



wwPDB X-ray Structure Validation Summary Report ⓘ

May 18, 2020 – 03:59 am BST

PDB ID : 2I2X
Title : Crystal structure of methanol:cobalamin methyltransferase complex MtaBC from *Methanosarcina barkeri*
Authors : Hagemeyer, C.H.; Kruer, M.; Thauer, R.K.; Warkentin, E.; Ermler, U.
Deposited on : 2006-08-17
Resolution : 2.50 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

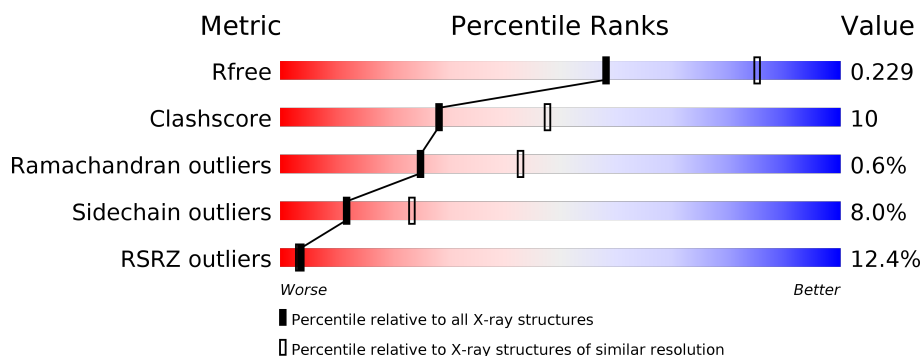
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on 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	461	<div> <div>82%</div> <div>14%</div> <div>.</div> </div>
1	C	461	<div> <div>82%</div> <div>15%</div> <div>.</div> </div>
1	E	461	<div> <div>6%</div> <div>80%</div> <div>18%</div> <div>.</div> </div>
1	G	461	<div> <div>2%</div> <div>79%</div> <div>18%</div> <div>.</div> </div>
1	I	461	<div> <div>%</div> <div>84%</div> <div>13%</div> <div>.</div> </div>
1	K	461	<div> <div>%</div> <div>82%</div> <div>15%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	M	461	<div><div></div><div>83%</div><div>13%</div><div></div></div>
1	O	461	<div><div></div><div>81%</div><div>16%</div><div></div></div>
2	B	258	<div><div>22%</div><div></div><div>66%</div><div>29%</div><div></div></div>
2	D	258	<div><div>28%</div><div></div><div>69%</div><div>29%</div><div></div></div>
2	F	258	<div><div>34%</div><div></div><div>72%</div><div>25%</div><div></div></div>
2	H	258	<div><div>45%</div><div></div><div>71%</div><div>26%</div><div></div></div>
2	J	258	<div><div>22%</div><div></div><div>70%</div><div>27%</div><div></div></div>
2	L	258	<div><div>38%</div><div></div><div>73%</div><div>23%</div><div></div></div>
2	N	258	<div><div>48%</div><div></div><div>71%</div><div>27%</div><div></div></div>
2	P	258	<div><div>20%</div><div></div><div>72%</div><div>23%</div><div></div></div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 45566 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 Methyltransferase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	459	Total	C	N	O	S	0	0	0
			3534	2216	589	695	34			
1	C	459	Total	C	N	O	S	0	0	0
			3534	2216	589	695	34			
1	E	459	Total	C	N	O	S	0	0	0
			3534	2216	589	695	34			
1	G	459	Total	C	N	O	S	0	0	0
			3534	2216	589	695	34			
1	I	459	Total	C	N	O	S	0	0	0
			3534	2216	589	695	34			
1	K	459	Total	C	N	O	S	0	0	0
			3534	2216	589	695	34			
1	M	459	Total	C	N	O	S	0	0	0
			3534	2216	589	695	34			
1	O	459	Total	C	N	O	S	0	0	0
			3534	2216	589	695	34			

- Molecule 2 is a protein called Methyltransferase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	258	Total	C	N	O	S	0	0	0
			1951	1238	311	389	13			
2	D	258	Total	C	N	O	S	0	0	0
			1951	1238	311	389	13			
2	F	258	Total	C	N	O	S	0	0	0
			1951	1238	311	389	13			
2	H	258	Total	C	N	O	S	0	0	0
			1951	1238	311	389	13			
2	J	258	Total	C	N	O	S	0	0	0
			1951	1238	311	389	13			
2	L	258	Total	C	N	O	S	0	0	0
			1951	1238	311	389	13			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	N	258	Total 1951	C 1238	N 311	O 389	S 13	0	0	0
2	P	258	Total 1951	C 1238	N 311	O 389	S 13	0	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	1	Total 1	Zn 1	0	0
3	K	1	Total 1	Zn 1	0	0
3	E	2	Total 2	Zn 2	0	0
3	I	2	Total 2	Zn 2	0	0
3	C	1	Total 1	Zn 1	0	0
3	A	2	Total 2	Zn 2	0	0
3	O	1	Total 1	Zn 1	0	0
3	M	2	Total 2	Zn 2	0	0

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

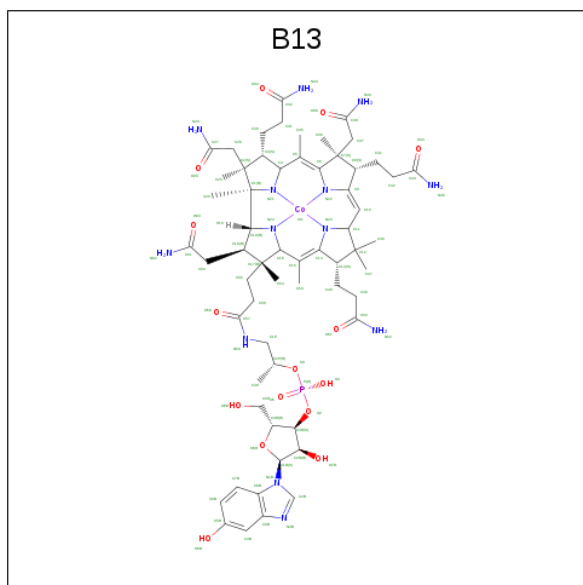
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	1	Total 1	K 1	0	0
4	K	1	Total 1	K 1	0	0
4	E	1	Total 1	K 1	0	0
4	I	1	Total 1	K 1	0	0
4	C	1	Total 1	K 1	0	0
4	A	1	Total 1	K 1	0	0
4	O	1	Total 1	K 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	M	1	Total K 1 1	0	0

- Molecule 5 is 5-HYDROXYBENZIMIDAZOLYLCOB(III)AMIDE (three-letter code: B13) (formula: $C_{60}H_{88}CoN_{13}O_{15}P$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	B	1	Total 90	C 60	Co 1	N 13	O 15	P 1	0	0
5	D	1	Total 90	C 60	Co 1	N 13	O 15	P 1	0	0
5	F	1	Total 90	C 60	Co 1	N 13	O 15	P 1	0	0
5	H	1	Total 90	C 60	Co 1	N 13	O 15	P 1	0	0
5	J	1	Total 90	C 60	Co 1	N 13	O 15	P 1	0	0
5	L	1	Total 90	C 60	Co 1	N 13	O 15	P 1	0	0
5	N	1	Total 90	C 60	Co 1	N 13	O 15	P 1	0	0
5	P	1	Total 90	C 60	Co 1	N 13	O 15	P 1	0	0

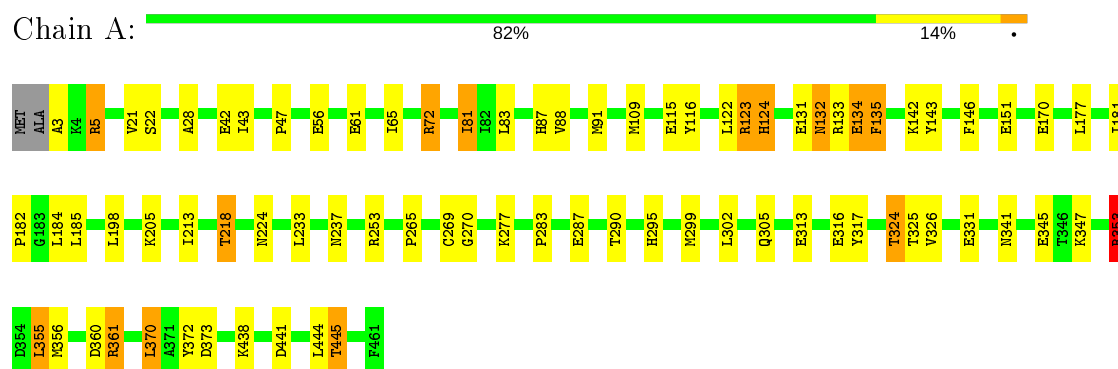
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	162	Total 162	O 162	0	0
6	B	36	Total 36	O 36	0	0
6	C	183	Total 183	O 183	0	0
6	D	27	Total 27	O 27	0	0
6	E	20	Total 20	O 20	0	0
6	F	6	Total 6	O 6	0	0
6	G	47	Total 47	O 47	0	0
6	H	1	Total 1	O 1	0	0
6	I	93	Total 93	O 93	0	0
6	J	15	Total 15	O 15	0	0
6	K	99	Total 99	O 99	0	0
6	L	18	Total 18	O 18	0	0
6	M	95	Total 95	O 95	0	0
6	N	18	Total 18	O 18	0	0
6	O	111	Total 111	O 111	0	0
6	P	15	Total 15	O 15	0	0

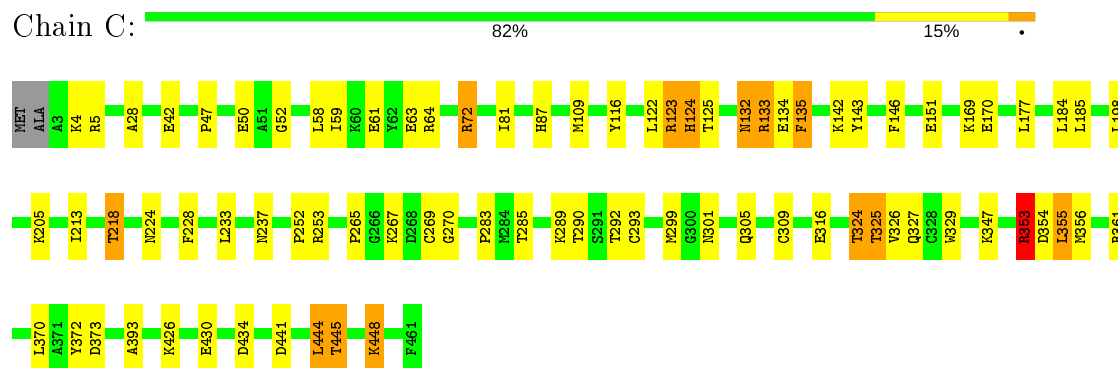
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

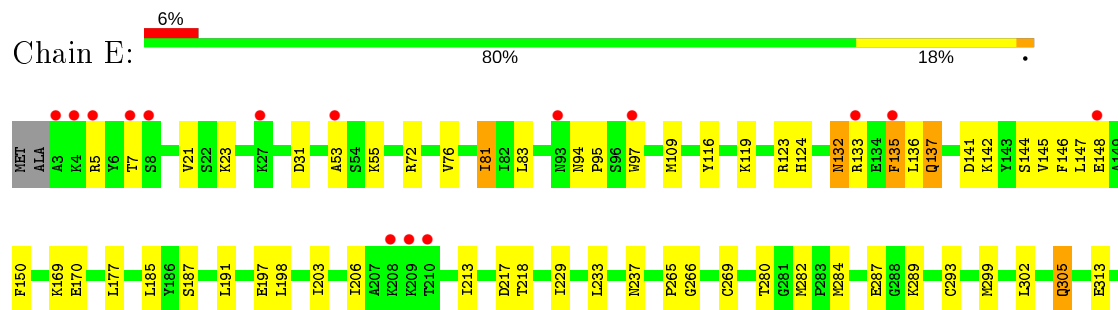
• Molecule 1: Methyltransferase 1

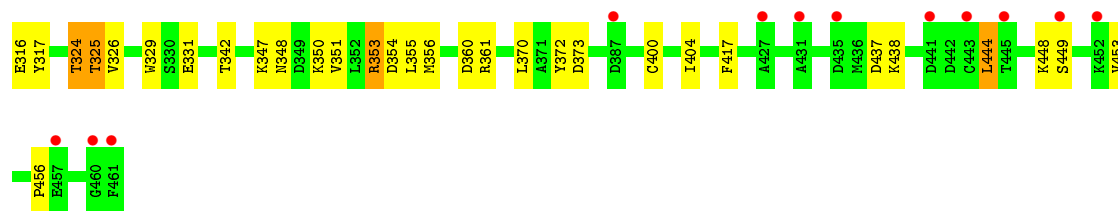


• Molecule 1: Methyltransferase 1

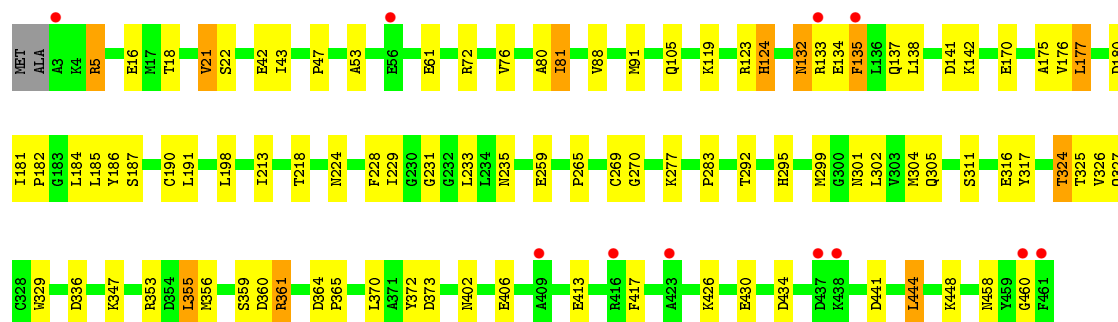
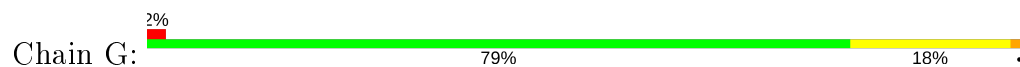


• Molecule 1: Methyltransferase 1

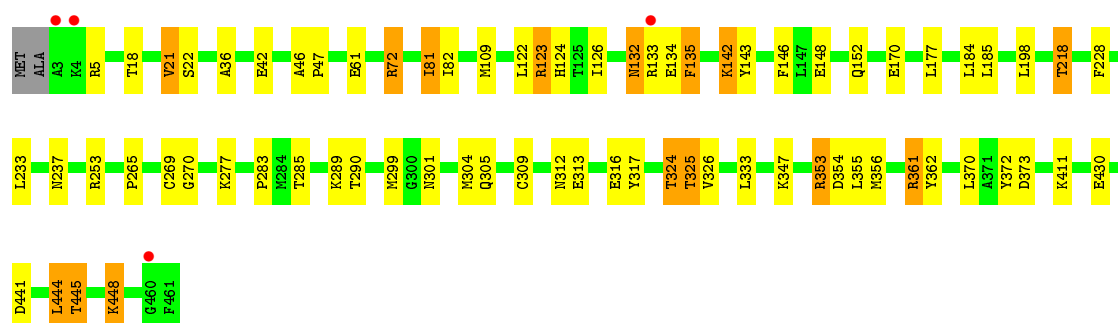
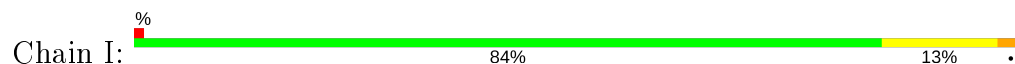




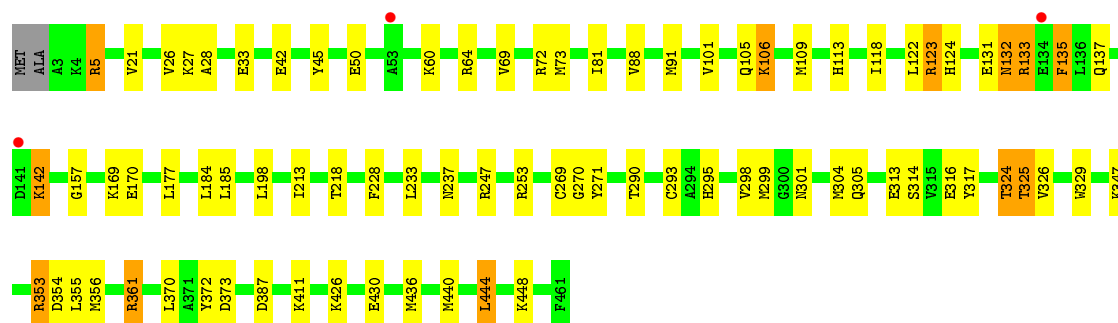
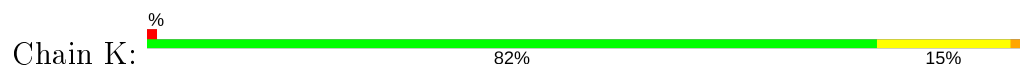
• Molecule 1: Methyltransferase 1




• Molecule 1: Methyltransferase 1

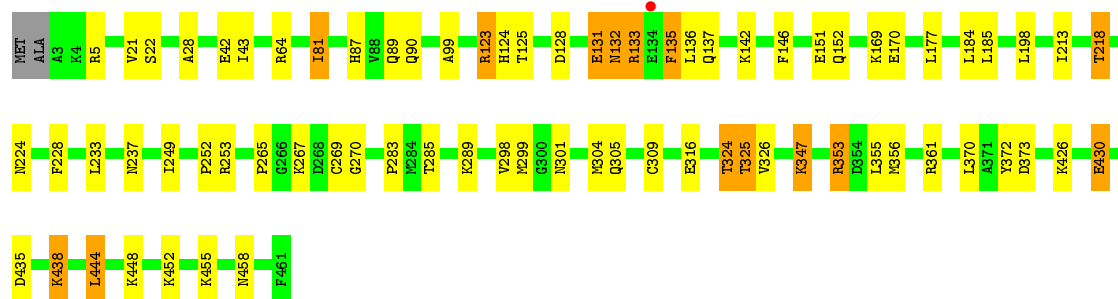


• Molecule 1: Methyltransferase 1




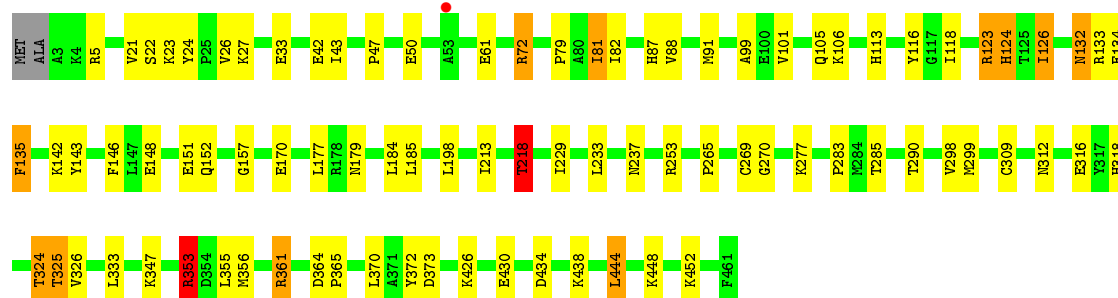
• Molecule 1: Methyltransferase 1

Chain M:  83% 13%



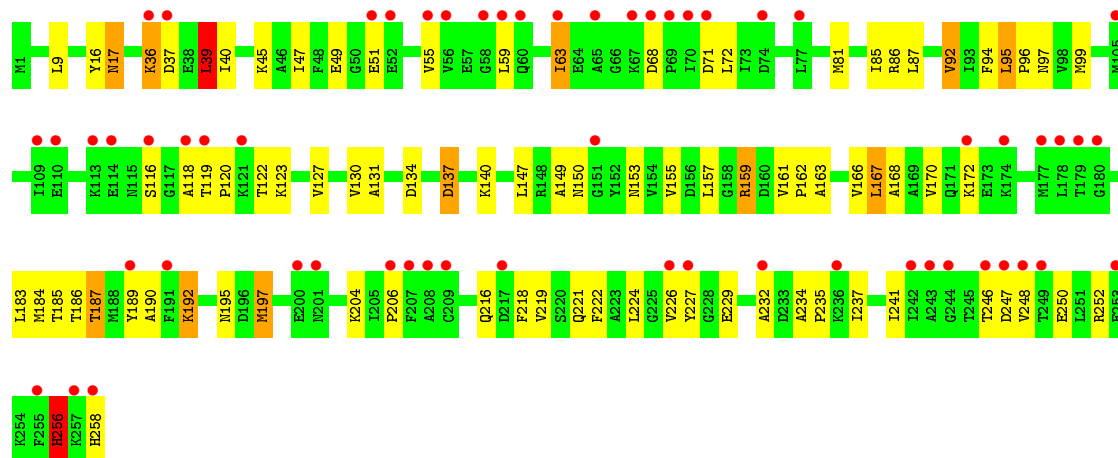
• Molecule 1: Methyltransferase 1

Chain O:  81% 16%



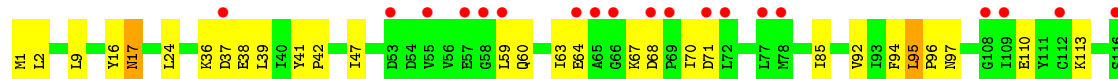
• Molecule 2: Methyltransferase 1

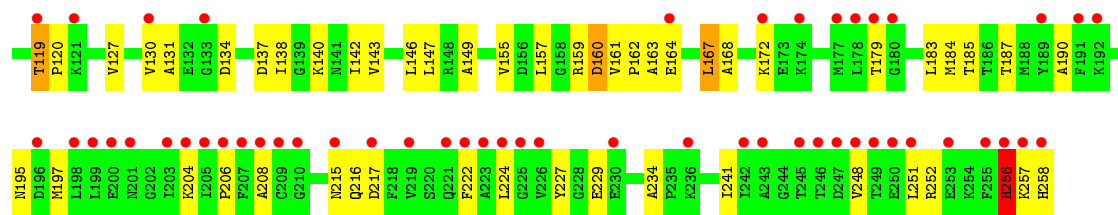
Chain B:  22% 66% 29%



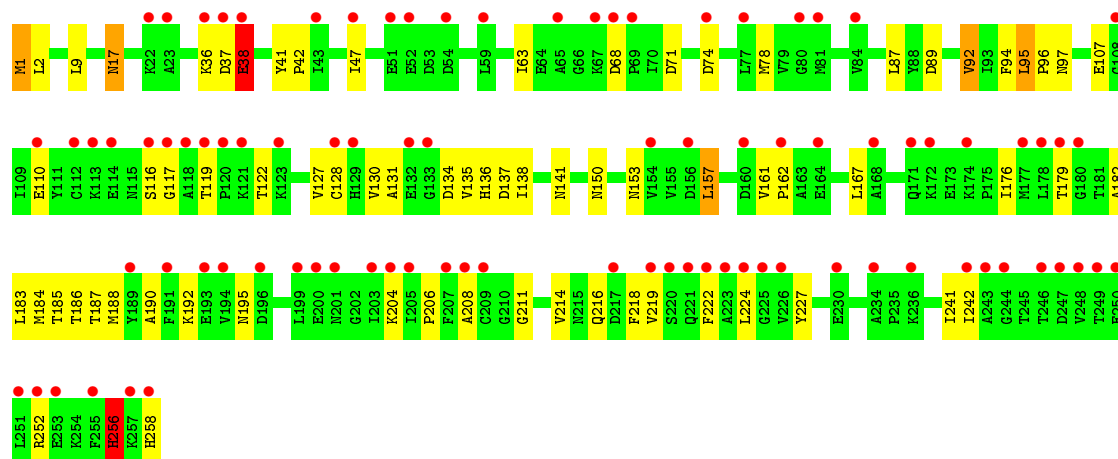
• Molecule 2: Methyltransferase 1

Chain D:  28% 69% 29%

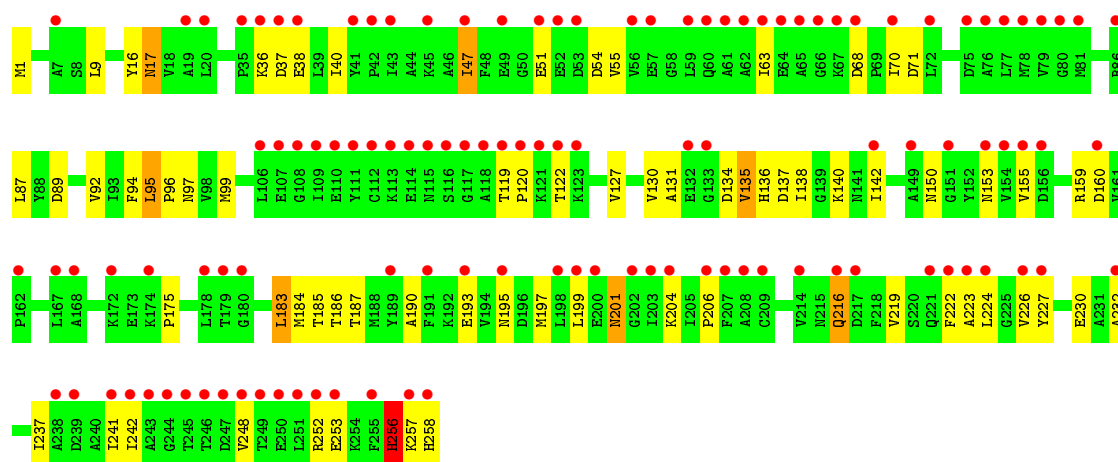




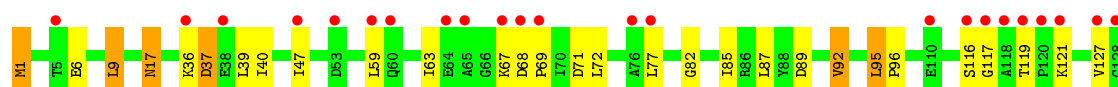
• Molecule 2: Methyltransferase 1

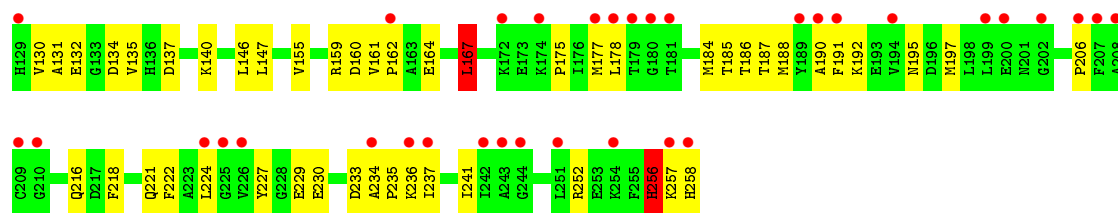


• Molecule 2: Methyltransferase 1

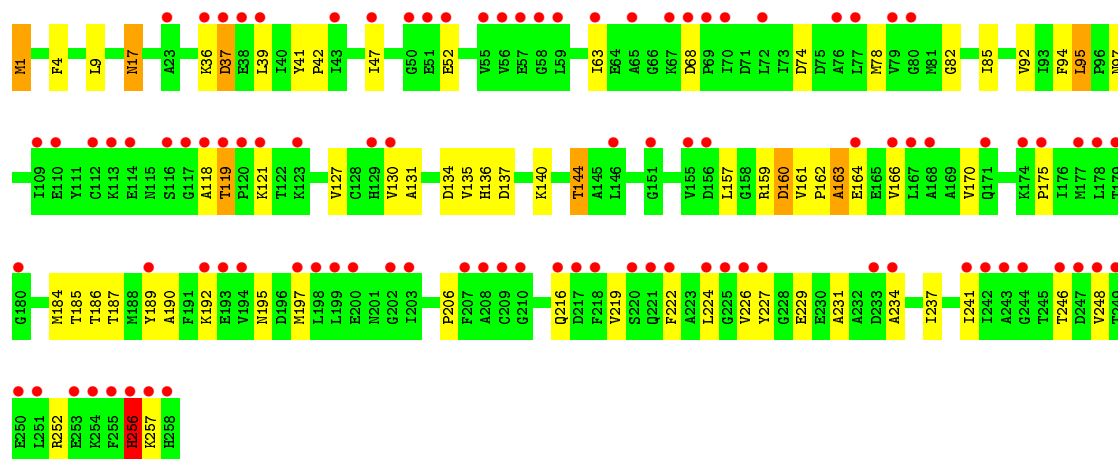
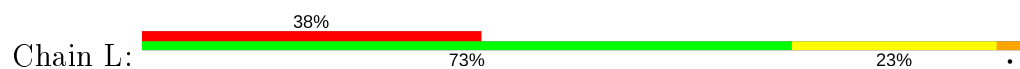


• Molecule 2: Methyltransferase 1

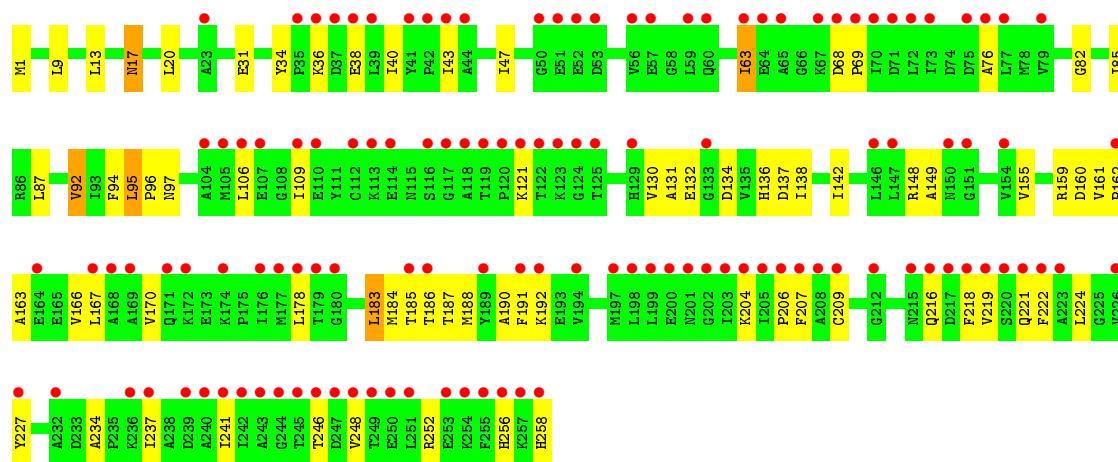




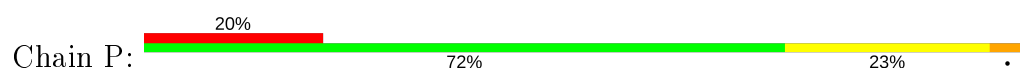
• Molecule 2: Methyltransferase 1

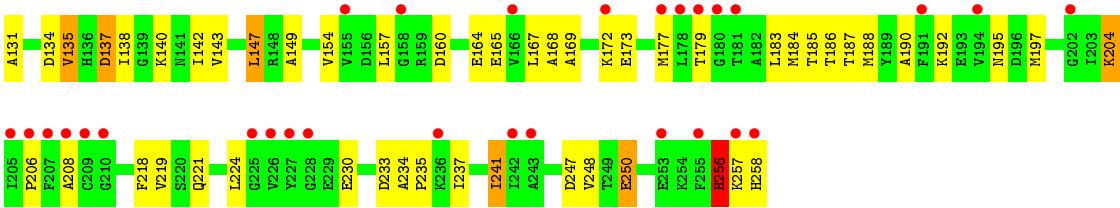


• Molecule 2: Methyltransferase 1



• Molecule 2: Methyltransferase 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	101.75Å 172.85Å 190.54Å 90.00° 98.86° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 20.02 – 2.51	Depositor EDS
% Data completeness (in resolution range)	98.5 (20.00-2.50) 98.5 (20.02-2.51)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.182 , 0.231 0.182 , 0.229	Depositor DCC
R_{free} test set	10921 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	36.3	Xtriage
Anisotropy	0.103	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 52.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	45566	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.35% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, K, B13

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	0.72	1/3595 (0.0%)	0.78	5/4852 (0.1%)
1	C	0.70	0/3595	0.78	5/4852 (0.1%)
1	E	0.51	0/3595	0.62	0/4852
1	G	0.54	0/3595	0.64	1/4852 (0.0%)
1	I	0.60	0/3595	0.70	3/4852 (0.1%)
1	K	0.60	0/3595	0.68	2/4852 (0.0%)
1	M	0.60	0/3595	0.69	2/4852 (0.0%)
1	O	0.62	0/3595	0.72	6/4852 (0.1%)
2	B	0.48	0/1980	0.66	1/2682 (0.0%)
2	D	0.47	0/1980	0.65	0/2682
2	F	0.46	0/1980	0.59	0/2682
2	H	0.45	0/1980	0.59	0/2682
2	J	0.47	0/1980	0.63	1/2682 (0.0%)
2	L	0.46	0/1980	0.60	0/2682
2	N	0.48	0/1980	0.61	0/2682
2	P	0.48	0/1980	0.65	0/2682
All	All	0.57	1/44600 (0.0%)	0.68	26/60272 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	56	GLU	CG-CD	5.18	1.59	1.51

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	O	361	ARG	NE-CZ-NH2	-7.96	116.32	120.30
1	A	361	ARG	NE-CZ-NH2	-7.96	116.32	120.30
1	C	353	ARG	NE-CZ-NH2	-7.86	116.37	120.30
1	M	123	ARG	NE-CZ-NH2	-7.65	116.48	120.30
1	I	361	ARG	NE-CZ-NH2	-6.96	116.82	120.30

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	3534	0	3462	49	0
1	C	3534	0	3462	56	0
1	E	3534	0	3462	54	0
1	G	3534	0	3462	63	0
1	I	3534	0	3462	51	0
1	K	3534	0	3462	61	0
1	M	3534	0	3462	54	0
1	O	3534	0	3462	57	0
2	B	1951	0	1952	64	0
2	D	1951	0	1952	55	0
2	F	1951	0	1952	54	0
2	H	1951	0	1952	52	0
2	J	1951	0	1952	53	0
2	L	1951	0	1952	49	0
2	N	1951	0	1952	50	0
2	P	1951	0	1952	47	0
3	A	2	0	0	0	0
3	C	1	0	0	0	0
3	E	2	0	0	0	0
3	G	1	0	0	0	0
3	I	2	0	0	0	0
3	K	1	0	0	0	0
3	M	2	0	0	0	0
3	O	1	0	0	0	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
4	I	1	0	0	0	0
4	K	1	0	0	0	0
4	M	1	0	0	0	0
4	O	1	0	0	0	0
5	B	90	0	81	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	90	0	81	13	0
5	F	90	0	81	7	0
5	H	90	0	81	10	0
5	J	90	0	81	13	0
5	L	90	0	81	10	0
5	N	90	0	81	11	0
5	P	90	0	81	9	0
6	A	162	0	0	4	0
6	B	36	0	0	1	0
6	C	183	0	0	3	0
6	D	27	0	0	0	0
6	E	20	0	0	0	0
6	F	6	0	0	0	0
6	G	47	0	0	3	0
6	H	1	0	0	0	0
6	I	93	0	0	3	0
6	J	15	0	0	0	0
6	K	99	0	0	4	0
6	L	18	0	0	1	0
6	M	95	0	0	4	0
6	N	18	0	0	0	0
6	O	111	0	0	4	0
6	P	15	0	0	0	0
All	All	45566	0	43960	865	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 10.

The worst 5 of 865 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:233:ASP:O	2:P:237:ILE:HG22	1.56	1.05
1:M:353:ARG:HA	1:M:356:MET:CE	1.92	0.99
1:K:353:ARG:HA	1:K:356:MET:CE	1.95	0.97
2:L:134:ASP:HB2	2:L:187:THR:HG21	1.46	0.94
2:B:17:ASN:HD22	2:B:17:ASN:H	1.14	0.91

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	457/461 (99%)	442 (97%)	15 (3%)	0	100	100
1	C	457/461 (99%)	440 (96%)	17 (4%)	0	100	100
1	E	457/461 (99%)	433 (95%)	21 (5%)	3 (1%)	22	39
1	G	457/461 (99%)	434 (95%)	22 (5%)	1 (0%)	47	68
1	I	457/461 (99%)	439 (96%)	17 (4%)	1 (0%)	47	68
1	K	457/461 (99%)	439 (96%)	18 (4%)	0	100	100
1	M	457/461 (99%)	439 (96%)	18 (4%)	0	100	100
1	O	457/461 (99%)	439 (96%)	18 (4%)	0	100	100
2	B	256/258 (99%)	239 (93%)	13 (5%)	4 (2%)	9	17
2	D	256/258 (99%)	224 (88%)	28 (11%)	4 (2%)	9	17
2	F	256/258 (99%)	227 (89%)	26 (10%)	3 (1%)	13	24
2	H	256/258 (99%)	235 (92%)	18 (7%)	3 (1%)	13	24
2	J	256/258 (99%)	237 (93%)	14 (6%)	5 (2%)	7	12
2	L	256/258 (99%)	235 (92%)	15 (6%)	6 (2%)	6	10
2	N	256/258 (99%)	229 (90%)	23 (9%)	4 (2%)	9	17
2	P	256/258 (99%)	240 (94%)	13 (5%)	3 (1%)	13	24
All	All	5704/5752 (99%)	5371 (94%)	296 (5%)	37 (1%)	25	43

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	256	HIS
2	F	256	HIS
2	H	256	HIS
2	L	37	ASP
2	L	256	HIS

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	373/374 (100%)	344 (92%)	29 (8%)	12	24
1	C	373/374 (100%)	344 (92%)	29 (8%)	12	24
1	E	373/374 (100%)	339 (91%)	34 (9%)	9	18
1	G	373/374 (100%)	346 (93%)	27 (7%)	14	28
1	I	373/374 (100%)	345 (92%)	28 (8%)	13	26
1	K	373/374 (100%)	348 (93%)	25 (7%)	16	31
1	M	373/374 (100%)	344 (92%)	29 (8%)	12	24
1	O	373/374 (100%)	343 (92%)	30 (8%)	12	23
2	B	206/206 (100%)	183 (89%)	23 (11%)	6	11
2	D	206/206 (100%)	192 (93%)	14 (7%)	16	30
2	F	206/206 (100%)	189 (92%)	17 (8%)	11	22
2	H	206/206 (100%)	190 (92%)	16 (8%)	12	24
2	J	206/206 (100%)	190 (92%)	16 (8%)	12	24
2	L	206/206 (100%)	190 (92%)	16 (8%)	12	24
2	N	206/206 (100%)	189 (92%)	17 (8%)	11	22
2	P	206/206 (100%)	184 (89%)	22 (11%)	6	13
All	All	4632/4640 (100%)	4260 (92%)	372 (8%)	12	23

5 of 372 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	370	LEU
1	I	325	THR
1	O	347	LYS
2	H	9	LEU
2	H	256	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 112 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	195	ASN
2	J	17	ASN
1	O	156	ASN
2	H	216	GLN
1	I	124	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 28 ligands modelled in this entry, 20 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	B13	F	500	2	78,100,100	2.10	17 (21%)	100,164,164	1.87	24 (24%)
5	B13	B	500	2	78,100,100	2.08	17 (21%)	100,164,164	1.78	18 (18%)
5	B13	H	500	2	78,100,100	2.13	17 (21%)	100,164,164	1.86	19 (19%)
5	B13	N	500	2	78,100,100	2.11	17 (21%)	100,164,164	1.84	22 (22%)
5	B13	D	500	2	78,100,100	2.14	20 (25%)	100,164,164	1.86	24 (24%)
5	B13	J	500	2,6	78,100,100	2.08	16 (20%)	100,164,164	1.78	18 (18%)
5	B13	P	500	2	78,100,100	2.04	16 (20%)	100,164,164	1.96	24 (24%)
5	B13	L	500	2,6	78,100,100	2.11	18 (23%)	100,164,164	1.78	22 (22%)

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	B13	F	500	2	-	17/52/223/223	0/3/11/11
5	B13	B	500	2	-	16/52/223/223	0/3/11/11
5	B13	H	500	2	-	19/52/223/223	0/3/11/11
5	B13	N	500	2	-	22/52/223/223	0/3/11/11
5	B13	D	500	2	-	18/52/223/223	0/3/11/11
5	B13	J	500	2,6	-	20/52/223/223	0/3/11/11
5	B13	P	500	2	-	18/52/223/223	0/3/11/11
5	B13	L	500	2,6	-	19/52/223/223	0/3/11/11

The worst 5 of 138 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	500	B13	C5R-C4R	-8.92	1.21	1.51
5	D	500	B13	C5R-C4R	-8.89	1.22	1.51
5	P	500	B13	C5R-C4R	-8.78	1.22	1.51
5	J	500	B13	C5R-C4R	-8.78	1.22	1.51
5	L	500	B13	C5R-C4R	-8.77	1.22	1.51

The worst 5 of 171 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	500	B13	O6R-C4R-C5R	7.95	126.41	109.21
5	N	500	B13	O6R-C4R-C5R	7.94	126.38	109.21
5	B	500	B13	O6R-C4R-C5R	7.90	126.29	109.21
5	J	500	B13	O6R-C4R-C5R	7.57	125.58	109.21
5	P	500	B13	O6R-C4R-C5R	7.52	125.48	109.21

There are no chirality outliers.

5 of 149 torsion outliers are listed below:

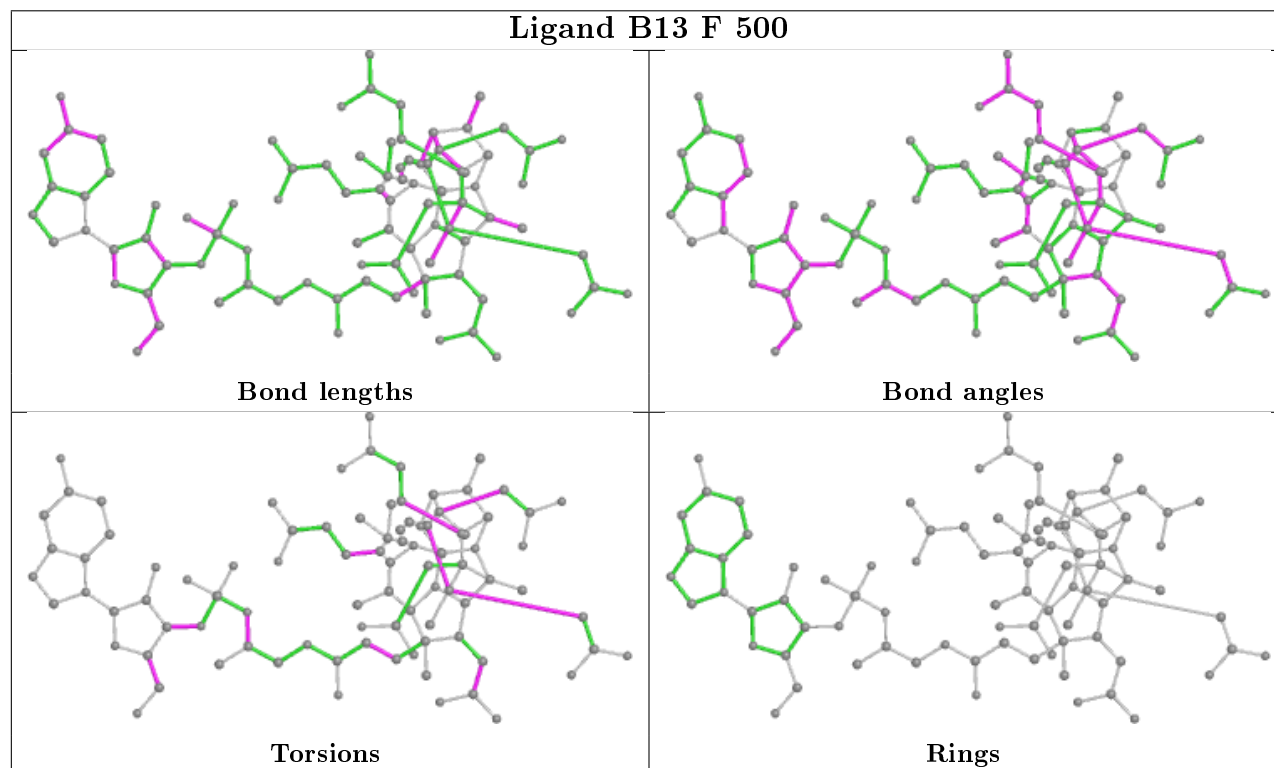
Mol	Chain	Res	Type	Atoms
5	P	500	B13	C3P-C2P-O3-P
5	P	500	B13	C1P-C2P-O3-P
5	P	500	B13	N59-C1P-C2P-O3
5	P	500	B13	N59-C1P-C2P-C3P
5	P	500	B13	C18-C60-C61-N62

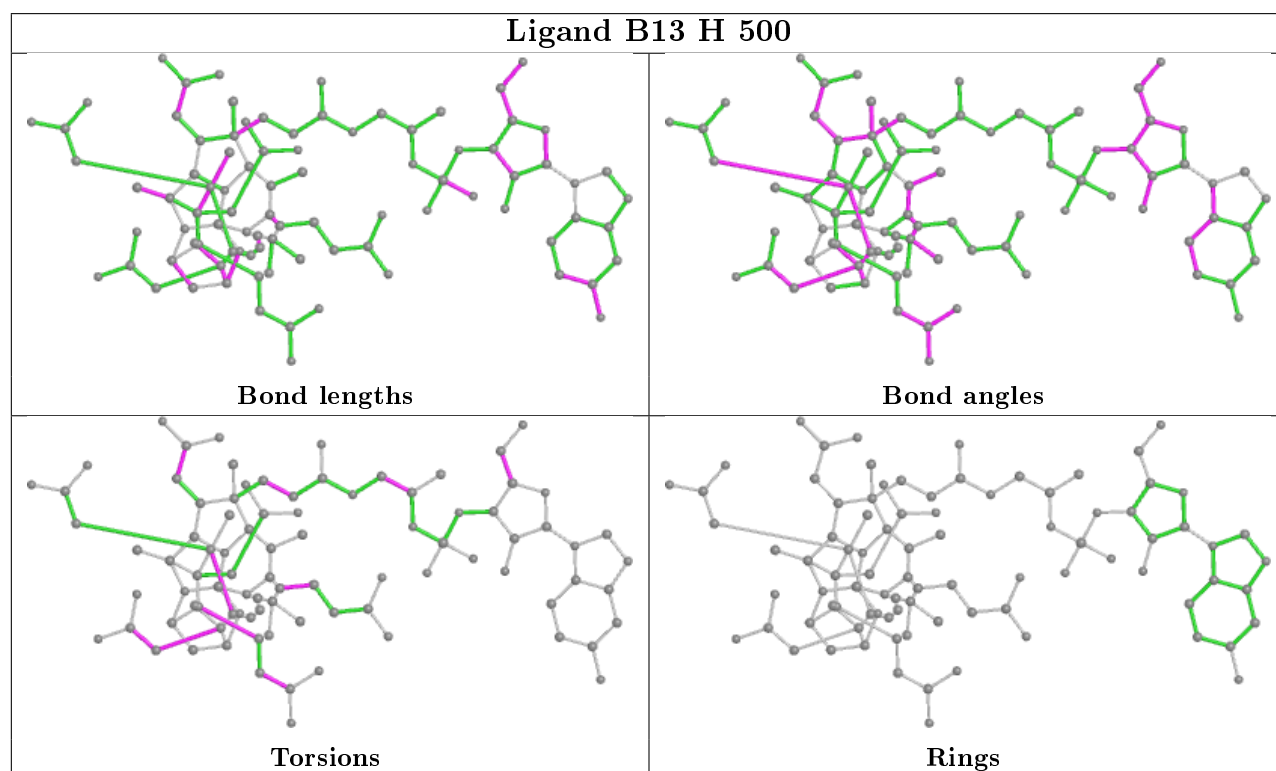
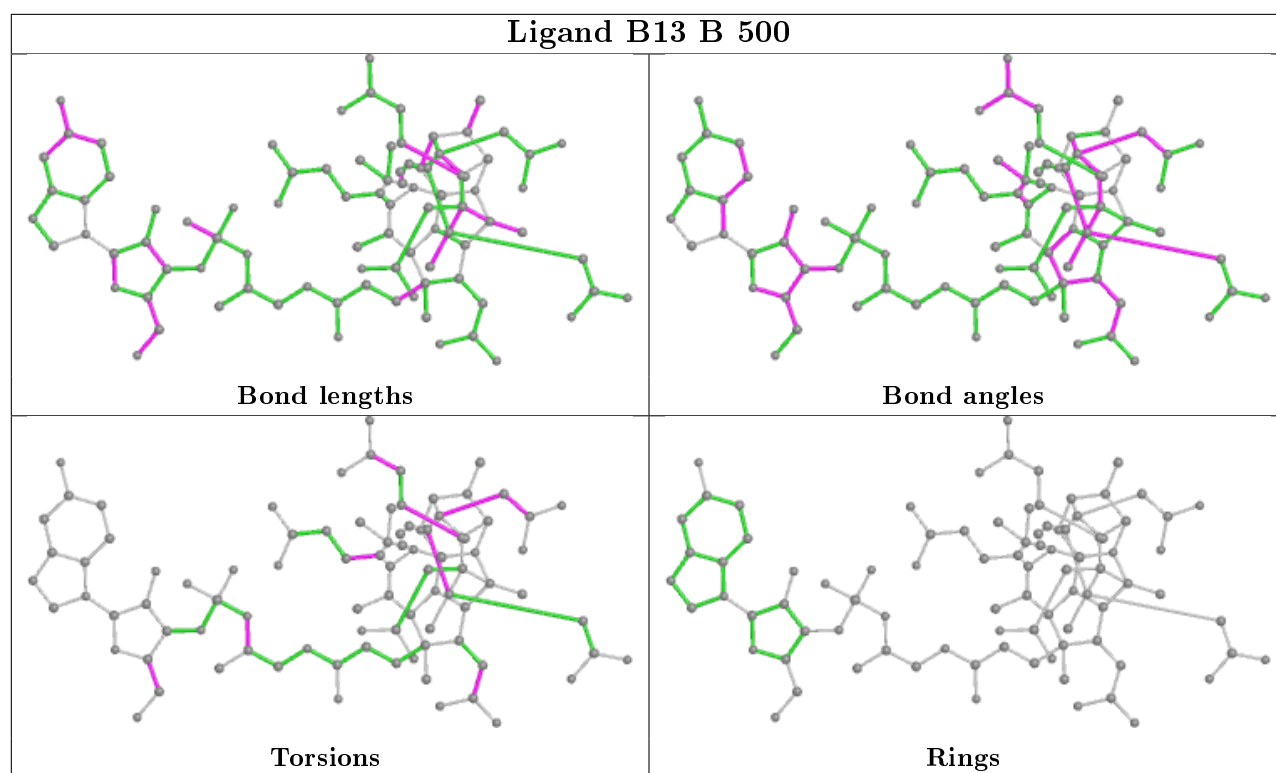
There are no ring outliers.

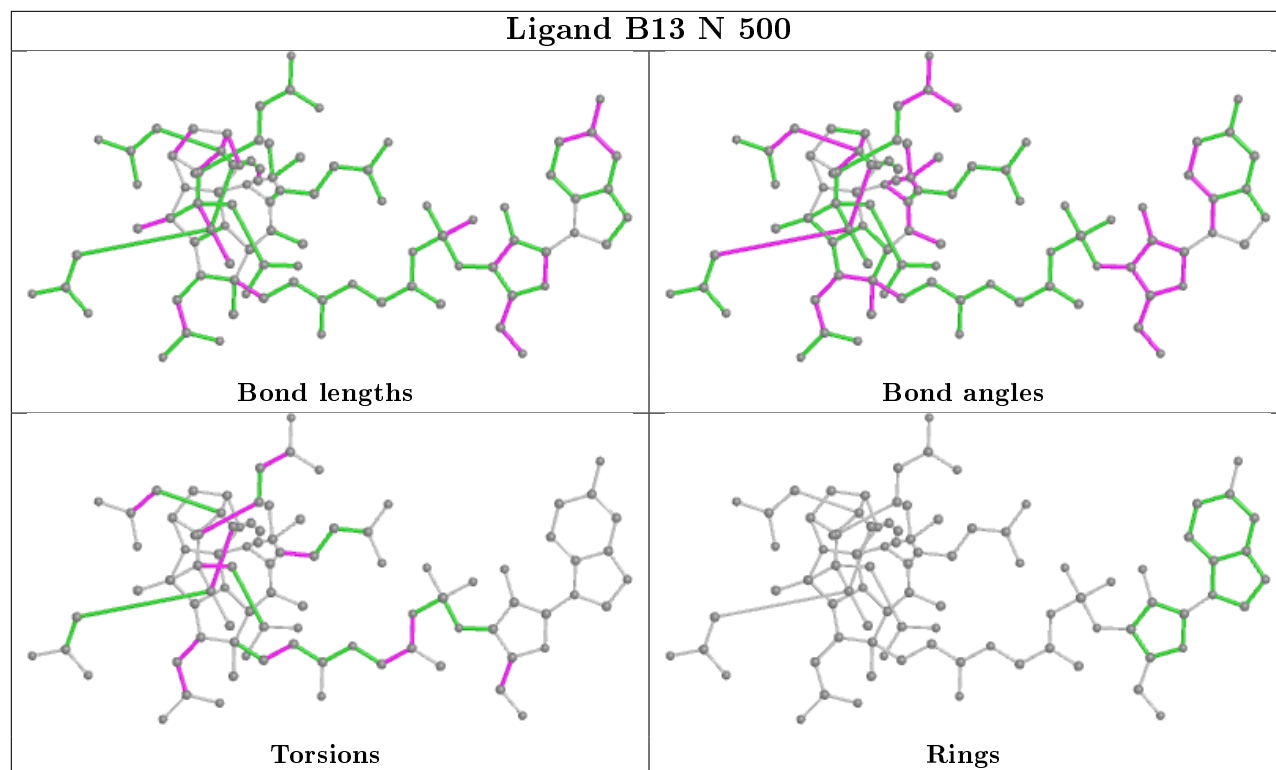
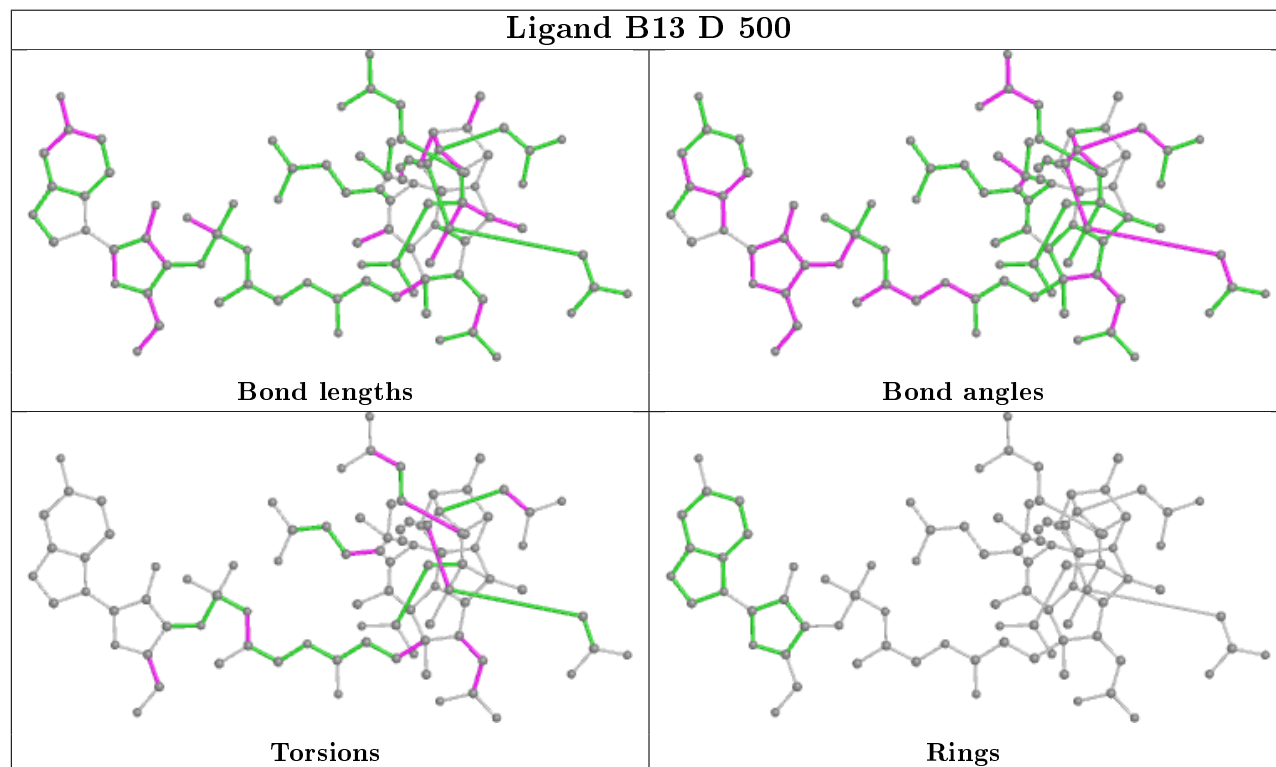
8 monomers are involved in 82 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	F	500	B13	7	0
5	B	500	B13	9	0
5	H	500	B13	10	0
5	N	500	B13	11	0
5	D	500	B13	13	0
5	J	500	B13	13	0
5	P	500	B13	9	0
5	L	500	B13	10	0

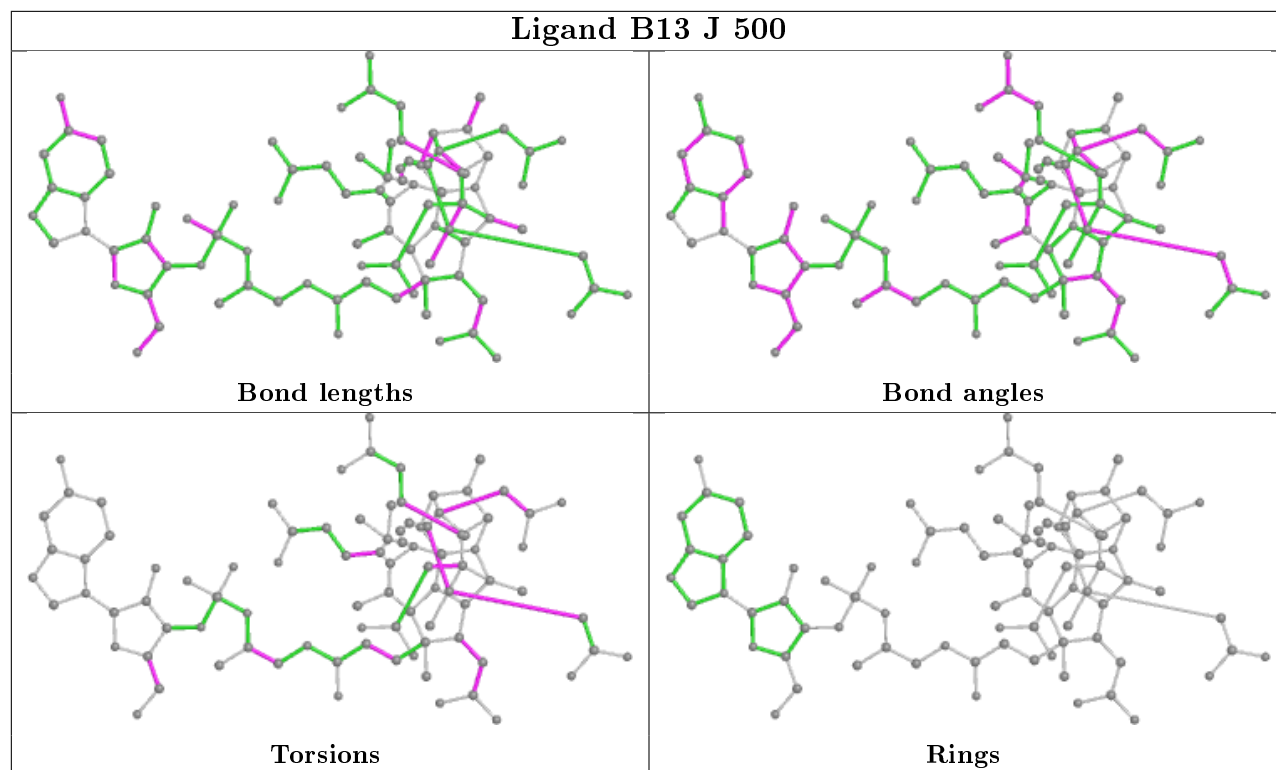
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



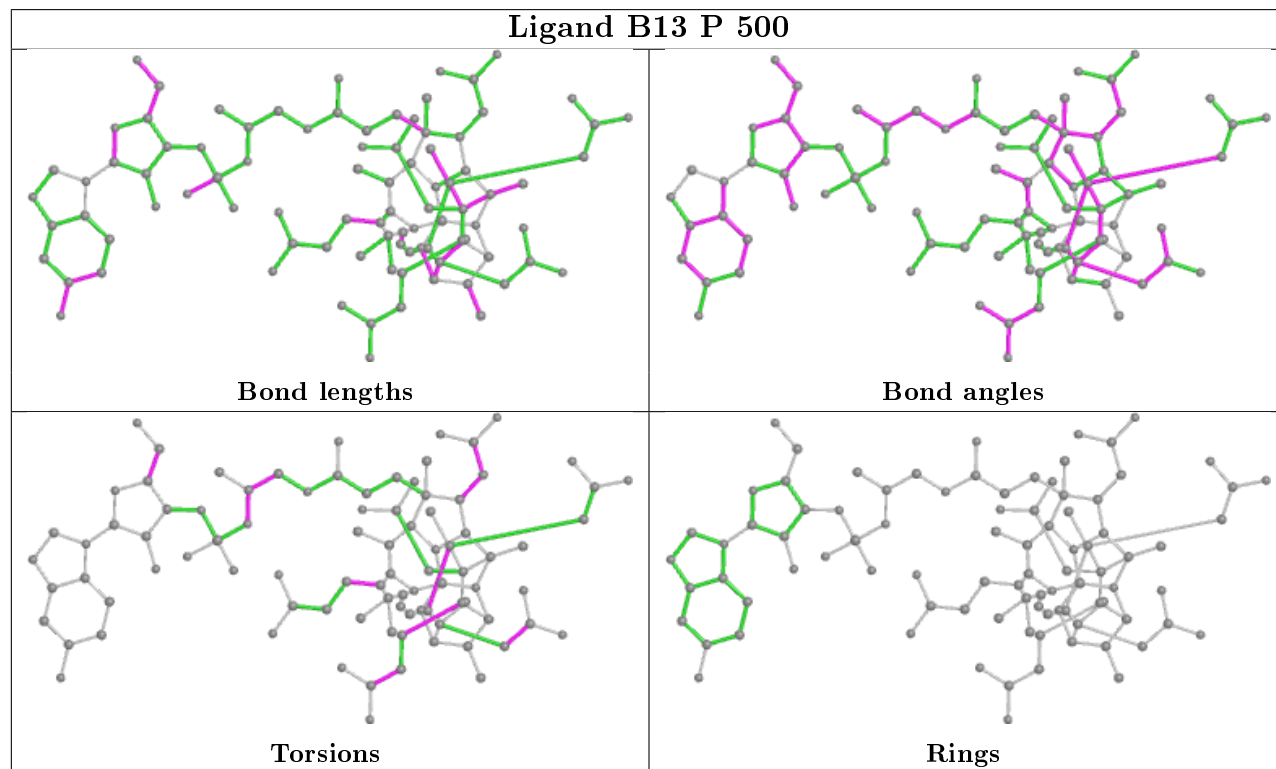


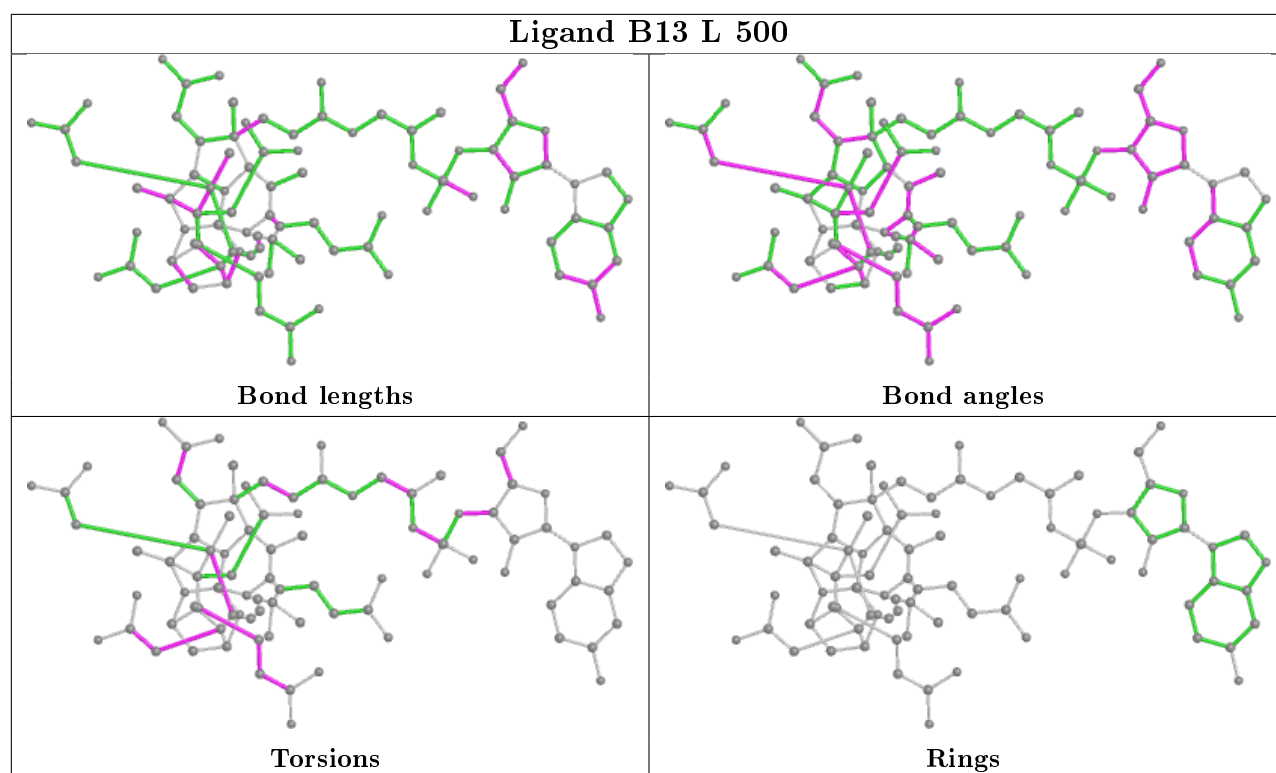
Ligand B13 N 500**Ligand B13 D 500**

Ligand B13 J 500



Ligand B13 P 500





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	459/461 (99%)	-0.25	0 100 100	3, 11, 26, 38	0
1	C	459/461 (99%)	-0.25	0 100 100	3, 10, 23, 39	0
1	E	459/461 (99%)	0.33	27 (5%) 22 23	25, 33, 42, 49	0
1	G	459/461 (99%)	0.02	11 (2%) 59 62	18, 29, 40, 49	0
1	I	459/461 (99%)	-0.17	4 (0%) 84 86	9, 20, 34, 50	0
1	K	459/461 (99%)	-0.16	3 (0%) 87 89	12, 20, 33, 46	0
1	M	459/461 (99%)	-0.20	1 (0%) 95 95	10, 20, 34, 48	0
1	O	459/461 (99%)	-0.20	1 (0%) 95 95	7, 18, 32, 45	0
2	B	258/258 (100%)	1.22	58 (22%) 0 0	4, 67, 100, 107	0
2	D	258/258 (100%)	1.31	71 (27%) 0 0	5, 66, 100, 110	0
2	F	258/258 (100%)	1.67	89 (34%) 0 0	18, 72, 102, 112	0
2	H	258/258 (100%)	2.10	116 (44%) 0 0	28, 73, 104, 110	0
2	J	258/258 (100%)	1.21	57 (22%) 0 0	17, 64, 97, 107	0
2	L	258/258 (100%)	1.63	97 (37%) 0 0	12, 71, 102, 113	0
2	N	258/258 (100%)	2.11	124 (48%) 0 0	12, 73, 103, 110	0
2	P	258/258 (100%)	1.25	51 (19%) 1 1	17, 67, 98, 108	0
All	All	5736/5752 (99%)	0.49	710 (12%) 4 3	3, 29, 92, 113	0

The worst 5 of 710 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	J	207	PHE	8.7
2	L	118	ALA	8.7
2	J	178	LEU	8.5
2	P	207	PHE	8.2
2	H	207	PHE	8.2

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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
4	K	G	514	1/1	0.82	0.20	39,39,39,39	1
5	B13	N	500	90/90	0.91	0.22	60,66,72,73	0
3	ZN	E	503	1/1	0.91	0.11	36,36,36,36	1
4	K	E	513	1/1	0.91	0.12	33,33,33,33	1
4	K	O	518	1/1	0.92	0.12	35,35,35,35	1
4	K	I	515	1/1	0.92	0.09	28,28,28,28	1
5	B13	F	500	90/90	0.92	0.21	53,63,71,72	0
5	B13	L	500	90/90	0.94	0.21	41,47,58,59	0
5	B13	H	500	90/90	0.94	0.18	45,58,68,69	0
5	B13	P	500	90/90	0.94	0.18	31,40,45,52	0
4	K	M	517	1/1	0.95	0.11	33,33,33,33	1
4	K	C	512	1/1	0.95	0.15	22,22,22,22	1
5	B13	J	500	90/90	0.95	0.17	32,37,50,57	0
5	B13	D	500	90/90	0.96	0.17	20,30,40,42	0
3	ZN	O	508	1/1	0.96	0.07	33,33,33,33	0
4	K	A	511	1/1	0.97	0.09	23,23,23,23	1
5	B13	B	500	90/90	0.97	0.14	9,24,48,49	0
3	ZN	G	504	1/1	0.97	0.09	33,33,33,33	1
3	ZN	I	505	1/1	0.98	0.09	30,30,30,30	0
3	ZN	A	501	1/1	0.98	0.11	20,20,20,20	0
3	ZN	C	502	1/1	0.99	0.11	19,19,19,19	0
3	ZN	K	506	1/1	0.99	0.11	33,33,33,33	0
3	ZN	E	522	1/1	0.99	0.08	37,37,37,37	0
3	ZN	M	523	1/1	0.99	0.10	21,21,21,21	0
3	ZN	M	507	1/1	0.99	0.13	33,33,33,33	0
3	ZN	I	521	1/1	0.99	0.08	16,16,16,16	0
4	K	K	516	1/1	0.99	0.07	31,31,31,31	1

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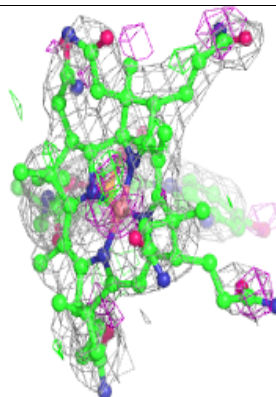
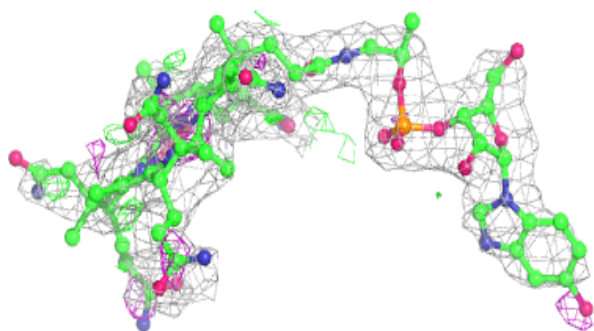
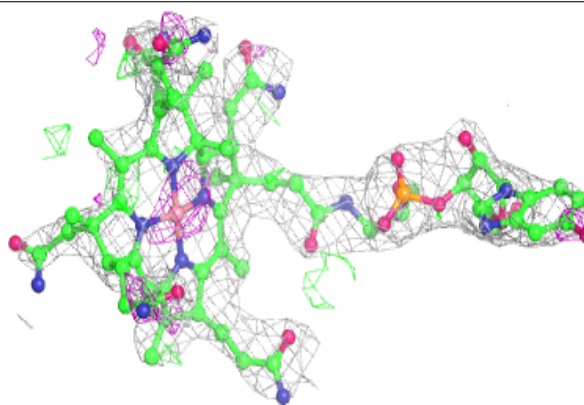
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	ZN	A	524	1/1	1.00	0.09	9,9,9,9	0

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.

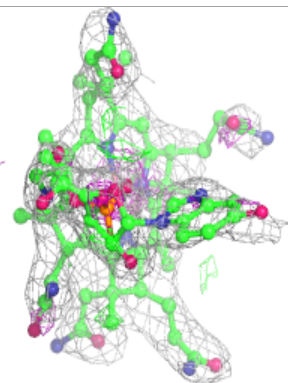
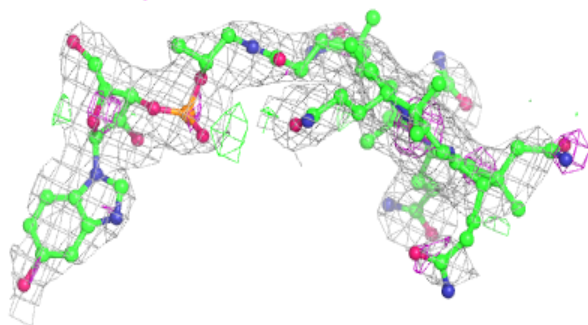
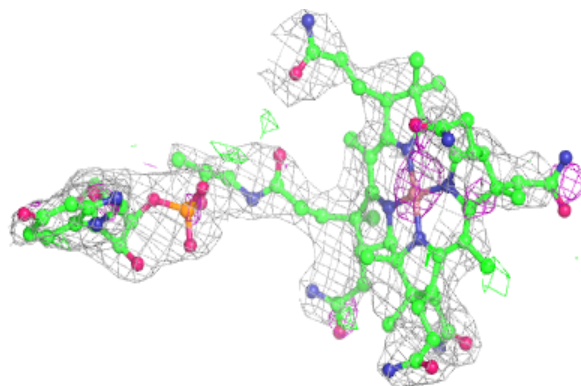
Electron density around B13 N 500:

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

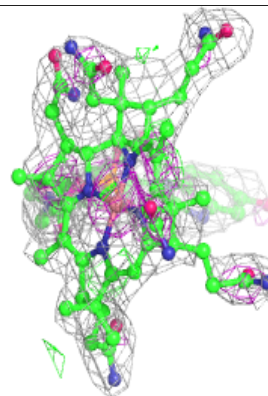
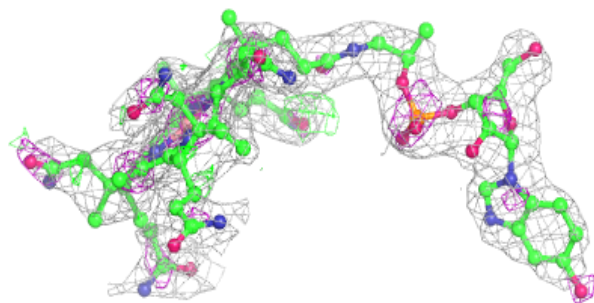
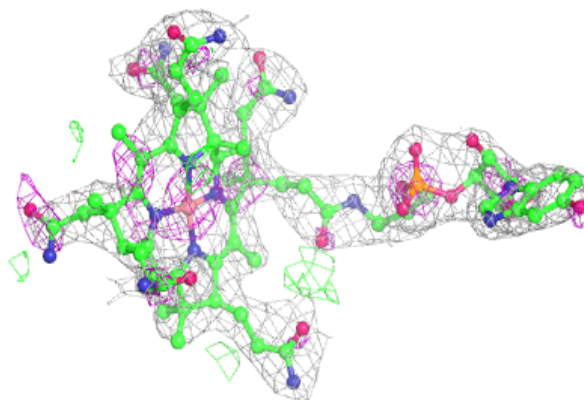


Electron density around B13 F 500:

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

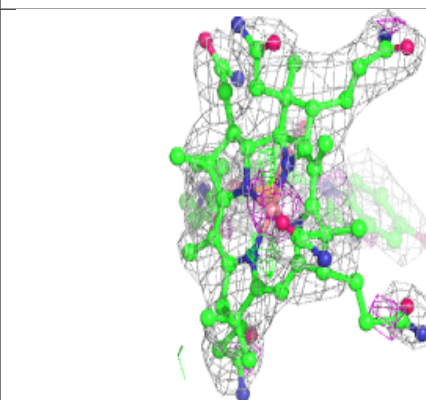
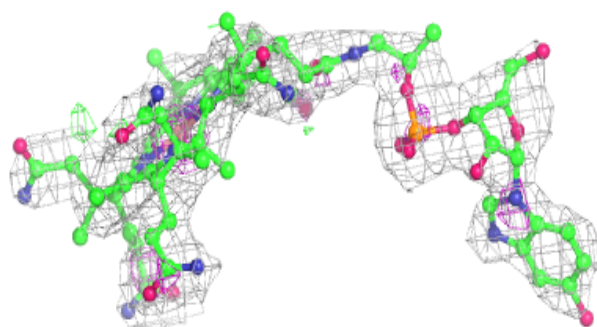
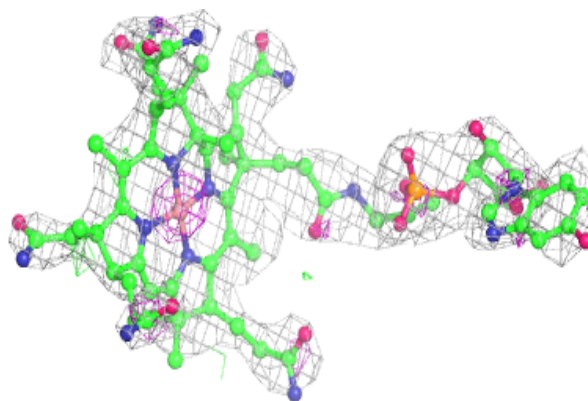
**Electron density around B13 L 500:**

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

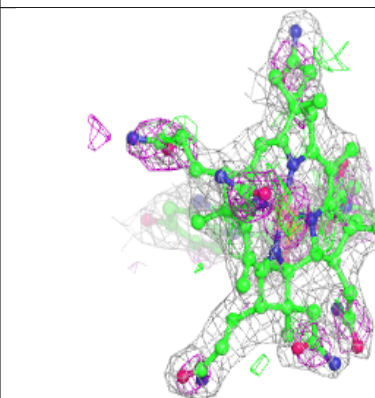
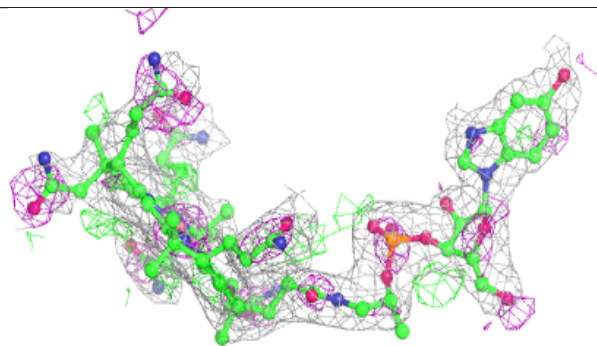
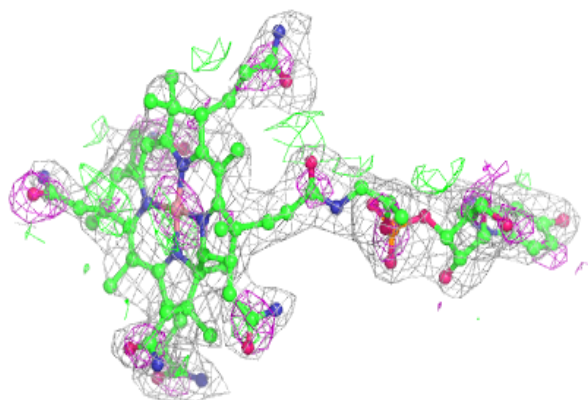


Electron density around B13 H 500:

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

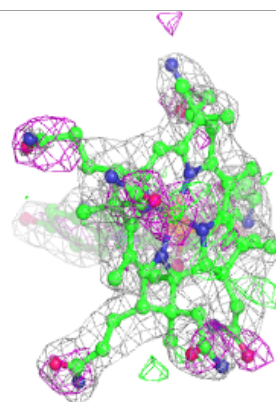
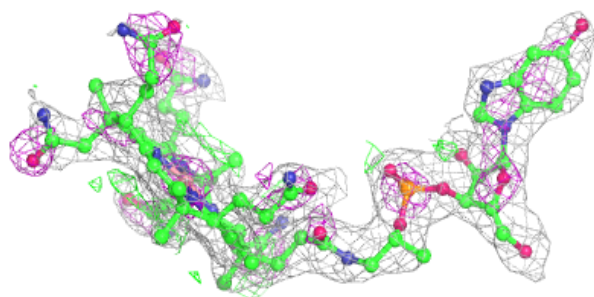
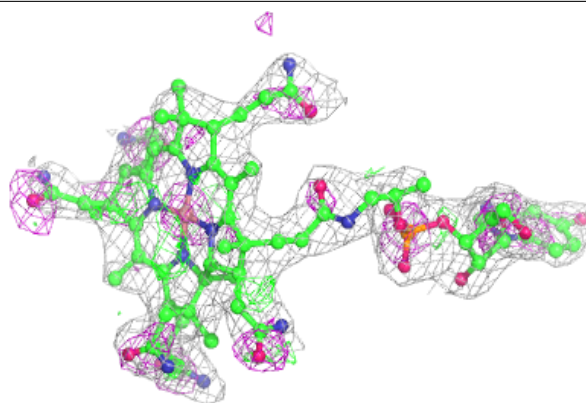
**Electron density around B13 P 500:**

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

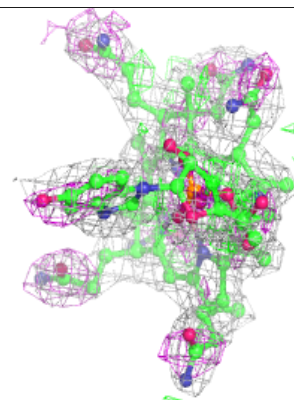
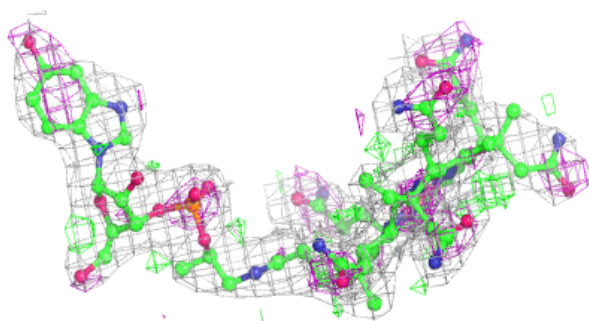
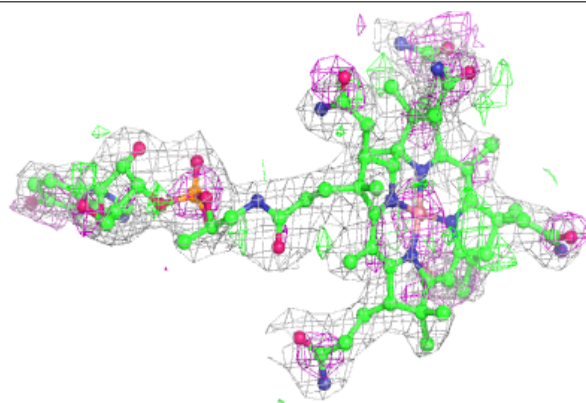


Electron density around B13 J 500:

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

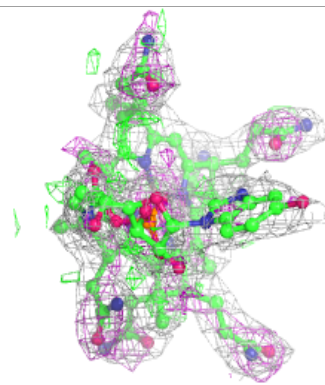
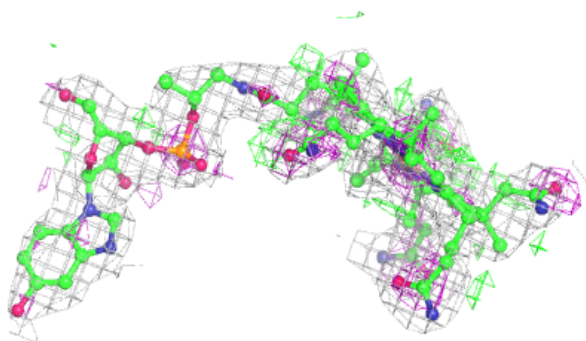
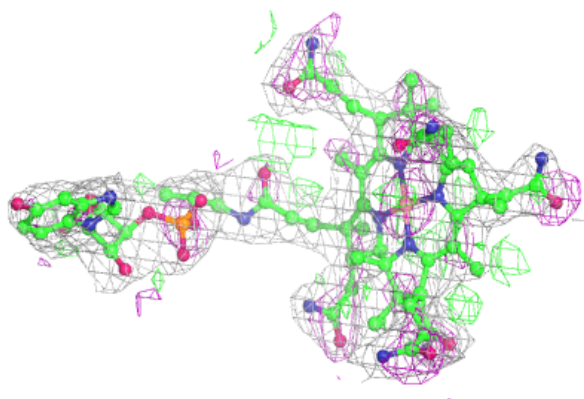
**Electron density around B13 D 500:**

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



Electron density around B13 B 500:

$2mF_o-DF_c$ (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.