



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 01:10 am BST

PDB ID : 2E74
Title : Crystal Structure of the Cytochrome b6f Complex from *M.laminosus*
Authors : Cramer, W.A.; Yamashita, E.; Zhang, H.
Deposited on : 2007-01-05
Resolution : 3.00 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 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

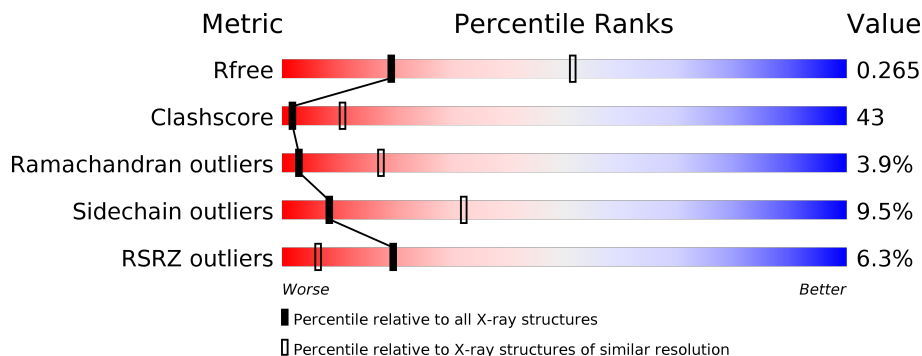
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	215	
2	B	160	
3	C	289	
4	D	179	
5	E	32	
6	F	35	

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Mol	Chain	Length	Quality of chain
7	G	37	
8	H	29	

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
11	UMQ	A	1101	X	-	-	-
11	UMQ	A	1102	X	-	-	-
11	UMQ	A	1103	X	-	-	-
11	UMQ	A	1104	X	-	-	-
12	CLA	B	201	X	-	-	-
13	OPC	H	1002	-	-	X	-
14	FES	D	200	-	-	X	-
15	SQD	D	201	X	-	-	-
16	BCR	G	101	-	-	-	X

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 8025 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Cytochrome b6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	215	1711	1140	272	288	11	0	0	0

- Molecule 2 is a protein called Cytochrome b6-f complex subunit 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	160	1249	841	193	209	6	0	0	0

- Molecule 3 is a protein called Apocytochrome f.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	288	2216	1415	369	424	8	0	0	0

- Molecule 4 is a protein called Cytochrome b6-f complex iron-sulfur subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	166	1260	805	218	230	7	0	0	0

- Molecule 5 is a protein called Cytochrome b6-f complex subunit 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	32	248	179	34	34	1	0	0	0

- Molecule 6 is a protein called Cytochrome b6-f complex subunit 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	F	32	242	165	35	40	2	0	0	0

- Molecule 7 is a protein called Cytochrome b6-f complex subunit 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
7	G	37	283	188	44	50	1	0	0	0

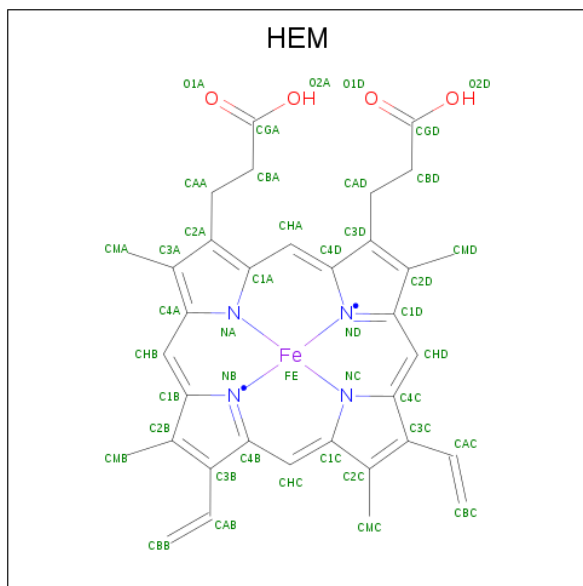
- Molecule 8 is a protein called Cytochrome b6-f complex subunit 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
8	H	29	230	156	36	36	2	0	0	0

- Molecule 9 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	1	Total	Cd	0	0
			1	1		
9	A	1	Total	Cd	0	0
			1	1		

- Molecule 10 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



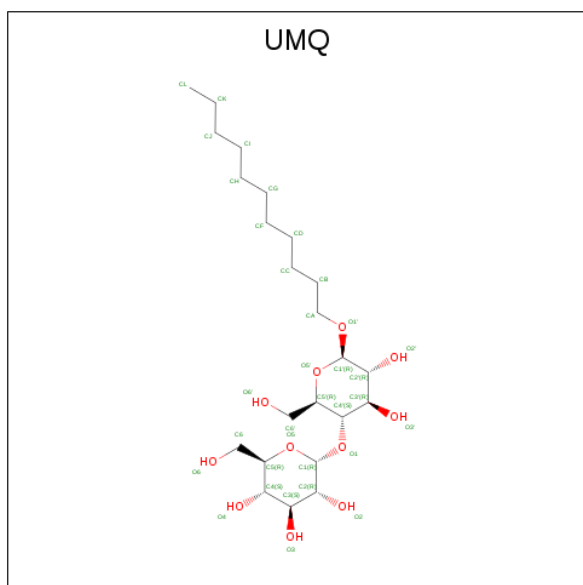
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Fe	N	O		
10	A	1	43	34	1	4	4	0	0
10	A	1	43	34	1	4	4	0	0

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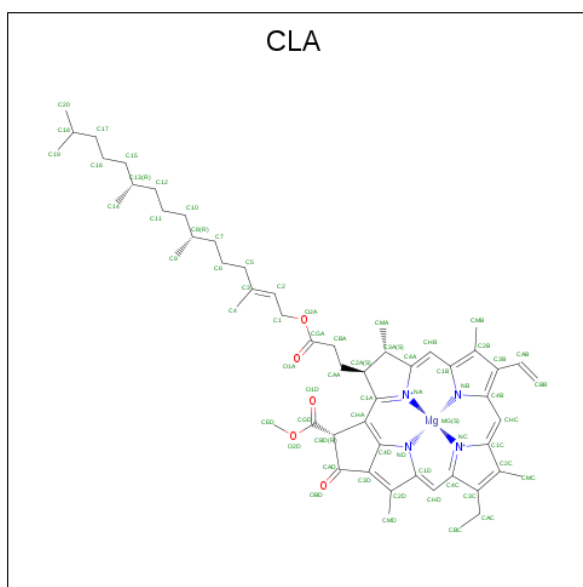
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
10	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
10	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 11 is UNDECYL-MALTOSE (three-letter code: UMQ) (formula: $C_{23}H_{44}O_{11}$).



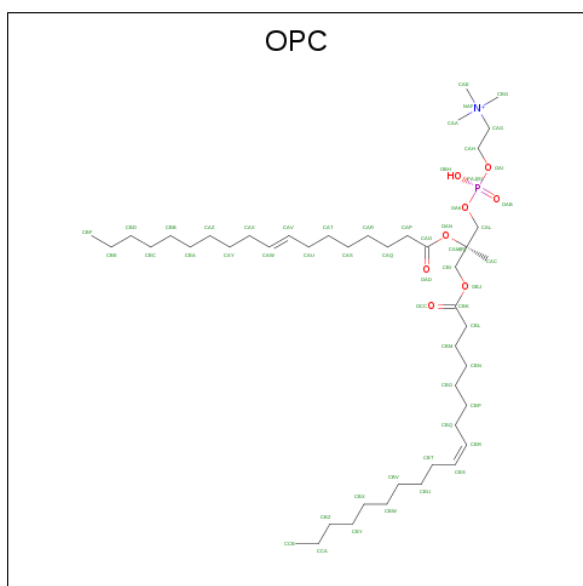
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			34	23	11		
11	A	1	Total	C	O	0	0
			34	23	11		
11	A	1	Total	C	O	0	0
			34	23	11		
11	A	1	Total	C	O	0	0
			34	23	11		

- Molecule 12 is CHLOROPHYLL A (three-letter code: CLA) (formula: $C_{55}H_{72}MgN_4O_5$).



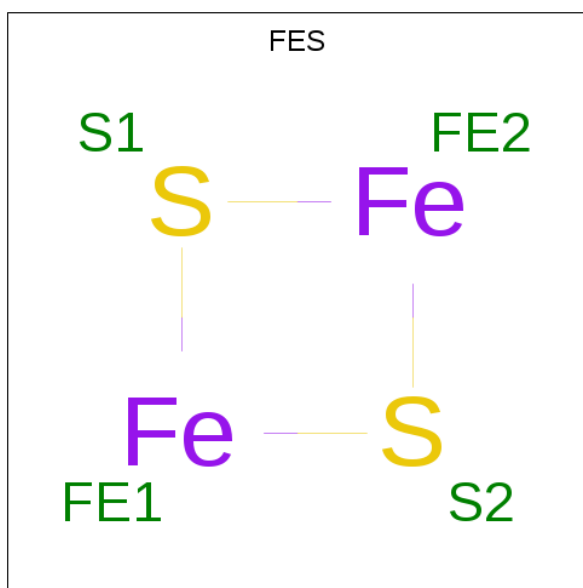
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	Mg	N			O
12	B	1	65	55	1	4	5	0	0

- Molecule 13 is (7R,17E)-4-HYDROXY-N,N,N,7-TETRAMETHYL-7-[(8E)-OCTADEC-8-ENOYLOXY]-10-OXO-3,5,9-TRIOXA-4-PHOSPHAHEPTACOS-17-EN-1-AMINIUM 4-OXIDE (three-letter code: OPC) (formula: C₄₅H₈₇NO₈P).



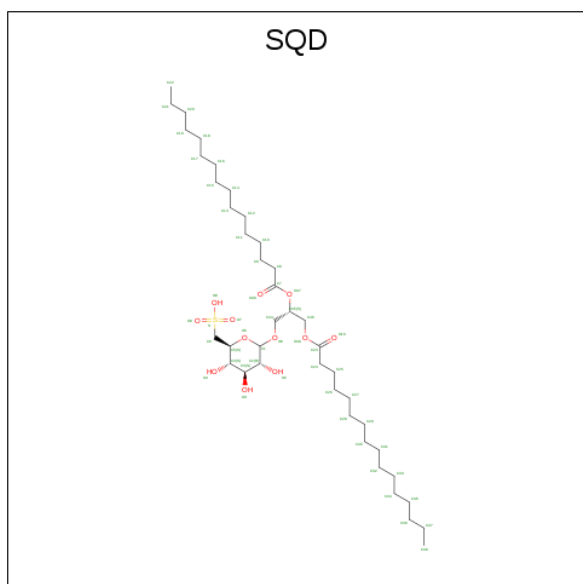
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
13	B	1	54	44	1	8	1	0	0
13	H	1	54	44	1	8	1	0	0

- Molecule 14 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



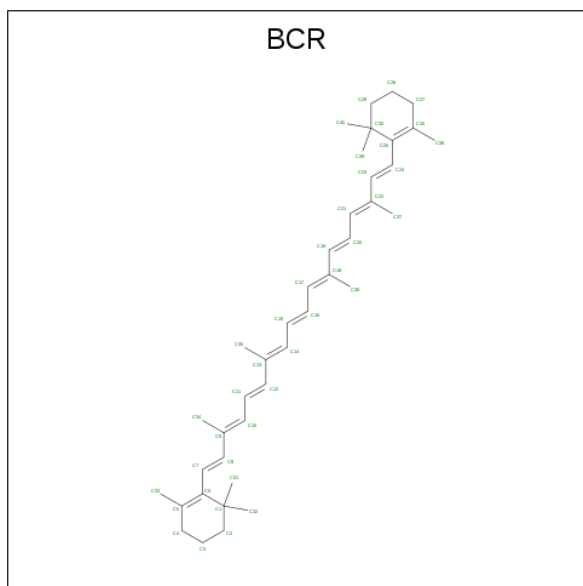
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
14	D	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 15 is 1,2-DI-O-ACYL-3-O-[6-DEOXY-6-SULFO-ALPHA-D-GLUCOPYRANOSYL]-SN-GLYCEROL (three-letter code: SQD) (formula: C₄₁H₇₈O₁₂S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
15	D	1	Total	C	O	S	0	0
			54	41	12	1		

- Molecule 16 is BETA-CAROTENE (three-letter code: BCR) (formula: C₄₀H₅₆).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	1	Total C 40 40	0	0

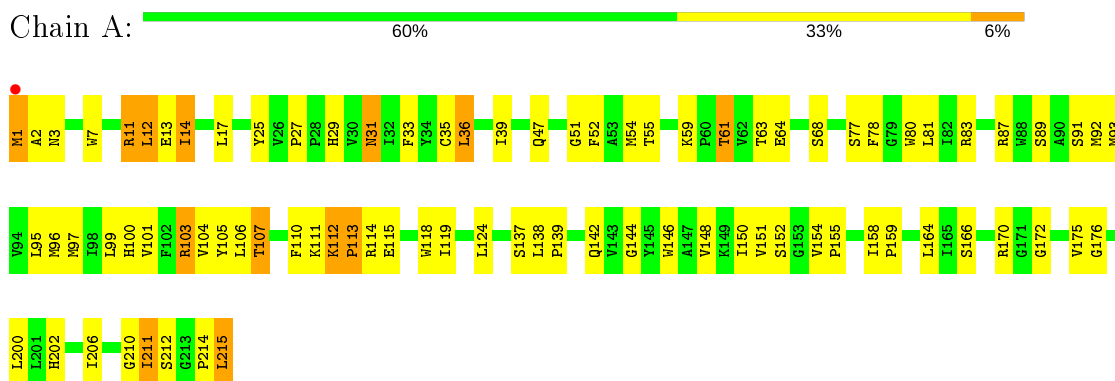
- Molecule 17 is water.

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

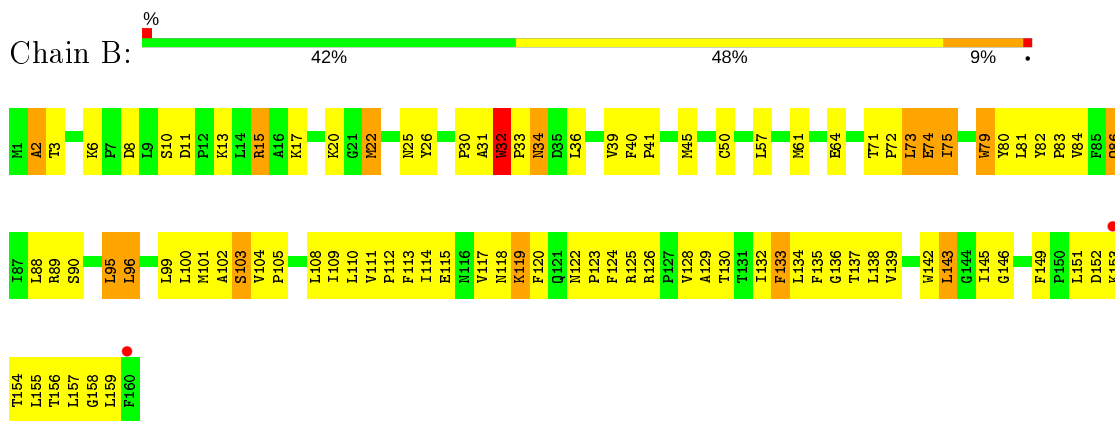
3 Residue-property plots [i](#)

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 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.

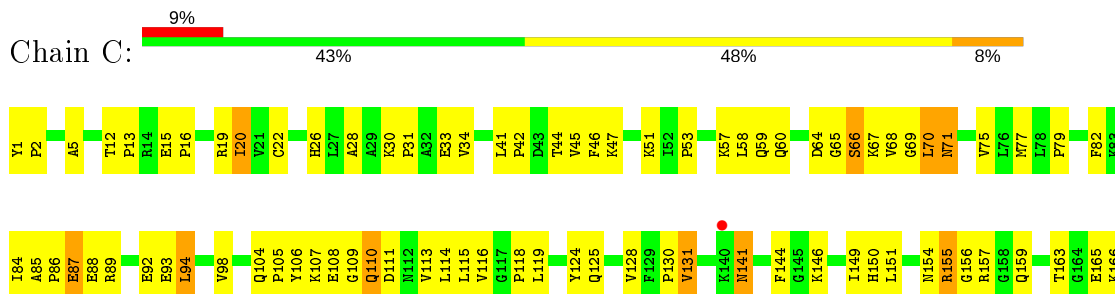
- Molecule 1: Cytochrome b6

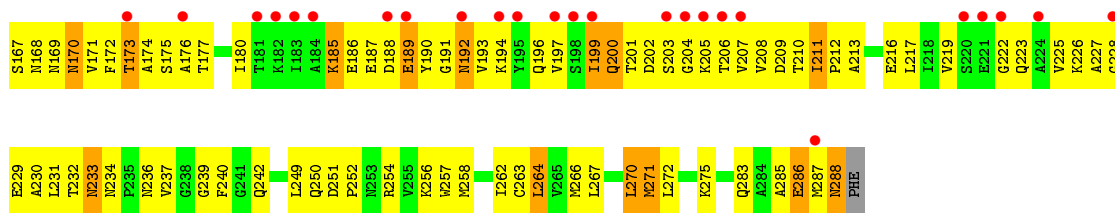


- Molecule 2: Cytochrome b6-f complex subunit 4



- Molecule 3: Apocytochrome f

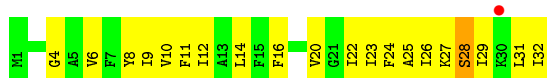




• Molecule 4: Cytochrome b6-f complex iron-sulfur subunit



• Molecule 5: Cytochrome b6-f complex subunit 6



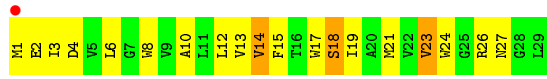
• Molecule 6: Cytochrome b6-f complex subunit 7



• Molecule 7: Cytochrome b6-f complex subunit 5



• Molecule 8: Cytochrome b6-f complex subunit 8



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	158.34Å 158.34Å 361.09Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.30 – 3.00 39.27 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (39.30-3.00) 99.7 (39.27-3.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.71 (at 3.01Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.222 , 0.268 0.219 , 0.265	Depositor DCC
R_{free} test set	2740 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	89.0	Xtrriage
Anisotropy	0.204	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 92.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8025	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.80% 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: UMQ, CLA, CD, FES, OPC, HEM, BCR, SQD

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	0.78	1/1763 (0.1%)	0.81	1/2405 (0.0%)
2	B	0.75	0/1288	0.87	3/1765 (0.2%)
3	C	0.57	1/2264 (0.0%)	0.66	0/3082
4	D	0.45	0/1292	0.57	0/1760
5	E	0.55	0/253	0.76	0/340
6	F	0.66	0/246	0.74	0/331
7	G	0.67	0/289	0.73	0/391
8	H	0.79	0/236	0.78	0/323
All	All	0.65	2/7631 (0.0%)	0.74	4/10397 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1
8	H	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	87	GLU	CG-CD	5.81	1.60	1.51
1	A	113	PRO	CB-CG	5.09	1.75	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	15	ARG	NE-CZ-NH2	-5.49	117.56	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	126	ARG	NE-CZ-NH2	-5.41	117.60	120.30
1	A	113	PRO	CA-N-CD	5.15	118.92	111.70
2	B	126	ARG	NE-CZ-NH1	5.13	122.86	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	32	TRP	Peptide
8	H	27	ASN	Peptide

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	1711	0	1736	138	1
2	B	1249	0	1308	135	0
3	C	2216	0	2232	199	2
4	D	1260	0	1243	121	0
5	E	248	0	284	27	0
6	F	242	0	260	27	0
7	G	283	0	289	42	1
8	H	230	0	239	21	0
9	A	1	0	0	0	0
9	B	1	0	0	0	0
10	A	129	0	90	24	0
10	C	43	0	30	8	0
11	A	136	0	164	13	0
12	B	65	0	72	4	0
13	B	54	0	83	2	0
13	H	54	0	83	24	0
14	D	4	0	0	2	0
15	D	54	0	57	12	0
16	G	40	0	52	11	0
17	A	2	0	0	0	0
17	B	2	0	0	0	0
17	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8025	0	8222	692	2

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 43.

All (692) 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)
15:D:201:SQD:C4	15:D:201:SQD:C3	1.85	1.54
1:A:113:PRO:CG	1:A:113:PRO:CB	1.75	1.41
15:D:201:SQD:C2	15:D:201:SQD:C4	2.11	1.27
2:B:151:LEU:O	2:B:154:THR:HG22	1.25	1.25
2:B:151:LEU:O	2:B:154:THR:CG2	1.86	1.23
2:B:139:VAL:O	2:B:143:LEU:HD12	1.43	1.19
7:G:30:LYS:O	7:G:32:PRO:HD3	1.43	1.17
3:C:65:GLY:O	3:C:66:SER:O	1.64	1.14
3:C:70:LEU:N	3:C:70:LEU:HD23	1.63	1.13
3:C:107:LYS:CE	3:C:110:GLN:NE2	2.12	1.12
4:D:78:ARG:HG2	4:D:92:VAL:HG22	1.26	1.12
4:D:166:THR:O	4:D:167:GLU:O	1.63	1.12
2:B:128:VAL:O	2:B:132:ILE:HD12	1.48	1.12
15:D:201:SQD:H2	15:D:201:SQD:C4	1.75	1.08
3:C:70:LEU:H	3:C:70:LEU:HD23	1.07	1.07
4:D:131:SER:CB	4:D:142:GLY:HA3	1.84	1.07
1:A:211:ILE:HD12	1:A:212:SER:H	1.19	1.07
4:D:109:THR:HG21	4:D:146:LEU:HB3	1.38	1.05
2:B:88:LEU:HD12	2:B:101:MET:SD	1.95	1.05
3:C:107:LYS:HE2	3:C:110:GLN:NE2	1.70	1.04
3:C:107:LYS:HE2	3:C:110:GLN:HE22	1.23	1.03
4:D:131:SER:HB3	4:D:142:GLY:HA3	1.39	1.02
2:B:158:GLY:O	2:B:159:LEU:HD23	1.57	1.02
1:A:111:LYS:O	1:A:113:PRO:HD2	1.59	1.02
2:B:128:VAL:O	2:B:132:ILE:CD1	2.09	1.01
10:A:301:HEM:HBB2	10:A:301:HEM:HMB2	1.39	0.98
4:D:133:TYR:CD2	4:D:139:VAL:HG12	1.98	0.98
15:D:201:SQD:H82	15:D:201:SQD:H241	1.45	0.98
3:C:107:LYS:HE3	3:C:110:GLN:NE2	1.78	0.98
1:A:112:LYS:HB3	1:A:113:PRO:HD3	1.46	0.97
3:C:232:THR:O	3:C:233:ASN:HB3	1.64	0.96
16:G:101:BCR:H333	13:H:1002:OPC:HBZ1	1.47	0.96
2:B:73:LEU:O	2:B:74:GLU:HB3	1.66	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:107:LYS:HE3	3:C:110:GLN:HE21	1.31	0.94
4:D:129:HIS:HB2	14:D:200:FES:S1	2.07	0.94
2:B:139:VAL:O	2:B:143:LEU:CD1	2.14	0.94
4:D:133:TYR:CE2	4:D:139:VAL:HG12	2.03	0.94
3:C:175:SER:HB2	3:C:209:ASP:OD1	1.67	0.93
1:A:7:TRP:CE2	1:A:11:ARG:NH2	2.35	0.93
3:C:188:ASP:O	3:C:190:TYR:N	2.00	0.93
4:D:131:SER:HA	4:D:142:GLY:HA3	1.49	0.93
7:G:30:LYS:C	7:G:32:PRO:HD3	1.88	0.93
4:D:131:SER:CA	4:D:142:GLY:HA3	1.98	0.93
2:B:32:TRP:CD1	2:B:33:PRO:HD3	2.04	0.92
4:D:15:ARG:HB3	5:E:31:LEU:HD23	1.51	0.92
3:C:206:THR:O	3:C:206:THR:HG22	1.69	0.91
15:D:201:SQD:H2	15:D:201:SQD:H4	1.49	0.91
3:C:262:ILE:HG23	8:H:14:VAL:HG13	1.52	0.91
3:C:199:ILE:HG22	3:C:200:GLN:H	1.36	0.90
3:C:199:ILE:O	3:C:200:GLN:HG3	1.72	0.90
4:D:155:VAL:C	4:D:156:GLN:HE21	1.73	0.90
2:B:22:MET:O	2:B:22:MET:HG2	1.72	0.90
5:E:8:TYR:CZ	5:E:12:ILE:HD11	2.07	0.90
2:B:123:PRO:HD2	7:G:25:ALA:HB1	1.54	0.90
15:D:201:SQD:C8	15:D:201:SQD:H241	2.01	0.90
4:D:67:SER:O	4:D:71:GLU:HG3	1.73	0.89
4:D:133:TYR:CE2	4:D:139:VAL:CG1	2.56	0.89
2:B:118:ASN:HD22	2:B:120:PHE:H	1.20	0.89
1:A:47:GLN:NE2	1:A:89:SER:HB3	1.86	0.89
4:D:77:ASP:O	4:D:92:VAL:HA	1.70	0.88
3:C:174:ALA:HB2	3:C:231:LEU:HD23	1.54	0.88
1:A:1:MET:H3	1:A:1:MET:HE3	1.38	0.87
3:C:70:LEU:N	3:C:70:LEU:CD2	2.37	0.87
3:C:231:LEU:HD12	3:C:231:LEU:O	1.73	0.87
3:C:155:ARG:HD2	3:C:155:ARG:H	1.39	0.87
1:A:211:ILE:HD12	1:A:212:SER:N	1.90	0.86
1:A:112:LYS:HB3	1:A:113:PRO:CD	2.06	0.86
3:C:94:LEU:O	3:C:94:LEU:HD23	1.76	0.86
11:A:1101:UMQ:HL3	4:D:37:PRO:HG2	1.58	0.85
1:A:92:MET:CE	13:H:1002:OPC:HBY1	2.05	0.85
1:A:103:ARG:NH1	1:A:104:VAL:HA	1.92	0.85
2:B:73:LEU:O	2:B:74:GLU:CB	2.24	0.85
2:B:109:ILE:O	2:B:112:PRO:HD2	1.77	0.84
15:D:201:SQD:C5	15:D:201:SQD:C3	2.55	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:301:HEM:HBB2	10:A:301:HEM:CMB	2.06	0.84
1:A:211:ILE:CD1	1:A:212:SER:H	1.91	0.83
2:B:45:MET:HE3	4:D:27:VAL:HG13	1.61	0.83
7:G:2:VAL:CG1	7:G:3:GLU:N	2.42	0.83
4:D:156:GLN:N	4:D:156:GLN:HE21	1.76	0.82
5:E:16:PHE:CD2	6:F:22:LEU:HD21	2.14	0.82
5:E:4:GLY:HA3	13:H:1002:OPC:HAS1	1.60	0.82
4:D:133:TYR:CD2	4:D:139:VAL:CG1	2.63	0.82
1:A:1:MET:CE	1:A:1:MET:N	2.43	0.82
1:A:215:LEU:H	1:A:215:LEU:HD23	1.45	0.82
4:D:131:SER:HB3	4:D:143:PRO:HD2	1.62	0.81
7:G:2:VAL:HG12	7:G:3:GLU:N	1.93	0.81
3:C:225:VAL:CG1	3:C:229:GLU:HG2	2.10	0.81
7:G:5:LEU:HD11	13:H:1002:OPC:HBN1	1.62	0.81
4:D:135:GLU:OE2	4:D:135:GLU:N	2.14	0.81
3:C:5:ALA:HB2	10:C:301:HEM:HBB2	1.62	0.81
7:G:28:GLN:O	7:G:32:PRO:HB3	1.81	0.80
10:A:302:HEM:CMB	10:A:302:HEM:HBB2	2.12	0.80
3:C:180:ILE:CG2	3:C:222:GLY:H	1.94	0.80
1:A:111:LYS:O	1:A:113:PRO:CD	2.28	0.80
6:F:20:TRP:CZ3	16:G:101:BCR:H19C	2.17	0.80
1:A:112:LYS:O	1:A:115:GLU:OE1	1.99	0.80
3:C:30:LYS:HB3	3:C:31:PRO:HD2	1.64	0.80
1:A:92:MET:HE1	13:H:1002:OPC:HBY1	1.64	0.79
10:A:302:HEM:HMB1	10:A:302:HEM:HBB2	1.64	0.79
2:B:84:VAL:HG13	2:B:101:MET:HG2	1.61	0.79
7:G:2:VAL:CG1	7:G:3:GLU:H	1.95	0.79
1:A:215:LEU:N	1:A:215:LEU:HD23	1.98	0.79
1:A:137:SER:HB2	1:A:148:VAL:HG21	1.64	0.79
7:G:30:LYS:O	7:G:32:PRO:CD	2.29	0.79
3:C:216:GLU:O	3:C:217:LEU:HD23	1.82	0.79
3:C:34:VAL:HG22	3:C:151:LEU:HD22	1.65	0.79
15:D:201:SQD:O3	15:D:201:SQD:C4	2.30	0.79
3:C:201:THR:HG22	3:C:202:ASP:N	1.97	0.78
2:B:143:LEU:H	2:B:143:LEU:HD12	1.48	0.78
3:C:199:ILE:O	3:C:200:GLN:CG	2.30	0.78
2:B:32:TRP:HB3	2:B:33:PRO:CD	2.13	0.78
1:A:11:ARG:HB2	1:A:12:LEU:HD22	1.66	0.78
2:B:99:LEU:O	2:B:103:SER:OG	2.01	0.78
7:G:5:LEU:HD11	13:H:1002:OPC:CBN	2.13	0.78
1:A:36:LEU:HD23	1:A:99:LEU:C	2.05	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:20:TRP:HZ3	16:G:101:BCR:H19C	1.48	0.77
3:C:232:THR:O	3:C:233:ASN:CB	2.30	0.77
1:A:29:HIS:CD2	1:A:214:PRO:HA	2.20	0.76
3:C:188:ASP:C	3:C:190:TYR:H	1.87	0.76
4:D:131:SER:HA	4:D:142:GLY:CA	2.14	0.76
3:C:155:ARG:HD2	3:C:155:ARG:N	1.97	0.76
3:C:22:CYS:SG	3:C:240:PHE:CD1	2.76	0.76
3:C:177:THR:HG23	3:C:226:LYS:HG2	1.68	0.76
1:A:83:ARG:NH2	2:B:61:MET:O	2.16	0.75
2:B:118:ASN:ND2	2:B:120:PHE:H	1.84	0.75
1:A:92:MET:CE	13:H:1002:OPC:CBY	2.64	0.75
3:C:196:GLN:NE2	3:C:210:THR:OG1	2.18	0.75
6:F:25:LEU:O	6:F:29:ILE:HG22	1.87	0.75
1:A:1:MET:N	1:A:1:MET:HE3	2.01	0.75
3:C:211:ILE:HD12	3:C:212:PRO:O	1.87	0.74
4:D:138:LYS:HA	4:D:147:SER:OG	1.86	0.74
2:B:31:ALA:O	2:B:32:TRP:O	2.04	0.74
4:D:67:SER:O	4:D:71:GLU:CG	2.36	0.74
1:A:7:TRP:NE1	1:A:11:ARG:NH2	2.36	0.74
2:B:82:TYR:HB2	2:B:83:PRO:HD3	1.70	0.74
1:A:61:THR:HG22	1:A:64:GLU:H	1.51	0.73
6:F:13:PHE:CE2	6:F:17:PHE:HE1	2.06	0.73
4:D:108:CYS:HB2	4:D:133:TYR:OH	1.88	0.73
3:C:19:ARG:O	3:C:20:ILE:HB	1.89	0.73
1:A:202:HIS:O	1:A:206:ILE:HG13	1.88	0.73
1:A:47:GLN:HE22	1:A:89:SER:HB3	1.51	0.72
1:A:103:ARG:HH11	1:A:104:VAL:HA	1.51	0.72
2:B:34:ASN:HD21	3:C:283:GLN:HE22	1.35	0.72
7:G:29:TYR:CD2	7:G:29:TYR:O	2.43	0.72
3:C:68:VAL:HG22	3:C:69:GLY:H	1.53	0.72
2:B:119:LYS:O	2:B:119:LYS:CG	2.37	0.72
3:C:199:ILE:O	3:C:200:GLN:CB	2.37	0.72
3:C:206:THR:O	3:C:206:THR:CG2	2.37	0.72
7:G:34:GLU:O	7:G:35:LEU:HB2	1.88	0.71
4:D:155:VAL:C	4:D:156:GLN:NE2	2.43	0.71
1:A:54:MET:CE	10:A:301:HEM:HBD1	2.20	0.71
3:C:185:LYS:HD3	3:C:185:LYS:O	1.90	0.71
3:C:98:VAL:HG21	3:C:130:PRO:HG3	1.73	0.71
3:C:176:ALA:HA	3:C:227:ALA:HB2	1.73	0.70
16:G:101:BCR:C32	8:H:19:ILE:HG12	2.21	0.70
2:B:135:PHE:O	2:B:139:VAL:HG23	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:154:THR:HG23	2:B:155:LEU:H	1.56	0.70
2:B:32:TRP:CG	2:B:33:PRO:HD3	2.26	0.70
3:C:286:GLU:OE1	3:C:286:GLU:N	2.24	0.70
4:D:92:VAL:HB	4:D:100:ARG:HD2	1.73	0.70
2:B:32:TRP:CB	2:B:33:PRO:CD	2.69	0.70
3:C:177:THR:HG23	3:C:226:LYS:HA	1.74	0.70
3:C:94:LEU:HD23	3:C:94:LEU:C	2.12	0.70
3:C:58:LEU:HD13	3:C:59:GLN:N	2.07	0.70
3:C:94:LEU:CD2	3:C:98:VAL:HG23	2.22	0.69
2:B:118:ASN:ND2	2:B:120:PHE:CD1	2.60	0.69
3:C:94:LEU:HD23	3:C:98:VAL:HG23	1.74	0.69
1:A:92:MET:CE	13:H:1002:OPC:HCB3	2.22	0.69
5:E:22:ILE:O	5:E:26:ILE:HB	1.92	0.69
3:C:28:ALA:HB3	3:C:239:GLY:HA2	1.72	0.69
1:A:104:VAL:O	1:A:107:THR:HG22	1.92	0.69
6:F:13:PHE:CE2	6:F:17:PHE:CE1	2.80	0.69
4:D:131:SER:HB3	4:D:142:GLY:CA	2.20	0.68
1:A:80:TRP:HE1	11:A:1101:UMQ:H6'1	1.57	0.68
7:G:2:VAL:HG13	7:G:3:GLU:H	1.59	0.68
3:C:163:THR:OG1	3:C:165:GLU:HG2	1.94	0.68
4:D:109:THR:HG21	4:D:146:LEU:CB	2.21	0.68
3:C:13:PRO:O	3:C:20:ILE:HA	1.93	0.68
4:D:15:ARG:HB3	5:E:31:LEU:CD2	2.23	0.68
3:C:189:GLU:OE1	3:C:189:GLU:N	2.26	0.68
3:C:288:ASN:H	3:C:288:ASN:HD22	1.40	0.68
6:F:7:TYR:O	6:F:11:LEU:HD12	1.94	0.68
1:A:105:TYR:CD1	12:B:201:CLA:HMB1	2.29	0.67
3:C:286:GLU:OE1	3:C:286:GLU:CA	2.41	0.67
3:C:79:PRO:HG2	3:C:82:PHE:CD1	2.29	0.67
2:B:32:TRP:HB3	2:B:33:PRO:HD3	1.76	0.67
1:A:114:ARG:NH1	1:A:210:GLY:O	2.27	0.67
3:C:46:PHE:CE2	3:C:131:VAL:HG22	2.30	0.67
4:D:57:LYS:HB3	4:D:61:GLY:HA2	1.76	0.67
1:A:155:PRO:HB2	1:A:166:SER:OG	1.94	0.67
3:C:219:VAL:HG21	3:C:231:LEU:HB2	1.77	0.66
1:A:1:MET:H1	1:A:1:MET:HE2	1.60	0.66
3:C:180:ILE:HG23	3:C:222:GLY:H	1.61	0.66
4:D:99:ILE:HG13	4:D:100:ARG:H	1.60	0.66
4:D:99:ILE:HG23	4:D:100:ARG:N	2.09	0.66
3:C:60:GLN:HE22	3:C:156:GLY:HA2	1.60	0.66
3:C:194:LYS:HB2	3:C:194:LYS:NZ	2.11	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:167:SER:OG	3:C:168:ASN:N	2.27	0.66
3:C:177:THR:N	3:C:227:ALA:HB2	2.10	0.66
5:E:6:VAL:O	5:E:10:VAL:HG23	1.95	0.66
10:A:303:HEM:HHA	10:A:303:HEM:HBD1	1.76	0.66
1:A:92:MET:HE2	13:H:1002:OPC:CBY	2.26	0.66
5:E:23:ILE:O	5:E:27:LYS:N	2.29	0.66
1:A:137:SER:HB2	1:A:148:VAL:CG2	2.26	0.65
4:D:122:ASN:HB3	4:D:135:GLU:OE1	1.95	0.65
6:F:18:VAL:O	6:F:22:LEU:HB2	1.96	0.65
3:C:201:THR:CG2	3:C:202:ASP:H	2.09	0.65
3:C:177:THR:CG2	3:C:226:LYS:HG2	2.26	0.65
4:D:63:ASN:HB3	4:D:159:ASN:HD21	1.61	0.65
4:D:109:THR:O	4:D:109:THR:HG22	1.95	0.65
4:D:63:ASN:HB3	4:D:159:ASN:ND2	2.11	0.65
3:C:201:THR:CG2	3:C:202:ASP:N	2.59	0.65
4:D:107:VAL:HG12	4:D:112:GLY:HA2	1.77	0.65
1:A:36:LEU:HB3	1:A:100:HIS:HB2	1.78	0.65
3:C:59:GLN:OE1	3:C:67:LYS:O	2.15	0.65
1:A:83:ARG:HD2	10:A:301:HEM:O1D	1.97	0.65
5:E:16:PHE:HD2	6:F:22:LEU:HD21	1.61	0.65
2:B:142:TRP:CZ2	2:B:155:LEU:O	2.50	0.64
3:C:201:THR:HG22	3:C:202:ASP:H	1.59	0.64
1:A:1:MET:CE	1:A:1:MET:H3	2.03	0.64
3:C:141:ASN:HD22	3:C:141:ASN:C	2.00	0.64
3:C:229:GLU:OE1	3:C:229:GLU:HA	1.97	0.64
7:G:20:GLY:N	16:G:101:BCR:H363	2.13	0.64
1:A:92:MET:HE2	13:H:1002:OPC:HBY2	1.79	0.64
3:C:251:ASP:HB3	3:C:254:ARG:HD3	1.79	0.64
1:A:1:MET:H1	1:A:1:MET:CE	2.10	0.64
2:B:45:MET:CE	4:D:27:VAL:HG13	2.27	0.64
3:C:94:LEU:CD2	3:C:94:LEU:C	2.66	0.64
2:B:151:LEU:O	2:B:154:THR:HG21	1.96	0.64
2:B:22:MET:CG	2:B:22:MET:O	2.41	0.63
3:C:64:ASP:HB2	3:C:192:ASN:HD22	1.62	0.63
3:C:94:LEU:CD2	3:C:98:VAL:CG2	2.75	0.63
12:B:201:CLA:HAC1	13:B:202:OPC:HBW1	1.80	0.63
2:B:8:ASP:OD1	2:B:10:SER:HB3	1.98	0.63
2:B:119:LYS:O	2:B:119:LYS:HG3	1.97	0.63
3:C:68:VAL:HG22	3:C:69:GLY:N	2.13	0.63
4:D:116:PRO:HD2	4:D:125:LYS:O	1.98	0.63
1:A:111:LYS:C	1:A:113:PRO:HD2	2.19	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:ARG:HG3	1:A:172:GLY:O	1.99	0.63
1:A:110:PHE:HD1	2:B:112:PRO:HB3	1.63	0.62
3:C:176:ALA:C	3:C:227:ALA:HB2	2.19	0.62
4:D:169:ASP:OD1	4:D:176:PRO:HB3	1.98	0.62
4:D:130:GLY:O	4:D:141:ARG:NH2	2.31	0.62
11:A:1104:UMQ:HC1	2:B:32:TRP:CZ2	2.34	0.62
4:D:118:ASN:HD22	4:D:118:ASN:C	2.03	0.62
1:A:36:LEU:HD23	1:A:100:HIS:N	2.14	0.61
2:B:142:TRP:HZ2	2:B:155:LEU:O	1.84	0.61
3:C:275:LYS:HD3	4:D:19:MET:HB3	1.82	0.61
4:D:156:GLN:CA	4:D:156:GLN:HE21	2.13	0.61
1:A:63:THR:HG22	1:A:64:GLU:HG3	1.82	0.61
3:C:119:LEU:HD22	3:C:124:TYR:CE1	2.36	0.61
1:A:142:GLN:HG3	2:B:72:PRO:HG3	1.82	0.61
1:A:93:MET:SD	10:A:301:HEM:HBB1	2.41	0.61
3:C:171:VAL:HG12	3:C:233:ASN:O	2.01	0.61
3:C:176:ALA:HA	3:C:227:ALA:CB	2.30	0.61
2:B:75:ILE:O	2:B:75:ILE:HG12	2.00	0.61
2:B:88:LEU:CD1	2:B:101:MET:SD	2.83	0.61
4:D:131:SER:HB3	4:D:143:PRO:CD	2.31	0.61
1:A:100:HIS:HE1	10:A:302:HEM:C1A	2.19	0.61
2:B:156:THR:O	2:B:157:LEU:HB2	2.01	0.60
2:B:32:TRP:CB	2:B:33:PRO:HD3	2.31	0.60
2:B:114:ILE:O	2:B:117:VAL:HG23	2.01	0.60
1:A:103:ARG:HH12	1:A:104:VAL:HG22	1.66	0.60
10:A:302:HEM:HMB1	10:A:302:HEM:CBB	2.30	0.60
4:D:156:GLN:N	4:D:156:GLN:NE2	2.49	0.60
3:C:71:ASN:N	10:C:301:HEM:O2A	2.16	0.60
3:C:15:GLU:HB3	3:C:16:PRO:CD	2.31	0.60
3:C:57:LYS:HA	3:C:57:LYS:HE2	1.82	0.60
5:E:26:ILE:HG22	5:E:32:ILE:HD12	1.83	0.60
7:G:33:ASN:O	7:G:34:GLU:O	2.20	0.60
1:A:137:SER:CB	1:A:148:VAL:HG21	2.30	0.60
2:B:57:LEU:HD13	8:H:8:TRP:HA	1.83	0.60
11:A:1104:UMQ:H21	11:A:1104:UMQ:H62	1.83	0.59
4:D:78:ARG:CG	4:D:92:VAL:HG22	2.15	0.59
3:C:211:ILE:HD12	3:C:211:ILE:C	2.23	0.59
1:A:31:ASN:C	1:A:31:ASN:HD22	2.05	0.59
2:B:118:ASN:ND2	2:B:120:PHE:HD1	2.00	0.59
4:D:145:PRO:O	4:D:146:LEU:HB2	2.02	0.59
15:D:201:SQD:H81	15:D:201:SQD:H241	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:VAL:HB	1:A:155:PRO:HD3	1.85	0.59
7:G:5:LEU:CD1	13:H:1002:OPC:HBN1	2.31	0.59
5:E:29:ILE:O	5:E:29:ILE:HG22	2.01	0.59
2:B:152:ASP:OD2	2:B:153:LYS:HG2	2.03	0.59
1:A:114:ARG:NH2	1:A:212:SER:HA	2.17	0.59
2:B:139:VAL:HG12	2:B:143:LEU:HD11	1.83	0.59
2:B:79:TRP:CG	2:B:80:TYR:N	2.70	0.59
5:E:25:ALA:O	5:E:29:ILE:HG13	2.02	0.59
1:A:137:SER:CB	1:A:148:VAL:CG2	2.80	0.59
3:C:176:ALA:CA	3:C:227:ALA:HB2	2.32	0.59
2:B:123:PRO:CD	7:G:25:ALA:HB1	2.31	0.59
2:B:2:ALA:O	2:B:3:THR:OG1	2.16	0.59
3:C:199:ILE:O	3:C:200:GLN:HB2	2.03	0.59
4:D:121:GLU:O	4:D:122:ASN:HB2	2.02	0.59
1:A:12:LEU:O	1:A:13:GLU:HB2	2.03	0.59
3:C:64:ASP:HB2	3:C:192:ASN:ND2	2.17	0.59
1:A:158:ILE:HG23	1:A:159:PRO:HD2	1.83	0.58
4:D:108:CYS:HB3	4:D:115:VAL:CG2	2.34	0.58
1:A:92:MET:HE3	13:H:1002:OPC:HCB3	1.86	0.58
11:A:1101:UMQ:HD2	3:C:257:TRP:HB2	1.85	0.58
2:B:95:LEU:HD22	2:B:99:LEU:CD1	2.33	0.58
4:D:118:ASN:ND2	4:D:120:ALA:H	2.02	0.58
4:D:176:PRO:HD2	4:D:179:VAL:HG22	1.86	0.58
3:C:204:GLY:O	3:C:205:LYS:HB2	2.03	0.58
4:D:105:ASN:HB2	4:D:149:ALA:HB3	1.86	0.58
7:G:31:ARG:HG2	7:G:31:ARG:O	2.02	0.58
4:D:36:TYR:HB3	4:D:37:PRO:HD3	1.86	0.57
1:A:103:ARG:O	1:A:107:THR:HB	2.03	0.57
4:D:133:TYR:N	4:D:133:TYR:CD1	2.71	0.57
1:A:103:ARG:HH11	1:A:104:VAL:CA	2.17	0.57
10:A:303:HEM:CHA	10:A:303:HEM:HBD1	2.33	0.57
3:C:42:PRO:HG3	3:C:144:PHE:HE2	1.68	0.57
3:C:5:ALA:HB2	10:C:301:HEM:CBB	2.34	0.57
1:A:92:MET:HE2	13:H:1002:OPC:HCB3	1.86	0.57
3:C:71:ASN:N	3:C:71:ASN:HD22	2.03	0.57
5:E:8:TYR:OH	6:F:15:LEU:HD22	2.03	0.57
2:B:151:LEU:O	2:B:154:THR:CB	2.53	0.57
6:F:11:LEU:HD21	13:H:1002:OPC:HAV	1.86	0.57
1:A:115:GLU:O	1:A:119:ILE:HG13	2.04	0.56
2:B:84:VAL:HG13	2:B:101:MET:CG	2.32	0.56
1:A:103:ARG:HD2	1:A:103:ARG:O	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:82:TYR:HB2	2:B:83:PRO:CD	2.35	0.56
5:E:28:SER:O	5:E:29:ILE:HG12	2.05	0.56
13:H:1002:OPC:HBC1	13:H:1002:OPC:HAY1	1.86	0.56
11:A:1104:UMQ:H21	11:A:1104:UMQ:C6	2.35	0.56
1:A:39:ILE:HD11	16:G:101:BCR:H312	1.87	0.56
1:A:61:THR:HG22	1:A:64:GLU:N	2.21	0.56
3:C:194:LYS:HB2	3:C:194:LYS:HZ2	1.71	0.56
1:A:106:LEU:HD12	7:G:21:LEU:HD23	1.86	0.56
2:B:110:LEU:O	2:B:111:VAL:C	2.43	0.56
4:D:118:ASN:HD22	4:D:120:ALA:H	1.52	0.56
1:A:29:HIS:CD2	1:A:214:PRO:CA	2.89	0.56
3:C:71:ASN:N	3:C:71:ASN:ND2	2.53	0.56
1:A:115:GLU:N	1:A:115:GLU:OE1	2.39	0.56
6:F:25:LEU:O	6:F:29:ILE:CG2	2.52	0.56
3:C:187:GLU:O	3:C:187:GLU:HG3	2.06	0.56
2:B:134:LEU:HD11	7:G:22:PHE:CZ	2.40	0.56
4:D:133:TYR:CD2	4:D:148:LEU:HG	2.41	0.56
1:A:1:MET:O	1:A:2:ALA:HB3	2.06	0.55
3:C:199:ILE:HG22	3:C:200:GLN:N	2.13	0.55
4:D:138:LYS:HA	4:D:147:SER:CB	2.36	0.55
2:B:71:THR:HG22	2:B:72:PRO:O	2.06	0.55
3:C:175:SER:HB2	3:C:209:ASP:CG	2.25	0.55
2:B:128:VAL:O	2:B:132:ILE:HD13	2.02	0.55
3:C:216:GLU:HG3	3:C:217:LEU:H	1.71	0.55
4:D:89:THR:HG23	4:D:104:ILE:C	2.27	0.55
1:A:47:GLN:NE2	1:A:89:SER:CB	2.65	0.55
2:B:11:ASP:OD1	2:B:13:LYS:HB2	2.07	0.55
3:C:270:LEU:HA	8:H:21:MET:HE2	1.87	0.55
6:F:13:PHE:CD2	6:F:17:PHE:HE1	2.25	0.54
2:B:57:LEU:CD1	8:H:8:TRP:HA	2.36	0.54
3:C:79:PRO:HG2	3:C:82:PHE:CE1	2.41	0.54
3:C:286:GLU:HA	3:C:286:GLU:OE1	2.06	0.54
3:C:41:LEU:HD22	3:C:252:PRO:HG3	1.88	0.54
3:C:173:THR:HB	3:C:228:GLY:HA2	1.88	0.54
1:A:100:HIS:CE1	10:A:302:HEM:C1A	2.95	0.54
3:C:174:ALA:CB	3:C:231:LEU:HD23	2.34	0.54
3:C:258:MET:O	3:C:262:ILE:HD13	2.07	0.54
4:D:56:ALA:HB1	4:D:81:VAL:HG11	1.90	0.54
5:E:10:VAL:O	5:E:14:LEU:HB2	2.08	0.54
6:F:29:ILE:HD12	6:F:29:ILE:O	2.08	0.54
3:C:169:ASN:O	3:C:236:ASN:HB2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:15:GLU:HB3	3:C:16:PRO:HD2	1.90	0.53
4:D:109:THR:O	4:D:109:THR:CG2	2.55	0.53
2:B:45:MET:HE1	4:D:27:VAL:HA	1.91	0.53
4:D:55:THR:HG22	4:D:56:ALA:N	2.22	0.53
3:C:197:VAL:O	3:C:208:VAL:HG13	2.08	0.53
3:C:288:ASN:ND2	3:C:288:ASN:H	2.06	0.53
1:A:170:ARG:CG	1:A:172:GLY:O	2.57	0.53
2:B:6:LYS:NZ	2:B:6:LYS:HB2	2.24	0.53
6:F:3:GLU:O	6:F:7:TYR:HB2	2.09	0.53
7:G:29:TYR:O	7:G:29:TYR:CG	2.61	0.53
3:C:172:PHE:O	3:C:232:THR:OG1	2.27	0.53
2:B:34:ASN:HD22	2:B:34:ASN:N	2.07	0.53
3:C:34:VAL:CG2	3:C:151:LEU:HD22	2.35	0.53
15:D:201:SQD:C8	15:D:201:SQD:C24	2.83	0.53
3:C:172:PHE:H	3:C:232:THR:CB	2.20	0.53
3:C:262:ILE:HG23	8:H:14:VAL:CG1	2.34	0.53
3:C:285:ALA:C	3:C:286:GLU:OE1	2.47	0.53
7:G:3:GLU:OE1	7:G:3:GLU:C	2.47	0.53
2:B:32:TRP:CG	2:B:33:PRO:CD	2.90	0.53
15:D:201:SQD:C4	15:D:201:SQD:HO3	2.21	0.52
3:C:199:ILE:C	3:C:200:GLN:HG3	2.29	0.52
1:A:138:LEU:N	1:A:139:PRO:CD	2.71	0.52
2:B:124:PHE:CE1	7:G:26:TYR:HB2	2.45	0.52
8:H:15:PHE:CG	13:H:1002:OPC:HBT1	2.44	0.52
1:A:144:GLY:O	1:A:148:VAL:HG23	2.10	0.52
3:C:22:CYS:HB2	10:C:301:HEM:CAB	2.40	0.52
3:C:172:PHE:N	3:C:232:THR:OG1	2.39	0.52
1:A:215:LEU:HB2	2:B:122:ASN:HB2	1.90	0.52
2:B:17:LYS:HE3	2:B:26:TYR:OH	2.10	0.52
2:B:32:TRP:HD1	2:B:33:PRO:HD3	1.70	0.52
3:C:107:LYS:CE	3:C:110:GLN:HE22	1.93	0.52
7:G:34:GLU:O	7:G:35:LEU:CB	2.59	0.51
2:B:86:GLN:HG2	2:B:143:LEU:HB3	1.93	0.51
3:C:194:LYS:CB	3:C:194:LYS:NZ	2.74	0.51
1:A:110:PHE:H	1:A:110:PHE:HD2	1.57	0.51
1:A:103:ARG:C	1:A:103:ARG:HD2	2.30	0.51
3:C:94:LEU:HD21	3:C:98:VAL:CG2	2.40	0.51
1:A:150:ILE:HG22	1:A:151:VAL:N	2.26	0.51
3:C:191:GLY:O	3:C:192:ASN:O	2.29	0.51
3:C:33:GLU:HB3	3:C:51:LYS:HB2	1.93	0.51
4:D:105:ASN:CB	4:D:149:ALA:HB3	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:77:ASP:N	4:D:77:ASP:OD2	2.44	0.51
1:A:215:LEU:N	1:A:215:LEU:CD2	2.73	0.51
1:A:35:CYS:SG	10:A:303:HEM:HMB1	2.51	0.51
3:C:84:ILE:HG12	3:C:114:LEU:HD11	1.93	0.50
4:D:90:TYR:CD1	4:D:106:ALA:HB2	2.46	0.50
1:A:111:LYS:HE2	2:B:115:GLU:O	2.10	0.50
4:D:141:ARG:HE	4:D:142:GLY:H	1.59	0.50
3:C:271:MET:HB3	4:D:23:ALA:HA	1.93	0.50
2:B:82:TYR:CB	2:B:83:PRO:HD3	2.41	0.50
3:C:231:LEU:CD1	3:C:231:LEU:O	2.53	0.50
11:A:1104:UMQ:C6	11:A:1104:UMQ:C2	2.88	0.50
2:B:32:TRP:O	2:B:33:PRO:C	2.49	0.50
15:D:201:SQD:H81	15:D:201:SQD:C24	2.41	0.50
10:A:301:HEM:CBB	10:A:301:HEM:HMB2	2.29	0.50
2:B:118:ASN:HD22	2:B:120:PHE:N	1.98	0.50
3:C:225:VAL:HG11	3:C:229:GLU:HG2	1.93	0.50
1:A:211:ILE:CD1	1:A:212:SER:N	2.63	0.50
2:B:74:GLU:O	2:B:74:GLU:HG3	2.11	0.50
3:C:211:ILE:O	3:C:211:ILE:HD12	2.11	0.50
3:C:193:VAL:O	3:C:213:ALA:HB2	2.12	0.49
3:C:109:GLY:O	3:C:111:ASP:N	2.44	0.49
3:C:30:LYS:HB3	3:C:31:PRO:CD	2.39	0.49
1:A:170:ARG:HD2	1:A:172:GLY:O	2.12	0.49
3:C:13:PRO:HB3	3:C:106:TYR:CE1	2.47	0.49
4:D:133:TYR:CD2	4:D:139:VAL:HG13	2.48	0.49
2:B:132:ILE:HD12	2:B:132:ILE:H	1.76	0.49
2:B:11:ASP:O	2:B:15:ARG:HG3	2.13	0.49
3:C:270:LEU:HA	8:H:21:MET:CE	2.41	0.49
5:E:24:PHE:O	5:E:25:ALA:C	2.50	0.49
8:H:8:TRP:CE3	13:H:1002:OPC:HBL1	2.47	0.49
16:G:101:BCR:H323	8:H:19:ILE:CG1	2.43	0.49
1:A:47:GLN:NE2	1:A:47:GLN:HA	2.27	0.49
4:D:38:LEU:O	4:D:41:TYR:HB3	2.12	0.49
4:D:56:ALA:HB1	4:D:81:VAL:CG1	2.43	0.49
8:H:15:PHE:CD1	13:H:1002:OPC:HBW1	2.48	0.49
3:C:203:SER:O	3:C:205:LYS:HG3	2.13	0.48
3:C:157:ARG:HE	10:C:301:HEM:CGD	2.25	0.48
4:D:55:THR:CG2	4:D:56:ALA:N	2.76	0.48
3:C:288:ASN:N	3:C:288:ASN:HD22	2.02	0.48
4:D:81:VAL:O	4:D:88:PRO:HA	2.14	0.48
2:B:50:CYS:HB3	13:H:1002:OPC:HBX1	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:23:VAL:O	8:H:24:TRP:C	2.50	0.48
2:B:61:MET:HG3	3:C:146:LYS:HB3	1.94	0.48
3:C:75:VAL:O	3:C:75:VAL:HG13	2.14	0.48
4:D:77:ASP:OD1	4:D:92:VAL:O	2.30	0.48
4:D:156:GLN:HB2	4:D:161:VAL:CG2	2.43	0.48
1:A:114:ARG:CZ	1:A:212:SER:HA	2.43	0.48
2:B:104:VAL:HB	2:B:105:PRO:HD3	1.94	0.48
1:A:106:LEU:HD21	2:B:133:PHE:CE1	2.48	0.48
5:E:16:PHE:HZ	6:F:25:LEU:HD22	1.78	0.48
6:F:25:LEU:HD23	6:F:29:ILE:HG22	1.94	0.48
5:E:24:PHE:O	5:E:28:SER:N	2.44	0.48
3:C:225:VAL:CG1	3:C:229:GLU:CG	2.87	0.48
5:E:16:PHE:HE1	5:E:20:VAL:HG21	1.79	0.48
2:B:128:VAL:HG12	2:B:132:ILE:CD1	2.44	0.48
3:C:5:ALA:CB	10:C:301:HEM:HBB2	2.39	0.48
1:A:27:PRO:HB2	1:A:29:HIS:ND1	2.29	0.48
1:A:52:PHE:N	10:A:301:HEM:CBC	2.76	0.48
3:C:19:ARG:O	3:C:20:ILE:CB	2.53	0.48
3:C:28:ALA:HB2	3:C:236:ASN:ND2	2.28	0.48
1:A:39:ILE:HG22	1:A:96:MET:HG3	1.94	0.48
8:H:10:ALA:O	8:H:14:VAL:HG22	2.13	0.48
2:B:95:LEU:O	2:B:95:LEU:HD23	2.14	0.47
3:C:77:MET:HB2	3:C:150:HIS:HB2	1.95	0.47
3:C:65:GLY:C	3:C:66:SER:O	2.44	0.47
8:H:17:TRP:O	8:H:21:MET:HB2	2.14	0.47
2:B:82:TYR:CB	2:B:83:PRO:CD	2.91	0.47
6:F:8:ALA:HB2	7:G:5:LEU:HD12	1.96	0.47
2:B:32:TRP:CG	2:B:33:PRO:N	2.82	0.47
3:C:116:VAL:O	3:C:116:VAL:HG12	2.15	0.47
6:F:20:TRP:CD1	6:F:20:TRP:C	2.87	0.47
6:F:6:LEU:O	6:F:10:LEU:HD23	2.14	0.47
2:B:134:LEU:HD11	7:G:22:PHE:HZ	1.77	0.47
3:C:60:GLN:NE2	3:C:70:LEU:HB3	2.29	0.47
1:A:77:SER:O	1:A:78:PHE:HB2	2.15	0.47
3:C:104:GLN:HA	3:C:105:PRO:HD3	1.71	0.47
3:C:1:TYR:CD2	3:C:118:PRO:HG3	2.49	0.47
1:A:158:ILE:HA	1:A:159:PRO:HD3	1.63	0.47
3:C:171:VAL:HG13	3:C:234:ASN:HD22	1.79	0.47
4:D:118:ASN:HD21	4:D:120:ALA:HB3	1.79	0.47
4:D:131:SER:CB	4:D:143:PRO:HD2	2.39	0.47
6:F:30:GLN:HG3	6:F:31:GLY:N	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:G:101:BCR:H323	8:H:19:ILE:HG12	1.95	0.47
1:A:112:LYS:CB	1:A:113:PRO:CD	2.82	0.47
2:B:152:ASP:C	2:B:154:THR:H	2.17	0.47
3:C:288:ASN:ND2	3:C:288:ASN:N	2.62	0.47
3:C:42:PRO:HG3	3:C:144:PHE:CE2	2.50	0.47
4:D:75:ALA:O	4:D:76:GLY:C	2.53	0.47
7:G:11:LEU:O	7:G:12:GLY:C	2.50	0.47
2:B:11:ASP:OD1	2:B:13:LYS:N	2.46	0.47
2:B:129:ALA:O	2:B:130:THR:C	2.52	0.47
2:B:137:THR:HG21	7:G:18:LEU:HD11	1.96	0.47
2:B:154:THR:HG23	2:B:155:LEU:N	2.27	0.47
3:C:199:ILE:CG2	3:C:200:GLN:H	2.12	0.47
4:D:115:VAL:HG13	4:D:125:LYS:C	2.35	0.47
4:D:165:TRP:CH2	4:D:170:PHE:HD1	2.33	0.47
4:D:57:LYS:HG3	4:D:62:ASN:O	2.15	0.47
2:B:119:LYS:HG2	2:B:119:LYS:O	2.14	0.46
2:B:34:ASN:HD22	2:B:34:ASN:H	1.62	0.46
3:C:199:ILE:HD12	3:C:207:VAL:HG23	1.97	0.46
5:E:24:PHE:CZ	6:F:29:ILE:HD11	2.50	0.46
3:C:1:TYR:HD2	3:C:118:PRO:HG3	1.81	0.46
1:A:97:MET:O	1:A:100:HIS:HB3	2.15	0.46
2:B:32:TRP:CD1	2:B:33:PRO:CD	2.89	0.46
3:C:45:VAL:HG21	3:C:89:ARG:O	2.16	0.46
4:D:169:ASP:C	4:D:171:ARG:H	2.19	0.46
6:F:26:LEU:HA	6:F:26:LEU:HD13	1.77	0.46
10:A:302:HEM:HBA1	10:A:302:HEM:HHA	1.98	0.46
2:B:122:ASN:HA	2:B:123:PRO:HD3	1.88	0.46
3:C:68:VAL:CG2	3:C:69:GLY:H	2.26	0.46
1:A:17:LEU:HD13	1:A:17:LEU:O	2.15	0.46
1:A:106:LEU:HD21	2:B:133:PHE:CD1	2.51	0.46
4:D:152:HIS:O	4:D:162:LEU:HA	2.16	0.46
4:D:141:ARG:CG	4:D:142:GLY:H	2.28	0.46
1:A:11:ARG:HG2	1:A:11:ARG:H	1.45	0.46
6:F:24:VAL:O	6:F:27:LEU:N	2.49	0.46
1:A:29:HIS:CB	7:G:28:GLN:HE22	2.29	0.46
1:A:211:ILE:HG23	1:A:212:SER:O	2.16	0.46
2:B:89:ARG:HG3	2:B:90:SER:N	2.31	0.46
3:C:53:PRO:HA	3:C:125:GLN:OE1	2.15	0.46
3:C:47:LYS:HG3	3:C:128:VAL:HG13	1.98	0.46
5:E:8:TYR:CZ	5:E:12:ILE:CD1	2.91	0.46
2:B:95:LEU:HD22	2:B:99:LEU:HD11	1.96	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:26:TYR:O	7:G:28:GLN:N	2.48	0.45
13:H:1002:OPC:HBM1	13:H:1002:OPC:HBP1	1.61	0.45
1:A:93:MET:SD	10:A:301:HEM:CBB	3.04	0.45
4:D:139:VAL:HG13	4:D:147:SER:HA	1.98	0.45
4:D:169:ASP:OD1	4:D:176:PRO:CB	2.63	0.45
5:E:8:TYR:CE2	5:E:12:ILE:HD11	2.50	0.45
1:A:54:MET:HE1	10:A:301:HEM:HBD1	1.96	0.45
1:A:54:MET:HE3	10:A:301:HEM:HBD1	1.97	0.45
3:C:34:VAL:CG2	3:C:151:LEU:CB	2.95	0.45
3:C:22:CYS:SG	3:C:240:PHE:CE1	3.08	0.45
1:A:211:ILE:CD1	10:A:302:HEM:O2D	2.65	0.45
3:C:60:GLN:CD	3:C:70:LEU:HB3	2.37	0.45
4:D:101:ASP:O	4:D:153:ALA:N	2.49	0.45
2:B:6:LYS:HG2	7:G:35:LEU:HD22	1.97	0.45
5:E:8:TYR:CE2	5:E:12:ILE:CD1	2.99	0.45
3:C:60:GLN:HE22	3:C:156:GLY:CA	2.28	0.45
1:A:92:MET:HB3	13:H:1002:OPC:CCB	2.47	0.45
2:B:6:LYS:HZ3	2:B:6:LYS:HB2	1.81	0.45
3:C:34:VAL:HG21	3:C:151:LEU:HB2	1.99	0.45
4:D:102:TYR:HA	4:D:151:CYS:O	2.16	0.45
2:B:96:LEU:O	2:B:100:LEU:HD12	2.16	0.45
2:B:124:PHE:HE1	7:G:26:TYR:HB2	1.82	0.44
2:B:128:VAL:HG12	2:B:132:ILE:HD13	1.98	0.44
1:A:80:TRP:CZ2	3:C:254:ARG:HG2	2.52	0.44
4:D:124:PHE:CE1	4:D:134:ASP:O	2.70	0.44
7:G:17:THR:O	7:G:18:LEU:C	2.55	0.44
3:C:119:LEU:HD22	3:C:124:TYR:CD1	2.53	0.44
7:G:13:LEU:HA	7:G:13:LEU:HD23	1.89	0.44
2:B:79:TRP:C	2:B:79:TRP:CD1	2.89	0.44
3:C:2:PRO:HD3	10:C:301:HEM:CHB	2.48	0.44
3:C:285:ALA:HB2	4:D:10:VAL:HG21	1.98	0.44
2:B:109:ILE:O	2:B:112:PRO:CD	2.59	0.44
1:A:105:TYR:C	1:A:107:THR:H	2.21	0.44
3:C:2:PRO:HD3	10:C:301:HEM:C1B	2.52	0.44
11:A:1102:UMQ:O3'	11:A:1102:UMQ:H11	2.13	0.44
1:A:111:LYS:O	1:A:113:PRO:N	2.50	0.44
3:C:79:PRO:HD3	3:C:149:ILE:HG12	1.98	0.44
6:F:20:TRP:HZ3	16:G:101:BCR:C19	2.22	0.44
1:A:110:PHE:HB3	1:A:118:TRP:CE3	2.53	0.44
2:B:32:TRP:O	2:B:34:ASN:N	2.51	0.44
1:A:151:VAL:CG2	1:A:152:SER:N	2.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:110:LEU:O	2:B:113:PHE:N	2.51	0.44
4:D:152:HIS:CE1	4:D:165:TRP:CD1	3.06	0.44
4:D:152:HIS:CE1	4:D:165:TRP:NE1	2.86	0.43
4:D:174:GLU:O	4:D:175:LYS:C	2.57	0.43
4:D:80:LEU:HA	4:D:80:LEU:HD23	1.84	0.43
1:A:101:VAL:CG2	10:A:302:HEM:HMC3	2.47	0.43
2:B:36:LEU:HA	2:B:36:LEU:HD23	1.70	0.43
2:B:81:LEU:HA	2:B:81:LEU:HD23	1.80	0.43
3:C:225:VAL:HG11	3:C:229:GLU:CG	2.49	0.43
3:C:144:PHE:CZ	3:C:251:ASP:HB2	2.52	0.43
5:E:20:VAL:HA	5:E:23:ILE:HG13	2.00	0.43
5:E:27:LYS:C	5:E:29:ILE:H	2.22	0.43
3:C:26:HIS:CE1	3:C:154:ASN:OD1	2.72	0.43
4:D:166:THR:C	4:D:167:GLU:O	2.45	0.43
4:D:129:HIS:CB	14:D:200:FES:S1	2.94	0.43
7:G:9:LEU:HD22	13:H:1002:OPC:HBV1	2.01	0.43
2:B:154:THR:O	2:B:157:LEU:HD12	2.18	0.43
3:C:263:CYS:HA	3:C:266:MET:HE2	1.99	0.43
3:C:34:VAL:CG2	3:C:151:LEU:HB2	2.49	0.43
4:D:117:TRP:CZ3	4:D:122:ASN:O	2.72	0.43
1:A:150:ILE:O	1:A:151:VAL:C	2.55	0.43
3:C:92:GLU:O	3:C:93:GLU:C	2.57	0.43
3:C:42:PRO:HD3	3:C:250:GLN:O	2.19	0.43
5:E:16:PHE:C	5:E:16:PHE:CD1	2.93	0.43
6:F:24:VAL:O	6:F:27:LEU:HB2	2.18	0.43
2:B:156:THR:O	2:B:157:LEU:CB	2.64	0.42
3:C:225:VAL:HG12	3:C:229:GLU:HG2	1.98	0.42
4:D:177:TRP:CE2	4:D:178:TRP:HE3	2.37	0.42
4:D:57:LYS:HB3	4:D:61:GLY:CA	2.48	0.42
6:F:22:LEU:O	6:F:26:LEU:HD22	2.19	0.42
11:A:1102:UMQ:H3'1	11:A:1102:UMQ:H11	1.72	0.42
4:D:90:TYR:OH	4:D:116:PRO:HA	2.19	0.42
7:G:28:GLN:C	7:G:30:LYS:H	2.22	0.42
1:A:137:SER:HB3	1:A:148:VAL:CG2	2.50	0.42
2:B:138:LEU:O	2:B:139:VAL:C	2.58	0.42
3:C:199:ILE:CG2	3:C:200:GLN:N	2.80	0.42
4:D:101:ASP:O	4:D:153:ALA:HB3	2.19	0.42
1:A:14:ILE:HG23	11:A:1103:UMQ:HD1	2.01	0.42
2:B:102:ALA:O	2:B:105:PRO:HD2	2.20	0.42
16:G:101:BCR:H20C	16:G:101:BCR:H361	1.61	0.42
3:C:19:ARG:O	3:C:242:GLN:OE1	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:44:THR:HG21	8:H:1:MET:SD	2.59	0.42
4:D:123:LYS:HE2	4:D:132:GLN:NE2	2.35	0.42
4:D:53:GLY:HA3	4:D:163:THR:HA	2.02	0.42
2:B:133:PHE:O	2:B:136:GLY:N	2.53	0.42
3:C:157:ARG:H	3:C:157:ARG:HG2	1.58	0.42
4:D:174:GLU:O	4:D:175:LYS:O	2.37	0.42
8:H:14:VAL:O	8:H:18:SER:HB2	2.19	0.42
1:A:139:PRO:HG3	10:A:301:HEM:O2A	2.19	0.42
3:C:266:MET:SD	8:H:13:VAL:HG12	2.60	0.42
2:B:41:PRO:HB2	3:C:272:LEU:HD13	2.02	0.42
4:D:124:PHE:CD1	4:D:134:ASP:O	2.73	0.42
7:G:16:ALA:O	16:G:101:BCR:H16C	2.19	0.42
1:A:51:GLY:O	1:A:55:THR:HG23	2.20	0.42
1:A:215:LEU:HB2	2:B:122:ASN:H	1.85	0.42
3:C:159:GLN:HB3	3:C:170:ASN:HD22	1.85	0.42
2:B:101:MET:O	2:B:104:VAL:HG23	2.19	0.42
2:B:158:GLY:O	2:B:159:LEU:CD2	2.48	0.42
3:C:144:PHE:CE2	3:C:251:ASP:HB2	2.55	0.42
4:D:144:ALA:HA	4:D:145:PRO:HD3	1.93	0.42
1:A:17:LEU:HD13	1:A:17:LEU:C	2.39	0.41
1:A:31:ASN:HD22	1:A:33:PHE:H	1.68	0.41
1:A:25:TYR:CD2	2:B:30:PRO:HA	2.54	0.41
1:A:146:TRP:CD1	2:B:72:PRO:CD	3.03	0.41
2:B:89:ARG:NH2	2:B:146:GLY:O	2.53	0.41
4:D:141:ARG:HG2	4:D:142:GLY:H	1.85	0.41
4:D:78:ARG:HD2	4:D:117:TRP:CE2	2.55	0.41
1:A:103:ARG:NH1	1:A:104:VAL:HG22	2.33	0.41
1:A:112:LYS:O	1:A:113:PRO:C	2.57	0.41
12:B:201:CLA:HHD	13:B:202:OPC:HBW2	2.02	0.41
1:A:146:TRP:CG	2:B:72:PRO:HD2	2.55	0.41
3:C:58:LEU:CD1	3:C:237:VAL:HG21	2.50	0.41
11:A:1101:UMQ:HK1	4:D:34:ALA:HA	2.02	0.41
4:D:34:ALA:O	4:D:37:PRO:HD2	2.20	0.41
1:A:59:LYS:HG3	1:A:68:SER:HB3	2.02	0.41
2:B:124:PHE:HE1	7:G:26:TYR:CA	2.33	0.41
8:H:12:LEU:HG	8:H:12:LEU:H	1.64	0.41
8:H:3:ILE:HG23	8:H:4:ASP:N	2.34	0.41
1:A:31:ASN:HD21	1:A:33:PHE:HB2	1.84	0.41
3:C:180:ILE:O	3:C:180:ILE:HG23	2.20	0.41
11:A:1101:UMQ:HB1	3:C:254:ARG:HA	2.01	0.41
2:B:86:GLN:NE2	2:B:86:GLN:HA	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:264:LEU:HA	3:C:264:LEU:HD23	1.86	0.41
3:C:28:ALA:HB3	3:C:239:GLY:CA	2.44	0.41
4:D:106:ALA:O	4:D:114:VAL:HA	2.19	0.41
4:D:115:VAL:HG11	4:D:124:PHE:HB3	2.02	0.41
1:A:78:PHE:HE2	11:A:1101:UMQ:HC2	1.86	0.41
3:C:211:ILE:HA	3:C:212:PRO:HD3	1.94	0.41
1:A:112:LYS:O	1:A:115:GLU:CD	2.59	0.41
1:A:7:TRP:CD1	1:A:11:ARG:NH2	2.89	0.41
1:A:124:LEU:HA	1:A:124:LEU:HD23	1.87	0.41
1:A:111:LYS:NZ	2:B:120:PHE:O	2.35	0.41
4:D:18:PHE:CZ	4:D:22:LEU:HD21	2.55	0.41
7:G:18:LEU:HA	7:G:18:LEU:HD23	1.81	0.41
1:A:36:LEU:N	1:A:36:LEU:CD1	2.84	0.41
2:B:17:LYS:HB3	2:B:22:MET:O	2.21	0.41
4:D:165:TRP:HZ3	4:D:169:ASP:HA	1.86	0.41
3:C:114:LEU:HD23	3:C:114:LEU:HA	1.73	0.41
7:G:21:LEU:HA	7:G:21:LEU:HD12	1.84	0.41
3:C:75:VAL:HG23	3:C:115:LEU:HD23	2.02	0.41
4:D:156:GLN:CA	4:D:156:GLN:NE2	2.83	0.41
2:B:57:LEU:HD13	8:H:8:TRP:CD2	2.56	0.41
1:A:175:VAL:CG1	1:A:176:GLY:N	2.84	0.41
10:A:303:HEM:C4B	2:B:40:PHE:CZ	3.09	0.41
3:C:77:MET:HG2	3:C:113:VAL:HG13	2.03	0.41
3:C:172:PHE:O	3:C:173:THR:O	2.39	0.41
4:D:105:ASN:O	4:D:148:LEU:HD22	2.21	0.41
4:D:177:TRP:NE1	4:D:178:TRP:CE3	2.89	0.41
13:H:1002:OPC:HBC1	13:H:1002:OPC:CAY	2.51	0.40
10:A:303:HEM:NB	2:B:40:PHE:CZ	2.90	0.40
4:D:68:LYS:HE3	4:D:68:LYS:HB2	1.77	0.40
1:A:31:ASN:ND2	1:A:33:PHE:HD2	2.20	0.40
3:C:271:MET:HG3	4:D:22:LEU:HB3	2.03	0.40
4:D:118:ASN:C	4:D:118:ASN:ND2	2.73	0.40
2:B:123:PRO:HD2	7:G:25:ALA:CB	2.37	0.40
2:B:145:ILE:HG22	2:B:149:PHE:HE1	1.86	0.40
12:B:201:CLA:O2A	12:B:201:CLA:C4	2.69	0.40
2:B:32:TRP:HB3	2:B:33:PRO:HD2	2.01	0.40
3:C:180:ILE:HD11	3:C:197:VAL:HG13	2.04	0.40
3:C:85:ALA:HA	3:C:86:PRO:HD2	1.91	0.40
1:A:112:LYS:O	1:A:114:ARG:N	2.55	0.40
1:A:92:MET:HE3	13:H:1002:OPC:CCB	2.51	0.40
3:C:12:THR:OG1	3:C:13:PRO:HD2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:180:ILE:HG22	3:C:223:GLN:H	1.87	0.40
5:E:22:ILE:O	5:E:26:ILE:CB	2.64	0.40
7:G:26:TYR:C	7:G:28:GLN:N	2.75	0.40

All (2) 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)
3:C:108:GLU:OE1	7:G:33:ASN:CB[8_565]	1.89	0.31
1:A:112:LYS:CE	3:C:87:GLU:OE1[8_665]	2.14	0.06

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	213/215 (99%)	185 (87%)	26 (12%)	2 (1%)	17	55
2	B	158/160 (99%)	126 (80%)	25 (16%)	7 (4%)	2	15
3	C	286/289 (99%)	244 (85%)	31 (11%)	11 (4%)	3	18
4	D	162/179 (90%)	124 (76%)	28 (17%)	10 (6%)	1	8
5	E	30/32 (94%)	23 (77%)	6 (20%)	1 (3%)	4	21
6	F	30/35 (86%)	25 (83%)	5 (17%)	0	100	100
7	G	35/37 (95%)	16 (46%)	14 (40%)	5 (14%)	0	1
8	H	27/29 (93%)	24 (89%)	2 (7%)	1 (4%)	3	19
All	All	941/976 (96%)	767 (82%)	137 (15%)	37 (4%)	3	17

All (37) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	112	LYS

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Mol	Chain	Res	Type
2	B	32	TRP
2	B	74	GLU
2	B	125	ARG
3	C	66	SER
3	C	173	THR
3	C	189	GLU
3	C	192	ASN
3	C	200	GLN
3	C	230	ALA
4	D	77	ASP
4	D	167	GLU
7	G	34	GLU
1	A	3	ASN
2	B	22	MET
3	C	110	GLN
4	D	47	GLY
4	D	73	HIS
7	G	31	ARG
3	C	186	GLU
7	G	27	GLN
2	B	133	PHE
3	C	20	ILE
3	C	233	ASN
4	D	146	LEU
7	G	35	LEU
2	B	86	GLN
4	D	166	THR
4	D	170	PHE
4	D	175	LYS
5	E	28	SER
2	B	2	ALA
7	G	32	PRO
8	H	23	VAL
3	C	199	ILE
4	D	99	ILE
4	D	145	PRO

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	184/184 (100%)	167 (91%)	17 (9%)	9	34
2	B	137/137 (100%)	123 (90%)	14 (10%)	7	28
3	C	242/243 (100%)	222 (92%)	20 (8%)	11	39
4	D	134/146 (92%)	126 (94%)	8 (6%)	19	53
5	E	25/25 (100%)	23 (92%)	2 (8%)	12	40
6	F	24/27 (89%)	17 (71%)	7 (29%)	0	2
7	G	28/28 (100%)	25 (89%)	3 (11%)	6	26
8	H	24/24 (100%)	19 (79%)	5 (21%)	1	5
All	All	798/814 (98%)	722 (90%)	76 (10%)	8	32

All (76) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	11	ARG
1	A	12	LEU
1	A	14	ILE
1	A	31	ASN
1	A	36	LEU
1	A	61	THR
1	A	81	LEU
1	A	87	ARG
1	A	91	SER
1	A	95	LEU
1	A	103	ARG
1	A	107	THR
1	A	164	LEU
1	A	200	LEU
1	A	211	ILE
1	A	215	LEU
2	B	20	LYS
2	B	25	ASN
2	B	34	ASN
2	B	39	VAL
2	B	64	GLU
2	B	73	LEU
2	B	75	ILE

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Mol	Chain	Res	Type
2	B	79	TRP
2	B	95	LEU
2	B	96	LEU
2	B	103	SER
2	B	108	LEU
2	B	119	LYS
2	B	143	LEU
3	C	70	LEU
3	C	71	ASN
3	C	88	GLU
3	C	94	LEU
3	C	131	VAL
3	C	141	ASN
3	C	155	ARG
3	C	166	LYS
3	C	170	ASN
3	C	185	LYS
3	C	211	ILE
3	C	249	LEU
3	C	256	LYS
3	C	264	LEU
3	C	267	LEU
3	C	270	LEU
3	C	271	MET
3	C	286	GLU
3	C	287	MET
3	C	288	ASN
4	D	59	LYS
4	D	72	SER
4	D	118	ASN
4	D	125	LYS
4	D	133	TYR
4	D	154	THR
4	D	156	GLN
4	D	165	TRP
5	E	9	ILE
5	E	11	PHE
6	F	1	MET
6	F	2	THR
6	F	7	TYR
6	F	22	LEU
6	F	26	LEU

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Mol	Chain	Res	Type
6	F	29	ILE
6	F	30	GLN
7	G	3	GLU
7	G	6	LEU
7	G	21	LEU
8	H	2	GLU
8	H	6	LEU
8	H	14	VAL
8	H	18	SER
8	H	26	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	ASN
1	A	31	ASN
1	A	47	GLN
2	B	25	ASN
2	B	34	ASN
2	B	118	ASN
3	C	6	GLN
3	C	59	GLN
3	C	60	GLN
3	C	71	ASN
3	C	110	GLN
3	C	123	GLN
3	C	141	ASN
3	C	192	ASN
3	C	196	GLN
3	C	234	ASN
3	C	242	GLN
3	C	250	GLN
3	C	288	ASN
4	D	62	ASN
4	D	118	ASN
4	D	132	GLN
4	D	156	GLN
4	D	159	ASN
7	G	27	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 16 ligands modelled in this entry, 2 are monoatomic - leaving 14 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
11	UMQ	A	1103	-	35,35,35	1.51	4 (11%)	46,46,46	2.09	8 (17%)
11	UMQ	A	1102	-	35,35,35	1.63	4 (11%)	46,46,46	2.23	10 (21%)
13	OPC	H	1002	-	53,53,54	2.06	14 (26%)	59,61,64	2.32	17 (28%)
10	HEM	A	303	1	27,50,50	2.24	6 (22%)	17,82,82	1.83	5 (29%)
13	OPC	B	202	-	53,53,54	1.99	14 (26%)	59,61,64	2.44	13 (22%)
11	UMQ	A	1104	-	35,35,35	1.42	3 (8%)	46,46,46	2.06	7 (15%)
11	UMQ	A	1101	-	35,35,35	1.48	4 (11%)	46,46,46	2.13	9 (19%)
10	HEM	A	302	1	27,50,50	2.31	5 (18%)	17,82,82	2.18	6 (35%)
14	FES	D	200	4	0,4,4	0.00	-	-	-	-
15	SQD	D	201	-	53,54,54	3.08	24 (45%)	62,65,65	4.54	23 (37%)
10	HEM	C	301	3	27,50,50	2.24	5 (18%)	17,82,82	1.94	6 (35%)
10	HEM	A	301	1	27,50,50	1.96	7 (25%)	17,82,82	2.43	8 (47%)
12	CLA	B	201	-	59,73,73	1.89	13 (22%)	67,113,113	2.20	19 (28%)
16	BCR	G	101	-	41,41,41	2.81	13 (31%)	56,56,56	6.87	17 (30%)

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
11	UMQ	A	1103	-	2/2/10/10	5/20/60/60	0/2/2/2
11	UMQ	A	1102	-	2/2/10/10	11/20/60/60	0/2/2/2
13	OPC	H	1002	-	-	26/57/57/60	-
10	HEM	A	303	1	-	3/6/54/54	-
13	OPC	B	202	-	-	23/57/57/60	-
11	UMQ	A	1104	-	2/2/10/10	11/20/60/60	0/2/2/2
11	UMQ	A	1101	-	2/2/10/10	13/20/60/60	0/2/2/2
10	HEM	A	302	1	-	0/6/54/54	-
14	FES	D	200	4	-	-	0/1/1/1
15	SQD	D	201	-	1/1/9/9	28/49/69/69	0/1/1/1
10	HEM	C	301	3	-	0/6/54/54	-
10	HEM	A	301	1	-	1/6/54/54	-
12	CLA	B	201	-	4/4/20/25	16/37/135/135	-
16	BCR	G	101	-	-	10/29/63/63	0/2/2/2

All (116) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	D	201	SQD	C4-C3	12.95	1.85	1.52
16	G	101	BCR	C8-C9	-8.93	1.26	1.45
16	G	101	BCR	C23-C22	-8.50	1.27	1.45
11	A	1102	UMQ	C1'-C2'	-6.68	1.33	1.52
11	A	1103	UMQ	C1'-C2'	-6.21	1.34	1.52
11	A	1104	UMQ	C1'-C2'	-6.17	1.34	1.52
11	A	1101	UMQ	C1'-C2'	-6.08	1.35	1.52
10	A	302	HEM	C3C-C2C	-5.86	1.32	1.40
10	A	303	HEM	C3B-C2B	-5.56	1.32	1.40
13	B	202	OPC	CAG-CAH	-5.55	1.33	1.51
10	A	302	HEM	C3B-C2B	-5.55	1.32	1.40
13	H	1002	OPC	CAG-CAH	-5.55	1.33	1.51
10	C	301	HEM	C3B-C2B	-5.50	1.32	1.40
15	D	201	SQD	C17-C16	-5.48	1.20	1.51
10	C	301	HEM	C3D-C2D	5.44	1.53	1.37
15	D	201	SQD	C12-C11	-5.31	1.21	1.51
12	B	201	CLA	OBD-CAD	5.23	1.29	1.22
10	A	303	HEM	C3D-C2D	5.17	1.53	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	303	HEM	C3C-C2C	-5.11	1.33	1.40
13	B	202	OPC	OBJ-CBK	5.11	1.48	1.33
15	D	201	SQD	C6-S	-5.10	1.58	1.77
16	G	101	BCR	C24-C25	-4.97	1.27	1.45
13	H	1002	OPC	CAQ-CAP	-4.94	1.34	1.52
10	A	301	HEM	C3D-C2D	4.93	1.52	1.37
13	B	202	OPC	CAQ-CAP	-4.90	1.34	1.52
16	G	101	BCR	C7-C6	-4.87	1.27	1.45
13	H	1002	OPC	OBJ-CBK	4.83	1.47	1.33
12	B	201	CLA	C3C-C2C	4.83	1.47	1.36
12	B	201	CLA	CHC-C1C	4.79	1.47	1.35
13	H	1002	OPC	CBP-CBQ	-4.79	1.33	1.52
15	D	201	SQD	O48-C23	4.77	1.47	1.33
10	A	302	HEM	C3D-C2D	4.73	1.51	1.37
13	H	1002	OPC	OAN-CAO	4.63	1.47	1.34
12	B	201	CLA	C3D-C2D	4.57	1.47	1.39
16	G	101	BCR	C12-C13	-4.57	1.36	1.45
12	B	201	CLA	C3B-C2B	4.49	1.46	1.40
16	G	101	BCR	C19-C18	-4.48	1.36	1.45
16	G	101	BCR	C8-C7	-4.44	1.19	1.33
15	D	201	SQD	C18-C17	-4.44	1.26	1.51
15	D	201	SQD	O47-C7	4.42	1.46	1.34
16	G	101	BCR	C24-C23	-4.41	1.19	1.33
11	A	1102	UMQ	O1'-C1'	4.35	1.47	1.40
15	D	201	SQD	C16-C15	-4.35	1.27	1.51
12	B	201	CLA	O2D-CGD	4.33	1.43	1.33
10	C	301	HEM	C3C-C2C	-4.32	1.34	1.40
15	D	201	SQD	C11-C10	-4.31	1.27	1.51
11	A	1101	UMQ	O2'-C2'	-4.31	1.32	1.43
13	B	202	OPC	CBP-CBQ	-4.30	1.35	1.52
15	D	201	SQD	C13-C12	-4.27	1.27	1.51
12	B	201	CLA	O2A-CGA	4.21	1.45	1.33
11	A	1103	UMQ	O1'-C1'	4.09	1.47	1.40
13	B	202	OPC	OAN-CAO	4.02	1.45	1.34
11	A	1102	UMQ	O2'-C2'	-3.99	1.33	1.43
10	A	301	HEM	C3B-C2B	-3.93	1.34	1.40
11	A	1103	UMQ	O2'-C2'	-3.83	1.33	1.43
11	A	1104	UMQ	O2'-C2'	-3.82	1.34	1.43
13	B	202	OPC	CAV-CAW	3.81	1.53	1.31
10	C	301	HEM	C3B-CAB	3.67	1.55	1.47
13	H	1002	OPC	CAV-CAW	3.66	1.53	1.31
12	B	201	CLA	C1D-C2D	3.60	1.50	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	302	HEM	C3C-CAC	3.55	1.55	1.47
15	D	201	SQD	C21-C20	-3.54	1.26	1.51
13	H	1002	OPC	CBP-CBO	-3.48	1.32	1.51
10	A	303	HEM	C3C-CAC	3.46	1.54	1.47
10	A	301	HEM	C3C-C2C	-3.41	1.35	1.40
11	A	1101	UMQ	O1'-C1'	3.32	1.45	1.40
11	A	1104	UMQ	O1'-C1'	3.29	1.45	1.40
13	H	1002	OPC	CAQ-CAR	-3.27	1.33	1.51
13	H	1002	OPC	CAR-CAS	-3.26	1.33	1.51
13	H	1002	OPC	CBQ-CBR	-3.25	1.31	1.50
10	C	301	HEM	C3C-CAC	3.22	1.54	1.47
15	D	201	SQD	C36-C35	-3.14	1.33	1.51
10	A	303	HEM	C3B-CAB	3.13	1.54	1.47
15	D	201	SQD	C19-C18	-3.13	1.34	1.51
15	D	201	SQD	C34-C33	-3.10	1.34	1.51
13	B	202	OPC	CBB-CBC	-3.09	1.34	1.51
15	D	201	SQD	C20-C19	-3.09	1.34	1.51
15	D	201	SQD	C32-C31	-3.08	1.34	1.51
13	H	1002	OPC	CBC-CBD	-3.08	1.34	1.51
13	B	202	OPC	CBC-CBD	-3.08	1.34	1.51
13	B	202	OPC	CAQ-CAR	-3.06	1.34	1.51
15	D	201	SQD	C33-C32	-3.04	1.34	1.51
15	D	201	SQD	C35-C34	-3.03	1.34	1.51
13	H	1002	OPC	CBB-CBC	-2.98	1.34	1.51
15	D	201	SQD	C15-C14	-2.98	1.34	1.51
13	B	202	OPC	CBP-CBO	-2.96	1.35	1.51
13	H	1002	OPC	CBT-CBS	-2.96	1.33	1.50
13	B	202	OPC	CAR-CAS	-2.92	1.35	1.51
15	D	201	SQD	C14-C13	-2.92	1.35	1.51
15	D	201	SQD	C22-C21	-2.85	1.26	1.49
10	A	302	HEM	C3B-CAB	2.82	1.53	1.47
10	A	301	HEM	C3B-CAB	2.81	1.53	1.47
16	G	101	BCR	C11-C10	-2.78	1.34	1.43
13	B	202	OPC	CBQ-CBR	-2.76	1.34	1.50
10	A	301	HEM	CMB-C2B	2.70	1.58	1.51
13	B	202	OPC	CBT-CBS	-2.66	1.35	1.50
13	H	1002	OPC	CAG-NAF	-2.64	1.42	1.51
10	A	301	HEM	C3C-CAC	2.57	1.53	1.47
16	G	101	BCR	C15-C14	-2.53	1.35	1.43
15	D	201	SQD	C37-C36	-2.51	1.33	1.51
16	G	101	BCR	C21-C22	2.43	1.39	1.35
16	G	101	BCR	C16-C17	-2.40	1.36	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	B	202	OPC	CAG-NAF	-2.38	1.43	1.51
12	B	201	CLA	CHD-C4C	2.38	1.47	1.41
15	D	201	SQD	O6-C1	2.32	1.44	1.40
12	B	201	CLA	C1C-C2C	2.30	1.49	1.44
12	B	201	CLA	C4B-CHC	2.22	1.47	1.41
12	B	201	CLA	C4C-C3C	2.14	1.48	1.45
12	B	201	CLA	C1B-CHB	2.14	1.46	1.41
16	G	101	BCR	C20-C21	-2.14	1.36	1.43
10	A	303	HEM	C1D-ND	2.11	1.40	1.36
15	D	201	SQD	C38-C37	-2.11	1.32	1.49
11	A	1102	UMQ	O5'-C1'	2.09	1.47	1.41
11	A	1101	UMQ	O5'-C1'	2.07	1.47	1.41
11	A	1103	UMQ	O5'-C1'	2.07	1.47	1.41
10	A	301	HEM	CAD-C3D	2.01	1.55	1.52

All (148) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	G	101	BCR	C24-C23-C22	33.07	176.20	126.23
16	G	101	BCR	C7-C8-C9	29.00	170.05	126.23
15	D	201	SQD	C4-C3-C2	-19.52	76.74	110.82
16	G	101	BCR	C23-C24-C25	16.98	174.90	127.20
16	G	101	BCR	C8-C7-C6	16.47	173.47	127.20
15	D	201	SQD	C18-C17-C16	11.24	171.49	114.42
15	D	201	SQD	C12-C11-C10	10.91	169.79	114.42
15	D	201	SQD	C17-C16-C15	10.68	168.62	114.42
15	D	201	SQD	C13-C12-C11	10.60	168.26	114.42
15	D	201	SQD	O3-C3-C4	-9.73	87.85	110.35
13	B	202	OPC	CAA-NAF-CBG	-9.08	85.62	108.97
13	B	202	OPC	CAA-NAF-CAE	-8.68	86.67	108.97
13	H	1002	OPC	CAA-NAF-CAE	-8.65	86.75	108.97
13	H	1002	OPC	CAA-NAF-CBG	-8.42	87.33	108.97
15	D	201	SQD	C22-C21-C20	8.41	177.30	113.42
11	A	1103	UMQ	O1'-C1'-C2'	7.47	119.96	108.30
11	A	1101	UMQ	O1'-C1'-C2'	7.32	119.74	108.30
11	A	1102	UMQ	O1'-C1'-C2'	6.94	119.14	108.30
11	A	1104	UMQ	O1'-C1'-C2'	6.90	119.08	108.30
12	B	201	CLA	C2C-C1C-NC	6.79	116.33	109.97
15	D	201	SQD	C3-C4-C5	-6.44	98.76	110.24
11	A	1104	UMQ	O5'-C1'-C2'	6.18	123.44	110.35
15	D	201	SQD	O7-S-C6	5.89	113.94	106.94
12	B	201	CLA	O2D-CGD-CBD	5.82	121.61	111.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	A	1104	UMQ	C1'-C2'-C3'	5.59	121.63	110.00
13	B	202	OPC	CAA-NAF-CAG	-5.52	87.35	109.92
13	H	1002	OPC	CAA-NAF-CAG	-5.47	87.55	109.92
10	A	302	HEM	C1D-C2D-C3D	-5.34	103.28	107.00
15	D	201	SQD	O9-S-C6	5.30	113.24	106.94
11	A	1102	UMQ	O5'-C1'-O1'	5.28	122.49	109.97
13	B	202	OPC	OAN-CAO-CAP	5.21	122.72	111.50
10	A	303	HEM	CBA-CAA-C2A	-5.02	103.23	112.49
11	A	1101	UMQ	O5'-C1'-C2'	5.00	120.93	110.35
11	A	1101	UMQ	C1'-C2'-C3'	4.99	120.39	110.00
11	A	1101	UMQ	O2'-C2'-C1'	4.97	122.12	110.05
11	A	1103	UMQ	C1'-C2'-C3'	4.95	120.30	110.00
11	A	1102	UMQ	CA-O1'-C1'	4.93	122.01	113.84
11	A	1104	UMQ	CA-O1'-C1'	4.92	121.99	113.84
11	A	1102	UMQ	C1'-C2'-C3'	4.90	120.19	110.00
15	D	201	SQD	O5-C5-C4	4.80	118.41	109.69
11	A	1103	UMQ	O5'-C1'-C2'	4.79	120.49	110.35
11	A	1103	UMQ	CA-O1'-C1'	4.72	121.67	113.84
12	B	201	CLA	C3C-C4C-NC	4.69	115.83	110.57
16	G	101	BCR	C8-C9-C10	4.68	126.13	118.94
13	B	202	OPC	CAR-CAQ-CAP	4.67	129.97	113.19
11	A	1103	UMQ	O2'-C2'-C1'	4.63	121.30	110.05
12	B	201	CLA	O2D-CGD-O1D	-4.58	114.89	123.84
10	A	301	HEM	CMA-C3A-C4A	-4.53	121.51	128.46
15	D	201	SQD	O47-C7-C8	4.52	121.24	111.50
13	H	1002	OPC	CBG-NAF-CAE	4.51	120.57	108.97
12	B	201	CLA	CHD-C4C-C3C	-4.50	118.22	124.84
10	A	302	HEM	CAA-CBA-CGA	4.48	120.19	112.67
13	B	202	OPC	CBG-NAF-CAE	4.41	120.32	108.97
12	B	201	CLA	O2A-CGA-CBA	4.33	125.50	111.91
11	A	1104	UMQ	O2'-C2'-C1'	4.30	120.49	110.05
11	A	1102	UMQ	O2'-C2'-C1'	4.26	120.40	110.05
16	G	101	BCR	C34-C9-C10	-4.25	116.97	122.92
12	B	201	CLA	C1C-C2C-C3C	-4.10	102.65	106.96
11	A	1103	UMQ	O5'-C1'-O1'	4.04	119.54	109.97
10	A	301	HEM	CAD-CBD-CGD	-3.97	106.01	112.67
11	A	1101	UMQ	O5'-C1'-O1'	3.94	119.31	109.97
11	A	1102	UMQ	O2'-C2'-C3'	3.92	119.40	110.35
16	G	101	BCR	C38-C26-C25	-3.88	120.17	124.53
11	A	1101	UMQ	CA-O1'-C1'	3.88	120.28	113.84
10	C	301	HEM	C1D-C2D-C3D	-3.85	104.32	107.00
11	A	1102	UMQ	O5'-C1'-C2'	3.79	118.37	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	B	202	OPC	OAN-CAO-OAD	-3.76	114.62	123.70
10	A	301	HEM	C4A-C3A-C2A	3.74	109.60	107.00
12	B	201	CLA	C3B-C4B-NB	3.67	113.95	109.21
10	C	301	HEM	CBD-CAD-C3D	-3.66	105.74	112.48
12	B	201	CLA	C4-C3-C5	3.65	121.41	115.27
16	G	101	BCR	C3-C4-C5	-3.58	107.69	114.08
15	D	201	SQD	O6-C1-C2	3.51	113.79	108.30
11	A	1103	UMQ	O2'-C2'-C3'	3.48	118.40	110.35
10	A	301	HEM	CBA-CAA-C2A	-3.47	106.08	112.49
10	C	301	HEM	CBA-CAA-C2A	-3.38	106.25	112.49
12	B	201	CLA	O2A-CGA-O1A	-3.37	115.08	123.59
13	H	1002	OPC	OAN-CAO-CAP	3.33	118.67	111.50
16	G	101	BCR	C32-C1-C6	-3.32	104.92	110.30
10	A	301	HEM	C4C-C3C-C2C	3.30	109.20	106.90
11	A	1104	UMQ	O2'-C2'-C3'	3.26	117.88	110.35
11	A	1104	UMQ	O5'-C1'-O1'	3.17	117.48	109.97
12	B	201	CLA	CAA-CBA-CGA	-3.16	104.03	113.25
11	A	1101	UMQ	O2'-C2'-C3'	3.09	117.50	110.35
15	D	201	SQD	C15-C14-C13	3.06	129.96	114.42
10	A	302	HEM	CAD-CBD-CGD	-2.94	107.74	112.67
12	B	201	CLA	C4D-C3D-CAD	2.90	110.09	108.47
12	B	201	CLA	CHB-C4A-NA	2.88	128.50	124.51
10	C	301	HEM	CMD-C2D-C3D	2.88	130.37	124.94
13	H	1002	OPC	OBJ-CBK-CBL	2.85	120.84	111.91
13	H	1002	OPC	CBO-CBP-CBQ	2.84	126.18	113.79
12	B	201	CLA	C4C-C3C-C2C	-2.83	102.77	106.90
16	G	101	BCR	C33-C5-C6	-2.81	121.38	124.53
15	D	201	SQD	O4-C4-C3	-2.76	103.98	110.35
15	D	201	SQD	C14-C13-C12	2.75	128.38	114.42
13	B	202	OPC	OBJ-CBK-CBL	2.74	120.50	111.91
12	B	201	CLA	O2A-C1-C2	2.71	115.76	108.64
13	B	202	OPC	CBU-CBT-CBS	2.71	127.95	112.43
11	A	1102	UMQ	C3-C4-C5	2.71	115.06	110.24
10	A	301	HEM	CAA-CBA-CGA	-2.70	108.14	112.67
13	B	202	OPC	CBG-NAF-CAG	2.68	120.90	109.92
11	A	1102	UMQ	O1-C1-C2	2.63	114.92	108.10
10	A	303	HEM	C4C-C3C-C2C	2.62	108.73	106.90
13	H	1002	OPC	CBV-CBU-CBT	-2.61	102.42	113.79
10	A	302	HEM	CBD-CAD-C3D	-2.56	107.75	112.48
13	H	1002	OPC	CAR-CAS-CAT	2.55	127.36	114.42
15	D	201	SQD	C45-O47-C7	-2.54	111.54	117.79
15	D	201	SQD	C16-C15-C14	2.54	127.30	114.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	303	HEM	CAA-CBA-CGA	-2.47	108.52	112.67
15	D	201	SQD	O48-C23-C24	2.47	119.64	111.91
15	D	201	SQD	O9-S-O7	-2.46	105.44	113.95
15	D	201	SQD	O3-C3-C2	-2.46	104.67	110.35
11	A	1101	UMQ	C1'-O5'-C5'	-2.46	108.86	113.69
13	H	1002	OPC	OAI-CAH-CAG	2.44	122.01	109.16
11	A	1101	UMQ	C1-O1-C4'	-2.41	111.99	117.96
13	H	1002	OPC	CAE-NAF-CAG	2.39	119.71	109.92
16	G	101	BCR	C38-C26-C27	2.39	118.21	113.62
13	B	202	OPC	CAR-CAS-CAT	2.39	126.55	114.42
13	H	1002	OPC	CAQ-CAP-CAO	2.37	122.23	113.62
16	G	101	BCR	C1-C6-C5	-2.32	119.35	122.61
16	G	101	BCR	C2-C1-C6	2.31	114.04	110.48
13	H	1002	OPC	CAQ-CAR-CAS	2.28	126.01	114.42
16	G	101	BCR	C11-C10-C9	2.25	130.52	127.31
12	B	201	CLA	CHC-C1C-C2C	-2.24	120.53	126.72
12	B	201	CLA	CMC-C2C-C1C	2.24	128.44	125.04
13	H	1002	OPC	CBG-NAF-CAG	2.22	119.01	109.92
13	H	1002	OPC	CBP-CBQ-CBR	2.20	125.07	112.43
10	A	303	HEM	C3C-C4C-NC	-2.20	106.79	110.94
10	A	302	HEM	CMD-C2D-C3D	2.20	129.09	124.94
13	B	202	OPC	CAM-OAN-CAO	-2.20	112.38	117.79
10	C	301	HEM	CMA-C3A-C4A	-2.18	125.11	128.46
15	D	201	SQD	O47-C7-O49	-2.18	118.44	123.70
10	A	303	HEM	CMA-C3A-C4A	-2.17	125.12	128.46
15	D	201	SQD	C1-C2-C3	2.17	114.52	110.00
16	G	101	BCR	C24-C25-C26	-2.13	116.29	121.46
10	A	302	HEM	CBA-CAA-C2A	-2.13	108.56	112.49
13	H	1002	OPC	CBW-CBV-CBU	-2.13	103.63	114.42
10	A	301	HEM	CBD-CAD-C3D	-2.12	108.57	112.48
13	H	1002	OPC	CAS-CAT-CAU	-2.11	104.59	113.79
11	A	1103	UMQ	C1-O1-C4'	-2.10	112.75	117.96
10	A	301	HEM	CMA-C3A-C2A	2.09	128.89	124.94
16	G	101	BCR	C20-C19-C18	-2.08	120.58	126.42
12	B	201	CLA	CAA-C2A-C3A	-2.07	107.12	112.78
11	A	1102	UMQ	O3'-C3'-C2'	-2.06	105.59	110.35
10	C	301	HEM	CMD-C2D-C1D	-2.05	125.31	128.46
12	B	201	CLA	CMB-C2B-C3B	2.05	128.52	124.68
13	B	202	OPC	CBP-CBO-CBN	2.03	124.75	114.42
16	G	101	BCR	C10-C11-C12	-2.00	116.97	123.22

All (13) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
11	A	1103	UMQ	C2'
11	A	1103	UMQ	C1'
11	A	1102	UMQ	C2'
11	A	1102	UMQ	C1'
15	D	201	SQD	C5
11	A	1104	UMQ	C2'
11	A	1104	UMQ	C1'
11	A	1101	UMQ	C2'
11	A	1101	UMQ	C1'
12	B	201	CLA	C8
12	B	201	CLA	NC
12	B	201	CLA	ND
12	B	201	CLA	NA

All (147) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	A	1103	UMQ	CB-CA-O1'-C1'
11	A	1102	UMQ	C2'-C1'-O1'-CA
13	H	1002	OPC	CAL-OAK-PAJ-OBH
13	H	1002	OPC	CAL-OAK-PAJ-OAB
13	H	1002	OPC	CAL-OAK-PAJ-OAI
13	H	1002	OPC	NAF-CAG-CAH-OAI
13	H	1002	OPC	CBO-CBP-CBQ-CBR
10	A	303	HEM	C2D-C3D-CAD-CBD
10	A	303	HEM	C4D-C3D-CAD-CBD
13	B	202	OPC	NAF-CAG-CAH-OAI
13	B	202	OPC	CBO-CBP-CBQ-CBR
15	D	201	SQD	C2-C1-O6-C44
15	D	201	SQD	O5-C1-O6-C44
15	D	201	SQD	O47-C45-C46-O48
15	D	201	SQD	O5-C5-C6-S
15	D	201	SQD	C5-C6-S-O7
15	D	201	SQD	C5-C6-S-O8
15	D	201	SQD	C5-C6-S-O9
11	A	1104	UMQ	O5'-C1'-O1'-CA
10	A	301	HEM	C3D-CAD-CBD-CGD
12	B	201	CLA	O2A-C1-C2-C3
16	G	101	BCR	C6-C7-C8-C9
16	G	101	BCR	C22-C23-C24-C25
11	A	1102	UMQ	C3'-C4'-O1-C1
12	B	201	CLA	CBD-CGD-O2D-CED
13	H	1002	OPC	CAQ-CAR-CAS-CAT

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Mol	Chain	Res	Type	Atoms
15	D	201	SQD	C12-C13-C14-C15
15	D	201	SQD	C13-C14-C15-C16
15	D	201	SQD	C31-C32-C33-C34
15	D	201	SQD	C33-C34-C35-C36
11	A	1102	UMQ	O5'-C5'-C6'-O6'
15	D	201	SQD	C9-C10-C11-C12
11	A	1101	UMQ	O5-C5-C6-O6
11	A	1104	UMQ	O5-C5-C6-O6
11	A	1102	UMQ	C4-C5-C6-O6
15	D	201	SQD	C10-C11-C12-C13
15	D	201	SQD	C16-C17-C18-C19
11	A	1101	UMQ	O5'-C5'-C6'-O6'
11	A	1103	UMQ	O5'-C1'-O1'-CA
11	A	1101	UMQ	C4-C5-C6-O6
13	H	1002	OPC	OAN-CAM-CBI-OBJ
11	A	1102	UMQ	O5-C5-C6-O6
11	A	1104	UMQ	C4-C5-C6-O6
16	G	101	BCR	C7-C8-C9-C34
16	G	101	BCR	C7-C8-C9-C10
15	D	201	SQD	C8-C7-O47-C45
11	A	1101	UMQ	C4'-C5'-C6'-O6'
12	B	201	CLA	C15-C16-C17-C18
13	B	202	OPC	CAP-CAO-OAN-CAM
12	B	201	CLA	C6-C7-C8-C10
12	B	201	CLA	O1D-CGD-O2D-CED
11	A	1102	UMQ	O1'-CA-CB-CC
12	B	201	CLA	C8-C10-C11-C12
13	B	202	OPC	CBL-CBK-OBJ-CBI
13	B	202	OPC	CBK-CBL-CBM-CBN
15	D	201	SQD	C23-C24-C25-C26
13	B	202	OPC	OAD-CAO-OAN-CAM
15	D	201	SQD	O49-C7-O47-C45
11	A	1102	UMQ	C4'-C5'-C6'-O6'
12	B	201	CLA	C10-C11-C12-C13
13	B	202	OPC	CAH-CAG-NAF-CBG
13	B	202	OPC	CBM-CBN-CBO-CBP
11	A	1101	UMQ	CB-CC-CD-CF
13	B	202	OPC	CAZ-CBA-CBB-CBC
11	A	1104	UMQ	CB-CC-CD-CF
13	B	202	OPC	OAK-CAL-CAM-OAN
11	A	1101	UMQ	C2'-C1'-O1'-CA
12	B	201	CLA	C4-C3-C5-C6

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Mol	Chain	Res	Type	Atoms
12	B	201	CLA	C2-C3-C5-C6
13	H	1002	OPC	CBX-CBY-CBZ-CCA
13	B	202	OPC	OCC-CBK-OBJ-CBI
13	H	1002	OPC	CBW-CBX-CBY-CBZ
15	D	201	SQD	C26-C27-C28-C29
11	A	1102	UMQ	CH-CI-CJ-CK
13	H	1002	OPC	CAH-CAG-NAF-CBG
13	H	1002	OPC	CBL-CBM-CBN-CBO
13	B	202	OPC	CAY-CAZ-CBA-CBB
11	A	1101	UMQ	CH-CI-CJ-CK
12	B	201	CLA	C3A-C2A-CAA-CBA
13	H	1002	OPC	CBM-CBN-CBO-CBP
11	A	1104	UMQ	CD-CF-CG-CH
13	H	1002	OPC	CBS-CBT-CBU-CBV
13	B	202	OPC	CAS-CAT-CAU-CAV
11	A	1101	UMQ	CA-CB-CC-CD
16	G	101	BCR	C23-C24-C25-C26
15	D	201	SQD	C25-C26-C27-C28
15	D	201	SQD	C28-C29-C30-C31
13	H	1002	OPC	CAX-CAY-CAZ-CBA
13	B	202	OPC	CAH-CAG-NAF-CAA
13	H	1002	OPC	CAW-CAX-CAY-CAZ
13	H	1002	OPC	CAS-CAT-CAU-CAV
12	B	201	CLA	C6-C7-C8-C9
16	G	101	BCR	C37-C22-C23-C24
16	G	101	BCR	C21-C22-C23-C24
12	B	201	CLA	C1A-C2A-CAA-CBA
11	A	1104	UMQ	CH-CI-CJ-CK
13	H	1002	OPC	CAL-CAM-CBI-OBJ
13	B	202	OPC	CBT-CBU-CBV-CBW
11	A	1104	UMQ	CF-CG-CH-CI
11	A	1104	UMQ	O5'-C5'-C6'-O6'
15	D	201	SQD	C24-C25-C26-C27
12	B	201	CLA	C3-C5-C6-C7
13	B	202	OPC	CAR-CAS-CAT-CAU
13	B	202	OPC	CBC-CBD-CBE-CBF
15	D	201	SQD	C24-C23-O48-C46
13	B	202	OPC	OAK-CAL-CAM-CBI
11	A	1102	UMQ	CB-CA-O1'-C1'
11	A	1101	UMQ	CB-CA-O1'-C1'
15	D	201	SQD	C44-C45-C46-O48
13	H	1002	OPC	CBU-CBV-CBW-CBX

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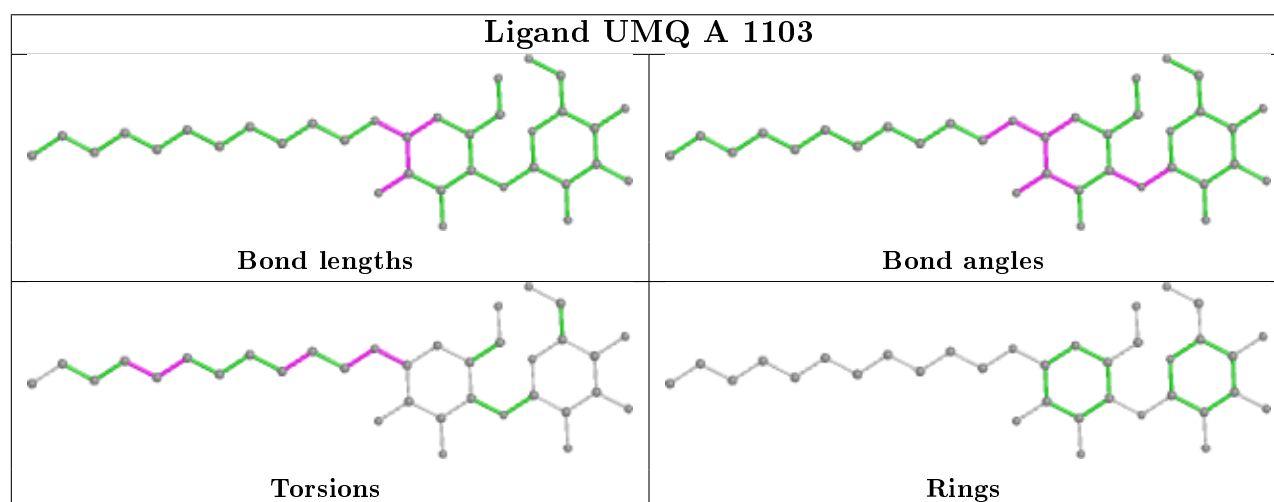
Mol	Chain	Res	Type	Atoms
11	A	1104	UMQ	O1'-CA-CB-CC
15	D	201	SQD	O6-C44-C45-O47
11	A	1103	UMQ	CF-CG-CH-CI
15	D	201	SQD	O10-C23-O48-C46
13	H	1002	OPC	CAM-CAL-OAK-PAJ
13	B	202	OPC	CAL-CAM-CBI-OBJ
13	H	1002	OPC	OAK-CAL-CAM-OAN
11	A	1103	UMQ	CA-CB-CC-CD
13	H	1002	OPC	CBV-CBW-CBX-CBY
13	B	202	OPC	CBL-CBM-CBN-CBO
11	A	1101	UMQ	CF-CG-CH-CI
11	A	1104	UMQ	CC-CD-CF-CG
13	B	202	OPC	CBP-CBQ-CBR-CBS
15	D	201	SQD	C15-C16-C17-C18
13	H	1002	OPC	CBC-CBD-CBE-CBF
13	H	1002	OPC	CBP-CBQ-CBR-CBS
13	B	202	OPC	CAL-OAK-PAJ-OAI
15	D	201	SQD	O6-C44-C45-C46
13	H	1002	OPC	OAK-CAL-CAM-CBI
16	G	101	BCR	C11-C10-C9-C34
11	A	1102	UMQ	CC-CD-CF-CG
16	G	101	BCR	C11-C10-C9-C8
12	B	201	CLA	C2-C1-O2A-CGA
16	G	101	BCR	C23-C24-C25-C30
15	D	201	SQD	C45-C44-O6-C1
11	A	1104	UMQ	CG-CH-CI-CJ
12	B	201	CLA	C11-C12-C13-C15
11	A	1103	UMQ	CG-CH-CI-CJ
12	B	201	CLA	CAD-CBD-CGD-O2D
13	B	202	OPC	CBR-CBS-CBT-CBU
11	A	1102	UMQ	C5'-C4'-O1-C1
11	A	1101	UMQ	CC-CD-CF-CG
10	A	303	HEM	C3D-CAD-CBD-CGD
13	H	1002	OPC	CBR-CBS-CBT-CBU
11	A	1101	UMQ	O5'-C1'-O1'-CA
11	A	1101	UMQ	CI-CJ-CK-CL
13	H	1002	OPC	CBY-CBZ-CCA-CCB

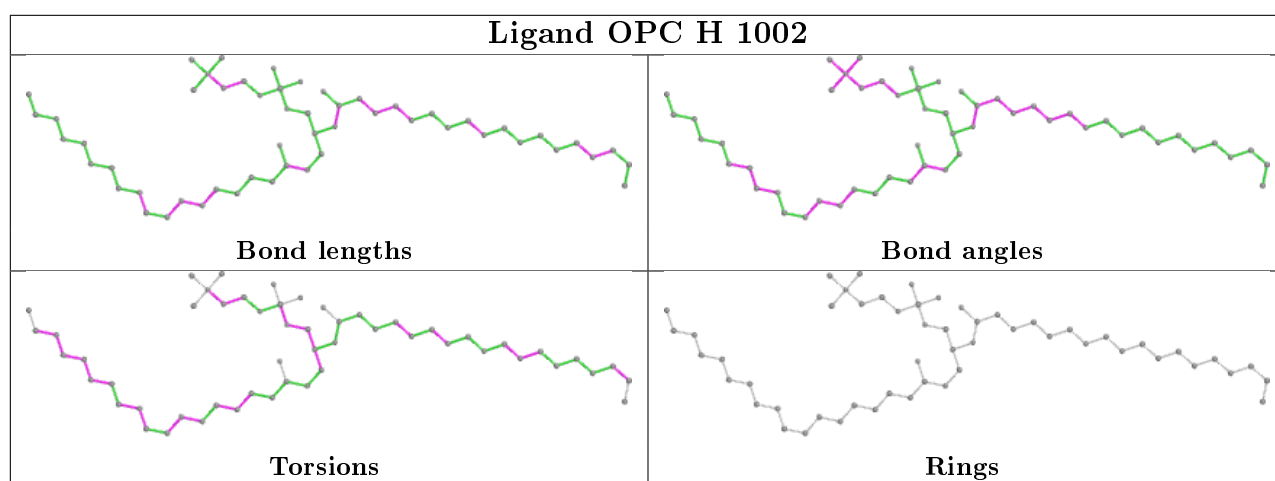
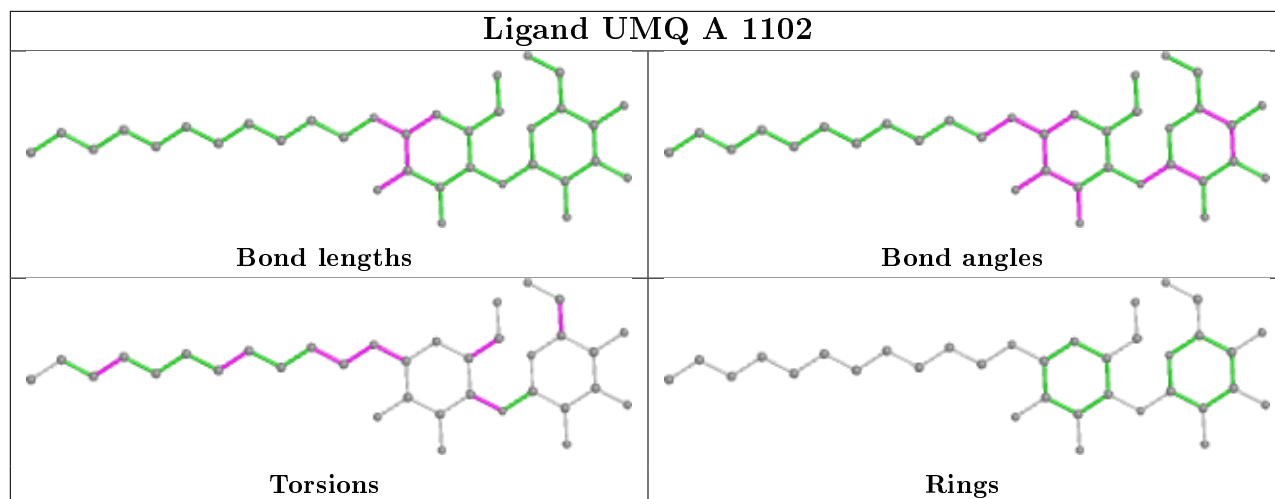
There are no ring outliers.

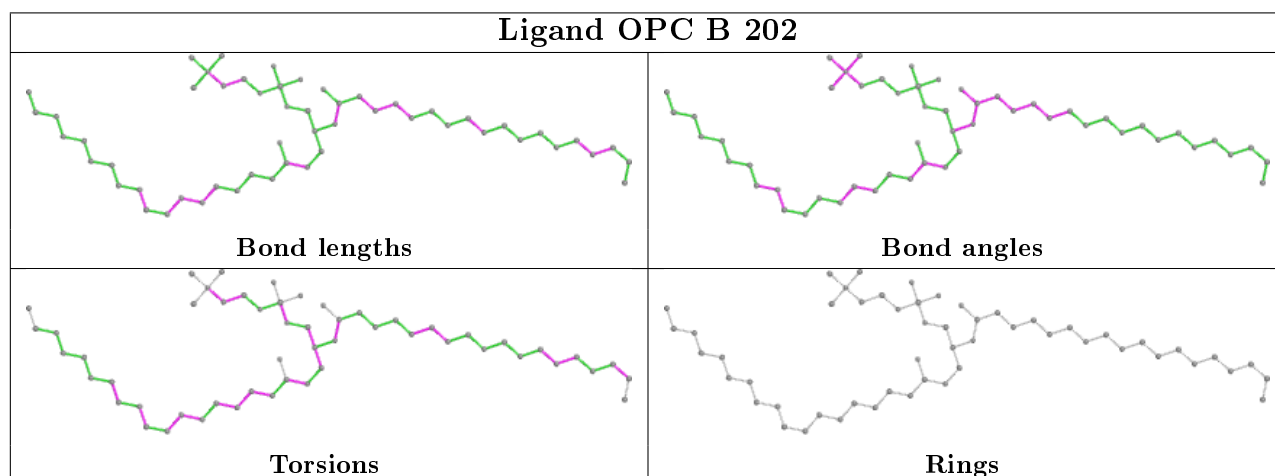
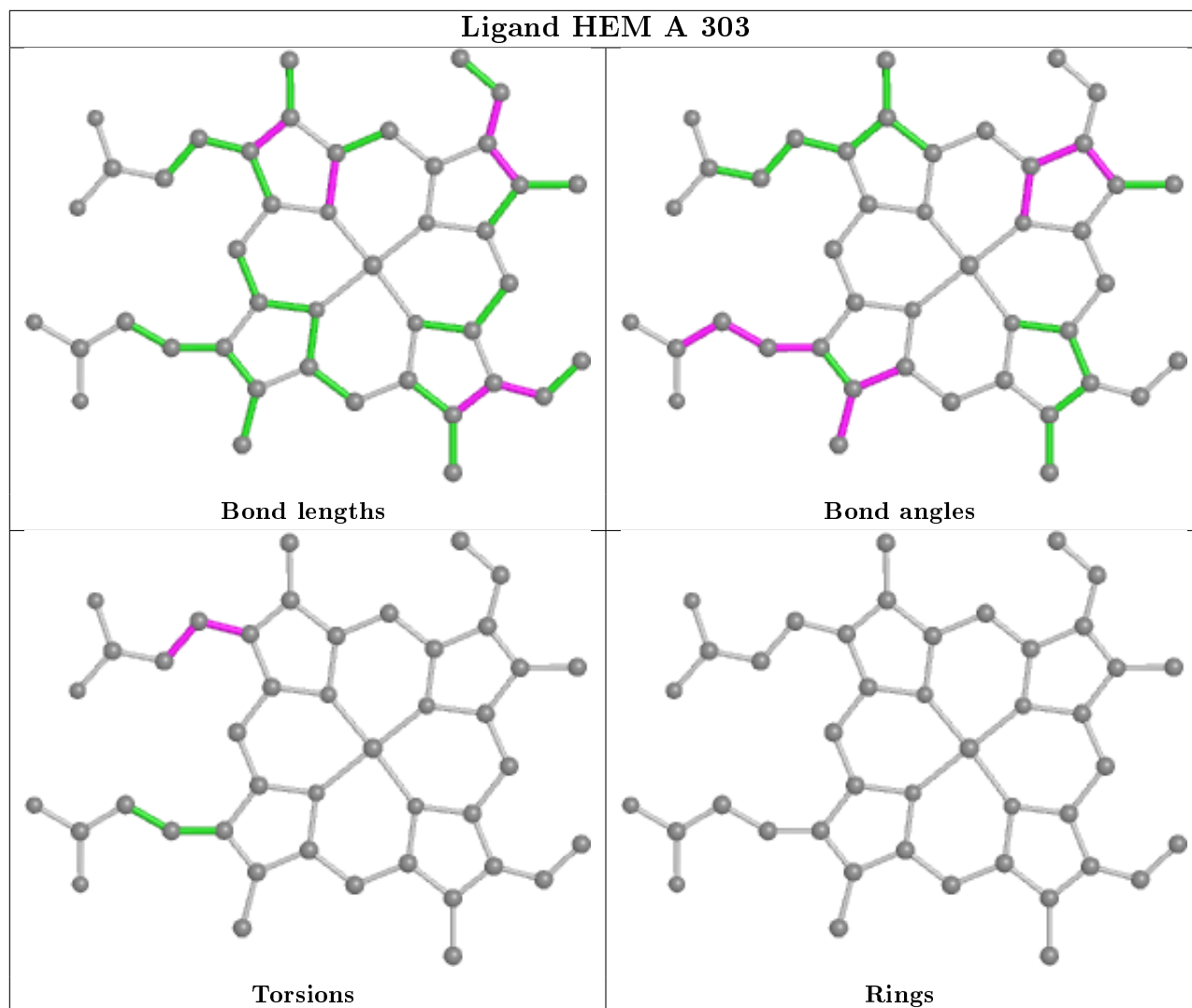
14 monomers are involved in 97 short contacts:

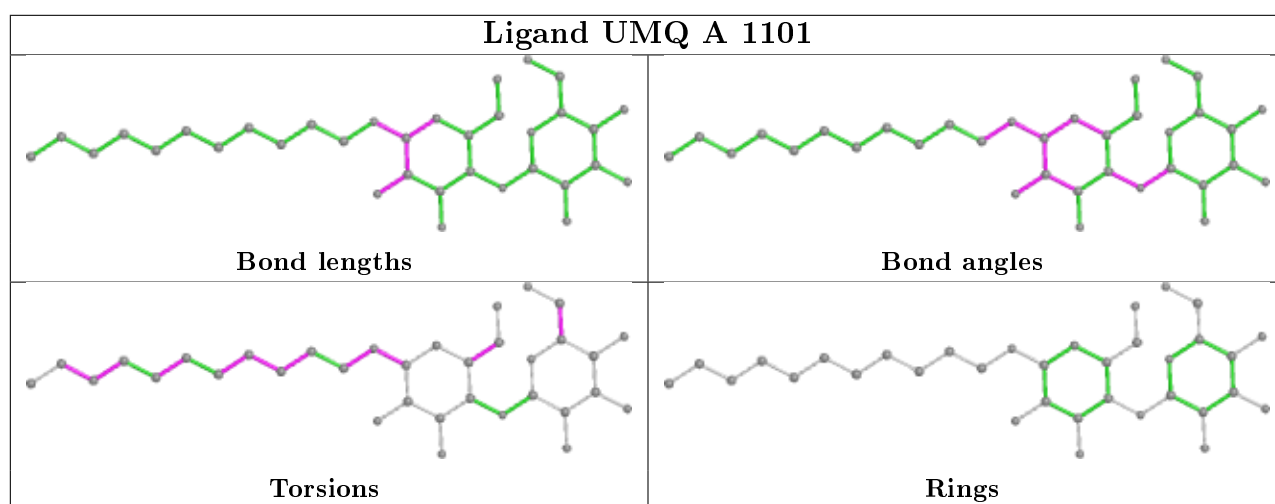
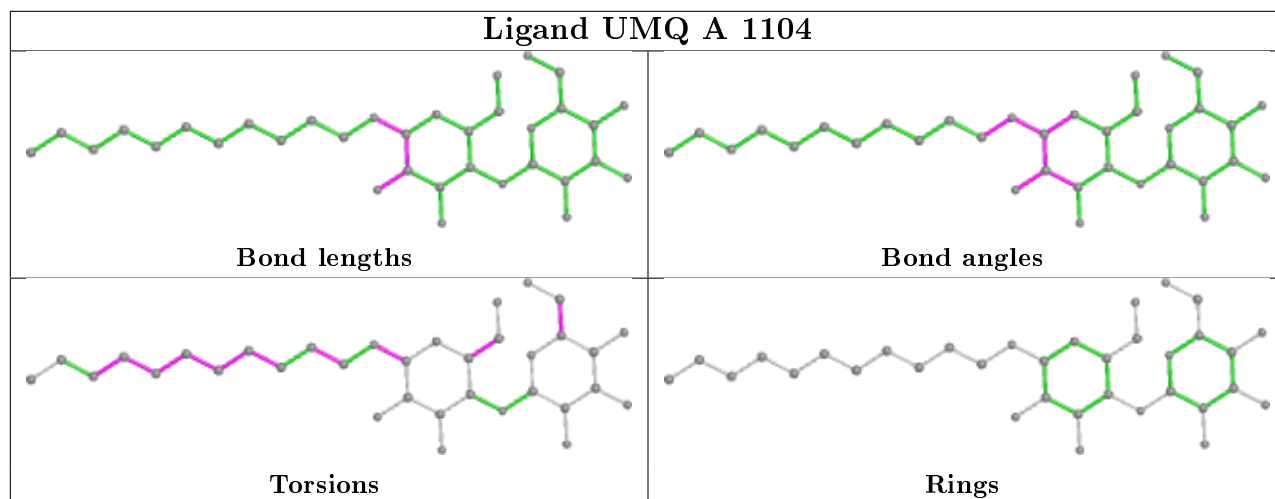
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	A	1103	UMQ	1	0
11	A	1102	UMQ	2	0
13	H	1002	OPC	24	0
10	A	303	HEM	5	0
13	B	202	OPC	2	0
11	A	1104	UMQ	4	0
11	A	1101	UMQ	6	0
10	A	302	HEM	8	0
14	D	200	FES	2	0
15	D	201	SQD	12	0
10	C	301	HEM	8	0
10	A	301	HEM	11	0
12	B	201	CLA	4	0
16	G	101	BCR	11	0

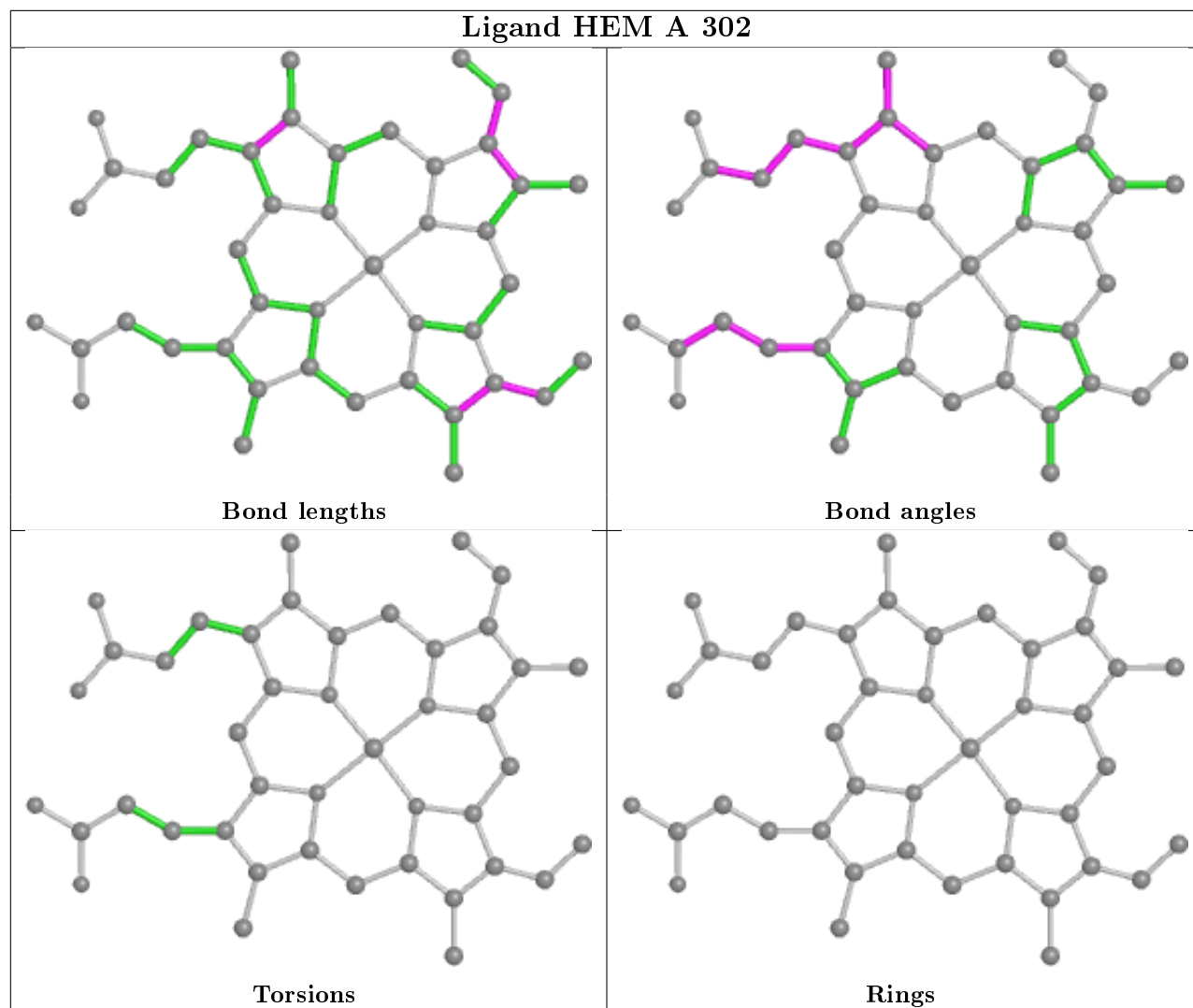
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

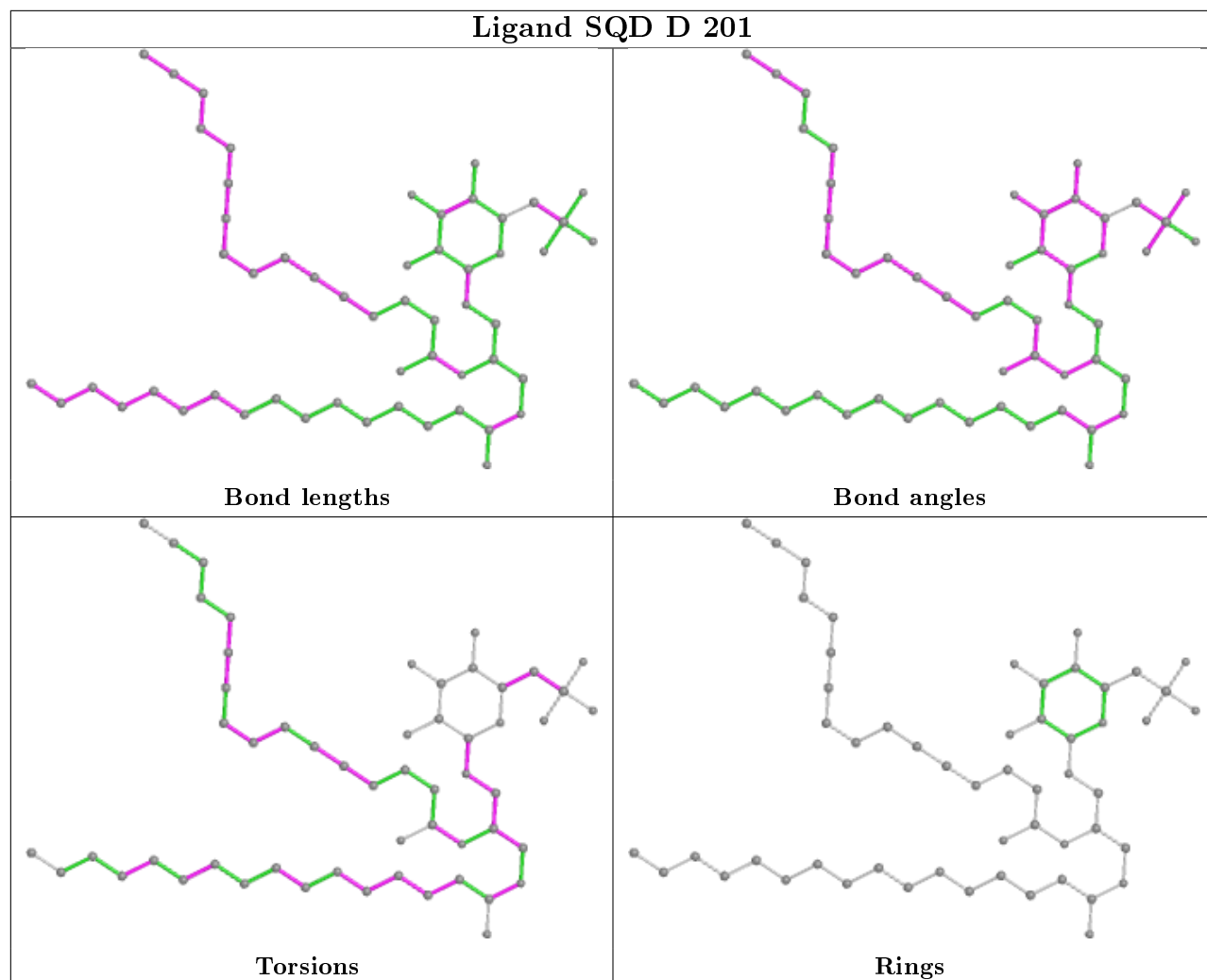


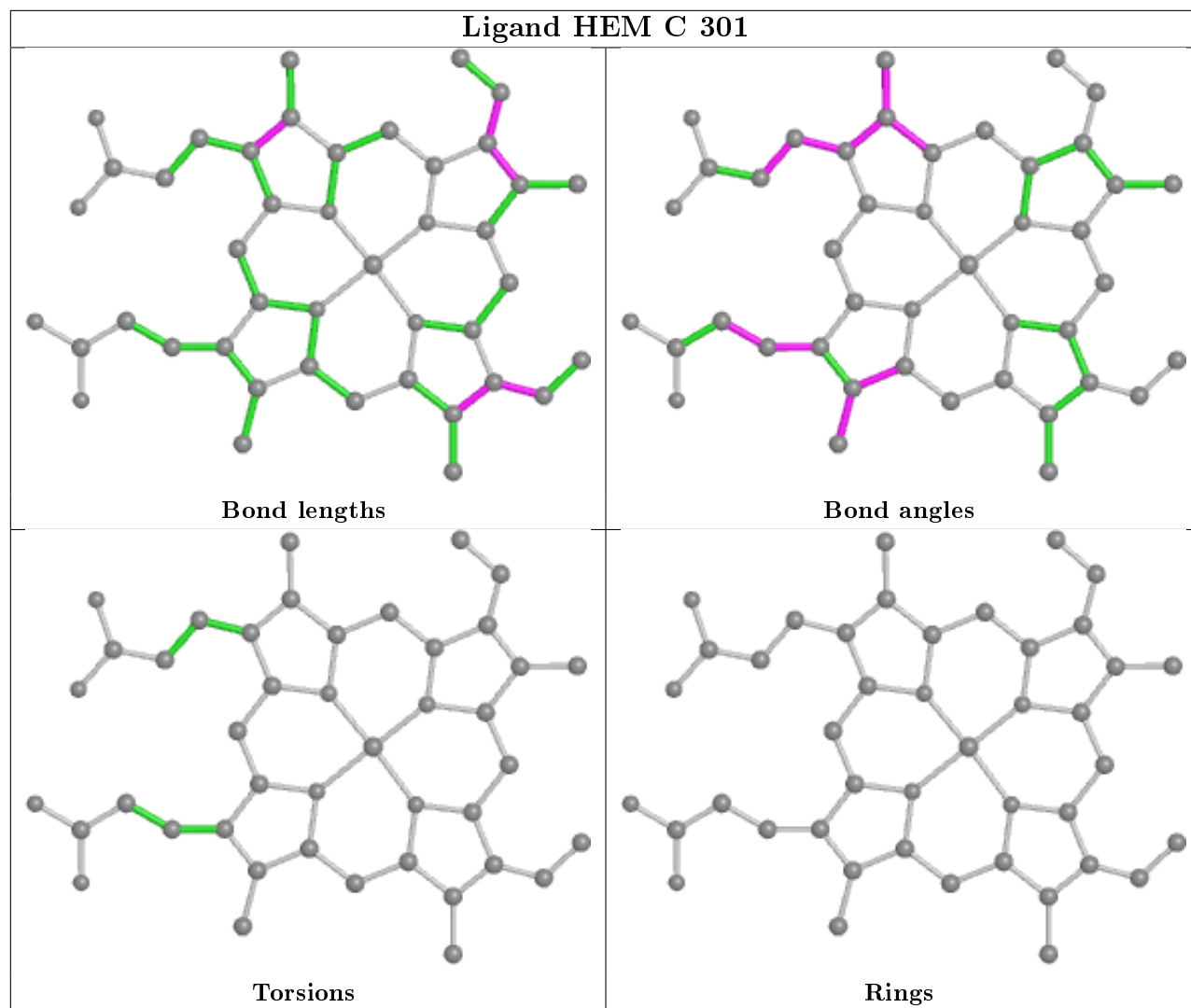


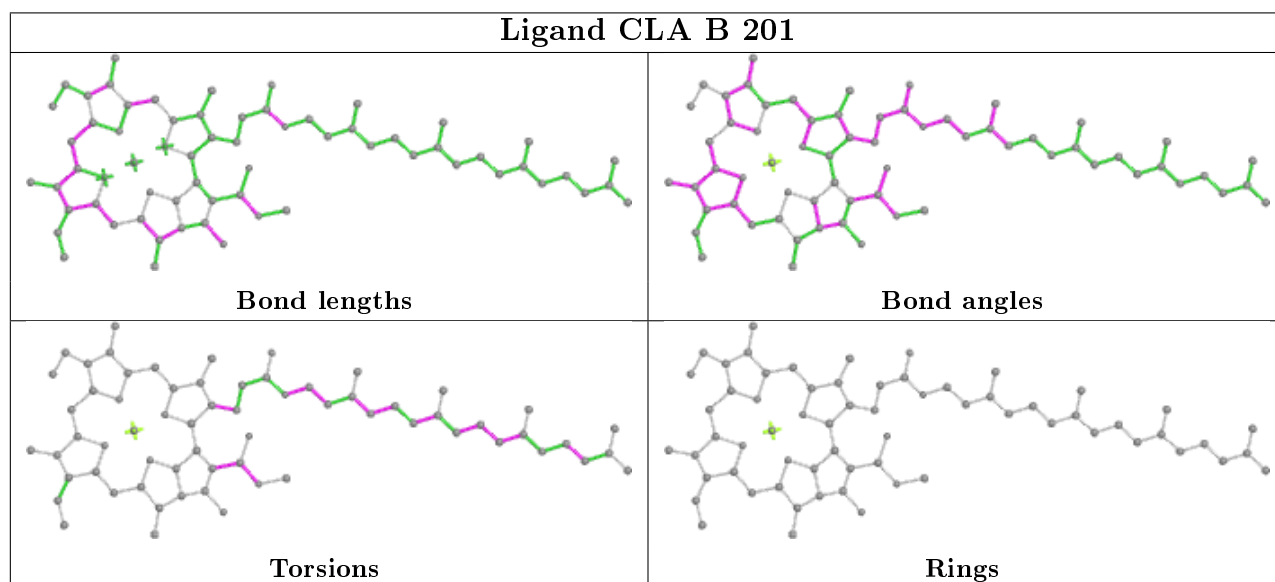
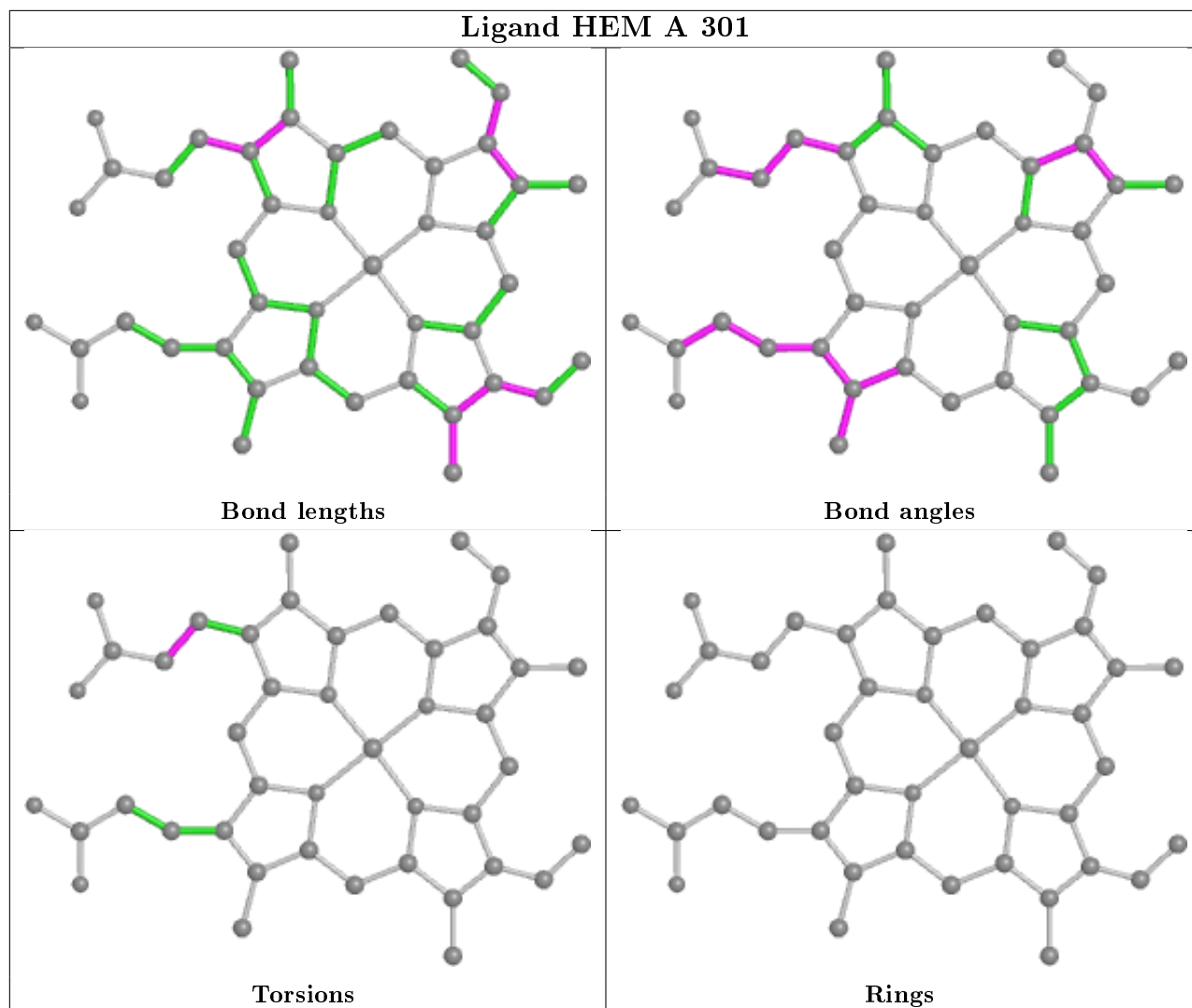


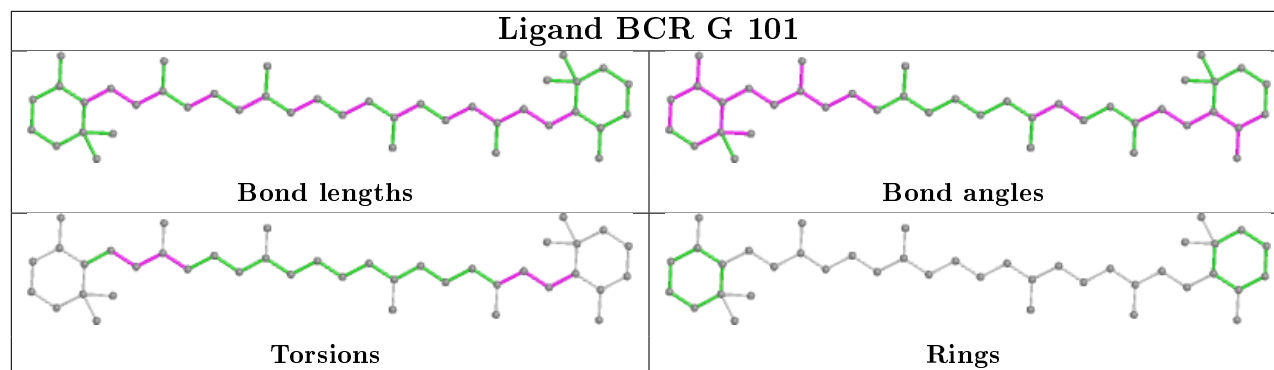












5.7 Other polymers [i](#)

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	215/215 (100%)	-0.52	1 (0%) 91 75	21, 41, 72, 160	0
2	B	160/160 (100%)	-0.41	2 (1%) 77 51	32, 57, 103, 135	0
3	C	288/289 (99%)	0.42	26 (9%) 9 3	20, 54, 114, 130	1 (0%)
4	D	166/179 (92%)	0.82	27 (16%) 1 0	38, 91, 125, 171	0
5	E	32/32 (100%)	-0.28	1 (3%) 49 21	60, 75, 106, 122	0
6	F	32/35 (91%)	-0.39	2 (6%) 20 6	47, 69, 124, 139	0
7	G	37/37 (100%)	-0.26	0 100 100	42, 57, 123, 131	0
8	H	29/29 (100%)	-0.32	1 (3%) 45 19	40, 52, 76, 118	0
All	All	959/976 (98%)	0.04	60 (6%) 20 6	20, 57, 115, 171	1 (0%)

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	220	SER	7.6
3	C	184	ALA	6.4
3	C	206	THR	6.2
4	D	159	ASN	6.1
4	D	50	VAL	6.0
4	D	179	VAL	5.2
3	C	222	GLY	5.1
3	C	181	THR	5.1
3	C	183	ILE	4.8
3	C	182	LYS	4.5
4	D	49	ALA	4.3
4	D	56	ALA	4.1
3	C	205	LYS	4.0
3	C	198	SER	3.9
4	D	158	ASP	3.9
2	B	160	PHE	3.8

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Mol	Chain	Res	Type	RSRZ
3	C	176	ALA	3.7
3	C	199	ILE	3.7
4	D	160	ILE	3.5
4	D	173	GLY	3.5
3	C	203	SER	3.4
4	D	70	LEU	3.2
3	C	207	VAL	3.1
4	D	157	ASP	3.1
3	C	221	GLU	3.0
3	C	197	VAL	2.9
4	D	166	THR	2.9
3	C	204	GLY	2.8
4	D	175	LYS	2.8
4	D	17	GLN	2.7
4	D	172	THR	2.7
3	C	194	LYS	2.7
4	D	72	SER	2.7
4	D	67	SER	2.6
3	C	287	MET	2.6
4	D	13	MET	2.6
4	D	62	ASN	2.6
4	D	170	PHE	2.5
3	C	195	TYR	2.5
4	D	10	VAL	2.5
8	H	1	MET	2.4
4	D	98	ALA	2.4
4	D	168	THR	2.3
6	F	31	GLY	2.3
3	C	224	ALA	2.3
4	D	156	GLN	2.3
6	F	32	ALA	2.3
1	A	1	MET	2.2
3	C	192	ASN	2.2
3	C	228	GLY	2.2
3	C	188	ASP	2.2
5	E	30	LYS	2.2
4	D	92	VAL	2.1
4	D	141	ARG	2.1
4	D	11	PRO	2.1
4	D	143	PRO	2.1
3	C	140	LYS	2.1
2	B	153	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
3	C	173	THR	2.0
3	C	189	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

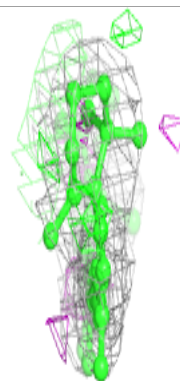
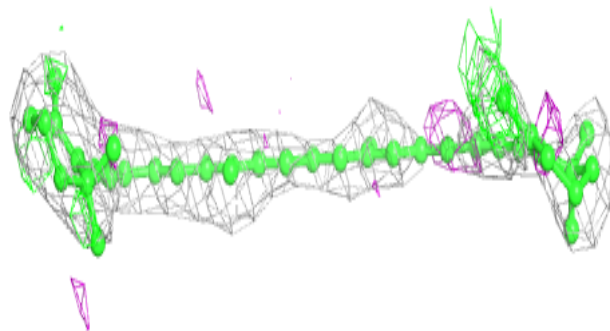
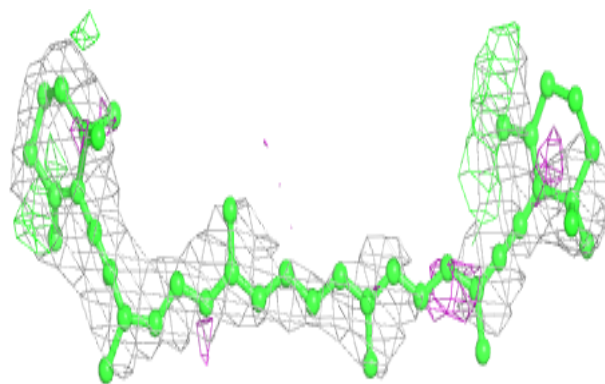
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
16	BCR	G	101	40/40	0.69	0.43	33,70,131,136	0
11	UMQ	A	1101	34/34	0.78	0.39	35,109,146,149	0
11	UMQ	A	1102	34/34	0.80	0.39	62,119,148,149	0
13	OPC	H	1002	54/55	0.82	0.27	41,93,187,196	0
11	UMQ	A	1104	34/34	0.84	0.32	86,134,171,175	0
15	SQD	D	201	54/54	0.86	0.58	67,164,194,196	0
11	UMQ	A	1103	34/34	0.88	0.33	76,112,134,135	0
9	CD	B	161	1/1	0.91	0.19	166,166,166,166	0
13	OPC	B	202	54/55	0.92	0.27	48,82,157,162	0
12	CLA	B	201	65/65	0.96	0.18	41,60,91,99	0
14	FES	D	200	4/4	0.96	0.08	96,101,102,113	0
10	HEM	C	301	43/43	0.97	0.21	29,54,89,97	0
10	HEM	A	303	43/43	0.97	0.19	26,59,68,76	0
9	CD	A	1001	1/1	0.97	0.15	65,65,65,65	0
10	HEM	A	301	43/43	0.98	0.18	9,32,51,75	0
10	HEM	A	302	43/43	0.98	0.21	9,34,57,74	0

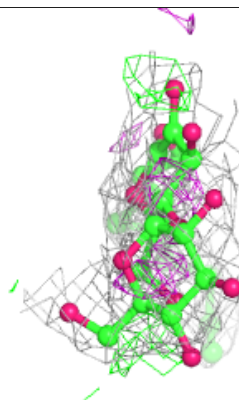
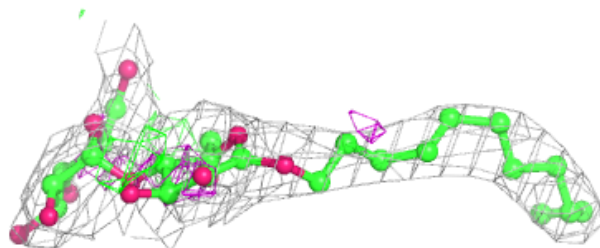
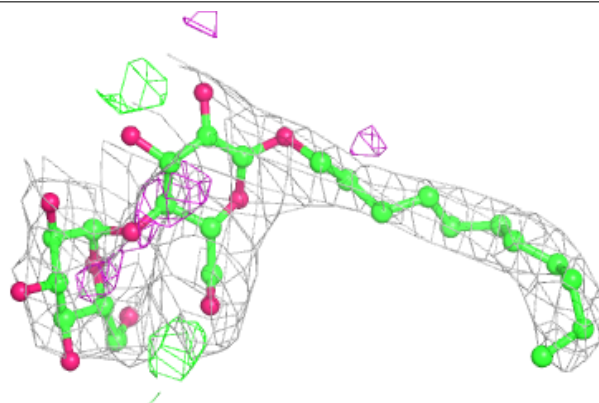
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around BCR G 101:

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

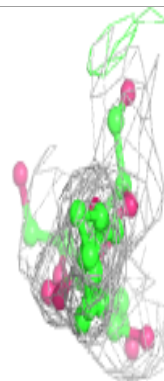
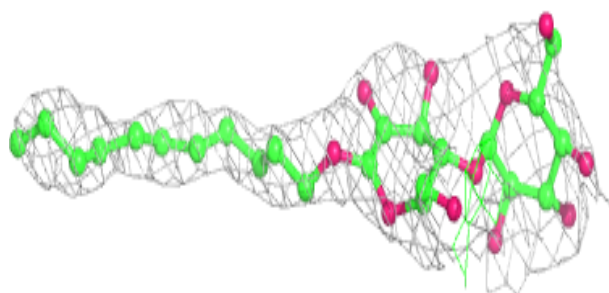
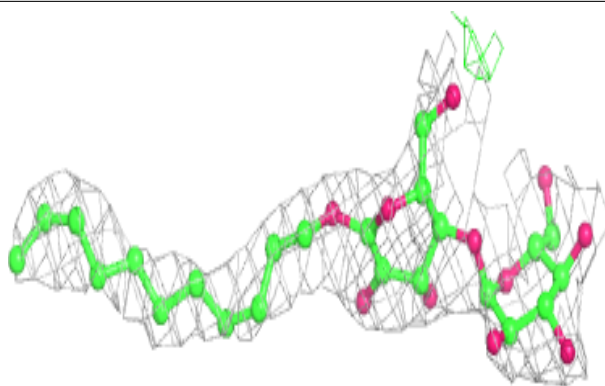
**Electron density around UMQ A 1101:**

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

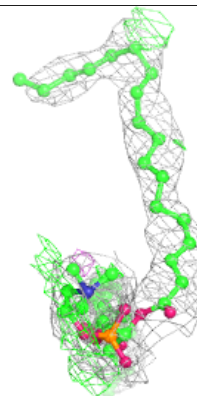
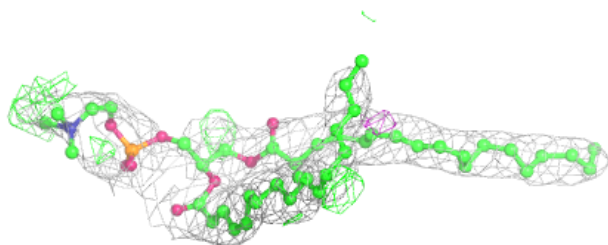
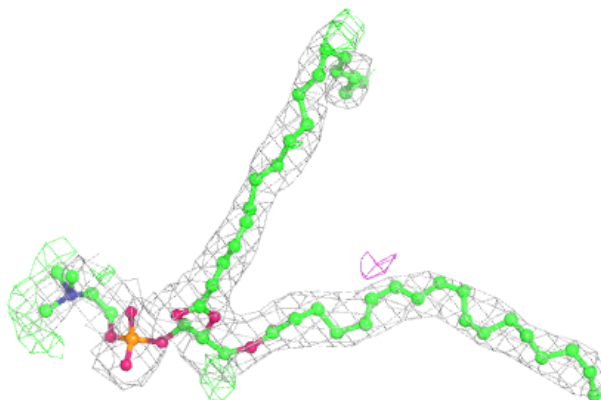


Electron density around UMQ A 1102:

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

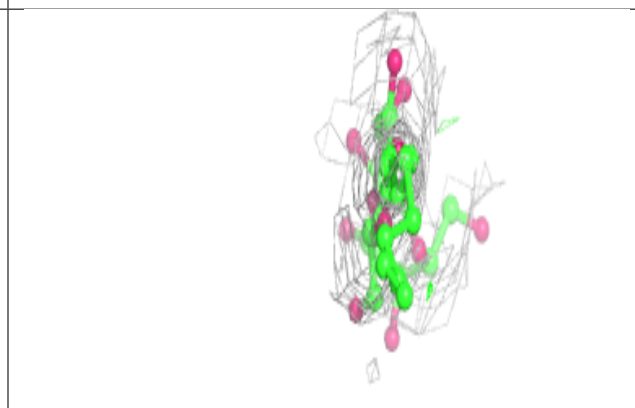
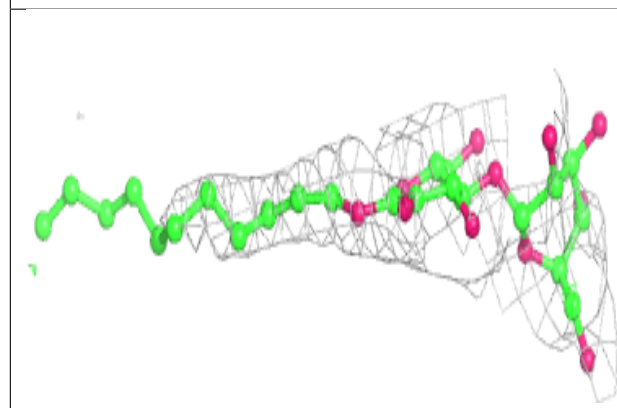
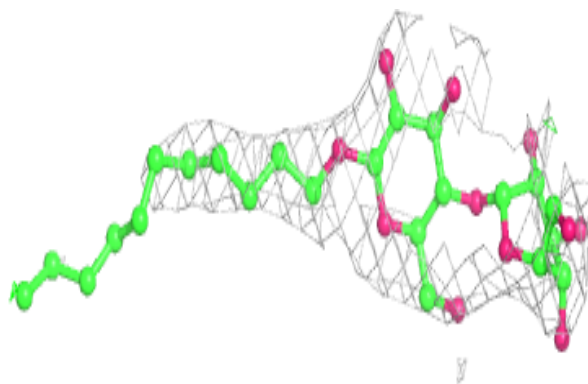
**Electron density around OPC H 1002:**

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

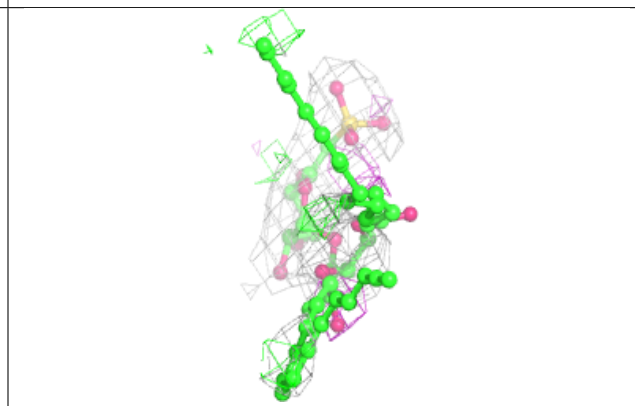
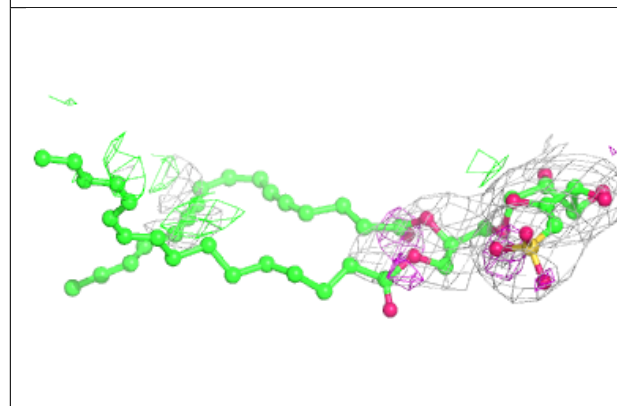
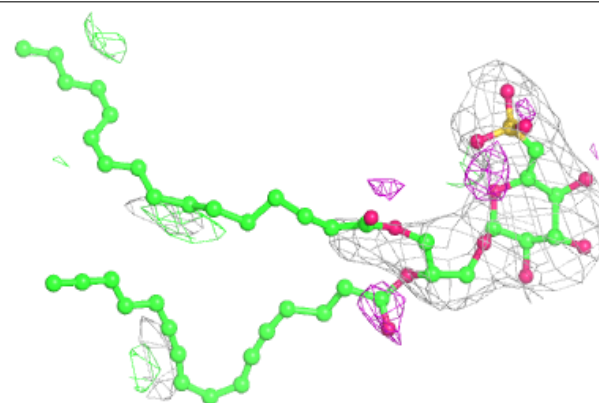


Electron density around UMQ A 1104:

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

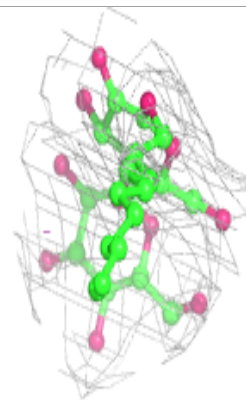
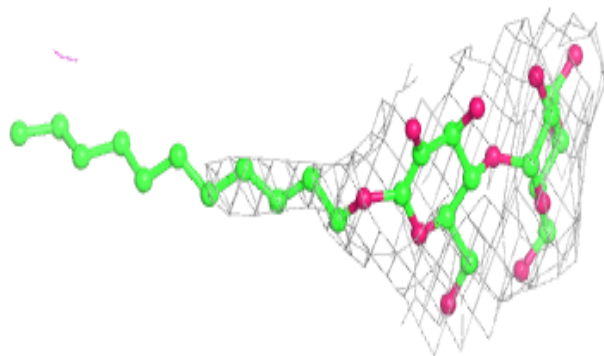
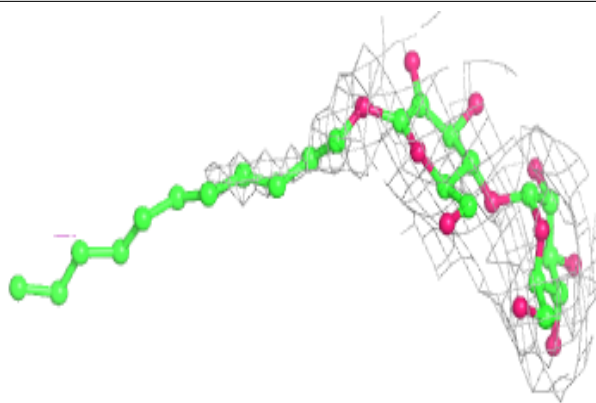
**Electron density around SQD D 201:**

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

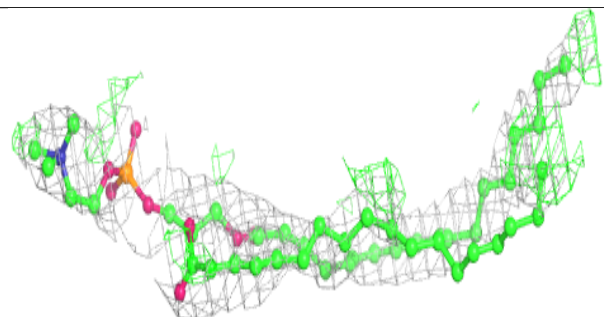
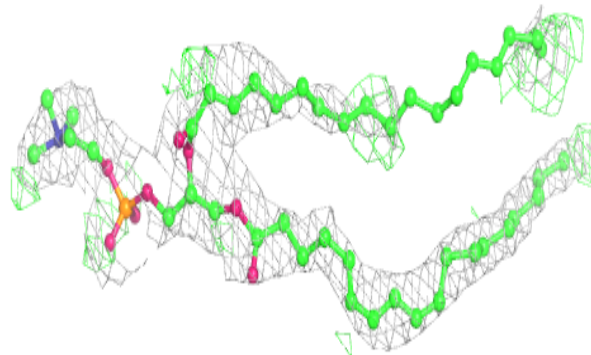


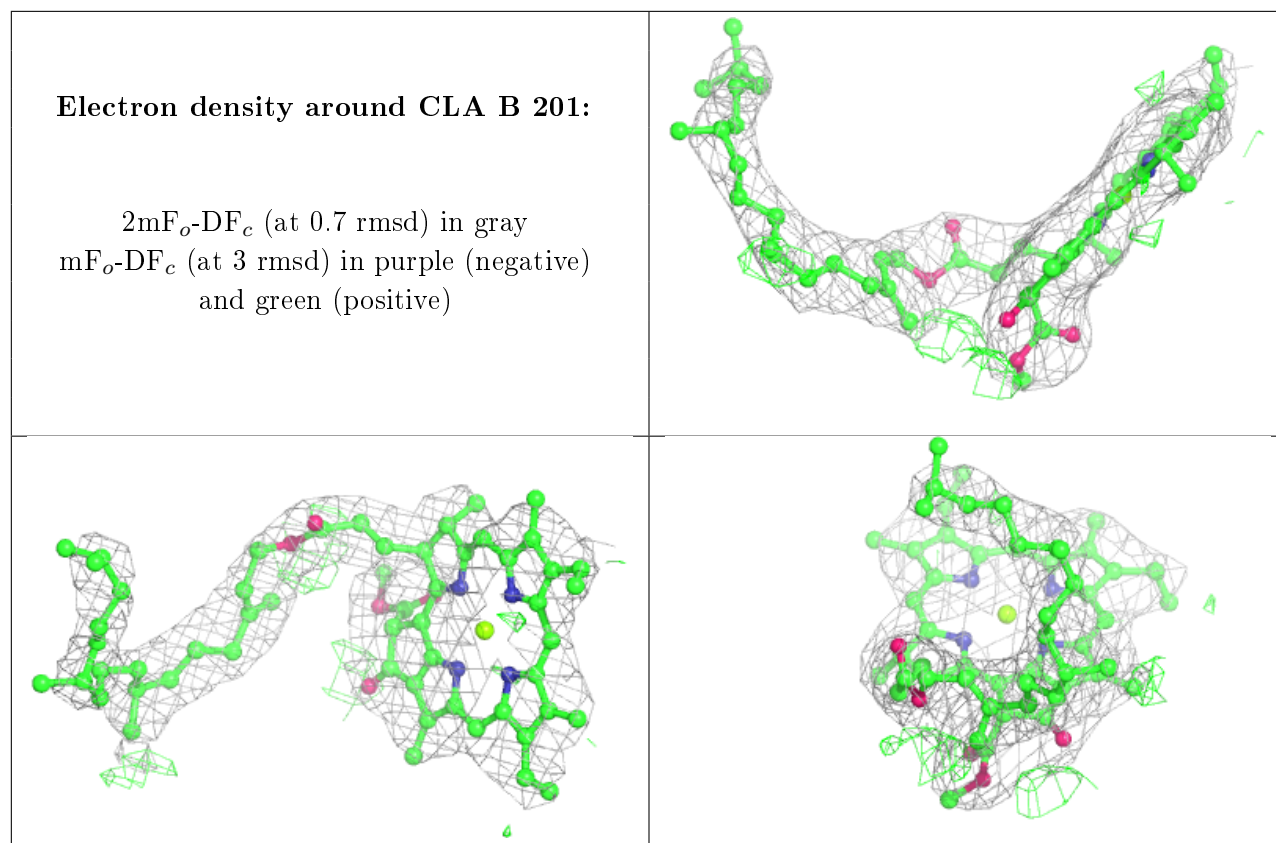
Electron density around UMQ A 1103:

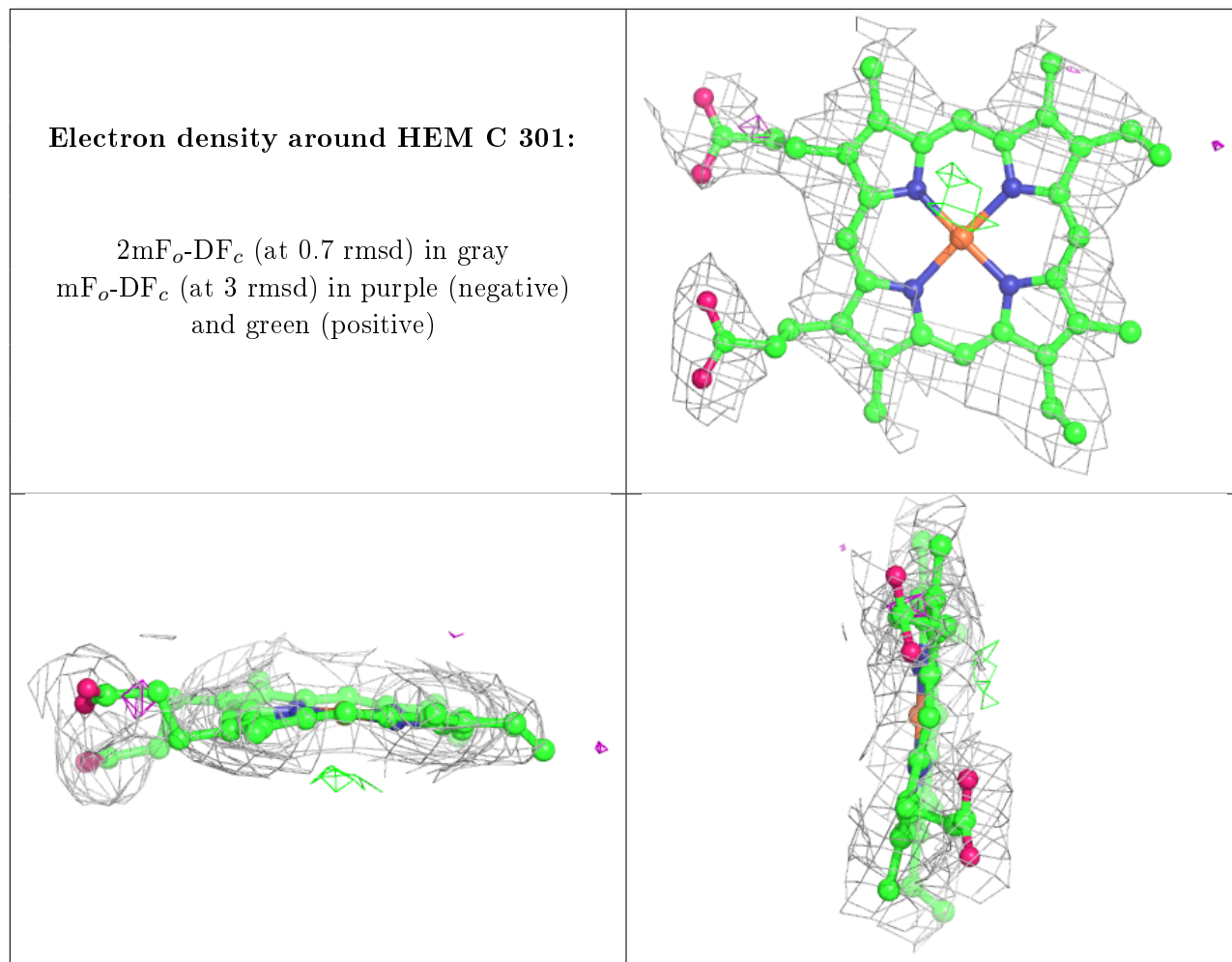
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around OPC B 202:**

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

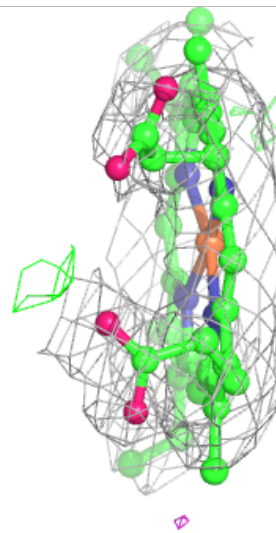
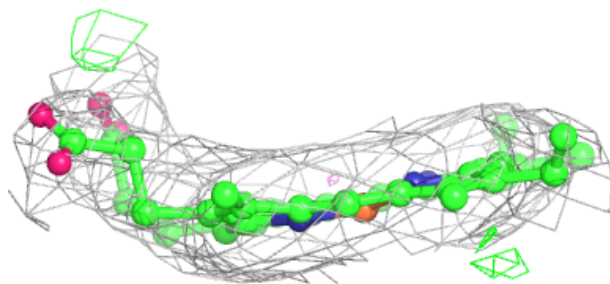
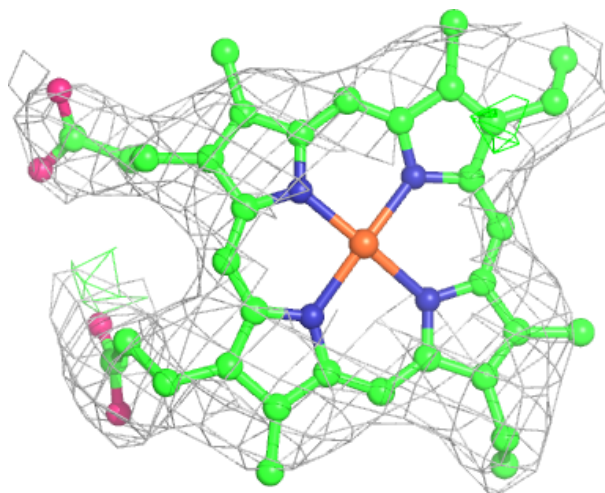


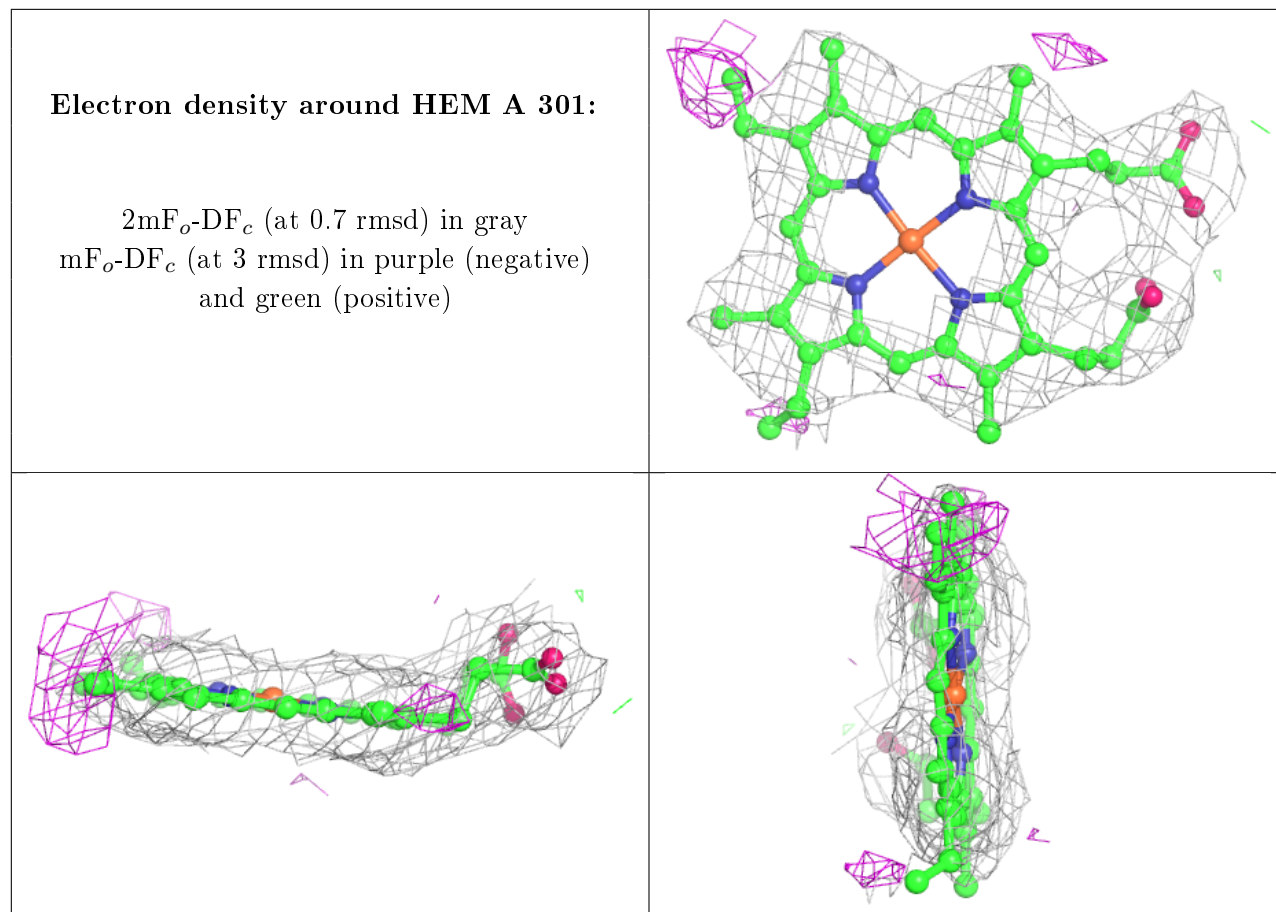


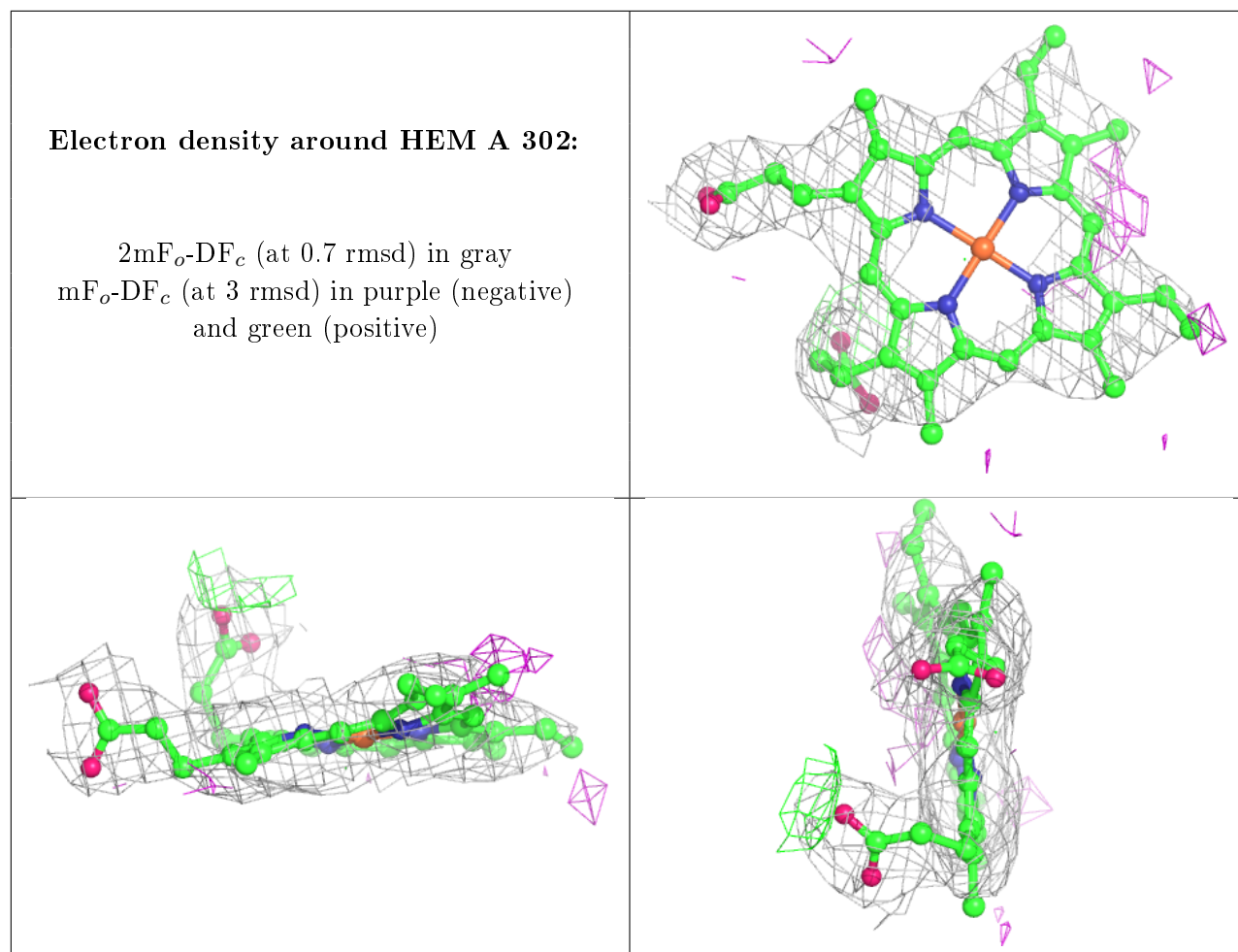


Electron density around HEM A 303:

$2mF_o-DF_c$ (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.