBD-CAD-C3D	-2.29	108.09	112.47
3	B	760	H4B	C6-C7-N8	-2.14	107.61	111.01
2	B	750	HEM	CMD-C2D-C3D	2.00	128.72	124.94
2	A	750	HEM	CMC-C2C-C3C	2.02	128.65	124.89
2	A	750	HEM	C4A-C3A-C2A	2.06	108.43	107.00
3	B	760	H4B	C2-N1-C8A	2.87	120.99	114.51
4	A	800	7M3	C11-O12-C25	2.89	124.80	117.61
3	A	760	H4B	C2-N1-C8A	2.99	121.24	114.51
3	B	760	H4B	C4-N3-C2	3.24	120.72	116.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	760	H4B	C4-N3-C2	3.27	120.76	116.06
3	A	760	H4B	C4-C4A-C8A	4.90	119.00	114.56
3	B	760	H4B	C4-C4A-C8A	5.05	119.14	114.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	750	HEM	2	0
4	A	800	7M3	1	0
2	B	750	HEM	4	0
4	B	800	7M3	5	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

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	408/422 (96%)	0.55	42 (10%) 7 7	15, 39, 85, 119	0
1	B	411/422 (97%)	-0.05	11 (2%) 55 54	12, 31, 64, 94	0
All	All	819/844 (97%)	0.25	53 (6%) 20 20	12, 35, 77, 119	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	717	LYS	11.5
1	A	488	PRO	8.9
1	B	348	VAL	7.7
1	A	716	TRP	6.4
1	A	486	LYS	6.3
1	B	300	PHE	6.2
1	A	715	VAL	6.1
1	A	352	ASP	5.6
1	B	619	ARG	4.6
1	A	551	PHE	4.6
1	A	507	GLN	4.5
1	A	508	GLN	4.5
1	A	351	LYS	4.2
1	B	620	LYS	4.2
1	A	490	GLY	4.2
1	A	389	GLU	4.0
1	A	515	GLY	3.9
1	A	506	ILE	3.9
1	A	713	THR	3.8
1	A	712	ASN	3.7
1	A	487	GLN	3.5
1	A	514	ARG	3.5
1	A	489	ASP	3.3
1	B	718	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	499	VAL	3.3
1	B	616	LEU	3.2
1	A	550	LYS	3.2
1	A	511	LYS	3.0
1	A	388	ILE	2.9
1	A	355	PHE	2.8
1	A	503	GLU	2.8
1	B	299	ARG	2.8
1	A	469	LYS	2.8
1	A	553	TRP	2.7
1	A	470	HIS	2.6
1	A	386	LYS	2.5
1	A	385	ASN	2.4
1	A	552	ASP	2.4
1	A	714	HIS	2.4
1	A	493	LEU	2.4
1	A	667	ARG	2.4
1	A	390	SER	2.3
1	A	391	THR	2.3
1	A	711	TRP	2.2
1	A	321	THR	2.2
1	B	302	LYS	2.2
1	B	349	ARG	2.2
1	A	350	THR	2.2
1	A	392	SER	2.1
1	B	615	ASP	2.1
1	A	492	THR	2.1
1	A	322	LEU	2.0
1	B	352	ASP	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 [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
4	7M3	B	800	23/23	0.91	0.23	4.53	12,39,95,98	0
4	7M3	A	800	23/23	0.90	0.29	3.98	19,33,99,100	0
5	ACT	B	860	4/4	0.94	0.14	3.21	33,40,45,60	0
2	HEM	B	750	43/43	0.98	0.15	2.29	9,22,44,62	0
3	H4B	B	760	17/17	0.91	0.20	1.46	26,42,55,56	0
5	ACT	A	860	4/4	0.92	0.14	1.21	30,45,46,52	0
2	HEM	A	750	43/43	0.98	0.17	0.74	9,22,49,61	0
3	H4B	A	760	17/17	0.94	0.17	0.65	31,44,55,58	0
6	ZN	B	900	1/1	1.00	0.07	-1.24	26,26,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.