



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 15, 2026 – 01:19 AM UTC

PDB ID : 9O5I / pdb_00009o5i
Title : Crystal structure of GutD2774
Authors : Gering, H.E.; Phan, H.N.; Makris, T.M.
Deposited on : 2025-04-10
Resolution : 2.00 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

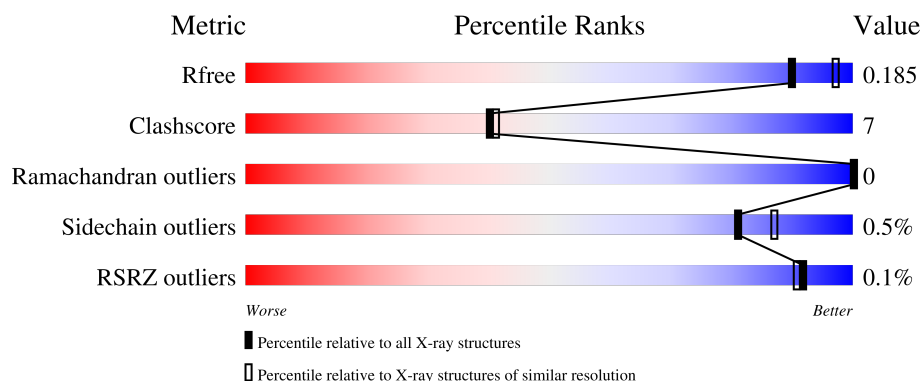
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 of 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	414	 84% 11% 5%
1	B	414	 86% 9% 5%

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	EDO	B	511	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7658 atoms, of which 314 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 P450 121.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	394	Total	C	N	O	S	0	10	0
			3134	1983	572	567	12			
1	B	394	Total	C	N	O	S	0	11	0
			3127	1979	570	566	12			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP A0A918H2T3
A	1	GLY	-	expression tag	UNP A0A918H2T3
A	109	ALA	ASP	conflict	UNP A0A918H2T3
A	399	LEU	-	expression tag	UNP A0A918H2T3
A	400	VAL	-	expression tag	UNP A0A918H2T3
A	401	PRO	-	expression tag	UNP A0A918H2T3
A	402	ARG	-	expression tag	UNP A0A918H2T3
A	403	GLY	-	expression tag	UNP A0A918H2T3
A	404	SER	-	expression tag	UNP A0A918H2T3
A	405	GLY	-	expression tag	UNP A0A918H2T3
A	406	SER	-	expression tag	UNP A0A918H2T3
A	407	SER	-	expression tag	UNP A0A918H2T3
A	408	HIS	-	expression tag	UNP A0A918H2T3
A	409	HIS	-	expression tag	UNP A0A918H2T3
A	410	HIS	-	expression tag	UNP A0A918H2T3
A	411	HIS	-	expression tag	UNP A0A918H2T3
A	412	HIS	-	expression tag	UNP A0A918H2T3
A	413	HIS	-	expression tag	UNP A0A918H2T3
B	0	MET	-	initiating methionine	UNP A0A918H2T3
B	1	GLY	-	expression tag	UNP A0A918H2T3
B	109	ALA	ASP	conflict	UNP A0A918H2T3
B	399	LEU	-	expression tag	UNP A0A918H2T3
B	400	VAL	-	expression tag	UNP A0A918H2T3
B	401	PRO	-	expression tag	UNP A0A918H2T3
B	402	ARG	-	expression tag	UNP A0A918H2T3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	403	GLY	-	expression tag	UNP A0A918H2T3
B	404	SER	-	expression tag	UNP A0A918H2T3
B	405	GLY	-	expression tag	UNP A0A918H2T3
B	406	SER	-	expression tag	UNP A0A918H2T3
B	407	SER	-	expression tag	UNP A0A918H2T3
B	408	HIS	-	expression tag	UNP A0A918H2T3
B	409	HIS	-	expression tag	UNP A0A918H2T3
B	410	HIS	-	expression tag	UNP A0A918H2T3
B	411	HIS	-	expression tag	UNP A0A918H2T3
B	412	HIS	-	expression tag	UNP A0A918H2T3
B	413	HIS	-	expression tag	UNP A0A918H2T3

- # HEM

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

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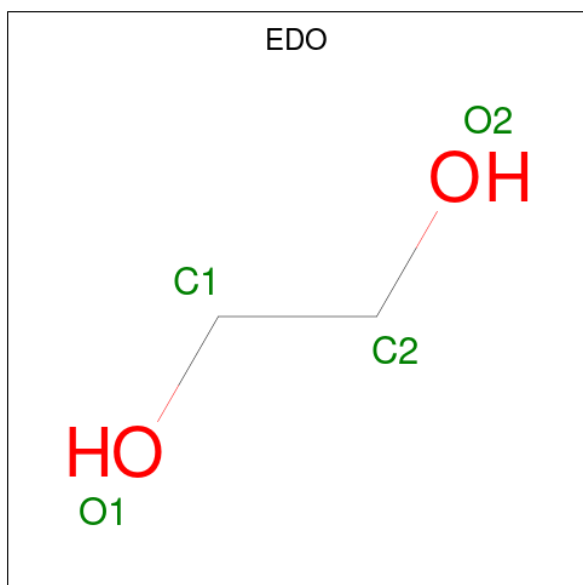
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mg	0	0
			1	1		
6	B	1	Total	Mg	0	0
			1	1		

- Molecule 7 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Ni	0	0
			1	1		


- Molecule 8 is water.

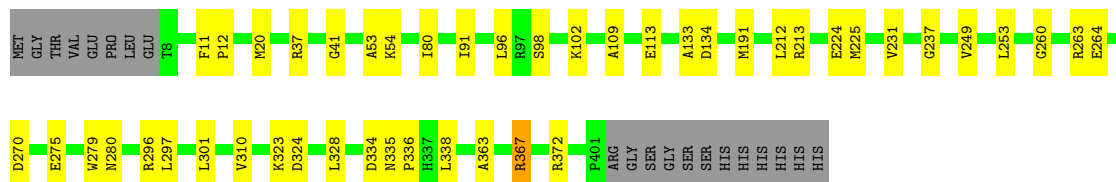
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	365	Total	O	0	0
			365	365		
8	B	408	Total	O	0	0
			408	408		

3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

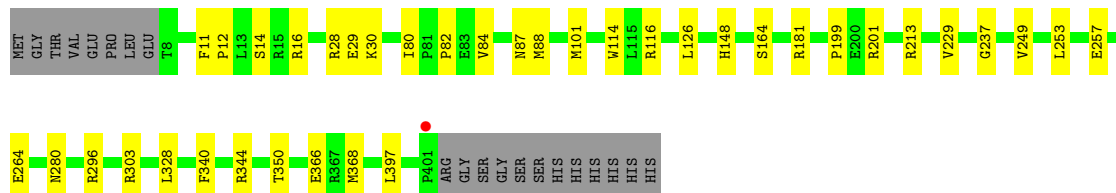
• Molecule 1: Cytochrome P450 121

Chain A: 



• Molecule 1: Cytochrome P450 121

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	75.95Å 108.39Å 120.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	17.70 – 2.00 17.70 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.6 (17.70-2.00) 99.4 (17.70-2.00)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.23 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.147 , 0.186 0.147 , 0.185	Depositor DCC
R_{free} test set	2000 reflections (2.96%)	wwPDB-VP
Wilson B-factor (Å ²)	22.4	Xtriage
Anisotropy	0.271	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 60.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7658	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.12% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, CL, EDO, MG, NI, GOL

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	0.29	0/3201	0.42	0/4353
1	B	0.31	0/3203	0.46	0/4355
All	All	0.30	0/6404	0.44	0/8708

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	3134	0	3162	42	0
1	B	3127	0	3163	39	0
2	A	43	0	30	1	0
2	B	43	0	30	4	0
3	A	48	64	64	3	0
3	B	48	64	64	6	0
4	A	52	78	78	11	0
4	B	72	108	108	14	0
5	A	1	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	1	0	0	0	0
8	A	365	0	0	6	0
8	B	408	0	0	8	0
All	All	7344	314	6699	88	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 7.

All (88) 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:191:MET:HG3	1:A:231:VAL:HG23	1.66	0.76
1:A:91:ILE:HG12	1:A:225:MET:HG2	1.76	0.68
1:A:301:LEU:H	4:A:507:EDO:H12	1.61	0.66
1:B:213:ARG:HB3	4:B:525:EDO:H11	1.77	0.66
1:B:296:ARG:HG3	4:B:508:EDO:O1	1.96	0.65
1:B:328:LEU:H	4:B:511:EDO:H22	1.61	0.64
1:A:301:LEU:HB3	4:A:507:EDO:H22	1.80	0.63
1:A:335:ASN:H	4:A:514:EDO:H11	1.65	0.61
1:B:82:PRO:HD2	1:B:181:ARG:HH22	1.65	0.61
1:B:303[A]:ARG:HG2	8:B:774:HOH:O	2.01	0.60
2:B:502:HEM:HMC1	2:B:502:HEM:HBC2	1.83	0.59
4:B:526:EDO:H22	8:B:646:HOH:O	2.02	0.58
1:B:14:SER:HB2	3:B:527:GOL:H2	1.87	0.57
1:A:109:ALA:O	1:A:113:GLU:HG3	2.05	0.56
1:A:134:ASP:H	3:A:521:GOL:C3	2.19	0.56
1:B:229:VAL:HG22	4:B:515:EDO:H22	1.86	0.56
1:B:11:PHE:CG	1:B:12:PRO:HA	2.41	0.56
1:A:224:GLU:HB2	8:A:601:HOH:O	2.05	0.56
1:B:16:ARG:HH12	3:B:520:GOL:H31	1.71	0.55
4:A:520:EDO:H21	8:B:828:HOH:O	2.06	0.55
1:A:323:LYS:HD3	1:A:324[A]:ASP:H	1.71	0.55
1:B:87:ASN:HB3	8:B:645:HOH:O	2.06	0.55
1:B:116:ARG:HD3	8:B:680:HOH:O	2.07	0.55
1:A:323:LYS:HD3	1:A:324[A]:ASP:N	2.21	0.54
1:B:328:LEU:H	4:B:511:EDO:C2	2.19	0.54
1:A:98:SER:O	1:A:102:LYS:HG2	2.07	0.54
1:A:372:ARG:HB3	4:A:510:EDO:C2	2.38	0.53
1:A:11:PHE:CG	1:A:12:PRO:HA	2.43	0.53
1:A:263:ARG:HD3	8:A:817:HOH:O	2.08	0.53
1:A:191:MET:HG3	1:A:231:VAL:CG2	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:28:ARG:HH21	4:B:513:EDO:H12	1.74	0.52
1:A:323:LYS:HD3	1:A:324[B]:ASP:N	2.23	0.52
1:A:338:LEU:HD23	4:A:519:EDO:H22	1.91	0.52
1:A:213:ARG:HD2	4:A:511:EDO:H21	1.92	0.52
1:A:372:ARG:HB3	4:A:510:EDO:H21	1.91	0.52
1:B:199:PRO:C	1:B:201:ARG:H	2.18	0.51
1:A:260:GLY:O	1:A:264:GLU:HG3	2.11	0.51
1:A:96:LEU:HA	1:A:212:LEU:HD11	1.92	0.50
3:A:521:GOL:H2	1:B:164:SER:CB	2.42	0.50
1:A:80:ILE:HD11	4:A:517:EDO:H12	1.93	0.50
1:B:264:GLU:O	1:B:264:GLU:HG3	2.12	0.49
1:B:16:ARG:HH22	3:B:520:GOL:H31	1.77	0.49
1:A:11:PHE:CD1	1:A:12:PRO:HA	2.47	0.49
1:A:323:LYS:HD3	1:A:324[B]:ASP:H	1.77	0.49
1:A:296:ARG:HG2	4:A:518:EDO:H11	1.94	0.49
1:B:328:LEU:H	4:B:511:EDO:C1	2.25	0.49
1:B:11:PHE:CD1	1:B:12:PRO:HA	2.48	0.48
1:A:372:ARG:NH2	8:A:608:HOH:O	2.46	0.48
1:A:279:TRP:CD2	1:A:328:LEU:HD13	2.49	0.48
1:A:336:PRO:O	4:A:519:EDO:H21	2.13	0.48
1:B:29:GLU:OE2	1:B:30:LYS:HE2	2.14	0.48
1:B:397:LEU:C	1:B:397:LEU:HD12	2.39	0.47
1:A:133:ALA:HA	3:A:521:GOL:H32	1.97	0.47
1:A:237:GLY:HA2	2:A:501:HEM:C2C	2.50	0.47
1:B:80:ILE:HG13	3:B:504:GOL:O2	2.16	0.45
1:A:102:LYS:N	1:A:102:LYS:HD3	2.31	0.45
1:B:237:GLY:HA2	2:B:502:HEM:C2C	2.51	0.45
1:B:249:VAL:O	1:B:253:LEU:HG	2.17	0.44
1:A:270:ASP:HB2	8:A:729:HOH:O	2.17	0.44
1:B:114:TRP:HA	4:B:526:EDO:H11	2.00	0.44
1:B:257:GLU:OE2	4:B:514:EDO:O2	2.34	0.44
1:B:126:LEU:HD13	1:B:368:MET:HE1	1.99	0.43
1:A:334:ASP:HB2	8:A:774:HOH:O	2.18	0.43
1:B:101:MET:HG2	8:B:928:HOH:O	2.18	0.43
1:A:249:VAL:O	1:A:253:LEU:HG	2.18	0.43
2:B:502:HEM:HMB2	2:B:502:HEM:HBB2	2.01	0.43
1:A:20:MET:HE2	1:A:20:MET:HB2	1.87	0.43
1:B:148:HIS:NE2	1:B:237:GLY:HA3	2.34	0.43
1:A:54:LYS:NZ	8:A:614:HOH:O	2.52	0.42
1:B:16:ARG:HH22	3:B:520:GOL:H12	1.83	0.42
1:B:328:LEU:HB3	4:B:511:EDO:H12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:344:ARG:HB2	3:B:507:GOL:H12	2.02	0.42
1:A:37:ARG:CZ	1:A:41:GLY:HA2	2.50	0.42
1:A:91:ILE:CG1	1:A:225:MET:HG2	2.46	0.41
1:B:82:PRO:HD2	1:B:181:ARG:NH2	2.32	0.41
1:A:53:ALA:HB1	1:A:310:VAL:HG13	2.02	0.41
1:B:84:VAL:O	1:B:88:MET:HG2	2.20	0.41
1:B:116:ARG:CD	8:B:680:HOH:O	2.68	0.41
1:A:363:ALA:O	1:A:367:ARG:HG3	2.21	0.41
1:B:237:GLY:CA	2:B:502:HEM:HMC3	2.50	0.41
1:A:275:GLU:HA	1:A:335:ASN:HD21	1.85	0.41
1:B:340:PHE:CG	1:B:350:THR:HG22	2.56	0.41
1:A:297:LEU:HD12	1:A:297:LEU:HA	1.92	0.40
1:B:199:PRO:C	1:B:201:ARG:N	2.79	0.40
1:B:366:GLU:HG2	8:B:875:HOH:O	2.20	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	402/414 (97%)	394 (98%)	8 (2%)	0	100	100
1	B	403/414 (97%)	397 (98%)	6 (2%)	0	100	100
All	All	805/828 (97%)	791 (98%)	14 (2%)	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	327/334 (98%)	325 (99%)	2 (1%)	78	85
1	B	328/334 (98%)	327 (100%)	1 (0%)	86	91
All	All	655/668 (98%)	652 (100%)	3 (0%)	81	87

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	280	ASN
1	A	367	ARG
1	B	280	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	ASN
1	A	265	HIS
1	B	86	ASN
1	B	90	ASN
1	B	265	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 53 ligands modelled in this entry, 4 are monoatomic - leaving 49 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	B	502	1	50,50,50	1.42	7 (14%)	67,82,82	0.89	3 (4%)
4	EDO	A	507	-	3,3,3	0.41	0	2,2,2	0.69	0
4	EDO	A	518	-	3,3,3	0.44	0	2,2,2	0.31	0
3	GOL	A	521	-	5,5,5	0.60	0	5,5,5	0.67	0
4	EDO	A	512	-	3,3,3	0.44	0	2,2,2	0.34	0
4	EDO	B	509	-	3,3,3	0.44	0	2,2,2	0.35	0
3	GOL	A	504	-	5,5,5	0.67	0	5,5,5	0.22	0
3	GOL	A	503	-	5,5,5	0.61	0	5,5,5	0.42	0
4	EDO	B	525	-	3,3,3	0.46	0	2,2,2	0.67	0
4	EDO	A	514	-	3,3,3	0.43	0	2,2,2	0.35	0
4	EDO	A	520	-	3,3,3	0.52	0	2,2,2	0.28	0
3	GOL	A	516	-	5,5,5	0.65	0	5,5,5	0.29	0
4	EDO	B	526	-	3,3,3	0.51	0	2,2,2	0.14	0
2	HEM	A	501	1	50,50,50	1.44	7 (14%)	67,82,82	0.79	0
4	EDO	B	524	-	3,3,3	0.50	0	2,2,2	0.36	0
4	EDO	A	508	-	3,3,3	0.44	0	2,2,2	0.40	0
4	EDO	B	518	-	3,3,3	0.43	0	2,2,2	0.44	0
3	GOL	B	520	-	5,5,5	0.58	0	5,5,5	0.22	0
4	EDO	A	519	-	3,3,3	0.38	0	2,2,2	0.60	0
4	EDO	B	512	-	3,3,3	0.43	0	2,2,2	0.62	0
4	EDO	B	510	-	3,3,3	0.42	0	2,2,2	0.39	0
4	EDO	B	516	-	3,3,3	0.45	0	2,2,2	0.48	0
4	EDO	B	508	-	3,3,3	0.42	0	2,2,2	0.68	0
4	EDO	B	515	-	3,3,3	0.46	0	2,2,2	0.51	0
4	EDO	B	519	-	3,3,3	0.44	0	2,2,2	0.32	0
3	GOL	A	505	-	5,5,5	0.56	0	5,5,5	0.43	0
3	GOL	B	527	-	5,5,5	0.52	0	5,5,5	0.35	0
3	GOL	B	506	-	5,5,5	0.59	0	5,5,5	0.72	0
3	GOL	B	507	-	5,5,5	0.53	0	5,5,5	0.52	0
4	EDO	A	522	-	3,3,3	0.44	0	2,2,2	0.39	0
4	EDO	B	521	-	3,3,3	0.47	0	2,2,2	0.22	0
3	GOL	B	504	-	5,5,5	0.50	0	5,5,5	0.62	0
4	EDO	A	517	-	3,3,3	0.48	0	2,2,2	0.24	0
4	EDO	B	501	-	3,3,3	0.54	0	2,2,2	0.17	0
4	EDO	B	514	-	3,3,3	0.37	0	2,2,2	0.59	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	A	511	-	3,3,3	0.43	0	2,2,2	0.46	0
4	EDO	B	517	-	3,3,3	0.44	0	2,2,2	0.69	0
4	EDO	A	513	-	3,3,3	0.45	0	2,2,2	0.37	0
4	EDO	A	509	-	3,3,3	0.49	0	2,2,2	0.24	0
3	GOL	B	505	-	5,5,5	0.74	0	5,5,5	0.70	0
3	GOL	A	515	-	5,5,5	0.59	0	5,5,5	0.62	0
4	EDO	A	510	-	3,3,3	0.52	0	2,2,2	0.22	0
4	EDO	B	522	-	3,3,3	0.44	0	2,2,2	0.70	0
3	GOL	A	502	-	5,5,5	0.52	0	5,5,5	0.34	0
3	GOL	B	503	-	5,5,5	0.68	0	5,5,5	0.38	0
3	GOL	A	506	-	5,5,5	0.57	0	5,5,5	0.20	0
4	EDO	B	511	-	3,3,3	0.48	0	2,2,2	0.34	0
4	EDO	B	513	-	3,3,3	0.36	0	2,2,2	0.64	0
3	GOL	B	523	-	5,5,5	0.63	0	5,5,5	0.90	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	B	502	1	-	2/14/54/54	-
4	EDO	A	507	-	-	1/1/1/1	-
4	EDO	A	518	-	-	0/1/1/1	-
3	GOL	A	521	-	-	2/4/4/4	-
4	EDO	A	512	-	-	0/1/1/1	-
4	EDO	B	509	-	-	1/1/1/1	-
3	GOL	A	504	-	-	2/4/4/4	-
3	GOL	A	503	-	-	3/4/4/4	-
4	EDO	B	525	-	-	1/1/1/1	-
4	EDO	A	514	-	-	1/1/1/1	-
4	EDO	A	520	-	-	1/1/1/1	-
3	GOL	A	516	-	-	2/4/4/4	-
4	EDO	B	526	-	-	1/1/1/1	-
2	HEM	A	501	1	-	0/14/54/54	-
4	EDO	B	524	-	-	1/1/1/1	-
4	EDO	A	508	-	-	0/1/1/1	-
4	EDO	B	518	-	-	1/1/1/1	-
3	GOL	B	520	-	-	2/4/4/4	-
4	EDO	A	519	-	-	0/1/1/1	-
4	EDO	B	512	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	B	510	-	-	0/1/1/1	-
4	EDO	B	516	-	-	1/1/1/1	-
4	EDO	B	508	-	-	0/1/1/1	-
4	EDO	B	515	-	-	0/1/1/1	-
4	EDO	B	519	-	-	0/1/1/1	-
3	GOL	A	505	-	-	0/4/4/4	-
3	GOL	B	527	-	-	2/4/4/4	-
3	GOL	B	506	-	-	2/4/4/4	-
3	GOL	B	507	-	-	0/4/4/4	-
4	EDO	A	522	-	-	0/1/1/1	-
4	EDO	B	521	-	-	0/1/1/1	-
3	GOL	B	504	-	-	0/4/4/4	-
4	EDO	A	517	-	-	1/1/1/1	-
4	EDO	B	501	-	-	0/1/1/1	-
4	EDO	B	514	-	-	1/1/1/1	-
4	EDO	A	511	-	-	0/1/1/1	-
4	EDO	B	517	-	-	1/1/1/1	-
4	EDO	A	513	-	-	1/1/1/1	-
4	EDO	A	509	-	-	1/1/1/1	-
3	GOL	B	505	-	-	4/4/4/4	-
3	GOL	A	515	-	-	0/4/4/4	-
4	EDO	A	510	-	-	1/1/1/1	-
4	EDO	B	522	-	-	0/1/1/1	-
3	GOL	A	502	-	-	4/4/4/4	-
3	GOL	B	503	-	-	2/4/4/4	-
3	GOL	A	506	-	-	0/4/4/4	-
4	EDO	B	511	-	-	1/1/1/1	-
4	EDO	B	513	-	-	1/1/1/1	-
3	GOL	B	523	-	-	2/4/4/4	-

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	HEM	FE-NB	4.65	2.09	1.94
2	B	502	HEM	FE-NB	4.45	2.08	1.94
2	B	502	HEM	FE-NC	3.76	2.07	1.95
2	A	501	HEM	FE-NC	3.47	2.06	1.95
2	B	502	HEM	FE-NA	3.14	2.05	1.95
2	A	501	HEM	FE-NA	3.07	2.05	1.95
2	B	502	HEM	C4C-NC	-2.52	1.34	1.39
2	A	501	HEM	C4C-NC	-2.40	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	HEM	C4D-ND	-2.36	1.36	1.40
2	A	501	HEM	FE-ND	2.34	2.02	1.94
2	B	502	HEM	FE-ND	2.30	2.02	1.94
2	A	501	HEM	C1C-NC	-2.26	1.35	1.39
2	B	502	HEM	C4D-ND	-2.08	1.36	1.40
2	B	502	HEM	C4A-C3A	2.04	1.47	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	502	HEM	CAD-C3D-C4D	2.33	128.75	124.70
2	B	502	HEM	C1B-NB-C4B	2.16	107.77	105.21
2	B	502	HEM	C3B-C2B-C1B	-2.03	104.88	106.41

There are no chirality outliers.

All (47) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	GOL	O1-C1-C2-C3
3	A	502	GOL	C1-C2-C3-O3
3	A	521	GOL	C1-C2-C3-O3
3	A	521	GOL	O2-C2-C3-O3
3	B	520	GOL	O1-C1-C2-O2
3	B	527	GOL	O2-C2-C3-O3
3	B	506	GOL	O1-C1-C2-O2
3	B	523	GOL	O1-C1-C2-O2
3	A	503	GOL	C1-C2-C3-O3
3	A	516	GOL	O1-C1-C2-C3
3	B	503	GOL	C1-C2-C3-O3
3	B	505	GOL	O1-C1-C2-C3
3	B	505	GOL	C1-C2-C3-O3
3	B	506	GOL	O1-C1-C2-C3
3	B	520	GOL	O1-C1-C2-C3
3	B	523	GOL	O1-C1-C2-C3
3	B	527	GOL	C1-C2-C3-O3
3	A	502	GOL	O1-C1-C2-O2
3	A	502	GOL	O2-C2-C3-O3
3	A	516	GOL	O1-C1-C2-O2
3	B	505	GOL	O2-C2-C3-O3
4	A	510	EDO	O1-C1-C2-O2
4	B	514	EDO	O1-C1-C2-O2
4	B	524	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
4	A	509	EDO	O1-C1-C2-O2
4	A	513	EDO	O1-C1-C2-O2
3	A	503	GOL	O2-C2-C3-O3
3	B	503	GOL	O2-C2-C3-O3
3	A	504	GOL	O1-C1-C2-O2
3	B	505	GOL	O1-C1-C2-O2
4	B	509	EDO	O1-C1-C2-O2
4	B	513	EDO	O1-C1-C2-O2
4	B	518	EDO	O1-C1-C2-O2
3	A	504	GOL	C1-C2-C3-O3
4	B	526	EDO	O1-C1-C2-O2
4	A	514	EDO	O1-C1-C2-O2
4	B	516	EDO	O1-C1-C2-O2
2	B	502	HEM	CAD-CBD-CGD-O2D
4	A	507	EDO	O1-C1-C2-O2
4	A	517	EDO	O1-C1-C2-O2
4	B	511	EDO	O1-C1-C2-O2
4	B	517	EDO	O1-C1-C2-O2
4	B	525	EDO	O1-C1-C2-O2
4	B	512	EDO	O1-C1-C2-O2
2	B	502	HEM	CAD-CBD-CGD-O1D
3	A	503	GOL	O1-C1-C2-O2
4	A	520	EDO	O1-C1-C2-O2

There are no ring outliers.

23 monomers are involved in 39 short contacts:

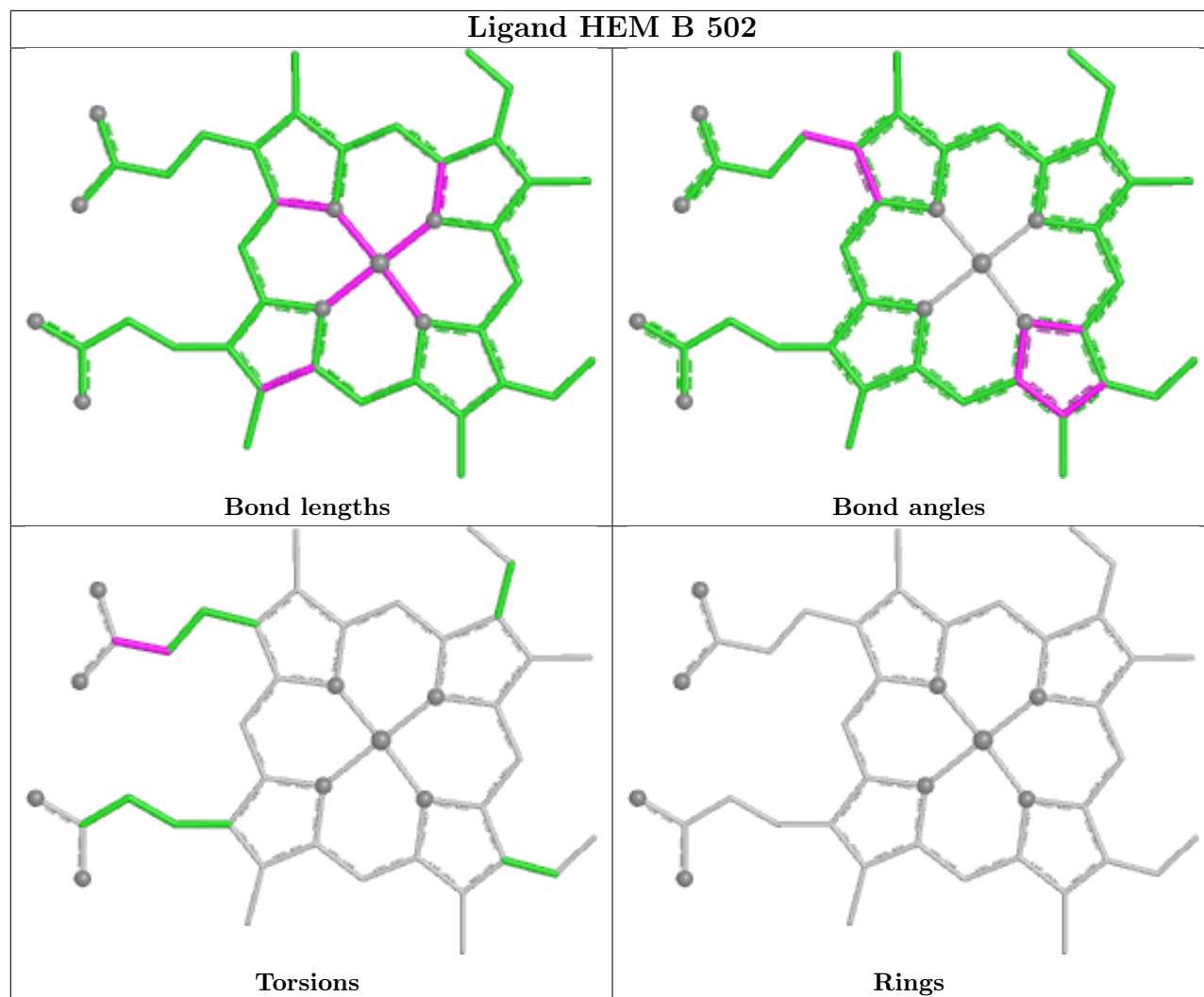
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	502	HEM	4	0
4	A	507	EDO	2	0
4	A	518	EDO	1	0
3	A	521	GOL	3	0
4	B	525	EDO	1	0
4	A	514	EDO	1	0
4	A	520	EDO	1	0
4	B	526	EDO	2	0
2	A	501	HEM	1	0
3	B	520	GOL	3	0
4	A	519	EDO	2	0
4	B	508	EDO	1	0
4	B	515	EDO	1	0
3	B	527	GOL	1	0

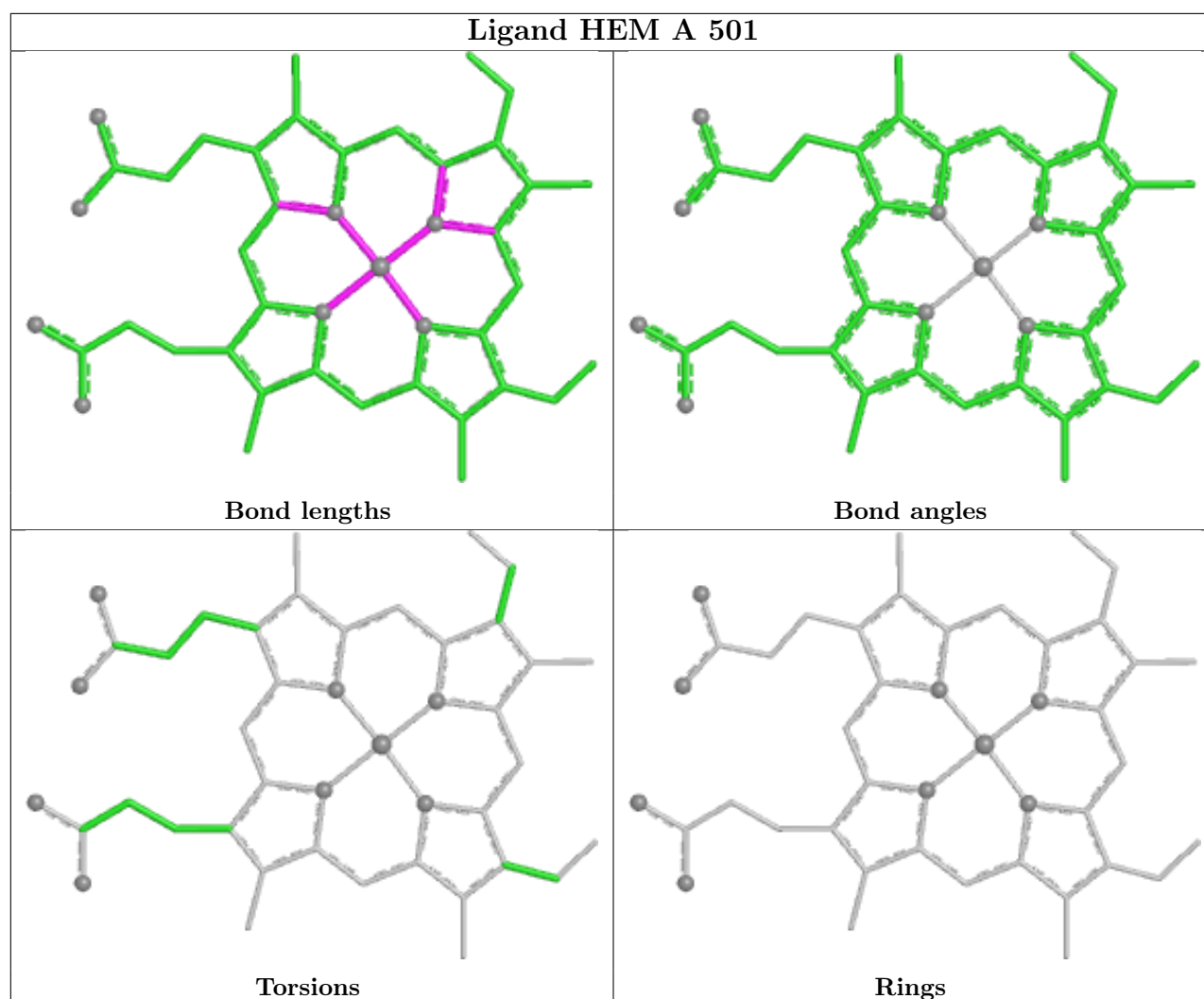
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	507	GOL	1	0
3	B	504	GOL	1	0
4	A	517	EDO	1	0
4	B	501	EDO	3	0
4	B	514	EDO	1	0
4	A	511	EDO	1	0
4	A	510	EDO	2	0
4	B	511	EDO	4	0
4	B	513	EDO	1	0

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 [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	394/414 (95%)	-0.69	0	100	100	9, 23, 47, 60	10 (2%)
1	B	394/414 (95%)	-0.79	1 (0%)	90	89	8, 20, 41, 64	11 (2%)
All	All	788/828 (95%)	-0.74	1 (0%)	92	91	8, 22, 44, 64	21 (2%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	401	PRO	2.3

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 oligosaccharides 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(Å ²)	Q<0.9
4	EDO	A	522	4/4	0.64	0.14	53,63,73,73	10
3	GOL	B	520	6/6	0.66	0.13	52,63,77,78	14
4	EDO	A	520	4/4	0.71	0.16	39,59,71,75	0
3	GOL	B	527	6/6	0.71	0.16	33,45,59,62	14

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	EDO	B	521	4/4	0.71	0.16	42,56,70,70	10
4	EDO	B	514	4/4	0.73	0.16	37,52,65,65	0
4	EDO	A	508	4/4	0.73	0.14	39,54,65,72	10
3	GOL	A	503	6/6	0.74	0.14	31,46,67,67	14
4	EDO	B	518	4/4	0.75	0.16	28,37,45,54	10
3	GOL	B	506	6/6	0.75	0.13	28,35,44,45	14
4	EDO	B	512	4/4	0.76	0.15	25,31,38,46	10
3	GOL	A	515	6/6	0.77	0.13	32,52,68,69	14
4	EDO	B	509	4/4	0.77	0.12	58,71,79,85	0
3	GOL	B	505	6/6	0.78	0.14	30,40,52,52	14
4	EDO	A	518	4/4	0.78	0.15	32,41,55,66	10
4	EDO	B	501	4/4	0.78	0.15	17,28,39,47	10
4	EDO	A	519	4/4	0.78	0.13	30,36,45,54	10
4	EDO	A	510	4/4	0.79	0.14	24,33,44,53	10
4	EDO	B	526	4/4	0.79	0.22	42,51,84,101	0
4	EDO	B	524	4/4	0.80	0.14	38,46,57,69	0
4	EDO	A	517	4/4	0.80	0.14	44,53,62,75	0
4	EDO	B	510	4/4	0.81	0.11	36,46,55,64	10
4	EDO	B	525	4/4	0.81	0.11	45,56,66,78	10
4	EDO	B	515	4/4	0.81	0.11	53,63,65,70	0
4	EDO	B	522	4/4	0.82	0.15	45,55,68,68	0
3	GOL	B	507	6/6	0.82	0.18	29,50,61,61	0
4	EDO	B	508	4/4	0.82	0.15	36,44,47,51	10
3	GOL	A	506	6/6	0.82	0.15	34,60,77,77	0
4	EDO	A	511	4/4	0.83	0.14	46,58,69,71	0
4	EDO	A	512	4/4	0.83	0.09	50,61,68,75	0
4	EDO	B	517	4/4	0.83	0.11	54,65,67,75	0
4	EDO	B	519	4/4	0.84	0.13	37,49,58,70	10
3	GOL	B	503	6/6	0.84	0.12	21,35,41,42	14
4	EDO	A	507	4/4	0.84	0.11	37,45,53,53	10
4	EDO	A	509	4/4	0.85	0.16	46,60,67,72	0
4	EDO	B	516	4/4	0.86	0.10	50,60,71,78	0
4	EDO	A	513	4/4	0.86	0.12	31,45,60,72	10
4	EDO	B	513	4/4	0.86	0.15	35,45,65,78	0
3	GOL	A	505	6/6	0.87	0.13	29,47,65,65	0
3	GOL	B	523	6/6	0.87	0.14	21,39,47,47	14
4	EDO	A	514	4/4	0.87	0.11	31,43,52,61	10
3	GOL	A	502	6/6	0.87	0.10	32,39,56,56	0
3	GOL	B	504	6/6	0.87	0.11	24,40,51,54	14
3	GOL	A	521	6/6	0.88	0.12	17,31,41,49	14
6	MG	B	528	1/1	0.88	0.13	58,58,58,58	0
4	EDO	B	511	4/4	0.89	0.14	31,41,75,77	0

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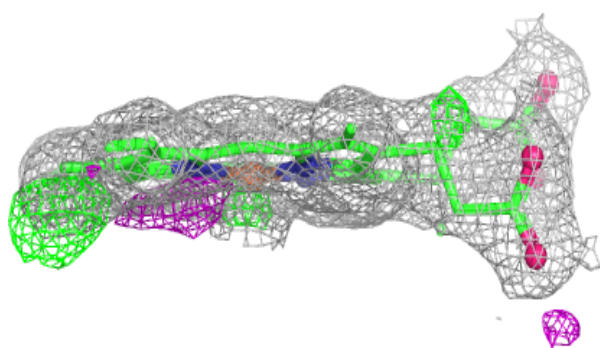
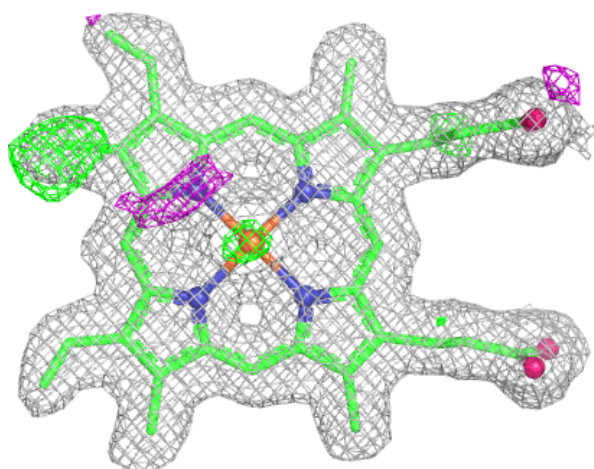
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	GOL	A	516	6/6	0.90	0.13	18,45,55,55	14
5	CL	A	523	1/1	0.94	0.19	41,41,41,41	0
6	MG	A	524	1/1	0.94	0.08	45,45,45,45	0
3	GOL	A	504	6/6	0.94	0.07	28,39,50,58	0
2	HEM	B	502	43/43	0.97	0.06	11,16,25,27	0
7	NI	B	529	1/1	0.97	0.12	51,51,51,51	0
2	HEM	A	501	43/43	0.98	0.06	14,18,26,29	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.

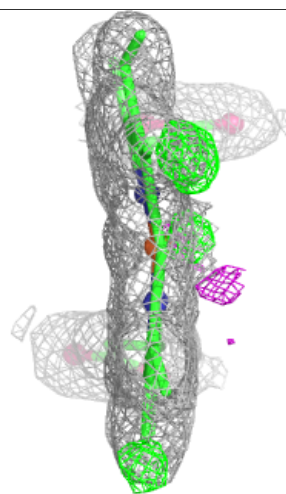
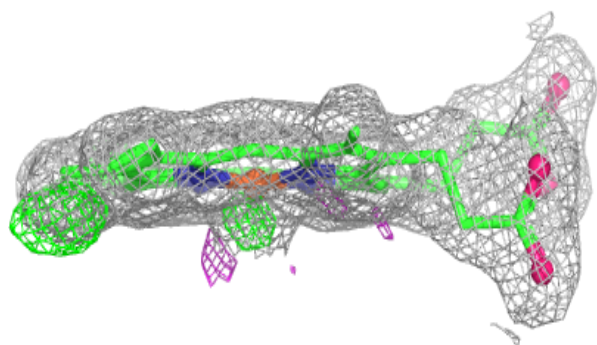
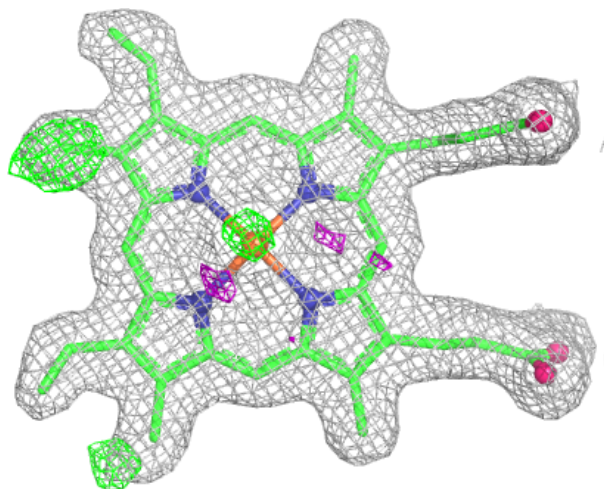
Electron density around HEM B 502:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM A 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.