



wwPDB EM Validation Summary Report ⓘ

May 31, 2023 – 10:25 PM JST

PDB ID : 7VXU
EMDB ID : EMD-32188
Title : Matrix arm of deactive state CI from Q10 dataset
Authors : Gu, J.K.; Yang, M.J.
Deposited on : 2021-11-13
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

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

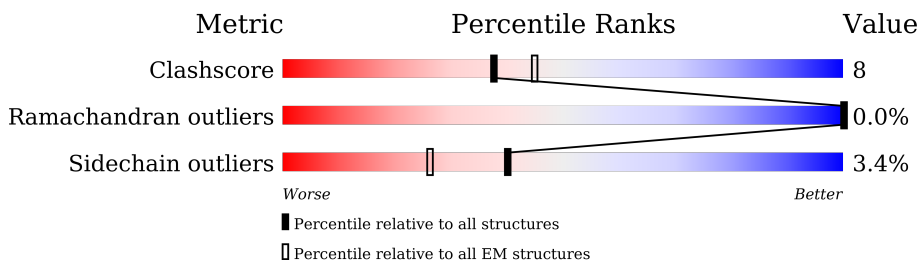
EMDB validation analysis : 0.0.1.dev50
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.33

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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.











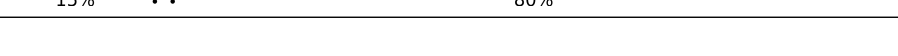

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	458	
2	B	212	
3	C	196	
4	E	128	
5	F	99	
6	G	156	
7	H	116	
8	I	113	

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Mol	Chain	Length	Quality of chain
9	J	376	
10	K	110	
11	L	175	
12	M	718	
13	N	145	
14	O	249	
15	P	264	
16	Q	473	
17	T	123	
18	W	144	

2 Entry composition [i](#)

There are 28 unique types of molecules in this entry. The entry contains 27965 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 dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	431	3318	2095	591	612	20	0	0

- Molecule 2 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	176	1412	887	243	269	13	0	0

- Molecule 3 is a protein called Complex I-20kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	156	1244	792	227	211	14	0	0

- Molecule 4 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	115	971	619	179	168	5	0	0

- Molecule 5 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	86	691	434	129	126	2	0	0

- Molecule 6 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	88	678	438	102	133	5	0	0

- Molecule 7 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	H	112	910	588	154	165	3	0	0

- Molecule 8 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	I	97	780	491	147	139	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	J	297	2356	1513	421	414	8	0	0

- Molecule 10 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	K	42	355	219	67	68	1	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	L	125	1016	642	181	190	3	0	0

- Molecule 12 is a protein called NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	M	690	5296	3320	923	1014	39	0	0

- Molecule 13 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	N	144	1204	770	218	212	4	0	0

- Molecule 14 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	O	217	1671	1065	281	315	10	0	0

- Molecule 15 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	P	208	1738	1124	298	314	2	0	0

- Molecule 16 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	Q	379	3044	1945	522	554	23	0	0

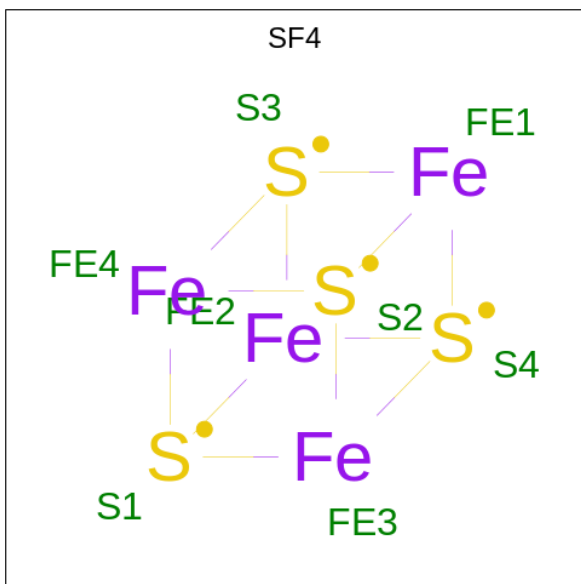
- Molecule 17 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	T	96	741	452	140	146	3	0	0

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

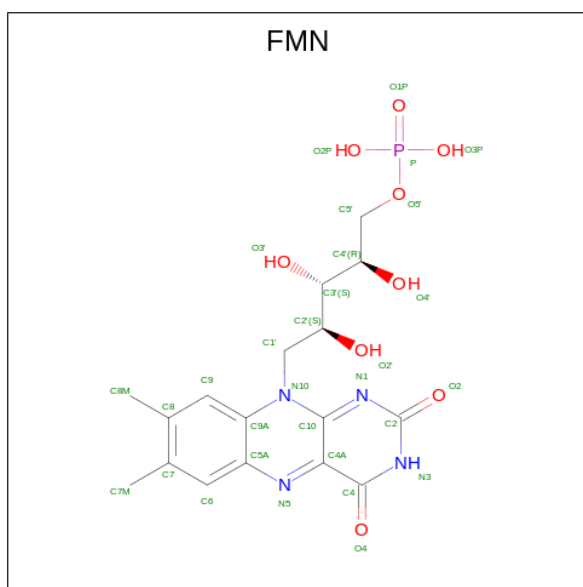
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	W	29	218	138	40	39	1	0	0

- Molecule 19 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄) (labeled as "Ligand of Interest" by depositor).



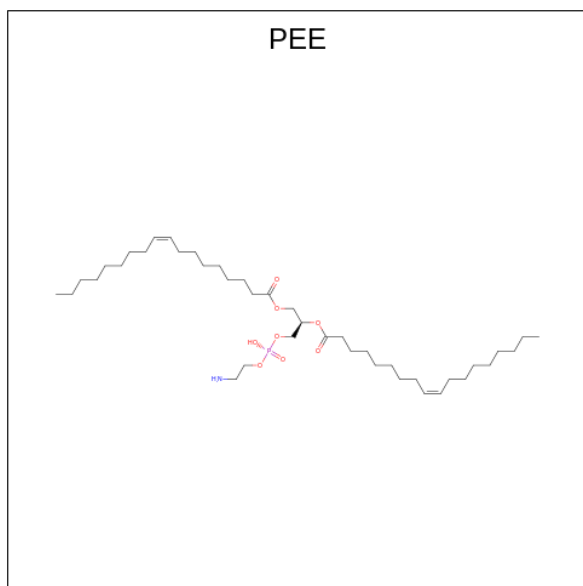
Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
19	A	1	8	4	4	0
19	B	1	8	4	4	0
19	B	1	8	4	4	0
19	C	1	8	4	4	0
19	M	1	8	4	4	0
19	M	1	8	4	4	0

- Molecule 20 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	
20	A	1	31	17	4	9	1	0

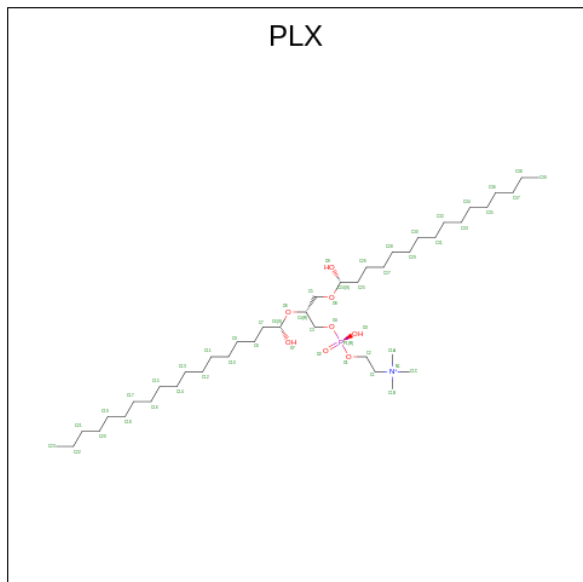
- Molecule 21 is 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (three-letter code: PEE) (formula: $C_{41}H_{78}NO_8P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
21	C	1	47	37	1	8	1	0

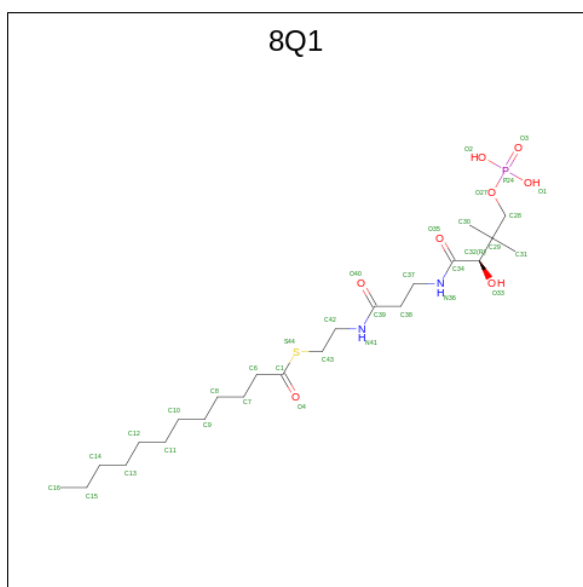
- Molecule 22 is (9R,11S)-9-({[(1S)-1-HYDROXYHEXADECYL]OXY}METHYL)-2,2-DIMETHYL-5,7,10-TRIOXA-2LAMBDA 5 -AZA-6LAMBDA 5 -PHOSPHAOCTACOSA

NE-6,6,11-TRIOL (three-letter code: PLX) (formula: $C_{42}H_{89}NO_8P$) (labeled as "Ligand of Interest" by depositor).



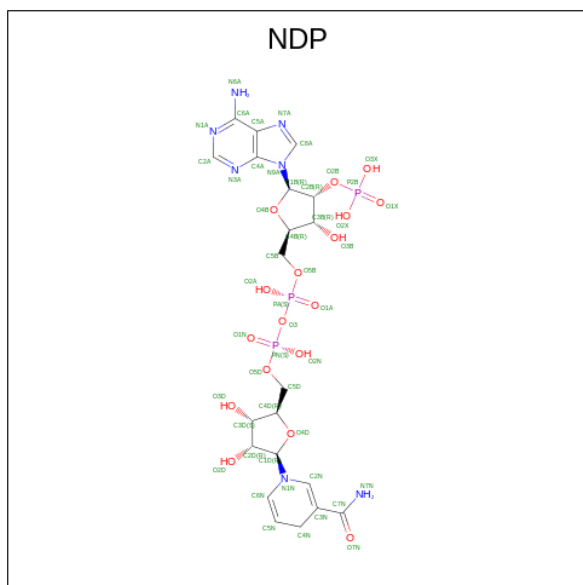
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
22	C	1	52	42	1	8	1	0

- Molecule 23 is S-[2-({N-[(2R)-2-hydroxy-3,3-dimethyl-4-(phosphonoxy)butanoyl]-beta-alanyl}amino)ethyl] dodecanethioate (three-letter code: 8Q1) (formula: $C_{23}H_{45}N_2O_8PS$) (labeled as "Ligand of Interest" by depositor).



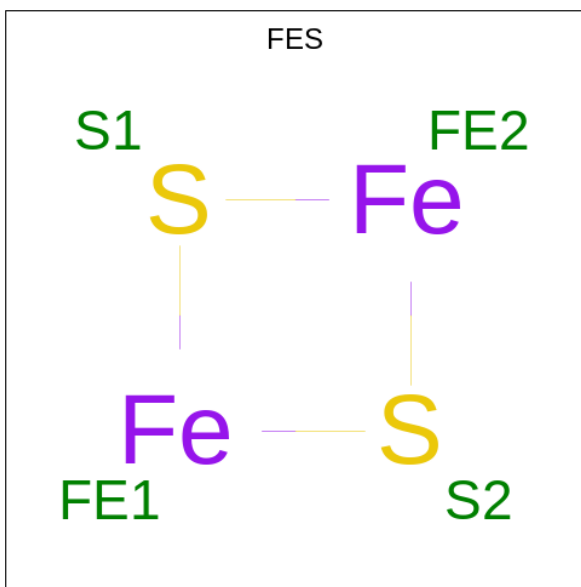
Mol	Chain	Residues	Atoms					AltConf	
			Total	C	N	O	P		S
23	G	1	35	23	2	8	1	1	0

- Molecule 24 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	
24	J	1	48	21	7	17	3	0

- Molecule 25 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2) (labeled as "Ligand of Interest" by depositor).

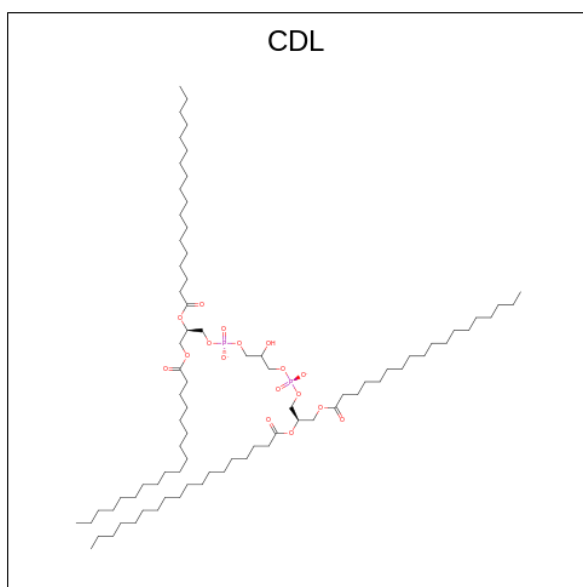


Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
25	M	1	4	2	2	0
25	O	1	4	2	2	0

- Molecule 26 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
26	M	1	1	1	0

- Molecule 27 is CARDIOLIPIN (three-letter code: CDL) (formula: C₈₁H₁₅₆O₁₇P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
27	N	1	51	32	17	2	0

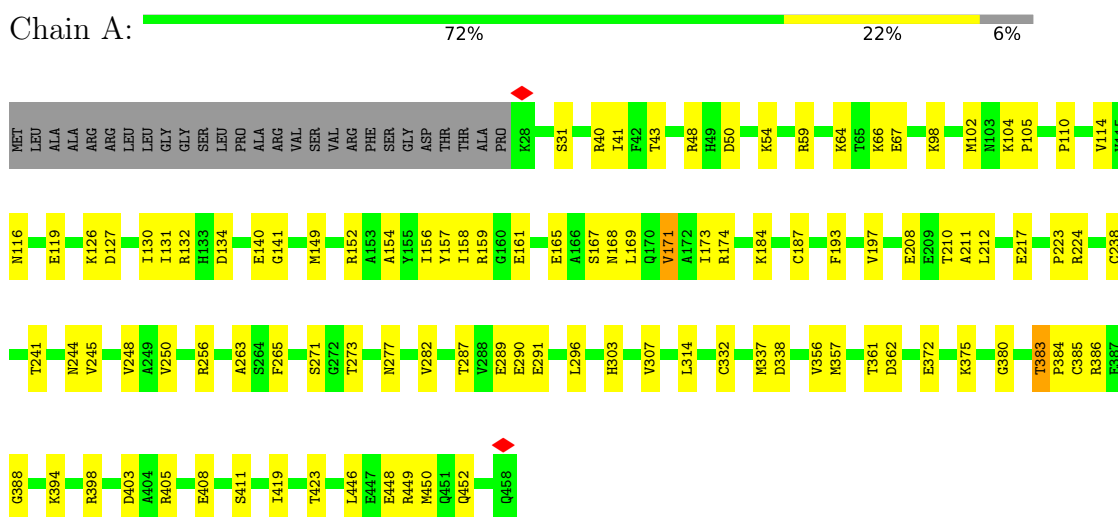
- Molecule 28 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
28	T	1	1	1	0

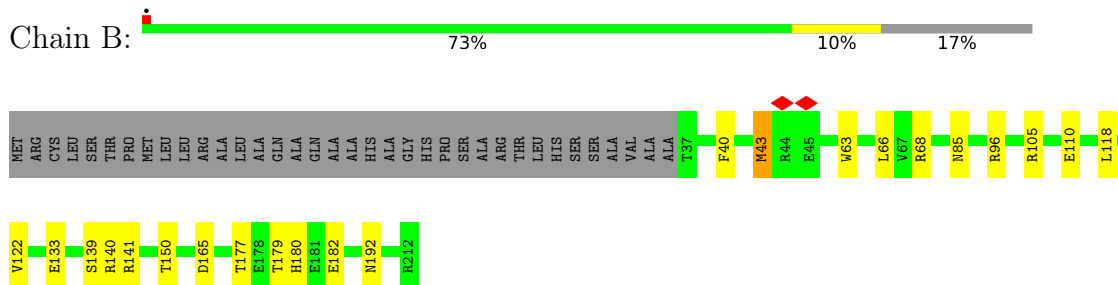
3 Residue-property plots [i](#)

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.

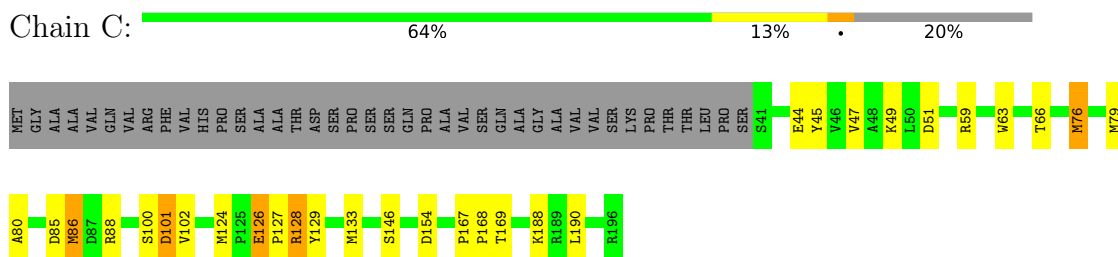
- Molecule 1: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial



- Molecule 2: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial



- Molecule 3: Complex I-20kD



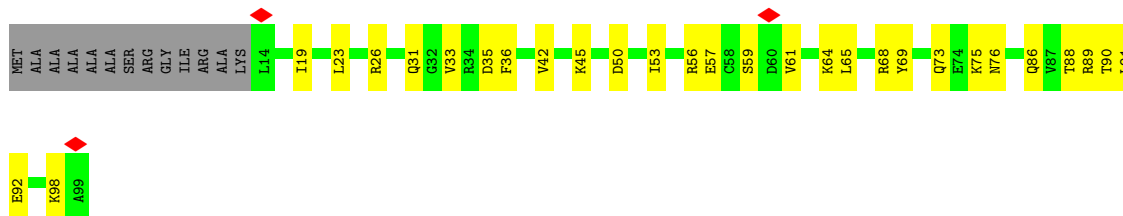
- Molecule 4: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6

Chain E:  71% 17% 10%

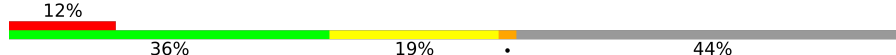


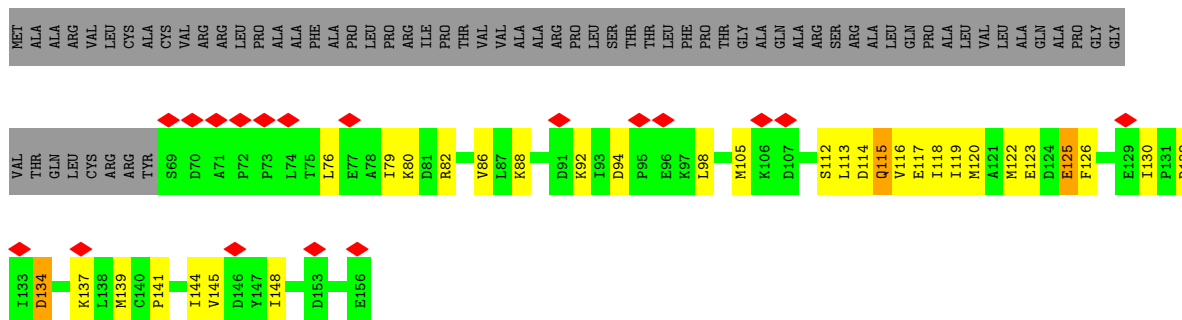
- Molecule 5: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2

Chain F:  58% 29% 13%




- Molecule 6: Acyl carrier protein, mitochondrial

Chain G:  12% 36% 19% 44%



- Molecule 7: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5

Chain H:  79% 16% 5%

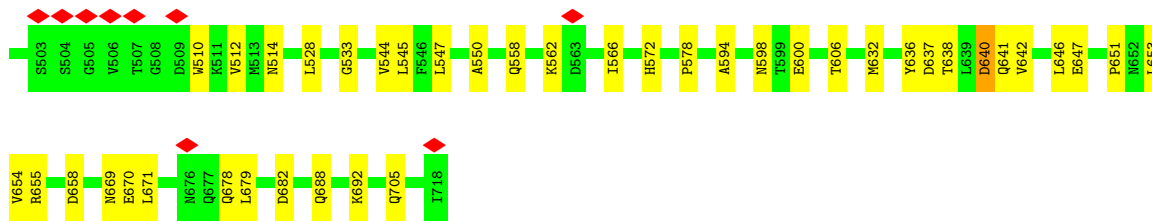


- Molecule 8: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7

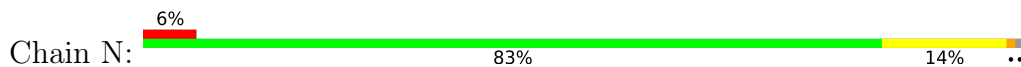
Chain I:  5% 71% 12% 14%



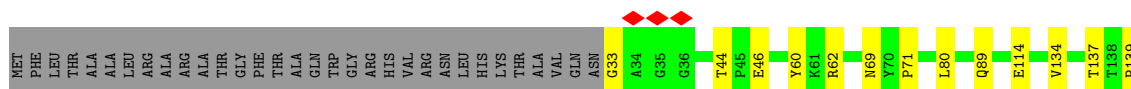
- Molecule 9: NADH dehydrogenase ubiquinone 1 alpha subcomplex subunit 9, mitochondrial



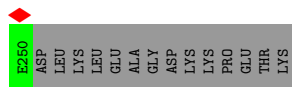
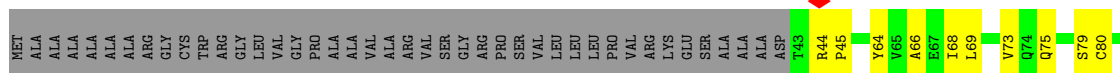
- Molecule 13: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12



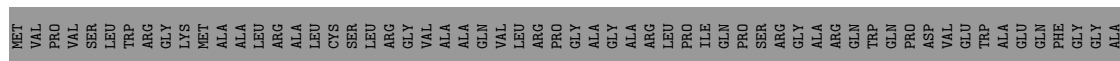
- Molecule 14: NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial

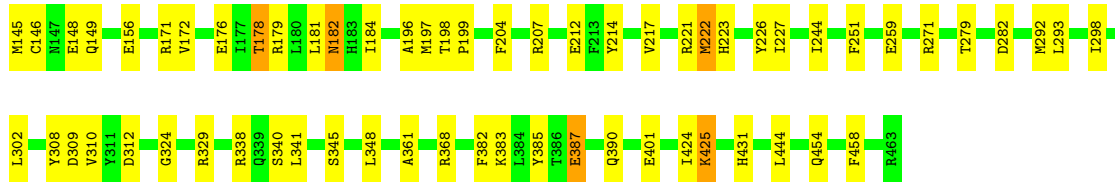


- Molecule 15: NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial

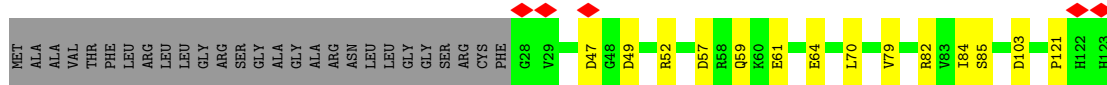


- Molecule 16: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial

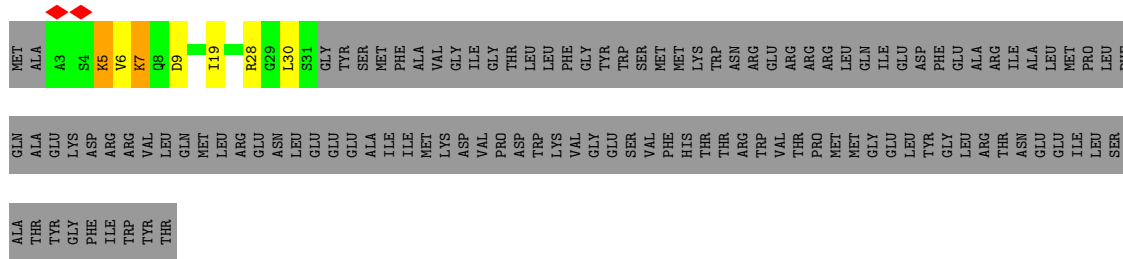




- Molecule 17: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial



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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	193234	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.230	Depositor
Minimum map value	-0.083	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0236	Depositor
Map size (Å)	354.48602, 354.48602, 354.48602	wwPDB
Map dimensions	330, 330, 330	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0742, 1.0742, 1.0742	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PEE, SF4, 2MR, MG, FES, 8Q1, NDP, CDL, PLX, FMN, ZN

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	0.25	0/3393	0.48	0/4584
2	B	0.25	0/1443	0.50	0/1952
3	C	0.27	0/1275	0.52	0/1725
4	E	0.25	0/995	0.51	0/1340
5	F	0.26	0/702	0.56	0/945
6	G	0.26	0/689	0.53	0/935
7	H	0.25	0/929	0.44	0/1258
8	I	0.25	0/798	0.53	0/1079
9	J	0.25	0/2408	0.49	0/3250
10	K	0.25	0/365	0.52	0/493
11	L	0.25	0/1039	0.50	0/1403
12	M	0.25	0/5384	0.50	0/7295
13	N	0.24	0/1245	0.49	0/1694
14	O	0.25	0/1711	0.46	0/2328
15	P	0.26	0/1789	0.50	0/2436
16	Q	0.26	0/3101	0.49	0/4189
17	T	0.26	0/755	0.51	0/1018
18	W	0.30	0/224	0.56	0/302
All	All	0.25	0/28245	0.50	0/38226

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3318	0	3280	79	0
2	B	1412	0	1363	14	0
3	C	1244	0	1250	25	0
4	E	971	0	975	17	0
5	F	691	0	704	26	0
6	G	678	0	655	42	0
7	H	910	0	950	12	0
8	I	780	0	808	13	0
9	J	2356	0	2400	32	0
10	K	355	0	329	12	0
11	L	1016	0	1016	24	0
12	M	5296	0	5326	87	0
13	N	1204	0	1162	12	0
14	O	1671	0	1673	24	0
15	P	1738	0	1693	30	0
16	Q	3044	0	3018	57	0
17	T	741	0	702	10	0
18	W	218	0	219	7	0
19	A	8	0	0	1	0
19	B	16	0	0	0	0
19	C	8	0	0	1	0
19	M	16	0	0	0	0
20	A	31	0	19	3	0
21	C	47	0	71	0	0
22	C	52	0	88	3	0
23	G	35	0	0	5	0
24	J	48	0	25	2	0
25	M	4	0	0	0	0
25	O	4	0	0	0	0
26	M	1	0	0	0	0
27	N	51	0	46	0	0
28	T	1	0	0	0	0
All	All	27965	0	27772	451	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.

The worst 5 of 451 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)
6:G:112:SER:CB	23:G:201:8Q1:O1	1.70	1.38
3:C:126:GLU:CB	3:C:127:PRO:CD	2.19	1.18
24:J:401:NDP:O4D	24:J:401:NDP:C4D	1.68	1.18
6:G:86:VAL:HG21	6:G:122:MET:HE1	1.25	1.12
6:G:114:ASP:O	6:G:118:ILE:HD12	1.51	1.09

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	429/458 (94%)	422 (98%)	7 (2%)	0	100	100
2	B	174/212 (82%)	172 (99%)	2 (1%)	0	100	100
3	C	154/196 (79%)	149 (97%)	4 (3%)	1 (1%)	25	56
4	E	113/128 (88%)	110 (97%)	3 (3%)	0	100	100
5	F	84/99 (85%)	80 (95%)	4 (5%)	0	100	100
6	G	86/156 (55%)	82 (95%)	4 (5%)	0	100	100
7	H	110/116 (95%)	103 (94%)	7 (6%)	0	100	100
8	I	93/113 (82%)	83 (89%)	10 (11%)	0	100	100
9	J	289/376 (77%)	280 (97%)	9 (3%)	0	100	100
10	K	40/110 (36%)	40 (100%)	0	0	100	100
11	L	123/175 (70%)	120 (98%)	3 (2%)	0	100	100
12	M	688/718 (96%)	669 (97%)	19 (3%)	0	100	100
13	N	142/145 (98%)	138 (97%)	4 (3%)	0	100	100
14	O	215/249 (86%)	209 (97%)	6 (3%)	0	100	100
15	P	206/264 (78%)	195 (95%)	11 (5%)	0	100	100
16	Q	374/473 (79%)	360 (96%)	14 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	T	94/123 (76%)	92 (98%)	2 (2%)	0	100	100
18	W	27/144 (19%)	26 (96%)	1 (4%)	0	100	100
All	All	3441/4255 (81%)	3330 (97%)	110 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	126	GLU

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	345/365 (94%)	340 (99%)	5 (1%)	67	90
2	B	151/176 (86%)	147 (97%)	4 (3%)	46	79
3	C	131/163 (80%)	125 (95%)	6 (5%)	27	60
4	E	107/112 (96%)	102 (95%)	5 (5%)	26	59
5	F	76/82 (93%)	74 (97%)	2 (3%)	46	79
6	G	72/132 (54%)	66 (92%)	6 (8%)	11	32
7	H	99/101 (98%)	93 (94%)	6 (6%)	18	48
8	I	87/98 (89%)	83 (95%)	4 (5%)	27	60
9	J	254/322 (79%)	243 (96%)	11 (4%)	29	62
10	K	41/92 (45%)	38 (93%)	3 (7%)	14	38
11	L	113/152 (74%)	109 (96%)	4 (4%)	36	70
12	M	580/602 (96%)	566 (98%)	14 (2%)	49	81
13	N	130/131 (99%)	122 (94%)	8 (6%)	18	47
14	O	183/207 (88%)	178 (97%)	5 (3%)	44	78
15	P	190/228 (83%)	184 (97%)	6 (3%)	39	73
16	Q	327/401 (82%)	318 (97%)	9 (3%)	43	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	T	79/97 (81%)	79 (100%)	0	100	100
18	W	23/124 (18%)	20 (87%)	3 (13%)	4	13
All	All	2988/3585 (83%)	2887 (97%)	101 (3%)	40	71

5 of 101 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	M	283	GLU
13	N	27	LEU
18	W	7	LYS
12	M	336	ASN
12	M	562	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	185	ASN
12	M	260	ASN
12	M	604	GLN
17	T	63	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](#)

1 non-standard protein/DNA/RNA residue is 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
16	2MR	Q	118	16	10,12,13	1.95	1 (10%)	5,13,15	6.15	3 (60%)

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
16	2MR	Q	118	16	-	3/10/13/15	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	Q	118	2MR	CZ-NE	5.60	1.46	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Q	118	2MR	NE-CZ-NH2	12.59	131.03	119.48
16	Q	118	2MR	CD-NE-CZ	4.52	131.88	123.41
16	Q	118	2MR	CQ2-NH2-CZ	3.03	130.56	123.86

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
16	Q	118	2MR	NE-CD-CG-CB
16	Q	118	2MR	CA-CB-CG-CD
16	Q	118	2MR	N-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	Q	118	2MR	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 2 are monoatomic - leaving 14 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
19	SF4	B	301	2	0,12,12	-	-	-		
19	SF4	M	802	12	0,12,12	-	-	-		
23	8Q1	G	201	-	31,34,34	1.71	6 (19%)	40,43,43	1.63	6 (15%)
19	SF4	B	302	2	0,12,12	-	-	-		
25	FES	M	803	12	0,4,4	-	-	-		
22	PLX	C	303	-	51,51,51	1.14	4 (7%)	55,59,59	0.62	1 (1%)
19	SF4	M	801	12	0,12,12	-	-	-		
20	FMN	A	502	-	33,33,33	1.09	2 (6%)	48,50,50	1.20	7 (14%)
25	FES	O	301	14	0,4,4	-	-	-		
27	CDL	N	201	-	50,50,99	1.41	9 (18%)	56,62,111	1.12	4 (7%)
21	PEE	C	302	-	46,46,50	1.21	6 (13%)	49,51,55	0.97	2 (4%)
24	NDP	J	401	-	45,52,52	4.57	20 (44%)	53,80,80	1.93	6 (11%)
19	SF4	A	501	1	0,12,12	-	-	-		
19	SF4	C	301	16,3	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 Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
19	SF4	B	301	2	-	-	0/6/5/5
19	SF4	M	802	12	-	-	0/6/5/5
23	8Q1	G	201	-	-	14/41/41/41	-
19	SF4	B	302	2	-	-	0/6/5/5
25	FES	M	803	12	-	-	0/1/1/1
22	PLX	C	303	-	-	27/55/55/55	-
19	SF4	M	801	12	-	-	0/6/5/5
20	FMN	A	502	-	-	5/18/18/18	0/3/3/3
25	FES	O	301	14	-	-	0/1/1/1
27	CDL	N	201	-	-	33/61/61/110	-
21	PEE	C	302	-	-	21/50/50/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	NDP	J	401	-	-	7/30/77/77	0/4/5/5
19	SF4	A	501	1	-	-	0/6/5/5
19	SF4	C	301	16,3	-	-	0/6/5/5

The worst 5 of 47 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	J	401	NDP	C3B-C2B	-12.98	1.24	1.52
24	J	401	NDP	C6N-C5N	12.41	1.55	1.33
24	J	401	NDP	O4D-C4D	10.71	1.68	1.45
24	J	401	NDP	C3D-C4D	-9.84	1.27	1.53
24	J	401	NDP	O4B-C1B	8.57	1.53	1.41

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	J	401	NDP	C3N-C2N-N1N	-7.92	111.80	123.10
24	J	401	NDP	C1D-N1N-C2N	-6.90	109.62	121.11
23	G	201	8Q1	C6-C1-S44	6.15	120.62	113.46
24	J	401	NDP	C1D-N1N-C6N	-5.08	109.89	120.83
24	J	401	NDP	N3A-C2A-N1A	-4.10	122.28	128.68

There are no chirality outliers.

5 of 107 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
20	A	502	FMN	N10-C1'-C2'-O2'
20	A	502	FMN	N10-C1'-C2'-C3'
22	C	303	PLX	O7-C6-O6-C4
22	C	303	PLX	C3-C4-O6-C6
22	C	303	PLX	N1-C1-C2-O1

There are no ring outliers.

6 monomers are involved in 15 short contacts:

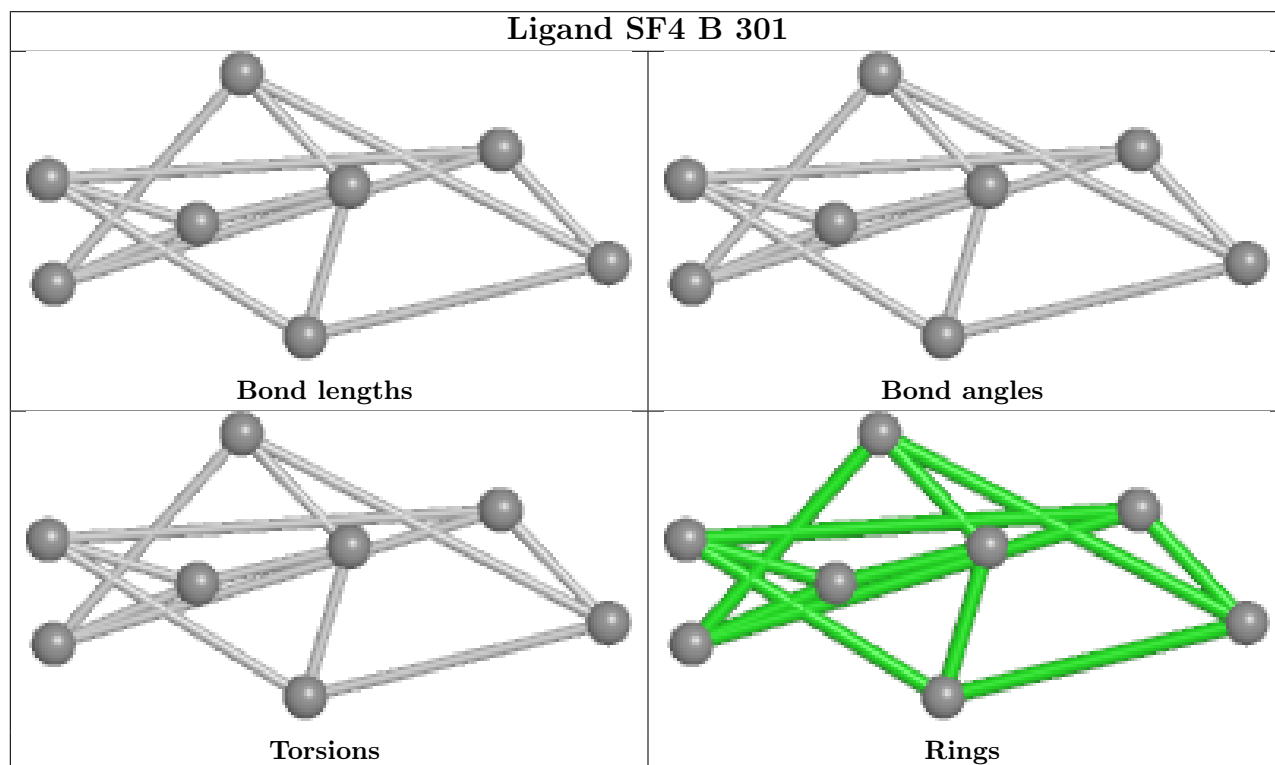
Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	G	201	8Q1	5	0
22	C	303	PLX	3	0
20	A	502	FMN	3	0
24	J	401	NDP	2	0
19	A	501	SF4	1	0

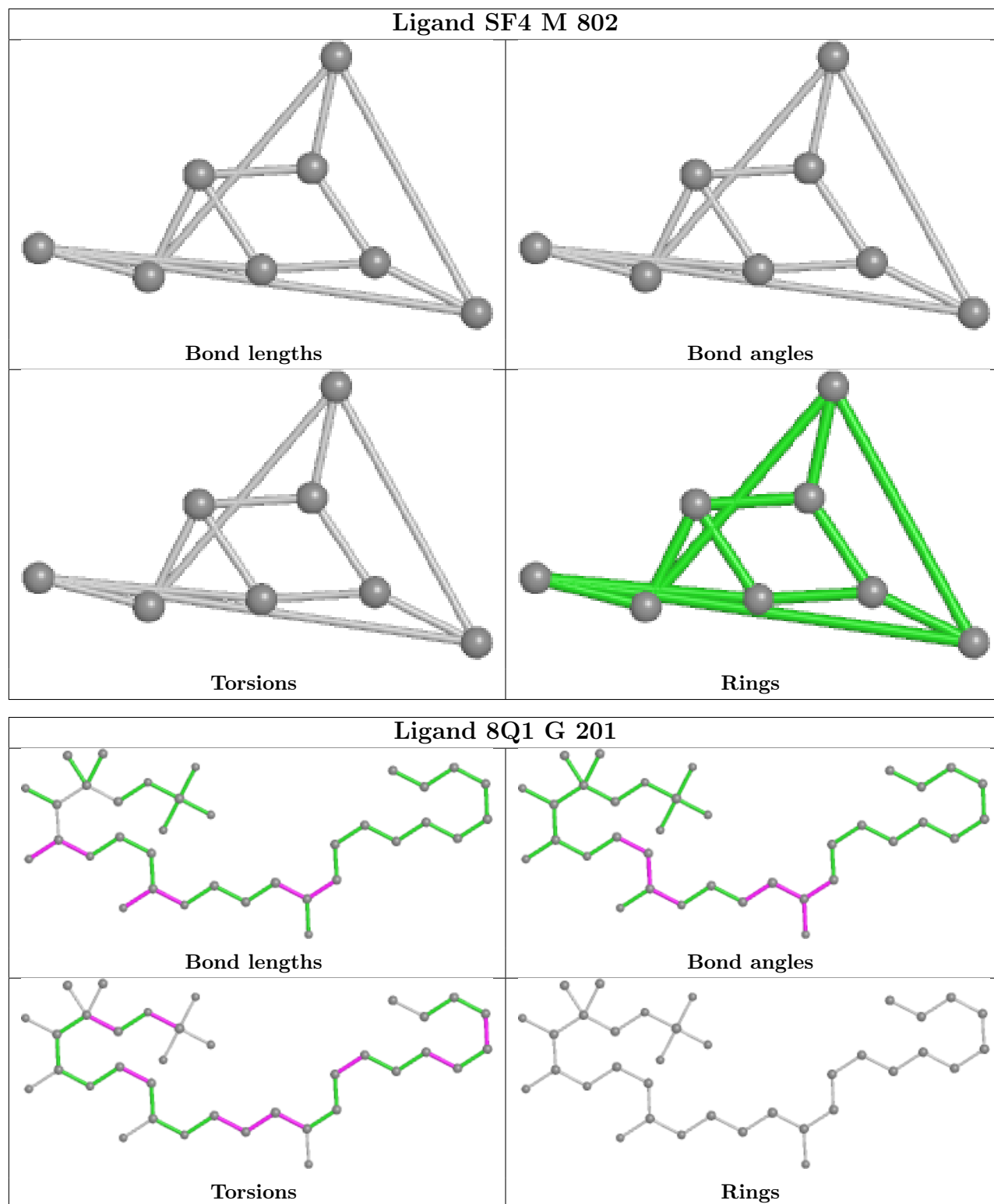
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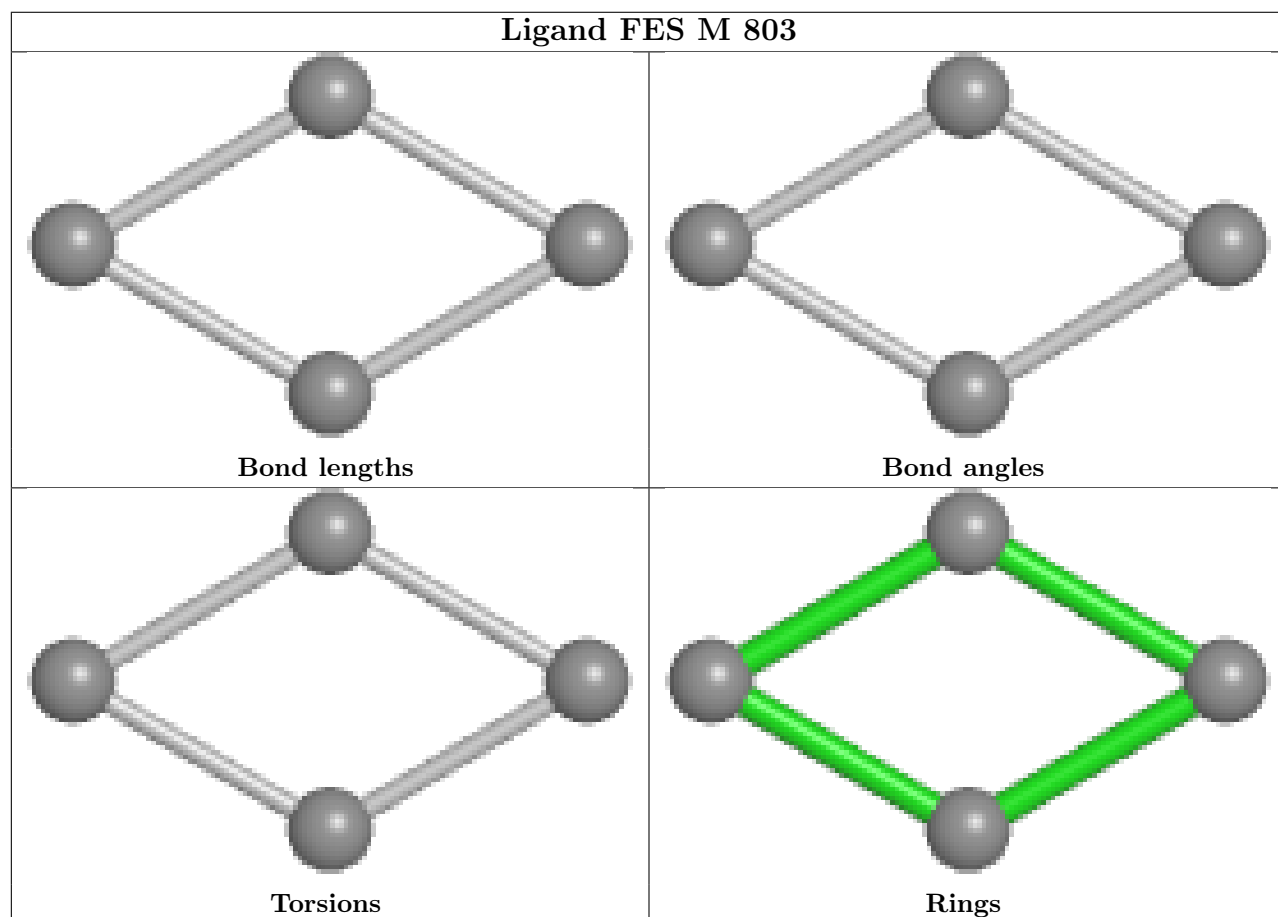
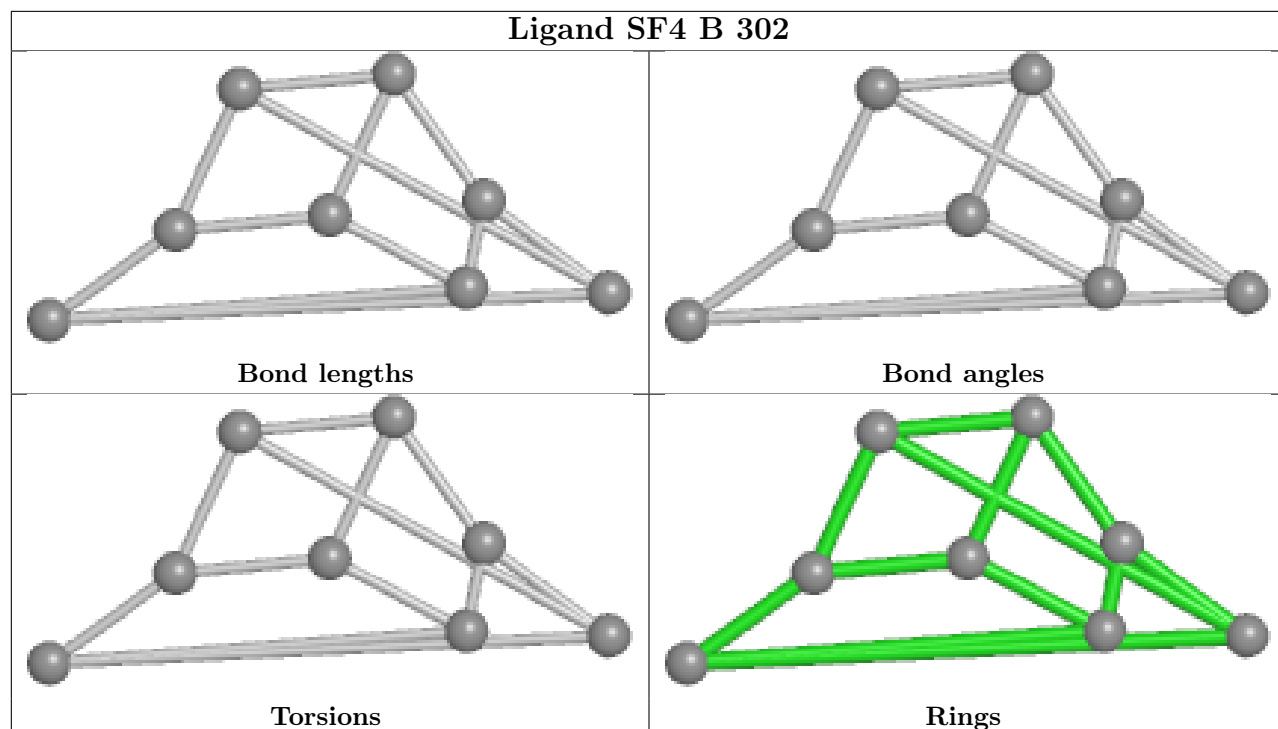
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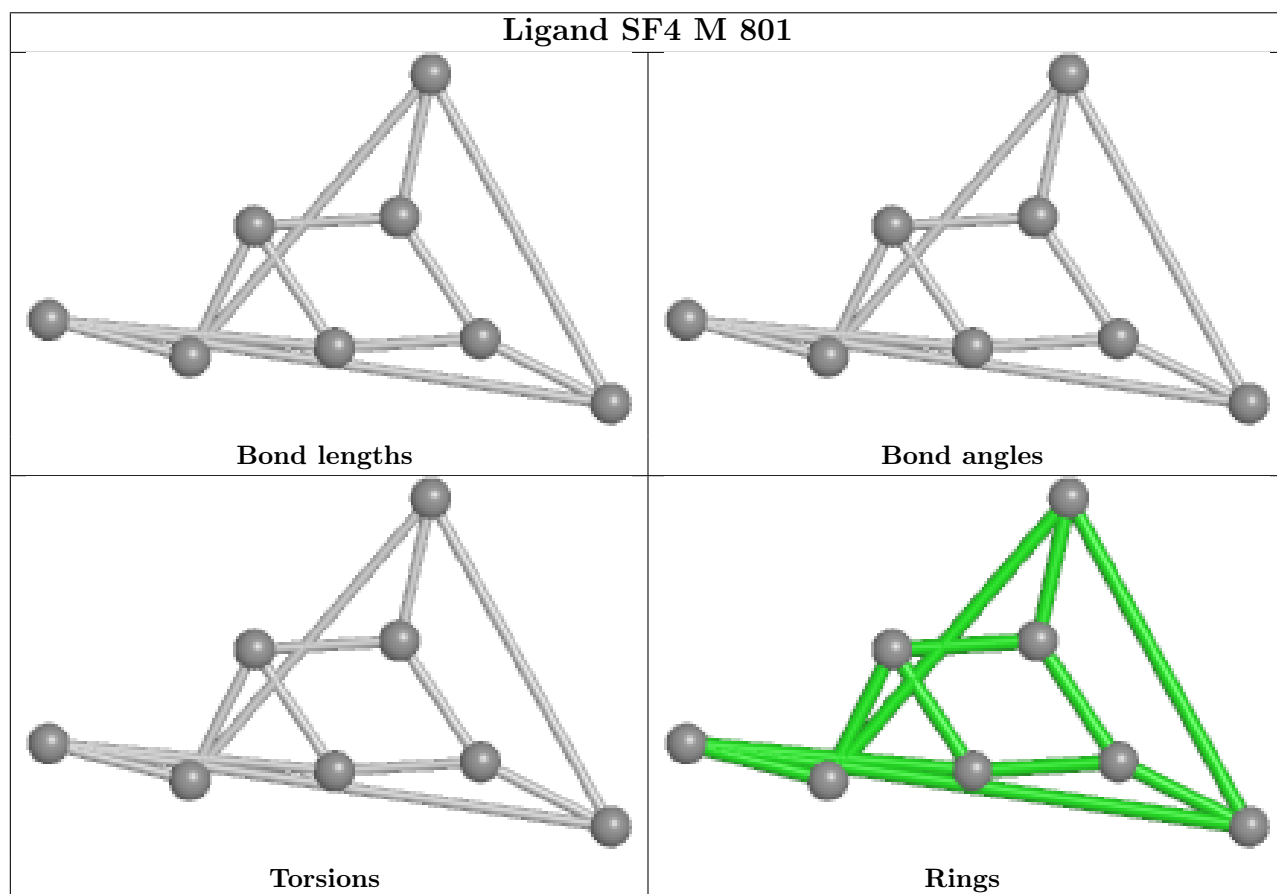
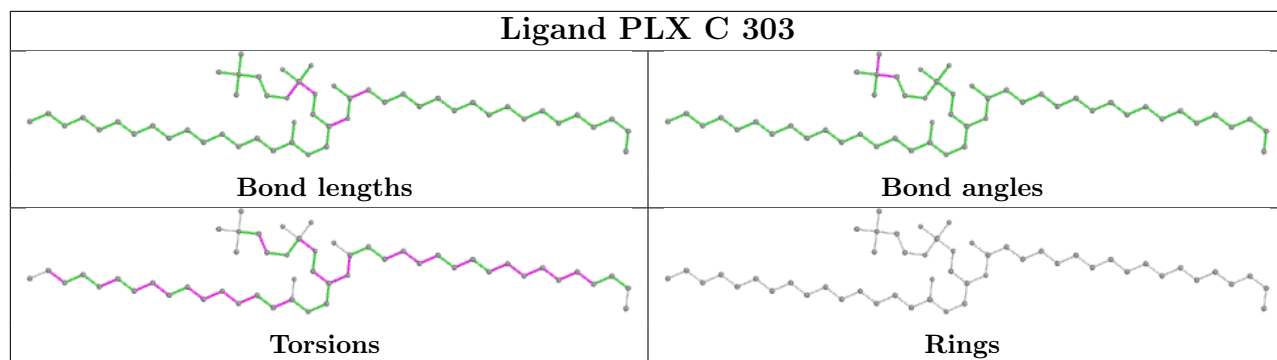
Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	C	301	SF4	1	0

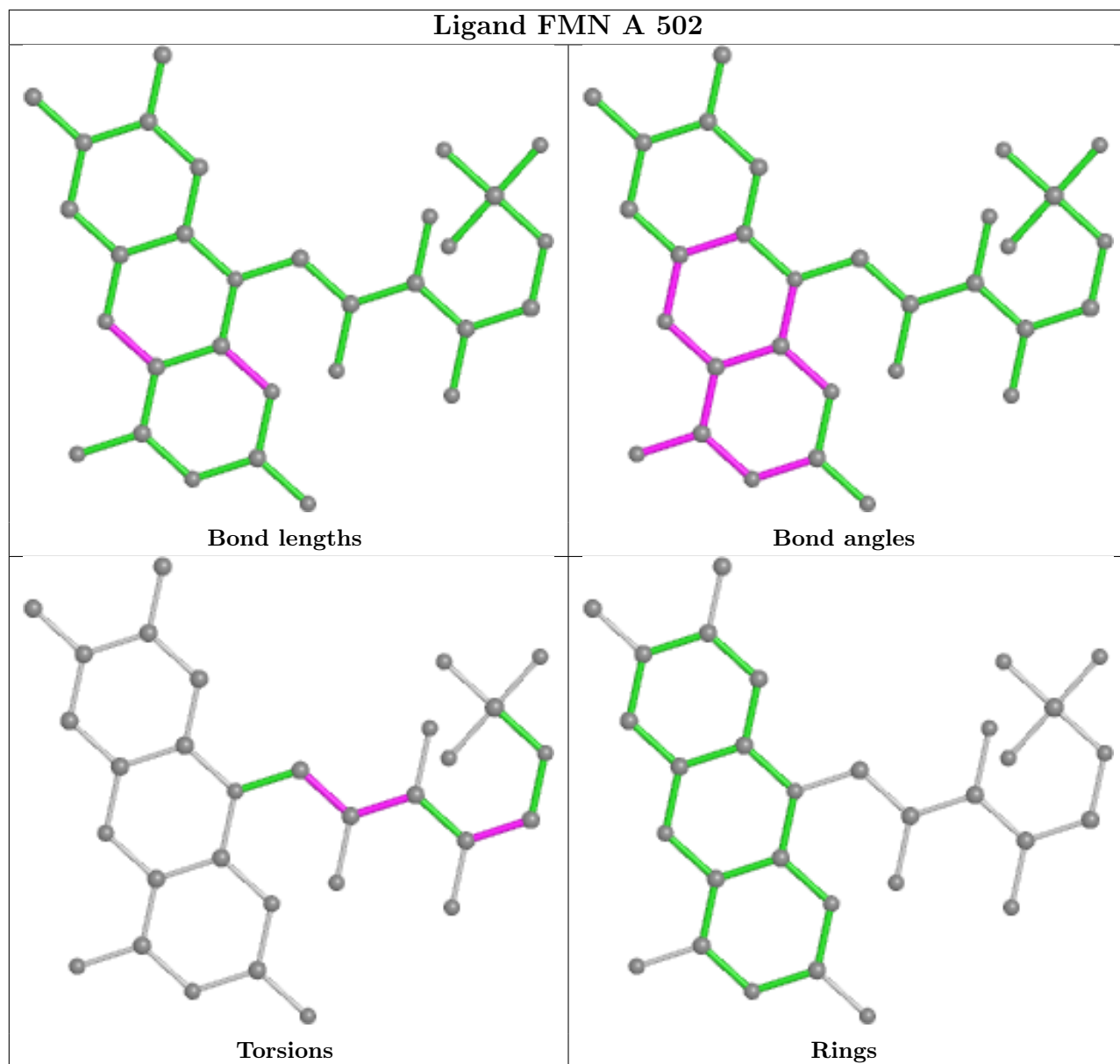
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

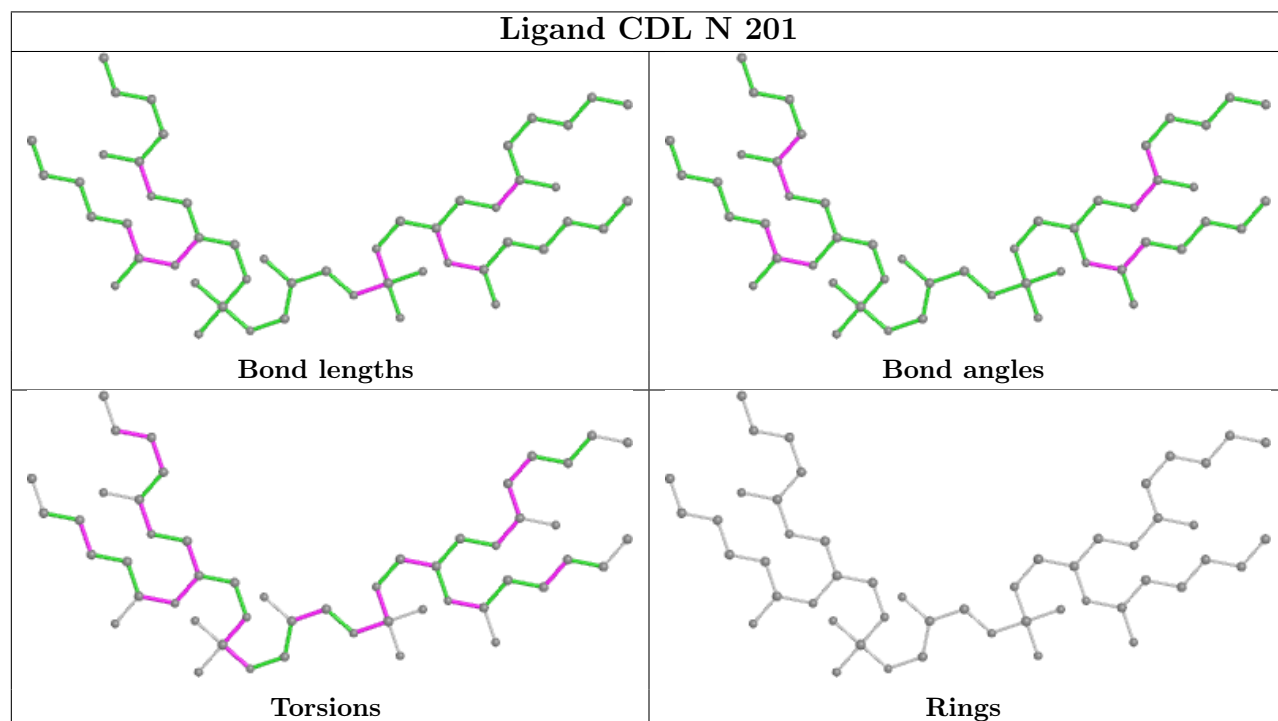
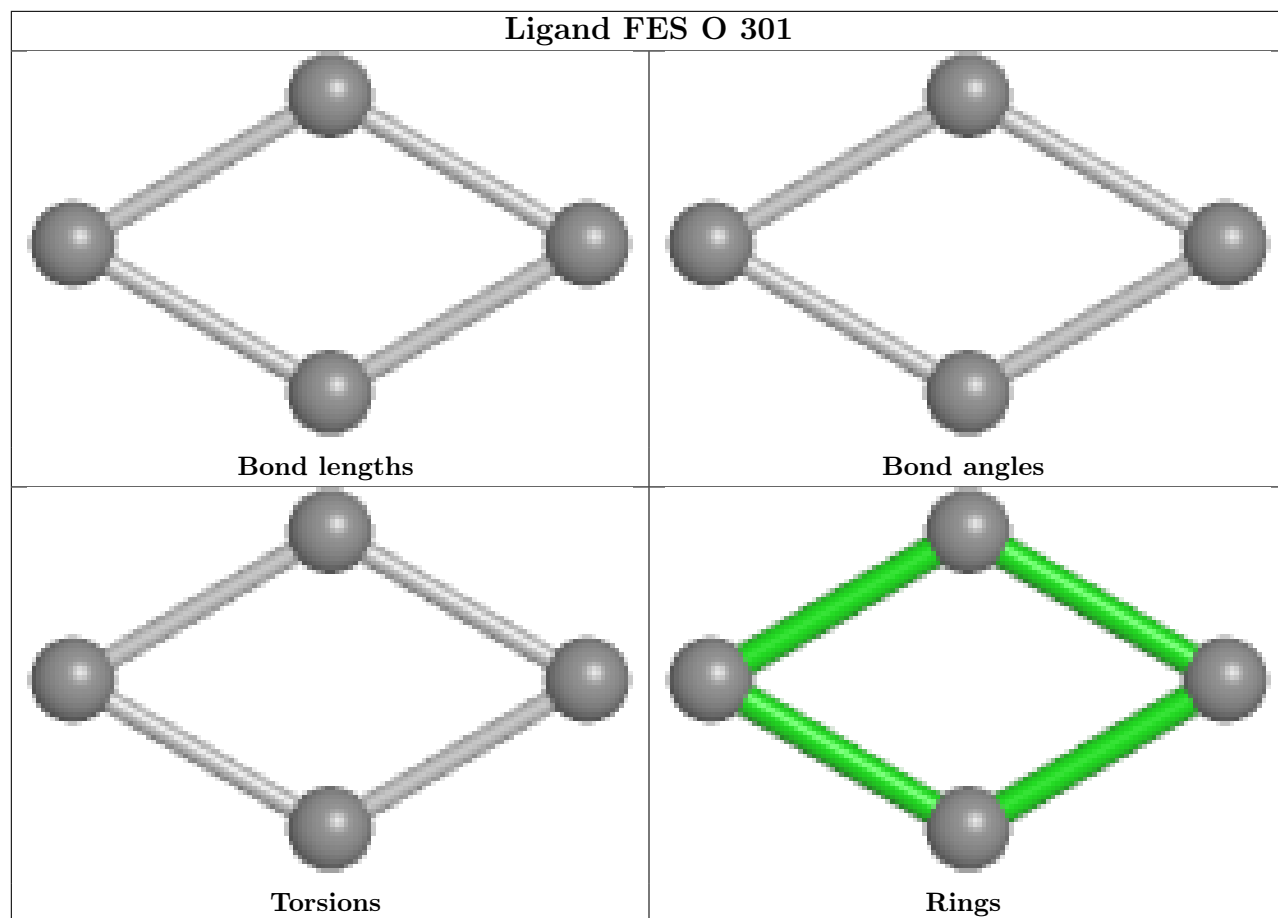


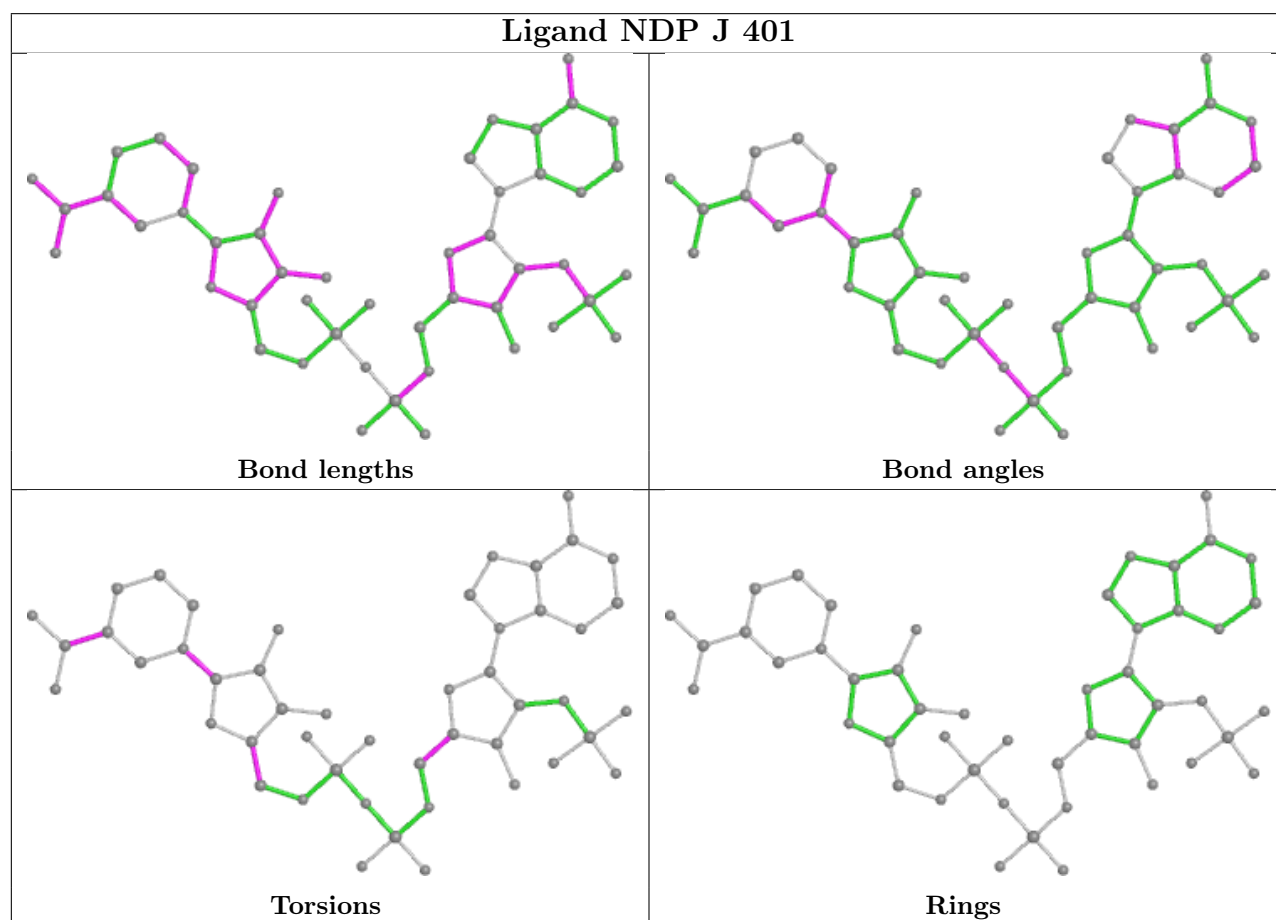
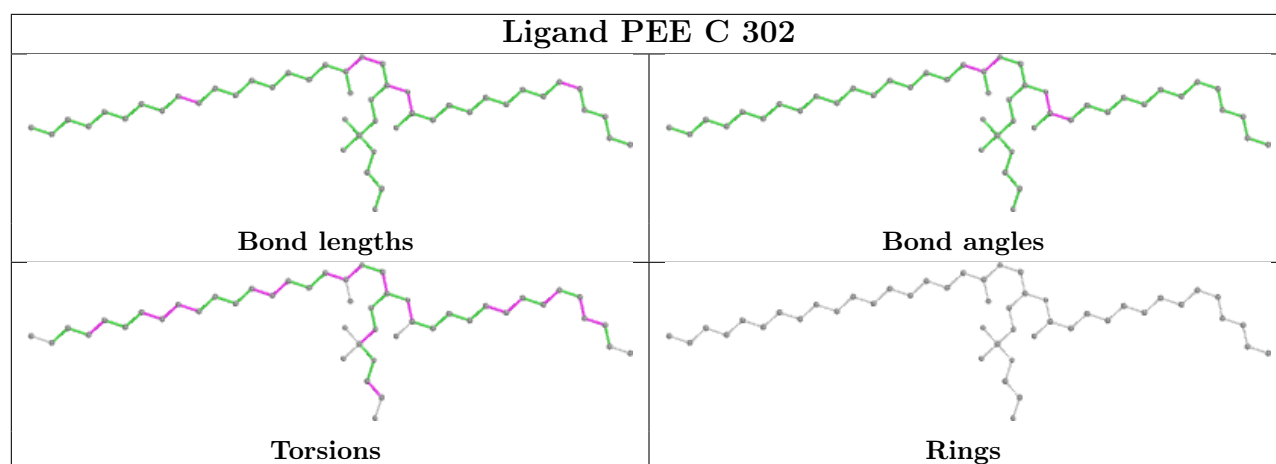


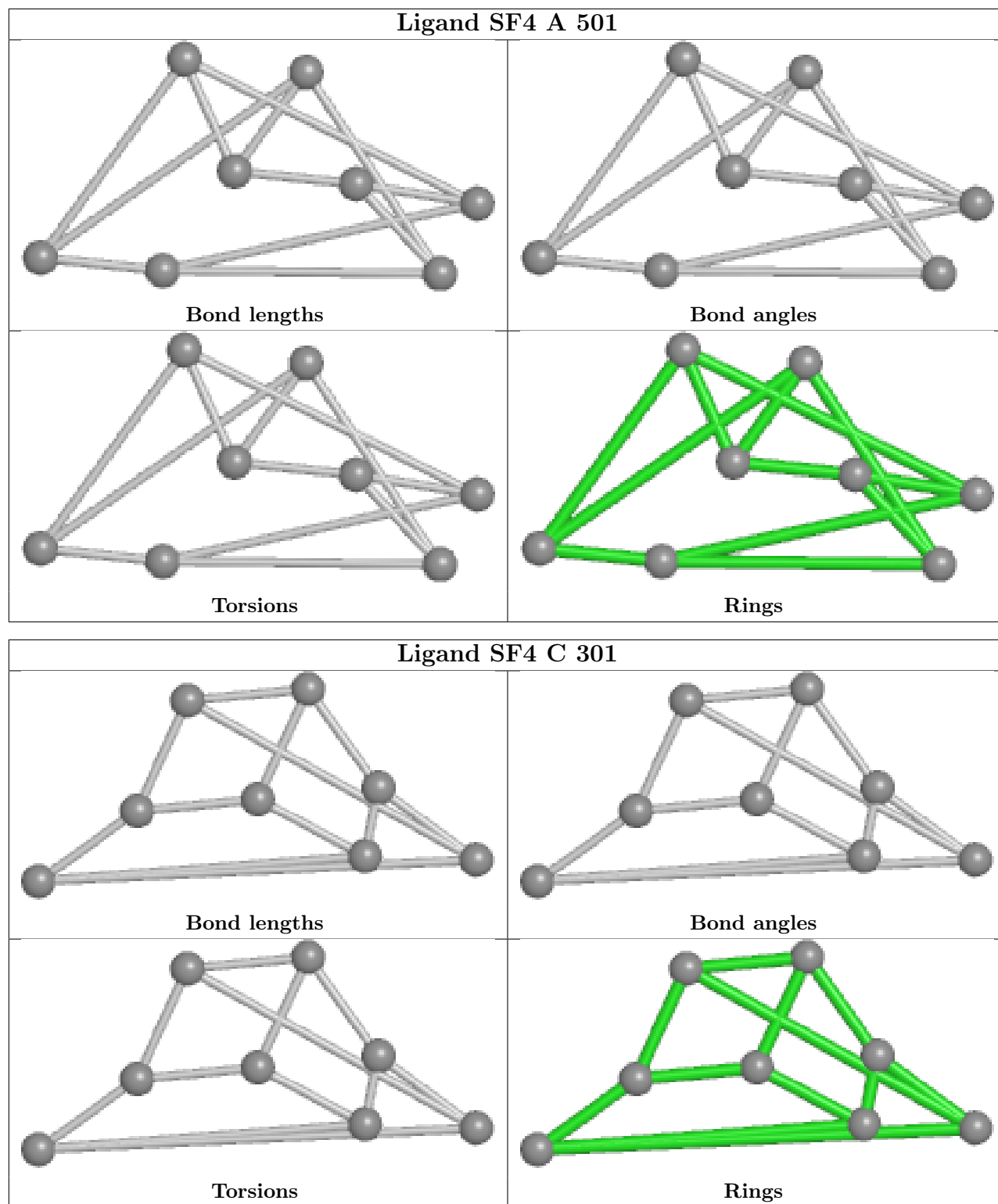












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

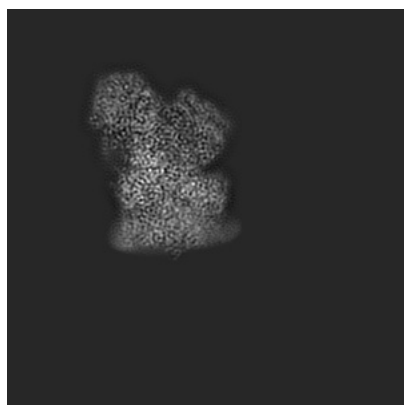
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32188. These allow visual inspection of the internal detail of the map and identification of artifacts.

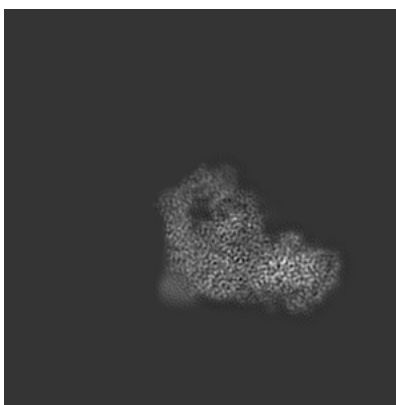
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

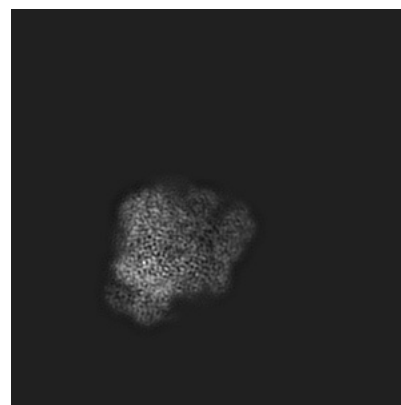
6.1.1 Primary map



X



Y

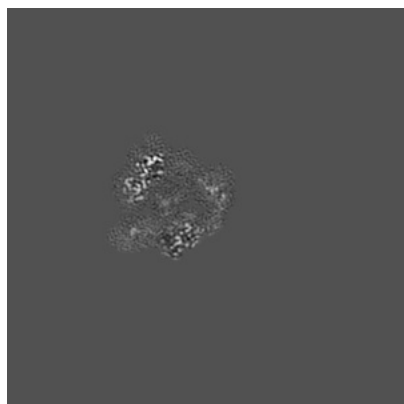


Z

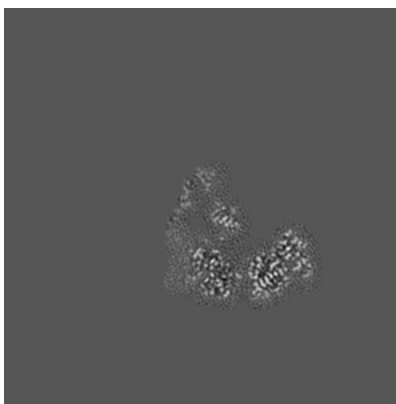
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

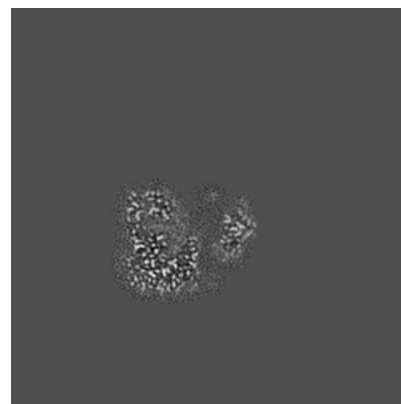
6.2.1 Primary map



X Index: 165



Y Index: 165

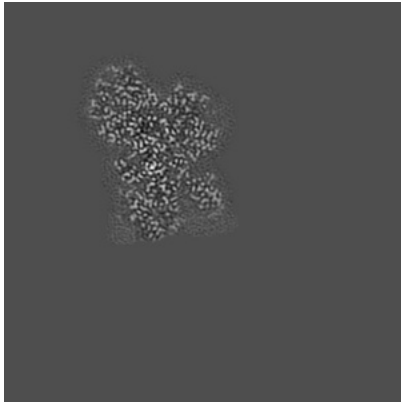


Z Index: 165

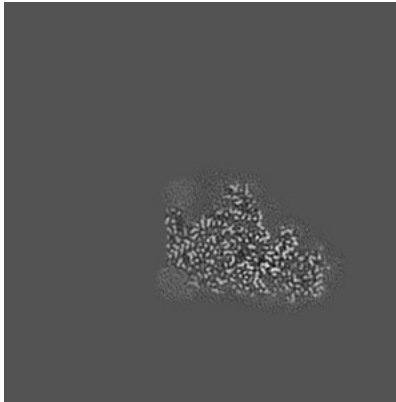
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

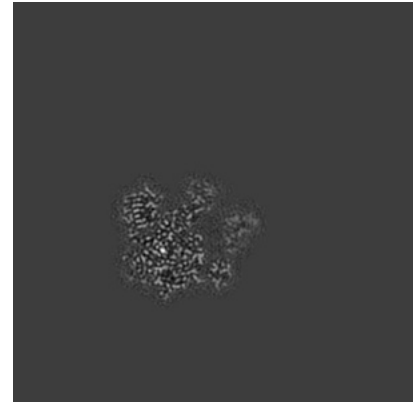
6.3.1 Primary map



X Index: 117



Y Index: 115

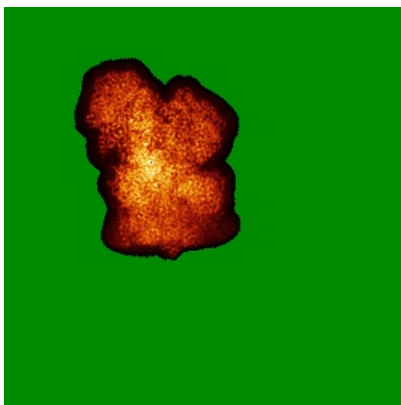


Z Index: 183

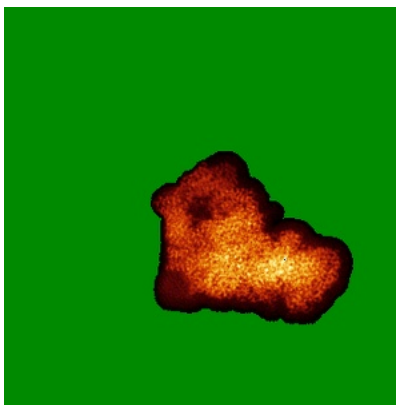
The images above show the largest variance slices of the map in three orthogonal directions.

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

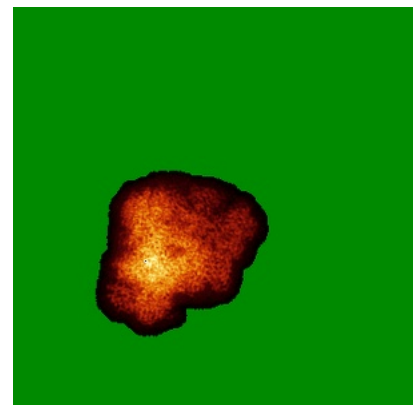
6.4.1 Primary map



X



Y

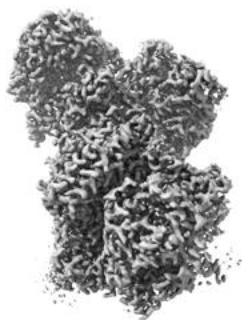


Z

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

6.5 Orthogonal surface views [i](#)

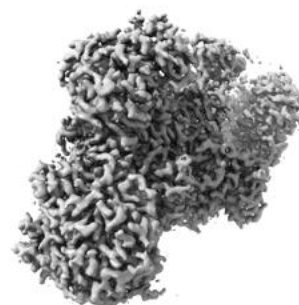
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0236. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

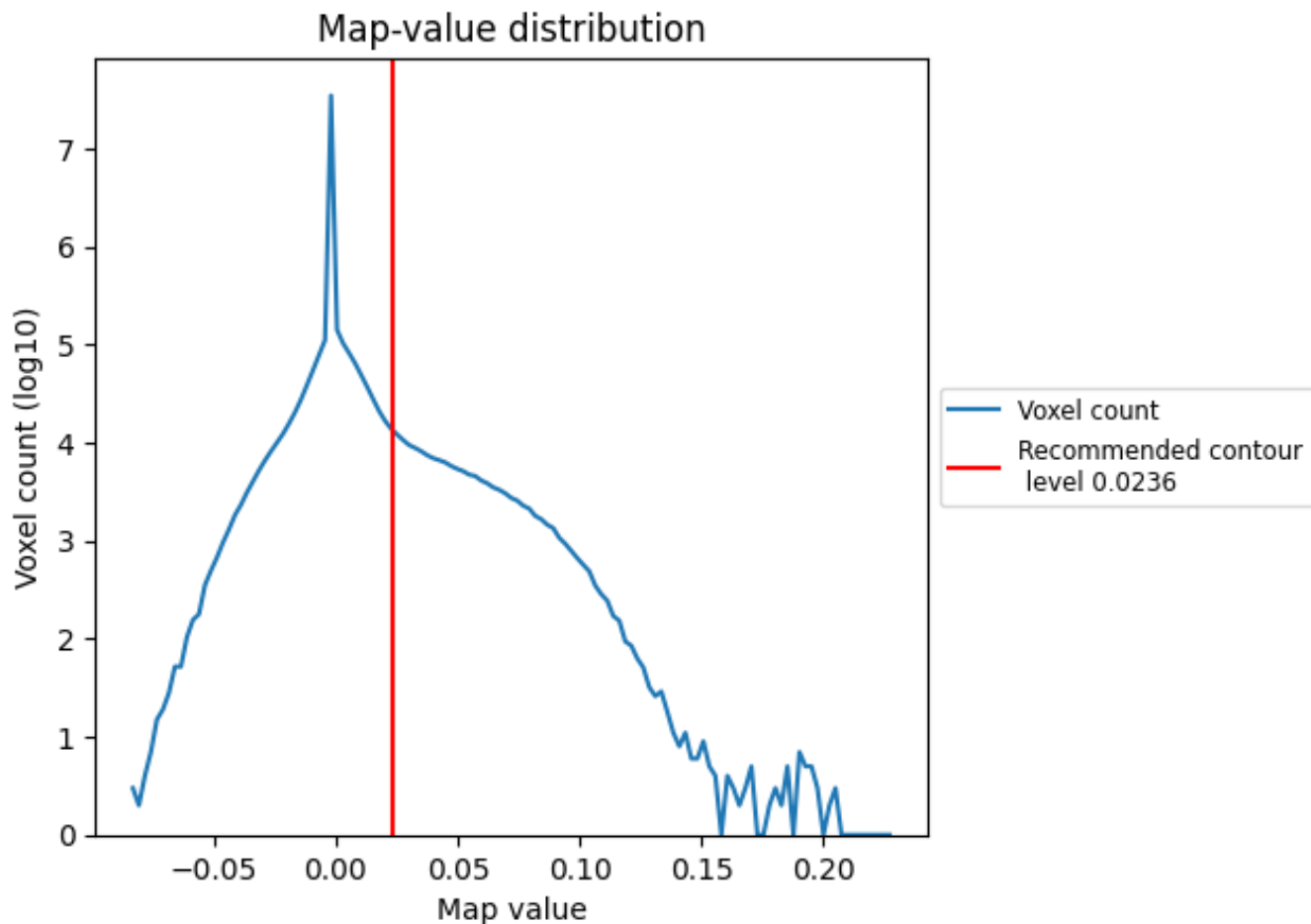
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

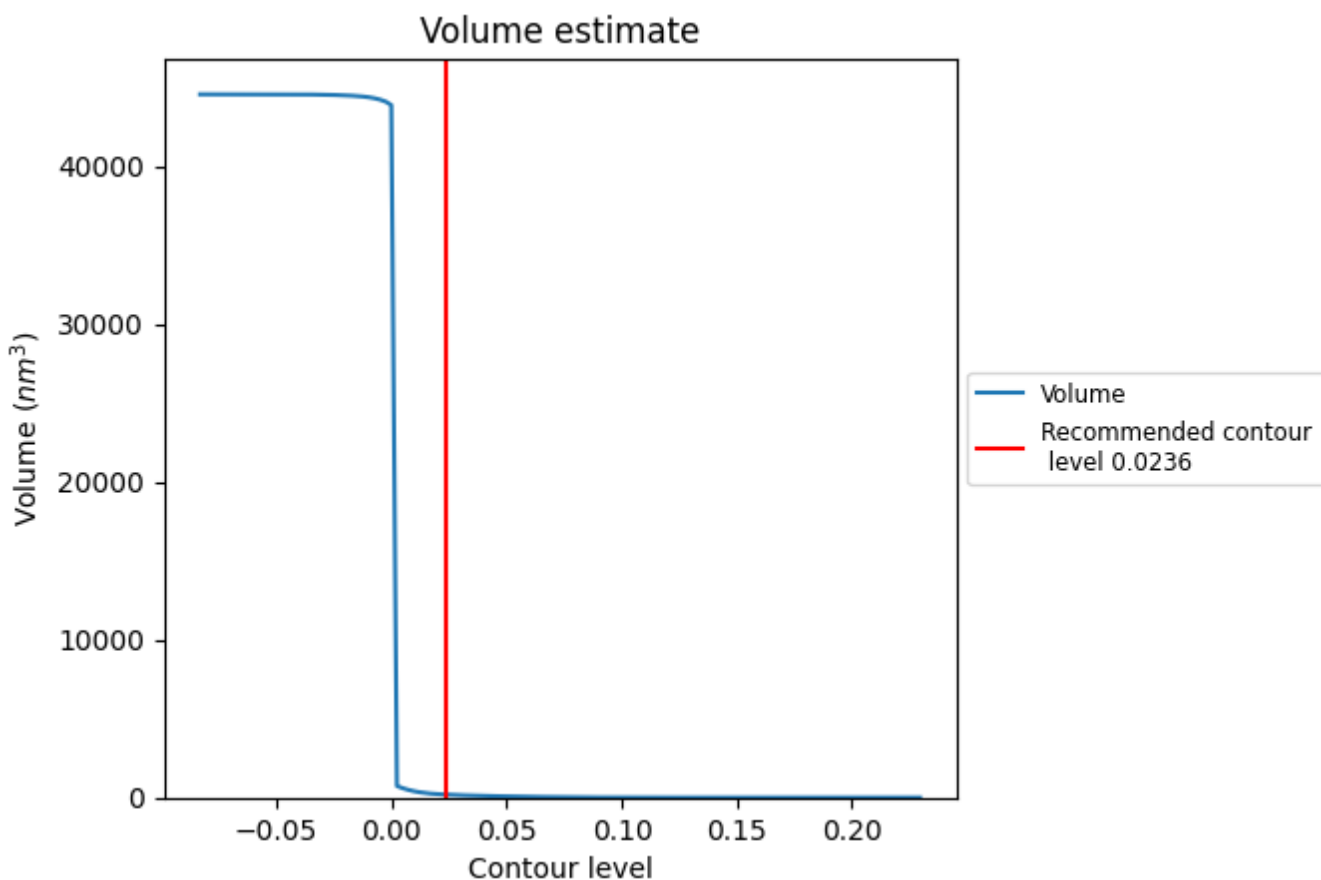
This section contains the results of statistical analysis of the map.

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.

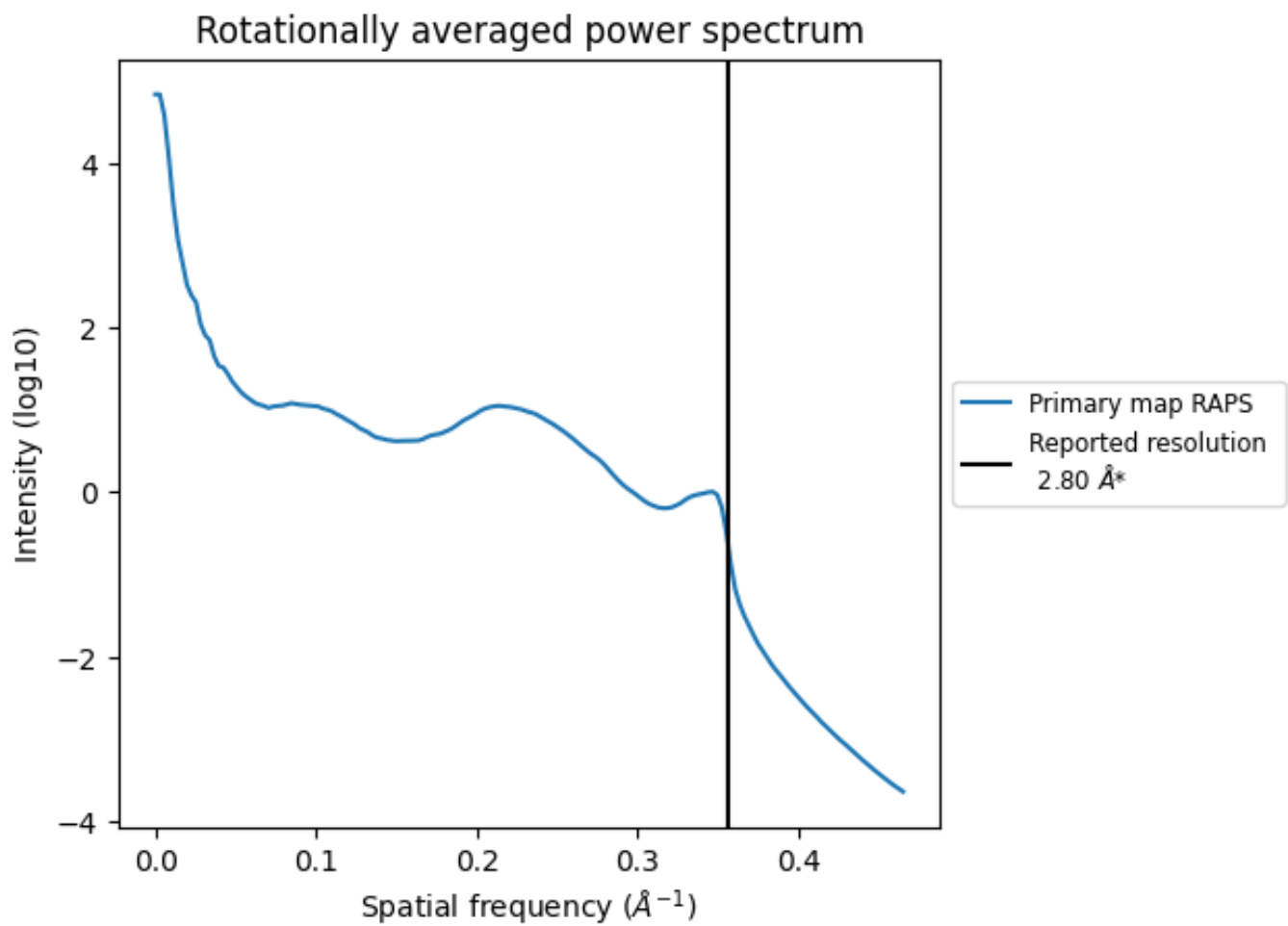
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 188 nm^3 ; this corresponds to an approximate mass of 169 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 0.357\AA^{-1}

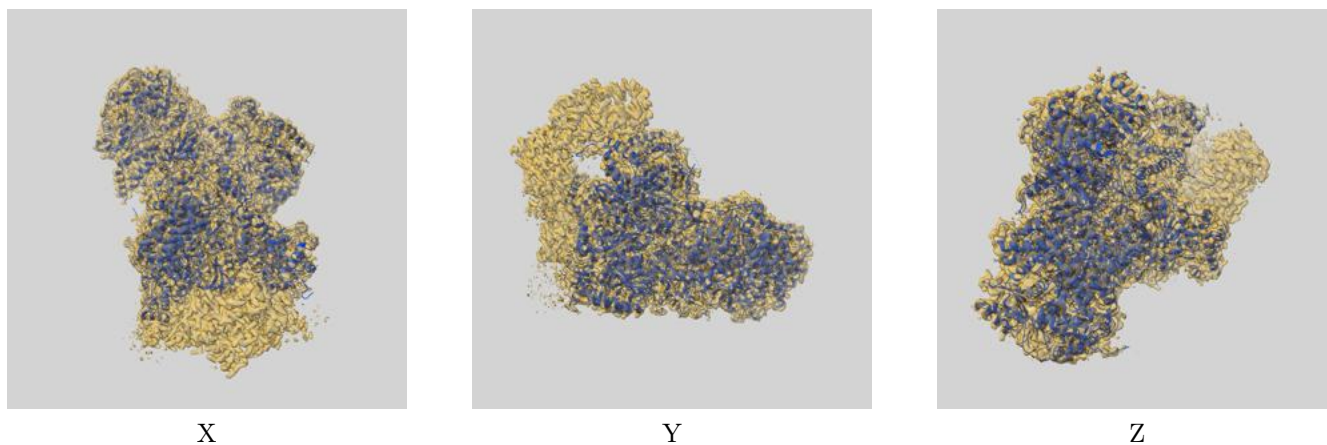
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

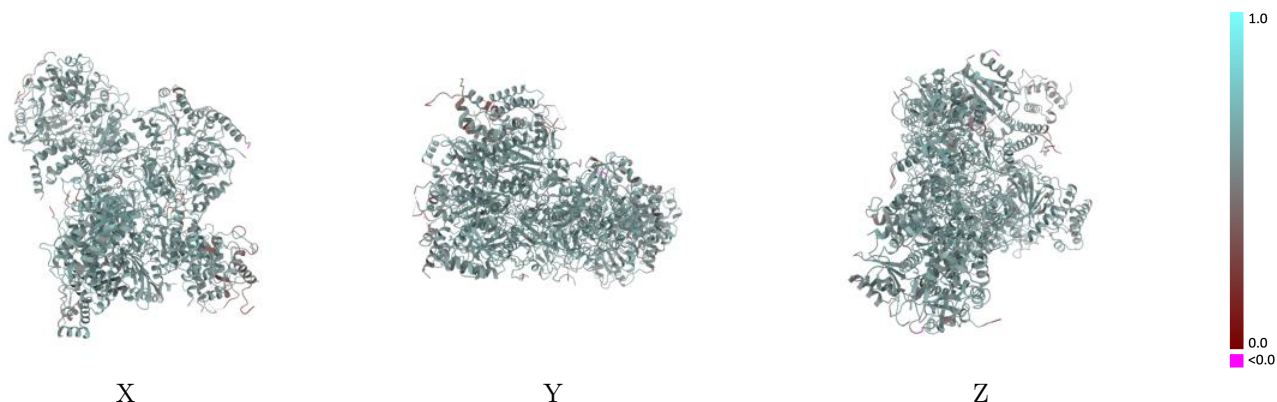
This section contains information regarding the fit between EMDB map EMD-32188 and PDB model 7VXU. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



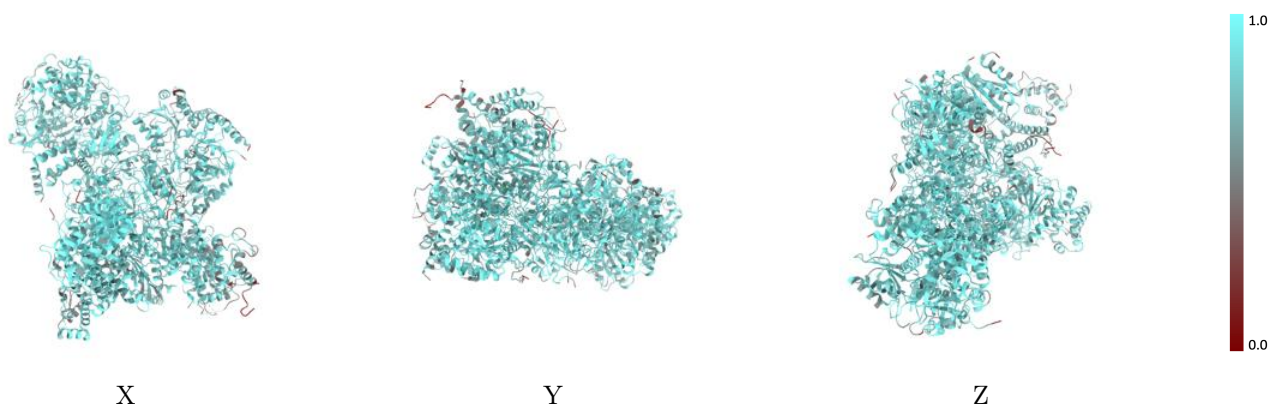
The images above show the 3D surface view of the map at the recommended contour level 0.0236 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



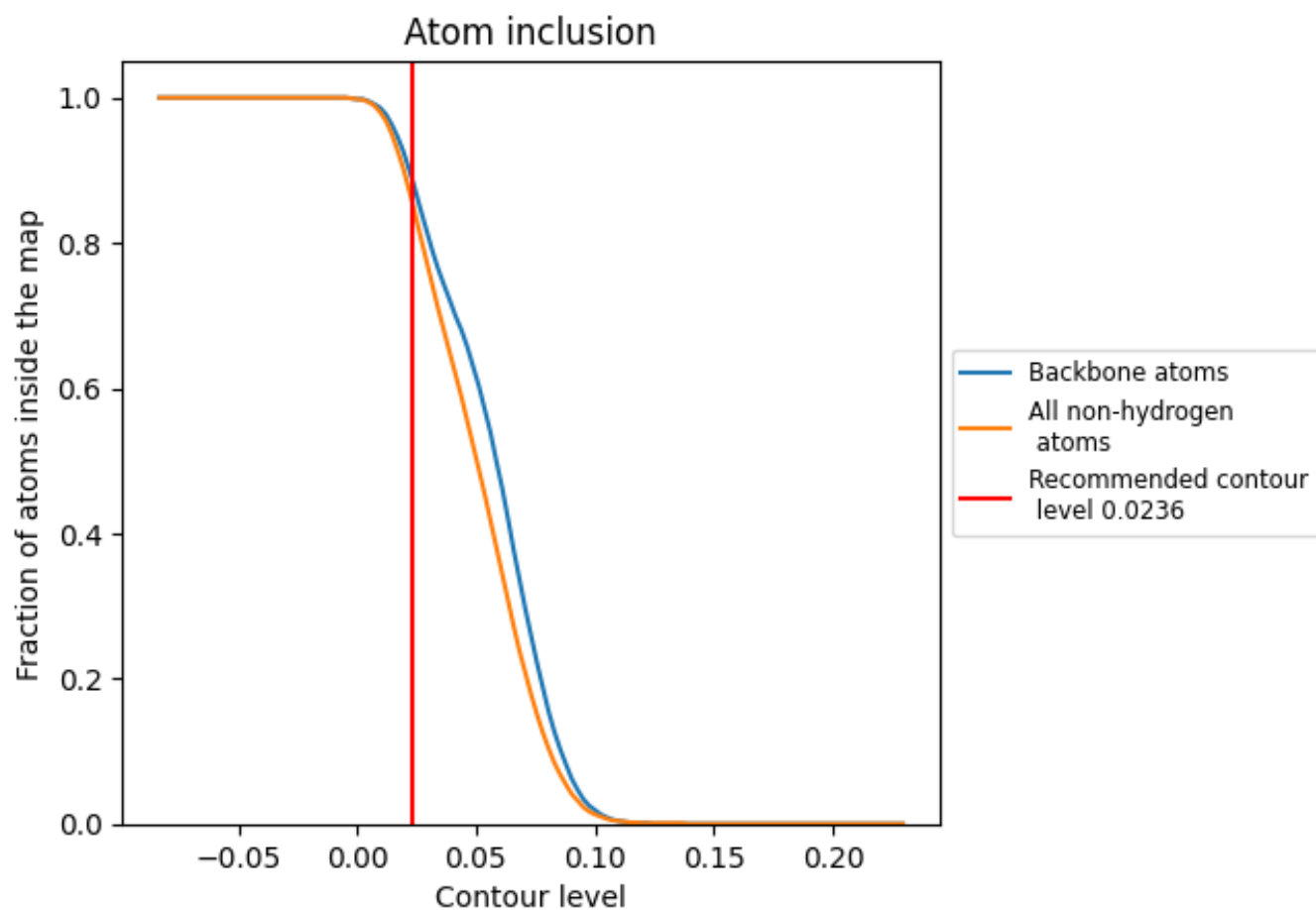
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0236).







































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 85% 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 (0.0236) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8510	 0.5820
A	 0.8620	 0.5800
B	 0.9180	 0.6070
C	 0.8660	 0.5940
E	 0.8290	 0.5790
F	 0.7980	 0.5530
G	 0.6470	 0.4840
H	 0.8340	 0.5650
I	 0.7960	 0.5570
J	 0.8310	 0.5710
K	 0.8400	 0.5710
L	 0.8450	 0.5900
M	 0.8710	 0.5910
N	 0.7780	 0.5680
O	 0.8210	 0.5590
P	 0.9070	 0.6110
Q	 0.8900	 0.6030
T	 0.8280	 0.5920
W	 0.8300	 0.5490

