



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:45 AM UTC

PDB ID : 1DS8 / pdb_00001ds8
Title : PHOTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES IN THE CHARGE-NEUTRAL DQAQB STATE WITH THE PROTON TRANSFER INHIBITOR CD2+
Authors : Axelrod, H.L.; Abresch, E.C.; Paddock, M.L.; Okamura, M.Y.; Feher, G.
Deposited on : 2000-01-07
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

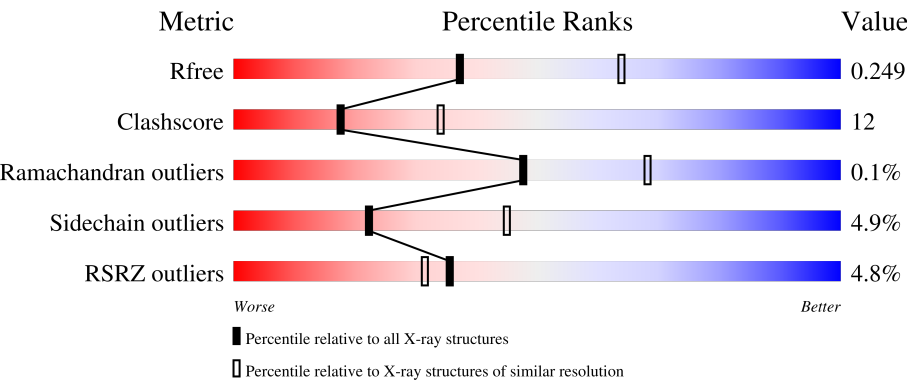
1 Overall quality at a glance i

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	L	281	12% 71%26%..
1	R	281	5% 71%26%..
2	M	307	2% 76%19%..
2	S	307	% 77%19%..

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Mol	Chain	Length	Quality of chain
3	H	260	4% 70% 23% • 5%
3	T	260	5% 69% 24% • 5%

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 14529 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 L CHAIN.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	299	Total	C	N	O	S	0	0	0
			2390	1597	391	392	10			
2	S	299	Total	C	N	O	S	0	0	0
			2390	1597	391	392	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	307	ALA	ASN	conflict	UNP P02953
S	307	ALA	ASN	conflict	UNP P02953

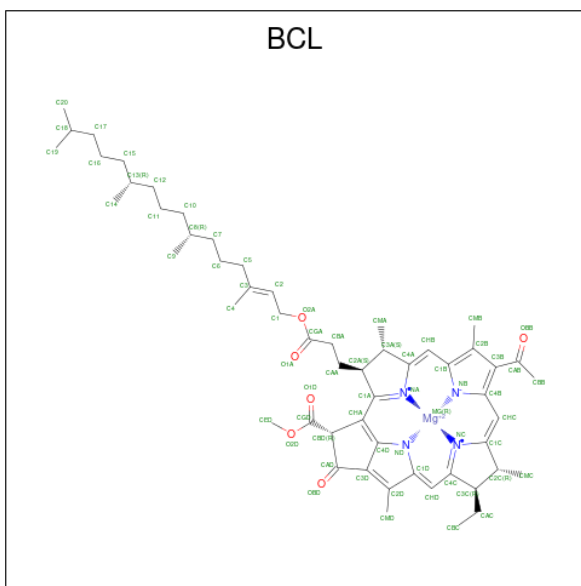
- Molecule 3 is a protein called REACTION CENTER PROTEIN H CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	246	Total	C	N	O	S	0	0	0
			1869	1196	320	343	10			
3	T	246	Total	C	N	O	S	0	0	0
			1869	1196	320	343	10			

There are 2 discrepancies between the modelled and reference sequences:

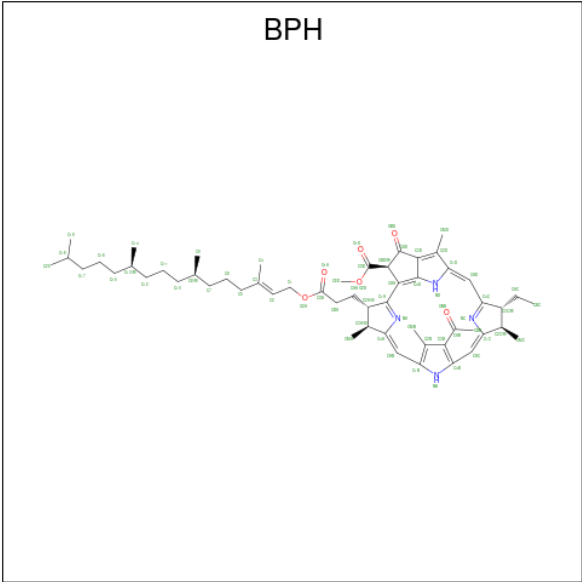
Chain	Residue	Modelled	Actual	Comment	Reference
H	8	GLN	GLY	conflict	UNP P11846
T	8	GLN	GLY	conflict	UNP P11846

- Molecule 4 is BACTERIOCHLOROPHYLL A (CCD ID: BCL) (formula: $\text{C}_{55}\text{H}_{74}\text{MgN}_4\text{O}_6$).



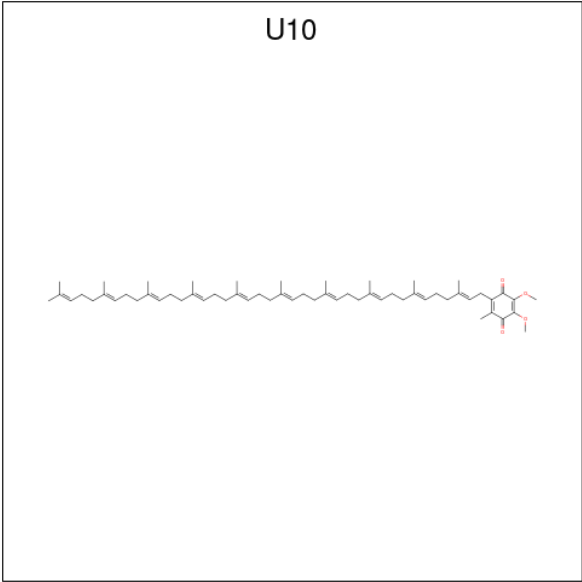
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	L	1	Total 51	C 40	Mg 1	N 4	O 6	0	0
4	L	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
4	L	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
4	M	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
4	R	1	Total 51	C 40	Mg 1	N 4	O 6	0	0
4	R	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
4	R	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
4	S	1	Total 66	C 55	Mg 1	N 4	O 6	0	0

- Molecule 5 is BACTERIOPHEOPHYTIN A (CCD ID: BPH) (formula: $C_{55}H_{76}N_4O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	L	1	Total	C	N	O	0	0
			65	55	4	6		
5	M	1	Total	C	N	O	0	0
			51	41	4	6		
5	R	1	Total	C	N	O	0	0
			65	55	4	6		
5	S	1	Total	C	N	O	0	0
			52	42	4	6		

- Molecule 6 is UBIQUINONE-10 (CCD ID: U10) (formula: C₅₉H₉₀O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	L	1	Total	C	O	0	0
			44	40	4		
6	M	1	Total	C	O	0	0
			38	34	4		
6	R	1	Total	C	O	0	0
			18	14	4		
6	S	1	Total	C	O	0	0
			32	28	4		

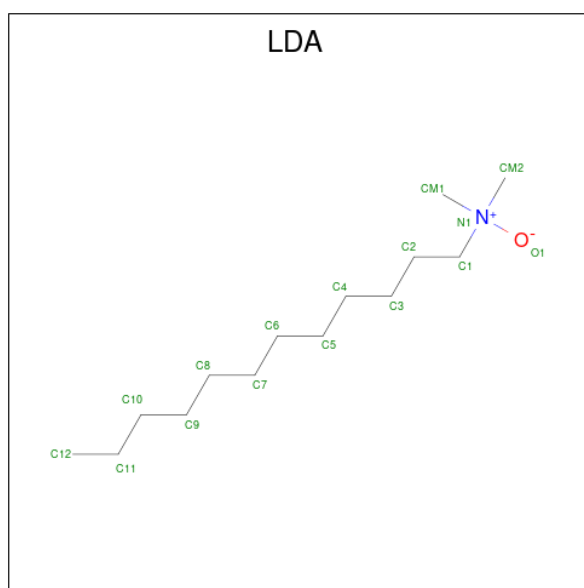
- Molecule 7 is FE (II) ION (CCD ID: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	M	1	Total	Fe	0	0
			1	1		
7	S	1	Total	Fe	0	0
			1	1		

- Molecule 8 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	M	1	Total	Cl	0	0
			1	1		
8	S	1	Total	Cl	0	0
			1	1		

- Molecule 9 is LAURYL DIMETHYLAMINE-N-OXIDE (CCD ID: LDA) (formula: C₁₄H₃₁NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	M	1	Total	C	N	O	0	0
			16	14	1	1		
9	M	1	Total	C	N	O	0	0
			16	14	1	1		
9	M	1	Total	C	N	O	0	0
			16	14	1	1		
9	S	1	Total	C	N	O	0	0
			16	14	1	1		
9	S	1	Total	C	N	O	0	0
			16	14	1	1		
9	S	1	Total	C	N	O	0	0
			16	14	1	1		

- Molecule 10 is CADMIUM ION (CCD ID: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	H	1	Total	Cd	0	0
			1	1		
10	T	1	Total	Cd	0	0
			1	1		

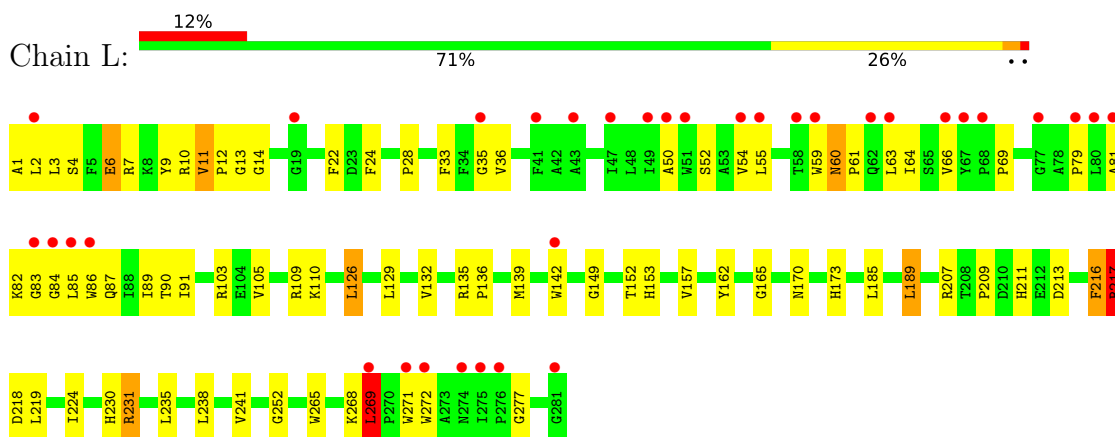
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	L	88	Total	O	0	0
			88	88		
11	M	133	Total	O	0	0
			133	133		
11	H	122	Total	O	0	0
			122	122		
11	R	62	Total	O	0	0
			62	62		
11	S	92	Total	O	0	0
			92	92		
11	T	85	Total	O	0	0
			85	85		

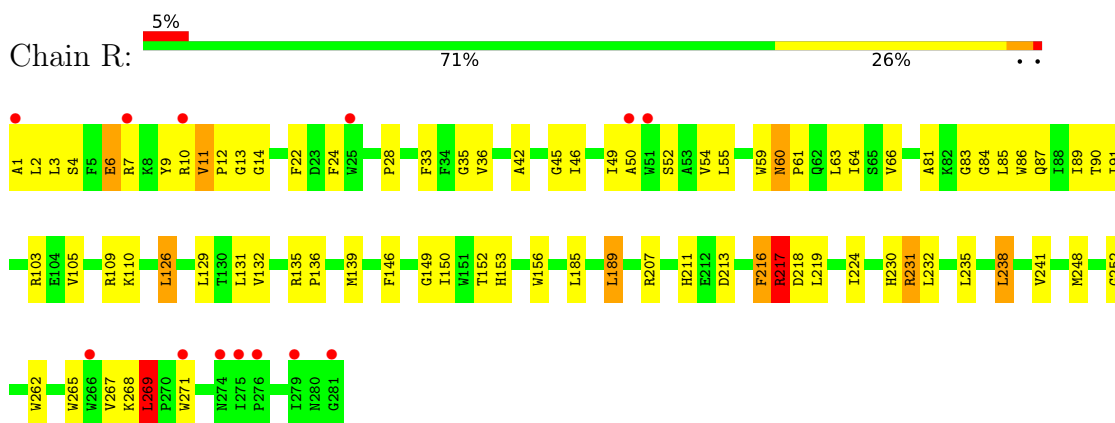
3 Residue-property plots [i](#)

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.

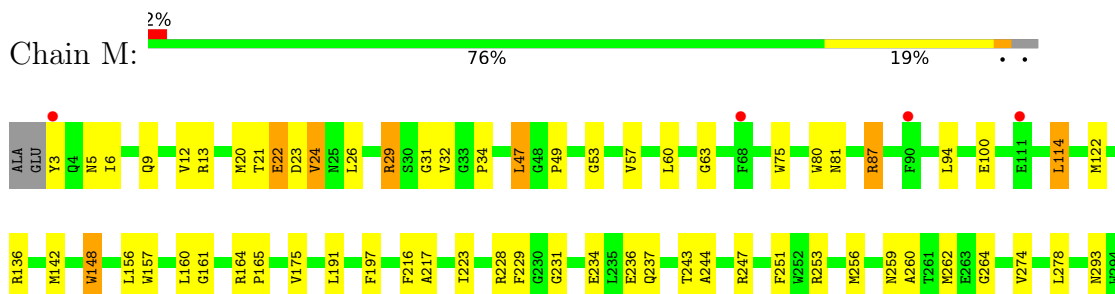
• Molecule 1: REACTION CENTER PROTEIN L CHAIN



• Molecule 1: REACTION CENTER PROTEIN L CHAIN

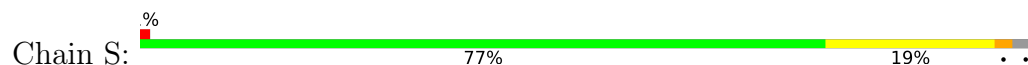


• Molecule 2: REACTION CENTER PROTEIN M CHAIN

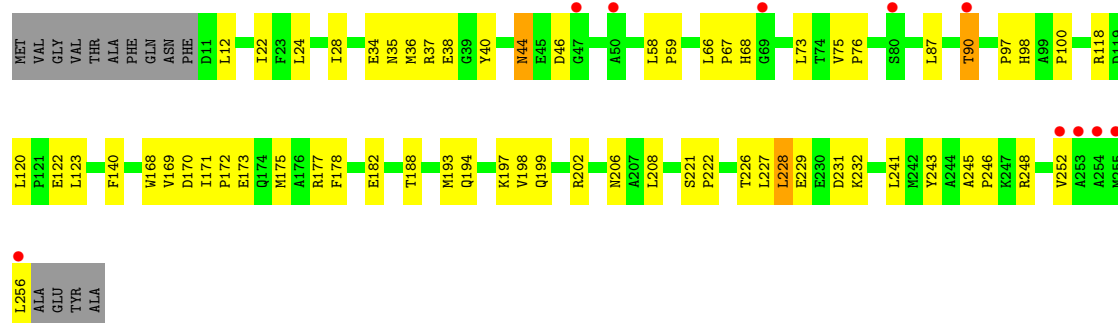




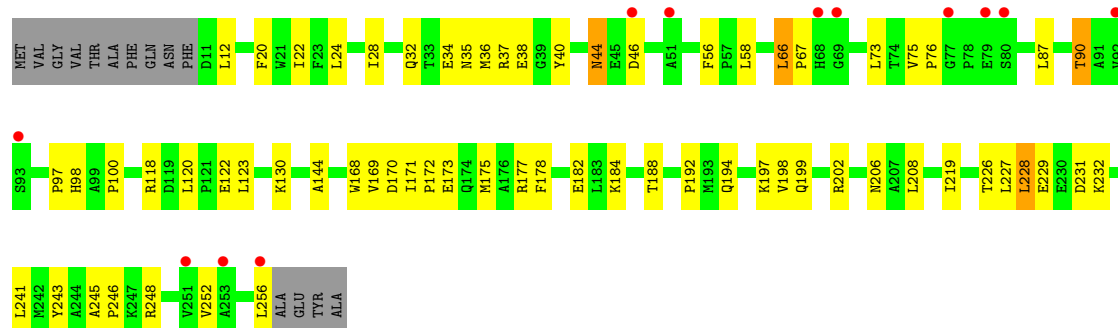
• Molecule 2: REACTION CENTER PROTEIN M CHAIN



• Molecule 3: REACTION CENTER PROTEIN H CHAIN



• Molecule 3: REACTION CENTER PROTEIN H CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	139.59Å 139.59Å 272.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.50 50.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-2.50) 99.8 (50.00-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.90 (at 2.51Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.227 , 0.256 0.219 , 0.249	Depositor DCC
R_{free} test set	4428 reflections (4.69%)	wwPDB-VP
Wilson B-factor (Å ²)	43.2	Xtriage
Anisotropy	0.124	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 42.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14529	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% 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: BCL, U10, CL, CD, LDA, FE2, BPH

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	L	0.45	0/2320	0.90	9/3175 (0.3%)
1	R	0.43	0/2320	0.91	10/3175 (0.3%)
2	M	0.47	0/2482	0.89	7/3389 (0.2%)
2	S	0.43	0/2482	0.89	7/3389 (0.2%)
3	H	0.44	0/1917	0.91	7/2608 (0.3%)
3	T	0.41	0/1917	0.91	6/2608 (0.2%)
All	All	0.44	0/13438	0.90	46/18344 (0.3%)

There are no bond length outliers.

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	231	GLY	N-CA-C	6.91	121.26	112.83
2	S	231	GLY	N-CA-C	6.81	121.14	112.83
1	R	269	LEU	CA-C-N	6.64	128.14	119.84
1	R	269	LEU	C-N-CA	6.64	128.14	119.84
2	S	217	ALA	N-CA-C	-6.62	104.00	111.14
1	L	269	LEU	CA-C-N	6.55	128.03	119.84
1	L	269	LEU	C-N-CA	6.55	128.03	119.84
2	M	217	ALA	N-CA-C	-6.53	104.09	111.14
1	R	271	TRP	N-CA-C	5.94	118.55	111.71
3	T	44	ASN	N-CA-C	-5.93	101.75	110.52
3	H	44	ASN	N-CA-C	-5.89	101.80	110.52
2	S	6	ILE	N-CA-C	-5.86	105.37	111.58
1	L	271	TRP	N-CA-C	5.82	118.40	111.71
2	S	234	GLU	N-CA-C	5.78	117.58	111.28
1	R	3	LEU	N-CA-C	-5.68	102.50	110.50
3	T	169	VAL	N-CA-C	5.66	117.48	108.89
2	M	234	GLU	N-CA-C	5.61	117.40	111.28
1	L	6	GLU	N-CA-C	5.60	118.57	111.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	6	ILE	N-CA-C	-5.51	105.74	111.58
1	L	219	LEU	N-CA-C	5.49	117.07	111.14
3	H	169	VAL	N-CA-C	5.47	117.21	108.89
3	H	22	ILE	N-CA-C	-5.47	105.00	110.30
1	L	217	ARG	N-CA-C	-5.45	105.25	111.14
2	M	160	LEU	N-CA-C	5.45	116.90	111.07
1	L	3	LEU	N-CA-C	-5.41	102.87	110.50
3	T	22	ILE	N-CA-C	-5.41	105.06	110.30
1	R	6	GLU	N-CA-C	5.31	118.22	111.69
3	H	243	TYR	N-CA-C	5.29	119.36	113.01
1	L	60	ASN	CA-C-N	5.28	124.91	119.05
1	L	60	ASN	C-N-CA	5.28	124.91	119.05
1	R	219	LEU	N-CA-C	5.22	116.78	111.14
3	T	243	TYR	N-CA-C	5.21	119.27	113.01
1	R	217	ARG	N-CA-C	-5.17	105.55	111.14
2	S	81	ASN	CA-C-N	5.14	124.58	119.24
2	S	81	ASN	C-N-CA	5.14	124.58	119.24
3	T	66	LEU	CA-C-N	5.14	125.12	120.03
3	T	66	LEU	C-N-CA	5.14	125.12	120.03
1	R	60	ASN	CA-C-N	5.12	124.73	119.05
1	R	60	ASN	C-N-CA	5.12	124.73	119.05
2	S	267	ARG	N-CA-C	-5.09	105.43	111.69
2	M	81	ASN	CA-C-N	5.08	124.53	119.24
2	M	81	ASN	C-N-CA	5.08	124.53	119.24
3	H	170	ASP	N-CA-C	-5.07	100.25	108.41
3	H	66	LEU	CA-C-N	5.03	125.01	120.03
3	H	66	LEU	C-N-CA	5.03	125.01	120.03
1	R	150	ILE	N-CA-C	5.02	115.64	110.36

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L	2232	0	2187	60	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	2232	0	2187	63	0
2	M	2390	0	2304	57	0
2	S	2390	0	2304	51	0
3	H	1869	0	1884	52	0
3	T	1869	0	1884	49	0
4	L	183	0	189	16	0
4	M	66	0	73	7	0
4	R	183	0	189	15	0
4	S	66	0	74	5	0
5	L	65	0	76	8	0
5	M	51	0	45	5	0
5	R	65	0	76	15	0
5	S	52	0	47	3	0
6	L	44	0	57	2	0
6	M	38	0	47	3	0
6	R	18	0	15	3	0
6	S	32	0	39	2	0
7	M	1	0	0	0	0
7	S	1	0	0	0	0
8	M	1	0	0	0	0
8	S	1	0	0	0	0
9	M	48	0	93	8	0
9	S	48	0	93	5	0
10	H	1	0	0	0	0
10	T	1	0	0	0	0
11	H	122	0	0	6	0
11	L	88	0	0	7	0
11	M	133	0	0	3	0
11	R	62	0	0	2	0
11	S	92	0	0	4	0
11	T	85	0	0	3	0
All	All	14529	0	13863	344	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (344) 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:M:122:MET:HE3	2:M:157:TRP:HE1	1.32	0.92
2:M:197:PHE:HZ	4:M:1003:BCL:HBB2	1.34	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:122:MET:HE3	2:S:157:TRP:HE1	1.34	0.91
2:M:197:PHE:CZ	4:M:1003:BCL:HBB2	2.11	0.86
1:L:217:ARG:HD2	11:M:1108:HOH:O	1.77	0.85
2:M:161:GLY:HA3	9:M:1014:LDA:HM12	1.62	0.82
1:R:131:LEU:HD21	4:R:2002:BCL:HED2	1.64	0.80
5:R:2006:BPH:HHC	5:R:2006:BPH:HBB3	1.68	0.76
2:S:197:PHE:HZ	4:S:2003:BCL:HBB2	1.51	0.75
4:R:2001:BCL:HHC	4:R:2001:BCL:HBB3	1.69	0.74
2:S:228:ARG:HA	3:T:194:GLN:CG	2.18	0.73
2:M:9:GLN:NE2	3:H:198:VAL:H	1.86	0.73
2:M:9:GLN:HE22	3:H:197:LYS:HA	1.54	0.72
11:L:1019:HOH:O	2:M:253:ARG:HD3	1.90	0.71
2:S:243:THR:O	2:S:247:ARG:HG3	1.90	0.71
2:M:161:GLY:CA	9:M:1014:LDA:HM12	2.20	0.71
2:S:228:ARG:HA	3:T:194:GLN:HG2	1.73	0.70
1:R:217:ARG:HD2	11:S:2024:HOH:O	1.91	0.70
1:L:224:ILE:HG22	6:L:1009:U10:H3M3	1.72	0.69
2:S:63:GLY:HA3	5:S:2005:BPH:H5C2	1.73	0.69
3:T:90:THR:HB	3:T:97:PRO:O	1.92	0.69
2:M:122:MET:CE	2:M:157:TRP:HE1	2.04	0.69
1:R:224:ILE:HG22	6:R:2009:U10:H3M3	1.74	0.69
2:M:122:MET:HE3	2:M:157:TRP:NE1	2.08	0.68
1:L:105:VAL:O	1:L:109:ARG:HG3	1.93	0.68
4:R:2001:BCL:HHC	4:R:2001:BCL:CBB	2.23	0.67
3:H:90:THR:HB	3:H:97:PRO:O	1.94	0.67
2:S:122:MET:CE	2:S:157:TRP:HE1	2.06	0.67
3:H:173:GLU:HG3	11:H:1088:HOH:O	1.94	0.67
2:S:197:PHE:CZ	4:S:2003:BCL:HBB2	2.29	0.67
1:R:189:LEU:HB3	6:R:2009:U10:H4M3	1.75	0.67
5:R:2006:BPH:HBB2	2:S:210:TYR:HB3	1.76	0.67
1:R:105:VAL:O	1:R:109:ARG:HG3	1.94	0.67
2:S:21:THR:O	2:S:24:VAL:HG13	1.93	0.67
1:L:55:LEU:HD13	1:L:81:ALA:HB2	1.75	0.67
1:R:55:LEU:HD13	1:R:81:ALA:HB2	1.77	0.66
3:T:194:GLN:CD	3:T:194:GLN:H	2.03	0.65
2:S:122:MET:HE3	2:S:157:TRP:NE1	2.10	0.65
3:H:194:GLN:CD	3:H:194:GLN:H	2.04	0.65
1:R:218:ASP:OD1	2:S:29:ARG:HD2	1.97	0.65
3:T:87:LEU:HD23	3:T:100:PRO:HA	1.80	0.64
2:M:21:THR:O	2:M:24:VAL:HG13	1.96	0.64
3:H:87:LEU:HD23	3:H:100:PRO:HA	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:231:ARG:HD2	2:S:5:ASN:O	1.98	0.63
2:M:243:THR:O	2:M:247:ARG:HG3	1.99	0.63
1:R:265:TRP:O	1:R:269:LEU:HD13	2.00	0.62
4:M:1003:BCL:CBB	4:M:1003:BCL:HHC	2.29	0.62
5:R:2006:BPH:HHC	5:R:2006:BPH:CBB	2.29	0.61
2:S:77:GLN:HG2	11:S:2029:HOH:O	2.00	0.61
3:H:252:VAL:O	3:H:256:LEU:HD13	2.02	0.60
1:L:60:ASN:HB3	1:L:63:LEU:HD23	1.84	0.60
2:M:9:GLN:HE22	3:H:198:VAL:H	1.49	0.60
2:M:161:GLY:HA3	9:M:1014:LDA:HM23	1.83	0.60
1:L:265:TRP:O	1:L:269:LEU:HD13	2.00	0.60
1:L:60:ASN:O	1:L:64:ILE:HG13	2.02	0.60
11:S:2020:HOH:O	3:T:173:GLU:HG2	2.01	0.59
1:L:218:ASP:OD1	2:M:29:ARG:HD2	2.02	0.59
1:R:238:LEU:HD12	5:R:2006:BPH:CBC	2.33	0.59
1:R:28:PRO:HB3	2:S:253:ARG:NH1	2.18	0.59
3:T:226:THR:OG1	3:T:229:GLU:HG3	2.03	0.59
4:L:1001:BCL:CBB	4:L:1001:BCL:HHC	2.33	0.58
1:R:60:ASN:HB3	1:R:63:LEU:HD23	1.84	0.58
2:M:63:GLY:HA3	5:M:1005:BPH:H5C2	1.84	0.58
3:T:252:VAL:O	3:T:256:LEU:HD13	2.03	0.58
6:M:1008:U10:H4M2	6:M:1008:U10:H3M3	1.83	0.58
1:R:60:ASN:O	1:R:64:ILE:HG13	2.02	0.58
1:R:86:TRP:CH2	1:R:132:VAL:HG13	2.39	0.58
1:L:86:TRP:CH2	1:L:132:VAL:HG13	2.38	0.58
1:L:272:TRP:CD2	2:M:87:ARG:HB3	2.38	0.58
3:T:118:ARG:HD3	3:T:120:LEU:HD12	1.86	0.58
4:S:2003:BCL:CBB	4:S:2003:BCL:HHC	2.34	0.58
5:S:2005:BPH:HBB3	5:S:2005:BPH:HMB1	1.85	0.58
1:R:13:GLY:O	1:R:110:LYS:HE2	2.04	0.57
1:L:13:GLY:O	1:L:110:LYS:HE2	2.04	0.57
2:S:256:MET:CE	6:S:2008:U10:H102	2.35	0.57
1:R:248:MET:HG3	4:R:2002:BCL:HED2	1.85	0.57
3:H:118:ARG:HD3	3:H:120:LEU:HD12	1.86	0.57
5:M:1005:BPH:HBB3	5:M:1005:BPH:HMB1	1.87	0.57
1:L:211:HIS:CE1	2:M:20:MET:HE2	2.40	0.56
2:S:148:TRP:HD1	9:S:2013:LDA:H12	1.70	0.56
6:L:1009:U10:H311	2:M:31:GLY:O	2.06	0.56
2:S:20:MET:HA	11:T:2085:HOH:O	2.04	0.56
1:L:189:LEU:HG	1:L:216:PHE:HZ	1.72	0.55
1:R:135:ARG:HB3	1:R:136:PRO:HD3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:28:PRO:HB3	2:M:253:ARG:NH1	2.22	0.55
1:R:267:VAL:HG13	2:S:87:ARG:HD2	1.90	0.54
2:M:228:ARG:HA	3:H:194:GLN:HG2	1.88	0.54
1:R:139:MET:HE3	1:R:252:GLY:HA3	1.90	0.54
2:S:9:GLN:HE22	3:T:198:VAL:H	1.55	0.54
4:L:1004:BCL:O1D	9:M:1013:LDA:H21	2.08	0.54
1:L:139:MET:HE3	1:L:252:GLY:HA3	1.90	0.54
1:R:211:HIS:CE1	2:S:20:MET:HE2	2.43	0.54
1:L:231:ARG:HD2	2:M:5:ASN:O	2.08	0.54
4:L:1001:BCL:HBB3	4:M:1003:BCL:H41	1.90	0.54
1:R:189:LEU:HG	1:R:216:PHE:HZ	1.72	0.54
2:S:100:GLU:H	2:S:100:GLU:CD	2.15	0.54
2:S:164:ARG:HB3	2:S:165:PRO:HD3	1.90	0.53
1:R:230:HIS:CD2	2:S:223:ILE:HG13	2.44	0.53
2:M:13:ARG:O	3:H:140:PHE:HA	2.07	0.53
1:R:54:VAL:HA	11:R:2068:HOH:O	2.09	0.53
1:L:14:GLY:O	1:L:109:ARG:HD3	2.08	0.53
1:R:14:GLY:O	1:R:109:ARG:HD3	2.08	0.53
1:R:87:GLN:O	1:R:91:ILE:HG12	2.08	0.53
3:T:199:GLN:HE22	3:T:202:ARG:NH1	2.07	0.53
11:L:1054:HOH:O	3:H:67:PRO:HG2	2.08	0.53
2:M:100:GLU:CD	2:M:100:GLU:H	2.17	0.53
5:L:1006:BPH:HMB3	5:L:1006:BPH:HBB3	1.91	0.53
5:L:1006:BPH:HMB3	5:L:1006:BPH:CBB	2.40	0.52
3:H:199:GLN:HE22	3:H:202:ARG:NH1	2.08	0.52
1:L:241:VAL:HG21	5:L:1006:BPH:HAC1	1.91	0.52
3:T:34:GLU:O	3:T:37:ARG:HD3	2.09	0.52
2:M:164:ARG:HB3	2:M:165:PRO:HD3	1.90	0.52
3:H:175:MET:HE3	11:H:1028:HOH:O	2.10	0.52
11:R:2018:HOH:O	2:S:233:ARG:HA	2.10	0.52
4:S:2003:BCL:HBB2	4:S:2003:BCL:HHC	1.91	0.52
1:L:135:ARG:HB3	1:L:136:PRO:HD3	1.91	0.52
3:H:37:ARG:HH11	3:H:76:PRO:HD3	1.75	0.51
3:H:34:GLU:O	3:H:37:ARG:HD3	2.09	0.51
4:R:2002:BCL:H122	5:R:2006:BPH:H3A	1.93	0.51
4:R:2002:BCL:H192	5:R:2006:BPH:HMA2	1.92	0.51
1:L:52:SER:HB2	1:L:85:LEU:HD23	1.91	0.51
1:L:83:GLY:O	1:L:87:GLN:HG3	2.10	0.51
1:R:6:GLU:OE2	1:R:10:ARG:HD3	2.10	0.51
1:L:28:PRO:HB3	2:M:253:ARG:HH11	1.75	0.51
1:L:272:TRP:CE2	2:M:87:ARG:HB3	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:226:THR:OG1	3:H:229:GLU:HG3	2.11	0.51
1:R:42:ALA:HA	5:R:2006:BPH:H9C2	1.93	0.51
2:S:9:GLN:NE2	3:T:198:VAL:H	2.07	0.51
2:M:32:VAL:HG22	2:M:49:PRO:HD3	1.92	0.51
2:M:228:ARG:HA	3:H:194:GLN:CG	2.41	0.51
3:T:87:LEU:HD22	3:T:98:HIS:O	2.11	0.51
1:R:45:GLY:HA3	5:R:2006:BPH:H9C1	1.93	0.50
3:T:37:ARG:HH11	3:T:76:PRO:HD3	1.75	0.50
2:M:148:TRP:HA	2:M:148:TRP:CE3	2.47	0.50
2:M:3:TYR:CE1	2:M:9:GLN:HG3	2.47	0.50
1:L:87:GLN:O	1:L:91:ILE:HG12	2.11	0.50
3:H:75:VAL:HA	3:H:76:PRO:C	2.36	0.50
1:R:232:LEU:HD21	6:R:2009:U10:H8	1.92	0.50
2:M:148:TRP:HA	2:M:148:TRP:HE3	1.77	0.50
1:R:83:GLY:O	1:R:87:GLN:HG3	2.12	0.50
3:T:199:GLN:NE2	3:T:202:ARG:NH1	2.60	0.50
2:S:148:TRP:HA	2:S:148:TRP:CE3	2.47	0.50
1:R:28:PRO:HB3	2:S:253:ARG:HH11	1.76	0.49
2:S:32:VAL:HG22	2:S:49:PRO:HD3	1.94	0.49
3:H:199:GLN:NE2	3:H:202:ARG:NH1	2.60	0.49
2:S:148:TRP:HA	2:S:148:TRP:HE3	1.77	0.49
1:R:50:ALA:O	1:R:54:VAL:HG23	2.12	0.49
1:L:277:GLY:HA3	11:L:1085:HOH:O	2.12	0.49
1:R:52:SER:HB2	1:R:85:LEU:HD23	1.94	0.49
4:R:2004:BCL:HED1	9:S:2014:LDA:H11	1.94	0.49
4:L:1002:BCL:H122	5:L:1006:BPH:H3A	1.95	0.49
1:L:50:ALA:O	1:L:54:VAL:HG23	2.13	0.49
2:M:274:VAL:HG11	9:M:1012:LDA:H61	1.95	0.49
3:H:228:LEU:CD2	3:H:232:LYS:HE3	2.43	0.48
2:S:3:TYR:CE1	2:S:9:GLN:HG3	2.47	0.48
3:T:75:VAL:HA	3:T:76:PRO:C	2.37	0.48
3:T:168:TRP:HB2	3:T:178:PHE:HB2	1.95	0.48
4:L:1002:BCL:HMB3	4:L:1002:BCL:CBB	2.43	0.48
3:H:87:LEU:HD22	3:H:98:HIS:O	2.13	0.48
3:H:199:GLN:NE2	3:H:202:ARG:HH11	2.12	0.48
2:M:136:ARG:CZ	2:M:136:ARG:HA	2.44	0.48
2:M:236:GLU:HB3	11:H:1012:HOH:O	2.13	0.48
3:T:122:GLU:HB2	3:T:227:LEU:HD21	1.95	0.48
3:T:241:LEU:O	3:T:248:ARG:NH2	2.46	0.48
1:L:6:GLU:OE2	1:L:10:ARG:HD3	2.13	0.48
1:L:209:PRO:HG3	11:M:1113:HOH:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:136:ARG:HA	2:M:136:ARG:NE	2.28	0.48
3:H:175:MET:CE	11:H:1028:HOH:O	2.61	0.48
3:H:241:LEU:O	3:H:248:ARG:NH2	2.47	0.48
3:T:228:LEU:CD2	3:T:232:LYS:HE3	2.43	0.48
3:H:168:TRP:HB2	3:H:178:PHE:HB2	1.96	0.47
2:S:71:GLY:HA2	9:S:2012:LDA:HM11	1.95	0.47
1:R:35:GLY:HA2	1:R:103:ARG:HD2	1.97	0.47
3:T:130:LYS:HZ2	3:T:170:ASP:CG	2.23	0.47
3:T:184:LYS:HG3	11:T:2090:HOH:O	2.14	0.47
1:L:59:TRP:HA	1:L:59:TRP:CE3	2.49	0.47
3:H:24:LEU:O	3:H:28:ILE:HG13	2.15	0.47
5:M:1005:BPH:HBC3	5:M:1005:BPH:HHD	1.96	0.47
1:R:11:VAL:HG13	1:R:12:PRO:HD2	1.97	0.47
1:R:189:LEU:HG	1:R:216:PHE:CZ	2.50	0.47
2:S:136:ARG:HA	2:S:136:ARG:NE	2.30	0.47
1:L:35:GLY:HA2	1:L:103:ARG:HD2	1.97	0.47
2:M:34:PRO:O	2:M:47:LEU:HB2	2.15	0.47
1:R:1:ALA:C	1:R:2:LEU:HD12	2.40	0.47
1:L:1:ALA:C	1:L:2:LEU:HD12	2.40	0.47
2:M:229:PHE:HB2	2:M:244:ALA:HB2	1.97	0.47
1:R:59:TRP:HA	1:R:59:TRP:CE3	2.50	0.47
3:H:122:GLU:HB2	3:H:227:LEU:HD21	1.97	0.46
1:L:189:LEU:HG	1:L:216:PHE:CZ	2.50	0.46
3:T:199:GLN:NE2	3:T:202:ARG:HH11	2.12	0.46
2:M:175:VAL:HB	9:M:1014:LDA:H11	1.97	0.46
3:H:206:ASN:O	3:H:248:ARG:NH1	2.49	0.46
1:R:42:ALA:O	1:R:46:ILE:HG13	2.16	0.46
2:S:204:LEU:HD13	3:T:20:PHE:CE2	2.51	0.46
3:T:206:ASN:O	3:T:248:ARG:NH1	2.49	0.46
5:R:2006:BPH:H151	5:R:2006:BPH:H192	1.97	0.46
3:T:87:LEU:HD23	3:T:100:PRO:CA	2.44	0.46
4:R:2002:BCL:C19	5:R:2006:BPH:HMA2	2.46	0.46
4:L:1002:BCL:HAA2	4:L:1002:BCL:HBD	1.97	0.46
2:M:3:TYR:CZ	2:M:5:ASN:HA	2.51	0.46
3:T:171:ILE:HB	3:T:172:PRO:HD3	1.98	0.46
4:R:2004:BCL:H193	5:R:2006:BPH:H102	1.97	0.46
2:S:53:GLY:O	2:S:57:VAL:HG23	2.16	0.46
2:S:3:TYR:CZ	2:S:5:ASN:HA	2.51	0.45
3:H:37:ARG:C	3:H:38:GLU:HG2	2.41	0.45
4:R:2002:BCL:CGA	4:R:2004:BCL:HBC1	2.47	0.45
1:L:207:ARG:HG2	2:M:142:MET:HG2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:T:228:LEU:HD22	3:T:232:LYS:HE3	1.98	0.45
1:L:2:LEU:HB3	1:L:6:GLU:HB3	1.98	0.45
2:S:136:ARG:HA	2:S:136:ARG:CZ	2.46	0.45
4:L:1001:BCL:HHC	4:L:1001:BCL:HBB2	1.99	0.45
3:H:175:MET:HE2	3:H:177:ARG:HG2	1.97	0.45
4:R:2004:BCL:CBB	4:R:2004:BCL:HMB1	2.47	0.45
3:T:40:TYR:HB3	3:T:58:LEU:HD21	1.99	0.45
1:R:85:LEU:O	1:R:89:ILE:HG13	2.16	0.45
1:L:11:VAL:HG13	1:L:12:PRO:HD2	1.99	0.45
11:L:1028:HOH:O	3:H:173:GLU:HG2	2.16	0.45
4:L:1002:BCL:CGA	4:L:1004:BCL:HBC1	2.47	0.45
2:M:256:MET:CE	6:M:1008:U10:H102	2.46	0.45
5:M:1005:BPH:HBB3	5:M:1005:BPH:CMB	2.47	0.45
1:R:149:GLY:HA3	1:R:152:THR:OG1	2.17	0.45
3:H:171:ILE:HB	3:H:172:PRO:HD3	1.99	0.44
1:R:90:THR:HG23	1:R:132:VAL:HG11	1.99	0.44
3:T:24:LEU:O	3:T:28:ILE:HG13	2.17	0.44
1:R:153:HIS:CE1	5:R:2006:BPH:H201	2.53	0.44
1:R:238:LEU:HD12	5:R:2006:BPH:HBC3	1.99	0.44
2:M:278:LEU:HD12	2:M:278:LEU:HA	1.88	0.44
2:S:34:PRO:O	2:S:47:LEU:HB2	2.18	0.44
2:M:260:ALA:HB1	3:H:35:ASN:OD1	2.18	0.44
2:M:264:GLY:HA3	3:H:35:ASN:OD1	2.16	0.44
3:H:87:LEU:HD23	3:H:100:PRO:CA	2.44	0.44
3:H:44:ASN:HB2	3:H:46:ASP:OD1	2.18	0.44
4:R:2004:BCL:HED1	9:S:2014:LDA:O1	2.18	0.44
3:T:194:GLN:H	3:T:194:GLN:NE2	2.15	0.44
1:L:90:THR:HG23	1:L:132:VAL:HG11	2.00	0.44
4:L:1002:BCL:C19	5:L:1006:BPH:HMA2	2.47	0.44
3:H:40:TYR:HB3	3:H:58:LEU:HD21	2.00	0.44
3:T:37:ARG:C	3:T:38:GLU:HG2	2.42	0.44
2:S:264:GLY:HA3	3:T:35:ASN:OD1	2.18	0.44
3:T:182:GLU:HA	3:T:188:THR:HG22	2.00	0.43
1:L:9:TYR:O	1:L:11:VAL:N	2.50	0.43
3:T:44:ASN:HB2	3:T:46:ASP:OD1	2.19	0.43
3:H:194:GLN:H	3:H:194:GLN:NE2	2.16	0.43
11:S:2073:HOH:O	3:T:175:MET:HE1	2.18	0.43
3:H:206:ASN:HD21	3:H:248:ARG:HD2	1.83	0.43
3:T:219:ILE:HG12	11:T:2062:HOH:O	2.19	0.43
1:L:66:VAL:HG12	1:L:86:TRP:HB2	2.00	0.43
1:R:213:ASP:O	1:R:217:ARG:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:268:LYS:HA	1:R:268:LYS:HD3	1.83	0.43
4:L:1002:BCL:HBD	4:L:1004:BCL:HAC1	2.00	0.43
1:R:2:LEU:HB3	1:R:6:GLU:HB3	1.99	0.43
1:L:84:GLY:HA2	1:L:87:GLN:HE21	1.83	0.43
1:L:185:LEU:HD13	5:M:1005:BPH:ND	2.32	0.43
1:L:213:ASP:O	1:L:217:ARG:HB2	2.19	0.43
3:H:177:ARG:HG2	3:H:177:ARG:NH1	2.33	0.43
2:S:55:LEU:HD12	2:S:55:LEU:HA	1.89	0.43
4:S:2003:BCL:HBC2	4:S:2003:BCL:H2C	1.88	0.43
1:L:33:PHE:O	1:L:36:VAL:HG22	2.19	0.43
4:L:1004:BCL:CBB	4:L:1004:BCL:HMB1	2.49	0.43
1:R:22:PHE:HA	1:R:24:PHE:CE2	2.54	0.43
2:S:11:GLN:HB2	3:T:144:ALA:HB3	2.01	0.43
2:S:253:ARG:HB2	2:S:259:ASN:OD1	2.19	0.43
1:R:60:ASN:HA	1:R:61:PRO:HD3	1.85	0.43
4:R:2002:BCL:HMB3	4:R:2002:BCL:CBB	2.49	0.43
1:R:9:TYR:O	1:R:11:VAL:N	2.49	0.43
1:R:84:GLY:HA2	1:R:87:GLN:HE21	1.83	0.43
1:R:207:ARG:HG3	1:R:211:HIS:CG	2.54	0.43
1:L:162:TYR:HA	1:L:165:GLY:O	2.19	0.42
1:L:185:LEU:HD12	1:L:189:LEU:HD22	2.01	0.42
1:R:238:LEU:HD12	5:R:2006:BPH:HBC1	2.00	0.42
1:R:33:PHE:O	1:R:36:VAL:HG22	2.18	0.42
1:R:45:GLY:O	1:R:49:ILE:HG13	2.20	0.42
2:S:237:GLN:HB2	2:S:262:MET:HG2	2.02	0.42
2:S:260:ALA:HB1	3:T:35:ASN:OD1	2.19	0.42
3:T:245:ALA:N	3:T:246:PRO:CD	2.82	0.42
2:M:253:ARG:HB2	2:M:259:ASN:OD1	2.20	0.42
4:L:1001:BCL:HBC1	4:M:1003:BCL:HAA2	2.02	0.42
4:L:1002:BCL:CBA	4:L:1004:BCL:HBC1	2.50	0.42
2:M:237:GLN:HB2	2:M:262:MET:HG2	2.02	0.42
3:H:228:LEU:HD22	3:H:232:LYS:HE3	2.00	0.42
3:T:36:MET:HE2	3:T:58:LEU:HD23	2.02	0.42
3:T:37:ARG:NH1	3:T:76:PRO:HD3	2.35	0.42
1:L:85:LEU:O	1:L:89:ILE:HG13	2.19	0.42
2:M:53:GLY:O	2:M:57:VAL:HG23	2.19	0.42
4:M:1003:BCL:HBB2	4:M:1003:BCL:HHC	2.00	0.42
3:H:34:GLU:HG3	11:H:1021:HOH:O	2.20	0.42
3:H:245:ALA:N	3:H:246:PRO:CD	2.82	0.42
1:L:11:VAL:HG13	11:L:1086:HOH:O	2.19	0.42
1:L:149:GLY:HA3	1:L:152:THR:OG1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:293:ASN:OD1	2:M:295:TYR:HB3	2.20	0.42
3:H:221:SER:HA	3:H:222:PRO:HD3	1.84	0.42
1:R:241:VAL:HG21	5:R:2006:BPH:HAC2	2.01	0.42
1:L:241:VAL:HG21	5:L:1006:BPH:CAC	2.50	0.42
4:M:1003:BCL:HHC	4:M:1003:BCL:HBB3	2.02	0.42
3:H:182:GLU:HA	3:H:188:THR:HG22	2.01	0.42
1:R:66:VAL:HG12	1:R:86:TRP:HB2	2.01	0.42
1:R:185:LEU:HD12	1:R:189:LEU:HD22	2.01	0.42
9:M:1014:LDA:HM11	9:M:1014:LDA:H22	1.68	0.42
1:R:185:LEU:HD13	5:S:2005:BPH:ND	2.35	0.42
2:S:251:PHE:CD2	2:S:251:PHE:C	2.98	0.42
1:L:60:ASN:HA	1:L:61:PRO:HD3	1.84	0.41
1:L:152:THR:HG23	11:L:1081:HOH:O	2.20	0.41
1:L:268:LYS:HA	1:L:268:LYS:HD3	1.81	0.41
11:L:1069:HOH:O	2:M:29:ARG:HD2	2.20	0.41
2:M:114:LEU:HD12	2:M:114:LEU:HA	1.92	0.41
3:T:175:MET:HE2	3:T:177:ARG:HG2	2.02	0.41
4:L:1002:BCL:OBB	4:L:1002:BCL:HHC	2.20	0.41
1:L:126:LEU:HD12	1:L:126:LEU:HA	1.87	0.41
2:M:122:MET:HE1	9:M:1014:LDA:HM21	2.02	0.41
3:H:68:HIS:HD2	11:H:1030:HOH:O	2.04	0.41
1:R:262:TRP:O	1:R:265:TRP:HD1	2.03	0.41
2:S:278:LEU:HA	2:S:278:LEU:HD12	1.86	0.41
4:L:1002:BCL:H192	5:L:1006:BPH:HMA2	2.02	0.41
3:T:206:ASN:HD21	3:T:248:ARG:HD2	1.85	0.41
11:M:1062:HOH:O	3:H:193:MET:HE3	2.20	0.41
3:H:36:MET:HE2	3:H:58:LEU:HD23	2.02	0.41
4:R:2001:BCL:HBB2	9:S:2012:LDA:H123	2.03	0.41
2:S:114:LEU:HD12	2:S:114:LEU:HA	1.91	0.41
2:S:229:PHE:HB2	2:S:244:ALA:HB2	2.02	0.41
3:T:66:LEU:HA	3:T:67:PRO:HD3	1.77	0.41
1:L:60:ASN:CB	1:L:63:LEU:HD23	2.49	0.41
1:L:69:PRO:HD2	1:L:142:TRP:HB2	2.03	0.41
3:H:177:ARG:HG2	3:H:177:ARG:HH11	1.86	0.41
1:R:207:ARG:HG2	2:S:142:MET:HG2	2.03	0.41
4:R:2002:BCL:H203	6:S:2008:U10:H252	2.03	0.41
2:S:75:TRP:HB3	2:S:80:TRP:CE3	2.56	0.41
1:L:79:PRO:HB2	1:L:82:LYS:HB2	2.02	0.40
1:L:153:HIS:O	1:L:157:VAL:HG23	2.21	0.40
1:L:170:ASN:HB3	1:L:173:HIS:CB	2.51	0.40
2:M:251:PHE:CD2	2:M:251:PHE:C	3.00	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:37:ARG:NH1	3:H:76:PRO:HD3	2.36	0.40
1:R:126:LEU:HD12	1:R:126:LEU:HA	1.87	0.40
1:L:22:PHE:HA	1:L:24:PHE:CE2	2.55	0.40
4:L:1004:BCL:H193	5:L:1006:BPH:H102	2.02	0.40
2:S:9:GLN:HE22	3:T:197:LYS:HA	1.87	0.40
1:L:207:ARG:HG3	1:L:211:HIS:CG	2.56	0.40
2:M:75:TRP:HB3	2:M:80:TRP:CE3	2.56	0.40
3:T:32:GLN:HG2	3:T:56:PHE:CD2	2.57	0.40
3:T:192:PRO:HB3	3:T:194:GLN:HE21	1.87	0.40
3:H:37:ARG:HD2	3:H:59:PRO:HG3	2.03	0.40
1:L:230:HIS:CD2	2:M:223:ILE:HG13	2.56	0.40
2:M:22:GLU:HB3	2:M:23:ASP:H	1.69	0.40
2:M:260:ALA:C	6:M:1008:U10:H4M3	2.47	0.40
1:R:146:PHE:HB3	1:R:156:TRP:CD2	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L	279/281 (99%)	266 (95%)	12 (4%)	1 (0%)	30	49
1	R	279/281 (99%)	266 (95%)	12 (4%)	1 (0%)	30	49
2	M	297/307 (97%)	288 (97%)	9 (3%)	0	100	100
2	S	297/307 (97%)	289 (97%)	8 (3%)	0	100	100
3	H	244/260 (94%)	236 (97%)	8 (3%)	0	100	100
3	T	244/260 (94%)	234 (96%)	10 (4%)	0	100	100
All	All	1640/1696 (97%)	1579 (96%)	59 (4%)	2 (0%)	48	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	R	4	SER
1	L	4	SER

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	L	220/220 (100%)	209 (95%)	11 (5%)	22	44
1	R	220/220 (100%)	209 (95%)	11 (5%)	22	44
2	M	235/239 (98%)	221 (94%)	14 (6%)	17	36
2	S	235/239 (98%)	221 (94%)	14 (6%)	17	36
3	H	199/209 (95%)	192 (96%)	7 (4%)	32	58
3	T	199/209 (95%)	192 (96%)	7 (4%)	32	58
All	All	1308/1336 (98%)	1244 (95%)	64 (5%)	22	45

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	7	ARG
1	L	11	VAL
1	L	126	LEU
1	L	129	LEU
1	L	189	LEU
1	L	216	PHE
1	L	217	ARG
1	L	231	ARG
1	L	235	LEU
1	L	238	LEU
1	L	269	LEU
2	M	12	VAL
2	M	22	GLU
2	M	24	VAL
2	M	26	LEU
2	M	29	ARG
2	M	47	LEU

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Mol	Chain	Res	Type
2	M	60	LEU
2	M	87	ARG
2	M	94	LEU
2	M	114	LEU
2	M	148	TRP
2	M	156	LEU
2	M	191	LEU
2	M	216	PHE
3	H	12	LEU
3	H	73	LEU
3	H	90	THR
3	H	123	LEU
3	H	208	LEU
3	H	228	LEU
3	H	231	ASP
1	R	7	ARG
1	R	11	VAL
1	R	126	LEU
1	R	129	LEU
1	R	189	LEU
1	R	216	PHE
1	R	217	ARG
1	R	231	ARG
1	R	235	LEU
1	R	238	LEU
1	R	269	LEU
2	S	12	VAL
2	S	22	GLU
2	S	24	VAL
2	S	26	LEU
2	S	29	ARG
2	S	47	LEU
2	S	60	LEU
2	S	87	ARG
2	S	94	LEU
2	S	114	LEU
2	S	148	TRP
2	S	156	LEU
2	S	191	LEU
2	S	216	PHE
3	T	12	LEU
3	T	73	LEU

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Mol	Chain	Res	Type
3	T	90	THR
3	T	123	LEU
3	T	208	LEU
3	T	228	LEU
3	T	231	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	87	GLN
1	L	183	ASN
1	L	258	GLN
2	M	4	GLN
2	M	9	GLN
2	M	300	ASN
3	H	68	HIS
3	H	194	GLN
3	H	199	GLN
3	H	206	ASN
1	R	87	GLN
1	R	183	ASN
1	R	258	GLN
1	R	274	ASN
2	S	4	GLN
2	S	9	GLN
2	S	300	ASN
3	T	194	GLN
3	T	199	GLN
3	T	206	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 28 ligands modelled in this entry, 6 are monoatomic - leaving 22 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$
9	LDA	S	2014	-	13,15,15	2.37	1 (7%)	14,17,17	1.37	1 (7%)
6	U10	R	2009	-	18,18,63	2.04	3 (16%)	24,25,79	1.48	5 (20%)
9	LDA	M	1014	-	13,15,15	2.26	1 (7%)	14,17,17	1.41	3 (21%)
6	U10	L	1009	-	44,44,63	1.71	9 (20%)	54,56,79	1.43	8 (14%)
4	BCL	L	1004	1	69,74,74	1.14	9 (13%)	79,115,115	1.85	21 (26%)
4	BCL	R	2004	1	69,74,74	0.96	5 (7%)	79,115,115	1.91	18 (22%)
5	BPH	S	2005	-	46,57,70	1.36	6 (13%)	42,85,101	2.88	21 (50%)
4	BCL	R	2001	2	54,59,74	1.05	5 (9%)	61,97,115	2.06	19 (31%)
9	LDA	S	2012	-	13,15,15	2.31	1 (7%)	14,17,17	1.36	1 (7%)
4	BCL	M	1003	2	69,74,74	0.95	5 (7%)	79,115,115	1.70	19 (24%)
4	BCL	R	2002	1	69,74,74	1.01	4 (5%)	79,115,115	1.86	16 (20%)
9	LDA	M	1012	-	13,15,15	2.13	2 (15%)	14,17,17	1.42	2 (14%)
5	BPH	M	1005	-	45,56,70	1.32	6 (13%)	41,84,101	2.88	20 (48%)
4	BCL	L	1001	2	54,59,74	1.14	4 (7%)	61,97,115	2.10	21 (34%)
5	BPH	L	1006	-	59,70,70	1.18	5 (8%)	59,101,101	2.26	16 (27%)
9	LDA	M	1013	-	13,15,15	2.25	1 (7%)	14,17,17	1.37	2 (14%)
9	LDA	S	2013	-	13,15,15	2.19	1 (7%)	14,17,17	1.40	1 (7%)
4	BCL	S	2003	2	69,74,74	1.01	4 (5%)	79,115,115	1.73	16 (20%)
6	U10	S	2008	-	32,32,63	1.72	7 (21%)	40,41,79	1.17	4 (10%)
5	BPH	R	2006	-	59,70,70	1.17	6 (10%)	59,101,101	2.20	16 (27%)
4	BCL	L	1002	1	69,74,74	1.01	4 (5%)	79,115,115	1.67	18 (22%)
6	U10	M	1008	-	38,38,63	1.90	11 (28%)	48,49,79	1.27	5 (10%)

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
9	LDA	S	2014	-	-	7/13/13/13	-
6	U10	R	2009	-	-	2/9/33/87	0/1/1/1
9	LDA	M	1014	-	-	8/13/13/13	-
6	U10	L	1009	-	-	14/41/65/87	0/1/1/1
4	BCL	L	1004	1	-	2/41/137/137	-
4	BCL	R	2004	1	-	7/41/137/137	-
5	BPH	S	2005	-	-	7/22/90/105	0/5/6/6
4	BCL	R	2001	2	-	1/23/119/137	-
9	LDA	S	2012	-	-	5/13/13/13	-
4	BCL	M	1003	2	-	4/41/137/137	-
4	BCL	R	2002	1	-	6/41/137/137	-
9	LDA	M	1012	-	-	7/13/13/13	-
5	BPH	M	1005	-	-	2/21/89/105	0/5/6/6
4	BCL	L	1001	2	-	0/23/119/137	-
5	BPH	L	1006	-	-	8/37/105/105	0/5/6/6
9	LDA	M	1013	-	-	4/13/13/13	-
9	LDA	S	2013	-	-	9/13/13/13	-
4	BCL	S	2003	2	-	2/41/137/137	-
6	U10	S	2008	-	-	2/26/50/87	0/1/1/1
5	BPH	R	2006	-	-	6/37/105/105	0/5/6/6
4	BCL	L	1002	1	-	2/41/137/137	-
6	U10	M	1008	-	-	2/33/57/87	0/1/1/1

All (100) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	S	2014	LDA	O1-N1	-8.12	1.22	1.42
9	S	2012	LDA	O1-N1	-7.81	1.23	1.42
9	M	1014	LDA	O1-N1	-7.79	1.23	1.42
9	M	1013	LDA	O1-N1	-7.60	1.23	1.42
9	S	2013	LDA	O1-N1	-7.52	1.23	1.42
9	M	1012	LDA	O1-N1	-7.12	1.24	1.42
6	M	1008	U10	C6-C1	6.78	1.47	1.35
6	R	2009	U10	C6-C1	5.79	1.45	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	S	2008	U10	C6-C1	5.37	1.44	1.35
6	L	1009	U10	C6-C1	5.29	1.44	1.35
5	L	1006	BPH	C3D-CAD	-4.33	1.39	1.47
5	S	2005	BPH	C3D-CAD	-4.11	1.39	1.47
5	R	2006	BPH	C3D-CAD	-4.04	1.40	1.47
4	L	1004	BCL	C1D-C2D	-3.83	1.37	1.45
6	M	1008	U10	C13-C14	3.69	1.41	1.33
5	M	1005	BPH	C3D-CAD	-3.60	1.40	1.47
4	S	2003	BCL	C2-C3	3.53	1.41	1.33
4	L	1001	BCL	C1D-C2D	-3.44	1.38	1.45
6	S	2008	U10	C18-C19	3.44	1.41	1.33
4	R	2002	BCL	C2-C3	3.43	1.41	1.33
5	L	1006	BPH	C2-C3	3.40	1.40	1.33
6	L	1009	U10	C28-C29	3.33	1.40	1.33
4	R	2004	BCL	O2D-CGD	-3.30	1.25	1.33
6	R	2009	U10	C7-C6	3.26	1.57	1.51
4	L	1001	BCL	O2D-CGD	-3.26	1.25	1.33
6	L	1009	U10	C33-C34	3.22	1.40	1.33
6	L	1009	U10	C8-C9	3.21	1.40	1.33
5	S	2005	BPH	C2-C3	3.18	1.40	1.33
4	R	2002	BCL	O2D-CGD	-3.14	1.25	1.33
6	R	2009	U10	C8-C9	3.12	1.41	1.32
5	R	2006	BPH	O2D-CGD	-3.07	1.25	1.33
5	S	2005	BPH	O2D-CGD	-3.05	1.25	1.33
6	M	1008	U10	C18-C19	3.02	1.40	1.33
4	S	2003	BCL	O2D-CGD	-3.01	1.25	1.33
4	L	1002	BCL	C1D-C2D	-2.99	1.39	1.45
4	L	1004	BCL	O2D-CGD	-2.99	1.25	1.33
5	R	2006	BPH	C2-C3	2.98	1.39	1.33
4	R	2001	BCL	O2D-CGD	-2.94	1.26	1.33
4	R	2004	BCL	C2-C3	2.90	1.39	1.33
5	S	2005	BPH	C3B-CAB	-2.90	1.41	1.49
5	L	1006	BPH	O2A-CGA	-2.90	1.24	1.33
4	L	1001	BCL	O2A-CGA	-2.88	1.25	1.33
6	S	2008	U10	C8-C9	2.87	1.39	1.33
4	M	1003	BCL	O2D-CGD	-2.86	1.26	1.33
5	M	1005	BPH	O2A-CGA	-2.84	1.25	1.33
4	L	1002	BCL	O2D-CGD	-2.84	1.26	1.33
4	L	1004	BCL	C1D-ND	-2.83	1.34	1.37
5	R	2006	BPH	C3B-CAB	-2.81	1.41	1.49
6	L	1009	U10	C7-C8	-2.77	1.46	1.50
5	M	1005	BPH	C3A-C2A	-2.75	1.52	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	M	1003	BCL	O2A-CGA	-2.74	1.25	1.33
4	L	1001	BCL	C1D-ND	-2.71	1.34	1.37
4	R	2002	BCL	O2A-CGA	-2.71	1.25	1.33
5	S	2005	BPH	O2A-CGA	-2.67	1.25	1.33
6	S	2008	U10	C7-C8	-2.67	1.46	1.50
5	L	1006	BPH	O2D-CGD	-2.66	1.26	1.33
5	M	1005	BPH	O2D-CGD	-2.65	1.26	1.33
6	L	1009	U10	C13-C14	2.64	1.39	1.33
4	S	2003	BCL	O2A-CGA	-2.63	1.25	1.33
4	R	2002	BCL	C1D-C2D	-2.63	1.40	1.45
4	R	2001	BCL	O2A-CGA	-2.61	1.25	1.33
6	L	1009	U10	C18-C19	2.58	1.39	1.33
4	M	1003	BCL	C1D-C2D	-2.57	1.40	1.45
4	L	1002	BCL	O2A-CGA	-2.57	1.25	1.33
5	R	2006	BPH	C3A-C2A	-2.56	1.52	1.54
4	L	1004	BCL	O2A-CGA	-2.54	1.26	1.33
5	R	2006	BPH	O2A-CGA	-2.54	1.26	1.33
6	M	1008	U10	C7-C6	2.54	1.56	1.51
4	R	2004	BCL	C3D-CAD	-2.53	1.36	1.45
6	M	1008	U10	C7-C8	-2.52	1.46	1.50
4	S	2003	BCL	C1D-C2D	-2.51	1.40	1.45
5	M	1005	BPH	C3B-CAB	-2.50	1.42	1.49
4	L	1004	BCL	C1B-NB	-2.48	1.34	1.37
6	M	1008	U10	C8-C9	2.48	1.38	1.33
4	R	2001	BCL	C1D-C2D	-2.45	1.40	1.45
4	L	1002	BCL	C2-C3	2.44	1.38	1.33
5	S	2005	BPH	C3A-C2A	-2.42	1.52	1.54
4	R	2004	BCL	C1D-C2D	-2.41	1.40	1.45
6	M	1008	U10	O3-C3	2.40	1.42	1.36
6	S	2008	U10	C4-C3	2.38	1.45	1.36
6	S	2008	U10	C4-C5	-2.37	1.42	1.48
4	R	2001	BCL	C2-C3	2.29	1.39	1.32
4	R	2004	BCL	O2A-CGA	-2.29	1.26	1.33
6	L	1009	U10	C23-C24	2.26	1.38	1.33
4	L	1004	BCL	C2-C3	2.24	1.38	1.33
5	M	1005	BPH	C2-C3	2.23	1.38	1.33
4	M	1003	BCL	C3D-CAD	-2.23	1.37	1.45
6	S	2008	U10	C13-C14	2.21	1.38	1.33
4	L	1004	BCL	C3D-C4D	-2.21	1.39	1.44
4	M	1003	BCL	C2-C3	2.20	1.38	1.33
4	L	1004	BCL	C1-C2	-2.20	1.43	1.49
6	M	1008	U10	C27-C28	-2.20	1.43	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L	1006	BPH	CBB-CAB	2.19	1.56	1.49
6	L	1009	U10	C4-C3	2.12	1.44	1.36
4	L	1004	BCL	C3D-CAD	-2.11	1.38	1.45
9	M	1012	LDA	C1-N1	-2.09	1.49	1.51
6	M	1008	U10	C3-C2	-2.09	1.42	1.48
6	M	1008	U10	C28-C29	2.03	1.38	1.32
6	M	1008	U10	C4-C3	2.02	1.43	1.36
4	R	2001	BCL	CMB-C2B	2.00	1.54	1.50

All (253) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	1006	BPH	C4D-CHA-CBD	-7.42	104.89	108.45
5	S	2005	BPH	C3D-C4D-ND	7.12	116.83	107.71
5	M	1005	BPH	C4D-CHA-CBD	-7.07	105.06	108.45
4	R	2001	BCL	C1C-NC-C4C	7.06	109.90	106.68
4	R	2002	BCL	C1C-NC-C4C	6.91	109.83	106.68
5	R	2006	BPH	C4D-CHA-CBD	-6.88	105.15	108.45
5	M	1005	BPH	C4-C3-C5	6.49	123.77	116.13
4	L	1004	BCL	C1C-NC-C4C	6.36	109.58	106.68
5	R	2006	BPH	C3D-C4D-ND	6.22	115.68	107.71
5	R	2006	BPH	O2D-CGD-CBD	6.22	117.78	110.95
5	S	2005	BPH	C4D-CHA-CBD	-6.00	105.58	108.45
5	S	2005	BPH	O2D-CGD-CBD	5.81	117.33	110.95
4	R	2002	BCL	C1D-ND-C4D	-5.76	102.27	106.31
5	L	1006	BPH	O2D-CGD-CBD	5.65	117.16	110.95
4	R	2004	BCL	C1C-NC-C4C	5.63	109.25	106.68
5	L	1006	BPH	C3D-C4D-ND	5.43	114.67	107.71
4	S	2003	BCL	C1C-NC-C4C	5.36	109.12	106.68
5	R	2006	BPH	C4D-ND-C1D	-5.33	102.48	108.87
4	L	1002	BCL	C1C-NC-C4C	5.27	109.08	106.68
4	L	1001	BCL	C4A-NA-C1A	5.21	109.06	106.68
4	R	2004	BCL	C1D-ND-C4D	-5.16	102.69	106.31
5	S	2005	BPH	C2B-C1B-NB	5.15	113.15	109.43
4	S	2003	BCL	C4D-CHA-C1A	5.10	127.33	121.24
4	L	1001	BCL	C1C-NC-C4C	5.08	109.00	106.68
4	M	1003	BCL	C4A-NA-C1A	5.02	108.97	106.68
4	M	1003	BCL	C4D-CHA-C1A	4.97	127.18	121.24
5	L	1006	BPH	C4D-ND-C1D	-4.93	102.96	108.87
5	M	1005	BPH	O2D-CGD-CBD	4.88	116.30	110.95
5	L	1006	BPH	C3D-CAD-CBD	4.86	114.00	107.61
5	S	2005	BPH	C1-O2A-CGA	4.85	128.40	116.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	S	2005	BPH	C4D-ND-C1D	-4.85	103.06	108.87
4	L	1004	BCL	C4D-C3D-CAD	-4.85	102.84	108.11
4	R	2002	BCL	C4D-CHA-C1A	4.77	126.93	121.24
4	R	2004	BCL	C4A-NA-C1A	4.70	108.82	106.68
4	S	2003	BCL	C4D-C3D-CAD	-4.69	103.01	108.11
5	M	1005	BPH	C3D-C4D-ND	4.69	113.72	107.71
4	R	2004	BCL	OBD-CAD-C3D	-4.68	117.48	128.42
4	L	1004	BCL	C4A-NA-C1A	4.66	108.81	106.68
4	L	1002	BCL	C4D-CHA-C1A	4.65	126.79	121.24
4	L	1004	BCL	C4D-CHA-C1A	4.63	126.76	121.24
5	M	1005	BPH	C2B-C1B-NB	4.62	112.77	109.43
4	R	2004	BCL	C4D-CHA-C1A	4.59	126.72	121.24
5	R	2006	BPH	C3D-CAD-CBD	4.57	113.62	107.61
4	R	2001	BCL	C4D-CHA-C1A	4.48	126.59	121.24
4	R	2004	BCL	C4D-C3D-CAD	-4.47	103.25	108.11
5	M	1005	BPH	C3D-CAD-CBD	4.47	113.49	107.61
5	L	1006	BPH	OBD-CAD-C3D	-4.38	121.06	127.89
5	M	1005	BPH	C1-O2A-CGA	4.31	127.09	116.65
4	R	2002	BCL	C3D-C4D-ND	4.30	116.98	109.99
4	L	1001	BCL	C4D-CHA-C1A	4.28	126.34	121.24
5	M	1005	BPH	C4D-ND-C1D	-4.21	103.83	108.87
5	S	2005	BPH	C3D-CAD-CBD	4.18	113.11	107.61
5	S	2005	BPH	C4C-C3C-C2C	4.14	106.78	102.84
5	S	2005	BPH	C4-C3-C5	4.12	122.37	115.23
6	L	1009	U10	C25-C24-C26	4.11	122.36	115.23
4	L	1001	BCL	C1-O2A-CGA	4.10	126.58	116.65
4	R	2001	BCL	C4D-C3D-CAD	-4.09	103.66	108.11
4	R	2001	BCL	C1-O2A-CGA	4.07	126.49	116.65
5	L	1006	BPH	C2B-C1B-NB	4.00	112.32	109.43
4	L	1001	BCL	C4D-C3D-CAD	-3.92	103.84	108.11
4	L	1001	BCL	C1D-ND-C4D	-3.92	103.56	106.31
5	L	1006	BPH	CMA-C3A-C4A	-3.92	106.17	114.61
4	L	1002	BCL	C1D-ND-C4D	-3.84	103.62	106.31
4	R	2004	BCL	C3D-C4D-ND	3.80	116.17	109.99
4	R	2001	BCL	C4A-NA-C1A	3.79	108.41	106.68
4	L	1002	BCL	C3D-C4D-ND	3.71	116.02	109.99
4	L	1001	BCL	C2A-C3A-C4A	3.70	107.84	101.87
4	L	1001	BCL	C3D-C4D-ND	3.69	115.98	109.99
4	S	2003	BCL	C3D-C4D-ND	3.66	115.94	109.99
5	S	2005	BPH	C1B-NB-C4B	-3.65	103.50	108.82
4	L	1002	BCL	C4D-C3D-CAD	-3.64	104.15	108.11
4	L	1004	BCL	C3D-C4D-ND	3.57	115.78	109.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	M	1003	BCL	C7-C6-C5	-3.56	103.77	113.26
4	M	1003	BCL	C3D-C4D-ND	3.56	115.78	109.99
5	M	1005	BPH	C1B-NB-C4B	-3.55	103.64	108.82
4	R	2001	BCL	C3D-C2D-C1D	3.52	110.64	105.83
5	M	1005	BPH	CED-O2D-CGD	3.50	123.85	115.92
4	R	2001	BCL	O2D-CGD-CBD	3.49	117.34	111.23
4	M	1003	BCL	C1C-NC-C4C	3.49	108.27	106.68
5	S	2005	BPH	CMA-C3A-C4A	-3.36	107.36	114.61
5	R	2006	BPH	CMA-C3A-C4A	-3.33	107.44	114.61
4	S	2003	BCL	CED-O2D-CGD	3.32	123.44	115.92
4	R	2001	BCL	C3D-C4D-ND	3.31	115.37	109.99
4	L	1002	BCL	CED-O2D-CGD	3.31	123.41	115.92
5	M	1005	BPH	O1D-CGD-CBD	-3.30	119.72	124.72
5	L	1006	BPH	CMC-C2C-C1C	-3.30	107.50	114.61
4	S	2003	BCL	C1D-ND-C4D	-3.28	104.01	106.31
4	L	1004	BCL	O2D-CGD-CBD	3.28	116.96	111.23
4	L	1004	BCL	C2A-C3A-C4A	3.26	107.13	101.87
5	R	2006	BPH	CMC-C2C-C1C	-3.23	107.65	114.61
4	L	1004	BCL	C1-C2-C3	-3.22	120.93	126.20
5	S	2005	BPH	C3B-C4B-NB	3.17	112.67	108.05
5	M	1005	BPH	CMA-C3A-C4A	-3.15	107.81	114.61
5	M	1005	BPH	O2A-C1-C2	-3.14	96.02	108.11
5	L	1006	BPH	O1D-CGD-CBD	-3.14	119.97	124.72
5	R	2006	BPH	C1-O2A-CGA	3.13	124.23	116.65
5	M	1005	BPH	C3B-C4B-NB	3.12	112.60	108.05
9	S	2013	LDA	O1-N1-C1	3.10	116.89	109.27
4	S	2003	BCL	C3D-C2D-C1D	3.07	110.02	105.83
4	R	2002	BCL	CHD-C1D-ND	-3.07	120.49	124.80
4	L	1002	BCL	C4-C3-C5	3.05	120.53	115.23
4	M	1003	BCL	C4D-C3D-CAD	-3.05	104.79	108.11
4	R	2004	BCL	C7-C6-C5	-3.05	105.14	113.26
4	R	2002	BCL	CHA-C4D-ND	-3.02	126.31	132.55
4	R	2002	BCL	C4D-C3D-CAD	-3.02	104.82	108.11
6	L	1009	U10	C30-C29-C31	2.97	120.39	115.23
4	M	1003	BCL	C1D-ND-C4D	-2.94	104.25	106.31
4	M	1003	BCL	C15-C13-C12	2.90	126.77	112.07
4	R	2004	BCL	CED-O2D-CGD	-2.88	109.38	115.92
4	R	2004	BCL	CHA-C4D-ND	-2.88	126.61	132.55
5	M	1005	BPH	C4A-C3A-C2A	2.86	105.56	102.84
5	S	2005	BPH	O1D-CGD-CBD	-2.86	120.39	124.72
5	R	2006	BPH	C2D-C1D-ND	2.86	111.50	109.43
4	R	2002	BCL	C3D-C2D-C1D	2.85	109.73	105.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	R	2009	U10	C3M-O3-C3	2.85	126.49	116.47
4	R	2002	BCL	CED-O2D-CGD	2.85	122.37	115.92
5	S	2005	BPH	O2A-C1-C2	-2.84	97.19	108.11
9	M	1012	LDA	O1-N1-C1	2.83	116.22	109.27
6	R	2009	U10	C8-C7-C6	2.83	119.06	112.08
4	S	2003	BCL	O2D-CGD-CBD	2.82	116.16	111.23
4	L	1004	BCL	C1D-ND-C4D	-2.82	104.33	106.31
4	R	2004	BCL	O2D-CGD-CBD	2.82	116.15	111.23
6	R	2009	U10	C1-C6-C5	-2.81	116.89	119.62
5	R	2006	BPH	O1D-CGD-CBD	-2.81	120.47	124.72
5	L	1006	BPH	C2D-C1D-ND	2.80	111.46	109.43
4	L	1001	BCL	CMA-C3A-C4A	-2.80	104.25	111.77
4	L	1002	BCL	CMA-C3A-C4A	-2.79	104.27	111.77
5	L	1006	BPH	C7-C6-C5	-2.79	105.84	113.26
4	L	1001	BCL	OBD-CAD-C3D	-2.78	121.93	128.42
4	L	1001	BCL	C3D-C2D-C1D	2.76	109.60	105.83
6	M	1008	U10	C31-C29-C30	2.75	120.92	114.59
9	S	2012	LDA	O1-N1-C1	2.74	115.99	109.27
6	M	1008	U10	O5-C5-C6	-2.73	116.50	121.79
5	R	2006	BPH	OBD-CAD-C3D	-2.73	123.63	127.89
6	L	1009	U10	C7-C6-C1	-2.70	120.26	124.89
4	L	1004	BCL	C3D-C2D-C1D	2.70	109.51	105.83
5	L	1006	BPH	CMB-C2B-C3B	2.70	130.07	124.68
4	L	1001	BCL	OBb-CAB-CBB	-2.67	113.80	119.77
6	M	1008	U10	C17-C18-C19	-2.65	121.55	127.62
4	L	1001	BCL	CBB-CAB-C3B	2.65	126.00	120.40
9	M	1013	LDA	O1-N1-C1	2.65	115.78	109.27
5	S	2005	BPH	C1C-C2C-C3C	-2.65	100.32	102.84
6	M	1008	U10	C1M-C1-C6	-2.65	120.10	124.45
4	R	2001	BCL	OBD-CAD-C3D	-2.64	122.23	128.42
4	M	1003	BCL	CED-O2D-CGD	2.64	121.91	115.92
4	L	1002	BCL	CHA-C1A-NA	-2.64	120.41	126.39
5	M	1005	BPH	CMB-C2B-C3B	2.64	129.96	124.68
5	M	1005	BPH	OBD-CAD-CBD	-2.63	121.96	125.82
4	L	1004	BCL	C4-C3-C5	2.63	119.79	115.23
4	L	1004	BCL	CAC-C3C-C4C	-2.63	106.75	112.58
4	L	1001	BCL	CHA-C1A-NA	-2.62	120.46	126.39
6	R	2009	U10	C1M-C1-C6	-2.60	120.18	124.45
4	R	2001	BCL	C1-C2-C3	2.60	130.97	126.76
5	R	2006	BPH	C7-C6-C5	-2.59	106.35	113.26
4	S	2003	BCL	C2B-C1B-NB	2.59	113.01	110.33
4	R	2002	BCL	CMA-C3A-C4A	-2.56	104.90	111.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L	1001	BCL	CHA-C4D-ND	-2.56	127.28	132.55
4	S	2003	BCL	CHA-C1A-NA	-2.55	120.61	126.39
4	M	1003	BCL	C3D-C2D-C1D	2.55	109.31	105.83
6	S	2008	U10	C15-C14-C16	2.55	119.66	115.23
4	S	2003	BCL	CAC-C3C-C4C	-2.55	106.93	112.58
4	R	2004	BCL	CAC-C3C-C4C	-2.54	106.95	112.58
4	L	1004	BCL	CHA-C4D-ND	-2.53	127.32	132.55
6	M	1008	U10	C12-C13-C14	-2.52	121.85	127.62
4	L	1001	BCL	O2D-CGD-CBD	2.51	115.62	111.23
4	R	2001	BCL	C2A-C3A-C4A	2.50	105.92	101.87
4	R	2001	BCL	CMD-C2D-C3D	-2.50	121.95	127.69
4	M	1003	BCL	CHA-C4D-ND	-2.49	127.40	132.55
6	S	2008	U10	C10-C9-C11	2.49	119.55	115.23
5	S	2005	BPH	C4A-C3A-C2A	2.49	105.21	102.84
5	M	1005	BPH	C1C-C2C-C3C	2.48	105.20	102.84
4	R	2001	BCL	CMA-C3A-C4A	-2.46	105.15	111.77
5	R	2006	BPH	CMB-C2B-C3B	2.46	129.60	124.68
6	S	2008	U10	C4M-O4-C4	2.46	125.11	116.47
4	L	1002	BCL	CHA-C4D-ND	-2.46	127.48	132.55
5	R	2006	BPH	C2B-C1B-NB	2.44	111.19	109.43
4	L	1002	BCL	C3D-C2D-C1D	2.43	109.15	105.83
9	M	1014	LDA	O1-N1-C1	2.41	115.19	109.27
4	L	1001	BCL	O2A-C1-C2	-2.41	98.83	108.11
4	M	1003	BCL	C2C-C3C-C4C	2.41	104.94	101.34
4	S	2003	BCL	O2A-CGA-CBA	2.41	119.17	111.83
4	S	2003	BCL	CHA-C4D-ND	-2.39	127.61	132.55
4	M	1003	BCL	OBD-CAD-C3D	-2.39	122.83	128.42
4	R	2002	BCL	C6-C5-C3	2.39	119.29	113.47
4	L	1004	BCL	CHA-C1A-NA	-2.38	121.00	126.39
5	S	2005	BPH	OBD-CAD-CBD	-2.36	122.36	125.82
9	M	1014	LDA	C6-C5-C4	-2.35	102.48	114.37
4	L	1004	BCL	C3B-C4B-NB	2.34	112.85	109.76
4	M	1003	BCL	CAC-C3C-C4C	-2.33	107.41	112.58
4	R	2002	BCL	CHA-C1A-NA	-2.33	121.11	126.39
6	L	1009	U10	C1M-C1-C6	-2.33	120.62	124.45
5	L	1006	BPH	C1-O2A-CGA	2.33	122.29	116.65
6	S	2008	U10	C1M-C1-C6	-2.33	120.63	124.45
5	L	1006	BPH	C1B-NB-C4B	-2.32	105.43	108.82
5	S	2005	BPH	CMB-C2B-C3B	2.31	129.29	124.68
5	S	2005	BPH	CMC-C2C-C1C	-2.29	109.69	114.61
4	L	1001	BCL	CHB-C4A-NA	2.28	127.69	124.40
4	L	1002	BCL	CAC-C3C-C4C	-2.28	107.52	112.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	M	1003	BCL	CMD-C2D-C3D	-2.28	122.46	127.69
5	M	1005	BPH	CMC-C2C-C1C	-2.27	109.72	114.61
4	L	1004	BCL	O2A-C1-C2	-2.26	99.39	108.11
4	M	1003	BCL	O2D-CGD-CBD	2.26	115.18	111.23
4	L	1004	BCL	OBD-CAD-C3D	-2.26	123.14	128.42
4	R	2002	BCL	C4A-NA-C1A	2.25	107.71	106.68
4	R	2002	BCL	CAC-C3C-C4C	-2.25	107.58	112.58
4	R	2001	BCL	CHA-C4D-ND	-2.24	127.92	132.55
4	M	1003	BCL	CHA-C1A-NA	-2.23	121.33	126.39
4	R	2004	BCL	C2B-C1B-NB	2.23	112.64	110.33
4	R	2001	BCL	CHC-C4B-NB	-2.23	120.70	124.05
9	M	1013	LDA	C6-C5-C4	-2.23	103.09	114.37
5	M	1005	BPH	OBD-CAD-C3D	-2.23	124.42	127.89
4	L	1001	BCL	CHB-C1B-NB	-2.23	120.71	124.05
4	R	2004	BCL	C6-C5-C3	-2.22	108.05	113.47
5	L	1006	BPH	CED-O2D-CGD	2.22	120.95	115.92
6	L	1009	U10	C7-C6-C5	2.20	121.08	118.52
6	L	1009	U10	C15-C14-C16	2.20	119.05	115.23
9	M	1012	LDA	C6-C5-C4	-2.20	103.24	114.37
5	S	2005	BPH	OBD-CAD-C3D	-2.20	124.46	127.89
4	S	2003	BCL	C1-O2A-CGA	2.19	121.96	116.65
6	L	1009	U10	C3-C2-C1	2.19	122.42	118.10
4	R	2004	BCL	C3B-C4B-NB	2.19	112.64	109.76
4	R	2002	BCL	CMC-C2C-C3C	-2.18	105.57	113.98
4	M	1003	BCL	C1-O2A-CGA	2.17	121.91	116.65
4	L	1002	BCL	C2B-C1B-NB	2.17	112.57	110.33
4	R	2001	BCL	C2C-C3C-C4C	2.17	104.58	101.34
4	L	1002	BCL	C6-C5-C3	2.16	118.73	113.47
4	L	1004	BCL	C15-C13-C12	-2.15	101.18	112.07
4	L	1001	BCL	C2C-C3C-C4C	2.15	104.55	101.34
5	R	2006	BPH	C1B-NB-C4B	-2.14	105.70	108.82
5	S	2005	BPH	CED-O2D-CGD	2.13	120.75	115.92
4	R	2002	BCL	C2C-C3C-C4C	2.12	104.52	101.34
4	S	2003	BCL	C7-C6-C5	-2.11	107.63	113.26
4	L	1004	BCL	O1D-CGD-CBD	-2.11	120.36	124.52
4	R	2004	BCL	CHD-C1D-ND	-2.10	121.85	124.80
4	M	1003	BCL	C2A-C1A-CHA	2.10	127.50	123.87
5	R	2006	BPH	OBD-CAD-CBD	-2.10	122.75	125.82
4	L	1002	BCL	C2C-C3C-C4C	2.08	104.45	101.34
4	R	2001	BCL	CHA-C1A-NA	-2.08	121.69	126.39
4	L	1004	BCL	C2B-C1B-NB	2.07	112.47	110.33
4	R	2004	BCL	CMC-C2C-C3C	-2.06	106.01	113.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	M	1014	LDA	C4-C3-C2	-2.06	103.97	114.37
6	R	2009	U10	C3-C2-C1	2.05	122.16	118.10
4	R	2001	BCL	C1D-ND-C4D	-2.05	104.88	106.31
9	S	2014	LDA	C4-C3-C2	-2.04	104.04	114.37
4	L	1002	BCL	CAA-C2A-C1A	-2.04	105.29	111.97
6	L	1009	U10	C30-C29-C28	-2.04	118.39	123.63
4	L	1002	BCL	C2A-C3A-C4A	2.04	105.16	101.87
4	R	2004	BCL	CHA-C1A-NA	-2.04	121.78	126.39
4	L	1002	BCL	CHD-C1D-ND	-2.03	121.94	124.80
4	L	1004	BCL	CHB-C4A-NA	2.03	127.33	124.40
4	L	1001	BCL	C1-C2-C3	2.03	130.04	126.76
4	R	2001	BCL	O1D-CGD-CBD	-2.03	120.52	124.52
4	S	2003	BCL	CHC-C4B-NB	-2.01	121.03	124.05

There are no chirality outliers.

All (107) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	R	2002	BCL	CBD-CGD-O2D-CED
4	R	2004	BCL	CBD-CGD-O2D-CED
5	M	1005	BPH	C2-C3-C5-C6
5	R	2006	BPH	C4C-C3C-CAC-CBC
5	R	2006	BPH	C2C-C3C-CAC-CBC
5	S	2005	BPH	C4C-C3C-CAC-CBC
5	S	2005	BPH	C2-C3-C5-C6
5	S	2005	BPH	C4-C3-C5-C6
5	S	2005	BPH	C3-C5-C6-C7
9	M	1012	LDA	C2-C1-N1-CM2
9	M	1013	LDA	N1-C1-C2-C3
9	M	1014	LDA	C2-C1-N1-O1
9	M	1014	LDA	C2-C1-N1-CM1
9	M	1014	LDA	N1-C1-C2-C3
9	S	2012	LDA	N1-C1-C2-C3
9	S	2013	LDA	C2-C1-N1-CM1
9	S	2013	LDA	N1-C1-C2-C3
9	S	2014	LDA	C2-C1-N1-O1
9	S	2014	LDA	C2-C1-N1-CM1
4	R	2002	BCL	O1D-CGD-O2D-CED
4	R	2004	BCL	O1D-CGD-O2D-CED
6	L	1009	U10	C14-C16-C17-C18
6	L	1009	U10	C19-C21-C22-C23
6	M	1008	U10	C24-C26-C27-C28

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Mol	Chain	Res	Type	Atoms
5	L	1006	BPH	C10-C11-C12-C13
4	R	2002	BCL	C4-C3-C5-C6
9	S	2013	LDA	C2-C3-C4-C5
9	M	1012	LDA	C4-C5-C6-C7
9	S	2012	LDA	C6-C7-C8-C9
9	S	2012	LDA	C2-C3-C4-C5
9	M	1014	LDA	C6-C7-C8-C9
4	R	2002	BCL	C2-C3-C5-C6
9	M	1014	LDA	C1-C2-C3-C4
9	M	1014	LDA	C11-C10-C9-C8
9	S	2012	LDA	C1-C2-C3-C4
9	S	2014	LDA	C11-C10-C9-C8
5	S	2005	BPH	C2C-C3C-CAC-CBC
6	L	1009	U10	C18-C19-C21-C22
5	R	2006	BPH	C2-C3-C5-C6
9	M	1012	LDA	C1-C2-C3-C4
9	S	2013	LDA	C1-C2-C3-C4
5	R	2006	BPH	C4-C3-C5-C6
9	S	2014	LDA	C1-C2-C3-C4
9	S	2014	LDA	C9-C10-C11-C12
9	S	2014	LDA	C7-C8-C9-C10
9	S	2014	LDA	C4-C5-C6-C7
4	S	2003	BCL	C14-C13-C15-C16
9	S	2013	LDA	C9-C10-C11-C12
4	L	1002	BCL	C15-C16-C17-C18
5	M	1005	BPH	C4-C3-C5-C6
9	S	2012	LDA	C11-C10-C9-C8
9	M	1013	LDA	C4-C5-C6-C7
6	L	1009	U10	C20-C19-C21-C22
5	L	1006	BPH	C15-C16-C17-C18
9	M	1012	LDA	C6-C7-C8-C9
4	R	2002	BCL	C15-C16-C17-C18
9	S	2013	LDA	C6-C7-C8-C9
5	L	1006	BPH	C2-C3-C5-C6
4	S	2003	BCL	C12-C13-C15-C16
5	R	2006	BPH	C15-C16-C17-C18
6	L	1009	U10	C2-C3-O3-C3M
5	L	1006	BPH	C4-C3-C5-C6
9	M	1013	LDA	C2-C3-C4-C5
6	R	2009	U10	C5-C6-C7-C8
9	M	1014	LDA	C2-C1-N1-CM2
9	S	2013	LDA	C2-C1-N1-CM2

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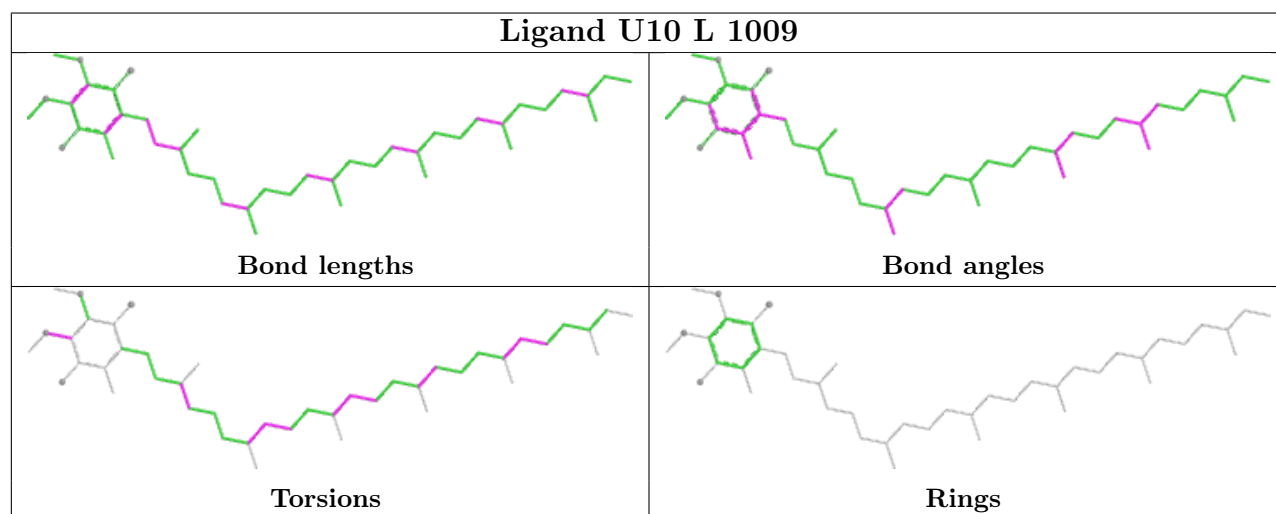
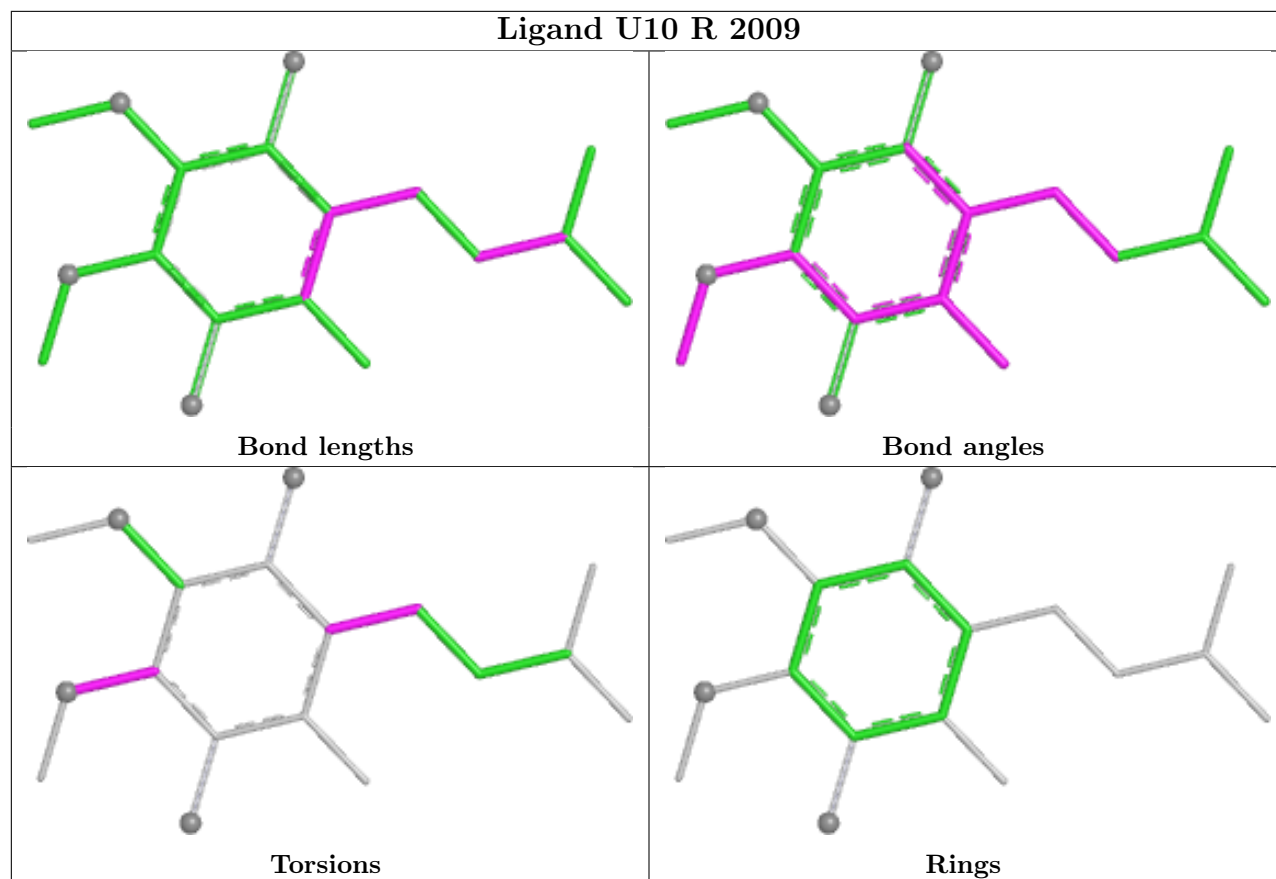
Mol	Chain	Res	Type	Atoms
5	L	1006	BPH	C16-C17-C18-C20
6	L	1009	U10	C12-C11-C9-C10
9	M	1012	LDA	C2-C1-N1-O1
6	M	1008	U10	C5-C4-O4-C4M
6	R	2009	U10	C2-C3-O3-C3M
5	L	1006	BPH	C16-C17-C18-C19
4	M	1003	BCL	C14-C13-C15-C16
4	R	2004	BCL	C3-C5-C6-C7
6	L	1009	U10	C29-C31-C32-C33
6	L	1009	U10	C4-C3-O3-C3M
4	R	2001	BCL	C3A-C2A-CAA-CBA
6	L	1009	U10	C12-C11-C9-C8
6	S	2008	U10	C5-C4-O4-C4M
4	L	1004	BCL	C12-C13-C15-C16
6	L	1009	U10	C15-C14-C16-C17
6	L	1009	U10	C28-C29-C31-C32
5	L	1006	BPH	C8-C10-C11-C12
5	S	2005	BPH	O1A-CGA-O2A-C1
4	R	2004	BCL	C13-C15-C16-C17
9	M	1013	LDA	C11-C10-C9-C8
9	M	1012	LDA	C2-C3-C4-C5
5	S	2005	BPH	CBA-CGA-O2A-C1
9	M	1012	LDA	C9-C10-C11-C12
6	L	1009	U10	C25-C24-C26-C27
4	L	1004	BCL	C14-C13-C15-C16
6	L	1009	U10	C23-C24-C26-C27
4	R	2002	BCL	C2A-CAA-CBA-CGA
4	R	2004	BCL	C12-C13-C15-C16
6	S	2008	U10	C21-C22-C23-C24
9	S	2013	LDA	C4-C5-C6-C7
4	M	1003	BCL	C11-C12-C13-C15
4	R	2004	BCL	C2C-C3C-CAC-CBC
6	L	1009	U10	C30-C29-C31-C32
4	R	2004	BCL	C14-C13-C15-C16
9	M	1014	LDA	C4-C5-C6-C7
9	S	2013	LDA	C2-C1-N1-O1
4	L	1002	BCL	CAD-CBD-CGD-O2D
5	L	1006	BPH	CAD-CBD-CGD-O2D
5	R	2006	BPH	CAD-CBD-CGD-O2D
4	M	1003	BCL	C5-C6-C7-C8
4	M	1003	BCL	C13-C15-C16-C17

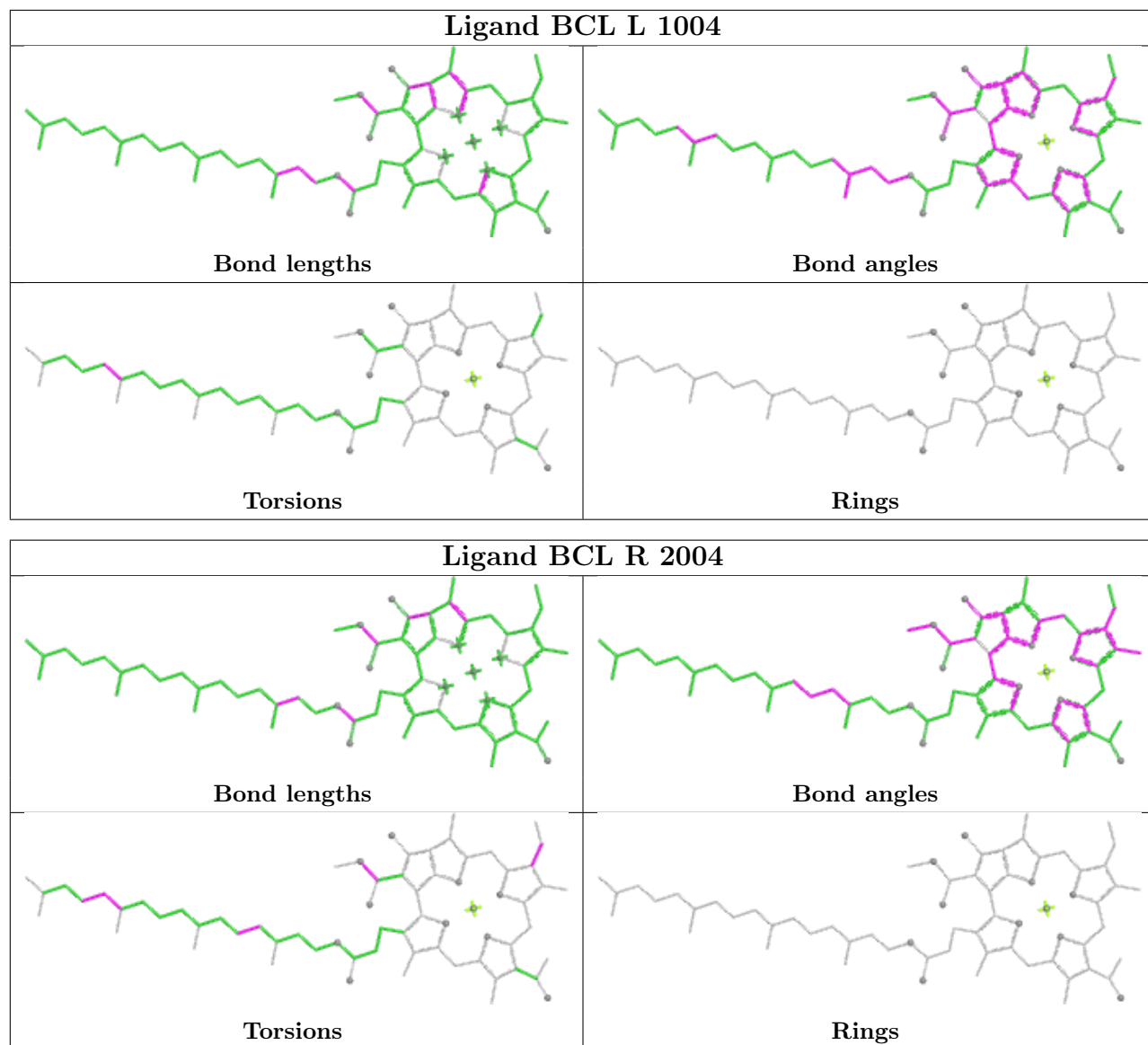
There are no ring outliers.

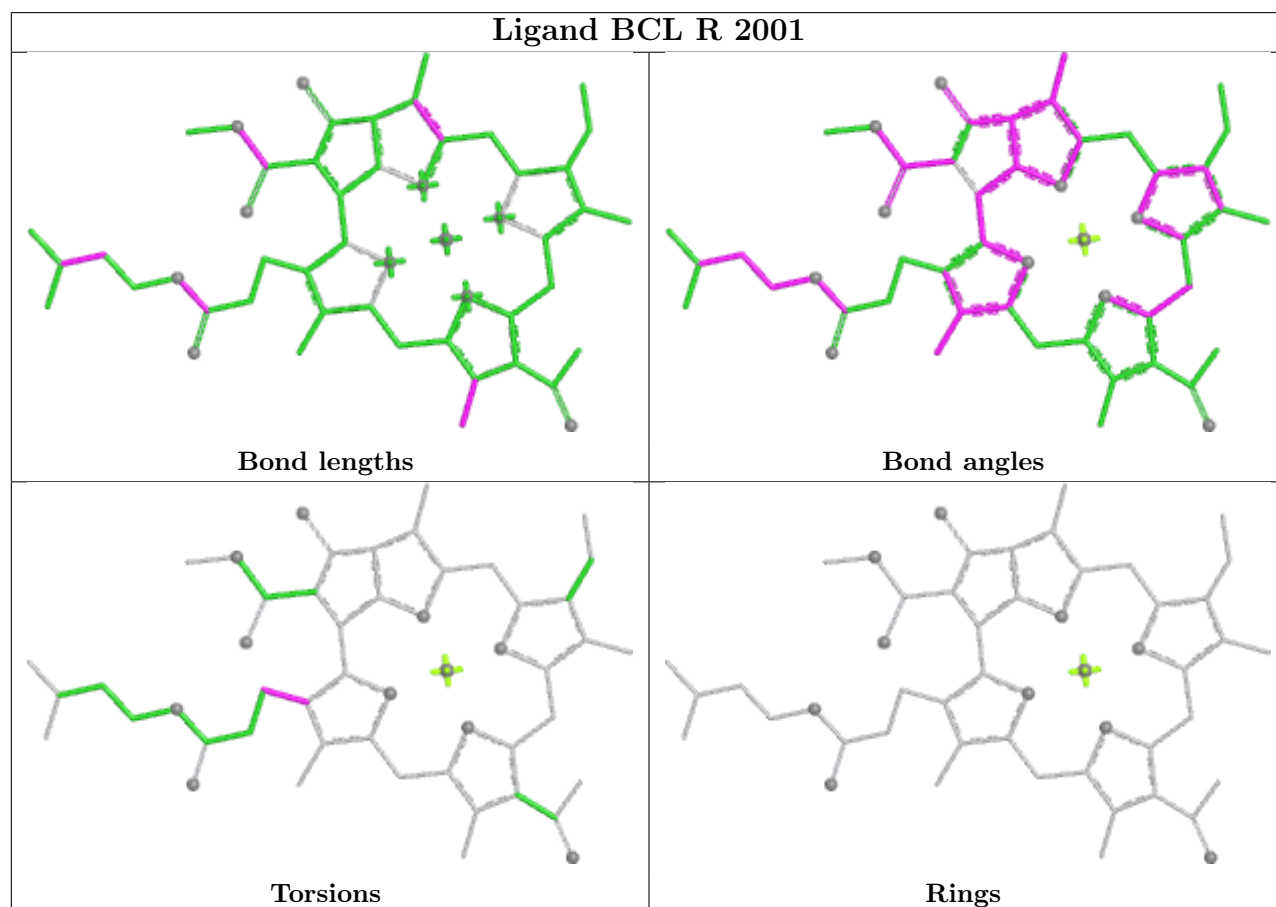
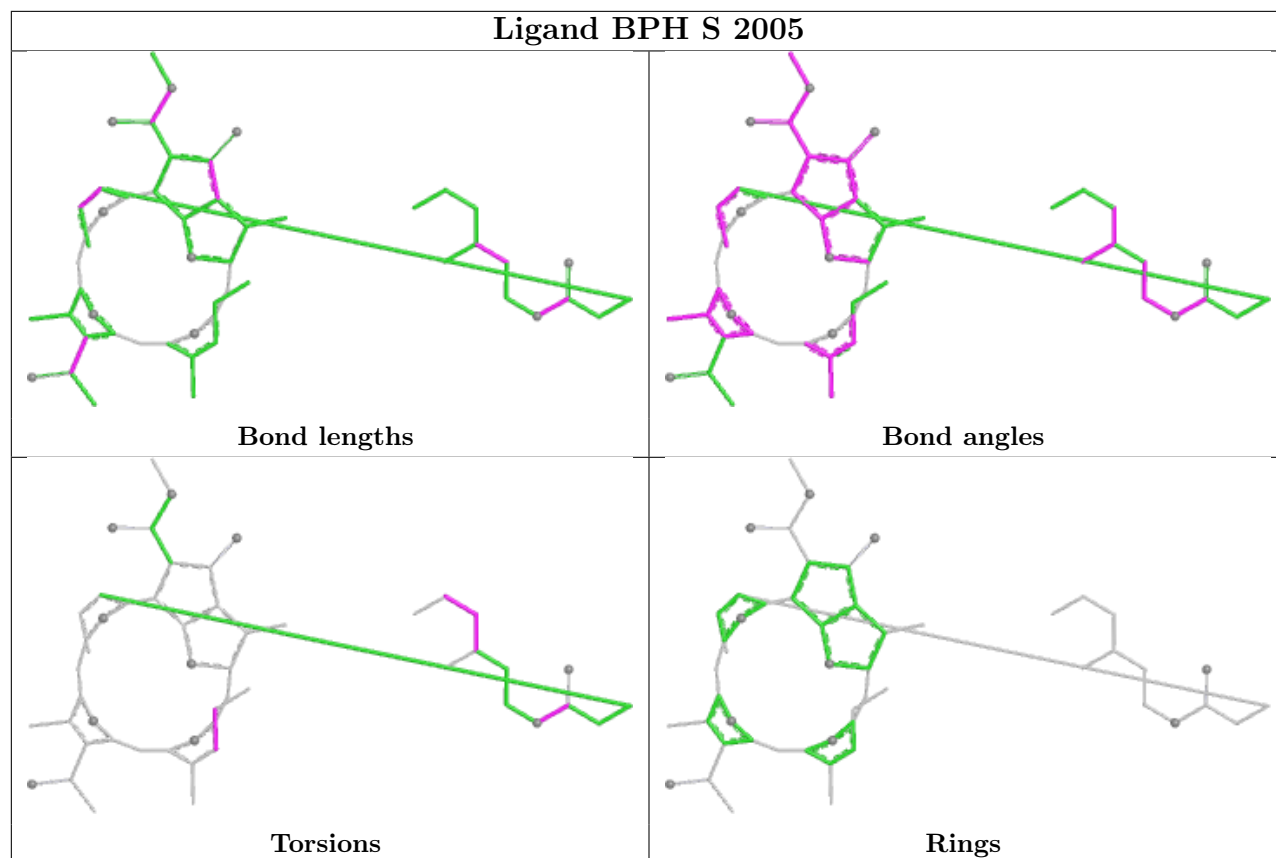
22 monomers are involved in 82 short contacts:

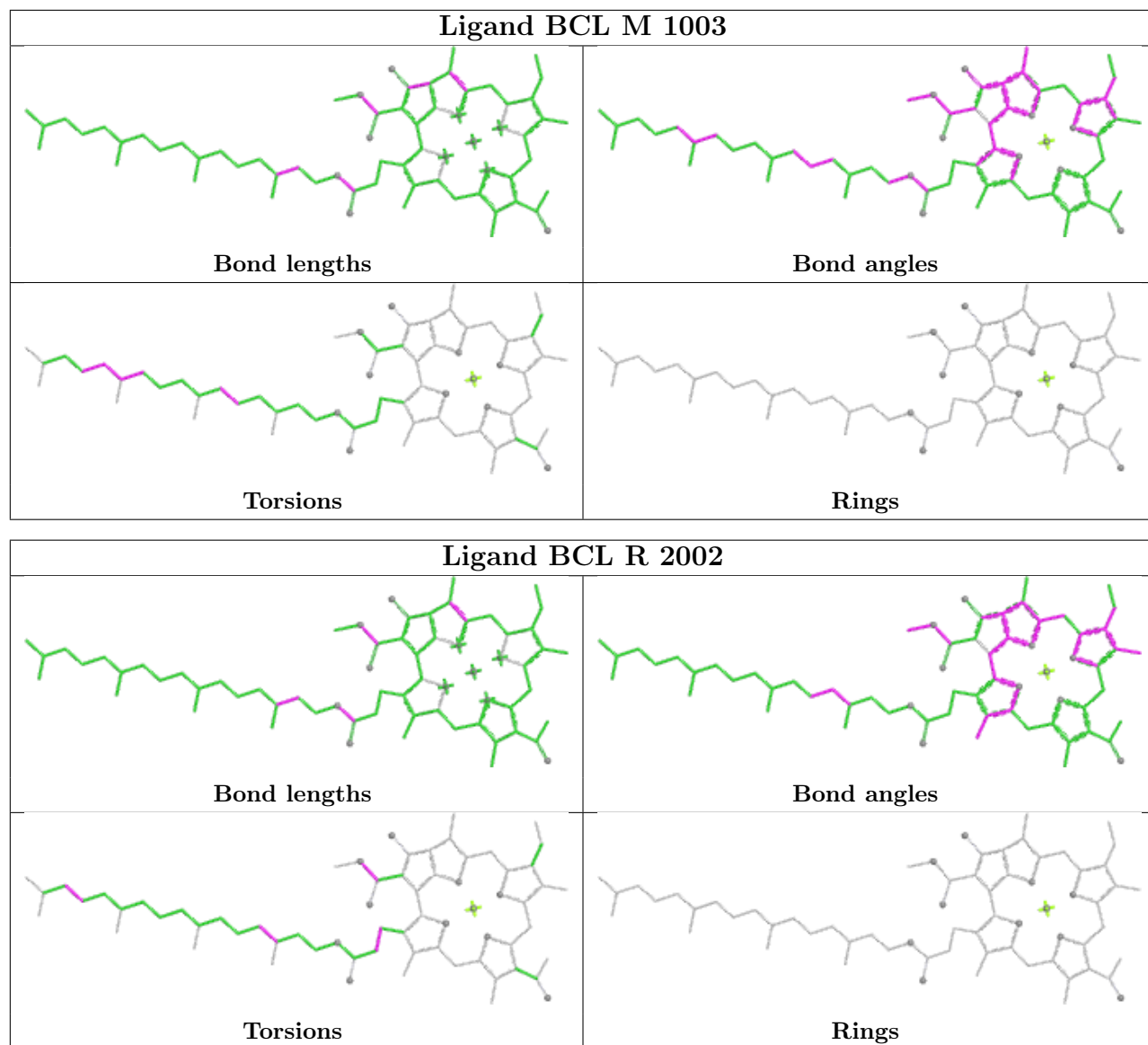
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	S	2014	LDA	2	0
6	R	2009	U10	3	0
9	M	1014	LDA	6	0
6	L	1009	U10	2	0
4	L	1004	BCL	6	0
4	R	2004	BCL	5	0
5	S	2005	BPH	3	0
4	R	2001	BCL	3	0
9	S	2012	LDA	2	0
4	M	1003	BCL	7	0
4	R	2002	BCL	8	0
9	M	1012	LDA	1	0
5	M	1005	BPH	5	0
4	L	1001	BCL	4	0
5	L	1006	BPH	8	0
9	M	1013	LDA	1	0
9	S	2013	LDA	1	0
4	S	2003	BCL	5	0
6	S	2008	U10	2	0
5	R	2006	BPH	15	0
4	L	1002	BCL	9	0
6	M	1008	U10	3	0

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

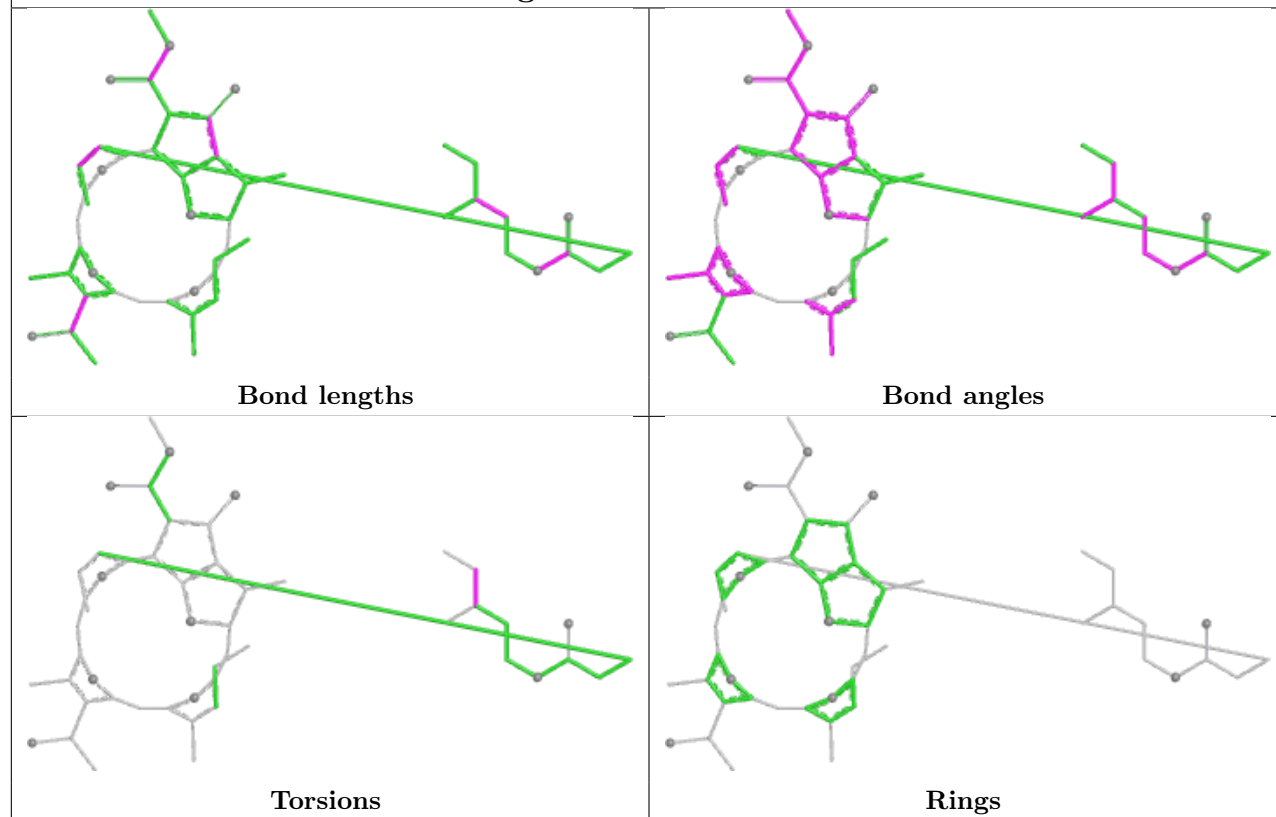




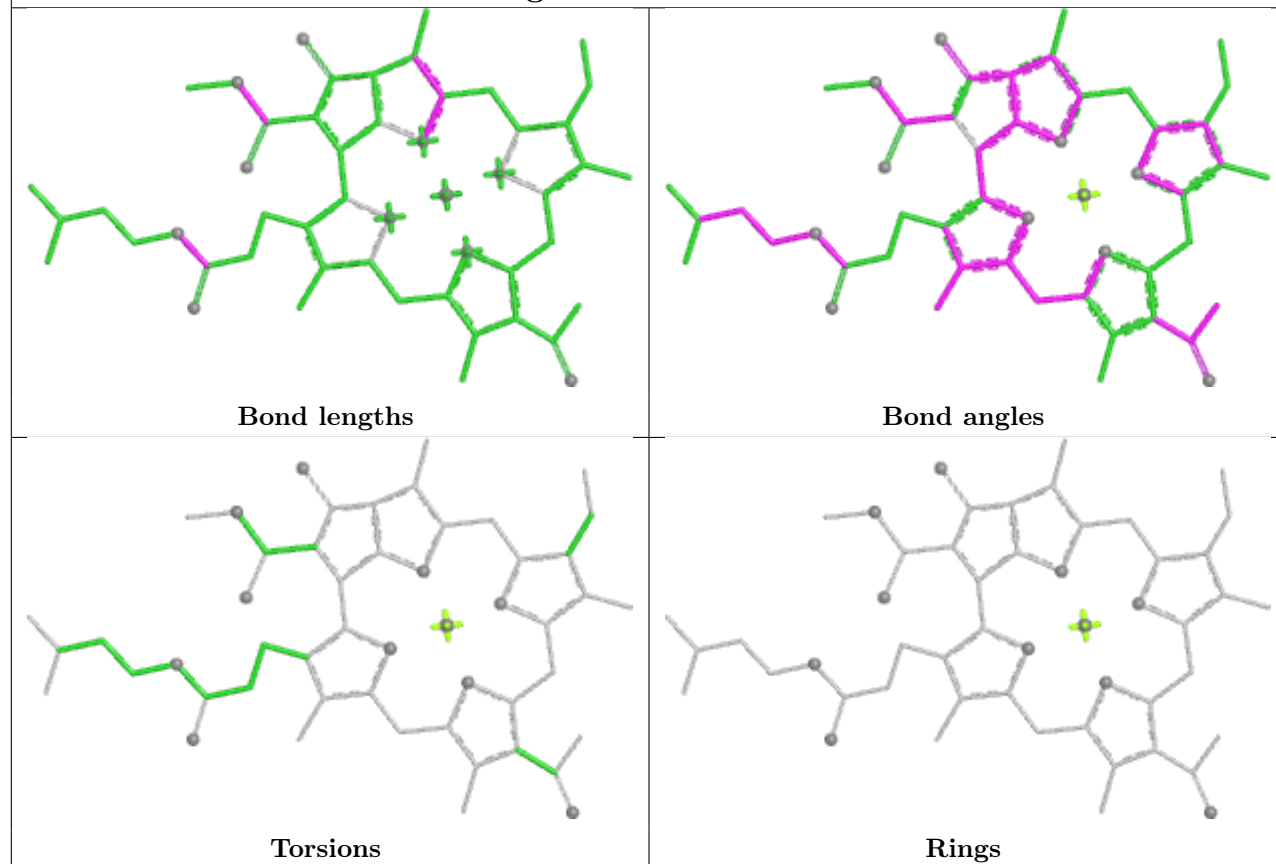


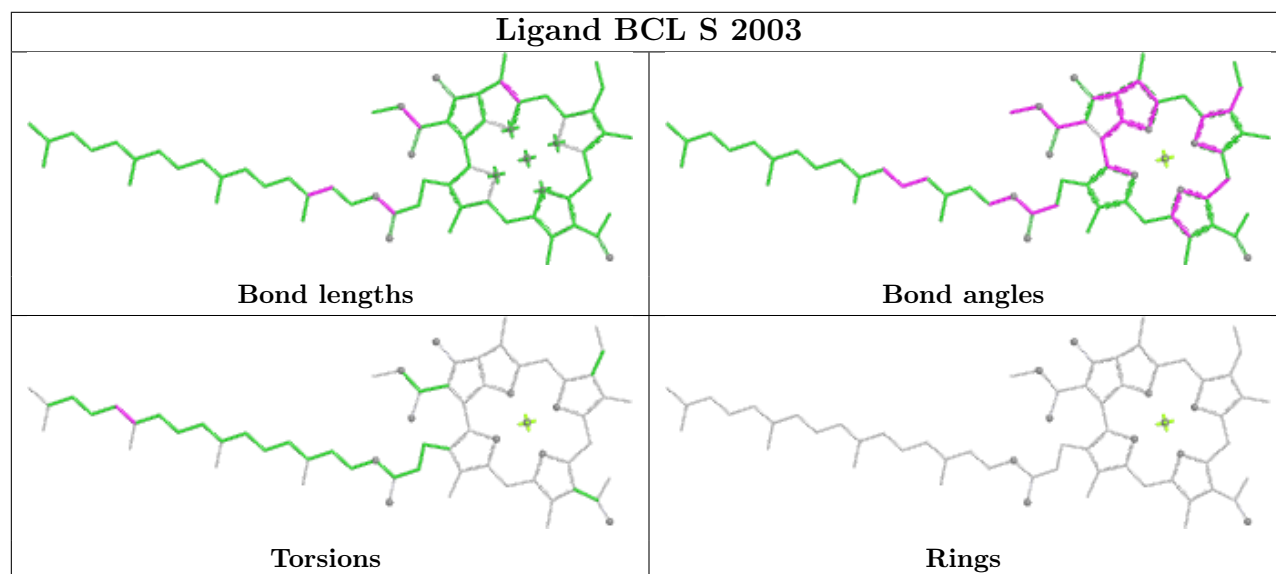
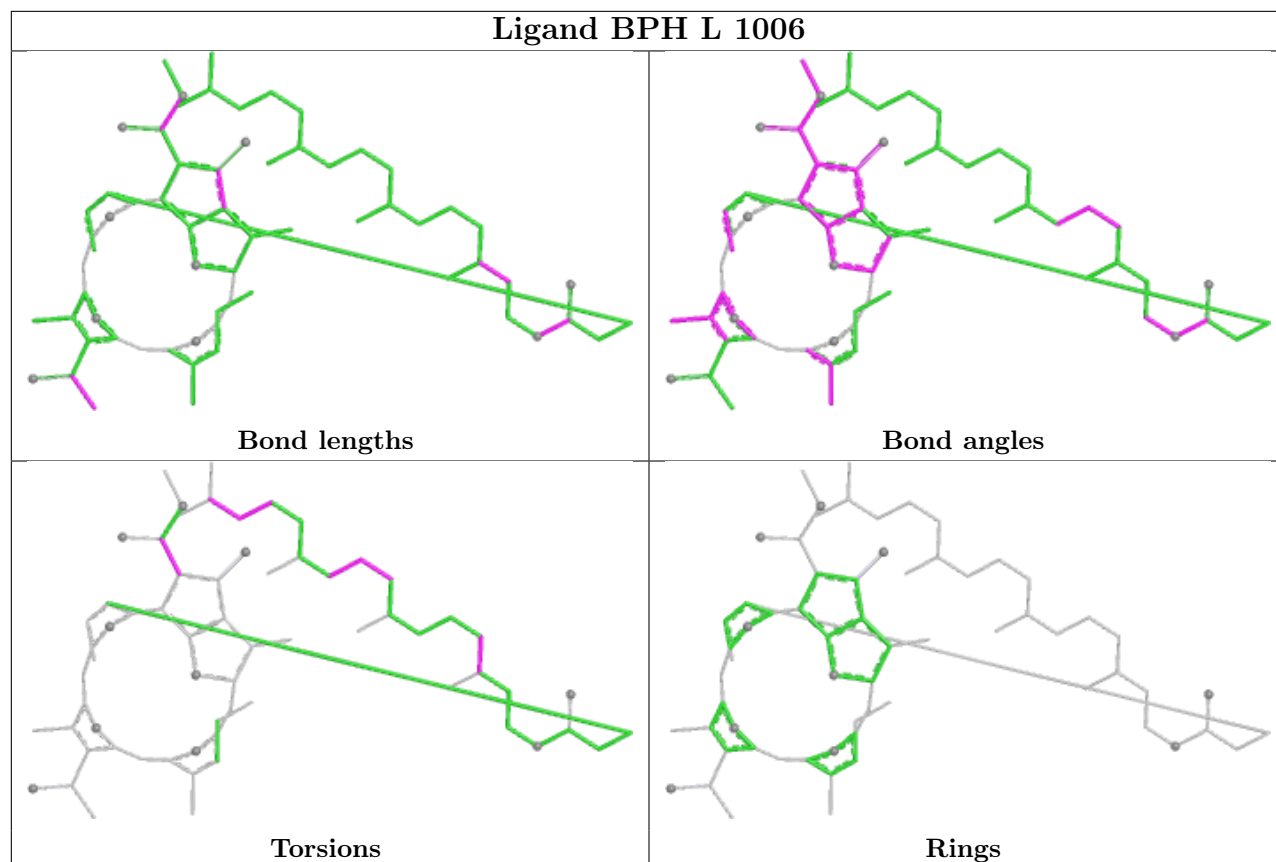


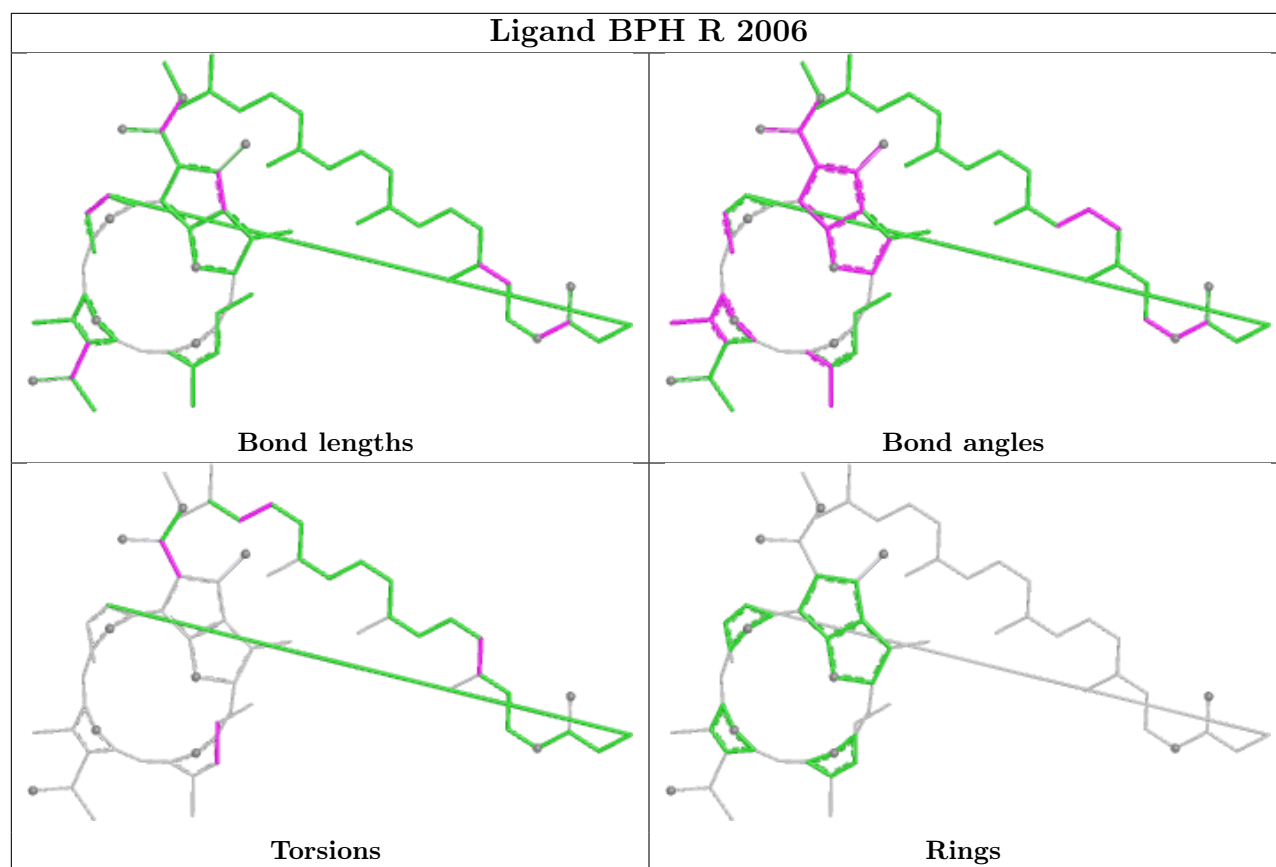
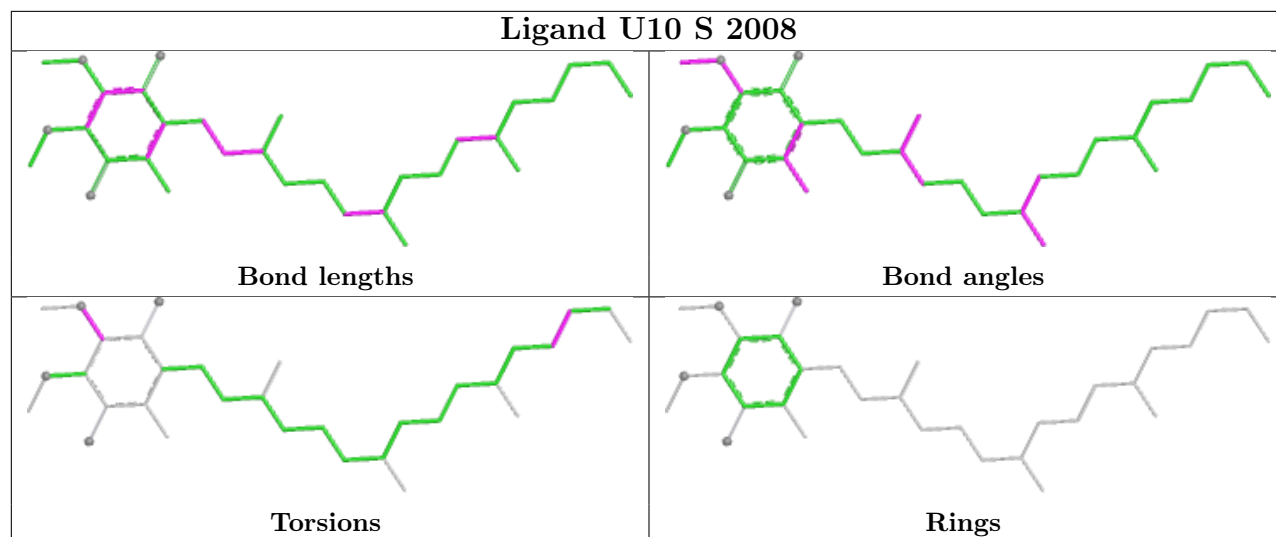
Ligand BPH M 1005

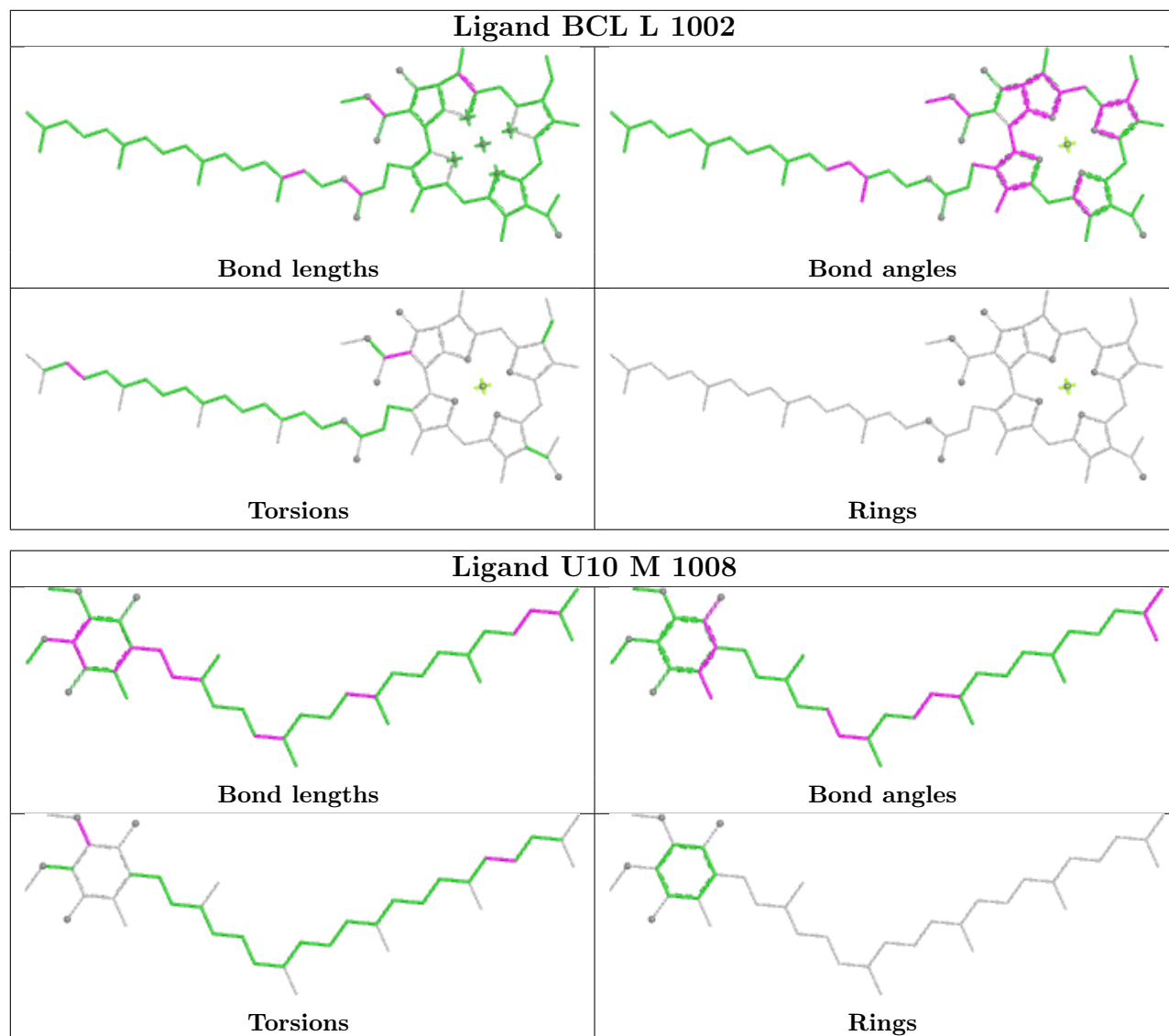


Ligand BCL L 1001









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	L	281/281 (100%)	0.69	34 (12%) 8 7	26, 43, 67, 74	0
1	R	281/281 (100%)	0.52	13 (4%) 37 33	26, 44, 67, 74	0
2	M	299/307 (97%)	0.17	6 (2%) 65 61	28, 36, 48, 67	0
2	S	299/307 (97%)	0.15	4 (1%) 75 71	29, 37, 49, 67	0
3	H	246/260 (94%)	0.40	10 (4%) 41 37	33, 43, 66, 82	0
3	T	246/260 (94%)	0.42	12 (4%) 35 31	34, 44, 66, 82	0
All	All	1652/1696 (97%)	0.39	79 (4%) 35 31	26, 40, 65, 82	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	M	301	HIS	5.3
1	L	84	GLY	4.4
3	T	69	GLY	4.3
1	R	1	ALA	4.3
2	S	301	HIS	4.0
3	H	252	VAL	3.8
3	T	256	LEU	3.8
1	L	55	LEU	3.6
3	H	253	ALA	3.5
1	L	275	ILE	3.5
3	H	256	LEU	3.5
1	L	79	PRO	3.5
1	L	51	TRP	3.4
1	R	276	PRO	3.3
2	S	77	GLN	3.2
1	L	83	GLY	3.2
1	R	281	GLY	3.2
1	R	275	ILE	3.2
2	M	111	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
3	H	254	ALA	3.1
1	L	58	THR	3.1
2	M	68	PHE	3.1
3	T	79	GLU	3.0
3	T	68	HIS	3.0
2	M	3	TYR	3.0
1	R	271	TRP	2.9
3	H	80	SER	2.9
1	L	81	ALA	2.9
2	M	90	PHE	2.9
1	L	85	LEU	2.8
1	L	269	LEU	2.8
1	L	59	TRP	2.8
1	L	80	LEU	2.8
3	T	80	SER	2.7
3	H	69	GLY	2.7
1	R	51	TRP	2.7
3	H	255	MET	2.7
1	L	272	TRP	2.6
1	L	281	GLY	2.6
1	L	271	TRP	2.6
1	R	266	TRP	2.6
1	R	274	ASN	2.5
1	L	49	ILE	2.4
1	L	68	PRO	2.4
1	R	50	ALA	2.4
3	T	253	ALA	2.4
3	T	93	SER	2.4
1	L	35	GLY	2.4
1	L	62	GLN	2.4
3	T	92	VAL	2.4
1	L	67	TYR	2.4
3	T	51	ALA	2.4
1	L	77	GLY	2.3
1	R	7	ARG	2.3
1	L	2	LEU	2.3
1	L	66	VAL	2.3
1	R	10	ARG	2.3
1	L	50	ALA	2.2
2	S	3	TYR	2.3
1	L	276	PRO	2.2
3	T	251	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	L	43	ALA	2.2
1	L	274	ASN	2.2
3	H	90	THR	2.1
2	S	87	ARG	2.1
1	L	63	LEU	2.1
3	H	47	GLY	2.1
3	T	77	GLY	2.1
2	M	300	ASN	2.1
1	L	54	VAL	2.1
1	L	86	TRP	2.1
1	L	142	TRP	2.1
1	L	19	GLY	2.1
3	T	46	ASP	2.1
1	L	41	PHE	2.0
1	R	279	ILE	2.0
3	H	50	ALA	2.0
1	L	47	ILE	2.0
1	R	25	TRP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	LDA	S	2013	16/16	0.70	0.23	58,59,63,63	0
6	U10	L	1009	44/63	0.71	0.26	67,78,87,87	0
9	LDA	S	2012	16/16	0.75	0.25	50,54,58,58	0
9	LDA	M	1014	16/16	0.75	0.28	51,52,55,55	0
9	LDA	S	2014	16/16	0.75	0.18	54,57,60,60	0

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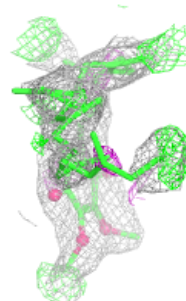
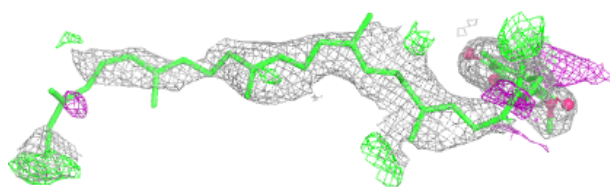
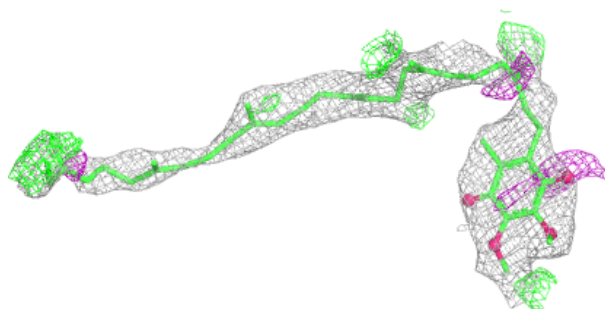
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	LDA	M	1013	16/16	0.76	0.17	47,51,55,55	0
9	LDA	M	1012	16/16	0.78	0.20	54,56,59,59	0
6	U10	R	2009	18/63	0.78	0.19	61,62,63,63	0
5	BPH	L	1006	65/65	0.91	0.10	26,30,39,39	0
5	BPH	R	2006	65/65	0.91	0.11	42,45,51,51	0
4	BCL	R	2002	66/66	0.92	0.10	36,38,43,44	0
4	BCL	R	2004	66/66	0.92	0.10	30,33,53,54	0
6	U10	M	1008	38/63	0.92	0.10	27,30,45,45	0
4	BCL	S	2003	66/66	0.92	0.10	33,34,48,49	0
4	BCL	R	2001	51/66	0.92	0.09	30,32,41,43	0
6	U10	S	2008	32/63	0.93	0.10	41,43,46,47	0
4	BCL	L	1002	66/66	0.94	0.09	27,32,33,36	0
5	BPH	S	2005	52/65	0.94	0.07	30,32,41,41	0
4	BCL	M	1003	66/66	0.95	0.09	27,29,39,43	0
4	BCL	L	1001	51/66	0.95	0.07	26,28,33,34	0
4	BCL	L	1004	66/66	0.95	0.08	25,27,43,44	0
5	BPH	M	1005	51/65	0.96	0.06	23,25,33,34	0
8	CL	S	2011	1/1	0.96	0.15	59,59,59,59	0
8	CL	M	1011	1/1	0.97	0.14	48,48,48,48	0
7	FE2	M	1007	1/1	0.99	0.03	28,28,28,28	0
10	CD	T	2010	1/1	0.99	0.07	53,53,53,53	0
10	CD	H	1010	1/1	1.00	0.01	41,41,41,41	0
7	FE2	S	2007	1/1	1.00	0.03	32,32,32,32	0

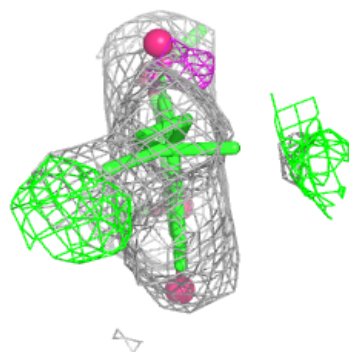
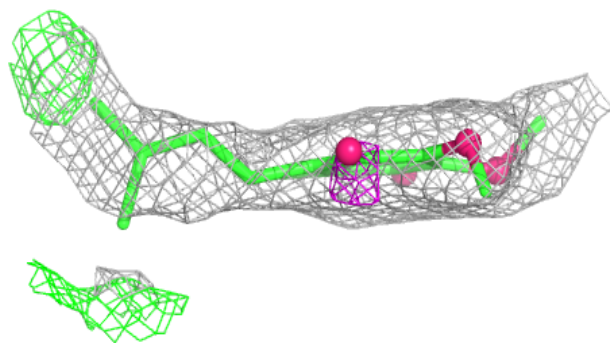
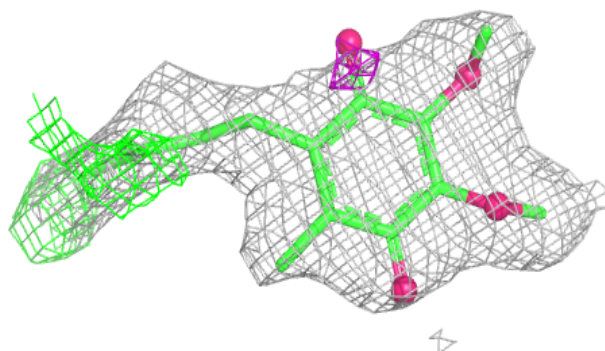
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around U10 L 1009:

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

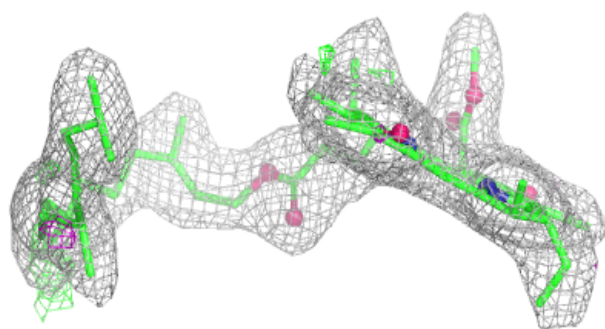
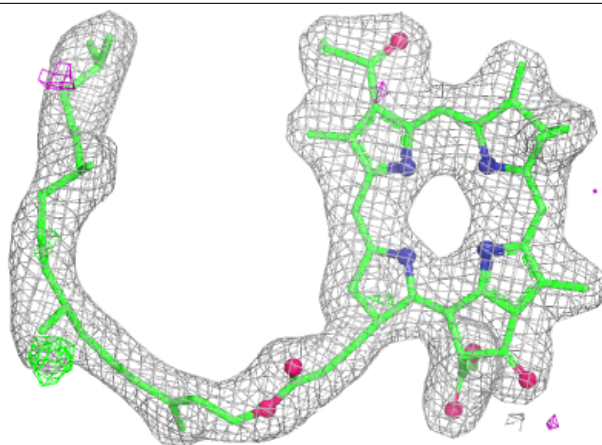
**Electron density around U10 R 2009:**

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



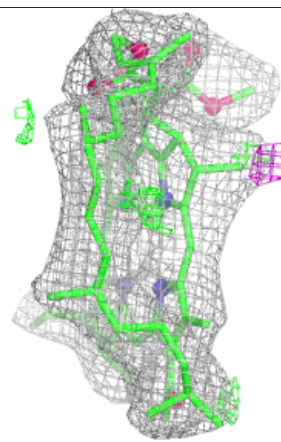
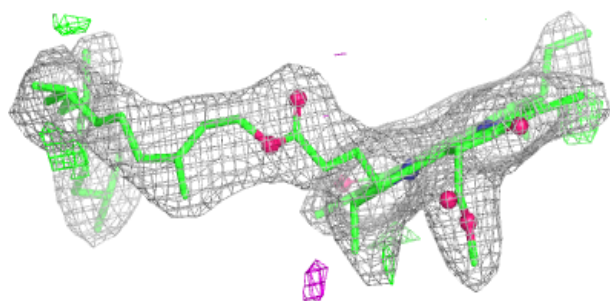
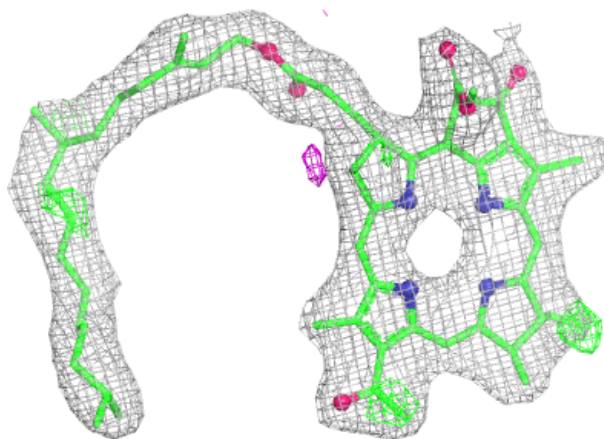
Electron density around BPH L 1006:

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



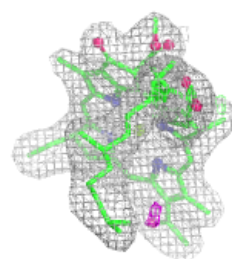
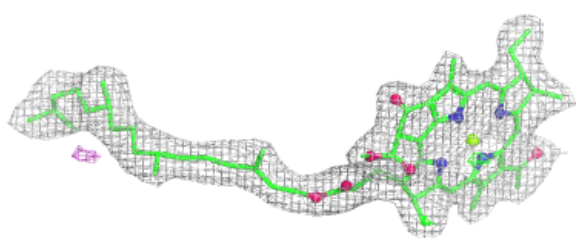
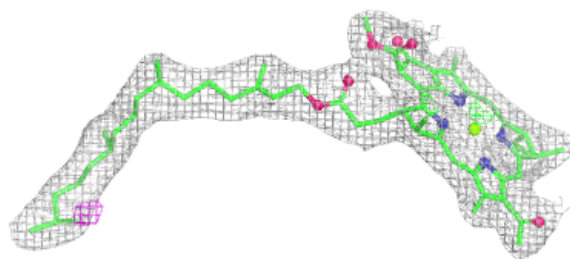
Electron density around BPH R 2006:

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

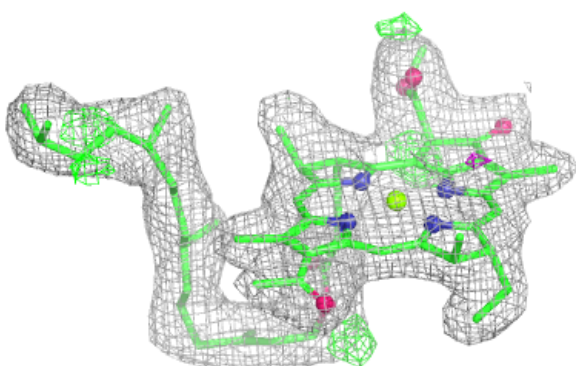
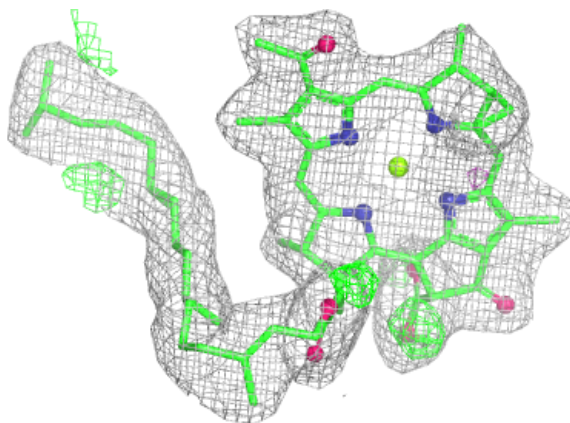


Electron density around BCL R 2002:

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

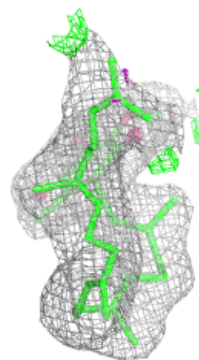
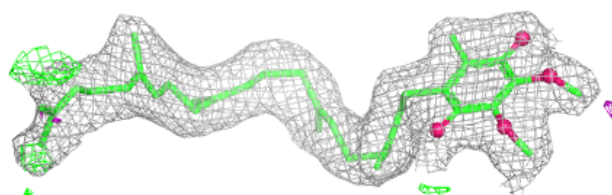
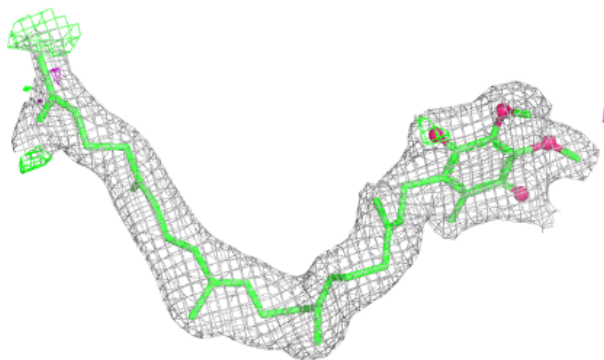
**Electron density around BCL R 2004:**

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

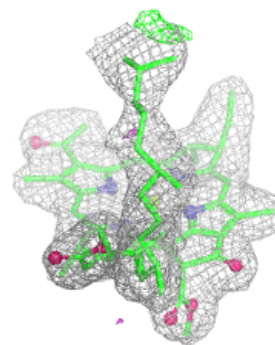
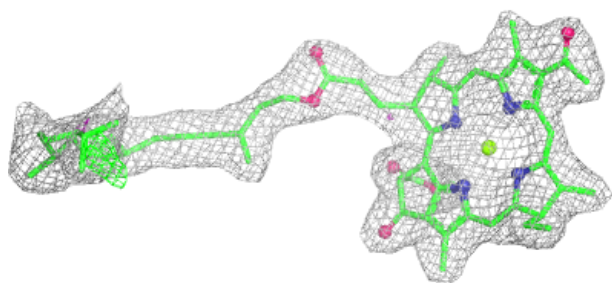
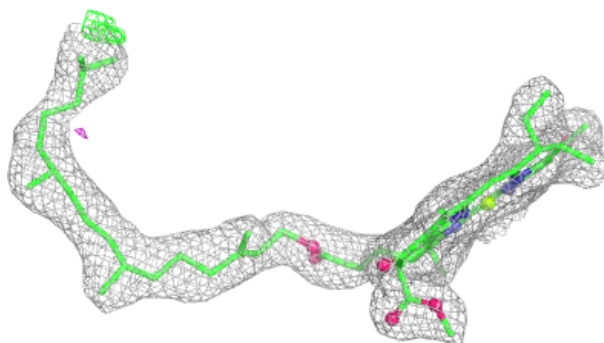


Electron density around U10 M 1008:

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

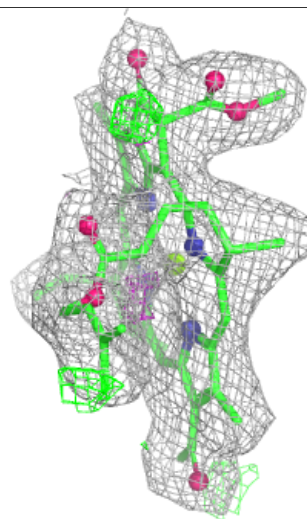
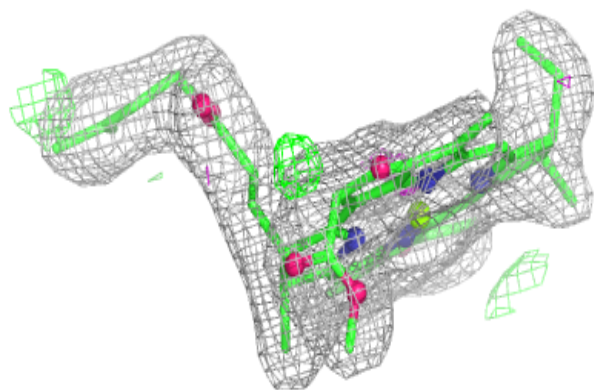
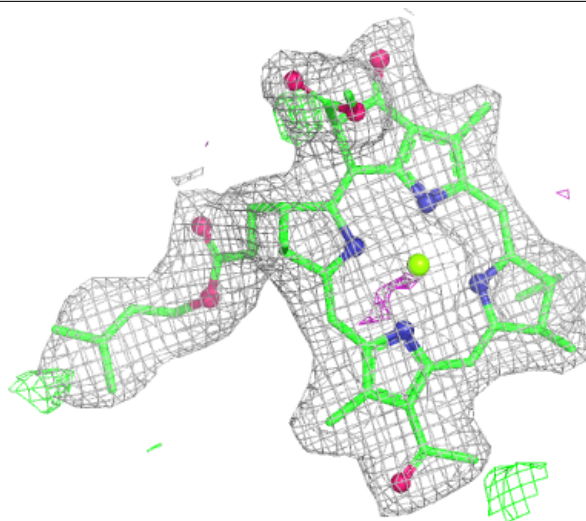
**Electron density around BCL S 2003:**

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



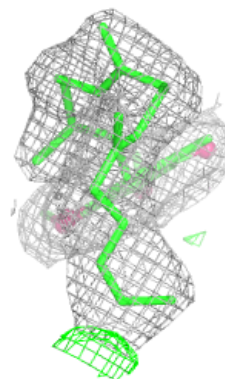
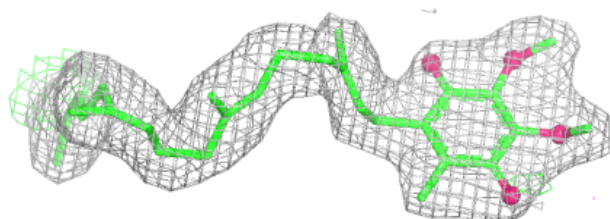
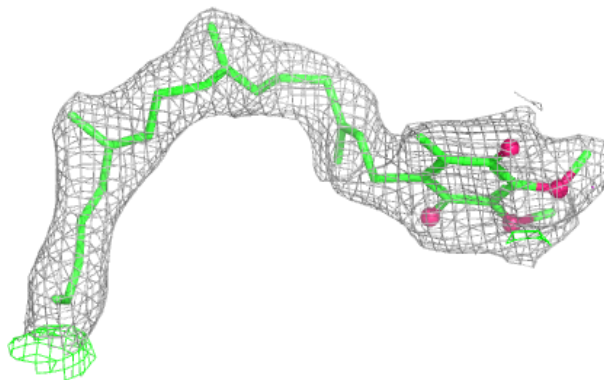
Electron density around BCL R 2001:

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

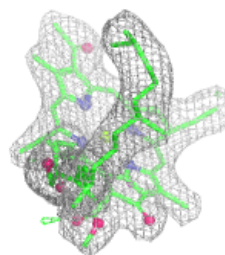
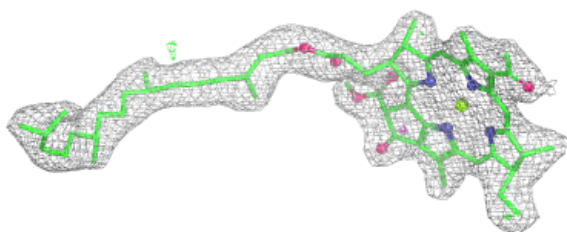
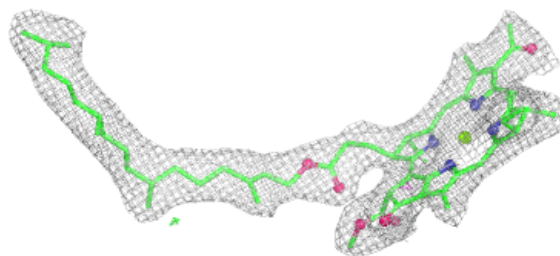


Electron density around U10 S 2008:

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

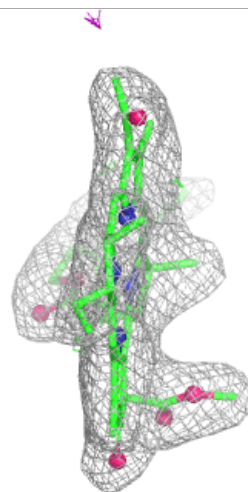
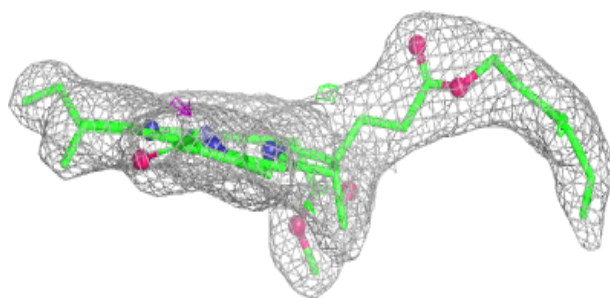
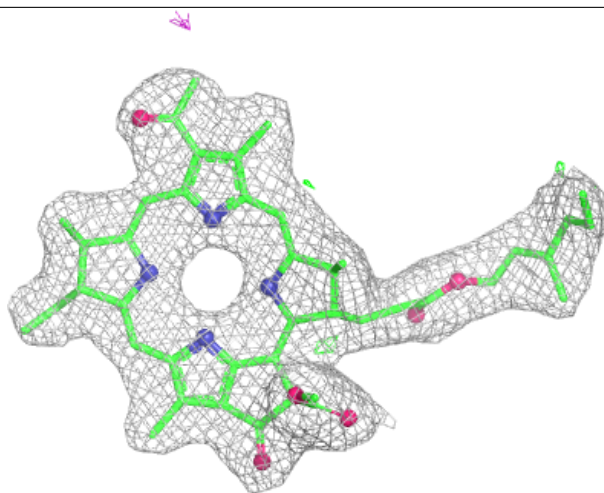
**Electron density around BCL L 1002:**

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



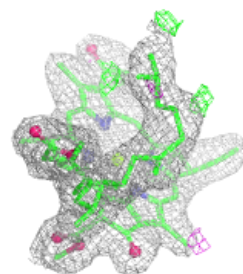
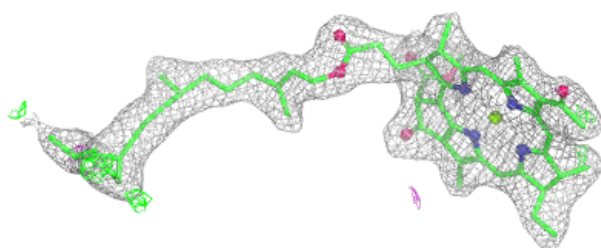
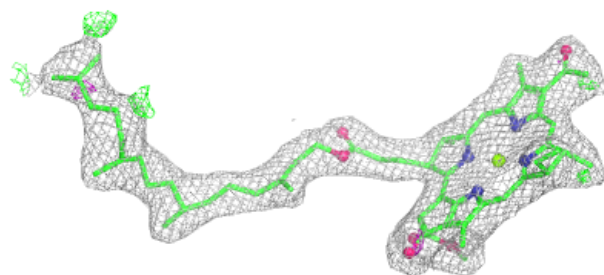
Electron density around BPH S 2005:

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



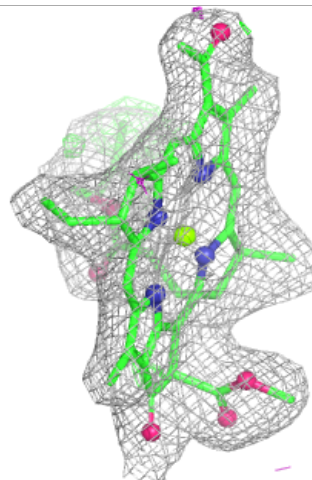
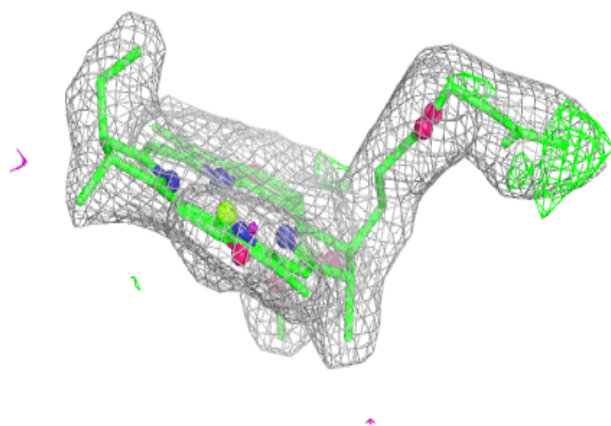
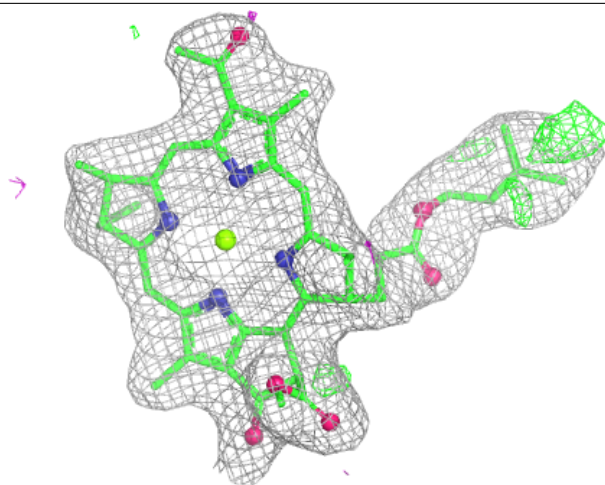
Electron density around BCL M 1003:

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



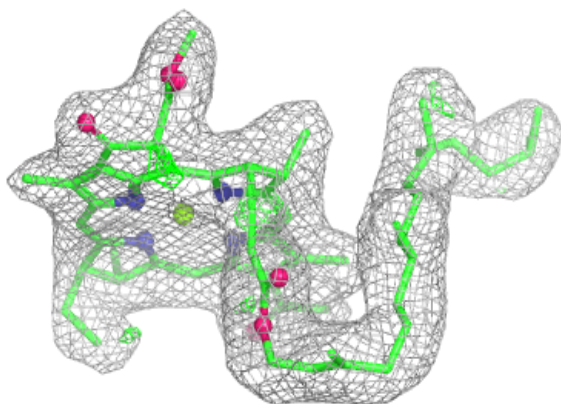
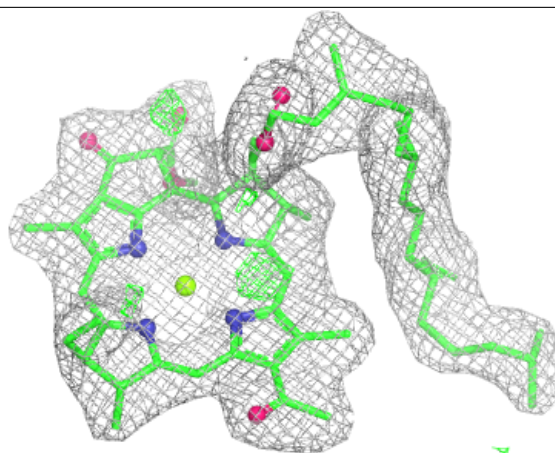
Electron density around BCL L 1001:

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



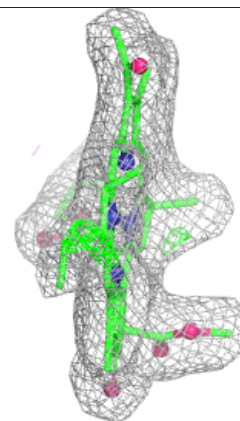
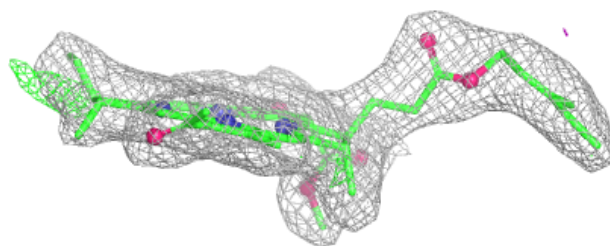
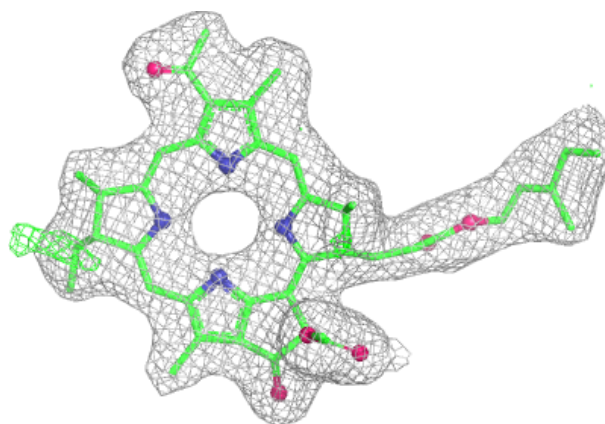
Electron density around BCL L 1004:

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



Electron density around BPH M 1005:

$2mF_o-DF_c$ (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.