



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:39 PM UTC

PDB ID : 5LI7 / pdb_00005li7
Title : Crystal structure of Mycobacterium tuberculosis CYP126A1 in complex with
1-(3-(1H-imidazol-1-yl)propyl)-3-((3s,5s,7s)-adamantan-1-yl)urea
Authors : Levy, C.; Munro, A.W.; Leys, D.
Deposited on : 2016-07-14
Resolution : 1.58 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

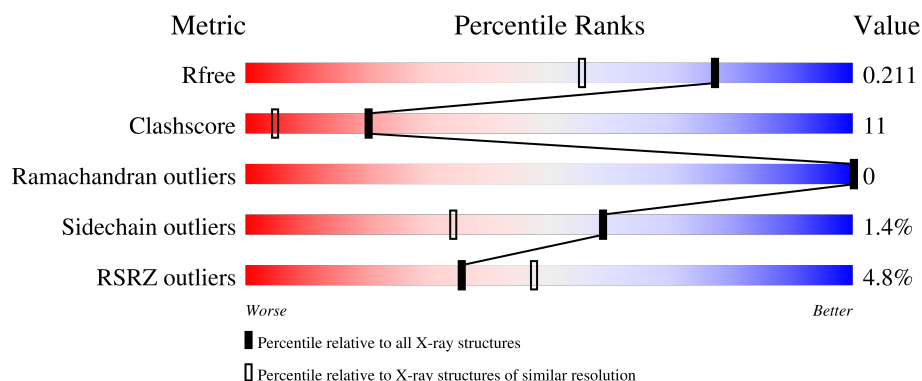
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.58 Å.

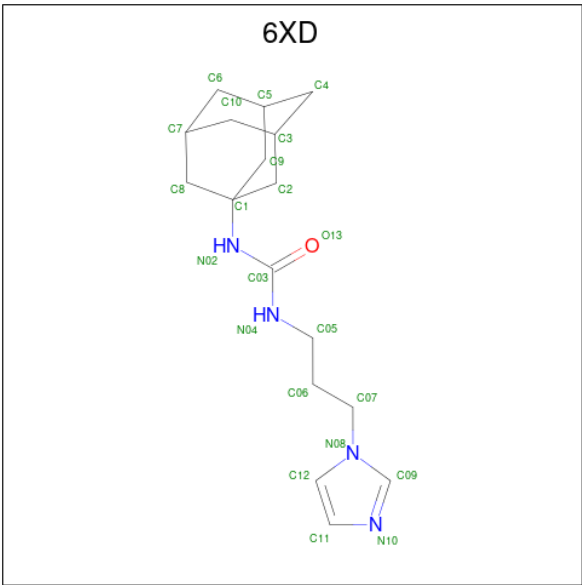
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1094 (1.58-1.58)
Clashscore	190562	1105 (1.58-1.58)
Ramachandran outliers	187476	1082 (1.58-1.58)
Sidechain outliers	187428	1081 (1.58-1.58)
RSRZ outliers	180081	1094 (1.58-1.58)

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	 3% 73% 15% • 10%
1	B	414	 5% 74% 14% • 10%



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			22	17	4	1		
3	B	1	Total	C	N	O	0	0
			22	17	4	1		

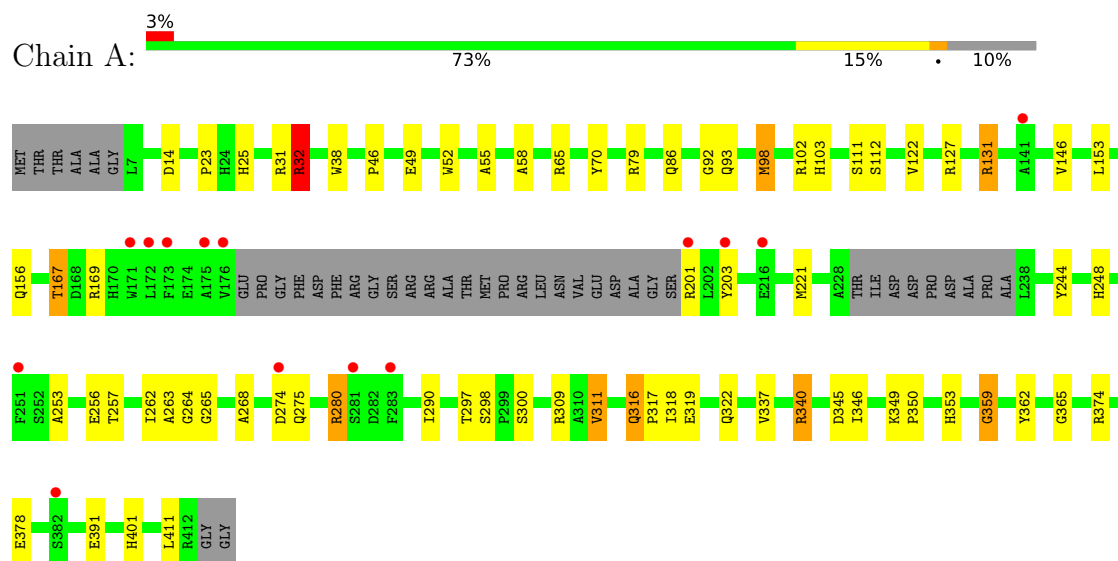
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	545	Total	O	0	0
			545	545		
4	B	453	Total	O	0	0
			453	453		

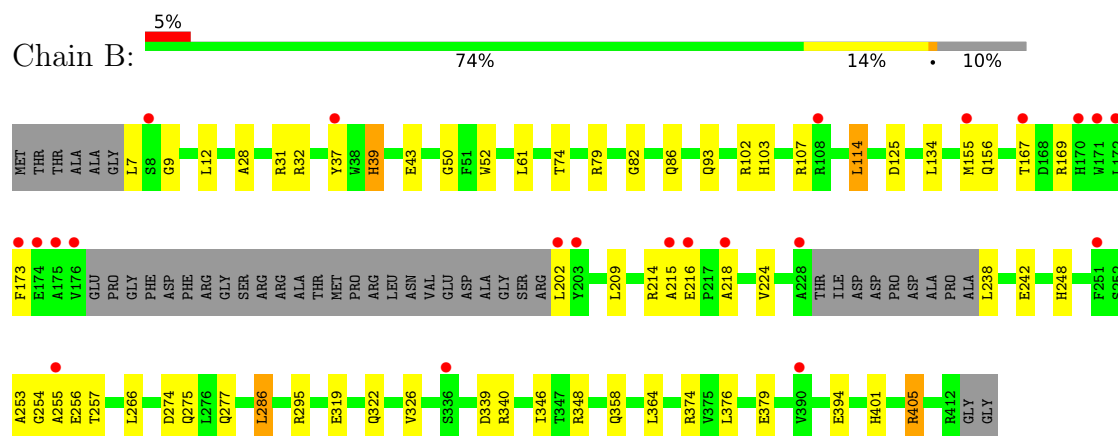
3 Residue-property plots [i](#)

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: Putative cytochrome P450 126



• Molecule 1: Putative cytochrome P450 126



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.25Å 69.91Å 226.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	57.31 – 1.58 57.31 – 1.58	Depositor EDS
% Data completeness (in resolution range)	100.0 (57.31-1.58) 99.8 (57.31-1.58)	Depositor EDS
R_{merge}	0.02	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 1.58Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.170 , 0.203 0.178 , 0.211	Depositor DCC
R_{free} test set	6486 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	17.2	Xtriage
Anisotropy	0.011	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 42.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7108	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% 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, 6XD

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	1.57	19/3080 (0.6%)	1.30	13/4183 (0.3%)
1	B	1.42	6/3048 (0.2%)	1.14	3/4141 (0.1%)
All	All	1.50	25/6128 (0.4%)	1.23	16/8324 (0.2%)

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	98	MET	CB-CG	-8.36	1.27	1.52
1	A	318	ILE	CG1-CD1	-8.21	1.19	1.51
1	A	38	TRP	C-O	6.98	1.32	1.24
1	A	316	GLN	CD-OE1	6.54	1.35	1.23
1	A	49	GLU	CB-CG	-6.53	1.32	1.52
1	A	127	ARG	CB-CG	-6.42	1.33	1.52
1	B	254	GLY	C-O	6.34	1.32	1.23
1	A	23	PRO	CA-CB	-6.14	1.47	1.53
1	B	39	HIS	N-CA	-5.75	1.39	1.46
1	A	262	ILE	CA-CB	-5.72	1.47	1.54
1	A	378	GLU	N-CA	5.69	1.53	1.46
1	A	268	ALA	CA-CB	5.69	1.62	1.53
1	B	218	ALA	CA-CB	-5.68	1.43	1.53
1	A	265	GLY	CA-C	5.62	1.58	1.52
1	A	411	LEU	N-CA	-5.58	1.39	1.46
1	B	74	THR	CA-CB	5.58	1.61	1.53
1	A	92	GLY	C-O	5.57	1.32	1.24
1	A	359	GLY	N-CA	5.34	1.53	1.45
1	A	146	VAL	CA-CB	-5.25	1.48	1.54
1	A	112	SER	N-CA	5.25	1.53	1.46
1	A	14	ASP	N-CA	5.20	1.53	1.46
1	A	290	ILE	CA-CB	-5.18	1.48	1.54
1	B	224	VAL	N-CA	-5.18	1.40	1.46
1	A	317	PRO	N-CA	-5.13	1.41	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	326	VAL	CA-C	-5.06	1.46	1.52

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	127	ARG	CG-CD-NE	-8.22	93.90	112.00
1	A	153	LEU	CA-C-N	-6.60	112.97	119.64
1	A	153	LEU	C-N-CA	-6.60	112.97	119.64
1	A	340	ARG	NE-CZ-NH1	5.73	127.23	121.50
1	A	311	VAL	CA-C-O	-5.66	116.21	120.96
1	A	25	HIS	N-CA-C	5.58	117.37	111.28
1	A	391	GLU	CA-C-N	-5.49	114.11	119.76
1	A	391	GLU	C-N-CA	-5.49	114.11	119.76
1	A	263	ALA	O-C-N	-5.45	116.45	122.07
1	A	55	ALA	N-CA-C	5.31	120.03	113.50
1	A	32	ARG	CB-CG-CD	5.23	123.33	111.30
1	A	280	ARG	CG-CD-NE	-5.15	100.67	112.00
1	A	374	ARG	CG-CD-NE	-5.12	100.74	112.00
1	B	214	ARG	CA-C-N	5.06	127.02	120.44
1	B	214	ARG	C-N-CA	5.06	127.02	120.44
1	B	209	LEU	N-CA-C	-5.05	105.68	111.14

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	3006	0	2957	77	0
1	B	2974	0	2929	68	0
2	A	43	0	30	2	0
2	B	43	0	30	2	0
3	A	22	0	0	3	0
3	B	22	0	0	1	0
4	A	545	0	0	36	3
4	B	453	0	0	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	7108	0	5946	136	3

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 11.

All (136) 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:B:274:ASP:HB3	4:B:932:HOH:O	1.32	1.21
1:A:316:GLN:HG3	4:A:895:HOH:O	1.43	1.14
1:A:274:ASP:HB3	4:A:982:HOH:O	1.47	1.11
1:A:65:ARG:NE	4:A:603:HOH:O	1.80	1.09
1:A:350:PRO:O	4:A:601:HOH:O	1.71	1.07
1:A:79:ARG:HH21	1:B:93:GLN:NE2	1.53	1.06
1:B:82:GLY:O	4:B:601:HOH:O	1.75	1.03
1:A:353:HIS:O	4:A:602:HOH:O	1.79	1.01
1:A:401:HIS:HD2	4:A:646:HOH:O	1.44	0.99
1:B:7:LEU:N	4:B:604:HOH:O	1.97	0.98
1:A:337:VAL:HG23	4:A:904:HOH:O	1.63	0.95
1:A:58:ALA:HB1	4:A:1028:HOH:O	1.67	0.93
1:A:264:GLY:O	4:A:604:HOH:O	1.87	0.92
1:A:340:ARG:NH2	4:A:606:HOH:O	2.02	0.91
1:A:221:MET:HE2	4:A:974:HOH:O	1.74	0.87
1:B:12:LEU:H	1:B:39:HIS:HE1	1.23	0.85
1:A:248[B]:HIS:HD2	3:A:502:6XD:C7	1.88	0.85
1:A:79:ARG:NH2	1:B:93:GLN:NE2	2.24	0.85
1:A:79:ARG:HH21	1:B:93:GLN:HE22	1.20	0.84
1:B:50:GLY:O	4:B:602:HOH:O	1.94	0.84
1:A:122:VAL:HG13	4:A:927:HOH:O	1.78	0.83
1:A:221:MET:CE	4:A:974:HOH:O	2.27	0.83
1:A:70:TYR:OH	4:A:605:HOH:O	1.98	0.81
1:A:401:HIS:CD2	4:A:646:HOH:O	2.22	0.81
1:A:221:MET:HB3	4:A:974:HOH:O	1.80	0.81
1:B:238:LEU:N	4:B:607:HOH:O	2.13	0.79
1:B:103:HIS:HE1	2:B:501:HEM:O1D	1.67	0.77
1:A:274:ASP:OD1	4:A:607:HOH:O	2.03	0.76
1:A:244:TYR:OH	1:A:248[A]:HIS:HE1	1.69	0.76
1:A:362:TYR:OH	4:A:608:HOH:O	2.03	0.75
1:A:65:ARG:HA	4:A:980:HOH:O	1.84	0.75
1:B:238:LEU:N	4:B:609:HOH:O	2.21	0.74
1:A:244:TYR:CZ	1:A:248[A]:HIS:HE1	2.05	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:TYR:CZ	1:A:248[A]:HIS:CE1	2.76	0.73
1:B:86:GLN:HG2	4:B:621:HOH:O	1.88	0.73
1:B:155:MET:HE1	1:B:255:ALA:HB2	1.70	0.73
1:B:277:GLN:NE2	4:B:603:HOH:O	1.97	0.72
1:A:201:ARG:NH2	4:A:610:HOH:O	2.23	0.72
1:B:7:LEU:CA	4:B:604:HOH:O	2.38	0.71
1:B:253:ALA:HA	1:B:257[B]:THR:HG22	1.72	0.71
1:B:202:LEU:N	4:B:610:HOH:O	2.25	0.70
1:A:79:ARG:NH1	4:A:609:HOH:O	2.21	0.70
1:A:79:ARG:NH2	1:B:242:GLU:OE2	2.25	0.69
1:B:295:ARG:O	4:B:605:HOH:O	2.11	0.68
1:B:9:GLY:O	4:B:606:HOH:O	2.11	0.68
1:A:79:ARG:NH2	1:B:93:GLN:HE22	1.90	0.67
1:B:7:LEU:C	4:B:604:HOH:O	2.37	0.67
1:B:202:LEU:N	4:B:612:HOH:O	2.30	0.65
1:A:248[B]:HIS:CD2	3:A:502:6XD:C7	2.77	0.64
1:A:103:HIS:HE1	2:A:501:HEM:O1D	1.81	0.64
1:A:31:ARG:HH21	1:A:32:ARG:NH2	1.95	0.64
1:A:359:GLY:HA3	4:A:980:HOH:O	1.98	0.64
1:B:86:GLN:CG	4:B:621:HOH:O	2.45	0.63
1:B:43:GLU:HG2	4:B:619:HOH:O	1.99	0.62
1:B:319:GLU:H	1:B:322:GLN:NE2	1.98	0.62
1:A:275:GLN:NE2	1:A:346:ILE:H	1.99	0.61
1:B:102[A]:ARG:HH11	1:B:102[A]:ARG:HG3	1.64	0.61
1:B:156:GLN:NE2	1:B:169:ARG:HH11	1.99	0.60
1:B:52:TRP:HE1	1:B:322:GLN:NE2	1.99	0.60
1:B:156:GLN:HE22	1:B:169:ARG:HH11	1.50	0.59
1:A:253:ALA:HA	1:A:257[B]:THR:HG22	1.82	0.59
1:A:31:ARG:HH21	1:A:32:ARG:HH22	1.49	0.58
1:A:131:ARG:NH2	4:A:617:HOH:O	2.36	0.58
1:B:275:GLN:NE2	1:B:346:ILE:H	2.01	0.58
1:A:31:ARG:HE	1:A:32:ARG:NH1	2.01	0.58
1:A:79:ARG:HH21	1:B:93:GLN:HE21	1.46	0.58
1:A:103:HIS:HD2	4:A:654:HOH:O	1.86	0.58
1:A:203:TYR:HD1	1:A:244:TYR:CZ	2.22	0.57
1:A:253:ALA:O	1:A:257[B]:THR:HG22	2.05	0.57
1:B:253:ALA:O	1:B:257[B]:THR:HG22	2.03	0.57
1:B:376:LEU:C	1:B:376:LEU:HD13	2.30	0.56
1:B:155:MET:CE	1:B:255:ALA:HB2	2.35	0.56
1:A:274:ASP:OD1	1:A:274:ASP:N	2.39	0.56
1:B:102[A]:ARG:HG3	1:B:102[A]:ARG:NH1	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:ARG:HE	1:A:32:ARG:HH12	1.53	0.56
1:B:12:LEU:H	1:B:39:HIS:CE1	2.14	0.56
1:A:65:ARG:CZ	4:A:603:HOH:O	2.38	0.55
1:A:52:TRP:HE1	1:A:322:GLN:NE2	2.04	0.55
1:A:79:ARG:HH22	1:B:242:GLU:CD	2.14	0.54
1:B:125:ASP:OD2	4:B:608:HOH:O	2.18	0.54
1:B:394:GLU:OE1	1:B:405:ARG:NH1	2.40	0.54
1:B:275:GLN:HE21	1:B:346:ILE:HG12	1.72	0.54
1:A:93:GLN:HE22	1:B:79:ARG:HE	1.55	0.54
1:A:111[A]:SER:HB2	4:A:753:HOH:O	2.08	0.53
1:A:221:MET:CB	4:A:974:HOH:O	2.48	0.51
1:B:253:ALA:HB2	3:B:502:6XD:C11	2.40	0.51
1:A:365:GLY:HA3	2:A:501:HEM:C3C	2.46	0.51
1:A:275:GLN:HE22	1:A:345:ASP:HA	1.77	0.50
1:B:155:MET:HG2	1:B:173:PHE:CE1	2.46	0.50
1:A:79:ARG:NH2	1:B:93:GLN:HE21	2.05	0.50
1:A:311:VAL:CG2	4:A:605:HOH:O	2.59	0.50
1:A:319:GLU:H	1:A:322:GLN:NE2	2.10	0.50
1:B:61:LEU:HD11	1:B:358:GLN:HG2	1.93	0.50
1:A:79:ARG:HG3	1:A:79:ARG:HH11	1.78	0.49
1:A:311:VAL:HG22	4:A:605:HOH:O	2.12	0.49
1:A:65:ARG:NH2	4:A:603:HOH:O	2.46	0.49
1:A:256[B]:GLU:HG2	1:A:401:HIS:CD2	2.47	0.49
1:A:316:GLN:NE2	4:A:623:HOH:O	2.46	0.48
1:B:256[B]:GLU:HG2	1:B:401:HIS:CD2	2.49	0.48
1:A:300:SER:C	4:A:612:HOH:O	2.57	0.47
1:B:215:ALA:HB2	4:B:819:HOH:O	2.13	0.47
1:A:167:THR:HB	4:A:931:HOH:O	2.13	0.47
1:B:31:ARG:HH21	1:B:32:ARG:NH2	2.11	0.47
1:A:309:ARG:NH2	4:A:624:HOH:O	2.48	0.47
1:B:107:ARG:HG3	1:B:364[A]:LEU:HD11	1.97	0.46
1:A:46:PRO:HB3	1:A:86[B]:GLN:CG	2.45	0.46
1:A:349:LYS:HE3	4:A:653:HOH:O	2.15	0.46
1:B:253:ALA:O	1:B:257[B]:THR:CG2	2.64	0.46
1:B:7:LEU:HD13	1:B:37:TYR:CE2	2.50	0.46
1:A:297:THR:O	1:A:298:SER:C	2.59	0.46
1:B:253:ALA:CA	1:B:257[B]:THR:HG22	2.43	0.45
1:B:348:ARG:HB3	4:B:623:HOH:O	2.16	0.45
1:B:134:LEU:HD13	1:B:379:GLU:C	2.42	0.45
1:A:156:GLN:NE2	1:A:169:ARG:HH11	2.15	0.45
1:B:286:LEU:HD13	1:B:374:ARG:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:31:ARG:HE	1:B:32:ARG:HH12	1.65	0.44
1:B:102[A]:ARG:HH11	1:B:102[A]:ARG:CG	2.24	0.44
1:B:340:ARG:NH2	4:B:620:HOH:O	2.50	0.44
1:A:221:MET:CG	4:A:974:HOH:O	2.66	0.43
1:A:253:ALA:O	1:A:257[B]:THR:CG2	2.66	0.43
1:B:266:LEU:HD12	1:B:266:LEU:HA	1.81	0.43
1:B:202:LEU:HD21	1:B:248[A]:HIS:CE1	2.53	0.43
1:B:31:ARG:HE	1:B:32:ARG:NH1	2.17	0.43
1:A:275:GLN:HE22	1:A:346:ILE:H	1.64	0.42
1:B:31:ARG:HH21	1:B:32:ARG:HH22	1.68	0.42
1:B:61:LEU:HD11	1:B:358:GLN:CG	2.49	0.42
1:A:253:ALA:HB2	3:A:502:6XD:C11	2.50	0.42
1:B:103:HIS:CE1	2:B:501:HEM:O1D	2.58	0.42
1:A:79:ARG:NH1	1:A:79:ARG:CG	2.82	0.42
1:B:339:ASP:O	1:B:340:ARG:C	2.63	0.41
1:B:114:LEU:HD23	1:B:114:LEU:HA	1.90	0.41
1:A:79:ARG:HH11	1:A:79:ARG:CG	2.33	0.41
1:A:98:MET:HE2	1:A:102[B]:ARG:NH1	2.36	0.41
1:B:28:ALA:O	1:B:32:ARG:HG2	2.21	0.40
1:A:203:TYR:CD1	1:A:244:TYR:CE2	3.09	0.40
1:A:244:TYR:OH	1:A:248[A]:HIS:CE1	2.60	0.40

All (3) 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)
4:A:749:HOH:O	4:A:844:HOH:O[4_555]	2.05	0.15
4:A:689:HOH:O	4:A:805:HOH:O[4_555]	2.13	0.07
4:A:1065:HOH:O	4:A:1103:HOH:O[4_545]	2.15	0.05

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	375/414 (91%)	363 (97%)	12 (3%)	0	100	100
1	B	371/414 (90%)	359 (97%)	12 (3%)	0	100	100
All	All	746/828 (90%)	722 (97%)	24 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	320/342 (94%)	316 (99%)	4 (1%)	61	37
1	B	316/342 (92%)	311 (98%)	5 (2%)	55	28
All	All	636/684 (93%)	627 (99%)	9 (1%)	59	34

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	ARG
1	A	131	ARG
1	A	167	THR
1	A	280	ARG
1	B	114	LEU
1	B	167	THR
1	B	216	GLU
1	B	286	LEU
1	B	405	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	HIS
1	A	93	GLN
1	A	103	HIS
1	A	156	GLN

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Mol	Chain	Res	Type
1	A	227	ASN
1	A	272	ASN
1	A	275	GLN
1	A	322	GLN
1	A	358	GLN
1	A	401	HIS
1	B	39	HIS
1	B	93	GLN
1	B	103	HIS
1	B	156	GLN
1	B	227	ASN
1	B	275	GLN
1	B	322	GLN
1	B	401	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](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	6XD	A	502	2	25,25,25	1.56	6 (24%)	36,36,36	2.05	9 (25%)
3	6XD	B	502	2	25,25,25	1.65	6 (24%)	36,36,36	2.60	13 (36%)
2	HEM	A	501	3,1	50,50,50	1.70	13 (26%)	67,82,82	1.78	14 (20%)
2	HEM	B	501	3,1	50,50,50	1.54	10 (20%)	67,82,82	1.62	15 (22%)

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
3	6XD	A	502	2	-	0/12/39/39	0/5/4/4
3	6XD	B	502	2	-	1/12/39/39	0/5/4/4
2	HEM	A	501	3,1	-	0/14/54/54	-
2	HEM	B	501	3,1	-	2/14/54/54	-

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	HEM	FE-NB	5.30	2.11	1.94
3	B	502	6XD	C03-N04	4.32	1.44	1.35
2	B	501	HEM	FE-ND	3.72	2.06	1.94
2	B	501	HEM	C3D-C2D	3.36	1.44	1.36
2	A	501	HEM	FE-ND	3.34	2.05	1.94
3	A	502	6XD	C03-N04	3.25	1.41	1.35
2	A	501	HEM	CHA-C1A	-3.02	1.32	1.39
3	A	502	6XD	O13-C03	-2.95	1.17	1.23
2	A	501	HEM	FE-NA	2.90	2.04	1.95
2	A	501	HEM	C1B-NB	-2.82	1.35	1.40
3	B	502	6XD	C11-N10	2.81	1.47	1.37
2	B	501	HEM	FE-NB	2.80	2.03	1.94
3	B	502	6XD	C03-N02	2.70	1.40	1.35
2	A	501	HEM	C3C-C4C	2.69	1.50	1.46
3	B	502	6XD	C09-N08	2.64	1.41	1.35
2	A	501	HEM	C3D-C2D	2.52	1.42	1.36
3	A	502	6XD	C07-N08	2.49	1.55	1.47
2	A	501	HEM	C4D-C3D	-2.42	1.40	1.45
3	B	502	6XD	C6-C5	-2.38	1.46	1.52
2	B	501	HEM	CMD-C2D	2.34	1.55	1.50
3	A	502	6XD	C03-N02	2.31	1.40	1.35
2	A	501	HEM	C1C-C2C	-2.28	1.40	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	6XD	C8-C1	-2.22	1.48	1.53
2	A	501	HEM	CAA-C2A	2.21	1.57	1.51
2	B	501	HEM	CMA-C3A	2.19	1.55	1.50
2	B	501	HEM	C3B-C2B	-2.15	1.32	1.37
2	B	501	HEM	CMB-C2B	2.15	1.55	1.50
2	A	501	HEM	CMC-C2C	2.13	1.55	1.50
3	B	502	6XD	C8-C1	-2.12	1.49	1.53
2	A	501	HEM	FE-NC	2.06	2.02	1.95
2	A	501	HEM	C4C-NC	-2.06	1.35	1.39
2	B	501	HEM	CMC-C2C	2.04	1.54	1.50
2	B	501	HEM	C4B-NB	-2.02	1.34	1.38
3	A	502	6XD	C11-N10	2.02	1.44	1.37
2	B	501	HEM	CAB-C3B	2.01	1.52	1.47

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502	6XD	C9-C1-C2	6.22	116.82	108.95
3	B	502	6XD	C10-C3-C4	-6.17	97.97	109.69
3	B	502	6XD	C6-C5-C9	6.04	122.31	109.05
3	B	502	6XD	C1-C9-C5	-6.02	103.51	109.92
2	B	501	HEM	C4D-ND-C1D	4.85	110.95	105.21
3	B	502	6XD	C9-C1-C2	4.60	114.77	108.95
2	A	501	HEM	C3C-C2C-C1C	4.57	111.37	107.05
3	B	502	6XD	C7-C6-C5	-4.51	100.50	109.90
2	A	501	HEM	C3B-C4B-NB	-4.44	106.28	109.47
2	A	501	HEM	C4D-ND-C1D	4.40	110.42	105.21
3	A	502	6XD	C6-C5-C9	3.87	117.53	109.05
2	B	501	HEM	C3B-C2B-C1B	3.65	109.15	106.41
3	A	502	6XD	C1-C9-C5	-3.64	106.03	109.92
2	A	501	HEM	C4C-C3C-C2C	-3.64	103.66	106.81
2	A	501	HEM	CHB-C1B-NB	3.42	128.59	124.37
2	B	501	HEM	C4A-C3A-C2A	3.36	110.67	106.82
2	A	501	HEM	CHD-C4C-NC	3.35	128.10	124.45
2	A	501	HEM	C1B-NB-C4B	3.34	109.16	105.21
3	B	502	6XD	C10-C3-C2	-3.27	101.87	109.05
3	B	502	6XD	C3-C4-C5	3.22	116.61	109.90
3	A	502	6XD	C10-C3-C2	-3.19	102.04	109.05
2	B	501	HEM	O2A-CGA-CBA	3.14	123.93	114.00
3	B	502	6XD	C3-C10-C7	3.01	116.18	109.90
3	B	502	6XD	C4-C5-C9	-2.94	102.58	109.05
2	A	501	HEM	O1D-CGD-CBD	-2.93	113.79	123.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502	6XD	C10-C7-C8	2.93	115.47	109.05
2	B	501	HEM	C2D-C1D-ND	-2.86	106.59	109.90
3	A	502	6XD	C10-C3-C4	-2.84	104.30	109.69
2	B	501	HEM	CHD-C1D-ND	2.83	127.47	124.42
2	B	501	HEM	CHA-C4D-ND	2.83	127.87	124.37
2	A	501	HEM	CHC-C4B-C3B	2.81	130.67	125.07
2	A	501	HEM	C2D-C1D-ND	-2.76	106.71	109.90
2	A	501	HEM	C4B-C3B-C2B	2.71	109.77	107.28
3	B	502	6XD	C8-C1-N02	-2.68	102.85	109.87
2	B	501	HEM	C3D-C4D-ND	-2.65	107.26	110.17
3	B	502	6XD	C12-C11-N10	-2.61	104.95	109.92
3	A	502	6XD	C12-N08-C09	2.60	109.95	106.71
2	B	501	HEM	CMB-C2B-C1B	-2.48	121.16	125.03
3	A	502	6XD	C4-C5-C9	-2.47	103.62	109.05
2	A	501	HEM	CHA-C4D-C3D	2.44	129.72	125.23
2	B	501	HEM	CHC-C1C-NC	-2.44	121.80	124.45
2	A	501	HEM	C3D-C4D-ND	-2.42	107.51	110.17
3	B	502	6XD	O13-C03-N02	-2.23	119.92	123.79
2	B	501	HEM	C3C-C2C-C1C	2.22	109.14	107.05
3	A	502	6XD	C10-C7-C6	-2.14	105.61	109.69
2	B	501	HEM	C1D-C2D-C3D	2.13	109.22	106.98
2	A	501	HEM	CHD-C1D-ND	2.11	126.70	124.42
2	B	501	HEM	C1A-C2A-C3A	-2.09	103.64	106.87
2	B	501	HEM	O2A-CGA-O1A	-2.06	118.04	123.33
3	B	502	6XD	C10-C7-C8	2.05	113.54	109.05
2	B	501	HEM	C1B-NB-C4B	2.03	107.61	105.21

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	501	HEM	C2C-C3C-CAC-CBC
2	B	501	HEM	CAD-CBD-CGD-O2D
3	B	502	6XD	C06-C05-N04-C03

There are no ring outliers.

4 monomers are involved in 8 short contacts:

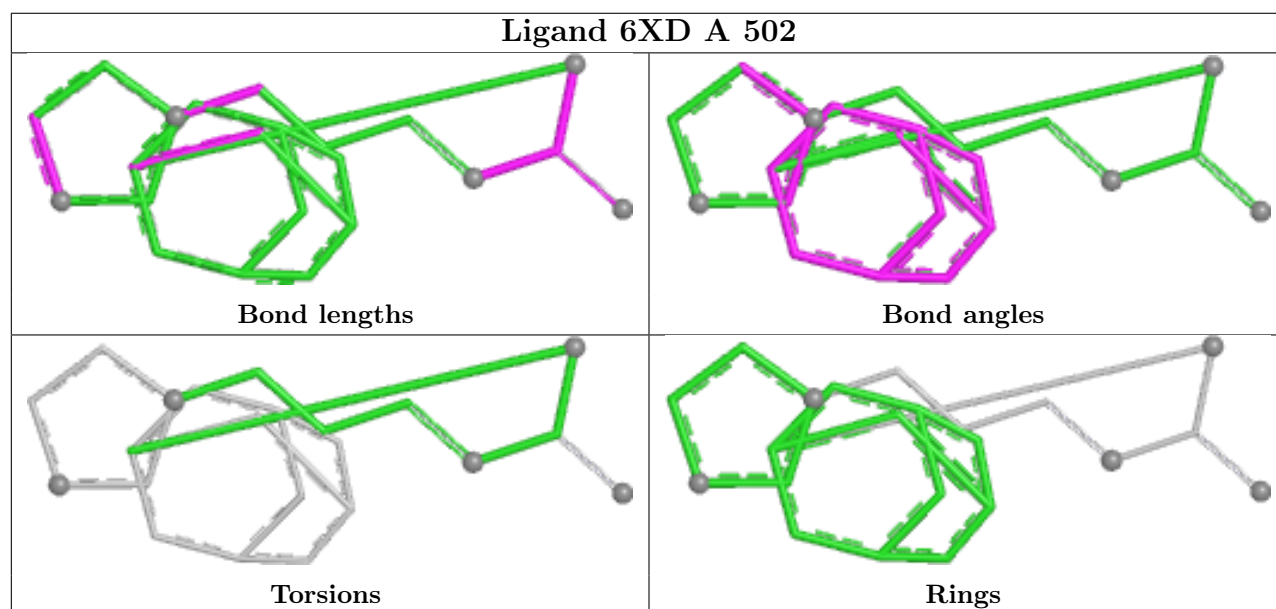
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	502	6XD	3	0
3	B	502	6XD	1	0

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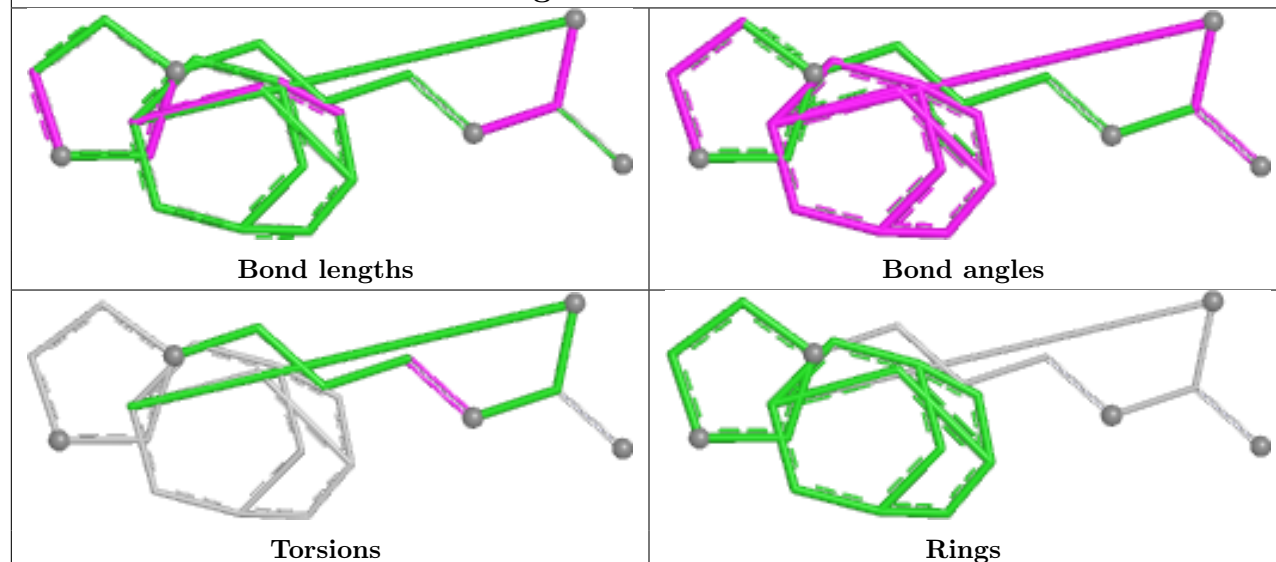
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	HEM	2	0
2	B	501	HEM	2	0

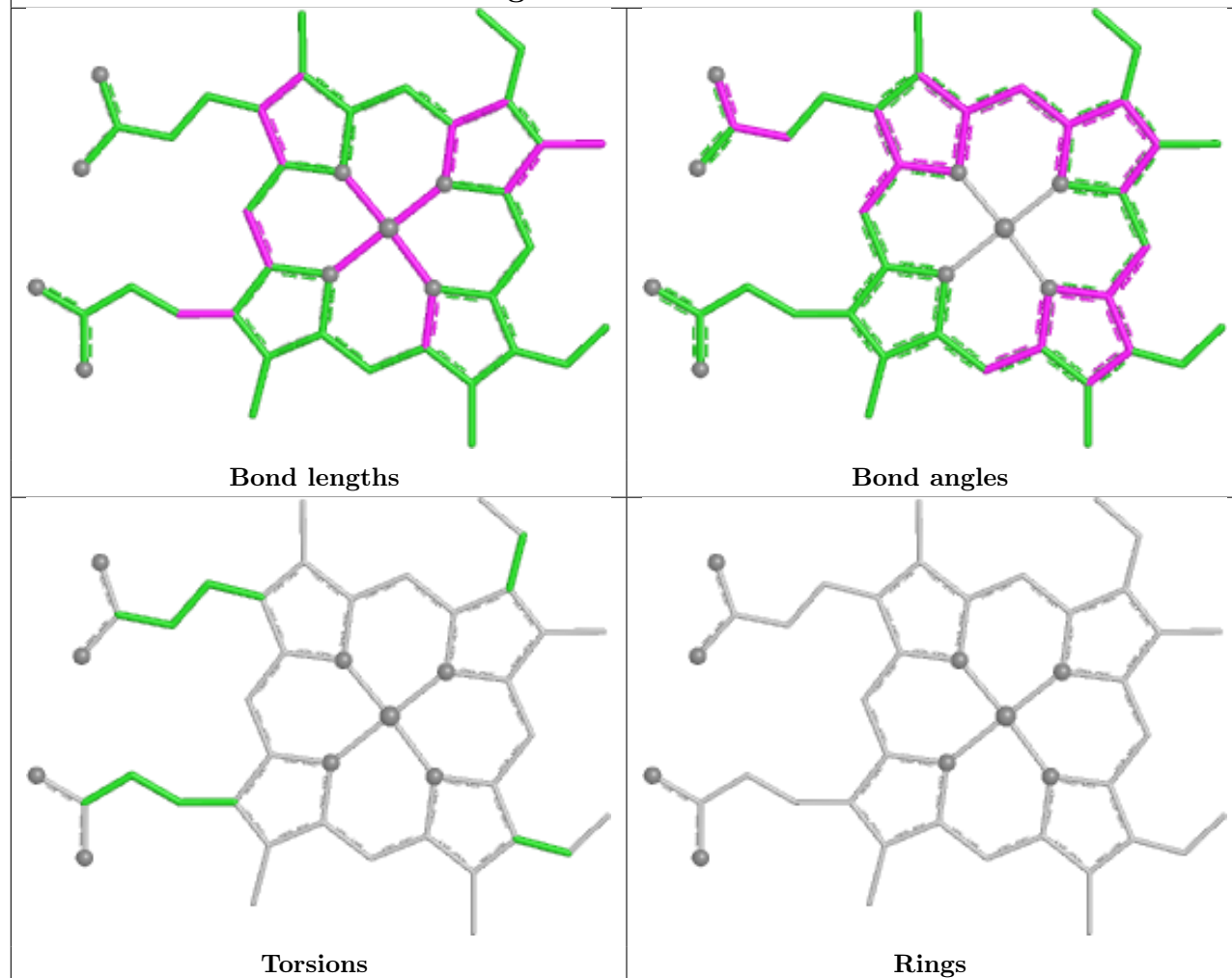
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

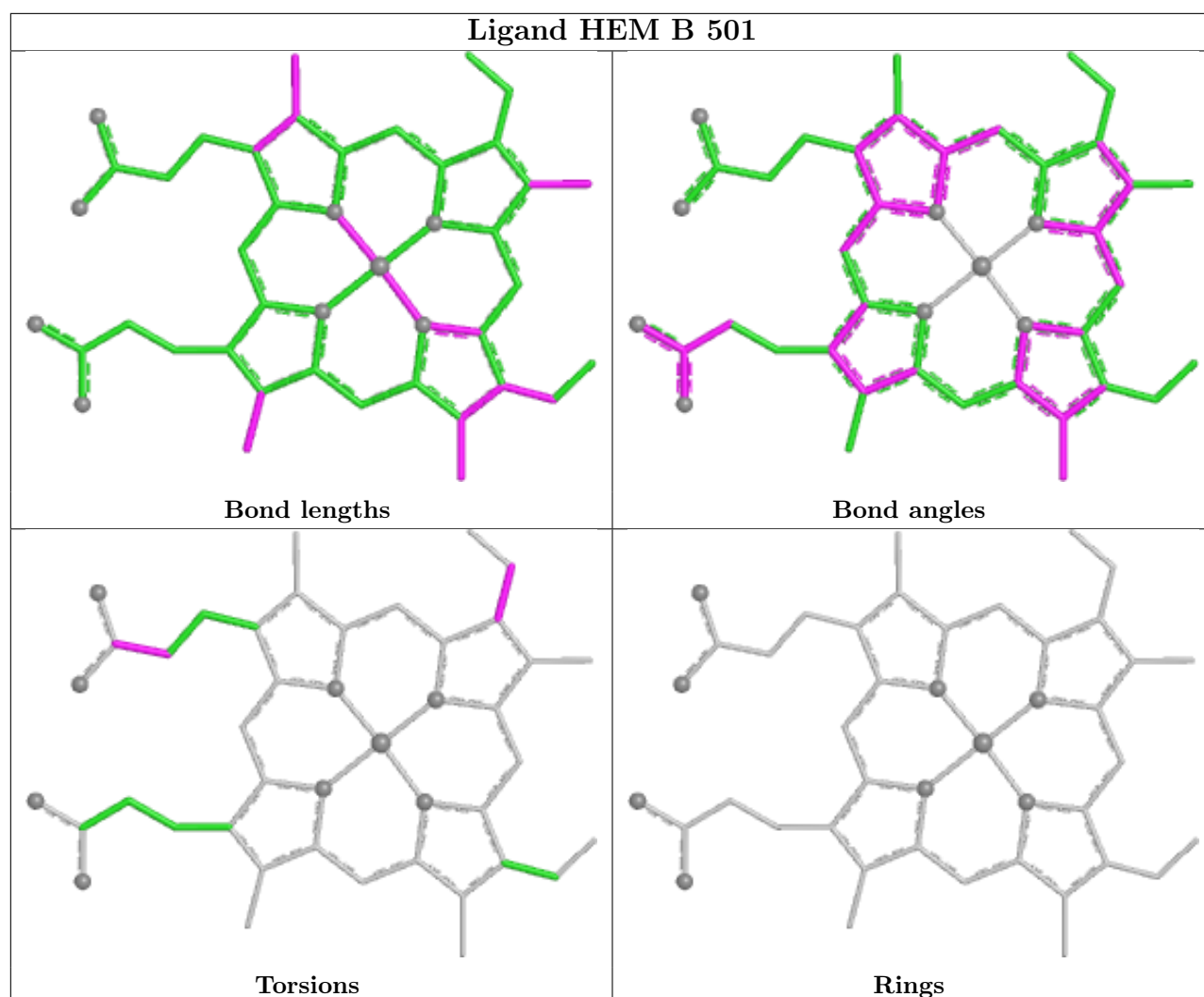


Ligand 6XD B 502



Ligand HEM A 501





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, 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	373/414 (90%)	0.00	14 (3%)	44 55	6, 16, 32, 48	8 (2%)
1	B	372/414 (89%)	0.29	22 (5%)	28 38	9, 20, 36, 65	5 (1%)
All	All	745/828 (89%)	0.15	36 (4%)	35 47	6, 18, 34, 65	13 (1%)

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	171	TRP	6.9
1	B	176	VAL	5.5
1	B	172	LEU	5.0
1	B	173	PHE	4.5
1	A	173	PHE	4.4
1	B	202	LEU	4.3
1	B	215	ALA	4.2
1	B	251	PHE	4.1
1	B	203	TYR	3.9
1	B	170	HIS	3.8
1	A	176	VAL	3.5
1	A	203	TYR	3.5
1	B	228	ALA	3.3
1	A	171	TRP	3.2
1	A	382	SER	3.0
1	A	172	LEU	3.0
1	B	255	ALA	3.0
1	A	283	PHE	2.7
1	B	175	ALA	2.6
1	B	216	GLU	2.6
1	B	37	TYR	2.6
1	A	281	SER	2.5
1	A	175	ALA	2.4
1	B	8	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	336	SER	2.4
1	B	155	MET	2.4
1	B	167	THR	2.3
1	A	141	ALA	2.2
1	A	274	ASP	2.2
1	A	216	GLU	2.1
1	B	218	ALA	2.1
1	B	174	GLU	2.1
1	A	251	PHE	2.0
1	B	390	VAL	2.0
1	A	201	ARG	2.0
1	B	108	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

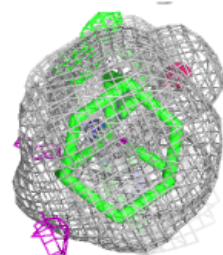
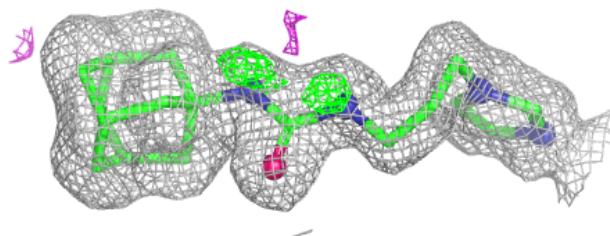
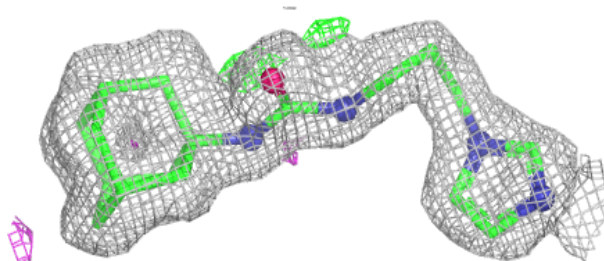
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	6XD	B	502	22/22	0.92	0.09	17,26,30,34	0
3	6XD	A	502	22/22	0.96	0.06	11,20,23,27	0
2	HEM	A	501	43/43	0.99	0.04	5,7,10,13	0
2	HEM	B	501	43/43	0.99	0.04	10,13,15,17	0

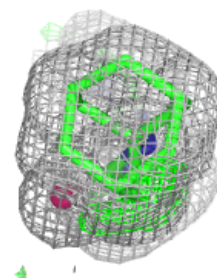
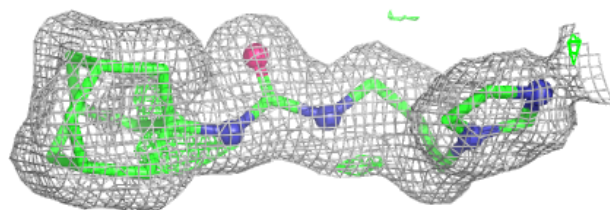
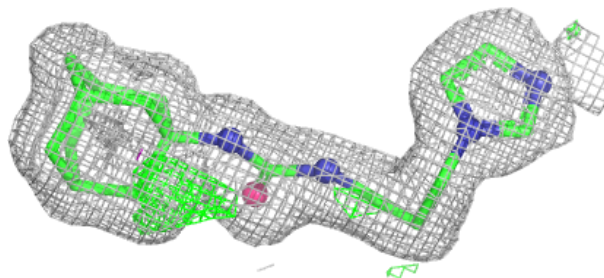
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 6XD 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)

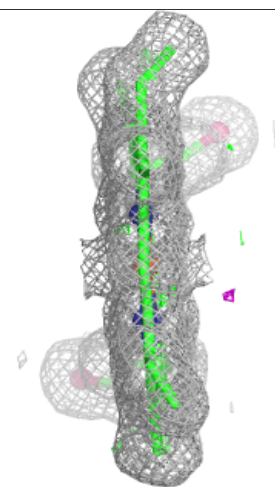
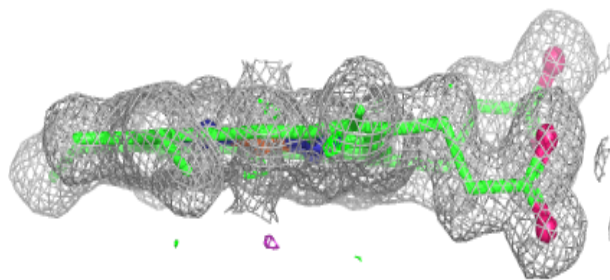
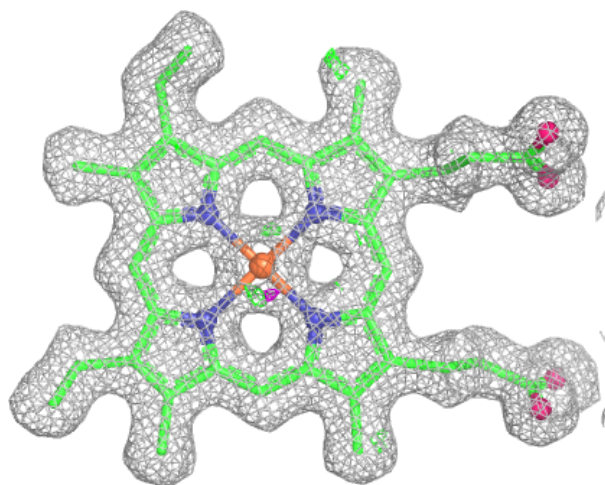
**Electron density around 6XD A 502:**

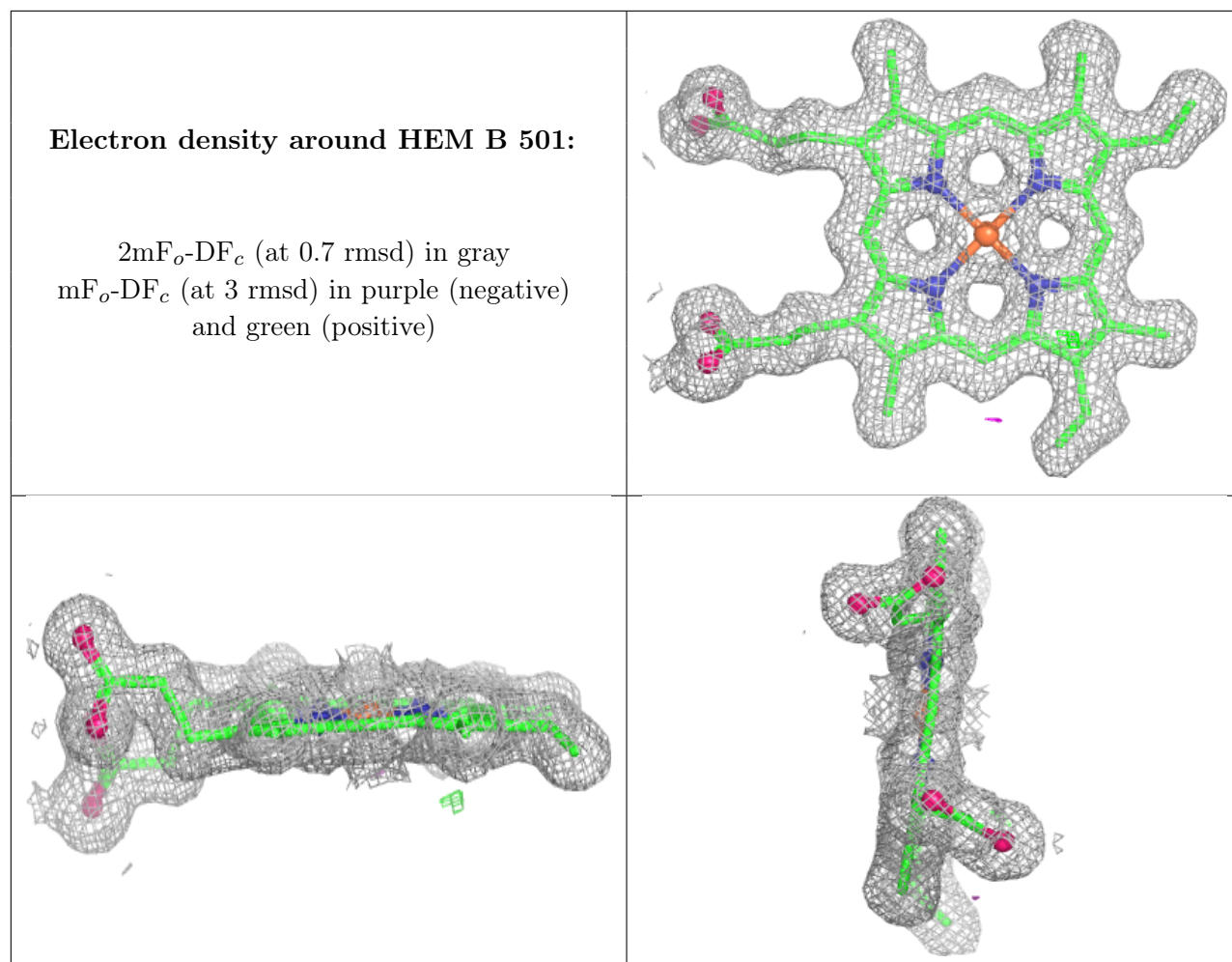
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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 ⓘ

There are no such residues in this entry.