



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 01:27 am BST

PDB ID : 3A16
Title : Crystal Structure of Aldoxime Dehydratase (OxdRE) in Complex with Propionaldoxime
Authors : Sawai, H.; Sugimoto, H.; Kato, Y.; Asano, Y.; Shiro, Y.; Aono, S.
Deposited on : 2009-03-26
Resolution : 1.60 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

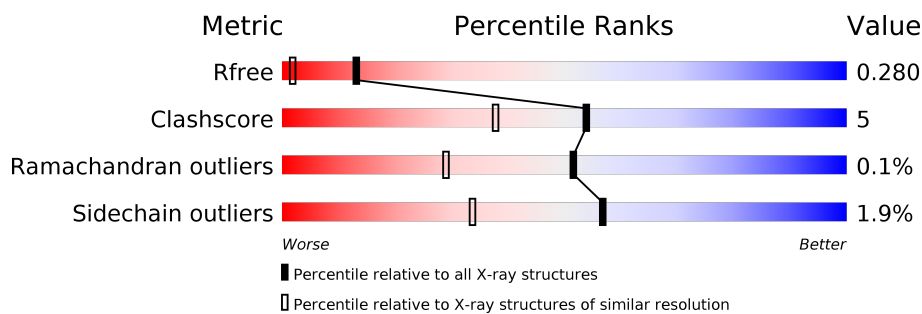
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	373	87% 8% 5%
1	B	373	85% 10% 5%
1	C	373	86% 8% 5%
1	D	373	83% 11% 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
3	PXO	C	355	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12699 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 Aldoxime dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	353	Total	C	N	O	S	0	4	0
			2840	1786	502	540	12			
1	B	353	Total	C	N	O	S	0	23	0
			3001	1893	531	565	12			
1	C	353	Total	C	N	O	S	0	2	0
			2827	1778	498	539	12			
1	D	353	Total	C	N	O	S	0	24	0
			3006	1896	531	567	12			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	INITIATING METHIONINE	UNP Q76K71
A	-18	GLY	-	EXPRESSION TAG	UNP Q76K71
A	-17	SER	-	EXPRESSION TAG	UNP Q76K71
A	-16	SER	-	EXPRESSION TAG	UNP Q76K71
A	-15	HIS	-	EXPRESSION TAG	UNP Q76K71
A	-14	HIS	-	EXPRESSION TAG	UNP Q76K71
A	-13	HIS	-	EXPRESSION TAG	UNP Q76K71
A	-12	HIS	-	EXPRESSION TAG	UNP Q76K71
A	-11	HIS	-	EXPRESSION TAG	UNP Q76K71
A	-10	HIS	-	EXPRESSION TAG	UNP Q76K71
A	-9	SER	-	EXPRESSION TAG	UNP Q76K71
A	-8	SER	-	EXPRESSION TAG	UNP Q76K71
A	-7	GLY	-	EXPRESSION TAG	UNP Q76K71
A	-6	LEU	-	EXPRESSION TAG	UNP Q76K71
A	-5	VAL	-	EXPRESSION TAG	UNP Q76K71
A	-4	PRO	-	EXPRESSION TAG	UNP Q76K71
A	-3	ARG	-	EXPRESSION TAG	UNP Q76K71
A	-2	GLY	-	EXPRESSION TAG	UNP Q76K71
A	-1	SER	-	EXPRESSION TAG	UNP Q76K71
A	0	HIS	-	EXPRESSION TAG	UNP Q76K71
B	-19	MET	-	INITIATING METHIONINE	UNP Q76K71

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	EXPRESSION TAG	UNP Q76K71
B	-17	SER	-	EXPRESSION TAG	UNP Q76K71
B	-16	SER	-	EXPRESSION TAG	UNP Q76K71
B	-15	HIS	-	EXPRESSION TAG	UNP Q76K71
B	-14	HIS	-	EXPRESSION TAG	UNP Q76K71
B	-13	HIS	-	EXPRESSION TAG	UNP Q76K71
B	-12	HIS	-	EXPRESSION TAG	UNP Q76K71
B	-11	HIS	-	EXPRESSION TAG	UNP Q76K71
B	-10	HIS	-	EXPRESSION TAG	UNP Q76K71
B	-9	SER	-	EXPRESSION TAG	UNP Q76K71
B	-8	SER	-	EXPRESSION TAG	UNP Q76K71
B	-7	GLY	-	EXPRESSION TAG	UNP Q76K71
B	-6	LEU	-	EXPRESSION TAG	UNP Q76K71
B	-5	VAL	-	EXPRESSION TAG	UNP Q76K71
B	-4	PRO	-	EXPRESSION TAG	UNP Q76K71
B	-3	ARG	-	EXPRESSION TAG	UNP Q76K71
B	-2	GLY	-	EXPRESSION TAG	UNP Q76K71
B	-1	SER	-	EXPRESSION TAG	UNP Q76K71
B	0	HIS	-	EXPRESSION TAG	UNP Q76K71
C	-19	MET	-	INITIATING METHIONINE	UNP Q76K71
C	-18	GLY	-	EXPRESSION TAG	UNP Q76K71
C	-17	SER	-	EXPRESSION TAG	UNP Q76K71
C	-16	SER	-	EXPRESSION TAG	UNP Q76K71
C	-15	HIS	-	EXPRESSION TAG	UNP Q76K71
C	-14	HIS	-	EXPRESSION TAG	UNP Q76K71
C	-13	HIS	-	EXPRESSION TAG	UNP Q76K71
C	-12	HIS	-	EXPRESSION TAG	UNP Q76K71
C	-11	HIS	-	EXPRESSION TAG	UNP Q76K71
C	-10	HIS	-	EXPRESSION TAG	UNP Q76K71
C	-9	SER	-	EXPRESSION TAG	UNP Q76K71
C	-8	SER	-	EXPRESSION TAG	UNP Q76K71
C	-7	GLY	-	EXPRESSION TAG	UNP Q76K71
C	-6	LEU	-	EXPRESSION TAG	UNP Q76K71
C	-5	VAL	-	EXPRESSION TAG	UNP Q76K71
C	-4	PRO	-	EXPRESSION TAG	UNP Q76K71
C	-3	ARG	-	EXPRESSION TAG	UNP Q76K71
C	-2	GLY	-	EXPRESSION TAG	UNP Q76K71
C	-1	SER	-	EXPRESSION TAG	UNP Q76K71
C	0	HIS	-	EXPRESSION TAG	UNP Q76K71
D	-19	MET	-	INITIATING METHIONINE	UNP Q76K71
D	-18	GLY	-	EXPRESSION TAG	UNP Q76K71
D	-17	SER	-	EXPRESSION TAG	UNP Q76K71

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	EXPRESSION TAG	UNP Q76K71
D	-15	HIS	-	EXPRESSION TAG	UNP Q76K71
D	-14	HIS	-	EXPRESSION TAG	UNP Q76K71
D	-13	HIS	-	EXPRESSION TAG	UNP Q76K71
D	-12	HIS	-	EXPRESSION TAG	UNP Q76K71
D	-11	HIS	-	EXPRESSION TAG	UNP Q76K71
D	-10	HIS	-	EXPRESSION TAG	UNP Q76K71
D	-9	SER	-	EXPRESSION TAG	UNP Q76K71
D	-8	SER	-	EXPRESSION TAG	UNP Q76K71
D	-7	GLY	-	EXPRESSION TAG	UNP Q76K71
D	-6	LEU	-	EXPRESSION TAG	UNP Q76K71
D	-5	VAL	-	EXPRESSION TAG	UNP Q76K71
D	-4	PRO	-	EXPRESSION TAG	UNP Q76K71
D	-3	ARG	-	EXPRESSION TAG	UNP Q76K71
D	-2	GLY	-	EXPRESSION TAG	UNP Q76K71
D	-1	SER	-	EXPRESSION TAG	UNP Q76K71
D	0	HIS	-	EXPRESSION TAG	UNP Q76K71

- # 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

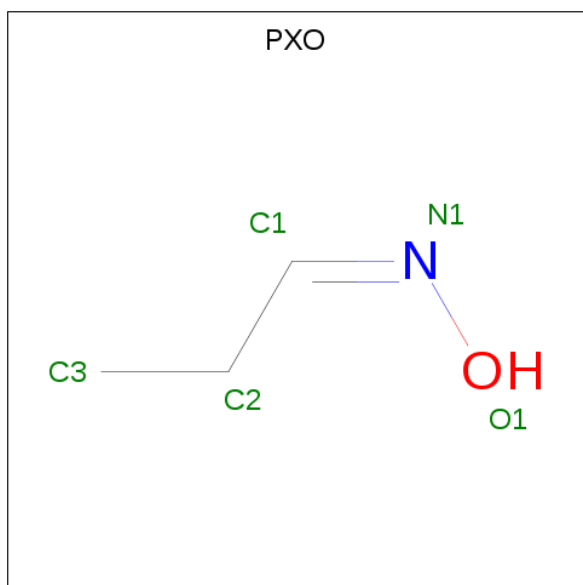


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PDB
PROTEIN DATA BANK

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

- Molecule 3 is (1Z)-propanal oxime (three-letter code: PXO) (formula: C₃H₇NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			5	3	1	1		
3	B	1	Total	C	N	O	0	0
			5	3	1	1		
3	C	1	Total	C	N	O	0	0
			5	3	1	1		
3	D	1	Total	C	N	O	0	0
			5	3	1	1		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	D	1	Total	Mg	0	0
			1	1		

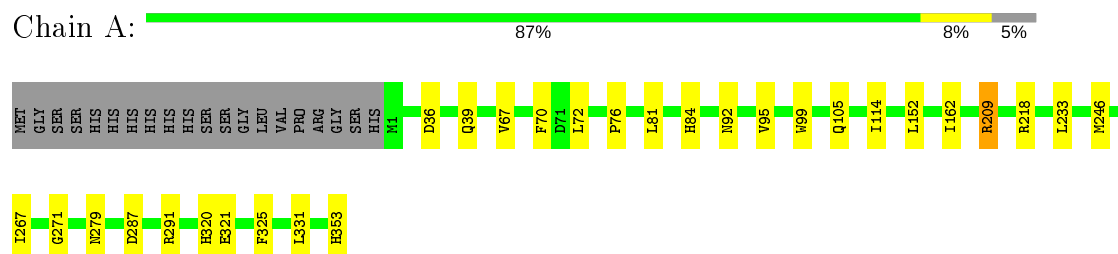
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	235	Total 235	O 235	0	0
5	B	208	Total 208	O 208	0	0
5	C	208	Total 208	O 208	0	0
5	D	180	Total 180	O 180	0	0

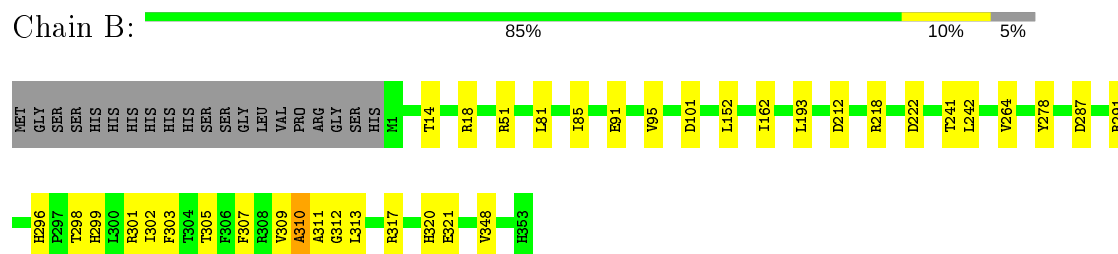
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

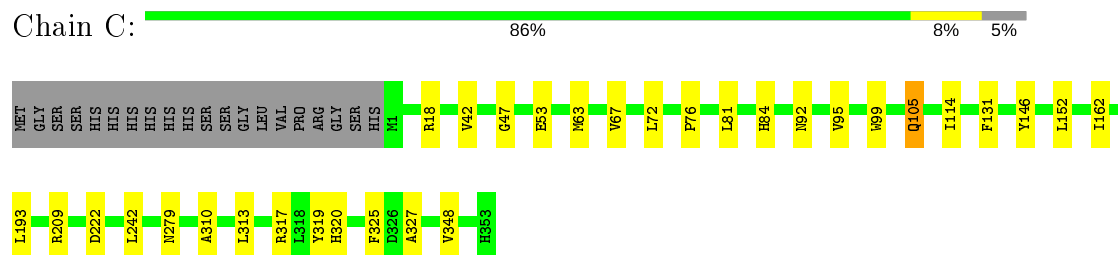
- Molecule 1: Aldoxime dehydratase



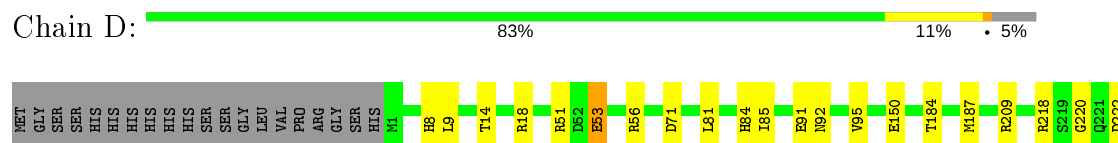
- Molecule 1: Aldoxime dehydratase

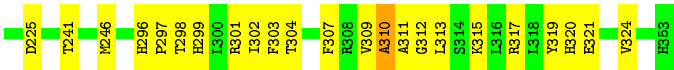


- Molecule 1: Aldoxime dehydratase



- Molecule 1: Aldoxime dehydratase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	62.71Å 147.67Å 78.91Å 90.00° 90.01° 90.00°	Depositor
Resolution (Å)	19.81 – 1.60 19.81 – 1.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.81-1.60) 99.9 (19.81-1.60)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.97 (at 1.60Å)	Xtriage
Refinement program	REFMAC refmac _5.2.0019	Depositor
R, R_{free}	0.248 , 0.274 0.256 , 0.280	Depositor DCC
R_{free} test set	9497 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	14.2	Xtriage
Anisotropy	0.620	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 22.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	0.460 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12699	wwPDB-VP
Average B, all atoms (Å ²)	10.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% 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, MG, PXO

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	0.45	0/2926	0.60	0/3979
1	B	0.44	0/3084	0.60	0/4194
1	C	0.46	0/2907	0.61	0/3954
1	D	0.43	0/3092	0.60	0/4205
All	All	0.44	0/12009	0.60	0/16332

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	2840	0	2675	17	0
1	B	3001	0	2835	29	0
1	C	2827	0	2656	16	0
1	D	3006	0	2839	60	0
2	A	43	0	30	3	0
2	B	43	0	30	2	0
2	C	43	0	30	3	0
2	D	43	0	30	2	0
3	A	5	0	7	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	5	0	7	0	0
3	C	5	0	7	0	0
3	D	5	0	7	1	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
5	A	235	0	0	0	0
5	B	208	0	0	0	0
5	C	208	0	0	0	0
5	D	180	0	0	1	0
All	All	12699	0	11153	122	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 5.

All (122) 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:D:299[B]:HIS:O	1:D:302[B]:ILE:HG13	1.36	1.20
1:A:209:ARG:CD	1:D:14:THR:HG21	1.80	1.12
1:D:299[B]:HIS:HA	1:D:302[B]:ILE:HD11	1.31	1.09
1:D:296[B]:HIS:CE1	1:D:298[B]:THR:HG23	1.96	1.00
1:D:299[B]:HIS:HA	1:D:302[B]:ILE:CD1	1.92	0.98
1:B:299[B]:HIS:O	1:B:302[B]:ILE:HG13	1.65	0.95
1:A:209:ARG:HD2	1:D:14:THR:HG21	1.44	0.95
1:B:299[B]:HIS:HA	1:B:302[B]:ILE:HD11	1.48	0.93
1:A:209:ARG:HD3	1:D:14:THR:HG21	1.53	0.90
1:A:209:ARG:HD2	1:D:14:THR:CG2	2.06	0.85
1:D:51:ARG:HG2	1:D:51:ARG:HH11	1.42	0.84
1:D:296[B]:HIS:CE1	1:D:298[B]:THR:CG2	2.61	0.82
1:D:299[B]:HIS:HA	1:D:302[B]:ILE:CG1	2.09	0.82
1:B:309[B]:VAL:O	1:B:311[B]:ALA:N	2.13	0.82
1:B:299[B]:HIS:HA	1:B:302[B]:ILE:CD1	2.08	0.81
1:B:296[B]:HIS:CE1	1:B:298[B]:THR:HG23	2.16	0.81
1:D:299[B]:HIS:CA	1:D:302[B]:ILE:HD11	2.09	0.81
1:D:299[B]:HIS:O	1:D:302[B]:ILE:CG1	2.27	0.81
1:D:309[B]:VAL:O	1:D:311[B]:ALA:N	2.14	0.80
1:B:299[B]:HIS:HA	1:B:302[B]:ILE:CG1	2.19	0.72
1:D:296[B]:HIS:HE1	1:D:298[B]:THR:HG23	1.55	0.69
1:D:296[B]:HIS:ND1	1:D:298[B]:THR:HG23	2.09	0.67
1:D:299[B]:HIS:CD2	1:D:302[B]:ILE:HD11	2.30	0.67
1:D:81:LEU:HD23	1:D:95:VAL:HG13	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:222:ASP:HB3	1:B:317:ARG:HB2	1.78	0.65
1:A:209:ARG:CD	1:D:14:THR:CG2	2.63	0.64
1:D:299[B]:HIS:CD2	1:D:302[B]:ILE:CD1	2.81	0.64
1:D:241:THR:HG22	1:D:301[A]:ARG:HE	1.63	0.63
1:D:299[B]:HIS:C	1:D:302[B]:ILE:HG13	2.18	0.63
1:D:85:ILE:HG12	1:D:91:GLU:HG2	1.79	0.63
1:B:296[B]:HIS:HE1	1:B:298[B]:THR:HG23	1.65	0.62
1:D:309[B]:VAL:O	1:D:310[B]:ALA:C	2.39	0.60
1:C:152:LEU:HD21	1:C:162:ILE:HD13	1.82	0.60
1:B:310[B]:ALA:HA	1:B:313[B]:LEU:HD12	1.82	0.60
1:C:222:ASP:HB3	1:C:317:ARG:HB2	1.83	0.59
1:B:309[B]:VAL:O	1:B:310[B]:ALA:C	2.41	0.59
1:B:299[B]:HIS:C	1:B:302[B]:ILE:HG13	2.24	0.59
1:A:152:LEU:HD21	1:A:162:ILE:HD13	1.85	0.57
3:D:355:PXO:H3A	5:D:398:HOH:O	2.03	0.57
1:D:299[B]:HIS:CA	1:D:302[B]:ILE:CG1	2.82	0.57
1:D:299[B]:HIS:HA	1:D:302[B]:ILE:HG12	1.86	0.56
1:D:296[B]:HIS:ND1	1:D:298[B]:THR:CG2	2.67	0.56
1:B:296[B]:HIS:CE1	1:B:298[B]:THR:CG2	2.89	0.56
1:D:51:ARG:HH11	1:D:51:ARG:CG	2.17	0.56
1:B:299[B]:HIS:HA	1:B:302[B]:ILE:HG13	1.88	0.55
1:C:81:LEU:HD23	1:C:95:VAL:HG13	1.89	0.55
1:D:296[B]:HIS:HE1	1:D:298[B]:THR:CG2	2.10	0.55
1:A:84:HIS:CE1	1:A:92:ASN:HB2	2.44	0.53
1:D:218:ARG:HB3	1:D:321:GLU:HG2	1.91	0.52
1:B:241:THR:HG22	1:B:301[A]:ARG:CZ	2.40	0.52
2:D:354:HEM:HMB2	2:D:354:HEM:HBB2	1.92	0.52
1:C:310:ALA:HA	1:C:313:LEU:HD12	1.91	0.51
1:B:85:ILE:HG12	1:B:91:GLU:HG2	1.93	0.51
1:C:84:HIS:CE1	1:C:92:ASN:HB2	2.46	0.51
1:C:18:ARG:HD2	1:D:18:ARG:HD2	1.93	0.51
1:A:76:PRO:HD3	1:A:99:TRP:CZ2	2.47	0.50
1:B:298[B]:THR:O	1:B:302[B]:ILE:HG12	2.12	0.50
1:B:81:LEU:HD23	1:B:95:VAL:HG13	1.94	0.49
1:D:303[B]:PHE:CE1	1:D:307[B]:PHE:CE1	3.00	0.49
1:D:303[B]:PHE:CZ	1:D:307[B]:PHE:CE1	3.01	0.49
1:D:299[A]:HIS:HA	1:D:302[A]:ILE:HD12	1.93	0.49
1:D:299[B]:HIS:CD2	1:D:302[B]:ILE:HD12	2.47	0.49
1:D:222:ASP:HB3	1:D:317:ARG:HB2	1.93	0.49
1:B:218:ARG:HB3	1:B:321:GLU:HG2	1.95	0.49
1:D:296[B]:HIS:CE1	1:D:298[B]:THR:HG21	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:ARG:HB3	1:A:321:GLU:HG2	1.94	0.48
1:C:279:ASN:OD1	2:C:354:HEM:HAC	2.14	0.48
1:B:193:LEU:O	1:B:348:VAL:HG22	2.14	0.48
1:D:299[B]:HIS:CG	1:D:302[B]:ILE:HD11	2.50	0.47
1:A:246:MET:CE	2:A:354:HEM:HMC1	2.44	0.47
1:B:309[B]:VAL:O	1:B:312[B]:GLY:N	2.46	0.47
1:D:310[B]:ALA:HA	1:D:313[B]:LEU:HD12	1.95	0.47
1:D:296[B]:HIS:CG	1:D:297[B]:PRO:HD2	2.49	0.47
1:D:309[B]:VAL:O	1:D:312[B]:GLY:N	2.46	0.47
2:A:354:HEM:HHD	2:A:354:HEM:HBC2	1.97	0.46
1:D:301[B]:ARG:O	1:D:304[B]:THR:CG2	2.63	0.46
1:B:303[B]:PHE:CZ	1:B:307[B]:PHE:CE1	3.04	0.46
1:D:220:GLY:HA3	1:D:319:TYR:CE1	2.50	0.46
1:B:299[B]:HIS:CA	1:B:302[B]:ILE:HG13	2.45	0.46
1:A:36[A]:ASP:OD2	1:D:209:ARG:NH1	2.49	0.46
1:D:299[B]:HIS:C	1:D:302[B]:ILE:CG1	2.81	0.46
2:D:354:HEM:CMB	2:D:354:HEM:HBB2	2.46	0.46
1:D:299[B]:HIS:CB	1:D:302[B]:ILE:HD11	2.46	0.45
1:D:14:THR:OG1	1:D:184:THR:HA	2.16	0.45
1:D:84:HIS:CE1	1:D:92:ASN:HB2	2.52	0.45
1:A:279:ASN:OD1	2:A:354:HEM:HAC	2.17	0.44
1:D:299[B]:HIS:HD2	1:D:302[B]:ILE:CD1	2.28	0.44
1:B:296[B]:HIS:ND1	1:B:298[B]:THR:HG23	2.32	0.44
1:B:242:LEU:HA	1:B:302[A]:ILE:HD11	1.99	0.44
1:A:81:LEU:HD22	1:A:95:VAL:HG22	1.99	0.44
1:C:193:LEU:O	1:C:348:VAL:HG22	2.17	0.44
2:B:354:HEM:HMB2	2:B:354:HEM:HBB2	2.00	0.43
1:D:241:THR:HG22	1:D:301[A]:ARG:NE	2.30	0.43
2:B:354:HEM:CMB	2:B:354:HEM:HBB2	2.48	0.43
1:C:47:GLY:HA3	1:C:131:PHE:CZ	2.54	0.43
1:D:187:MET:SD	1:D:324:VAL:HG21	2.58	0.43
1:D:53:GLU:CD	1:D:56:ARG:HE	2.22	0.43
1:B:152:LEU:HD21	1:B:162:ILE:HD13	2.00	0.42
1:D:51:ARG:HG2	1:D:51:ARG:NH1	2.21	0.42
1:A:67:VAL:O	1:A:70:PHE:HB2	2.19	0.42
1:C:76:PRO:HD3	1:C:99:TRP:CZ2	2.55	0.42
1:D:246:MET:HA	1:D:246:MET:HE2	2.02	0.42
1:C:146:TYR:CD1	1:C:319:TYR:HB2	2.55	0.41
1:A:72:LEU:HD12	1:A:114:ILE:HD11	2.02	0.41
2:C:354:HEM:HHD	2:C:354:HEM:HBC2	2.03	0.41
1:C:63:MET:O	1:C:67:VAL:HG23	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:ASP:O	1:A:291:ARG:HG2	2.20	0.41
1:B:287:ASP:O	1:B:291:ARG:HG2	2.20	0.41
1:C:242:LEU:HD22	2:C:354:HEM:HBB1	2.02	0.41
1:D:225:ASP:O	1:D:315[B]:LYS:HD3	2.21	0.41
1:C:42:VAL:HG11	1:C:105:GLN:HG3	2.01	0.41
1:D:8:HIS:CE1	1:D:9:LEU:HG	2.56	0.41
1:D:301[B]:ARG:HA	1:D:304[B]:THR:HG22	2.02	0.41
1:A:267:ILE:HD12	1:A:271:GLY:HA2	2.03	0.41
1:B:309[B]:VAL:C	1:B:311[B]:ALA:N	2.72	0.41
1:B:305[B]:THR:O	1:B:309[B]:VAL:HG22	2.21	0.40
1:D:301[B]:ARG:O	1:D:304[B]:THR:HG22	2.21	0.40
1:C:209:ARG:HE	1:C:327:ALA:HB1	1.86	0.40
1:D:298[B]:THR:O	1:D:302[B]:ILE:HG12	2.21	0.40
1:D:310[A]:ALA:HA	1:D:313[A]:LEU:HD12	2.04	0.40
1:B:264:VAL:HG22	1:B:278:TYR:O	2.21	0.40
1:C:72:LEU:HD12	1:C:114:ILE:HD11	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	355/373 (95%)	349 (98%)	6 (2%)	0	100	100
1	B	374/373 (100%)	365 (98%)	7 (2%)	2 (0%)	29	11
1	C	353/373 (95%)	348 (99%)	5 (1%)	0	100	100
1	D	375/373 (100%)	362 (96%)	11 (3%)	2 (0%)	29	11
All	All	1457/1492 (98%)	1424 (98%)	29 (2%)	4 (0%)	51	21

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	310[A]	ALA
1	B	310[B]	ALA
1	D	310[A]	ALA
1	D	310[B]	ALA

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	299/312 (96%)	290 (97%)	9 (3%)	41	16
1	B	315/312 (101%)	309 (98%)	6 (2%)	57	34
1	C	297/312 (95%)	293 (99%)	4 (1%)	69	50
1	D	316/312 (101%)	312 (99%)	4 (1%)	69	50
All	All	1227/1248 (98%)	1204 (98%)	23 (2%)	57	34

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

Mol	Chain	Res	Type
1	A	39[A]	GLN
1	A	39[B]	GLN
1	A	105	GLN
1	A	209	ARG
1	A	233	LEU
1	A	320	HIS
1	A	325	PHE
1	A	331	LEU
1	A	353	HIS
1	B	14	THR
1	B	18	ARG
1	B	51	ARG
1	B	101	ASP
1	B	212	ASP
1	B	320	HIS
1	C	53	GLU
1	C	105	GLN
1	C	320	HIS

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Mol	Chain	Res	Type
1	C	325	PHE
1	D	53	GLU
1	D	71	ASP
1	D	150	GLU
1	D	320	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	106	HIS
1	B	105	GLN
1	B	252	ASN
1	C	39	GLN
1	C	105	GLN
1	D	39	GLN
1	D	105	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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
3	PXO	B	355	2	4,4,4	1.33	1 (25%)	3,3,3	4.58	1 (33%)
2	HEM	D	354	1,3	27,50,50	2.04	6 (22%)	17,82,82	1.62	4 (23%)
2	HEM	B	354	1,3	27,50,50	2.06	7 (25%)	17,82,82	1.67	4 (23%)
2	HEM	C	354	1,3	27,50,50	2.09	6 (22%)	17,82,82	1.70	3 (17%)
3	PXO	C	355	2	4,4,4	2.00	2 (50%)	3,3,3	5.27	2 (66%)
3	PXO	A	355	2	4,4,4	1.15	1 (25%)	3,3,3	7.65	1 (33%)
3	PXO	D	355	2	4,4,4	1.07	1 (25%)	3,3,3	5.66	2 (66%)
2	HEM	A	354	1,3	27,50,50	2.11	6 (22%)	17,82,82	1.70	6 (35%)

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	PXO	B	355	2	-	0/0/2/2	-
2	HEM	D	354	1,3	-	0/6/54/54	-
2	HEM	B	354	1,3	-	0/6/54/54	-
2	HEM	C	354	1,3	-	0/6/54/54	-
3	PXO	C	355	2	-	0/0/2/2	-
3	PXO	A	355	2	-	0/0/2/2	-
3	PXO	D	355	2	-	0/0/2/2	-
2	HEM	A	354	1,3	-	0/6/54/54	-

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	354	HEM	C3D-C2D	5.11	1.52	1.37
2	C	354	HEM	C3D-C2D	5.04	1.52	1.37
2	D	354	HEM	C3D-C2D	4.91	1.52	1.37
2	B	354	HEM	C3D-C2D	4.90	1.52	1.37
2	C	354	HEM	C3C-C2C	-4.58	1.34	1.40
2	A	354	HEM	C3C-C2C	-4.29	1.34	1.40
2	A	354	HEM	C3B-C2B	-4.21	1.34	1.40
2	C	354	HEM	C3B-C2B	-4.16	1.34	1.40
2	B	354	HEM	C3B-C2B	-4.14	1.34	1.40
2	D	354	HEM	C3C-C2C	-3.81	1.35	1.40
2	D	354	HEM	C3C-CAC	3.75	1.55	1.47
2	B	354	HEM	C3C-CAC	3.75	1.55	1.47
2	C	354	HEM	C3B-CAB	3.59	1.55	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	354	HEM	C3C-C2C	-3.55	1.35	1.40
2	B	354	HEM	C3B-CAB	3.53	1.55	1.47
2	A	354	HEM	C3B-CAB	3.44	1.55	1.47
2	C	354	HEM	C3C-CAC	3.41	1.54	1.47
2	D	354	HEM	C3B-CAB	3.38	1.54	1.47
2	A	354	HEM	C3C-CAC	3.28	1.54	1.47
2	D	354	HEM	C3B-C2B	-3.27	1.35	1.40
3	C	355	PXO	C2-C1	3.16	1.52	1.49
2	D	354	HEM	CAA-C2A	2.62	1.55	1.52
3	B	355	PXO	C2-C1	2.42	1.51	1.49
3	C	355	PXO	C1-N1	2.28	1.28	1.26
2	A	354	HEM	CAA-C2A	2.25	1.55	1.52
3	A	355	PXO	C2-C1	2.23	1.51	1.49
2	B	354	HEM	C1D-ND	2.20	1.40	1.36
2	C	354	HEM	CAA-C2A	2.19	1.55	1.52
2	B	354	HEM	CAA-C2A	2.17	1.55	1.52
3	D	355	PXO	C2-C1	2.03	1.51	1.49

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	355	PXO	O1-N1-C1	13.22	124.09	111.70
3	D	355	PXO	O1-N1-C1	8.91	120.05	111.70
3	C	355	PXO	O1-N1-C1	8.75	119.90	111.70
3	B	355	PXO	O1-N1-C1	7.69	118.91	111.70
3	D	355	PXO	C3-C2-C1	-4.06	106.59	113.75
2	D	354	HEM	CBA-CAA-C2A	-3.49	106.06	112.49
2	C	354	HEM	CBA-CAA-C2A	-3.42	106.18	112.49
2	B	354	HEM	CBA-CAA-C2A	-3.23	106.54	112.49
2	D	354	HEM	CAD-CBD-CGD	-3.03	107.58	112.67
2	A	354	HEM	CBA-CAA-C2A	-2.95	107.05	112.49
2	C	354	HEM	CAD-CBD-CGD	-2.89	107.82	112.67
2	B	354	HEM	CAD-CBD-CGD	-2.81	107.95	112.67
2	B	354	HEM	C4A-C3A-C2A	2.80	108.94	107.00
2	A	354	HEM	CMA-C3A-C4A	-2.57	124.51	128.46
2	C	354	HEM	CMA-C3A-C4A	-2.55	124.55	128.46
2	A	354	HEM	C1D-C2D-C3D	-2.41	105.32	107.00
2	D	354	HEM	C4A-C3A-C2A	2.26	108.56	107.00
3	C	355	PXO	C3-C2-C1	-2.22	109.83	113.75
2	A	354	HEM	CAD-CBD-CGD	-2.14	109.07	112.67
2	A	354	HEM	C4A-C3A-C2A	2.14	108.49	107.00
2	A	354	HEM	CMC-C2C-C3C	2.14	128.68	124.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	354	HEM	CMA-C3A-C4A	-2.11	125.21	128.46
2	B	354	HEM	CMD-C2D-C3D	2.01	128.74	124.94

There are no chirality outliers.

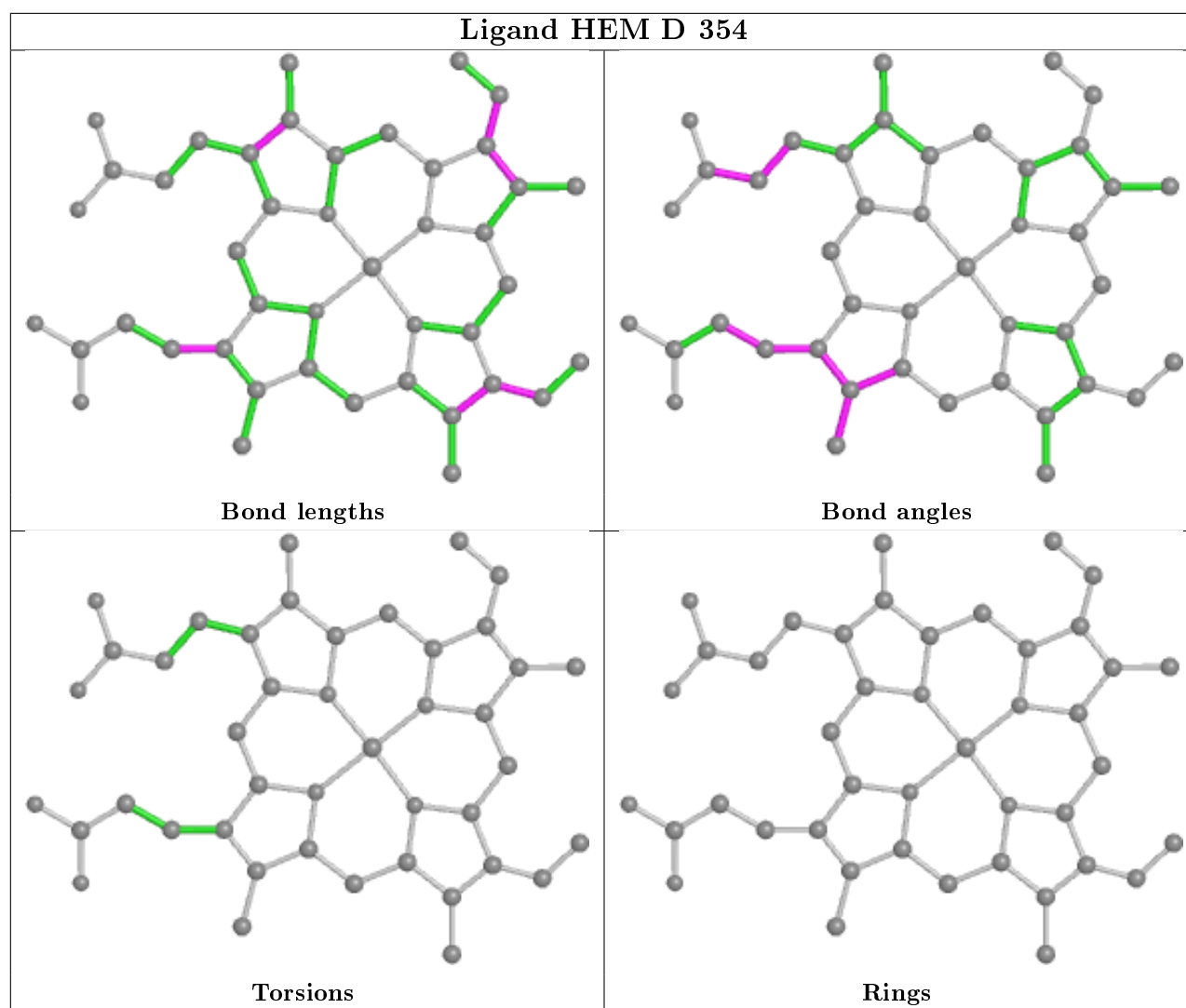
There are no torsion outliers.

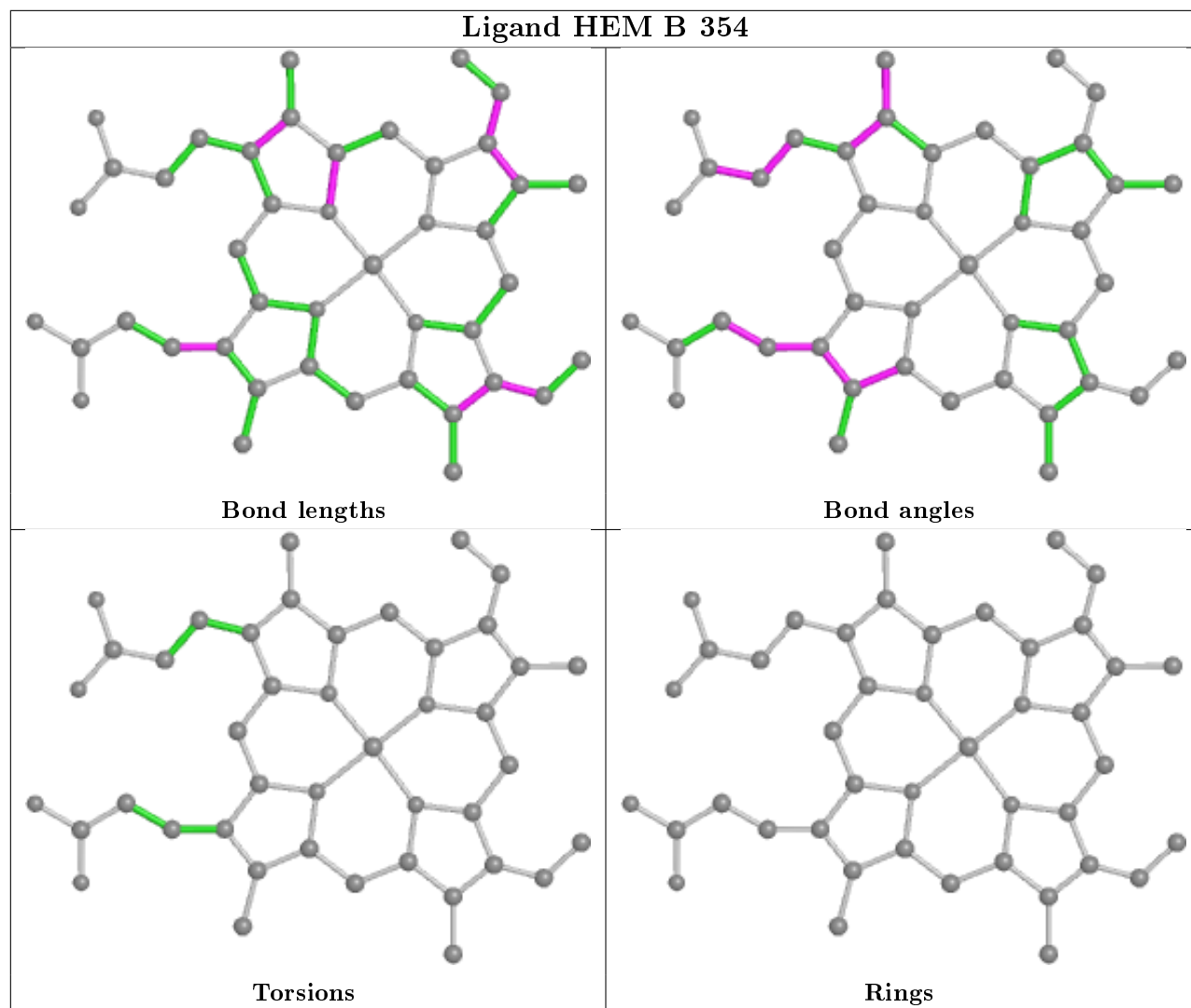
There are no ring outliers.

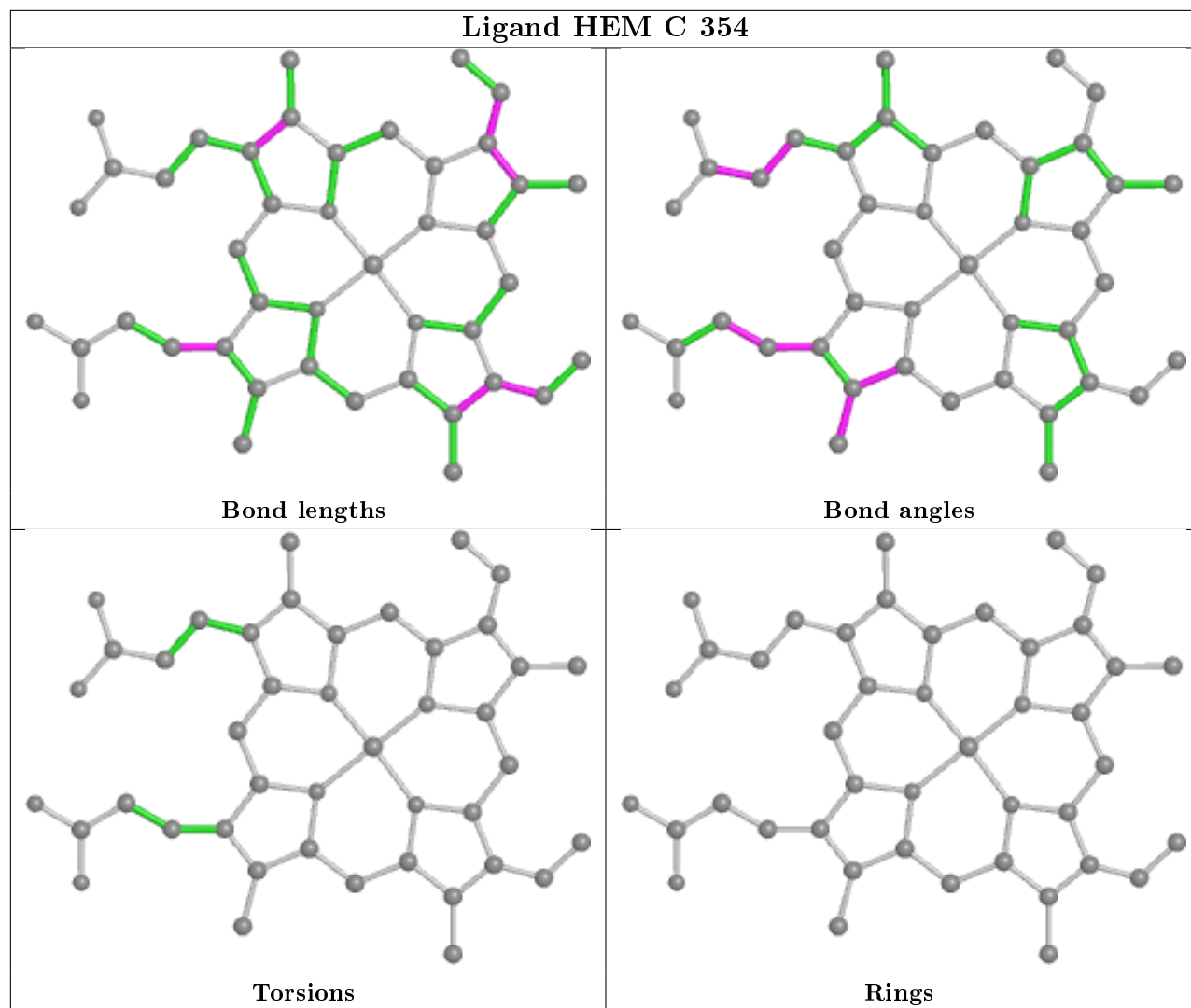
5 monomers are involved in 11 short contacts:

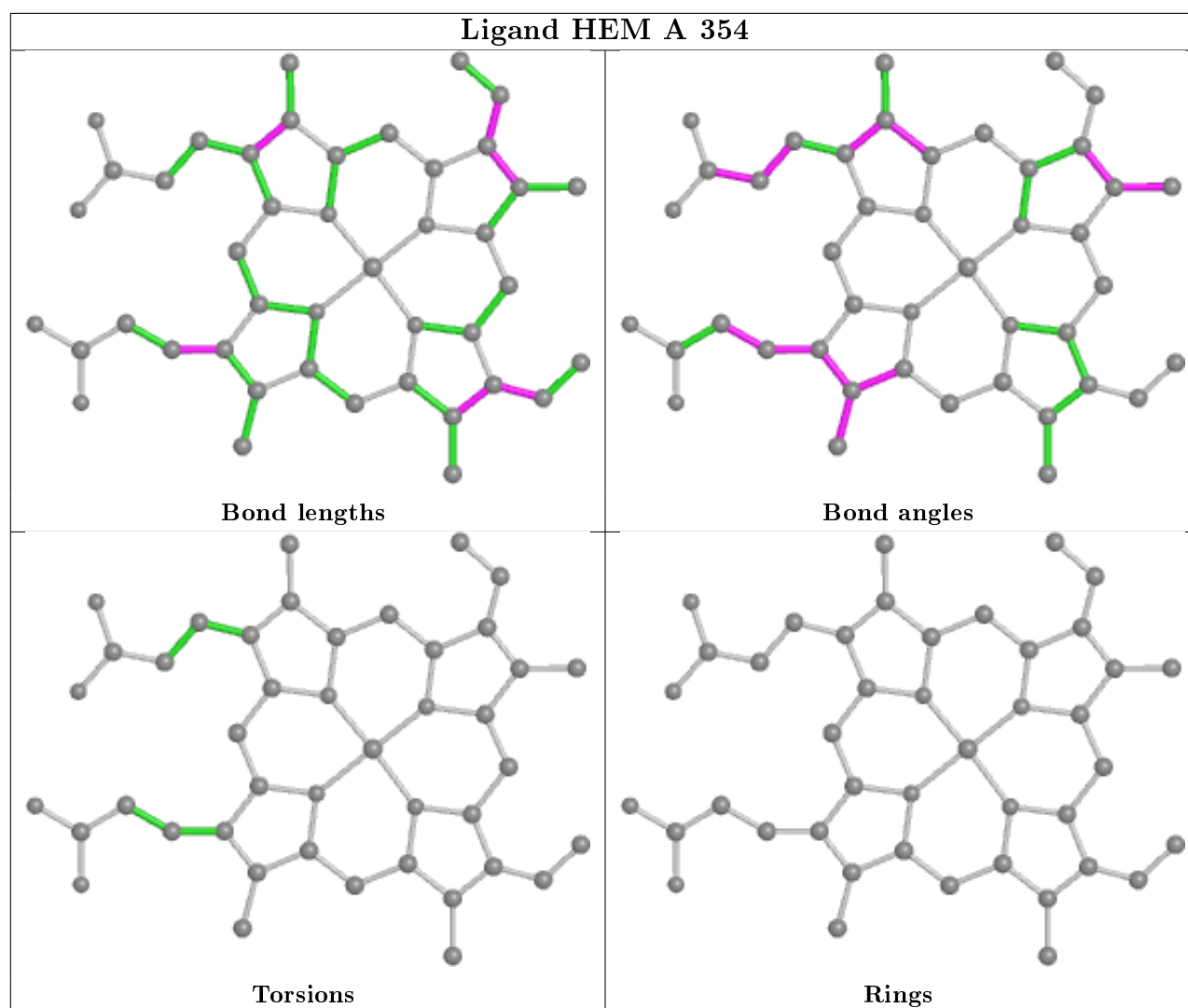
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	354	HEM	2	0
2	B	354	HEM	2	0
2	C	354	HEM	3	0
3	D	355	PXO	1	0
2	A	354	HEM	3	0

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

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

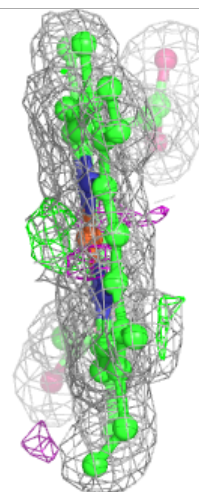
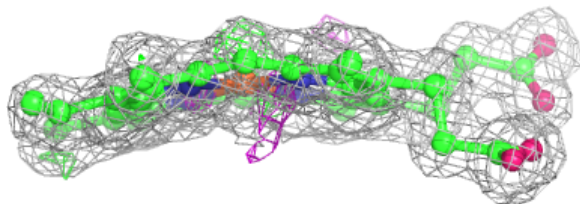
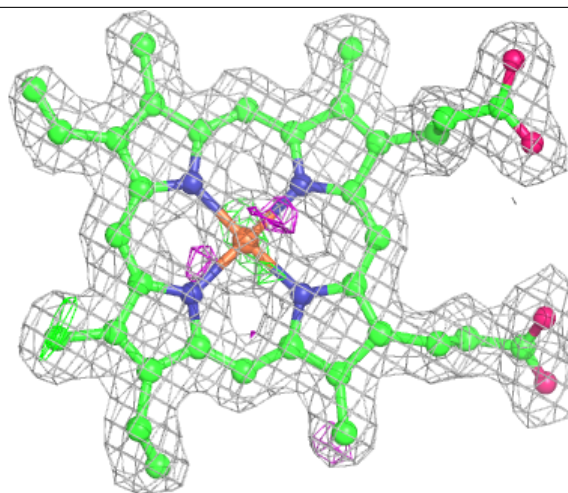
6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

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.

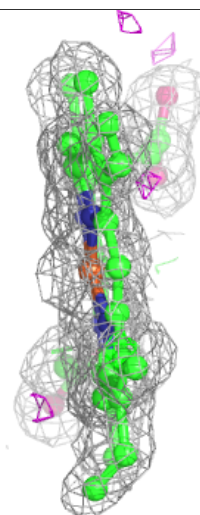
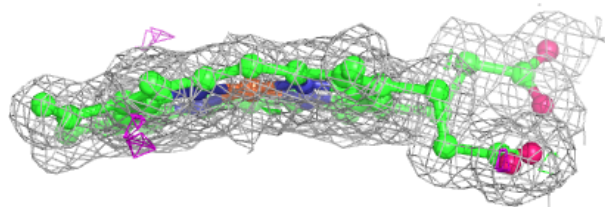
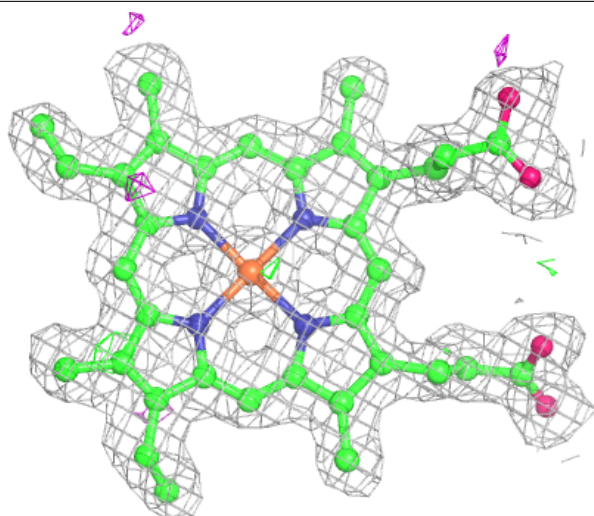
Electron density around HEM D 354:

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



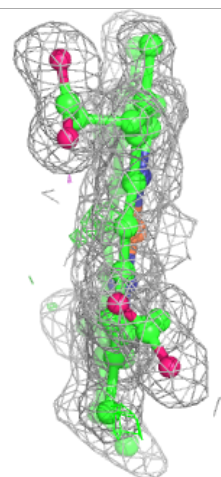
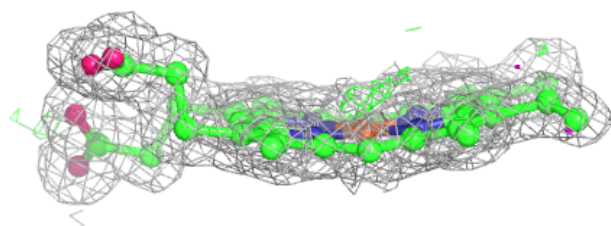
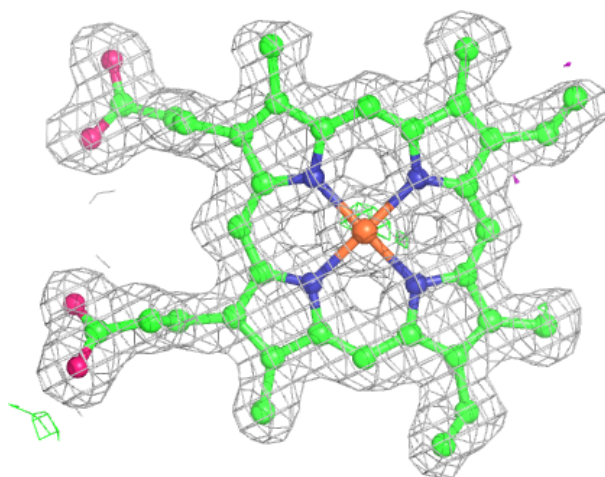
Electron density around HEM B 354:

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



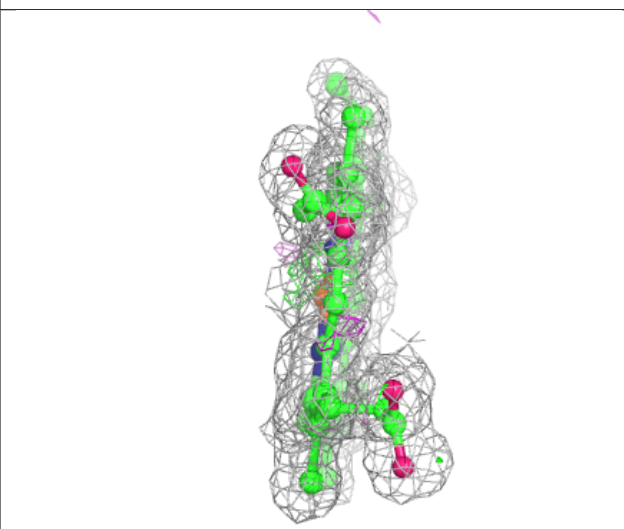
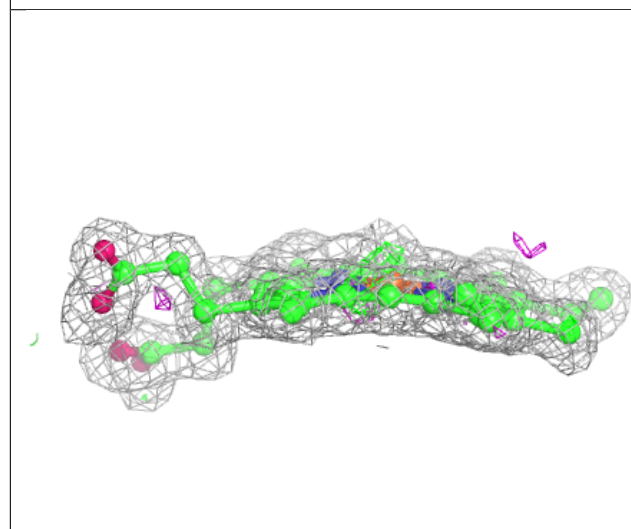
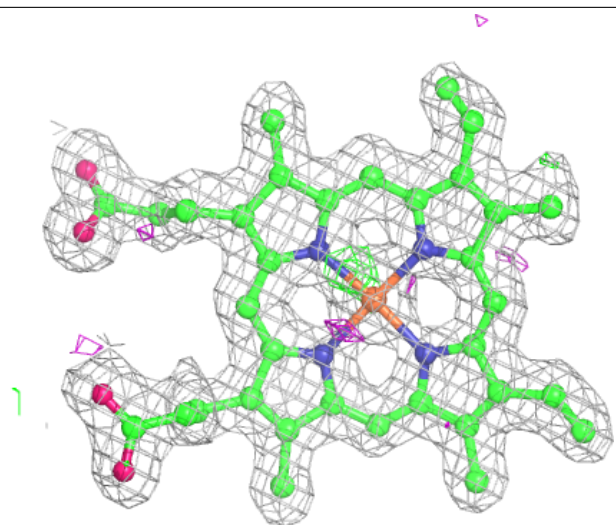
Electron density around HEM C 354:

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



Electron density around HEM A 354:

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



6.5 Other polymers [i](#)

Unable to reproduce the depositor's R factor - this section is therefore empty.