



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 10:23 AM UTC

PDB ID : 6YX7 / pdb_00006yx7
Title : The high resolution structure of allophycocyanin from cyanobacterium Nostoc sp. WR13, the P21212 crystal form.
Authors : Patel, H.M.; Roszak, A.W.; Madamwar, D.; Cogdell, R.J.
Deposited on : 2020-04-30
Resolution : 1.42 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

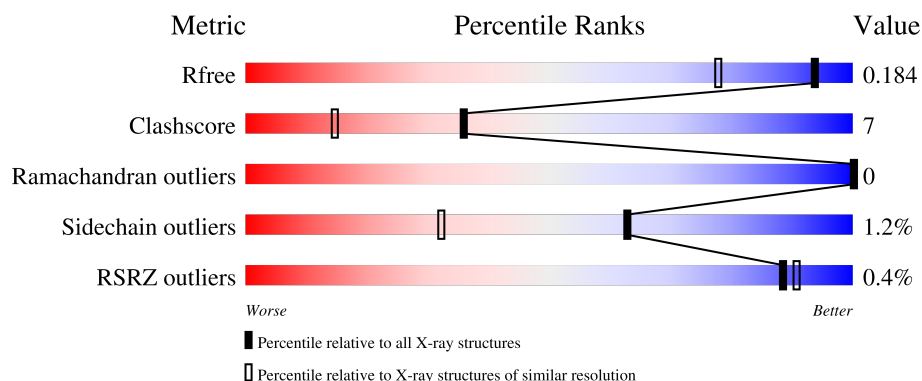
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.42 Å.

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



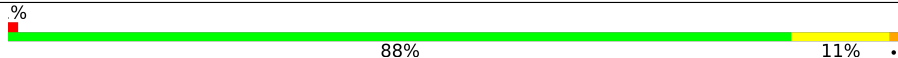
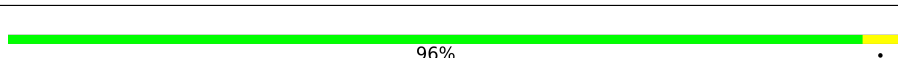
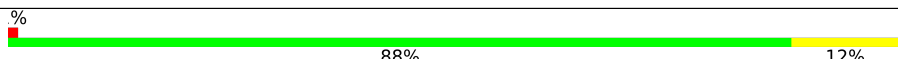
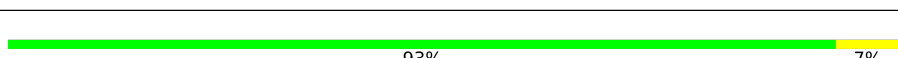
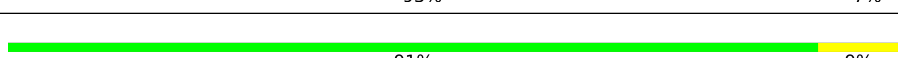
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4041 (1.44-1.40)
Clashscore	190562	4154 (1.44-1.40)
Ramachandran outliers	187476	4083 (1.44-1.40)
Sidechain outliers	187428	4082 (1.44-1.40)
RSRZ outliers	180081	4039 (1.44-1.40)

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

Mol	Chain	Length	Quality of chain
1	AAA	160	88% 12%
1	CCC	160	88% 12%
1	EEE	160	89% 11%
1	GGG	160	86% 12%
1	III	160	91% 9%

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Mol	Chain	Length	Quality of chain	
1	KKK	160		
2	BBB	161		
2	DDD	161		
2	FFF	161		
2	HHH	161		
2	JJJ	161		
2	LLL	161		

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	P6G	CCC	202	-	-	-	X
15	PGE	GGG	203	-	-	X	-
4	PG4	AAA	202	-	-	X	-
4	PG4	FFF	204	-	-	-	X
8	PEG	BBB	205	-	-	X	-
8	PEG	CCC	204	-	-	X	-

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 19418 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

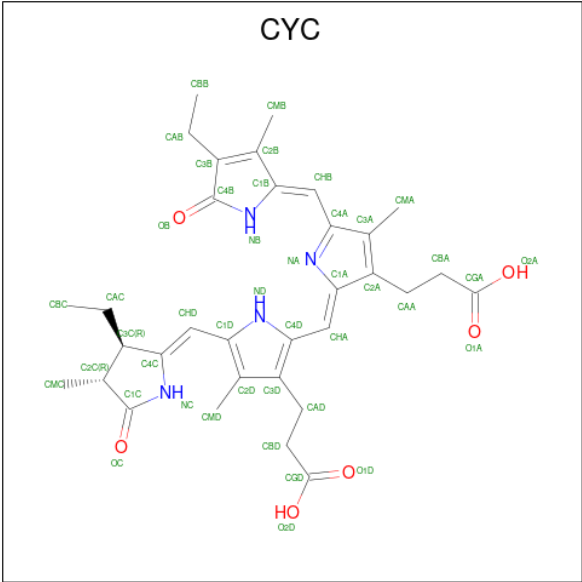
- Molecule 1 is a protein called Allophycocyanin alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	160	Total	C	N	O	S	0	10	0
			1272	800	222	243	7			
1	CCC	160	Total	C	N	O	S	0	15	0
			1292	820	223	243	6			
1	EEE	160	Total	C	N	O	S	0	12	0
			1285	808	226	245	6			
1	GGG	160	Total	C	N	O	S	0	13	0
			1272	803	220	243	6			
1	III	160	Total	C	N	O	S	0	8	0
			1247	785	215	241	6			
1	KKK	160	Total	C	N	O	S	0	16	0
			1319	830	230	252	7			

- Molecule 2 is a protein called Allophycocyanin beta.

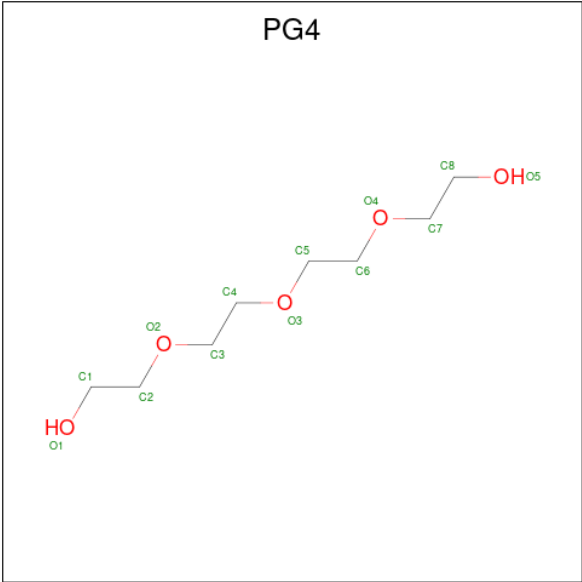
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	BBB	161	Total	C	N	O	S	0	15	0
			1303	831	213	253	6			
2	DDD	161	Total	C	N	O	S	0	19	0
			1309	837	210	256	6			
2	FFF	161	Total	C	N	O	S	0	3	0
			1236	779	207	244	6			
2	HHH	161	Total	C	N	O	S	0	13	0
			1290	818	210	256	6			
2	JJJ	161	Total	C	N	O	S	0	9	0
			1258	797	209	246	6			
2	LLL	161	Total	C	N	O	S	0	11	0
			1280	813	213	248	6			

- Molecule 3 is PHYCOCYANOBILIN (CCD ID: CYC) (formula: $C_{33}H_{40}N_4O_6$) (labeled as "Ligand of Interest" by depositor).



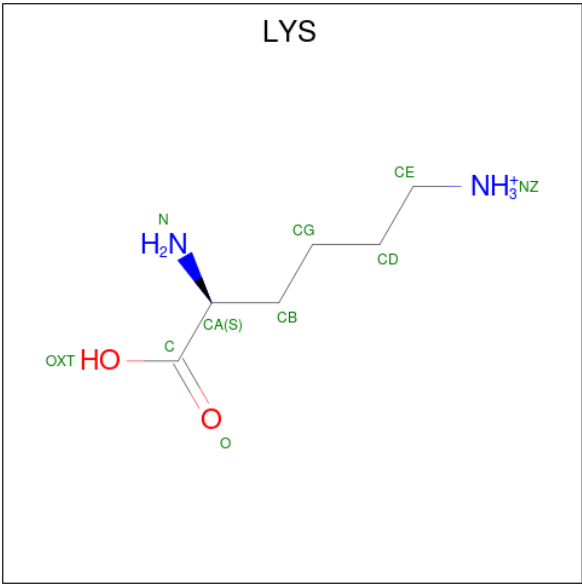
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	AAA	1	Total	C	N	O	0	0
			43	33	4	6		
3	BBB	1	Total	C	N	O	0	0
			43	33	4	6		
3	CCC	1	Total	C	N	O	0	0
			43	33	4	6		
3	DDD	1	Total	C	N	O	0	0
			43	33	4	6		
3	EEE	1	Total	C	N	O	0	0
			43	33	4	6		
3	FFF	1	Total	C	N	O	0	0
			43	33	4	6		
3	GGG	1	Total	C	N	O	0	0
			43	33	4	6		
3	HHH	1	Total	C	N	O	0	0
			43	33	4	6		
3	III	1	Total	C	N	O	0	0
			43	33	4	6		
3	JJJ	1	Total	C	N	O	0	0
			43	33	4	6		
3	KKK	1	Total	C	N	O	0	0
			43	33	4	6		
3	LLL	1	Total	C	N	O	0	0
			43	33	4	6		

- Molecule 4 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



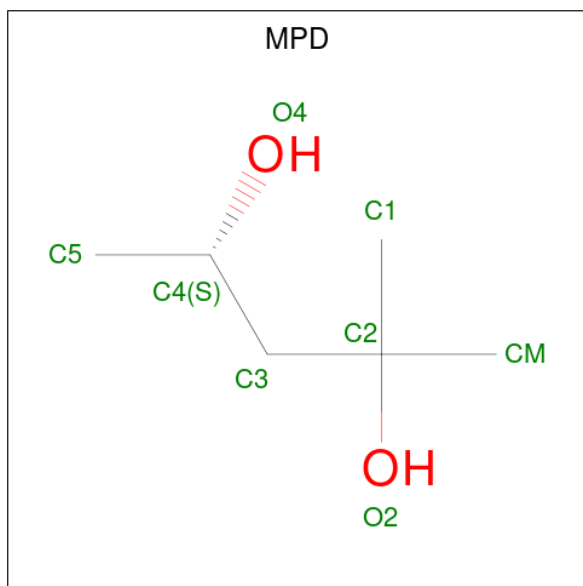
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	AAA	1	Total	C	O	0	0
			13	8	5		
4	CCC	1	Total	C	O	0	0
			13	8	5		
4	FFF	1	Total	C	O	0	0
			13	8	5		
4	JJJ	1	Total	C	O	0	0
			13	8	5		

- Molecule 5 is LYSINE (CCD ID: LYS) (formula: C₆H₁₅N₂O₂).



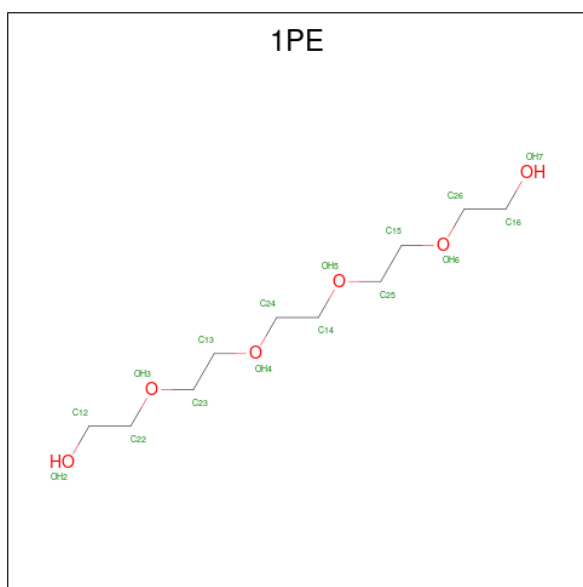
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	BBB	1	Total	C	N	O	0	1
			16	11	3	2		
5	III	1	Total	C	N	O	0	0
			10	6	2	2		
5	KKK	1	Total	C	N	O	0	0
			10	6	2	2		

- Molecule 6 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: $C_6H_{14}O_2$).



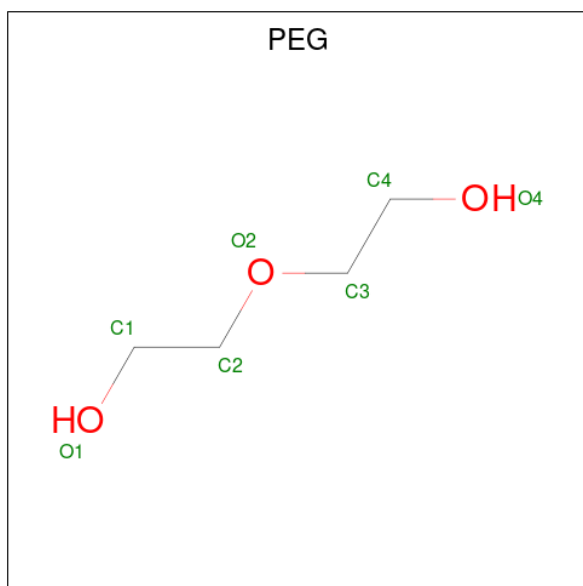
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	BBB	1	Total	C	O	0	0
			8	6	2		
6	DDD	1	Total	C	O	0	0
			8	6	2		
6	EEE	1	Total	C	O	0	0
			8	6	2		
6	FFF	1	Total	C	O	0	0
			8	6	2		
6	HHH	1	Total	C	O	0	0
			8	6	2		
6	JJJ	1	Total	C	O	0	0
			8	6	2		
6	LLL	1	Total	C	O	0	0
			8	6	2		

- Molecule 7 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	BBB	1	Total	C	O	0	0
			16	10	6		

- Molecule 8 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



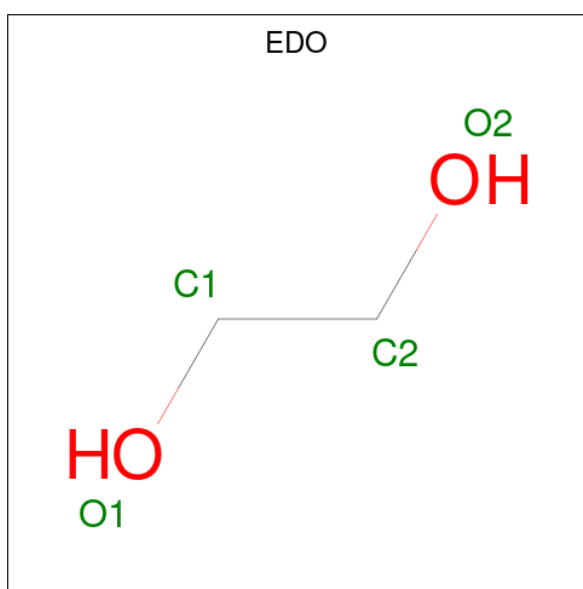
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	BBB	1	Total	C	O	0	0
			7	4	3		
8	BBB	1	Total	C	O	0	0
			7	4	3		
8	BBB	1	Total	C	O	0	0
			7	4	3		

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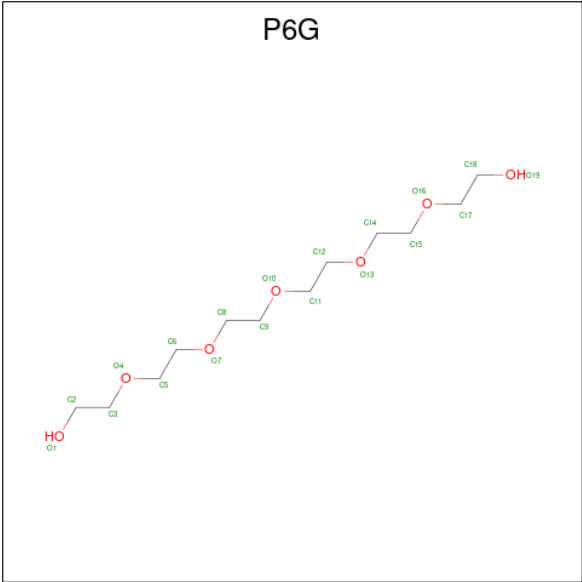
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	CCC	1	Total	C	O	0	0
			7	4	3		
8	GGG	1	Total	C	O	0	0
			7	4	3		
8	HHH	1	Total	C	O	0	0
			7	4	3		
8	JJJ	1	Total	C	O	0	0
			7	4	3		

- Molecule 9 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



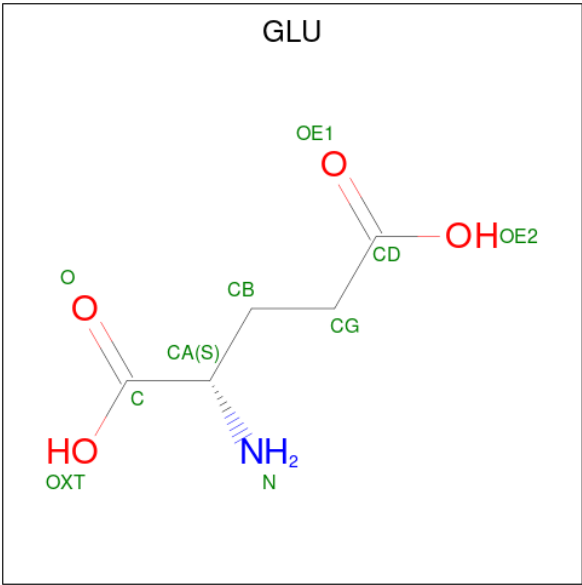
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	BBB	1	Total	C	O	0	0
			4	2	2		
9	CCC	1	Total	C	O	0	0
			4	2	2		
9	CCC	1	Total	C	O	0	0
			4	2	2		
9	KKK	1	Total	C	O	0	0
			4	2	2		
9	KKK	1	Total	C	O	0	0
			4	2	2		

- Molecule 10 is HEXAETHYLENE GLYCOL (CCD ID: P6G) (formula: $C_{12}H_{26}O_7$).



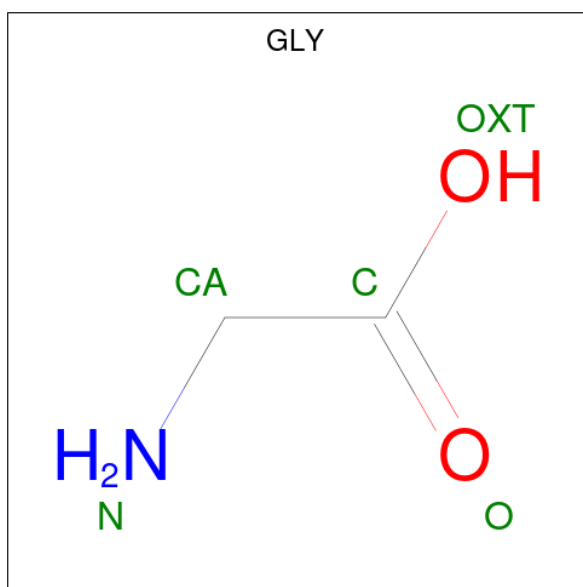
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	CCC	1	Total	C	O	0	0
			19	12	7		

- Molecule 11 is GLUTAMIC ACID (CCD ID: GLU) (formula: C₅H₉NO₄).



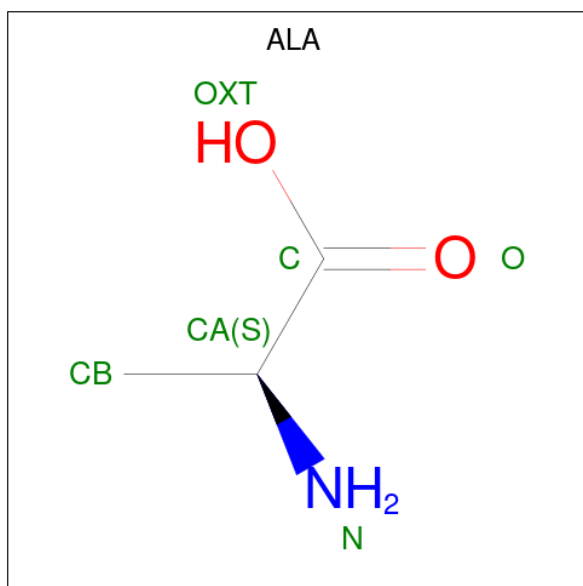
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	DDD	1	Total	C	N	O	0	0
			10	5	1	4		
11	HHH	1	Total	C	N	O	0	0
			10	5	1	4		

- Molecule 12 is GLYCINE (CCD ID: GLY) (formula: C₂H₅NO₂).



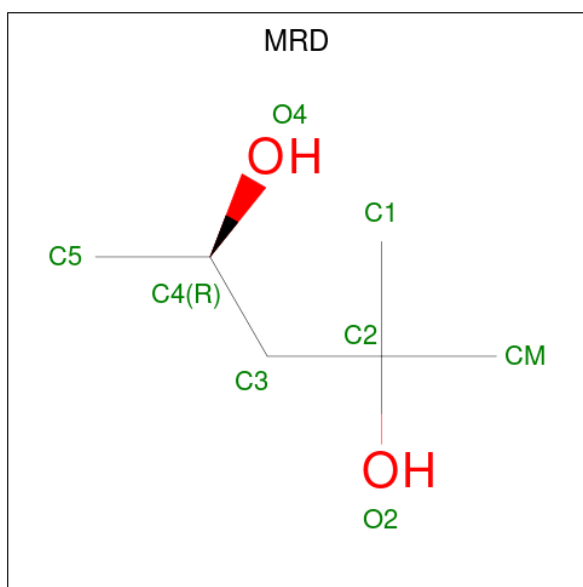
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	EEE	1	Total	C	N	O	0	0
			5	2	1	2		

- Molecule 13 is ALANINE (CCD ID: ALA) (formula: $C_3H_7NO_2$).



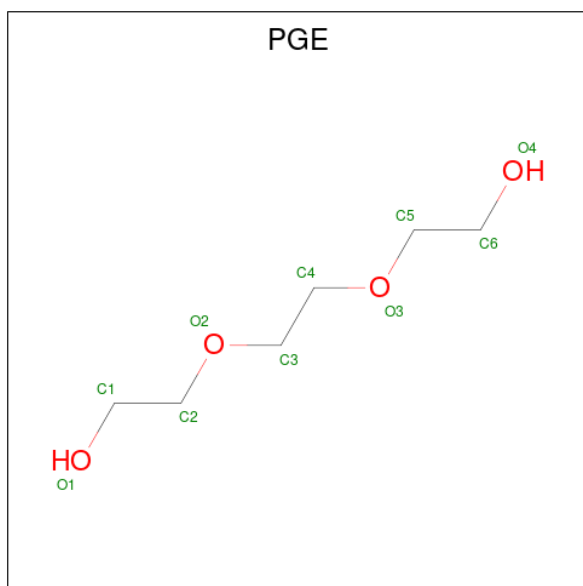
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
13	FFF	1	Total	C	N	O	0	0
			6	3	1	2		

- Molecule 14 is (4R)-2-METHYLPENTANE-2,4-DIOL (CCD ID: MRD) (formula: $C_6H_{14}O_2$).



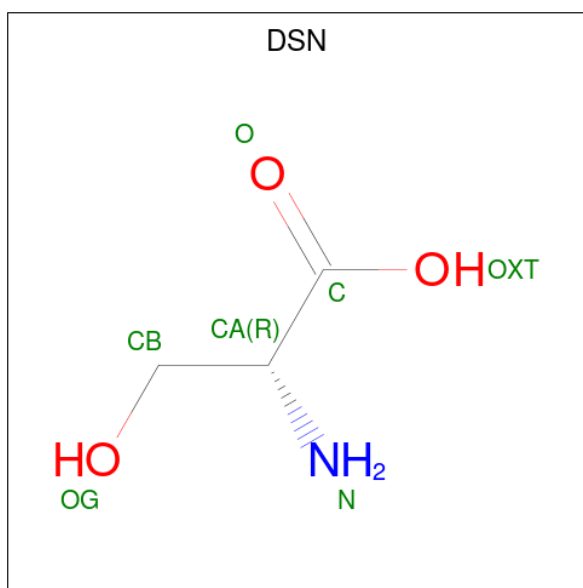
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
14	GGG	1	Total	C	O	0	0
			8	6	2		

- Molecule 15 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
15	GGG	1	Total	C	O	0	0
			10	6	4		
15	GGG	1	Total	C	O	0	0
			10	6	4		
15	LLL	1	Total	C	O	0	0
			10	6	4		

- Molecule 16 is D-SERINE (CCD ID: DSN) (formula: $C_3H_7NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
16	JJJ	1	Total	C	N	O	0	0
			7	3	1	3		
16	LLL	1	Total	C	N	O	0	0
			7	3	1	3		

- Molecule 17 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	AAA	230	Total	O	0	0
			230	230		
17	BBB	281	Total	O	0	0
			281	281		
17	CCC	299	Total	O	0	0
			299	299		
17	DDD	303	Total	O	0	0
			303	303		
17	EEE	246	Total	O	0	0
			246	246		
17	FFF	286	Total	O	0	0
			286	286		
17	GGG	241	Total	O	0	0
			241	241		
17	HHH	284	Total	O	0	0
			284	284		
17	III	252	Total	O	0	0
			252	252		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	JJJ	284	Total 284	O 284	0	0
17	KKK	238	Total 238	O 238	0	0
17	LLL	264	Total 264	O 264	0	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 electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Allophycocyanin alpha



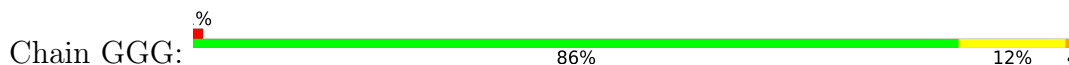
- Molecule 1: Allophycocyanin alpha



- Molecule 1: Allophycocyanin alpha



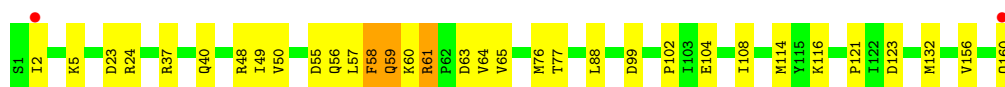
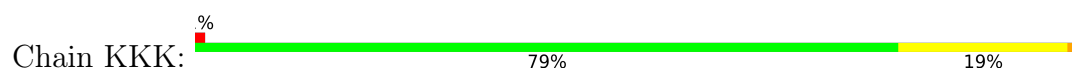
- Molecule 1: Allophycocyanin alpha



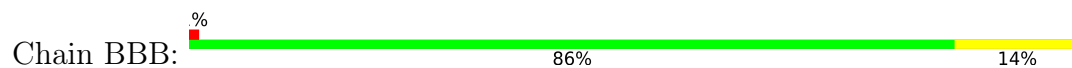
- Molecule 1: Allophycocyanin alpha



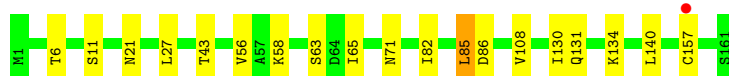
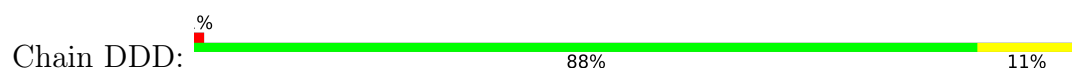
- Molecule 1: Allophycocyanin alpha



- Molecule 2: Allophycocyanin beta



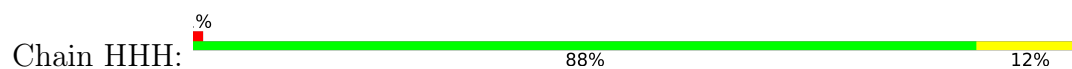
- Molecule 2: Allophycocyanin beta



- Molecule 2: Allophycocyanin beta



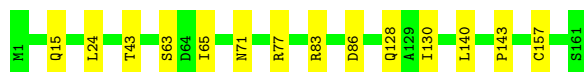
- Molecule 2: Allophycocyanin beta



- Molecule 2: Allophycocyanin beta



- Molecule 2: Allophycocyanin beta



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	123.69Å 177.73Å 106.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	106.37 – 1.42 106.37 – 1.42	Depositor EDS
% Data completeness (in resolution range)	87.3 (106.37-1.42) 87.3 (106.37-1.42)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.54 (at 1.42Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.126 , 0.175 0.141 , 0.184	Depositor DCC
R_{free} test set	19133 reflections (4.36%)	wwPDB-VP
Wilson B-factor (Å ²)	20.1	Xtriage
Anisotropy	0.014	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 64.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	19418	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 48.78 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 8.1971e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: P6G, MRD, MEN, EDO, 1PE, PEG, CYC, PGE, DSN, PG4, MPD

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	AAA	0.95	0/1320	1.27	1/1780 (0.1%)
1	CCC	0.99	0/1358	1.23	0/1831
1	EEE	0.97	0/1342	1.22	0/1808
1	GGG	0.98	0/1326	1.26	1/1790 (0.1%)
1	III	1.01	0/1286	1.22	1/1735 (0.1%)
1	KKK	0.99	0/1358	1.26	3/1834 (0.2%)
2	BBB	0.94	0/1358	1.16	0/1836
2	DDD	1.02	1/1373 (0.1%)	1.18	2/1857 (0.1%)
2	FFF	0.95	0/1249	1.21	1/1689 (0.1%)
2	HHH	1.01	2/1333 (0.2%)	1.17	0/1804
2	JJJ	0.93	0/1292	1.22	0/1746
2	LLL	0.93	0/1317	1.17	1/1781 (0.1%)
All	All	0.97	3/15912 (0.0%)	1.21	10/21491 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	HHH	90	ARG	C-O	6.38	1.31	1.24
2	DDD	108	VAL	N-CA	5.41	1.51	1.46
2	HHH	108	VAL	N-CA	5.35	1.51	1.46

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	KKK	99	ASP	CA-CB-CG	7.77	120.37	112.60
1	AAA	99	ASP	CA-CB-CG	6.39	118.99	112.60
2	FFF	86	ASP	CA-CB-CG	5.64	118.24	112.60
2	DDD	86[A]	ASP	CA-CB-CG	5.51	118.11	112.60
2	DDD	86[B]	ASP	CA-CB-CG	5.51	118.11	112.60

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	AAA	1272	0	1312	25	0
1	CCC	1292	0	1370	24	0
1	EEE	1285	0	1333	25	0
1	GGG	1272	0	1324	30	0
1	III	1247	0	1282	11	0
1	KKK	1319	0	1349	41	0
2	BBB	1303	0	1359	33	0
2	DDD	1309	0	1372	12	0
2	FFF	1236	0	1247	7	0
2	HHH	1290	0	1322	17	0
2	JJJ	1258	0	1292	11	0
2	LLL	1280	0	1322	9	0
3	AAA	43	0	37	1	0
3	BBB	43	0	37	1	0
3	CCC	43	0	37	1	0
3	DDD	43	0	37	1	0
3	EEE	43	0	37	1	0
3	FFF	43	0	37	1	0
3	GGG	43	0	37	1	0
3	HHH	43	0	37	1	0
3	III	43	0	37	1	0
3	JJJ	43	0	37	0	0
3	KKK	43	0	37	1	0
3	LLL	43	0	37	1	0
4	AAA	13	0	18	8	0
4	CCC	13	0	18	0	0
4	FFF	13	0	18	0	0
4	JJJ	13	0	18	2	0
5	BBB	16	0	24	0	0
5	III	10	0	12	0	0
5	KKK	10	0	12	1	0
6	BBB	8	0	14	0	0
6	DDD	8	0	14	0	0
6	EEE	8	0	14	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	FFF	8	0	14	0	0
6	HHH	8	0	14	1	0
6	JJJ	8	0	14	0	0
6	LLL	8	0	14	0	0
7	BBB	16	0	22	5	0
8	BBB	21	0	30	7	0
8	CCC	7	0	10	4	0
8	GGG	7	0	10	0	0
8	HHH	7	0	10	1	0
8	JJJ	7	0	10	2	0
9	BBB	4	0	6	1	0
9	CCC	8	0	12	0	0
9	KKK	8	0	12	2	0
10	CCC	19	0	26	0	0
11	DDD	10	0	5	0	0
11	HHH	10	0	5	0	0
12	EEE	5	0	2	0	0
13	FFF	6	0	4	2	0
14	GGG	8	0	14	0	0
15	GGG	20	0	28	9	0
15	LLL	10	0	14	1	0
16	JJJ	7	0	6	0	0
16	LLL	7	0	6	0	0
17	AAA	230	0	0	4	0
17	BBB	281	0	0	13	0
17	CCC	299	0	0	5	0
17	DDD	303	0	0	1	0
17	EEE	246	0	0	4	0
17	FFF	286	0	0	2	0
17	GGG	241	0	0	8	0
17	HHH	284	0	0	6	0
17	III	252	0	0	5	1
17	JJJ	284	0	0	2	0
17	KKK	238	0	0	11	0
17	LLL	264	0	0	2	1
All	All	19418	0	16778	241	1

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

The worst 5 of 241 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:46[B]:ARG:HG3	1:AAA:46[B]:ARG:HH11	1.18	1.08
17:CCC:308:HOH:O	2:DDD:6[A]:THR:HG22	1.63	0.98
1:GGG:76[A]:MET:HE1	17:GGG:505:HOH:O	1.65	0.95
1:GGG:133:LYS:HE2	15:GGG:203:PGE:H3	1.49	0.93
1:AAA:48[A]:ARG:HH21	1:AAA:139:LEU:HD21	1.38	0.87

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:III:428:HOH:O	17:LLL:475:HOH:O[4_454]	2.19	0.01

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AAA	170/160 (106%)	169 (99%)	1 (1%)	0	100	100
1	CCC	176/160 (110%)	176 (100%)	0	0	100	100
1	EEE	172/160 (108%)	172 (100%)	0	0	100	100
1	GGG	172/160 (108%)	172 (100%)	0	0	100	100
1	III	167/160 (104%)	167 (100%)	0	0	100	100
1	KKK	175/160 (109%)	175 (100%)	0	0	100	100
2	BBB	174/161 (108%)	172 (99%)	2 (1%)	0	100	100
2	DDD	177/161 (110%)	175 (99%)	2 (1%)	0	100	100
2	FFF	161/161 (100%)	159 (99%)	2 (1%)	0	100	100
2	HHH	172/161 (107%)	170 (99%)	2 (1%)	0	100	100
2	JJJ	167/161 (104%)	164 (98%)	3 (2%)	0	100	100
2	LLL	169/161 (105%)	167 (99%)	2 (1%)	0	100	100
All	All	2052/1926 (106%)	2038 (99%)	14 (1%)	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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AAA	134/122 (110%)	132 (98%)	2 (2%)	57	24
1	CCC	140/122 (115%)	136 (97%)	4 (3%)	37	8
1	EEE	136/122 (112%)	135 (99%)	1 (1%)	76	52
1	GGG	136/122 (112%)	132 (97%)	4 (3%)	37	8
1	III	131/122 (107%)	126 (96%)	5 (4%)	29	4
1	KKK	139/122 (114%)	135 (97%)	4 (3%)	37	8
2	BBB	141/125 (113%)	140 (99%)	1 (1%)	76	52
2	DDD	144/125 (115%)	139 (96%)	5 (4%)	32	5
2	FFF	128/125 (102%)	128 (100%)	0	100	100
2	HHH	139/125 (111%)	139 (100%)	0	100	100
2	JJJ	133/125 (106%)	133 (100%)	0	100	100
2	LLL	136/125 (109%)	135 (99%)	1 (1%)	76	52
All	All	1637/1482 (110%)	1610 (98%)	27 (2%)	63	22

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	GGG	23[B]	ASP
1	III	23	ASP
1	KKK	61[A]	ARG
1	GGG	143	GLU
1	III	51	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 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	HHH	71	2	7,8,9	1.34	1 (14%)	4,9,11	0.93	0
2	MEN	JJJ	71	2	7,8,9	0.39	0	4,9,11	0.44	0
2	MEN	FFF	71	2	7,8,9	0.53	0	4,9,11	0.51	0
2	MEN	LLL	71	2	7,8,9	1.06	0	4,9,11	1.33	1 (25%)
2	MEN	BBB	71	2	7,8,9	0.84	0	4,9,11	1.01	0
2	MEN	DDD	71	2	7,8,9	1.34	1 (14%)	4,9,11	0.50	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	HHH	71	2	-	2/7/8/10	-
2	MEN	JJJ	71	2	-	2/7/8/10	-
2	MEN	FFF	71	2	-	2/7/8/10	-
2	MEN	LLL	71	2	-	2/7/8/10	-
2	MEN	BBB	71	2	-	2/7/8/10	-
2	MEN	DDD	71	2	-	2/7/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	DDD	71	MEN	OD1-CG	2.63	1.28	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	HHH	71	MEN	CE2-ND2	2.47	1.50	1.45

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	LLL	71	MEN	OD1-CG-CB	2.55	125.26	121.54

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	BBB	71	MEN	CA-CB-CG-OD1
2	FFF	71	MEN	CA-CB-CG-OD1
2	JJJ	71	MEN	CA-CB-CG-OD1
2	DDD	71	MEN	CA-CB-CG-OD1
2	BBB	71	MEN	CA-CB-CG-ND2

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](#)

51 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	$\# Z > 2$
14	MRD	GGG	202	-	7,7,7	0.37	0	9,10,10	0.57	0
11	GLU	DDD	202	-	8,9,9	1.01	1 (12%)	8,11,11	1.18	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PG4	AAA	202	-	12,12,12	0.14	0	11,11,11	0.32	0
3	CYC	III	201	1	46,46,46	0.77	0	63,67,67	1.22	7 (11%)
8	PEG	CCC	204	-	6,6,6	0.16	0	5,5,5	0.18	0
9	EDO	KKK	204	-	3,3,3	0.16	0	2,2,2	0.51	0
15	PGE	LLL	204	-	9,9,9	0.16	0	8,8,8	0.12	0
3	CYC	GGG	201	1	46,46,46	0.73	1 (2%)	63,67,67	1.28	8 (12%)
8	PEG	BBB	208	-	6,6,6	0.29	0	5,5,5	0.29	0
5	LYS	III	202	-	8,9,9	0.74	0	7,10,10	0.77	0
9	EDO	BBB	207	-	3,3,3	0.26	0	2,2,2	0.48	0
5	LYS	BBB	202[A]	-	8,9,9	0.84	1 (12%)	7,10,10	1.18	1 (14%)
6	MPD	HHH	203	-	7,7,7	0.47	0	9,10,10	0.51	0
4	PG4	CCC	203	-	12,12,12	0.15	0	11,11,11	0.10	0
12	GLY	EEE	202	-	4,4,4	1.00	0	3,4,4	1.52	1 (33%)
15	PGE	GGG	204	-	9,9,9	0.17	0	8,8,8	0.19	0
16	DSN	JJJ	202	-	4,6,6	1.31	1 (25%)	2,7,7	1.34	0
8	PEG	JJJ	205	-	6,6,6	0.51	0	5,5,5	0.36	0
6	MPD	EEE	203	-	7,7,7	0.21	0	9,10,10	0.47	0
6	MPD	LLL	203	-	7,7,7	0.26	0	9,10,10	0.28	0
8	PEG	HHH	204	-	6,6,6	0.27	0	5,5,5	0.16	0
3	CYC	BBB	201	2	46,46,46	0.84	2 (4%)	63,67,67	1.12	4 (6%)
13	ALA	FFF	202	-	5,5,5	1.14	1 (20%)	6,6,6	0.94	0
8	PEG	BBB	205	-	6,6,6	0.19	0	5,5,5	0.24	0
6	MPD	BBB	203	-	7,7,7	0.18	0	9,10,10	0.34	0
3	CYC	LLL	201	2	46,46,46	0.75	0	63,67,67	1.07	3 (4%)
15	PGE	GGG	203	-	9,9,9	0.26	0	8,8,8	0.23	0
8	PEG	BBB	206	-	6,6,6	0.13	0	5,5,5	0.10	0
3	CYC	EEE	201	1	46,46,46	0.65	0	63,67,67	1.27	7 (11%)
6	MPD	JJJ	203	-	7,7,7	0.23	0	9,10,10	0.48	0
3	CYC	HHH	201	2	46,46,46	0.72	1 (2%)	63,67,67	1.05	1 (1%)
9	EDO	KKK	203	-	3,3,3	0.27	0	2,2,2	0.25	0
4	PG4	FFF	204	-	12,12,12	0.13	0	11,11,11	0.15	0
9	EDO	CCC	206	-	3,3,3	0.30	0	2,2,2	0.59	0
3	CYC	AAA	201	1	46,46,46	0.84	0	63,67,67	1.24	7 (11%)
5	LYS	BBB	202[B]	-	8,9,9	0.84	1 (12%)	7,10,10	1.18	1 (14%)
3	CYC	FFF	201	2	46,46,46	0.84	2 (4%)	63,67,67	1.13	5 (7%)
3	CYC	DDD	201	2	46,46,46	0.75	0	63,67,67	1.03	1 (1%)
8	PEG	GGG	205	-	6,6,6	0.18	0	5,5,5	0.08	0
3	CYC	JJJ	201	2	46,46,46	0.84	2 (4%)	63,67,67	1.09	5 (7%)
3	CYC	KKK	201	1	46,46,46	0.72	0	63,67,67	1.24	8 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PG4	JJJ	204	-	12,12,12	0.15	0	11,11,11	0.16	0
3	CYC	CCC	201	1	46,46,46	0.70	0	63,67,67	1.22	6 (9%)
5	LYS	KKK	202	-	8,9,9	0.80	1 (12%)	7,10,10	1.07	1 (14%)
6	MPD	FFF	203	-	7,7,7	0.26	0	9,10,10	0.35	0
9	EDO	CCC	205	-	3,3,3	0.10	0	2,2,2	0.60	0
10	P6G	CCC	202	-	18,18,18	0.86	1 (5%)	17,17,17	0.83	1 (5%)
7	1PE	BBB	204	-	15,15,15	0.77	0	14,14,14	0.77	0
6	MPD	DDD	203	-	7,7,7	0.38	0	9,10,10	0.40	0
11	GLU	HHH	202	-	8,9,9	1.11	1 (12%)	8,11,11	1.22	1 (12%)
16	DSN	LLL	202	-	4,6,6	1.13	1 (25%)	2,7,7	1.88	1 (50%)

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
14	MRD	GGG	202	-	-	0/5/5/5	-
11	GLU	DDD	202	-	-	1/9/9/9	-
4	PG4	AAA	202	-	-	4/10/10/10	-
3	CYC	III	201	1	-	8/26/74/74	0/4/4/4
8	PEG	CCC	204	-	-	3/4/4/4	-
9	EDO	KKK	204	-	-	0/1/1/1	-
15	PGE	LLL	204	-	-	4/7/7/7	-
3	CYC	GGG	201	1	-	6/26/74/74	0/4/4/4
8	PEG	BBB	208	-	-	1/4/4/4	-
5	LYS	III	202	-	-	5/9/9/9	-
9	EDO	BBB	207	-	-	1/1/1/1	-
5	LYS	BBB	202[A]	-	-	6/9/9/9	-
6	MPD	HHH	203	-	-	0/5/5/5	-
4	PG4	CCC	203	-	-	10/10/10/10	-
12	GLY	EEE	202	-	-	0/2/2/2	-
15	PGE	GGG	204	-	-	5/7/7/7	-
16	DSN	JJJ	202	-	-	4/6/6/6	-
8	PEG	JJJ	205	-	-	2/4/4/4	-
6	MPD	EEE	203	-	-	1/5/5/5	-
6	MPD	LLL	203	-	-	0/5/5/5	-
8	PEG	HHH	204	-	-	3/4/4/4	-
3	CYC	BBB	201	2	-	8/26/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	ALA	FFF	202	-	-	2/4/4/4	-
8	PEG	BBB	205	-	-	2/4/4/4	-
6	MPD	BBB	203	-	-	0/5/5/5	-
3	CYC	LLL	201	2	-	8/26/74/74	0/4/4/4
15	PGE	GGG	203	-	-	5/7/7/7	-
8	PEG	BBB	206	-	-	3/4/4/4	-
3	CYC	EEE	201	1	-	7/26/74/74	0/4/4/4
6	MPD	JJJ	203	-	-	0/5/5/5	-
3	CYC	HHH	201	2	-	8/26/74/74	0/4/4/4
9	EDO	KKK	203	-	-	1/1/1/1	-
4	PG4	FFF	204	-	-	4/10/10/10	-
9	EDO	CCC	206	-	-	1/1/1/1	-
3	CYC	AAA	201	1	-	8/26/74/74	0/4/4/4
5	LYS	BBB	202[B]	-	-	7/9/9/9	-
3	CYC	FFF	201	2	-	8/26/74/74	0/4/4/4
3	CYC	DDD	201	2	-	8/26/74/74	0/4/4/4
8	PEG	GGG	205	-	-	3/4/4/4	-
3	CYC	JJJ	201	2	-	8/26/74/74	0/4/4/4
3	CYC	KKK	201	1	-	6/26/74/74	0/4/4/4
4	PG4	JJJ	204	-	-	6/10/10/10	-
3	CYC	CCC	201	1	-	6/26/74/74	0/4/4/4
5	LYS	KKK	202	-	-	2/9/9/9	-
6	MPD	FFF	203	-	-	0/5/5/5	-
9	EDO	CCC	205	-	-	1/1/1/1	-
10	P6G	CCC	202	-	-	11/16/16/16	-
7	1PE	BBB	204	-	-	8/13/13/13	-
6	MPD	DDD	203	-	-	0/5/5/5	-
11	GLU	HHH	202	-	-	5/9/9/9	-
16	DSN	LLL	202	-	-	2/6/6/6	-

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	CCC	202	P6G	O10-C11	3.03	1.55	1.42
16	JJJ	202	DSN	OXT-C	-2.59	1.22	1.30
3	FFF	201	CYC	O2D-CGD	-2.57	1.22	1.30
3	BBB	201	CYC	CHD-C1D	2.56	1.46	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	JJJ	201	CYC	O2D-CGD	-2.41	1.22	1.30

The worst 5 of 69 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	CCC	201	CYC	C1B-CHB-C4A	4.09	138.10	128.06
3	HHH	201	CYC	C1D-CHD-C4C	4.03	134.65	127.76
3	EEE	201	CYC	C1B-CHB-C4A	3.92	137.68	128.06
3	DDD	201	CYC	C1D-CHD-C4C	3.91	134.44	127.76
3	III	201	CYC	C1B-CHB-C4A	3.88	137.57	128.06

There are no chirality outliers.

5 of 202 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	BBB	201	CYC	NA-C4A-CHB-C1B
3	BBB	201	CYC	C3A-C4A-CHB-C1B
3	CCC	201	CYC	NA-C4A-CHB-C1B
3	CCC	201	CYC	C3A-C4A-CHB-C1B
3	DDD	201	CYC	NA-C4A-CHB-C1B

There are no ring outliers.

27 monomers are involved in 57 short contacts:

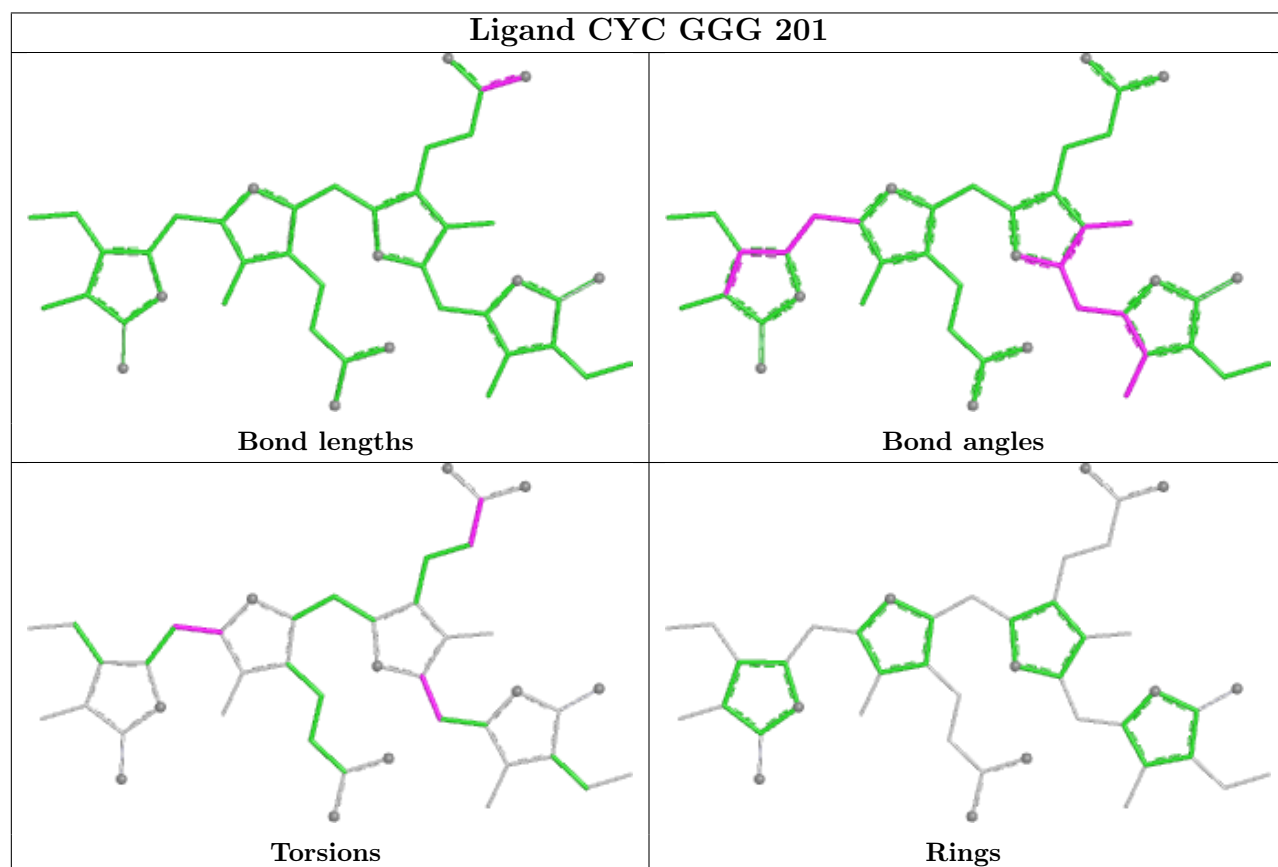
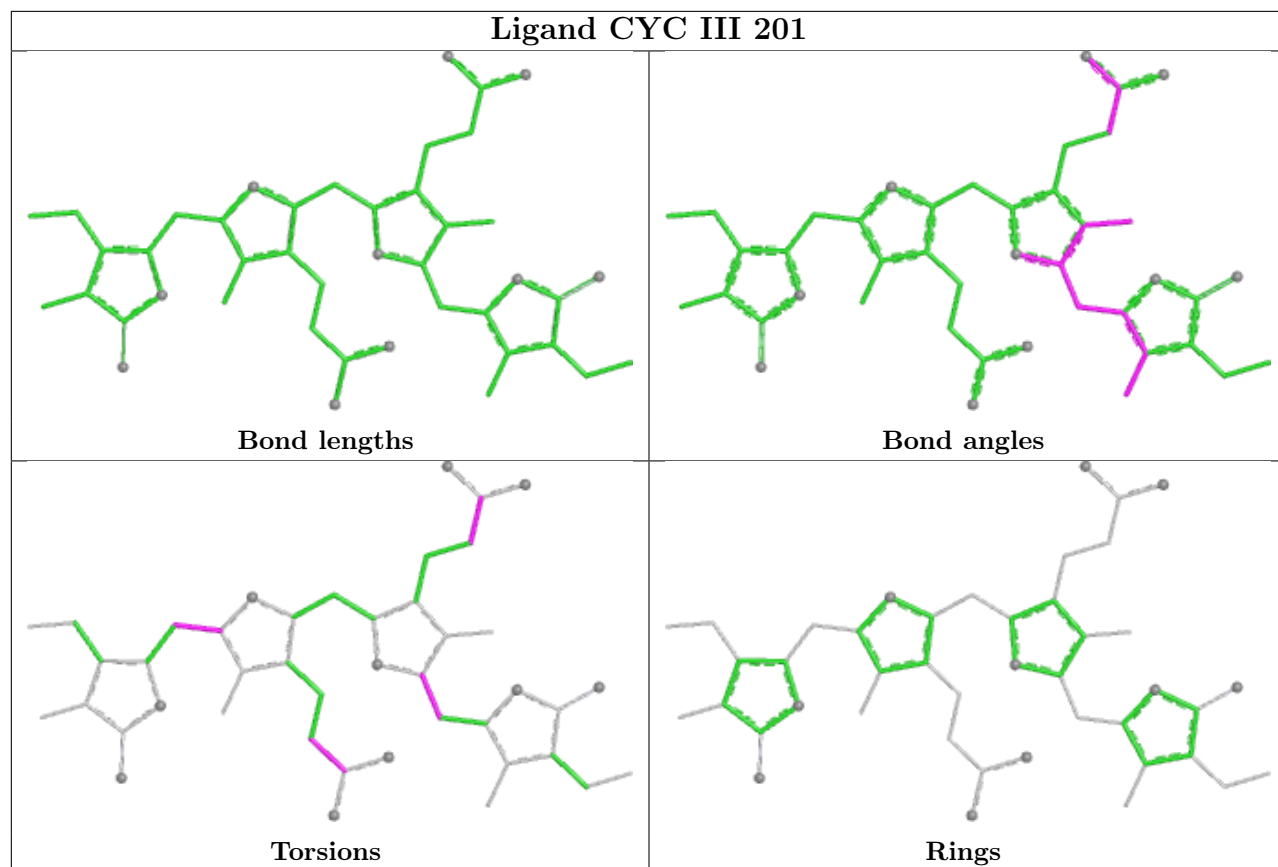
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	AAA	202	PG4	8	0
3	III	201	CYC	1	0
8	CCC	204	PEG	4	0
9	KKK	204	EDO	2	0
15	LLL	204	PGE	1	0
3	GGG	201	CYC	1	0
8	BBB	208	PEG	3	0
9	BBB	207	EDO	1	0
6	HHH	203	MPD	1	0
8	JJJ	205	PEG	2	0
6	EEE	203	MPD	1	0
8	HHH	204	PEG	1	0
3	BBB	201	CYC	1	0
13	FFF	202	ALA	2	0
8	BBB	205	PEG	4	0
3	LLL	201	CYC	1	0

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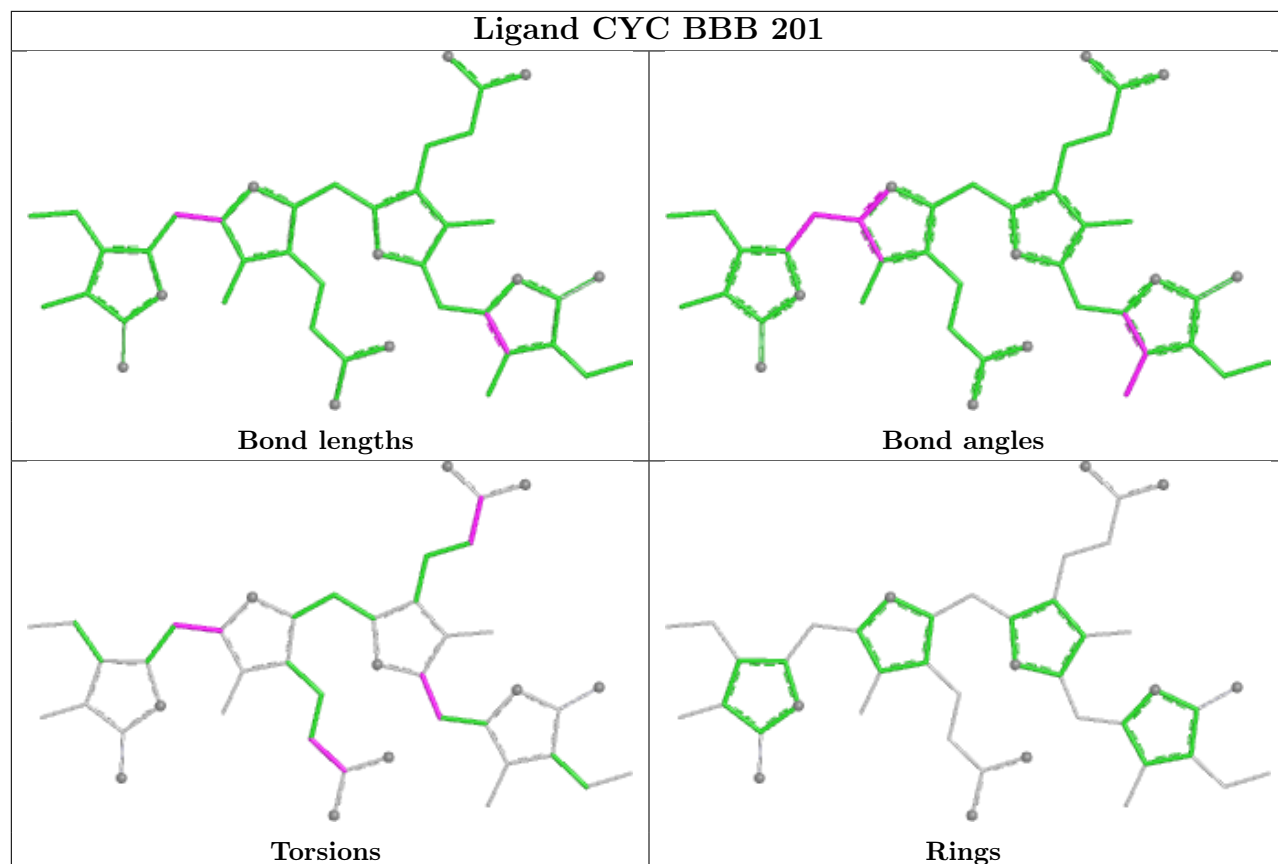
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	GGG	203	PGE	9	0
3	EEE	201	CYC	1	0
3	HHH	201	CYC	1	0
3	AAA	201	CYC	1	0
3	FFF	201	CYC	1	0
3	DDD	201	CYC	1	0
3	KKK	201	CYC	1	0
4	JJJ	204	PG4	2	0
3	CCC	201	CYC	1	0
5	KKK	202	LYS	1	0
7	BBB	204	1PE	5	0

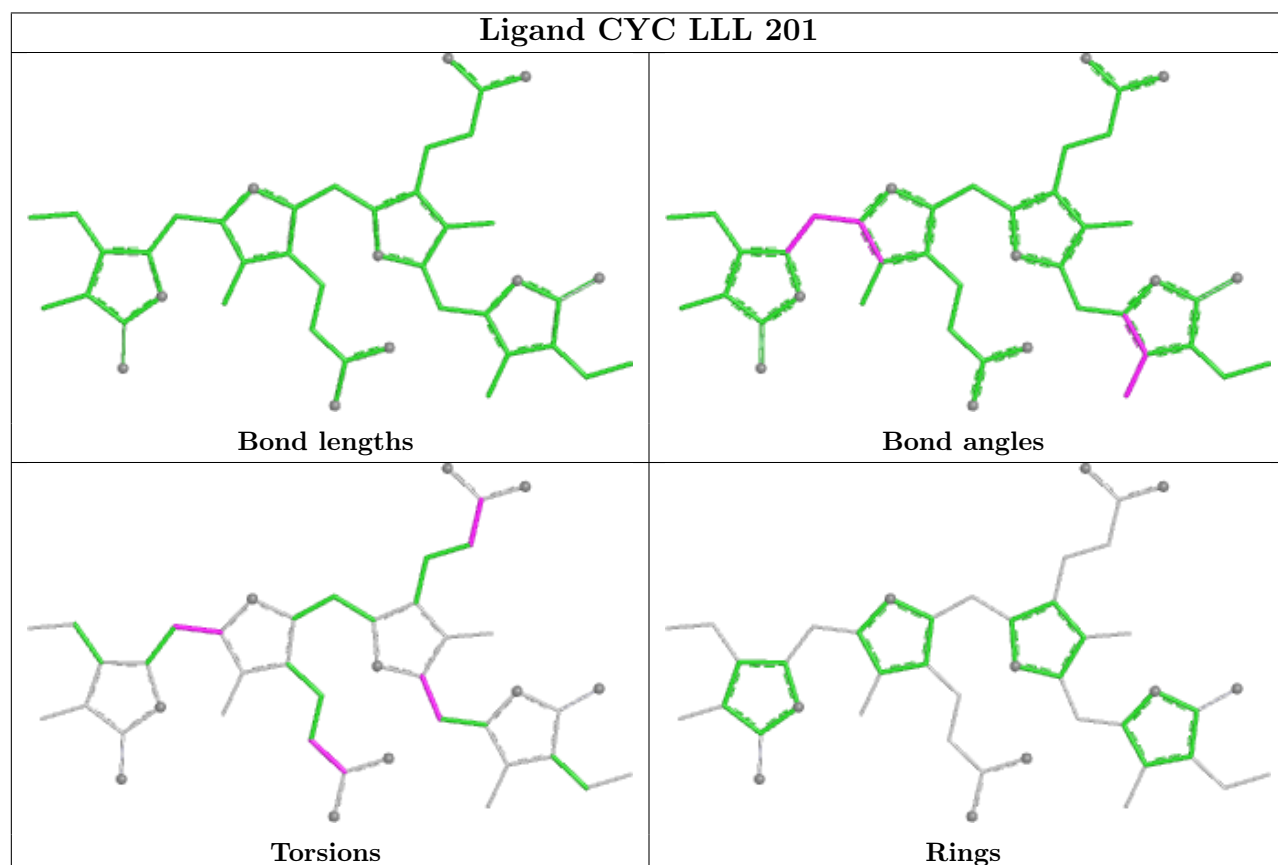
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



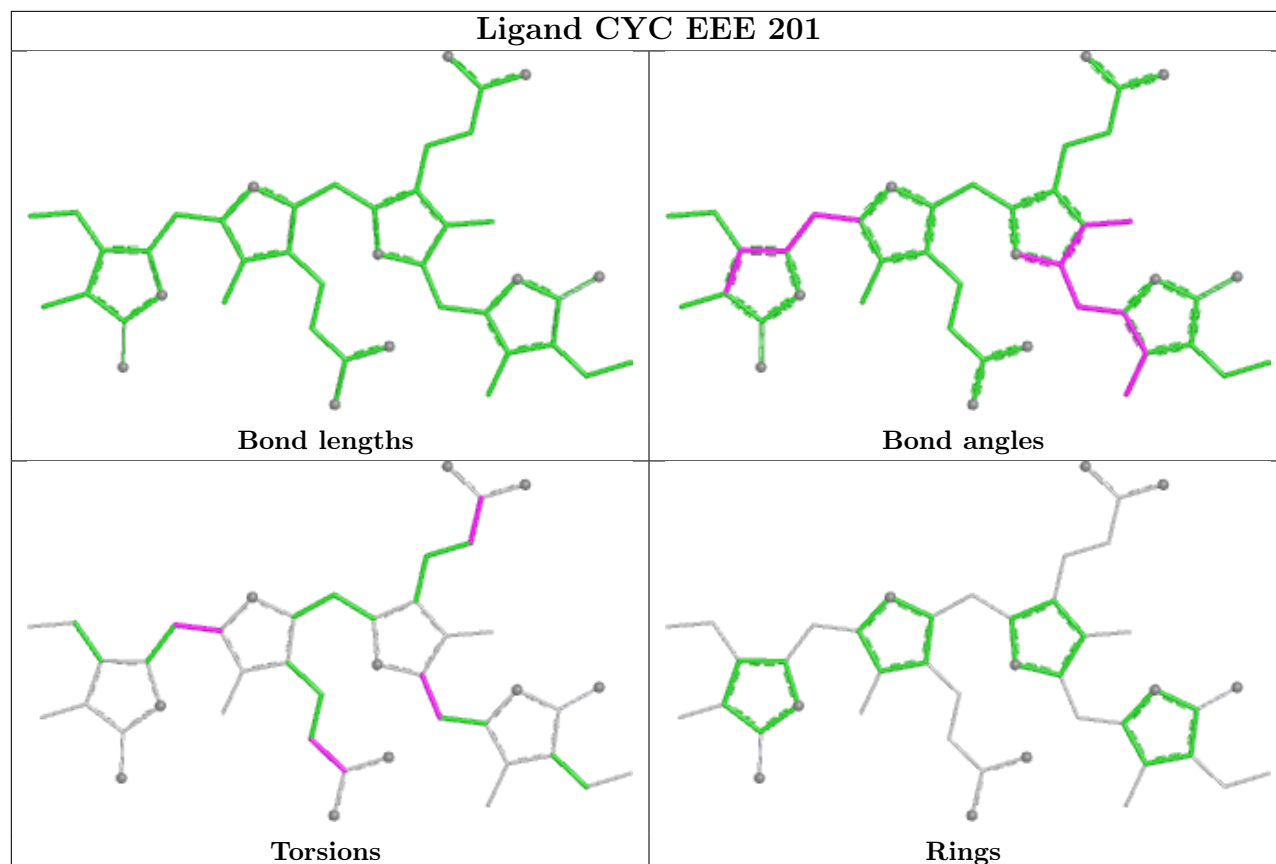
Ligand CYC BBB 201



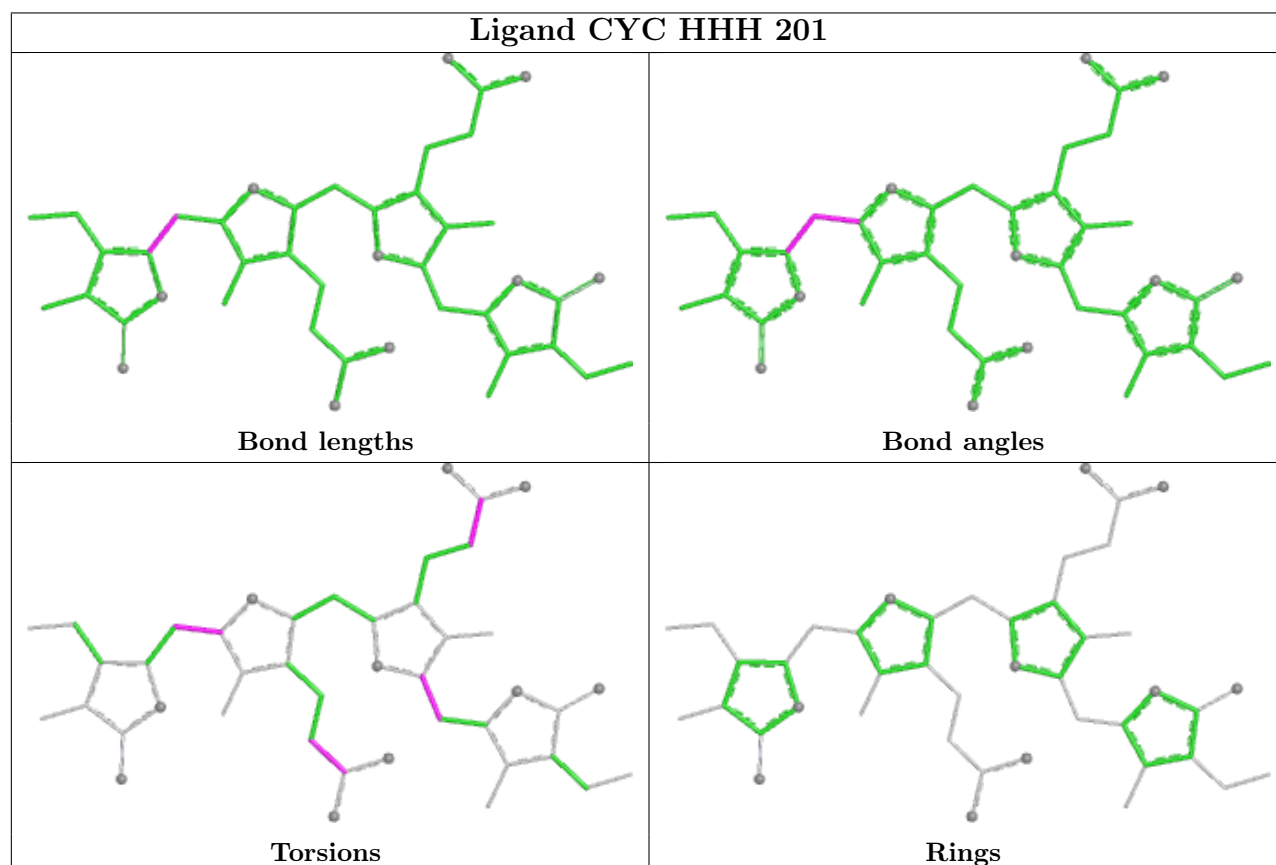
Ligand CYC LLL 201



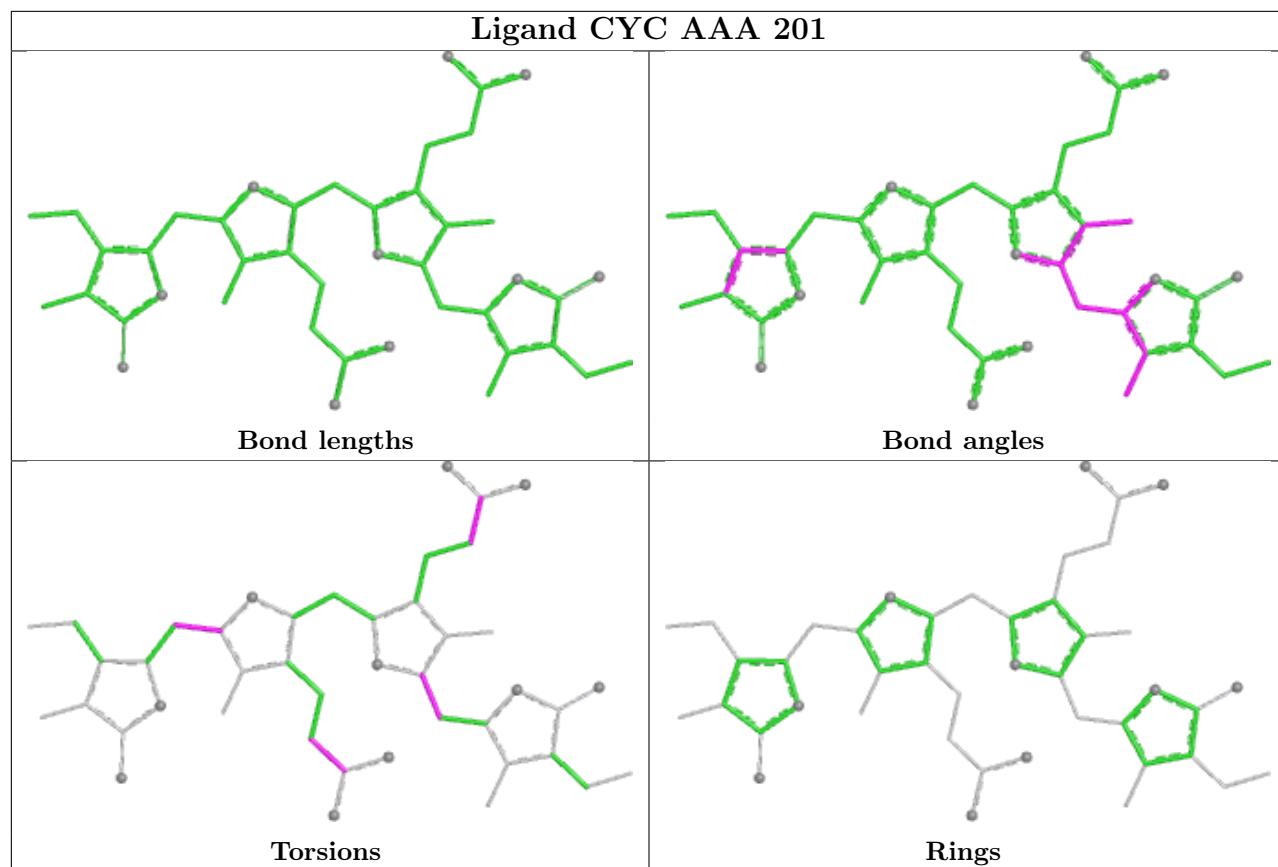
Ligand CYC EEE 201



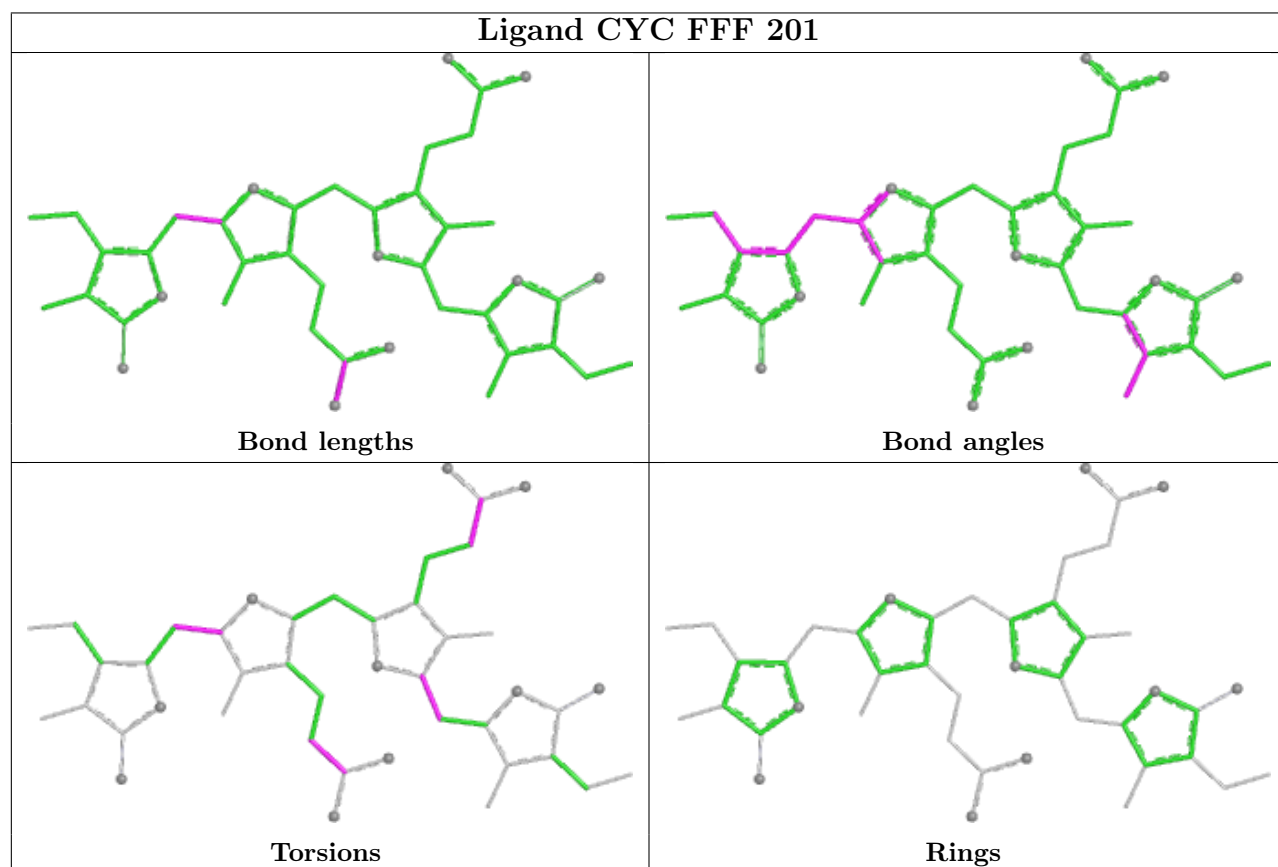
Ligand CYC HHH 201



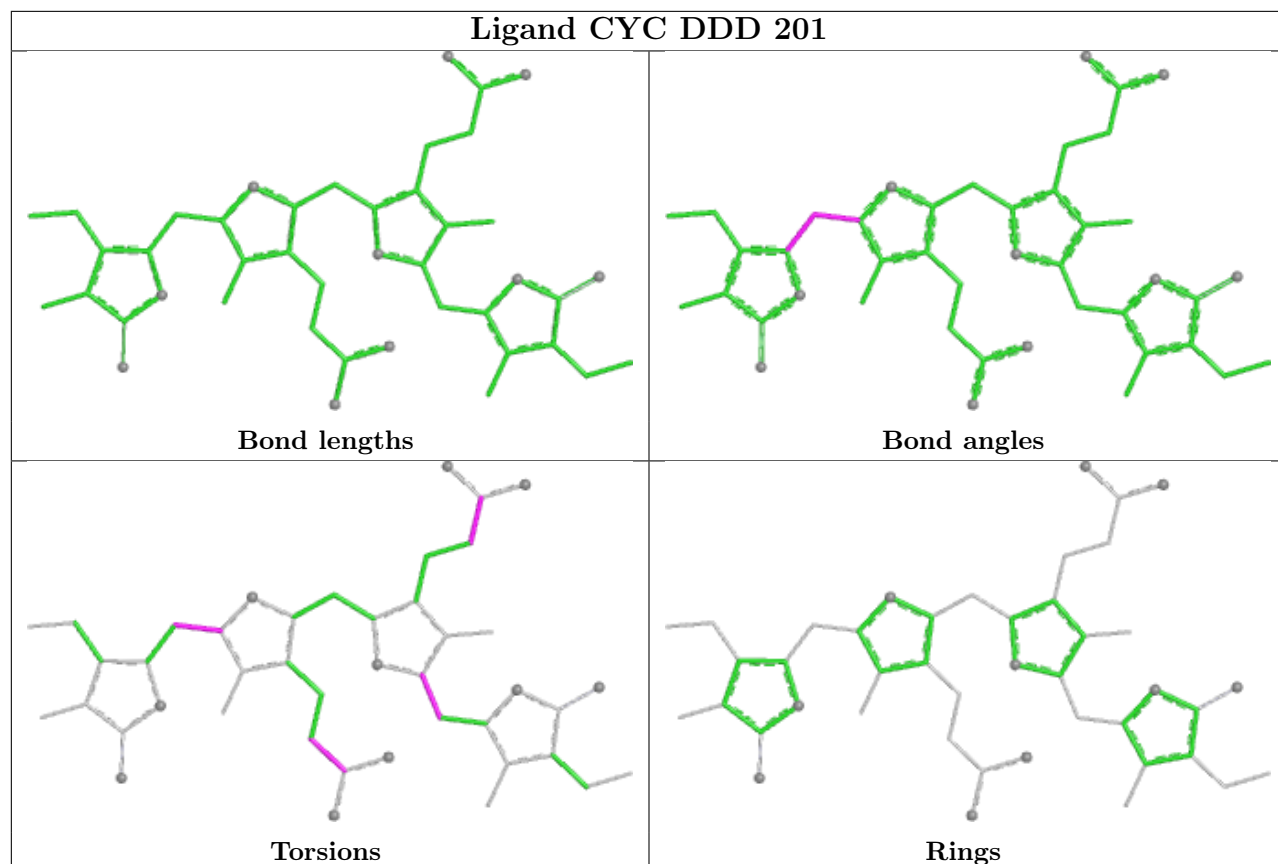
Ligand CYC AAA 201



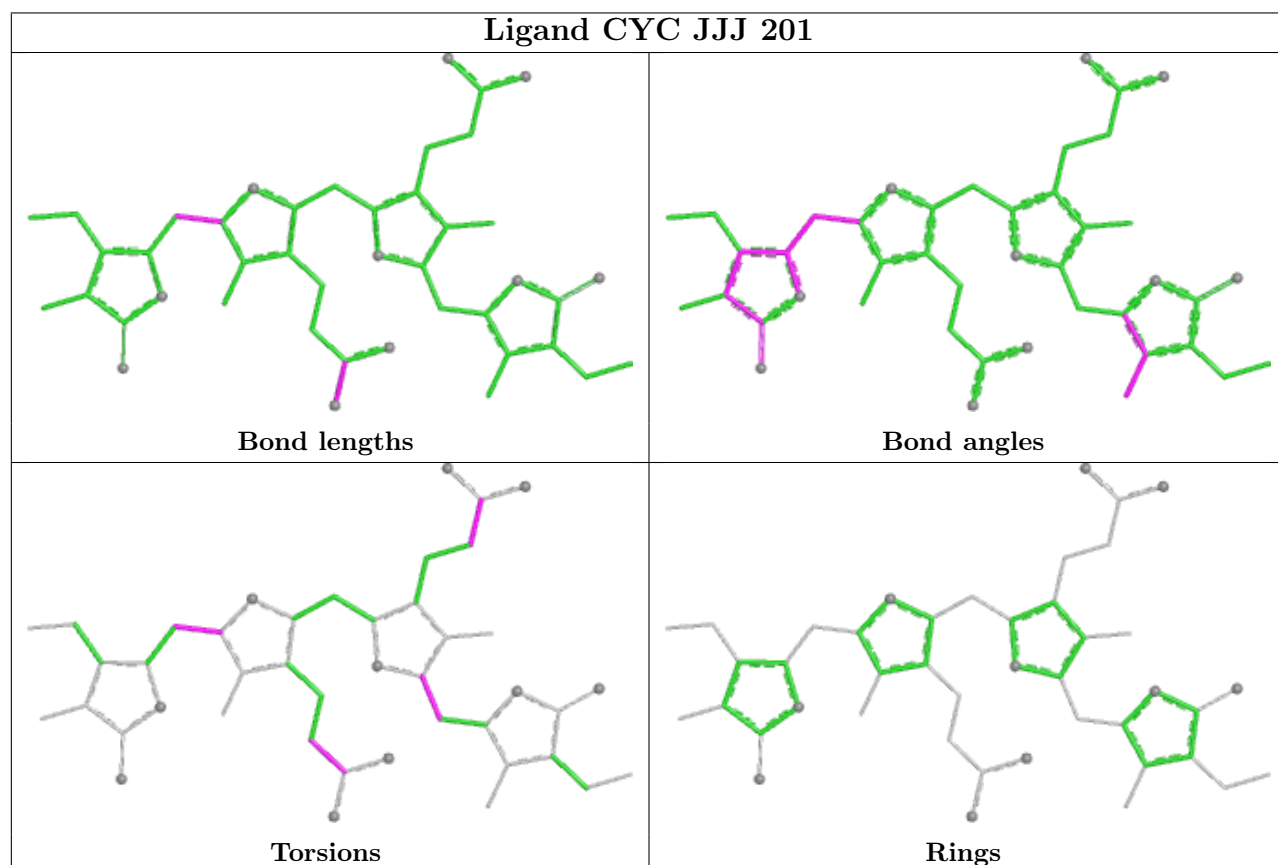
Ligand CYC FFF 201



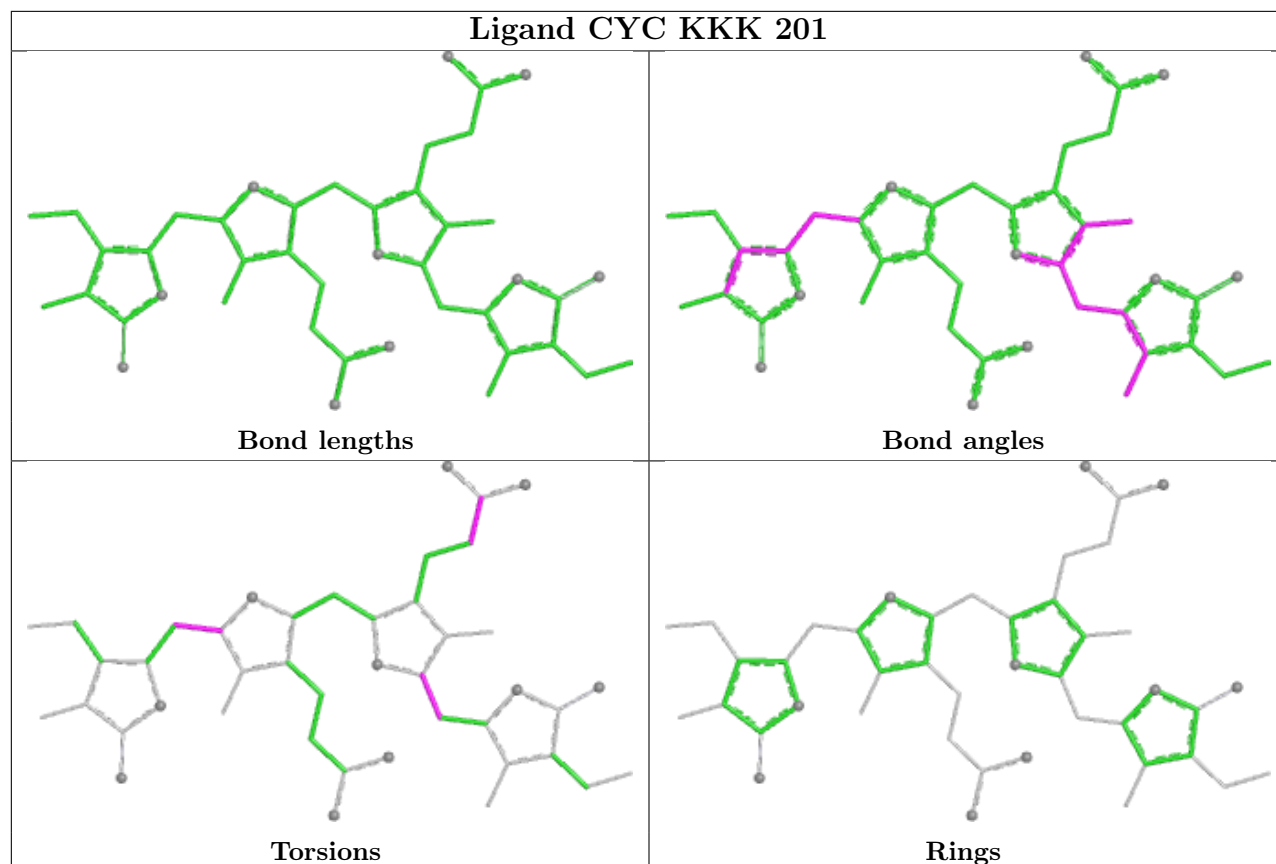
Ligand CYC DDD 201



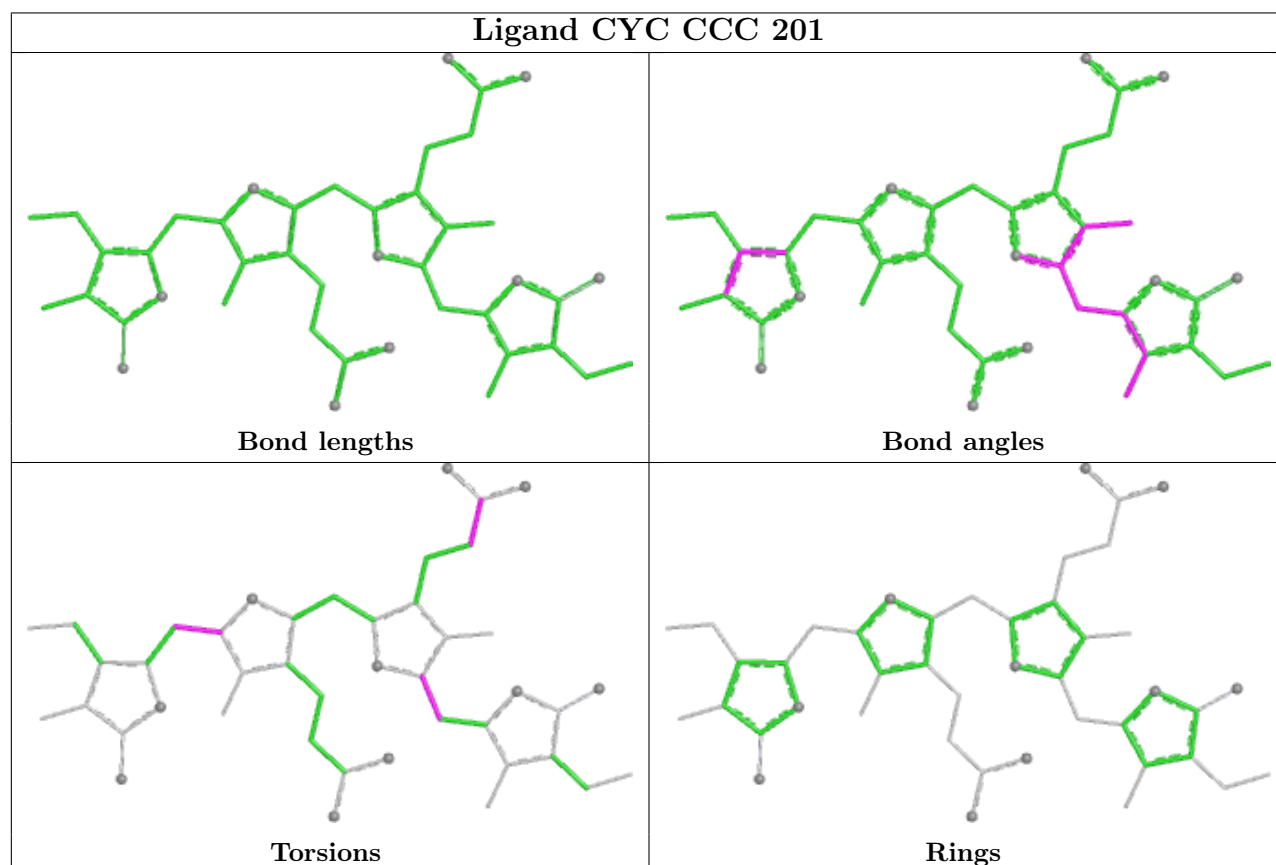
Ligand CYC JJJ 201

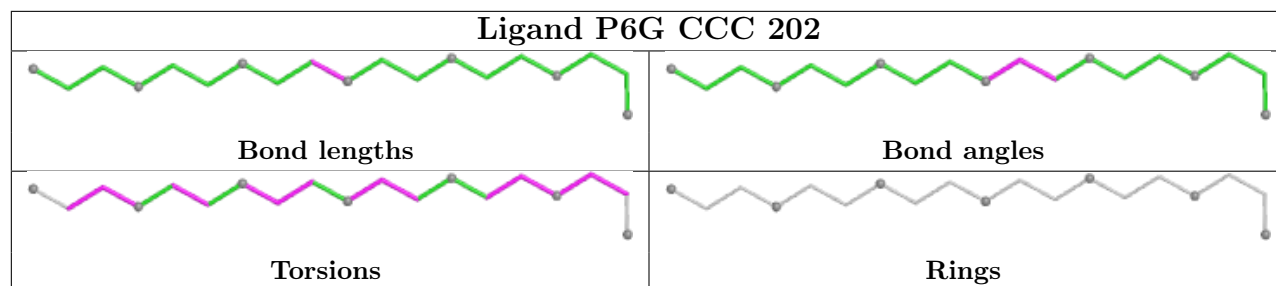


Ligand CYC KKK 201



Ligand CYC CCC 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 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å ²)	Q < 0.9
1	AAA	160/160 (100%)	0.06	1 (0%) 85 88	12, 30, 55, 71	10 (6%)
1	CCC	160/160 (100%)	-0.29	0 100 100	11, 21, 36, 50	15 (9%)
1	EEE	160/160 (100%)	-0.33	0 100 100	10, 22, 36, 57	12 (7%)
1	GGG	160/160 (100%)	-0.15	1 (0%) 85 88	10, 22, 38, 48	13 (8%)
1	III	160/160 (100%)	-0.15	1 (0%) 85 88	12, 24, 38, 60	8 (5%)
1	KKK	160/160 (100%)	0.07	2 (1%) 75 79	10, 28, 44, 65	16 (10%)
2	BBB	160/161 (99%)	-0.27	1 (0%) 85 88	10, 22, 39, 69	15 (9%)
2	DDD	160/161 (99%)	-0.45	1 (0%) 85 88	10, 20, 35, 62	19 (11%)
2	FFF	160/161 (99%)	-0.34	0 100 100	10, 22, 35, 58	3 (1%)
2	HHH	160/161 (99%)	-0.37	1 (0%) 85 88	9, 21, 37, 60	13 (8%)
2	JJJ	160/161 (99%)	-0.39	0 100 100	11, 20, 33, 56	9 (5%)
2	LLL	160/161 (99%)	-0.30	0 100 100	9, 21, 35, 65	11 (6%)
All	All	1920/1926 (99%)	-0.24	8 (0%) 88 91	9, 22, 40, 71	144 (7%)

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	160	GLN	3.4
1	KKK	2	ILE	2.6
2	HHH	157	CYS	2.5
1	III	123	ASP	2.4
1	GGG	20	GLY	2.4

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MEN	LLL	71	9/10	0.97	0.06	16,18,21,22	0
2	MEN	DDD	71	9/10	0.98	0.05	20,21,26,28	0
2	MEN	HHH	71	9/10	0.98	0.05	21,24,30,30	0
2	MEN	JJJ	71	9/10	0.98	0.04	13,14,17,20	0
2	MEN	BBB	71	9/10	0.98	0.04	15,17,20,22	0
2	MEN	FFF	71	9/10	0.99	0.03	14,15,18,18	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
15	PGE	GGG	204	10/10	0.59	0.23	35,38,43,43	10
12	GLY	EEE	202	5/5	0.64	0.21	30,31,33,34	5
7	1PE	BBB	204	16/16	0.71	0.24	25,38,43,44	16
6	MPD	EEE	203	8/8	0.72	0.27	28,30,31,32	8
8	PEG	BBB	205	7/7	0.74	0.25	28,34,38,39	7
11	GLU	HHH	202	10/10	0.74	0.23	37,43,47,47	10
10	P6G	CCC	202	19/19	0.75	0.42	33,37,39,41	19
5	LYS	III	202	10/10	0.75	0.20	35,37,40,43	10
8	PEG	BBB	206	7/7	0.77	0.24	35,36,37,38	7
8	PEG	BBB	208	7/7	0.78	0.20	32,33,35,37	7
8	PEG	JJJ	205	7/7	0.78	0.20	24,25,30,32	7
15	PGE	LLL	204	10/10	0.78	0.34	32,38,40,42	10
11	GLU	DDD	202	10/10	0.79	0.25	35,38,40,41	10
4	PG4	FFF	204	13/13	0.80	0.41	20,27,33,37	13
8	PEG	GGG	205	7/7	0.80	0.20	30,32,37,38	7
4	PG4	CCC	203	13/13	0.80	0.44	30,32,34,34	13
16	DSN	JJJ	202	7/7	0.83	0.22	34,37,39,40	7
14	MRD	GGG	202	8/8	0.84	0.15	28,29,32,36	8
8	PEG	CCC	204	7/7	0.84	0.16	28,34,37,38	7
4	PG4	AAA	202	13/13	0.85	0.20	25,29,34,36	13

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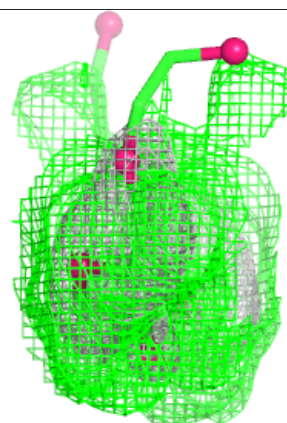
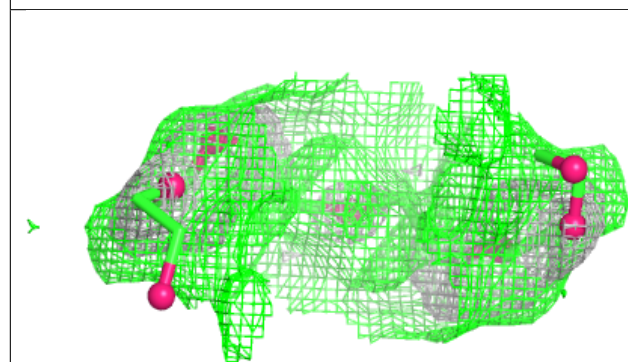
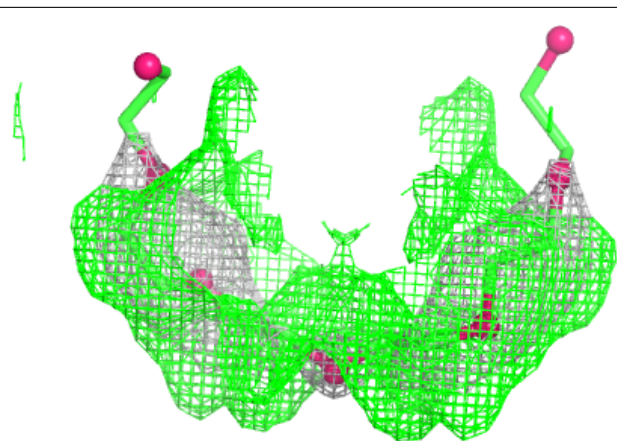
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	PG4	JJJ	204	13/13	0.85	0.21	28,34,41,43	13
15	PGE	GGG	203	10/10	0.85	0.18	24,31,34,36	10
16	DSN	LLL	202	7/7	0.86	0.21	33,36,37,38	7
13	ALA	FFF	202	6/6	0.87	0.25	37,37,40,43	6
9	EDO	CCC	205	4/4	0.88	0.16	29,29,30,31	4
8	PEG	HHH	204	7/7	0.89	0.17	25,29,32,34	7
5	LYS	KKK	202	10/10	0.89	0.17	21,33,40,43	10
6	MPD	BBB	203	8/8	0.90	0.18	24,27,32,33	8
9	EDO	KKK	204	4/4	0.91	0.22	27,27,27,28	4
5	LYS	BBB	202[A]	10/10	0.91	0.17	26,36,39,39	10
5	LYS	BBB	202[B]	10/10	0.91	0.17	25,36,39,39	10
6	MPD	HHH	203	8/8	0.91	0.15	26,29,35,36	8
9	EDO	BBB	207	4/4	0.92	0.13	28,32,33,33	4
6	MPD	DDD	203	8/8	0.92	0.14	26,29,34,37	8
6	MPD	LLL	203	8/8	0.94	0.16	23,26,32,33	8
9	EDO	CCC	206	4/4	0.94	0.09	24,26,27,27	4
9	EDO	KKK	203	4/4	0.95	0.11	28,29,31,33	4
6	MPD	JJJ	203	8/8	0.96	0.08	23,26,29,34	0
6	MPD	FFF	203	8/8	0.96	0.08	26,29,31,36	8
3	CYC	FFF	201	43/43	0.97	0.06	14,21,35,39	0
3	CYC	HHH	201	43/43	0.97	0.06	20,25,36,43	0
3	CYC	III	201	43/43	0.97	0.05	14,17,23,28	0
3	CYC	GGG	201	43/43	0.98	0.05	13,15,21,25	0
3	CYC	BBB	201	43/43	0.98	0.05	14,19,34,43	0
3	CYC	CCC	201	43/43	0.98	0.04	13,15,22,25	0
3	CYC	JJJ	201	43/43	0.98	0.05	14,22,36,40	0
3	CYC	KKK	201	43/43	0.98	0.05	14,18,26,29	0
3	CYC	LLL	201	43/43	0.98	0.05	14,18,31,40	0
3	CYC	DDD	201	43/43	0.98	0.05	17,22,33,37	0
3	CYC	EEE	201	43/43	0.98	0.04	14,16,22,28	0
3	CYC	AAA	201	43/43	0.98	0.04	17,19,26,31	0

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

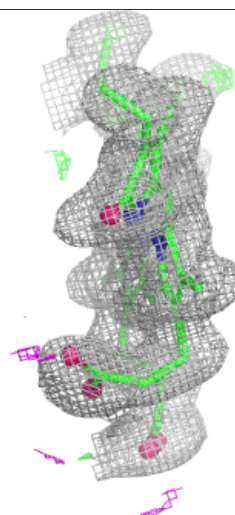
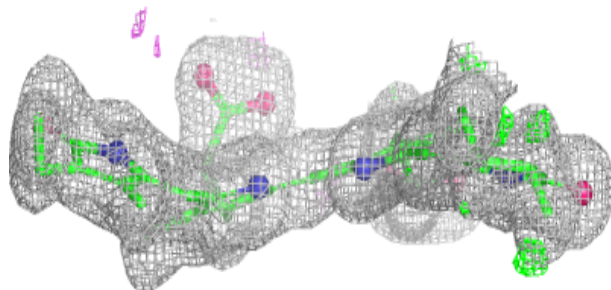
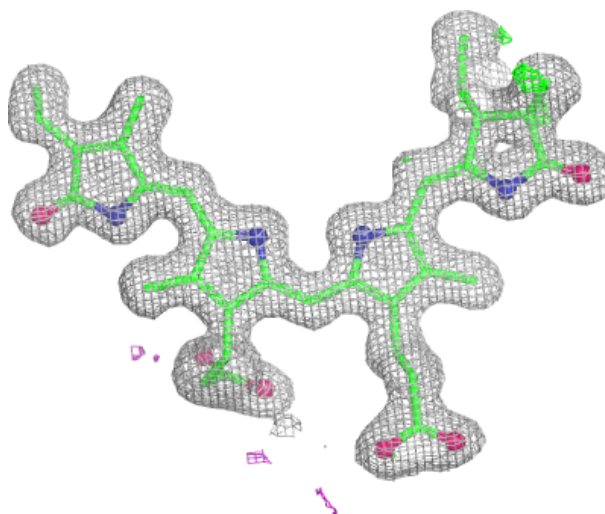
Electron density around P6G CCC 202:

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



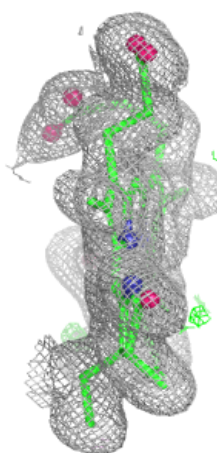
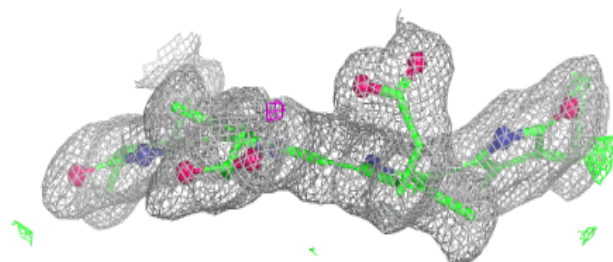
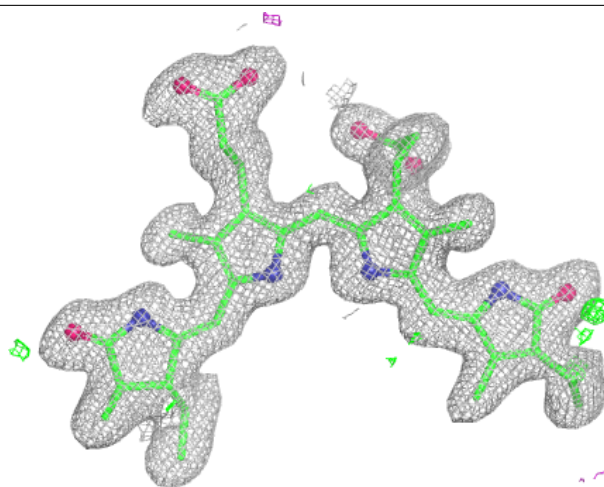
Electron density around CYC FFF 201:

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and green (positive)



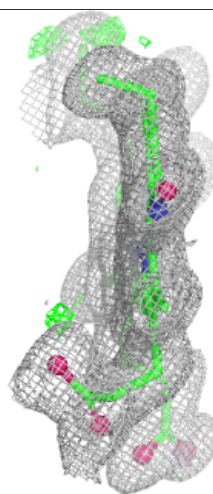
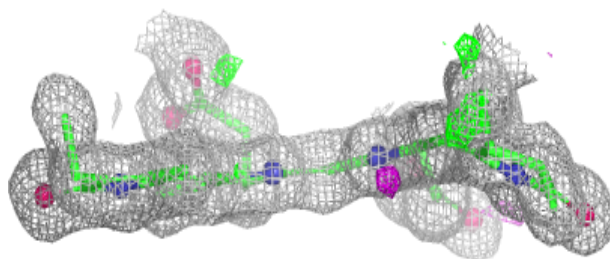
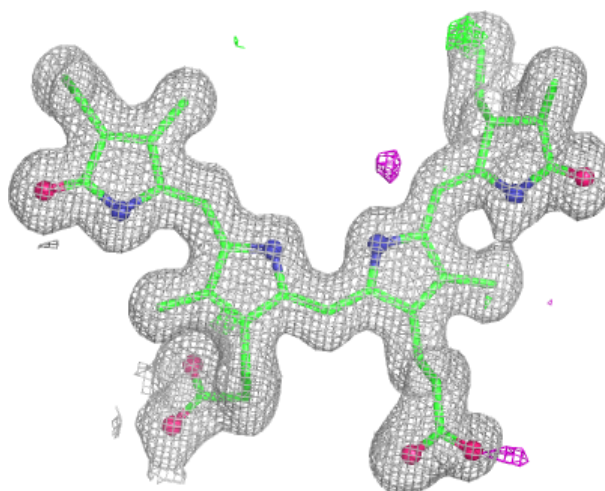
Electron density around CYC HHH 201:

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and green (positive)



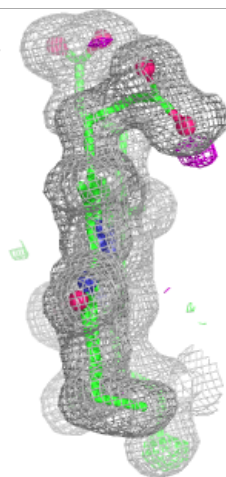
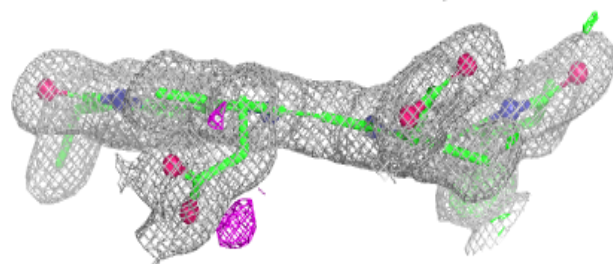
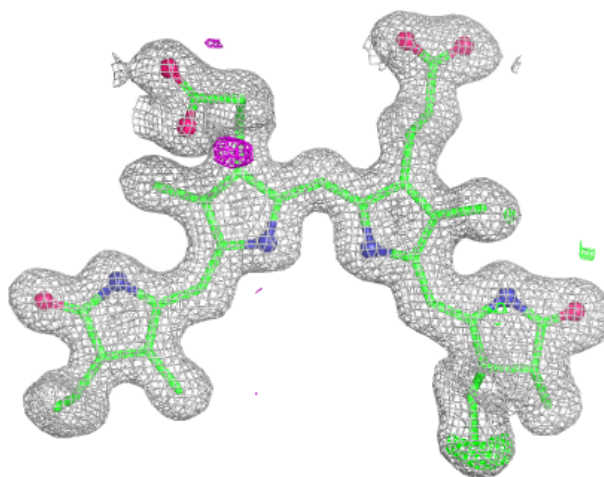
Electron density around CYC III 201:

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and green (positive)



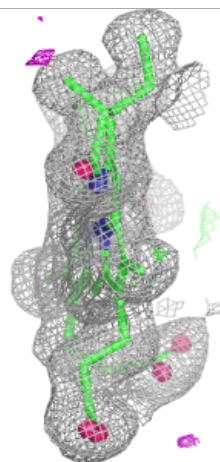
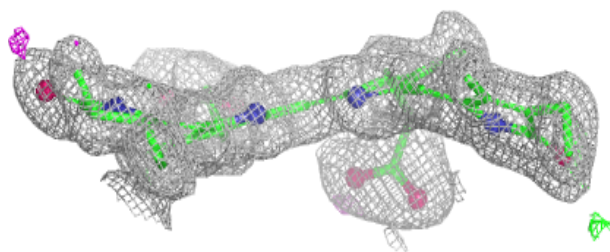
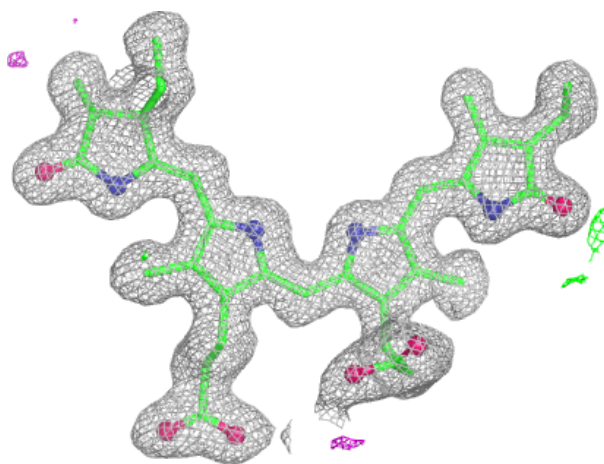
Electron density around CYC GGG 201:

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and green (positive)



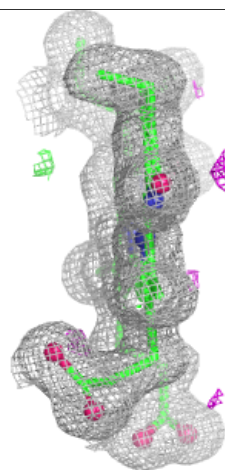
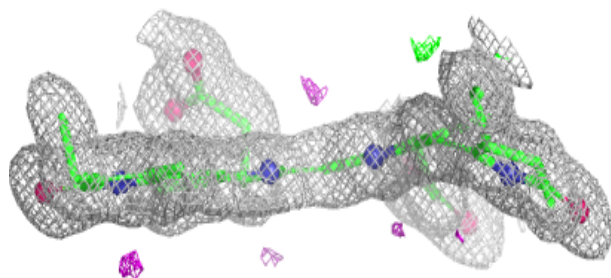
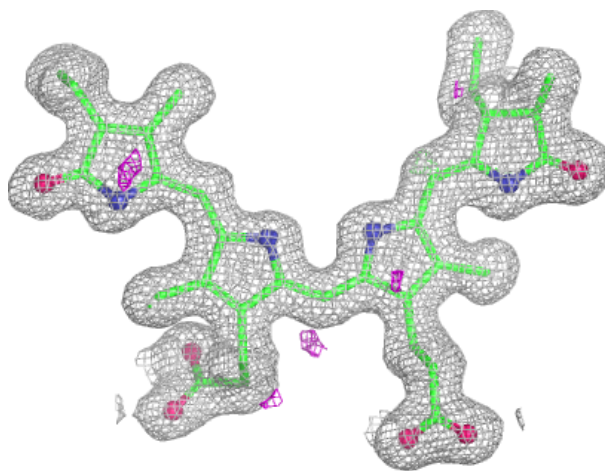
Electron density around CYC BBB 201:

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



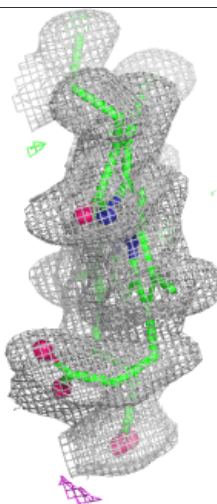
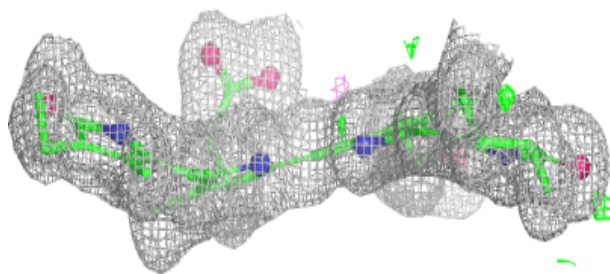
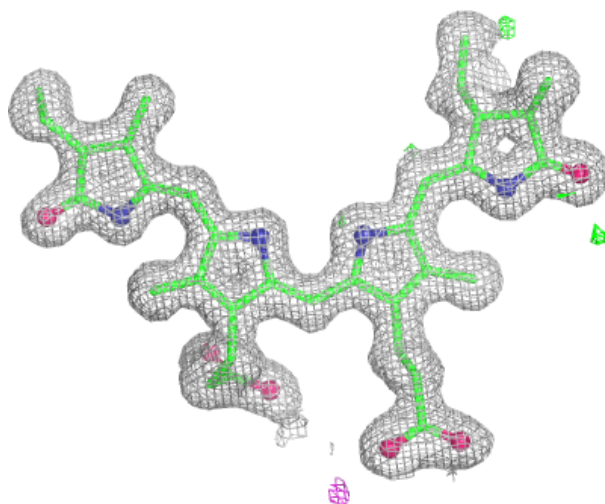
Electron density around CYC CCC 201:

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



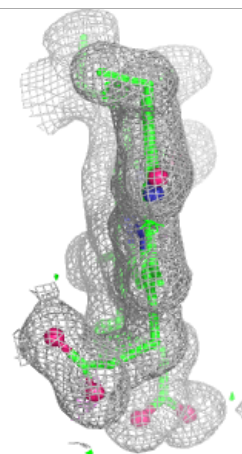
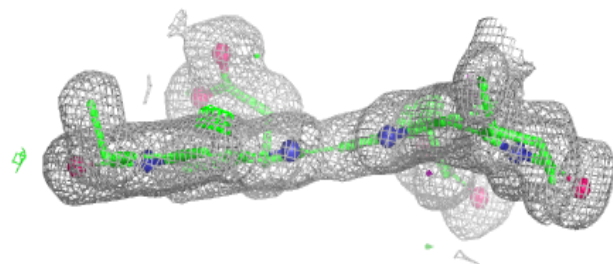
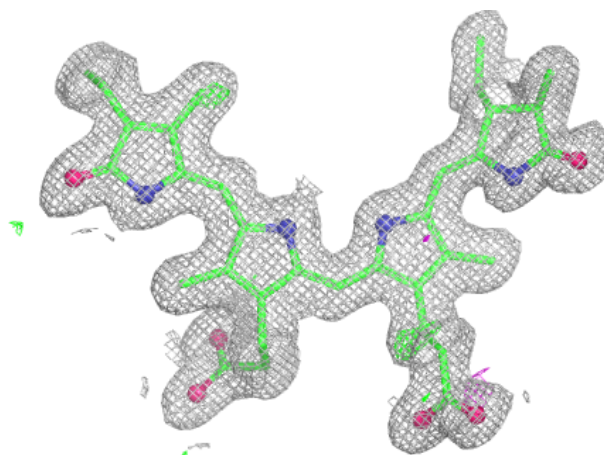
Electron density around CYC JJJ 201:

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



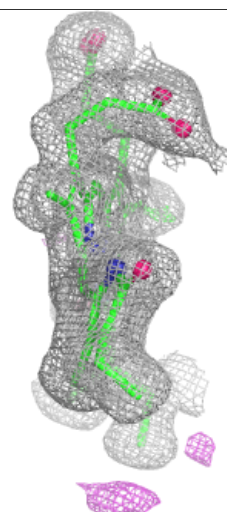
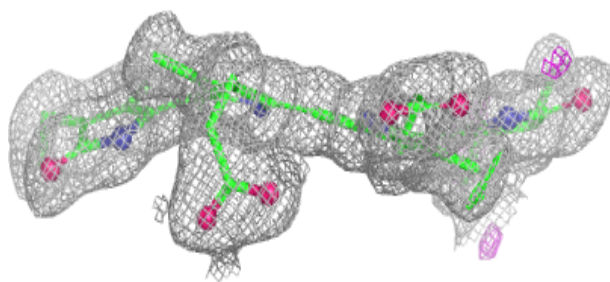
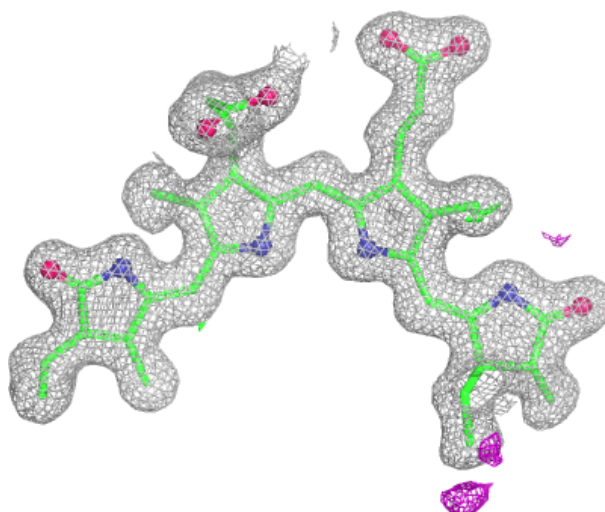
Electron density around CYC KKK 201:

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



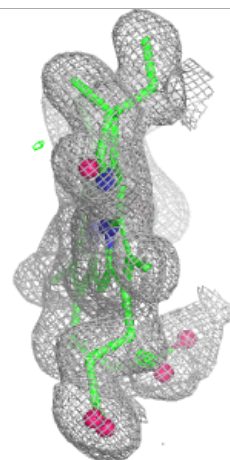
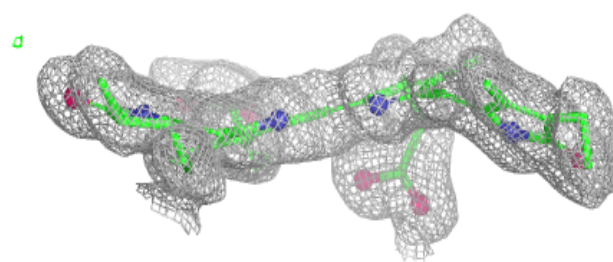
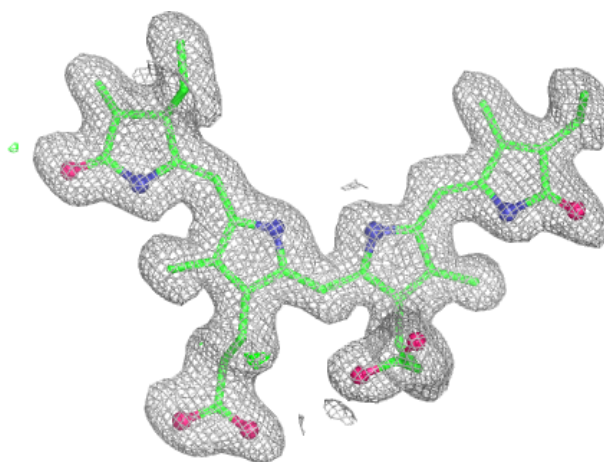
Electron density around CYC LLL 201:

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



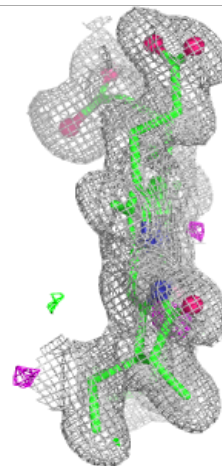
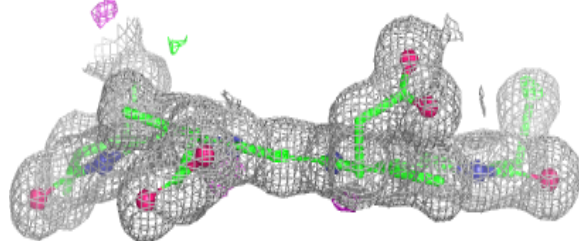
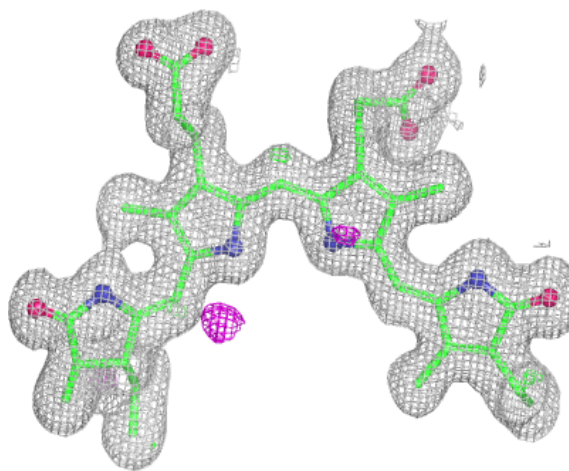
Electron density around CYC DDD 201:

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



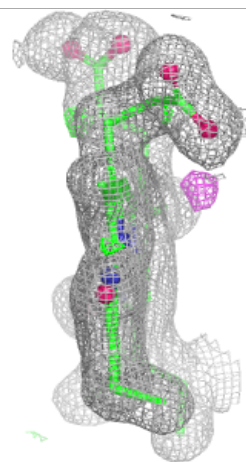
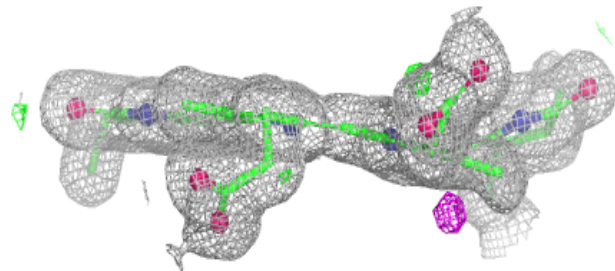
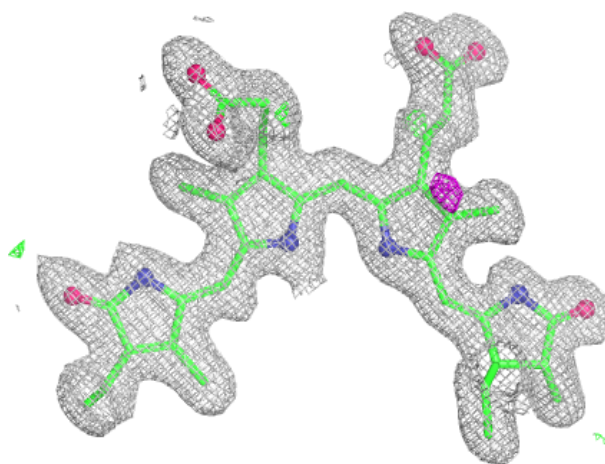
Electron density around CYC EEE 201:

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



Electron density around CYC AAA 201:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.