



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:02 PM GMT

PDB ID : 4UPQ  
Title : Structure of bovine endothelial nitric oxide synthase heme domain in complex with N',N'-{[(2R)-3-aminopropane-1,2-diyl]bis(oxymethanediylbenzene-3,1-diyl)}dithiophene-2-carboximidamide  
Authors : Li, H.; Poulos, T.L.  
Deposited on : 2014-06-17  
Resolution : 2.03 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 (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

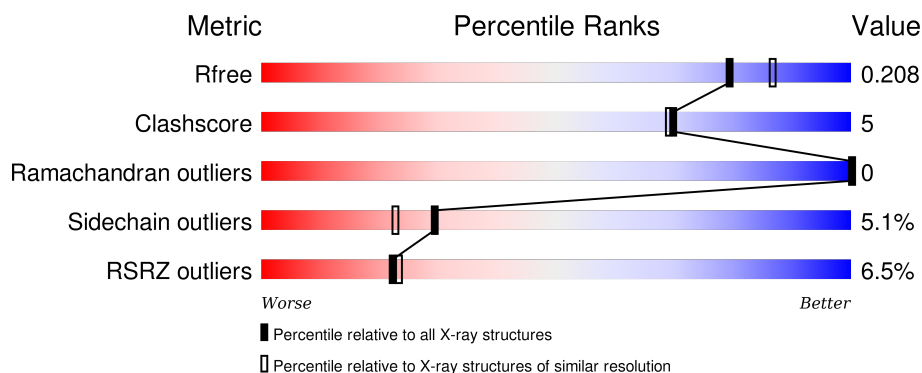
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.03 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	7858 (2.04-2.00)
Clashscore	102246	9060 (2.04-2.00)
Ramachandran outliers	100387	8952 (2.04-2.00)
Sidechain outliers	100360	8951 (2.04-2.00)
RSRZ outliers	91569	7873 (2.04-2.00)

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  $\geq 3$ , 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	
1	B	443	

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	I5U	A	800	-	-	-	X
4	I5U	B	800	-	-	-	X
5	ACT	B	860	-	-	-	X
6	GOL	A	880	-	-	-	X



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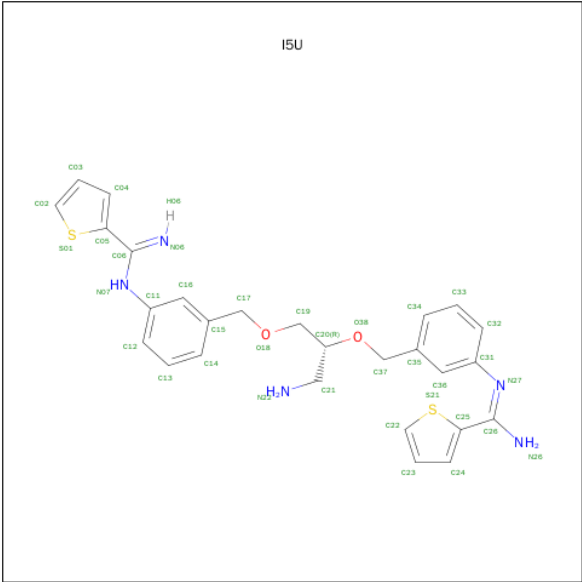
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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



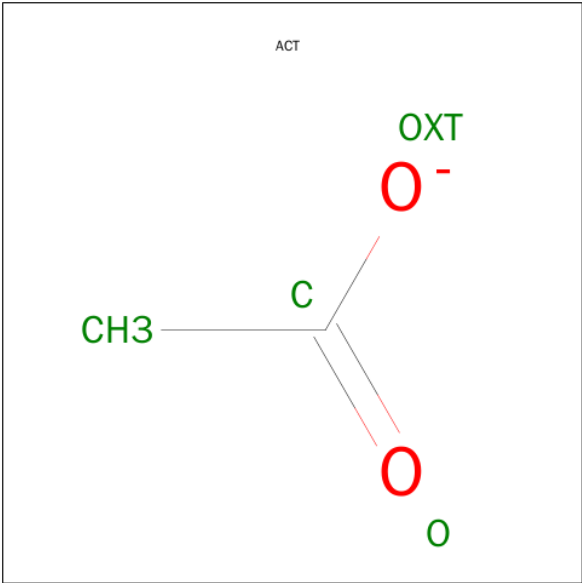
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			17	9	5	3		
3	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 4 is N',N'-{[(2R)-3-AMINOPROPANE-1,2-DIYL]BIS(OXYMETHANEDIYLBENZENE-3,1-DIYL)}DITHIOPHENE-2-CARBOXIMIDAMIDE (three-letter code: I5U) (formula:  $C_{27}H_{29}N_5O_2S_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			36	27	5	2	2		
4	B	1	Total	C	N	O	S	0	0
			36	27	5	2	2		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



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		

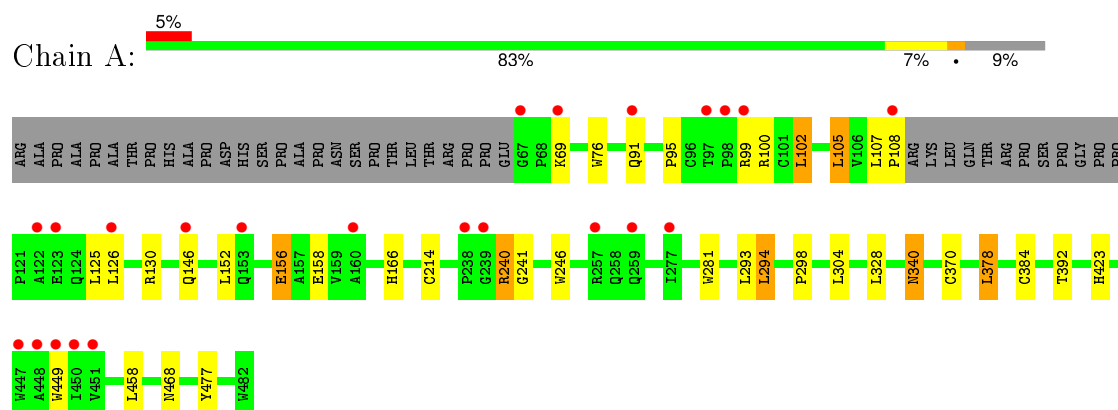
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	200	Total	O	0	0
			200	200		
8	B	171	Total	O	0	0
			171	171		

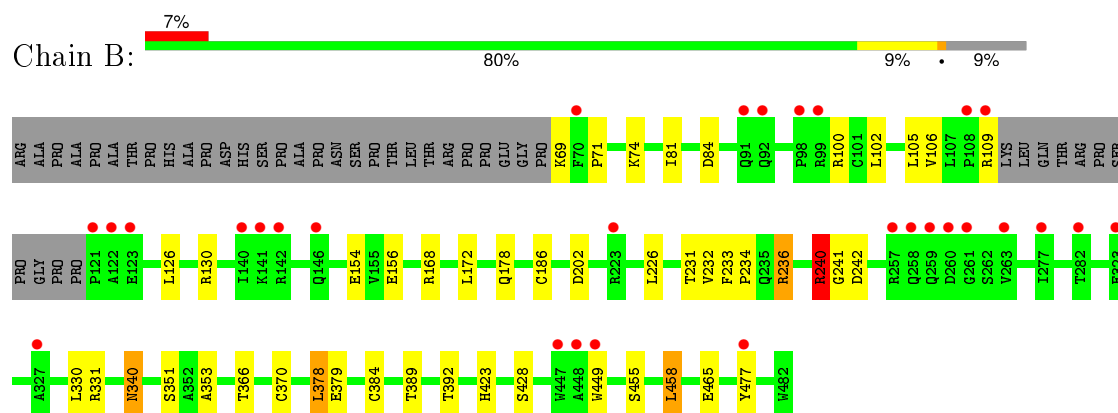
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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, 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, $\alpha$ , $\beta$ , $\gamma$	57.63Å 106.01Å 156.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.88 – 2.03 46.84 – 2.02	Depositor EDS
% Data completeness (in resolution range)	97.3 (46.88-2.03) 96.7 (46.84-2.02)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.87 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.168 , 0.209 0.167 , 0.208	Depositor DCC
$R_{free}$ test set	3045 reflections (5.23%)	DCC
Wilson B-factor (Å <sup>2</sup> )	35.1	Xtriage
Anisotropy	0.383	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 45.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 62027 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	7024	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.40% 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, 0.375 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, I5U

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	A	0.61	0/3306	0.71	2/4502 (0.0%)
1	B	0.61	0/3291	0.72	2/4480 (0.0%)
All	All	0.61	0/6597	0.71	4/8982 (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	B	240	ARG	NE-CZ-NH2	-9.83	115.38	120.30
1	B	240	ARG	NE-CZ-NH1	8.82	124.71	120.30
1	A	240	ARG	NE-CZ-NH1	5.93	123.27	120.30
1	A	240	ARG	NE-CZ-NH2	-5.62	117.49	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	3220	0	3123	26	0
1	B	3212	0	3117	30	1
2	A	43	0	30	2	0
2	B	43	0	30	4	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	1	0
4	A	36	0	28	4	0
4	B	36	0	28	4	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	200	0	0	3	1
8	B	171	0	0	2	0
All	All	7024	0	6414	59	1

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 (59) 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	2.52	1.27
1:B:384:CAS:AS	1:B:384:CAS:SG	2.57	1.22
1:A:240:ARG:HD3	1:A:298:PRO:HB3	1.42	0.99
1:A:240:ARG:HD3	1:A:298:PRO:CB	2.16	0.74
1:B:236:ARG:HD3	1:B:351:SER:HB3	1.75	0.69
1:B:428:SER:OG	8:B:2049:HOH:O	2.11	0.69
1:A:214:CYS:SG	8:A:2078:HOH:O	2.53	0.67
2:B:500:HEM:HHC	2:B:500:HEM:HBB2	1.79	0.65
1:A:152:LEU:O	1:A:156:GLU:HG2	1.98	0.64
2:A:500:HEM:HBB2	2:A:500:HEM:HHC	1.81	0.62
4:A:800:I5U:H32	4:A:800:I5U:S21	2.39	0.62
1:B:240:ARG:HD2	1:B:241:GLY:O	2.01	0.61
1:A:384:CAS:AS	1:A:384:CAS:CB	3.09	0.60
1:A:378:LEU:HB2	8:A:2143:HOH:O	2.03	0.59
1:B:126:LEU:HD21	1:B:130:ARG:HH21	1.69	0.58
1:A:246:TRP:HB2	1:A:294:LEU:HB3	1.86	0.56
1:A:384:CAS:CE2	1:A:384:CAS:SG	2.93	0.56
1:A:126:LEU:HD11	1:A:156:GLU:HA	1.87	0.56
1:A:449:TRP:HA	3:A:600:H4B:N1	2.22	0.55
1:B:370:CYS:SG	1:B:378:LEU:HD13	2.47	0.55
1:A:370:CYS:SG	1:A:378:LEU:HD13	2.46	0.54
1:B:384:CAS:CE2	1:B:384:CAS:SG	2.97	0.53
1:B:233:PHE:HB3	1:B:234:PRO:CD	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:LEU:HD23	1:A:130:ARG:NH2	2.26	0.50
1:A:240:ARG:HD2	1:A:241:GLY:O	2.12	0.50
1:B:477:TYR:CE1	4:B:800:I5U:H34	2.47	0.50
1:B:130:ARG:NH2	1:B:156:GLU:OE1	2.45	0.50
4:B:800:I5U:H32	4:B:800:I5U:N26	2.26	0.50
1:A:102:LEU:HD11	1:B:71:PRO:HB3	1.94	0.50
1:B:186:CYS:HB2	2:B:500:HEM:ND	2.27	0.49
1:B:340:ASN:HD22	1:B:340:ASN:H	1.60	0.49
4:B:800:I5U:C32	4:B:800:I5U:N26	2.75	0.49
1:A:340:ASN:HD22	1:A:340:ASN:H	1.61	0.48
1:A:95:PRO:HB3	1:A:108:PRO:HB2	1.94	0.48
1:B:236:ARG:HD2	1:B:242:ASP:OD1	2.13	0.48
1:B:366:THR:O	1:B:370:CYS:HB2	2.13	0.48
4:B:800:I5U:H262	4:B:800:I5U:C32	2.27	0.47
1:A:76:TRP:CZ2	1:B:106:VAL:HB	2.49	0.47
1:A:477:TYR:CE1	4:A:800:I5U:H34	2.50	0.47
1:A:105:LEU:HD22	1:B:465:GLU:HB3	1.97	0.47
1:B:154:GLU:OE1	1:B:168:ARG:NH2	2.47	0.47
1:B:231:THR:O	1:B:353:ALA:HA	2.15	0.46
1:B:71:PRO:HG2	1:B:84:ASP:HB3	1.98	0.46
1:A:158:GLU:OE2	1:A:166:HIS:HD2	1.99	0.46
1:B:378:LEU:HB2	8:B:2134:HOH:O	2.16	0.45
2:A:500:HEM:CBB	2:A:500:HEM:HHC	2.45	0.45
1:A:240:ARG:N	8:A:2093:HOH:O	2.49	0.44
2:B:500:HEM:HBC2	2:B:500:HEM:CMC	2.48	0.44
1:B:186:CYS:HB2	2:B:500:HEM:C4D	2.52	0.43
1:B:455:SER:HB3	1:B:458:LEU:HD22	1.98	0.43
4:A:800:I5U:H24	1:B:74:LYS:NZ	2.33	0.43
1:B:172:LEU:HD11	1:B:232:VAL:HG11	2.00	0.43
1:A:423:HIS:HB2	1:B:392:THR:HB	2.01	0.43
1:A:384:CAS:HB2	1:A:384:CAS:AS	2.78	0.43
1:B:449:TRP:HA	3:B:600:H4B:N1	2.33	0.42
4:A:800:I5U:H24	1:B:74:LYS:HZ3	1.85	0.42
1:B:384:CAS:AS	1:B:384:CAS:CB	3.28	0.42
1:A:281:TRP:HB2	1:A:304:LEU:HD21	2.04	0.40
1:A:392:THR:HB	1:B:423:HIS:HB2	2.02	0.40

All (1) 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)
1:B:240:ARG:NH2	8:A:2069:HOH:O[2_555]	2.05	0.15

## 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	401/443 (90%)	390 (97%)	11 (3%)	0	100	100
1	B	398/443 (90%)	385 (97%)	13 (3%)	0	100	100
All	All	799/886 (90%)	775 (97%)	24 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	344/375 (92%)	327 (95%)	17 (5%)	31	24
1	B	342/375 (91%)	324 (95%)	18 (5%)	28	21
All	All	686/750 (92%)	651 (95%)	35 (5%)	29	23

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

Mol	Chain	Res	Type
1	A	69	LYS
1	A	91	GLN
1	A	99	ARG

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Mol	Chain	Res	Type
1	A	100	ARG
1	A	102	LEU
1	A	105	LEU
1	A	107	LEU
1	A	125	LEU
1	A	146	GLN
1	A	156	GLU
1	A	293	LEU
1	A	294	LEU
1	A	328	LEU
1	A	340	ASN
1	A	378	LEU
1	A	458	LEU
1	A	468	ASN
1	B	69	LYS
1	B	81	ILE
1	B	100	ARG
1	B	102	LEU
1	B	105	LEU
1	B	109	ARG
1	B	178	GLN
1	B	202	ASP
1	B	226	LEU
1	B	236	ARG
1	B	240	ARG
1	B	330	LEU
1	B	331	ARG
1	B	340	ASN
1	B	378	LEU
1	B	379	GLU
1	B	389	THR
1	B	458	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	146	GLN
1	A	153	GLN
1	A	166	HIS
1	A	191	GLN
1	A	340	ASN
1	A	376	ASN

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Mol	Chain	Res	Type
1	A	468	ASN
1	B	178	GLN
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	5,8,9	0.95	0	2,9,11	1.37	0
1	CAS	B	384	1	5,8,9	1.28	1 (20%)	2,9,11	1.71	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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	384	CAS	AS-CE1	2.08	2.01	1.96

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	384	CAS	O-C-CA	-2.34	119.39	125.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	384	CAS	4	0
1	B	384	CAS	3	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	500	1	30,50,50	2.00	8 (26%)	24,82,82	2.41	9 (37%)
3	H4B	A	600	-	13,18,18	0.83	0	11,26,26	2.63	6 (54%)
4	I5U	A	800	-	38,39,39	1.42	5 (13%)	36,51,51	1.95	4 (11%)
5	ACT	A	860	-	1,3,3	1.97	0	0,3,3	0.00	-
5	ACT	A	861	-	1,3,3	1.21	0	0,3,3	0.00	-
6	GOL	A	880	-	5,5,5	0.28	0	5,5,5	0.67	0



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	HEM	B	500	1	30,50,50	2.07	6 (20%)	24,82,82	2.45	10 (41%)
3	H4B	B	600	-	13,18,18	0.85	0	11,26,26	2.24	6 (54%)
4	I5U	B	800	-	38,39,39	1.47	7 (18%)	36,51,51	1.82	5 (13%)
5	ACT	B	860	-	1,3,3	1.42	0	0,3,3	0.00	-
5	ACT	B	861	-	1,3,3	1.98	0	0,3,3	0.00	-
6	GOL	B	880	-	5,5,5	0.32	0	5,5,5	0.98	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	-	0/10/54/54	0/0/8/8
3	H4B	A	600	-	-	0/8/17/17	0/2/2/2
4	I5U	A	800	-	-	1/21/29/29	0/4/4/4
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	-	0/10/54/54	0/0/8/8
3	H4B	B	600	-	-	0/8/17/17	0/2/2/2
4	I5U	B	800	-	-	0/21/29/29	0/4/4/4
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 (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	HEM	C2D-C3D	-6.60	1.34	1.54
2	A	500	HEM	C2D-C3D	-6.28	1.35	1.54
2	B	500	HEM	C2C-C1C	-5.57	1.42	1.52
2	A	500	HEM	C2C-C1C	-4.76	1.43	1.52
4	A	800	I5U	C31-N27	-3.41	1.36	1.42
2	B	500	HEM	C3D-C4D	-3.40	1.47	1.51
4	B	800	I5U	C31-N27	-3.23	1.37	1.42
4	B	800	I5U	C06-N07	-3.21	1.32	1.39
2	A	500	HEM	C3B-C4B	-3.12	1.49	1.51
4	A	800	I5U	C06-N07	-2.87	1.33	1.39
4	B	800	I5U	C11-N07	-2.78	1.36	1.41
2	A	500	HEM	C3D-C4D	-2.59	1.48	1.51
2	B	500	HEM	C3B-C4B	-2.53	1.49	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	HEM	C2B-C1B	-2.44	1.43	1.51
2	A	500	HEM	C2B-C1B	-2.17	1.44	1.51
4	B	800	I5U	C05-C06	2.16	1.48	1.45
4	B	800	I5U	C05-S01	2.18	1.75	1.72
2	A	500	HEM	CHC-C1C	2.35	1.41	1.36
2	A	500	HEM	FE-NB	2.61	2.11	1.97
2	A	500	HEM	FE-NC	2.81	2.06	1.95
2	B	500	HEM	FE-NC	3.14	2.08	1.95
4	A	800	I5U	C26-N27	3.44	1.35	1.30
4	A	800	I5U	C05-C06	3.50	1.50	1.45
4	A	800	I5U	C25-C26	3.75	1.50	1.45
4	B	800	I5U	C25-C26	3.79	1.50	1.45
4	B	800	I5U	C26-N27	3.92	1.35	1.30

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	800	I5U	C03-C02-S01	-7.09	105.38	113.23
4	A	800	I5U	C23-C22-S21	-5.93	106.67	113.23
4	B	800	I5U	C23-C22-S21	-5.85	106.75	113.23
4	B	800	I5U	C03-C02-S01	-5.47	107.18	113.23
2	B	500	HEM	CBA-CAA-C2A	-4.03	105.31	112.53
2	B	500	HEM	C3C-CAC-CBC	-3.87	118.53	124.46
2	B	500	HEM	C1D-CHD-C4C	-3.44	120.07	125.82
3	A	600	H4B	N3-C2-N1	-3.27	120.18	125.53
2	A	500	HEM	C1D-CHD-C4C	-3.26	120.38	125.82
3	B	600	H4B	N3-C2-N1	-3.12	120.41	125.53
2	A	500	HEM	C3B-C4B-NB	-2.32	107.19	111.63
2	B	500	HEM	C3B-C4B-NB	-2.25	107.32	111.63
3	B	600	H4B	C8A-C4A-N5	2.02	121.40	118.85
4	B	800	I5U	C17-O18-C19	2.13	117.91	112.81
4	A	800	I5U	C31-N27-C26	2.19	126.76	121.46
3	A	600	H4B	C4A-C8A-N8	2.26	121.09	118.43
2	A	500	HEM	C2D-C3D-C4D	2.33	105.44	101.50
3	B	600	H4B	N2-C2-N3	2.44	121.24	117.20
2	B	500	HEM	C2D-C3D-C4D	2.44	105.64	101.50
2	A	500	HEM	CAA-CBA-CGA	2.46	117.26	112.75
3	B	600	H4B	C2-N1-C8A	2.55	120.27	114.54
2	B	500	HEM	CMD-C2D-C3D	2.55	125.63	114.35
4	A	800	I5U	O38-C37-C35	2.62	116.23	109.99
3	A	600	H4B	N2-C2-N3	2.64	121.57	117.20
3	A	600	H4B	C2-N1-C8A	2.65	120.50	114.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	800	I5U	C37-O38-C20	2.80	118.66	114.04
2	B	500	HEM	CMB-C2B-C3B	2.95	123.90	116.53
2	A	500	HEM	CMD-C2D-C3D	3.03	127.77	114.35
3	B	600	H4B	C4-N3-C2	3.20	120.38	115.94
2	A	500	HEM	CAD-C3D-C4D	3.89	126.19	112.47
3	B	600	H4B	C4-C4A-C8A	3.91	118.10	114.56
2	B	500	HEM	CMC-C2C-C3C	3.97	126.43	116.53
4	B	800	I5U	O38-C37-C35	3.97	119.45	109.99
2	A	500	HEM	CMB-C2B-C3B	3.99	126.48	116.53
3	A	600	H4B	C4-N3-C2	4.22	121.80	115.94
2	B	500	HEM	CAD-C3D-C4D	4.24	127.43	112.47
2	A	500	HEM	CMC-C2C-C3C	4.53	127.84	116.53
2	B	500	HEM	CAD-C3D-C2D	4.77	126.94	113.22
3	A	600	H4B	C4-C4A-C8A	5.17	119.25	114.56
2	A	500	HEM	CAD-C3D-C2D	5.23	128.26	113.22

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	800	I5U	N26-C26-N27-C31

There are no ring outliers.

6 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	HEM	2	0
3	A	600	H4B	1	0
4	A	800	I5U	4	0
2	B	500	HEM	4	0
3	B	600	H4B	1	0
4	B	800	I5U	4	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, 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	403/443 (90%)	0.19	23 (5%) 27 29	26, 37, 65, 90	0
1	B	402/443 (90%)	0.26	29 (7%) 18 20	26, 40, 68, 108	0
All	All	805/886 (90%)	0.23	52 (6%) 22 23	26, 38, 67, 108	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	109	ARG	7.8
1	B	259	GLN	6.9
1	B	261	GLY	5.2
1	B	122	ALA	4.6
1	B	146	GLN	4.4
1	A	123	GLU	4.0
1	A	122	ALA	3.8
1	A	259	GLN	3.6
1	A	450	ILE	3.5
1	B	263	VAL	3.3
1	A	448	ALA	3.3
1	B	448	ALA	3.3
1	B	123	GLU	3.3
1	B	121	PRO	3.3
1	A	99	ARG	3.3
1	A	91	GLN	3.2
1	A	97	THR	3.1
1	A	69	LYS	2.8
1	B	449	TRP	2.8
1	B	142	ARG	2.8
1	B	70	PHE	2.7
1	B	258	GLN	2.7
1	B	447	TRP	2.7
1	B	260	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	239	GLY	2.6
1	A	257	ARG	2.6
1	A	146	GLN	2.6
1	B	91	GLN	2.6
1	B	282	THR	2.6
1	A	277	ILE	2.5
1	B	99	ARG	2.5
1	A	449	TRP	2.5
1	B	140	ILE	2.5
1	A	447	TRP	2.5
1	A	160	ALA	2.4
1	B	223	ARG	2.4
1	A	108	PRO	2.4
1	A	67	GLY	2.4
1	B	141	LYS	2.4
1	A	238	PRO	2.3
1	B	98	PRO	2.3
1	A	451	VAL	2.3
1	B	108	PRO	2.3
1	A	98	PRO	2.2
1	B	327	ALA	2.1
1	B	277	ILE	2.1
1	B	477	TYR	2.1
1	A	153	GLN	2.1
1	B	257	ARG	2.1
1	A	126	LEU	2.1
1	B	323	GLU	2.0
1	B	92	GLN	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	A	384	9/10	0.97	0.09	-	37,38,55,63	0
1	CAS	B	384	9/10	0.94	0.11	-	46,48,62,68	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	0.97	0.16	3.66	47,47,50,51	0
4	I5U	B	800	36/36	0.95	0.23	2.43	26,78,151,158	0
4	I5U	A	800	36/36	0.94	0.22	2.17	26,67,140,147	0
6	GOL	A	880	6/6	0.87	0.23	2.16	56,64,69,72	0
6	GOL	B	880	6/6	0.90	0.21	1.42	51,60,62,64	0
2	HEM	A	500	43/43	0.97	0.18	1.05	26,30,36,37	0
3	H4B	B	600	17/17	0.97	0.21	0.60	30,32,36,36	0
2	HEM	B	500	43/43	0.98	0.16	0.34	27,30,39,41	0
5	ACT	A	860	4/4	0.96	0.13	0.23	39,43,44,46	0
3	H4B	A	600	17/17	0.98	0.18	0.14	29,32,35,35	0
5	ACT	A	861	4/4	0.98	0.09	-0.36	34,35,35,36	0
5	ACT	B	861	4/4	0.98	0.08	-1.32	38,40,41,42	0
7	ZN	A	900	1/1	1.00	0.03	-3.36	47,47,47,47	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.