



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:52 PM GMT

PDB ID : 4JSL
Title : Structure of bovine endothelial nitric oxide synthase heme domain in complex with 6,6'-(heptane-1,7-diyl)bis(4-methylpyridin-2-amine)
Authors : Li, H.; Poulos, T.L.
Deposited on : 2013-03-22
Resolution : 2.04 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

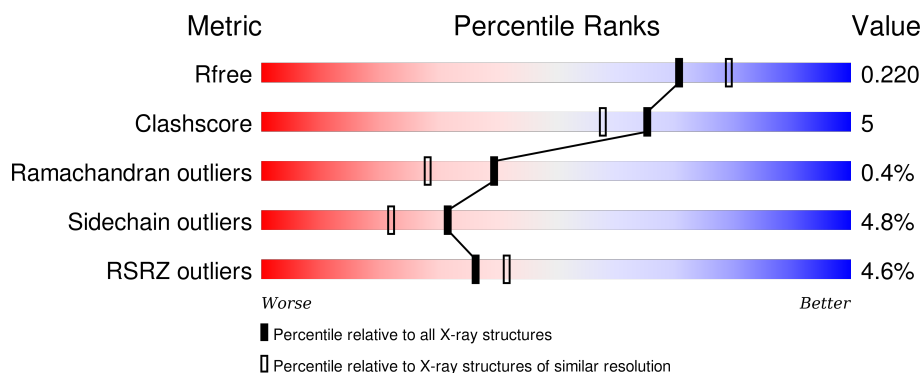
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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	1192 (2.04-2.04)
Clashscore	102246	1269 (2.04-2.04)
Ramachandran outliers	100387	1258 (2.04-2.04)
Sidechain outliers	100360	1258 (2.04-2.04)
RSRZ outliers	91569	1194 (2.04-2.04)

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	443	<div> <div>5%</div> <div> <div></div> <div>81%</div> <div>10%</div> <div>9%</div> </div> </div>
1	B	443	<div> <div>4%</div> <div> <div></div> <div>81%</div> <div>9%</div> <div>9%</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	504	-	-	-	X

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 7104 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, endothelial.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	405	Total	As	C	N	O	S	0	2	0
			3234	1	2056	569	592	16			
1	B	403	Total	As	C	N	O	S	0	1	0
			3218	1	2046	567	588	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	100	ARG	CYS	CONFLICT	UNP P29473
B	100	ARG	CYS	CONFLICT	UNP P29473

- 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		

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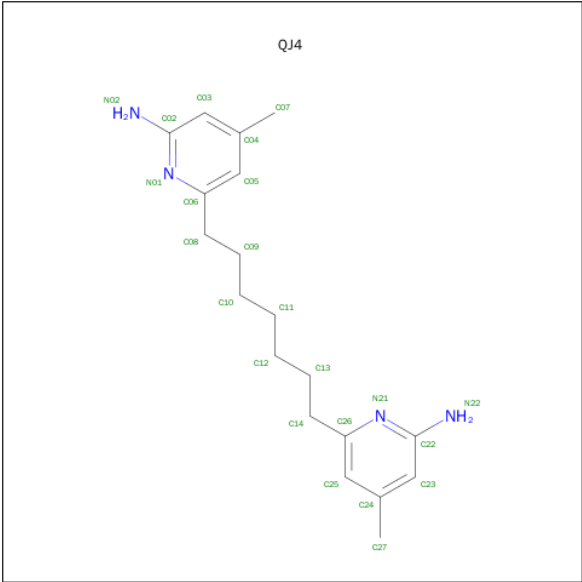
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- 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 6,6'-HEPTANE-1,7-DIYLBIS(4-METHYLPYRIDIN-2-AMINE) (three-letter code: QJ4) (formula: $C_{19}H_{28}N_4$).



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

- 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	A	1	Total	C	O	0	0
			4	2	2		

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

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 7 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	228	Total	O	0	0
			228	228		
8	B	229	Total	O	0	0
			229	229		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.86Å 106.58Å 157.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.97 – 2.04 46.97 – 2.04	Depositor EDS
% Data completeness (in resolution range)	99.3 (46.97-2.04) 99.3 (46.97-2.04)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.169 , 0.208 0.178 , 0.220	Depositor DCC
R_{free} test set	3109 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	35.1	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 40.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 62232 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7104	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ZN, H4B, CAS, ACT, HEM, QJ4

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	0.69	0/3320	0.70	1/4520 (0.0%)
1	B	0.69	1/3300 (0.0%)	0.69	1/4492 (0.0%)
All	All	0.69	1/6620 (0.0%)	0.69	2/9012 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	203	CYS	CB-SG	-6.61	1.71	1.82

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	240	ARG	NE-CZ-NH2	-5.95	117.32	120.30
1	A	294	LEU	CB-CG-CD1	5.31	120.02	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	3234	0	3139	30	0
1	B	3218	0	3125	26	0
2	A	43	0	30	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	43	0	30	3	0
3	A	17	0	15	2	0
3	B	17	0	15	1	0
4	A	23	0	28	4	0
4	B	23	0	28	3	0
5	A	8	0	6	0	0
5	B	8	0	6	0	0
6	A	6	0	8	1	0
6	B	6	0	8	1	0
7	A	1	0	0	0	0
8	A	228	0	0	2	0
8	B	229	0	0	4	0
All	All	7104	0	6438	65	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 (65) 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:384:CAS:AS	1:A:384:CAS:SG	2.58	1.22
1:A:240:ARG:HD3	1:A:298:PRO:HB3	1.65	0.78
3:A:502:H4B:O4	6:A:506:GOL:H32	1.86	0.75
1:A:236:ARG:HH12	1:A:342:LEU:CD1	2.03	0.71
1:A:69:LYS:HE2	1:A:69:LYS:HA	1.75	0.69
1:A:69:LYS:CE	1:A:69:LYS:HA	2.26	0.66
1:A:236:ARG:HH12	1:A:342:LEU:HD11	1.63	0.62
1:B:378:LEU:HB2	8:B:616:HOH:O	2.02	0.60
1:B:236:ARG:CD	1:B:351:SER:HB3	2.34	0.58
1:B:236:ARG:HG3	1:B:349:GLU:O	2.05	0.56
1:B:178:GLN:HE22	1:B:181:ARG:HH11	1.54	0.56
1:A:99:ARG:HG2	8:B:756:HOH:O	2.06	0.56
1:B:236:ARG:HD3	1:B:351:SER:HB3	1.89	0.55
1:A:370:CYS:SG	1:A:378:LEU:HD13	2.47	0.54
1:B:340:ASN:HD22	1:B:340:ASN:H	1.56	0.54
1:B:145:SER:O	1:B:149:GLU:HG2	2.08	0.53
1:A:236:ARG:HH12	1:A:342:LEU:HD12	1.73	0.52
1:A:246:TRP:HB2	1:A:294:LEU:HB3	1.90	0.52
1:B:236:ARG:NH1	1:B:242:ASP:OD1	2.41	0.52
1:A:378:LEU:HB2	8:A:606:HOH:O	2.11	0.51
2:A:501:HEM:C1C	4:A:503:QJ4:H28	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:323:GLU:CD	1:B:323:GLU:H	2.15	0.49
2:A:501:HEM:HBB2	2:A:501:HEM:HHC	1.96	0.48
1:B:330:LEU:HB2	8:B:615:HOH:O	2.13	0.48
1:B:281:TRP:HB2	1:B:304:LEU:HD21	1.95	0.48
1:A:236:ARG:NH1	1:A:342:LEU:HD11	2.29	0.48
1:B:233:PHE:HB3	1:B:234:PRO:CD	2.43	0.48
1:B:231:THR:O	1:B:353:ALA:HA	2.14	0.47
1:A:449:TRP:HA	3:A:502:H4B:N1	2.30	0.47
6:B:506:GOL:H2	8:B:649:HOH:O	2.15	0.47
1:B:240:ARG:HD2	1:B:241:GLY:O	2.15	0.47
1:A:340:ASN:HD22	1:A:340:ASN:H	1.61	0.47
1:A:384:CAS:CB	1:A:384:CAS:AS	3.22	0.47
1:A:338:VAL:HG23	4:A:503:QJ4:H25	1.96	0.47
2:B:501:HEM:O2D	4:B:503:QJ4:H11	2.16	0.46
1:A:455:SER:O	1:A:458:LEU:HB2	2.15	0.46
1:A:390:ARG:HB2	1:A:390:ARG:HE	1.42	0.45
1:A:126:LEU:HD11	1:A:156:GLU:HA	1.99	0.45
2:A:501:HEM:O2D	4:A:503:QJ4:N21	2.50	0.45
1:A:196:GLN:OE1	8:A:817:HOH:O	2.21	0.45
2:A:501:HEM:HBA2	4:A:503:QJ4:H18	2.00	0.44
1:B:172:LEU:HD11	1:B:232:VAL:HG11	1.99	0.44
1:B:167:LEU:HG	1:B:348:LEU:HD12	2.00	0.44
1:A:423:HIS:HB2	1:B:392:THR:HB	1.98	0.44
1:A:472:SER:HA	1:A:473:PRO:C	2.38	0.43
1:B:218:LYS:HD3	1:B:218:LYS:C	2.38	0.43
1:B:236:ARG:HG3	1:B:349:GLU:HB2	2.01	0.43
1:A:70:PHE:HB3	1:A:84:ASP:O	2.19	0.43
2:B:501:HEM:HBC2	2:B:501:HEM:CMC	2.49	0.43
2:A:501:HEM:HHC	2:A:501:HEM:CBB	2.49	0.43
1:B:449:TRP:HA	3:B:502:H4B:N1	2.34	0.42
1:B:384:CAS:HA	1:B:384:CAS:CE1	2.49	0.42
1:A:185:ARG:HD3	1:A:449:TRP:CD2	2.54	0.42
1:A:355:PHE:CD1	2:A:501:HEM:CAC	3.03	0.42
1:A:67:GLY:HA3	1:A:68:PRO:HD2	1.86	0.41
1:B:236:ARG:HD2	1:B:351:SER:HB3	2.01	0.41
1:B:99:ARG:HG2	1:B:100:ARG:HD2	2.03	0.41
1:A:68:PRO:HG2	1:A:83:TYR:CD2	2.55	0.41
1:A:158:GLU:OE1	1:A:166:HIS:HD2	2.04	0.41
1:B:340:ASN:N	1:B:340:ASN:HD22	2.16	0.41
1:B:338:VAL:CG2	4:B:503:QJ4:H18	2.51	0.41
2:B:501:HEM:C1C	4:B:503:QJ4:H28	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:447:TRP:CZ2	1:A:451:VAL:HG21	2.55	0.41
1:B:478:GLN:HB2	1:B:479:PRO:HD2	2.02	0.40
1:A:107:LEU:HD21	1:A:477:TYR:CD2	2.57	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	402/443 (91%)	390 (97%)	10 (2%)	2 (0%)	34	22
1	B	399/443 (90%)	388 (97%)	10 (2%)	1 (0%)	46	36
All	All	801/886 (90%)	778 (97%)	20 (2%)	3 (0%)	39	28

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	122	ALA
1	B	260	ASP
1	A	238	PRO

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	345/375 (92%)	331 (96%)	14 (4%)	37	28
1	B	343/375 (92%)	324 (94%)	19 (6%)	27	16
All	All	688/750 (92%)	655 (95%)	33 (5%)	31	22

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	LYS
1	A	100	ARG
1	A	102	LEU
1	A	109	ARG
1	A	123	GLU
1	A	125	LEU
1	A	154	GLU
1	A	293	LEU
1	A	294	LEU
1	A	328	LEU
1	A	340	ASN
1	A	378	LEU
1	A	391	THR
1	A	468	ASN
1	B	69	LYS
1	B	100	ARG
1	B	102	LEU
1	B	105	LEU
1	B	124	GLN
1	B	143	SER
1	B	178	GLN
1	B	223	ARG
1	B	225	ASN
1	B	236	ARG
1	B	240	ARG
1	B	259	GLN
1	B	323	GLU
1	B	330	LEU
1	B	340	ASN
1	B	378	LEU
1	B	389	THR
1	B	391	THR
1	B	458	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	153	GLN
1	A	166	HIS
1	A	340	ASN
1	A	376	ASN
1	A	413	GLN
1	A	468	ASN
1	B	178	GLN
1	B	222	ASN
1	B	225	ASN
1	B	340	ASN
1	B	376	ASN
1	B	405	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CAS	A	384	1	5,8,9	1.08	0	2,9,11	1.37	0
1	CAS	B	384	1	5,8,9	1.29	0	2,9,11	1.75	1 (50%)

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
1	CAS	A	384	1	-	0/0/7/9	0/0/0/0
1	CAS	B	384	1	-	0/0/7/9	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	384	CAS	O-C-CA	-2.34	119.40	125.49

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
1	A	384	CAS	2	0
1	B	384	CAS	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 1 is monoatomic - leaving 12 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	501	1	30,50,50	2.09	8 (26%)	24,82,82	2.36	10 (41%)
3	H4B	A	502	-	13,18,18	0.70	0	11,26,26	2.55	5 (45%)
4	QJ4	A	503	-	24,24,24	0.59	0	31,31,31	1.84	8 (25%)
5	ACT	A	504	-	1,3,3	1.31	0	0,3,3	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	ACT	A	505	-	1,3,3	2.49	1 (100%)	0,3,3	0.00	-
6	GOL	A	506	-	5,5,5	0.35	0	5,5,5	0.70	0
2	HEM	B	501	1	30,50,50	2.02	8 (26%)	24,82,82	2.34	10 (41%)
3	H4B	B	502	-	13,18,18	0.84	0	11,26,26	2.06	4 (36%)
4	QJ4	B	503	-	24,24,24	0.79	1 (4%)	31,31,31	2.48	10 (32%)
5	ACT	B	504	-	1,3,3	1.50	0	0,3,3	0.00	-
5	ACT	B	505	-	1,3,3	2.06	1 (100%)	0,3,3	0.00	-
6	GOL	B	506	-	5,5,5	0.60	0	5,5,5	0.59	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	1	-	0/10/54/54	0/0/8/8
3	H4B	A	502	-	-	0/8/17/17	0/2/2/2
4	QJ4	A	503	-	-	0/10/10/10	0/2/2/2
5	ACT	A	504	-	-	0/0/0/0	0/0/0/0
5	ACT	A	505	-	-	0/0/0/0	0/0/0/0
6	GOL	A	506	-	-	0/4/4/4	0/0/0/0
2	HEM	B	501	1	-	0/10/54/54	0/0/8/8
3	H4B	B	502	-	-	0/8/17/17	0/2/2/2
4	QJ4	B	503	-	-	0/10/10/10	0/2/2/2
5	ACT	B	504	-	-	0/0/0/0	0/0/0/0
5	ACT	B	505	-	-	0/0/0/0	0/0/0/0
6	GOL	B	506	-	-	0/4/4/4	0/0/0/0

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	HEM	C3B-C4B	-6.76	1.45	1.51
2	A	501	HEM	C3B-C4B	-6.18	1.46	1.51
2	A	501	HEM	C3D-C4D	-5.13	1.45	1.51
2	B	501	HEM	C3D-C4D	-4.37	1.46	1.51
2	B	501	HEM	C2C-C1C	-3.14	1.46	1.52
2	A	501	HEM	C2C-C1C	-3.10	1.46	1.52
2	B	501	HEM	C2D-C1D	-2.08	1.45	1.51
2	A	501	HEM	CMA-C3A	2.00	1.55	1.51
4	B	503	QJ4	C26-N21	2.05	1.38	1.34
5	B	505	ACT	CH3-C	2.06	1.51	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	HEM	FE-NB	2.10	2.08	1.97
2	A	501	HEM	C3C-CAC	2.18	1.55	1.51
2	B	501	HEM	C3B-CAB	2.28	1.55	1.51
2	B	501	HEM	CAA-C2A	2.31	1.56	1.52
5	A	505	ACT	CH3-C	2.49	1.52	1.48
2	B	501	HEM	FE-NC	2.61	2.06	1.95
2	A	501	HEM	CAA-C2A	2.73	1.56	1.52
2	A	501	HEM	C1C-NC	3.09	1.39	1.36
2	A	501	HEM	C4C-NC	3.21	1.40	1.36

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	503	QJ4	C04-C05-C06	-4.20	117.65	120.28
4	B	503	QJ4	C14-C26-C25	-3.52	116.19	121.13
4	A	503	QJ4	C04-C05-C06	-3.40	118.15	120.28
3	B	502	H4B	N3-C2-N1	-3.40	119.96	125.53
2	A	501	HEM	CAA-C2A-C1A	-3.24	123.50	127.01
2	B	501	HEM	CBA-CAA-C2A	-3.22	106.76	112.53
3	A	502	H4B	N3-C2-N1	-3.21	120.28	125.53
2	A	501	HEM	CMA-C3A-C4A	-3.13	123.18	128.36
4	B	503	QJ4	C25-C26-N21	-3.03	119.54	122.96
2	A	501	HEM	C3C-CAC-CBC	-2.79	120.17	124.46
2	B	501	HEM	C3C-CAC-CBC	-2.62	120.44	124.46
2	A	501	HEM	CBA-CAA-C2A	-2.60	107.86	112.53
4	B	503	QJ4	C05-C06-N01	-2.40	120.25	122.96
4	A	503	QJ4	C12-C13-C14	-2.38	103.86	113.90
4	A	503	QJ4	C05-C06-N01	-2.22	120.45	122.96
2	B	501	HEM	CBD-CAD-C3D	-2.14	107.32	113.55
4	A	503	QJ4	C10-C09-C08	-2.05	105.23	113.90
2	A	501	HEM	CMA-C3A-C2A	2.13	129.69	125.24
3	A	502	H4B	C2-N1-C8A	2.22	119.53	114.54
4	B	503	QJ4	C09-C08-C06	2.26	120.73	112.79
4	B	503	QJ4	C05-C04-C03	2.36	121.09	118.08
2	B	501	HEM	C3B-C4B-CHC	2.39	126.52	123.16
3	A	502	H4B	C4A-C8A-N8	2.46	121.32	118.43
4	A	503	QJ4	C14-C26-N21	2.61	119.55	115.69
4	B	503	QJ4	N22-C22-N21	2.66	121.35	116.50
2	A	501	HEM	CMD-C2D-C3D	2.68	126.19	114.35
3	B	502	H4B	C4-N3-C2	2.68	119.66	115.94
4	A	503	QJ4	C22-N21-C26	2.76	120.19	118.23
3	B	502	H4B	C2-N1-C8A	2.80	120.82	114.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	HEM	CMD-C2D-C3D	2.91	127.20	114.35
3	B	502	H4B	C4-C4A-C8A	2.95	117.23	114.56
2	B	501	HEM	C2D-C3D-C4D	3.01	106.61	101.50
4	A	503	QJ4	C08-C06-C05	3.13	125.52	121.13
2	A	501	HEM	CMC-C2C-C3C	3.32	124.81	116.53
2	A	501	HEM	CMB-C2B-C3B	3.45	125.14	116.53
2	B	501	HEM	CMC-C2C-C3C	3.51	125.29	116.53
2	B	501	HEM	CAD-C3D-C2D	4.11	125.05	113.22
2	B	501	HEM	CMB-C2B-C3B	4.30	127.26	116.53
2	B	501	HEM	CAD-C3D-C4D	4.49	128.31	112.47
3	A	502	H4B	C4-C4A-C8A	4.50	118.63	114.56
2	A	501	HEM	CAD-C3D-C4D	4.58	128.61	112.47
2	A	501	HEM	CAD-C3D-C2D	4.75	126.87	113.22
3	A	502	H4B	C4-N3-C2	4.84	122.65	115.94
4	B	503	QJ4	C22-N21-C26	5.73	122.30	118.23
4	A	503	QJ4	C02-N01-C06	5.73	122.30	118.23
4	B	503	QJ4	C14-C26-N21	5.81	124.27	115.69
4	B	503	QJ4	C02-N01-C06	6.36	122.75	118.23

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	HEM	6	0
3	A	502	H4B	2	0
4	A	503	QJ4	4	0
6	A	506	GOL	1	0
2	B	501	HEM	3	0
3	B	502	H4B	1	0
4	B	503	QJ4	3	0
6	B	506	GOL	1	0

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	404/443 (91%)	0.07	21 (5%) 31 36	24, 36, 58, 77	0
1	B	402/443 (90%)	0.09	16 (3%) 42 48	23, 38, 62, 84	0
All	All	806/886 (90%)	0.08	37 (4%) 36 41	23, 37, 60, 84	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	259	GLN	6.2
1	A	67	GLY	5.9
1	A	259	GLN	4.7
1	A	239	GLY	4.3
1	B	121	PRO	4.1
1	A	69	LYS	3.8
1	A	123	GLU	3.6
1	B	448	ALA	3.4
1	B	123	GLU	3.4
1	B	260	ASP	3.3
1	A	109	ARG	3.2
1	B	449	TRP	3.2
1	A	450	ILE	3.1
1	B	447	TRP	2.9
1	A	257	ARG	2.9
1	A	448	ALA	2.9
1	A	451	VAL	2.9
1	B	261	GLY	2.8
1	A	449	TRP	2.7
1	B	146	GLN	2.7
1	B	258	GLN	2.7
1	B	144	GLY	2.7
1	A	91	GLN	2.6
1	B	106	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	105	LEU	2.5
1	A	106	VAL	2.5
1	B	142	ARG	2.4
1	B	477	TYR	2.4
1	A	447	TRP	2.4
1	A	153	GLN	2.3
1	A	121	PRO	2.3
1	A	187	VAL	2.2
1	B	282	THR	2.1
1	A	104	SER	2.1
1	A	122	ALA	2.1
1	A	258	GLN	2.0
1	B	451	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	CAS	B	384	9/10	0.96	0.11	-	46,47,63,65	0
1	CAS	A	384	9/10	0.95	0.11	-	37,37,66,66	0

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
5	ACT	B	504	4/4	0.96	0.20	6.03	44,45,46,46	0
6	GOL	A	506	6/6	0.85	0.23	1.50	55,57,57,60	0
6	GOL	B	506	6/6	0.86	0.23	1.35	51,52,54,54	0
4	QJ4	B	503	23/23	0.92	0.21	1.02	28,38,49,49	0
2	HEM	A	501	43/43	0.98	0.18	0.80	24,27,36,42	0
4	QJ4	A	503	23/23	0.94	0.18	0.61	24,33,45,46	0
2	HEM	B	501	43/43	0.98	0.16	0.58	25,27,35,38	0
5	ACT	A	505	4/4	0.97	0.10	0.50	29,29,29,31	0
5	ACT	B	505	4/4	0.98	0.09	0.16	32,34,34,35	0
3	H4B	B	502	17/17	0.96	0.20	0.10	27,29,31,33	0
3	H4B	A	502	17/17	0.98	0.20	0.02	25,29,31,32	0
5	ACT	A	504	4/4	0.95	0.12	-0.24	43,44,45,46	0
7	ZN	A	507	1/1	1.00	0.10	-1.65	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.