



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:05 PM GMT

PDB ID : 5AGL
Title : Structure of rat neuronal nitric oxide synthase heme domain in complex with
(S)-2-Amino-5-(2-(methylsulfonyl)acetimidamido)pentanoic acid
Authors : Li, H.; Poulos, T.L.
Deposited on : 2015-02-02
Resolution : 1.94 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) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

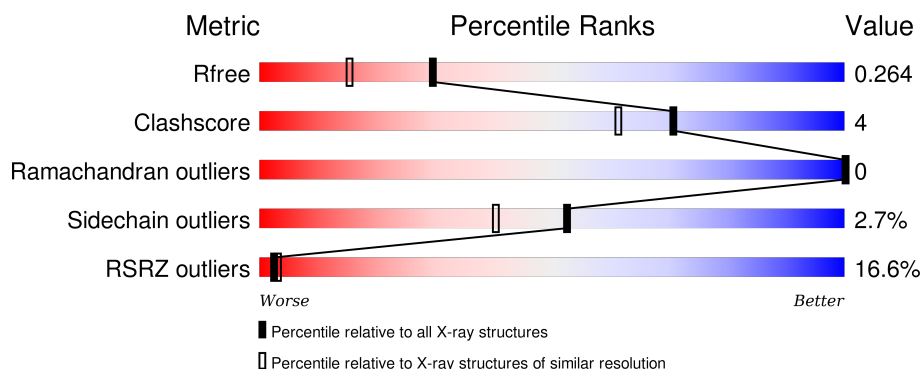
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.94 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	2910 (1.96-1.92)
Clashscore	102246	3095 (1.96-1.92)
Ramachandran outliers	100387	3062 (1.96-1.92)
Sidechain outliers	100360	3062 (1.96-1.92)
RSRZ outliers	91569	2915 (1.96-1.92)

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>24%</div> <div>85%</div> <div>11%</div> <div>..</div> </div>
1	B	422	<div> <div>8%</div> <div>88%</div> <div>9%</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
5	ACT	B	860	-	-	-	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7220 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 NITRIC OXIDE SYNTHASE, BRAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	408	Total	C	N	O	S	0	5	1
			3339	2138	569	610	22			
1	B	411	Total	C	N	O	S	0	4	0
			3360	2150	574	614	22			

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



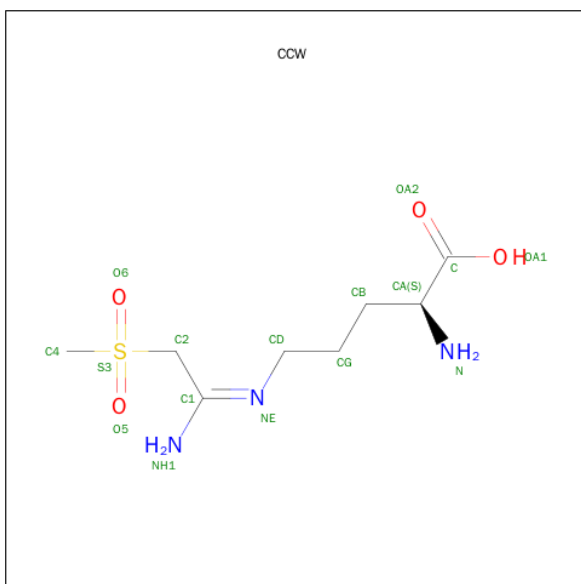
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- 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	0	0
			17	9	5	3		
3	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 4 is (S)-2-AMINO-5-(2-(METHYLSULFONYL)ACETIMIDAMIDO)PENTANOIC ACID (three-letter code: CCW) (formula: C₈H₁₇N₃O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			16	8	3	4	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			16	8	3	4	1		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



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		

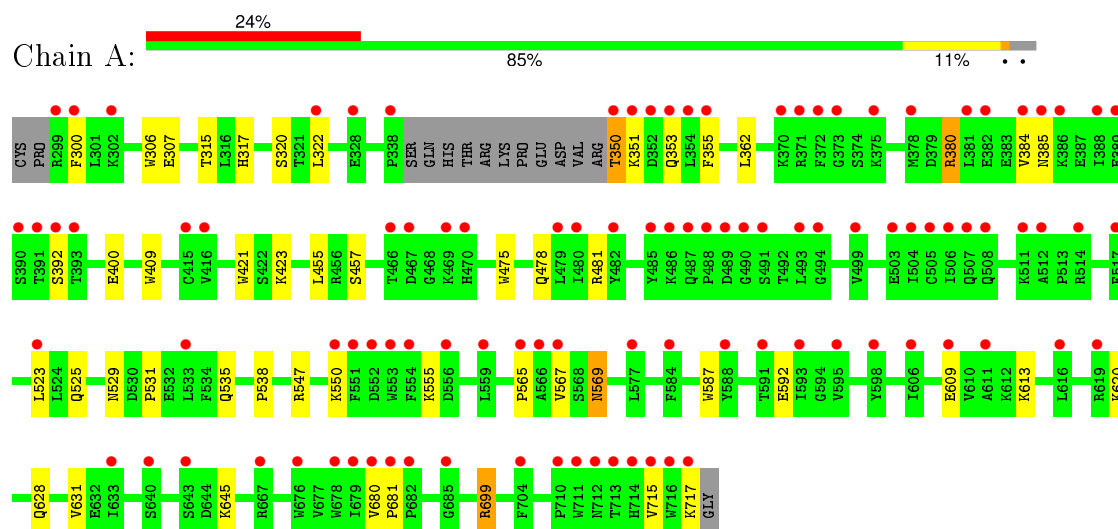
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	154	Total	O	0	0
			154	154		
7	B	206	Total	O	0	0
			206	206		

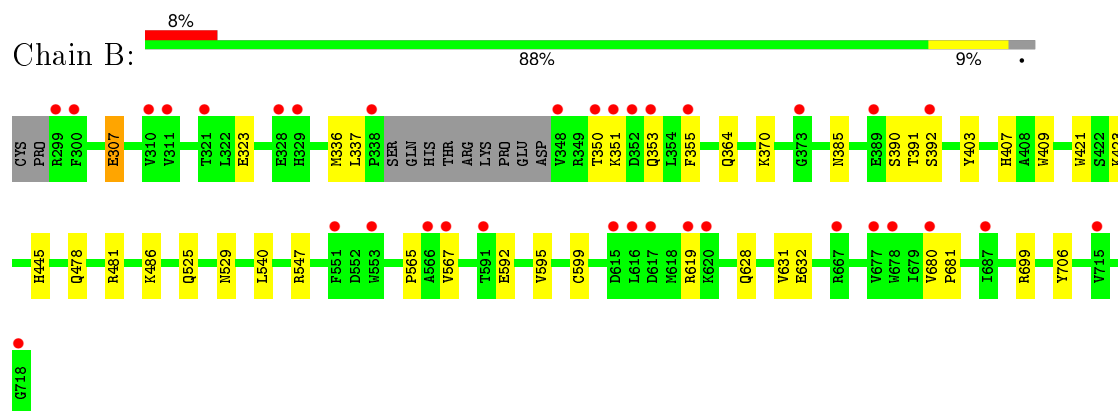
3 Residue-property plots

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: 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	52.01Å 111.34Å 164.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.59 – 1.94 38.59 – 1.94	Depositor EDS
% Data completeness (in resolution range)	99.6 (38.59-1.94) 99.6 (38.59-1.94)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 1.94Å)	Xtriage
Refinement program	REFMAC 5.5.0089	Depositor
R, R_{free}	0.179 , 0.210 0.237 , 0.264	Depositor DCC
R_{free} test set	3532 reflections (5.20%)	DCC
Wilson B-factor (Å ²)	29.5	Xtriage
Anisotropy	0.677	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 71517 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7220	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CCW, 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	0.61	0/3444	0.64	0/4672
1	B	0.64	0/3465	0.65	0/4697
All	All	0.62	0/6909	0.65	0/9369

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	3339	0	3256	33	0
1	B	3360	0	3280	24	0
2	A	43	0	30	3	0
2	B	43	0	30	4	0
3	A	17	0	15	0	0
3	B	17	0	15	0	0
4	A	16	0	16	4	0
4	B	16	0	16	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	154	0	0	2	0
7	B	206	0	0	2	0
All	All	7220	0	6664	60	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 (60) 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:565:PRO:HB2	4:A:800:CCW:H42C	1.37	1.06
1:B:565:PRO:HB2	4:B:800:CCW:H42C	1.52	0.89
1:A:350:THR:N	1:A:353:GLN:HE21	1.79	0.80
1:B:706:TYR:OH	2:B:750:HEM:O1D	2.09	0.71
1:A:350:THR:N	1:A:353:GLN:NE2	2.41	0.67
4:A:800:CCW:HD2C	4:A:800:CCW:H41C	1.77	0.64
1:B:567:VAL:HG23	4:B:800:CCW:H41C	1.80	0.63
1:A:628:GLN:HG2	1:B:631:VAL:HG11	1.80	0.62
1:A:322:LEU:HD13	1:A:699:ARG:HH21	1.66	0.61
4:B:800:CCW:H41C	4:B:800:CCW:HD2C	1.83	0.60
1:A:478:GLN:HB2	1:A:481:ARG:HG3	1.85	0.59
2:B:750:HEM:HHC	2:B:750:HEM:HBB2	1.85	0.58
1:A:380:ARG:HD3	1:A:400:GLU:OE2	2.07	0.55
1:A:300:PHE:HD1	1:A:315:THR:HG22	1.72	0.54
2:A:750:HEM:HBB2	2:A:750:HEM:HHC	1.91	0.53
2:B:750:HEM:HBC2	2:B:750:HEM:CMC	2.40	0.52
1:A:355:PHE:CE1	1:A:385:ASN:HB2	2.45	0.52
1:A:306:TRP:CE2	1:B:336:MET:HE3	2.45	0.52
1:B:478:GLN:HB2	1:B:481:ARG:HG3	1.91	0.52
1:B:403:TYR:CE1	1:B:407:HIS:CE1	2.98	0.51
1:A:609:GLU:HG3	7:A:2119:HOH:O	2.10	0.51
1:A:362:LEU:HD11	1:A:384:VAL:HG21	1.91	0.51
1:B:351:LYS:HE3	1:B:392:SER:OG	2.11	0.51
1:A:306:TRP:CD2	1:B:336:MET:HE3	2.46	0.50
1:A:567:VAL:HG23	4:A:800:CCW:H41C	1.92	0.50
1:B:355:PHE:CE1	1:B:385:ASN:HB2	2.46	0.50
1:A:592:GLU:OE1	4:A:800:CCW:NE	2.45	0.50
2:A:750:HEM:CMC	2:A:750:HEM:HBC2	2.42	0.49
1:A:475:TRP:CZ2	1:A:531:PRO:HG3	2.47	0.49
1:B:323:GLU:O	1:B:699:ARG:HD3	2.14	0.48
1:A:317:HIS:O	1:A:320:SER:HB3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:595:VAL:O	1:B:599:CYS:HB2	2.16	0.46
1:A:455:LEU:HD12	1:A:587:TRP:HB3	1.98	0.46
1:A:523:LEU:HD22	1:A:531:PRO:HB2	1.98	0.45
1:A:569:ASN:H	1:A:569:ASN:HD22	1.64	0.45
1:A:717:LYS:N	7:A:2096:HOH:O	2.48	0.45
1:A:628:GLN:NE2	1:B:632:GLU:OE2	2.50	0.45
2:A:750:HEM:HMC1	2:A:750:HEM:HBC2	1.99	0.45
1:A:535:GLN:HE21	1:A:538:PRO:HD3	1.82	0.45
1:B:364:GLN:NE2	7:B:2018:HOH:O	2.47	0.45
1:B:619:ARG:HE	1:B:619:ARG:HB2	1.49	0.44
1:B:307[B]:GLU:OE1	7:B:2003:HOH:O	2.21	0.44
1:B:680:VAL:HA	1:B:681:PRO:HD3	1.88	0.44
1:A:423[B]:LYS:O	1:A:457[B]:SER:OG	2.35	0.44
1:A:525:GLN:HG3	1:A:529:ASN:O	2.18	0.44
1:A:351:LYS:HE2	1:A:392:SER:HB3	2.00	0.43
1:A:409:TRP:CE3	1:A:421:TRP:HA	2.53	0.43
1:A:550:LYS:HB2	1:A:550:LYS:HE3	1.73	0.43
1:A:306:TRP:CD1	1:B:336:MET:HE2	2.54	0.43
1:A:609:GLU:O	1:A:613:LYS:HG2	2.19	0.42
1:B:409:TRP:CE3	1:B:421:TRP:HA	2.54	0.42
1:B:525:GLN:HG3	1:B:529:ASN:O	2.19	0.42
1:B:445:HIS:C	1:B:445:HIS:CD2	2.93	0.42
1:A:475:TRP:CE2	1:A:531:PRO:HG3	2.55	0.41
1:A:680:VAL:HA	1:A:681:PRO:HD3	1.89	0.41
1:B:391:THR:O	1:B:392:SER:HB2	2.20	0.41
4:B:800:CCW:HD2C	4:B:800:CCW:C4	2.49	0.41
2:B:750:HEM:HBC2	2:B:750:HEM:HMC1	2.02	0.41
1:A:631:VAL:HG11	1:B:628:GLN:CG	2.51	0.40
1:B:592:GLU:OE1	4:B:800:CCW:NE	2.55	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	409/422 (97%)	398 (97%)	11 (3%)	0	100	100
1	B	411/422 (97%)	405 (98%)	6 (2%)	0	100	100
All	All	820/844 (97%)	803 (98%)	17 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	368/377 (98%)	357 (97%)	11 (3%)	48	35
1	B	370/377 (98%)	359 (97%)	11 (3%)	48	35
All	All	738/754 (98%)	716 (97%)	22 (3%)	52	35

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	307[A]	GLU
1	A	307[B]	GLU
1	A	350	THR
1	A	380	ARG
1	A	547	ARG
1	A	555	LYS
1	A	569	ASN
1	A	620	LYS
1	A	645	LYS
1	A	699	ARG
1	A	715	VAL
1	B	307[A]	GLU
1	B	307[B]	GLU
1	B	337	LEU
1	B	350	THR
1	B	353	GLN
1	B	370	LYS
1	B	390	SER

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Mol	Chain	Res	Type
1	B	423	LYS
1	B	486	LYS
1	B	540	LEU
1	B	547	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	425	GLN
1	A	454	ASN
1	A	508	GLN
1	A	535	GLN
1	A	569	ASN
1	A	605	ASN
1	A	628	GLN
1	A	697	ASN
1	B	364	GLN
1	B	454	ASN
1	B	507	GLN
1	B	529	ASN
1	B	535	GLN
1	B	601	ASN
1	B	605	ASN
1	B	628	GLN
1	B	697	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 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	30,50,50	2.31	8 (26%)	24,82,82	2.78	10 (41%)
3	H4B	A	760	-	13,18,18	0.87	0	11,26,26	2.81	6 (54%)
4	CCW	A	800	-	10,15,15	1.18	1 (10%)	10,20,20	3.12	7 (70%)
5	ACT	A	860	-	1,3,3	1.20	0	0,3,3	0.00	-
2	HEM	B	750	1	30,50,50	2.27	7 (23%)	24,82,82	2.79	9 (37%)
3	H4B	B	760	-	13,18,18	1.05	0	11,26,26	2.38	4 (36%)
4	CCW	B	800	-	10,15,15	1.26	2 (20%)	10,20,20	3.06	7 (70%)
5	ACT	B	860	-	1,3,3	1.26	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	-	0/10/54/54	0/0/8/8
3	H4B	A	760	-	-	0/8/17/17	0/2/2/2
4	CCW	A	800	-	-	0/8/16/16	0/0/0/0
5	ACT	A	860	-	-	0/0/0/0	0/0/0/0
2	HEM	B	750	1	-	0/10/54/54	0/0/8/8
3	H4B	B	760	-	-	0/8/17/17	0/2/2/2
4	CCW	B	800	-	-	0/8/16/16	0/0/0/0
5	ACT	B	860	-	-	0/0/0/0	0/0/0/0

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	750	HEM	C3B-C4B	-7.20	1.45	1.51
2	B	750	HEM	C3B-C4B	-6.42	1.46	1.51
2	B	750	HEM	C3D-C4D	-6.32	1.43	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	750	HEM	C3D-C4D	-5.75	1.44	1.51
2	B	750	HEM	C2C-C1C	-5.08	1.42	1.52
2	A	750	HEM	C2C-C1C	-4.07	1.44	1.52
4	B	800	CCW	C1-NH1	-3.00	1.28	1.34
4	A	800	CCW	C1-NH1	-2.70	1.28	1.34
2	B	750	HEM	C2B-C1B	-2.49	1.43	1.51
2	B	750	HEM	C2D-C1D	-2.19	1.44	1.51
4	B	800	CCW	C4-S3	-2.14	1.65	1.75
2	A	750	HEM	C2D-C1D	-2.06	1.45	1.51
2	A	750	HEM	C2B-C1B	-2.05	1.45	1.51
2	A	750	HEM	C3B-CAB	2.05	1.55	1.51
2	A	750	HEM	FE-ND	2.10	2.08	1.97
2	B	750	HEM	FE-NC	2.11	2.04	1.95
2	B	750	HEM	C1C-NC	2.72	1.39	1.36
2	A	750	HEM	FE-NC	3.57	2.09	1.95

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	750	HEM	CBA-CAA-C2A	-7.28	99.48	112.53
2	A	750	HEM	CBA-CAA-C2A	-6.87	100.21	112.53
4	B	800	CCW	O5-S3-C2	-4.92	104.19	107.94
2	A	750	HEM	C3C-CAC-CBC	-4.18	118.05	124.46
3	A	760	H4B	N3-C2-N1	-4.00	118.97	125.53
4	A	800	CCW	O5-S3-C4	-3.63	104.91	108.92
2	B	750	HEM	C3C-CAC-CBC	-3.41	119.23	124.46
3	B	760	H4B	N3-C2-N1	-3.24	120.23	125.53
2	B	750	HEM	CBD-CAD-C3D	-2.99	104.84	113.55
4	B	800	CCW	O5-S3-C4	-2.94	105.68	108.92
2	A	750	HEM	CBD-CAD-C3D	-2.91	105.08	113.55
4	B	800	CCW	O6-S3-C2	-2.76	105.83	107.94
4	A	800	CCW	O6-S3-C2	-2.62	105.94	107.94
4	A	800	CCW	O5-S3-O6	-2.57	110.11	116.85
4	A	800	CCW	C4-S3-C2	2.01	112.29	105.34
3	B	760	H4B	C2-N1-C8A	2.03	119.10	114.54
2	B	750	HEM	C2D-C3D-C4D	2.15	105.15	101.50
4	B	800	CCW	C4-S3-C2	2.24	113.10	105.34
2	A	750	HEM	C3B-C4B-CHC	2.29	126.38	123.16
2	A	750	HEM	C2D-C3D-C4D	2.42	105.60	101.50
4	A	800	CCW	C2-C1-NH1	2.56	120.53	117.23
2	A	750	HEM	CMD-C2D-C3D	2.63	125.97	114.35
4	B	800	CCW	C2-C1-NH1	2.69	120.69	117.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	760	H4B	N2-C2-N3	2.70	121.67	117.20
2	B	750	HEM	CMD-C2D-C3D	2.81	126.78	114.35
3	A	760	H4B	C2-N1-C8A	3.06	121.42	114.54
4	B	800	CCW	CG-CD-NE	3.15	115.87	110.73
2	A	750	HEM	CMB-C2B-C3B	3.33	124.83	116.53
3	A	760	H4B	C4A-C8A-N8	3.36	122.39	118.43
4	A	800	CCW	CG-CD-NE	3.98	117.22	110.73
2	B	750	HEM	CMB-C2B-C3B	4.17	126.93	116.53
3	B	760	H4B	C4-C4A-C8A	4.21	118.38	114.56
3	A	760	H4B	C4-C4A-C8A	4.38	118.53	114.56
2	A	750	HEM	CAD-C3D-C4D	4.38	127.93	112.47
3	B	760	H4B	C4-N3-C2	4.43	122.08	115.94
3	A	760	H4B	C4-N3-C2	4.49	122.17	115.94
2	B	750	HEM	CAD-C3D-C2D	4.54	126.27	113.22
2	B	750	HEM	CAD-C3D-C4D	4.56	128.56	112.47
2	A	750	HEM	CAD-C3D-C2D	4.58	126.39	113.22
2	B	750	HEM	CMC-C2C-C3C	4.86	128.66	116.53
4	B	800	CCW	O6-S3-C4	5.29	114.77	108.92
2	A	750	HEM	CMC-C2C-C3C	5.30	129.76	116.53
4	A	800	CCW	O6-S3-C4	6.52	116.14	108.92

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	750	HEM	3	0
4	A	800	CCW	4	0
2	B	750	HEM	4	0
4	B	800	CCW	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%)	1.39	102 (25%) 1 1	23, 48, 93, 117	0
1	B	411/422 (97%)	0.58	34 (8%) 14 21	22, 35, 60, 81	0
All	All	819/844 (97%)	0.99	136 (16%) 2 3	22, 40, 85, 117	0

All (136) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	300	PHE	9.7
1	A	488	PRO	8.7
1	A	716	TRP	8.3
1	A	355	PHE	7.5
1	A	352	ASP	6.5
1	B	350	THR	6.0
1	A	300	PHE	5.8
1	B	348	VAL	5.4
1	A	388	ILE	5.2
1	A	715	VAL	5.2
1	A	350	THR	5.0
1	B	718	GLY	4.9
1	A	712	ASN	4.8
1	A	503	GLU	4.7
1	B	619	ARG	4.5
1	A	384	VAL	4.3
1	A	486	LYS	4.2
1	A	351	LYS	4.2
1	A	551	PHE	4.1
1	A	373	GLY	4.1
1	A	490	GLY	4.0
1	A	381	LEU	4.0
1	A	470	HIS	3.8
1	B	620	LYS	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	299	ARG	3.8
1	A	392	SER	3.8
1	A	567	VAL	3.8
1	A	385	ASN	3.7
1	B	352	ASP	3.6
1	A	469	LYS	3.6
1	A	506	ILE	3.6
1	A	489	ASP	3.5
1	A	507	GLN	3.5
1	A	678	TRP	3.5
1	A	714	HIS	3.5
1	A	550	LYS	3.5
1	A	487	GLN	3.4
1	A	593	ILE	3.3
1	A	386	LYS	3.3
1	B	715	VAL	3.3
1	A	393	THR	3.3
1	B	299	ARG	3.2
1	A	554	PHE	3.2
1	A	679	ILE	3.1
1	B	615	ASP	3.1
1	A	523	LEU	3.0
1	A	643	SER	3.0
1	A	619	ARG	3.0
1	A	552	ASP	3.0
1	A	717	LYS	3.0
1	A	584	PHE	3.0
1	A	391	THR	2.9
1	A	389	GLU	2.9
1	A	338	PRO	2.9
1	A	511	LYS	2.9
1	A	491	SER	2.8
1	A	517	PHE	2.8
1	A	505	CYS	2.8
1	B	616	LEU	2.8
1	A	480	ILE	2.8
1	A	595	VAL	2.7
1	B	351	LYS	2.7
1	A	482	TYR	2.7
1	A	479	LEU	2.7
1	B	353	GLN	2.7
1	A	680	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	378	MET	2.6
1	A	371	ARG	2.6
1	A	711	TRP	2.6
1	A	616	LEU	2.6
1	A	588	TYR	2.6
1	A	533	LEU	2.6
1	B	355	PHE	2.6
1	B	389	GLU	2.6
1	A	713	THR	2.6
1	A	633	ILE	2.5
1	A	682	PRO	2.5
1	A	467	ASP	2.5
1	B	567	VAL	2.5
1	A	710	PRO	2.5
1	A	485	TYR	2.5
1	A	514	ARG	2.5
1	A	606	ILE	2.5
1	B	329	HIS	2.5
1	A	493	LEU	2.5
1	A	415	CYS	2.4
1	B	677	VAL	2.4
1	A	302	LYS	2.4
1	A	466	THR	2.4
1	A	416	VAL	2.4
1	A	553	TRP	2.4
1	A	372	PHE	2.4
1	A	370	LYS	2.4
1	A	354	LEU	2.4
1	A	559	LEU	2.4
1	B	667	ARG	2.4
1	A	499	VAL	2.4
1	A	609	GLU	2.3
1	A	322	LEU	2.3
1	A	390	SER	2.3
1	A	328	GLU	2.3
1	B	551	PHE	2.3
1	A	565	PRO	2.3
1	A	382	GLU	2.3
1	A	375	LYS	2.3
1	A	676	TRP	2.3
1	B	321	THR	2.3
1	B	553	TRP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	353	GLN	2.3
1	B	310	VAL	2.3
1	A	598	TYR	2.3
1	A	681	PRO	2.2
1	B	392	SER	2.2
1	A	504	ILE	2.2
1	B	566	ALA	2.2
1	B	311	VAL	2.2
1	B	328	GLU	2.2
1	B	591	THR	2.2
1	A	512	ALA	2.2
1	A	508	GLN	2.2
1	A	611	ALA	2.2
1	B	373	GLY	2.2
1	B	680	VAL	2.2
1	B	678	TRP	2.1
1	A	591	THR	2.1
1	B	338	PRO	2.1
1	B	687	ILE	2.1
1	B	617	ASP	2.1
1	A	494	GLY	2.1
1	A	640	SER	2.1
1	A	667	ARG	2.1
1	A	685	GLY	2.1
1	A	566	ALA	2.0
1	A	704	PHE	2.0
1	A	577	LEU	2.0
1	A	556	ASP	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
5	ACT	B	860	4/4	0.97	0.15	3.65	39,40,41,43	0
5	ACT	A	860	4/4	0.96	0.15	1.60	52,52,53,53	0
2	HEM	A	750	43/43	0.97	0.21	0.99	24,27,34,39	0
2	HEM	B	750	43/43	0.97	0.15	0.57	22,25,30,40	0
3	H4B	A	760	17/17	0.95	0.17	0.49	23,27,30,31	0
3	H4B	B	760	17/17	0.98	0.16	0.40	21,24,28,30	0
4	CCW	A	800	16/16	0.93	0.19	-0.04	36,39,41,42	0
4	CCW	B	800	16/16	0.94	0.14	-0.63	32,35,41,44	0
6	ZN	B	900	1/1	0.99	0.07	-1.47	31,31,31,31	0

6.5 Other polymers ⓘ

There are no such residues in this entry.