



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:27 PM GMT

PDB ID : 1FOJ  
Title : BOVINE ENDOTHELIAL NITRIC OXIDE SYNTHASE HEME DOMAIN  
COMPLEXED WITH 7-NITROINDAZOLE-2-CARBOXAMIDINE (H4B  
PRESENT)  
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Deposited on : 2000-08-28  
Resolution : 2.10 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

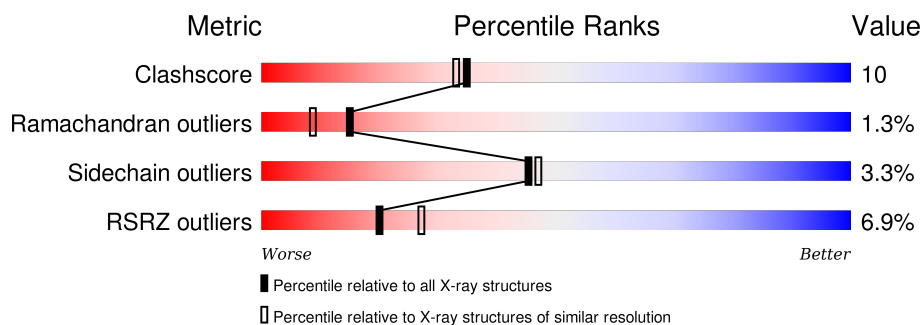
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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))
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	444	
1	B	444	

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 7128 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.

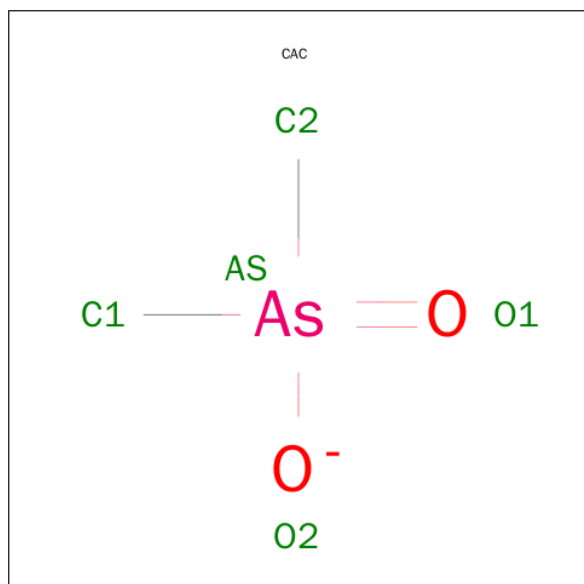
- Molecule 1 is a protein called NITRIC-OXIDE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	416	Total	C	N	O	S	0	0	0
			3302	2099	584	603	16			
1	B	414	Total	C	N	O	S	0	0	0
			3291	2092	582	601	16			

There are 2 discrepancies between the modelled and reference sequences:

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

- Molecule 2 is CACODYLATE ION (three-letter code: CAC) (formula:  $\text{C}_2\text{H}_6\text{AsO}_2$ ).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	As C	0	0
			3	1 2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	As	C	0	0
			3	1	2		

- 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	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

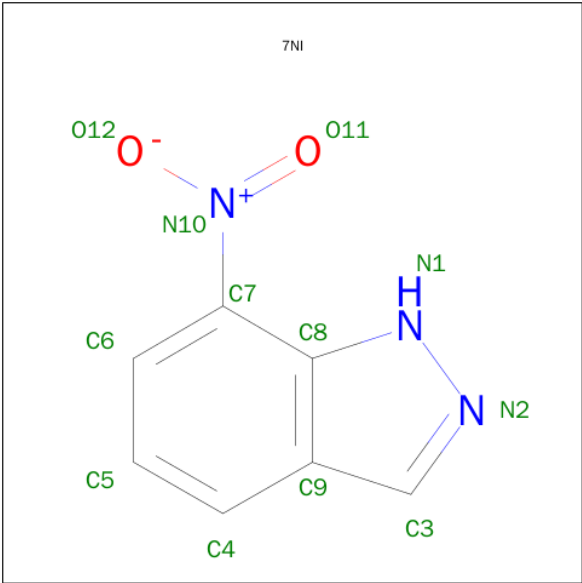
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		

- Molecule 5 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



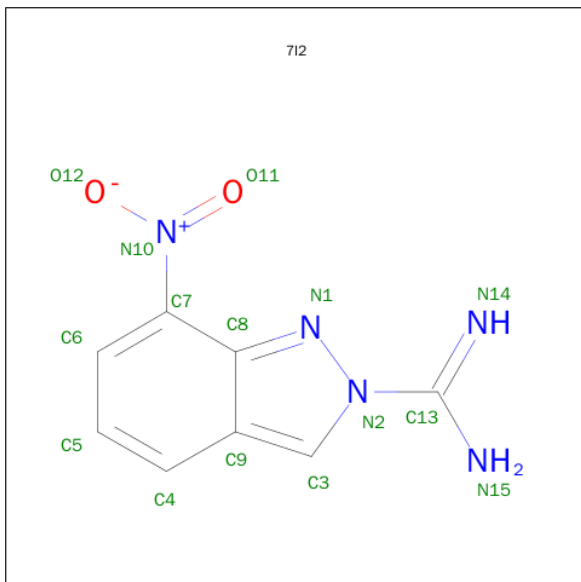
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
5	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 6 is 7-NITROINDAZOLE (three-letter code: 7NI) (formula: C<sub>7</sub>H<sub>5</sub>N<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			12	7	3	2		
6	B	1	Total	C	N	O	0	0
			12	7	3	2		

- Molecule 7 is 7-NITROINDAZOLE-2-CARBOXAMIDINE (three-letter code: 7I2) (formula:  $C_8H_7N_5O_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	N	O	0	0
			15	8	5	2		
7	B	1	Total	C	N	O	0	0
			15	8	5	2		

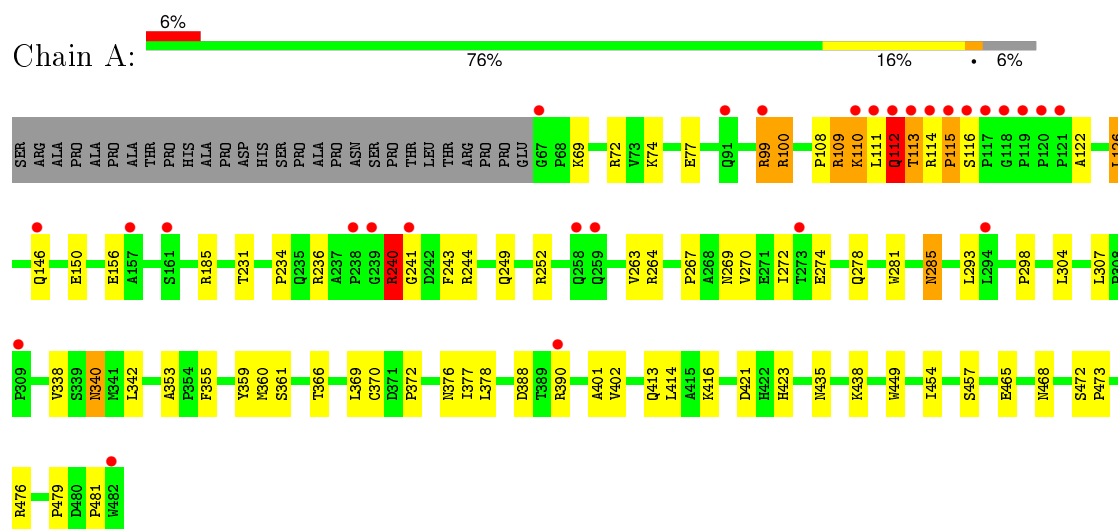
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	183	Total	O	0	0
			183	183		
8	B	189	Total	O	0	0
			189	189		

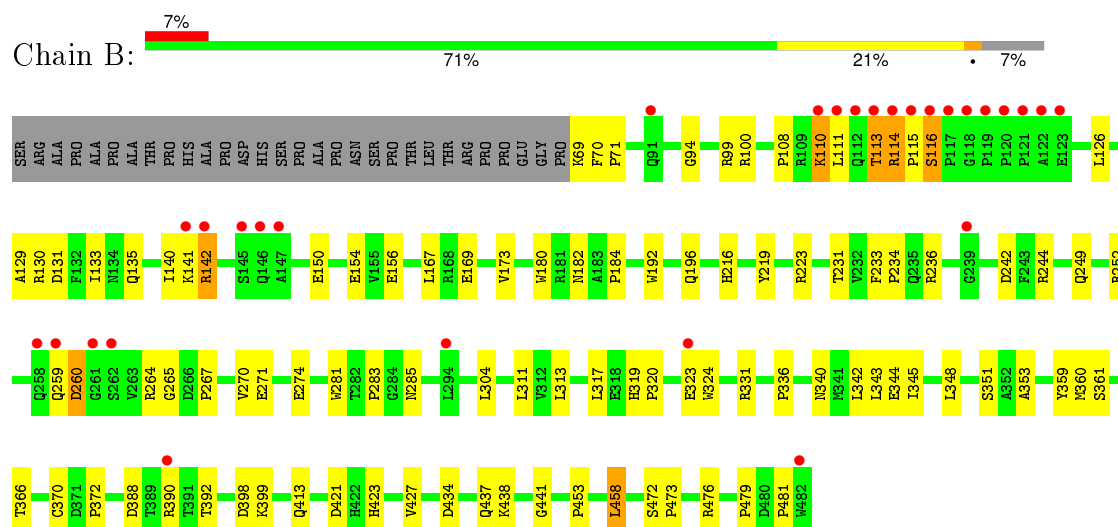
### 3 Residue-property plots

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



#### • Molecule 1: NITRIC-OXIDE SYNTHASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	58.38Å 106.49Å 155.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.85 – 2.10 19.84 – 2.09	Depositor EDS
% Data completeness (in resolution range)	88.4 (19.85-2.10) 76.2 (19.84-2.09)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.80 (at 2.09Å)	Xtriage
Refinement program	CNS 0.9	Depositor
R, $R_{free}$	0.227 , 0.259 0.218 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	32.5	Xtriage
Anisotropy	0.609	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 52.3	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 49747 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7128	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.23% 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: ZN, 7NI, 7I2, ACT, CAC, 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	0.34	0/3397	0.61	1/4631 (0.0%)
1	B	0.34	0/3385	0.63	1/4614 (0.0%)
All	All	0.34	0/6782	0.62	2/9245 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	360	MET	N-CA-C	-5.86	95.18	111.00
1	B	360	MET	N-CA-C	-5.61	95.86	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	3302	0	3215	67	0
1	B	3291	0	3205	70	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
3	A	8	0	6	0	0
3	B	8	0	6	1	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	43	0	30	0	0
5	B	43	0	30	0	0
6	A	12	0	5	1	0
6	B	12	0	5	1	0
7	B	30	0	12	0	0
8	A	183	0	0	1	0
8	B	189	0	0	0	0
All	All	7128	0	6514	131	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 10.

All (131) 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:435:ASN:HA	1:A:438:LYS:HE3	1.45	0.94
1:A:126:LEU:HD11	1:A:156:GLU:HG2	1.47	0.92
1:B:126:LEU:HD11	1:B:156:GLU:HG2	1.56	0.87
1:B:116:SER:H	1:B:236:ARG:HH22	1.18	0.86
1:A:111:LEU:H	1:A:111:LEU:HD12	1.42	0.84
1:A:416:LYS:HE2	1:A:416:LYS:HA	1.64	0.80
1:A:115:PRO:HA	1:A:236:ARG:HH22	1.48	0.79
1:B:270:VAL:O	1:B:274:GLU:HG2	1.82	0.79
1:B:114:ARG:HH11	1:B:114:ARG:HA	1.48	0.78
1:A:240:ARG:HD3	1:A:298:PRO:HB3	1.67	0.77
1:A:77:GLU:HG3	1:B:372:PRO:HG2	1.71	0.72
1:B:260:ASP:OD2	1:B:260:ASP:N	2.23	0.71
1:B:140:ILE:HG13	1:B:142:ARG:HG2	1.72	0.70
1:A:69:LYS:HE3	1:A:69:LYS:O	1.92	0.70
1:B:236:ARG:HD3	1:B:351:SER:HB3	1.72	0.70
1:B:126:LEU:O	1:B:130:ARG:HG3	1.95	0.67
1:A:285:ASN:C	1:A:285:ASN:HD22	1.98	0.65
1:B:110:LYS:O	1:B:110:LYS:HG2	1.99	0.63
1:A:234:PRO:HB2	1:A:243:PHE:CE1	2.34	0.63
1:B:344:GLU:HG3	1:B:476:ARG:HH12	1.64	0.63
1:A:378:LEU:HB2	8:A:2118:HOH:O	1.99	0.62
1:B:236:ARG:HD2	1:B:242:ASP:CG	2.20	0.62
1:A:472:SER:HA	1:A:473:PRO:C	2.20	0.61
1:B:264:ARG:NE	1:B:285:ASN:O	2.33	0.61
1:A:366:THR:O	1:A:370:CYS:HB2	2.02	0.60
1:A:249:GLN:HB2	1:A:252:ARG:CG	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:ASN:C	1:A:285:ASN:ND2	2.55	0.59
1:B:244:ARG:NH2	1:B:481:PRO:HD3	2.18	0.59
1:A:281:TRP:HB2	1:A:304:LEU:HD21	1.83	0.58
1:A:108:PRO:O	1:A:110:LYS:N	2.36	0.58
1:A:423:HIS:HB2	1:B:392:THR:HB	1.84	0.58
1:B:114:ARG:HH12	1:B:479:PRO:HG3	1.69	0.57
1:A:249:GLN:HB2	1:A:252:ARG:HG3	1.85	0.57
1:B:265:GLY:O	1:B:267:PRO:HD3	2.04	0.57
1:B:130:ARG:HB3	1:B:130:ARG:NH1	2.19	0.57
1:A:369:LEU:O	1:A:377:ILE:HG12	2.06	0.55
1:A:108:PRO:C	1:A:110:LYS:H	2.10	0.55
1:A:340:ASN:HD22	1:A:340:ASN:H	1.55	0.55
1:B:167:LEU:HG	1:B:348:LEU:HD12	1.89	0.54
1:B:317:LEU:HG	1:B:331:ARG:HA	1.88	0.54
1:B:366:THR:O	1:B:370:CYS:HB2	2.07	0.54
1:A:77:GLU:HG3	1:B:372:PRO:CG	2.36	0.53
1:A:390:ARG:HH11	1:A:390:ARG:HG2	1.73	0.53
1:A:366:THR:HG21	1:A:454:ILE:HG23	1.90	0.53
1:A:274:GLU:O	1:A:278:GLN:HG3	2.08	0.53
1:B:116:SER:H	1:B:236:ARG:NH2	1.97	0.53
1:B:281:TRP:HB2	1:B:304:LEU:HD21	1.90	0.52
1:B:388:ASP:OD1	1:B:390:ARG:HB2	2.09	0.52
1:B:196:GLN:HG2	1:B:219:TYR:CZ	2.45	0.52
1:B:94:GLY:HA2	1:B:111:LEU:HD21	1.92	0.51
1:B:140:ILE:O	1:B:141:LYS:HB2	2.09	0.51
1:A:69:LYS:CE	1:A:69:LYS:O	2.59	0.51
1:B:359:TYR:CE1	3:B:2850:ACT:H3	2.46	0.51
1:B:114:ARG:HA	1:B:114:ARG:NH1	2.22	0.49
1:B:223:ARG:HH22	1:B:313:LEU:HD13	1.76	0.49
1:A:74:LYS:O	1:A:465:GLU:HG3	2.12	0.49
1:B:114:ARG:HH12	1:B:479:PRO:CG	2.25	0.49
1:A:338:VAL:HB	1:A:355:PHE:CZ	2.48	0.49
1:B:437:GLN:O	1:B:441:GLY:HA2	2.13	0.49
1:A:111:LEU:O	1:A:112:GLN:C	2.51	0.48
1:A:99:ARG:HG2	1:A:100:ARG:HD2	1.94	0.48
1:A:115:PRO:HA	1:A:236:ARG:NH2	2.21	0.48
1:B:472:SER:HA	1:B:473:PRO:C	2.34	0.48
1:A:111:LEU:O	1:A:113:THR:N	2.46	0.48
1:A:472:SER:HA	1:A:473:PRO:O	2.13	0.48
1:A:372:PRO:HA	1:A:376:ASN:ND2	2.28	0.48
1:A:113:THR:OG1	1:A:342:LEU:HD13	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:434:ASP:OD1	1:B:438:LYS:HE3	2.14	0.47
1:B:344:GLU:CG	1:B:476:ARG:HH12	2.28	0.47
1:A:146:GLN:HG2	1:A:150:GLU:OE2	2.14	0.46
1:A:416:LYS:HE2	1:A:416:LYS:CA	2.38	0.46
1:A:231:THR:O	1:A:353:ALA:HA	2.15	0.46
1:B:259:GLN:HG3	1:B:260:ASP:OD2	2.15	0.46
1:B:150:GLU:O	1:B:154:GLU:HG3	2.16	0.46
1:A:126:LEU:HD11	1:A:156:GLU:CG	2.34	0.45
1:B:108:PRO:CB	1:B:111:LEU:HB2	2.46	0.45
1:B:236:ARG:HD2	1:B:242:ASP:OD1	2.16	0.45
1:A:421:ASP:OD2	1:A:423:HIS:HB2	2.15	0.45
1:B:359:TYR:HA	6:B:2750:7NI:O12	2.16	0.45
1:B:423:HIS:O	1:B:427:VAL:HG23	2.17	0.45
1:A:270:VAL:O	1:A:274:GLU:HG3	2.17	0.45
1:B:271:GLU:O	1:B:274:GLU:HB2	2.16	0.45
1:B:319:HIS:CG	1:B:320:PRO:HD2	2.52	0.45
1:A:340:ASN:HD22	1:A:340:ASN:N	2.13	0.45
1:A:435:ASN:O	1:A:438:LYS:HG2	2.17	0.44
1:A:114:ARG:HD2	1:A:479:PRO:HG2	1.99	0.44
1:A:185:ARG:HD3	1:A:449:TRP:CD2	2.52	0.44
1:B:249:GLN:HB2	1:B:252:ARG:CG	2.48	0.44
1:A:113:THR:HG23	1:A:476:ARG:HD2	1.98	0.44
1:A:264:ARG:HH11	1:A:264:ARG:HG3	1.82	0.44
1:B:130:ARG:HH11	1:B:130:ARG:CB	2.31	0.44
1:A:244:ARG:NH2	1:A:481:PRO:HD3	2.32	0.44
1:A:99:ARG:CG	1:A:100:ARG:HD2	2.47	0.44
1:B:180:TRP:CE3	1:B:192:TRP:HA	2.53	0.44
1:A:401:ALA:CB	1:B:458:LEU:HD21	2.48	0.43
1:B:182:ASN:O	1:B:184:PRO:HD3	2.19	0.43
1:B:438:LYS:NZ	1:B:438:LYS:HB2	2.33	0.43
1:B:169:GLU:O	1:B:173:VAL:HG23	2.17	0.43
1:A:112:GLN:O	1:A:114:ARG:N	2.52	0.43
1:B:233:PHE:HB3	1:B:234:PRO:HD2	2.01	0.43
1:A:413:GLN:O	1:A:416:LYS:HE3	2.18	0.43
1:B:281:TRP:O	1:B:283:PRO:HD3	2.19	0.43
1:A:457:SER:OG	1:B:453:PRO:HB2	2.19	0.43
1:B:130:ARG:HB3	1:B:130:ARG:HH11	1.84	0.42
1:A:359:TYR:HA	6:A:1750:7NI:O12	2.19	0.42
1:A:111:LEU:CD1	1:A:111:LEU:H	2.21	0.42
1:A:388:ASP:OD1	1:A:390:ARG:HB2	2.20	0.42
1:B:223:ARG:HA	1:B:223:ARG:NE	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:VAL:HG11	1:A:267:PRO:HA	2.02	0.42
1:A:402:VAL:HG11	1:B:399:LYS:HG2	2.01	0.42
1:B:336:PRO:HB3	1:B:359:TYR:CZ	2.54	0.42
1:B:131:ASP:OD2	1:B:135:GLN:NE2	2.53	0.42
1:B:70:PHE:HA	1:B:71:PRO:HD3	1.84	0.42
1:A:146:GLN:NE2	1:A:150:GLU:OE2	2.44	0.42
1:B:242:ASP:HB3	1:B:351:SER:OG	2.19	0.41
1:A:240:ARG:HD3	1:A:298:PRO:CB	2.46	0.41
1:A:269:ASN:HB3	1:A:272:ILE:CG2	2.50	0.41
1:A:114:ARG:O	1:A:116:SER:N	2.53	0.41
1:B:129:ALA:O	1:B:133:ILE:HG12	2.20	0.41
1:A:361:SER:OG	1:A:421:ASP:HA	2.20	0.41
1:A:108:PRO:HB2	1:A:110:LYS:HG2	2.02	0.41
1:A:293:LEU:HD11	1:A:307:LEU:HD21	2.02	0.41
1:B:236:ARG:HH11	1:B:242:ASP:CG	2.24	0.41
1:B:323:GLU:HG3	1:B:324:TRP:N	2.36	0.41
1:B:361:SER:OG	1:B:421:ASP:HA	2.20	0.41
1:B:113:THR:HG21	1:B:342:LEU:HD22	2.03	0.41
1:B:113:THR:HG23	1:B:476:ARG:HD2	2.02	0.41
1:B:343:LEU:HD21	1:B:345:ILE:HD11	2.03	0.41
1:A:390:ARG:NH1	1:A:390:ARG:HG2	2.35	0.41
1:B:231:THR:O	1:B:353:ALA:HA	2.20	0.41
1:B:216:HIS:C	1:B:216:HIS:CD2	2.94	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	414/444 (93%)	384 (93%)	23 (6%)	7 (2%)	11	5
1	B	412/444 (93%)	382 (93%)	26 (6%)	4 (1%)	19	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	826/888 (93%)	766 (93%)	49 (6%)	11 (1%)	15 9

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	109	ARG
1	A	112	GLN
1	A	113	THR
1	A	115	PRO
1	A	241	GLY
1	B	113	THR
1	A	122	ALA
1	A	240	ARG
1	B	110	LYS
1	B	115	PRO
1	B	116	SER

### 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	354/377 (94%)	342 (97%)	12 (3%)	44 45
1	B	353/377 (94%)	342 (97%)	11 (3%)	47 50
All	All	707/754 (94%)	684 (97%)	23 (3%)	45 47

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

Mol	Chain	Res	Type
1	A	72	ARG
1	A	99	ARG
1	A	100	ARG
1	A	109	ARG
1	A	110	LYS
1	A	112	GLN
1	A	126	LEU

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Mol	Chain	Res	Type
1	A	240	ARG
1	A	285	ASN
1	A	340	ASN
1	A	414	LEU
1	A	468	ASN
1	B	69	LYS
1	B	99	ARG
1	B	100	ARG
1	B	114	ARG
1	B	142	ARG
1	B	260	ASP
1	B	311	LEU
1	B	340	ASN
1	B	398	ASP
1	B	413	GLN
1	B	458	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	GLN
1	A	112	GLN
1	A	153	GLN
1	A	191	GLN
1	A	259	GLN
1	A	278	GLN
1	A	285	ASN
1	A	340	ASN
1	A	376	ASN
1	A	413	GLN
1	A	468	ASN
1	B	146	GLN
1	B	191	GLN
1	B	222	ASN
1	B	225	ASN
1	B	340	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 ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

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$
6	7NI	A	1750	-	11,13,13	2.87	3 (27%)	7,18,18	1.56	2 (28%)
3	ACT	A	1850	-	1,3,3	3.13	1 (100%)	0,3,3	0.00	-
3	ACT	A	1860	-	1,3,3	2.78	1 (100%)	0,3,3	0.00	-
2	CAC	A	1950	1	0,2,4	0.00	-	0,1,6	0.00	-
5	HEM	A	500	1	30,50,50	2.83	9 (30%)	24,82,82	2.17	7 (29%)
7	7I2	B	1770	-	9,16,16	0.96	1 (11%)	8,23,23	1.88	3 (37%)
6	7NI	B	2750	-	11,13,13	2.87	3 (27%)	7,18,18	1.51	2 (28%)
7	7I2	B	2770	-	9,16,16	1.14	1 (11%)	8,23,23	2.02	3 (37%)
3	ACT	B	2850	-	1,3,3	2.51	1 (100%)	0,3,3	0.00	-
3	ACT	B	2860	-	1,3,3	2.76	1 (100%)	0,3,3	0.00	-
2	CAC	B	2950	1	0,2,4	0.00	-	0,1,6	0.00	-
5	HEM	B	500	1	30,50,50	2.55	7 (23%)	24,82,82	2.05	7 (29%)

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	7NI	A	1750	-	-	0/3/4/4	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ACT	A	1850	-	-	0/0/0/0	0/0/0/0
3	ACT	A	1860	-	-	0/0/0/0	0/0/0/0
2	CAC	A	1950	1	-	0/0/0/0	0/0/0/0
5	HEM	A	500	1	-	0/10/54/54	0/0/8/8
7	7I2	B	1770	-	-	0/3/8/8	0/2/2/2
6	7NI	B	2750	-	-	0/3/4/4	0/2/2/2
7	7I2	B	2770	-	-	0/3/8/8	0/2/2/2
3	ACT	B	2850	-	-	0/0/0/0	0/0/0/0
3	ACT	B	2860	-	-	0/0/0/0	0/0/0/0
2	CAC	B	2950	1	-	0/0/0/0	0/0/0/0
5	HEM	B	500	1	-	0/10/54/54	0/0/8/8

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	500	HEM	C2D-C3D	-6.81	1.34	1.54
5	B	500	HEM	C3B-C4B	-6.43	1.46	1.51
5	A	500	HEM	C3B-CAB	-6.32	1.39	1.51
5	A	500	HEM	C3B-C4B	-5.95	1.46	1.51
5	A	500	HEM	C3C-CAC	-5.87	1.40	1.51
5	B	500	HEM	C2D-C3D	-5.70	1.37	1.54
5	A	500	HEM	C3D-C4D	-5.67	1.44	1.51
5	B	500	HEM	C3B-CAB	-5.36	1.41	1.51
5	B	500	HEM	C3D-C4D	-5.09	1.45	1.51
5	B	500	HEM	C3C-CAC	-5.01	1.41	1.51
5	B	500	HEM	C2C-C1C	-3.76	1.45	1.52
5	A	500	HEM	C2C-C1C	-3.60	1.45	1.52
6	B	2750	7NI	C9-C8	-3.07	1.38	1.43
6	A	1750	7NI	C9-C8	-2.99	1.38	1.43
7	B	2770	7I2	C9-C8	-2.95	1.38	1.43
7	B	1770	7I2	C9-C8	-2.38	1.39	1.43
6	B	2750	7NI	C8-N1	-2.29	1.31	1.37
6	A	1750	7NI	C8-N1	-2.29	1.31	1.37
5	A	500	HEM	C2B-C1B	-2.25	1.44	1.51
5	A	500	HEM	C2D-C1D	-2.01	1.45	1.51
3	B	2850	ACT	CH3-C	2.51	1.52	1.48
5	B	500	HEM	C4C-NC	2.51	1.39	1.36
3	B	2860	ACT	CH3-C	2.76	1.52	1.48
3	A	1860	ACT	CH3-C	2.78	1.52	1.48
3	A	1850	ACT	CH3-C	3.13	1.53	1.48
5	A	500	HEM	C4C-NC	3.41	1.40	1.36
6	B	2750	7NI	C3-N2	8.45	1.51	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1750	7NI	C3-N2	8.65	1.51	1.33

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1750	7NI	C9-C3-N2	-3.02	103.88	111.38
6	B	2750	7NI	C9-C3-N2	-3.00	103.92	111.38
7	B	2770	7I2	C6-C7-N10	2.27	119.53	116.59
6	B	2750	7NI	C6-C7-N10	2.49	119.82	116.59
7	B	1770	7I2	C6-C7-N10	2.50	119.83	116.59
5	B	500	HEM	C2D-C3D-C4D	2.54	105.81	101.50
5	A	500	HEM	CMD-C2D-C3D	2.61	125.90	114.35
6	A	1750	7NI	C6-C7-N10	2.68	120.06	116.59
5	B	500	HEM	C3C-CAC-CBC	2.87	128.85	124.46
5	B	500	HEM	CMB-C2B-C3B	2.88	123.73	116.53
5	B	500	HEM	CMD-C2D-C3D	2.88	127.11	114.35
7	B	1770	7I2	C13-N2-N1	2.99	127.02	118.96
5	A	500	HEM	C3C-CAC-CBC	3.03	129.10	124.46
7	B	2770	7I2	C13-N2-N1	3.06	127.21	118.96
7	B	1770	7I2	C3-C9-C8	3.17	109.59	104.92
5	B	500	HEM	CAD-C3D-C4D	3.31	124.13	112.47
5	A	500	HEM	CAD-C3D-C4D	3.39	124.43	112.47
5	A	500	HEM	CMC-C2C-C3C	3.55	125.38	116.53
7	B	2770	7I2	C3-C9-C8	3.56	110.17	104.92
5	A	500	HEM	C2D-C3D-C4D	4.15	108.53	101.50
5	B	500	HEM	CMC-C2C-C3C	4.46	127.67	116.53
5	A	500	HEM	CMB-C2B-C3B	4.59	128.00	116.53
5	A	500	HEM	CAD-C3D-C2D	4.79	126.98	113.22
5	B	500	HEM	CAD-C3D-C2D	5.69	129.58	113.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1750	7NI	1	0
6	B	2750	7NI	1	0
3	B	2850	ACT	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, 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	416/444 (93%)	0.42	28 (6%) 21 28	29, 41, 67, 93	0
1	B	414/444 (93%)	0.52	29 (7%) 19 26	28, 43, 65, 96	0
All	All	830/888 (93%)	0.47	57 (6%) 20 27	28, 42, 67, 96	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	113	THR	8.6
1	B	115	PRO	8.3
1	B	117	PRO	8.2
1	B	114	ARG	8.1
1	B	113	THR	7.9
1	A	115	PRO	7.6
1	A	117	PRO	7.5
1	B	116	SER	7.4
1	B	111	LEU	7.0
1	A	118	GLY	6.9
1	B	119	PRO	6.8
1	B	118	GLY	6.4
1	A	112	GLN	6.0
1	B	259	GLN	5.7
1	A	111	LEU	5.7
1	A	110	LYS	5.6
1	B	120	PRO	5.2
1	A	116	SER	5.0
1	A	114	ARG	5.0
1	A	119	PRO	4.8
1	B	121	PRO	4.8
1	A	120	PRO	4.7
1	A	259	GLN	4.6
1	B	110	LYS	4.5

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Mol	Chain	Res	Type	RSRZ
1	B	239	GLY	4.4
1	B	112	GLN	4.0
1	A	239	GLY	3.7
1	A	91	GLN	3.4
1	A	390	ARG	3.4
1	A	157	ALA	3.3
1	A	482	TRP	3.2
1	B	262	SER	3.2
1	B	261	GLY	3.1
1	B	142	ARG	3.1
1	B	122	ALA	3.0
1	A	67	GLY	2.9
1	A	238	PRO	2.9
1	A	258	GLN	2.7
1	B	147	ALA	2.5
1	B	91	GLN	2.5
1	A	99	ARG	2.5
1	B	390	ARG	2.5
1	B	323	GLU	2.4
1	B	146	GLN	2.4
1	B	294	LEU	2.4
1	B	258	GLN	2.3
1	A	146	GLN	2.3
1	B	123	GLU	2.3
1	A	294	LEU	2.3
1	B	482	TRP	2.2
1	A	309	PRO	2.2
1	A	121	PRO	2.2
1	A	161	SER	2.1
1	A	273	THR	2.1
1	B	141	LYS	2.1
1	B	145	SER	2.1
1	A	241	GLY	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 [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	HEM	A	500	43/43	0.96	0.14	0.57	26,32,45,47	0
3	ACT	B	2850	4/4	0.94	0.14	0.09	49,50,50,51	0
3	ACT	B	2860	4/4	0.96	0.11	0.08	42,42,44,46	0
5	HEM	B	500	43/43	0.97	0.11	-0.10	26,31,44,48	0
3	ACT	A	1860	4/4	0.95	0.11	-0.38	49,51,51,51	0
7	7I2	B	1770	15/15	0.94	0.12	-0.43	44,45,50,51	0
2	CAC	A	1950	3/5	0.99	0.08	-0.66	56,56,58,62	0
7	7I2	B	2770	15/15	0.96	0.10	-0.80	34,37,43,44	0
6	7NI	A	1750	12/12	0.95	0.12	-1.04	32,36,39,40	0
6	7NI	B	2750	12/12	0.96	0.10	-1.45	31,36,43,43	0
2	CAC	B	2950	3/5	0.99	0.09	-1.59	73,73,73,74	0
4	ZN	A	900	1/1	0.99	0.05	-1.79	34,34,34,34	0
3	ACT	A	1850	4/4	0.97	0.09	-1.87	45,46,46,48	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.