



Full wwPDB EM Validation Report ⓘ

Nov 5, 2024 – 08:03 pm GMT

PDB ID : 7Z5J
EMDB ID : EMD-14522
Title : The molybdenum storage protein loaded with tungstate
Authors : Ermler, U.; Aziz, I.; Kaltwasser, S.; Kayastha, K.; Vonck, J.
Deposited on : 2022-03-09
Resolution : 2.58 Å(reported)
Based on initial model : 6RKE

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

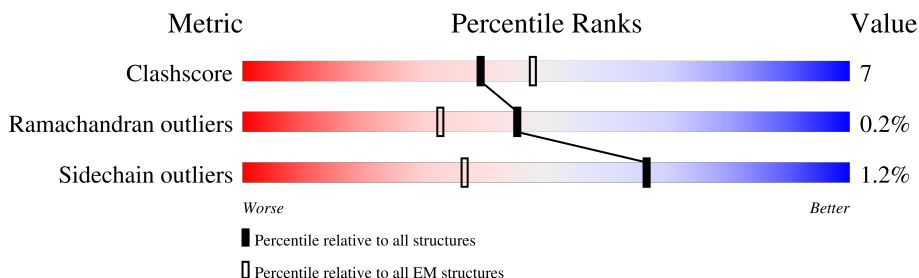
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY








The reported resolution of this entry is 2.58 Å.

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





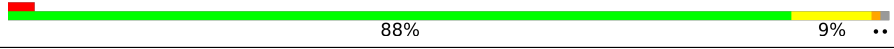

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	B	269	 80% 19% ..
1	D	269	 85% 13% ..
1	F	269	 84% 14% ..
1	H	269	 84% 14% ...
1	J	269	 83% 16% ..
1	L	269	 80% 18% ..
2	A	275	 84% 14% ..
2	C	275	 87% 11% ..

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Mol	Chain	Length	Quality of chain
2	E	275	 84% 14% .
2	G	275	 85% 13% .
2	I	275	 88% 9% ..
2	K	275	 88% 10% .

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
3	MOO	B	301	-	-	X	-
3	MOO	D	301	-	-	X	-
3	MOO	F	301	-	-	X	-
3	MOO	H	301	-	-	X	-
3	MOO	J	301	-	-	X	-
3	MOO	L	301	-	-	X	-

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 25576 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

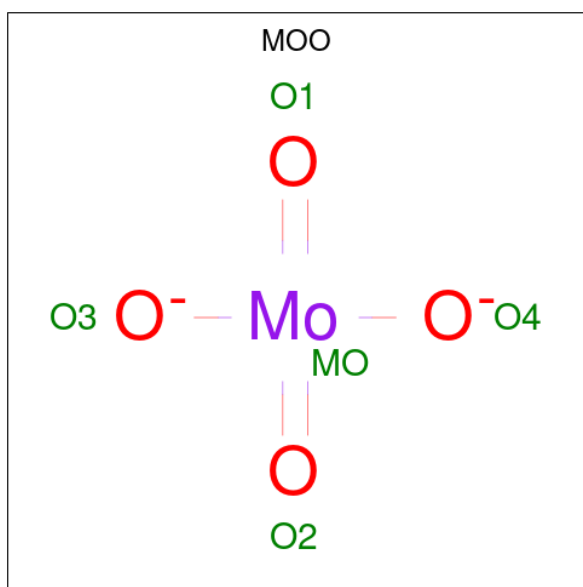
- Molecule 1 is a protein called Molybdenum storage protein subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	267	Total	C	N	O	S	4	0
			1986	1262	346	370	8		
1	D	267	Total	C	N	O	S	3	0
			1983	1260	346	369	8		
1	F	267	Total	C	N	O	S	3	0
			1983	1260	346	369	8		
1	H	267	Total	C	N	O	S	3	0
			1984	1261	346	369	8		
1	J	267	Total	C	N	O	S	3	0
			1983	1260	346	369	8		
1	L	267	Total	C	N	O	S	2	0
			1981	1259	346	368	8		

- Molecule 2 is a protein called Molybdenum storage protein subunit alpha.

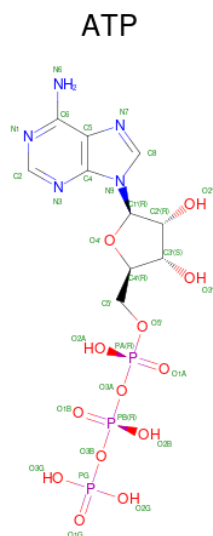
Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	272	Total	C	N	O	S	2	0
			2048	1292	386	367	3		
2	C	272	Total	C	N	O	S	3	0
			2059	1298	390	368	3		
2	E	272	Total	C	N	O	S	2	0
			2048	1292	386	367	3		
2	I	272	Total	C	N	O	S	2	0
			2048	1292	386	367	3		
2	G	272	Total	C	N	O	S	3	0
			2059	1298	390	368	3		
2	K	272	Total	C	N	O	S	2	0
			2048	1292	386	367	3		

- Molecule 3 is MOLYBDATE ION (three-letter code: MOO) (formula: MoO_4) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
3	B	1	Total	Mo	O	0
			5	1	4	
3	D	1	Total	Mo	O	0
			5	1	4	
3	F	1	Total	Mo	O	0
			5	1	4	
3	H	1	Total	Mo	O	0
			5	1	4	
3	J	1	Total	Mo	O	0
			5	1	4	
3	L	1	Total	Mo	O	0
			5	1	4	

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).

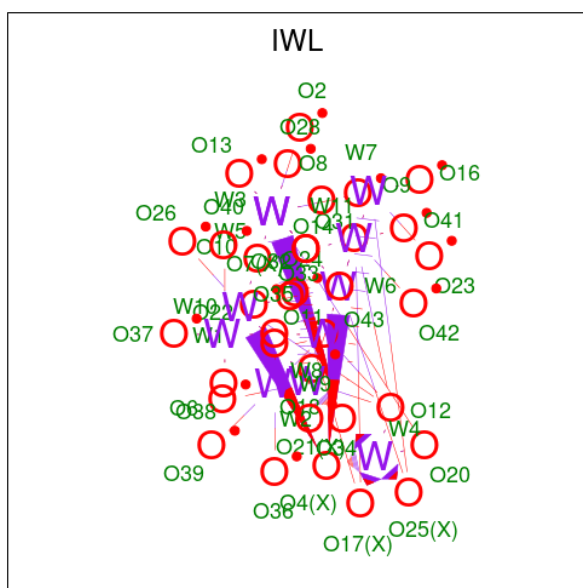


Mol	Chain	Residues	Atoms					AltConf
4	B	1	Total 31	C 10	N 5	O 13	P 3	0
4	A	1	Total 31	C 10	N 5	O 13	P 3	0
4	D	1	Total 31	C 10	N 5	O 13	P 3	0
4	C	1	Total 31	C 10	N 5	O 13	P 3	0
4	F	1	Total 31	C 10	N 5	O 13	P 3	0
4	E	1	Total 31	C 10	N 5	O 13	P 3	0
4	H	1	Total 31	C 10	N 5	O 13	P 3	0
4	I	1	Total 31	C 10	N 5	O 13	P 3	0
4	J	1	Total 31	C 10	N 5	O 13	P 3	0
4	G	1	Total 31	C 10	N 5	O 13	P 3	0
4	L	1	Total 31	C 10	N 5	O 13	P 3	0
4	K	1	Total 31	C 10	N 5	O 13	P 3	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

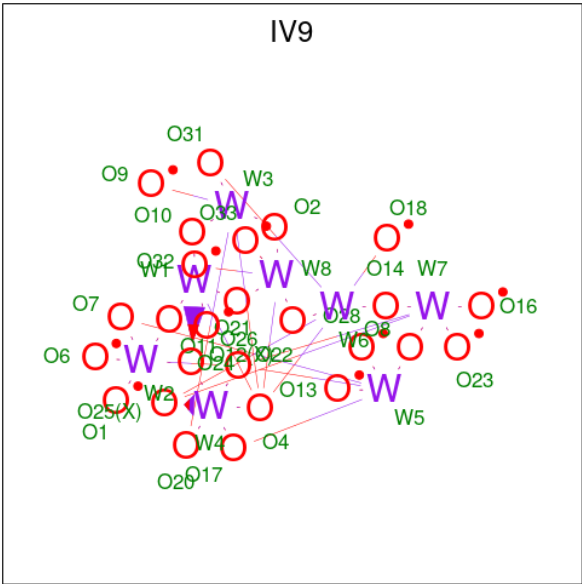
Mol	Chain	Residues	Atoms		AltConf
5	B	1	Total 1	Mg 1	0
5	A	1	Total 1	Mg 1	0
5	D	1	Total 1	Mg 1	0
5	C	1	Total 1	Mg 1	0
5	F	1	Total 1	Mg 1	0
5	E	1	Total 1	Mg 1	0
5	H	1	Total 1	Mg 1	0
5	I	1	Total 1	Mg 1	0
5	J	1	Total 1	Mg 1	0
5	G	1	Total 1	Mg 1	0
5	L	1	Total 1	Mg 1	0
5	K	1	Total 1	Mg 1	0

- Molecule 6 is W11-O35 cluster (three-letter code: IWL) (formula: $\text{O}_{35}\text{W}_{11}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
6	B	1	Total	O	W	0
			46	35	11	
6	D	1	Total	O	W	0
			46	35	11	
6	F	1	Total	O	W	0
			46	35	11	
6	H	1	Total	O	W	0
			46	35	11	
6	J	1	Total	O	W	0
			46	35	11	
6	L	1	Total	O	W	0
			46	35	11	

- Molecule 7 is 1,1,3,3,5,7,7,9,11,15,15-undecakis($\text{1}^{\{1\}}$ -oxidanyl)-2 $\text{1}^{\{4\}}$,4 $\text{1}^{\{3\}}$,6 $\text{1}^{\{5\}}$,8,10,12,14,16,17,18,19 $\text{1}^{\{3\}}$,20,21,22,23-pentadecaoxa-1 $\text{1}^{\{6\}}$,3 $\text{1}^{\{6\}}$,5 $\text{1}^{\{6\}}$,7 $\text{1}^{\{6\}}$,9 $\text{1}^{\{6\}}$,11 $\text{1}^{\{6\}}$,13 $\text{1}^{\{6\}}$,15 $\text{1}^{\{6\}}$ -octatungstapentadecacyclo[7.7.1.1 $^{\{1,13\}}$.1 $^{\{3,5\}}$.1 $^{\{3,15\}}$.1 $^{\{5,7\}}$.1 $^{\{5,11\}}$.1 $^{\{7,11\}}$.0 $^{\{2,13\}}$.0 $^{\{2,15\}}$.0 $^{\{4,13\}}$.0 $^{\{6,9\}}$.0 $^{\{6,11\}}$.0 $^{\{6,13\}}$.0 $^{\{9,19\}}$]tricosane (three-letter code: IV9) (formula: O_{26}W_8) (labeled as "Ligand of Interest" by depositor).



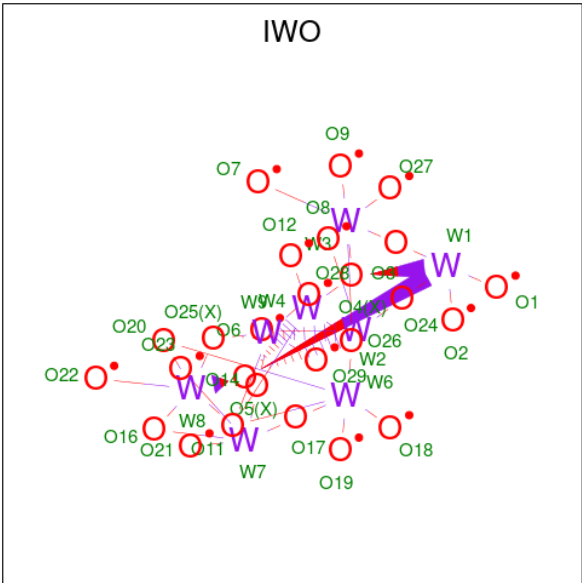
Mol	Chain	Residues	Atoms			AltConf
7	A	1	Total	O	W	0
			34	26	8	
7	C	1	Total	O	W	0
			34	26	8	
7	E	1	Total	O	W	0
			34	26	8	

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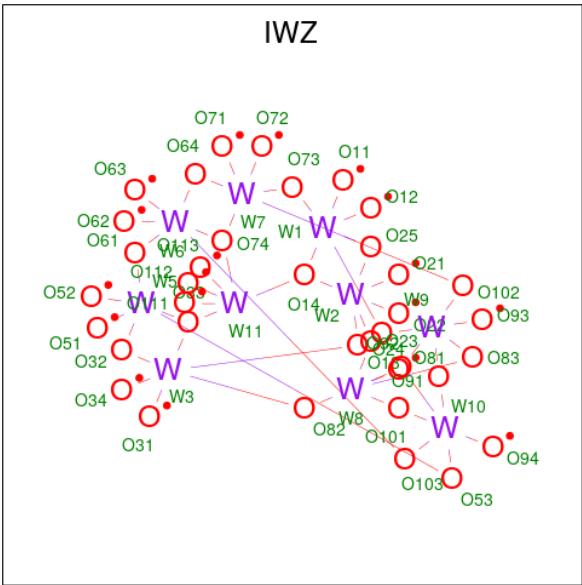
Mol	Chain	Residues	Atoms			AltConf
			Total	O	W	
7	I	1	34	26	8	0
7	G	1	34	26	8	0
7	K	1	34	26	8	0

- Molecule 8 is W8-O26 cluster (three-letter code: IWO) (formula: $O_{26}W_8$) (labeled as "Ligand of Interest" by depositor).



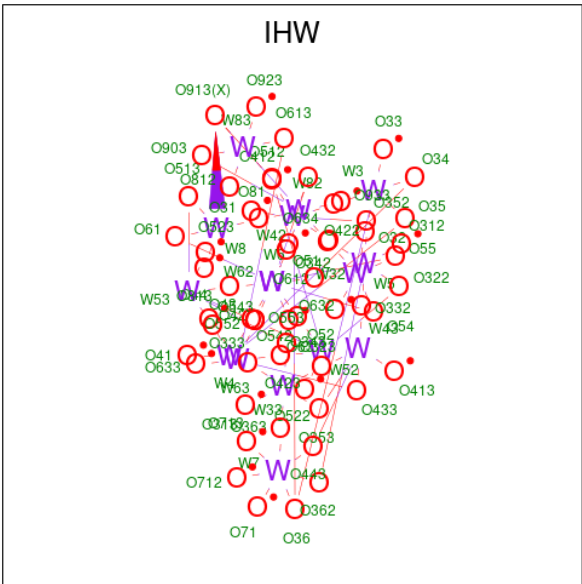
Mol	Chain	Residues	Atoms			AltConf
			Total	O	W	
8	A	1	34	26	8	0
8	C	1	34	26	8	0
8	E	1	34	26	8	0
8	I	1	34	26	8	0
8	G	1	34	26	8	0
8	K	1	34	26	8	0

- Molecule 9 is W10-O37 cluster (three-letter code: IWZ) (formula: $O_{37}W_{10}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
9	C	1	Total	O	W	0
			47	37	10	
9	K	1	Total	O	W	0
			47	37	10	

- Molecule 10 is tungstate cluster (three-letter code: IHW) (formula: $O_{58}W_{16}$) (labeled as "Ligand of Interest" by depositor).



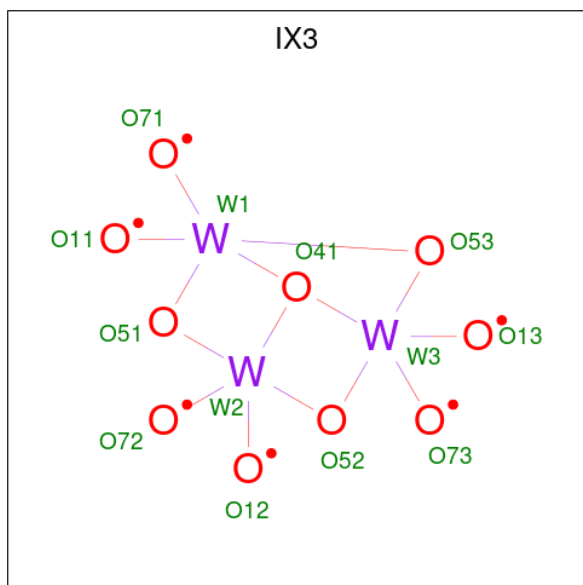
Mol	Chain	Residues	Atoms			AltConf
10	F	1	Total	O	W	0
			74	58	16	

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Mol	Chain	Residues	Atoms			AltConf
10	L	1	Total	O	W	0
			74	58	16	

- Molecule 11 is W3-O10 cluster (three-letter code: IX3) (formula: $O_{10}W_3$) (labeled as "Ligand of Interest" by depositor).

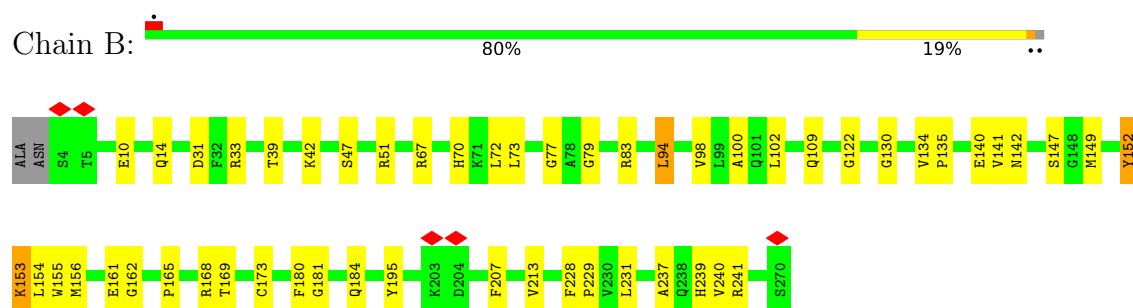


Mol	Chain	Residues	Atoms			AltConf
11	E	1	Total	O	W	0
			13	10	3	
11	I	1	Total	O	W	0
			13	10	3	

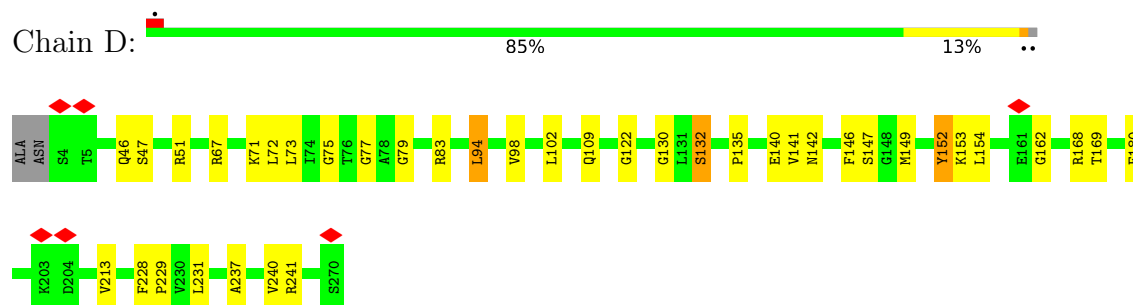
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

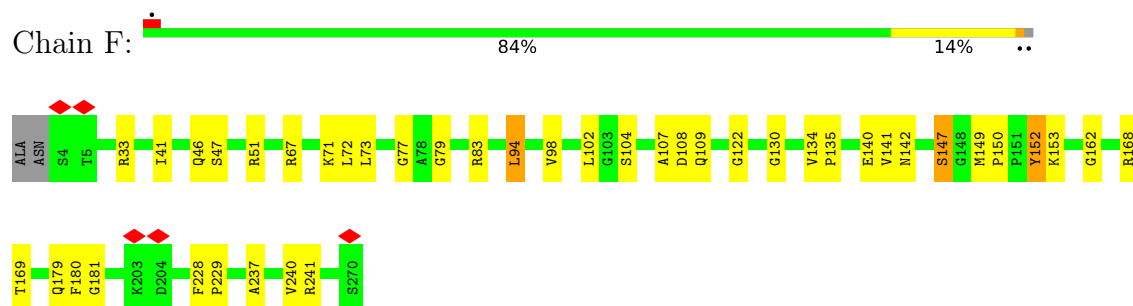
- Molecule 1: Molybdenum storage protein subunit beta



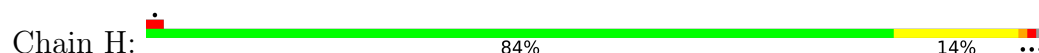
- Molecule 1: Molybdenum storage protein subunit beta

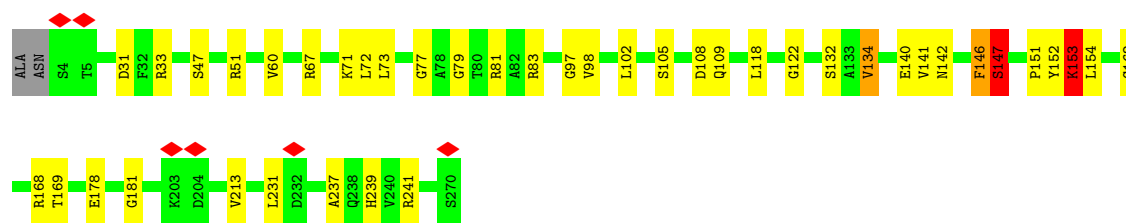


- Molecule 1: Molybdenum storage protein subunit beta

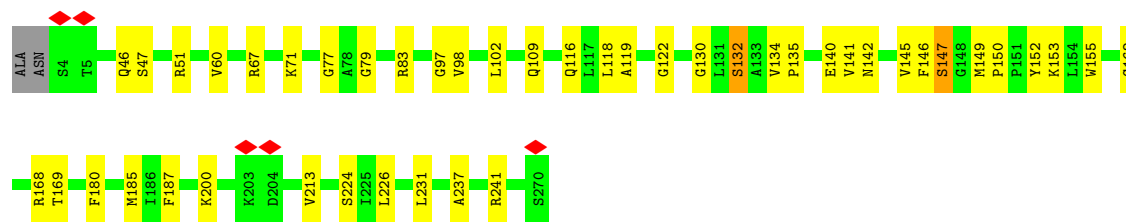
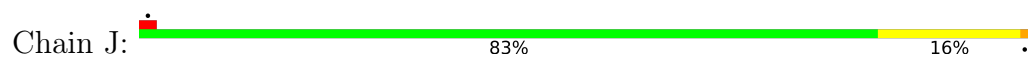


- Molecule 1: Molybdenum storage protein subunit beta

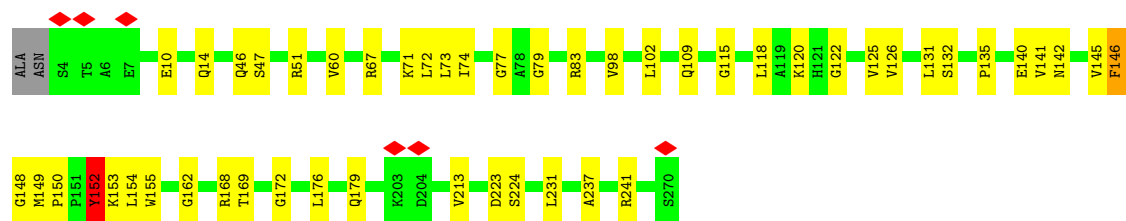
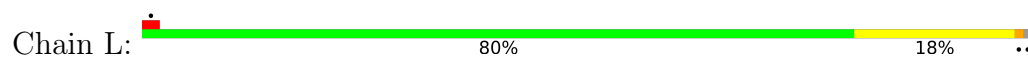




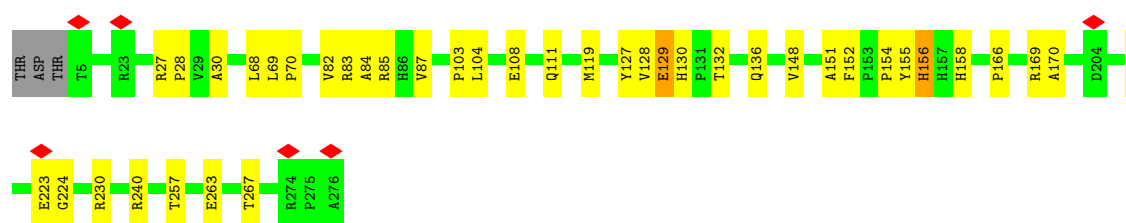
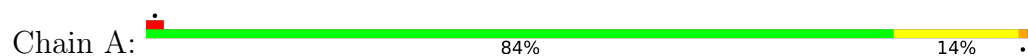
- Molecule 1: Molybdenum storage protein subunit beta



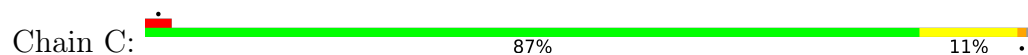
- Molecule 1: Molybdenum storage protein subunit beta



- Molecule 2: Molybdenum storage protein subunit alpha



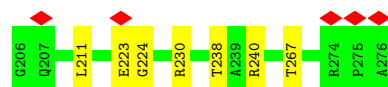
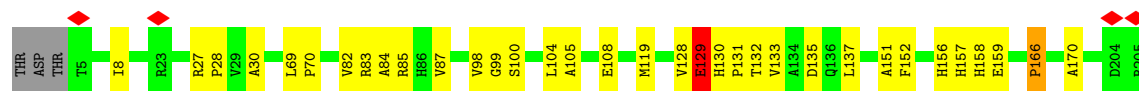
- Molecule 2: Molybdenum storage protein subunit alpha





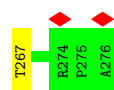
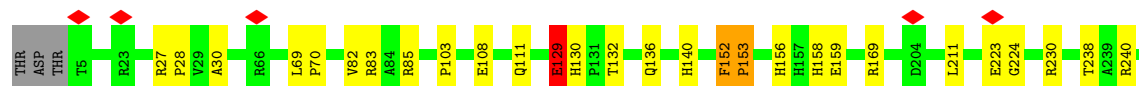
- Molecule 2: Molybdenum storage protein subunit alpha

Chain E: 84% 14%



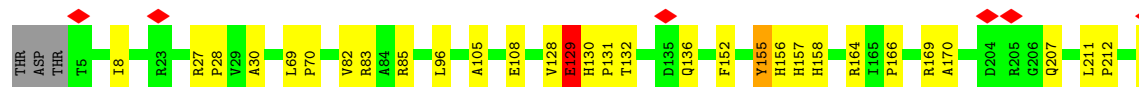
- Molecule 2: Molybdenum storage protein subunit alpha

Chain I: 88% 9%



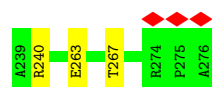
- Molecule 2: Molybdenum storage protein subunit alpha

Chain G: 85% 13%



- Molecule 2: Molybdenum storage protein subunit alpha

Chain K: 88% 10%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D3	Depositor
Number of particles used	674283	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42.6	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2100	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.066	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0082	Depositor
Map size (Å)	232.68, 232.68, 232.68	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.831, 0.831, 0.831	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MOO, IWZ, IX3, IV9, IWO, ATP, MG, IHW, IWL

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	B	0.86	3/2034 (0.1%)	0.65	2/2763 (0.1%)
1	D	0.88	3/2028 (0.1%)	0.65	2/2755 (0.1%)
1	F	0.90	4/2028 (0.2%)	0.61	2/2755 (0.1%)
1	H	0.87	1/2028 (0.0%)	0.64	4/2755 (0.1%)
1	J	0.81	0/2028	0.59	3/2755 (0.1%)
1	L	0.83	0/2022	0.64	3/2747 (0.1%)
2	A	0.89	0/2097	0.59	0/2857
2	C	0.96	3/2108 (0.1%)	0.64	2/2871 (0.1%)
2	E	0.98	4/2097 (0.2%)	0.86	8/2857 (0.3%)
2	G	0.88	1/2108 (0.0%)	0.60	0/2871
2	I	0.89	1/2097 (0.0%)	0.62	0/2857
2	K	0.88	0/2097	0.60	2/2857 (0.1%)
All	All	0.89	20/24772 (0.1%)	0.64	28/33700 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1
1	F	0	1
1	H	0	1
1	L	0	2
2	C	0	1
2	G	0	1
2	I	0	2
2	K	0	1
All	All	0	10

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	166	PRO	N-CA	12.65	1.68	1.47
2	E	166	PRO	N-CA	11.92	1.67	1.47
1	D	149	MET	C-N	10.54	1.54	1.34
1	F	134	VAL	C-N	10.34	1.53	1.34
1	B	147	SER	CA-CB	-10.20	1.37	1.52
2	E	130	HIS	C-N	9.03	1.51	1.34
2	E	166	PRO	C-N	8.77	1.50	1.34
1	H	134	VAL	C-N	8.70	1.50	1.34
1	B	149	MET	C-N	8.61	1.50	1.34
2	C	130	HIS	C-N	8.51	1.50	1.34
1	F	149	MET	C-N	8.51	1.50	1.34
2	I	153	PRO	C-N	8.20	1.49	1.34
1	D	94	LEU	C-N	8.16	1.49	1.34
1	F	94	LEU	C-N	8.15	1.49	1.34
1	B	94	LEU	C-N	8.10	1.49	1.34
1	D	147	SER	CA-CB	-7.97	1.41	1.52
1	F	147	SER	CA-CB	-7.45	1.41	1.52
2	C	165	ILE	C-N	5.44	1.44	1.34
2	G	155	TYR	C-N	-5.30	1.21	1.34
2	E	135	ASP	C-N	-5.28	1.22	1.34

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	128	VAL	O-C-N	17.02	149.94	122.70
2	E	128	VAL	C-N-CA	-16.82	79.66	121.70
2	E	128	VAL	CA-C-N	-12.05	90.69	117.20
2	E	130	HIS	N-CA-CB	10.29	129.12	110.60
1	L	147	SER	CA-C-O	8.36	137.66	120.10
2	E	130	HIS	CB-CA-C	-7.90	94.60	110.40
1	H	108	ASP	CB-CA-C	-7.76	94.87	110.40
2	E	166	PRO	N-CA-C	-7.70	92.09	112.10
2	K	129	GLU	CB-CA-C	7.65	125.70	110.40
2	K	129	GLU	N-CA-CB	-7.29	97.47	110.60
2	E	129	GLU	O-C-N	6.54	133.17	122.70
1	D	147	SER	CB-CA-C	6.23	121.94	110.10
2	C	166	PRO	CA-N-CD	-5.86	103.30	111.50
1	B	152	TYR	CB-CA-C	-5.74	98.92	110.40
1	J	147	SER	CA-C-N	-5.73	104.73	116.20
2	E	130	HIS	CA-C-N	5.72	133.11	117.10
1	L	147	SER	CA-C-N	-5.61	104.98	116.20
1	L	152	TYR	CB-CA-C	-5.58	99.24	110.40
1	D	152	TYR	CB-CA-C	-5.54	99.32	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	147	SER	CA-C-O	5.52	131.69	120.10
1	J	145	VAL	O-C-N	5.50	131.50	122.70
1	H	147	SER	CA-C-N	-5.46	105.27	116.20
1	F	147	SER	N-CA-CB	5.43	118.64	110.50
2	C	166	PRO	N-CA-C	-5.25	98.45	112.10
1	H	146	PHE	C-N-CA	-5.24	108.60	121.70
1	H	147	SER	O-C-N	-5.17	114.42	123.20
1	B	152	TYR	O-C-N	5.13	130.91	122.70
1	F	152	TYR	CB-CA-C	-5.01	100.39	110.40

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	127	TYR	Mainchain
1	D	152	TYR	Mainchain
1	F	152	TYR	Mainchain
2	G	129	GLU	Mainchain
1	H	147	SER	Mainchain
2	I	129	GLU	Mainchain
2	I	169	ARG	Sidechain
2	K	127	TYR	Mainchain
1	L	152	TYR	Mainchain
1	L	153	LYS	Mainchain

5.2 Too-close contacts [i](#)

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	B	1986	0	2046	32	0
1	D	1983	0	2041	28	0
1	F	1983	0	2041	30	0
1	H	1984	0	2045	30	0
1	J	1983	0	2041	38	0
1	L	1981	0	2040	44	0
2	A	2048	0	2105	28	0
2	C	2059	0	2117	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	2048	0	2105	30	0
2	G	2059	0	2116	25	0
2	I	2048	0	2105	22	0
2	K	2048	0	2105	23	0
3	B	5	0	0	4	0
3	D	5	0	0	5	0
3	F	5	0	0	6	0
3	H	5	0	0	7	0
3	J	5	0	0	6	0
3	L	5	0	0	6	0
4	A	31	0	12	1	0
4	B	31	0	12	0	0
4	C	31	0	12	1	0
4	D	31	0	12	1	0
4	E	31	0	12	2	0
4	F	31	0	12	1	0
4	G	31	0	12	1	0
4	H	31	0	12	1	0
4	I	31	0	12	2	0
4	J	31	0	12	2	0
4	K	31	0	12	2	0
4	L	31	0	12	1	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	0	0
5	H	1	0	0	0	0
5	I	1	0	0	0	0
5	J	1	0	0	0	0
5	K	1	0	0	0	0
5	L	1	0	0	0	0
6	B	46	0	0	0	0
6	D	46	0	0	0	0
6	F	46	0	0	0	0
6	H	46	0	0	0	0
6	J	46	0	0	0	0
6	L	46	0	0	0	0
7	A	34	0	0	0	0
7	C	34	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	E	34	0	0	0	0
7	G	34	0	0	0	0
7	I	34	0	0	0	0
7	K	34	0	0	0	0
8	A	34	0	0	1	0
8	C	34	0	0	0	0
8	E	34	0	0	0	0
8	G	34	0	0	0	0
8	I	34	0	0	0	0
8	K	34	0	0	0	0
9	C	47	0	0	0	0
9	K	47	0	0	0	0
10	F	74	0	0	0	0
10	L	74	0	0	0	0
11	E	13	0	0	0	0
11	I	13	0	0	0	0
All	All	25576	0	25051	351	0

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

All (351) 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:C:166:PRO:N	2:C:166:PRO:CA	1.68	1.32
2:E:166:PRO:N	2:E:166:PRO:CA	1.67	1.29
1:J:185:MET:HE2	1:J:187:PHE:CZ	1.83	1.13
1:J:185:MET:CE	1:J:187:PHE:CZ	2.47	0.96
1:B:130:GLY:HA3	1:B:180:PHE:CZ	2.05	0.92
2:K:129:GLU:OE2	2:K:129:GLU:HA	1.70	0.90
2:A:127:TYR:HE1	2:A:129:GLU:OE1	1.56	0.88
1:F:130:GLY:HA3	1:F:180:PHE:CZ	2.12	0.84
2:E:166:PRO:N	2:E:166:PRO:C	2.30	0.84
2:C:224:GLY:O	2:C:230:ARG:NH2	2.13	0.82
1:J:130:GLY:HA3	1:J:180:PHE:CZ	2.15	0.82
2:G:166:PRO:O	2:G:169:ARG:NH1	2.14	0.80
1:D:130:GLY:HA3	1:D:180:PHE:CZ	2.18	0.79
2:G:129:GLU:OE2	2:G:129:GLU:HA	1.82	0.78
2:A:166:PRO:O	2:A:169:ARG:NH1	2.16	0.78
1:B:195:TYR:CE1	1:B:207:PHE:HD1	2.03	0.76
2:I:129:GLU:HA	2:I:129:GLU:OE2	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:33:ARG:NH1	1:H:181:GLY:O	2.21	0.74
1:F:33:ARG:NH1	1:F:181:GLY:O	2.22	0.73
1:D:168:ARG:NE	3:D:301:MOO:O2	2.18	0.71
2:E:129:GLU:O	2:E:132:THR:HB	1.90	0.71
2:C:166:PRO:N	2:C:166:PRO:C	2.43	0.71
1:B:33:ARG:NH1	1:B:181:GLY:O	2.24	0.70
1:J:200:LYS:HE3	4:J:302:ATP:O3'	1.92	0.69
1:J:185:MET:CE	1:J:187:PHE:CE2	2.75	0.69
2:A:224:GLY:O	2:A:230:ARG:NH2	2.25	0.69
1:D:75:GLY:HA2	1:D:146:PHE:O	1.92	0.69
2:E:224:GLY:O	2:E:230:ARG:NH2	2.27	0.68
2:K:263:GLU:OE1	2:K:263:GLU:N	2.27	0.68
1:J:109:GLN:NE2	2:K:108:GLU:OE1	2.27	0.67
1:J:185:MET:HE3	1:J:187:PHE:CE2	2.29	0.67
2:I:108:GLU:OE1	1:L:109:GLN:NE2	2.28	0.66
1:J:224:SER:OG	1:J:226:LEU:O	2.12	0.66
1:H:146:PHE:CD2	1:H:147:SER:O	2.49	0.65
3:F:301:MOO:MO	3:F:301:MOO:O1	1.68	0.65
2:G:224:GLY:O	2:G:230:ARG:NH2	2.28	0.65
2:I:224:GLY:O	2:I:230:ARG:NH2	2.29	0.65
3:B:301:MOO:O1	3:B:301:MOO:MO	1.68	0.65
3:D:301:MOO:O1	3:D:301:MOO:MO	1.68	0.65
3:J:301:MOO:O3	3:J:301:MOO:MO	1.68	0.65
3:D:301:MOO:MO	3:D:301:MOO:O3	1.68	0.64
3:H:301:MOO:MO	3:H:301:MOO:O1	1.68	0.64
3:L:301:MOO:MO	3:L:301:MOO:O3	1.69	0.64
2:A:119:MET:SD	1:F:94:LEU:HD21	2.37	0.63
2:G:223:GLU:N	2:G:223:GLU:OE1	2.31	0.63
3:L:301:MOO:MO	3:L:301:MOO:O1	1.68	0.63
2:A:83:ARG:NE	2:A:108:GLU:OE2	2.31	0.63
3:H:301:MOO:MO	3:H:301:MOO:O4	1.70	0.63
3:B:301:MOO:MO	3:B:301:MOO:O3	1.69	0.63
3:B:301:MOO:MO	3:B:301:MOO:O4	1.70	0.63
3:J:301:MOO:MO	3:J:301:MOO:O1	1.68	0.63
3:F:301:MOO:MO	3:F:301:MOO:O3	1.69	0.63
1:L:155:TRP:CH2	2:K:130:HIS:HB3	2.34	0.62
1:F:79:GLY:O	1:F:83:ARG:NH1	2.32	0.62
1:J:237:ALA:O	1:J:241:ARG:NH1	2.32	0.62
3:L:301:MOO:MO	3:L:301:MOO:O2	1.70	0.62
1:H:237:ALA:O	1:H:241:ARG:NH1	2.32	0.62
3:D:301:MOO:O2	3:D:301:MOO:MO	1.70	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:223:GLU:N	2:C:223:GLU:OE1	2.32	0.62
2:A:263:GLU:OE1	2:A:263:GLU:N	2.33	0.62
2:C:83:ARG:NE	2:C:108:GLU:OE2	2.32	0.62
1:F:71:LYS:HG2	1:F:142:ASN:OD1	1.99	0.62
3:H:301:MOO:MO	3:H:301:MOO:O3	1.69	0.62
3:J:301:MOO:MO	3:J:301:MOO:O4	1.70	0.62
3:D:301:MOO:MO	3:D:301:MOO:O4	1.70	0.61
3:J:301:MOO:MO	3:J:301:MOO:O2	1.70	0.61
3:F:301:MOO:MO	3:F:301:MOO:O4	1.70	0.61
3:F:301:MOO:MO	3:F:301:MOO:O2	1.70	0.61
1:L:71:LYS:HG2	1:L:142:ASN:OD1	1.99	0.61
1:B:165:PRO:O	1:B:168:ARG:NH2	2.29	0.61
2:E:238:THR:O	2:E:240:ARG:NH1	2.33	0.61
1:H:79:GLY:O	1:H:83:ARG:NH1	2.34	0.61
3:B:301:MOO:MO	3:B:301:MOO:O2	1.70	0.61
2:I:103:PRO:HD3	2:I:156:HIS:HB3	1.82	0.61
1:D:79:GLY:O	1:D:83:ARG:NH1	2.34	0.61
2:E:83:ARG:NE	2:E:108:GLU:OE2	2.30	0.61
3:L:301:MOO:MO	3:L:301:MOO:O4	1.70	0.61
2:I:238:THR:O	2:I:240:ARG:NH1	2.33	0.61
2:G:238:THR:O	2:G:240:ARG:NH1	2.34	0.60
3:H:301:MOO:MO	3:H:301:MOO:O2	1.71	0.60
1:H:146:PHE:HD2	1:H:147:SER:O	1.84	0.60
1:F:237:ALA:O	1:F:241:ARG:NH1	2.34	0.60
1:L:146:PHE:CD1	1:L:146:PHE:N	2.70	0.60
1:L:74:ILE:C	1:L:146:PHE:HE1	2.04	0.60
1:L:146:PHE:CE2	1:L:176:LEU:HD22	2.38	0.59
1:F:122:GLY:O	1:F:141:VAL:HG13	2.02	0.59
1:L:67:ARG:O	1:L:142:ASN:ND2	2.34	0.59
2:I:83:ARG:NE	2:I:108:GLU:OE2	2.35	0.59
2:G:83:ARG:NE	2:G:108:GLU:OE2	2.32	0.59
1:B:237:ALA:O	1:B:241:ARG:NH1	2.36	0.58
1:F:107:ALA:HB1	1:F:147:SER:HB2	1.85	0.58
1:J:168:ARG:NE	3:J:301:MOO:O2	2.31	0.58
1:B:70:HIS:O	1:B:142:ASN:ND2	2.37	0.58
1:J:122:GLY:O	1:J:141:VAL:HG13	2.04	0.58
1:L:74:ILE:C	1:L:146:PHE:CE1	2.77	0.58
2:C:127:TYR:HE1	2:C:129:GLU:OE2	1.87	0.57
1:D:122:GLY:O	1:D:141:VAL:HG13	2.04	0.57
2:I:223:GLU:N	2:I:223:GLU:OE1	2.37	0.57
2:K:224:GLY:O	2:K:230:ARG:NH2	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:152:PHE:CE1	2:E:170:ALA:HB2	2.40	0.57
1:D:47:SER:O	1:D:51:ARG:NE	2.36	0.57
1:F:104:SER:O	1:F:108:ASP:OD1	2.23	0.56
1:H:71:LYS:HG3	1:H:142:ASN:OD1	2.05	0.56
2:K:238:THR:O	2:K:240:ARG:NH1	2.38	0.56
1:B:67:ARG:NH1	1:B:140:GLU:O	2.38	0.56
1:D:154:LEU:O	1:D:154:LEU:HG	2.05	0.56
1:J:79:GLY:O	1:J:83:ARG:NH1	2.38	0.56
1:J:185:MET:CE	1:J:187:PHE:CE1	2.87	0.56
1:L:79:GLY:O	1:L:83:ARG:NH1	2.38	0.56
1:F:67:ARG:NH1	1:F:140:GLU:O	2.37	0.56
1:J:116:GLN:HG2	1:L:131:LEU:HD11	1.86	0.56
1:B:79:GLY:O	1:B:83:ARG:NH1	2.38	0.56
1:F:77:GLY:HA2	1:F:169:THR:HG21	1.88	0.56
1:L:168:ARG:NE	3:L:301:MOO:O3	2.35	0.56
1:F:67:ARG:O	1:F:142:ASN:ND2	2.38	0.55
1:D:237:ALA:O	1:D:241:ARG:NH1	2.38	0.55
1:L:74:ILE:O	1:L:146:PHE:CD1	2.59	0.55
1:H:152:TYR:O	1:H:154:LEU:N	2.40	0.55
1:J:47:SER:O	1:J:51:ARG:NE	2.35	0.55
1:L:146:PHE:N	1:L:146:PHE:HD1	2.05	0.55
1:B:77:GLY:HA2	1:B:169:THR:HG21	1.89	0.54
1:H:77:GLY:HA2	1:H:169:THR:HG21	1.90	0.54
1:J:98:VAL:O	1:J:102:LEU:HG	2.08	0.54
2:K:83:ARG:NE	2:K:108:GLU:OE2	2.33	0.54
1:J:155:TRP:O	2:G:155:TYR:OH	2.20	0.54
2:I:159:GLU:HA	2:I:159:GLU:OE1	2.07	0.54
1:B:47:SER:O	1:B:51:ARG:NE	2.37	0.53
2:G:152:PHE:CE1	2:G:170:ALA:HB2	2.44	0.53
1:B:98:VAL:O	1:B:102:LEU:HG	2.09	0.53
1:H:168:ARG:NE	3:H:301:MOO:O2	2.37	0.53
1:D:94:LEU:HD21	2:E:119:MET:SD	2.48	0.53
2:E:159:GLU:OE1	2:E:159:GLU:HA	2.07	0.53
1:D:109:GLN:OE1	2:E:104:LEU:O	2.26	0.53
1:F:168:ARG:NE	3:F:301:MOO:O3	2.35	0.53
1:F:98:VAL:O	1:F:102:LEU:HG	2.09	0.53
1:F:130:GLY:HA3	1:F:180:PHE:CE2	2.43	0.53
2:C:129:GLU:HB3	2:C:131:PRO:HD2	1.91	0.53
1:B:195:TYR:CE1	1:B:207:PHE:CD1	2.93	0.52
2:A:127:TYR:CE1	2:A:129:GLU:OE1	2.48	0.52
1:L:98:VAL:O	1:L:102:LEU:HG	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:162:GLY:O	2:G:240:ARG:NH2	2.39	0.52
1:L:237:ALA:O	1:L:241:ARG:NH1	2.43	0.52
2:I:103:PRO:HA	2:I:156:HIS:HD2	1.74	0.52
1:L:122:GLY:O	1:L:141:VAL:HG13	2.08	0.52
1:B:122:GLY:O	1:B:141:VAL:HG13	2.10	0.52
2:A:130:HIS:CE1	2:A:152:PHE:O	2.63	0.52
2:C:85:ARG:NH2	4:C:302:ATP:O1A	2.42	0.52
1:B:162:GLY:O	2:A:240:ARG:NH2	2.38	0.52
1:H:122:GLY:O	1:H:141:VAL:HG13	2.09	0.52
1:D:98:VAL:O	1:D:102:LEU:HG	2.10	0.52
1:H:72:LEU:C	1:H:73:LEU:HD12	2.30	0.52
2:K:152:PHE:CE1	2:K:170:ALA:HB2	2.46	0.51
2:A:85:ARG:NH2	4:A:302:ATP:O1A	2.42	0.51
1:D:71:LYS:HG2	1:D:142:ASN:OD1	2.10	0.51
2:A:130:HIS:HE1	2:A:152:PHE:O	1.94	0.51
1:B:72:LEU:C	1:B:73:LEU:HD12	2.30	0.51
1:H:98:VAL:O	1:H:102:LEU:HG	2.11	0.51
1:B:31:ASP:OD1	1:B:239:HIS:NE2	2.44	0.51
2:E:152:PHE:HE1	2:E:170:ALA:HB2	1.76	0.50
1:B:94:LEU:HD21	2:C:119:MET:SD	2.51	0.50
1:H:67:ARG:O	1:H:142:ASN:ND2	2.45	0.50
2:I:129:GLU:OE2	2:I:129:GLU:CA	2.57	0.50
2:E:98:VAL:HG23	2:E:166:PRO:N	2.26	0.50
1:D:77:GLY:HA2	1:D:169:THR:HG21	1.94	0.50
2:A:104:LEU:O	1:F:109:GLN:OE1	2.29	0.50
1:L:132:SER:O	1:L:132:SER:OG	2.25	0.50
1:D:72:LEU:C	1:D:73:LEU:HD12	2.32	0.50
1:J:71:LYS:HG2	1:J:142:ASN:OD1	2.11	0.50
1:D:162:GLY:O	2:C:240:ARG:NH2	2.39	0.49
2:I:136:GLN:O	2:I:140:HIS:ND1	2.28	0.49
1:B:154:LEU:O	1:B:154:LEU:HG	2.11	0.49
1:H:47:SER:O	1:H:51:ARG:NE	2.35	0.49
1:F:107:ALA:CB	1:F:147:SER:HB2	2.42	0.49
2:C:99:GLY:O	2:C:157:HIS:CD2	2.66	0.49
1:L:115:GLY:HA3	1:L:125:VAL:CG2	2.42	0.48
1:J:67:ARG:NH1	1:J:140:GLU:O	2.45	0.48
2:G:211:LEU:O	2:G:267:THR:HG23	2.13	0.48
1:H:67:ARG:NH1	1:H:140:GLU:O	2.45	0.48
1:L:135:PRO:HB3	1:L:141:VAL:HG11	1.95	0.48
2:C:211:LEU:O	2:C:267:THR:HG23	2.13	0.48
2:A:103:PRO:HB3	2:A:156:HIS:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:85:ARG:NH2	4:E:302:ATP:O1A	2.47	0.48
1:L:146:PHE:HE2	1:L:176:LEU:HD22	1.77	0.48
1:H:132:SER:O	1:H:132:SER:OG	2.27	0.48
1:L:155:TRP:HH2	2:K:130:HIS:HB3	1.79	0.48
1:H:162:GLY:HA2	2:I:30:ALA:O	2.14	0.48
2:G:152:PHE:HE1	2:G:170:ALA:HB2	1.78	0.48
2:A:152:PHE:CE1	2:A:170:ALA:HB2	2.49	0.47
1:J:46:GLN:O	2:G:8:ILE:HD13	2.14	0.47
1:J:185:MET:HE2	1:J:187:PHE:CE2	2.38	0.47
1:L:77:GLY:HA2	1:L:169:THR:HG21	1.97	0.47
2:A:223:GLU:OE1	2:A:223:GLU:N	2.48	0.47
1:H:31:ASP:OD1	1:H:239:HIS:NE2	2.43	0.47
1:F:47:SER:O	1:F:51:ARG:NE	2.36	0.47
2:E:211:LEU:O	2:E:267:THR:HG23	2.15	0.47
1:F:46:GLN:O	2:E:8:ILE:HD13	2.14	0.47
1:D:146:PHE:O	1:D:146:PHE:CD1	2.68	0.47
2:A:130:HIS:HB2	8:A:304:IWO:O29	2.13	0.46
1:F:240:VAL:HG13	1:F:240:VAL:O	2.15	0.46
1:B:73:LEU:HD12	1:B:73:LEU:N	2.29	0.46
2:K:211:LEU:O	2:K:267:THR:HG23	2.15	0.46
1:B:240:VAL:O	1:B:240:VAL:HG13	2.14	0.46
2:C:99:GLY:O	2:C:157:HIS:HD2	1.98	0.46
1:J:152:TYR:OH	2:G:158:HIS:O	2.32	0.46
1:L:74:ILE:O	1:L:146:PHE:CE1	2.68	0.46
2:E:98:VAL:HG23	2:E:166:PRO:CD	2.45	0.46
2:G:130:HIS:HB2	2:G:131:PRO:HD3	1.96	0.46
1:L:179:GLN:NE2	2:K:100:SER:OG	2.48	0.46
1:J:119:ALA:HB2	1:L:131:LEU:HD22	1.96	0.46
1:J:132:SER:O	1:J:132:SER:OG	2.22	0.46
1:B:100:ALA:HB2	1:B:156:MET:HE2	1.97	0.46
2:I:103:PRO:CD	2:I:156:HIS:HB3	2.45	0.46
1:D:140:GLU:N	1:D:140:GLU:OE1	2.49	0.46
2:E:105:ALA:HB1	2:E:152:PHE:HE2	1.81	0.46
1:J:77:GLY:HA2	1:J:169:THR:HG21	1.98	0.46
1:L:125:VAL:HA	1:L:145:VAL:O	2.15	0.46
1:D:67:ARG:NH1	1:D:140:GLU:O	2.49	0.45
2:C:152:PHE:CE1	2:C:170:ALA:HB2	2.51	0.45
2:A:154:PRO:HA	2:A:156:HIS:CE1	2.51	0.45
1:L:140:GLU:OE1	1:L:140:GLU:N	2.50	0.45
1:L:146:PHE:HD1	1:L:146:PHE:H	1.63	0.45
1:B:109:GLN:OE1	2:C:104:LEU:O	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:73:LEU:HD12	1:D:73:LEU:N	2.31	0.45
2:C:130:HIS:CE1	2:C:152:PHE:O	2.69	0.45
2:A:211:LEU:O	2:A:267:THR:HG23	2.17	0.45
1:J:152:TYR:O	1:J:153:LYS:C	2.55	0.45
2:G:128:VAL:HG23	2:G:128:VAL:O	2.16	0.45
1:F:72:LEU:C	1:F:73:LEU:HD12	2.37	0.45
1:H:73:LEU:HD12	1:H:73:LEU:N	2.31	0.45
1:B:213:VAL:HG13	1:B:231:LEU:HB3	1.99	0.45
2:E:223:GLU:N	2:E:223:GLU:OE1	2.49	0.45
1:H:151:PRO:C	1:H:153:LYS:H	2.21	0.45
1:F:179:GLN:NE2	2:E:100:SER:OG	2.50	0.45
1:J:168:ARG:NH1	3:J:301:MOO:O2	2.50	0.45
1:D:146:PHE:O	1:D:146:PHE:CG	2.70	0.44
2:C:207:GLN:OE1	2:C:207:GLN:N	2.50	0.44
1:J:140:GLU:OE1	1:J:140:GLU:N	2.50	0.44
1:L:213:VAL:HG13	1:L:231:LEU:HB3	1.98	0.44
1:L:168:ARG:NH1	3:L:301:MOO:O3	2.49	0.44
2:K:99:GLY:O	2:K:157:HIS:HD2	1.99	0.44
1:B:134:VAL:HB	1:B:135:PRO:HD3	1.99	0.44
1:B:152:TYR:O	1:B:155:TRP:N	2.50	0.44
4:D:302:ATP:H2'	4:D:302:ATP:N3	2.32	0.44
1:H:97:GLY:O	1:H:153:LYS:O	2.35	0.44
1:H:168:ARG:NH1	3:H:301:MOO:O2	2.48	0.44
2:I:85:ARG:NH2	4:I:302:ATP:O1A	2.51	0.44
4:J:302:ATP:H2'	4:J:302:ATP:N3	2.33	0.44
2:A:68:LEU:HD21	2:A:257:THR:HG23	2.01	0.43
1:F:168:ARG:NH1	3:F:301:MOO:O3	2.48	0.43
1:F:228:PHE:N	1:F:229:PRO:CD	2.81	0.43
1:J:134:VAL:HB	1:J:135:PRO:HD3	1.99	0.43
2:C:155:TYR:N	2:C:155:TYR:CD1	2.86	0.43
2:E:99:GLY:O	2:E:156:HIS:O	2.35	0.43
2:E:133:VAL:O	2:E:137:LEU:HB2	2.18	0.43
2:I:153:PRO:O	2:I:153:PRO:HG2	2.18	0.43
2:I:211:LEU:O	2:I:267:THR:HG23	2.19	0.43
2:G:82:VAL:HA	2:G:85:ARG:HG2	2.01	0.43
2:G:85:ARG:NH2	4:G:302:ATP:O1A	2.52	0.43
2:E:82:VAL:HA	2:E:85:ARG:HG2	1.99	0.43
1:L:60:VAL:HG13	1:L:118:LEU:CD2	2.49	0.43
2:G:105:ALA:HB1	2:G:152:PHE:HE2	1.84	0.43
1:B:228:PHE:N	1:B:229:PRO:CD	2.82	0.43
1:H:81:ARG:HE	1:H:109:GLN:HE22	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:155:TYR:N	2:G:155:TYR:CD1	2.87	0.43
2:E:99:GLY:O	2:E:157:HIS:CD2	2.72	0.43
1:J:213:VAL:HG13	1:J:231:LEU:HB3	2.00	0.43
1:L:72:LEU:C	1:L:73:LEU:HD12	2.39	0.43
1:D:213:VAL:HG13	1:D:231:LEU:HB3	2.01	0.43
1:D:228:PHE:N	1:D:229:PRO:CD	2.82	0.43
1:L:47:SER:O	1:L:51:ARG:NE	2.39	0.43
1:H:213:VAL:HG13	1:H:231:LEU:HB3	2.01	0.42
2:K:141:LEU:HD23	2:K:141:LEU:HA	1.77	0.42
1:H:134:VAL:HG21	1:L:135:PRO:HG3	2.01	0.42
2:I:69:LEU:N	2:I:70:PRO:HD2	2.34	0.42
1:B:162:GLY:HA2	2:A:30:ALA:O	2.19	0.42
1:D:67:ARG:O	1:D:142:ASN:ND2	2.53	0.42
2:E:151:ALA:HB3	2:E:170:ALA:HB1	2.02	0.42
1:L:162:GLY:HA2	2:K:30:ALA:O	2.19	0.42
1:L:223:ASP:OD1	1:L:224:SER:N	2.52	0.42
4:L:302:ATP:N3	4:L:302:ATP:H2'	2.34	0.42
1:H:152:TYR:O	1:H:153:LYS:C	2.57	0.42
2:G:96:LEU:O	2:G:164:ARG:NH2	2.46	0.42
2:A:82:VAL:HA	2:A:85:ARG:HG2	2.01	0.42
1:B:102:LEU:HD23	2:C:111:GLN:OE1	2.19	0.42
1:D:162:GLY:HA2	2:C:30:ALA:O	2.20	0.42
2:I:111:GLN:OE1	1:L:102:LEU:HD23	2.19	0.42
1:J:149:MET:SD	1:J:150:PRO:HD2	2.60	0.42
2:K:85:ARG:NH2	4:K:302:ATP:O1A	2.52	0.42
1:B:39:THR:HG23	1:B:184:GLN:HG3	2.02	0.42
1:F:41:ILE:HG21	1:F:41:ILE:HD13	1.83	0.42
1:L:10:GLU:O	1:L:14[B]:GLN:HG2	2.20	0.42
2:C:69:LEU:N	2:C:70:PRO:HD2	2.35	0.42
2:C:82:VAL:HA	2:C:85:ARG:HG2	2.01	0.42
2:C:130:HIS:HE1	2:C:152:PHE:O	2.03	0.42
1:F:162:GLY:HA2	2:E:30:ALA:O	2.20	0.42
1:H:178:GLU:O	1:H:239:HIS:ND1	2.53	0.42
2:I:103:PRO:CG	2:I:156:HIS:HB3	2.50	0.41
1:J:60:VAL:HG13	1:J:118:LEU:CD2	2.50	0.41
1:J:162:GLY:HA2	2:G:30:ALA:O	2.19	0.41
2:G:69:LEU:N	2:G:70:PRO:HD2	2.35	0.41
2:K:82:VAL:HA	2:K:85:ARG:HG2	2.02	0.41
2:K:152:PHE:HE1	2:K:170:ALA:HB2	1.83	0.41
1:D:135:PRO:HB3	1:D:141:VAL:HG11	2.01	0.41
1:H:169:THR:OG1	3:H:301:MOO:O3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:71:LYS:CG	1:J:142:ASN:OD1	2.68	0.41
1:J:102:LEU:HD23	2:K:111:GLN:OE1	2.20	0.41
2:G:207:GLN:N	2:G:207:GLN:OE1	2.53	0.41
1:L:149:MET:SD	1:L:150:PRO:HD2	2.59	0.41
1:J:97:GLY:O	1:J:153:LYS:O	2.38	0.41
1:L:154:LEU:O	1:L:154:LEU:HG	2.20	0.41
2:K:96:LEU:O	2:K:164:ARG:NH2	2.47	0.41
1:H:60:VAL:HG13	1:H:118:LEU:CD2	2.50	0.41
1:L:46:GLN:O	2:K:8:ILE:HD13	2.20	0.41
1:L:152:TYR:O	1:L:155:TRP:N	2.52	0.41
2:A:69:LEU:N	2:A:70:PRO:HD2	2.36	0.41
4:E:302:ATP:N3	4:E:302:ATP:H2'	2.35	0.41
1:B:130:GLY:CA	1:B:180:PHE:CZ	2.91	0.41
2:A:111:GLN:OE1	1:F:102:LEU:HD23	2.21	0.41
2:A:128:VAL:HG22	2:A:148:VAL:O	2.20	0.41
2:A:151:ALA:HB3	2:A:170:ALA:HB1	2.02	0.41
2:C:238:THR:O	2:C:240:ARG:NH1	2.53	0.41
1:F:162:GLY:O	2:E:240:ARG:NH2	2.40	0.41
4:H:302:ATP:N3	4:H:302:ATP:H2'	2.34	0.41
1:L:162:GLY:O	2:K:240:ARG:NH2	2.41	0.41
2:K:69:LEU:N	2:K:70:PRO:HD2	2.36	0.41
2:E:69:LEU:N	2:E:70:PRO:HD2	2.36	0.41
2:E:84:ALA:O	2:E:87:VAL:HG12	2.21	0.41
4:K:302:ATP:H2'	4:K:302:ATP:N3	2.36	0.41
1:B:42:LYS:HG3	1:B:173:CYS:SG	2.61	0.41
2:A:155:TYR:N	2:A:155:TYR:HD1	2.19	0.41
1:D:46:GLN:O	2:C:8:ILE:HD13	2.21	0.41
1:D:240:VAL:O	1:D:240:VAL:HG13	2.20	0.41
4:F:302:ATP:N3	4:F:302:ATP:H2'	2.35	0.41
2:I:130:HIS:CE1	2:I:152:PHE:O	2.73	0.41
2:K:12:ILE:HD12	2:K:12:ILE:H	1.86	0.41
1:B:10:GLU:O	1:B:14[B]:GLN:HG2	2.21	0.40
2:C:148:VAL:HG12	2:C:149:GLY:N	2.36	0.40
1:F:150:PRO:HB3	2:E:158:HIS:HD2	1.86	0.40
2:A:84:ALA:O	2:A:87:VAL:HG12	2.21	0.40
1:D:132:SER:O	1:D:132:SER:OG	2.22	0.40
1:F:135:PRO:HB3	1:F:141:VAL:HG11	2.02	0.40
1:H:81:ARG:HE	1:H:109:GLN:NE2	2.18	0.40
2:I:82:VAL:HA	2:I:85:ARG:HG2	2.03	0.40
1:L:148:GLY:O	1:L:172:GLY:HA3	2.21	0.40
2:G:212:PRO:O	2:G:264:HIS:NE2	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:27:ARG:N	2:A:28:PRO:CD	2.84	0.40
4:I:302:ATP:N3	4:I:302:ATP:H2'	2.36	0.40
1:J:146:PHE:CD1	1:J:146:PHE:N	2.89	0.40
2:E:27:ARG:N	2:E:28:PRO:CD	2.84	0.40
2:I:27:ARG:N	2:I:28:PRO:CD	2.84	0.40
2:G:27:ARG:N	2:G:28:PRO:CD	2.84	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	269/269 (100%)	256 (95%)	12 (4%)	1 (0%)	30	50
1	D	268/269 (100%)	254 (95%)	12 (4%)	2 (1%)	19	36
1	F	268/269 (100%)	250 (93%)	18 (7%)	0	100	100
1	H	268/269 (100%)	256 (96%)	11 (4%)	1 (0%)	30	50
1	J	268/269 (100%)	250 (93%)	17 (6%)	1 (0%)	30	50
1	L	267/269 (99%)	250 (94%)	17 (6%)	0	100	100
2	A	272/275 (99%)	263 (97%)	8 (3%)	1 (0%)	30	50
2	C	273/275 (99%)	261 (96%)	11 (4%)	1 (0%)	30	50
2	E	272/275 (99%)	264 (97%)	8 (3%)	0	100	100
2	G	273/275 (99%)	261 (96%)	11 (4%)	1 (0%)	30	50
2	I	272/275 (99%)	262 (96%)	10 (4%)	0	100	100
2	K	272/275 (99%)	262 (96%)	10 (4%)	0	100	100
All	All	3242/3264 (99%)	3089 (95%)	145 (4%)	8 (0%)	45	64

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	153	LYS
2	G	156	HIS
2	A	156	HIS
1	D	153	LYS
2	C	166	PRO
1	H	153	LYS
1	J	132	SER
1	D	132	SER

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	208/205 (102%)	206 (99%)	2 (1%)	73	87
1	D	207/205 (101%)	207 (100%)	0	100	100
1	F	207/205 (101%)	206 (100%)	1 (0%)	86	95
1	H	207/205 (101%)	204 (99%)	3 (1%)	62	81
1	J	207/205 (101%)	206 (100%)	1 (0%)	86	95
1	L	206/205 (100%)	202 (98%)	4 (2%)	52	74
2	A	213/215 (99%)	209 (98%)	4 (2%)	52	74
2	C	214/215 (100%)	213 (100%)	1 (0%)	86	95
2	E	213/215 (99%)	211 (99%)	2 (1%)	75	89
2	G	214/215 (100%)	210 (98%)	4 (2%)	52	74
2	I	213/215 (99%)	209 (98%)	4 (2%)	52	74
2	K	213/215 (99%)	210 (99%)	3 (1%)	62	81
All	All	2522/2520 (100%)	2493 (99%)	29 (1%)	66	86

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	153	LYS
1	B	161	GLU
2	A	129	GLU

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Mol	Chain	Res	Type
2	A	132	THR
2	A	136	GLN
2	A	158	HIS
2	C	166	PRO
1	F	153	LYS
2	E	129	GLU
2	E	131	PRO
1	H	105	SER
1	H	147	SER
1	H	153	LYS
2	I	129	GLU
2	I	132	THR
2	I	152	PHE
2	I	158	HIS
1	J	147	SER
2	G	129	GLU
2	G	132	THR
2	G	136	GLN
2	G	157	HIS
1	L	120	LYS
1	L	126	VAL
1	L	146	PHE
1	L	147	SER
2	K	129	GLU
2	K	135	ASP
2	K	157	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	101	GLN
2	A	130	HIS
2	A	156	HIS
2	A	157	HIS
2	A	158	HIS
2	C	130	HIS
2	C	157	HIS
2	E	156	HIS
2	E	157	HIS
2	E	158	HIS
2	E	207	GLN
1	H	109	GLN

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Mol	Chain	Res	Type
2	I	130	HIS
2	I	156	HIS
2	K	114	HIS
2	K	157	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 54 ligands modelled in this entry, 12 are monoatomic - leaving 42 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	$\# Z > 2$
4	ATP	J	302	5	26,33,33	0.90	0	31,52,52	1.64	5 (16%)
6	IWL	J	304	1	22,64,64	3.53	4 (18%)	-		
10	IHW	L	305	-	68,98,98	3.45	46 (67%)	-		
8	IWO	I	304	2	13,45,45	2.18	2 (15%)	-		
11	IX3	E	305	-	0,15,15	-	-	-		
3	MOO	L	301	-	2,4,4	2.05	1 (50%)	-		
7	IV9	G	301	2	17,48,48	4.38	6 (35%)	-		
6	IWL	F	304	1	22,64,64	3.19	8 (36%)	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	IV9	A	301	-	17,48,48	4.62	6 (35%)	-		
4	ATP	A	302	5	26,33,33	0.93	0	31,52,52	1.62	6 (19%)
8	IWO	G	304	2	13,45,45	2.62	3 (23%)	-		
4	ATP	I	302	5	26,33,33	0.95	0	31,52,52	1.64	5 (16%)
7	IV9	E	301	-	17,48,48	4.30	6 (35%)	-		
8	IWO	K	304	2	13,45,45	2.22	2 (15%)	-		
8	IWO	C	304	2	13,45,45	2.84	3 (23%)	-		
10	IHW	F	305	-	68,98,98	3.34	44 (64%)	-		
4	ATP	G	302	5	26,33,33	0.95	0	31,52,52	1.64	5 (16%)
3	MOO	D	301	-	2,4,4	2.00	1 (50%)	-		
11	IX3	I	305	2	0,15,15	-	-	-		
4	ATP	L	302	5	26,33,33	0.93	0	31,52,52	1.65	4 (12%)
3	MOO	B	301	-	2,4,4	2.05	1 (50%)	-		
3	MOO	F	301	-	2,4,4	2.07	1 (50%)	-		
4	ATP	C	302	5	26,33,33	0.95	0	31,52,52	1.64	6 (19%)
6	IWL	B	304	1	22,64,64	4.09	7 (31%)	-		
8	IWO	A	304	2	13,45,45	2.21	2 (15%)	-		
6	IWL	L	304	1	22,64,64	3.48	7 (31%)	-		
4	ATP	F	302	5	26,33,33	0.92	0	31,52,52	1.64	5 (16%)
4	ATP	K	302	5	26,33,33	0.95	0	31,52,52	1.65	6 (19%)
7	IV9	I	301	-	17,48,48	4.62	6 (35%)	-		
3	MOO	J	301	-	2,4,4	2.01	1 (50%)	-		
9	IWZ	K	305	-	33,60,60	2.44	6 (18%)	-		
4	ATP	B	302	5	26,33,33	0.92	0	31,52,52	1.64	4 (12%)
9	IWZ	C	305	-	33,60,60	2.87	6 (18%)	-		
3	MOO	H	301	-	2,4,4	2.03	1 (50%)	-		
4	ATP	D	302	5	26,33,33	0.91	0	31,52,52	1.64	5 (16%)
4	ATP	H	302	5	26,33,33	0.93	0	31,52,52	1.65	4 (12%)
6	IWL	H	304	1	22,64,64	3.40	7 (31%)	-		
8	IWO	E	304	2	13,45,45	2.25	2 (15%)	-		
7	IV9	C	301	-	17,48,48	4.63	6 (35%)	-		
7	IV9	K	301	-	17,48,48	4.64	7 (41%)	-		
4	ATP	E	302	5	26,33,33	0.94	0	31,52,52	1.64	6 (19%)
6	IWL	D	304	1	22,64,64	3.40	6 (27%)	-		

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
4	ATP	B	302	5	-	4/18/38/38	0/3/3/3
4	ATP	A	302	5	-	3/18/38/38	0/3/3/3
4	ATP	L	302	5	-	4/18/38/38	0/3/3/3
4	ATP	J	302	5	-	6/18/38/38	0/3/3/3
4	ATP	C	302	5	-	4/18/38/38	0/3/3/3
4	ATP	D	302	5	-	6/18/38/38	0/3/3/3
11	IX3	E	305	-	-	-	0/3/3/3
4	ATP	H	302	5	-	3/18/38/38	0/3/3/3
4	ATP	I	302	5	-	4/18/38/38	0/3/3/3
4	ATP	F	302	5	-	4/18/38/38	0/3/3/3
4	ATP	K	302	5	-	4/18/38/38	0/3/3/3
4	ATP	G	302	5	-	4/18/38/38	0/3/3/3
4	ATP	E	302	5	-	3/18/38/38	0/3/3/3
11	IX3	I	305	2	-	-	0/3/3/3

All (198) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	304	IWL	W11-O12	-14.70	1.79	2.30
9	C	305	IWZ	W7-O74	11.70	2.33	2.10
6	H	304	IWL	W11-O12	-11.34	1.91	2.30
6	D	304	IWL	W11-O12	-10.86	1.92	2.30
6	J	304	IWL	W11-O12	-10.84	1.92	2.30
7	I	301	IV9	W1-O4	-10.55	1.93	2.30
7	A	301	IV9	W1-O4	-10.55	1.93	2.30
7	K	301	IV9	W1-O4	-10.54	1.93	2.30
7	C	301	IV9	W1-O4	-10.54	1.93	2.30
7	G	301	IV9	W1-O4	-10.53	1.94	2.30
7	I	301	IV9	W3-O4	-10.00	1.95	2.30
7	A	301	IV9	W3-O4	-9.99	1.95	2.30
7	C	301	IV9	W3-O4	-9.99	1.95	2.30
7	E	301	IV9	W3-O4	-9.99	1.95	2.30
7	K	301	IV9	W3-O4	-9.98	1.95	2.30
7	K	301	IV9	W6-O4	-9.80	1.96	2.30
7	E	301	IV9	W6-O4	-9.78	1.96	2.30
7	C	301	IV9	W6-O4	-9.76	1.96	2.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	301	IV9	W6-O4	-9.76	1.96	2.30
7	I	301	IV9	W6-O4	-9.75	1.96	2.30
7	G	301	IV9	W6-O4	-9.75	1.96	2.30
9	K	305	IWZ	W6-O74	9.41	2.29	2.10
7	E	301	IV9	W1-O4	-9.24	1.98	2.30
6	J	304	IWL	W2-O12	-9.14	1.98	2.30
6	L	304	IWL	W11-O12	-8.65	2.00	2.30
6	L	304	IWL	W2-O12	7.88	2.57	2.30
6	F	304	IWL	W2-O12	-7.79	2.03	2.30
7	G	301	IV9	W3-O4	-7.10	2.05	2.30
10	L	305	IHW	W63-O433	-6.98	1.59	1.91
10	F	305	IHW	W6-O54	-6.82	1.64	1.92
10	L	305	IHW	W6-O54	-6.82	1.64	1.92
9	C	305	IWZ	W1-O14	6.70	2.23	2.10
6	B	304	IWL	W3-O4	-6.52	1.86	2.25
7	G	301	IV9	W8-O4	-6.35	2.08	2.30
8	C	304	IWO	W3-O7	6.29	3.71	2.14
6	F	304	IWL	W3-O4	-6.26	1.88	2.25
10	L	305	IHW	W53-O553	-6.19	1.67	1.92
10	F	305	IHW	W53-O553	-6.19	1.67	1.92
6	H	304	IWL	W3-O4	-5.98	1.89	2.25
6	L	304	IWL	W3-O4	-5.97	1.89	2.25
6	D	304	IWL	W2-O12	-5.90	2.09	2.30
6	L	304	IWL	W1-O12	-5.87	2.10	2.30
6	H	304	IWL	W2-O12	-5.87	2.10	2.30
6	B	304	IWL	W2-O12	-5.86	2.10	2.30
10	L	305	IHW	W43-O343	-5.64	1.69	1.92
10	F	305	IHW	W43-O343	-5.63	1.69	1.92
8	G	304	IWO	W6-O11	-5.59	2.10	2.30
10	L	305	IHW	W43-O353	-5.53	1.69	1.92
10	F	305	IHW	W43-O353	-5.52	1.69	1.92
6	D	304	IWL	W3-O4	-5.49	1.92	2.25
7	C	301	IV9	W8-O4	-5.45	2.11	2.30
7	A	301	IV9	W8-O4	-5.43	2.11	2.30
7	I	301	IV9	W8-O4	-5.43	2.11	2.30
7	K	301	IV9	W8-O4	-5.41	2.11	2.30
10	L	305	IHW	W6-O55	-5.34	1.70	1.92
10	F	305	IHW	W6-O55	-5.34	1.70	1.92
6	F	304	IWL	W1-O12	-5.25	2.12	2.30
10	L	305	IHW	W32-O342	5.20	2.14	1.92
10	F	305	IHW	W32-O342	5.18	2.14	1.92
10	F	305	IHW	W63-O433	-5.15	1.67	1.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	K	305	IWZ	W2-O14	5.02	2.20	2.10
9	C	305	IWZ	W2-O14	5.00	2.20	2.10
10	L	305	IHW	W32-O352	4.99	2.13	1.92
10	L	305	IHW	W6-O43	-4.98	1.68	1.91
10	F	305	IHW	W6-O43	-4.98	1.68	1.91
10	F	305	IHW	W32-O352	4.97	2.13	1.92
8	C	304	IWO	W7-O11	-4.96	2.13	2.30
8	G	304	IWO	W7-O11	-4.95	2.13	2.30
8	E	304	IWO	W7-O11	-4.95	2.13	2.30
8	K	304	IWO	W7-O11	-4.94	2.13	2.30
10	L	305	IHW	W62-O552	-4.94	1.72	1.92
8	A	304	IWO	W7-O11	-4.93	2.13	2.30
10	F	305	IHW	W62-O552	-4.92	1.72	1.92
8	I	304	IWO	W7-O11	-4.92	2.13	2.30
8	K	304	IWO	W6-O11	-4.89	2.13	2.30
8	E	304	IWO	W6-O11	-4.88	2.13	2.30
8	A	304	IWO	W6-O11	-4.87	2.13	2.30
8	I	304	IWO	W6-O11	-4.86	2.13	2.30
10	L	305	IHW	W5-O54	4.86	2.12	1.92
10	F	305	IHW	W5-O54	4.86	2.12	1.92
10	L	305	IHW	W63-O553	4.85	2.12	1.92
10	F	305	IHW	W63-O553	4.85	2.12	1.92
8	C	304	IWO	W6-O11	-4.84	2.13	2.30
6	F	304	IWL	W8-O12	-4.75	2.13	2.30
9	C	305	IWZ	W9-O91	-4.71	1.72	1.94
6	L	304	IWL	W8-O12	-4.71	2.14	2.30
9	K	305	IWZ	W9-O91	-4.70	1.72	1.94
6	B	304	IWL	W8-O12	-4.66	2.14	2.30
6	H	304	IWL	W4-O12	-4.64	2.14	2.30
10	F	305	IHW	W53-O323	-4.63	1.70	1.91
10	L	305	IHW	W53-O323	-4.63	1.70	1.91
10	L	305	IHW	W62-O612	-4.63	1.58	1.97
10	L	305	IHW	W33-O353	-4.62	1.73	1.92
10	F	305	IHW	W33-O353	-4.61	1.73	1.92
8	G	304	IWO	W3-O7	4.61	3.29	2.14
10	L	305	IHW	W83-O812	4.60	2.15	1.94
6	F	304	IWL	W4-O12	-4.52	2.14	2.30
10	L	305	IHW	W63-O423	-4.50	1.59	1.97
10	F	305	IHW	W63-O423	-4.50	1.59	1.97
6	J	304	IWL	W8-O12	-4.49	2.14	2.30
6	D	304	IWL	W8-O12	-4.48	2.14	2.30
6	F	304	IWL	W11-O12	-4.45	2.14	2.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	304	IWL	W4-O12	-4.27	2.15	2.30
6	D	304	IWL	W4-O12	-4.24	2.15	2.30
10	L	305	IHW	W33-O333	-4.22	1.72	1.91
6	J	304	IWL	W4-O12	-4.21	2.15	2.30
10	F	305	IHW	W33-O333	-4.21	1.72	1.91
10	L	305	IHW	W52-O542	-4.19	1.75	1.92
10	F	305	IHW	W52-O542	-4.19	1.75	1.92
10	F	305	IHW	W6-O61	-4.18	1.62	1.97
10	F	305	IHW	W43-O433	-4.14	1.72	1.91
10	L	305	IHW	W3-O34	-4.12	1.75	1.94
10	F	305	IHW	W3-O34	-4.11	1.75	1.94
9	K	305	IWZ	W5-O33	-4.04	2.02	2.10
10	L	305	IHW	W43-O433	-4.00	1.73	1.91
10	L	305	IHW	W43-O443	-3.88	1.67	1.94
10	F	305	IHW	W62-O612	-3.74	1.66	1.97
10	F	305	IHW	W32-O322	-3.72	1.74	1.91
10	L	305	IHW	W32-O322	-3.72	1.74	1.91
10	F	305	IHW	W3-O422	-3.64	1.77	1.94
10	L	305	IHW	W3-O422	-3.63	1.77	1.94
10	F	305	IHW	W33-O323	3.62	2.07	1.91
10	L	305	IHW	W33-O323	3.61	2.07	1.91
10	L	305	IHW	W8-O81	-3.59	1.77	1.94
10	F	305	IHW	W83-O812	3.53	2.10	1.94
10	L	305	IHW	W82-O903	3.48	2.10	1.94
10	F	305	IHW	W43-O443	-3.48	1.70	1.94
10	F	305	IHW	W43-O332	-3.38	1.69	1.97
10	L	305	IHW	W43-O332	-3.37	1.69	1.97
10	L	305	IHW	W6-O42	-3.34	1.69	1.97
10	F	305	IHW	W6-O42	-3.34	1.69	1.97
10	F	305	IHW	W62-O632	-3.26	1.70	1.97
10	L	305	IHW	W62-O632	-3.26	1.70	1.97
10	F	305	IHW	W5-O55	3.19	2.05	1.92
10	F	305	IHW	W53-O42	-3.18	1.70	1.97
10	L	305	IHW	W53-O42	-3.18	1.70	1.97
10	F	305	IHW	W63-O613	-3.17	1.71	1.97
10	L	305	IHW	W5-O55	3.17	2.05	1.92
10	L	305	IHW	W63-O613	-3.17	1.71	1.97
10	L	305	IHW	W6-O61	-3.12	1.71	1.97
10	L	305	IHW	W3-O35	-3.05	1.80	1.94
10	F	305	IHW	W3-O35	-3.05	1.80	1.94
10	F	305	IHW	W42-O422	-3.00	1.64	1.93
10	L	305	IHW	W42-O422	-3.00	1.64	1.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	L	305	IHW	W62-O432	-2.99	1.77	1.91
10	F	305	IHW	W62-O432	-2.99	1.77	1.91
10	L	305	IHW	W62-O542	-2.92	1.80	1.92
10	F	305	IHW	W62-O542	-2.92	1.80	1.92
9	K	305	IWZ	W1-O14	2.85	2.16	2.10
9	C	305	IWZ	W6-O74	2.73	2.16	2.10
10	F	305	IHW	W82-O81	2.72	2.07	1.94
6	D	304	IWL	W3-O2	-2.69	1.65	2.19
9	C	305	IWZ	W8-O83	2.69	2.06	1.94
10	L	305	IHW	W52-O423	-2.68	1.75	1.97
9	K	305	IWZ	W8-O83	2.67	2.06	1.94
10	F	305	IHW	W52-O423	-2.67	1.75	1.97
6	L	304	IWL	W9-O36	-2.63	1.49	2.14
3	B	301	MOO	O1-MO	-2.60	1.68	1.73
3	H	301	MOO	O1-MO	-2.58	1.68	1.73
7	E	301	IV9	W8-O4	-2.57	2.21	2.30
3	F	301	MOO	O1-MO	-2.57	1.68	1.73
3	L	301	MOO	O1-MO	-2.55	1.68	1.73
10	F	305	IHW	W63-O543	2.54	2.03	1.92
10	L	305	IHW	W63-O543	2.52	2.03	1.92
10	F	305	IHW	W42-O352	-2.51	1.69	1.93
10	L	305	IHW	W42-O352	-2.51	1.69	1.93
10	F	305	IHW	W42-O342	-2.51	1.69	1.93
3	J	301	MOO	O1-MO	-2.51	1.68	1.73
10	L	305	IHW	W42-O342	-2.50	1.69	1.93
10	F	305	IHW	W8-O812	-2.50	1.82	1.94
3	D	301	MOO	O1-MO	-2.49	1.68	1.73
10	F	305	IHW	W5-O632	-2.48	1.76	1.97
10	L	305	IHW	W5-O632	-2.48	1.76	1.97
6	B	304	IWL	W3-O2	-2.48	1.69	2.19
10	L	305	IHW	W8-O812	2.46	2.05	1.94
6	F	304	IWL	W9-O36	-2.41	1.54	2.14
7	K	301	IV9	W4-O4	2.40	2.38	2.30
7	E	301	IV9	W4-O4	2.40	2.38	2.30
7	C	301	IV9	W4-O4	2.40	2.38	2.30
7	G	301	IV9	W4-O4	2.40	2.38	2.30
6	H	304	IWL	W9-O39	-2.39	1.55	2.14
7	A	301	IV9	W4-O4	2.38	2.38	2.30
7	I	301	IV9	W4-O4	2.37	2.38	2.30
6	F	304	IWL	W3-O2	-2.36	1.71	2.19
6	H	304	IWL	W9-O36	-2.27	1.58	2.14
6	H	304	IWL	W3-O2	-2.22	1.74	2.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	F	305	IHW	W33-O343	-2.20	1.83	1.92
10	L	305	IHW	W33-O343	-2.20	1.83	1.92
6	B	304	IWL	W9-O39	-2.19	1.60	2.14
7	I	301	IV9	W5-O13	-2.13	1.76	2.19
7	C	301	IV9	W5-O13	-2.13	1.76	2.19
7	G	301	IV9	W5-O13	-2.12	1.76	2.19
7	A	301	IV9	W5-O13	-2.12	1.76	2.19
7	E	301	IV9	W5-O13	-2.12	1.76	2.19
7	K	301	IV9	W5-O13	-2.12	1.76	2.19
10	L	305	IHW	W8-O61	-2.06	1.70	2.04
6	L	304	IWL	W9-O39	-2.06	1.63	2.14
7	K	301	IV9	W2-O1	-2.02	1.64	2.14

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	302	ATP	PB-O3B-PG	-4.07	118.87	132.83
4	K	302	ATP	PB-O3B-PG	-4.06	118.91	132.83
4	E	302	ATP	PB-O3B-PG	-4.04	118.98	132.83
4	C	302	ATP	PB-O3B-PG	-4.03	119.01	132.83
4	G	302	ATP	PB-O3B-PG	-4.02	119.05	132.83
4	I	302	ATP	PB-O3B-PG	-3.98	119.17	132.83
4	F	302	ATP	PA-O3A-PB	-3.94	119.31	132.83
4	H	302	ATP	PA-O3A-PB	-3.93	119.34	132.83
4	L	302	ATP	PA-O3A-PB	-3.93	119.35	132.83
4	B	302	ATP	PA-O3A-PB	-3.92	119.36	132.83
4	H	302	ATP	PB-O3B-PG	-3.85	119.60	132.83
4	J	302	ATP	PB-O3B-PG	-3.85	119.61	132.83
4	D	302	ATP	PB-O3B-PG	-3.83	119.67	132.83
4	L	302	ATP	PB-O3B-PG	-3.81	119.76	132.83
4	B	302	ATP	PB-O3B-PG	-3.79	119.82	132.83
4	D	302	ATP	PA-O3A-PB	-3.79	119.83	132.83
4	J	302	ATP	PA-O3A-PB	-3.76	119.93	132.83
4	F	302	ATP	PB-O3B-PG	-3.74	119.99	132.83
4	K	302	ATP	PA-O3A-PB	-3.63	120.37	132.83
4	A	302	ATP	PA-O3A-PB	-3.60	120.47	132.83
4	G	302	ATP	PA-O3A-PB	-3.58	120.53	132.83
4	E	302	ATP	C3'-C2'-C1'	3.56	106.34	100.98
4	C	302	ATP	PA-O3A-PB	-3.55	120.63	132.83
4	E	302	ATP	PA-O3A-PB	-3.55	120.65	132.83
4	I	302	ATP	PA-O3A-PB	-3.55	120.65	132.83
4	I	302	ATP	C3'-C2'-C1'	3.55	106.32	100.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	302	ATP	C3'-C2'-C1'	3.54	106.31	100.98
4	K	302	ATP	C3'-C2'-C1'	3.52	106.28	100.98
4	C	302	ATP	C3'-C2'-C1'	3.50	106.25	100.98
4	D	302	ATP	C3'-C2'-C1'	3.34	106.00	100.98
4	J	302	ATP	C3'-C2'-C1'	3.30	105.94	100.98
4	J	302	ATP	N3-C2-N1	-3.27	123.57	128.68
4	F	302	ATP	C3'-C2'-C1'	3.26	105.89	100.98
4	H	302	ATP	N3-C2-N1	-3.26	123.59	128.68
4	B	302	ATP	N3-C2-N1	-3.24	123.61	128.68
4	D	302	ATP	N3-C2-N1	-3.23	123.62	128.68
4	L	302	ATP	N3-C2-N1	-3.23	123.63	128.68
4	F	302	ATP	N3-C2-N1	-3.21	123.66	128.68
4	B	302	ATP	C3'-C2'-C1'	3.20	105.79	100.98
4	A	302	ATP	N3-C2-N1	-3.17	123.73	128.68
4	E	302	ATP	N3-C2-N1	-3.16	123.73	128.68
4	C	302	ATP	N3-C2-N1	-3.15	123.75	128.68
4	G	302	ATP	N3-C2-N1	-3.14	123.76	128.68
4	H	302	ATP	C3'-C2'-C1'	3.13	105.69	100.98
4	L	302	ATP	C3'-C2'-C1'	3.12	105.67	100.98
4	K	302	ATP	N3-C2-N1	-3.10	123.83	128.68
4	I	302	ATP	N3-C2-N1	-3.10	123.84	128.68
4	A	302	ATP	C3'-C2'-C1'	3.02	105.53	100.98
4	I	302	ATP	C1'-N9-C4	2.44	130.93	126.64
4	G	302	ATP	C1'-N9-C4	2.44	130.92	126.64
4	K	302	ATP	C1'-N9-C4	2.43	130.91	126.64
4	A	302	ATP	C1'-N9-C4	2.42	130.89	126.64
4	C	302	ATP	C1'-N9-C4	2.36	130.79	126.64
4	E	302	ATP	C1'-N9-C4	2.34	130.76	126.64
4	D	302	ATP	C4-C5-N7	-2.13	107.18	109.40
4	F	302	ATP	C4-C5-N7	-2.11	107.20	109.40
4	J	302	ATP	C4-C5-N7	-2.08	107.23	109.40
4	E	302	ATP	C4-C5-N7	-2.04	107.27	109.40
4	C	302	ATP	C4-C5-N7	-2.04	107.27	109.40
4	A	302	ATP	C4-C5-N7	-2.01	107.30	109.40
4	K	302	ATP	C4-C5-N7	-2.00	107.31	109.40

There are no chirality outliers.

All (49) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	302	ATP	C5'-O5'-PA-O1A
4	D	302	ATP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
4	D	302	ATP	C5'-O5'-PA-O3A
4	F	302	ATP	C5'-O5'-PA-O1A
4	H	302	ATP	C5'-O5'-PA-O1A
4	J	302	ATP	C5'-O5'-PA-O1A
4	J	302	ATP	C5'-O5'-PA-O3A
4	L	302	ATP	C5'-O5'-PA-O1A
4	J	302	ATP	PB-O3A-PA-O1A
4	B	302	ATP	C4'-C5'-O5'-PA
4	F	302	ATP	C4'-C5'-O5'-PA
4	H	302	ATP	C4'-C5'-O5'-PA
4	L	302	ATP	C4'-C5'-O5'-PA
4	B	302	ATP	C5'-O5'-PA-O3A
4	F	302	ATP	C5'-O5'-PA-O3A
4	H	302	ATP	C5'-O5'-PA-O3A
4	L	302	ATP	C5'-O5'-PA-O3A
4	A	302	ATP	PA-O3A-PB-O1B
4	D	302	ATP	PB-O3A-PA-O1A
4	C	302	ATP	PA-O3A-PB-O1B
4	E	302	ATP	PA-O3A-PB-O1B
4	I	302	ATP	PA-O3A-PB-O1B
4	G	302	ATP	PA-O3A-PB-O1B
4	K	302	ATP	PA-O3A-PB-O1B
4	D	302	ATP	C4'-C5'-O5'-PA
4	J	302	ATP	C4'-C5'-O5'-PA
4	D	302	ATP	PB-O3A-PA-O2A
4	F	302	ATP	PB-O3A-PA-O1A
4	K	302	ATP	PG-O3B-PB-O1B
4	B	302	ATP	PB-O3A-PA-O2A
4	A	302	ATP	PA-O3A-PB-O2B
4	A	302	ATP	PB-O3A-PA-O1A
4	C	302	ATP	PG-O3B-PB-O2B
4	C	302	ATP	PA-O3A-PB-O2B
4	C	302	ATP	PB-O3A-PA-O1A
4	E	302	ATP	PA-O3A-PB-O2B
4	E	302	ATP	PB-O3A-PA-O1A
4	I	302	ATP	PG-O3B-PB-O2B
4	I	302	ATP	PA-O3A-PB-O2B
4	I	302	ATP	PB-O3A-PA-O1A
4	J	302	ATP	PB-O3A-PA-O2A
4	G	302	ATP	PG-O3B-PB-O1B
4	G	302	ATP	PA-O3A-PB-O2B
4	G	302	ATP	PB-O3A-PA-O1A

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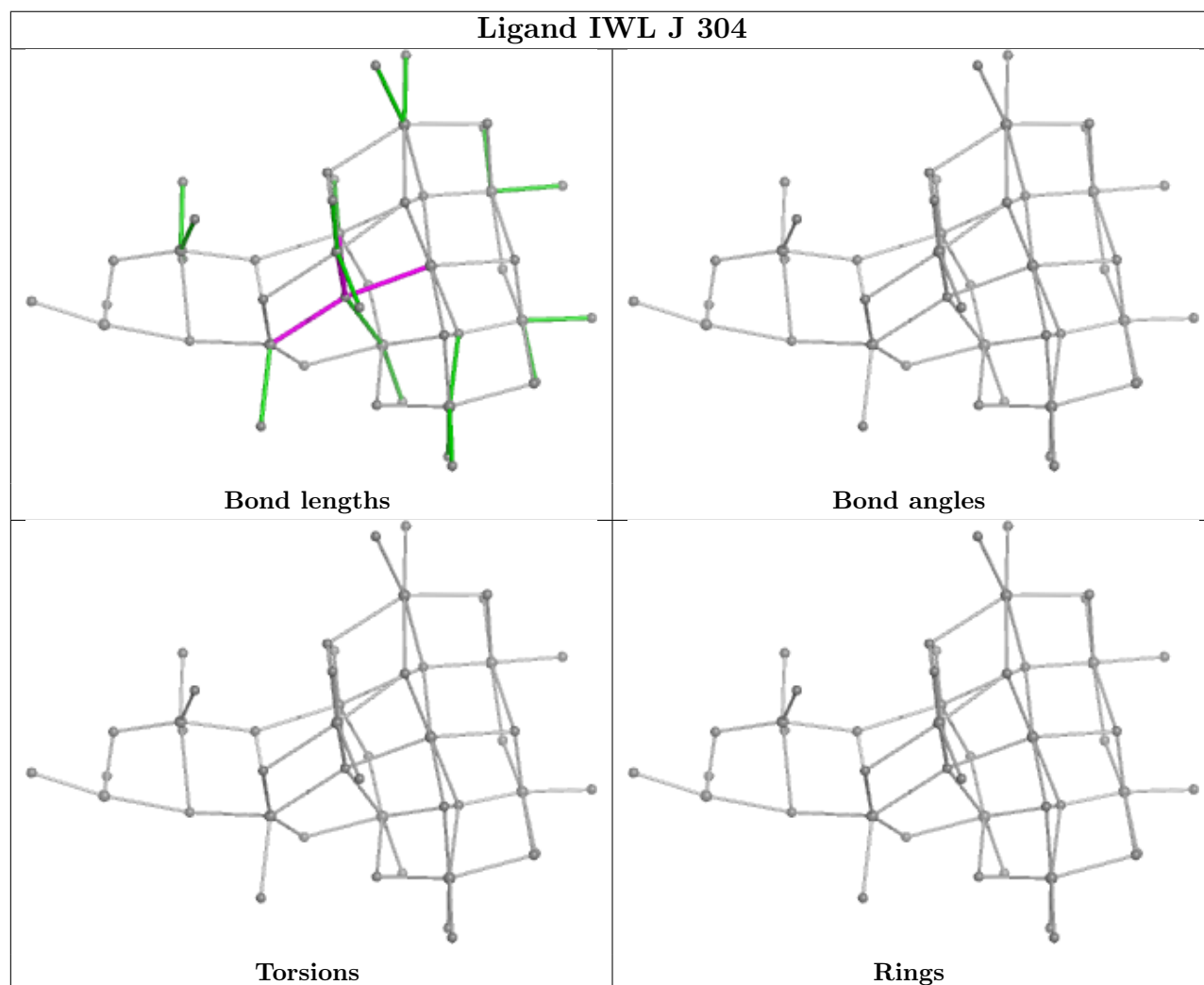
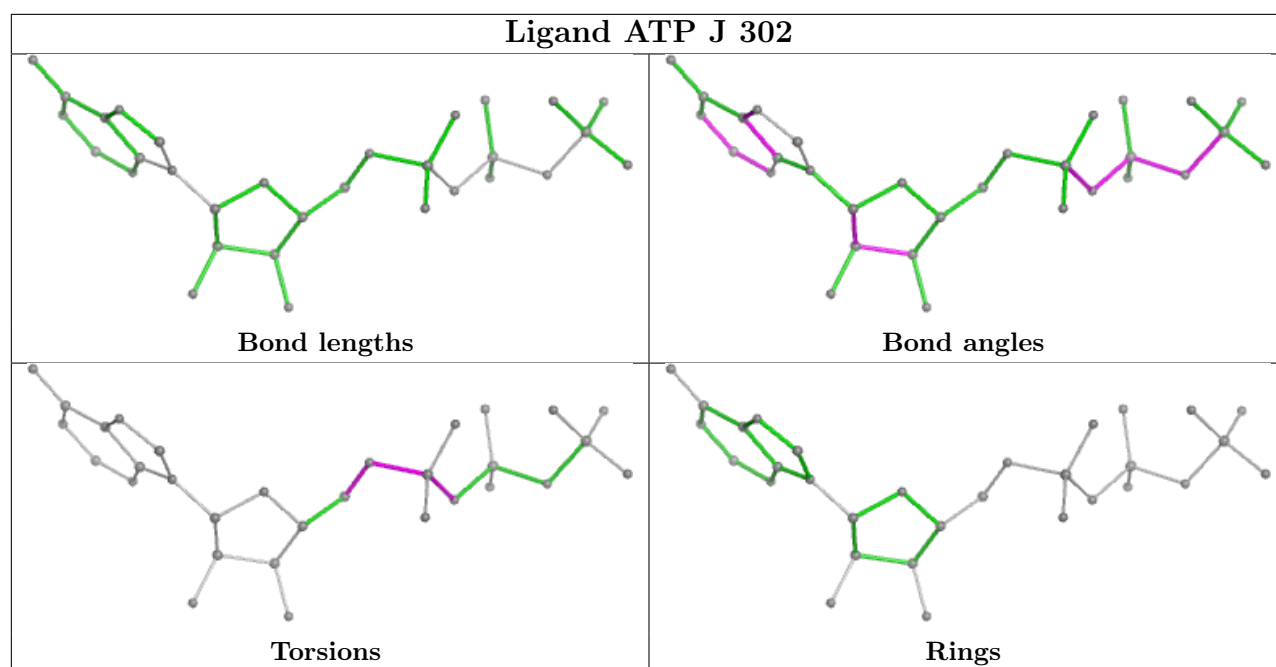
Mol	Chain	Res	Type	Atoms
4	L	302	ATP	PB-O3A-PA-O2A
4	K	302	ATP	PA-O3A-PB-O2B
4	K	302	ATP	PB-O3A-PA-O1A
4	D	302	ATP	C5'-O5'-PA-O2A
4	J	302	ATP	C5'-O5'-PA-O2A

There are no ring outliers.

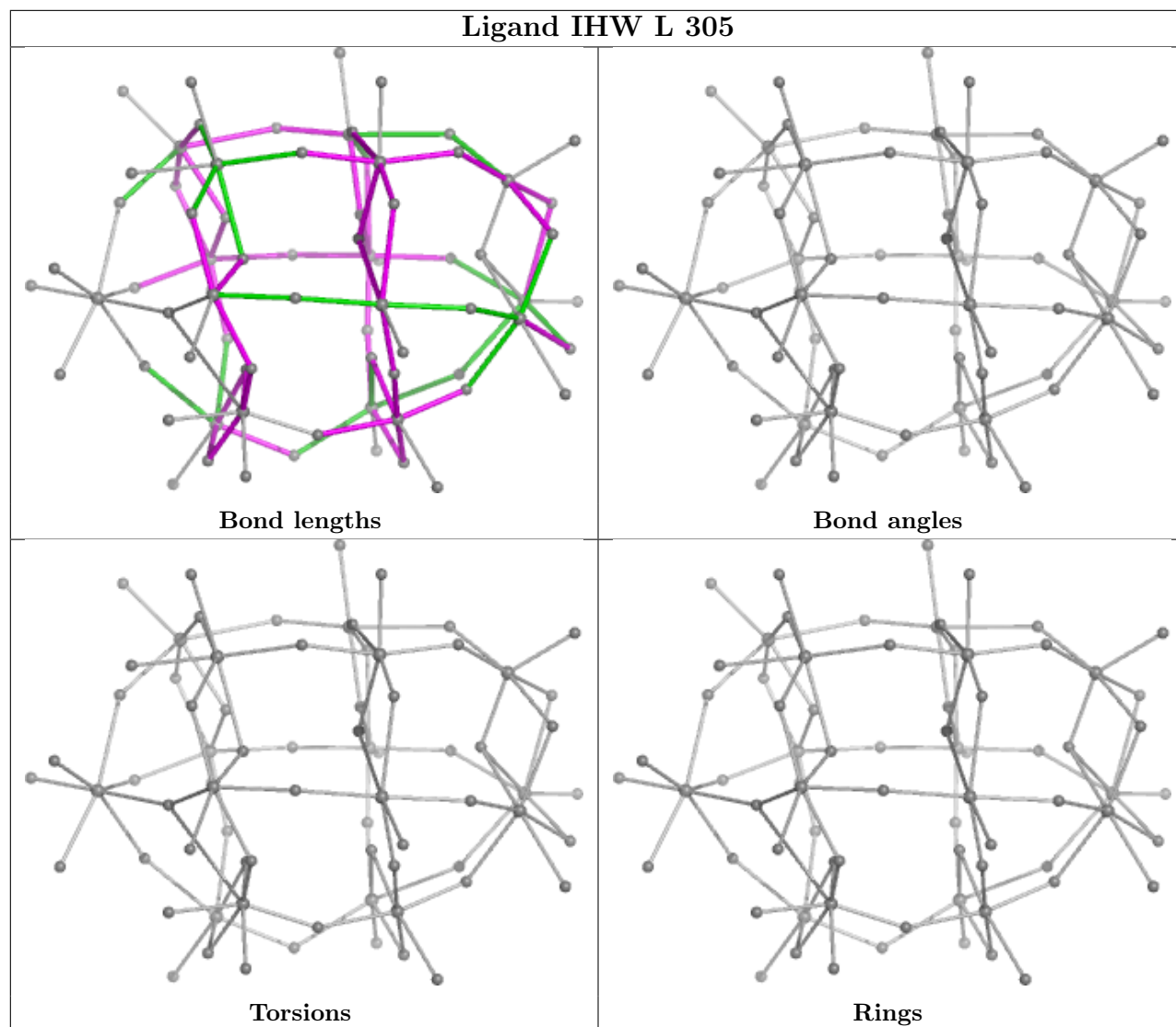
18 monomers are involved in 50 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	J	302	ATP	2	0
3	L	301	MOO	6	0
4	A	302	ATP	1	0
4	I	302	ATP	2	0
4	G	302	ATP	1	0
3	D	301	MOO	5	0
4	L	302	ATP	1	0
3	B	301	MOO	4	0
3	F	301	MOO	6	0
4	C	302	ATP	1	0
8	A	304	IWO	1	0
4	F	302	ATP	1	0
4	K	302	ATP	2	0
3	J	301	MOO	6	0
3	H	301	MOO	7	0
4	D	302	ATP	1	0
4	H	302	ATP	1	0
4	E	302	ATP	2	0

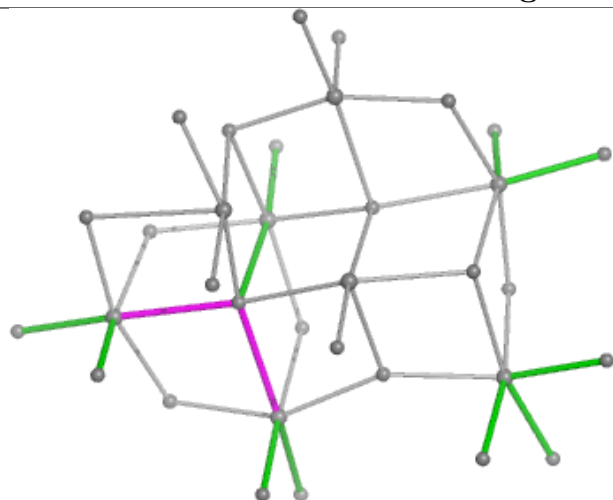
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



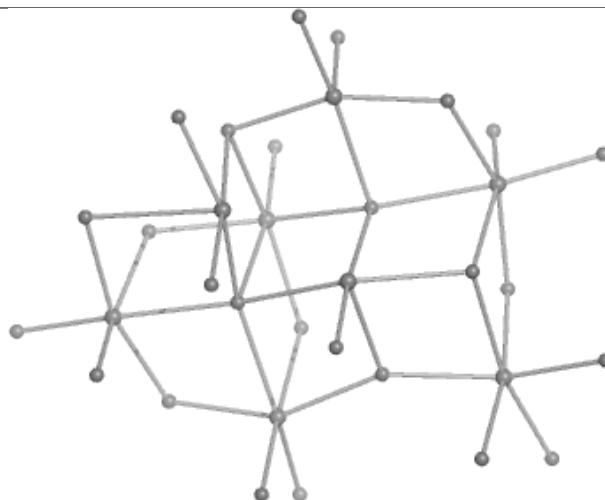
Ligand IHW L 305



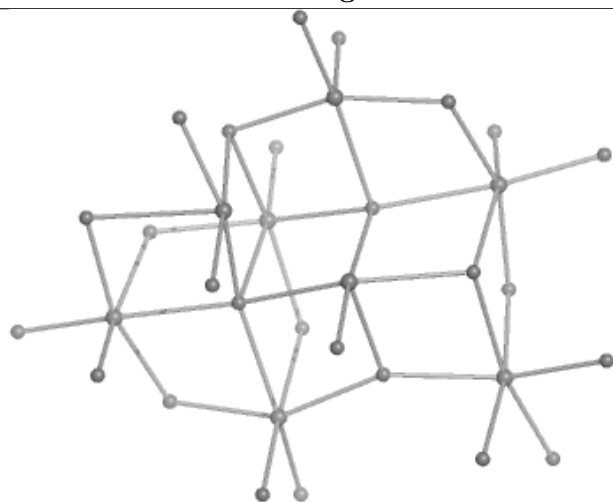
Ligand IWO I 304



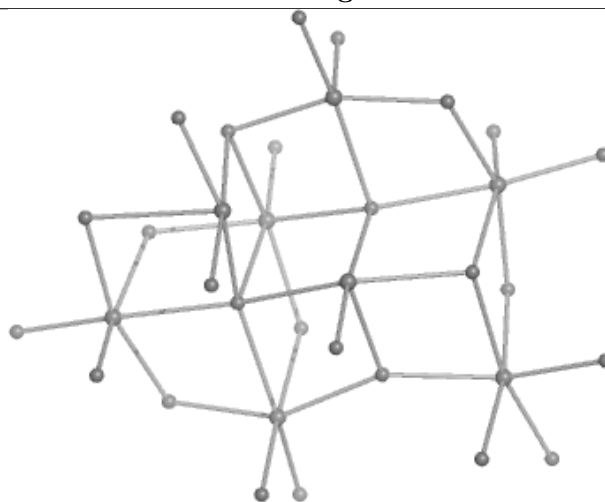
Bond lengths



Bond angles

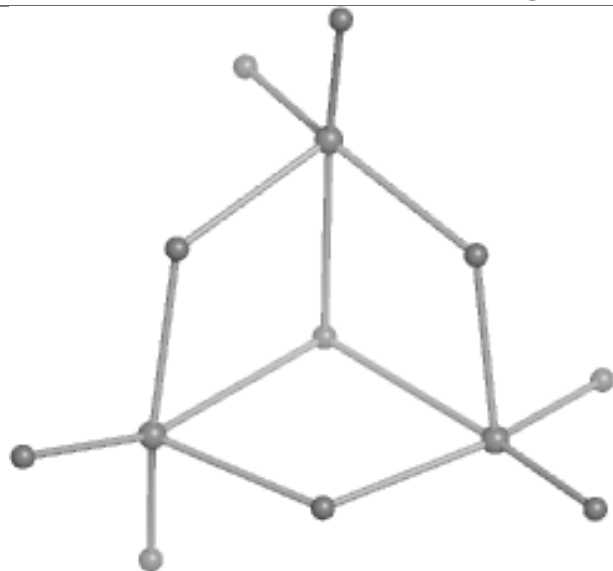


Torsions

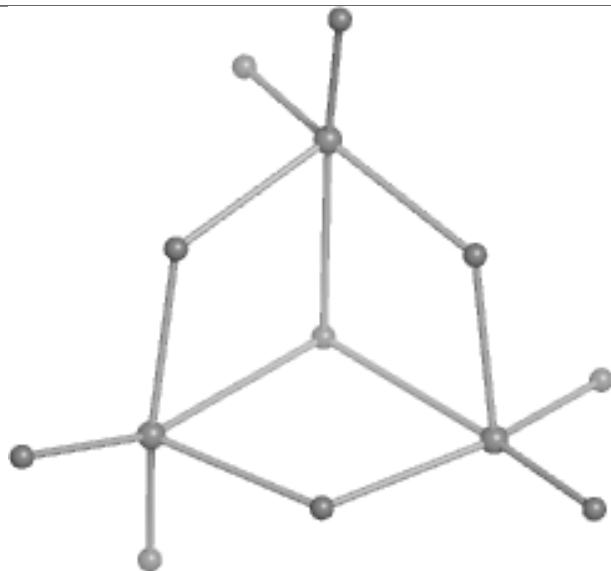


Rings

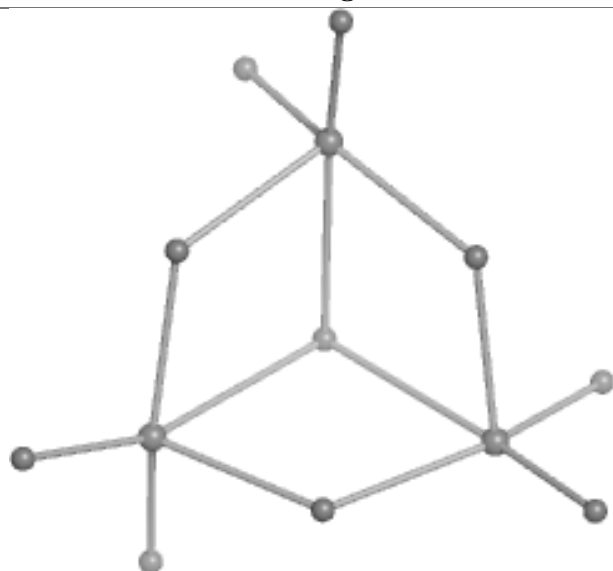
Ligand IX3 E 305



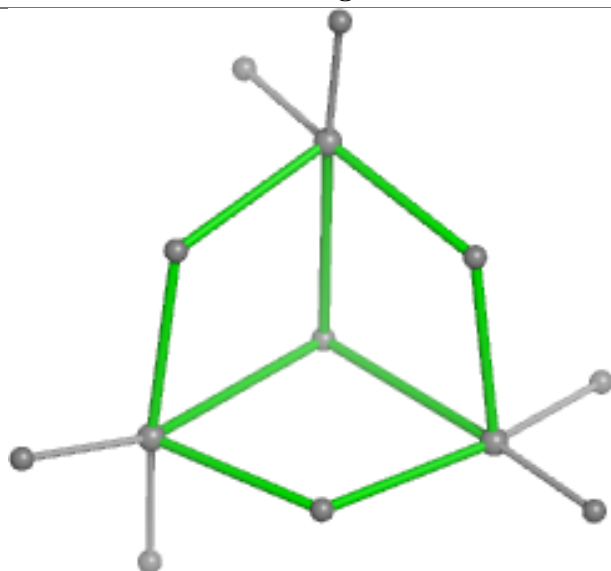
Bond lengths



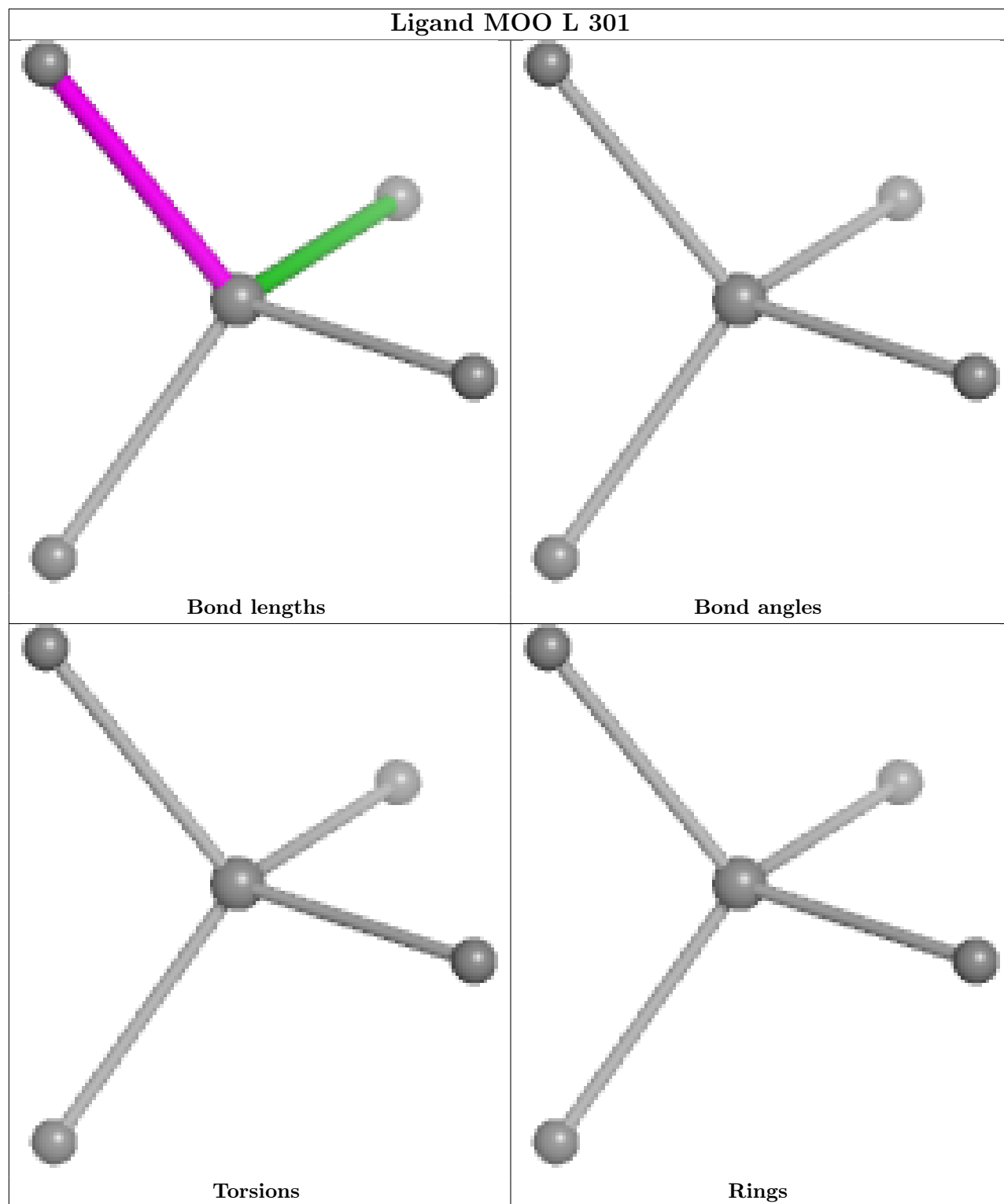
Bond angles



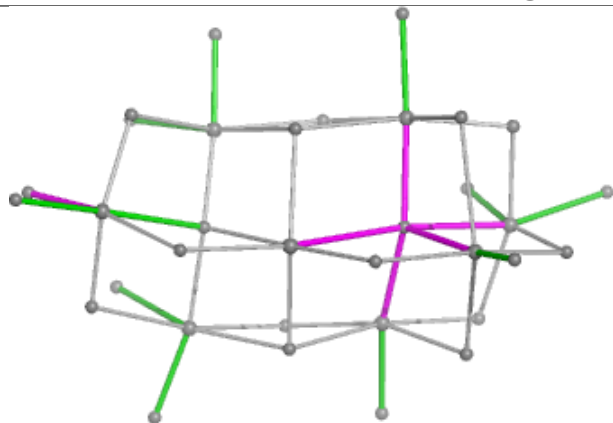
Torsions



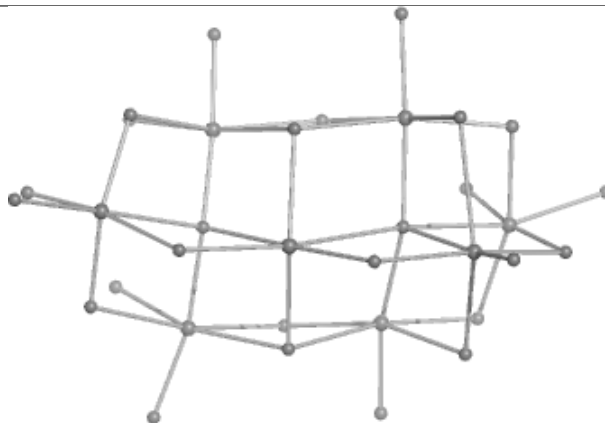
Rings



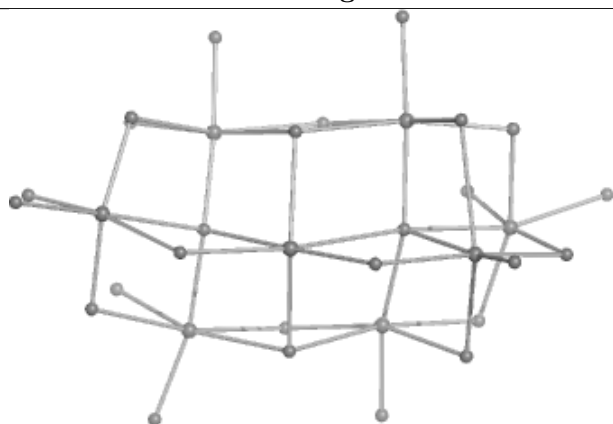
Ligand IV9 G 301



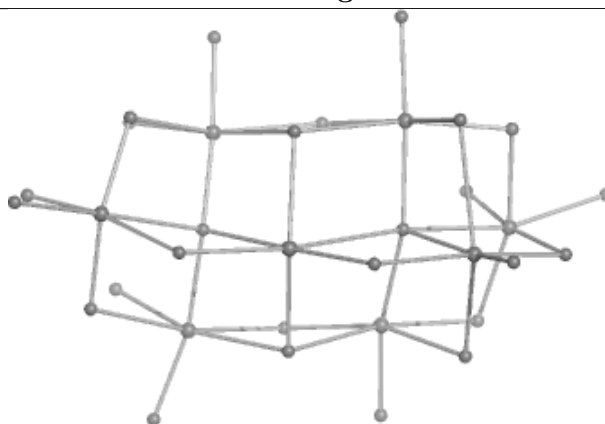
Bond lengths



Bond angles

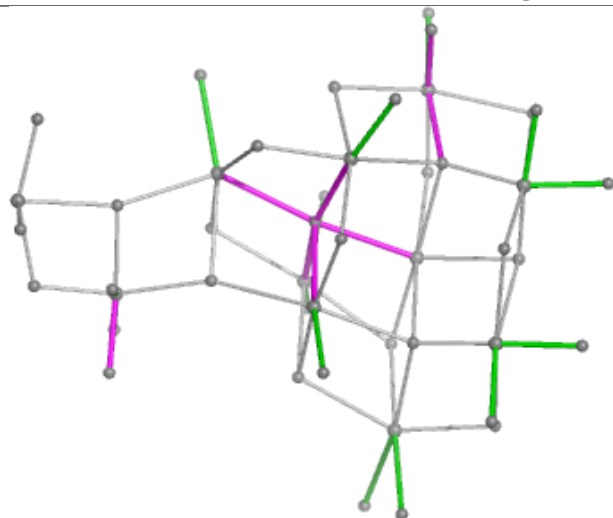


Torsions

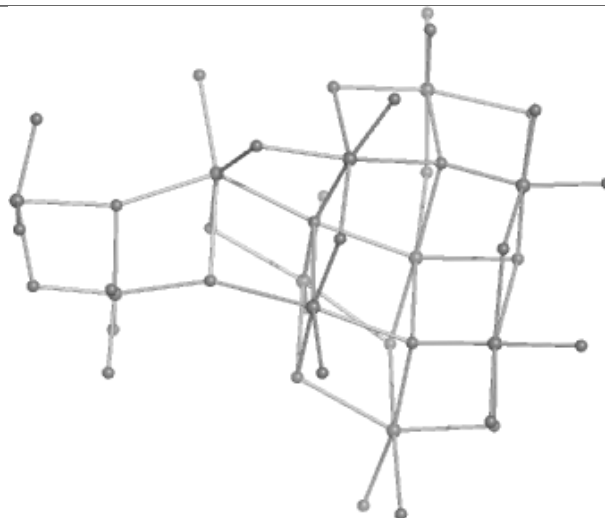


Rings

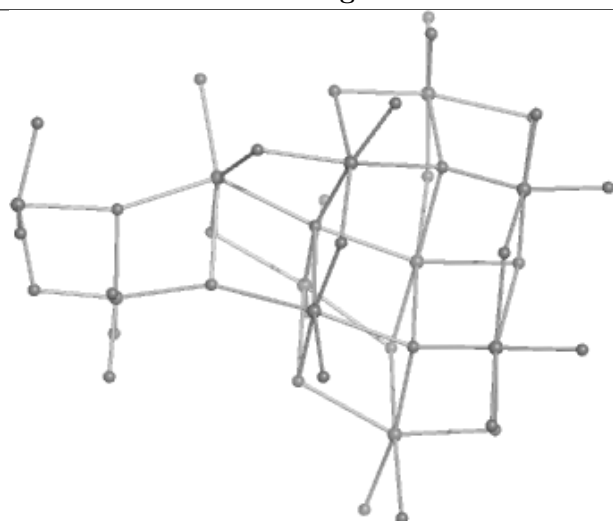
Ligand IWL F 304



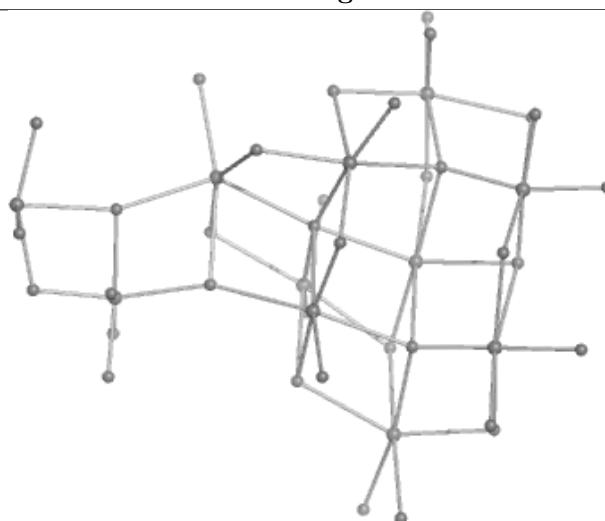
Bond lengths



Bond angles

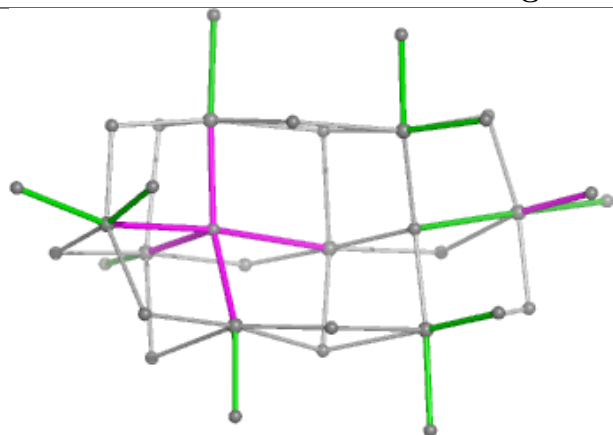


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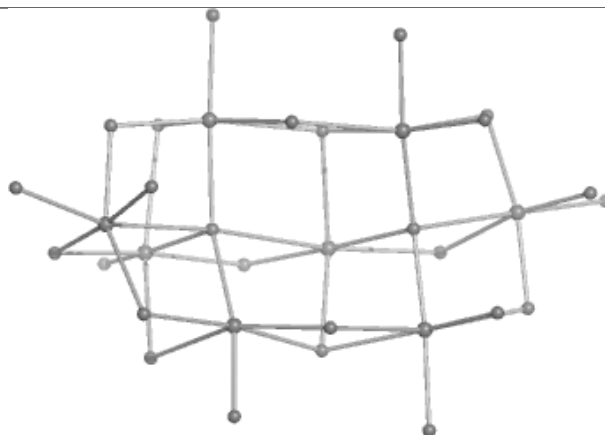


Rings

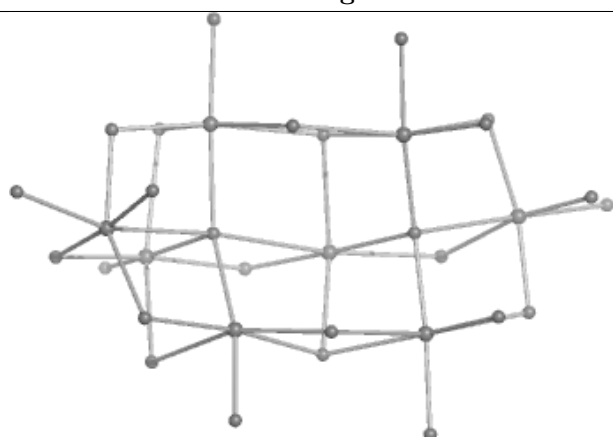
Ligand IV9 A 301



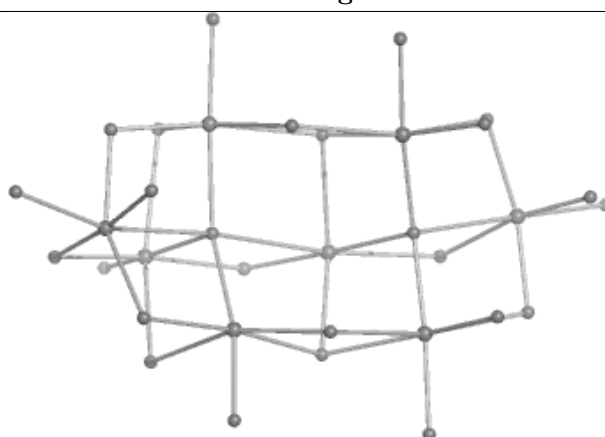
Bond lengths



Bond angles

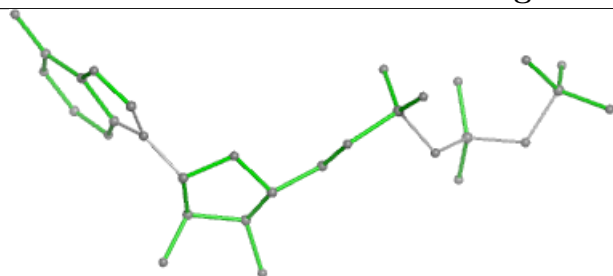


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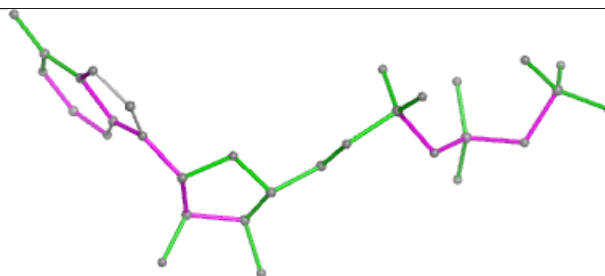


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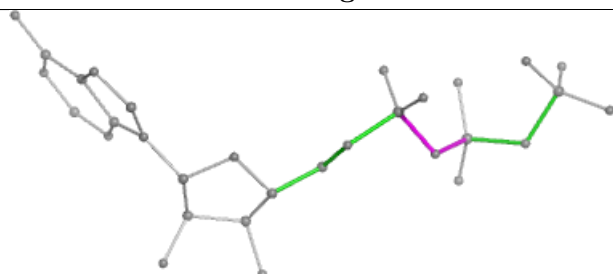
Ligand ATP A 302



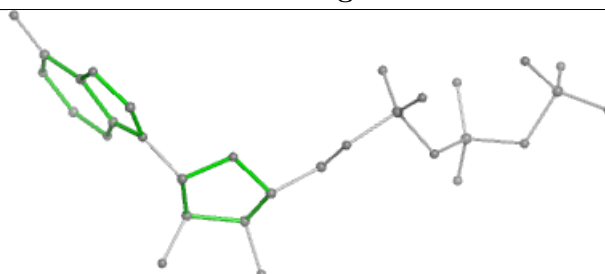
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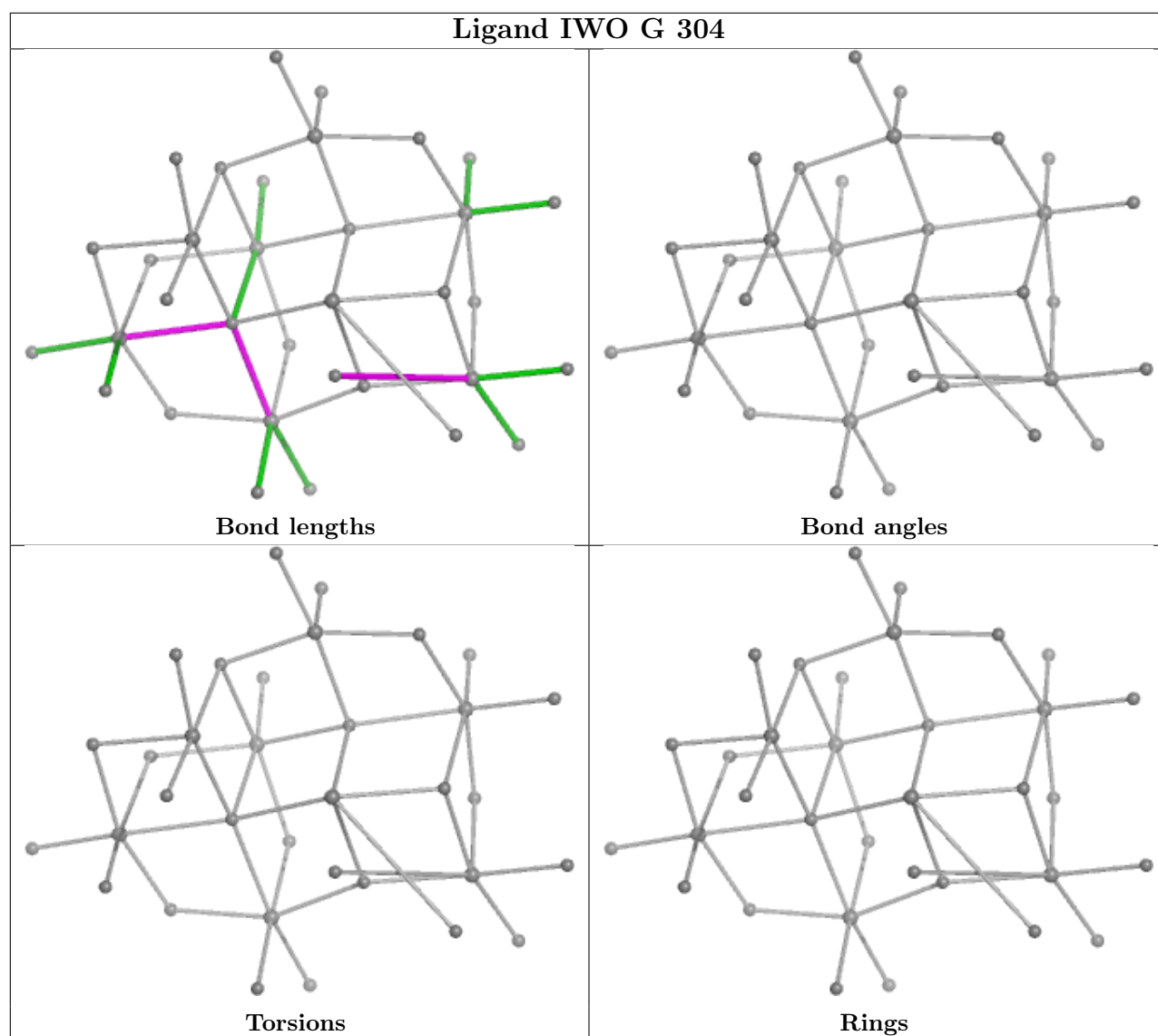
Bond angles



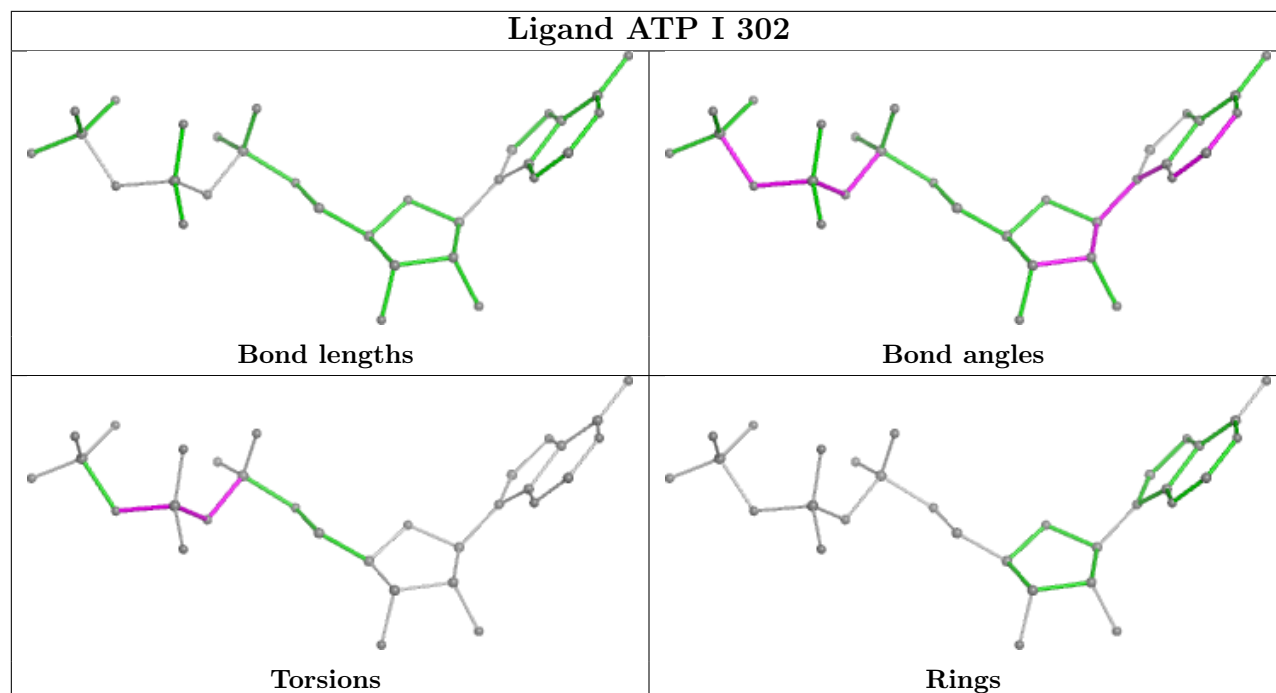
Torsions



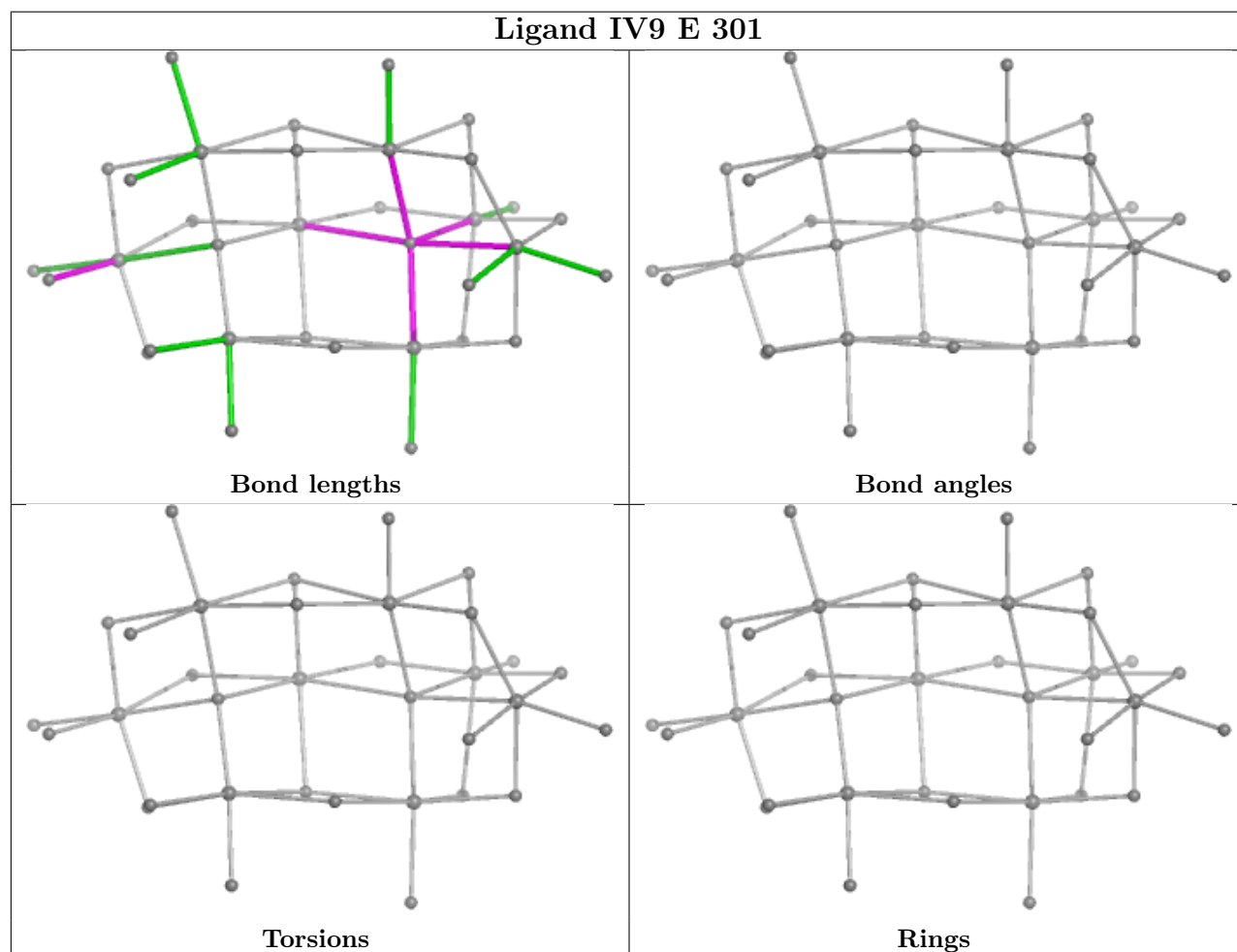
Rings

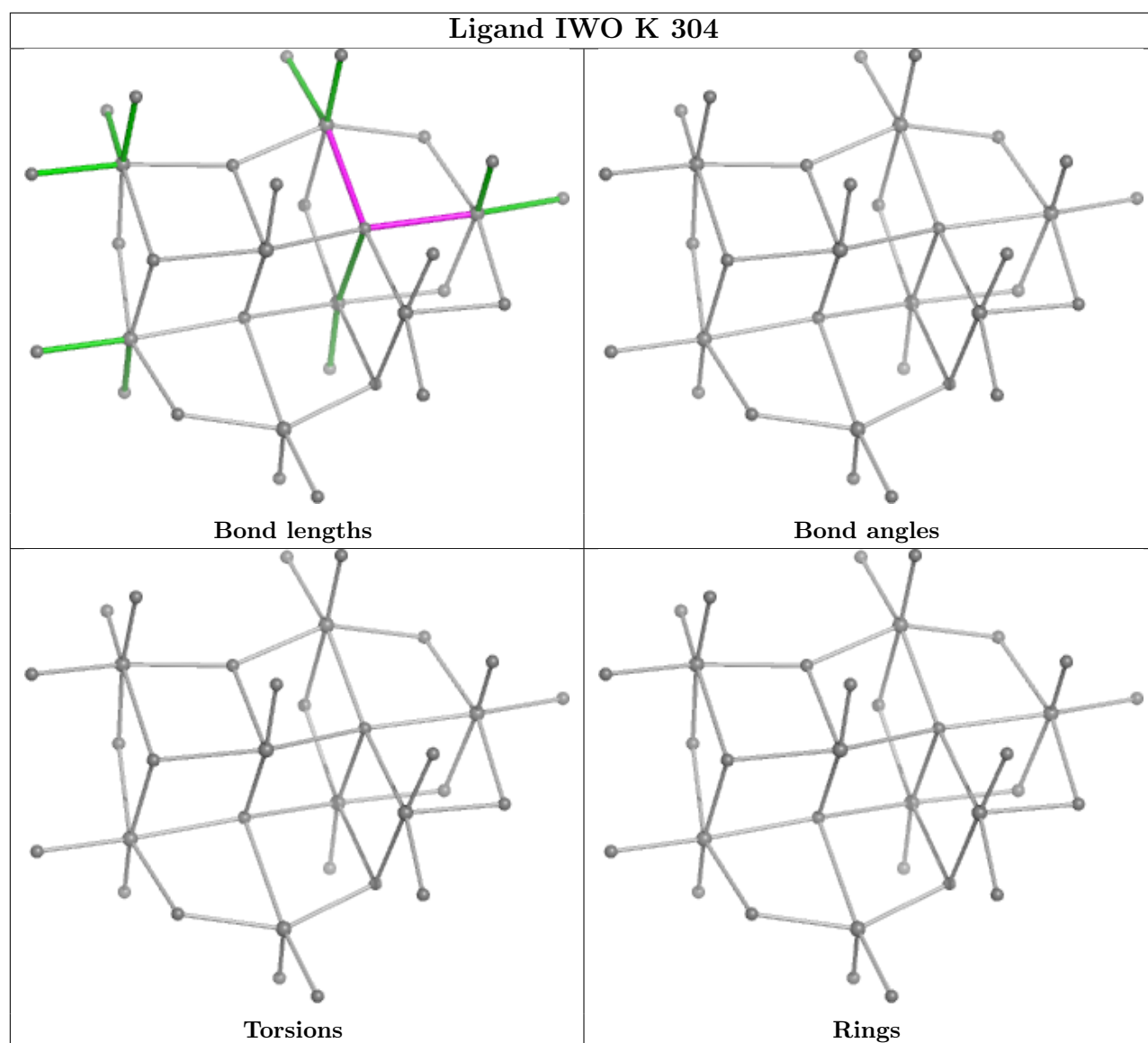


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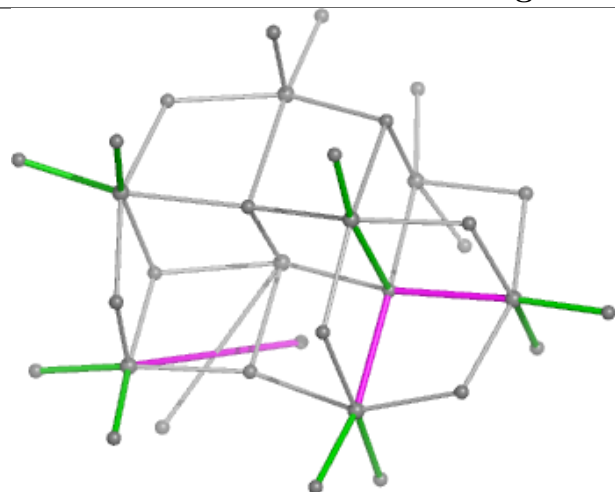


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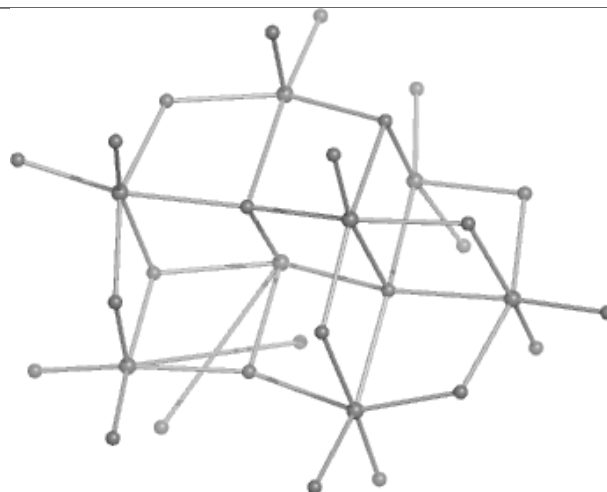




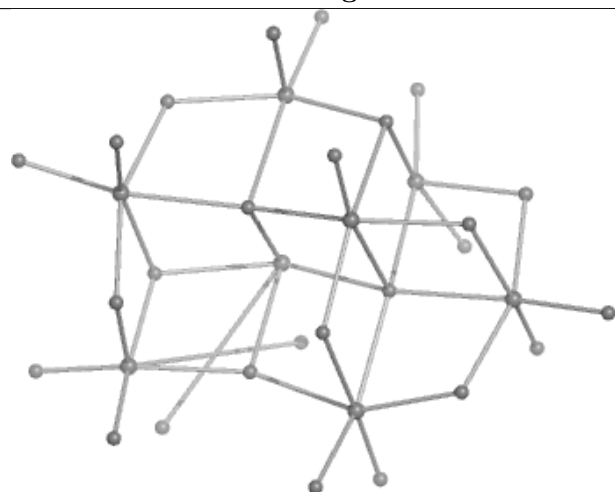
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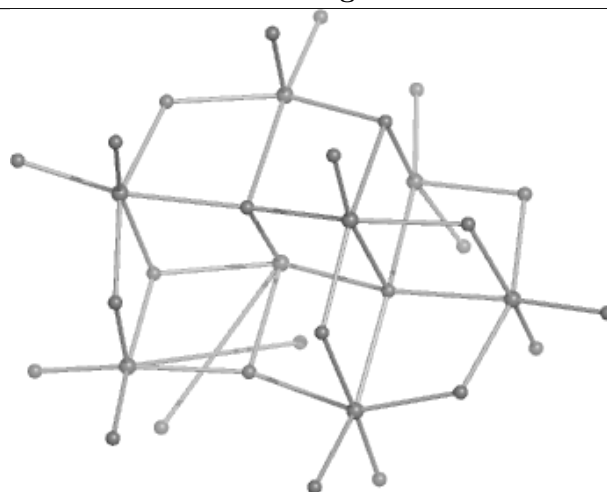
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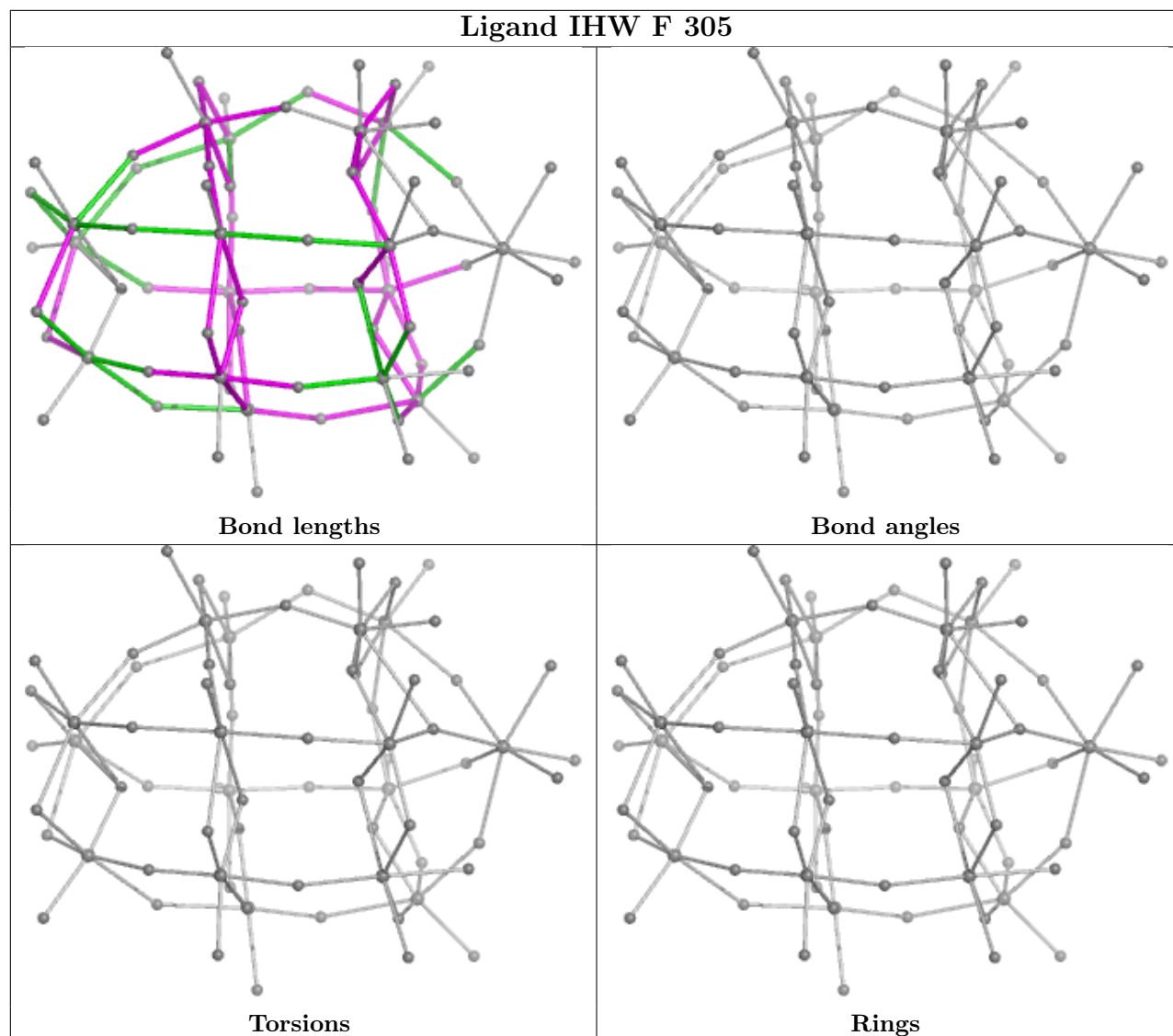
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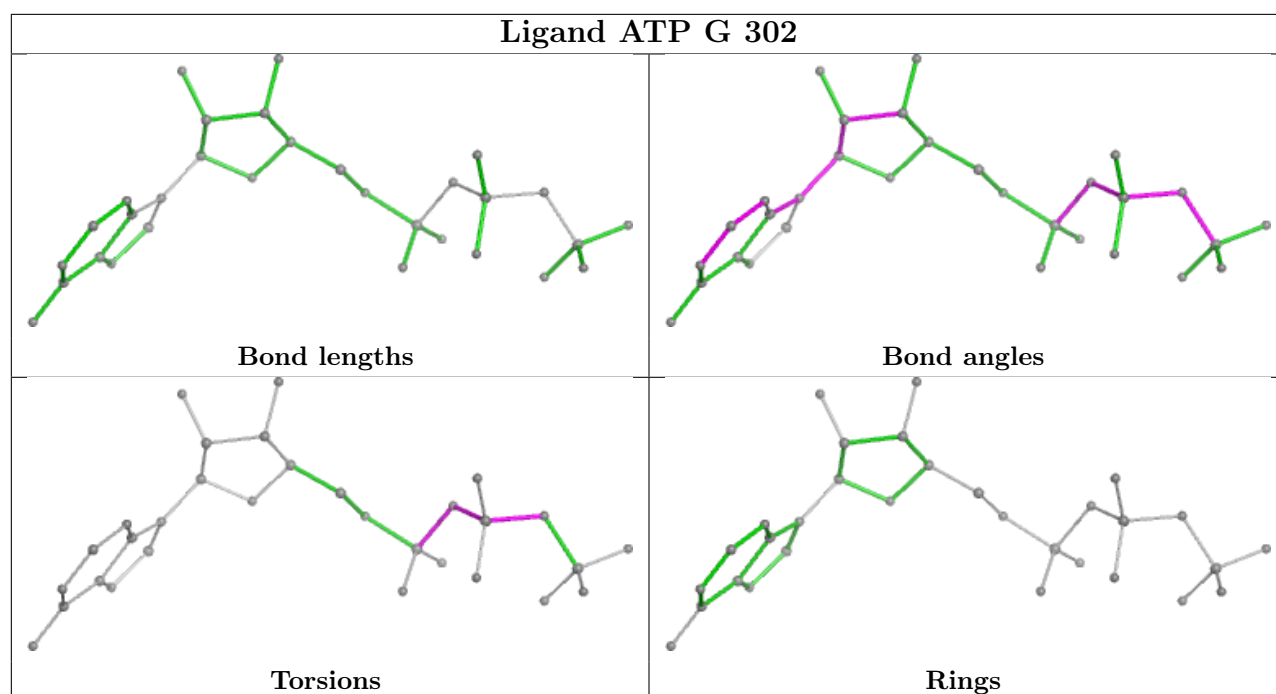


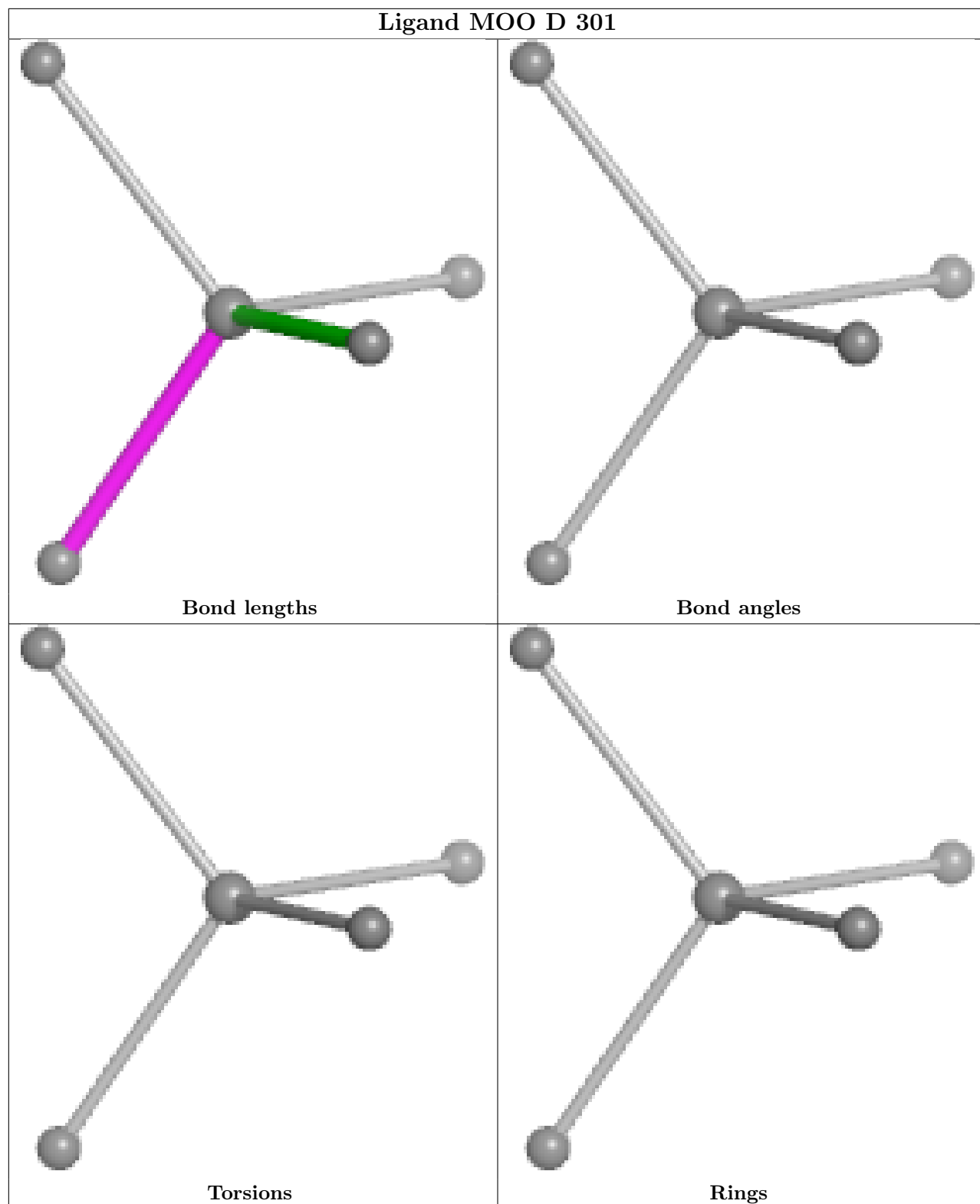
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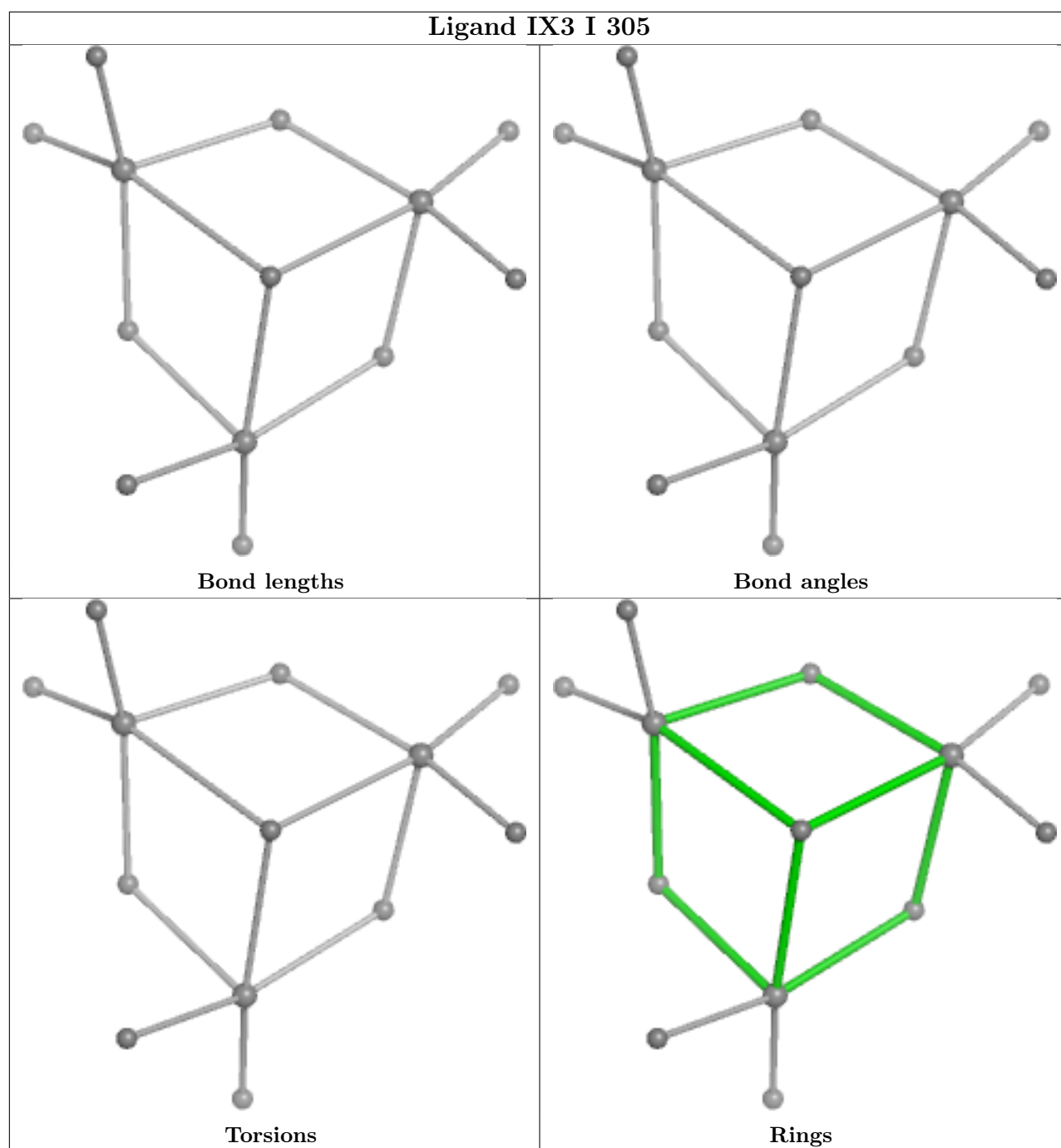


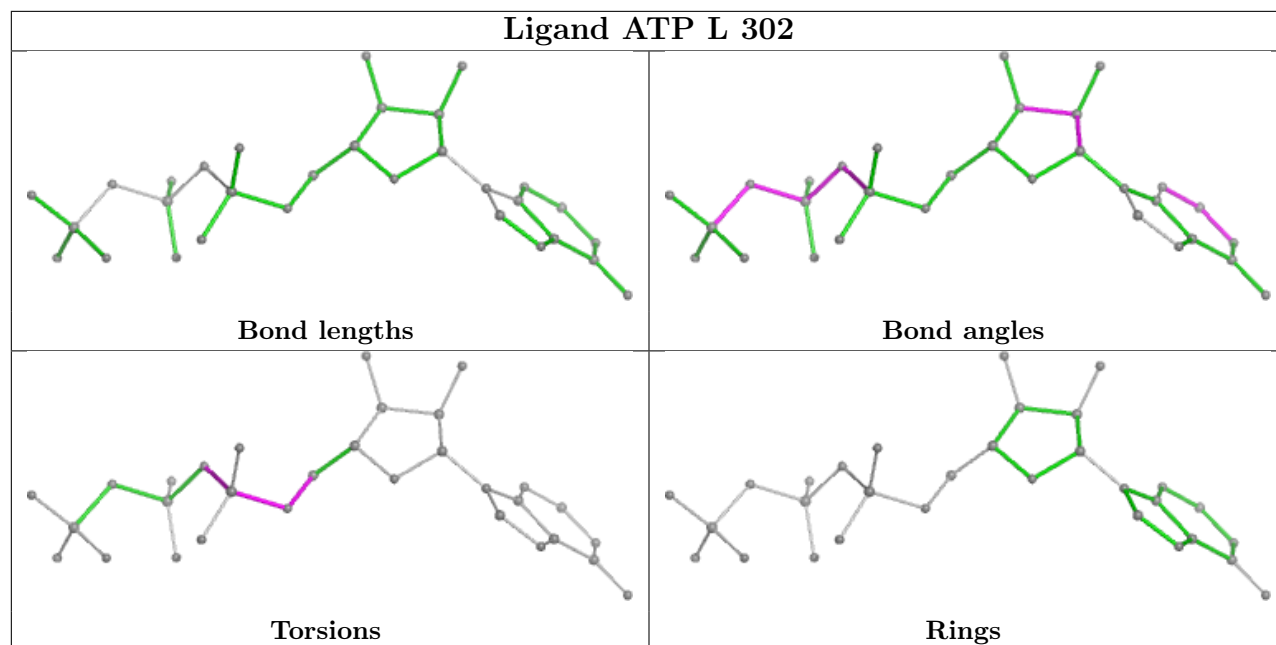
Rings

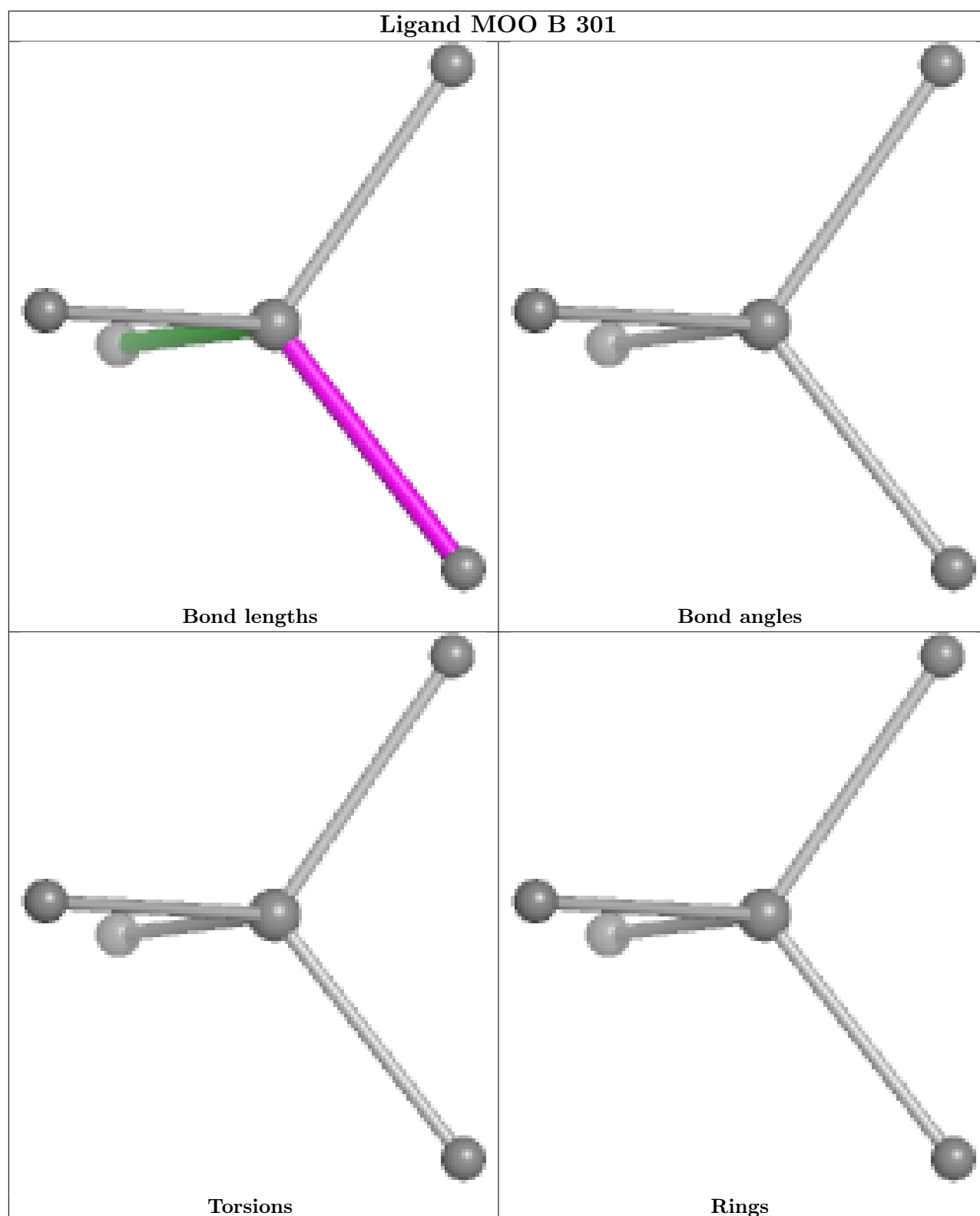


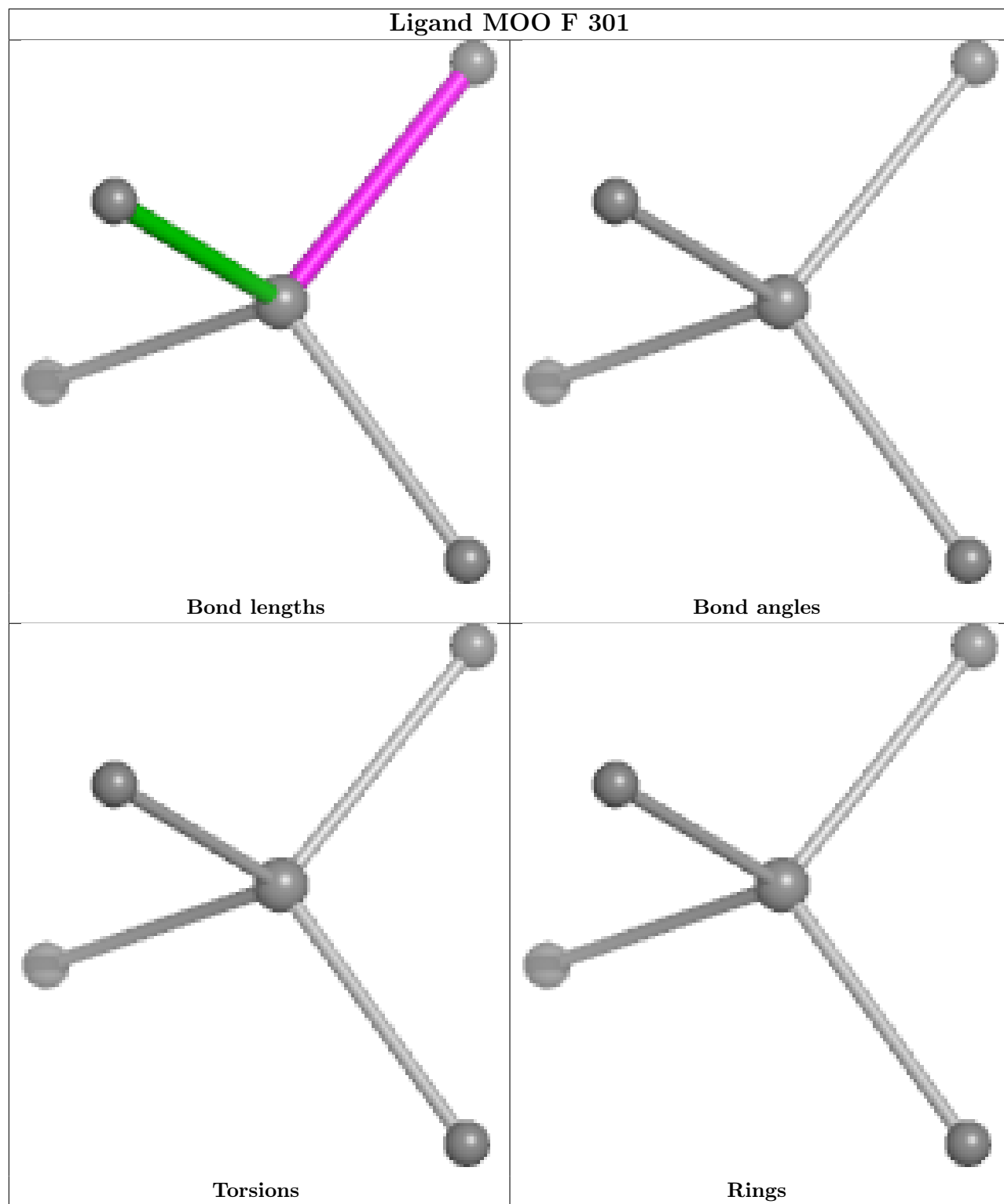




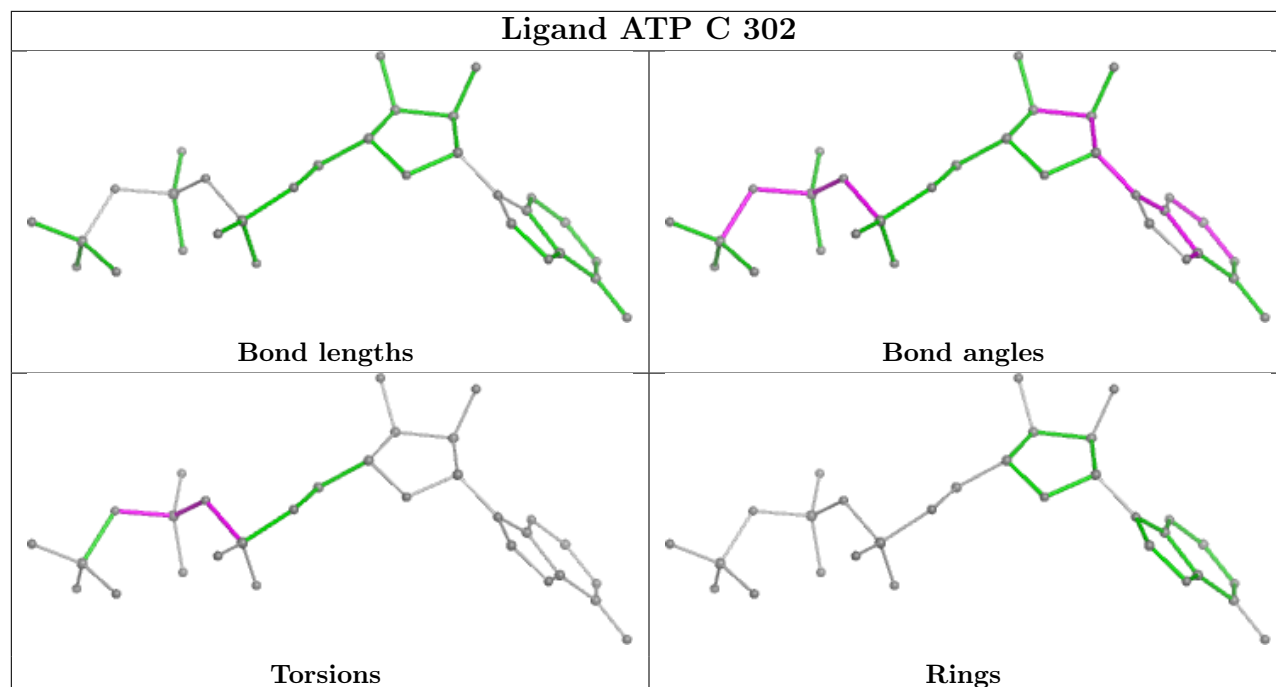




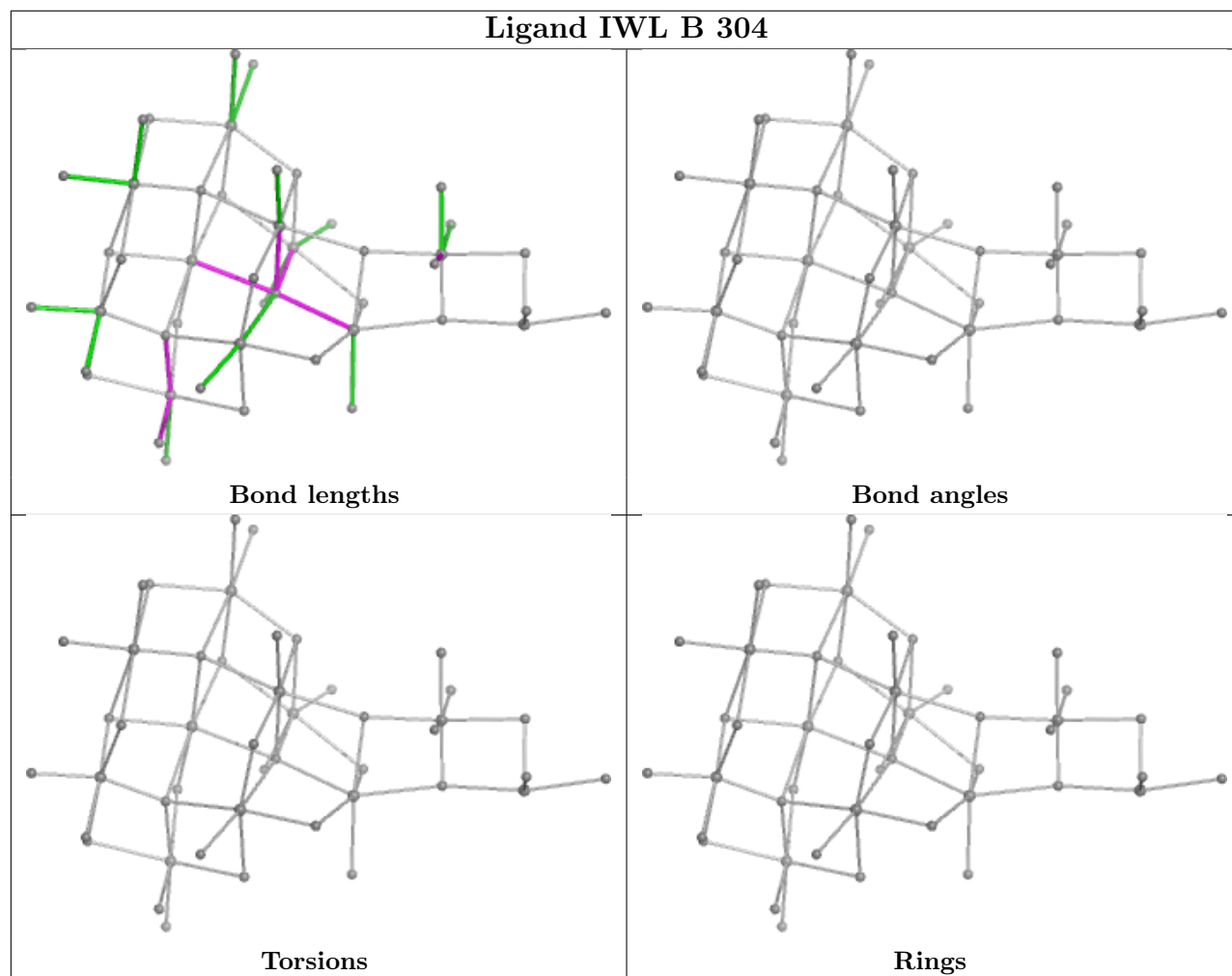


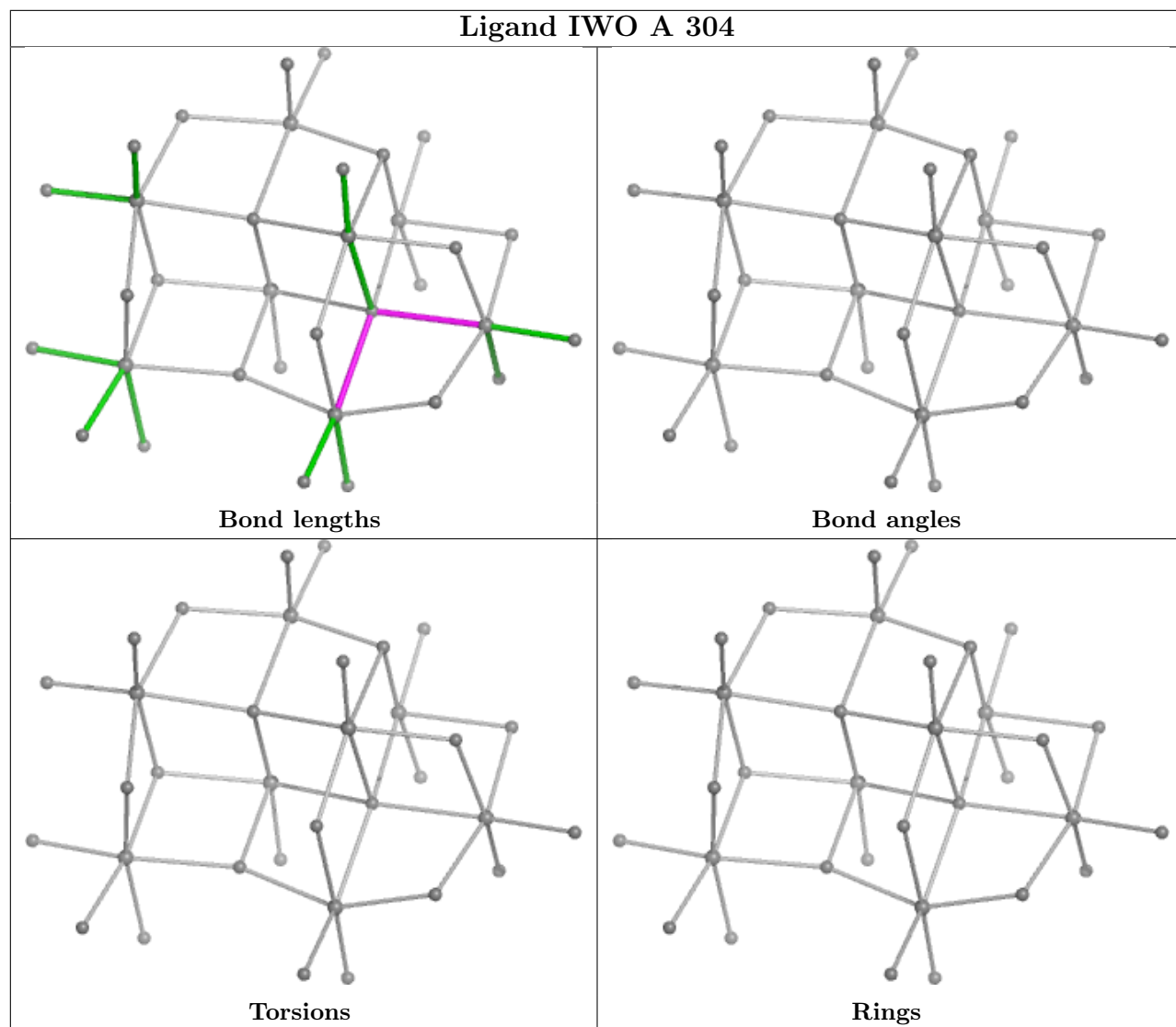


Ligand ATP C 302

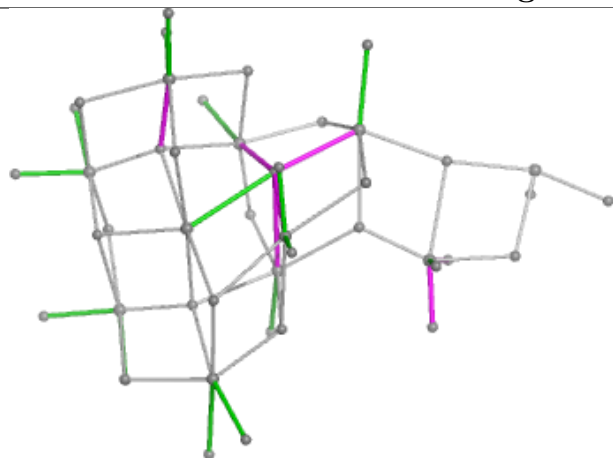


Ligand IWL B 304

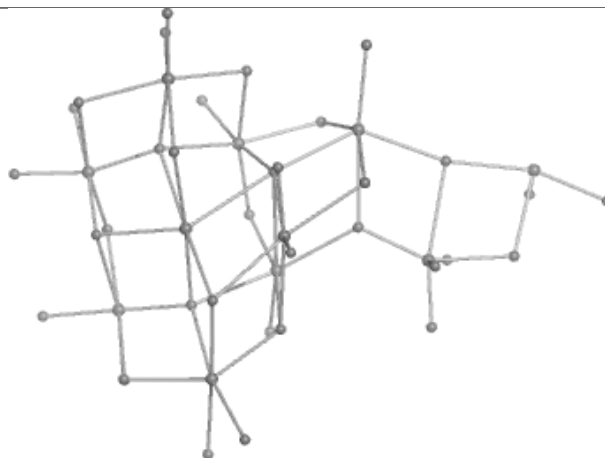




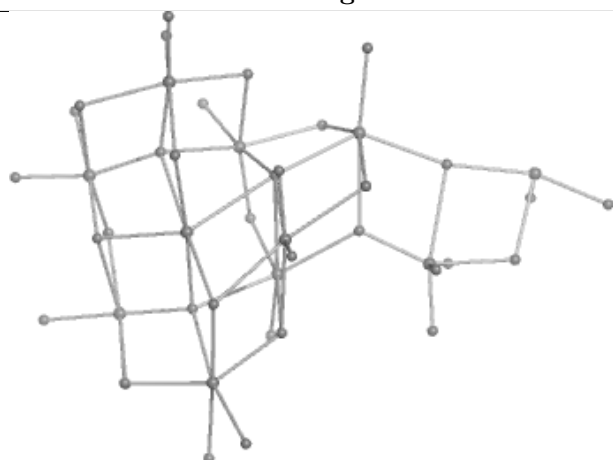
Ligand IWL L 304



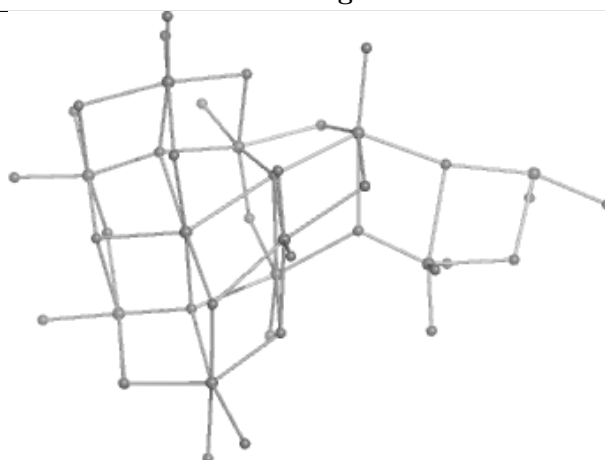
Bond lengths



Bond angles

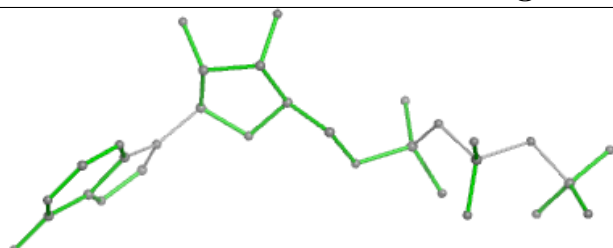


Torsions

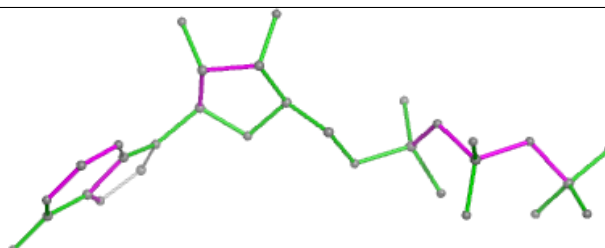


Rings

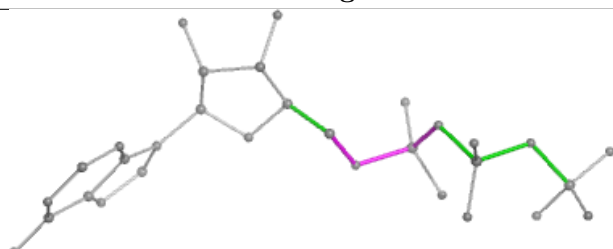
Ligand ATP F 302



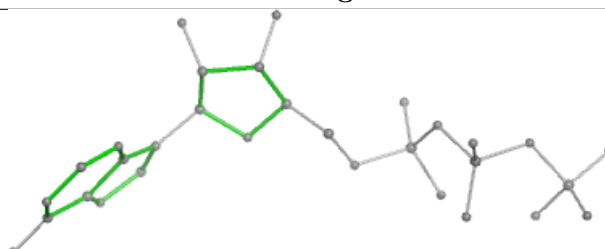
Bond lengths



Bond angles

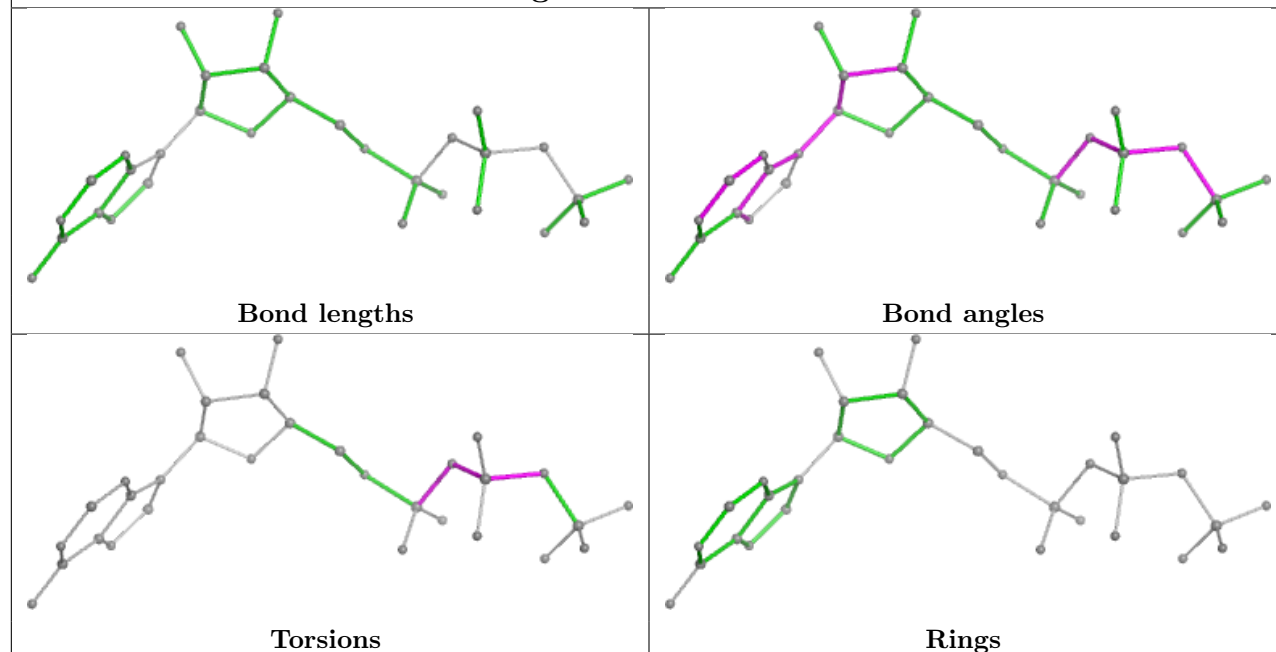


Torsions

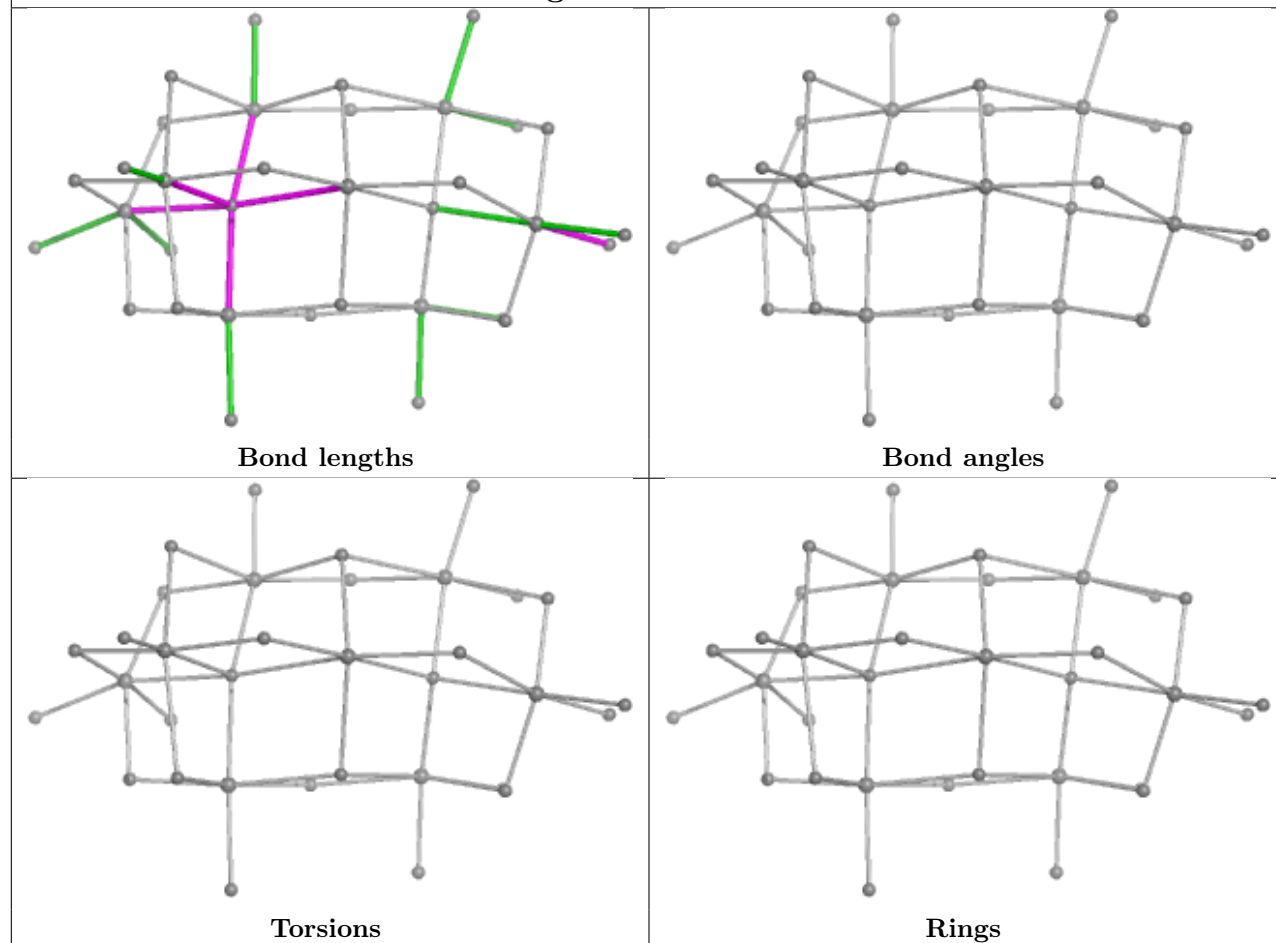


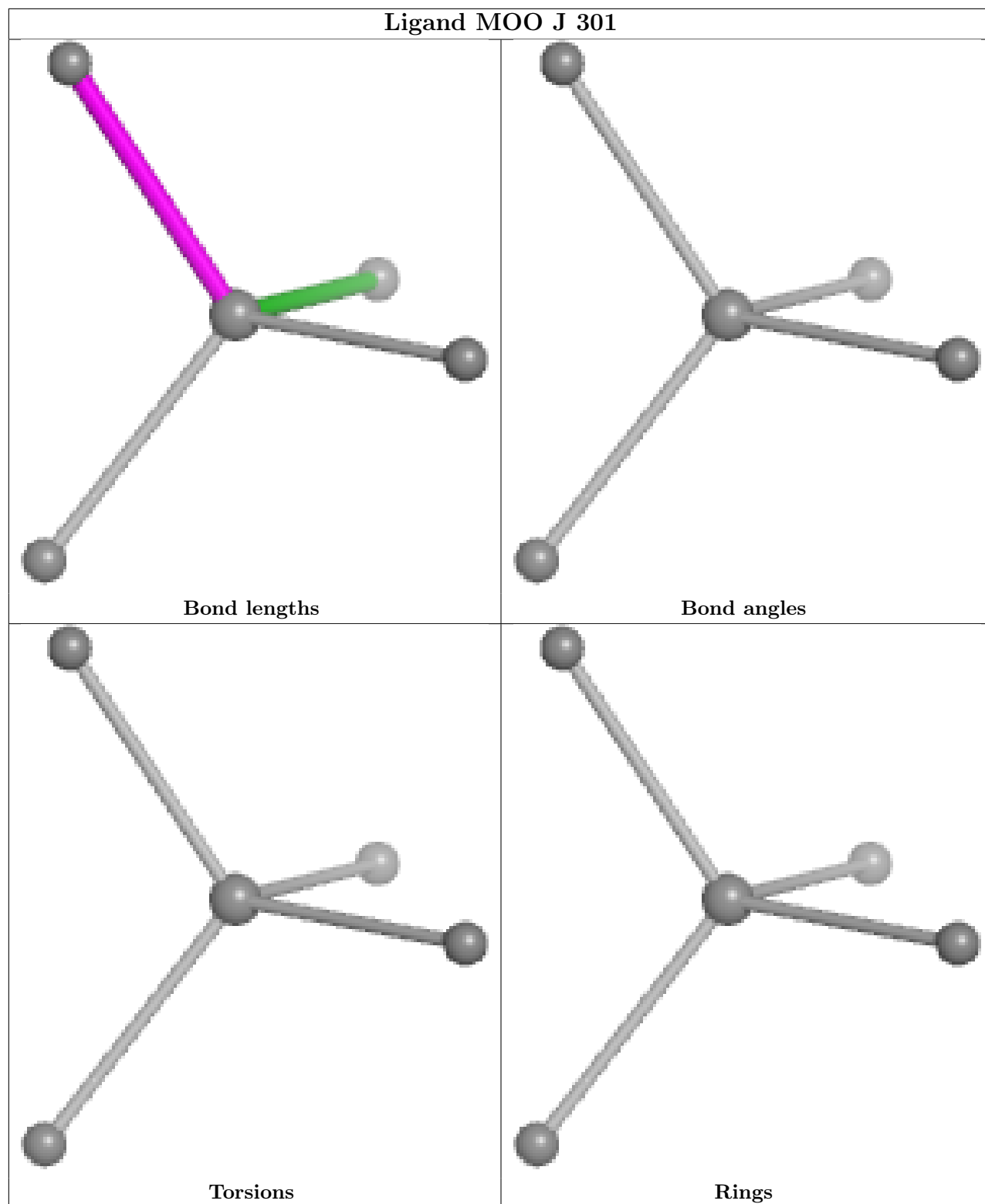
Rings

Ligand ATP K 302

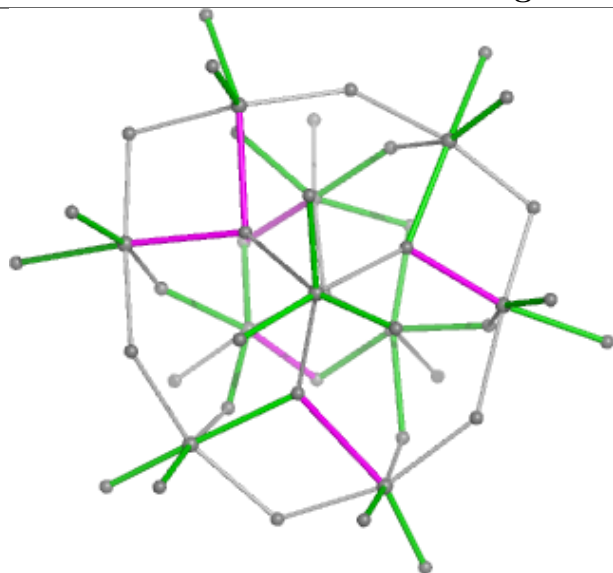


Ligand IV9 I 301

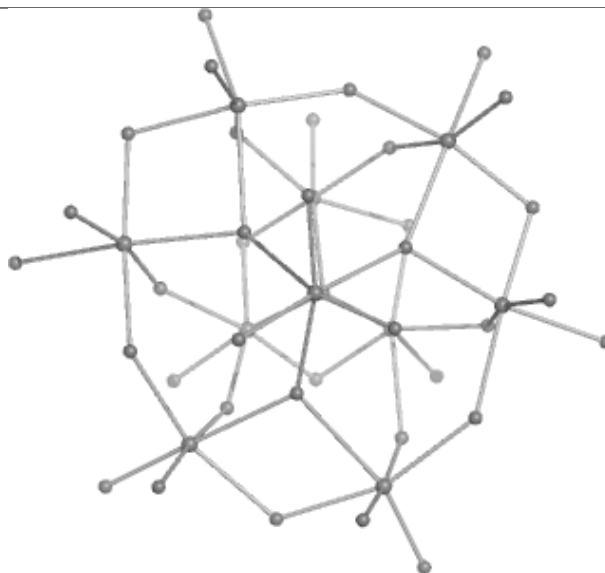




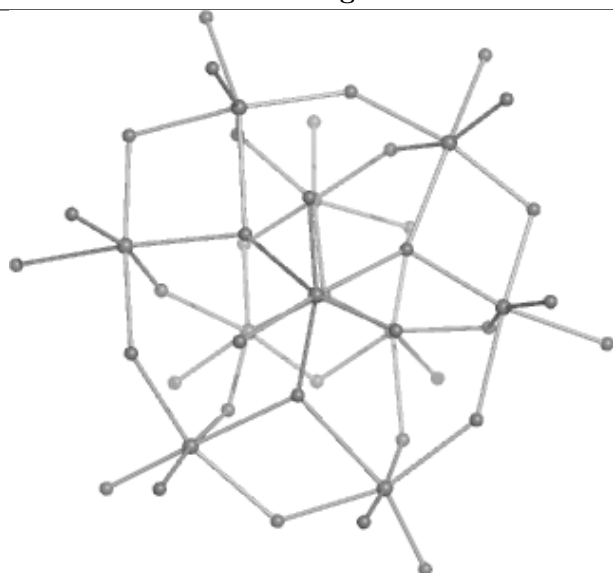
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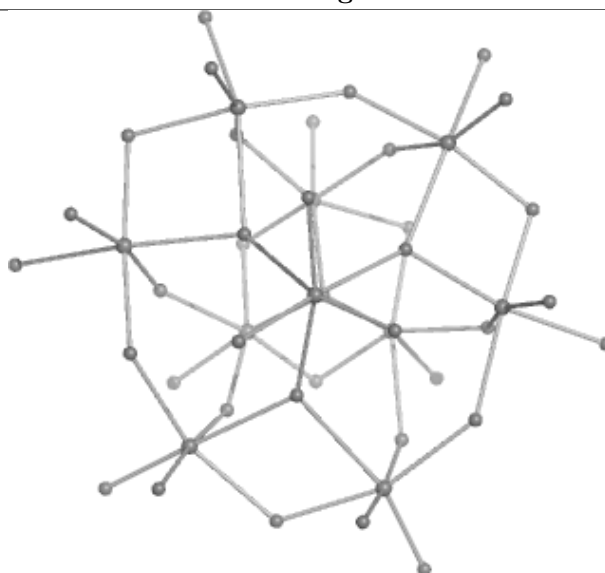
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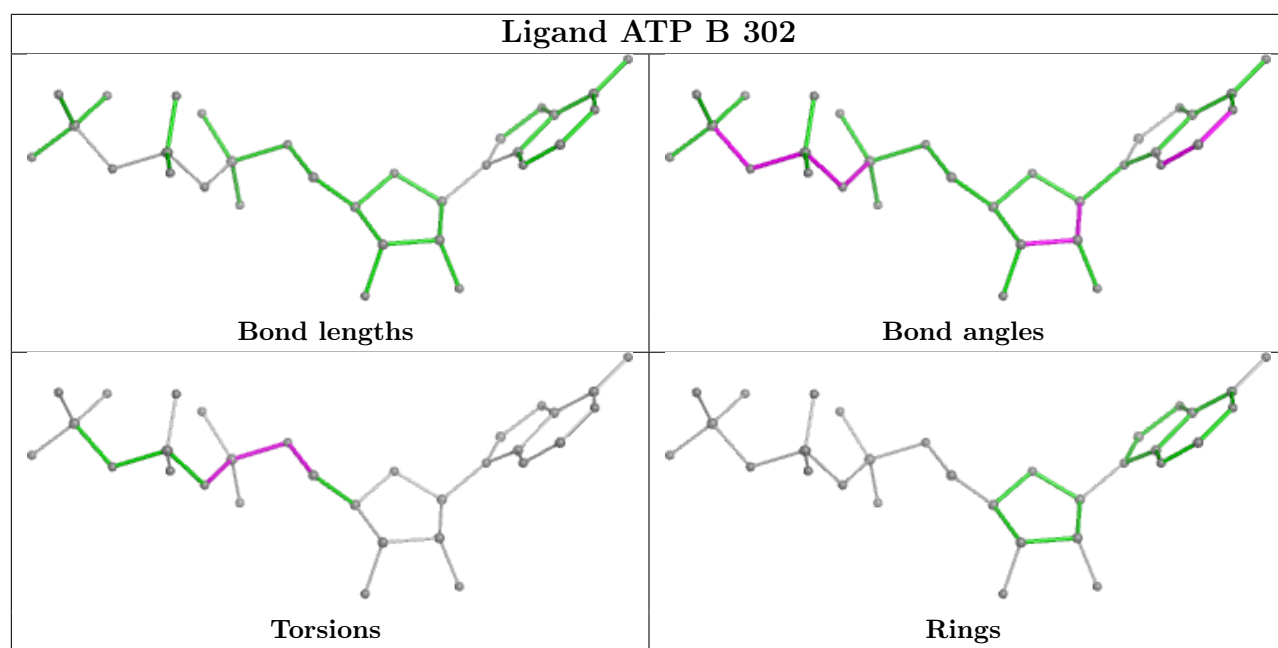
Bond angles



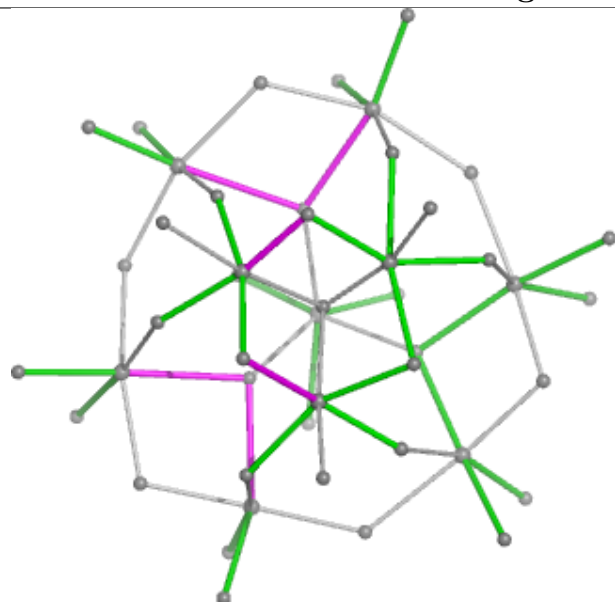
Torsions



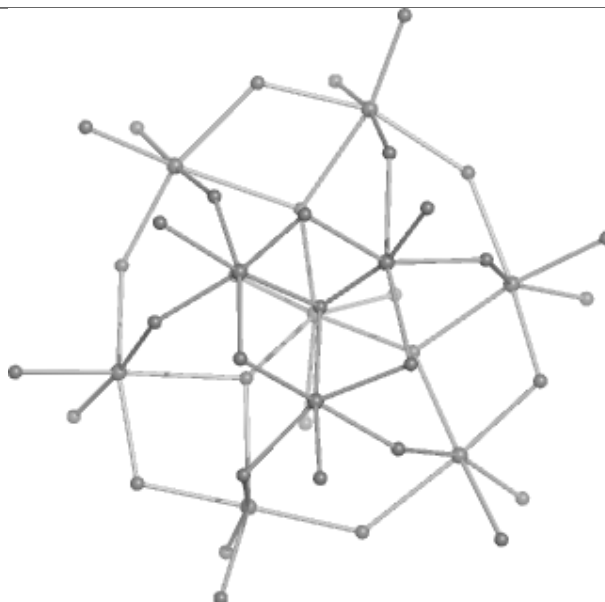
Rings



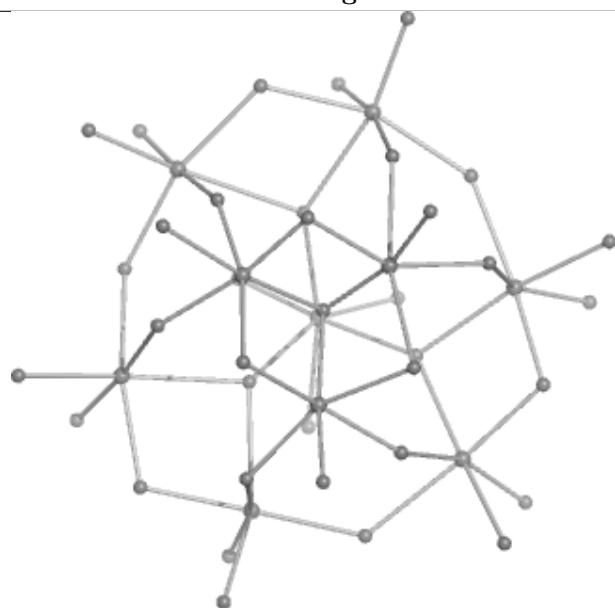
Ligand IWZ C 305



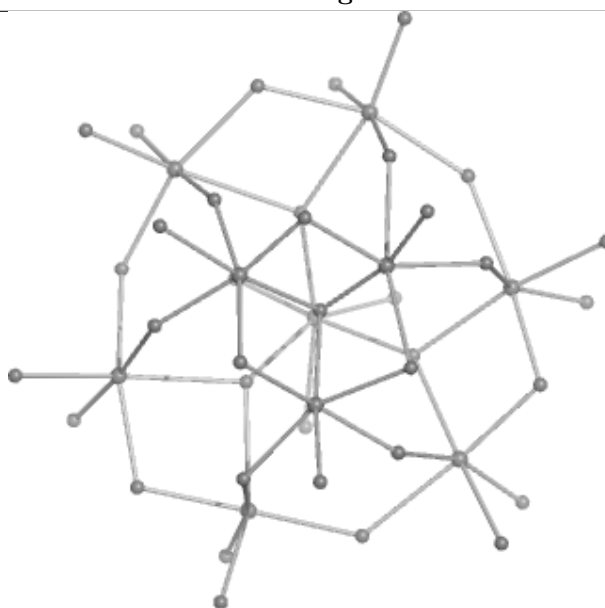
Bond lengths



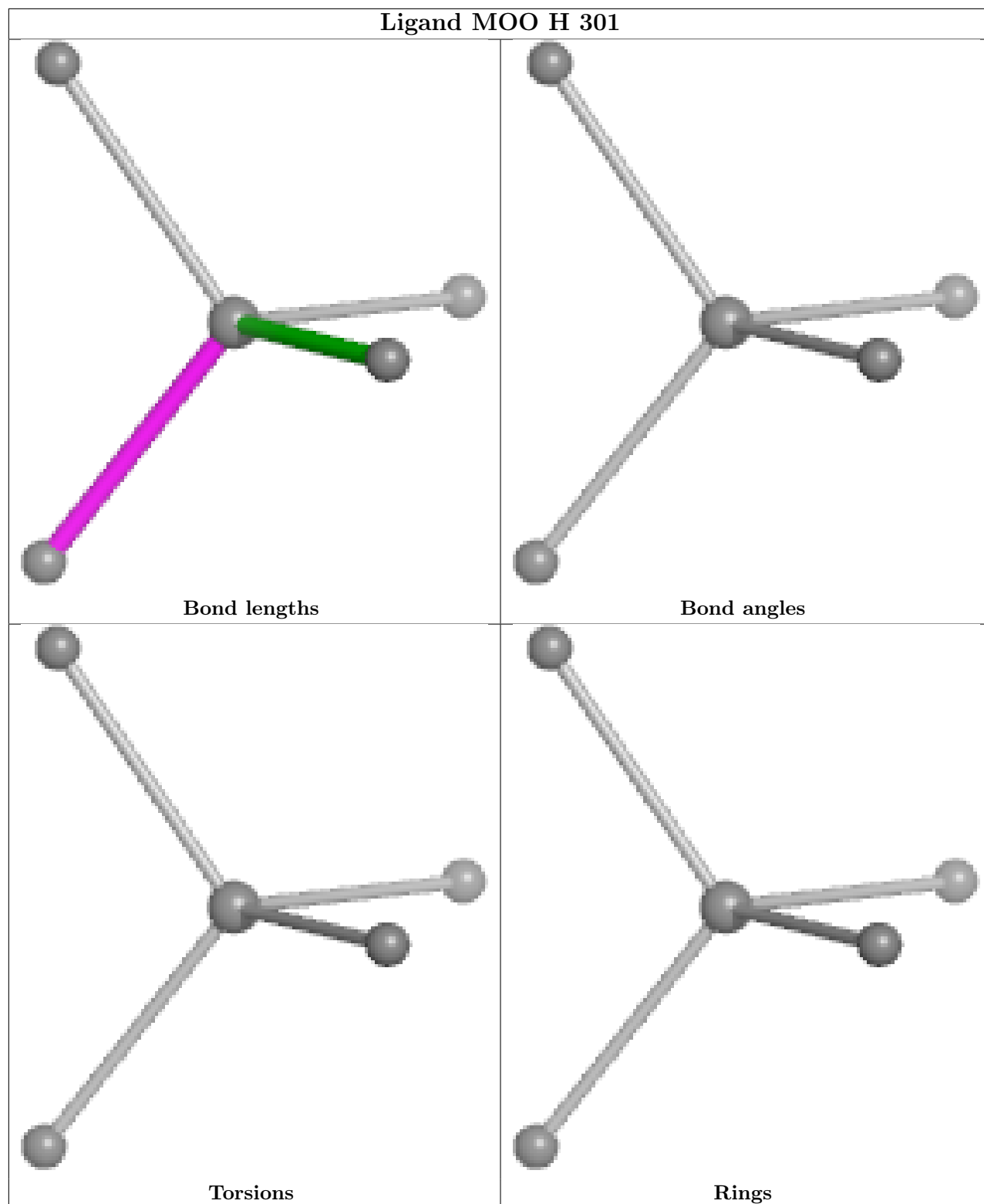
Bond angles

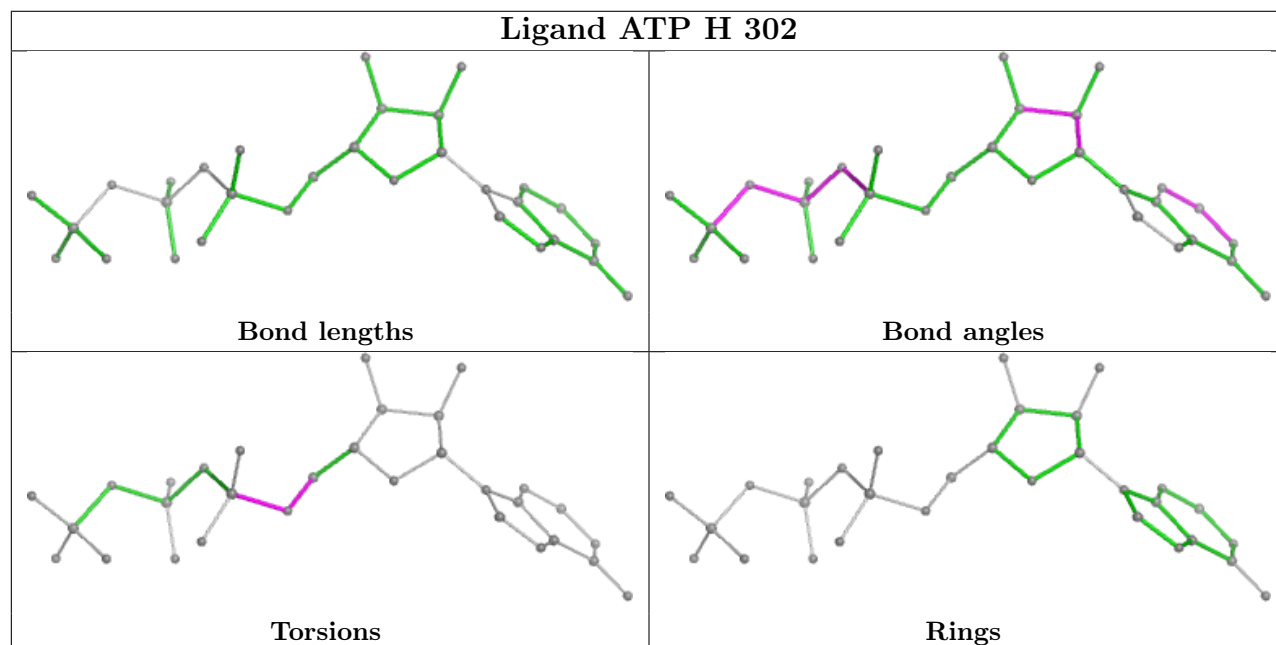
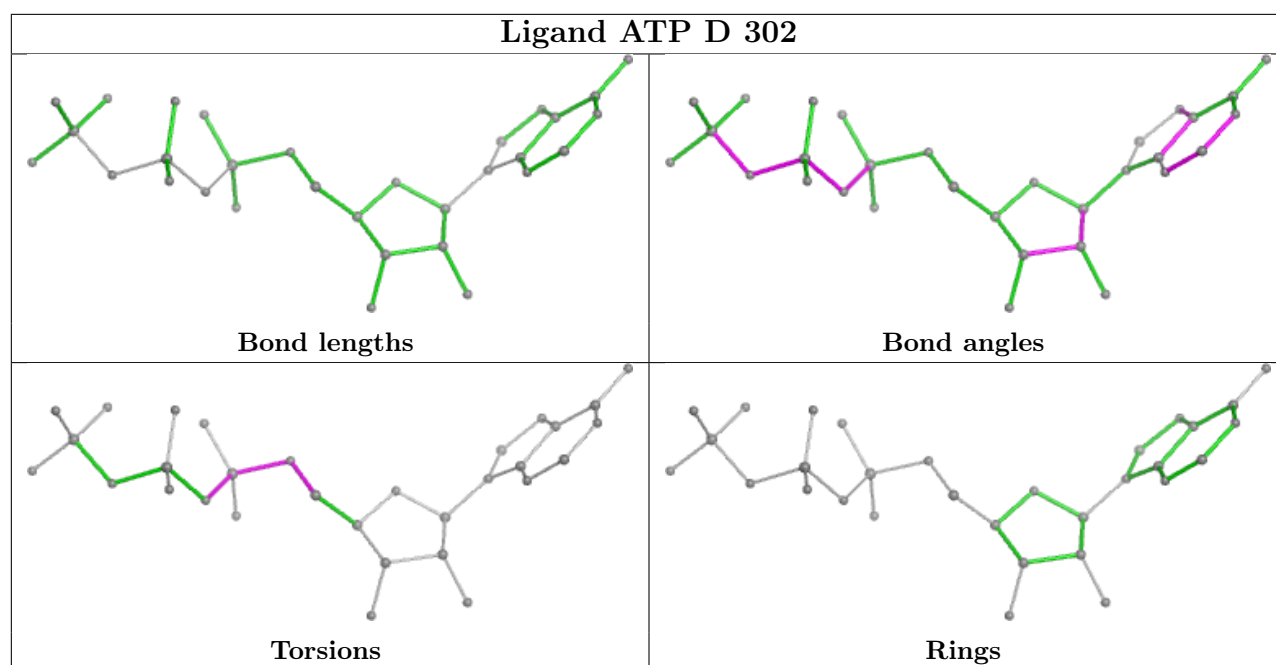


Torsions

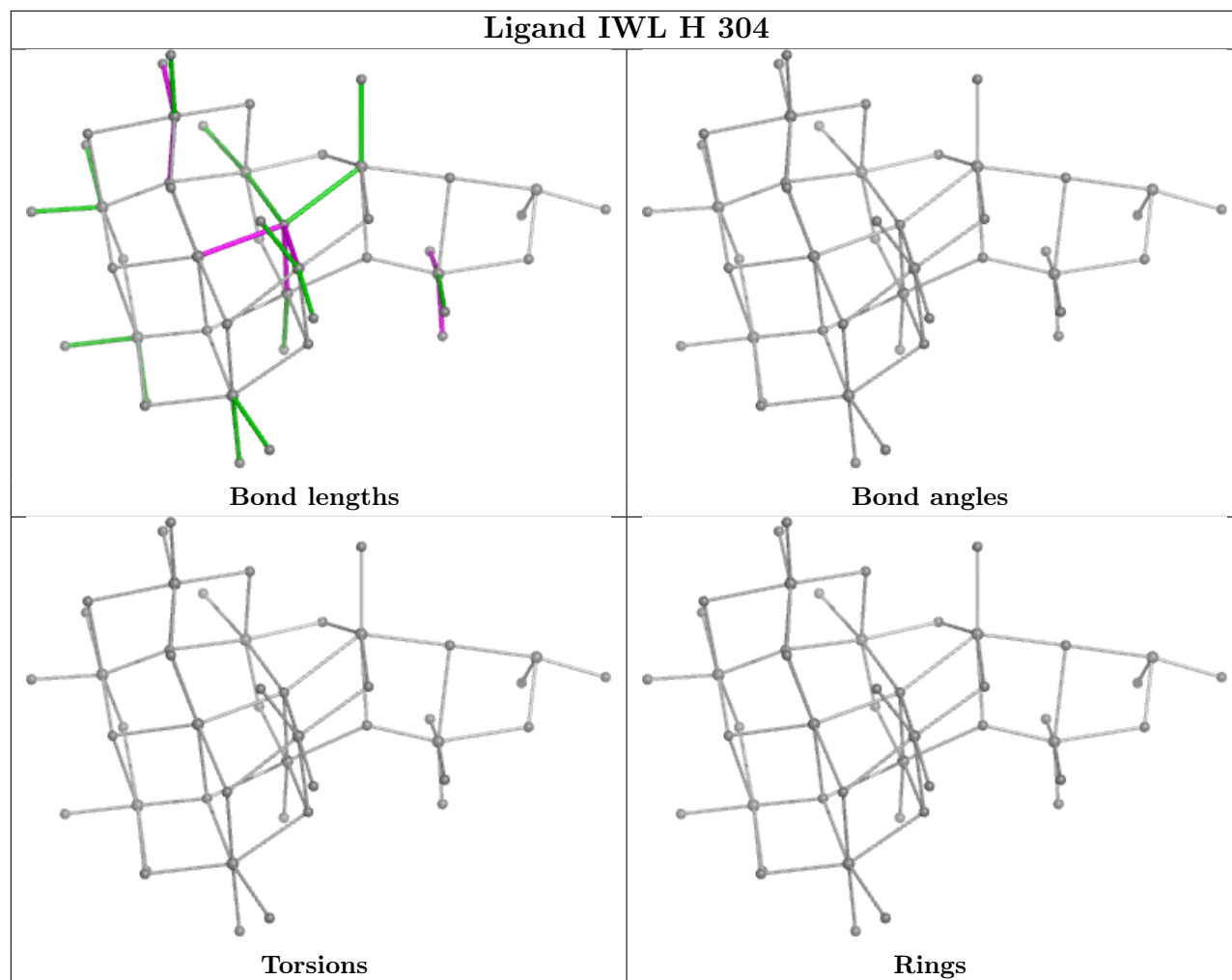


Rings

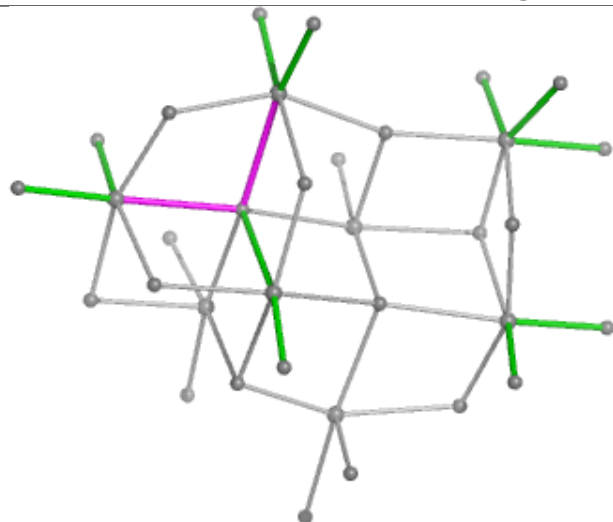




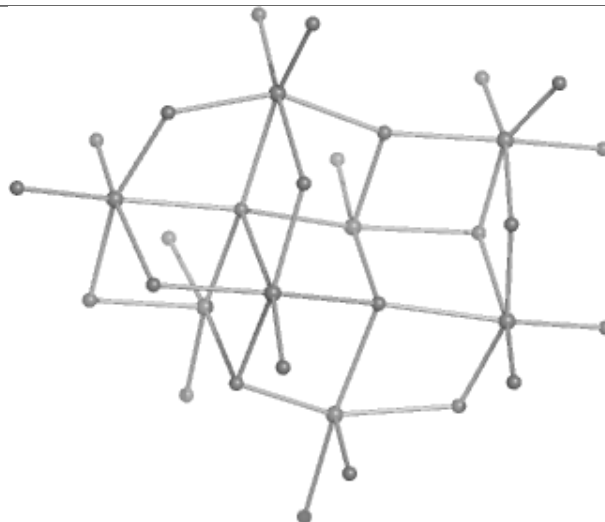
Ligand IWL H 304



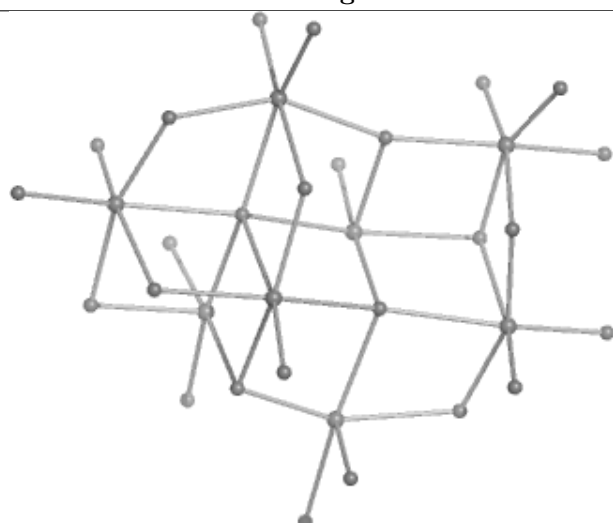
Ligand IWO E 304



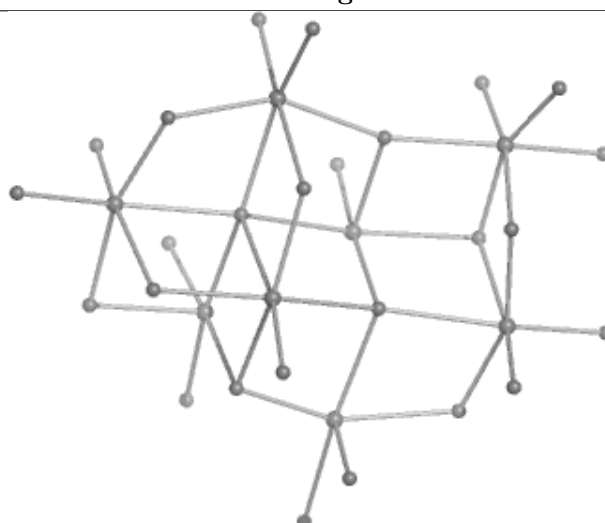
Bond lengths



Bond angles

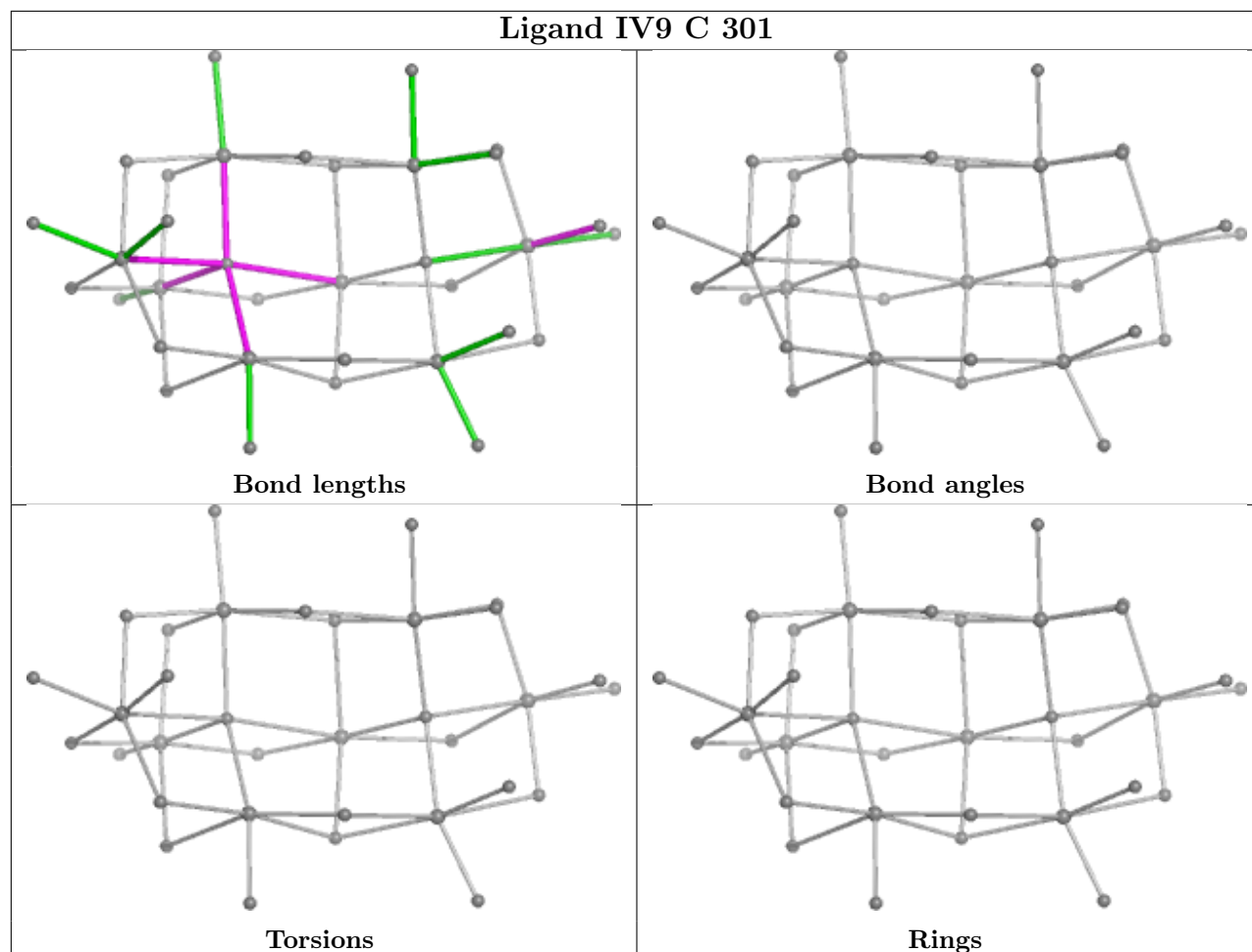


Torsions

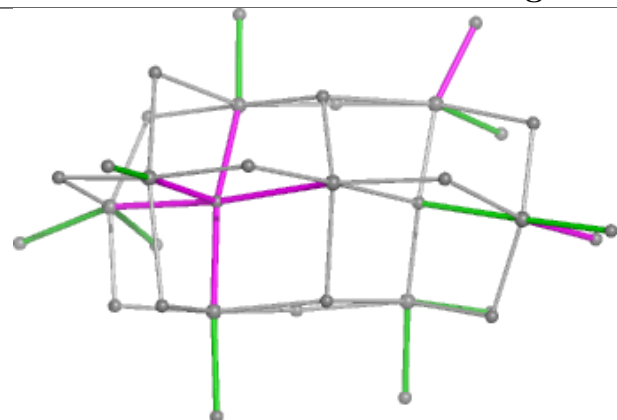


Rings

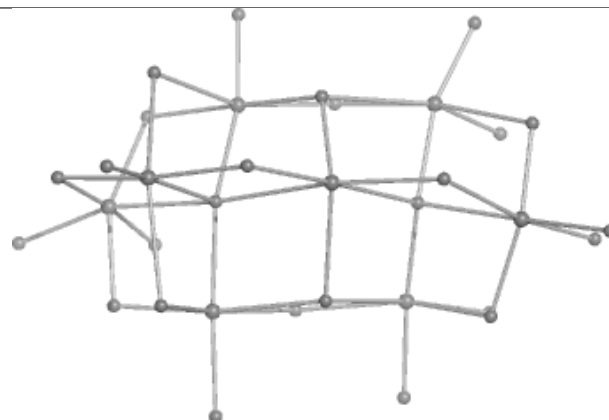
Ligand IV9 C 301



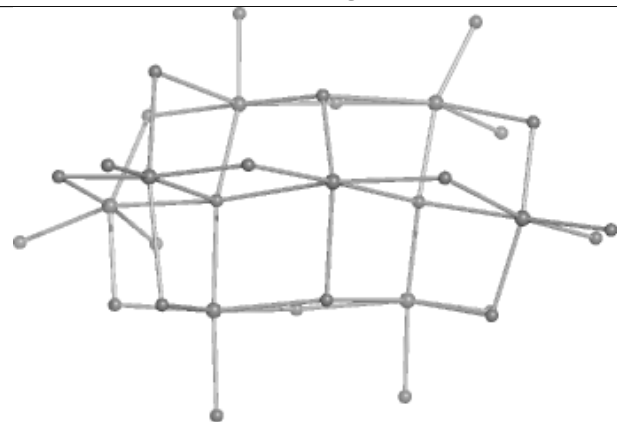
Ligand IV9 K 301



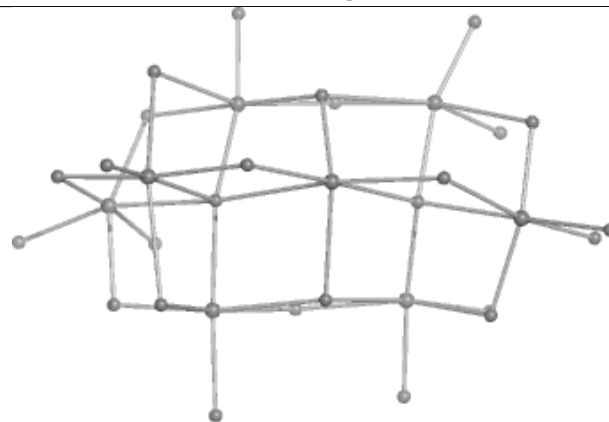
Bond lengths



Bond angles

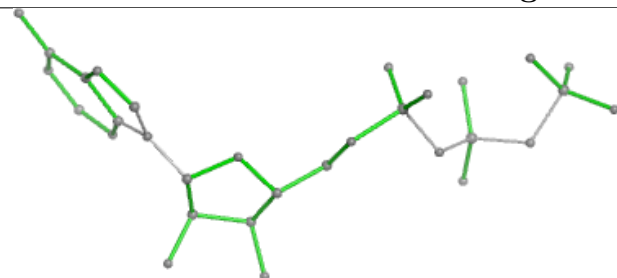


Torsions

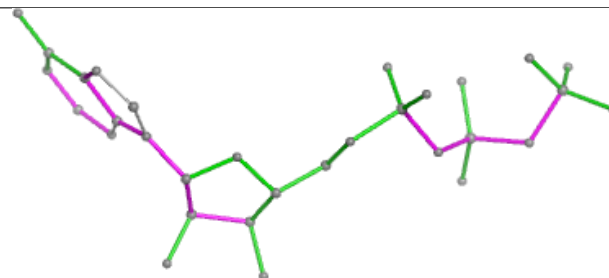


Rings

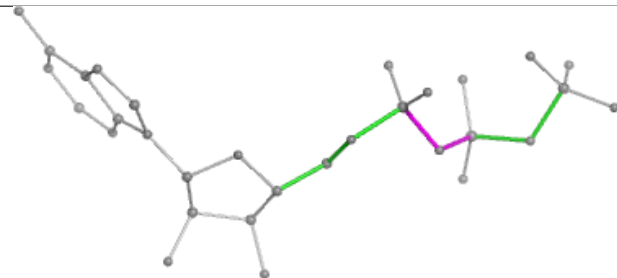
Ligand ATP E 302



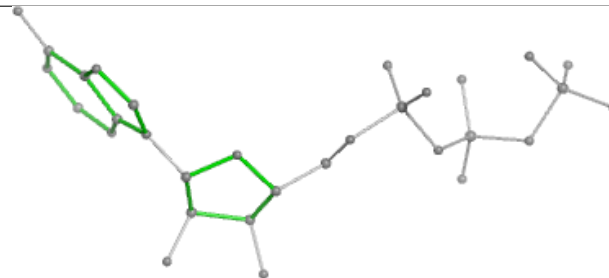
Bond lengths



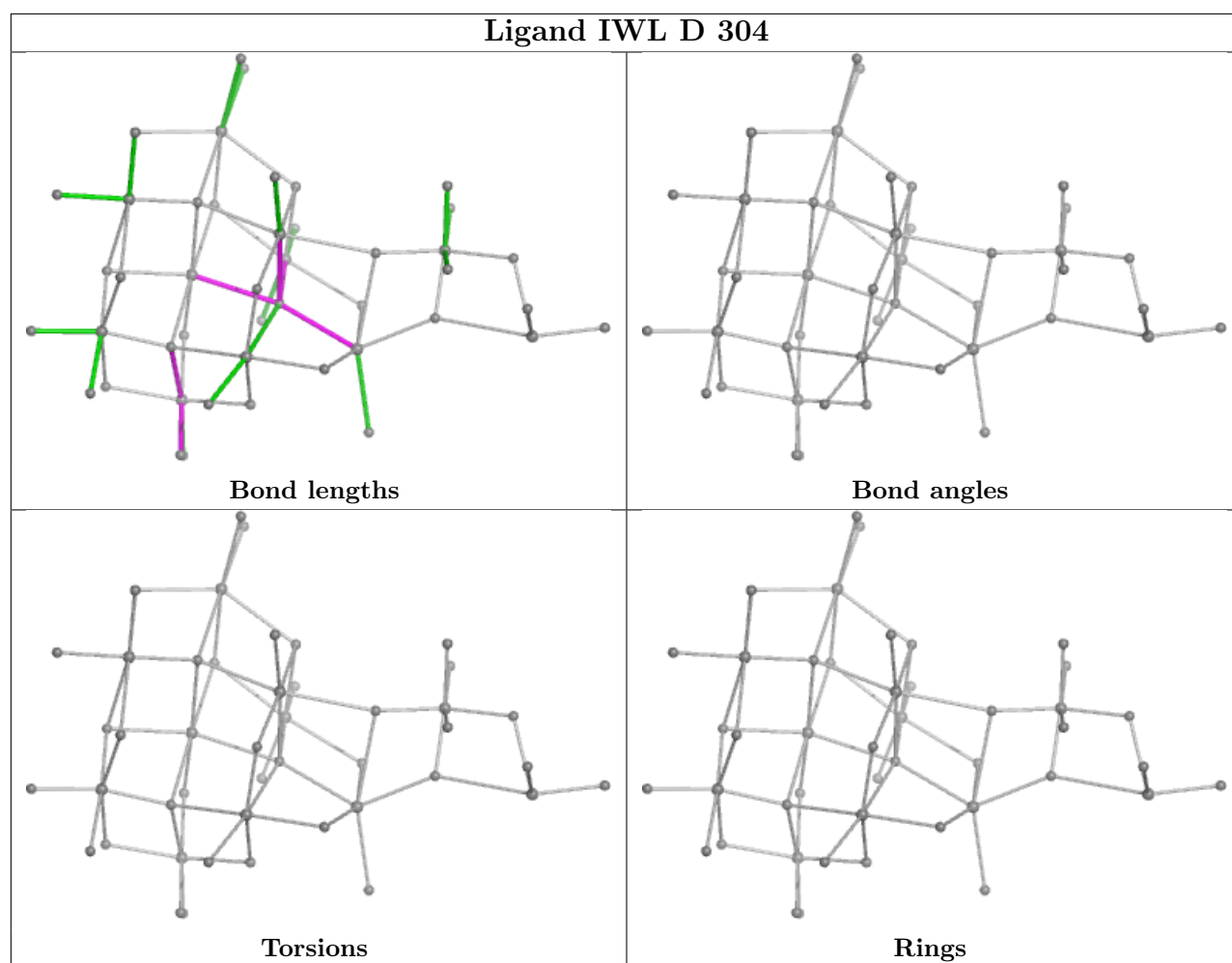
Bond angles



Torsions



Rings



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

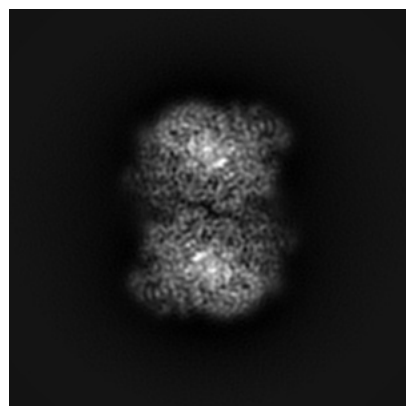
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14522. These allow visual inspection of the internal detail of the map and identification of artifacts.

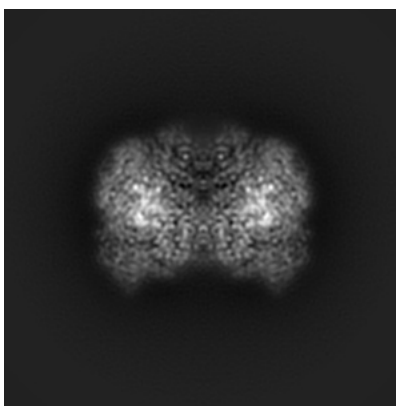
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

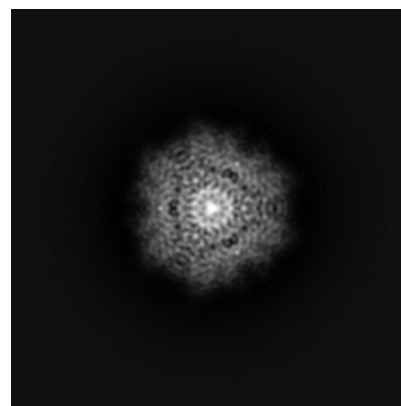
6.1.1 Primary map



X

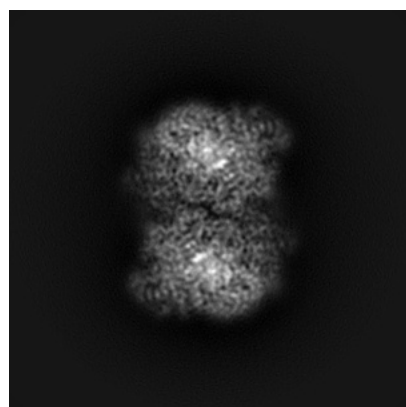


Y

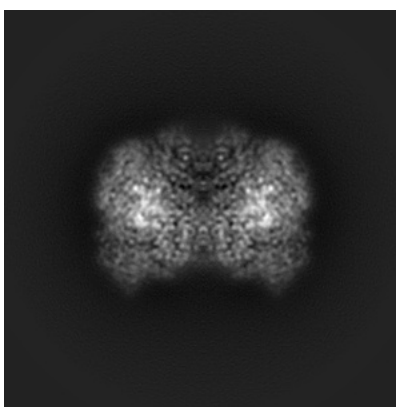


Z

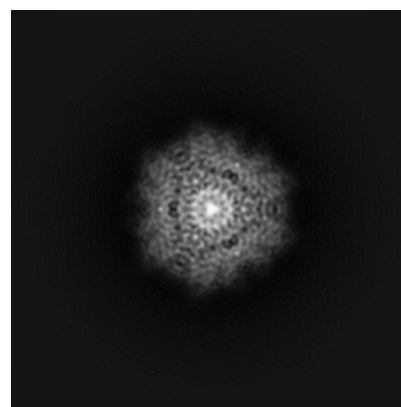
6.1.2 Raw map



X



Y

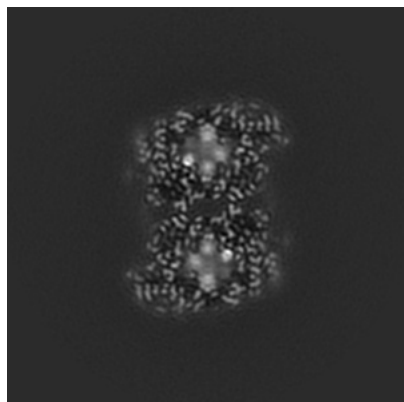


Z

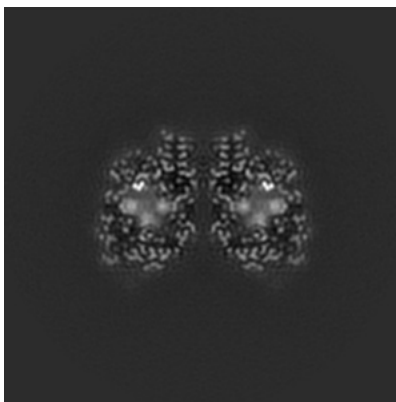
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

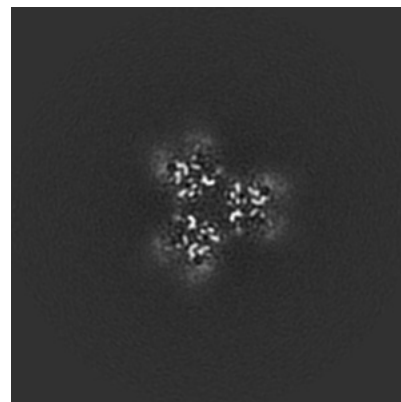
6.2.1 Primary map



X Index: 140

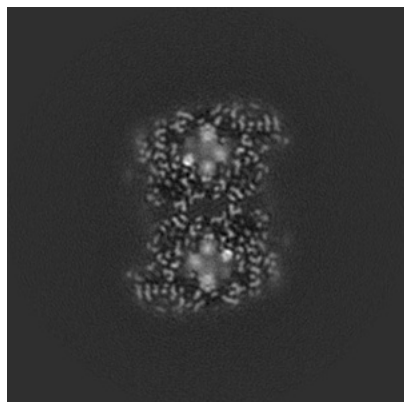


Y Index: 140

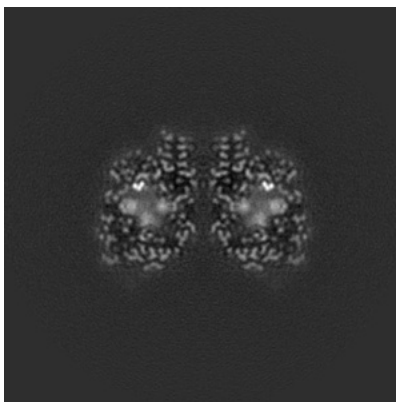


Z Index: 140

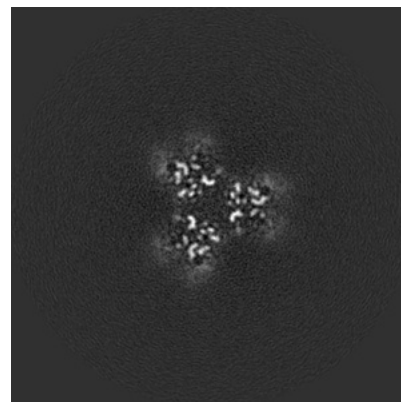
6.2.2 Raw map



X Index: 140



Y Index: 140

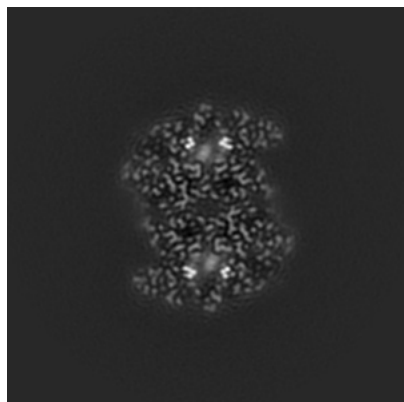


Z Index: 140

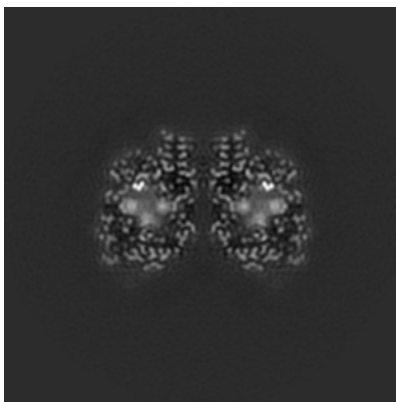
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

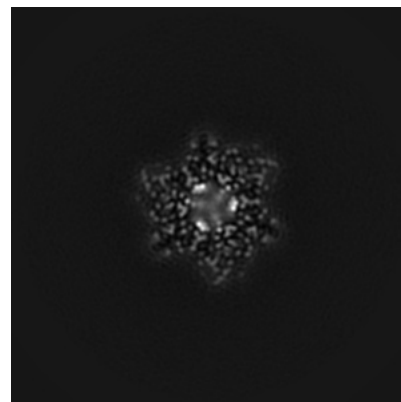
6.3.1 Primary map



X Index: 133

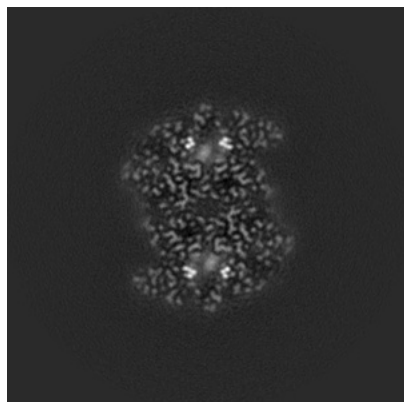


Y Index: 140

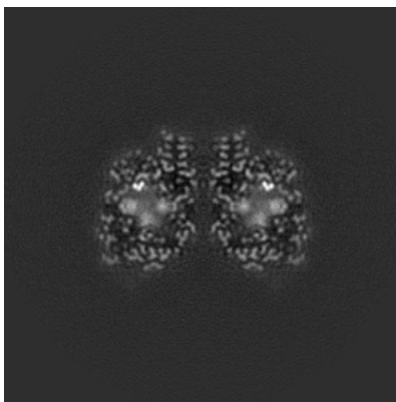


Z Index: 96

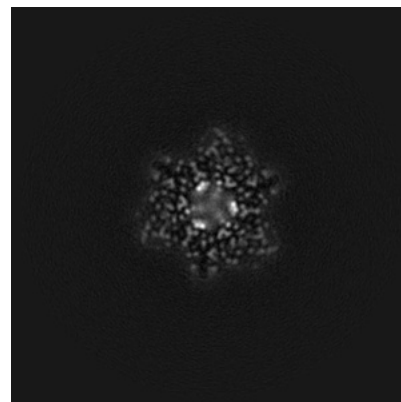
6.3.2 Raw map



X Index: 133



Y Index: 140

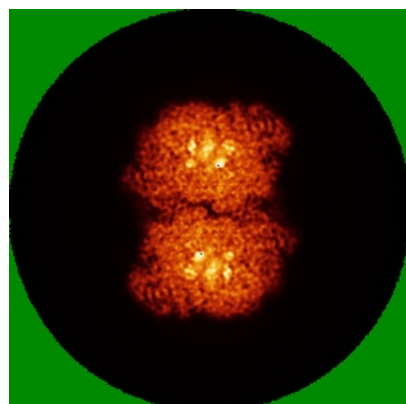


Z Index: 182

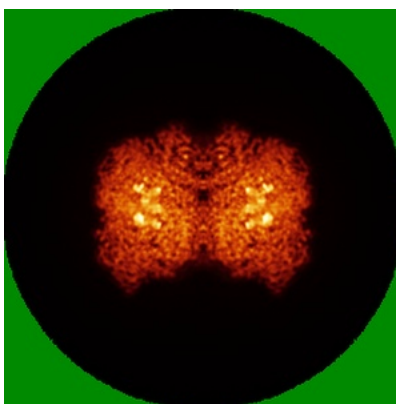
The images above show the largest variance slices of the map in three orthogonal directions.

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

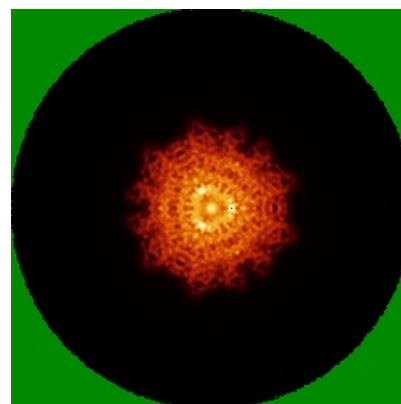
6.4.1 Primary map



X

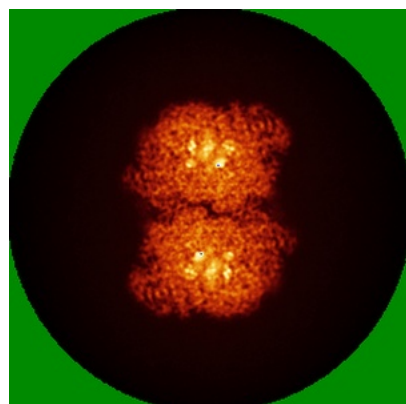


Y

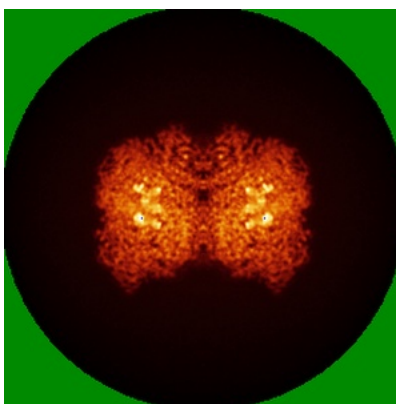


Z

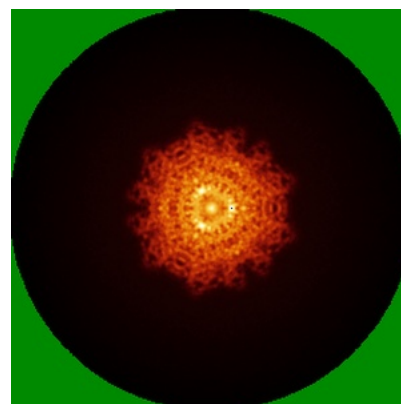
6.4.2 Raw map



X



Y

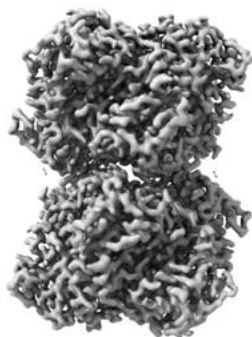


Z

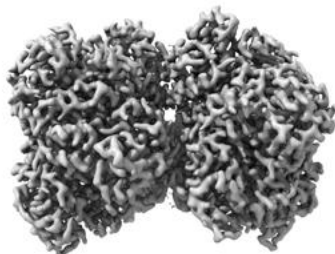
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



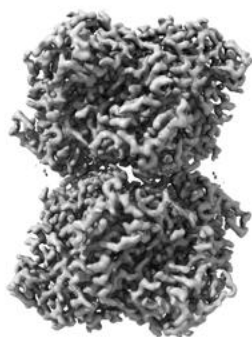
Y



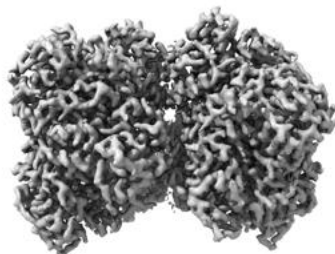
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0082. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

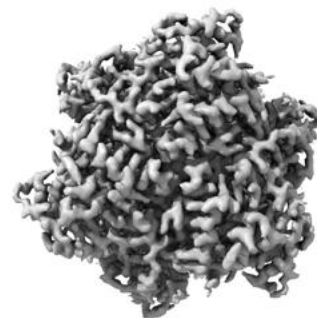
6.5.2 Raw map



X



Y



Z

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

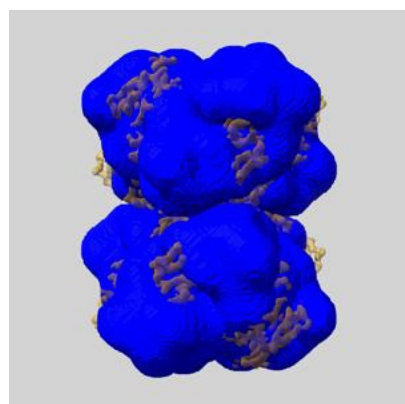
6.6 Mask visualisation [i](#)

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

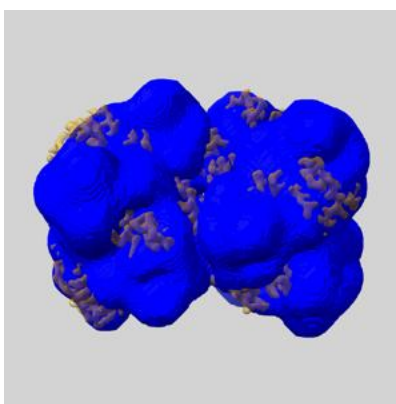
A mask typically either:

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

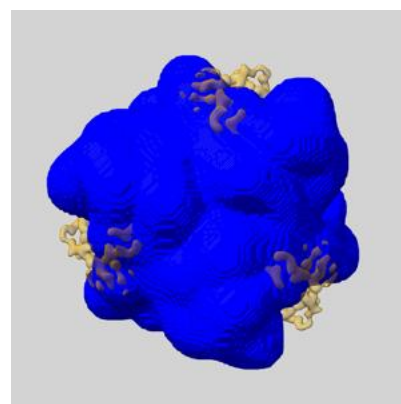
6.6.1 emd_14522_msk_1.map [i](#)



X



Y

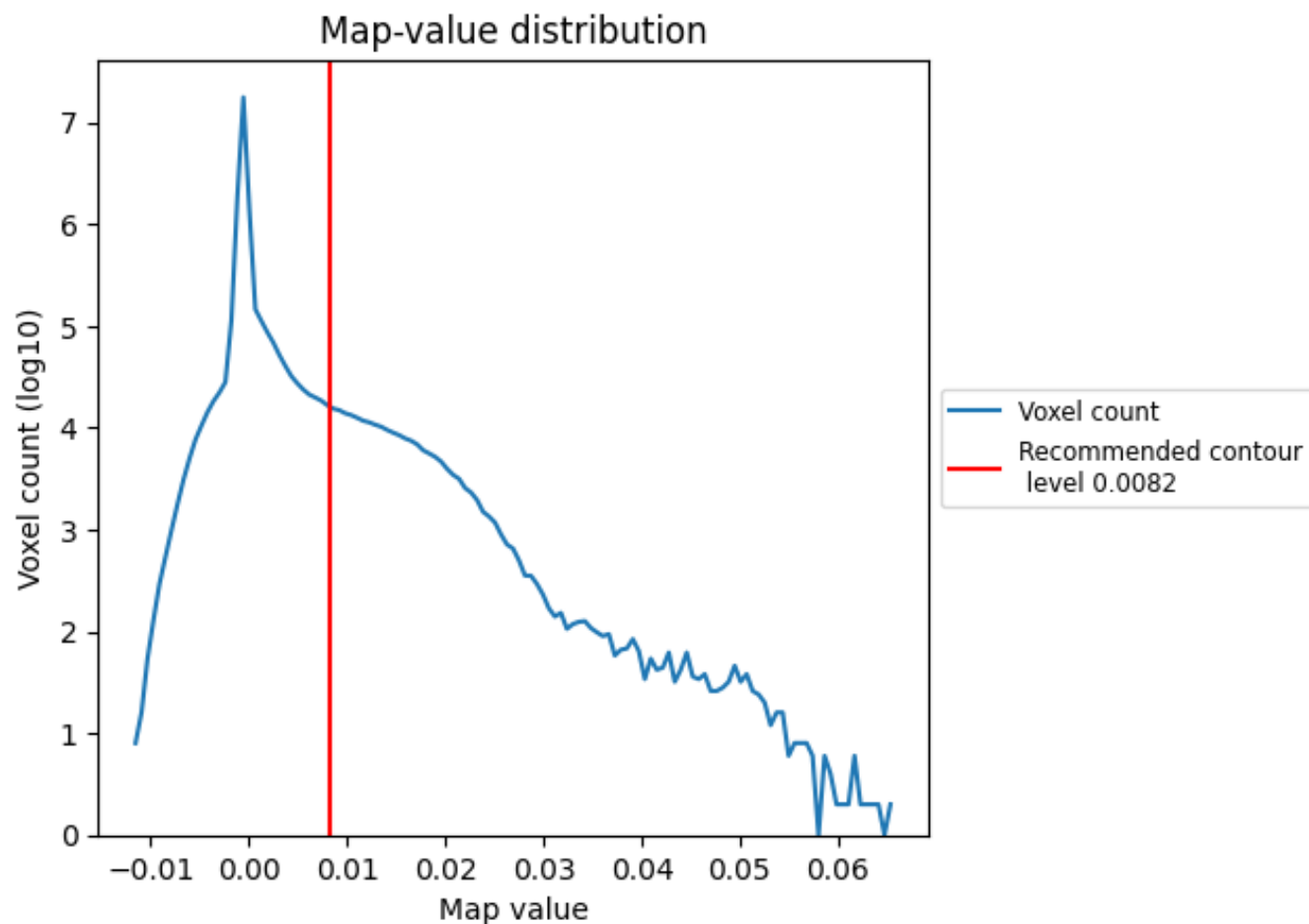


Z

7 Map analysis [i](#)

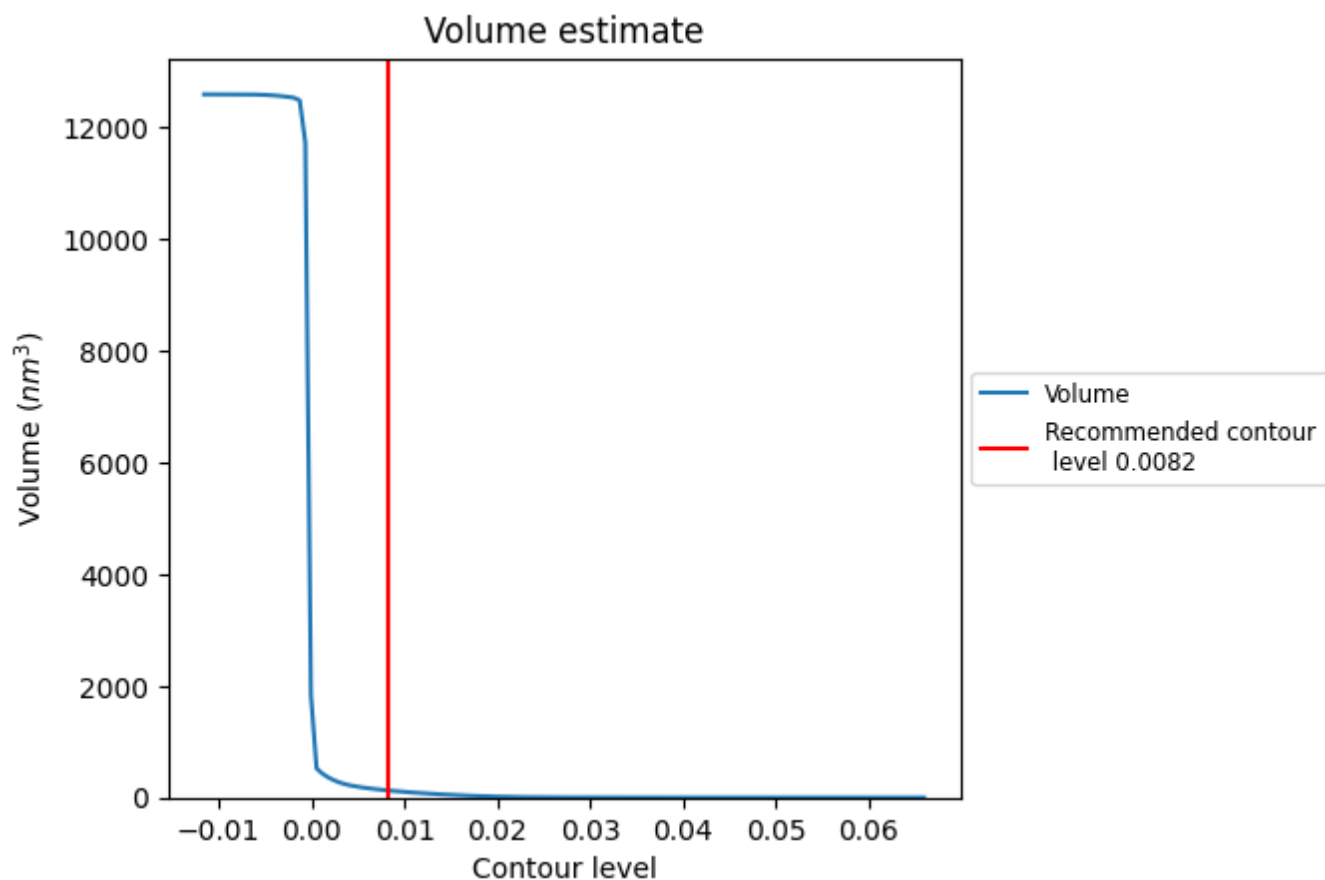
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

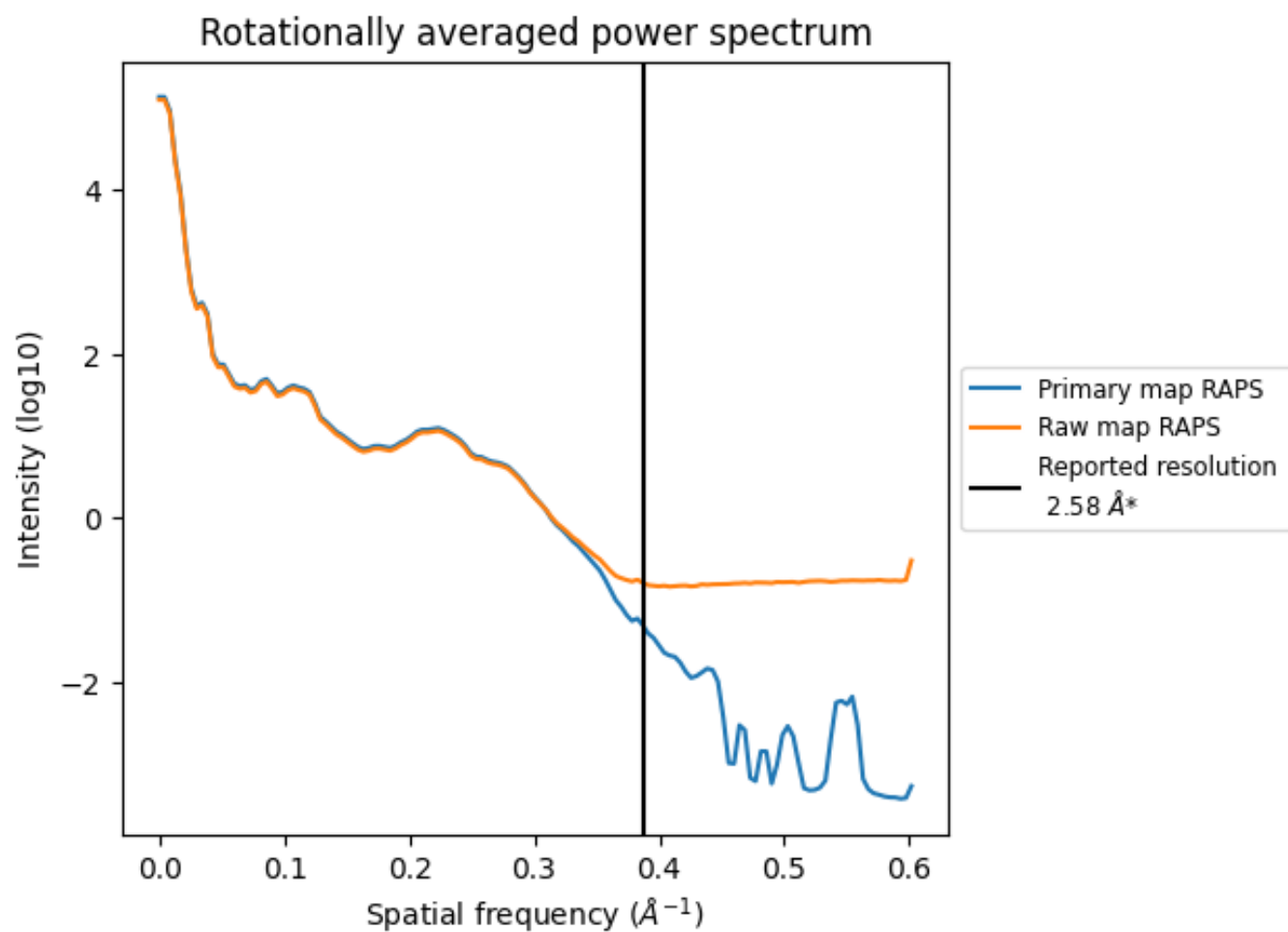
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 128 nm³; this corresponds to an approximate mass of 116 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

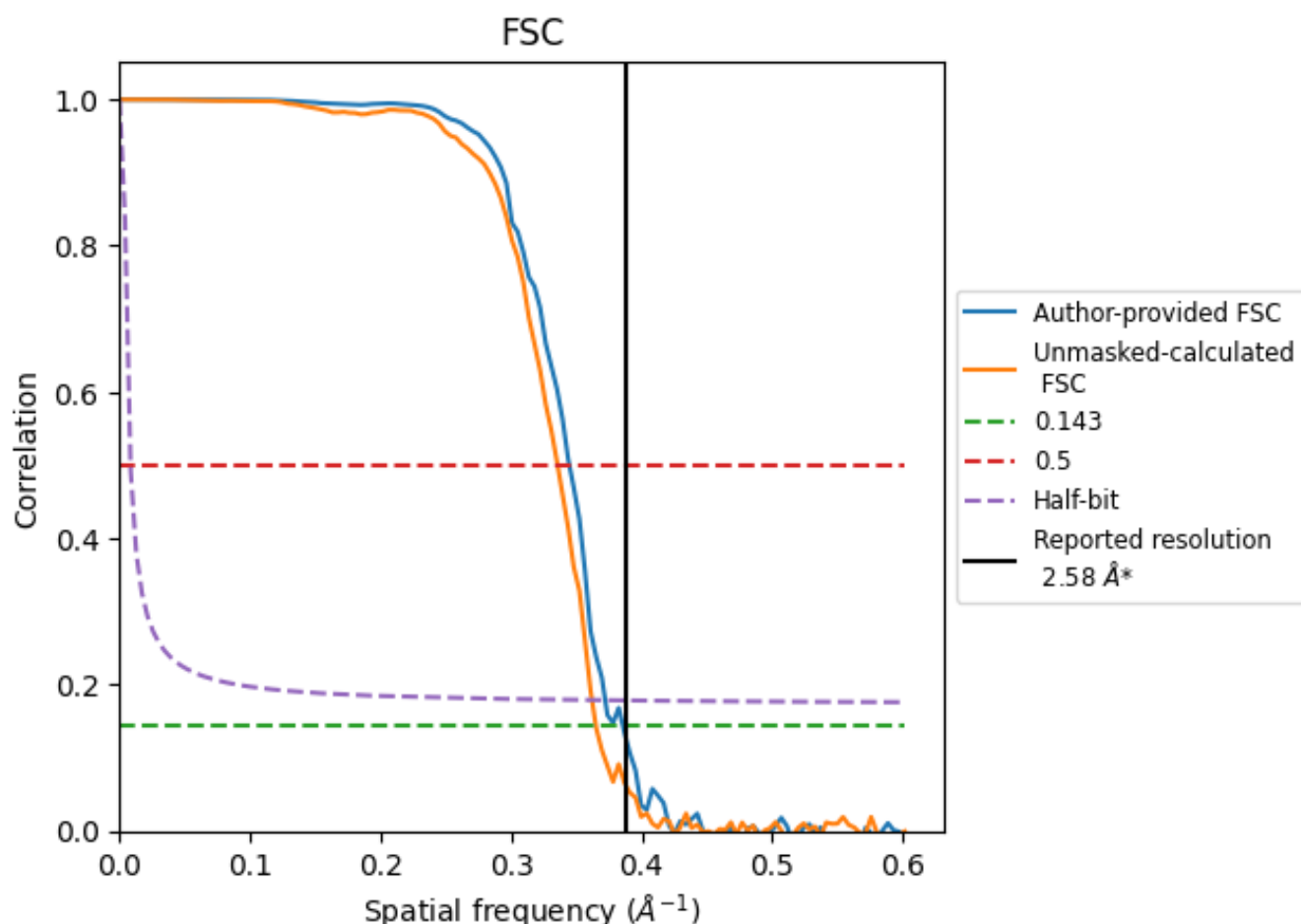


*Reported resolution corresponds to spatial frequency of 0.388 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.388 Å⁻¹

8.2 Resolution estimates [i](#)

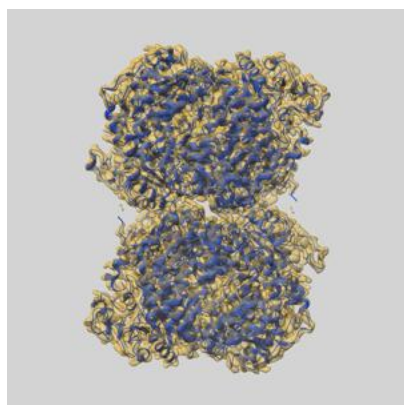
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.58	-	-
Author-provided FSC curve	2.59	2.90	2.69
Unmasked-calculated*	2.74	2.98	2.76

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

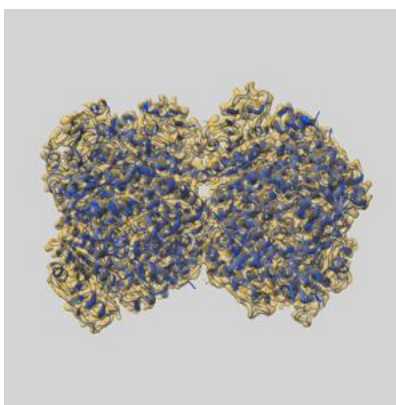
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14522 and PDB model 7Z5J. Per-residue inclusion information can be found in section 3 on page 12.

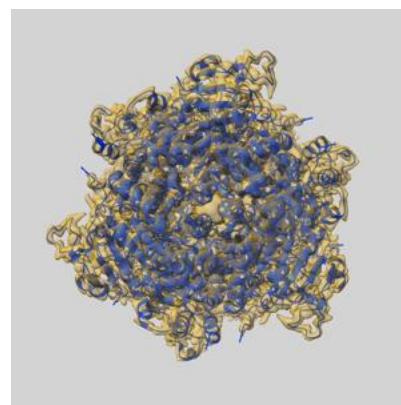
9.1 Map-model overlay [i](#)



X



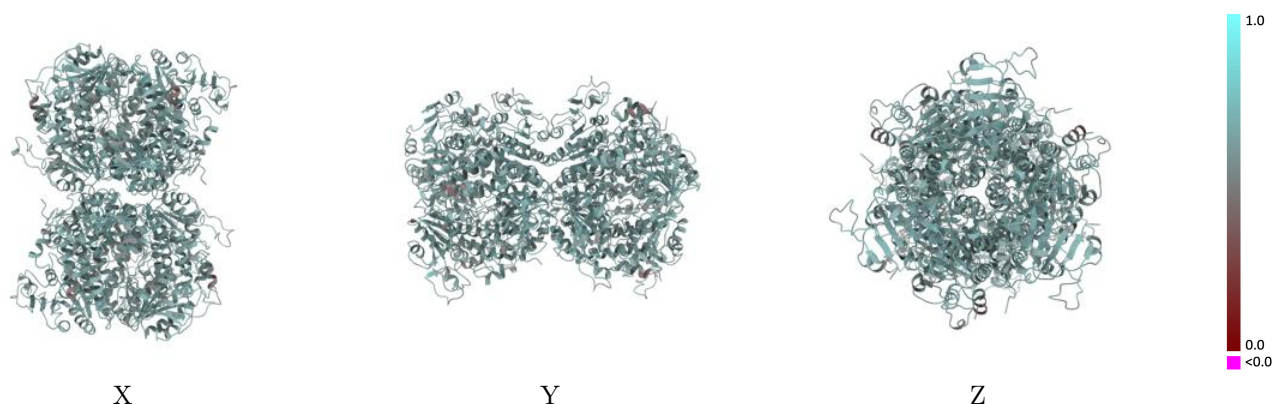
Y



Z

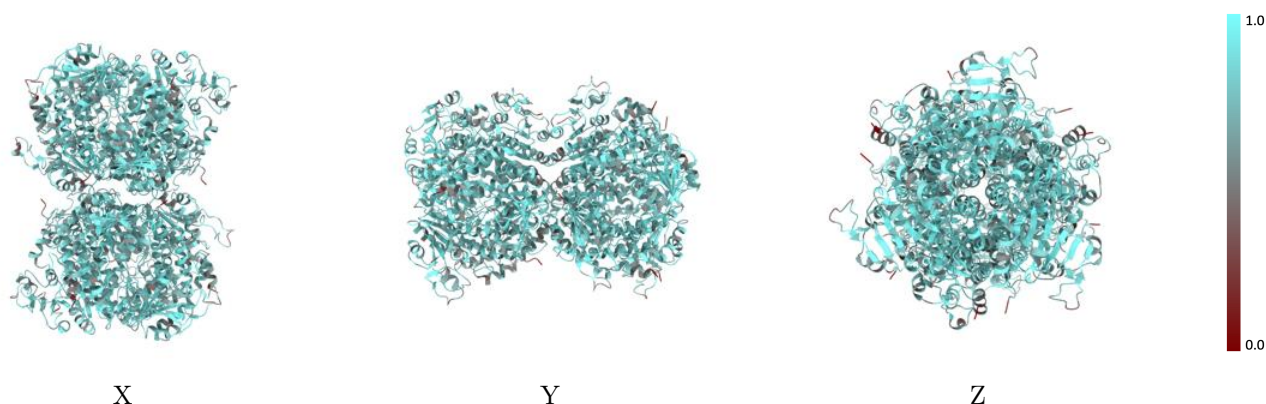
The images above show the 3D surface view of the map at the recommended contour level 0.0082 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



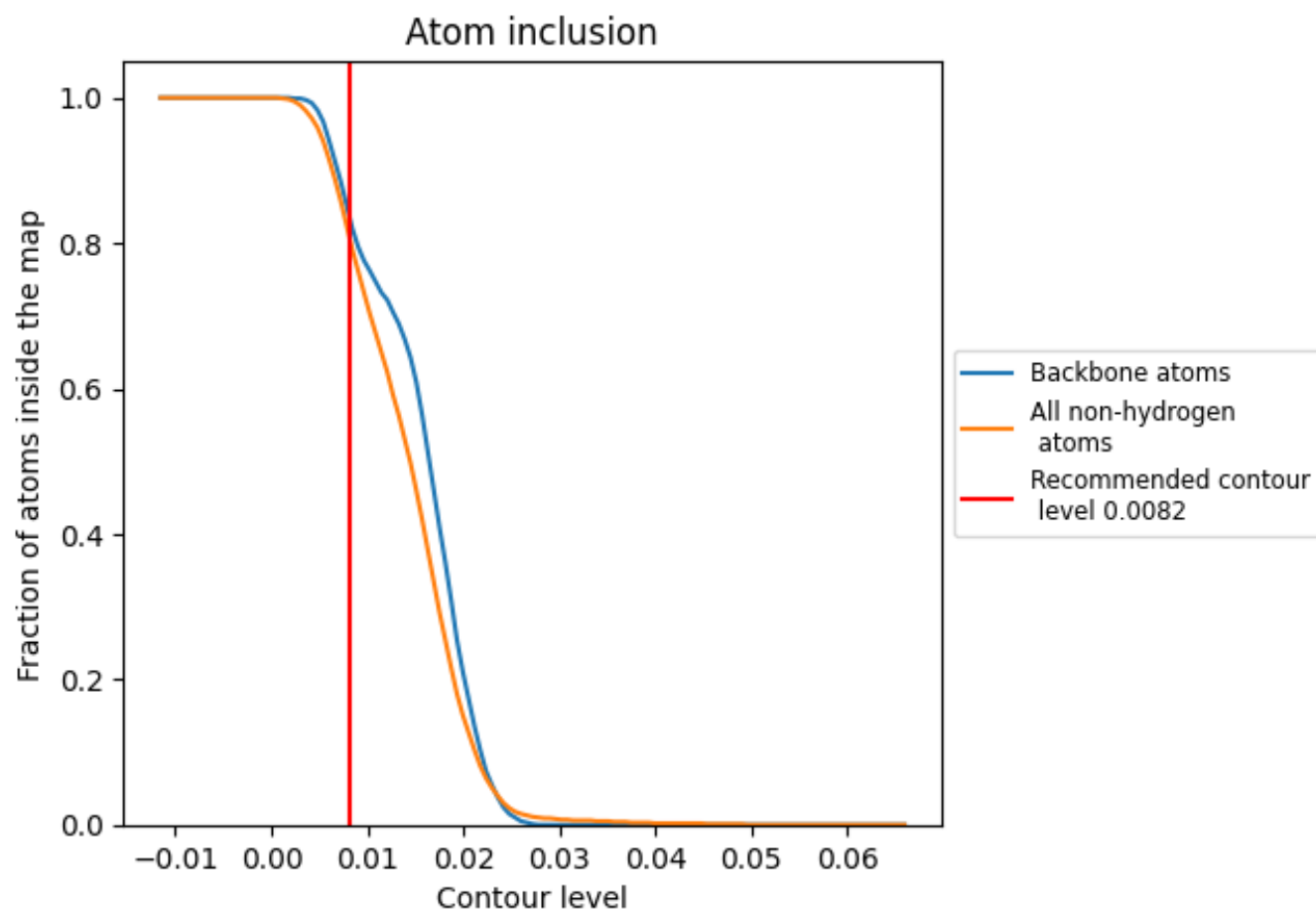
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0082).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0082) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8050</div>	<div><div></div>0.5940</div>
A	<div><div></div>0.8150</div>	<div><div></div>0.6010</div>
B	<div><div></div>0.7970</div>	<div><div></div>0.5950</div>
C	<div><div></div>0.8170</div>	<div><div></div>0.5940</div>
D	<div><div></div>0.7960</div>	<div><div></div>0.5930</div>
E	<div><div></div>0.8100</div>	<div><div></div>0.6000</div>
F	<div><div></div>0.7970</div>	<div><div></div>0.5810</div>
G	<div><div></div>0.8080</div>	<div><div></div>0.6010</div>
H	<div><div></div>0.7940</div>	<div><div></div>0.5920</div>
I	<div><div></div>0.8100</div>	<div><div></div>0.6010</div>
J	<div><div></div>0.7900</div>	<div><div></div>0.5940</div>
K	<div><div></div>0.8140</div>	<div><div></div>0.5930</div>
L	<div><div></div>0.8030</div>	<div><div></div>0.5810</div>

1.0

0.0

<0.0