wwPDB EM Validation Summary Report

Jun 13, 2024 – 12:12 PM EDT

PDB ID	:	8UER
EMDB ID	:	EMD-42168
Title	:	In-situ complex I with Q10 (State-gamma)
Authors	:	Zheng, W.; Zhu, J.; Zhang, K.
Deposited on	:	2023-10-02
Resolution	:	3.50 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:

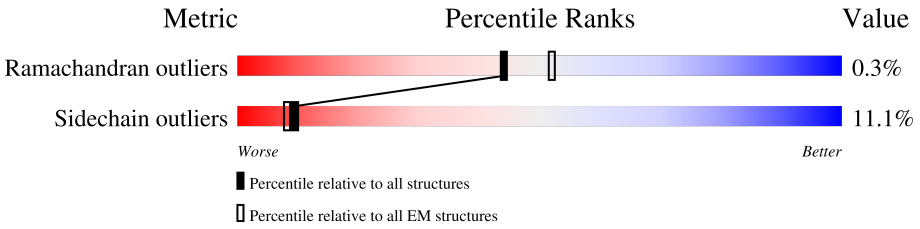
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	43% 85% 15%
2	1B	255	8% 55% 5% 39%
3	1C	264	11% 74% 5% 21%
4	1D	476	17% 83% 8% 10%
5	1E	249	47% 77% 9% 14%
6	1F	464	52% 86% 6% 7%
7	1G	727	13% 89% 7% .
8	1H	318	16% 91% 9%
9	1I	239	5% 67% 6% 26%

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Mol	Chain	Length	Quality of chain
10	1J	175	50% 85% 15%
11	1K	98	39% 87% 13%
12	1L	606	92% 91% 9%
13	1M	459	56% 89% 11%
14	1N	347	19% 92% 8%
15	1O	357	68% 81% 9% 10%
16	1P	377	28% 83% 8% 9%
17	1Q	175	21% 66% 7% 26%
18	1R	123	15% 68% 10% 22%
19	1S	99	22% 75% 13% 12%
20	1T	156	45% 49% 6% 46%
20	1U	156	55% 46% 8% 45%
21	1V	116	38% 90% 9%
22	1W	128	41% 77% 13% 10%
23	1X	172	28% 92% 7%
24	1Y	141	66% 91% 8%
25	1Z	144	23% 86% 12%
26	1a	70	16% 93% 7%
27	1b	84	37% 89% 10%
28	1c	76	38% 53% 12% 36%
29	1d	123	30% 89% 10%
30	1e	106	23% 84% 9% 7%
31	1f	135	31% 34% 8% 58%
32	1g	154	60% 52% 11% 35%
33	1h	189	48% 66% 7% 27%

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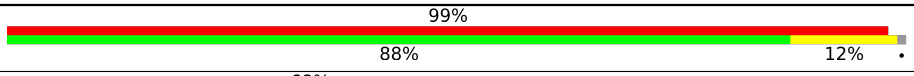
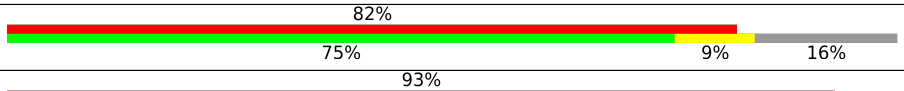
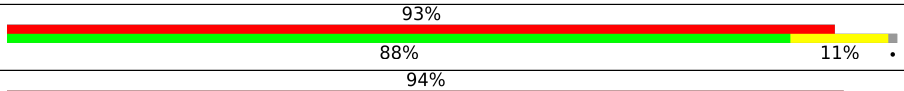
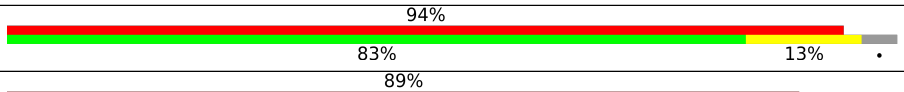
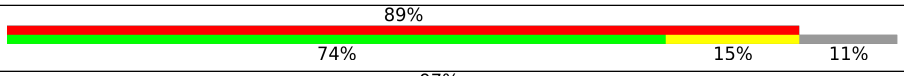
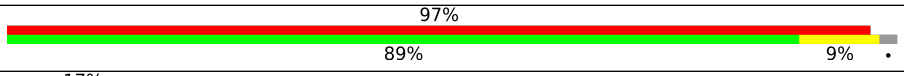
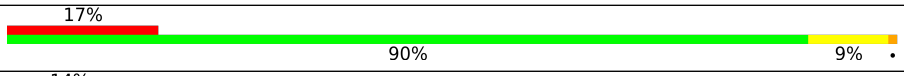
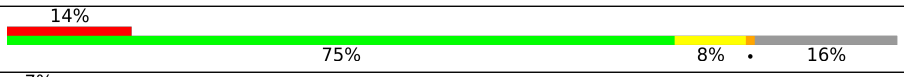
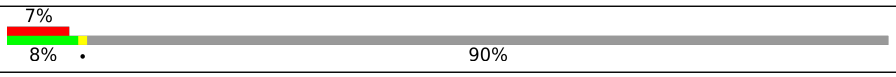
Mol	Chain	Length	Quality of chain
34	1i	128	
35	1j	105	
36	1k	98	
37	1l	186	
38	1m	129	
39	1n	179	
40	1o	137	
41	1p	176	
42	1q	145	
43	1r	114	
44	1s	471	

2 Entry composition (i)

There are 58 unique types of molecules in this entry. The entry contains 67436 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	1A	115	916	616	134	159	7	0	0

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

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

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
			Total	C	N	O	S		
3	1C	209	1740	1125	297	316	2	0	0

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	429	Total	C	N	O	S	0	0
			3452	2207	593	628	24		

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	318	Total	C	N	O	S	0	0
			2504	1673	385	425	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	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		

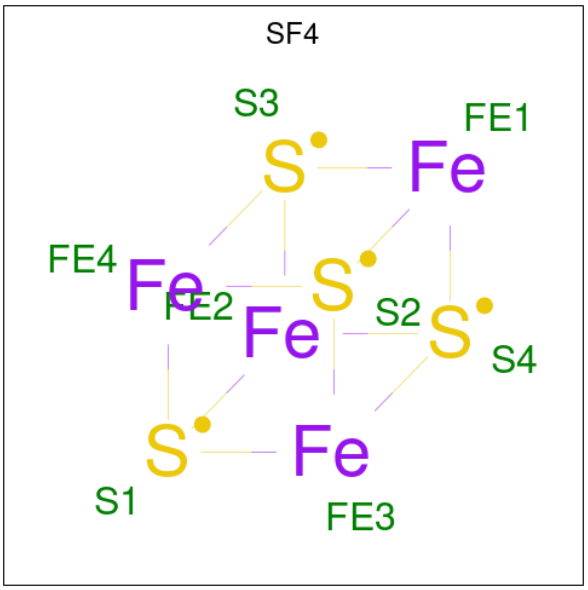
There is a discrepancy between the modelled and reference sequences:

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 IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			AltConf
45	1B	1	Total	Fe	S	0
			8	4	4	
45	1F	1	Total	Fe	S	0
			8	4	4	
45	1G	1	Total	Fe	S	0
			8	4	4	
45	1G	1	Total	Fe	S	0
			8	4	4	

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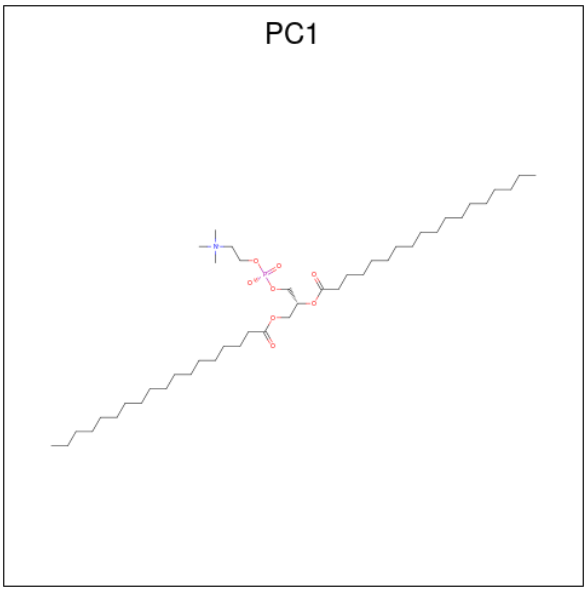
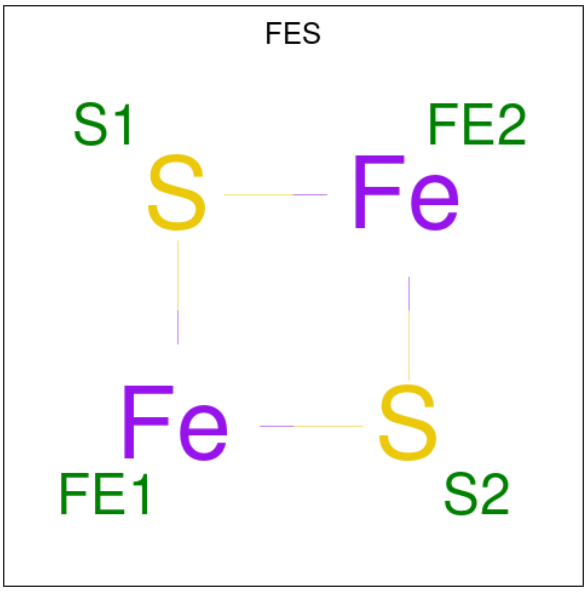
Mol	Chain	Residues	Atoms	AltConf
45	1I	1	Total Fe S 8 4 4	0
45	1I	1	Total Fe S 8 4 4	0

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



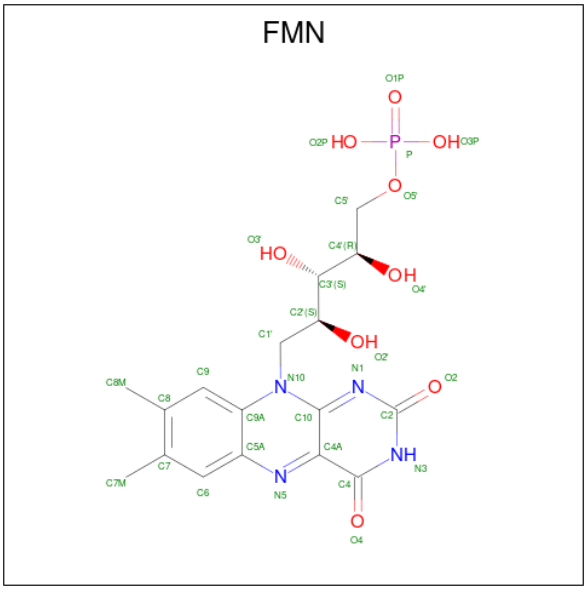
Mol	Chain	Residues	Atoms	AltConf
46	1B	1	Total C N O P 34 24 1 8 1	0
46	1Y	1	Total C N O P 35 25 1 8 1	0
46	1d	1	Total C N O P 39 29 1 8 1	0
46	1h	1	Total C N O P 34 24 1 8 1	0
46	1m	1	Total C N O P 46 36 1 8 1	0
46	1q	1	Total C N O P 48 38 1 8 1	0

- Molecule 47 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



Mol	Chain	Residues	Atoms			AltConf
47	1E	1	Total	Fe	S	0
			4	2	2	
47	1G	1	Total	Fe	S	0
			4	2	2	

- Molecule 48 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: $C_{17}H_{21}N_4O_9P$).

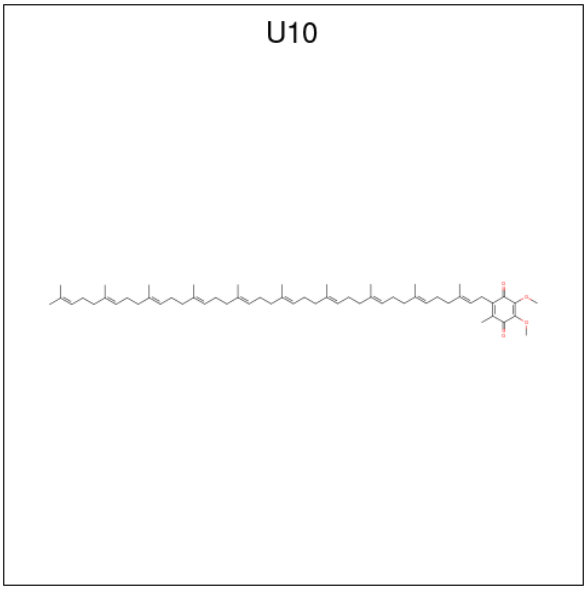


Mol	Chain	Residues	Atoms					AltConf
48	1F	1	Total	C	N	O	P	0
			31	17	4	9	1	

- Molecule 49 is POTASSIUM ION (three-letter code: K) (formula: K).

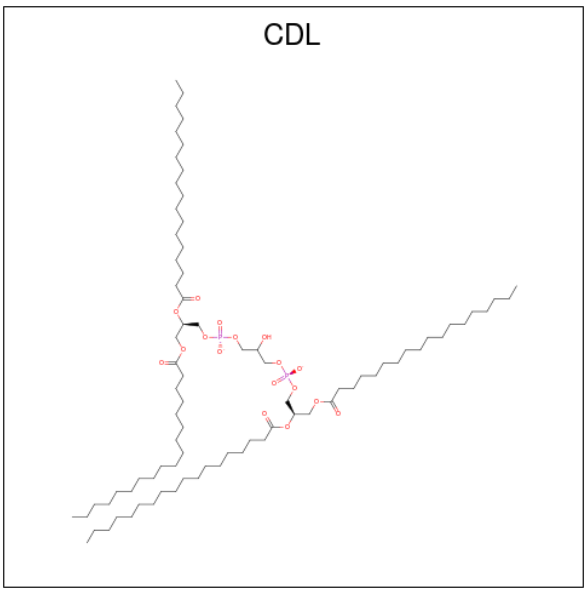
Mol	Chain	Residues	Atoms	AltConf
49	1G	1	Total K 1 1	0

- Molecule 50 is UBIQUINONE-10 (three-letter code: U10) (formula: $C_{59}H_{90}O_4$) (labeled as "Ligand of Interest" by depositor).



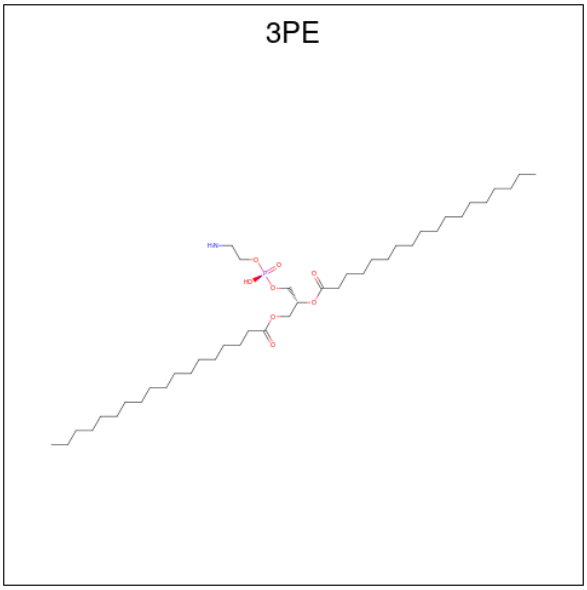
Mol	Chain	Residues	Atoms	AltConf
50	1H	1	Total C O 63 59 4	0

- Molecule 51 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



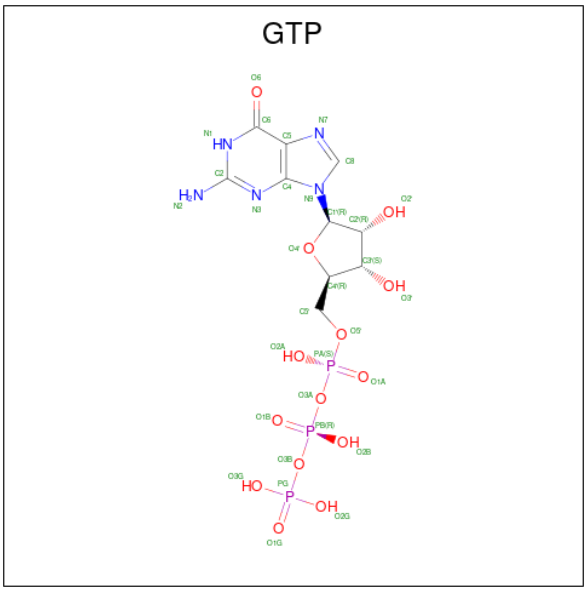
Mol	Chain	Residues	Atoms				AltConf
51	1H	1	Total	C	O	P	0
			51	32	17	2	
51	1O	1	Total	C	O	P	0
			67	48	17	2	
51	1a	1	Total	C	O	P	0
			61	42	17	2	

- Molecule 52 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (three-letter code: 3PE) (formula: $C_{41}H_{82}NO_8P$).



Mol	Chain	Residues	Atoms					AltConf
52	1N	1	Total	C	N	O	P	0
			38	28	1	8	1	
52	1Y	1	Total	C	N	O	P	0
			35	25	1	8	1	
52	1g	1	Total	C	N	O	P	0
			51	41	1	8	1	
52	1n	1	Total	C	N	O	P	0
			42	32	1	8	1	

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

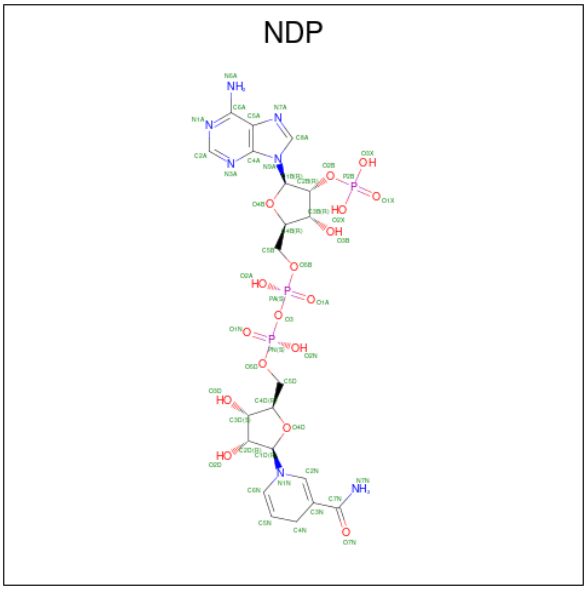


Mol	Chain	Residues	Atoms					AltConf
53	1O	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 54 is MAGNESIUM ION (three-letter code: 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 (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).

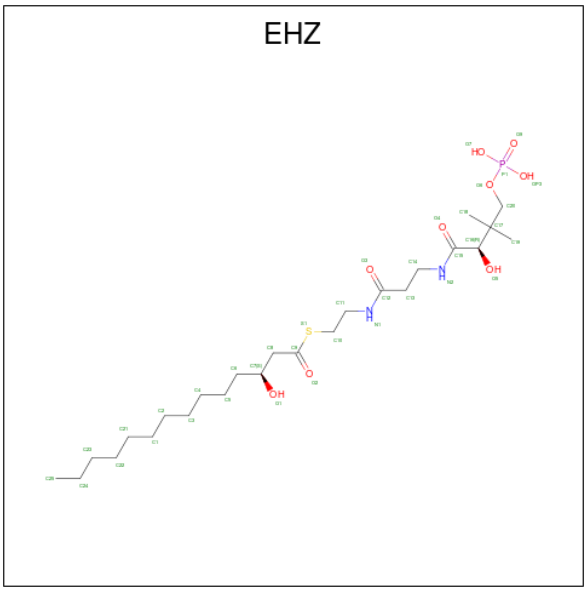


Mol	Chain	Residues	Atoms					AltConf
55	1P	1	Total	C	N	O	P	0
			48	21	7	17	3	

- Molecule 56 is ZINC ION (three-letter code: ZN) (formula: Zn).

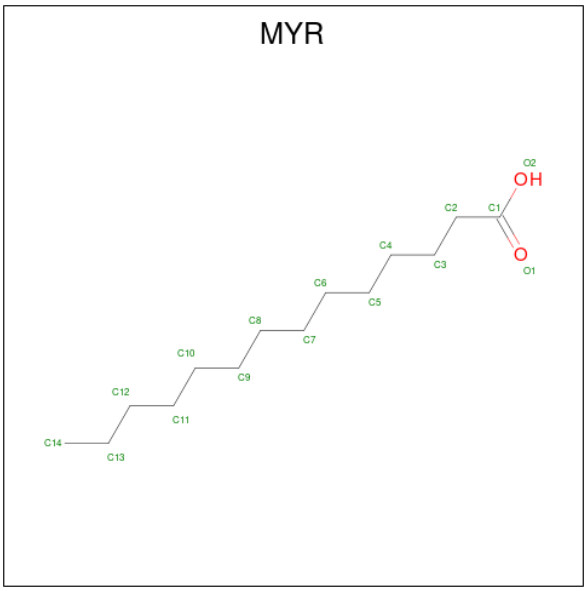
Mol	Chain	Residues	Atoms		AltConf
56	1R	1	Total	Zn	0
			1	1	

- Molecule 57 is {S}-[2-[3-[[(2 {R})-3,3-dimethyl-2-oxidanyl-4-phosphonooxy-butanoyl]amino]propanoylamino]ethyl] (3 {S})-3-oxidanyltetradecanethioate (three-letter code: EHZ) (formula: $C_{25}H_{49}N_2O_9PS$).



Mol	Chain	Residues	Atoms						AltConf
57	1W	1	Total	C	N	O	P	S	0
			37	25	2	8	1	1	
57	1n	1	Total	C	N	O	P	S	0
			37	25	2	8	1	1	

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



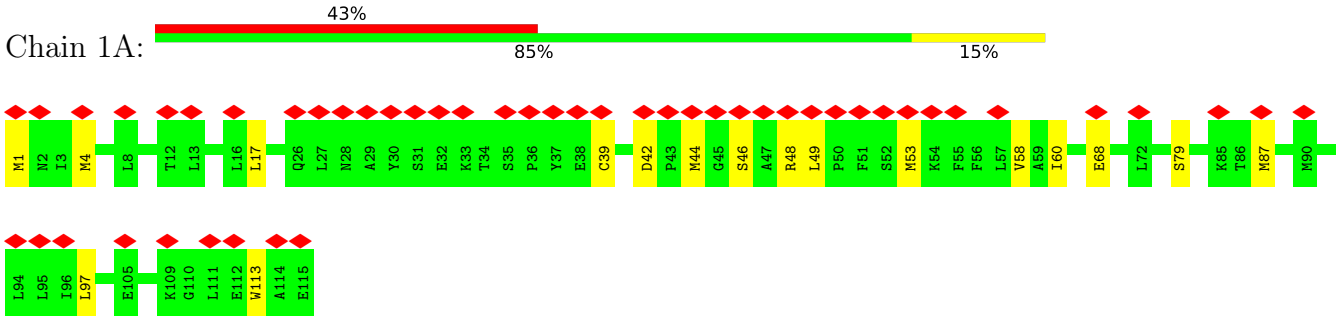
Mol	Chain	Residues	Atoms			AltConf
58	1l	1	Total	C	O	0
			15	14	1	

3 Residue-property plots (i)

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

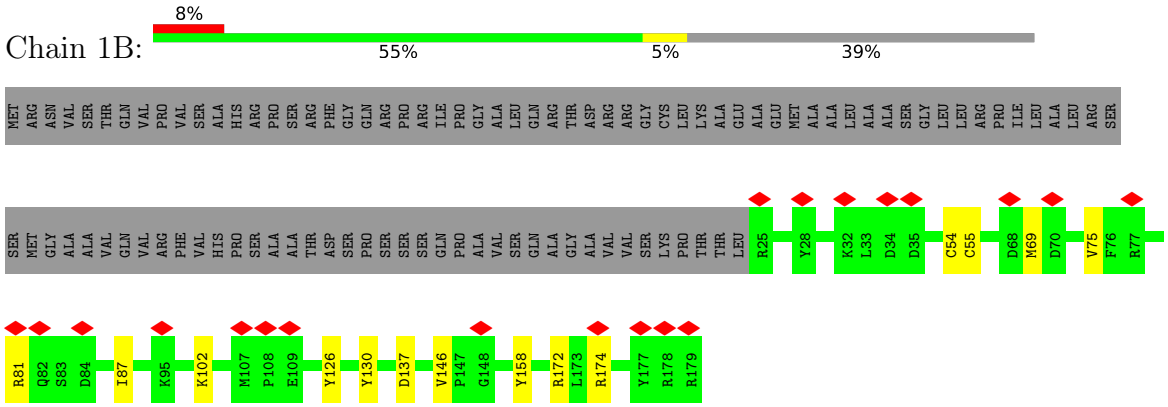
• Molecule 1: NADH-ubiquinone oxidoreductase chain 3

Chain 1A:



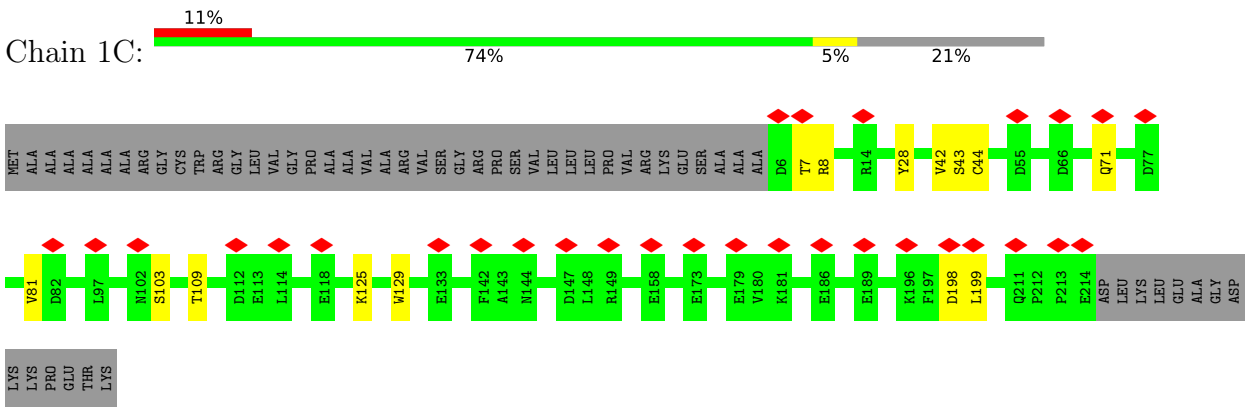
• Molecule 2: NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial

Chain 1B:



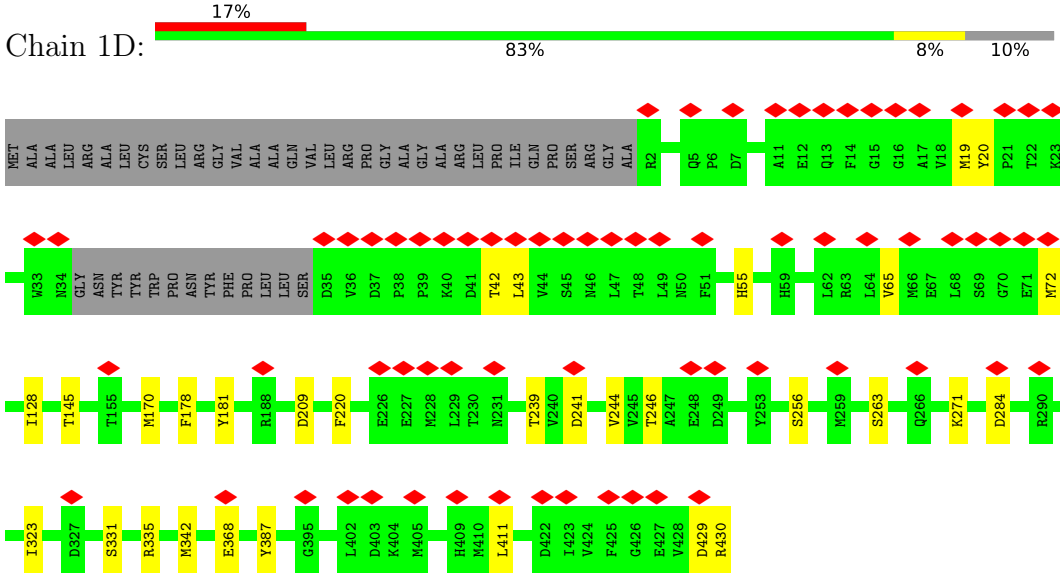
• Molecule 3: NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial

Chain 1C:



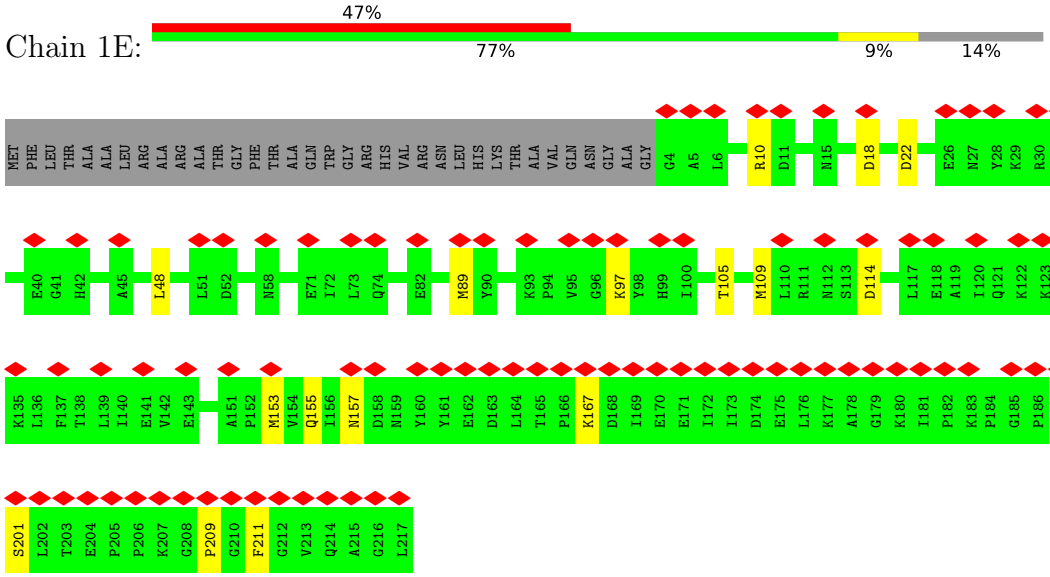
• Molecule 4: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial

Chain 1D:



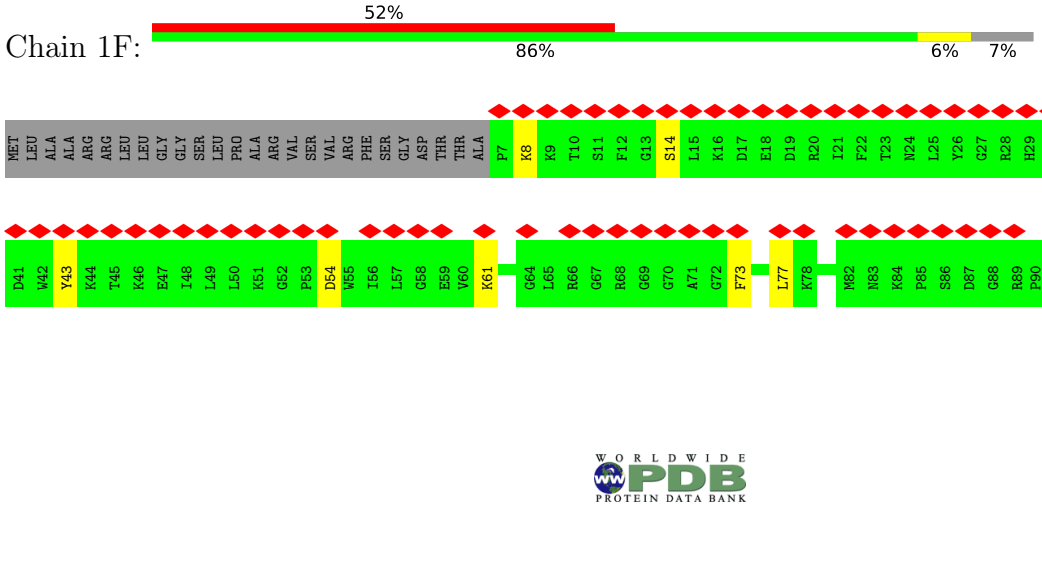
• Molecule 5: NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial

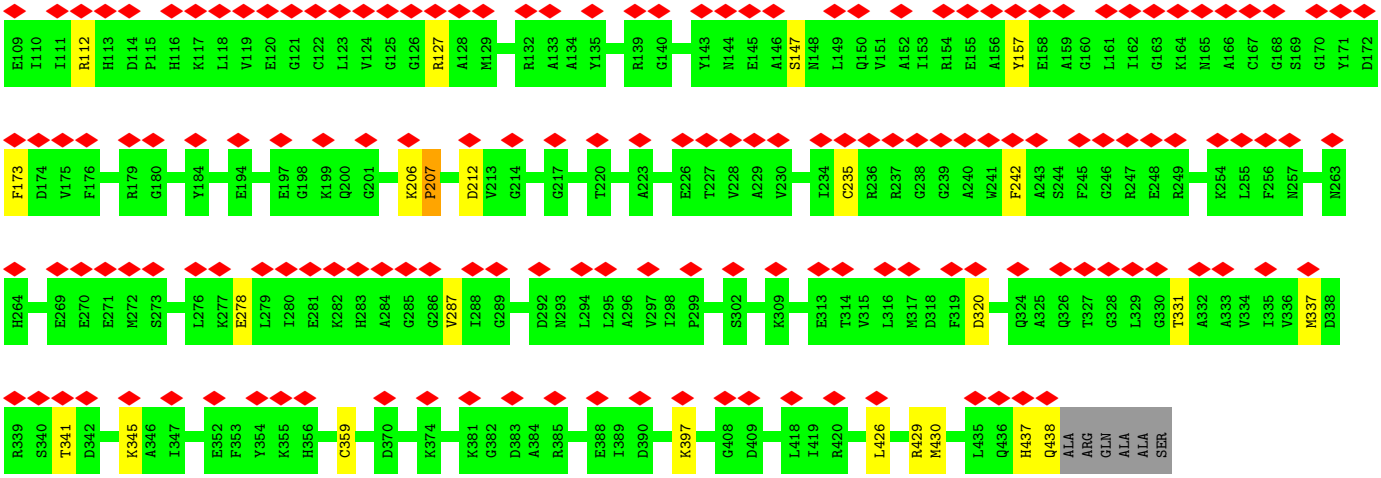
Chain 1E:



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

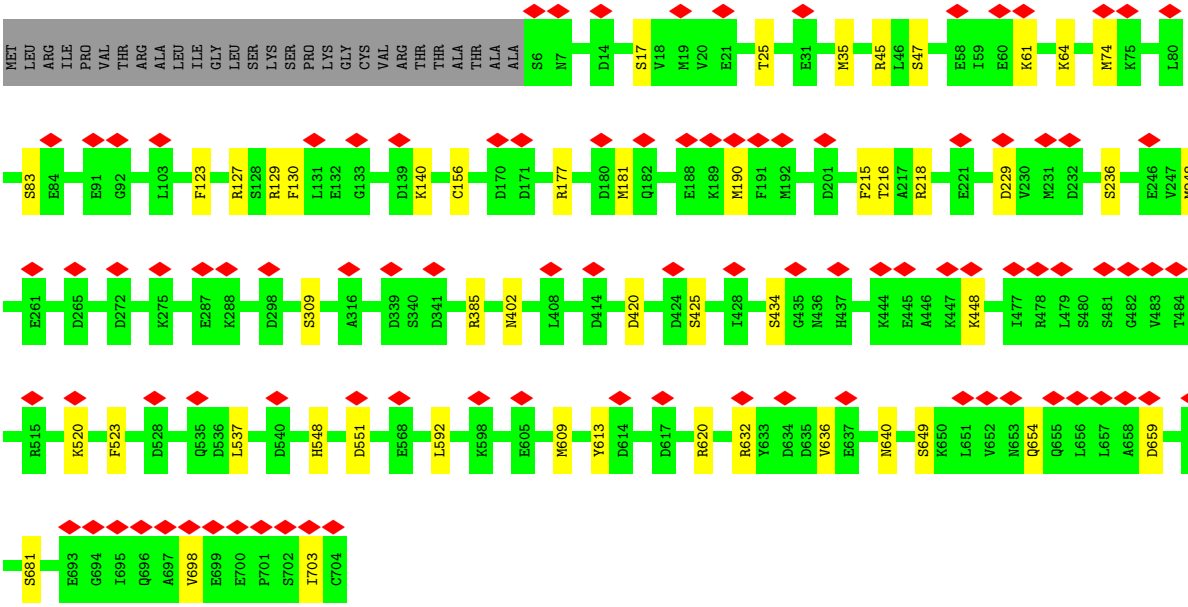
Chain 1F:





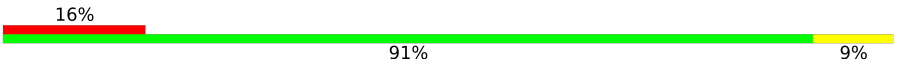
• Molecule 7: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial

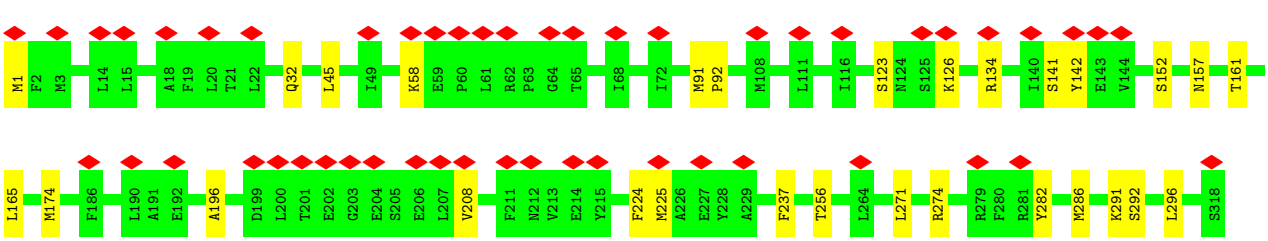
Chain 1G:



• Molecule 8: NADH-ubiquinone oxidoreductase chain 1

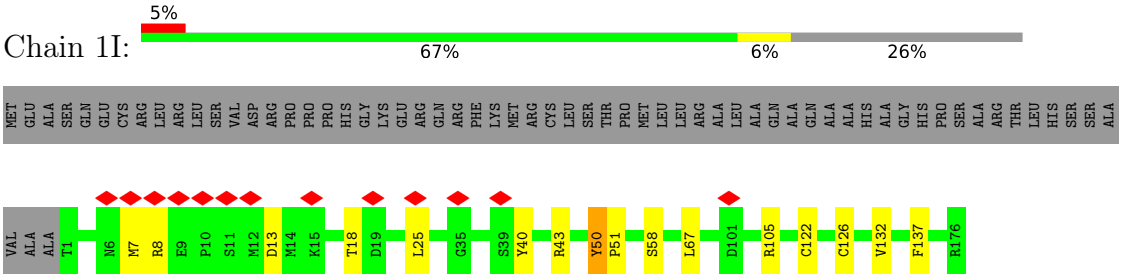
Chain 1H:





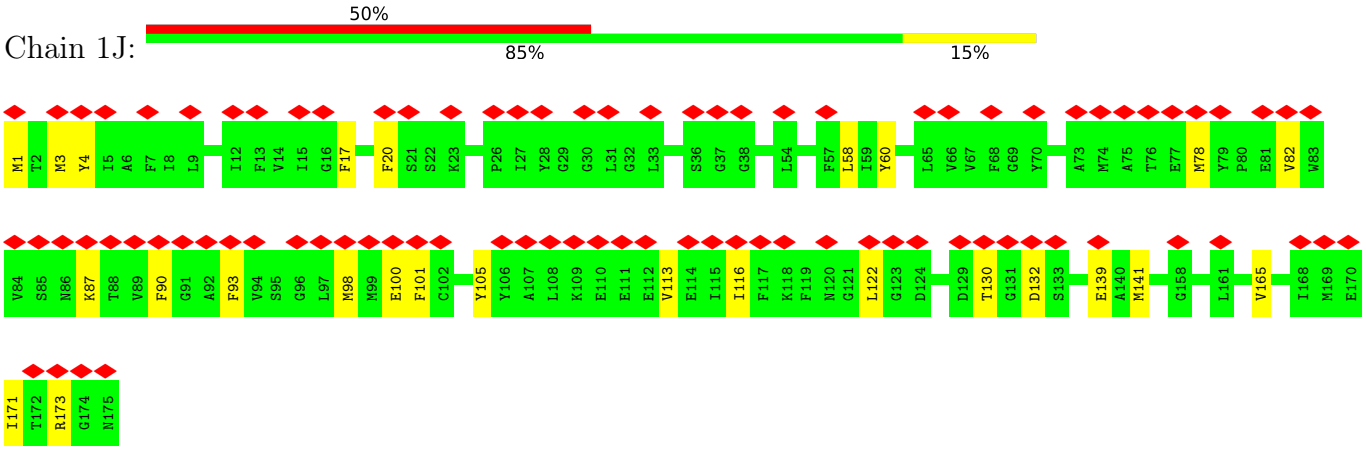
• Molecule 9: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial

Chain 1I:



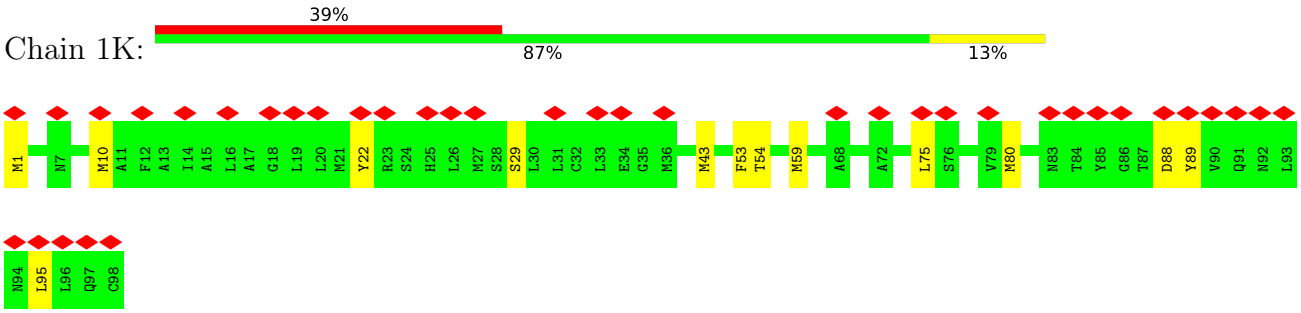
• Molecule 10: NADH-ubiquinone oxidoreductase chain 6

Chain 1J:



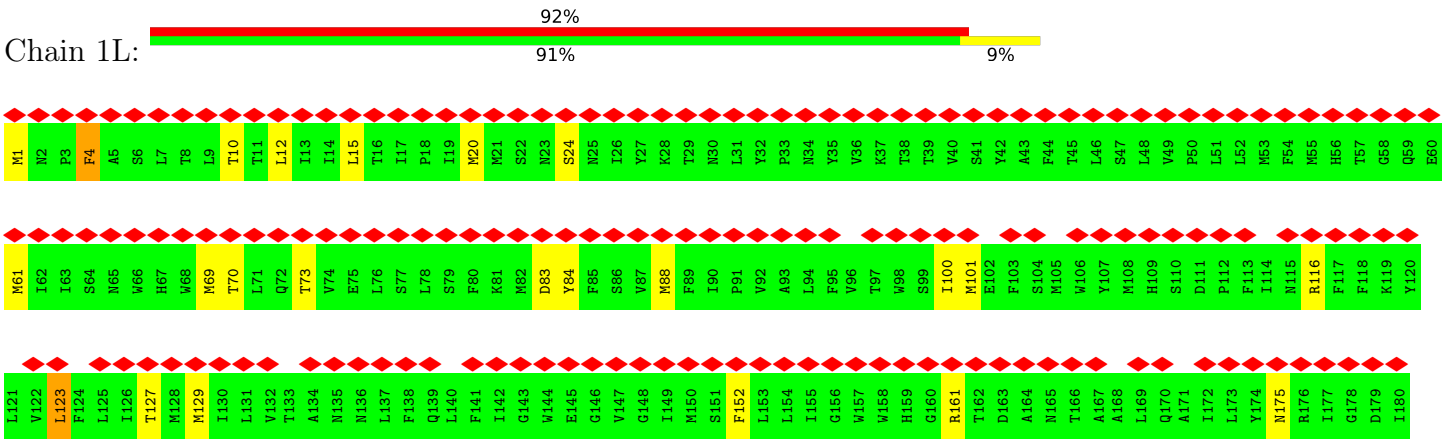
• Molecule 11: NADH-ubiquinone oxidoreductase chain 4L

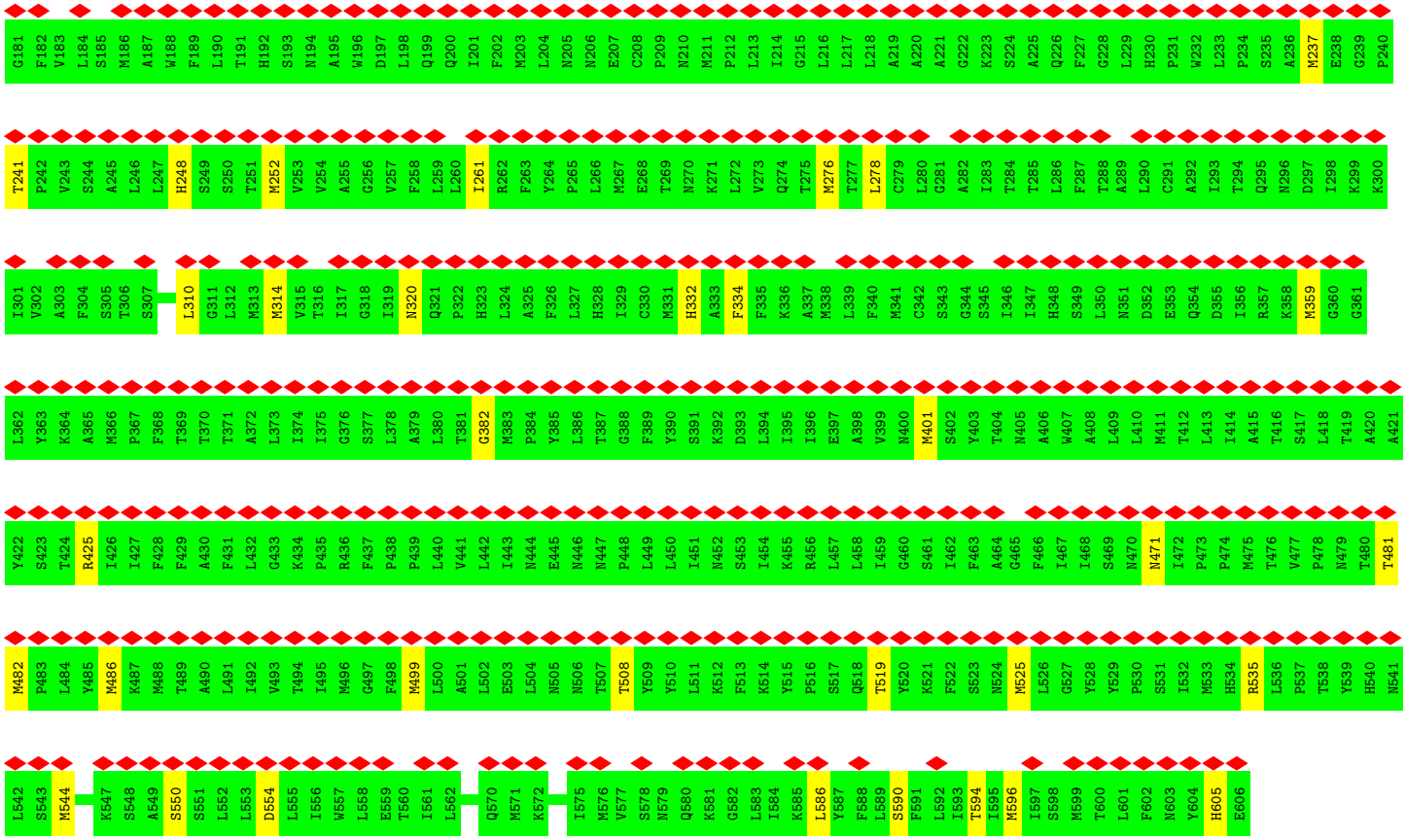
Chain 1K:



• Molecule 12: NADH-ubiquinone oxidoreductase chain 5

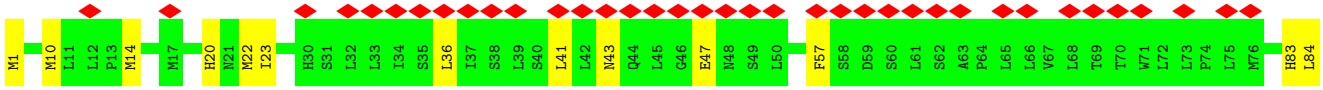
Chain 1L:

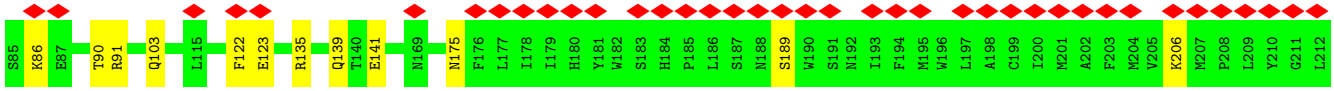


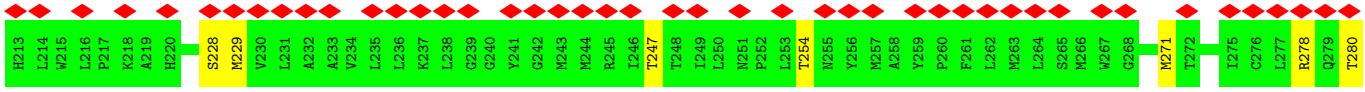


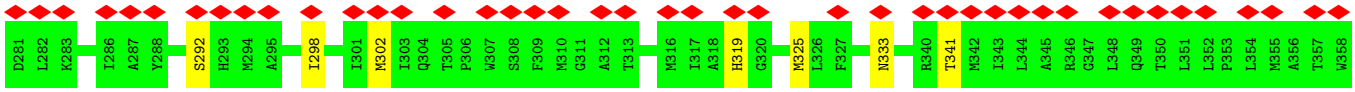
• Molecule 13: NADH-ubiquinone oxidoreductase chain 4

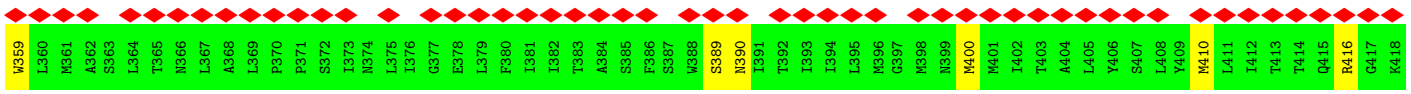
Chain 1M:

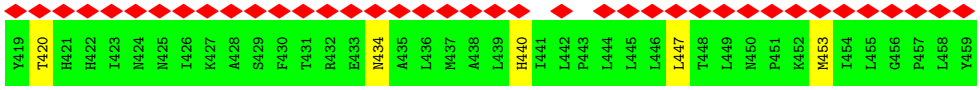






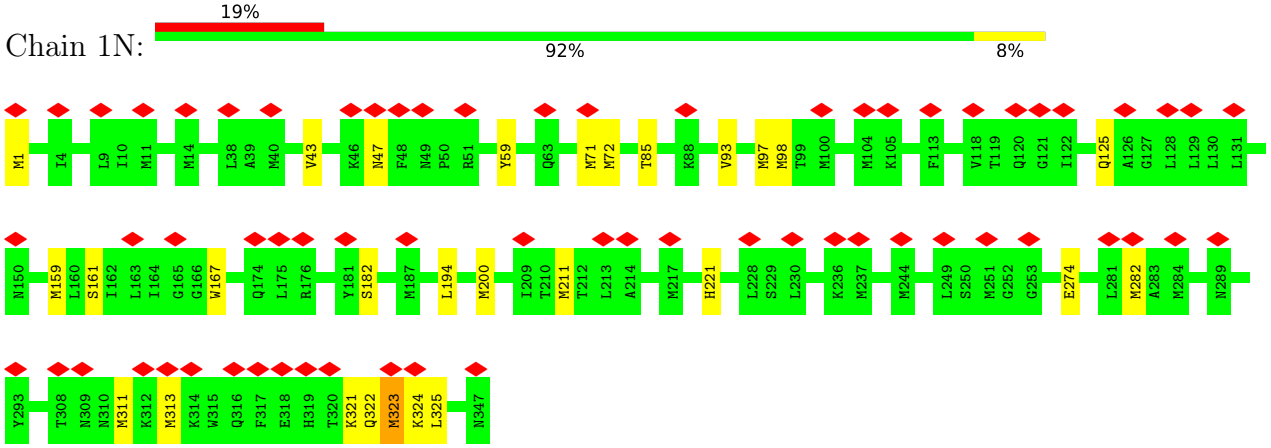






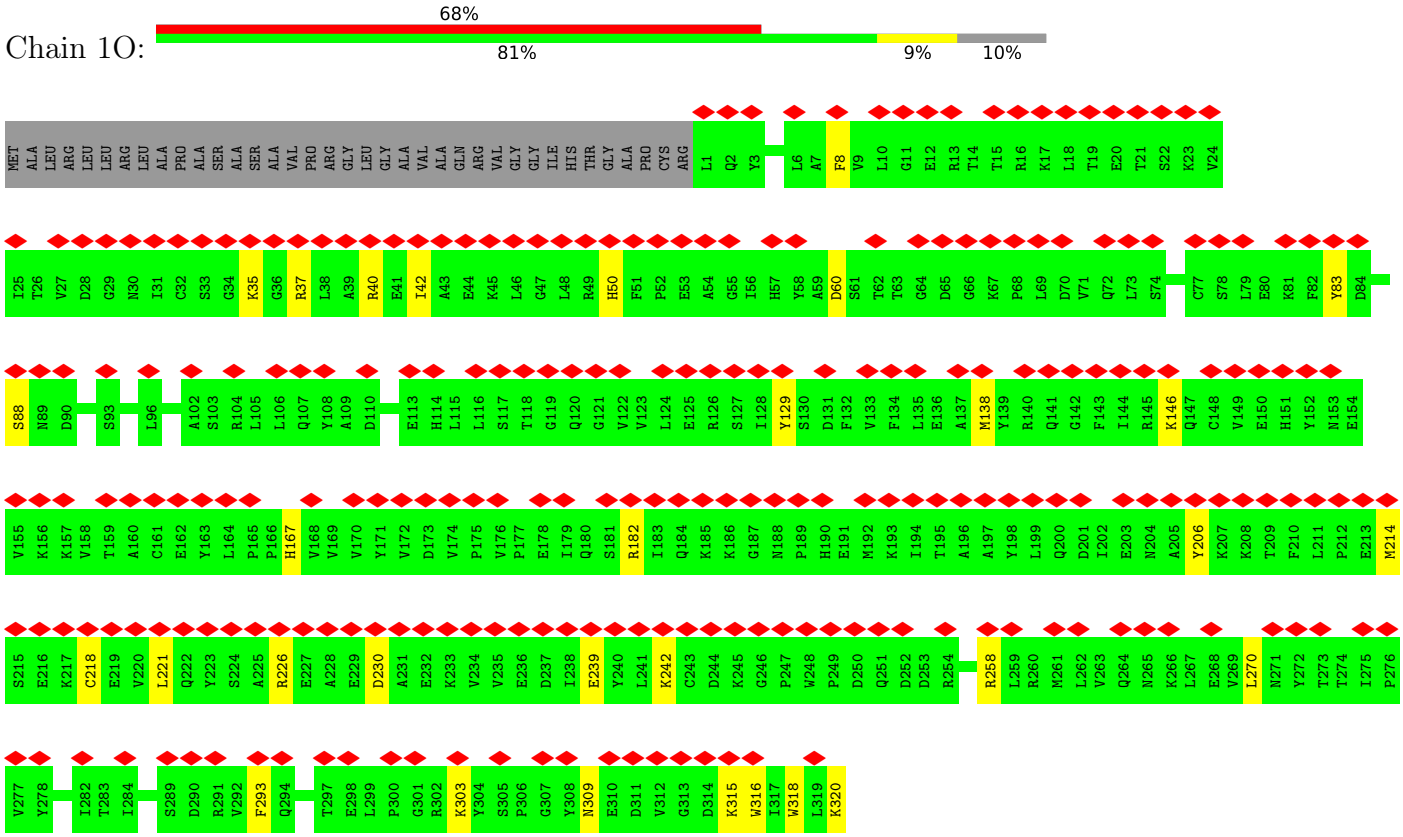
• Molecule 14: NADH-ubiquinone oxidoreductase chain 2

Chain 1N:



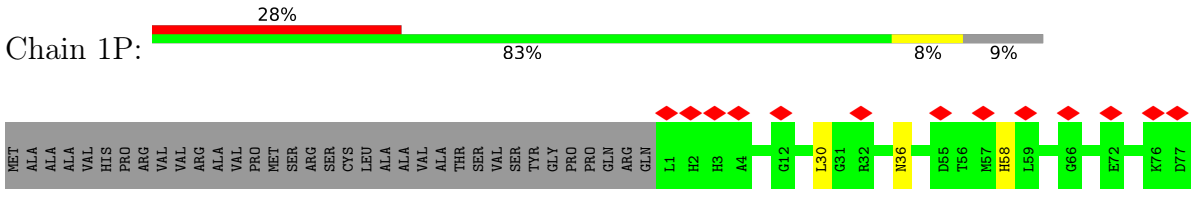
• Molecule 15: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial

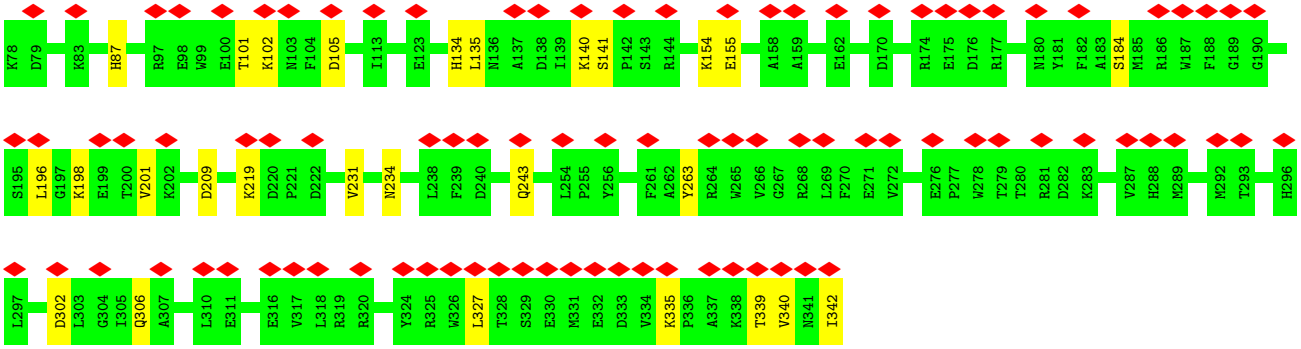
Chain 1O:



• Molecule 16: NADH:ubiquinone oxidoreductase subunit A9

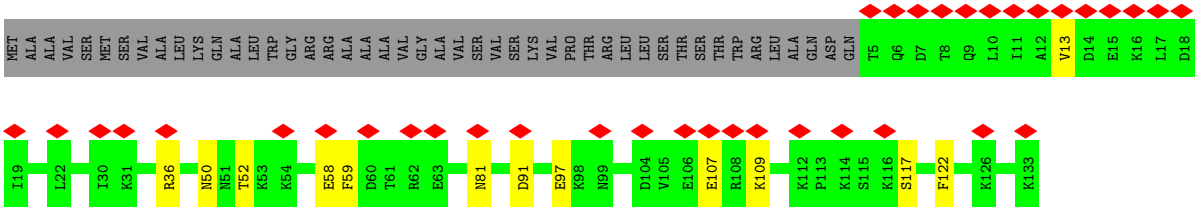
Chain 1P:





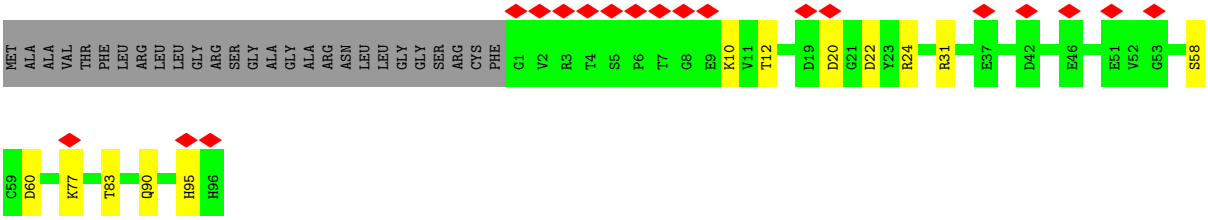
• Molecule 17: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial

Chain 1Q:



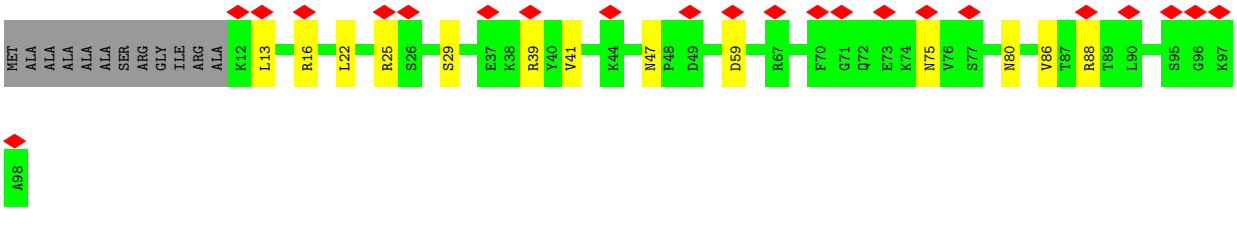
• Molecule 18: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial

Chain 1R:



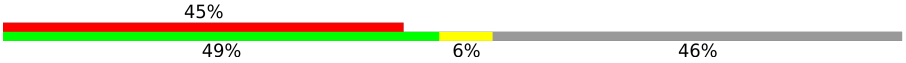
• Molecule 19: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2

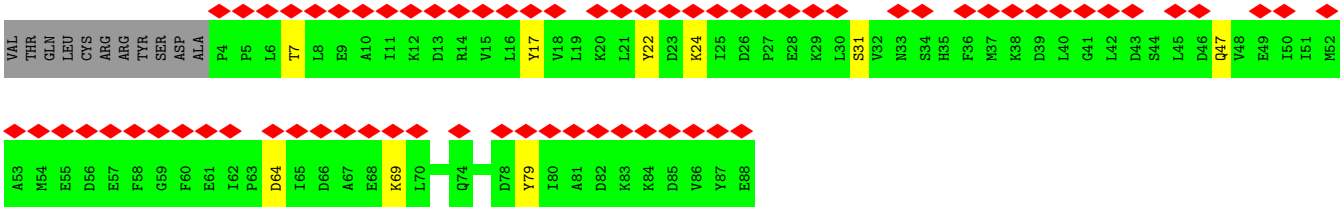
Chain 1S:



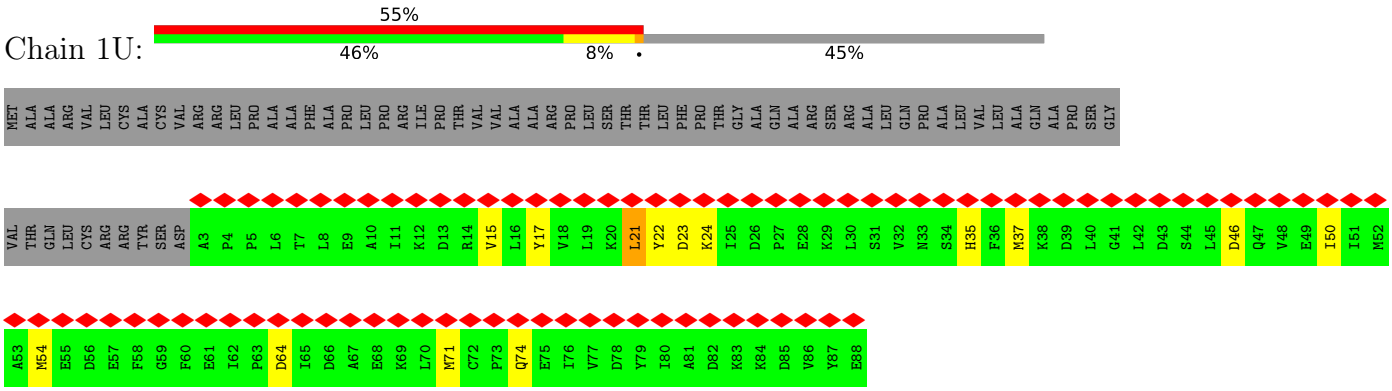
• Molecule 20: NADH:ubiquinone oxidoreductase subunit AB1

Chain 1T:

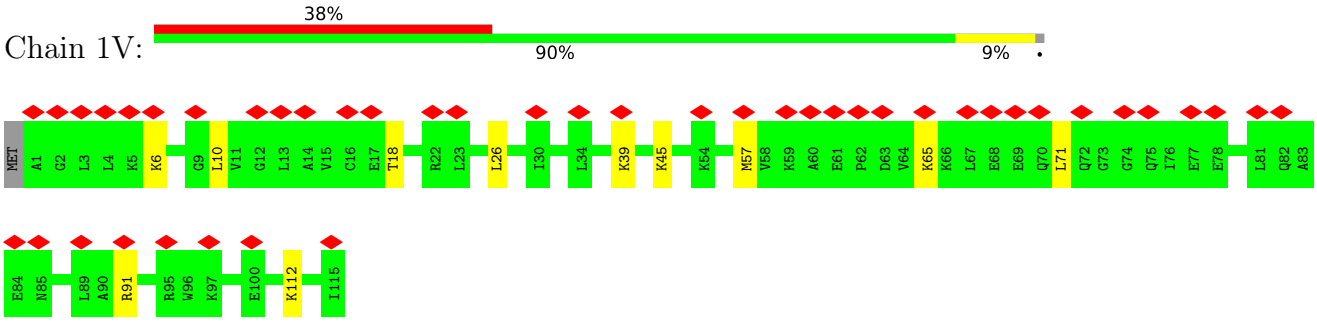




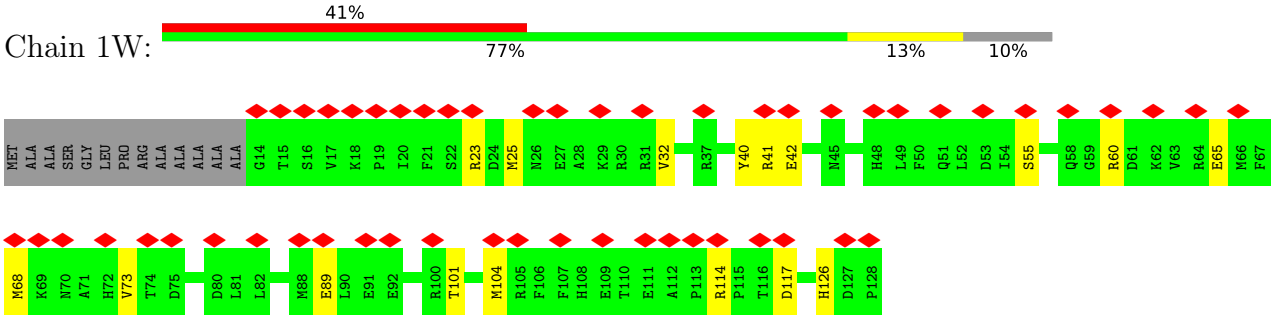
• Molecule 20: NADH:ubiquinone oxidoreductase subunit AB1



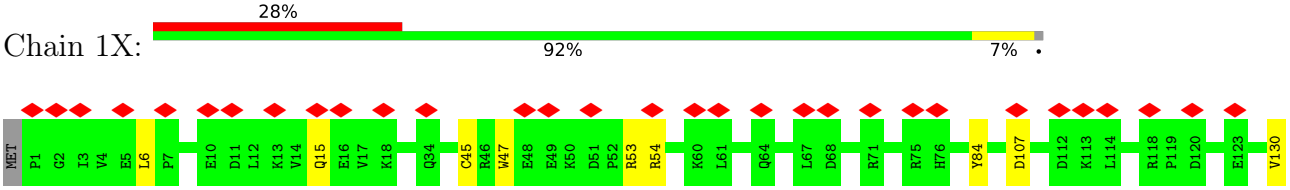
• Molecule 21: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 isoform X1



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

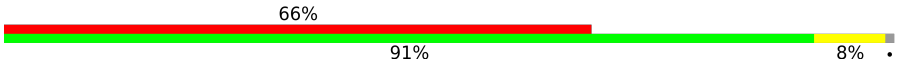


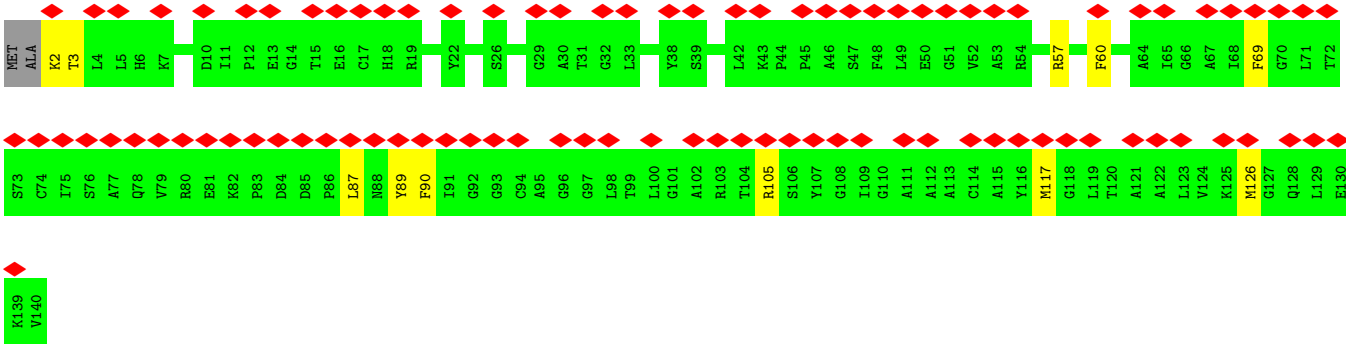
• Molecule 23: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8



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

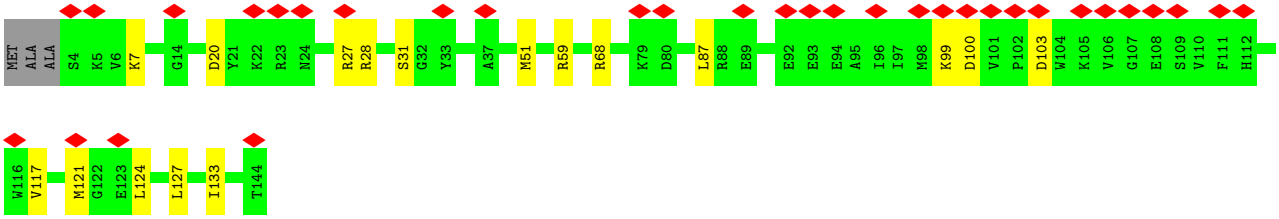
Chain 1Y:





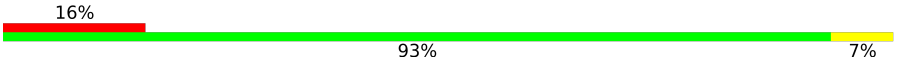
• Molecule 25: NADH:ubiquinone oxidoreductase subunit A13

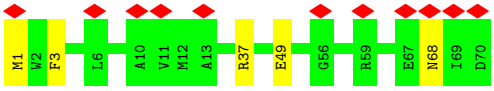
Chain 1Z:



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

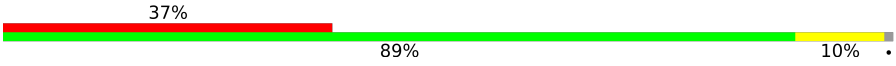
Chain 1a:

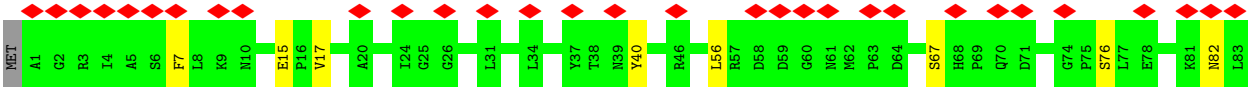




• Molecule 27: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3

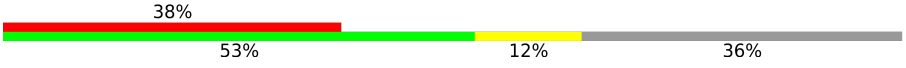
Chain 1b:



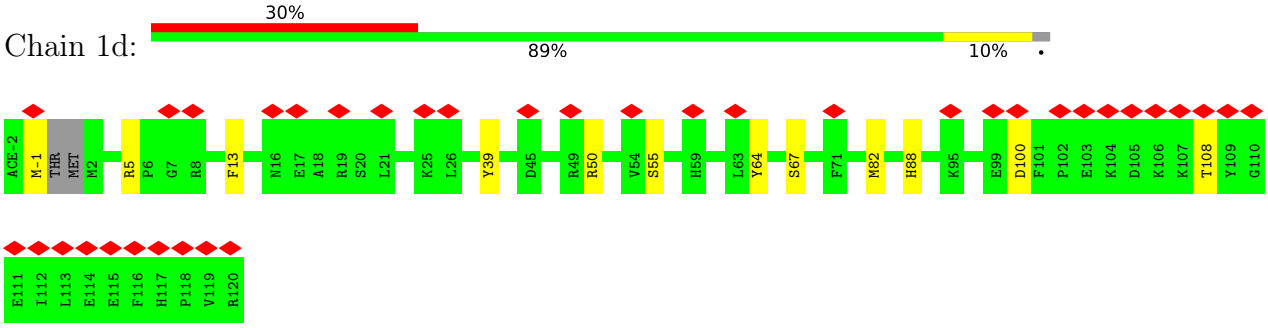


• Molecule 28: NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial

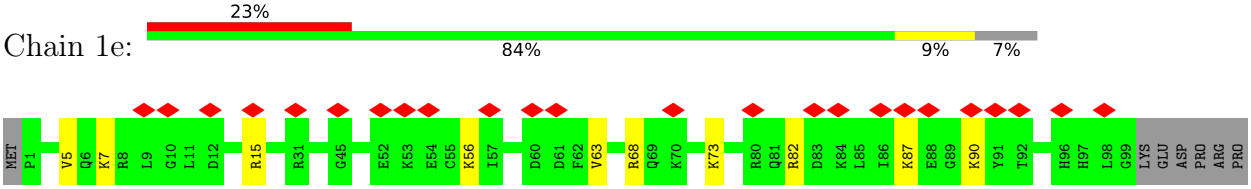
Chain 1c:



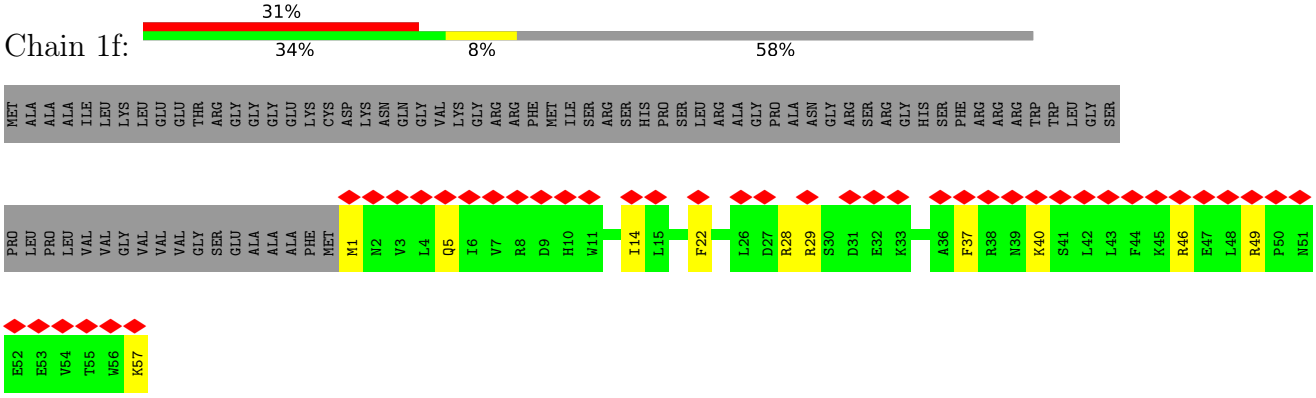
• Molecule 29: NADH dehydrogenase [ubiquinone] 1 subunit C2



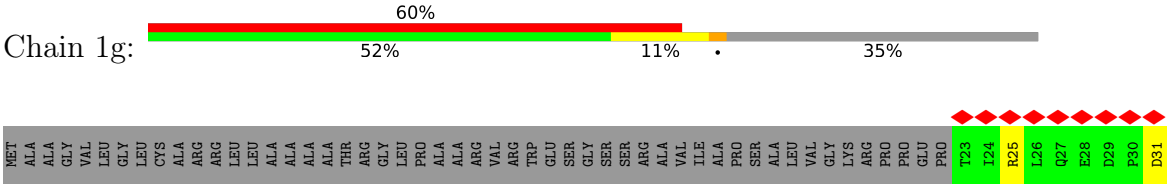
• Molecule 30: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5

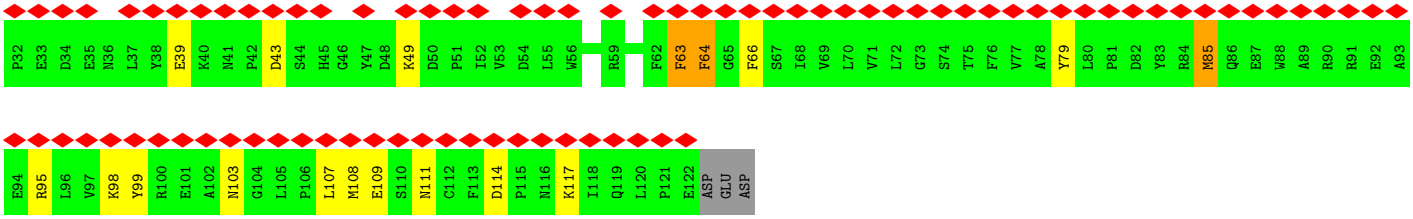


• Molecule 31: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1 [Sus scrofa]



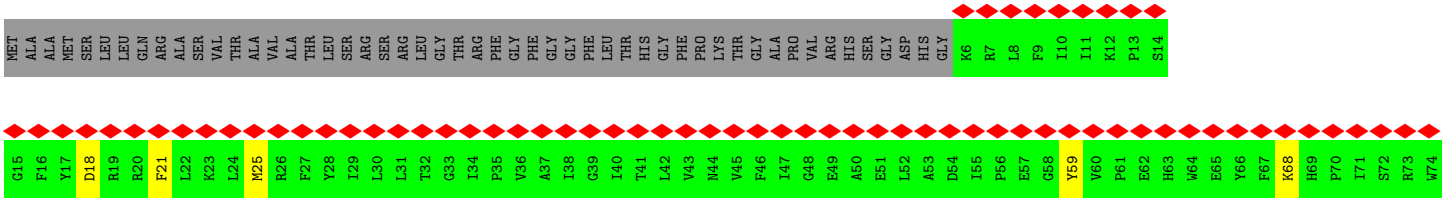
• Molecule 32: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial





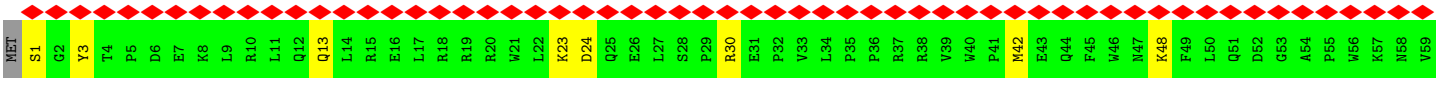
• Molecule 33: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial

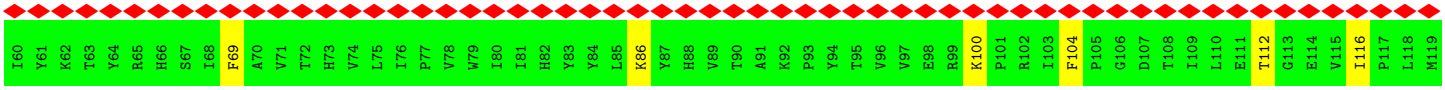
Chain 1h:

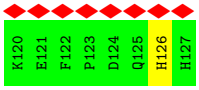


• Molecule 34: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6

Chain 1i:

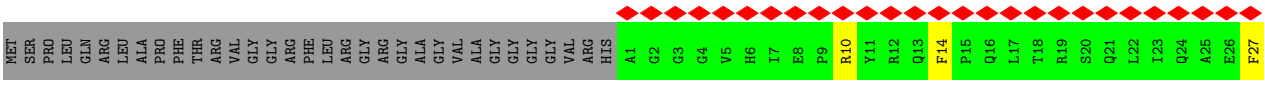


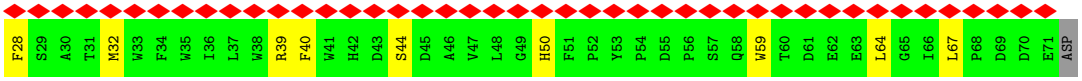




• Molecule 35: NADH:ubiquinone oxidoreductase subunit B2

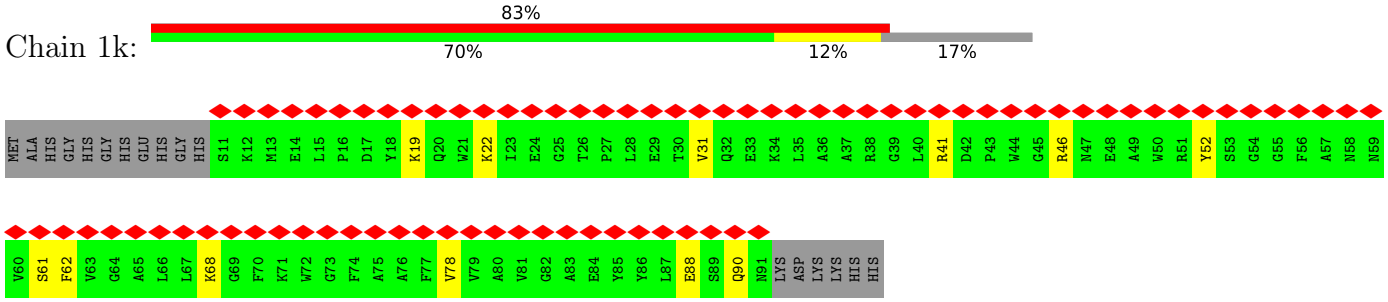
Chain 1j:





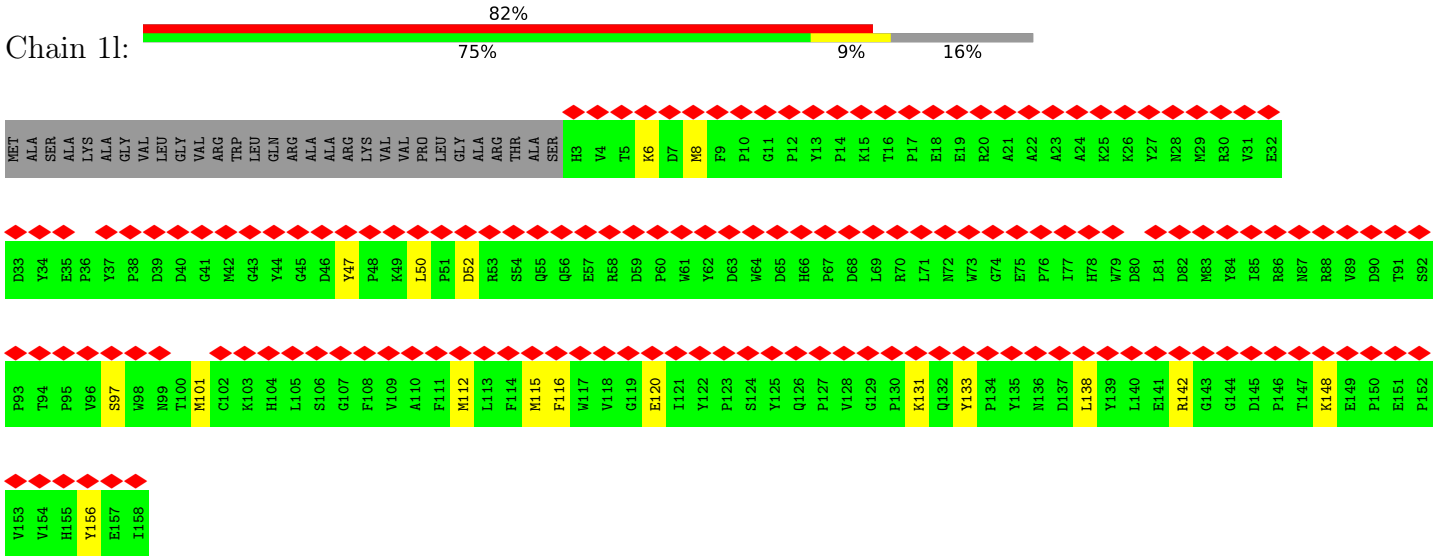
• Molecule 36: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3

Chain 1k:



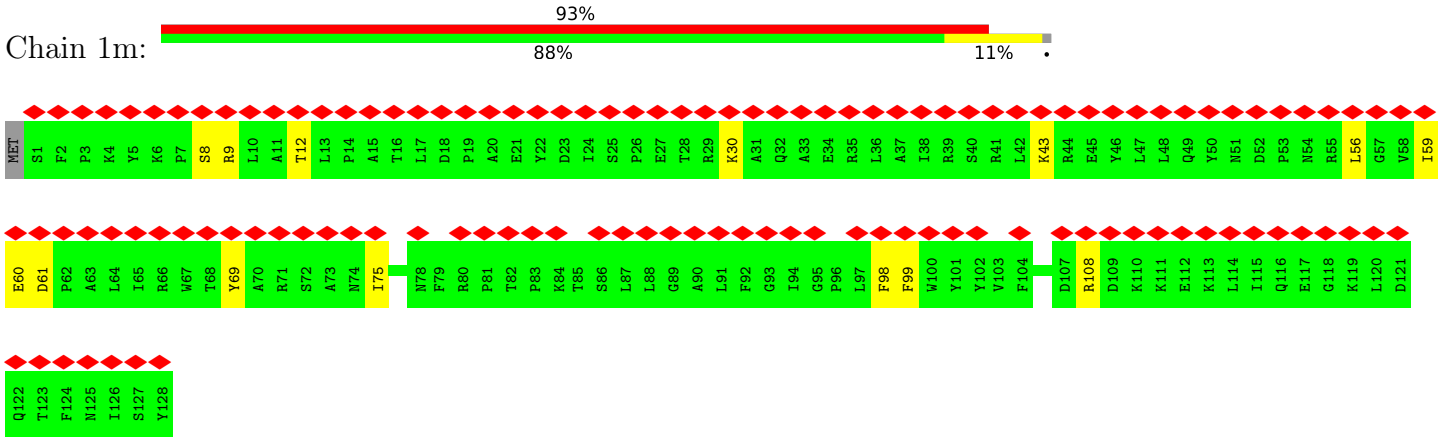
• Molecule 37: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial

Chain 1l:



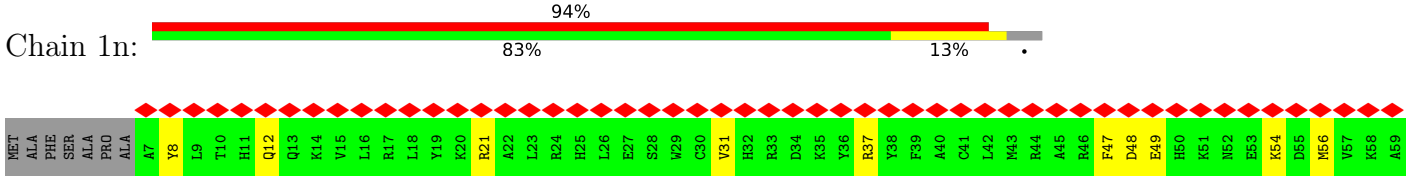
• Molecule 38: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4

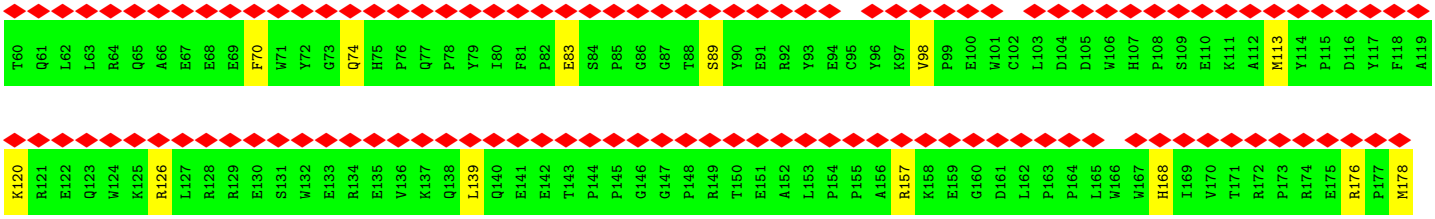
Chain 1m:



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

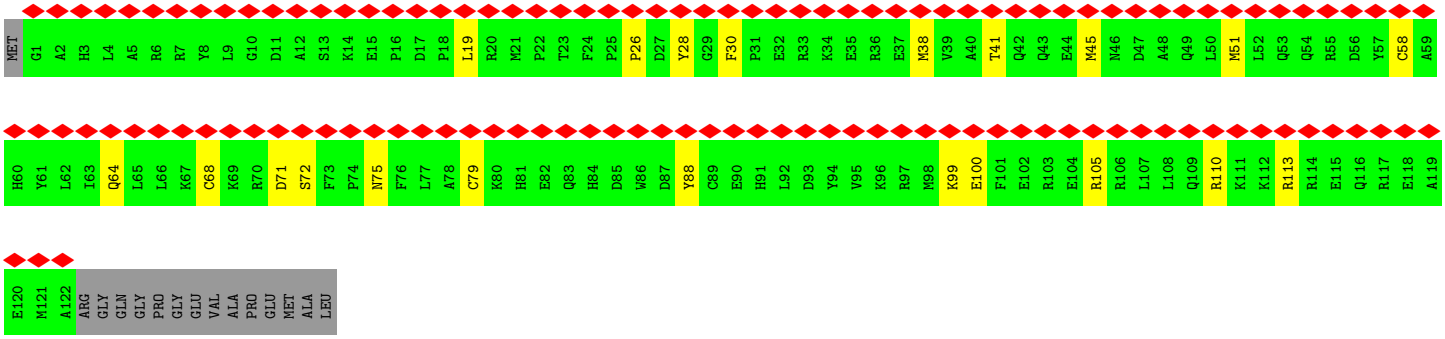
Chain 1n:





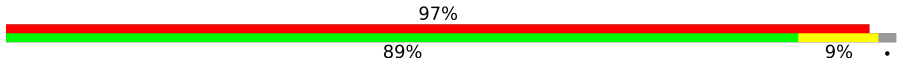
• Molecule 40: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7

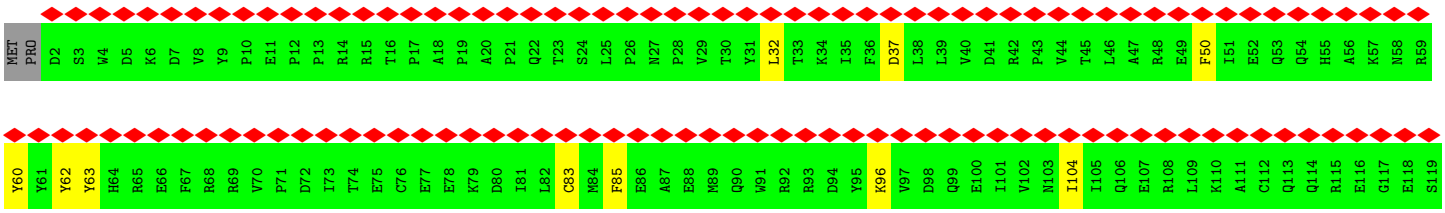
Chain 1o:



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

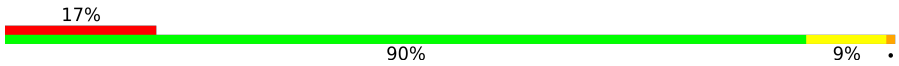
Chain 1p:

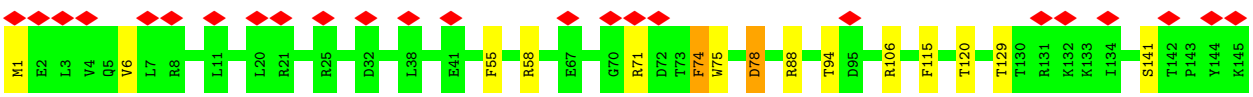




• Molecule 42: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12

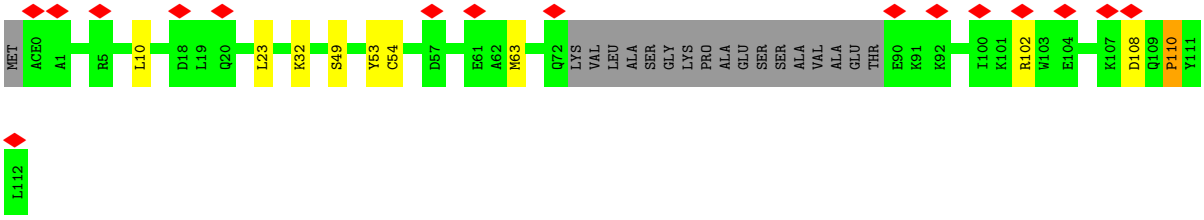
Chain 1q:





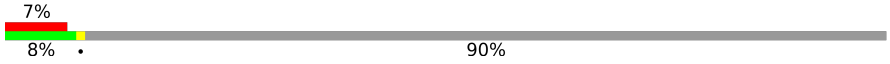
• Molecule 43: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7

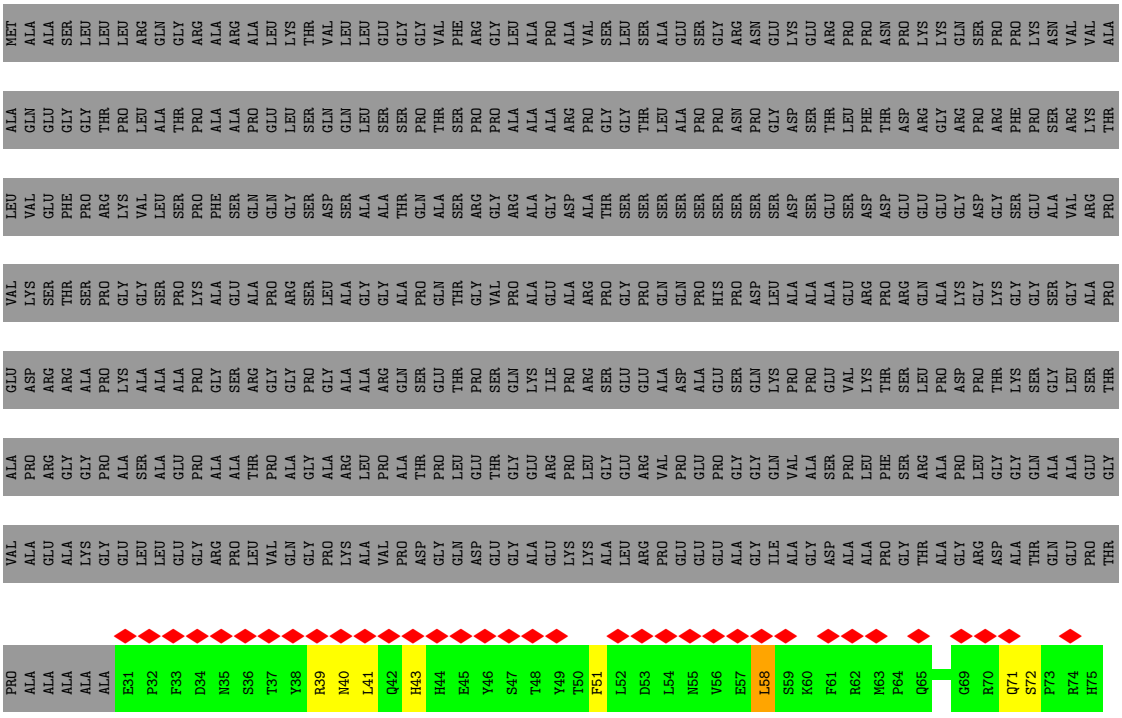
Chain 1r:



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

Chain 1s:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45000	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 ($e^-/Å^2$)	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	0.924	Depositor
Minimum map value	-0.272	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	444.8, 444.8, 444.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MYR, U10, MG, FES, 3PE, FMN, NDP, SF4, ACE, FME, SAC, GTP, K, PC1, CDL, ZN, EHZ

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	0.29	0/930	0.62	0/1271
2	1B	0.32	0/1273	0.62	0/1722
3	1C	0.29	0/1791	0.54	0/2439
4	1D	0.29	0/3545	0.53	0/4806
5	1E	0.28	0/1698	0.55	0/2311
6	1F	0.27	0/3401	0.53	0/4595
7	1G	0.27	0/5451	0.54	0/7387
8	1H	0.28	0/2566	0.54	0/3509
9	1I	0.30	0/1443	0.52	0/1952
10	1J	0.30	0/1364	0.59	0/1850
11	1K	0.28	0/751	0.68	0/1018
12	1L	0.26	0/4939	0.59	5/6718 (0.1%)
13	1M	0.26	0/3713	0.62	1/5063 (0.0%)
14	1N	0.30	0/2765	0.62	3/3758 (0.1%)
15	1O	0.29	0/2650	0.57	0/3588
16	1P	0.27	0/2828	0.52	0/3834
17	1Q	0.29	0/1070	0.56	1/1446 (0.1%)
18	1R	0.28	0/755	0.60	0/1018
19	1S	0.27	0/711	0.61	0/956
20	1T	0.30	0/701	0.72	0/946
20	1U	0.31	0/706	0.71	1/954 (0.1%)
21	1V	0.28	0/946	0.54	0/1281
22	1W	0.30	0/995	0.65	0/1340
23	1X	0.26	0/1436	0.50	0/1938
24	1Y	0.27	0/1037	0.60	0/1404
25	1Z	0.28	0/1199	0.59	0/1617
26	1a	0.26	0/577	0.49	0/777
27	1b	0.26	0/664	0.56	0/912
28	1c	0.28	0/430	0.67	0/581
29	1d	0.29	0/1024	0.55	0/1383
30	1e	0.28	0/836	0.57	0/1118
31	1f	0.29	0/499	0.70	0/673

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	1g	0.34	0/858	0.71	1/1165 (0.1%)
33	1h	0.26	0/1184	0.56	0/1603
34	1i	0.29	0/1131	0.67	0/1541
35	1j	0.27	0/627	0.63	0/858
36	1k	0.26	0/668	0.54	0/903
37	1l	0.27	0/1365	0.58	1/1867 (0.1%)
38	1m	0.28	0/1092	0.55	0/1481
39	1n	0.28	0/1549	0.62	0/2098
40	1o	0.33	1/1069 (0.1%)	0.73	3/1430 (0.2%)
41	1p	0.27	0/1481	0.55	1/1997 (0.1%)
42	1q	0.29	0/1253	0.59	1/1704 (0.1%)
43	1r	0.31	0/782	0.70	1/1057 (0.1%)
44	1s	0.28	0/394	0.69	1/533 (0.2%)
All	All	0.28	1/68147 (0.0%)	0.58	20/92402 (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	2
8	1H	0	1
9	1I	0	1
14	1N	0	1
42	1q	0	1
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	1o	26	PRO	CG-CD	-6.41	1.29	1.50

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
40	1o	26	PRO	N-CD-CG	-10.96	86.76	103.20
13	1M	84	LEU	CA-CB-CG	8.82	135.59	115.30
20	1U	21	LEU	CA-CB-CG	8.31	134.42	115.30
43	1r	110	PRO	CA-N-CD	-7.87	100.48	111.50
32	1g	85	MET	CB-CG-SD	7.38	134.54	112.40

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	1F	206	LYS	Peptide
6	1F	207	PRO	Peptide
8	1H	141	SER	Peptide
9	1I	50	TYR	Peptide
14	1N	322	GLN	Peptide

5.2 Too-close contacts (i)

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

5.3 Torsion angles (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	113/115 (98%)	102 (90%)	10 (9%)	1 (1%)	17	56
2	1B	153/255 (60%)	138 (90%)	14 (9%)	1 (1%)	22	61
3	1C	207/264 (78%)	196 (95%)	11 (5%)	0	100	100
4	1D	427/476 (90%)	407 (95%)	20 (5%)	0	100	100
5	1E	212/249 (85%)	192 (91%)	19 (9%)	1 (0%)	29	68
6	1F	430/464 (93%)	401 (93%)	28 (6%)	1 (0%)	47	81
7	1G	697/727 (96%)	633 (91%)	62 (9%)	2 (0%)	41	75
8	1H	316/318 (99%)	299 (95%)	14 (4%)	3 (1%)	17	56
9	1I	174/239 (73%)	160 (92%)	12 (7%)	2 (1%)	14	52
10	1J	173/175 (99%)	161 (93%)	9 (5%)	3 (2%)	9	42
11	1K	96/98 (98%)	88 (92%)	8 (8%)	0	100	100
12	1L	604/606 (100%)	541 (90%)	62 (10%)	1 (0%)	47	81
13	1M	457/459 (100%)	431 (94%)	25 (6%)	1 (0%)	47	81

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
14	1N	345/347 (99%)	320 (93%)	23 (7%)	2 (1%)	25 64
15	1O	318/357 (89%)	287 (90%)	31 (10%)	0	100 100
16	1P	340/377 (90%)	316 (93%)	24 (7%)	0	100 100
17	1Q	127/175 (73%)	119 (94%)	8 (6%)	0	100 100
18	1R	94/123 (76%)	81 (86%)	13 (14%)	0	100 100
19	1S	85/99 (86%)	68 (80%)	17 (20%)	0	100 100
20	1T	83/156 (53%)	77 (93%)	6 (7%)	0	100 100
20	1U	84/156 (54%)	77 (92%)	7 (8%)	0	100 100
21	1V	113/116 (97%)	104 (92%)	8 (7%)	1 (1%)	17 56
22	1W	113/128 (88%)	107 (95%)	6 (5%)	0	100 100
23	1X	169/172 (98%)	162 (96%)	7 (4%)	0	100 100
24	1Y	137/141 (97%)	132 (96%)	5 (4%)	0	100 100
25	1Z	139/144 (96%)	130 (94%)	9 (6%)	0	100 100
26	1a	68/70 (97%)	65 (96%)	3 (4%)	0	100 100
27	1b	81/84 (96%)	74 (91%)	7 (9%)	0	100 100
28	1c	47/76 (62%)	44 (94%)	3 (6%)	0	100 100
29	1d	117/123 (95%)	112 (96%)	5 (4%)	0	100 100
30	1e	97/106 (92%)	87 (90%)	10 (10%)	0	100 100
31	1f	55/135 (41%)	50 (91%)	5 (9%)	0	100 100
32	1g	98/154 (64%)	84 (86%)	12 (12%)	2 (2%)	7 39
33	1h	136/189 (72%)	129 (95%)	7 (5%)	0	100 100
34	1i	124/128 (97%)	116 (94%)	8 (6%)	0	100 100
35	1j	69/105 (66%)	58 (84%)	11 (16%)	0	100 100
36	1k	79/98 (81%)	71 (90%)	8 (10%)	0	100 100
37	1l	154/186 (83%)	130 (84%)	24 (16%)	0	100 100
38	1m	126/129 (98%)	122 (97%)	4 (3%)	0	100 100
39	1n	170/179 (95%)	157 (92%)	12 (7%)	1 (1%)	25 64
40	1o	120/137 (88%)	114 (95%)	6 (5%)	0	100 100
41	1p	171/176 (97%)	166 (97%)	5 (3%)	0	100 100
42	1q	143/145 (99%)	136 (95%)	6 (4%)	1 (1%)	22 61
43	1r	90/114 (79%)	85 (94%)	4 (4%)	1 (1%)	14 52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
44	1s	43/471 (9%)	41 (95%)	2 (5%)	0	100 100
All	All	8194/9741 (84%)	7570 (92%)	600 (7%)	24 (0%)	44 75

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1A	46	SER
8	1H	92	PRO
8	1H	196	ALA
10	1J	113	VAL
10	1J	122	LEU

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	1A	99/99 (100%)	84 (85%)	15 (15%)	3 17
2	1B	131/209 (63%)	118 (90%)	13 (10%)	8 33
3	1C	190/227 (84%)	176 (93%)	14 (7%)	13 44
4	1D	371/405 (92%)	335 (90%)	36 (10%)	8 33
5	1E	183/207 (88%)	161 (88%)	22 (12%)	5 24
6	1F	346/368 (94%)	317 (92%)	29 (8%)	11 40
7	1G	588/610 (96%)	538 (92%)	50 (8%)	10 39
8	1H	274/274 (100%)	250 (91%)	24 (9%)	10 38
9	1I	151/201 (75%)	137 (91%)	14 (9%)	9 35
10	1J	140/140 (100%)	118 (84%)	22 (16%)	2 15
11	1K	84/84 (100%)	72 (86%)	12 (14%)	3 19
12	1L	539/539 (100%)	488 (90%)	51 (10%)	8 34
13	1M	408/408 (100%)	361 (88%)	47 (12%)	5 26
14	1N	310/310 (100%)	287 (93%)	23 (7%)	13 44
15	1O	283/307 (92%)	252 (89%)	31 (11%)	6 29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
16	1P	296/323 (92%)	266 (90%)	30 (10%)	7 32
17	1Q	117/152 (77%)	105 (90%)	12 (10%)	7 32
18	1R	79/97 (81%)	67 (85%)	12 (15%)	3 17
19	1S	77/82 (94%)	64 (83%)	13 (17%)	2 12
20	1T	79/133 (59%)	70 (89%)	9 (11%)	5 26
20	1U	79/133 (59%)	65 (82%)	14 (18%)	2 10
21	1V	100/101 (99%)	90 (90%)	10 (10%)	7 32
22	1W	107/112 (96%)	90 (84%)	17 (16%)	2 14
23	1X	153/154 (99%)	141 (92%)	12 (8%)	12 42
24	1Y	101/102 (99%)	90 (89%)	11 (11%)	6 29
25	1Z	123/124 (99%)	106 (86%)	17 (14%)	3 20
26	1a	58/58 (100%)	53 (91%)	5 (9%)	10 38
27	1b	69/70 (99%)	61 (88%)	8 (12%)	5 26
28	1c	45/66 (68%)	36 (80%)	9 (20%)	1 7
29	1d	107/109 (98%)	95 (89%)	12 (11%)	6 27
30	1e	87/94 (93%)	77 (88%)	10 (12%)	5 26
31	1f	54/113 (48%)	43 (80%)	11 (20%)	1 6
32	1g	92/129 (71%)	72 (78%)	20 (22%)	1 5
33	1h	121/158 (77%)	108 (89%)	13 (11%)	6 30
34	1i	119/120 (99%)	105 (88%)	14 (12%)	5 25
35	1j	62/84 (74%)	50 (81%)	12 (19%)	1 7
36	1k	63/76 (83%)	51 (81%)	12 (19%)	1 8
37	1l	141/161 (88%)	125 (89%)	16 (11%)	6 27
38	1m	113/114 (99%)	99 (88%)	14 (12%)	4 23
39	1n	156/160 (98%)	134 (86%)	22 (14%)	3 19
40	1o	110/120 (92%)	90 (82%)	20 (18%)	1 9
41	1p	154/156 (99%)	139 (90%)	15 (10%)	8 33
42	1q	131/131 (100%)	117 (89%)	14 (11%)	6 30
43	1r	85/98 (87%)	76 (89%)	9 (11%)	6 30
44	1s	44/351 (12%)	36 (82%)	8 (18%)	1 9
All	All	7219/8269 (87%)	6415 (89%)	804 (11%)	9 28

5 of 804 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	1S	41	VAL
28	1c	1	LYS
44	1s	43	HIS
20	1T	64	ASP
19	1S	39	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
25	1Z	8	GLN
39	1n	107	HIS
26	1a	68	ASN
33	1h	124	GLN
39	1n	168	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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	$\#\|Z\| > 2$
14	FME	1N	1	14	8,9,10	0.56	0	7,9,11	1.02	1 (14%)
34	SAC	1i	1	-	7,8,9	0.55	0	8,9,11	1.06	1 (12%)
1	FME	1A	1	1	8,9,10	0.51	0	7,9,11	1.04	1 (14%)
10	FME	1J	1	10	8,9,10	0.52	0	7,9,11	0.93	1 (14%)
13	FME	1M	1	13	8,9,10	0.51	0	7,9,11	0.91	1 (14%)
12	FME	1L	1	12	8,9,10	0.53	0	7,9,11	0.99	1 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
11	FME	1K	1	11	8,9,10	0.47	0	7,9,11	1.04	1 (14%)
8	FME	1H	1	8	8,9,10	0.51	0	7,9,11	1.15	1 (14%)

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
14	FME	1N	1	14	-	3/7/9/11	-
34	SAC	1i	1	-	-	0/7/8/10	-
1	FME	1A	1	1	-	1/7/9/11	-
10	FME	1J	1	10	-	1/7/9/11	-
13	FME	1M	1	13	-	1/7/9/11	-
12	FME	1L	1	12	-	1/7/9/11	-
11	FME	1K	1	11	-	1/7/9/11	-
8	FME	1H	1	8	-	0/7/9/11	-

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
34	1i	1	SAC	O-C-CA	-2.91	117.15	124.78
8	1H	1	FME	O-C-CA	-2.76	117.56	124.78
11	1K	1	FME	O-C-CA	-2.59	117.99	124.78
12	1L	1	FME	O-C-CA	-2.54	118.12	124.78
1	1A	1	FME	O-C-CA	-2.51	118.19	124.78

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	1K	1	FME	O1-CN-N-CA
14	1N	1	FME	O1-CN-N-CA
14	1N	1	FME	N-CA-CB-CG
14	1N	1	FME	C-CA-CB-CG
10	1J	1	FME	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides 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	$\#\|Z\|>2$
57	EHZ	1n	201	-	29,36,37	0.16	0	35,44,47	1.17	1 (2%)
58	MYR	1l	201	-	14,14,15	0.34	0	13,13,15	0.38	0
45	SF4	1I	201	9	0,12,12	-	-	-		
51	CDL	1O	403	-	66,66,99	0.36	0	72,78,111	0.53	0
45	SF4	1F	502	6	0,12,12	-	-	-		
47	FES	1G	803	7	0,4,4	-	-	-		
46	PC1	1h	201	-	33,33,53	0.31	0	39,41,61	0.44	0
46	PC1	1m	201	-	45,45,53	0.28	0	51,53,61	0.36	0
57	EHZ	1W	201	-	29,36,37	0.16	0	35,44,47	1.23	1 (2%)
46	PC1	1B	202	-	33,33,53	0.32	0	39,41,61	0.33	0
45	SF4	1G	802	7	0,12,12	-	-	-		
46	PC1	1q	201	-	47,47,53	0.37	0	53,55,61	0.54	1 (1%)
52	3PE	1g	201	-	50,50,50	0.27	0	53,55,55	0.98	3 (5%)
52	3PE	1n	202	-	41,41,50	0.29	0	44,46,55	0.43	0
51	CDL	1H	402	-	50,50,99	0.36	0	56,62,111	0.54	1 (1%)
48	FMN	1F	501	-	33,33,33	0.58	0	48,50,50	0.66	1 (2%)
50	U10	1H	401	-	63,63,63	0.56	1 (1%)	76,79,79	0.82	4 (5%)
45	SF4	1B	201	2	0,12,12	-	-	-		
55	NDP	1P	501	-	45,52,52	0.60	0	53,80,80	0.70	1 (1%)
45	SF4	1G	801	7	0,12,12	-	-	-		
47	FES	1E	301	5	0,4,4	-	-	-		
52	3PE	1Y	202	-	34,34,50	0.30	0	37,39,55	0.56	1 (2%)
51	CDL	1a	101	-	60,60,99	0.33	0	66,72,111	0.53	0
46	PC1	1d	201	-	38,38,53	0.31	0	44,46,61	0.50	0
52	3PE	1N	401	-	37,37,50	0.32	0	40,42,55	0.39	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
45	SF4	1I	202	9	0,12,12	-	-	-		
53	GTP	1O	401	54	26,34,34	0.95	2 (7%)	32,54,54	0.84	0
46	PC1	1Y	201	-	34,34,53	0.33	0	40,42,61	0.37	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
57	EHZ	1n	201	-	-	2/42/44/45	-
58	MYR	1l	201	-	-	1/11/12/13	-
45	SF4	1I	201	9	-	-	0/6/5/5
51	CDL	1O	403	-	-	15/76/76/110	-
45	SF4	1F	502	6	-	-	0/6/5/5
47	FES	1G	803	7	-	-	0/1/1/1
46	PC1	1h	201	-	-	4/36/36/57	-
57	EHZ	1W	201	-	-	17/42/44/45	-
46	PC1	1m	201	-	-	9/49/49/57	-
46	PC1	1B	202	-	-	13/37/37/57	-
45	SF4	1G	802	7	-	-	0/6/5/5
46	PC1	1q	201	-	-	18/51/51/57	-
52	3PE	1g	201	-	-	12/54/54/54	-
52	3PE	1n	202	-	-	7/45/45/54	-
51	CDL	1H	402	-	-	8/61/61/110	-
48	FMN	1F	501	-	-	2/18/18/18	0/3/3/3
50	U10	1H	401	-	-	6/63/87/87	0/1/1/1
55	NDP	1P	501	-	-	5/30/77/77	0/5/5/5
45	SF4	1B	201	2	-	-	0/6/5/5
45	SF4	1G	801	7	-	-	0/6/5/5
47	FES	1E	301	5	-	-	0/1/1/1
52	3PE	1Y	202	-	-	14/38/38/54	-
51	CDL	1a	101	-	-	18/71/71/110	-
46	PC1	1d	201	-	-	13/42/42/57	-
52	3PE	1N	401	-	-	4/41/41/54	-
45	SF4	1I	202	9	-	-	0/6/5/5
53	GTP	1O	401	54	-	3/18/38/38	0/3/3/3
46	PC1	1Y	201	-	-	11/38/38/57	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	1O	401	GTP	C5-C6	-2.58	1.42	1.47
50	1H	401	U10	C4-C5	-2.50	1.41	1.48
53	1O	401	GTP	C8-N7	-2.12	1.31	1.35

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	1W	201	EHZ	C10-S1-C9	6.71	122.76	101.87
57	1n	201	EHZ	C10-S1-C9	6.49	122.07	101.87
52	1g	201	3PE	O21-C21-C22	4.52	121.23	111.50
52	1g	201	3PE	O21-C2-C3	3.44	120.86	108.40
52	1g	201	3PE	O21-C21-O22	-2.77	117.01	123.70

There are no chirality outliers.

5 of 182 torsion outliers are listed below:

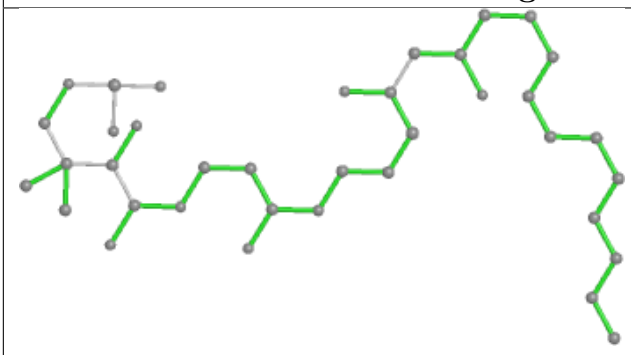
Mol	Chain	Res	Type	Atoms
46	1B	202	PC1	C11-O13-P-O14
46	1B	202	PC1	C2-C1-O11-P
46	1B	202	PC1	O32-C31-O31-C3
46	1B	202	PC1	C32-C31-O31-C3
46	1Y	201	PC1	C1-O11-P-O14

There are no ring outliers.

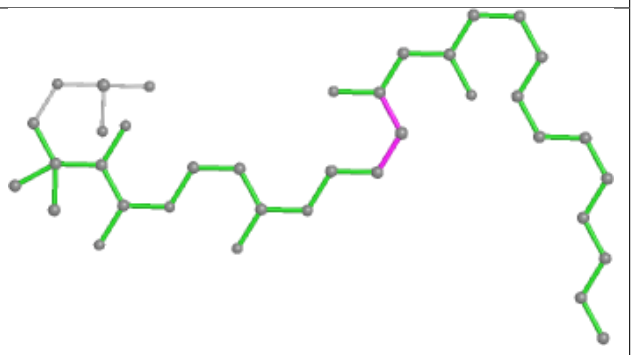
No monomer is involved in short contacts.

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

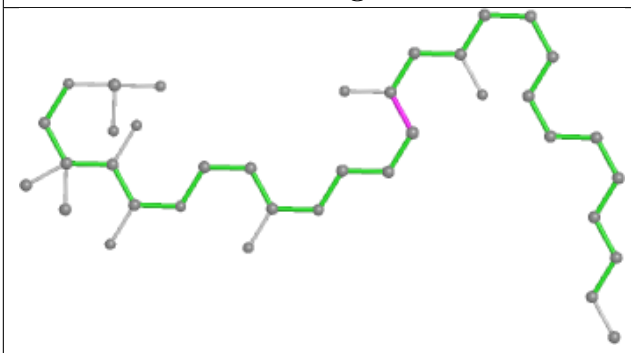
Ligand EHZ 1n 201



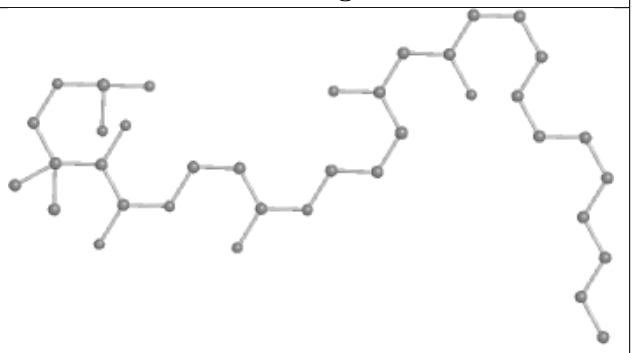
Bond lengths



Bond angles

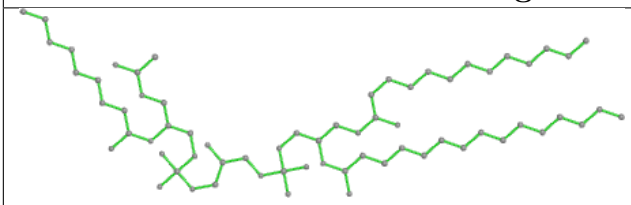


Torsions

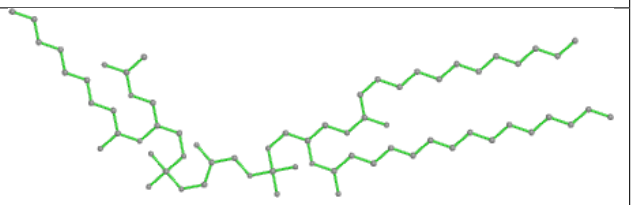


Rings

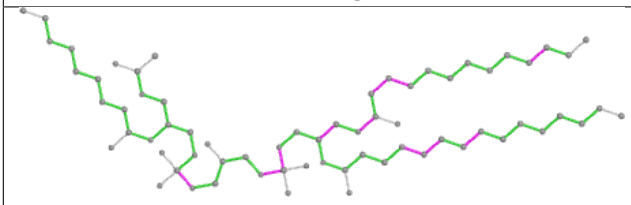
Ligand CDL 1O 403



Bond lengths



Bond angles



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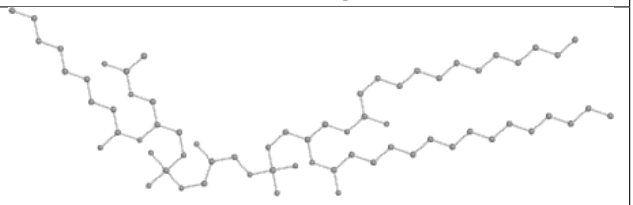
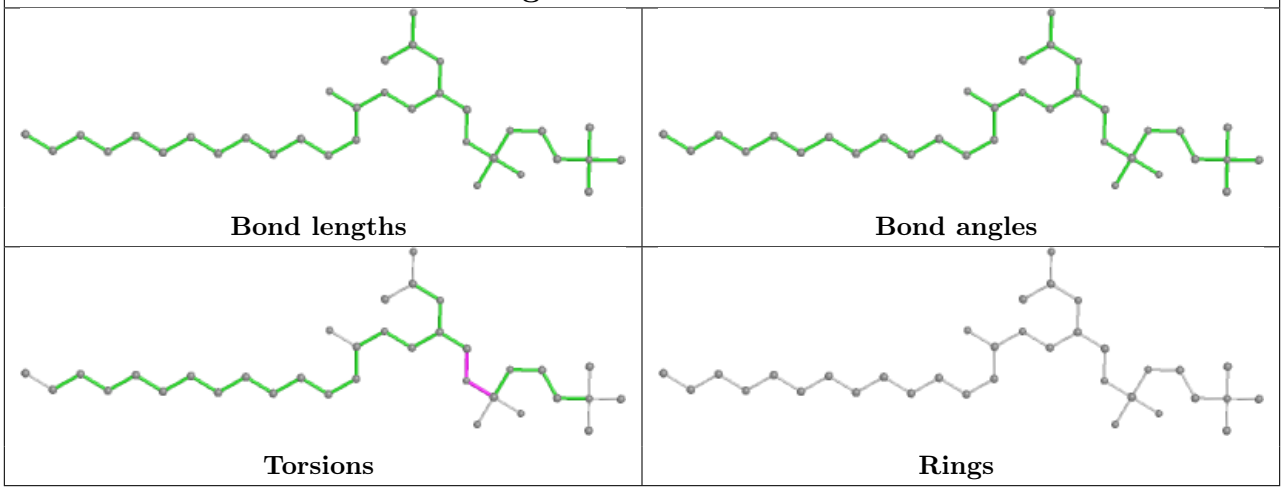
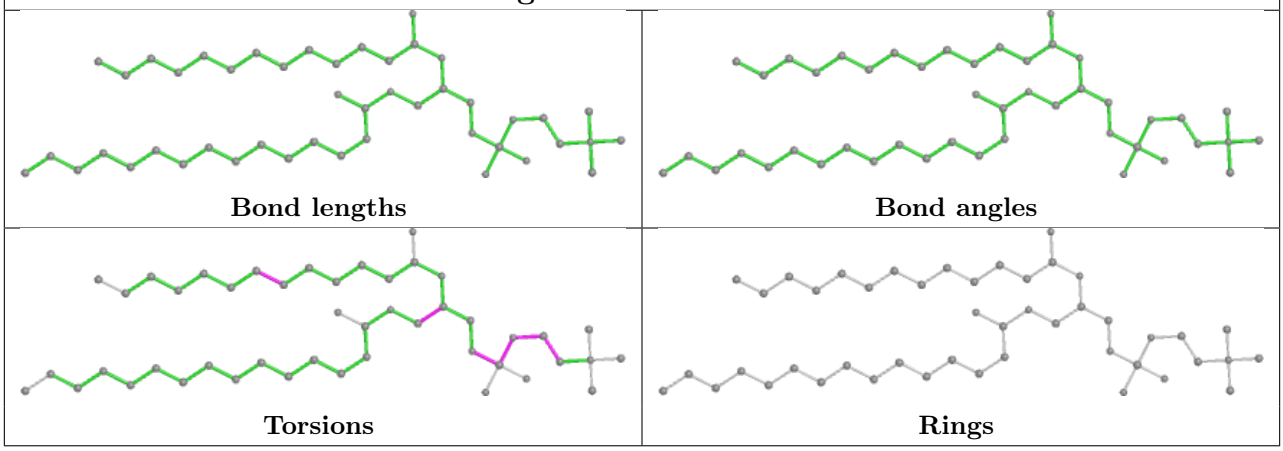


Rings

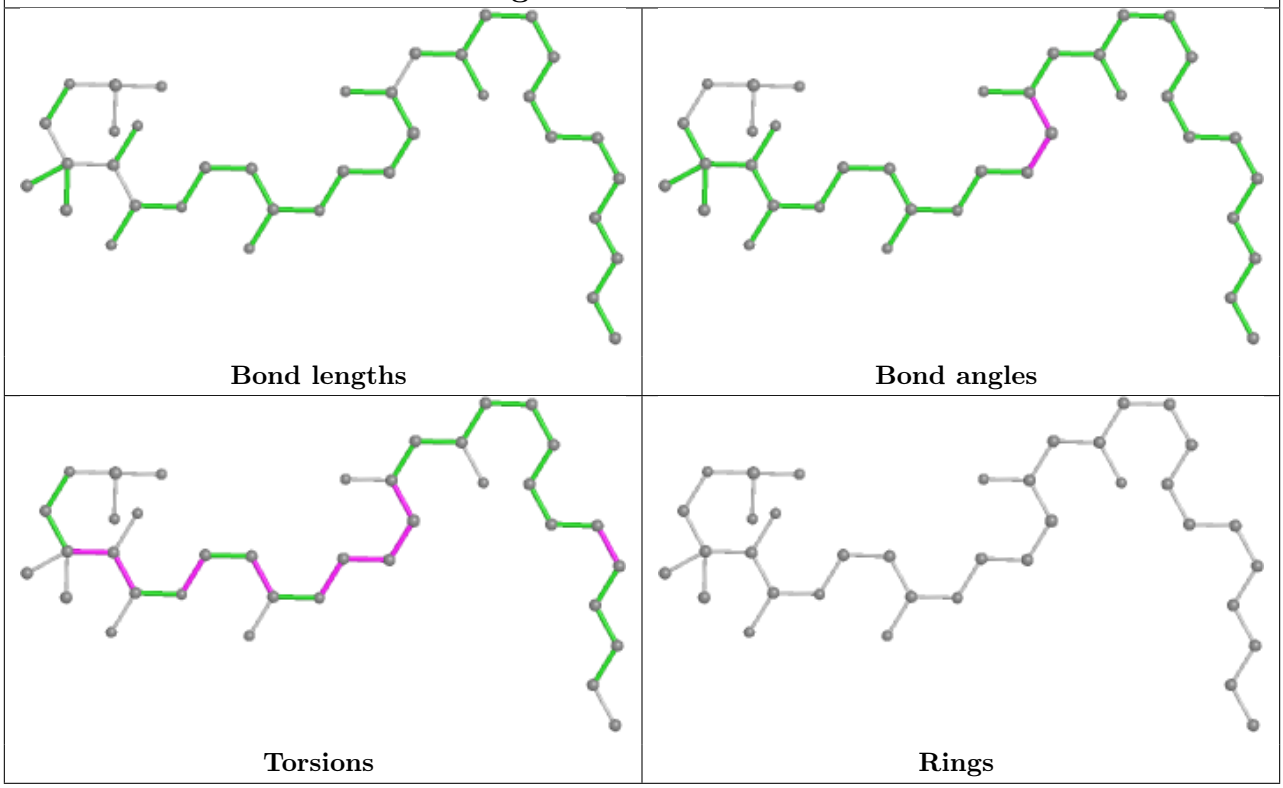
Ligand PC1 1h 201



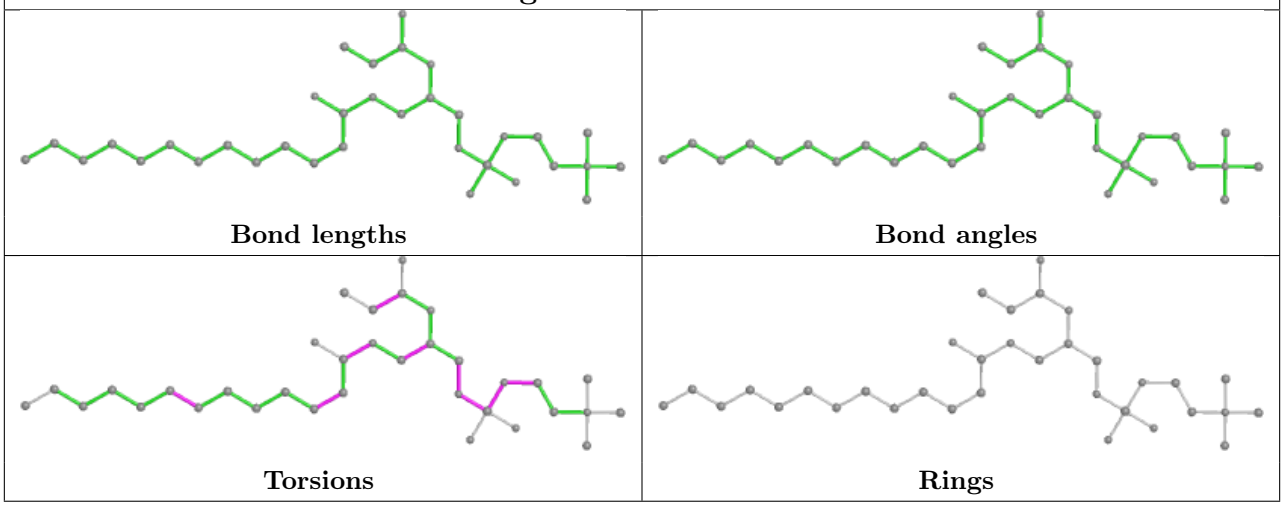
Ligand PC1 1m 201



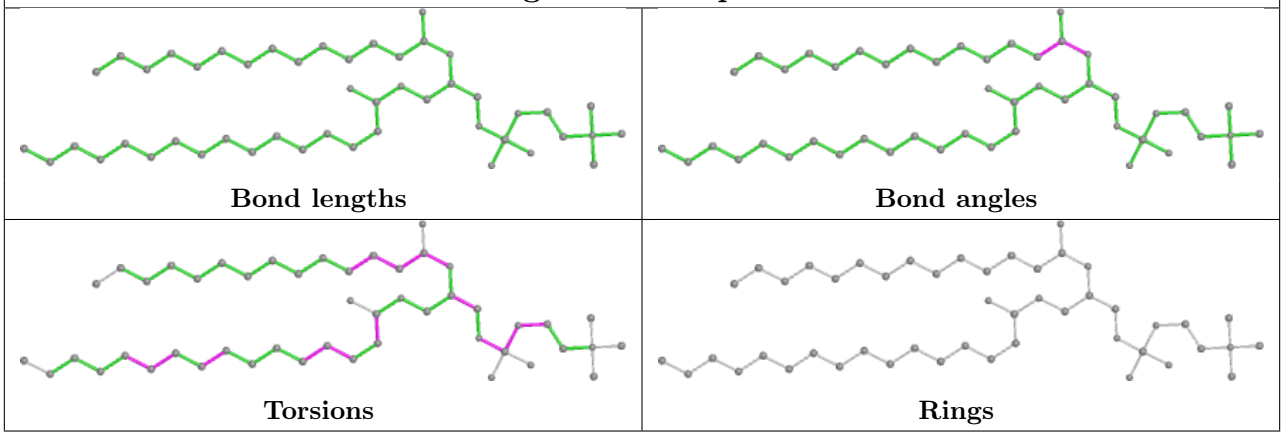
Ligand EHZ 1W 201



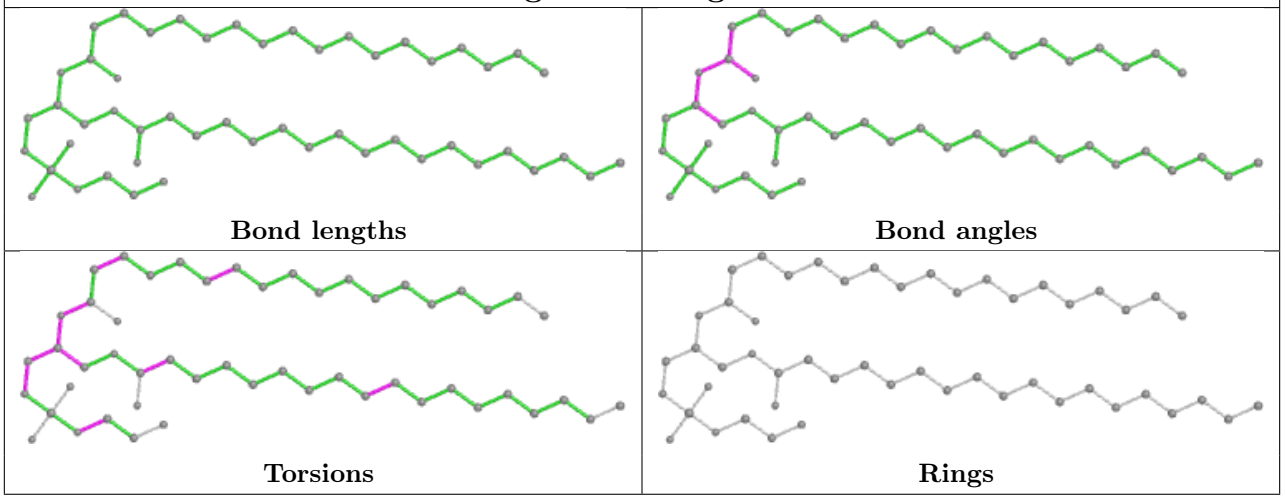
Ligand PC1 1B 202



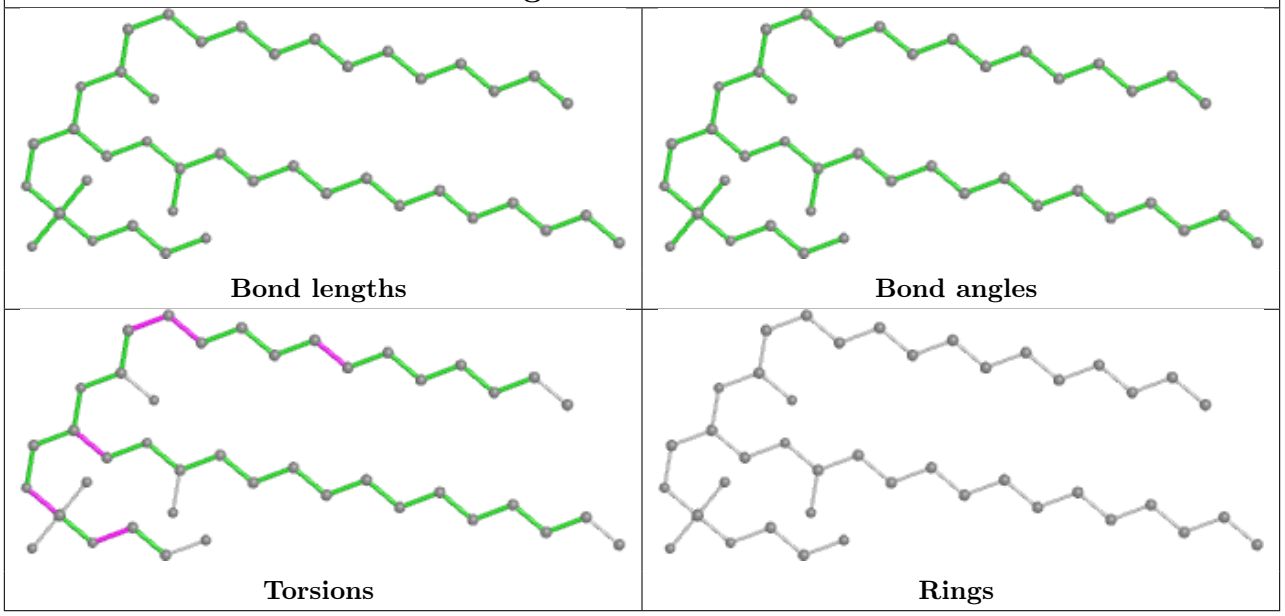
Ligand PC1 1q 201



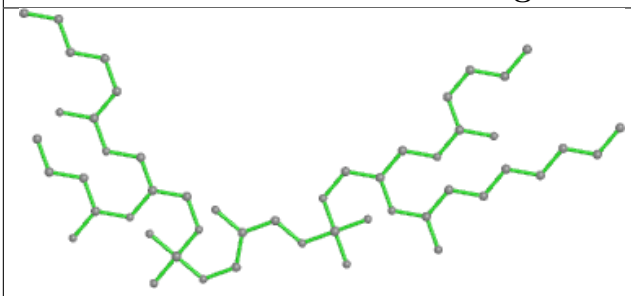
Ligand 3PE 1g 201



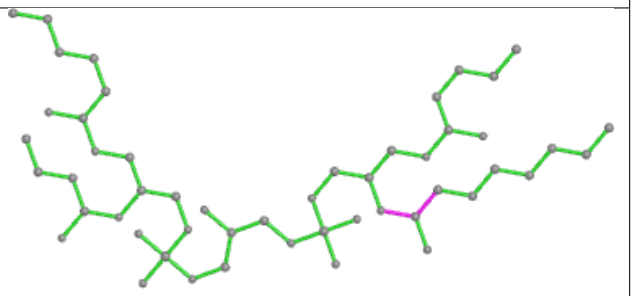
Ligand 3PE 1n 202



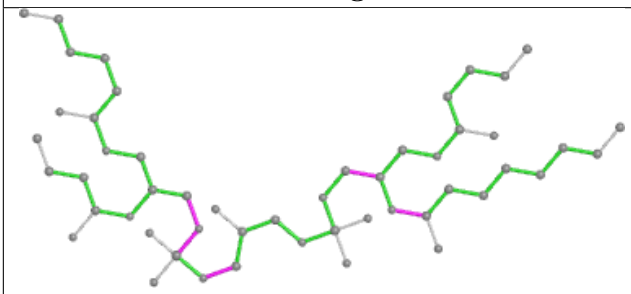
Ligand CDL 1H 402



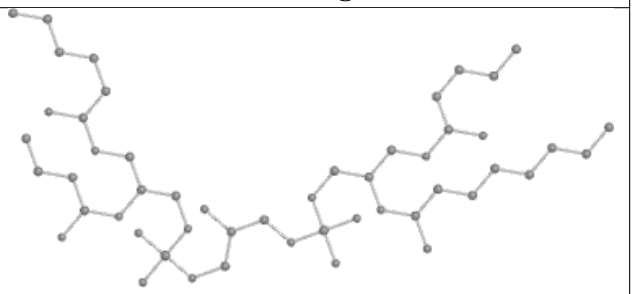
Bond lengths



Bond angles

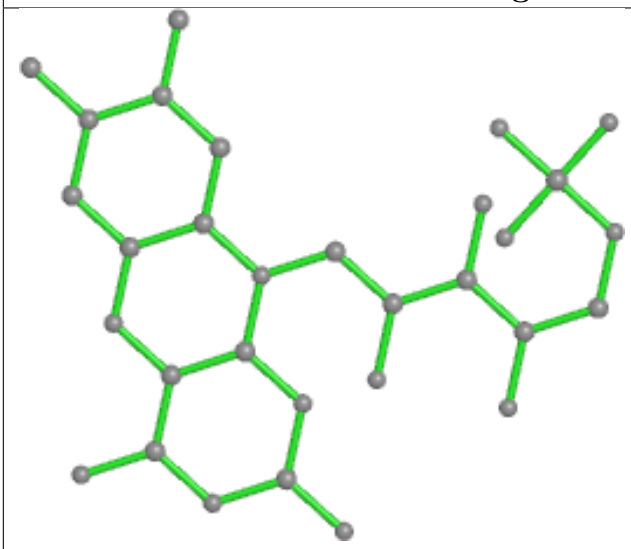


Torsions

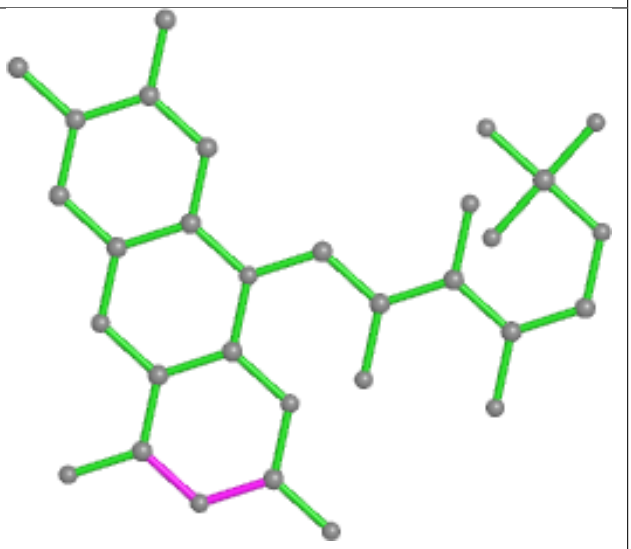


Rings

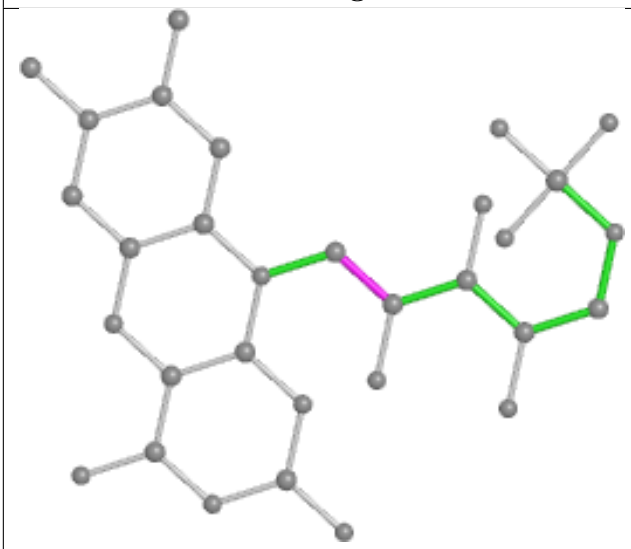
Ligand FMN 1F 501



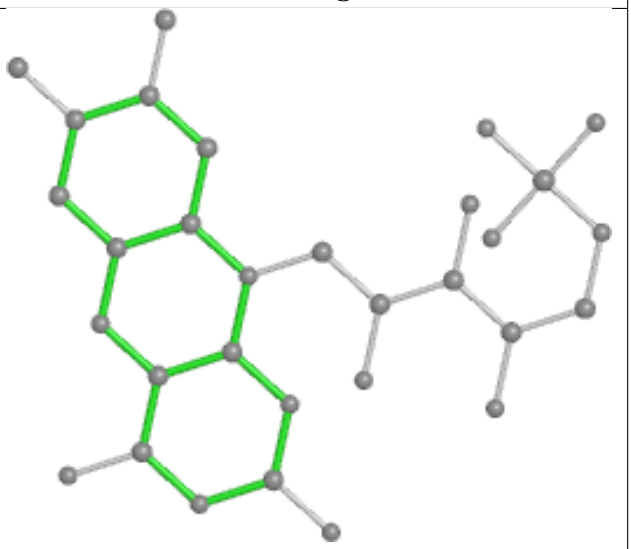
Bond lengths



Bond angles

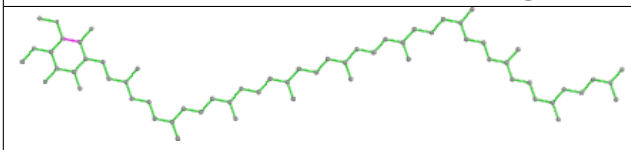


Torsions

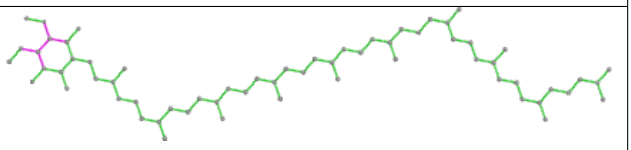


Rings

Ligand U10 1H 401

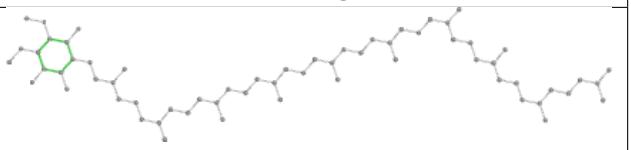


Bond lengths



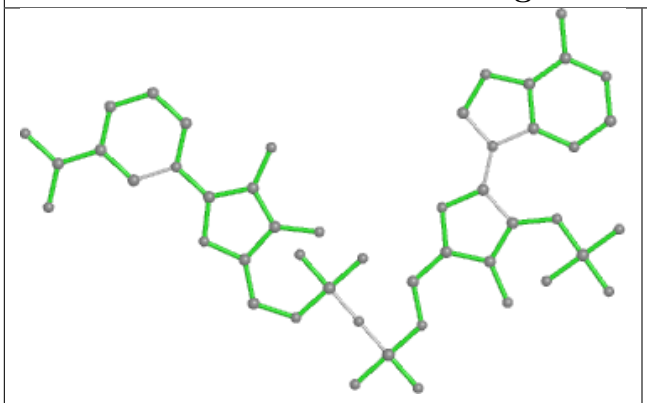
Bond angles

Torsions

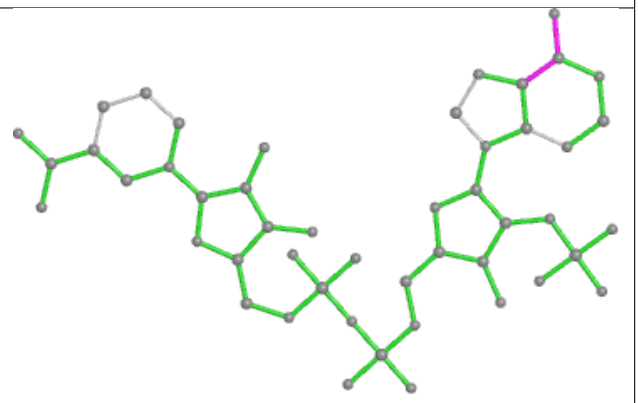


Rings

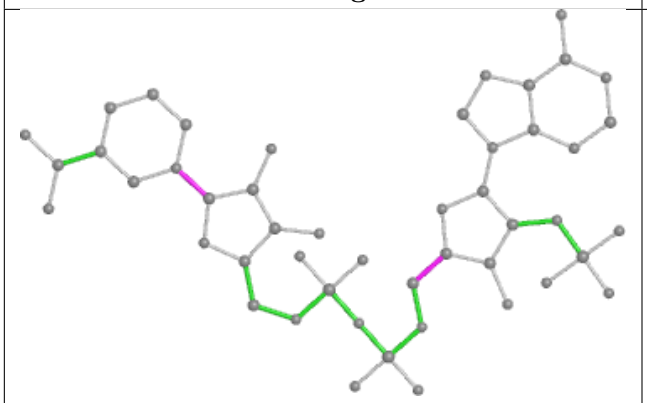
Ligand NDP 1P 501



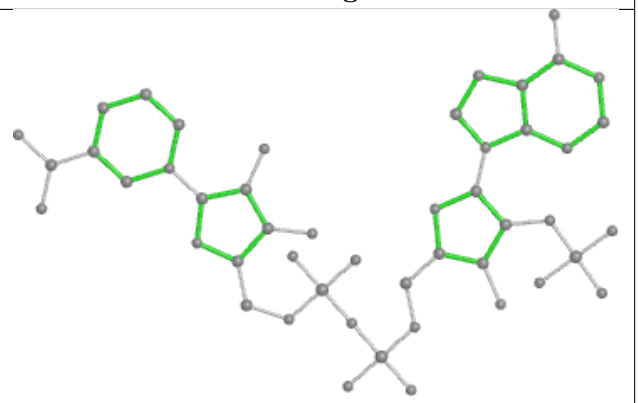
Bond lengths



Bond angles

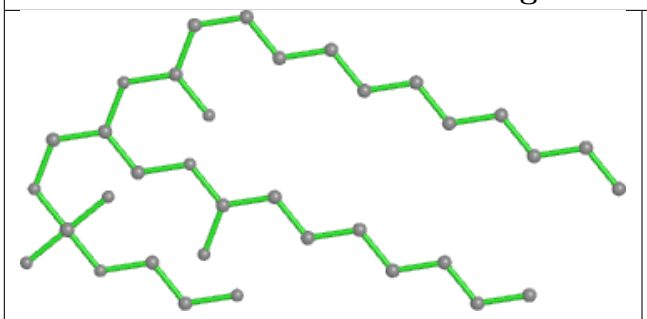


Torsions

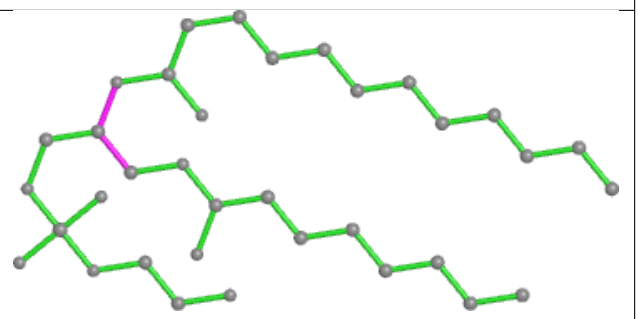


Rings

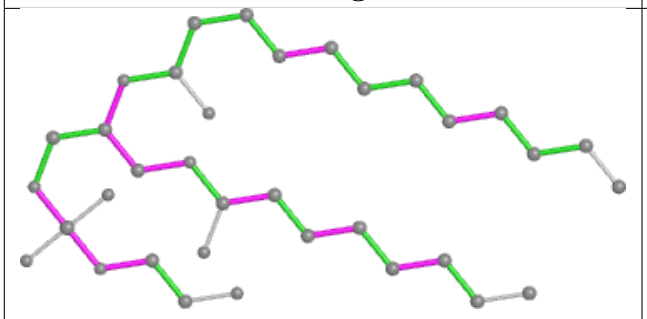
Ligand 3PE 1Y 202



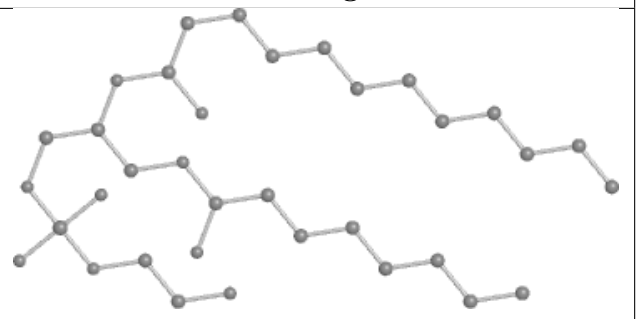
Bond lengths



Bond angles

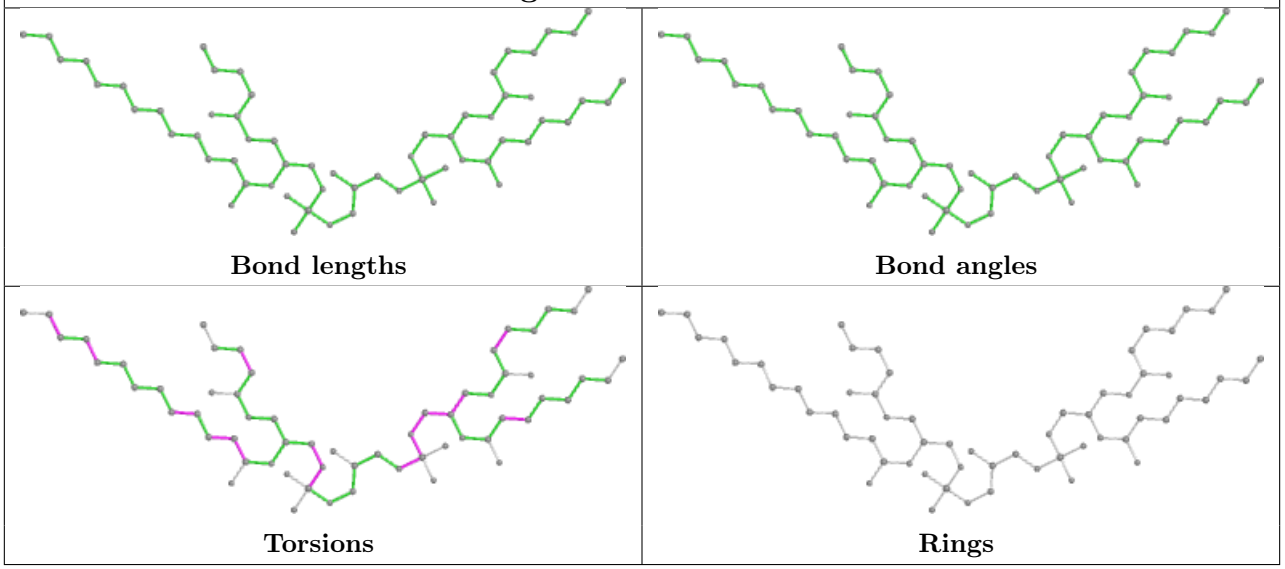


Torsions

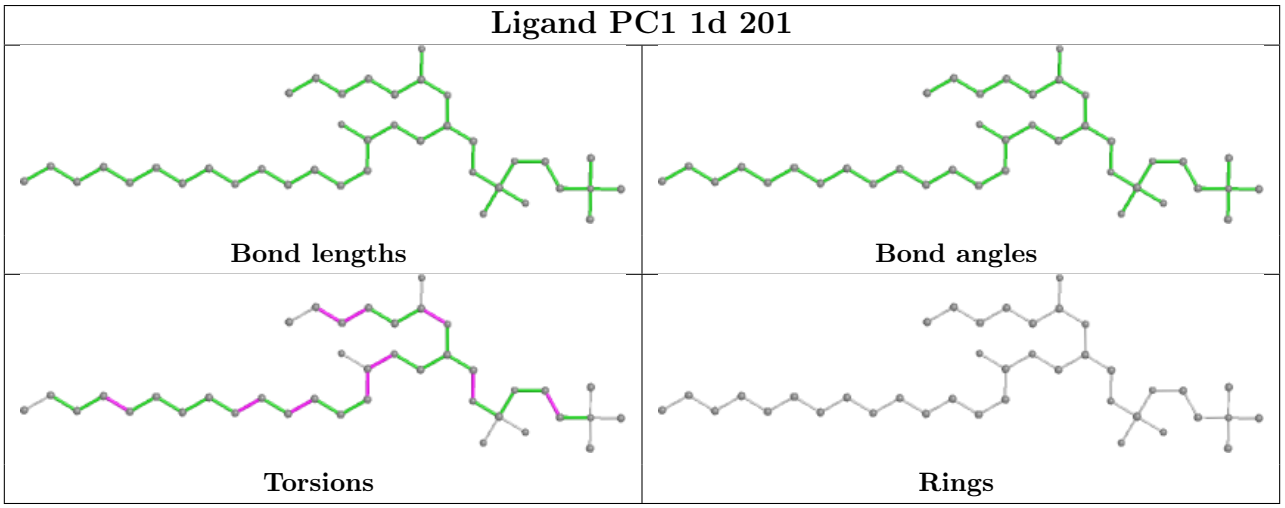


Rings

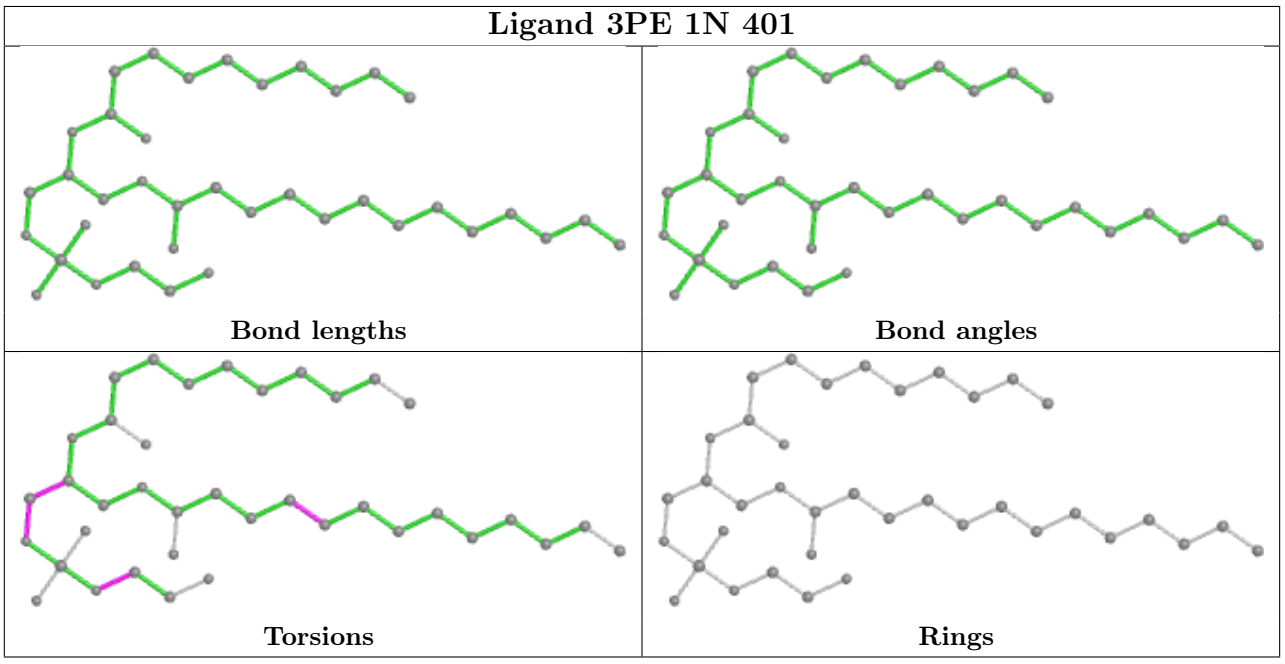
Ligand CDL 1a 101



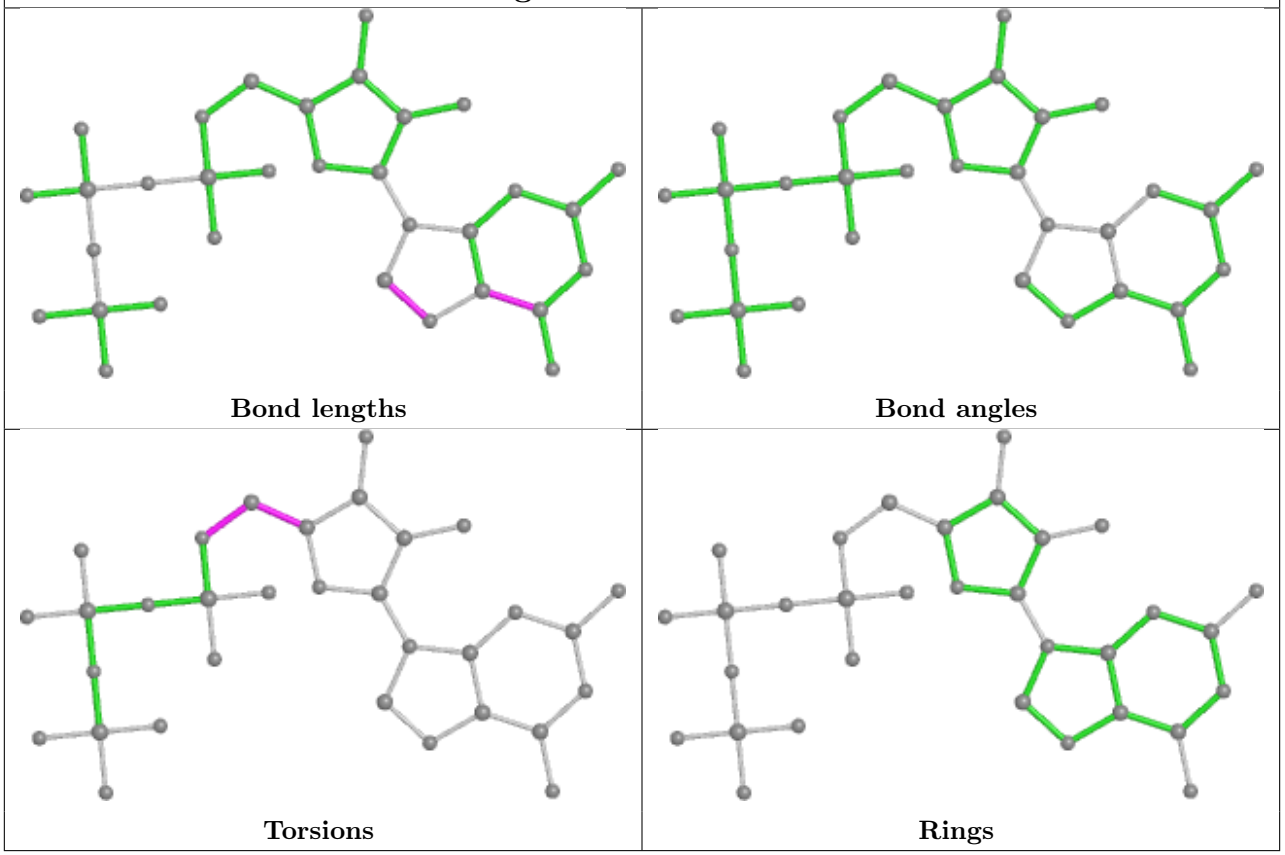
Ligand PC1 1d 201



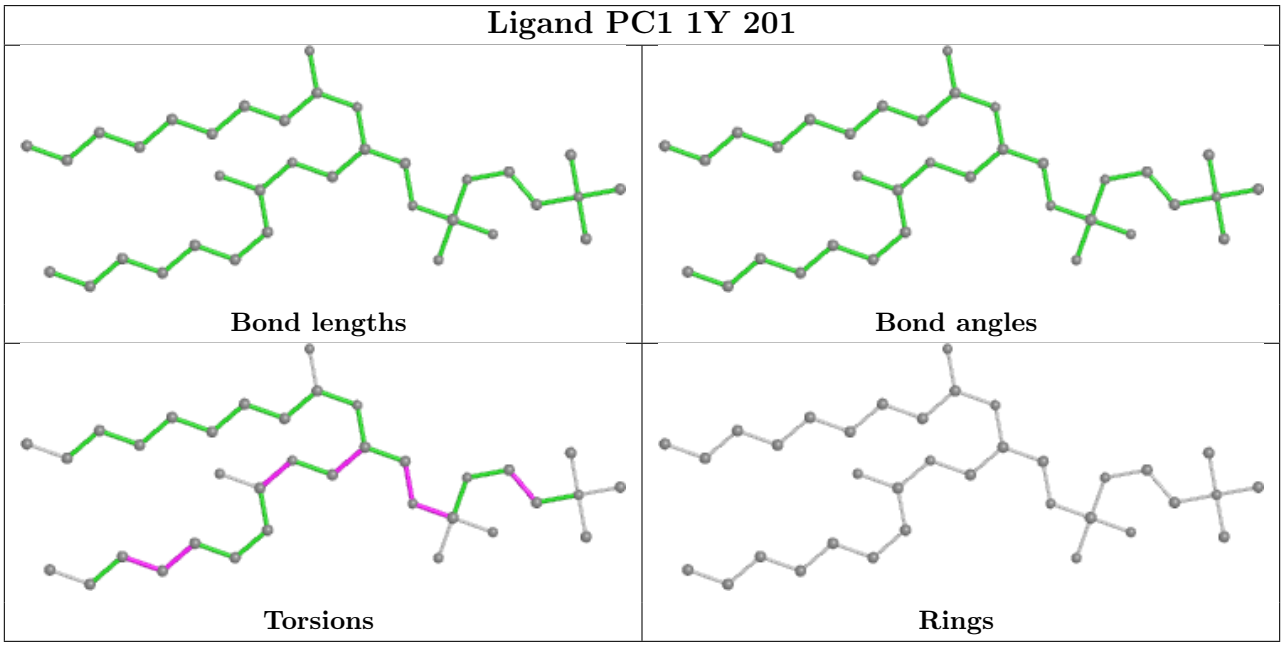
Ligand 3PE 1N 401



Ligand GTP 1O 401



Ligand PC1 1Y 201



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
43	1r	1
34	1i	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1r	1:ALA	C	2:SER	N	7.02
1	1i	1:SAC	C	2:GLY	N	4.04

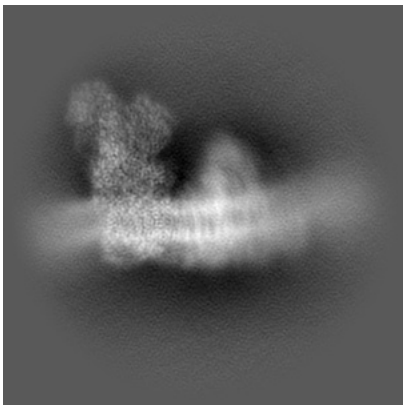
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-42168. These allow visual inspection of the internal detail of the map and identification of artifacts.

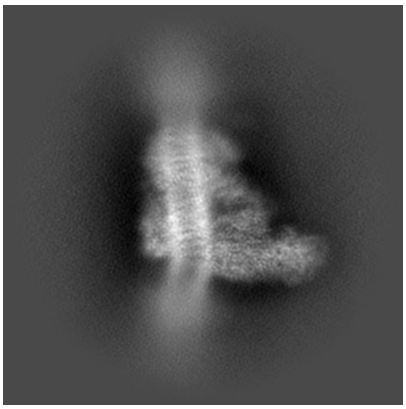
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

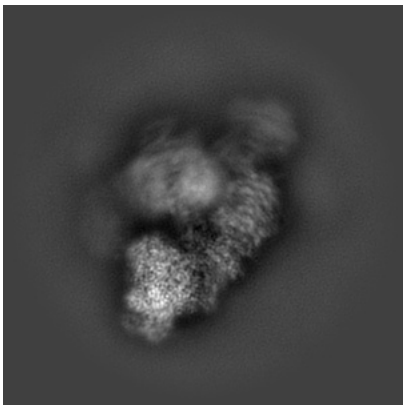
6.1.1 Primary map



X

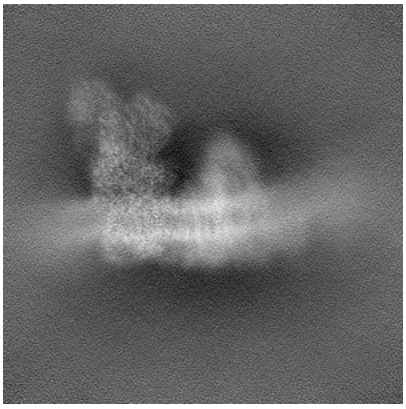


Y

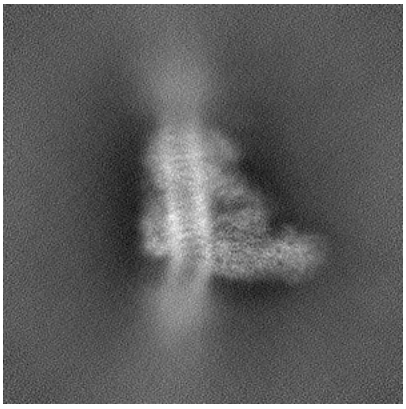


Z

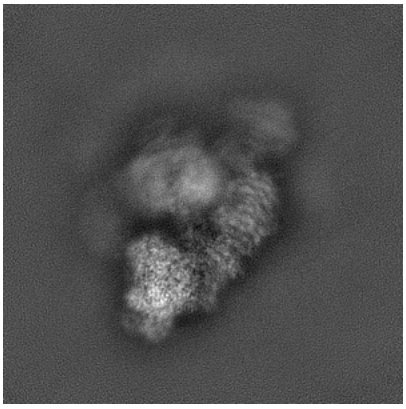
6.1.2 Raw map



X



Y

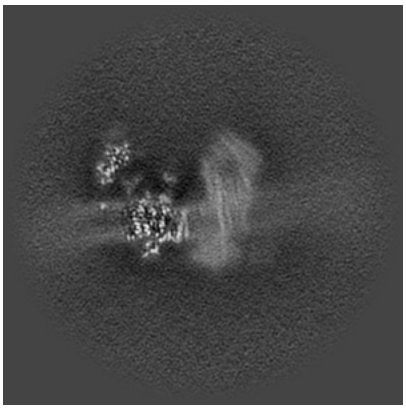


Z

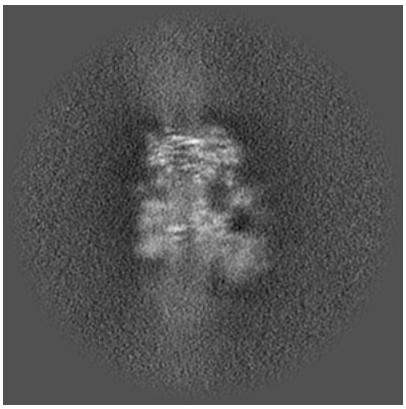
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

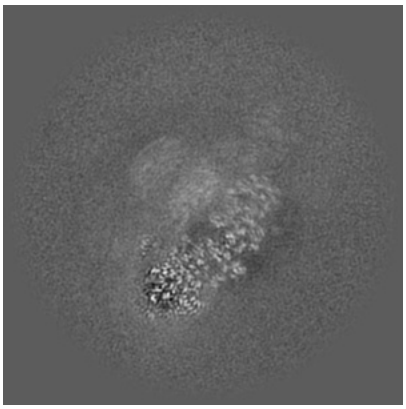
6.2.1 Primary map



X Index: 160

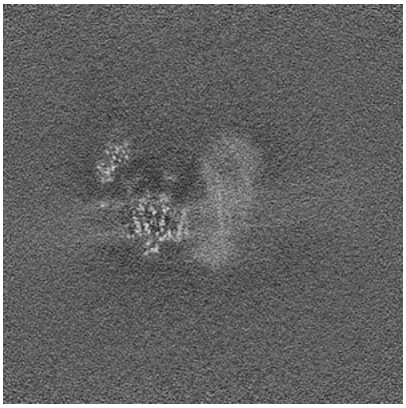


Y Index: 160

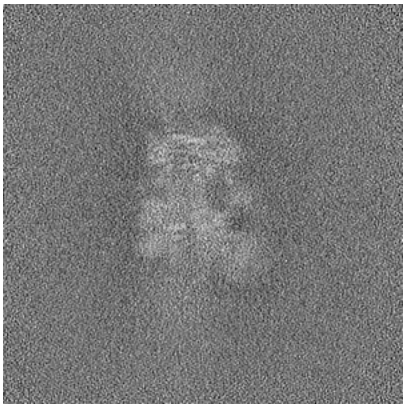


Z Index: 160

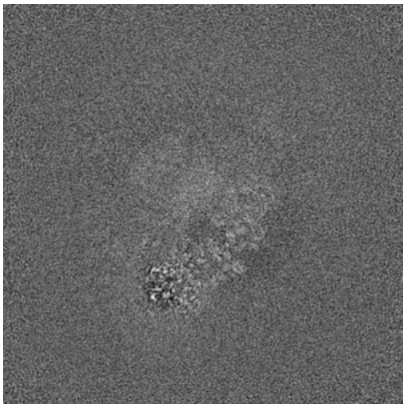
6.2.2 Raw map



X Index: 160



Y Index: 160

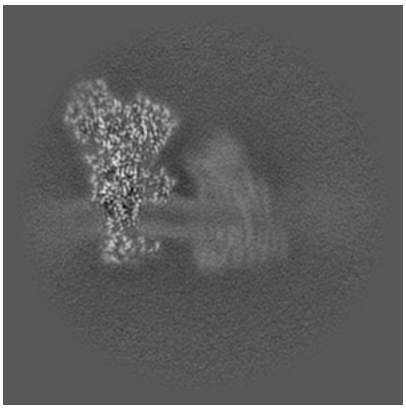


Z Index: 160

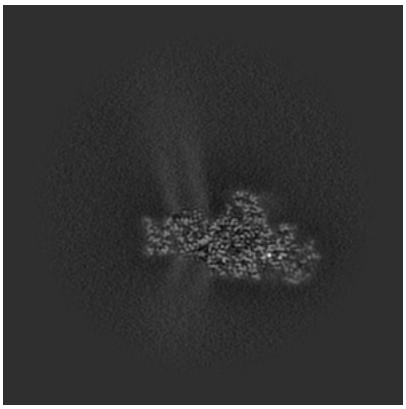
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

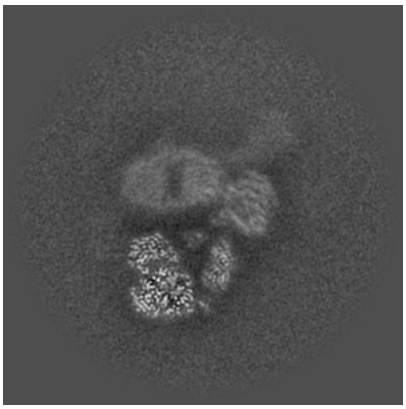
6.3.1 Primary map



X Index: 123

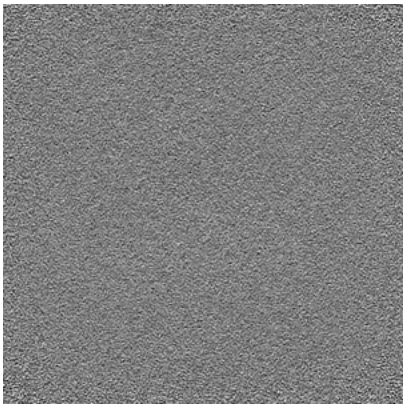


Y Index: 87

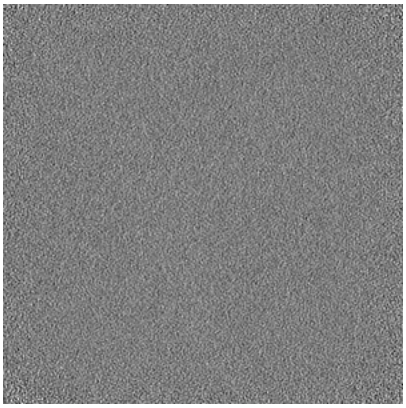


Z Index: 177

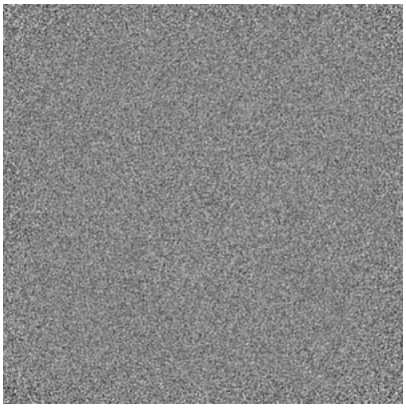
6.3.2 Raw map



X Index: 0



Y Index: 0

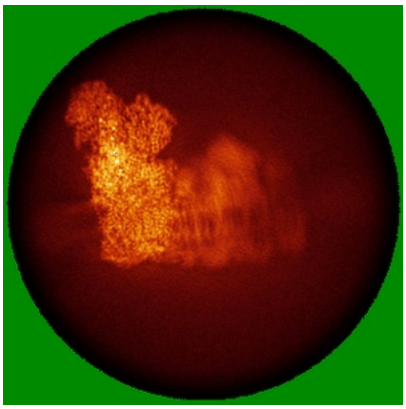


Z Index: 0

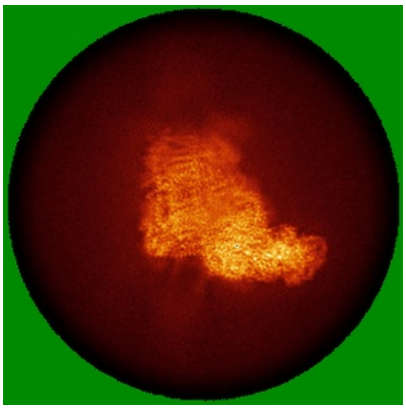
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

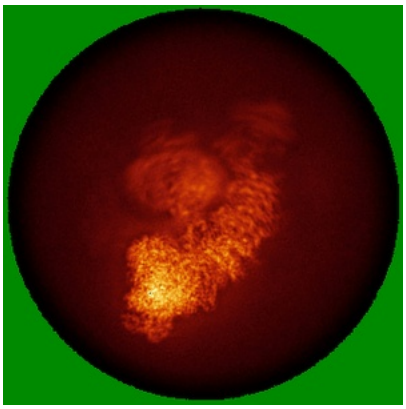
6.4.1 Primary map



X

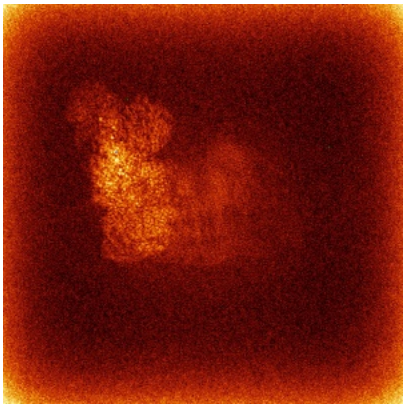


Y

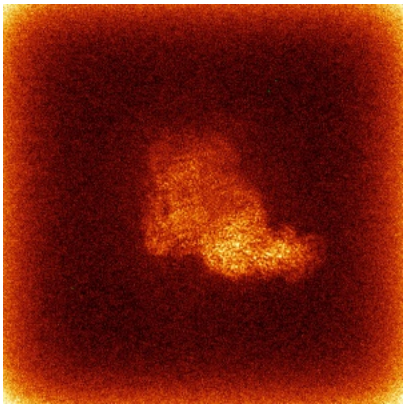


Z

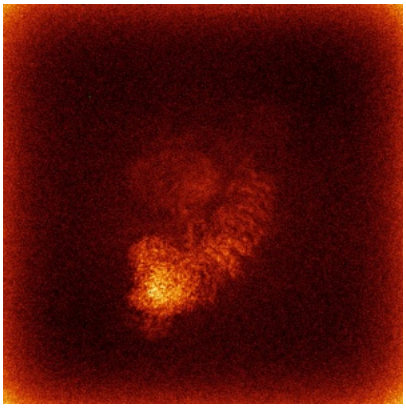
6.4.2 Raw map



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.

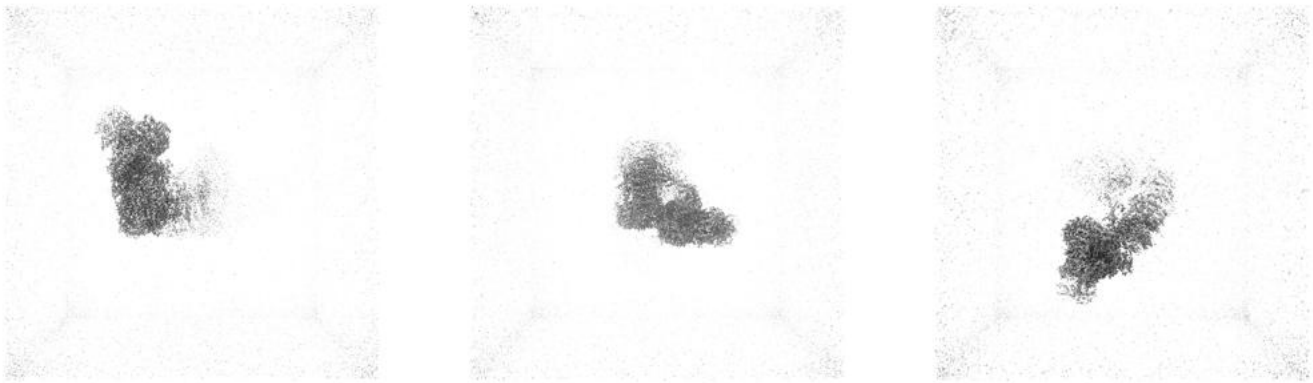
6.5 Orthogonal surface views (i)

6.5.1 Primary map

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.

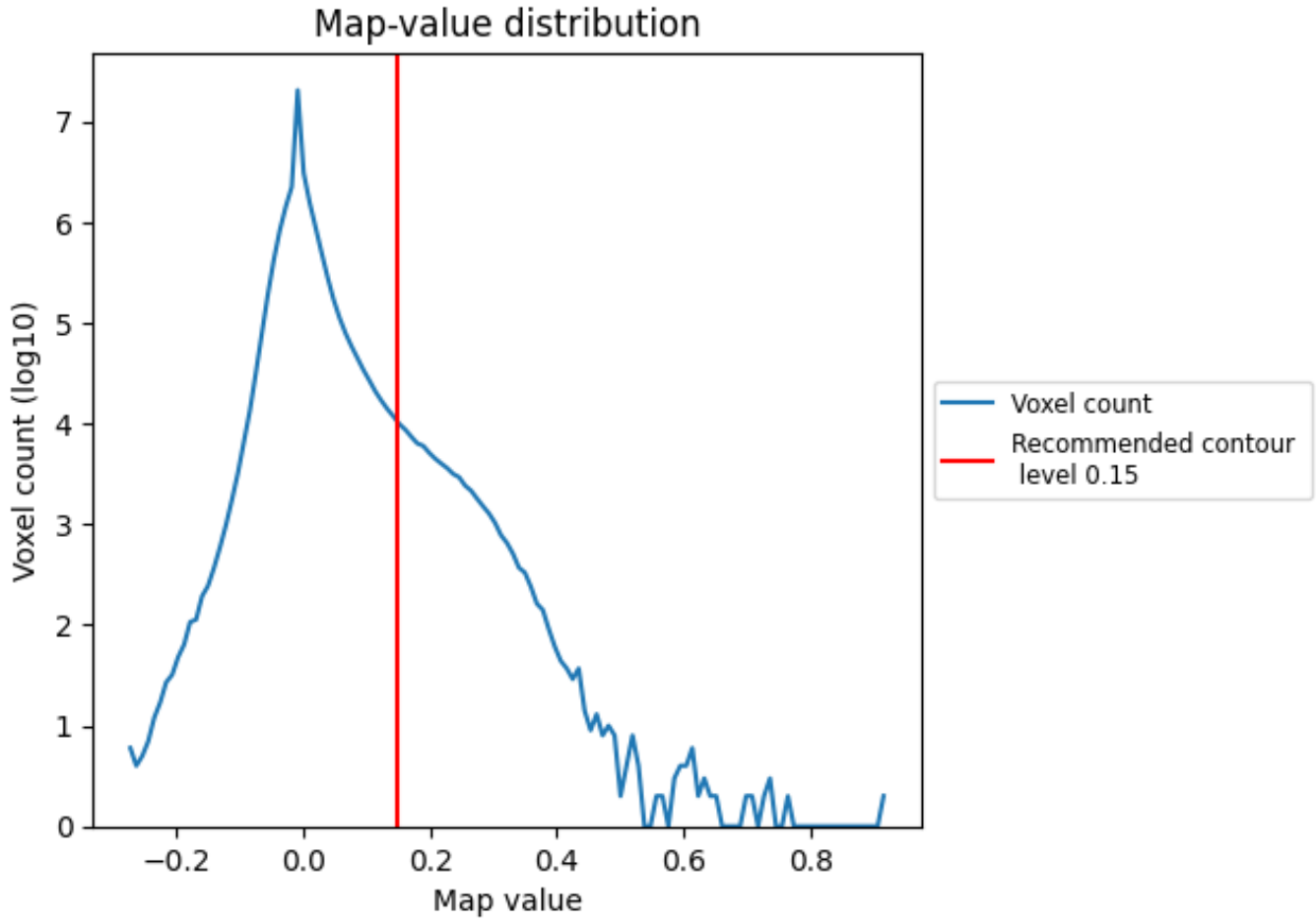
6.6 Mask visualisation (i)

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

7 Map analysis

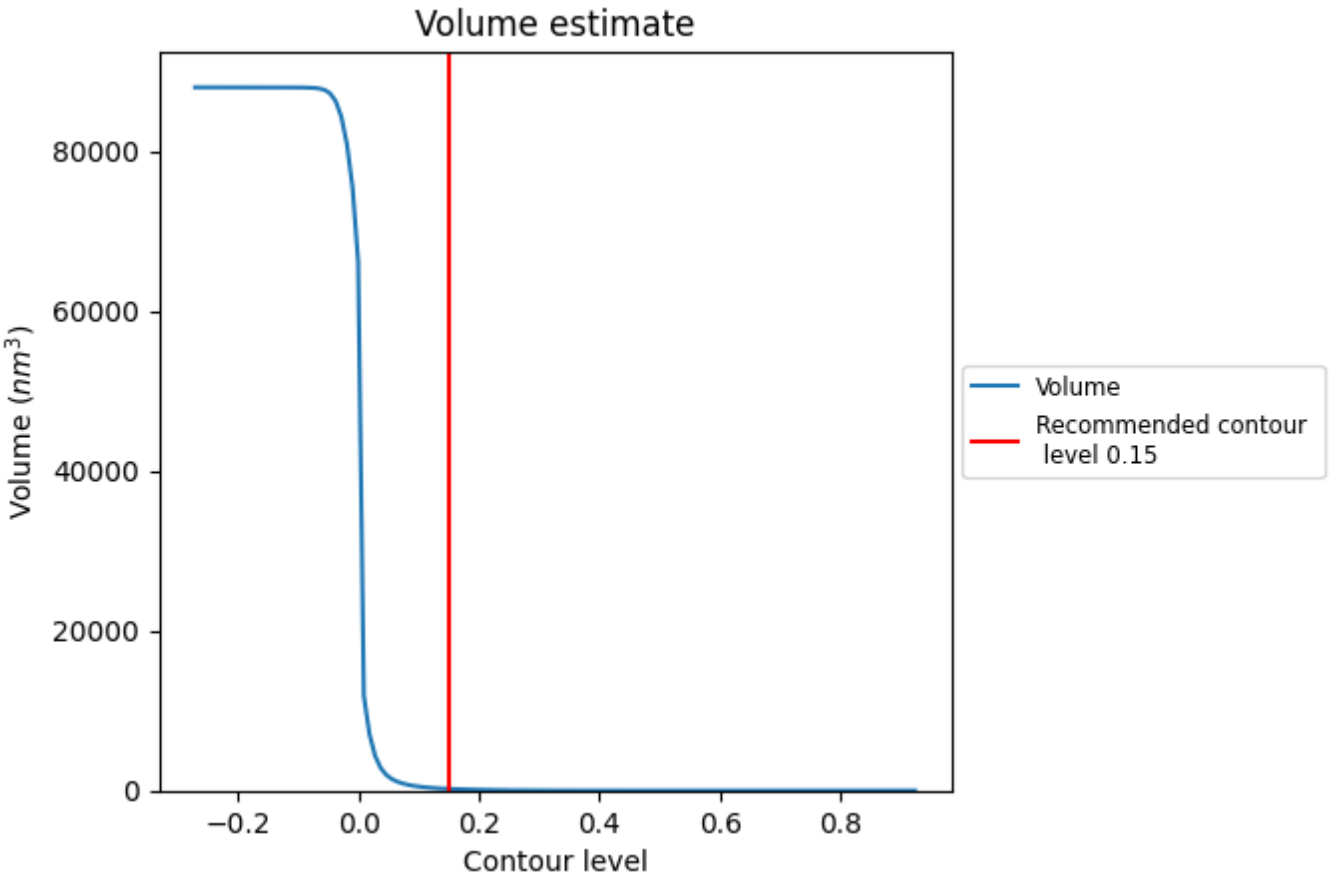
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

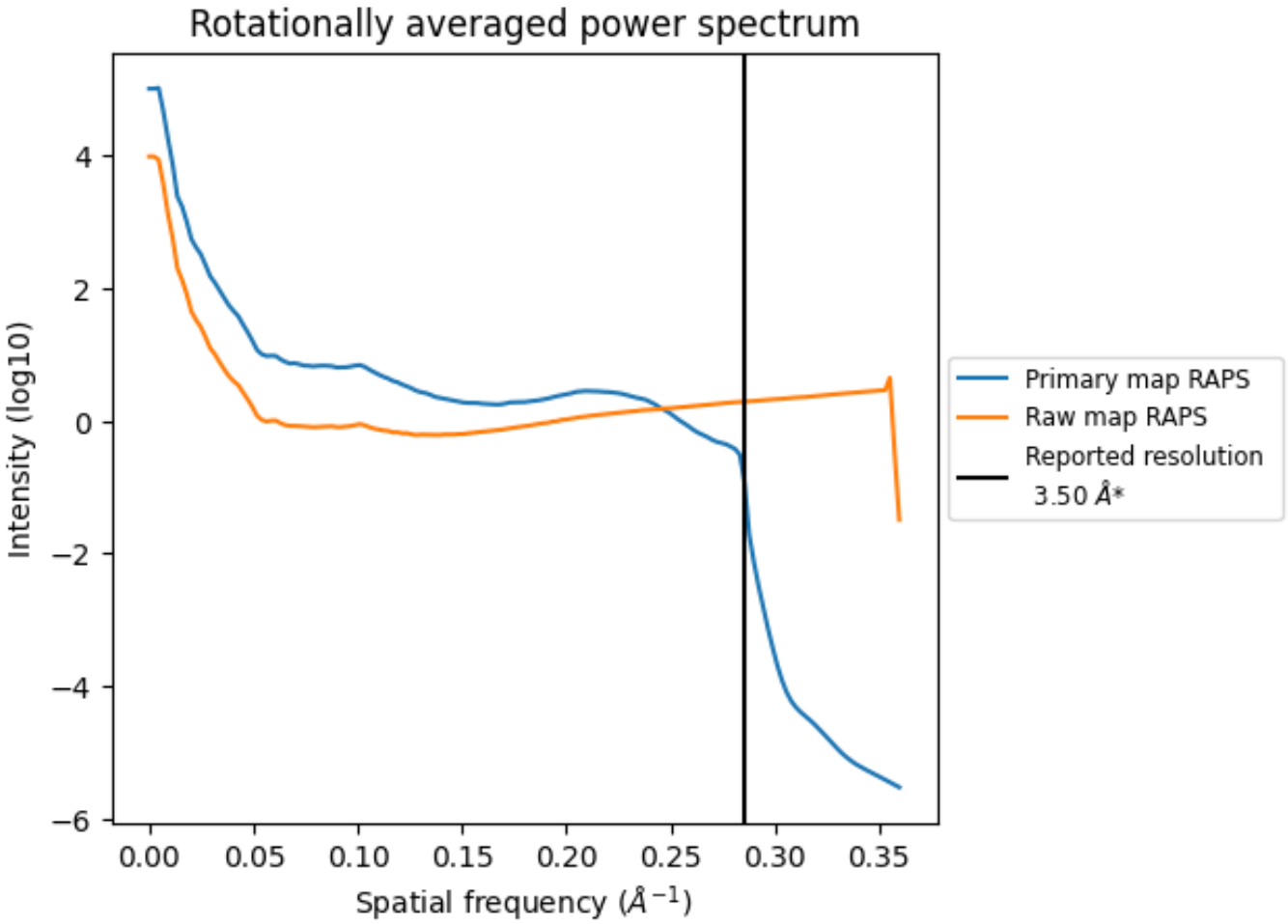
7.2 Volume estimate (i)



The volume at the recommended contour level is 210 nm^3; this corresponds to an approximate mass of 190 kDa.

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

7.3 Rotationally averaged power spectrum (i)

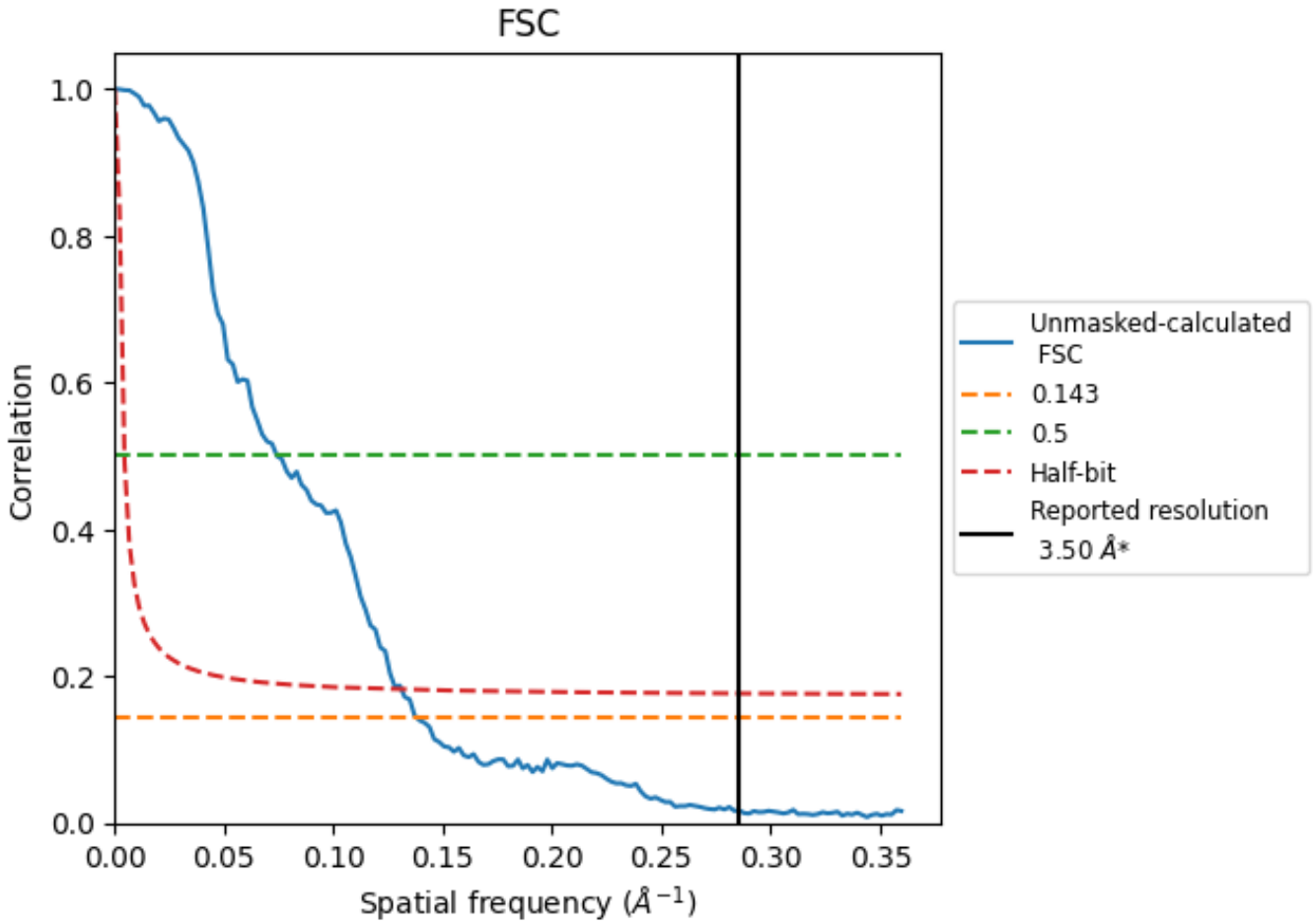


*Reported resolution corresponds to spatial frequency of 0.286 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.286 Å^{-1}

8.2 Resolution estimates (i)

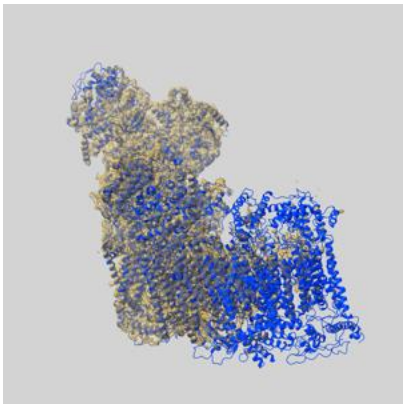
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.24	13.48	7.63

*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 7.24 differs from the reported value 3.5 by more than 10 %

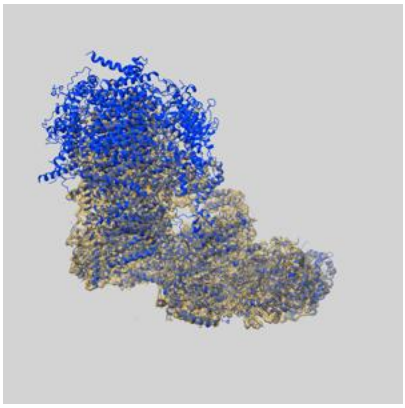
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-42168 and PDB model 8UER. Per-residue inclusion information can be found in section 3 on page 21.

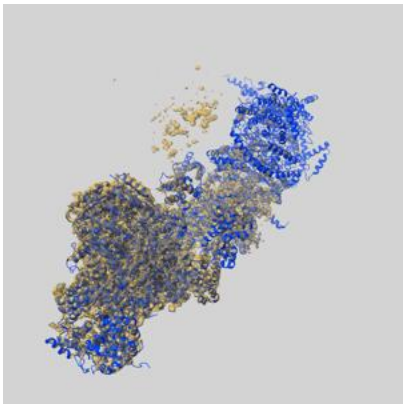
9.1 Map-model overlay



X



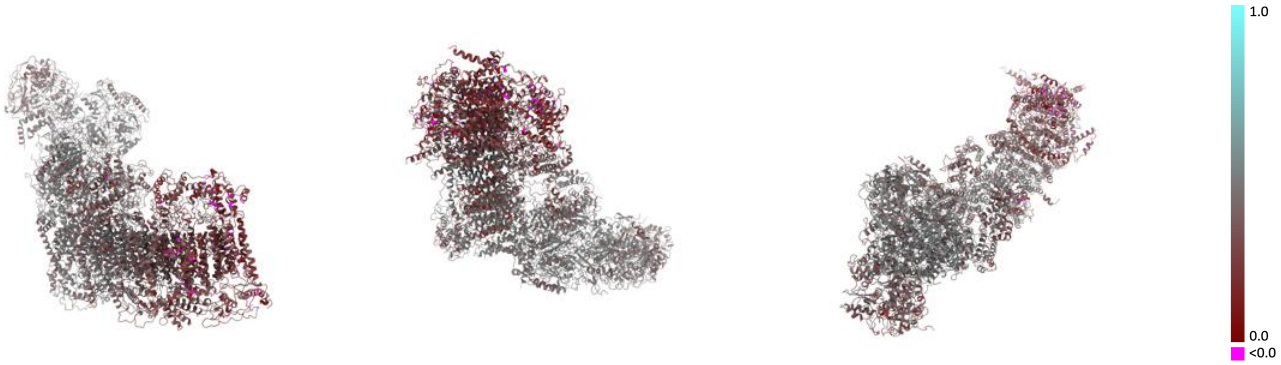
Y



Z

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.

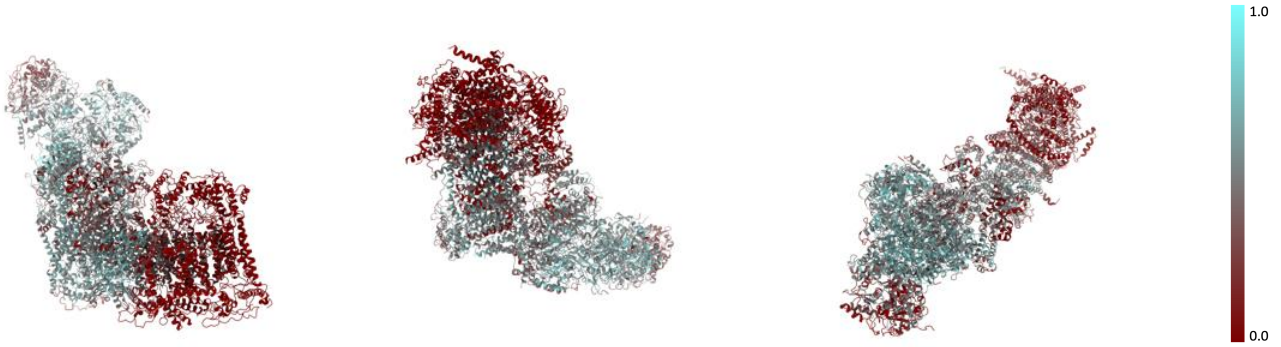
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

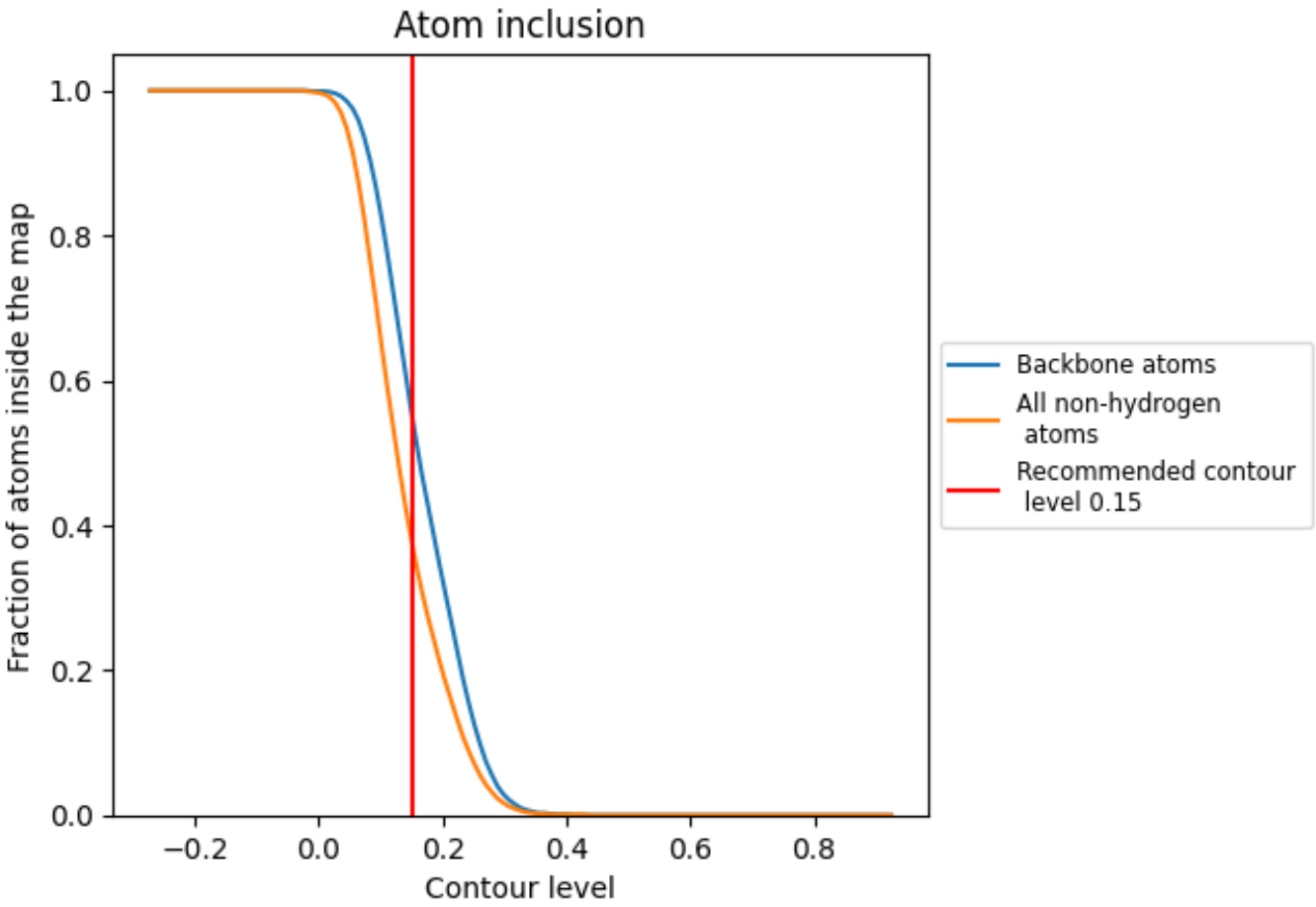
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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, 56% of all backbone atoms, 38% 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	0.3800	0.3880
1A	0.4340	0.4320
1B	0.6100	0.4560
1C	0.5770	0.4740
1D	0.5810	0.4590
1E	0.3490	0.3930
1F	0.3610	0.3930
1G	0.5870	0.4470
1H	0.5560	0.4510
1I	0.6800	0.4600
1J	0.4030	0.4130
1K	0.4480	0.4110
1L	0.1050	0.2710
1M	0.3520	0.3820
1N	0.5370	0.4410
1O	0.2470	0.3480
1P	0.5000	0.4580
1Q	0.4720	0.4510
1R	0.5400	0.4590
1S	0.5320	0.4170
1T	0.2300	0.3430
1U	0.0020	0.2200
1V	0.4610	0.4300
1W	0.4200	0.4200
1X	0.5060	0.4250
1Y	0.2750	0.3430
1Z	0.5740	0.4340
1a	0.5880	0.4480
1b	0.4780	0.4270
1c	0.3100	0.3700
1d	0.4660	0.4150
1e	0.5380	0.4350
1f	0.2250	0.3370
1g	0.1330	0.3280
1h	0.2770	0.3750

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Chain	Atom inclusion	Q-score
1i	0.0090	0.2600
1j	0.0000	0.2620
1k	0.0000	0.2080
1l	0.0550	0.2770
1m	0.1150	0.2940
1n	0.0290	0.2450
1o	0.0020	0.2220
1p	0.0430	0.3140
1q	0.6100	0.4560
1r	0.5980	0.4600
1s	0.2210	0.3810