



Full wwPDB EM Validation Report ⓘ

Mar 18, 2023 – 07:01 am GMT

PDB ID : 7Q4V
EMDB ID : EMD-13818
Title : Electron bifurcating hydrogenase - HydABC from *A. woodii*
Authors : Katsyv, A.; Kumar, A.; Saura, P.; Poeverlein, M.C.; Freibert, S.A.; Stripp, S.; Jain, S.; Gamiz-Hernandez, A.P.; Kaila, V.R.I.; Mueller, V.; Schuller, J.M.
Deposited on : 2021-11-02
Resolution : 4.70 Å(reported)

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.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.32.1

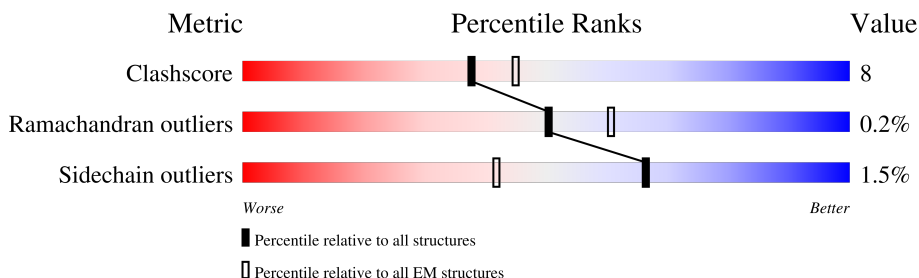
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.70 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	A	583	
1	E	583	
2	B	599	
2	F	599	
3	C	156	
3	G	156	

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
4	SF4	A	603	-	-	X	-
4	SF4	B	606	-	-	X	-
5	FES	C	201	-	-	X	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 19303 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 Iron hydrogenase HydA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	583	Total	C	N	O	S	0	0
			4442	2774	766	865	37		
1	E	583	Total	C	N	O	S	0	0
			4442	2774	766	865	37		

- Molecule 2 is a protein called Iron hydrogenase HydB.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	599	Total	C	N	O	S	0	0
			4510	2849	762	862	37		
2	F	470	Total	C	N	O	S	0	0
			3513	2216	592	676	29		

- Molecule 3 is a protein called Iron hydrogenase HydC.

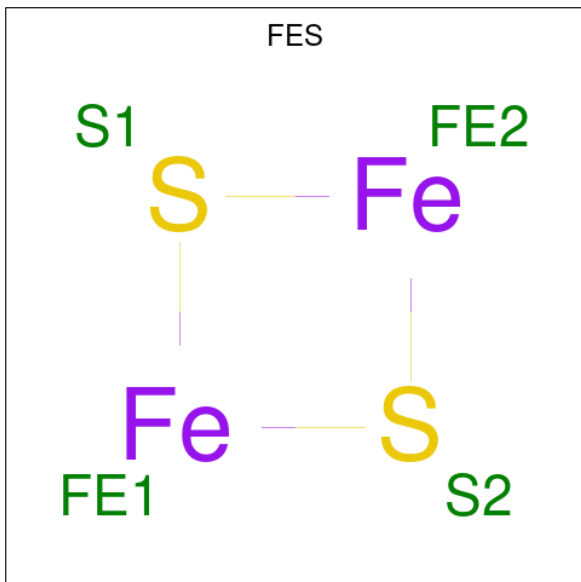
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	156	Total	C	N	O	S	0	0
			1188	761	190	228	9		
3	G	129	Total	C	N	O	S	0	0
			968	620	156	183	9		

- Molecule 4 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
4	A	1	Total	Fe	S	0
			8	4	4	
4	A	1	Total	Fe	S	0
			8	4	4	
4	A	1	Total	Fe	S	0
			8	4	4	
4	A	1	Total	Fe	S	0
			8	4	4	
4	B	1	Total	Fe	S	0
			8	4	4	
4	B	1	Total	Fe	S	0
			8	4	4	
4	B	1	Total	Fe	S	0
			8	4	4	
4	E	1	Total	Fe	S	0
			8	4	4	
4	E	1	Total	Fe	S	0
			8	4	4	
4	E	1	Total	Fe	S	0
			8	4	4	
4	E	1	Total	Fe	S	0
			8	4	4	
4	F	1	Total	Fe	S	0
			8	4	4	
4	F	1	Total	Fe	S	0
			8	4	4	
4	F	1	Total	Fe	S	0
			8	4	4	

- Molecule 5 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	AltConf
5	A	1	Total Fe S 4 2 2	0
5	B	1	Total Fe S 4 2 2	0
5	C	1	Total Fe S 4 2 2	0
5	E	1	Total Fe S 4 2 2	0
5	G	1	Total Fe S 4 2 2	0

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

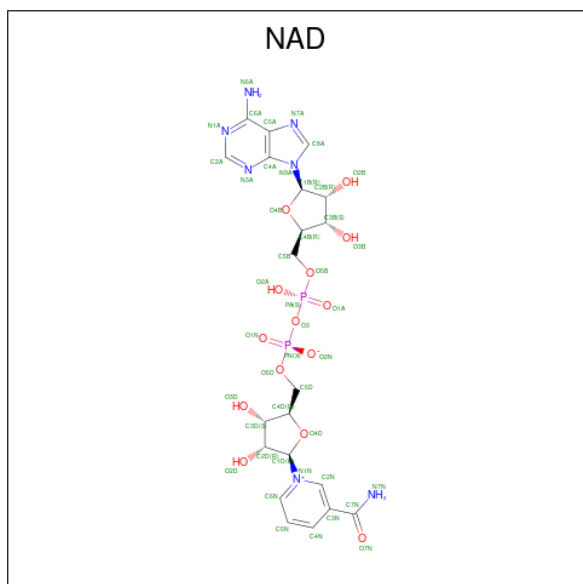
Mol	Chain	Residues	Atoms	AltConf
6	B	1	Total Zn 1 1	0
6	F	1	Total Zn 1 1	0

- Molecule 7 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C₁₇H₂₁N₄O₉P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
7	B	1	Total	C	N	O	P	0
			31	17	4	9	1	
7	F	1	Total	C	N	O	P	0
			31	17	4	9	1	

- Molecule 8 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).



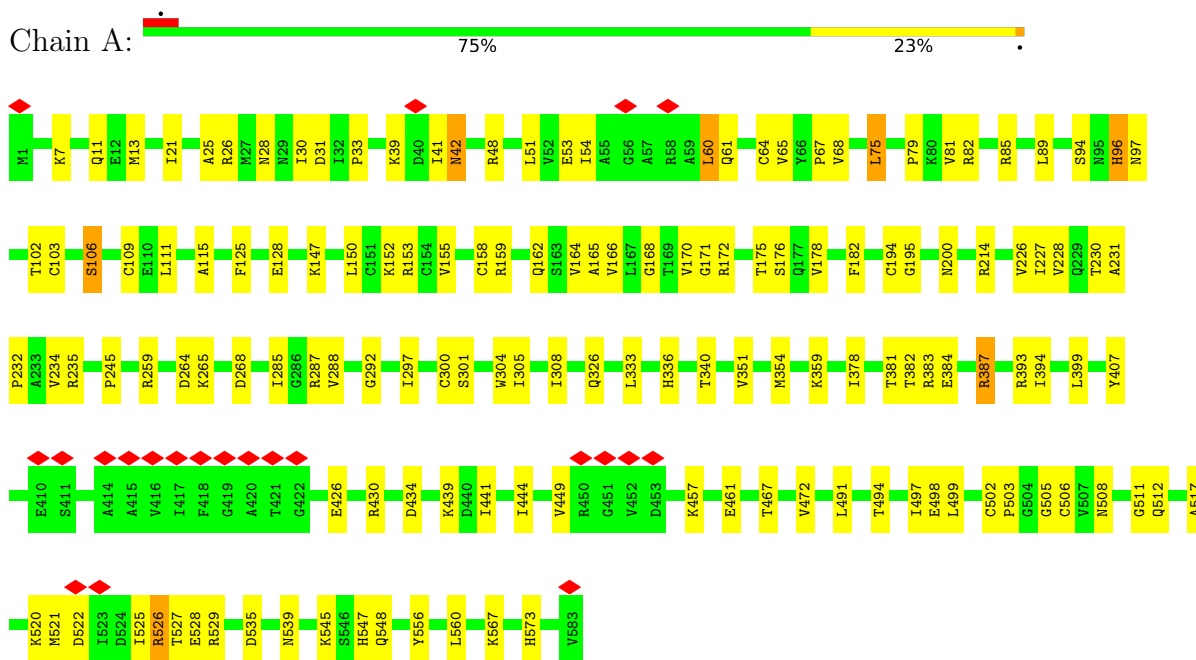
Mol	Chain	Residues	Atoms					AltConf
8	F	1	Total	C	N	O	P	0
			44	21	7	14	2	

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and 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.

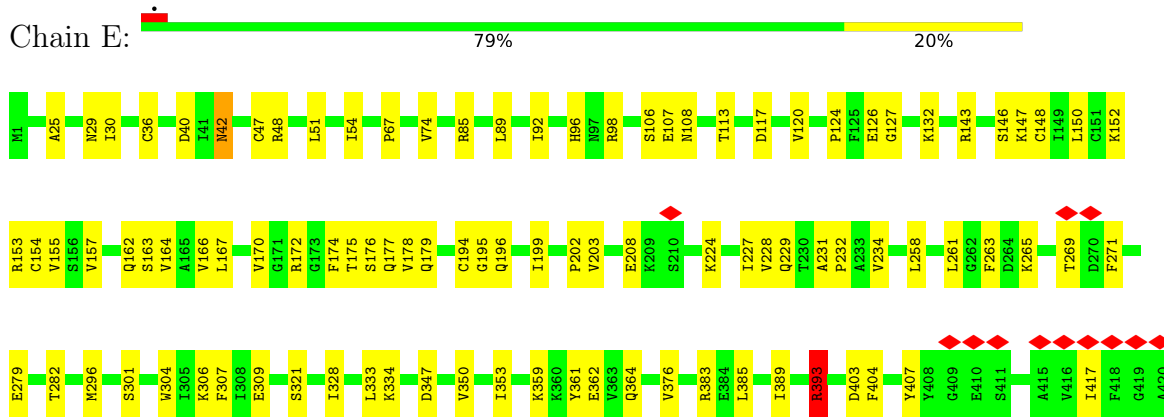
- Molecule 1: Iron hydrogenase HydA1

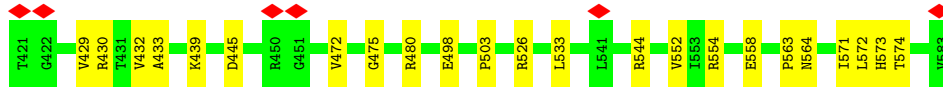
Chain A:



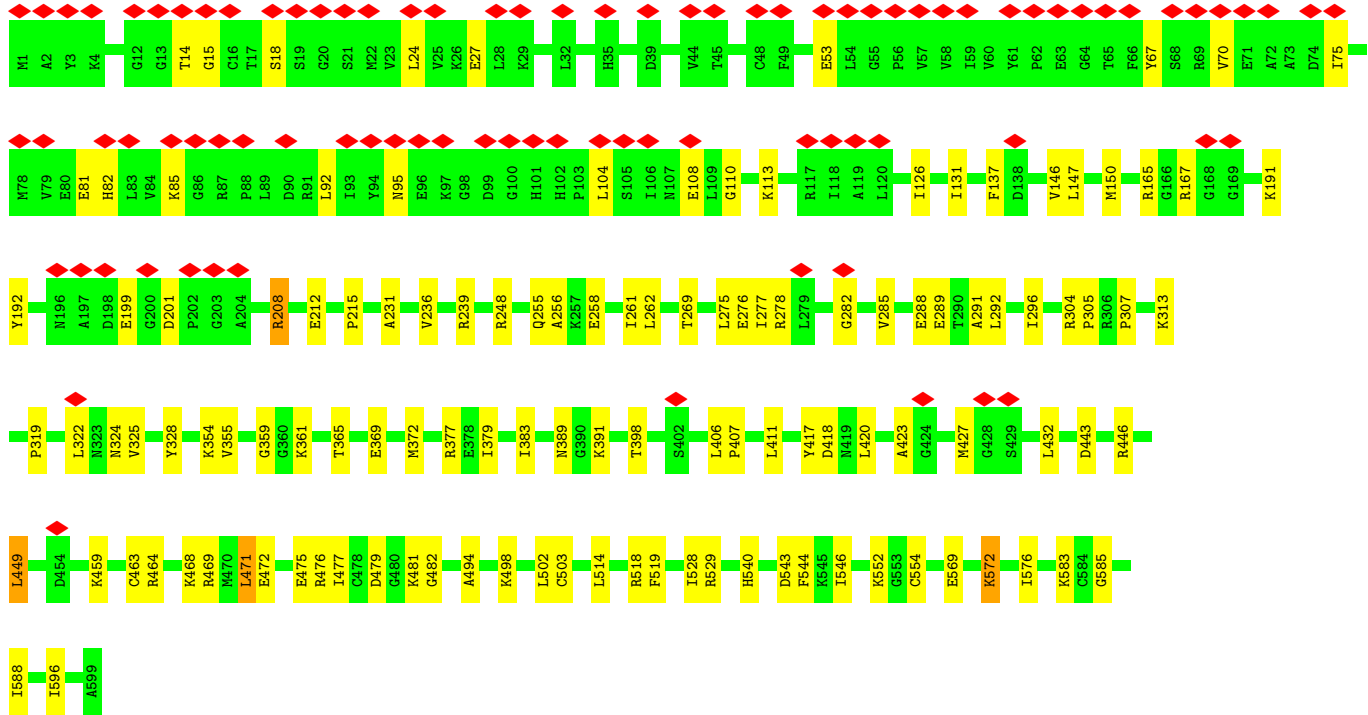
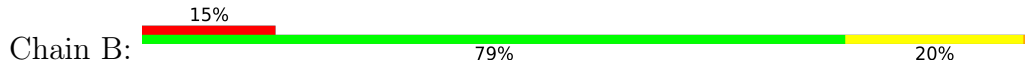
- Molecule 1: Iron hydrogenase HydA1

Chain E:

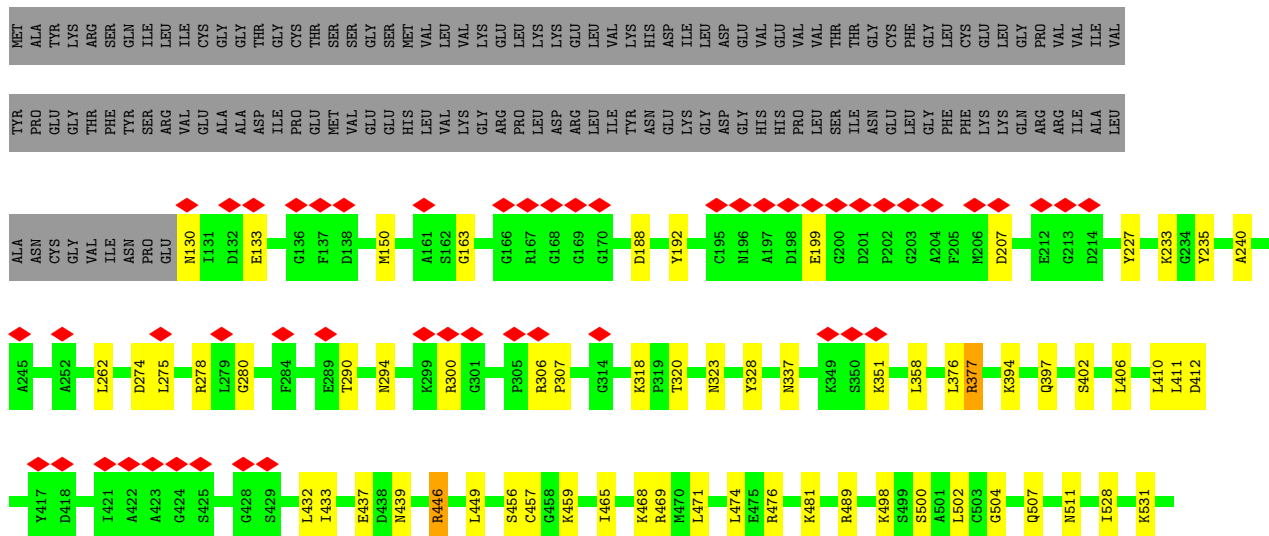


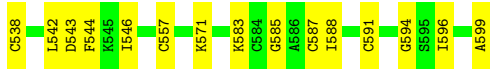


• Molecule 2: Iron hydrogenase HydB

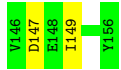
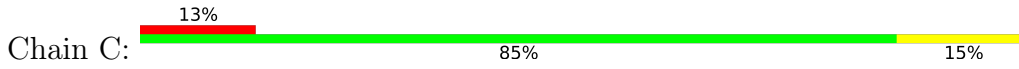


• Molecule 2: Iron hydrogenase HydB

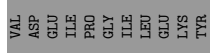
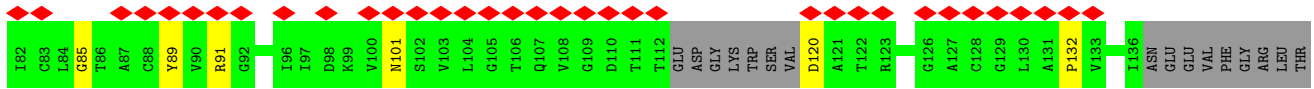
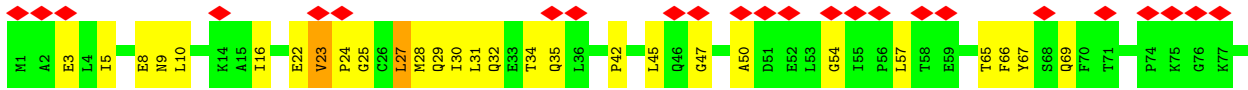
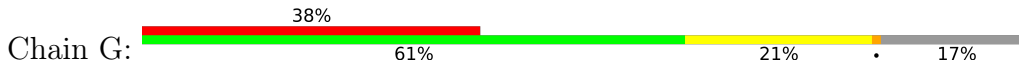




• Molecule 3: Iron hydrogenase HydC



• Molecule 3: Iron hydrogenase HydC



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	559245	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 ($e^-/\text{\AA}^2$)	55	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.025	Depositor
Minimum map value	-0.007	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00114	Depositor
Map size (Å)	218.0, 218.0, 218.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: NAD, FES, ZN, FMN, SF4

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	0.41	1/4507 (0.0%)	0.71	6/6105 (0.1%)
1	E	0.34	0/4507	0.65	2/6105 (0.0%)
2	B	0.32	0/4592	0.59	2/6195 (0.0%)
2	F	0.30	0/3577	0.59	1/4825 (0.0%)
3	C	0.30	0/1207	0.64	0/1638
3	G	0.36	0/981	0.71	2/1330 (0.2%)
All	All	0.34	1/19371 (0.0%)	0.64	13/26198 (0.0%)

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	A	0	2
1	E	0	2
2	F	0	1
3	G	0	1
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	245	PRO	CG-CD	-8.17	1.23	1.50

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	245	PRO	CA-N-CD	-11.25	95.75	111.50
1	A	245	PRO	N-CD-CG	-8.94	89.79	103.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	449	LEU	CA-CB-CG	8.46	134.75	115.30
3	G	23	VAL	CG1-CB-CG2	-6.58	100.38	110.90
2	F	459	LYS	C-N-CA	-6.10	106.44	121.70
1	A	75	LEU	CA-CB-CG	6.04	129.20	115.30
1	E	393	ARG	CG-CD-NE	-5.66	99.92	111.80
1	A	573	HIS	N-CA-CB	-5.42	100.85	110.60
1	A	245	PRO	CA-CB-CG	-5.37	93.79	104.00
1	A	393	ARG	CA-CB-CG	5.18	124.80	113.40
2	B	471	LEU	CA-CB-CG	5.08	126.99	115.30
1	E	40	ASP	CB-CG-OD1	5.07	122.86	118.30
3	G	27	LEU	CA-CB-CG	5.03	126.88	115.30

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	407	TYR	Peptide
1	A	96	HIS	Sidechain
1	E	393	ARG	Sidechain
1	E	407	TYR	Peptide
2	F	538	CYS	Peptide
3	G	23	VAL	Peptide

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	A	4442	0	4463	93	0
1	E	4442	0	4462	76	0
2	B	4510	0	4495	80	0
2	F	3513	0	3481	49	0
3	C	1188	0	1211	14	0
3	G	968	0	1000	22	0
4	A	32	0	0	4	0
4	B	24	0	0	3	0
4	E	32	0	0	2	0
4	F	24	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	4	0	0	0	0
5	B	4	0	0	0	0
5	C	4	0	0	2	0
5	E	4	0	0	0	0
5	G	4	0	0	0	0
6	B	1	0	0	0	0
6	F	1	0	0	0	0
7	B	31	0	19	3	0
7	F	31	0	19	1	0
8	F	44	0	26	0	0
All	All	19303	0	19176	313	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 8.

All (313) 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)
3:G:3:GLU:HB2	3:G:8:GLU:OE2	1.56	1.05
1:A:545:LYS:HB2	1:A:548:GLN:OE1	1.56	1.05
1:E:170:VAL:O	1:E:176:SER:HA	1.59	1.03
1:A:170:VAL:O	1:A:176:SER:HA	1.61	0.97
1:A:103:CYS:HB2	4:A:603:SF4:S4	2.05	0.96
2:B:503:CYS:HB2	4:B:606:SF4:S1	2.09	0.92
3:G:3:GLU:CB	3:G:8:GLU:OE2	2.18	0.91
1:A:545:LYS:HB2	1:A:548:GLN:CD	1.97	0.83
2:B:468:LYS:HA	2:B:471:LEU:HD13	1.67	0.74
1:E:279:GLU:OE1	1:E:573:HIS:CE1	2.42	0.73
3:C:128:CYS:HB3	5:C:201:FES:S2	2.28	0.72
2:B:569:GLU:H	2:B:572:LYS:HE3	1.57	0.69
2:F:446:ARG:HB3	2:F:474:LEU:HD11	1.74	0.69
1:E:328:ILE:HD12	1:E:572:LEU:CD1	2.23	0.68
1:E:279:GLU:OE1	1:E:573:HIS:HE1	1.77	0.68
2:B:110:GLY:HA2	2:B:113:LYS:HD3	1.74	0.68
1:A:526:ARG:NH1	1:A:527:THR:OG1	2.27	0.67
2:B:463:CYS:HB2	4:B:606:SF4:S2	2.35	0.67
1:E:147:LYS:NZ	4:E:603:SF4:S2	2.66	0.67
1:A:109:CYS:HB2	4:A:603:SF4:S3	2.35	0.67
3:G:5:ILE:O	3:G:9:ASN:OD1	2.13	0.66
1:A:81:VAL:HG23	1:A:85:ARG:HH22	1.60	0.65
2:B:503:CYS:CB	4:B:606:SF4:S1	2.86	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:3:GLU:HB2	3:G:8:GLU:CD	2.18	0.64
2:F:468:LYS:HA	2:F:471:LEU:HD13	1.79	0.63
1:A:89:LEU:HD21	1:A:115:ALA:HA	1.81	0.63
1:E:433:ALA:HB1	1:E:439:LYS:HB3	1.79	0.63
2:F:498:LYS:HD2	2:F:507:GLN:HB2	1.79	0.63
2:F:476:ARG:HB3	2:F:481:LYS:HB3	1.81	0.63
2:B:546:ILE:HG23	2:B:576:ILE:HD11	1.80	0.62
2:B:423:ALA:O	2:B:518:ARG:NH2	2.32	0.62
2:B:239:ARG:HE	2:B:282:GLY:HA2	1.64	0.62
2:F:163:GLY:HA3	2:F:351:LYS:HD2	1.80	0.62
1:E:472:VAL:HA	1:E:498:GLU:HB3	1.80	0.62
2:B:292:LEU:HD11	2:B:322:LEU:HD11	1.82	0.62
1:E:430:ARG:NH2	1:E:544:ARG:O	2.33	0.62
1:E:67:PRO:HD2	2:F:307:PRO:HG2	1.81	0.62
2:B:191:LYS:NZ	2:B:192:TYR:O	2.33	0.61
3:C:128:CYS:CB	5:C:201:FES:S2	2.88	0.61
1:A:125:PHE:HB3	2:B:469:ARG:HH12	1.65	0.61
3:G:28:MET:HA	3:G:31:LEU:HD12	1.82	0.61
1:E:124:PRO:O	2:F:489:ARG:NH2	2.34	0.61
1:E:143:ARG:HH12	1:E:179:GLN:HA	1.64	0.61
1:A:194:CYS:SG	1:A:195:GLY:N	2.74	0.60
1:E:417:ILE:HA	1:E:533:LEU:HD21	1.84	0.60
1:E:258:LEU:HD13	1:E:261:LEU:HD12	1.83	0.59
2:B:146:VAL:HA	2:B:150:MET:HB2	1.85	0.59
1:E:126:GLU:O	2:F:469:ARG:NH1	2.35	0.59
1:E:153:ARG:HH22	1:E:202:PRO:HB3	1.68	0.59
1:E:389:ILE:O	1:E:393:ARG:N	2.34	0.58
2:B:389:ASN:HB3	2:B:391:LYS:HE2	1.85	0.58
1:E:571:ILE:HG13	1:E:572:LEU:HD22	1.86	0.57
1:A:103:CYS:O	1:A:106:SER:OG	2.21	0.57
3:C:21:ARG:HH12	3:C:53:LEU:HA	1.69	0.57
1:A:430:ARG:HH21	1:A:444:ILE:HD12	1.69	0.57
1:A:384:GLU:OE2	1:A:387:ARG:NH1	2.38	0.57
1:A:434:ASP:OD2	1:A:547:HIS:NE2	2.37	0.57
1:E:194:CYS:N	4:E:601:SF4:S3	2.76	0.57
3:G:22:GLU:HB3	3:G:25:GLY:HA3	1.86	0.57
1:A:556:TYR:HA	1:A:560:LEU:HB2	1.85	0.57
2:B:528:ILE:HG22	2:B:529:ARG:HE	1.70	0.57
2:F:397:GLN:HB3	2:F:433:ILE:HB	1.86	0.56
3:G:3:GLU:HB3	3:G:8:GLU:OE2	2.05	0.56
1:A:81:VAL:HB	1:A:85:ARG:HH12	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:CYS:SG	1:A:301:SER:N	2.79	0.56
1:E:148:CYS:HA	1:E:203:VAL:HG21	1.86	0.56
1:E:232:PRO:HD3	1:E:269:THR:HB	1.88	0.56
2:F:290:THR:O	2:F:294:ASN:ND2	2.37	0.56
2:B:476:ARG:HD3	2:B:482:GLY:HA2	1.88	0.56
1:A:525:ILE:HG23	1:A:529:ARG:HH12	1.70	0.56
2:B:305:PRO:HG3	2:B:502:LEU:HD21	1.86	0.56
2:F:588:ILE:HA	2:F:596:ILE:HD12	1.88	0.56
2:B:262:LEU:HD21	2:B:275:LEU:HB2	1.88	0.56
2:F:233:LYS:HD2	2:F:274:ASP:HB2	1.88	0.56
1:A:172:ARG:N	1:A:175:THR:OG1	2.37	0.55
1:E:127:GLY:HA3	2:F:469:ARG:HH22	1.70	0.55
1:E:150:LEU:HD11	1:E:177:GLN:HA	1.89	0.55
2:F:543:ASP:O	2:F:599:ALA:N	2.39	0.55
1:A:94:SER:OG	2:B:469:ARG:NH1	2.40	0.55
1:A:354:MET:HG3	1:A:359:LYS:HG2	1.88	0.55
2:B:191:LYS:HB3	2:B:231:ALA:HA	1.88	0.55
3:G:31:LEU:O	3:G:34:THR:OG1	2.17	0.55
1:A:54:ILE:HD13	1:A:61:GLN:HB2	1.88	0.55
2:F:358:LEU:HA	2:F:432:LEU:HB3	1.88	0.55
3:G:50:ALA:O	3:G:54:GLY:N	2.38	0.55
1:E:321:SER:OG	1:E:573:HIS:HB3	2.07	0.55
1:A:228:VAL:HG23	1:A:228:VAL:O	2.06	0.55
1:E:224:LYS:NZ	1:E:347:ASP:OD1	2.40	0.54
1:E:51:LEU:O	1:E:85:ARG:NH2	2.41	0.54
1:A:382:THR:OG1	1:A:511:GLY:O	2.22	0.54
2:B:131:ILE:HD12	2:B:255:GLN:HB3	1.89	0.54
3:C:145:THR:HG23	3:C:147:ASP:H	1.73	0.54
2:B:379:ILE:HA	2:B:383:ILE:HD12	1.90	0.54
1:E:170:VAL:HA	3:G:65:THR:HG21	1.90	0.54
2:B:126:ILE:HG22	2:B:137:PHE:HD2	1.73	0.53
2:F:394:LYS:HE2	2:F:437:GLU:HA	1.90	0.53
2:F:150:MET:O	2:F:227:TYR:OH	2.24	0.53
1:E:196:GLN:HA	1:E:199:ILE:HG22	1.91	0.53
2:B:377:ARG:N	2:B:411:LEU:O	2.43	0.52
3:G:91:ARG:HG2	3:G:132:PRO:HD3	1.92	0.52
2:F:588:ILE:HG13	2:F:596:ILE:HB	1.92	0.52
2:B:288:GLU:OE1	2:B:291:ALA:N	2.42	0.52
1:E:36:CYS:HB3	1:E:47:CYS:H	1.74	0.52
1:A:159:ARG:HA	1:A:165:ALA:HB2	1.92	0.52
1:A:545:LYS:CB	1:A:548:GLN:OE1	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:439:LYS:HE2	1:A:441:ILE:HD11	1.92	0.52
2:B:81:GLU:HA	2:B:85:LYS:HD2	1.92	0.52
1:A:64:CYS:SG	1:A:65:VAL:N	2.83	0.52
1:E:350:VAL:HG13	1:E:376:VAL:HG23	1.92	0.52
2:F:544:PHE:HE2	2:F:585:GLY:HA2	1.75	0.52
1:A:259:ARG:HH22	1:A:265:LYS:HA	1.74	0.52
1:A:158:CYS:HA	1:A:162:GLN:HG3	1.92	0.51
2:B:27:GLU:HB3	2:B:75:ILE:HG21	1.93	0.51
3:G:42:PRO:HB2	3:G:45:LEU:HB2	1.93	0.51
1:A:39:LYS:NZ	1:A:520:LYS:O	2.44	0.51
2:B:494:ALA:HB1	2:B:514:LEU:HD21	1.92	0.51
1:A:491:LEU:HD12	1:A:494:THR:HB	1.91	0.51
1:E:328:ILE:HD12	1:E:572:LEU:HD12	1.91	0.51
3:G:85:GLY:O	3:G:89:TYR:N	2.41	0.51
1:E:48:ARG:NH1	2:F:500:SER:O	2.44	0.51
2:F:377:ARG:HB3	2:F:411:LEU:HB3	1.93	0.51
2:B:544:PHE:HE2	2:B:585:GLY:HA2	1.76	0.50
2:F:402:SER:O	2:F:511:ASN:ND2	2.39	0.50
2:B:147:LEU:HB3	2:B:269:THR:HG21	1.93	0.50
2:B:546:ILE:HG22	2:B:596:ILE:HG12	1.94	0.50
1:E:163:SER:O	1:E:480:ARG:NH2	2.44	0.50
1:E:429:VAL:HA	1:E:432:VAL:HG12	1.93	0.50
1:A:67:PRO:HD2	2:B:307:PRO:HG2	1.92	0.50
1:A:25:ALA:HB1	1:A:30:ILE:HB	1.92	0.50
1:A:305:ILE:HA	1:A:308:ILE:HG22	1.93	0.50
2:B:53:GLU:HB2	2:B:365:THR:H	1.77	0.50
3:C:141:PHE:HB2	3:C:144:LEU:HD11	1.94	0.50
1:A:26:ARG:NH2	1:A:522:ASP:OD1	2.44	0.49
2:B:70:VAL:HG22	2:B:92:LEU:HD13	1.93	0.49
2:B:201:ASP:OD1	2:B:201:ASP:N	2.46	0.49
1:A:232:PRO:HA	1:A:235:ARG:HH22	1.77	0.49
1:E:132:LYS:HE2	1:E:146:SER:HB2	1.93	0.49
1:E:227:ILE:HG12	1:E:265:LYS:HB3	1.93	0.49
3:G:29:GLN:O	3:G:32:GLN:NE2	2.44	0.49
2:B:191:LYS:HE2	2:B:319:PRO:HB2	1.93	0.49
3:G:27:LEU:HA	3:G:30:ILE:HG12	1.95	0.49
1:E:282:THR:HG21	1:E:563:PRO:HB2	1.95	0.49
1:A:297:ILE:HG22	1:A:497:ILE:HB	1.94	0.48
2:F:406:LEU:HB3	2:F:410:LEU:HD11	1.95	0.48
2:B:476:ARG:O	2:B:481:LYS:N	2.45	0.48
2:B:552:LYS:HD2	2:B:554:CYS:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:377:ARG:HD2	2:F:412:ASP:HA	1.95	0.48
1:A:226:VAL:HG23	1:A:264:ASP:H	1.77	0.48
2:B:276:GLU:HG2	2:B:278:ARG:HH12	1.77	0.48
2:B:543:ASP:N	2:B:543:ASP:OD1	2.46	0.48
1:E:167:LEU:HD12	1:E:178:VAL:HG22	1.95	0.48
1:E:445:ASP:OD1	1:E:445:ASP:N	2.46	0.48
2:B:199:GLU:O	2:B:239:ARG:NH1	2.47	0.48
2:B:398:THR:HG21	2:B:420:LEU:HD21	1.95	0.48
2:B:14:THR:HG22	3:C:127:ALA:HB2	1.95	0.48
3:C:35:GLN:NE2	3:C:39:GLY:O	2.46	0.48
1:E:25:ALA:HB1	1:E:30:ILE:HB	1.94	0.48
1:E:403:ASP:OD1	1:E:404:PHE:N	2.45	0.48
1:A:439:LYS:NZ	1:A:461:GLU:OE2	2.40	0.48
2:B:355:VAL:HG13	2:B:369:GLU:HG3	1.96	0.48
2:B:354:LYS:NZ	2:B:372:MET:SD	2.87	0.48
2:B:406:LEU:HD21	2:B:420:LEU:HD11	1.96	0.48
1:E:282:THR:HG22	1:E:564:ASN:HD22	1.79	0.48
2:F:300:ARG:HD2	3:G:66:PHE:HB2	1.96	0.48
2:B:324:ASN:ND2	7:B:605:FMN:O2	2.47	0.48
2:B:359:GLY:N	2:B:432:LEU:O	2.47	0.48
1:E:54:ILE:HA	1:E:74:VAL:HG12	1.96	0.48
2:F:235:TYR:HB3	2:F:278:ARG:HG2	1.96	0.47
2:B:199:GLU:OE2	2:B:208:ARG:NH1	2.43	0.47
1:A:526:ARG:HA	1:A:529:ARG:HG2	1.96	0.47
1:E:157:VAL:O	1:E:162:GLN:HG2	2.15	0.47
1:A:155:VAL:O	1:A:159:ARG:HB2	2.14	0.47
1:A:33:PRO:HD3	1:E:393:ARG:CZ	2.45	0.47
2:B:24:LEU:HD22	2:B:75:ILE:HD11	1.97	0.47
2:B:304:ARG:HD2	2:B:305:PRO:HD2	1.97	0.47
2:B:459:LYS:O	2:B:464:ARG:NH2	2.35	0.47
2:B:278:ARG:HD3	2:B:296:ILE:HD12	1.97	0.46
2:F:262:LEU:HD21	2:F:275:LEU:HB2	1.97	0.46
2:F:278:ARG:NH2	3:G:22:GLU:OE2	2.48	0.46
1:A:301:SER:HB3	1:A:304:TRP:CD1	2.50	0.46
2:B:588:ILE:HG13	2:B:596:ILE:HB	1.96	0.46
2:B:104:LEU:N	2:B:108:GLU:OE1	2.48	0.46
1:E:361:TYR:O	1:E:364:GLN:HB3	2.16	0.46
1:A:31:ASP:O	1:E:393:ARG:NH2	2.48	0.46
2:B:472:GLU:HA	2:B:475:GLU:HG3	1.97	0.46
2:B:477:ILE:HD12	2:B:528:ILE:HG12	1.96	0.46
1:A:336:HIS:O	1:A:340:THR:OG1	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:228:VAL:HG12	1:A:351:VAL:CG1	2.45	0.46
2:F:557:CYS:HB2	2:F:587:CYS:HB2	1.97	0.46
1:A:79:PRO:HA	1:A:82:ARG:HD2	1.98	0.46
1:E:571:ILE:HG13	1:E:572:LEU:CD2	2.45	0.46
1:A:381:THR:OG1	1:A:382:THR:N	2.48	0.46
3:C:125:VAL:HG13	3:C:127:ALA:H	1.80	0.46
1:E:359:LYS:O	1:E:362:GLU:HG3	2.16	0.45
2:F:476:ARG:O	2:F:481:LYS:N	2.46	0.45
3:G:101:ASN:OD1	3:G:101:ASN:O	2.34	0.45
1:A:164:VAL:HG12	1:A:166:VAL:HG13	1.97	0.45
1:E:475:GLY:HA2	1:E:503:PRO:HG3	1.98	0.45
1:A:53:GLU:OE2	1:A:75:LEU:HB3	2.16	0.45
1:A:150:LEU:HB3	1:A:152:LYS:HZ2	1.82	0.45
1:A:535:ASP:O	1:A:539:ASN:HB2	2.17	0.45
1:A:287:ARG:HD3	1:A:292:GLY:HA3	1.97	0.45
1:E:301:SER:HB3	1:E:304:TRP:CD1	2.51	0.45
2:F:188:ASP:OD1	2:F:188:ASP:N	2.50	0.45
3:G:67:TYR:HB3	3:G:69:GLN:HG3	1.99	0.45
1:A:60:LEU:N	1:A:60:LEU:HD22	2.31	0.45
1:E:42:ASN:C	1:E:42:ASN:HD22	2.19	0.45
1:E:89:LEU:HA	1:E:92:ILE:HG22	1.98	0.45
1:E:328:ILE:HD12	1:E:572:LEU:HD13	1.99	0.45
2:F:542:LEU:O	2:F:583:LYS:NZ	2.35	0.45
1:E:172:ARG:HH21	2:F:457:CYS:HA	1.81	0.45
1:A:41:ILE:HD12	1:A:42:ASN:HB2	1.98	0.44
1:A:383:ARG:NH1	1:A:512:GLN:O	2.51	0.44
2:B:427:MET:SD	2:B:427:MET:N	2.90	0.44
1:E:208:GLU:OE2	1:E:383:ARG:NH2	2.38	0.44
2:F:337:ASN:O	2:F:337:ASN:ND2	2.50	0.44
3:G:120:ASP:N	3:G:120:ASP:OD1	2.50	0.44
1:A:472:VAL:HG22	1:A:498:GLU:HB3	1.99	0.44
1:E:306:LYS:HA	1:E:309:GLU:HG2	1.98	0.44
2:F:199:GLU:OE2	2:F:207:ASP:N	2.50	0.44
2:B:165:ARG:HE	2:B:417:TYR:HE1	1.64	0.44
2:B:446:ARG:HA	2:B:449:LEU:HB3	2.00	0.44
1:E:113:THR:O	1:E:117:ASP:HB2	2.17	0.44
1:A:13:MET:SD	1:A:28:ASN:ND2	2.85	0.44
1:E:194:CYS:SG	1:E:195:GLY:N	2.91	0.44
2:F:504:GLY:HA3	7:F:604:FMN:HM83	2.00	0.44
1:A:168:GLY:O	1:A:178:VAL:HA	2.18	0.44
3:G:47:GLY:HA2	3:G:57:LEU:HD21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:525:ILE:O	1:A:528:GLU:HG3	2.17	0.43
1:A:567:LYS:HA	1:A:567:LYS:HD3	1.78	0.43
1:E:271:PHE:HE1	1:E:552:VAL:HB	1.83	0.43
1:A:171:GLY:O	1:A:172:ARG:NH1	2.51	0.43
1:A:234:VAL:HG13	1:A:235:ARG:HG3	2.00	0.43
1:A:503:PRO:O	1:A:508:ASN:HB2	2.19	0.43
2:B:67:TYR:OH	2:B:82:HIS:ND1	2.45	0.43
2:B:255:GLN:HA	2:B:258:GLU:HB2	2.00	0.43
1:E:154:CYS:SG	1:E:155:VAL:N	2.92	0.43
2:F:240:ALA:N	2:F:280:GLY:O	2.52	0.43
1:A:7:LYS:HA	1:A:11:GLN:O	2.18	0.43
2:F:528:ILE:O	2:F:531:LYS:NZ	2.36	0.43
3:C:112:THR:OG1	3:C:114:ASP:OD1	2.35	0.43
1:E:48:ARG:HH22	2:F:502:LEU:HA	1.83	0.43
1:E:164:VAL:HG12	1:E:166:VAL:HG13	2.00	0.43
1:E:150:LEU:O	1:E:152:LYS:NZ	2.52	0.43
2:F:130:ASN:HB3	2:F:133:GLU:HB2	2.00	0.43
1:E:227:ILE:HG21	1:E:333:LEU:HD21	2.00	0.43
1:A:449:VAL:HG22	1:A:457:LYS:HZ2	1.84	0.43
1:A:60:LEU:N	1:A:60:LEU:CD2	2.82	0.43
1:A:545:LYS:O	1:A:548:GLN:HG2	2.19	0.43
2:F:323:ASN:HB2	2:F:328:TYR:CZ	2.54	0.43
1:A:304:TRP:CE3	1:A:499:LEU:HD22	2.54	0.43
1:A:502:CYS:SG	1:A:505:GLY:O	2.78	0.42
1:A:21:ILE:HG13	1:A:68:VAL:HG12	2.01	0.42
1:A:517:ALA:O	1:A:521:MET:HG2	2.19	0.42
2:B:208:ARG:O	2:B:212:GLU:N	2.38	0.42
2:B:325:VAL:HA	2:B:328:TYR:HD2	1.84	0.42
2:F:446:ARG:HA	2:F:449:LEU:HG	2.00	0.42
2:B:285:VAL:HA	7:B:605:FMN:HM72	2.01	0.42
1:E:228:VAL:HG11	1:E:263:PHE:CD2	2.54	0.42
1:A:103:CYS:SG	1:A:147:LYS:NZ	2.72	0.42
2:B:540:HIS:O	2:B:583:LYS:NZ	2.39	0.42
3:C:29:GLN:O	3:C:32:GLN:HG3	2.19	0.42
1:A:301:SER:HB3	1:A:304:TRP:HD1	1.85	0.42
2:B:15:GLY:O	2:B:18:SER:OG	2.34	0.42
2:B:167:ARG:NH2	2:B:427:MET:HB2	2.34	0.42
2:B:215:PRO:HD3	2:B:248:ARG:HH21	1.84	0.42
2:B:443:ASP:OD1	2:B:443:ASP:N	2.53	0.42
1:A:383:ARG:HH22	1:A:511:GLY:HA2	1.85	0.42
1:A:394:ILE:HG22	1:A:399:LEU:HD21	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:420:LEU:HD12	2:B:423:ALA:HB3	2.00	0.42
1:E:328:ILE:HG23	1:E:572:LEU:HD11	2.01	0.42
1:A:231:ALA:O	1:A:235:ARG:NH1	2.49	0.42
1:A:301:SER:OG	4:A:605:SF4:S1	2.67	0.41
2:F:192:TYR:HB2	2:F:320:THR:HG22	2.02	0.41
1:A:96:HIS:CD2	1:A:111:LEU:HD23	2.55	0.41
1:E:172:ARG:NH2	2:F:456:SER:O	2.48	0.41
1:E:304:TRP:HA	1:E:307:PHE:HB3	2.02	0.41
2:F:192:TYR:HH	2:F:235:TYR:HH	1.67	0.41
1:A:426:GLU:O	1:A:430:ARG:HG2	2.19	0.41
1:E:174:PHE:HE1	2:F:465:ILE:HA	1.84	0.41
3:G:32:GLN:HA	3:G:35:GLN:HG3	2.01	0.41
2:B:407:PRO:HG2	2:B:519:PHE:CD1	2.55	0.41
1:E:554:ARG:O	1:E:558:GLU:HB2	2.20	0.41
1:A:426:GLU:OE1	1:A:430:ARG:NH2	2.53	0.41
2:B:236:VAL:HG23	2:B:277:ILE:HD12	2.02	0.41
2:B:262:LEU:HD11	2:B:275:LEU:HD23	2.03	0.41
3:C:75:LYS:HE3	3:C:75:LYS:HA	2.02	0.41
1:E:42:ASN:C	1:E:42:ASN:ND2	2.74	0.41
2:B:479:ASP:HA	2:B:540:HIS:HB3	2.03	0.41
2:F:376:LEU:HB2	2:F:411:LEU:HA	2.02	0.41
1:E:172:ARG:N	1:E:175:THR:OG1	2.52	0.41
1:A:48:ARG:HE	1:A:51:LEU:HD21	1.86	0.41
1:A:227:ILE:HG21	1:A:333:LEU:HD21	2.03	0.41
2:B:256:ALA:O	2:B:261:ILE:N	2.54	0.41
2:B:361:LYS:HE2	2:B:361:LYS:HB2	1.89	0.41
2:F:591:CYS:SG	2:F:594:GLY:N	2.92	0.41
1:A:102:THR:HG22	1:E:120:VAL:HG13	2.02	0.41
1:A:128:GLU:HB2	2:B:468:LYS:NZ	2.35	0.41
1:A:214:ARG:HG2	1:A:378:ILE:HD11	2.03	0.41
3:C:109:GLY:H	3:C:119:VAL:HG13	1.86	0.40
1:A:285:ILE:HA	1:A:288:VAL:HG22	2.02	0.40
1:A:461:GLU:HB3	1:A:467:THR:HG22	2.03	0.40
3:C:96:ILE:HD13	3:C:149:ILE:HD11	2.02	0.40
1:E:231:ALA:HB3	1:E:234:VAL:HG13	2.03	0.40
2:B:588:ILE:HA	2:B:596:ILE:HD12	2.03	0.40
1:A:153:ARG:NH2	1:A:200:ASN:O	2.54	0.40
1:E:334:LYS:HB3	1:E:334:LYS:HE2	1.83	0.40
1:A:103:CYS:CB	4:A:603:SF4:S4	2.87	0.40
1:A:182:PHE:CZ	3:C:43:LEU:HB3	2.56	0.40
1:A:230:THR:HG22	1:A:268:ASP:HA	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:289:GLU:OE1	7:B:605:FMN:O2'	2.38	0.40
1:E:353:ILE:HG21	1:E:385:LEU:HD12	2.03	0.40
2:F:546:ILE:HD12	2:F:546:ILE:HA	1.92	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	A	581/583 (100%)	547 (94%)	32 (6%)	2 (0%)	41	76
1	E	581/583 (100%)	556 (96%)	24 (4%)	1 (0%)	47	81
2	B	597/599 (100%)	587 (98%)	10 (2%)	0	100	100
2	F	468/599 (78%)	454 (97%)	14 (3%)	0	100	100
3	C	154/156 (99%)	146 (95%)	8 (5%)	0	100	100
3	G	125/156 (80%)	105 (84%)	19 (15%)	1 (1%)	19	60
All	All	2506/2676 (94%)	2395 (96%)	107 (4%)	4 (0%)	50	81

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	106	SER
1	E	106	SER
1	A	97	ASN
3	G	24	PRO

5.3.2 Protein sidechains [i](#)

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	A	492/492 (100%)	486 (99%)	6 (1%)	71	84
1	E	492/492 (100%)	482 (98%)	10 (2%)	55	73
2	B	480/480 (100%)	474 (99%)	6 (1%)	69	82
2	F	369/480 (77%)	363 (98%)	6 (2%)	62	79
3	C	130/130 (100%)	128 (98%)	2 (2%)	65	80
3	G	106/130 (82%)	104 (98%)	2 (2%)	57	75
All	All	2069/2204 (94%)	2037 (98%)	32 (2%)	66	80

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	ASN
1	A	60	LEU
1	A	326	GLN
1	A	387	ARG
1	A	506	CYS
1	A	526	ARG
2	B	95	ASN
2	B	208	ARG
2	B	313	LYS
2	B	418	ASP
2	B	498	LYS
2	B	572	LYS
3	C	30	ILE
3	C	143	ARG
1	E	29	ASN
1	E	42	ASN
1	E	96	HIS
1	E	98	ARG
1	E	107	GLU
1	E	108	ASN
1	E	229	GLN
1	E	296	MET
1	E	526	ARG
1	E	574	THR
2	F	306	ARG
2	F	318	LYS

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Mol	Chain	Res	Type
2	F	377	ARG
2	F	439	ASN
2	F	446	ARG
2	F	571	LYS
3	G	10	LEU
3	G	16	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	ASN
2	B	397	GLN
1	E	29	ASN
1	E	42	ASN
1	E	564	ASN
1	E	573	HIS
2	F	337	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 2 are monoatomic - leaving 22 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	SF4	E	602	1	0,12,12	-	-	-		
5	FES	E	604	1	0,4,4	-	-	-		
4	SF4	B	603	2	0,12,12	-	-	-		
4	SF4	E	605	1	0,12,12	-	-	-		
5	FES	G	201	3	0,4,4	-	-	-		
4	SF4	B	602	2	0,12,12	-	-	-		
4	SF4	E	601	1	0,12,12	-	-	-		
7	FMN	F	604	-	33,33,33	2.12	12 (36%)	48,50,50	2.82	17 (35%)
5	FES	C	201	3	0,4,4	-	-	-		
4	SF4	A	601	1	0,12,12	-	-	-		
4	SF4	B	606	2	0,12,12	-	-	-		
4	SF4	F	602	2	0,12,12	-	-	-		
4	SF4	F	606	2	0,12,12	-	-	-		
4	SF4	E	603	1	0,12,12	-	-	-		
4	SF4	A	602	1	0,12,12	-	-	-		
7	FMN	B	605	-	33,33,33	2.14	13 (39%)	48,50,50	2.83	16 (33%)
8	NAD	F	605	-	42,48,48	1.50	5 (11%)	50,73,73	1.54	5 (10%)
4	SF4	A	603	1	0,12,12	-	-	-		
4	SF4	A	605	1	0,12,12	-	-	-		
5	FES	A	604	1	0,4,4	-	-	-		
5	FES	B	601	2	0,4,4	-	-	-		
4	SF4	F	601	2	0,12,12	-	-	-		

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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SF4	E	602	1	-	-	0/6/5/5
5	FES	E	604	1	-	-	0/1/1/1
4	SF4	B	603	2	-	-	0/6/5/5
4	SF4	E	605	1	-	-	0/6/5/5
5	FES	G	201	3	-	-	0/1/1/1
4	SF4	B	602	2	-	-	0/6/5/5
4	SF4	E	601	1	-	-	0/6/5/5
7	FMN	F	604	-	-	7/18/18/18	0/3/3/3
5	FES	C	201	3	-	-	0/1/1/1
4	SF4	A	601	1	-	-	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SF4	B	606	2	-	-	0/6/5/5
4	SF4	F	602	2	-	-	0/6/5/5
4	SF4	F	606	2	-	-	0/6/5/5
4	SF4	E	603	1	-	-	0/6/5/5
4	SF4	A	602	1	-	-	0/6/5/5
7	FMN	B	605	-	-	11/18/18/18	0/3/3/3
8	NAD	F	605	-	-	11/26/62/62	0/5/5/5
4	SF4	A	603	1	-	-	0/6/5/5
4	SF4	A	605	1	-	-	0/6/5/5
5	FES	A	604	1	-	-	0/1/1/1
5	FES	B	601	2	-	-	0/1/1/1
4	SF4	F	601	2	-	-	0/6/5/5

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	F	605	NAD	C4N-C3N	6.42	1.50	1.39
8	F	605	NAD	C5N-C4N	4.75	1.48	1.38
7	F	604	FMN	C10-N1	4.61	1.42	1.33
7	B	605	FMN	C10-N1	4.57	1.42	1.33
7	B	605	FMN	C9A-C5A	3.67	1.47	1.41
7	F	604	FMN	C9A-C5A	3.55	1.47	1.41
7	F	604	FMN	C4-N3	-3.45	1.32	1.38
7	B	605	FMN	C4-N3	-3.41	1.32	1.38
7	B	605	FMN	C2-N3	-3.30	1.31	1.39
7	F	604	FMN	C2-N3	-3.16	1.31	1.39
7	B	605	FMN	C4A-C4	3.10	1.55	1.44
7	F	604	FMN	C4A-C4	3.05	1.55	1.44
7	F	604	FMN	C2-N1	2.89	1.43	1.36
7	B	605	FMN	C2-N1	2.75	1.43	1.36
8	F	605	NAD	C3N-C7N	-2.65	1.46	1.50
7	B	605	FMN	C9-C8	-2.52	1.35	1.39
8	F	605	NAD	C6N-C5N	-2.51	1.33	1.38
7	F	604	FMN	C1'-C2'	-2.37	1.49	1.52
8	F	605	NAD	C2N-C3N	-2.31	1.35	1.39
7	F	604	FMN	C9-C8	-2.29	1.36	1.39
7	F	604	FMN	C5A-N5	-2.23	1.35	1.39
7	B	605	FMN	C5A-N5	-2.20	1.35	1.39
7	B	605	FMN	C9A-N10	-2.11	1.37	1.41
7	B	605	FMN	C1'-C2'	-2.07	1.49	1.52
7	B	605	FMN	P-O2P	-2.07	1.46	1.54
7	B	605	FMN	C4A-C10	2.07	1.50	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	F	604	FMN	P-O2P	-2.05	1.46	1.54
7	F	604	FMN	C4A-C10	2.04	1.50	1.44
7	B	605	FMN	C6-C7	-2.03	1.36	1.39
7	F	604	FMN	C2'-C3'	-2.02	1.49	1.53

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	F	604	FMN	C4A-C10-N1	-9.40	102.91	124.73
7	B	605	FMN	C4A-C10-N1	-9.32	103.11	124.73
7	B	605	FMN	C10-N1-C2	8.83	134.55	116.90
7	F	604	FMN	C10-N1-C2	8.78	134.45	116.90
8	F	605	NAD	C5N-C4N-C3N	-8.56	110.21	120.34
7	B	605	FMN	C4A-C10-N10	6.98	126.69	116.48
7	F	604	FMN	C4A-C10-N10	6.97	126.67	116.48
7	F	604	FMN	C10-C4A-N5	-4.67	114.94	124.86
7	B	605	FMN	C10-C4A-N5	-4.63	115.04	124.86
7	F	604	FMN	N10-C10-N1	4.20	130.42	118.35
7	B	605	FMN	N10-C10-N1	4.12	130.21	118.35
7	B	605	FMN	C4A-C4-N3	3.56	122.23	113.19
7	B	605	FMN	C9A-N10-C10	-3.52	115.29	120.77
7	F	604	FMN	O2'-C2'-C1'	-3.52	101.30	109.80
7	F	604	FMN	C9A-N10-C10	-3.51	115.30	120.77
7	F	604	FMN	C4-C4A-C10	3.44	122.58	116.79
7	B	605	FMN	C1'-N10-C9A	3.42	126.21	120.51
7	F	604	FMN	C4A-C4-N3	3.41	121.84	113.19
7	F	604	FMN	C1'-N10-C9A	3.38	126.16	120.51
7	B	605	FMN	C4-N3-C2	-3.36	119.44	125.64
7	B	605	FMN	C4-C4A-N5	3.32	122.95	118.23
7	F	604	FMN	C4-N3-C2	-3.24	119.65	125.64
7	B	605	FMN	C4-C4A-C10	3.10	122.01	116.79
7	F	604	FMN	C4-C4A-N5	2.98	122.48	118.23
8	F	605	NAD	C2N-C3N-C4N	2.97	121.63	118.26
7	B	605	FMN	O2'-C2'-C1'	-2.94	102.69	109.80
8	F	605	NAD	C6N-C5N-C4N	2.70	123.36	119.44
7	F	604	FMN	O2'-C2'-C3'	-2.60	102.77	109.10
7	B	605	FMN	O2'-C2'-C3'	-2.47	103.09	109.10
7	B	605	FMN	C1'-C2'-C3'	2.29	116.19	109.79
8	F	605	NAD	C5A-C6A-N6A	2.25	123.78	120.35
7	F	604	FMN	C1'-C2'-C3'	2.20	115.93	109.79
8	F	605	NAD	C6N-N1N-C2N	-2.15	120.02	121.97
7	F	604	FMN	O3'-C3'-C2'	-2.07	103.82	108.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	F	604	FMN	O3P-P-O2P	2.03	115.41	107.64
7	F	604	FMN	O4-C4-C4A	-2.03	121.23	126.60
7	B	605	FMN	O3'-C3'-C2'	-2.02	103.92	108.81
7	B	605	FMN	C4'-C3'-C2'	2.02	117.57	113.36

There are no chirality outliers.

All (29) torsion outliers are listed below:

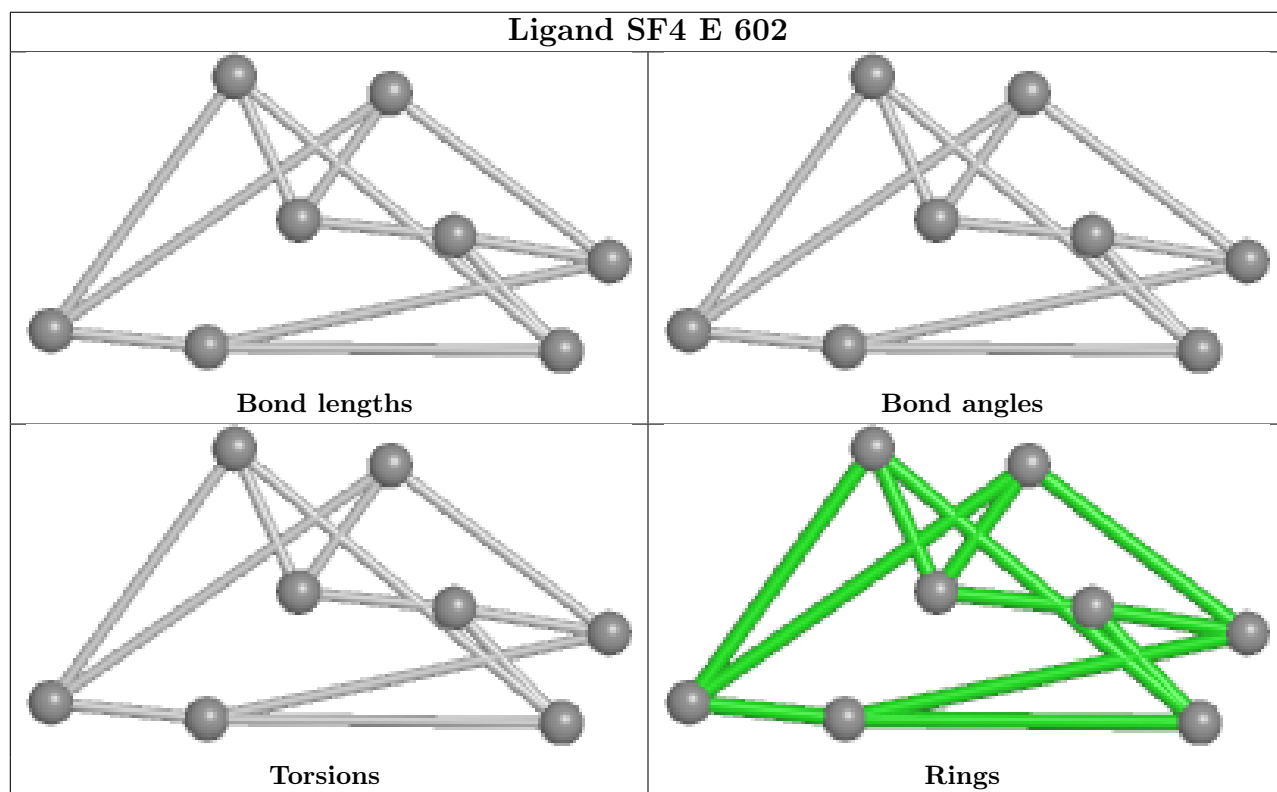
Mol	Chain	Res	Type	Atoms
7	B	605	FMN	N10-C1'-C2'-O2'
7	B	605	FMN	N10-C1'-C2'-C3'
7	B	605	FMN	C1'-C2'-C3'-O3'
7	B	605	FMN	C1'-C2'-C3'-C4'
7	B	605	FMN	C3'-C4'-C5'-O5'
7	B	605	FMN	O4'-C4'-C5'-O5'
7	B	605	FMN	C5'-O5'-P-O1P
7	B	605	FMN	C5'-O5'-P-O3P
7	F	604	FMN	N10-C1'-C2'-O2'
7	F	604	FMN	N10-C1'-C2'-C3'
7	F	604	FMN	C3'-C4'-C5'-O5'
7	F	604	FMN	O4'-C4'-C5'-O5'
7	F	604	FMN	C5'-O5'-P-O1P
7	F	604	FMN	C5'-O5'-P-O2P
7	F	604	FMN	C5'-O5'-P-O3P
8	F	605	NAD	O4B-C4B-C5B-O5B
8	F	605	NAD	C3B-C4B-C5B-O5B
8	F	605	NAD	O4D-C1D-N1N-C2N
8	F	605	NAD	C2D-C1D-N1N-C2N
8	F	605	NAD	O4D-C4D-C5D-O5D
8	F	605	NAD	C3D-C4D-C5D-O5D
7	B	605	FMN	C5'-O5'-P-O2P
8	F	605	NAD	C4B-C5B-O5B-PA
8	F	605	NAD	C4D-C5D-O5D-PN
8	F	605	NAD	PA-O3-PN-O2N
7	B	605	FMN	O2'-C2'-C3'-C4'
7	B	605	FMN	O2'-C2'-C3'-O3'
8	F	605	NAD	C2D-C1D-N1N-C6N
8	F	605	NAD	PA-O3-PN-O1N

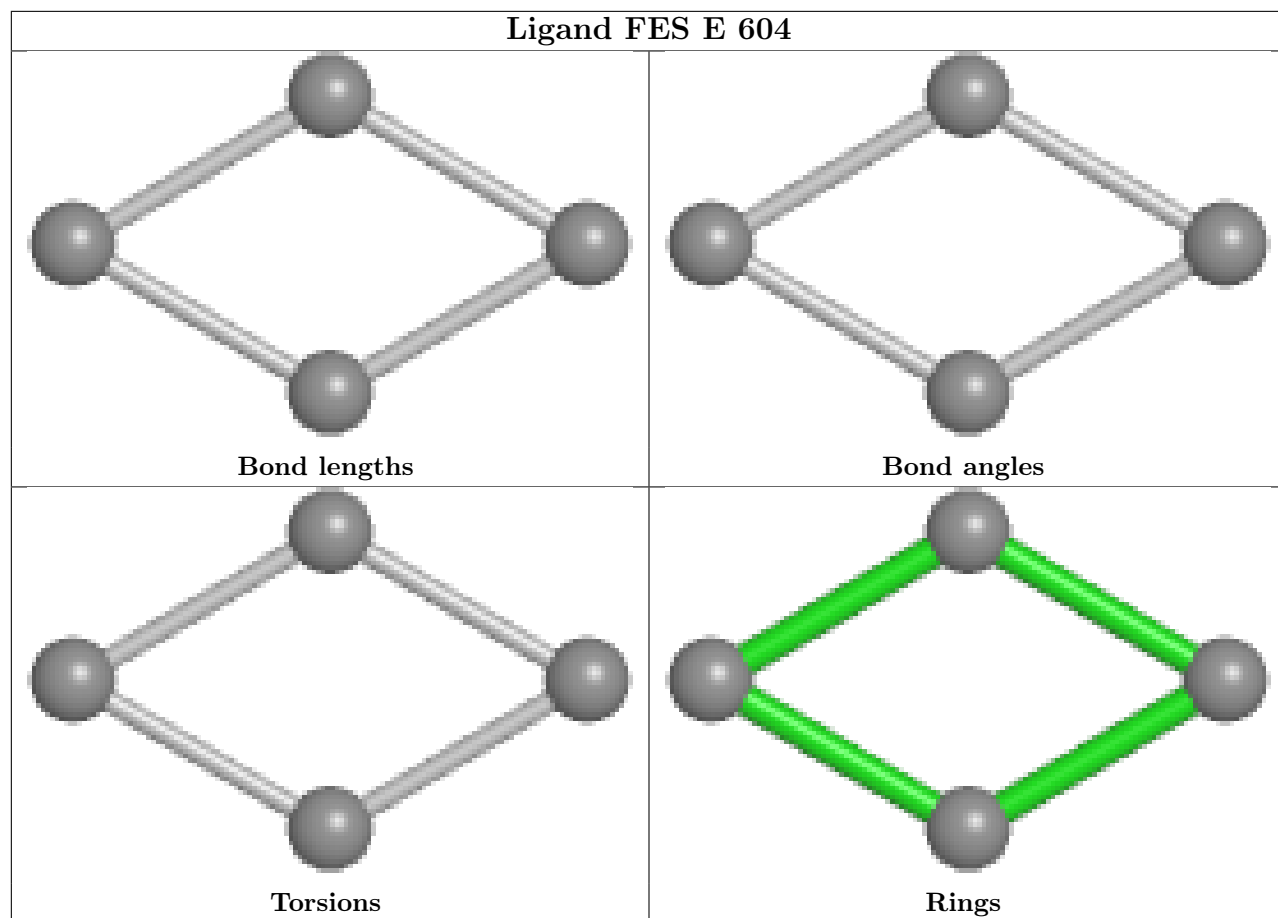
There are no ring outliers.

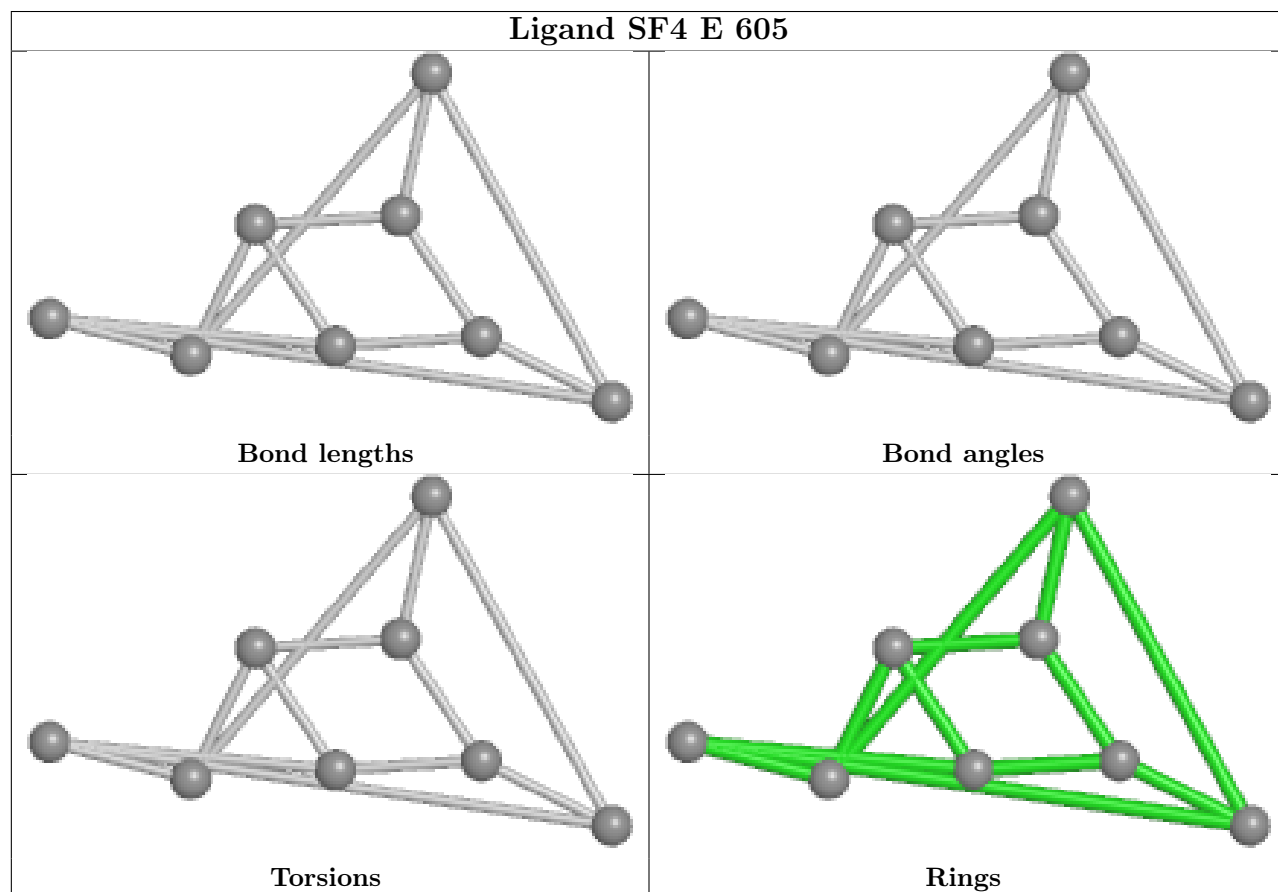
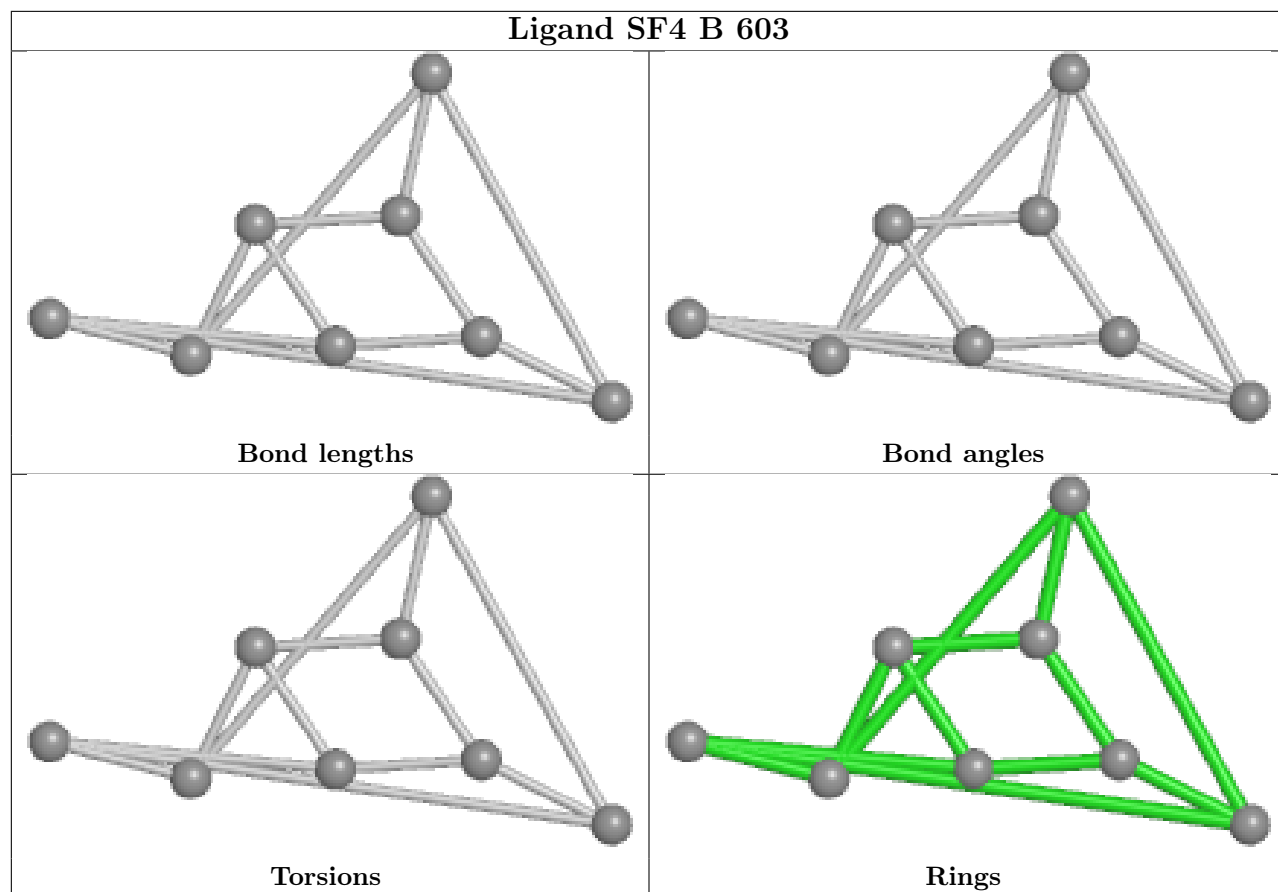
8 monomers are involved in 15 short contacts:

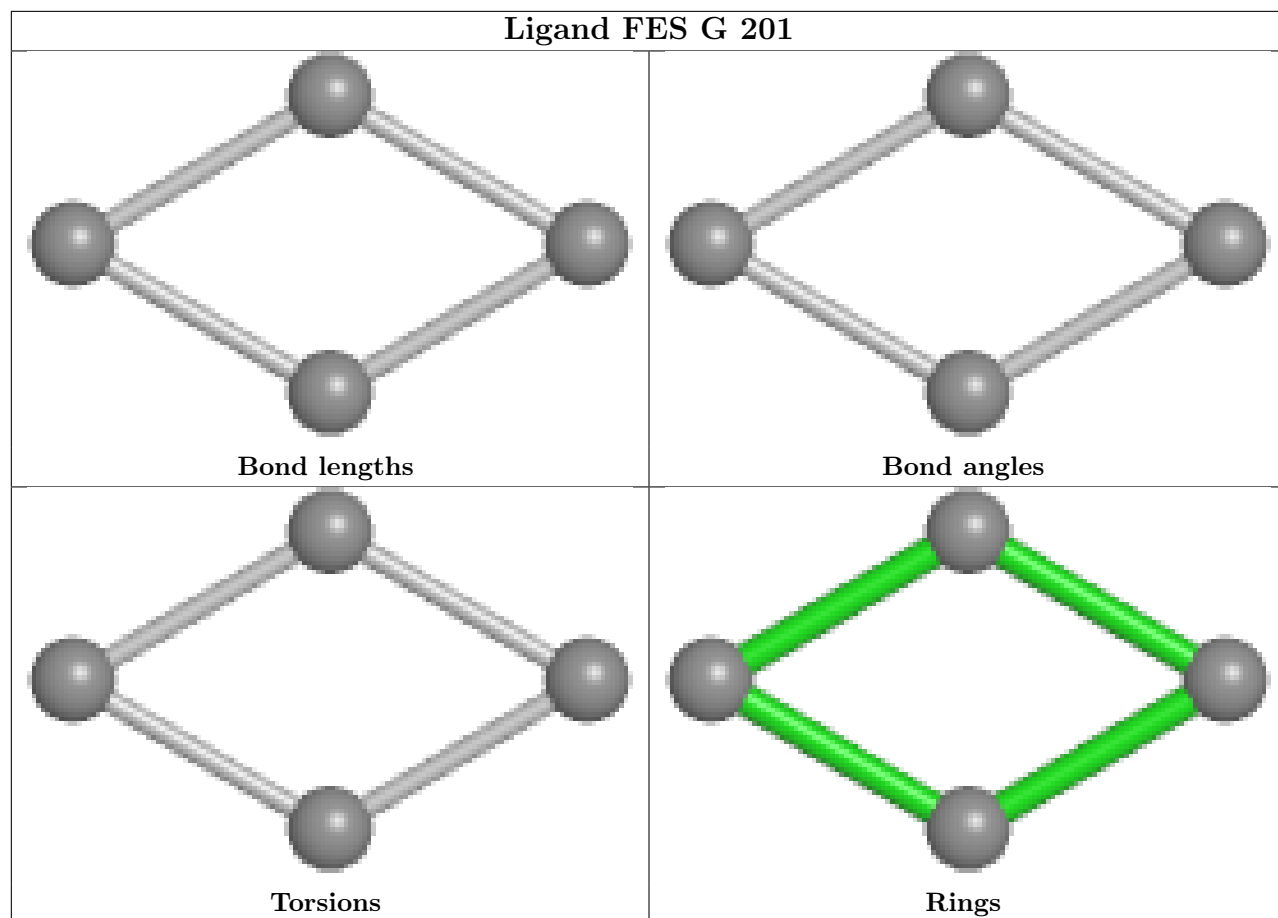
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	601	SF4	1	0
7	F	604	FMN	1	0
5	C	201	FES	2	0
4	B	606	SF4	3	0
4	E	603	SF4	1	0
7	B	605	FMN	3	0
4	A	603	SF4	3	0
4	A	605	SF4	1	0

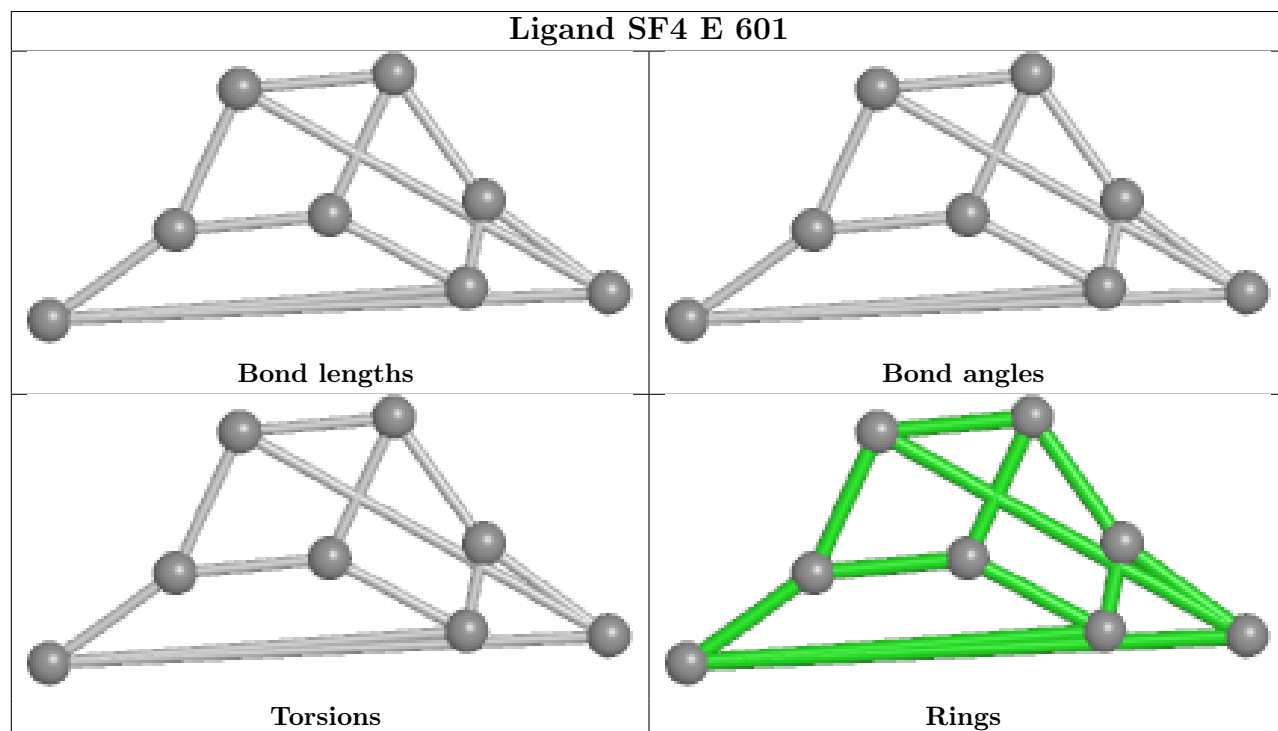
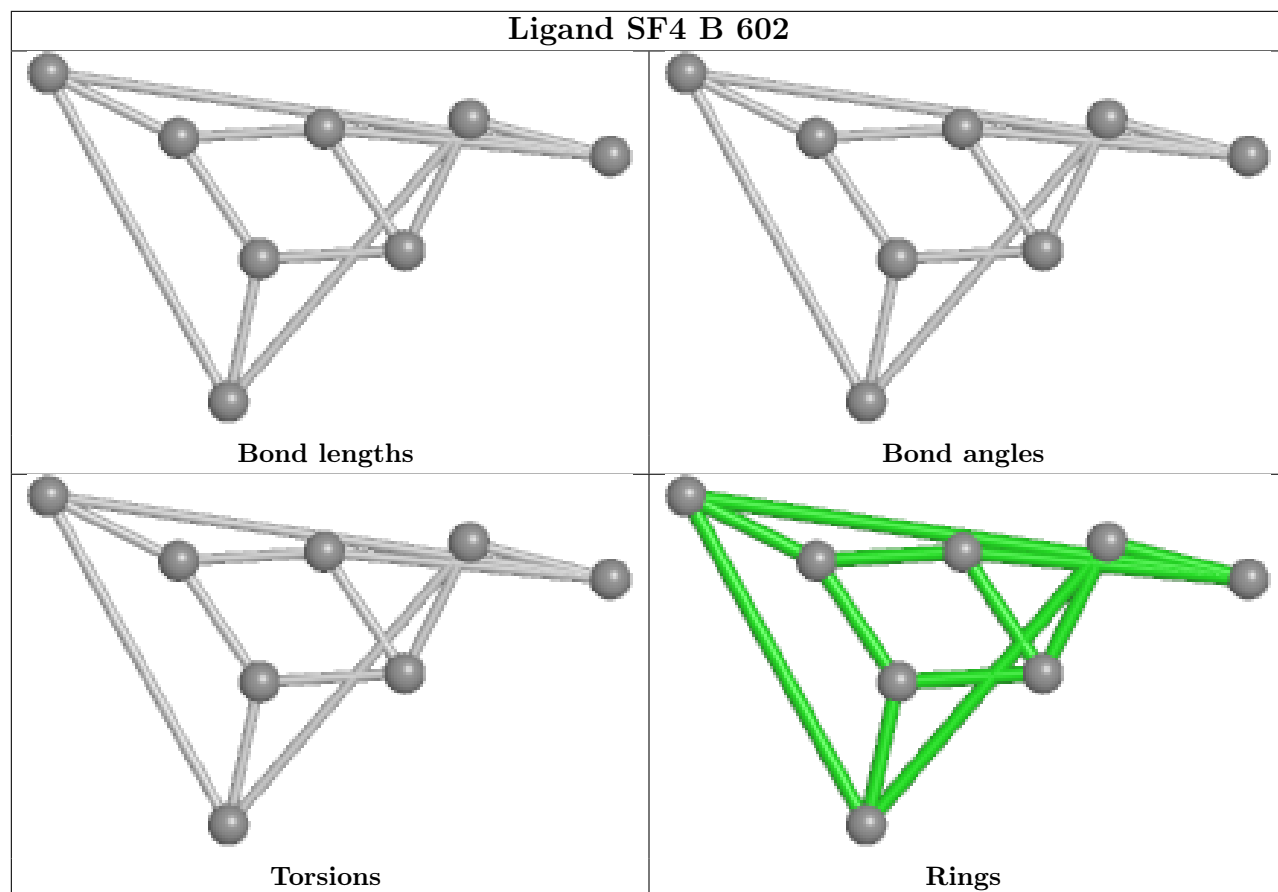
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

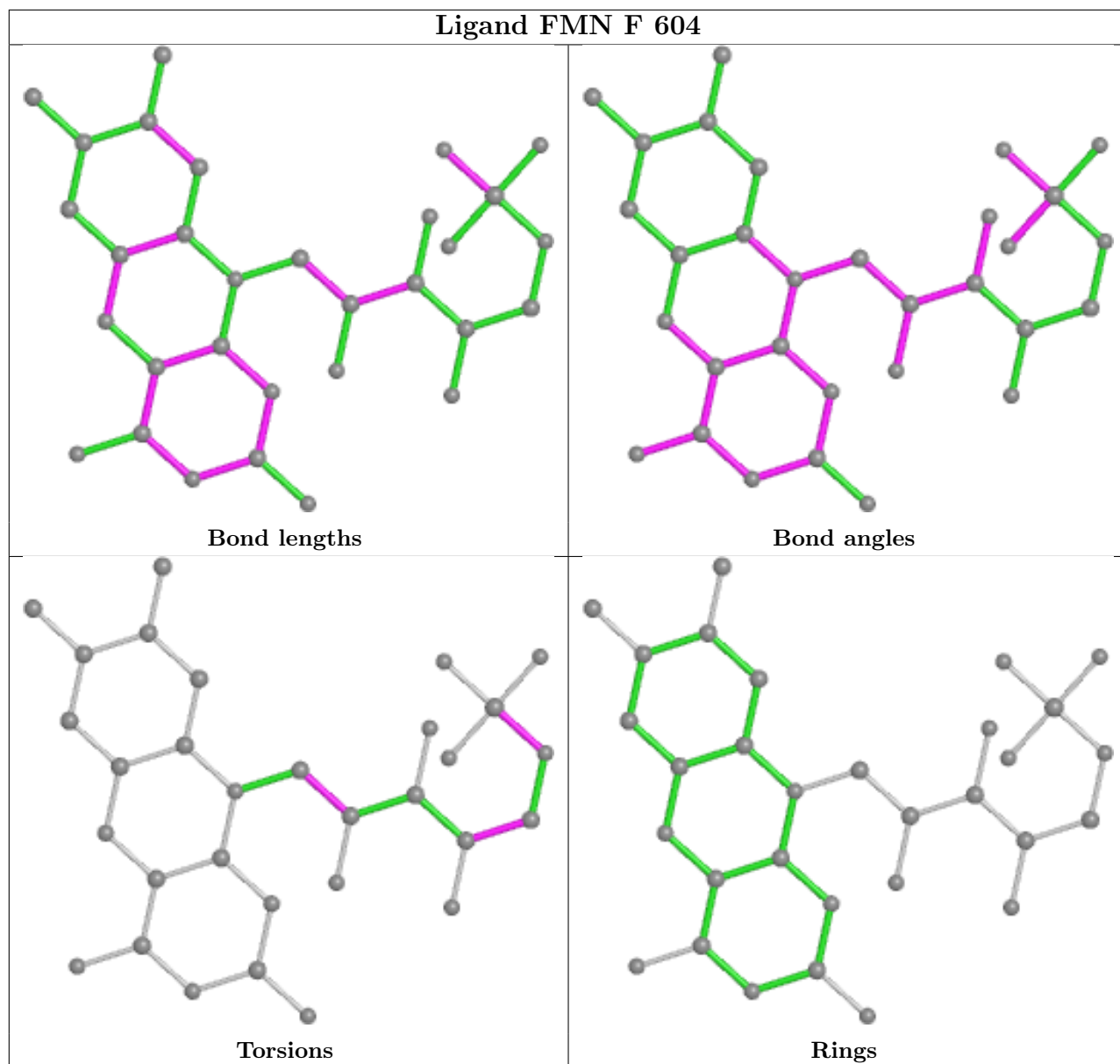


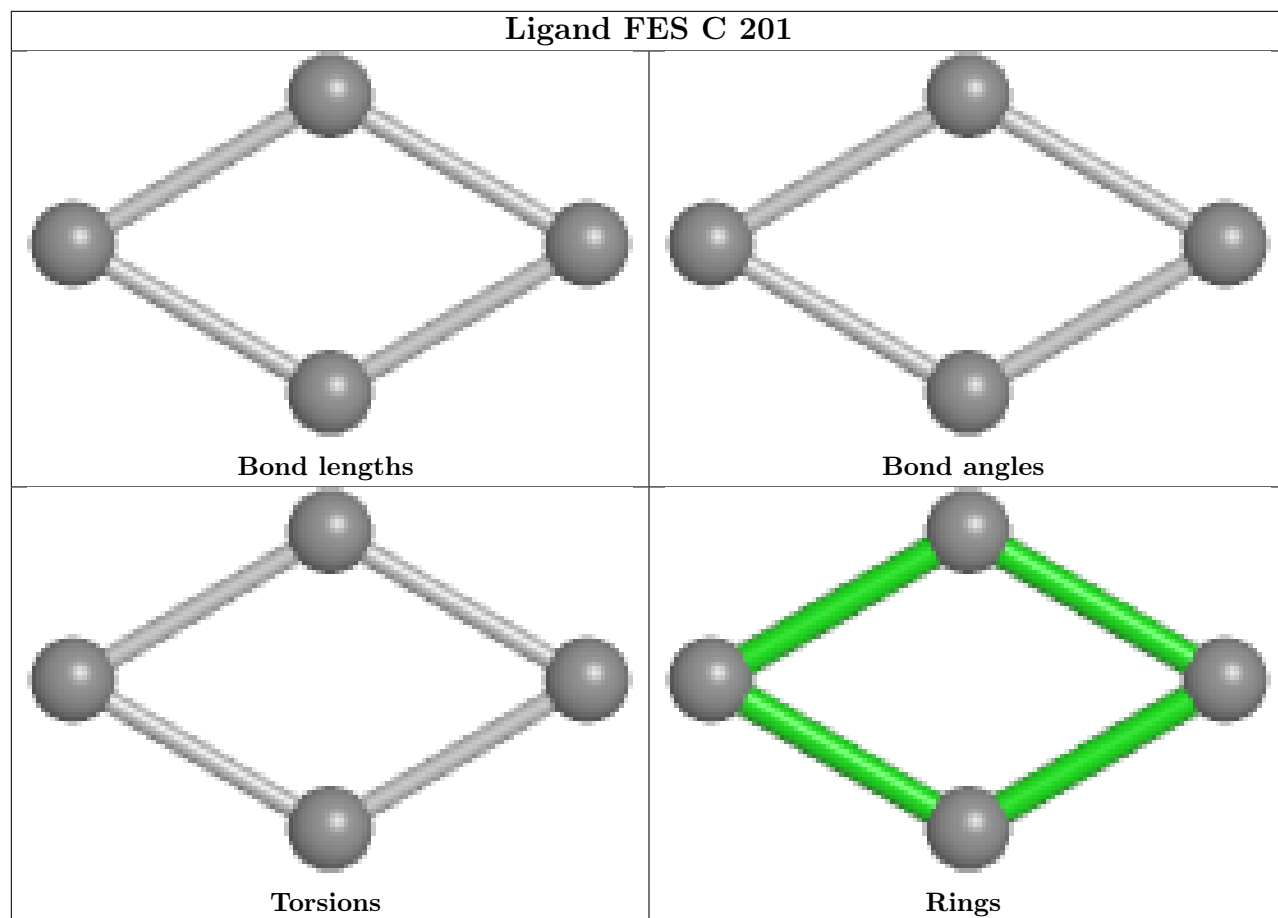


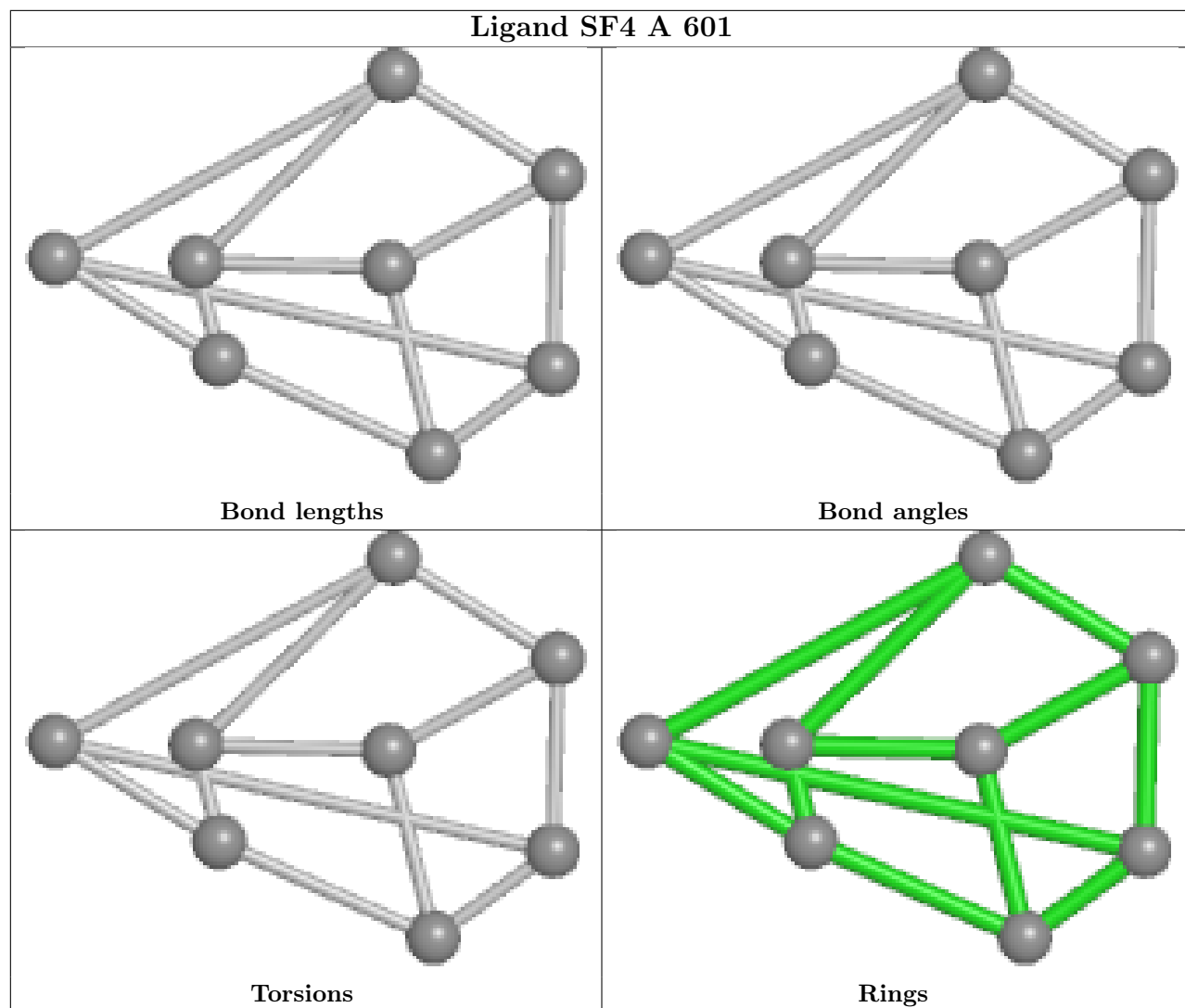


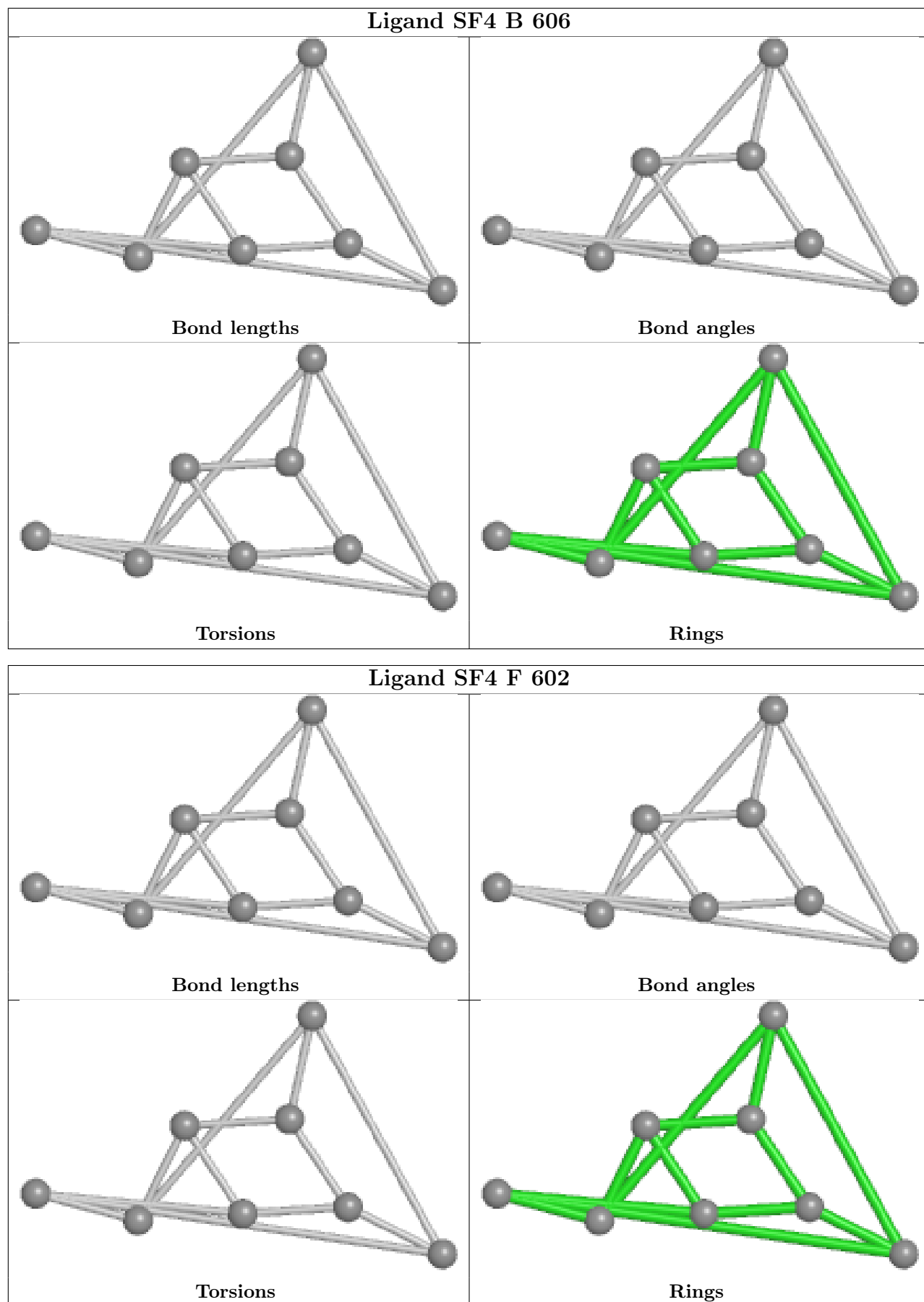


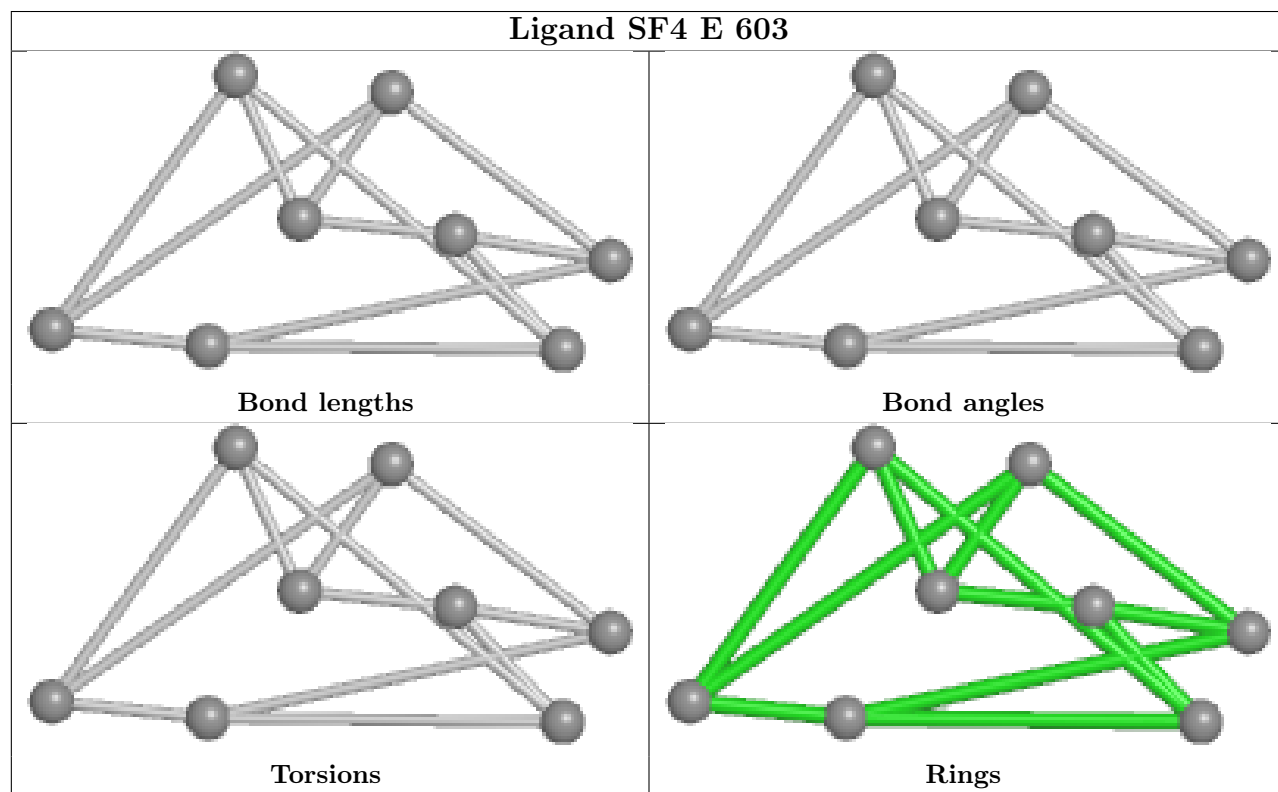
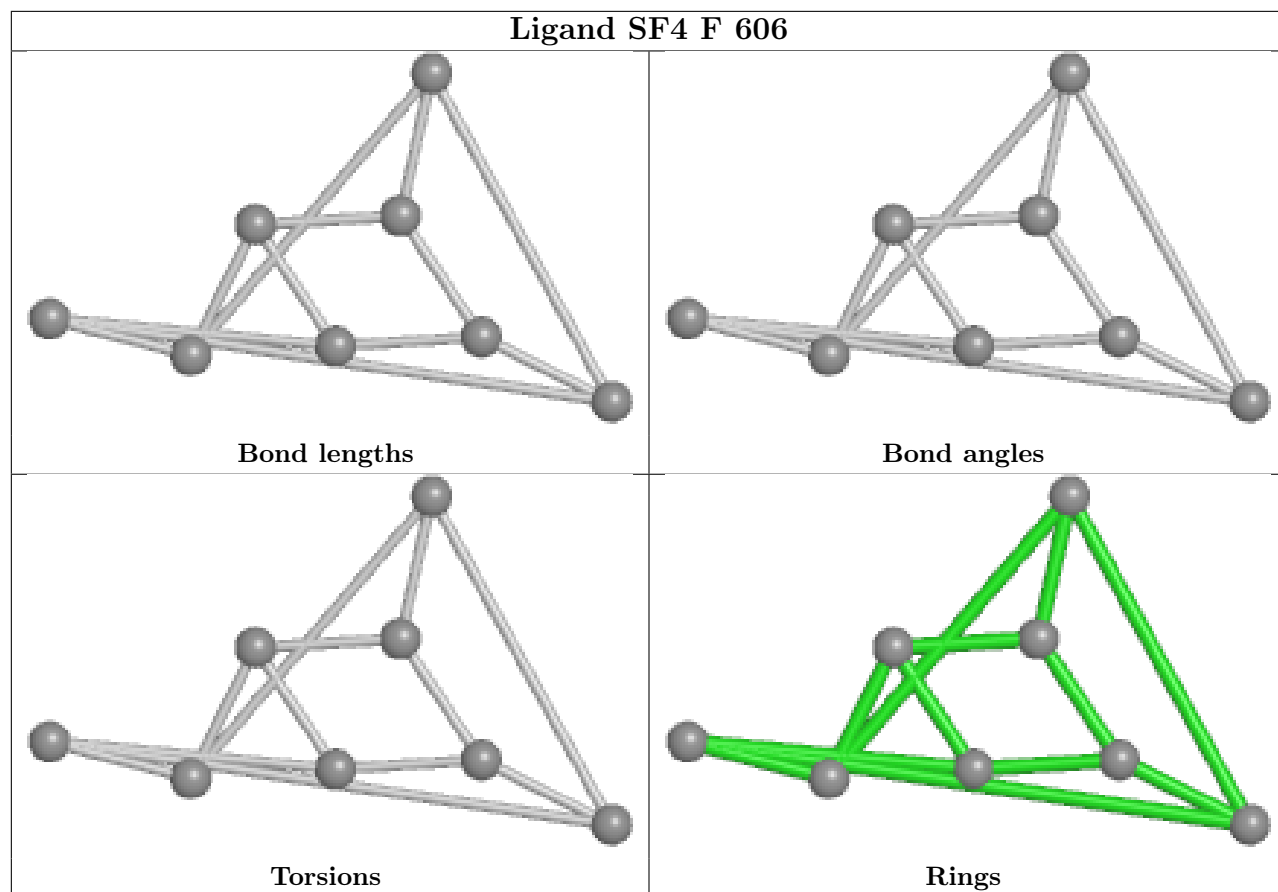


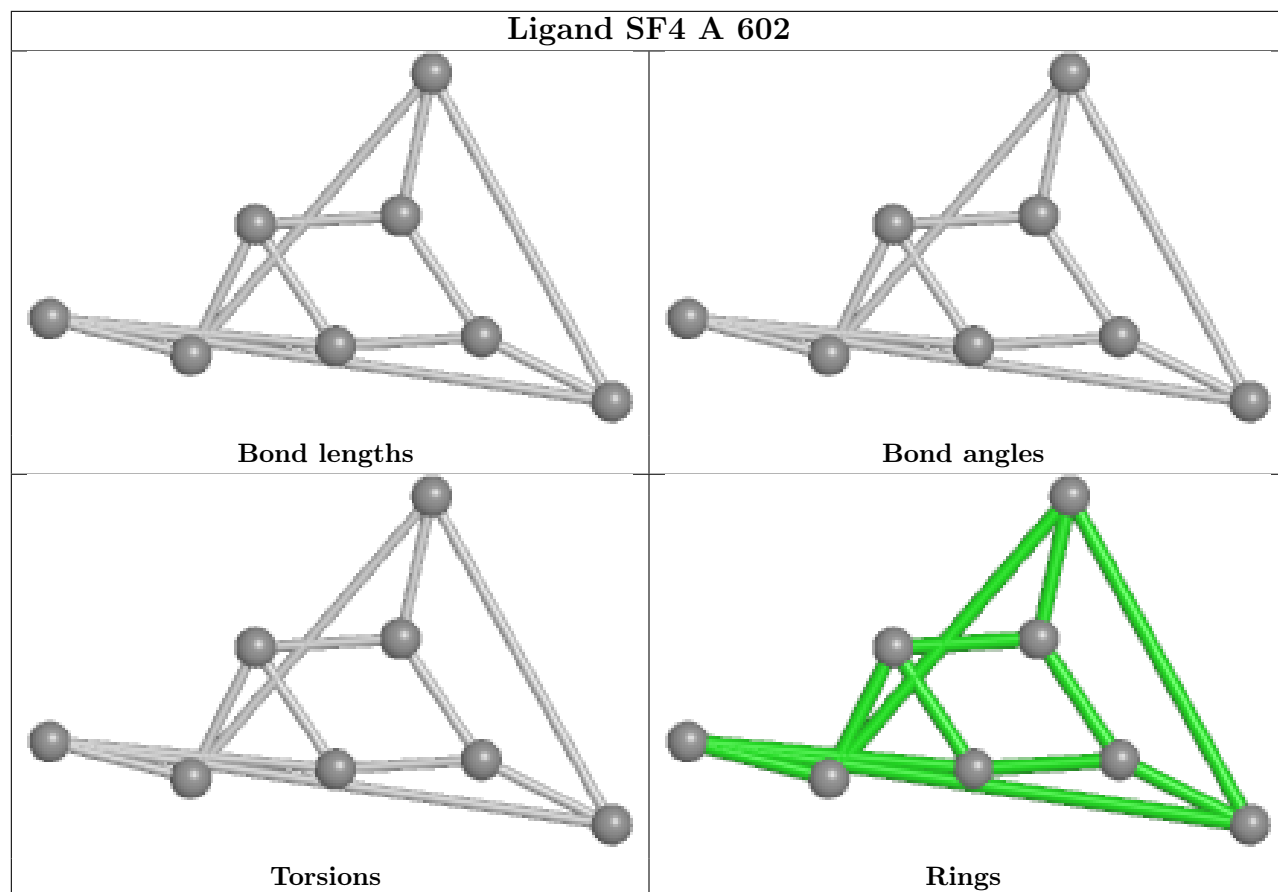


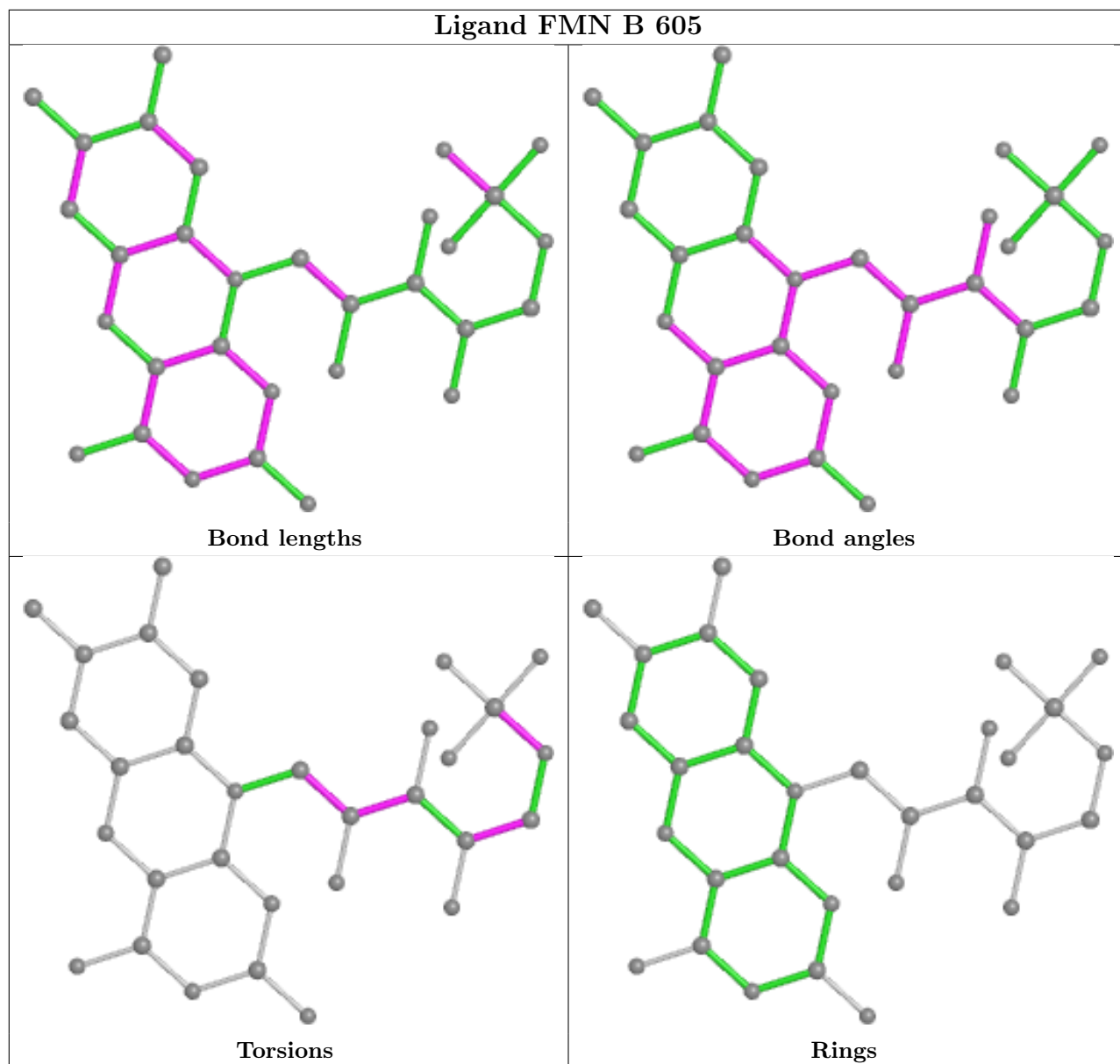


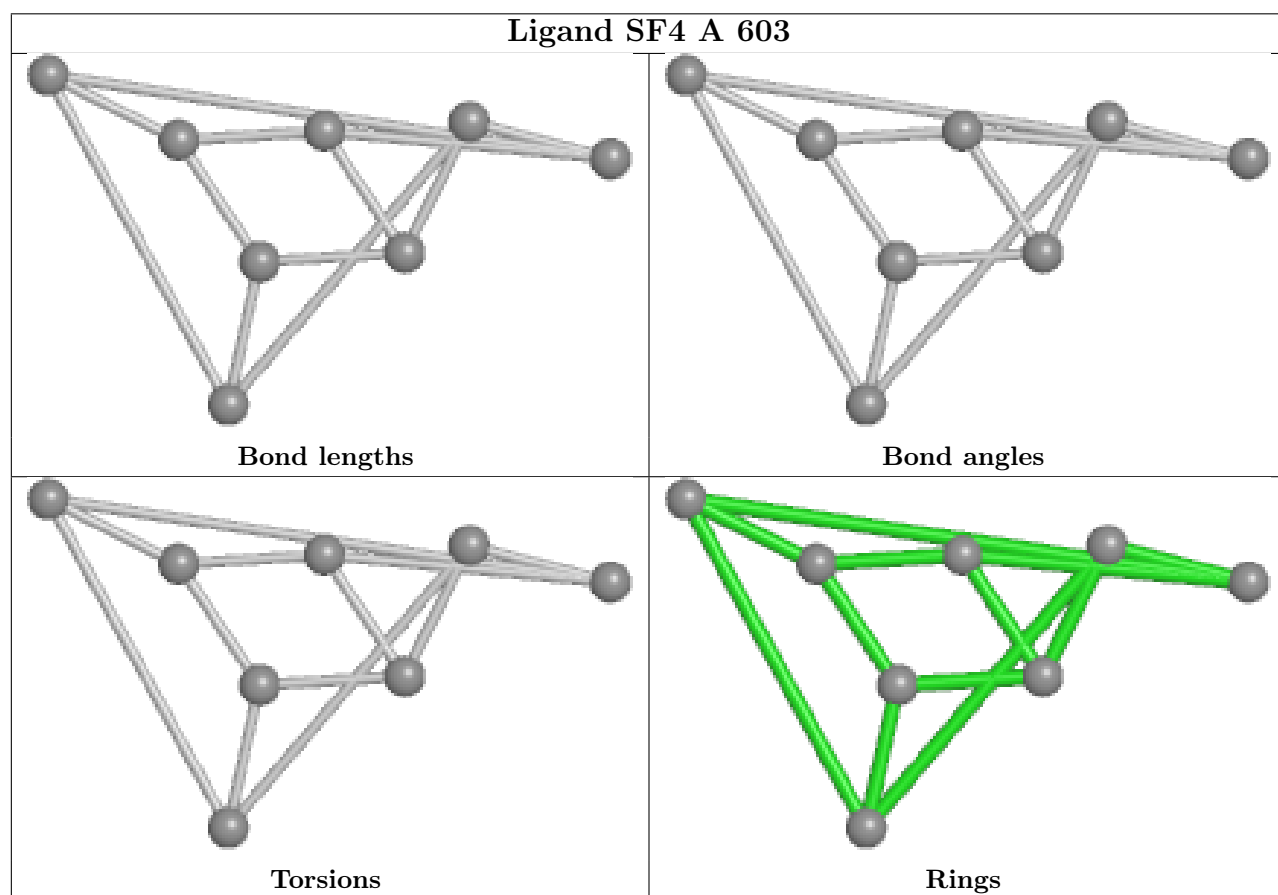
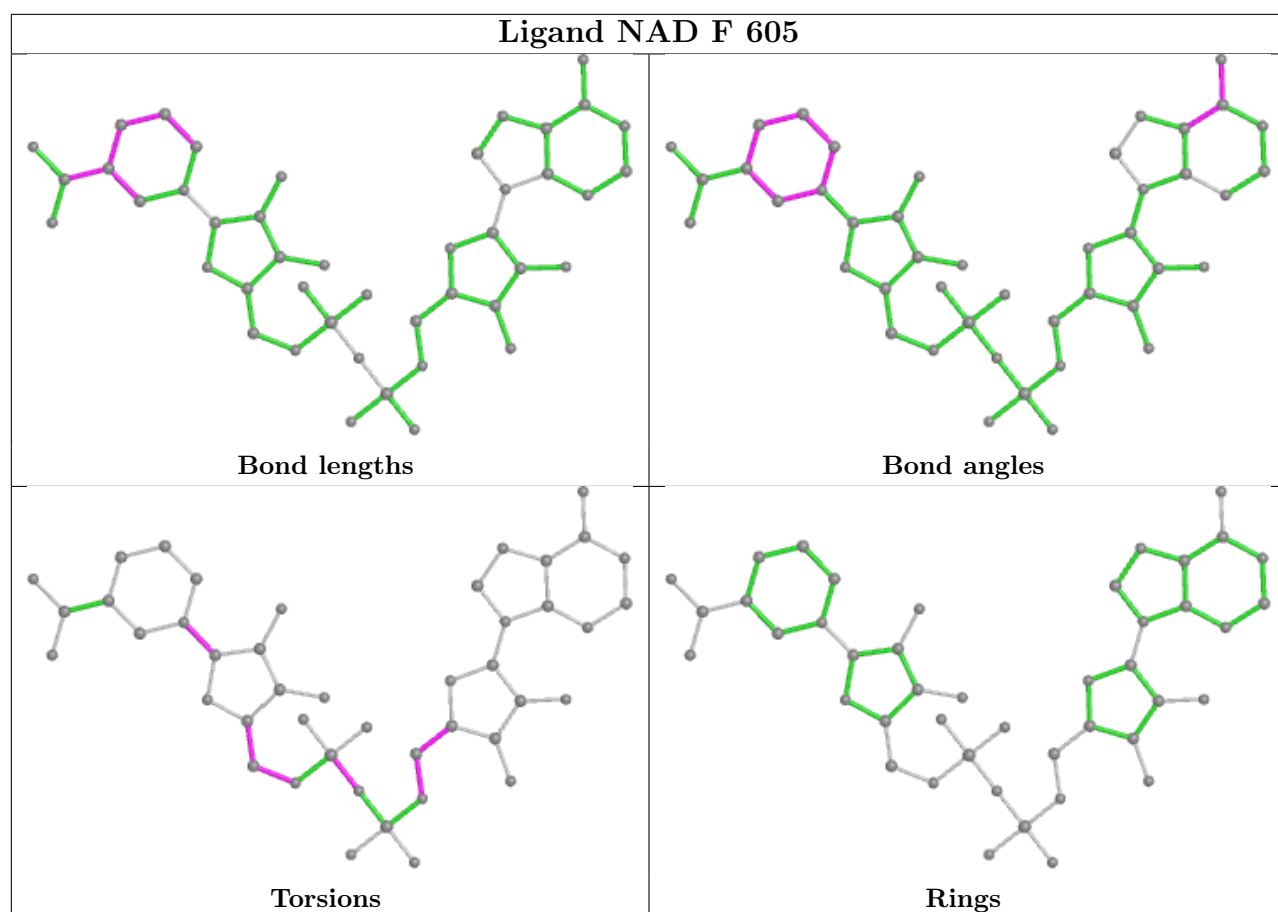


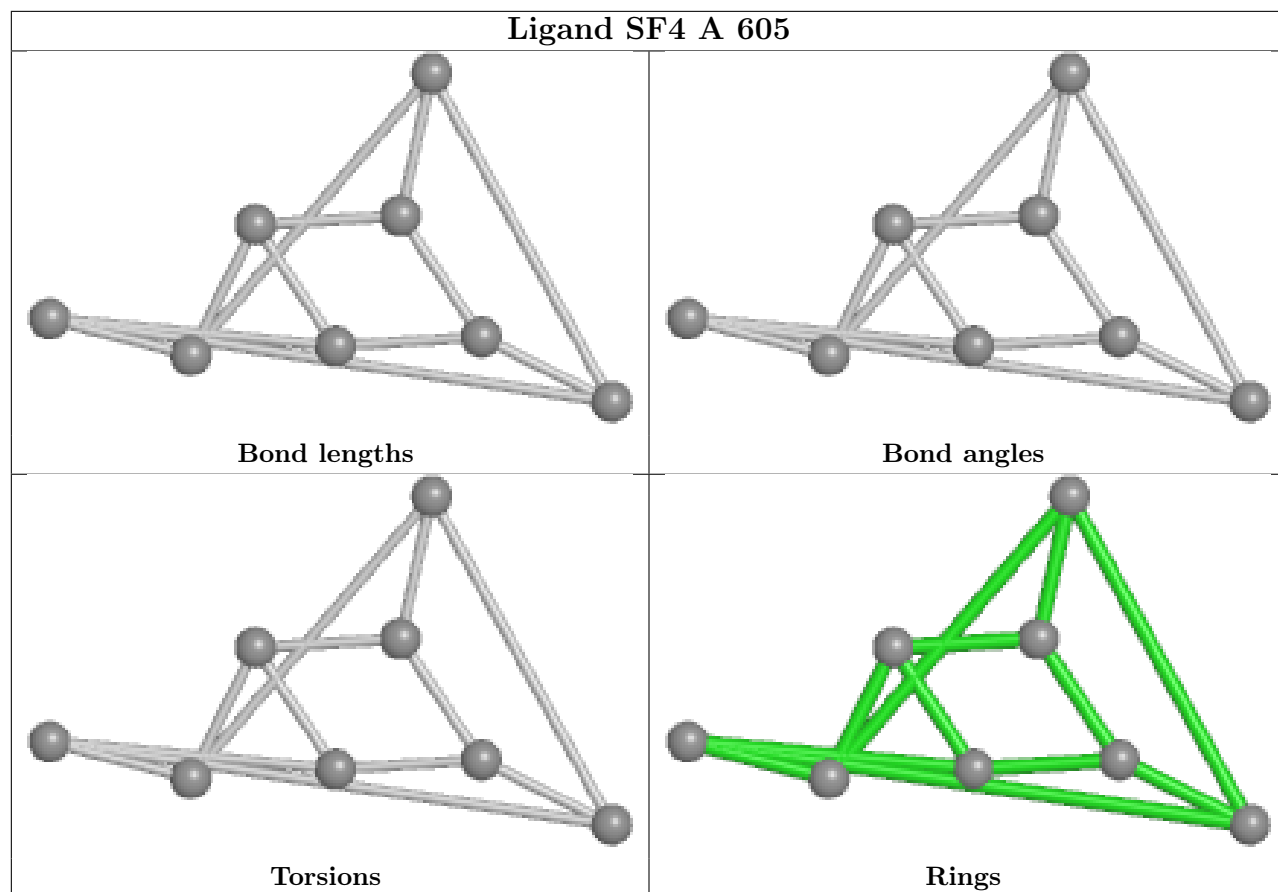


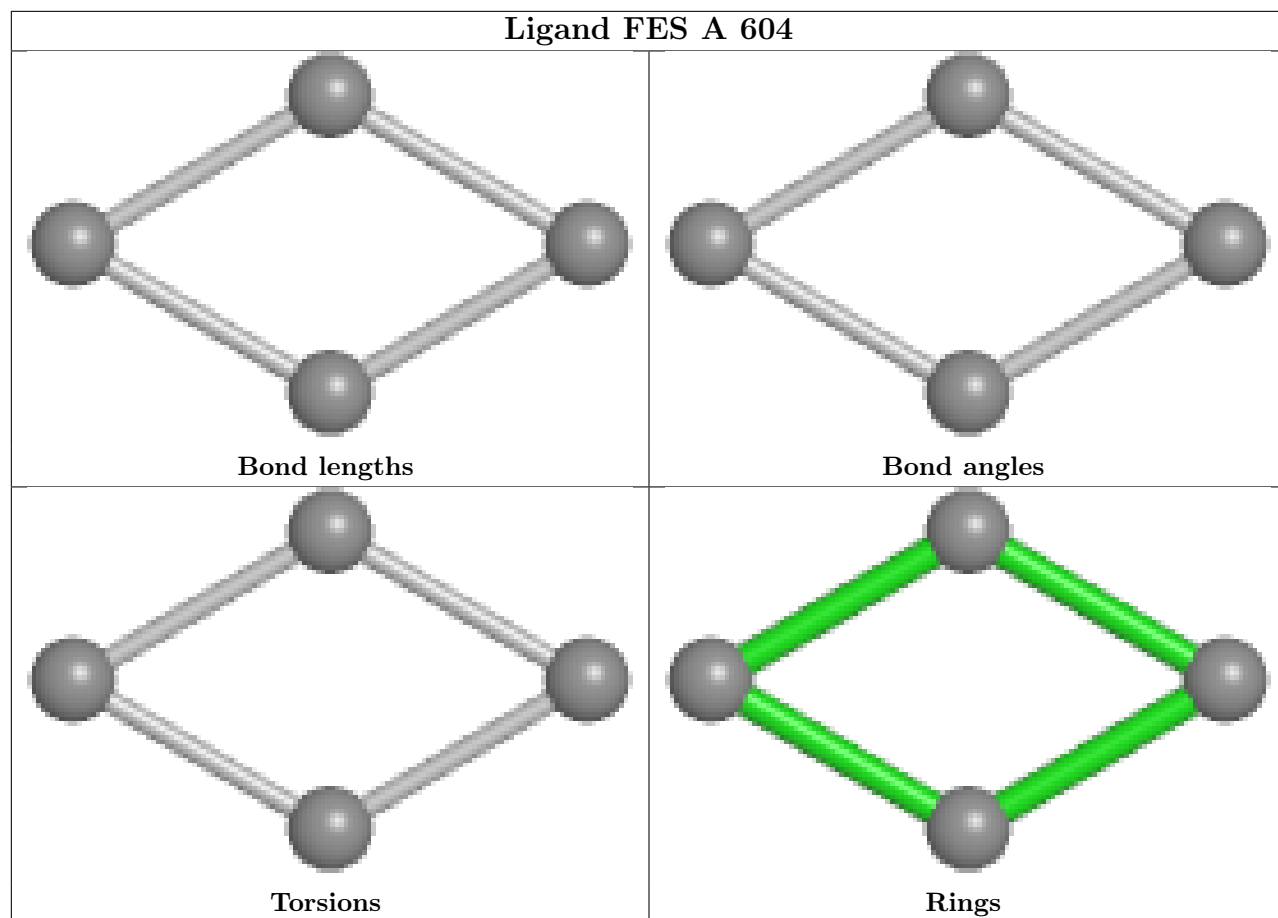


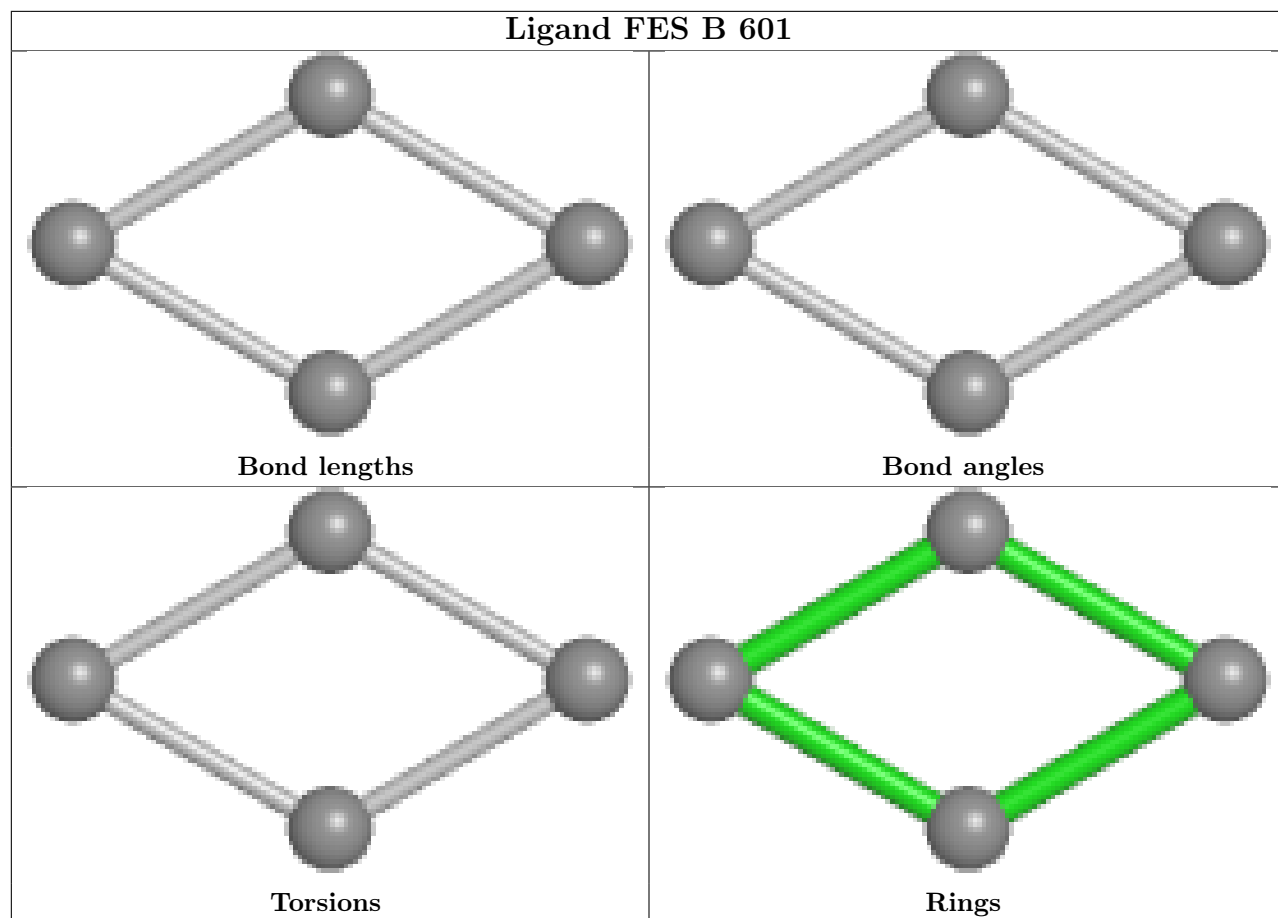


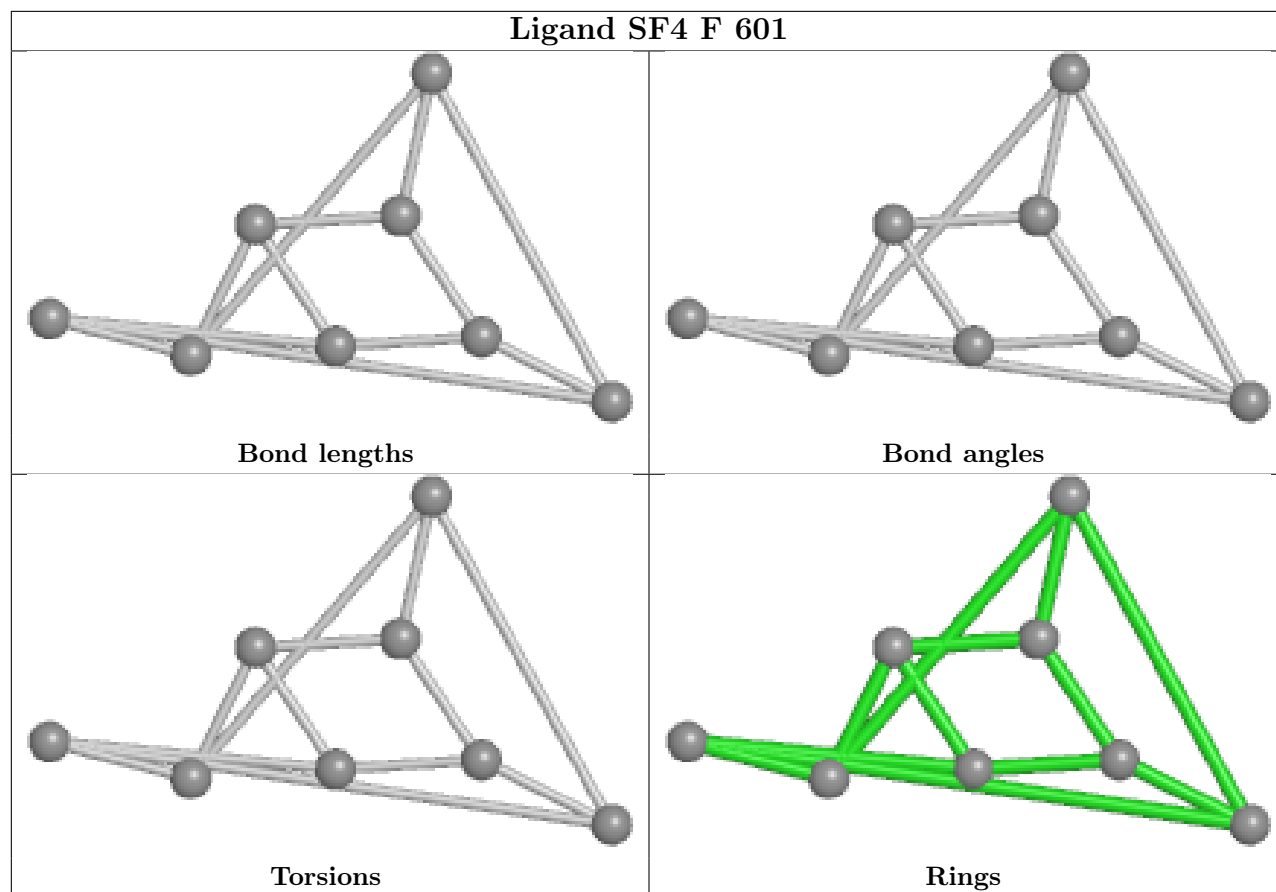












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

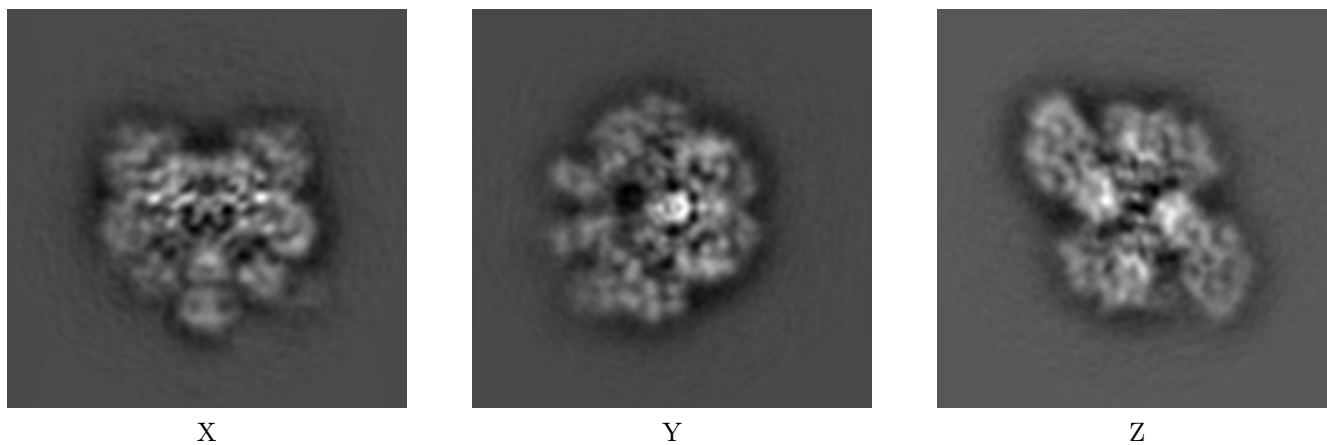
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13818. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

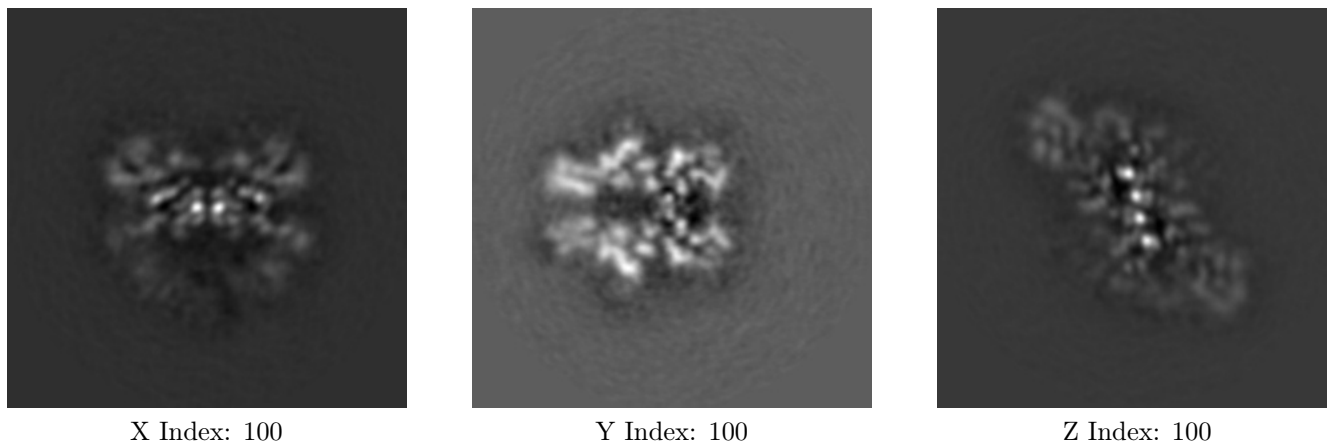
6.1.1 Primary map



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

6.2 Central slices [i](#)

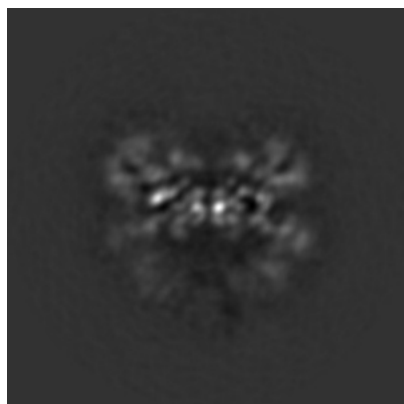
6.2.1 Primary map



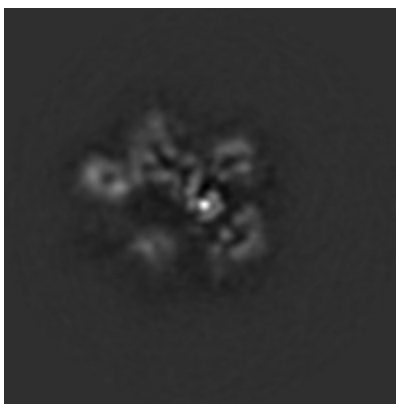
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

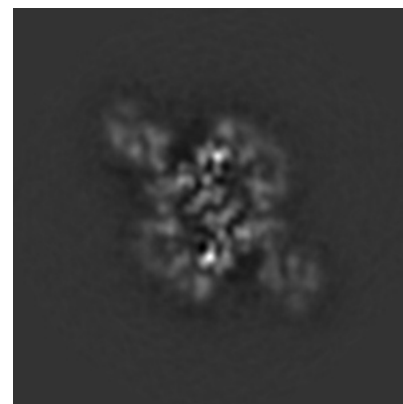
6.3.1 Primary map



X Index: 99



Y Index: 94

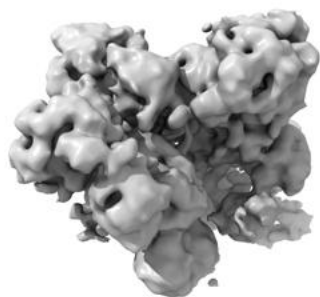


Z Index: 105

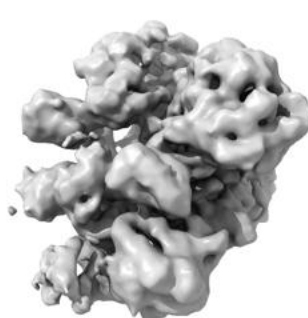
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

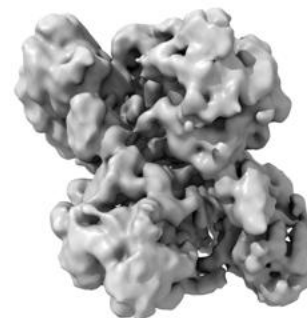
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.00114. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

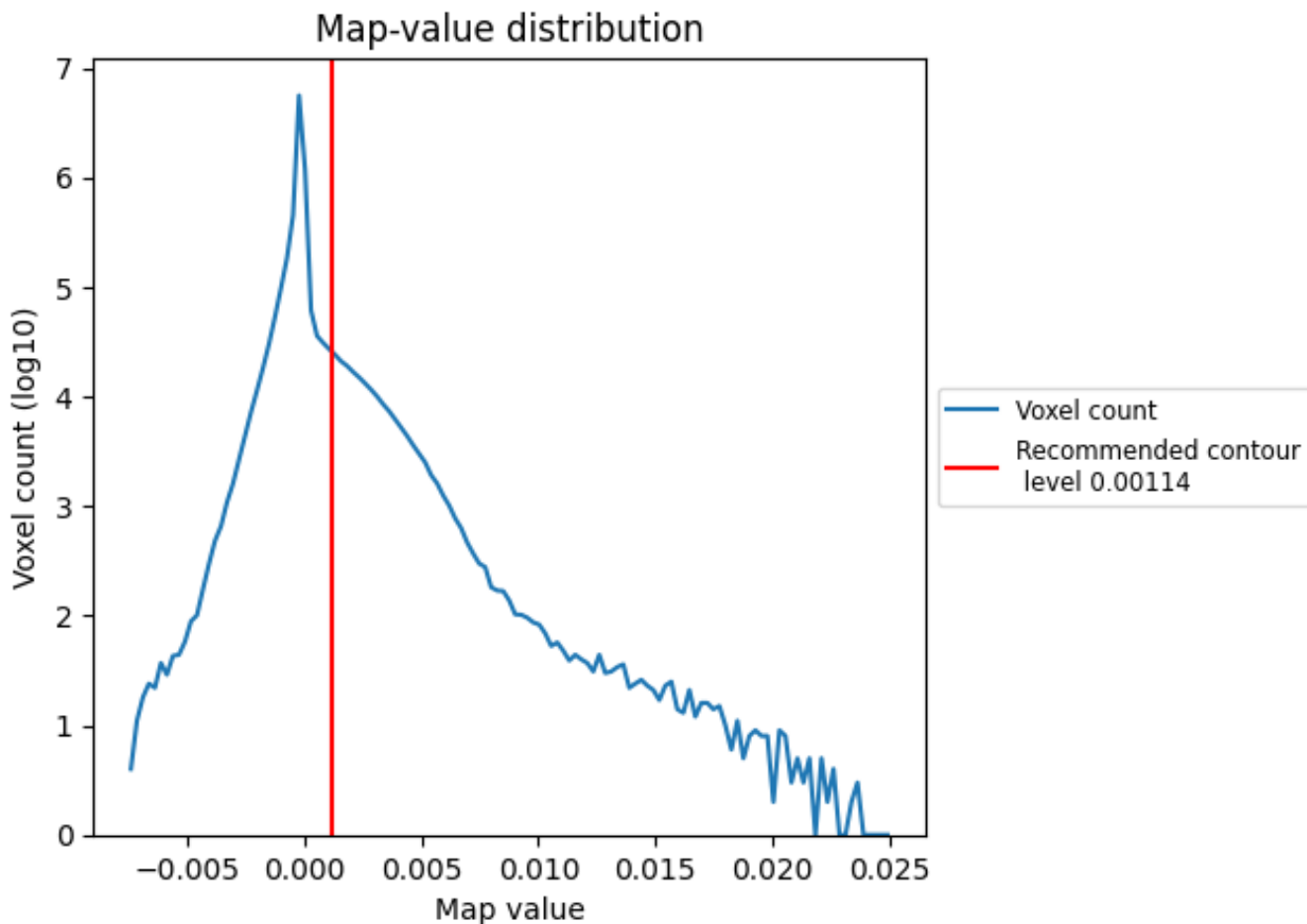
6.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

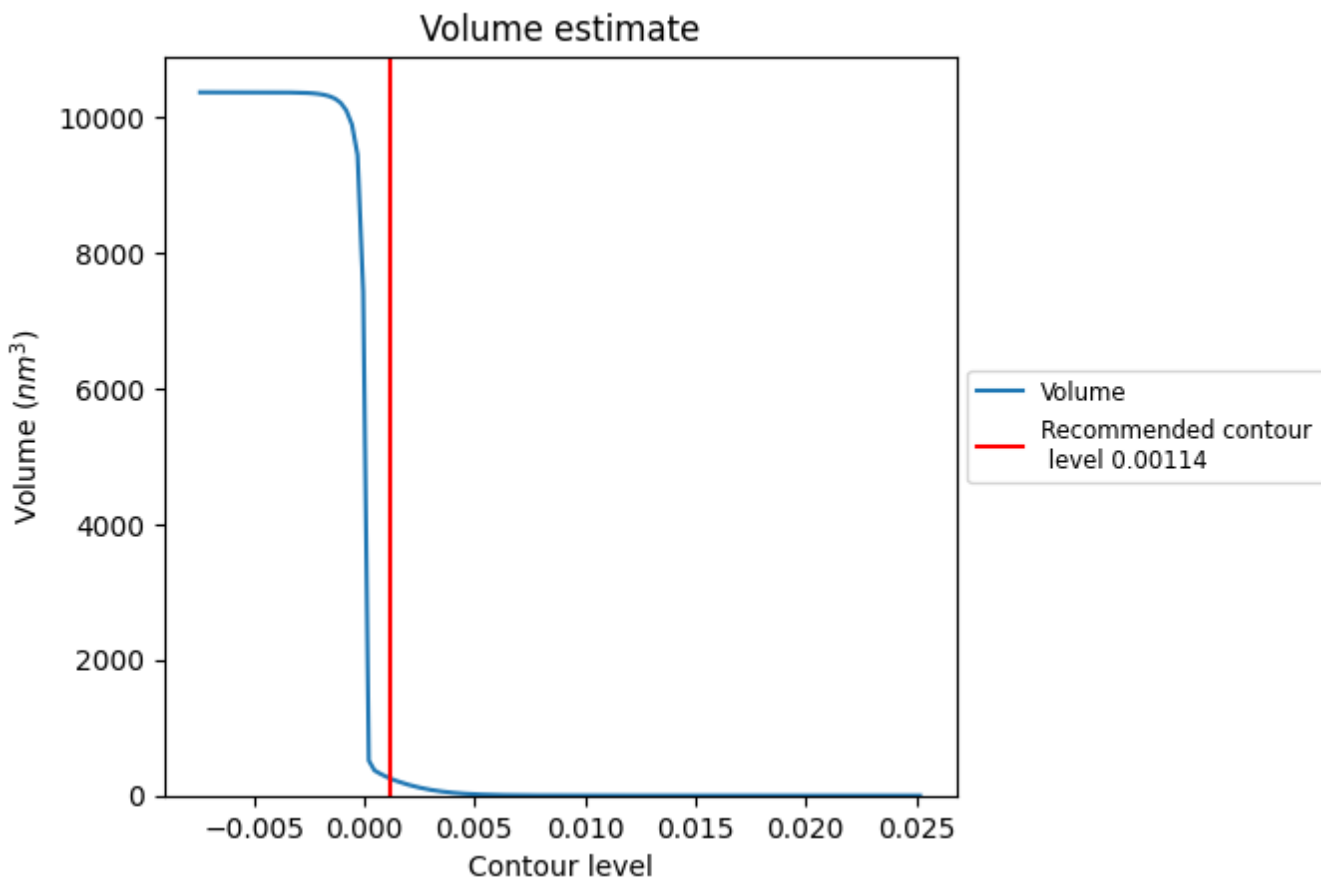
This section contains the results of statistical analysis of the map.

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.

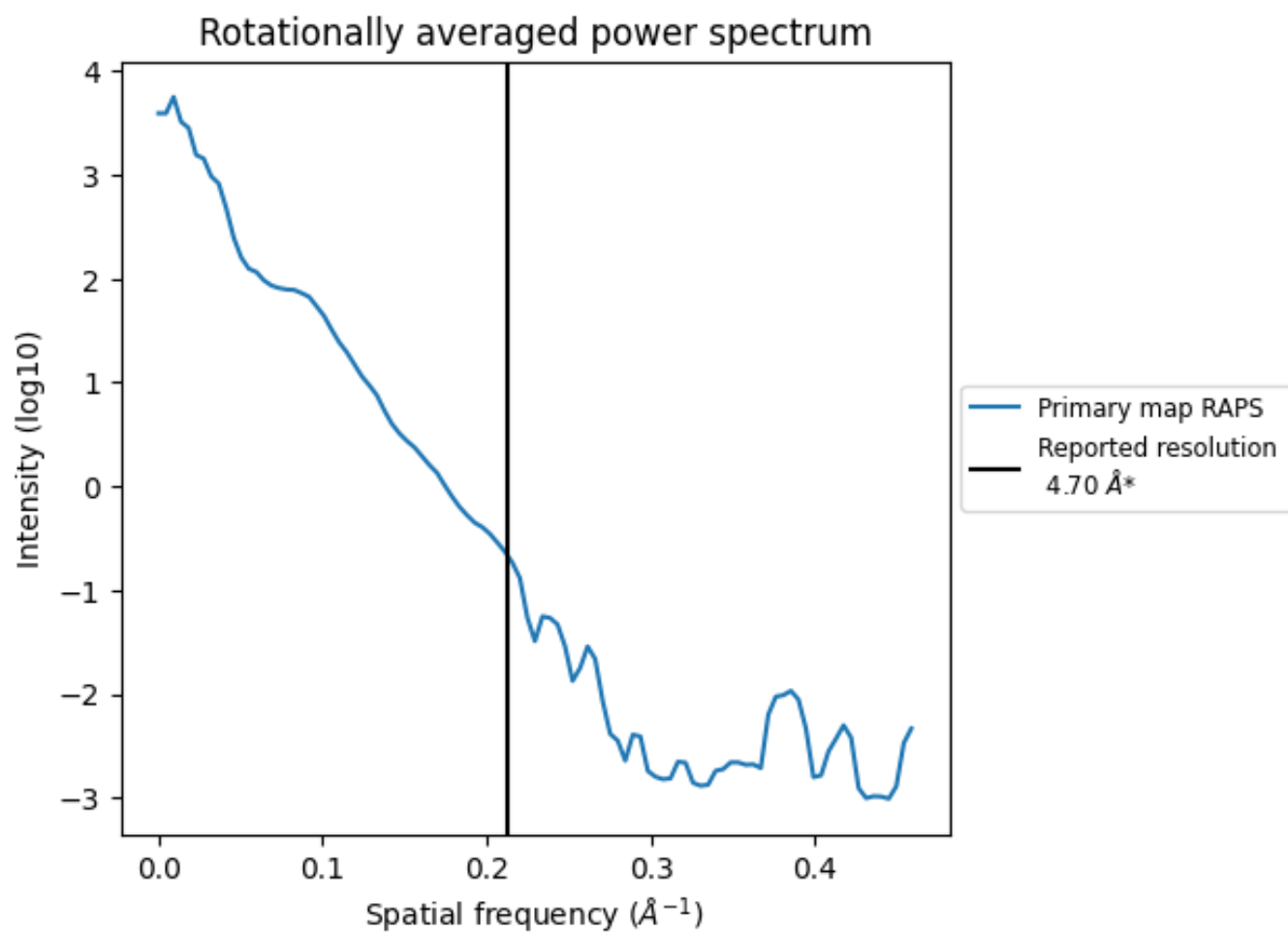
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 259 nm^3 ; this corresponds to an approximate mass of 234 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.213\AA^{-1}

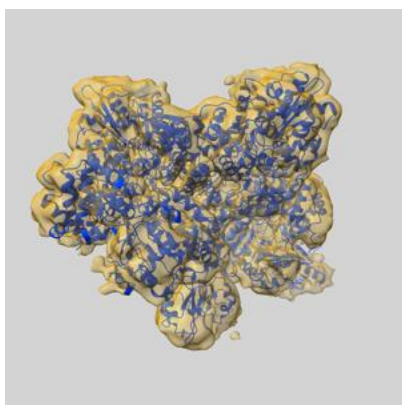
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

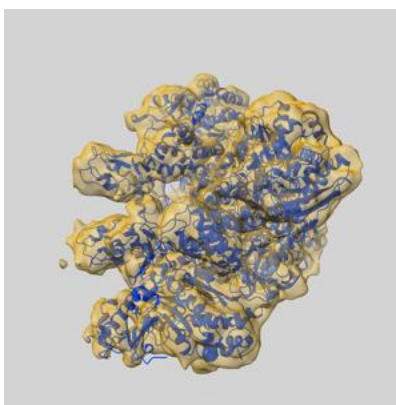
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13818 and PDB model 7Q4V. Per-residue inclusion information can be found in section 3 on page 8.

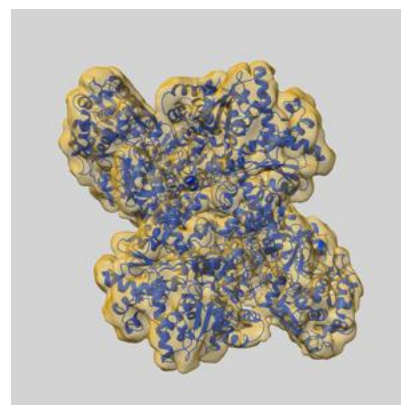
9.1 Map-model overlay [i](#)



X



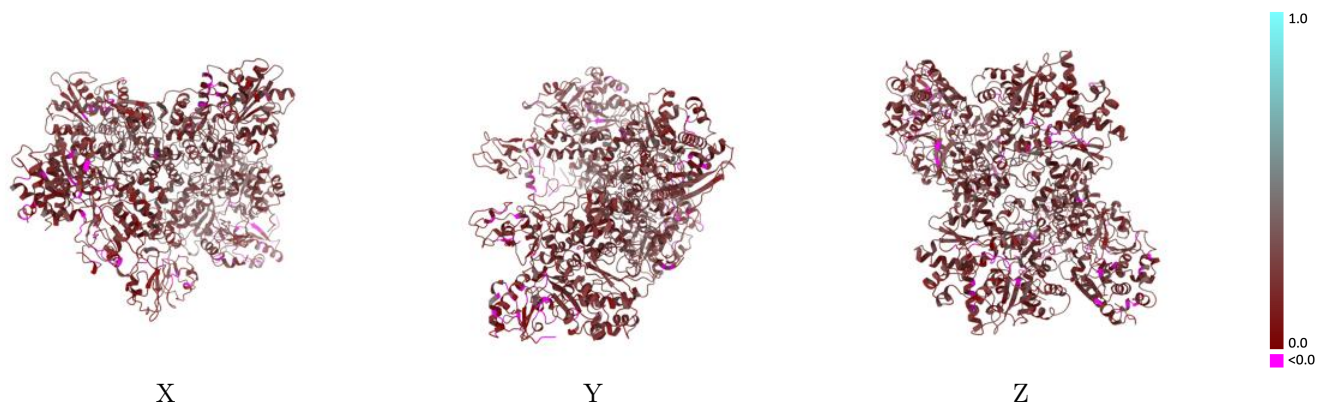
Y



Z

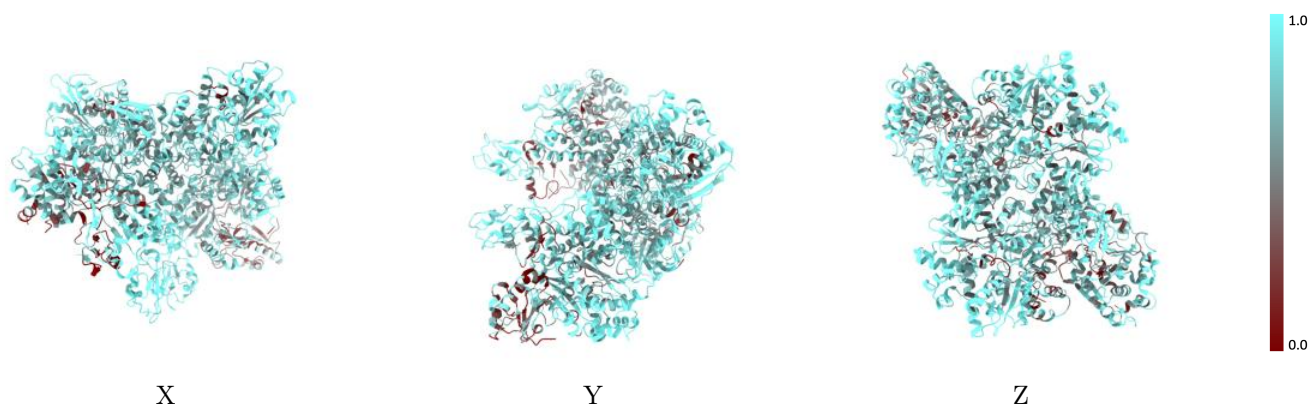
The images above show the 3D surface view of the map at the recommended contour level 0.00114 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



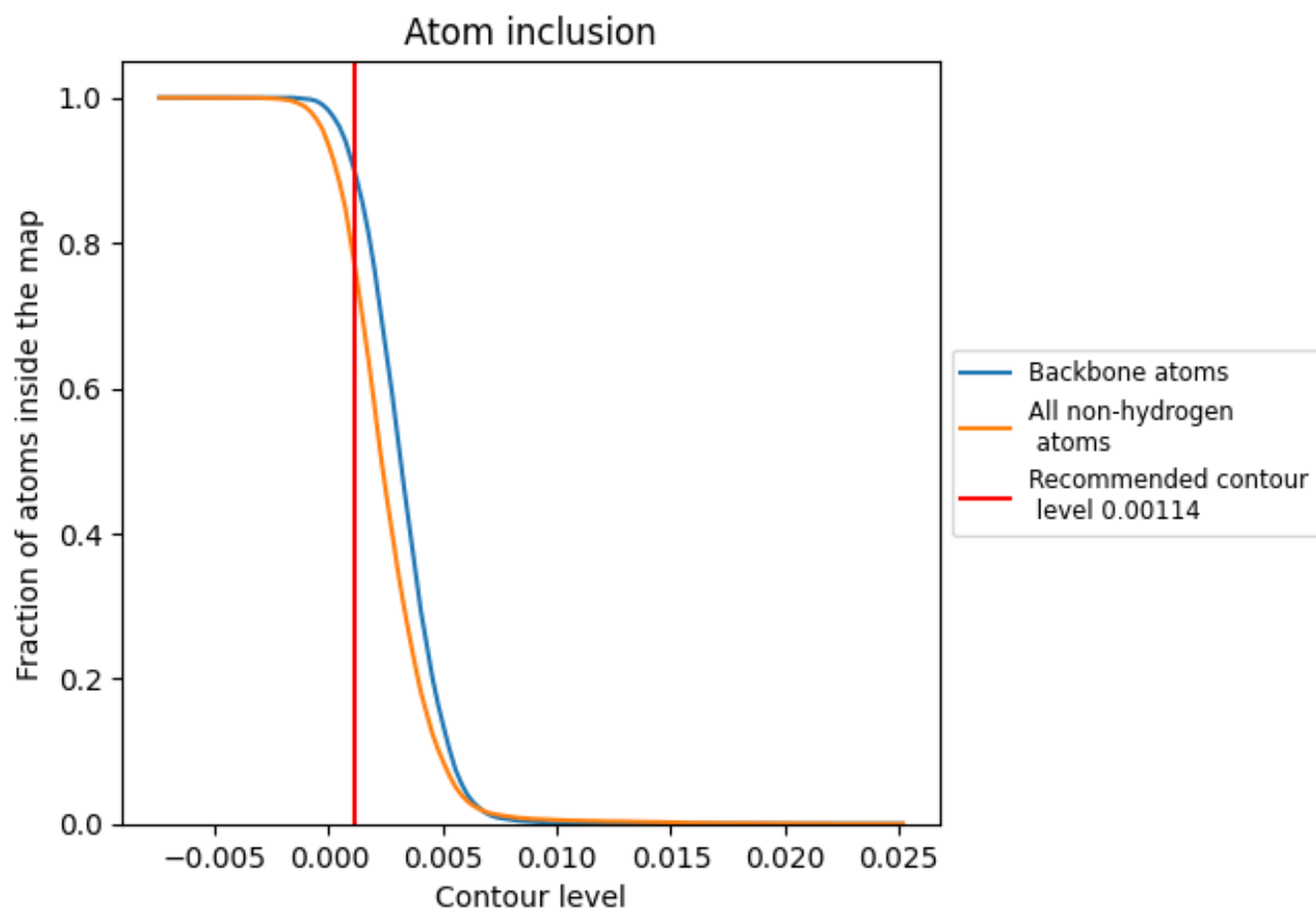
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00114).















9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 77% 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 (0.00114) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7701	 0.2110
A	 0.8066	 0.2400
B	 0.7519	 0.1860
C	 0.7713	 0.2090
E	 0.8229	 0.2340
F	 0.7656	 0.1970
G	 0.4604	 0.1530

