



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:31 PM GMT

PDB ID : 1XME  
Title : Structure of Recombinant Cytochrome ba3 Oxidase from *Thermus thermophilus*  
Authors : Hunsicker-Wang, L.M.; Pacoma, R.L.; Chen, Y.; Fee, J.A.; Stout, C.D.  
Deposited on : 2004-10-01  
Resolution : 2.30 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

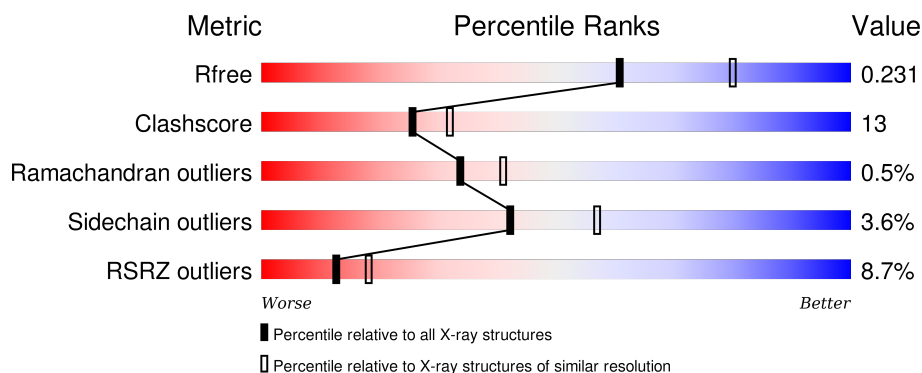
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	568	<div> <div>7%</div> <div>73%</div> <div>23%</div> <div>• •</div> </div>
2	B	168	<div> <div>15%</div> <div>72%</div> <div>26%</div> <div>• •</div> </div>
3	C	34	<div> <div>9%</div> <div>71%</div> <div>24%</div> <div>• •</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	BNG	A	805	-	-	-	X
9	GOL	A	804	-	X	-	-

## 2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 6177 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 Cytochrome c oxidase polypeptide I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	557	Total	C	N	O	S	0	0	0
			4407	2985	707	699	16			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	EXPRESSION TAG	UNP Q56408
A	-4	HIS	-	EXPRESSION TAG	UNP Q56408
A	-3	HIS	-	EXPRESSION TAG	UNP Q56408
A	-2	HIS	-	EXPRESSION TAG	UNP Q56408
A	-1	HIS	-	EXPRESSION TAG	UNP Q56408
A	0	HIS	-	EXPRESSION TAG	UNP Q56408
A	1	HIS	-	EXPRESSION TAG	UNP Q56408

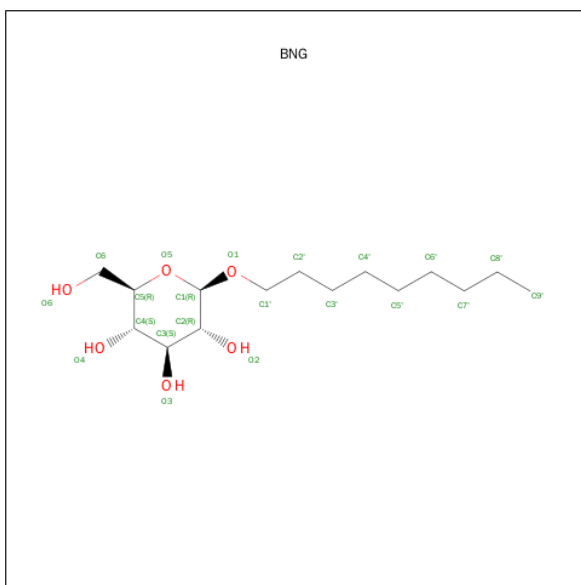
- Molecule 2 is a protein called Cytochrome c oxidase polypeptide II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	166	Total	C	N	O	S	0	0	0
			1298	844	216	234	4			

- Molecule 3 is a protein called Cytochrome c oxidase polypeptide IIA.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	33	Total	C	N	O	0	0	0
			259	179	39	41			

- Molecule 4 is SUGAR (B-NONYLGLUCOSIDE) (three-letter code: BNG) (formula: C<sub>15</sub>H<sub>30</sub>O<sub>6</sub>).

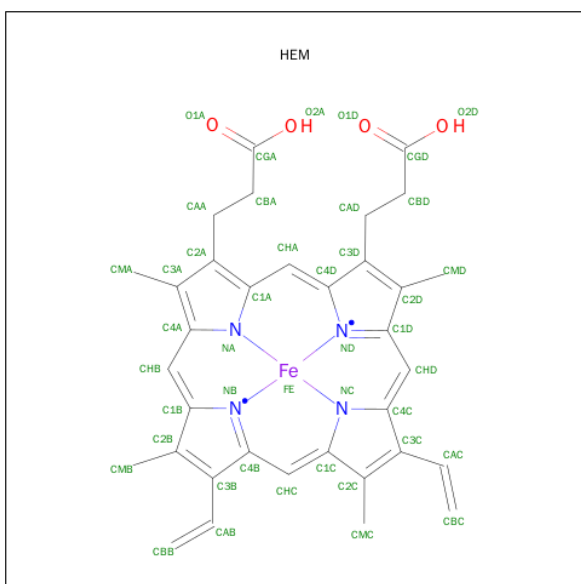


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			21	15	6		

- Molecule 5 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

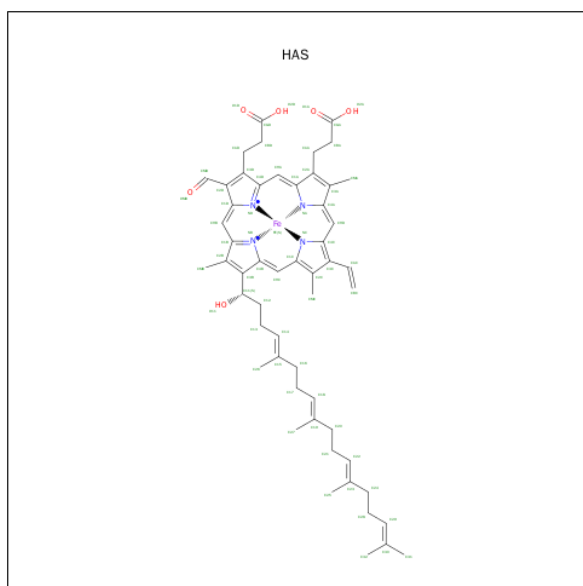
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Cu 1 1	0	0

- Molecule 6 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



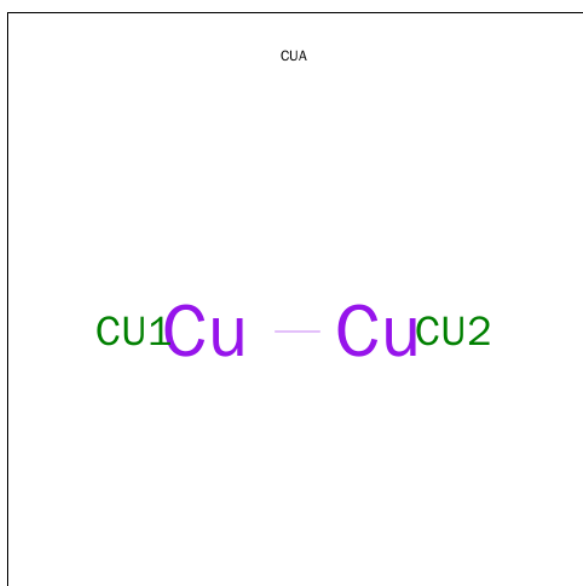
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 7 is HEME-AS (three-letter code: HAS) (formula:  $C_{54}H_{64}FeN_4O_6$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	Fe	N	O	0	0
			65	54	1	4	6		

- Molecule 8 is DINUCLEAR COPPER ION (three-letter code: CUA) (formula:  $Cu_2$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	B	1	Total Cu 2 2	0	0

- Molecule 9 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total C O 6 3 3	0	0

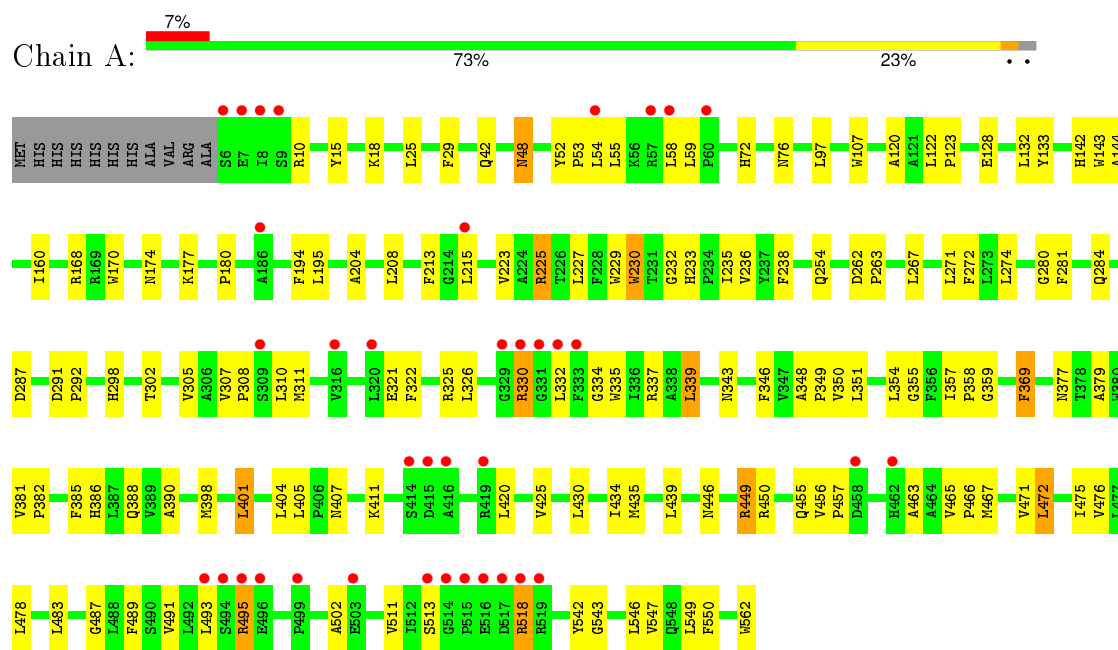
- Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	62	Total O 62 62	0	0
10	B	13	Total O 13 13	0	0

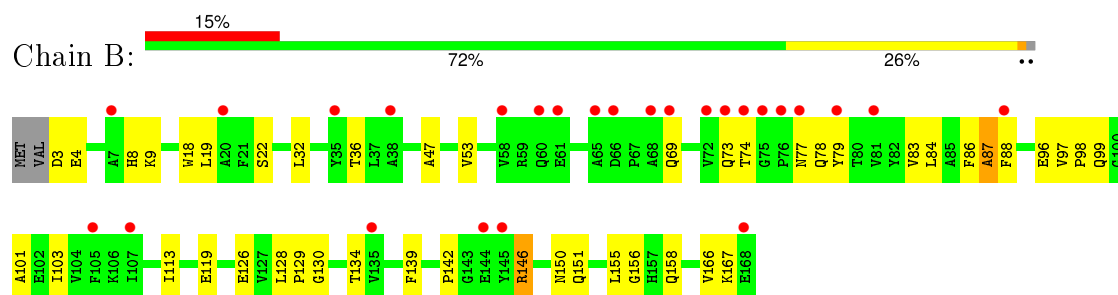
### 3 Residue-property plots [i](#)

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

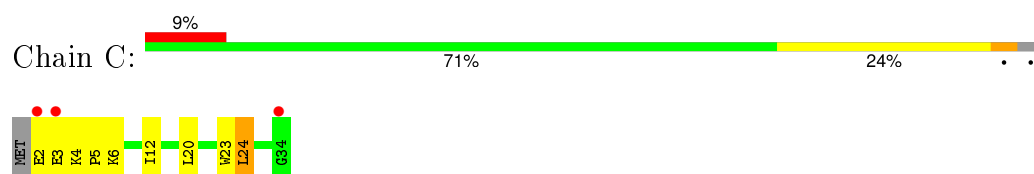
#### • Molecule 1: Cytochrome c oxidase polypeptide I



#### • Molecule 2: Cytochrome c oxidase polypeptide II



#### • Molecule 3: Cytochrome c oxidase polypeptide IIA





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	114.90Å 114.90Å 177.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	21.42 – 2.30 24.10 – 2.30	Depositor EDS
% Data completeness (in resolution range)	92.7 (21.42-2.30) 92.8 (24.10-2.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.34 (at 2.31Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.217 , 0.236 0.213 , 0.231	Depositor DCC
$R_{free}$ test set	2480 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	49.7	Xtriage
Anisotropy	0.003	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 59.3	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 49414 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6177	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.82% 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, CUA, HEM, HAS, BNG, CU

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	0.42	0/4564	0.60	0/6263
2	B	0.36	0/1335	0.59	0/1822
3	C	0.39	0/265	0.50	0/359
All	All	0.41	0/6164	0.59	0/8444

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [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	4407	0	4515	114	0
2	B	1298	0	1280	37	0
3	C	259	0	279	9	0
4	A	21	0	30	2	0
5	A	1	0	0	0	0
6	A	43	0	30	1	0
7	A	65	0	62	2	0
8	B	2	0	0	0	0
9	A	6	0	4	0	0
10	A	62	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	B	13	0	0	0	0
All	All	6177	0	6200	154	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 13.

All (154) 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:262:ASP:HB2	1:A:511:VAL:HG11	1.52	0.90
3:C:3:GLU:HG3	3:C:4:LYS:H	1.36	0.89
2:B:9:LYS:HE2	2:B:9:LYS:HA	1.55	0.88
1:A:449:ARG:HD2	1:A:450:ARG:HG3	1.56	0.88
1:A:122:LEU:HB2	1:A:123:PRO:HD3	1.64	0.79
1:A:357:ILE:HB	1:A:358:PRO:HD3	1.67	0.76
2:B:142:PRO:HA	2:B:166:VAL:HG23	1.65	0.76
1:A:465:VAL:HG23	1:A:466:PRO:HD3	1.69	0.74
3:C:3:GLU:CG	3:C:4:LYS:H	2.05	0.70
1:A:18:LYS:HE2	1:A:502:ALA:O	1.93	0.68
1:A:379:ALA:HB1	1:A:439:LEU:HD12	1.75	0.67
1:A:302:THR:O	1:A:305:VAL:HG12	1.94	0.66
1:A:330:ARG:HG2	1:A:330:ARG:HH21	1.61	0.66
1:A:463:ALA:O	1:A:467:MET:HG3	1.95	0.66
1:A:54:LEU:O	1:A:58:LEU:HD13	1.96	0.65
1:A:262:ASP:HB3	1:A:263:PRO:HD3	1.77	0.65
1:A:254:GLN:NE2	1:A:343:ASN:HD21	1.94	0.65
1:A:18:LYS:HE3	1:A:407:ASN:O	1.97	0.64
1:A:435:MET:HG2	1:A:439:LEU:HD23	1.80	0.63
1:A:335:TRP:O	1:A:339:LEU:HD22	1.99	0.62
1:A:449:ARG:HH12	7:A:801:HAS:CGA	2.12	0.62
2:B:18:TRP:CE3	3:C:12:ILE:HD12	2.35	0.62
1:A:434:ILE:HD13	1:A:472:LEU:HD13	1.82	0.62
1:A:381:VAL:HB	1:A:382:PRO:HD3	1.82	0.62
1:A:281:PHE:H	1:A:298:HIS:HD2	1.48	0.61
3:C:2:GLU:HG3	3:C:3:GLU:H	1.64	0.61
1:A:97:LEU:HD22	1:A:170:TRP:CD1	2.37	0.60
1:A:229:TRP:CE3	1:A:232:GLY:HA3	2.36	0.60
1:A:281:PHE:H	1:A:298:HIS:CD2	2.19	0.60
1:A:120:ALA:O	1:A:123:PRO:HD2	2.01	0.60
2:B:99:GLN:OE1	2:B:142:PRO:HD3	2.01	0.60
1:A:435:MET:HG2	1:A:439:LEU:CD2	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:801:HAS:HBC1	7:A:801:HAS:HMC1	1.84	0.60
1:A:15:TYR:O	1:A:18:LYS:HB2	2.03	0.59
1:A:271:LEU:CB	1:A:308:PRO:HG3	2.33	0.58
2:B:113:ILE:HG22	2:B:151:GLN:HG2	1.84	0.58
1:A:267:LEU:HD23	1:A:311:MET:HE1	1.86	0.57
1:A:42:GLN:HE22	1:A:72:HIS:CD2	2.21	0.57
1:A:322:PHE:O	1:A:326:LEU:HD13	2.05	0.57
2:B:142:PRO:HA	2:B:166:VAL:CG2	2.34	0.57
2:B:88:PHE:N	2:B:88:PHE:CD2	2.70	0.57
1:A:355:GLY:O	1:A:358:PRO:HD2	2.05	0.56
1:A:15:TYR:HB2	1:A:18:LYS:HD2	1.87	0.56
1:A:465:VAL:HG23	1:A:466:PRO:CD	2.35	0.55
1:A:223:VAL:HG12	1:A:549:LEU:HB3	1.89	0.55
1:A:204:ALA:HA	1:A:208:LEU:HB2	1.88	0.55
1:A:267:LEU:HD23	1:A:311:MET:CE	2.37	0.54
1:A:449:ARG:HD3	10:A:834:HOH:O	2.08	0.54
1:A:52:TYR:N	1:A:53:PRO:HD2	2.24	0.53
1:A:330:ARG:NH2	1:A:330:ARG:HG2	2.24	0.53
1:A:160:ILE:HD13	1:A:194:PHE:HB2	1.90	0.53
1:A:230:TRP:C	1:A:230:TRP:CD1	2.82	0.52
3:C:3:GLU:HG3	3:C:4:LYS:N	2.14	0.52
1:A:305:VAL:O	1:A:308:PRO:HD2	2.10	0.52
1:A:254:GLN:HE21	1:A:343:ASN:HD21	1.55	0.52
1:A:377:ASN:HB3	2:B:150:ASN:HB2	1.91	0.52
1:A:321:GLU:HA	1:A:335:TRP:CE3	2.45	0.52
4:A:805:BNG:O2	4:A:805:BNG:H1'1	2.10	0.51
1:A:420:LEU:HD11	1:A:483:LEU:HD22	1.92	0.51
1:A:330:ARG:HB2	1:A:334:GLY:HA3	1.91	0.51
1:A:325:ARG:HG3	1:A:325:ARG:HH21	1.76	0.51
1:A:377:ASN:HB3	2:B:150:ASN:O	2.11	0.50
1:A:478:LEU:O	1:A:478:LEU:HD23	2.10	0.50
1:A:382:PRO:HA	1:A:385:PHE:CE2	2.46	0.50
1:A:471:VAL:O	1:A:475:ILE:HG13	2.12	0.50
1:A:271:LEU:HB3	1:A:308:PRO:HG3	1.93	0.50
2:B:101:ALA:O	2:B:103:ILE:HD12	2.12	0.49
1:A:489:PHE:O	1:A:493:LEU:HD13	2.12	0.49
2:B:166:VAL:HG23	2:B:166:VAL:O	2.12	0.49
1:A:143:TRP:HB2	1:A:213:PHE:CE2	2.48	0.49
1:A:546:LEU:O	1:A:550:PHE:HD1	1.95	0.49
1:A:472:LEU:O	1:A:476:VAL:HG23	2.12	0.49
1:A:233:HIS:O	1:A:236:VAL:HG22	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:74:THR:HG23	2:B:78:GLN:OE1	2.13	0.48
1:A:398:MET:O	1:A:401:LEU:HB2	2.14	0.48
1:A:307:VAL:HB	1:A:308:PRO:HD3	1.95	0.48
2:B:139:PHE:CG	2:B:166:VAL:HG11	2.49	0.48
1:A:55:LEU:HD11	1:A:59:LEU:HD12	1.95	0.47
1:A:18:LYS:CE	1:A:502:ALA:O	2.63	0.47
1:A:359:GLY:HA3	1:A:388:GLN:NE2	2.29	0.47
1:A:123:PRO:HG2	1:A:144:ALA:HB3	1.96	0.47
1:A:455:GLN:C	1:A:457:PRO:HD3	2.34	0.47
2:B:97:VAL:O	2:B:166:VAL:HA	2.14	0.46
2:B:103:ILE:HD12	2:B:103:ILE:N	2.29	0.46
2:B:69:GLN:HA	2:B:69:GLN:HE21	1.79	0.46
1:A:174:ASN:HB3	1:A:177:LYS:HD3	1.98	0.46
1:A:543:GLY:O	1:A:547:VAL:HG23	2.16	0.46
2:B:53:VAL:O	2:B:130:GLY:HA2	2.16	0.46
2:B:86:PHE:O	2:B:88:PHE:N	2.49	0.46
1:A:76:ASN:HB3	6:A:800:HEM:CAC	2.46	0.46
1:A:337:ARG:HD2	1:A:337:ARG:HA	1.81	0.46
1:A:271:LEU:HB2	1:A:308:PRO:HG3	1.97	0.46
1:A:280:GLY:HA3	1:A:542:TYR:OH	2.16	0.46
1:A:332:LEU:HD13	3:C:6:LYS:HE2	1.98	0.45
2:B:83:VAL:HG12	2:B:84:LEU:N	2.31	0.45
1:A:562:TRP:HA	2:B:155:LEU:HG	1.97	0.45
1:A:254:GLN:HE21	1:A:343:ASN:ND2	2.14	0.45
1:A:446:ASN:OD1	2:B:119:GLU:HG3	2.17	0.45
1:A:29:PHE:CE1	1:A:401:LEU:HD11	2.52	0.45
1:A:225:ARG:HD3	1:A:287:ASP:OD1	2.16	0.45
1:A:382:PRO:HA	1:A:385:PHE:CZ	2.51	0.45
1:A:128:GLU:HB3	1:A:142:HIS:HB2	1.99	0.45
1:A:487:GLY:O	1:A:491:VAL:HG23	2.17	0.45
1:A:235:ILE:O	1:A:238:PHE:HB3	2.17	0.44
2:B:73:GLN:HB2	2:B:79:TYR:CE1	2.52	0.44
3:C:20:LEU:O	3:C:24:LEU:HB2	2.18	0.44
1:A:355:GLY:C	1:A:358:PRO:HD2	2.38	0.44
2:B:79:TYR:CE2	2:B:98:PRO:HG3	2.53	0.44
2:B:8:HIS:HD2	2:B:9:LYS:HE3	1.82	0.44
1:A:346:PHE:CZ	1:A:350:VAL:HG21	2.52	0.44
1:A:456:VAL:N	1:A:457:PRO:HD3	2.32	0.44
2:B:158:GLN:CD	2:B:158:GLN:H	2.21	0.44
1:A:54:LEU:C	1:A:54:LEU:HD13	2.39	0.44
1:A:215:LEU:N	1:A:215:LEU:HD22	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:405:LEU:HD12	1:A:405:LEU:HA	1.83	0.44
1:A:518:ARG:HH21	1:A:518:ARG:HG2	1.82	0.44
1:A:170:TRP:CH2	1:A:180:PRO:HD3	2.53	0.43
1:A:48:ASN:HD21	1:A:457:PRO:HA	1.82	0.43
1:A:465:VAL:N	1:A:466:PRO:HD2	2.33	0.43
1:A:25:LEU:HD11	1:A:404:LEU:CD2	2.49	0.43
1:A:123:PRO:CG	1:A:144:ALA:HB3	2.48	0.43
1:A:379:ALA:C	1:A:382:PRO:HD2	2.39	0.43
2:B:3:ASP:O	2:B:4:GLU:HB3	2.18	0.43
1:A:339:LEU:HG	1:A:346:PHE:CZ	2.53	0.43
1:A:489:PHE:O	1:A:493:LEU:HB2	2.18	0.43
2:B:69:GLN:HA	2:B:69:GLN:NE2	2.33	0.42
2:B:96:GLU:CD	2:B:167:LYS:HZ1	2.22	0.42
3:C:4:LYS:HA	3:C:5:PRO:HD3	1.83	0.42
2:B:9:LYS:HE2	2:B:9:LYS:CA	2.39	0.42
1:A:351:LEU:HD12	1:A:425:VAL:HG12	2.02	0.42
1:A:357:ILE:CB	1:A:358:PRO:HD3	2.46	0.42
1:A:272:PHE:CZ	1:A:308:PRO:HB2	2.53	0.42
1:A:232:GLY:O	1:A:235:ILE:HG22	2.20	0.42
1:A:310:LEU:HD13	2:B:22:SER:HB3	2.02	0.42
1:A:495:ARG:HD3	1:A:495:ARG:HA	1.39	0.42
3:C:2:GLU:HG3	3:C:3:GLU:N	2.33	0.42
1:A:107:TRP:HB3	4:A:805:BNG:H1'2	2.02	0.42
1:A:132:LEU:HD13	1:A:450:ARG:NE	2.35	0.42
2:B:87:ALA:C	2:B:88:PHE:CG	2.93	0.42
1:A:225:ARG:HG3	1:A:284:GLN:NE2	2.34	0.42
1:A:230:TRP:C	1:A:230:TRP:HD1	2.22	0.41
2:B:119:GLU:OE2	2:B:146:ARG:HD2	2.21	0.41
2:B:156:GLY:HA2	2:B:158:GLN:HE22	1.84	0.41
1:A:411:LYS:NZ	1:A:495:ARG:NH2	2.69	0.41
1:A:348:ALA:HB3	1:A:349:PRO:CD	2.51	0.41
2:B:47:ALA:HB2	2:B:134:THR:HB	2.03	0.41
1:A:386:HIS:HA	1:A:390:ALA:HB3	2.02	0.41
1:A:291:ASP:HA	1:A:292:PRO:HD3	1.88	0.41
1:A:287:ASP:OD2	2:B:126:GLU:HG3	2.21	0.41
1:A:227:LEU:O	1:A:230:TRP:HB3	2.21	0.40
2:B:128:LEU:HA	2:B:129:PRO:HD3	1.93	0.40
2:B:32:LEU:O	2:B:36:THR:HG23	2.22	0.40
1:A:465:VAL:CG2	1:A:466:PRO:HD3	2.43	0.40
1:A:465:VAL:CG2	1:A:466:PRO:CD	3.00	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	555/568 (98%)	530 (96%)	22 (4%)	3 (0%)	34	41
2	B	164/168 (98%)	154 (94%)	9 (6%)	1 (1%)	30	36
3	C	31/34 (91%)	29 (94%)	2 (6%)	0	100	100
All	All	750/770 (97%)	713 (95%)	33 (4%)	4 (0%)	34	41

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	330	ARG
2	B	87	ALA
1	A	369	PHE
1	A	518	ARG

### 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	453/462 (98%)	436 (96%)	17 (4%)	40	54
2	B	136/138 (99%)	133 (98%)	3 (2%)	60	77
3	C	26/27 (96%)	24 (92%)	2 (8%)	16	20
All	All	615/627 (98%)	593 (96%)	22 (4%)	42	57

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ARG
1	A	48	ASN
1	A	133	TYR
1	A	168	ARG
1	A	195	LEU
1	A	225	ARG
1	A	230	TRP
1	A	274	LEU
1	A	339	LEU
1	A	354	LEU
1	A	369	PHE
1	A	401	LEU
1	A	430	LEU
1	A	449	ARG
1	A	472	LEU
1	A	495	ARG
1	A	513	SER
2	B	19	LEU
2	B	77	ASN
2	B	146	ARG
3	C	23	TRP
3	C	24	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	GLN
1	A	48	ASN
1	A	76	ASN
1	A	254	GLN
1	A	284	GLN
1	A	298	HIS
1	A	388	GLN
2	B	8	HIS
2	B	60	GLN
2	B	69	GLN
2	B	77	ASN
2	B	117	HIS
2	B	122	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 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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	HEM	A	800	1	30,50,50	2.54	7 (23%)	24,82,82	2.36	9 (37%)
7	HAS	A	801	1,10	45,72,72	1.84	10 (22%)	47,109,109	1.00	3 (6%)
9	GOL	A	804	-	5,5,5	4.91	5 (100%)	5,5,5	5.67	3 (60%)
4	BNG	A	805	-	21,21,21	1.62	5 (23%)	26,26,26	0.97	1 (3%)
8	CUA	B	802	2	0,1,1	0.00	-	0,0,0	0.00	-

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	HEM	A	800	1	-	0/10/54/54	0/0/8/8
7	HAS	A	801	1,10	-	0/30/82/82	0/0/8/8
9	GOL	A	804	-	-	0/4/4/4	0/0/0/0
4	BNG	A	805	-	-	0/12/32/32	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	CUA	B	802	2	-	0/0/0/0	0/0/0/0

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	804	GOL	C3-C2	-8.57	1.19	1.52
6	A	800	HEM	C3B-C4B	-6.53	1.46	1.51
6	A	800	HEM	C3D-C4D	-5.73	1.44	1.51
6	A	800	HEM	CMC-C2C	-5.41	1.40	1.53
6	A	800	HEM	C2D-C3D	-4.99	1.39	1.54
6	A	800	HEM	C2D-C1D	-4.47	1.37	1.51
7	A	801	HAS	C2D-C3D	-3.79	1.35	1.40
6	A	800	HEM	C2C-C1C	-3.49	1.46	1.52
9	A	804	GOL	C1-C2	-3.39	1.39	1.52
9	A	804	GOL	O2-C2	-2.86	1.34	1.43
7	A	801	HAS	C3C-CAC	-2.55	1.42	1.47
4	A	805	BNG	C3'-C2'	-2.43	1.37	1.51
7	A	801	HAS	C4B-NB	2.02	1.39	1.36
4	A	805	BNG	O1-C1'	2.39	1.49	1.42
7	A	801	HAS	C4C-NC	2.67	1.40	1.36
4	A	805	BNG	O5-C1	2.79	1.49	1.41
7	A	801	HAS	C29-C30	2.87	1.41	1.32
4	A	805	BNG	C4-C5	2.99	1.59	1.53
4	A	805	BNG	O1-C1	3.02	1.45	1.40
7	A	801	HAS	C1B-NB	3.05	1.40	1.36
9	A	804	GOL	O3-C3	3.10	1.55	1.42
6	A	800	HEM	FE-NC	3.25	2.08	1.95
7	A	801	HAS	C14-C15	3.98	1.40	1.33
7	A	801	HAS	C18-C19	4.04	1.40	1.33
9	A	804	GOL	O1-C1	4.22	1.60	1.42
7	A	801	HAS	C22-C23	4.66	1.42	1.33
7	A	801	HAS	C3C-C2C	4.85	1.46	1.40

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	805	BNG	C4-C3-C2	-2.30	106.51	110.79
6	A	800	HEM	CMA-C3A-C4A	-2.12	124.86	128.36
7	A	801	HAS	CMA-C3A-C4A	-2.00	125.05	128.36
7	A	801	HAS	CMC-C2C-C3C	2.20	129.39	125.09
6	A	800	HEM	C3B-CAB-CBB	2.39	128.12	124.46
6	A	800	HEM	C2D-C3D-C4D	2.72	106.11	101.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	801	HAS	C4B-C3B-C11	2.79	130.03	127.01
6	A	800	HEM	CMD-C2D-C3D	2.80	126.74	114.35
6	A	800	HEM	C3C-CAC-CBC	2.84	128.81	124.46
9	A	804	GOL	O1-C1-C2	3.09	125.16	110.18
6	A	800	HEM	CAD-C3D-C4D	4.12	127.00	112.47
6	A	800	HEM	CMB-C2B-C3B	4.67	128.20	116.53
6	A	800	HEM	CAD-C3D-C2D	4.75	126.89	113.22
6	A	800	HEM	CMC-C2C-C3C	5.02	129.07	116.53
9	A	804	GOL	O2-C2-C3	6.60	138.92	108.65
9	A	804	GOL	O3-C3-C2	10.34	160.31	110.18

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
6	A	800	HEM	1	0
7	A	801	HAS	2	0
4	A	805	BNG	2	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	557/568 (98%)	0.21	37 (6%) 22 29	32, 46, 74, 93	0
2	B	166/168 (98%)	0.78	26 (15%) 3 4	36, 62, 87, 98	0
3	C	33/34 (97%)	0.27	3 (9%) 11 17	48, 57, 83, 96	0
All	All	756/770 (98%)	0.34	66 (8%) 13 18	32, 50, 80, 98	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	68	ALA	6.3
2	B	76	PRO	5.3
2	B	69	GLN	5.1
1	A	331	GLY	4.9
2	B	168	GLU	4.8
1	A	493	LEU	4.7
1	A	330	ARG	4.7
1	A	60	PRO	4.6
1	A	515	PRO	4.4
1	A	462	HIS	4.0
1	A	329	GLY	3.9
2	B	35	TYR	3.9
1	A	496	GLU	3.7
2	B	38	ALA	3.7
1	A	57	ARG	3.6
1	A	458	ASP	3.6
3	C	3	GLU	3.5
2	B	77	ASN	3.5
2	B	20	ALA	3.5
1	A	495	ARG	3.4
3	C	34	GLY	3.4
2	B	65	ALA	3.4
2	B	74	THR	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	414	SER	3.3
1	A	516	GLU	3.3
1	A	513	SER	3.3
1	A	415	ASP	3.2
1	A	518	ARG	3.2
1	A	58	LEU	3.2
3	C	2	GLU	3.2
1	A	8	ILE	3.2
1	A	215	LEU	3.0
1	A	6	SER	3.0
2	B	60	GLN	2.9
2	B	61	GLU	2.9
1	A	320	LEU	2.8
2	B	7	ALA	2.7
1	A	499	PRO	2.7
1	A	332	LEU	2.6
2	B	135	VAL	2.6
2	B	107	ILE	2.6
1	A	514	GLY	2.5
2	B	73	GLN	2.5
1	A	333	PHE	2.5
2	B	72	VAL	2.5
2	B	81	VAL	2.5
1	A	503	GLU	2.5
2	B	105	PHE	2.4
1	A	416	ALA	2.4
1	A	54	LEU	2.3
1	A	7	GLU	2.3
1	A	316	VAL	2.2
2	B	144	GLU	2.2
2	B	58	VAL	2.2
2	B	79	TYR	2.2
1	A	494	SER	2.1
2	B	145	TYR	2.1
2	B	88	PHE	2.1
2	B	75	GLY	2.1
1	A	9	SER	2.1
2	B	66	ASP	2.1
1	A	309	SER	2.0
1	A	517	ASP	2.0
1	A	186	ALA	2.0
1	A	419	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	519	ARG	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, 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
4	BNG	A	805	21/21	0.81	0.40	3.27	59,62,64,65	0
9	GOL	A	804	6/6	0.92	0.17	0.21	44,51,52,52	0
6	HEM	A	800	43/43	0.97	0.16	0.13	31,39,41,46	0
7	HAS	A	801	65/65	0.95	0.13	-0.35	31,39,53,60	0
8	CUA	B	802	2/2	0.99	0.06	-2.44	44,44,44,47	0
5	CU	A	803	1/1	0.98	0.06	-	38,38,38,38	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.