



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 06:25 am GMT

PDB ID : 3E7M
Title : Structure of murine iNOS oxygenase domain with inhibitor AR-C95791
Authors : Garcin, E.D.; Arvai, A.S.; Rosenfeld, R.J.; Kroeger, M.D.; Crane, B.R.; Andersson, G.; Andrews, G.; Hamley, P.J.; Mallinder, P.R.; Nicholls, D.J.; St-Gallay, S.A.; Tinker, A.C.; Gensmantel, N.P.; Mete, A.; Cheshire, D.R.; Connolly, S.; Stuehr, D.J.; Aberg, A.; Wallace, A.V.; Tainer, J.A.; Getzoff, E.D.
Deposited on : 2008-08-18
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

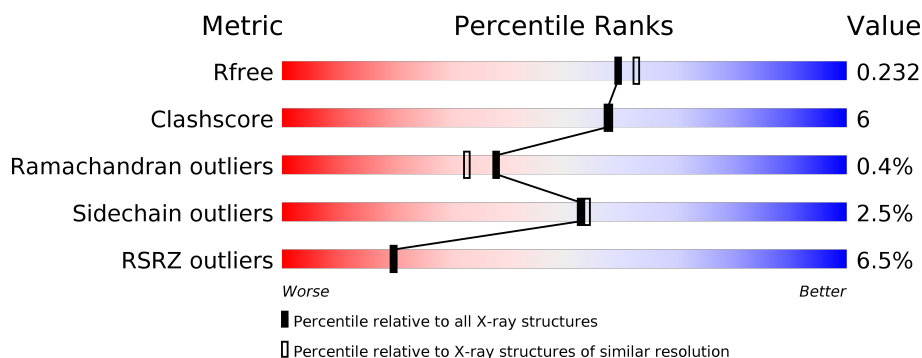
1 Overall quality at a glance

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.



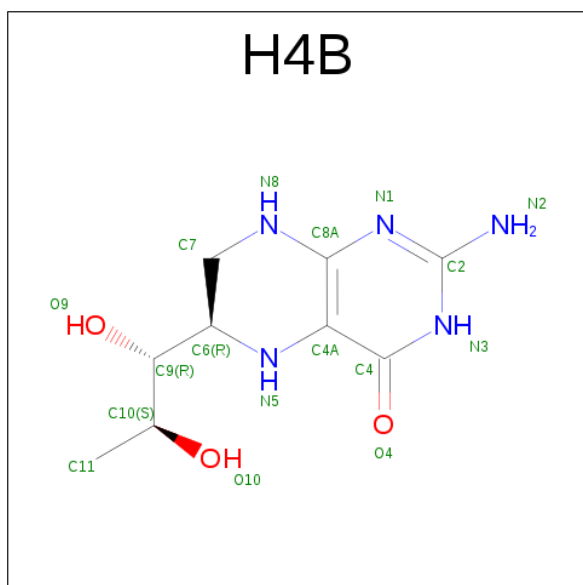
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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	433	<div> <div>6%</div> <div> <div></div> <div>84%</div> <div>10%</div> <div>• •</div> </div> </div>
1	B	433	<div> <div>7%</div> <div> <div></div> <div>86%</div> <div>10%</div> <div>• •</div> </div> </div>

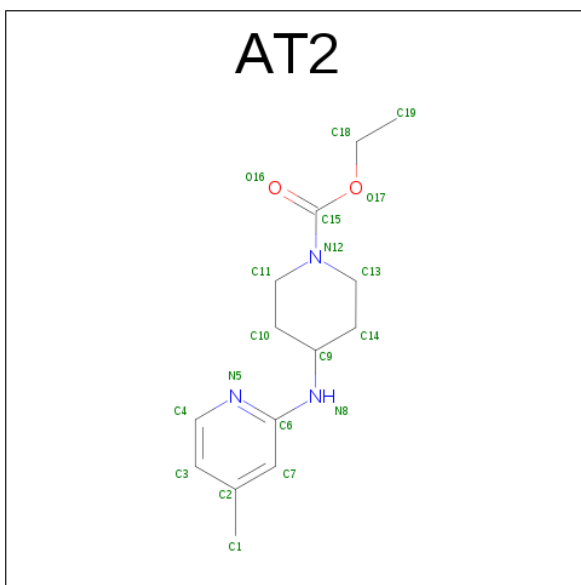
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 4 is 5,6,7,8-TETRAHYDROBIOPTERIN (three-letter code: H4B) (formula: $C_9H_{15}N_5O_3$).



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

- Molecule 5 is ETHYL 4-[(4-METHYLPYRIDIN-2-YL)AMINO]PIPERIDINE-1-CARBOXYLATE (three-letter code: AT2) (formula: $C_{14}H_{21}N_3O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			19	14	3	2		
5	B	1	Total	C	N	O	0	0
			19	14	3	2		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

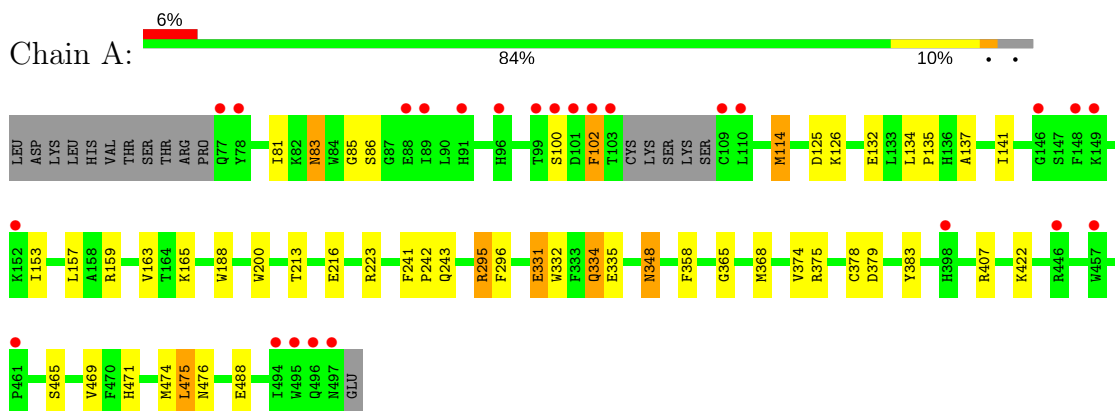
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	228	Total 228	O 228	0	0
7	B	278	Total 278	O 278	0	0

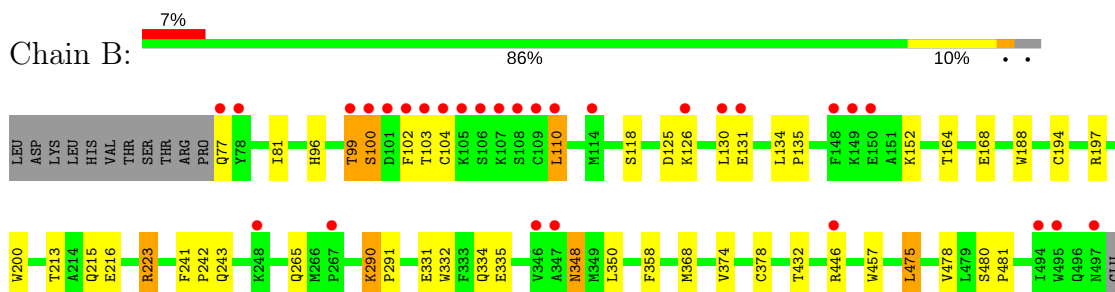
3 Residue-property plots [i](#)

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, inducible



- Molecule 1: Nitric oxide synthase, inducible



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	213.85Å 213.85Å 116.64Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.96 – 2.00 39.41 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.7 (19.96-2.00) 98.7 (39.41-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.03	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.37 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.223 , 0.237 0.218 , 0.232	Depositor DCC
R_{free} test set	5249 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	30.3	Xtriage
Anisotropy	0.707	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 51.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7484	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.90% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: HEM, ZN, AT2, H4B, EDO

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	0.33	0/3488	0.59	2/4743 (0.0%)
1	B	0.36	0/3521	0.63	1/4787 (0.0%)
All	All	0.34	0/7009	0.61	3/9530 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	365	GLY	N-CA-C	-5.39	99.64	113.10
1	B	368	MET	N-CA-C	-5.19	96.98	111.00
1	A	368	MET	N-CA-C	-5.14	97.13	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	3389	0	3276	36	0
1	B	3421	0	3310	41	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	43	0	30	0	0
3	B	43	0	30	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	17	0	15	0	0
4	B	17	0	15	1	0
5	A	19	0	21	0	0
5	B	19	0	21	0	0
6	A	8	0	12	0	0
7	A	228	0	0	5	2
7	B	278	0	0	5	1
All	All	7484	0	6730	77	3

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 (77) 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:B:103:THR:O	1:B:110:LEU:HD23	1.62	1.00
1:B:81:ILE:HD11	1:B:475:LEU:HD13	1.44	0.97
1:A:81:ILE:HD11	1:A:475:LEU:HD13	1.62	0.79
1:A:83:ASN:HD22	1:A:85:GLY:H	1.35	0.75
1:A:83:ASN:ND2	1:A:85:GLY:H	1.86	0.72
1:A:331:GLU:H	1:A:331:GLU:CD	1.93	0.72
1:B:432:THR:CG2	7:B:1158:HOH:O	2.39	0.70
1:B:290:LYS:HE2	1:B:291:PRO:HD2	1.76	0.68
1:B:223:ARG:HH21	1:B:223:ARG:CG	2.07	0.67
1:B:215:GLN:OE1	7:B:1476:HOH:O	2.12	0.66
1:B:223:ARG:HH21	1:B:223:ARG:HG3	1.61	0.66
1:B:290:LYS:HE2	1:B:291:PRO:CD	2.31	0.61
1:B:81:ILE:HD11	1:B:475:LEU:CD1	2.26	0.60
1:B:102:PHE:HE1	1:B:478:VAL:HG23	1.66	0.60
1:B:194:CYS:HB3	1:B:197:ARG:HD2	1.83	0.60
1:A:465:SER:O	1:A:471:HIS:HE1	1.85	0.59
1:A:469:VAL:HG13	1:A:474:MET:HE3	1.86	0.58
1:B:194:CYS:O	1:B:197:ARG:HD3	2.04	0.58
1:B:432:THR:HG21	7:B:1158:HOH:O	1.99	0.57
1:A:469:VAL:HG13	1:A:474:MET:CE	2.35	0.56
1:A:295:ARG:HD2	1:A:296:PHE:CE2	2.42	0.55
1:A:488:GLU:HG2	7:A:1379:HOH:O	2.08	0.54
1:B:102:PHE:CE1	1:B:478:VAL:HG23	2.42	0.54
1:A:134:LEU:HB3	1:A:135:PRO:HD3	1.91	0.52
1:B:188:TRP:CE3	1:B:200:TRP:HA	2.44	0.52
1:A:223:ARG:HH21	1:A:223:ARG:HG3	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:103:THR:HG22	1:B:118:SER:OG	2.10	0.52
1:A:348:ASN:HB2	7:A:1221:HOH:O	2.09	0.52
1:A:83:ASN:ND2	1:A:86:SER:H	2.08	0.52
1:B:104:CYS:SG	1:B:110:LEU:N	2.81	0.51
1:A:188:TRP:CE3	1:A:200:TRP:HA	2.45	0.51
1:A:125:ASP:OD1	1:A:126:LYS:HG3	2.10	0.51
1:B:446:ARG:HH21	1:B:446:ARG:HG2	1.77	0.49
1:A:348:ASN:H	1:A:348:ASN:HD22	1.61	0.48
1:A:114:MET:HE3	7:A:1011:HOH:O	2.14	0.47
1:B:348:ASN:H	1:B:348:ASN:HD22	1.63	0.47
1:A:102:PHE:HE2	1:A:476:ASN:O	1.97	0.46
1:A:153:ILE:O	1:A:157:LEU:HD23	2.14	0.46
1:A:407:ARG:HD2	7:A:1364:HOH:O	2.15	0.46
1:B:125:ASP:OD1	1:B:126:LYS:HG3	2.16	0.46
1:B:152:LYS:HB3	7:B:1410:HOH:O	2.15	0.46
1:B:213:THR:OG1	1:B:216:GLU:HG3	2.15	0.46
1:A:295:ARG:HD3	1:A:383:TYR:HE2	1.81	0.45
1:B:194:CYS:O	1:B:197:ARG:CD	2.63	0.45
1:A:331:GLU:N	1:A:331:GLU:CD	2.66	0.45
1:A:332:TRP:O	1:A:335:GLU:HB2	2.16	0.45
1:B:134:LEU:HB3	1:B:135:PRO:HD3	1.99	0.44
1:A:348:ASN:HD22	1:A:348:ASN:N	2.16	0.44
1:B:332:TRP:O	1:B:335:GLU:HB2	2.16	0.44
1:A:348:ASN:H	1:A:348:ASN:ND2	2.16	0.44
1:A:241:PHE:HB3	1:A:242:PRO:CD	2.48	0.44
1:B:243:GLN:HB3	1:B:358:PHE:CE2	2.53	0.44
1:A:243:GLN:HB3	1:A:358:PHE:CE2	2.52	0.43
1:B:241:PHE:HB3	1:B:242:PRO:CD	2.49	0.43
1:B:241:PHE:HB3	1:B:242:PRO:HD2	2.00	0.43
1:B:457:TRP:HA	4:B:1902:H4B:N1	2.34	0.43
1:B:374:VAL:O	1:B:378:CYS:HB2	2.19	0.42
1:B:348:ASN:N	1:B:348:ASN:HD22	2.17	0.42
1:A:165:LYS:HD2	1:A:165:LYS:N	2.34	0.42
1:A:334:GLN:OE1	1:A:335:GLU:N	2.53	0.42
1:A:132:GLU:O	1:A:135:PRO:HD2	2.20	0.42
1:A:374:VAL:O	1:A:378:CYS:HB2	2.20	0.42
1:A:422:LYS:NZ	7:A:1357:HOH:O	2.53	0.41
1:B:99:THR:HG23	1:B:478:VAL:O	2.21	0.41
1:A:213:THR:OG1	1:A:216:GLU:HG3	2.21	0.41
1:B:81:ILE:HA	1:B:81:ILE:HD13	1.92	0.41
1:A:137:ALA:O	1:A:141:ILE:HG12	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:77:GLN:O	1:B:96:HIS:HE1	2.04	0.41
1:B:350:LEU:C	1:B:350:LEU:HD23	2.40	0.41
1:A:159:ARG:O	1:A:163:VAL:HG23	2.21	0.41
1:A:375:ARG:O	1:A:379:ASP:HB2	2.21	0.40
1:B:99:THR:HB	1:B:100:SER:H	1.51	0.40
1:B:223:ARG:HD3	7:B:1189:HOH:O	2.20	0.40
1:B:102:PHE:CG	1:B:103:THR:N	2.86	0.40
1:B:348:ASN:H	1:B:348:ASN:ND2	2.20	0.40
1:B:164:THR:O	1:B:168:GLU:HG3	2.22	0.40
1:B:480:SER:HA	1:B:481:PRO:C	2.41	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1082:HOH:O	7:A:1082:HOH:O[11_655]	0.98	1.22
7:A:1376:HOH:O	7:A:1376:HOH:O[11_655]	1.19	1.01
7:B:1215:HOH:O	7:B:1303:HOH:O[9_766]	2.00	0.20

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	412/433 (95%)	393 (95%)	18 (4%)	1 (0%)	51	48
1	B	419/433 (97%)	402 (96%)	15 (4%)	2 (0%)	32	26
All	All	831/866 (96%)	795 (96%)	33 (4%)	3 (0%)	38	33

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	100	SER

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Mol	Chain	Res	Type
1	B	100	SER
1	B	99	THR

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	362/381 (95%)	354 (98%)	8 (2%)	57	60
1	B	366/381 (96%)	356 (97%)	10 (3%)	50	51
All	All	728/762 (96%)	710 (98%)	18 (2%)	53	54

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	83	ASN
1	A	102	PHE
1	A	114	MET
1	A	295	ARG
1	A	331	GLU
1	A	334	GLN
1	A	348	ASN
1	A	475	LEU
1	B	110	LEU
1	B	130	LEU
1	B	131	GLU
1	B	223	ARG
1	B	265	GLN
1	B	290	LYS
1	B	331	GLU
1	B	334	GLN
1	B	348	ASN
1	B	475	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	ASN
1	A	96	HIS
1	A	215	GLN
1	A	219	GLN
1	A	348	ASN
1	A	421	GLN
1	A	442	GLN
1	A	471	HIS
1	B	96	HIS
1	B	143	GLN
1	B	215	GLN
1	B	219	GLN
1	B	348	ASN
1	B	421	GLN

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 10 ligands modelled in this entry, 2 are 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	$\# Z > 2$
6	EDO	A	5001	-	3,3,3	0.58	0	2,2,2	0.59	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	EDO	A	5002	-	3,3,3	0.50	0	2,2,2	0.67	0
3	HEM	A	901	-	28,50,50	1.43	3 (10%)	17,82,82	1.09	1 (5%)
4	H4B	A	902	-	14,18,18	1.10	2 (14%)	12,26,26	2.02	5 (41%)
5	AT2	A	906	-	20,20,20	1.86	5 (25%)	26,26,26	1.45	4 (15%)
3	HEM	B	1901	-	28,50,50	1.51	4 (14%)	17,82,82	1.24	2 (11%)
4	H4B	B	1902	-	14,18,18	1.35	3 (21%)	12,26,26	1.94	4 (33%)
5	AT2	B	1906	-	20,20,20	1.79	4 (20%)	26,26,26	1.43	4 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	EDO	A	5001	-	-	0/1/1/1	0/0/0/0
6	EDO	A	5002	-	-	0/1/1/1	0/0/0/0
3	HEM	A	901	-	-	0/6/54/54	0/0/8/8
4	H4B	A	902	-	-	0/8/17/17	0/2/2/2
5	AT2	A	906	-	-	0/11/21/21	0/2/2/2
3	HEM	B	1901	-	-	0/6/54/54	0/0/8/8
4	H4B	B	1902	-	-	0/8/17/17	0/2/2/2
5	AT2	B	1906	-	-	0/11/21/21	0/2/2/2

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	901	HEM	C3B-CAB	-3.78	1.40	1.47
3	B	1901	HEM	C3B-CAB	-3.63	1.40	1.47
3	B	1901	HEM	C3C-CAC	-3.15	1.41	1.47
3	A	901	HEM	C3C-CAC	-2.88	1.42	1.47
3	B	1901	HEM	C3B-C2B	-2.72	1.36	1.40
3	A	901	HEM	C4C-NC	2.02	1.39	1.36
5	A	906	AT2	C10-C9	2.04	1.57	1.51
3	B	1901	HEM	C1C-NC	2.05	1.39	1.36
4	A	902	H4B	C6-N5	2.13	1.50	1.45
4	B	1902	H4B	C4A-C8A	2.19	1.45	1.41
4	A	902	H4B	C4A-C8A	2.22	1.45	1.41
5	A	906	AT2	C3-C4	2.22	1.43	1.38
4	B	1902	H4B	C4-C4A	2.22	1.43	1.41
5	B	1906	AT2	C3-C4	2.27	1.43	1.38
5	B	1906	AT2	C4-N5	2.49	1.40	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1902	H4B	C6-N5	2.50	1.50	1.45
5	A	906	AT2	C4-N5	2.81	1.40	1.34
5	B	1906	AT2	C6-N5	3.97	1.41	1.34
5	A	906	AT2	C6-N5	4.02	1.41	1.34
5	B	1906	AT2	O16-C15	4.49	1.28	1.21
5	A	906	AT2	O16-C15	4.88	1.28	1.21

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	906	AT2	C3-C4-N5	-2.97	120.49	123.92
5	B	1906	AT2	C3-C4-N5	-2.81	120.67	123.92
4	A	902	H4B	N3-C2-N1	-2.61	121.21	125.45
4	B	1902	H4B	N3-C2-N1	-2.51	121.38	125.45
5	A	906	AT2	C7-C6-N5	-2.33	119.47	122.73
5	B	1906	AT2	C7-C6-N5	-2.33	119.47	122.73
5	B	1906	AT2	O16-C15-N12	-2.30	120.25	124.36
5	A	906	AT2	O16-C15-N12	-2.16	120.51	124.36
3	A	901	HEM	CMC-C2C-C3C	2.04	128.67	124.89
4	A	902	H4B	C4-C4A-C8A	2.06	116.43	114.56
3	B	1901	HEM	CMC-C2C-C3C	2.32	129.20	124.89
4	A	902	H4B	C6-C7-N8	2.66	115.24	111.01
4	B	1902	H4B	C6-C7-N8	2.75	115.39	111.01
3	B	1901	HEM	C4A-C3A-C2A	2.77	108.92	107.00
4	B	1902	H4B	C2-N1-C8A	2.97	121.20	114.51
4	A	902	H4B	C2-N1-C8A	3.02	121.31	114.51
5	A	906	AT2	O17-C15-N12	3.31	114.51	111.66
4	B	1902	H4B	C4-N3-C2	3.40	120.95	116.06
4	A	902	H4B	C4-N3-C2	3.48	121.07	116.06
5	B	1906	AT2	O17-C15-N12	3.48	114.67	111.66

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1902	H4B	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	416/433 (96%)	0.18	25 (6%) 23 23	23, 35, 51, 64	2 (0%)
1	B	421/433 (97%)	0.26	29 (6%) 18 18	22, 33, 50, 67	7 (1%)
All	All	837/866 (96%)	0.22	54 (6%) 20 20	22, 34, 50, 67	9 (1%)

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	102	PHE	12.2
1	B	100	SER	9.5
1	A	102	PHE	7.8
1	B	109	CYS	7.3
1	B	105	LYS	7.2
1	B	101	ASP	7.0
1	A	103	THR	6.9
1	A	109	CYS	6.9
1	B	103	THR	6.6
1	B	497	ASN	6.5
1	A	78	TYR	6.4
1	A	101	ASP	6.0
1	A	100	SER	5.6
1	B	108	SER	4.9
1	B	107	LYS	4.9
1	B	78	TYR	4.7
1	B	494	ILE	4.6
1	A	497	ASN	4.4
1	A	496	GLN	4.4
1	B	149	LYS	3.9
1	A	494	ILE	3.8
1	B	104	CYS	3.7
1	A	495	TRP	3.7
1	A	149	LYS	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	106	SER	3.3
1	A	99	THR	3.2
1	B	495	TRP	3.2
1	B	110	LEU	3.1
1	B	446	ARG	3.0
1	B	131	GLU	2.9
1	A	110	LEU	2.9
1	B	99	THR	2.8
1	A	398	HIS	2.7
1	B	267	PRO	2.7
1	A	446	ARG	2.5
1	A	91	HIS	2.5
1	B	130	LEU	2.5
1	A	152	LYS	2.4
1	B	114	MET	2.4
1	B	148	PHE	2.4
1	A	146	GLY	2.4
1	B	150	GLU	2.4
1	A	77	GLN	2.4
1	A	457	TRP	2.3
1	B	347	ALA	2.3
1	B	77	GLN	2.2
1	A	148	PHE	2.2
1	B	248	LYS	2.2
1	A	461	PRO	2.2
1	B	126	LYS	2.2
1	A	89	ILE	2.1
1	A	96	HIS	2.1
1	A	88	GLU	2.0
1	B	346	VAL	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	AT2	B	1906	19/19	0.96	0.20	1.36	18,22,28,30	0
4	H4B	A	902	17/17	0.94	0.21	1.20	23,25,29,29	0
5	AT2	A	906	19/19	0.96	0.17	1.08	20,22,29,30	0
3	HEM	A	901	43/43	0.98	0.16	1.03	21,24,26,29	0
3	HEM	B	1901	43/43	0.98	0.18	0.83	18,22,25,26	0
4	H4B	B	1902	17/17	0.94	0.18	0.77	22,25,28,29	0
6	EDO	A	5002	4/4	0.83	0.14	-	55,55,55,55	0
2	ZN	A	900	1/1	0.90	0.15	-	45,45,45,45	1
6	EDO	A	5001	4/4	0.85	0.10	-	52,54,55,55	0
2	ZN	B	1900	1/1	0.97	0.20	-	34,34,34,34	1

6.5 Other polymers [i](#)

There are no such residues in this entry.