



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 07:18 AM UTC

PDB ID : 8UEY / pdb_00008uey
EMDB ID : EMD-42175
Title : In-situ complex I, Deactive class07
Authors : Zheng, W.; Zhu, J.; Zhang, K.
Deposited on : 2023-10-02
Resolution : 3.60 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:

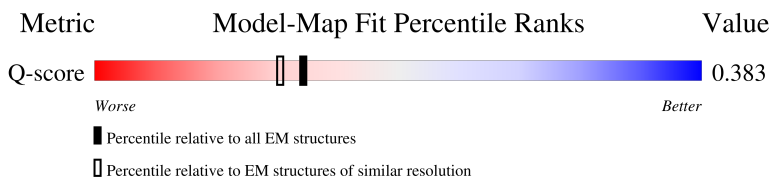
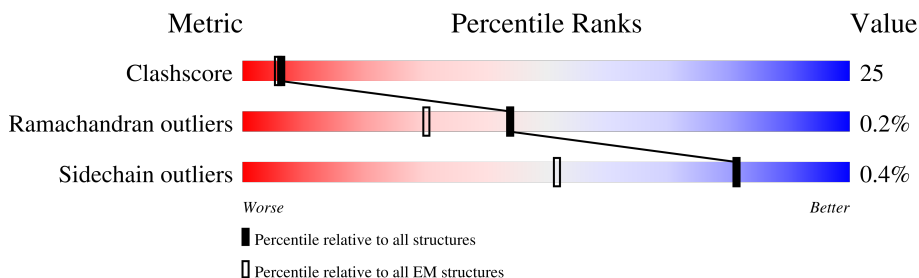
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.60 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	12797 (3.10 - 4.10)

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	1A	115	10% 36% 40% 23%
2	1B	255	15% 29% 31% 39%
3	1C	264	33% 34% 45% 21%
4	1D	476	15% 46% 37% 17%

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Mol	Chain	Length	Quality of chain
5	1E	249	
6	1F	464	
7	1G	727	
8	1H	318	
9	1I	239	
10	1J	175	
11	1K	98	
12	1L	606	
13	1M	459	
14	1N	347	
15	1O	357	
16	1P	377	
17	1Q	175	
18	1R	123	
19	1S	99	
20	1T	156	
20	1U	156	
21	1V	116	
22	1W	128	
23	1X	172	
24	1Y	141	
25	1Z	144	
26	1a	70	
27	1b	84	
28	1c	76	

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Mol	Chain	Length	Quality of chain
29	1d	123	
30	1e	106	
31	1f	135	
32	1g	154	
33	1h	189	
34	1i	128	
35	1j	105	
36	1k	98	
37	1l	186	
38	1m	129	
39	1n	179	
40	1o	137	
41	1p	176	
42	1q	145	
43	1r	114	
44	1s	471	

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
47	SF4	1B	201	-	-	X	-
47	SF4	1G	801	-	-	X	-
48	FES	1E	301	-	-	X	-

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 66812 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1A	88	Total	C	N	O	S	0	0
			707	484	101	117	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1B	155	Total	C	N	O	S	0	0
			1242	791	226	211	14		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1B	?	-	PRO	deletion	UNP A0A4X1VVS8
1B	?	-	SER	deletion	UNP A0A4X1VVS8
1B	?	-	SER	deletion	UNP A0A4X1VVS8

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1C	209	Total	C	N	O	S	0	0
			1740	1125	297	316	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1C	104	GLN	ARG	conflict	UNP A0A286ZNN4
1C	154	GLY	ASP	conflict	UNP A0A286ZNN4

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1D	394	Total	C	N	O	S	0	0
			3189	2040	547	580	22		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1D	0	GLY	GLU	conflict	UNP A0A8D0QM68

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1E	214	Total	C	N	O	S	0	0
			1658	1058	278	312	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1F	432	Total	C	N	O	S	0	0
			3325	2100	592	613	20		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	1G	699	Total	C	N	O	S	0	0
			5362	3360	933	1029	40		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	1H	293	Total	C	N	O	S	0	0
			2316	1556	355	384	21		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	1I	176	Total	C	N	O	S	0	0
			1412	887	243	269	13		

- Molecule 10 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	1J	175	Total	C	N	O	S	0	0
			1339	898	190	238	13		

- Molecule 11 is a protein called NADH-ubiquinone oxidoreductase chain 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	1K	98	Total	C	N	O	S	0	0
			750	494	113	129	14		

- Molecule 12 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	1L	606	Total	C	N	O	S	0	0
			4818	3195	746	826	51		

- Molecule 13 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	1M	459	Total	C	N	O	S	0	0
			3632	2411	572	610	39		

- Molecule 14 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	1N	347	Total	C	N	O	S	0	0
			2712	1783	420	463	46		

- Molecule 15 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	1O	320	Total	C	N	O	S	0	0
			2590	1649	440	491	10		

- Molecule 16 is a protein called NADH:ubiquinone oxidoreductase subunit A9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	1P	342	Total	C	N	O	S	0	0
			2751	1783	481	478	9		

- Molecule 17 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	1Q	129	Total	C	N	O	S	0	0
			1047	659	186	199	3		

- Molecule 18 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	1R	96	Total	C	N	O	S	0	0
			741	452	140	146	3		

- Molecule 19 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	1S	87	Total	C	N	O	S	0	0
			700	440	131	127	2		

- Molecule 20 is a protein called NADH:ubiquinone oxidoreductase subunit AB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	1T	85	Total	C	N	O	S	0	0
			689	445	101	138	5		
20	1U	86	Total	C	N	O	S	0	0
			694	448	102	139	5		

- Molecule 21 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 isoform X1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	1V	115	Total	C	N	O	S	0	0
			927	599	157	168	3		

- Molecule 22 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1W	115	Total	C	N	O	S	0	0
			971	619	179	168	5		

- Molecule 23 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	1X	171	Total	C	N	O	S	0	0
			1398	887	250	251	10		

- Molecule 24 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	1Y	139	Total	C	N	O	S	0	0
			1016	648	173	189	6		

- Molecule 25 is a protein called NADH:ubiquinone oxidoreductase subunit A13.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	1Z	141	Total	C	N	O	S	0	0
			1168	752	202	205	9		

- Molecule 26 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	1a	70	Total	C	N	O	S	0	0
			562	361	101	94	6		

- Molecule 27 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	1b	83	Total	C	N	O	S	0	0
			643	417	110	115	1		

- Molecule 28 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	1c	49	Total	C	N	O	0	0
			417	276	71	70		

- Molecule 29 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	1d	121	Total	C	N	O	S	0	0
			996	648	172	170	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1d	-2	ACE	-	acetylation	UNP A0A480JRW3

- Molecule 30 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	1e	99	Total	C	N	O	S	0	0
			816	519	151	140	6		

- Molecule 31 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1 [Sus scrofa].

Mol	Chain	Residues	Atoms					AltConf	Trace
31	1f	57	Total	C	N	O	S	0	0
			487	316	89	80	2		

There are 29 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1f	-77	MET	-	initiating methionine	UNP A0A8D1IZ33
1f	-76	ALA	-	expression tag	UNP A0A8D1IZ33
1f	-75	ALA	-	expression tag	UNP A0A8D1IZ33
1f	-74	ALA	-	expression tag	UNP A0A8D1IZ33
1f	-73	ILE	-	expression tag	UNP A0A8D1IZ33
1f	-72	LEU	-	expression tag	UNP A0A8D1IZ33
1f	-71	LYS	-	expression tag	UNP A0A8D1IZ33
1f	-70	LEU	-	expression tag	UNP A0A8D1IZ33
1f	-69	GLU	-	expression tag	UNP A0A8D1IZ33
1f	-68	GLU	-	expression tag	UNP A0A8D1IZ33
1f	-67	THR	-	expression tag	UNP A0A8D1IZ33
1f	-66	ARG	-	expression tag	UNP A0A8D1IZ33
1f	-65	GLY	-	expression tag	UNP A0A8D1IZ33
1f	-64	GLY	-	expression tag	UNP A0A8D1IZ33
1f	-63	GLY	-	expression tag	UNP A0A8D1IZ33
1f	-62	GLU	-	expression tag	UNP A0A8D1IZ33
1f	-61	LYS	-	expression tag	UNP A0A8D1IZ33
1f	-60	CYS	-	expression tag	UNP A0A8D1IZ33
1f	-59	ASP	-	expression tag	UNP A0A8D1IZ33
1f	-58	LYS	-	expression tag	UNP A0A8D1IZ33
1f	-57	ASN	-	expression tag	UNP A0A8D1IZ33
1f	-56	GLN	-	expression tag	UNP A0A8D1IZ33
1f	-55	GLY	-	expression tag	UNP A0A8D1IZ33

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Chain	Residue	Modelled	Actual	Comment	Reference
1f	-54	VAL	-	expression tag	UNP A0A8D1IZ33
1f	-53	LYS	-	expression tag	UNP A0A8D1IZ33
1f	-52	GLY	-	expression tag	UNP A0A8D1IZ33
1f	-51	ARG	-	expression tag	UNP A0A8D1IZ33
1f	-50	ARG	-	expression tag	UNP A0A8D1IZ33
1f	-49	PHE	-	expression tag	UNP A0A8D1IZ33

- Molecule 32 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	1g	100	Total	C	N	O	S	0	0
			835	535	138	158	4		

- Molecule 33 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	1h	138	Total	C	N	O	S	0	0
			1151	754	195	199	3		

- Molecule 34 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	1i	127	Total	C	N	O	S	0	0
			1100	723	194	181	2		

- Molecule 35 is a protein called NADH:ubiquinone oxidoreductase subunit B2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	1j	71	Total	C	N	O	S	0	0
			601	394	99	107	1		

- Molecule 36 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	1k	81	Total	C	N	O	S	0	0
			649	422	110	116	1		

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

8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	1l	156	Total	C	N	O	S	0	0
			1310	847	213	242	8		

- Molecule 38 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	1m	128	Total	C	N	O	S	0	0
			1062	691	182	189			

- Molecule 39 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	1n	172	Total	C	N	O	S	0	0
			1495	956	273	258	8		

- Molecule 40 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	1o	122	Total	C	N	O	S	0	0
			1045	650	198	187	10		

- Molecule 41 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	1p	173	Total	C	N	O	S	0	0
			1449	908	263	270	8		

- Molecule 42 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	1q	145	Total	C	N	O	S	0	0
			1212	775	219	213	5		

- Molecule 43 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	1r	96	Total	C	N	O	S	0	0
			767	483	144	137	3		

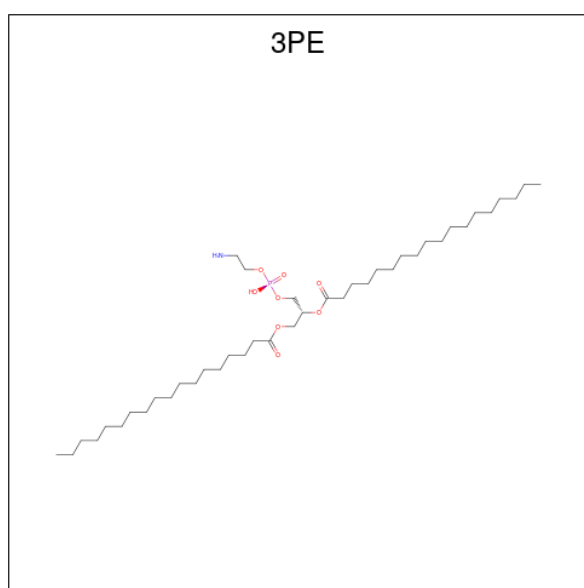
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1r	0	ACE	-	insertion	UNP A0A8W4F7N8

- Molecule 44 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	1s	45	Total	C	N	O	S	0	0
			382	238	70	73	1		

- Molecule 45 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: $C_{41}H_{82}NO_8P$).



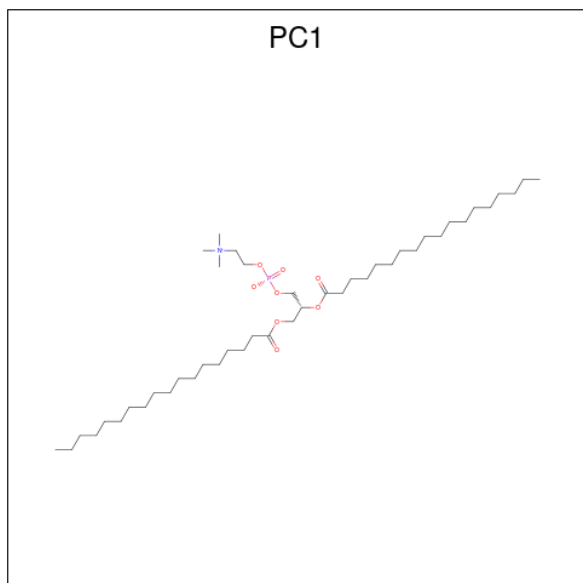
Mol	Chain	Residues	Atoms					AltConf
45	1A	1	Total	C	N	O	P	0
			47	37	1	8	1	
45	1L	1	Total	C	N	O	P	0
			46	36	1	8	1	
45	1L	1	Total	C	N	O	P	0
			42	32	1	8	1	
45	1N	1	Total	C	N	O	P	0
			51	41	1	8	1	

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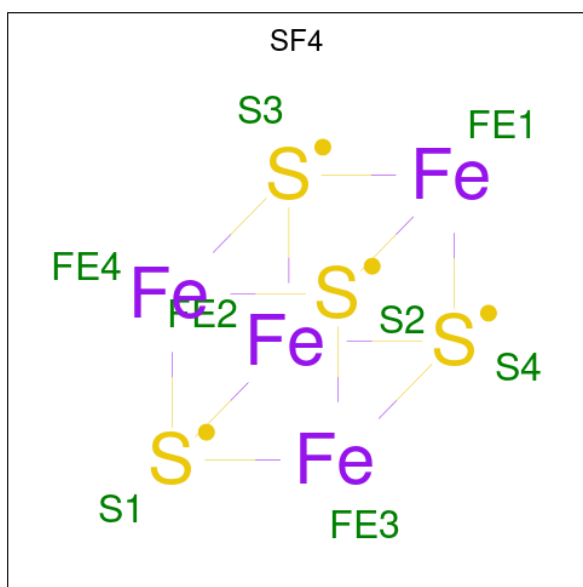
Mol	Chain	Residues	Atoms					AltConf
45	1Y	1	Total	C	N	O	P	0
			31	21	1	8	1	
45	1Y	1	Total	C	N	O	P	0
			51	41	1	8	1	

- Molecule 46 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: $C_{44}H_{88}NO_8P$).



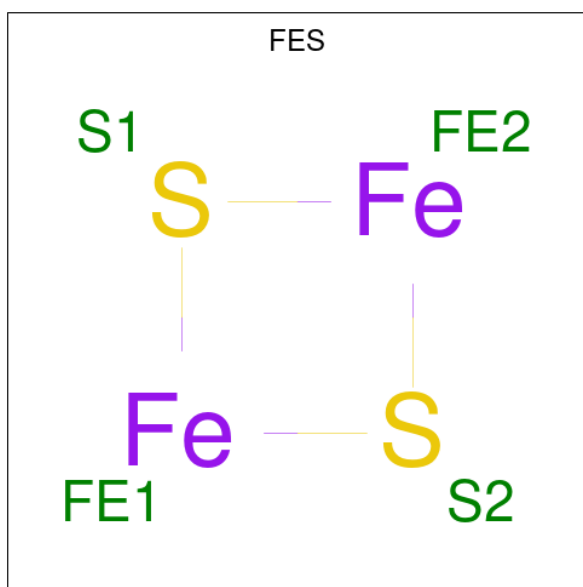
Mol	Chain	Residues	Atoms					AltConf
46	1A	1	Total	C	N	O	P	0
			35	25	1	8	1	
46	1I	1	Total	C	N	O	P	0
			54	44	1	8	1	
46	1I	1	Total	C	N	O	P	0
			44	34	1	8	1	
46	1L	1	Total	C	N	O	P	0
			44	34	1	8	1	
46	1f	1	Total	C	N	O	P	0
			46	36	1	8	1	

- Molecule 47 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



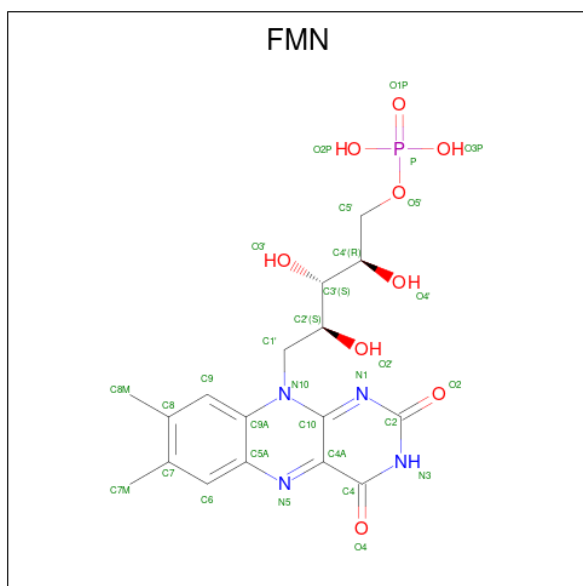
Mol	Chain	Residues	Atoms			AltConf
47	1B	1	Total	Fe	S	0
			8	4	4	
47	1F	1	Total	Fe	S	0
			8	4	4	
47	1G	1	Total	Fe	S	0
			8	4	4	
47	1G	1	Total	Fe	S	0
			8	4	4	
47	1I	1	Total	Fe	S	0
			8	4	4	
47	1I	1	Total	Fe	S	0
			8	4	4	

- Molecule 48 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



Mol	Chain	Residues	Atoms			AltConf
48	1E	1	Total	Fe	S	0
			4	2	2	
48	1G	1	Total	Fe	S	0
			4	2	2	

- Molecule 49 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).

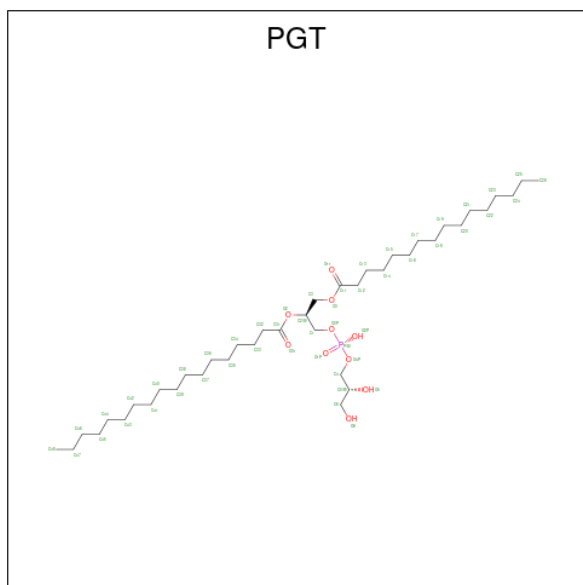


Mol	Chain	Residues	Atoms					AltConf
49	1F	1	Total	C	N	O	P	0
			31	17	4	9	1	

- Molecule 50 is POTASSIUM ION (CCD ID: K) (formula: K).

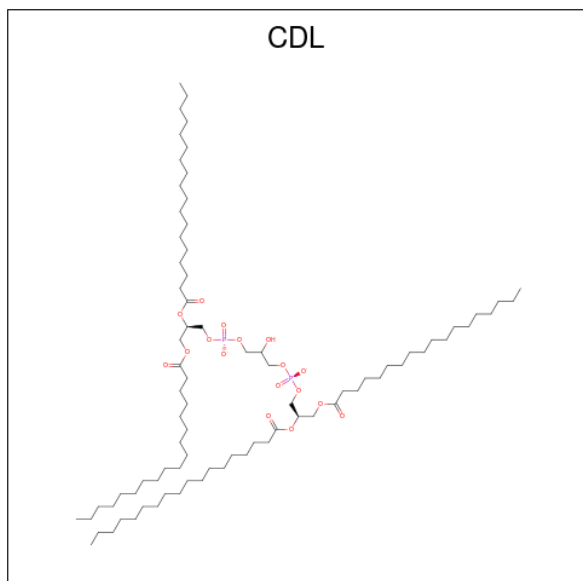
Mol	Chain	Residues	Atoms		AltConf
50	1G	1	Total	K	0
			1	1	

- Molecule 51 is (1S)-2-{{[[(2R)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL STEARATE (CCD ID: PGT) (formula: C₄₀H₇₉O₁₀P).



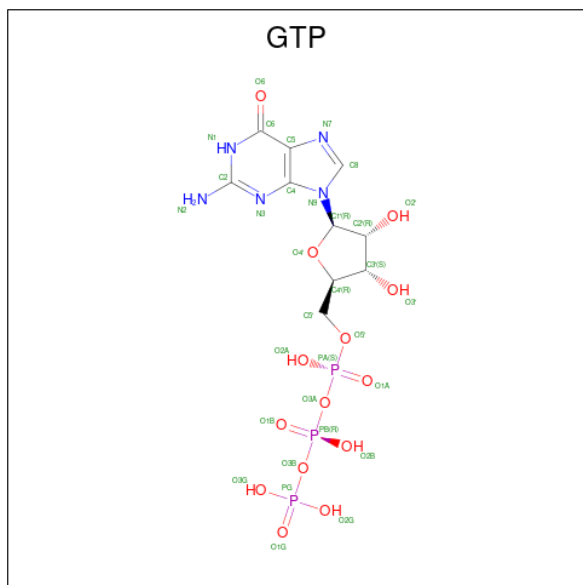
Mol	Chain	Residues	Atoms				AltConf
51	1M	1	Total	C	O	P	0
			51	40	10	1	

- Molecule 52 is CARDIOLIPIN (CCD ID: CDL) (formula: C₈₁H₁₅₆O₁₇P₂).



Mol	Chain	Residues	Atoms				AltConf
52	1N	1	Total	C	O	P	0
			77	58	17	2	
52	1q	1	Total	C	O	P	0
			61	42	17	2	

- Molecule 53 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
53	1O	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	1O	1	Total	Mg	0
			1	1	

- Molecule 55 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
55	1P	1	Total	C	N	O	P	0
			48	21	7	17	3	

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

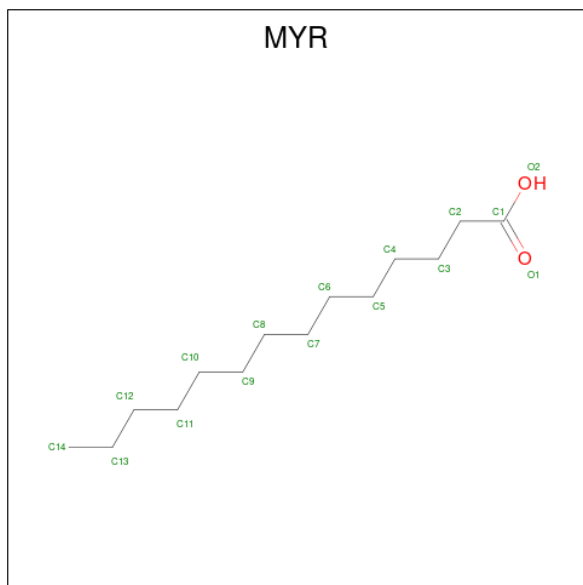
Mol	Chain	Residues	Atoms	AltConf
56	1R	1	Total Zn 1 1	0

- Molecule 57 is {S}-[2-[3-[(2 {R})-3,3-dimethyl-2-oxidanyl-4-phosphonooxy-butanoyl]amino]propanoylamino]ethyl] (3 {S})-3-oxidanyltetradecanethioate (CCD ID: EHZ) (formula: C₂₅H₄₉N₂O₉PS).



Mol	Chain	Residues	Atoms					AltConf
57	1W	1	Total	C	N	O	P	S
			37	25	2	8	1	1
57	1n	1	Total	C	N	O	P	S
			37	25	2	8	1	1

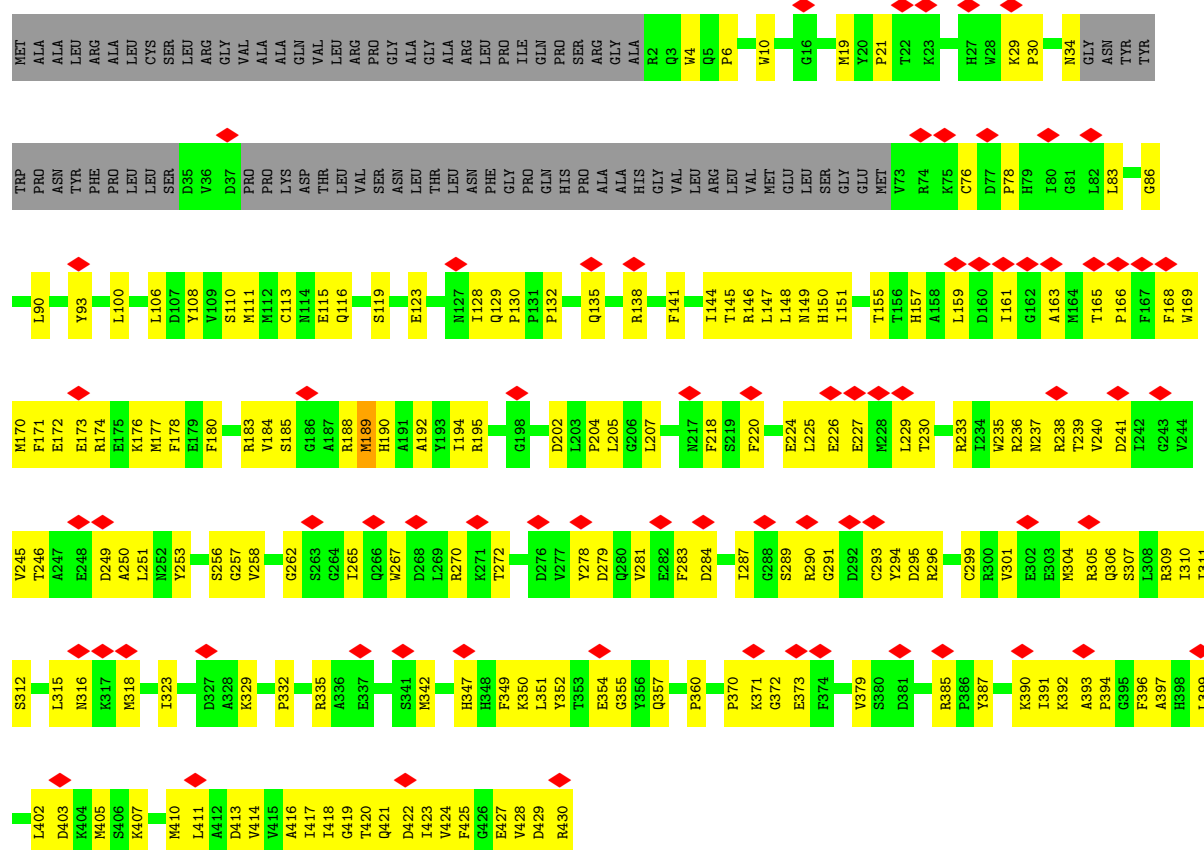
- Molecule 58 is MYRISTIC ACID (CCD ID: MYR) (formula: $C_{14}H_{28}O_2$).



Mol	Chain	Residues	Atoms			AltConf
58	1l	1	Total	C	O	
			15	14	1	0

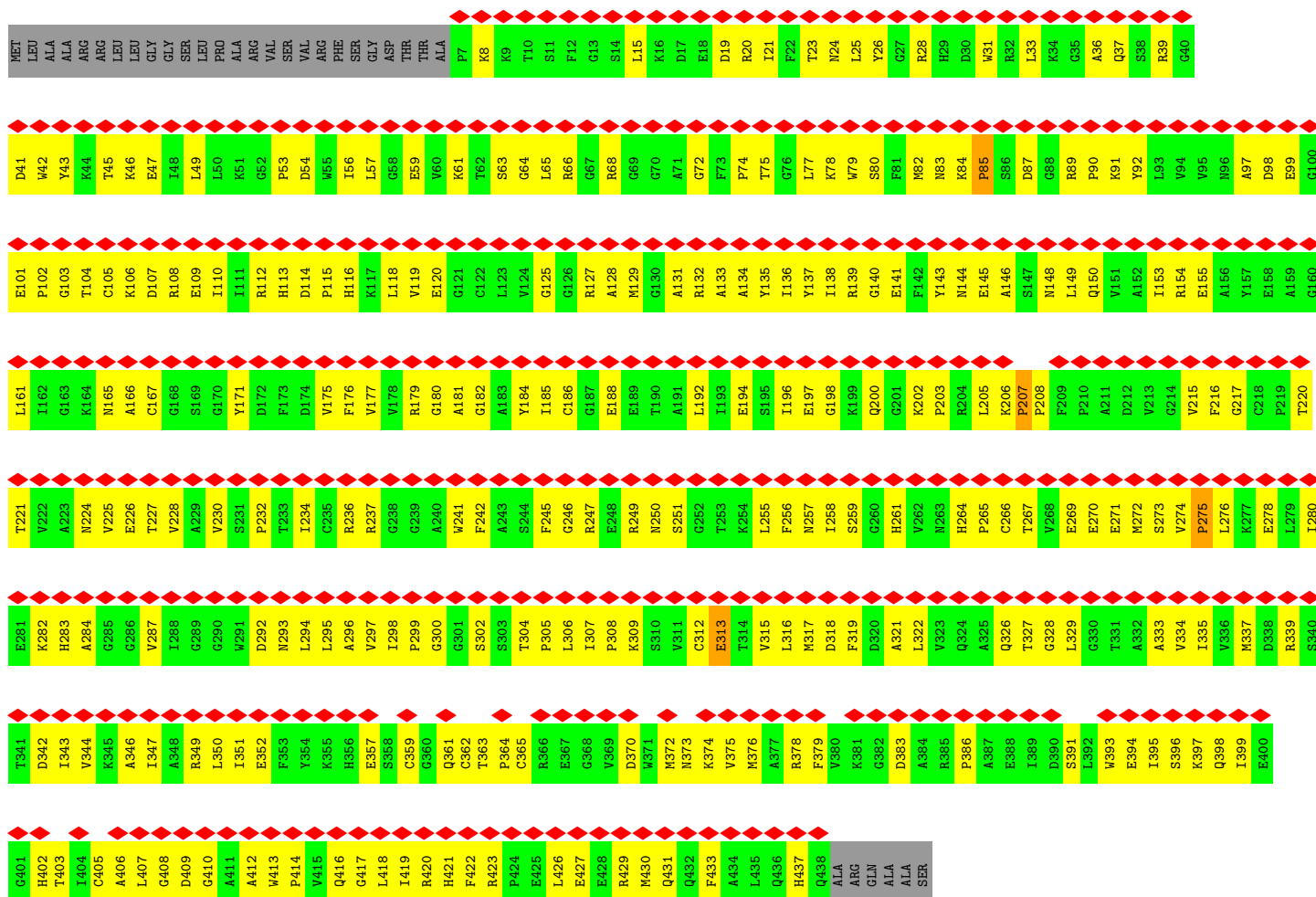
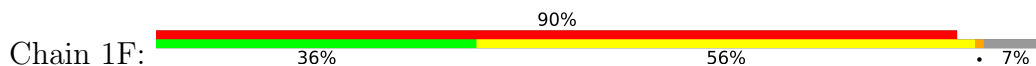


• Molecule 4: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial



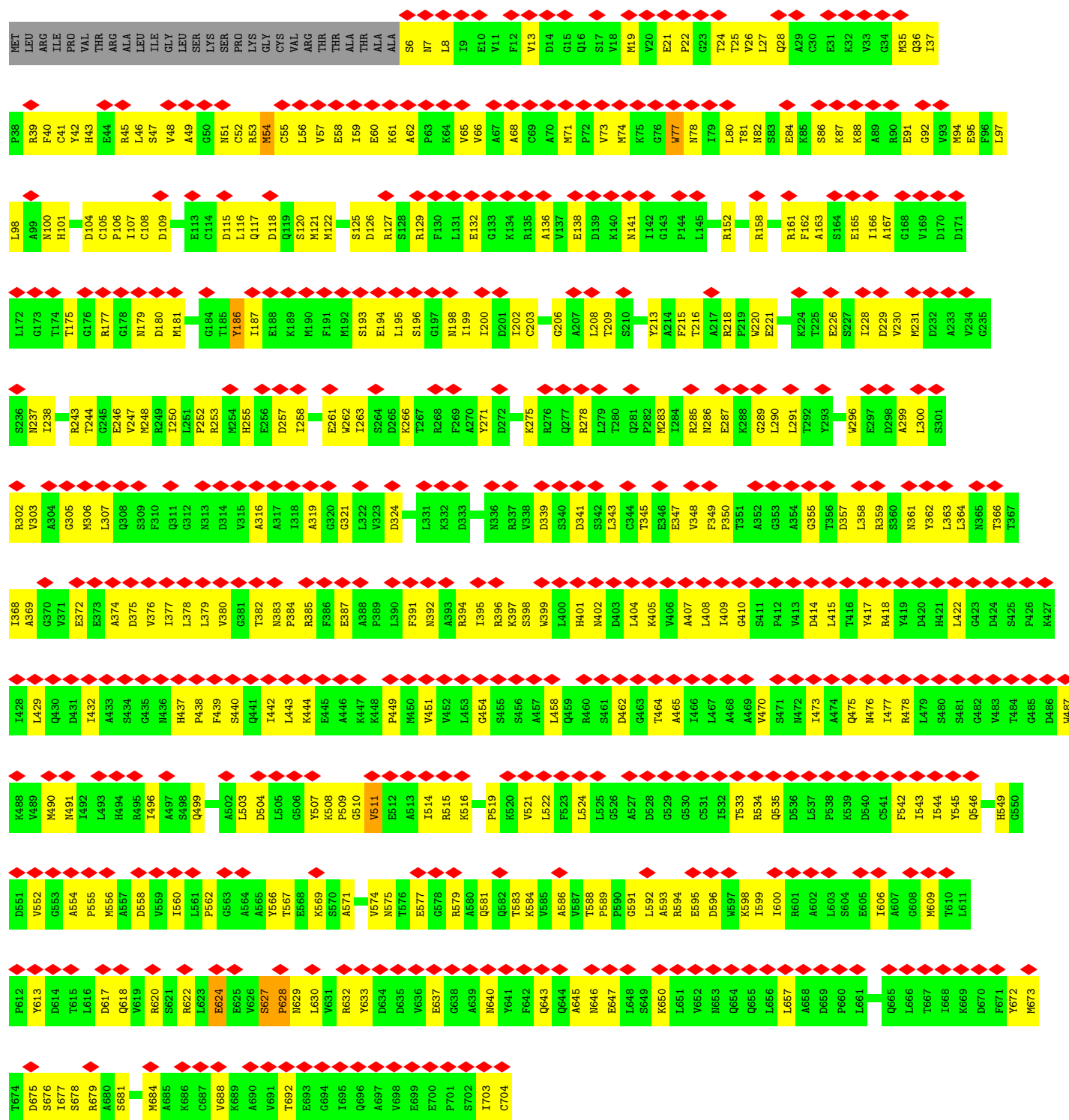


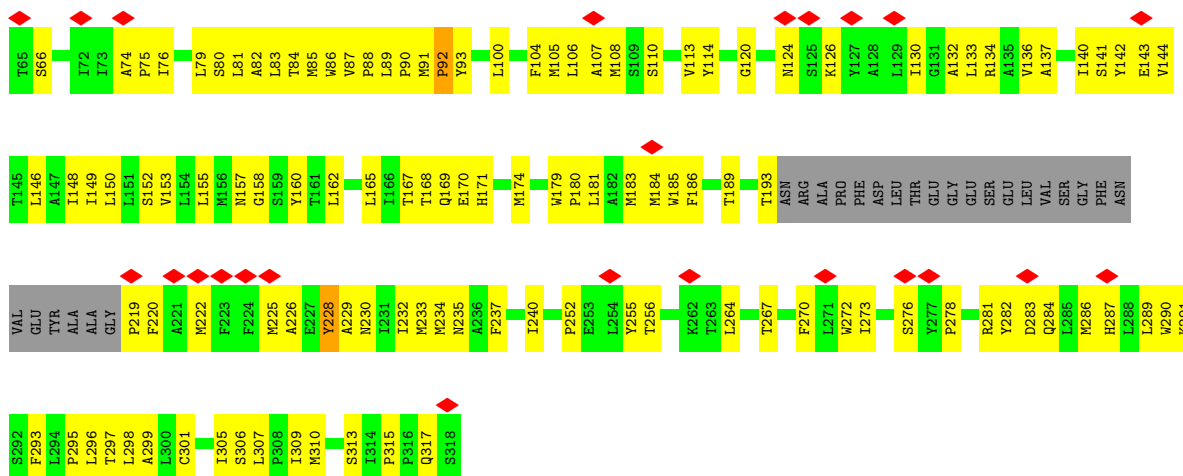
• Molecule 6: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial



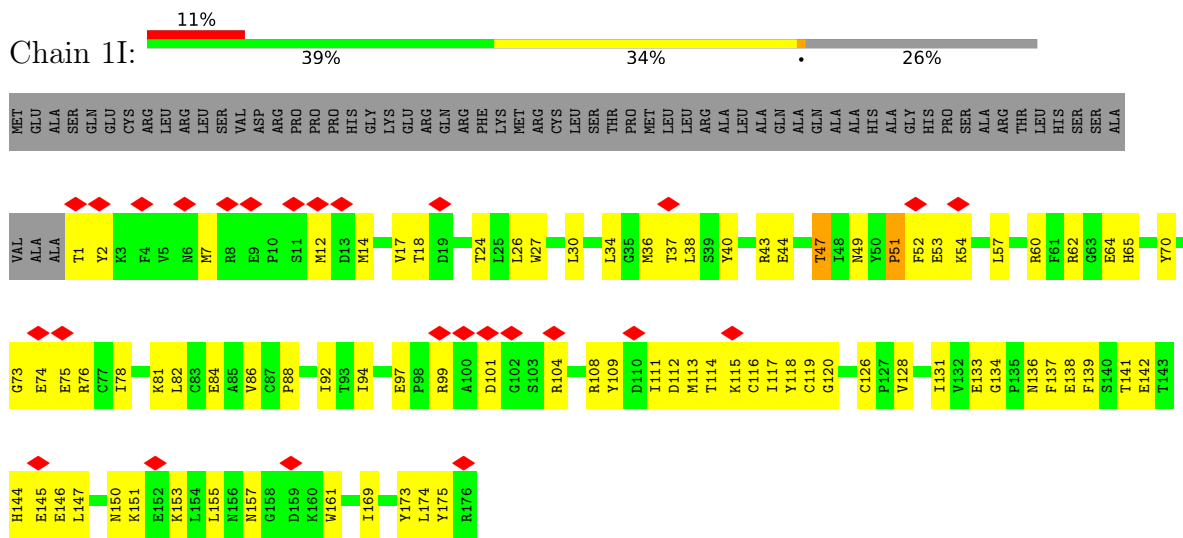
• Molecule 7: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial



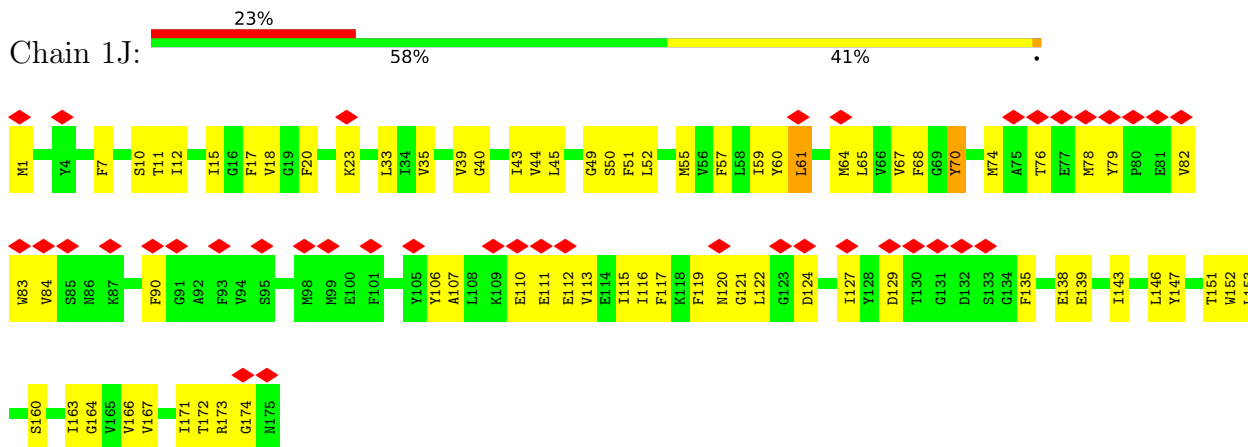




- Molecule 9: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial

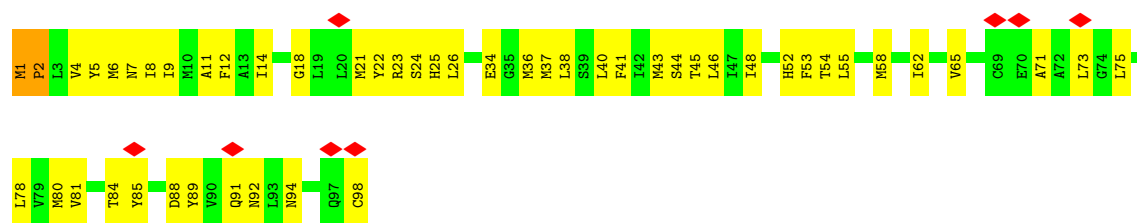


- Molecule 10: NADH-ubiquinone oxidoreductase chain 6

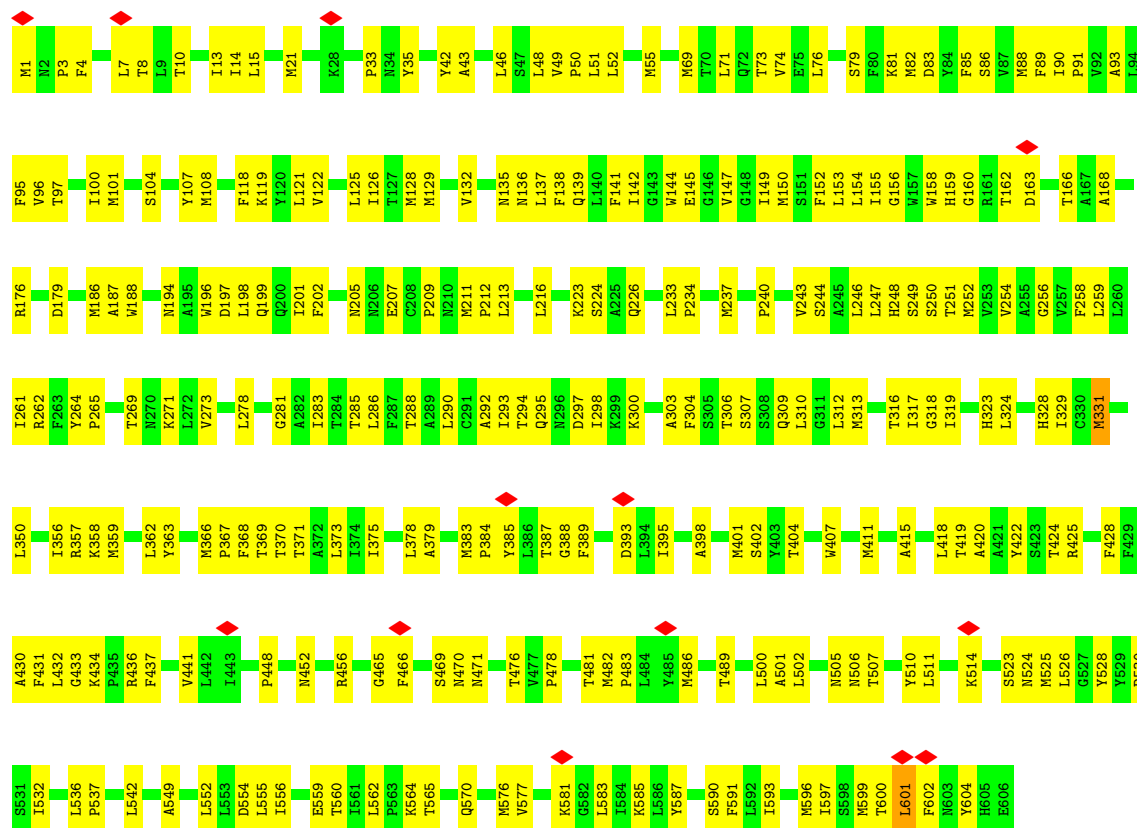


- Molecule 11: NADH-ubiquinone oxidoreductase chain 4L



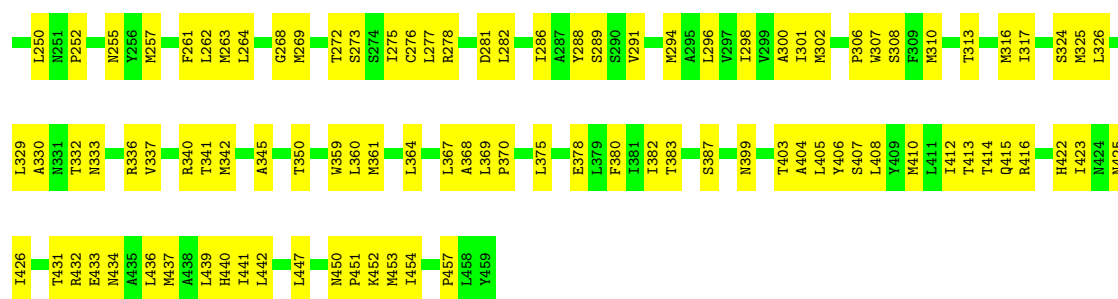


• Molecule 12: NADH-ubiquinone oxidoreductase chain 5

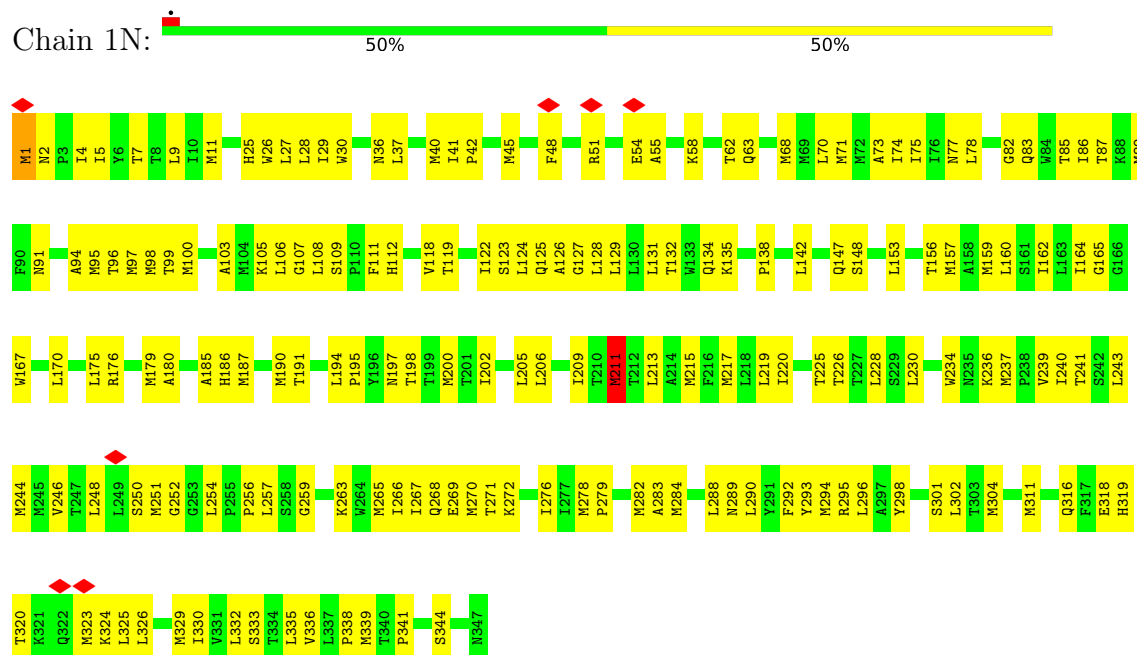


• Molecule 13: NADH-ubiquinone oxidoreductase chain 4

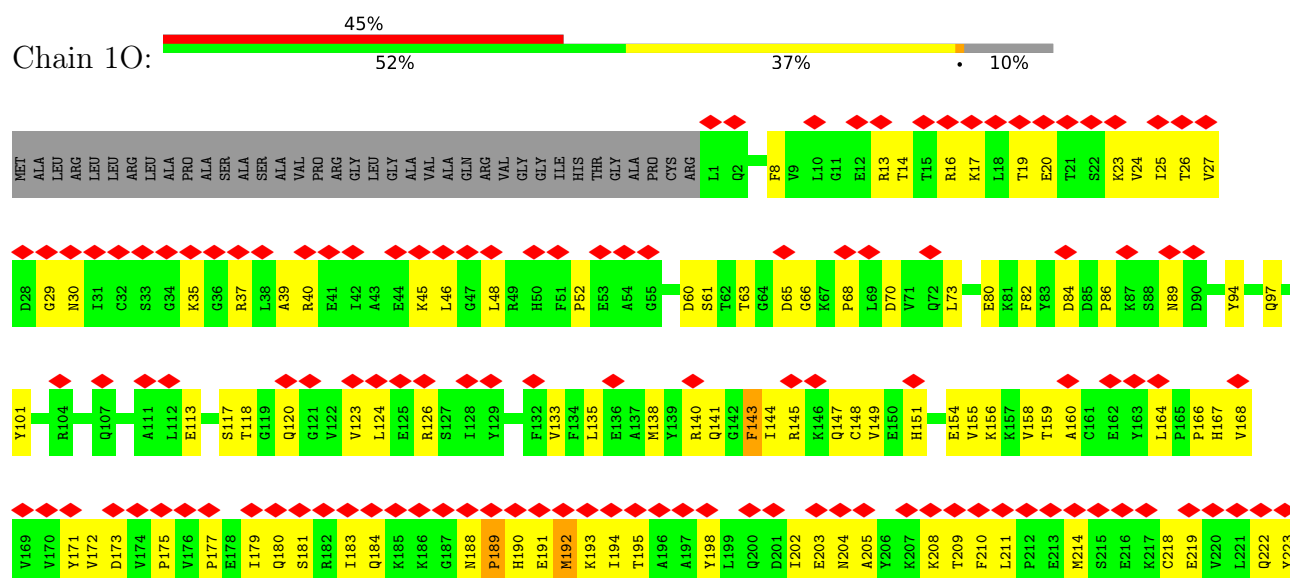


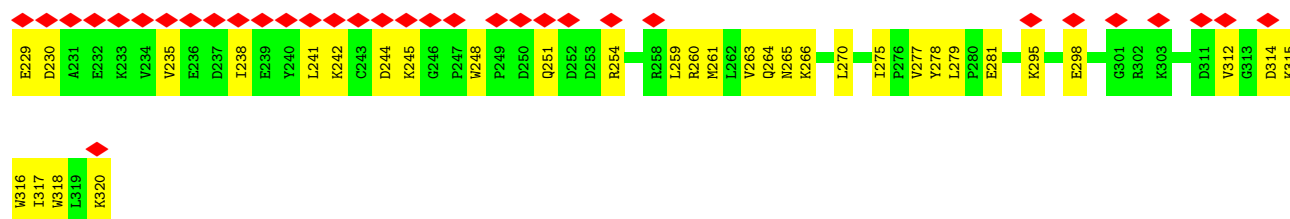


• Molecule 14: NADH-ubiquinone oxidoreductase chain 2

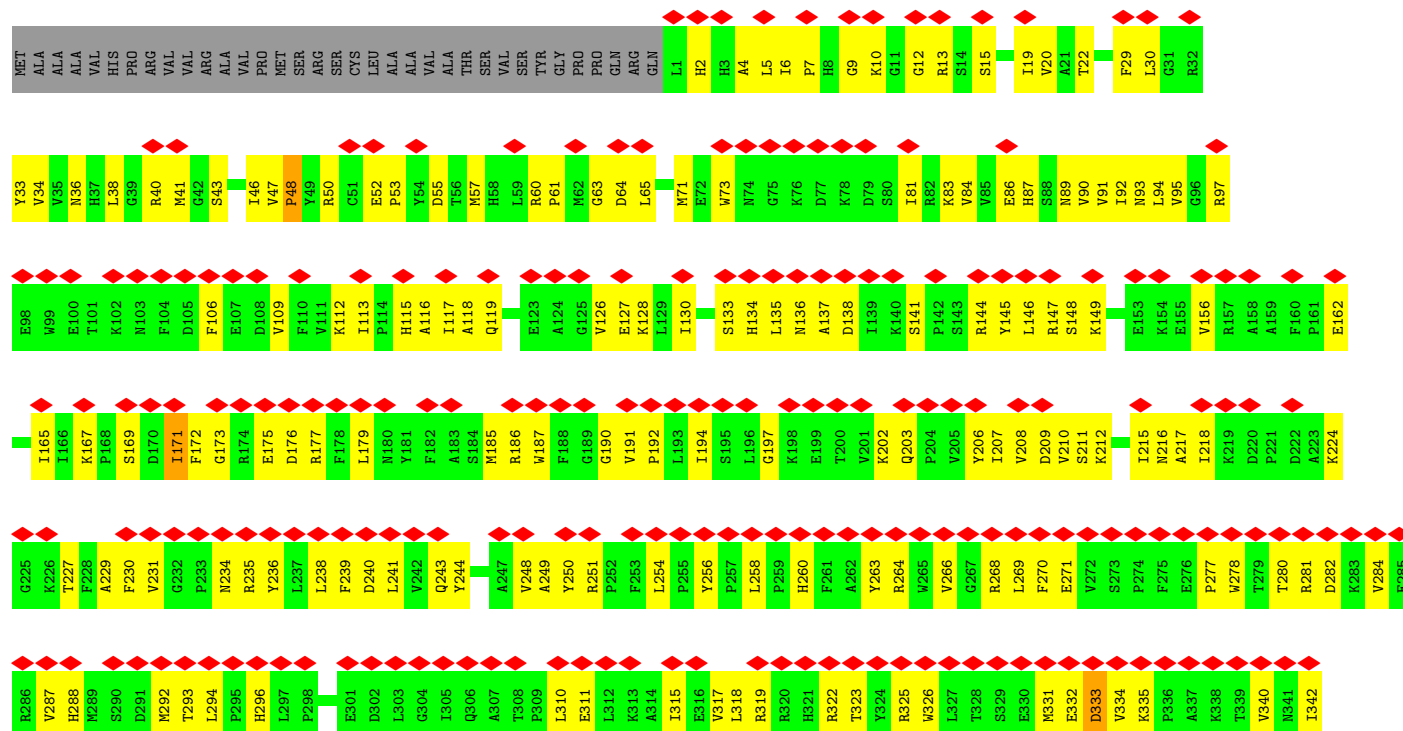


• Molecule 15: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial

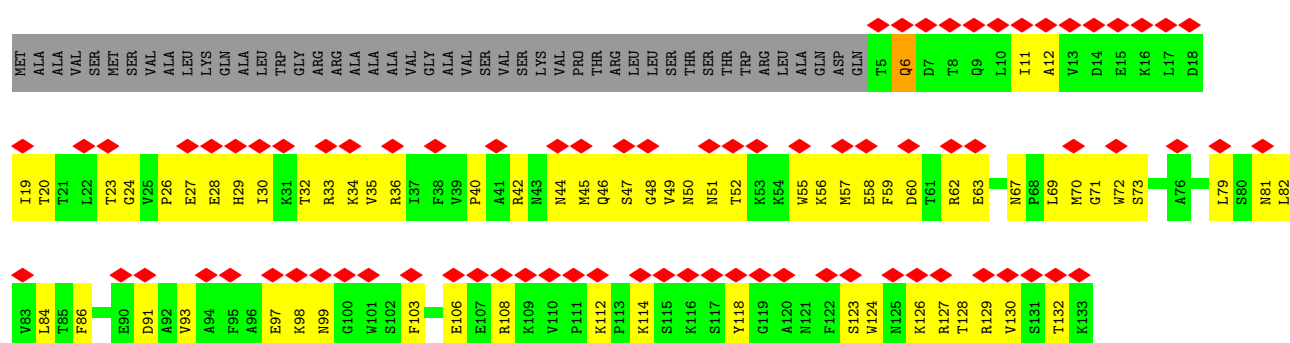




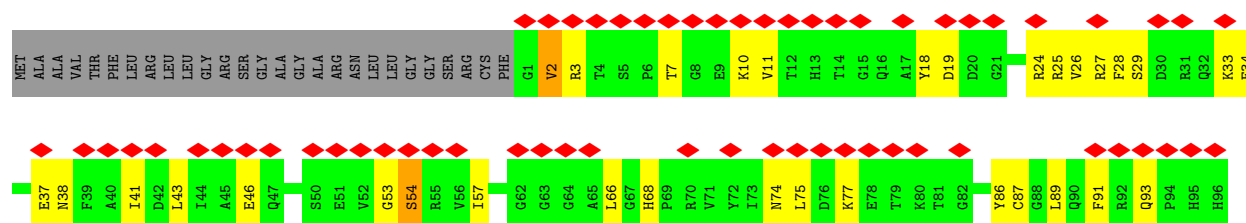
• Molecule 16: NADH:ubiquinone oxidoreductase subunit A9



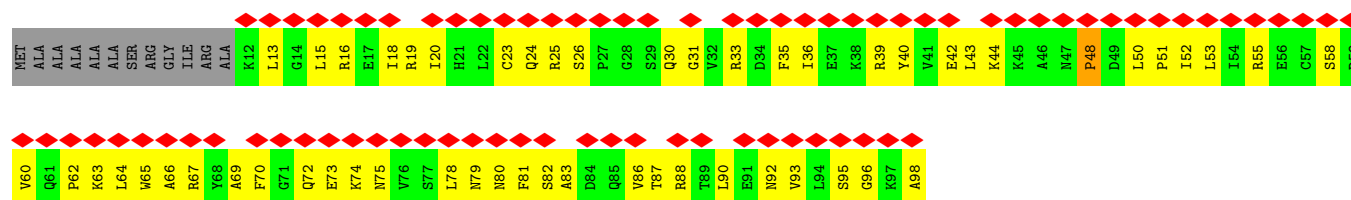
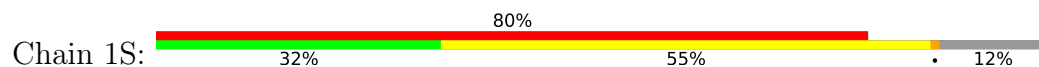
• Molecule 17: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial



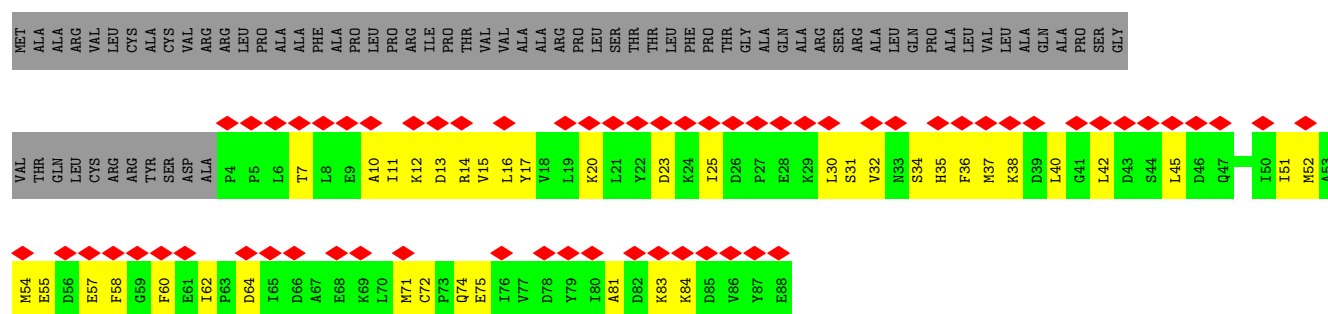
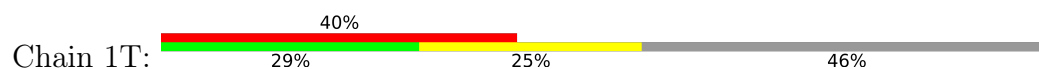
• Molecule 18: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial



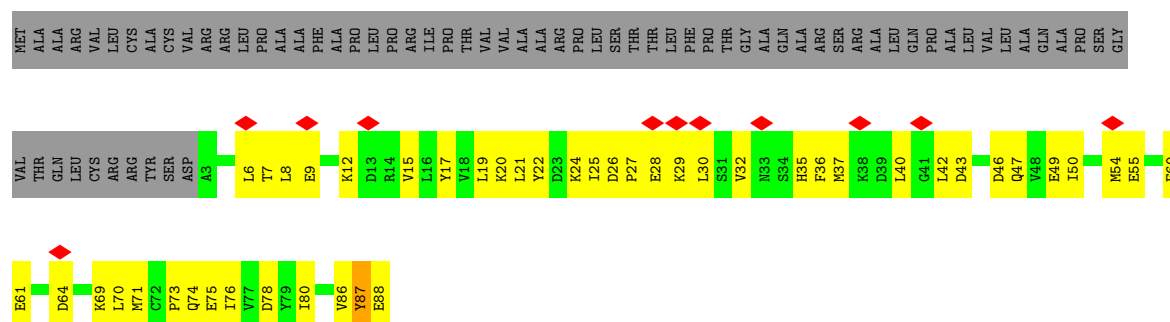
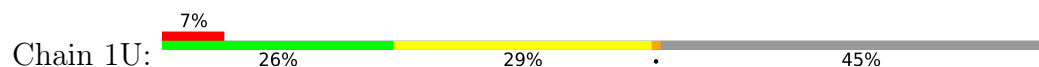
- Molecule 19: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2



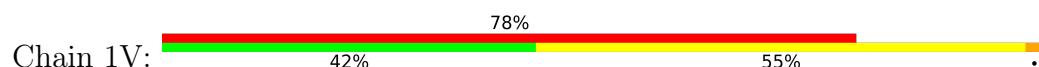
- Molecule 20: NADH:ubiquinone oxidoreductase subunit AB1

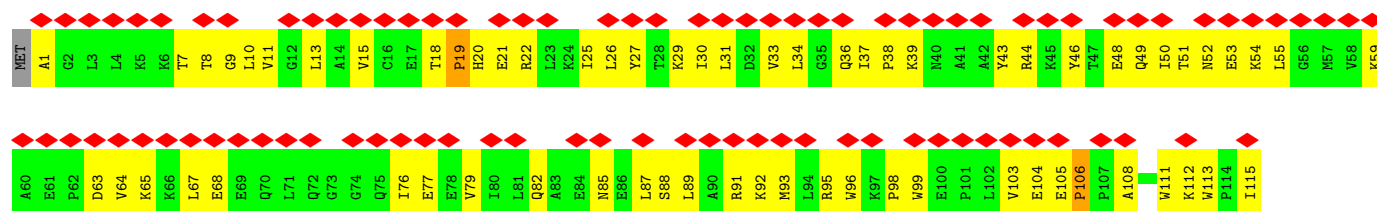


- Molecule 20: NADH:ubiquinone oxidoreductase subunit AB1

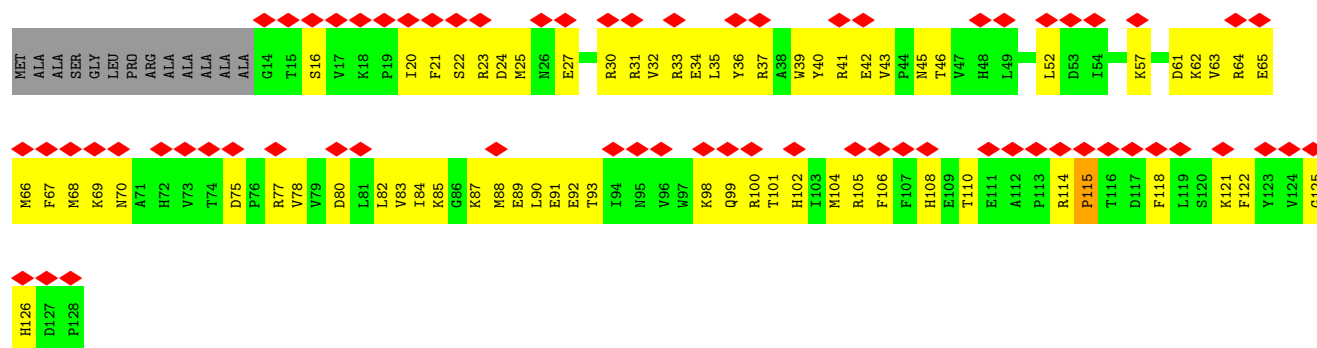


- Molecule 21: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 isoform X1

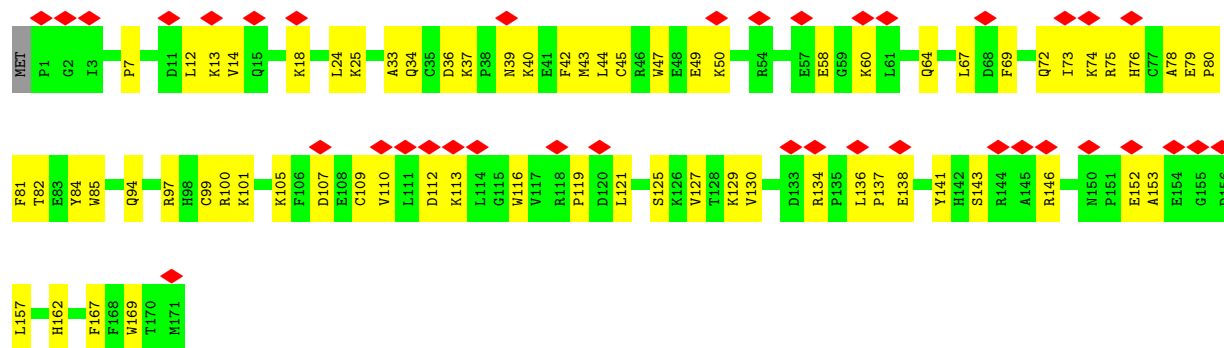




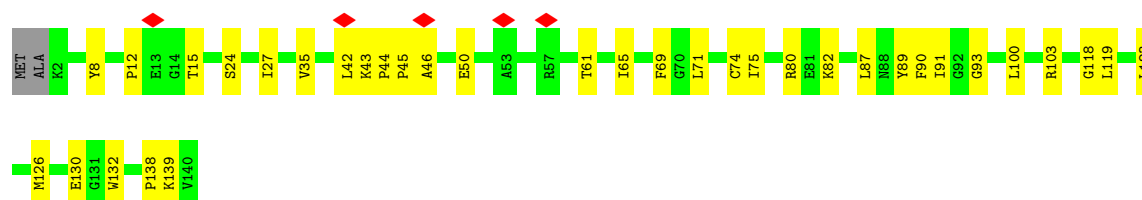
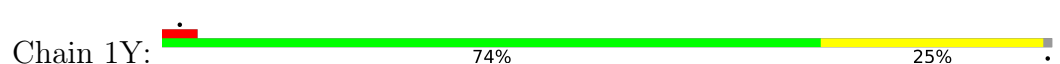
• Molecule 22: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6



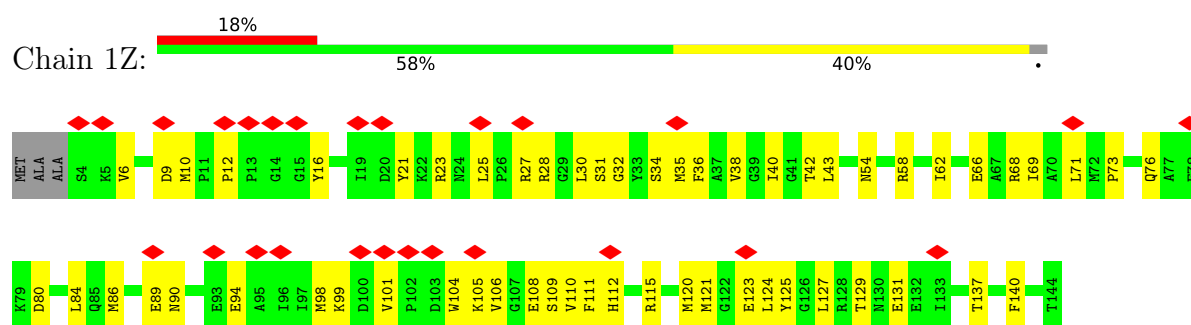
• Molecule 23: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8



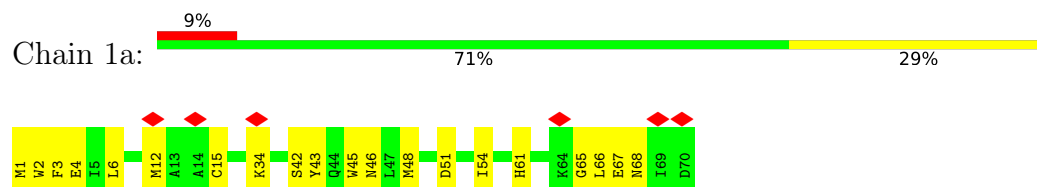
• Molecule 24: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11



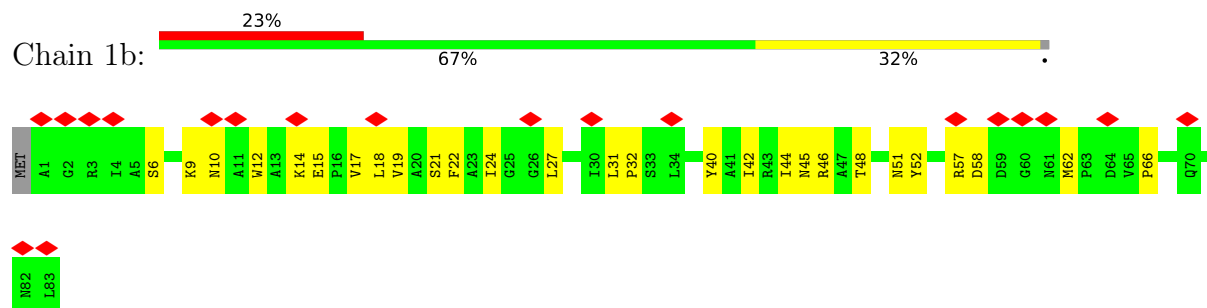
• Molecule 25: NADH:ubiquinone oxidoreductase subunit A13



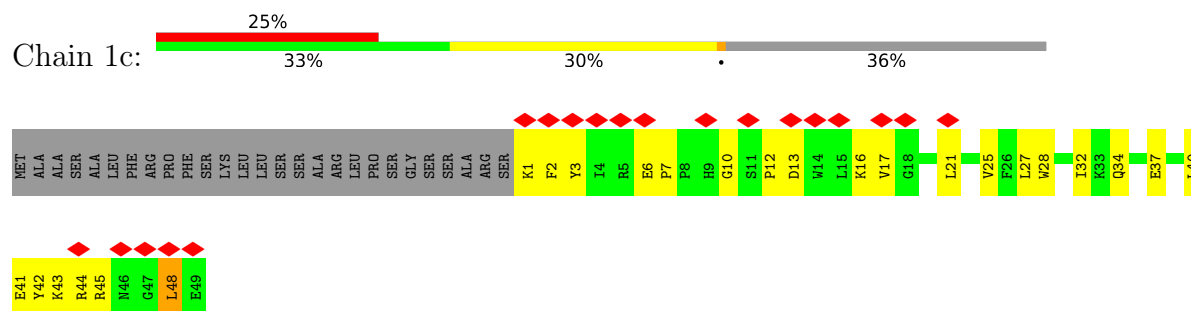
- Molecule 26: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1



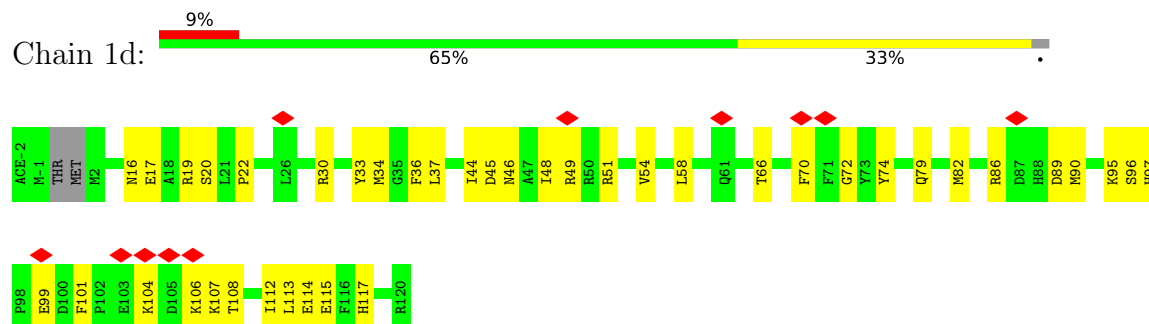
- Molecule 27: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3



- Molecule 28: NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial

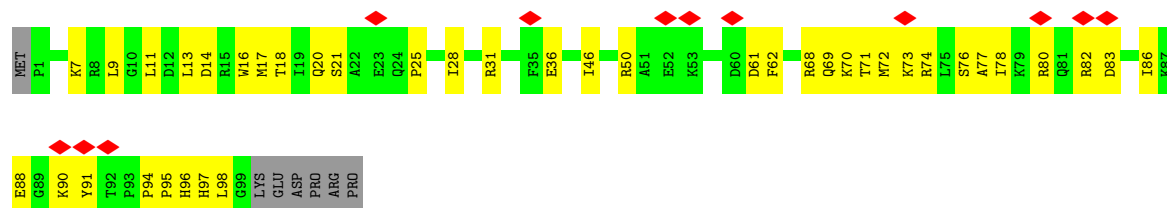


- Molecule 29: NADH dehydrogenase [ubiquinone] 1 subunit C2



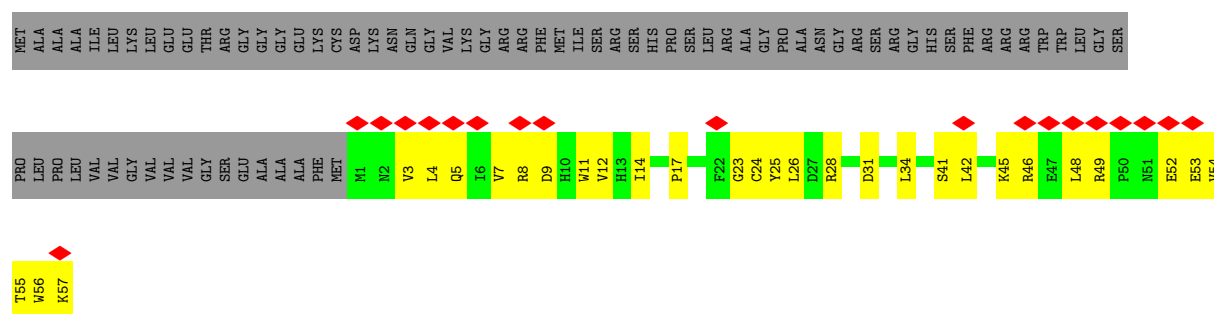
- Molecule 30: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5

Chain 1e: 

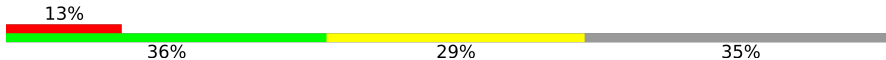


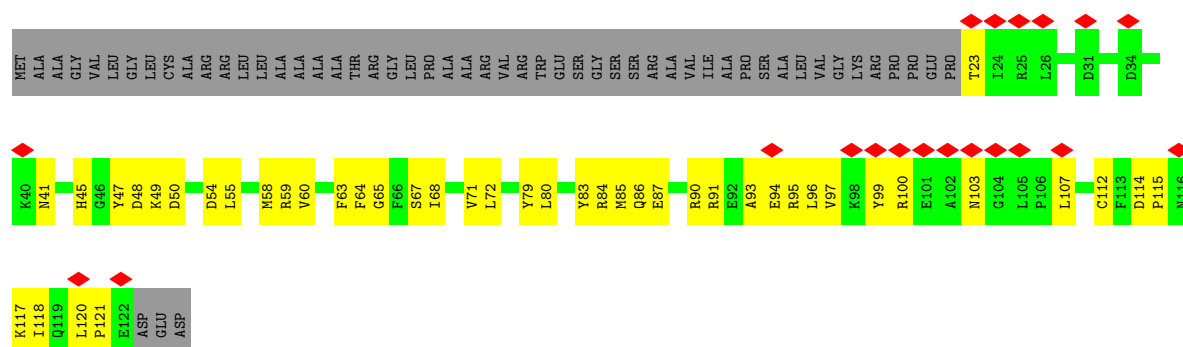
- Molecule 31: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1 [Sus scrofa]

Chain 1f: 

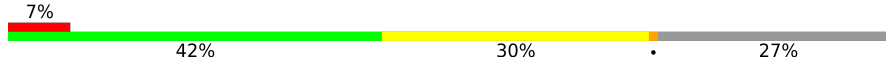


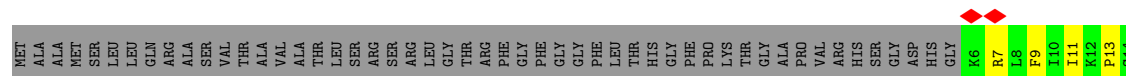
- Molecule 32: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial

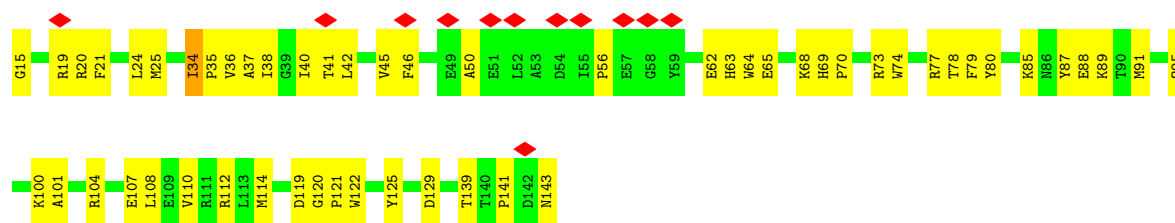
Chain 1g: 



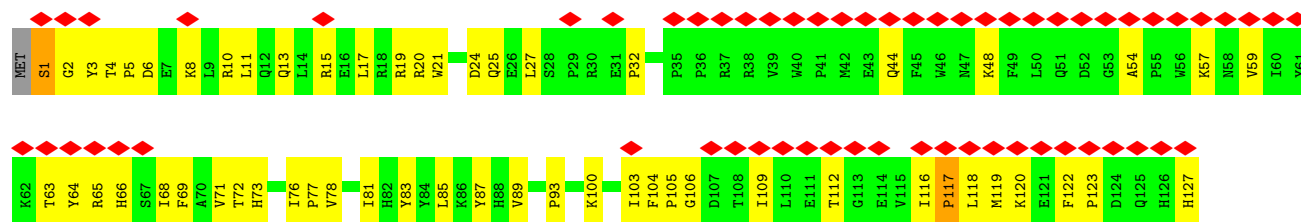
- Molecule 33: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial

Chain 1h: 

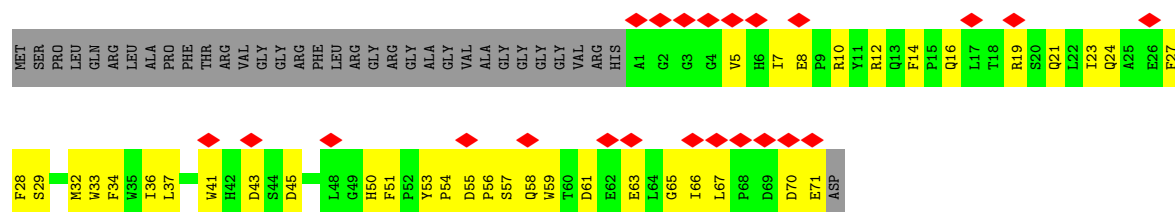




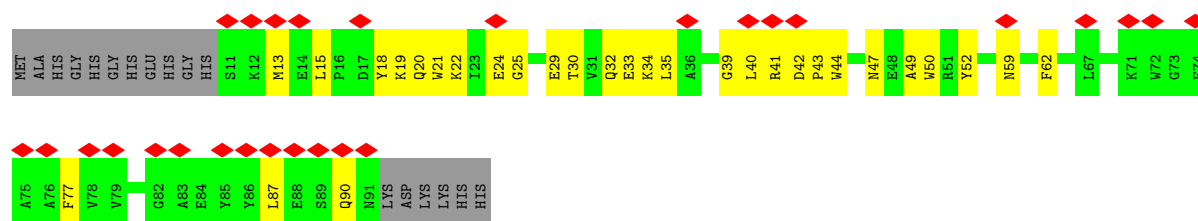
- Molecule 34: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6



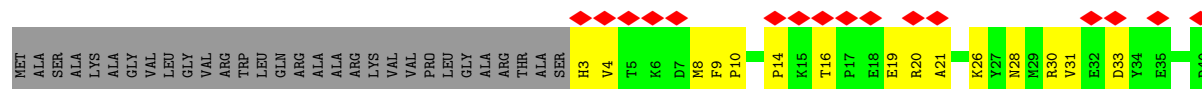
- Molecule 35: NADH:ubiquinone oxidoreductase subunit B2

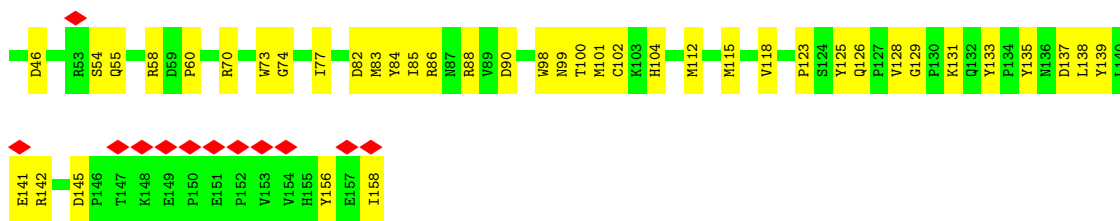


- Molecule 36: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3

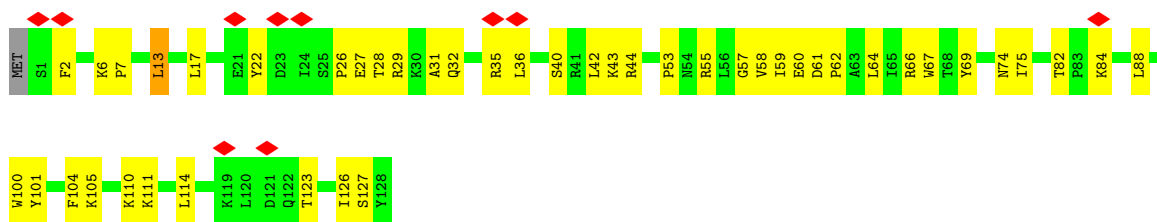


- Molecule 37: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial

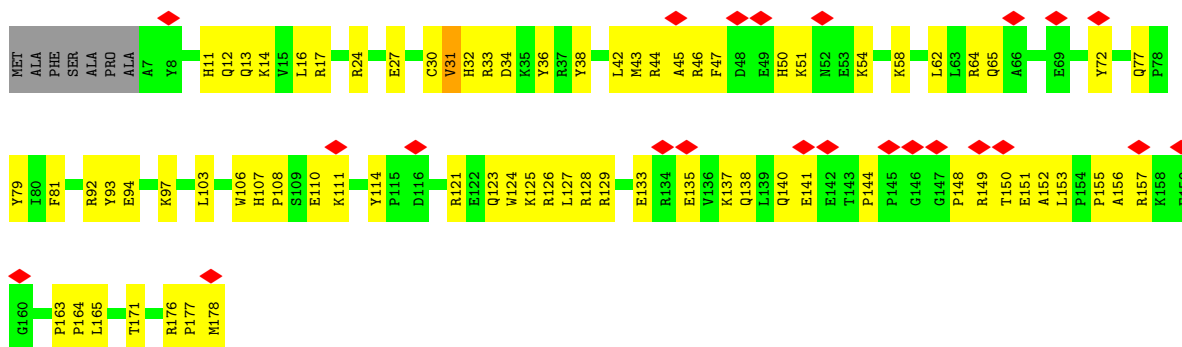




- Molecule 38: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4



- Molecule 39: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9



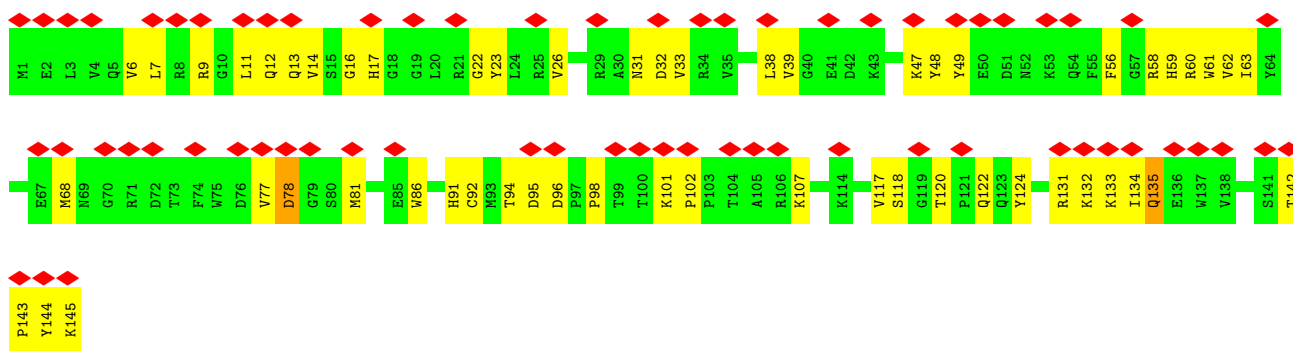
- Molecule 40: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7



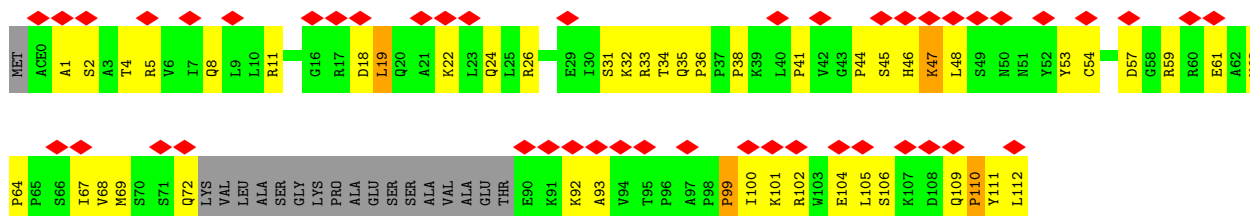
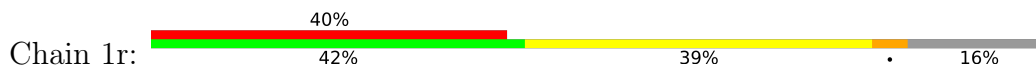
- Molecule 41: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10



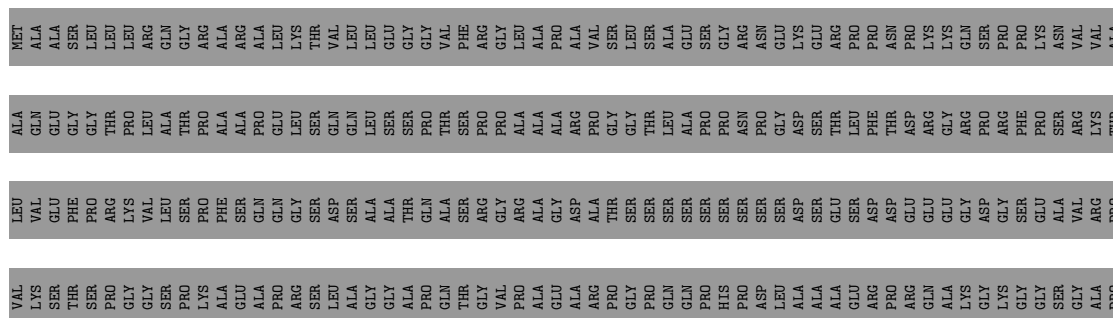
- Molecule 42: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12



- Molecule 43: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7



- Molecule 44: NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	29000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.973	Depositor
Minimum map value	-0.458	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	425.6, 425.6, 425.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33, 1.33, 1.33	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ACE, EHZ, 3PE, CDL, FES, MYR, SF4, FME, SAC, FMN, MG, NDP, PGT, K, GTP, PC1, 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	1A	0.15	0/713	0.37	0/975
2	1B	0.23	0/1273	0.50	0/1722
3	1C	0.16	0/1791	0.40	0/2439
4	1D	0.17	0/3274	0.37	0/4434
5	1E	0.25	1/1698 (0.1%)	0.45	0/2311
6	1F	0.22	0/3401	0.50	2/4595 (0.0%)
7	1G	0.48	5/5451 (0.1%)	0.63	8/7387 (0.1%)
8	1H	0.28	1/2373 (0.0%)	0.43	0/3244
9	1I	0.21	0/1443	0.50	2/1952 (0.1%)
10	1J	0.24	0/1364	0.39	0/1850
11	1K	0.21	0/751	0.47	0/1018
12	1L	0.15	0/4939	0.39	0/6718
13	1M	0.19	0/3713	0.37	0/5063
14	1N	0.42	2/2765 (0.1%)	0.64	4/3758 (0.1%)
15	1O	0.20	0/2650	0.36	1/3588 (0.0%)
16	1P	0.60	4/2828 (0.1%)	0.76	7/3834 (0.2%)
17	1Q	0.19	0/1070	0.43	0/1446
18	1R	0.21	0/755	0.46	1/1018 (0.1%)
19	1S	0.29	0/711	0.63	1/956 (0.1%)
20	1T	0.20	0/701	0.51	0/946
20	1U	0.25	0/706	0.49	0/954
21	1V	0.31	0/946	0.66	5/1281 (0.4%)
22	1W	0.35	0/995	0.64	1/1340 (0.1%)
23	1X	0.14	0/1436	0.36	0/1938
24	1Y	0.09	0/1037	0.28	0/1404
25	1Z	0.17	0/1199	0.37	0/1617
26	1a	0.13	0/577	0.36	0/777
27	1b	0.17	0/664	0.38	0/912
28	1c	0.11	0/430	0.29	0/581
29	1d	0.13	0/1024	0.31	0/1383
30	1e	0.12	0/836	0.32	0/1118
31	1f	0.14	0/499	0.41	0/673

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	1g	0.17	0/858	0.38	0/1165
33	1h	0.16	0/1184	0.35	0/1603
34	1i	0.22	0/1131	0.58	2/1541 (0.1%)
35	1j	0.15	0/627	0.38	0/858
36	1k	0.14	0/668	0.37	0/903
37	1l	0.22	0/1365	0.38	0/1867
38	1m	0.14	0/1092	0.32	0/1481
39	1n	0.20	0/1549	0.33	0/2098
40	1o	0.19	0/1069	0.42	0/1430
41	1p	0.14	0/1481	0.29	0/1997
42	1q	0.18	0/1253	0.43	0/1704
43	1r	0.36	1/782 (0.1%)	0.71	2/1057 (0.2%)
44	1s	0.28	0/394	0.76	1/533 (0.2%)
All	All	0.27	14/67466 (0.0%)	0.48	37/91469 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	1F	0	1

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	1G	628	PRO	CG-CD	-23.83	0.69	1.50
16	1P	48	PRO	CG-CD	-23.00	0.72	1.50
7	1G	628	PRO	CB-CG	16.20	2.30	1.49
16	1P	48	PRO	CB-CG	15.73	2.28	1.49
14	1N	11	MET	CG-SD	-13.35	1.47	1.80

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	1G	628	PRO	CB-CG-CD	-33.13	0.07	106.10
14	1N	11	MET	CG-SD-CE	-27.56	40.27	100.90
16	1P	48	PRO	CB-CG-CD	-23.73	30.18	106.10
16	1P	48	PRO	N-CD-CG	-16.41	78.59	103.20
7	1G	628	PRO	CA-N-CD	-15.75	89.95	112.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	1F	207	PRO	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	707	0	755	47	0
2	1B	1242	0	1249	99	0
3	1C	1740	0	1691	134	0
4	1D	3189	0	3121	191	0
5	1E	1658	0	1662	118	0
6	1F	3325	0	3288	269	0
7	1G	5362	0	5387	333	0
8	1H	2316	0	2434	179	0
9	1I	1412	0	1364	89	0
10	1J	1339	0	1337	91	0
11	1K	750	0	798	56	0
12	1L	4818	0	4956	234	0
13	1M	3632	0	3836	220	0
14	1N	2712	0	2873	168	0
15	1O	2590	0	2556	124	0
16	1P	2751	0	2776	159	0
17	1Q	1047	0	1042	70	0
18	1R	741	0	704	34	0
19	1S	700	0	719	67	0
20	1T	689	0	687	47	0
20	1U	694	0	691	48	0
21	1V	927	0	972	80	0
22	1W	971	0	975	98	0
23	1X	1398	0	1378	63	0
24	1Y	1016	0	1020	29	0
25	1Z	1168	0	1161	63	0
26	1a	562	0	557	25	0
27	1b	643	0	645	28	0
28	1c	417	0	425	27	0
29	1d	996	0	990	42	0
30	1e	816	0	823	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	1f	487	0	496	31	0
32	1g	835	0	795	42	0
33	1h	1151	0	1164	70	0
34	1i	1100	0	1106	57	0
35	1j	601	0	546	45	0
36	1k	649	0	626	32	0
37	1l	1310	0	1204	70	0
38	1m	1062	0	1075	53	0
39	1n	1495	0	1434	78	0
40	1o	1045	0	1018	74	0
41	1p	1449	0	1416	61	0
42	1q	1212	0	1172	69	0
43	1r	767	0	791	71	0
44	1s	382	0	351	36	0
45	1A	47	0	71	2	0
45	1L	88	0	127	8	0
45	1N	51	0	79	2	0
45	1Y	82	0	118	11	0
46	1A	35	0	42	1	0
46	1I	98	0	147	9	0
46	1L	44	0	65	4	0
46	1f	46	0	69	6	0
47	1B	8	0	0	2	0
47	1F	8	0	0	1	0
47	1G	16	0	0	2	0
47	1I	16	0	0	1	0
48	1E	4	0	0	2	0
48	1G	4	0	0	1	0
49	1F	31	0	19	0	0
50	1G	1	0	0	1	0
51	1M	51	0	78	8	0
52	1N	77	0	98	6	0
52	1q	61	0	66	11	0
53	1O	32	0	12	0	0
54	1O	1	0	0	0	0
55	1P	48	0	26	6	0
56	1R	1	0	0	0	0
57	1W	37	0	0	1	0
57	1n	37	0	0	0	0
58	1l	15	0	27	1	0
All	All	66812	0	67110	3413	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 25.

The worst 5 of 3413 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)
52:1N:402:CDL:C14	52:1N:402:CDL:C15	1.79	1.58
7:1G:628:PRO:N	7:1G:628:PRO:CG	1.72	1.42
7:1G:54:MET:HE1	7:1G:94:MET:HB2	1.18	1.18
8:1H:20:LEU:HB3	8:1H:228:TYR:OH	1.50	1.10
7:1G:628:PRO:CG	7:1G:628:PRO:CB	2.30	1.08

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	1A	84/115 (73%)	78 (93%)	6 (7%)	0	100	100
2	1B	153/255 (60%)	138 (90%)	14 (9%)	1 (1%)	18	51
3	1C	207/264 (78%)	191 (92%)	16 (8%)	0	100	100
4	1D	390/476 (82%)	364 (93%)	26 (7%)	0	100	100
5	1E	212/249 (85%)	195 (92%)	16 (8%)	1 (0%)	24	57
6	1F	430/464 (93%)	401 (93%)	28 (6%)	1 (0%)	43	72
7	1G	697/727 (96%)	648 (93%)	48 (7%)	1 (0%)	48	79
8	1H	289/318 (91%)	270 (93%)	17 (6%)	2 (1%)	18	51
9	1I	174/239 (73%)	166 (95%)	8 (5%)	0	100	100
10	1J	173/175 (99%)	158 (91%)	14 (8%)	1 (1%)	21	54
11	1K	96/98 (98%)	90 (94%)	5 (5%)	1 (1%)	12	45
12	1L	604/606 (100%)	541 (90%)	61 (10%)	2 (0%)	36	65
13	1M	457/459 (100%)	441 (96%)	16 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	1N	345/347 (99%)	323 (94%)	22 (6%)	0	100	100
15	1O	318/357 (89%)	302 (95%)	16 (5%)	0	100	100
16	1P	340/377 (90%)	314 (92%)	25 (7%)	1 (0%)	36	65
17	1Q	127/175 (73%)	113 (89%)	13 (10%)	1 (1%)	16	49
18	1R	94/123 (76%)	87 (93%)	7 (7%)	0	100	100
19	1S	85/99 (86%)	73 (86%)	12 (14%)	0	100	100
20	1T	83/156 (53%)	79 (95%)	3 (4%)	1 (1%)	10	41
20	1U	84/156 (54%)	79 (94%)	5 (6%)	0	100	100
21	1V	113/116 (97%)	106 (94%)	7 (6%)	0	100	100
22	1W	113/128 (88%)	108 (96%)	5 (4%)	0	100	100
23	1X	169/172 (98%)	158 (94%)	11 (6%)	0	100	100
24	1Y	137/141 (97%)	131 (96%)	6 (4%)	0	100	100
25	1Z	139/144 (96%)	122 (88%)	17 (12%)	0	100	100
26	1a	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
27	1b	81/84 (96%)	71 (88%)	10 (12%)	0	100	100
28	1c	47/76 (62%)	44 (94%)	3 (6%)	0	100	100
29	1d	117/123 (95%)	106 (91%)	11 (9%)	0	100	100
30	1e	97/106 (92%)	92 (95%)	5 (5%)	0	100	100
31	1f	55/135 (41%)	47 (86%)	8 (14%)	0	100	100
32	1g	98/154 (64%)	90 (92%)	7 (7%)	1 (1%)	12	45
33	1h	136/189 (72%)	124 (91%)	12 (9%)	0	100	100
34	1i	124/128 (97%)	117 (94%)	7 (6%)	0	100	100
35	1j	69/105 (66%)	65 (94%)	4 (6%)	0	100	100
36	1k	79/98 (81%)	71 (90%)	8 (10%)	0	100	100
37	1l	154/186 (83%)	143 (93%)	11 (7%)	0	100	100
38	1m	126/129 (98%)	119 (94%)	7 (6%)	0	100	100
39	1n	170/179 (95%)	163 (96%)	5 (3%)	2 (1%)	10	41
40	1o	120/137 (88%)	111 (92%)	8 (7%)	1 (1%)	16	49
41	1p	171/176 (97%)	167 (98%)	4 (2%)	0	100	100
42	1q	143/145 (99%)	130 (91%)	11 (8%)	2 (1%)	9	38
43	1r	90/114 (79%)	77 (86%)	13 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	1s	43/471 (9%)	37 (86%)	6 (14%)	0	100	100
All	All	8101/9741 (83%)	7516 (93%)	566 (7%)	19 (0%)	44	72

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	1F	313	GLU
8	1H	92	PRO
8	1H	170	GLU
20	1T	23	ASP
42	1q	142	THR

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	1A	76/99 (77%)	76 (100%)	0	100	100
2	1B	131/209 (63%)	130 (99%)	1 (1%)	73	77
3	1C	190/227 (84%)	188 (99%)	2 (1%)	65	74
4	1D	341/405 (84%)	339 (99%)	2 (1%)	78	79
5	1E	183/207 (88%)	183 (100%)	0	100	100
6	1F	346/368 (94%)	346 (100%)	0	100	100
7	1G	588/610 (96%)	585 (100%)	3 (0%)	81	80
8	1H	255/274 (93%)	255 (100%)	0	100	100
9	1I	151/201 (75%)	151 (100%)	0	100	100
10	1J	140/140 (100%)	138 (99%)	2 (1%)	59	71
11	1K	84/84 (100%)	84 (100%)	0	100	100
12	1L	539/539 (100%)	536 (99%)	3 (1%)	78	79
13	1M	408/408 (100%)	408 (100%)	0	100	100
14	1N	310/310 (100%)	309 (100%)	1 (0%)	86	83
15	1O	283/307 (92%)	281 (99%)	2 (1%)	76	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	1P	296/323 (92%)	295 (100%)	1 (0%)	86	83
17	1Q	117/152 (77%)	116 (99%)	1 (1%)	70	76
18	1R	79/97 (81%)	78 (99%)	1 (1%)	61	72
19	1S	77/82 (94%)	77 (100%)	0	100	100
20	1T	79/133 (59%)	79 (100%)	0	100	100
20	1U	79/133 (59%)	78 (99%)	1 (1%)	61	72
21	1V	100/101 (99%)	100 (100%)	0	100	100
22	1W	107/112 (96%)	107 (100%)	0	100	100
23	1X	153/154 (99%)	153 (100%)	0	100	100
24	1Y	101/102 (99%)	100 (99%)	1 (1%)	68	75
25	1Z	123/124 (99%)	123 (100%)	0	100	100
26	1a	58/58 (100%)	58 (100%)	0	100	100
27	1b	69/70 (99%)	69 (100%)	0	100	100
28	1c	45/66 (68%)	44 (98%)	1 (2%)	45	65
29	1d	107/109 (98%)	107 (100%)	0	100	100
30	1e	87/94 (93%)	87 (100%)	0	100	100
31	1f	54/113 (48%)	54 (100%)	0	100	100
32	1g	92/129 (71%)	91 (99%)	1 (1%)	65	74
33	1h	121/158 (77%)	120 (99%)	1 (1%)	73	77
34	1i	119/120 (99%)	119 (100%)	0	100	100
35	1j	62/84 (74%)	62 (100%)	0	100	100
36	1k	63/76 (83%)	63 (100%)	0	100	100
37	1l	141/161 (88%)	141 (100%)	0	100	100
38	1m	113/114 (99%)	112 (99%)	1 (1%)	70	76
39	1n	156/160 (98%)	156 (100%)	0	100	100
40	1o	110/120 (92%)	110 (100%)	0	100	100
41	1p	154/156 (99%)	153 (99%)	1 (1%)	78	79
42	1q	131/131 (100%)	129 (98%)	2 (2%)	57	70
43	1r	85/98 (87%)	84 (99%)	1 (1%)	63	73
44	1s	44/351 (12%)	44 (100%)	0	100	100
All	All	7147/8269 (86%)	7118 (100%)	29 (0%)	81	81

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	1O	143	PHE
42	1q	135	GLN
17	1Q	6	GLN
38	1m	13	LEU
16	1P	171	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
21	1V	49	GLN
39	1n	140	GLN
22	1W	126	HIS
34	1i	25	GLN
41	1p	27	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

8 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
12	FME	1L	1	12	8,9,10	0.56	0	8,9,11	1.05	1 (12%)
14	FME	1N	1	14	8,9,10	0.52	0	8,9,11	1.03	1 (12%)
8	FME	1H	1	8	8,9,10	0.55	0	8,9,11	1.09	1 (12%)
10	FME	1J	1	10	8,9,10	0.56	0	8,9,11	0.96	1 (12%)
11	FME	1K	1	11	8,9,10	0.54	0	8,9,11	1.72	2 (25%)
1	FME	1A	1	1	8,9,10	0.53	0	8,9,11	0.99	1 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	SAC	1i	1	-	7,8,9	0.53	0	7,9,11	1.54	1 (14%)
13	FME	1M	1	13	8,9,10	0.56	0	8,9,11	0.99	1 (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
12	FME	1L	1	12	-	0/7/9/11	-
14	FME	1N	1	14	-	0/7/9/11	-
8	FME	1H	1	8	-	0/7/9/11	-
10	FME	1J	1	10	-	0/7/9/11	-
11	FME	1K	1	11	-	0/7/9/11	-
1	FME	1A	1	1	-	2/7/9/11	-
34	SAC	1i	1	-	-	5/7/8/10	-
13	FME	1M	1	13	-	1/7/9/11	-

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	1K	1	FME	CA-N-CN	3.72	128.54	122.82
34	1i	1	SAC	O-C-CA	-2.98	117.10	124.77
8	1H	1	FME	O-C-CA	-2.80	117.57	124.77
12	1L	1	FME	O-C-CA	-2.71	117.81	124.77
14	1N	1	FME	O-C-CA	-2.66	117.94	124.77

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1A	1	FME	N-CA-CB-CG
13	1M	1	FME	C-CA-CB-CG
34	1i	1	SAC	C-CA-CB-OG
34	1i	1	SAC	C2A-C1A-N-CA
34	1i	1	SAC	OAC-C1A-N-CA

There are no ring outliers.

5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	1N	1	FME	3	0
11	1K	1	FME	1	0
1	1A	1	FME	1	0
34	1i	1	SAC	2	0
13	1M	1	FME	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 31 ligands modelled in this entry, 3 are monoatomic - leaving 28 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	$\# Z > 2$
46	PC1	1f	101	-	45,45,53	0.27	0	51,53,61	0.35	0
47	SF4	1G	801	7	0,12,12	-	-	-		
45	3PE	1A	201	-	46,46,50	0.28	0	49,51,55	0.38	0
45	3PE	1Y	201	-	30,30,50	0.34	0	33,35,55	0.60	1 (3%)
52	CDL	1q	201	-	60,60,99	0.34	0	66,72,111	0.43	0
45	3PE	1L	703	-	41,41,50	0.31	0	44,46,55	1.27	5 (11%)
55	NDP	1P	501	-	51,52,52	0.53	0	71,80,80	0.73	1 (1%)
52	CDL	1N	402	-	76,76,99	0.85	2 (2%)	82,88,111	0.63	2 (2%)
47	SF4	1I	202	9	0,12,12	-	-	-		
57	EHZ	1W	201	-	31,36,37	0.21	0	36,44,47	1.09	1 (2%)
57	EHZ	1n	201	-	31,36,37	0.18	0	36,44,47	1.26	1 (2%)
46	PC1	1L	702	-	43,43,53	0.30	0	49,51,61	0.38	0
47	SF4	1I	201	9	0,12,12	-	-	-		
45	3PE	1L	701	-	45,45,50	0.29	0	48,50,55	0.31	0
45	3PE	1Y	202	-	50,50,50	0.26	0	53,55,55	0.41	0
46	PC1	1I	204	-	43,43,53	0.30	0	49,51,61	0.35	0
47	SF4	1G	802	7	0,12,12	-	-	-		
46	PC1	1A	202	-	34,34,53	0.32	0	40,42,61	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
53	GTP	1O	401	54	33,34,34	0.59	0	50,54,54	0.61	0
58	MYR	1l	201	-	13,14,15	0.30	0	12,13,15	0.30	0
51	PGT	1M	501	-	50,50,50	0.50	0	53,56,56	0.50	0
49	FMN	1F	501	-	33,33,33	0.61	0	48,50,50	0.66	1 (2%)
47	SF4	1B	201	2	0,12,12	-	-	-	-	-
45	3PE	1N	401	-	50,50,50	0.27	0	53,55,55	0.41	0
47	SF4	1F	502	6	0,12,12	-	-	-	-	-
48	FES	1G	803	7	0,4,4	-	-	-	-	-
48	FES	1E	301	5	0,4,4	-	-	-	-	-
46	PC1	1I	203	-	53,53,53	0.27	0	59,61,61	0.30	0

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
46	PC1	1f	101	-	-	5/49/49/57	-
47	SF4	1G	801	7	-	-	0/6/5/5
45	3PE	1A	201	-	-	2/50/50/54	-
45	3PE	1Y	201	-	-	7/34/34/54	-
52	CDL	1q	201	-	-	16/71/71/110	-
45	3PE	1L	703	-	-	6/45/45/54	-
55	NDP	1P	501	-	-	6/34/77/77	0/5/5/5
52	CDL	1N	402	-	-	10/87/87/110	-
47	SF4	1I	202	9	-	-	0/6/5/5
57	EHZ	1W	201	-	-	14/42/44/45	-
46	PC1	1L	702	-	-	4/47/47/57	-
47	SF4	1I	201	9	-	-	0/6/5/5
45	3PE	1L	701	-	-	3/49/49/54	-
45	3PE	1Y	202	-	-	8/54/54/54	-
46	PC1	1I	204	-	-	4/47/47/57	-
47	SF4	1G	802	7	-	-	0/6/5/5
46	PC1	1A	202	-	-	4/38/38/57	-
53	GTP	1O	401	54	-	0/22/38/38	0/3/3/3
58	MYR	1l	201	-	-	1/12/12/13	-
48	FES	1E	301	5	-	-	0/1/1/1
51	PGT	1M	501	-	-	22/55/55/55	-
49	FMN	1F	501	-	-	1/18/18/18	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
47	SF4	1B	201	2	-	-	0/6/5/5
45	3PE	1N	401	-	-	5/54/54/54	-
47	SF4	1F	502	6	-	-	0/6/5/5
48	FES	1G	803	7	-	-	0/1/1/1
57	EHZ	1n	201	-	-	3/42/44/45	-
46	PC1	1I	203	-	-	3/57/57/57	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	1N	402	CDL	C15-C14	5.64	1.79	1.51
52	1N	402	CDL	C16-C15	3.03	1.66	1.51

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	1n	201	EHZ	C10-S1-C9	7.14	122.94	101.84
57	1W	201	EHZ	C10-S1-C9	6.18	120.11	101.84
45	1L	703	3PE	O21-C21-C22	6.09	124.66	111.48
55	1P	501	NDP	P2B-O2B-C2B	-3.91	112.99	123.43
52	1N	402	CDL	C17-C16-C15	2.82	139.96	115.25

There are no chirality outliers.

5 of 124 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
45	1L	703	3PE	O22-C21-O21-C2
45	1L	703	3PE	C22-C21-O21-C2
45	1Y	201	3PE	O32-C31-O31-C3
45	1Y	201	3PE	C32-C31-O31-C3
45	1Y	201	3PE	O22-C21-O21-C2

There are no ring outliers.

23 monomers are involved in 85 short contacts:

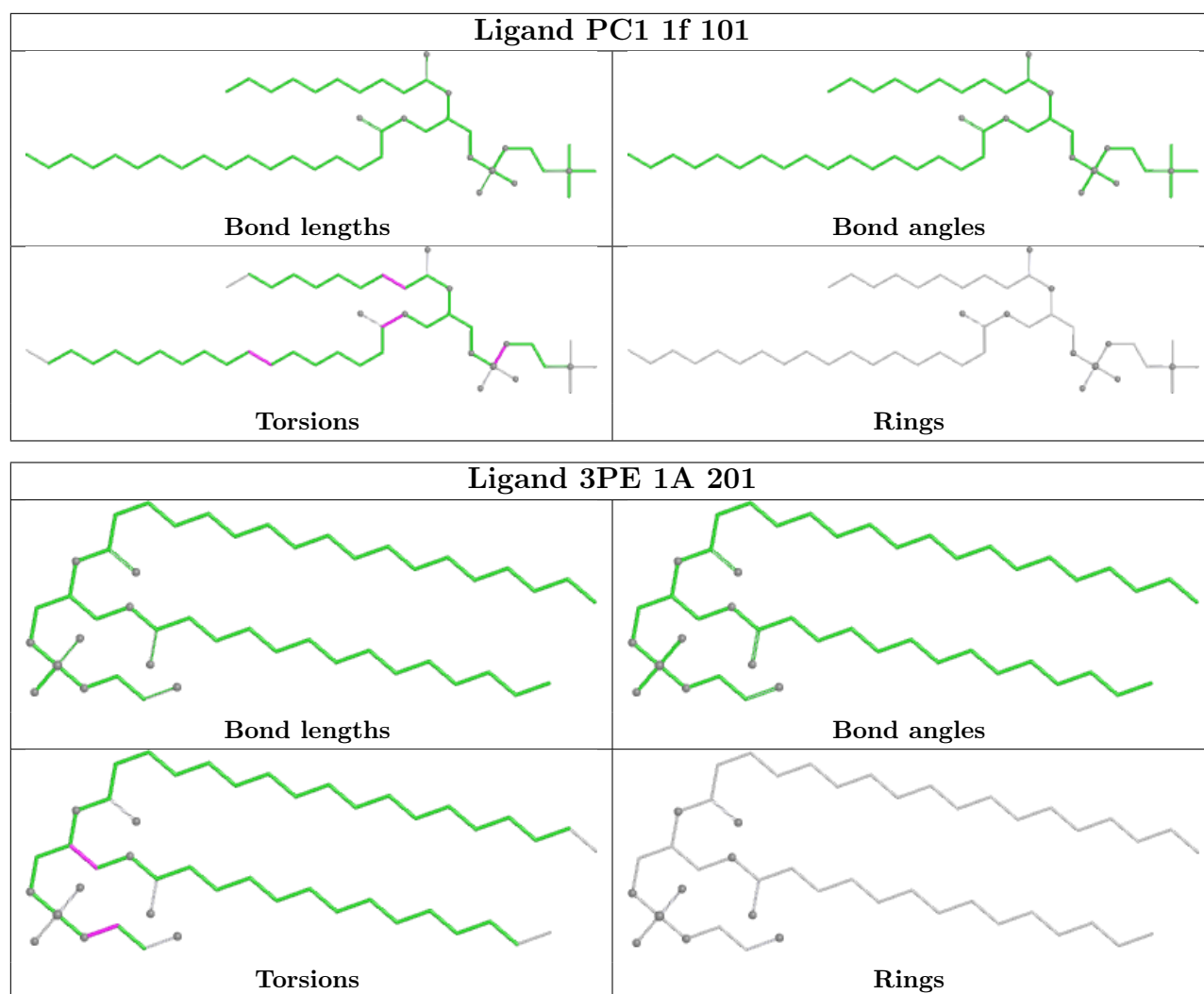
Mol	Chain	Res	Type	Clashes	Symm-Clashes
46	1f	101	PC1	6	0
47	1G	801	SF4	2	0
45	1A	201	3PE	2	0
45	1Y	201	3PE	7	0

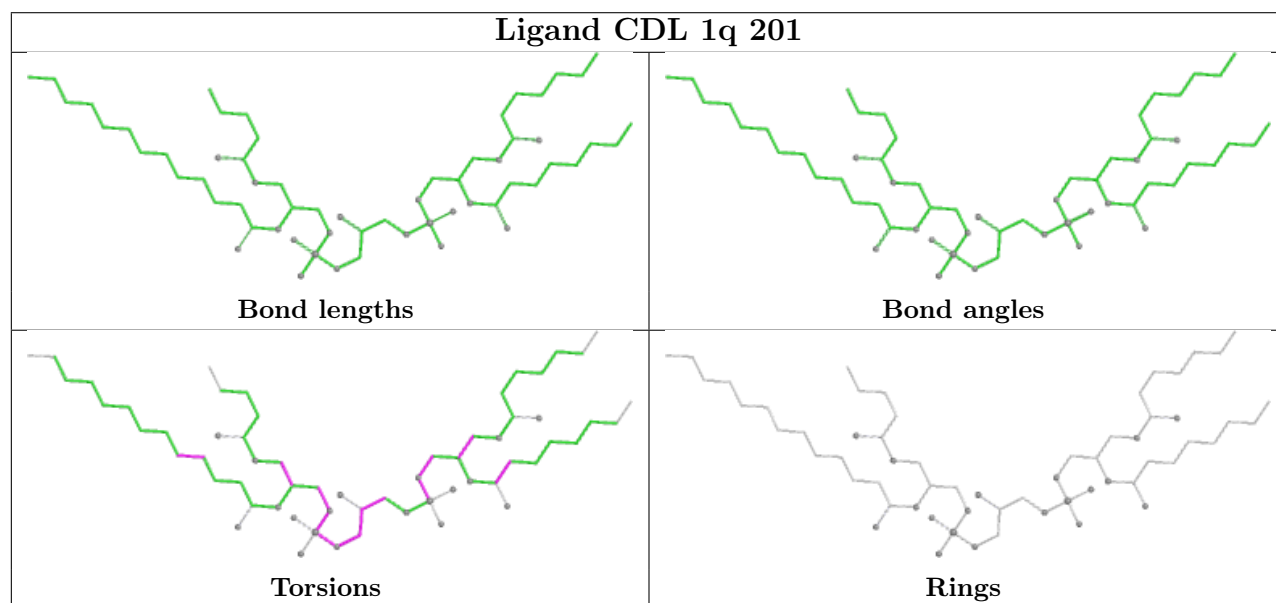
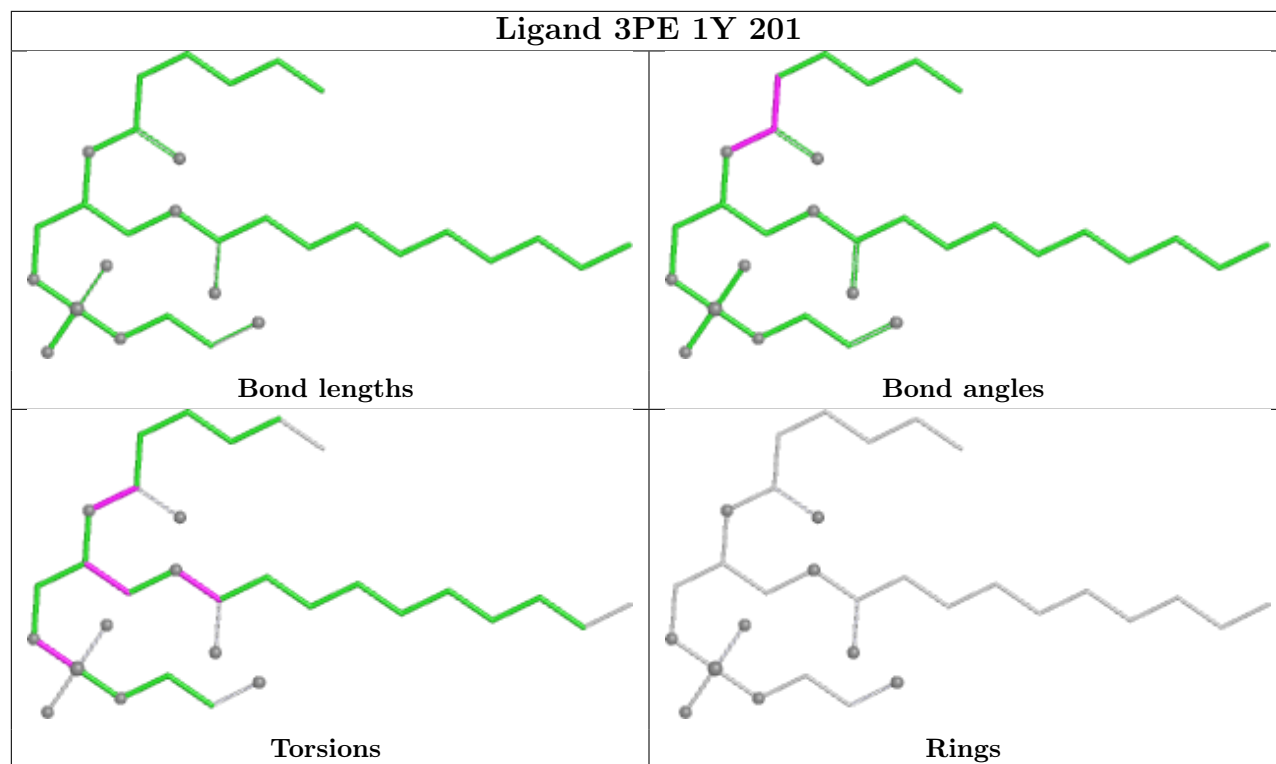
Continued on next page...

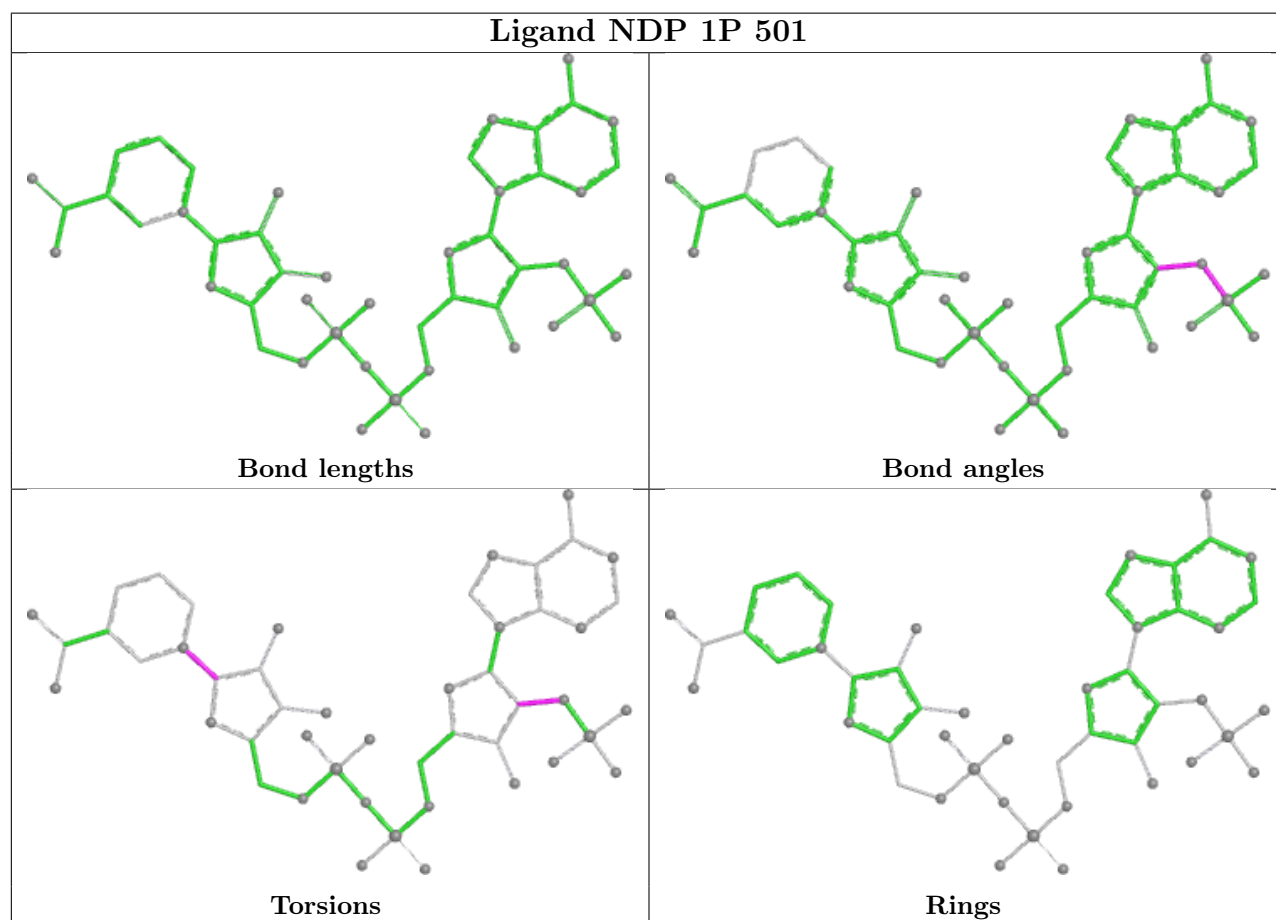
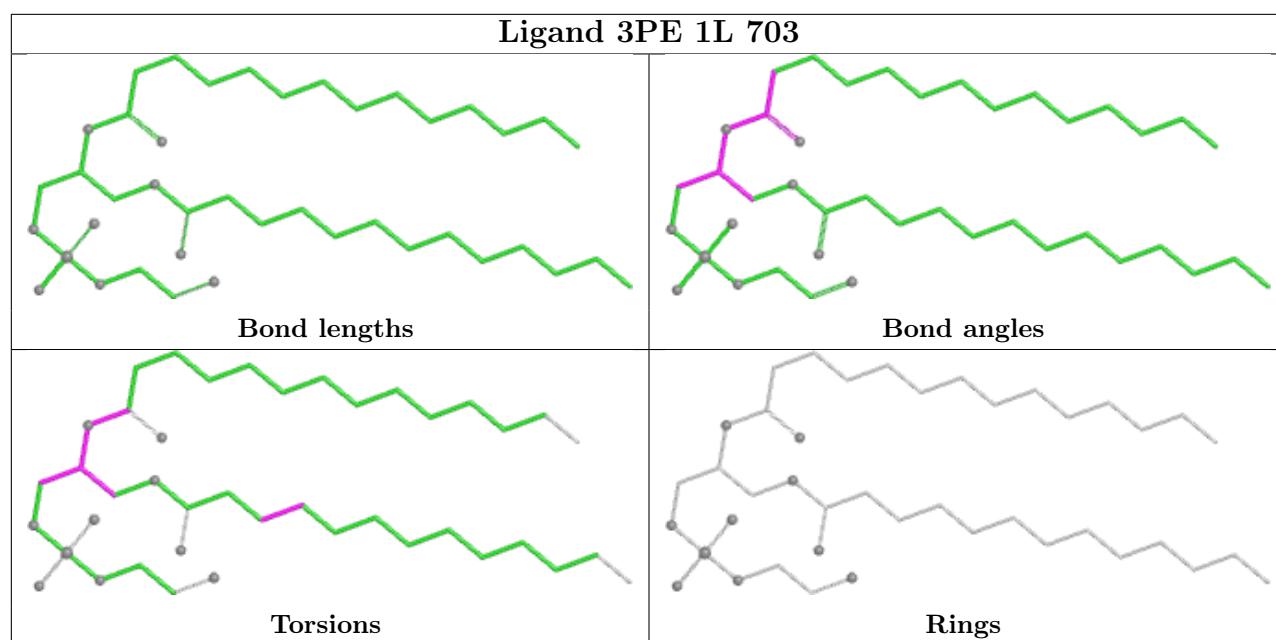
Continued from previous page...

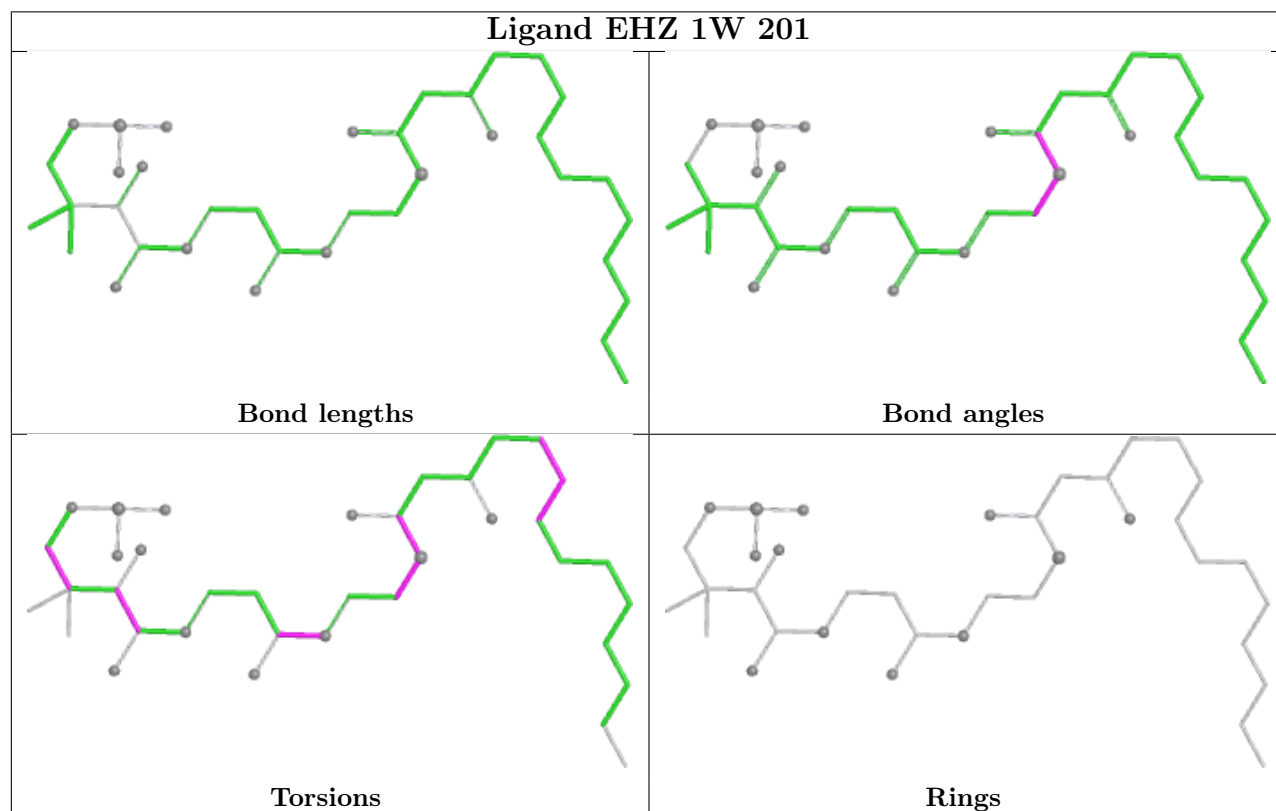
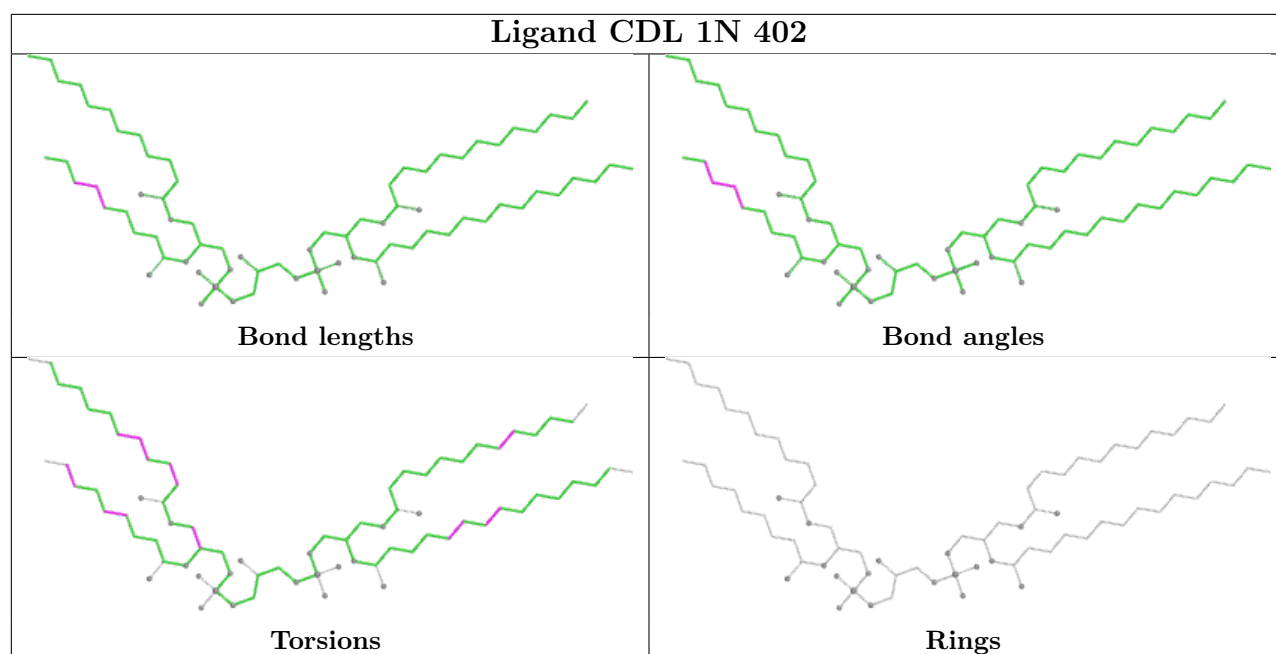
Mol	Chain	Res	Type	Clashes	Symm-Clashes
52	1q	201	CDL	11	0
45	1L	703	3PE	4	0
55	1P	501	NDP	6	0
52	1N	402	CDL	6	0
57	1W	201	EHZ	1	0
46	1L	702	PC1	4	0
47	1I	201	SF4	1	0
45	1L	701	3PE	4	0
45	1Y	202	3PE	4	0
46	1I	204	PC1	5	0
46	1A	202	PC1	1	0
58	1I	201	MYR	1	0
51	1M	501	PGT	8	0
47	1B	201	SF4	2	0
45	1N	401	3PE	2	0
47	1F	502	SF4	1	0
48	1G	803	FES	1	0
48	1E	301	FES	2	0
46	1I	203	PC1	4	0

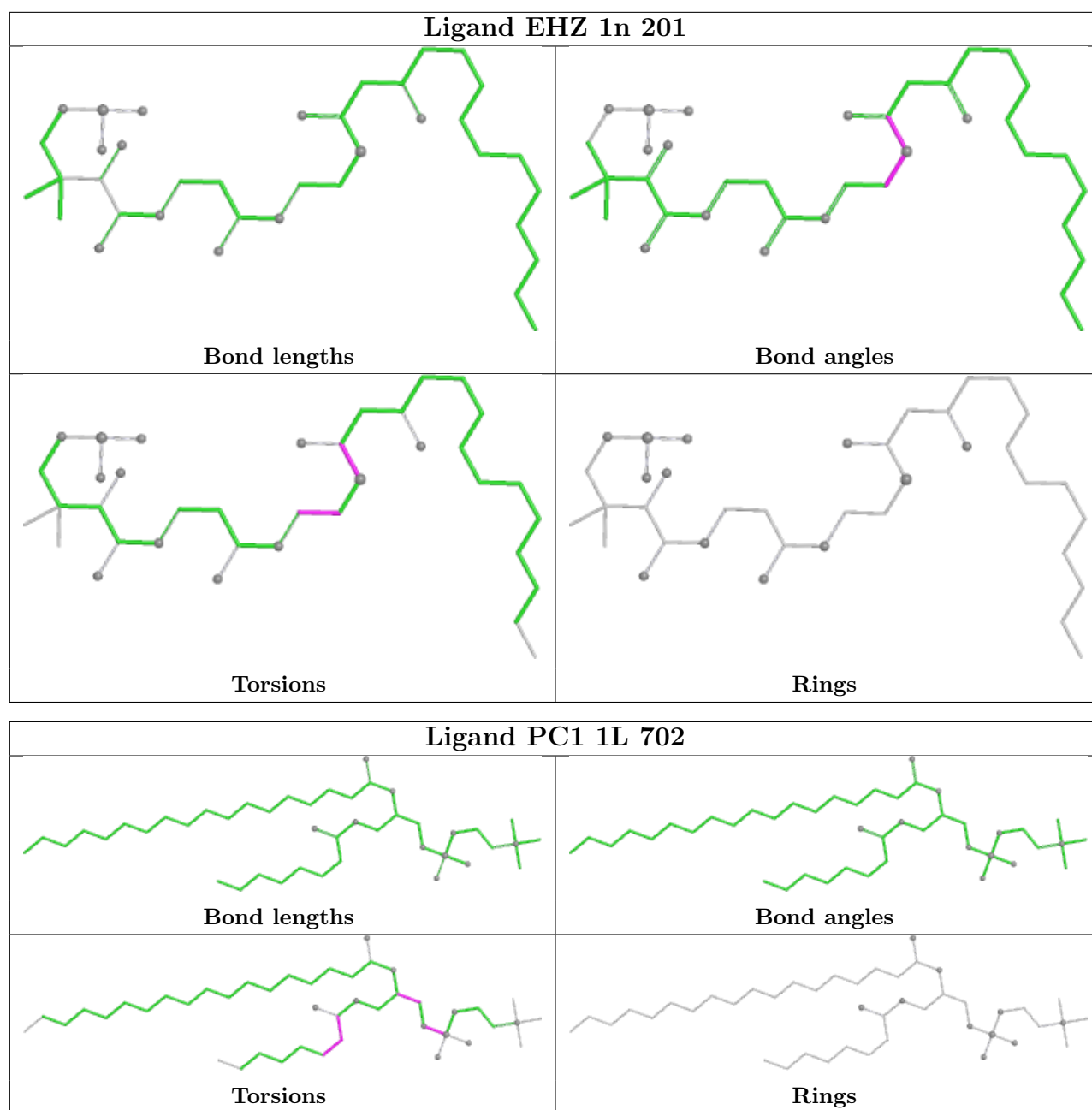
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

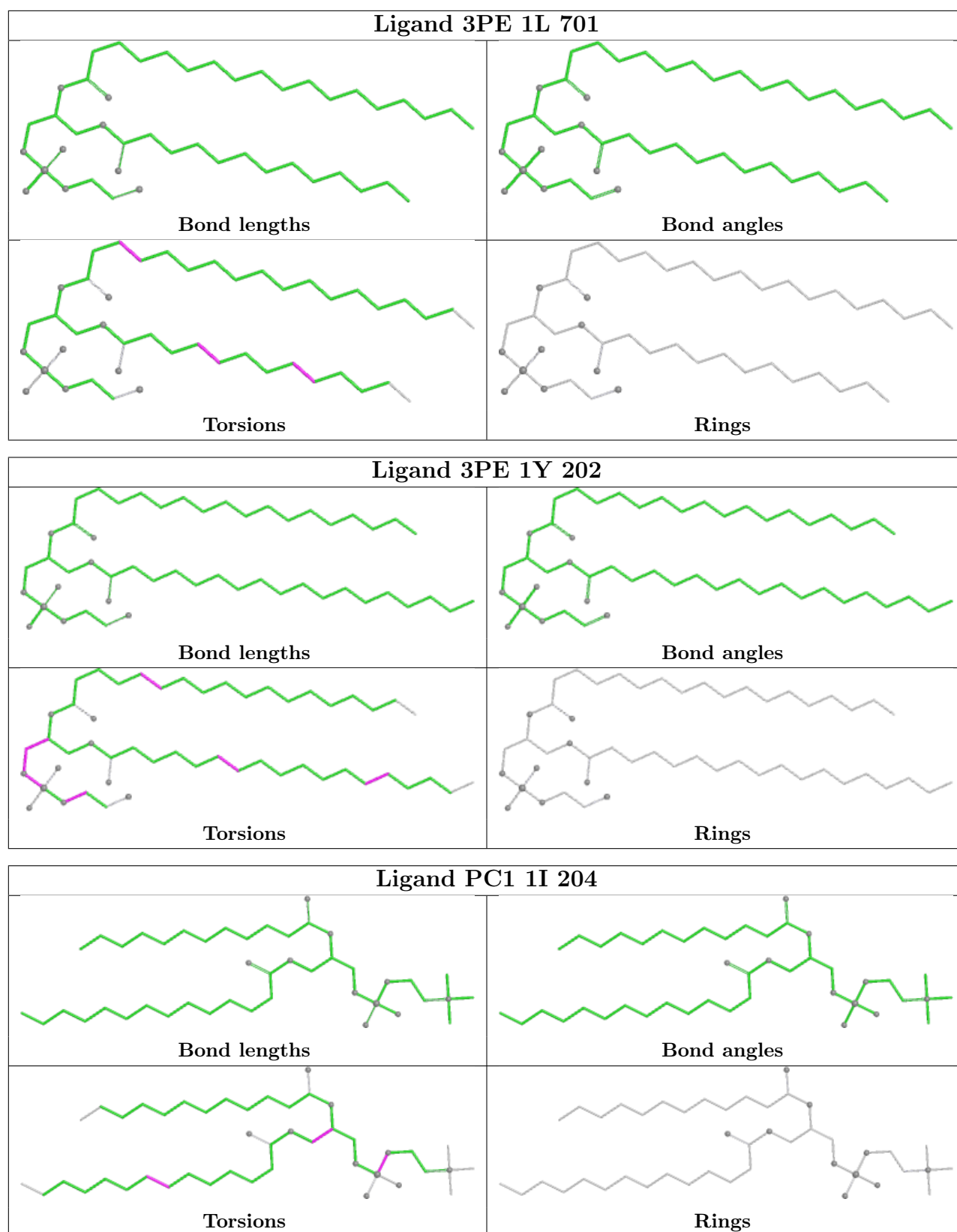


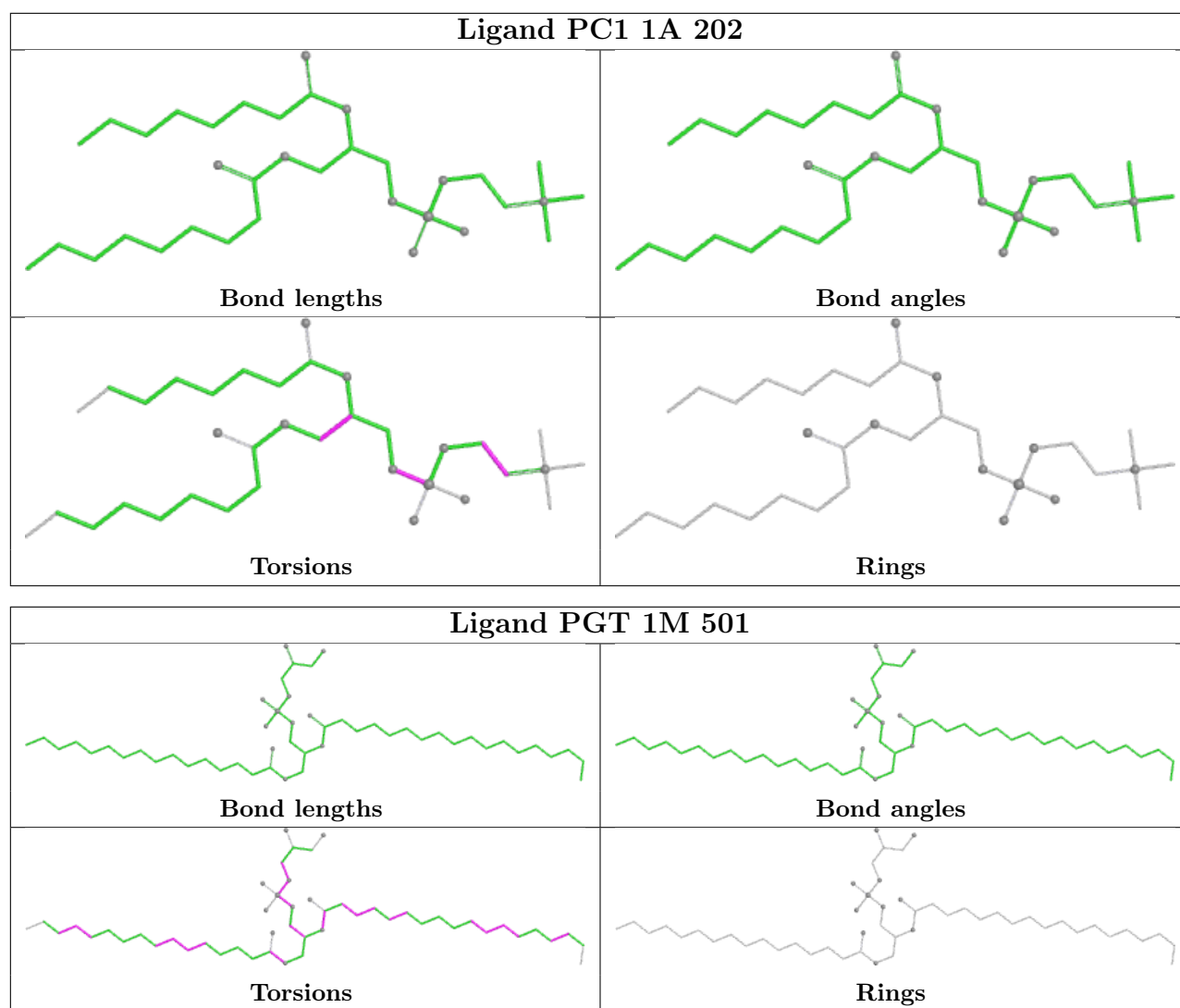


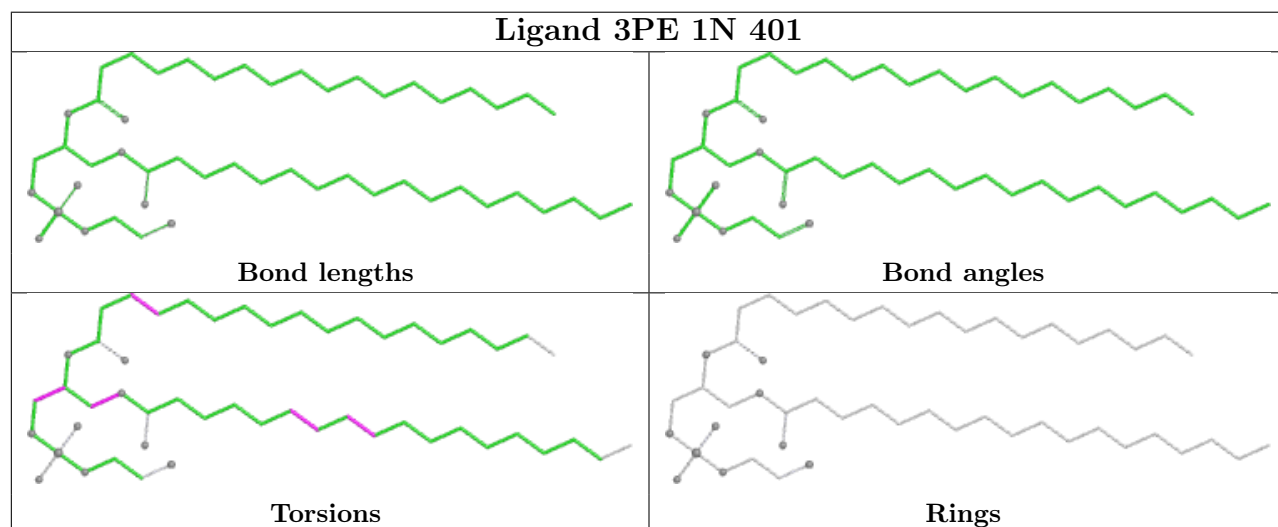
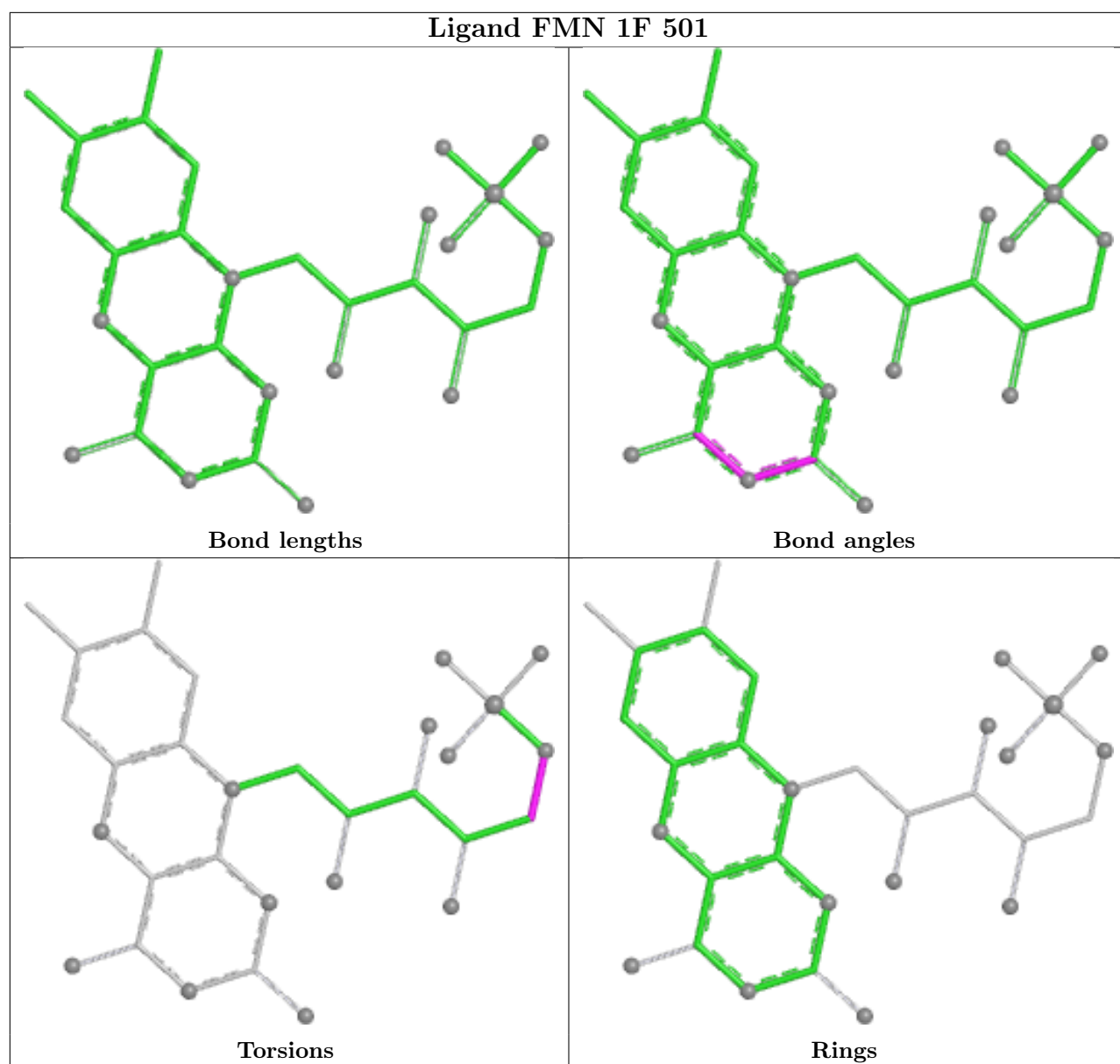


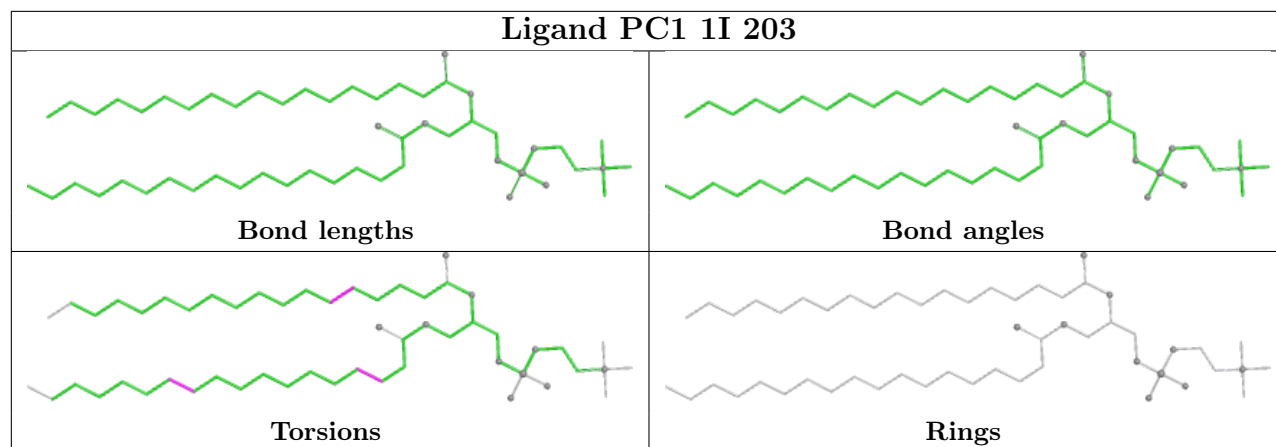












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
34	1i	1
43	1r	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1i	1:SAC	C	2:GLY	N	3.75
1	1r	1:ALA	C	2:SER	N	3.09

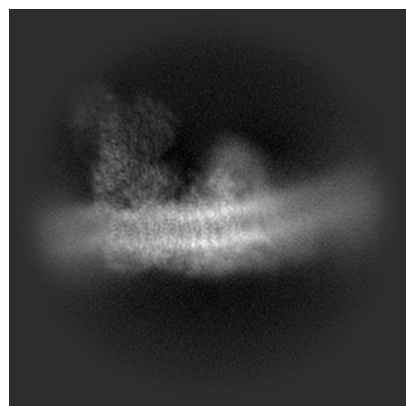
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42175. These allow visual inspection of the internal detail of the map and identification of artifacts.

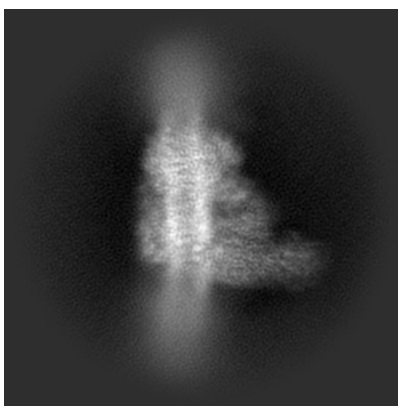
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

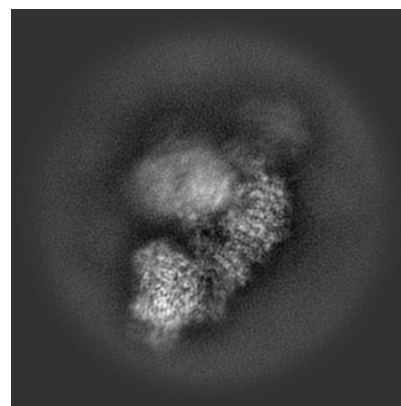
6.1.1 Primary map



X

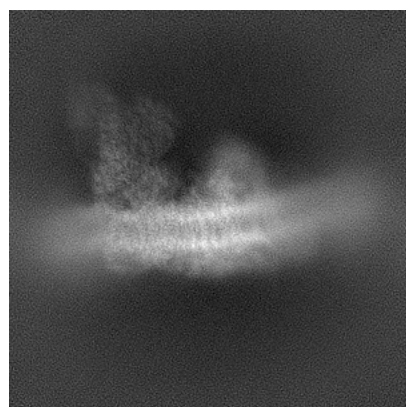


Y

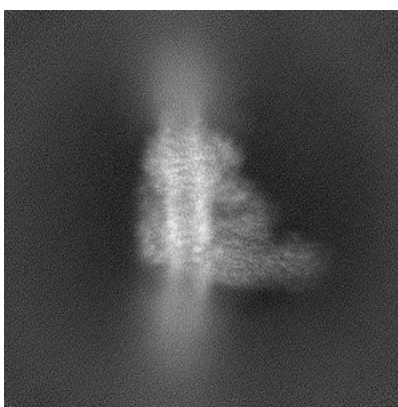


Z

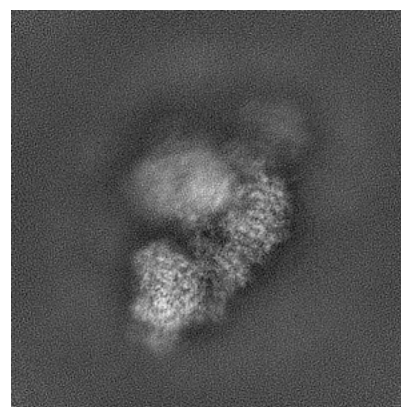
6.1.2 Raw map



X



Y

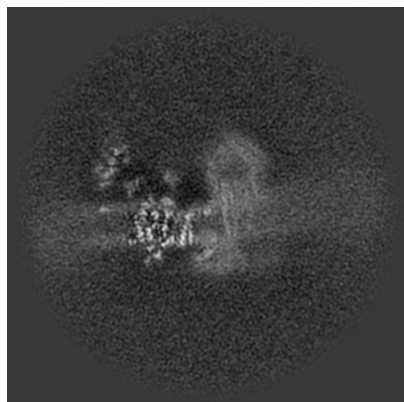


Z

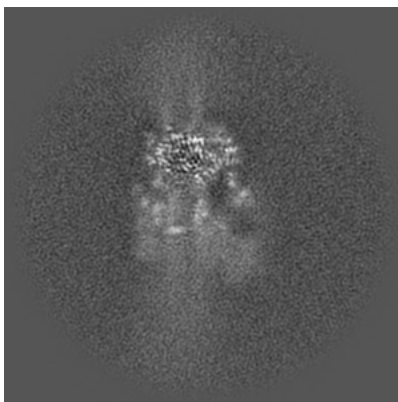
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

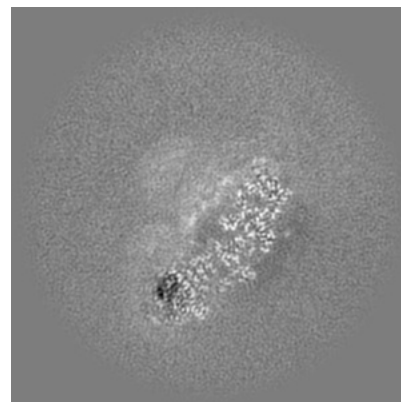
6.2.1 Primary map



X Index: 160



Y Index: 160

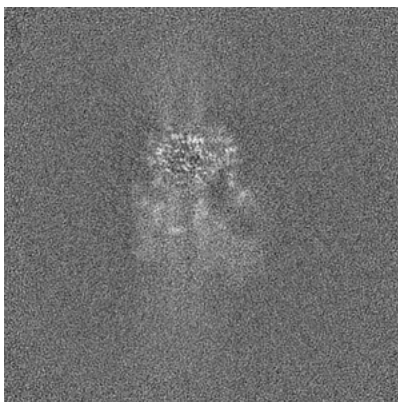


Z Index: 160

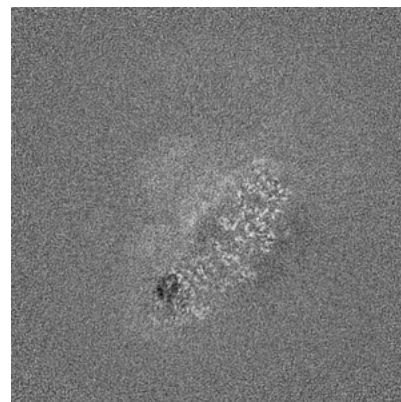
6.2.2 Raw map



X Index: 160



Y Index: 160

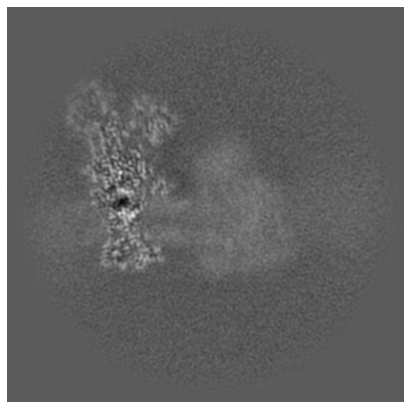


Z Index: 160

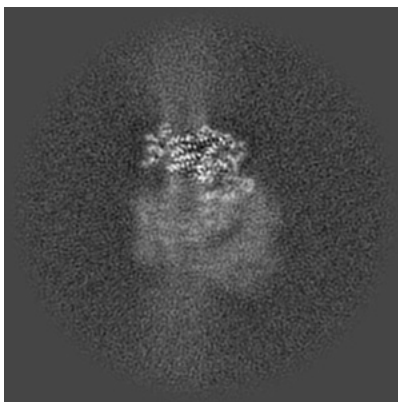
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

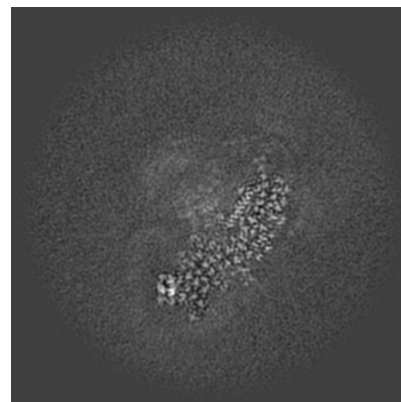
6.3.1 Primary map



X Index: 127

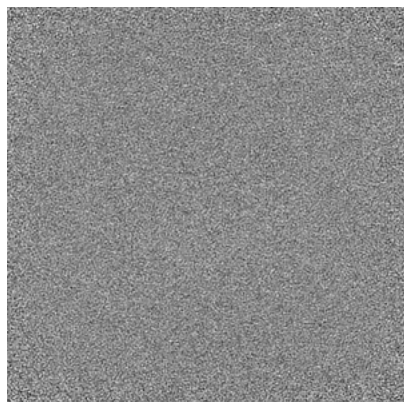


Y Index: 171

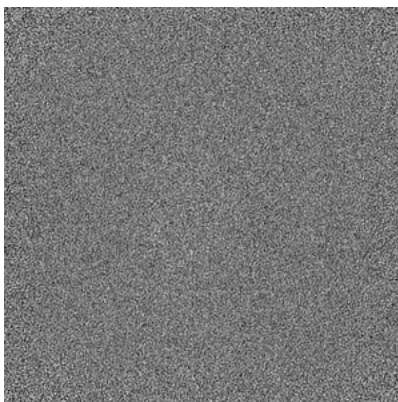


Z Index: 155

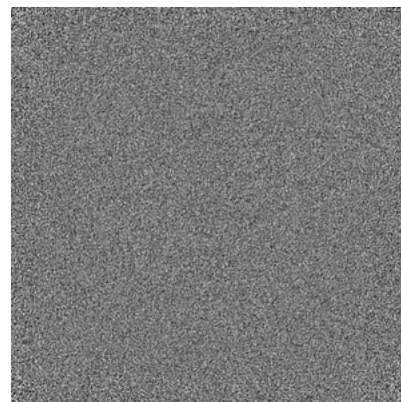
6.3.2 Raw map



X Index: 0



Y Index: 0

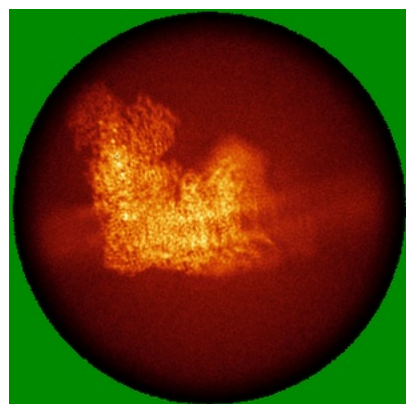


Z Index: 0

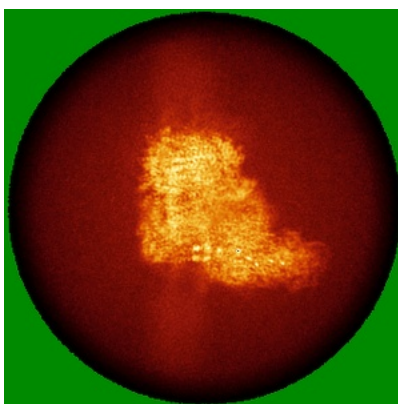
The images above show the largest variance slices of the map in three orthogonal directions.

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

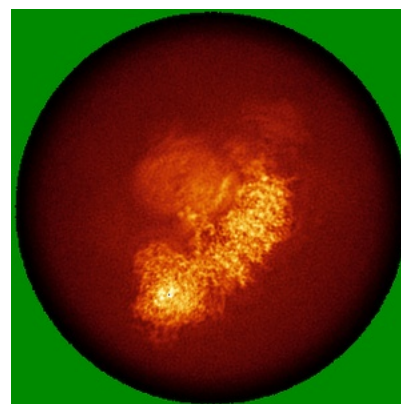
6.4.1 Primary map



X

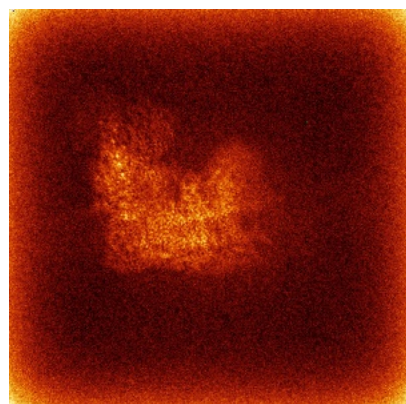


Y

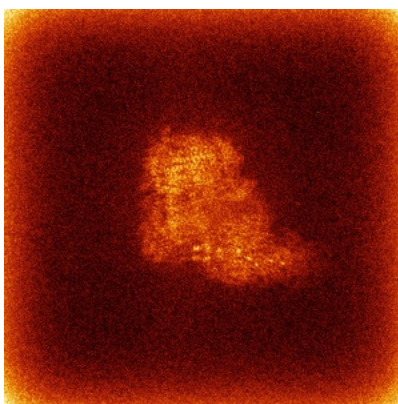


Z

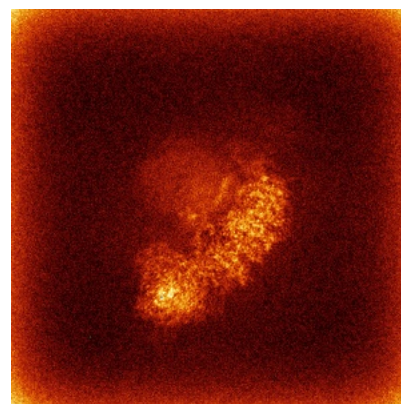
6.4.2 Raw map



X



Y



Z

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

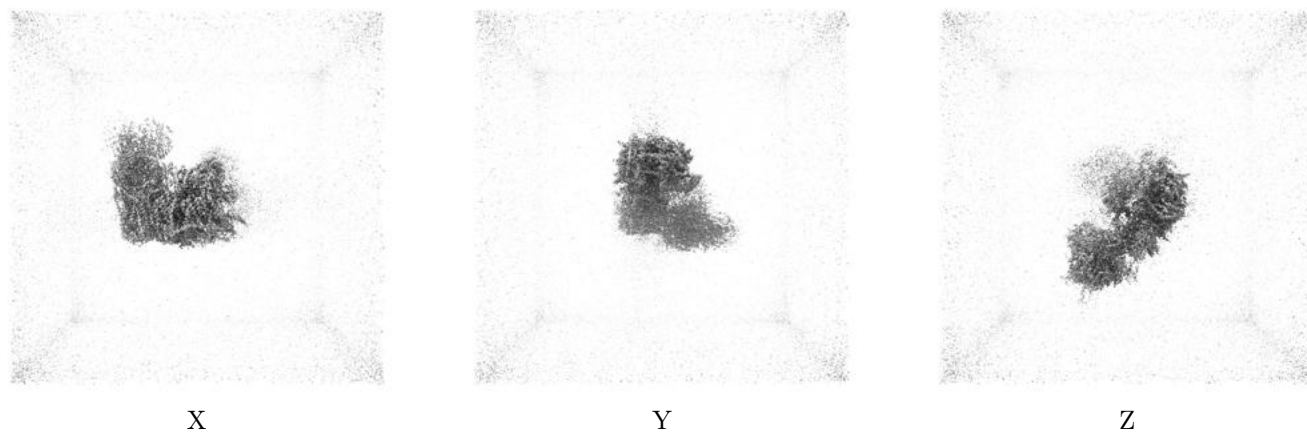
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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



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

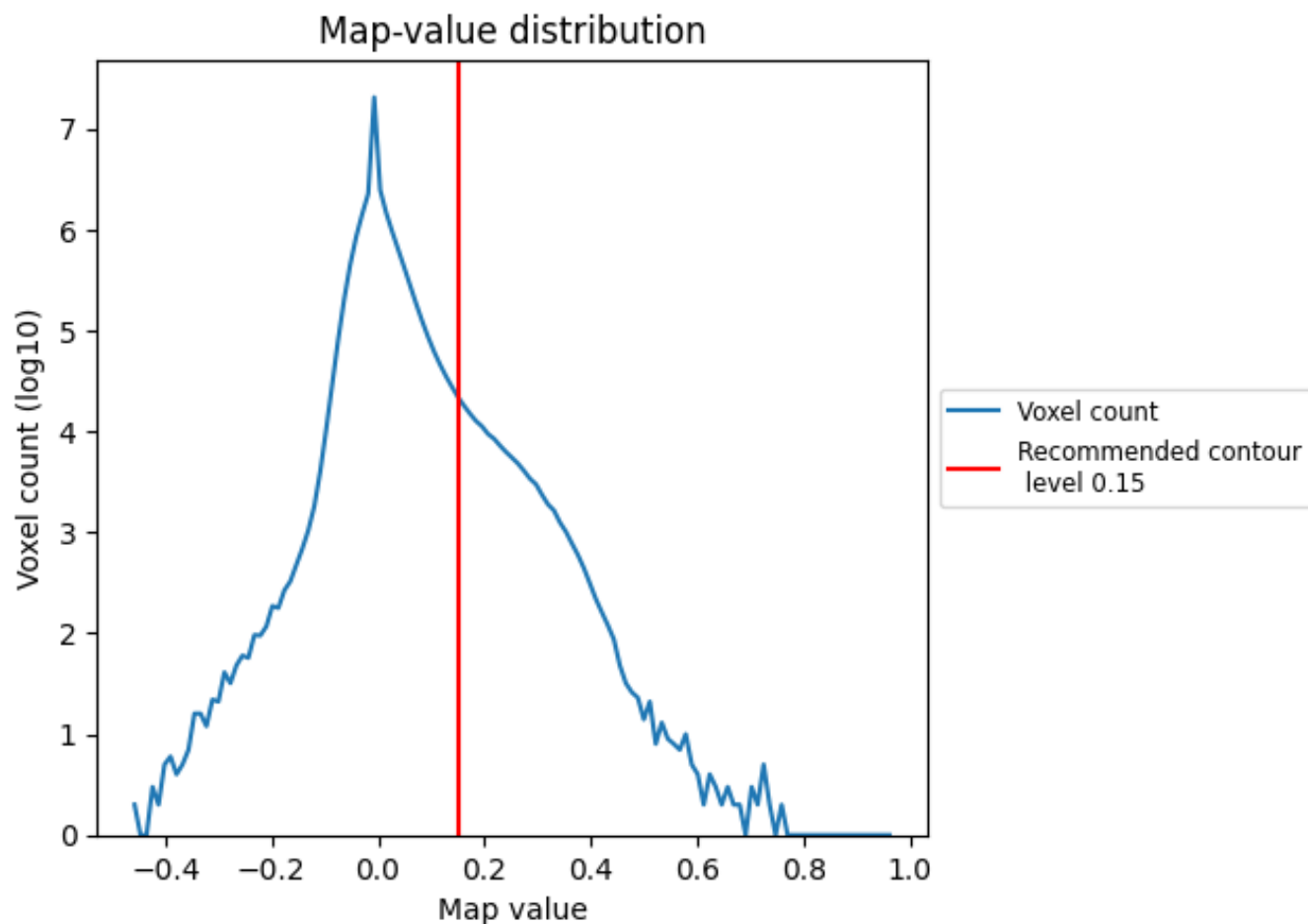
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

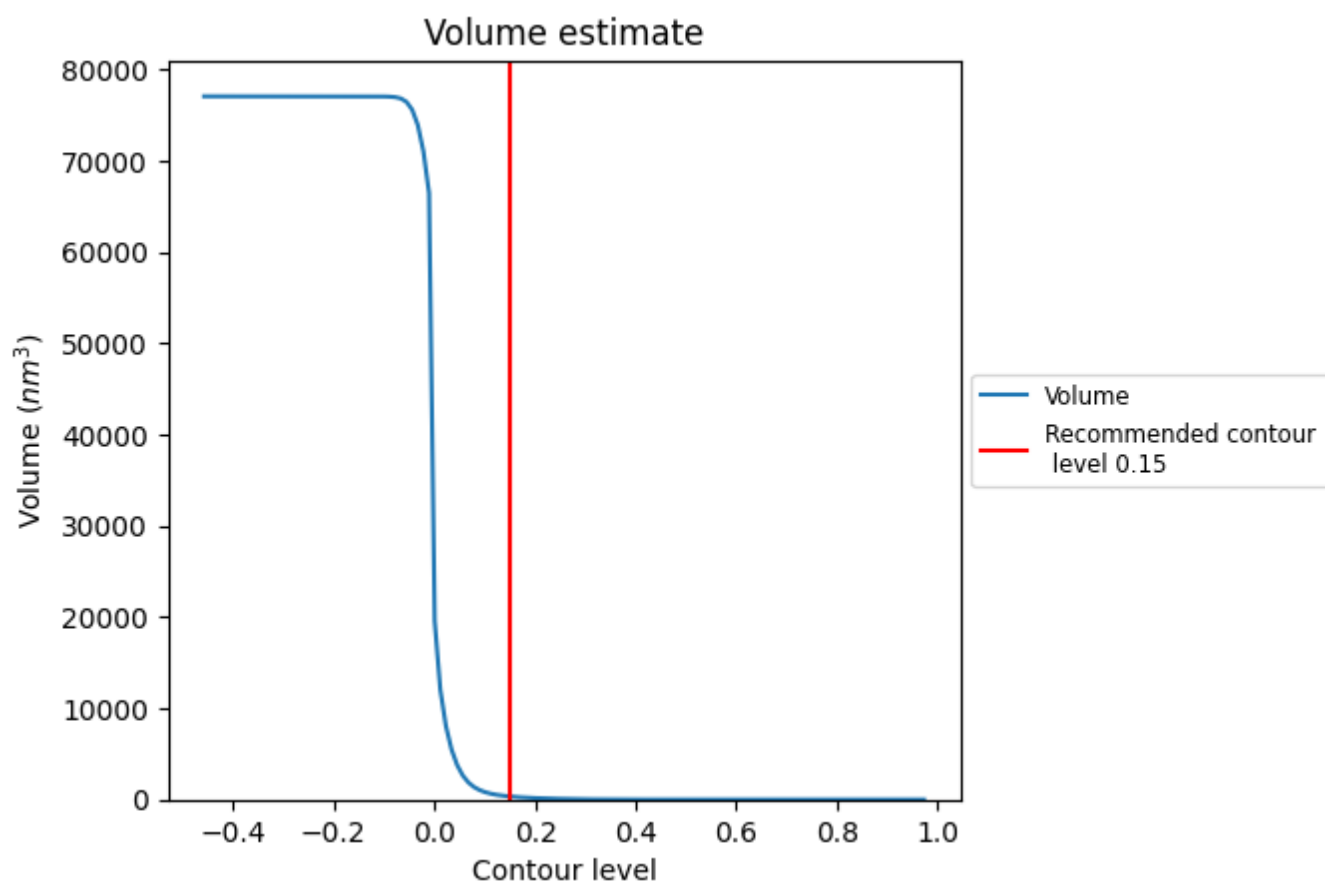
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

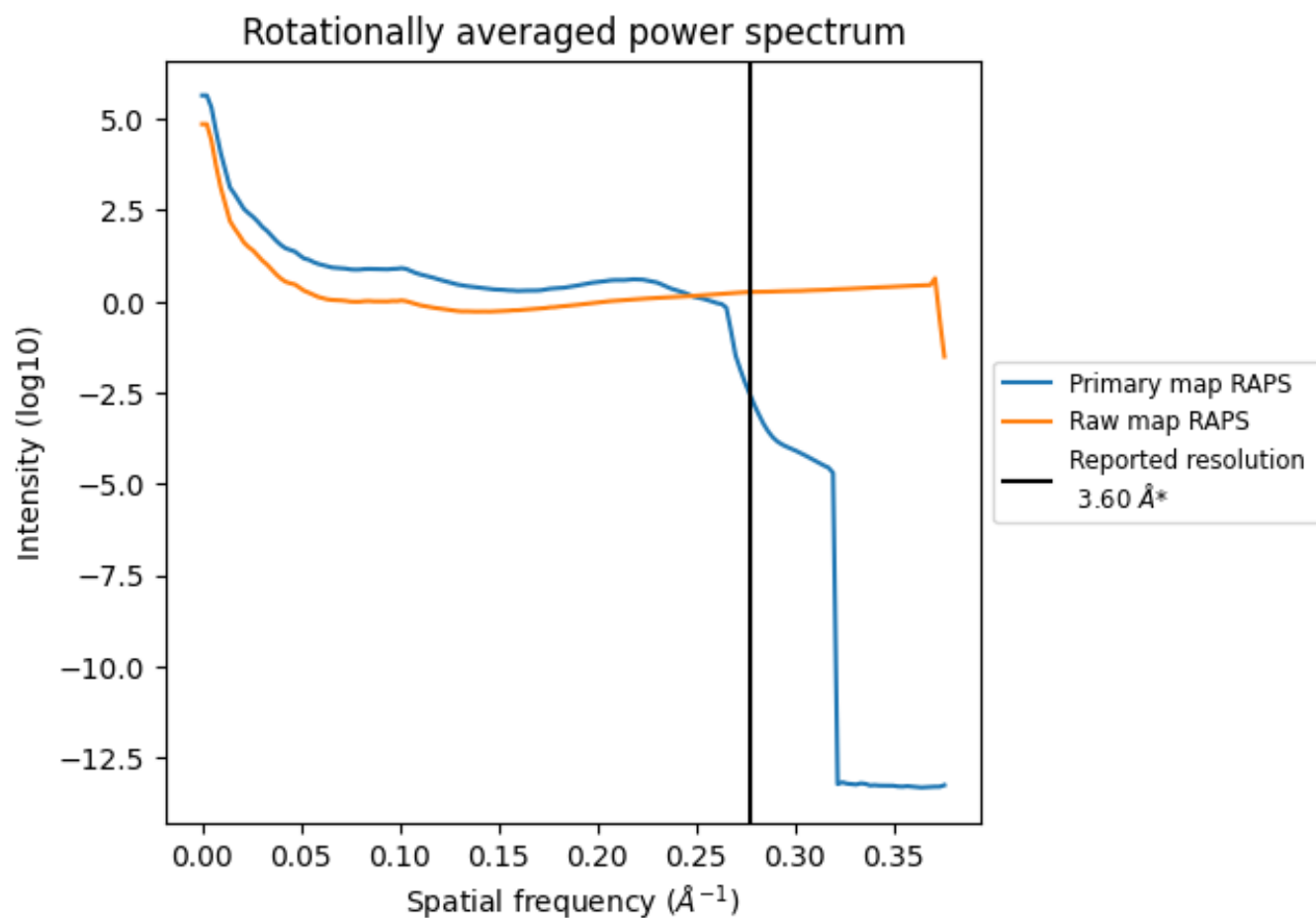
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 338 nm³; this corresponds to an approximate mass of 306 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 ⓘ

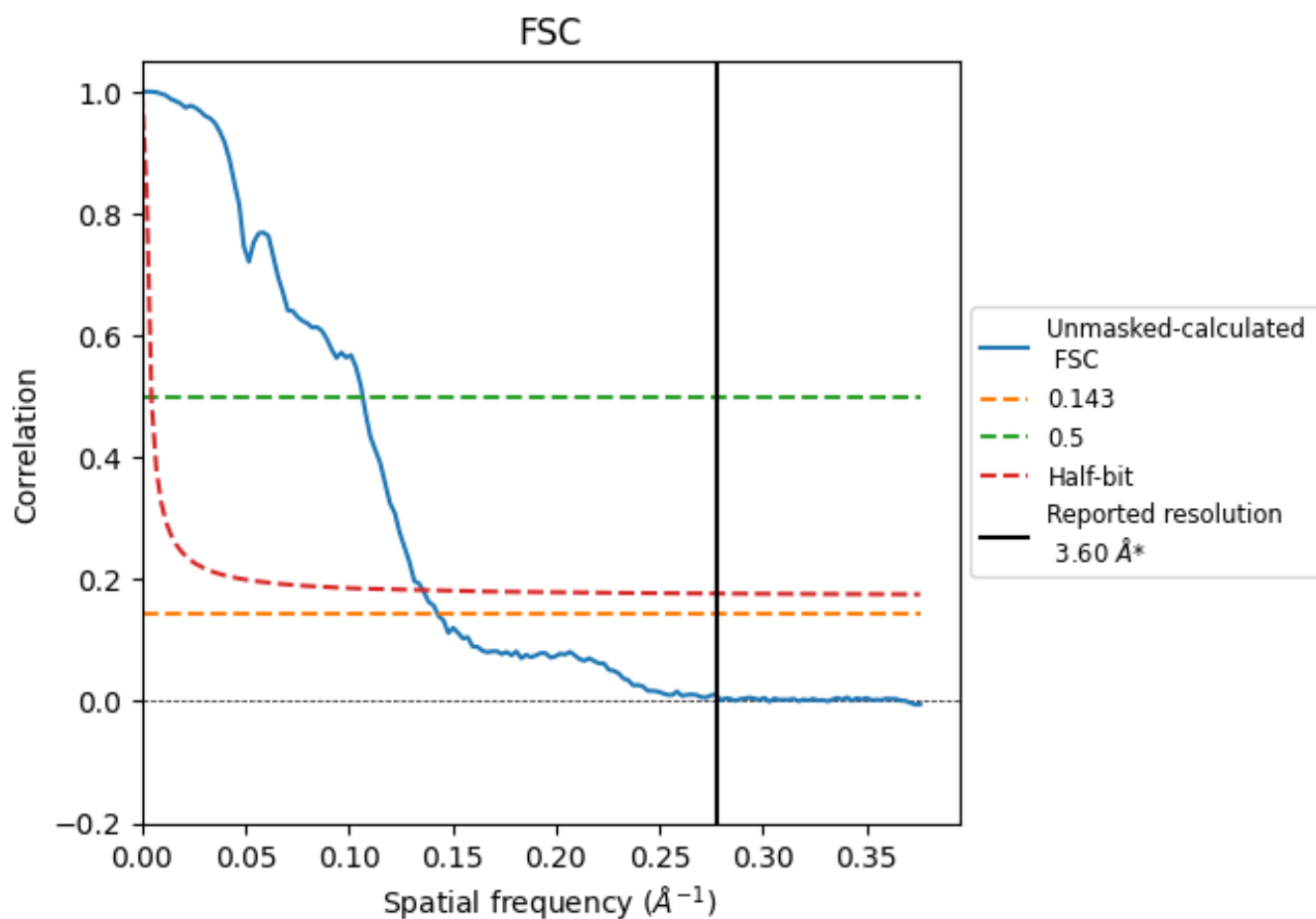


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

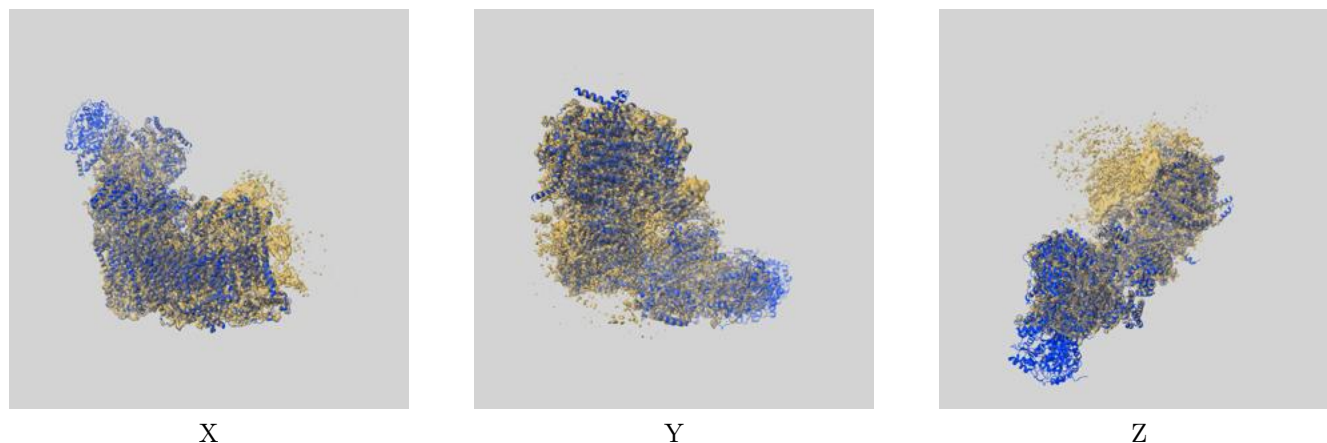
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.00	9.37	7.36

*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 7.00 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

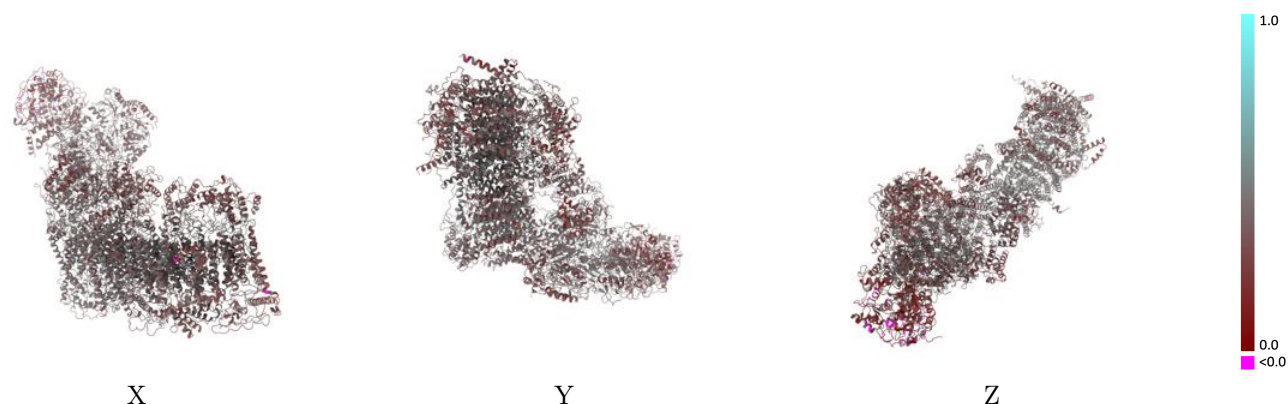
This section contains information regarding the fit between EMDB map EMD-42175 and PDB model 8UEY. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



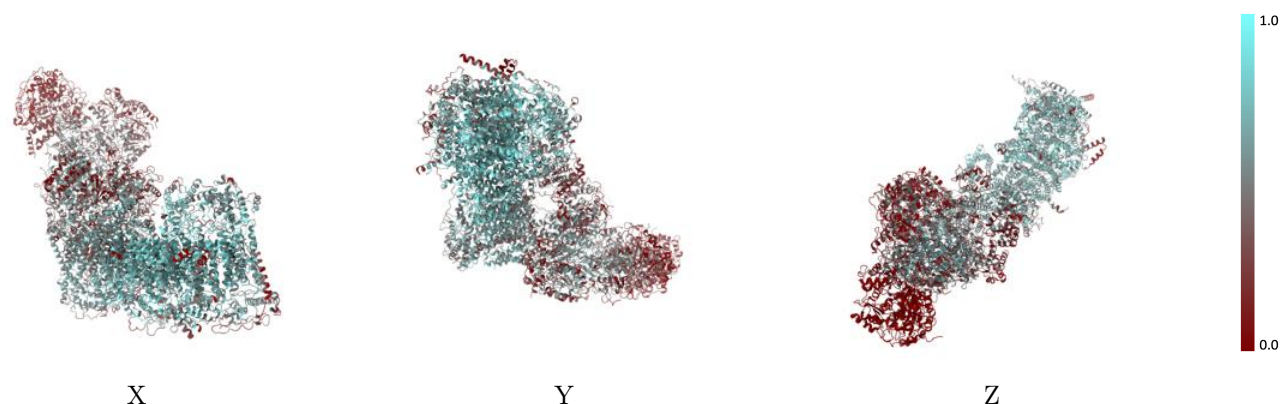
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



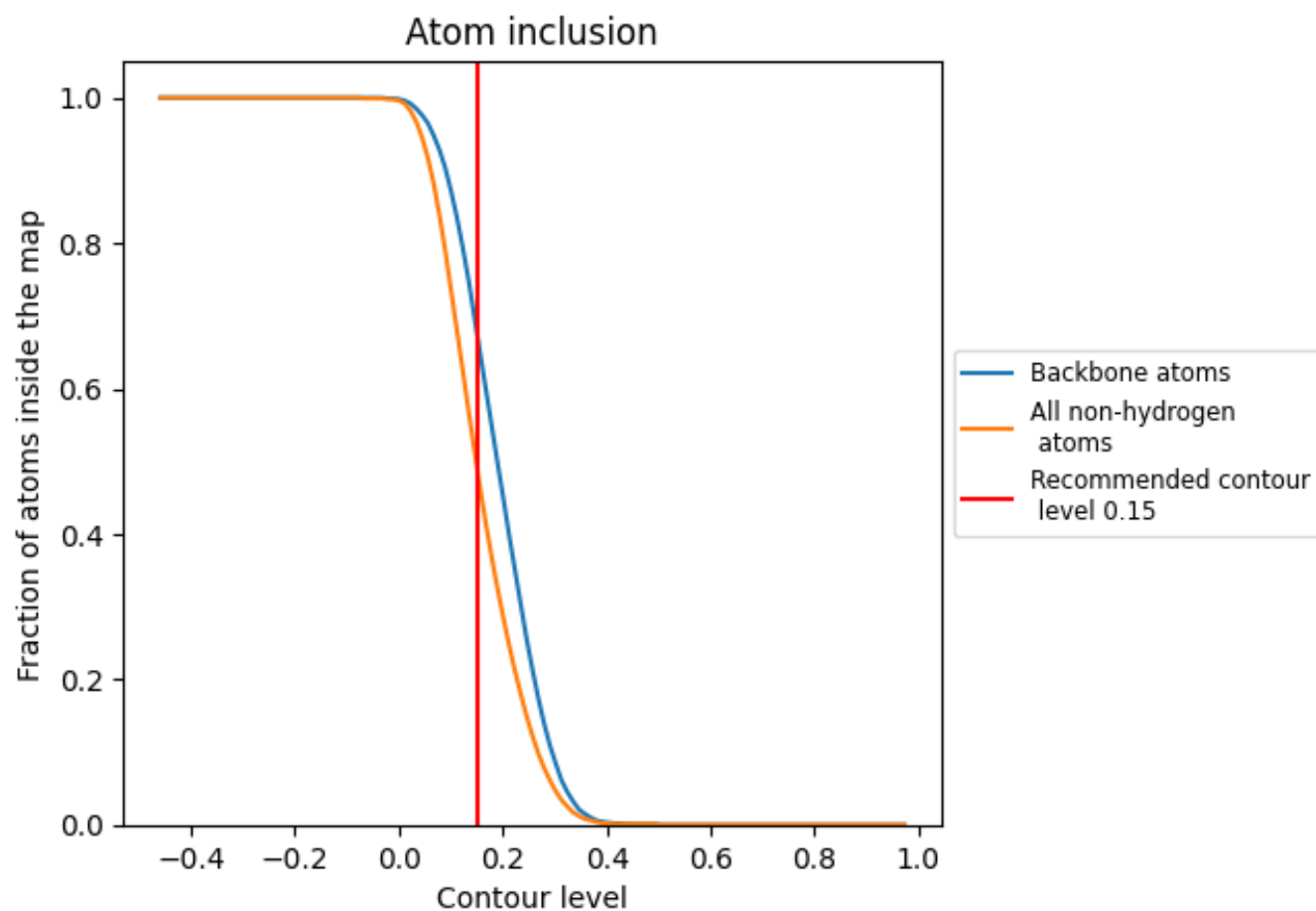
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



At the recommended contour level, 68% of all backbone atoms, 50% 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	 0.4950	 0.3830
1A	 0.5300	 0.4180
1B	 0.5860	 0.4290
1C	 0.4340	 0.4060
1D	 0.5590	 0.4080
1E	 0.0450	 0.2950
1F	 0.0480	 0.2570
1G	 0.3120	 0.3680
1H	 0.5930	 0.4130
1I	 0.5670	 0.4210
1J	 0.5290	 0.3800
1K	 0.6290	 0.4090
1L	 0.7110	 0.4100
1M	 0.7630	 0.4420
1N	 0.6850	 0.4310
1O	 0.4050	 0.3700
1P	 0.3270	 0.3470
1Q	 0.3250	 0.3840
1R	 0.3320	 0.4040
1S	 0.1620	 0.3070
1T	 0.2640	 0.2940
1U	 0.6120	 0.3580
1V	 0.2440	 0.3400
1W	 0.3370	 0.3580
1X	 0.5630	 0.4110
1Y	 0.6790	 0.3880
1Z	 0.5820	 0.4200
1a	 0.6840	 0.4140
1b	 0.5690	 0.4180
1c	 0.4460	 0.3740
1d	 0.6800	 0.4180
1e	 0.6120	 0.4290
1f	 0.4740	 0.3860
1g	 0.5960	 0.4040
1h	 0.6890	 0.4230



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Chain	Atom inclusion	Q-score
1i	 0.4070	 0.3590
1j	 0.5220	 0.3630
1k	 0.5200	 0.3610
1l	 0.6540	 0.3940
1m	 0.6900	 0.3870
1n	 0.6560	 0.3760
1o	 0.5350	 0.3320
1p	 0.6210	 0.3920
1q	 0.4310	 0.4050
1r	 0.4140	 0.3990
1s	 0.0000	 0.2350