



Full wwPDB EM Validation Report ⓘ

Oct 22, 2024 – 10:35 AM JST

PDB ID : 8XO0
EMDB ID : EMD-38521
Title : Respiratory complex Peripheral Arm of CI, close form B, focus-refined map of type I, PERK -/- mouse under Cold Acclimation
Authors : Shin, Y.-C.; Liao, M.
Deposited on : 2023-12-30
Resolution : 4.20 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:

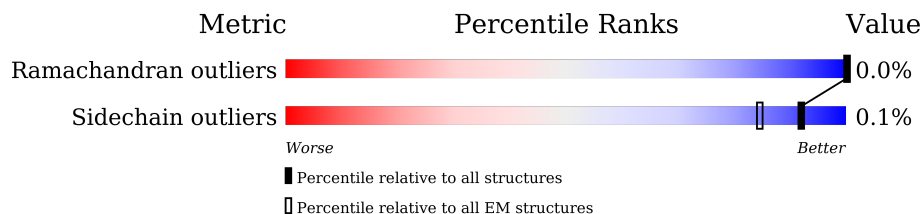
EMDB validation analysis : 0.0.1.dev113
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (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 4.20 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.




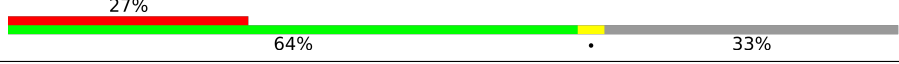



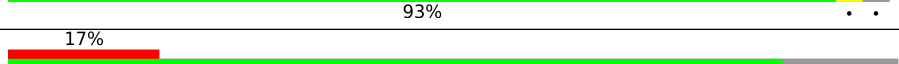
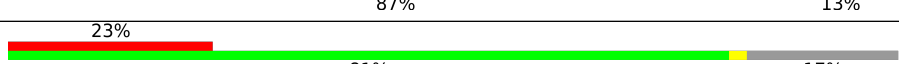
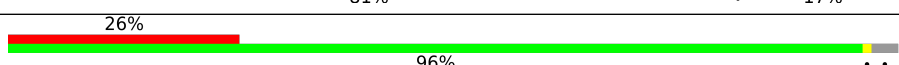
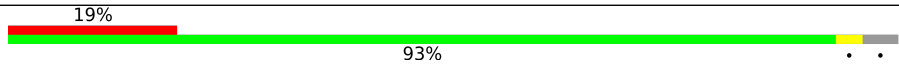
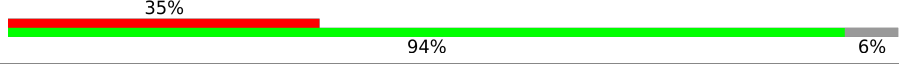
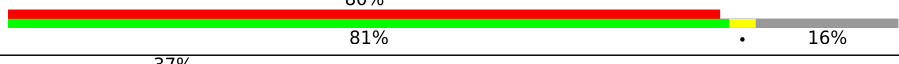



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	A	115	
2	B	224	
3	C	263	
4	D	463	
5	E	248	
6	F	464	
7	G	727	
8	H	318	
9	I	212	

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Mol	Chain	Length	Quality of chain
10	P	377	
11	Q	175	
12	R	116	
13	S	99	
14	T	156	
15	V	116	
16	W	131	
17	X	172	
18	Z	144	
19	a	70	
20	b	84	
21	q	145	
22	r	113	
23	s	104	

2 Entry composition

There are 30 unique types of molecules in this entry. The entry contains 33729 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 NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	91	737	511	102	118	6	0	0

- Molecule 2 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	156	1247	796	223	214	14	0	0

- Molecule 3 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	198	1641	1060	279	299	3	0	0

- Molecule 4 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	385	3088	1970	533	562	23	0	0

- Molecule 5 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	210	1635	1039	275	310	11	0	0

- Molecule 6 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	424	3273	2062	586	603	22	0	0

- Molecule 7 is a protein called NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	687	5287	3316	918	1012	41	0	0

- Molecule 8 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	317	2531	1701	383	425	22	0	0

- Molecule 9 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	173	1389	875	239	263	12	0	0

- Molecule 10 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	P	339	2720	1759	476	478	7	0	0

- Molecule 11 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	Q	118	957	608	165	180	4	0	0

- Molecule 12 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	R	74	587	366	109	109	3	0	0

- Molecule 13 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	S	83	667	419	126	119	3	0	0

- Molecule 14 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	T	75	604	388	89	122	5	0	0

- Molecule 15 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	V	112	915	596	152	164	3	0	0

- Molecule 16 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	W	114	970	619	180	165	6	0	0

- Molecule 17 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	X	142	1164	736	209	209	10	0	0

- Molecule 18 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	Z	139	1152	741	204	199	8	0	0

- Molecule 19 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	a	67	548	356	97	91	4	0	0

- Molecule 20 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	b	79	620	408	98	110	4	0	0

- Molecule 21 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	q	122	1020	655	180	181	4	0	0

- Molecule 22 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	r	51	418	266	78	73	1	0	0

- Molecule 23 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial.

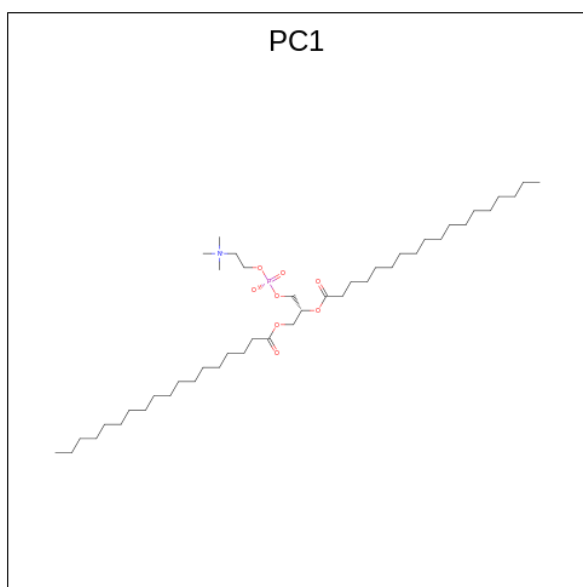
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
23	s	29	238	151	39	48	0	0

- Molecule 24 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄) (labeled as "Ligand of Interest" by depositor).



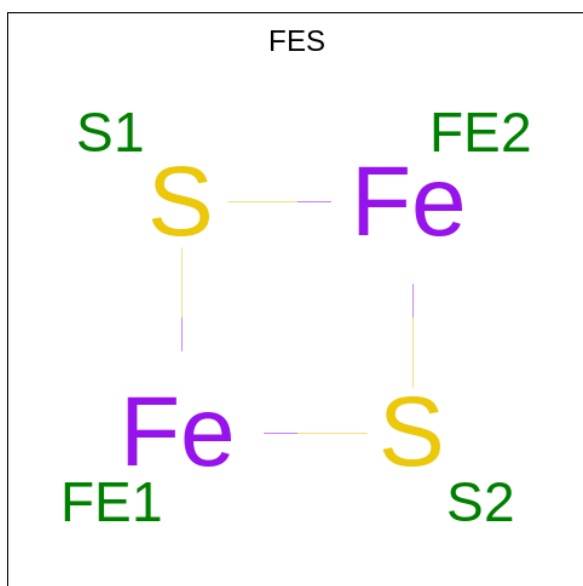
Mol	Chain	Residues	Atoms			AltConf
24	B	1	Total	Fe	S	0
			8	4	4	
24	F	1	Total	Fe	S	0
			8	4	4	
24	G	1	Total	Fe	S	0
			8	4	4	
24	G	1	Total	Fe	S	0
			8	4	4	
24	I	1	Total	Fe	S	0
			8	4	4	
24	I	1	Total	Fe	S	0
			8	4	4	

- Molecule 25 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PC1) (formula: C₄₄H₈₈NO₈P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
25	B	1	35	25	1	8	1	0
25	I	1	43	33	1	8	1	0

- Molecule 26 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂) (labeled as "Ligand of Interest" by depositor).



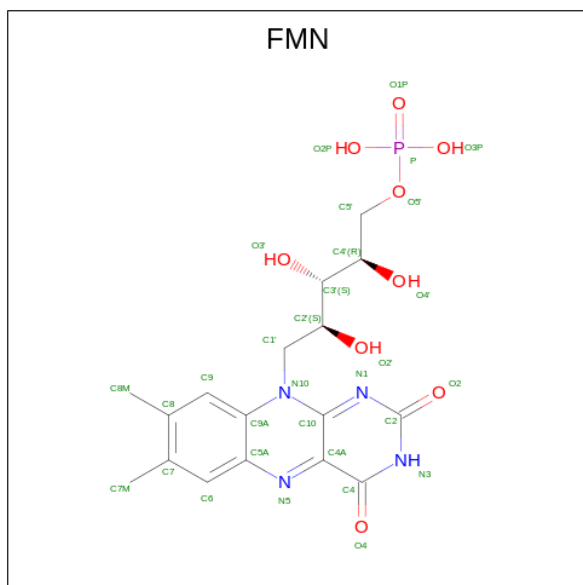
Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
26	E	1	4	2	2	0

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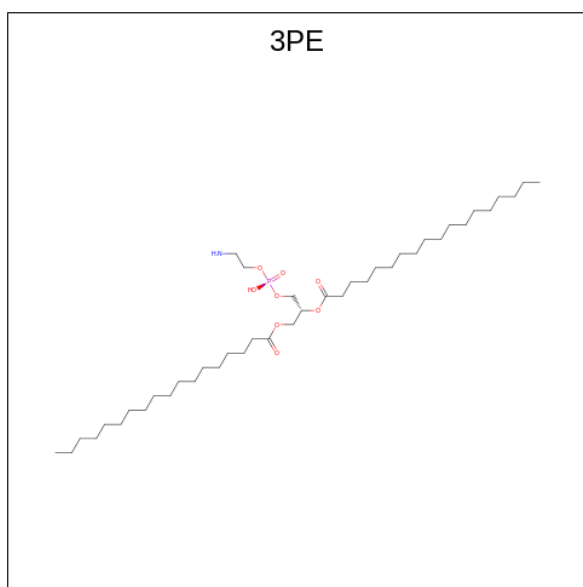
Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
26	G	1	4	2	2	0

- Molecule 27 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C₁₇H₂₁N₄O₉P) (labeled as "Ligand of Interest" by depositor).



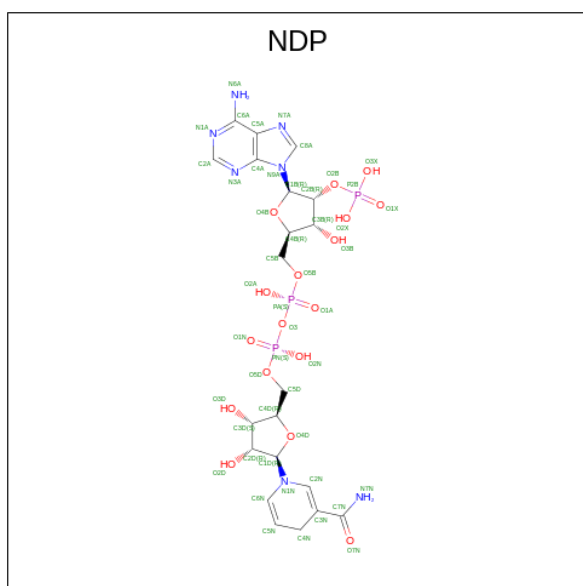
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
27	F	1	31	17	4	9	1	0

- Molecule 28 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (three-letter code: 3PE) (formula: C₄₁H₈₂NO₈P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
28	H	1	51	41	1	8	1	0

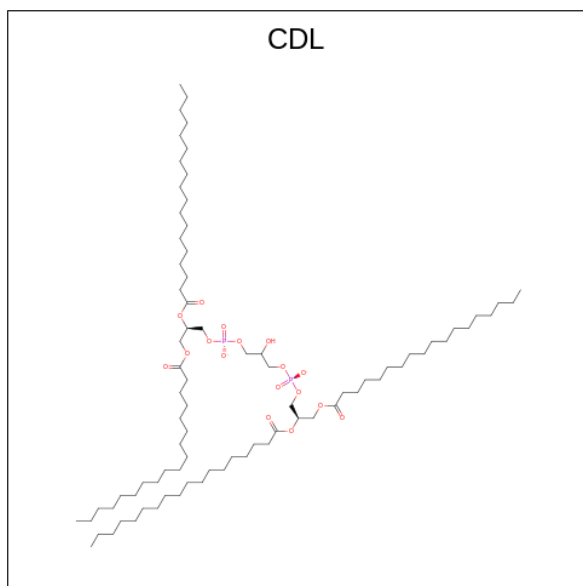
- Molecule 29 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
29	P	1	48	21	7	17	3	0

- Molecule 30 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$) (labeled

as "Ligand of Interest" by depositor).

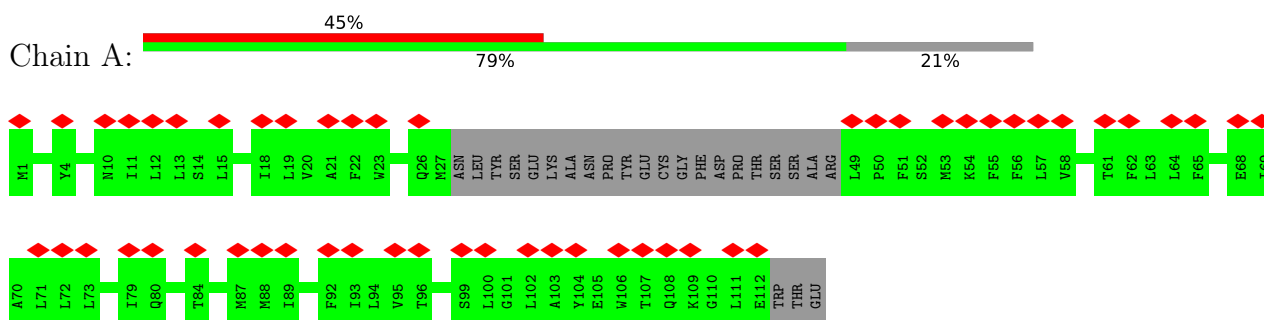


Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
30	q	1	57	38	17	2	0

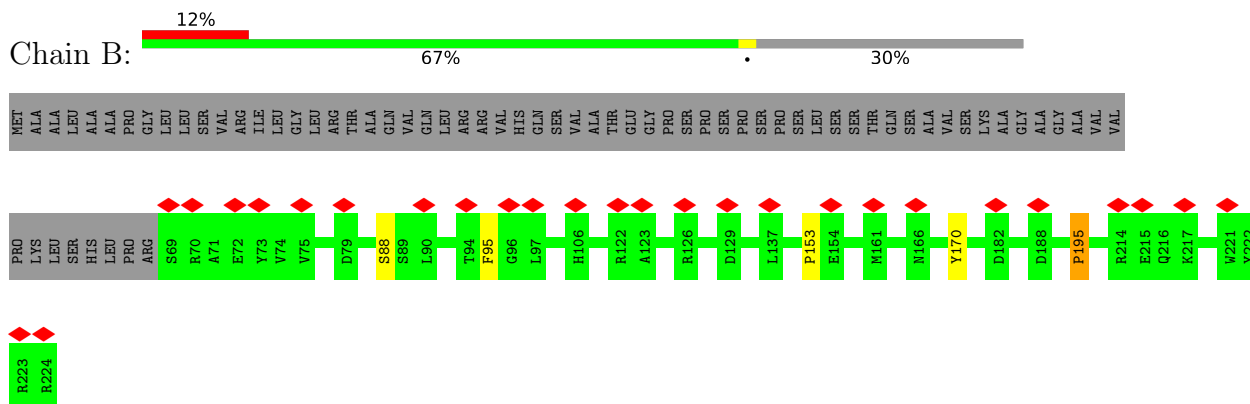
3 Residue-property plots [i](#)

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

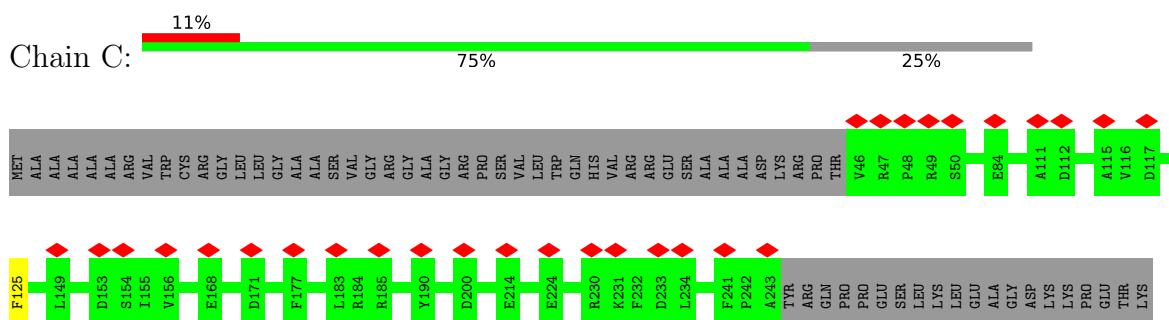
- Molecule 1: NADH-ubiquinone oxidoreductase chain 3



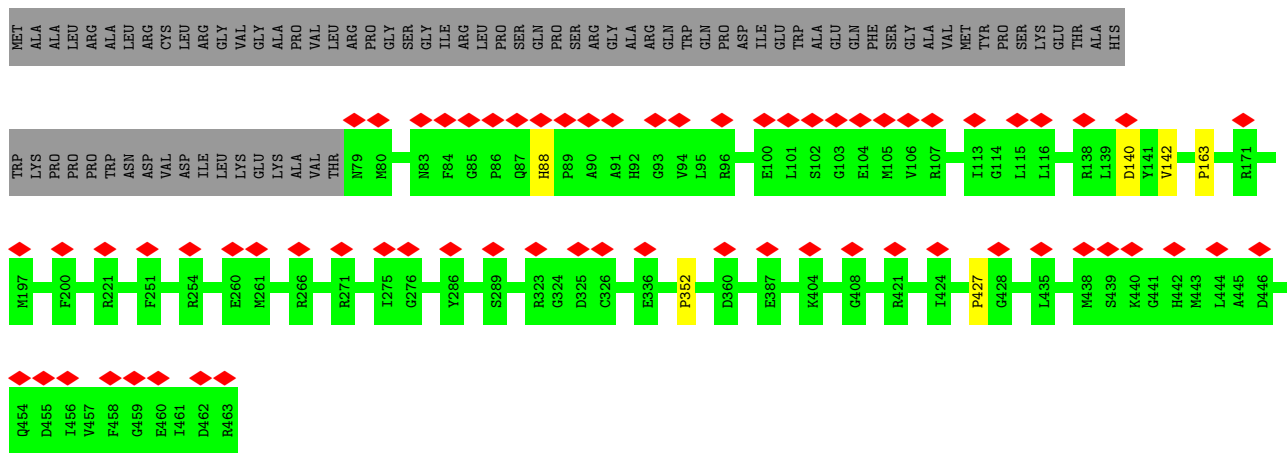
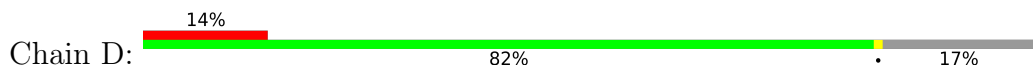
- Molecule 2: NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial



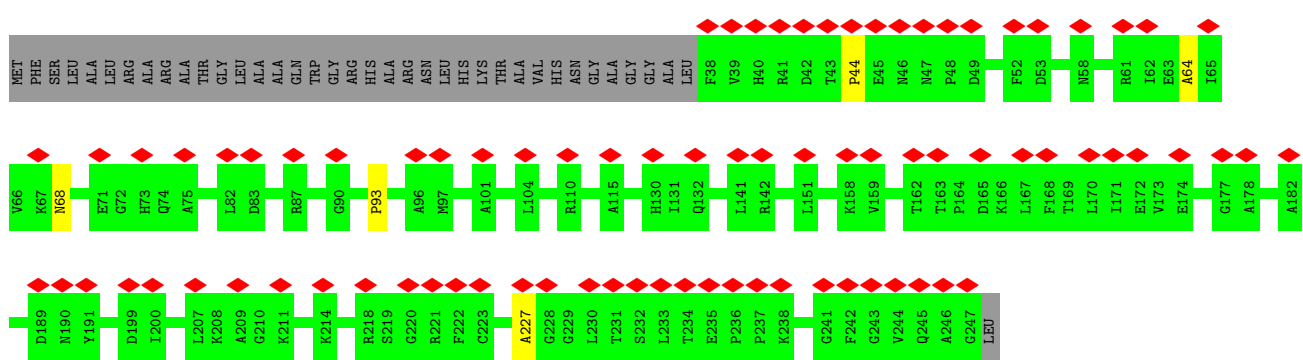
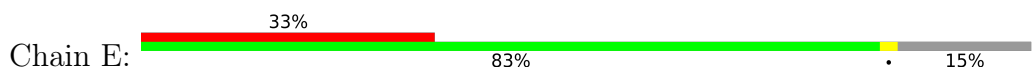
- Molecule 3: NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial



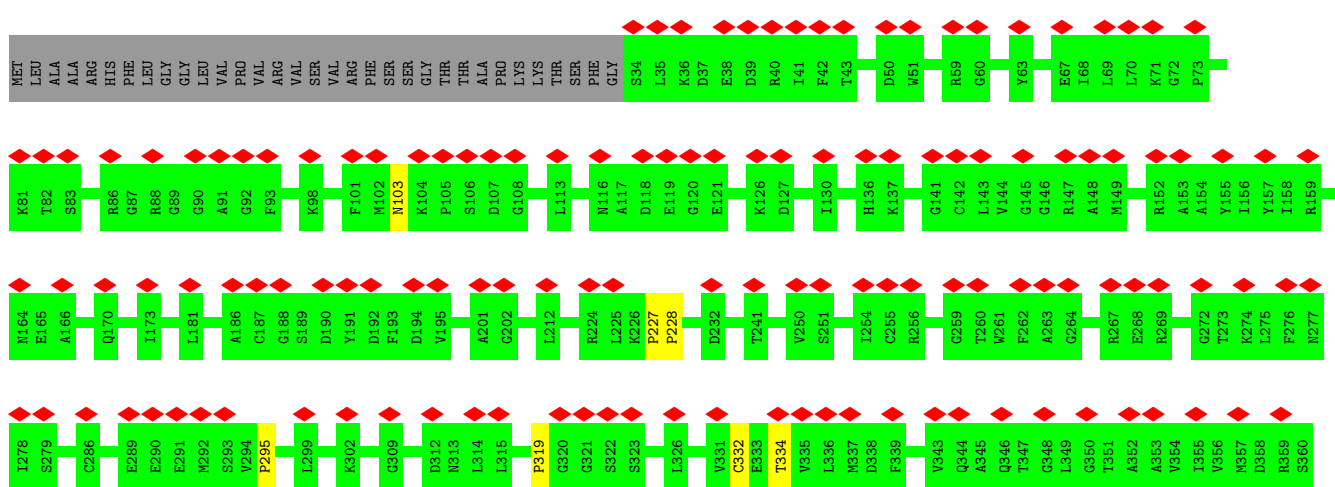
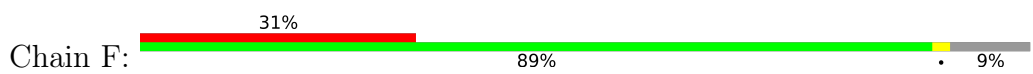
- Molecule 4: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial

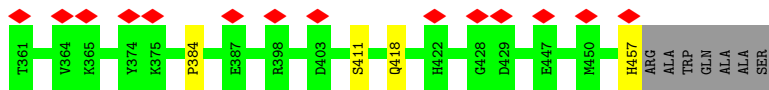


• Molecule 5: NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial



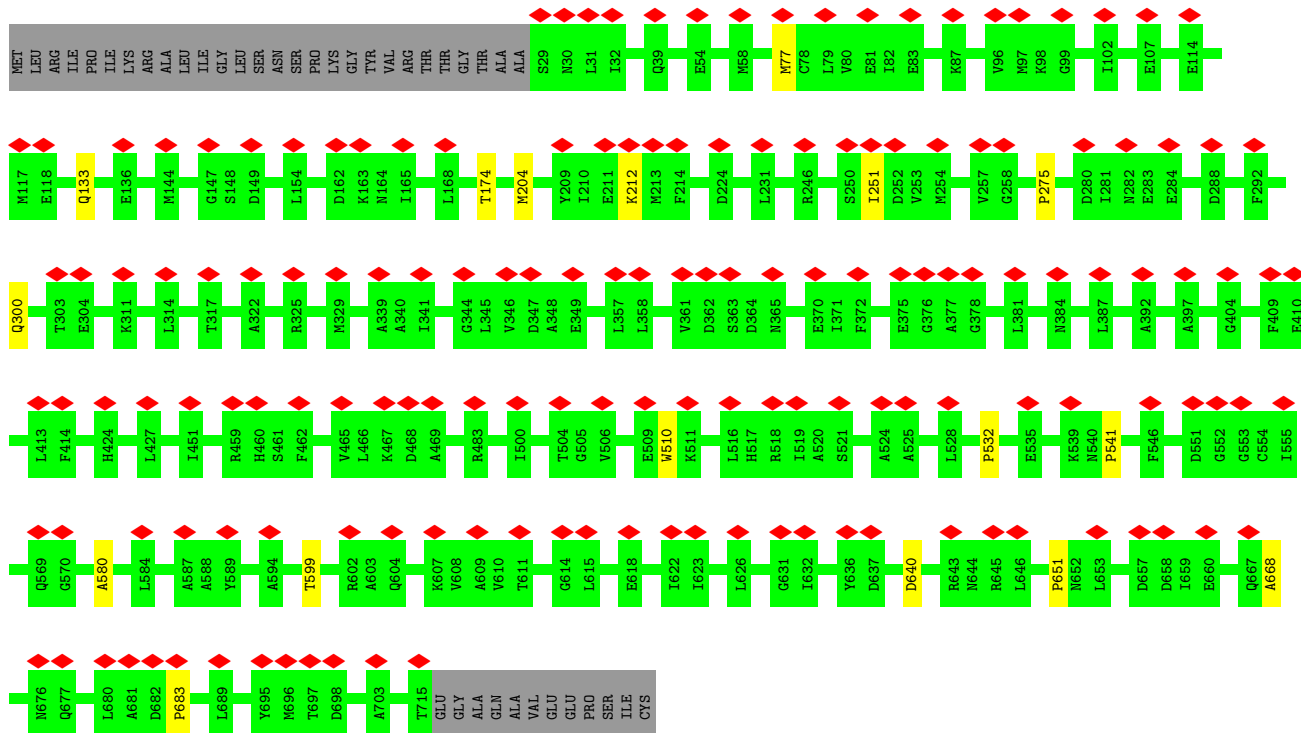
• Molecule 6: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial





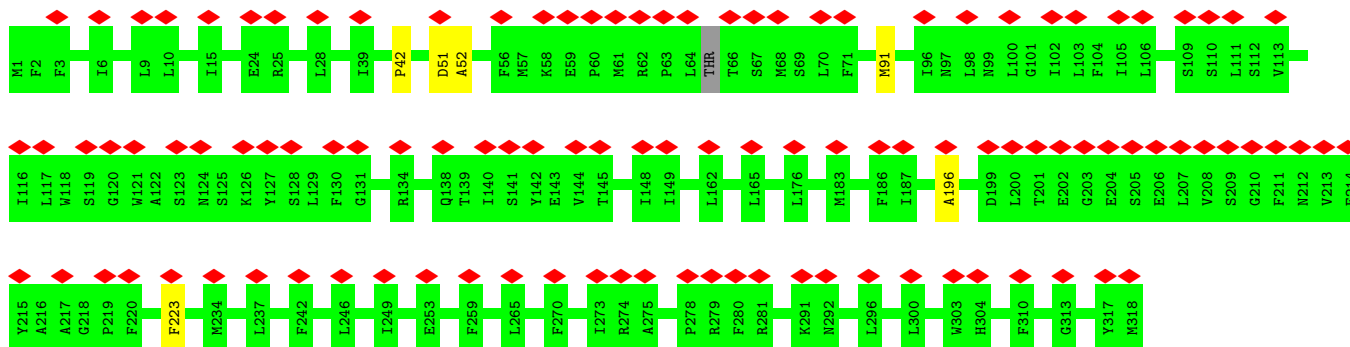
- Molecule 7: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial

Chain G: 21% 92% 6%



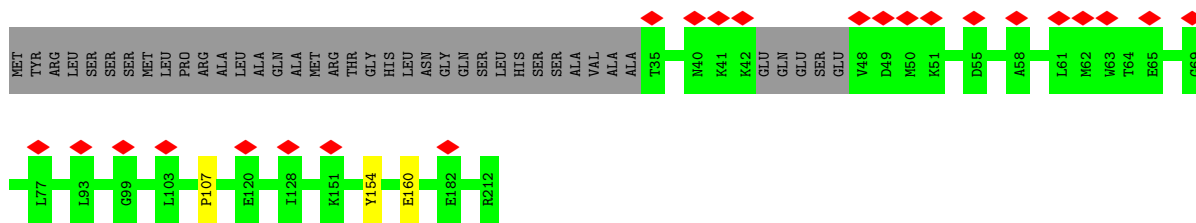
- Molecule 8: NADH-ubiquinone oxidoreductase chain 1

Chain H: 34% 98%

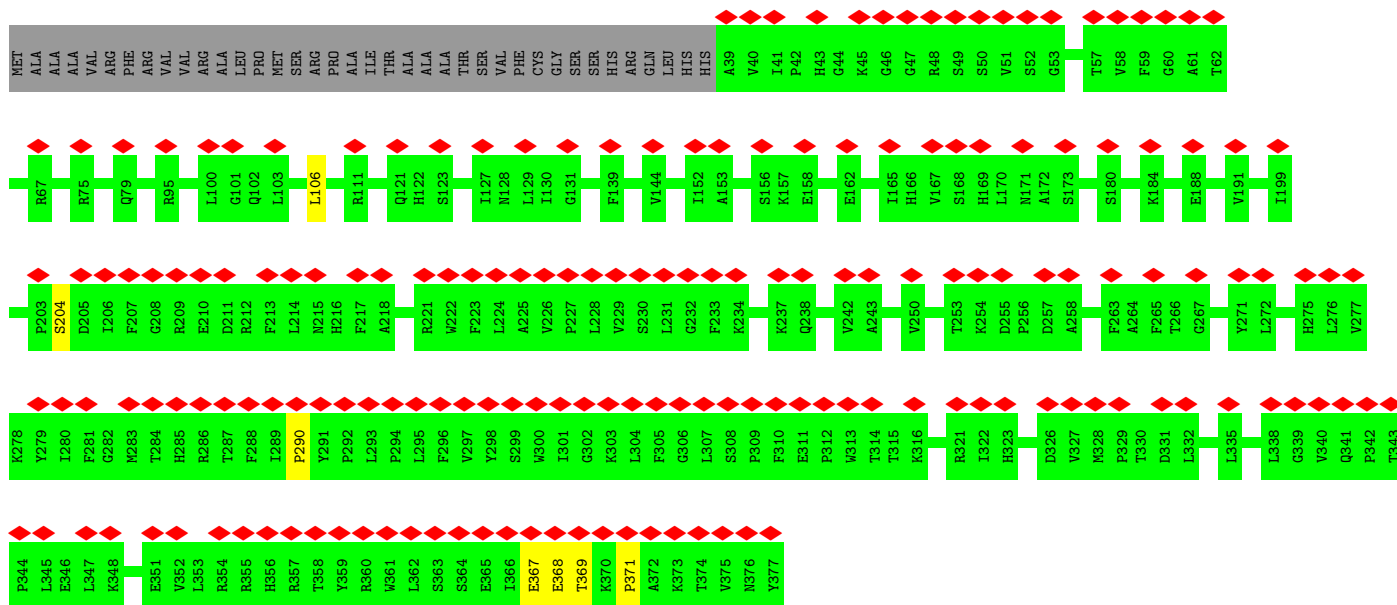
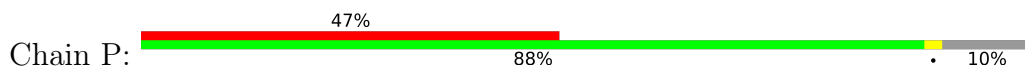


- Molecule 9: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial

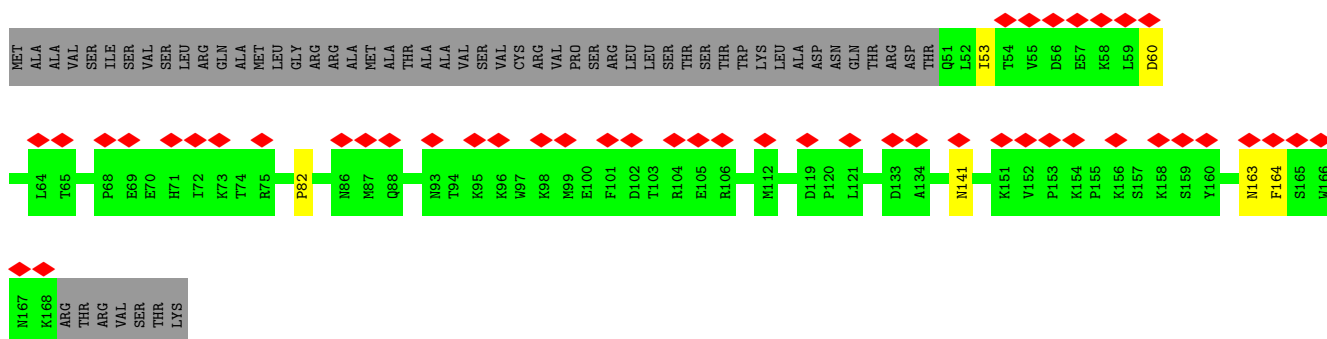
Chain I: 11% 80% 18%



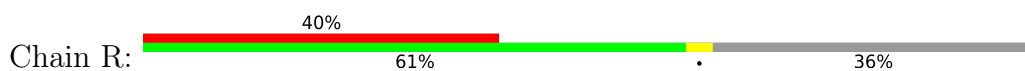
• Molecule 10: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial

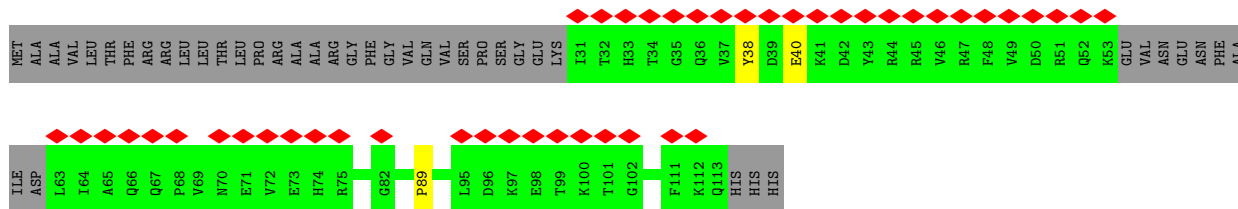


• Molecule 11: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial

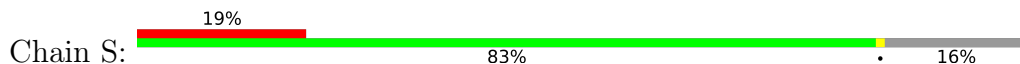


• Molecule 12: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial





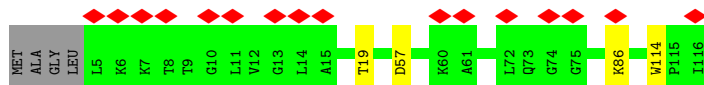
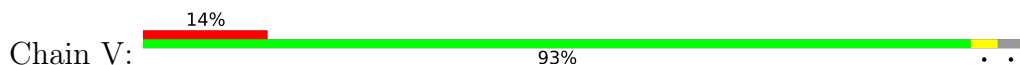
• Molecule 13: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2



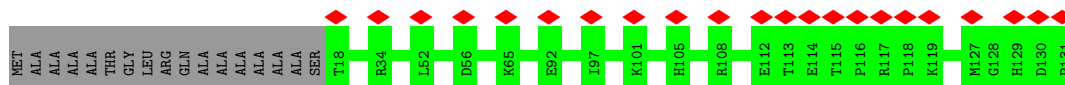
• Molecule 14: Acyl carrier protein, mitochondrial



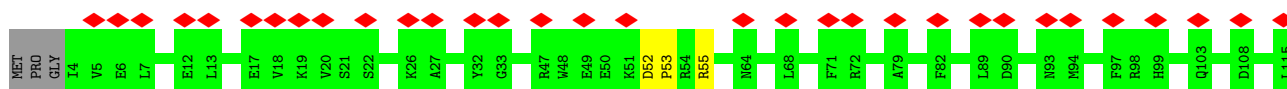
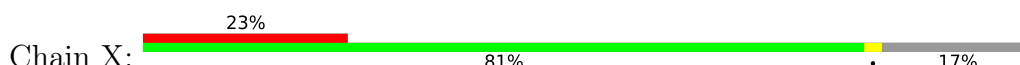
• Molecule 15: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5

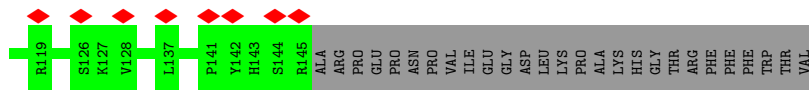


• Molecule 16: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6

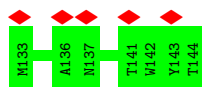
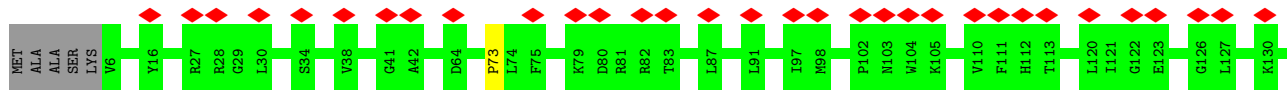


• Molecule 17: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8

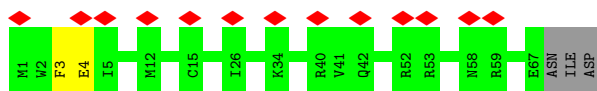
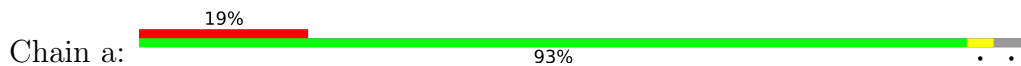




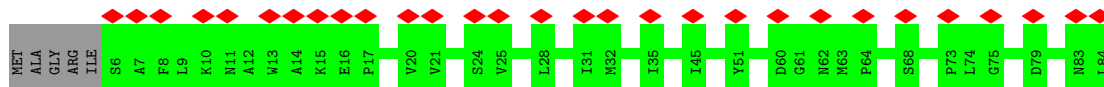
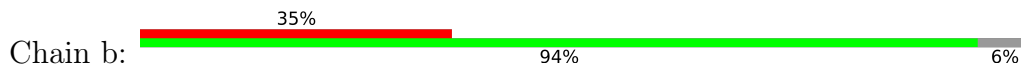
• Molecule 18: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13



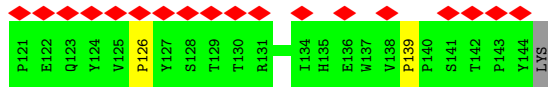
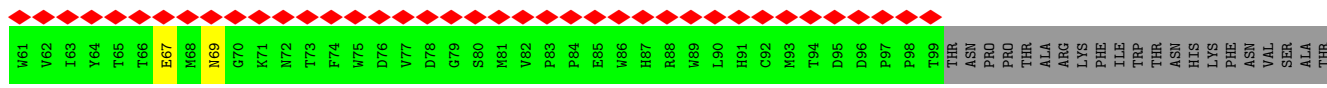
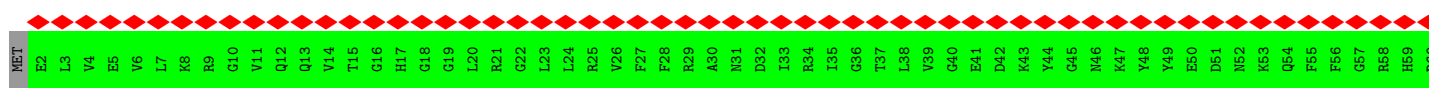
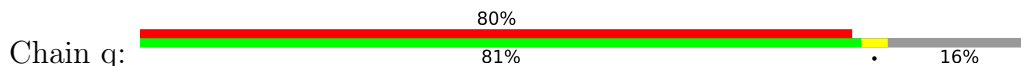
• Molecule 19: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1



• Molecule 20: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3

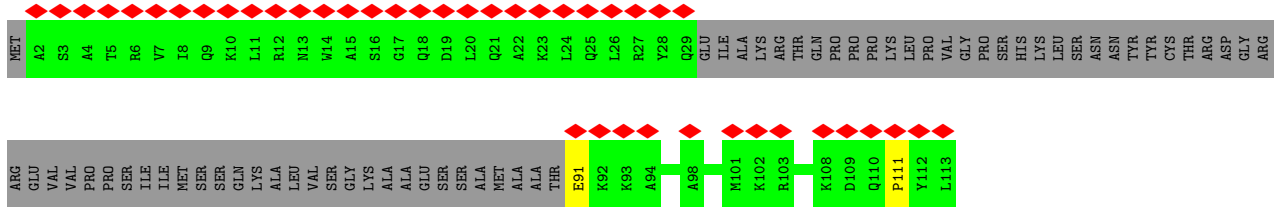


• Molecule 21: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12

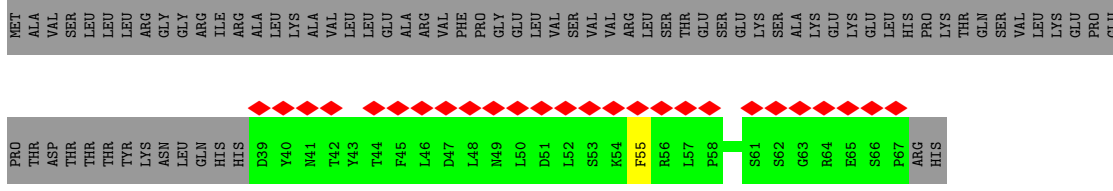


• Molecule 22: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7





● Molecule 23: NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	7071	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.2	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.664	Depositor
Minimum map value	-0.623	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.064	Depositor
Recommended contour level	0.4	Depositor
Map size (\AA)	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.83, 0.83, 0.83	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: CDL, FMN, 3PE, FES, NDP, SF4, PC1

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	0.42	0/755	0.56	0/1029
2	B	0.62	2/1278 (0.2%)	0.78	1/1730 (0.1%)
3	C	0.55	0/1687	0.79	1/2297 (0.0%)
4	D	0.63	2/3162 (0.1%)	0.86	6/4276 (0.1%)
5	E	0.59	3/1675 (0.2%)	0.68	3/2282 (0.1%)
6	F	0.59	4/3347 (0.1%)	0.79	9/4522 (0.2%)
7	G	0.62	4/5374 (0.1%)	0.93	16/7281 (0.2%)
8	H	0.55	1/2607 (0.0%)	0.71	5/3561 (0.1%)
9	I	0.61	1/1418 (0.1%)	0.87	2/1915 (0.1%)
10	P	0.57	3/2793 (0.1%)	0.71	6/3787 (0.2%)
11	Q	0.58	2/980 (0.2%)	0.80	4/1324 (0.3%)
12	R	0.83	2/596 (0.3%)	0.83	2/799 (0.3%)
13	S	0.66	1/678 (0.1%)	0.90	1/915 (0.1%)
14	T	0.76	1/613 (0.2%)	0.89	4/826 (0.5%)
15	V	0.57	0/937	0.85	4/1270 (0.3%)
16	W	0.47	0/993	0.54	0/1335
17	X	0.76	1/1191 (0.1%)	0.96	6/1605 (0.4%)
18	Z	0.57	1/1183 (0.1%)	0.69	0/1597
19	a	0.57	0/561	0.81	2/755 (0.3%)
20	b	0.45	0/643	0.53	0/884
21	q	0.76	2/1054 (0.2%)	0.95	4/1431 (0.3%)
22	r	0.87	2/426 (0.5%)	1.17	2/573 (0.3%)
23	s	0.31	0/244	0.71	1/331 (0.3%)
All	All	0.61	32/34195 (0.1%)	0.81	79/46325 (0.2%)

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	X	53	PRO	N-CD	-19.25	1.20	1.47
12	R	89	PRO	N-CD	-15.26	1.26	1.47
21	q	139	PRO	N-CD	-13.69	1.28	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	P	371	PRO	N-CD	12.78	1.65	1.47
7	G	532	PRO	N-CD	-12.69	1.30	1.47
14	T	141	PRO	N-CD	11.77	1.64	1.47
6	F	295	PRO	N-CD	-11.32	1.32	1.47
8	H	42	PRO	N-CD	10.78	1.62	1.47
5	E	227	ALA	C-O	10.01	1.42	1.23
6	F	227	PRO	N-CD	9.79	1.61	1.47
5	E	44	PRO	N-CD	-9.61	1.34	1.47
7	G	275	PRO	N-CD	-9.55	1.34	1.47
10	P	290	PRO	N-CD	9.53	1.61	1.47
22	r	91	GLU	N-CA	9.42	1.65	1.46
6	F	319	PRO	N-CD	8.95	1.60	1.47
9	I	107	PRO	N-CD	8.44	1.59	1.47
4	D	163	PRO	N-CD	-8.42	1.36	1.47
13	S	63	PRO	N-CD	-8.04	1.36	1.47
18	Z	73	PRO	N-CD	7.96	1.58	1.47
4	D	352	PRO	N-CD	-7.88	1.36	1.47
22	r	111	PRO	N-CD	-7.46	1.37	1.47
7	G	541	PRO	N-CD	-6.95	1.38	1.47
2	B	153	PRO	N-CD	-6.36	1.39	1.47
6	F	384	PRO	N-CD	-6.29	1.39	1.47
5	E	93	PRO	N-CD	-6.00	1.39	1.47
2	B	88	SER	C-N	-5.77	1.20	1.34
7	G	683	PRO	N-CD	-5.57	1.40	1.47
11	Q	53	ILE	C-O	5.37	1.33	1.23
21	q	126	PRO	N-CD	5.27	1.55	1.47
12	R	40	GLU	N-CA	5.05	1.56	1.46
10	P	204	SER	C-O	-5.02	1.13	1.23
11	Q	82	PRO	N-CD	-5.01	1.40	1.47

All (79) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	r	91	GLU	N-CA-CB	13.68	135.22	110.60
17	X	53	PRO	CA-N-CD	13.07	130.00	111.70
17	X	53	PRO	N-CA-CB	-11.17	89.89	103.30
19	a	3	PHE	CB-CA-C	-10.38	89.64	110.40
21	q	139	PRO	CA-N-CD	9.61	125.15	111.70
4	D	142	VAL	N-CA-CB	9.53	132.46	111.50
6	F	334	THR	N-CA-CB	8.90	127.22	110.30
7	G	532	PRO	CA-N-CD	8.56	123.68	111.70
7	G	174	THR	N-CA-C	-8.11	89.10	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	F	295	PRO	CA-N-CD	7.74	122.53	111.70
11	Q	60	ASP	N-CA-C	-7.68	90.27	111.00
6	F	411	SER	N-CA-CB	7.53	121.79	110.50
17	X	55	ARG	N-CA-CB	-7.43	97.22	110.60
17	X	53	PRO	N-CD-CG	-7.28	92.28	103.20
7	G	204	MET	N-CA-C	-7.27	91.37	111.00
10	P	371	PRO	N-CA-CB	7.08	111.80	103.30
17	X	55	ARG	N-CA-C	7.07	130.07	111.00
6	F	332	CYS	N-CA-C	7.04	130.01	111.00
10	P	369	THR	N-CA-CB	6.89	123.39	110.30
4	D	142	VAL	N-CA-C	-6.85	92.51	111.00
5	E	44	PRO	CA-N-CD	6.83	121.26	111.70
7	G	275	PRO	CA-N-CD	6.61	120.95	111.70
7	G	300	GLN	N-CA-CB	6.56	122.41	110.60
10	P	106	LEU	N-CA-C	6.54	128.67	111.00
5	E	64	ALA	N-CA-CB	6.49	119.19	110.10
8	H	52	ALA	N-CA-CB	6.40	119.06	110.10
21	q	139	PRO	N-CA-CB	-6.38	95.58	102.60
9	I	154	TYR	N-CA-CB	-6.33	99.21	110.60
8	H	196	ALA	N-CA-C	6.31	128.03	111.00
10	P	371	PRO	CA-N-CD	-6.30	102.68	111.50
4	D	427	PRO	N-CA-C	-6.30	95.72	112.10
4	D	140	ASP	CB-CA-C	-6.21	97.98	110.40
14	T	141	PRO	CA-N-CD	-6.11	102.95	111.50
7	G	133	GLN	N-CA-CB	6.10	121.58	110.60
7	G	212	LYS	N-CA-C	-6.08	94.58	111.00
14	T	141	PRO	N-CA-CB	6.07	110.59	103.30
21	q	69	ASN	N-CA-CB	5.98	121.37	110.60
13	S	63	PRO	CA-N-CD	5.84	119.88	111.70
7	G	251	ILE	N-CA-C	5.81	126.69	111.00
6	F	103	ASN	N-CA-CB	5.81	121.06	110.60
14	T	135	ALA	N-CA-CB	5.79	118.20	110.10
5	E	68	ASN	N-CA-CB	5.78	121.01	110.60
11	Q	141	ASN	N-CA-CB	5.70	120.86	110.60
7	G	510	TRP	N-CA-CB	5.69	120.84	110.60
7	G	599	THR	N-CA-C	5.65	126.26	111.00
8	H	223	PHE	CB-CA-C	-5.65	99.11	110.40
15	V	57	ASP	N-CA-CB	5.64	120.75	110.60
11	Q	163	ASN	CB-CA-C	-5.55	99.30	110.40
3	C	125	PHE	N-CA-CB	-5.53	100.65	110.60
7	G	580	ALA	N-CA-CB	5.51	117.81	110.10
9	I	160	GLU	N-CA-CB	-5.49	100.71	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	V	19	THR	N-CA-CB	5.48	120.70	110.30
10	P	367	GLU	CB-CA-C	-5.46	99.49	110.40
23	s	55	PHE	N-CA-C	5.44	125.69	111.00
12	R	38	TYR	N-CA-C	-5.43	96.35	111.00
15	V	114	TRP	N-CA-CB	5.43	120.37	110.60
2	B	195	PRO	N-CA-C	-5.42	98.01	112.10
6	F	457	HIS	N-CA-CB	-5.41	100.87	110.60
7	G	651	PRO	CB-CA-C	-5.39	98.52	112.00
21	q	67	GLU	CB-CA-C	-5.38	99.64	110.40
8	H	91	MET	N-CA-C	-5.37	96.50	111.00
6	F	295	PRO	N-CA-CB	-5.36	96.71	102.60
22	r	111	PRO	CA-N-CD	5.35	119.19	111.70
4	D	140	ASP	N-CA-C	-5.35	96.57	111.00
6	F	418	GLN	N-CA-CB	5.30	120.14	110.60
8	H	51	ASP	CB-CA-C	-5.25	99.90	110.40
17	X	53	PRO	CB-CA-C	-5.23	98.92	112.00
7	G	640	ASP	N-CA-CB	5.21	119.97	110.60
11	Q	164	PHE	N-CA-CB	5.17	119.90	110.60
12	R	89	PRO	CA-N-CD	5.14	118.90	111.70
10	P	368	GLU	N-CA-CB	5.12	119.81	110.60
19	a	4	GLU	N-CA-C	5.09	124.75	111.00
6	F	228	PRO	N-CA-C	-5.09	98.88	112.10
4	D	352	PRO	CA-N-CD	5.08	118.81	111.70
15	V	86	LYS	N-CA-CB	5.07	119.72	110.60
7	G	668	ALA	N-CA-CB	5.06	117.19	110.10
7	G	77	MET	N-CA-C	-5.02	97.43	111.00
7	G	532	PRO	N-CA-CB	-5.01	97.08	102.60
14	T	139	MET	N-CA-C	-5.00	97.49	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	87/115 (76%)	83 (95%)	4 (5%)	0	100	100
2	B	154/224 (69%)	142 (92%)	11 (7%)	1 (1%)	22	59
3	C	196/263 (74%)	187 (95%)	9 (5%)	0	100	100
4	D	383/463 (83%)	356 (93%)	27 (7%)	0	100	100
5	E	208/248 (84%)	193 (93%)	15 (7%)	0	100	100
6	F	422/464 (91%)	402 (95%)	20 (5%)	0	100	100
7	G	685/727 (94%)	632 (92%)	53 (8%)	0	100	100
8	H	313/318 (98%)	295 (94%)	18 (6%)	0	100	100
9	I	169/212 (80%)	169 (100%)	0	0	100	100
10	P	337/377 (89%)	314 (93%)	23 (7%)	0	100	100
11	Q	116/175 (66%)	114 (98%)	2 (2%)	0	100	100
12	R	70/116 (60%)	64 (91%)	6 (9%)	0	100	100
13	S	81/99 (82%)	77 (95%)	4 (5%)	0	100	100
14	T	73/156 (47%)	72 (99%)	1 (1%)	0	100	100
15	V	110/116 (95%)	107 (97%)	3 (3%)	0	100	100
16	W	112/131 (86%)	111 (99%)	1 (1%)	0	100	100
17	X	140/172 (81%)	131 (94%)	9 (6%)	0	100	100
18	Z	137/144 (95%)	132 (96%)	5 (4%)	0	100	100
19	a	65/70 (93%)	61 (94%)	4 (6%)	0	100	100
20	b	77/84 (92%)	69 (90%)	8 (10%)	0	100	100
21	q	118/145 (81%)	115 (98%)	3 (2%)	0	100	100
22	r	47/113 (42%)	43 (92%)	4 (8%)	0	100	100
23	s	27/104 (26%)	27 (100%)	0	0	100	100
All	All	4127/5036 (82%)	3896 (94%)	230 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	195	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	83/104 (80%)	83 (100%)	0	100	100
2	B	132/185 (71%)	130 (98%)	2 (2%)	60	74
3	C	180/227 (79%)	180 (100%)	0	100	100
4	D	332/395 (84%)	331 (100%)	1 (0%)	91	92
5	E	182/206 (88%)	182 (100%)	0	100	100
6	F	340/370 (92%)	340 (100%)	0	100	100
7	G	579/610 (95%)	579 (100%)	0	100	100
8	H	279/280 (100%)	279 (100%)	0	100	100
9	I	147/178 (83%)	147 (100%)	0	100	100
10	P	296/325 (91%)	296 (100%)	0	100	100
11	Q	105/153 (69%)	105 (100%)	0	100	100
12	R	62/96 (65%)	62 (100%)	0	100	100
13	S	74/80 (92%)	74 (100%)	0	100	100
14	T	69/135 (51%)	69 (100%)	0	100	100
15	V	100/102 (98%)	100 (100%)	0	100	100
16	W	108/114 (95%)	108 (100%)	0	100	100
17	X	129/154 (84%)	128 (99%)	1 (1%)	79	84
18	Z	120/123 (98%)	120 (100%)	0	100	100
19	a	57/60 (95%)	57 (100%)	0	100	100
20	b	70/73 (96%)	70 (100%)	0	100	100
21	q	110/131 (84%)	110 (100%)	0	100	100
22	r	44/96 (46%)	44 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	s	28/95 (30%)	28 (100%)	0	100	100
All	All	3626/4292 (84%)	3622 (100%)	4 (0%)	92	94

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	95	PHE
2	B	170	TYR
4	D	88	HIS
17	X	52	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (85) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	106	HIS
2	B	151	GLN
2	B	209	GLN
3	C	54	HIS
3	C	73	GLN
3	C	88	HIS
3	C	123	ASN
3	C	179	ASN
3	C	180	HIS
3	C	195	HIS
3	C	227	GLN
3	C	235	ASN
4	D	87	GLN
4	D	117	HIS
4	D	131	GLN
4	D	147	ASN
4	D	182	ASN
4	D	233	HIS
4	D	339	GLN
4	D	346	GLN
4	D	381	HIS
5	E	245	GLN
6	F	168	ASN
6	F	270	ASN
6	F	283	ASN
6	F	303	HIS
6	F	346	GLN

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Mol	Chain	Res	Type
6	F	441	HIS
7	G	59	GLN
7	G	74	ASN
7	G	140	GLN
7	G	164	ASN
7	G	205	GLN
7	G	260	ASN
7	G	359	ASN
7	G	365	ASN
7	G	388	ASN
7	G	406	ASN
7	G	444	HIS
7	G	495	ASN
7	G	540	ASN
7	G	569	GLN
7	G	571	HIS
7	G	605	GLN
7	G	666	GLN
8	H	5	ASN
8	H	32	GLN
8	H	47	GLN
8	H	124	ASN
8	H	169	GLN
8	H	171	HIS
8	H	258	ASN
8	H	292	ASN
10	P	71	ASN
10	P	79	GLN
10	P	154	GLN
10	P	166	HIS
10	P	219	ASN
10	P	238	GLN
10	P	269	ASN
10	P	275	HIS
10	P	341	GLN
10	P	356	HIS
11	Q	51	GLN
11	Q	88	GLN
12	R	52	GLN
13	S	48	HIS
15	V	41	HIS
15	V	50	GLN

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Mol	Chain	Res	Type
16	W	54	GLN
16	W	105	HIS
17	X	30	HIS
17	X	77	HIS
17	X	140	ASN
19	a	31	ASN
20	b	69	HIS
20	b	71	GLN
20	b	83	ASN
21	q	13	GLN
21	q	31	ASN
21	q	54	GLN
21	q	87	HIS
21	q	91	HIS
22	r	21	GLN
22	r	110	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

14 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	PC1	B	302	-	34,34,53	1.14	2 (5%)	40,42,61	1.15	3 (7%)
24	SF4	G	801	7	0,12,12	-	-	-	-	-
26	FES	E	301	5	0,4,4	-	-	-	-	-
30	CDL	q	201	-	56,56,99	1.20	4 (7%)	62,68,111	1.20	5 (8%)
24	SF4	I	303	9	0,12,12	-	-	-	-	-
27	FMN	F	501	-	33,33,33	1.38	5 (15%)	48,50,50	1.22	6 (12%)
24	SF4	G	802	7	0,12,12	-	-	-	-	-
26	FES	G	803	7	0,4,4	-	-	-	-	-
24	SF4	I	302	9	0,12,12	-	-	-	-	-
24	SF4	B	301	2	0,12,12	-	-	-	-	-
28	3PE	H	401	-	50,50,50	0.92	2 (4%)	53,55,55	1.01	2 (3%)
29	NDP	P	401	-	45,52,52	0.96	2 (4%)	53,80,80	1.17	4 (7%)
24	SF4	F	502	6	0,12,12	-	-	-	-	-
25	PC1	I	301	-	42,42,53	1.04	2 (4%)	48,50,61	1.04	3 (6%)

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
25	PC1	B	302	-	-	11/38/38/57	-
24	SF4	G	801	7	-	-	0/6/5/5
26	FES	E	301	5	-	-	0/1/1/1
30	CDL	q	201	-	-	20/67/67/110	-
27	FMN	F	501	-	-	1/18/18/18	0/3/3/3
24	SF4	I	303	9	-	-	0/6/5/5
24	SF4	G	802	7	-	-	0/6/5/5
26	FES	G	803	7	-	-	0/1/1/1
24	SF4	I	302	9	-	-	0/6/5/5
24	SF4	B	301	2	-	-	0/6/5/5
28	3PE	H	401	-	-	11/54/54/54	-
29	NDP	P	401	-	-	4/30/77/77	0/5/5/5
24	SF4	F	502	6	-	-	0/6/5/5
25	PC1	I	301	-	-	9/46/46/57	-

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	F	501	FMN	C9A-C5A	4.88	1.49	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	q	201	CDL	OB8-CB7	4.25	1.45	1.33
30	q	201	CDL	OA8-CA7	4.24	1.45	1.33
25	B	302	PC1	O31-C31	4.21	1.45	1.33
25	I	301	PC1	O31-C31	4.21	1.45	1.33
28	H	401	3PE	O31-C31	4.20	1.45	1.33
28	H	401	3PE	O21-C21	4.08	1.45	1.34
25	I	301	PC1	O21-C21	4.08	1.45	1.34
30	q	201	CDL	OB6-CB5	4.08	1.45	1.34
25	B	302	PC1	O21-C21	4.02	1.45	1.34
30	q	201	CDL	OA6-CA5	4.01	1.45	1.34
29	P	401	NDP	C6N-C5N	3.23	1.39	1.33
27	F	501	FMN	C8-C7	3.13	1.48	1.40
27	F	501	FMN	C4-N3	-2.54	1.34	1.38
29	P	401	NDP	C5A-C4A	2.34	1.47	1.40
27	F	501	FMN	C5A-N5	-2.15	1.35	1.39
27	F	501	FMN	C4A-N5	2.10	1.34	1.30

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	B	302	PC1	O21-C21-C22	4.24	120.64	111.50
25	I	301	PC1	O21-C21-C22	3.89	119.88	111.50
30	q	201	CDL	OA6-CA5-C11	3.85	119.80	111.50
30	q	201	CDL	OB6-CB5-C51	3.81	119.70	111.50
29	P	401	NDP	PN-O3-PA	-3.44	121.02	132.83
28	H	401	3PE	O21-C21-C22	3.35	118.73	111.50
29	P	401	NDP	N3A-C2A-N1A	-3.19	123.69	128.68
29	P	401	NDP	C4A-C5A-N7A	-2.75	106.53	109.40
30	q	201	CDL	OB8-CB7-C71	2.71	120.40	111.91
25	I	301	PC1	C2-O21-C21	-2.68	111.20	117.79
28	H	401	3PE	O31-C31-C32	2.67	120.30	111.91
27	F	501	FMN	O4-C4-C4A	-2.65	119.58	126.60
27	F	501	FMN	C4A-C10-N1	-2.62	118.66	124.73
25	I	301	PC1	O31-C31-C32	2.49	119.73	111.91
30	q	201	CDL	OA8-CA7-C31	2.49	119.71	111.91
25	B	302	PC1	O31-C31-C32	2.38	119.39	111.91
25	B	302	PC1	C2-O21-C21	-2.29	112.16	117.79
30	q	201	CDL	CA4-OA6-CA5	-2.28	112.18	117.79
27	F	501	FMN	C10-N1-C2	2.22	121.34	116.90
27	F	501	FMN	C4-C4A-N5	2.20	121.36	118.23
29	P	401	NDP	C3D-C2D-C1D	2.13	105.47	101.43
27	F	501	FMN	C4A-C4-N3	2.11	118.54	113.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	F	501	FMN	O2-C2-N1	-2.05	118.44	121.83

There are no chirality outliers.

All (56) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
25	B	302	PC1	C1-O11-P-O12
25	B	302	PC1	C1-O11-P-O14
25	B	302	PC1	C1-O11-P-O13
25	B	302	PC1	O22-C21-O21-C2
28	H	401	3PE	C1-O11-P-O12
28	H	401	3PE	C1-O11-P-O13
28	H	401	3PE	C1-O11-P-O14
28	H	401	3PE	C11-O13-P-O14
29	P	401	NDP	C2B-O2B-P2B-O2X
29	P	401	NDP	C2N-C3N-C7N-N7N
30	q	201	CDL	CA2-OA2-PA1-OA3
30	q	201	CDL	OA7-CA5-OA6-CA4
30	q	201	CDL	C11-CA5-OA6-CA4
30	q	201	CDL	CB2-OB2-PB2-OB3
30	q	201	CDL	CB2-OB2-PB2-OB4
30	q	201	CDL	CB2-OB2-PB2-OB5
30	q	201	CDL	CB3-OB5-PB2-OB2
30	q	201	CDL	CB3-OB5-PB2-OB4
25	I	301	PC1	O22-C21-O21-C2
25	B	302	PC1	C22-C21-O21-C2
25	I	301	PC1	C22-C21-O21-C2
28	H	401	3PE	C32-C31-O31-C3
30	q	201	CDL	C31-CA7-OA8-CA6
28	H	401	3PE	O32-C31-O31-C3
30	q	201	CDL	C51-CB5-OB6-CB4
30	q	201	CDL	OA9-CA7-OA8-CA6
30	q	201	CDL	OB7-CB5-OB6-CB4
28	H	401	3PE	C11-O13-P-O11
30	q	201	CDL	CA3-OA5-PA1-OA2
25	I	301	PC1	C32-C31-O31-C3
30	q	201	CDL	CB6-CB4-OB6-CB5
25	I	301	PC1	O32-C31-O31-C3
25	B	302	PC1	C32-C33-C34-C35
25	B	302	PC1	C23-C24-C25-C26
30	q	201	CDL	CA2-OA2-PA1-OA5
28	H	401	3PE	C3E-C3F-C3G-C3H

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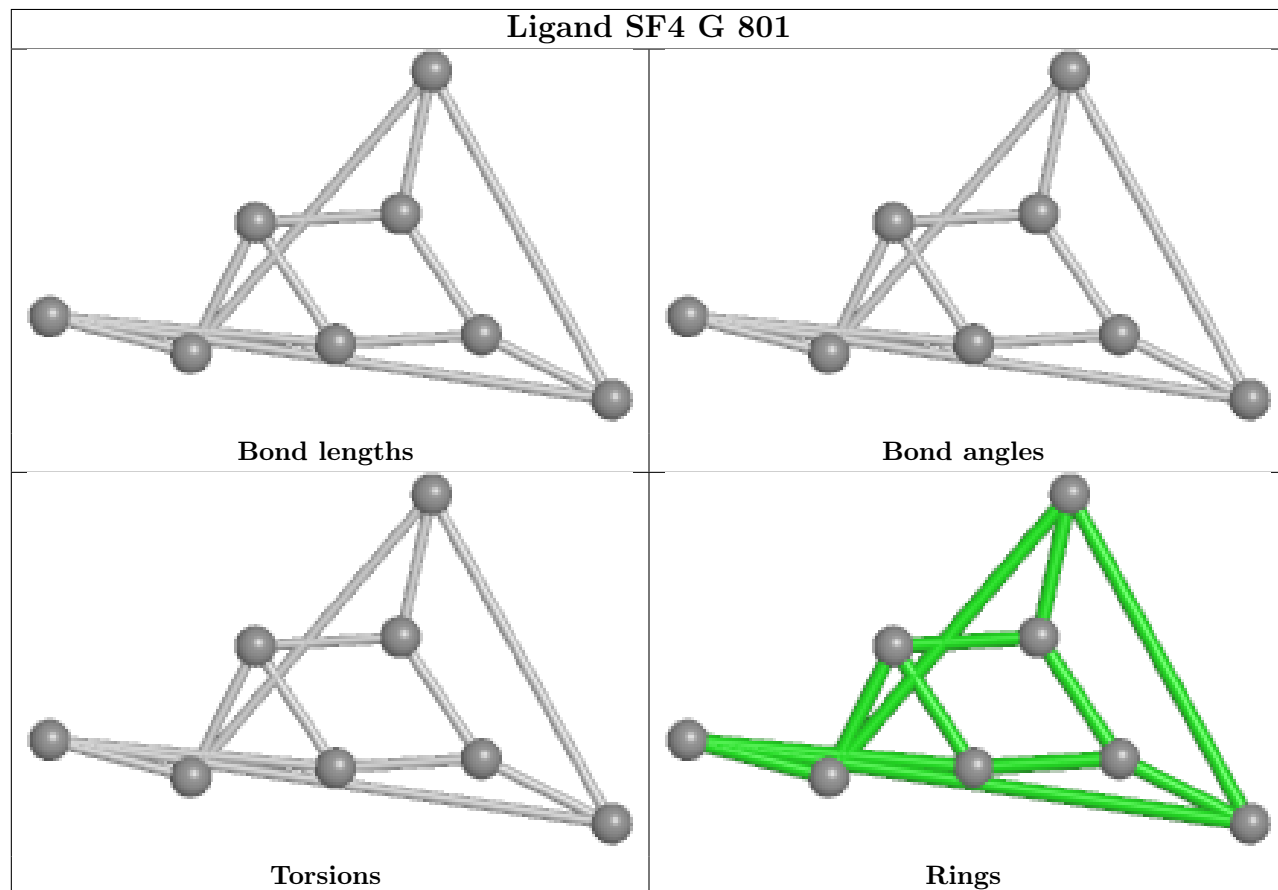
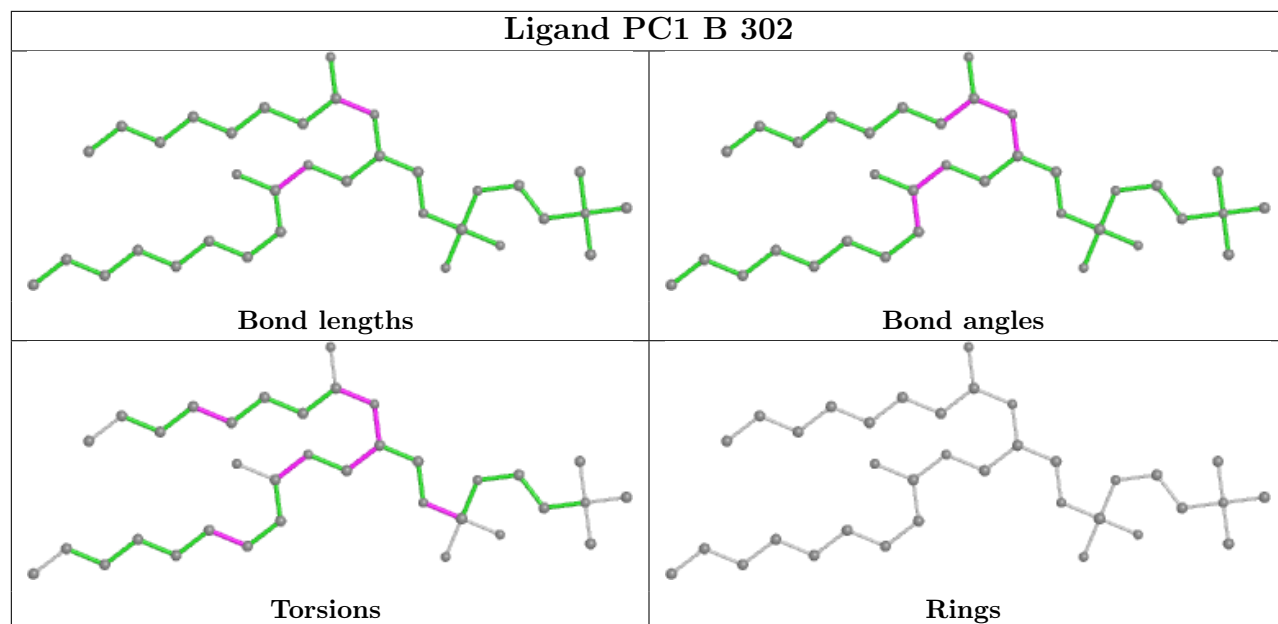
Continued from previous page...

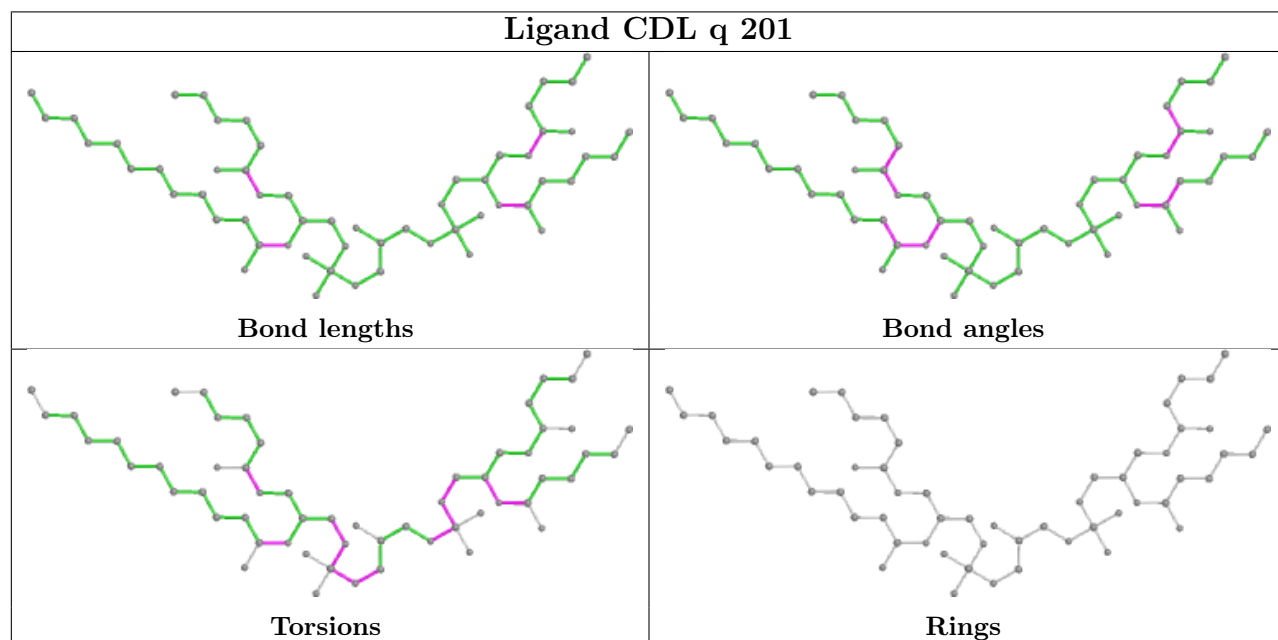
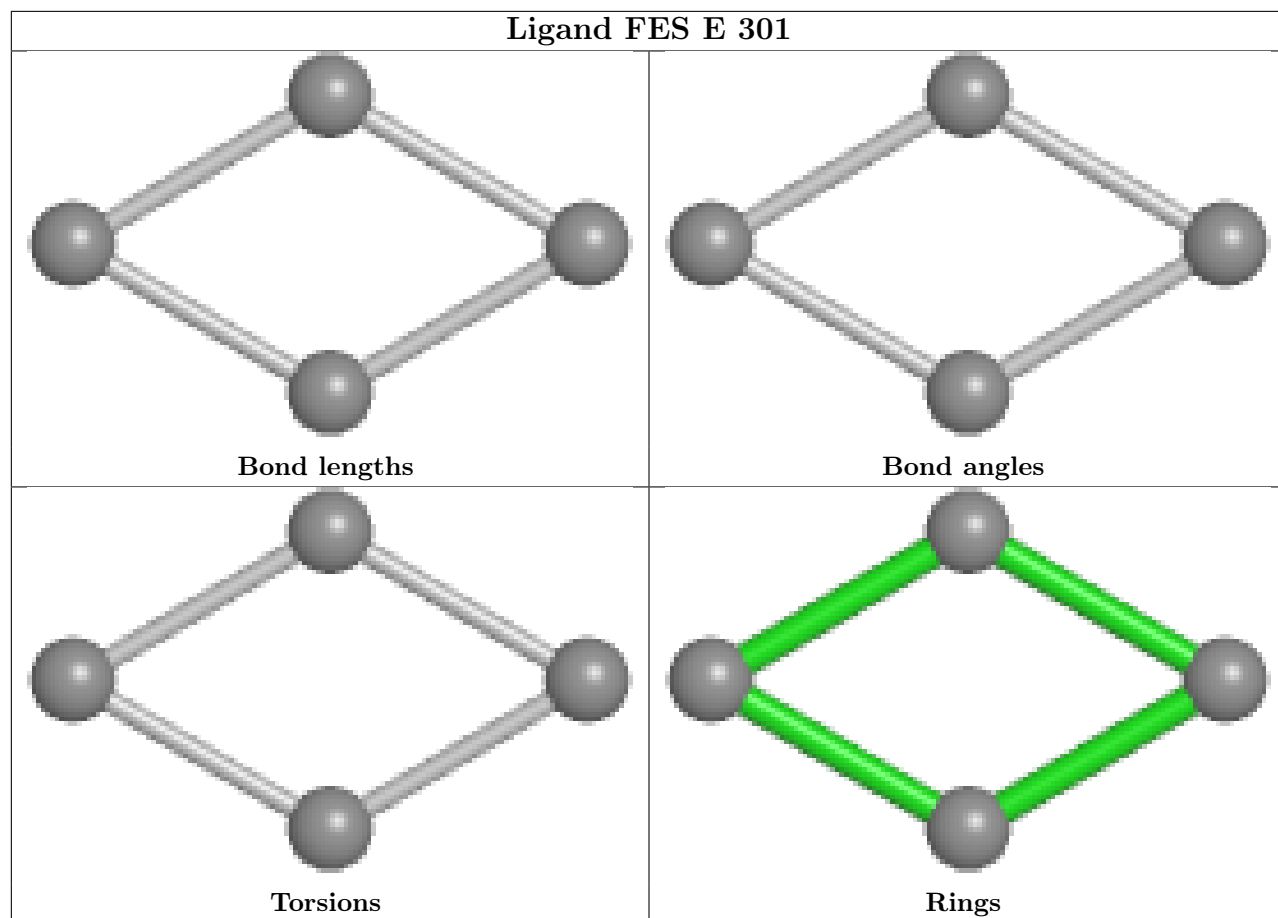
Mol	Chain	Res	Type	Atoms
28	H	401	3PE	C37-C38-C39-C3A
25	I	301	PC1	C11-C12-N-C13
29	P	401	NDP	PN-O3-PA-O2A
29	P	401	NDP	O4D-C1D-N1N-C6N
30	q	201	CDL	C1-CA2-OA2-PA1
25	I	301	PC1	C11-C12-N-C15
28	H	401	3PE	C11-O13-P-O12
30	q	201	CDL	CA3-OA5-PA1-OA3
30	q	201	CDL	CB3-OB5-PB2-OB3
27	F	501	FMN	C5'-O5'-P-O1P
25	I	301	PC1	C1-O11-P-O13
28	H	401	3PE	C24-C25-C26-C27
25	B	302	PC1	C1-C2-C3-O31
25	I	301	PC1	C11-C12-N-C14
25	I	301	PC1	C32-C33-C34-C35
30	q	201	CDL	CA4-CA3-OA5-PA1
25	B	302	PC1	C32-C31-O31-C3
25	B	302	PC1	O32-C31-O31-C3
30	q	201	CDL	CB4-CB3-OB5-PB2
25	B	302	PC1	C3-C2-O21-C21

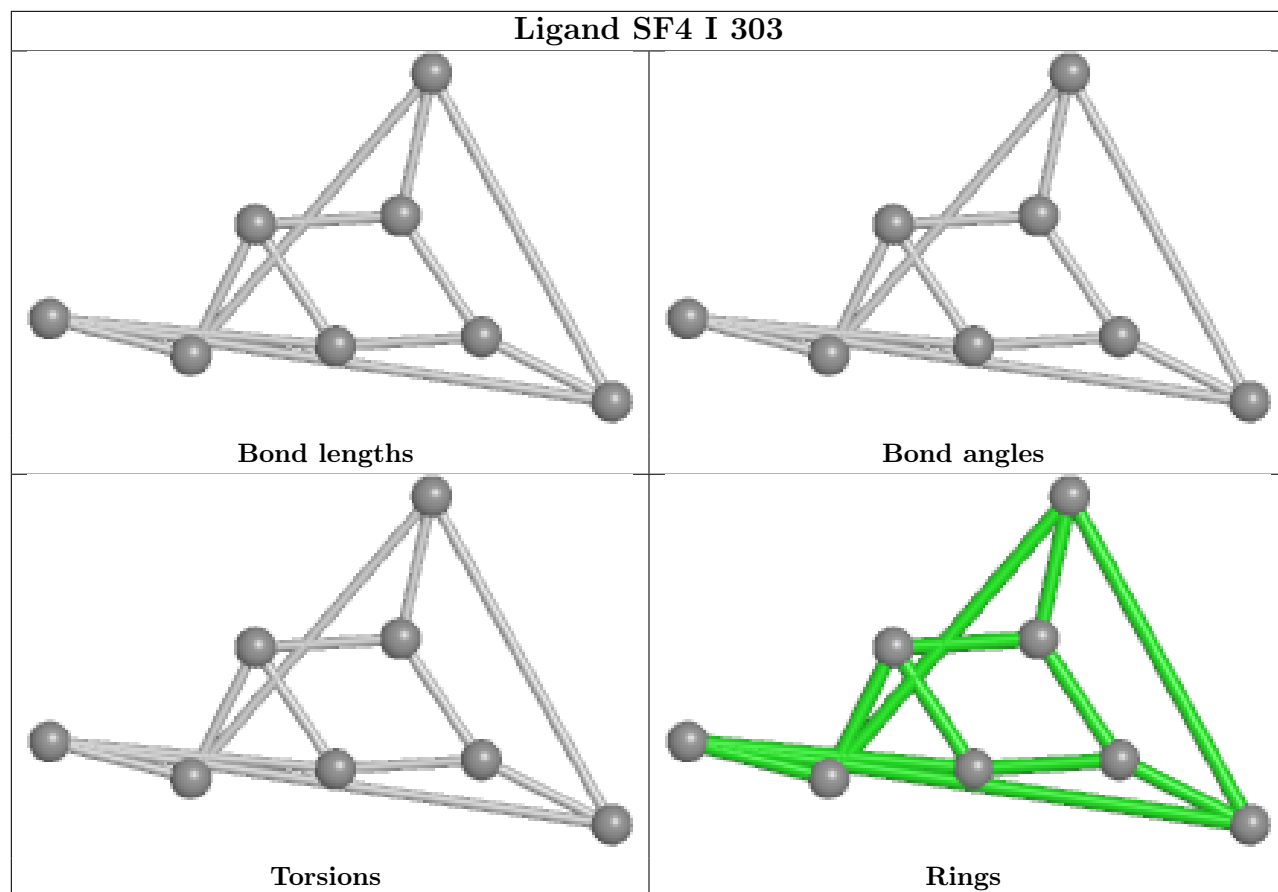
There are no ring outliers.

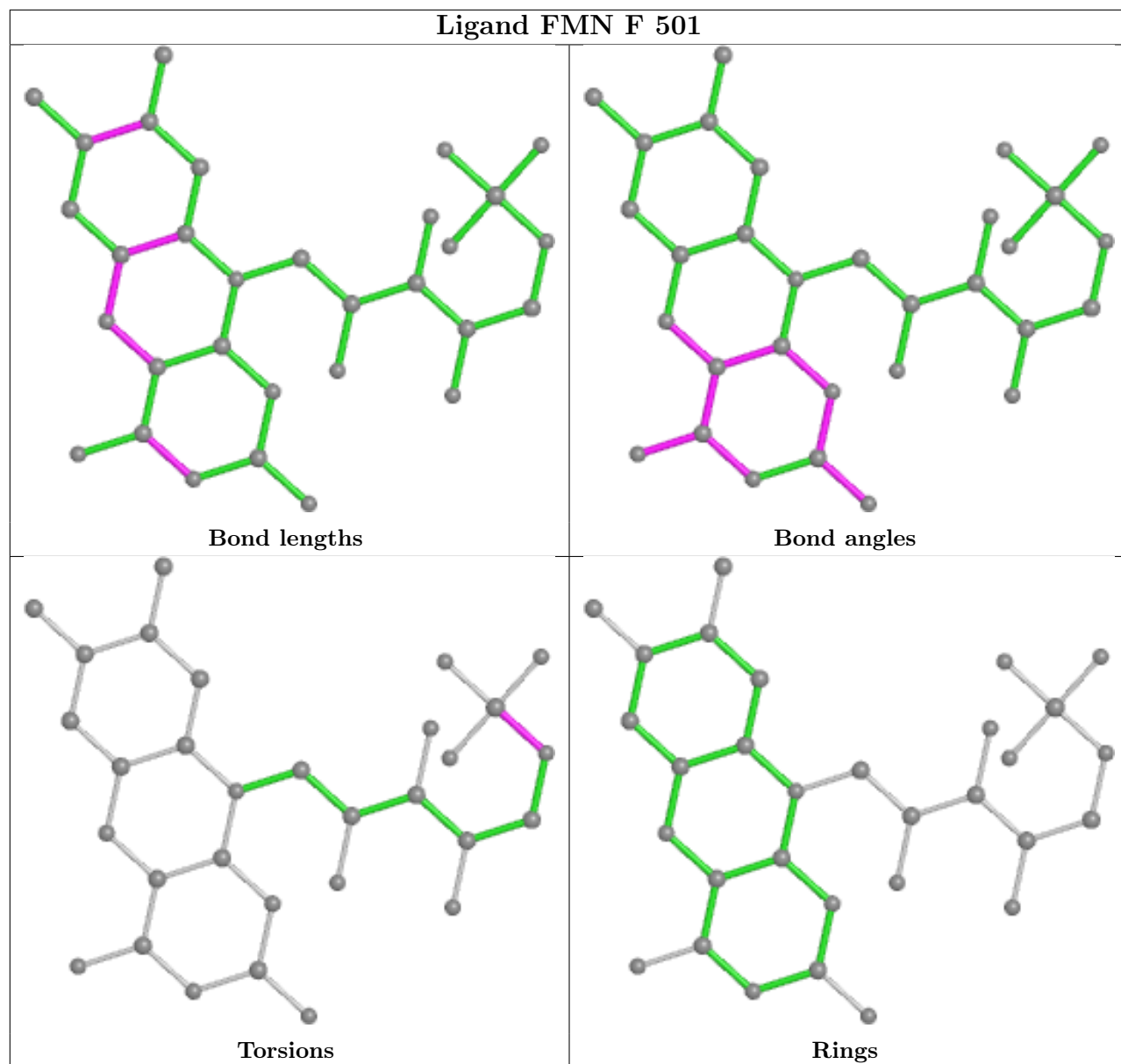
No monomer is involved in short contacts.

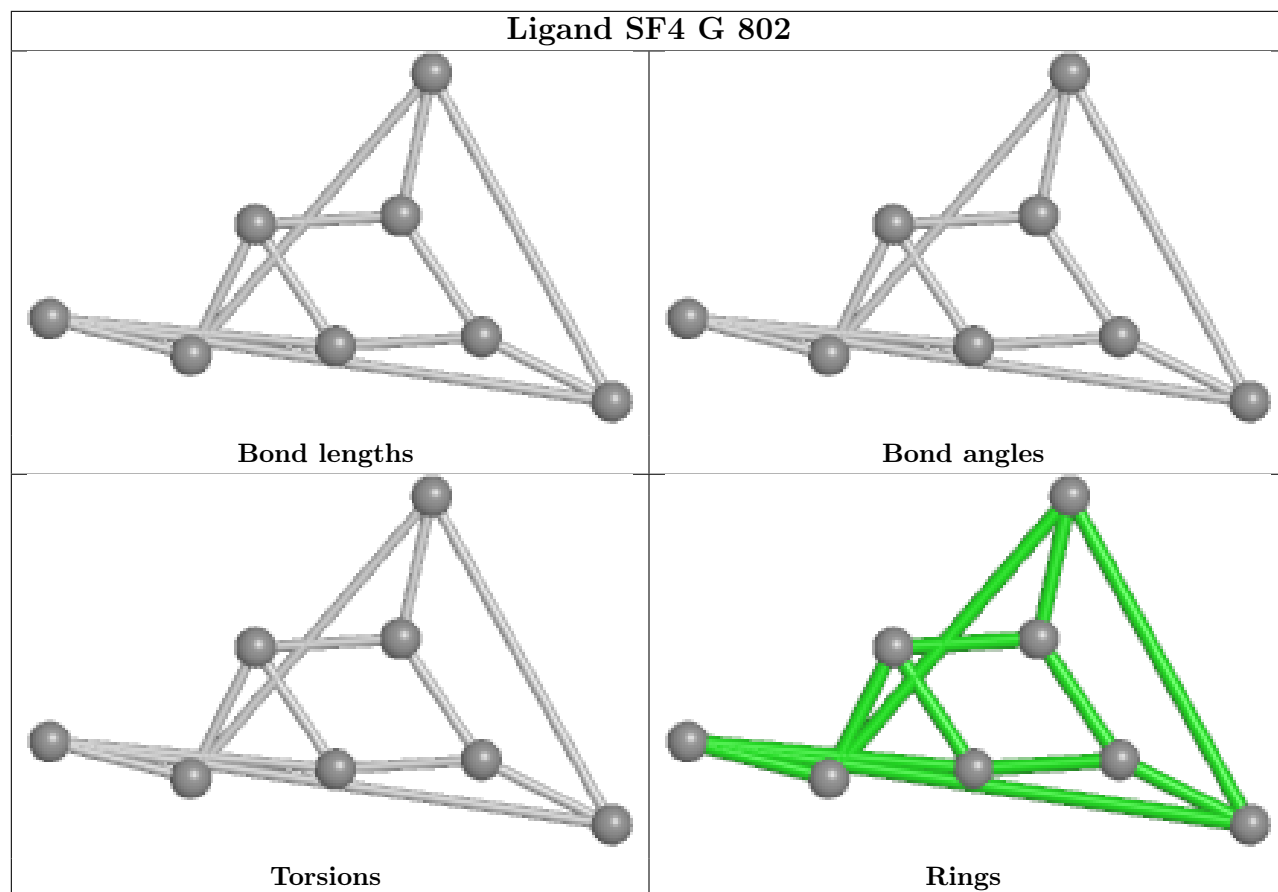
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

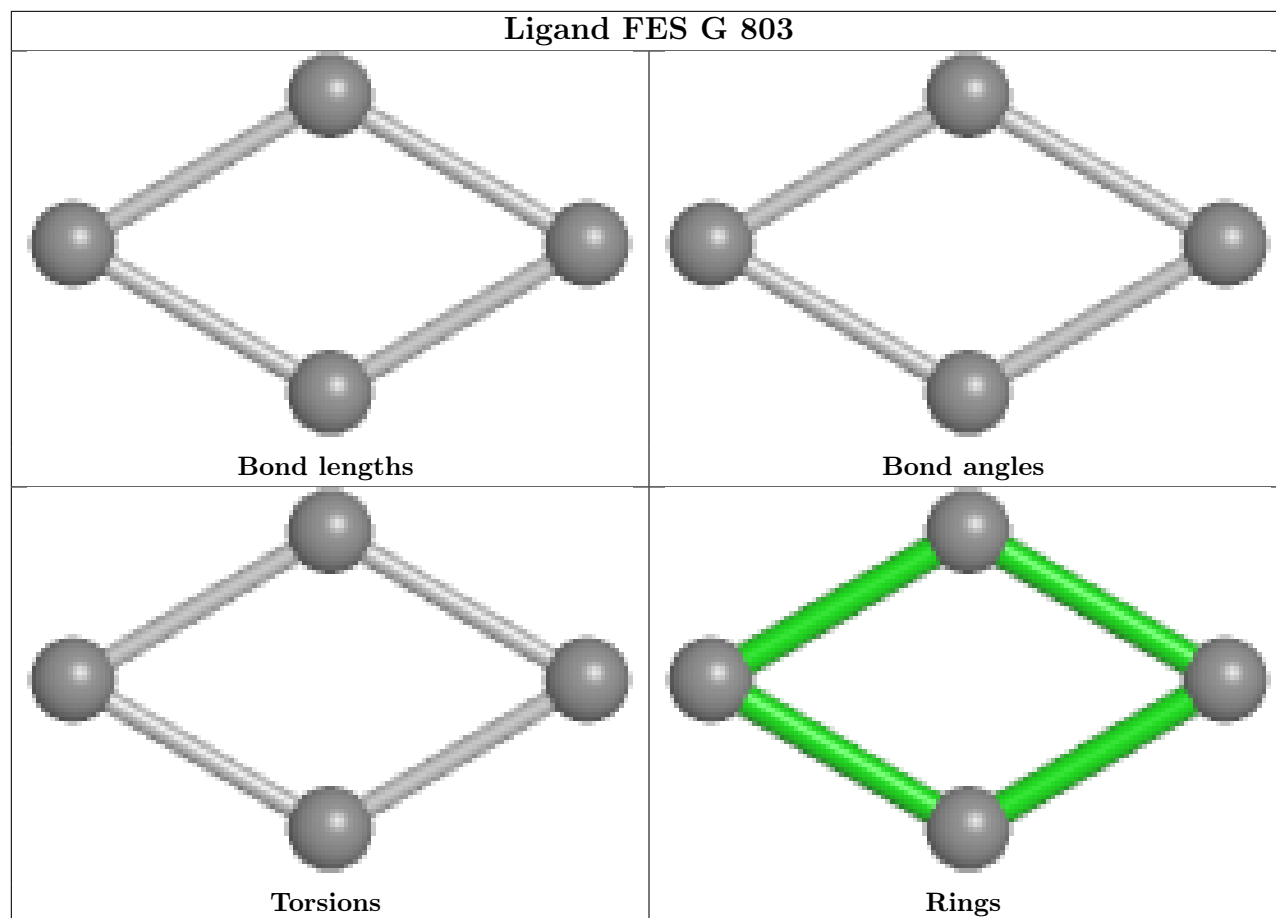


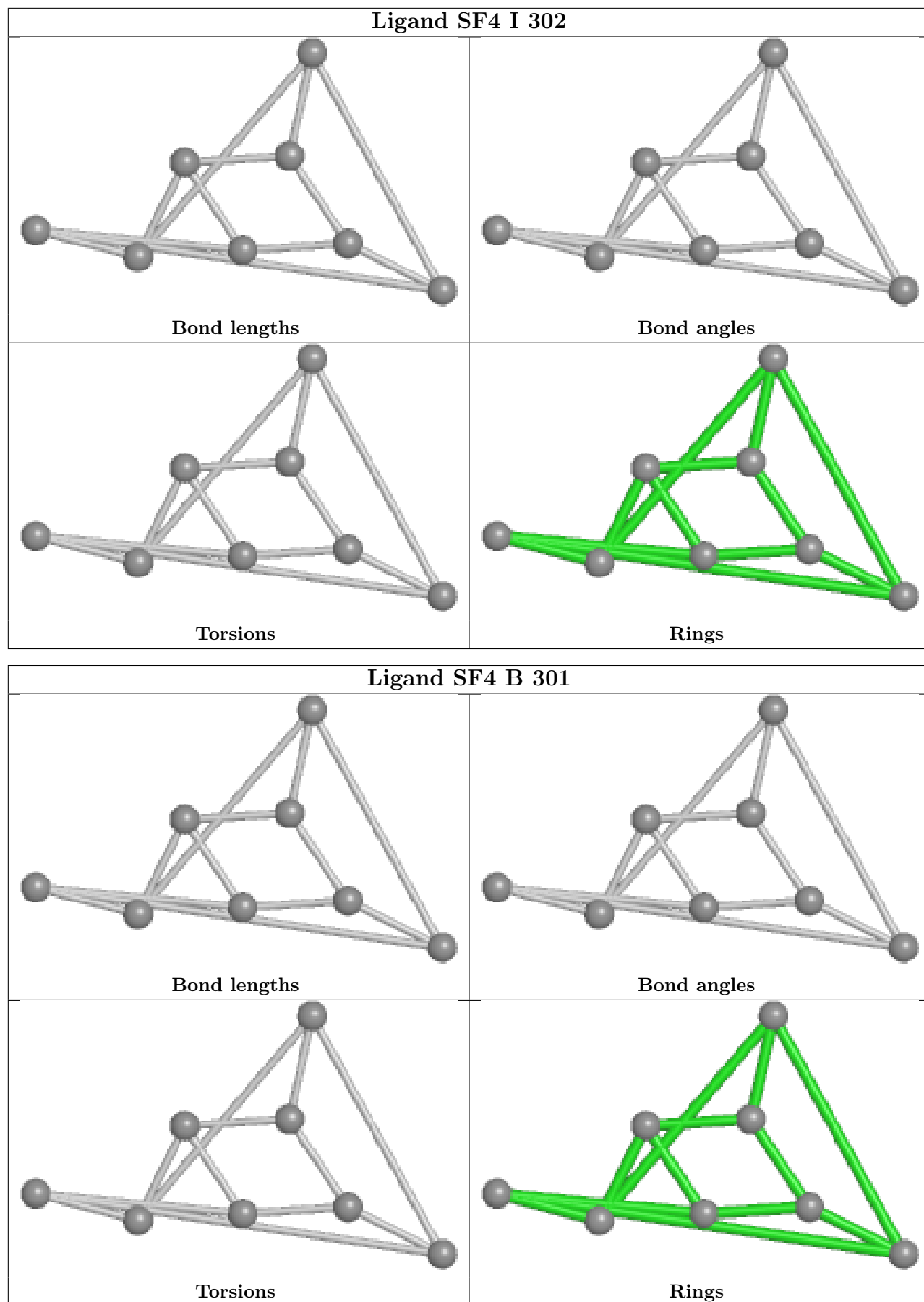


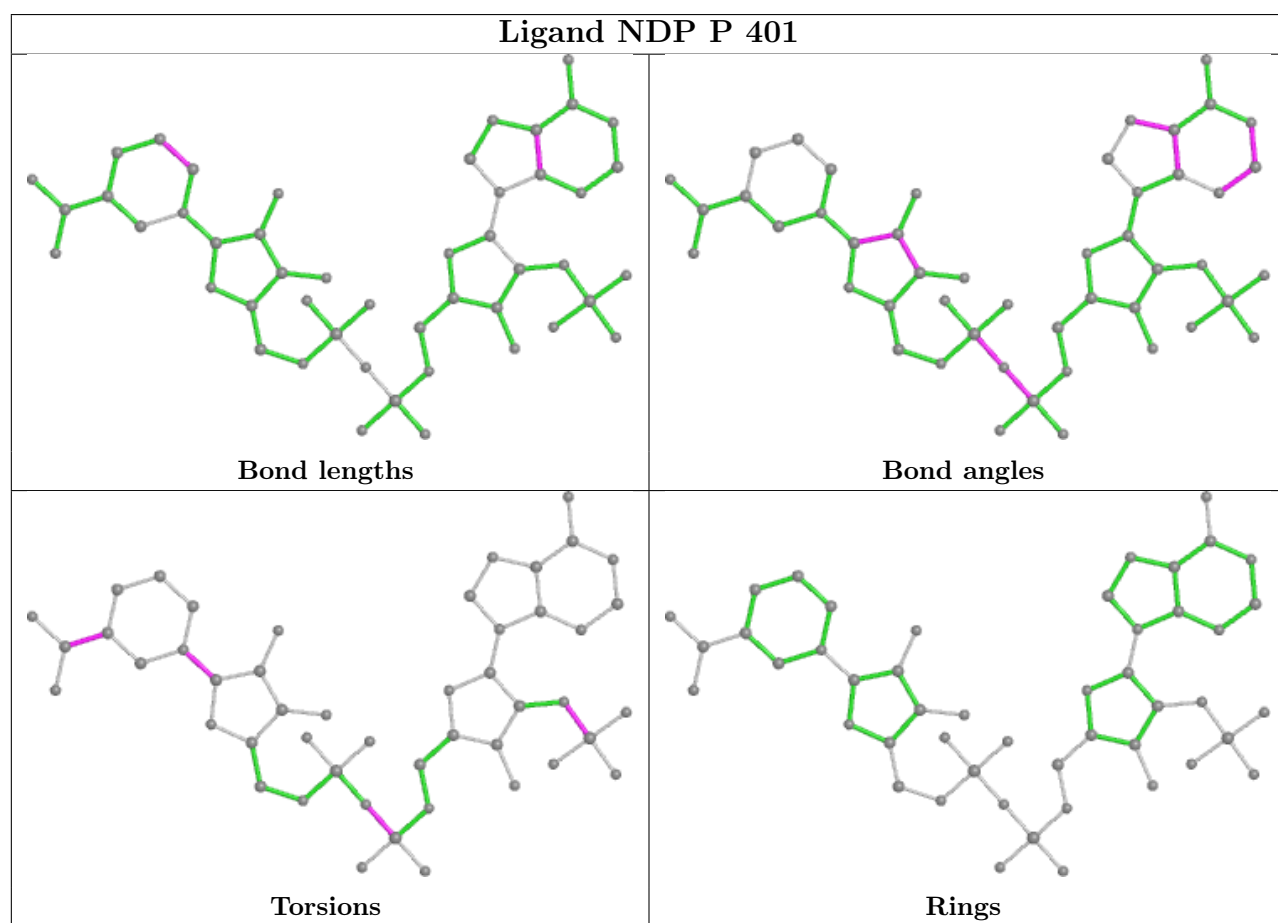
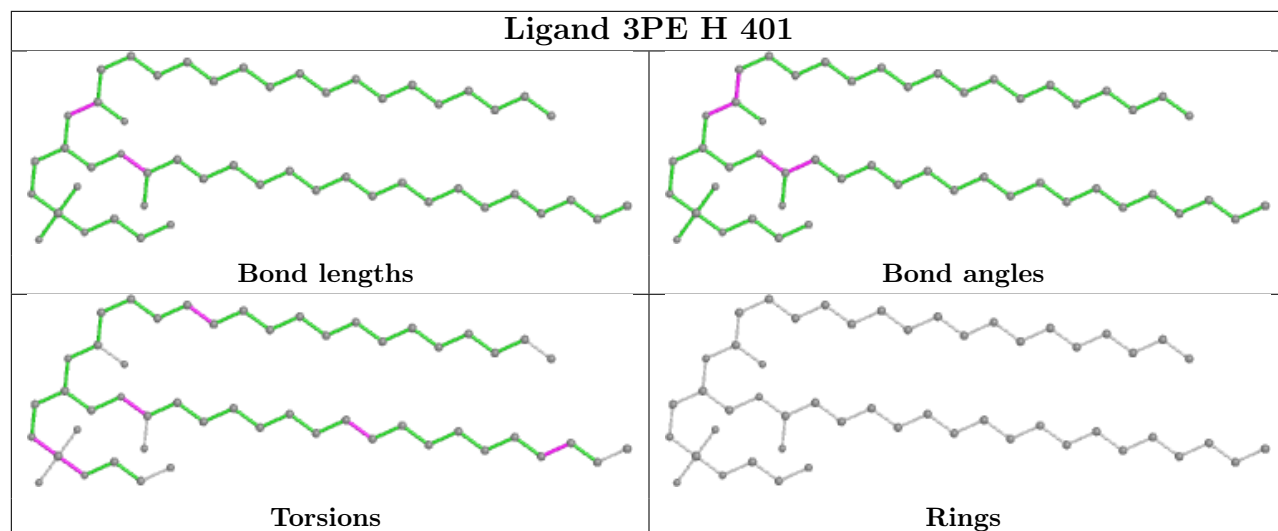


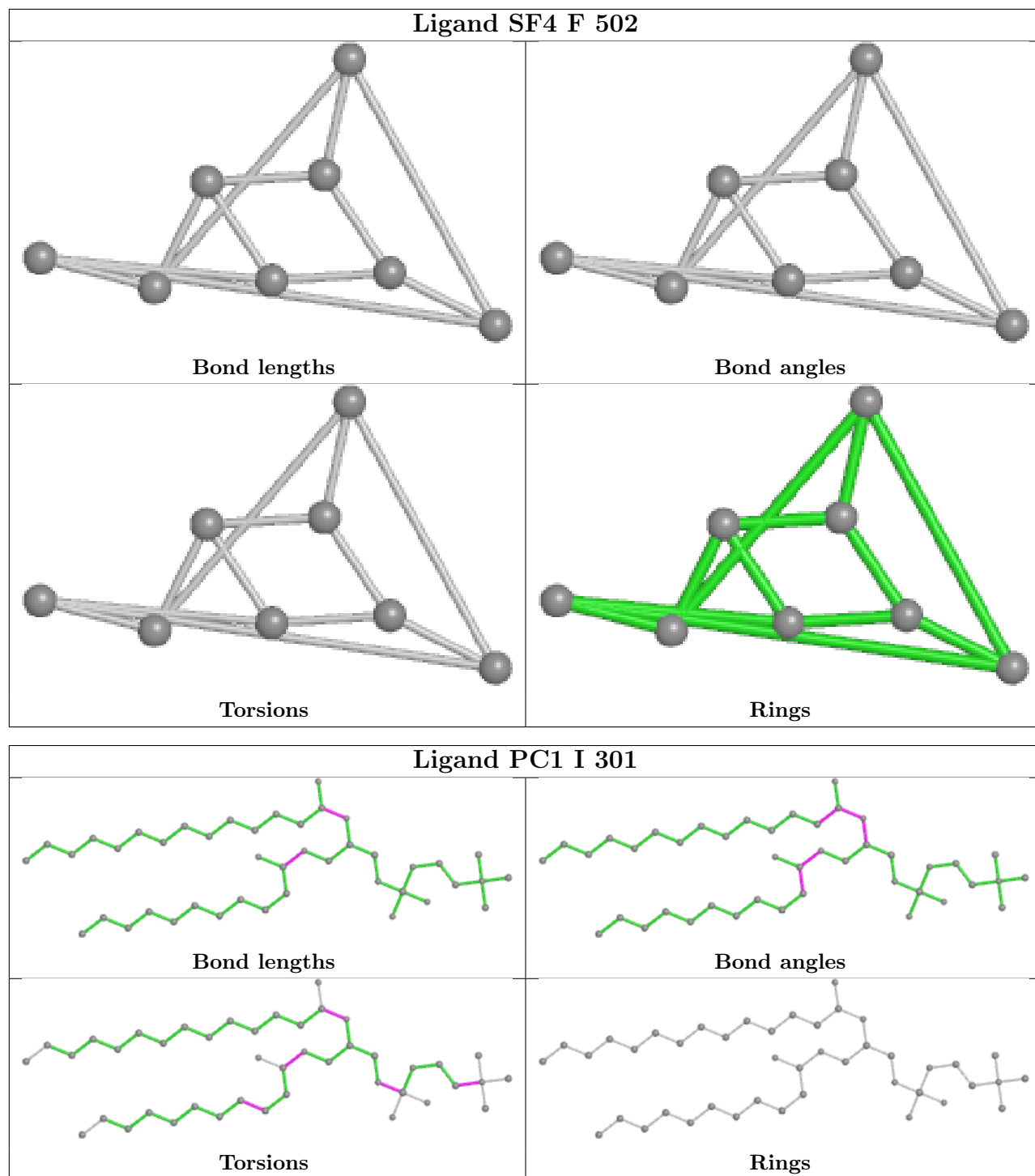












5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

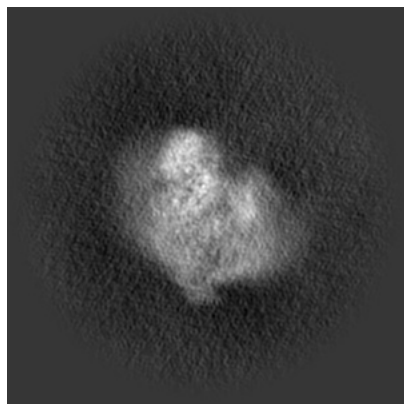
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38521. These allow visual inspection of the internal detail of the map and identification of artifacts.

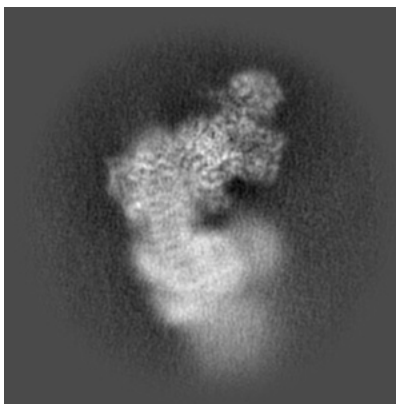
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

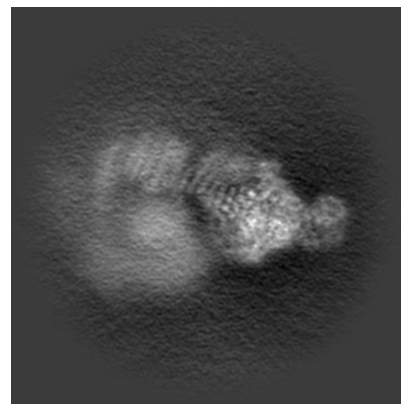
6.1.1 Primary map



X

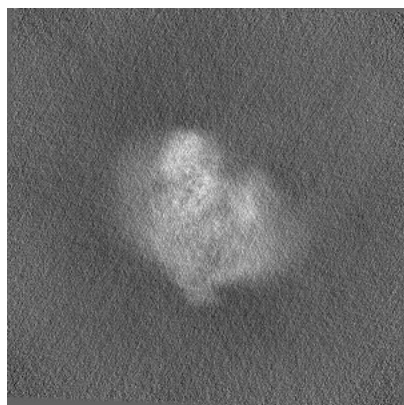


Y

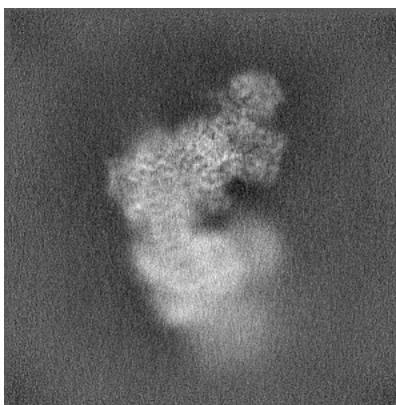


Z

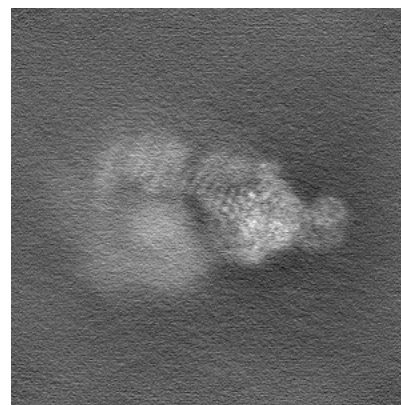
6.1.2 Raw map



X



Y

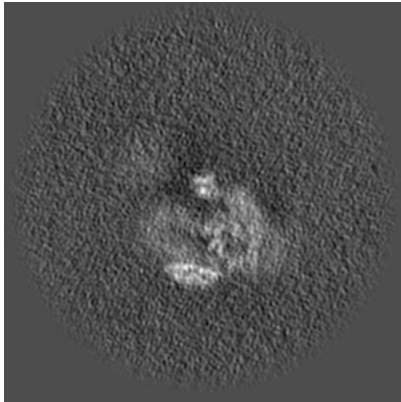


Z

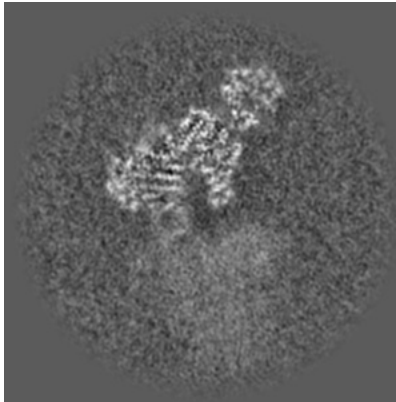
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

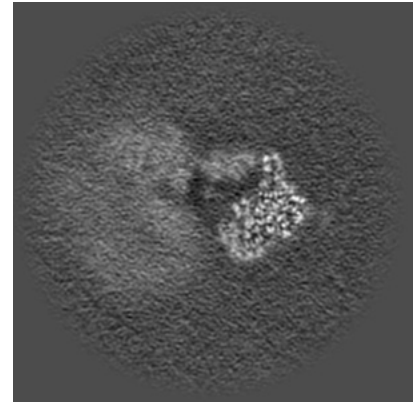
6.2.1 Primary map



X Index: 256

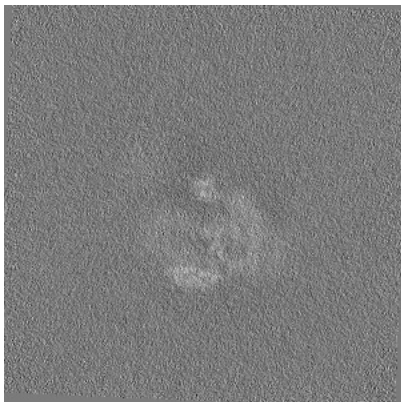


Y Index: 256

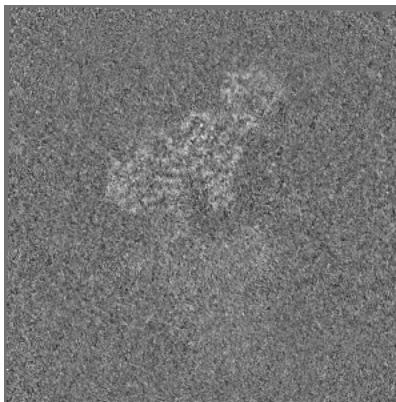


Z Index: 256

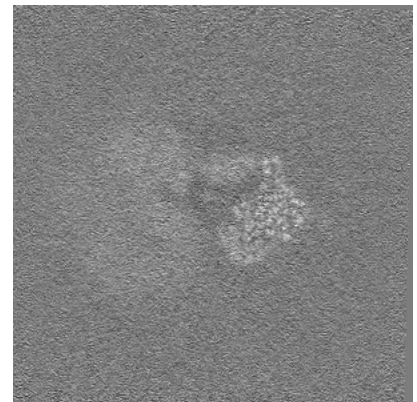
6.2.2 Raw map



X Index: 256



Y Index: 256

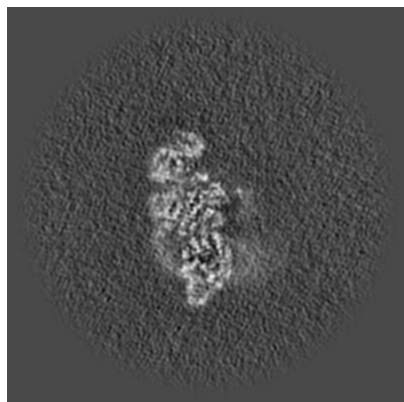


Z Index: 256

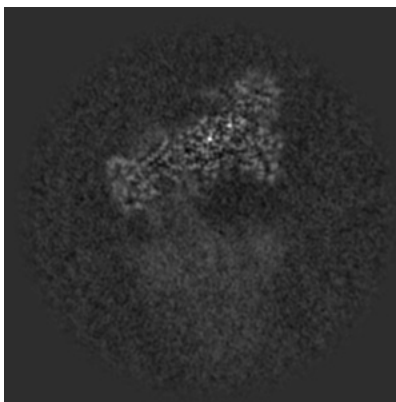
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

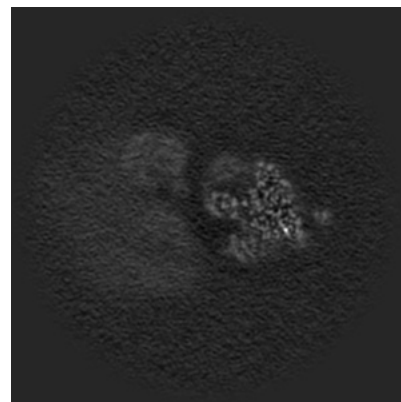
6.3.1 Primary map



X Index: 311

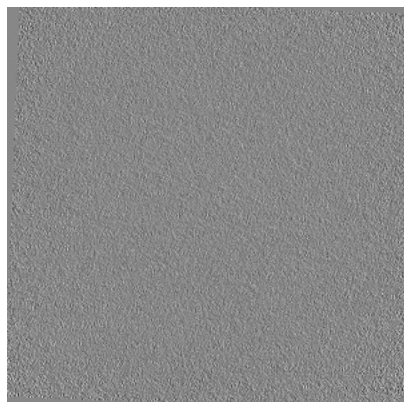


Y Index: 234

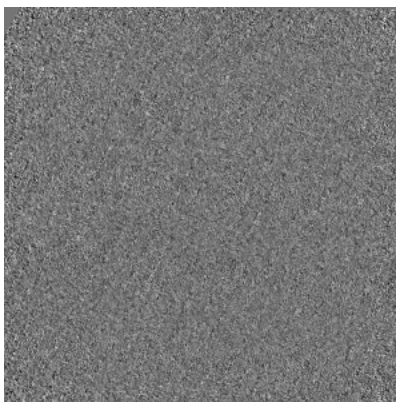


Z Index: 272

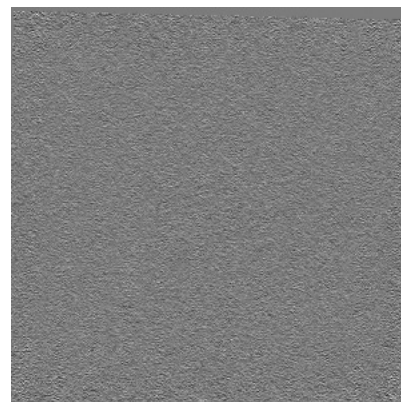
6.3.2 Raw map



X Index: 3



Y Index: 495

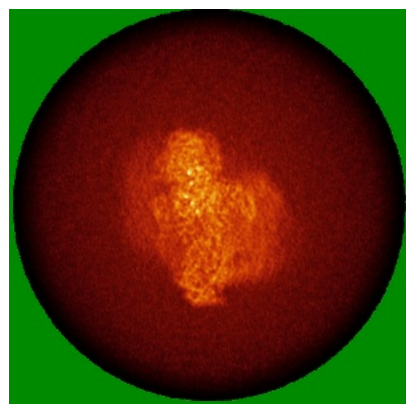


Z Index: 18

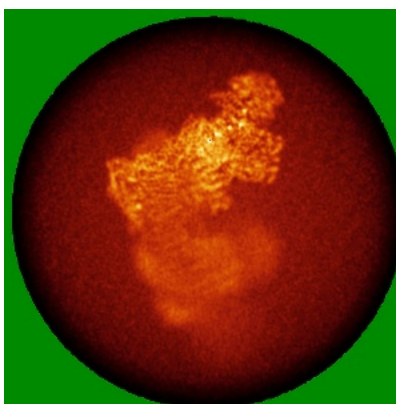
The images above show the largest variance slices of the map in three orthogonal directions.

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

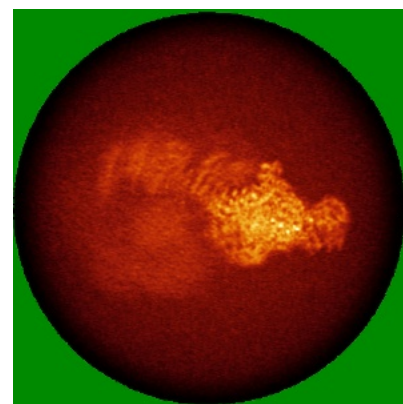
6.4.1 Primary map



X

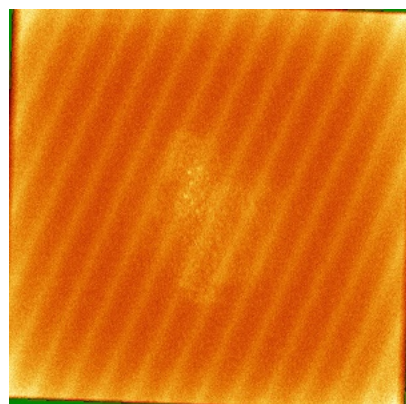


Y

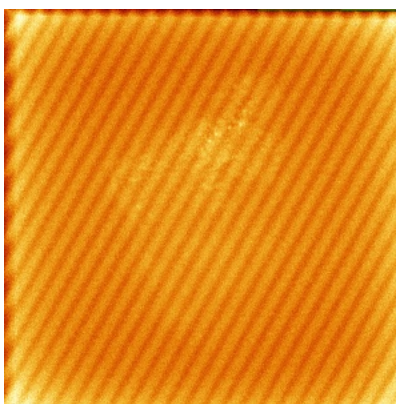


Z

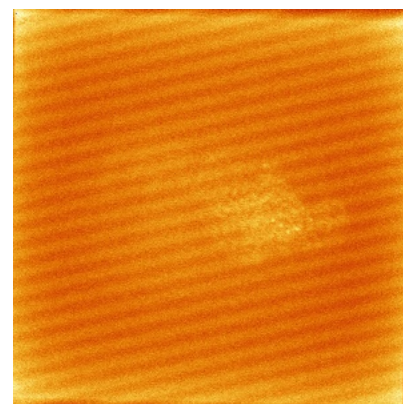
6.4.2 Raw map



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.

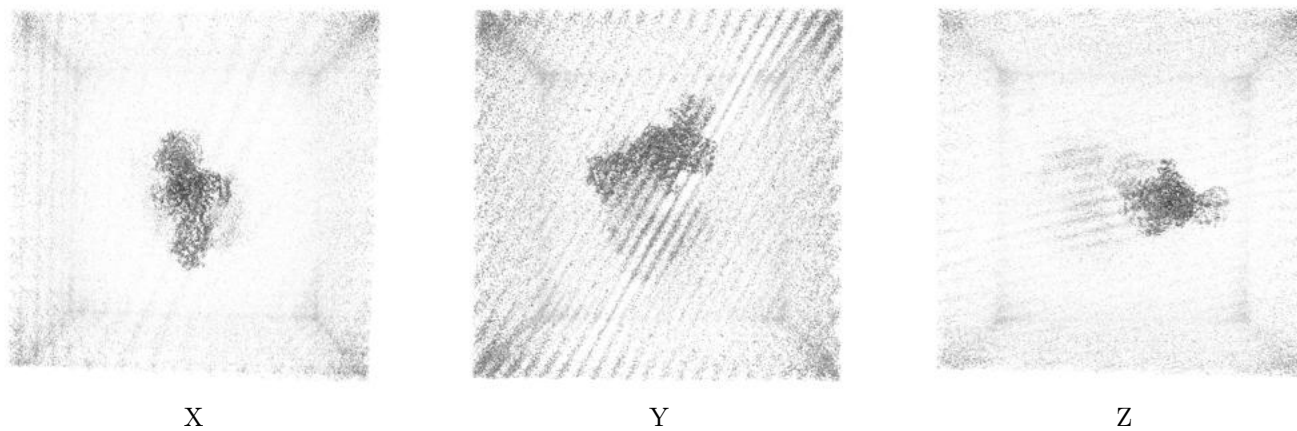
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.4. 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



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.

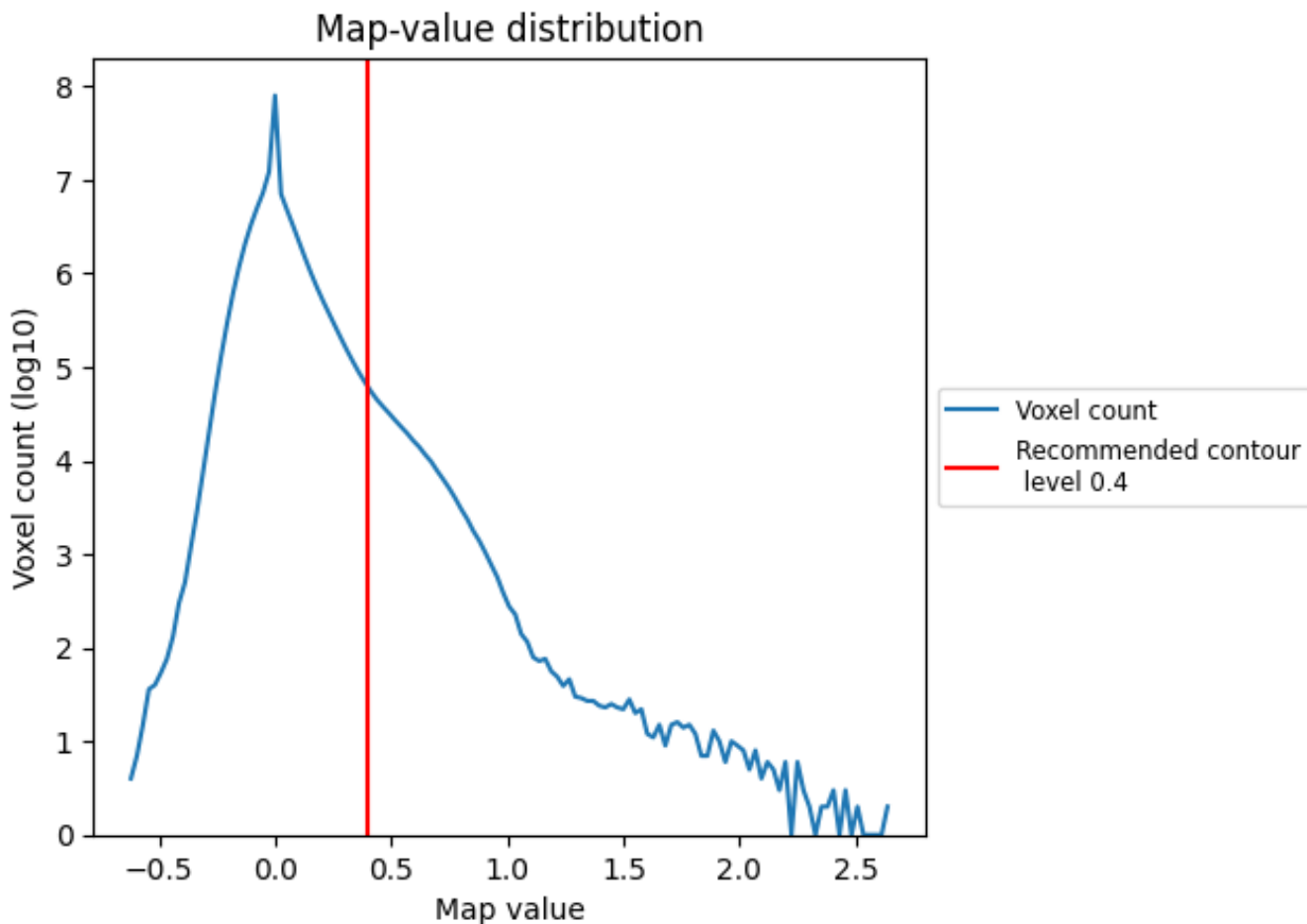
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

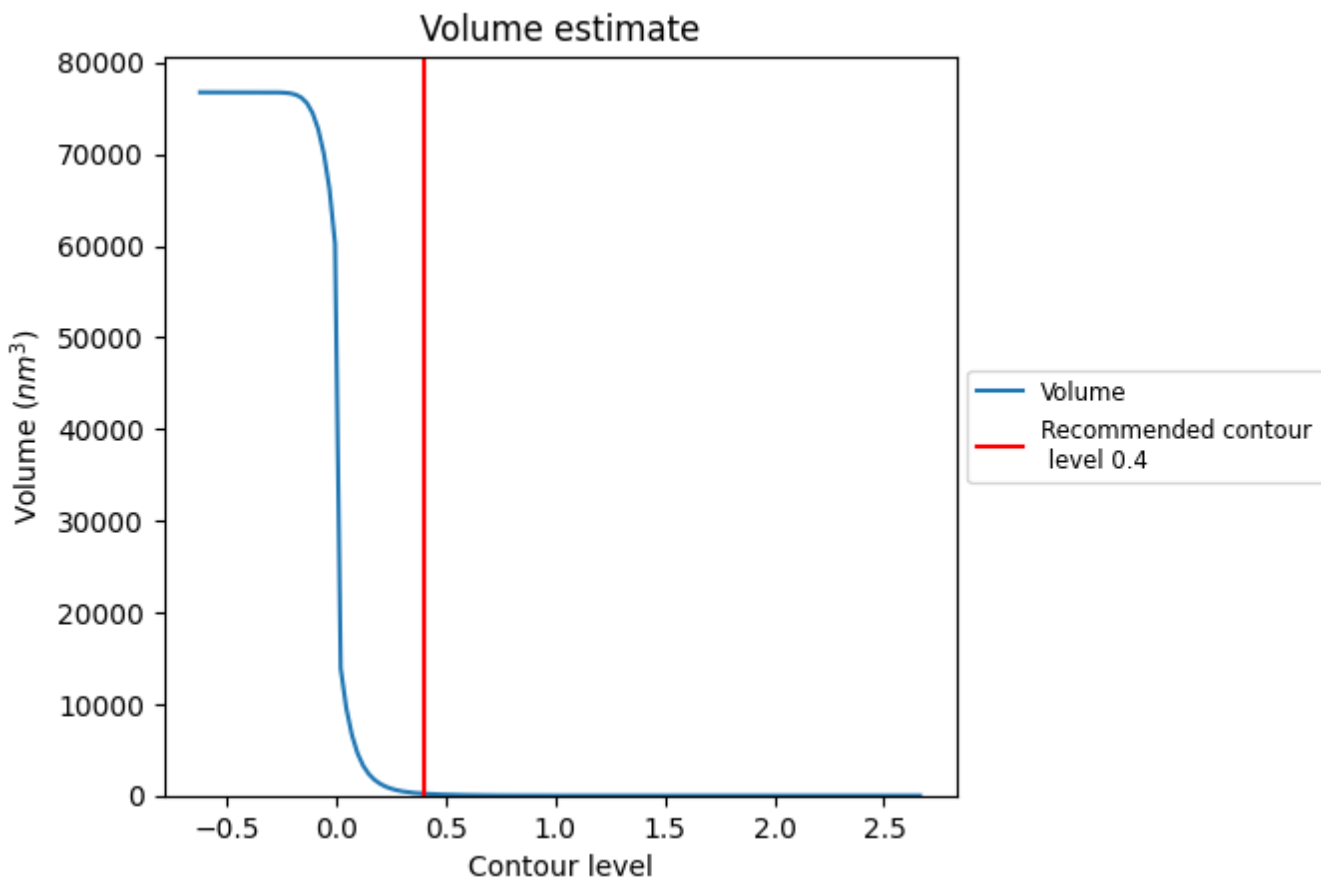
This section contains the results of statistical analysis of the map.

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.

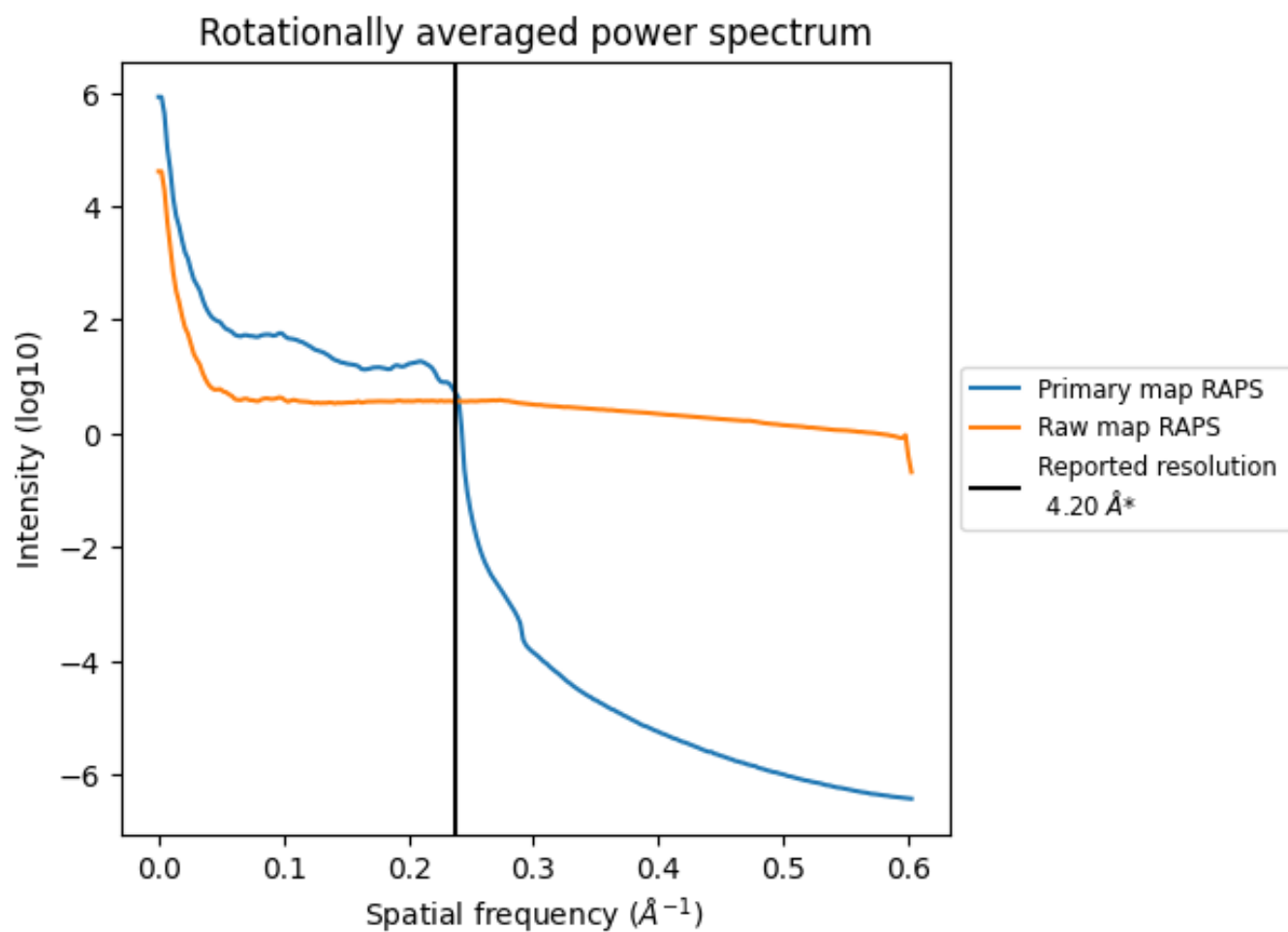
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 205 nm³; this corresponds to an approximate mass of 185 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](#)

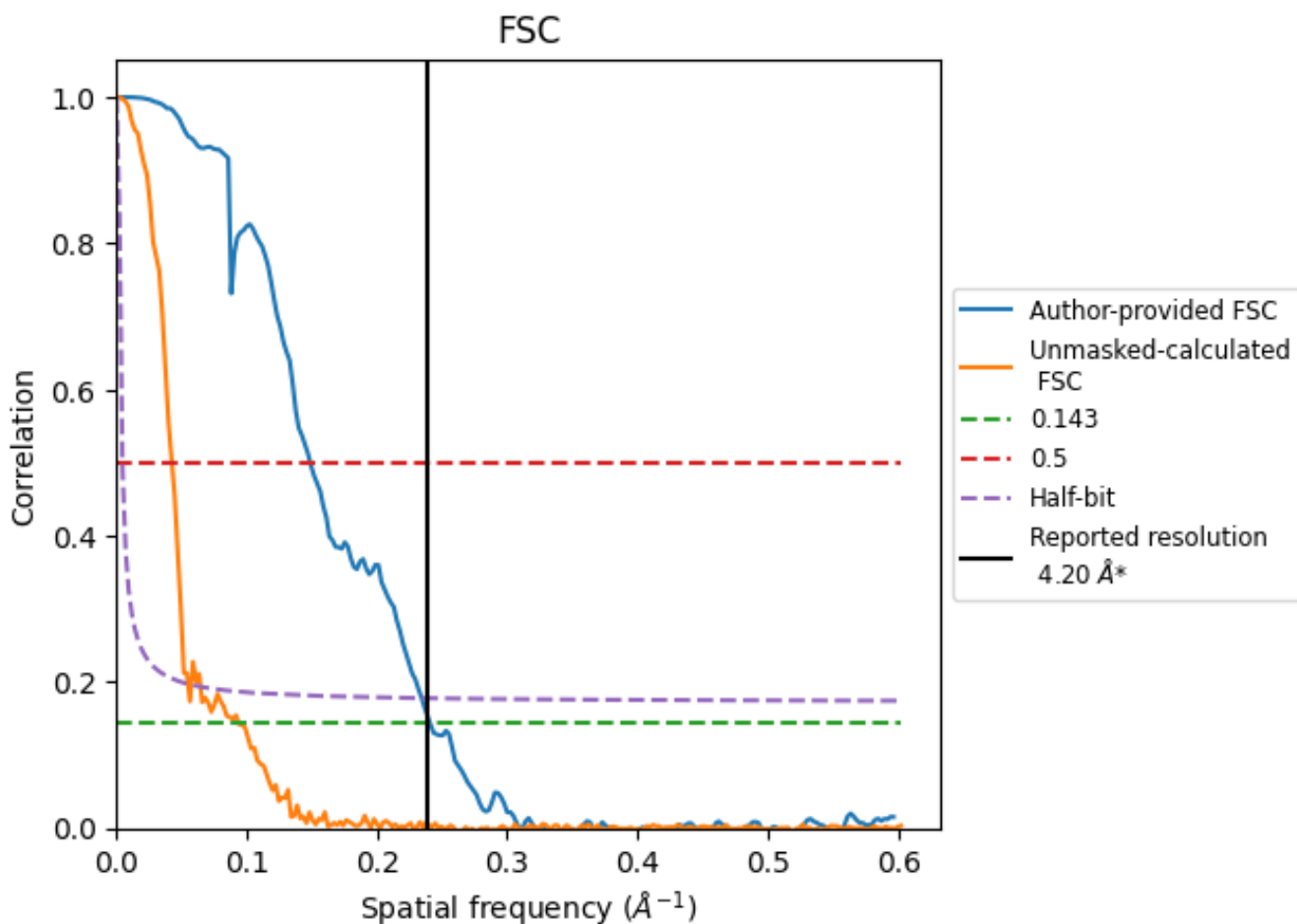


*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

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 0.238 Å⁻¹

8.2 Resolution estimates [i](#)

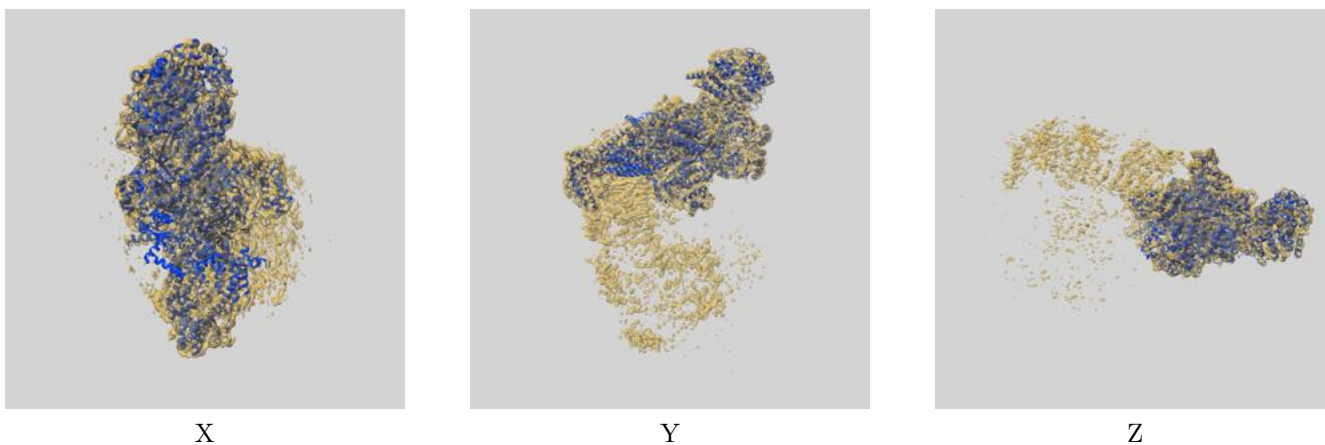
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.15	6.72	4.27
Unmasked-calculated*	10.65	23.47	18.18

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 10.65 differs from the reported value 4.2 by more than 10 %

9 Map-model fit [i](#)

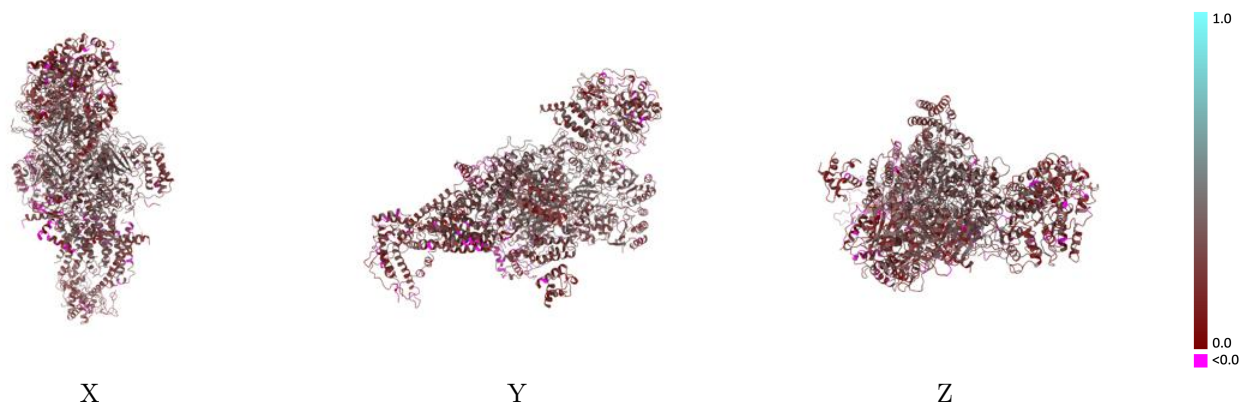
This section contains information regarding the fit between EMDB map EMD-38521 and PDB model 8XO0. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



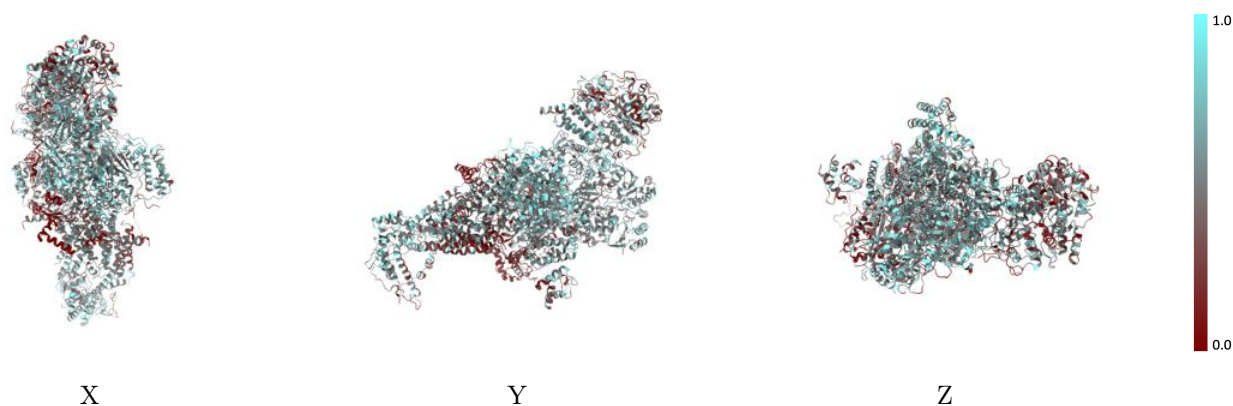
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



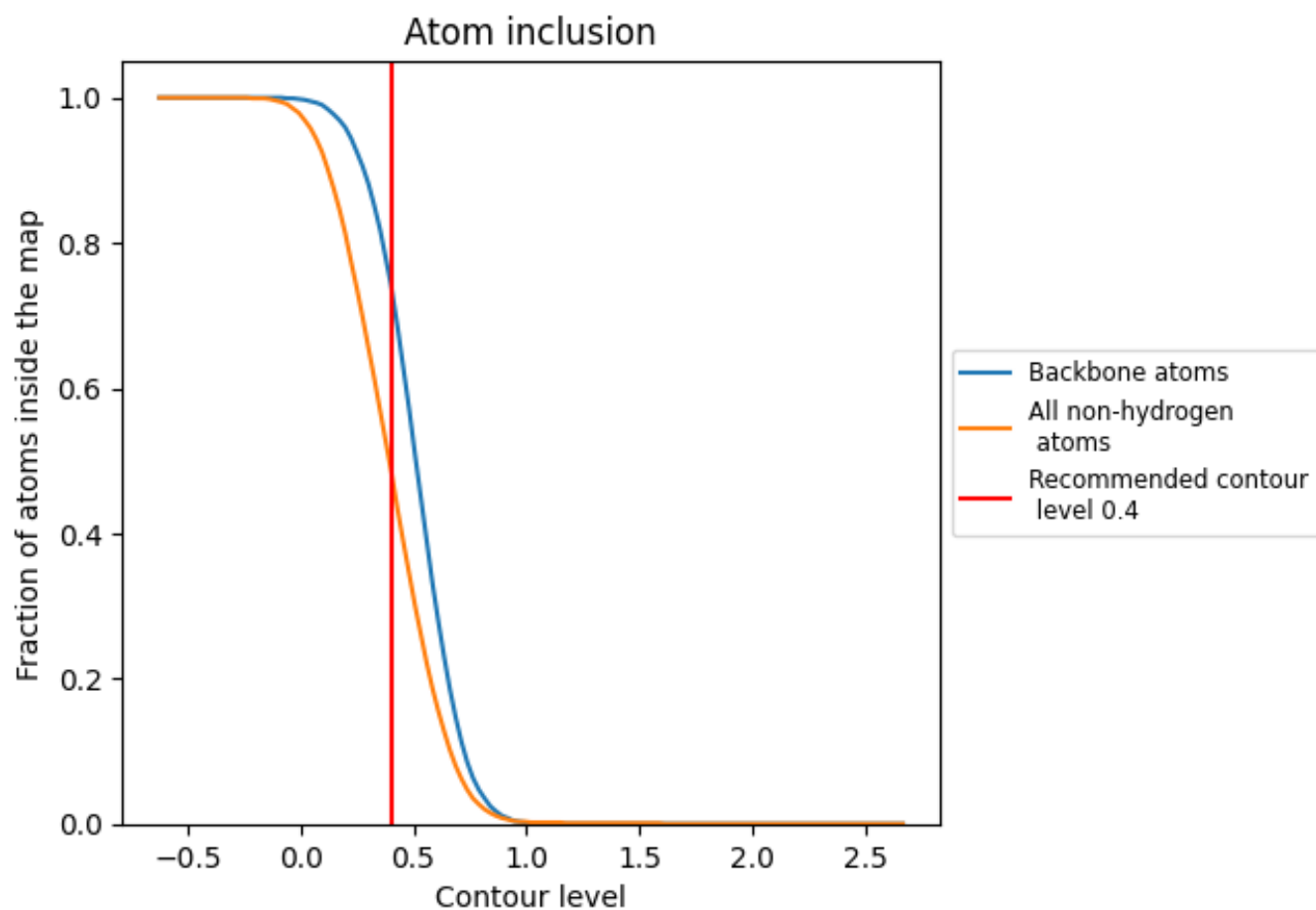
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

















































9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 49% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4890	 0.2590
A	 0.3740	 0.1970
B	 0.5780	 0.3090
C	 0.5990	 0.3290
D	 0.5900	 0.3300
E	 0.4370	 0.2310
F	 0.4840	 0.2510
G	 0.5620	 0.2930
H	 0.4610	 0.2800
I	 0.6190	 0.3180
P	 0.3660	 0.2040
Q	 0.4320	 0.3000
R	 0.2740	 0.2010
S	 0.5560	 0.2570
T	 0.4470	 0.1740
V	 0.5710	 0.2460
W	 0.5250	 0.2630
X	 0.5420	 0.1810
Z	 0.5350	 0.2170
a	 0.5690	 0.2540
b	 0.4750	 0.2130
q	 0.0630	 0.1260
r	 0.1950	 0.1580
s	 0.1120	 0.1380

