



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 5, 2026 – 09:23 PM EDT

PDB ID : 3SOM / pdb_00003som
Title : crystal structure of human MMACHC
Authors : Krojer, T.; Froese, D.S.; von Delft, F.; Muniz, J.R.; Gileadi, C.; Vollmar, M.; Bountra, C.; Arrowsmith, C.H.; Weigelt, J.; Edwards, A.; Gravel, R.A.; Yue, W.W.; Oppermann, U.; Structural Genomics Consortium (SGC)
Deposited on : 2011-06-30
Resolution : 2.40 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	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

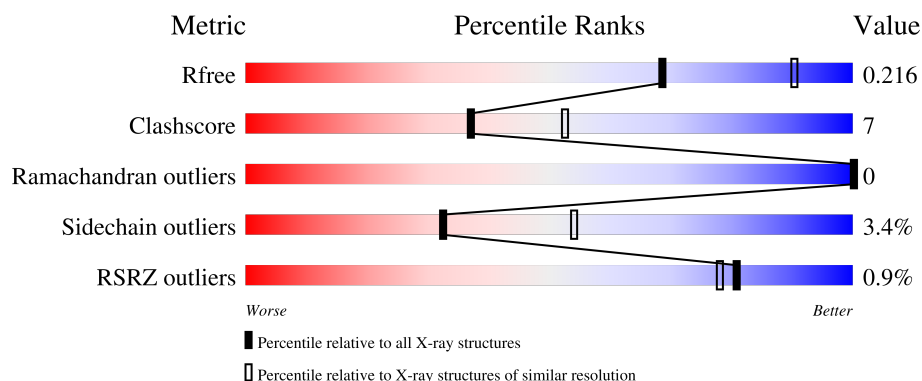
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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

Mol	Chain	Length	Quality of chain
1	A	286	
1	B	286	
1	C	286	
1	D	286	

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Mol	Chain	Length	Quality of chain
1	E	286	
1	F	286	
1	G	286	
1	H	286	
1	I	286	
1	J	286	
1	K	286	
1	L	286	
1	M	286	
1	N	286	
1	O	286	
1	P	286	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	5AD	A	401	X	-	-	-
5	5AD	B	401	X	-	-	-
5	5AD	C	401	X	-	-	-
5	5AD	D	401	X	-	-	-
5	5AD	E	401	X	-	-	-
5	5AD	F	401	X	-	-	-
5	5AD	G	283	X	-	-	-
5	5AD	G	401	X	-	-	-
5	5AD	H	401	X	-	-	-
5	5AD	I	283	X	-	-	-
5	5AD	I	401	X	-	-	-
5	5AD	J	401	X	-	-	-
5	5AD	K	401	X	-	-	-
5	5AD	L	401	X	-	-	-
5	5AD	M	401	X	-	-	-
5	5AD	N	401	X	-	-	-
5	5AD	O	401	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	5AD	P	401	X	-	-	-
6	EDO	P	284	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 33236 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 Methylmalonic aciduria and homocystinuria type C protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	227	Total	C	N	O	S	Se	0	0	0
			1837	1193	319	318	5	2			
1	B	228	Total	C	N	O	S	Se	0	0	0
			1837	1193	319	318	5	2			
1	C	228	Total	C	N	O	S	Se	0	2	0
			1832	1190	318	316	6	2			
1	D	229	Total	C	N	O	S	Se	0	1	0
			1848	1200	320	320	6	2			
1	E	230	Total	C	N	O	S	Se	0	1	0
			1849	1201	321	319	6	2			
1	F	228	Total	C	N	O	S	Se	0	3	0
			1857	1203	324	322	6	2			
1	G	228	Total	C	N	O	S	Se	0	0	0
			1843	1195	322	319	5	2			
1	H	227	Total	C	N	O	S	Se	0	0	0
			1833	1190	317	319	5	2			
1	I	228	Total	C	N	O	S	Se	0	1	0
			1844	1196	321	319	6	2			
1	J	227	Total	C	N	O	S	Se	0	2	0
			1844	1196	321	319	5	3			
1	K	227	Total	C	N	O	S	Se	0	1	0
			1832	1189	318	318	5	2			
1	L	231	Total	C	N	O	S	Se	0	2	0
			1868	1213	325	322	6	2			
1	M	231	Total	C	N	O	S	Se	0	1	0
			1861	1206	321	326	6	2			
1	N	232	Total	C	N	O	S	Se	0	0	0
			1853	1204	324	318	5	2			
1	O	228	Total	C	N	O	S	Se	0	1	0
			1836	1194	316	318	6	2			
1	P	230	Total	C	N	O	S	Se	0	0	0
			1860	1208	322	323	5	2			

There are 64 discrepancies between the modelled and reference sequences:

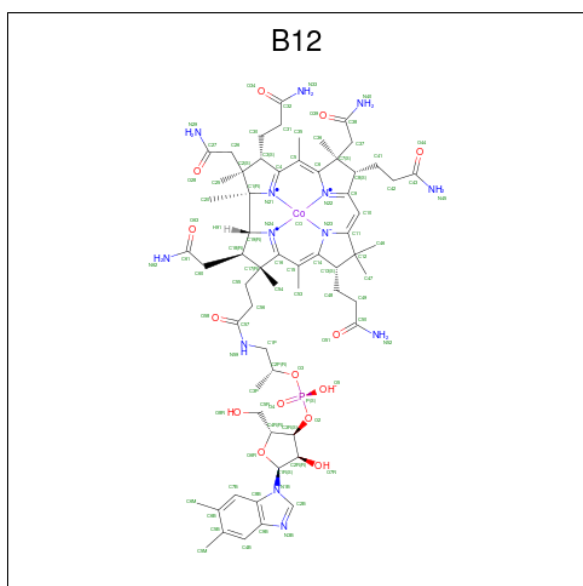
Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	TYR	-	expression tag	UNP Q9Y4U1
A	-2	PHE	-	expression tag	UNP Q9Y4U1
A	-1	GLN	-	expression tag	UNP Q9Y4U1
A	0	SER	-	expression tag	UNP Q9Y4U1
B	-3	TYR	-	expression tag	UNP Q9Y4U1
B	-2	PHE	-	expression tag	UNP Q9Y4U1
B	-1	GLN	-	expression tag	UNP Q9Y4U1
B	0	SER	-	expression tag	UNP Q9Y4U1
C	-3	TYR	-	expression tag	UNP Q9Y4U1
C	-2	PHE	-	expression tag	UNP Q9Y4U1
C	-1	GLN	-	expression tag	UNP Q9Y4U1
C	0	SER	-	expression tag	UNP Q9Y4U1
D	-3	TYR	-	expression tag	UNP Q9Y4U1
D	-2	PHE	-	expression tag	UNP Q9Y4U1
D	-1	GLN	-	expression tag	UNP Q9Y4U1
D	0	SER	-	expression tag	UNP Q9Y4U1
E	-3	TYR	-	expression tag	UNP Q9Y4U1
E	-2	PHE	-	expression tag	UNP Q9Y4U1
E	-1	GLN	-	expression tag	UNP Q9Y4U1
E	0	SER	-	expression tag	UNP Q9Y4U1
F	-3	TYR	-	expression tag	UNP Q9Y4U1
F	-2	PHE	-	expression tag	UNP Q9Y4U1
F	-1	GLN	-	expression tag	UNP Q9Y4U1
F	0	SER	-	expression tag	UNP Q9Y4U1
G	-3	TYR	-	expression tag	UNP Q9Y4U1
G	-2	PHE	-	expression tag	UNP Q9Y4U1
G	-1	GLN	-	expression tag	UNP Q9Y4U1
G	0	SER	-	expression tag	UNP Q9Y4U1
H	-3	TYR	-	expression tag	UNP Q9Y4U1
H	-2	PHE	-	expression tag	UNP Q9Y4U1
H	-1	GLN	-	expression tag	UNP Q9Y4U1
H	0	SER	-	expression tag	UNP Q9Y4U1
I	-3	TYR	-	expression tag	UNP Q9Y4U1
I	-2	PHE	-	expression tag	UNP Q9Y4U1
I	-1	GLN	-	expression tag	UNP Q9Y4U1
I	0	SER	-	expression tag	UNP Q9Y4U1
J	-3	TYR	-	expression tag	UNP Q9Y4U1
J	-2	PHE	-	expression tag	UNP Q9Y4U1
J	-1	GLN	-	expression tag	UNP Q9Y4U1
J	0	SER	-	expression tag	UNP Q9Y4U1
K	-3	TYR	-	expression tag	UNP Q9Y4U1
K	-2	PHE	-	expression tag	UNP Q9Y4U1

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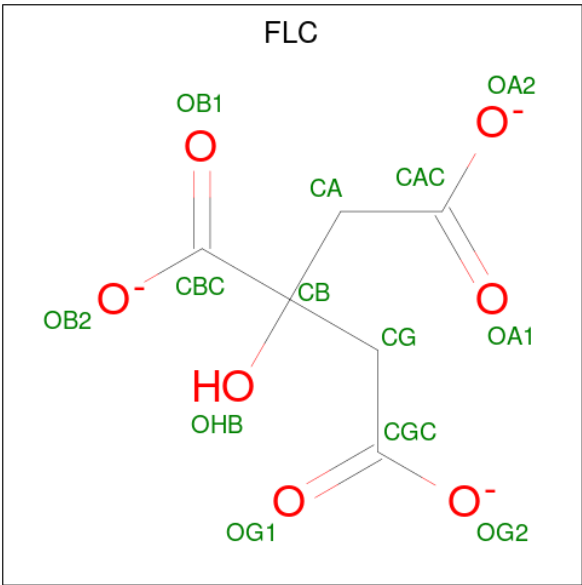
Chain	Residue	Modelled	Actual	Comment	Reference
K	-1	GLN	-	expression tag	UNP Q9Y4U1
K	0	SER	-	expression tag	UNP Q9Y4U1
L	-3	TYR	-	expression tag	UNP Q9Y4U1
L	-2	PHE	-	expression tag	UNP Q9Y4U1
L	-1	GLN	-	expression tag	UNP Q9Y4U1
L	0	SER	-	expression tag	UNP Q9Y4U1
M	-3	TYR	-	expression tag	UNP Q9Y4U1
M	-2	PHE	-	expression tag	UNP Q9Y4U1
M	-1	GLN	-	expression tag	UNP Q9Y4U1
M	0	SER	-	expression tag	UNP Q9Y4U1
N	-3	TYR	-	expression tag	UNP Q9Y4U1
N	-2	PHE	-	expression tag	UNP Q9Y4U1
N	-1	GLN	-	expression tag	UNP Q9Y4U1
N	0	SER	-	expression tag	UNP Q9Y4U1
O	-3	TYR	-	expression tag	UNP Q9Y4U1
O	-2	PHE	-	expression tag	UNP Q9Y4U1
O	-1	GLN	-	expression tag	UNP Q9Y4U1
O	0	SER	-	expression tag	UNP Q9Y4U1
P	-3	TYR	-	expression tag	UNP Q9Y4U1
P	-2	PHE	-	expression tag	UNP Q9Y4U1
P	-1	GLN	-	expression tag	UNP Q9Y4U1
P	0	SER	-	expression tag	UNP Q9Y4U1

- Molecule 2 is COBALAMIN (CCD ID: B12) (formula: $C_{62}H_{89}CoN_{13}O_{14}P$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
2	B	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
2	C	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
2	D	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
2	E	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
2	F	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
2	G	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
2	H	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
2	I	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
2	J	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
2	K	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
2	L	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
2	M	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
2	N	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
2	O	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0
2	P	1	Total 91	C 62	Co 1	N 13	O 14	P 1	0	0

- Molecule 3 is CITRATE ANION (CCD ID: FLC) (formula: $C_6H_5O_7$).



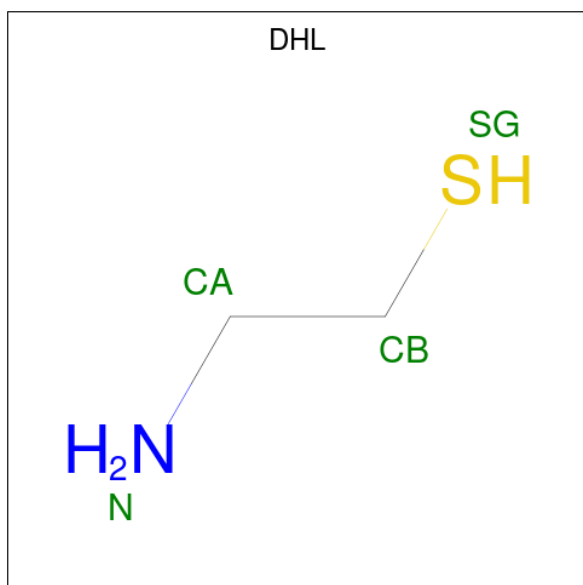
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		
3	B	1	Total	C	O	0	0
			13	6	7		
3	C	1	Total	C	O	0	0
			13	6	7		
3	D	1	Total	C	O	0	0
			13	6	7		
3	E	1	Total	C	O	0	0
			13	6	7		
3	F	1	Total	C	O	0	0
			13	6	7		
3	G	1	Total	C	O	0	0
			13	6	7		
3	H	1	Total	C	O	0	0
			13	6	7		
3	I	1	Total	C	O	0	0
			13	6	7		
3	J	1	Total	C	O	0	0
			13	6	7		
3	K	1	Total	C	O	0	0
			13	6	7		
3	L	1	Total	C	O	0	0
			13	6	7		
3	M	1	Total	C	O	0	0
			13	6	7		
3	N	1	Total	C	O	0	0
			13	6	7		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	O	1	Total	C	O	0	0
			13	6	7		
3	P	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is 2-AMINO-ETHANETHIOL (CCD ID: DHL) (formula: C₂H₇NS).



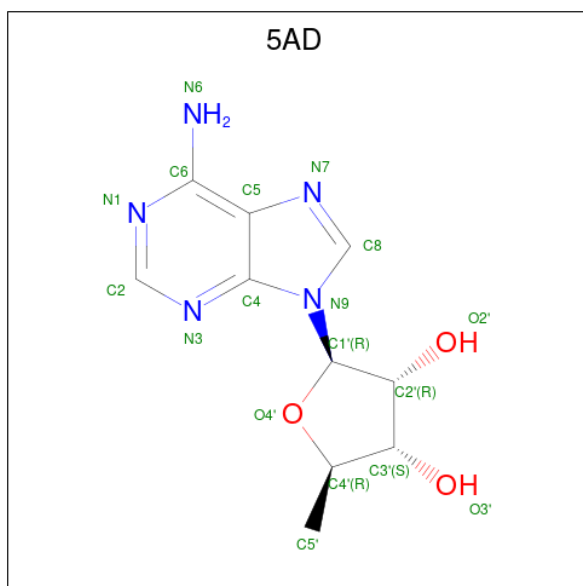
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	S	0	0
			4	2	1	1		
4	C	1	Total	C	N	S	0	0
			4	2	1	1		
4	D	1	Total	C	N	S	0	0
			4	2	1	1		
4	F	1	Total	C	N	S	0	0
			4	2	1	1		
4	G	1	Total	C	N	S	0	0
			4	2	1	1		
4	H	1	Total	C	N	S	0	0
			4	2	1	1		
4	I	1	Total	C	N	S	0	0
			4	2	1	1		
4	J	1	Total	C	N	S	0	0
			4	2	1	1		
4	K	1	Total	C	N	S	0	0
			4	2	1	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	L	1	Total	C	N	S	0	0
			4	2	1	1		
4	M	1	Total	C	N	S	0	0
			4	2	1	1		
4	N	1	Total	C	N	S	0	0
			4	2	1	1		
4	O	1	Total	C	N	S	0	0
			4	2	1	1		
4	P	1	Total	C	N	S	0	0
			4	2	1	1		

- Molecule 5 is 5'-DEOXYADENOSINE (CCD ID: 5AD) (formula: $C_{10}H_{13}N_5O_3$).



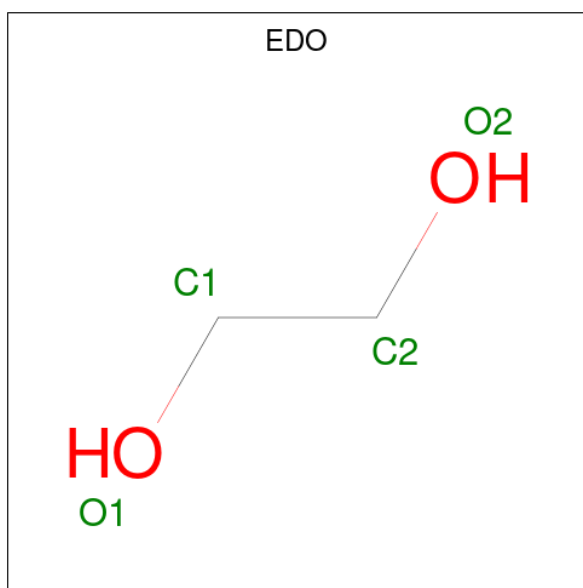
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			18	10	5	3		
5	B	1	Total	C	N	O	0	0
			18	10	5	3		
5	C	1	Total	C	N	O	0	0
			18	10	5	3		
5	D	1	Total	C	N	O	0	0
			18	10	5	3		
5	E	1	Total	C	N	O	0	0
			18	10	5	3		
5	F	1	Total	C	N	O	0	0
			18	10	5	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	G	1	Total	C	N	O	0	0
			18	10	5	3		
5	G	1	Total	C	N	O	0	0
			18	10	5	3		
5	H	1	Total	C	N	O	0	0
			18	10	5	3		
5	I	1	Total	C	N	O	0	0
			18	10	5	3		
5	I	1	Total	C	N	O	0	0
			18	10	5	3		
5	J	1	Total	C	N	O	0	0
			18	10	5	3		
5	K	1	Total	C	N	O	0	0
			18	10	5	3		
5	L	1	Total	C	N	O	0	0
			18	10	5	3		
5	M	1	Total	C	N	O	0	0
			18	10	5	3		
5	N	1	Total	C	N	O	0	0
			18	10	5	3		
5	O	1	Total	C	N	O	0	0
			18	10	5	3		
5	P	1	Total	C	N	O	0	0
			18	10	5	3		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	E	1	Total C O 4 2 2	0	0
6	P	1	Total C O 4 2 2	0	0
6	P	1	Total C O 4 2 2	0	0

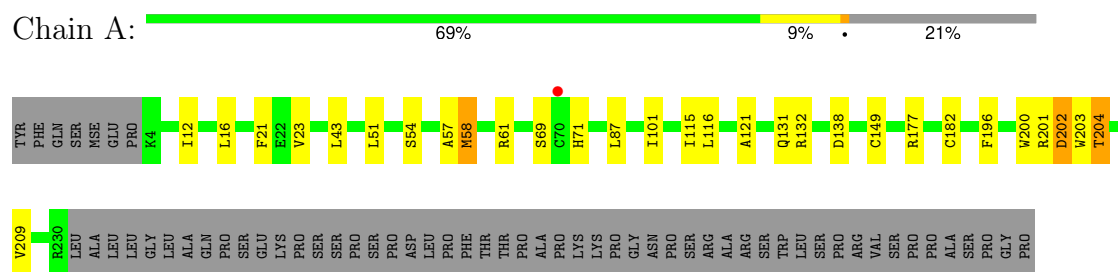
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	70	Total O 70 70	0	0
7	B	63	Total O 63 63	0	0
7	C	63	Total O 63 63	0	0
7	D	79	Total O 79 79	0	0
7	E	105	Total O 105 105	0	0
7	F	111	Total O 111 111	0	0
7	G	125	Total O 125 125	0	0
7	H	124	Total O 124 124	0	0
7	I	122	Total O 122 122	0	0
7	J	111	Total O 111 111	0	0
7	K	100	Total O 100 100	0	0
7	L	130	Total O 130 130	0	0
7	M	125	Total O 125 125	0	0
7	N	100	Total O 100 100	0	0
7	O	124	Total O 124 124	0	0
7	P	94	Total O 94 94	0	0

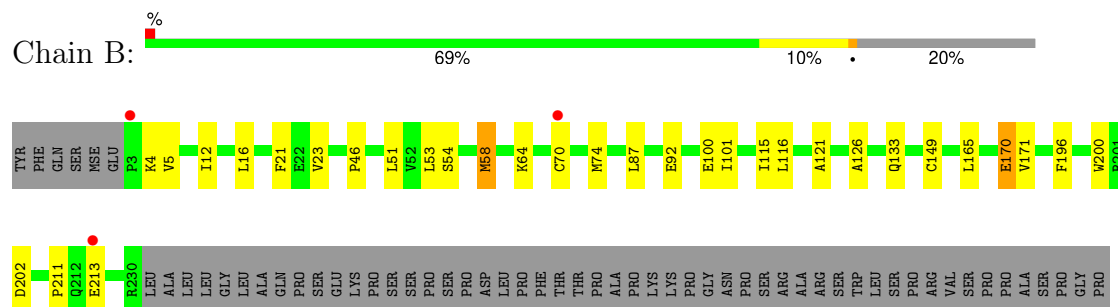
3 Residue-property plots [i](#)

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.

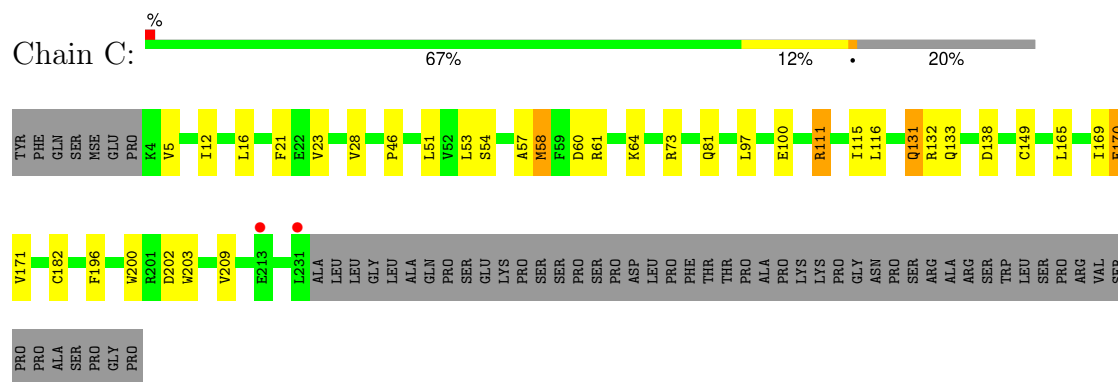
- Molecule 1: Methylmalonic aciduria and homocystinuria type C protein



- Molecule 1: Methylmalonic aciduria and homocystinuria type C protein

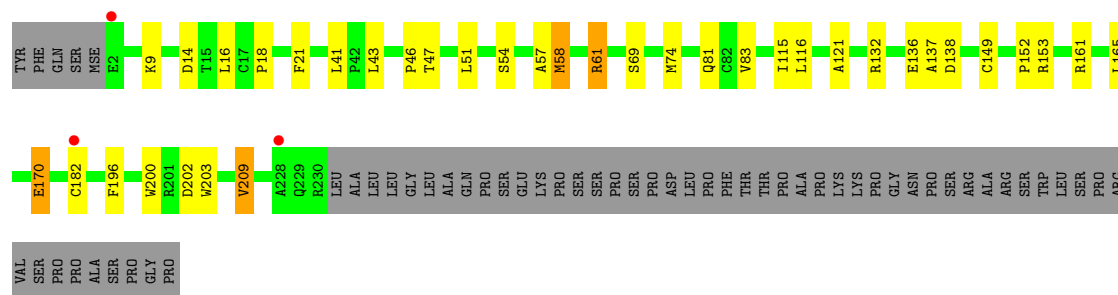


- Molecule 1: Methylmalonic aciduria and homocystinuria type C protein



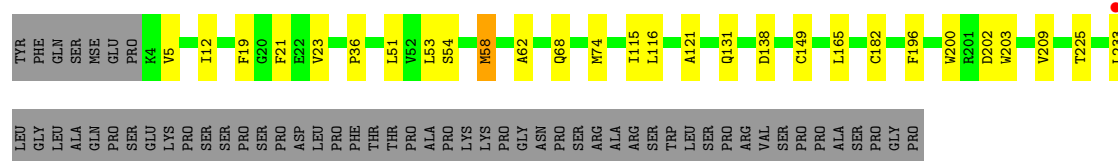
- Molecule 1: Methylmalonic aciduria and homocystinuria type C protein





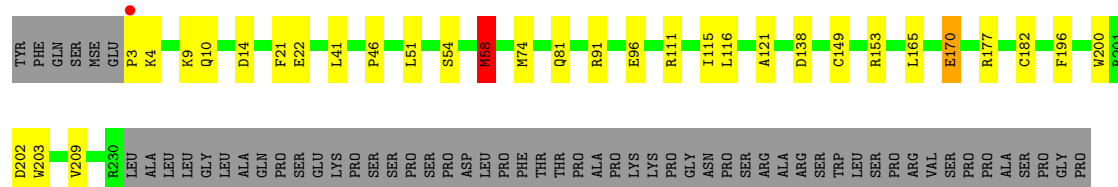
- Molecule 1: Methylmalonic aciduria and homocystinuria type C protein

Chain E: 71% 9% 20%



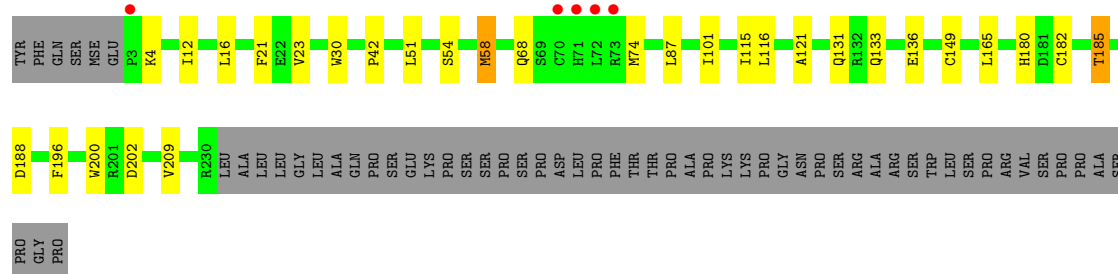
- Molecule 1: Methylmalonic aciduria and homocystinuria type C protein

Chain F: 69% 10% 20%



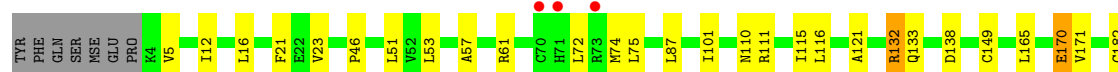
- Molecule 1: Methylmalonic aciduria and homocystinuria type C protein

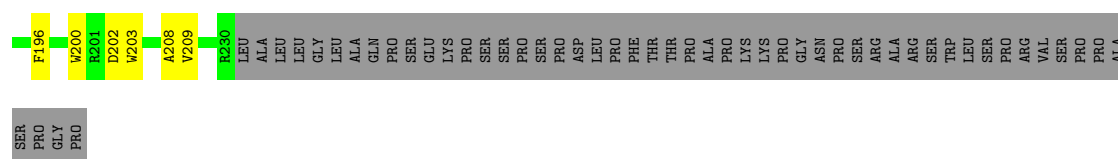
Chain G: 69% 10% 20%



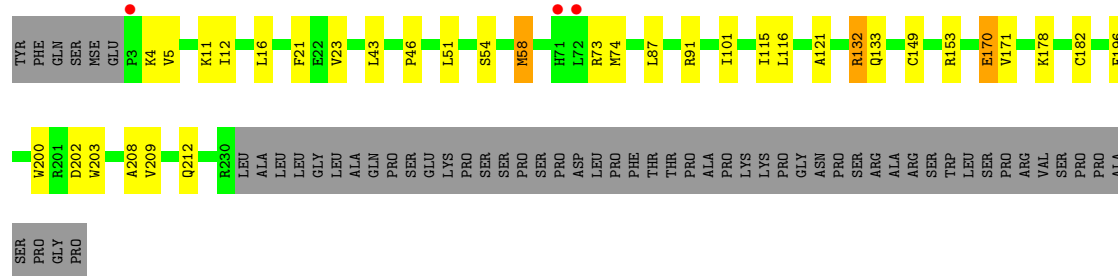
- Molecule 1: Methylmalonic aciduria and homocystinuria type C protein

Chain H: 67% 11% 21%

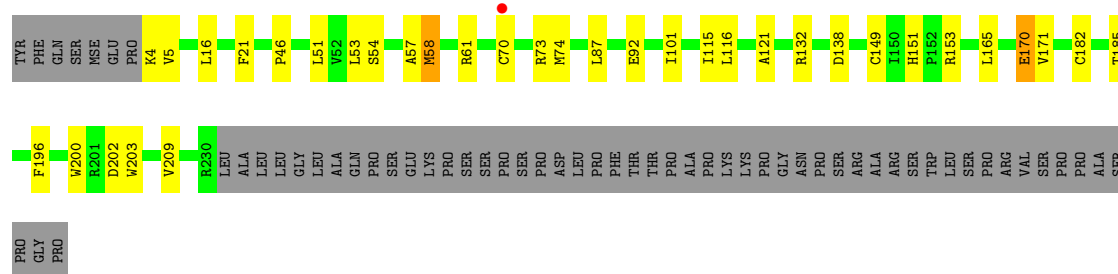




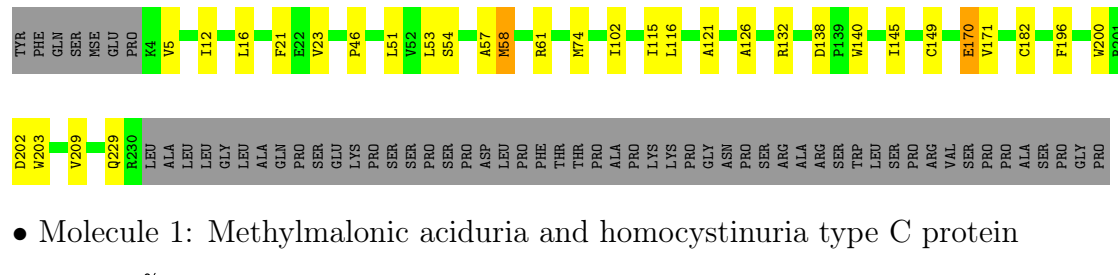
- Molecule 1: Methylmalonic aciduria and homocystinuria type C protein



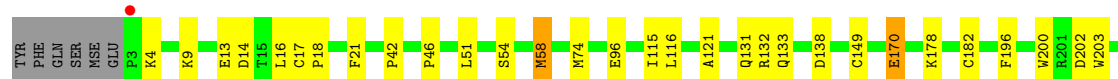
- Molecule 1: Methylmalonic aciduria and homocystinuria type C protein

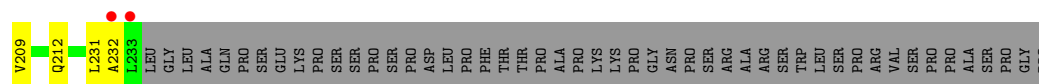


- Molecule 1: Methylmalonic aciduria and homocystinuria type C protein

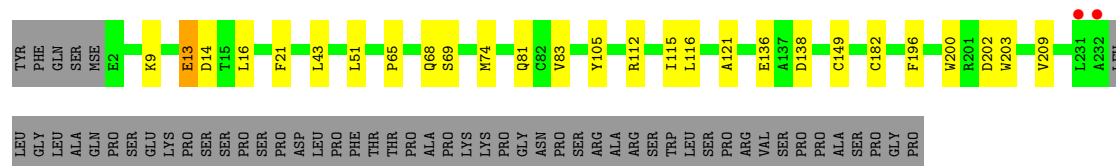


- Molecule 1: Methylmalonic aciduria and homocystinuria type C protein

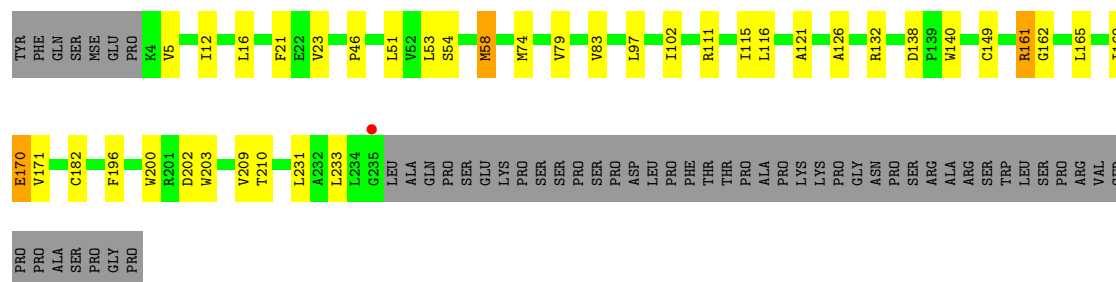




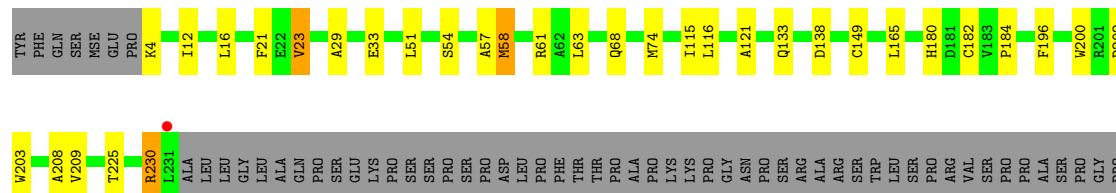
- Molecule 1: Methylmalonic aciduria and homocystinuria type C protein



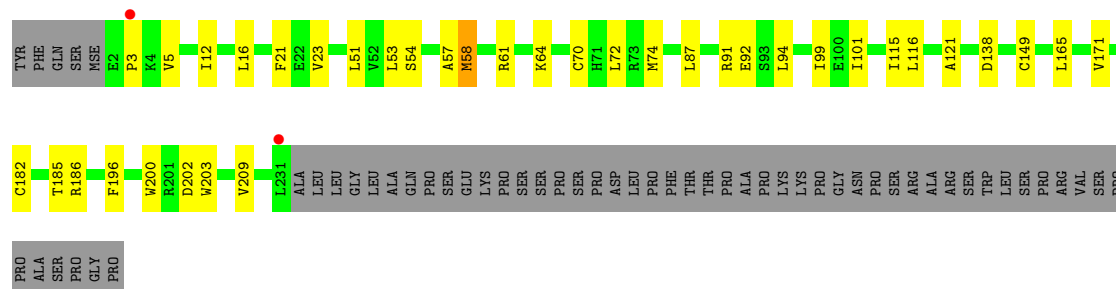
- Molecule 1: Methylmalonic aciduria and homocystinuria type C protein



- Molecule 1: Methylmalonic aciduria and homocystinuria type C protein



- Molecule 1: Methylmalonic aciduria and homocystinuria type C protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	71.66Å 71.96Å 300.06Å 88.53° 85.25° 83.76°	Depositor
Resolution (Å)	19.86 – 2.40 19.86 – 2.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) (19.86-2.40) 98.6 (19.86-2.40)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 2.41Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.182 , 0.206 0.190 , 0.216	Depositor DCC
R_{free} test set	11473 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	30.7	Xtriage
Anisotropy	0.112	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.007 for -h,-k,-h+l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	33236	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.16% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FLC, 5AD, B12, DHL, EDO

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	0.79	0/1898	1.18	6/2592 (0.2%)
1	B	0.79	0/1899	1.21	5/2595 (0.2%)
1	C	0.79	0/1899	1.21	10/2598 (0.4%)
1	D	0.81	0/1913	1.21	8/2616 (0.3%)
1	E	0.80	0/1913	1.22	8/2615 (0.3%)
1	F	0.84	1/1928 (0.1%)	1.22	8/2635 (0.3%)
1	G	0.80	0/1905	1.20	5/2603 (0.2%)
1	H	0.79	0/1894	1.22	10/2588 (0.4%)
1	I	0.77	0/1909	1.20	11/2609 (0.4%)
1	J	0.81	0/1911	1.22	11/2610 (0.4%)
1	K	0.81	0/1899	1.22	7/2596 (0.3%)
1	L	0.82	0/1936	1.25	11/2646 (0.4%)
1	M	0.82	0/1926	1.23	6/2635 (0.2%)
1	N	0.81	0/1914	1.26	10/2618 (0.4%)
1	O	0.81	0/1900	1.23	8/2596 (0.3%)
1	P	0.80	0/1922	1.22	9/2626 (0.3%)
All	All	0.80	1/30566 (0.0%)	1.22	133/41778 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	58	MSE	SE-CE	-5.35	1.79	1.95

The worst 5 of 133 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	138	ASP	CA-CB-CG	8.72	121.32	112.60
1	N	138	ASP	CA-CB-CG	8.72	121.33	112.60
1	O	138	ASP	CA-CB-CG	8.71	121.31	112.60
1	H	202	ASP	CA-CB-CG	7.41	120.01	112.60
1	P	138	ASP	CA-CB-CG	7.14	119.74	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	A	1837	0	1791	15	0
1	B	1837	0	1792	15	0
1	C	1832	0	1779	18	0
1	D	1848	0	1798	20	0
1	E	1849	0	1802	18	0
1	F	1857	0	1813	19	0
1	G	1843	0	1797	22	0
1	H	1833	0	1782	22	0
1	I	1844	0	1796	19	0
1	J	1844	0	1804	16	0
1	K	1832	0	1783	21	0
1	L	1868	0	1826	17	0
1	M	1861	0	1800	19	0
1	N	1853	0	1806	21	0
1	O	1836	0	1786	23	0
1	P	1860	0	1817	22	0
2	A	91	0	88	14	0
2	B	91	0	88	13	0
2	C	91	0	88	15	0
2	D	91	0	88	12	0
2	E	91	0	88	14	0
2	F	91	0	88	13	0
2	G	91	0	88	15	0
2	H	91	0	88	13	0
2	I	91	0	88	14	0
2	J	91	0	88	12	0
2	K	91	0	88	12	0
2	L	91	0	88	13	0
2	M	91	0	88	12	0
2	N	91	0	88	13	0
2	O	91	0	88	15	0
2	P	91	0	88	16	0
3	A	13	0	5	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	13	0	5	0	0
3	C	13	0	5	0	0
3	D	13	0	5	0	0
3	E	13	0	5	0	0
3	F	13	0	5	0	0
3	G	13	0	5	0	0
3	H	13	0	5	0	0
3	I	13	0	5	0	0
3	J	13	0	5	0	0
3	K	13	0	5	0	0
3	L	13	0	5	0	0
3	M	13	0	5	0	0
3	N	13	0	5	0	0
3	O	13	0	5	0	0
3	P	13	0	5	0	0
4	A	4	0	6	0	0
4	C	4	0	6	0	0
4	D	4	0	6	2	0
4	F	4	0	6	0	0
4	G	4	0	6	1	0
4	H	4	0	6	0	0
4	I	4	0	7	0	0
4	J	4	0	7	1	0
4	K	4	0	7	3	0
4	L	4	0	6	0	0
4	M	4	0	6	0	0
4	N	4	0	7	1	0
4	O	4	0	6	1	0
4	P	4	0	6	0	0
5	A	18	0	13	3	0
5	B	18	0	13	3	0
5	C	18	0	13	4	0
5	D	18	0	13	3	0
5	E	18	0	13	3	0
5	F	18	0	13	3	0
5	G	36	0	26	5	0
5	H	18	0	13	4	0
5	I	36	0	26	4	0
5	J	18	0	13	3	0
5	K	18	0	13	3	0
5	L	18	0	13	3	0
5	M	18	0	13	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	N	18	0	13	4	0
5	O	18	0	13	3	0
5	P	18	0	13	3	0
6	E	4	0	6	2	0
6	P	8	0	12	7	0
7	A	70	0	0	0	0
7	B	63	0	0	1	0
7	C	63	0	0	0	0
7	D	79	0	0	0	0
7	E	105	0	0	0	0
7	F	111	0	0	0	0
7	G	125	0	0	1	0
7	H	124	0	0	0	0
7	I	122	0	0	2	0
7	J	111	0	0	0	0
7	K	100	0	0	0	0
7	L	130	0	0	0	0
7	M	125	0	0	3	0
7	N	100	0	0	0	0
7	O	124	0	0	1	0
7	P	94	0	0	0	0
All	All	33236	0	30600	440	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 7.

The worst 5 of 440 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:D:182:CYS:SG	4:D:601:DHL:SG	2.33	1.26
2:A:301:B12:H362	2:A:301:B12:H351	1.37	1.06
2:P:301:B12:H362	2:P:301:B12:H351	1.37	1.05
2:D:301:B12:H362	2:D:301:B12:H351	1.39	1.03
2:G:301:B12:H362	2:G:301:B12:H351	1.37	1.03

There are no symmetry-related clashes.

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	A	225/286 (79%)	222 (99%)	3 (1%)	0	100	100
1	B	226/286 (79%)	222 (98%)	4 (2%)	0	100	100
1	C	228/286 (80%)	226 (99%)	2 (1%)	0	100	100
1	D	228/286 (80%)	224 (98%)	4 (2%)	0	100	100
1	E	229/286 (80%)	227 (99%)	2 (1%)	0	100	100
1	F	229/286 (80%)	225 (98%)	4 (2%)	0	100	100
1	G	226/286 (79%)	223 (99%)	3 (1%)	0	100	100
1	H	225/286 (79%)	224 (100%)	1 (0%)	0	100	100
1	I	227/286 (79%)	223 (98%)	4 (2%)	0	100	100
1	J	227/286 (79%)	224 (99%)	3 (1%)	0	100	100
1	K	226/286 (79%)	224 (99%)	2 (1%)	0	100	100
1	L	231/286 (81%)	228 (99%)	3 (1%)	0	100	100
1	M	230/286 (80%)	228 (99%)	2 (1%)	0	100	100
1	N	230/286 (80%)	229 (100%)	1 (0%)	0	100	100
1	O	227/286 (79%)	224 (99%)	3 (1%)	0	100	100
1	P	228/286 (80%)	227 (100%)	1 (0%)	0	100	100
All	All	3642/4576 (80%)	3600 (99%)	42 (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	A	193/243 (79%)	187 (97%)	6 (3%)	35	57
1	B	193/243 (79%)	187 (97%)	6 (3%)	35	57
1	C	192/243 (79%)	182 (95%)	10 (5%)	21	36
1	D	194/243 (80%)	184 (95%)	10 (5%)	21	36
1	E	193/243 (79%)	188 (97%)	5 (3%)	40	63
1	F	197/243 (81%)	190 (96%)	7 (4%)	31	52
1	G	194/243 (80%)	188 (97%)	6 (3%)	35	57
1	H	192/243 (79%)	185 (96%)	7 (4%)	31	52
1	I	194/243 (80%)	189 (97%)	5 (3%)	40	63
1	J	195/243 (80%)	189 (97%)	6 (3%)	35	57
1	K	192/243 (79%)	188 (98%)	4 (2%)	47	69
1	L	196/243 (81%)	188 (96%)	8 (4%)	27	46
1	M	195/243 (80%)	191 (98%)	4 (2%)	47	69
1	N	192/243 (79%)	185 (96%)	7 (4%)	31	52
1	O	192/243 (79%)	185 (96%)	7 (4%)	31	52
1	P	196/243 (81%)	190 (97%)	6 (3%)	35	57
All	All	3100/3888 (80%)	2996 (97%)	104 (3%)	32	54

5 of 104 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	58	MSE
1	K	229	GLN
1	P	58	MSE
1	I	115	ILE
1	J	70	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	180	HIS
1	P	71	HIS
1	J	81	GLN
1	P	180	HIS
1	N	180	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

67 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	$\# Z > 2$
4	DHL	G	601	-	2,3,3	0.48	0	1,2,2	0.19	0
5	5AD	E	401	-	20,20,20	1.63	5 (25%)	28,30,30	2.21	10 (35%)
5	5AD	I	401	-	20,20,20	1.69	5 (25%)	28,30,30	2.11	7 (25%)
4	DHL	C	601	-	2,3,3	0.61	0	1,2,2	0.42	0
5	5AD	P	401	-	20,20,20	1.69	4 (20%)	28,30,30	2.14	7 (25%)
5	5AD	D	401	-	20,20,20	1.69	4 (20%)	28,30,30	2.14	8 (28%)
3	FLC	G	501	-	12,12,12	1.52	4 (33%)	17,17,17	1.35	3 (17%)
4	DHL	M	601	-	2,3,3	1.13	0	1,2,2	0.03	0
5	5AD	L	401	-	20,20,20	1.67	5 (25%)	28,30,30	2.10	8 (28%)
5	5AD	B	401	-	20,20,20	1.62	4 (20%)	28,30,30	2.08	9 (32%)
5	5AD	N	401	-	20,20,20	1.57	5 (25%)	28,30,30	2.16	8 (28%)
5	5AD	O	401	-	20,20,20	1.65	4 (20%)	28,30,30	2.07	8 (28%)
2	B12	E	301	-	94,101,101	1.60	11 (11%)	149,166,166	2.00	27 (18%)
2	B12	M	301	-	94,101,101	1.55	11 (11%)	149,166,166	2.01	26 (17%)
4	DHL	A	601	-	2,3,3	1.04	0	1,2,2	0.17	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	DHL	D	601	-	2,3,3	1.26	0	1,2,2	0.34	0
4	DHL	I	601	-	2,3,3	0.67	0	1,2,2	0.67	0
4	DHL	J	601	-	2,3,3	1.62	1 (50%)	1,2,2	0.77	0
3	FLC	H	501	-	12,12,12	1.38	3 (25%)	17,17,17	1.41	2 (11%)
2	B12	J	301	-	94,101,101	1.59	13 (13%)	149,166,166	1.97	26 (17%)
4	DHL	P	601	-	2,3,3	0.89	0	1,2,2	0.13	0
3	FLC	C	501	-	12,12,12	1.51	3 (25%)	17,17,17	1.42	2 (11%)
2	B12	G	301	-	94,101,101	1.55	12 (12%)	149,166,166	2.02	26 (17%)
3	FLC	D	501	-	12,12,12	1.80	2 (16%)	17,17,17	1.38	3 (17%)
3	FLC	A	501	-	12,12,12	1.49	3 (25%)	17,17,17	1.35	3 (17%)
5	5AD	F	401	-	20,20,20	1.68	5 (25%)	28,30,30	2.03	8 (28%)
3	FLC	I	501	-	12,12,12	1.62	4 (33%)	17,17,17	1.42	2 (11%)
2	B12	D	301	-	94,101,101	1.54	13 (13%)	149,166,166	2.01	26 (17%)
3	FLC	L	501	-	12,12,12	1.51	2 (16%)	17,17,17	1.43	3 (17%)
3	FLC	P	501	-	12,12,12	1.46	2 (16%)	17,17,17	1.47	3 (17%)
4	DHL	N	601	-	2,3,3	0.45	0	1,2,2	0.80	0
5	5AD	G	283	-	20,20,20	1.60	4 (20%)	28,30,30	2.28	8 (28%)
5	5AD	M	401	-	20,20,20	1.64	5 (25%)	28,30,30	2.10	8 (28%)
6	EDO	E	283	-	3,3,3	0.50	0	2,2,2	0.17	0
5	5AD	J	401	-	20,20,20	1.60	5 (25%)	28,30,30	2.13	10 (35%)
2	B12	K	301	-	94,101,101	1.55	12 (12%)	149,166,166	2.04	26 (17%)
5	5AD	H	401	-	20,20,20	1.60	4 (20%)	28,30,30	2.20	9 (32%)
4	DHL	F	601	-	2,3,3	0.84	0	1,2,2	0.06	0
2	B12	I	301	-	94,101,101	1.58	13 (13%)	149,166,166	2.00	27 (18%)
6	EDO	P	284	-	3,3,3	0.37	0	2,2,2	0.19	0
6	EDO	P	283	-	3,3,3	0.52	0	2,2,2	0.16	0
2	B12	F	301	-	94,101,101	1.56	12 (12%)	149,166,166	1.99	26 (17%)
3	FLC	B	501	-	12,12,12	1.47	4 (33%)	17,17,17	1.49	4 (23%)
5	5AD	A	401	-	20,20,20	1.67	4 (20%)	28,30,30	2.05	7 (25%)
2	B12	N	301	-	94,101,101	1.60	12 (12%)	149,166,166	2.01	25 (16%)
3	FLC	E	501	-	12,12,12	1.57	3 (25%)	17,17,17	1.33	2 (11%)
5	5AD	C	401	-	20,20,20	1.72	5 (25%)	28,30,30	2.10	8 (28%)
5	5AD	I	283	-	20,20,20	1.66	3 (15%)	28,30,30	2.29	8 (28%)
4	DHL	H	601	-	2,3,3	0.64	0	1,2,2	1.53	0
2	B12	C	301	-	94,101,101	1.59	13 (13%)	149,166,166	2.04	27 (18%)
2	B12	H	301	-	94,101,101	1.56	13 (13%)	149,166,166	2.04	24 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	FLC	F	501	-	12,12,12	1.61	3 (25%)	17,17,17	1.23	2 (11%)
5	5AD	K	401	-	20,20,20	1.71	5 (25%)	28,30,30	2.10	8 (28%)
4	DHL	L	601	-	2,3,3	1.77	1 (50%)	1,2,2	0.69	0
2	B12	A	301	-	94,101,101	1.58	12 (12%)	149,166,166	1.98	24 (16%)
5	5AD	G	401	-	20,20,20	1.68	4 (20%)	28,30,30	2.20	7 (25%)
3	FLC	K	501	-	12,12,12	1.64	3 (25%)	17,17,17	1.44	2 (11%)
2	B12	L	301	-	94,101,101	1.55	11 (11%)	149,166,166	2.00	22 (14%)
2	B12	B	301	-	94,101,101	1.58	13 (13%)	149,166,166	2.00	24 (16%)
2	B12	P	301	-	94,101,101	1.56	13 (13%)	149,166,166	2.02	26 (17%)
2	B12	O	301	-	94,101,101	1.55	12 (12%)	149,166,166	1.98	27 (18%)
3	FLC	J	501	-	12,12,12	1.67	4 (33%)	17,17,17	1.26	2 (11%)
3	FLC	O	501	-	12,12,12	1.45	3 (25%)	17,17,17	1.34	2 (11%)
4	DHL	O	601	-	2,3,3	0.72	0	1,2,2	0.08	0
3	FLC	N	501	-	12,12,12	1.34	2 (16%)	17,17,17	1.37	2 (11%)
4	DHL	K	601	-	2,3,3	1.34	0	1,2,2	0.02	0
3	FLC	M	501	-	12,12,12	1.63	3 (25%)	17,17,17	1.47	2 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	5AD	E	401	-	1/1/4/4	2/4/20/20	0/3/3/3
5	5AD	I	401	-	1/1/4/4	1/4/20/20	0/3/3/3
4	DHL	G	601	-	-	1/1/1/1	-
4	DHL	C	601	-	-	0/1/1/1	-
5	5AD	P	401	-	1/1/4/4	1/4/20/20	0/3/3/3
5	5AD	D	401	-	1/1/4/4	2/4/20/20	0/3/3/3
3	FLC	G	501	-	-	0/16/16/16	-
5	5AD	L	401	-	1/1/4/4	2/4/20/20	0/3/3/3
5	5AD	N	401	-	1/1/4/4	2/4/20/20	0/3/3/3
5	5AD	B	401	-	1/1/4/4	1/4/20/20	0/3/3/3
4	DHL	M	601	-	-	0/1/1/1	-
5	5AD	O	401	-	1/1/4/4	1/4/20/20	0/3/3/3
2	B12	E	301	-	-	7/56/223/223	0/3/11/11
2	B12	M	301	-	-	7/56/223/223	0/3/11/11
4	DHL	A	601	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	DHL	D	601	-	-	1/1/1/1	-
4	DHL	I	601	-	-	1/1/1/1	-
4	DHL	J	601	-	-	0/1/1/1	-
3	FLC	H	501	-	-	0/16/16/16	-
2	B12	J	301	-	-	8/56/223/223	0/3/11/11
4	DHL	P	601	-	-	1/1/1/1	-
3	FLC	C	501	-	-	0/16/16/16	-
5	5AD	F	401	-	1/1/4/4	2/4/20/20	0/3/3/3
2	B12	G	301	-	-	7/56/223/223	0/3/11/11
3	FLC	A	501	-	-	0/16/16/16	-
3	FLC	D	501	-	-	0/16/16/16	-
3	FLC	I	501	-	-	0/16/16/16	-
2	B12	D	301	-	-	8/56/223/223	0/3/11/11
3	FLC	L	501	-	-	0/16/16/16	-
3	FLC	P	501	-	-	0/16/16/16	-
4	DHL	N	601	-	-	1/1/1/1	-
5	5AD	G	283	-	1/1/4/4	2/4/20/20	0/3/3/3
5	5AD	M	401	-	1/1/4/4	2/4/20/20	0/3/3/3
6	EDO	E	283	-	-	1/1/1/1	-
5	5AD	J	401	-	1/1/4/4	1/4/20/20	0/3/3/3
5	5AD	H	401	-	1/1/4/4	2/4/20/20	0/3/3/3
2	B12	K	301	-	-	6/56/223/223	0/3/11/11
4	DHL	F	601	-	-	1/1/1/1	-
2	B12	I	301	-	-	7/56/223/223	0/3/11/11
6	EDO	P	284	-	-	0/1/1/1	-
6	EDO	P	283	-	-	1/1/1/1	-
2	B12	F	301	-	-	7/56/223/223	0/3/11/11
3	FLC	B	501	-	-	0/16/16/16	-
5	5AD	A	401	-	1/1/4/4	1/4/20/20	0/3/3/3
2	B12	N	301	-	-	7/56/223/223	0/3/11/11
3	FLC	E	501	-	-	0/16/16/16	-
5	5AD	C	401	-	1/1/4/4	2/4/20/20	0/3/3/3
5	5AD	I	283	-	1/1/4/4	2/4/20/20	0/3/3/3
4	DHL	H	601	-	-	1/1/1/1	-
2	B12	C	301	-	-	6/56/223/223	0/3/11/11
2	B12	H	301	-	-	7/56/223/223	0/3/11/11
3	FLC	F	501	-	-	0/16/16/16	-
5	5AD	K	401	-	1/1/4/4	2/4/20/20	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	DHL	L	601	-	-	0/1/1/1	-
2	B12	A	301	-	-	7/56/223/223	0/3/11/11
5	5AD	G	401	-	1/1/4/4	1/4/20/20	0/3/3/3
3	FLC	K	501	-	-	0/16/16/16	-
2	B12	L	301	-	-	8/56/223/223	0/3/11/11
2	B12	B	301	-	-	6/56/223/223	0/3/11/11
2	B12	P	301	-	-	7/56/223/223	0/3/11/11
2	B12	O	301	-	-	6/56/223/223	0/3/11/11
3	FLC	J	501	-	-	0/16/16/16	-
3	FLC	O	501	-	-	0/16/16/16	-
4	DHL	O	601	-	-	1/1/1/1	-
3	FLC	N	501	-	-	0/16/16/16	-
4	DHL	K	601	-	-	0/1/1/1	-
3	FLC	M	501	-	-	0/16/16/16	-

The worst 5 of 326 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	N	301	B12	C19-N24	-7.89	1.39	1.49
2	E	301	B12	C19-N24	-7.73	1.39	1.49
2	A	301	B12	C19-N24	-7.61	1.39	1.49
2	C	301	B12	C19-N24	-7.58	1.39	1.49
2	H	301	B12	C19-N24	-7.49	1.39	1.49

The worst 5 of 594 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	301	B12	C20-C1-C19	-8.93	100.75	109.35
2	K	301	B12	C20-C1-C19	-8.41	101.25	109.35
2	H	301	B12	C20-C1-C19	-8.38	101.28	109.35
2	B	301	B12	C20-C1-C19	-8.27	101.39	109.35
2	C	301	B12	C2-C1-C19	8.18	131.34	118.61

5 of 18 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	A	401	5AD	C4'
5	B	401	5AD	C4'
5	C	401	5AD	C4'
5	D	401	5AD	C4'
5	E	401	5AD	C4'

5 of 150 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	301	B12	C1P-C2P-O3-P
2	D	301	B12	C1P-C2P-O3-P
2	E	301	B12	C1P-C2P-O3-P
2	F	301	B12	C1P-C2P-O3-P
2	K	301	B12	C1P-C2P-O3-P

There are no ring outliers.

43 monomers are involved in 239 short contacts:

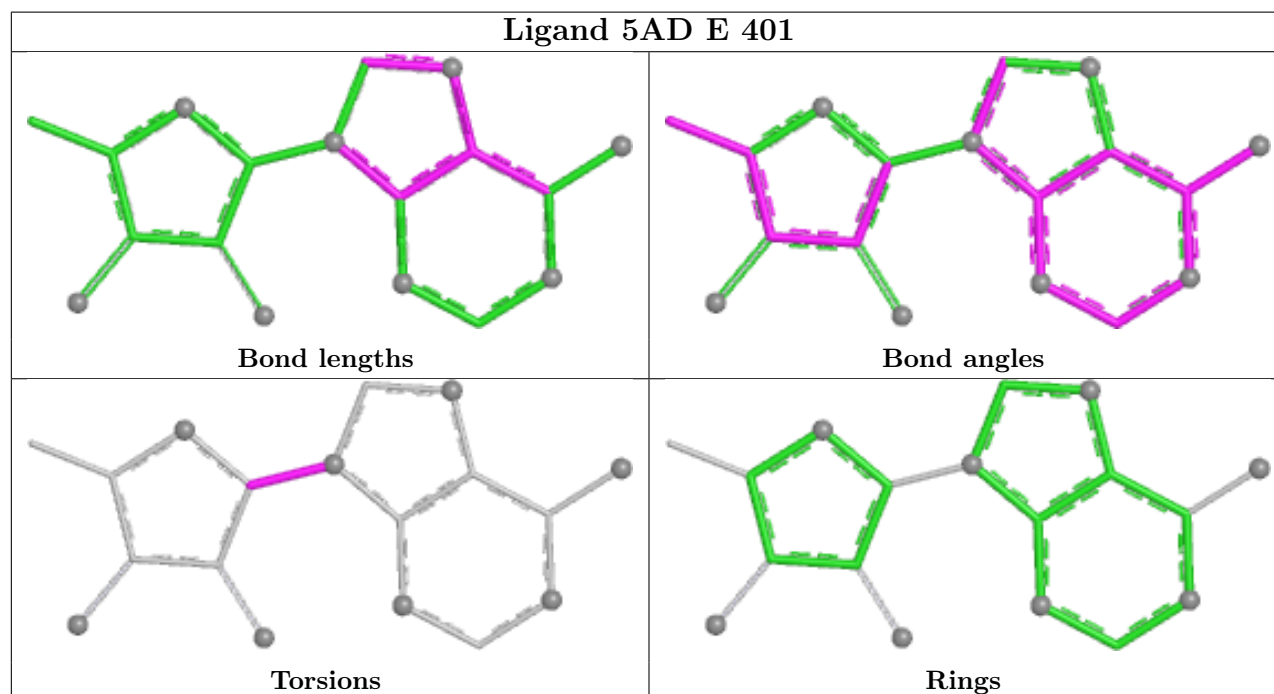
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	601	DHL	1	0
5	E	401	5AD	3	0
5	I	401	5AD	3	0
5	P	401	5AD	3	0
5	D	401	5AD	3	0
5	L	401	5AD	3	0
5	B	401	5AD	3	0
5	N	401	5AD	4	0
5	O	401	5AD	3	0
2	E	301	B12	14	0
2	M	301	B12	12	0
4	D	601	DHL	2	0
4	J	601	DHL	1	0
2	J	301	B12	12	0
2	G	301	B12	15	0
5	F	401	5AD	3	0
2	D	301	B12	12	0
4	N	601	DHL	1	0
5	G	283	5AD	2	0
5	M	401	5AD	3	0
6	E	283	EDO	2	0
5	J	401	5AD	3	0
2	K	301	B12	12	0
5	H	401	5AD	4	0
2	I	301	B12	14	0
6	P	284	EDO	5	0
6	P	283	EDO	2	0
2	F	301	B12	13	0
5	A	401	5AD	3	0
2	N	301	B12	13	0
5	C	401	5AD	4	0

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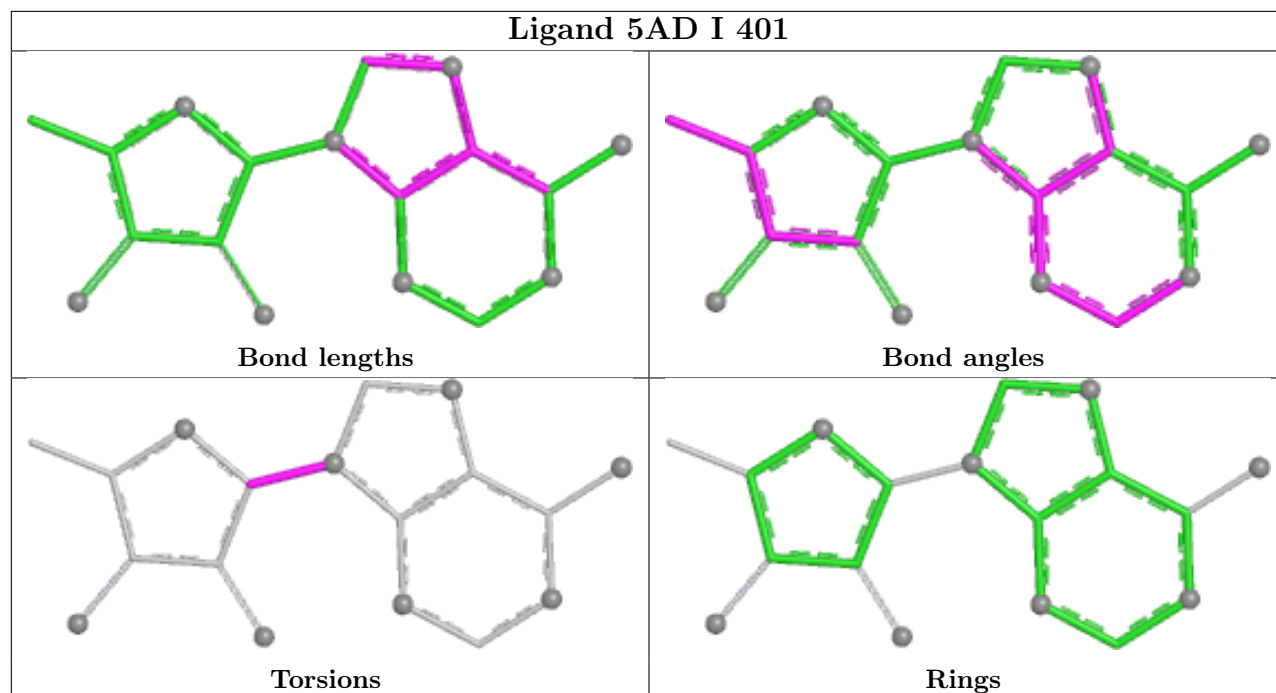
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	I	283	5AD	1	0
2	C	301	B12	15	0
2	H	301	B12	13	0
5	K	401	5AD	3	0
2	A	301	B12	14	0
5	G	401	5AD	3	0
2	L	301	B12	13	0
2	B	301	B12	13	0
2	P	301	B12	16	0
2	O	301	B12	15	0
4	O	601	DHL	1	0
4	K	601	DHL	3	0

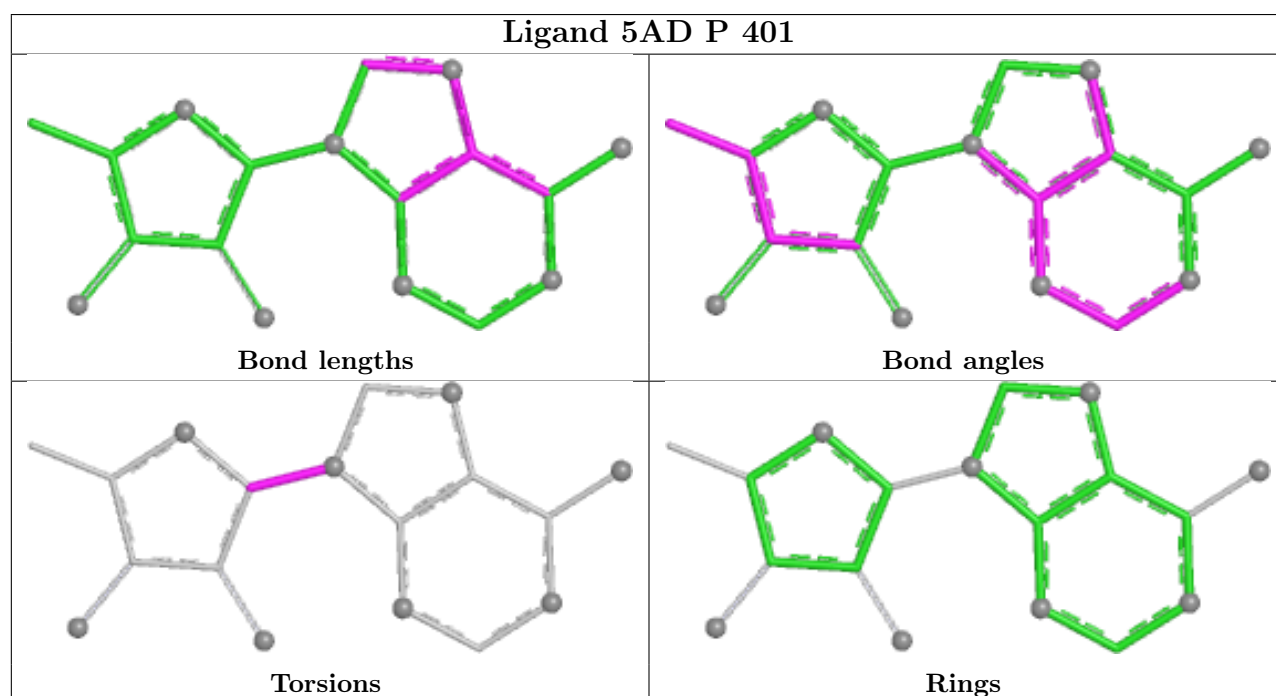
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



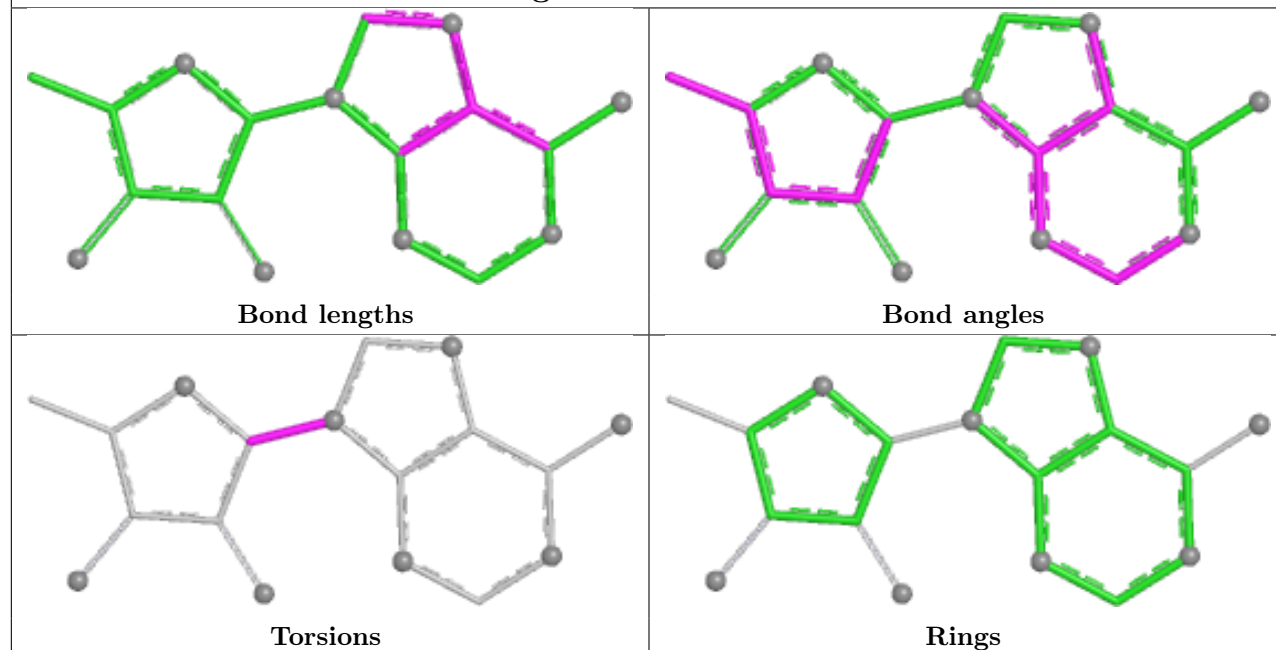
Ligand 5AD I 401



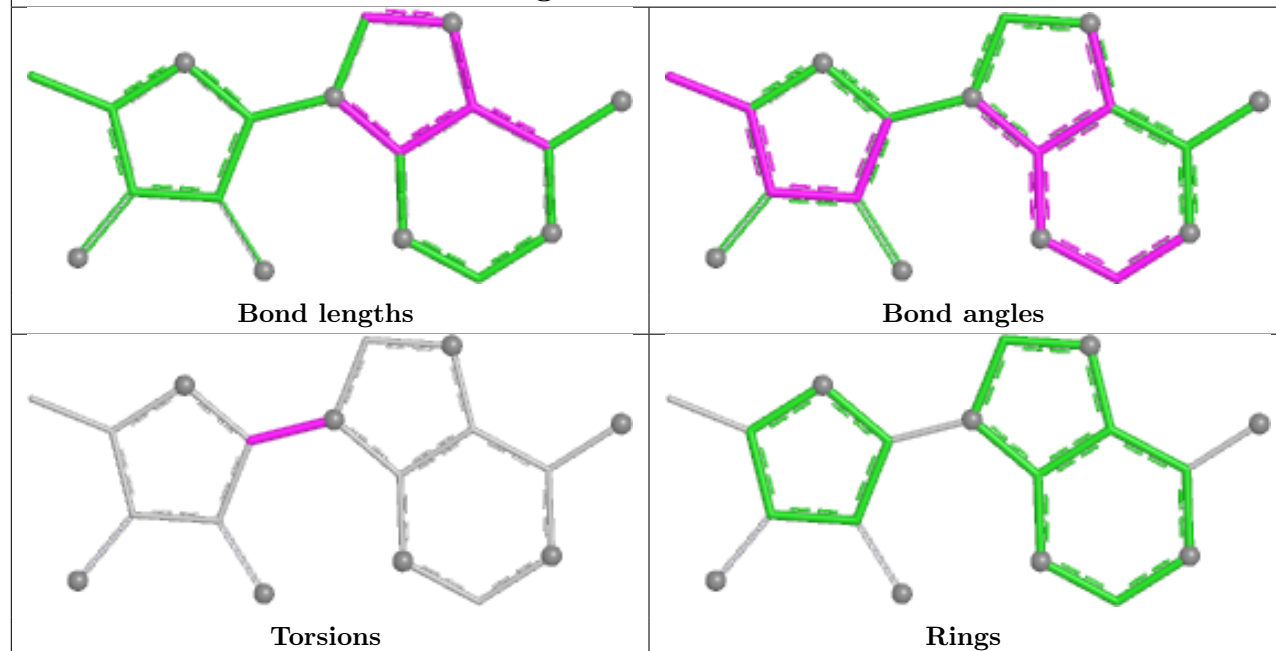
Ligand 5AD P 401



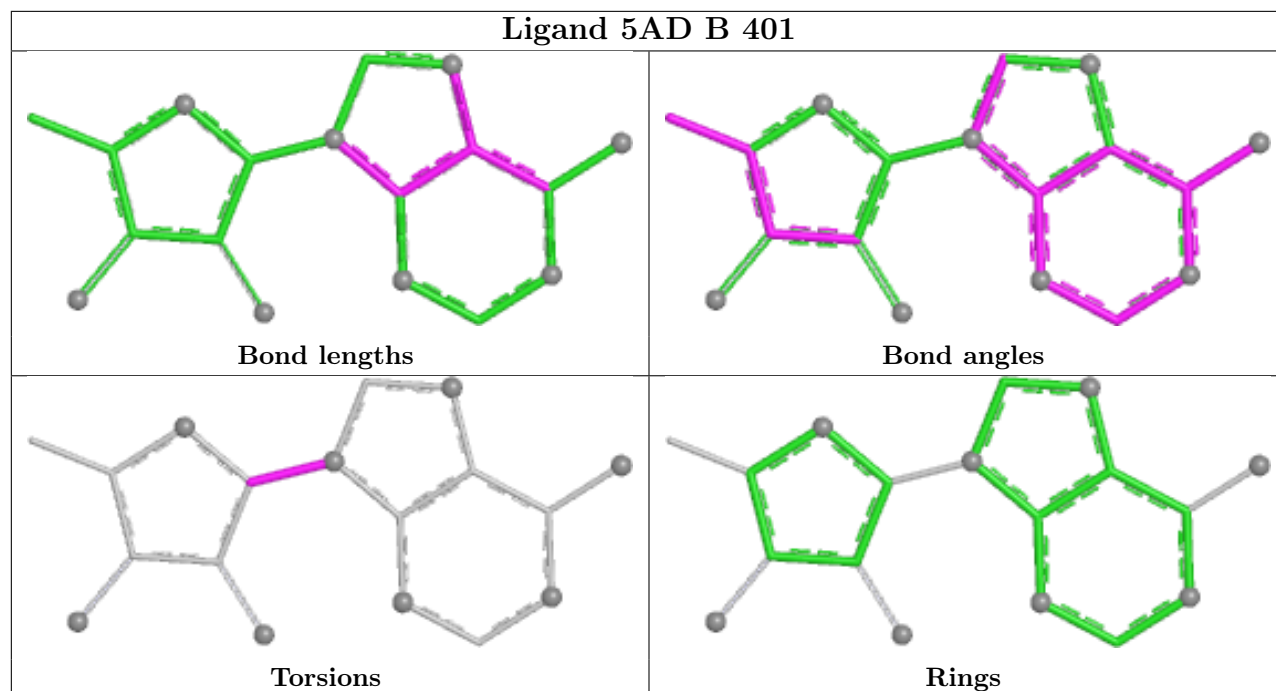
Ligand 5AD D 401



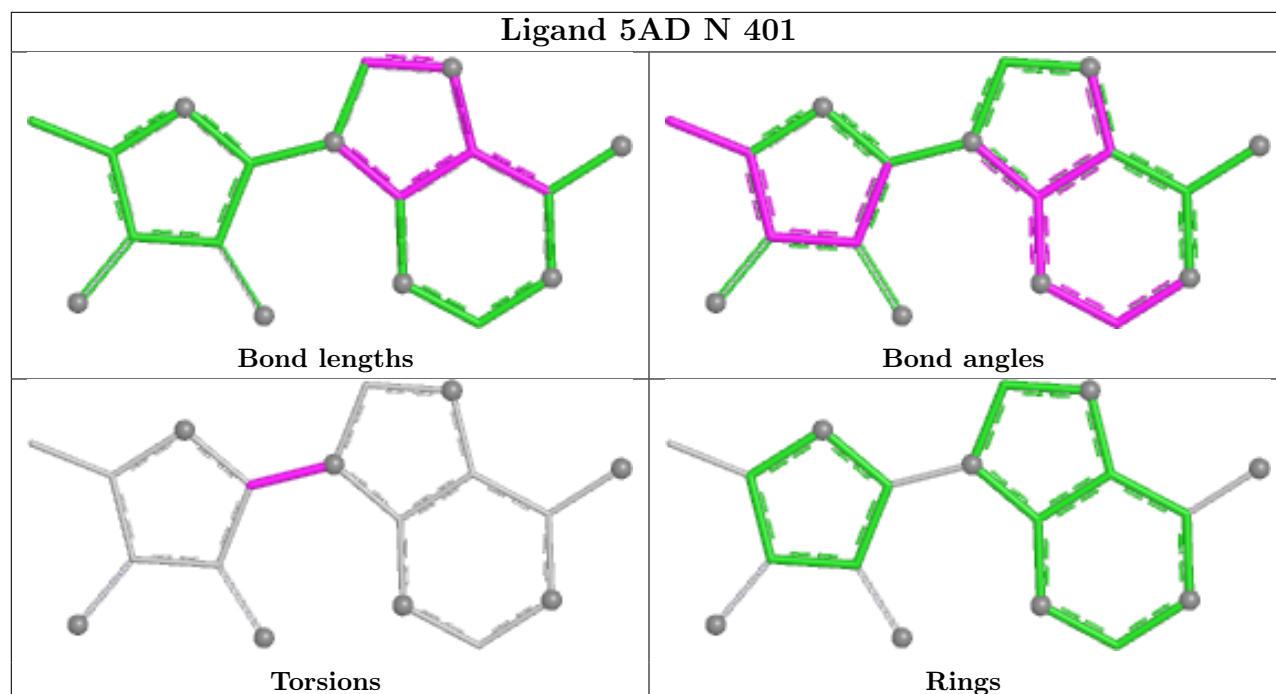
Ligand 5AD L 401



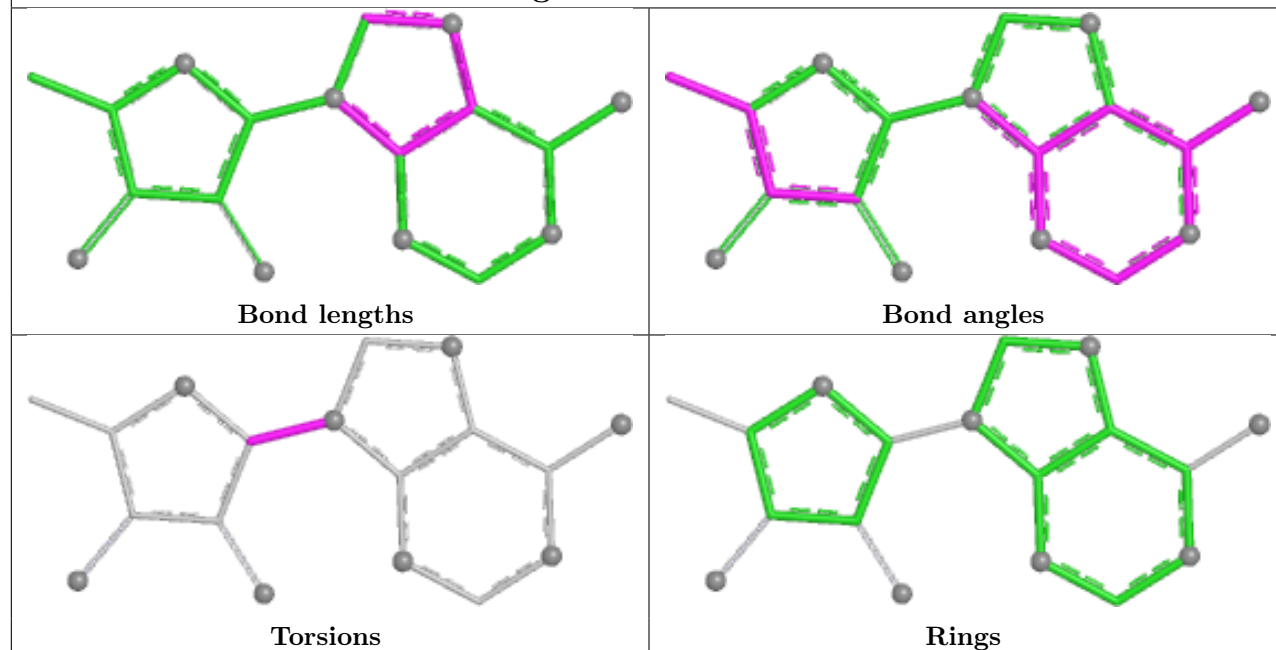
Ligand 5AD B 401



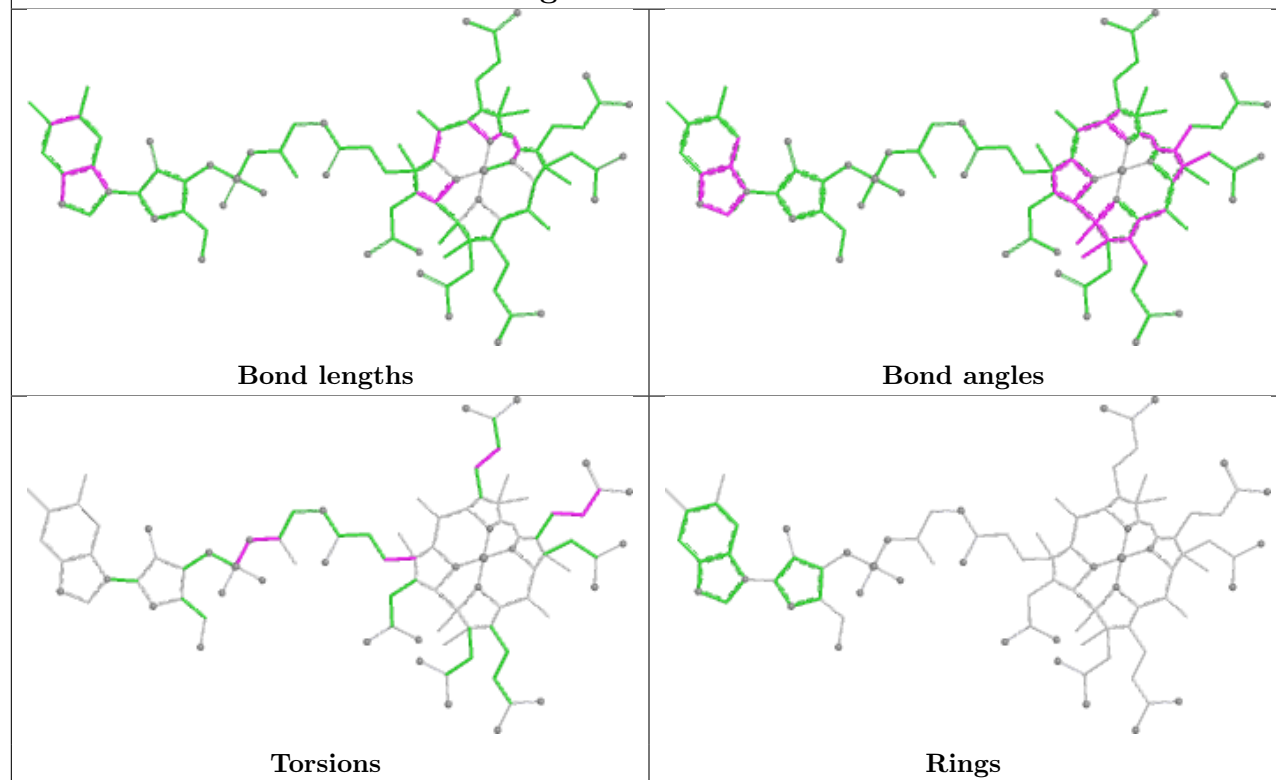
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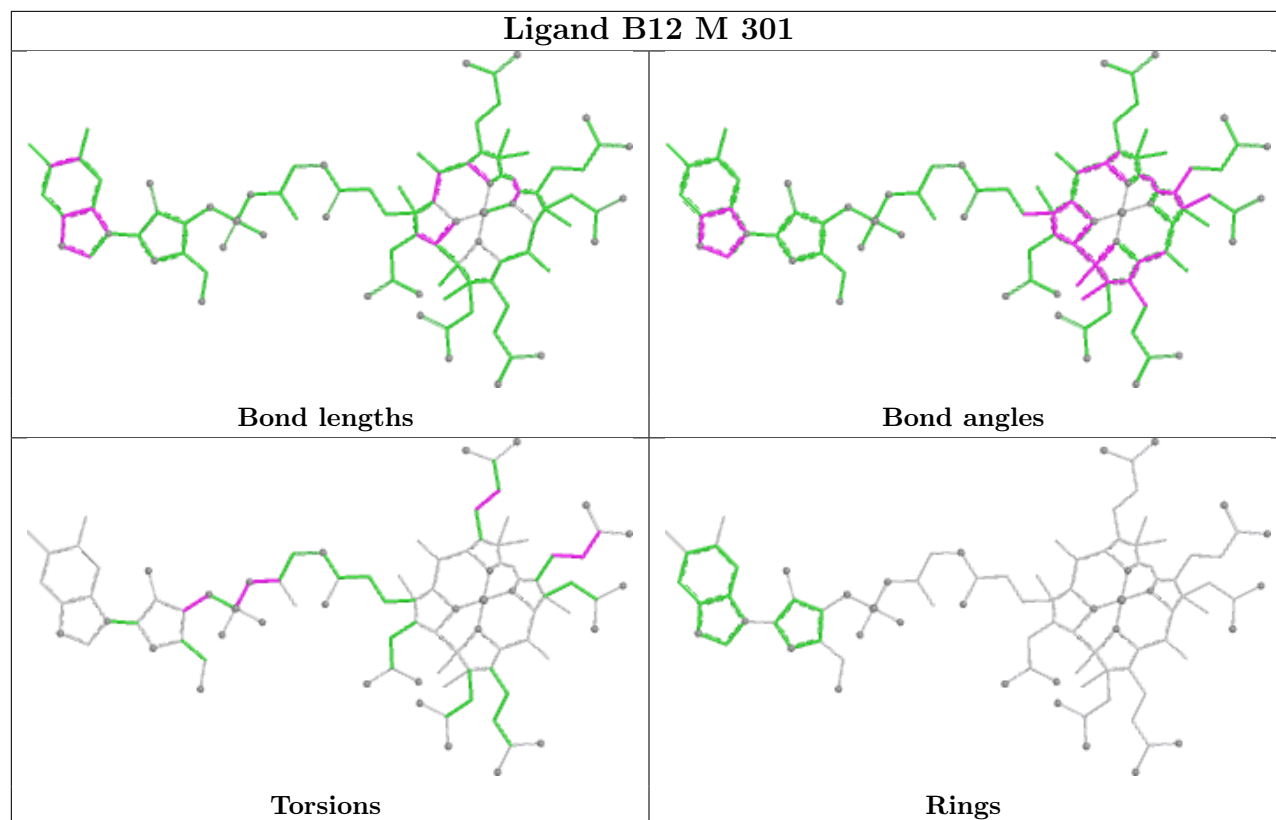
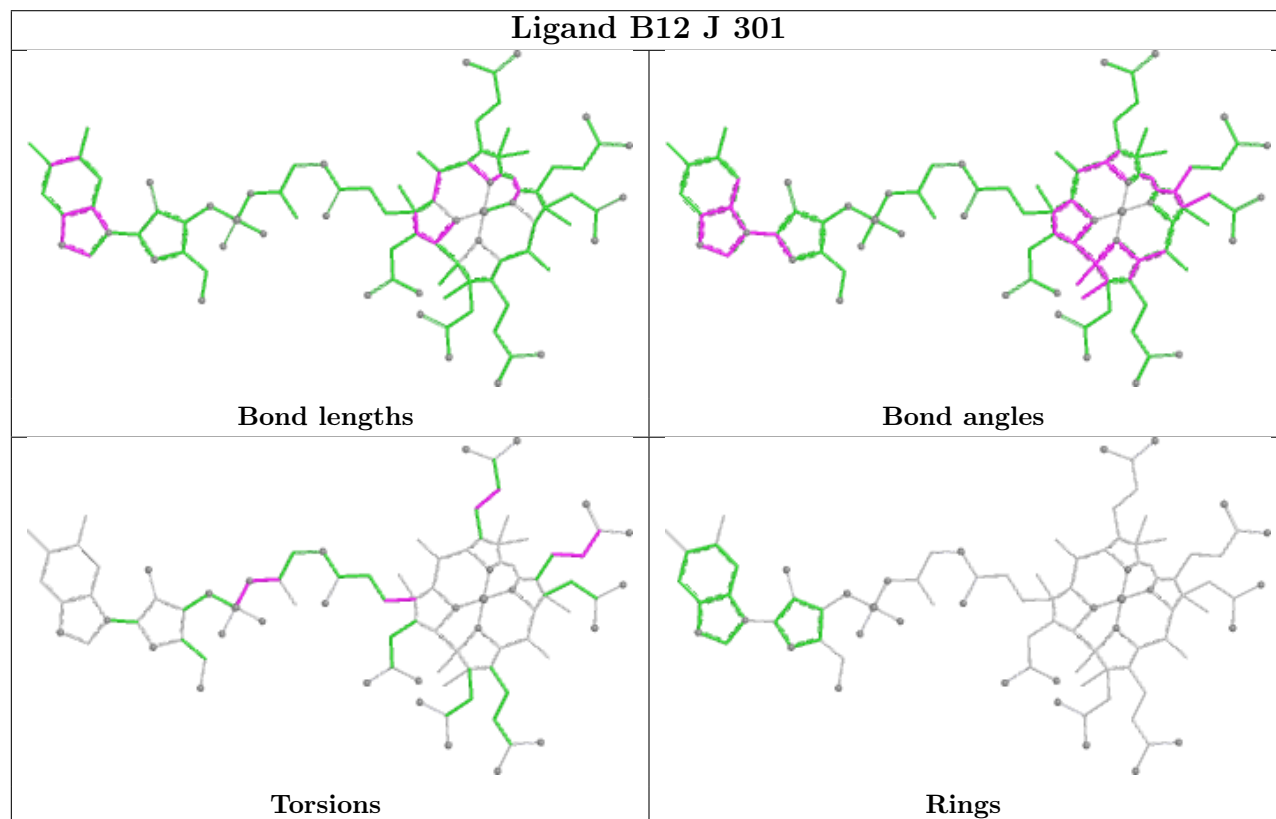


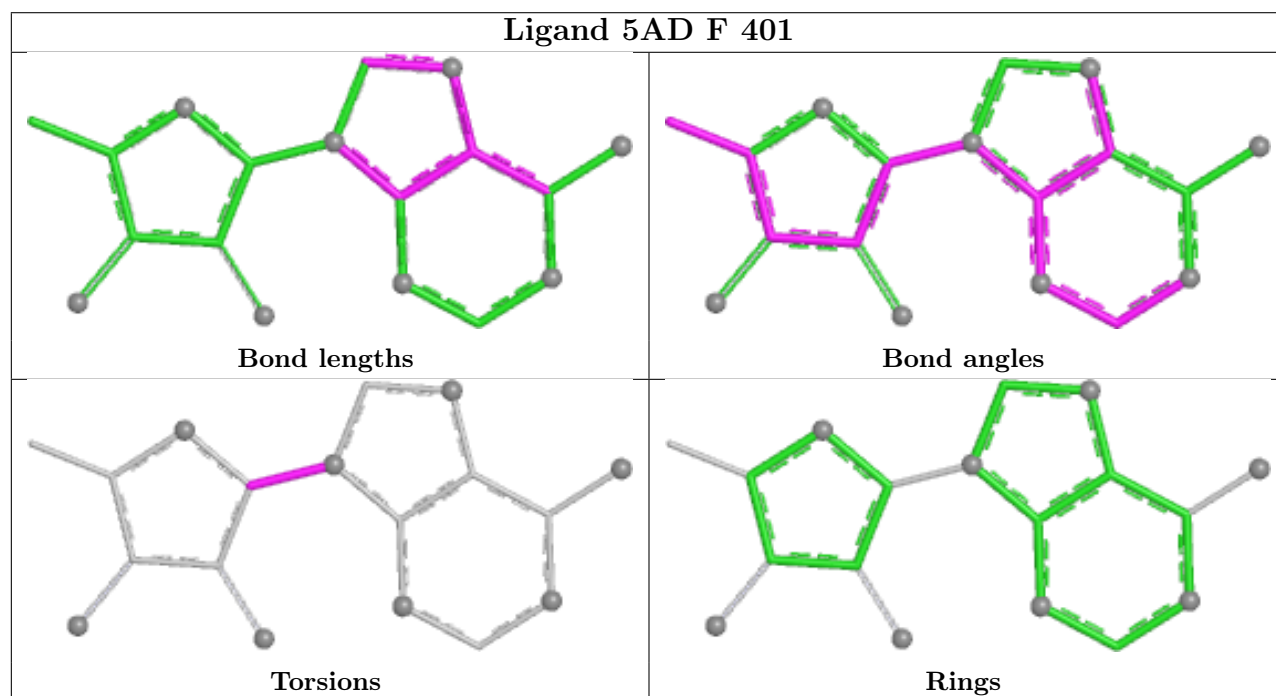
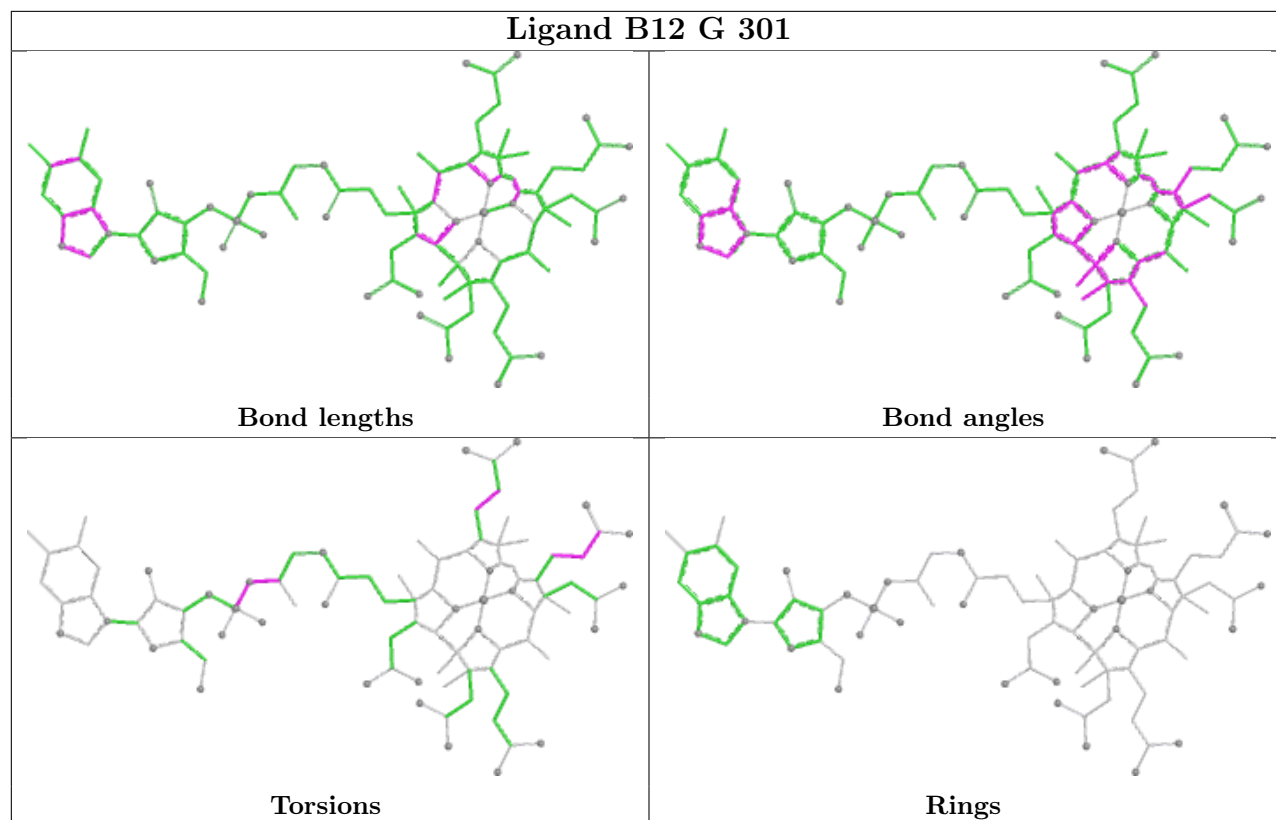
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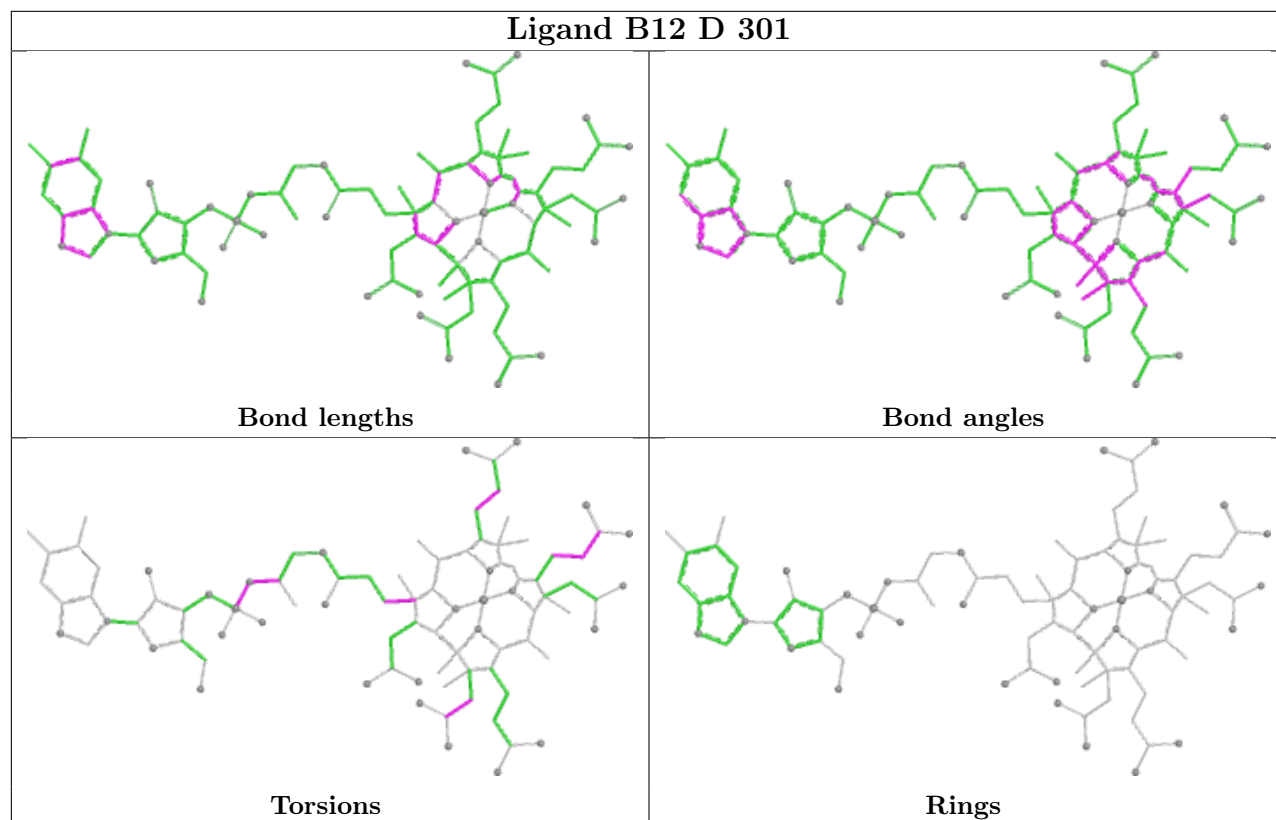
Ligand B12 E 301



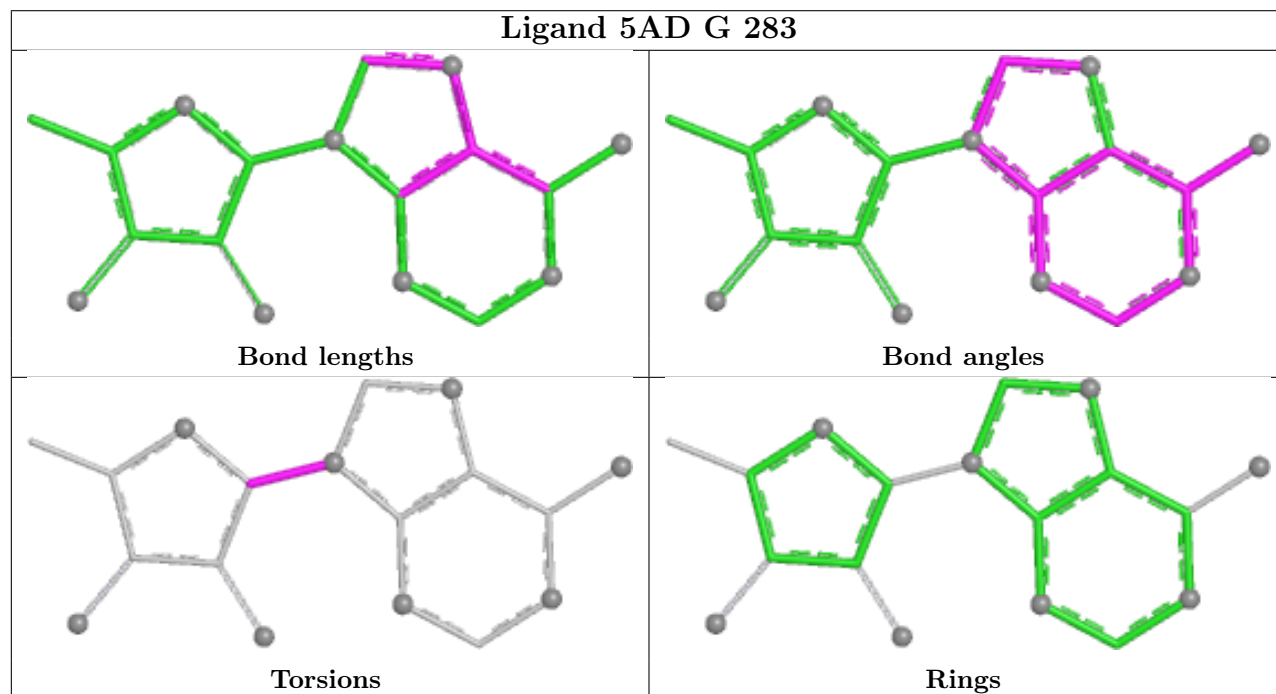
Ligand B12 M 301**Ligand B12 J 301**

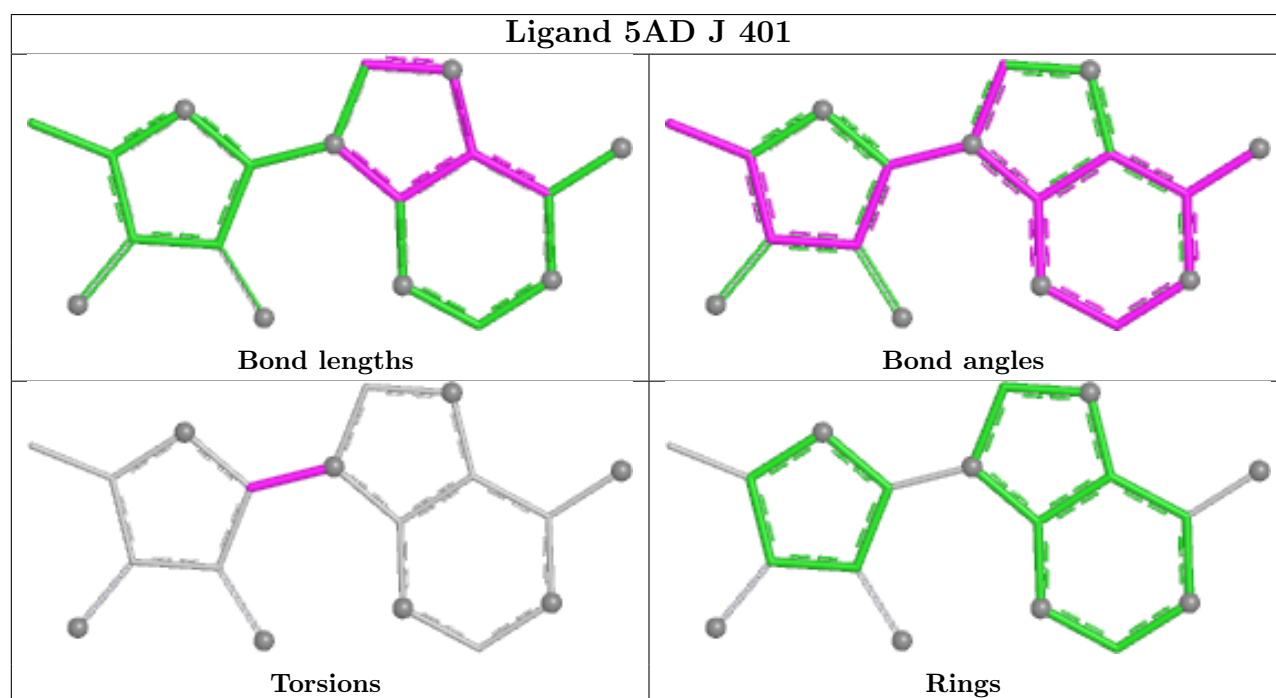
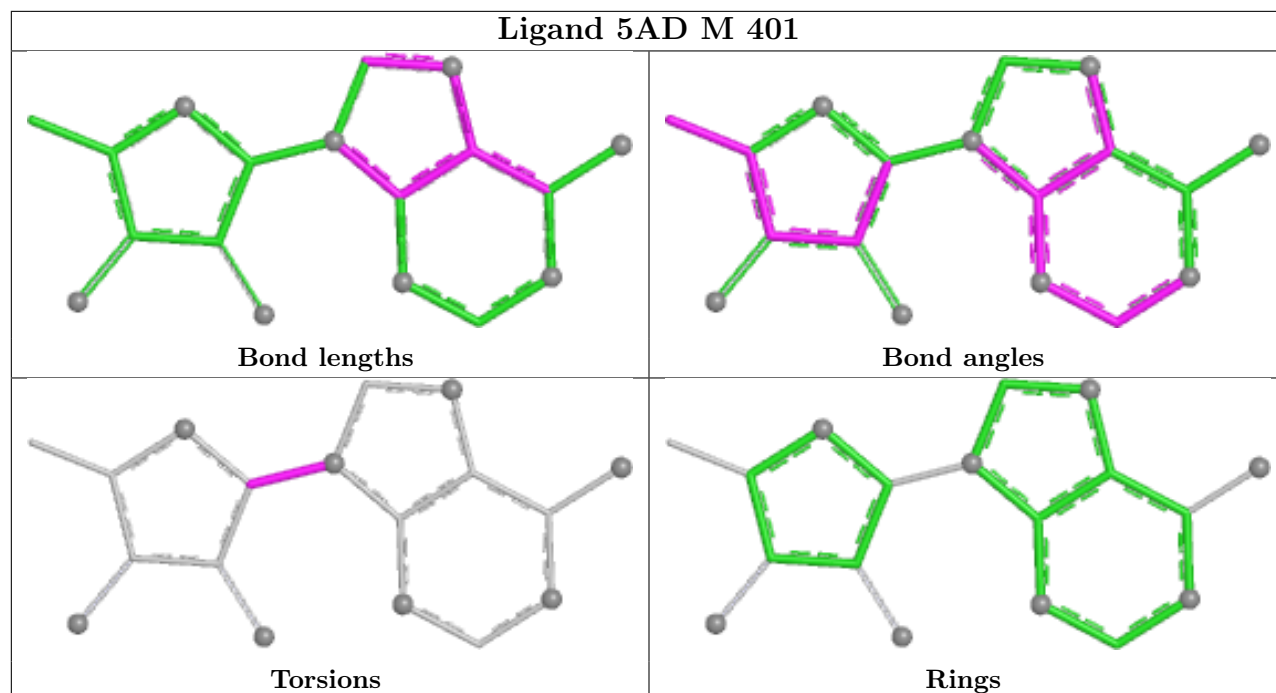


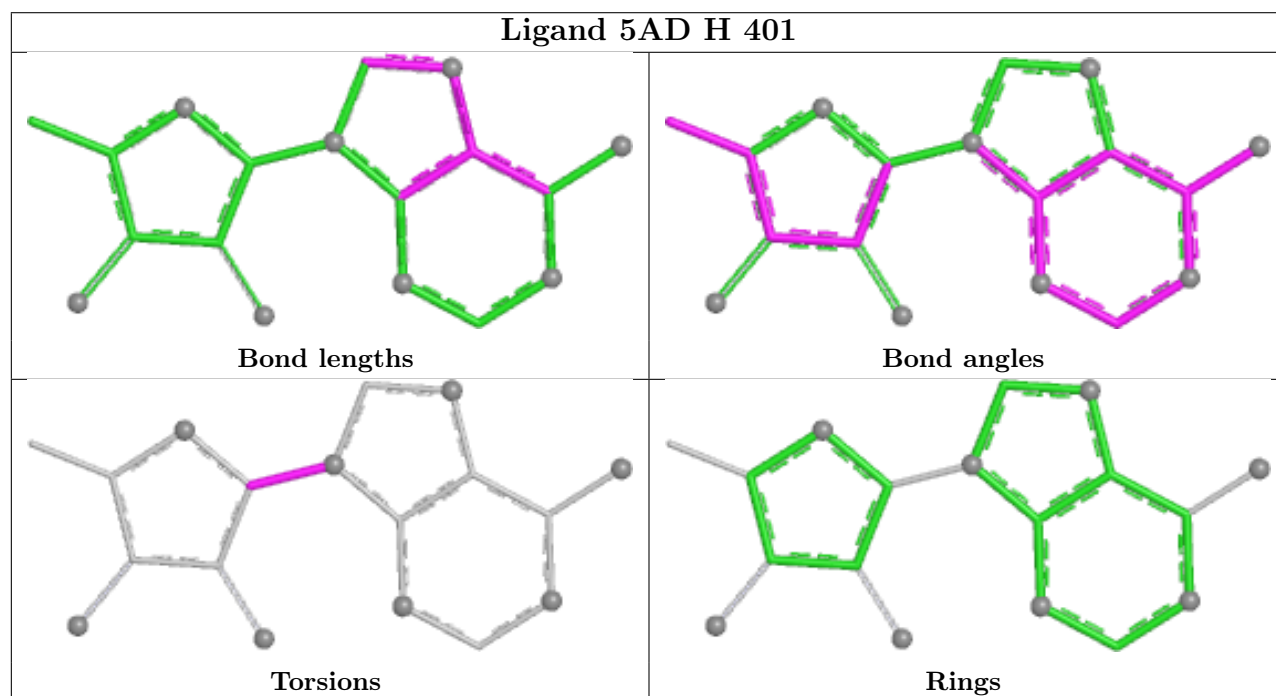
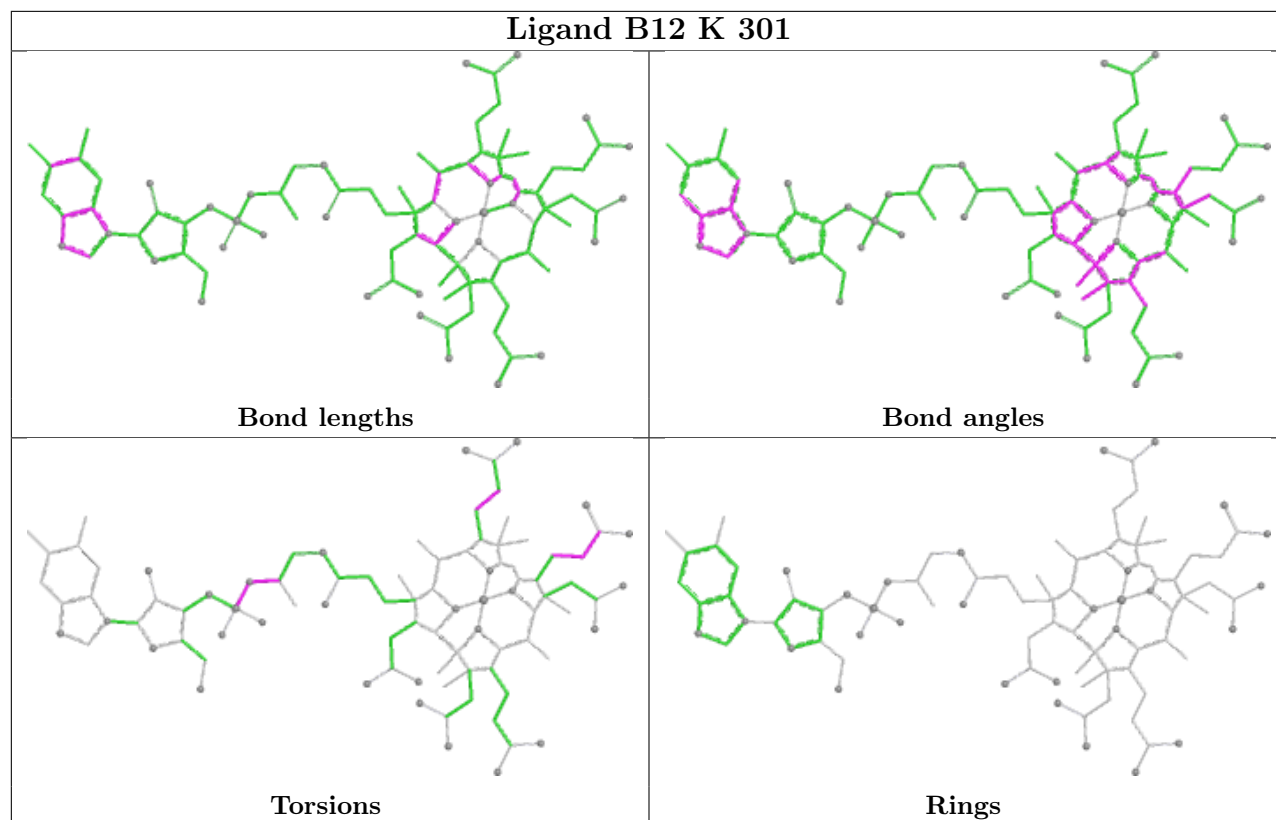
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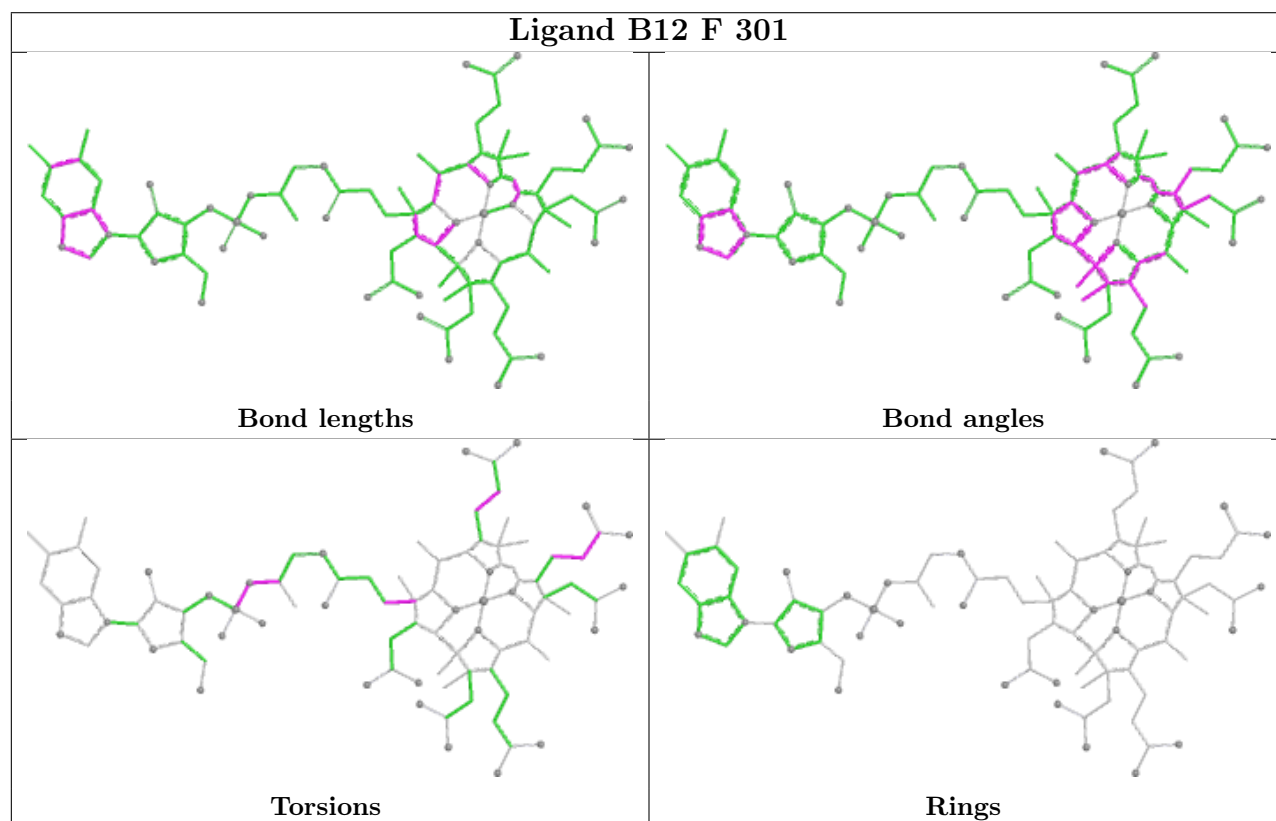
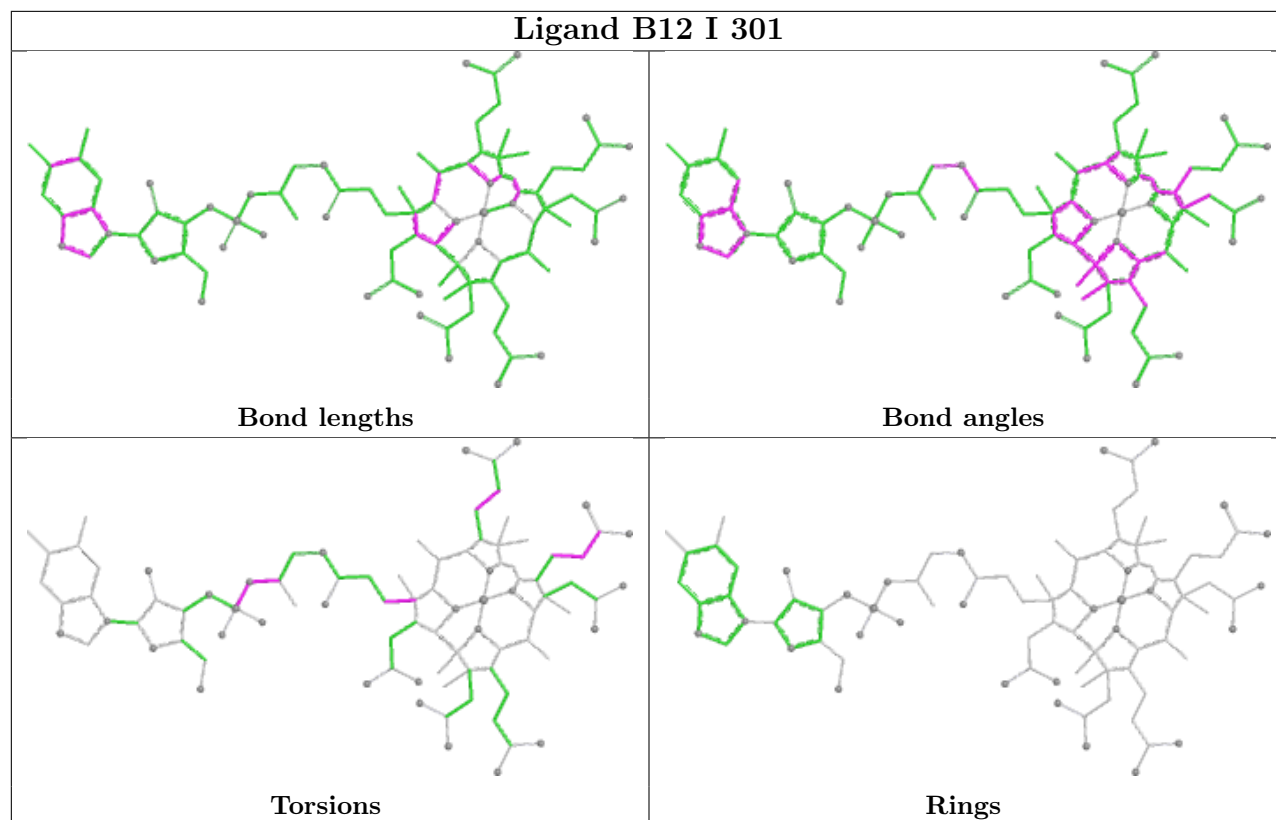


Ligand 5AD G 283

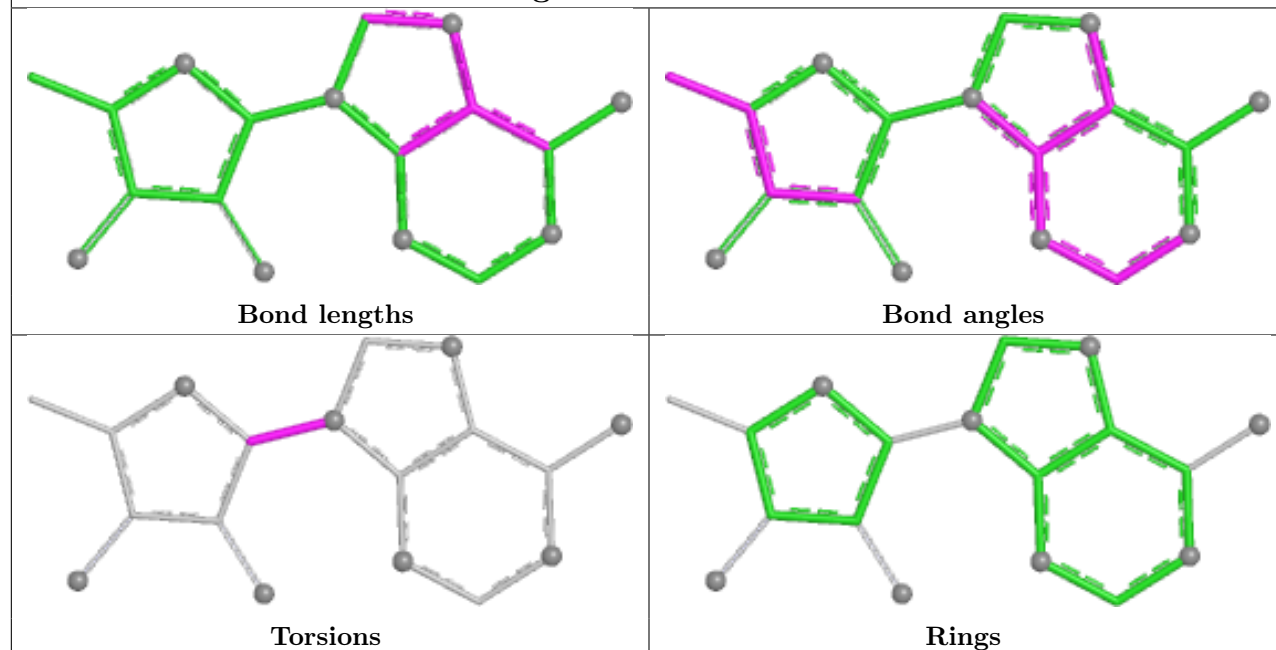




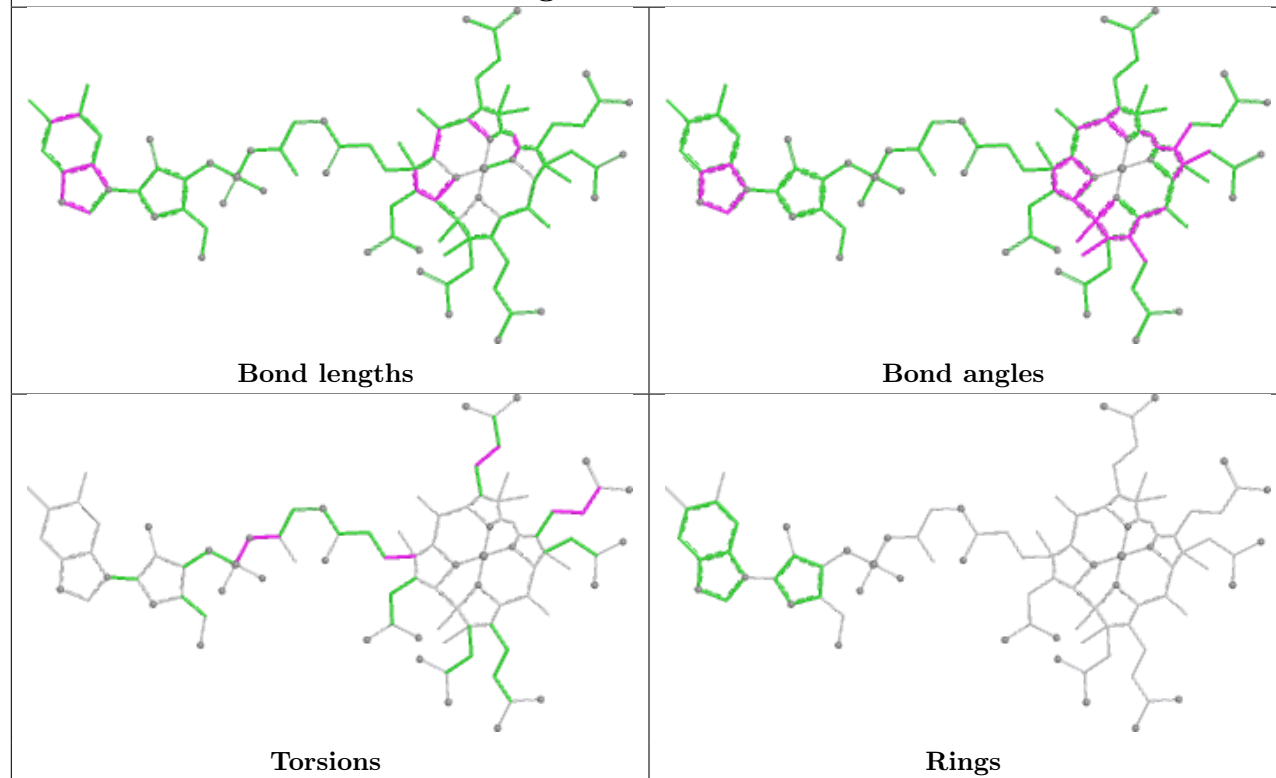




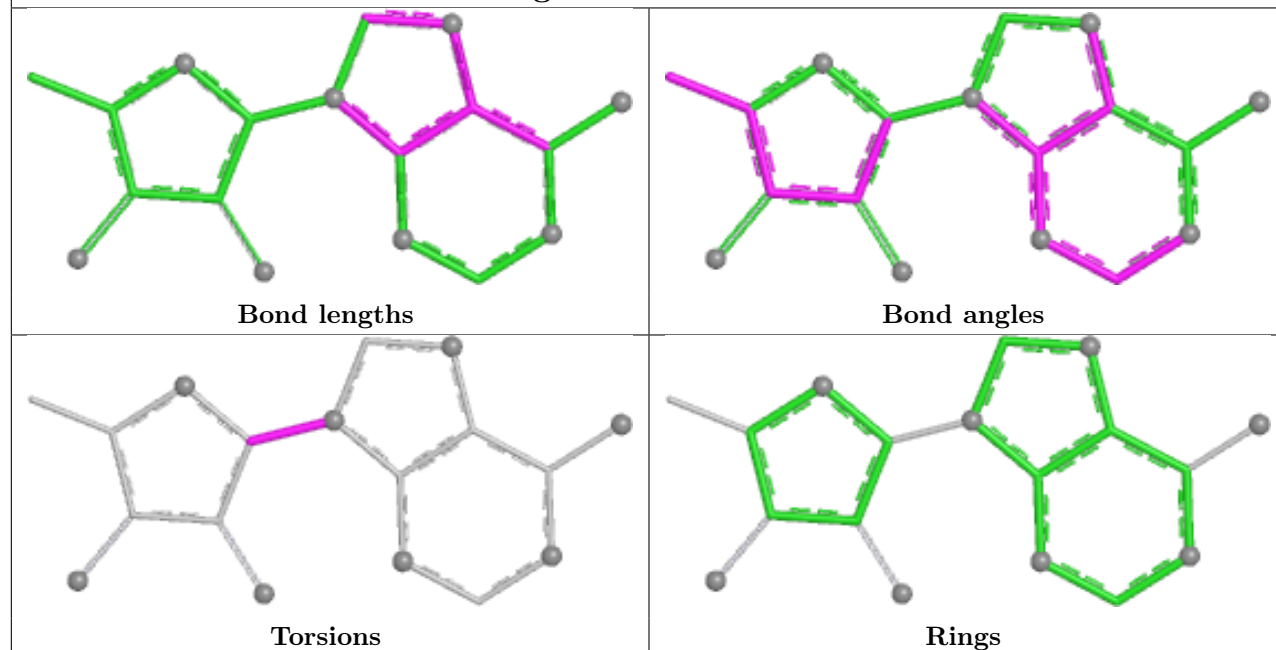
Ligand 5AD A 401



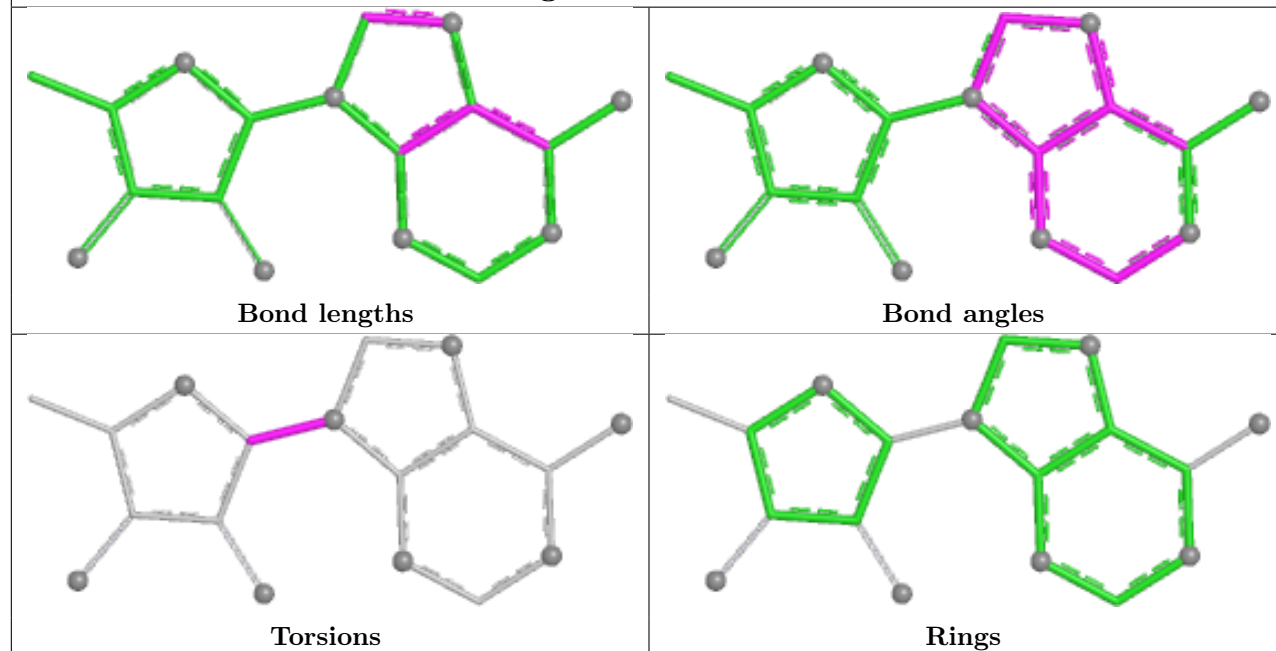
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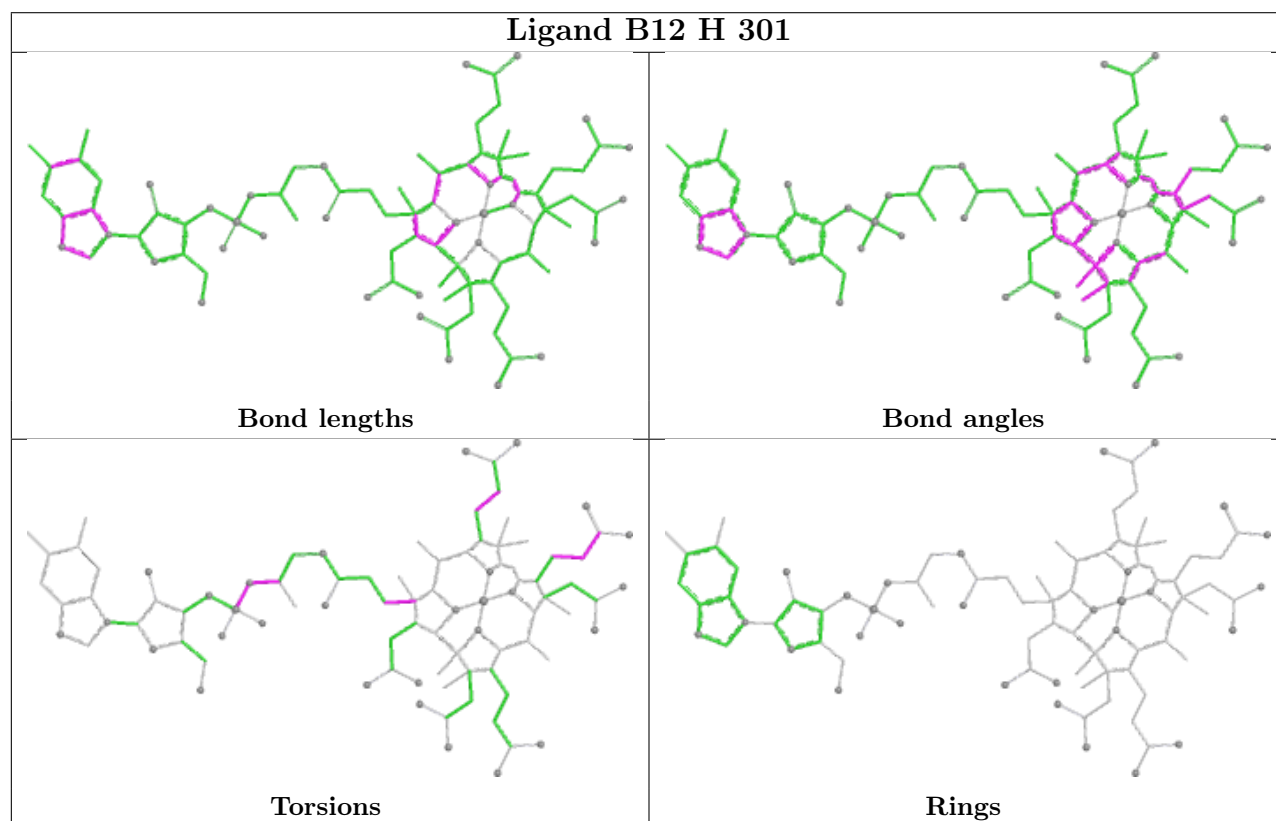
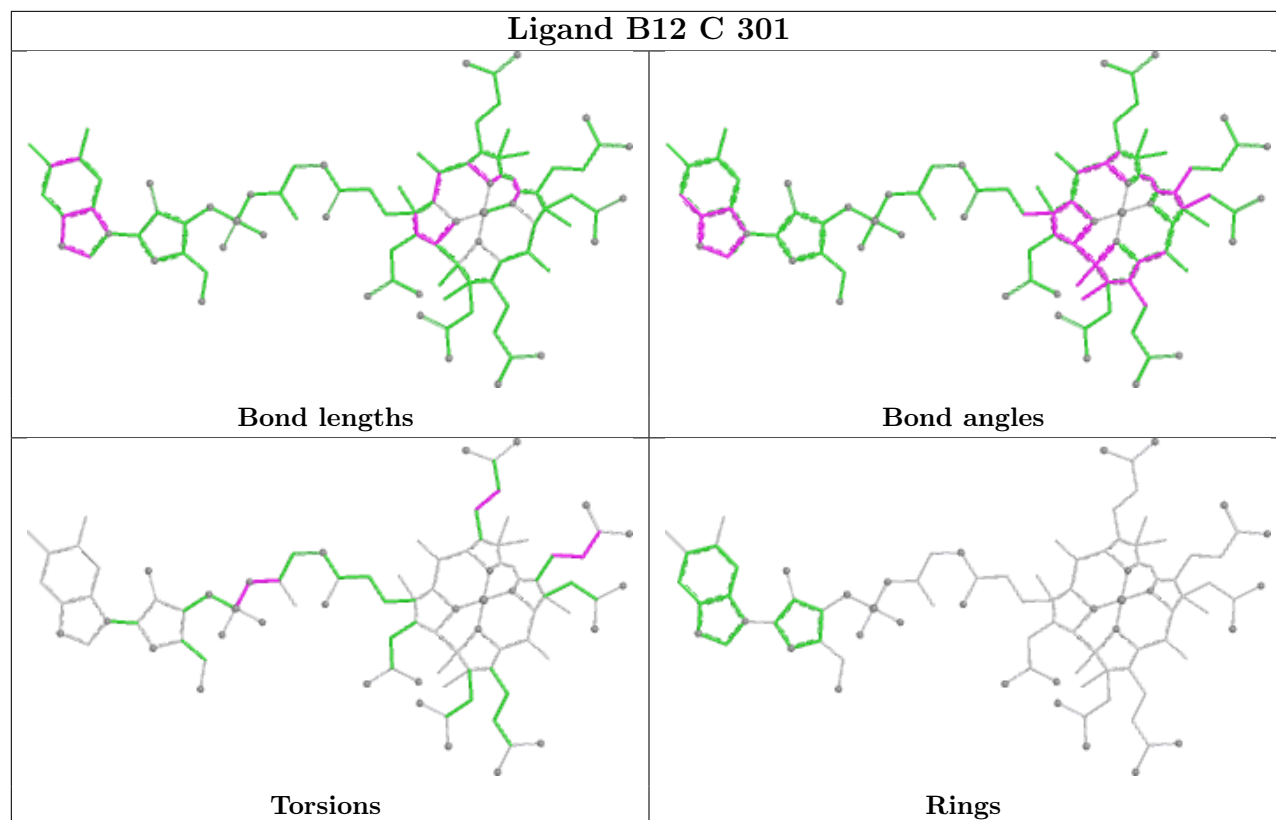


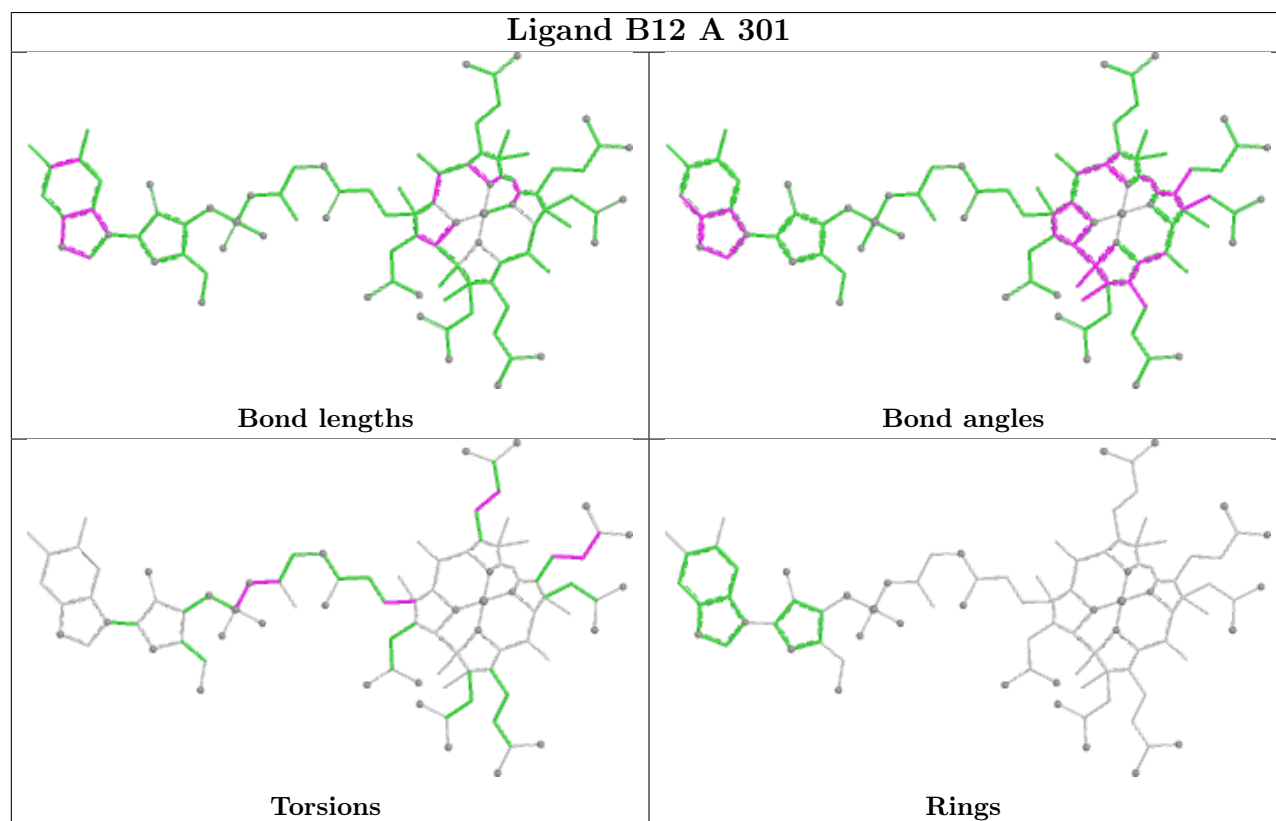
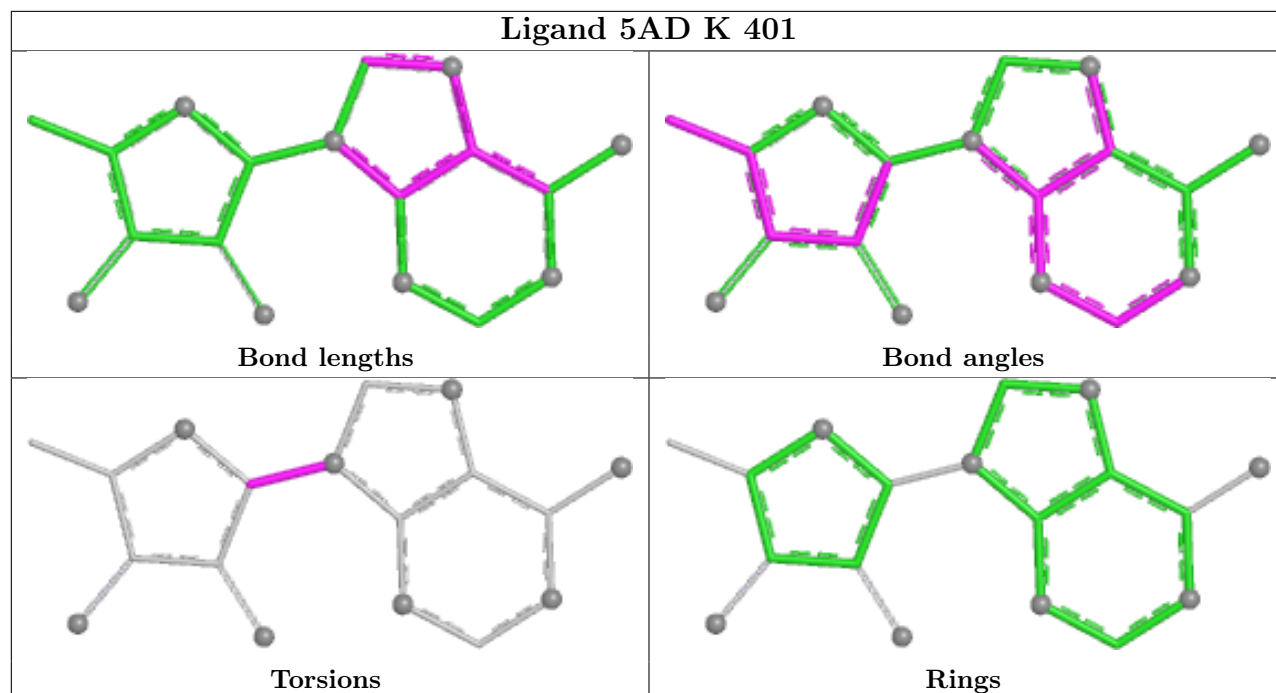
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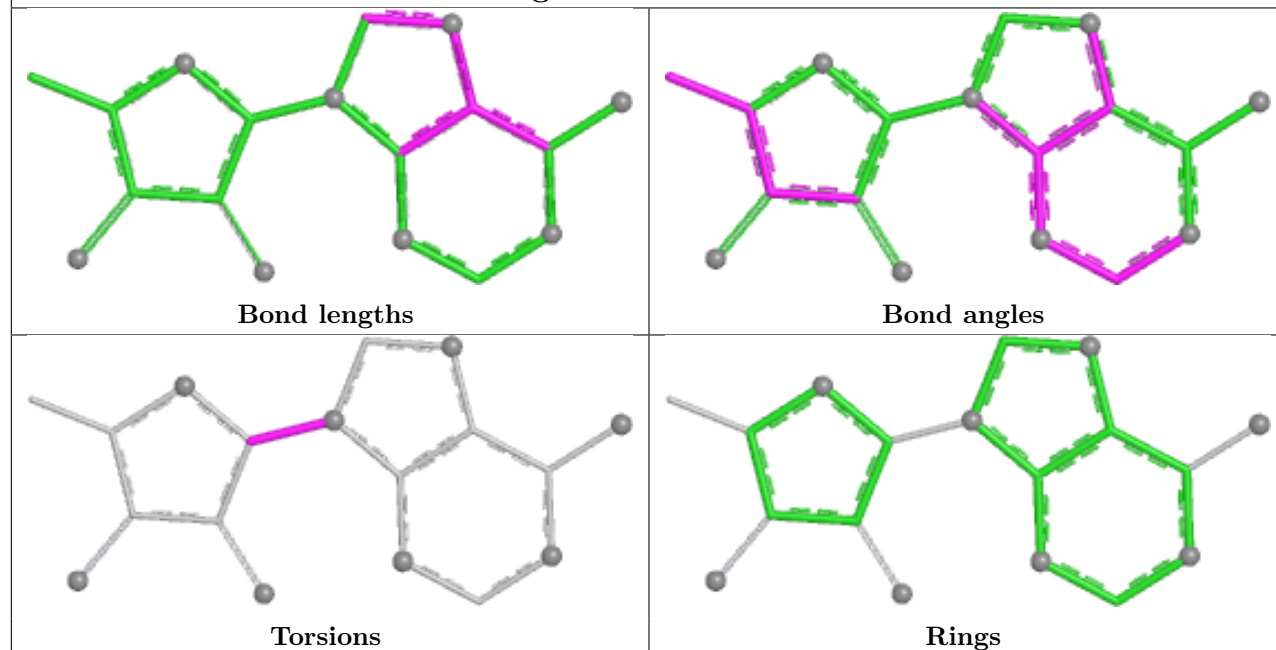
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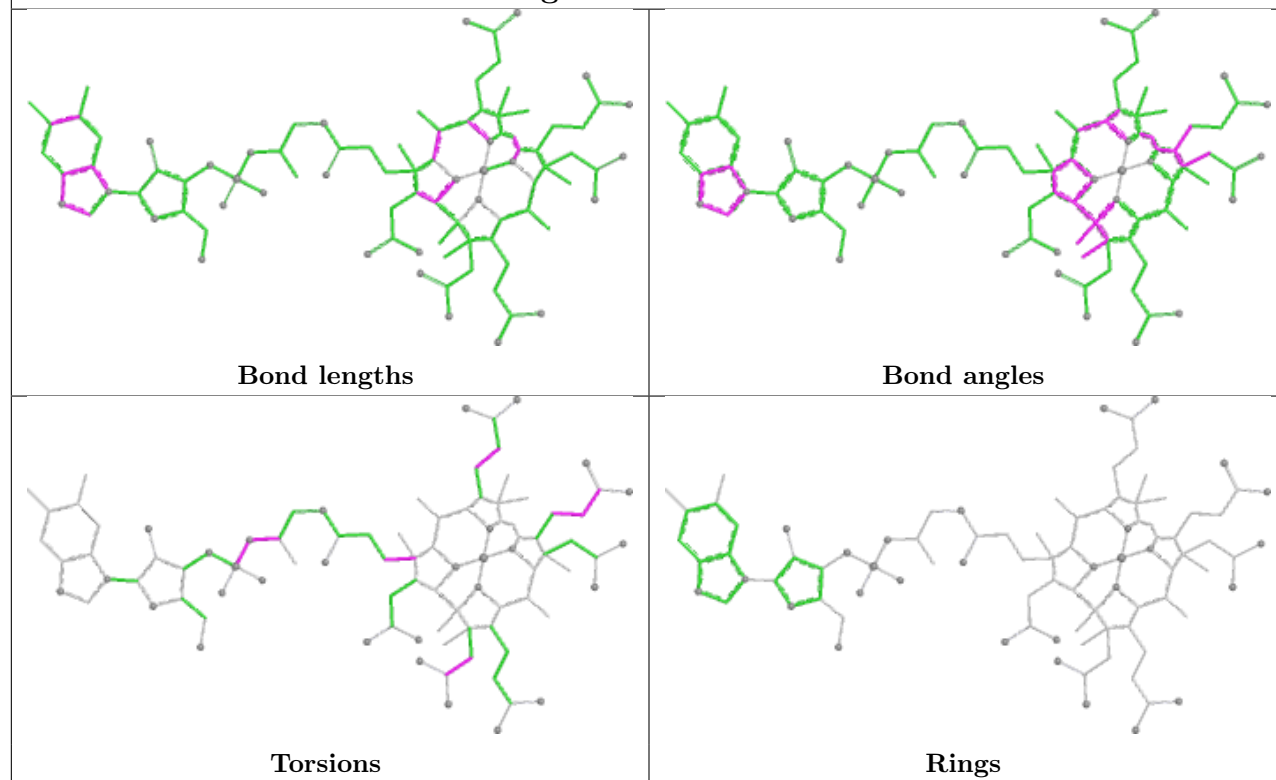


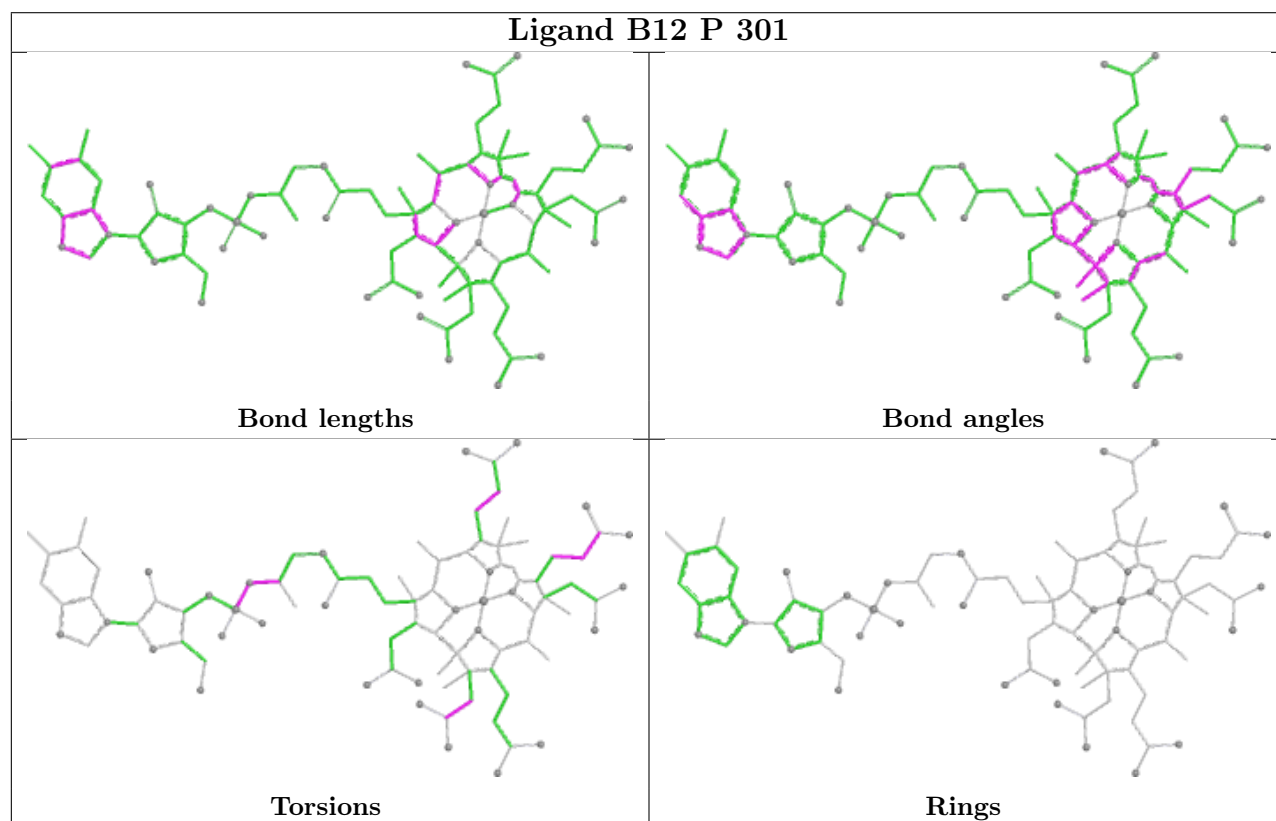
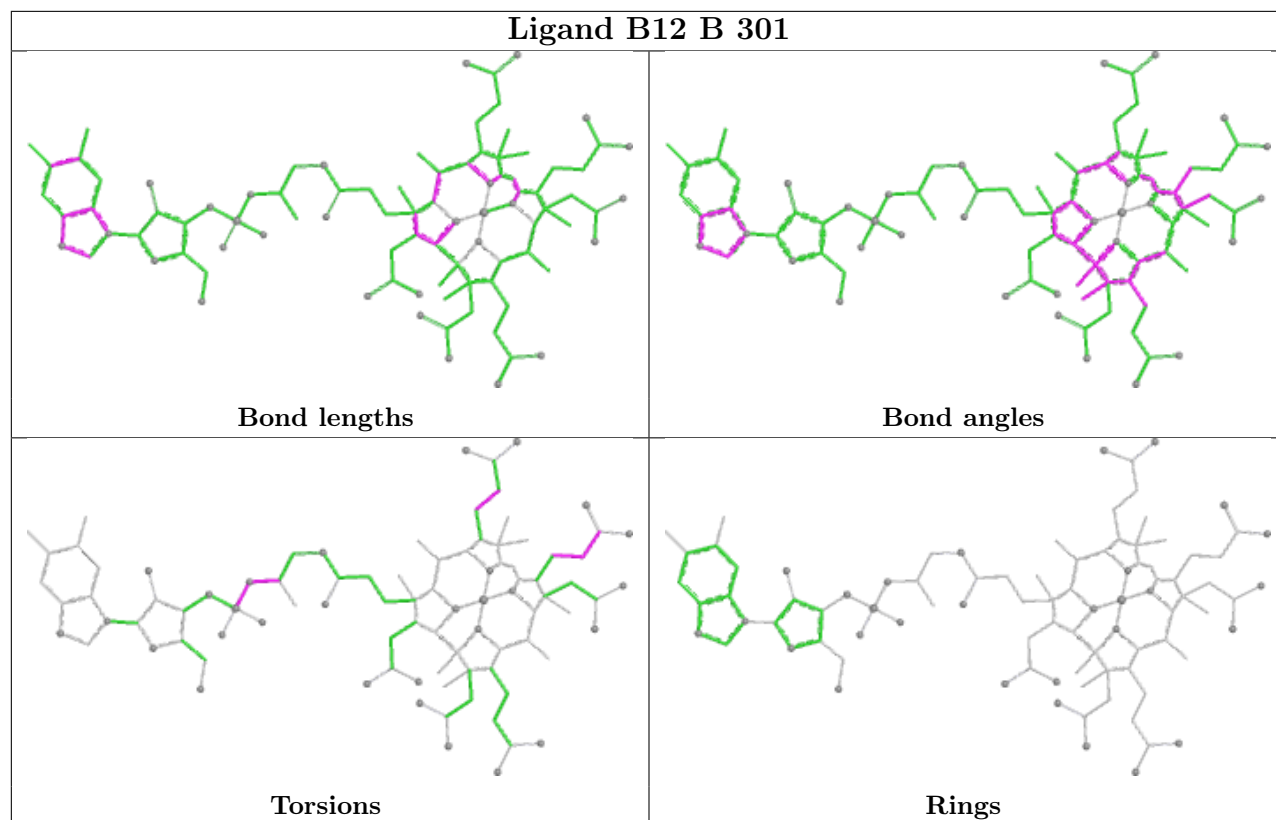


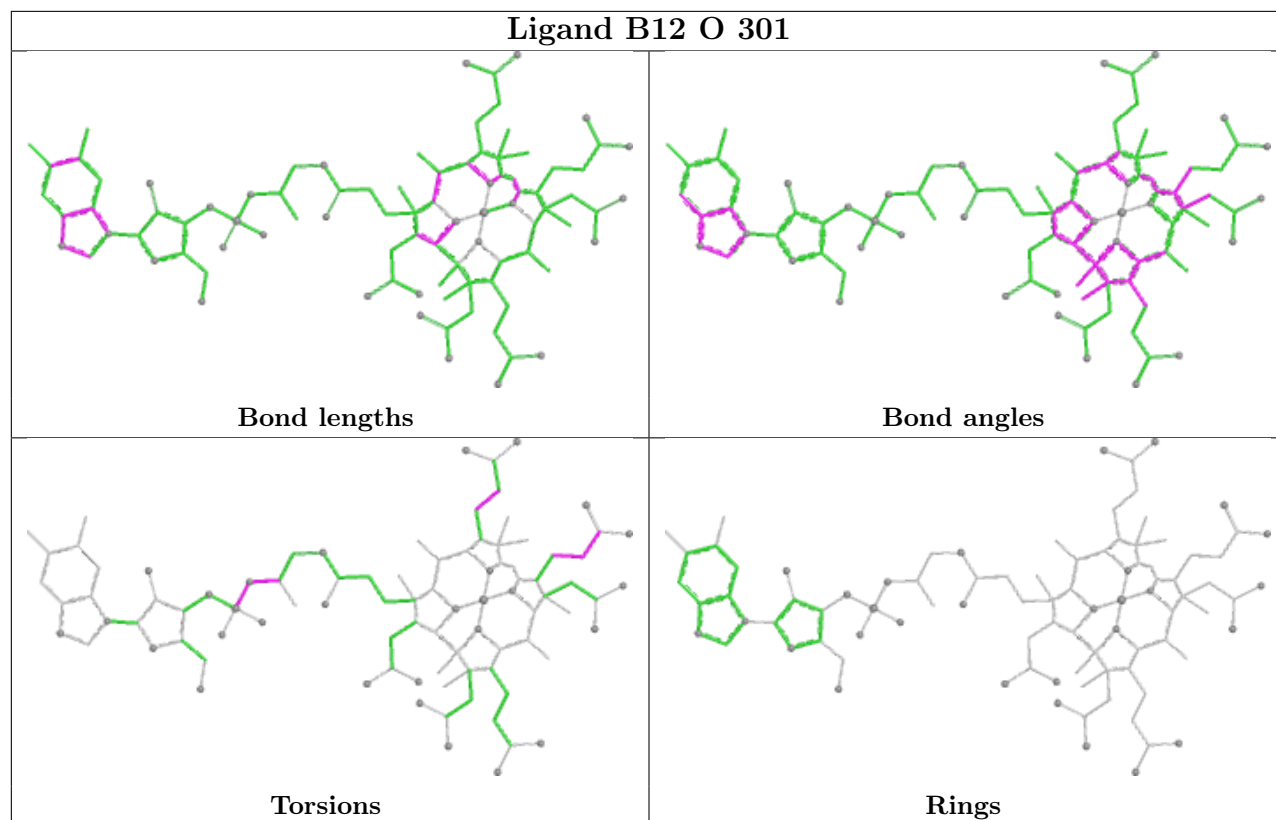
Ligand 5AD G 401



Ligand B12 L 301







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	A	225/286 (78%)	-0.04	1 (0%) 88 86	24, 40, 57, 70	0
1	B	226/286 (79%)	0.04	3 (1%) 75 71	26, 40, 59, 70	0
1	C	226/286 (79%)	0.22	2 (0%) 81 78	29, 42, 60, 76	2 (0%)
1	D	227/286 (79%)	-0.21	3 (1%) 75 71	23, 35, 52, 73	1 (0%)
1	E	228/286 (79%)	-0.37	1 (0%) 88 86	18, 31, 51, 72	1 (0%)
1	F	226/286 (79%)	-0.47	1 (0%) 88 86	16, 28, 47, 63	3 (1%)
1	G	226/286 (79%)	-0.47	5 (2%) 62 58	16, 27, 48, 68	0
1	H	225/286 (78%)	-0.46	3 (1%) 75 71	17, 27, 47, 66	0
1	I	226/286 (79%)	-0.40	3 (1%) 75 71	19, 30, 51, 71	1 (0%)
1	J	225/286 (78%)	-0.47	1 (0%) 88 86	19, 28, 50, 71	1 (0%)
1	K	225/286 (78%)	-0.32	0 100 100	19, 32, 51, 67	1 (0%)
1	L	229/286 (80%)	-0.46	3 (1%) 75 71	16, 28, 45, 71	2 (0%)
1	M	229/286 (80%)	-0.51	2 (0%) 81 78	16, 28, 45, 63	1 (0%)
1	N	230/286 (80%)	-0.26	1 (0%) 88 86	20, 33, 51, 76	0
1	O	226/286 (79%)	-0.44	1 (0%) 88 86	18, 30, 47, 68	1 (0%)
1	P	228/286 (79%)	-0.39	2 (0%) 81 78	18, 31, 51, 68	0
All	All	3627/4576 (79%)	-0.31	32 (0%) 81 78	16, 32, 54, 76	14 (0%)

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3	PRO	4.8
1	P	231	LEU	4.7
1	F	3	PRO	4.3
1	C	231	LEU	4.2
1	O	231	LEU	4.2

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	DHL	G	601	4/4	0.67	0.27	57,59,61,64	0
4	DHL	A	601	4/4	0.68	0.26	79,79,79,80	0
4	DHL	O	601	4/4	0.70	0.34	29,30,32,35	4
5	5AD	G	283	18/18	0.72	0.19	55,68,72,72	0
5	5AD	I	283	18/18	0.75	0.18	59,64,71,73	0
4	DHL	I	601	4/4	0.76	0.34	41,42,42,42	4
4	DHL	D	601	4/4	0.77	0.25	62,62,63,64	0
4	DHL	M	601	4/4	0.81	0.21	54,55,56,56	0
6	EDO	E	283	4/4	0.83	0.20	55,55,55,59	0
4	DHL	C	601	4/4	0.85	0.28	22,23,25,30	4
4	DHL	L	601	4/4	0.88	0.15	51,51,51,51	0
4	DHL	F	601	4/4	0.88	0.16	52,52,53,54	0
5	5AD	C	401	18/18	0.89	0.12	31,39,46,46	0
4	DHL	N	601	4/4	0.89	0.17	51,55,58,61	0
3	FLC	D	501	13/13	0.90	0.10	43,44,45,45	0
4	DHL	K	601	4/4	0.90	0.15	50,51,51,53	0
3	FLC	C	501	13/13	0.90	0.13	61,62,63,63	0
5	5AD	O	401	18/18	0.90	0.11	25,31,35,39	0
5	5AD	B	401	18/18	0.90	0.11	35,40,43,43	0
6	EDO	P	284	4/4	0.90	0.21	48,49,49,53	0
4	DHL	J	601	4/4	0.91	0.13	43,47,51,54	0
5	5AD	K	401	18/18	0.91	0.11	23,32,34,35	0
5	5AD	L	401	18/18	0.91	0.11	24,32,44,47	0
3	FLC	B	501	13/13	0.91	0.10	53,54,55,55	0
5	5AD	E	401	18/18	0.91	0.10	24,31,38,38	0
6	EDO	P	283	4/4	0.91	0.18	43,44,45,48	0
5	5AD	A	401	18/18	0.91	0.09	41,44,47,49	0

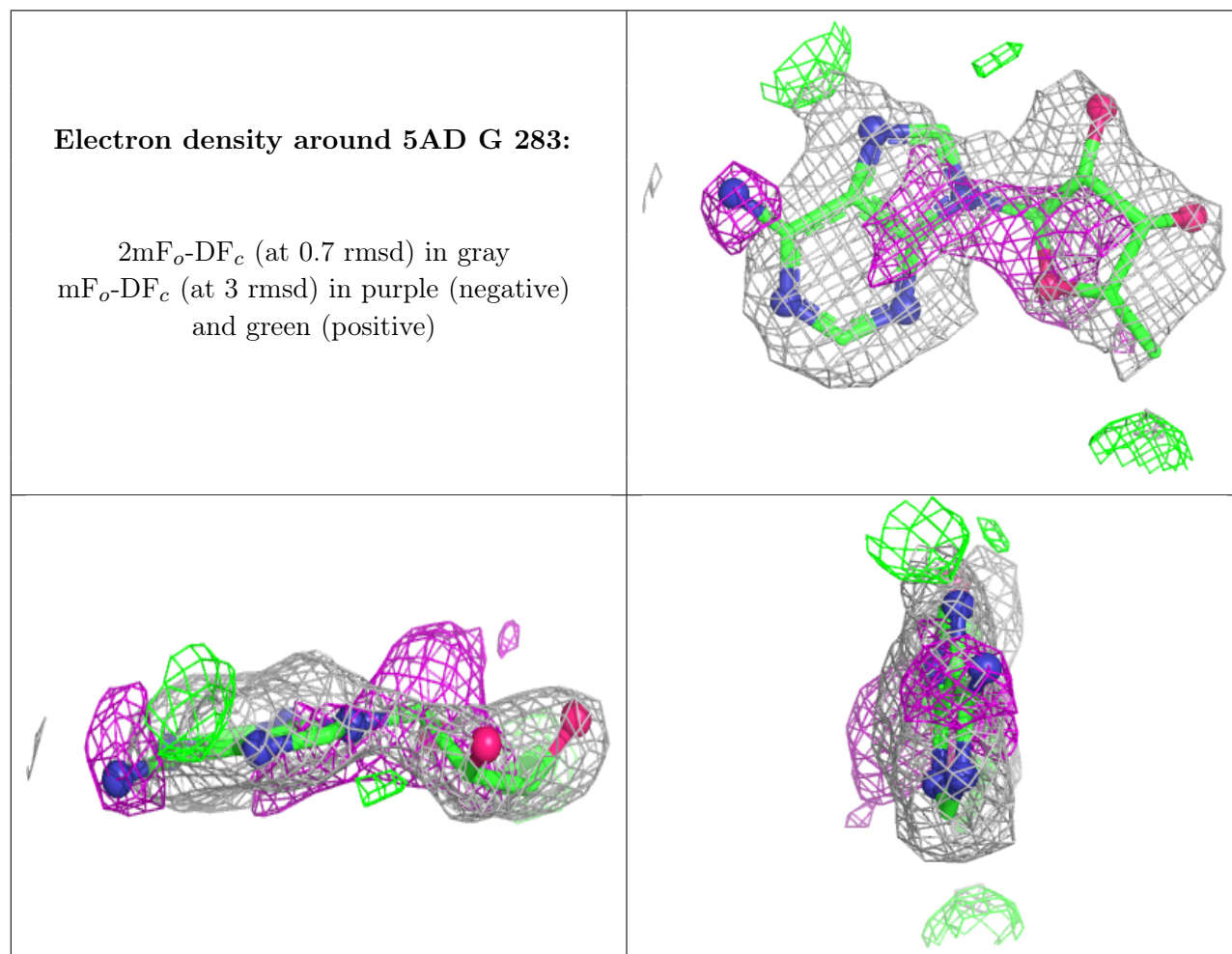
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	FLC	P	501	13/13	0.92	0.10	39,40,41,42	0
5	5AD	F	401	18/18	0.92	0.10	24,31,35,38	0
5	5AD	M	401	18/18	0.92	0.10	26,34,40,43	0
5	5AD	N	401	18/18	0.92	0.10	22,31,39,40	0
3	FLC	K	501	13/13	0.92	0.10	37,38,39,39	0
5	5AD	H	401	18/18	0.92	0.10	23,29,38,38	0
5	5AD	I	401	18/18	0.92	0.10	28,34,38,39	0
5	5AD	D	401	18/18	0.92	0.09	31,35,47,48	0
3	FLC	N	501	13/13	0.93	0.09	38,39,40,41	0
3	FLC	G	501	13/13	0.93	0.09	33,34,35,36	0
5	5AD	G	401	18/18	0.93	0.09	28,32,38,39	0
5	5AD	J	401	18/18	0.94	0.09	22,28,37,38	0
3	FLC	F	501	13/13	0.94	0.08	31,32,33,33	0
3	FLC	L	501	13/13	0.94	0.09	35,35,36,37	0
3	FLC	M	501	13/13	0.94	0.08	35,36,37,37	0
3	FLC	E	501	13/13	0.94	0.09	36,37,38,38	0
4	DHL	P	601	4/4	0.94	0.12	38,38,38,40	0
5	5AD	P	401	18/18	0.94	0.09	26,32,36,37	0
3	FLC	O	501	13/13	0.94	0.08	36,37,38,38	0
3	FLC	H	501	13/13	0.94	0.08	37,38,39,39	0
3	FLC	J	501	13/13	0.94	0.07	35,36,37,38	0
4	DHL	H	601	4/4	0.95	0.11	39,40,41,42	0
3	FLC	A	501	13/13	0.95	0.07	43,44,45,46	0
3	FLC	I	501	13/13	0.95	0.08	34,34,35,36	0
2	B12	C	301	91/91	0.96	0.09	28,35,46,55	0
2	B12	B	301	91/91	0.96	0.08	29,35,42,49	0
2	B12	G	301	91/91	0.97	0.07	15,21,28,29	0
2	B12	H	301	91/91	0.97	0.07	16,22,26,29	0
2	B12	I	301	91/91	0.97	0.07	17,23,30,33	0
2	B12	J	301	91/91	0.97	0.07	18,23,30,32	0
2	B12	K	301	91/91	0.97	0.07	17,25,29,34	0
2	B12	M	301	91/91	0.97	0.07	10,21,28,31	0
2	B12	N	301	91/91	0.97	0.07	15,23,29,32	0
2	B12	O	301	91/91	0.97	0.07	15,22,29,32	0
2	B12	P	301	91/91	0.97	0.07	17,24,29,31	0
2	B12	A	301	91/91	0.97	0.07	27,33,41,44	0
2	B12	D	301	91/91	0.97	0.08	17,28,37,38	0
2	B12	F	301	91/91	0.97	0.07	12,21,28,30	0
2	B12	L	301	91/91	0.98	0.07	14,20,28,30	0
2	B12	E	301	91/91	0.98	0.07	17,23,30,32	0

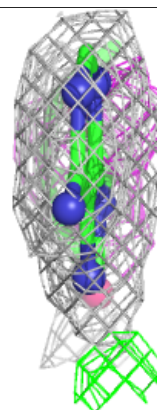
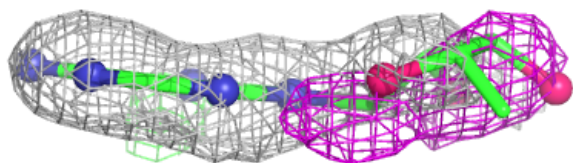
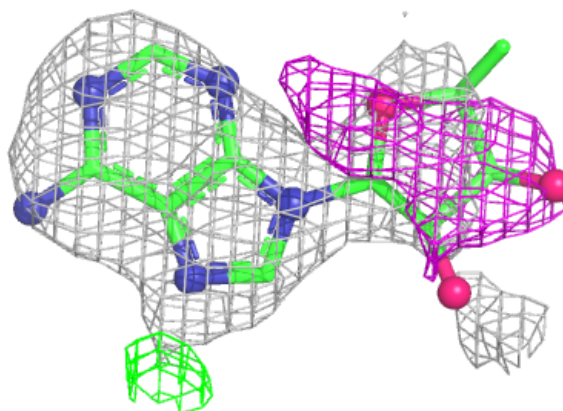
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

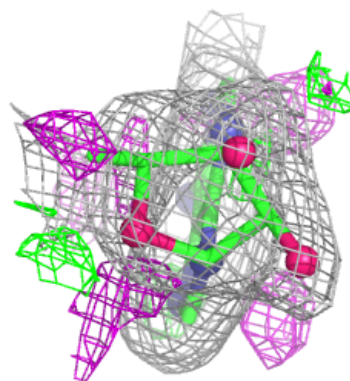
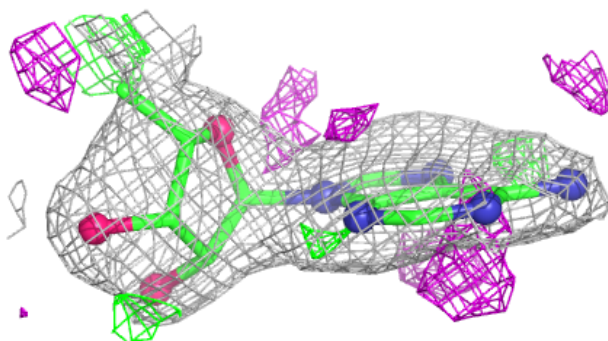
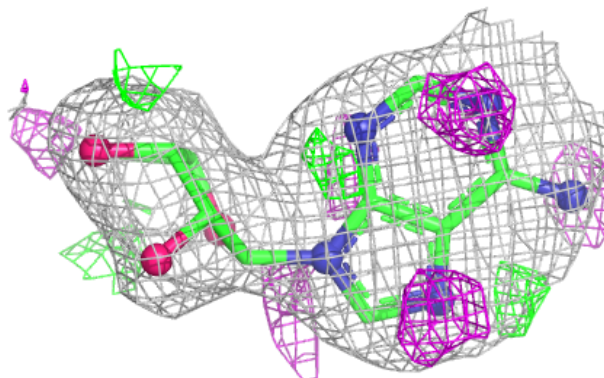


Electron density around 5AD I 283:

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

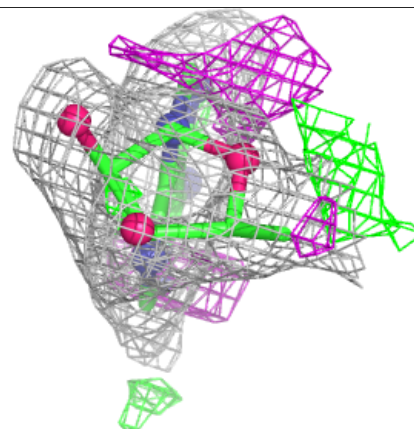
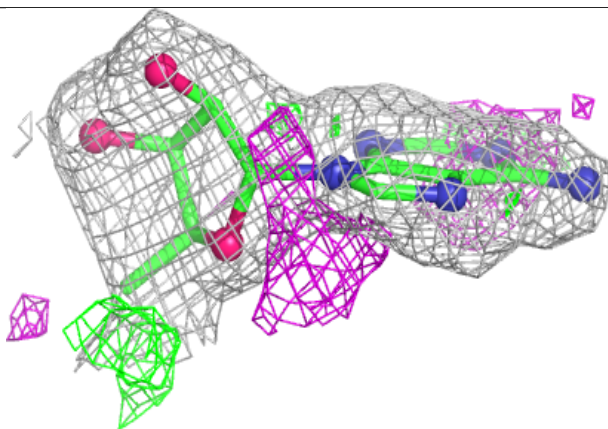
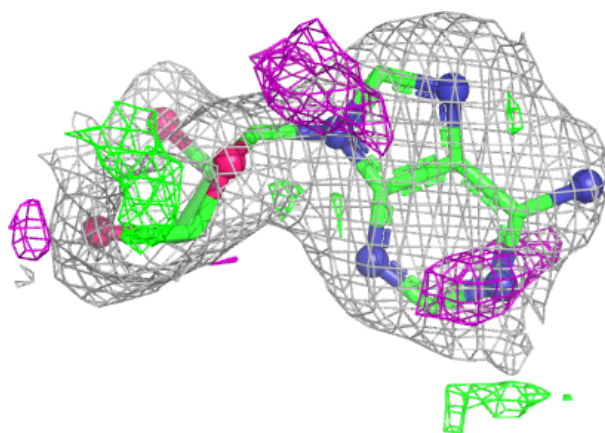
**Electron density around 5AD C 401:**

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

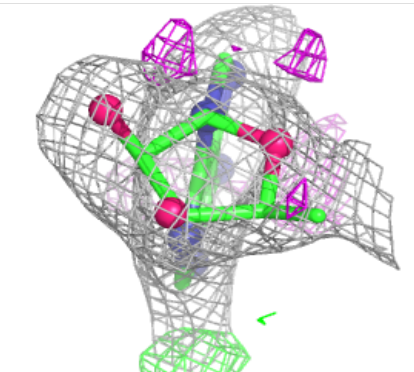
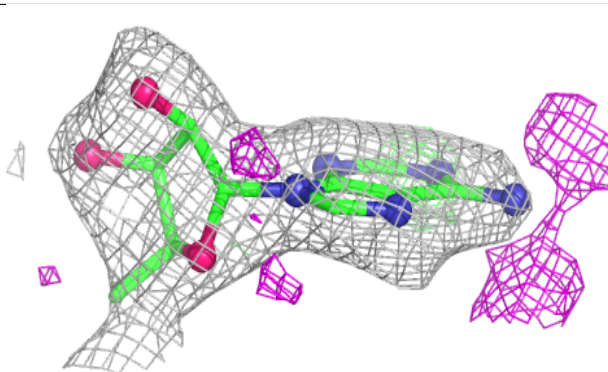
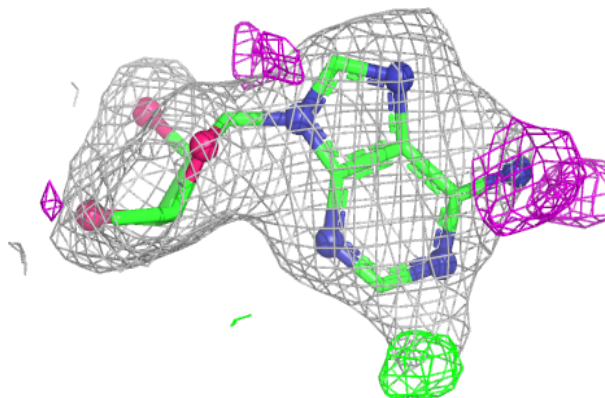


Electron density around 5AD O 401:

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

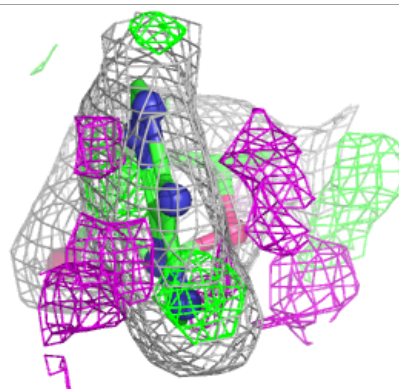
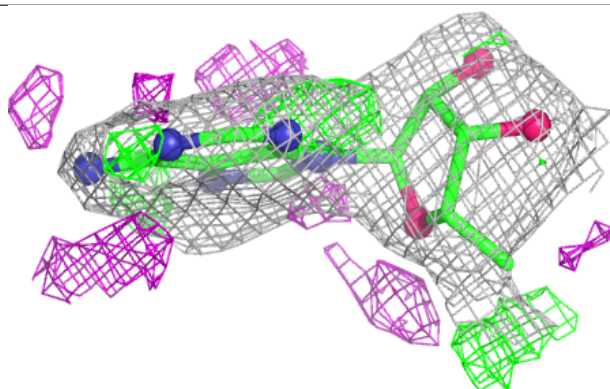
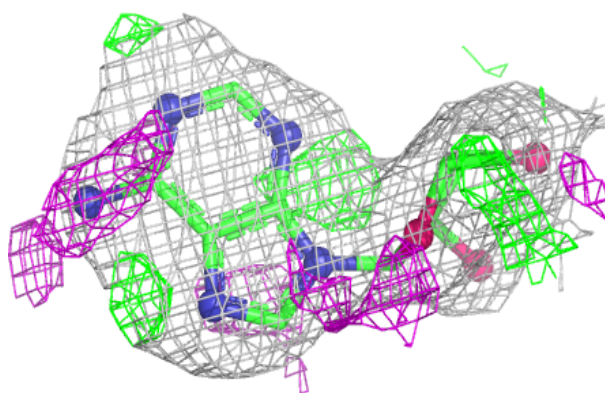
**Electron density around 5AD B 401:**

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and green (positive)

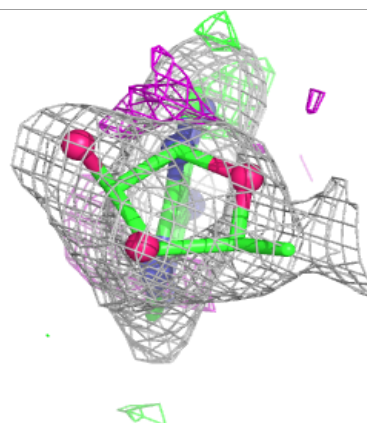
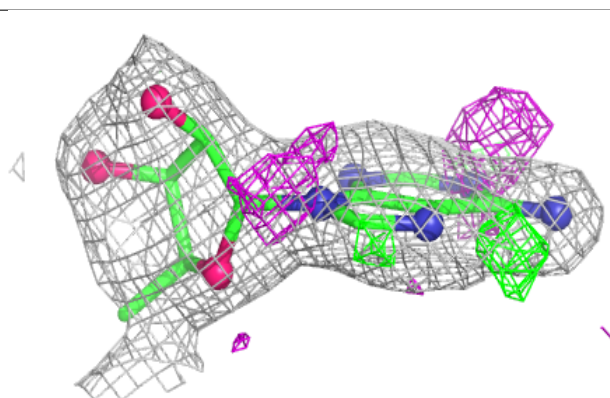
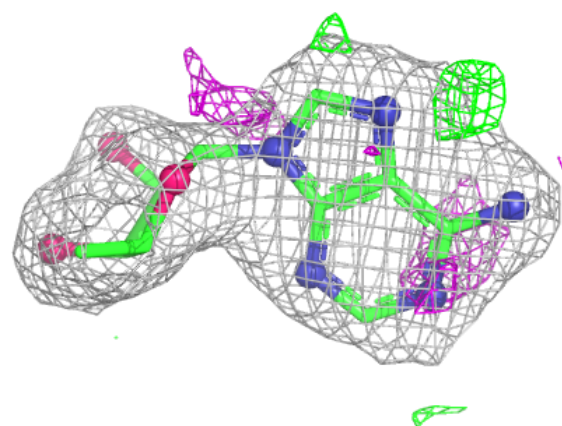


Electron density around 5AD K 401:

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

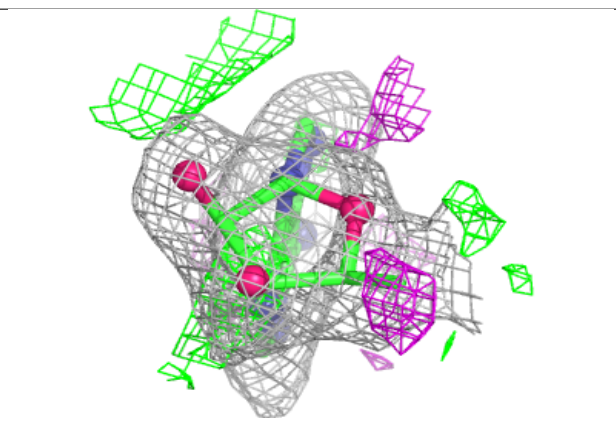
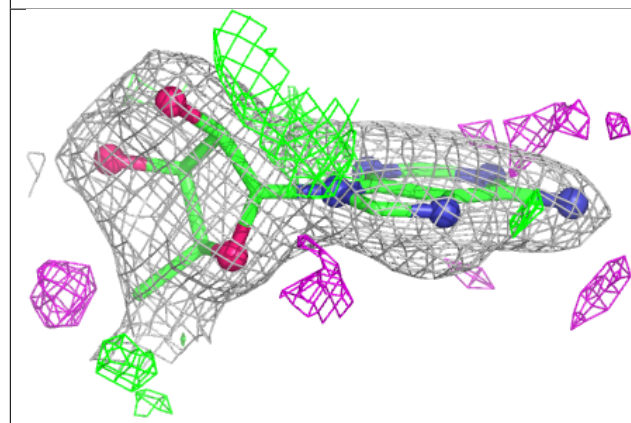
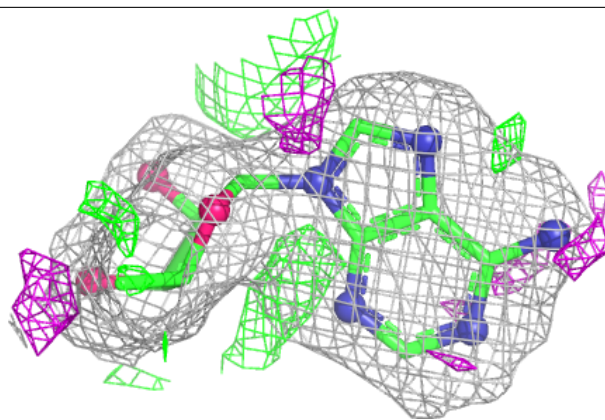
**Electron density around 5AD L 401:**

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



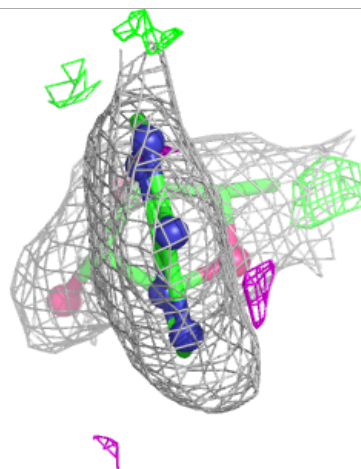
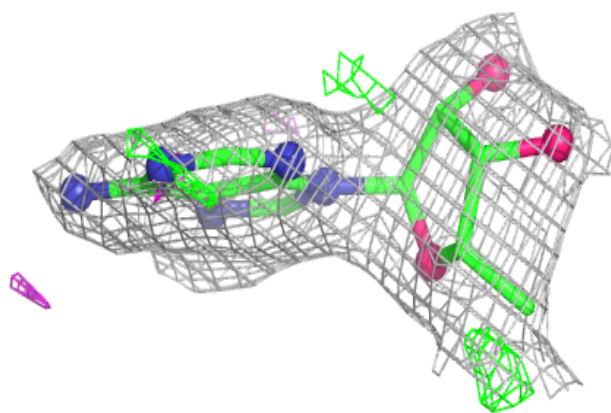
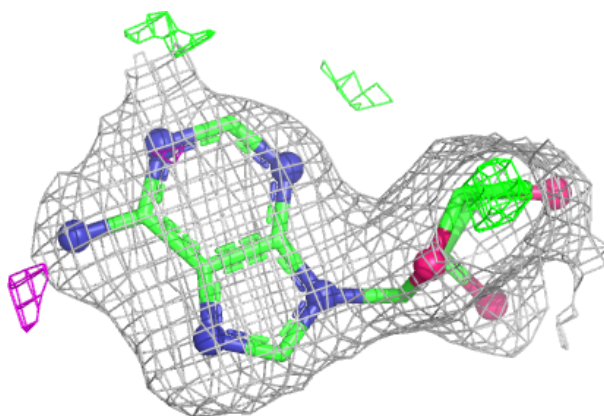
Electron density around 5AD E 401:

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



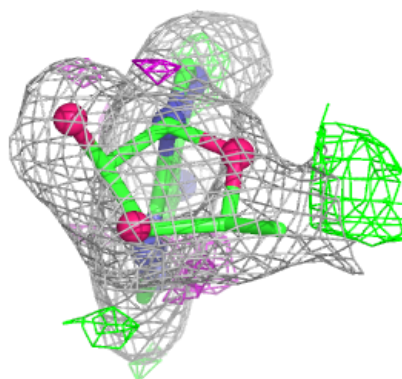
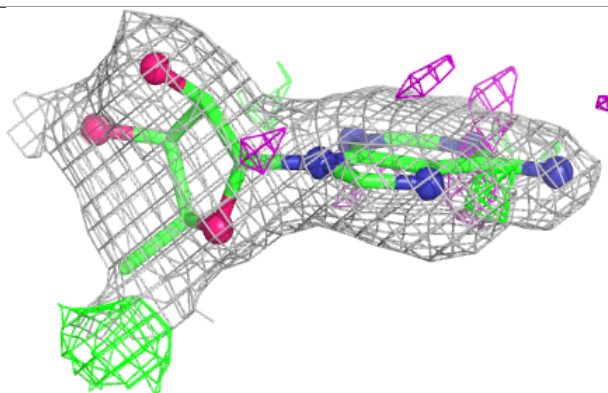
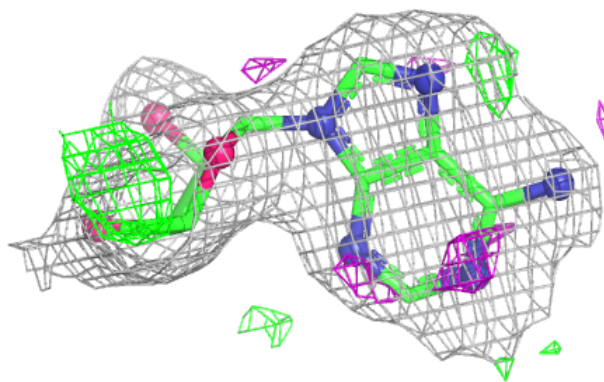
Electron density around 5AD A 401:

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and green (positive)



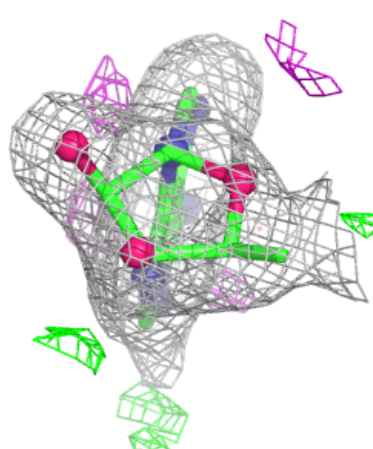
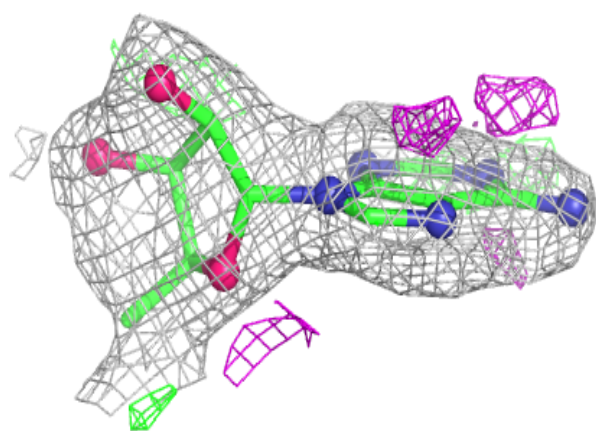
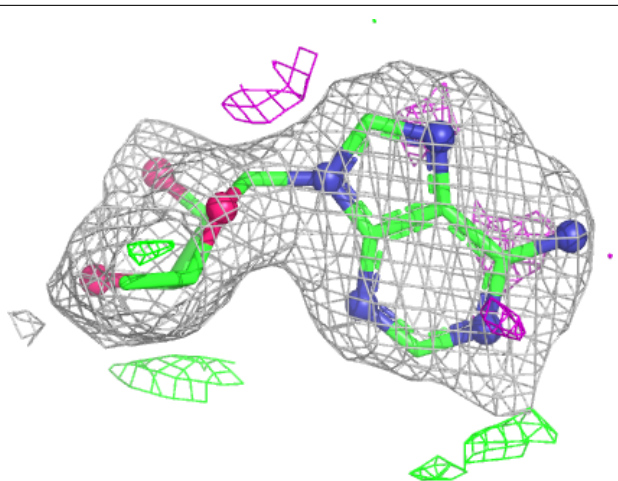
Electron density around 5AD F 401:

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and green (positive)



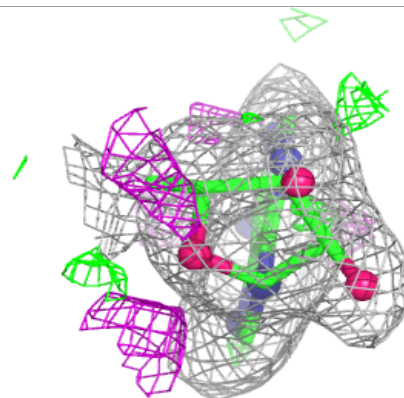
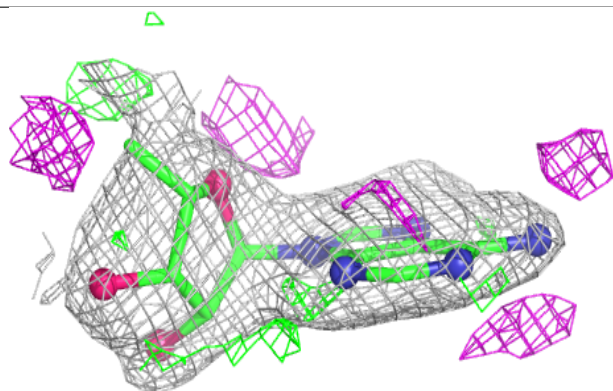
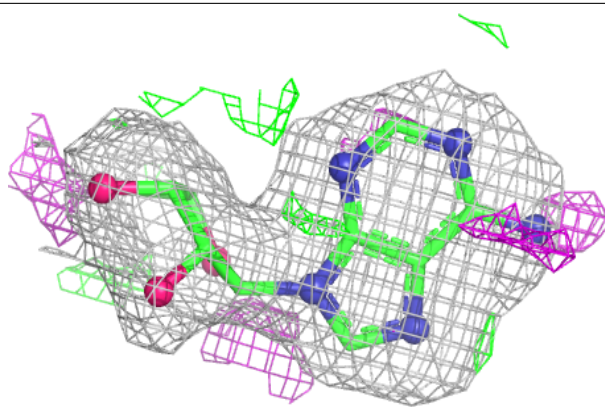
Electron density around 5AD M 401:

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and green (positive)



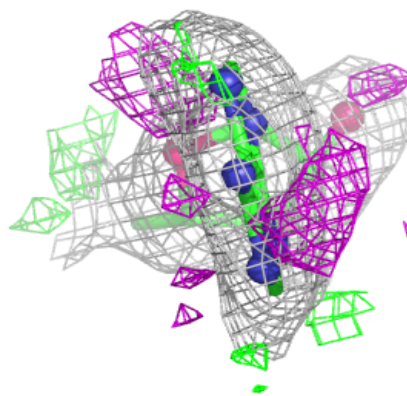
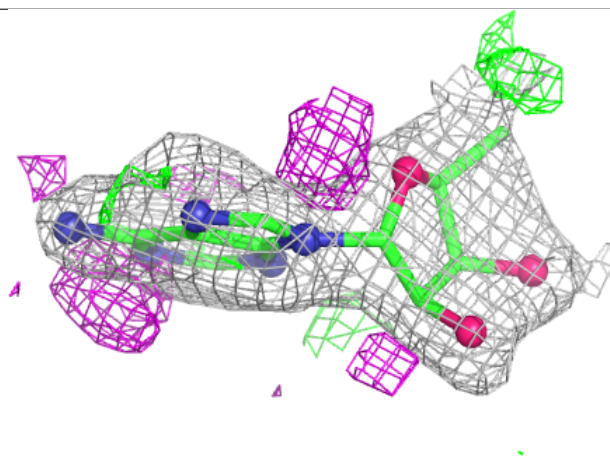
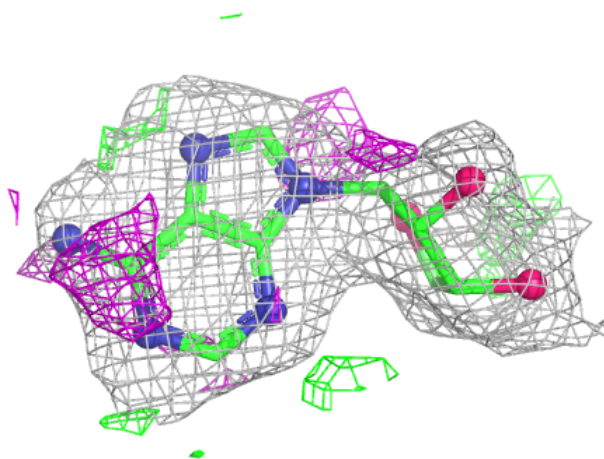
Electron density around 5AD N 401:

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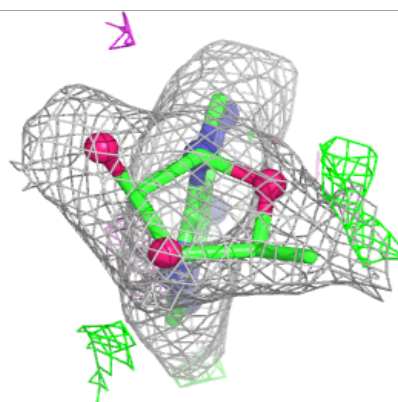
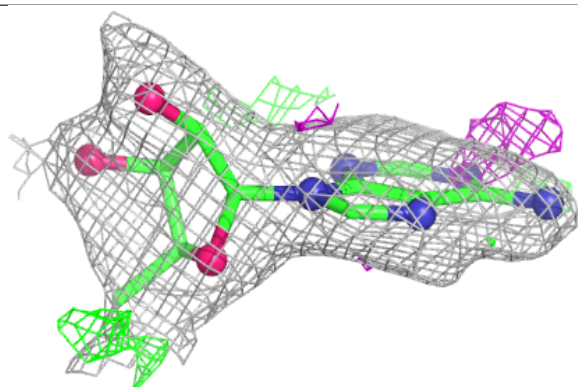
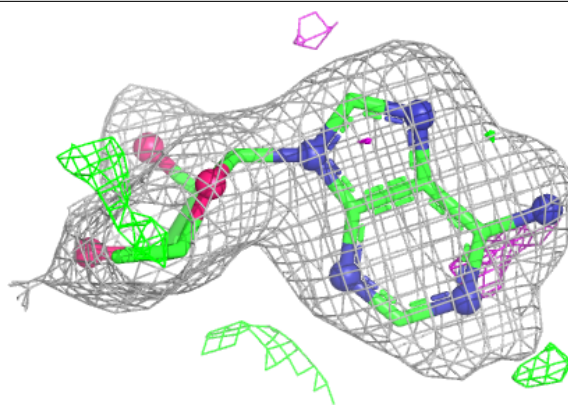
Electron density around 5AD H 401:

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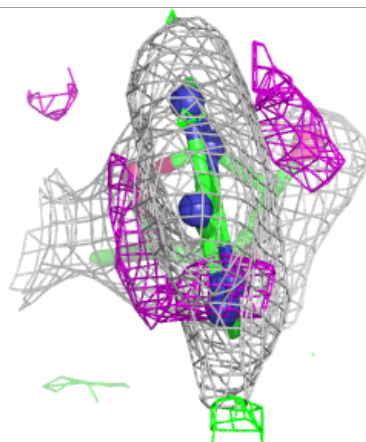
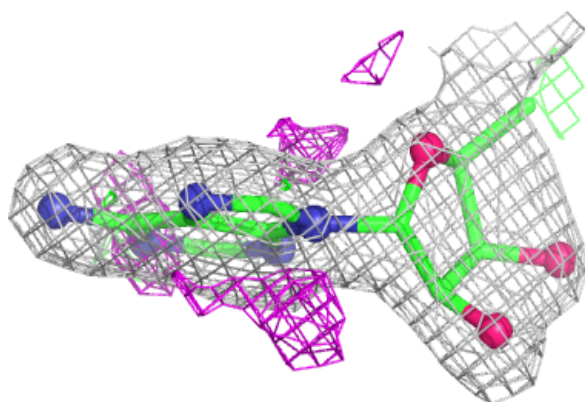
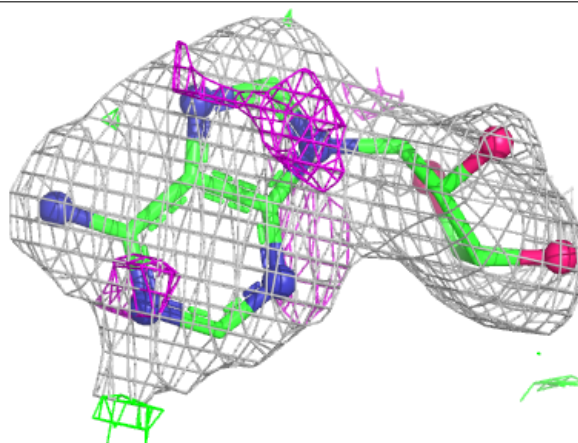


Electron density around 5AD I 401:

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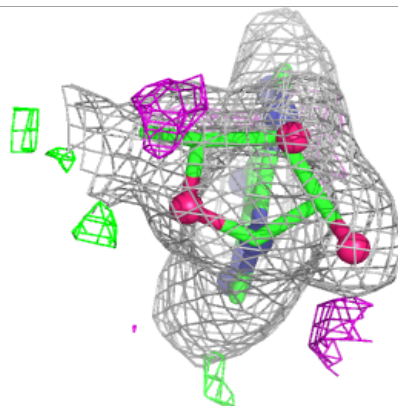
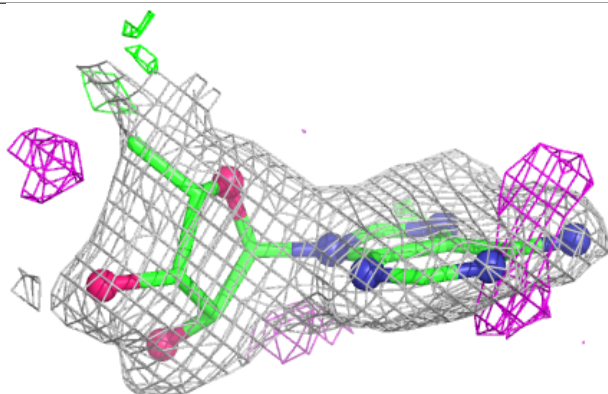
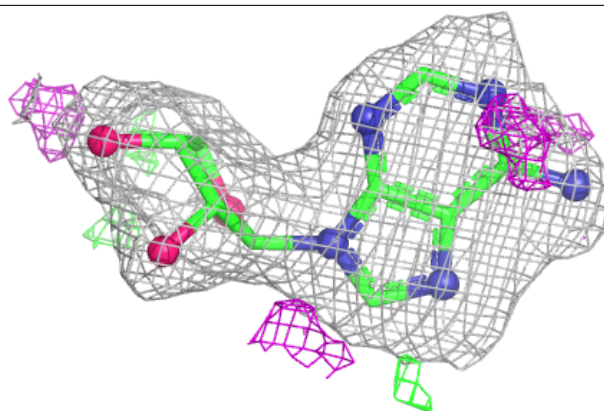
**Electron density around 5AD D 401:**

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and green (positive)

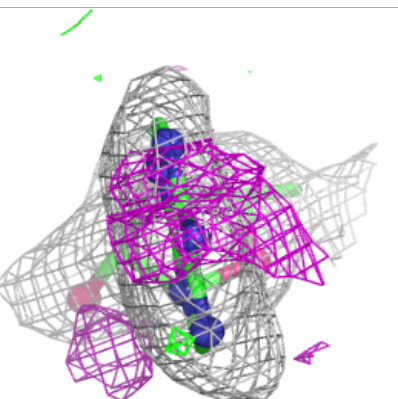
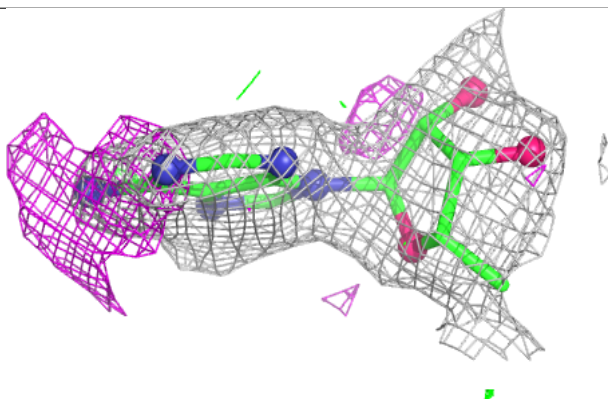
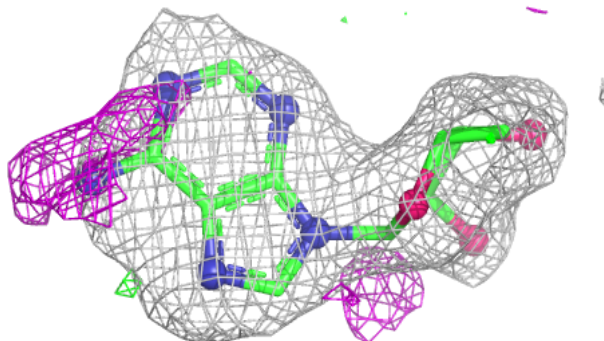


Electron density around 5AD G 401:

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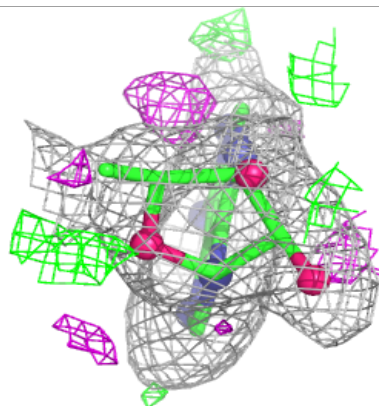
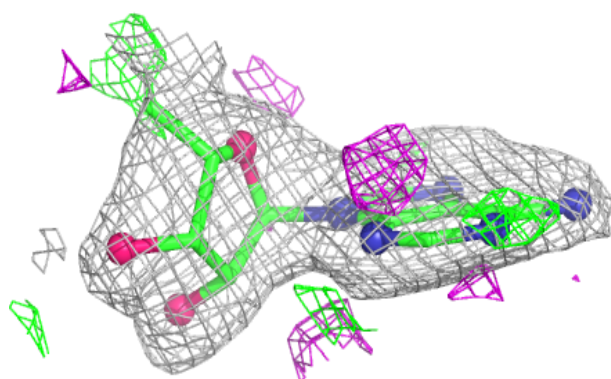
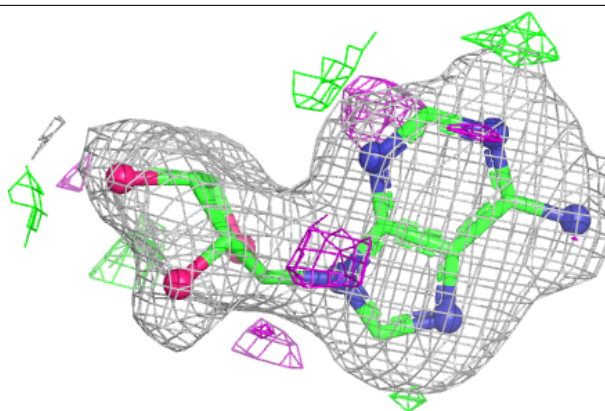
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and green (positive)

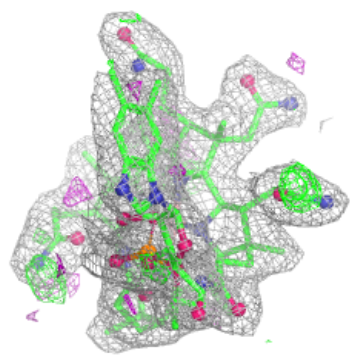
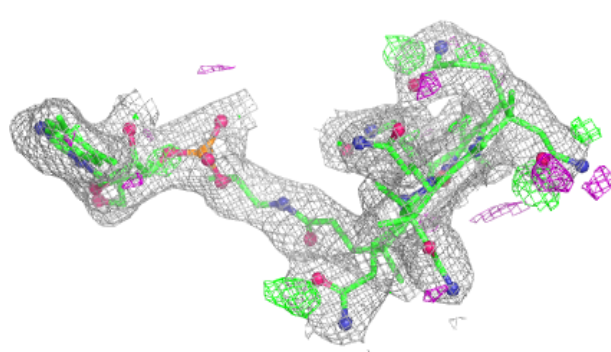
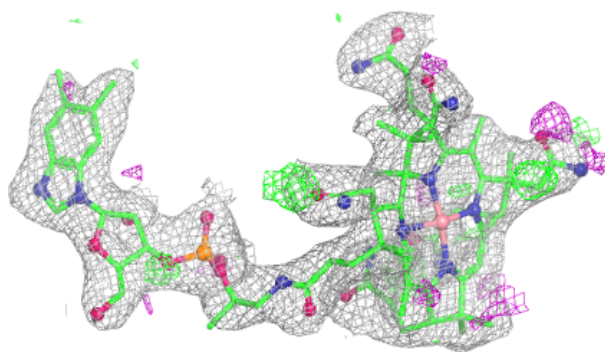


Electron density around 5AD P 401:

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and green (positive)

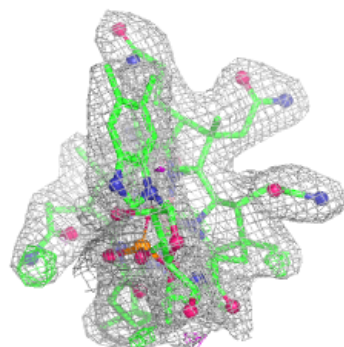
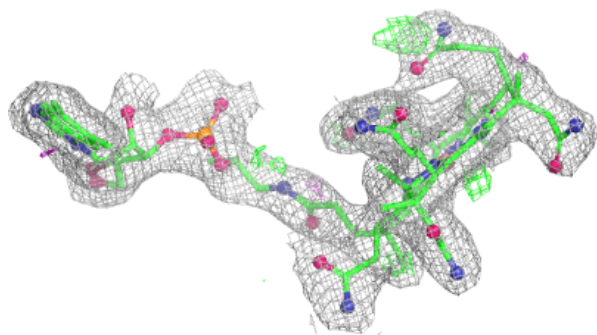
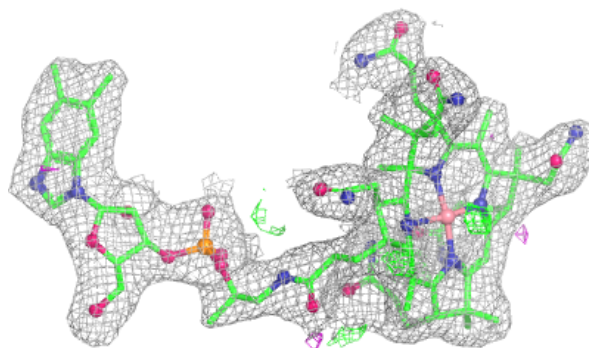
**Electron density around B12 C 301:**

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

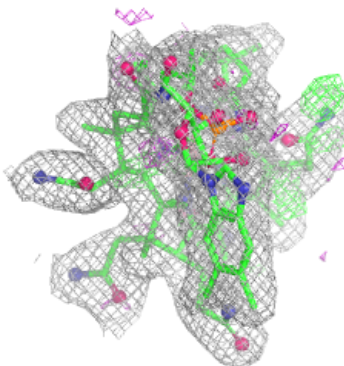
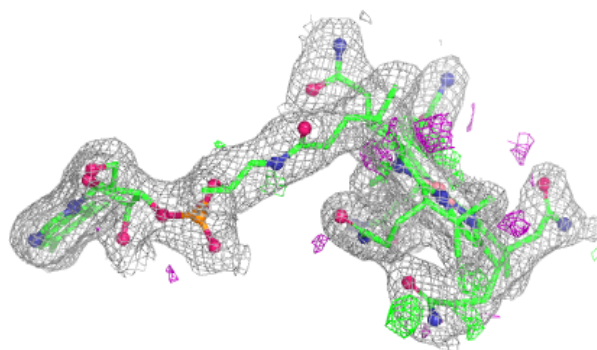
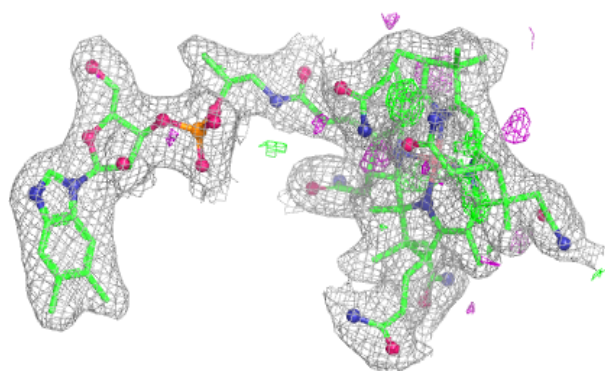


Electron density around B12 B 301:

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

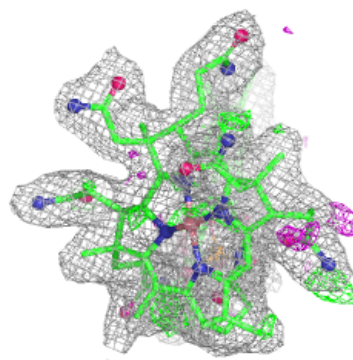
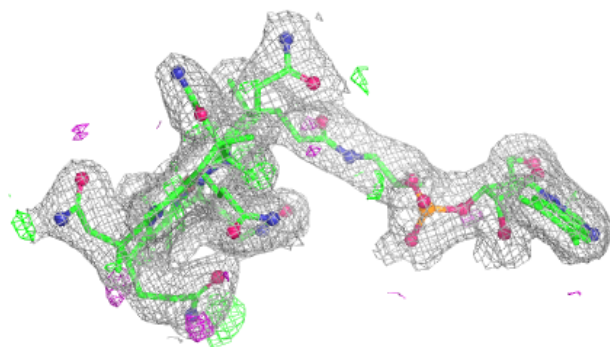
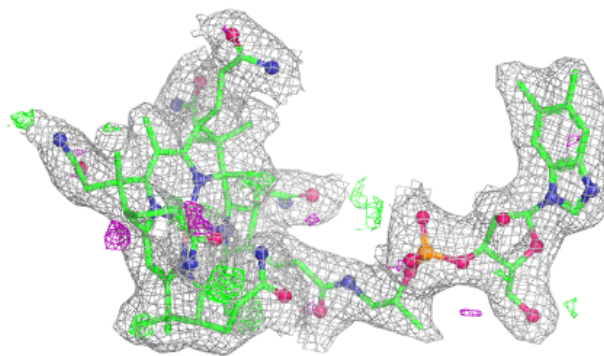
**Electron density around B12 G 301:**

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

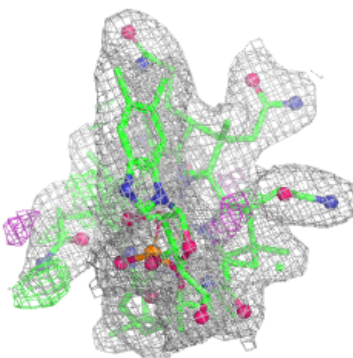
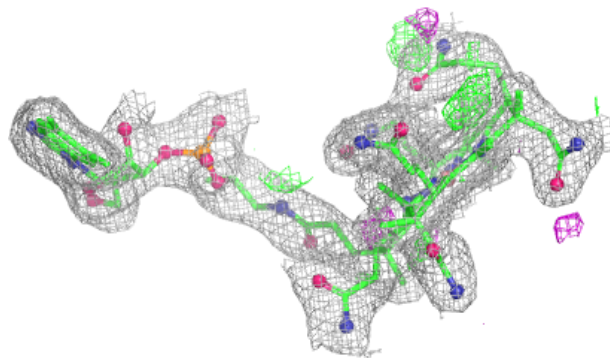
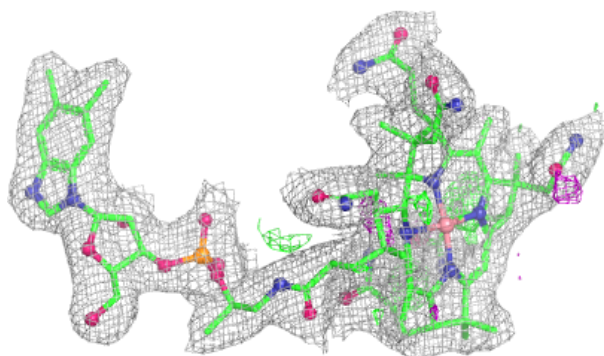


Electron density around B12 H 301:

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

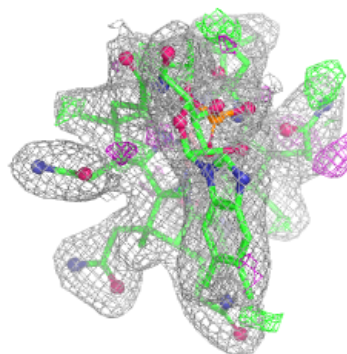
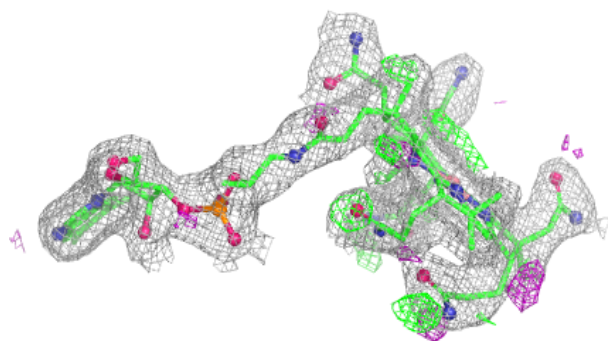
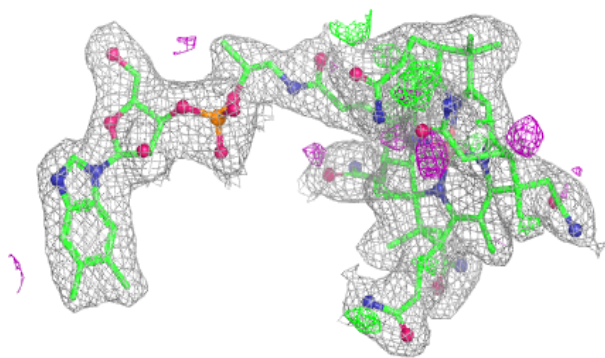
**Electron density around B12 I 301:**

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

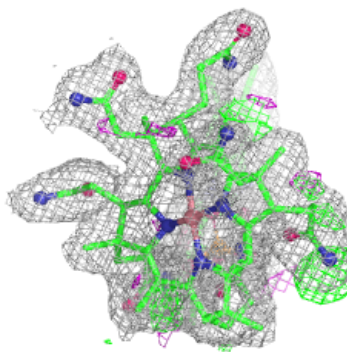
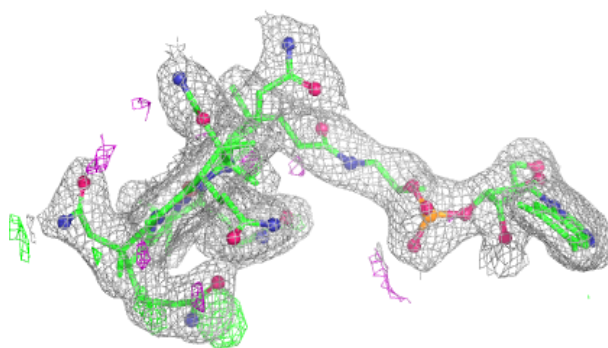
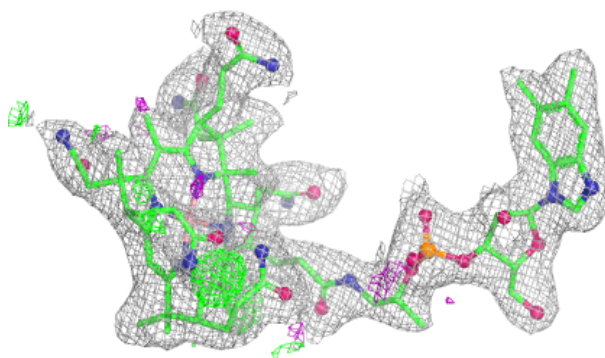


Electron density around B12 J 301:

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

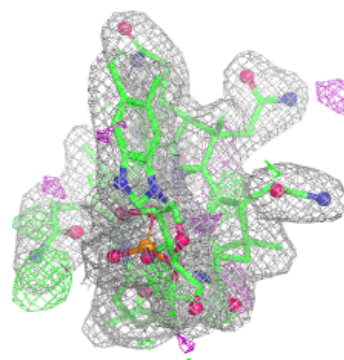
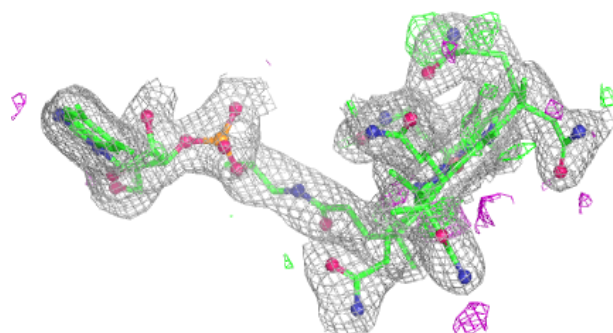
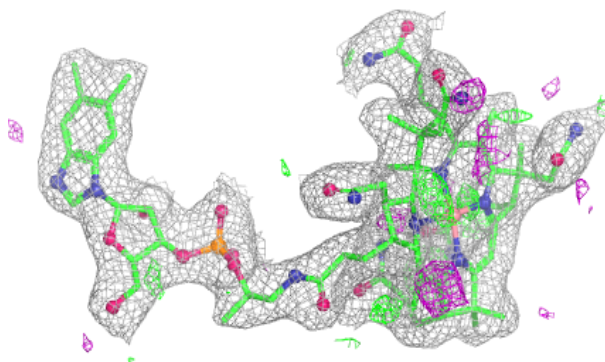
**Electron density around B12 K 301:**

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

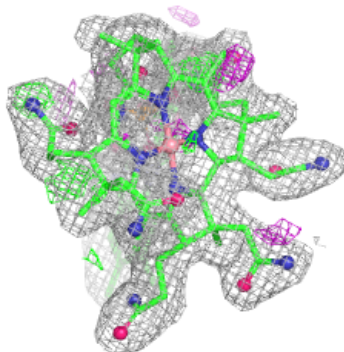
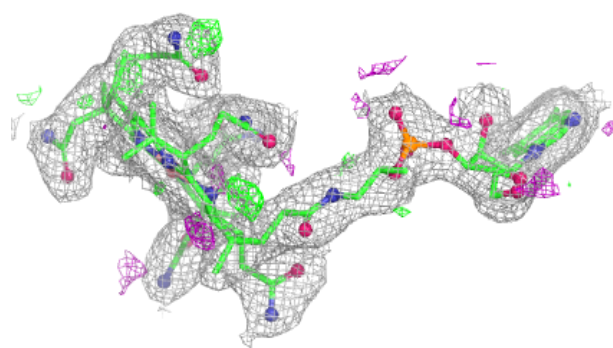
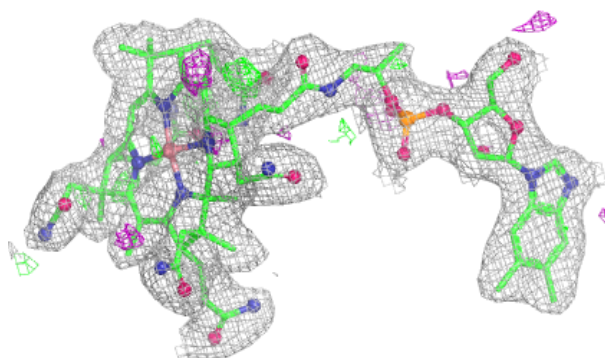


Electron density around B12 M 301:

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

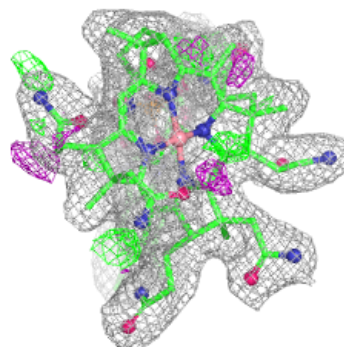
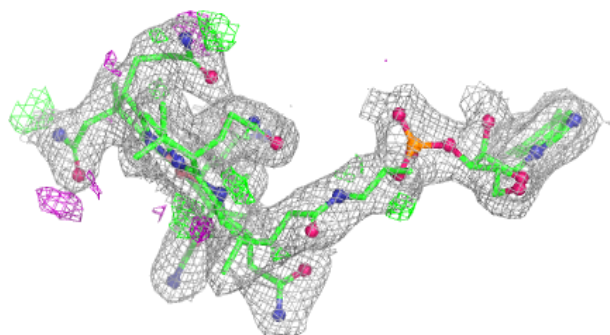
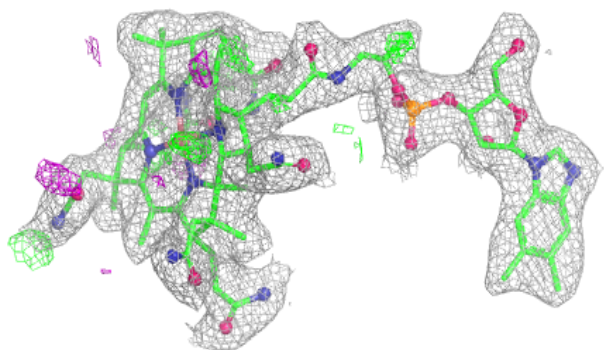
**Electron density around B12 N 301:**

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

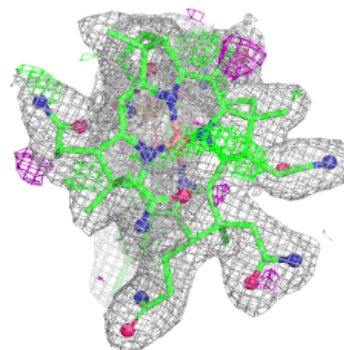
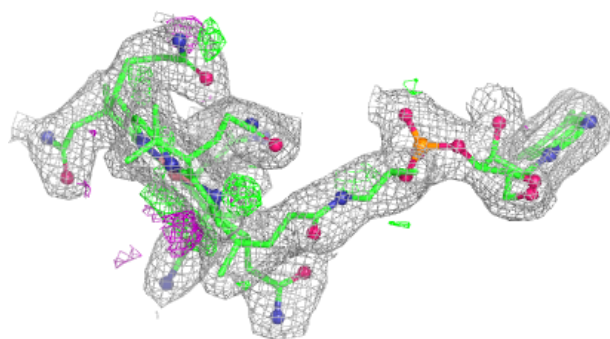
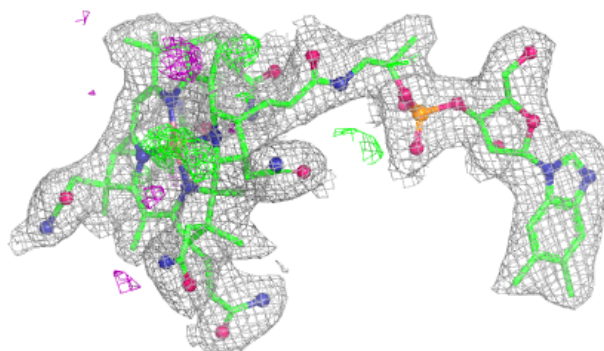


Electron density around B12 O 301:

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

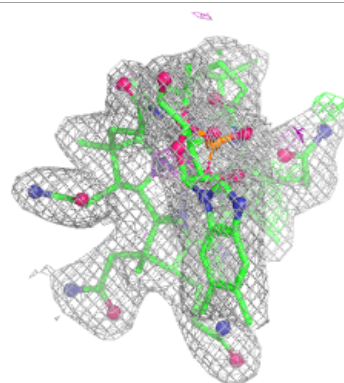
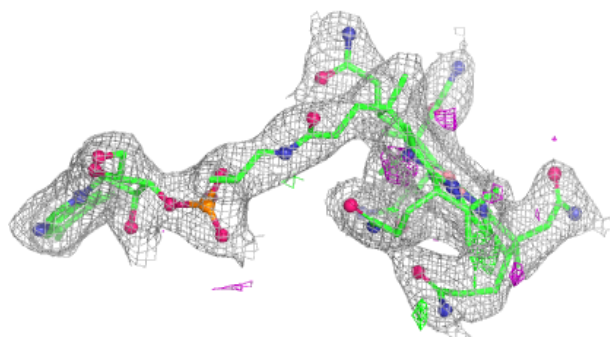
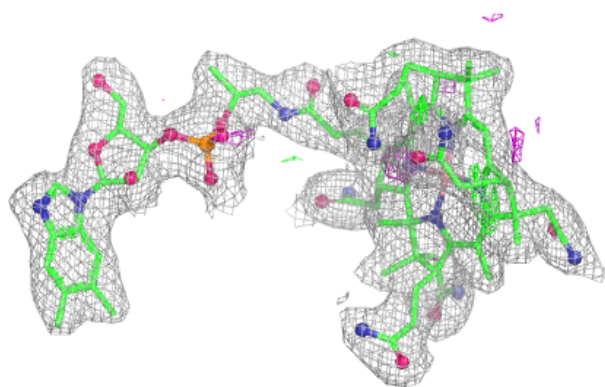
**Electron density around B12 P 301:**

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

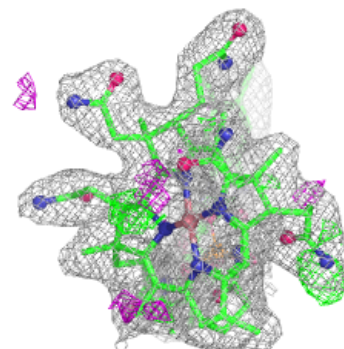
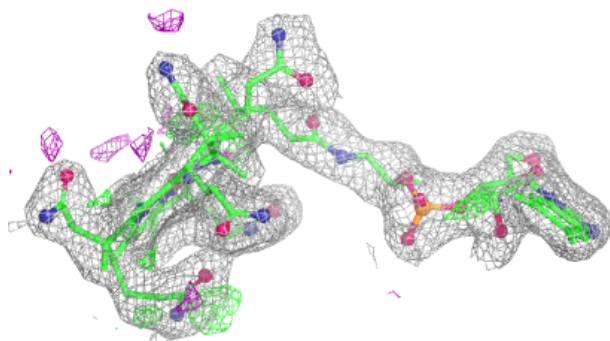
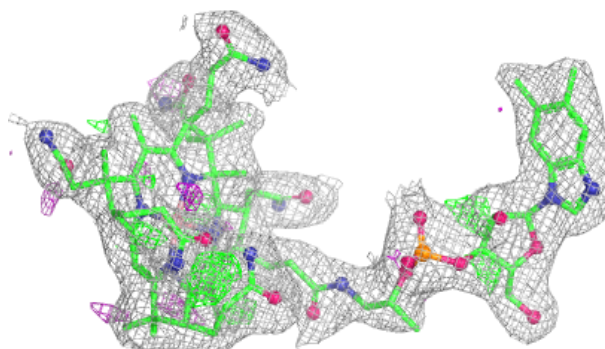


Electron density around B12 A 301:

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

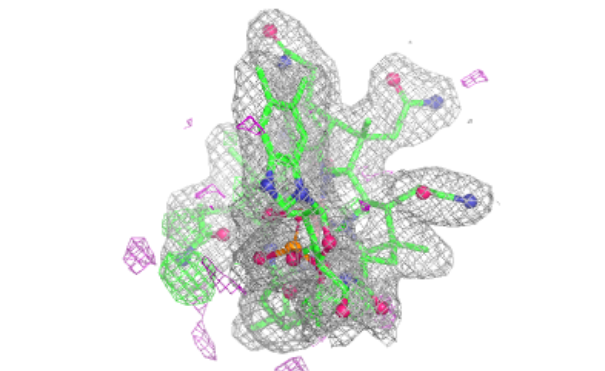
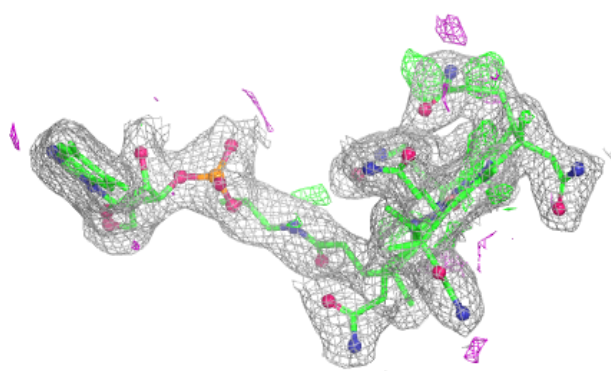
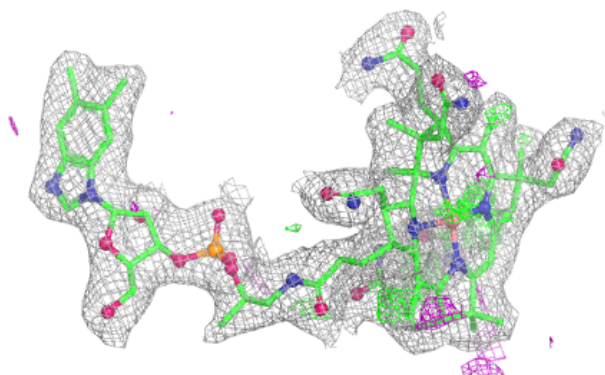
**Electron density around B12 D 301:**

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

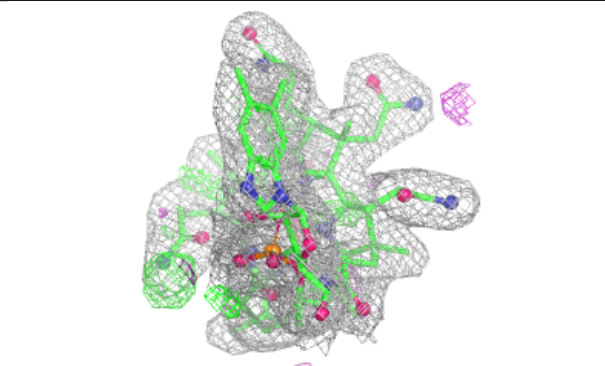
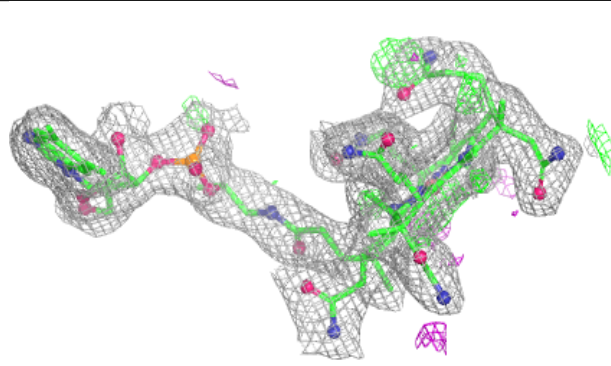
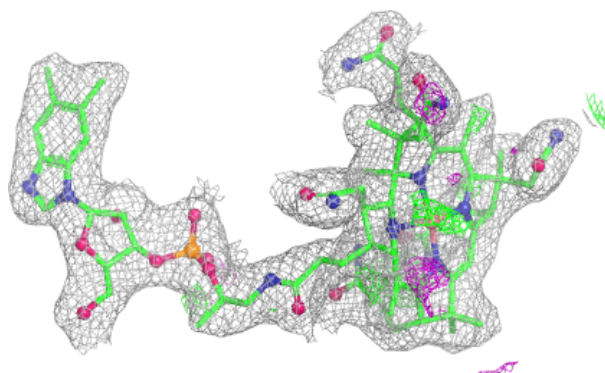


Electron density around B12 F 301:

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

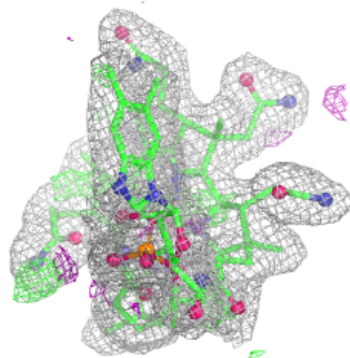
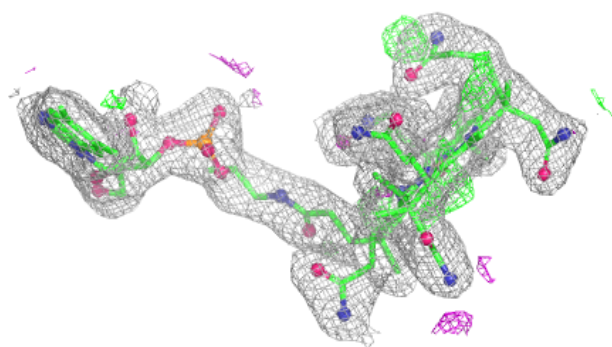
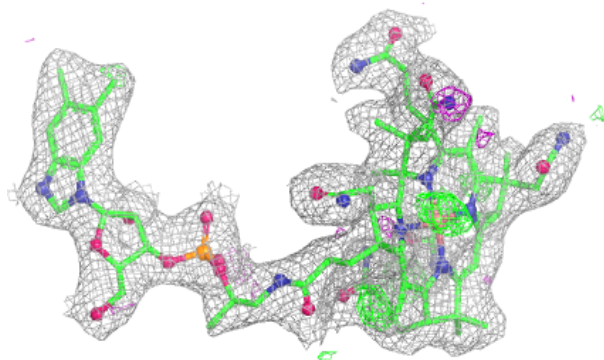
**Electron density around B12 L 301:**

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



Electron density around B12 E 301:

$2mF_o-DF_c$ (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.