



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 06:04 PM UTC

PDB ID : 2UX3 / pdb_00002ux3
Title : X-ray high resolution structure of the photosynthetic reaction center from Rb. sphaeroides at pH 9 in the neutral state
Authors : Koepke, J.; Diehm, R.; Fritzsche, G.
Deposited on : 2007-03-26
Resolution : 2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

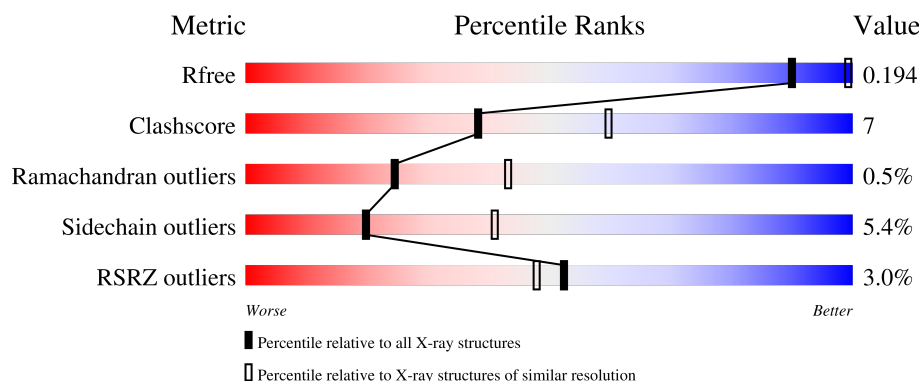
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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

Mol	Chain	Length	Quality of chain
1	H	260	 4% 82% 10% 7%
2	L	281	 2% 85% 14% .
3	M	307	 3% 81% 16% ..

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
5	BCL	L	1282	X	-	-	-
5	BCL	L	1286	X	-	-	-
5	BCL	M	1303	X	-	-	-
5	BCL	M	1304	X	-	-	-

2 Entry composition [i](#)

There are 15 unique types of molecules in this entry. The entry contains 7606 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 REACTION CENTER PROTEIN H CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	241	Total	C	N	O	S	0	3	1
			1846	1181	319	337	9			

- Molecule 2 is a protein called REACTION CENTER PROTEIN L CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	281	Total	C	N	O	S	0	0	0
			2232	1507	355	362	8			

- Molecule 3 is a protein called REACTION CENTER PROTEIN M CHAIN.

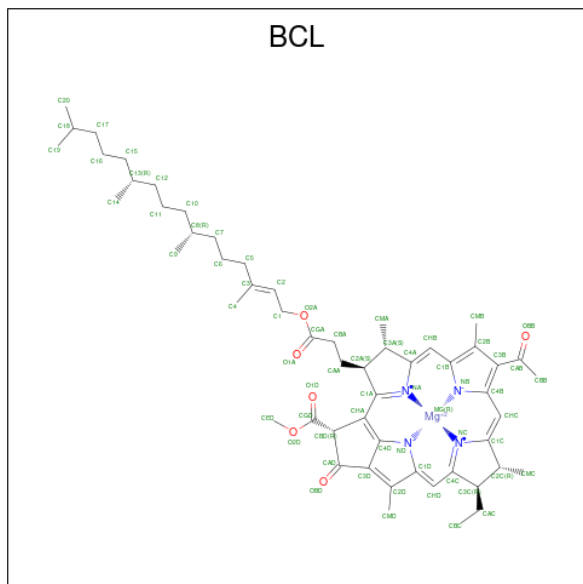
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	303	Total	C	N	O	S	0	1	1
			2419	1616	396	397	10			

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



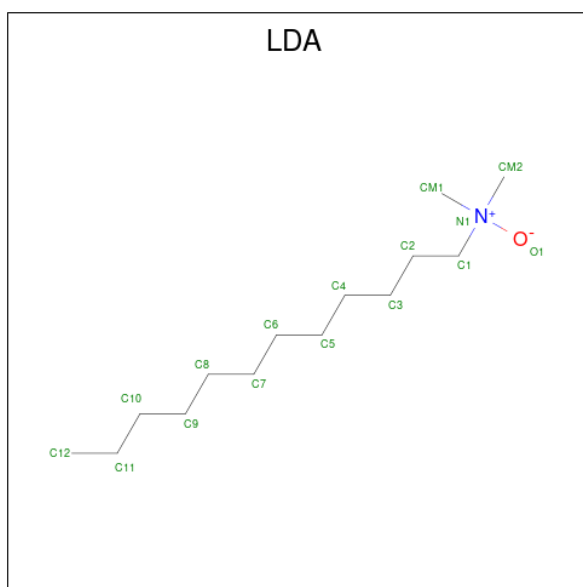
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	L	1	Total	C	O	0	0
			6	3	3		
4	L	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is BACTERIOCHLOROPHYLL A (CCD ID: BCL) (formula: $C_{55}H_{74}MgN_4O_6$).



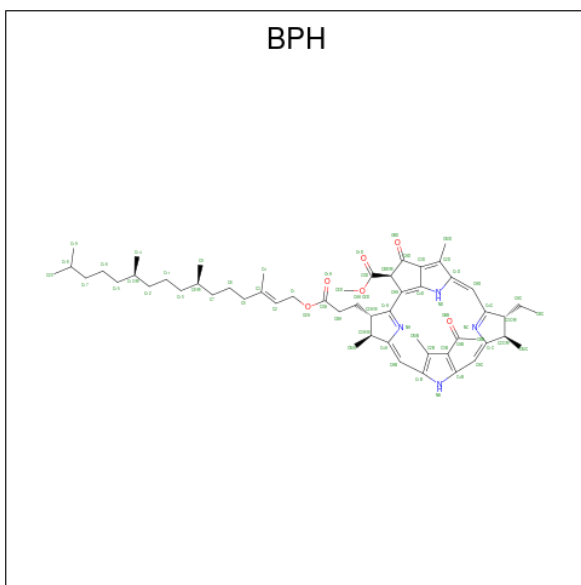
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
5	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
5	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
5	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		

- Molecule 6 is LAURYL DIMETHYLAMINE-N-OXIDE (CCD ID: LDA) (formula: $C_{14}H_{31}NO$).



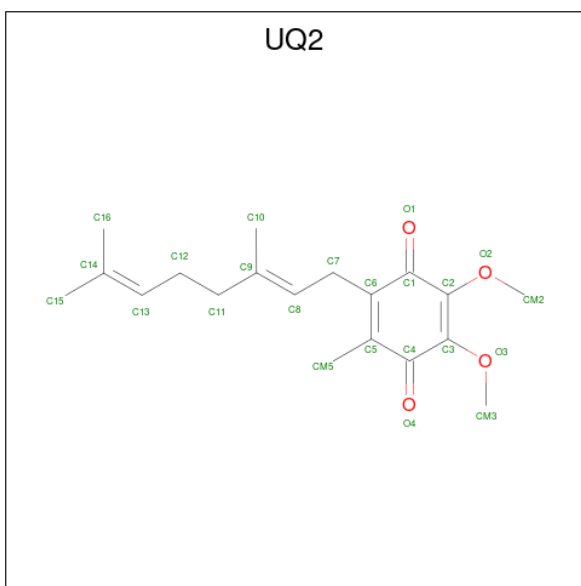
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	L	1	Total	C	N	O	0	0
			16	14	1	1		
6	L	1	Total	C	N	O	0	0
			16	14	1	1		
6	M	1	Total	C	N	O	0	0
			16	14	1	1		
6	M	1	Total	C	N	O	0	0
			16	14	1	1		
6	M	1	Total	C	N	O	0	0
			16	14	1	1		
6	M	1	Total	C	N	O	0	0
			16	14	1	1		
6	M	1	Total	C	N	O	0	0
			16	14	1	1		
6	M	1	Total	C	N	O	0	0
			16	14	1	1		

- Molecule 7 is BACTERIOPHEOPHYTIN A (CCD ID: BPH) (formula: $C_{55}H_{76}N_4O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	L	1	Total	C	N	O	0	0
			65	55	4	6		
7	M	1	Total	C	N	O	0	0
			65	55	4	6		

- Molecule 8 is UBIQUINONE-2 (CCD ID: UQ2) (formula: $C_{19}H_{26}O_4$).



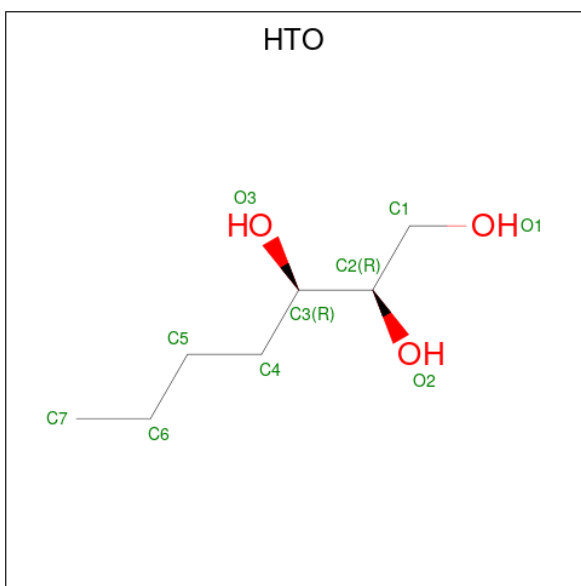
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	L	1	Total	C	O	0	1
			46	38	8		

- Molecule 9 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	L	1	Total	O	P	0	0
			5	4	1		

- Molecule 10 is HEPTANE-1,2,3-TRIOL (CCD ID: HTO) (formula: $C_7H_{16}O_3$).

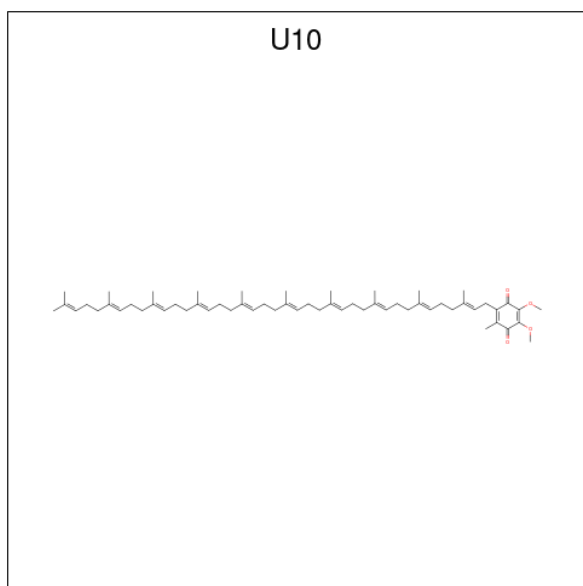


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	L	1	Total	C	O	0	0
			10	7	3		

- Molecule 11 is FE (III) ION (CCD ID: FE) (formula: Fe).

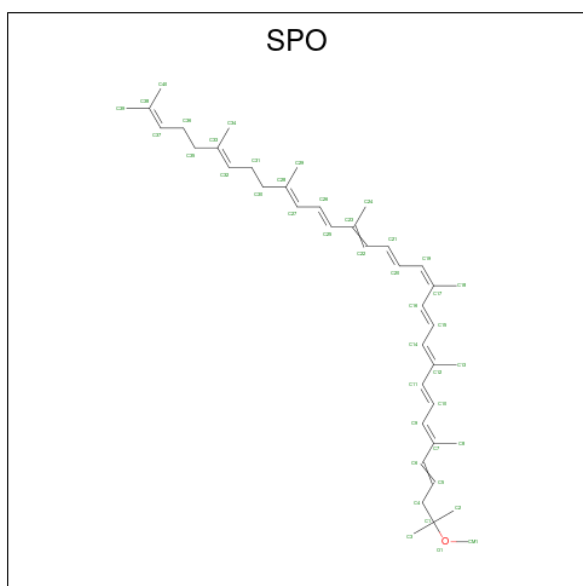
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	M	1	Total	Fe	0	0
			1	1		

- Molecule 12 is UBIQUINONE-10 (CCD ID: U10) (formula: $C_{59}H_{90}O_4$).



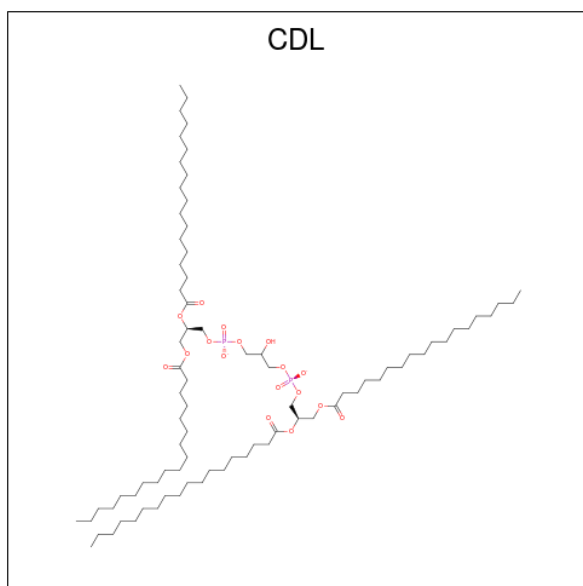
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	M	1	Total	C	O	0	0
			48	44	4		

- Molecule 13 is SPHEROIDENE (CCD ID: SPO) (formula: $C_{41}H_{60}O$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	M	1	Total	C	O	0	0
			42	41	1		

- Molecule 14 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
14	M	1	Total	C	O	P	0	0
			81	62	17	2		

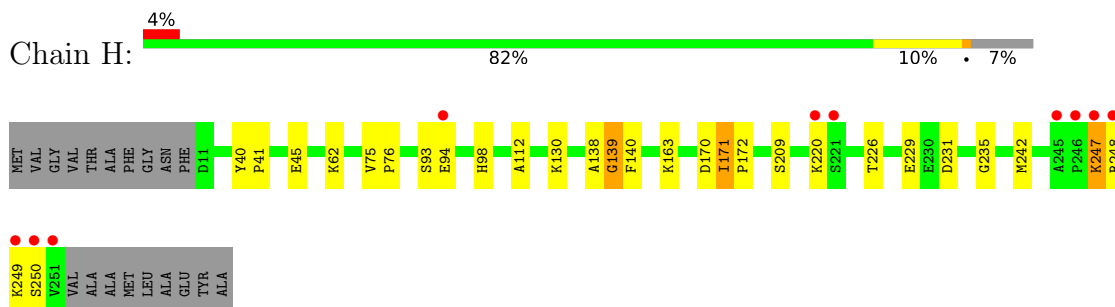
- Molecule 15 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	H	114	Total	O	0	0
			114	114		
15	L	92	Total	O	0	0
			92	92		
15	M	96	Total	O	0	0
			96	96		

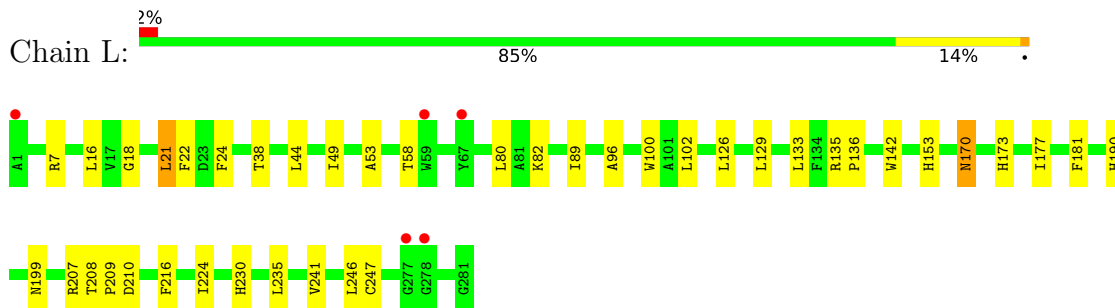
3 Residue-property plots [i](#)

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

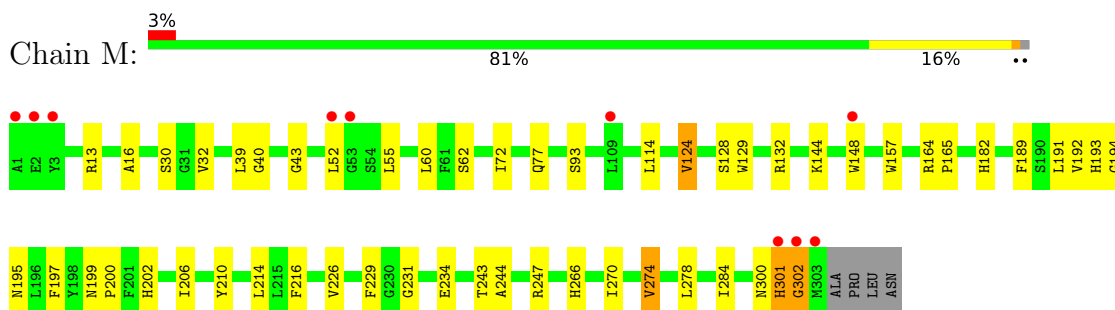
• Molecule 1: REACTION CENTER PROTEIN H CHAIN



• Molecule 2: REACTION CENTER PROTEIN L CHAIN



• Molecule 3: REACTION CENTER PROTEIN M CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	139.45Å 139.45Å 184.58Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	119.52 – 2.50 119.52 – 2.50	Depositor EDS
% Data completeness (in resolution range)	92.1 (119.52-2.50) 86.6 (119.52-2.50)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.79 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.185 , 0.221 (Not available) , 0.194	Depositor DCC
R_{free} test set	2004 reflections (3.01%)	wwPDB-VP
Wilson B-factor (Å ²)	44.7	Xtriage
Anisotropy	0.190	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 40.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.021 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7606	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UQ2, CDL, FE, HTO, SPO, U10, LDA, BPH, BCL, PO4, GOL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	H	0.76	2/1906 (0.1%)	0.91	1/2591 (0.0%)
2	L	0.77	0/2320	0.91	0/3175
3	M	0.72	1/2517 (0.0%)	0.93	1/3438 (0.0%)
All	All	0.75	3/6743 (0.0%)	0.92	2/9204 (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
3	M	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	M	302	GLY	C-N	-6.50	1.24	1.33
1	H	250	SER	C-N	-6.42	1.24	1.33
1	H	242	MET	SD-CE	5.00	1.92	1.79

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	139	GLY	N-CA-C	-5.23	98.13	113.30
3	M	302	GLY	O-C-N	-5.19	114.70	123.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	M	300	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	H	1846	0	1861	14	0
2	L	2232	0	2187	27	0
3	M	2419	0	2327	31	0
4	H	24	0	32	1	0
4	L	12	0	16	1	0
5	L	132	0	148	7	0
5	M	132	0	148	19	0
6	L	32	0	62	2	0
6	M	112	0	217	2	0
7	L	65	0	76	9	0
7	M	65	0	76	13	0
8	L	46	0	52	6	0
9	L	5	0	0	0	0
10	L	10	0	16	2	0
11	M	1	0	0	0	0
12	M	48	0	63	2	0
13	M	42	0	60	3	0
14	M	81	0	82	3	0
15	H	114	0	0	0	1
15	L	92	0	0	0	0
15	M	96	0	0	0	0
All	All	7606	0	7423	101	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (101) 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)
2:L:224:ILE:HG22	8:L:1285[A]:UQ2:H8	1.61	0.83
8:L:1285[A]:UQ2:H161	6:L:1711:LDA:H121	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:197:PHE:HZ	5:M:1304:BCL:HBB2	1.46	0.79
2:L:181:PHE:CD2	7:M:1313:BPH:HBB1	2.18	0.78
3:M:197:PHE:CZ	5:M:1304:BCL:HBB2	2.18	0.78
1:H:62:LYS:HE3	4:H:1251:GOL:H11	1.64	0.78
3:M:16:ALA:HB1	3:M:32:VAL:HG11	1.66	0.75
7:L:1284:BPH:HBB2	3:M:210:TYR:HB3	1.75	0.69
7:L:1284:BPH:HHC	7:L:1284:BPH:CBB	2.22	0.69
2:L:181:PHE:HB3	7:M:1313:BPH:HBB2	1.74	0.69
2:L:170:ASN:HD22	2:L:170:ASN:C	2.01	0.68
7:L:1284:BPH:HHC	7:L:1284:BPH:HBB3	1.76	0.66
7:M:1313:BPH:HBB3	7:M:1313:BPH:HHC	1.76	0.65
3:M:144:LYS:N	14:M:1316:CDL:OB3	2.26	0.65
3:M:157:TRP:HB2	5:M:1304:BCL:H71	1.78	0.65
5:M:1303:BCL:H62	7:M:1313:BPH:HMB2	1.79	0.63
3:M:77:GLN:HE22	3:M:93:SER:H	1.44	0.63
5:M:1303:BCL:HBB3	5:M:1304:BCL:H41	1.79	0.62
7:M:1313:BPH:HHD	7:M:1313:BPH:HBC2	1.80	0.62
2:L:199:ASN:HA	4:L:1289:GOL:H31	1.82	0.61
2:L:199:ASN:O	14:M:1316:CDL:HB22	2.00	0.60
3:M:199:ASN:HD22	3:M:199:ASN:C	2.09	0.59
5:M:1303:BCL:H62	7:M:1313:BPH:CMB	2.32	0.59
2:L:181:PHE:HB3	7:M:1313:BPH:CBB	2.33	0.59
1:H:140:PHE:HA	3:M:13:ARG:O	2.03	0.58
2:L:190:HIS:HA	8:L:1285[A]:UQ2:O4	2.04	0.58
5:M:1303:BCL:CBB	13:M:1315:SPO:H243	2.34	0.57
8:L:1285[B]:UQ2:H5M3	8:L:1285[B]:UQ2:H8	1.87	0.57
3:M:197:PHE:CE1	5:M:1304:BCL:HHC	2.40	0.57
8:L:1285[A]:UQ2:C16	6:L:1711:LDA:H121	2.34	0.56
6:M:1308:LDA:H71	12:M:1314:U10:H23	1.88	0.56
5:M:1304:BCL:HBB2	5:M:1304:BCL:HHC	1.90	0.54
3:M:62:SER:OG	3:M:124:VAL:HG22	2.07	0.54
3:M:189:PHE:O	3:M:193:HIS:HD2	1.90	0.53
5:L:1282:BCL:HMD2	3:M:206:ILE:HD13	1.91	0.52
5:M:1303:BCL:HBB2	13:M:1315:SPO:H243	1.90	0.52
3:M:194:GLY:O	3:M:195:ASN:HB3	2.10	0.51
1:H:75:VAL:HA	1:H:76:PRO:C	2.36	0.51
7:L:1284:BPH:HBB1	3:M:210:TYR:CD2	2.46	0.51
7:L:1284:BPH:HBB3	7:L:1284:BPH:CHC	2.40	0.51
7:M:1313:BPH:HHC	7:M:1313:BPH:CBB	2.38	0.51
5:M:1304:BCL:HAA2	5:M:1304:BCL:HBD	1.93	0.51
2:L:135:ARG:HB3	2:L:136:PRO:HD3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:M:1304:BCL:CHC	5:M:1304:BCL:CBB	2.90	0.49
3:M:55:LEU:HD22	3:M:128:SER:HB2	1.95	0.48
2:L:133:LEU:HD13	10:L:1288:HTO:H62	1.95	0.47
5:L:1282:BCL:HBB3	5:L:1286:BCL:H52	1.95	0.47
1:H:98:HIS:CD2	2:L:7:ARG:HH21	2.32	0.47
7:L:1284:BPH:CBB	7:L:1284:BPH:CHC	2.91	0.47
3:M:243:THR:O	3:M:247:ARG:HG3	2.14	0.47
2:L:224:ILE:CG2	8:L:1285[A]:UQ2:H8	2.40	0.46
3:M:164:ARG:HB3	3:M:165:PRO:HD3	1.98	0.46
7:M:1313:BPH:HBC2	7:M:1313:BPH:CHD	2.44	0.46
3:M:284:ILE:HG12	5:M:1304:BCL:HED3	1.97	0.46
1:H:209:SER:OG	1:H:247:LYS:HD3	2.16	0.46
3:M:229:PHE:HB2	3:M:244:ALA:HB2	1.98	0.46
2:L:38:THR:HG21	2:L:100:TRP:HE3	1.80	0.45
2:L:22:PHE:HA	2:L:24:PHE:CE2	2.52	0.45
3:M:129:TRP:O	3:M:132:ARG:HB3	2.16	0.45
2:L:49:ILE:HG13	2:L:89:ILE:HD13	1.98	0.45
6:M:1307:LDA:H112	12:M:1314:U10:H202	1.98	0.45
5:M:1304:BCL:HHC	5:M:1304:BCL:CBB	2.47	0.45
1:H:226:THR:OG1	1:H:229:GLU:HG3	2.17	0.45
1:H:45:GLU:HG3	1:H:94:GLU:OE1	2.16	0.45
5:L:1282:BCL:HBB2	5:L:1282:BCL:HHC	1.98	0.44
5:M:1303:BCL:C6	7:M:1313:BPH:HMB2	2.46	0.44
2:L:96:ALA:HB1	7:L:1284:BPH:H2	2.00	0.44
7:M:1313:BPH:HBB3	7:M:1313:BPH:CHC	2.47	0.44
2:L:241:VAL:HG21	7:L:1284:BPH:HBC3	2.00	0.44
2:L:170:ASN:C	2:L:170:ASN:ND2	2.74	0.44
5:M:1303:BCL:HBB1	13:M:1315:SPO:H243	2.00	0.43
1:H:98:HIS:HD2	2:L:7:ARG:HH21	1.67	0.43
1:H:171:ILE:N	1:H:172:PRO:HD2	2.33	0.43
5:L:1282:BCL:H161	5:L:1282:BCL:H122	1.64	0.43
5:M:1304:BCL:H61	7:M:1313:BPH:C4B	2.49	0.43
7:L:1284:BPH:ND	3:M:214:LEU:HD13	2.34	0.43
5:M:1303:BCL:H102	5:M:1303:BCL:H13	1.82	0.43
1:H:112:ALA:HA	1:H:235:GLY:O	2.19	0.42
3:M:189:PHE:O	3:M:193:HIS:CD2	2.71	0.42
2:L:190:HIS:CE1	2:L:230:HIS:CE1	3.07	0.42
3:M:234:GLU:CD	3:M:266:HIS:HE1	2.27	0.42
1:H:138:ALA:HA	1:H:139:GLY:HA2	1.82	0.42
2:L:173:HIS:CE1	2:L:177:ILE:HD11	2.55	0.42
1:H:98:HIS:CD2	2:L:7:ARG:HE	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:40:GLY:HA2	3:M:43:GLY:O	2.20	0.42
3:M:199:ASN:HD22	3:M:200:PRO:N	2.18	0.42
7:M:1313:BPH:H142	7:M:1313:BPH:H111	1.95	0.42
1:H:130:LYS:HE3	1:H:170:ASP:OD2	2.19	0.42
3:M:202:HIS:CE1	3:M:206:ILE:HD11	2.55	0.41
2:L:53:ALA:HB1	2:L:58:THR:O	2.19	0.41
3:M:148[B]:TRP:CD1	14:M:1316:CDL:HB62	2.56	0.41
5:L:1282:BCL:O1A	5:L:1282:BCL:H43	2.21	0.41
3:M:226:VAL:HG23	3:M:231:GLY:HA3	2.03	0.41
2:L:142:TRP:CZ2	10:L:1288:HTO:H3	2.54	0.41
5:L:1286:BCL:C1C	5:M:1304:BCL:HBB3	2.51	0.41
3:M:270:ILE:O	3:M:274:VAL:HG13	2.21	0.41
1:H:40:TYR:HA	1:H:41:PRO:C	2.46	0.41
2:L:18:GLY:O	2:L:21:LEU:HB2	2.20	0.40
2:L:153:HIS:CD2	5:L:1282:BCL:NC	2.89	0.40
2:L:208:THR:HB	2:L:209:PRO:HD2	2.04	0.40
3:M:199:ASN:C	3:M:199:ASN:ND2	2.78	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:2033:HOH:O	15:H:2033:HOH:O[4_555]	2.10	0.10

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	H	242/260 (93%)	234 (97%)	7 (3%)	1 (0%)	30	49
2	L	279/281 (99%)	270 (97%)	9 (3%)	0	100	100
3	M	302/307 (98%)	286 (95%)	13 (4%)	3 (1%)	12	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	823/848 (97%)	790 (96%)	29 (4%)	4 (0%)	24 43

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	M	301	HIS
1	H	248	ARG
3	M	30	SER
3	M	302	GLY

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	H	198/208 (95%)	190 (96%)	8 (4%)	28 54
2	L	220/220 (100%)	205 (93%)	15 (7%)	14 31
3	M	237/240 (99%)	224 (94%)	13 (6%)	19 40
All	All	655/668 (98%)	619 (94%)	36 (6%)	20 40

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	93	SER
1	H	163	LYS
1	H	171	ILE
1	H	220[A]	LYS
1	H	220[B]	LYS
1	H	231	ASP
1	H	247	LYS
1	H	249	LYS
2	L	16	LEU
2	L	21	LEU
2	L	44	LEU
2	L	80	LEU

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Mol	Chain	Res	Type
2	L	82	LYS
2	L	102	LEU
2	L	126	LEU
2	L	129	LEU
2	L	170	ASN
2	L	207	ARG
2	L	210	ASP
2	L	216	PHE
2	L	235	LEU
2	L	246	LEU
2	L	247	CYS
3	M	39	LEU
3	M	52	LEU
3	M	60	LEU
3	M	72	ILE
3	M	114	LEU
3	M	124	VAL
3	M	182	HIS
3	M	191	LEU
3	M	192	VAL
3	M	216	PHE
3	M	274	VAL
3	M	278	LEU
3	M	301	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	98	HIS
2	L	159	ASN
2	L	170	ASN
2	L	183	ASN
2	L	258	GLN
3	M	4	GLN
3	M	77	GLN
3	M	187	ASN
3	M	193	HIS
3	M	199	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 29 ligands modelled in this entry, 1 is monoatomic - leaving 28 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
5	BCL	L	1286	2	69,74,74	1.81	7 (10%)	79,115,115	2.18	19 (24%)
5	BCL	M	1304	3	69,74,74	1.83	7 (10%)	79,115,115	1.89	19 (24%)
6	LDA	M	1307	-	13,15,15	2.37	2 (15%)	14,17,17	0.67	0
6	LDA	M	1308	-	13,15,15	2.18	2 (15%)	14,17,17	0.44	0
6	LDA	M	1310	-	13,15,15	2.22	2 (15%)	14,17,17	0.46	0
4	GOL	H	1252	-	5,5,5	0.41	0	5,5,5	0.35	0
5	BCL	M	1303	3	69,74,74	1.87	9 (13%)	79,115,115	2.09	22 (27%)
6	LDA	M	1306	-	13,15,15	2.18	2 (15%)	14,17,17	0.56	0
6	LDA	L	1283	-	13,15,15	2.10	2 (15%)	14,17,17	0.45	0
6	LDA	M	1305	-	13,15,15	2.09	2 (15%)	14,17,17	0.63	0
12	U10	M	1314	-	48,48,63	2.77	13 (27%)	60,61,79	1.57	15 (25%)
5	BCL	L	1282	2	69,74,74	1.85	6 (8%)	79,115,115	2.17	24 (30%)
4	GOL	H	1254	-	5,5,5	0.34	0	5,5,5	0.37	0
7	BPH	M	1313	-	59,70,70	2.86	13 (22%)	59,101,101	2.50	19 (32%)
4	GOL	H	1251	-	5,5,5	0.59	0	5,5,5	0.63	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	UQ2	L	1285[A]	-	23,23,23	2.65	7 (30%)	30,31,31	1.86	9 (30%)
7	BPH	L	1284	-	59,70,70	2.83	12 (20%)	59,101,101	2.52	18 (30%)
4	GOL	H	1253	-	5,5,5	0.37	0	5,5,5	0.29	0
10	HTO	L	1288	-	9,9,9	0.41	0	10,10,10	0.83	0
6	LDA	L	1711	-	13,15,15	2.27	2 (15%)	14,17,17	0.57	0
9	PO4	L	1287	-	4,4,4	0.91	0	6,6,6	0.51	0
4	GOL	L	1289	-	5,5,5	0.36	0	5,5,5	0.31	0
4	GOL	L	1290	-	5,5,5	0.37	0	5,5,5	0.28	0
14	CDL	M	1316	-	80,80,99	2.53	18 (22%)	86,92,111	3.79	16 (18%)
6	LDA	M	1311	-	13,15,15	2.15	2 (15%)	14,17,17	0.46	0
13	SPO	M	1315	-	41,41,41	2.75	12 (29%)	47,50,50	2.13	17 (36%)
6	LDA	M	1309	-	13,15,15	2.24	2 (15%)	14,17,17	0.52	0
8	UQ2	L	1285[B]	-	23,23,23	2.76	7 (30%)	30,31,31	1.26	2 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	BCL	L	1286	2	2/2/21/25	8/41/137/137	-
5	BCL	M	1304	3	2/2/21/25	9/41/137/137	-
6	LDA	M	1307	-	-	4/13/13/13	-
6	LDA	M	1308	-	-	7/13/13/13	-
6	LDA	M	1310	-	-	6/13/13/13	-
4	GOL	H	1252	-	-	2/4/4/4	-
5	BCL	M	1303	3	2/2/21/25	16/41/137/137	-
6	LDA	M	1306	-	-	4/13/13/13	-
6	LDA	L	1283	-	-	10/13/13/13	-
6	LDA	M	1305	-	-	6/13/13/13	-
12	U10	M	1314	-	-	7/45/69/87	0/1/1/1
5	BCL	L	1282	2	2/2/21/25	12/41/137/137	-
4	GOL	H	1254	-	-	0/4/4/4	-
7	BPH	M	1313	-	-	16/37/105/105	0/5/6/6
4	GOL	H	1251	-	-	2/4/4/4	-
8	UQ2	L	1285[A]	-	-	6/15/39/39	0/1/1/1
7	BPH	L	1284	-	-	6/37/105/105	0/5/6/6

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	H	1253	-	-	2/4/4/4	-
10	HTO	L	1288	-	-	8/10/10/10	-
6	LDA	L	1711	-	-	7/13/13/13	-
4	GOL	L	1289	-	-	2/4/4/4	-
4	GOL	L	1290	-	-	4/4/4/4	-
14	CDL	M	1316	-	-	38/91/91/110	-
6	LDA	M	1311	-	-	7/13/13/13	-
13	SPO	M	1315	-	-	18/47/47/47	-
6	LDA	M	1309	-	-	9/13/13/13	-
8	UQ2	L	1285[B]	-	-	9/15/39/39	0/1/1/1

All (129) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	M	1313	BPH	OBD-CAD	14.05	1.40	1.22
7	L	1284	BPH	OBD-CAD	13.45	1.40	1.22
5	L	1282	BCL	OBD-CAD	11.04	1.41	1.22
5	L	1286	BCL	OBD-CAD	10.65	1.40	1.22
5	M	1304	BCL	OBD-CAD	10.56	1.40	1.22
5	M	1303	BCL	OBD-CAD	10.39	1.40	1.22
14	M	1316	CDL	C11-CA5	-8.03	1.27	1.50
7	L	1284	BPH	O1D-CGD	7.73	1.40	1.21
7	M	1313	BPH	O1D-CGD	7.10	1.39	1.21
12	M	1314	U10	C33-C34	7.07	1.49	1.33
12	M	1314	U10	C13-C14	7.01	1.49	1.33
14	M	1316	CDL	C12-C11	-6.98	1.26	1.52
14	M	1316	CDL	C32-C31	-6.95	1.26	1.52
8	L	1285[B]	UQ2	C8-C9	6.94	1.49	1.33
6	L	1711	LDA	O1-N1	-6.90	1.25	1.42
7	L	1284	BPH	OBB-CAB	6.87	1.42	1.22
13	M	1315	SPO	C32-C33	6.80	1.48	1.33
6	M	1309	LDA	O1-N1	-6.72	1.25	1.42
6	M	1308	LDA	O1-N1	-6.64	1.25	1.42
6	L	1283	LDA	O1-N1	-6.63	1.25	1.42
6	M	1310	LDA	O1-N1	-6.62	1.25	1.42
8	L	1285[A]	UQ2	C8-C9	6.60	1.48	1.33
6	M	1307	LDA	O1-N1	-6.58	1.26	1.42
6	M	1311	LDA	O1-N1	-6.58	1.26	1.42
12	M	1314	U10	C8-C9	6.56	1.48	1.33
7	M	1313	BPH	C2-C3	6.52	1.48	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	M	1306	LDA	O1-N1	-6.52	1.26	1.42
6	M	1305	LDA	O1-N1	-6.51	1.26	1.42
14	M	1316	CDL	C33-C32	-6.47	1.19	1.51
7	M	1313	BPH	OB6-CAB	6.30	1.41	1.22
7	L	1284	BPH	O1A-CGA	6.29	1.41	1.22
5	M	1303	BCL	O1A-CGA	6.20	1.41	1.22
12	M	1314	U10	C23-C24	6.17	1.47	1.33
7	L	1284	BPH	C2-C3	6.15	1.47	1.33
14	M	1316	CDL	C34-C33	-6.14	1.21	1.51
7	M	1313	BPH	C3D-C2D	6.08	1.50	1.39
12	M	1314	U10	C28-C29	6.01	1.46	1.33
5	M	1304	BCL	O1A-CGA	5.93	1.40	1.22
12	M	1314	U10	C18-C19	5.90	1.46	1.33
5	L	1282	BCL	O1A-CGA	5.88	1.40	1.22
7	M	1313	BPH	O1A-CGA	5.83	1.39	1.22
13	M	1315	SPO	C37-C38	5.59	1.49	1.32
5	L	1286	BCL	O1A-CGA	5.56	1.39	1.22
8	L	1285[A]	UQ2	O2-C2	-5.41	1.23	1.36
6	M	1307	LDA	C1-N1	-5.41	1.45	1.51
7	L	1284	BPH	C3D-C2D	5.37	1.48	1.39
13	M	1315	SPO	C9-C7	5.35	1.48	1.35
8	L	1285[B]	UQ2	C13-C14	5.26	1.48	1.32
8	L	1285[A]	UQ2	C13-C14	5.22	1.48	1.32
13	M	1315	SPO	C22-C23	5.20	1.47	1.35
12	M	1314	U10	C38-C39	5.17	1.47	1.32
13	M	1315	SPO	C19-C17	5.16	1.47	1.35
14	M	1316	CDL	C16-C15	-5.09	1.26	1.51
8	L	1285[B]	UQ2	O2-C2	-5.08	1.24	1.36
13	M	1315	SPO	C6-C5	5.07	1.46	1.32
14	M	1316	CDL	C17-C16	-5.01	1.26	1.51
14	M	1316	CDL	C20-C19	-4.99	1.27	1.51
14	M	1316	CDL	C19-C18	-4.91	1.27	1.51
14	M	1316	CDL	OB6-CB5	4.89	1.48	1.34
8	L	1285[B]	UQ2	O3-C3	-4.88	1.25	1.36
14	M	1316	CDL	OA8-CA7	4.81	1.47	1.33
8	L	1285[A]	UQ2	O3-C3	-4.79	1.25	1.36
13	M	1315	SPO	C14-C12	4.76	1.46	1.35
12	M	1314	U10	O4-C4	-4.74	1.25	1.36
13	M	1315	SPO	C10-C11	4.64	1.46	1.34
14	M	1316	CDL	OB8-CB7	4.60	1.46	1.33
14	M	1316	CDL	OA6-CA5	4.55	1.47	1.34
13	M	1315	SPO	C15-C16	4.55	1.46	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	L	1284	BPH	C3D-CAD	-4.44	1.39	1.47
6	M	1310	LDA	C1-N1	-4.39	1.47	1.51
12	M	1314	U10	O3-C3	-4.37	1.26	1.36
6	M	1309	LDA	C1-N1	-4.33	1.47	1.51
6	M	1306	LDA	C1-N1	-4.26	1.47	1.51
6	L	1711	LDA	C1-N1	-4.23	1.47	1.51
13	M	1315	SPO	C26-C25	4.17	1.45	1.34
5	M	1303	BCL	C3D-C4D	-4.14	1.34	1.44
14	M	1316	CDL	C13-C12	-4.06	1.31	1.51
6	M	1308	LDA	C1-N1	-4.02	1.47	1.51
13	M	1315	SPO	C27-C28	3.95	1.47	1.35
7	M	1313	BPH	C3D-C4D	-3.93	1.35	1.41
6	M	1311	LDA	C1-N1	-3.90	1.47	1.51
5	L	1286	BCL	C3D-C4D	-3.86	1.35	1.44
5	M	1304	BCL	C3D-C4D	-3.82	1.35	1.44
5	L	1286	BCL	C2-C3	3.80	1.41	1.33
7	M	1313	BPH	C3D-CAD	-3.76	1.40	1.47
8	L	1285[B]	UQ2	C6-C5	3.73	1.41	1.35
13	M	1315	SPO	C21-C20	3.64	1.46	1.36
5	L	1282	BCL	C3D-C4D	-3.63	1.36	1.44
14	M	1316	CDL	C37-C36	-3.58	1.34	1.51
12	M	1314	U10	C6-C1	3.57	1.41	1.35
14	M	1316	CDL	C79-C78	-3.47	1.34	1.51
6	L	1283	LDA	C1-N1	-3.44	1.47	1.51
14	M	1316	CDL	C22-C21	-3.43	1.34	1.51
5	M	1303	BCL	C2-C3	3.42	1.40	1.33
14	M	1316	CDL	C80-C79	-3.37	1.35	1.51
6	M	1305	LDA	C1-N1	-3.36	1.48	1.51
5	L	1282	BCL	C2-C3	3.16	1.40	1.33
8	L	1285[A]	UQ2	C3-C4	-3.14	1.39	1.48
12	M	1314	U10	C4-C5	-3.09	1.39	1.48
8	L	1285[B]	UQ2	C3-C4	-3.06	1.40	1.48
5	M	1304	BCL	C2-C3	3.06	1.40	1.33
7	L	1284	BPH	C3D-C4D	-3.02	1.37	1.41
7	L	1284	BPH	O2D-CGD	-2.85	1.26	1.33
7	M	1313	BPH	O2A-CGA	-2.84	1.25	1.33
7	M	1313	BPH	O2D-CGD	-2.80	1.26	1.33
5	M	1303	BCL	CHD-C4C	2.80	1.47	1.39
5	M	1303	BCL	C1D-C2D	-2.80	1.39	1.45
5	M	1303	BCL	O2D-CGD	-2.69	1.26	1.33
12	M	1314	U10	C3-C2	-2.67	1.41	1.48
8	L	1285[A]	UQ2	C6-C5	2.67	1.40	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L	1282	BCL	O2A-CGA	-2.66	1.25	1.33
8	L	1285[A]	UQ2	C6-C1	-2.65	1.39	1.46
8	L	1285[B]	UQ2	C2-C1	-2.62	1.41	1.48
7	L	1284	BPH	C2C-C3C	-2.55	1.52	1.54
5	M	1304	BCL	CHD-C4C	2.52	1.46	1.39
5	M	1304	BCL	C3C-C4C	-2.50	1.48	1.51
5	L	1282	BCL	O2D-CGD	-2.46	1.27	1.33
5	M	1304	BCL	O2D-CGD	-2.41	1.27	1.33
5	L	1286	BCL	CHD-C4C	2.39	1.45	1.39
7	M	1313	BPH	C3A-C2A	-2.37	1.52	1.54
5	L	1286	BCL	O2D-CGD	-2.27	1.27	1.33
7	M	1313	BPH	C1B-NB	-2.24	1.34	1.38
7	M	1313	BPH	C4D-ND	-2.22	1.35	1.38
7	L	1284	BPH	O2D-CED	-2.17	1.40	1.45
5	M	1303	BCL	O2A-CGA	-2.17	1.27	1.33
7	L	1284	BPH	O2A-CGA	-2.16	1.27	1.33
12	M	1314	U10	C6-C5	-2.13	1.40	1.46
5	L	1286	BCL	O2A-CGA	-2.07	1.27	1.33
5	M	1303	BCL	MG-ND	-2.06	2.01	2.05

All (180) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	M	1316	CDL	C33-C32-C31	17.50	177.43	113.13
14	M	1316	CDL	C12-C11-CA5	13.02	161.41	113.69
14	M	1316	CDL	C17-C16-C15	11.88	174.41	114.37
14	M	1316	CDL	C20-C19-C18	11.60	173.01	114.37
7	M	1313	BPH	O2D-CGD-CBD	10.87	122.89	110.95
14	M	1316	CDL	C34-C33-C32	10.72	168.54	114.37
14	M	1316	CDL	C13-C12-C11	10.66	152.29	113.13
14	M	1316	CDL	C35-C34-C33	10.64	168.17	114.37
7	L	1284	BPH	O2D-CGD-CBD	8.54	120.33	110.95
5	L	1286	BCL	C1D-ND-C4D	7.47	111.55	106.31
5	M	1303	BCL	C1D-ND-C4D	7.27	111.41	106.31
7	M	1313	BPH	C2B-C1B-NB	7.01	114.50	109.43
7	L	1284	BPH	C2B-C1B-NB	7.01	114.50	109.43
5	L	1286	BCL	C2D-C1D-ND	-6.18	104.00	110.13
5	L	1282	BCL	O2D-CGD-CBD	6.11	121.90	111.23
5	M	1304	BCL	CMB-C2B-C1B	-5.96	116.35	125.42
5	L	1286	BCL	CMB-C2B-C1B	-5.93	116.39	125.42
5	M	1303	BCL	O2D-CGD-CBD	5.74	121.26	111.23
5	L	1282	BCL	C4A-NA-C1A	5.52	109.20	106.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	1282	BCL	CMB-C2B-C1B	-5.50	117.05	125.42
5	M	1303	BCL	CHC-C4B-NB	-5.42	115.92	124.05
5	L	1282	BCL	C1D-ND-C4D	5.33	110.05	106.31
13	M	1315	SPO	C20-C19-C17	-5.21	119.97	127.28
7	L	1284	BPH	C3D-C4D-ND	5.19	114.36	107.71
5	M	1303	BCL	C2D-C1D-ND	-5.18	105.00	110.13
7	L	1284	BPH	OBD-CAD-C3D	-5.14	119.88	127.89
7	M	1313	BPH	C2D-C1D-ND	5.07	113.09	109.43
14	M	1316	CDL	OA6-CA5-C11	5.06	122.44	111.48
5	L	1282	BCL	CMD-C2D-C1D	5.04	133.60	124.73
5	M	1303	BCL	CMB-C2B-C1B	-4.96	117.87	125.42
7	M	1313	BPH	C3D-C4D-ND	4.83	113.90	107.71
5	M	1303	BCL	C4A-NA-C1A	4.82	108.88	106.68
7	L	1284	BPH	C2D-C1D-ND	4.78	112.88	109.43
13	M	1315	SPO	C21-C22-C23	-4.68	120.72	127.28
13	M	1315	SPO	C10-C9-C7	-4.63	120.79	127.28
5	M	1304	BCL	C1D-ND-C4D	4.62	109.55	106.31
7	M	1313	BPH	OBD-CAD-CBD	-4.59	119.09	125.82
5	M	1304	BCL	CMD-C2D-C1D	4.58	132.79	124.73
7	L	1284	BPH	OBD-CAD-CBD	-4.57	119.12	125.82
12	M	1314	U10	C30-C29-C31	4.57	123.15	115.23
5	L	1286	BCL	O2D-CGD-CBD	4.51	119.12	111.23
5	M	1304	BCL	O2D-CGD-CBD	4.49	119.08	111.23
5	L	1286	BCL	C4A-NA-C1A	4.47	108.72	106.68
14	M	1316	CDL	OB6-CB5-C51	4.46	121.14	111.48
13	M	1315	SPO	C26-C27-C28	-4.38	121.53	127.69
5	L	1282	BCL	C2D-C1D-ND	-4.36	105.81	110.13
7	L	1284	BPH	O1D-CGD-CBD	-4.35	118.13	124.72
5	L	1282	BCL	C1C-NC-C4C	-4.22	104.75	106.68
5	L	1286	BCL	CMD-C2D-C1D	4.20	132.12	124.73
8	L	1285[A]	UQ2	CM5-C5-C6	-4.19	117.57	124.45
13	M	1315	SPO	C15-C14-C12	-3.94	121.75	127.28
5	L	1282	BCL	C2B-C1B-NB	-3.92	106.26	110.33
5	M	1304	BCL	C2D-C1D-ND	-3.90	106.27	110.13
8	L	1285[A]	UQ2	CM3-O3-C3	3.87	130.06	116.47
5	M	1303	BCL	C1-O2A-CGA	3.86	126.00	116.65
7	L	1284	BPH	C1B-NB-C4B	-3.86	103.19	108.82
5	M	1304	BCL	C1C-NC-C4C	3.84	108.43	106.68
5	M	1303	BCL	C2B-C1B-NB	-3.81	106.37	110.33
7	L	1284	BPH	C4D-ND-C1D	-3.81	104.31	108.87
5	L	1282	BCL	O1D-CGD-CBD	-3.73	117.17	124.52
5	L	1282	BCL	CMD-C2D-C3D	-3.64	119.34	127.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	1286	BCL	C2B-C1B-NB	-3.62	106.57	110.33
5	L	1286	BCL	CHD-C1D-ND	-3.62	119.71	124.80
8	L	1285[A]	UQ2	O1-C1-C6	-3.61	114.80	121.79
5	L	1286	BCL	O2A-CGA-CBA	3.59	122.77	111.83
5	M	1304	BCL	O2A-CGA-CBA	3.57	122.71	111.83
7	M	1313	BPH	O1D-CGD-CBD	-3.48	119.44	124.72
7	M	1313	BPH	C4D-ND-C1D	-3.37	104.84	108.87
5	M	1303	BCL	CMD-C2D-C1D	3.36	130.65	124.73
7	L	1284	BPH	C4D-CHA-CBD	-3.35	106.85	108.45
13	M	1315	SPO	C29-C28-C30	3.31	120.98	115.23
5	L	1286	BCL	C1-O2A-CGA	3.29	124.62	116.65
12	M	1314	U10	C27-C28-C29	-3.27	120.14	127.62
5	L	1282	BCL	C4-C3-C5	3.22	120.82	115.23
7	L	1284	BPH	C1-C2-C3	-3.20	120.95	126.20
5	L	1286	BCL	CMD-C2D-C3D	-3.19	120.37	127.69
7	M	1313	BPH	O2D-CGD-O1D	-3.19	117.64	123.85
13	M	1315	SPO	C4-C5-C6	-3.19	120.44	124.91
5	M	1304	BCL	CED-O2D-CGD	3.17	123.09	115.92
5	L	1286	BCL	CHC-C4B-NB	-3.11	119.39	124.05
12	M	1314	U10	C10-C9-C11	3.11	120.62	115.23
14	M	1316	CDL	OB8-CB7-C71	3.10	121.28	111.83
5	L	1286	BCL	C2A-C3A-C4A	3.08	106.85	101.87
7	L	1284	BPH	O2A-CGA-CBA	3.07	121.19	111.83
7	L	1284	BPH	CED-O2D-CGD	3.07	122.87	115.92
5	L	1286	BCL	CED-O2D-CGD	3.06	122.86	115.92
12	M	1314	U10	C22-C23-C24	-3.03	120.68	127.62
7	M	1313	BPH	C1C-C2C-C3C	-3.03	99.96	102.84
7	L	1284	BPH	C1C-C2C-C3C	-3.01	99.97	102.84
5	M	1304	BCL	CMD-C2D-C3D	-2.98	120.85	127.69
13	M	1315	SPO	C5-C6-C7	-2.97	121.40	125.89
7	M	1313	BPH	CED-O2D-CGD	2.95	122.61	115.92
5	L	1286	BCL	CMA-C3A-C4A	-2.93	103.91	111.77
5	L	1282	BCL	CHA-C1A-NA	-2.92	119.77	126.39
5	M	1304	BCL	C2B-C1B-NB	-2.89	107.33	110.33
12	M	1314	U10	C25-C24-C26	2.88	120.22	115.23
5	L	1282	BCL	CHC-C4B-NB	-2.87	119.74	124.05
5	L	1282	BCL	C1-C2-C3	-2.87	121.50	126.20
7	M	1313	BPH	O2A-CGA-CBA	2.85	120.53	111.83
5	M	1303	BCL	O2A-CGA-CBA	2.79	120.34	111.83
7	M	1313	BPH	C1-C2-C3	-2.78	121.65	126.20
5	M	1304	BCL	O2D-CGD-O1D	-2.77	118.45	123.85
14	M	1316	CDL	OA8-CA7-C31	2.75	120.22	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	1303	BCL	CMA-C3A-C4A	-2.74	104.40	111.77
7	M	1313	BPH	OBD-CAD-C3D	-2.73	123.64	127.89
7	M	1313	BPH	C1B-NB-C4B	-2.72	104.85	108.82
5	M	1304	BCL	CMB-C2B-C3B	2.71	134.21	125.67
7	L	1284	BPH	CMA-C3A-C4A	-2.68	108.83	114.61
5	M	1304	BCL	C4-C3-C5	2.68	119.88	115.23
5	M	1304	BCL	C1-C2-C3	-2.67	121.83	126.20
12	M	1314	U10	C35-C34-C36	2.65	119.84	115.23
12	M	1314	U10	C17-C18-C19	-2.62	121.63	127.62
5	L	1286	BCL	CMB-C2B-C3B	2.59	133.84	125.67
5	M	1304	BCL	CHC-C4B-NB	-2.58	120.18	124.05
5	M	1303	BCL	O2D-CGD-O1D	-2.57	118.84	123.85
8	L	1285[B]	UQ2	C10-C9-C11	2.57	119.69	115.23
5	M	1304	BCL	C7-C6-C5	-2.56	106.44	113.26
13	M	1315	SPO	C14-C15-C16	-2.56	115.79	123.20
5	M	1304	BCL	C16-C15-C13	-2.53	107.54	115.97
5	M	1303	BCL	CHA-C1A-NA	-2.53	120.67	126.39
5	M	1304	BCL	CAC-C3C-C4C	-2.52	106.99	112.58
5	L	1286	BCL	CHC-C1C-NC	-2.52	120.76	124.40
5	L	1282	BCL	O2A-CGA-CBA	2.49	119.43	111.83
5	M	1303	BCL	C1D-CHD-C4C	-2.49	120.61	126.62
7	M	1313	BPH	C4A-C3A-C2A	-2.46	100.49	102.84
13	M	1315	SPO	C31-C32-C33	-2.46	121.99	127.62
14	M	1316	CDL	C32-C31-CA7	2.46	122.72	113.69
13	M	1315	SPO	C34-C33-C35	2.45	119.49	115.23
8	L	1285[A]	UQ2	C16-C14-C15	2.45	120.23	114.59
5	M	1303	BCL	CHC-C4B-C3B	-2.41	122.13	131.72
5	L	1282	BCL	O2A-CGA-O1A	-2.41	117.60	123.63
7	M	1313	BPH	CMD-C2D-C3D	-2.41	119.87	124.68
5	L	1282	BCL	C2A-C3A-C4A	2.40	105.74	101.87
5	L	1282	BCL	CMB-C2B-C3B	2.38	133.18	125.67
5	L	1286	BCL	CHA-C4D-ND	2.37	137.45	132.55
7	L	1284	BPH	O2A-CGA-O1A	-2.37	117.70	123.63
5	M	1303	BCL	CMB-C2B-C3B	2.37	133.14	125.67
12	M	1314	U10	C15-C14-C16	2.36	119.33	115.23
12	M	1314	U10	C1M-C1-C6	-2.36	120.58	124.45
8	L	1285[B]	UQ2	C5-C6-C1	-2.36	117.33	119.62
5	L	1282	BCL	CHB-C4A-NA	-2.35	121.00	124.40
5	M	1303	BCL	O1D-CGD-CBD	-2.35	119.89	124.52
13	M	1315	SPO	C8-C7-C6	2.35	121.68	118.09
7	L	1284	BPH	C4A-C3A-C2A	-2.28	100.67	102.84
13	M	1315	SPO	C27-C26-C25	-2.28	116.59	123.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	L	1285[A]	UQ2	O4-C4-C3	-2.26	116.25	121.03
5	M	1303	BCL	CAA-C2A-C3A	-2.24	106.94	113.00
12	M	1314	U10	C32-C33-C34	-2.24	122.49	127.62
12	M	1314	U10	C41-C39-C40	2.23	119.72	114.59
12	M	1314	U10	C30-C29-C28	-2.22	117.93	123.63
8	L	1285[A]	UQ2	C10-C9-C11	2.22	119.08	115.23
12	M	1314	U10	C20-C19-C21	2.20	119.06	115.23
5	L	1282	BCL	CAA-CBA-CGA	2.20	119.46	113.21
13	M	1315	SPO	C40-C38-C39	2.20	119.66	114.59
14	M	1316	CDL	OB8-CB7-OB9	-2.19	118.15	123.63
5	L	1286	BCL	O2D-CGD-O1D	-2.19	119.59	123.85
14	M	1316	CDL	C80-C79-C78	2.18	125.37	114.37
12	M	1314	U10	C3M-O3-C3	2.17	124.10	116.47
5	M	1303	BCL	CMD-C2D-C3D	-2.17	122.72	127.69
13	M	1315	SPO	C18-C17-C16	2.16	121.39	118.09
14	M	1316	CDL	OA6-CA5-OA7	-2.16	118.66	123.70
5	L	1282	BCL	C1-O2A-CGA	2.15	121.85	116.65
8	L	1285[A]	UQ2	C6-C5-C4	2.15	120.86	119.17
5	M	1303	BCL	CAB-C3B-C2B	-2.13	123.32	127.74
5	L	1282	BCL	C1D-CHD-C4C	-2.12	121.50	126.62
8	L	1285[A]	UQ2	C2-C3-C4	-2.12	116.80	120.69
13	M	1315	SPO	C13-C12-C11	2.12	121.33	118.09
14	M	1316	CDL	C81-C80-C79	2.11	125.05	114.37
12	M	1314	U10	C4M-O4-C4	2.11	123.88	116.47
5	M	1303	BCL	CHA-C4D-ND	2.11	136.90	132.55
5	M	1303	BCL	C2A-C3A-C4A	2.08	105.23	101.87
7	M	1313	BPH	O2A-CGA-O1A	-2.06	118.48	123.63
5	M	1304	BCL	C1-O2A-CGA	2.05	121.61	116.65
7	L	1284	BPH	CMC-C2C-C1C	-2.04	110.22	114.61
5	L	1282	BCL	C3C-C4C-CHD	-2.04	119.09	123.39
7	M	1313	BPH	CMC-C2C-C1C	-2.03	110.24	114.61
8	L	1285[A]	UQ2	O3-C3-C2	-2.03	115.97	123.64
7	M	1313	BPH	CMA-C3A-C4A	-2.02	110.26	114.61
13	M	1315	SPO	C36-C37-C38	-2.02	120.91	127.64
5	L	1282	BCL	CAA-C2A-C3A	-2.00	107.59	113.00

All (8) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	L	1282	BCL	C8
5	L	1282	BCL	C13
5	L	1286	BCL	C8

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Mol	Chain	Res	Type	Atom
5	L	1286	BCL	C13
5	M	1303	BCL	C8
5	M	1303	BCL	C13
5	M	1304	BCL	C8
5	M	1304	BCL	C13

All (225) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	1252	GOL	C1-C2-C3-O3
4	L	1289	GOL	C1-C2-C3-O3
4	L	1290	GOL	O1-C1-C2-C3
4	L	1290	GOL	C1-C2-C3-O3
4	L	1290	GOL	O2-C2-C3-O3
5	L	1282	BCL	CHA-CBD-CGD-O1D
5	L	1282	BCL	CHA-CBD-CGD-O2D
5	M	1303	BCL	C1-C2-C3-C4
5	M	1303	BCL	C1-C2-C3-C5
6	M	1305	LDA	C2-C1-N1-CM2
6	M	1309	LDA	C2-C1-N1-CM1
7	M	1313	BPH	C4C-C3C-CAC-CBC
7	M	1313	BPH	C2C-C3C-CAC-CBC
8	L	1285[A]	UQ2	C7-C8-C9-C10
8	L	1285[A]	UQ2	C7-C8-C9-C11
8	L	1285[B]	UQ2	C7-C8-C9-C10
8	L	1285[B]	UQ2	C7-C8-C9-C11
10	L	1288	HTO	O1-C1-C2-O2
10	L	1288	HTO	C1-C2-C3-O3
10	L	1288	HTO	C1-C2-C3-C4
10	L	1288	HTO	O2-C2-C3-O3
10	L	1288	HTO	O2-C2-C3-C4
10	L	1288	HTO	O3-C3-C4-C5
12	M	1314	U10	C27-C28-C29-C30
12	M	1314	U10	C27-C28-C29-C31
13	M	1315	SPO	C11-C12-C14-C15
13	M	1315	SPO	C13-C12-C14-C15
13	M	1315	SPO	C15-C16-C17-C18
13	M	1315	SPO	C15-C16-C17-C19
13	M	1315	SPO	C36-C37-C38-C39
14	M	1316	CDL	CB3-OB5-PB2-OB4
14	M	1316	CDL	C51-CB5-OB6-CB4
8	L	1285[A]	UQ2	C12-C13-C14-C15

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Mol	Chain	Res	Type	Atoms
8	L	1285[A]	UQ2	C12-C13-C14-C16
13	M	1315	SPO	C36-C37-C38-C40
14	M	1316	CDL	OB9-CB7-OB8-CB6
14	M	1316	CDL	OB7-CB5-OB6-CB4
14	M	1316	CDL	C71-CB7-OB8-CB6
14	M	1316	CDL	C78-C79-C80-C81
14	M	1316	CDL	C20-C21-C22-C23
5	L	1282	BCL	C3-C5-C6-C7
5	M	1303	BCL	C10-C11-C12-C13
8	L	1285[B]	UQ2	C9-C11-C12-C13
12	M	1314	U10	C29-C31-C32-C33
13	M	1315	SPO	C33-C35-C36-C37
14	M	1316	CDL	C31-CA7-OA8-CA6
8	L	1285[B]	UQ2	C12-C11-C9-C10
8	L	1285[B]	UQ2	C12-C11-C9-C8
5	L	1282	BCL	C11-C10-C8-C9
5	L	1286	BCL	C11-C12-C13-C14
14	M	1316	CDL	OA9-CA7-OA8-CA6
4	H	1252	GOL	O2-C2-C3-O3
4	L	1289	GOL	O2-C2-C3-O3
10	L	1288	HTO	O1-C1-C2-C3
5	L	1286	BCL	C13-C15-C16-C17
14	M	1316	CDL	CA7-C31-C32-C33
7	M	1313	BPH	C5-C6-C7-C8
5	L	1282	BCL	C5-C6-C7-C8
5	M	1304	BCL	C15-C16-C17-C18
5	L	1286	BCL	C15-C16-C17-C18
13	M	1315	SPO	C8-C7-C9-C10
13	M	1315	SPO	C18-C17-C19-C20
13	M	1315	SPO	C21-C22-C23-C24
4	H	1251	GOL	O1-C1-C2-C3
4	H	1253	GOL	O1-C1-C2-C3
7	L	1284	BPH	O2A-C1-C2-C3
7	M	1313	BPH	C16-C17-C18-C20
13	M	1315	SPO	C16-C17-C19-C20
13	M	1315	SPO	C21-C22-C23-C25
6	L	1283	LDA	C11-C10-C9-C8
7	M	1313	BPH	C10-C11-C12-C13
6	L	1283	LDA	C5-C6-C7-C8
6	M	1310	LDA	C7-C8-C9-C10
14	M	1316	CDL	C16-C17-C18-C19
4	H	1253	GOL	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
4	L	1290	GOL	O1-C1-C2-O2
6	L	1711	LDA	C4-C5-C6-C7
6	M	1309	LDA	C6-C7-C8-C9
7	M	1313	BPH	C16-C17-C18-C19
14	M	1316	CDL	O1-C1-CB2-OB2
14	M	1316	CDL	C71-C72-C73-C74
6	M	1311	LDA	C6-C7-C8-C9
6	L	1711	LDA	C2-C3-C4-C5
6	M	1310	LDA	C3-C4-C5-C6
6	M	1311	LDA	C4-C5-C6-C7
6	M	1307	LDA	C6-C7-C8-C9
6	L	1711	LDA	C5-C6-C7-C8
14	M	1316	CDL	OA7-CA5-OA6-CA4
6	M	1307	LDA	C4-C5-C6-C7
6	M	1307	LDA	C7-C8-C9-C10
13	M	1315	SPO	C9-C10-C11-C12
7	M	1313	BPH	C13-C15-C16-C17
14	M	1316	CDL	C80-C81-C82-C83
6	L	1283	LDA	C6-C7-C8-C9
6	M	1309	LDA	C7-C8-C9-C10
6	M	1311	LDA	C11-C10-C9-C8
5	L	1282	BCL	C16-C17-C18-C20
14	M	1316	CDL	C11-CA5-OA6-CA4
6	M	1309	LDA	C1-C2-C3-C4
6	M	1307	LDA	C1-C2-C3-C4
5	M	1303	BCL	C15-C16-C17-C18
6	M	1305	LDA	C2-C3-C4-C5
6	M	1311	LDA	C3-C4-C5-C6
5	M	1303	BCL	C8-C10-C11-C12
5	M	1304	BCL	C13-C15-C16-C17
6	M	1308	LDA	C2-C3-C4-C5
5	L	1282	BCL	C1A-C2A-CAA-CBA
5	M	1303	BCL	C6-C7-C8-C10
7	L	1284	BPH	C4-C3-C5-C6
8	L	1285[B]	UQ2	C12-C13-C14-C15
6	L	1283	LDA	C2-C3-C4-C5
5	M	1303	BCL	C6-C7-C8-C9
7	M	1313	BPH	C11-C10-C8-C9
6	L	1711	LDA	C11-C10-C9-C8
14	M	1316	CDL	CA3-CA4-CA6-OA8
6	L	1283	LDA	C1-C2-C3-C4
6	M	1308	LDA	C7-C8-C9-C10

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Mol	Chain	Res	Type	Atoms
7	L	1284	BPH	C2-C3-C5-C6
7	L	1284	BPH	C8-C10-C11-C12
6	M	1310	LDA	C11-C10-C9-C8
7	M	1313	BPH	O2A-C1-C2-C3
6	M	1308	LDA	C5-C6-C7-C8
5	L	1282	BCL	C16-C17-C18-C19
13	M	1315	SPO	C6-C7-C9-C10
6	L	1711	LDA	C9-C10-C11-C12
6	M	1310	LDA	C9-C10-C11-C12
14	M	1316	CDL	C74-C75-C76-C77
6	L	1283	LDA	N1-C1-C2-C3
6	L	1283	LDA	C9-C10-C11-C12
14	M	1316	CDL	C81-C82-C83-C84
6	M	1308	LDA	C11-C10-C9-C8
7	M	1313	BPH	C15-C16-C17-C18
6	M	1306	LDA	C9-C10-C11-C12
14	M	1316	CDL	C21-C22-C23-C24
5	M	1303	BCL	C11-C12-C13-C15
7	M	1313	BPH	C11-C10-C8-C7
6	M	1311	LDA	C5-C6-C7-C8
10	L	1288	HTO	C4-C5-C6-C7
6	M	1311	LDA	C9-C10-C11-C12
14	M	1316	CDL	CB3-CB4-CB6-OB8
5	L	1282	BCL	C15-C16-C17-C18
6	M	1306	LDA	C7-C8-C9-C10
14	M	1316	CDL	OB5-CB3-CB4-OB6
14	M	1316	CDL	C19-C20-C21-C22
6	L	1283	LDA	C4-C5-C6-C7
6	M	1308	LDA	C4-C5-C6-C7
7	L	1284	BPH	C1-C2-C3-C5
5	M	1303	BCL	C11-C12-C13-C14
12	M	1314	U10	C34-C36-C37-C38
5	L	1286	BCL	C10-C11-C12-C13
6	M	1305	LDA	C9-C10-C11-C12
14	M	1316	CDL	CA2-C1-CB2-OB2
7	M	1313	BPH	C12-C13-C15-C16
5	L	1286	BCL	C2A-CAA-CBA-CGA
6	M	1305	LDA	C4-C5-C6-C7
5	M	1303	BCL	C3-C5-C6-C7
6	M	1309	LDA	C4-C5-C6-C7
8	L	1285[B]	UQ2	C12-C13-C14-C16
8	L	1285[B]	UQ2	C1-C6-C7-C8

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Mol	Chain	Res	Type	Atoms
14	M	1316	CDL	OA6-CA4-CA6-OA8
7	M	1313	BPH	C14-C13-C15-C16
5	M	1303	BCL	C2-C1-O2A-CGA
5	M	1304	BCL	C16-C17-C18-C19
6	M	1305	LDA	C2-C1-N1-CM1
6	M	1309	LDA	C2-C1-N1-CM2
5	M	1303	BCL	C4-C3-C5-C6
6	L	1711	LDA	C6-C7-C8-C9
6	M	1310	LDA	C1-C2-C3-C4
14	M	1316	CDL	OB5-CB3-CB4-CB6
7	M	1313	BPH	C6-C7-C8-C10
6	M	1305	LDA	C2-C1-N1-O1
6	M	1309	LDA	C2-C1-N1-O1
14	M	1316	CDL	OB6-CB4-CB6-OB8
14	M	1316	CDL	C40-C41-C42-C43
8	L	1285[B]	UQ2	C1-C2-O2-CM2
14	M	1316	CDL	CB3-OB5-PB2-OB2
14	M	1316	CDL	CB3-OB5-PB2-OB3
5	M	1303	BCL	C2-C3-C5-C6
4	H	1251	GOL	O1-C1-C2-O2
6	M	1311	LDA	C7-C8-C9-C10
6	M	1306	LDA	C6-C7-C8-C9
5	L	1286	BCL	C11-C12-C13-C15
8	L	1285[A]	UQ2	C4-C3-O3-CM3
6	M	1310	LDA	N1-C1-C2-C3
7	M	1313	BPH	C8-C10-C11-C12
12	M	1314	U10	C31-C32-C33-C34
5	L	1286	BCL	C8-C10-C11-C12
13	M	1315	SPO	C12-C14-C15-C16
13	M	1315	SPO	C19-C20-C21-C22
6	M	1306	LDA	C4-C5-C6-C7
6	M	1308	LDA	C6-C7-C8-C9
14	M	1316	CDL	C12-C13-C14-C15
7	L	1284	BPH	C1-C2-C3-C4
6	L	1711	LDA	C1-C2-C3-C4
5	L	1282	BCL	C11-C10-C8-C7
5	L	1286	BCL	C11-C10-C8-C7
12	M	1314	U10	C5-C4-O4-C4M
6	M	1309	LDA	C9-C10-C11-C12
5	M	1303	BCL	C11-C10-C8-C9
8	L	1285[A]	UQ2	C9-C11-C12-C13
5	M	1303	BCL	C4C-C3C-CAC-CBC

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Mol	Chain	Res	Type	Atoms
12	M	1314	U10	C25-C24-C26-C27
14	M	1316	CDL	C17-C18-C19-C20
14	M	1316	CDL	C11-C12-C13-C14
14	M	1316	CDL	C37-C38-C39-C40
5	M	1304	BCL	CAA-CBA-CGA-O2A
14	M	1316	CDL	CA5-C11-C12-C13
5	M	1303	BCL	C11-C10-C8-C7
5	M	1304	BCL	C8-C10-C11-C12
6	L	1283	LDA	C3-C4-C5-C6
6	L	1283	LDA	C7-C8-C9-C10
5	L	1282	BCL	C11-C12-C13-C14
7	M	1313	BPH	C6-C7-C8-C9
5	M	1304	BCL	C12-C13-C15-C16
6	M	1308	LDA	C2-C1-N1-CM2
5	M	1304	BCL	C3-C5-C6-C7
13	M	1315	SPO	C24-C23-C25-C26
14	M	1316	CDL	C1-CB2-OB2-PB2
14	M	1316	CDL	C72-C71-CB7-OB8
13	M	1315	SPO	C22-C23-C25-C26
5	M	1304	BCL	C16-C17-C18-C20
5	M	1304	BCL	C14-C13-C15-C16
14	M	1316	CDL	C72-C71-CB7-OB9
5	L	1282	BCL	C1-C2-C3-C4
6	M	1309	LDA	C11-C10-C9-C8

There are no ring outliers.

17 monomers are involved in 58 short contacts:

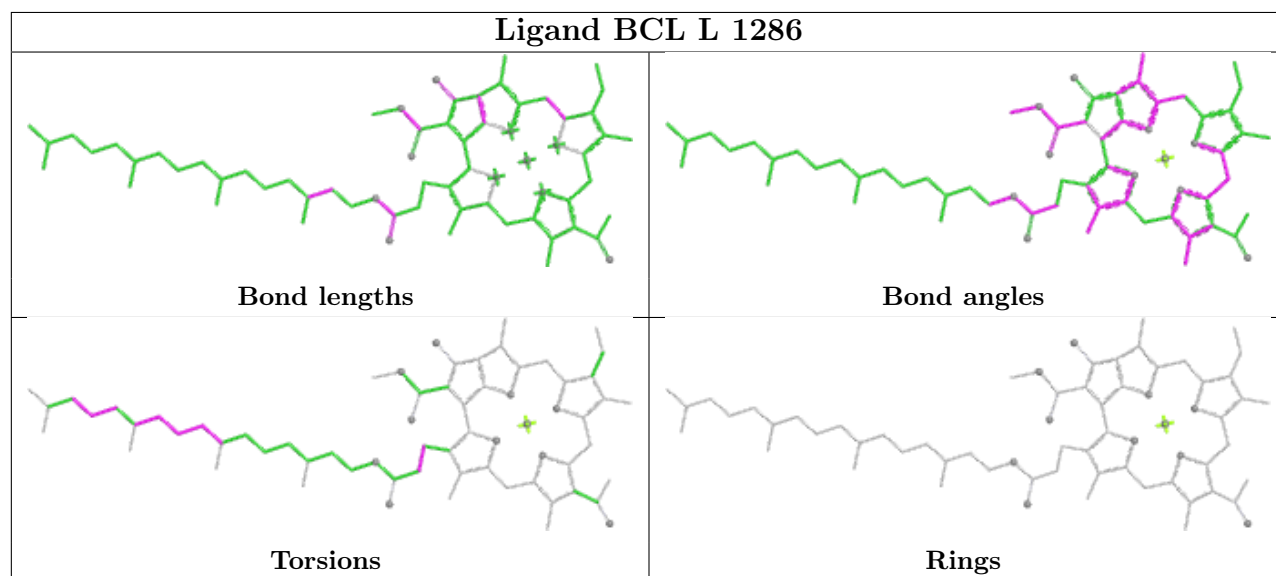
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	L	1286	BCL	2	0
5	M	1304	BCL	12	0
6	M	1307	LDA	1	0
6	M	1308	LDA	1	0
5	M	1303	BCL	8	0
12	M	1314	U10	2	0
5	L	1282	BCL	6	0
7	M	1313	BPH	13	0
4	H	1251	GOL	1	0
8	L	1285[A]	UQ2	5	0
7	L	1284	BPH	9	0
10	L	1288	HTO	2	0
6	L	1711	LDA	2	0

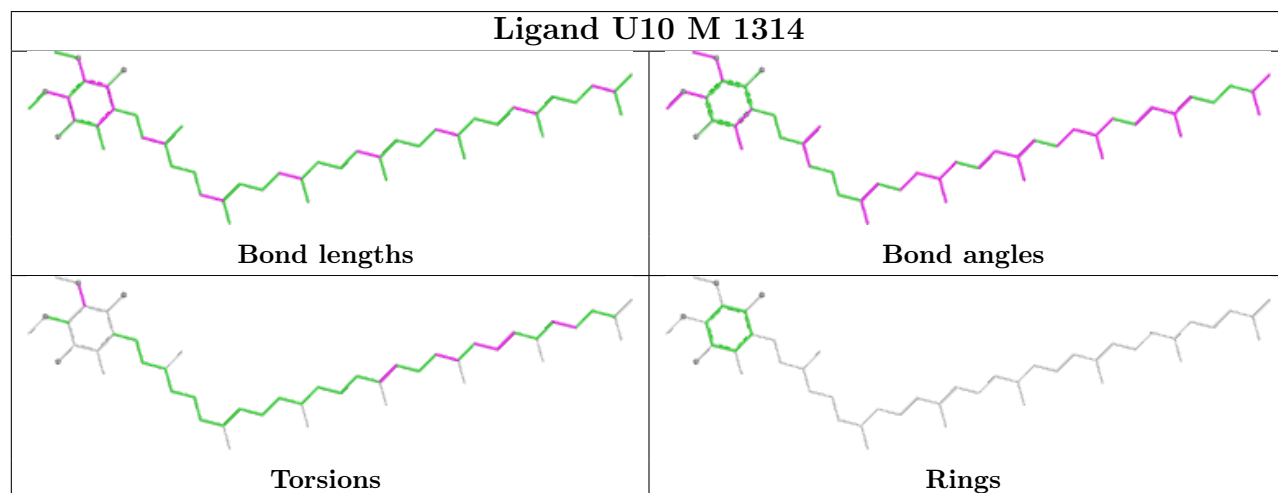
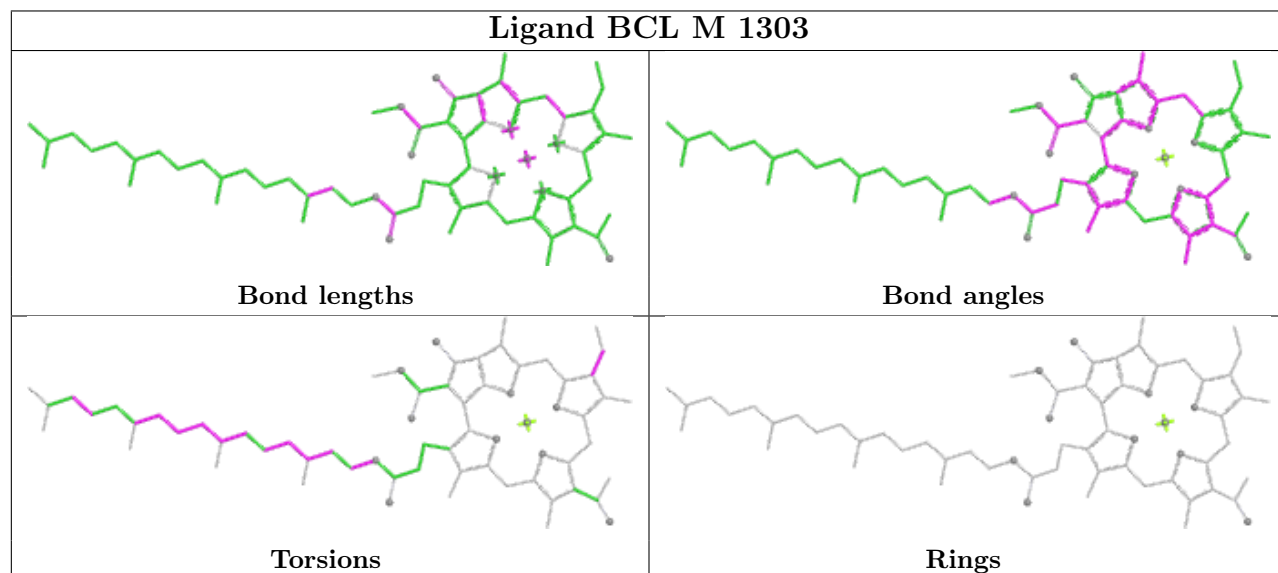
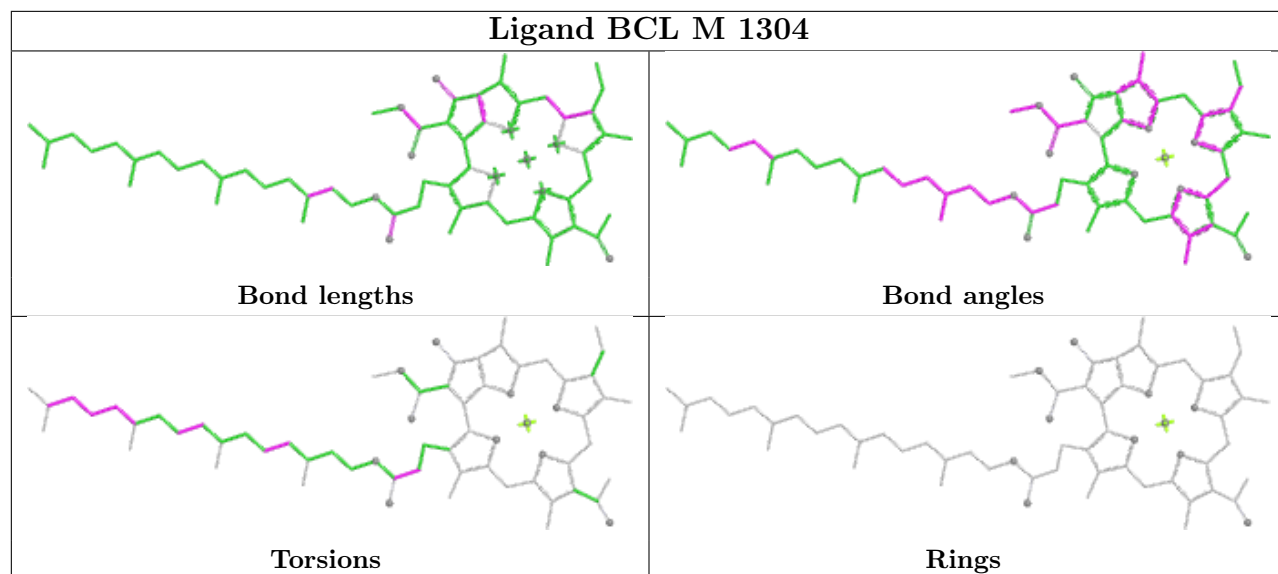
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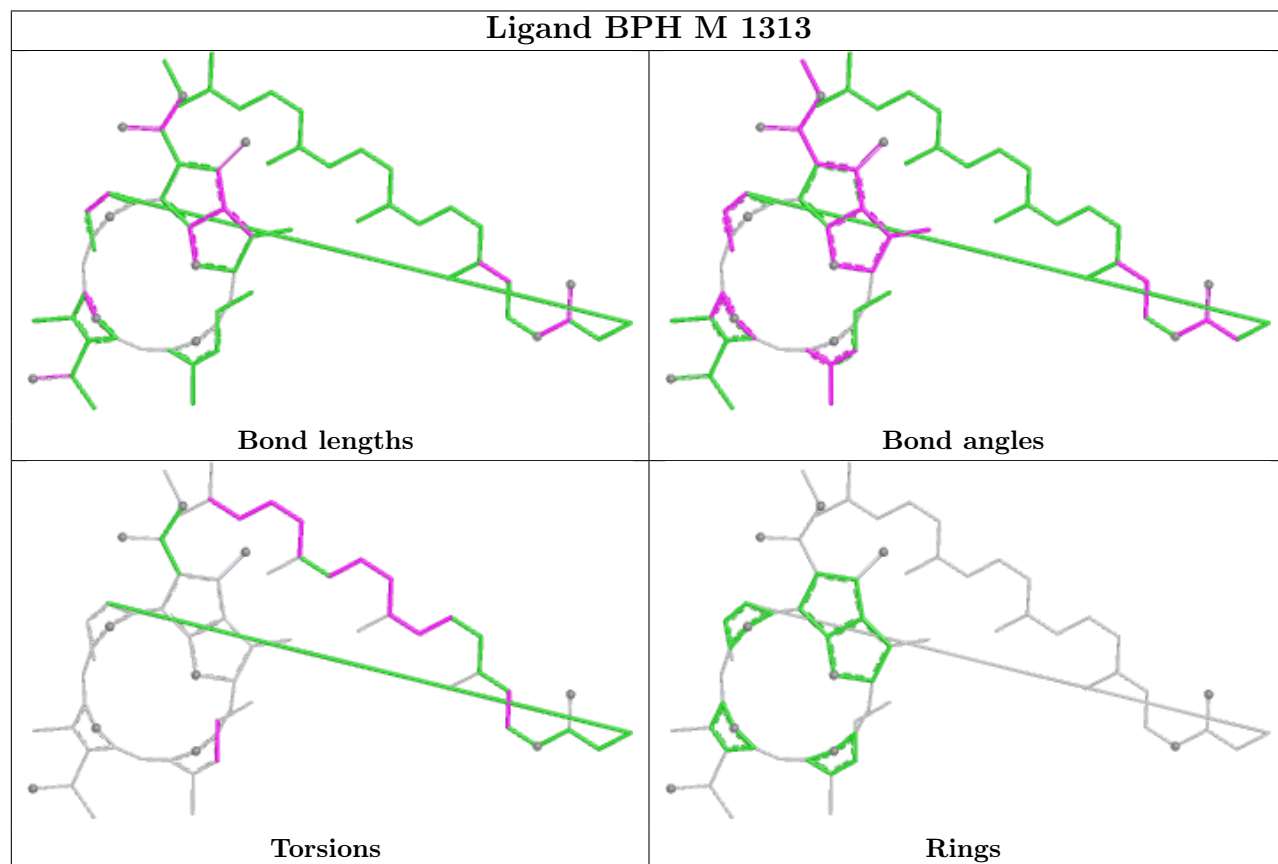
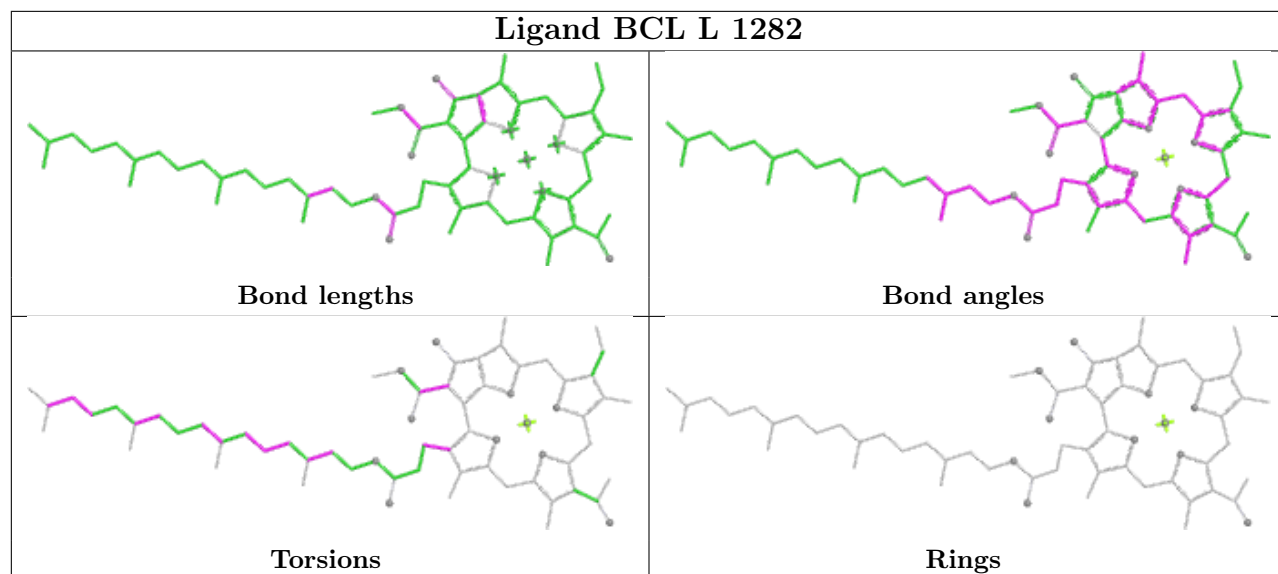
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	L	1289	GOL	1	0
14	M	1316	CDL	3	0
13	M	1315	SPO	3	0
8	L	1285[B]	UQ2	1	0

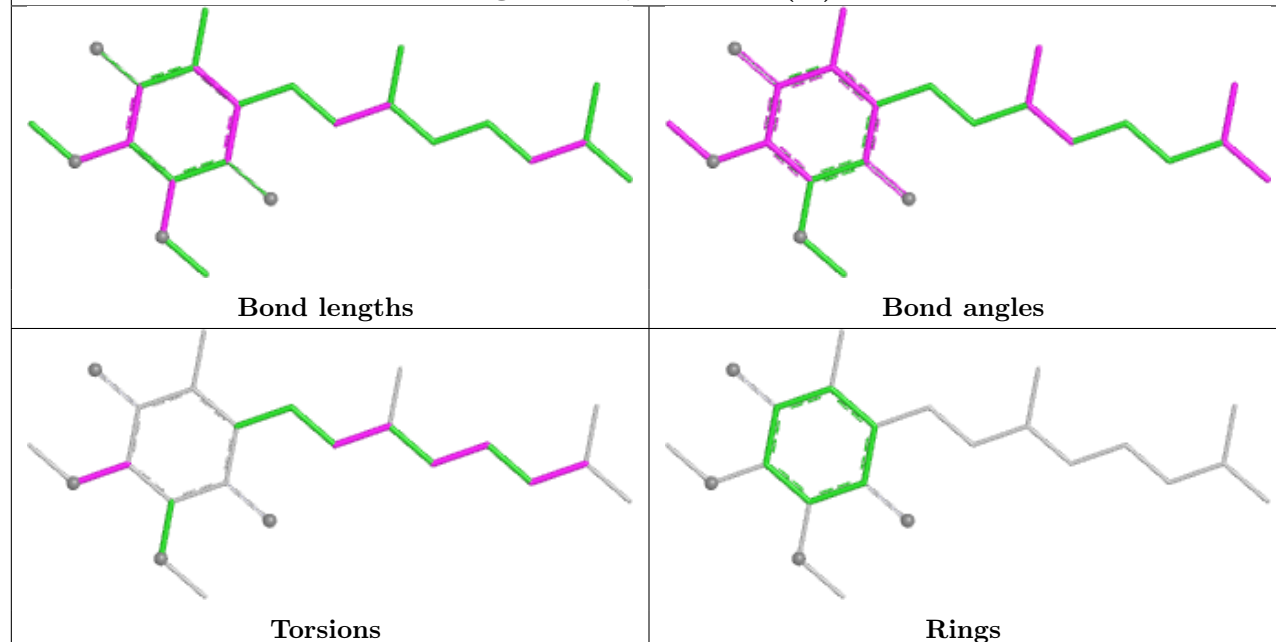
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



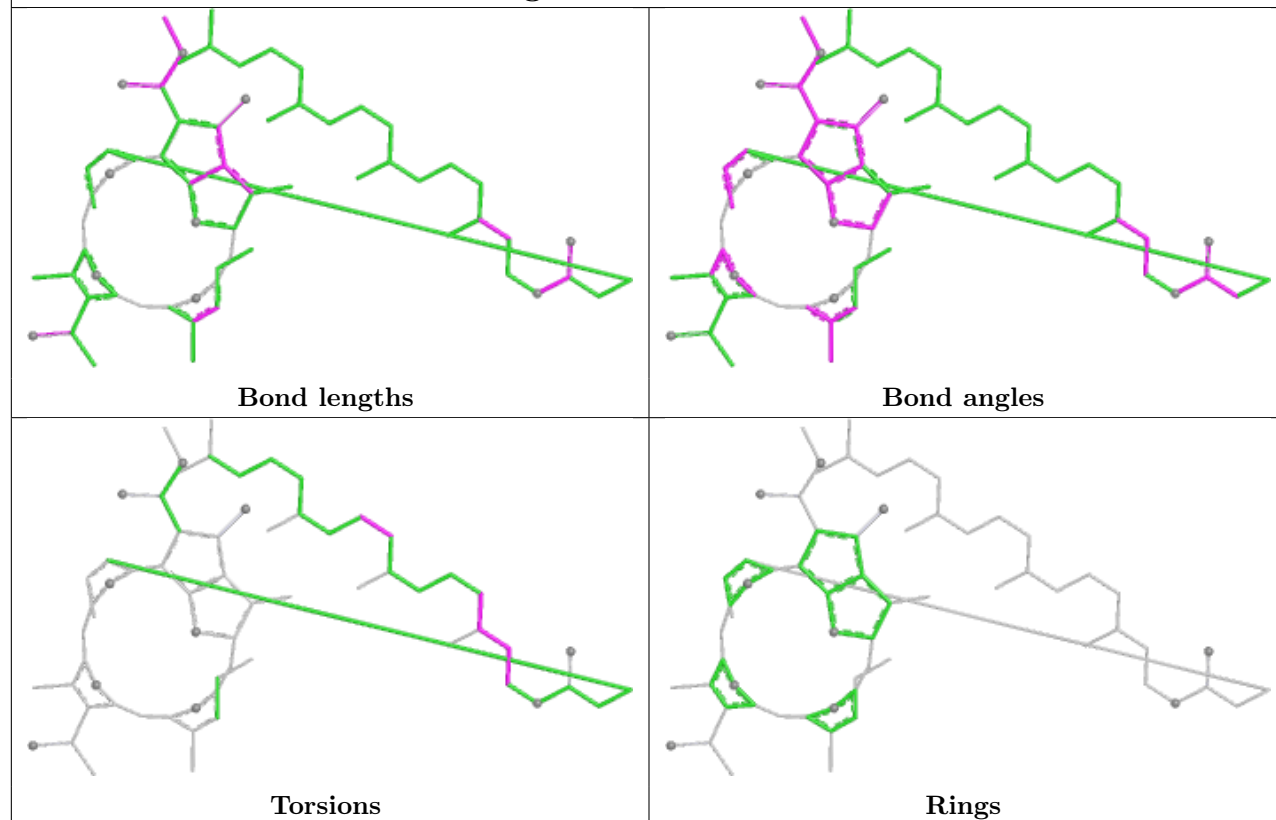


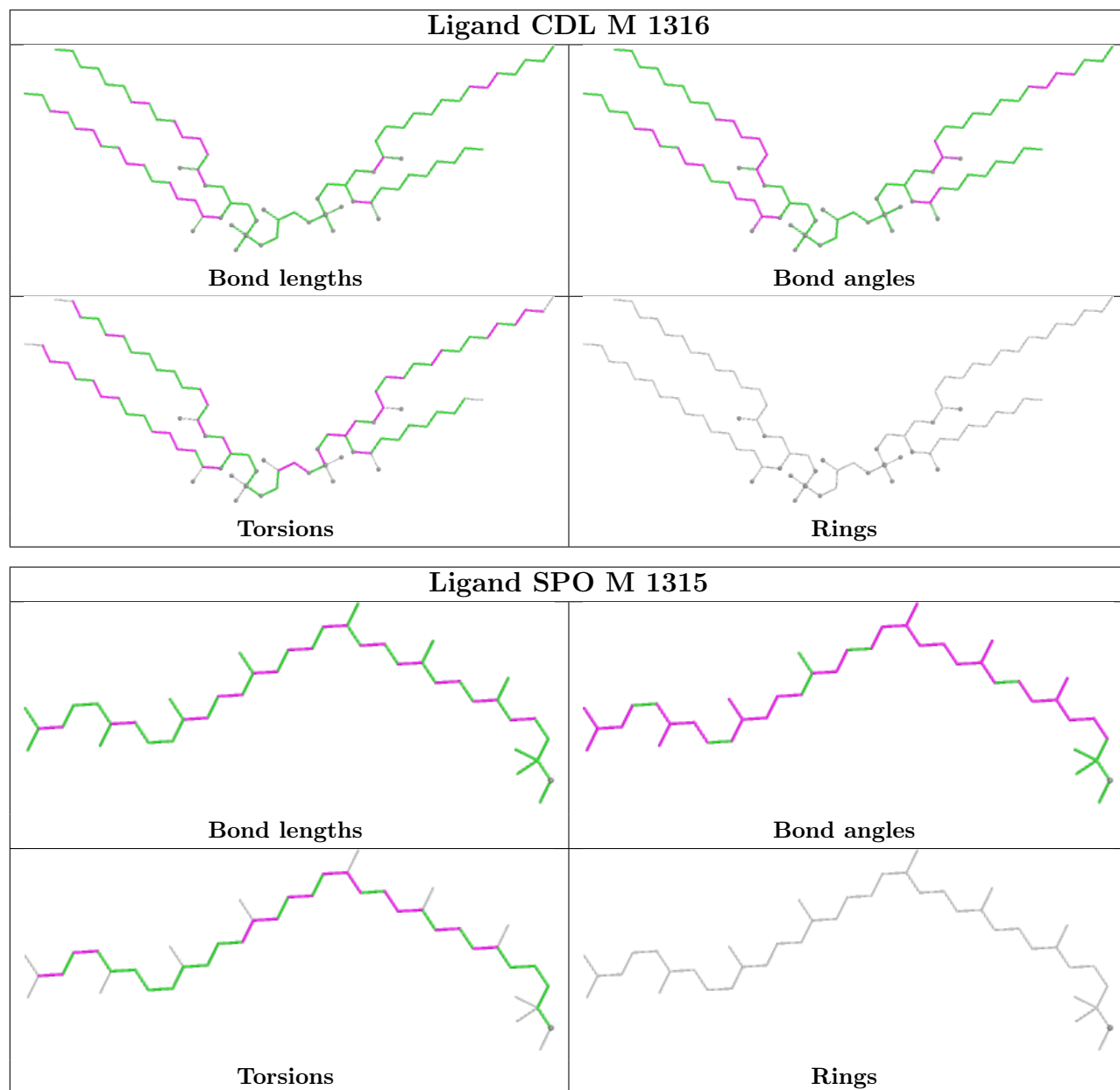


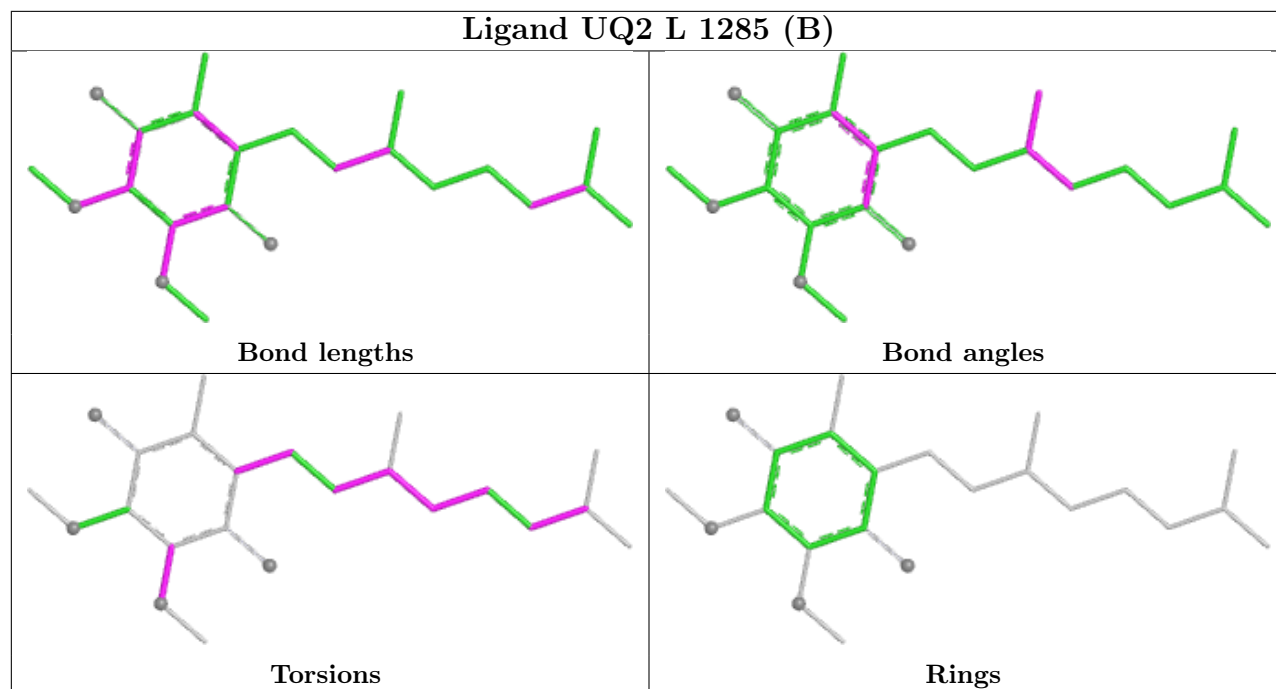
Ligand UQ2 L 1285 (A)



Ligand BPH L 1284







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	H	241/260 (92%)	0.11	10 (4%) 41 37	28, 48, 61, 105	3 (1%)
2	L	281/281 (100%)	0.06	5 (1%) 67 64	35, 44, 69, 77	0
3	M	303/307 (98%)	0.13	10 (3%) 49 45	30, 49, 73, 86	1 (0%)
All	All	825/848 (97%)	0.10	25 (3%) 52 48	28, 47, 72, 105	4 (0%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	246	PRO	6.6
1	H	249	LYS	5.0
3	M	1	ALA	4.7
2	L	277	GLY	4.2
3	M	302	GLY	3.9
3	M	301	HIS	3.8
3	M	3	TYR	3.8
3	M	2	GLU	3.5
2	L	278	GLY	3.3
1	H	248	ARG	3.2
1	H	250	SER	3.0
1	H	247	LYS	2.8
1	H	245	ALA	2.8
3	M	148[A]	TRP	2.8
1	H	251	VAL	2.8
3	M	109	LEU	2.6
1	H	221	SER	2.6
2	L	59	TRP	2.4
1	H	220[A]	LYS	2.4
3	M	52	LEU	2.4
2	L	1	ALA	2.2
2	L	67	TYR	2.2
3	M	53	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	H	94	GLU	2.1
3	M	303	MET	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
14	CDL	M	1316	81/100	0.71	0.34	91,107,125,126	0
4	GOL	H	1251	6/6	0.75	0.24	70,75,76,76	0
6	LDA	M	1309	16/16	0.76	0.39	118,120,126,126	0
6	LDA	M	1311	16/16	0.80	0.38	115,118,122,122	0
10	HTO	L	1288	10/10	0.80	0.29	83,85,85,86	0
6	LDA	M	1310	16/16	0.80	0.32	101,111,118,118	0
8	UQ2	L	1285[A]	23/23	0.83	0.19	38,44,54,55	23
8	UQ2	L	1285[B]	23/23	0.83	0.19	42,47,53,54	23
6	LDA	L	1711	16/16	0.84	0.30	108,112,117,117	0
6	LDA	M	1308	16/16	0.85	0.29	96,99,107,108	0
4	GOL	H	1253	6/6	0.85	0.21	103,104,106,106	0
6	LDA	L	1283	16/16	0.86	0.24	78,103,114,115	0
6	LDA	M	1305	16/16	0.86	0.20	70,80,85,85	0
6	LDA	M	1306	16/16	0.87	0.21	70,74,86,87	0
4	GOL	H	1254	6/6	0.89	0.13	92,93,93,93	0
4	GOL	L	1290	6/6	0.90	0.18	98,99,99,100	0
9	PO4	L	1287	5/5	0.90	0.09	100,100,101,101	0
4	GOL	L	1289	6/6	0.92	0.17	65,69,70,73	0
6	LDA	M	1307	16/16	0.93	0.17	68,70,76,77	0
4	GOL	H	1252	6/6	0.93	0.15	93,94,94,95	0
13	SPO	M	1315	42/42	0.94	0.13	44,57,77,80	0

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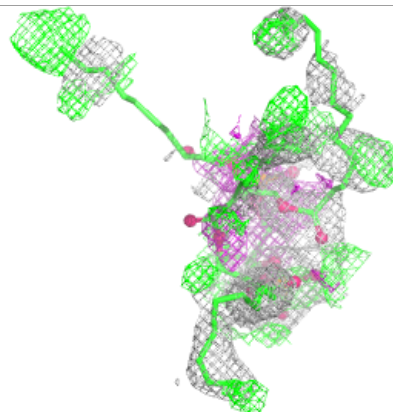
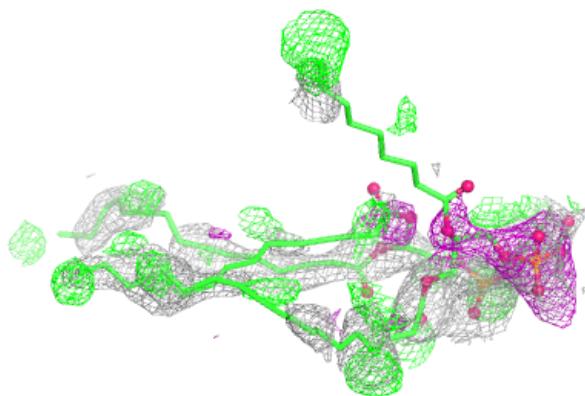
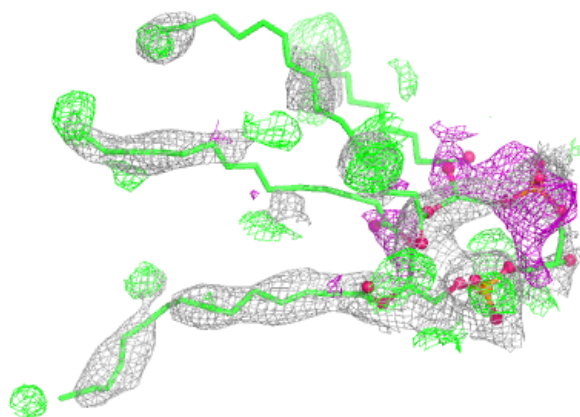
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
12	U10	M	1314	48/63	0.94	0.14	36,47,75,78	0
7	BPH	M	1313	65/65	0.95	0.12	38,45,98,99	0
5	BCL	M	1303	66/66	0.96	0.10	30,36,89,90	0
5	BCL	L	1282	66/66	0.96	0.08	29,35,58,61	0
7	BPH	L	1284	65/65	0.97	0.07	29,36,45,48	0
5	BCL	M	1304	66/66	0.97	0.08	30,36,58,65	0
5	BCL	L	1286	66/66	0.97	0.07	30,38,51,56	0
11	FE	M	1312	1/1	1.00	0.05	34,34,34,34	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.

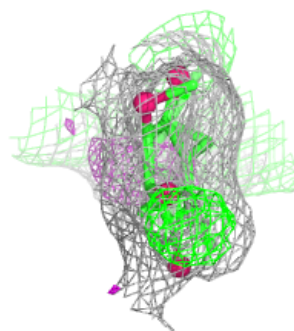
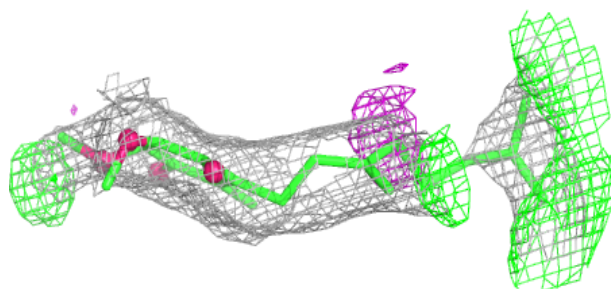
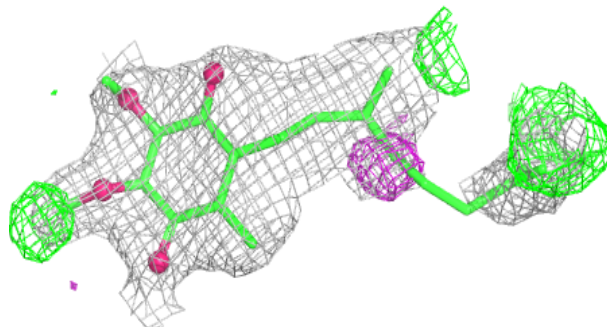
Electron density around CDL M 1316:

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

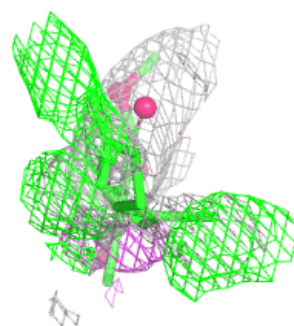
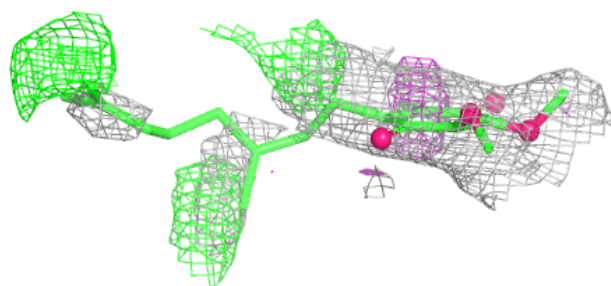
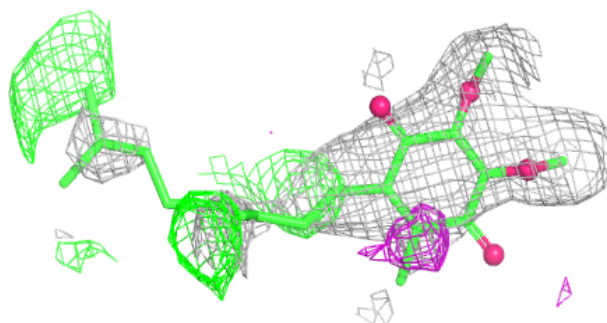


Electron density around UQ2 L 1285 (A):

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

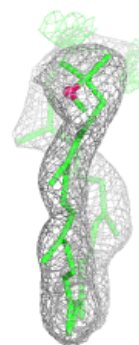
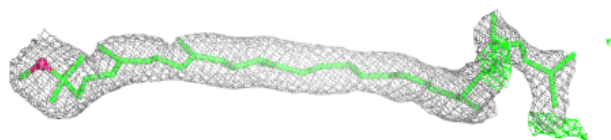
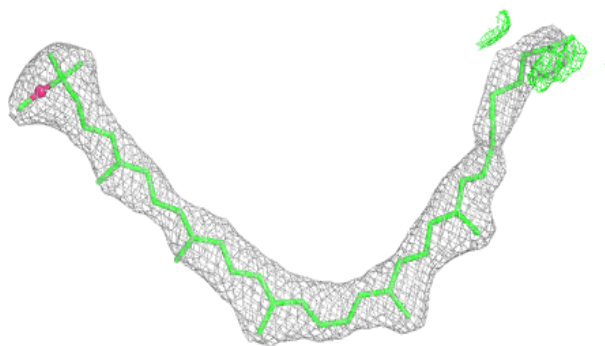
**Electron density around UQ2 L 1285 (B):**

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

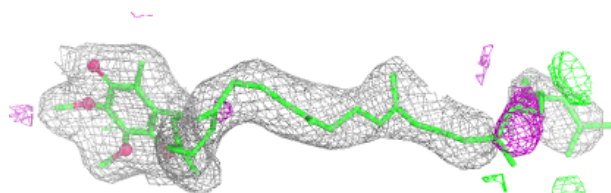
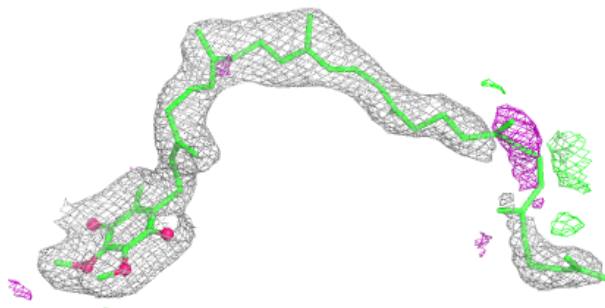


Electron density around SPO M 1315:

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

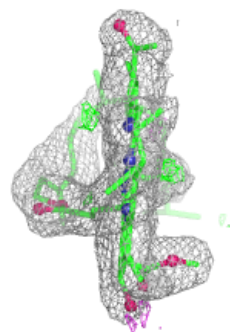
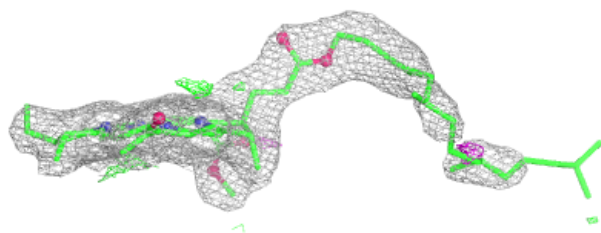
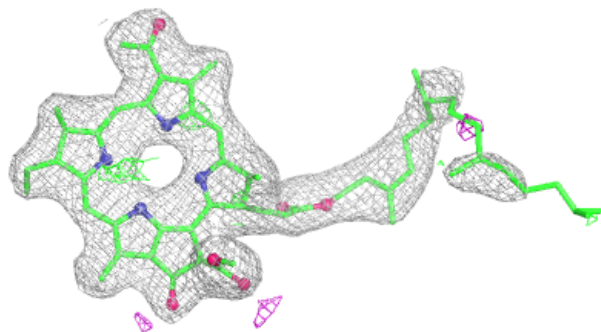
**Electron density around U10 M 1314:**

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



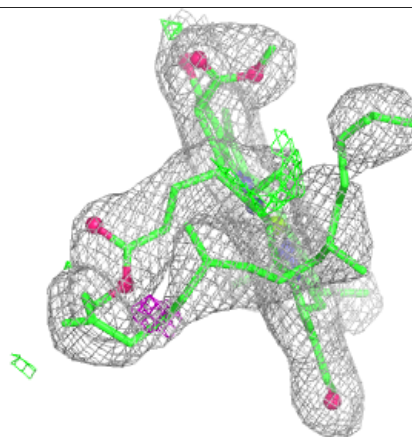
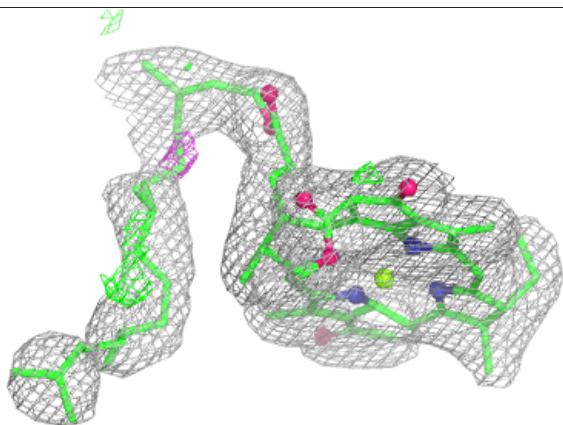
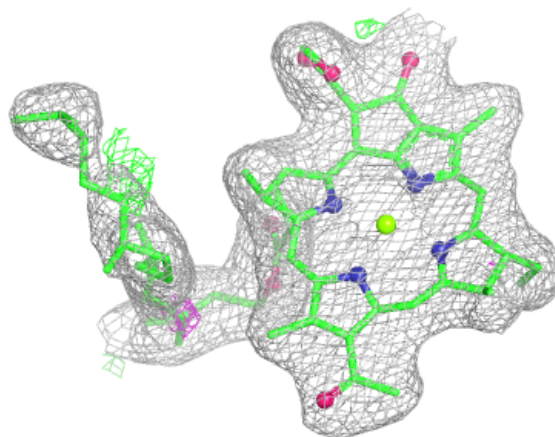
Electron density around BPH M 1313:

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



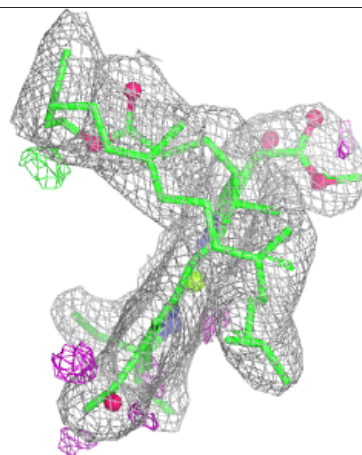
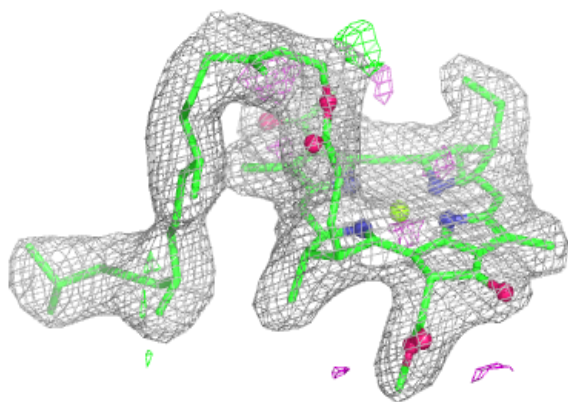
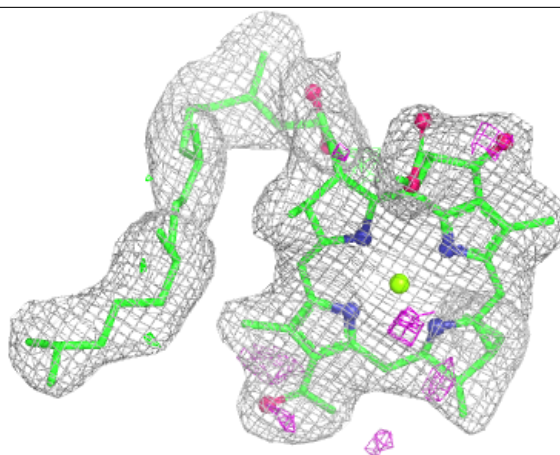
Electron density around BCL M 1303:

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



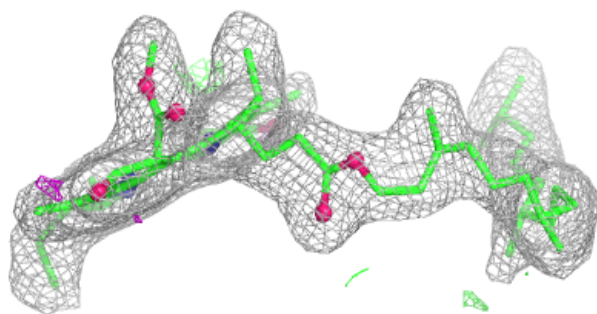
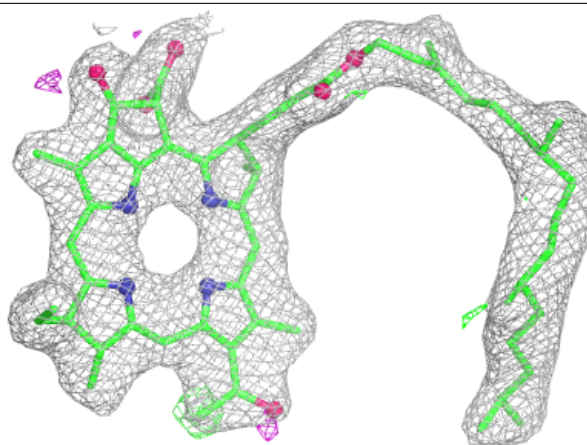
Electron density around BCL L 1282:

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

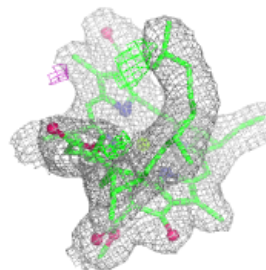
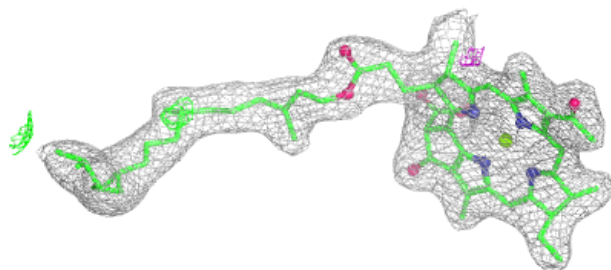
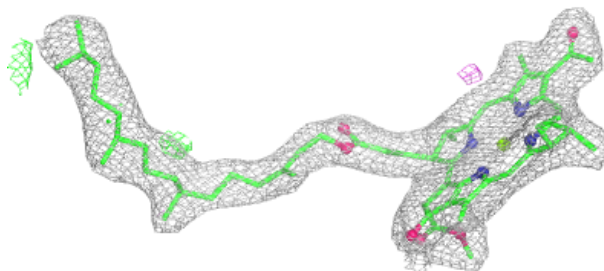


Electron density around BPH L 1284:

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

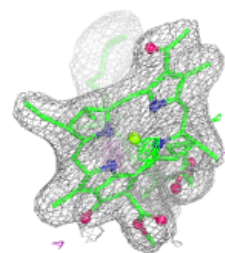
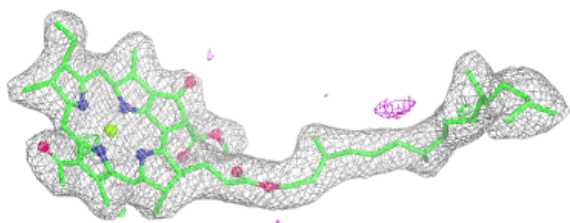
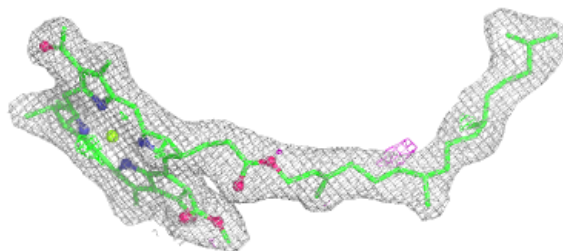
**Electron density around BCL M 1304:**

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



Electron density around BCL L 1286:

$2mF_o-DF_c$ (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.