



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:52 PM GMT

PDB ID : 4JSE
Title : Structure of rat neuronal nitric oxide synthase heme domain in complex with
6,6'-(pentane-1,5-diyl)bis(4-methylpyridin-2-amine)
Authors : Li, H.; Poulos, T.L.
Deposited on : 2013-03-22
Resolution : 1.97 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

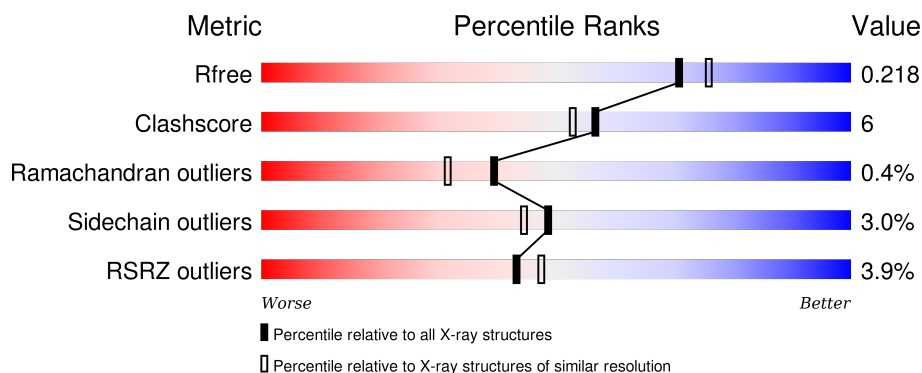
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.97 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	8664 (2.00-1.96)
Clashscore	102246	9905 (2.00-1.96)
Ramachandran outliers	100387	9792 (2.00-1.96)
Sidechain outliers	100360	9791 (2.00-1.96)
RSRZ outliers	91569	8679 (2.00-1.96)

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>5%</div> <div>86%</div> <div>9%</div> <div>• •</div> </div>
1	B	422	<div> <div>3%</div> <div>87%</div> <div>10%</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
4	QJ2	A	803	-	-	-	X
4	QJ2	A	805	-	-	-	X
4	QJ2	B	805	-	-	-	X
5	H4B	A	804	-	-	-	X
5	H4B	B	802	-	-	-	X

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 7377 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	6	0
			3348	2144	570	611	23			
1	B	412	Total	C	N	O	S	0	6	0
			3379	2162	578	616	23			

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



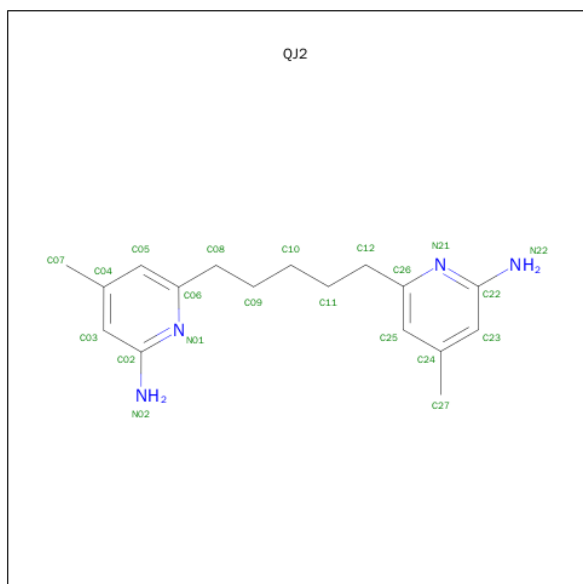
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 4 is 6,6'-PENTANE-1,5-DIYLBIS(4-METHYLPYRIDIN-2-AMINE) (three-letter code: QJ2) (formula: C₁₇H₂₄N₄).



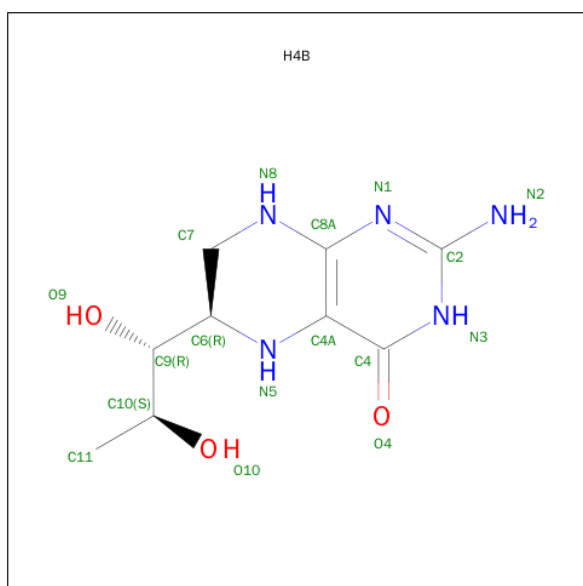
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	0
			21	17	4		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	0
			21	17	4		
4	B	1	Total	C	N	0	0
			21	17	4		
4	B	1	Total	C	N	0	0
			21	17	4		

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



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

- 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		
6	A	2	Total	Zn	0	1
			2	2		

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	2	Total 2	Cl 2	0	0
7	A	2	Total 2	Cl 2	0	2

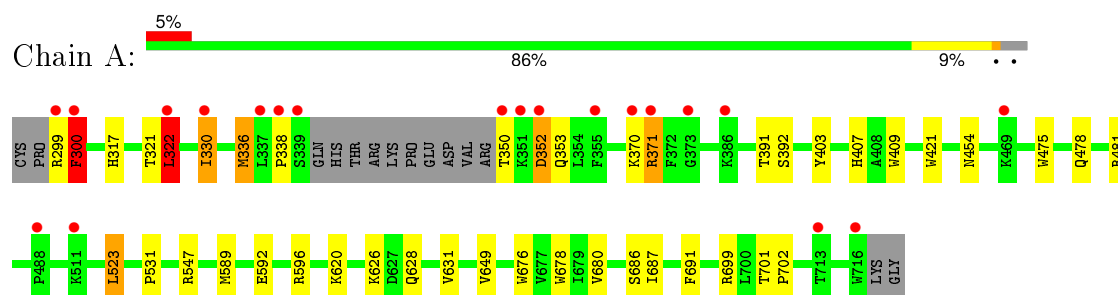
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	178	Total 178	O 178	0	0
8	B	253	Total 253	O 253	0	0

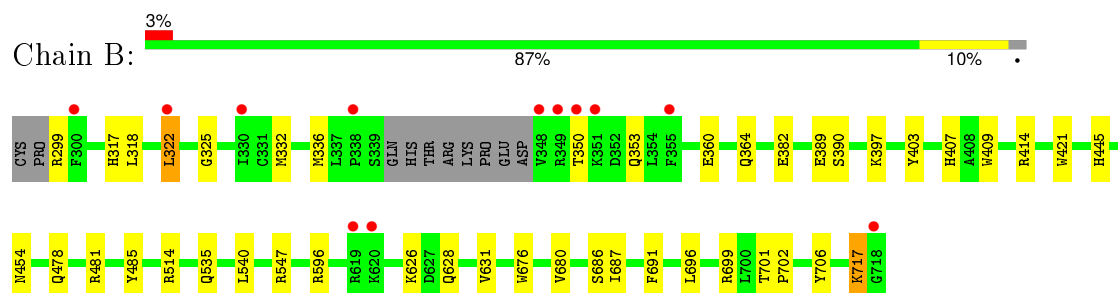
3 Residue-property plots

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	51.74Å 110.25Å 163.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.34 – 1.97 49.34 – 1.97	Depositor EDS
% Data completeness (in resolution range)	98.9 (49.34-1.97) 98.9 (49.34-1.97)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.65 (at 1.97Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.170 , 0.205 0.183 , 0.218	Depositor DCC
R_{free} test set	3286 reflections (5.21%)	DCC
Wilson B-factor (Å ²)	29.3	Xtriage
Anisotropy	0.733	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 43.6	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 66557 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7377	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 3.90% 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: ZN, H4B, CL, ACT, HEM, QJ2

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	0.67	0/3459	0.68	0/4692
1	B	0.70	0/3490	0.69	0/4729
All	All	0.68	0/6949	0.68	0/9421

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	3348	0	3271	39	0
1	B	3379	0	3307	34	0
2	A	43	0	30	6	0
2	B	43	0	30	6	0
3	A	4	0	3	0	0
3	B	4	0	3	0	0
4	A	42	0	48	5	0
4	B	42	0	48	3	0
5	A	17	0	15	6	0
5	B	17	0	15	6	0
6	A	2	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	1	0	0	0	0
7	A	2	0	0	0	0
7	B	2	0	0	0	0
8	A	178	0	0	4	0
8	B	253	0	0	7	0
All	All	7377	0	6770	83	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 6.

All (83) 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:336[A]:MET:HE2	1:A:336[A]:MET:HA	1.31	1.09
1:A:336[A]:MET:CE	1:A:336[A]:MET:HA	1.97	0.94
1:A:371:ARG:HH21	1:A:371:ARG:HG2	1.33	0.93
1:A:371:ARG:CG	1:A:371:ARG:HH21	1.92	0.82
1:A:371:ARG:HG2	1:A:371:ARG:NH2	1.91	0.82
2:A:801:HEM:HHC	2:A:801:HEM:HBB2	1.70	0.73
1:A:701[A]:THR:HG22	1:A:702:PRO:HA	1.70	0.73
2:B:801:HEM:O1A	5:B:802:H4B:N2	2.23	0.72
5:B:802:H4B:H71	5:B:802:H4B:O10	1.89	0.72
1:A:299:ARG:N	1:A:317:HIS:NE2	2.39	0.70
2:A:801:HEM:O1A	5:A:804:H4B:N3	2.27	0.66
1:A:330:ILE:HD11	1:B:696:LEU:HD22	1.77	0.64
1:A:336[A]:MET:SD	5:A:804:H4B:H6	2.38	0.63
1:B:336[A]:MET:SD	5:B:802:H4B:H6	2.38	0.62
1:A:321:THR:HG23	1:A:699:ARG:HH11	1.63	0.62
1:B:336[A]:MET:HE2	1:B:336[A]:MET:HA	1.81	0.61
1:A:336[A]:MET:CA	1:A:336[A]:MET:CE	2.77	0.60
1:A:478:GLN:HG3	4:A:805:QJ2:H5	1.84	0.60
2:B:801:HEM:O1A	5:B:802:H4B:N3	2.36	0.59
2:B:801:HEM:HBB2	2:B:801:HEM:HHC	1.85	0.58
1:A:336[A]:MET:HE1	1:A:678:TRP:HE1	1.68	0.58
1:A:628:GLN:HG2	1:B:631:VAL:HG11	1.86	0.58
1:A:523:LEU:HD22	1:A:531:PRO:HB2	1.86	0.58
1:B:299:ARG:HB3	1:B:318:LEU:HD21	1.87	0.57
1:B:299:ARG:HG2	1:B:317:HIS:NE2	2.21	0.56
1:A:336[A]:MET:SD	5:A:804:H4B:H9	2.46	0.56
1:A:478:GLN:HB2	1:A:481:ARG:HG3	1.87	0.55
1:B:364:GLN:NE2	8:B:967:HOH:O	2.39	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:478:GLN:HB2	1:B:481:ARG:HG3	1.91	0.53
2:A:801:HEM:O1A	5:A:804:H4B:N2	2.39	0.53
1:B:336[A]:MET:CE	8:B:1153:HOH:O	0.82	0.52
1:A:336[A]:MET:CE	1:A:678:TRP:HE1	2.22	0.52
2:B:801:HEM:C1C	4:B:805:QJ2:H24	2.45	0.52
1:A:321:THR:HG23	1:A:322:LEU:N	2.23	0.52
1:B:336[A]:MET:HE1	8:B:1153:HOH:O	0.78	0.51
1:A:596[B]:ARG:HG3	8:A:906:HOH:O	2.10	0.50
1:B:299:ARG:HD2	1:B:317:HIS:NE2	2.27	0.49
1:B:336[A]:MET:CE	1:B:336[A]:MET:HA	2.44	0.48
1:B:350:THR:O	1:B:353:GLN:HG2	2.13	0.47
1:A:676:TRP:CE2	1:A:680:VAL:HG21	2.50	0.47
1:B:596[B]:ARG:HG3	8:B:976:HOH:O	2.14	0.47
1:A:403:TYR:CE1	1:A:407:HIS:CE1	3.02	0.47
1:B:325:GLY:O	1:B:332:MET:HG3	2.15	0.47
2:B:801:HEM:HBA2	4:B:805:QJ2:H14	1.96	0.46
1:B:596[A]:ARG:NE	8:B:1098:HOH:O	2.49	0.46
4:A:803:QJ2:H20	8:A:1006:HOH:O	2.16	0.46
2:B:801:HEM:O1A	5:B:802:H4B:C2	2.64	0.45
1:B:336[A]:MET:SD	5:B:802:H4B:H9	2.56	0.45
1:A:701[A]:THR:HG22	8:A:923:HOH:O	2.17	0.45
5:A:804:H4B:H71	5:A:804:H4B:O10	2.16	0.44
1:A:687:ILE:HD12	1:B:626:LYS:HB3	2.00	0.44
1:B:409:TRP:CE3	1:B:421:TRP:HA	2.52	0.44
1:B:322:LEU:HB2	1:B:699:ARG:HD3	1.99	0.44
1:A:699:ARG:HD2	4:A:803:QJ2:H15	2.00	0.44
1:A:475:TRP:HB2	1:A:523:LEU:HB3	1.99	0.44
1:A:352:ASP:N	1:A:352:ASP:OD2	2.51	0.44
1:A:686:SER:HA	1:A:691:PHE:CG	2.52	0.44
1:B:485:TYR:CE1	1:B:514:ARG:HA	2.52	0.44
1:B:701:THR:HA	1:B:702:PRO:C	2.38	0.43
1:A:589:MET:HA	1:A:649:VAL:O	2.18	0.43
1:A:409:TRP:CE3	1:A:421:TRP:HA	2.53	0.43
2:A:801:HEM:CMC	2:A:801:HEM:HBC2	2.49	0.43
1:A:701[A]:THR:CG2	1:A:702:PRO:HA	2.42	0.43
1:A:475:TRP:CZ2	1:A:531:PRO:HG3	2.54	0.42
1:A:391:THR:O	1:A:392:SER:OG	2.25	0.42
2:A:801:HEM:O1A	5:A:804:H4B:C2	2.67	0.42
1:A:592:GLU:OE1	4:A:805:QJ2:N01	2.52	0.42
1:B:717:LYS:N	1:B:717:LYS:HD2	2.35	0.42
1:B:414:ARG:NH1	1:B:706:TYR:OH	2.52	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:445:HIS:C	1:B:445:HIS:CD2	2.94	0.41
1:B:596[A]:ARG:NH1	8:B:1119:HOH:O	2.52	0.41
1:A:626:LYS:HB3	1:B:687:ILE:HD12	2.03	0.41
1:B:478:GLN:HG3	4:B:805:QJ2:H5	2.01	0.41
1:A:631:VAL:HG11	1:B:628:GLN:HG2	2.02	0.41
1:A:321:THR:HG23	1:A:699:ARG:NH1	2.30	0.41
1:A:300:PHE:HB3	8:A:1059:HOH:O	2.20	0.41
1:B:403:TYR:CE1	1:B:407:HIS:CE1	3.08	0.41
2:A:801:HEM:C1C	4:A:805:QJ2:H24	2.56	0.41
1:B:676:TRP:CE2	1:B:680:VAL:HG21	2.56	0.40
1:B:535:GLN:HG3	8:B:1117:HOH:O	2.21	0.40
1:B:397:LYS:HA	1:B:397:LYS:HD2	1.79	0.40
1:A:322:LEU:HB2	1:A:699:ARG:NH1	2.37	0.40
1:B:686:SER:HA	1:B:691:PHE:CG	2.57	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	410/422 (97%)	398 (97%)	9 (2%)	3 (1%)	26	17
1	B	414/422 (98%)	407 (98%)	7 (2%)	0	100	100
All	All	824/844 (98%)	805 (98%)	16 (2%)	3 (0%)	39	31

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	322	LEU
1	A	300	PHE
1	A	338	PRO

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	370/377 (98%)	356 (96%)	14 (4%)	40	33
1	B	373/377 (99%)	364 (98%)	9 (2%)	57	55
All	All	743/754 (98%)	720 (97%)	23 (3%)	48	43

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	300	PHE
1	A	322	LEU
1	A	330	ILE
1	A	336[A]	MET
1	A	336[B]	MET
1	A	350	THR
1	A	352	ASP
1	A	353	GLN
1	A	370	LYS
1	A	371	ARG
1	A	454	ASN
1	A	523	LEU
1	A	547	ARG
1	A	620	LYS
1	B	322	LEU
1	B	360	GLU
1	B	382	GLU
1	B	389	GLU
1	B	390	SER
1	B	454	ASN
1	B	540	LEU
1	B	547	ARG
1	B	717	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	425	GLN
1	A	436	HIS
1	A	440	ASN
1	A	454	ASN
1	A	527	ASN
1	A	605	ASN
1	A	628	GLN
1	A	642	GLN
1	A	697	ASN
1	B	364	GLN
1	B	440	ASN
1	B	454	ASN
1	B	507	GLN
1	B	527	ASN
1	B	601	ASN
1	B	605	ASN
1	B	642	GLN
1	B	697	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 7 are monoatomic - leaving 10 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	30,50,50	2.28	9 (30%)	24,82,82	2.74	11 (45%)
3	ACT	A	802	-	1,3,3	1.02	0	0,3,3	0.00	-
4	QJ2	A	803	-	22,22,22	0.77	0	29,29,29	1.90	8 (27%)
5	H4B	A	804	-	13,18,18	0.83	0	11,26,26	2.71	7 (63%)
4	QJ2	A	805	-	22,22,22	0.62	0	29,29,29	1.92	6 (20%)
2	HEM	B	801	1	30,50,50	2.12	9 (30%)	24,82,82	2.59	14 (58%)
5	H4B	B	802	-	13,18,18	0.87	0	11,26,26	2.52	5 (45%)
4	QJ2	B	803	-	22,22,22	0.88	0	29,29,29	2.18	6 (20%)
3	ACT	B	804	-	1,3,3	1.01	0	0,3,3	0.00	-
4	QJ2	B	805	-	22,22,22	0.73	0	29,29,29	2.15	9 (31%)

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	-	0/10/54/54	0/0/8/8
3	ACT	A	802	-	-	0/0/0/0	0/0/0/0
4	QJ2	A	803	-	-	0/8/8/8	0/2/2/2
5	H4B	A	804	-	-	0/8/17/17	0/2/2/2
4	QJ2	A	805	-	-	0/8/8/8	0/2/2/2
2	HEM	B	801	1	-	0/10/54/54	0/0/8/8
5	H4B	B	802	-	-	0/8/17/17	0/2/2/2
4	QJ2	B	803	-	-	0/8/8/8	0/2/2/2
3	ACT	B	804	-	-	0/0/0/0	0/0/0/0
4	QJ2	B	805	-	-	0/8/8/8	0/2/2/2

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEM	C3B-C4B	-6.91	1.45	1.51
2	B	801	HEM	C3D-C4D	-5.86	1.44	1.51
2	A	801	HEM	C3D-C4D	-5.72	1.44	1.51
2	B	801	HEM	C3B-C4B	-5.24	1.47	1.51
2	A	801	HEM	C2C-C1C	-3.54	1.45	1.52
2	B	801	HEM	C2C-C1C	-3.31	1.46	1.52
2	B	801	HEM	C2B-C1B	-2.40	1.44	1.51
2	B	801	HEM	C2D-C1D	-2.34	1.44	1.51
2	A	801	HEM	C2D-C1D	-2.18	1.44	1.51

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEM	CAA-C2A	2.09	1.55	1.52
2	B	801	HEM	CMA-C3A	2.14	1.56	1.51
2	A	801	HEM	FE-ND	2.21	2.09	1.97
2	A	801	HEM	FE-NC	2.22	2.04	1.95
2	B	801	HEM	C1C-NC	2.25	1.38	1.36
2	A	801	HEM	CMA-C3A	2.40	1.56	1.51
2	A	801	HEM	C1C-NC	2.54	1.39	1.36
2	B	801	HEM	FE-NC	2.61	2.06	1.95
2	B	801	HEM	CAA-C2A	2.62	1.56	1.52

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	HEM	CBA-CAA-C2A	-6.30	101.24	112.53
5	A	804	H4B	N3-C2-N1	-4.40	118.32	125.53
4	B	805	QJ2	C05-C06-N01	-4.16	118.26	122.96
4	A	805	QJ2	C05-C06-N01	-4.07	118.36	122.96
5	B	802	H4B	N3-C2-N1	-3.97	119.03	125.53
4	B	803	QJ2	C25-C26-N21	-3.58	118.92	122.96
4	B	803	QJ2	C05-C06-N01	-3.46	119.05	122.96
2	B	801	HEM	CBA-CAA-C2A	-3.43	106.37	112.53
2	A	801	HEM	CBD-CAD-C3D	-3.24	104.14	113.55
4	A	803	QJ2	C25-C26-N21	-2.94	119.64	122.96
4	B	805	QJ2	C27-C24-C25	-2.85	116.63	120.95
4	A	803	QJ2	C05-C06-N01	-2.77	119.84	122.96
2	B	801	HEM	CBD-CAD-C3D	-2.58	106.04	113.55
2	A	801	HEM	CAA-C2A-C1A	-2.52	124.27	127.01
4	B	805	QJ2	C25-C26-N21	-2.44	120.21	122.96
2	B	801	HEM	C3B-C4B-NB	-2.44	106.97	111.63
2	B	801	HEM	CAA-C2A-C1A	-2.39	124.41	127.01
2	A	801	HEM	C3C-CAC-CBC	-2.37	120.82	124.46
2	B	801	HEM	CMA-C3A-C4A	-2.36	124.46	128.36
2	B	801	HEM	C3B-CAB-CBB	-2.29	120.94	124.46
4	A	805	QJ2	C24-C25-C26	-2.28	118.85	120.28
4	B	805	QJ2	C11-C12-C26	-2.18	105.10	112.79
4	A	805	QJ2	C25-C26-N21	-2.11	120.58	122.96
4	B	805	QJ2	C24-C25-C26	-2.06	118.99	120.28
5	A	804	H4B	N2-C2-N3	2.03	120.55	117.20
4	A	803	QJ2	N02-C02-N01	2.09	120.31	116.50
5	B	802	H4B	N2-C2-N1	2.17	120.80	117.20
4	A	803	QJ2	N22-C22-N21	2.25	120.60	116.50
5	A	804	H4B	N2-C2-N1	2.37	121.12	117.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	HEM	C2D-C3D-C4D	2.39	105.55	101.50
4	B	803	QJ2	C12-C26-C25	2.44	124.55	121.13
4	A	805	QJ2	C04-C05-C06	2.46	121.82	120.28
4	B	805	QJ2	C12-C26-N21	2.49	119.37	115.69
5	A	804	H4B	C4A-C8A-N8	2.49	121.36	118.43
2	B	801	HEM	C2C-C1C-CHC	2.51	127.50	123.68
2	A	801	HEM	CMD-C2D-C3D	2.53	125.55	114.35
5	B	802	H4B	C2-N1-C8A	2.61	120.41	114.54
4	A	803	QJ2	C08-C06-N01	2.66	119.62	115.69
4	B	805	QJ2	C08-C06-N01	2.69	119.67	115.69
2	B	801	HEM	CMD-C2D-C3D	2.84	126.90	114.35
4	A	803	QJ2	C12-C26-N21	3.07	120.22	115.69
2	B	801	HEM	C3B-C4B-CHC	3.11	127.53	123.16
5	A	804	H4B	C4-C4A-C8A	3.11	117.38	114.56
2	A	801	HEM	C3B-C4B-CHC	3.20	127.67	123.16
5	A	804	H4B	C2-N1-C8A	3.33	122.02	114.54
2	A	801	HEM	C2D-C3D-C4D	3.36	107.20	101.50
5	B	802	H4B	C4-C4A-C8A	3.62	117.84	114.56
4	B	803	QJ2	C08-C06-N01	3.63	121.06	115.69
2	A	801	HEM	CMB-C2B-C3B	3.86	126.17	116.53
2	A	801	HEM	CAD-C3D-C4D	3.95	126.39	112.47
2	B	801	HEM	CAD-C3D-C2D	4.35	125.71	113.22
2	A	801	HEM	CAD-C3D-C2D	4.56	126.32	113.22
2	B	801	HEM	CMB-C2B-C3B	4.57	127.94	116.53
2	B	801	HEM	CAD-C3D-C4D	4.61	128.74	112.47
2	B	801	HEM	CMC-C2C-C3C	4.62	128.07	116.53
4	A	803	QJ2	C22-N21-C26	4.68	121.56	118.23
5	A	804	H4B	C4-N3-C2	4.70	122.47	115.94
5	B	802	H4B	C4-N3-C2	4.77	122.55	115.94
4	A	805	QJ2	C02-N01-C06	4.78	121.62	118.23
2	A	801	HEM	CMC-C2C-C3C	4.87	128.69	116.53
4	A	805	QJ2	C22-N21-C26	5.12	121.87	118.23
4	B	805	QJ2	C02-N01-C06	5.34	122.02	118.23
4	B	803	QJ2	C02-N01-C06	5.54	122.16	118.23
4	A	803	QJ2	C02-N01-C06	5.71	122.29	118.23
4	B	805	QJ2	C22-N21-C26	5.98	122.48	118.23
4	B	803	QJ2	C22-N21-C26	6.53	122.87	118.23

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	HEM	6	0
4	A	803	QJ2	2	0
5	A	804	H4B	6	0
4	A	805	QJ2	3	0
2	B	801	HEM	6	0
5	B	802	H4B	6	0
4	B	805	QJ2	3	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%)	0.41	20 (4%) 33 37	24, 39, 63, 85	0
1	B	412/422 (97%)	0.34	12 (2%) 55 58	21, 33, 54, 80	0
All	All	820/844 (97%)	0.37	32 (3%) 43 47	21, 36, 61, 85	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	300	PHE	9.0
1	A	322	LEU	8.7
1	A	351	LYS	8.0
1	B	322	LEU	7.8
1	B	348	VAL	7.0
1	A	299	ARG	5.4
1	B	300	PHE	4.5
1	B	718	GLY	4.3
1	A	352	ASP	3.9
1	A	339	SER	3.8
1	A	373	GLY	3.5
1	A	355	PHE	3.4
1	A	350	THR	3.3
1	B	350	THR	2.9
1	B	619	ARG	2.9
1	A	338	PRO	2.8
1	A	716	TRP	2.8
1	B	355	PHE	2.7
1	B	351	LYS	2.7
1	A	713	THR	2.7
1	B	349	ARG	2.7
1	A	371	ARG	2.6
1	A	488	PRO	2.6
1	A	370	LYS	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	330	ILE	2.4
1	B	338	PRO	2.4
1	B	620	LYS	2.2
1	A	330	ILE	2.2
1	A	337	LEU	2.1
1	A	469	LYS	2.1
1	A	511	LYS	2.1
1	A	386	LYS	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 ⓘ

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	H4B	A	804	17/17	0.81	0.24	5.33	37,43,48,49	0
5	H4B	B	802	17/17	0.86	0.21	4.82	44,51,55,56	0
4	QJ2	A	805	21/21	0.93	0.16	2.83	21,35,45,46	0
4	QJ2	A	803	21/21	0.78	0.42	2.81	37,54,72,72	0
4	QJ2	B	805	21/21	0.91	0.16	2.54	20,36,48,48	0
2	HEM	A	801	43/43	0.98	0.13	1.17	25,29,41,50	0
2	HEM	B	801	43/43	0.98	0.15	1.04	22,25,38,48	0
3	ACT	A	802	4/4	0.96	0.13	0.85	41,42,42,43	0
4	QJ2	B	803	21/21	0.88	0.22	0.72	35,50,71,73	0
6	ZN	A	809	1/1	1.00	0.11	0.10	32,32,32,32	0
3	ACT	B	804	4/4	0.97	0.12	-0.68	37,38,39,40	0
6	ZN	A	806[A]	1/1	0.98	0.10	-1.23	31,31,31,31	1
7	CL	B	808	1/1	1.00	0.11	-1.32	42,42,42,42	1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
7	CL	A	808[A]	1/1	0.98	0.08	-2.49	40,40,40,40	1
6	ZN	B	806	1/1	0.99	0.08	-2.72	36,36,36,36	1
7	CL	B	807	1/1	0.99	0.15	-	45,45,45,45	1
7	CL	A	807[A]	1/1	0.99	0.11	-	35,35,35,35	1

6.5 Other polymers [i](#)

There are no such residues in this entry.