



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 08:49 AM UTC

PDB ID : 6QC8 / pdb_00006qc8
EMDB ID : EMD-4500
Title : Ovine respiratory complex I FRC open class 2
Authors : Letts, J.A.; Sazanov, L.A.
Deposited on : 2018-12-27
Resolution : 4.20 Å(reported)
Based on initial model : 5LNK

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:

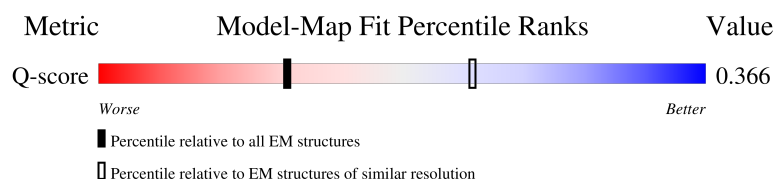
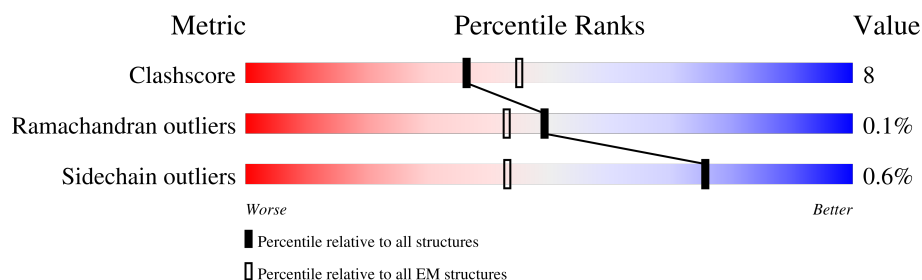
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5410 (3.70 - 4.70)

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	V1	445	14% 76% 20% ..
2	V2	217	16% 77% 19% ..
3	S1	704	14% 74% 23% ..
4	S2	430	20% 80% 20% ..

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Mol	Chain	Length	Quality of chain
5	S3	228	
6	S7	179	
7	S8	176	
8	V3	75	
9	S6	96	
10	S4	133	
11	A9	338	
12	A2	98	
13	A5	115	
14	A6	127	
15	A7	112	
16	AL	145	
17	AA	88	
17	AB	88	
18	D3	115	
19	D1	318	
20	D6	175	
21	4L	98	
22	D5	606	
23	D4	459	
24	D2	347	
25	AK	140	
26	B5	143	
27	A8	171	
28	BJ	175	

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Mol	Chain	Length	Quality of chain
29	AJ	320	
30	S5	105	
31	A3	83	
32	B3	97	
33	C2	120	
34	B4	128	
35	AM	143	
36	B6	127	
37	B7	136	
38	B9	178	
39	B2	72	
40	B8	158	
41	BK	125	
42	C1	49	
43	B1	57	
44	A1	70	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
45	SF4	S1	801	-	-	X	-

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 65394 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
1	V1	430	Total	C	N	O	S	0	0
			3312	2086	593	613	20		

- Molecule 2 is a protein called NDUFV2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	V2	212	Total	C	N	O	S	0	0
			1647	1052	277	308	10		

- Molecule 3 is a protein called NADH:ubiquinone oxidoreductase core subunit S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	S1	688	Total	C	N	O	S	0	0
			5275	3301	922	1011	41		

- Molecule 4 is a protein called NADH:ubiquinone oxidoreductase core subunit S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	S2	430	Total	C	N	O	S	0	0
			3455	2205	594	631	25		

- Molecule 5 is a protein called NADH:ubiquinone oxidoreductase core subunit S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	S3	208	Total	C	N	O	S	0	0
			1726	1112	296	315	3		

- Molecule 6 is a protein called NADH:ubiquinone oxidoreductase core subunit S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	S7	156	Total	C	N	O	S	0	0
			1247	795	225	213	14		

- Molecule 7 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	S8	176	Total	C	N	O	S	0	0
			1414	889	243	270	12		

- Molecule 8 is a protein called NADH:ubiquinone oxidoreductase subunit V3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	V3	41	Total	C	N	O	S	0	0
			345	215	63	66	1		

- Molecule 9 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	S6	95	Total	C	N	O	S	0	0
			737	451	139	144	3		

- Molecule 10 is a protein called NADH:ubiquinone oxidoreductase subunit S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	S4	126	Total	C	N	O	S	0	0
			1024	646	182	193	3		

- Molecule 11 is a protein called NADH:ubiquinone oxidoreductase subunit A9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A9	287	Total	C	N	O	S	0	0
			2293	1464	419	405	5		

- Molecule 12 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	A2	82	Total	C	N	O	S	0	0
			665	419	124	120	2		

- Molecule 13 is a protein called NDUFA5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A5	111	Total	C	N	O	S	0	0
			901	583	151	165	2		

- Molecule 14 is a protein called NADH:ubiquinone oxidoreductase subunit A6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	A6	114	Total	C	N	O	S	0	0
			969	619	180	166	4		

- Molecule 15 is a protein called NDUFA7.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	A7	96	Total	C	N	O	S	0	0
			766	478	146	139	3		

- Molecule 16 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AL	144	Total	C	N	O	S	0	0
			1201	773	215	209	4		

- Molecule 17 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AA	80	Total	C	N	O	S	0	0
			645	416	96	128	5		
17	AB	87	Total	C	N	O	S	0	0
			702	451	103	143	5		

- Molecule 18 is a protein called NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	D3	90	Total	C	N	O	S	0	0
			728	500	103	120	5		

- Molecule 19 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	D1	303	Total	C	N	O	S	0	0
			2415	1633	368	395	19		

- Molecule 20 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	D6	171	Total	C	N	O	S	0	0
			1308	878	187	230	13		

- Molecule 21 is a protein called NADH-ubiquinone oxidoreductase chain 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	4L	98	Total	C	N	O	S	0	0
			748	489	112	132	15		

- Molecule 22 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	D5	606	Total	C	N	O	S	0	0
			4805	3187	746	828	44		

- Molecule 23 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	D4	459	Total	C	N	O	S	0	0
			3646	2428	571	607	40		

- Molecule 24 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	D2	347	Total	C	N	O	S	0	0
			2724	1808	416	460	40		

- Molecule 25 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AK	140	Total	C	N	O	S	0	0
			1025	654	175	190	6		

- Molecule 26 is a protein called NADH:ubiquinone oxidoreductase subunit B5.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B5	139	Total	C	N	O	S	0	0
			1156	761	194	199	2		

- Molecule 27 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A8	171	Total	C	N	O	S	0	0
			1404	889	253	252	10		

- Molecule 28 is a protein called NADH:ubiquinone oxidoreductase subunit B10.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BJ	171	Total	C	N	O	S	0	0
			1441	905	266	262	8		

- Molecule 29 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AJ	319	Total	C	N	O	S	0	0
			2583	1653	430	490	10		

- Molecule 30 is a protein called NADH:ubiquinone oxidoreductase subunit S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	S5	99	Total	C	N	O	S	0	0
			822	520	154	142	6		

- Molecule 31 is a protein called NADH:ubiquinone oxidoreductase subunit A3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	A3	74	Total	C	N	O	S	0	0
			582	379	96	105	2		

- Molecule 32 is a protein called NADH:ubiquinone oxidoreductase subunit B3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B3	73	Total	C	N	O	S	0	0
			578	378	100	98	2		

- Molecule 33 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	C2	119	Total	C	N	O	S	0	0
			997	647	174	172	4		

- Molecule 34 is a protein called NADH:ubiquinone oxidoreductase subunit B4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B4	128	Total	C	N	O	S	0	0
			1059	675	189	194	1		

- Molecule 35 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AM	139	Total	C	N	O	S	0	0
			1143	733	200	201	9		

- Molecule 36 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B6	96	Total	C	N	O	S	0	0
			815	536	139	139	1		

- Molecule 37 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	B7	119	Total	C	N	O	S	0	0
			1026	641	196	181	8		

- Molecule 38 is a protein called NADH:ubiquinone oxidoreductase subunit B9.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	B9	176	Total	C	N	O	S	0	0
			1515	970	278	261	6		

- Molecule 39 is a protein called NADH:ubiquinone oxidoreductase subunit B2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	B2	65	Total	C	N	O	S	0	0
			563	372	93	97	1		

- Molecule 40 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	B8	157	Total	C	N	O	S	0	0
			1324	855	217	243	9		

- Molecule 41 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BK	102	Total	C	N	O	S	0	0
			853	547	141	161	4		

- Molecule 42 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	C1	46	Total	C	N	O		0	0
			391	258	67	66			

- Molecule 43 is a protein called NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 1, 7kDa.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	B1	52	Total	C	N	O		0	0
			449	296	79	74			

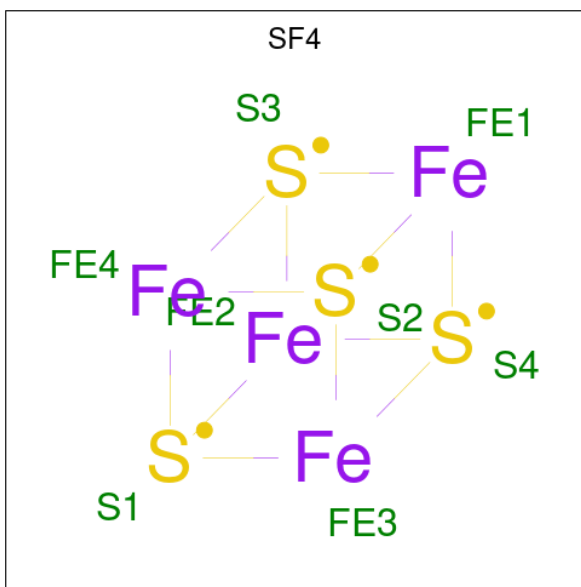
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B1	16	VAL	GLY	conflict	UNP W5QG39
B1	35	ALA	THR	conflict	UNP W5QG39
B1	38	ARG	TRP	conflict	UNP W5QG39

- Molecule 44 is a protein called NADH dehydrogenase 1 alpha subcomplex.

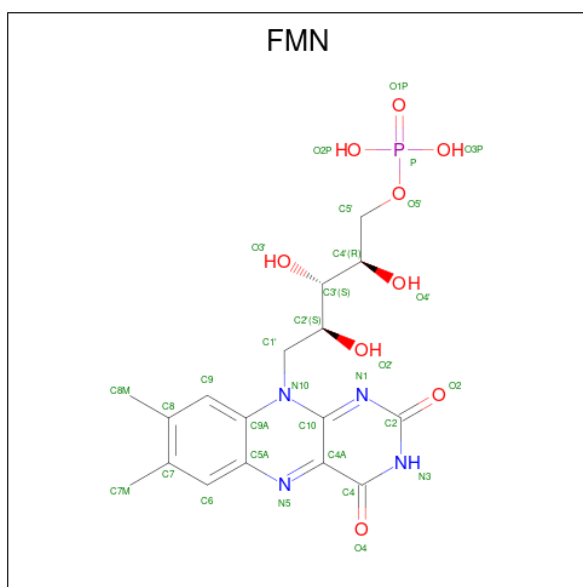
Mol	Chain	Residues	Atoms					AltConf	Trace
44	A1	70	Total	C	N	O	S	0	0
			577	369	106	97	5		

- Molecule 45 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



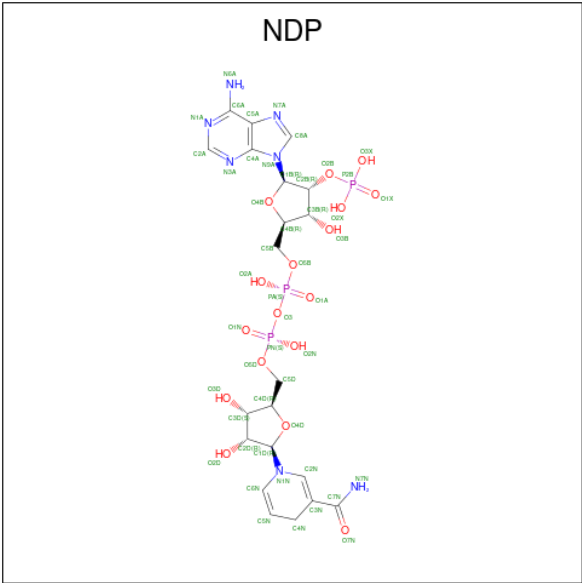
Mol	Chain	Residues	Atoms			AltConf
45	V1	1	Total	Fe	S	0
			8	4	4	
45	S1	1	Total	Fe	S	0
			8	4	4	
45	S1	1	Total	Fe	S	0
			8	4	4	
45	S7	1	Total	Fe	S	0
			8	4	4	
45	S8	1	Total	Fe	S	0
			8	4	4	
45	S8	1	Total	Fe	S	0
			8	4	4	

- Molecule 46 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



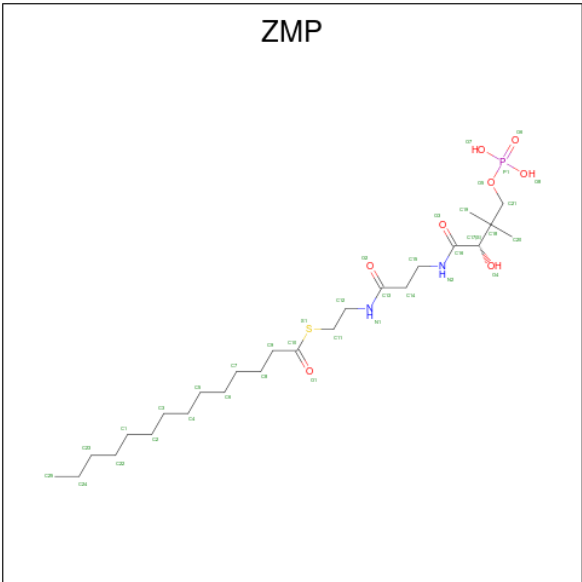
Mol	Chain	Residues	Atoms		AltConf
48	S6	1	Total	Zn	0
			1	1	

- Molecule 49 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



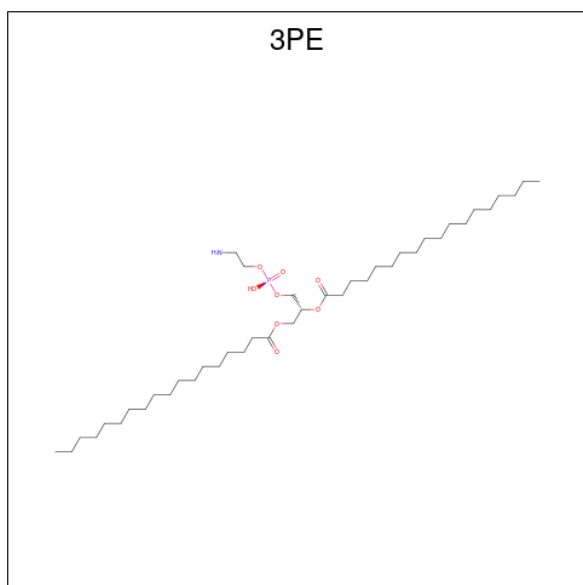
Mol	Chain	Residues	Atoms					AltConf
49	A9	1	Total	C	N	O	P	0
			48	21	7	17	3	

- Molecule 50 is S-[2-({N-[(2S)-2-hydroxy-3,3-dimethyl-4-(phosphonooxy)butanoyl]-beta-alanyl} amino)ethyl] tetradecanethioate (CCD ID: ZMP) (formula: $C_{25}H_{49}N_2O_8PS$).



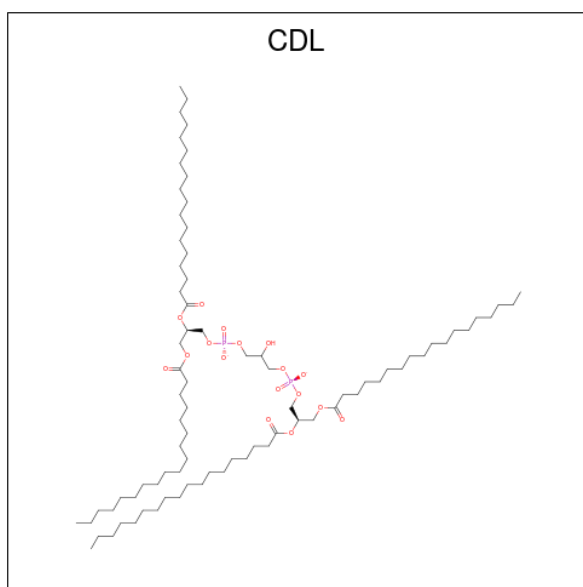
Mol	Chain	Residues	Atoms						AltConf
50	AA	1	Total	C	N	O	P	S	0
			34	23	2	7	1	1	
50	AB	1	Total	C	N	O	P	S	0
			31	20	2	7	1	1	

- Molecule 51 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: $C_{41}H_{82}NO_8P$).



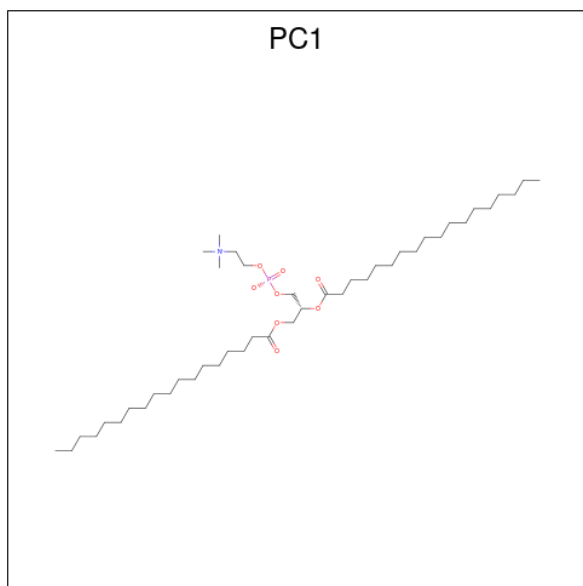
Mol	Chain	Residues	Atoms					AltConf
51	D1	1	Total	C	N	O	P	0
			26	16	1	8	1	
51	D5	1	Total	C	N	O	P	0
			38	28	1	8	1	
51	D4	1	Total	C	N	O	P	0
			40	30	1	8	1	

- Molecule 52 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
52	D5	1	60	41	17	2	0

- Molecule 53 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: $C_{44}H_{88}NO_8P$).

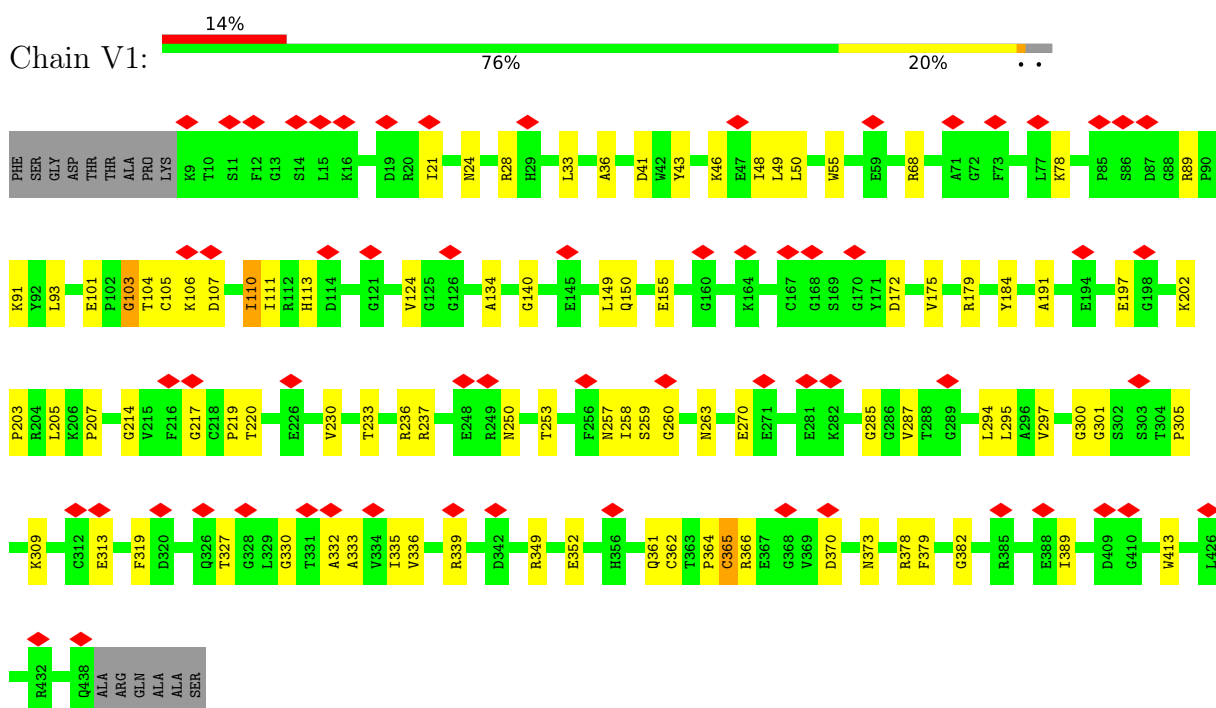


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
53	AK	1	28	18	1	8	1	0

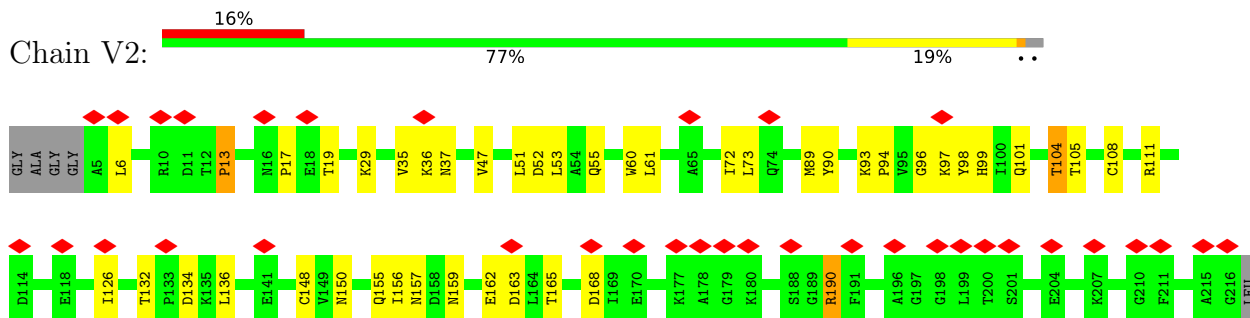
3 Residue-property plots

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

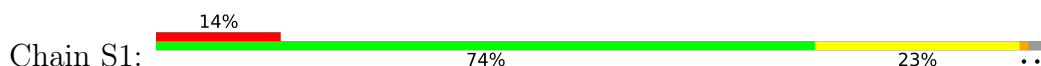
- Molecule 1: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial



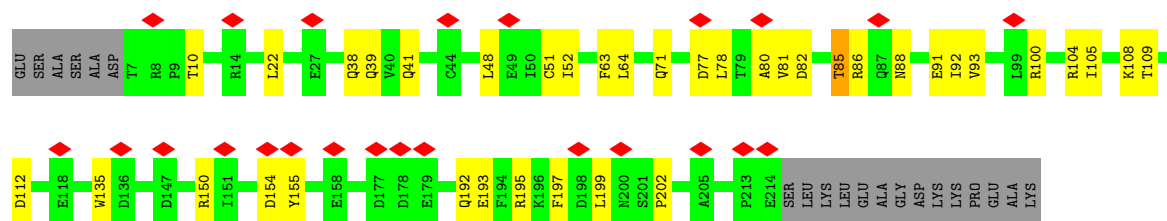
- Molecule 2: NDUFV2



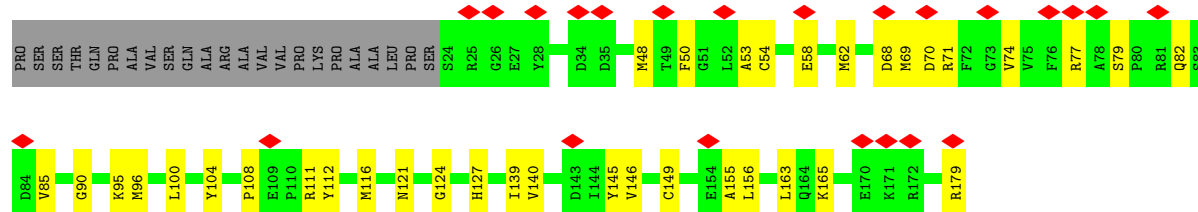
- Molecule 3: NADH:ubiquinone oxidoreductase core subunit S1



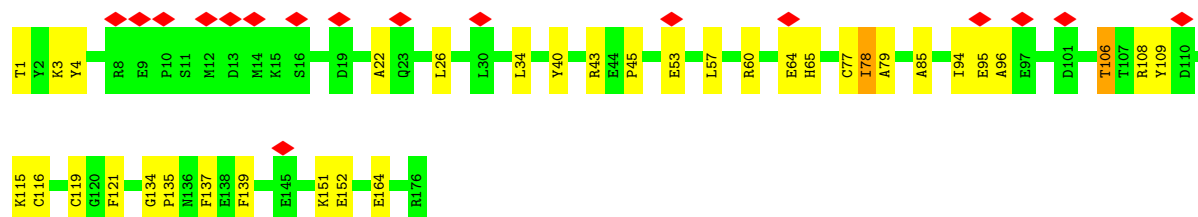
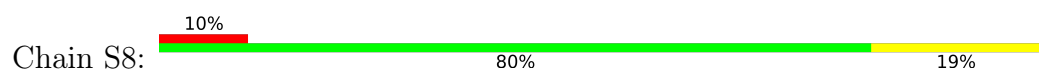




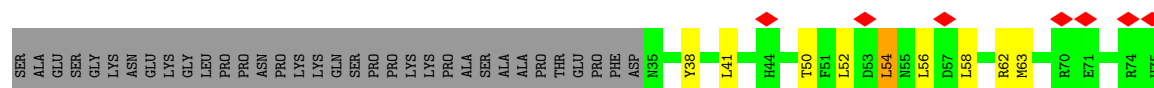
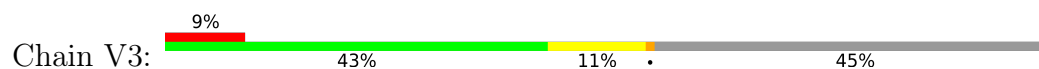
- Molecule 6: NADH:ubiquinone oxidoreductase core subunit S7



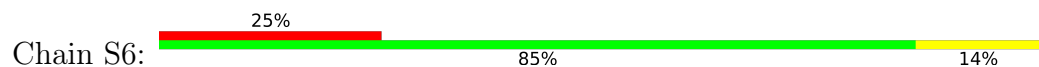
- Molecule 7: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial



- Molecule 8: NADH:ubiquinone oxidoreductase subunit V3

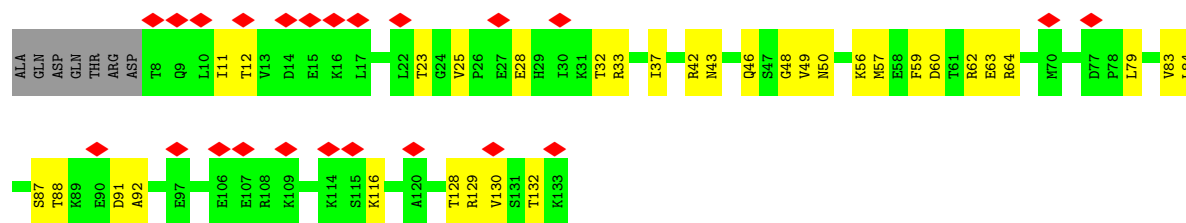


- Molecule 9: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial

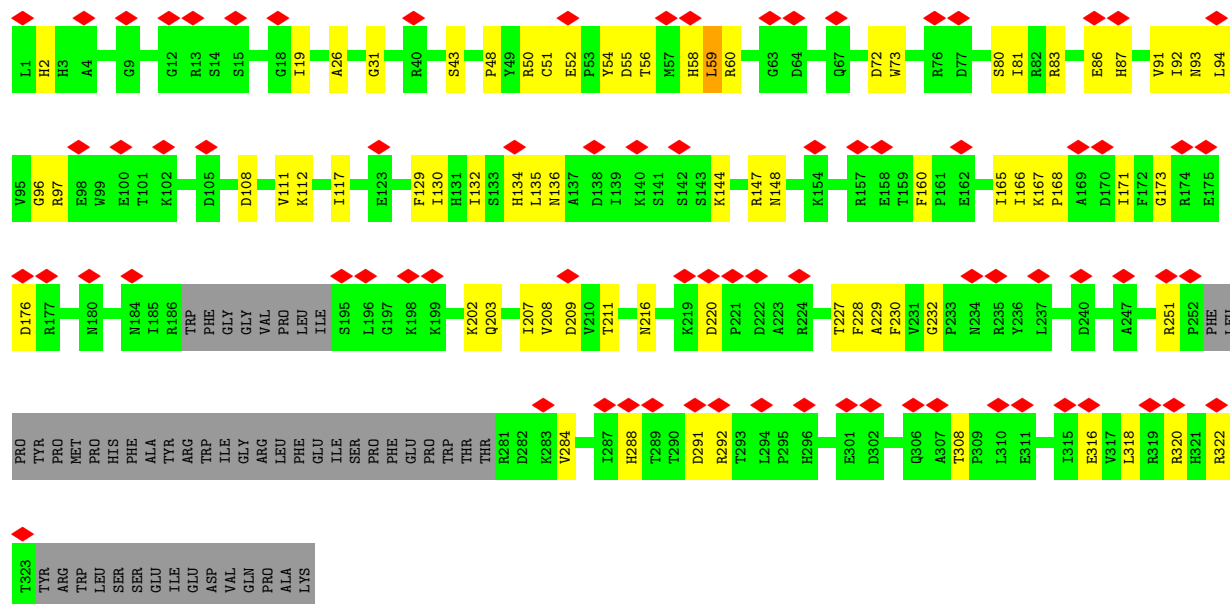


- Molecule 10: NADH:ubiquinone oxidoreductase subunit S4

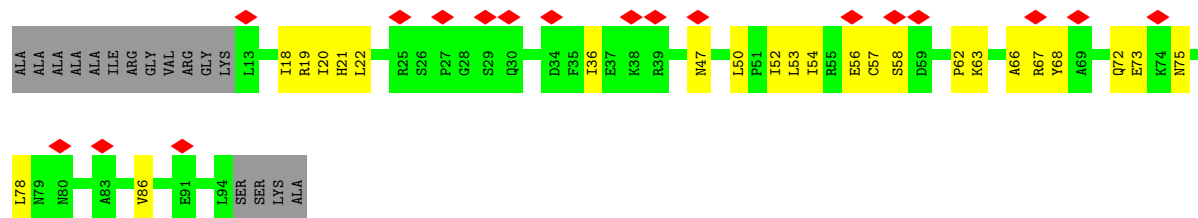




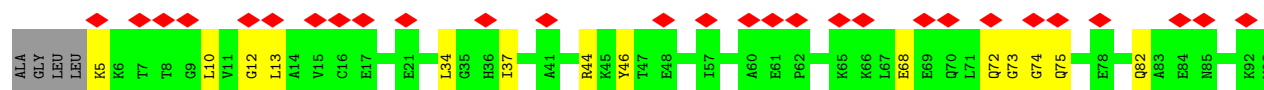
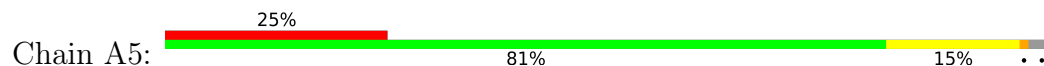
• Molecule 11: NADH:ubiquinone oxidoreductase subunit A9

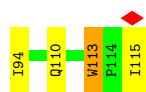


• Molecule 12: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2

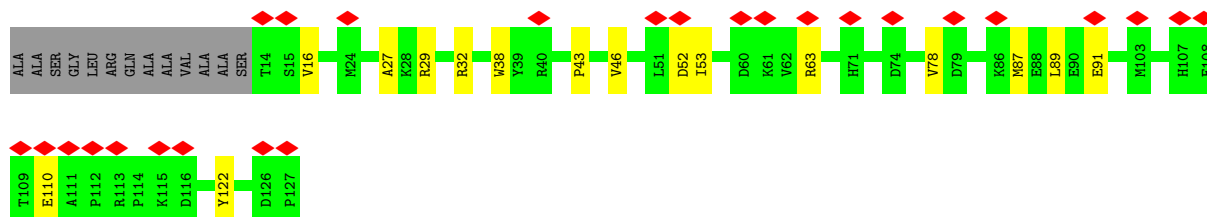
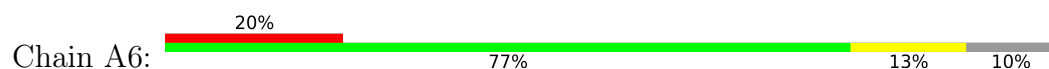


• Molecule 13: NDUFA5





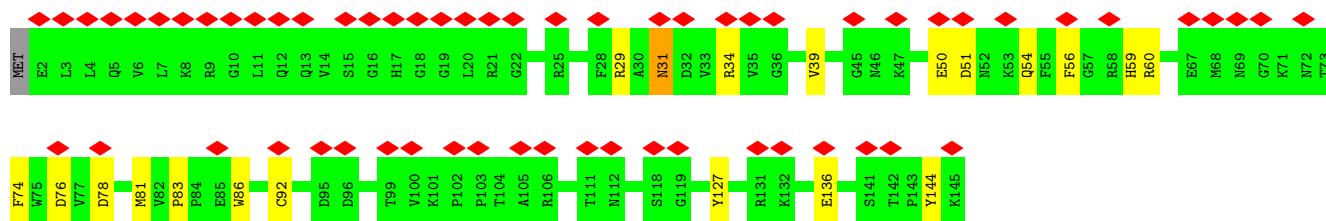
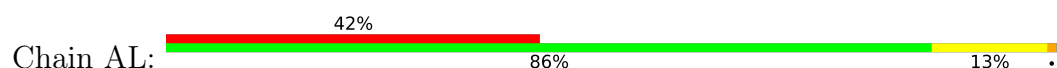
- Molecule 14: NADH:ubiquinone oxidoreductase subunit A6



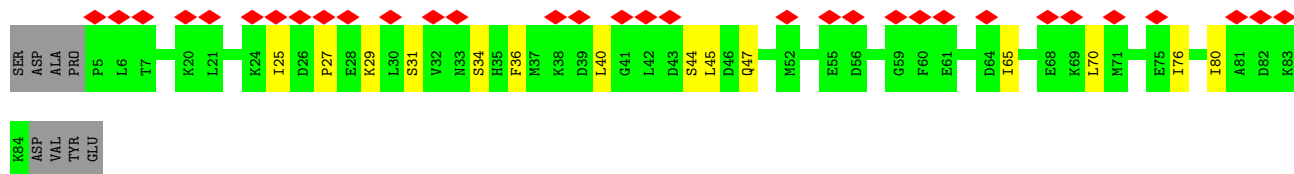
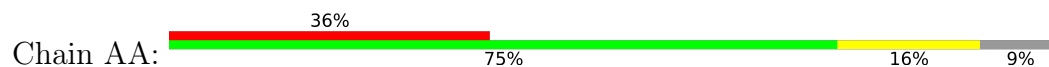
- Molecule 15: NDUFA7



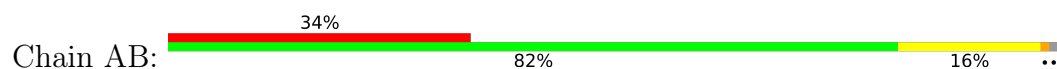
- Molecule 16: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12

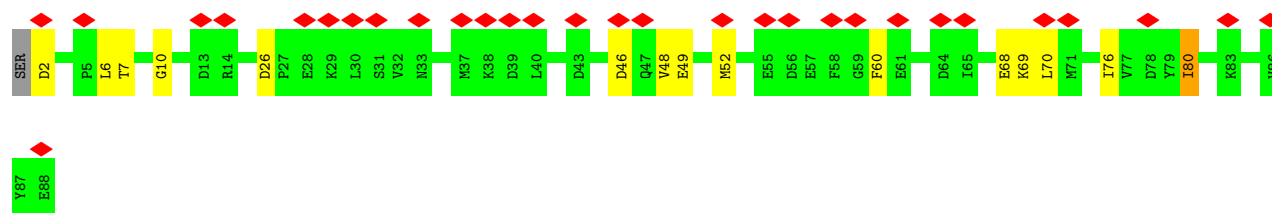


- Molecule 17: Acyl carrier protein

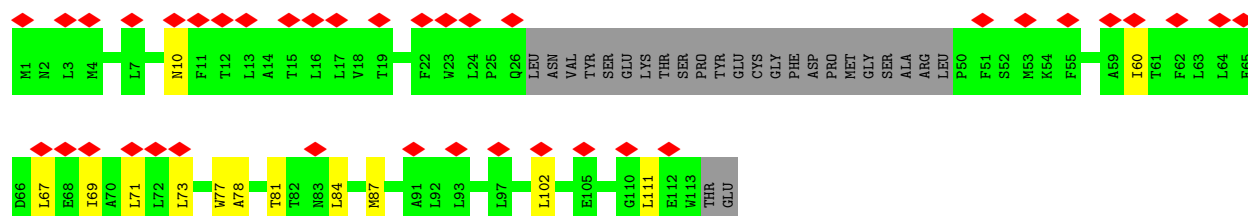


- Molecule 17: Acyl carrier protein

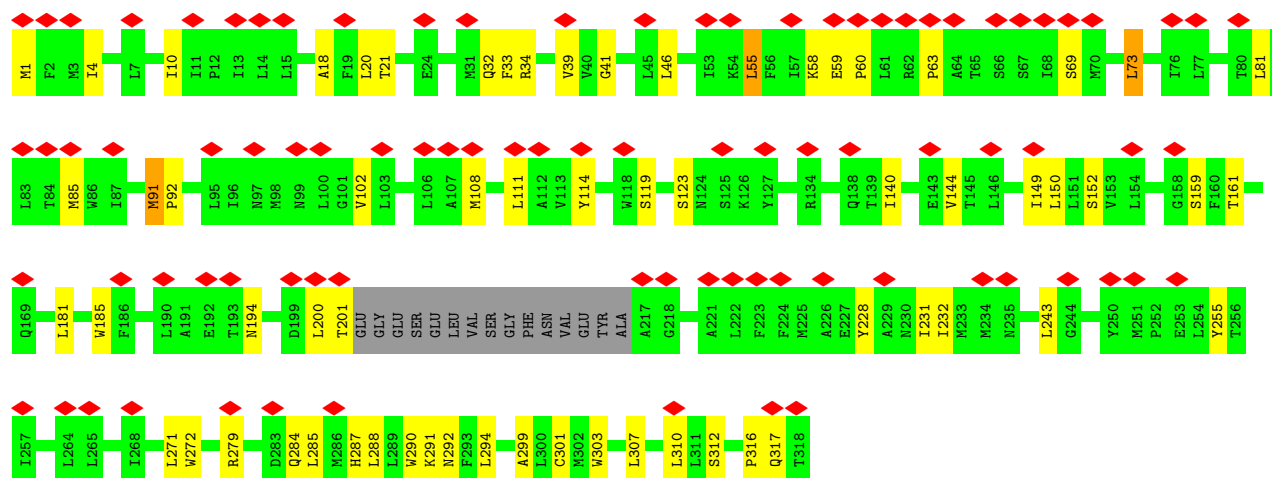
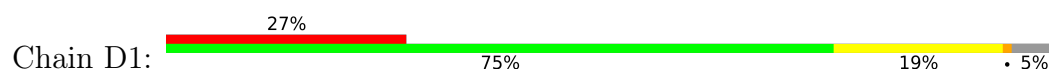




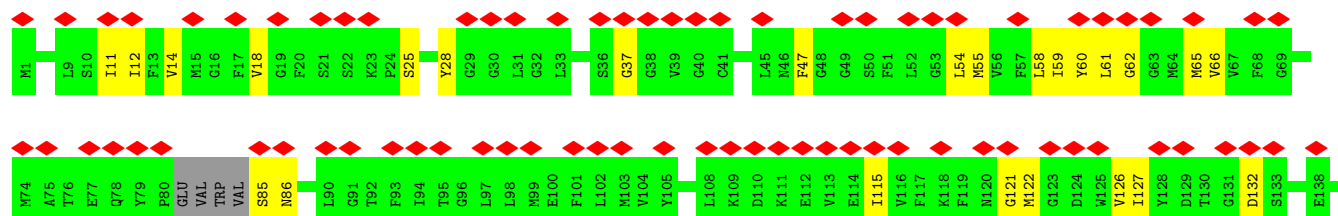
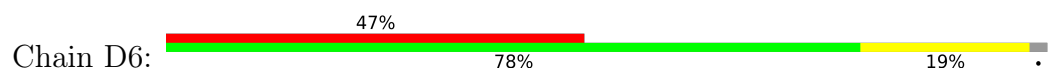
• Molecule 18: NADH-ubiquinone oxidoreductase chain 3



• Molecule 19: NADH-ubiquinone oxidoreductase chain 1

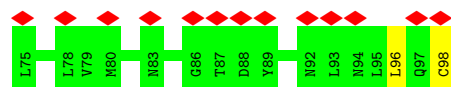
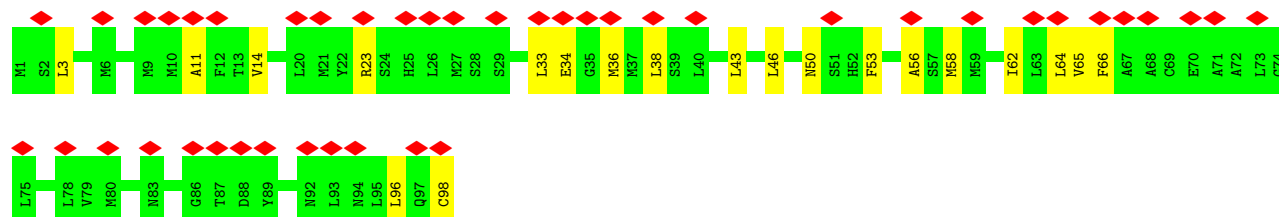
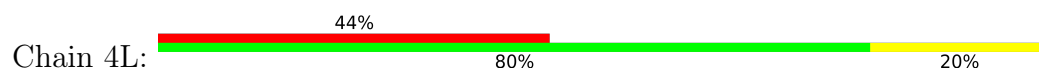


• Molecule 20: NADH-ubiquinone oxidoreductase chain 6

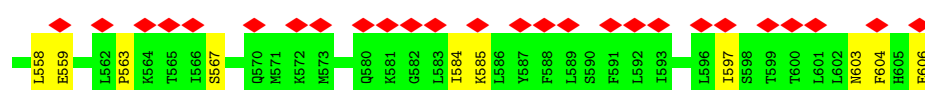
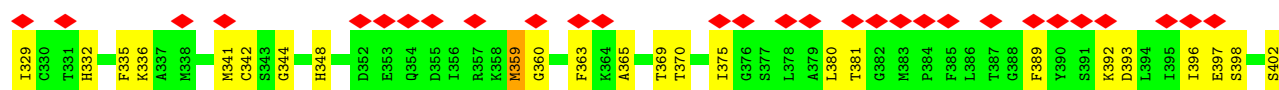
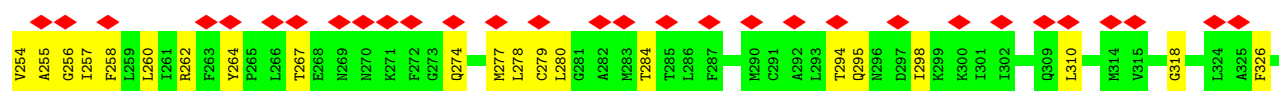
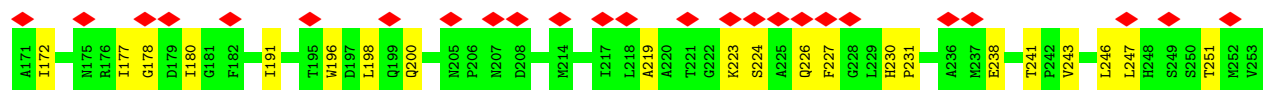
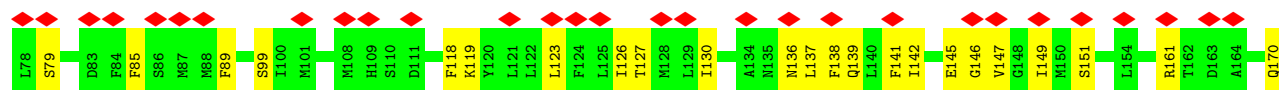
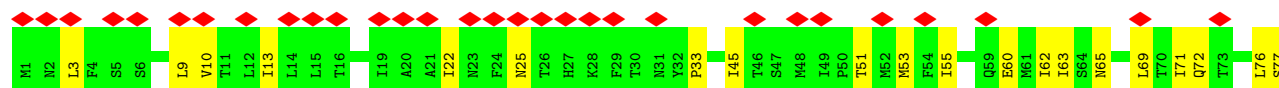
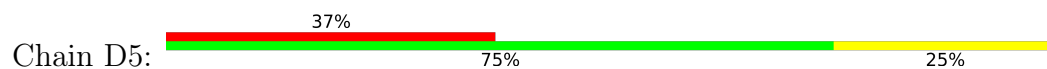




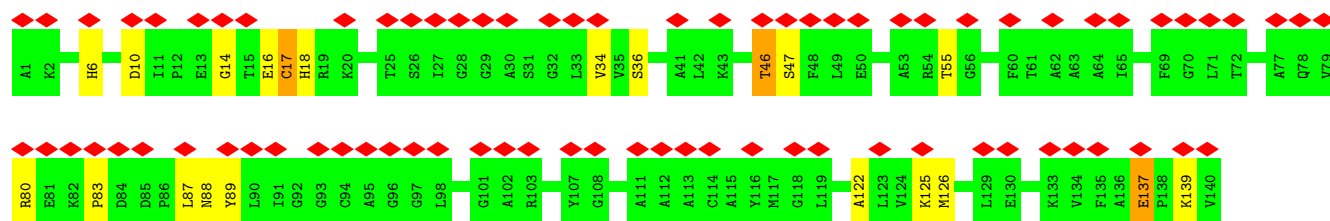
- Molecule 21: NADH-ubiquinone oxidoreductase chain 4L



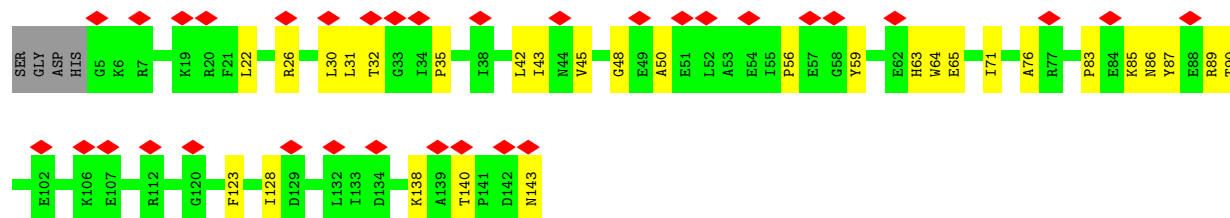
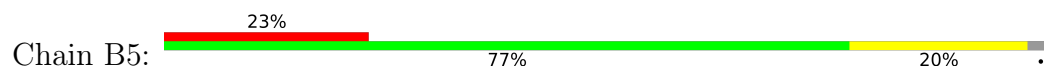
- Molecule 22: NADH-ubiquinone oxidoreductase chain 5



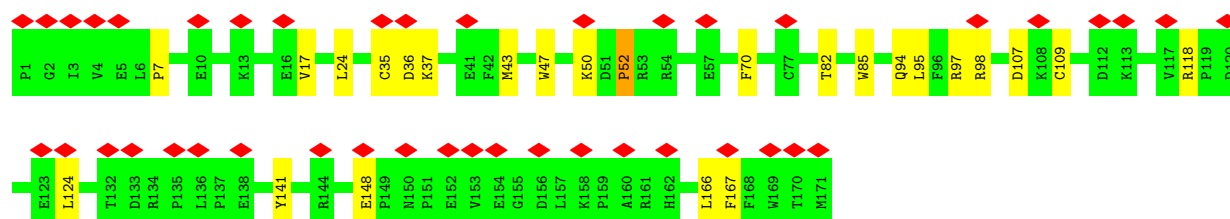
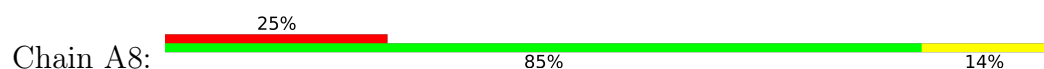
- Molecule 23: NADH-ubiquinone oxidoreductase chain 4



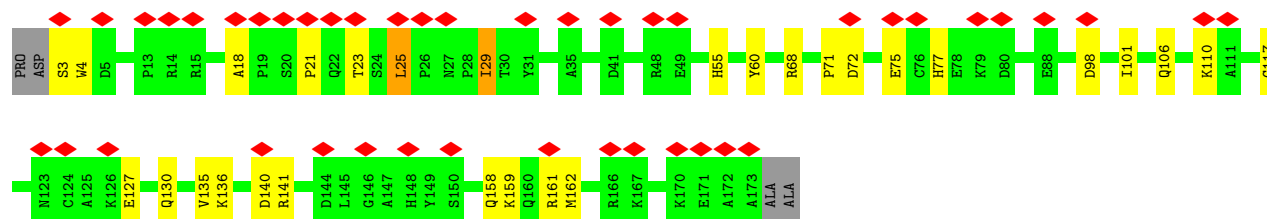
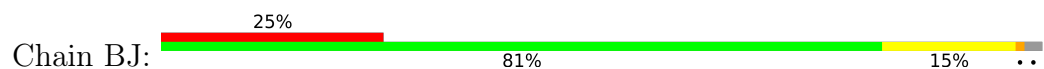
• Molecule 26: NADH:ubiquinone oxidoreductase subunit B5



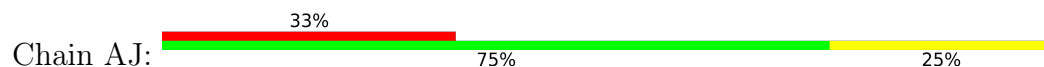
• Molecule 27: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8

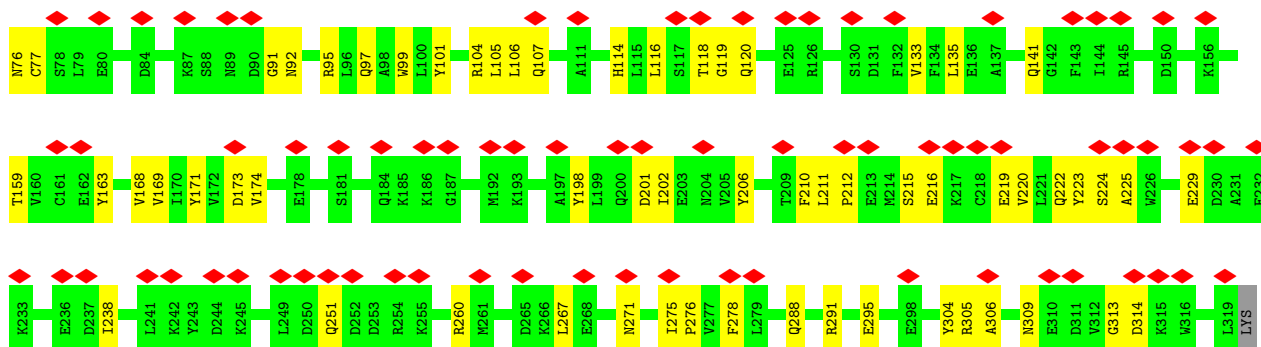


• Molecule 28: NADH:ubiquinone oxidoreductase subunit B10

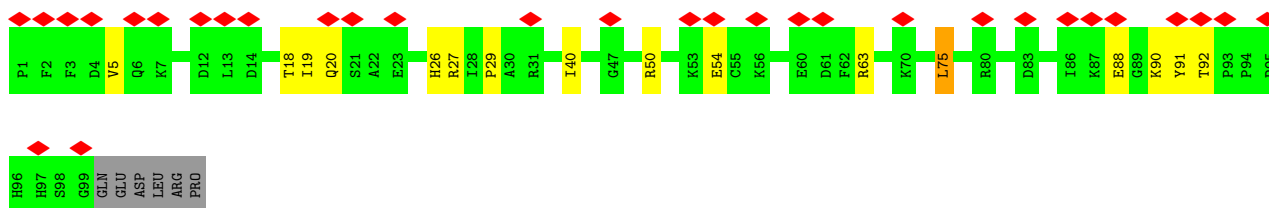
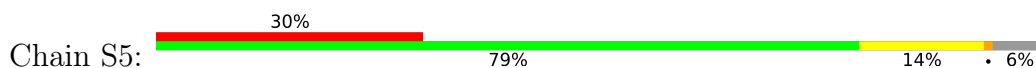


• Molecule 29: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial

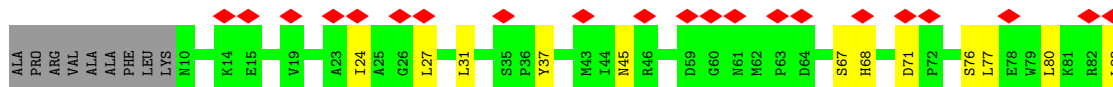
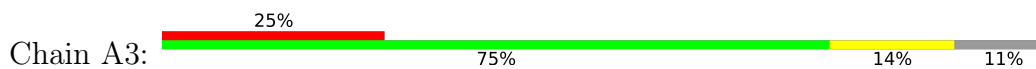




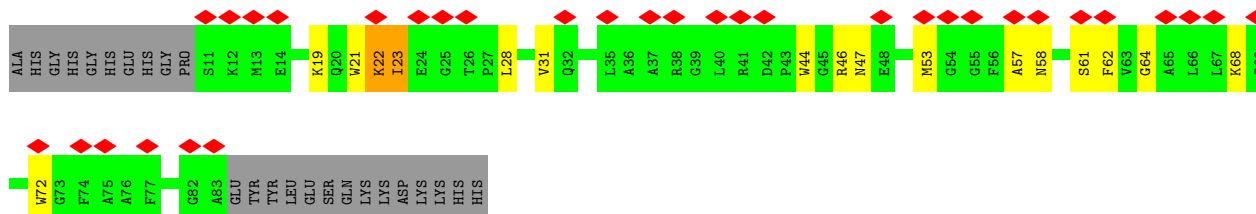
• Molecule 30: NADH:ubiquinone oxidoreductase subunit S5



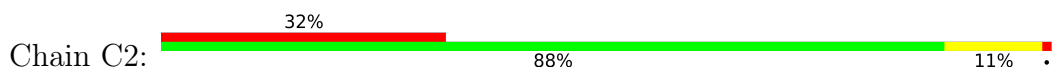
• Molecule 31: NADH:ubiquinone oxidoreductase subunit A3



• Molecule 32: NADH:ubiquinone oxidoreductase subunit B3

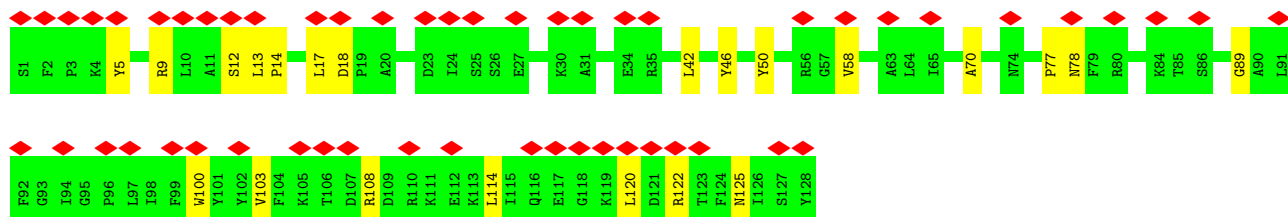
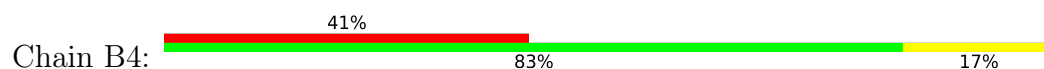


• Molecule 33: NADH dehydrogenase [ubiquinone] 1 subunit C2

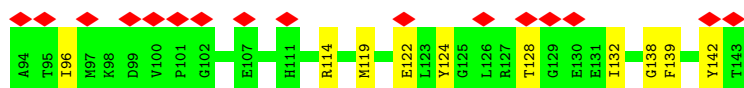
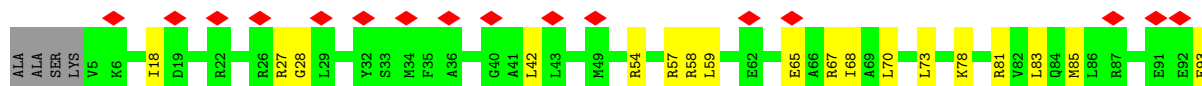
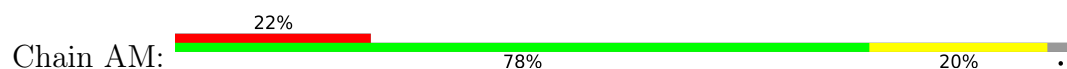




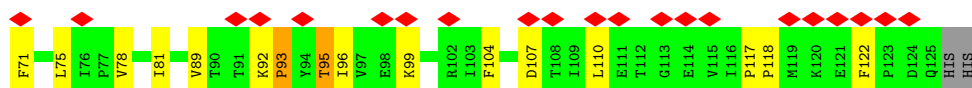
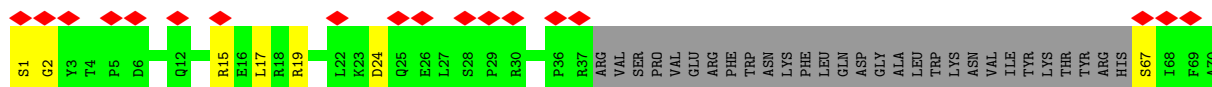
- Molecule 34: NADH:ubiquinone oxidoreductase subunit B4



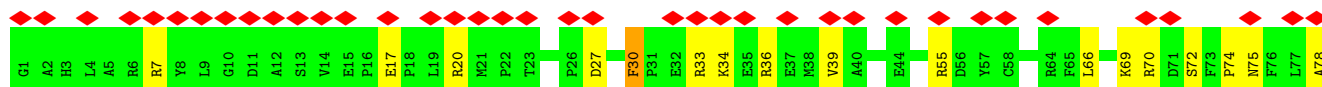
- Molecule 35: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13



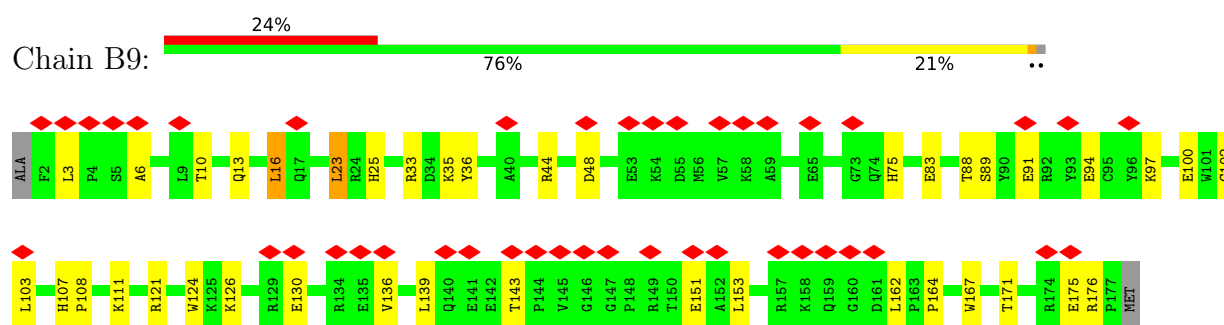
- Molecule 36: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6



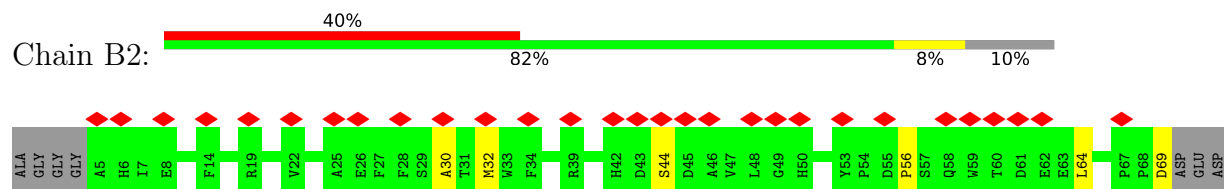
- Molecule 37: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7



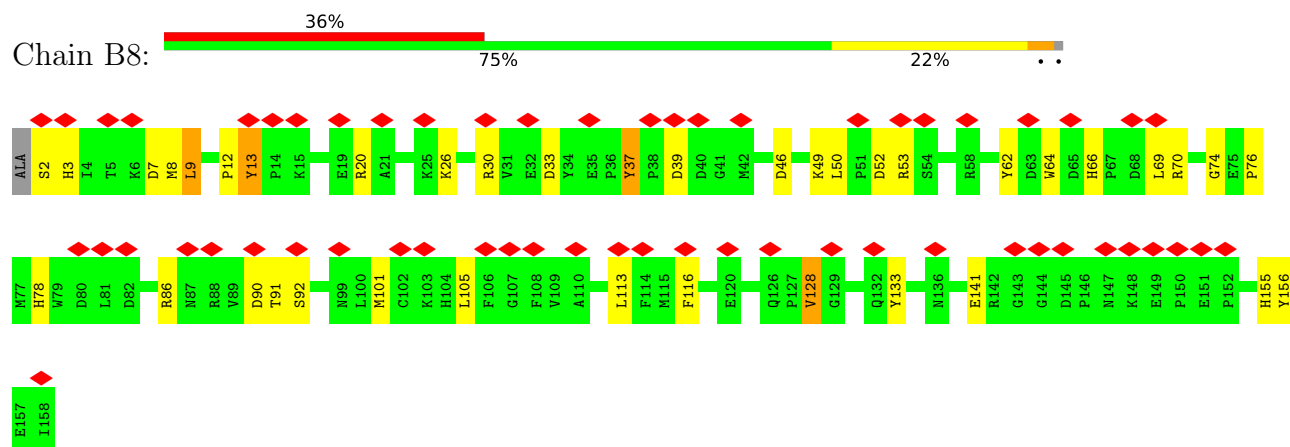
- Molecule 38: NADH:ubiquinone oxidoreductase subunit B9



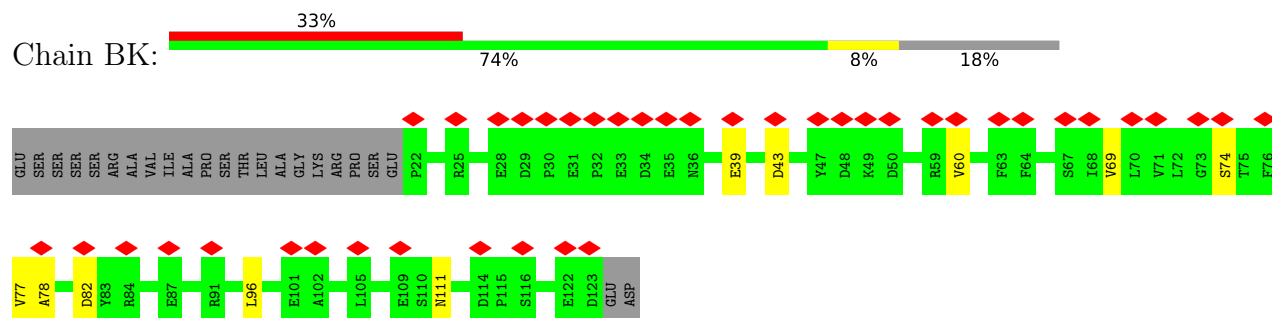
- Molecule 39: NADH:ubiquinone oxidoreductase subunit B2



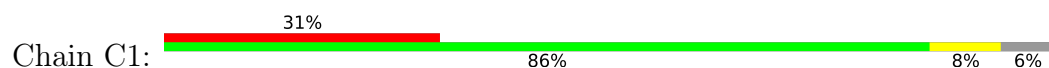
- Molecule 40: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial

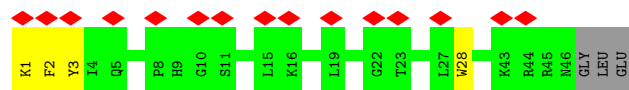


- Molecule 41: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial

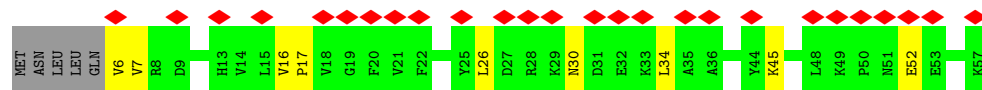
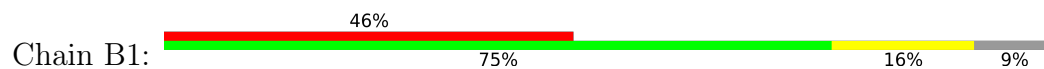


- Molecule 42: NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial

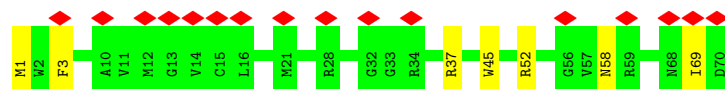




- Molecule 43: NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 1, 7kDa



- Molecule 44: NADH dehydrogenase 1 alpha subcomplex



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	25404	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 ($e^-/\text{\AA}^2$)	51	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	100000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	1.367	Depositor
Minimum map value	-0.381	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	716.8, 716.8, 716.8	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4, 1.4, 1.4	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 3PE, SF4, FMN, PC1, FES, CDL, ZMP, NDP

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	V1	0.37	0/3386	0.68	0/4575
2	V2	0.36	0/1687	0.81	4/2295 (0.2%)
3	S1	0.37	0/5362	0.66	0/7266
4	S2	0.40	0/3547	0.68	2/4808 (0.0%)
5	S3	0.39	0/1776	0.74	0/2417
6	S7	0.41	0/1278	0.70	0/1728
7	S8	0.45	0/1445	0.70	0/1956
8	V3	0.29	0/355	0.71	0/480
9	S6	0.31	0/749	0.58	0/1009
10	S4	0.34	0/1047	0.60	0/1415
11	A9	0.32	0/2343	0.71	3/3164 (0.1%)
12	A2	0.30	0/676	0.65	0/911
13	A5	0.33	0/921	0.69	0/1249
14	A6	0.31	0/993	0.68	2/1336 (0.1%)
15	A7	0.28	0/784	0.68	0/1060
16	AL	0.30	0/1242	0.68	0/1688
17	AA	0.28	0/655	0.74	0/881
17	AB	0.29	0/714	0.59	0/963
18	D3	0.33	0/747	0.67	0/1022
19	D1	0.39	0/2487	0.76	3/3401 (0.1%)
20	D6	0.31	0/1339	0.68	0/1810
21	4L	0.37	0/758	0.70	0/1024
22	D5	0.36	0/4933	0.73	1/6710 (0.0%)
23	D4	0.40	0/3740	0.77	2/5095 (0.0%)
24	D2	0.39	0/2788	0.70	2/3795 (0.1%)
25	AK	0.29	0/1046	0.72	4/1419 (0.3%)
26	B5	0.30	0/1189	0.59	0/1607
27	A8	0.32	0/1441	0.69	2/1942 (0.1%)
28	BJ	0.32	0/1475	0.70	3/1989 (0.2%)
29	AJ	0.31	0/2644	0.69	8/3579 (0.2%)
30	S5	0.34	0/843	0.69	0/1128
31	A3	0.30	0/602	0.70	0/828

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	B3	0.32	0/595	0.80	0/803
33	C2	0.32	0/1028	0.71	4/1388 (0.3%)
34	B4	0.30	0/1085	0.65	0/1467
35	AM	0.33	0/1172	0.69	0/1579
36	B6	0.32	0/841	0.77	1/1144 (0.1%)
37	B7	0.33	0/1051	0.71	1/1408 (0.1%)
38	B9	0.31	0/1568	0.68	0/2123
39	B2	0.31	0/590	0.75	2/810 (0.2%)
40	B8	0.32	0/1379	0.82	6/1884 (0.3%)
41	BK	0.31	0/880	0.67	0/1196
42	C1	0.25	0/404	0.58	0/548
43	B1	0.27	0/462	0.64	0/624
44	A1	0.29	0/592	0.68	0/795
All	All	0.35	0/66639	0.70	50/90319 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	V1	0	2
2	V2	0	2
3	S1	0	7
4	S2	0	3
7	S8	0	1
8	V3	0	1
10	S4	0	1
13	A5	0	1
15	A7	0	3
16	AL	0	1
17	AB	0	1
19	D1	0	1
20	D6	0	1
22	D5	0	2
23	D4	0	3
24	D2	0	1
25	AK	0	2
27	A8	0	1
29	AJ	0	2
30	S5	0	1
32	B3	0	2

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Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
33	C2	0	1
35	AM	0	1
37	B7	0	1
39	B2	0	1
40	B8	0	1
41	BK	0	1
43	B1	0	1
All	All	0	46

There are no bond length outliers.

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	V2	36	LYS	N-CA-C	-7.66	104.83	114.56
29	AJ	229	GLU	CA-C-N	7.57	135.32	121.70
29	AJ	229	GLU	C-N-CA	7.57	135.32	121.70
28	BJ	21	PRO	CA-C-N	7.47	135.15	121.70
28	BJ	21	PRO	C-N-CA	7.47	135.15	121.70

There are no chirality outliers.

5 of 46 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	S1	213	TYR	Peptide
1	V1	103	GLY	Peptide
1	V1	207	PRO	Peptide
2	V2	13	PRO	Peptide
2	V2	35	VAL	Peptide

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	V1	3312	0	3266	62	0
2	V2	1647	0	1657	30	0
3	S1	5275	0	5300	113	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	S2	3455	0	3395	59	0
5	S3	1726	0	1676	39	0
6	S7	1247	0	1256	26	0
7	S8	1414	0	1371	29	0
8	V3	345	0	323	7	0
9	S6	737	0	710	8	0
10	S4	1024	0	1023	24	0
11	A9	2293	0	2326	49	0
12	A2	665	0	678	14	0
13	A5	901	0	936	13	0
14	A6	969	0	980	12	0
15	A7	766	0	779	17	0
16	AL	1201	0	1170	15	0
17	AA	645	0	649	8	0
17	AB	702	0	692	11	0
18	D3	728	0	773	14	0
19	D1	2415	0	2542	41	0
20	D6	1308	0	1329	30	0
21	4L	748	0	794	22	0
22	D5	4805	0	4950	107	0
23	D4	3646	0	3850	83	0
24	D2	2724	0	2930	70	0
25	AK	1025	0	1033	12	0
26	B5	1156	0	1177	25	0
27	A8	1404	0	1384	18	0
28	BJ	1441	0	1417	21	0
29	AJ	2583	0	2547	44	0
30	S5	822	0	820	14	0
31	A3	582	0	583	13	0
32	B3	578	0	570	11	0
33	C2	997	0	983	11	0
34	B4	1059	0	1062	16	0
35	AM	1143	0	1137	22	0
36	B6	815	0	837	20	0
37	B7	1026	0	995	22	0
38	B9	1515	0	1469	30	0
39	B2	563	0	509	7	0
40	B8	1324	0	1219	29	0
41	BK	853	0	800	9	0
42	C1	391	0	391	3	0
43	B1	449	0	453	6	0
44	A1	577	0	570	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	S1	16	0	0	2	0
45	S7	8	0	0	1	0
45	S8	16	0	0	0	0
45	V1	8	0	0	1	0
46	V1	31	0	19	3	0
47	S1	4	0	0	0	0
47	V2	4	0	0	0	0
48	S6	1	0	0	0	0
49	A9	48	0	26	7	0
50	AA	34	0	40	1	0
50	AB	31	0	34	0	0
51	D1	26	0	26	0	0
51	D4	40	0	54	4	0
51	D5	38	0	50	3	0
52	D5	60	0	64	2	0
53	AK	28	0	30	0	0
All	All	65394	0	65654	1013	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 1013 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)
5:S3:80:ALA:HA	5:S3:91:GLU:O	1.17	1.32
5:S3:38:GLN:O	15:A7:70:SER:HA	1.44	1.14
5:S3:80:ALA:CA	5:S3:91:GLU:O	2.07	1.01
3:S1:449:PRO:O	3:S1:489:VAL:HA	1.60	1.01
5:S3:38:GLN:O	15:A7:70:SER:CA	2.21	0.88

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	V1	428/445 (96%)	389 (91%)	39 (9%)	0	100	100
2	V2	210/217 (97%)	171 (81%)	39 (19%)	0	100	100
3	S1	686/704 (97%)	609 (89%)	77 (11%)	0	100	100
4	S2	428/430 (100%)	378 (88%)	50 (12%)	0	100	100
5	S3	206/228 (90%)	177 (86%)	29 (14%)	0	100	100
6	S7	154/179 (86%)	137 (89%)	17 (11%)	0	100	100
7	S8	174/176 (99%)	160 (92%)	14 (8%)	0	100	100
8	V3	39/75 (52%)	33 (85%)	6 (15%)	0	100	100
9	S6	93/96 (97%)	85 (91%)	8 (9%)	0	100	100
10	S4	124/133 (93%)	112 (90%)	12 (10%)	0	100	100
11	A9	281/338 (83%)	244 (87%)	37 (13%)	0	100	100
12	A2	80/98 (82%)	70 (88%)	10 (12%)	0	100	100
13	A5	109/115 (95%)	93 (85%)	16 (15%)	0	100	100
14	A6	112/127 (88%)	105 (94%)	7 (6%)	0	100	100
15	A7	92/112 (82%)	76 (83%)	15 (16%)	1 (1%)	11	45
16	AL	142/145 (98%)	117 (82%)	25 (18%)	0	100	100
17	AA	78/88 (89%)	67 (86%)	11 (14%)	0	100	100
17	AB	85/88 (97%)	76 (89%)	9 (11%)	0	100	100
18	D3	86/115 (75%)	81 (94%)	5 (6%)	0	100	100
19	D1	299/318 (94%)	269 (90%)	30 (10%)	0	100	100
20	D6	167/175 (95%)	147 (88%)	20 (12%)	0	100	100
21	4L	96/98 (98%)	89 (93%)	7 (7%)	0	100	100
22	D5	604/606 (100%)	536 (89%)	68 (11%)	0	100	100
23	D4	457/459 (100%)	417 (91%)	39 (8%)	1 (0%)	43	77
24	D2	345/347 (99%)	319 (92%)	26 (8%)	0	100	100
25	AK	138/140 (99%)	129 (94%)	9 (6%)	0	100	100
26	B5	137/143 (96%)	119 (87%)	18 (13%)	0	100	100
27	A8	169/171 (99%)	138 (82%)	31 (18%)	0	100	100
28	BJ	169/175 (97%)	150 (89%)	18 (11%)	1 (1%)	21	58
29	AJ	317/320 (99%)	275 (87%)	42 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	S5	97/105 (92%)	80 (82%)	17 (18%)	0	100	100
31	A3	72/83 (87%)	59 (82%)	13 (18%)	0	100	100
32	B3	71/97 (73%)	54 (76%)	16 (22%)	1 (1%)	9	39
33	C2	117/120 (98%)	104 (89%)	13 (11%)	0	100	100
34	B4	126/128 (98%)	109 (86%)	17 (14%)	0	100	100
35	AM	137/143 (96%)	123 (90%)	14 (10%)	0	100	100
36	B6	92/127 (72%)	81 (88%)	10 (11%)	1 (1%)	11	45
37	B7	117/136 (86%)	102 (87%)	15 (13%)	0	100	100
38	B9	174/178 (98%)	147 (84%)	27 (16%)	0	100	100
39	B2	63/72 (88%)	58 (92%)	5 (8%)	0	100	100
40	B8	155/158 (98%)	115 (74%)	40 (26%)	0	100	100
41	BK	100/125 (80%)	85 (85%)	15 (15%)	0	100	100
42	C1	44/49 (90%)	40 (91%)	4 (9%)	0	100	100
43	B1	50/57 (88%)	43 (86%)	7 (14%)	0	100	100
44	A1	68/70 (97%)	64 (94%)	4 (6%)	0	100	100
All	All	7988/8509 (94%)	7032 (88%)	951 (12%)	5 (0%)	49	82

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	D4	53	SER
15	A7	69	MET
28	BJ	71	PRO
32	B3	23	ILE
36	B6	93	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	V1	344/354 (97%)	341 (99%)	3 (1%)	70	75
2	V2	182/183 (100%)	181 (100%)	1 (0%)	81	81
3	S1	578/588 (98%)	574 (99%)	4 (1%)	76	78
4	S2	371/371 (100%)	368 (99%)	3 (1%)	73	77
5	S3	189/204 (93%)	188 (100%)	1 (0%)	81	81
6	S7	132/150 (88%)	131 (99%)	1 (1%)	73	77
7	S8	151/151 (100%)	150 (99%)	1 (1%)	76	78
8	V3	40/68 (59%)	39 (98%)	1 (2%)	42	62
9	S6	79/80 (99%)	79 (100%)	0	100	100
10	S4	113/119 (95%)	113 (100%)	0	100	100
11	A9	246/292 (84%)	246 (100%)	0	100	100
12	A2	73/81 (90%)	73 (100%)	0	100	100
13	A5	99/101 (98%)	98 (99%)	1 (1%)	68	75
14	A6	107/113 (95%)	107 (100%)	0	100	100
15	A7	84/94 (89%)	84 (100%)	0	100	100
16	AL	130/131 (99%)	130 (100%)	0	100	100
17	AA	74/81 (91%)	73 (99%)	1 (1%)	59	70
17	AB	80/81 (99%)	79 (99%)	1 (1%)	61	71
18	D3	81/103 (79%)	81 (100%)	0	100	100
19	D1	266/278 (96%)	262 (98%)	4 (2%)	57	70
20	D6	140/144 (97%)	138 (99%)	2 (1%)	59	70
21	4L	87/87 (100%)	86 (99%)	1 (1%)	65	73
22	D5	539/539 (100%)	538 (100%)	1 (0%)	87	85
23	D4	412/412 (100%)	411 (100%)	1 (0%)	87	85
24	D2	315/315 (100%)	313 (99%)	2 (1%)	78	80
25	AK	101/101 (100%)	101 (100%)	0	100	100
26	B5	122/125 (98%)	122 (100%)	0	100	100
27	A8	154/154 (100%)	153 (99%)	1 (1%)	78	80
28	BJ	155/157 (99%)	153 (99%)	2 (1%)	61	71
29	AJ	283/284 (100%)	282 (100%)	1 (0%)	84	82
30	S5	88/94 (94%)	87 (99%)	1 (1%)	65	73
31	A3	65/71 (92%)	65 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	B3	55/75 (73%)	55 (100%)	0	100	100
33	C2	106/107 (99%)	106 (100%)	0	100	100
34	B4	114/114 (100%)	114 (100%)	0	100	100
35	AM	119/121 (98%)	119 (100%)	0	100	100
36	B6	92/121 (76%)	90 (98%)	2 (2%)	45	64
37	B7	108/119 (91%)	108 (100%)	0	100	100
38	B9	159/160 (99%)	157 (99%)	2 (1%)	61	71
39	B2	59/62 (95%)	59 (100%)	0	100	100
40	B8	142/142 (100%)	140 (99%)	2 (1%)	59	70
41	BK	93/112 (83%)	93 (100%)	0	100	100
42	C1	42/44 (96%)	42 (100%)	0	100	100
43	B1	48/53 (91%)	48 (100%)	0	100	100
44	A1	59/59 (100%)	59 (100%)	0	100	100
All	All	7076/7395 (96%)	7036 (99%)	40 (1%)	76	80

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	AB	80	ILE
36	B6	95	THR
27	A8	109	CYS
29	AJ	31	ILE
38	B9	23	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 124 such sidechains are listed below:

Mol	Chain	Res	Type
22	D5	113	ASN
35	AM	89	ASN
23	D4	293	HIS
35	AM	53	ASN
39	B2	58	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 1 is monoatomic - leaving 17 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	$\# Z > 2$
50	ZMP	AA	101	17	28,33,36	0.63	1 (3%)	32,40,45	1.12	3 (9%)
45	SF4	S8	202	7	0,12,12	-	-	-		
51	3PE	D5	902	-	37,37,50	0.35	0	40,42,55	0.34	0
51	3PE	D4	501	-	39,39,50	0.33	0	42,44,55	0.33	0
53	PC1	AK	201	-	27,27,53	0.39	0	33,35,61	0.37	0
45	SF4	S8	201	7	0,12,12	-	-	-		
45	SF4	S1	802	3	0,12,12	-	-	-		
50	ZMP	AB	101	17	25,30,36	0.77	1 (4%)	29,37,45	1.07	2 (6%)
46	FMN	V1	501	-	33,33,33	0.36	0	48,50,50	0.35	0
49	NDP	A9	401	-	51,52,52	0.50	1 (1%)	71,80,80	0.57	1 (1%)
51	3PE	D1	501	-	25,25,50	0.40	0	28,30,55	0.45	0
52	CDL	D5	901	-	59,59,99	0.40	0	65,71,111	0.54	2 (3%)
47	FES	V2	300	2	0,4,4	-	-	-		
45	SF4	V1	500	1	0,12,12	-	-	-		
45	SF4	S1	801	3	0,12,12	-	-	-		
47	FES	S1	803	3	0,4,4	-	-	-		
45	SF4	S7	300	6	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
50	ZMP	AA	101	17	-	14/38/40/43	-
51	3PE	D5	902	-	-	7/41/41/54	-
51	3PE	D4	501	-	-	5/43/43/54	-
53	PC1	AK	201	-	-	9/31/31/57	-
45	SF4	S8	202	7	-	-	0/6/5/5
45	SF4	S8	201	7	-	-	0/6/5/5
45	SF4	S1	802	3	-	-	0/6/5/5
50	ZMP	AB	101	17	-	11/35/37/43	-
49	NDP	A9	401	-	-	10/34/77/77	0/5/5/5
51	3PE	D1	501	-	-	11/28/28/54	-
46	FMN	V1	501	-	-	6/18/18/18	0/3/3/3
52	CDL	D5	901	-	-	18/70/70/110	-
47	FES	V2	300	2	-	-	0/1/1/1
45	SF4	V1	500	1	-	-	0/6/5/5
45	SF4	S1	801	3	-	-	0/6/5/5
47	FES	S1	803	3	-	-	0/1/1/1
45	SF4	S7	300	6	-	-	0/6/5/5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	AA	101	ZMP	C9-C10	2.34	1.53	1.50
50	AB	101	ZMP	C9-C10	2.32	1.53	1.50
49	A9	401	NDP	P2B-O2B	2.01	1.63	1.59

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	AB	101	ZMP	O1-C10-C9	-3.13	120.37	123.98
50	AA	101	ZMP	O1-C10-C9	-2.81	120.74	123.98
49	A9	401	NDP	P2B-O2B-C2B	2.66	130.54	123.43
52	D5	901	CDL	CB4-OB6-CB5	2.28	123.24	117.80
50	AA	101	ZMP	C15-C14-C13	-2.22	108.69	112.39

There are no chirality outliers.

5 of 91 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
46	V1	501	FMN	C2'-C3'-C4'-O4'

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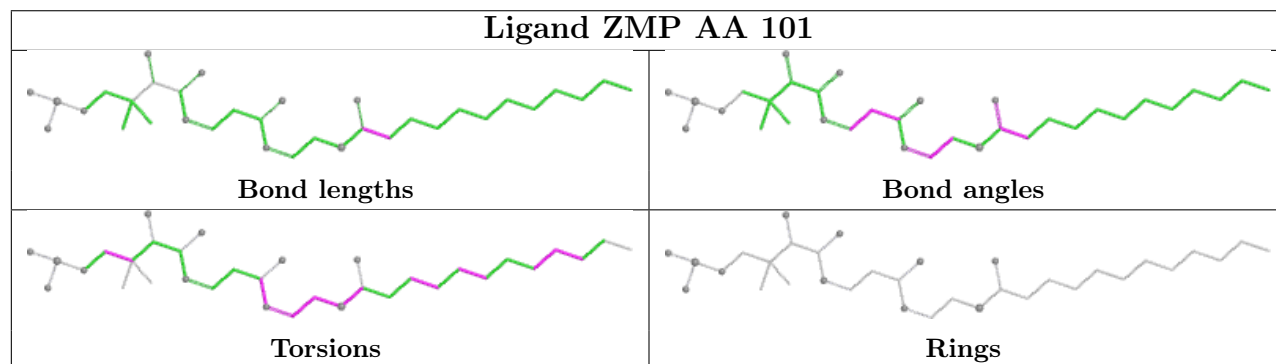
Mol	Chain	Res	Type	Atoms
46	V1	501	FMN	C2'-C3'-C4'-C5'
46	V1	501	FMN	O3'-C3'-C4'-O4'
46	V1	501	FMN	O3'-C3'-C4'-C5'
49	A9	401	NDP	C1B-C2B-O2B-P2B

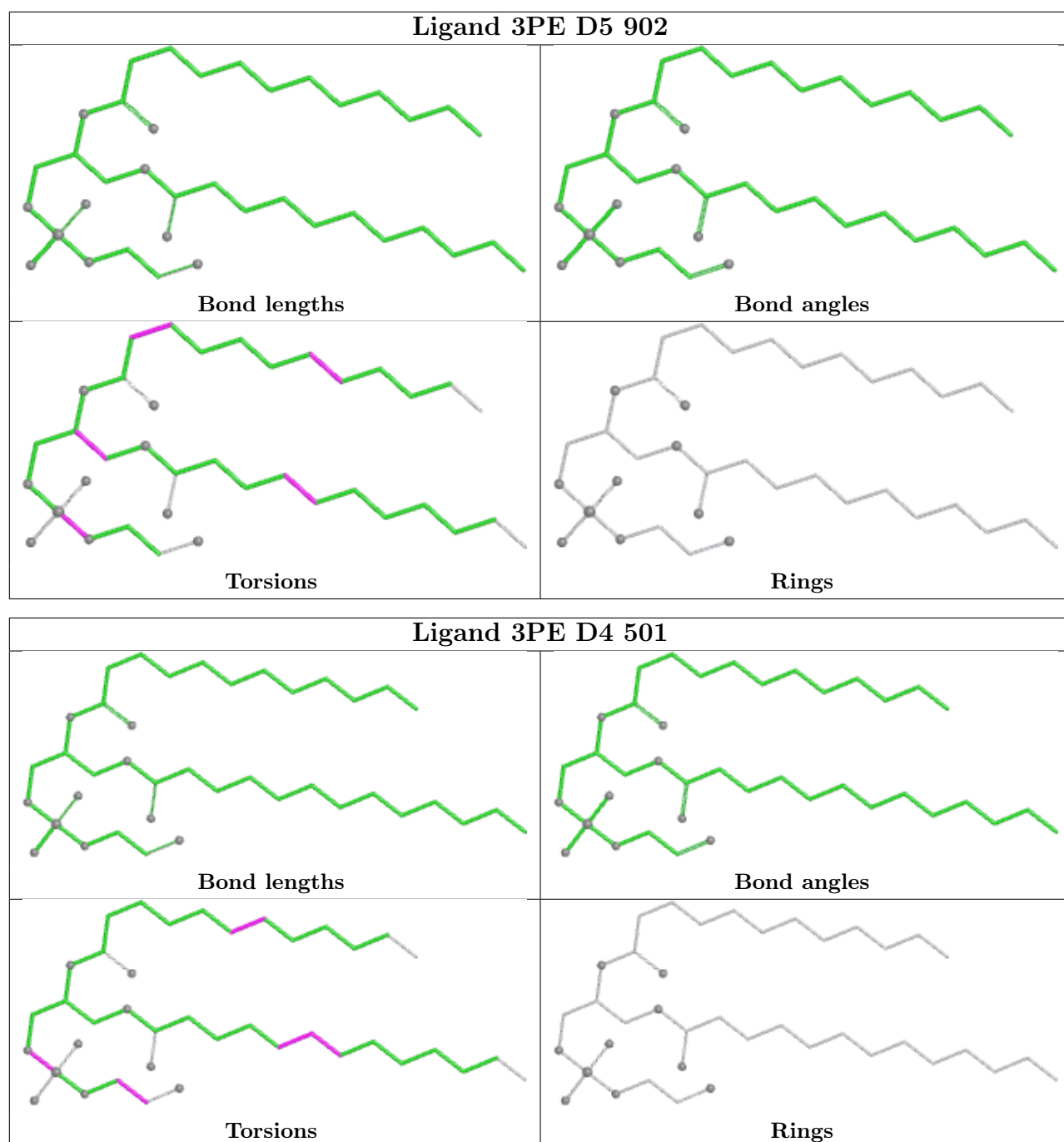
There are no ring outliers.

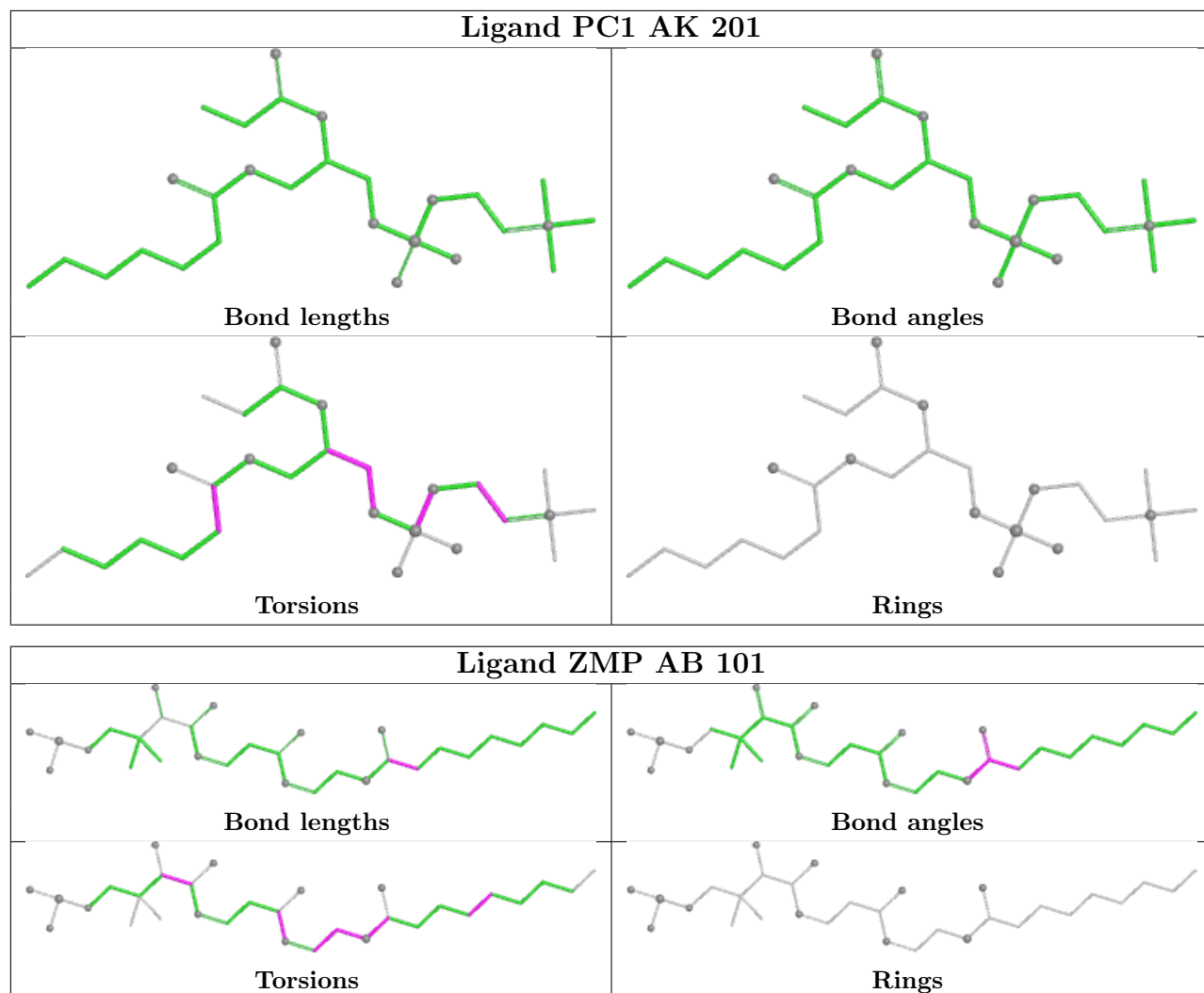
9 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
50	AA	101	ZMP	1	0
51	D5	902	3PE	3	0
51	D4	501	3PE	4	0
46	V1	501	FMN	3	0
49	A9	401	NDP	7	0
52	D5	901	CDL	2	0
45	V1	500	SF4	1	0
45	S1	801	SF4	2	0
45	S7	300	SF4	1	0

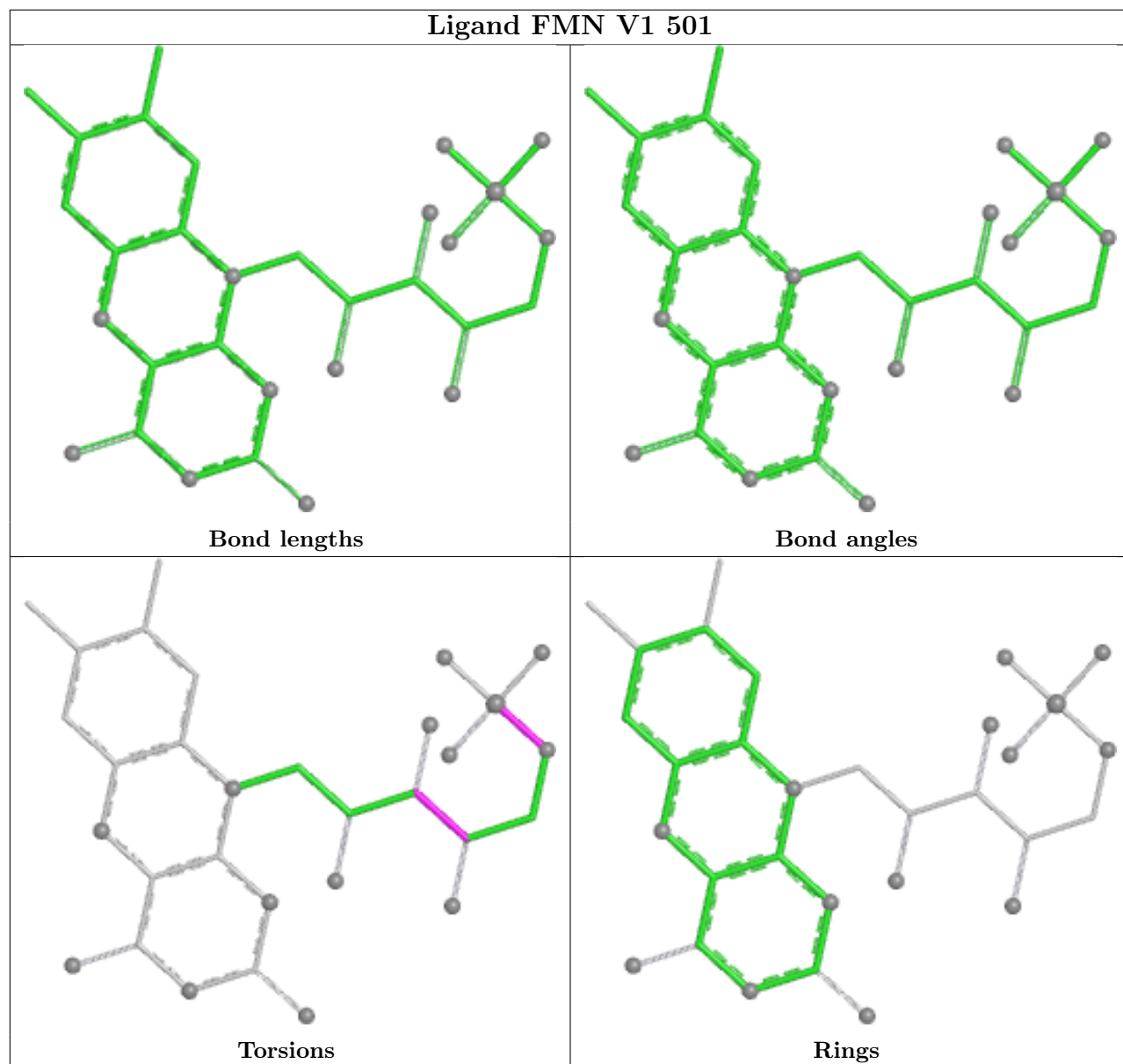
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

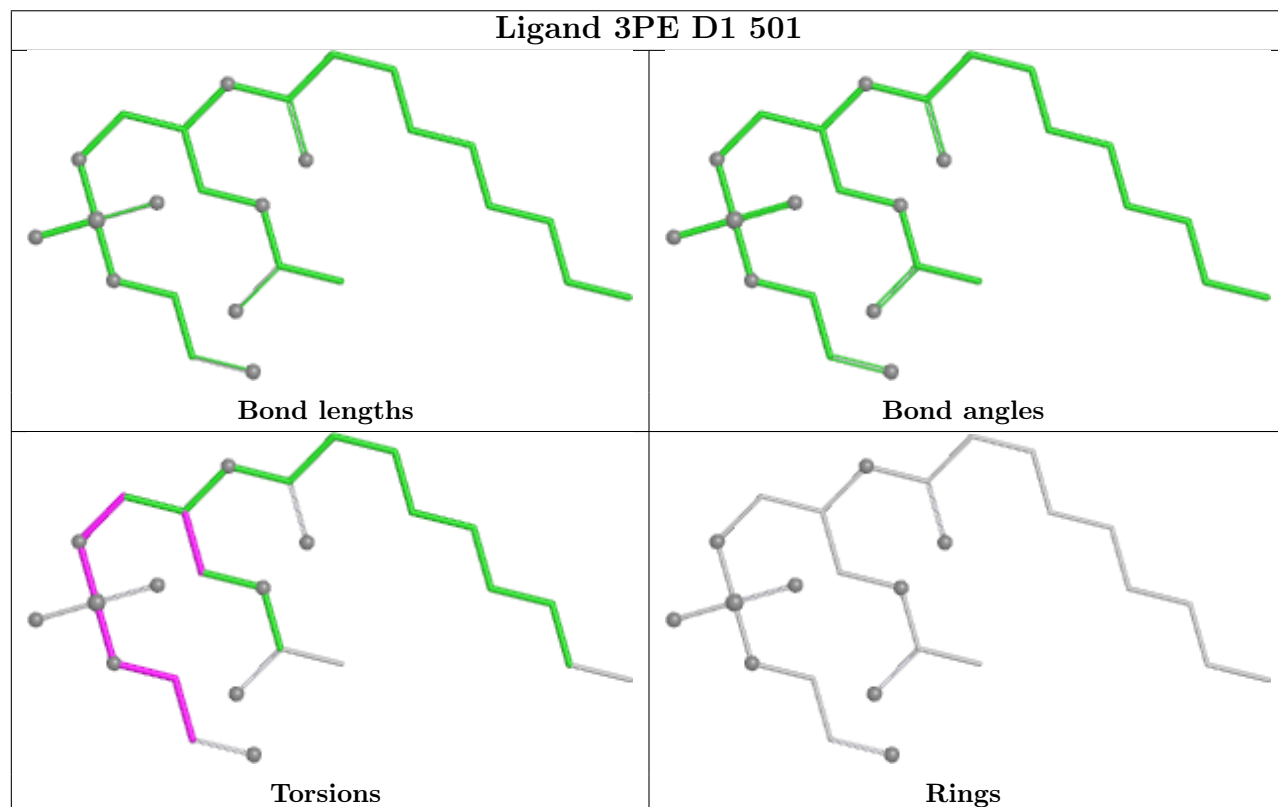
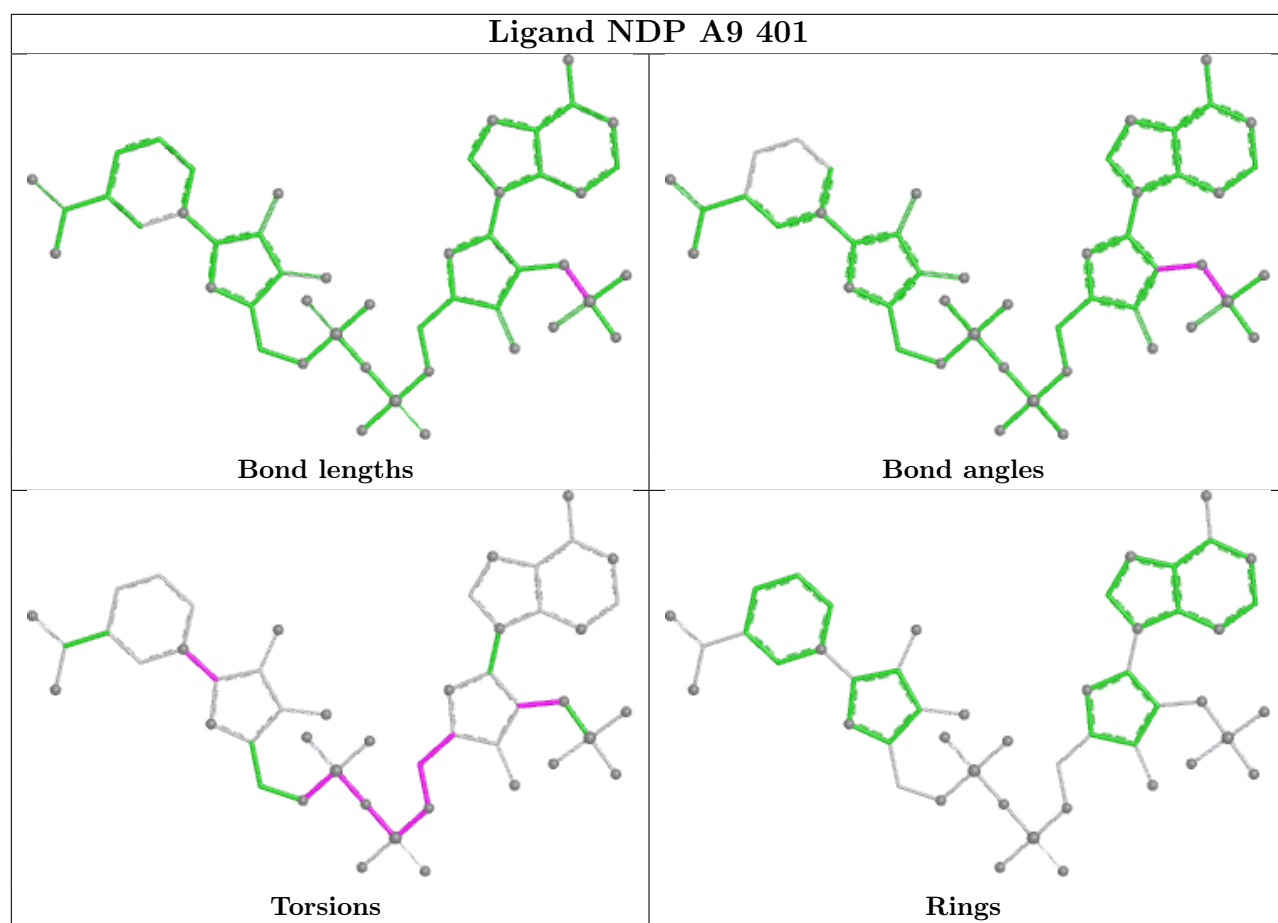


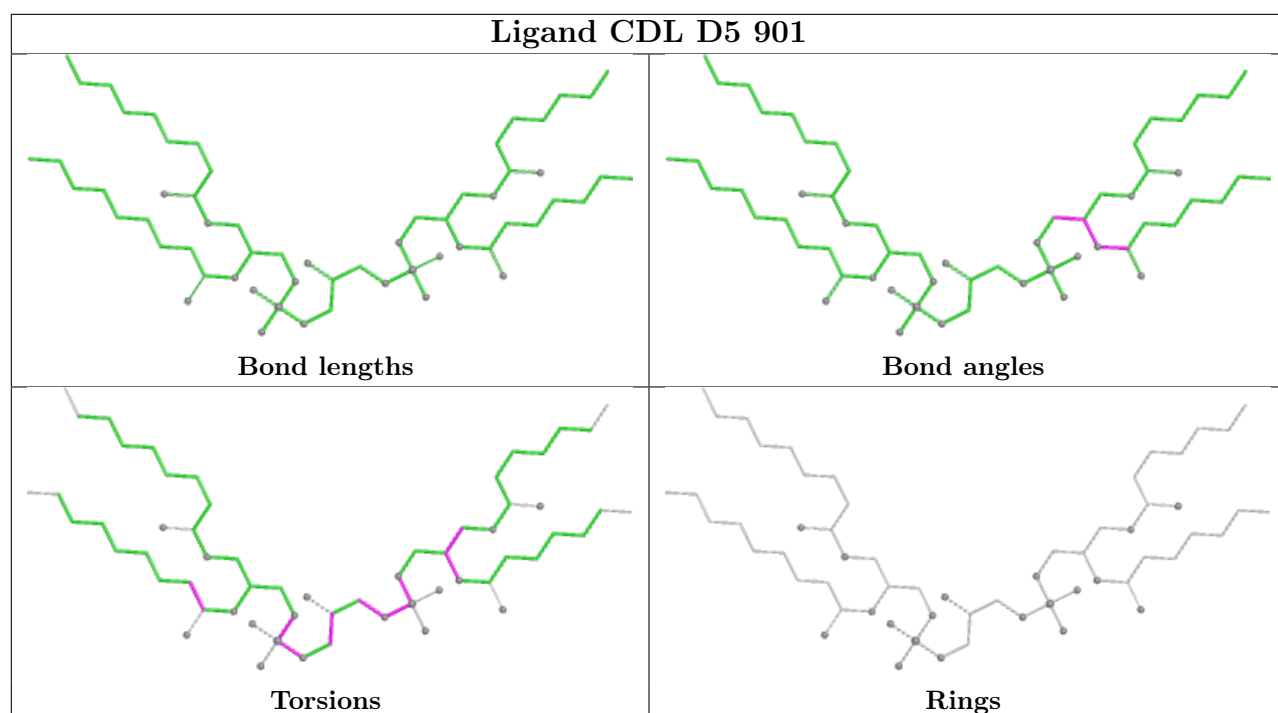




Ligand FMN V1 501







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

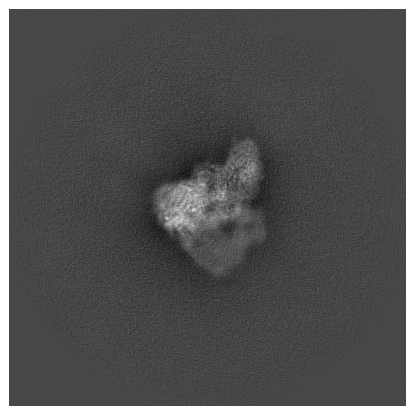
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4500. These allow visual inspection of the internal detail of the map and identification of artifacts.

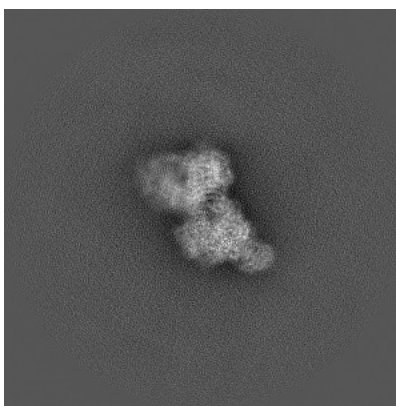
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

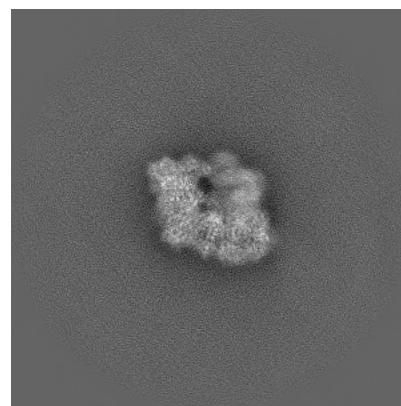
6.1.1 Primary map



X

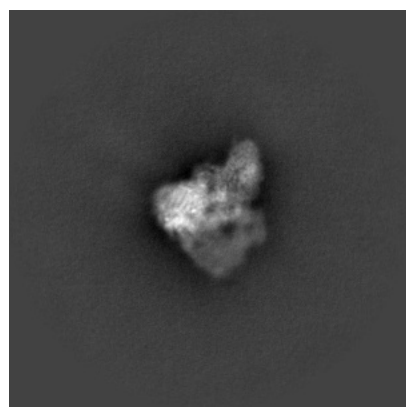


Y

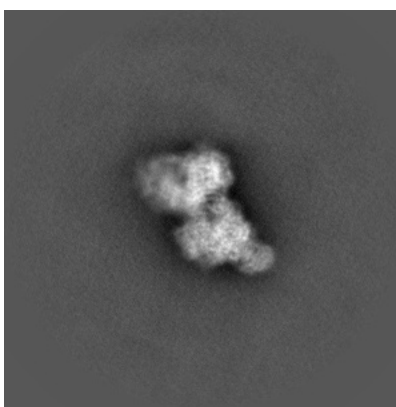


Z

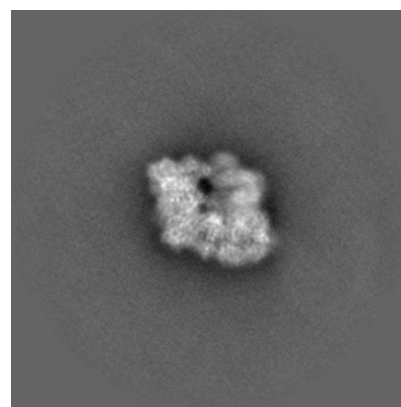
6.1.2 Raw map



X



Y

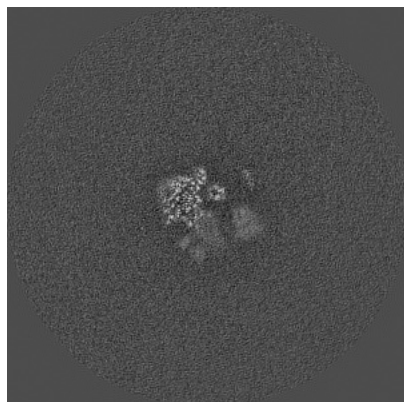


Z

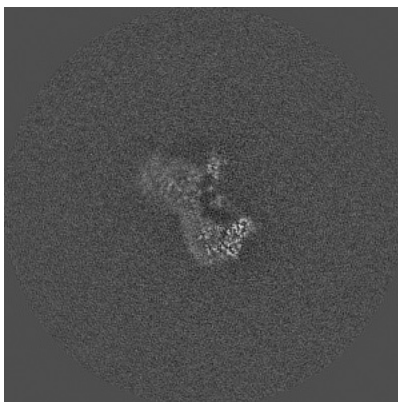
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

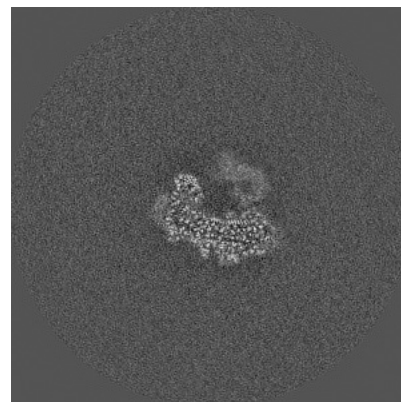
6.2.1 Primary map



X Index: 256

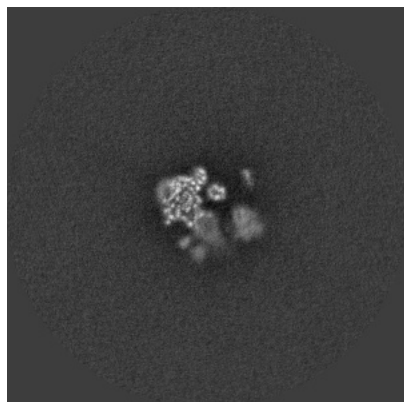


Y Index: 256

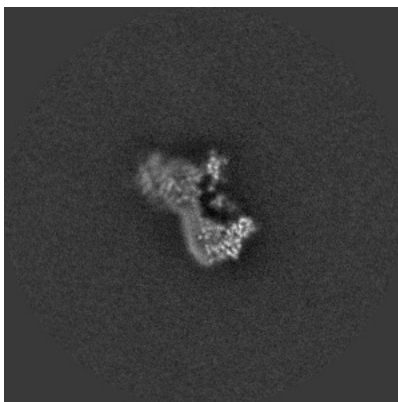


Z Index: 256

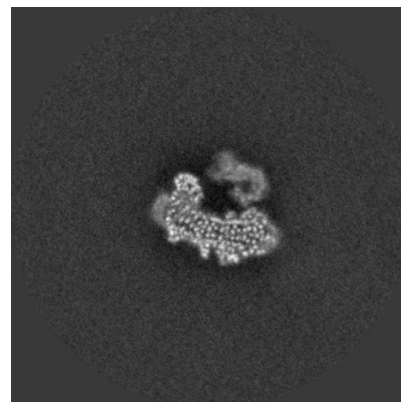
6.2.2 Raw map



X Index: 256



Y Index: 256

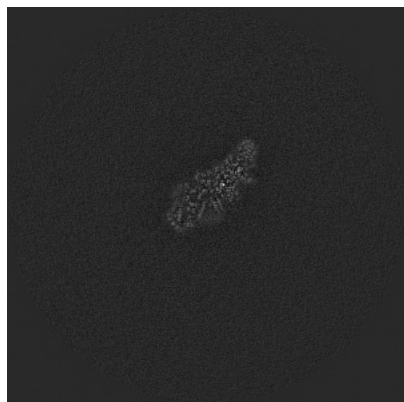


Z Index: 256

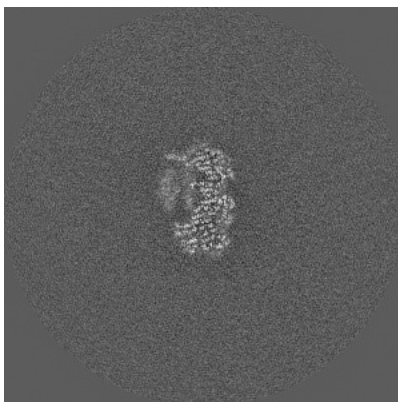
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

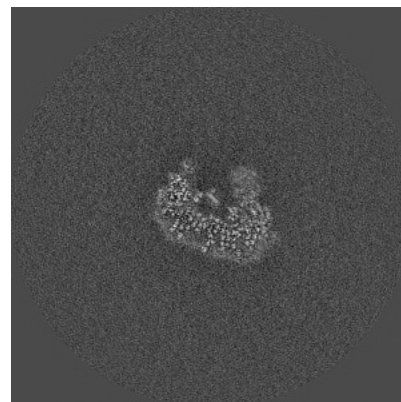
6.3.1 Primary map



X Index: 208

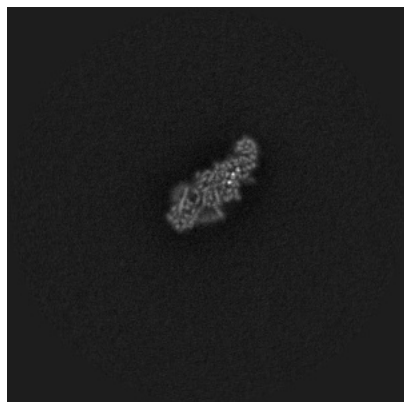


Y Index: 229

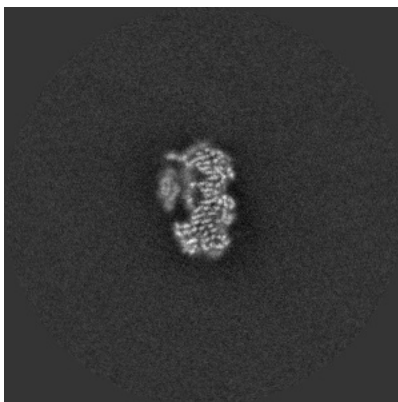


Z Index: 268

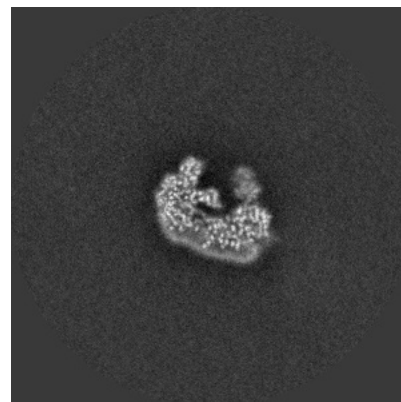
6.3.2 Raw map



X Index: 205



Y Index: 229

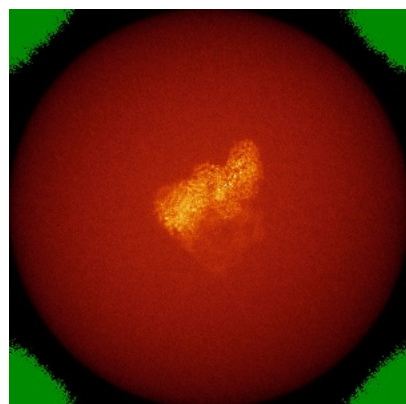


Z Index: 274

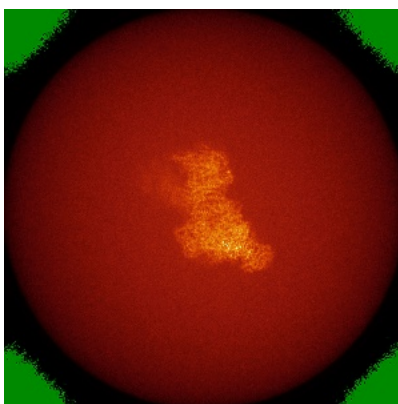
The images above show the largest variance slices of the map in three orthogonal directions.

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

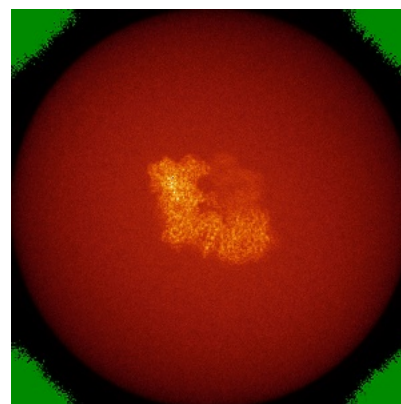
6.4.1 Primary map



X

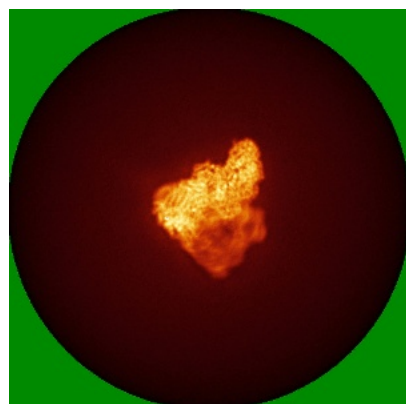


Y

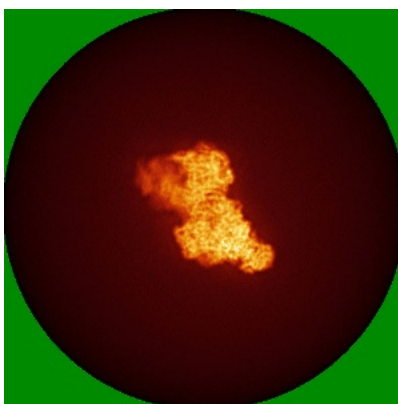


Z

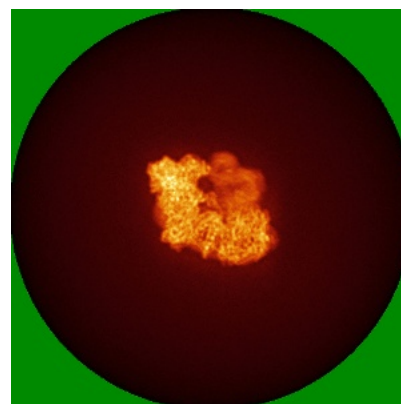
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

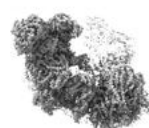
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

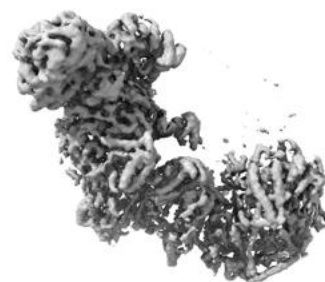
6.5.2 Raw map



X



Y



Z

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

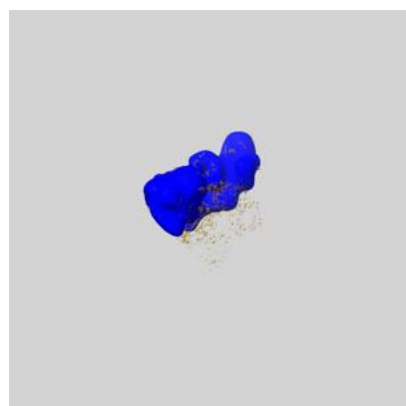
6.6 Mask visualisation [i](#)

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

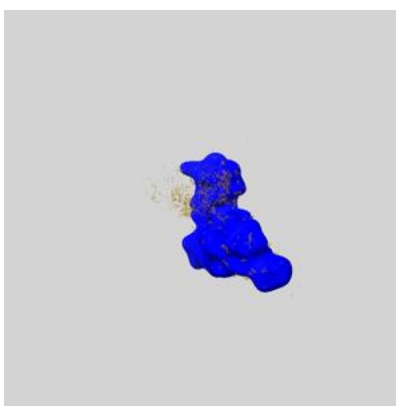
A mask typically either:

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

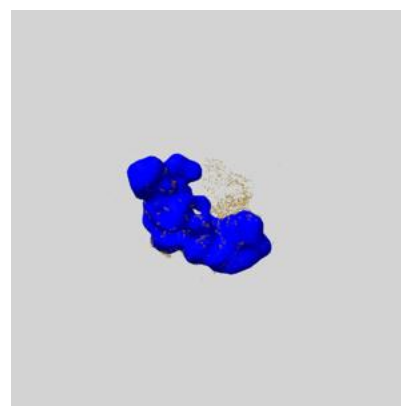
6.6.1 emd_4500_msk_1.map [i](#)



X



Y

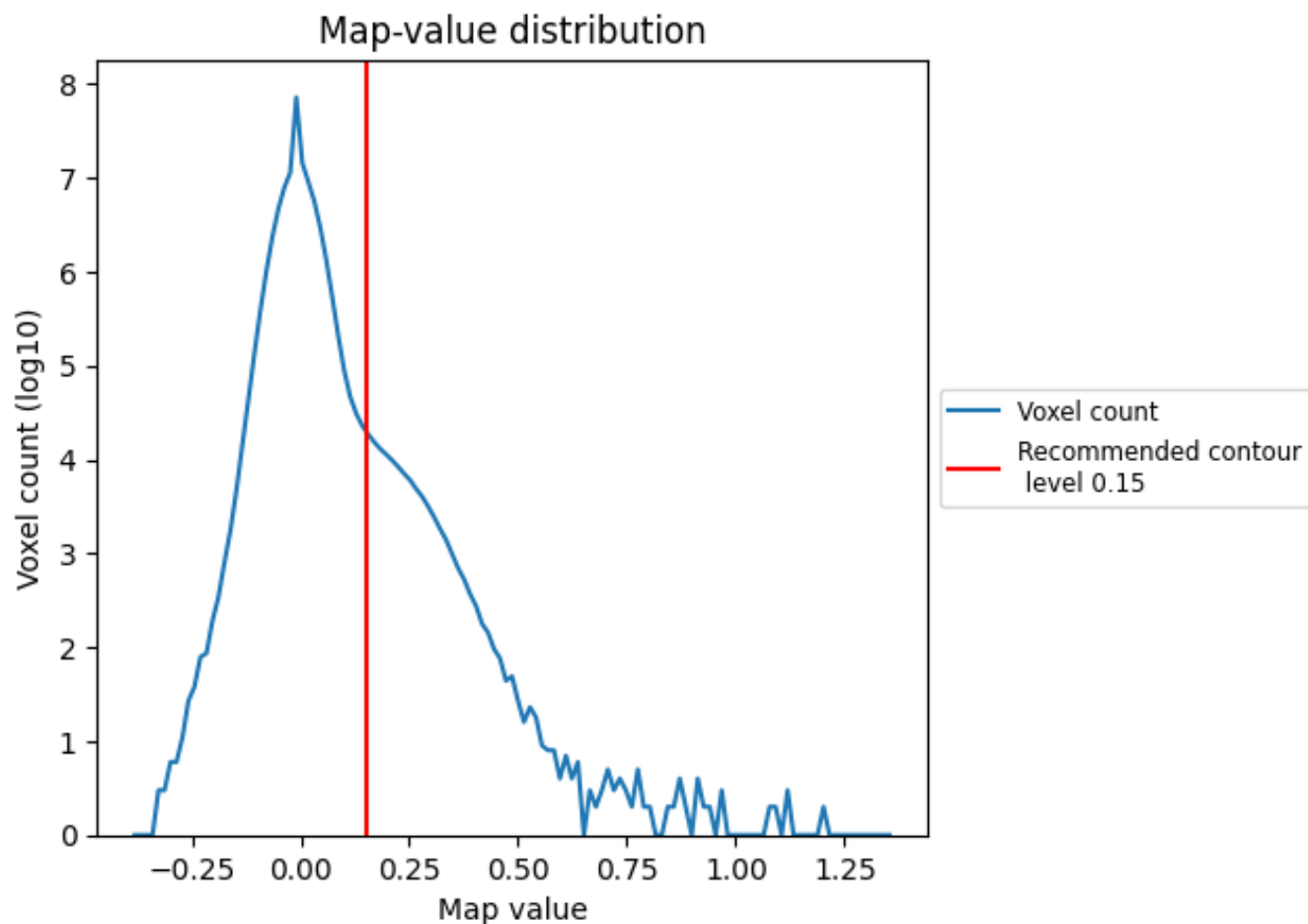


Z

7 Map analysis [i](#)

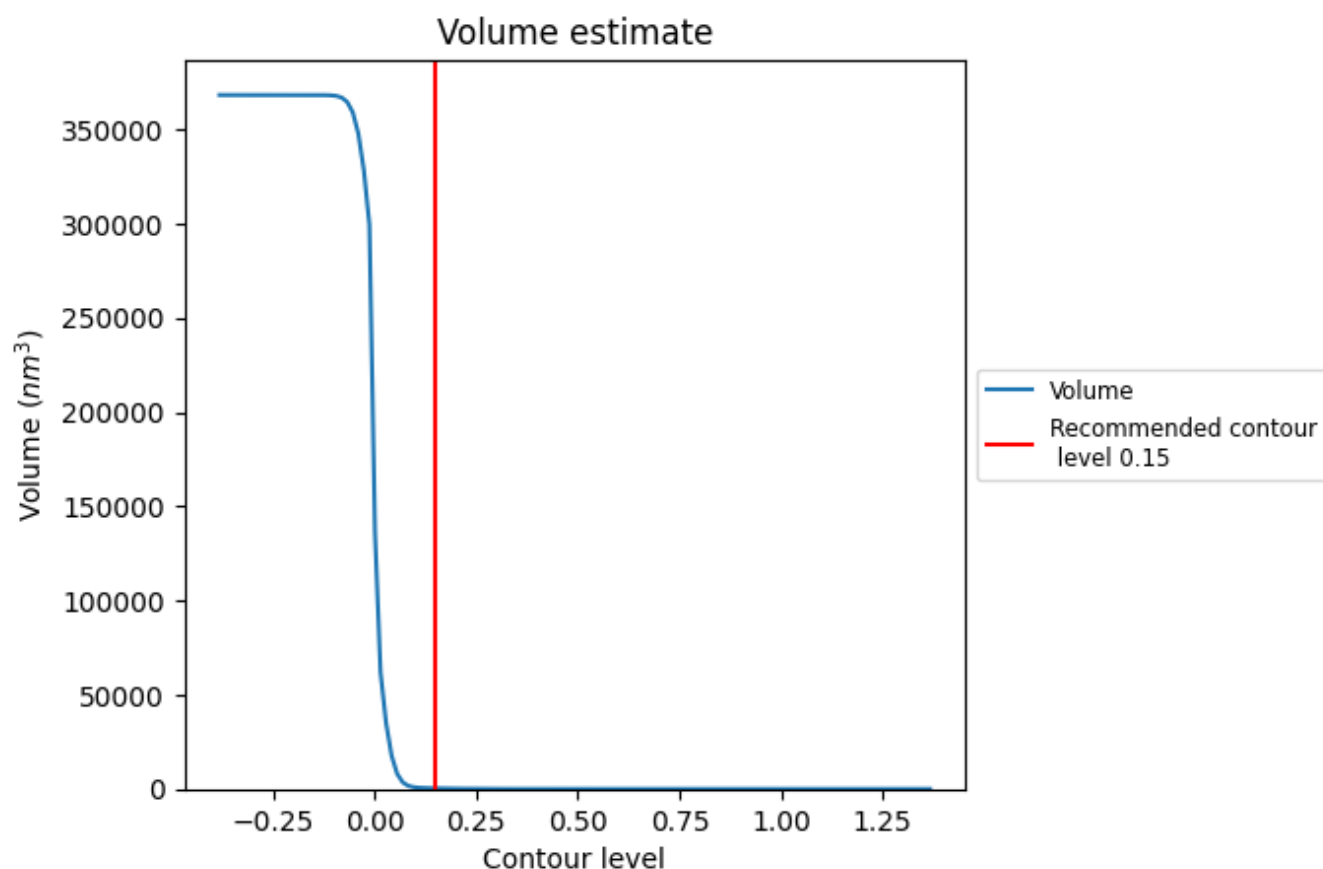
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

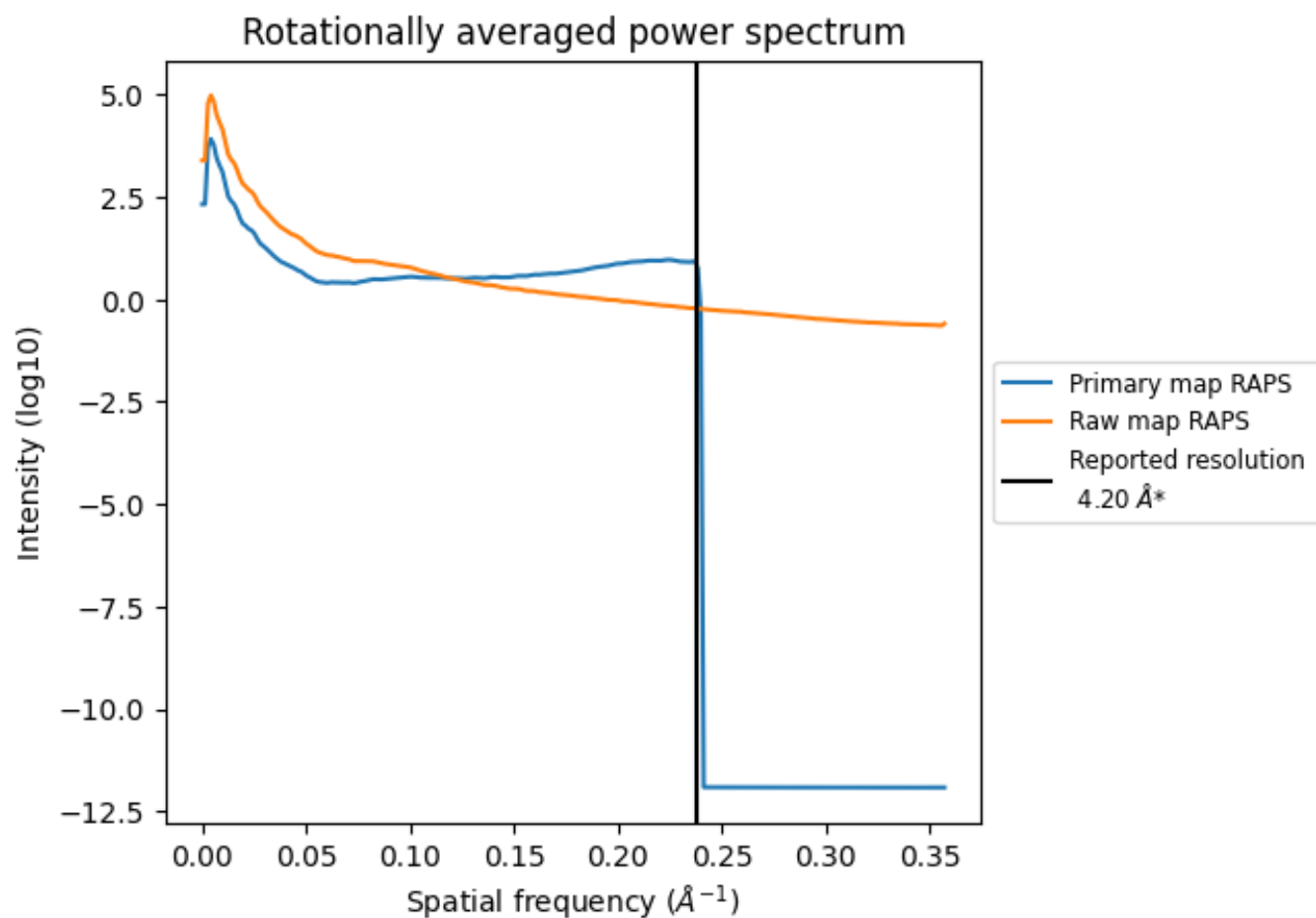
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 328 nm^3 ; this corresponds to an approximate mass of 296 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

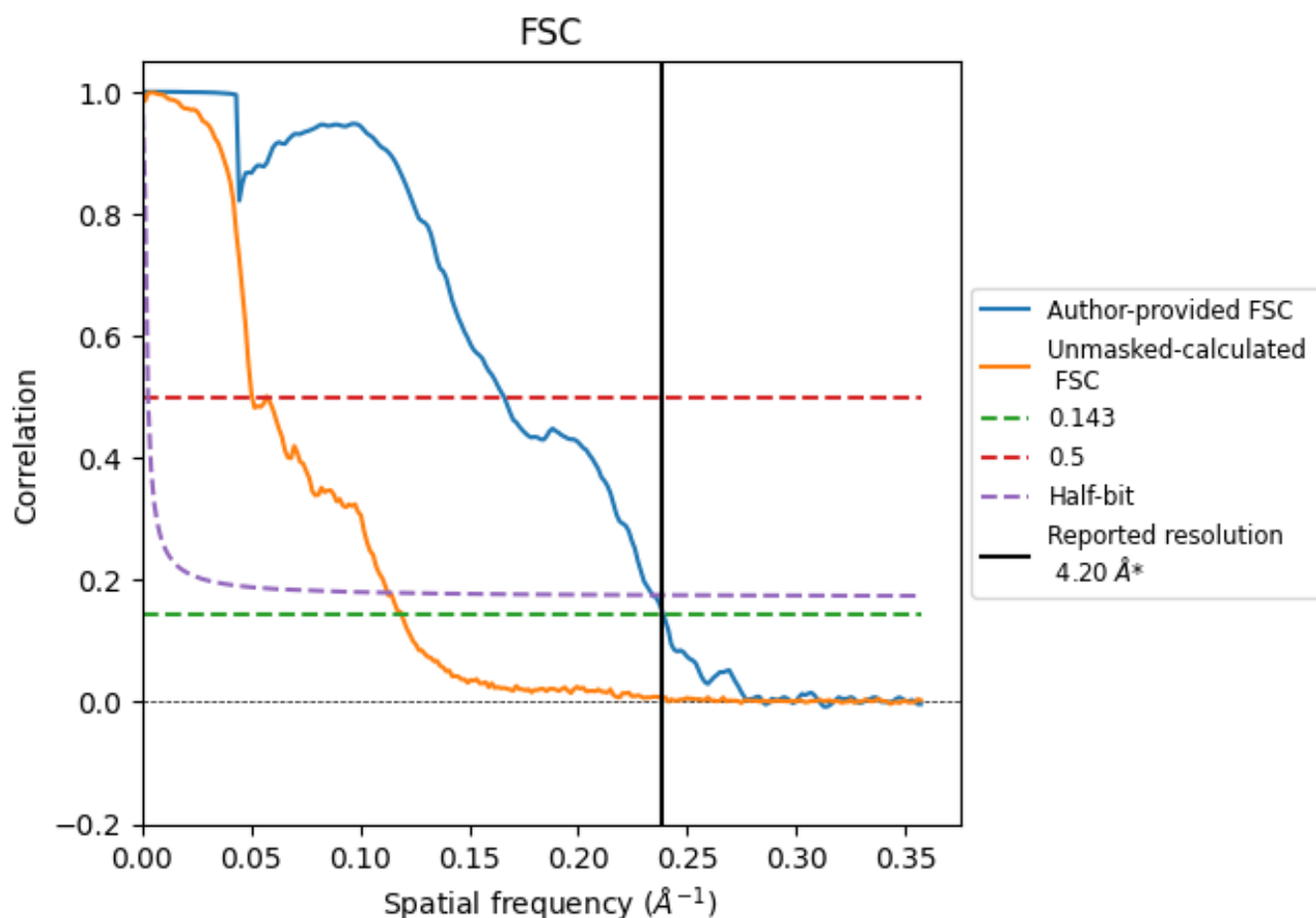


*Reported resolution corresponds to spatial frequency of 0.238 $\text{\AA}^{-1}$

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 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

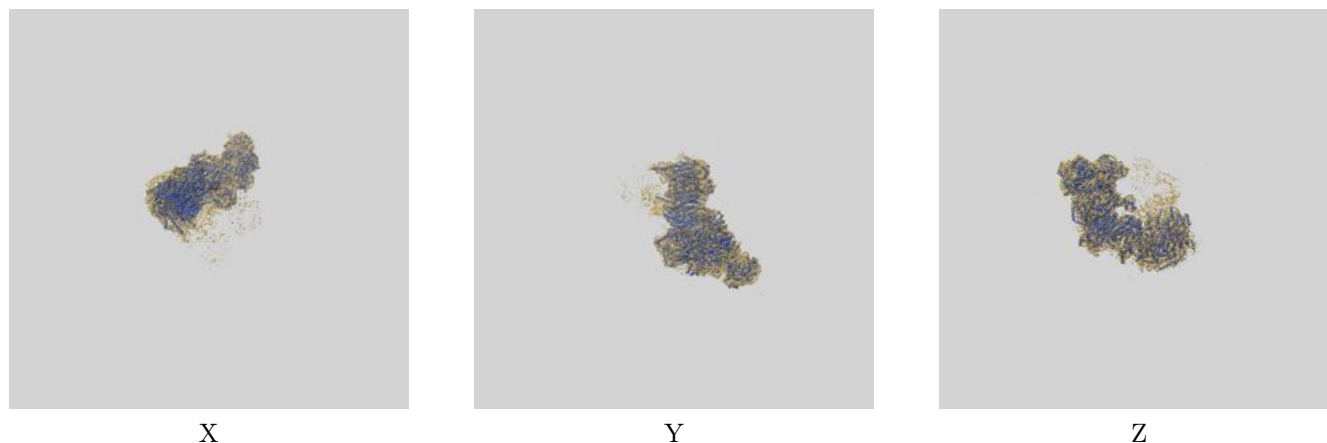
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.18	6.02	4.27
Unmasked-calculated*	8.40	19.80	8.88

*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 8.40 differs from the reported value 4.2 by more than 10 %

9 Map-model fit [i](#)

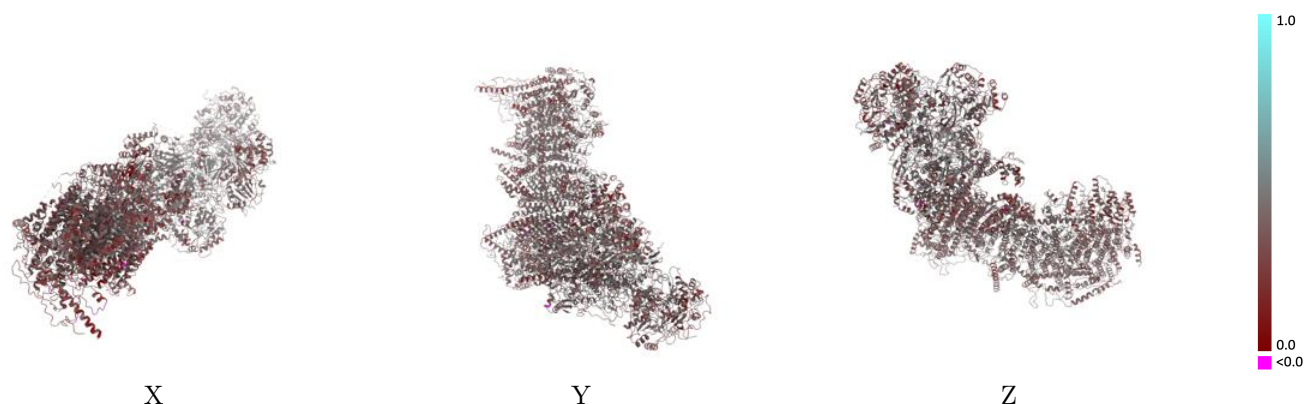
This section contains information regarding the fit between EMDB map EMD-4500 and PDB model 6QC8. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



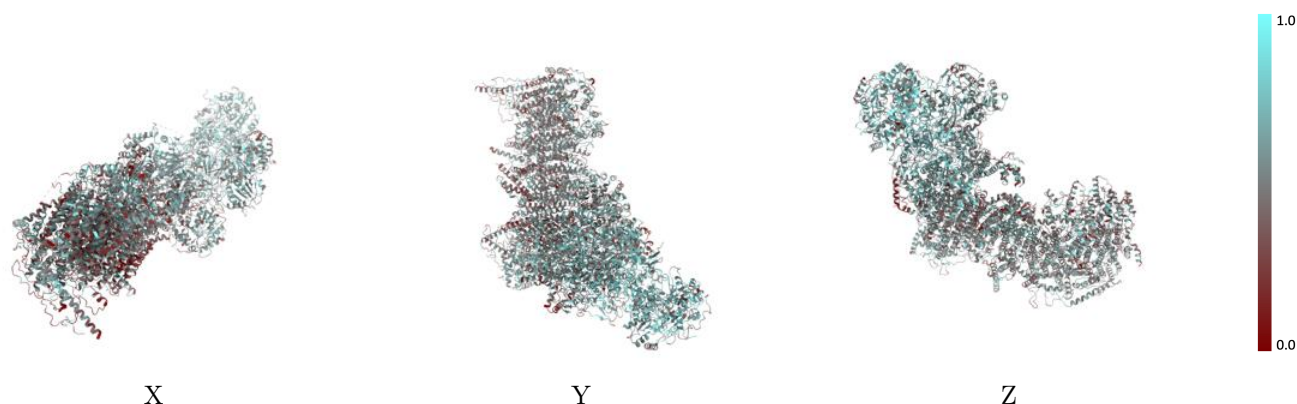
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



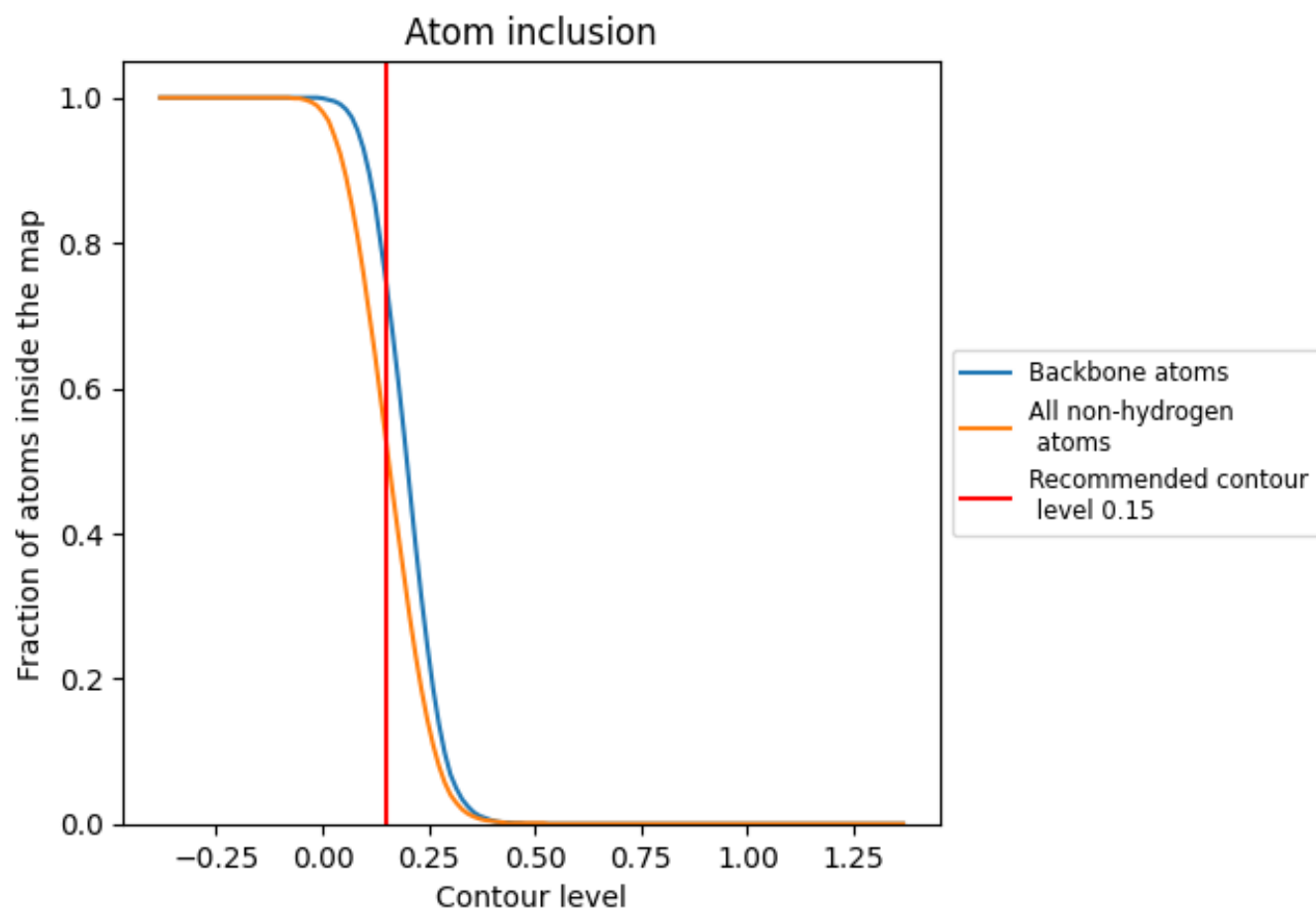
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion ⓘ



At the recommended contour level, 75% of all backbone atoms, 53% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5270	 0.3660
4L	 0.4380	 0.3710
A1	 0.5610	 0.3710
A2	 0.5840	 0.3360
A3	 0.5330	 0.3650
A5	 0.5660	 0.3570
A6	 0.5380	 0.3820
A7	 0.4620	 0.3790
A8	 0.5290	 0.3540
A9	 0.5410	 0.3710
AA	 0.4660	 0.3170
AB	 0.4690	 0.3300
AJ	 0.5010	 0.3510
AK	 0.3700	 0.3230
AL	 0.4570	 0.3780
AM	 0.5230	 0.3490
B1	 0.4010	 0.3520
B2	 0.4560	 0.3120
B3	 0.4330	 0.3230
B4	 0.4800	 0.3470
B5	 0.5330	 0.3730
B6	 0.4710	 0.3370
B7	 0.4630	 0.2820
B8	 0.4770	 0.3460
B9	 0.5400	 0.3490
BJ	 0.5300	 0.3450
BK	 0.4650	 0.3640
C1	 0.4870	 0.3290
C2	 0.5130	 0.3720
D1	 0.4980	 0.3700
D2	 0.5130	 0.3830
D3	 0.4250	 0.3530
D4	 0.4970	 0.3860
D5	 0.4540	 0.3490
D6	 0.3950	 0.3430



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Chain	Atom inclusion	Q-score
S1	 0.6050	 0.3940
S2	 0.5680	 0.3870
S3	 0.6270	 0.4090
S4	 0.5850	 0.4010
S5	 0.5250	 0.3370
S6	 0.5840	 0.4050
S7	 0.6200	 0.4000
S8	 0.6480	 0.4010
V1	 0.6300	 0.3680
V2	 0.6110	 0.3640
V3	 0.6070	 0.3810