



Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 09:58 am BST

PDB ID : 4O4S
Title : Crystal structure of phycobiliprotein lyase CpcT complexed with phycocyanobilin (PCB)
Authors : Zhou, W.; Ding, W.-L.; Zeng, X.-l.; Dong, L.-L.; Zhao, B.; Zhou, M.; Scheer, H.; Zhao, K.-H.; Yang, X.
Deposited on : 2013-12-19
Resolution : 2.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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

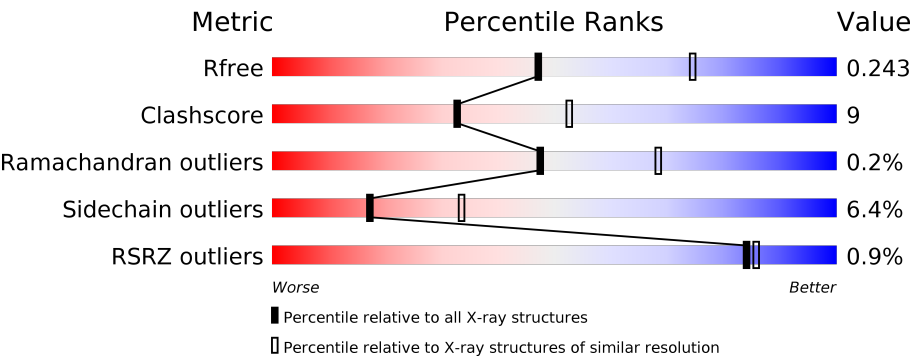
1 Overall quality at a glance i

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	207	<div><div></div><div><div></div><div>78%</div><div>17%</div><div>• •</div></div></div>
1	B	207	<div><div>%</div><div><div></div><div>72%</div><div>20%</div><div>• 5%</div></div></div>
1	C	207	<div><div></div><div><div></div><div>70%</div><div>25%</div><div>• •</div></div></div>
1	D	207	<div><div>%</div><div><div></div><div>70%</div><div>24%</div><div>• 5%</div></div></div>
1	E	207	<div><div></div><div><div></div><div>78%</div><div>17%</div><div>5%</div></div></div>
1	F	207	<div><div>%</div><div><div></div><div>76%</div><div>19%</div><div>5%</div></div></div>

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Mol	Chain	Length	Quality of chain
1	G	207	
1	H	207	
1	I	207	
1	J	207	
1	K	207	
1	L	207	

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
2	CYC	A	301	X	-	-	-
2	CYC	B	301	X	-	-	-
2	CYC	C	301	X	-	-	-
2	CYC	D	301	X	-	-	-
2	CYC	E	301	X	-	-	-
2	CYC	F	301	X	-	-	-
2	CYC	G	301	X	-	-	-
2	CYC	H	301	X	-	-	-
2	CYC	I	301	X	-	-	-
2	CYC	J	301	X	-	-	-
2	CYC	K	301	X	-	-	-
2	CYC	L	301	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 19721 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 Phycocyanobilin lyase CpcT.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	199	Total	C	N	O	S	Se	0	0	0
			1608	1026	274	300	3	5			
1	B	197	Total	C	N	O	S	Se	0	0	0
			1594	1018	272	296	3	5			
1	I	197	Total	C	N	O	S	Se	0	1	0
			1600	1021	273	298	3	5			
1	J	197	Total	C	N	O	S	Se	0	0	0
			1594	1018	272	296	3	5			
1	C	199	Total	C	N	O	S	Se	0	0	0
			1608	1026	274	300	3	5			
1	D	197	Total	C	N	O	S	Se	0	0	0
			1594	1018	272	296	3	5			
1	E	197	Total	C	N	O	S	Se	0	1	0
			1600	1021	273	298	3	5			
1	F	197	Total	C	N	O	S	Se	0	0	0
			1594	1018	272	296	3	5			
1	G	199	Total	C	N	O	S	Se	0	0	0
			1608	1026	274	300	3	5			
1	H	197	Total	C	N	O	S	Se	0	0	0
			1594	1018	272	296	3	5			
1	K	197	Total	C	N	O	S	Se	0	1	0
			1600	1021	273	298	3	5			
1	L	197	Total	C	N	O	S	Se	0	0	0
			1594	1018	272	296	3	5			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	200	LEU	-	EXPRESSION TAG	UNP Q8YLF9
A	201	GLU	-	EXPRESSION TAG	UNP Q8YLF9
A	202	HIS	-	EXPRESSION TAG	UNP Q8YLF9
A	203	HIS	-	EXPRESSION TAG	UNP Q8YLF9
A	204	HIS	-	EXPRESSION TAG	UNP Q8YLF9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	205	HIS	-	EXPRESSION TAG	UNP Q8YLF9
A	206	HIS	-	EXPRESSION TAG	UNP Q8YLF9
A	207	HIS	-	EXPRESSION TAG	UNP Q8YLF9
B	200	LEU	-	EXPRESSION TAG	UNP Q8YLF9
B	201	GLU	-	EXPRESSION TAG	UNP Q8YLF9
B	202	HIS	-	EXPRESSION TAG	UNP Q8YLF9
B	203	HIS	-	EXPRESSION TAG	UNP Q8YLF9
B	204	HIS	-	EXPRESSION TAG	UNP Q8YLF9
B	205	HIS	-	EXPRESSION TAG	UNP Q8YLF9
B	206	HIS	-	EXPRESSION TAG	UNP Q8YLF9
B	207	HIS	-	EXPRESSION TAG	UNP Q8YLF9
I	200	LEU	-	EXPRESSION TAG	UNP Q8YLF9
I	201	GLU	-	EXPRESSION TAG	UNP Q8YLF9
I	202	HIS	-	EXPRESSION TAG	UNP Q8YLF9
I	203	HIS	-	EXPRESSION TAG	UNP Q8YLF9
I	204	HIS	-	EXPRESSION TAG	UNP Q8YLF9
I	205	HIS	-	EXPRESSION TAG	UNP Q8YLF9
I	206	HIS	-	EXPRESSION TAG	UNP Q8YLF9
I	207	HIS	-	EXPRESSION TAG	UNP Q8YLF9
J	200	LEU	-	EXPRESSION TAG	UNP Q8YLF9
J	201	GLU	-	EXPRESSION TAG	UNP Q8YLF9
J	202	HIS	-	EXPRESSION TAG	UNP Q8YLF9
J	203	HIS	-	EXPRESSION TAG	UNP Q8YLF9
J	204	HIS	-	EXPRESSION TAG	UNP Q8YLF9
J	205	HIS	-	EXPRESSION TAG	UNP Q8YLF9
J	206	HIS	-	EXPRESSION TAG	UNP Q8YLF9
J	207	HIS	-	EXPRESSION TAG	UNP Q8YLF9
C	200	LEU	-	EXPRESSION TAG	UNP Q8YLF9
C	201	GLU	-	EXPRESSION TAG	UNP Q8YLF9
C	202	HIS	-	EXPRESSION TAG	UNP Q8YLF9
C	203	HIS	-	EXPRESSION TAG	UNP Q8YLF9
C	204	HIS	-	EXPRESSION TAG	UNP Q8YLF9
C	205	HIS	-	EXPRESSION TAG	UNP Q8YLF9
C	206	HIS	-	EXPRESSION TAG	UNP Q8YLF9
C	207	HIS	-	EXPRESSION TAG	UNP Q8YLF9
D	200	LEU	-	EXPRESSION TAG	UNP Q8YLF9
D	201	GLU	-	EXPRESSION TAG	UNP Q8YLF9
D	202	HIS	-	EXPRESSION TAG	UNP Q8YLF9
D	203	HIS	-	EXPRESSION TAG	UNP Q8YLF9
D	204	HIS	-	EXPRESSION TAG	UNP Q8YLF9
D	205	HIS	-	EXPRESSION TAG	UNP Q8YLF9
D	206	HIS	-	EXPRESSION TAG	UNP Q8YLF9

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Chain	Residue	Modelled	Actual	Comment	Reference
D	207	HIS	-	EXPRESSION TAG	UNP Q8YLF9
E	200	LEU	-	EXPRESSION TAG	UNP Q8YLF9
E	201	GLU	-	EXPRESSION TAG	UNP Q8YLF9
E	202	HIS	-	EXPRESSION TAG	UNP Q8YLF9
E	203	HIS	-	EXPRESSION TAG	UNP Q8YLF9
E	204	HIS	-	EXPRESSION TAG	UNP Q8YLF9
E	205	HIS	-	EXPRESSION TAG	UNP Q8YLF9
E	206	HIS	-	EXPRESSION TAG	UNP Q8YLF9
E	207	HIS	-	EXPRESSION TAG	UNP Q8YLF9
F	200	LEU	-	EXPRESSION TAG	UNP Q8YLF9
F	201	GLU	-	EXPRESSION TAG	UNP Q8YLF9
F	202	HIS	-	EXPRESSION TAG	UNP Q8YLF9
F	203	HIS	-	EXPRESSION TAG	UNP Q8YLF9
F	204	HIS	-	EXPRESSION TAG	UNP Q8YLF9
F	205	HIS	-	EXPRESSION TAG	UNP Q8YLF9
F	206	HIS	-	EXPRESSION TAG	UNP Q8YLF9
F	207	HIS	-	EXPRESSION TAG	UNP Q8YLF9
G	200	LEU	-	EXPRESSION TAG	UNP Q8YLF9
G	201	GLU	-	EXPRESSION TAG	UNP Q8YLF9
G	202	HIS	-	EXPRESSION TAG	UNP Q8YLF9
G	203	HIS	-	EXPRESSION TAG	UNP Q8YLF9
G	204	HIS	-	EXPRESSION TAG	UNP Q8YLF9
G	205	HIS	-	EXPRESSION TAG	UNP Q8YLF9
G	206	HIS	-	EXPRESSION TAG	UNP Q8YLF9
G	207	HIS	-	EXPRESSION TAG	UNP Q8YLF9
H	200	LEU	-	EXPRESSION TAG	UNP Q8YLF9
H	201	GLU	-	EXPRESSION TAG	UNP Q8YLF9
H	202	HIS	-	EXPRESSION TAG	UNP Q8YLF9
H	203	HIS	-	EXPRESSION TAG	UNP Q8YLF9
H	204	HIS	-	EXPRESSION TAG	UNP Q8YLF9
H	205	HIS	-	EXPRESSION TAG	UNP Q8YLF9
H	206	HIS	-	EXPRESSION TAG	UNP Q8YLF9
H	207	HIS	-	EXPRESSION TAG	UNP Q8YLF9
K	200	LEU	-	EXPRESSION TAG	UNP Q8YLF9
K	201	GLU	-	EXPRESSION TAG	UNP Q8YLF9
K	202	HIS	-	EXPRESSION TAG	UNP Q8YLF9
K	203	HIS	-	EXPRESSION TAG	UNP Q8YLF9
K	204	HIS	-	EXPRESSION TAG	UNP Q8YLF9
K	205	HIS	-	EXPRESSION TAG	UNP Q8YLF9
K	206	HIS	-	EXPRESSION TAG	UNP Q8YLF9
K	207	HIS	-	EXPRESSION TAG	UNP Q8YLF9
L	200	LEU	-	EXPRESSION TAG	UNP Q8YLF9

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Chain	Residue	Modelled	Actual	Comment	Reference
L	201	GLU	-	EXPRESSION TAG	UNP Q8YLF9
L	202	HIS	-	EXPRESSION TAG	UNP Q8YLF9
L	203	HIS	-	EXPRESSION TAG	UNP Q8YLF9
L	204	HIS	-	EXPRESSION TAG	UNP Q8YLF9
L	205	HIS	-	EXPRESSION TAG	UNP Q8YLF9
L	206	HIS	-	EXPRESSION TAG	UNP Q8YLF9
L	207	HIS	-	EXPRESSION TAG	UNP Q8YLF9

-
- The chemical structure of Cyclosporin A (CYC) is shown, a cyclic peptide consisting of 11 amino acid residues. The structure is a macrocyclic ring with a central nitrogen atom (N1) and a carbonyl group (C1=O). The residues are labeled with their corresponding amino acid abbreviations: C1 (Proline), C2 (Valine), C3 (Isoleucine), C4 (Threonine), C5 (Proline), C6 (Valine), C7 (Isoleucine), C8 (Threonine), C9 (Proline), C10 (Valine), and C11 (Isoleucine). The structure is shown in a 3D representation with stereochemistry indicated by wedges and dashes.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 43	C 33	N 4	O 6	0	0
2	B	1	Total 43	C 33	N 4	O 6	0	0
2	I	1	Total 43	C 33	N 4	O 6	0	0
2	J	1	Total 43	C 33	N 4	O 6	0	0
2	C	1	Total 43	C 33	N 4	O 6	0	0
2	D	1	Total 43	C 33	N 4	O 6	0	0
2	E	1	Total 43	C 33	N 4	O 6	0	0
2	F	1	Total 43	C 33	N 4	O 6	0	0



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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	G	1	Total	C	N	O	0	0
			43	33	4	6		
2	H	1	Total	C	N	O	0	0
			43	33	4	6		
2	K	1	Total	C	N	O	0	0
			43	33	4	6		
2	L	1	Total	C	N	O	0	0
			43	33	4	6		

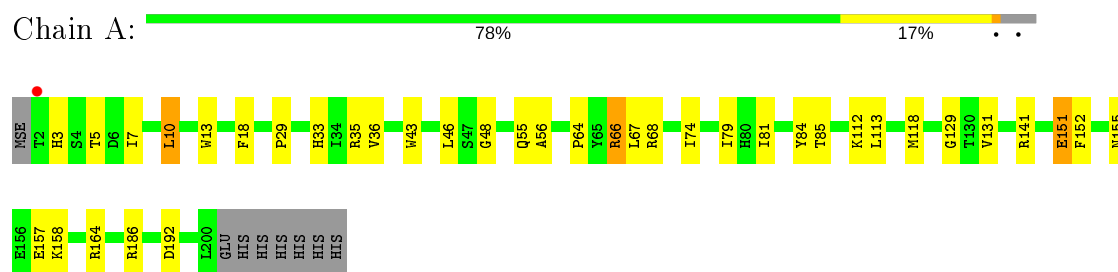
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	O	0	0
			2	2		
3	B	1	Total	O	0	0
			1	1		
3	I	2	Total	O	0	0
			2	2		
3	J	1	Total	O	0	0
			1	1		
3	C	1	Total	O	0	0
			1	1		
3	D	1	Total	O	0	0
			1	1		
3	E	2	Total	O	0	0
			2	2		
3	F	1	Total	O	0	0
			1	1		
3	G	2	Total	O	0	0
			2	2		
3	H	1	Total	O	0	0
			1	1		
3	K	2	Total	O	0	0
			2	2		
3	L	1	Total	O	0	0
			1	1		

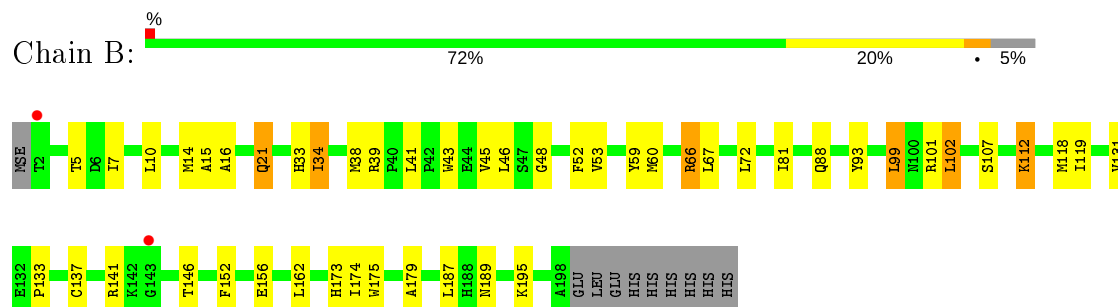
3 Residue-property plots [i](#)

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.

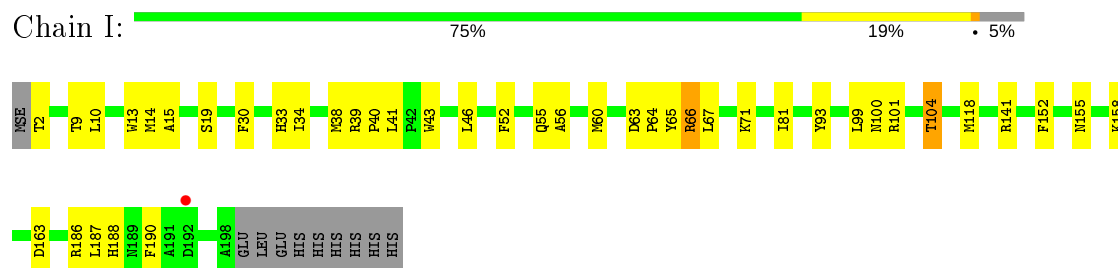
• Molecule 1: Phycocyanobilin lyase CpcT



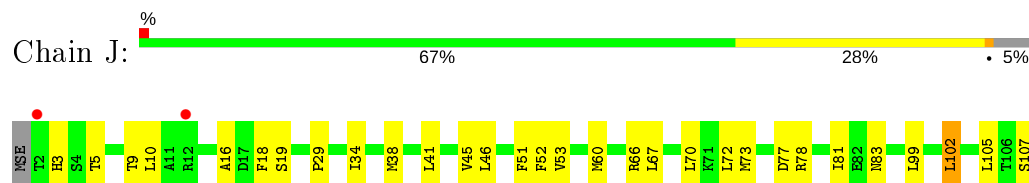
• Molecule 1: Phycocyanobilin lyase CpcT



• Molecule 1: Phycocyanobilin lyase CpcT



• Molecule 1: Phycocyanobilin lyase CpcT

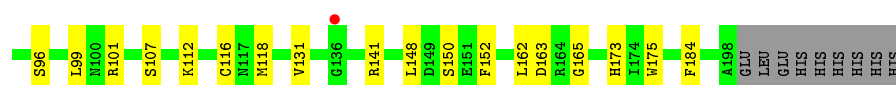




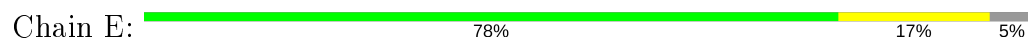
• Molecule 1: Phycocyanobilin lyase CpcT



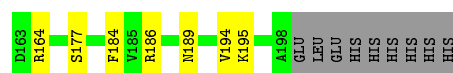
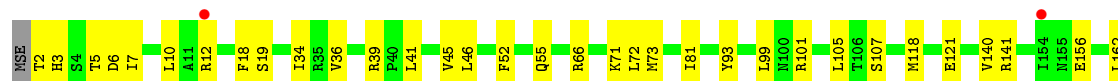
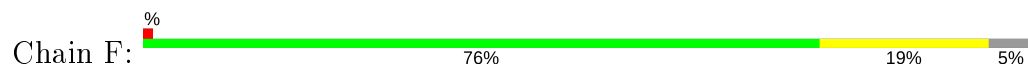
• Molecule 1: Phycocyanobilin lyase CpcT



• Molecule 1: Phycocyanobilin lyase CpcT

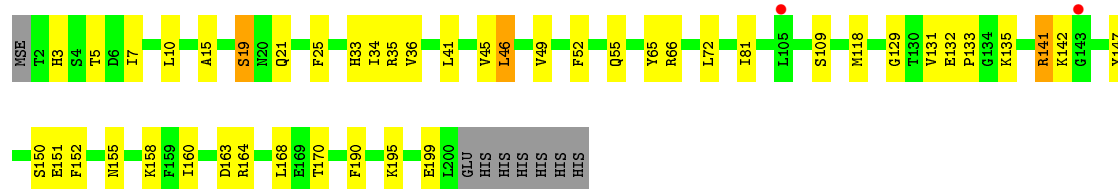


• Molecule 1: Phycocyanobilin lyase CpcT

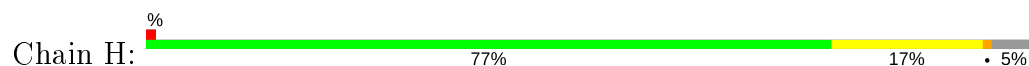


• Molecule 1: Phycocyanobilin lyase CpcT

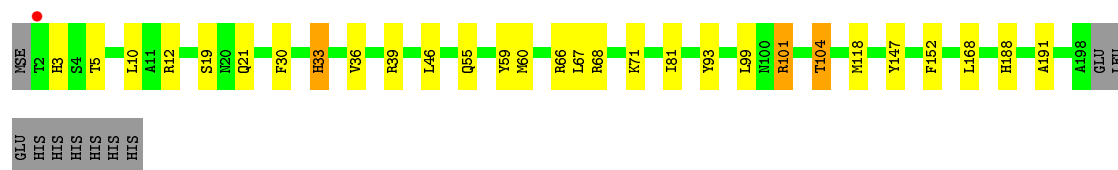
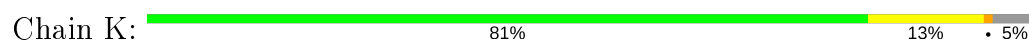




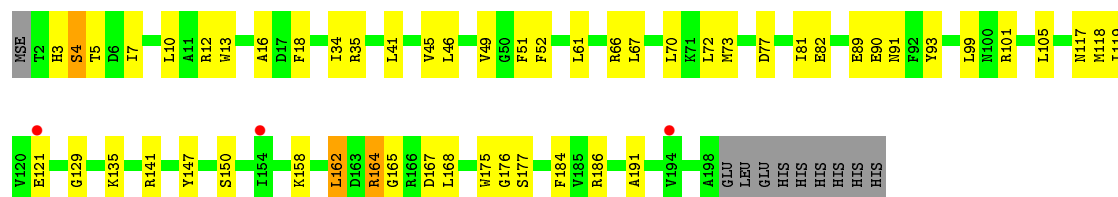
• Molecule 1: Phycocyanobilin lyase CpcT



• Molecule 1: Phycocyanobilin lyase CpcT



• Molecule 1: Phycocyanobilin lyase CpcT



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	69.75Å 69.60Å 162.59Å 90.21° 90.28° 60.12°	Depositor
Resolution (Å)	29.75 – 2.50 40.65 – 2.49	Depositor EDS
% Data completeness (in resolution range)	80.2 (29.75-2.50) 81.4 (40.65-2.49)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 2.48Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.180 , 0.248 0.178 , 0.243	Depositor DCC
R_{free} test set	3880 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	63.2	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 17.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.012 for h-k,h,l 0.012 for k,-h+k,l 0.447 for -k,h-k,l 0.447 for -h+k,-h,l 0.457 for -h+k,k,-l 0.447 for h,h-k,-l 0.013 for -h,-k,l 0.014 for k,h,-l 0.459 for -k,-h,-l 0.011 for h-k,-k,-l 0.014 for -h,-h+k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	19721	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.66% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: CYC

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.54	0/1643	0.67	0/2217
1	B	0.52	0/1629	0.62	0/2198
1	C	0.53	0/1643	0.65	0/2217
1	D	0.48	0/1629	0.59	0/2198
1	E	0.49	0/1635	0.66	0/2206
1	F	0.48	0/1629	0.63	0/2198
1	G	0.49	0/1643	0.65	0/2217
1	H	0.46	0/1629	0.60	0/2198
1	I	0.50	0/1635	0.65	0/2206
1	J	0.50	0/1629	0.64	0/2198
1	K	0.48	0/1635	0.64	0/2206
1	L	0.49	0/1629	0.62	0/2198
All	All	0.50	0/19608	0.64	0/26457

There are no bond length outliers.

There are no bond angle outliers.

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	1608	0	1549	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1594	0	1541	28	0
1	C	1608	0	1549	31	0
1	D	1594	0	1541	31	0
1	E	1600	0	1545	25	0
1	F	1594	0	1541	24	0
1	G	1608	0	1549	30	0
1	H	1594	0	1541	17	0
1	I	1600	0	1545	29	0
1	J	1594	0	1541	40	0
1	K	1600	0	1545	22	0
1	L	1594	0	1541	34	0
2	A	43	0	36	1	0
2	B	43	0	36	6	0
2	C	43	0	36	3	0
2	D	43	0	36	9	0
2	E	43	0	36	6	0
2	F	43	0	36	10	0
2	G	43	0	36	2	0
2	H	43	0	36	6	0
2	I	43	0	36	5	0
2	J	43	0	36	11	0
2	K	43	0	36	2	0
2	L	43	0	36	7	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	2	0	0	1	0
3	F	1	0	0	0	0
3	G	2	0	0	0	0
3	H	1	0	0	0	0
3	I	2	0	0	0	0
3	J	1	0	0	0	0
3	K	2	0	0	0	0
3	L	1	0	0	0	0
All	All	19721	0	18960	337	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 9.

All (337) 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:L:118:MSE:HG3	2:L:301:CYC:HMB2	1.59	0.84
1:F:118:MSE:HG3	2:F:301:CYC:HMB2	1.59	0.84
1:H:118:MSE:HG3	2:H:301:CYC:HMB2	1.62	0.82
1:H:173:HIS:HB2	1:K:104:THR:HG21	1.63	0.81
1:G:55:GLN:OE1	1:G:66:ARG:NH1	2.15	0.79
1:I:55:GLN:OE1	1:I:66:ARG:NH1	2.16	0.78
1:J:66:ARG:HH22	2:J:301:CYC:CGA	1.99	0.76
1:C:55:GLN:OE1	1:C:66:ARG:NH1	2.19	0.75
1:E:93:TYR:O	1:E:101:ARG:NH2	2.20	0.74
1:F:66:ARG:HH22	2:F:301:CYC:CGA	2.00	0.73
1:J:141:ARG:NH1	2:J:301:CYC:O1D	2.22	0.71
1:G:141:ARG:HH11	1:G:141:ARG:CG	2.04	0.70
1:I:93:TYR:O	1:I:101:ARG:NH2	2.15	0.69
1:J:77:ASP:O	1:J:78:ARG:NH1	2.26	0.69
1:B:93:TYR:O	1:B:101:ARG:NH2	2.19	0.68
1:F:66:ARG:NH2	2:F:301:CYC:O1A	2.26	0.68
1:E:39:ARG:NH2	1:E:99:LEU:HD11	2.09	0.68
1:J:38:MSE:HG2	1:J:53:VAL:HG22	1.76	0.68
1:K:81:ILE:HB	1:K:118:MSE:HB2	1.76	0.66
1:B:66:ARG:NH2	2:B:301:CYC:O2A	2.22	0.66
1:B:99:LEU:HD12	1:B:99:LEU:H	1.61	0.65
1:G:45:VAL:HG12	1:G:46:LEU:HD13	1.79	0.65
1:A:55:GLN:OE1	1:A:66:ARG:NH1	2.29	0.65
1:F:66:ARG:HH21	2:F:301:CYC:HBD2	1.62	0.65
1:C:151:GLU:OE1	1:C:164:ARG:NH2	2.29	0.65
1:H:38:MSE:HG2	1:H:53:VAL:HG22	1.80	0.64
1:J:66:ARG:HH21	2:J:301:CYC:HBD2	1.62	0.64
1:B:179:ALA:O	1:I:100:ASN:ND2	2.29	0.64
1:D:67:LEU:HD13	1:D:89:GLU:HB2	1.79	0.64
1:G:141:ARG:NH1	2:G:301:CYC:O2D	2.31	0.64
1:A:56:ALA:HB2	1:A:64:PRO:HA	1.78	0.64
1:I:81:ILE:HB	1:I:118:MSE:HB2	1.80	0.63
1:G:141:ARG:HH11	1:G:141:ARG:HG3	1.64	0.63
1:A:36:VAL:HG22	1:A:55:GLN:HG2	1.81	0.63
2:A:301:CYC:HD	2:A:301:CYC:HC	1.47	0.62
1:D:41:LEU:HD21	1:D:52:PHE:HB2	1.80	0.62
1:K:147:TYR:HD2	1:K:168:LEU:HD23	1.64	0.62
1:L:66:ARG:NH2	2:L:301:CYC:O1A	2.33	0.62
1:L:141:ARG:NH1	2:L:301:CYC:O1D	2.32	0.62
1:L:66:ARG:HH22	2:L:301:CYC:CGA	2.13	0.62
1:G:36:VAL:HG22	1:G:55:GLN:HG2	1.82	0.61
1:F:156:GLU:O	1:F:186:ARG:NH1	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:36:VAL:HG22	1:K:55:GLN:HG2	1.83	0.60
1:I:118:MSE:HE3	1:I:152:PHE:HD1	1.66	0.60
1:K:55:GLN:OE1	1:K:66:ARG:NH1	2.34	0.60
1:D:173:HIS:HB2	1:E:104:THR:HG21	1.84	0.60
1:E:55:GLN:OE1	1:E:66:ARG:NH1	2.34	0.60
1:D:99:LEU:H	1:D:99:LEU:HD12	1.66	0.60
1:F:12:ARG:HA	1:F:194:VAL:HG21	1.83	0.60
1:D:36:VAL:HG22	1:D:55:GLN:HG2	1.83	0.59
1:K:93:TYR:O	1:K:101:ARG:NH1	2.35	0.59
2:E:301:CYC:HD	2:E:301:CYC:HC	1.51	0.59
1:B:173:HIS:HB2	1:I:104:THR:HG21	1.83	0.59
1:E:36:VAL:HG22	1:E:55:GLN:HG2	1.85	0.59
1:A:151:GLU:OE1	1:A:164:ARG:NH2	2.36	0.59
1:C:36:VAL:HG22	1:C:55:GLN:HG2	1.84	0.59
1:H:93:TYR:O	1:H:101:ARG:NH2	2.25	0.58
1:J:135:LYS:HB3	1:J:147:TYR:CG	2.38	0.58
1:B:118:MSE:HG3	2:B:301:CYC:HMB2	1.85	0.58
1:A:155:ASN:HD21	1:A:158:LYS:HE2	1.68	0.58
1:A:67:LEU:O	1:A:68:ARG:NH1	2.37	0.58
1:B:39:ARG:HH22	1:B:99:LEU:HD11	1.69	0.58
1:F:41:LEU:HD21	1:F:52:PHE:HB2	1.86	0.58
1:L:99:LEU:HD12	1:L:99:LEU:H	1.70	0.57
1:D:150:SER:OG	1:D:163:ASP:OD2	2.21	0.57
1:F:99:LEU:H	1:F:99:LEU:HD12	1.70	0.57
1:J:99:LEU:H	1:J:99:LEU:HD12	1.70	0.57
1:B:152:PHE:CE2	2:B:301:CYC:HAB1	2.40	0.56
2:C:301:CYC:HC	2:C:301:CYC:HD	1.52	0.56
2:I:301:CYC:HD	2:I:301:CYC:HC	1.53	0.56
1:D:141:ARG:HG3	1:D:175:TRP:CD1	2.41	0.56
1:J:45:VAL:O	1:J:107:SER:HB3	2.05	0.56
1:C:81:ILE:HB	1:C:118:MSE:HB2	1.87	0.56
1:J:72:LEU:HD23	1:J:81:ILE:HG12	1.88	0.56
1:G:118:MSE:HE2	1:G:152:PHE:HD1	1.70	0.56
1:H:41:LEU:HD21	1:H:52:PHE:HB2	1.87	0.56
1:J:66:ARG:NH2	2:J:301:CYC:HBD2	2.20	0.56
1:C:192:ASP:OD1	1:C:192:ASP:N	2.33	0.55
1:H:36:VAL:HG22	1:H:55:GLN:HG2	1.88	0.55
2:G:301:CYC:HD	2:G:301:CYC:HC	1.55	0.55
1:G:151:GLU:OE1	1:G:164:ARG:NH2	2.40	0.55
2:K:301:CYC:HC	2:K:301:CYC:HD	1.55	0.55
1:B:39:ARG:NH2	1:B:99:LEU:HD11	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:118:MSE:HG3	2:D:301:CYC:HMB2	1.89	0.54
1:A:13:TRP:O	1:A:186:ARG:NH2	2.33	0.54
1:J:174:ILE:HG22	1:J:175:TRP:HD1	1.73	0.54
1:I:187:LEU:HB3	1:I:188:HIS:CD2	2.42	0.54
1:B:41:LEU:HD23	1:B:102:LEU:HD11	1.88	0.53
1:C:141:ARG:NH1	2:C:301:CYC:O2D	2.41	0.53
1:I:163:ASP:OD1	2:I:301:CYC:HAC2	2.08	0.53
1:E:118:MSE:HE3	1:E:152:PHE:HD1	1.73	0.53
1:C:118:MSE:HE2	1:C:152:PHE:HD1	1.72	0.53
1:E:46:LEU:HD13	1:E:71:LYS:HB2	1.90	0.53
1:A:129:GLY:HA3	1:A:152:PHE:CE1	2.43	0.53
1:K:21:GLN:HB2	1:K:33:HIS:CE1	2.44	0.53
1:A:81:ILE:HB	1:A:118:MSE:HB2	1.91	0.52
2:D:301:CYC:HD	2:D:301:CYC:HC	1.57	0.52
1:H:41:LEU:HD13	1:H:45:VAL:HG11	1.92	0.52
1:J:118:MSE:HG3	2:J:301:CYC:HMB2	1.91	0.52
1:F:66:ARG:NH2	2:F:301:CYC:HBD2	2.25	0.52
1:K:118:MSE:HE3	1:K:152:PHE:HD1	1.74	0.52
1:K:39:ARG:HH22	1:K:99:LEU:HD11	1.74	0.52
1:F:45:VAL:O	1:F:107:SER:HB3	2.10	0.52
1:H:141:ARG:HG3	1:H:175:TRP:CD1	2.44	0.52
1:H:99:LEU:H	1:H:99:LEU:HD12	1.75	0.52
1:C:118:MSE:HE2	1:C:152:PHE:CD1	2.45	0.52
1:J:164:ARG:HB2	1:J:175:TRP:O	2.10	0.52
1:L:18:PHE:HB3	1:L:184:PHE:HB3	1.92	0.52
1:L:49:VAL:HB	1:L:72:LEU:HB2	1.92	0.52
1:D:93:TYR:O	1:D:101:ARG:NH2	2.36	0.51
1:J:116:CYS:HB3	2:J:301:CYC:HMA2	1.93	0.51
2:L:301:CYC:HD	2:L:301:CYC:HC	1.58	0.51
1:B:112:LYS:N	1:E:169:GLU:OE2	2.43	0.51
1:H:66:ARG:NH2	2:H:301:CYC:O2A	2.39	0.51
1:E:41:LEU:HD21	1:E:52:PHE:HB2	1.92	0.51
1:I:155:ASN:HD21	1:I:158:LYS:HE2	1.75	0.51
1:A:118:MSE:HE2	1:A:152:PHE:HD1	1.75	0.51
1:I:155:ASN:ND2	1:I:158:LYS:HE2	2.26	0.51
1:J:72:LEU:CD2	1:J:81:ILE:HG12	2.40	0.51
1:A:13:TRP:CZ3	1:A:155:ASN:HA	2.46	0.51
1:C:52:PHE:CZ	1:C:67:LEU:HD11	2.46	0.51
1:B:137:CYS:SG	2:B:301:CYC:HAA1	2.50	0.50
1:F:72:LEU:HD23	1:F:81:ILE:HG12	1.93	0.50
1:H:152:PHE:CE2	2:H:301:CYC:HAB1	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3:HIS:NE2	1:G:5:THR:OG1	2.45	0.50
1:K:118:MSE:HE3	1:K:152:PHE:CD1	2.47	0.50
1:L:4:SER:HB3	1:L:77:ASP:O	2.12	0.50
1:G:49:VAL:HB	1:G:72:LEU:HB2	1.94	0.49
1:I:39:ARG:HH22	1:I:99:LEU:HD11	1.77	0.49
1:I:46:LEU:HD13	1:I:71:LYS:HB2	1.94	0.49
1:E:167:ASP:HB2	1:E:174:ILE:HD11	1.93	0.49
1:D:69:VAL:HB	1:D:84:TYR:HB2	1.95	0.49
1:F:39:ARG:HH22	1:F:99:LEU:HD11	1.76	0.49
1:J:66:ARG:NH2	2:J:301:CYC:CGA	2.73	0.49
1:F:141:ARG:NH1	2:F:301:CYC:O1D	2.39	0.49
1:F:3:HIS:NE2	1:F:5:THR:OG1	2.45	0.49
1:I:56:ALA:HB2	1:I:64:PRO:HA	1.95	0.49
1:A:192:ASP:OD1	1:A:192:ASP:N	2.46	0.49
1:B:41:LEU:HD21	1:B:52:PHE:HB2	1.94	0.48
2:F:301:CYC:HD	2:F:301:CYC:HC	1.61	0.48
1:C:195:LYS:HE3	1:C:199:GLU:OE2	2.13	0.48
1:E:152:PHE:HB3	2:E:301:CYC:HBB3	1.94	0.48
1:G:21:GLN:HG3	1:G:25:PHE:CD2	2.48	0.48
1:A:10:LEU:HD12	1:A:79:ILE:HG21	1.95	0.48
1:I:118:MSE:HE2	2:I:301:CYC:C3B	2.43	0.48
1:C:142:LYS:HZ1	1:D:26:GLU:HB3	1.79	0.48
2:F:301:CYC:HBA1	2:F:301:CYC:HMA3	1.96	0.48
1:I:39:ARG:NH2	1:I:99:LEU:HD11	2.28	0.48
1:K:59:TYR:CD2	1:K:60:MSE:HG3	2.47	0.48
1:L:41:LEU:HD21	1:L:52:PHE:HB2	1.95	0.48
1:L:167:ASP:OD1	1:L:168:LEU:N	2.47	0.48
1:L:3:HIS:NE2	1:L:5:THR:OG1	2.45	0.48
1:C:158:LYS:HD2	1:C:160:ILE:HD11	1.96	0.48
1:L:91:ASN:O	1:L:101:ARG:NH2	2.47	0.48
1:E:12:ARG:HG3	1:E:191:ALA:HB1	1.96	0.48
1:G:118:MSE:HE2	1:G:152:PHE:CD1	2.49	0.48
1:G:15:ALA:HB1	1:G:190:PHE:HB2	1.96	0.48
1:H:101:ARG:O	1:H:104:THR:OG1	2.22	0.48
1:I:60:MSE:HE2	1:I:63:ASP:HB2	1.95	0.48
1:E:187:LEU:HB3	1:E:188:HIS:CD2	2.49	0.47
1:K:55:GLN:HE22	2:K:301:CYC:C4C	2.27	0.47
1:D:51:PHE:HB2	1:D:70:LEU:HB2	1.95	0.47
1:J:127:PHE:O	1:J:153:GLU:HA	2.15	0.47
1:A:18:PHE:O	1:A:35:ARG:HD2	2.15	0.47
1:C:187:LEU:HB3	1:C:188:HIS:ND1	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:39:ARG:NH2	1:K:99:LEU:HD11	2.30	0.47
1:E:81:ILE:HB	1:E:118:MSE:HB2	1.96	0.47
1:E:129:GLY:HA3	1:E:152:PHE:CE1	2.50	0.47
1:K:67:LEU:O	1:K:68:ARG:NH1	2.46	0.47
1:K:99:LEU:H	1:K:99:LEU:HD12	1.79	0.47
1:F:36:VAL:HG22	1:F:55:GLN:HG2	1.95	0.47
1:C:129:GLY:HA3	1:C:152:PHE:CE1	2.50	0.47
1:L:135:LYS:HB3	1:L:147:TYR:CG	2.50	0.46
1:A:29:PRO:HB2	1:B:34:ILE:HG21	1.97	0.46
2:H:301:CYC:HD	2:H:301:CYC:HC	1.63	0.46
1:J:167:ASP:OD1	1:J:168:LEU:N	2.49	0.46
1:D:39:ARG:HH22	1:D:99:LEU:HD11	1.80	0.46
1:E:39:ARG:HH22	1:E:99:LEU:HD11	1.78	0.46
1:J:174:ILE:HG22	1:J:175:TRP:CD1	2.51	0.46
1:D:148:LEU:HG	1:D:150:SER:H	1.81	0.46
1:D:41:LEU:HD13	1:D:45:VAL:HG11	1.97	0.46
1:E:67:LEU:HD22	1:E:89:GLU:HB2	1.98	0.46
1:J:137:CYS:SG	2:J:301:CYC:HAA1	2.55	0.46
1:C:116:CYS:HB3	2:C:301:CYC:HMA2	1.97	0.46
1:J:66:ARG:NH2	2:J:301:CYC:O1A	2.48	0.46
1:G:19:SER:HB2	1:G:35:ARG:HD2	1.98	0.46
1:L:12:ARG:HE	1:L:12:ARG:HB2	1.54	0.46
1:C:51:PHE:HB2	1:C:70:LEU:HB2	1.98	0.45
1:C:5:THR:HB	1:C:74:ILE:HD13	1.97	0.45
1:G:41:LEU:HD21	1:G:52:PHE:HB2	1.98	0.45
1:L:165:GLY:HA3	1:L:175:TRP:NE1	2.31	0.45
1:E:18:PHE:HB3	1:E:184:PHE:HB3	1.99	0.45
1:F:93:TYR:O	1:F:101:ARG:NH2	2.45	0.45
2:J:301:CYC:HD	2:J:301:CYC:HC	1.62	0.45
1:C:141:ARG:NH2	1:D:28:PRO:O	2.49	0.45
1:F:3:HIS:CE1	1:F:5:THR:HG1	2.34	0.45
1:L:119:ILE:O	1:L:129:GLY:HA2	2.15	0.45
2:B:301:CYC:HC	2:B:301:CYC:HD	1.63	0.45
1:I:65:TYR:CZ	1:J:29:PRO:HG3	2.51	0.45
1:B:119:ILE:HD12	1:B:133:PRO:HD3	1.98	0.45
1:G:142:LYS:NZ	1:H:26:GLU:HB3	2.31	0.45
1:G:65:TYR:CZ	1:H:29:PRO:HG3	2.52	0.45
1:D:66:ARG:NH2	2:D:301:CYC:O2A	2.45	0.45
1:E:105:LEU:HA	1:E:105:LEU:HD12	1.76	0.45
1:E:16:ALA:HB3	1:E:18:PHE:CE1	2.51	0.45
1:J:41:LEU:HD21	1:J:52:PHE:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:18:PHE:HB3	1:F:184:PHE:HB3	1.98	0.45
1:L:164:ARG:HB2	1:L:175:TRP:O	2.17	0.45
1:D:38:MSE:HG2	1:D:53:VAL:HG22	1.99	0.44
1:B:141:ARG:HG3	1:B:175:TRP:CD1	2.52	0.44
1:B:72:LEU:HD12	1:B:81:ILE:HG12	2.00	0.44
1:K:3:HIS:NE2	1:K:5:THR:OG1	2.50	0.44
1:G:129:GLY:HA3	1:G:152:PHE:CE1	2.52	0.44
1:H:66:ARG:NH2	1:H:68:ARG:HG3	2.32	0.44
1:K:168:LEU:HD23	1:K:168:LEU:HA	1.68	0.44
1:L:82:GLU:HG2	1:L:117:ASN:ND2	2.33	0.44
1:L:13:TRP:O	1:L:186:ARG:NH2	2.41	0.44
1:C:65:TYR:CZ	1:D:29:PRO:HG3	2.52	0.44
2:F:301:CYC:HMA1	2:F:301:CYC:HHB	1.79	0.44
1:L:16:ALA:HB3	1:L:18:PHE:CZ	2.52	0.44
1:G:135:LYS:HG2	1:G:147:TYR:CE1	2.53	0.44
1:C:18:PHE:HB3	1:C:184:PHE:HB3	2.00	0.44
1:D:39:ARG:NH1	1:D:96:SER:O	2.48	0.44
1:J:168:LEU:HA	1:J:168:LEU:HD23	1.71	0.44
1:D:118:MSE:HE2	1:D:152:PHE:CE2	2.53	0.43
1:G:21:GLN:HG3	1:G:25:PHE:CE2	2.53	0.43
1:E:118:MSE:HE2	2:E:301:CYC:C3B	2.47	0.43
1:G:81:ILE:HB	1:G:118:MSE:HB2	1.99	0.43
1:L:90:GLU:HA	1:L:93:TYR:CE2	2.53	0.43
1:B:146:THR:HG22	1:B:174:ILE:HD12	2.00	0.43
1:D:165:GLY:HA3	1:D:175:TRP:CE2	2.53	0.43
1:E:101:ARG:HG2	3:E:402:HOH:O	2.18	0.43
1:G:158:LYS:HD2	1:G:160:ILE:HD11	2.00	0.43
1:B:156:GLU:H	1:B:156:GLU:CD	2.22	0.43
1:C:165:GLY:HA3	1:C:175:TRP:CE2	2.52	0.43
1:E:116:CYS:HB3	2:E:301:CYC:HMA2	1.99	0.43
1:G:170:THR:HG22	1:K:188:HIS:CE1	2.53	0.43
1:E:55:GLN:HE22	2:E:301:CYC:C3C	2.31	0.43
1:F:72:LEU:CD2	1:F:81:ILE:HG12	2.49	0.43
1:B:187:LEU:HA	1:B:187:LEU:HD23	1.90	0.43
1:J:118:MSE:HE2	1:J:152:PHE:CE2	2.53	0.43
1:B:21:GLN:HB2	1:B:33:HIS:NE2	2.34	0.43
1:D:18:PHE:HB3	1:D:184:PHE:HB3	2.01	0.43
1:G:155:ASN:HD21	1:G:158:LYS:HE2	1.84	0.43
1:J:116:CYS:HB3	2:J:301:CYC:CMA	2.48	0.43
1:F:46:LEU:HD23	1:F:71:LYS:HG3	2.00	0.43
1:L:16:ALA:HB3	1:L:18:PHE:CE2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:THR:HG23	1:A:113:LEU:HD11	1.99	0.43
1:D:43:TRP:CH2	1:D:48:GLY:HA2	2.53	0.43
1:F:81:ILE:HB	1:F:118:MSE:HB2	2.01	0.43
1:G:19:SER:HB2	1:G:35:ARG:CD	2.49	0.43
1:I:13:TRP:O	1:I:186:ARG:NH2	2.49	0.43
1:I:152:PHE:HB3	2:I:301:CYC:HBB3	2.00	0.43
1:J:53:VAL:HG21	1:J:70:LEU:CD1	2.49	0.43
1:B:38:MSE:HG2	1:B:53:VAL:HG22	2.01	0.43
1:G:150:SER:OG	1:G:163:ASP:HA	2.18	0.43
1:I:15:ALA:HB1	1:I:190:PHE:HB2	2.01	0.43
1:J:83:ASN:HB3	1:J:113:LEU:HD12	2.01	0.43
1:J:161:SER:OG	1:J:163:ASP:OD1	2.36	0.42
1:A:5:THR:HG22	1:A:74:ILE:HG23	2.00	0.42
1:C:115:GLY:O	1:C:137:CYS:HB2	2.19	0.42
1:I:39:ARG:HA	1:I:40:PRO:HD3	1.75	0.42
1:L:67:LEU:HD13	1:L:89:GLU:HB2	2.02	0.42
1:I:55:GLN:HE22	2:I:301:CYC:C3C	2.32	0.42
1:K:12:ARG:HG3	1:K:191:ALA:HB1	2.02	0.42
1:J:132:GLU:HA	1:J:133:PRO:HD3	1.86	0.42
1:J:41:LEU:HD23	1:J:102:LEU:HD11	2.01	0.42
1:D:152:PHE:CE2	2:D:301:CYC:HAB1	2.55	0.42
1:H:39:ARG:HA	1:H:39:ARG:HD2	1.87	0.42
1:J:119:ILE:O	1:J:129:GLY:HA2	2.20	0.42
1:L:168:LEU:HA	1:L:168:LEU:HD23	1.87	0.42
1:L:51:PHE:HB2	1:L:70:LEU:HB2	2.01	0.42
1:G:132:GLU:HA	1:G:133:PRO:HD3	1.84	0.42
1:L:141:ARG:HG3	1:L:175:TRP:CD1	2.55	0.42
1:L:12:ARG:HG3	1:L:191:ALA:HB1	2.01	0.42
1:L:72:LEU:HD23	1:L:81:ILE:HG12	2.01	0.42
1:B:45:VAL:O	1:B:107:SER:HB3	2.20	0.42
1:C:39:ARG:HA	1:C:40:PRO:HD3	1.90	0.42
1:C:56:ALA:HB2	1:C:64:PRO:HA	2.02	0.42
1:J:51:PHE:HB2	1:J:70:LEU:HB2	2.00	0.42
1:D:39:ARG:NH2	1:D:99:LEU:HD11	2.34	0.42
1:I:14:MSE:O	1:I:38:MSE:HB2	2.20	0.42
1:C:141:ARG:O	1:C:142:LYS:HB2	2.20	0.41
1:H:162:LEU:HD11	1:H:164:ARG:NH1	2.34	0.41
1:B:43:TRP:CH2	1:B:48:GLY:HA2	2.55	0.41
1:J:72:LEU:HD23	1:J:72:LEU:HA	1.87	0.41
1:D:10:LEU:HD13	1:D:72:LEU:HD21	2.01	0.41
1:G:168:LEU:HD23	1:G:168:LEU:HA	1.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:39:ARG:HD2	1:I:190:PHE:CE2	2.55	0.41
1:E:13:TRP:CZ3	1:E:155:ASN:HA	2.55	0.41
1:I:41:LEU:HD21	1:I:52:PHE:HB2	2.02	0.41
1:J:157:GLU:O	1:J:158:LYS:HD3	2.21	0.41
1:F:2:THR:HG22	1:F:6:ASP:OD1	2.20	0.41
2:L:301:CYC:HMA3	2:L:301:CYC:HBA1	2.02	0.41
1:L:72:LEU:CD2	1:L:81:ILE:HG12	2.51	0.41
1:A:43:TRP:CH2	1:A:48:GLY:HA2	2.56	0.41
1:C:105:LEU:HA	1:C:105:LEU:HD12	1.79	0.41
2:E:301:CYC:HMA1	2:E:301:CYC:HBB	1.88	0.41
1:G:141:ARG:NH1	1:G:141:ARG:CG	2.74	0.41
1:J:9:THR:HG22	1:J:127:PHE:HE1	1.85	0.41
1:B:39:ARG:HD2	1:B:39:ARG:HA	1.78	0.41
1:C:45:VAL:HG12	1:C:46:LEU:HD13	2.03	0.41
1:C:2:THR:HG21	1:C:9:THR:HG21	2.02	0.41
1:D:116:CYS:HB3	2:D:301:CYC:HMA2	2.02	0.41
1:D:55:GLN:HE22	2:D:301:CYC:C1C	2.34	0.41
2:D:301:CYC:HMA1	2:D:301:CYC:HBB	1.86	0.41
1:D:66:ARG:NH2	1:D:68:ARG:HG3	2.36	0.41
2:F:301:CYC:HHA	2:F:301:CYC:HAA2	1.85	0.41
2:H:301:CYC:HHA	2:H:301:CYC:HBD1	2.03	0.41
1:I:52:PHE:CZ	1:I:67:LEU:HD11	2.55	0.41
1:J:165:GLY:HA3	1:J:175:TRP:CE2	2.55	0.41
1:L:66:ARG:NH2	2:L:301:CYC:CGA	2.82	0.41
1:D:61:LEU:HD12	1:D:61:LEU:HA	1.77	0.41
1:F:195:LYS:HA	1:F:195:LYS:HD3	1.96	0.41
1:C:22:ALA:O	1:C:26:GLU:HG3	2.21	0.41
1:A:84:TYR:CE1	1:A:112:LYS:HG3	2.56	0.40
1:B:14:MSE:O	1:B:16:ALA:N	2.54	0.40
1:C:13:TRP:CZ3	1:C:155:ASN:HA	2.56	0.40
1:I:13:TRP:CE3	1:I:155:ASN:HA	2.56	0.40
1:L:35:ARG:HG3	1:L:61:LEU:HD21	2.03	0.40
1:C:52:PHE:HZ	1:C:67:LEU:HD11	1.86	0.40
2:D:301:CYC:HHA	2:D:301:CYC:HAA2	1.93	0.40
2:D:301:CYC:C4B	2:D:301:CYC:OC	2.70	0.40
1:F:140:VAL:O	1:F:141:ARG:HG2	2.21	0.40
1:I:30:PHE:CZ	1:J:176:GLY:HA2	2.56	0.40
1:K:147:TYR:CD2	1:K:168:LEU:HD23	2.50	0.40
1:L:150:SER:HA	1:L:162:LEU:O	2.20	0.40
2:H:301:CYC:HAA2	2:H:301:CYC:HHA	1.90	0.40
1:K:46:LEU:HD13	1:K:71:LYS:HB2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:59:TYR:CE2	1:B:60:MSE:HG3	2.57	0.40
1:J:16:ALA:HB3	1:J:18:PHE:CZ	2.55	0.40
1:K:30:PHE:CE1	1:L:176:GLY:HA2	2.56	0.40
1:L:41:LEU:HD13	1:L:45:VAL:HG11	2.02	0.40
1:B:118:MSE:CG	2:B:301:CYC:HMB2	2.50	0.40
1:G:195:LYS:HE3	1:G:199:GLU:OE2	2.21	0.40
1:I:2:THR:HG22	1:I:9:THR:OG1	2.22	0.40
1:J:130:THR:HG22	1:J:151:GLU:HB3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	197/207 (95%)	187 (95%)	10 (5%)	0	100	100
1	B	195/207 (94%)	180 (92%)	13 (7%)	2 (1%)	15	28
1	C	197/207 (95%)	184 (93%)	13 (7%)	0	100	100
1	D	195/207 (94%)	178 (91%)	16 (8%)	1 (0%)	29	48
1	E	196/207 (95%)	186 (95%)	9 (5%)	1 (0%)	29	48
1	F	195/207 (94%)	183 (94%)	12 (6%)	0	100	100
1	G	197/207 (95%)	189 (96%)	8 (4%)	0	100	100
1	H	195/207 (94%)	185 (95%)	10 (5%)	0	100	100
1	I	196/207 (95%)	186 (95%)	9 (5%)	1 (0%)	29	48
1	J	195/207 (94%)	182 (93%)	13 (7%)	0	100	100
1	K	196/207 (95%)	188 (96%)	8 (4%)	0	100	100
1	L	195/207 (94%)	185 (95%)	10 (5%)	0	100	100
All	All	2349/2484 (95%)	2213 (94%)	131 (6%)	5 (0%)	47	68

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	99	LEU
1	I	43	TRP
1	D	21	GLN
1	B	15	ALA
1	E	15	ALA

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	172/175 (98%)	162 (94%)	10 (6%)	20	38
1	B	171/175 (98%)	156 (91%)	15 (9%)	10	19
1	C	172/175 (98%)	158 (92%)	14 (8%)	11	23
1	D	171/175 (98%)	156 (91%)	15 (9%)	10	19
1	E	172/175 (98%)	168 (98%)	4 (2%)	50	76
1	F	171/175 (98%)	160 (94%)	11 (6%)	17	33
1	G	172/175 (98%)	163 (95%)	9 (5%)	23	44
1	H	171/175 (98%)	155 (91%)	16 (9%)	8	17
1	I	172/175 (98%)	165 (96%)	7 (4%)	30	55
1	J	171/175 (98%)	157 (92%)	14 (8%)	11	22
1	K	172/175 (98%)	167 (97%)	5 (3%)	42	69
1	L	171/175 (98%)	159 (93%)	12 (7%)	15	29
All	All	2058/2100 (98%)	1926 (94%)	132 (6%)	17	33

All (132) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	HIS
1	A	7	ILE
1	A	10	LEU
1	A	33	HIS

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Mol	Chain	Res	Type
1	A	46	LEU
1	A	66	ARG
1	A	131	VAL
1	A	141	ARG
1	A	151	GLU
1	A	157	GLU
1	B	5	THR
1	B	7	ILE
1	B	10	LEU
1	B	21	GLN
1	B	34	ILE
1	B	46	LEU
1	B	66	ARG
1	B	67	LEU
1	B	88	GLN
1	B	102	LEU
1	B	112	LYS
1	B	131	VAL
1	B	162	LEU
1	B	189	ASN
1	B	195	LYS
1	I	10	LEU
1	I	19	SER
1	I	33	HIS
1	I	34	ILE
1	I	66	ARG
1	I	104	THR
1	I	141	ARG
1	J	3	HIS
1	J	5	THR
1	J	10	LEU
1	J	19	SER
1	J	34	ILE
1	J	46	LEU
1	J	60	MSE
1	J	67	LEU
1	J	73	MSE
1	J	102	LEU
1	J	105	LEU
1	J	162	LEU
1	J	164	ARG
1	J	177	SER

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Mol	Chain	Res	Type
1	C	3	HIS
1	C	7	ILE
1	C	10	LEU
1	C	19	SER
1	C	33	HIS
1	C	34	ILE
1	C	46	LEU
1	C	66	ARG
1	C	109	SER
1	C	112	LYS
1	C	131	VAL
1	C	151	GLU
1	C	168	LEU
1	C	192	ASP
1	D	4	SER
1	D	5	THR
1	D	7	ILE
1	D	10	LEU
1	D	21	GLN
1	D	33	HIS
1	D	34	ILE
1	D	46	LEU
1	D	67	LEU
1	D	80	HIS
1	D	88	GLN
1	D	107	SER
1	D	112	LYS
1	D	131	VAL
1	D	162	LEU
1	E	10	LEU
1	E	19	SER
1	E	78	ARG
1	E	104	THR
1	F	7	ILE
1	F	10	LEU
1	F	19	SER
1	F	34	ILE
1	F	73	MSE
1	F	105	LEU
1	F	121	GLU
1	F	162	LEU
1	F	164	ARG

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Mol	Chain	Res	Type
1	F	177	SER
1	F	189	ASN
1	G	7	ILE
1	G	10	LEU
1	G	19	SER
1	G	33	HIS
1	G	34	ILE
1	G	46	LEU
1	G	109	SER
1	G	131	VAL
1	G	141	ARG
1	H	5	THR
1	H	7	ILE
1	H	10	LEU
1	H	21	GLN
1	H	33	HIS
1	H	46	LEU
1	H	47	SER
1	H	66	ARG
1	H	67	LEU
1	H	88	GLN
1	H	107	SER
1	H	112	LYS
1	H	131	VAL
1	H	162	LEU
1	H	177	SER
1	H	197	SER
1	K	10	LEU
1	K	19	SER
1	K	33	HIS
1	K	101	ARG
1	K	104	THR
1	L	4	SER
1	L	7	ILE
1	L	10	LEU
1	L	34	ILE
1	L	46	LEU
1	L	73	MSE
1	L	105	LEU
1	L	121	GLU
1	L	158	LYS
1	L	162	LEU

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Mol	Chain	Res	Type
1	L	164	ARG
1	L	177	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	55	GLN
1	H	55	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

12 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	$\# Z > 2$
2	CYC	K	301	-	36,46,46	3.13	9 (25%)	44,67,67	2.93	14 (31%)
2	CYC	B	301	-	36,46,46	3.22	11 (30%)	44,67,67	2.85	16 (36%)
2	CYC	D	301	-	36,46,46	3.27	10 (27%)	44,67,67	2.85	18 (40%)
2	CYC	F	301	-	36,46,46	3.24	9 (25%)	44,67,67	2.79	15 (34%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CYC	H	301	-	36,46,46	3.17	9 (25%)	44,67,67	2.87	17 (38%)
2	CYC	J	301	-	36,46,46	3.14	9 (25%)	44,67,67	2.89	18 (40%)
2	CYC	L	301	-	36,46,46	3.20	9 (25%)	44,67,67	2.91	18 (40%)
2	CYC	A	301	-	36,46,46	3.22	9 (25%)	44,67,67	2.90	17 (38%)
2	CYC	C	301	-	36,46,46	3.17	8 (22%)	44,67,67	2.98	17 (38%)
2	CYC	E	301	-	36,46,46	3.21	8 (22%)	44,67,67	2.97	17 (38%)
2	CYC	G	301	-	36,46,46	3.18	9 (25%)	44,67,67	2.87	18 (40%)
2	CYC	I	301	-	36,46,46	3.17	8 (22%)	44,67,67	2.75	15 (34%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CYC	K	301	-	2/2/14/19	6/21/74/74	0/4/4/4
2	CYC	B	301	-	2/2/14/19	4/21/74/74	0/4/4/4
2	CYC	D	301	-	2/2/14/19	5/21/74/74	0/4/4/4
2	CYC	F	301	-	2/2/14/19	5/21/74/74	0/4/4/4
2	CYC	H	301	-	2/2/14/19	5/21/74/74	0/4/4/4
2	CYC	J	301	-	2/2/14/19	4/21/74/74	0/4/4/4
2	CYC	L	301	-	2/2/14/19	5/21/74/74	0/4/4/4
2	CYC	A	301	-	2/2/14/19	5/21/74/74	0/4/4/4
2	CYC	C	301	-	2/2/14/19	4/21/74/74	0/4/4/4
2	CYC	E	301	-	2/2/14/19	6/21/74/74	0/4/4/4
2	CYC	G	301	-	2/2/14/19	5/21/74/74	0/4/4/4
2	CYC	I	301	-	2/2/14/19	4/21/74/74	0/4/4/4

All (108) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	301	CYC	CAC-C3C	-9.95	1.34	1.54
2	C	301	CYC	CAC-C3C	-9.91	1.34	1.54
2	A	301	CYC	CAC-C3C	-9.83	1.34	1.54
2	L	301	CYC	CAC-C3C	-9.66	1.34	1.54
2	F	301	CYC	CAC-C3C	-9.61	1.35	1.54
2	G	301	CYC	CAC-C3C	-9.58	1.35	1.54
2	E	301	CYC	CAC-C3C	-9.49	1.35	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	301	CYC	CAC-C3C	-9.32	1.35	1.54
2	K	301	CYC	CAC-C3C	-9.27	1.35	1.54
2	D	301	CYC	CAC-C3C	-9.23	1.35	1.54
2	B	301	CYC	CAC-C3C	-9.06	1.36	1.54
2	H	301	CYC	CAC-C3C	-8.94	1.36	1.54
2	B	301	CYC	C4B-C3B	-7.85	1.33	1.48
2	E	301	CYC	OB-C4B	7.67	1.38	1.23
2	D	301	CYC	C1A-C2A	-7.60	1.33	1.45
2	D	301	CYC	C4B-C3B	-7.59	1.33	1.48
2	F	301	CYC	C1A-C2A	-7.58	1.33	1.45
2	L	301	CYC	C4B-C3B	-7.53	1.33	1.48
2	H	301	CYC	C1A-C2A	-7.48	1.33	1.45
2	F	301	CYC	C4B-C3B	-7.45	1.34	1.48
2	J	301	CYC	C1A-C2A	-7.43	1.33	1.45
2	L	301	CYC	C1A-C2A	-7.38	1.34	1.45
2	H	301	CYC	C4B-C3B	-7.37	1.34	1.48
2	C	301	CYC	C1A-C2A	-7.20	1.34	1.45
2	J	301	CYC	C4B-C3B	-7.20	1.34	1.48
2	K	301	CYC	OB-C4B	7.13	1.37	1.23
2	G	301	CYC	C1A-C2A	-7.10	1.34	1.45
2	H	301	CYC	OB-C4B	7.10	1.37	1.23
2	B	301	CYC	C1A-C2A	-7.07	1.34	1.45
2	B	301	CYC	OB-C4B	7.02	1.36	1.23
2	G	301	CYC	C4B-C3B	-6.99	1.34	1.48
2	C	301	CYC	C4B-C3B	-6.97	1.34	1.48
2	A	301	CYC	C1A-C2A	-6.96	1.34	1.45
2	I	301	CYC	OB-C4B	6.95	1.36	1.23
2	I	301	CYC	C4B-C3B	-6.92	1.35	1.48
2	D	301	CYC	OB-C4B	6.91	1.36	1.23
2	G	301	CYC	OB-C4B	6.87	1.36	1.23
2	E	301	CYC	C1A-C2A	-6.85	1.34	1.45
2	A	301	CYC	OB-C4B	6.82	1.36	1.23
2	J	301	CYC	OB-C4B	6.80	1.36	1.23
2	A	301	CYC	C4B-C3B	-6.79	1.35	1.48
2	K	301	CYC	C1A-C2A	-6.71	1.35	1.45
2	K	301	CYC	C4B-C3B	-6.69	1.35	1.48
2	I	301	CYC	C1A-C2A	-6.65	1.35	1.45
2	I	301	CYC	C1B-C2B	-6.58	1.33	1.45
2	A	301	CYC	C1B-C2B	-6.57	1.33	1.45
2	C	301	CYC	OB-C4B	6.54	1.36	1.23
2	F	301	CYC	OB-C4B	6.52	1.36	1.23
2	E	301	CYC	C4B-C3B	-6.46	1.35	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	301	CYC	OB-C4B	6.44	1.35	1.23
2	B	301	CYC	C1B-C2B	-6.36	1.33	1.45
2	E	301	CYC	C4A-C3A	-6.30	1.32	1.45
2	D	301	CYC	C1B-C2B	-6.28	1.33	1.45
2	E	301	CYC	C1B-C2B	-6.24	1.33	1.45
2	G	301	CYC	C1B-C2B	-6.14	1.34	1.45
2	F	301	CYC	C1B-C2B	-6.13	1.34	1.45
2	C	301	CYC	C1B-C2B	-6.06	1.34	1.45
2	K	301	CYC	C1B-C2B	-6.04	1.34	1.45
2	L	301	CYC	C1B-C2B	-5.91	1.34	1.45
2	H	301	CYC	C1B-C2B	-5.85	1.34	1.45
2	J	301	CYC	C4A-C3A	-5.85	1.33	1.45
2	D	301	CYC	C4A-C3A	-5.85	1.33	1.45
2	F	301	CYC	C4A-C3A	-5.84	1.33	1.45
2	L	301	CYC	C4A-C3A	-5.78	1.33	1.45
2	B	301	CYC	C4A-C3A	-5.56	1.33	1.45
2	K	301	CYC	C4A-C3A	-5.55	1.33	1.45
2	A	301	CYC	C4A-C3A	-5.53	1.33	1.45
2	I	301	CYC	C4A-C3A	-5.52	1.33	1.45
2	C	301	CYC	C4A-C3A	-5.47	1.34	1.45
2	H	301	CYC	C4A-C3A	-5.44	1.34	1.45
2	G	301	CYC	C4A-C3A	-5.41	1.34	1.45
2	J	301	CYC	C1B-C2B	-5.32	1.35	1.45
2	B	301	CYC	CAD-C3D	3.18	1.56	1.52
2	H	301	CYC	CAD-C3D	2.86	1.56	1.52
2	E	301	CYC	CHB-C4A	-2.61	1.34	1.40
2	F	301	CYC	C1B-NB	-2.61	1.33	1.37
2	A	301	CYC	C2C-C1C	2.59	1.54	1.52
2	J	301	CYC	C1C-NC	-2.59	1.34	1.37
2	G	301	CYC	C1C-NC	-2.53	1.34	1.37
2	D	301	CYC	CAD-C3D	2.53	1.55	1.52
2	I	301	CYC	CHB-C4A	-2.42	1.34	1.40
2	D	301	CYC	CHB-C4A	-2.39	1.34	1.40
2	A	301	CYC	CHB-C4A	-2.39	1.34	1.40
2	G	301	CYC	CHB-C4A	-2.38	1.34	1.40
2	B	301	CYC	C1B-NB	-2.35	1.33	1.37
2	K	301	CYC	CMD-C2D	2.35	1.56	1.51
2	L	301	CYC	C1B-NB	-2.34	1.33	1.37
2	L	301	CYC	CHB-C4A	-2.34	1.35	1.40
2	D	301	CYC	C1C-NC	-2.32	1.34	1.37
2	L	301	CYC	C1C-NC	-2.28	1.34	1.37
2	C	301	CYC	CHB-C4A	-2.28	1.35	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	301	CYC	C1B-NB	-2.22	1.34	1.37
2	H	301	CYC	CHB-C4A	-2.18	1.35	1.40
2	J	301	CYC	CMB-C2B	2.16	1.55	1.50
2	K	301	CYC	CHB-C4A	-2.16	1.35	1.40
2	B	301	CYC	C1C-NC	-2.10	1.34	1.37
2	C	301	CYC	C1C-NC	-2.09	1.34	1.37
2	B	301	CYC	C3B-C2B	-2.09	1.32	1.36
2	K	301	CYC	C1C-NC	-2.08	1.34	1.37
2	A	301	CYC	C1C-NC	-2.07	1.34	1.37
2	H	301	CYC	C1C-NC	-2.05	1.34	1.37
2	J	301	CYC	CHB-C4A	-2.05	1.35	1.40
2	F	301	CYC	C1C-NC	-2.03	1.35	1.37
2	I	301	CYC	C3C-C4C	2.03	1.53	1.50
2	F	301	CYC	CHB-C4A	-2.01	1.35	1.40
2	B	301	CYC	CHB-C4A	-2.01	1.35	1.40
2	G	301	CYC	C1B-NB	-2.01	1.34	1.37
2	E	301	CYC	CHB-C1B	-2.00	1.33	1.38

All (200) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	CYC	CAC-C3C-C2C	8.77	136.18	114.26
2	F	301	CYC	CAC-C3C-C2C	8.60	135.76	114.26
2	J	301	CYC	CAC-C3C-C2C	8.59	135.72	114.26
2	D	301	CYC	CAC-C3C-C2C	8.31	135.03	114.26
2	L	301	CYC	CAC-C3C-C2C	8.16	134.65	114.26
2	H	301	CYC	CAC-C3C-C2C	8.04	134.34	114.26
2	G	301	CYC	CAC-C3C-C2C	7.88	133.96	114.26
2	C	301	CYC	CAC-C3C-C2C	7.85	133.86	114.26
2	A	301	CYC	CAC-C3C-C2C	7.70	133.49	114.26
2	C	301	CYC	C2C-C1C-NC	7.54	114.78	108.27
2	K	301	CYC	CAC-C3C-C2C	7.53	133.08	114.26
2	E	301	CYC	CAC-C3C-C2C	7.47	132.91	114.26
2	I	301	CYC	CAC-C3C-C2C	7.02	131.81	114.26
2	H	301	CYC	C2C-C1C-NC	6.86	114.18	108.27
2	A	301	CYC	C2C-C1C-NC	6.85	114.18	108.27
2	G	301	CYC	CMC-C2C-C1C	6.78	127.01	112.40
2	C	301	CYC	CMC-C2C-C1C	6.61	126.66	112.40
2	E	301	CYC	C4D-CHA-C1A	-6.60	120.93	128.81
2	G	301	CYC	C2C-C1C-NC	6.55	113.92	108.27
2	A	301	CYC	CMC-C2C-C1C	6.48	126.38	112.40
2	I	301	CYC	C4D-CHA-C1A	-6.38	121.19	128.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	301	CYC	C2C-C1C-NC	6.35	113.75	108.27
2	D	301	CYC	C2C-C1C-NC	6.31	113.71	108.27
2	H	301	CYC	CMC-C2C-C1C	6.27	125.91	112.40
2	J	301	CYC	C4D-CHA-C1A	-6.25	121.35	128.81
2	C	301	CYC	C4D-CHA-C1A	-6.23	121.37	128.81
2	H	301	CYC	C4D-CHA-C1A	-6.19	121.42	128.81
2	B	301	CYC	CMC-C2C-C1C	6.18	125.72	112.40
2	F	301	CYC	C4D-CHA-C1A	-6.15	121.46	128.81
2	L	301	CYC	C4D-CHA-C1A	-6.14	121.48	128.81
2	K	301	CYC	CMC-C2C-C1C	6.12	125.61	112.40
2	A	301	CYC	C4D-CHA-C1A	-6.11	121.50	128.81
2	D	301	CYC	C4D-CHA-C1A	-6.10	121.53	128.81
2	B	301	CYC	C4D-CHA-C1A	-6.09	121.53	128.81
2	E	301	CYC	CMC-C2C-C1C	6.09	125.52	112.40
2	J	301	CYC	CMC-C2C-C1C	6.08	125.52	112.40
2	L	301	CYC	C2C-C1C-NC	6.05	113.49	108.27
2	B	301	CYC	C2C-C1C-NC	6.04	113.48	108.27
2	K	301	CYC	C2C-C1C-NC	6.02	113.46	108.27
2	F	301	CYC	CMC-C2C-C1C	5.91	125.15	112.40
2	G	301	CYC	C4D-CHA-C1A	-5.88	121.79	128.81
2	H	301	CYC	OC-C1C-C2C	-5.87	121.51	126.17
2	D	301	CYC	CMC-C2C-C1C	5.85	125.01	112.40
2	K	301	CYC	OC-C1C-C2C	-5.83	121.54	126.17
2	I	301	CYC	C2C-C1C-NC	5.78	113.26	108.27
2	E	301	CYC	C2C-C1C-NC	5.76	113.24	108.27
2	L	301	CYC	CMC-C2C-C1C	5.73	124.76	112.40
2	L	301	CYC	OC-C1C-C2C	-5.73	121.62	126.17
2	K	301	CYC	C4D-CHA-C1A	-5.66	122.05	128.81
2	I	301	CYC	CMC-C2C-C1C	5.63	124.53	112.40
2	D	301	CYC	OC-C1C-C2C	-5.60	121.72	126.17
2	E	301	CYC	CAB-C3B-C4B	5.60	130.22	121.38
2	F	301	CYC	C2C-C1C-NC	5.53	113.04	108.27
2	I	301	CYC	OC-C1C-C2C	-5.53	121.77	126.17
2	K	301	CYC	CAB-C3B-C4B	5.53	130.12	121.38
2	C	301	CYC	OC-C1C-C2C	-5.47	121.82	126.17
2	I	301	CYC	CMC-C2C-C3C	5.43	135.72	113.83
2	L	301	CYC	CMC-C2C-C3C	5.33	135.32	113.83
2	C	301	CYC	CMC-C2C-C3C	5.24	134.95	113.83
2	A	301	CYC	CMC-C2C-C3C	5.20	134.80	113.83
2	D	301	CYC	CMC-C2C-C3C	5.17	134.70	113.83
2	E	301	CYC	CMC-C2C-C3C	5.15	134.62	113.83
2	J	301	CYC	CMC-C2C-C3C	5.13	134.51	113.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	301	CYC	CMC-C2C-C3C	5.11	134.43	113.83
2	K	301	CYC	CMC-C2C-C3C	5.10	134.42	113.83
2	E	301	CYC	OC-C1C-C2C	-5.08	122.13	126.17
2	H	301	CYC	CMC-C2C-C3C	5.06	134.23	113.83
2	B	301	CYC	OC-C1C-C2C	-5.04	122.17	126.17
2	A	301	CYC	CAB-C3B-C4B	5.00	129.28	121.38
2	B	301	CYC	CMC-C2C-C3C	4.99	133.97	113.83
2	A	301	CYC	OC-C1C-C2C	-4.98	122.21	126.17
2	G	301	CYC	CMC-C2C-C3C	4.97	133.86	113.83
2	C	301	CYC	CAB-C3B-C4B	4.87	129.07	121.38
2	J	301	CYC	OC-C1C-C2C	-4.79	122.36	126.17
2	L	301	CYC	CBD-CAD-C3D	-4.54	104.11	112.49
2	G	301	CYC	CBD-CAD-C3D	-4.53	104.13	112.49
2	J	301	CYC	CAB-C3B-C4B	4.40	128.32	121.38
2	F	301	CYC	OC-C1C-C2C	-4.39	122.69	126.17
2	G	301	CYC	CAB-C3B-C4B	4.36	128.27	121.38
2	E	301	CYC	CBD-CAD-C3D	-4.36	104.44	112.49
2	C	301	CYC	CBD-CAD-C3D	-4.23	104.69	112.49
2	G	301	CYC	OC-C1C-C2C	-4.20	122.83	126.17
2	I	301	CYC	CAB-C3B-C4B	4.12	127.89	121.38
2	F	301	CYC	CAB-C3B-C4B	4.12	127.89	121.38
2	E	301	CYC	CAB-C3B-C2B	-4.10	120.51	127.53
2	K	301	CYC	CBD-CAD-C3D	-4.08	104.96	112.49
2	L	301	CYC	CAB-C3B-C4B	4.04	127.77	121.38
2	J	301	CYC	CBD-CAD-C3D	-4.04	105.03	112.49
2	D	301	CYC	CAB-C3B-C4B	3.99	127.68	121.38
2	K	301	CYC	CAB-C3B-C2B	-3.93	120.81	127.53
2	K	301	CYC	CMB-C2B-C1B	3.90	129.03	124.17
2	B	301	CYC	CAB-C3B-C4B	3.89	127.52	121.38
2	E	301	CYC	OB-C4B-C3B	3.76	132.12	128.04
2	H	301	CYC	CAB-C3B-C4B	3.74	127.29	121.38
2	K	301	CYC	C1B-CHB-C4A	-3.64	119.20	128.08
2	I	301	CYC	CAC-C3C-C4C	3.62	121.97	112.67
2	C	301	CYC	C2C-C3C-C4C	3.56	106.68	101.34
2	D	301	CYC	CBD-CAD-C3D	3.52	118.97	112.49
2	E	301	CYC	CMB-C2B-C1B	3.51	128.55	124.17
2	E	301	CYC	C1B-CHB-C4A	-3.49	119.56	128.08
2	F	301	CYC	C1B-NB-C4B	-3.41	106.32	110.67
2	K	301	CYC	CAC-C3C-C4C	3.40	121.39	112.67
2	A	301	CYC	C2C-C3C-C4C	3.39	106.42	101.34
2	I	301	CYC	C1B-CHB-C4A	-3.37	119.85	128.08
2	K	301	CYC	OB-C4B-C3B	3.34	131.66	128.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	301	CYC	CBD-CAD-C3D	-3.31	106.38	112.49
2	A	301	CYC	CBD-CAD-C3D	-3.31	106.39	112.49
2	H	301	CYC	CBD-CAD-C3D	3.31	118.58	112.49
2	E	301	CYC	CAC-C3C-C4C	3.27	121.06	112.67
2	I	301	CYC	C2C-C3C-C4C	3.26	106.22	101.34
2	G	301	CYC	C2C-C3C-C4C	3.22	106.16	101.34
2	B	301	CYC	CHD-C4C-NC	3.17	128.97	125.20
2	B	301	CYC	CAA-CBA-CGA	-3.14	107.40	112.67
2	F	301	CYC	CHB-C4A-NA	3.14	131.50	124.93
2	D	301	CYC	C1B-NB-C4B	-3.11	106.71	110.67
2	E	301	CYC	C2C-C3C-C4C	3.10	105.98	101.34
2	J	301	CYC	CHB-C4A-NA	3.10	131.42	124.93
2	F	301	CYC	CMB-C2B-C1B	3.09	128.02	124.17
2	L	301	CYC	C1B-NB-C4B	-3.08	106.74	110.67
2	B	301	CYC	C1B-NB-C4B	-3.05	106.79	110.67
2	A	301	CYC	CHB-C1B-C2B	-3.01	120.98	126.95
2	J	301	CYC	CHD-C4C-NC	3.01	128.78	125.20
2	L	301	CYC	CMB-C2B-C1B	2.99	127.91	124.17
2	G	301	CYC	CAA-CBA-CGA	-2.98	107.67	112.67
2	L	301	CYC	CHB-C4A-NA	2.97	131.15	124.93
2	H	301	CYC	CAC-C3C-C4C	2.96	120.27	112.67
2	H	301	CYC	C1B-NB-C4B	-2.95	106.92	110.67
2	B	301	CYC	CMB-C2B-C1B	2.88	127.77	124.17
2	A	301	CYC	CAC-C3C-C4C	2.88	120.07	112.67
2	B	301	CYC	CHB-C4A-NA	2.88	130.96	124.93
2	L	301	CYC	C2C-C3C-C4C	2.86	105.63	101.34
2	C	301	CYC	C1B-NB-C4B	-2.85	107.04	110.67
2	J	301	CYC	CMB-C2B-C1B	2.84	127.72	124.17
2	J	301	CYC	C1B-NB-C4B	-2.84	107.06	110.67
2	I	301	CYC	C1B-NB-C4B	-2.83	107.06	110.67
2	H	301	CYC	CMB-C2B-C1B	2.83	127.70	124.17
2	G	301	CYC	CAC-C3C-C4C	2.81	119.88	112.67
2	K	301	CYC	C2C-C3C-C4C	2.80	105.53	101.34
2	D	301	CYC	CAC-C3C-C4C	2.79	119.85	112.67
2	J	301	CYC	C2C-C3C-C4C	2.79	105.51	101.34
2	A	301	CYC	CAB-C3B-C2B	-2.79	122.76	127.53
2	C	301	CYC	CAB-C3B-C2B	-2.78	122.77	127.53
2	L	301	CYC	CAC-C3C-C4C	2.70	119.61	112.67
2	A	301	CYC	CAD-CBD-CGD	-2.70	108.14	112.67
2	D	301	CYC	CHB-C4A-NA	2.69	130.55	124.93
2	G	301	CYC	C1B-CHB-C4A	-2.68	121.53	128.08
2	F	301	CYC	C2C-C3C-C4C	2.67	105.33	101.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	301	CYC	C2C-C3C-C4C	2.66	105.33	101.34
2	A	301	CYC	OB-C4B-C3B	2.66	130.93	128.04
2	G	301	CYC	C1B-NB-C4B	-2.66	107.29	110.67
2	C	301	CYC	CAC-C3C-C4C	2.64	119.46	112.67
2	I	301	CYC	OB-C4B-C3B	2.63	130.90	128.04
2	H	301	CYC	CHB-C4A-NA	2.62	130.42	124.93
2	B	301	CYC	CBD-CAD-C3D	2.62	117.31	112.49
2	D	301	CYC	CMB-C2B-C1B	2.59	127.41	124.17
2	F	301	CYC	CBD-CAD-C3D	-2.53	107.82	112.49
2	F	301	CYC	C3B-C4B-NB	2.52	108.81	106.78
2	G	301	CYC	CMB-C2B-C1B	2.51	127.30	124.17
2	L	301	CYC	OB-C4B-C3B	2.50	130.75	128.04
2	A	301	CYC	C1B-CHB-C4A	-2.47	122.04	128.08
2	H	301	CYC	CAA-CBA-CGA	-2.45	108.56	112.67
2	J	301	CYC	C3B-C4B-NB	2.45	108.75	106.78
2	A	301	CYC	CHB-C4A-NA	2.44	130.05	124.93
2	D	301	CYC	C2C-C3C-C4C	2.44	105.00	101.34
2	F	301	CYC	CAC-C3C-C4C	2.41	118.86	112.67
2	I	301	CYC	CHB-C1B-C2B	-2.40	122.19	126.95
2	B	301	CYC	C2C-C3C-C4C	2.39	104.93	101.34
2	B	301	CYC	CAC-C3C-C4C	2.39	118.82	112.67
2	A	301	CYC	C1B-NB-C4B	-2.39	107.63	110.67
2	E	301	CYC	CHB-C4A-NA	2.38	129.92	124.93
2	G	301	CYC	CHD-C4C-NC	2.38	128.04	125.20
2	J	301	CYC	CAC-C3C-C4C	2.36	118.73	112.67
2	L	301	CYC	CAA-CBA-CGA	-2.34	108.75	112.67
2	C	301	CYC	CHB-C4A-NA	2.33	129.82	124.93
2	J	301	CYC	C4A-C3A-C2A	2.33	109.19	106.51
2	G	301	CYC	CHB-C4A-NA	2.31	129.76	124.93
2	C	301	CYC	OB-C4B-C3B	2.30	130.54	128.04
2	H	301	CYC	C4A-C3A-C2A	2.30	109.14	106.51
2	E	301	CYC	CHB-C1B-C2B	-2.27	122.46	126.95
2	L	301	CYC	C3B-C4B-NB	2.26	108.60	106.78
2	G	301	CYC	OB-C4B-C3B	2.24	130.47	128.04
2	B	301	CYC	CAB-C3B-C2B	-2.22	123.73	127.53
2	J	301	CYC	CHB-C1B-C2B	-2.20	122.59	126.95
2	G	301	CYC	CAB-C3B-C2B	-2.19	123.79	127.53
2	E	301	CYC	C1B-NB-C4B	-2.17	107.91	110.67
2	C	301	CYC	C1B-CHB-C4A	-2.17	122.79	128.08
2	I	301	CYC	CHB-C4A-NA	2.16	129.46	124.93
2	D	301	CYC	CBC-CAC-C3C	2.15	118.24	113.47
2	L	301	CYC	CHB-C1B-C2B	-2.14	122.71	126.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	301	CYC	CAB-C3B-C2B	-2.13	123.89	127.53
2	C	301	CYC	CHB-C1B-C2B	-2.13	122.74	126.95
2	F	301	CYC	CHD-C4C-NC	2.12	127.72	125.20
2	H	301	CYC	OB-C4B-C3B	2.11	130.33	128.04
2	D	301	CYC	CAA-CBA-CGA	-2.10	109.14	112.67
2	D	301	CYC	C1B-CHB-C4A	-2.07	123.03	128.08
2	J	301	CYC	CAB-C3B-C2B	-2.06	124.01	127.53
2	D	301	CYC	CAB-C3B-C2B	-2.05	124.03	127.53
2	H	301	CYC	CAB-C3B-C2B	-2.03	124.06	127.53
2	D	301	CYC	CHB-C1B-C2B	-2.01	122.96	126.95
2	C	301	CYC	CHD-C4C-NC	2.01	127.59	125.20

All (24) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	K	301	CYC	C3C
2	K	301	CYC	C2C
2	B	301	CYC	C3C
2	B	301	CYC	C2C
2	D	301	CYC	C3C
2	D	301	CYC	C2C
2	F	301	CYC	C3C
2	F	301	CYC	C2C
2	H	301	CYC	C3C
2	H	301	CYC	C2C
2	J	301	CYC	C3C
2	J	301	CYC	C2C
2	L	301	CYC	C3C
2	L	301	CYC	C2C
2	A	301	CYC	C3C
2	A	301	CYC	C2C
2	C	301	CYC	C3C
2	C	301	CYC	C2C
2	E	301	CYC	C3C
2	E	301	CYC	C2C
2	G	301	CYC	C3C
2	G	301	CYC	C2C
2	I	301	CYC	C3C
2	I	301	CYC	C2C

All (58) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	K	301	CYC	C2B-C3B-CAB-CBB
2	K	301	CYC	C4B-C3B-CAB-CBB
2	K	301	CYC	C2C-C3C-CAC-CBC
2	B	301	CYC	C2B-C3B-CAB-CBB
2	B	301	CYC	C4B-C3B-CAB-CBB
2	B	301	CYC	C2C-C3C-CAC-CBC
2	D	301	CYC	C2B-C3B-CAB-CBB
2	D	301	CYC	C4B-C3B-CAB-CBB
2	D	301	CYC	C2C-C3C-CAC-CBC
2	D	301	CYC	C2D-C3D-CAD-CBD
2	F	301	CYC	C2B-C3B-CAB-CBB
2	F	301	CYC	C4B-C3B-CAB-CBB
2	F	301	CYC	C2C-C3C-CAC-CBC
2	H	301	CYC	C2B-C3B-CAB-CBB
2	H	301	CYC	C4B-C3B-CAB-CBB
2	H	301	CYC	C2C-C3C-CAC-CBC
2	J	301	CYC	C2B-C3B-CAB-CBB
2	J	301	CYC	C4B-C3B-CAB-CBB
2	J	301	CYC	C2C-C3C-CAC-CBC
2	L	301	CYC	C2B-C3B-CAB-CBB
2	L	301	CYC	C4B-C3B-CAB-CBB
2	L	301	CYC	C2C-C3C-CAC-CBC
2	A	301	CYC	C2B-C3B-CAB-CBB
2	A	301	CYC	C4B-C3B-CAB-CBB
2	A	301	CYC	C2C-C3C-CAC-CBC
2	C	301	CYC	C2B-C3B-CAB-CBB
2	C	301	CYC	C4B-C3B-CAB-CBB
2	C	301	CYC	C2C-C3C-CAC-CBC
2	E	301	CYC	C2B-C3B-CAB-CBB
2	E	301	CYC	C4B-C3B-CAB-CBB
2	E	301	CYC	C2C-C3C-CAC-CBC
2	G	301	CYC	C2B-C3B-CAB-CBB
2	G	301	CYC	C4B-C3B-CAB-CBB
2	G	301	CYC	C2C-C3C-CAC-CBC
2	I	301	CYC	C2B-C3B-CAB-CBB
2	I	301	CYC	C4B-C3B-CAB-CBB
2	I	301	CYC	C2C-C3C-CAC-CBC
2	F	301	CYC	C3A-C2A-CAA-CBA
2	E	301	CYC	C2B-C1B-CHB-C4A
2	L	301	CYC	C3A-C2A-CAA-CBA
2	L	301	CYC	C1A-C2A-CAA-CBA
2	C	301	CYC	C3A-C2A-CAA-CBA
2	E	301	CYC	C3A-C2A-CAA-CBA

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Mol	Chain	Res	Type	Atoms
2	G	301	CYC	C3A-C2A-CAA-CBA
2	F	301	CYC	C1A-C2A-CAA-CBA
2	A	301	CYC	C3A-C2A-CAA-CBA
2	B	301	CYC	C2D-C3D-CAD-CBD
2	H	301	CYC	C2D-C3D-CAD-CBD
2	J	301	CYC	C3A-C2A-CAA-CBA
2	K	301	CYC	C3A-C4A-CHB-C1B
2	K	301	CYC	C2B-C1B-CHB-C4A
2	K	301	CYC	C3A-C2A-CAA-CBA
2	E	301	CYC	C1A-C2A-CAA-CBA
2	D	301	CYC	C3A-C2A-CAA-CBA
2	A	301	CYC	C2B-C1B-CHB-C4A
2	I	301	CYC	C3A-C2A-CAA-CBA
2	H	301	CYC	C3A-C2A-CAA-CBA
2	G	301	CYC	C1A-C2A-CAA-CBA

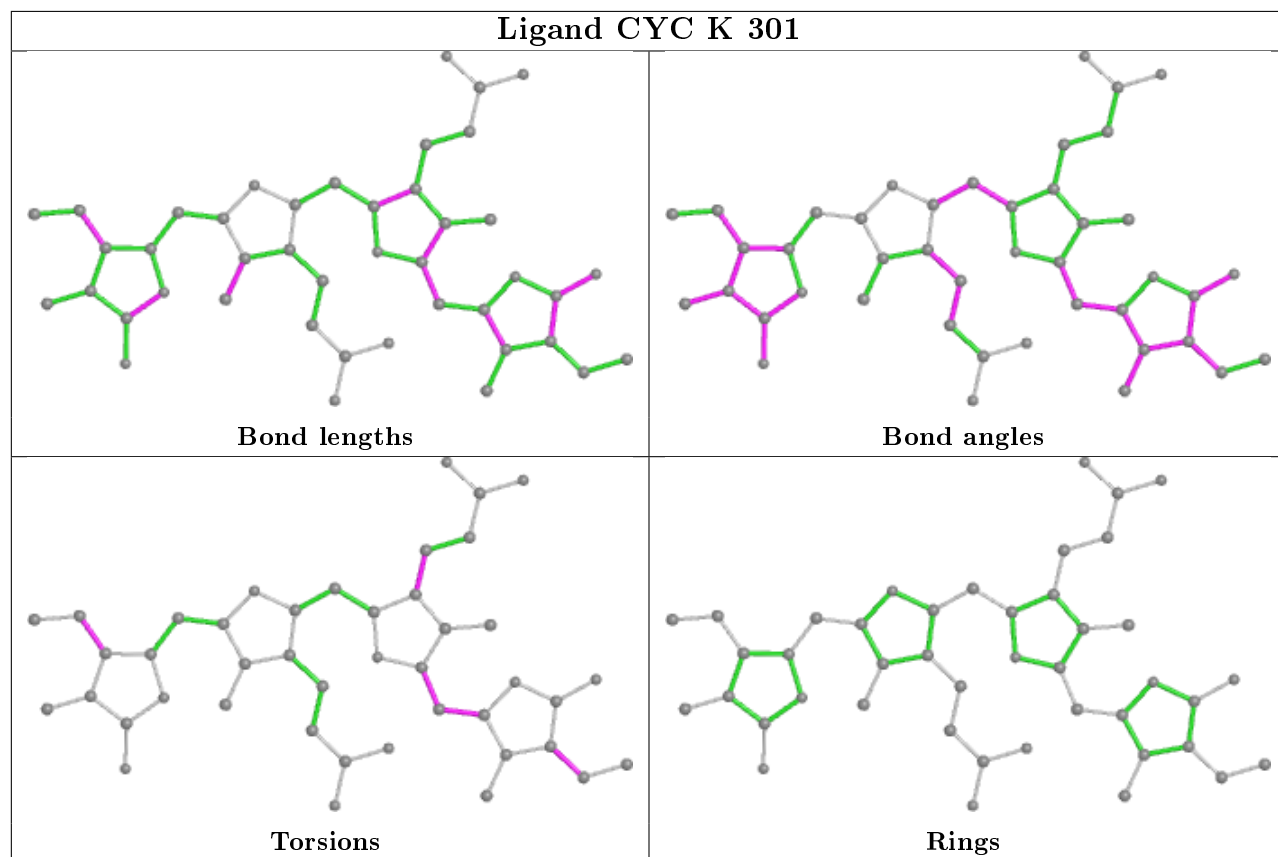
There are no ring outliers.

12 monomers are involved in 68 short contacts:

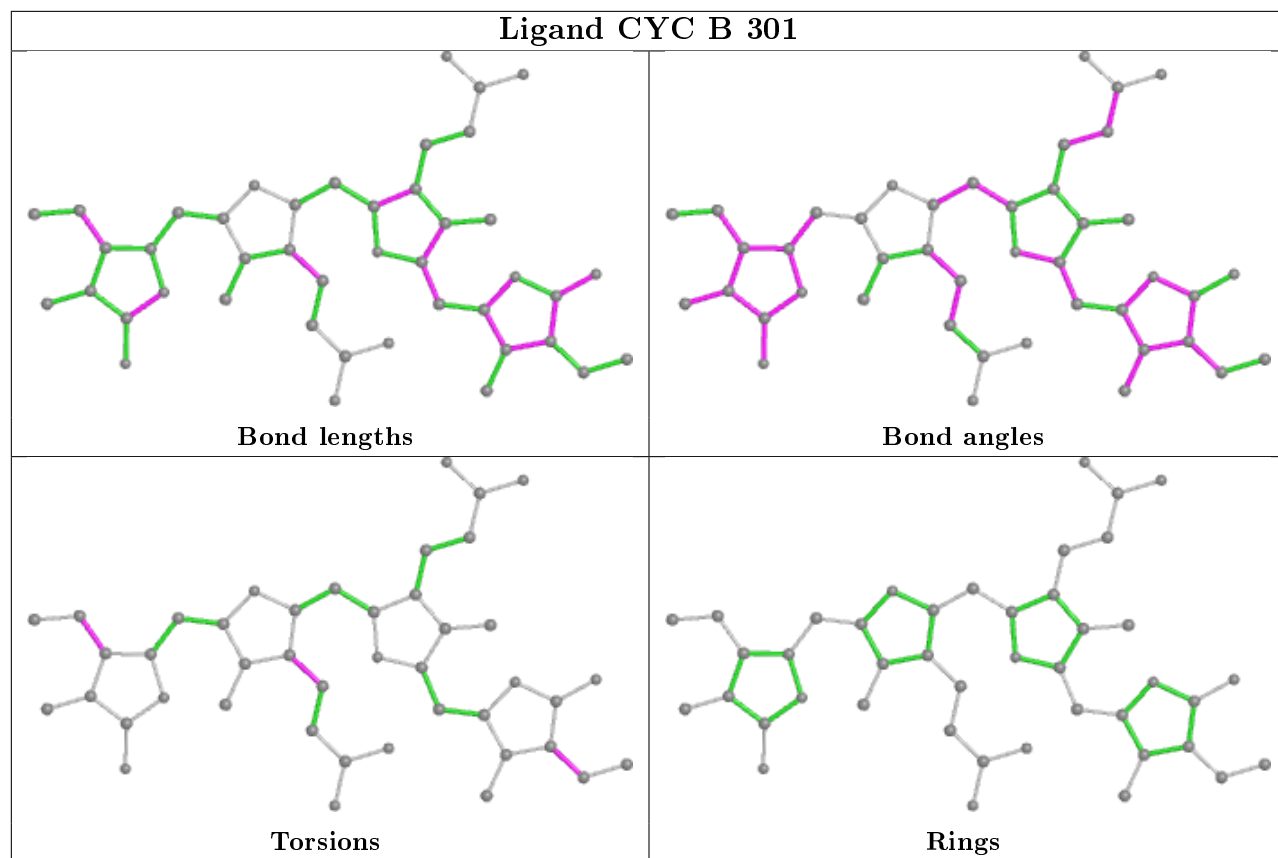
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	K	301	CYC	2	0
2	B	301	CYC	6	0
2	D	301	CYC	9	0
2	F	301	CYC	10	0
2	H	301	CYC	6	0
2	J	301	CYC	11	0
2	L	301	CYC	7	0
2	A	301	CYC	1	0
2	C	301	CYC	3	0
2	E	301	CYC	6	0
2	G	301	CYC	2	0
2	I	301	CYC	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

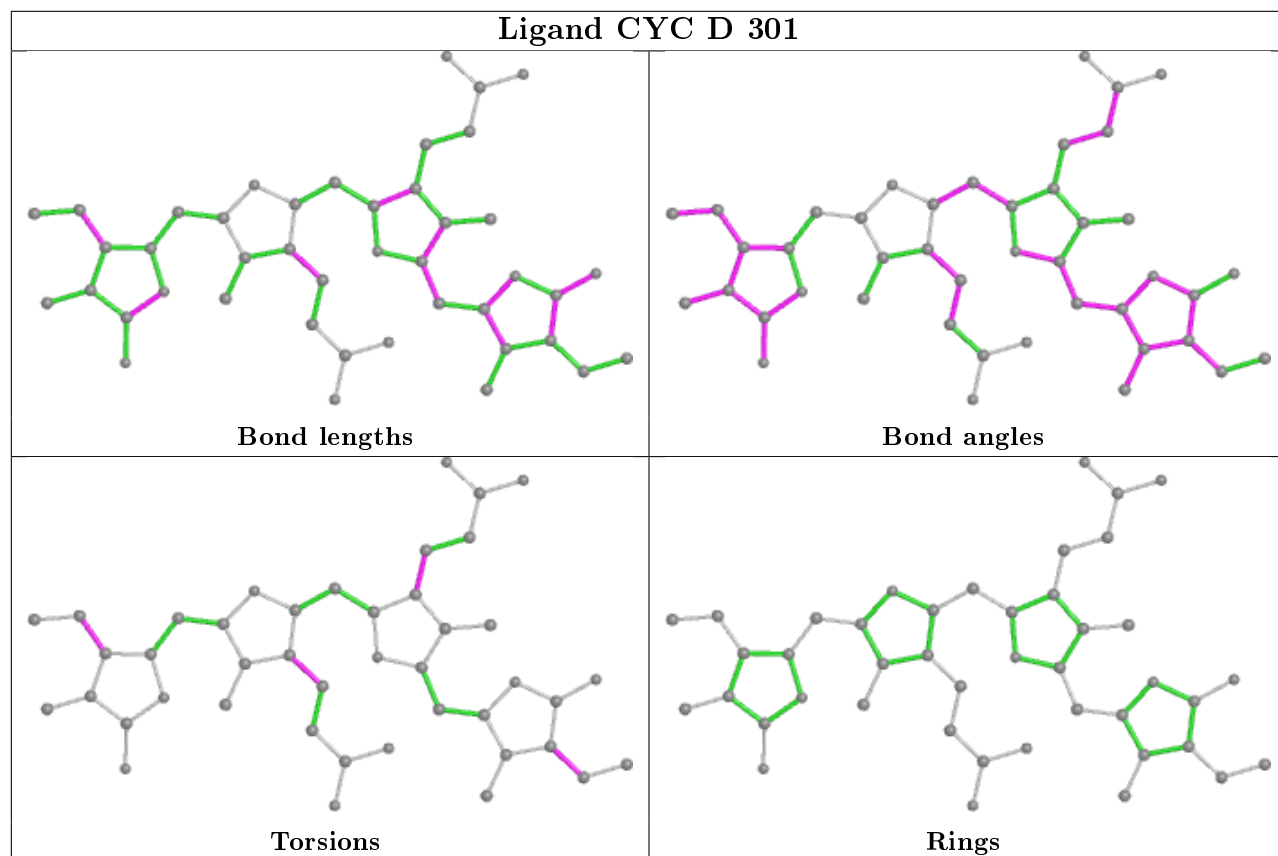
any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



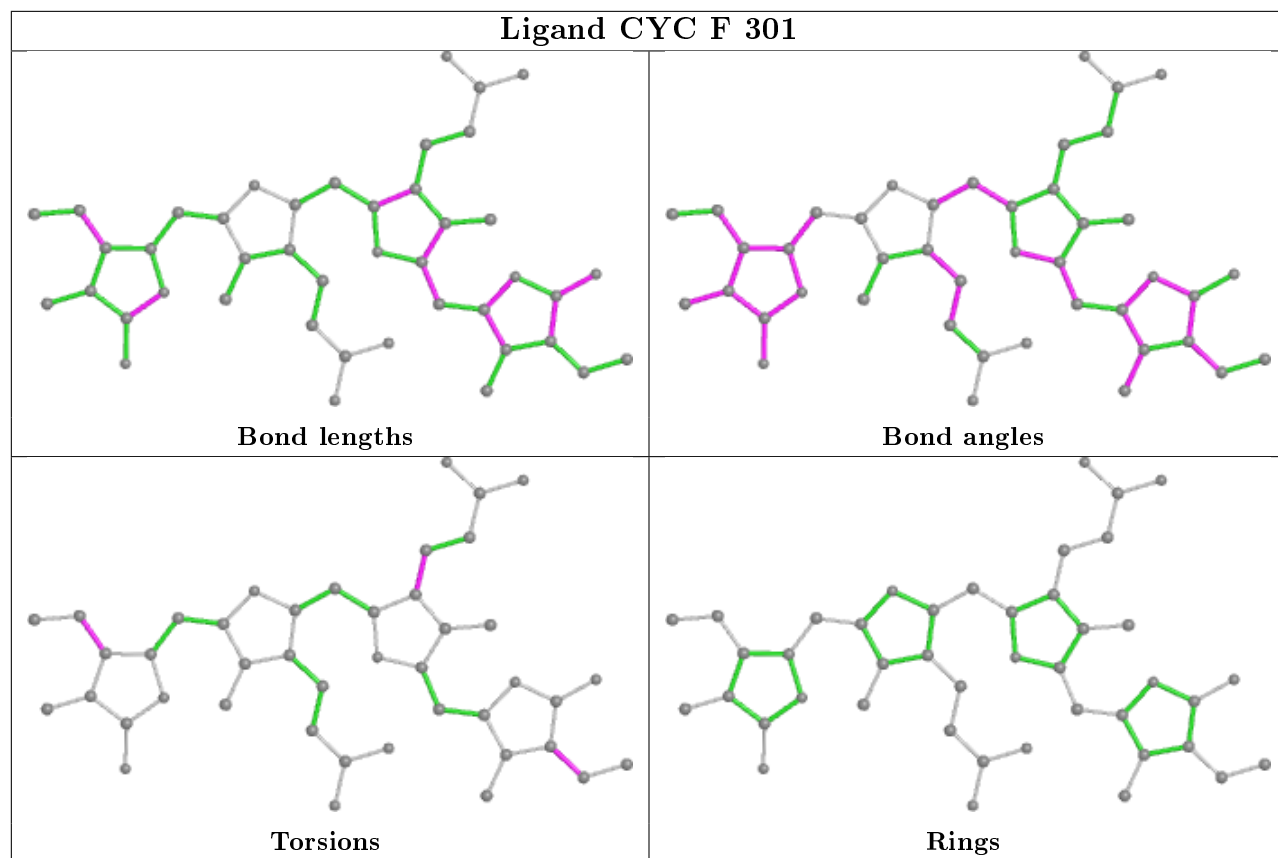
Ligand CYC B 301



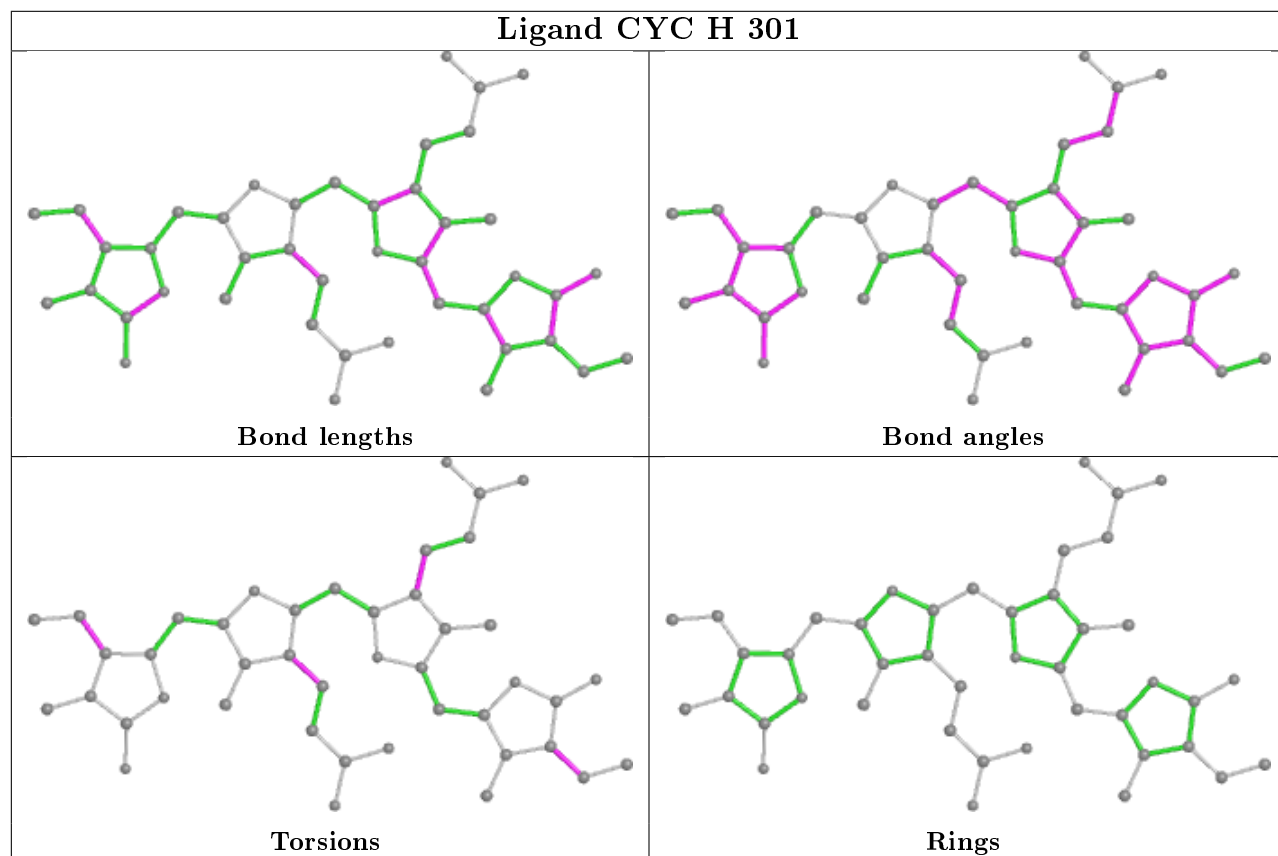
Ligand CYC D 301



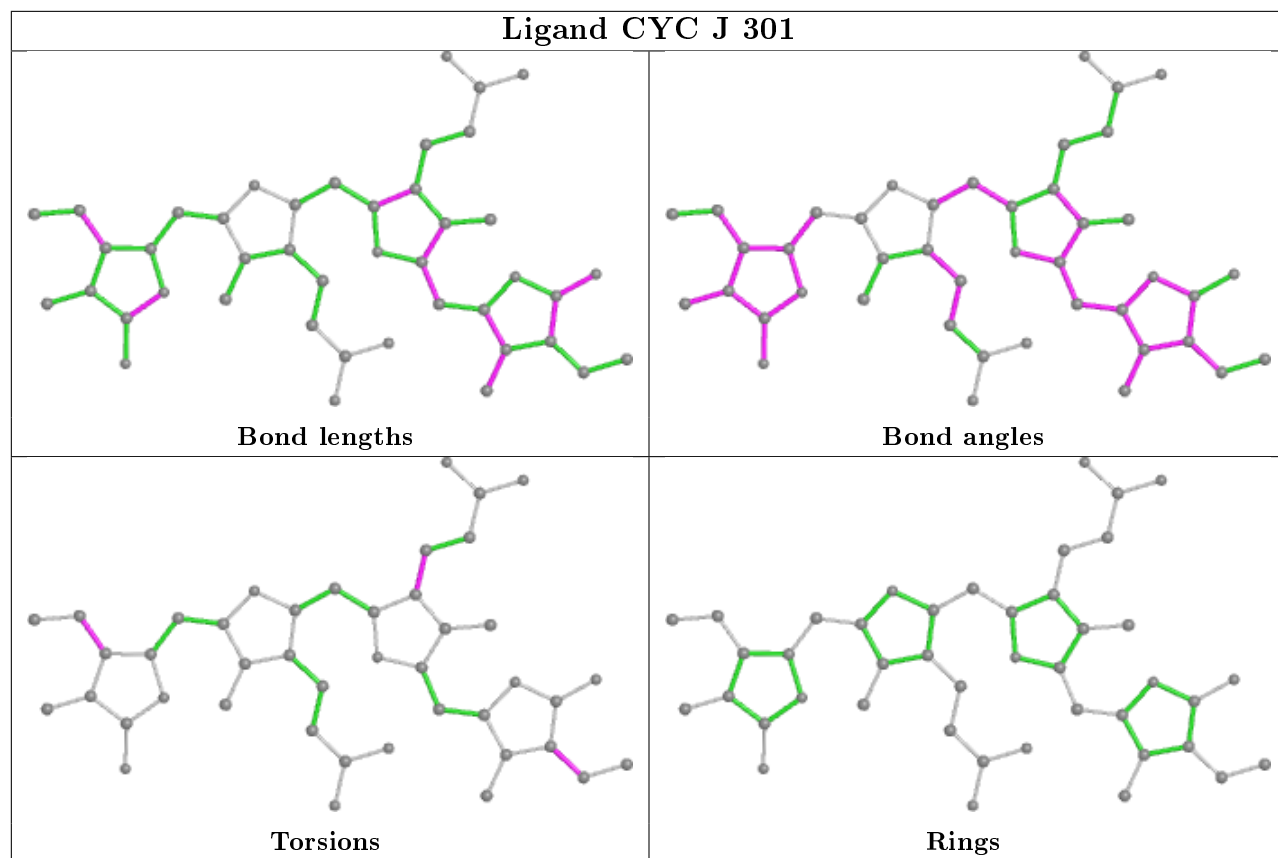
Ligand CYC F 301



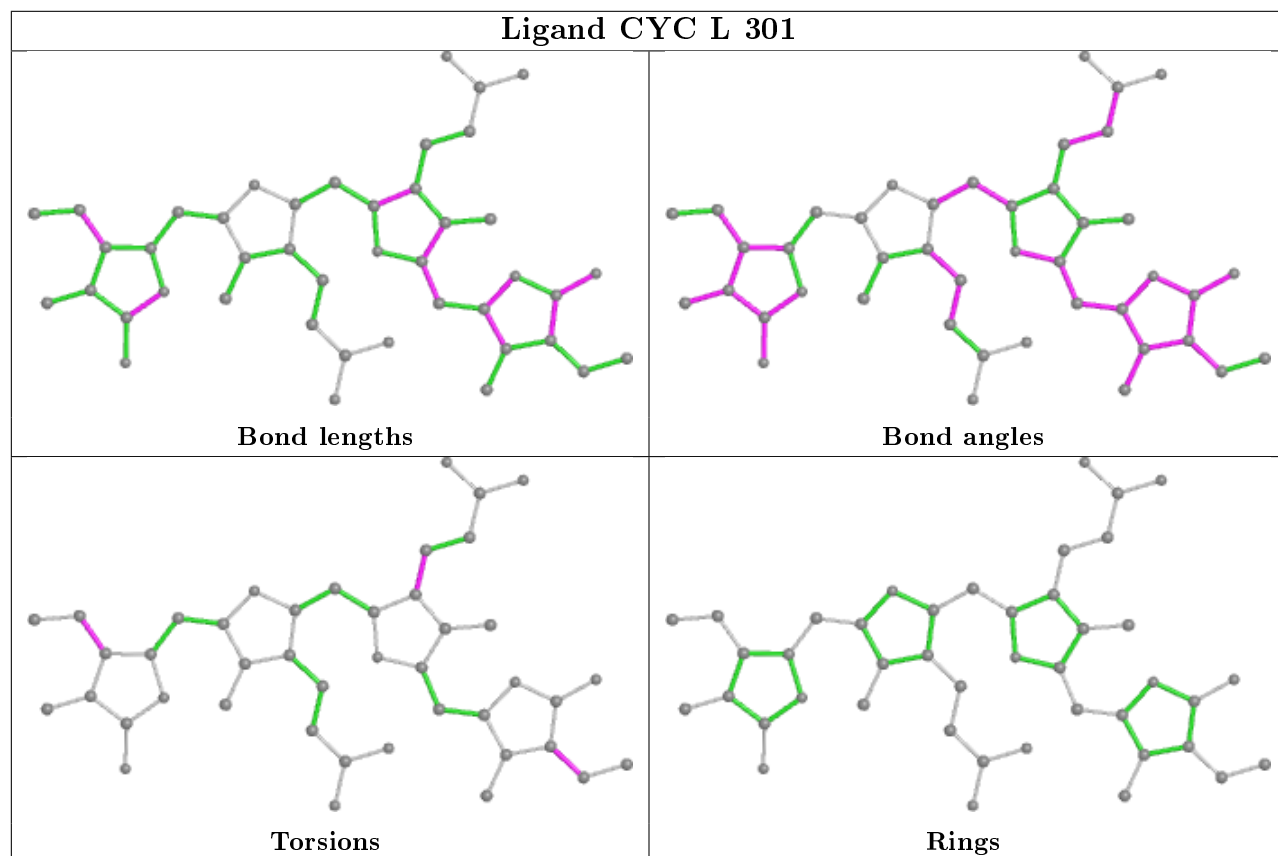
Ligand CYC H 301

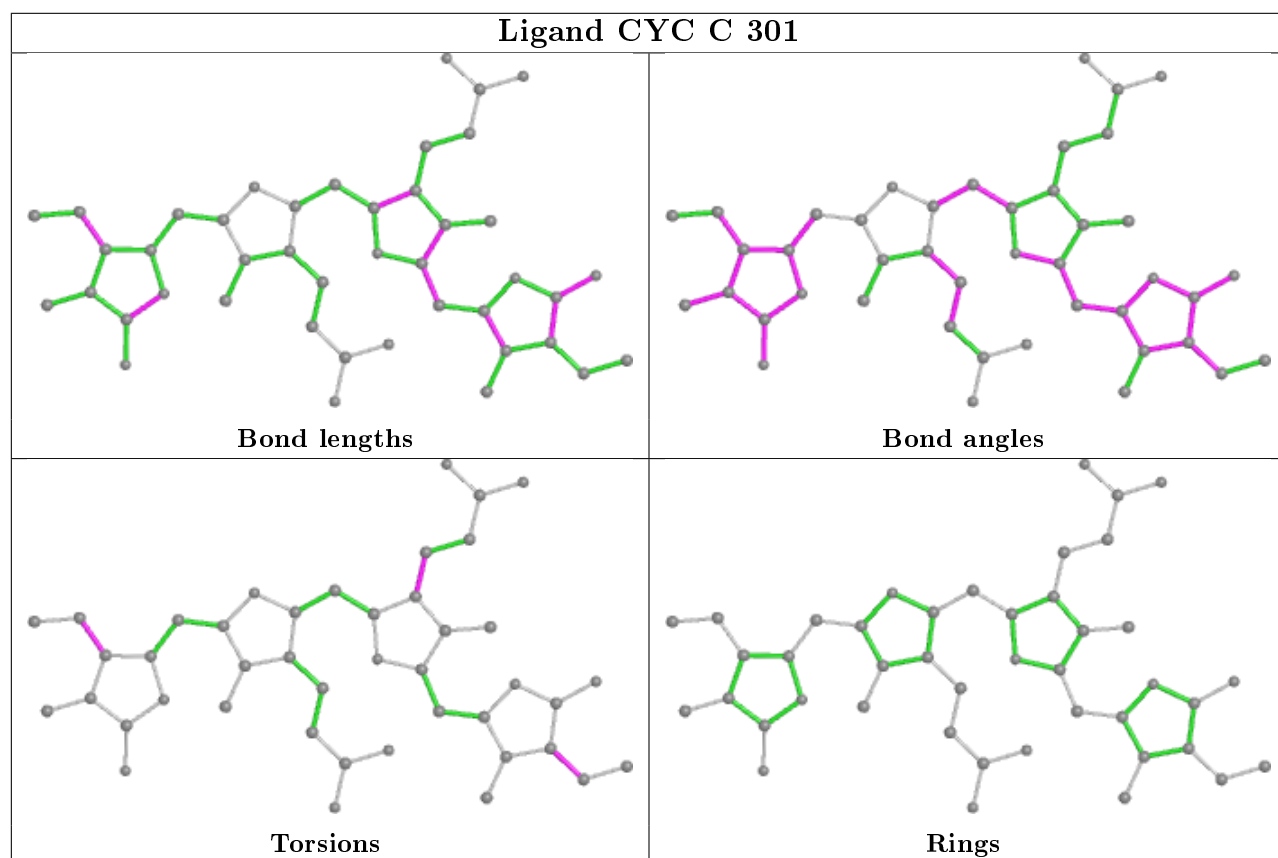
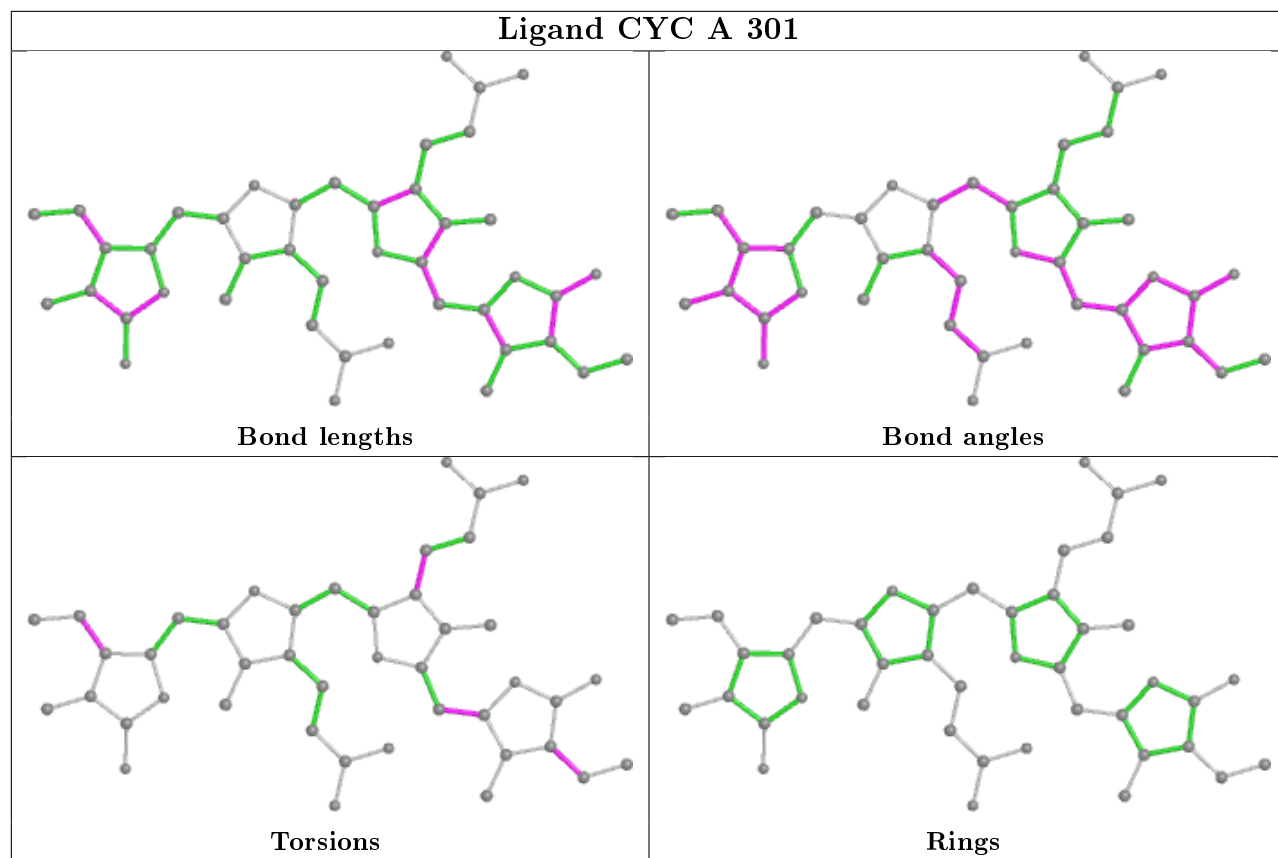


Ligand CYC J 301

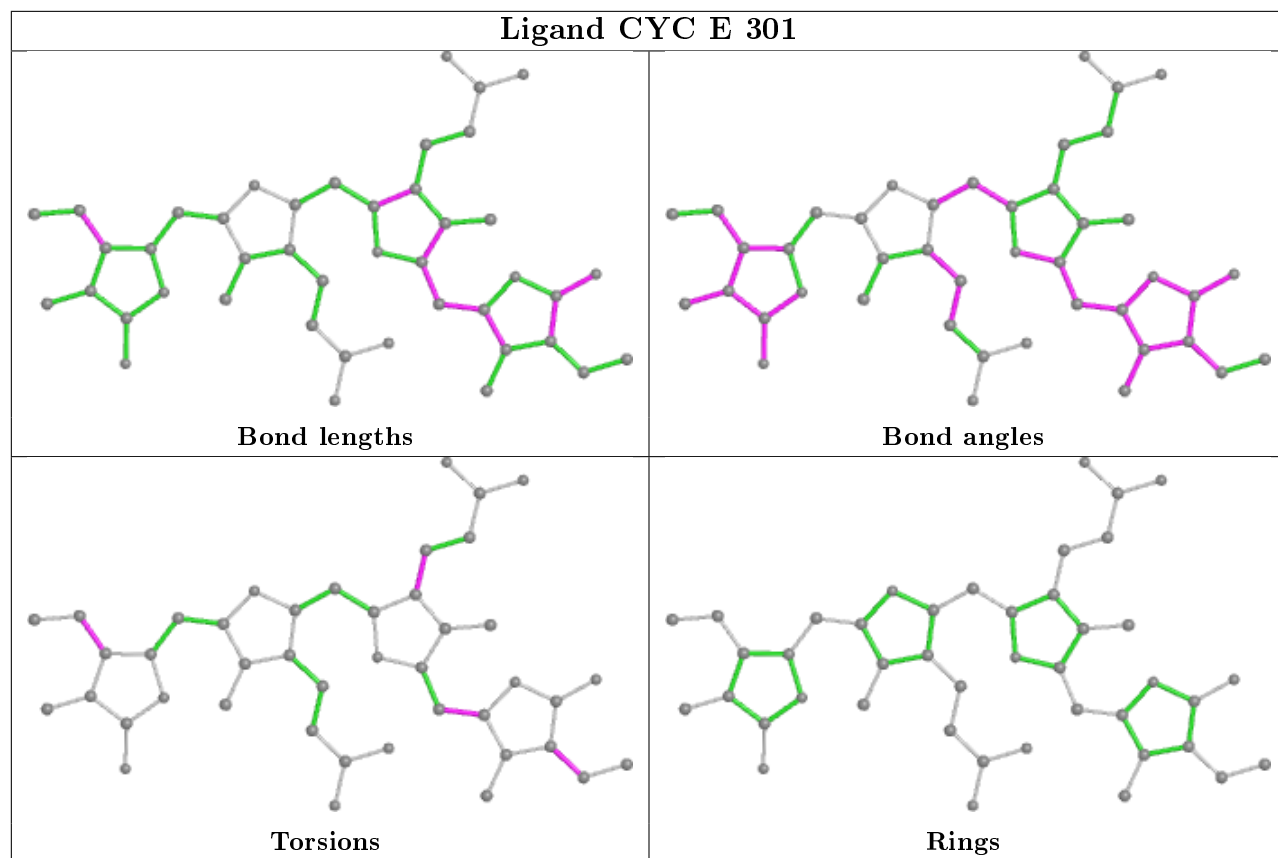


Ligand CYC L 301

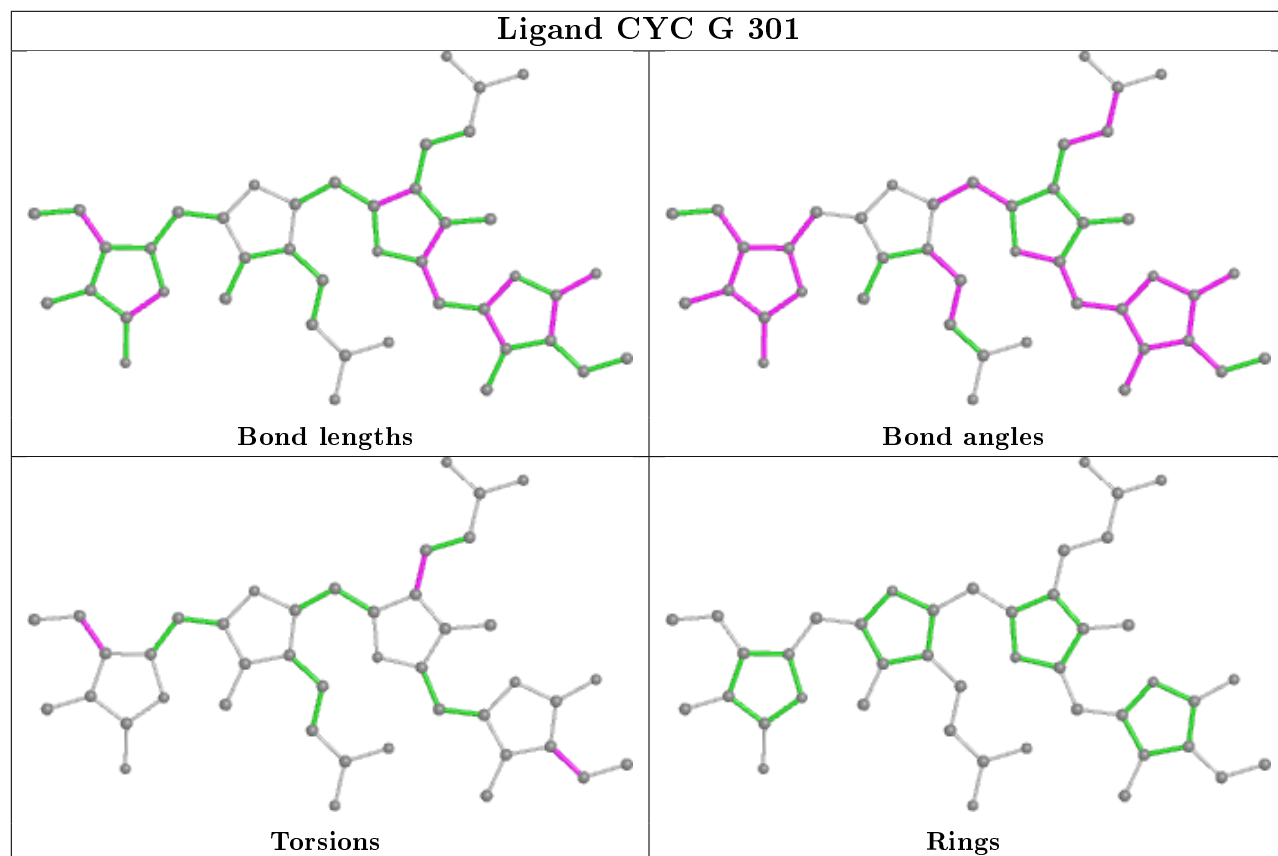


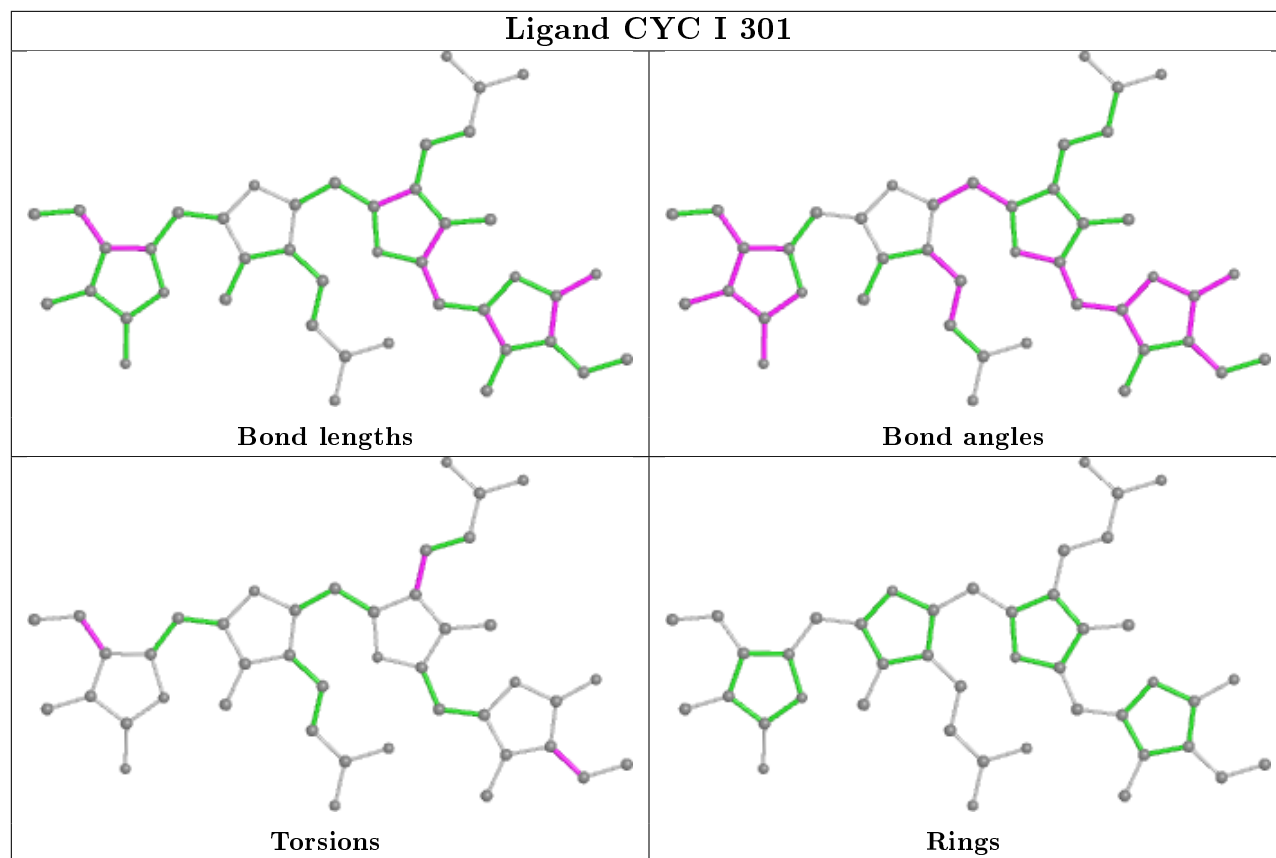


Ligand CYC E 301



Ligand CYC G 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 ⓘ

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	194/207 (93%)	-0.17	1 (0%) 91 91	38, 56, 94, 123	0
1	B	192/207 (92%)	-0.05	2 (1%) 82 84	37, 70, 104, 133	0
1	C	194/207 (93%)	-0.19	1 (0%) 91 91	36, 59, 93, 113	0
1	D	192/207 (92%)	-0.02	2 (1%) 82 84	35, 69, 102, 125	0
1	E	192/207 (92%)	-0.18	0 100 100	38, 57, 88, 117	0
1	F	192/207 (92%)	-0.17	2 (1%) 82 84	35, 69, 102, 124	0
1	G	194/207 (93%)	-0.16	2 (1%) 82 84	36, 57, 90, 122	0
1	H	192/207 (92%)	-0.15	2 (1%) 82 84	38, 69, 106, 128	0
1	I	192/207 (92%)	-0.11	1 (0%) 91 91	38, 59, 91, 121	0
1	J	192/207 (92%)	-0.00	3 (1%) 72 74	35, 69, 107, 120	0
1	K	192/207 (92%)	-0.20	1 (0%) 91 91	37, 57, 92, 121	0
1	L	192/207 (92%)	-0.13	3 (1%) 72 74	33, 68, 103, 129	0
All	All	2310/2484 (92%)	-0.13	20 (0%) 84 86	33, 63, 101, 133	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	THR	3.5
1	D	2	THR	3.4
1	J	12	ARG	3.3
1	F	154	ILE	2.8
1	J	2	THR	2.8
1	C	2	THR	2.7
1	G	143	GLY	2.7
1	H	46	LEU	2.6
1	L	194	VAL	2.6
1	I	192	ASP	2.4
1	F	12	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	143	GLY	2.3
1	D	136	GLY	2.3
1	K	2	THR	2.3
1	L	121	GLU	2.2
1	H	2	THR	2.2
1	G	105	LEU	2.2
1	B	2	THR	2.1
1	L	154	ILE	2.0
1	J	127	PHE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

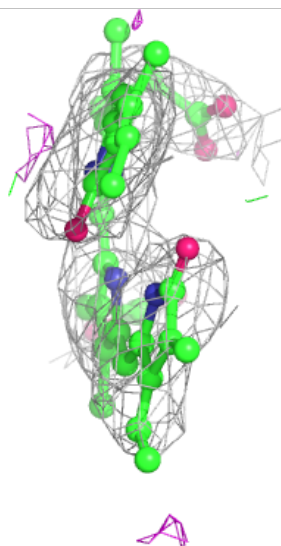
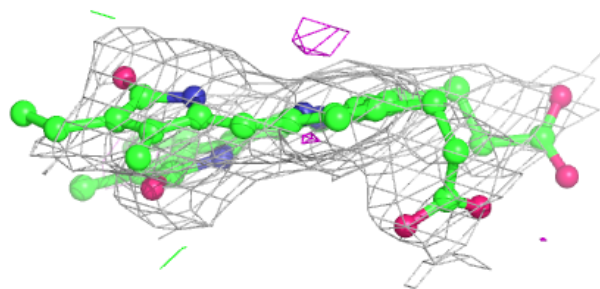
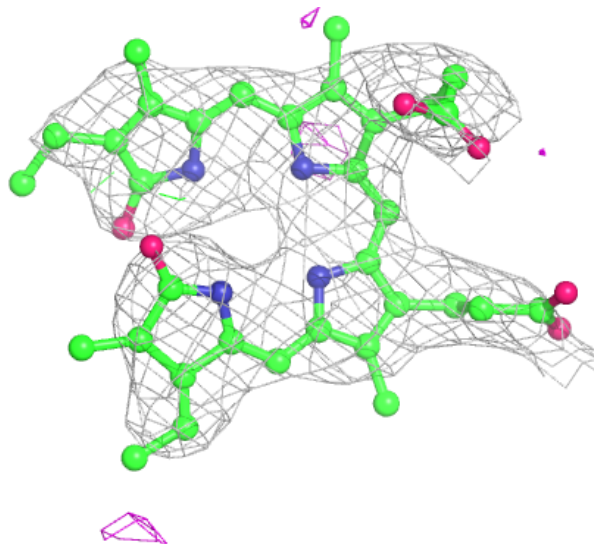
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CYC	G	301	43/43	0.89	0.28	65,92,100,105	0
2	CYC	E	301	43/43	0.90	0.24	64,80,100,111	0
2	CYC	A	301	43/43	0.90	0.25	47,79,95,103	0
2	CYC	C	301	43/43	0.91	0.23	52,81,92,93	0
2	CYC	L	301	43/43	0.91	0.19	53,74,91,98	0
2	CYC	K	301	43/43	0.91	0.25	38,80,98,102	0
2	CYC	J	301	43/43	0.92	0.17	41,63,82,91	0
2	CYC	H	301	43/43	0.92	0.20	49,75,118,120	0
2	CYC	I	301	43/43	0.92	0.22	68,81,93,97	0
2	CYC	D	301	43/43	0.93	0.16	63,74,117,119	0
2	CYC	F	301	43/43	0.93	0.18	49,68,81,87	0
2	CYC	B	301	43/43	0.94	0.18	52,70,108,111	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.

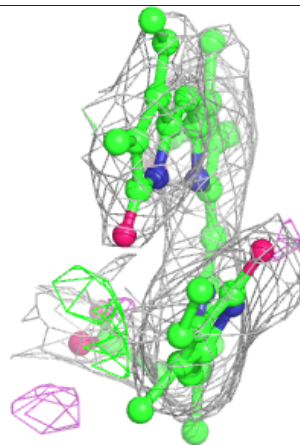
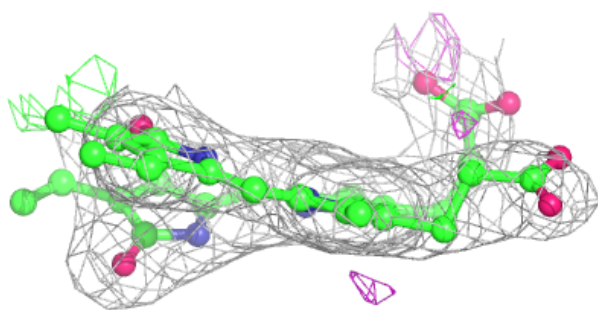
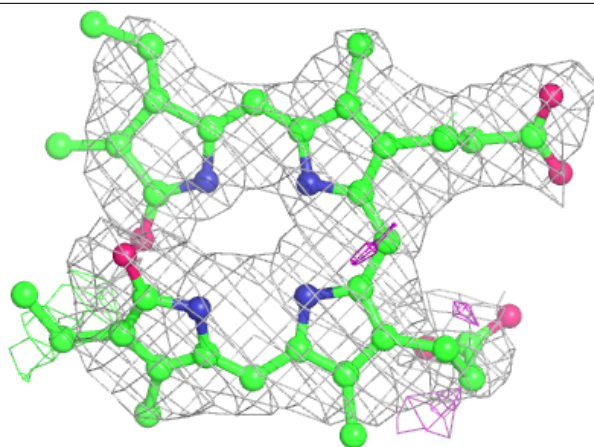
Electron density around CYC G 301:

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



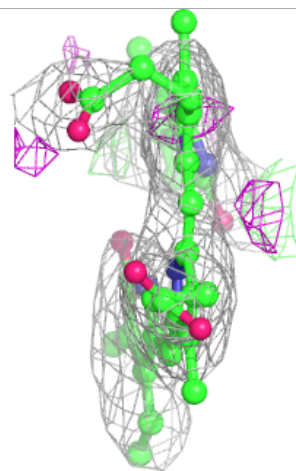
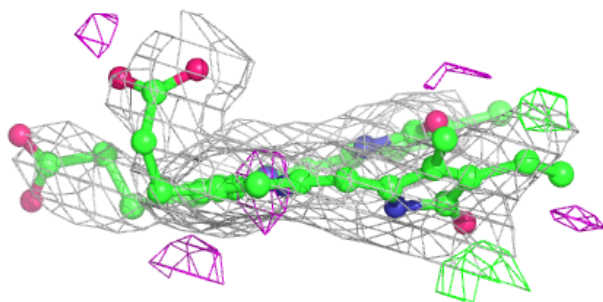
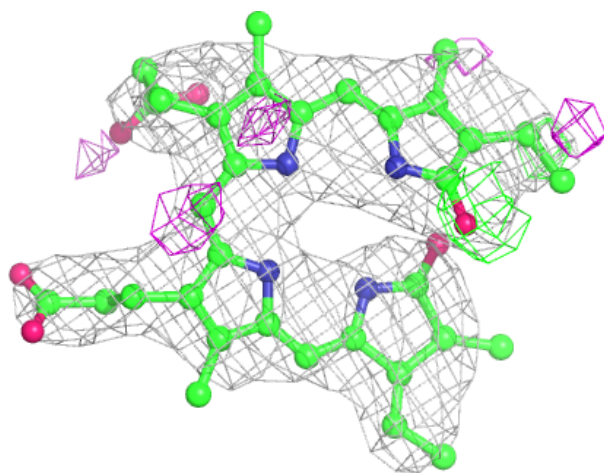
Electron density around CYC E 301:

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



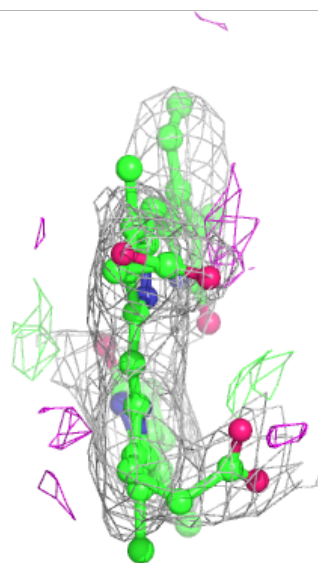
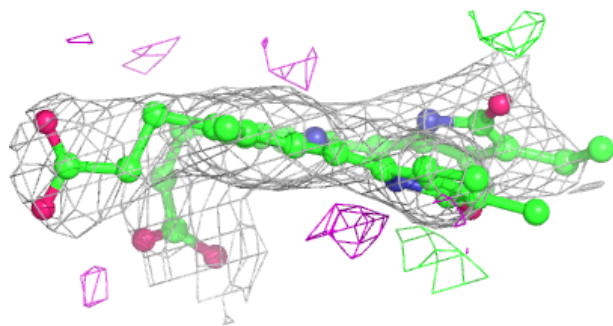
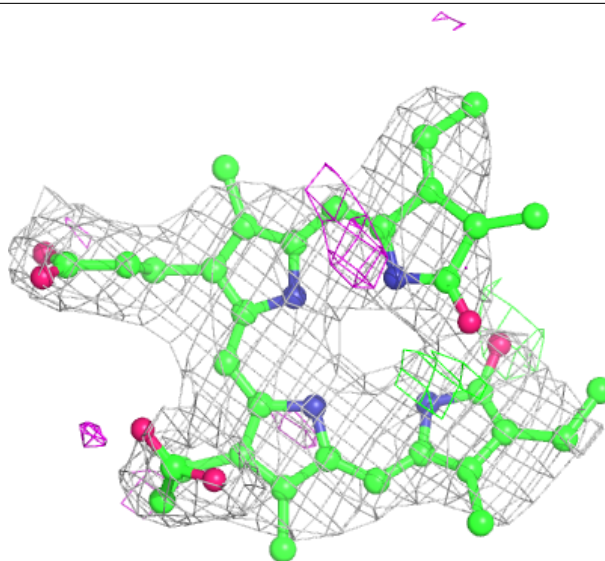
Electron density around CYC A 301:

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



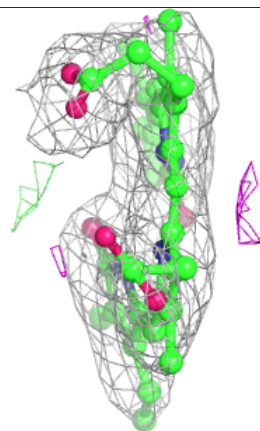
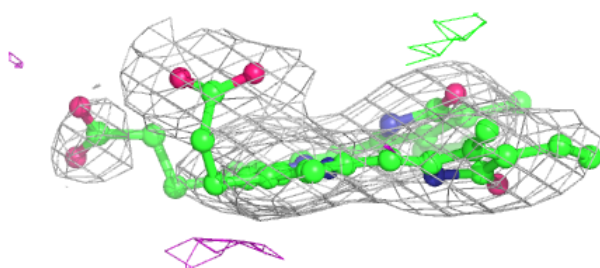
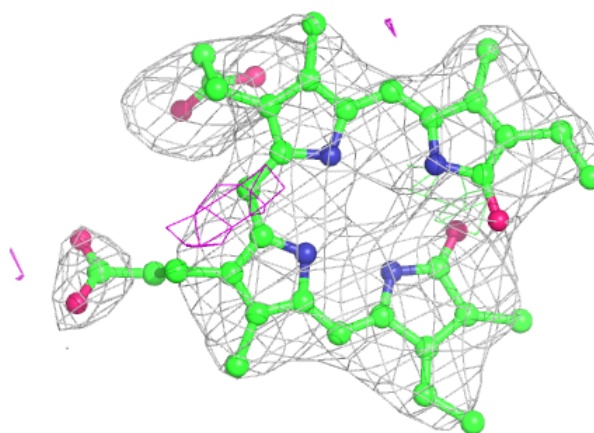
Electron density around CYC C 301:

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



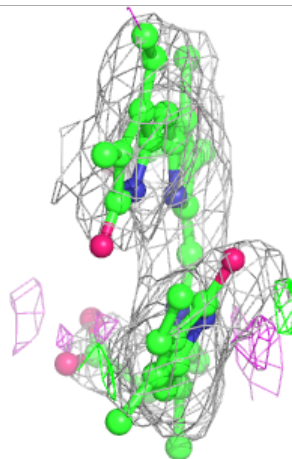
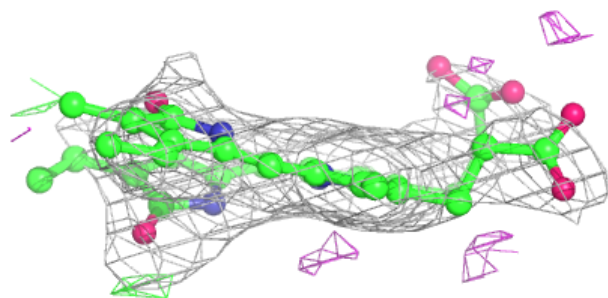
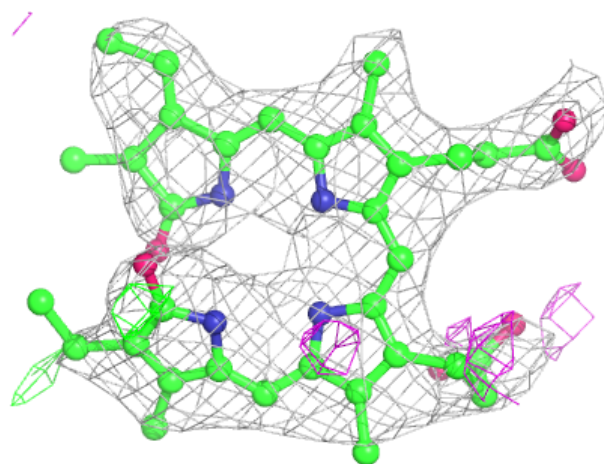
Electron density around CYC L 301:

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



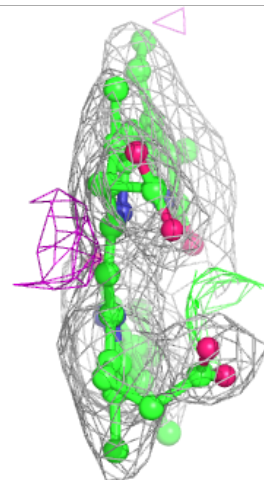
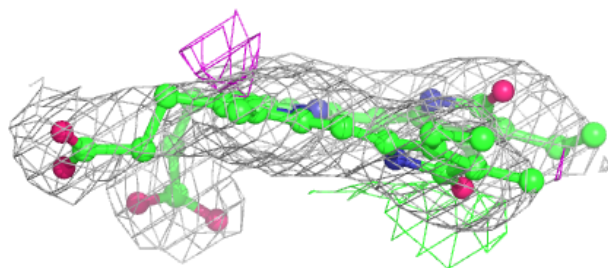
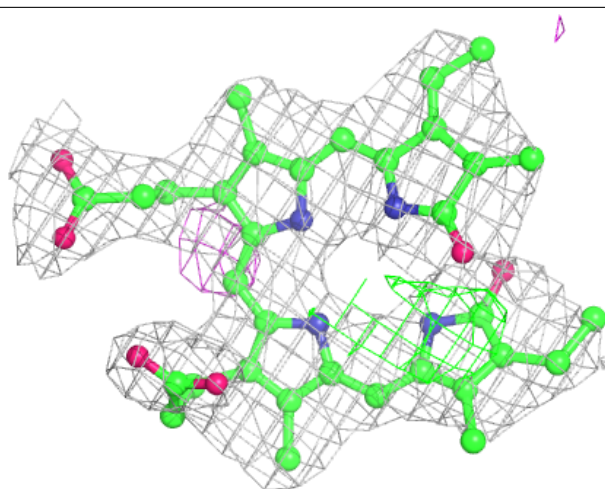
Electron density around CYC K 301:

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



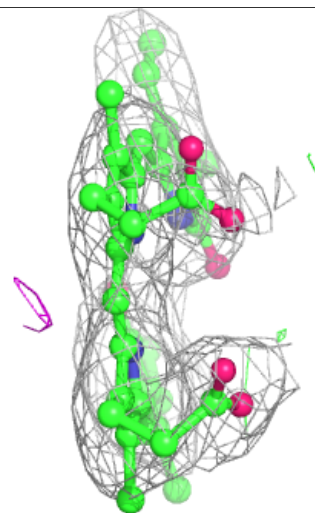
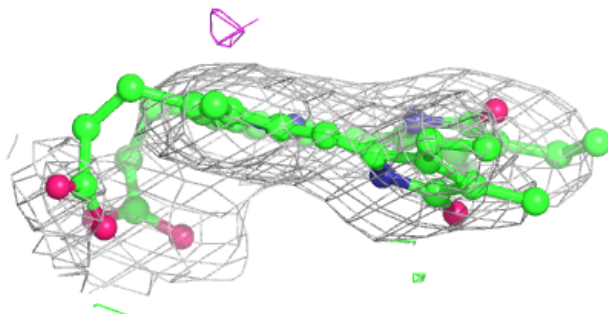
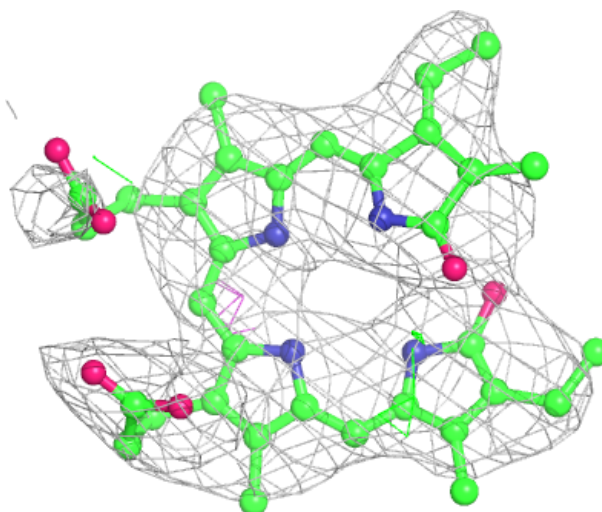
Electron density around CYC J 301:

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



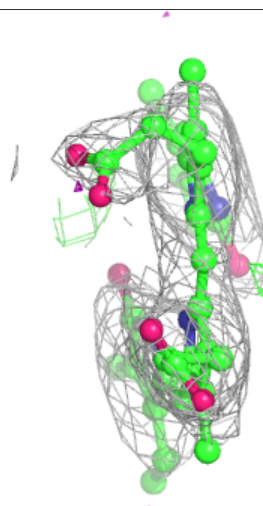
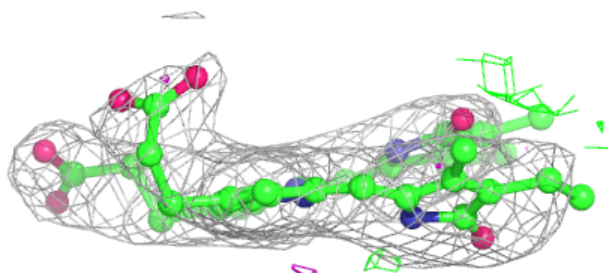
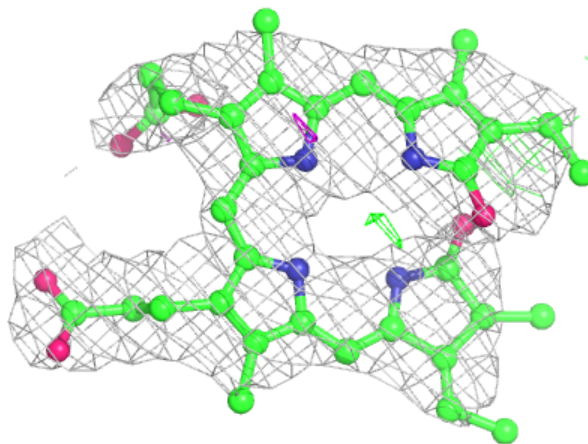
Electron density around CYC H 301:

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



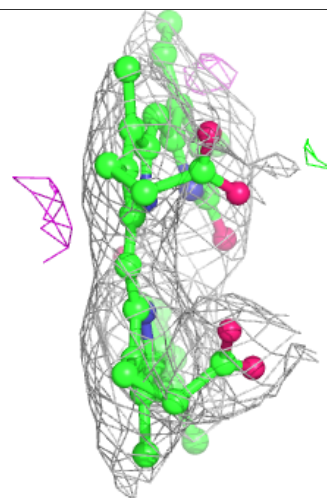
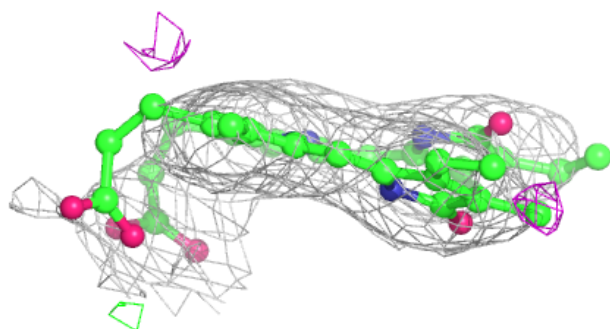
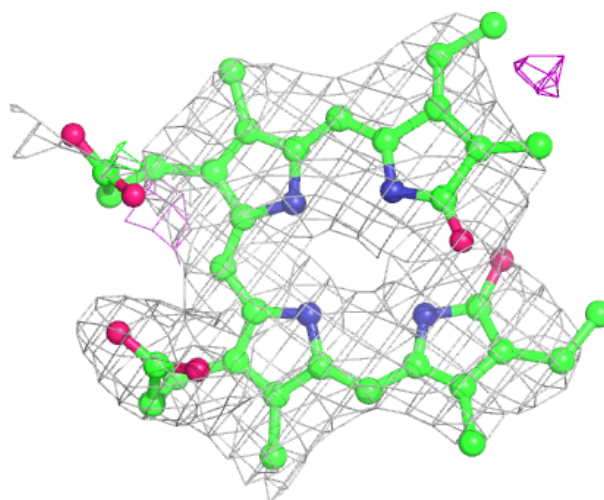
Electron density around CYC I 301:

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



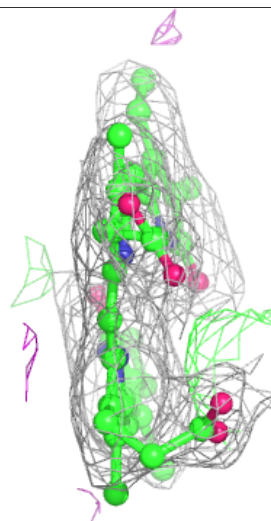
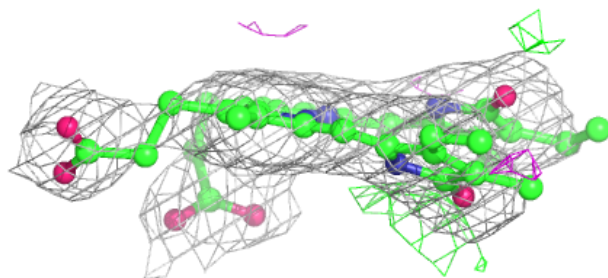
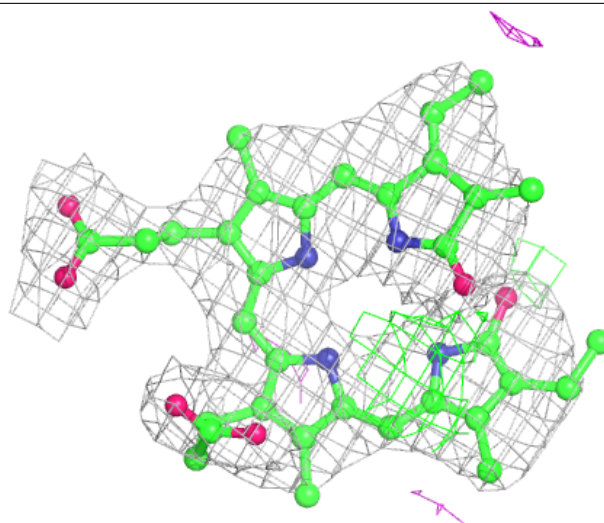
Electron density around CYC D 301:

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



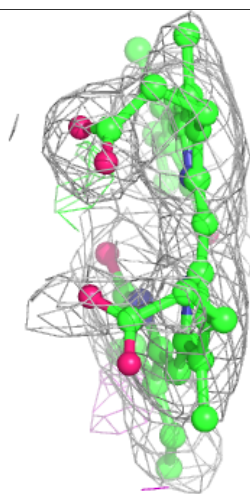
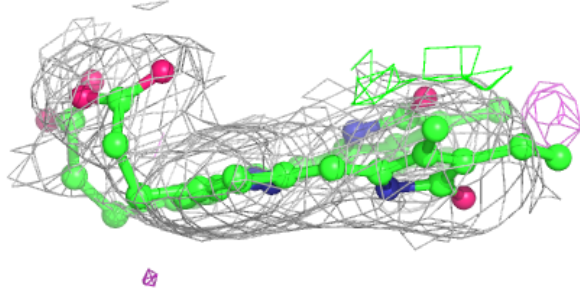
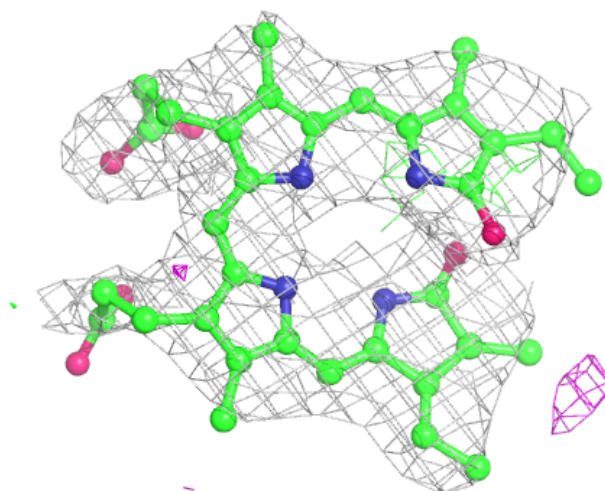
Electron density around CYC F 301:

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



Electron density around CYC 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.