



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 10:37 AM UTC

PDB ID : 7EH7 / pdb_00007eh7
EMDB ID : EMD-31089
Title : Cryo-EM structure of the octameric state of C-phycocyanin from *Thermoleptolyngbya* sp. O-77
Authors : Minato, T.; Teramoto, T.; Adachi, N.; Hung, N.K.; Yamada, K.; Kawasaki, M.; Akutsu, M.; Moriya, T.; Senda, T.; Ogo, S.; Kakuta, Y.; Yoon, K.S.
Deposited on : 2021-03-28
Resolution : 3.71 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>
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:

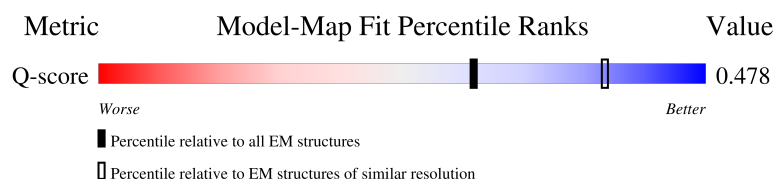
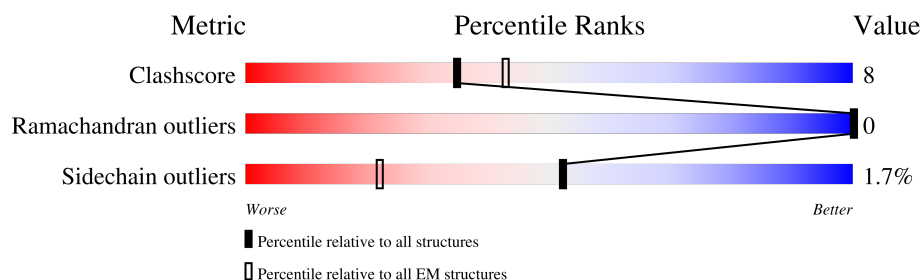
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.71 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.



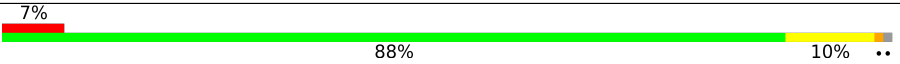
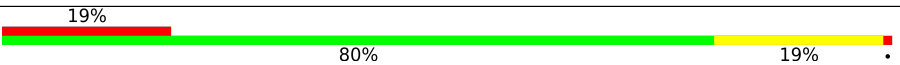
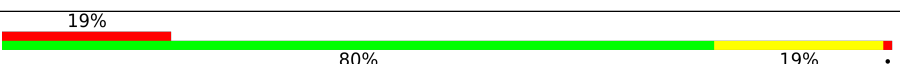
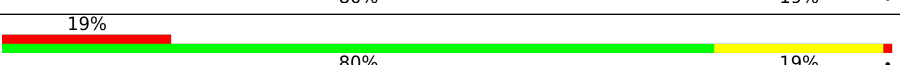
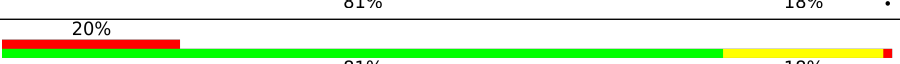
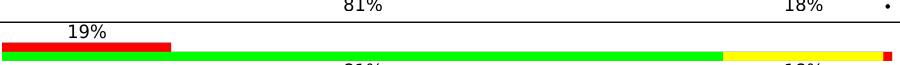
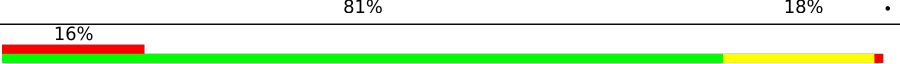
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10534 (3.21 - 4.21)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	162	7% 86% 12% ..
1	C	162	9% 87% 11% ..
1	E	162	6% 85% 14% ..
1	G	162	7% 87% 11% ..

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Mol	Chain	Length	Quality of chain
1	I	162	
1	K	162	
1	M	162	
1	O	162	
2	B	172	
2	D	172	
2	F	172	
2	H	172	
2	J	172	
2	L	172	
2	N	172	
2	P	172	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 20904 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 C-phycocyanin alpha chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	160	Total	C	N	O	S	0	0
			1221	764	212	241	4		
1	C	160	Total	C	N	O	S	0	0
			1221	764	212	241	4		
1	E	160	Total	C	N	O	S	0	0
			1221	764	212	241	4		
1	G	160	Total	C	N	O	S	0	0
			1221	764	212	241	4		
1	I	160	Total	C	N	O	S	0	0
			1221	764	212	241	4		
1	K	160	Total	C	N	O	S	0	0
			1221	764	212	241	4		
1	M	160	Total	C	N	O	S	0	0
			1221	764	212	241	4		
1	O	160	Total	C	N	O	S	0	0
			1221	764	212	241	4		

- Molecule 2 is a protein called C-phycocyanin beta chain.

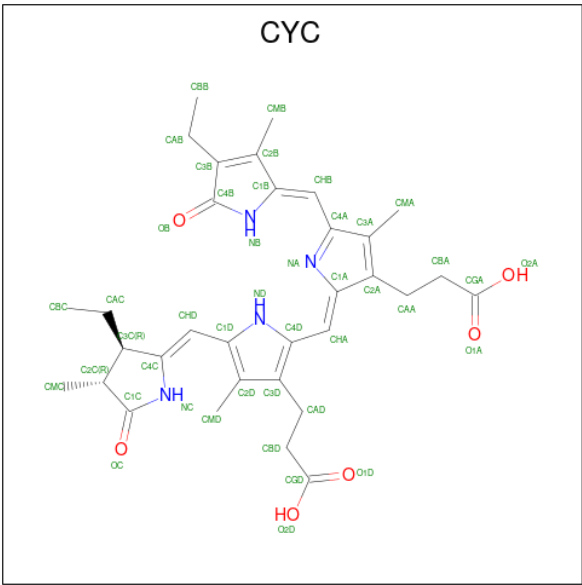
Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	172	Total	C	N	O	S	0	0
			1263	779	224	252	8		
2	D	172	Total	C	N	O	S	0	0
			1263	779	224	252	8		
2	F	172	Total	C	N	O	S	0	0
			1263	779	224	252	8		
2	H	172	Total	C	N	O	S	0	0
			1263	779	224	252	8		
2	J	172	Total	C	N	O	S	0	0
			1263	779	224	252	8		
2	L	172	Total	C	N	O	S	0	0
			1263	779	224	252	8		
2	N	172	Total	C	N	O	S	0	0
			1263	779	224	252	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	172	Total	C	N	O	S	0	0
			1263	779	224	252	8		

- Molecule 3 is PHYCOCYANOBILIN (CCD ID: CYC) (formula: C₃₃H₄₀N₄O₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			43	33	4	6	
3	B	1	Total	C	N	O	0
			43	33	4	6	
3	B	1	Total	C	N	O	0
			43	33	4	6	
3	C	1	Total	C	N	O	0
			43	33	4	6	
3	D	1	Total	C	N	O	0
			43	33	4	6	
3	D	1	Total	C	N	O	0
			43	33	4	6	
3	E	1	Total	C	N	O	0
			43	33	4	6	
3	F	1	Total	C	N	O	0
			43	33	4	6	
3	F	1	Total	C	N	O	0
			43	33	4	6	
3	G	1	Total	C	N	O	0
			43	33	4	6	

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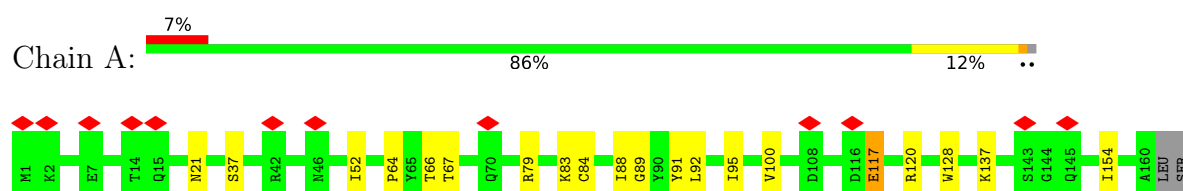
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Mol	Chain	Residues	Atoms				AltConf
3	H	1	Total 43	C 33	N 4	O 6	0
3	H	1	Total 43	C 33	N 4	O 6	0
3	I	1	Total 43	C 33	N 4	O 6	0
3	J	1	Total 43	C 33	N 4	O 6	0
3	J	1	Total 43	C 33	N 4	O 6	0
3	K	1	Total 43	C 33	N 4	O 6	0
3	L	1	Total 43	C 33	N 4	O 6	0
3	L	1	Total 43	C 33	N 4	O 6	0
3	M	1	Total 43	C 33	N 4	O 6	0
3	N	1	Total 43	C 33	N 4	O 6	0
3	N	1	Total 43	C 33	N 4	O 6	0
3	O	1	Total 43	C 33	N 4	O 6	0
3	P	1	Total 43	C 33	N 4	O 6	0
3	P	1	Total 43	C 33	N 4	O 6	0

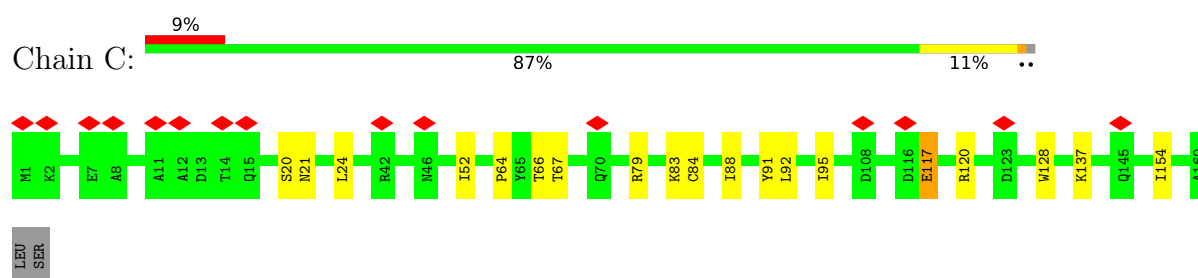
3 Residue-property plots [i](#)

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

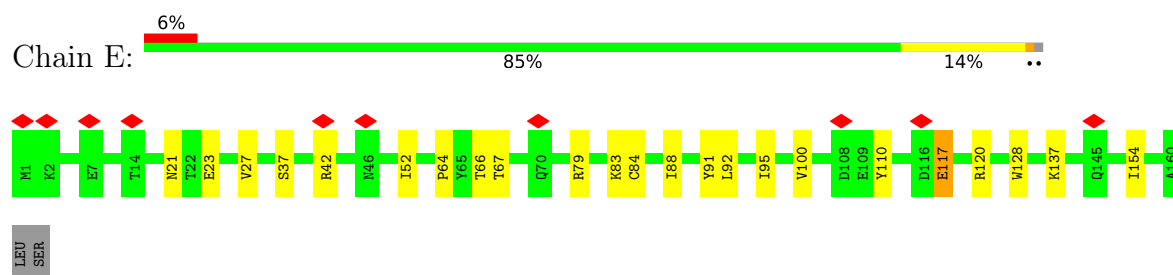
- Molecule 1: C-phycocyanin alpha chain



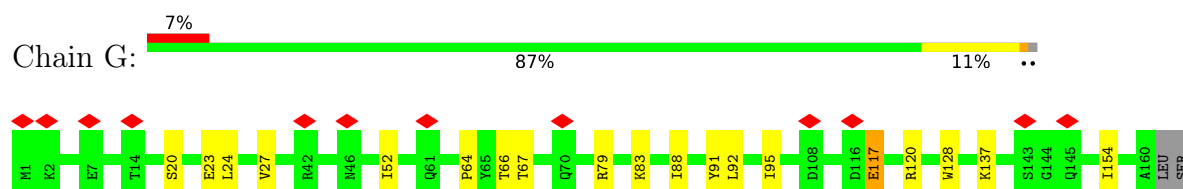
- Molecule 1: C-phycocyanin alpha chain



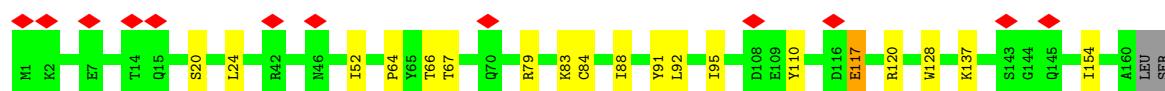
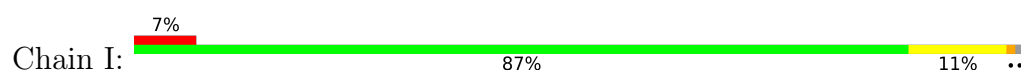
- Molecule 1: C-phycocyanin alpha chain



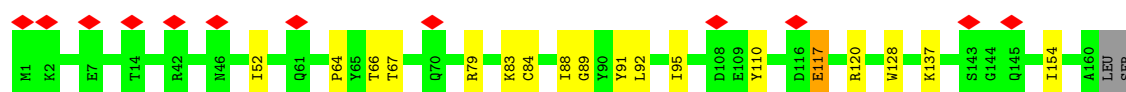
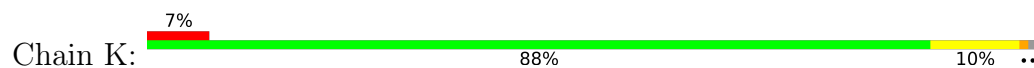
- Molecule 1: C-phycocyanin alpha chain



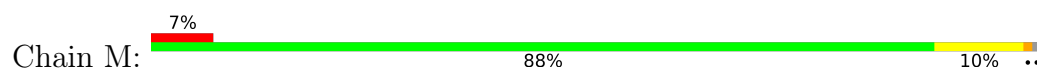
- Molecule 1: C-phycocyanin alpha chain



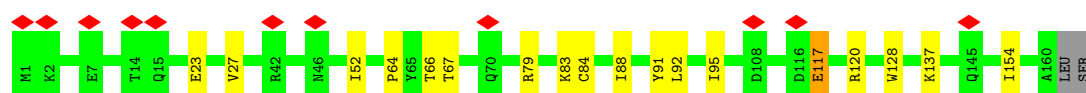
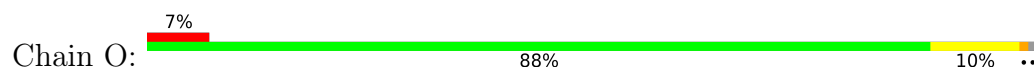
- Molecule 1: C-phycoerythrin alpha chain



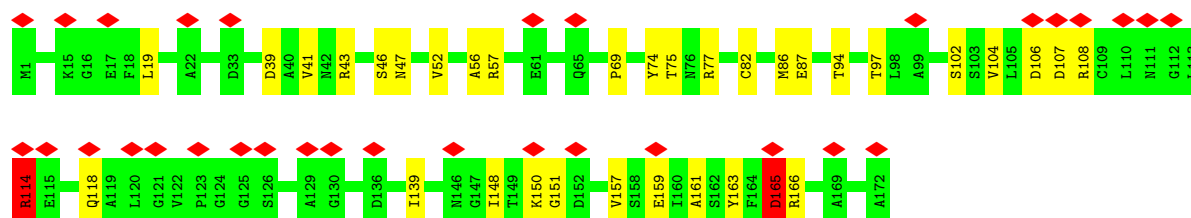
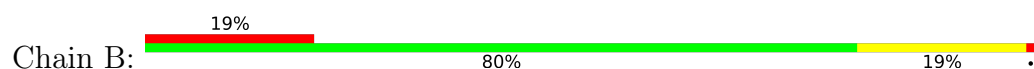
- Molecule 1: C-phycoerythrin alpha chain



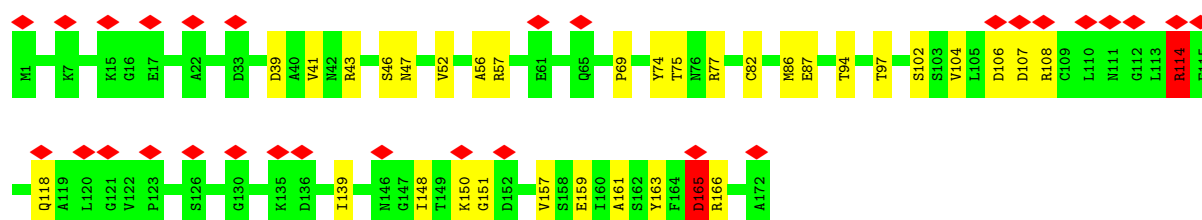
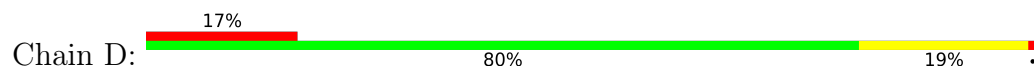
- Molecule 1: C-phycoerythrin alpha chain



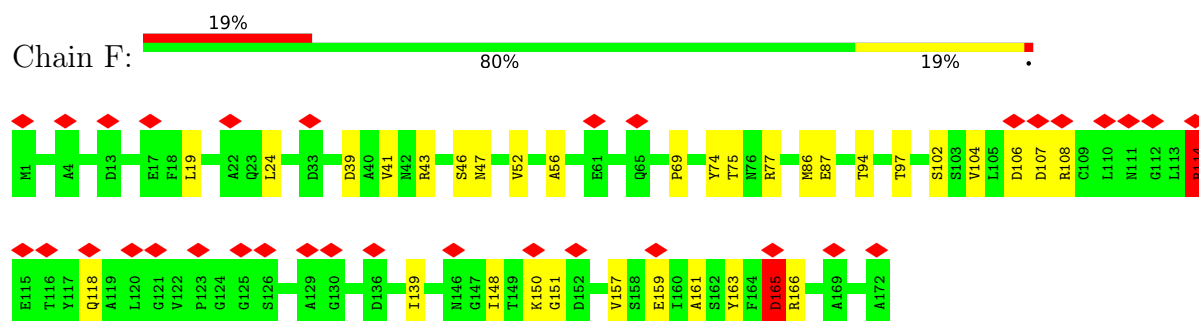
- Molecule 2: C-phycoerythrin beta chain



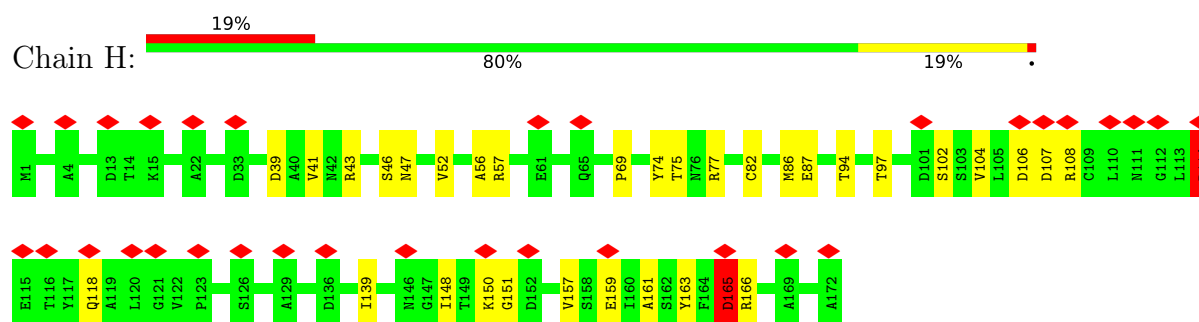
- Molecule 2: C-phycoerythrin beta chain



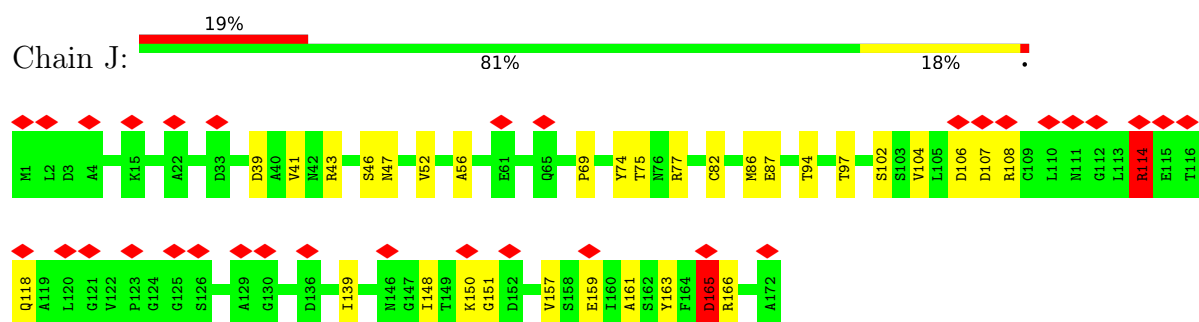
- Molecule 2: C-phycoerythrin beta chain



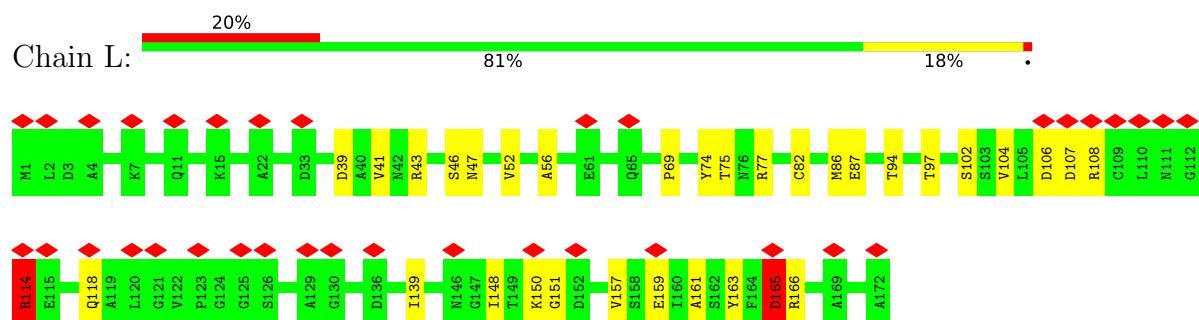
- Molecule 2: C-phycoerythrin beta chain



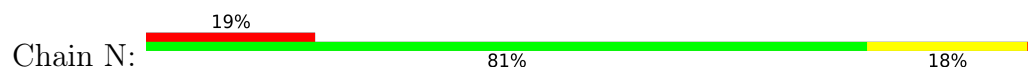
- Molecule 2: C-phycoerythrin beta chain

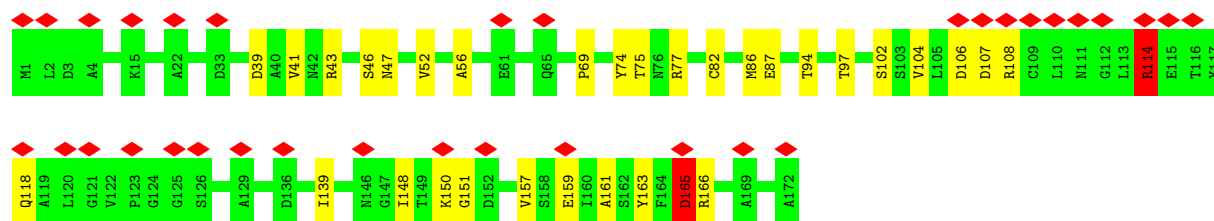


- Molecule 2: C-phycoerythrin beta chain

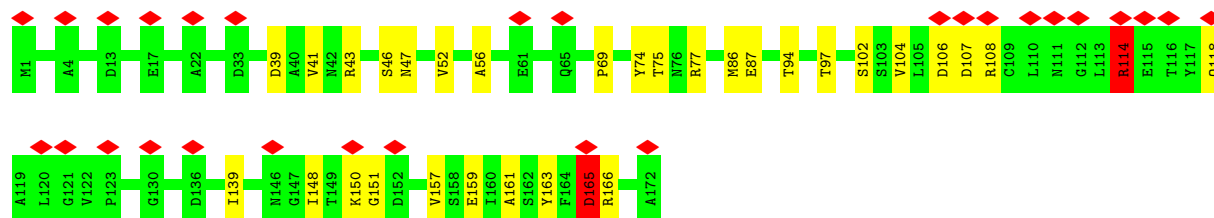
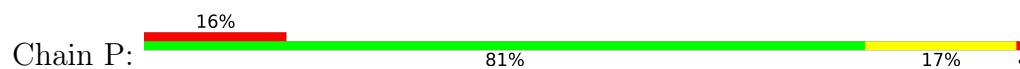


- Molecule 2: C-phycoerythrin beta chain





• Molecule 2: C-phycocyanin beta chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D4	Depositor
Number of particles used	10402	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS TALOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.0	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	120000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.144	Depositor
Minimum map value	-0.074	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.041	Depositor
Map size (Å)	352.0, 352.0, 352.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.88, 0.88, 0.88	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MEN, CYC

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.20	0/1242	0.48	0/1684
1	C	0.20	0/1242	0.48	0/1684
1	E	0.20	0/1242	0.48	0/1684
1	G	0.20	0/1242	0.48	0/1684
1	I	0.20	0/1242	0.48	0/1684
1	K	0.20	0/1242	0.48	0/1684
1	M	0.20	0/1242	0.48	0/1684
1	O	0.20	0/1242	0.48	0/1684
2	B	0.24	0/1265	0.55	2/1710 (0.1%)
2	D	0.24	0/1265	0.55	2/1710 (0.1%)
2	F	0.24	0/1265	0.55	2/1710 (0.1%)
2	H	0.24	0/1265	0.55	2/1710 (0.1%)
2	J	0.24	0/1265	0.55	2/1710 (0.1%)
2	L	0.24	0/1265	0.55	2/1710 (0.1%)
2	N	0.24	0/1265	0.55	2/1710 (0.1%)
2	P	0.24	0/1265	0.55	2/1710 (0.1%)
All	All	0.22	0/20056	0.52	16/27152 (0.1%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	N	114	ARG	CG-CD-NE	5.29	123.64	112.00
2	N	165	ASP	N-CA-CB	5.29	118.47	110.28
2	F	114	ARG	CG-CD-NE	5.28	123.62	112.00
2	H	114	ARG	CG-CD-NE	5.28	123.61	112.00
2	D	165	ASP	N-CA-CB	5.27	118.45	110.28
2	B	165	ASP	N-CA-CB	5.27	118.45	110.28
2	B	114	ARG	CG-CD-NE	5.27	123.60	112.00
2	F	165	ASP	N-CA-CB	5.26	118.44	110.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	114	ARG	CG-CD-NE	5.26	123.57	112.00
2	H	165	ASP	N-CA-CB	5.26	118.43	110.28
2	J	114	ARG	CG-CD-NE	5.26	123.57	112.00
2	J	165	ASP	N-CA-CB	5.25	118.42	110.28
2	L	114	ARG	CG-CD-NE	5.25	123.56	112.00
2	P	114	ARG	CG-CD-NE	5.25	123.54	112.00
2	L	165	ASP	N-CA-CB	5.24	118.39	110.28
2	P	165	ASP	N-CA-CB	5.23	118.39	110.28

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	A	1221	0	1187	15	0
1	C	1221	0	1187	14	0
1	E	1221	0	1187	17	0
1	G	1221	0	1187	13	0
1	I	1221	0	1187	14	0
1	K	1221	0	1187	14	0
1	M	1221	0	1187	12	0
1	O	1221	0	1187	13	0
2	B	1263	0	1267	27	0
2	D	1263	0	1267	25	0
2	F	1263	0	1267	25	0
2	H	1263	0	1267	26	0
2	J	1263	0	1267	25	0
2	L	1263	0	1267	24	0
2	N	1263	0	1267	25	0
2	P	1263	0	1267	23	0
3	A	43	0	37	4	0
3	B	86	0	74	7	0
3	C	43	0	37	4	0
3	D	86	0	74	6	0
3	E	43	0	37	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	86	0	74	6	0
3	G	43	0	37	2	0
3	H	86	0	74	5	0
3	I	43	0	37	5	0
3	J	86	0	74	5	0
3	K	43	0	37	5	0
3	L	86	0	74	6	0
3	M	43	0	37	1	0
3	N	86	0	74	6	0
3	O	43	0	37	5	0
3	P	86	0	74	5	0
All	All	20904	0	20520	332	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 8.

All (332) 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:N:43:ARG:HH22	2:N:148:ILE:HD13	1.52	0.74
2:H:43:ARG:HH22	2:H:148:ILE:HD13	1.52	0.74
2:N:139:ILE:HD12	2:N:157:VAL:HG13	1.70	0.74
2:B:139:ILE:HD12	2:B:157:VAL:HG13	1.70	0.74
2:H:139:ILE:HD12	2:H:157:VAL:HG13	1.70	0.74
2:L:43:ARG:HH22	2:L:148:ILE:HD13	1.52	0.74
2:L:139:ILE:HD12	2:L:157:VAL:HG13	1.70	0.74
2:B:43:ARG:HH22	2:B:148:ILE:HD13	1.52	0.74
2:D:43:ARG:HH22	2:D:148:ILE:HD13	1.52	0.73
2:J:43:ARG:HH22	2:J:148:ILE:HD13	1.52	0.73
2:F:43:ARG:HH22	2:F:148:ILE:HD13	1.52	0.73
2:J:139:ILE:HD12	2:J:157:VAL:HG13	1.70	0.73
2:D:139:ILE:HD12	2:D:157:VAL:HG13	1.70	0.72
2:F:139:ILE:HD12	2:F:157:VAL:HG13	1.70	0.72
2:P:43:ARG:HH22	2:P:148:ILE:HD13	1.52	0.72
2:P:139:ILE:HD12	2:P:157:VAL:HG13	1.70	0.72
1:E:137:LYS:HB2	1:E:154:ILE:HG21	1.71	0.71
1:O:137:LYS:HB2	1:O:154:ILE:HG21	1.71	0.71
1:C:137:LYS:HB2	1:C:154:ILE:HG21	1.71	0.71
2:H:106:ASP:OD1	2:H:107:ASP:N	2.24	0.71
1:I:137:LYS:HB2	1:I:154:ILE:HG21	1.71	0.71
2:J:106:ASP:OD1	2:J:107:ASP:N	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:106:ASP:OD1	2:N:107:ASP:N	2.24	0.71
1:K:137:LYS:HB2	1:K:154:ILE:HG21	1.71	0.71
2:P:106:ASP:OD1	2:P:107:ASP:N	2.24	0.71
2:D:106:ASP:OD1	2:D:107:ASP:N	2.24	0.71
2:F:106:ASP:OD1	2:F:107:ASP:N	2.24	0.71
1:G:137:LYS:HB2	1:G:154:ILE:HG21	1.71	0.71
1:A:137:LYS:HB2	1:A:154:ILE:HG21	1.71	0.70
1:M:137:LYS:HB2	1:M:154:ILE:HG21	1.71	0.70
2:B:106:ASP:OD1	2:B:107:ASP:N	2.24	0.69
2:L:106:ASP:OD1	2:L:107:ASP:N	2.24	0.69
2:B:114:ARG:O	2:B:118:GLN:NE2	2.26	0.69
2:L:114:ARG:O	2:L:118:GLN:NE2	2.26	0.69
2:F:114:ARG:O	2:F:118:GLN:NE2	2.26	0.68
2:N:114:ARG:O	2:N:118:GLN:NE2	2.26	0.68
2:P:114:ARG:O	2:P:118:GLN:NE2	2.26	0.68
2:H:114:ARG:O	2:H:118:GLN:NE2	2.26	0.68
2:D:114:ARG:O	2:D:118:GLN:NE2	2.26	0.67
2:J:114:ARG:O	2:J:118:GLN:NE2	2.26	0.67
2:N:114:ARG:HG3	2:N:118:GLN:HE22	1.63	0.63
2:H:114:ARG:HG3	2:H:118:GLN:HE22	1.63	0.63
2:L:114:ARG:HG3	2:L:118:GLN:HE22	1.63	0.63
2:B:114:ARG:HG3	2:B:118:GLN:HE22	1.63	0.63
2:P:114:ARG:HG3	2:P:118:GLN:HE22	1.63	0.63
2:F:114:ARG:HG3	2:F:118:GLN:HE22	1.63	0.62
2:J:114:ARG:HG3	2:J:118:GLN:HE22	1.63	0.62
2:D:114:ARG:HG3	2:D:118:GLN:HE22	1.63	0.61
1:A:117:GLU:OE1	1:A:120:ARG:NH1	2.34	0.61
1:K:117:GLU:OE1	1:K:120:ARG:NH1	2.34	0.61
1:E:117:GLU:OE1	1:E:120:ARG:NH1	2.34	0.61
1:G:117:GLU:OE1	1:G:120:ARG:NH1	2.34	0.61
1:M:117:GLU:OE1	1:M:120:ARG:NH1	2.34	0.61
1:C:117:GLU:OE1	1:C:120:ARG:NH1	2.34	0.61
1:I:117:GLU:OE1	1:I:120:ARG:NH1	2.34	0.61
1:O:117:GLU:OE1	1:O:120:ARG:NH1	2.34	0.61
2:B:52:VAL:HG21	2:B:87:GLU:HG2	1.84	0.59
2:L:52:VAL:HG21	2:L:87:GLU:HG2	1.84	0.59
2:P:52:VAL:HG21	2:P:87:GLU:HG2	1.84	0.59
2:D:52:VAL:HG21	2:D:87:GLU:HG2	1.84	0.59
2:F:52:VAL:HG21	2:F:87:GLU:HG2	1.84	0.59
2:J:52:VAL:HG21	2:J:87:GLU:HG2	1.84	0.59
2:H:52:VAL:HG21	2:H:87:GLU:HG2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:52:VAL:HG21	2:N:87:GLU:HG2	1.84	0.59
1:C:92:LEU:HD12	1:C:95:ILE:HD11	1.85	0.59
2:P:161:ALA:O	2:P:165:ASP:OD1	2.21	0.59
2:D:161:ALA:O	2:D:165:ASP:OD1	2.21	0.59
1:E:92:LEU:HD12	1:E:95:ILE:HD11	1.85	0.59
1:I:92:LEU:HD12	1:I:95:ILE:HD11	1.85	0.59
1:O:92:LEU:HD12	1:O:95:ILE:HD11	1.85	0.59
2:F:161:ALA:O	2:F:165:ASP:OD1	2.21	0.58
2:J:161:ALA:O	2:J:165:ASP:OD1	2.21	0.58
2:N:161:ALA:O	2:N:165:ASP:OD1	2.21	0.58
2:H:161:ALA:O	2:H:165:ASP:OD1	2.21	0.58
1:K:92:LEU:HD12	1:K:95:ILE:HD11	1.85	0.57
1:A:92:LEU:HD12	1:A:95:ILE:HD11	1.85	0.57
1:M:92:LEU:HD12	1:M:95:ILE:HD11	1.85	0.57
2:B:161:ALA:O	2:B:165:ASP:OD1	2.21	0.57
1:G:92:LEU:HD12	1:G:95:ILE:HD11	1.85	0.57
2:L:161:ALA:O	2:L:165:ASP:OD1	2.21	0.57
2:B:114:ARG:CG	2:B:118:GLN:HE22	2.18	0.57
2:N:56:ALA:HB2	2:N:86:MET:HE1	1.87	0.57
2:D:114:ARG:CG	2:D:118:GLN:HE22	2.18	0.56
2:J:114:ARG:CG	2:J:118:GLN:HE22	2.18	0.56
2:L:114:ARG:CG	2:L:118:GLN:HE22	2.18	0.56
2:H:56:ALA:HB2	2:H:86:MET:HE1	1.87	0.56
2:B:94:THR:HA	2:B:97:THR:HG22	1.87	0.56
2:L:94:THR:HA	2:L:97:THR:HG22	1.87	0.56
1:G:117:GLU:OE1	1:G:117:GLU:HA	2.06	0.56
1:M:117:GLU:OE1	1:M:117:GLU:HA	2.06	0.56
2:L:56:ALA:HB2	2:L:86:MET:HE1	1.87	0.56
1:A:117:GLU:OE1	1:A:117:GLU:HA	2.06	0.56
2:F:56:ALA:HB2	2:F:86:MET:HE1	1.87	0.56
1:K:117:GLU:OE1	1:K:117:GLU:HA	2.06	0.56
2:B:56:ALA:HB2	2:B:86:MET:HE1	1.87	0.56
2:P:56:ALA:HB2	2:P:86:MET:HE1	1.87	0.56
2:D:94:THR:HA	2:D:97:THR:HG22	1.87	0.55
1:E:117:GLU:OE1	1:E:117:GLU:HA	2.06	0.55
2:J:94:THR:HA	2:J:97:THR:HG22	1.87	0.55
2:P:114:ARG:CG	2:P:118:GLN:HE22	2.18	0.55
2:F:114:ARG:CG	2:F:118:GLN:HE22	2.18	0.55
2:H:94:THR:HA	2:H:97:THR:HG22	1.87	0.55
2:N:94:THR:HA	2:N:97:THR:HG22	1.87	0.55
2:H:114:ARG:CG	2:H:118:GLN:HE22	2.18	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:114:ARG:CG	2:N:118:GLN:HE22	2.18	0.55
1:O:117:GLU:OE1	1:O:117:GLU:HA	2.06	0.55
2:D:56:ALA:HB2	2:D:86:MET:HE1	1.87	0.55
2:J:56:ALA:HB2	2:J:86:MET:HE1	1.87	0.55
2:F:94:THR:HA	2:F:97:THR:HG22	1.87	0.55
2:P:94:THR:HA	2:P:97:THR:HG22	1.87	0.54
1:E:52:ILE:HD13	1:E:88:ILE:HG22	1.90	0.54
2:B:46:SER:C	2:B:47:ASN:HD22	2.16	0.54
1:C:52:ILE:HD13	1:C:88:ILE:HG22	1.90	0.54
2:H:102:SER:OG	2:H:166:ARG:NH1	2.41	0.54
2:L:46:SER:C	2:L:47:ASN:HD22	2.16	0.54
2:N:102:SER:OG	2:N:166:ARG:NH1	2.41	0.54
1:O:52:ILE:HD13	1:O:88:ILE:HG22	1.90	0.54
2:D:46:SER:C	2:D:47:ASN:HD22	2.16	0.54
2:F:102:SER:OG	2:F:166:ARG:NH1	2.41	0.54
1:I:52:ILE:HD13	1:I:88:ILE:HG22	1.90	0.54
2:P:102:SER:OG	2:P:166:ARG:NH1	2.41	0.54
1:C:117:GLU:OE1	1:C:117:GLU:HA	2.06	0.54
2:J:46:SER:C	2:J:47:ASN:HD22	2.16	0.54
2:D:165:ASP:OD1	2:D:165:ASP:N	2.41	0.54
1:I:117:GLU:OE1	1:I:117:GLU:HA	2.06	0.54
2:J:165:ASP:OD1	2:J:165:ASP:N	2.41	0.54
2:D:114:ARG:HG3	2:D:118:GLN:NE2	2.23	0.54
2:J:114:ARG:HG3	2:J:118:GLN:NE2	2.23	0.54
2:B:114:ARG:HG3	2:B:118:GLN:NE2	2.23	0.54
2:L:114:ARG:HG3	2:L:118:GLN:NE2	2.23	0.54
1:E:100:VAL:HG21	2:F:19:LEU:HD22	1.88	0.53
2:F:165:ASP:OD1	2:F:165:ASP:N	2.41	0.53
1:G:64:PRO:O	1:G:67:THR:HG22	2.08	0.53
2:N:46:SER:C	2:N:47:ASN:HD22	2.16	0.53
1:C:64:PRO:O	1:C:67:THR:HG22	2.08	0.53
2:H:46:SER:C	2:H:47:ASN:HD22	2.16	0.53
1:M:64:PRO:O	1:M:67:THR:HG22	2.08	0.53
2:D:102:SER:OG	2:D:166:ARG:NH1	2.41	0.53
1:I:64:PRO:O	1:I:67:THR:HG22	2.08	0.53
2:J:102:SER:OG	2:J:166:ARG:NH1	2.41	0.53
2:L:102:SER:OG	2:L:166:ARG:NH1	2.41	0.53
1:O:64:PRO:O	1:O:67:THR:HG22	2.08	0.53
2:B:165:ASP:OD1	2:B:165:ASP:N	2.41	0.53
1:E:64:PRO:O	1:E:67:THR:HG22	2.08	0.53
2:L:165:ASP:OD1	2:L:165:ASP:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:41:VAL:HG22	2:B:97:THR:HG23	1.90	0.53
2:B:102:SER:OG	2:B:166:ARG:NH1	2.41	0.53
2:L:41:VAL:HG22	2:L:97:THR:HG23	1.90	0.53
2:P:46:SER:C	2:P:47:ASN:HD22	2.16	0.53
2:F:46:SER:C	2:F:47:ASN:HD22	2.16	0.53
1:A:52:ILE:HD13	1:A:88:ILE:HG22	1.90	0.53
2:F:41:VAL:HG22	2:F:97:THR:HG23	1.90	0.53
1:K:52:ILE:HD13	1:K:88:ILE:HG22	1.90	0.53
2:D:41:VAL:HG22	2:D:97:THR:HG23	1.90	0.53
2:F:114:ARG:HG3	2:F:118:GLN:NE2	2.23	0.53
1:M:52:ILE:HD13	1:M:88:ILE:HG22	1.90	0.53
2:P:114:ARG:HG3	2:P:118:GLN:NE2	2.23	0.53
1:G:52:ILE:HD13	1:G:88:ILE:HG22	1.90	0.52
2:J:41:VAL:HG22	2:J:97:THR:HG23	1.90	0.52
1:A:64:PRO:O	1:A:67:THR:HG22	2.08	0.52
2:H:41:VAL:HG22	2:H:97:THR:HG23	1.90	0.52
2:H:114:ARG:HG3	2:H:118:GLN:NE2	2.23	0.52
2:N:114:ARG:HG3	2:N:118:GLN:NE2	2.23	0.52
1:K:64:PRO:O	1:K:67:THR:HG22	2.08	0.52
2:P:41:VAL:HG22	2:P:97:THR:HG23	1.90	0.52
2:H:165:ASP:OD1	2:H:165:ASP:N	2.41	0.52
2:N:41:VAL:HG22	2:N:97:THR:HG23	1.90	0.52
2:N:165:ASP:OD1	2:N:165:ASP:N	2.41	0.52
1:E:42:ARG:HG2	2:F:24:LEU:HD13	1.92	0.51
2:P:165:ASP:OD1	2:P:165:ASP:N	2.41	0.51
2:F:114:ARG:CG	2:F:114:ARG:HH11	2.25	0.49
2:N:114:ARG:CG	2:N:114:ARG:HH11	2.25	0.49
2:P:114:ARG:CG	2:P:114:ARG:HH11	2.25	0.49
2:H:114:ARG:CG	2:H:114:ARG:HH11	2.25	0.49
2:B:104:VAL:HG23	2:B:108:ARG:HD3	1.95	0.49
2:L:104:VAL:HG23	2:L:108:ARG:HD3	1.95	0.49
2:N:104:VAL:HG23	2:N:108:ARG:HD3	1.95	0.49
2:H:104:VAL:HG23	2:H:108:ARG:HD3	1.95	0.48
2:J:114:ARG:CG	2:J:114:ARG:HH11	2.25	0.48
2:L:114:ARG:CG	2:L:114:ARG:HH11	2.25	0.48
2:F:104:VAL:HG23	2:F:108:ARG:HD3	1.95	0.48
2:B:114:ARG:CG	2:B:114:ARG:HH11	2.25	0.48
2:D:114:ARG:CG	2:D:114:ARG:HH11	2.25	0.48
2:F:159:GLU:HG2	2:F:163:TYR:CE2	2.49	0.48
2:H:82:CYS:HA	3:H:201:CYC:HAC1	1.64	0.48
2:P:104:VAL:HG23	2:P:108:ARG:HD3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:159:GLU:HG2	2:J:163:TYR:CE2	2.49	0.48
2:P:159:GLU:HG2	2:P:163:TYR:CE2	2.49	0.48
2:D:104:VAL:HG23	2:D:108:ARG:HD3	1.95	0.48
2:D:159:GLU:HG2	2:D:163:TYR:CE2	2.49	0.48
2:H:159:GLU:HG2	2:H:163:TYR:CE2	2.49	0.48
2:J:104:VAL:HG23	2:J:108:ARG:HD3	1.95	0.48
2:N:159:GLU:HG2	2:N:163:TYR:CE2	2.49	0.48
2:N:82:CYS:HA	3:N:201:CYC:HAC1	1.64	0.47
2:B:159:GLU:HG2	2:B:163:TYR:CE2	2.49	0.47
3:D:201:CYC:HC	3:D:201:CYC:CMD	2.27	0.47
3:F:201:CYC:CMD	3:F:201:CYC:HC	2.27	0.47
3:J:201:CYC:HC	3:J:201:CYC:CMD	2.27	0.47
2:L:159:GLU:HG2	2:L:163:TYR:CE2	2.49	0.47
3:P:201:CYC:HC	3:P:201:CYC:CMD	2.27	0.47
2:D:82:CYS:HA	3:D:201:CYC:HAC1	1.64	0.47
3:I:201:CYC:HAC1	3:I:201:CYC:HHD	1.61	0.47
3:C:201:CYC:HAC1	3:C:201:CYC:HHD	1.61	0.47
2:J:82:CYS:HA	3:J:201:CYC:HAC1	1.64	0.47
3:N:201:CYC:HC	3:N:201:CYC:CMD	2.27	0.47
3:H:201:CYC:HC	3:H:201:CYC:CMD	2.27	0.47
3:H:202:CYC:HBD1	3:H:202:CYC:HAA1	1.97	0.47
3:B:202:CYC:HBD1	3:B:202:CYC:HAA1	1.97	0.46
3:N:202:CYC:HBD1	3:N:202:CYC:HAA1	1.97	0.46
1:G:92:LEU:O	1:G:95:ILE:HG12	2.16	0.46
3:L:202:CYC:HBD1	3:L:202:CYC:HAA1	1.97	0.46
1:M:92:LEU:O	1:M:95:ILE:HG12	2.16	0.46
3:B:201:CYC:HC	3:B:201:CYC:CMD	2.27	0.46
3:L:201:CYC:HC	3:L:201:CYC:CMD	2.27	0.46
1:E:92:LEU:O	1:E:95:ILE:HG12	2.16	0.46
1:O:92:LEU:O	1:O:95:ILE:HG12	2.16	0.46
1:K:92:LEU:O	1:K:95:ILE:HG12	2.16	0.46
3:F:202:CYC:HBD1	3:F:202:CYC:HAA1	1.98	0.45
1:A:92:LEU:O	1:A:95:ILE:HG12	2.16	0.45
3:P:202:CYC:HBD1	3:P:202:CYC:HAA1	1.97	0.45
2:B:77:ARG:HH22	1:I:110:TYR:HD1	1.65	0.45
3:D:202:CYC:HBD1	3:D:202:CYC:HAA1	1.97	0.45
3:J:202:CYC:HBD1	3:J:202:CYC:HAA1	1.97	0.45
1:C:92:LEU:O	1:C:95:ILE:HG12	2.16	0.45
1:I:92:LEU:O	1:I:95:ILE:HG12	2.16	0.45
1:E:84:CYS:HA	3:E:201:CYC:HAC1	1.79	0.45
1:G:79:ARG:CZ	1:G:83:LYS:HE2	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:79:ARG:CZ	1:M:83:LYS:HE2	2.47	0.44
1:O:84:CYS:HA	3:O:201:CYC:HAC1	1.79	0.44
3:O:201:CYC:HAC1	3:O:201:CYC:HHD	1.61	0.44
1:A:79:ARG:CZ	1:A:83:LYS:HE2	2.47	0.44
3:E:201:CYC:HAC1	3:E:201:CYC:HHD	1.61	0.44
1:K:79:ARG:CZ	1:K:83:LYS:HE2	2.47	0.44
1:C:79:ARG:CZ	1:C:83:LYS:HE2	2.47	0.44
1:I:79:ARG:CZ	1:I:83:LYS:HE2	2.47	0.44
2:D:39:ASP:OD1	3:D:202:CYC:HBB	2.18	0.44
2:D:74:TYR:CG	2:D:74:TYR:O	2.71	0.44
2:H:57:ARG:NH2	3:K:201:CYC:O1D	2.50	0.44
2:J:39:ASP:OD1	3:J:202:CYC:HBB	2.18	0.44
2:J:74:TYR:CG	2:J:74:TYR:O	2.71	0.44
2:P:39:ASP:OD1	3:P:202:CYC:HBB	2.18	0.44
2:F:39:ASP:OD1	3:F:202:CYC:HBB	2.18	0.44
1:M:13:ASP:OD2	2:N:108:ARG:NE	2.51	0.44
3:B:202:CYC:HHD	3:B:202:CYC:HAC1	1.87	0.43
3:A:201:CYC:HHD	3:A:201:CYC:HAC1	1.61	0.43
1:I:84:CYS:HA	3:I:201:CYC:HAC1	1.79	0.43
1:C:21:ASN:OD1	3:D:202:CYC:HBB1	2.18	0.43
1:C:84:CYS:HA	3:C:201:CYC:HAC1	1.79	0.43
3:K:201:CYC:HHD	3:K:201:CYC:HAC1	1.61	0.43
1:A:21:ASN:OD1	3:B:202:CYC:HBB1	2.17	0.43
2:B:74:TYR:O	2:B:74:TYR:CG	2.71	0.43
2:B:82:CYS:HA	3:B:201:CYC:HAC1	1.64	0.43
2:L:39:ASP:OD1	3:L:202:CYC:HBB	2.18	0.43
2:L:74:TYR:O	2:L:74:TYR:CG	2.71	0.43
3:L:202:CYC:HHD	3:L:202:CYC:HAC1	1.87	0.43
2:B:39:ASP:OD1	3:B:202:CYC:HBB	2.18	0.43
1:E:79:ARG:CZ	1:E:83:LYS:HE2	2.47	0.43
2:L:82:CYS:HA	3:L:201:CYC:HAC1	1.64	0.43
2:N:74:TYR:CG	2:N:74:TYR:O	2.71	0.43
1:O:79:ARG:CZ	1:O:83:LYS:HE2	2.47	0.43
2:H:74:TYR:CG	2:H:74:TYR:O	2.71	0.43
2:H:39:ASP:OD1	3:H:202:CYC:HBB	2.18	0.43
2:N:39:ASP:OD1	3:N:202:CYC:HBB	2.18	0.42
2:D:69:PRO:HA	2:D:74:TYR:CD2	2.55	0.42
2:B:69:PRO:HA	2:B:74:TYR:CD2	2.55	0.42
2:L:69:PRO:HA	2:L:74:TYR:CD2	2.55	0.42
2:P:74:TYR:CG	2:P:74:TYR:O	2.71	0.42
1:E:110:TYR:HD1	2:J:77:ARG:HH22	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:74:TYR:CG	2:F:74:TYR:O	2.71	0.42
2:J:69:PRO:HA	2:J:74:TYR:CD2	2.55	0.42
2:P:69:PRO:HA	2:P:74:TYR:CD2	2.54	0.42
2:D:75:THR:HG21	2:D:77:ARG:NH1	2.34	0.42
2:F:69:PRO:HA	2:F:74:TYR:CD2	2.55	0.42
2:H:69:PRO:HA	2:H:74:TYR:CD2	2.55	0.42
2:H:77:ARG:HH22	1:K:110:TYR:HD1	1.68	0.42
1:M:91:TYR:O	1:M:95:ILE:HG23	2.19	0.42
2:N:75:THR:HG21	2:N:77:ARG:NH1	2.34	0.42
2:B:57:ARG:NH2	3:I:201:CYC:O1D	2.53	0.42
2:F:75:THR:HG21	2:F:77:ARG:NH1	2.34	0.42
2:N:69:PRO:HA	2:N:74:TYR:CD2	2.55	0.42
2:P:75:THR:HG21	2:P:77:ARG:NH1	2.34	0.42
2:J:75:THR:HG21	2:J:77:ARG:NH1	2.34	0.42
1:K:91:TYR:O	1:K:95:ILE:HG23	2.19	0.42
1:E:91:TYR:O	1:E:95:ILE:HG23	2.19	0.42
1:G:91:TYR:O	1:G:95:ILE:HG23	2.19	0.42
2:H:75:THR:HG21	2:H:77:ARG:NH1	2.34	0.42
1:A:91:TYR:O	1:A:95:ILE:HG23	2.19	0.42
1:K:84:CYS:HA	3:K:201:CYC:HAC1	1.79	0.42
1:O:91:TYR:O	1:O:95:ILE:HG23	2.19	0.42
1:I:91:TYR:O	1:I:95:ILE:HG23	2.19	0.41
1:K:128:TRP:CE3	3:K:201:CYC:HMC3	2.55	0.41
1:A:128:TRP:CE3	3:A:201:CYC:HMC3	2.56	0.41
2:B:75:THR:HG21	2:B:77:ARG:NH1	2.34	0.41
2:L:75:THR:HG21	2:L:77:ARG:NH1	2.34	0.41
1:C:91:TYR:O	1:C:95:ILE:HG23	2.19	0.41
1:A:84:CYS:HA	3:A:201:CYC:HAC1	1.79	0.41
2:D:57:ARG:NH2	3:O:201:CYC:O1D	2.54	0.41
1:C:128:TRP:CE3	3:C:201:CYC:HMC3	2.56	0.41
1:I:128:TRP:CE3	3:I:201:CYC:HMC3	2.56	0.41
1:M:128:TRP:CE3	3:M:201:CYC:HMC3	2.56	0.41
1:A:66:THR:HG21	3:A:201:CYC:HMC2	2.03	0.41
1:G:128:TRP:CE3	3:G:201:CYC:HMC3	2.56	0.41
2:H:151:GLY:HA3	3:H:202:CYC:HMD2	2.03	0.41
1:K:66:THR:HG21	3:K:201:CYC:HMC2	2.03	0.41
2:N:151:GLY:HA3	3:N:202:CYC:HMD2	2.03	0.41
2:B:151:GLY:HA3	3:B:202:CYC:HMD2	2.03	0.41
1:G:20:SER:O	1:G:24:LEU:HD23	2.21	0.41
2:L:151:GLY:HA3	3:L:202:CYC:HMD2	2.03	0.41
1:A:100:VAL:HG21	2:B:19:LEU:HD22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:20:SER:O	1:C:24:LEU:HD23	2.22	0.40
1:E:23:GLU:O	1:E:27:VAL:HG23	2.21	0.40
2:F:151:GLY:HA3	3:F:202:CYC:HMD2	2.03	0.40
3:F:202:CYC:HHD	3:F:202:CYC:HAC1	1.87	0.40
1:I:20:SER:O	1:I:24:LEU:HD23	2.21	0.40
1:M:20:SER:O	1:M:24:LEU:HD23	2.21	0.40
1:C:66:THR:HG21	3:C:201:CYC:HMC2	2.03	0.40
1:E:21:ASN:OD1	3:F:202:CYC:HBB1	2.21	0.40
1:I:66:THR:HG21	3:I:201:CYC:HMC2	2.03	0.40
1:K:52:ILE:HD11	1:K:89:GLY:HA2	2.03	0.40
3:N:201:CYC:HAC1	3:N:201:CYC:HHD	1.90	0.40
1:A:52:ILE:HD11	1:A:89:GLY:HA2	2.03	0.40
1:G:23:GLU:O	1:G:27:VAL:HG23	2.21	0.40
1:O:23:GLU:O	1:O:27:VAL:HG23	2.21	0.40
2:D:151:GLY:HA3	3:D:202:CYC:HMD2	2.03	0.40
2:P:151:GLY:HA3	3:P:202:CYC:HMD2	2.03	0.40
1:E:66:THR:HG21	3:E:201:CYC:HMC2	2.03	0.40
1:E:128:TRP:CE3	3:E:201:CYC:HMC3	2.56	0.40
1:G:66:THR:HG21	3:G:201:CYC:HMC2	2.03	0.40
2:J:151:GLY:HA3	3:J:202:CYC:HMD2	2.03	0.40
1:O:66:THR:HG21	3:O:201:CYC:HMC2	2.03	0.40
1:O:128:TRP:CE3	3:O:201:CYC:HMC3	2.56	0.40
3:P:202:CYC:HHD	3:P:202:CYC:HAC1	1.87	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 PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	158/162 (98%)	154 (98%)	4 (2%)	0	100	100
1	C	158/162 (98%)	154 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	158/162 (98%)	154 (98%)	4 (2%)	0	100	100
1	G	158/162 (98%)	154 (98%)	4 (2%)	0	100	100
1	I	158/162 (98%)	154 (98%)	4 (2%)	0	100	100
1	K	158/162 (98%)	154 (98%)	4 (2%)	0	100	100
1	M	158/162 (98%)	154 (98%)	4 (2%)	0	100	100
1	O	158/162 (98%)	154 (98%)	4 (2%)	0	100	100
2	B	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
2	D	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
2	F	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
2	H	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
2	J	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
2	L	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
2	N	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
2	P	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
All	All	2616/2672 (98%)	2552 (98%)	64 (2%)	0	100	100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	121/123 (98%)	119 (98%)	2 (2%)	53	67
1	C	121/123 (98%)	120 (99%)	1 (1%)	73	76
1	E	121/123 (98%)	119 (98%)	2 (2%)	53	67
1	G	121/123 (98%)	120 (99%)	1 (1%)	73	76
1	I	121/123 (98%)	120 (99%)	1 (1%)	73	76
1	K	121/123 (98%)	120 (99%)	1 (1%)	73	76
1	M	121/123 (98%)	120 (99%)	1 (1%)	73	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	O	121/123 (98%)	120 (99%)	1 (1%)	73	76
2	B	130/130 (100%)	127 (98%)	3 (2%)	44	62
2	D	130/130 (100%)	127 (98%)	3 (2%)	44	62
2	F	130/130 (100%)	127 (98%)	3 (2%)	44	62
2	H	130/130 (100%)	127 (98%)	3 (2%)	44	62
2	J	130/130 (100%)	127 (98%)	3 (2%)	44	62
2	L	130/130 (100%)	127 (98%)	3 (2%)	44	62
2	N	130/130 (100%)	127 (98%)	3 (2%)	44	62
2	P	130/130 (100%)	127 (98%)	3 (2%)	44	62
All	All	2008/2024 (99%)	1974 (98%)	34 (2%)	52	67

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	SER
1	A	117	GLU
2	B	114	ARG
2	B	150	LYS
2	B	165	ASP
1	C	117	GLU
2	D	114	ARG
2	D	150	LYS
2	D	165	ASP
1	E	37	SER
1	E	117	GLU
2	F	114	ARG
2	F	150	LYS
2	F	165	ASP
1	G	117	GLU
2	H	114	ARG
2	H	150	LYS
2	H	165	ASP
1	I	117	GLU
2	J	114	ARG
2	J	150	LYS
2	J	165	ASP
1	K	117	GLU
2	L	114	ARG
2	L	150	LYS

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Mol	Chain	Res	Type
2	L	165	ASP
1	M	117	GLU
2	N	114	ARG
2	N	150	LYS
2	N	165	ASP
1	O	117	GLU
2	P	114	ARG
2	P	150	LYS
2	P	165	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	118	GLN
2	D	118	GLN
1	E	28	ASN
2	F	111	ASN
2	F	118	GLN
1	G	25	GLN
2	H	118	GLN
2	J	118	GLN
2	L	118	GLN
1	M	25	GLN
1	M	28	ASN
2	N	118	GLN
2	P	111	ASN
2	P	118	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\# Z > 2$
2	MEN	H	72	2	7,8,9	0.90	0	4,9,11	1.05	0
2	MEN	B	72	2	7,8,9	0.91	0	4,9,11	1.06	0
2	MEN	D	72	2	7,8,9	0.92	0	4,9,11	1.06	0
2	MEN	J	72	2	7,8,9	0.92	0	4,9,11	1.06	0
2	MEN	L	72	2	7,8,9	0.91	0	4,9,11	1.05	0
2	MEN	P	72	2	7,8,9	0.91	0	4,9,11	1.07	0
2	MEN	N	72	2	7,8,9	0.92	0	4,9,11	1.06	0
2	MEN	F	72	2	7,8,9	0.92	0	4,9,11	1.04	0

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
2	MEN	H	72	2	-	4/7/8/10	-
2	MEN	B	72	2	-	4/7/8/10	-
2	MEN	D	72	2	-	4/7/8/10	-
2	MEN	J	72	2	-	4/7/8/10	-
2	MEN	L	72	2	-	4/7/8/10	-
2	MEN	P	72	2	-	4/7/8/10	-
2	MEN	N	72	2	-	4/7/8/10	-
2	MEN	F	72	2	-	4/7/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	72	MEN	O-C-CA-CB
2	D	72	MEN	O-C-CA-CB
2	F	72	MEN	O-C-CA-CB
2	H	72	MEN	O-C-CA-CB
2	J	72	MEN	O-C-CA-CB
2	L	72	MEN	O-C-CA-CB

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Mol	Chain	Res	Type	Atoms
2	N	72	MEN	O-C-CA-CB
2	P	72	MEN	O-C-CA-CB
2	B	72	MEN	CA-CB-CG-OD1
2	D	72	MEN	CA-CB-CG-OD1
2	F	72	MEN	CA-CB-CG-OD1
2	H	72	MEN	CA-CB-CG-OD1
2	J	72	MEN	CA-CB-CG-OD1
2	L	72	MEN	CA-CB-CG-OD1
2	N	72	MEN	CA-CB-CG-OD1
2	P	72	MEN	CA-CB-CG-OD1
2	B	72	MEN	CA-CB-CG-ND2
2	D	72	MEN	CA-CB-CG-ND2
2	F	72	MEN	CA-CB-CG-ND2
2	H	72	MEN	CA-CB-CG-ND2
2	J	72	MEN	CA-CB-CG-ND2
2	L	72	MEN	CA-CB-CG-ND2
2	N	72	MEN	CA-CB-CG-ND2
2	P	72	MEN	CA-CB-CG-ND2
2	B	72	MEN	N-CA-CB-CG
2	D	72	MEN	N-CA-CB-CG
2	F	72	MEN	N-CA-CB-CG
2	H	72	MEN	N-CA-CB-CG
2	J	72	MEN	N-CA-CB-CG
2	L	72	MEN	N-CA-CB-CG
2	N	72	MEN	N-CA-CB-CG
2	P	72	MEN	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

24 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	CYC	J	202	2	46,46,46	3.78	22 (47%)	63,67,67	2.57	13 (20%)
3	CYC	D	202	2	46,46,46	3.76	22 (47%)	63,67,67	2.56	13 (20%)
3	CYC	F	202	2	46,46,46	3.77	22 (47%)	63,67,67	2.56	13 (20%)
3	CYC	H	201	2	46,46,46	3.81	21 (45%)	63,67,67	2.35	15 (23%)
3	CYC	L	202	2	46,46,46	3.76	23 (50%)	63,67,67	2.56	13 (20%)
3	CYC	C	201	1	46,46,46	3.78	22 (47%)	63,67,67	2.26	15 (23%)
3	CYC	D	201	2	46,46,46	3.81	22 (47%)	63,67,67	2.35	15 (23%)
3	CYC	M	201	1	46,46,46	3.78	23 (50%)	63,67,67	2.26	15 (23%)
3	CYC	P	202	2	46,46,46	3.77	22 (47%)	63,67,67	2.56	13 (20%)
3	CYC	I	201	1	46,46,46	3.77	22 (47%)	63,67,67	2.26	15 (23%)
3	CYC	G	201	1	46,46,46	3.78	22 (47%)	63,67,67	2.26	15 (23%)
3	CYC	K	201	1	46,46,46	3.78	23 (50%)	63,67,67	2.27	15 (23%)
3	CYC	N	201	2	46,46,46	3.80	22 (47%)	63,67,67	2.35	15 (23%)
3	CYC	H	202	2	46,46,46	3.77	21 (45%)	63,67,67	2.56	13 (20%)
3	CYC	N	202	2	46,46,46	3.77	22 (47%)	63,67,67	2.57	13 (20%)
3	CYC	O	201	1	46,46,46	3.78	22 (47%)	63,67,67	2.26	15 (23%)
3	CYC	P	201	2	46,46,46	3.80	21 (45%)	63,67,67	2.35	16 (25%)
3	CYC	B	202	2	46,46,46	3.77	23 (50%)	63,67,67	2.57	13 (20%)
3	CYC	J	201	2	46,46,46	3.80	22 (47%)	63,67,67	2.35	15 (23%)
3	CYC	B	201	2	46,46,46	3.80	22 (47%)	63,67,67	2.35	16 (25%)
3	CYC	F	201	2	46,46,46	3.80	22 (47%)	63,67,67	2.35	15 (23%)
3	CYC	A	201	1	46,46,46	3.77	23 (50%)	63,67,67	2.26	15 (23%)
3	CYC	L	201	2	46,46,46	3.80	21 (45%)	63,67,67	2.35	15 (23%)
3	CYC	E	201	1	46,46,46	3.77	22 (47%)	63,67,67	2.26	15 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CYC	J	202	2	-	14/26/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CYC	D	202	2	-	14/26/74/74	0/4/4/4
3	CYC	F	202	2	-	14/26/74/74	0/4/4/4
3	CYC	H	201	2	-	9/26/74/74	0/4/4/4
3	CYC	L	202	2	-	14/26/74/74	0/4/4/4
3	CYC	C	201	1	-	11/26/74/74	0/4/4/4
3	CYC	D	201	2	-	9/26/74/74	0/4/4/4
3	CYC	M	201	1	-	11/26/74/74	0/4/4/4
3	CYC	P	202	2	-	14/26/74/74	0/4/4/4
3	CYC	I	201	1	-	11/26/74/74	0/4/4/4
3	CYC	G	201	1	-	11/26/74/74	0/4/4/4
3	CYC	K	201	1	-	11/26/74/74	0/4/4/4
3	CYC	N	201	2	-	9/26/74/74	0/4/4/4
3	CYC	H	202	2	-	14/26/74/74	0/4/4/4
3	CYC	N	202	2	-	14/26/74/74	0/4/4/4
3	CYC	O	201	1	-	11/26/74/74	0/4/4/4
3	CYC	P	201	2	-	9/26/74/74	0/4/4/4
3	CYC	B	202	2	-	14/26/74/74	0/4/4/4
3	CYC	J	201	2	-	9/26/74/74	0/4/4/4
3	CYC	B	201	2	-	9/26/74/74	0/4/4/4
3	CYC	F	201	2	-	9/26/74/74	0/4/4/4
3	CYC	A	201	1	-	11/26/74/74	0/4/4/4
3	CYC	L	201	2	-	9/26/74/74	0/4/4/4
3	CYC	E	201	1	-	11/26/74/74	0/4/4/4

All (529) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	201	CYC	C4C-NC	10.27	1.57	1.37
3	H	201	CYC	C4C-NC	10.27	1.57	1.37
3	P	201	CYC	C4C-NC	10.26	1.57	1.37
3	L	201	CYC	C4C-NC	10.25	1.57	1.37
3	F	201	CYC	C4C-NC	10.24	1.57	1.37
3	B	201	CYC	C4C-NC	10.24	1.57	1.37
3	N	201	CYC	C4C-NC	10.24	1.57	1.37
3	J	202	CYC	C4C-NC	10.23	1.57	1.37
3	J	201	CYC	C4C-NC	10.21	1.57	1.37
3	F	202	CYC	C4C-NC	10.19	1.57	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	202	CYC	C4C-NC	10.18	1.57	1.37
3	N	202	CYC	C4C-NC	10.18	1.57	1.37
3	M	201	CYC	C4C-NC	10.17	1.57	1.37
3	K	201	CYC	C4C-NC	10.16	1.57	1.37
3	H	202	CYC	C4C-NC	10.16	1.57	1.37
3	A	201	CYC	C4C-NC	10.16	1.57	1.37
3	O	201	CYC	C4C-NC	10.15	1.57	1.37
3	E	201	CYC	C4C-NC	10.15	1.57	1.37
3	I	201	CYC	C4C-NC	10.15	1.57	1.37
3	P	202	CYC	C4C-NC	10.15	1.57	1.37
3	C	201	CYC	C4C-NC	10.15	1.57	1.37
3	G	201	CYC	C4C-NC	10.14	1.57	1.37
3	D	202	CYC	C4C-NC	10.13	1.57	1.37
3	L	202	CYC	C4C-NC	10.11	1.56	1.37
3	O	201	CYC	C1B-NB	9.88	1.54	1.37
3	M	201	CYC	C1B-NB	9.86	1.54	1.37
3	C	201	CYC	C1B-NB	9.85	1.54	1.37
3	E	201	CYC	C1B-NB	9.85	1.54	1.37
3	I	201	CYC	C1B-NB	9.84	1.54	1.37
3	A	201	CYC	C1B-NB	9.84	1.54	1.37
3	G	201	CYC	C1B-NB	9.83	1.54	1.37
3	J	202	CYC	C1B-NB	9.82	1.54	1.37
3	K	201	CYC	C1B-NB	9.82	1.54	1.37
3	B	202	CYC	C1B-NB	9.81	1.54	1.37
3	H	201	CYC	C1B-NB	9.80	1.54	1.37
3	F	202	CYC	C1B-NB	9.79	1.54	1.37
3	N	201	CYC	C1B-NB	9.78	1.54	1.37
3	B	201	CYC	C1B-NB	9.78	1.54	1.37
3	L	201	CYC	C1B-NB	9.78	1.54	1.37
3	J	201	CYC	C1B-NB	9.78	1.54	1.37
3	P	202	CYC	C1B-NB	9.78	1.54	1.37
3	F	201	CYC	C1B-NB	9.77	1.54	1.37
3	N	202	CYC	C1B-NB	9.77	1.54	1.37
3	P	201	CYC	C1B-NB	9.76	1.54	1.37
3	D	202	CYC	C1B-NB	9.76	1.54	1.37
3	H	202	CYC	C1B-NB	9.75	1.54	1.37
3	D	201	CYC	C1B-NB	9.74	1.54	1.37
3	L	202	CYC	C1B-NB	9.73	1.54	1.37
3	F	201	CYC	CHD-C1D	7.82	1.58	1.40
3	J	201	CYC	CHD-C1D	7.81	1.58	1.40
3	D	201	CYC	CHD-C1D	7.80	1.58	1.40
3	H	201	CYC	CHD-C1D	7.78	1.58	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	201	CYC	CHD-C1D	7.77	1.58	1.40
3	L	201	CYC	CHD-C1D	7.77	1.58	1.40
3	B	201	CYC	CHD-C1D	7.76	1.57	1.40
3	N	201	CYC	CHD-C1D	7.76	1.57	1.40
3	C	201	CYC	CHD-C1D	7.53	1.57	1.40
3	O	201	CYC	CHD-C1D	7.53	1.57	1.40
3	G	201	CYC	CHD-C1D	7.52	1.57	1.40
3	K	201	CYC	CHD-C1D	7.51	1.57	1.40
3	E	201	CYC	CHD-C1D	7.50	1.57	1.40
3	I	201	CYC	CHD-C1D	7.49	1.57	1.40
3	M	201	CYC	CHD-C1D	7.49	1.57	1.40
3	A	201	CYC	CHD-C1D	7.49	1.57	1.40
3	L	201	CYC	CHA-C4D	7.42	1.57	1.40
3	H	201	CYC	CHA-C4D	7.41	1.57	1.40
3	P	201	CYC	CHA-C4D	7.41	1.57	1.40
3	F	201	CYC	CHA-C4D	7.40	1.57	1.40
3	B	201	CYC	CHA-C4D	7.39	1.57	1.40
3	D	201	CYC	CHA-C4D	7.39	1.57	1.40
3	N	201	CYC	CHA-C4D	7.38	1.57	1.40
3	J	201	CYC	CHA-C4D	7.37	1.57	1.40
3	J	202	CYC	CHD-C1D	7.31	1.56	1.40
3	N	202	CYC	CHD-C1D	7.29	1.56	1.40
3	F	202	CYC	CHA-C4D	7.29	1.56	1.40
3	B	202	CYC	CHD-C1D	7.29	1.56	1.40
3	P	202	CYC	CHD-C1D	7.29	1.56	1.40
3	F	202	CYC	CHD-C1D	7.27	1.56	1.40
3	L	202	CYC	CHD-C1D	7.27	1.56	1.40
3	D	202	CYC	CHD-C1D	7.27	1.56	1.40
3	J	202	CYC	CHA-C4D	7.27	1.56	1.40
3	N	202	CYC	CHA-C4D	7.27	1.56	1.40
3	H	202	CYC	CHD-C1D	7.27	1.56	1.40
3	D	202	CYC	C4B-NB	7.26	1.54	1.38
3	P	202	CYC	CHA-C4D	7.26	1.56	1.40
3	N	202	CYC	C4B-NB	7.25	1.54	1.38
3	L	202	CYC	CHA-C4D	7.25	1.56	1.40
3	B	202	CYC	C4B-NB	7.24	1.54	1.38
3	H	202	CYC	CHA-C4D	7.24	1.56	1.40
3	H	202	CYC	C4B-NB	7.24	1.54	1.38
3	J	202	CYC	C4B-NB	7.24	1.54	1.38
3	F	202	CYC	C4B-NB	7.24	1.54	1.38
3	L	202	CYC	C4B-NB	7.24	1.54	1.38
3	K	201	CYC	CHA-C4D	7.23	1.56	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	202	CYC	CHA-C4D	7.23	1.56	1.40
3	P	202	CYC	C4B-NB	7.23	1.54	1.38
3	G	201	CYC	CHA-C4D	7.22	1.56	1.40
3	G	201	CYC	C4B-NB	7.22	1.54	1.38
3	D	202	CYC	CHA-C4D	7.22	1.56	1.40
3	O	201	CYC	CHA-C4D	7.21	1.56	1.40
3	M	201	CYC	CHA-C4D	7.21	1.56	1.40
3	C	201	CYC	CHA-C4D	7.21	1.56	1.40
3	I	201	CYC	CHA-C4D	7.20	1.56	1.40
3	A	201	CYC	CHA-C4D	7.20	1.56	1.40
3	E	201	CYC	CHA-C4D	7.20	1.56	1.40
3	K	201	CYC	C4B-NB	7.19	1.54	1.38
3	E	201	CYC	C4B-NB	7.19	1.54	1.38
3	D	201	CYC	C4B-NB	7.19	1.54	1.38
3	A	201	CYC	C4B-NB	7.18	1.54	1.38
3	M	201	CYC	C4B-NB	7.18	1.54	1.38
3	O	201	CYC	C4B-NB	7.17	1.54	1.38
3	I	201	CYC	C4B-NB	7.16	1.54	1.38
3	C	201	CYC	C4B-NB	7.16	1.54	1.38
3	J	201	CYC	C4B-NB	7.15	1.54	1.38
3	L	201	CYC	C4B-NB	7.15	1.54	1.38
3	H	201	CYC	C4B-NB	7.14	1.54	1.38
3	B	201	CYC	C4B-NB	7.14	1.54	1.38
3	F	201	CYC	C4B-NB	7.13	1.54	1.38
3	P	201	CYC	C4B-NB	7.12	1.54	1.38
3	N	201	CYC	C4B-NB	7.11	1.54	1.38
3	B	201	CYC	CHB-C4A	6.83	1.56	1.40
3	H	201	CYC	CHB-C4A	6.81	1.56	1.40
3	J	201	CYC	CHB-C4A	6.80	1.56	1.40
3	P	201	CYC	CHB-C4A	6.80	1.56	1.40
3	N	201	CYC	CHB-C4A	6.79	1.56	1.40
3	D	201	CYC	CHB-C4A	6.79	1.56	1.40
3	L	201	CYC	CHB-C4A	6.78	1.56	1.40
3	F	201	CYC	CHB-C4A	6.77	1.56	1.40
3	K	201	CYC	CHB-C4A	6.71	1.56	1.40
3	N	202	CYC	CHB-C4A	6.70	1.56	1.40
3	D	202	CYC	CHB-C4A	6.70	1.56	1.40
3	L	202	CYC	CHB-C4A	6.69	1.56	1.40
3	P	202	CYC	CHB-C4A	6.69	1.56	1.40
3	M	201	CYC	CHB-C4A	6.69	1.56	1.40
3	B	202	CYC	CHB-C4A	6.69	1.56	1.40
3	C	201	CYC	CHB-C4A	6.69	1.56	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	202	CYC	CHB-C4A	6.68	1.56	1.40
3	H	202	CYC	CHB-C4A	6.68	1.56	1.40
3	J	202	CYC	CHB-C4A	6.68	1.56	1.40
3	G	201	CYC	CHB-C4A	6.67	1.56	1.40
3	A	201	CYC	CHB-C4A	6.67	1.56	1.40
3	O	201	CYC	CHB-C4A	6.65	1.56	1.40
3	E	201	CYC	CHB-C4A	6.65	1.56	1.40
3	I	201	CYC	CHB-C4A	6.64	1.56	1.40
3	N	201	CYC	C1A-NA	6.40	1.52	1.38
3	D	201	CYC	C1A-NA	6.39	1.52	1.38
3	C	201	CYC	C1A-NA	6.38	1.52	1.38
3	H	201	CYC	C1A-NA	6.38	1.52	1.38
3	M	201	CYC	C1A-NA	6.37	1.52	1.38
3	E	201	CYC	C1A-NA	6.37	1.52	1.38
3	I	201	CYC	C1A-NA	6.36	1.52	1.38
3	G	201	CYC	C1A-NA	6.36	1.52	1.38
3	O	201	CYC	C1A-NA	6.36	1.52	1.38
3	B	201	CYC	C1A-NA	6.35	1.52	1.38
3	L	201	CYC	C1A-NA	6.35	1.52	1.38
3	P	201	CYC	C1A-NA	6.34	1.52	1.38
3	F	201	CYC	C1A-NA	6.33	1.52	1.38
3	A	201	CYC	C1A-NA	6.33	1.52	1.38
3	J	201	CYC	C1A-NA	6.33	1.52	1.38
3	K	201	CYC	C1A-NA	6.31	1.52	1.38
3	B	202	CYC	C1A-NA	6.22	1.51	1.38
3	H	202	CYC	C1A-NA	6.21	1.51	1.38
3	N	202	CYC	C1A-NA	6.21	1.51	1.38
3	J	202	CYC	C1A-NA	6.20	1.51	1.38
3	F	202	CYC	C1A-NA	6.19	1.51	1.38
3	L	202	CYC	C1A-NA	6.19	1.51	1.38
3	P	202	CYC	C1A-NA	6.18	1.51	1.38
3	D	202	CYC	C1A-NA	6.16	1.51	1.38
3	F	201	CYC	C4A-NA	6.07	1.50	1.36
3	D	201	CYC	C4A-NA	6.05	1.50	1.36
3	A	201	CYC	C4A-NA	6.05	1.50	1.36
3	N	201	CYC	C4A-NA	6.05	1.50	1.36
3	E	201	CYC	C4A-NA	6.05	1.50	1.36
3	M	201	CYC	C4A-NA	6.04	1.50	1.36
3	P	201	CYC	C4A-NA	6.04	1.50	1.36
3	O	201	CYC	C4A-NA	6.04	1.50	1.36
3	I	201	CYC	C4A-NA	6.03	1.50	1.36
3	J	201	CYC	C4A-NA	6.03	1.50	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	201	CYC	C4A-NA	6.02	1.50	1.36
3	K	201	CYC	C4A-NA	6.02	1.50	1.36
3	H	201	CYC	C4A-NA	6.02	1.50	1.36
3	G	201	CYC	C4A-NA	6.02	1.50	1.36
3	B	201	CYC	C4A-NA	6.01	1.50	1.36
3	L	201	CYC	C4A-NA	6.00	1.50	1.36
3	D	202	CYC	C4A-NA	5.88	1.50	1.36
3	L	202	CYC	C4A-NA	5.86	1.49	1.36
3	F	202	CYC	C4A-NA	5.85	1.49	1.36
3	H	202	CYC	C4A-NA	5.85	1.49	1.36
3	N	202	CYC	C4A-NA	5.84	1.49	1.36
3	J	202	CYC	C4A-NA	5.84	1.49	1.36
3	B	202	CYC	C4A-NA	5.83	1.49	1.36
3	P	202	CYC	C4A-NA	5.83	1.49	1.36
3	L	202	CYC	C1A-C2A	5.44	1.54	1.45
3	H	202	CYC	C1A-C2A	5.44	1.54	1.45
3	N	202	CYC	C1A-C2A	5.44	1.54	1.45
3	J	201	CYC	C1A-C2A	5.44	1.54	1.45
3	B	202	CYC	C1A-C2A	5.43	1.54	1.45
3	H	201	CYC	C1A-C2A	5.43	1.54	1.45
3	F	202	CYC	C2A-C3A	5.42	1.48	1.36
3	B	201	CYC	C1A-C2A	5.42	1.54	1.45
3	J	202	CYC	C1A-C2A	5.41	1.54	1.45
3	P	202	CYC	C1A-C2A	5.41	1.54	1.45
3	D	202	CYC	C1A-C2A	5.40	1.54	1.45
3	F	202	CYC	C1A-C2A	5.39	1.54	1.45
3	P	202	CYC	C2A-C3A	5.39	1.48	1.36
3	B	202	CYC	C2A-C3A	5.39	1.48	1.36
3	L	201	CYC	C1A-C2A	5.39	1.54	1.45
3	D	202	CYC	C2A-C3A	5.38	1.48	1.36
3	J	202	CYC	C2A-C3A	5.38	1.48	1.36
3	P	201	CYC	C1A-C2A	5.37	1.54	1.45
3	H	202	CYC	C2A-C3A	5.37	1.48	1.36
3	D	201	CYC	C1A-C2A	5.37	1.54	1.45
3	N	202	CYC	C2A-C3A	5.36	1.48	1.36
3	F	201	CYC	C1A-C2A	5.36	1.54	1.45
3	L	202	CYC	C2A-C3A	5.36	1.48	1.36
3	N	201	CYC	C1A-C2A	5.36	1.54	1.45
3	M	201	CYC	C1A-C2A	5.25	1.53	1.45
3	I	201	CYC	C1A-C2A	5.23	1.53	1.45
3	P	201	CYC	C2A-C3A	5.22	1.48	1.36
3	D	201	CYC	C2A-C3A	5.21	1.48	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	201	CYC	C1A-C2A	5.21	1.53	1.45
3	N	201	CYC	C2A-C3A	5.21	1.48	1.36
3	E	201	CYC	C1A-C2A	5.20	1.53	1.45
3	K	201	CYC	C1A-C2A	5.20	1.53	1.45
3	B	201	CYC	C2A-C3A	5.20	1.48	1.36
3	C	201	CYC	C1A-C2A	5.19	1.53	1.45
3	O	201	CYC	C2A-C3A	5.18	1.48	1.36
3	J	201	CYC	C2A-C3A	5.18	1.47	1.36
3	A	201	CYC	C1A-C2A	5.18	1.53	1.45
3	F	201	CYC	C2A-C3A	5.18	1.47	1.36
3	O	201	CYC	C1A-C2A	5.18	1.53	1.45
3	I	201	CYC	C2A-C3A	5.17	1.47	1.36
3	L	201	CYC	C2A-C3A	5.17	1.47	1.36
3	H	201	CYC	C2A-C3A	5.17	1.47	1.36
3	G	201	CYC	C2A-C3A	5.16	1.47	1.36
3	M	201	CYC	C2A-C3A	5.15	1.47	1.36
3	C	201	CYC	C2A-C3A	5.15	1.47	1.36
3	A	201	CYC	C2A-C3A	5.15	1.47	1.36
3	K	201	CYC	C2A-C3A	5.14	1.47	1.36
3	E	201	CYC	C2A-C3A	5.13	1.47	1.36
3	J	202	CYC	C3C-C4C	-3.75	1.42	1.50
3	D	202	CYC	C3C-C4C	-3.74	1.42	1.50
3	N	202	CYC	C3C-C4C	-3.74	1.42	1.50
3	H	202	CYC	C3C-C4C	-3.73	1.42	1.50
3	F	202	CYC	C3C-C4C	-3.73	1.42	1.50
3	L	202	CYC	C3C-C4C	-3.73	1.42	1.50
3	P	202	CYC	C3C-C4C	-3.73	1.42	1.50
3	B	202	CYC	C3C-C4C	-3.70	1.42	1.50
3	B	202	CYC	C2C-C1C	3.65	1.55	1.52
3	P	202	CYC	C2C-C1C	3.61	1.55	1.52
3	J	202	CYC	C2C-C1C	3.60	1.55	1.52
3	N	202	CYC	C2C-C1C	3.60	1.55	1.52
3	H	202	CYC	C2C-C1C	3.56	1.55	1.52
3	F	202	CYC	C2C-C1C	3.55	1.55	1.52
3	L	202	CYC	C2C-C1C	3.54	1.55	1.52
3	M	201	CYC	C3C-C4C	-3.50	1.43	1.50
3	E	201	CYC	C3C-C4C	-3.50	1.43	1.50
3	I	201	CYC	C3C-C4C	-3.49	1.43	1.50
3	C	201	CYC	C3C-C4C	-3.49	1.43	1.50
3	K	201	CYC	C3C-C4C	-3.48	1.43	1.50
3	A	201	CYC	C3C-C4C	-3.47	1.43	1.50
3	G	201	CYC	C3C-C4C	-3.46	1.43	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	O	201	CYC	C3C-C4C	-3.46	1.43	1.50
3	D	202	CYC	C2C-C1C	3.44	1.55	1.52
3	P	201	CYC	C3C-C4C	-3.39	1.43	1.50
3	B	201	CYC	C3C-C4C	-3.37	1.43	1.50
3	H	201	CYC	C3C-C4C	-3.36	1.43	1.50
3	F	201	CYC	C3C-C4C	-3.36	1.43	1.50
3	J	201	CYC	C3C-C4C	-3.36	1.43	1.50
3	L	201	CYC	C3C-C4C	-3.35	1.43	1.50
3	N	201	CYC	C3C-C4C	-3.35	1.43	1.50
3	D	201	CYC	C3C-C4C	-3.34	1.43	1.50
3	O	201	CYC	C2C-C1C	3.30	1.55	1.52
3	K	201	CYC	C2C-C1C	3.27	1.55	1.52
3	A	201	CYC	C2C-C1C	3.27	1.55	1.52
3	I	201	CYC	C2C-C1C	3.25	1.55	1.52
3	G	201	CYC	C2C-C1C	3.24	1.55	1.52
3	E	201	CYC	C2C-C1C	3.24	1.55	1.52
3	C	201	CYC	C2C-C1C	3.21	1.54	1.52
3	M	201	CYC	C2C-C1C	3.17	1.54	1.52
3	H	201	CYC	C2C-C1C	3.14	1.54	1.52
3	B	201	CYC	C3B-C2B	3.10	1.43	1.36
3	H	201	CYC	C3B-C2B	3.09	1.43	1.36
3	P	201	CYC	C3B-C2B	3.09	1.43	1.36
3	F	201	CYC	C3B-C2B	3.09	1.43	1.36
3	J	201	CYC	C3B-C2B	3.08	1.43	1.36
3	N	201	CYC	C2C-C1C	3.08	1.54	1.52
3	D	201	CYC	C3B-C2B	3.07	1.43	1.36
3	B	201	CYC	C2C-C1C	3.07	1.54	1.52
3	D	201	CYC	C2C-C1C	3.06	1.54	1.52
3	L	201	CYC	C3B-C2B	3.06	1.43	1.36
3	N	201	CYC	C3B-C2B	3.06	1.43	1.36
3	L	201	CYC	C2C-C1C	3.06	1.54	1.52
3	N	201	CYC	C1B-C2B	3.02	1.50	1.45
3	F	201	CYC	C2C-C1C	3.02	1.54	1.52
3	F	201	CYC	C1B-C2B	3.02	1.50	1.45
3	L	201	CYC	C1B-C2B	3.01	1.50	1.45
3	O	201	CYC	C3B-C2B	3.00	1.43	1.36
3	J	201	CYC	C1B-C2B	3.00	1.50	1.45
3	D	201	CYC	C1B-C2B	3.00	1.50	1.45
3	J	201	CYC	C2C-C1C	3.00	1.54	1.52
3	P	201	CYC	C2C-C1C	2.99	1.54	1.52
3	G	201	CYC	C3B-C2B	2.98	1.43	1.36
3	C	201	CYC	C3B-C2B	2.97	1.43	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	201	CYC	C3B-C2B	2.96	1.43	1.36
3	K	201	CYC	C3B-C2B	2.96	1.43	1.36
3	A	201	CYC	C3B-C2B	2.96	1.43	1.36
3	I	201	CYC	C3B-C2B	2.96	1.43	1.36
3	B	201	CYC	C1B-C2B	2.96	1.50	1.45
3	H	201	CYC	C1B-C2B	2.96	1.50	1.45
3	M	201	CYC	C3B-C2B	2.95	1.43	1.36
3	P	201	CYC	C1B-C2B	2.94	1.50	1.45
3	C	201	CYC	C1B-C2B	2.93	1.50	1.45
3	E	201	CYC	C1B-C2B	2.90	1.50	1.45
3	O	201	CYC	C4D-C3D	-2.89	1.36	1.42
3	L	202	CYC	C1B-C2B	2.89	1.50	1.45
3	I	201	CYC	C1B-C2B	2.89	1.50	1.45
3	H	202	CYC	C1B-C2B	2.89	1.50	1.45
3	K	201	CYC	C4D-C3D	-2.89	1.36	1.42
3	G	201	CYC	C1B-C2B	2.88	1.50	1.45
3	M	201	CYC	C1B-C2B	2.88	1.50	1.45
3	J	202	CYC	C1B-C2B	2.87	1.50	1.45
3	D	202	CYC	C1B-C2B	2.86	1.50	1.45
3	O	201	CYC	C1B-C2B	2.86	1.50	1.45
3	I	201	CYC	C4D-C3D	-2.86	1.36	1.42
3	M	201	CYC	C4D-C3D	-2.86	1.36	1.42
3	G	201	CYC	C4D-C3D	-2.86	1.36	1.42
3	N	202	CYC	C1B-C2B	2.85	1.50	1.45
3	E	201	CYC	C4D-C3D	-2.85	1.36	1.42
3	P	202	CYC	C1B-C2B	2.85	1.50	1.45
3	A	201	CYC	C1B-C2B	2.85	1.50	1.45
3	B	202	CYC	C1B-C2B	2.84	1.50	1.45
3	C	201	CYC	C4D-C3D	-2.84	1.36	1.42
3	F	202	CYC	C1B-C2B	2.84	1.50	1.45
3	K	201	CYC	C1B-C2B	2.83	1.50	1.45
3	A	201	CYC	C4D-C3D	-2.83	1.36	1.42
3	H	202	CYC	C3B-C2B	2.82	1.42	1.36
3	F	202	CYC	C3B-C2B	2.82	1.42	1.36
3	B	202	CYC	C3B-C2B	2.81	1.42	1.36
3	L	202	CYC	C3B-C2B	2.81	1.42	1.36
3	J	202	CYC	C3B-C2B	2.81	1.42	1.36
3	D	202	CYC	C3B-C2B	2.80	1.42	1.36
3	N	202	CYC	C3B-C2B	2.79	1.42	1.36
3	P	202	CYC	C3B-C2B	2.79	1.42	1.36
3	H	201	CYC	C4D-C3D	-2.69	1.36	1.42
3	L	201	CYC	C4D-C3D	-2.69	1.36	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	201	CYC	C4D-C3D	-2.68	1.36	1.42
3	J	201	CYC	C4D-C3D	-2.68	1.36	1.42
3	B	201	CYC	C4D-C3D	-2.68	1.36	1.42
3	F	201	CYC	C4D-C3D	-2.67	1.36	1.42
3	P	201	CYC	C4D-C3D	-2.67	1.36	1.42
3	N	201	CYC	C4D-C3D	-2.64	1.37	1.42
3	N	201	CYC	CMC-C2C	-2.53	1.47	1.53
3	B	201	CYC	CMC-C2C	-2.51	1.47	1.53
3	H	201	CYC	CMC-C2C	-2.51	1.47	1.53
3	D	201	CYC	CMC-C2C	-2.50	1.47	1.53
3	L	201	CYC	CMC-C2C	-2.49	1.47	1.53
3	J	201	CYC	CMC-C2C	-2.49	1.47	1.53
3	P	201	CYC	CMC-C2C	-2.48	1.48	1.53
3	F	201	CYC	CMC-C2C	-2.46	1.48	1.53
3	C	201	CYC	CMC-C2C	-2.43	1.48	1.53
3	A	201	CYC	CMC-C2C	-2.43	1.48	1.53
3	M	201	CYC	CMC-C2C	-2.42	1.48	1.53
3	E	201	CYC	CMC-C2C	-2.42	1.48	1.53
3	H	202	CYC	CMC-C2C	-2.41	1.48	1.53
3	F	202	CYC	CMC-C2C	-2.41	1.48	1.53
3	N	202	CYC	CMC-C2C	-2.41	1.48	1.53
3	G	201	CYC	CMC-C2C	-2.41	1.48	1.53
3	L	202	CYC	CMC-C2C	-2.41	1.48	1.53
3	P	202	CYC	CMC-C2C	-2.41	1.48	1.53
3	D	202	CYC	CMC-C2C	-2.40	1.48	1.53
3	J	202	CYC	CMC-C2C	-2.40	1.48	1.53
3	O	201	CYC	CMC-C2C	-2.40	1.48	1.53
3	B	202	CYC	CMC-C2C	-2.40	1.48	1.53
3	K	201	CYC	CMC-C2C	-2.39	1.48	1.53
3	I	201	CYC	CMC-C2C	-2.39	1.48	1.53
3	N	202	CYC	C4D-C3D	-2.35	1.37	1.42
3	F	202	CYC	C4D-C3D	-2.33	1.37	1.42
3	D	202	CYC	C4D-C3D	-2.33	1.37	1.42
3	P	202	CYC	C4D-C3D	-2.33	1.37	1.42
3	J	202	CYC	C4D-C3D	-2.33	1.37	1.42
3	L	202	CYC	C4D-C3D	-2.32	1.37	1.42
3	B	202	CYC	C4D-C3D	-2.32	1.37	1.42
3	H	202	CYC	C4D-C3D	-2.32	1.37	1.42
3	D	201	CYC	C4A-C3A	2.31	1.50	1.45
3	J	201	CYC	C4A-C3A	2.30	1.50	1.45
3	O	201	CYC	C4A-C3A	2.30	1.50	1.45
3	H	201	CYC	C4A-C3A	2.30	1.50	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	201	CYC	C4A-C3A	2.29	1.50	1.45
3	N	202	CYC	OB-C4B	-2.28	1.19	1.23
3	I	201	CYC	C4A-C3A	2.28	1.50	1.45
3	N	201	CYC	C4A-C3A	2.28	1.50	1.45
3	F	201	CYC	C4A-C3A	2.28	1.50	1.45
3	B	201	CYC	C4A-C3A	2.28	1.50	1.45
3	A	201	CYC	C4A-C3A	2.27	1.50	1.45
3	C	201	CYC	C1C-NC	-2.27	1.34	1.37
3	L	202	CYC	OB-C4B	-2.27	1.19	1.23
3	K	201	CYC	C4A-C3A	2.27	1.50	1.45
3	K	201	CYC	C1C-NC	-2.27	1.34	1.37
3	G	201	CYC	C4A-C3A	2.27	1.50	1.45
3	B	202	CYC	OB-C4B	-2.26	1.19	1.23
3	G	201	CYC	OC-C1C	-2.26	1.19	1.23
3	O	201	CYC	C1C-NC	-2.26	1.34	1.37
3	P	201	CYC	C4A-C3A	2.25	1.50	1.45
3	I	201	CYC	C1C-NC	-2.25	1.34	1.37
3	A	201	CYC	C1C-NC	-2.25	1.34	1.37
3	P	202	CYC	OB-C4B	-2.25	1.19	1.23
3	G	201	CYC	OB-C4B	-2.25	1.19	1.23
3	M	201	CYC	C4A-C3A	2.24	1.50	1.45
3	K	201	CYC	OB-C4B	-2.24	1.19	1.23
3	E	201	CYC	C4A-C3A	2.24	1.50	1.45
3	C	201	CYC	C4A-C3A	2.24	1.50	1.45
3	A	201	CYC	OB-C4B	-2.24	1.19	1.23
3	O	201	CYC	OC-C1C	-2.24	1.19	1.23
3	M	201	CYC	OB-C4B	-2.24	1.19	1.23
3	H	202	CYC	C4A-C3A	2.24	1.50	1.45
3	E	201	CYC	OB-C4B	-2.23	1.19	1.23
3	H	202	CYC	OB-C4B	-2.23	1.19	1.23
3	N	202	CYC	C4A-C3A	2.23	1.50	1.45
3	M	201	CYC	C1C-NC	-2.23	1.34	1.37
3	O	201	CYC	OB-C4B	-2.23	1.19	1.23
3	A	201	CYC	OC-C1C	-2.23	1.19	1.23
3	E	201	CYC	C1C-NC	-2.23	1.34	1.37
3	D	202	CYC	OB-C4B	-2.23	1.19	1.23
3	J	202	CYC	OB-C4B	-2.23	1.19	1.23
3	D	201	CYC	C1C-NC	-2.22	1.34	1.37
3	I	201	CYC	OC-C1C	-2.22	1.19	1.23
3	J	202	CYC	C4A-C3A	2.22	1.50	1.45
3	L	201	CYC	OB-C4B	-2.22	1.19	1.23
3	D	201	CYC	OB-C4B	-2.21	1.19	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	202	CYC	CMD-C2D	2.21	1.55	1.50
3	B	201	CYC	OB-C4B	-2.21	1.19	1.23
3	J	201	CYC	OB-C4B	-2.21	1.19	1.23
3	B	202	CYC	C4A-C3A	2.21	1.50	1.45
3	C	201	CYC	OB-C4B	-2.21	1.19	1.23
3	D	202	CYC	C4A-C3A	2.21	1.50	1.45
3	N	202	CYC	OC-C1C	-2.21	1.19	1.23
3	I	201	CYC	OB-C4B	-2.21	1.19	1.23
3	F	202	CYC	C4A-C3A	2.21	1.50	1.45
3	H	201	CYC	C1C-NC	-2.21	1.34	1.37
3	G	201	CYC	C1C-NC	-2.20	1.34	1.37
3	F	202	CYC	OB-C4B	-2.20	1.19	1.23
3	B	201	CYC	C1C-NC	-2.20	1.34	1.37
3	L	202	CYC	C4A-C3A	2.20	1.50	1.45
3	N	201	CYC	OB-C4B	-2.20	1.19	1.23
3	P	202	CYC	C4A-C3A	2.20	1.50	1.45
3	K	201	CYC	OC-C1C	-2.20	1.19	1.23
3	L	202	CYC	CMD-C2D	2.19	1.55	1.50
3	J	201	CYC	C1C-NC	-2.19	1.34	1.37
3	N	202	CYC	CMD-C2D	2.19	1.55	1.50
3	N	201	CYC	C1C-NC	-2.19	1.34	1.37
3	P	201	CYC	C1C-NC	-2.19	1.34	1.37
3	M	201	CYC	CMD-C2D	2.19	1.55	1.50
3	H	201	CYC	OB-C4B	-2.19	1.19	1.23
3	E	201	CYC	OC-C1C	-2.19	1.19	1.23
3	K	201	CYC	CMD-C2D	2.19	1.55	1.50
3	J	202	CYC	CMD-C2D	2.19	1.55	1.50
3	F	202	CYC	OC-C1C	-2.18	1.19	1.23
3	D	202	CYC	CMD-C2D	2.18	1.55	1.50
3	F	202	CYC	CMD-C2D	2.18	1.55	1.50
3	L	202	CYC	OC-C1C	-2.18	1.19	1.23
3	H	202	CYC	CMD-C2D	2.18	1.55	1.50
3	F	201	CYC	OB-C4B	-2.18	1.19	1.23
3	F	201	CYC	C1C-NC	-2.18	1.34	1.37
3	P	202	CYC	CMD-C2D	2.18	1.55	1.50
3	M	201	CYC	OC-C1C	-2.18	1.19	1.23
3	P	202	CYC	OC-C1C	-2.18	1.19	1.23
3	B	202	CYC	OC-C1C	-2.18	1.19	1.23
3	C	201	CYC	OC-C1C	-2.18	1.19	1.23
3	P	201	CYC	OB-C4B	-2.17	1.19	1.23
3	H	202	CYC	OC-C1C	-2.17	1.19	1.23
3	A	201	CYC	CMD-C2D	2.17	1.55	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	201	CYC	CMD-C2D	2.16	1.55	1.50
3	N	201	CYC	OC-C1C	-2.16	1.19	1.23
3	O	201	CYC	CMD-C2D	2.16	1.55	1.50
3	D	202	CYC	OC-C1C	-2.15	1.19	1.23
3	G	201	CYC	CMD-C2D	2.15	1.55	1.50
3	D	201	CYC	OC-C1C	-2.15	1.19	1.23
3	L	201	CYC	C1C-NC	-2.14	1.34	1.37
3	F	201	CYC	OC-C1C	-2.13	1.19	1.23
3	P	201	CYC	OC-C1C	-2.13	1.19	1.23
3	J	202	CYC	OC-C1C	-2.13	1.19	1.23
3	H	201	CYC	OC-C1C	-2.13	1.19	1.23
3	E	201	CYC	CMD-C2D	2.13	1.55	1.50
3	P	201	CYC	CMA-C3A	2.12	1.55	1.50
3	I	201	CYC	CMD-C2D	2.12	1.55	1.50
3	F	201	CYC	CMA-C3A	2.12	1.55	1.50
3	B	201	CYC	OC-C1C	-2.11	1.19	1.23
3	J	201	CYC	OC-C1C	-2.11	1.19	1.23
3	A	201	CYC	CMA-C3A	2.11	1.55	1.50
3	L	201	CYC	OC-C1C	-2.11	1.19	1.23
3	K	201	CYC	CMA-C3A	2.11	1.55	1.50
3	M	201	CYC	CMA-C3A	2.11	1.55	1.50
3	B	201	CYC	CMA-C3A	2.10	1.55	1.50
3	E	201	CYC	CMA-C3A	2.10	1.55	1.50
3	D	201	CYC	CMA-C3A	2.10	1.55	1.50
3	N	201	CYC	CMA-C3A	2.09	1.55	1.50
3	L	201	CYC	CMA-C3A	2.08	1.55	1.50
3	H	202	CYC	C1C-NC	-2.08	1.35	1.37
3	J	201	CYC	CMA-C3A	2.08	1.55	1.50
3	I	201	CYC	CMA-C3A	2.08	1.55	1.50
3	G	201	CYC	CMA-C3A	2.08	1.55	1.50
3	C	201	CYC	CMA-C3A	2.07	1.55	1.50
3	B	202	CYC	C1C-NC	-2.07	1.35	1.37
3	P	202	CYC	C1C-NC	-2.06	1.35	1.37
3	N	202	CYC	C1C-NC	-2.06	1.35	1.37
3	O	201	CYC	CMA-C3A	2.06	1.55	1.50
3	P	202	CYC	CMB-C2B	2.06	1.55	1.50
3	H	201	CYC	CMA-C3A	2.06	1.55	1.50
3	D	202	CYC	C1C-NC	-2.05	1.35	1.37
3	F	202	CYC	C1C-NC	-2.05	1.35	1.37
3	B	202	CYC	CMA-C3A	2.04	1.54	1.50
3	B	202	CYC	CMB-C2B	2.03	1.54	1.50
3	J	202	CYC	C1C-NC	-2.03	1.35	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	202	CYC	C1C-NC	-2.03	1.35	1.37
3	J	201	CYC	CMD-C2D	2.03	1.54	1.50
3	A	201	CYC	CMB-C2B	2.02	1.54	1.50
3	K	201	CYC	CMB-C2B	2.02	1.54	1.50
3	D	202	CYC	CMA-C3A	2.02	1.54	1.50
3	M	201	CYC	CMB-C2B	2.02	1.54	1.50
3	F	201	CYC	CMD-C2D	2.02	1.54	1.50
3	B	201	CYC	CMB-C2B	2.01	1.54	1.50
3	N	201	CYC	CMD-C2D	2.01	1.54	1.50
3	J	202	CYC	CMB-C2B	2.01	1.54	1.50
3	F	202	CYC	CMB-C2B	2.01	1.54	1.50
3	L	202	CYC	CMA-C3A	2.01	1.54	1.50
3	D	201	CYC	CMB-C2B	2.00	1.54	1.50
3	N	202	CYC	CMB-C2B	2.00	1.54	1.50
3	L	202	CYC	CMB-C2B	2.00	1.54	1.50

All (346) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	202	CYC	CHA-C4D-ND	-11.89	98.42	125.29
3	F	202	CYC	CHA-C4D-ND	-11.89	98.43	125.29
3	P	202	CYC	CHA-C4D-ND	-11.88	98.45	125.29
3	J	202	CYC	CHA-C4D-ND	-11.88	98.45	125.29
3	B	202	CYC	CHA-C4D-ND	-11.88	98.45	125.29
3	D	202	CYC	CHA-C4D-ND	-11.88	98.45	125.29
3	L	202	CYC	CHA-C4D-ND	-11.87	98.47	125.29
3	H	202	CYC	CHA-C4D-ND	-11.85	98.52	125.29
3	F	201	CYC	CHA-C4D-ND	-9.78	103.20	125.29
3	J	201	CYC	CHA-C4D-ND	-9.77	103.22	125.29
3	H	201	CYC	CHA-C4D-ND	-9.77	103.22	125.29
3	L	201	CYC	CHA-C4D-ND	-9.77	103.22	125.29
3	B	201	CYC	CHA-C4D-ND	-9.76	103.23	125.29
3	P	201	CYC	CHA-C4D-ND	-9.76	103.25	125.29
3	D	201	CYC	CHA-C4D-ND	-9.75	103.26	125.29
3	N	201	CYC	CHA-C4D-ND	-9.75	103.26	125.29
3	N	202	CYC	CHA-C4D-C3D	9.57	147.79	127.22
3	P	202	CYC	CHA-C4D-C3D	9.56	147.76	127.22
3	B	202	CYC	CHA-C4D-C3D	9.54	147.73	127.22
3	D	202	CYC	CHA-C4D-C3D	9.53	147.72	127.22
3	H	202	CYC	CHA-C4D-C3D	9.53	147.71	127.22
3	F	202	CYC	CHA-C4D-C3D	9.52	147.69	127.22
3	L	202	CYC	CHA-C4D-C3D	9.52	147.69	127.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	202	CYC	CHA-C4D-C3D	9.52	147.68	127.22
3	I	201	CYC	CHA-C4D-ND	-9.51	103.80	125.29
3	K	201	CYC	CHA-C4D-ND	-9.51	103.80	125.29
3	O	201	CYC	CHA-C4D-ND	-9.51	103.81	125.29
3	M	201	CYC	CHA-C4D-ND	-9.50	103.82	125.29
3	G	201	CYC	CHA-C4D-ND	-9.50	103.83	125.29
3	E	201	CYC	CHA-C4D-ND	-9.50	103.83	125.29
3	C	201	CYC	CHA-C4D-ND	-9.49	103.84	125.29
3	A	201	CYC	CHA-C4D-ND	-9.49	103.86	125.29
3	F	201	CYC	CHA-C4D-C3D	7.58	143.53	127.22
3	J	201	CYC	CHA-C4D-C3D	7.58	143.53	127.22
3	L	201	CYC	CHA-C4D-C3D	7.58	143.53	127.22
3	H	201	CYC	CHA-C4D-C3D	7.57	143.50	127.22
3	B	201	CYC	CHA-C4D-C3D	7.57	143.50	127.22
3	D	201	CYC	CHA-C4D-C3D	7.56	143.48	127.22
3	P	201	CYC	CHA-C4D-C3D	7.55	143.46	127.22
3	N	201	CYC	CHA-C4D-C3D	7.54	143.44	127.22
3	M	201	CYC	CHA-C4D-C3D	7.12	142.54	127.22
3	E	201	CYC	CHA-C4D-C3D	7.12	142.53	127.22
3	G	201	CYC	CHA-C4D-C3D	7.11	142.52	127.22
3	I	201	CYC	CHA-C4D-C3D	7.11	142.51	127.22
3	O	201	CYC	CHA-C4D-C3D	7.11	142.51	127.22
3	K	201	CYC	CHA-C4D-C3D	7.11	142.50	127.22
3	C	201	CYC	CHA-C4D-C3D	7.11	142.50	127.22
3	A	201	CYC	CHA-C4D-C3D	7.10	142.48	127.22
3	F	202	CYC	C3D-C4D-ND	5.02	113.87	107.57
3	J	202	CYC	C3D-C4D-ND	5.01	113.86	107.57
3	L	202	CYC	C3D-C4D-ND	4.99	113.83	107.57
3	D	202	CYC	C3D-C4D-ND	4.98	113.82	107.57
3	B	202	CYC	C3D-C4D-ND	4.98	113.81	107.57
3	H	201	CYC	C2C-C3C-C4C	4.97	108.78	101.34
3	N	202	CYC	C3D-C4D-ND	4.96	113.78	107.57
3	P	202	CYC	C3D-C4D-ND	4.95	113.77	107.57
3	H	202	CYC	C3D-C4D-ND	4.94	113.77	107.57
3	N	201	CYC	C2C-C3C-C4C	4.93	108.73	101.34
3	D	201	CYC	C2C-C3C-C4C	4.93	108.72	101.34
3	F	201	CYC	C2C-C3C-C4C	4.93	108.72	101.34
3	P	201	CYC	C2C-C3C-C4C	4.92	108.70	101.34
3	B	201	CYC	C2C-C3C-C4C	4.91	108.70	101.34
3	J	201	CYC	C2C-C3C-C4C	4.91	108.69	101.34
3	L	201	CYC	C2C-C3C-C4C	4.91	108.69	101.34
3	K	201	CYC	C3D-C4D-ND	4.88	113.69	107.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	201	CYC	C3D-C4D-ND	4.88	113.68	107.57
3	O	201	CYC	C3D-C4D-ND	4.87	113.68	107.57
3	A	201	CYC	C3D-C4D-ND	4.86	113.66	107.57
3	C	201	CYC	C3D-C4D-ND	4.86	113.66	107.57
3	G	201	CYC	C3D-C4D-ND	4.85	113.65	107.57
3	M	201	CYC	C3D-C4D-ND	4.85	113.64	107.57
3	E	201	CYC	C3D-C4D-ND	4.85	113.64	107.57
3	N	201	CYC	C3D-C4D-ND	4.57	113.30	107.57
3	P	201	CYC	C3D-C4D-ND	4.56	113.29	107.57
3	H	201	CYC	C3D-C4D-ND	4.55	113.27	107.57
3	F	201	CYC	C3D-C4D-ND	4.55	113.27	107.57
3	D	201	CYC	C3D-C4D-ND	4.55	113.27	107.57
3	B	201	CYC	C3D-C4D-ND	4.54	113.27	107.57
3	J	201	CYC	C3D-C4D-ND	4.53	113.25	107.57
3	L	201	CYC	C3D-C4D-ND	4.53	113.25	107.57
3	H	202	CYC	C1D-CHD-C4C	-4.09	120.78	127.76
3	B	202	CYC	C1D-CHD-C4C	-4.09	120.78	127.76
3	D	202	CYC	C1D-CHD-C4C	-4.09	120.79	127.76
3	J	202	CYC	C1D-CHD-C4C	-4.07	120.81	127.76
3	L	202	CYC	C1D-CHD-C4C	-4.07	120.81	127.76
3	N	202	CYC	C1D-CHD-C4C	-4.06	120.83	127.76
3	F	202	CYC	C1D-CHD-C4C	-4.06	120.83	127.76
3	P	202	CYC	C1D-CHD-C4C	-4.05	120.84	127.76
3	E	201	CYC	C3C-C4C-NC	-3.64	103.26	107.94
3	M	201	CYC	C3C-C4C-NC	-3.63	103.26	107.94
3	K	201	CYC	C3C-C4C-NC	-3.62	103.28	107.94
3	O	201	CYC	C3C-C4C-NC	-3.62	103.28	107.94
3	I	201	CYC	CHA-C1A-NA	3.62	132.20	124.60
3	A	201	CYC	C3C-C4C-NC	-3.61	103.29	107.94
3	C	201	CYC	C3C-C4C-NC	-3.61	103.30	107.94
3	K	201	CYC	CHA-C1A-NA	3.61	132.17	124.60
3	G	201	CYC	C3C-C4C-NC	-3.61	103.30	107.94
3	M	201	CYC	CHA-C1A-NA	3.60	132.16	124.60
3	I	201	CYC	C3C-C4C-NC	-3.60	103.31	107.94
3	G	201	CYC	CHA-C1A-NA	3.60	132.15	124.60
3	E	201	CYC	CHA-C1A-NA	3.60	132.15	124.60
3	A	201	CYC	CHA-C1A-NA	3.60	132.15	124.60
3	O	201	CYC	CHA-C1A-NA	3.59	132.13	124.60
3	C	201	CYC	CHA-C1A-NA	3.58	132.11	124.60
3	O	201	CYC	C4D-ND-C1D	-3.49	103.65	109.78
3	K	201	CYC	C4D-ND-C1D	-3.49	103.66	109.78
3	C	201	CYC	C4D-ND-C1D	-3.48	103.67	109.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	201	CYC	C4D-ND-C1D	-3.48	103.68	109.78
3	H	201	CYC	C2A-C1A-NA	-3.48	105.12	110.04
3	A	201	CYC	C4D-ND-C1D	-3.47	103.69	109.78
3	E	201	CYC	C4D-ND-C1D	-3.47	103.70	109.78
3	G	201	CYC	C4D-ND-C1D	-3.46	103.70	109.78
3	M	201	CYC	C4D-ND-C1D	-3.46	103.71	109.78
3	N	201	CYC	C2A-C1A-NA	-3.46	105.15	110.04
3	J	201	CYC	C2A-C1A-NA	-3.45	105.16	110.04
3	L	201	CYC	C2A-C1A-NA	-3.45	105.16	110.04
3	B	201	CYC	C2A-C1A-NA	-3.44	105.17	110.04
3	D	201	CYC	C2A-C1A-NA	-3.44	105.17	110.04
3	F	201	CYC	C2A-C1A-NA	-3.44	105.17	110.04
3	P	201	CYC	C2A-C1A-NA	-3.43	105.19	110.04
3	J	202	CYC	C4D-ND-C1D	-3.42	103.78	109.78
3	B	201	CYC	C1B-C2B-C3B	3.42	111.38	107.86
3	H	201	CYC	C1B-C2B-C3B	3.41	111.37	107.86
3	N	201	CYC	C1B-C2B-C3B	3.41	111.37	107.86
3	P	201	CYC	C1B-C2B-C3B	3.41	111.37	107.86
3	F	201	CYC	C1B-C2B-C3B	3.41	111.36	107.86
3	D	202	CYC	C4D-ND-C1D	-3.41	103.80	109.78
3	F	202	CYC	C4D-ND-C1D	-3.41	103.80	109.78
3	D	201	CYC	C1B-C2B-C3B	3.40	111.36	107.86
3	J	201	CYC	C1B-C2B-C3B	3.40	111.36	107.86
3	L	201	CYC	C1B-C2B-C3B	3.40	111.36	107.86
3	N	202	CYC	C4D-ND-C1D	-3.40	103.82	109.78
3	P	202	CYC	C4D-ND-C1D	-3.39	103.82	109.78
3	B	202	CYC	C4D-ND-C1D	-3.38	103.84	109.78
3	L	202	CYC	C4D-ND-C1D	-3.38	103.85	109.78
3	H	202	CYC	C4D-ND-C1D	-3.35	103.90	109.78
3	H	201	CYC	CHA-C1A-NA	3.28	131.48	124.60
3	L	201	CYC	CHA-C1A-NA	3.28	131.48	124.60
3	F	201	CYC	CAB-C3B-C4B	3.27	126.43	121.37
3	J	201	CYC	CHA-C1A-NA	3.27	131.47	124.60
3	B	201	CYC	CHA-C1A-NA	3.27	131.47	124.60
3	H	201	CYC	CAB-C3B-C4B	3.27	126.43	121.37
3	P	201	CYC	CHA-C1A-NA	3.27	131.46	124.60
3	F	201	CYC	CHA-C1A-NA	3.27	131.46	124.60
3	B	201	CYC	CAB-C3B-C4B	3.26	126.42	121.37
3	P	201	CYC	CAB-C3B-C4B	3.26	126.42	121.37
3	D	201	CYC	CAB-C3B-C4B	3.26	126.41	121.37
3	D	201	CYC	CHA-C1A-NA	3.25	131.43	124.60
3	N	201	CYC	CAB-C3B-C4B	3.25	126.40	121.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	201	CYC	CHA-C1A-NA	3.25	131.43	124.60
3	H	202	CYC	C2A-C1A-NA	-3.25	105.44	110.04
3	J	201	CYC	CAB-C3B-C4B	3.24	126.38	121.37
3	L	202	CYC	C2A-C1A-NA	-3.24	105.46	110.04
3	P	202	CYC	C2A-C1A-NA	-3.23	105.47	110.04
3	N	202	CYC	C2A-C1A-NA	-3.23	105.47	110.04
3	B	202	CYC	C2A-C1A-NA	-3.23	105.47	110.04
3	L	201	CYC	CAB-C3B-C4B	3.23	126.36	121.37
3	J	202	CYC	C2A-C1A-NA	-3.21	105.50	110.04
3	D	202	CYC	C2A-C1A-NA	-3.21	105.50	110.04
3	F	202	CYC	C2A-C1A-NA	-3.20	105.51	110.04
3	P	202	CYC	C1B-C2B-C3B	3.19	111.14	107.86
3	B	202	CYC	C1B-C2B-C3B	3.19	111.14	107.86
3	N	202	CYC	C1B-C2B-C3B	3.17	111.13	107.86
3	J	202	CYC	C1B-C2B-C3B	3.17	111.12	107.86
3	F	202	CYC	C1B-C2B-C3B	3.14	111.09	107.86
3	H	202	CYC	C1B-C2B-C3B	3.13	111.08	107.86
3	D	202	CYC	C1B-C2B-C3B	3.13	111.08	107.86
3	L	202	CYC	C1B-C2B-C3B	3.10	111.05	107.86
3	J	202	CYC	C2C-C3C-C4C	3.06	105.92	101.34
3	F	201	CYC	C4D-ND-C1D	-3.05	104.43	109.78
3	H	202	CYC	C2C-C3C-C4C	3.04	105.90	101.34
3	J	201	CYC	C4D-ND-C1D	-3.04	104.44	109.78
3	B	202	CYC	C2C-C3C-C4C	3.04	105.89	101.34
3	N	201	CYC	C4D-ND-C1D	-3.04	104.45	109.78
3	H	201	CYC	C4D-ND-C1D	-3.04	104.45	109.78
3	D	201	CYC	C4D-ND-C1D	-3.04	104.45	109.78
3	A	201	CYC	C1B-C2B-C3B	3.03	110.98	107.86
3	P	201	CYC	C4D-ND-C1D	-3.03	104.46	109.78
3	L	201	CYC	C4D-ND-C1D	-3.03	104.47	109.78
3	K	201	CYC	C1B-C2B-C3B	3.02	110.97	107.86
3	N	202	CYC	C2C-C3C-C4C	3.02	105.86	101.34
3	E	201	CYC	C2A-C1A-NA	-3.02	105.77	110.04
3	B	201	CYC	C4D-ND-C1D	-3.02	104.48	109.78
3	I	201	CYC	C2A-C1A-NA	-3.02	105.77	110.04
3	C	201	CYC	C2A-C1A-NA	-3.02	105.77	110.04
3	H	201	CYC	C1A-C2A-C3A	3.02	109.99	106.73
3	N	201	CYC	C1A-C2A-C3A	3.01	109.99	106.73
3	D	202	CYC	C2C-C3C-C4C	3.01	105.85	101.34
3	F	202	CYC	C2C-C3C-C4C	3.01	105.85	101.34
3	P	202	CYC	C2C-C3C-C4C	3.01	105.85	101.34
3	M	201	CYC	C2A-C1A-NA	-3.01	105.79	110.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	202	CYC	C2C-C3C-C4C	3.01	105.84	101.34
3	G	201	CYC	C2A-C1A-NA	-3.01	105.79	110.04
3	D	201	CYC	C1A-C2A-C3A	3.00	109.98	106.73
3	E	201	CYC	C1B-C2B-C3B	3.00	110.95	107.86
3	C	201	CYC	C1B-C2B-C3B	3.00	110.95	107.86
3	O	201	CYC	C2A-C1A-NA	-3.00	105.80	110.04
3	G	201	CYC	C1B-C2B-C3B	3.00	110.94	107.86
3	M	201	CYC	C1B-C2B-C3B	3.00	110.94	107.86
3	F	201	CYC	C1A-C2A-C3A	2.99	109.97	106.73
3	A	201	CYC	C2A-C1A-NA	-2.99	105.81	110.04
3	K	201	CYC	C2A-C1A-NA	-2.99	105.81	110.04
3	L	201	CYC	C1A-C2A-C3A	2.98	109.95	106.73
3	I	201	CYC	C1B-C2B-C3B	2.97	110.92	107.86
3	O	201	CYC	C1B-C2B-C3B	2.97	110.92	107.86
3	B	201	CYC	C1A-C2A-C3A	2.96	109.93	106.73
3	J	201	CYC	C1A-C2A-C3A	2.96	109.93	106.73
3	P	201	CYC	C1A-C2A-C3A	2.95	109.92	106.73
3	C	201	CYC	C1A-C2A-C3A	2.81	109.77	106.73
3	J	202	CYC	C4D-C3D-C2D	-2.80	104.36	107.62
3	A	201	CYC	C1A-C2A-C3A	2.80	109.75	106.73
3	O	201	CYC	C1A-C2A-C3A	2.80	109.75	106.73
3	L	202	CYC	C4D-C3D-C2D	-2.79	104.37	107.62
3	F	202	CYC	C4D-C3D-C2D	-2.79	104.37	107.62
3	I	201	CYC	C1A-C2A-C3A	2.79	109.74	106.73
3	G	201	CYC	C1A-C2A-C3A	2.79	109.74	106.73
3	B	202	CYC	C4D-C3D-C2D	-2.78	104.39	107.62
3	E	201	CYC	C1A-C2A-C3A	2.78	109.73	106.73
3	H	202	CYC	C4D-C3D-C2D	-2.77	104.39	107.62
3	K	201	CYC	C1A-C2A-C3A	2.77	109.72	106.73
3	M	201	CYC	C1A-C2A-C3A	2.76	109.72	106.73
3	E	201	CYC	C2C-C3C-C4C	2.76	105.47	101.34
3	D	202	CYC	C4D-C3D-C2D	-2.76	104.41	107.62
3	M	201	CYC	C2C-C3C-C4C	2.75	105.46	101.34
3	K	201	CYC	C2C-C3C-C4C	2.75	105.45	101.34
3	D	202	CYC	C1B-NB-C4B	-2.74	107.29	110.66
3	J	202	CYC	C1B-NB-C4B	-2.74	107.30	110.66
3	N	202	CYC	C4D-C3D-C2D	-2.74	104.43	107.62
3	F	202	CYC	C1B-NB-C4B	-2.74	107.30	110.66
3	O	201	CYC	C2C-C3C-C4C	2.73	105.44	101.34
3	P	202	CYC	C4D-C3D-C2D	-2.73	104.44	107.62
3	C	201	CYC	C2C-C3C-C4C	2.73	105.43	101.34
3	I	201	CYC	C2C-C3C-C4C	2.72	105.41	101.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	202	CYC	C1B-NB-C4B	-2.72	107.33	110.66
3	A	201	CYC	C2C-C3C-C4C	2.71	105.40	101.34
3	B	202	CYC	C1B-NB-C4B	-2.71	107.33	110.66
3	G	201	CYC	C2C-C3C-C4C	2.71	105.40	101.34
3	P	202	CYC	C1B-NB-C4B	-2.71	107.34	110.66
3	H	202	CYC	C1B-NB-C4B	-2.69	107.36	110.66
3	H	201	CYC	C3C-C4C-NC	-2.68	104.50	107.94
3	L	202	CYC	C1B-NB-C4B	-2.67	107.38	110.66
3	D	201	CYC	C3C-C4C-NC	-2.67	104.51	107.94
3	F	201	CYC	C3C-C4C-NC	-2.66	104.52	107.94
3	N	201	CYC	C3C-C4C-NC	-2.66	104.52	107.94
3	J	201	CYC	C3C-C4C-NC	-2.64	104.54	107.94
3	B	201	CYC	C3C-C4C-NC	-2.63	104.55	107.94
3	P	201	CYC	C3C-C4C-NC	-2.62	104.57	107.94
3	L	201	CYC	C3C-C4C-NC	-2.61	104.58	107.94
3	B	202	CYC	CAB-C3B-C4B	2.59	125.38	121.37
3	D	202	CYC	CAB-C3B-C4B	2.59	125.38	121.37
3	O	201	CYC	C1B-NB-C4B	-2.59	107.49	110.66
3	P	202	CYC	CAB-C3B-C4B	2.57	125.35	121.37
3	F	202	CYC	CAB-C3B-C4B	2.56	125.34	121.37
3	M	201	CYC	C1B-NB-C4B	-2.56	107.52	110.66
3	G	201	CYC	C1B-NB-C4B	-2.56	107.52	110.66
3	K	201	CYC	C1B-NB-C4B	-2.56	107.52	110.66
3	H	202	CYC	C1A-C2A-C3A	2.56	109.49	106.73
3	J	202	CYC	CAB-C3B-C4B	2.55	125.32	121.37
3	L	202	CYC	CAB-C3B-C4B	2.55	125.32	121.37
3	H	202	CYC	CAB-C3B-C4B	2.55	125.32	121.37
3	I	201	CYC	C1B-NB-C4B	-2.55	107.53	110.66
3	N	202	CYC	C1A-C2A-C3A	2.55	109.49	106.73
3	E	201	CYC	C1B-NB-C4B	-2.54	107.54	110.66
3	N	202	CYC	CAB-C3B-C4B	2.54	125.30	121.37
3	L	202	CYC	C1A-C2A-C3A	2.54	109.48	106.73
3	A	201	CYC	C1B-NB-C4B	-2.54	107.55	110.66
3	P	202	CYC	C1A-C2A-C3A	2.53	109.47	106.73
3	C	201	CYC	C1B-NB-C4B	-2.52	107.57	110.66
3	D	202	CYC	C1A-C2A-C3A	2.52	109.45	106.73
3	F	202	CYC	C1A-C2A-C3A	2.52	109.45	106.73
3	J	202	CYC	C1A-C2A-C3A	2.52	109.45	106.73
3	B	202	CYC	C1A-C2A-C3A	2.50	109.44	106.73
3	B	201	CYC	CMD-C2D-C1D	2.41	129.13	125.62
3	D	201	CYC	CMD-C2D-C1D	2.40	129.11	125.62
3	J	201	CYC	CMD-C2D-C1D	2.40	129.10	125.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	201	CYC	CMD-C2D-C1D	2.40	129.10	125.62
3	F	201	CYC	CMD-C2D-C1D	2.39	129.09	125.62
3	P	201	CYC	CMD-C2D-C1D	2.38	129.09	125.62
3	L	201	CYC	CMD-C2D-C1D	2.37	129.07	125.62
3	N	201	CYC	CMD-C2D-C1D	2.36	129.06	125.62
3	C	201	CYC	CBD-CAD-C3D	-2.32	106.12	112.53
3	D	201	CYC	CAB-C3B-C2B	-2.32	123.30	127.56
3	I	201	CYC	CBD-CAD-C3D	-2.32	106.13	112.53
3	J	201	CYC	CAB-C3B-C2B	-2.31	123.31	127.56
3	K	201	CYC	CBD-CAD-C3D	-2.31	106.15	112.53
3	O	201	CYC	CBD-CAD-C3D	-2.31	106.15	112.53
3	N	201	CYC	CAB-C3B-C2B	-2.31	123.32	127.56
3	H	201	CYC	CAB-C3B-C2B	-2.31	123.32	127.56
3	F	201	CYC	CAB-C3B-C2B	-2.30	123.33	127.56
3	P	201	CYC	CAB-C3B-C2B	-2.30	123.33	127.56
3	L	201	CYC	CAB-C3B-C2B	-2.30	123.33	127.56
3	E	201	CYC	CBD-CAD-C3D	-2.30	106.17	112.53
3	B	201	CYC	CAB-C3B-C2B	-2.30	123.33	127.56
3	G	201	CYC	CBD-CAD-C3D	-2.30	106.18	112.53
3	A	201	CYC	CBD-CAD-C3D	-2.30	106.18	112.53
3	M	201	CYC	CBD-CAD-C3D	-2.30	106.18	112.53
3	I	201	CYC	CMD-C2D-C1D	2.22	128.84	125.62
3	E	201	CYC	CMD-C2D-C1D	2.22	128.84	125.62
3	C	201	CYC	CMD-C2D-C1D	2.22	128.84	125.62
3	K	201	CYC	CMD-C2D-C1D	2.21	128.83	125.62
3	O	201	CYC	CMD-C2D-C1D	2.21	128.83	125.62
3	G	201	CYC	CMD-C2D-C1D	2.18	128.79	125.62
3	A	201	CYC	CMD-C2D-C1D	2.18	128.79	125.62
3	M	201	CYC	CMD-C2D-C1D	2.15	128.75	125.62
3	H	201	CYC	C1B-NB-C4B	-2.13	108.05	110.66
3	J	202	CYC	C1C-NC-C4C	-2.11	110.76	113.41
3	O	201	CYC	CAB-C3B-C4B	2.11	124.63	121.37
3	D	201	CYC	C1B-NB-C4B	-2.10	108.09	110.66
3	F	201	CYC	C1B-NB-C4B	-2.09	108.09	110.66
3	C	201	CYC	CAB-C3B-C4B	2.09	124.61	121.37
3	M	201	CYC	CAB-C3B-C4B	2.09	124.61	121.37
3	B	201	CYC	C1B-NB-C4B	-2.09	108.10	110.66
3	F	202	CYC	C1C-NC-C4C	-2.08	110.79	113.41
3	G	201	CYC	CAB-C3B-C4B	2.07	124.58	121.37
3	N	201	CYC	C4D-C3D-C2D	-2.07	105.21	107.62
3	P	201	CYC	C1B-NB-C4B	-2.07	108.12	110.66
3	P	202	CYC	C1C-NC-C4C	-2.07	110.81	113.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	201	CYC	CAB-C3B-C4B	2.06	124.56	121.37
3	D	202	CYC	C1C-NC-C4C	-2.06	110.82	113.41
3	J	201	CYC	C1B-NB-C4B	-2.06	108.13	110.66
3	N	201	CYC	C1B-NB-C4B	-2.06	108.13	110.66
3	K	201	CYC	CAB-C3B-C4B	2.06	124.56	121.37
3	E	201	CYC	CAB-C3B-C4B	2.06	124.56	121.37
3	H	202	CYC	C1C-NC-C4C	-2.06	110.82	113.41
3	A	201	CYC	CAB-C3B-C4B	2.06	124.56	121.37
3	N	202	CYC	C1C-NC-C4C	-2.06	110.83	113.41
3	L	202	CYC	C1C-NC-C4C	-2.06	110.83	113.41
3	K	201	CYC	C1D-CHD-C4C	-2.06	124.25	127.76
3	L	201	CYC	C1B-NB-C4B	-2.06	108.14	110.66
3	B	202	CYC	C1C-NC-C4C	-2.06	110.83	113.41
3	C	201	CYC	C1D-CHD-C4C	-2.05	124.27	127.76
3	P	201	CYC	C4D-C3D-C2D	-2.04	105.24	107.62
3	E	201	CYC	C1D-CHD-C4C	-2.03	124.29	127.76
3	B	201	CYC	C4D-C3D-C2D	-2.03	105.25	107.62
3	F	201	CYC	C4D-C3D-C2D	-2.03	105.25	107.62
3	I	201	CYC	C1D-CHD-C4C	-2.03	124.30	127.76
3	G	201	CYC	C1D-CHD-C4C	-2.03	124.30	127.76
3	J	201	CYC	C4D-C3D-C2D	-2.03	105.26	107.62
3	A	201	CYC	C1D-CHD-C4C	-2.02	124.32	127.76
3	D	201	CYC	C4D-C3D-C2D	-2.01	105.28	107.62
3	L	201	CYC	C4D-C3D-C2D	-2.01	105.28	107.62
3	B	201	CYC	CMA-C3A-C4A	2.01	128.22	125.10
3	O	201	CYC	C1D-CHD-C4C	-2.01	124.33	127.76
3	M	201	CYC	C1D-CHD-C4C	-2.01	124.33	127.76
3	H	201	CYC	C4D-C3D-C2D	-2.01	105.28	107.62
3	P	201	CYC	CMA-C3A-C4A	2.01	128.22	125.10

There are no chirality outliers.

All (272) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	201	CYC	NA-C4A-CHB-C1B
3	A	201	CYC	C3A-C4A-CHB-C1B
3	A	201	CYC	C2C-C3C-CAC-CBC
3	A	201	CYC	C4C-C3C-CAC-CBC
3	A	201	CYC	NC-C4C-CHD-C1D
3	B	201	CYC	NA-C4A-CHB-C1B
3	B	201	CYC	C3A-C4A-CHB-C1B
3	B	201	CYC	NC-C4C-CHD-C1D

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Mol	Chain	Res	Type	Atoms
3	B	202	CYC	NA-C1A-CHA-C4D
3	B	202	CYC	C2A-C1A-CHA-C4D
3	B	202	CYC	ND-C4D-CHA-C1A
3	B	202	CYC	C3D-C4D-CHA-C1A
3	B	202	CYC	NA-C4A-CHB-C1B
3	B	202	CYC	C3A-C4A-CHB-C1B
3	B	202	CYC	C2C-C3C-CAC-CBC
3	B	202	CYC	C4C-C3C-CAC-CBC
3	C	201	CYC	NA-C4A-CHB-C1B
3	C	201	CYC	C3A-C4A-CHB-C1B
3	C	201	CYC	C2C-C3C-CAC-CBC
3	C	201	CYC	C4C-C3C-CAC-CBC
3	C	201	CYC	NC-C4C-CHD-C1D
3	D	201	CYC	NA-C4A-CHB-C1B
3	D	201	CYC	C3A-C4A-CHB-C1B
3	D	201	CYC	NC-C4C-CHD-C1D
3	D	202	CYC	NA-C1A-CHA-C4D
3	D	202	CYC	C2A-C1A-CHA-C4D
3	D	202	CYC	ND-C4D-CHA-C1A
3	D	202	CYC	C3D-C4D-CHA-C1A
3	D	202	CYC	NA-C4A-CHB-C1B
3	D	202	CYC	C3A-C4A-CHB-C1B
3	D	202	CYC	C2C-C3C-CAC-CBC
3	D	202	CYC	C4C-C3C-CAC-CBC
3	E	201	CYC	NA-C4A-CHB-C1B
3	E	201	CYC	C3A-C4A-CHB-C1B
3	E	201	CYC	C2C-C3C-CAC-CBC
3	E	201	CYC	C4C-C3C-CAC-CBC
3	E	201	CYC	NC-C4C-CHD-C1D
3	F	201	CYC	NA-C4A-CHB-C1B
3	F	201	CYC	C3A-C4A-CHB-C1B
3	F	201	CYC	NC-C4C-CHD-C1D
3	F	202	CYC	NA-C1A-CHA-C4D
3	F	202	CYC	C2A-C1A-CHA-C4D
3	F	202	CYC	ND-C4D-CHA-C1A
3	F	202	CYC	C3D-C4D-CHA-C1A
3	F	202	CYC	NA-C4A-CHB-C1B
3	F	202	CYC	C3A-C4A-CHB-C1B
3	F	202	CYC	C2C-C3C-CAC-CBC
3	F	202	CYC	C4C-C3C-CAC-CBC
3	G	201	CYC	NA-C4A-CHB-C1B
3	G	201	CYC	C3A-C4A-CHB-C1B

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Mol	Chain	Res	Type	Atoms
3	G	201	CYC	C2C-C3C-CAC-CBC
3	G	201	CYC	C4C-C3C-CAC-CBC
3	G	201	CYC	NC-C4C-CHD-C1D
3	H	201	CYC	NA-C4A-CHB-C1B
3	H	201	CYC	C3A-C4A-CHB-C1B
3	H	201	CYC	NC-C4C-CHD-C1D
3	H	202	CYC	NA-C1A-CHA-C4D
3	H	202	CYC	C2A-C1A-CHA-C4D
3	H	202	CYC	ND-C4D-CHA-C1A
3	H	202	CYC	C3D-C4D-CHA-C1A
3	H	202	CYC	NA-C4A-CHB-C1B
3	H	202	CYC	C3A-C4A-CHB-C1B
3	H	202	CYC	C2C-C3C-CAC-CBC
3	H	202	CYC	C4C-C3C-CAC-CBC
3	I	201	CYC	NA-C4A-CHB-C1B
3	I	201	CYC	C3A-C4A-CHB-C1B
3	I	201	CYC	C2C-C3C-CAC-CBC
3	I	201	CYC	C4C-C3C-CAC-CBC
3	I	201	CYC	NC-C4C-CHD-C1D
3	J	201	CYC	NA-C4A-CHB-C1B
3	J	201	CYC	C3A-C4A-CHB-C1B
3	J	201	CYC	NC-C4C-CHD-C1D
3	J	202	CYC	NA-C1A-CHA-C4D
3	J	202	CYC	C2A-C1A-CHA-C4D
3	J	202	CYC	ND-C4D-CHA-C1A
3	J	202	CYC	C3D-C4D-CHA-C1A
3	J	202	CYC	NA-C4A-CHB-C1B
3	J	202	CYC	C3A-C4A-CHB-C1B
3	J	202	CYC	C2C-C3C-CAC-CBC
3	J	202	CYC	C4C-C3C-CAC-CBC
3	K	201	CYC	NA-C4A-CHB-C1B
3	K	201	CYC	C3A-C4A-CHB-C1B
3	K	201	CYC	C2C-C3C-CAC-CBC
3	K	201	CYC	C4C-C3C-CAC-CBC
3	K	201	CYC	NC-C4C-CHD-C1D
3	L	201	CYC	NA-C4A-CHB-C1B
3	L	201	CYC	C3A-C4A-CHB-C1B
3	L	201	CYC	NC-C4C-CHD-C1D
3	L	202	CYC	NA-C1A-CHA-C4D
3	L	202	CYC	C2A-C1A-CHA-C4D
3	L	202	CYC	ND-C4D-CHA-C1A
3	L	202	CYC	C3D-C4D-CHA-C1A

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Mol	Chain	Res	Type	Atoms
3	L	202	CYC	NA-C4A-CHB-C1B
3	L	202	CYC	C3A-C4A-CHB-C1B
3	L	202	CYC	C2C-C3C-CAC-CBC
3	L	202	CYC	C4C-C3C-CAC-CBC
3	M	201	CYC	NA-C4A-CHB-C1B
3	M	201	CYC	C3A-C4A-CHB-C1B
3	M	201	CYC	C2C-C3C-CAC-CBC
3	M	201	CYC	C4C-C3C-CAC-CBC
3	M	201	CYC	NC-C4C-CHD-C1D
3	N	201	CYC	NA-C4A-CHB-C1B
3	N	201	CYC	C3A-C4A-CHB-C1B
3	N	201	CYC	NC-C4C-CHD-C1D
3	N	202	CYC	NA-C1A-CHA-C4D
3	N	202	CYC	C2A-C1A-CHA-C4D
3	N	202	CYC	ND-C4D-CHA-C1A
3	N	202	CYC	C3D-C4D-CHA-C1A
3	N	202	CYC	NA-C4A-CHB-C1B
3	N	202	CYC	C3A-C4A-CHB-C1B
3	N	202	CYC	C2C-C3C-CAC-CBC
3	N	202	CYC	C4C-C3C-CAC-CBC
3	O	201	CYC	NA-C4A-CHB-C1B
3	O	201	CYC	C3A-C4A-CHB-C1B
3	O	201	CYC	C2C-C3C-CAC-CBC
3	O	201	CYC	C4C-C3C-CAC-CBC
3	O	201	CYC	NC-C4C-CHD-C1D
3	P	201	CYC	NA-C4A-CHB-C1B
3	P	201	CYC	C3A-C4A-CHB-C1B
3	P	201	CYC	NC-C4C-CHD-C1D
3	P	202	CYC	NA-C1A-CHA-C4D
3	P	202	CYC	C2A-C1A-CHA-C4D
3	P	202	CYC	ND-C4D-CHA-C1A
3	P	202	CYC	C3D-C4D-CHA-C1A
3	P	202	CYC	NA-C4A-CHB-C1B
3	P	202	CYC	C3A-C4A-CHB-C1B
3	P	202	CYC	C2C-C3C-CAC-CBC
3	P	202	CYC	C4C-C3C-CAC-CBC
3	B	201	CYC	C2B-C3B-CAB-CBB
3	D	201	CYC	C2B-C3B-CAB-CBB
3	F	201	CYC	C2B-C3B-CAB-CBB
3	H	201	CYC	C2B-C3B-CAB-CBB
3	J	201	CYC	C2B-C3B-CAB-CBB
3	L	201	CYC	C2B-C3B-CAB-CBB

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Mol	Chain	Res	Type	Atoms
3	N	201	CYC	C2B-C3B-CAB-CBB
3	P	201	CYC	C2B-C3B-CAB-CBB
3	B	202	CYC	ND-C1D-CHD-C4C
3	D	202	CYC	ND-C1D-CHD-C4C
3	F	202	CYC	ND-C1D-CHD-C4C
3	H	202	CYC	ND-C1D-CHD-C4C
3	J	202	CYC	ND-C1D-CHD-C4C
3	L	202	CYC	ND-C1D-CHD-C4C
3	N	202	CYC	ND-C1D-CHD-C4C
3	P	202	CYC	ND-C1D-CHD-C4C
3	B	201	CYC	C2D-C1D-CHD-C4C
3	D	201	CYC	C2D-C1D-CHD-C4C
3	F	201	CYC	C2D-C1D-CHD-C4C
3	H	201	CYC	C2D-C1D-CHD-C4C
3	J	201	CYC	C2D-C1D-CHD-C4C
3	L	201	CYC	C2D-C1D-CHD-C4C
3	N	201	CYC	C2D-C1D-CHD-C4C
3	P	201	CYC	C2D-C1D-CHD-C4C
3	A	201	CYC	ND-C1D-CHD-C4C
3	B	201	CYC	ND-C1D-CHD-C4C
3	C	201	CYC	ND-C1D-CHD-C4C
3	D	201	CYC	ND-C1D-CHD-C4C
3	E	201	CYC	ND-C1D-CHD-C4C
3	F	201	CYC	ND-C1D-CHD-C4C
3	G	201	CYC	ND-C1D-CHD-C4C
3	H	201	CYC	ND-C1D-CHD-C4C
3	I	201	CYC	ND-C1D-CHD-C4C
3	J	201	CYC	ND-C1D-CHD-C4C
3	K	201	CYC	ND-C1D-CHD-C4C
3	L	201	CYC	ND-C1D-CHD-C4C
3	M	201	CYC	ND-C1D-CHD-C4C
3	N	201	CYC	ND-C1D-CHD-C4C
3	O	201	CYC	ND-C1D-CHD-C4C
3	P	201	CYC	ND-C1D-CHD-C4C
3	A	201	CYC	C2D-C1D-CHD-C4C
3	C	201	CYC	C2D-C1D-CHD-C4C
3	E	201	CYC	C2D-C1D-CHD-C4C
3	G	201	CYC	C2D-C1D-CHD-C4C
3	I	201	CYC	C2D-C1D-CHD-C4C
3	K	201	CYC	C2D-C1D-CHD-C4C
3	M	201	CYC	C2D-C1D-CHD-C4C
3	O	201	CYC	C2D-C1D-CHD-C4C

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Mol	Chain	Res	Type	Atoms
3	B	202	CYC	C2D-C1D-CHD-C4C
3	D	202	CYC	C2D-C1D-CHD-C4C
3	F	202	CYC	C2D-C1D-CHD-C4C
3	H	202	CYC	C2D-C1D-CHD-C4C
3	J	202	CYC	C2D-C1D-CHD-C4C
3	L	202	CYC	C2D-C1D-CHD-C4C
3	N	202	CYC	C2D-C1D-CHD-C4C
3	P	202	CYC	C2D-C1D-CHD-C4C
3	B	201	CYC	C4B-C3B-CAB-CBB
3	D	201	CYC	C4B-C3B-CAB-CBB
3	F	201	CYC	C4B-C3B-CAB-CBB
3	H	201	CYC	C4B-C3B-CAB-CBB
3	J	201	CYC	C4B-C3B-CAB-CBB
3	L	201	CYC	C4B-C3B-CAB-CBB
3	N	201	CYC	C4B-C3B-CAB-CBB
3	P	201	CYC	C4B-C3B-CAB-CBB
3	B	202	CYC	C2B-C3B-CAB-CBB
3	D	202	CYC	C2B-C3B-CAB-CBB
3	P	202	CYC	C2B-C3B-CAB-CBB
3	F	202	CYC	C2B-C3B-CAB-CBB
3	H	202	CYC	C2B-C3B-CAB-CBB
3	J	202	CYC	C2B-C3B-CAB-CBB
3	L	202	CYC	C2B-C3B-CAB-CBB
3	N	202	CYC	C2B-C3B-CAB-CBB
3	B	202	CYC	C4D-C3D-CAD-CBD
3	D	202	CYC	C4D-C3D-CAD-CBD
3	F	202	CYC	C4D-C3D-CAD-CBD
3	H	202	CYC	C4D-C3D-CAD-CBD
3	J	202	CYC	C4D-C3D-CAD-CBD
3	L	202	CYC	C4D-C3D-CAD-CBD
3	N	202	CYC	C4D-C3D-CAD-CBD
3	P	202	CYC	C4D-C3D-CAD-CBD
3	A	201	CYC	CAA-CBA-CGA-O2A
3	G	201	CYC	CAA-CBA-CGA-O1A
3	I	201	CYC	CAA-CBA-CGA-O2A
3	K	201	CYC	CAA-CBA-CGA-O1A
3	M	201	CYC	CAA-CBA-CGA-O1A
3	C	201	CYC	CAA-CBA-CGA-O2A
3	E	201	CYC	CAA-CBA-CGA-O2A
3	G	201	CYC	CAA-CBA-CGA-O2A
3	K	201	CYC	CAA-CBA-CGA-O2A
3	M	201	CYC	CAA-CBA-CGA-O2A

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Mol	Chain	Res	Type	Atoms
3	O	201	CYC	CAA-CBA-CGA-O2A
3	A	201	CYC	CAA-CBA-CGA-O1A
3	C	201	CYC	CAA-CBA-CGA-O1A
3	E	201	CYC	CAA-CBA-CGA-O1A
3	I	201	CYC	CAA-CBA-CGA-O1A
3	O	201	CYC	CAA-CBA-CGA-O1A
3	B	201	CYC	CAA-CBA-CGA-O1A
3	D	201	CYC	CAA-CBA-CGA-O1A
3	H	201	CYC	CAA-CBA-CGA-O1A
3	J	201	CYC	CAA-CBA-CGA-O1A
3	L	201	CYC	CAA-CBA-CGA-O1A
3	F	201	CYC	CAA-CBA-CGA-O1A
3	N	201	CYC	CAA-CBA-CGA-O1A
3	P	201	CYC	CAA-CBA-CGA-O1A
3	B	201	CYC	CAA-CBA-CGA-O2A
3	D	201	CYC	CAA-CBA-CGA-O2A
3	J	201	CYC	CAA-CBA-CGA-O2A
3	L	201	CYC	CAA-CBA-CGA-O2A
3	F	201	CYC	CAA-CBA-CGA-O2A
3	H	201	CYC	CAA-CBA-CGA-O2A
3	N	201	CYC	CAA-CBA-CGA-O2A
3	P	201	CYC	CAA-CBA-CGA-O2A
3	J	202	CYC	CAA-CBA-CGA-O2A
3	D	202	CYC	CAA-CBA-CGA-O2A
3	F	202	CYC	CAA-CBA-CGA-O2A
3	H	202	CYC	CAA-CBA-CGA-O2A
3	L	202	CYC	CAA-CBA-CGA-O2A
3	N	202	CYC	CAA-CBA-CGA-O2A
3	B	202	CYC	CAA-CBA-CGA-O2A
3	P	202	CYC	CAA-CBA-CGA-O2A
3	B	202	CYC	CAA-CBA-CGA-O1A
3	D	202	CYC	CAA-CBA-CGA-O1A
3	F	202	CYC	CAA-CBA-CGA-O1A
3	H	202	CYC	CAA-CBA-CGA-O1A
3	J	202	CYC	CAA-CBA-CGA-O1A
3	L	202	CYC	CAA-CBA-CGA-O1A
3	N	202	CYC	CAA-CBA-CGA-O1A
3	P	202	CYC	CAA-CBA-CGA-O1A
3	A	201	CYC	CAD-CBD-CGD-O2D
3	C	201	CYC	CAD-CBD-CGD-O2D
3	E	201	CYC	CAD-CBD-CGD-O2D
3	G	201	CYC	CAD-CBD-CGD-O2D

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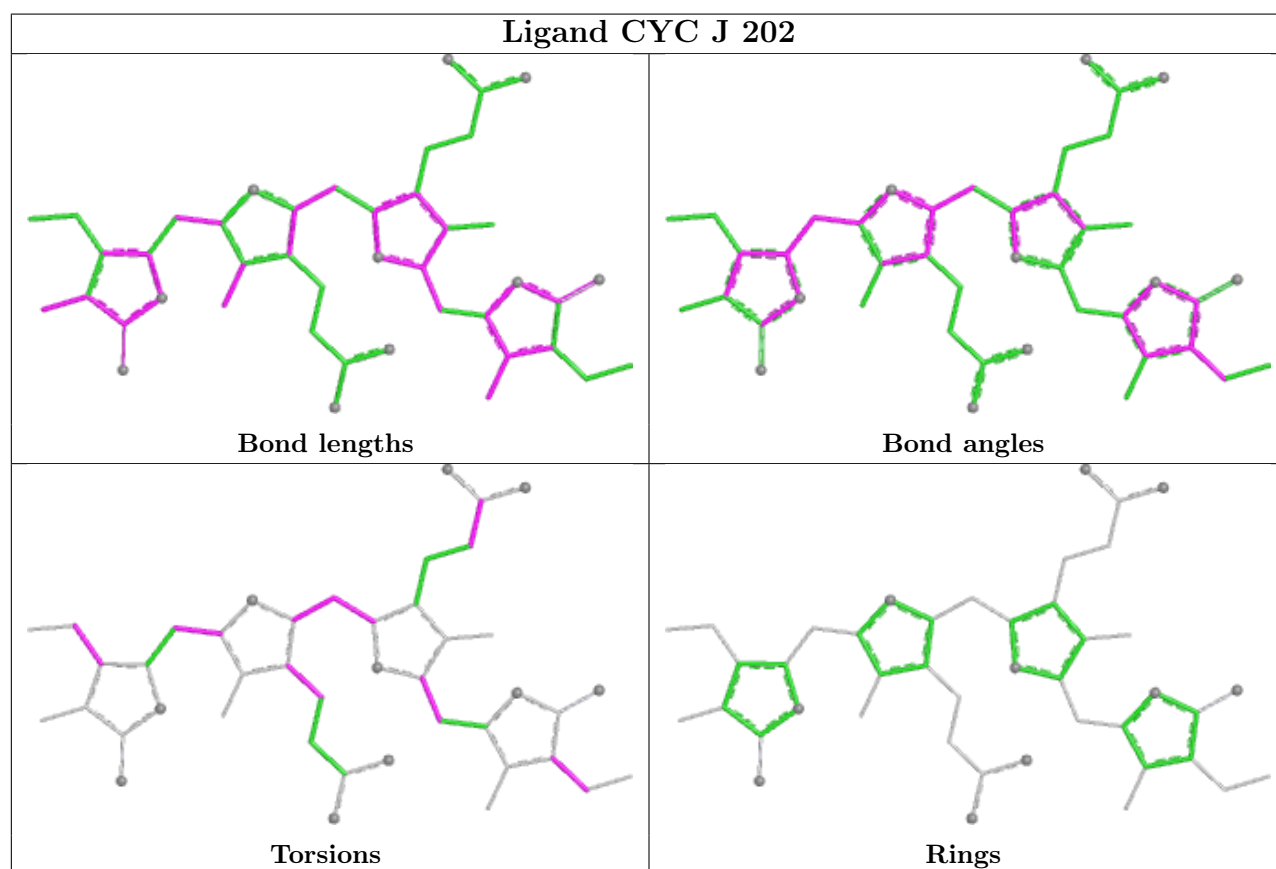
Mol	Chain	Res	Type	Atoms
3	I	201	CYC	CAD-CBD-CGD-O2D
3	K	201	CYC	CAD-CBD-CGD-O2D
3	M	201	CYC	CAD-CBD-CGD-O2D
3	O	201	CYC	CAD-CBD-CGD-O2D
3	M	201	CYC	CAD-CBD-CGD-O1D
3	A	201	CYC	CAD-CBD-CGD-O1D
3	C	201	CYC	CAD-CBD-CGD-O1D
3	E	201	CYC	CAD-CBD-CGD-O1D
3	G	201	CYC	CAD-CBD-CGD-O1D
3	I	201	CYC	CAD-CBD-CGD-O1D
3	K	201	CYC	CAD-CBD-CGD-O1D
3	O	201	CYC	CAD-CBD-CGD-O1D

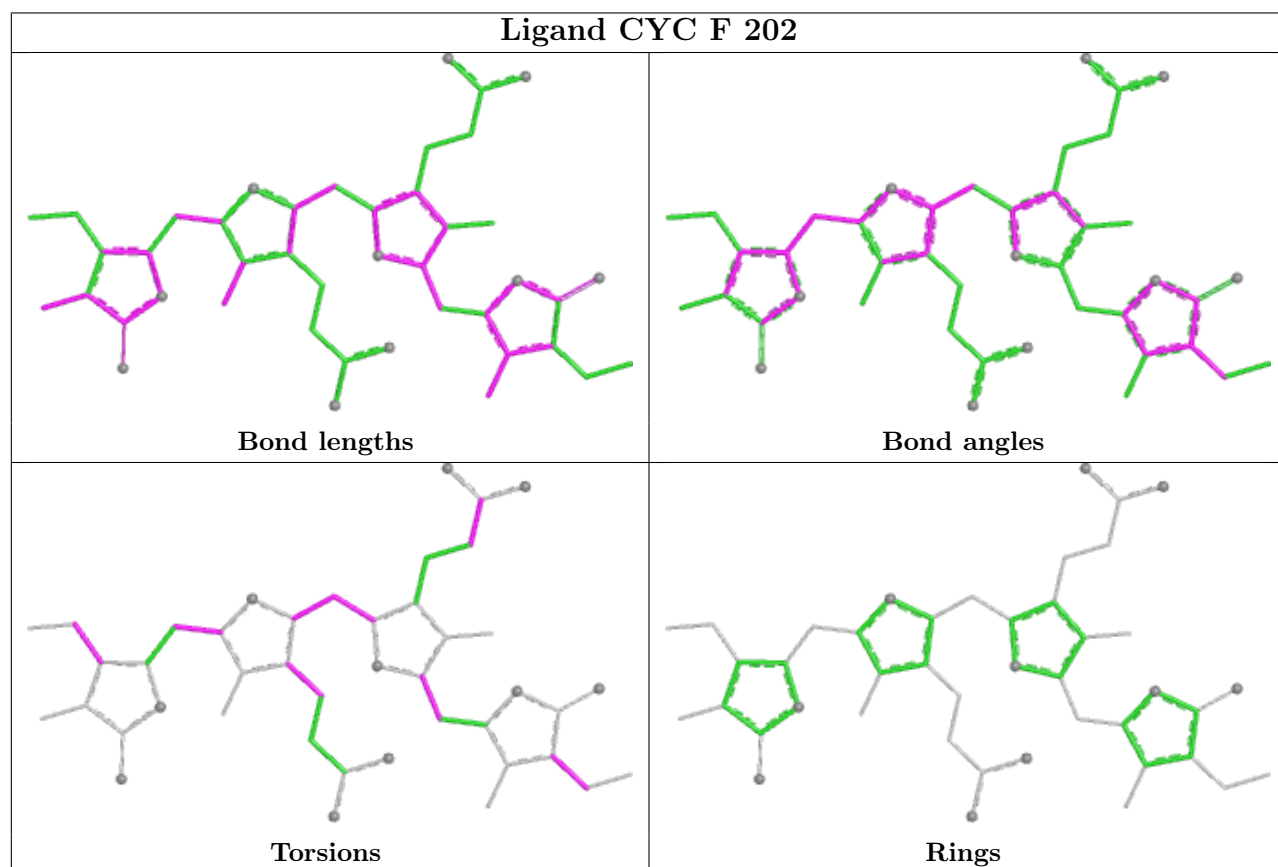
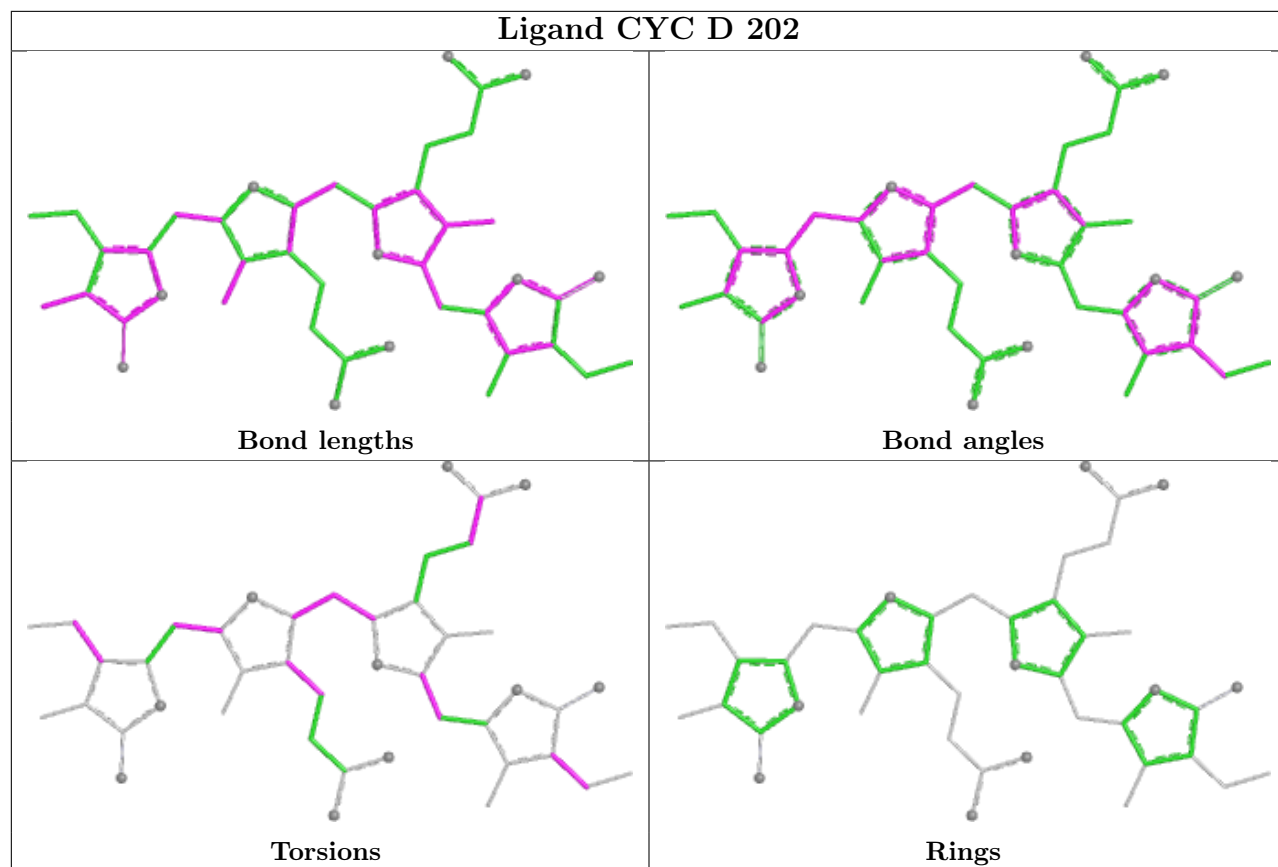
There are no ring outliers.

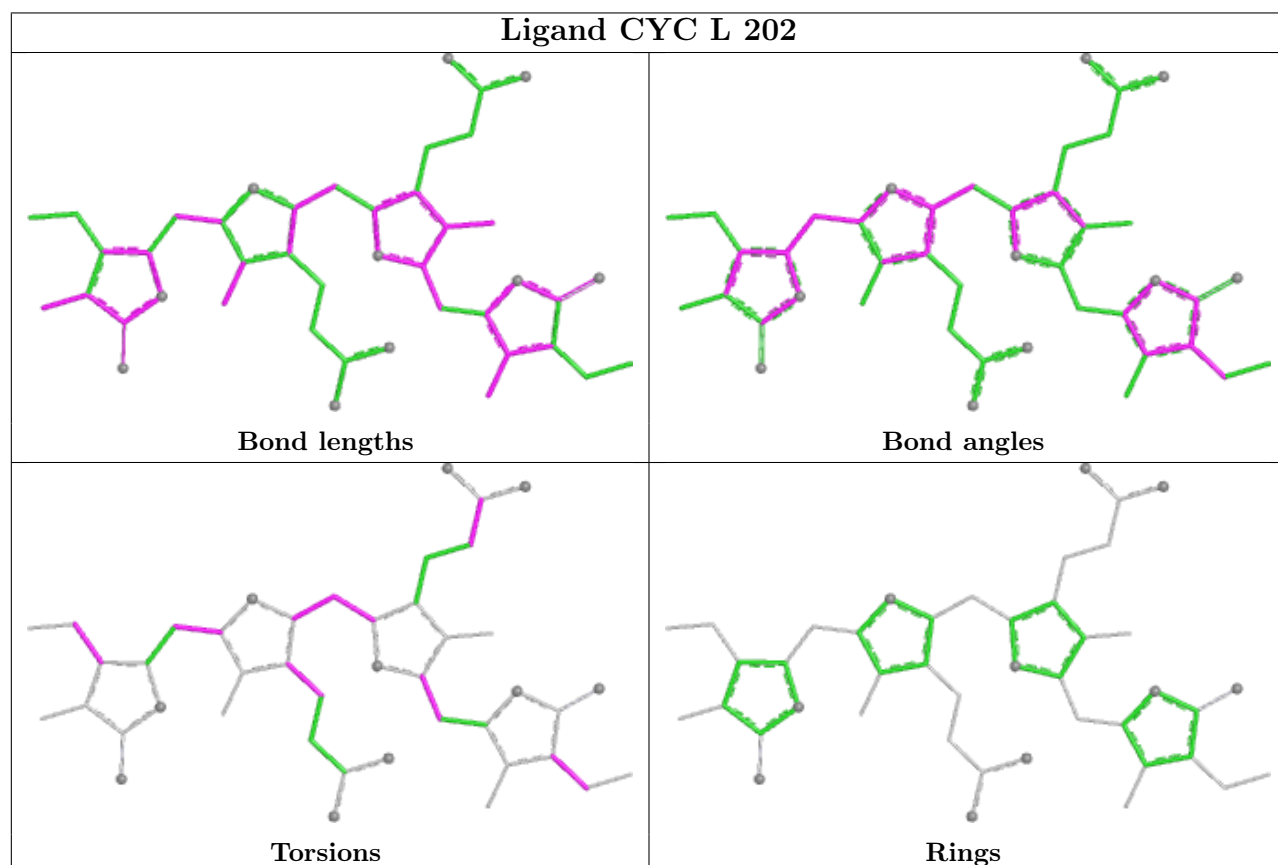
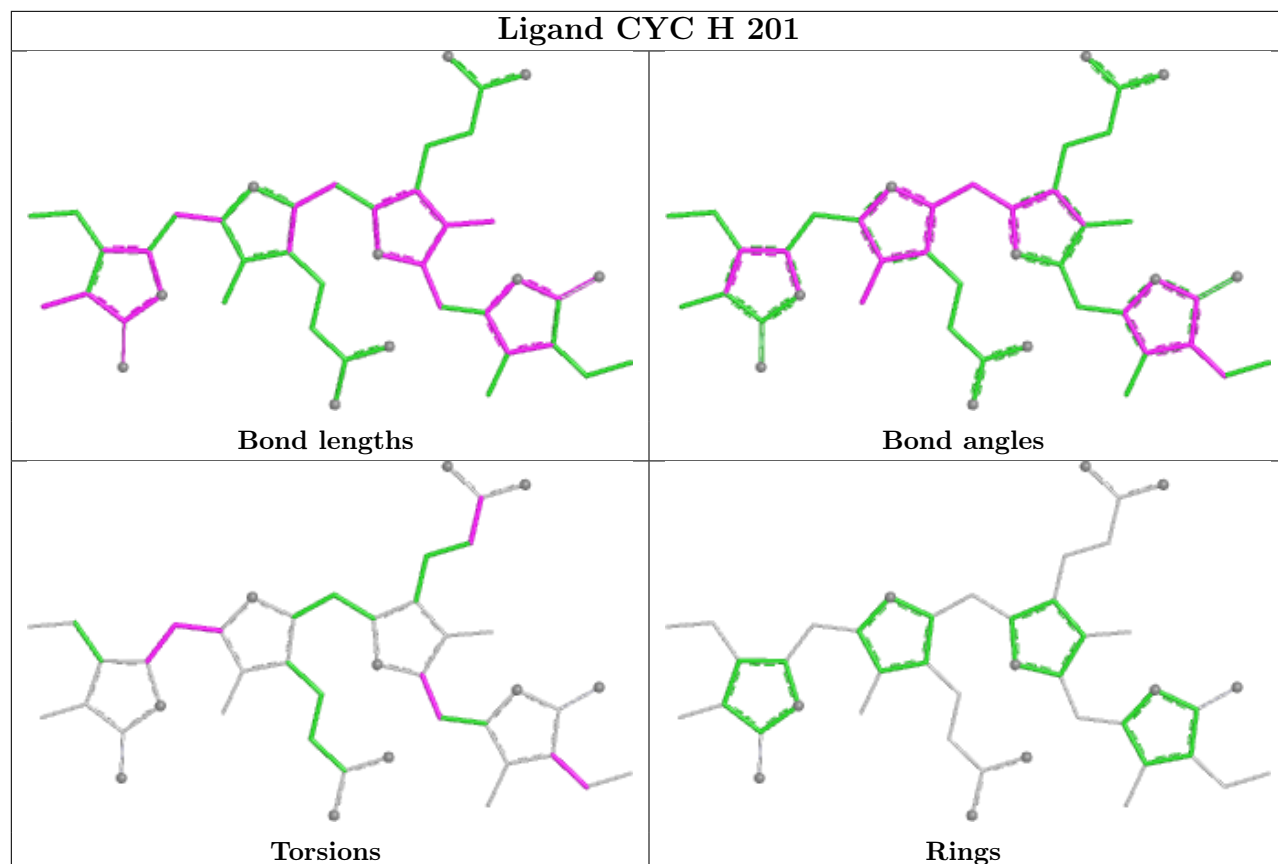
24 monomers are involved in 76 short contacts:

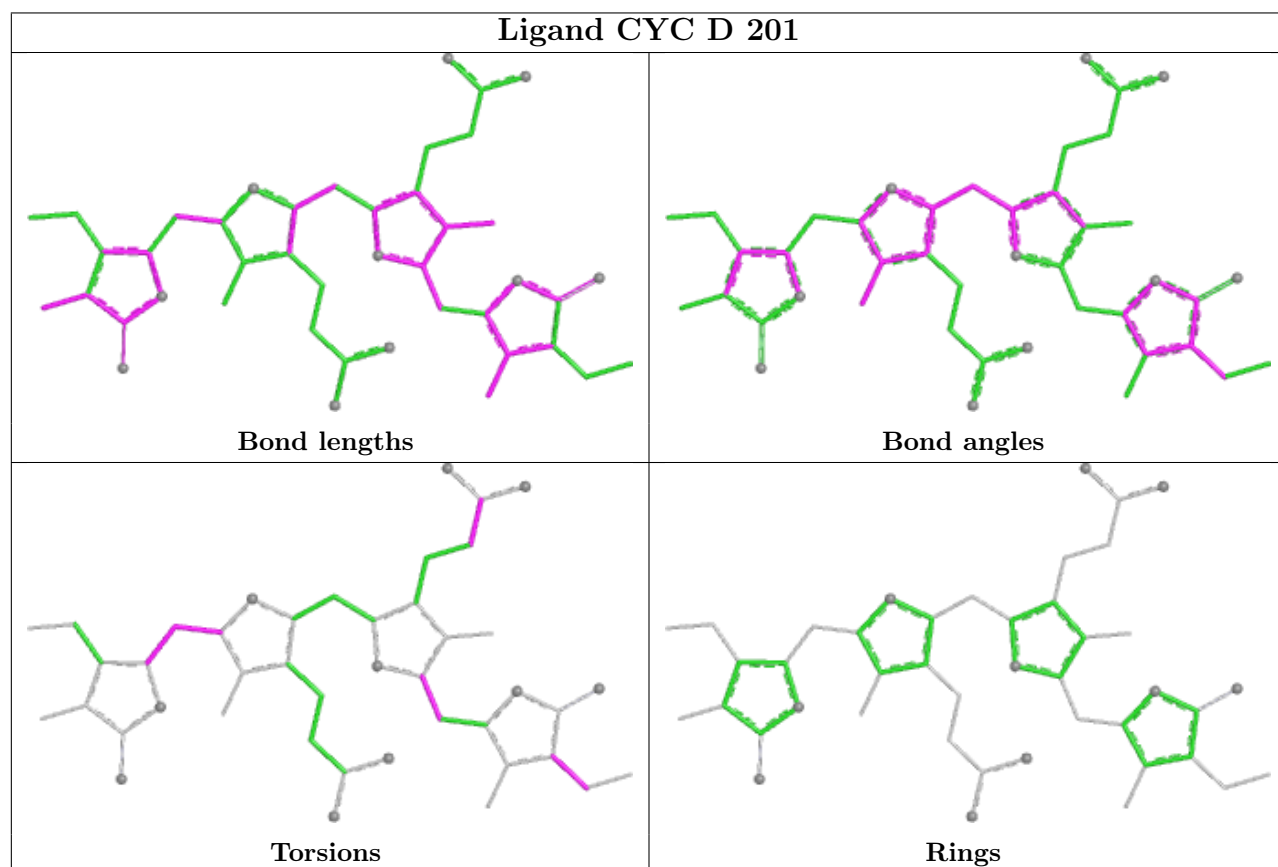
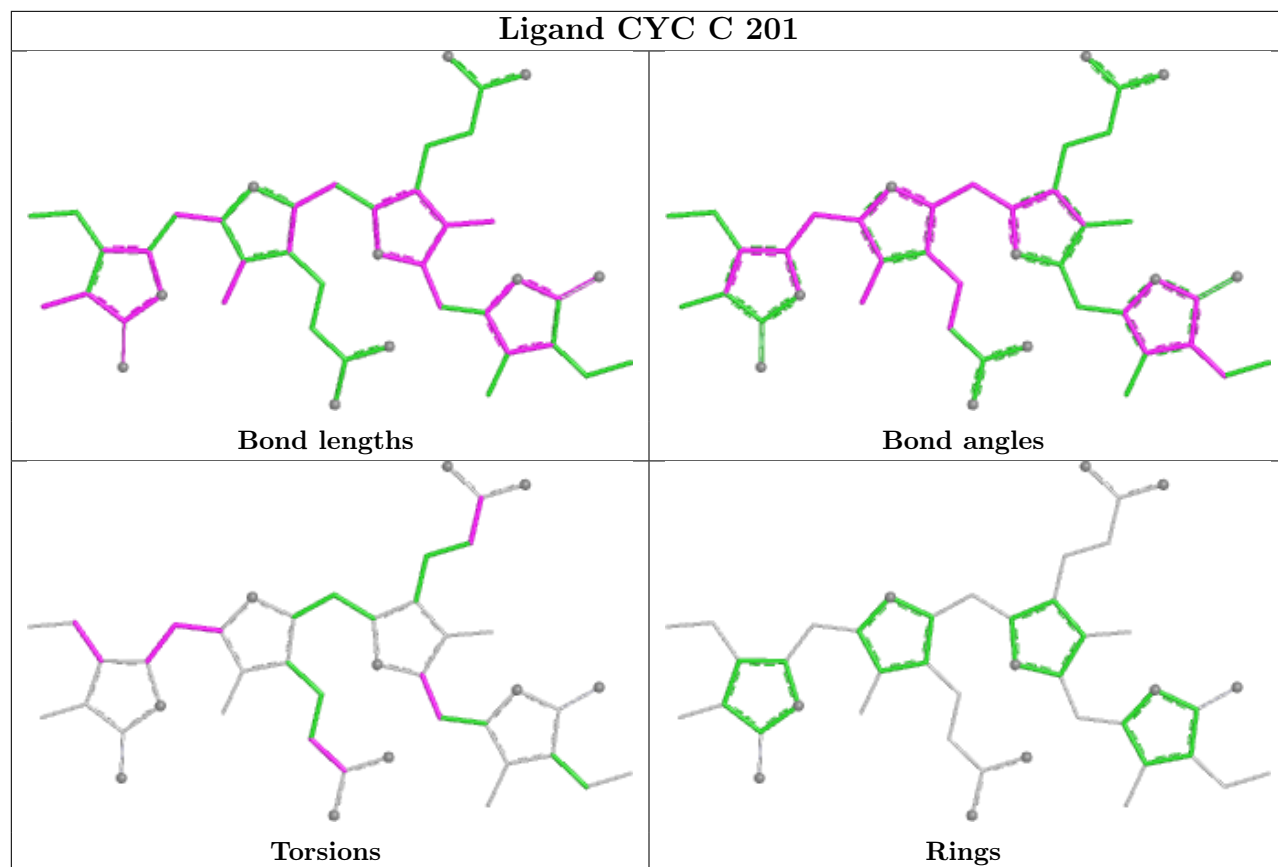
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	J	202	CYC	3	0
3	D	202	CYC	4	0
3	F	202	CYC	5	0
3	H	201	CYC	2	0
3	L	202	CYC	4	0
3	C	201	CYC	4	0
3	D	201	CYC	2	0
3	M	201	CYC	1	0
3	P	202	CYC	4	0
3	I	201	CYC	5	0
3	G	201	CYC	2	0
3	K	201	CYC	5	0
3	N	201	CYC	3	0
3	H	202	CYC	3	0
3	N	202	CYC	3	0
3	O	201	CYC	5	0
3	P	201	CYC	1	0
3	B	202	CYC	5	0
3	J	201	CYC	2	0
3	B	201	CYC	2	0
3	F	201	CYC	1	0
3	A	201	CYC	4	0
3	L	201	CYC	2	0
3	E	201	CYC	4	0

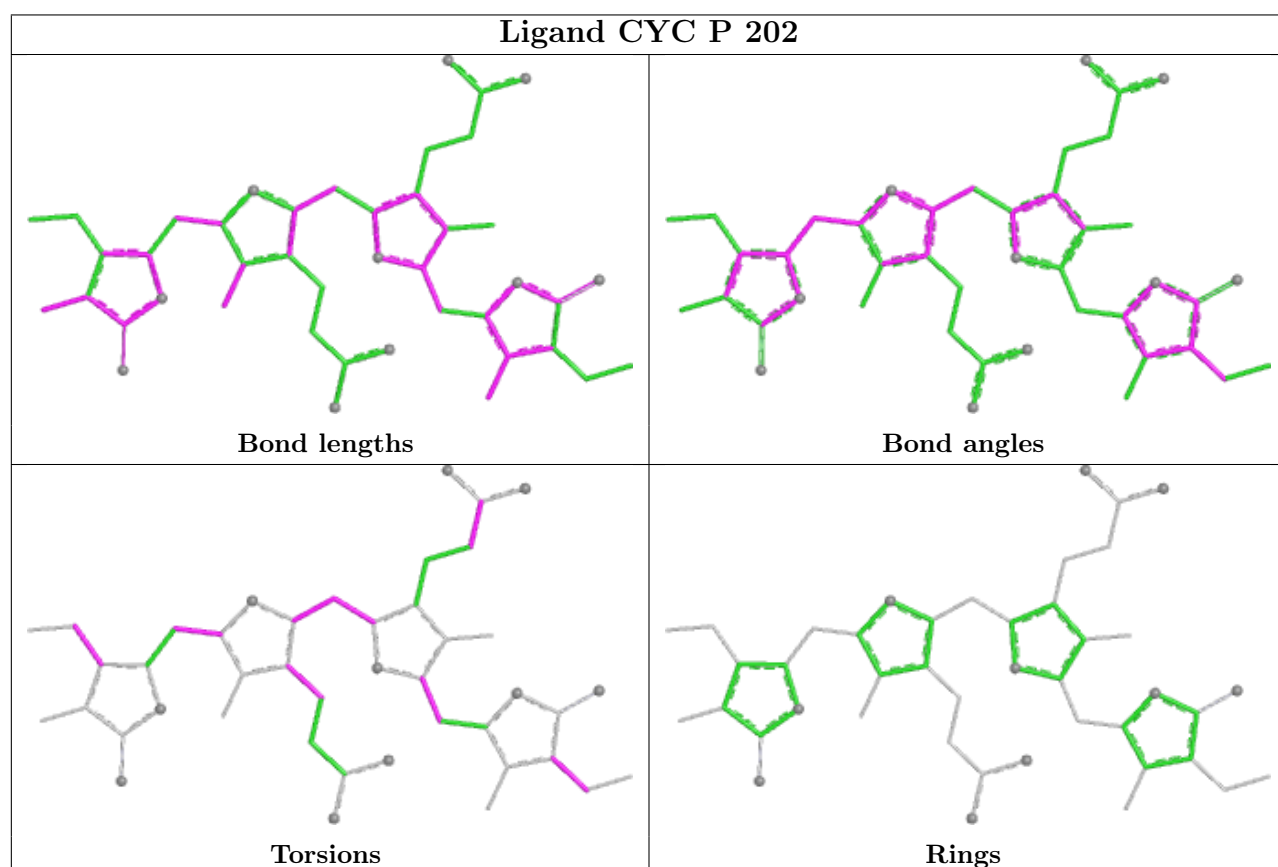
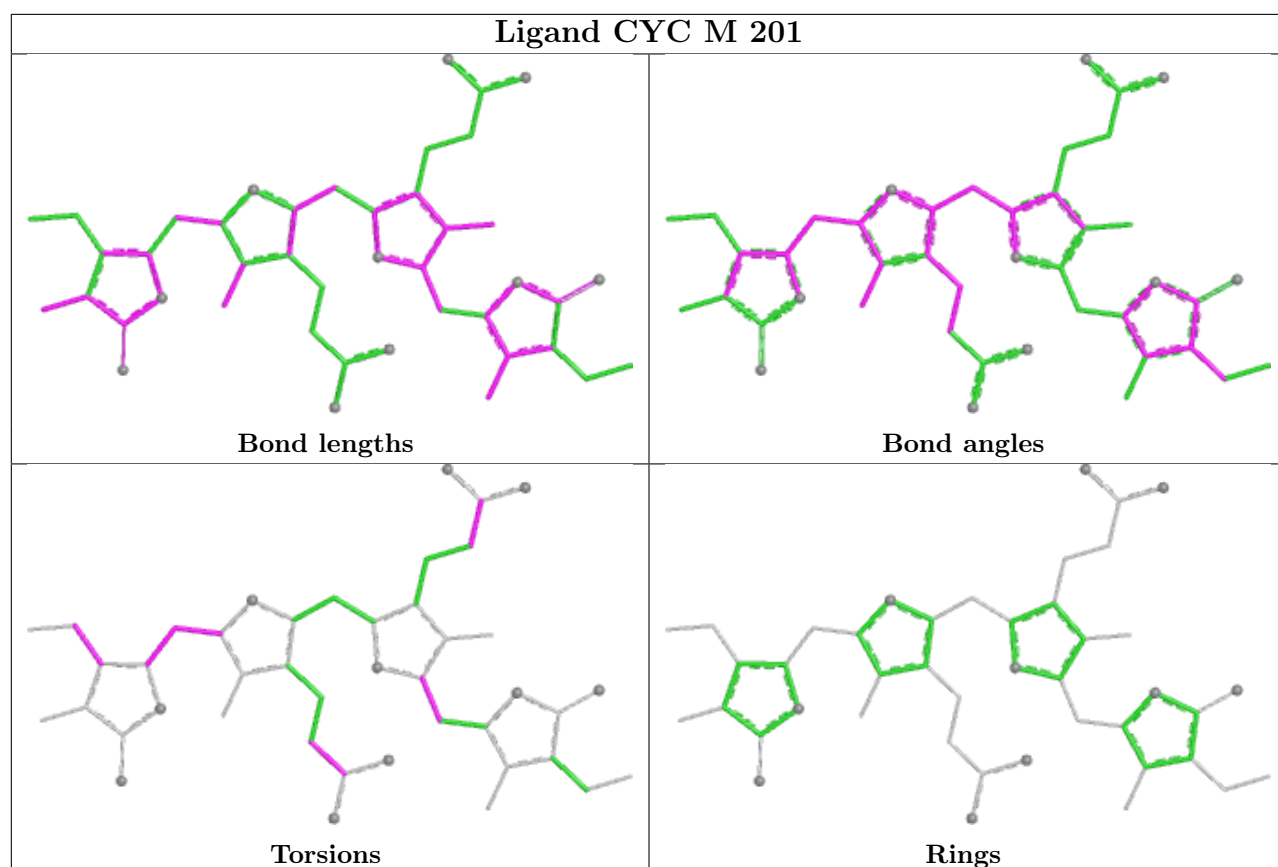
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



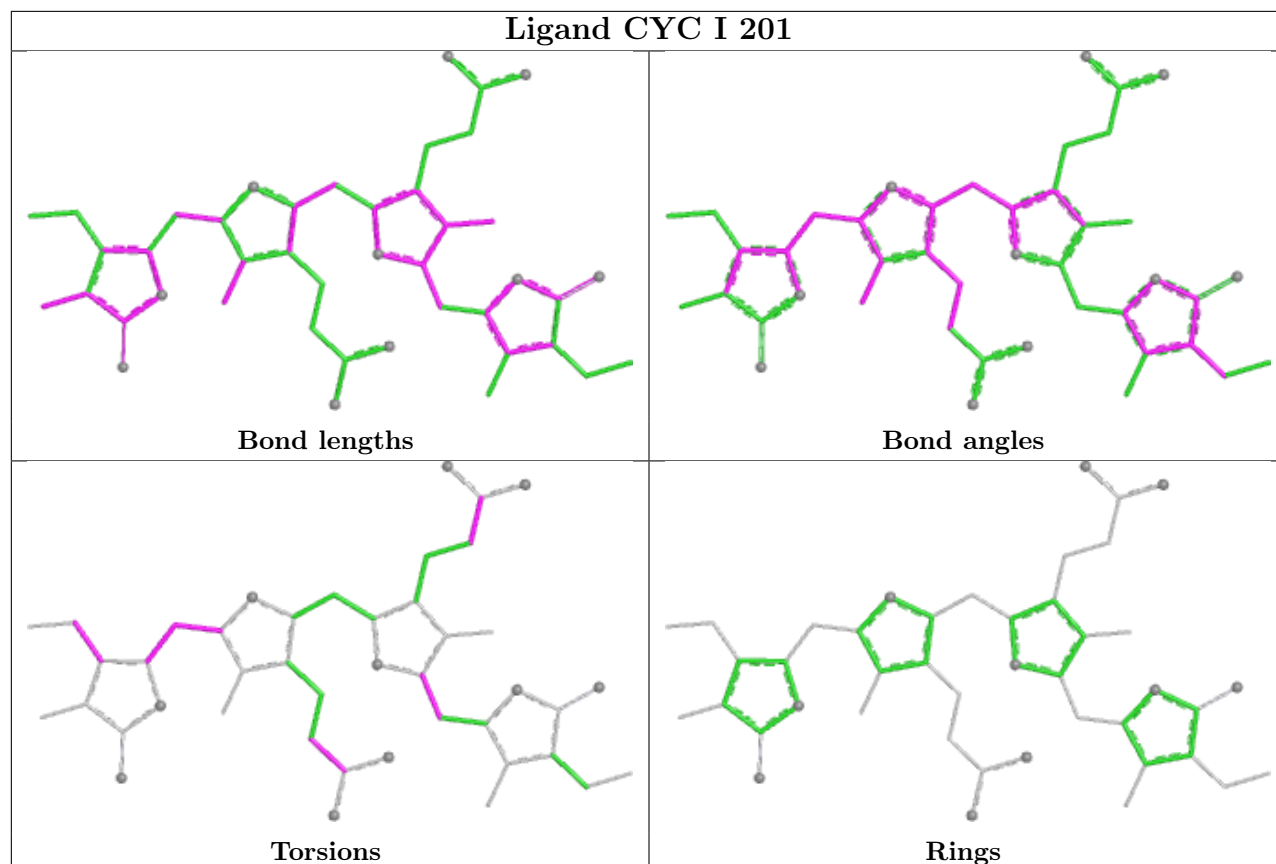




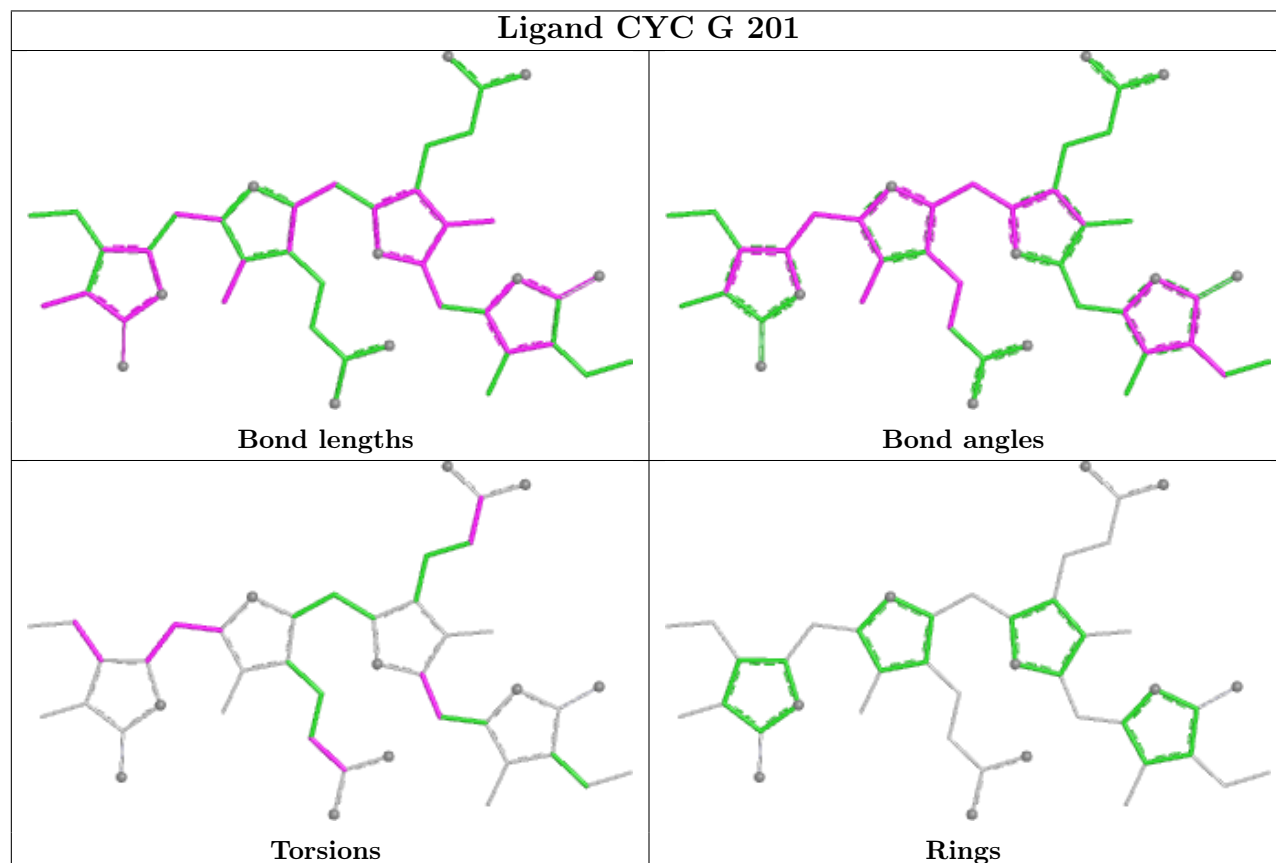


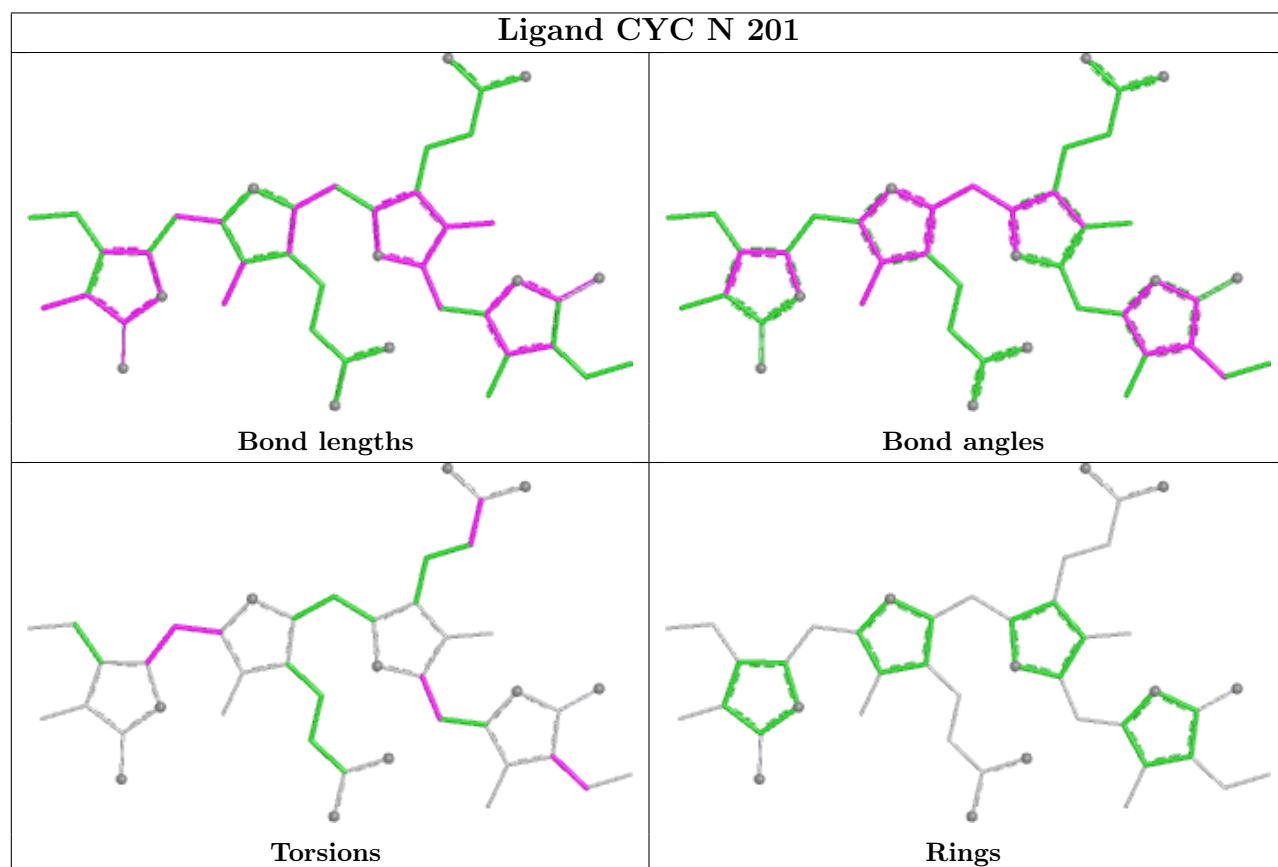
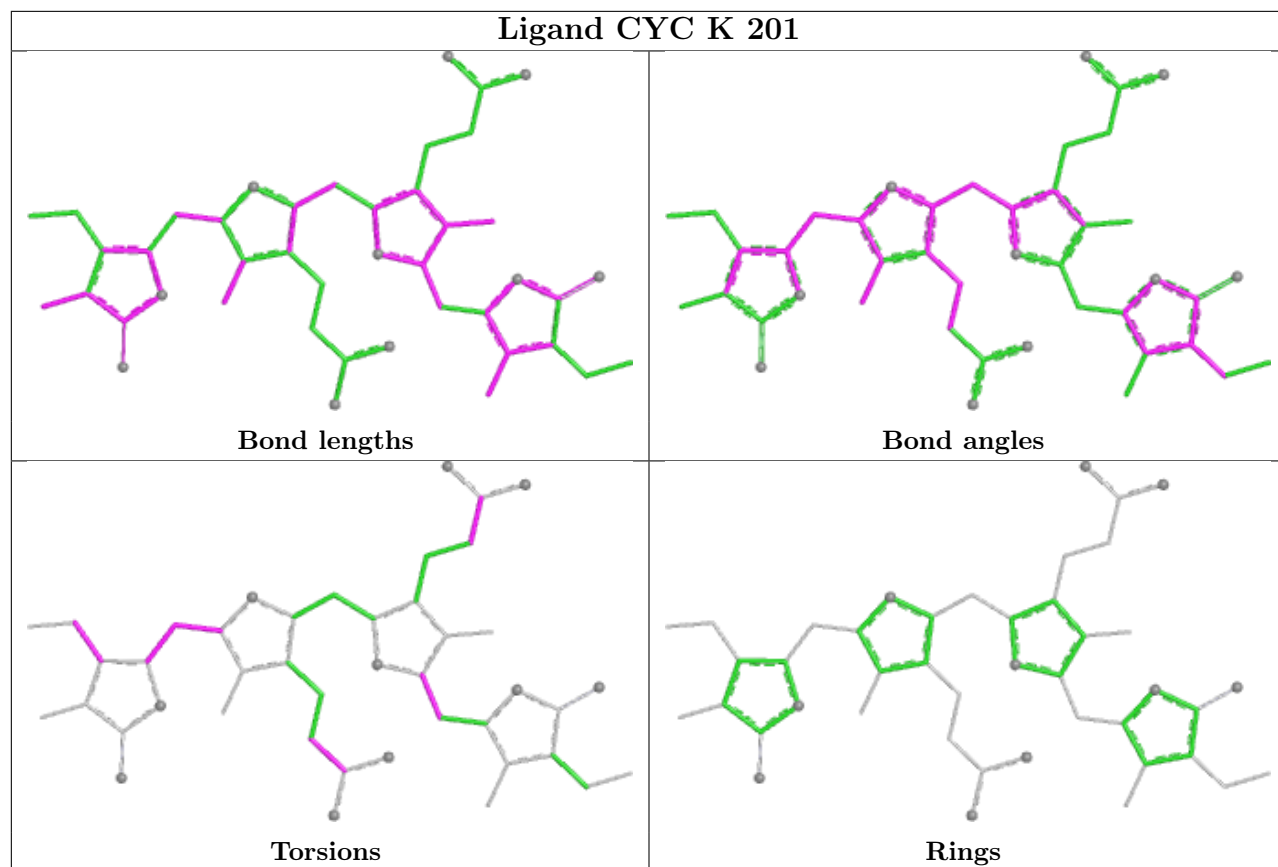


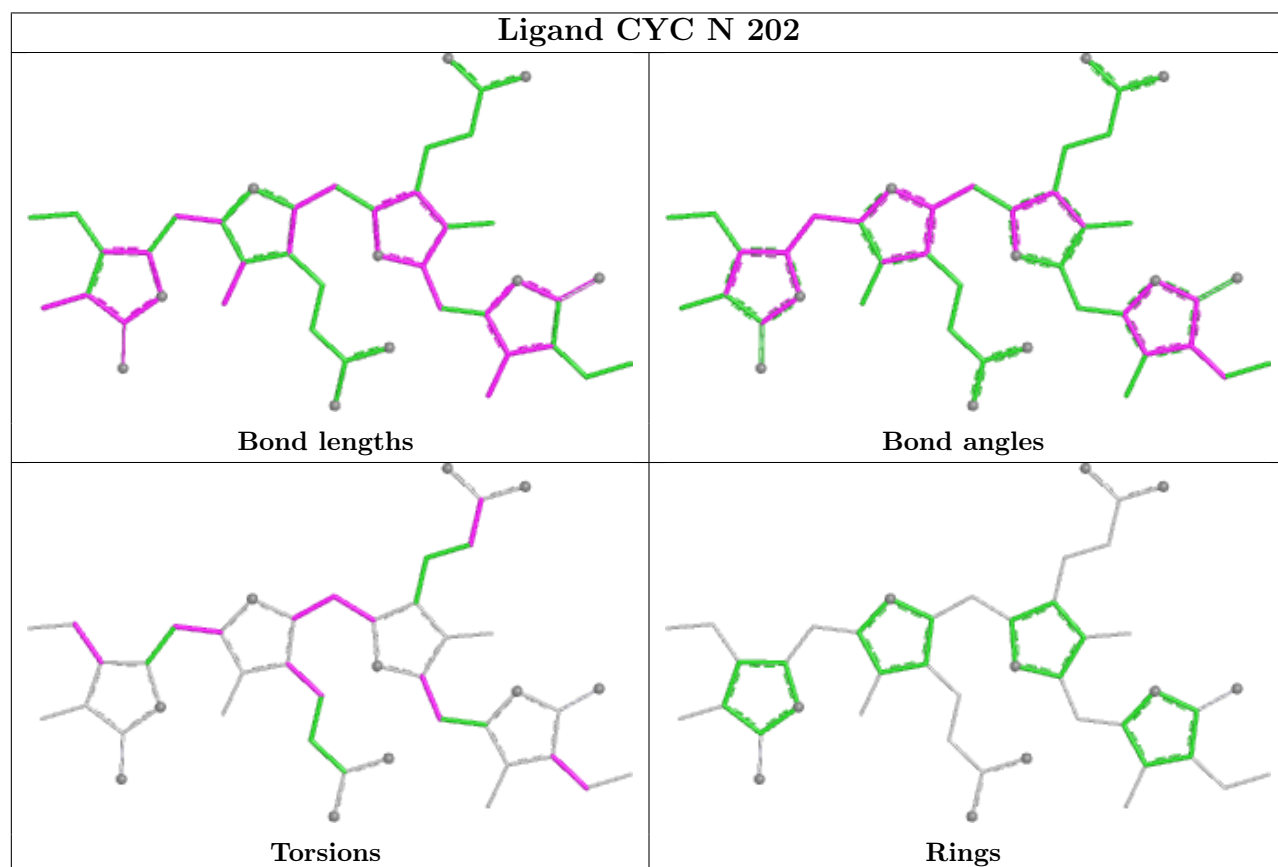
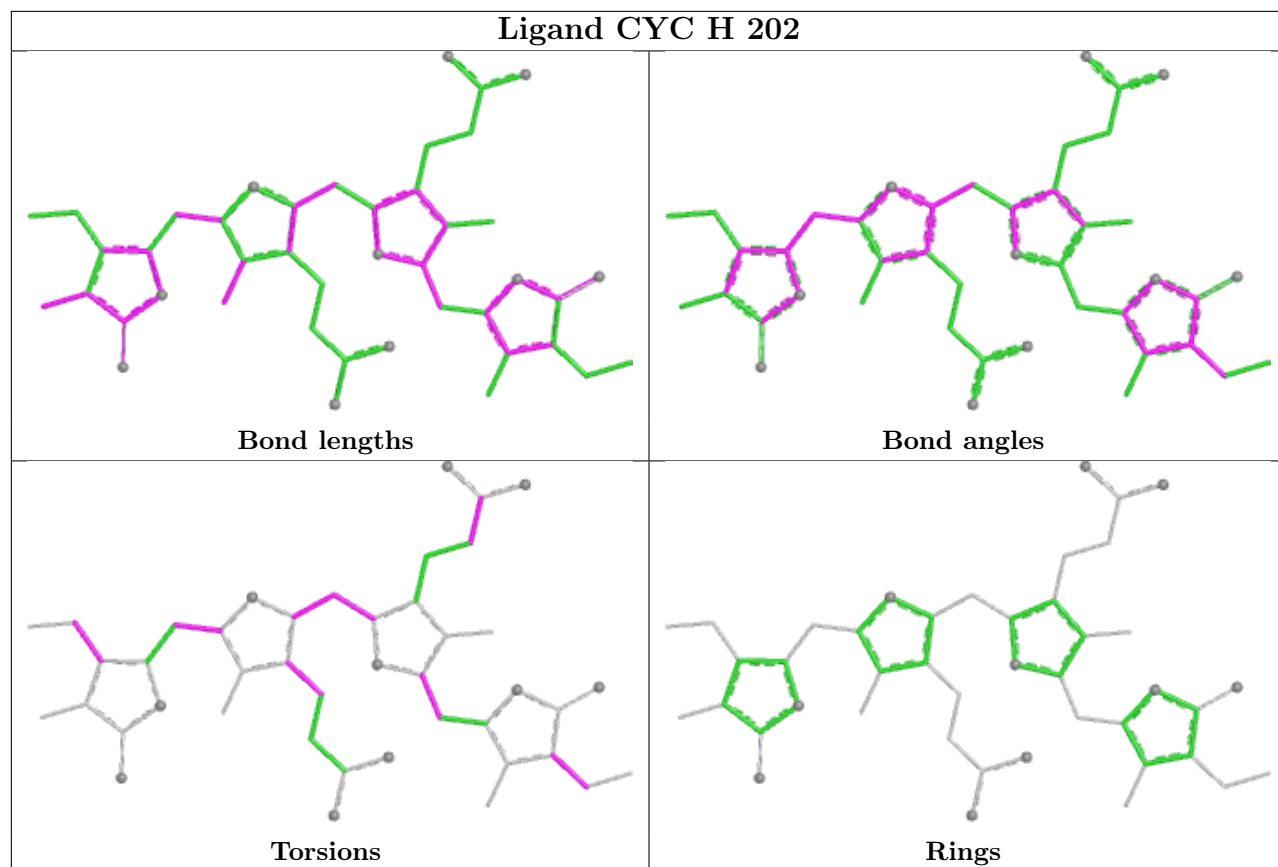
Ligand CYC I 201

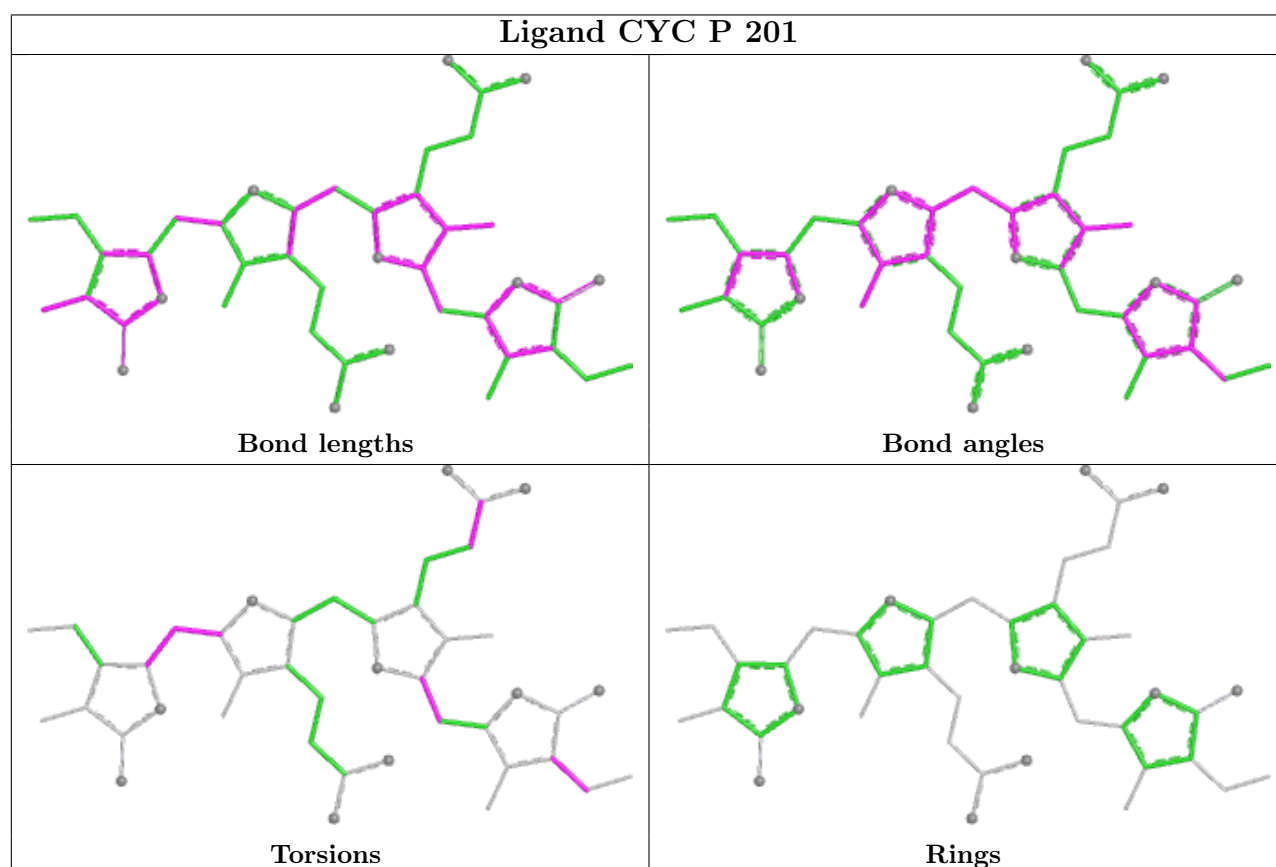
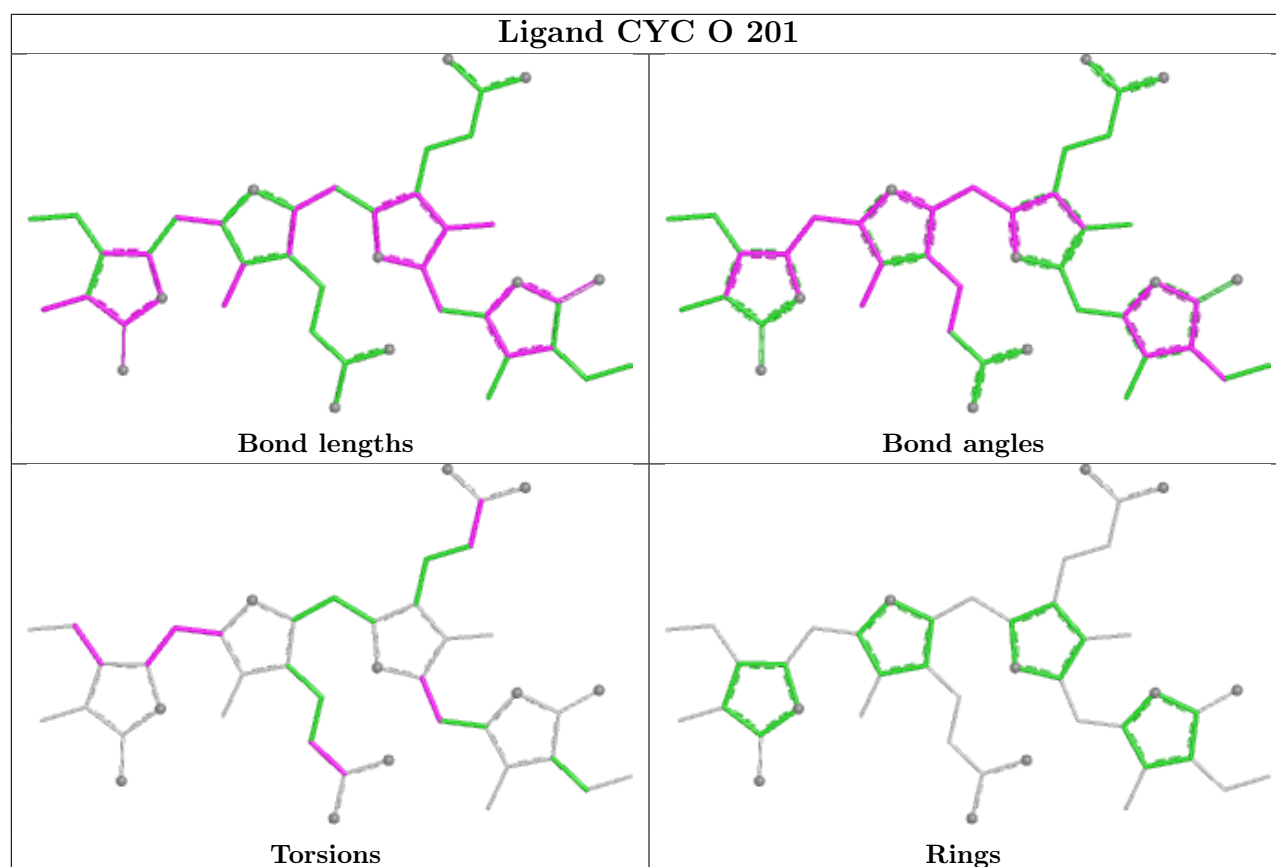


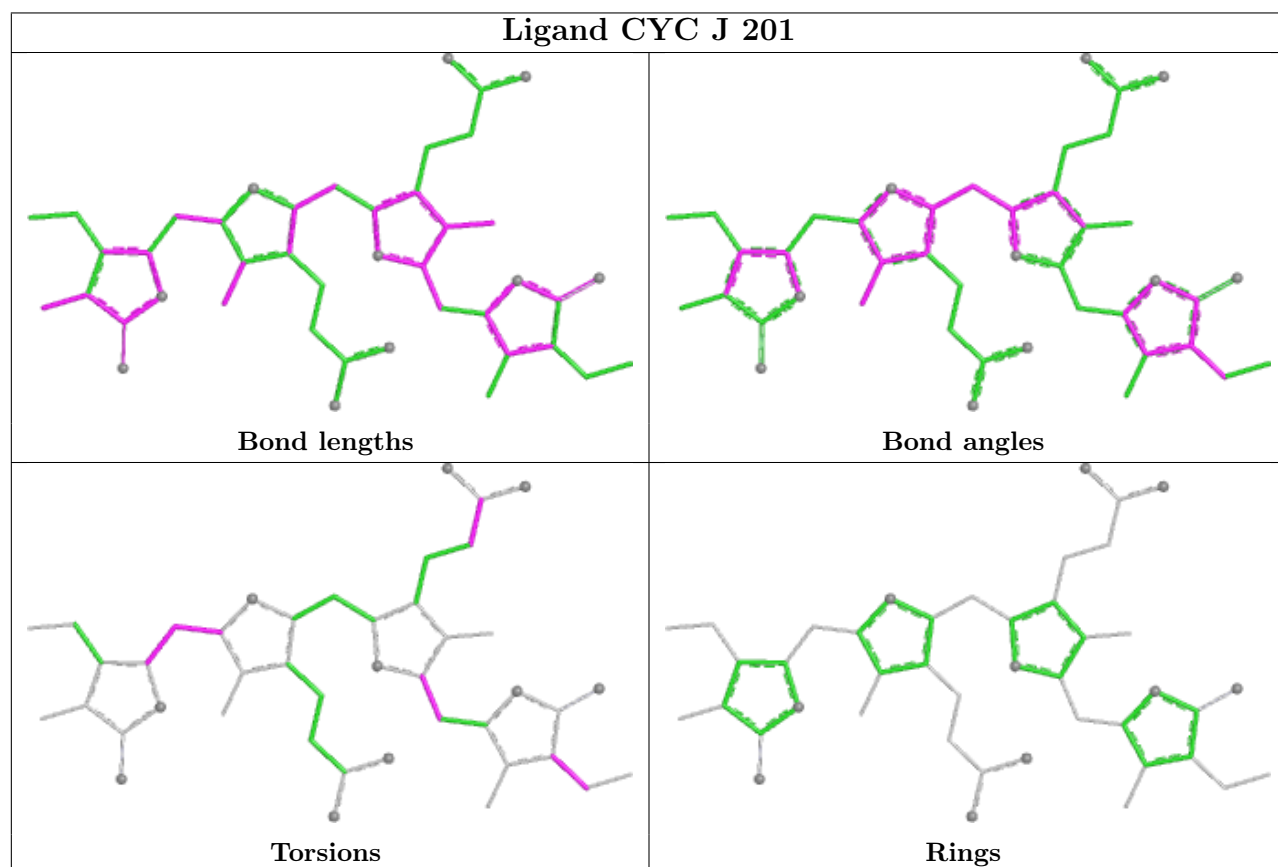
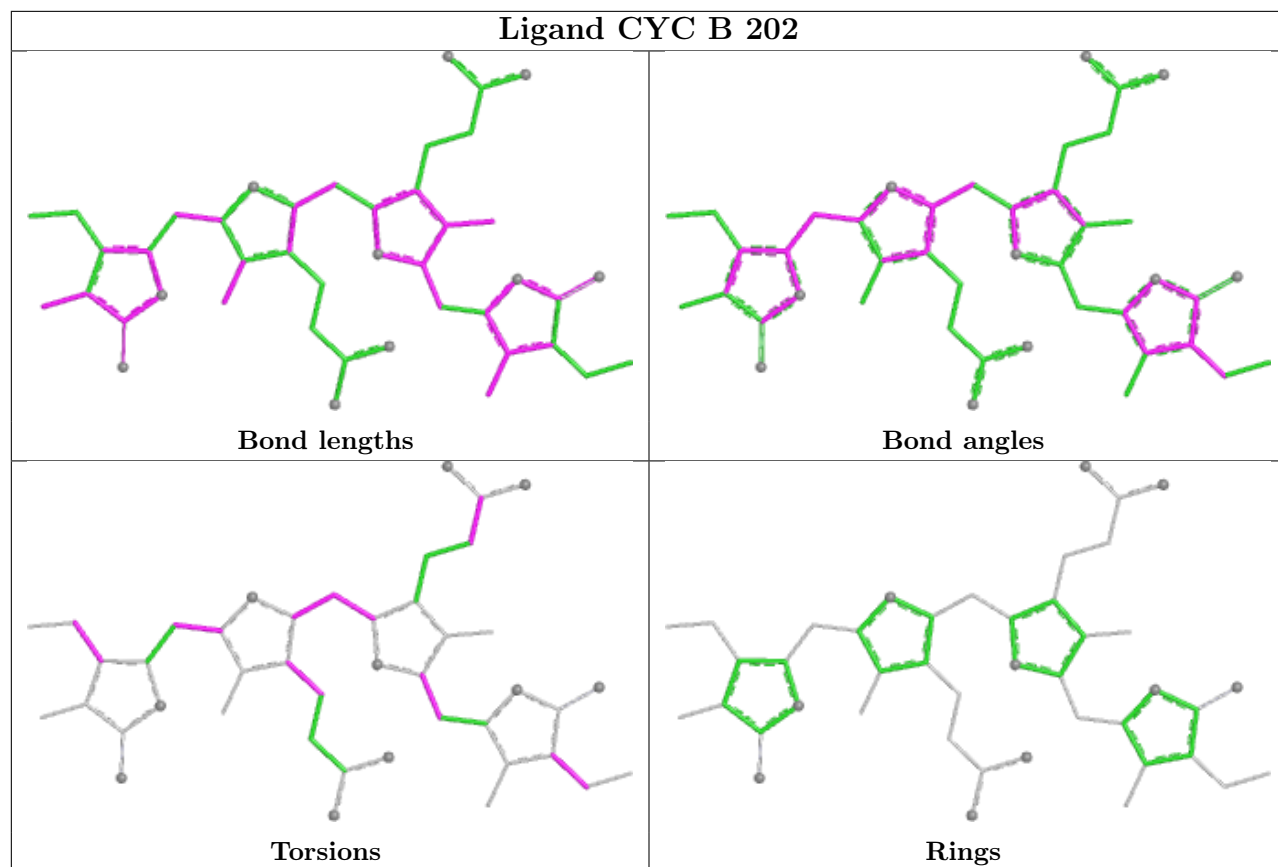
Ligand CYC G 201

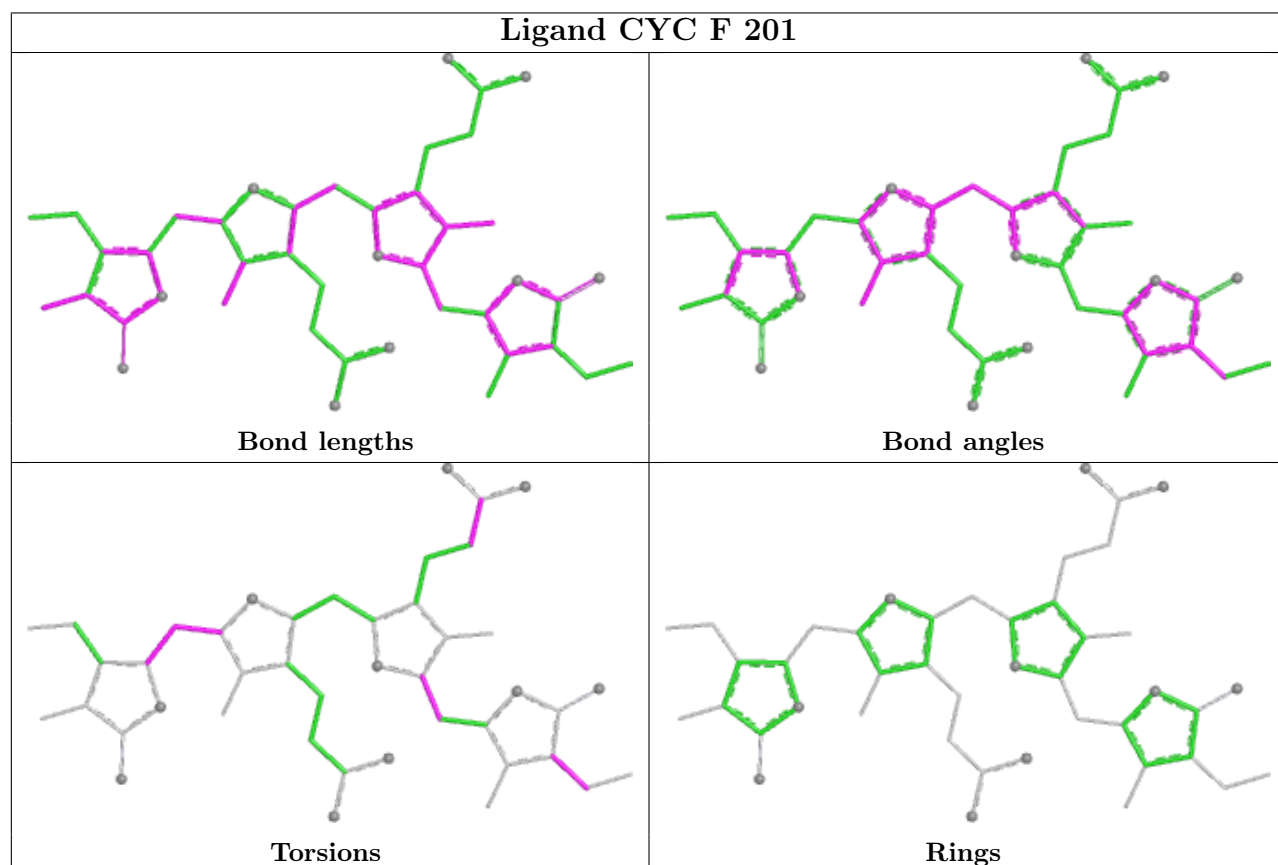
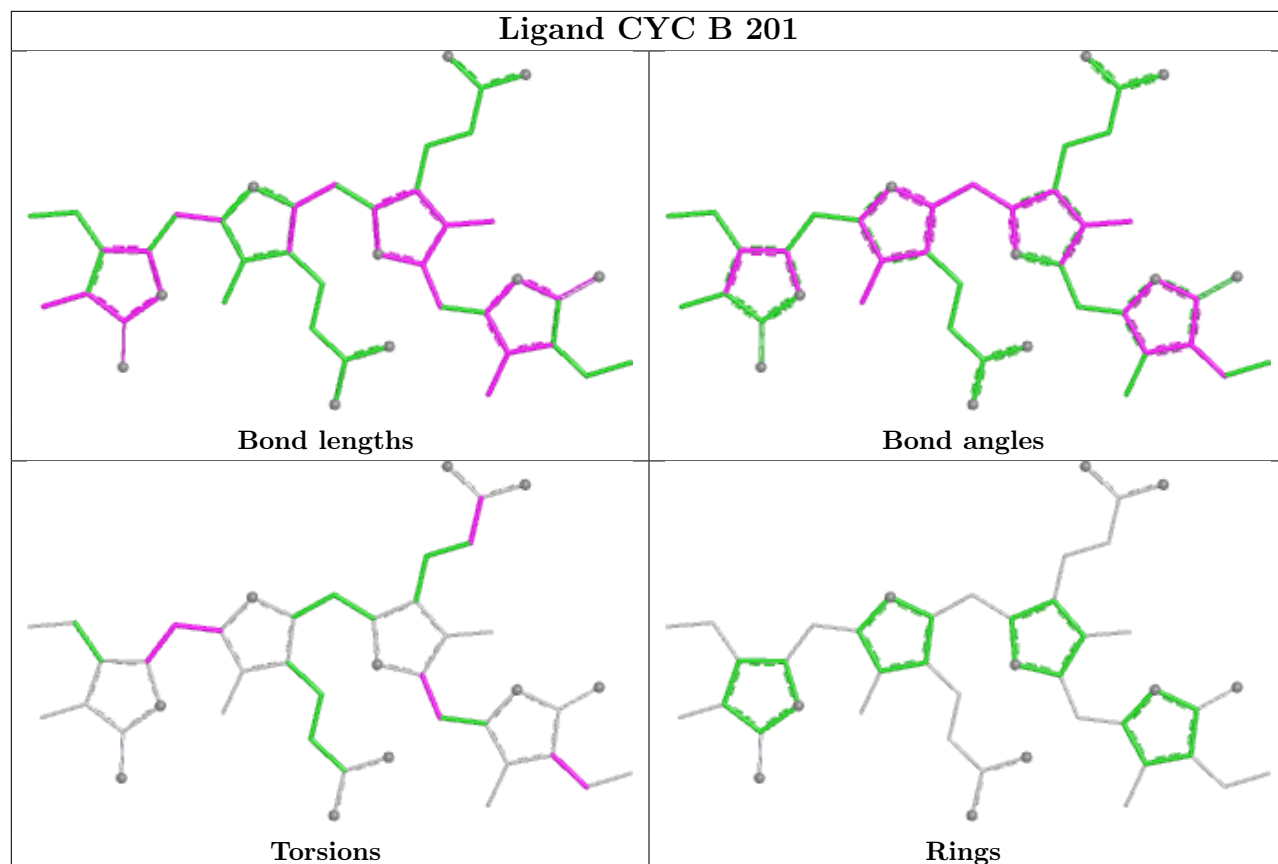


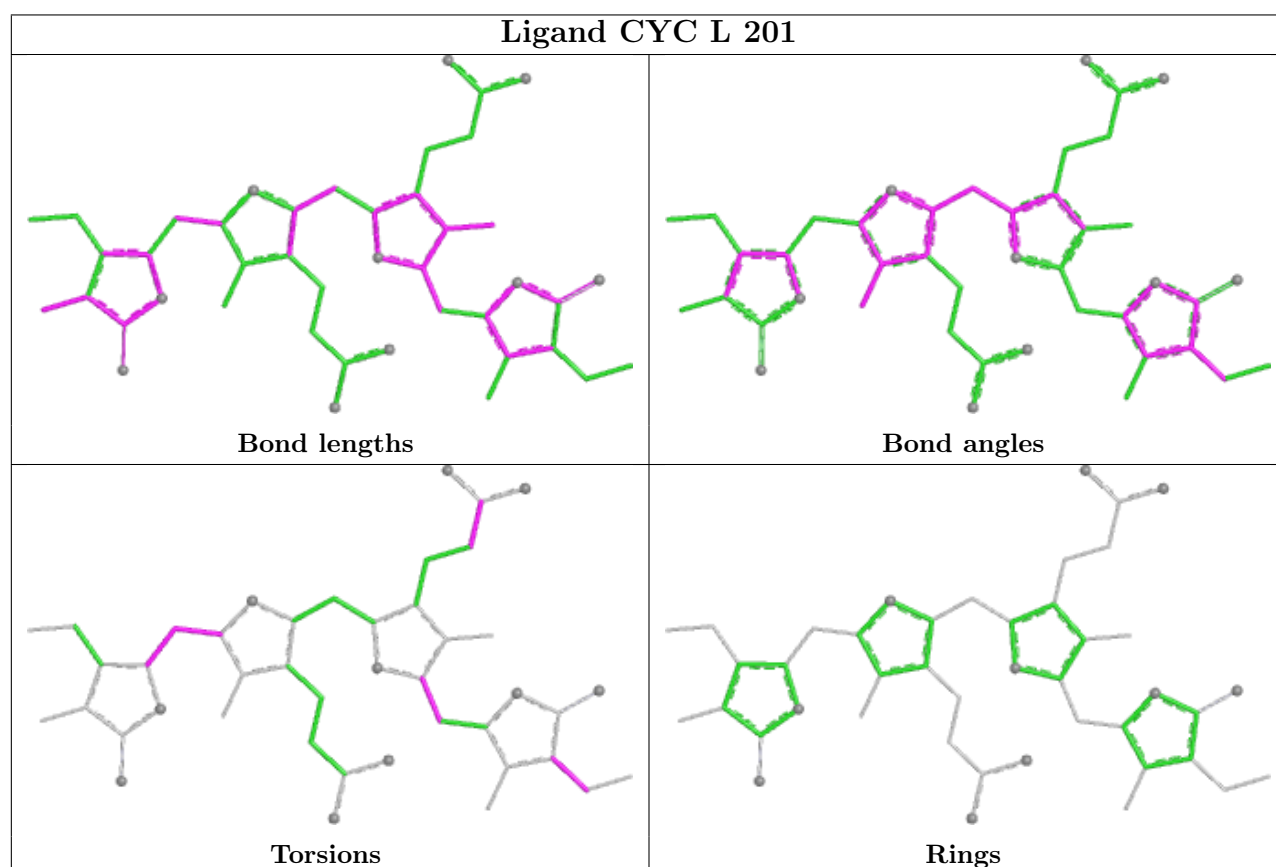
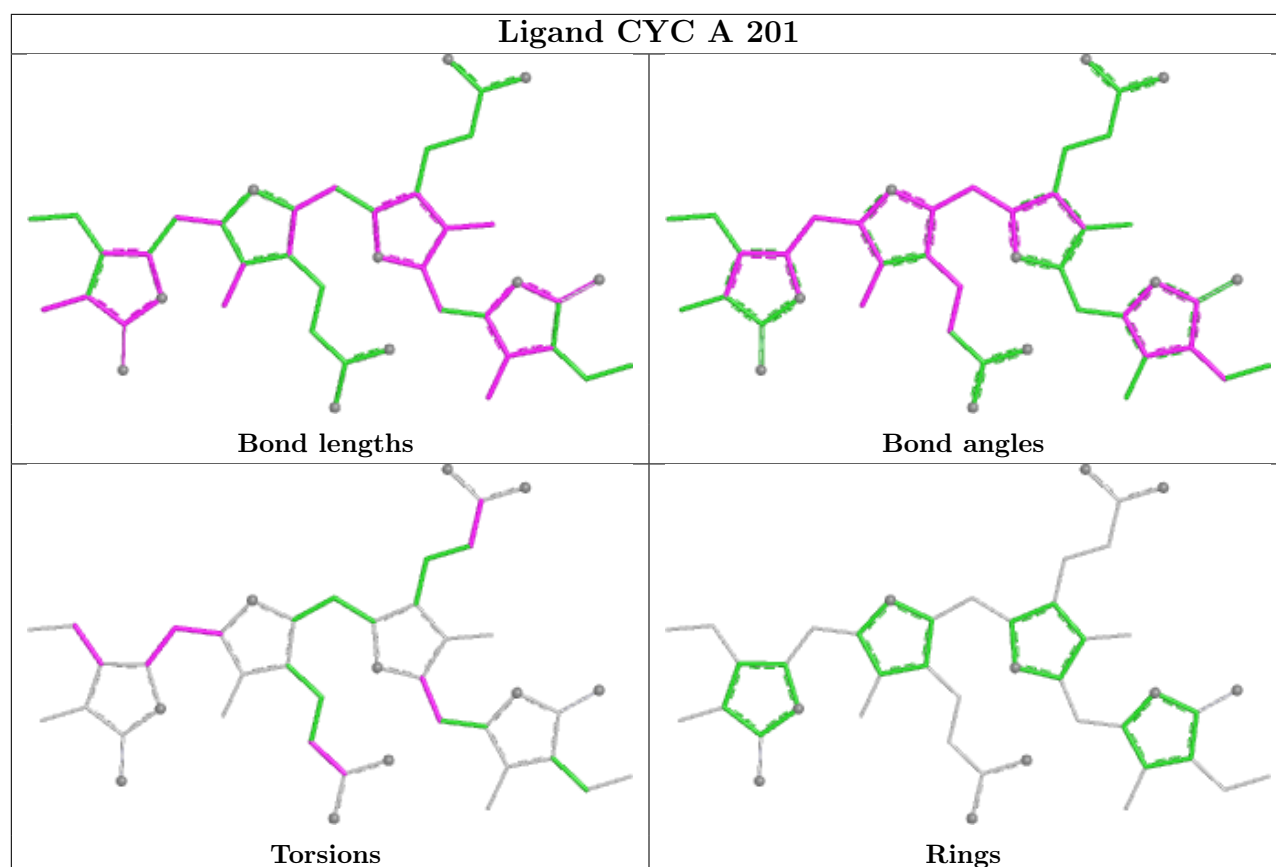


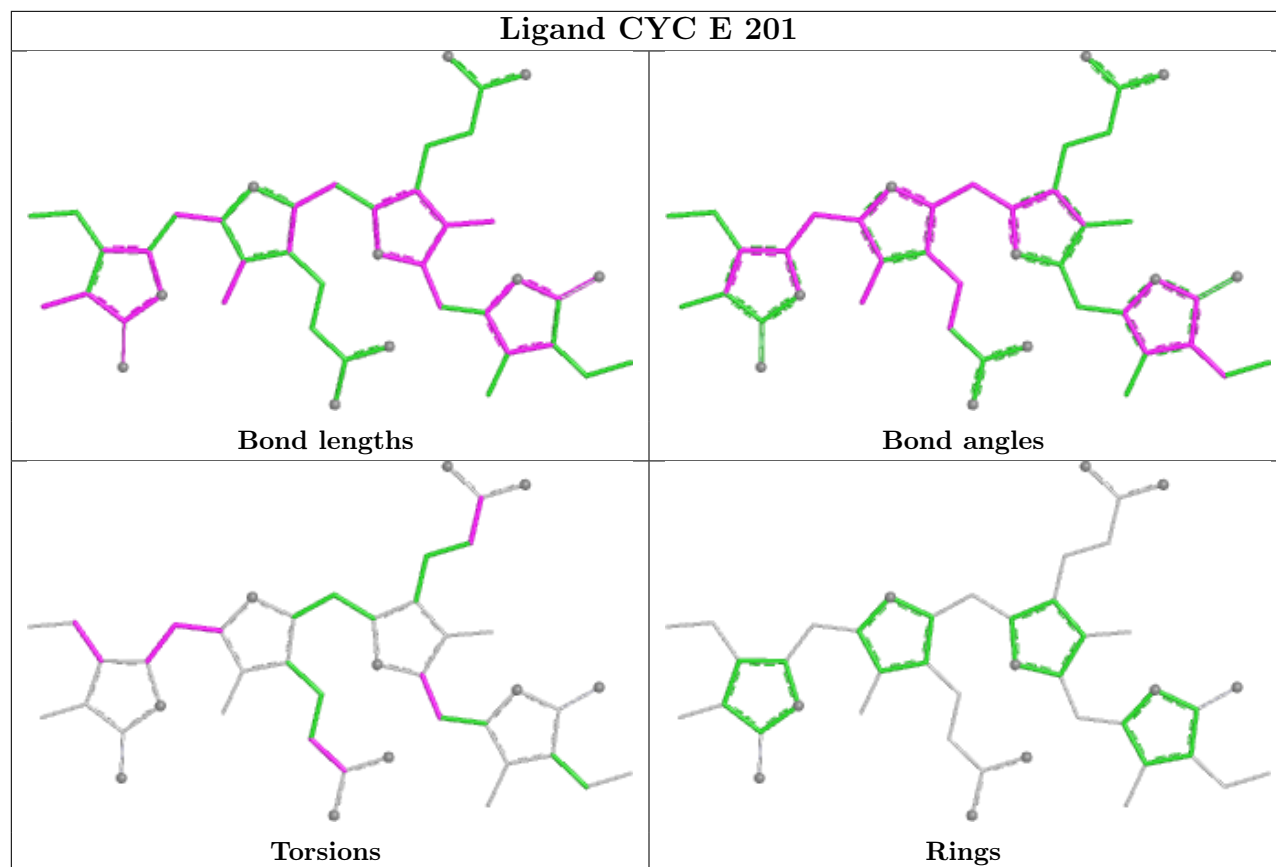












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

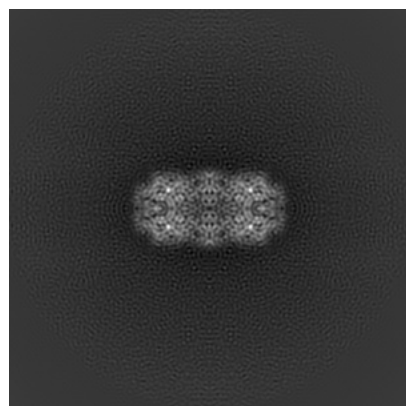
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31089. These allow visual inspection of the internal detail of the map and identification of artifacts.

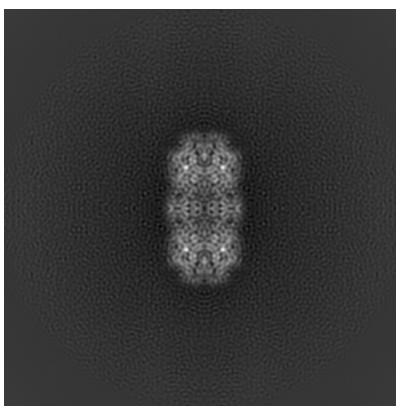
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

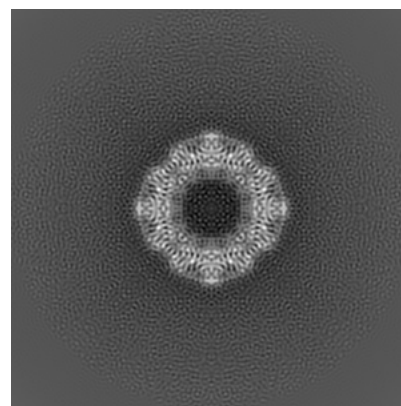
6.1.1 Primary map



X

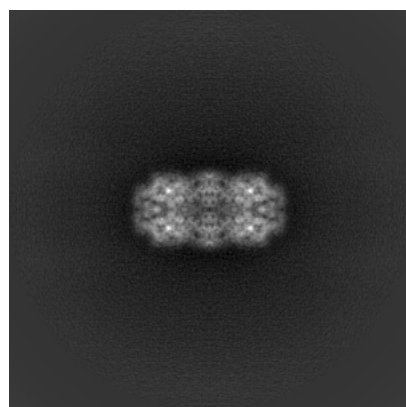


Y

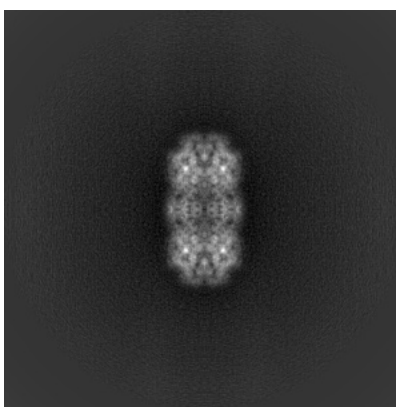


Z

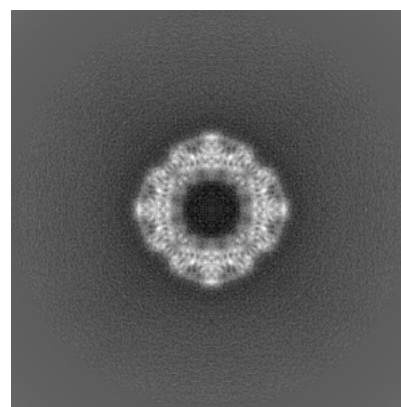
6.1.2 Raw map



X



Y

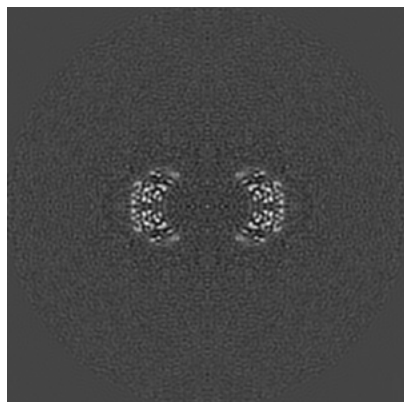


Z

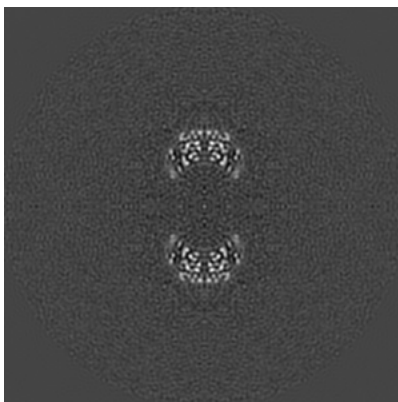
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

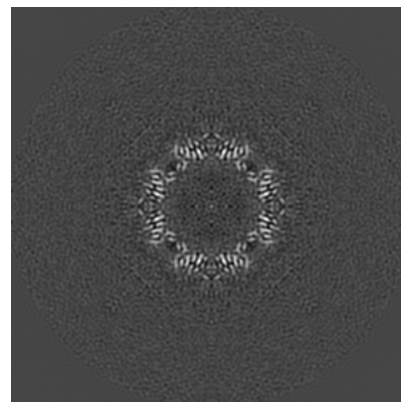
6.2.1 Primary map



X Index: 200

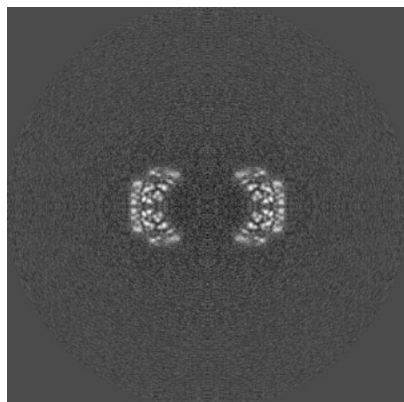


Y Index: 200

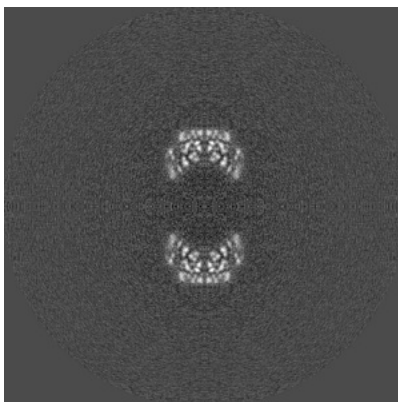


Z Index: 200

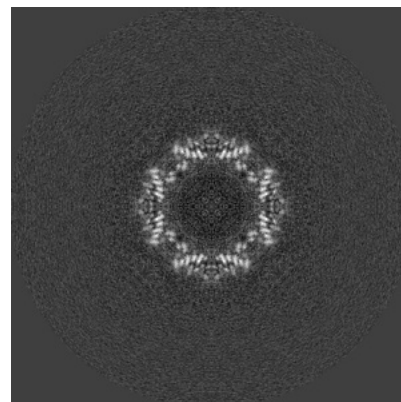
6.2.2 Raw map



X Index: 200



Y Index: 200

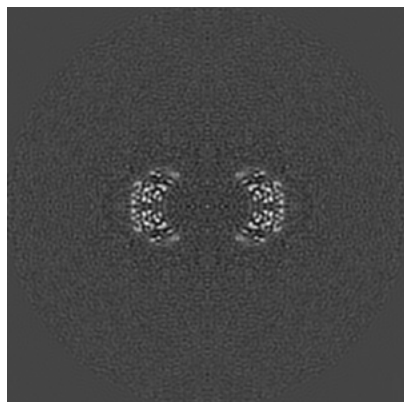


Z Index: 200

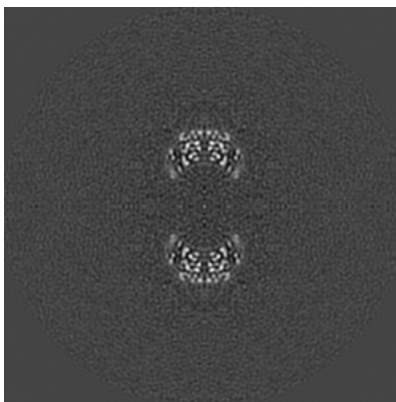
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

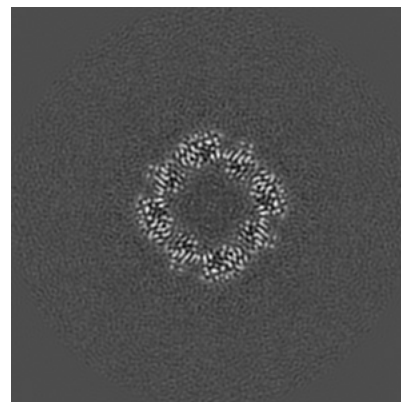
6.3.1 Primary map



X Index: 200

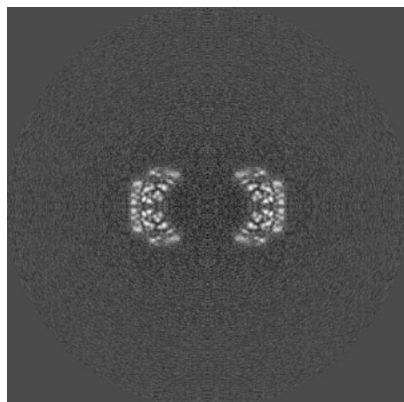


Y Index: 200

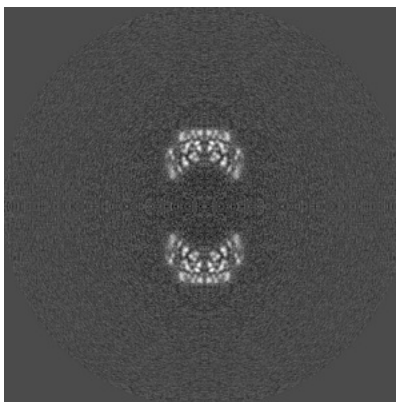


Z Index: 187

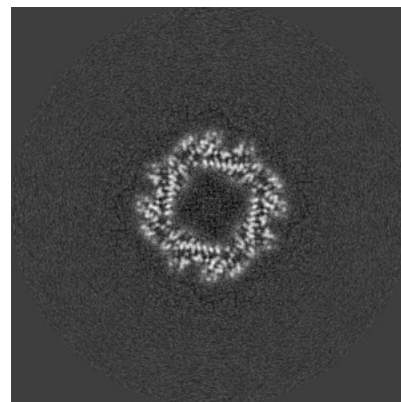
6.3.2 Raw map



X Index: 200



Y Index: 200

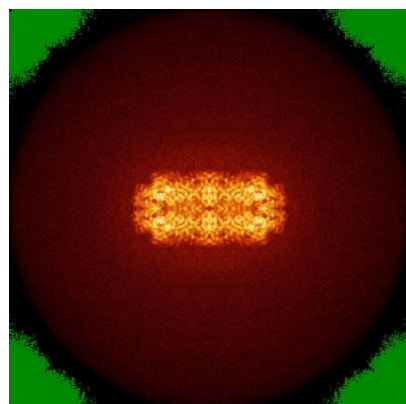


Z Index: 182

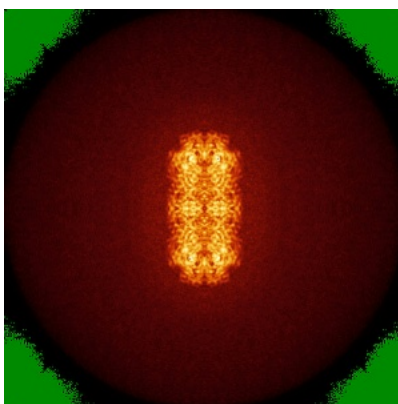
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

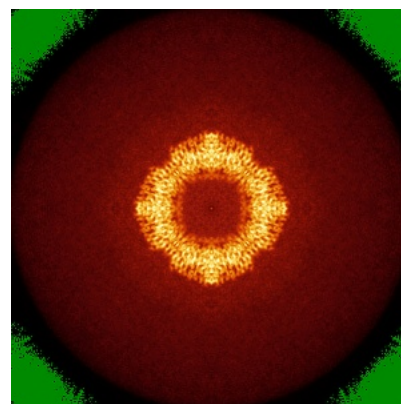
6.4.1 Primary map



X

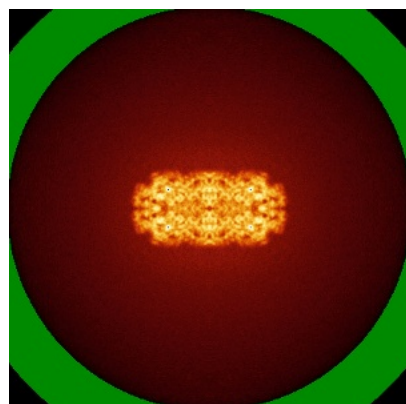


Y

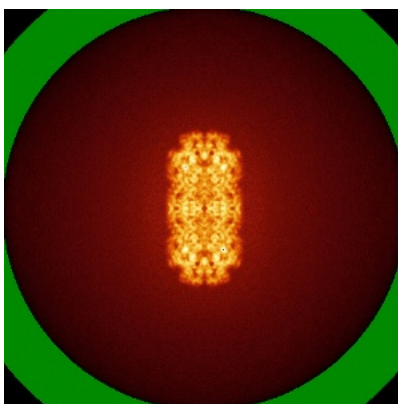


Z

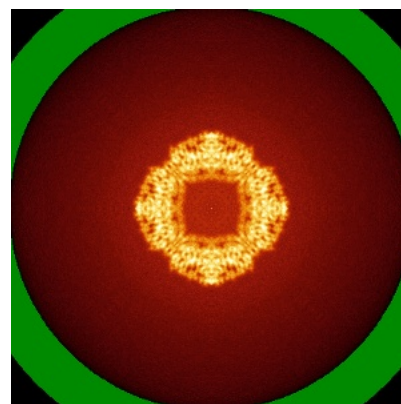
6.4.2 Raw map



X



Y

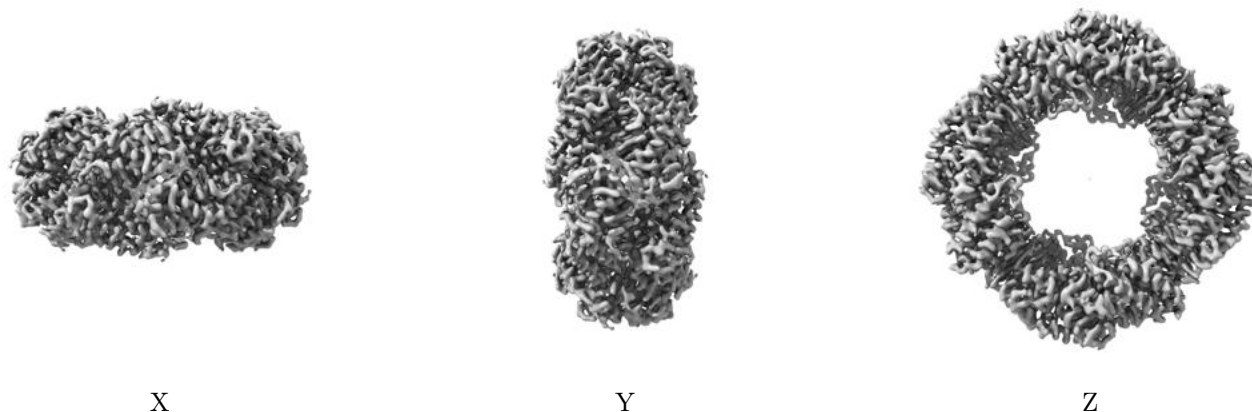


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

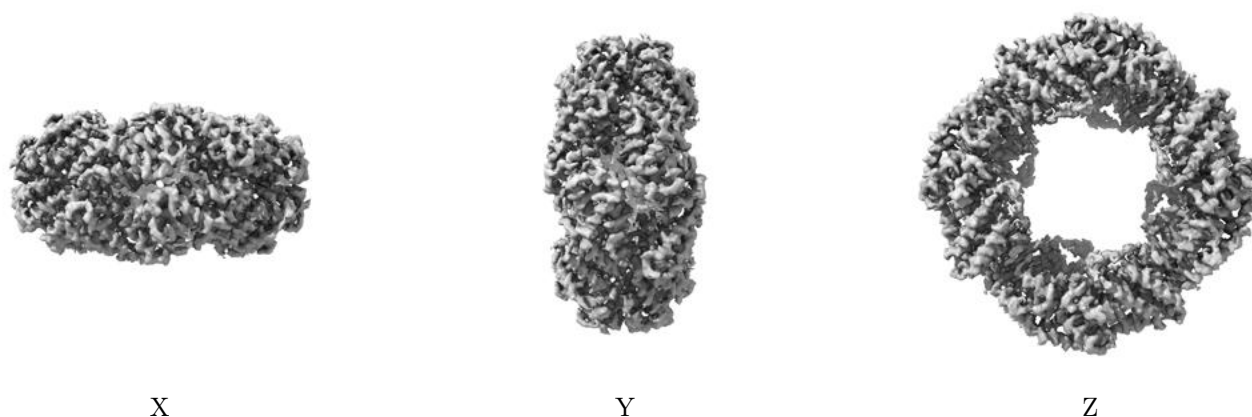
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.041. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

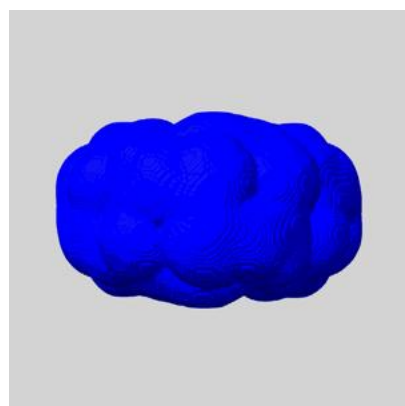
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

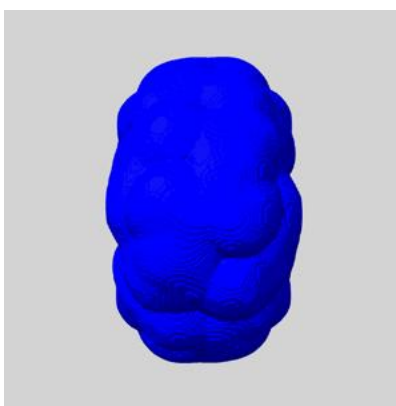
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

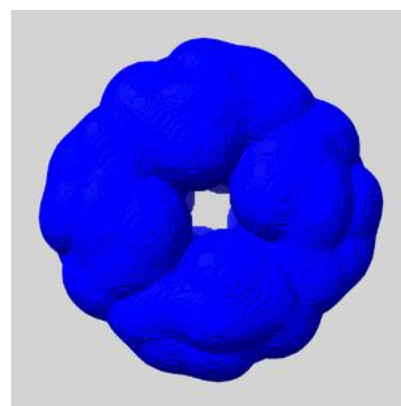
6.6.1 emd_31089_msk_1.map [i](#)



X



Y

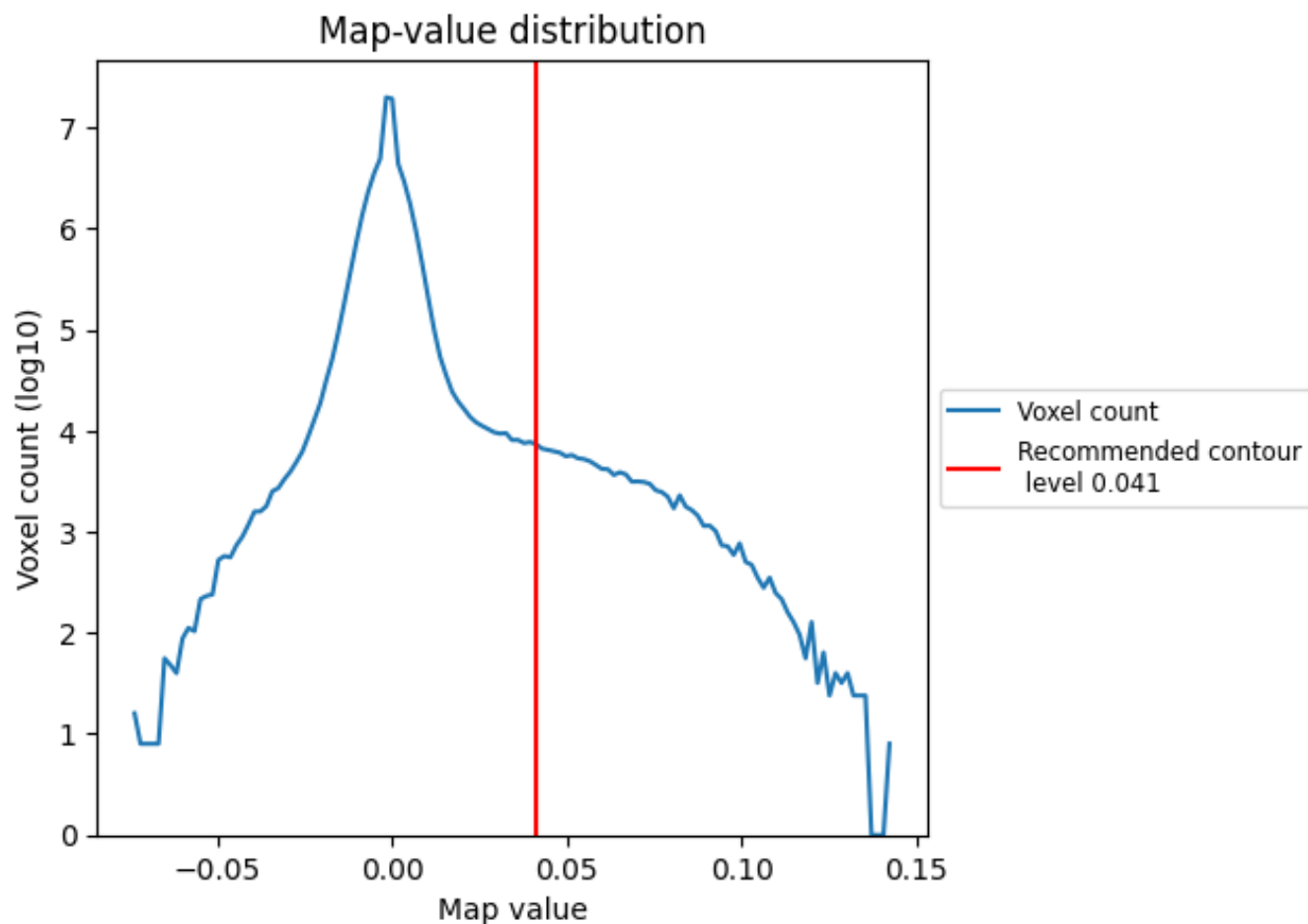


Z

7 Map analysis [i](#)

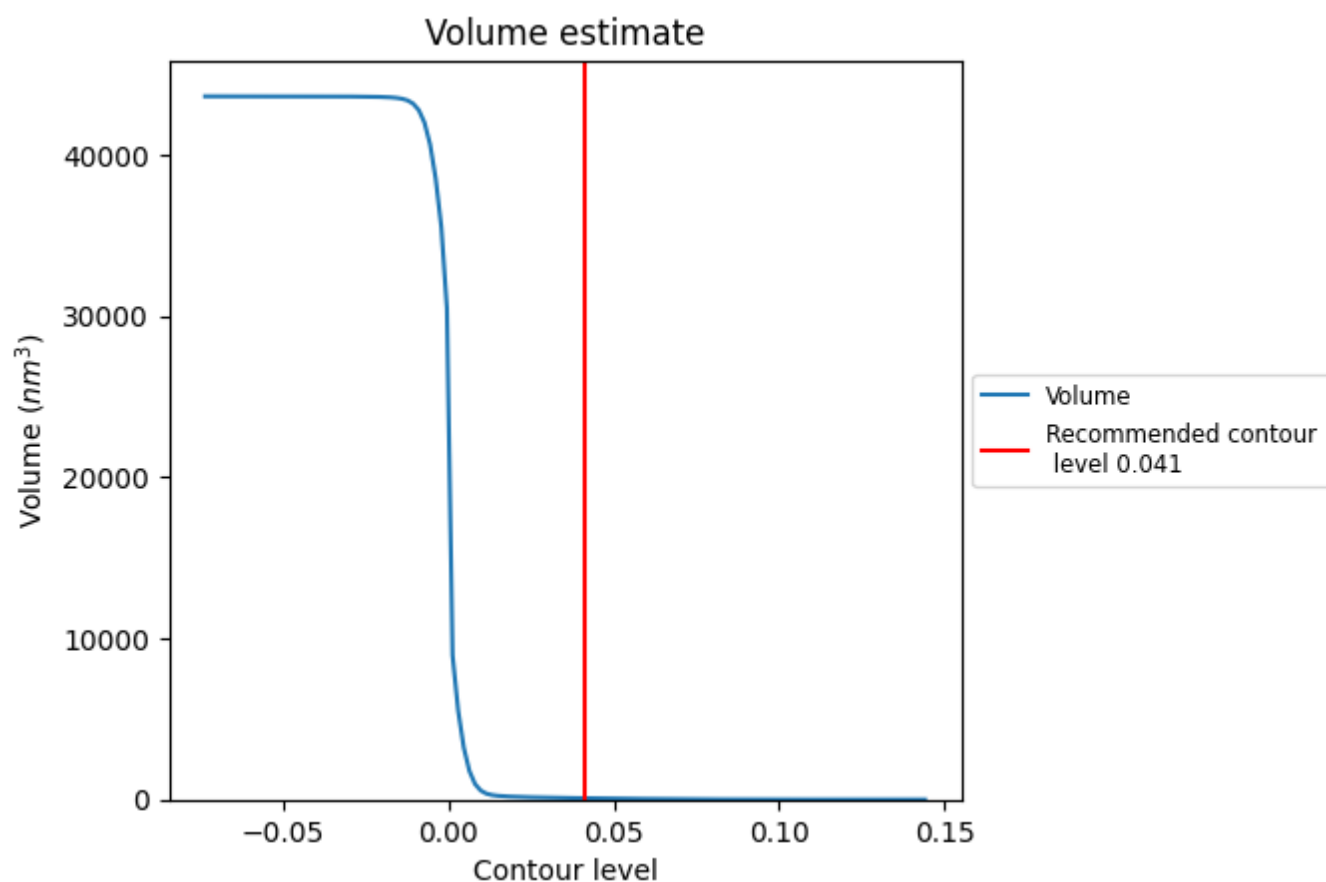
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

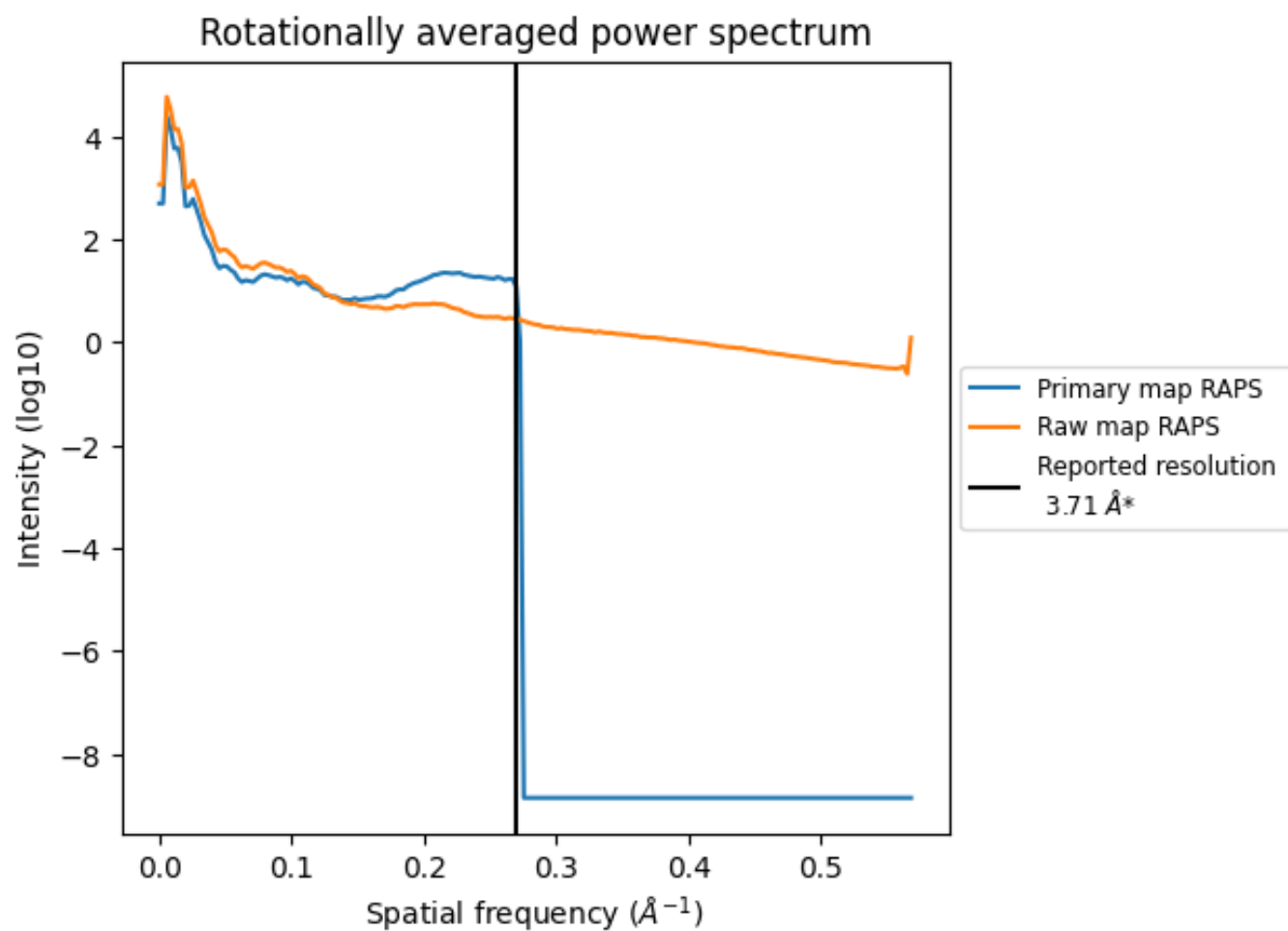
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 84 nm³; this corresponds to an approximate mass of 76 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

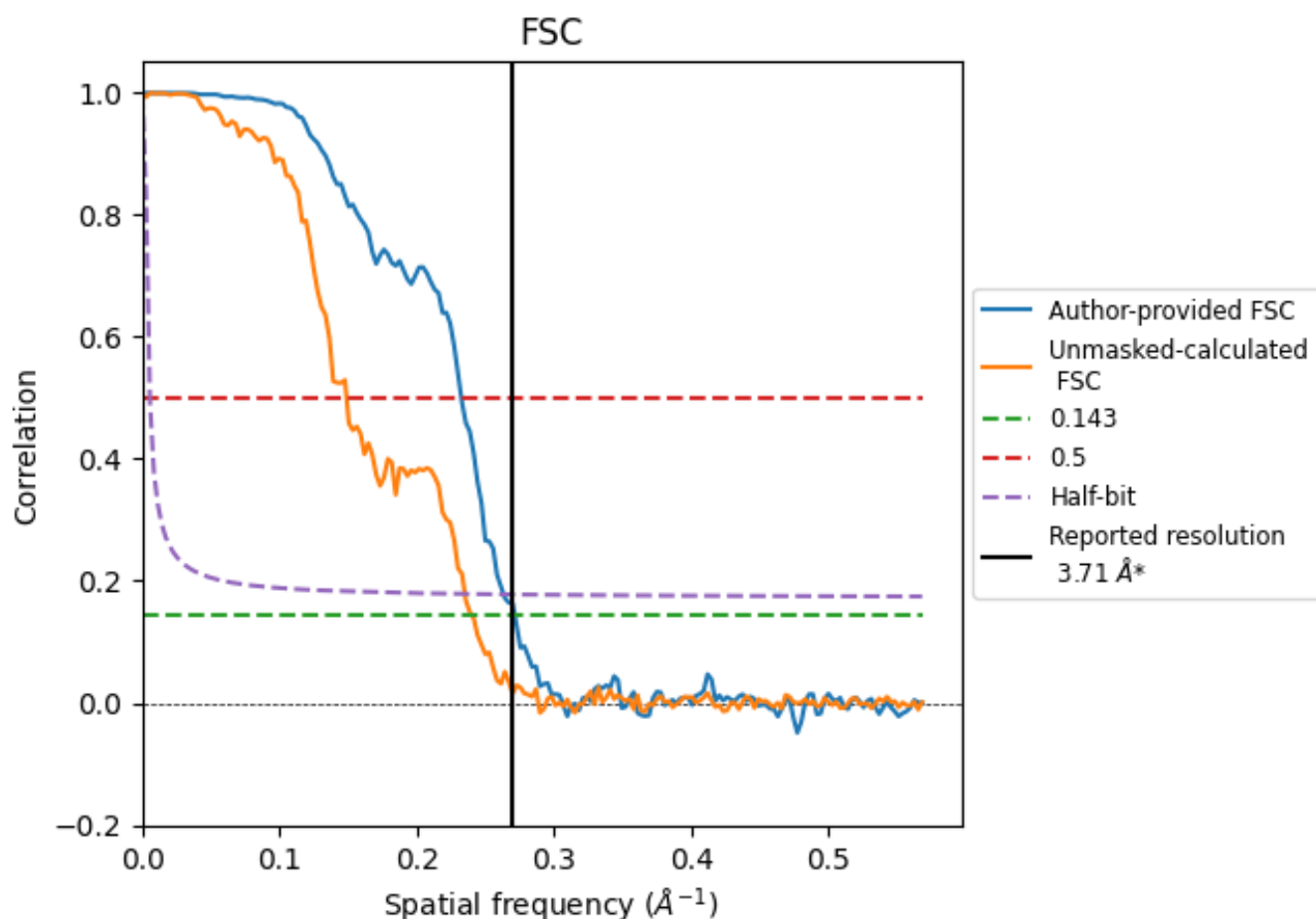


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

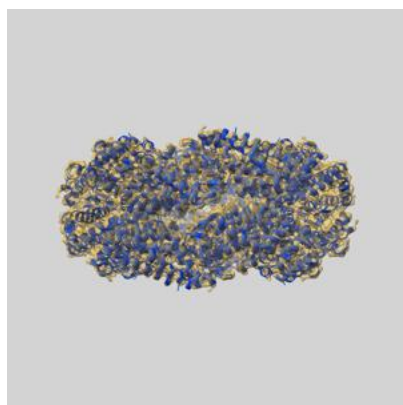
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.71	-	-
Author-provided FSC curve	3.68	4.30	3.80
Unmasked-calculated*	4.16	6.72	4.25

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.16 differs from the reported value 3.71 by more than 10 %

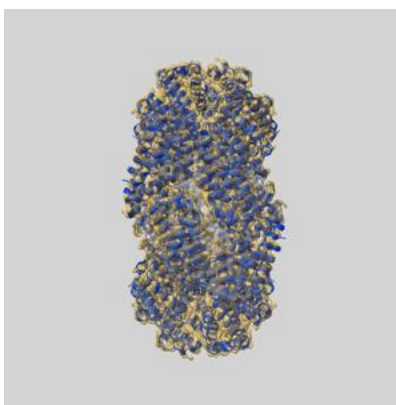
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-31089 and PDB model 7EH7. Per-residue inclusion information can be found in section [3](#) on page [7](#).

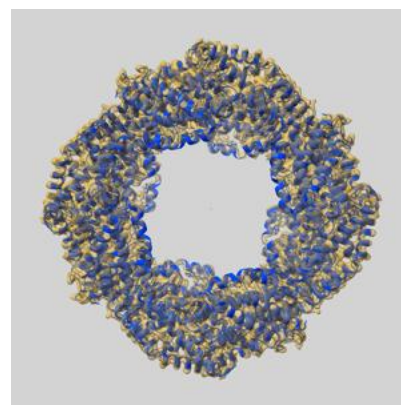
9.1 Map-model overlay [i](#)



X



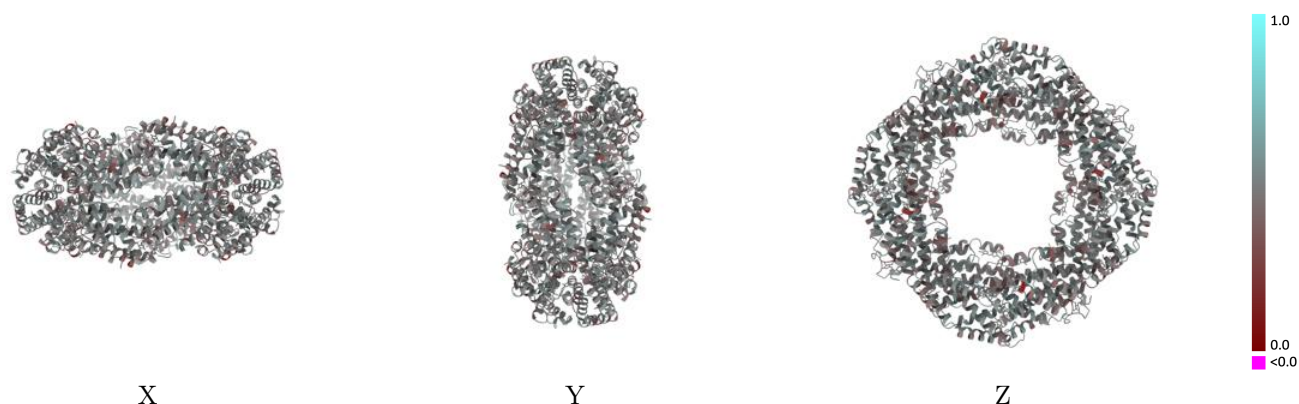
Y



Z

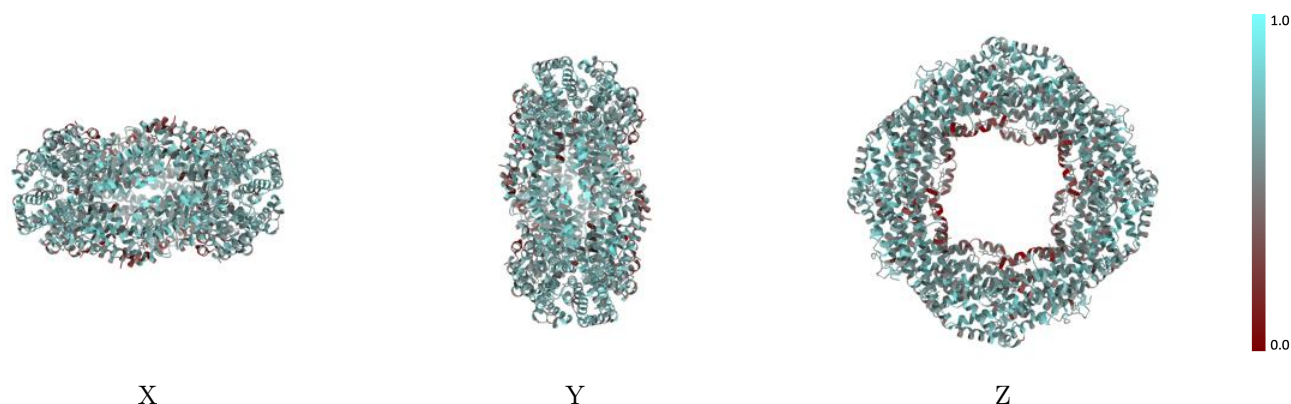
The images above show the 3D surface view of the map at the recommended contour level 0.041 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



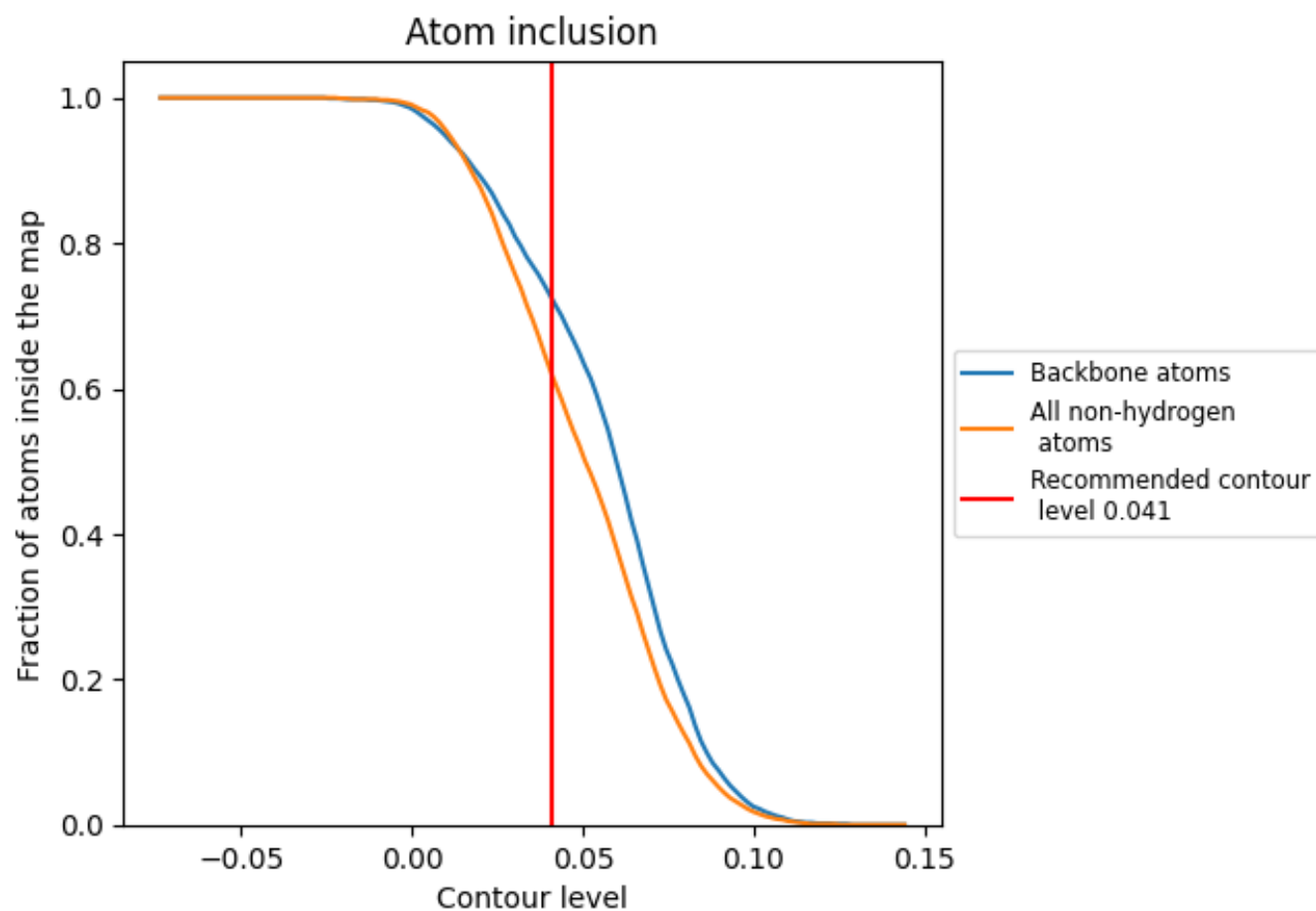
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.041).

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 62% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.041) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6180	0.4780
A	0.6590	0.4830
B	0.5830	0.4750
C	0.6490	0.4800
D	0.5850	0.4700
E	0.6560	0.4840
F	0.5830	0.4740
G	0.6550	0.4860
H	0.5830	0.4750
I	0.6530	0.4850
J	0.5860	0.4710
K	0.6530	0.4850
L	0.5810	0.4720
M	0.6590	0.4850
N	0.5890	0.4760
O	0.6560	0.4830
P	0.5840	0.4710

