



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 10:03 pm BST

PDB ID : 3QJR
Title : The structure of and photolytic induced changes of carbon monoxide binding to the cytochrome ba3-oxidase from *Thermus thermophilus*
Authors : Liu, B.; Zhang, Y.; Sage, J.T.; Doukov, T.; Chen, Y.; Stout, C.D.; Fee, J.A.
Deposited on : 2011-01-30
Resolution : 3.20 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

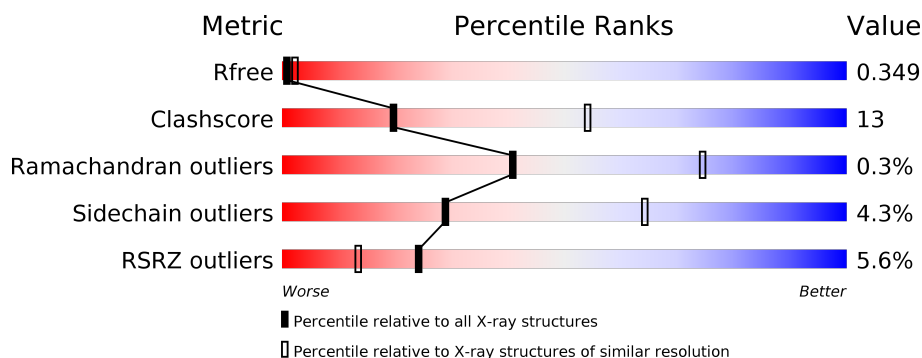
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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>5%</div> <div> <div></div> <div>74%</div> <div>21%</div> <div>• •</div> </div> </div>
2	B	168	<div> <div>7%</div> <div> <div></div> <div>74%</div> <div>23%</div> <div>• •</div> </div> </div>
3	C	34	<div> <div>6%</div> <div> <div></div> <div>56%</div> <div>41%</div> <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
7	CMO	A	563	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6037 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 subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	552	Total	C	N	O	S	0	0	0
			4367	2962	699	690	16			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	EXPRESSION TAG	UNP Q5SJ79
A	-4	HIS	-	EXPRESSION TAG	UNP Q5SJ79
A	-3	HIS	-	EXPRESSION TAG	UNP Q5SJ79
A	-2	HIS	-	EXPRESSION TAG	UNP Q5SJ79
A	-1	HIS	-	EXPRESSION TAG	UNP Q5SJ79
A	0	HIS	-	EXPRESSION TAG	UNP Q5SJ79
A	1	HIS	-	EXPRESSION TAG	UNP Q5SJ79

- Molecule 2 is a protein called Cytochrome c oxidase subunit 2.

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 2A.

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

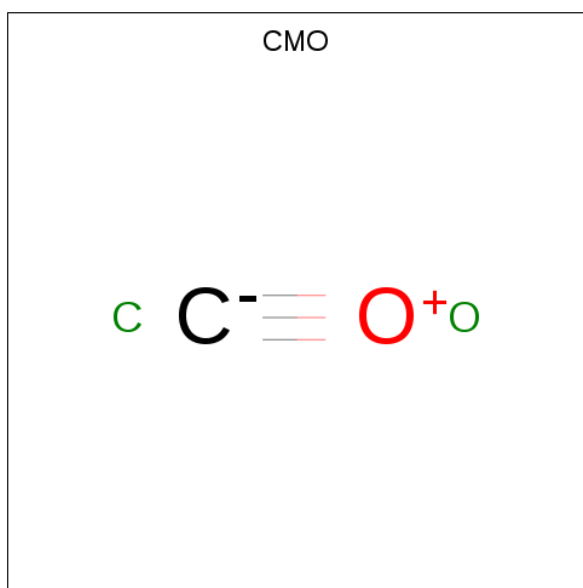
- Molecule 4 is COPPER (I) ION (three-letter code: CU1) (formula: Cu).

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

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

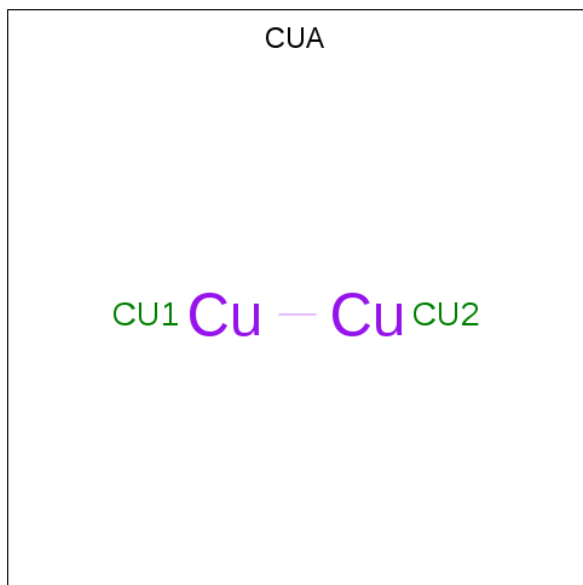


- Molecule 7 is CARBON MONOXIDE (three-letter code: CMO) (formula: CO).



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

- Molecule 8 is DINUCLEAR COPPER ION (three-letter code: CUA) (formula: Cu₂).

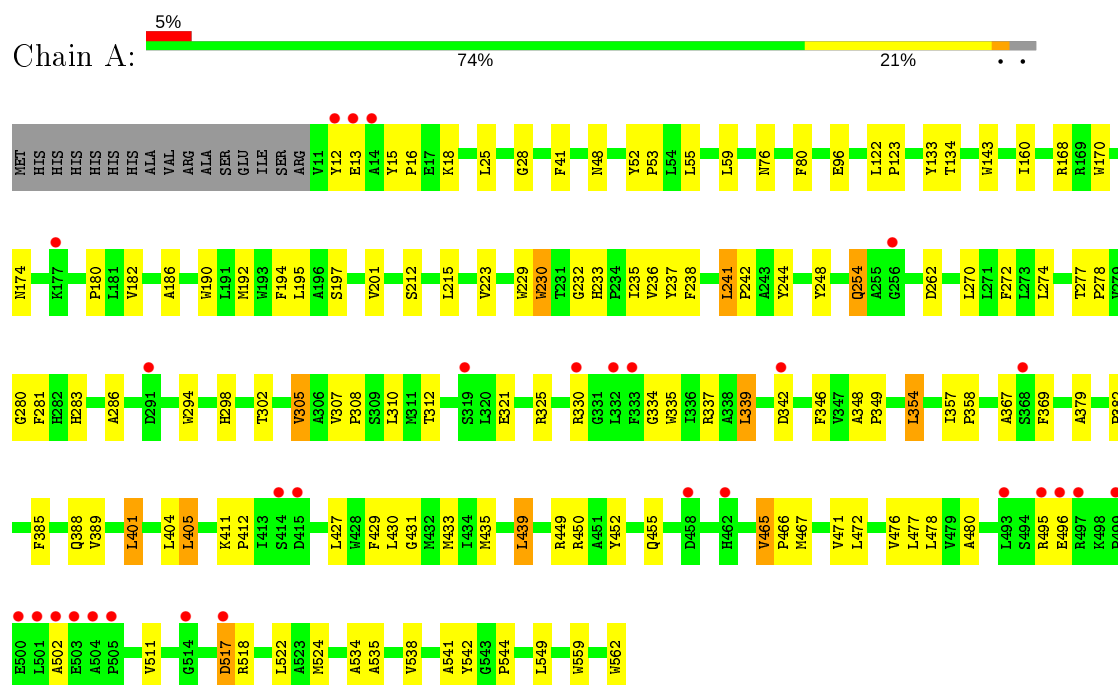


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	Cu	0	0
			2	2		

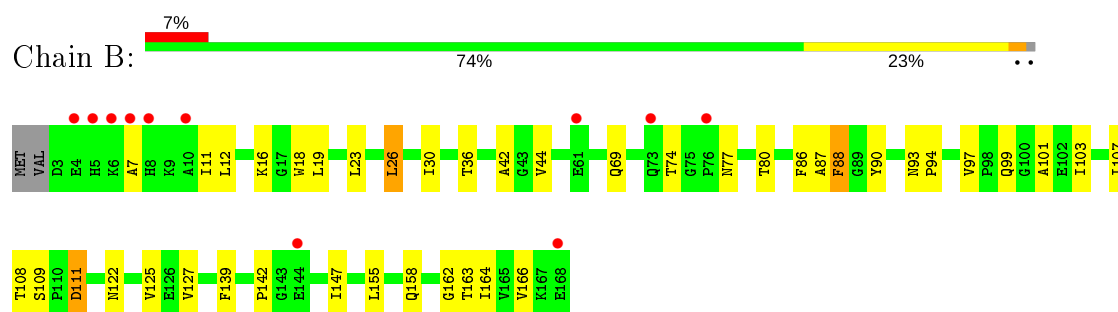
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Cytochrome c oxidase subunit 1

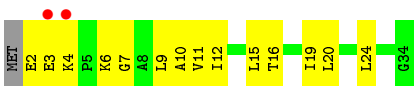


• Molecule 2: Cytochrome c oxidase subunit 2



• Molecule 3: Cytochrome c oxidase polypeptide 2A





4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	108.81Å 108.81Å 164.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.89 – 3.20 19.89 – 3.20	Depositor EDS
% Data completeness (in resolution range)	90.6 (19.89-3.20) 90.6 (19.89-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.15 (at 3.22Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.318 , 0.367 0.310 , 0.349	Depositor DCC
R_{free} test set	778 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	68.1	Xtriage
Anisotropy	0.164	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 59.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.79	EDS
Total number of atoms	6037	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.85% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CMO, HEM, HAS, CUA, CU1

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	0.57	0/4524	0.64	0/6210
2	B	0.55	0/1335	0.60	0/1822
3	C	0.58	0/265	0.59	0/359
All	All	0.56	0/6124	0.63	0/8391

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

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	4367	0	4476	112	1
2	B	1298	0	1280	33	1
3	C	259	0	279	14	0
4	A	1	0	0	0	0
5	A	43	0	30	2	0
6	A	65	0	62	11	0
7	A	2	0	0	2	0
8	B	2	0	0	0	0
All	All	6037	0	6127	155	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 13.

All (155) 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:233:HIS:NE2	1:A:237:TYR:CE2	1.78	1.50
1:A:233:HIS:NE2	1:A:237:TYR:HE2	0.89	1.37
2:B:99:GLN:OE1	2:B:142:PRO:HG3	1.44	1.17
1:A:233:HIS:CD2	1:A:237:TYR:HE2	1.75	1.04
3:C:3:GLU:HG3	3:C:4:LYS:H	1.32	0.95
2:B:142:PRO:HA	2:B:166:VAL:HG23	1.52	0.92
3:C:3:GLU:CG	3:C:4:LYS:H	1.85	0.88
1:A:233:HIS:CE1	1:A:237:TYR:HE2	1.91	0.87
1:A:379:ALA:HB1	1:A:439:LEU:HD12	1.54	0.86
1:A:122:LEU:HB2	1:A:123:PRO:HD3	1.57	0.85
1:A:233:HIS:CE1	1:A:237:TYR:CE2	2.65	0.83
2:B:142:PRO:HA	2:B:166:VAL:CG2	2.11	0.81
1:A:357:ILE:HB	1:A:358:PRO:HD3	1.64	0.79
2:B:97:VAL:O	2:B:166:VAL:HA	1.82	0.78
1:A:262:ASP:HB2	1:A:511:VAL:HG11	1.67	0.77
1:A:15:TYR:HB2	1:A:18:LYS:HD2	1.66	0.75
1:A:233:HIS:CD2	1:A:237:TYR:CE2	2.60	0.75
1:A:232:GLY:O	1:A:235:ILE:HG22	1.89	0.73
1:A:518:ARG:HG2	1:A:518:ARG:HH21	1.53	0.72
1:A:272:PHE:CZ	1:A:308:PRO:HB2	2.24	0.72
1:A:388:GLN:HB2	6:A:801:HAS:HAC	1.72	0.71
1:A:134:THR:CG2	1:A:450:ARG:HH12	2.03	0.70
2:B:166:VAL:HG23	2:B:166:VAL:O	1.93	0.68
1:A:254:GLN:HE21	1:A:254:GLN:HA	1.60	0.66
3:C:3:GLU:CG	3:C:4:LYS:N	2.59	0.66
1:A:160:ILE:HD13	1:A:194:PHE:HB2	1.78	0.65
2:B:69:GLN:HA	2:B:69:GLN:NE2	2.11	0.64
1:A:230:TRP:C	1:A:230:TRP:CD1	2.71	0.63
2:B:74:THR:HG21	2:B:80:THR:OG1	1.99	0.62
1:A:449:ARG:HH12	6:A:801:HAS:CGA	2.13	0.62
1:A:379:ALA:HB1	1:A:439:LEU:CD1	2.27	0.62
1:A:270:LEU:HD22	1:A:524:MET:HG2	1.82	0.61
2:B:93:ASN:HD21	2:B:162:GLY:HA2	1.66	0.61
2:B:147:ILE:HD11	2:B:164:ILE:HG13	1.83	0.61
1:A:76:ASN:HB3	5:A:800:HEM:CAC	2.31	0.60
2:B:26:LEU:O	2:B:30:ILE:HG13	2.02	0.60
1:A:294:TRP:CZ2	1:A:544:PRO:HG2	2.37	0.59
1:A:321:GLU:O	1:A:325:ARG:HG2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:THR:HG21	1:A:450:ARG:HH12	1.68	0.58
1:A:518:ARG:HG2	1:A:518:ARG:NH2	2.19	0.58
1:A:229:TRP:CE3	1:A:232:GLY:HA3	2.39	0.57
1:A:427:LEU:HB3	1:A:480:ALA:HB2	1.87	0.57
1:A:223:VAL:HG12	1:A:549:LEU:HB3	1.85	0.57
1:A:435:MET:HG2	1:A:439:LEU:HD23	1.87	0.57
1:A:302:THR:O	1:A:305:VAL:HG12	2.05	0.56
1:A:233:HIS:NE2	1:A:237:TYR:CZ	2.57	0.56
3:C:4:LYS:HE2	3:C:6:LYS:HG2	1.86	0.56
1:A:15:TYR:O	1:A:18:LYS:HB2	2.06	0.56
6:A:801:HAS:H253	3:C:11:VAL:HG11	1.87	0.56
1:A:235:ILE:O	1:A:238:PHE:HB3	2.05	0.56
1:A:25:LEU:HD11	1:A:404:LEU:CD2	2.36	0.56
1:A:195:LEU:HD21	1:A:535:ALA:HA	1.89	0.55
2:B:18:TRP:CE3	3:C:12:ILE:HD12	2.40	0.55
1:A:230:TRP:C	1:A:230:TRP:HD1	2.10	0.55
1:A:143:TRP:HA	1:A:212:SER:HB2	1.90	0.54
1:A:307:VAL:HA	1:A:310:LEU:HD12	1.90	0.54
1:A:233:HIS:O	1:A:236:VAL:HG22	2.08	0.53
1:A:122:LEU:HB2	1:A:123:PRO:CD	2.33	0.53
2:B:101:ALA:O	2:B:103:ILE:HD12	2.07	0.53
3:C:20:LEU:O	3:C:24:LEU:HB2	2.08	0.53
1:A:283:HIS:HE1	7:A:563:CMO:C	2.12	0.53
1:A:277:THR:N	1:A:278:PRO:HD2	2.24	0.53
1:A:298:HIS:CE1	1:A:541:ALA:HB1	2.44	0.52
2:B:99:GLN:OE1	2:B:142:PRO:CG	2.37	0.52
3:C:3:GLU:HG3	3:C:4:LYS:N	2.13	0.52
1:A:262:ASP:HB2	1:A:511:VAL:CG1	2.38	0.52
1:A:455:GLN:O	1:A:455:GLN:HG2	2.09	0.51
1:A:277:THR:N	1:A:278:PRO:CD	2.74	0.51
1:A:76:ASN:HB3	5:A:800:HEM:CBC	2.41	0.51
1:A:562:TRP:HA	2:B:155:LEU:HG	1.92	0.51
1:A:197:SER:O	1:A:201:VAL:HG23	2.11	0.50
2:B:44:VAL:HG11	2:B:122:ASN:HB2	1.93	0.50
2:B:90:TYR:O	2:B:93:ASN:HB2	2.11	0.50
3:C:2:GLU:HG3	3:C:3:GLU:H	1.77	0.50
1:A:286:ALA:HB1	2:B:125:VAL:HA	1.94	0.50
1:A:465:VAL:HG23	1:A:466:PRO:HD3	1.94	0.50
1:A:427:LEU:HD22	1:A:476:VAL:HG13	1.93	0.50
1:A:248:TYR:OH	1:A:312:THR:HA	2.11	0.50
1:A:280:GLY:HA3	1:A:542:TYR:OH	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:GLU:HA	1:A:335:TRP:CE3	2.48	0.49
1:A:170:TRP:CH2	1:A:180:PRO:HD3	2.46	0.49
1:A:18:LYS:HE2	1:A:502:ALA:O	2.12	0.49
1:A:335:TRP:O	1:A:339:LEU:HD22	2.12	0.49
1:A:122:LEU:CB	1:A:123:PRO:HD3	2.38	0.48
1:A:330:ARG:HB2	1:A:334:GLY:HA3	1.95	0.48
2:B:69:GLN:HA	2:B:69:GLN:HE21	1.78	0.48
1:A:330:ARG:HG3	1:A:334:GLY:HA3	1.94	0.48
1:A:41:PHE:CE2	1:A:55:LEU:HB2	2.48	0.48
6:A:801:HAS:ND	7:A:563:CMO:C	2.75	0.48
2:B:86:PHE:O	2:B:88:PHE:N	2.47	0.48
3:C:4:LYS:HE3	3:C:9:LEU:HD12	1.95	0.48
1:A:357:ILE:HG23	3:C:15:LEU:HD12	1.95	0.48
6:A:801:HAS:H161	3:C:15:LEU:HD11	1.96	0.47
1:A:467:MET:O	1:A:471:VAL:HG23	2.14	0.47
1:A:452:TYR:O	2:B:158:GLN:HG3	2.15	0.47
1:A:330:ARG:CB	1:A:334:GLY:HA3	2.44	0.47
1:A:192:MET:C	1:A:192:MET:SD	2.93	0.46
1:A:401:LEU:O	1:A:405:LEU:HB2	2.15	0.46
1:A:401:LEU:HG	1:A:405:LEU:HD22	1.97	0.46
1:A:134:THR:HG23	1:A:450:ARG:HH12	1.77	0.46
1:A:517:ASP:OD2	1:A:517:ASP:N	2.49	0.46
1:A:367:ALA:HB2	6:A:801:HAS:OMD	2.15	0.46
1:A:495:ARG:HD3	1:A:495:ARG:HA	1.76	0.46
1:A:382:PRO:HA	1:A:385:PHE:CE2	2.51	0.46
1:A:59:LEU:HD23	1:A:59:LEU:HA	1.70	0.46
1:A:357:ILE:HB	1:A:358:PRO:CD	2.43	0.46
1:A:534:ALA:O	1:A:538:VAL:HG23	2.16	0.46
1:A:388:GLN:HB2	6:A:801:HAS:CAC	2.45	0.46
1:A:12:TYR:O	1:A:16:PRO:CA	2.64	0.46
2:B:69:GLN:CA	2:B:69:GLN:HE21	2.28	0.45
1:A:241:LEU:N	1:A:242:PRO:CD	2.80	0.45
1:A:52:TYR:N	1:A:53:PRO:HD2	2.32	0.45
6:A:801:HAS:HHB	6:A:801:HAS:OMD	2.17	0.45
2:B:103:ILE:HD13	2:B:139:PHE:HD1	1.82	0.45
1:A:389:VAL:HB	6:A:801:HAS:HBC2	1.99	0.45
1:A:25:LEU:HD11	1:A:404:LEU:HD23	1.99	0.45
2:B:69:GLN:CA	2:B:69:GLN:NE2	2.77	0.44
3:C:7:GLY:O	3:C:10:ALA:HB3	2.18	0.44
1:A:281:PHE:H	1:A:298:HIS:HD2	1.65	0.44
1:A:28:GLY:O	1:A:80:PHE:HD1	2.01	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:ALA:C	1:A:382:PRO:HD2	2.37	0.44
1:A:429:PHE:O	1:A:433:MET:HG2	2.18	0.44
1:A:388:GLN:CB	6:A:801:HAS:CAC	2.95	0.44
1:A:449:ARG:HD2	1:A:450:ARG:HG3	2.00	0.44
2:B:7:ALA:O	2:B:11:ILE:HG13	2.17	0.44
1:A:411:LYS:HG2	1:A:496:GLU:O	2.19	0.43
1:A:388:GLN:CB	6:A:801:HAS:HAC	2.46	0.43
1:A:12:TYR:O	1:A:16:PRO:HA	2.19	0.43
1:A:281:PHE:H	1:A:298:HIS:CD2	2.37	0.43
1:A:96:GLU:OE2	1:A:182:VAL:HB	2.18	0.43
1:A:186:ALA:O	1:A:190:TRP:HD1	2.02	0.43
1:A:337:ARG:HA	1:A:337:ARG:HD2	1.82	0.43
1:A:348:ALA:HB3	1:A:349:PRO:HD3	2.01	0.42
1:A:339:LEU:HB3	1:A:346:PHE:CZ	2.54	0.42
1:A:330:ARG:HG3	1:A:334:GLY:CA	2.49	0.42
2:B:166:VAL:CG2	2:B:166:VAL:O	2.62	0.42
1:A:170:TRP:CE2	1:A:174:ASN:ND2	2.88	0.42
2:B:94:PRO:HB3	2:B:163:THR:HB	2.02	0.42
1:A:431:GLY:HA3	1:A:477:LEU:HG	2.01	0.42
3:C:16:THR:HA	3:C:19:ILE:HD12	2.02	0.42
1:A:559:TRP:CZ2	2:B:111:ASP:HB3	2.55	0.41
1:A:186:ALA:O	1:A:190:TRP:CD1	2.73	0.41
1:A:411:LYS:HA	1:A:412:PRO:HD2	1.85	0.41
2:B:12:LEU:O	2:B:16:LYS:HG3	2.20	0.41
2:B:97:VAL:CG2	2:B:166:VAL:HG12	2.50	0.41
1:A:342:ASP:OD1	1:A:342:ASP:N	2.40	0.41
1:A:354:LEU:HD12	1:A:354:LEU:HA	1.93	0.41
1:A:518:ARG:O	1:A:522:LEU:HB2	2.21	0.41
2:B:108:THR:OG1	2:B:109:SER:N	2.54	0.41
2:B:7:ALA:O	2:B:11:ILE:CG1	2.68	0.41
2:B:36:THR:O	2:B:42:ALA:HB2	2.20	0.41
1:A:241:LEU:HD12	1:A:241:LEU:HA	1.92	0.41
1:A:401:LEU:HA	1:A:401:LEU:HD12	1.80	0.41
1:A:325:ARG:HA	1:A:325:ARG:HD3	1.94	0.40
2:B:107:ILE:HG22	2:B:127:VAL:HG11	2.04	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:A:13:GLU:OE1	2:B:166:VAL:N[4_545]	1.91	0.29

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	550/568 (97%)	518 (94%)	32 (6%)	0	100	100
2	B	164/168 (98%)	154 (94%)	8 (5%)	2 (1%)	13	49
3	C	31/34 (91%)	30 (97%)	1 (3%)	0	100	100
All	All	745/770 (97%)	702 (94%)	41 (6%)	2 (0%)	41	74

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	87	ALA
2	B	88	PHE

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	448/462 (97%)	427 (95%)	21 (5%)	26	62
2	B	136/138 (99%)	131 (96%)	5 (4%)	34	68
3	C	26/27 (96%)	26 (100%)	0	100	100
All	All	610/627 (97%)	584 (96%)	26 (4%)	29	64

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	ASN

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Mol	Chain	Res	Type
1	A	133	TYR
1	A	168	ARG
1	A	215	LEU
1	A	230	TRP
1	A	241	LEU
1	A	244	TYR
1	A	254	GLN
1	A	274	LEU
1	A	305	VAL
1	A	339	LEU
1	A	354	LEU
1	A	369	PHE
1	A	401	LEU
1	A	405	LEU
1	A	430	LEU
1	A	439	LEU
1	A	465	VAL
1	A	472	LEU
1	A	478	LEU
1	A	517	ASP
2	B	19	LEU
2	B	23	LEU
2	B	26	LEU
2	B	77	ASN
2	B	111	ASP

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	174	ASN
1	A	254	GLN
1	A	298	HIS
1	A	388	GLN
2	B	8	HIS
2	B	69	GLN
2	B	77	ASN
2	B	93	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 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	$\# Z > 2$
5	HEM	A	800	1	27,50,50	2.15	6 (22%)	17,82,82	2.26	4 (23%)
7	CMO	A	563	4,6	0,1,1	0.00	-	-	-	-
6	HAS	A	801	1,7	56,72,72	4.19	16 (28%)	50,109,109	3.60	21 (42%)
8	CUA	B	802	2	0,1,1	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
5	HEM	A	800	1	-	0/6/54/54	-
6	HAS	A	801	1,7	-	3/35/122/122	-

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	801	HAS	C4D-ND	-11.06	1.34	1.49
6	A	801	HAS	C1D-ND	-11.01	1.34	1.49
6	A	801	HAS	C3D-C2D	10.55	1.47	1.34
6	A	801	HAS	C1D-C2D	-10.04	1.35	1.51
6	A	801	HAS	C1B-NB	-10.01	1.36	1.49
6	A	801	HAS	C4B-NB	-9.98	1.36	1.49
6	A	801	HAS	C1C-C2C	8.13	1.49	1.38
6	A	801	HAS	C4A-C3A	7.95	1.49	1.38
6	A	801	HAS	C1A-C2A	7.41	1.48	1.38
6	A	801	HAS	C2B-C3B	5.44	1.38	1.34
6	A	801	HAS	C3C-C2C	5.19	1.47	1.40
5	A	800	HEM	C3D-C2D	4.66	1.51	1.37
5	A	800	HEM	C3C-C2C	-4.53	1.34	1.40
5	A	800	HEM	C3B-C2B	-4.45	1.34	1.40
6	A	801	HAS	CHD-C4C	-4.05	1.47	1.51
5	A	800	HEM	C3B-CAB	3.83	1.55	1.47
5	A	800	HEM	C3C-CAC	3.79	1.55	1.47
6	A	801	HAS	C2A-C3A	3.49	1.48	1.37
6	A	801	HAS	CHD-C4A	-3.40	1.47	1.51
6	A	801	HAS	CHC-C4B	-2.77	1.48	1.53
6	A	801	HAS	CHA-C4D	-2.65	1.48	1.53
5	A	800	HEM	CAA-C2A	2.15	1.55	1.52

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	801	HAS	CHB-C1D-ND	11.37	125.07	110.94
6	A	801	HAS	CHD-C4C-C3C	-10.63	115.67	129.61
6	A	801	HAS	CHB-C1B-NB	8.74	121.81	110.94
6	A	801	HAS	C4C-C3C-C2C	-7.09	93.52	104.41
5	A	800	HEM	CAD-CBD-CGD	-6.31	102.08	112.67
6	A	801	HAS	C4C-CHD-C4A	5.61	126.56	112.87
6	A	801	HAS	C13-C12-C11	-5.20	106.54	114.35
6	A	801	HAS	CHC-C4B-NB	4.99	120.16	110.75
6	A	801	HAS	CHA-C4D-ND	4.80	119.81	110.75
5	A	800	HEM	C1D-C2D-C3D	-4.54	103.84	107.00
6	A	801	HAS	CHD-C4A-C3A	-4.22	122.47	129.53
6	A	801	HAS	OMD-CMD-C2D	-3.93	119.41	124.39
6	A	801	HAS	CMC-C2C-C3C	-3.88	117.41	124.68
6	A	801	HAS	C25-C23-C24	3.62	121.36	115.27
6	A	801	HAS	C1D-CHB-C1B	3.49	126.22	116.15
6	A	801	HAS	C4A-C3A-C2A	-3.06	102.55	105.81
5	A	800	HEM	CBA-CAA-C2A	-3.02	106.91	112.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	801	HAS	CHB-C1B-C2B	2.84	123.57	114.70
6	A	801	HAS	CAD-CBD-CGD	-2.81	107.95	112.67
6	A	801	HAS	CAA-CBA-CGA	-2.80	107.97	112.67
6	A	801	HAS	C26-C15-C16	2.34	119.20	115.27
5	A	800	HEM	CMA-C3A-C4A	-2.29	124.94	128.46
6	A	801	HAS	C32-C30-C31	2.21	119.49	114.60
6	A	801	HAS	C27-C19-C20	2.18	118.94	115.27
6	A	801	HAS	CBA-CAA-C2A	-2.17	108.48	112.49

There are no chirality outliers.

All (3) torsion outliers are listed below:

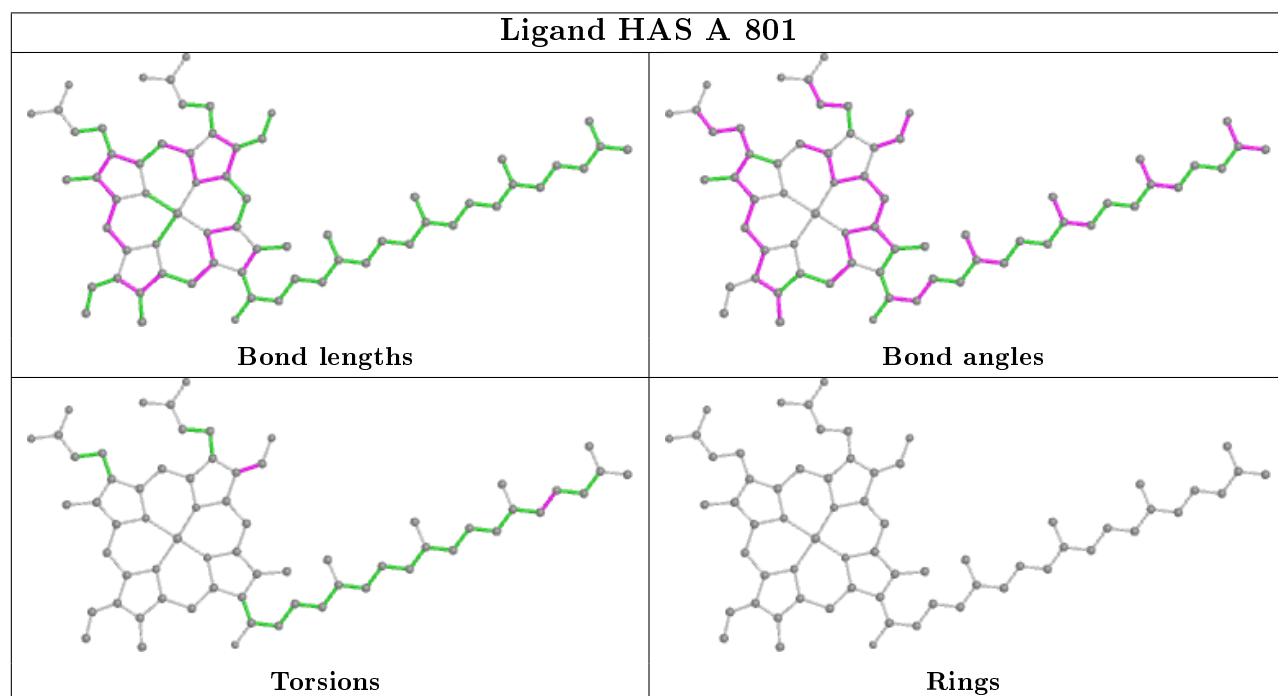
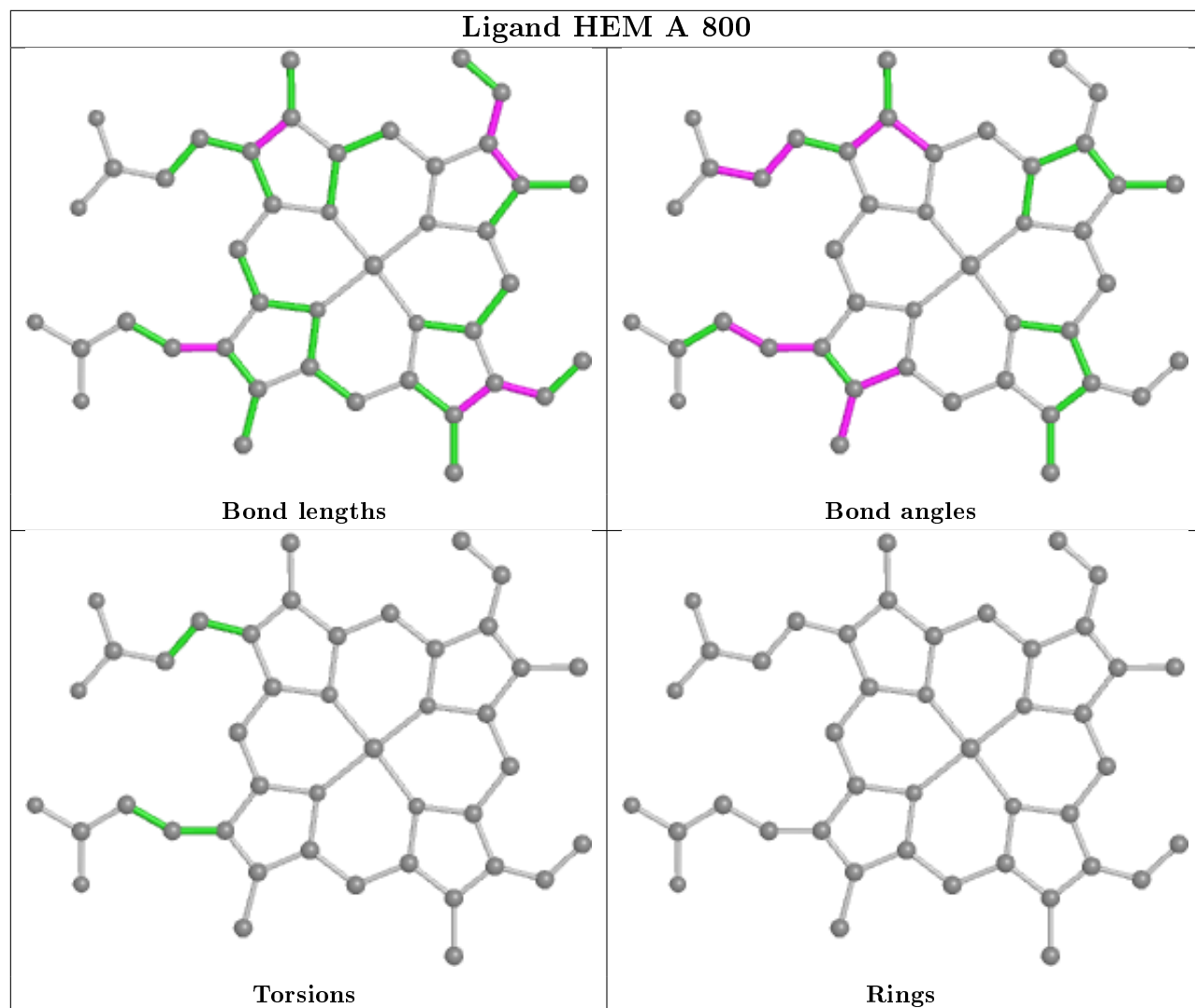
Mol	Chain	Res	Type	Atoms
6	A	801	HAS	C3D-C2D-CMD-OMD
6	A	801	HAS	C1D-C2D-CMD-OMD
6	A	801	HAS	C23-C24-C28-C29

There are no ring outliers.

3 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	800	HEM	2	0
7	A	563	CMO	2	0
6	A	801	HAS	11	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	552/568 (97%)	-0.04	29 (5%) 26 14	21, 24, 25, 27	0
2	B	166/168 (98%)	0.23	11 (6%) 18 11	22, 24, 25, 26	0
3	C	33/34 (97%)	0.18	2 (6%) 21 12	12, 21, 31, 37	0
All	All	751/770 (97%)	0.03	42 (5%) 24 13	12, 24, 25, 37	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	7	ALA	7.2
1	A	501	LEU	4.8
1	A	415	ASP	4.6
1	A	503	GLU	4.6
1	A	504	ALA	4.2
1	A	330	ARG	4.1
1	A	497	ARG	4.1
1	A	502	ALA	3.9
1	A	414	SER	3.9
2	B	6	LYS	3.8
1	A	493	LEU	3.6
1	A	496	GLU	3.5
1	A	14	ALA	3.4
1	A	499	PRO	3.2
2	B	76	PRO	3.1
1	A	495	ARG	3.1
1	A	256	GLY	3.1
1	A	12	TYR	2.9
1	A	458	ASP	2.8
2	B	4	GLU	2.7
1	A	505	PRO	2.7
3	C	3	GLU	2.7
1	A	332	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	342	ASP	2.7
1	A	177	LYS	2.7
2	B	61	GLU	2.7
1	A	500	GLU	2.7
1	A	368	SER	2.6
2	B	144	GLU	2.5
2	B	168	GLU	2.5
1	A	13	GLU	2.4
1	A	517	ASP	2.4
2	B	73	GLN	2.3
2	B	5	HIS	2.2
2	B	8	HIS	2.2
3	C	4	LYS	2.1
1	A	291	ASP	2.1
1	A	462	HIS	2.1
1	A	514	GLY	2.1
2	B	10	ALA	2.1
1	A	319	SER	2.1
1	A	333	PHE	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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

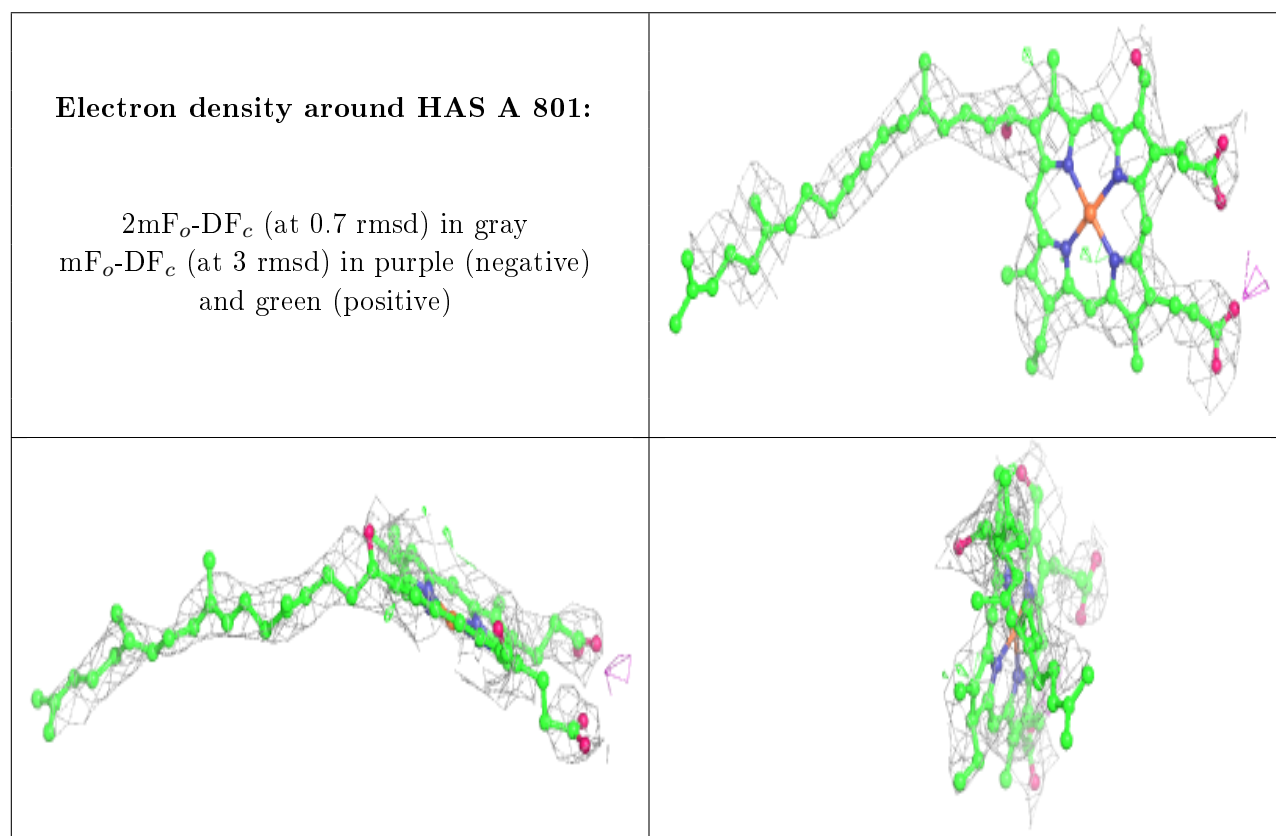
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	HAS	A	801	65/65	0.93	0.20	23,24,25,26	0
5	HEM	A	800	43/43	0.96	0.19	19,23,23,24	0
7	CMO	A	563	2/2	0.98	0.10	36,36,36,40	0
4	CU1	A	803	1/1	0.99	0.03	22,22,22,22	0

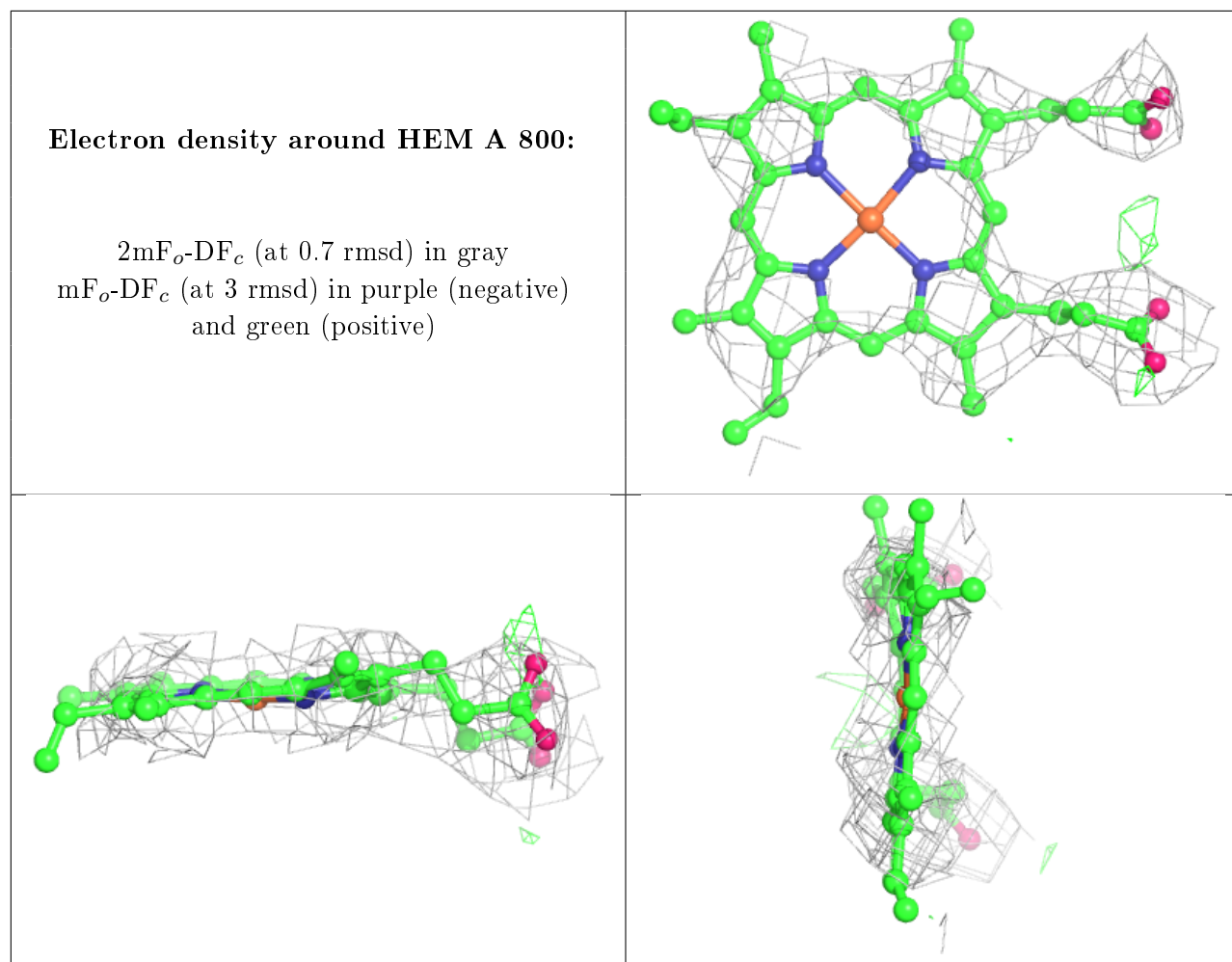
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	CUA	B	802	2/2	0.99	0.06	16,16,16,20	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers [i](#)

There are no such residues in this entry.