



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 07:43 am GMT

PDB ID : 4CX0  
Title : Structure of bovine endothelial nitric oxide synthase Y477A mutant heme domain in complex with 6-((((3S, 5R)-5-((((6-AMINO-4-METHYLPYRIDIN-2-YL)METHOXY)METHYL)PYRROLIDIN-3-YL)OXY)METHYL)-4-METHYLPYRIDIN-2-AMINE  
Authors : Li, H.; Poulos, T.L.  
Deposited on : 2014-04-03  
Resolution : 2.20 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](mailto: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.

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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

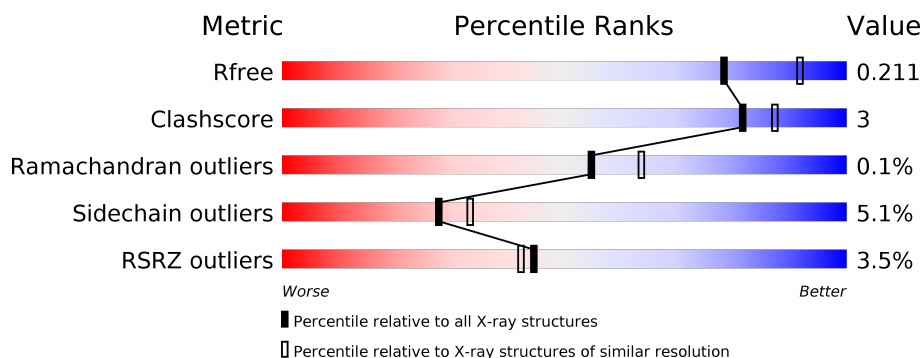
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	4002 (2.20-2.20)
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)

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  $\geq 3$ , 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>4%</div> <div> <div></div> <div>81%</div> <div>9%</div> <div>9%</div> </div> </div>
1	B	443	<div> <div>2%</div> <div> <div></div> <div>84%</div> <div>7%</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	A	860	-	-	-	X
5	ACT	A	861	-	-	-	X
5	ACT	B	860	-	-	-	X
6	GOL	A	880	-	-	-	X
6	GOL	B	880	-	-	-	X

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 7054 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.

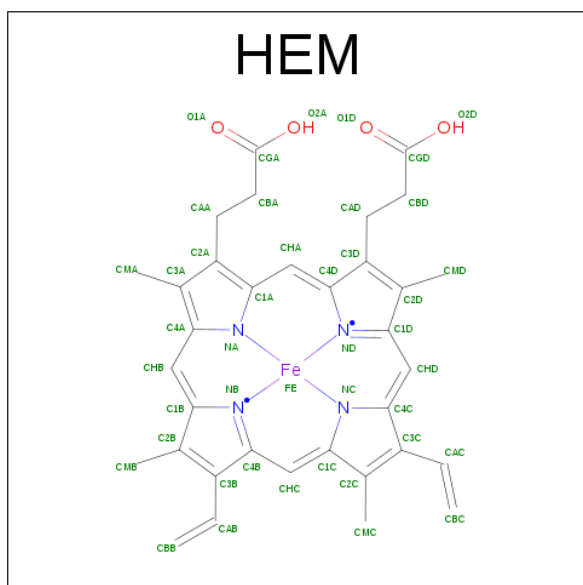
- Molecule 1 is a protein called NITRIC OXIDE SYNTHASE, ENDOTHELIAL.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	405	Total	As	C	N	O	S	0	1	0
			3221	1	2046	568	590	16			
1	B	403	Total	As	C	N	O	S	0	0	0
			3205	1	2036	566	586	16			

There are 4 discrepancies between the modelled and reference sequences:

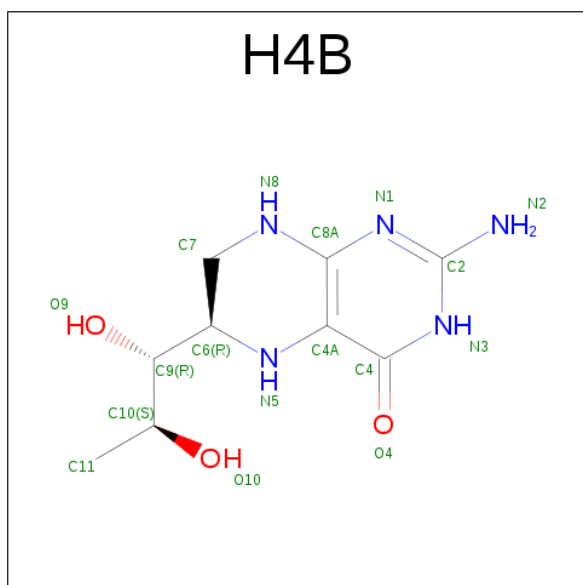
Chain	Residue	Modelled	Actual	Comment	Reference
A	100	ARG	CYS	SEE REMARK 999	UNP P29473
A	477	ALA	TYR	ENGINEERED MUTATION	UNP P29473
B	100	ARG	CYS	SEE REMARK 999	UNP P29473
B	477	ALA	TYR	ENGINEERED MUTATION	UNP P29473

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



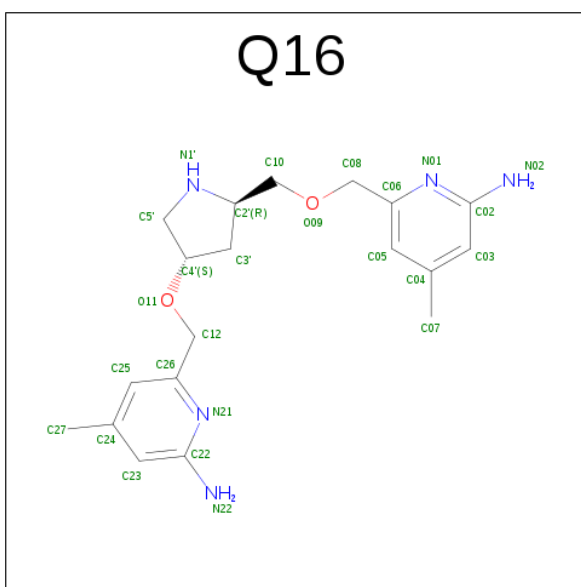
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is 5,6,7,8-TETRAHYDROBIOPTERIN (three-letter code: H4B) (formula:  $C_9H_{15}N_5O_3$ ).



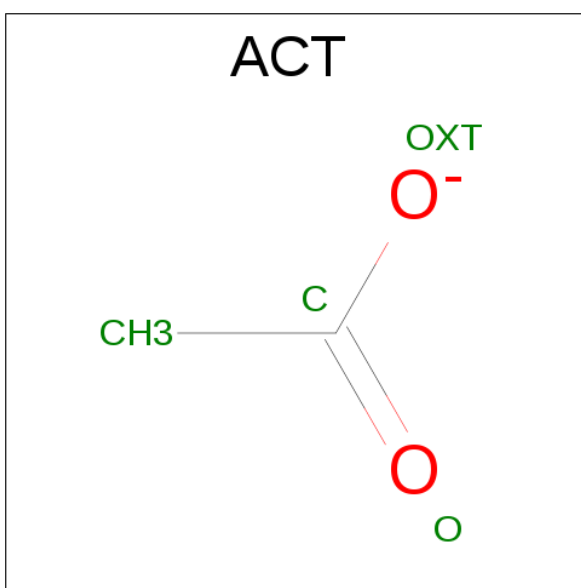
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			17	9	5	3		
3	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 4 is 6-((((3S, 5R)-5-(((6-AMINO-4-METHYLPYRIDIN-2-YL)METHOXY)METHYL)PYRROLIDIN-3-YL)OXY)METHYL)-4-METHYLPYRIDIN-2-AMINE (three-letter code: Q16) (formula:  $C_{19}H_{27}N_5O_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 26	C 19	N 5	O 2	0	0
4	B	1	Total 26	C 19	N 5	O 2	0	0

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula:  $\text{C}_2\text{H}_3\text{O}_2$ ).



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

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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		

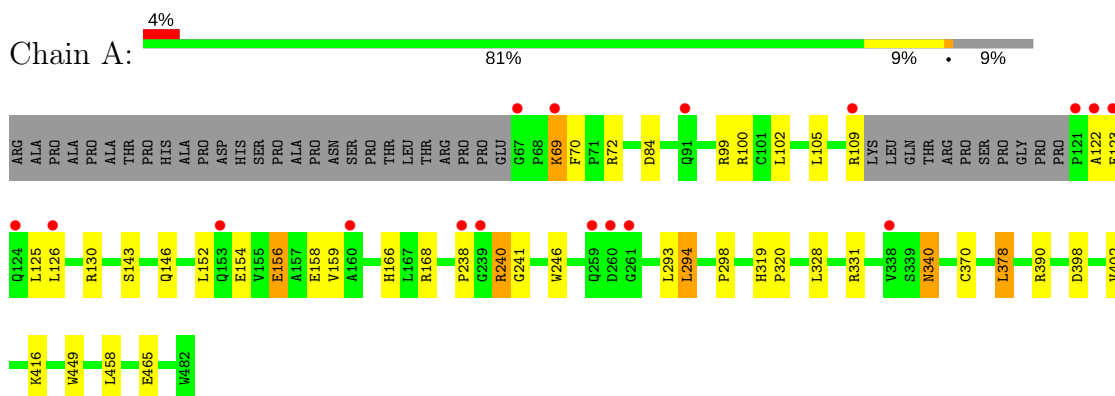
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	232	Total	O	0	0
			232	232		
8	B	195	Total	O	0	0
			195	195		

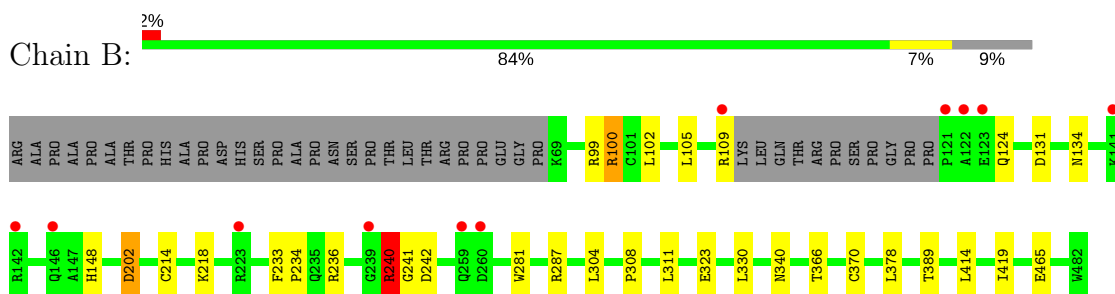
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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, ENDOTHELIAL



#### • Molecule 1: NITRIC OXIDE SYNTHASE, ENDOTHELIAL





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.71Å 106.46Å 156.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.68 – 2.20 38.65 – 2.18	Depositor EDS
% Data completeness (in resolution range)	99.4 (38.68-2.20) 98.8 (38.65-2.18)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.52 (at 2.18Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.155 , 0.203 0.164 , 0.211	Depositor DCC
$R_{free}$ test set	2466 reflections (5.25%)	DCC
Wilson B-factor (Å <sup>2</sup> )	31.7	Xtriage
Anisotropy	0.460	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 39.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	7054	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.57% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: GOL, ZN, H4B, CAS, Q16, ACT, HEM

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	0.64	0/3303	0.77	2/4497 (0.0%)
1	B	0.63	0/3283	0.76	2/4469 (0.0%)
All	All	0.64	0/6586	0.76	4/8966 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	331	ARG	NE-CZ-NH1	5.75	123.17	120.30
1	B	240	ARG	NE-CZ-NH2	-5.32	117.64	120.30
1	A	240	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	B	100	ARG	NE-CZ-NH1	5.16	122.88	120.30

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	3221	0	3127	23	0
1	B	3205	0	3113	14	0
2	A	43	0	30	1	0
2	B	43	0	30	3	0
3	A	17	0	15	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	17	0	15	0	0
4	A	26	0	27	0	0
4	B	26	0	27	0	0
5	A	8	0	6	0	0
5	B	8	0	6	0	0
6	A	6	0	8	0	0
6	B	6	0	8	0	0
7	A	1	0	0	0	0
8	A	232	0	0	1	0
8	B	195	0	0	3	0
All	All	7054	0	6412	39	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 3.

All (39) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:500:HEM:HMC2	2:B:500:HEM:HBC2	1.63	0.79
1:A:126:LEU:HD23	1:A:130:ARG:NH2	2.10	0.66
1:A:105:LEU:HD22	1:B:465:GLU:HB3	1.78	0.65
1:A:465:GLU:HB3	1:B:105:LEU:HD22	1.83	0.61
1:B:236:ARG:HD2	1:B:242:ASP:OD1	2.00	0.61
2:B:500:HEM:HHC	2:B:500:HEM:HBB2	1.84	0.60
1:B:287:ARG:HD3	8:B:2122:HOH:O	2.03	0.59
1:A:126:LEU:HD21	1:A:156:GLU:HB3	1.85	0.59
1:A:70:PHE:HB3	1:A:84:ASP:O	2.05	0.57
1:A:240:ARG:HD3	1:A:298:PRO:HB3	1.86	0.57
1:B:370:CYS:SG	1:B:378:LEU:HD13	2.43	0.57
1:B:240:ARG:HD2	1:B:241:GLY:O	2.05	0.56
1:A:240:ARG:HD2	1:A:241:GLY:O	2.06	0.55
1:B:308:PRO:HD2	1:B:311:LEU:HD12	1.88	0.55
1:A:449:TRP:HA	3:A:600:H4B:N1	2.23	0.54
1:A:152:LEU:O	1:A:156:GLU:HG2	2.07	0.53
1:B:233:PHE:HB3	1:B:234:PRO:CD	2.39	0.53
1:A:240:ARG:HD3	1:A:298:PRO:CB	2.39	0.52
1:A:69:LYS:HE2	1:A:69:LYS:HA	1.91	0.52
1:B:378:LEU:HB2	8:B:2152:HOH:O	2.10	0.51
1:A:370:CYS:SG	1:A:378:LEU:HD13	2.52	0.49
1:B:366:THR:O	1:B:370:CYS:HB2	2.12	0.49
2:A:500:HEM:HBB2	2:A:500:HEM:HHC	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:214:CYS:SG	8:B:2081:HOH:O	2.59	0.48
1:A:126:LEU:HD13	1:A:159:VAL:HG11	1.96	0.48
2:B:500:HEM:CMC	2:B:500:HEM:HBC2	2.41	0.47
1:A:246:TRP:HB2	1:A:294:LEU:HB3	1.97	0.46
1:A:378:LEU:HB2	8:A:2173:HOH:O	2.16	0.46
1:A:319:HIS:CG	1:A:320:PRO:HD2	2.51	0.46
1:A:158:GLU:OE2	1:A:166:HIS:HD2	1.99	0.46
1:B:134:ASN:OD1	1:B:148:HIS:NE2	2.50	0.45
1:A:340:ASN:HD22	1:A:340:ASN:H	1.66	0.44
1:A:126:LEU:HD12	1:A:159:VAL:HG21	2.00	0.44
1:B:281:TRP:HB2	1:B:304:LEU:HD21	2.01	0.42
1:B:202:ASP:O	1:B:202:ASP:CG	2.58	0.42
1:A:105:LEU:HD23	1:A:105:LEU:N	2.35	0.41
1:A:154:GLU:OE1	1:A:168:ARG:NH2	2.54	0.40
1:A:126:LEU:HD11	1:A:156:GLU:HA	2.04	0.40
1:A:398:ASP:O	1:A:402:VAL:HG23	2.22	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	401/443 (90%)	390 (97%)	10 (2%)	1 (0%)	51	58
1	B	398/443 (90%)	384 (96%)	14 (4%)	0	100	100
All	All	799/886 (90%)	774 (97%)	24 (3%)	1 (0%)	55	63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	122	ALA

### 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	343/374 (92%)	323 (94%)	20 (6%)	23	27
1	B	341/374 (91%)	326 (96%)	15 (4%)	33	40
All	All	684/748 (91%)	649 (95%)	35 (5%)	28	33

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	LYS
1	A	72	ARG
1	A	99	ARG
1	A	100	ARG
1	A	102	LEU
1	A	109	ARG
1	A	123	GLU
1	A	125	LEU
1	A	143	SER
1	A	146	GLN
1	A	156	GLU
1	A	238	PRO
1	A	293	LEU
1	A	294	LEU
1	A	328	LEU
1	A	340	ASN
1	A	378	LEU
1	A	390	ARG
1	A	416	LYS
1	A	458	LEU
1	B	99	ARG
1	B	100	ARG
1	B	102	LEU
1	B	109	ARG
1	B	124	GLN
1	B	131	ASP
1	B	202	ASP

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Mol	Chain	Res	Type
1	B	218	LYS
1	B	240	ARG
1	B	323	GLU
1	B	330	LEU
1	B	340	ASN
1	B	389	THR
1	B	414	LEU
1	B	419	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	166	HIS
1	A	191	GLN
1	A	340	ASN
1	A	376	ASN
1	A	468	ASN
1	B	191	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	6,8,9	1.04	0	2,9,11	1.05	0
1	CAS	B	384	1	6,8,9	1.32	0	2,9,11	1.31	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
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.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	500	1	28,50,50	1.11	3 (10%)	17,82,82	1.75	4 (23%)
3	H4B	A	600	-	14,18,18	0.90	0	12,26,26	2.60	7 (58%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	Q16	A	800	-	27,28,28	0.72	0	34,38,38	1.33	4 (11%)
5	ACT	A	860	-	1,3,3	1.46	0	0,3,3	0.00	-
5	ACT	A	861	-	1,3,3	1.94	0	0,3,3	0.00	-
6	GOL	A	880	-	5,5,5	0.38	0	5,5,5	0.71	0
2	HEM	B	500	1	28,50,50	1.27	2 (7%)	17,82,82	1.80	2 (11%)
3	H4B	B	600	-	14,18,18	0.80	0	12,26,26	1.98	5 (41%)
4	Q16	B	800	-	27,28,28	0.63	0	34,38,38	1.70	7 (20%)
5	ACT	B	860	-	1,3,3	1.84	0	0,3,3	0.00	-
5	ACT	B	861	-	1,3,3	2.26	1 (100%)	0,3,3	0.00	-
6	GOL	B	880	-	5,5,5	0.30	0	5,5,5	0.54	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	500	1	-	0/6/54/54	0/0/8/8
3	H4B	A	600	-	-	0/8/17/17	0/2/2/2
4	Q16	A	800	-	-	0/11/20/20	0/3/3/3
5	ACT	A	860	-	-	0/0/0/0	0/0/0/0
5	ACT	A	861	-	-	0/0/0/0	0/0/0/0
6	GOL	A	880	-	-	0/4/4/4	0/0/0/0
2	HEM	B	500	1	-	0/6/54/54	0/0/8/8
3	H4B	B	600	-	-	0/8/17/17	0/2/2/2
4	Q16	B	800	-	-	0/11/20/20	0/3/3/3
5	ACT	B	860	-	-	0/0/0/0	0/0/0/0
5	ACT	B	861	-	-	0/0/0/0	0/0/0/0
6	GOL	B	880	-	-	0/4/4/4	0/0/0/0

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	HEM	C1B-NB	-4.06	1.32	1.36
2	B	500	HEM	C3B-C2B	-3.25	1.36	1.40
2	A	500	HEM	C3B-C2B	-2.83	1.36	1.40
2	A	500	HEM	C4C-NC	2.14	1.39	1.36
2	A	500	HEM	C3C-C2C	2.18	1.43	1.40
5	B	861	ACT	CH3-C	2.26	1.51	1.48

All (29) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	500	HEM	CBA-CAA-C2A	-5.82	101.36	112.48
2	A	500	HEM	CBA-CAA-C2A	-3.79	105.24	112.48
4	A	800	Q16	C24-C25-C26	-3.51	118.06	120.26
3	A	600	H4B	N3-C2-N1	-3.15	120.34	125.45
4	B	800	Q16	C24-C25-C26	-2.97	118.40	120.26
3	B	600	H4B	N3-C2-N1	-2.88	120.78	125.45
2	A	500	HEM	CMA-C3A-C4A	-2.46	124.68	128.46
4	B	800	Q16	O09-C10-C2'	-2.44	102.01	109.39
4	B	800	Q16	C05-C06-N01	-2.38	120.33	122.91
4	A	800	Q16	C3'-C2'-C10	-2.37	109.14	113.37
3	A	600	H4B	C6-C7-N8	-2.34	107.30	111.01
3	A	600	H4B	C4A-C4-N3	-2.21	117.41	123.91
4	B	800	Q16	C04-C05-C06	-2.04	118.98	120.26
4	B	800	Q16	C08-C06-C05	2.09	123.96	121.04
2	A	500	HEM	CMC-C2C-C3C	2.18	128.94	124.89
3	A	600	H4B	N2-C2-N3	2.45	121.16	117.24
4	A	800	Q16	C3'-C2'-N1'	2.46	107.01	103.23
3	A	600	H4B	C2-N1-C8A	2.50	120.14	114.51
3	B	600	H4B	C2-N1-C8A	2.52	120.20	114.51
3	B	600	H4B	N2-C2-N3	2.92	121.91	117.24
3	B	600	H4B	C4-N3-C2	3.02	120.40	116.06
2	B	500	HEM	CAA-CBA-CGA	3.05	117.86	112.66
3	B	600	H4B	C4-C4A-C8A	3.17	117.44	114.56
4	A	800	Q16	C3'-C4'-C5'	3.26	106.55	103.60
2	A	500	HEM	CAA-CBA-CGA	3.49	118.62	112.66
3	A	600	H4B	C4-N3-C2	4.28	122.22	116.06
4	B	800	Q16	C3'-C4'-C5'	4.48	107.66	103.60
4	B	800	Q16	C02-N01-C06	5.16	121.82	118.17
3	A	600	H4B	C4-C4A-C8A	5.20	119.27	114.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	HEM	1	0
3	A	600	H4B	1	0
2	B	500	HEM	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	404/443 (91%)	-0.22	17 (4%) 37 35	23, 34, 60, 94	0
1	B	402/443 (90%)	-0.26	11 (2%) 55 52	23, 36, 64, 98	0
All	All	806/886 (90%)	-0.24	28 (3%) 44 42	23, 35, 62, 98	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	259	GLN	5.1
1	A	67	GLY	4.8
1	A	122	ALA	4.7
1	A	239	GLY	3.9
1	A	160	ALA	3.9
1	A	123	GLU	3.6
1	A	259	GLN	3.6
1	A	69	LYS	3.4
1	B	260	ASP	3.4
1	A	121	PRO	3.3
1	A	109	ARG	3.1
1	B	122	ALA	3.0
1	B	146	GLN	3.0
1	B	142	ARG	2.9
1	B	121	PRO	2.9
1	A	261	GLY	2.7
1	A	124	GLN	2.7
1	A	238	PRO	2.5
1	B	239	GLY	2.5
1	A	126	LEU	2.4
1	B	123	GLU	2.4
1	B	141	LYS	2.3
1	A	153	GLN	2.3
1	A	260	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	338	VAL	2.2
1	B	109	ARG	2.1
1	A	91	GLN	2.1
1	B	223	ARG	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	CAS	B	384	9/10	0.99	0.07	-	43,44,51,52	0
1	CAS	A	384	9/10	0.98	0.07	-	33,34,52,53	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
5	ACT	B	860	4/4	0.96	0.14	5.38	44,45,46,48	0
6	GOL	A	880	6/6	0.87	0.29	3.82	53,57,60,66	0
6	GOL	B	880	6/6	0.91	0.27	3.39	51,55,57,64	0
5	ACT	A	861	4/4	0.97	0.23	3.01	28,32,33,33	0
5	ACT	A	860	4/4	0.94	0.12	2.20	35,42,47,47	0
4	Q16	B	800	26/26	0.94	0.21	1.51	26,36,43,45	0
3	H4B	B	600	17/17	0.97	0.17	0.80	27,30,32,34	0
4	Q16	A	800	26/26	0.93	0.18	0.47	22,33,43,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	HEM	A	500	43/43	0.97	0.17	0.42	24,27,29,31	0
2	HEM	B	500	43/43	0.98	0.14	0.38	25,28,32,36	0
5	ACT	B	861	4/4	0.97	0.13	-0.03	27,28,29,30	0
3	H4B	A	600	17/17	0.98	0.15	-0.12	26,29,31,31	0
7	ZN	A	900	1/1	1.00	0.08	-0.80	28,28,28,28	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.