



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2026 – 01:00 AM EDT

PDB ID : 1RZZ / pdb_00001rzz
Title : PHOTOSYNTHETIC REACTION CENTER DOUBLE MUTANT FROM RHODOBACTER SPHAEROIDES WITH ASP L213 REPLACED WITH ASN AND ARG M233 REPLACED WITH CYS IN THE CHARGE-NEUTRAL DQAQB STATE (TETRAGONAL FORM)
Authors : Xu, Q.; Axelrod, H.L.; Abresch, E.C.; Paddock, M.L.; Okamura, M.Y.; Feher, G.
Deposited on : 2003-12-29
Resolution : 2.40 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:

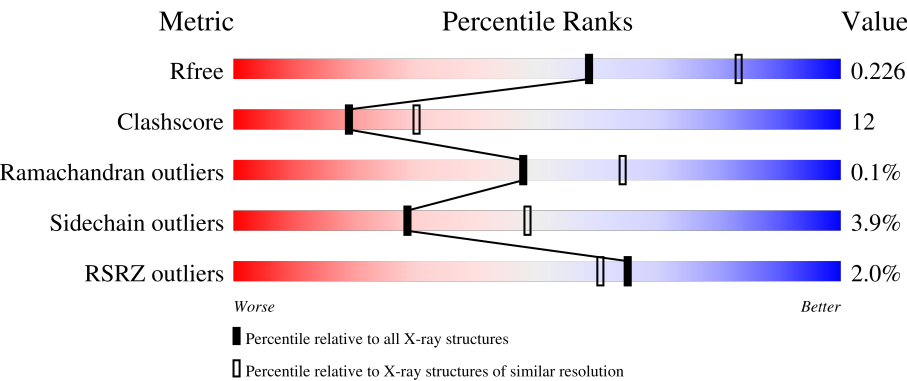
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)

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 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	76%21%.
1	R	281	% 73%23%.
2	M	307	% 75%22%..

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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Mol	Chain	Length	Quality of chain
2	S	307	
3	H	260	
3	T	260	

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
7	BPH	M	1005	X	-	-	-
7	BPH	M	1006	X	-	-	-
7	BPH	R	2006	X	-	-	-
7	BPH	S	2005	X	-	-	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 14481 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	356	361	8			
1	R	281	Total	C	N	O	S	0	0	0
			2232	1507	356	361	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	213	ASN	ASP	engineered mutation	UNP P02954
R	213	ASN	ASP	engineered mutation	UNP P02954

- 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
			2385	1594	388	392	11			
2	S	299	Total	C	N	O	S	0	0	0
			2385	1594	388	392	11			

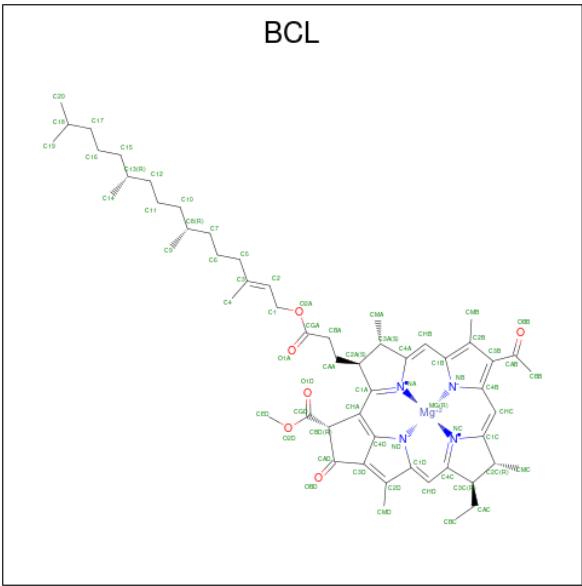
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	233	CYS	ARG	engineered mutation	UNP P02953
S	233	CYS	ARG	engineered mutation	UNP P02953

- Molecule 3 is a protein called Reaction center protein H chain.

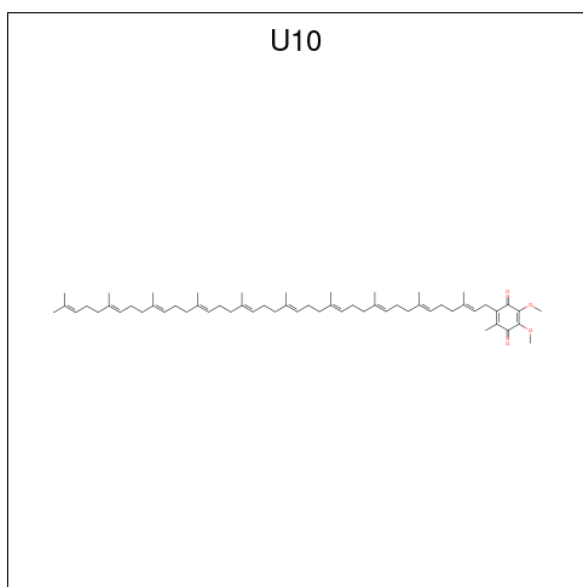
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	246	Total	C	N	O	S	0	0	0
			1869	1196	320	343	10			
3	T	246	Total	C	N	O	S	0	0	0
			1869	1196	320	343	10			

- Molecule 4 is BACTERIOCHLOROPHYLL A (CCD ID: BCL) (formula: C₅₅H₇₄MgN₄O₆).



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

- Molecule 5 is UBIQUINONE-10 (CCD ID: U10) (formula: C₅₉H₉₀O₄).

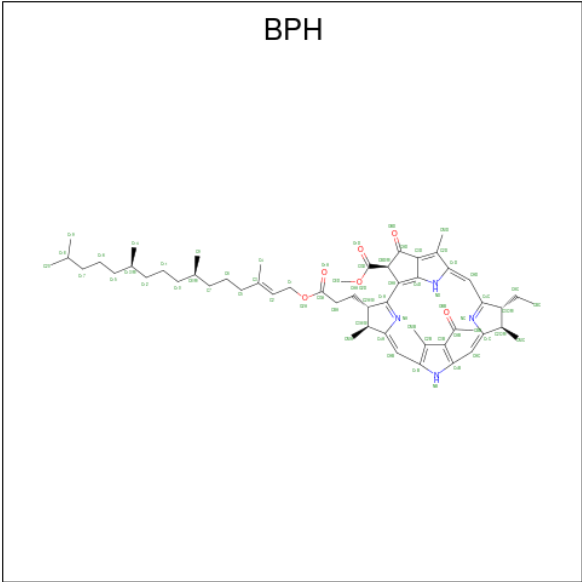


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	L	1	Total	C	O	0	0
			44	40	4		
5	M	1	Total	C	O	0	0
			38	34	4		
5	R	1	Total	C	O	0	0
			18	14	4		
5	S	1	Total	C	O	0	0
			32	28	4		

- Molecule 6 is FE (II) ION (CCD ID: FE2) (formula: Fe).

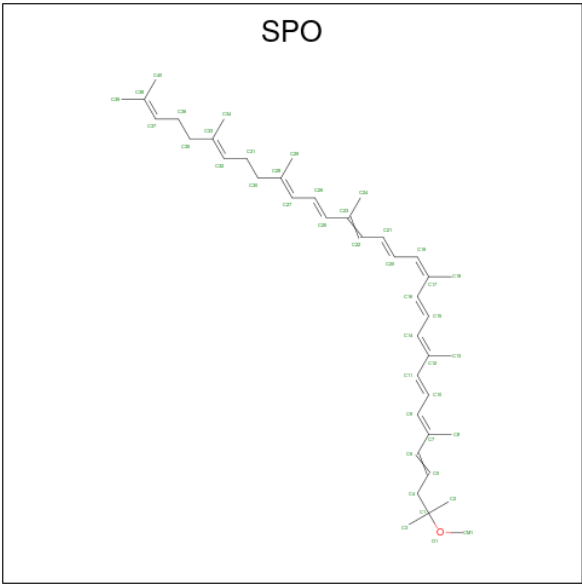
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	M	1	Total	Fe	0	0
			1	1		
6	S	1	Total	Fe	0	0
			1	1		

- Molecule 7 is BACTERIOPHEOPHYTIN A (CCD ID: BPH) (formula: C₅₅H₇₆N₄O₆).



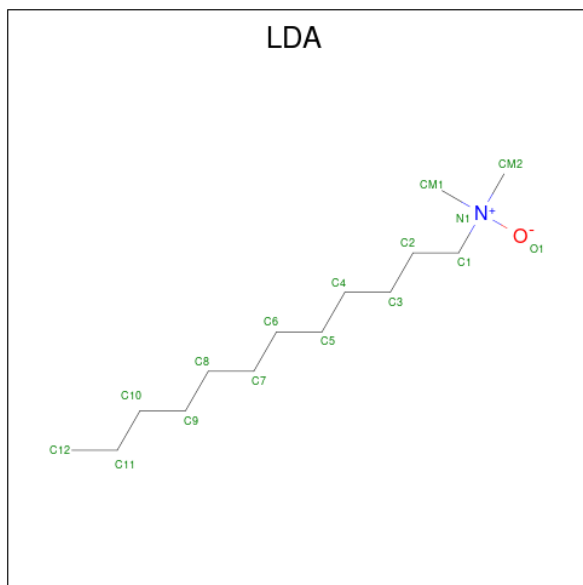
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	M	1	Total	C	N	O	0	0
			55	45	4	6		
7	M	1	Total	C	N	O	0	0
			65	55	4	6		
7	R	1	Total	C	N	O	0	0
			65	55	4	6		
7	S	1	Total	C	N	O	0	0
			55	45	4	6		

- Molecule 8 is SPHEROIDENE (CCD ID: SPO) (formula: C₄₁H₆₀O).



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

- Molecule 9 is LAURYL DIMETHYLAMINE-N-OXIDE (CCD ID: LDA) (formula: $C_{14}H_{31}NO$).



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	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		

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	L	72	Total	O	0	0
			72	72		
10	M	107	Total	O	0	0
			107	107		
10	H	109	Total	O	0	0
			109	109		

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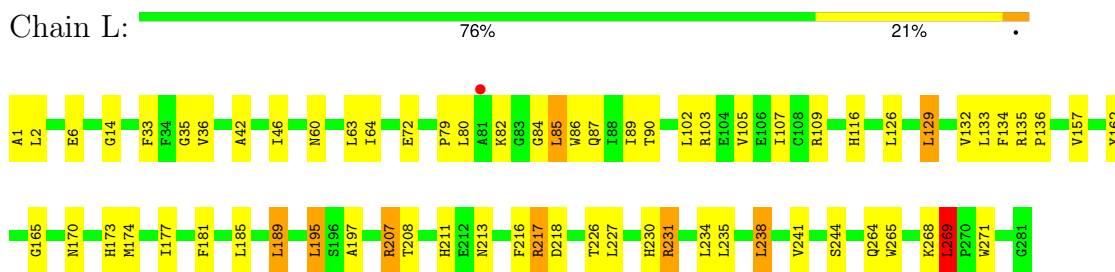
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	R	47	Total 47	O 47	0	0
10	S	75	Total 75	O 75	0	0
10	T	63	Total 63	O 63	0	0

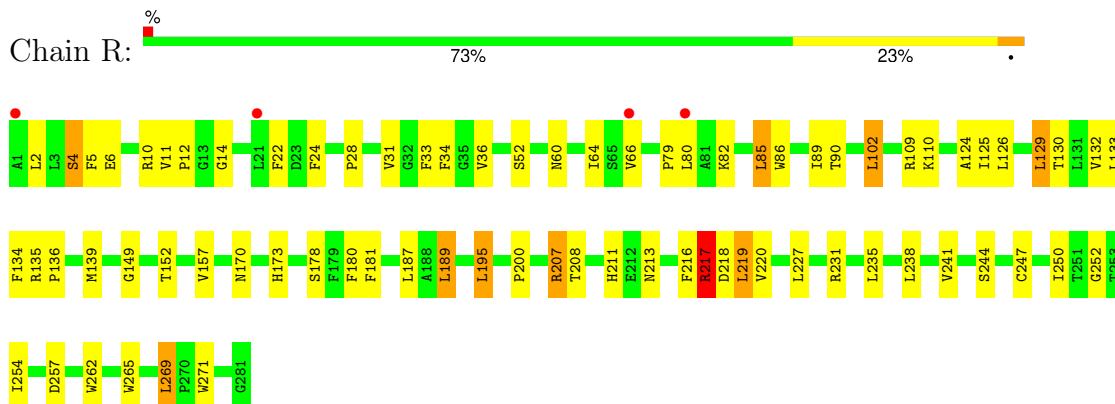
3 Residue-property plots

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.

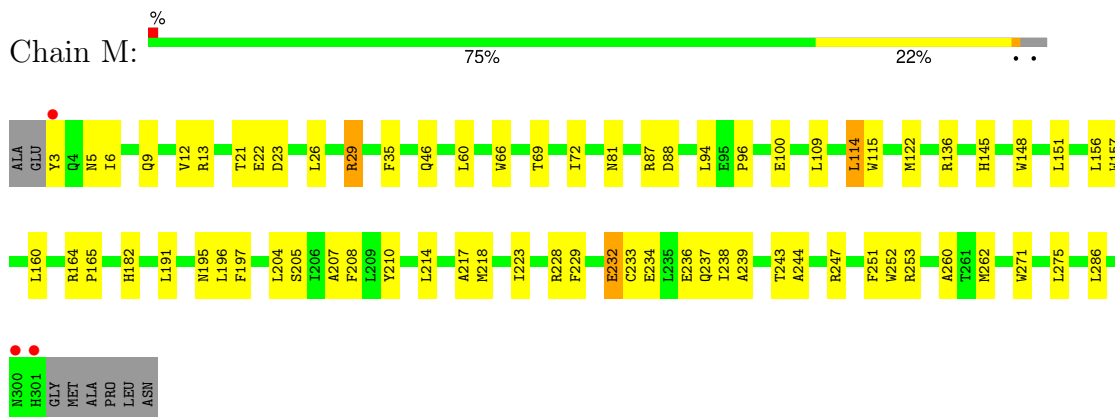
- Molecule 1: Reaction center protein L chain



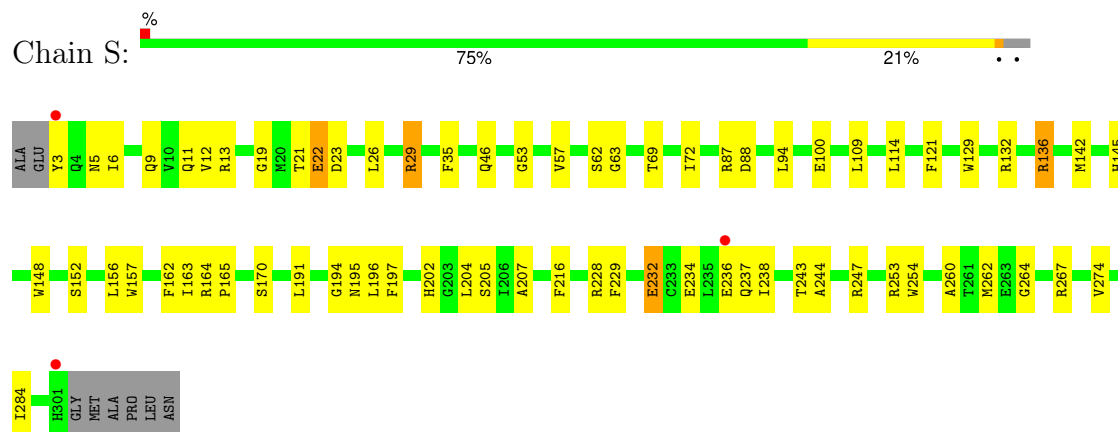
- Molecule 1: Reaction center protein L chain



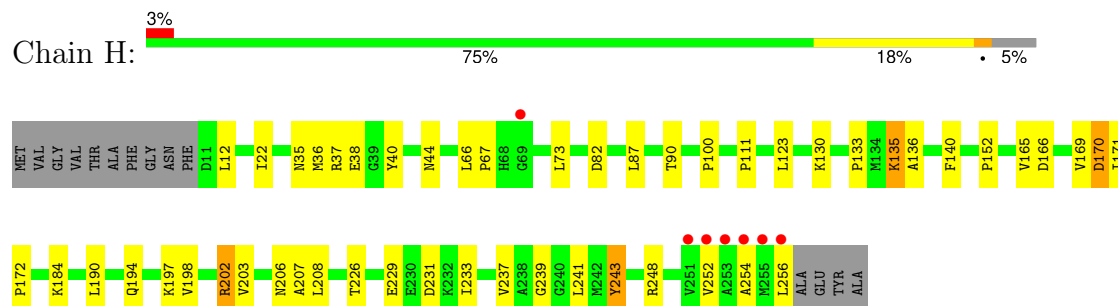
- Molecule 2: Reaction center protein M chain



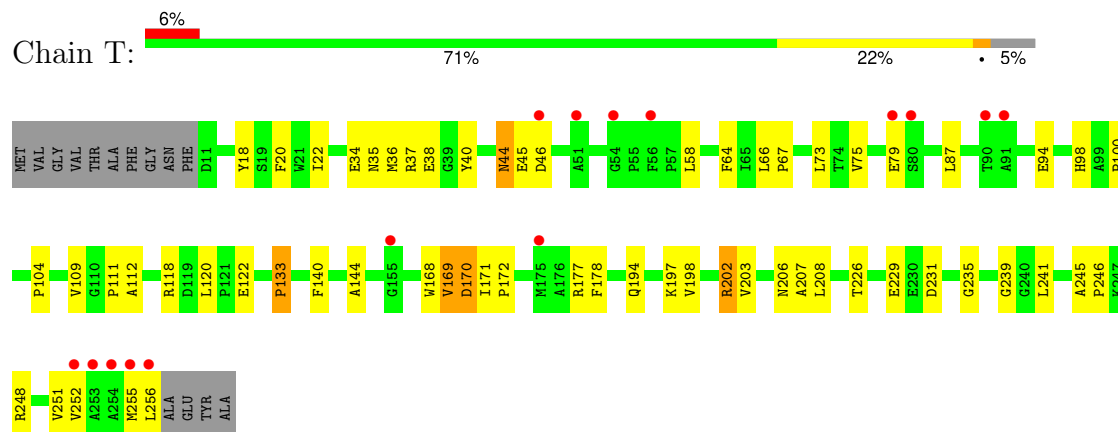
- Molecule 2: Reaction center protein M chain



- 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	139.58Å 139.58Å 274.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.76 – 2.40 39.76 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.2 (39.76-2.40) 98.3 (39.76-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.39Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.216 , 0.238 0.201 , 0.226	Depositor DCC
R_{free} test set	5283 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	36.9	Xtriage
Anisotropy	0.306	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 55.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14481	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.36% 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: SPO, FE2, U10, BPH, LDA, BCL

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	0.49	0/2320	0.90	6/3175 (0.2%)
1	R	0.41	0/2320	0.90	4/3175 (0.1%)
2	M	0.46	0/2477	0.90	7/3383 (0.2%)
2	S	0.41	0/2477	0.88	7/3383 (0.2%)
3	H	0.42	0/1917	0.87	6/2608 (0.2%)
3	T	0.36	0/1917	0.86	4/2608 (0.2%)
All	All	0.43	0/13428	0.89	34/18332 (0.2%)

There are no bond length outliers.

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	6	GLU	N-CA-C	7.51	120.93	111.69
3	H	44	ASN	N-CA-C	-7.29	100.70	110.55
1	R	219	LEU	N-CA-C	7.20	118.91	111.14
3	T	169	VAL	N-CA-C	6.68	118.22	108.53
3	T	44	ASN	N-CA-C	-6.53	101.73	110.55
1	L	134	PHE	N-CA-C	6.28	117.79	111.07
1	R	244	SER	N-CA-C	-6.23	104.12	111.03
3	H	170	ASP	N-CA-C	-6.21	99.09	108.96
2	M	217	ALA	N-CA-C	-6.02	104.80	111.36
3	H	22	ILE	N-CA-C	-6.01	104.65	110.42
1	R	217	ARG	N-CA-C	-6.00	104.65	111.14
3	H	133	PRO	N-CA-C	-5.97	101.89	111.38
3	H	243	TYR	N-CA-C	5.87	120.05	113.01
1	R	6	GLU	N-CA-C	5.69	120.35	112.90
1	L	269	LEU	CA-C-N	5.62	126.86	119.84
1	L	269	LEU	C-N-CA	5.62	126.86	119.84
2	S	267	ARG	N-CA-C	-5.53	104.89	111.69
3	T	133	PRO	N-CA-C	-5.47	102.51	111.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	6	ILE	N-CA-C	-5.33	105.92	111.58
2	S	22	GLU	CB-CA-C	-5.29	110.46	116.54
2	M	210	TYR	N-CA-C	-5.29	105.52	111.28
2	S	202	HIS	N-CA-C	-5.27	105.61	111.36
2	S	46	GLN	N-CA-C	5.27	117.87	109.96
2	M	81	ASN	CA-C-N	5.23	124.68	119.24
2	M	81	ASN	C-N-CA	5.23	124.68	119.24
2	M	160	LEU	N-CA-C	5.17	116.73	111.14
3	H	169	VAL	N-CA-C	5.15	116.39	108.71
1	L	244	SER	N-CA-C	-5.15	104.60	111.24
3	T	170	ASP	N-CA-C	-5.11	100.18	108.41
1	L	116	HIS	N-CA-C	5.09	116.83	111.28
2	M	46	GLN	N-CA-C	5.09	117.85	109.76
2	S	163	ILE	N-CA-C	5.06	115.21	110.30
2	S	6	ILE	N-CA-C	-5.06	106.22	111.58
2	S	19	GLY	N-CA-C	5.03	121.63	112.58

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	2189	57	0
1	R	2232	0	2189	62	0
2	M	2385	0	2296	55	0
2	S	2385	0	2296	66	0
3	H	1869	0	1884	39	0
3	T	1869	0	1884	54	0
4	L	183	0	189	20	0
4	M	66	0	74	14	0
4	R	66	0	74	6	0
4	S	183	0	189	22	0
5	L	44	0	56	3	0
5	M	38	0	47	4	0
5	R	18	0	15	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	S	32	0	39	1	0
6	M	1	0	0	0	0
6	S	1	0	0	0	0
7	M	120	0	127	6	0
7	R	65	0	74	5	0
7	S	55	0	53	2	0
8	M	42	0	60	4	0
8	S	42	0	60	3	0
9	M	64	0	124	3	0
9	S	16	0	31	0	0
10	H	109	0	0	1	0
10	L	72	0	0	1	0
10	M	107	0	0	2	0
10	R	47	0	0	2	0
10	S	75	0	0	3	0
10	T	63	0	0	1	0
All	All	14481	0	13950	330	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 (330) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:241:VAL:HG21	7:R:2006:BPH:HAC1	1.40	1.03
1:L:241:VAL:HG21	7:M:1006:BPH:HAC2	1.38	1.01
2:M:109:LEU:HD12	2:M:114:LEU:HD13	1.56	0.86
2:S:157:TRP:HB2	4:S:2003:BCL:H62	1.58	0.84
4:S:2001:BCL:HBC1	4:S:2003:BCL:CAD	2.09	0.82
1:R:79:PRO:HG2	1:R:82:LYS:HB2	1.61	0.82
1:R:208:THR:H	1:R:211:HIS:HD2	1.28	0.81
2:S:207:ALA:HA	4:S:2004:BCL:O1A	1.81	0.80
2:S:21:THR:HG23	2:S:26:LEU:HD11	1.63	0.80
1:R:227:LEU:HD13	2:S:232:GLU:HG2	1.64	0.80
2:S:13:ARG:HD2	2:S:35:PHE:CD2	2.18	0.79
1:R:208:THR:H	1:R:211:HIS:CD2	2.01	0.78
2:M:157:TRP:HB2	4:M:1003:BCL:H62	1.65	0.77
1:R:52:SER:HB2	1:R:85:LEU:HD23	1.66	0.77
1:L:189:LEU:HG	1:L:216:PHE:HZ	1.50	0.76
1:L:217:ARG:HD2	10:M:1043:HOH:O	1.85	0.75
5:M:1008:U10:H202	9:M:1012:LDA:H123	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:197:PHE:HZ	4:S:2003:BCL:HBB2	1.50	0.75
1:L:79:PRO:HG2	1:L:82:LYS:HB2	1.69	0.74
1:R:189:LEU:HG	1:R:216:PHE:HZ	1.53	0.73
1:R:2:LEU:HG	1:R:10:ARG:NH1	2.04	0.73
2:M:197:PHE:HZ	4:M:1003:BCL:HBB2	1.54	0.72
4:L:1001:BCL:HBB3	4:M:1003:BCL:H41	1.72	0.71
3:H:202:ARG:HG2	3:H:203:VAL:N	2.06	0.71
4:R:2002:BCL:HBD	4:S:2004:BCL:HBC1	1.73	0.70
1:R:217:ARG:HD2	10:S:2014:HOH:O	1.92	0.70
2:S:63:GLY:HA3	7:S:2005:BPH:H5C2	1.74	0.70
2:M:253:ARG:HD3	10:M:1016:HOH:O	1.91	0.69
4:L:1002:BCL:HBD	4:L:1004:BCL:CBC	2.21	0.69
2:S:136:ARG:HA	2:S:136:ARG:NE	2.07	0.69
3:H:252:VAL:O	3:H:256:LEU:HD13	1.92	0.68
3:H:171:ILE:HB	3:H:172:PRO:HD3	1.75	0.68
3:T:226:THR:OG1	3:T:229:GLU:HG3	1.94	0.68
3:T:44:ASN:HB2	3:T:46:ASP:OD1	1.94	0.67
3:T:202:ARG:HG2	3:T:203:VAL:N	2.09	0.67
10:R:2021:HOH:O	2:S:253:ARG:HD3	1.94	0.67
1:L:105:VAL:O	1:L:109:ARG:HG3	1.94	0.67
2:S:228:ARG:HA	3:T:194:GLN:CG	2.25	0.66
2:S:243:THR:O	2:S:247:ARG:HG3	1.94	0.66
3:T:73:LEU:HD11	3:T:75:VAL:HG13	1.77	0.66
1:R:135:ARG:HB3	1:R:136:PRO:HD3	1.77	0.66
2:M:229:PHE:HB2	2:M:244:ALA:HB2	1.77	0.66
2:S:9:GLN:NE2	3:T:198:VAL:H	1.94	0.66
2:M:9:GLN:NE2	3:H:198:VAL:H	1.93	0.65
3:H:87:LEU:HD23	3:H:100:PRO:HA	1.78	0.65
3:T:252:VAL:O	3:T:256:LEU:HD13	1.97	0.65
2:M:197:PHE:CZ	4:M:1003:BCL:HBB2	2.32	0.65
4:R:2002:BCL:HBD	4:S:2004:BCL:CBC	2.27	0.65
2:M:136:ARG:NE	2:M:136:ARG:HA	2.10	0.64
1:L:60:ASN:CG	1:L:63:LEU:HD23	2.22	0.64
1:L:86:TRP:CH2	1:L:132:VAL:HG13	2.33	0.64
1:L:80:LEU:H	1:L:80:LEU:HD22	1.61	0.64
1:R:14:GLY:O	1:R:109:ARG:HD3	1.97	0.64
1:L:208:THR:H	1:L:211:HIS:CD2	2.16	0.63
2:M:13:ARG:HD2	2:M:35:PHE:CD2	2.33	0.63
1:L:185:LEU:HD23	4:L:1001:BCL:H42	1.80	0.63
4:S:2001:BCL:HBB3	4:S:2003:BCL:H41	1.79	0.63
2:S:109:LEU:HD12	2:S:114:LEU:HD13	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:33:PHE:O	1:L:36:VAL:HG22	1.98	0.62
4:L:1004:BCL:O1A	2:M:207:ALA:HA	1.99	0.62
4:L:1001:BCL:HBC1	4:M:1003:BCL:CBD	2.29	0.62
3:T:118:ARG:HD3	3:T:120:LEU:HD12	1.80	0.62
3:T:194:GLN:CD	3:T:194:GLN:H	2.07	0.62
2:M:9:GLN:HE22	3:H:197:LYS:HA	1.64	0.61
1:L:189:LEU:HB3	5:L:1009:U10:H4M3	1.81	0.61
2:S:69:THR:O	2:S:72:ILE:HG22	2.00	0.61
2:S:195:ASN:ND2	2:S:197:PHE:H	1.98	0.61
4:L:1002:BCL:HBD	4:L:1004:BCL:HBC1	1.82	0.61
1:L:84:GLY:HA2	1:L:87:GLN:HE21	1.64	0.60
2:M:208:PHE:HE1	9:M:1014:LDA:H101	1.65	0.60
4:L:1004:BCL:H61	5:M:1008:U10:H203	1.84	0.60
1:L:86:TRP:CZ2	1:L:132:VAL:HG13	2.36	0.60
1:L:208:THR:H	1:L:211:HIS:HD2	1.48	0.60
2:S:236:GLU:HG3	3:T:122:GLU:OE2	2.01	0.60
2:M:243:THR:O	2:M:247:ARG:HG3	2.03	0.59
2:S:195:ASN:C	2:S:195:ASN:HD22	2.09	0.59
1:L:265:TRP:O	1:L:269:LEU:HD13	2.02	0.59
2:M:228:ARG:HA	3:H:194:GLN:HG2	1.85	0.59
2:S:9:GLN:HE22	3:T:198:VAL:H	1.50	0.59
3:T:87:LEU:HD23	3:T:100:PRO:HA	1.84	0.58
2:M:260:ALA:HB1	3:H:35:ASN:OD1	2.05	0.57
1:L:14:GLY:O	1:L:109:ARG:HD3	2.05	0.57
1:R:178:SER:HA	4:S:2001:BCL:O1A	2.05	0.57
2:M:69:THR:O	2:M:72:ILE:HG22	2.04	0.56
2:S:157:TRP:HB2	4:S:2003:BCL:C6	2.30	0.56
1:R:28:PRO:HB3	2:S:253:ARG:NH1	2.20	0.56
4:L:1002:BCL:HBD	4:L:1004:BCL:HBC3	1.85	0.56
3:H:135:LYS:NZ	3:H:135:LYS:HB3	2.20	0.56
3:T:37:ARG:O	3:T:38:GLU:HG2	2.06	0.56
3:T:133:PRO:HG3	3:T:168:TRP:CZ2	2.40	0.56
4:L:1001:BCL:HBC1	4:M:1003:BCL:HBD	1.88	0.56
2:S:228:ARG:HA	3:T:194:GLN:HG3	1.86	0.56
4:L:1001:BCL:HBC1	4:M:1003:BCL:CAD	2.36	0.56
1:L:218:ASP:OD1	2:M:29:ARG:HD2	2.05	0.56
2:S:197:PHE:CZ	4:S:2003:BCL:HBB2	2.35	0.56
3:T:133:PRO:HG3	3:T:168:TRP:CE2	2.41	0.56
1:L:60:ASN:O	1:L:64:ILE:HG13	2.06	0.56
2:M:157:TRP:HB2	4:M:1003:BCL:C6	2.35	0.56
1:L:157:VAL:HG11	4:M:1003:BCL:HBB1	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:194:GLN:CD	3:H:194:GLN:H	2.14	0.55
3:T:45:GLU:HG3	3:T:94:GLU:OE1	2.06	0.55
3:H:206:ASN:HD21	3:H:248:ARG:HD2	1.71	0.55
2:S:264:GLY:HA3	3:T:35:ASN:OD1	2.06	0.55
1:L:60:ASN:ND2	1:L:63:LEU:HD23	2.22	0.55
1:R:218:ASP:OD1	2:S:29:ARG:HD2	2.07	0.55
3:T:73:LEU:CD1	3:T:75:VAL:HG13	2.35	0.55
2:S:12:VAL:HG21	3:T:169:VAL:HG21	1.89	0.54
1:R:170:ASN:HB3	1:R:173:HIS:CB	2.38	0.54
1:R:265:TRP:O	1:R:269:LEU:HD13	2.08	0.54
2:S:152:SER:HB2	2:S:274:VAL:HG13	1.89	0.54
1:L:269:LEU:HD23	1:L:271:TRP:CZ2	2.44	0.53
3:T:36:MET:HE2	3:T:58:LEU:HD23	1.91	0.53
3:T:241:LEU:O	3:T:248:ARG:NH2	2.41	0.53
1:L:103:ARG:O	1:L:107:ILE:HG13	2.07	0.53
1:L:264:GLN:OE1	1:L:268:LYS:HE2	2.08	0.53
3:H:130:LYS:HE3	3:H:170:ASP:OD2	2.08	0.53
2:S:9:GLN:HE22	3:T:197:LYS:HA	1.73	0.53
1:L:1:ALA:C	1:L:2:LEU:HD12	2.34	0.53
3:T:37:ARG:HH11	3:T:37:ARG:HG2	1.73	0.53
1:R:213:ASN:O	1:R:217:ARG:HB2	2.08	0.53
3:T:251:VAL:O	3:T:255:MET:HG3	2.09	0.53
1:L:80:LEU:H	1:L:80:LEU:CD2	2.22	0.53
1:R:133:LEU:C	1:R:133:LEU:HD23	2.34	0.52
1:R:189:LEU:HG	1:R:216:PHE:CZ	2.41	0.52
2:M:195:ASN:HD22	2:M:195:ASN:C	2.17	0.52
4:L:1002:BCL:H122	7:M:1006:BPH:H3A	1.92	0.52
3:H:152:PRO:HG2	3:H:202:ARG:HB2	1.91	0.52
1:R:157:VAL:HG11	4:S:2003:BCL:HBB1	1.91	0.52
2:S:157:TRP:HD1	4:S:2001:BCL:HBB1	1.73	0.52
2:S:152:SER:CB	2:S:274:VAL:HG13	2.40	0.52
3:T:168:TRP:HB2	3:T:178:PHE:HB2	1.90	0.52
3:T:171:ILE:HB	3:T:172:PRO:HD3	1.92	0.52
3:H:66:LEU:HD22	3:H:66:LEU:N	2.25	0.52
1:L:213:ASN:O	1:L:217:ARG:HB2	2.10	0.51
1:L:238:LEU:HD12	7:M:1006:BPH:CB	2.41	0.51
1:R:269:LEU:HD23	1:R:271:TRP:CZ2	2.45	0.51
2:M:271:TRP:O	2:M:275:LEU:HG	2.11	0.51
1:R:33:PHE:O	1:R:36:VAL:HG22	2.10	0.51
3:H:241:LEU:O	3:H:248:ARG:NH2	2.44	0.51
1:R:22:PHE:HA	1:R:24:PHE:CE2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:257:ASP:HB3	10:R:2056:HOH:O	2.10	0.51
3:H:207:ALA:O	3:H:208:LEU:HD12	2.11	0.51
2:S:164:ARG:HB3	2:S:165:PRO:HD3	1.94	0.50
1:L:85:LEU:O	1:L:89:ILE:HG13	2.10	0.50
2:S:13:ARG:O	3:T:140:PHE:HA	2.11	0.50
2:S:284:ILE:HG12	4:S:2003:BCL:HED3	1.93	0.50
1:L:216:PHE:CE1	5:L:1009:U10:H4M2	2.46	0.50
2:M:9:GLN:HE22	3:H:198:VAL:H	1.57	0.50
4:R:2002:BCL:H122	7:R:2006:BPH:H3A	1.93	0.50
1:L:189:LEU:HG	1:L:216:PHE:CZ	2.40	0.50
1:R:85:LEU:O	1:R:89:ILE:HG13	2.12	0.50
4:S:2004:BCL:H121	4:S:2004:BCL:HMA1	1.93	0.50
1:R:80:LEU:HB3	1:R:85:LEU:HD13	1.92	0.50
2:S:21:THR:HG23	2:S:26:LEU:CD1	2.38	0.50
1:L:72:GLU:HG3	10:L:1062:HOH:O	2.11	0.49
4:L:1001:BCL:HBB2	8:M:1010:SPO:H243	1.94	0.49
3:H:135:LYS:NZ	3:H:135:LYS:CB	2.75	0.49
2:M:195:ASN:ND2	2:M:197:PHE:H	2.10	0.49
1:L:231:ARG:HD2	2:M:5:ASN:O	2.13	0.49
1:R:28:PRO:HB3	2:S:253:ARG:HH11	1.75	0.49
4:R:2002:BCL:H52	7:R:2006:BPH:HBB2	1.94	0.49
2:S:3:TYR:CE1	2:S:9:GLN:HG3	2.47	0.49
3:T:37:ARG:HG2	3:T:37:ARG:NH1	2.28	0.49
3:H:66:LEU:HD22	3:H:66:LEU:H	1.77	0.49
4:L:1001:BCL:HBB2	4:L:1001:BCL:HHC	1.95	0.48
2:M:208:PHE:CE1	9:M:1014:LDA:H101	2.46	0.48
2:M:3:TYR:CE1	2:M:9:GLN:HG3	2.47	0.48
1:R:80:LEU:O	1:R:85:LEU:HB2	2.12	0.48
1:R:195:LEU:HB3	2:S:145:HIS:CD2	2.47	0.48
1:L:162:TYR:HA	1:L:165:GLY:O	2.13	0.48
3:H:12:LEU:HD13	3:H:12:LEU:C	2.38	0.48
1:R:80:LEU:H	1:R:80:LEU:HD22	1.78	0.48
3:T:170:ASP:HB2	3:T:177:ARG:HG3	1.96	0.48
2:M:164:ARG:HB3	2:M:165:PRO:HD3	1.94	0.48
3:H:82:ASP:OD1	3:H:82:ASP:N	2.45	0.48
4:S:2001:BCL:HBB2	8:S:2010:SPO:H243	1.95	0.48
3:T:118:ARG:HG2	3:T:120:LEU:HB2	1.96	0.48
1:L:90:THR:CG2	1:L:132:VAL:HG11	2.44	0.48
3:T:206:ASN:HD21	3:T:248:ARG:HD2	1.79	0.47
2:M:114:LEU:HD12	2:M:114:LEU:HA	1.73	0.47
4:L:1002:BCL:HAA2	4:L:1004:BCL:HBC1	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:125:ILE:HG22	1:R:129:LEU:HD22	1.96	0.47
3:T:34:GLU:HA	3:T:34:GLU:OE1	2.13	0.47
1:R:139:MET:HE3	1:R:252:GLY:HA3	1.95	0.47
2:M:66:TRP:CD1	2:M:122:MET:HB2	2.50	0.47
2:M:237:GLN:HB2	2:M:262:MET:HG2	1.96	0.47
1:R:181:PHE:CZ	4:S:2003:BCL:O1A	2.68	0.47
1:R:241:VAL:CG2	7:R:2006:BPH:HAC1	2.30	0.47
4:R:2002:BCL:NC	4:S:2003:BCL:HBB3	2.30	0.47
1:R:170:ASN:HB3	1:R:173:HIS:HB2	1.96	0.47
1:L:170:ASN:HB3	1:L:173:HIS:CB	2.45	0.46
1:L:227:LEU:HD13	2:M:232:GLU:HG2	1.98	0.46
1:R:60:ASN:O	1:R:64:ILE:HG13	2.15	0.46
1:R:66:VAL:HG11	1:R:89:ILE:HD12	1.97	0.46
4:L:1001:BCL:CBC	4:M:1003:BCL:CAD	2.93	0.46
2:S:228:ARG:HA	3:T:194:GLN:HG2	1.96	0.46
2:M:234:GLU:O	2:M:238:ILE:HG13	2.14	0.46
3:T:111:PRO:HB2	3:T:239:GLY:HA2	1.98	0.46
3:H:111:PRO:HB2	3:H:239:GLY:HA2	1.97	0.46
2:S:205:SER:OG	4:S:2003:BCL:HMA3	2.15	0.46
4:S:2001:BCL:HBB3	4:S:2003:BCL:H61	1.97	0.46
1:R:11:VAL:HB	1:R:12:PRO:HD2	1.98	0.46
2:S:3:TYR:CZ	2:S:5:ASN:HA	2.51	0.46
1:R:80:LEU:H	1:R:80:LEU:CD2	2.29	0.46
2:S:204:LEU:HD13	3:T:20:PHE:CE2	2.51	0.46
3:T:73:LEU:HD13	3:T:73:LEU:C	2.41	0.46
3:T:87:LEU:HD22	3:T:98:HIS:O	2.15	0.46
3:H:233:ILE:O	3:H:237:VAL:HG23	2.16	0.46
1:L:35:GLY:HA2	1:L:103:ARG:HD2	1.98	0.46
1:L:80:LEU:HD22	1:L:80:LEU:N	2.28	0.45
4:L:1001:BCL:H41	5:L:1009:U10:H112	1.97	0.45
2:M:100:GLU:CD	2:M:100:GLU:H	2.25	0.45
3:H:135:LYS:HB3	3:H:135:LYS:HZ3	1.82	0.45
4:S:2001:BCL:HBB2	4:S:2001:BCL:HHC	1.99	0.45
3:H:111:PRO:HD2	3:H:243:TYR:CE2	2.52	0.45
3:H:165:VAL:O	3:H:166:ASP:HB2	2.17	0.45
2:M:228:ARG:HA	3:H:194:GLN:CG	2.45	0.45
2:S:237:GLN:HB2	2:S:262:MET:HG2	1.98	0.45
3:H:226:THR:OG1	3:H:229:GLU:HG3	2.16	0.45
2:S:194:GLY:O	2:S:195:ASN:HB3	2.17	0.45
3:T:40:TYR:HB3	3:T:58:LEU:HD21	1.98	0.45
1:L:185:LEU:HD13	7:M:1005:BPH:ND	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:1004:BCL:HBB3	7:M:1006:BPH:H152	1.99	0.45
2:M:286:LEU:CD2	3:H:12:LEU:HD12	2.48	0.44
1:R:170:ASN:HB3	1:R:173:HIS:HB3	1.97	0.44
1:R:149:GLY:HA3	1:R:152:THR:OG1	2.17	0.44
4:S:2001:BCL:CBB	8:S:2010:SPO:H243	2.47	0.44
2:M:195:ASN:HD22	2:M:197:PHE:H	1.64	0.44
1:R:34:PHE:CE1	1:R:102:LEU:HD23	2.52	0.44
1:R:211:HIS:HE1	2:S:22:GLU:OE1	2.00	0.44
1:L:207:ARG:HA	1:L:207:ARG:HD2	1.57	0.44
7:M:1005:BPH:HMB3	7:M:1005:BPH:HBB3	1.98	0.44
1:R:129:LEU:HB3	1:R:134:PHE:CE2	2.52	0.44
1:R:207:ARG:HG3	2:S:142:MET:HG2	1.99	0.44
2:S:148:TRP:HA	2:S:148:TRP:CE3	2.53	0.44
3:T:207:ALA:HA	3:T:241:LEU:HD23	2.00	0.44
1:L:226:THR:HG23	1:L:227:LEU:N	2.33	0.44
3:H:90:THR:HG22	10:H:290:HOH:O	2.16	0.44
2:S:229:PHE:HB2	2:S:244:ALA:HB2	2.00	0.44
3:H:66:LEU:HA	3:H:67:PRO:HD3	1.85	0.44
1:R:262:TRP:O	1:R:265:TRP:HD1	2.01	0.44
2:M:196:LEU:HD12	2:M:196:LEU:HA	1.85	0.44
3:H:36:MET:HE3	3:H:40:TYR:CD2	2.53	0.44
3:T:18:TYR:O	3:T:22:ILE:HG12	2.18	0.44
3:T:64:PHE:HD2	3:T:73:LEU:HD12	1.82	0.44
2:S:87:ARG:HG3	2:S:88:ASP:N	2.33	0.43
2:S:148:TRP:HA	2:S:148:TRP:HE3	1.82	0.43
2:M:96:PRO:HB3	2:M:115:TRP:CE2	2.53	0.43
2:S:11:GLN:HB2	3:T:144:ALA:HB3	2.00	0.43
2:S:53:GLY:O	2:S:57:VAL:HG23	2.18	0.43
2:S:129:TRP:O	2:S:132:ARG:HB3	2.17	0.43
2:S:62:SER:HB3	2:S:121:PHE:O	2.18	0.43
2:S:236:GLU:OE1	3:T:122:GLU:HG2	2.18	0.43
2:S:195:ASN:ND2	2:S:195:ASN:C	2.73	0.43
3:T:112:ALA:HA	3:T:235:GLY:O	2.19	0.43
2:S:63:GLY:CA	7:S:2005:BPH:H5C2	2.47	0.43
2:M:13:ARG:O	3:H:140:PHE:HA	2.19	0.43
1:L:80:LEU:HD12	1:L:85:LEU:HD13	2.00	0.43
2:M:22:GLU:HB3	2:M:23:ASP:H	1.67	0.43
1:R:90:THR:HG23	1:R:132:VAL:HG11	2.01	0.43
1:L:174:MET:HE3	4:L:1001:BCL:HED3	2.00	0.42
2:M:87:ARG:HG3	2:M:88:ASP:N	2.34	0.42
1:R:86:TRP:CH2	1:R:132:VAL:HG13	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:234:GLU:O	2:S:238:ILE:HG13	2.18	0.42
1:R:227:LEU:HD13	2:S:232:GLU:CG	2.43	0.42
3:T:66:LEU:HA	3:T:67:PRO:HD3	1.84	0.42
1:L:197:ALA:HA	1:L:207:ARG:HB2	2.01	0.42
1:L:230:HIS:CD2	2:M:223:ILE:HG13	2.54	0.42
1:R:130:THR:HA	1:R:134:PHE:HD2	1.84	0.42
1:L:170:ASN:HB3	1:L:173:HIS:HB3	2.01	0.42
4:L:1004:BCL:H3A	4:L:1004:BCL:HBA2	1.73	0.42
2:M:214:LEU:HD21	5:M:1008:U10:H172	2.00	0.42
2:S:22:GLU:HB3	2:S:23:ASP:H	1.61	0.42
3:T:104:PRO:HA	3:T:109:VAL:HG22	2.01	0.42
2:M:182:HIS:CG	8:M:1010:SPO:H181	2.54	0.42
4:M:1003:BCL:CBB	4:M:1003:BCL:HHC	2.49	0.42
1:L:129:LEU:HD12	1:L:129:LEU:HA	1.86	0.42
1:L:185:LEU:HD12	1:L:185:LEU:O	2.19	0.42
2:M:13:ARG:HD2	2:M:35:PHE:CE2	2.54	0.42
1:R:133:LEU:HD22	1:R:134:PHE:CD1	2.54	0.42
3:T:206:ASN:ND2	10:T:312:HOH:O	2.48	0.42
2:M:205:SER:OG	4:M:1003:BCL:HMA3	2.20	0.42
3:H:194:GLN:H	3:H:194:GLN:NE2	2.18	0.42
2:S:114:LEU:HD12	2:S:114:LEU:HA	1.94	0.42
1:L:211:HIS:HE1	2:M:22:GLU:OE1	2.02	0.42
2:M:21:THR:O	2:M:22:GLU:C	2.62	0.42
1:L:42:ALA:O	1:L:46:ILE:HG13	2.19	0.42
2:M:239:ALA:HB1	3:H:66:LEU:HD11	2.02	0.42
1:R:219:LEU:HG	1:R:220:VAL:HG13	2.01	0.42
2:S:162:PHE:C	2:S:165:PRO:HD2	2.44	0.42
2:S:170:SER:HB2	10:S:2022:HOH:O	2.20	0.42
5:M:1008:U10:H4M2	5:M:1008:U10:H3M3	2.02	0.41
1:L:195:LEU:HB3	2:M:145:HIS:CD2	2.55	0.41
1:R:250:ILE:HB	1:R:254:ILE:HD11	2.03	0.41
2:S:260:ALA:HB1	3:T:35:ASN:OD1	2.19	0.41
3:H:190:LEU:HB2	3:H:233:ILE:HD13	2.00	0.41
3:H:254:ALA:C	3:H:256:LEU:H	2.28	0.41
1:R:4:SER:O	3:T:79:GLU:HG2	2.20	0.41
1:R:110:LYS:HD2	2:S:254:TRP:CZ3	2.55	0.41
1:R:180:PHE:CD2	4:R:2002:BCL:HMA3	2.55	0.41
1:R:187:LEU:HD13	2:S:216:PHE:CG	2.55	0.41
2:S:195:ASN:HD22	2:S:196:LEU:N	2.18	0.41
8:S:2010:SPO:H15	8:S:2010:SPO:H131	1.85	0.41
1:R:5:PHE:CD1	1:R:5:PHE:C	2.98	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:S:2032:HOH:O	3:T:194:GLN:HB3	2.20	0.41
1:R:2:LEU:HG	1:R:10:ARG:HH12	1.83	0.41
2:M:148:TRP:HA	2:M:148:TRP:HE3	1.85	0.41
3:H:135:LYS:HG2	3:H:136:ALA:N	2.36	0.41
3:T:73:LEU:HD11	3:T:75:VAL:CG1	2.47	0.41
1:L:90:THR:HG23	1:L:132:VAL:HG11	2.01	0.41
1:L:234:LEU:O	1:L:238:LEU:HB2	2.21	0.41
2:M:233:CYS:O	2:M:236:GLU:HB3	2.21	0.41
2:S:100:GLU:H	2:S:100:GLU:CD	2.29	0.41
1:L:135:ARG:N	1:L:136:PRO:CD	2.84	0.41
2:M:204:LEU:O	2:M:207:ALA:HB3	2.20	0.41
2:M:218:MET:HE3	2:M:252:TRP:CZ3	2.56	0.41
8:M:1010:SPO:H15	8:M:1010:SPO:H131	1.88	0.41
3:T:245:ALA:N	3:T:246:PRO:CD	2.84	0.41
2:M:251:PHE:CD2	2:M:251:PHE:C	2.99	0.40
4:M:1003:BCL:H62	4:M:1003:BCL:H92	1.94	0.40
1:R:200:PRO:HB3	1:R:207:ARG:HD3	2.04	0.40
3:H:37:ARG:C	3:H:38:GLU:HG2	2.47	0.40
1:R:124:ALA:HB2	7:R:2006:BPH:HBC3	2.03	0.40
1:L:181:PHE:CZ	4:M:1003:BCL:O1A	2.74	0.40
2:M:148:TRP:HA	2:M:148:TRP:CE3	2.56	0.40
3:T:36:MET:HE3	3:T:40:TYR:CD2	2.56	0.40
4:L:1001:BCL:CBB	8:M:1010:SPO:H243	2.51	0.40
1:L:173:HIS:CE1	1:L:177:ILE:HD11	2.56	0.40
1:R:66:VAL:HG12	1:R:86:TRP:HB2	2.02	0.40
4:S:2004:BCL:H61	5:S:2008:U10:H203	2.03	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%)	269 (96%)	10 (4%)	0	100	100
1	R	279/281 (99%)	263 (94%)	14 (5%)	2 (1%)	18	28
2	M	297/307 (97%)	285 (96%)	12 (4%)	0	100	100
2	S	297/307 (97%)	287 (97%)	10 (3%)	0	100	100
3	H	244/260 (94%)	236 (97%)	8 (3%)	0	100	100
3	T	244/260 (94%)	235 (96%)	9 (4%)	0	100	100
All	All	1640/1696 (97%)	1575 (96%)	63 (4%)	2 (0%)	48	64

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	R	4	SER
1	R	31	VAL

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%)	207 (94%)	13 (6%)	18	31
1	R	220/220 (100%)	207 (94%)	13 (6%)	18	31
2	M	235/240 (98%)	225 (96%)	10 (4%)	26	44
2	S	235/240 (98%)	229 (97%)	6 (3%)	40	63
3	H	199/208 (96%)	193 (97%)	6 (3%)	36	58
3	T	199/208 (96%)	196 (98%)	3 (2%)	57	77
All	All	1308/1336 (98%)	1257 (96%)	51 (4%)	28	48

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	85	LEU
1	L	102	LEU
1	L	126	LEU

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Mol	Chain	Res	Type
1	L	129	LEU
1	L	133	LEU
1	L	189	LEU
1	L	195	LEU
1	L	207	ARG
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	26	LEU
2	M	29	ARG
2	M	60	LEU
2	M	94	LEU
2	M	114	LEU
2	M	151	LEU
2	M	156	LEU
2	M	191	LEU
2	M	232	GLU
3	H	73	LEU
3	H	123	LEU
3	H	135	LYS
3	H	184	LYS
3	H	202	ARG
3	H	231	ASP
1	R	85	LEU
1	R	102	LEU
1	R	126	LEU
1	R	129	LEU
1	R	189	LEU
1	R	195	LEU
1	R	207	ARG
1	R	217	ARG
1	R	231	ARG
1	R	235	LEU
1	R	238	LEU
1	R	247	CYS
1	R	269	LEU
2	S	29	ARG
2	S	94	LEU
2	S	136	ARG

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Mol	Chain	Res	Type
2	S	156	LEU
2	S	191	LEU
2	S	232	GLU
3	T	202	ARG
3	T	208	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	159	ASN
1	L	183	ASN
1	L	211	HIS
1	L	258	GLN
2	M	9	GLN
2	M	195	ASN
3	H	32	GLN
3	H	206	ASN
1	R	87	GLN
1	R	159	ASN
1	R	183	ASN
1	R	211	HIS
1	R	258	GLN
1	R	274	ASN
2	S	9	GLN
2	S	195	ASN
3	T	128	HIS
3	T	194	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 25 ligands modelled in this entry, 2 are monoatomic - leaving 23 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$
4	BCL	R	2002	1	69,74,74	1.82	11 (15%)	79,115,115	1.86	22 (27%)
4	BCL	L	1001	2	54,59,74	2.11	15 (27%)	61,97,115	1.96	14 (22%)
7	BPH	R	2006	-	59,70,70	2.21	15 (25%)	59,101,101	2.87	20 (33%)
9	LDA	M	1012	-	13,15,15	1.95	1 (7%)	14,17,17	1.71	4 (28%)
5	U10	L	1009	-	44,44,63	2.13	19 (43%)	54,56,79	3.01	18 (33%)
5	U10	M	1008	-	38,38,63	2.01	11 (28%)	48,49,79	1.88	11 (22%)
9	LDA	M	1013	-	13,15,15	1.93	1 (7%)	14,17,17	1.70	4 (28%)
9	LDA	M	1014	-	13,15,15	1.96	1 (7%)	14,17,17	1.74	5 (35%)
5	U10	S	2008	-	32,32,63	2.01	9 (28%)	40,41,79	1.93	11 (27%)
7	BPH	M	1006	-	59,70,70	2.13	13 (22%)	59,101,101	2.79	21 (35%)
7	BPH	M	1005	-	49,60,70	2.27	15 (30%)	47,89,101	3.02	21 (44%)
4	BCL	L	1002	1	69,74,74	1.75	10 (14%)	79,115,115	1.88	20 (25%)
4	BCL	M	1003	2	69,74,74	1.77	14 (20%)	79,115,115	1.85	23 (29%)
4	BCL	S	2004	1	69,74,74	1.83	15 (21%)	79,115,115	1.83	19 (24%)
4	BCL	S	2001	2	54,59,74	2.02	14 (25%)	61,97,115	1.97	13 (21%)
4	BCL	L	1004	1	69,74,74	1.81	13 (18%)	79,115,115	1.86	20 (25%)
9	LDA	S	2011	-	13,15,15	1.91	1 (7%)	14,17,17	1.71	4 (28%)
5	U10	R	2009	-	18,18,63	2.25	7 (38%)	24,25,79	2.27	8 (33%)
7	BPH	S	2005	-	49,60,70	2.32	14 (28%)	47,89,101	3.25	23 (48%)
4	BCL	S	2003	2	69,74,74	1.82	12 (17%)	79,115,115	1.93	25 (31%)
8	SPO	S	2010	-	41,41,41	3.10	22 (53%)	47,50,50	2.40	15 (31%)
8	SPO	M	1010	-	41,41,41	3.22	23 (56%)	47,50,50	2.30	14 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	LDA	M	1011	-	13,15,15	1.85	1 (7%)	14,17,17	1.66	4 (28%)

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
4	BCL	R	2002	1	-	6/41/137/137	-
4	BCL	L	1001	2	-	1/23/119/137	-
7	BPH	R	2006	-	2/2/18/22	12/37/105/105	0/5/6/6
9	LDA	M	1012	-	-	6/13/13/13	-
5	U10	L	1009	-	-	8/41/65/87	0/1/1/1
5	U10	M	1008	-	-	1/33/57/87	0/1/1/1
9	LDA	M	1013	-	-	4/13/13/13	-
9	LDA	M	1014	-	-	6/13/13/13	-
5	U10	S	2008	-	-	2/26/50/87	0/1/1/1
7	BPH	M	1006	-	2/2/18/22	13/37/105/105	0/5/6/6
7	BPH	M	1005	-	1/1/16/22	4/25/93/105	0/5/6/6
4	BCL	L	1002	1	-	5/41/137/137	-
4	BCL	M	1003	2	-	10/41/137/137	-
4	BCL	S	2004	1	-	8/41/137/137	-
4	BCL	S	2001	2	-	4/23/119/137	-
4	BCL	L	1004	1	-	10/41/137/137	-
9	LDA	S	2011	-	-	7/13/13/13	-
7	BPH	S	2005	-	1/1/16/22	10/25/93/105	0/5/6/6
5	U10	R	2009	-	-	1/9/33/87	0/1/1/1
4	BCL	S	2003	2	-	8/41/137/137	-
8	SPO	S	2010	-	-	12/47/47/47	-
8	SPO	M	1010	-	-	14/47/47/47	-
9	LDA	M	1011	-	-	6/13/13/13	-

All (257) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	M	1010	SPO	C6-C5	8.60	1.55	1.32
8	M	1010	SPO	C15-C16	8.45	1.56	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	S	2010	SPO	C6-C5	8.18	1.54	1.32
7	S	2005	BPH	C2C-C3C	-7.75	1.48	1.54
8	M	1010	SPO	C10-C11	7.72	1.54	1.34
8	S	2010	SPO	C10-C11	7.69	1.54	1.34
8	S	2010	SPO	C15-C16	7.57	1.54	1.34
4	S	2003	BCL	C3B-C4B	6.97	1.54	1.41
4	L	1002	BCL	C3B-C4B	6.95	1.54	1.41
7	M	1005	BPH	C2C-C3C	-6.93	1.48	1.54
4	R	2002	BCL	C3B-C4B	6.86	1.54	1.41
7	R	2006	BPH	C2C-C3C	-6.85	1.48	1.54
9	M	1012	LDA	O1-N1	-6.71	1.25	1.42
9	M	1014	LDA	O1-N1	-6.67	1.25	1.42
9	M	1013	LDA	O1-N1	-6.60	1.26	1.42
9	S	2011	LDA	O1-N1	-6.53	1.26	1.42
7	R	2006	BPH	C1D-C2D	6.48	1.46	1.39
7	M	1006	BPH	C2C-C3C	-6.46	1.49	1.54
4	S	2001	BCL	C3B-C4B	6.43	1.53	1.41
4	L	1004	BCL	C3B-C4B	6.37	1.53	1.41
7	S	2005	BPH	C1D-C2D	6.35	1.46	1.39
4	L	1001	BCL	C3B-C4B	6.34	1.53	1.41
4	M	1003	BCL	C3B-C4B	6.30	1.53	1.41
9	M	1011	LDA	O1-N1	-6.25	1.26	1.42
4	S	2004	BCL	C3B-C4B	6.17	1.53	1.41
7	M	1005	BPH	C1D-C2D	6.16	1.46	1.39
7	M	1006	BPH	C1D-C2D	6.12	1.46	1.39
4	R	2002	BCL	MG-ND	6.05	2.17	2.05
4	M	1003	BCL	MG-NB	-5.91	1.94	2.05
7	M	1005	BPH	C1B-C2B	5.83	1.45	1.39
7	M	1006	BPH	C1B-C2B	5.79	1.45	1.39
4	L	1002	BCL	MG-ND	5.68	2.17	2.05
4	L	1001	BCL	MG-NB	-5.55	1.94	2.05
7	S	2005	BPH	C1B-C2B	5.54	1.45	1.39
4	S	2004	BCL	MG-NB	-5.53	1.94	2.05
7	M	1006	BPH	C11-C10	-5.45	1.29	1.52
4	S	2001	BCL	MG-ND	5.44	2.16	2.05
7	R	2006	BPH	C11-C10	-5.43	1.29	1.52
4	S	2003	BCL	MG-NB	-5.42	1.95	2.05
4	M	1003	BCL	MG-ND	5.36	2.16	2.05
4	L	1001	BCL	MG-ND	5.35	2.16	2.05
4	R	2002	BCL	MG-NB	-5.26	1.95	2.05
4	S	2003	BCL	MG-ND	5.20	2.16	2.05
7	R	2006	BPH	C1B-C2B	5.19	1.45	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	S	2001	BCL	MG-NB	-5.14	1.95	2.05
4	S	2004	BCL	MG-ND	5.10	2.15	2.05
4	L	1004	BCL	MG-ND	5.08	2.15	2.05
8	M	1010	SPO	C21-C20	5.06	1.50	1.36
4	L	1001	BCL	C3C-C4C	-5.03	1.45	1.51
5	R	2009	U10	O4-C4	5.02	1.48	1.36
5	S	2008	U10	O4-C4	5.01	1.48	1.36
5	L	1009	U10	O4-C4	4.94	1.48	1.36
4	L	1002	BCL	MG-NB	-4.91	1.96	2.05
8	S	2010	SPO	C21-C20	4.87	1.49	1.36
4	L	1004	BCL	MG-NB	-4.85	1.96	2.05
5	M	1008	U10	O4-C4	4.65	1.48	1.36
8	S	2010	SPO	C26-C25	4.54	1.46	1.34
5	L	1009	U10	C13-C14	4.50	1.43	1.33
8	M	1010	SPO	C4-C1	4.49	1.60	1.52
7	M	1005	BPH	O2D-CGD	4.41	1.44	1.33
8	M	1010	SPO	C26-C25	4.33	1.46	1.34
7	S	2005	BPH	O2A-CGA	4.32	1.45	1.33
8	S	2010	SPO	O1-CM1	4.26	1.56	1.43
8	M	1010	SPO	O1-CM1	4.24	1.56	1.43
7	R	2006	BPH	O2A-CGA	4.23	1.45	1.33
7	M	1006	BPH	O2D-CGD	4.15	1.43	1.33
5	M	1008	U10	C7-C8	-4.15	1.44	1.50
7	R	2006	BPH	O2D-CGD	4.12	1.43	1.33
4	S	2001	BCL	C3C-C4C	-4.08	1.46	1.51
7	M	1005	BPH	O2A-CGA	3.91	1.44	1.33
7	S	2005	BPH	O2D-CGD	3.88	1.42	1.33
7	M	1006	BPH	O2A-CGA	3.83	1.44	1.33
4	S	2003	BCL	MG-NA	3.80	2.15	2.06
7	R	2006	BPH	C3B-C4B	3.78	1.47	1.41
5	M	1008	U10	C13-C14	3.77	1.41	1.33
5	L	1009	U10	C8-C9	3.76	1.41	1.33
5	S	2008	U10	C13-C14	3.75	1.41	1.33
4	S	2004	BCL	C1B-C2B	3.70	1.51	1.43
4	L	1001	BCL	MG-NC	-3.65	1.97	2.06
4	L	1004	BCL	C1B-C2B	3.63	1.51	1.43
7	M	1006	BPH	C3B-C4B	3.57	1.47	1.41
4	L	1004	BCL	MG-NC	-3.51	1.97	2.06
4	R	2002	BCL	CBB-CAB	3.50	1.57	1.50
5	R	2009	U10	C6-C1	3.50	1.41	1.35
5	L	1009	U10	C6-C1	3.48	1.41	1.35
5	L	1009	U10	O3-C3	3.46	1.45	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	S	2008	U10	O3-C3	3.45	1.45	1.36
7	M	1005	BPH	C3B-C4B	3.42	1.47	1.41
5	M	1008	U10	O3-C3M	-3.42	1.37	1.45
5	M	1008	U10	C6-C1	3.42	1.41	1.35
8	M	1010	SPO	C10-C9	3.38	1.53	1.43
5	R	2009	U10	O3-C3	3.38	1.44	1.36
8	S	2010	SPO	C4-C1	3.26	1.58	1.52
5	M	1008	U10	C23-C24	3.25	1.40	1.33
7	S	2005	BPH	C3B-C4B	3.25	1.46	1.41
7	R	2006	BPH	C1A-C2A	3.24	1.55	1.51
5	L	1009	U10	C23-C24	3.23	1.40	1.33
7	R	2006	BPH	CHA-CBD	3.21	1.55	1.51
4	L	1004	BCL	CBB-CAB	3.20	1.56	1.50
4	L	1001	BCL	C1B-C2B	3.18	1.50	1.43
8	S	2010	SPO	C10-C9	3.16	1.53	1.43
4	M	1003	BCL	MG-NA	3.16	2.13	2.06
7	S	2005	BPH	CHA-CBD	3.15	1.55	1.51
4	L	1002	BCL	MG-NA	3.12	2.13	2.06
7	M	1006	BPH	CHA-CBD	3.12	1.55	1.51
5	S	2008	U10	C6-C1	3.12	1.40	1.35
5	S	2008	U10	C7-C8	-3.10	1.45	1.50
5	R	2009	U10	O3-C3M	-3.10	1.38	1.45
4	S	2004	BCL	CBB-CAB	3.09	1.56	1.50
7	M	1005	BPH	O2D-CED	-3.08	1.38	1.45
4	R	2002	BCL	MG-NA	3.07	2.13	2.06
7	S	2005	BPH	C3A-C2A	-3.06	1.52	1.54
5	S	2008	U10	O3-C3M	-3.06	1.38	1.45
4	L	1004	BCL	C3C-C4C	-3.05	1.47	1.51
4	L	1002	BCL	CBB-CAB	3.04	1.56	1.50
4	S	2003	BCL	C3D-C4D	-3.04	1.37	1.44
7	M	1006	BPH	O2D-CED	-3.03	1.38	1.45
4	S	2001	BCL	C1B-C2B	3.03	1.50	1.43
5	M	1008	U10	O3-C3	3.01	1.44	1.36
7	M	1005	BPH	CHA-CBD	3.00	1.55	1.51
5	S	2008	U10	C18-C19	2.98	1.39	1.33
4	R	2002	BCL	C1B-C2B	2.98	1.50	1.43
7	R	2006	BPH	C2-C3	2.98	1.39	1.33
5	M	1008	U10	C18-C19	2.98	1.39	1.33
8	M	1010	SPO	C25-C23	-2.97	1.39	1.46
4	M	1003	BCL	C4B-NB	-2.96	1.34	1.37
8	M	1010	SPO	C14-C12	2.95	1.42	1.35
8	M	1010	SPO	C15-C14	2.95	1.52	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	M	1005	BPH	CAA-C2A	2.94	1.60	1.54
8	S	2010	SPO	C25-C23	-2.94	1.39	1.46
7	M	1006	BPH	CAA-C2A	2.93	1.60	1.54
5	S	2008	U10	C8-C9	2.92	1.39	1.33
5	L	1009	U10	O3-C3M	-2.90	1.38	1.45
8	S	2010	SPO	C14-C12	2.90	1.42	1.35
8	M	1010	SPO	C37-C38	2.89	1.41	1.32
4	S	2003	BCL	CHD-C1D	2.89	1.44	1.38
4	L	1002	BCL	CHD-C1D	2.89	1.44	1.38
4	S	2004	BCL	C3C-C4C	-2.87	1.48	1.51
4	S	2001	BCL	MG-NC	-2.87	1.99	2.06
7	M	1006	BPH	C4D-ND	-2.86	1.34	1.38
5	R	2009	U10	C8-C9	2.84	1.40	1.32
4	L	1001	BCL	C3D-C4D	-2.82	1.37	1.44
7	S	2005	BPH	C4D-ND	-2.82	1.34	1.38
8	M	1010	SPO	C32-C33	2.81	1.39	1.33
5	L	1009	U10	C18-C19	2.80	1.39	1.33
5	L	1009	U10	C31-C29	2.79	1.57	1.51
4	S	2001	BCL	C3D-C4D	-2.79	1.37	1.44
4	S	2004	BCL	MG-NA	2.78	2.12	2.06
8	S	2010	SPO	C8-C7	2.78	1.56	1.50
8	M	1010	SPO	O1-C1	2.78	1.57	1.41
7	R	2006	BPH	C4D-ND	-2.78	1.34	1.38
4	S	2004	BCL	CAA-C2A	2.77	1.59	1.54
4	S	2004	BCL	MG-NC	-2.77	1.99	2.06
8	S	2010	SPO	O1-C1	2.75	1.57	1.41
8	M	1010	SPO	C11-C12	-2.75	1.40	1.46
4	S	2001	BCL	MG-NA	2.73	2.12	2.06
4	S	2003	BCL	C4-C3	2.73	1.57	1.50
4	S	2003	BCL	C1B-C2B	2.71	1.49	1.43
7	R	2006	BPH	O2D-CED	-2.70	1.39	1.45
8	S	2010	SPO	C11-C12	-2.70	1.40	1.46
8	S	2010	SPO	C32-C33	2.69	1.39	1.33
7	S	2005	BPH	C1A-C2A	2.69	1.55	1.51
8	S	2010	SPO	C37-C38	2.67	1.40	1.32
5	R	2009	U10	C7-C8	-2.66	1.46	1.50
5	L	1009	U10	C7-C6	2.65	1.56	1.51
4	M	1003	BCL	C3D-C4D	-2.63	1.38	1.44
5	L	1009	U10	C7-C8	-2.62	1.46	1.50
7	M	1005	BPH	C2-C3	2.62	1.39	1.33
4	M	1003	BCL	C1B-C2B	2.61	1.49	1.43
4	L	1001	BCL	C4B-NB	-2.60	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	S	2010	SPO	C26-C27	2.59	1.51	1.43
7	M	1005	BPH	C3A-C2A	-2.58	1.52	1.54
7	S	2005	BPH	CAA-C2A	2.58	1.59	1.54
4	L	1002	BCL	C1B-C2B	2.56	1.49	1.43
5	R	2009	U10	C7-C6	2.56	1.56	1.51
4	S	2003	BCL	C4B-NB	-2.55	1.34	1.37
7	S	2005	BPH	C2-C3	2.55	1.38	1.33
4	R	2002	BCL	C3D-C4D	-2.53	1.38	1.44
4	M	1003	BCL	CMD-C2D	2.53	1.55	1.50
7	M	1005	BPH	C4D-ND	-2.53	1.34	1.38
8	S	2010	SPO	C13-C12	2.52	1.55	1.50
4	L	1004	BCL	C3D-C4D	-2.51	1.38	1.44
5	L	1009	U10	C32-C33	-2.51	1.42	1.50
5	L	1009	U10	C28-C29	2.51	1.38	1.33
7	S	2005	BPH	O2D-CED	-2.51	1.39	1.45
4	S	2004	BCL	C3D-C4D	-2.50	1.38	1.44
8	S	2010	SPO	C15-C14	2.48	1.50	1.43
4	S	2004	BCL	CAA-CBA	2.45	1.60	1.52
8	S	2010	SPO	C6-C7	-2.45	1.40	1.46
8	S	2010	SPO	C24-C23	2.45	1.55	1.50
8	M	1010	SPO	C13-C12	2.44	1.55	1.50
4	S	2004	BCL	C4-C3	2.44	1.56	1.50
4	L	1002	BCL	C3D-C4D	-2.43	1.38	1.44
4	R	2002	BCL	CHD-C1D	2.43	1.43	1.38
4	M	1003	BCL	C4-C3	2.42	1.56	1.50
5	M	1008	U10	C15-C14	2.42	1.56	1.50
4	S	2003	BCL	CBB-CAB	2.42	1.54	1.50
7	M	1006	BPH	O1D-CGD	2.41	1.27	1.21
4	L	1001	BCL	C1D-C2D	-2.40	1.40	1.45
4	L	1001	BCL	CAA-CBA	2.40	1.60	1.52
5	M	1008	U10	C27-C28	-2.40	1.43	1.50
4	L	1001	BCL	MG-NA	2.38	2.11	2.06
4	L	1004	BCL	C6-C5	2.38	1.60	1.52
4	R	2002	BCL	CMD-C2D	2.38	1.55	1.50
4	S	2003	BCL	MG-NC	-2.37	2.00	2.06
7	M	1005	BPH	O1D-CGD	2.36	1.27	1.21
4	R	2002	BCL	C4-C3	2.35	1.56	1.50
4	S	2003	BCL	CMD-C2D	2.35	1.55	1.50
4	S	2004	BCL	CHD-C1D	2.35	1.43	1.38
8	M	1010	SPO	C8-C7	2.34	1.55	1.50
4	L	1001	BCL	CBB-CAB	2.34	1.54	1.50
7	R	2006	BPH	CAA-C2A	2.34	1.58	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L	1009	U10	C20-C19	2.32	1.56	1.50
5	L	1009	U10	C30-C29	2.32	1.56	1.50
5	L	1009	U10	C15-C14	2.31	1.56	1.50
4	S	2001	BCL	CHD-C1D	2.31	1.42	1.38
8	M	1010	SPO	C26-C27	2.29	1.50	1.43
4	L	1004	BCL	CMD-C2D	2.29	1.55	1.50
8	S	2010	SPO	C35-C33	2.29	1.56	1.51
4	S	2004	BCL	C4B-NB	-2.28	1.34	1.37
4	L	1001	BCL	CAA-C2A	2.27	1.58	1.54
4	L	1004	BCL	MG-NA	2.27	2.11	2.06
4	S	2001	BCL	CBB-CAB	2.26	1.54	1.50
4	S	2001	BCL	C4B-NB	-2.26	1.34	1.37
7	R	2006	BPH	C3D-C2D	-2.25	1.35	1.39
5	S	2008	U10	C15-C14	2.25	1.56	1.50
7	M	1006	BPH	C3A-C2A	-2.24	1.52	1.54
4	L	1004	BCL	C4-C3	2.23	1.56	1.50
7	S	2005	BPH	C3B-C2B	-2.22	1.35	1.39
4	S	2001	BCL	CAA-CBA	2.22	1.59	1.52
7	R	2006	BPH	C3A-C2A	-2.21	1.52	1.54
4	L	1001	BCL	CMD-C2D	2.19	1.55	1.50
4	L	1002	BCL	C4-C3	2.19	1.56	1.50
4	S	2001	BCL	CMD-C2D	2.17	1.55	1.50
4	M	1003	BCL	C3C-C4C	-2.16	1.48	1.51
7	M	1005	BPH	C1A-C2A	2.16	1.54	1.51
7	M	1005	BPH	C3D-C2D	-2.15	1.36	1.39
8	M	1010	SPO	C19-C17	2.15	1.40	1.35
4	L	1004	BCL	C3B-CAB	2.14	1.53	1.46
4	M	1003	BCL	C3A-C2A	2.14	1.60	1.54
4	M	1003	BCL	CBB-CAB	2.14	1.54	1.50
5	L	1009	U10	C26-C24	2.12	1.55	1.51
5	M	1008	U10	C8-C9	2.12	1.37	1.33
8	M	1010	SPO	C40-C38	2.09	1.56	1.50
4	L	1002	BCL	CMD-C2D	2.09	1.55	1.50
4	R	2002	BCL	OBB-CAB	-2.08	1.18	1.23
8	M	1010	SPO	C24-C23	2.07	1.55	1.50
8	M	1010	SPO	C9-C7	2.07	1.40	1.35
5	L	1009	U10	C27-C28	-2.06	1.44	1.50
4	L	1001	BCL	C1-C2	2.06	1.55	1.49
8	M	1010	SPO	C35-C33	2.05	1.55	1.51
4	M	1003	BCL	MG-NC	-2.04	2.01	2.06
4	S	2004	BCL	C3B-CAB	2.03	1.53	1.46
8	S	2010	SPO	C19-C17	2.03	1.40	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	M	1003	BCL	CHD-C1D	2.03	1.42	1.38
5	L	1009	U10	C33-C34	2.01	1.37	1.33
4	S	2001	BCL	OBB-CAB	-2.01	1.18	1.23

All (339) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	1009	U10	C32-C33-C34	15.28	162.60	127.62
7	S	2005	BPH	O2D-CGD-CBD	14.78	127.18	110.95
7	R	2006	BPH	O2D-CGD-CBD	13.91	126.24	110.95
7	M	1005	BPH	O2D-CGD-CBD	13.54	125.83	110.95
7	M	1006	BPH	O2D-CGD-CBD	13.34	125.60	110.95
5	L	1009	U10	C27-C28-C29	8.06	146.07	127.62
4	S	2001	BCL	CBC-CAC-C3C	-6.73	99.14	113.41
5	R	2009	U10	C3M-O3-C3	6.54	139.47	116.47
5	L	1009	U10	C3M-O3-C3	6.44	139.10	116.47
4	L	1002	BCL	C4A-NA-C1A	-6.44	103.74	106.68
5	S	2008	U10	C3M-O3-C3	6.37	138.85	116.47
5	M	1008	U10	C3M-O3-C3	6.16	138.10	116.47
7	S	2005	BPH	C1-C2-C3	6.10	136.19	126.20
7	R	2006	BPH	C1-C2-C3	6.08	136.16	126.20
8	M	1010	SPO	C20-C21-C22	-6.06	111.12	123.52
4	R	2002	BCL	C4A-NA-C1A	-6.06	103.92	106.68
7	M	1006	BPH	C1-C2-C3	6.00	136.03	126.20
4	L	1001	BCL	CBC-CAC-C3C	-5.97	100.75	113.41
8	S	2010	SPO	C20-C21-C22	-5.97	111.31	123.52
7	R	2006	BPH	CBC-CAC-C3C	5.96	125.49	113.78
8	S	2010	SPO	C15-C14-C12	-5.91	118.99	127.28
7	M	1005	BPH	C1-C2-C3	5.64	135.44	126.20
4	S	2003	BCL	C4A-NA-C1A	-5.64	104.11	106.68
4	S	2001	BCL	C4A-NA-C1A	-5.46	104.19	106.68
8	M	1010	SPO	C15-C14-C12	-5.44	119.64	127.28
4	S	2004	BCL	C4A-NA-C1A	-5.23	104.29	106.68
7	S	2005	BPH	O1D-CGD-CBD	-5.21	116.81	124.72
4	L	1004	BCL	C4A-NA-C1A	-5.19	104.31	106.68
8	S	2010	SPO	C26-C27-C28	-5.08	120.54	127.69
7	M	1005	BPH	O1D-CGD-CBD	-5.06	117.04	124.72
7	R	2006	BPH	C4D-CHA-CBD	-5.05	106.03	108.45
8	S	2010	SPO	C25-C23-C22	-4.99	111.16	119.01
4	L	1001	BCL	C4A-NA-C1A	-4.97	104.41	106.68
7	S	2005	BPH	C4D-CHA-CBD	-4.88	106.11	108.45
4	S	2003	BCL	C1D-ND-C4D	4.87	109.73	106.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	M	1010	SPO	C26-C27-C28	-4.87	120.84	127.69
7	R	2006	BPH	O1D-CGD-CBD	-4.87	117.34	124.72
7	M	1006	BPH	O1D-CGD-CBD	-4.79	117.46	124.72
4	L	1004	BCL	C1-O2A-CGA	4.73	128.11	116.65
8	M	1010	SPO	C25-C23-C22	-4.66	111.67	119.01
4	M	1003	BCL	C4A-NA-C1A	-4.59	104.59	106.68
4	M	1003	BCL	C1D-ND-C4D	4.50	109.47	106.31
7	R	2006	BPH	C6-C5-C3	4.46	124.33	113.47
4	L	1001	BCL	C1D-ND-C4D	4.46	109.44	106.31
7	M	1006	BPH	C4D-CHA-CBD	-4.45	106.32	108.45
4	L	1002	BCL	C1D-ND-C4D	4.36	109.37	106.31
7	S	2005	BPH	C6-C5-C3	4.33	124.02	113.47
7	M	1006	BPH	CED-O2D-CGD	4.33	125.73	115.92
4	S	2001	BCL	C1D-ND-C4D	4.32	109.34	106.31
7	M	1005	BPH	C6-C5-C3	4.31	123.98	113.47
4	S	2004	BCL	C1D-ND-C4D	4.29	109.32	106.31
4	S	2003	BCL	C11-C12-C13	-4.27	101.77	115.97
5	M	1008	U10	C27-C28-C29	4.25	141.82	127.64
4	L	1004	BCL	C1D-ND-C4D	4.24	109.29	106.31
7	S	2005	BPH	CBC-CAC-C3C	4.24	122.11	113.78
7	M	1005	BPH	C4D-CHA-CBD	-4.23	106.43	108.45
4	R	2002	BCL	C1D-ND-C4D	4.20	109.26	106.31
8	S	2010	SPO	C24-C23-C25	4.18	124.47	118.09
7	R	2006	BPH	CED-O2D-CGD	4.17	125.37	115.92
7	S	2005	BPH	CED-O2D-CGD	4.08	125.17	115.92
7	M	1005	BPH	CED-O2D-CGD	4.08	125.17	115.92
4	L	1002	BCL	C1-C2-C3	-4.07	119.54	126.20
4	L	1001	BCL	C4D-CHA-C1A	4.05	126.08	121.24
4	M	1003	BCL	C11-C12-C13	-4.05	102.52	115.97
7	M	1006	BPH	C11-C10-C8	4.04	129.39	115.97
7	S	2005	BPH	O2D-CGD-O1D	-4.04	115.99	123.85
7	M	1006	BPH	C6-C5-C3	4.03	123.28	113.47
4	M	1003	BCL	C4D-CHA-C1A	4.01	126.03	121.24
7	M	1006	BPH	CBC-CAC-C3C	3.99	121.62	113.78
4	S	2004	BCL	C11-C12-C13	-3.92	102.93	115.97
4	R	2002	BCL	C7-C6-C5	-3.86	102.98	113.26
8	M	1010	SPO	C24-C23-C25	3.84	123.95	118.09
7	R	2006	BPH	C11-C10-C8	3.84	128.72	115.97
7	R	2006	BPH	O2D-CGD-O1D	-3.82	116.40	123.85
4	S	2001	BCL	C1-C2-C3	-3.78	120.64	126.76
4	S	2004	BCL	CBB-CAB-C3B	3.77	128.35	120.40
4	L	1002	BCL	C7-C6-C5	-3.77	103.22	113.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	R	2009	U10	O5-C5-C6	-3.73	114.58	121.79
8	M	1010	SPO	C18-C17-C19	-3.73	116.78	122.82
4	S	2004	BCL	C4D-CHA-C1A	3.71	125.66	121.24
5	M	1008	U10	C20-C19-C21	-3.69	108.82	115.23
5	L	1009	U10	O5-C5-C6	-3.68	114.68	121.79
4	L	1004	BCL	CBB-CAB-C3B	3.67	128.14	120.40
4	S	2003	BCL	C4D-CHA-C1A	3.66	125.61	121.24
4	S	2001	BCL	C4D-CHA-C1A	3.66	125.61	121.24
7	M	1005	BPH	CBC-CAC-C3C	3.65	120.96	113.78
4	L	1001	BCL	CAC-C3C-C4C	-3.65	104.49	112.58
8	S	2010	SPO	C4-C5-C6	-3.64	119.80	124.91
4	L	1004	BCL	CAC-C3C-C4C	-3.63	104.52	112.58
8	S	2010	SPO	C3-C1-C2	3.62	117.04	110.43
4	L	1004	BCL	OBB-CAB-CBB	-3.58	111.76	119.77
7	M	1006	BPH	O2D-CGD-O1D	-3.58	116.89	123.85
5	S	2008	U10	O5-C5-C6	-3.56	114.90	121.79
8	S	2010	SPO	C15-C16-C17	-3.55	116.63	126.36
4	L	1004	BCL	C4D-CHA-C1A	3.54	125.47	121.24
5	M	1008	U10	O5-C5-C6	-3.54	114.94	121.79
5	L	1009	U10	O2-C2-C3	-3.54	113.54	121.03
4	L	1002	BCL	C4D-CHA-C1A	3.53	125.45	121.24
4	L	1004	BCL	O2A-C1-C2	-3.52	94.55	108.11
9	S	2011	LDA	CM1-N1-C1	-3.52	102.84	110.23
8	S	2010	SPO	C18-C17-C19	-3.50	117.14	122.82
4	S	2004	BCL	CBC-CAC-C3C	-3.50	105.99	113.41
7	R	2006	BPH	C1C-C2C-C3C	3.49	106.16	102.84
4	S	2004	BCL	OBB-CAB-CBB	-3.49	111.96	119.77
4	S	2003	BCL	OBB-CAB-CBB	-3.49	111.96	119.77
4	L	1001	BCL	C2C-C3C-C4C	3.48	106.56	101.34
9	M	1012	LDA	CM1-N1-C1	-3.48	102.92	110.23
8	S	2010	SPO	C8-C7-C6	3.46	123.38	118.09
4	M	1003	BCL	CBB-CAB-C3B	3.46	127.69	120.40
9	M	1013	LDA	CM1-N1-C1	-3.45	102.98	110.23
7	M	1005	BPH	O2D-CGD-O1D	-3.45	117.13	123.85
4	S	2003	BCL	C4-C3-C5	3.45	121.22	115.23
7	S	2005	BPH	C1C-C2C-C3C	3.44	106.11	102.84
4	S	2003	BCL	CBB-CAB-C3B	3.44	127.66	120.40
8	M	1010	SPO	C3-C1-C2	3.44	116.72	110.43
9	M	1011	LDA	CM1-N1-C1	-3.42	103.06	110.23
4	R	2002	BCL	C4D-CHA-C1A	3.41	125.32	121.24
4	M	1003	BCL	OBB-CAB-CBB	-3.41	112.13	119.77
9	M	1014	LDA	CM1-N1-C1	-3.41	103.08	110.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	1009	U10	C1-C6-C5	-3.40	116.31	119.62
5	R	2009	U10	O2-C2-C3	-3.40	113.83	121.03
4	L	1001	BCL	OBB-CAB-CBB	-3.38	112.19	119.77
4	S	2001	BCL	OBB-CAB-CBB	-3.38	112.20	119.77
8	M	1010	SPO	C15-C16-C17	-3.37	117.11	126.36
4	L	1004	BCL	CBC-CAC-C3C	-3.37	106.26	113.41
5	S	2008	U10	O2-C2-C3	-3.37	113.89	121.03
4	S	2001	BCL	CAA-C2A-C3A	-3.37	103.89	113.00
4	L	1001	BCL	CAA-C2A-C3A	-3.37	103.90	113.00
4	R	2002	BCL	OBB-CAB-CBB	-3.36	112.25	119.77
4	L	1002	BCL	OBB-CAB-CBB	-3.36	112.25	119.77
8	M	1010	SPO	C8-C7-C6	3.34	123.19	118.09
8	S	2010	SPO	C6-C7-C9	-3.33	113.77	119.01
7	M	1006	BPH	C1C-C2C-C3C	3.32	106.00	102.84
4	M	1003	BCL	C4-C3-C5	3.32	121.00	115.23
4	L	1002	BCL	CBB-CAB-C3B	3.32	127.40	120.40
4	R	2002	BCL	CBB-CAB-C3B	3.31	127.39	120.40
4	S	2001	BCL	C2C-C3C-C4C	3.30	106.28	101.34
5	L	1009	U10	C20-C19-C21	-3.26	109.58	115.23
7	M	1006	BPH	CMA-C3A-C4A	-3.24	107.63	114.61
5	R	2009	U10	C1-C6-C5	-3.24	116.47	119.62
7	R	2006	BPH	C4C-C3C-C2C	3.24	105.92	102.84
4	S	2003	BCL	CAA-CBA-CGA	-3.23	104.04	113.21
4	L	1004	BCL	C2C-C3C-C4C	3.20	106.13	101.34
4	R	2002	BCL	O1D-CGD-CBD	3.16	130.75	124.52
4	S	2004	BCL	C2C-C3C-C4C	3.14	106.05	101.34
4	R	2002	BCL	C11-C12-C13	-3.14	105.53	115.97
5	M	1008	U10	O2-C2-C3	-3.14	114.38	121.03
4	M	1003	BCL	CAA-CBA-CGA	-3.13	104.31	113.21
4	S	2004	BCL	CAA-C2A-C3A	-3.12	104.58	113.00
4	L	1004	BCL	C11-C12-C13	-3.11	105.61	115.97
7	M	1005	BPH	CMA-C3A-C4A	-3.11	107.91	114.61
4	S	2004	BCL	CAC-C3C-C4C	-3.10	105.71	112.58
7	M	1005	BPH	C1C-C2C-C3C	3.07	105.76	102.84
4	R	2002	BCL	O2D-CGD-CBD	-3.05	105.90	111.23
4	L	1004	BCL	CHD-C1D-ND	-3.03	120.53	124.80
7	S	2005	BPH	CMA-C3A-C4A	-3.03	108.08	114.61
7	M	1006	BPH	C4C-C3C-C2C	3.02	105.72	102.84
4	L	1001	BCL	CBB-CAB-C3B	3.01	126.75	120.40
4	L	1002	BCL	C11-C12-C13	-2.98	106.07	115.97
7	M	1005	BPH	C4C-C3C-C2C	2.97	105.67	102.84
5	S	2008	U10	C20-C19-C21	-2.96	110.09	115.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	S	2001	BCL	CHD-C1D-ND	-2.95	120.64	124.80
4	S	2001	BCL	CBB-CAB-C3B	2.95	126.62	120.40
4	S	2003	BCL	CHA-C1A-NA	-2.94	119.73	126.39
4	L	1002	BCL	CHD-C1D-ND	-2.93	120.68	124.80
4	S	2004	BCL	C1-C2-C3	-2.92	121.41	126.20
7	S	2005	BPH	C4C-C3C-C2C	2.92	105.62	102.84
4	S	2004	BCL	CHA-C1A-NA	-2.92	119.79	126.39
4	R	2002	BCL	CHD-C1D-ND	-2.91	120.70	124.80
4	L	1001	BCL	CHA-C1A-NA	-2.88	119.88	126.39
4	M	1003	BCL	CHA-C1A-NA	-2.87	119.89	126.39
4	L	1001	BCL	CHD-C1D-ND	-2.84	120.80	124.80
7	R	2006	BPH	CMA-C3A-C4A	-2.84	108.49	114.61
8	M	1010	SPO	C6-C7-C9	-2.83	114.55	119.01
4	S	2001	BCL	CHA-C1A-NA	-2.82	120.01	126.39
4	L	1002	BCL	CAC-C3C-C4C	-2.81	106.34	112.58
4	S	2004	BCL	CHD-C1D-ND	-2.79	120.87	124.80
9	M	1013	LDA	O1-N1-C1	2.79	116.12	109.27
7	M	1006	BPH	C7-C6-C5	-2.79	105.84	113.26
9	M	1014	LDA	O1-N1-C1	2.78	116.10	109.27
9	M	1012	LDA	O1-N1-C1	2.78	116.09	109.27
4	R	2002	BCL	CAA-C2A-C3A	-2.77	105.50	113.00
4	S	2003	BCL	C4D-C3D-CAD	-2.77	105.10	108.11
9	S	2011	LDA	O1-N1-C1	2.77	116.06	109.27
7	R	2006	BPH	CMB-C2B-C3B	2.77	130.21	124.68
4	L	1002	BCL	O2D-CGD-CBD	-2.76	106.40	111.23
4	L	1002	BCL	CAA-C2A-C3A	-2.74	105.59	113.00
9	M	1011	LDA	O1-N1-C1	2.74	115.99	109.27
4	L	1002	BCL	CHA-C1A-NA	-2.74	120.19	126.39
7	S	2005	BPH	C4-C3-C5	2.72	119.95	115.23
4	R	2002	BCL	CHA-C1A-NA	-2.72	120.23	126.39
5	R	2009	U10	C8-C7-C6	2.71	118.75	112.08
7	M	1005	BPH	CMB-C2B-C3B	2.71	130.09	124.68
7	M	1006	BPH	C5-C3-C2	-2.71	115.09	121.17
7	M	1006	BPH	C4-C3-C5	2.70	119.91	115.23
4	L	1001	BCL	C4D-C3D-CAD	-2.69	105.18	108.11
4	M	1003	BCL	CBA-CAA-C2A	2.67	121.73	113.79
4	L	1004	BCL	C16-C15-C13	-2.66	107.11	115.97
7	M	1006	BPH	CMB-C2B-C3B	2.66	130.00	124.68
5	M	1008	U10	C21-C19-C18	2.66	127.14	121.17
7	M	1006	BPH	C2B-C1B-NB	2.66	111.35	109.43
4	R	2002	BCL	C1-C2-C3	-2.66	121.85	126.20
7	M	1006	BPH	O2A-CGA-O1A	-2.65	116.99	123.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	1009	U10	C16-C14-C13	2.65	127.11	121.17
5	S	2008	U10	C1-C6-C5	-2.64	117.06	119.62
4	L	1002	BCL	O1D-CGD-CBD	2.63	129.71	124.52
5	L	1009	U10	C8-C7-C6	2.62	118.54	112.08
4	M	1003	BCL	C4D-C3D-CAD	-2.62	105.26	108.11
4	S	2003	BCL	CGD-CBD-CAD	-2.60	102.42	110.85
5	L	1009	U10	C21-C19-C18	2.60	127.00	121.17
4	M	1003	BCL	C1-C2-C3	-2.59	121.95	126.20
7	S	2005	BPH	C1B-NB-C4B	-2.59	105.04	108.82
4	L	1004	BCL	CHA-C1A-NA	-2.59	120.53	126.39
7	S	2005	BPH	C2B-C1B-NB	2.58	111.30	109.43
9	M	1014	LDA	C6-C5-C4	-2.58	101.34	114.37
7	S	2005	BPH	CAA-C2A-C3A	-2.57	106.06	113.00
4	L	1002	BCL	C16-C15-C13	-2.57	107.43	115.97
4	M	1003	BCL	CBC-CAC-C3C	-2.56	107.97	113.41
4	R	2002	BCL	CAC-C3C-C4C	-2.56	106.89	112.58
7	R	2006	BPH	O2A-CGA-O1A	-2.56	117.22	123.63
4	L	1004	BCL	CBA-CAA-C2A	2.56	121.41	113.79
7	S	2005	BPH	C5-C3-C2	-2.55	115.44	121.17
4	S	2003	BCL	C7-C6-C5	-2.53	106.53	113.26
7	M	1005	BPH	C2B-C1B-NB	2.51	111.24	109.43
4	R	2002	BCL	C4D-C3D-CAD	-2.49	105.40	108.11
4	S	2003	BCL	CBA-CAA-C2A	2.49	121.21	113.79
7	R	2006	BPH	C7-C6-C5	-2.49	106.63	113.26
4	M	1003	BCL	CHD-C1D-ND	-2.49	121.30	124.80
8	M	1010	SPO	C10-C9-C7	-2.48	123.80	127.28
4	S	2003	BCL	CHD-C1D-ND	-2.48	121.32	124.80
7	S	2005	BPH	CMB-C2B-C3B	2.47	129.62	124.68
4	R	2002	BCL	C16-C15-C13	-2.47	107.76	115.97
4	R	2002	BCL	CBC-CAC-C3C	-2.47	108.18	113.41
4	L	1002	BCL	C4D-C3D-CAD	-2.47	105.43	108.11
7	M	1005	BPH	C1B-NB-C4B	-2.46	105.22	108.82
7	S	2005	BPH	CMD-C2D-C3D	2.45	129.57	124.68
4	S	2003	BCL	C1-C2-C3	-2.44	122.20	126.20
8	M	1010	SPO	C4-C5-C6	-2.43	121.50	124.91
7	S	2005	BPH	O2A-CGA-O1A	-2.42	117.56	123.63
8	S	2010	SPO	C20-C19-C17	-2.42	123.88	127.28
7	M	1006	BPH	C1B-NB-C4B	-2.42	105.30	108.82
5	L	1009	U10	C30-C29-C31	-2.41	111.05	115.23
4	L	1004	BCL	C12-C11-C10	-2.41	102.49	113.28
7	R	2006	BPH	C2B-C1B-NB	2.41	111.17	109.43
4	M	1003	BCL	C7-C6-C5	-2.40	106.88	113.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	S	2003	BCL	C11-C10-C8	-2.39	108.01	115.97
5	M	1008	U10	C7-C6-C5	-2.39	115.74	118.52
4	S	2001	BCL	C4D-C3D-CAD	-2.39	105.51	108.11
7	M	1005	BPH	CAA-C2A-C3A	-2.38	106.56	113.00
4	S	2003	BCL	CBC-CAC-C3C	-2.38	108.37	113.41
5	M	1008	U10	C16-C14-C13	2.37	126.49	121.17
9	M	1014	LDA	CM2-N1-C1	2.37	115.21	110.23
5	S	2008	U10	C16-C14-C13	2.36	126.47	121.17
5	S	2008	U10	C6-C1-C2	2.36	121.03	119.17
8	S	2010	SPO	C1-C4-C5	2.36	119.11	112.98
5	L	1009	U10	C31-C29-C28	2.36	126.47	121.17
5	L	1009	U10	C22-C21-C19	2.36	121.00	113.19
9	S	2011	LDA	CM2-N1-C1	2.36	115.19	110.23
9	M	1013	LDA	C9-C8-C7	-2.35	102.51	114.37
4	L	1002	BCL	C2C-C3C-C4C	2.34	104.85	101.34
4	S	2003	BCL	CAA-C2A-C3A	-2.34	106.67	113.00
5	M	1008	U10	C1-C6-C5	-2.34	117.34	119.62
5	S	2008	U10	C17-C18-C19	2.34	132.97	127.62
7	M	1006	BPH	CMD-C2D-C3D	2.33	129.34	124.68
4	L	1004	BCL	C4D-C3D-CAD	-2.32	105.58	108.11
8	M	1010	SPO	C1-C4-C5	2.32	119.01	112.98
7	M	1005	BPH	O2A-CGA-O1A	-2.31	117.84	123.63
5	R	2009	U10	C7-C6-C5	-2.31	115.83	118.52
9	M	1013	LDA	CM2-N1-C1	2.31	115.08	110.23
4	S	2001	BCL	CHD-C1D-C2D	2.31	130.29	125.49
4	M	1003	BCL	C11-C10-C8	-2.31	108.30	115.97
5	R	2009	U10	C6-C1-C2	2.30	120.98	119.17
9	S	2011	LDA	C9-C8-C7	-2.29	102.78	114.37
9	M	1012	LDA	C9-C8-C7	-2.29	102.78	114.37
4	L	1002	BCL	C12-C11-C10	-2.29	103.03	113.28
5	S	2008	U10	C7-C6-C5	-2.28	115.86	118.52
4	S	2003	BCL	C2C-C3C-C4C	2.28	104.75	101.34
4	S	2004	BCL	C16-C15-C13	-2.27	108.43	115.97
4	S	2003	BCL	O1D-CGD-CBD	2.26	128.98	124.52
9	M	1012	LDA	CM2-N1-C1	2.26	114.98	110.23
4	L	1002	BCL	CHD-C1D-C2D	2.26	130.19	125.49
7	R	2006	BPH	CAA-C2A-C3A	-2.24	106.95	113.00
4	M	1003	BCL	CAC-C3C-C4C	-2.24	107.61	112.58
4	M	1003	BCL	C16-C15-C13	-2.24	108.53	115.97
4	S	2003	BCL	C16-C15-C13	-2.23	108.54	115.97
4	R	2002	BCL	C2C-C3C-C4C	2.23	104.68	101.34
4	L	1004	BCL	CHD-C1D-C2D	2.23	130.13	125.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L	1001	BCL	CMD-C2D-C3D	2.23	132.80	127.69
4	S	2003	BCL	CHD-C1D-C2D	2.23	130.12	125.49
4	S	2003	BCL	O2A-CGA-O1A	-2.22	118.06	123.63
4	S	2004	BCL	C7-C6-C5	-2.22	107.34	113.26
9	M	1011	LDA	CM2-N1-C1	2.22	114.90	110.23
4	S	2004	BCL	CHD-C1D-C2D	2.22	130.11	125.49
8	S	2010	SPO	C10-C9-C7	-2.22	124.17	127.28
8	M	1010	SPO	C16-C17-C19	2.21	122.49	119.01
4	L	1004	BCL	C7-C6-C5	-2.21	107.37	113.26
5	L	1009	U10	C6-C1-C2	2.21	120.91	119.17
5	L	1009	U10	C7-C6-C5	-2.20	115.96	118.52
9	M	1011	LDA	C9-C8-C7	-2.20	103.25	114.37
7	S	2005	BPH	C4A-C3A-C2A	2.19	104.92	102.84
7	S	2005	BPH	C7-C6-C5	-2.16	107.50	113.26
4	S	2003	BCL	O2A-CGA-CBA	2.16	118.43	111.83
4	M	1003	BCL	O1D-CGD-CBD	2.14	128.74	124.52
5	S	2008	U10	C4-C3-C2	-2.13	116.78	120.69
4	R	2002	BCL	CHD-C1D-C2D	2.13	129.92	125.49
4	R	2002	BCL	C12-C11-C10	-2.13	103.74	113.28
5	R	2009	U10	C4-C3-C2	-2.12	116.81	120.69
4	M	1003	BCL	O2A-CGA-O1A	-2.12	118.33	123.63
5	L	1009	U10	C4-C3-C2	-2.12	116.81	120.69
7	R	2006	BPH	C1B-NB-C4B	-2.11	105.74	108.82
5	M	1008	U10	C6-C1-C2	2.11	120.84	119.17
4	L	1002	BCL	CBC-CAC-C3C	-2.11	108.95	113.41
5	M	1008	U10	C31-C29-C30	-2.10	109.75	114.59
5	S	2008	U10	C21-C19-C18	2.10	125.88	121.17
7	M	1005	BPH	CMD-C2D-C3D	2.10	128.88	124.68
4	S	2004	BCL	C4D-C3D-CAD	-2.10	105.83	108.11
7	R	2006	BPH	CMD-C2D-C3D	2.09	128.85	124.68
4	R	2002	BCL	C4-C3-C5	2.08	118.85	115.23
7	M	1005	BPH	C4A-C3A-C2A	2.08	104.82	102.84
4	L	1001	BCL	CHD-C1D-C2D	2.08	129.82	125.49
4	S	2004	BCL	C11-C10-C8	-2.08	109.05	115.97
4	S	2003	BCL	CAC-C3C-C4C	-2.07	107.98	112.58
4	S	2004	BCL	C14-C13-C15	-2.07	103.89	111.27
7	M	1006	BPH	OBD-CAD-CBD	-2.05	122.81	125.82
7	M	1005	BPH	CMA-C3A-C2A	-2.05	106.22	114.13
4	M	1003	BCL	C2C-C3C-C4C	2.05	104.40	101.34
5	L	1009	U10	C3-C2-C1	2.04	122.14	118.10
4	R	2002	BCL	CMD-C2D-C3D	2.04	132.37	127.69
7	S	2005	BPH	OBD-CAD-CBD	-2.04	122.83	125.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	S	2005	BPH	CMA-C3A-C2A	-2.04	106.25	114.13
7	M	1005	BPH	OBD-CAD-CBD	-2.04	122.83	125.82
9	M	1014	LDA	C9-C8-C7	-2.02	104.15	114.37
5	L	1009	U10	C10-C9-C11	-2.01	111.73	115.23
4	L	1004	BCL	C1-C2-C3	-2.01	122.91	126.20
7	M	1005	BPH	C7-C6-C5	-2.01	107.91	113.26
7	R	2006	BPH	OBD-CAD-CBD	-2.01	122.88	125.82
8	S	2010	SPO	C18-C17-C16	2.01	121.15	118.09
4	M	1003	BCL	C3D-C2D-C1D	-2.00	103.09	105.83
4	M	1003	BCL	CHD-C1D-C2D	2.00	129.66	125.49

All (6) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	M	1005	BPH	C8
7	M	1006	BPH	C13
7	M	1006	BPH	C8
7	R	2006	BPH	C13
7	R	2006	BPH	C8
7	S	2005	BPH	C8

All (158) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	L	1004	BCL	C1A-C2A-CAA-CBA
4	L	1004	BCL	C3A-C2A-CAA-CBA
4	M	1003	BCL	C4-C3-C5-C6
5	L	1009	U10	C24-C26-C27-C28
5	L	1009	U10	C31-C32-C33-C34
7	M	1006	BPH	C4C-C3C-CAC-CBC
7	M	1006	BPH	C2C-C3C-CAC-CBC
7	M	1006	BPH	C1-C2-C3-C4
7	M	1006	BPH	C1-C2-C3-C5
7	R	2006	BPH	C4C-C3C-CAC-CBC
7	R	2006	BPH	C2C-C3C-CAC-CBC
7	S	2005	BPH	C2-C3-C5-C6
7	S	2005	BPH	C4-C3-C5-C6
8	M	1010	SPO	C3-C1-O1-CM1
8	M	1010	SPO	C4-C5-C6-C7
8	S	2010	SPO	C3-C1-O1-CM1
8	S	2010	SPO	C1-C4-C5-C6
8	S	2010	SPO	C4-C5-C6-C7

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Mol	Chain	Res	Type	Atoms
8	S	2010	SPO	C36-C37-C38-C40
8	M	1010	SPO	C36-C37-C38-C39
8	S	2010	SPO	C36-C37-C38-C39
7	S	2005	BPH	CBD-CGD-O2D-CED
4	S	2003	BCL	C4-C3-C5-C6
4	M	1003	BCL	C2-C3-C5-C6
4	S	2003	BCL	C2-C3-C5-C6
8	M	1010	SPO	C36-C37-C38-C40
5	L	1009	U10	C29-C31-C32-C33
8	S	2010	SPO	C33-C35-C36-C37
7	M	1005	BPH	CBD-CGD-O2D-CED
7	S	2005	BPH	O1D-CGD-O2D-CED
7	M	1006	BPH	C10-C11-C12-C13
7	R	2006	BPH	C8-C10-C11-C12
7	R	2006	BPH	C10-C11-C12-C13
7	S	2005	BPH	C6-C7-C8-C9
7	S	2005	BPH	C6-C7-C8-C10
7	R	2006	BPH	C12-C13-C15-C16
9	M	1014	LDA	C6-C7-C8-C9
4	S	2003	BCL	C3-C5-C6-C7
4	L	1004	BCL	C2A-CAA-CBA-CGA
9	M	1012	LDA	C6-C7-C8-C9
7	M	1005	BPH	C5-C6-C7-C8
9	S	2011	LDA	C1-C2-C3-C4
9	M	1011	LDA	C4-C5-C6-C7
7	M	1005	BPH	O1D-CGD-O2D-CED
9	M	1012	LDA	C11-C10-C9-C8
4	S	2004	BCL	C1A-C2A-CAA-CBA
4	S	2003	BCL	C11-C10-C8-C7
9	M	1014	LDA	C1-C2-C3-C4
4	S	2003	BCL	C11-C10-C8-C9
7	M	1006	BPH	C11-C12-C13-C14
9	M	1013	LDA	C4-C5-C6-C7
4	R	2002	BCL	C15-C16-C17-C18
4	S	2003	BCL	C13-C15-C16-C17
4	L	1004	BCL	C13-C15-C16-C17
7	M	1006	BPH	C8-C10-C11-C12
7	R	2006	BPH	O2A-C1-C2-C3
5	L	1009	U10	C25-C24-C26-C27
8	M	1010	SPO	C33-C35-C36-C37
4	M	1003	BCL	C11-C10-C8-C9
7	R	2006	BPH	C14-C13-C15-C16

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Mol	Chain	Res	Type	Atoms
4	L	1002	BCL	C15-C16-C17-C18
4	L	1002	BCL	C12-C13-C15-C16
4	M	1003	BCL	C11-C10-C8-C7
4	S	2003	BCL	C11-C12-C13-C15
7	M	1006	BPH	C11-C12-C13-C15
9	S	2011	LDA	C9-C10-C11-C12
5	L	1009	U10	C12-C11-C9-C10
7	S	2005	BPH	C5-C6-C7-C8
8	S	2010	SPO	C20-C21-C22-C23
5	L	1009	U10	C12-C11-C9-C8
4	S	2001	BCL	C4B-C3B-CAB-CBB
9	M	1012	LDA	C9-C10-C11-C12
8	M	1010	SPO	C20-C21-C22-C23
4	M	1003	BCL	C3-C5-C6-C7
4	M	1003	BCL	C11-C12-C13-C15
4	R	2002	BCL	C12-C13-C15-C16
8	M	1010	SPO	C1-C4-C5-C6
9	M	1011	LDA	C11-C10-C9-C8
4	S	2001	BCL	C2B-C3B-CAB-OBB
4	S	2001	BCL	C2B-C3B-CAB-CBB
7	M	1005	BPH	O2A-C1-C2-C3
7	M	1006	BPH	O2A-C1-C2-C3
5	S	2008	U10	C5-C4-O4-C4M
4	M	1003	BCL	C13-C15-C16-C17
7	R	2006	BPH	C16-C17-C18-C20
9	M	1011	LDA	C2-C1-N1-CM1
9	M	1011	LDA	C2-C1-N1-CM2
9	M	1012	LDA	C2-C1-N1-CM1
9	M	1012	LDA	C2-C1-N1-CM2
9	M	1013	LDA	C2-C1-N1-CM1
9	M	1013	LDA	C2-C1-N1-CM2
9	M	1014	LDA	C2-C1-N1-CM1
9	M	1014	LDA	C2-C1-N1-CM2
9	S	2011	LDA	C2-C1-N1-CM1
9	S	2011	LDA	C2-C1-N1-CM2
4	L	1001	BCL	C1A-C2A-CAA-CBA
4	L	1004	BCL	C11-C12-C13-C15
7	R	2006	BPH	C4-C3-C5-C6
5	L	1009	U10	C23-C24-C26-C27
4	R	2002	BCL	C14-C13-C15-C16
7	M	1006	BPH	C15-C16-C17-C18
9	M	1011	LDA	C2-C1-N1-O1

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Mol	Chain	Res	Type	Atoms
9	M	1012	LDA	C2-C1-N1-O1
9	M	1013	LDA	C2-C1-N1-O1
9	M	1014	LDA	C2-C1-N1-O1
9	S	2011	LDA	C2-C1-N1-O1
4	L	1002	BCL	C2A-CAA-CBA-CGA
4	L	1004	BCL	CHA-CBD-CGD-O1D
4	L	1004	BCL	CHA-CBD-CGD-O2D
4	S	2004	BCL	CHA-CBD-CGD-O1D
4	S	2004	BCL	CHA-CBD-CGD-O2D
8	M	1010	SPO	C17-C19-C20-C21
8	S	2010	SPO	C17-C19-C20-C21
4	M	1003	BCL	C15-C16-C17-C18
7	R	2006	BPH	C2-C3-C5-C6
7	R	2006	BPH	C16-C17-C18-C19
5	S	2008	U10	C21-C22-C23-C24
5	M	1008	U10	C5-C4-O4-C4M
4	S	2004	BCL	C15-C16-C17-C18
4	S	2001	BCL	C4B-C3B-CAB-OBB
4	L	1002	BCL	C14-C13-C15-C16
4	L	1004	BCL	C11-C10-C8-C9
4	L	1004	BCL	C11-C12-C13-C14
4	S	2003	BCL	C11-C12-C13-C14
4	S	2004	BCL	C11-C10-C8-C9
8	M	1010	SPO	C19-C20-C21-C22
8	M	1010	SPO	C18-C17-C19-C20
8	S	2010	SPO	C18-C17-C19-C20
9	M	1011	LDA	C9-C10-C11-C12
8	M	1010	SPO	C16-C17-C19-C20
8	S	2010	SPO	C16-C17-C19-C20
7	M	1006	BPH	C12-C13-C15-C16
9	S	2011	LDA	C6-C7-C8-C9
4	R	2002	BCL	C4-C3-C5-C6
9	S	2011	LDA	C11-C10-C9-C8
9	M	1014	LDA	C11-C10-C9-C8
8	M	1010	SPO	C4-C1-O1-CM1
8	S	2010	SPO	C4-C1-O1-CM1
5	R	2009	U10	C2-C3-O3-C3M
7	R	2006	BPH	CHA-CBD-CGD-O2D
4	L	1002	BCL	C4-C3-C5-C6
4	S	2004	BCL	C11-C10-C8-C7
4	R	2002	BCL	C2A-CAA-CBA-CGA
7	S	2005	BPH	O2A-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
7	S	2005	BPH	C2A-CAA-CBA-CGA
4	L	1004	BCL	C11-C10-C8-C7
4	S	2004	BCL	CAA-CBA-CGA-O2A
4	M	1003	BCL	C5-C6-C7-C8
8	M	1010	SPO	C29-C28-C30-C31
4	R	2002	BCL	C2-C3-C5-C6
8	S	2010	SPO	C30-C31-C32-C33
4	M	1003	BCL	C11-C12-C13-C14
7	M	1006	BPH	C6-C7-C8-C9
7	M	1006	BPH	C14-C13-C15-C16
8	M	1010	SPO	C30-C31-C32-C33
4	S	2004	BCL	CAA-CBA-CGA-O1A
7	S	2005	BPH	C2-C1-O2A-CGA
5	L	1009	U10	C2-C3-O3-C3M

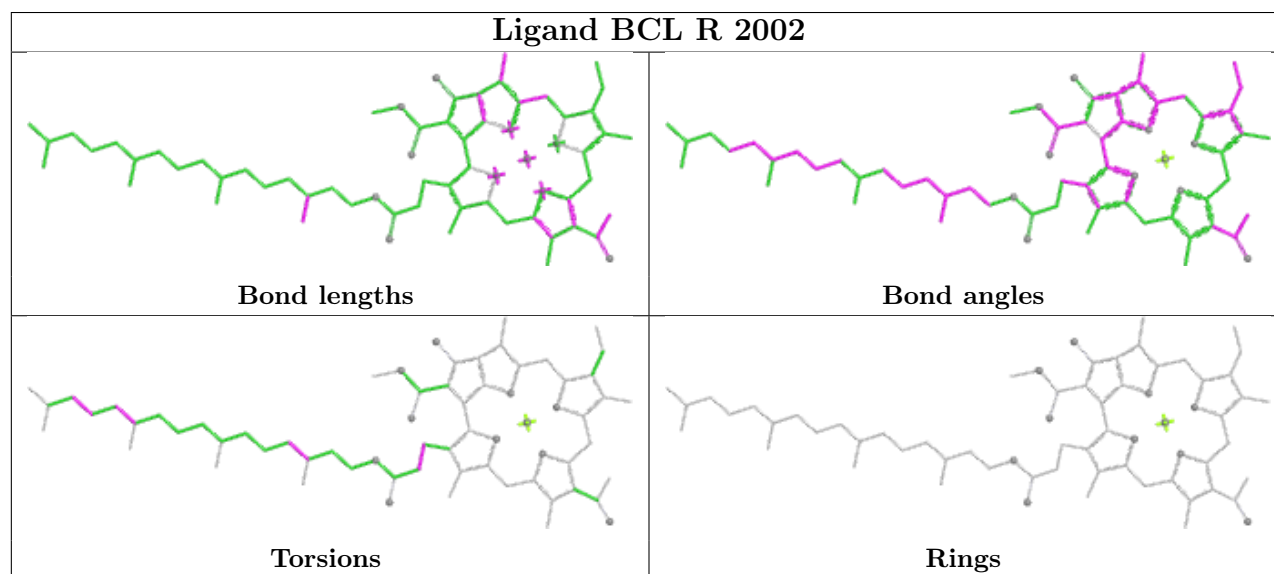
There are no ring outliers.

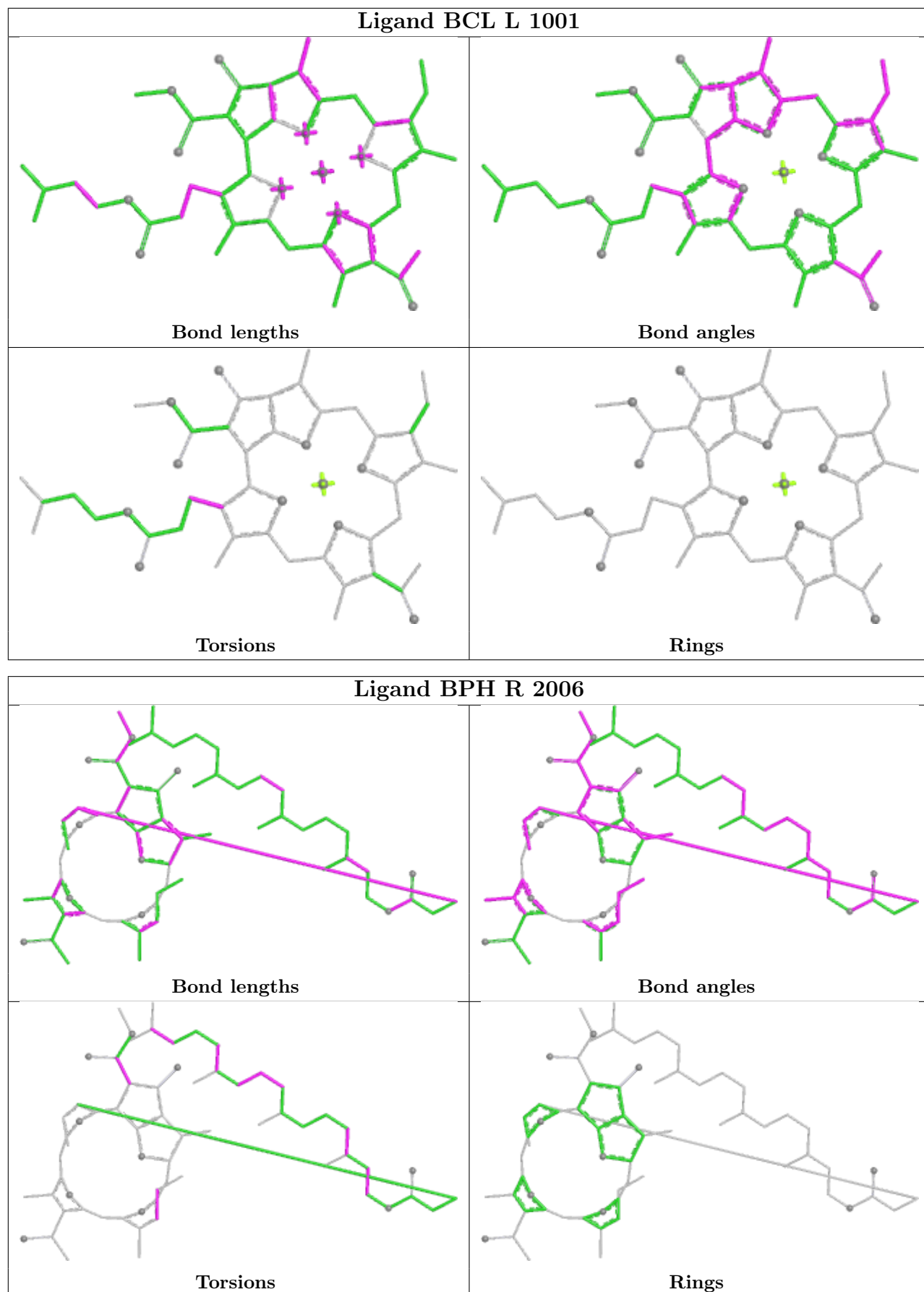
19 monomers are involved in 73 short contacts:

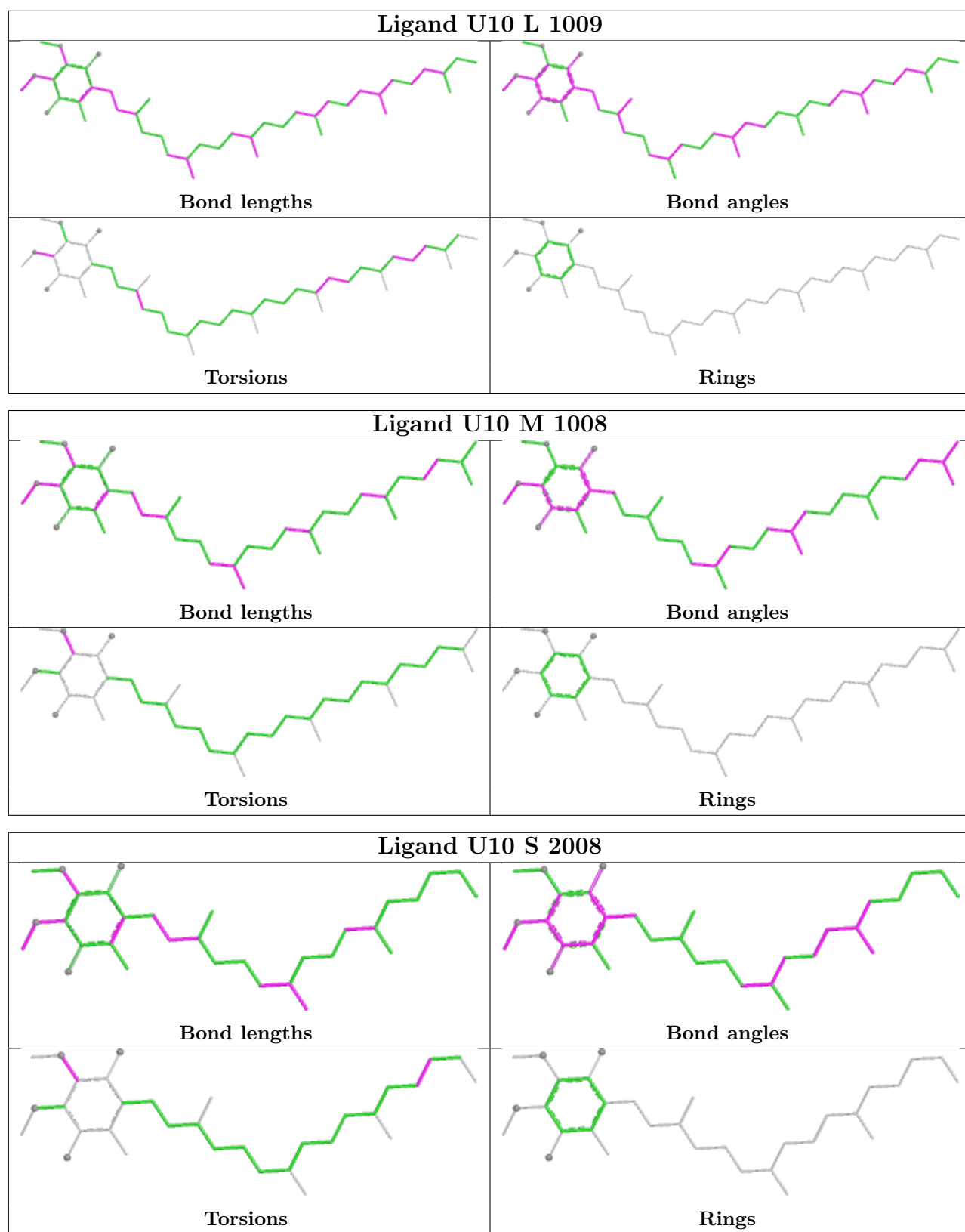
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	R	2002	BCL	6	0
4	L	1001	BCL	11	0
7	R	2006	BPH	5	0
9	M	1012	LDA	1	0
5	L	1009	U10	3	0
5	M	1008	U10	4	0
9	M	1014	LDA	2	0
5	S	2008	U10	1	0
7	M	1006	BPH	4	0
7	M	1005	BPH	2	0
4	L	1002	BCL	5	0
4	M	1003	BCL	14	0
4	S	2004	BCL	5	0
4	S	2001	BCL	8	0
4	L	1004	BCL	8	0
7	S	2005	BPH	2	0
4	S	2003	BCL	12	0
8	S	2010	SPO	3	0
8	M	1010	SPO	4	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

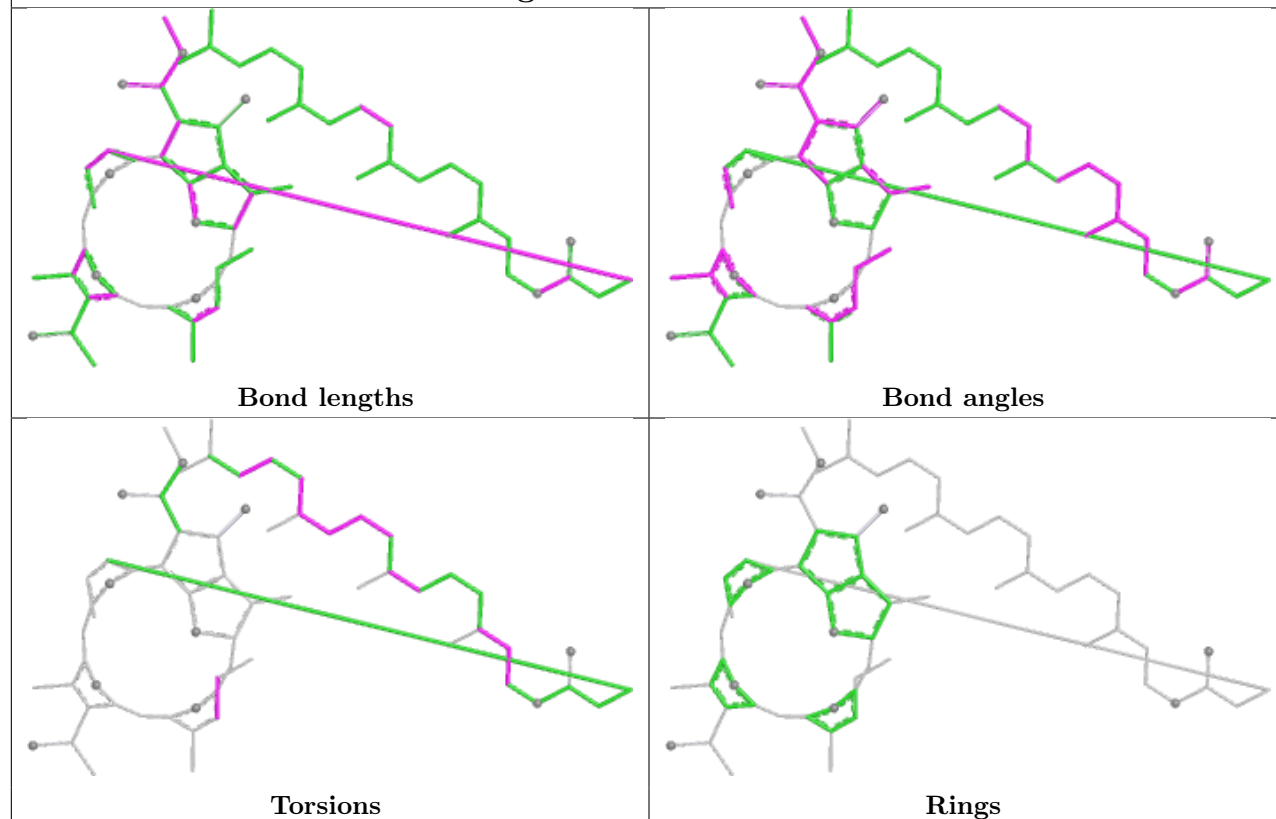
also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted 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.



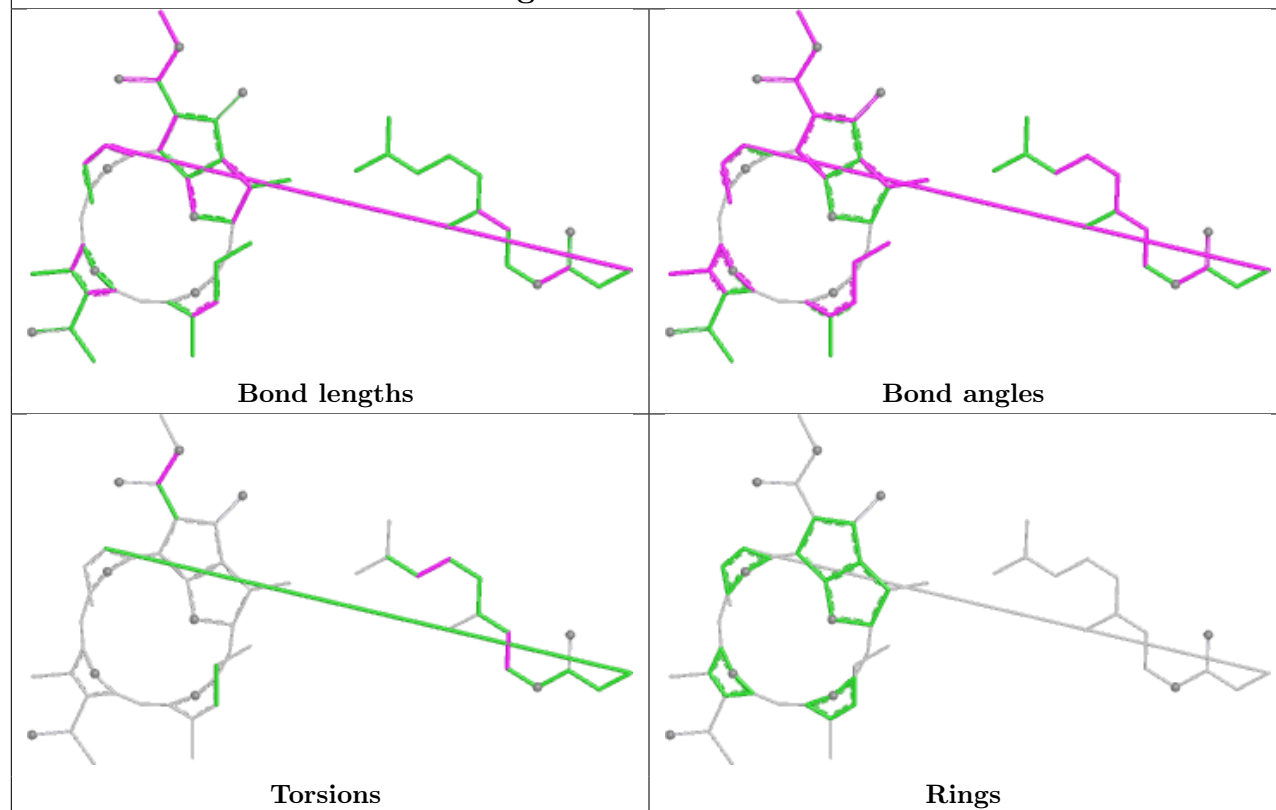


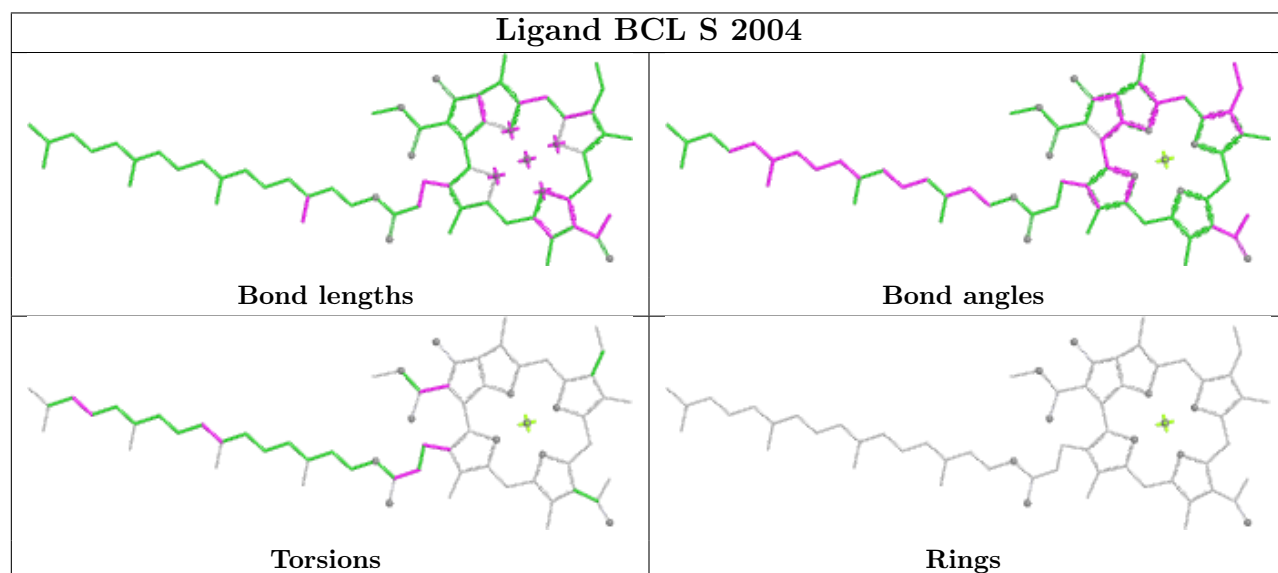
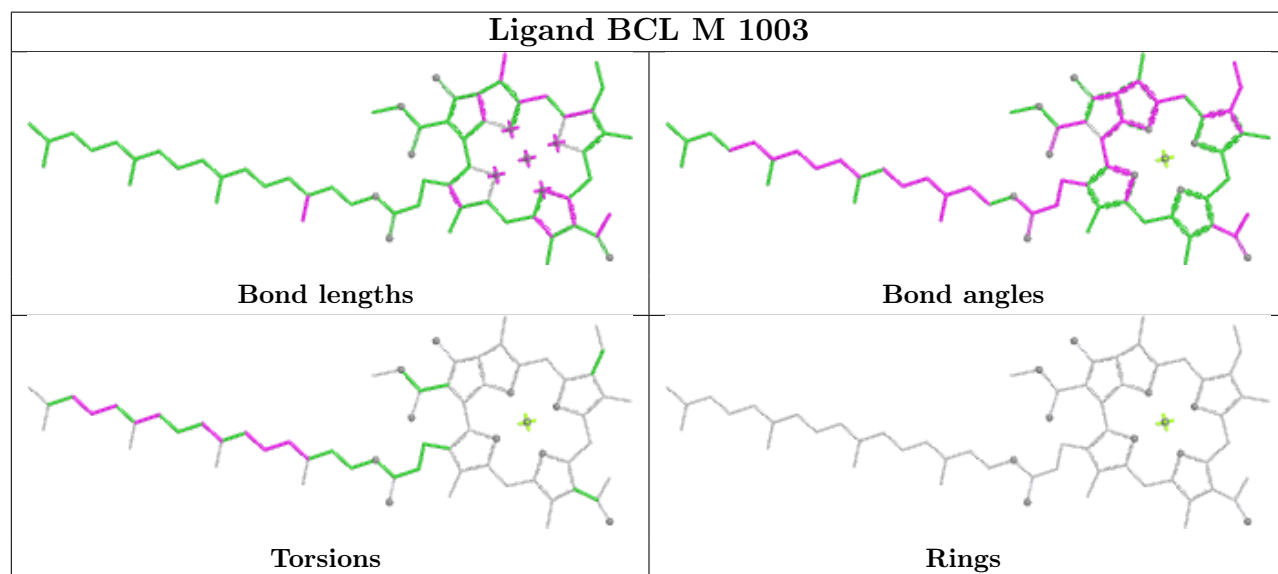
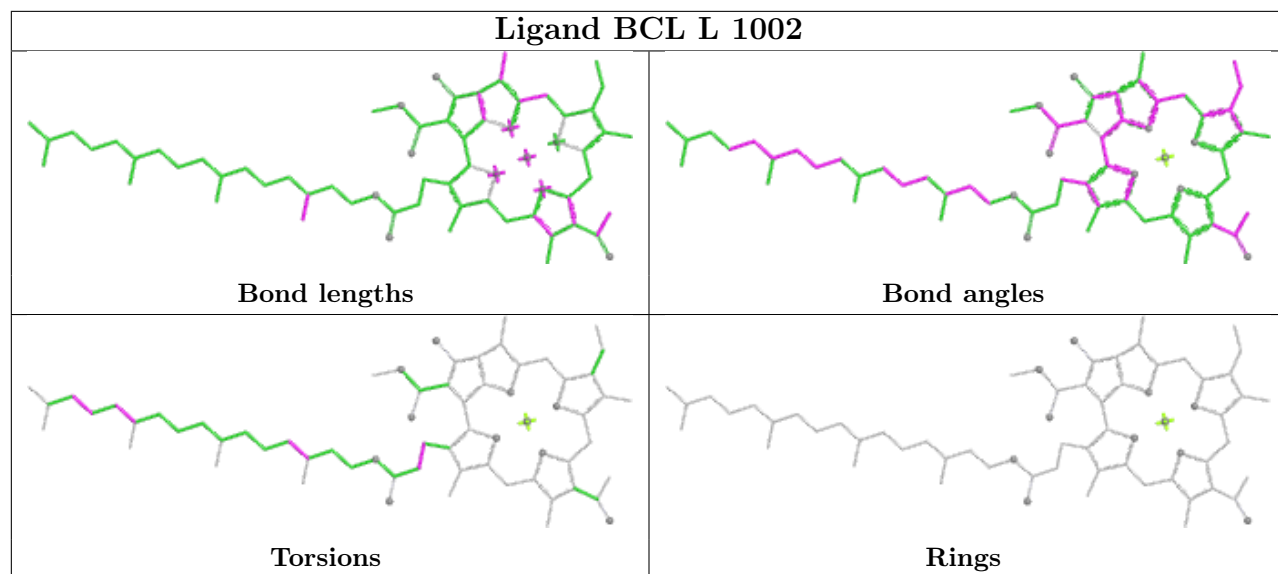


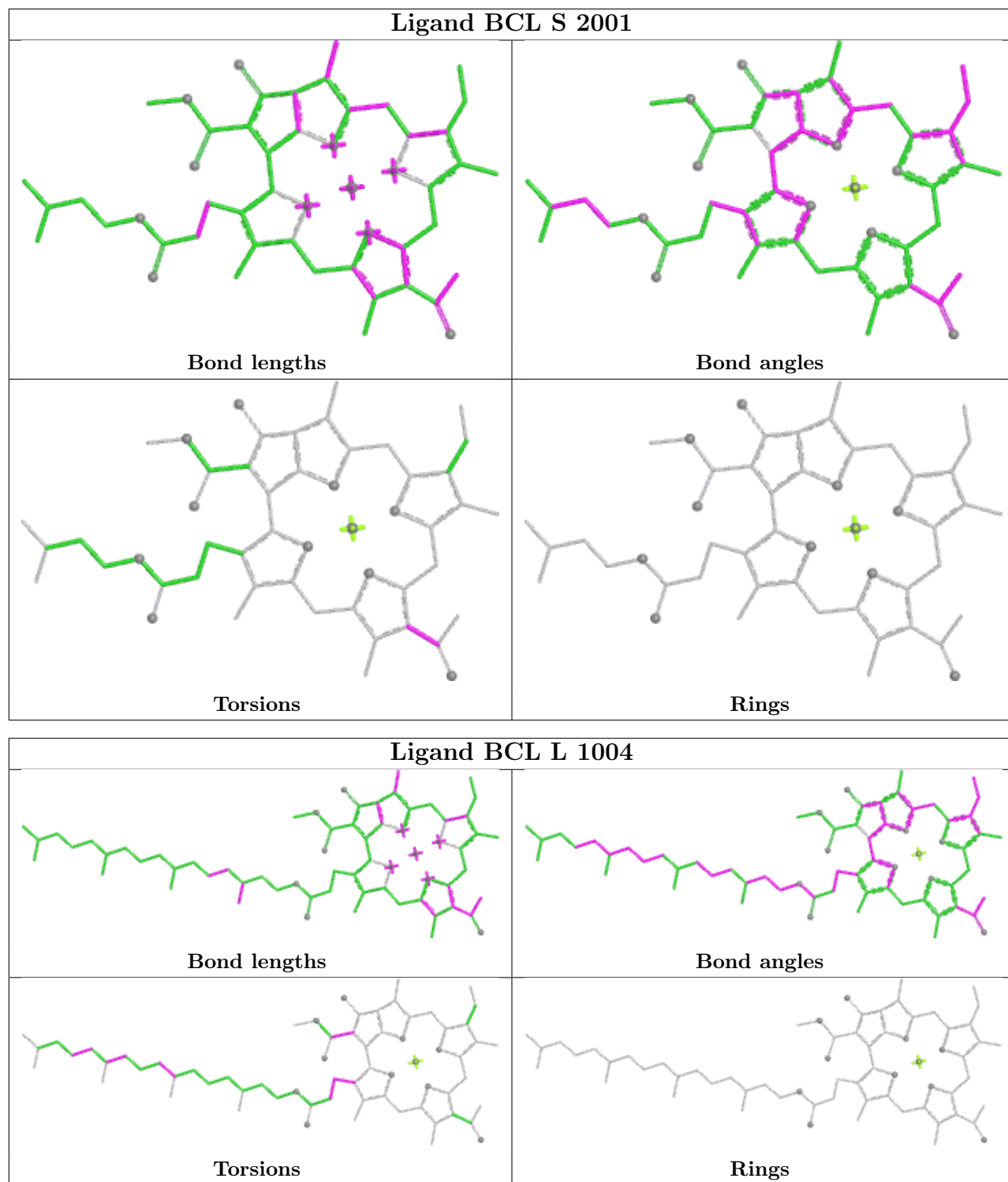
Ligand BPH M 1006

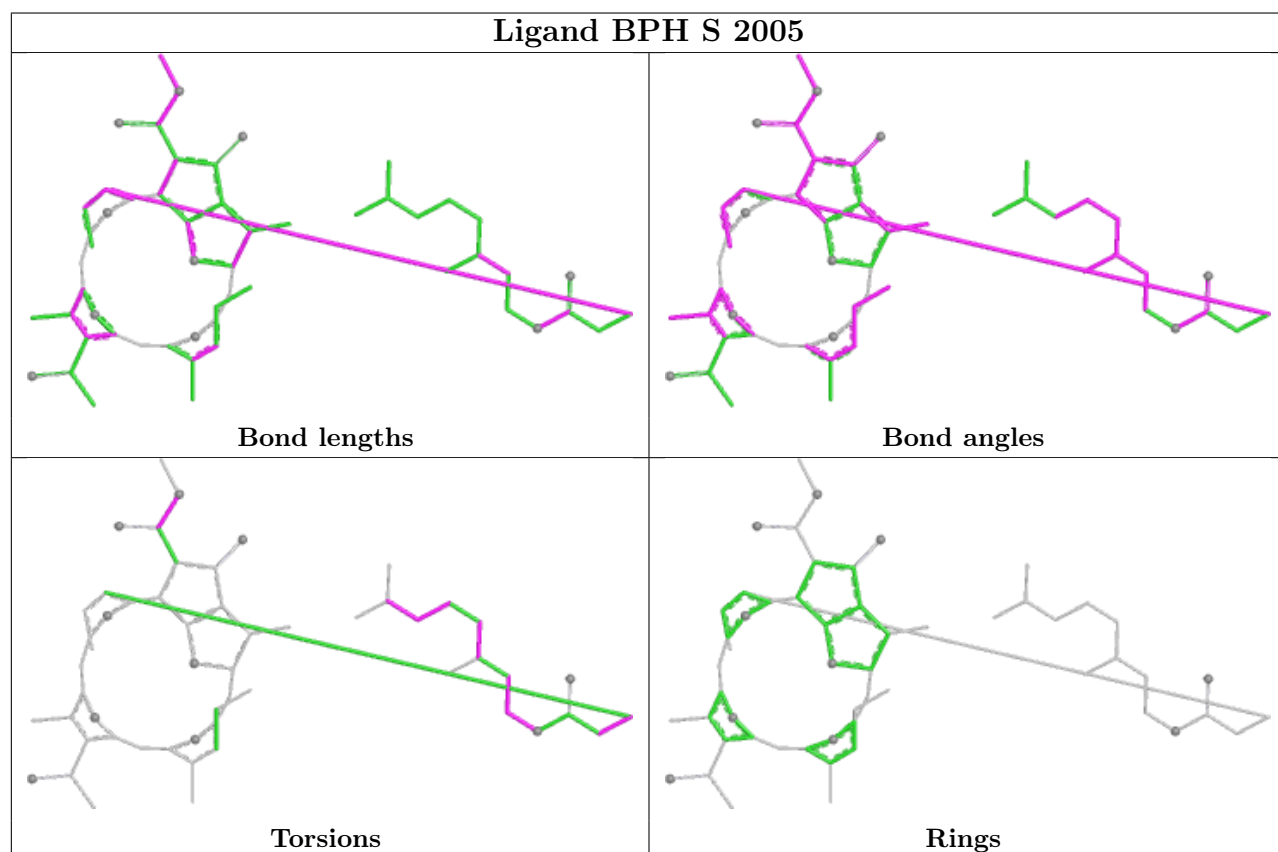
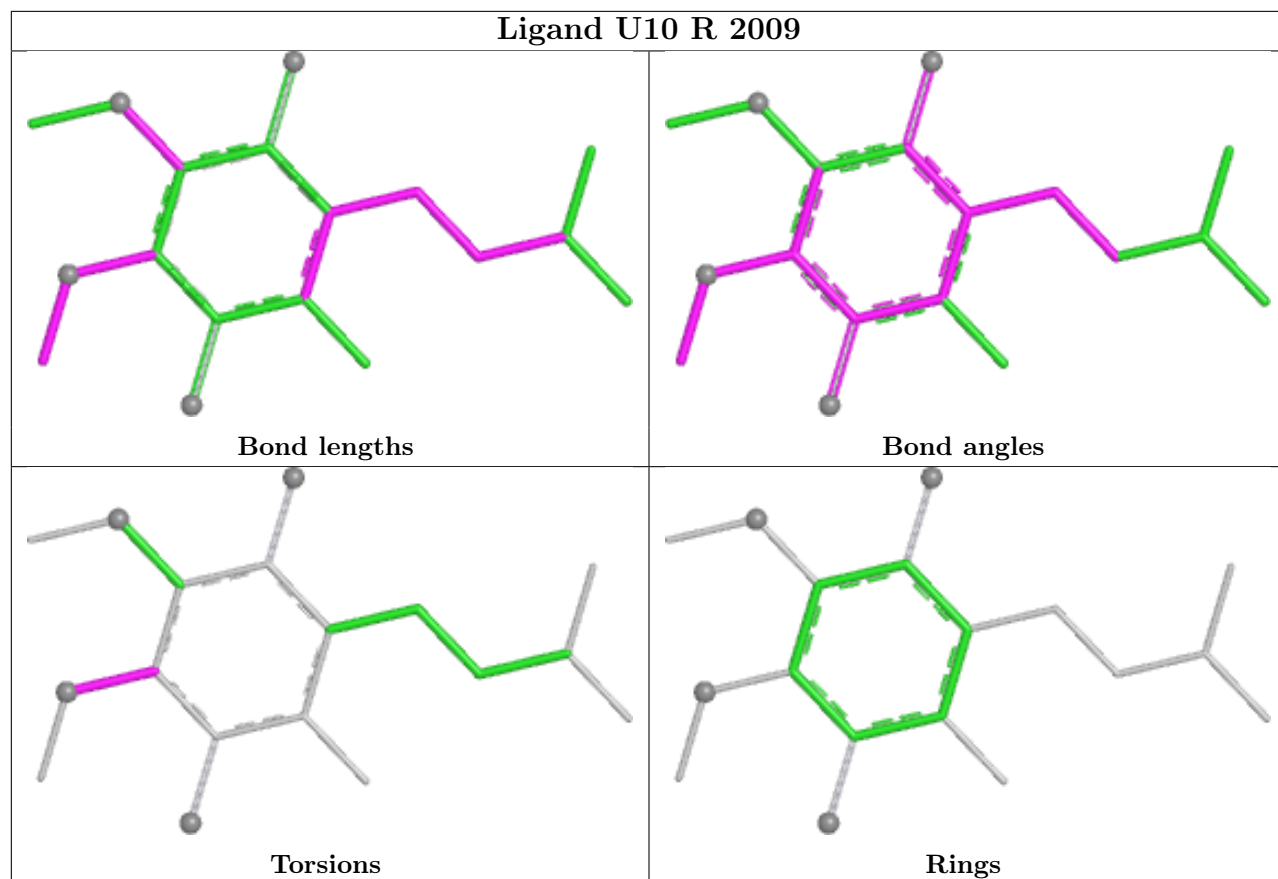


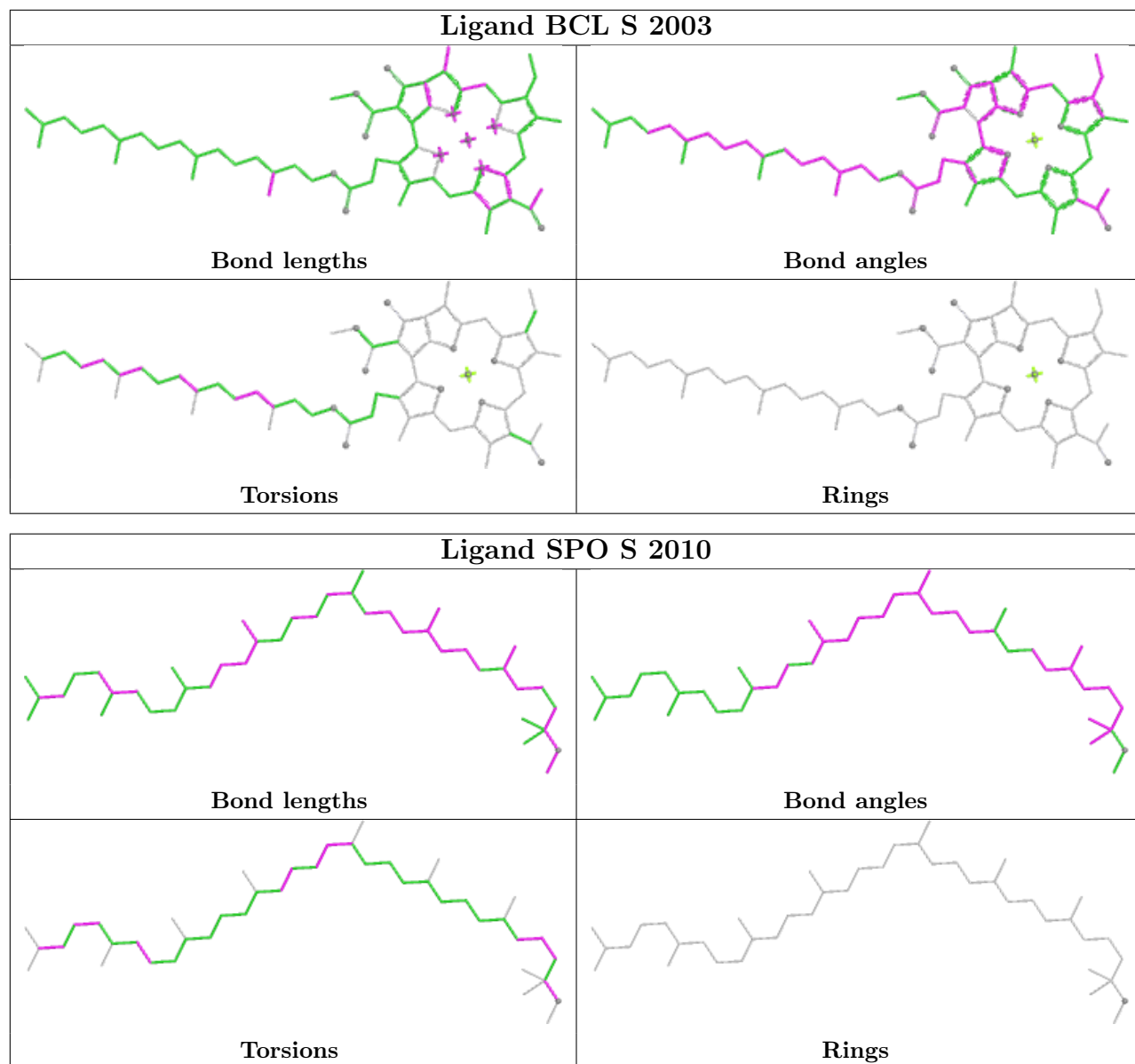
Ligand BPH M 1005

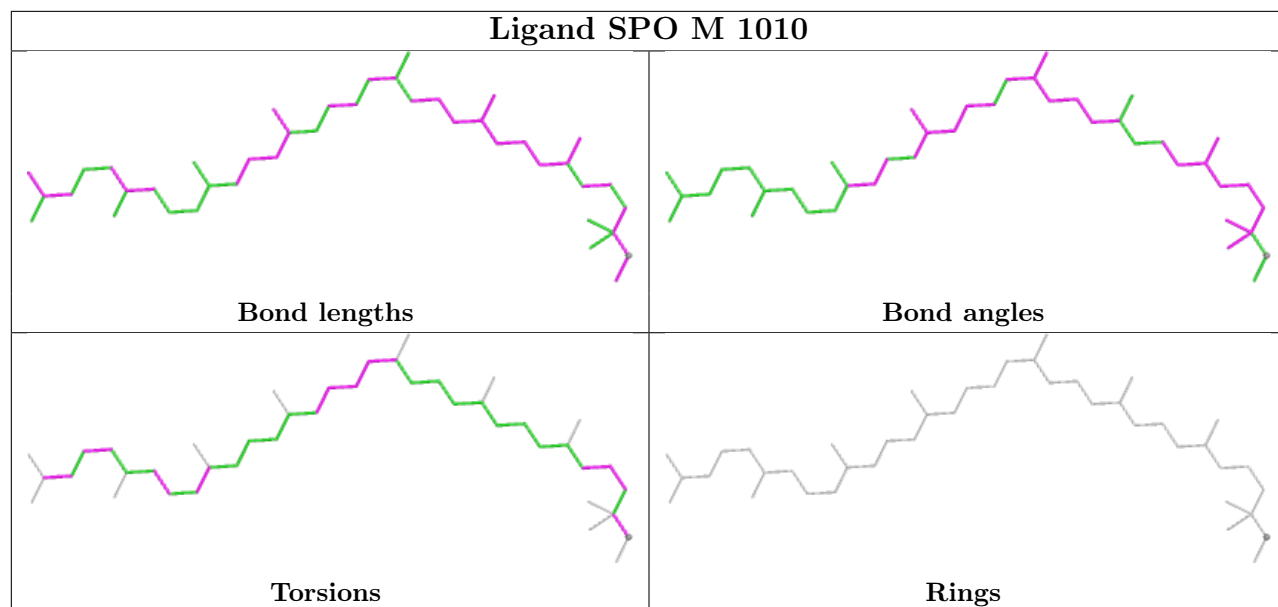












5.7 Other polymers [i](#)

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%)	-0.09	1 (0%) 88 86	17, 32, 49, 58	0
1	R	281/281 (100%)	0.30	4 (1%) 73 69	23, 41, 58, 69	0
2	M	299/307 (97%)	-0.35	3 (1%) 79 76	17, 27, 41, 67	0
2	S	299/307 (97%)	-0.08	3 (1%) 79 76	24, 35, 48, 69	0
3	H	246/260 (94%)	0.01	7 (2%) 55 51	22, 34, 54, 88	0
3	T	246/260 (94%)	0.49	15 (6%) 27 23	31, 45, 70, 80	0
All	All	1652/1696 (97%)	0.03	33 (1%) 65 60	17, 36, 57, 88	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	T	256	LEU	4.7
3	H	256	LEU	4.6
3	T	254	ALA	4.0
1	R	1	ALA	3.8
3	H	254	ALA	3.6
2	M	3	TYR	3.5
3	H	253	ALA	3.4
3	H	252	VAL	3.1
3	H	251	VAL	3.1
2	M	301	HIS	2.9
3	H	69	GLY	2.9
2	S	301	HIS	2.8
3	T	255	MET	2.8
3	H	255	MET	2.8
2	S	3	TYR	2.7
3	T	51	ALA	2.7
3	T	80	SER	2.6
1	L	81	ALA	2.5
3	T	253	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
3	T	91	ALA	2.4
3	T	46	ASP	2.3
3	T	252	VAL	2.3
2	M	300	ASN	2.3
2	S	236	GLU	2.2
1	R	80	LEU	2.2
3	T	175	MET	2.2
3	T	90	THR	2.2
1	R	21	LEU	2.1
3	T	155	GLY	2.1
3	T	56	PHE	2.1
3	T	54	GLY	2.0
1	R	66	VAL	2.0
3	T	79	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no 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.

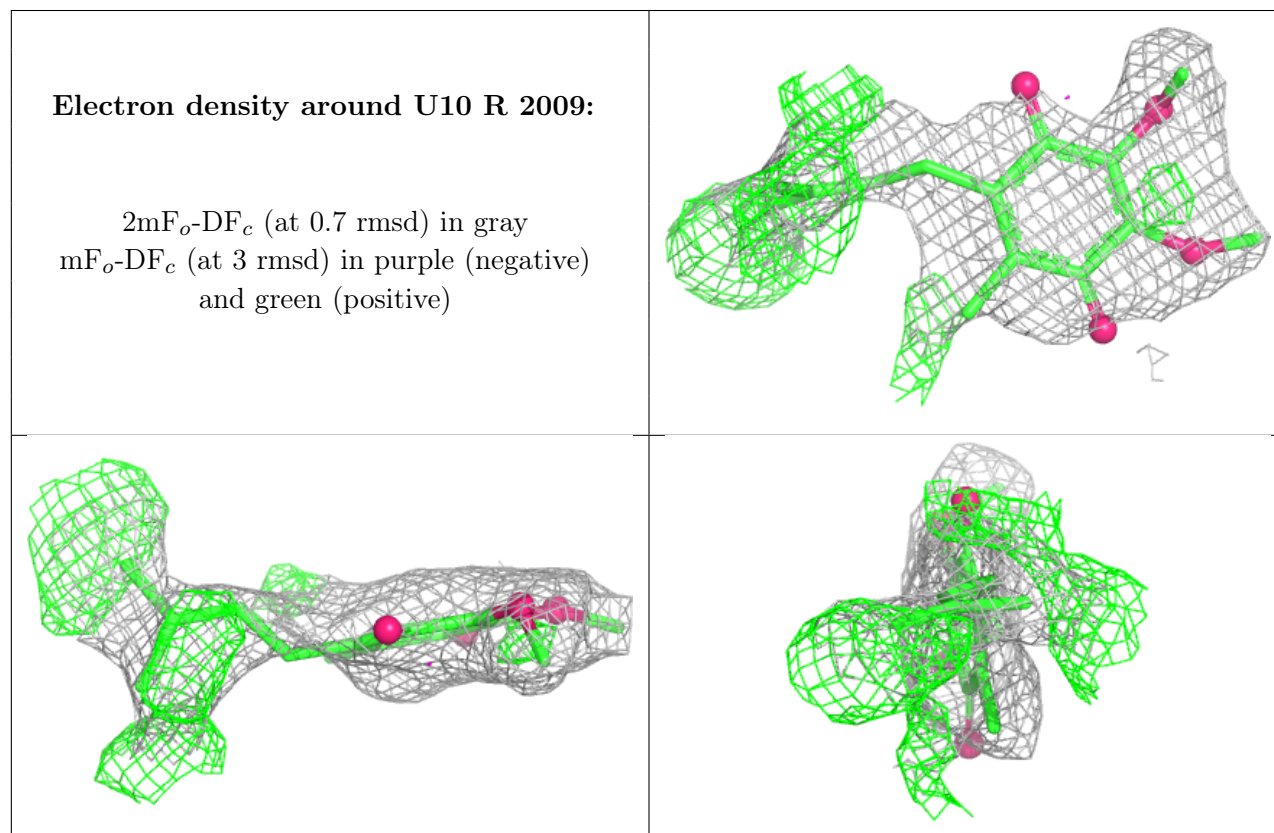
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	U10	R	2009	18/63	0.70	0.33	81,85,86,87	0
5	U10	L	1009	44/63	0.71	0.30	66,72,79,79	0
9	LDA	S	2011	16/16	0.76	0.26	74,79,85,85	0
9	LDA	M	1013	16/16	0.78	0.23	69,71,80,80	0
9	LDA	M	1011	16/16	0.79	0.24	49,57,74,74	0
9	LDA	M	1014	16/16	0.84	0.20	50,55,59,60	0
4	BCL	S	2001	51/66	0.88	0.12	28,31,41,43	0
9	LDA	M	1012	16/16	0.88	0.19	60,62,65,65	0
4	BCL	S	2003	66/66	0.88	0.13	27,33,48,55	0

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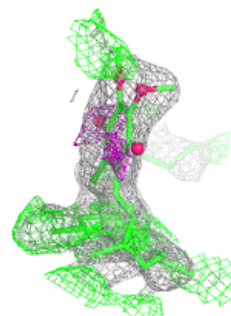
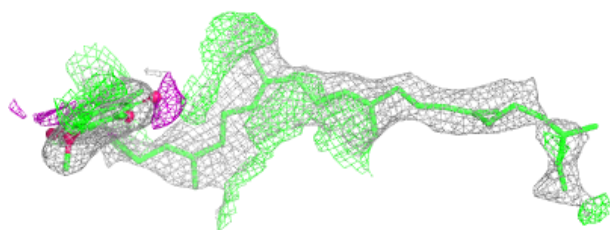
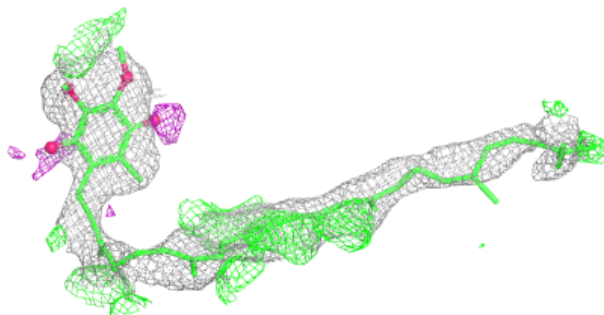
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	SPO	M	1010	42/42	0.88	0.14	16,28,47,51	0
8	SPO	S	2010	42/42	0.88	0.15	24,35,51,54	0
4	BCL	R	2002	66/66	0.89	0.12	29,35,44,48	0
4	BCL	L	1001	51/66	0.89	0.13	17,24,51,55	0
5	U10	S	2008	32/63	0.90	0.13	36,42,51,54	0
4	BCL	S	2004	66/66	0.90	0.14	26,34,58,60	0
4	BCL	M	1003	66/66	0.90	0.11	20,25,39,44	0
4	BCL	L	1004	66/66	0.90	0.11	16,25,45,52	0
7	BPH	R	2006	65/65	0.91	0.11	31,38,45,46	0
7	BPH	M	1006	65/65	0.92	0.10	23,28,37,40	0
4	BCL	L	1002	66/66	0.92	0.11	20,26,29,33	0
5	U10	M	1008	38/63	0.92	0.11	23,30,53,53	0
7	BPH	S	2005	55/65	0.93	0.10	25,30,55,58	0
7	BPH	M	1005	55/65	0.94	0.09	17,23,43,46	0
6	FE2	S	2007	1/1	0.99	0.02	30,30,30,30	0
6	FE2	M	1007	1/1	1.00	0.01	20,20,20,20	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.



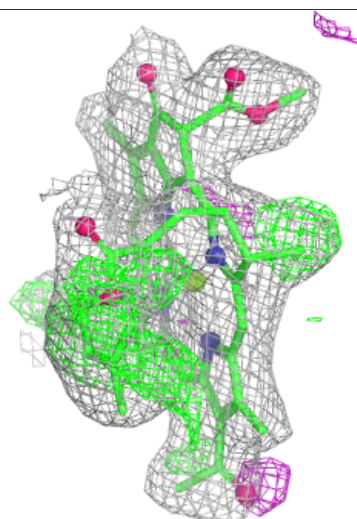
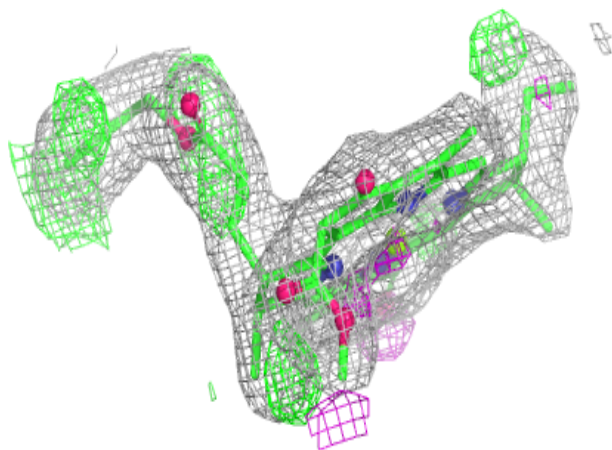
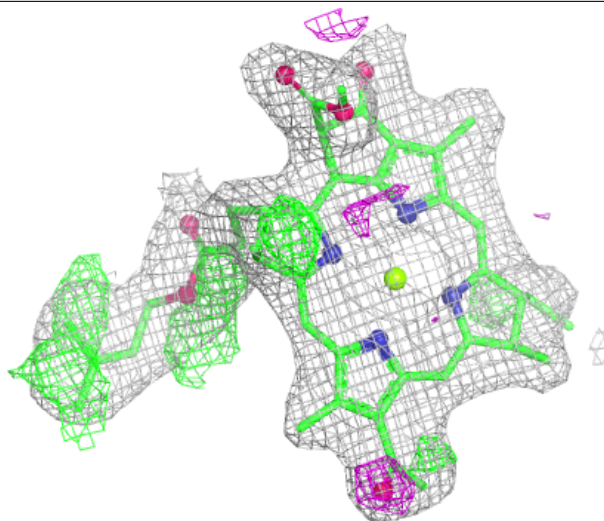
Electron density around U10 L 1009:

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



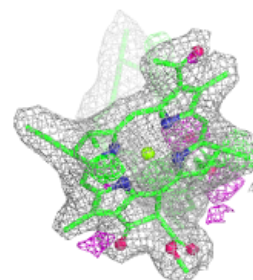
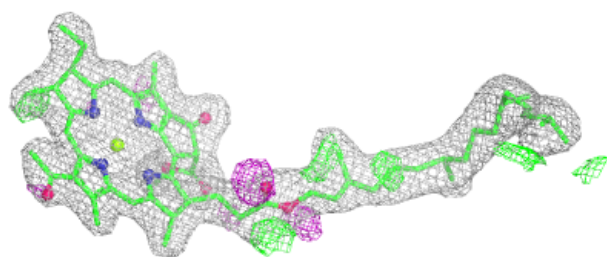
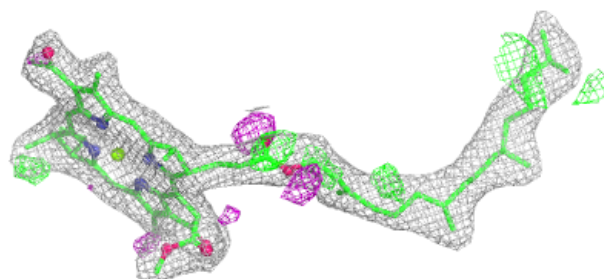
Electron density around BCL S 2001:

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

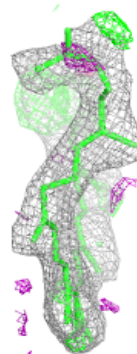
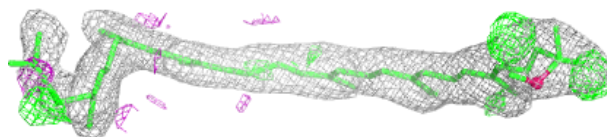
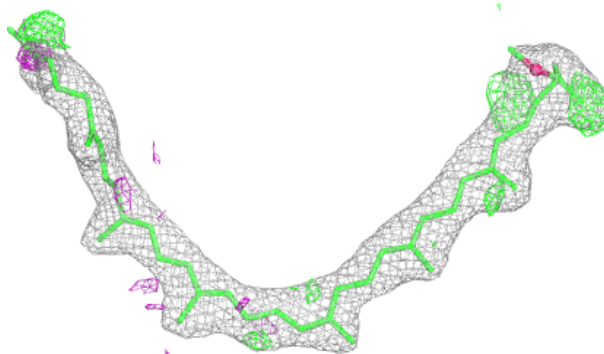


Electron density around BCL S 2003:

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

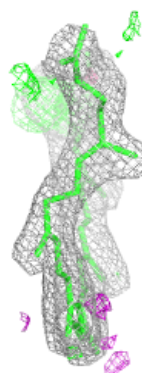
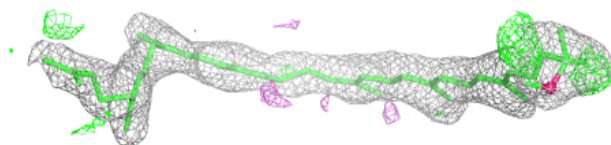
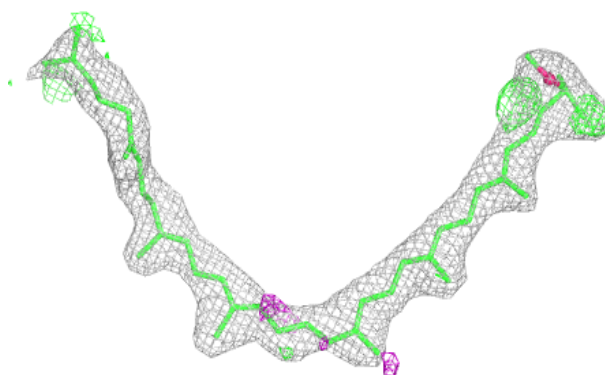
**Electron density around SPO M 1010:**

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

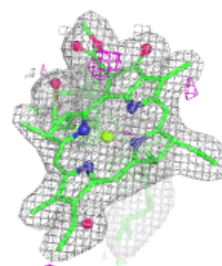
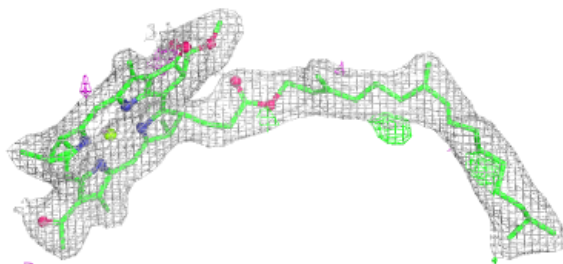


Electron density around SPO S 2010:

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

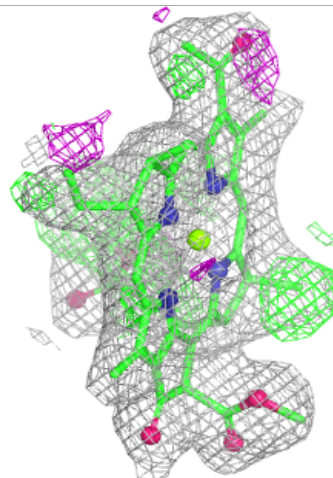
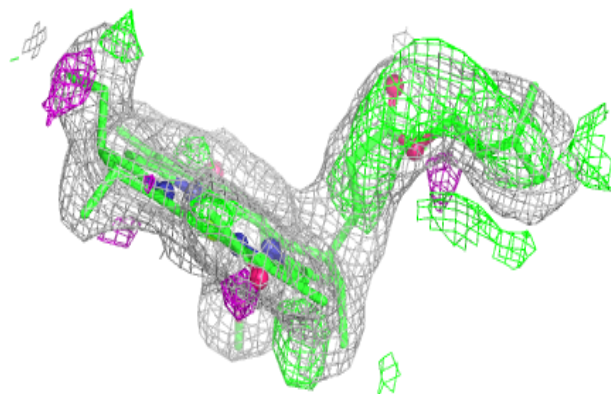
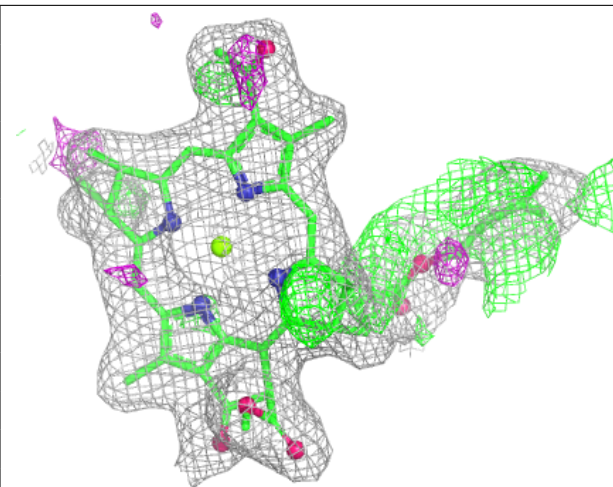
**Electron density around BCL R 2002:**

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



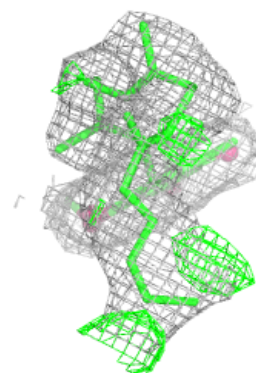
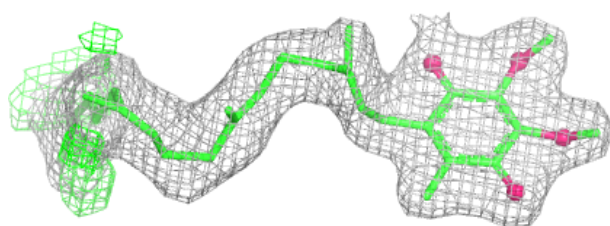
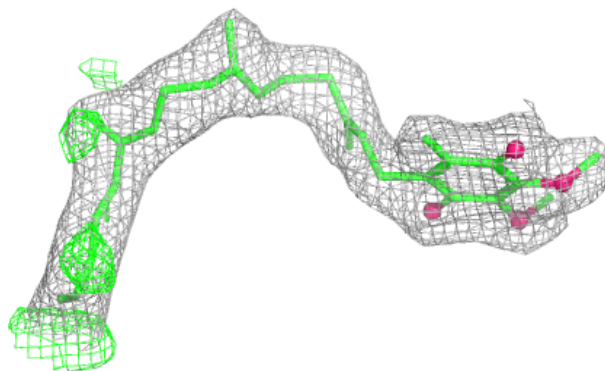
Electron density around BCL L 1001:

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



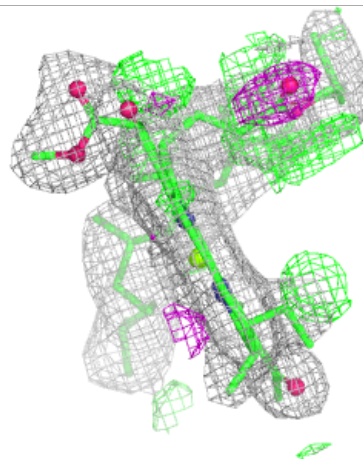
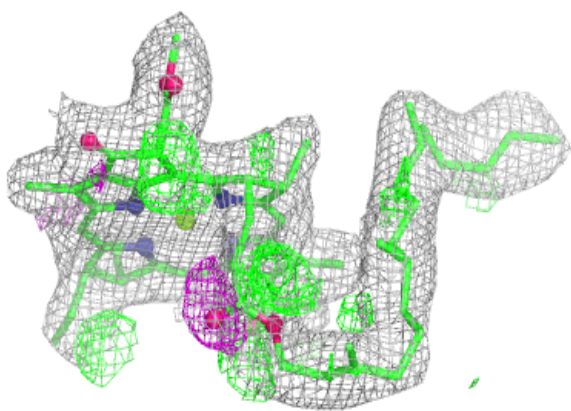
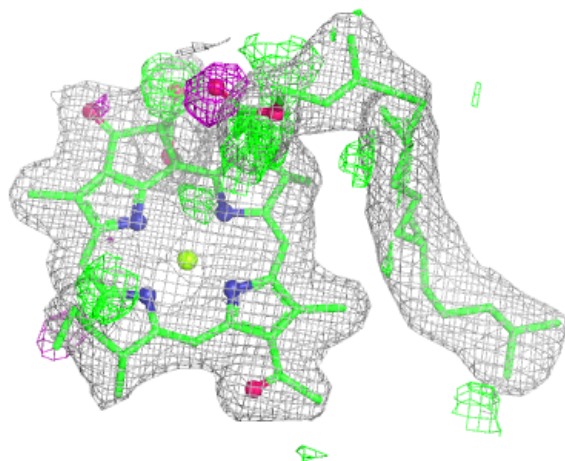
Electron density around U10 S 2008:

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



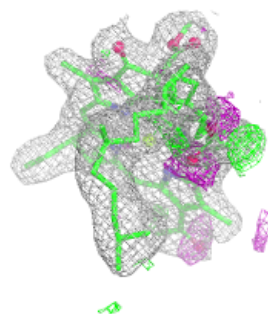
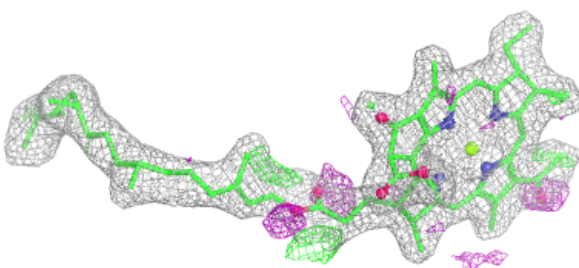
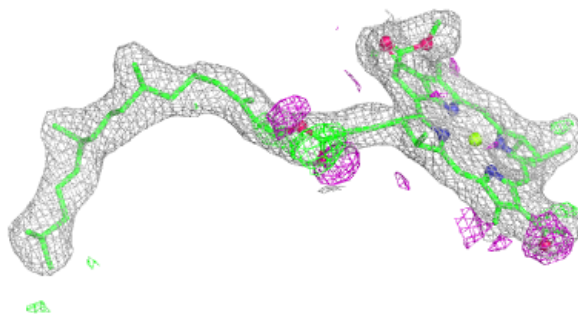
Electron density around BCL S 2004:

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



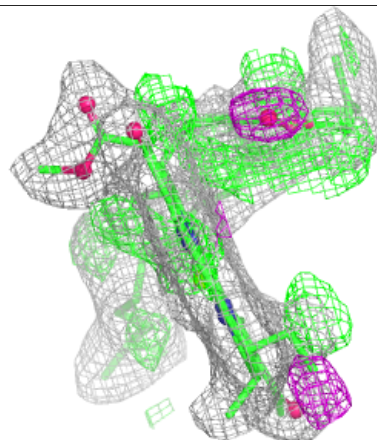
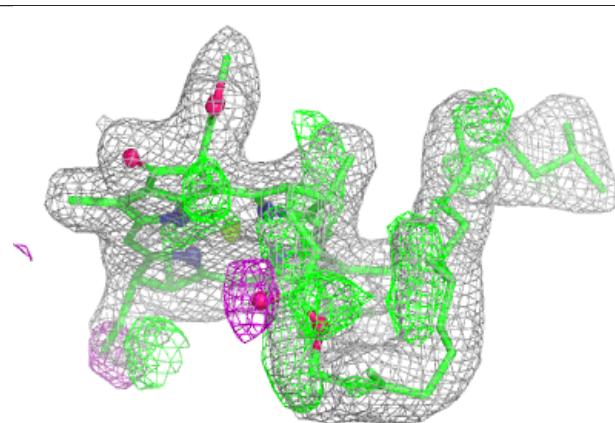
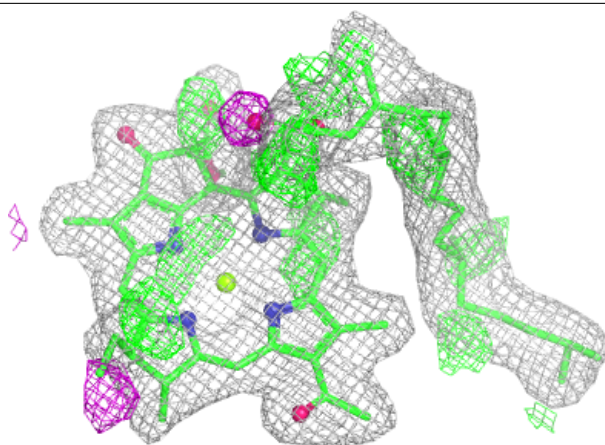
Electron density around BCL M 1003:

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



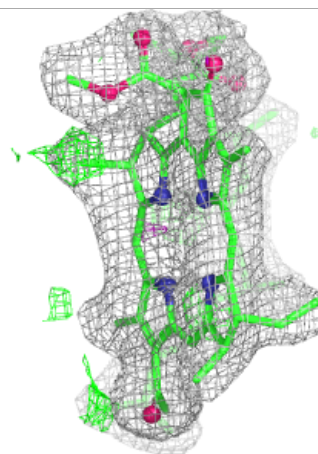
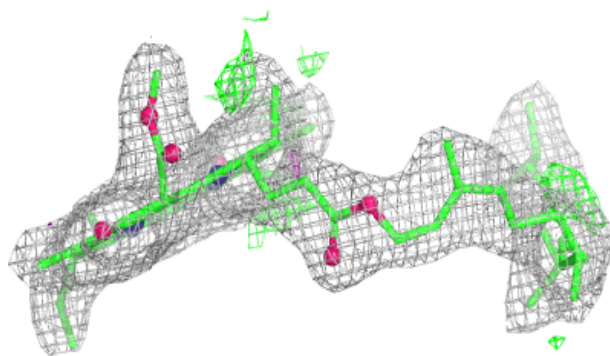
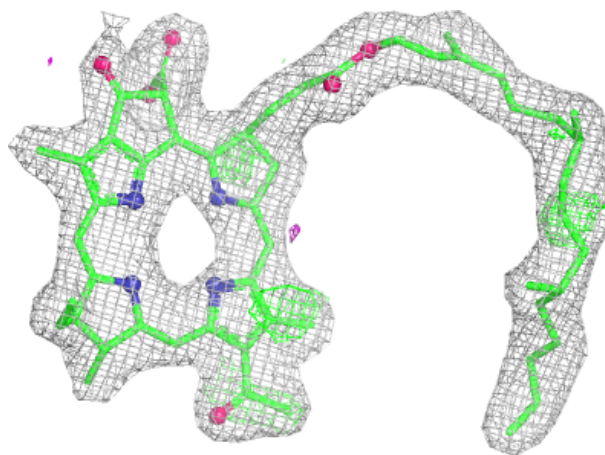
Electron density around BCL L 1004:

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



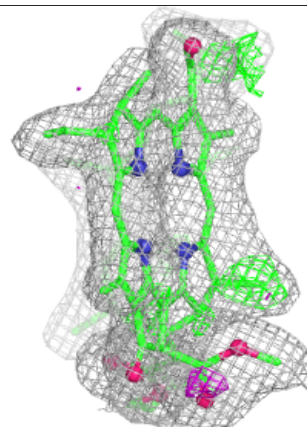
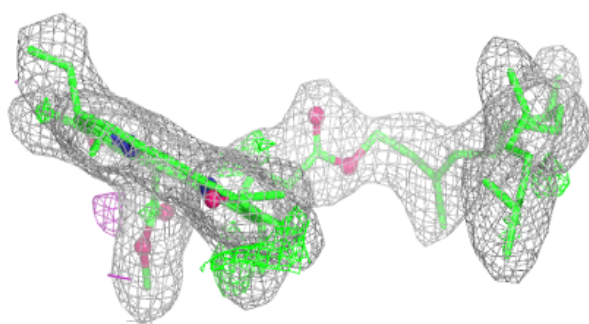
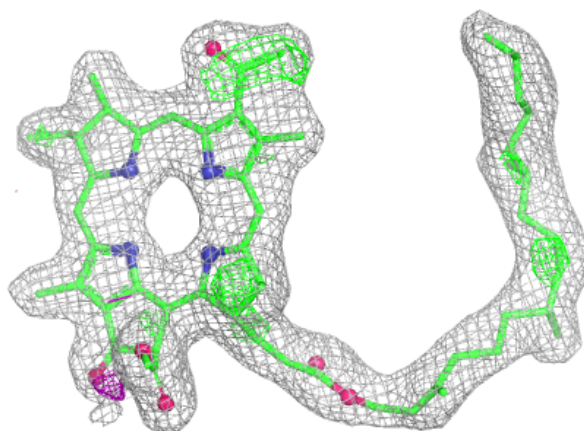
Electron density around BPH R 2006:

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

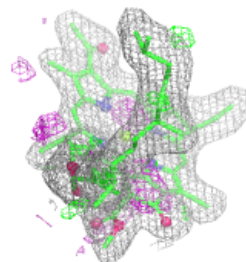
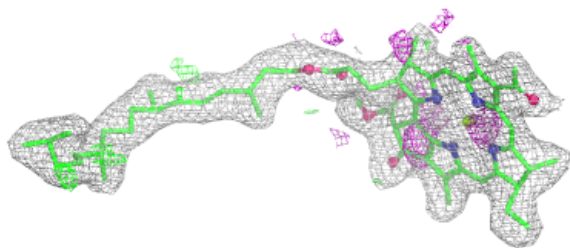
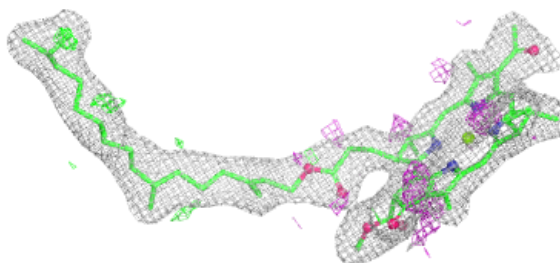


Electron density around BPH M 1006:

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

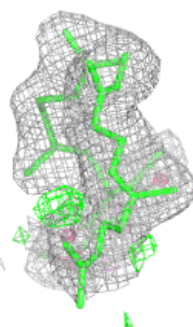
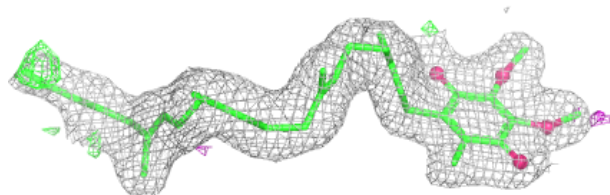
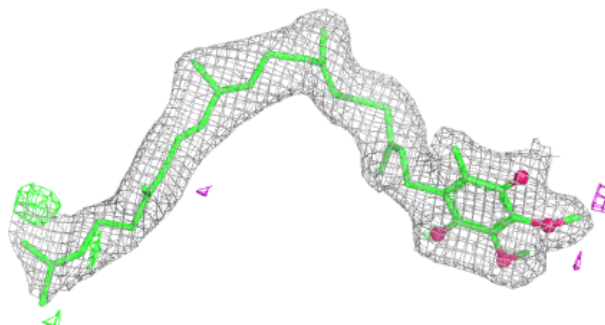
**Electron density around BCL L 1002:**

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

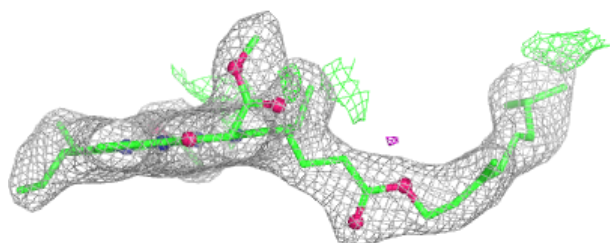
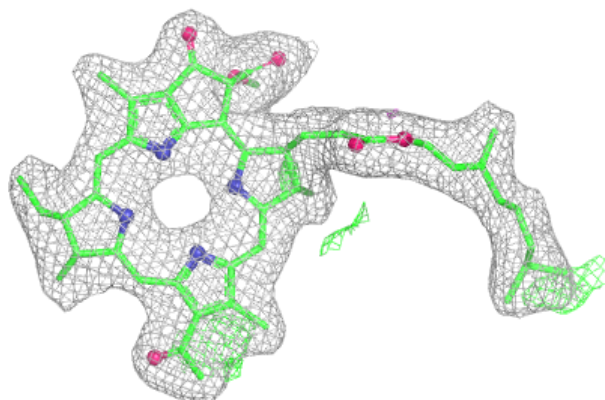


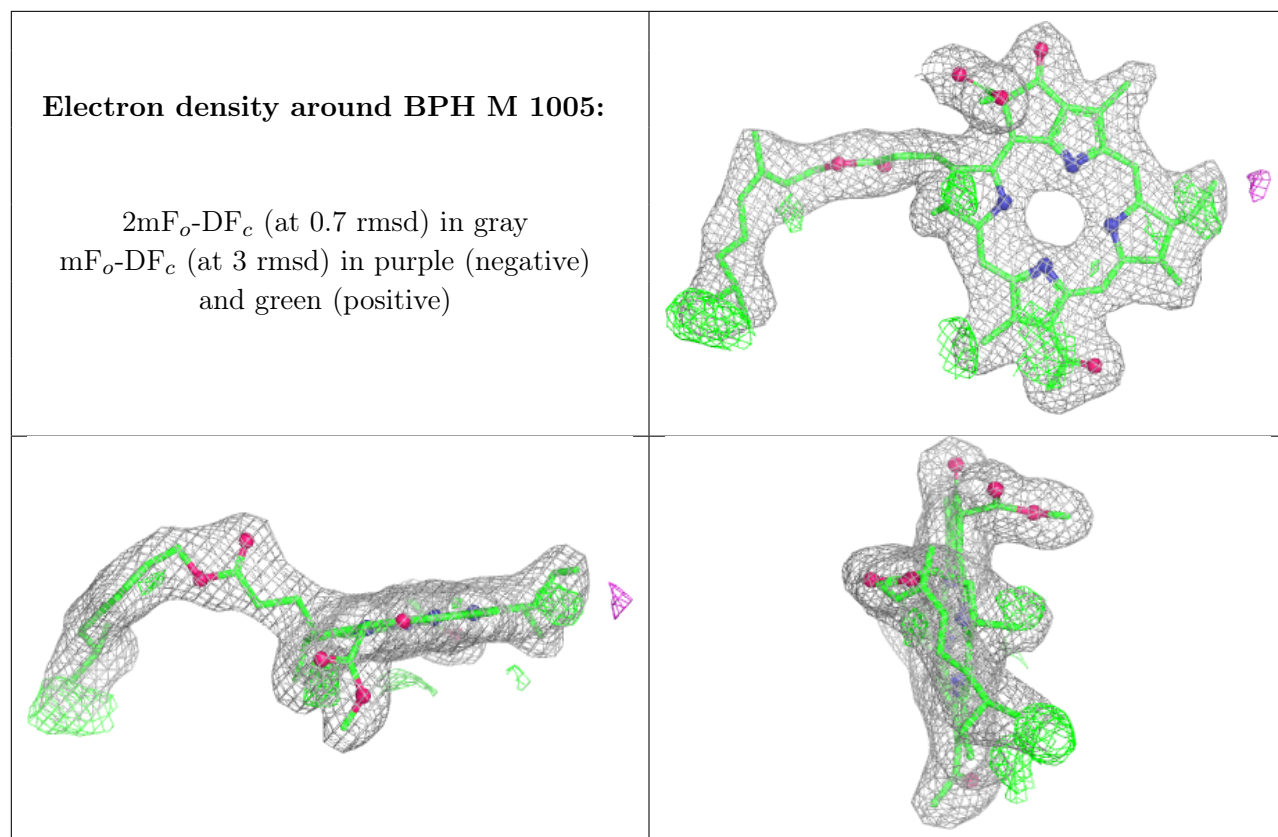
Electron density around U10 M 1008:

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

**Electron density around 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.