



wwPDB EM Validation Summary Report ⓘ

Aug 5, 2026 – 10:39 AM EDT

PDB ID : 9OLF / pdb_00009olf
EMDB ID : EMD-70592
Title : Membrane-associated human mitoribosome in complex with TACO1
Authors : Wang, S.; Xiong, Y.; Zhang, Y.
Deposited on : 2025-05-12
Resolution : 2.46 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:

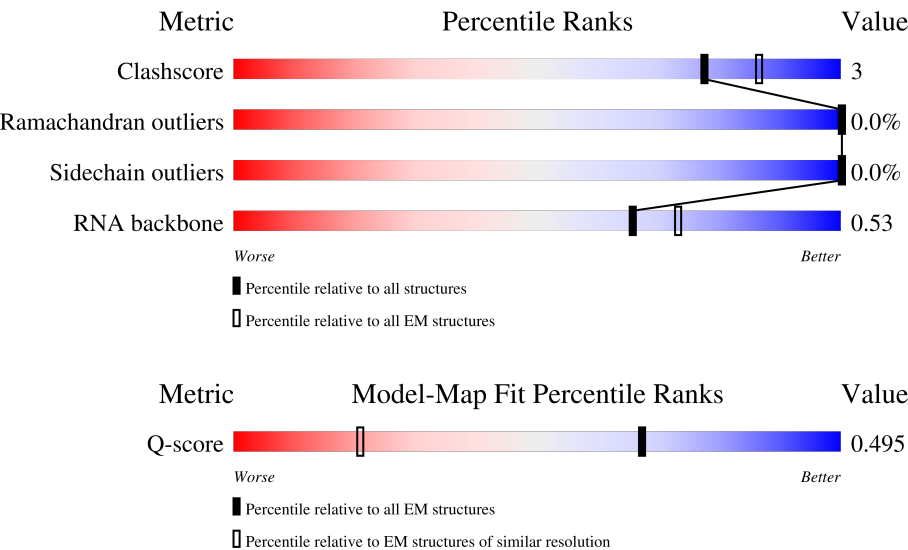
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

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 2.46 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.



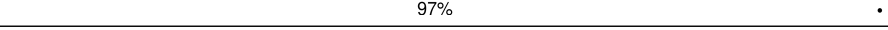
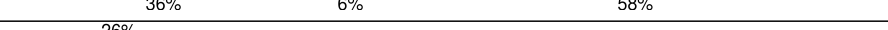
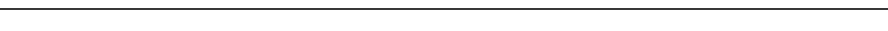
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	6014 (1.96 - 2.96)

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	0	188	57% 41%
2	1	65	75% 11% 14%
3	2	92	49% 50%

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Mol	Chain	Length	Quality of chain
4	3	188	
5	4	103	
6	5	423	
7	6	380	
8	7	338	
9	8	206	
10	9	137	
11	A	1558	
12	A0	217	
13	A1	323	
14	A2	118	
15	A3	199	
16	A4	689	
17	A5	1394	
18	A6	109	
19	AA	954	
20	AB	296	
21	AC	167	
22	AD	430	
23	AE	125	
24	AF	242	
25	AG	396	
26	AH	201	
27	AI	194	
28	AJ	138	

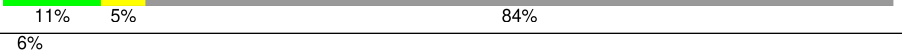
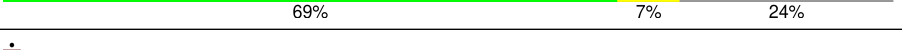
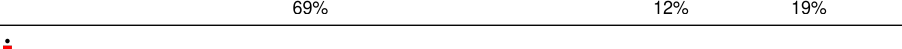
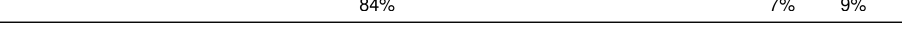
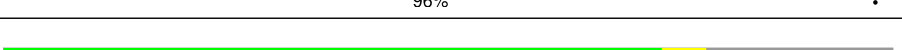
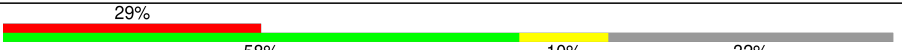
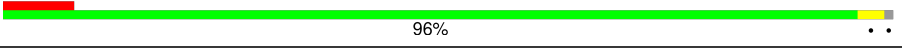
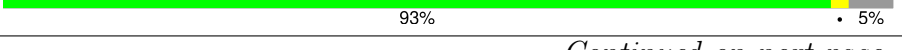
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Mol	Chain	Length	Quality of chain
29	AK	128	
30	AL	257	
31	AM	137	
32	AN	130	
33	AO	258	
34	AP	142	
35	AQ	87	
36	AR	360	
37	AS	190	
38	AT	173	
39	AU	205	
40	AV	414	
41	AW	187	
42	AX	398	
43	AY	395	
44	AZ	106	
45	Aw	76	
46	Ax	71	
47	Ay	76	
48	Az	34	
49	B	72	
50	C	297	
51	D	305	
52	E	348	
53	F	311	

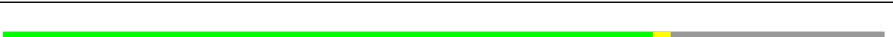
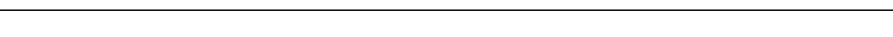
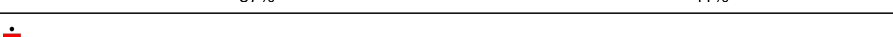
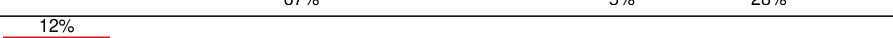
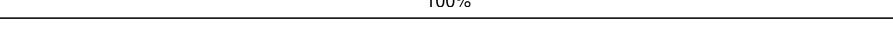
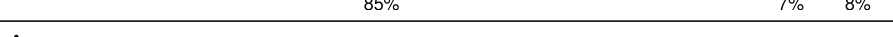
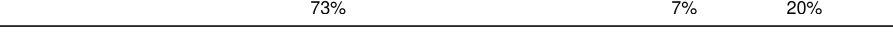
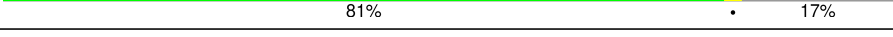
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Mol	Chain	Length	Quality of chain
54	G	198	
54	t	198	
54	u	198	
54	v	198	
54	w	198	
54	x	198	
54	y	198	
55	H	267	
56	I	261	
57	J	192	
58	K	178	
59	L	145	
60	M	296	
61	N	251	
62	O	175	
63	OX	435	
64	P	180	
65	Q	292	
66	R	149	
67	S	205	
68	T	206	
69	U	153	
70	V	216	
71	W	148	
72	X	256	

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Mol	Chain	Length	Quality of chain
73	Y	250	
74	Z	161	
75	a	142	
76	b	215	
77	c	332	
78	d	306	
79	e	279	
80	f	212	
81	g	166	
82	h	158	
83	i	128	
84	j	123	
85	k	112	
86	l	138	
87	m	128	
88	n	43	
89	o	102	
90	p	206	
91	q	222	
92	r	196	
93	s	439	
94	z	325	

2 Entry composition

There are 105 unique types of molecules in this entry. The entry contains 192936 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 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	110	Total	C	N	O	S	0	0
			898	554	176	162	6		

- Molecule 2 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	56	Total	C	N	O	S	0	0
			464	296	89	77	2		

- Molecule 3 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	233	83	60	1		

- Molecule 4 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	95	Total	C	N	O	S	0	0
			832	539	162	128	3		

- Molecule 5 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			342	217	72	49	4		

- Molecule 6 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	394	Total	C	N	O	S	0	0
			3210	2073	560	566	11		

- Molecule 7 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	354	Total	C	N	O	S	0	0
			2948	1881	525	533	9		

- Molecule 8 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	294	Total	C	N	O	S	0	0
			2390	1529	405	438	18		

- Molecule 9 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	157	Total	C	N	O	S	0	0
			1327	844	235	246	2		

- Molecule 10 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	9	124	Total	C	N	O	S	0	0
			997	644	170	181	2		

- Molecule 11 is a RNA chain called 16S mitochondrial rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A	1558	Total	C	N	O	P	0	0
			33070	14843	5963	10706	1558		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	A	deletion	GB 2756414513
A	?	-	C	deletion	GB 2756414513
A	?	-	U	deletion	GB 2756414513

- Molecule 12 is a protein called Small ribosomal subunit protein mS34.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	A0	215	Total	C	N	O	S	0	0
			1787	1130	339	313	5		

- Molecule 13 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A1	279	Total	C	N	O	S	0	0
			2265	1435	387	432	11		

- Molecule 14 is a protein called Small ribosomal subunit protein mS37.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	A2	118	Total	C	N	O	S	0	0
			935	579	182	166	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A2	1	ACE	-	acetylation	UNP Q96BP2

- Molecule 15 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	A3	70	Total	C	N	O	S	0	0
			625	401	134	89	1		

- Molecule 16 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	A4	588	Total	C	N	O	S	0	0
			4768	3053	808	879	28		

- Molecule 17 is a protein called Leucine-rich PPR motif-containing protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	A5	581	Total	C	N	O	S	0	0
			4646	2959	790	871	26		

- Molecule 18 is a protein called SRA stem-loop-interacting RNA-binding protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	A6	74	Total	C	N	O	S	0	0
			603	384	115	103	1		

- Molecule 19 is a RNA chain called 12S mitochondrial rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AA	954	Total	C	N	O	P	0	0
			20260	9088	3647	6571	954		

- Molecule 20 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AB	225	Total	C	N	O	S	0	0
			1828	1164	331	323	10		

- Molecule 21 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AC	132	Total	C	N	O	S	0	0
			1083	699	195	185	4		

- Molecule 22 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AD	343	Total	C	N	O	S	0	0
			2731	1713	518	487	13		

- Molecule 23 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AE	122	Total	C	N	O	S	0	0
			972	614	177	177	4		

- Molecule 24 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AF	208	Total	C	N	O	S	0	0
			1725	1104	312	298	11		

- Molecule 25 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AG	327	Total	C	N	O	S	0	0
			2688	1710	477	487	14		

- Molecule 26 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AH	140	Total	C	N	O	S	0	0
			1152	745	194	210	3		

- Molecule 27 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AI	137	Total	C	N	O	S	0	0
			1019	641	193	181	4		

- Molecule 28 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AJ	108	Total	C	N	O	S	0	0
			839	521	169	143	6		

- Molecule 29 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AK	101	Total	C	N	O	S	0	0
			862	537	179	141	5		

- Molecule 30 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AL	174	Total	C	N	O	S	0	0
			1453	925	270	251	7		

- Molecule 31 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AM	119	Total	C	N	O	S	0	0
			942	594	185	157	6		

- Molecule 32 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AN	110	Total	C	N	O	S	0	0
			868	562	156	147	3		

- Molecule 33 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AO	193	Total	C	N	O	S	0	0
			1592	1014	294	277	7		

- Molecule 34 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AP	97	Total	C	N	O	S	0	0
			781	501	134	138	8		

- Molecule 35 is a protein called Small ribosomal subunit protein bS21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AQ	87	Total	C	N	O	S	0	0
			744	460	150	126	8		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AQ	1	ACE	-	acetylation	UNP P82921
AQ	50	ARG	CYS	variant	UNP P82921

- Molecule 36 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AR	295	Total	C	N	O	S	0	0
			2409	1533	413	455	8		

- Molecule 37 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AS	135	Total	C	N	O	S	0	0
			1111	716	198	196	1		

- Molecule 38 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	AT	168	Total	C	N	O	S	0	0
			1371	877	239	244	11		

- Molecule 39 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	AU	176	Total	C	N	O	S	0	0
			1488	916	301	267	4		

- Molecule 40 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	AV	362	Total	C	N	O	S	0	0
			2969	1904	495	558	12		

- Molecule 41 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AW	100	Total	C	N	O	S	0	0
			789	498	141	146	4		

- Molecule 42 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AX	352	Total	C	N	O	S	0	0
			2849	1822	499	517	11		

- Molecule 43 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AY	221	Total	C	N	O	S	0	0
			1835	1159	319	352	5		

- Molecule 44 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AZ	100	Total	C	N	O	S	0	0
			839	534	153	148	4		

- Molecule 45 is a RNA chain called A/A-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Aw	68	Total	C	N	O	P	0	0
			1434	646	248	472	68		

- Molecule 46 is a RNA chain called P/P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ax	71	Total	C	N	O	P	0	0
			1498	673	264	491	70		

- Molecule 47 is a RNA chain called E/E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ay	70	Total	C	N	O	P	0	0
			1483	665	261	487	70		

- Molecule 48 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Az	34	Total	C	N	O	P	0	0
			719	324	123	238	34		

- Molecule 49 is a RNA chain called RNA (73-MER)mitochondrial tRNAVal.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	B	72	Total	C	N	O	P	0	0
			1524	685	269	498	72		

- Molecule 50 is a protein called Translational activator of cytochrome c oxidase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	C	223	Total	C	N	O	S	0	0
			1732	1072	310	340	10		

- Molecule 51 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	D	238	Total	C	N	O	S	0	0
			1859	1157	376	317	9		

- Molecule 52 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	E	305	Total	C	N	O	S	0	0
			2406	1545	418	432	11		

- Molecule 53 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	F	252	Total	C	N	O	S	0	0
			2031	1305	370	350	6		

- Molecule 54 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	G	72	Total	C	N	O		0	0
			558	358	97	103			
54	t	46	Total	C	N	O		0	0
			354	228	56	70			
54	u	32	Total	C	N	O		0	0
			257	168	40	49			
54	v	32	Total	C	N	O		0	0
			257	168	40	49			
54	w	31	Total	C	N	O		0	0
			245	159	39	47			
54	x	31	Total	C	N	O		0	0
			245	159	39	47			
54	y	31	Total	C	N	O		0	0
			245	159	39	47			

- Molecule 55 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	H	202	Total	C	N	O	S	0	0
			1661	1067	304	286	4		

- Molecule 56 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	I	212	Total	C	N	O	S	0	0
			1695	1088	304	292	11		

- Molecule 57 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	J	175	Total	C	N	O	S	0	0
			1330	847	237	244	2		

- Molecule 58 is a protein called Large ribosomal subunit protein uL13m.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	K	178	Total	C	N	O	S	0	0
			1455	936	259	253	7		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	1	ACE	-	acetylation	UNP H2QWN0
K	132	TYR	ASP	conflict	UNP H2QWN0

- Molecule 59 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	L	115	Total	C	N	O	S	0	0
			890	559	171	155	5		

- Molecule 60 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	M	291	Total	C	N	O	S	0	0
			2327	1483	430	408	6		

- Molecule 61 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	N	222	Total	C	N	O	S	0	0
			1786	1143	326	307	10		

- Molecule 62 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	O	154	Total	C	N	O	S	0	0
			1259	792	241	219	7		

- Molecule 63 is a protein called Mitochondrial inner membrane protein OXA1L.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	OX	297	Total	C	N	O	S	0	0
			2404	1568	417	405	14		

- Molecule 64 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	P	144	Total	C	N	O	S	0	0
			1173	733	224	211	5		

- Molecule 65 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Q	239	Total	C	N	O	S	0	0
			1990	1277	353	351	9		

- Molecule 66 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	R	140	Total	C	N	O	S	0	0
			1154	732	231	187	4		

- Molecule 67 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	S	161	Total	C	N	O	S	0	0
			1293	835	227	227	4		

- Molecule 68 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	T	166	Total	C	N	O	S	0	0
			1369	875	254	233	7		

- Molecule 69 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	U	152	Total	C	N	O	S	0	0
			1248	786	234	225	3		

- Molecule 70 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	V	205	Total	C	N	O	S	0	0
			1676	1068	298	302	8		

- Molecule 71 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	W	116	Total	C	N	O	S	0	0
			904	577	171	153	3		

- Molecule 72 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	X	244	Total	C	N	O	S	0	0
			2044	1322	352	365	5		

- Molecule 73 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Y	181	Total	C	N	O	S	0	0
			1556	995	298	259	4		

- Molecule 74 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Z	122	Total	C	N	O	S	0	0
			996	636	186	171	3		

- Molecule 75 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	a	103	Total	C	N	O	S	0	0
			865	543	155	162	5		

- Molecule 76 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	b	150	Total	C	N	O	S	0	0
			1193	742	231	217	3		

- Molecule 77 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	c	286	Total	C	N	O	S	0	0
			2299	1470	397	423	9		

- Molecule 78 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	d	259	Total	C	N	O	S	0	0
			2124	1357	369	384	14		

- Molecule 79 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	e	238	Total	C	N	O	S	0	0
			1931	1222	339	364	6		

- Molecule 80 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	f	157	Total	C	N	O	S	0	0
			1252	799	207	242	4		

- Molecule 81 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	g	134	Total	C	N	O	S	0	0
			1113	719	193	199	2		

- Molecule 82 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	h	110	Total	C	N	O	S	0	0
			895	568	156	168	3		

- Molecule 83 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	i	97	Total	C	N	O	S	0	0
			828	532	165	127	4		

- Molecule 84 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	j	94	Total	C	N	O	S	0	0
			745	463	144	136	2		

- Molecule 85 is a protein called Large ribosomal subunit protein mL53.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	k	102	Total	C	N	O	S	0	0
			774	479	148	142	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	1	ACE	-	acetylation	UNP Q96EL3

- Molecule 86 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	l	82	Total	C	N	O	S	0	0
			688	437	120	128	3		

- Molecule 87 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	m	92	Total	C	N	O	S	0	0
			791	488	159	142	2		

- Molecule 88 is a protein called Nascent polypeptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
88	n	43	Total	C	N	O	0	0
			215	129	43	43		

- Molecule 89 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	o	94	Total	C	N	O	S	0	0
			798	501	165	129	3		

- Molecule 90 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	p	147	Total	C	N	O	S	0	0
			1205	748	228	225	4		

- Molecule 91 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	q	177	Total	C	N	O	S	0	0
			1495	929	292	269	5		

- Molecule 92 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
92	r	162	Total	C	N	O	S	0	0
			1322	839	252	223	8		

- Molecule 93 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
93	s	385	Total	C	N	O	S	0	0
			3148	2018	558	558	14		

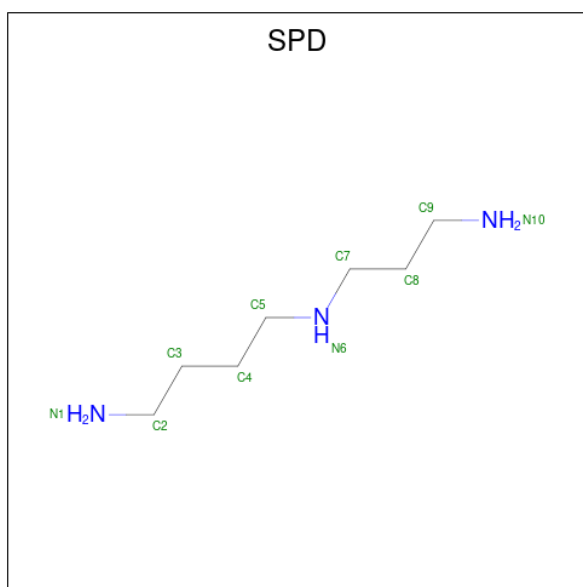
- Molecule 94 is a protein called Large ribosomal subunit protein uL1m.

Mol	Chain	Residues	Atoms					AltConf	Trace
94	z	252	Total	C	N	O	S	0	0
			2027	1304	336	381	6		

- Molecule 95 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
95	0	1	Total	Zn	0
			1	1	
95	4	1	Total	Zn	0
			1	1	
95	AO	1	Total	Zn	0
			1	1	

- Molecule 96 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
96	A	1	Total	C	N	0
			10	7	3	
96	A	1	Total	C	N	0
			10	7	3	
96	A	1	Total	C	N	0
			10	7	3	
96	A	1	Total	C	N	0
			10	7	3	
96	AA	1	Total	C	N	0
			10	7	3	
96	AA	1	Total	C	N	0
			10	7	3	
96	O	1	Total	C	N	0
			10	7	3	

- Molecule 97 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

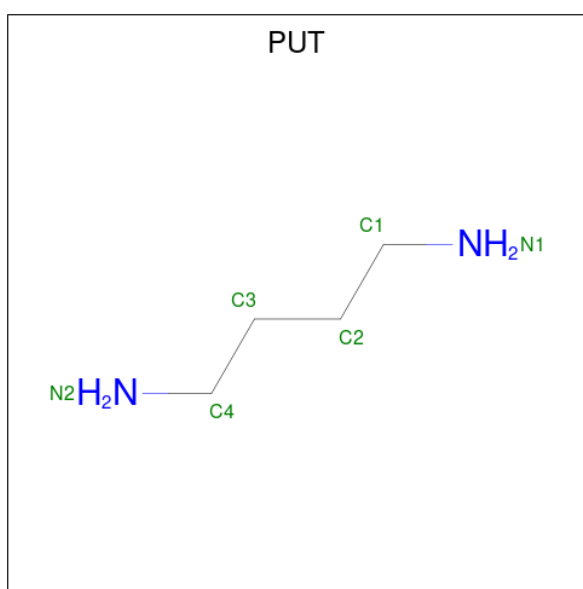
Mol	Chain	Residues	Atoms		AltConf
97	A	137	Total	Mg	0
			137	137	
97	A3	1	Total	Mg	0
			1	1	
97	AA	60	Total	Mg	0
			60	60	
97	AB	1	Total	Mg	0
			1	1	
97	AX	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
97	Az	1	Total	Mg	0
			1	1	
97	D	2	Total	Mg	0
			2	2	
97	E	1	Total	Mg	0
			1	1	
97	g	1	Total	Mg	0
			1	1	

- Molecule 98 is 1,4-DIAMINO BUTANE (CCD ID: PUT) (formula: $C_4H_{12}N_2$).



Mol	Chain	Residues	Atoms			AltConf
98	A	1	Total	C	N	0
			6	4	2	

- Molecule 99 is POTASSIUM ION (CCD ID: K) (formula: K).

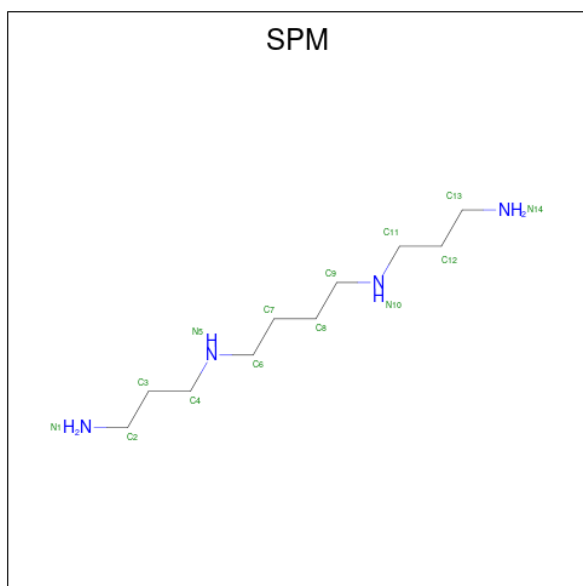
Mol	Chain	Residues	Atoms		AltConf
99	A	29	Total	K	0
			29	29	
99	AA	18	Total	K	0
			18	18	
99	D	1	Total	K	0
			1	1	
99	M	2	Total	K	0
			2	2	

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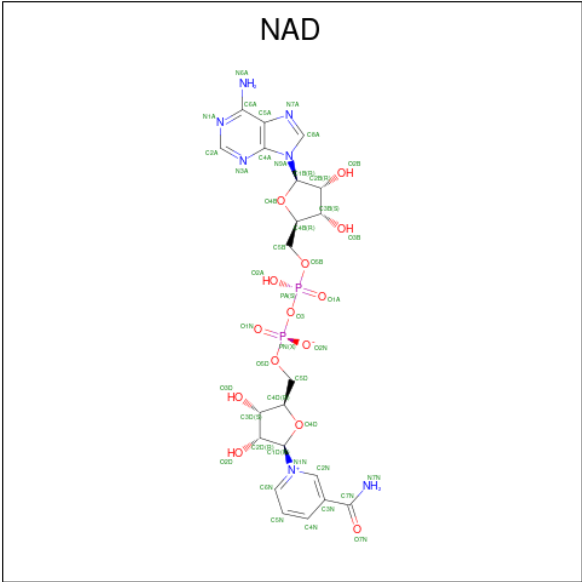
Mol	Chain	Residues	Atoms		AltConf
99	N	1	Total	K	0
			1	1	
99	P	1	Total	K	0
			1	1	
99	W	1	Total	K	0
			1	1	
99	o	1	Total	K	0
			1	1	

- Molecule 100 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$) (labeled as "Ligand of Interest" by depositor).



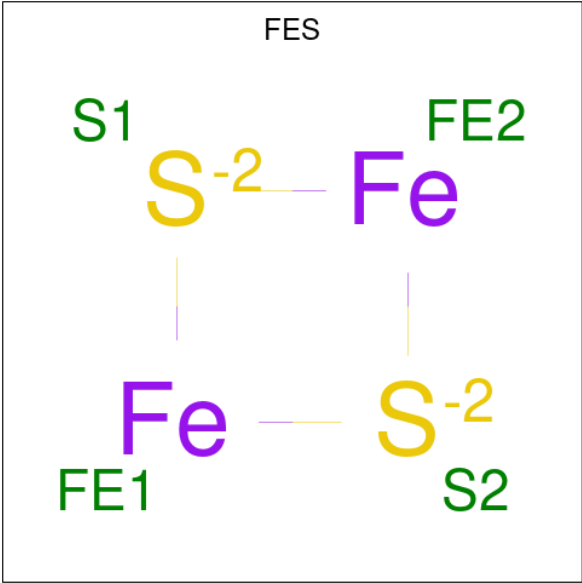
Mol	Chain	Residues	Atoms			AltConf
100	AA	1	Total	C	N	0
			14	10	4	
100	AA	1	Total	C	N	0
			14	10	4	

- Molecule 101 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
101	AA	1	Total	C	N	O	P	0
			44	21	7	14	2	

- Molecule 102 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂) (labeled as "Ligand of Interest" by depositor).



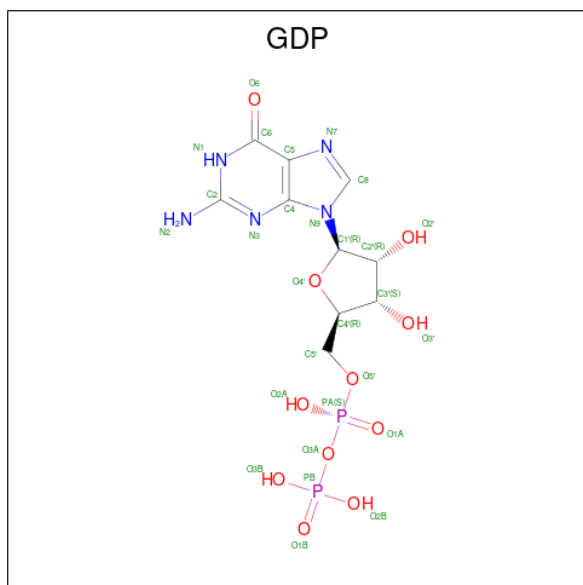
Mol	Chain	Residues	Atoms			AltConf
102	AP	1	Total	Fe	S	0
			4	2	2	
102	AT	1	Total	Fe	S	0
			4	2	2	

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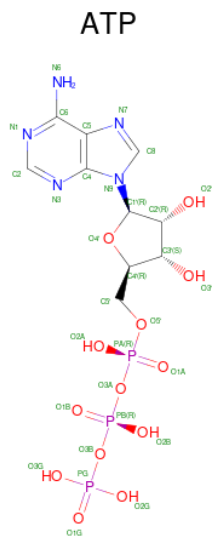
Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
102	r	1	4	2	2	0

- Molecule 103 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$) (labeled as "Ligand of Interest" by depositor).



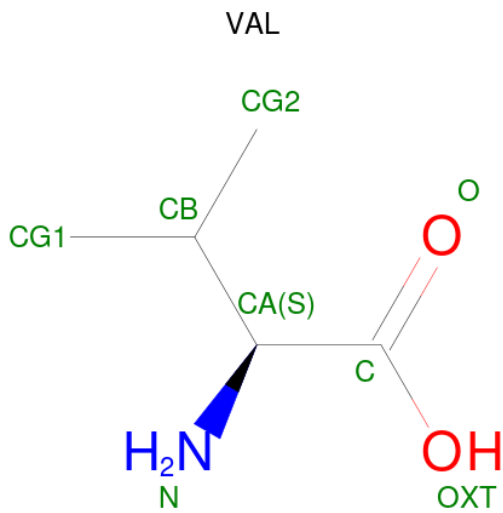
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
103	AX	1	28	10	5	11	2	0

- Molecule 104 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
104	AX	1	Total 31	C 10	N 5	O 13	P 3	0

- Molecule 105 is VALINE (CCD ID: VAL) (formula: $\text{C}_5\text{H}_{11}\text{NO}_2$).

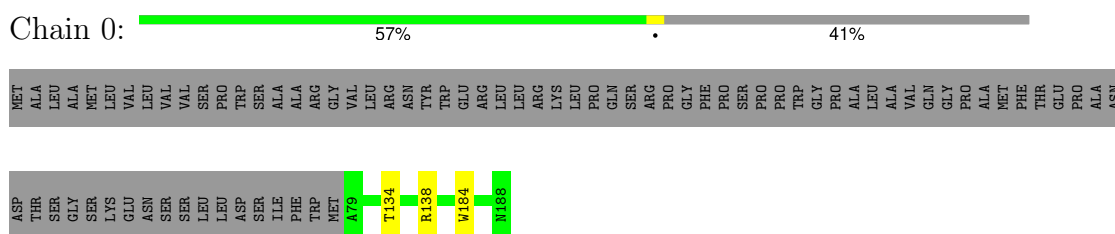


Mol	Chain	Residues	Atoms				AltConf
105	B	1	Total	C	N	O	0
			7	5	1	1	

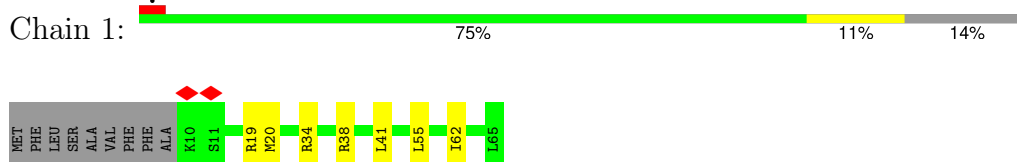
3 Residue-property plots [i](#)

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.

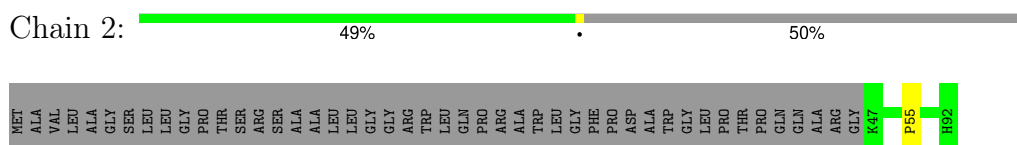
- Molecule 1: 39S ribosomal protein L32, mitochondrial



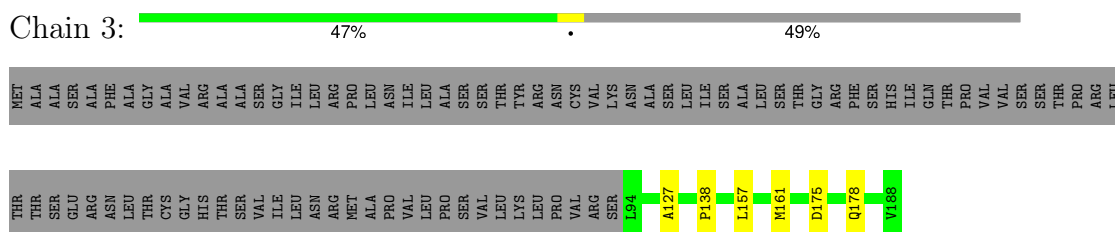
- Molecule 2: 39S ribosomal protein L33, mitochondrial



- Molecule 3: 39S ribosomal protein L34, mitochondrial



- Molecule 4: 39S ribosomal protein L35, mitochondrial



- Molecule 5: 39S ribosomal protein L36, mitochondrial



MET ALA ASN PHE ILE ARG LYS MET VAL ASN PRO LEU LEU TYR SER ARG HIS THR VAL LYS PRO ARG ALA LEU SER ARG PHE LEU PHE GLY SER ILE ARG GLY ALA ALA PRO VAL VAL GLU PRO GLY ALA VAL ARG SER LEU SER PRO GLY LEU LEU HIS LEU PRO HIS LEU

LEU PRO ALA LEU GLY F66 K69 L72 M103

- Molecule 6: 39S ribosomal protein L37, mitochondrial

Chain 5:  88% 5% 7%

MET ALA LEU ALA SER GLY PRO ALA ARG ARG ALA LEU ALA GLY SER GLY GLN LEU LEU GLY LEU GLY PHE PRO GLY ALA PRO ARG ARG GLY A30 P91 H96 P97 L98 E115 Q119 I129 P143 H146 Q165 T166 T167 T175 V179 R201 V204 T232

D272 L336 T362 L373 E409 R412 A423

- Molecule 7: 39S ribosomal protein L38, mitochondrial

Chain 6:  89% 7% 7%

MET ALA PRO TRP TRP ARG ALA ALA LEU CYS CYS ARG ARG TRP TRP ARG GLY R27 R106 V175 V187 V204 L217 H224 E227 H234 V235 L236 L255 P256 P257 F319 V327 I330 Y380

- Molecule 8: 39S ribosomal protein L39, mitochondrial

Chain 7:  80% 7% 13%

MET GLU ALA LEU ALA MET GLY SER ARG ALA LEU ARG LEU TRP LEU VAL ALA PRO GLY GLY ILE LYS TRP ARG PHE ILE ALA THR SER SER ALA SER Q34 P112 V113 D114 K117 N139 W143 R156 L166 V172 F173 V174 Y181 K204 F260 P267

L268 L269 L274 C275 F276 L286 E296 L302 P303 V304 H309 K315 L316 L317 D327 GLN SER LYS ALA THR GLU CYS THR SER THR

- Molecule 9: 39S ribosomal protein L40, mitochondrial

Chain 8:  69% 7% 24%

MET THR ALA SER VAL ARG ARG ILE SER LEU ALA LEU ARG PRO THR SER GLY LEU GLY THR TRP GLN THR GLN LEU ARG GLU THR HIS GLN ARG ALA SER LEU SER SER TRP PHE GLU ILE PRO MET ARG S47 K53 K54 L68 R99 L117 R129 R133

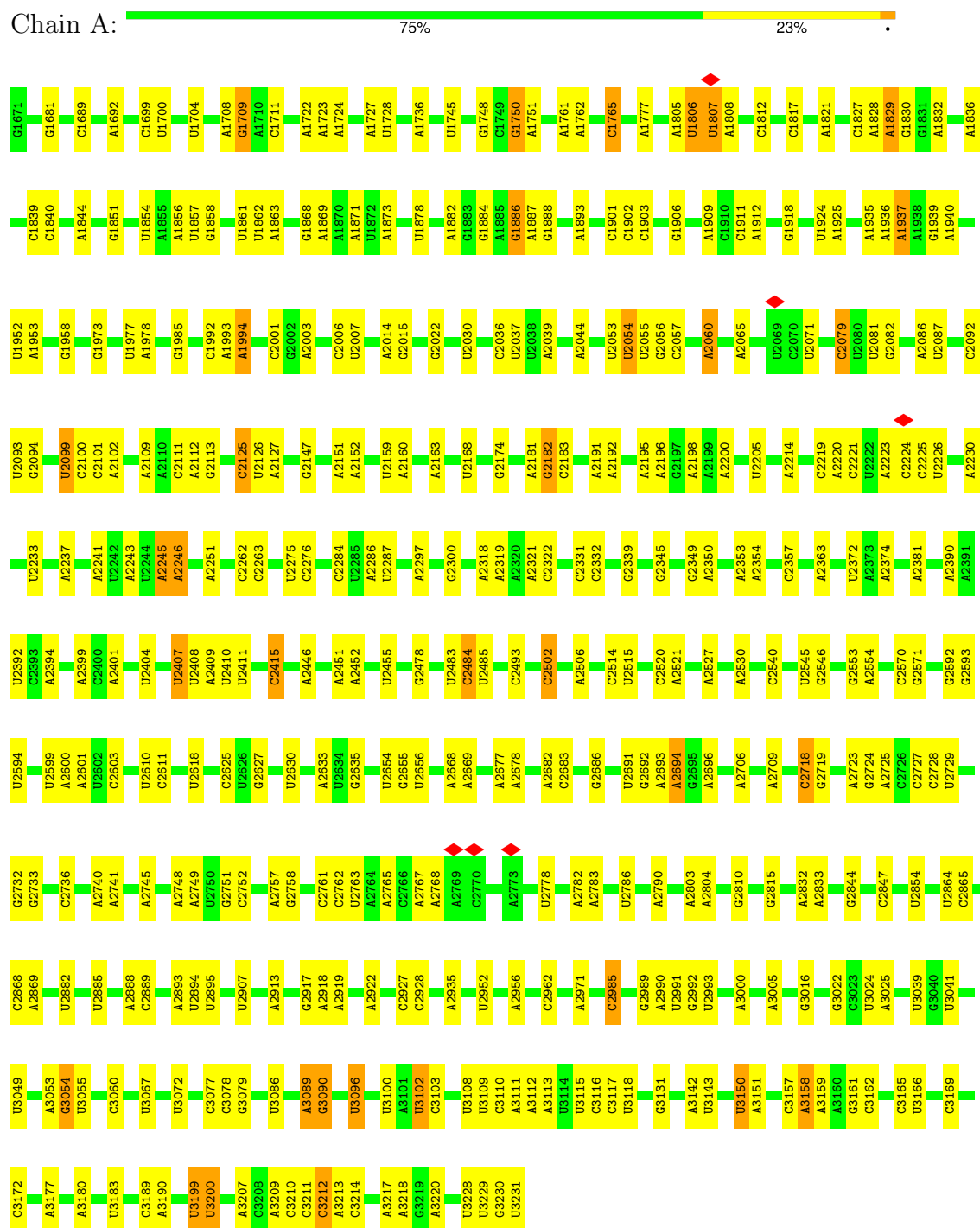
I136 E160 K163 R164 P170 K173 P187 Y192 Q201 V202 E203 PHE LYS ARG

- Molecule 10: 39S ribosomal protein L41, mitochondrial

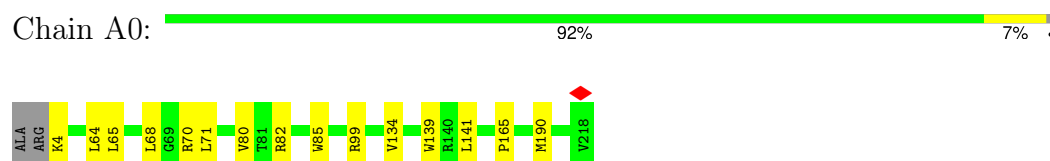
Chain 9:  86% 9% 9%

MET GLY VAL LEU ALA ALA ALA ARG CYS LEU VAL ARG G14 R36 F68 K69 L70 L86 L91 G118 R137

• Molecule 11: 16S mitochondrial rRNA



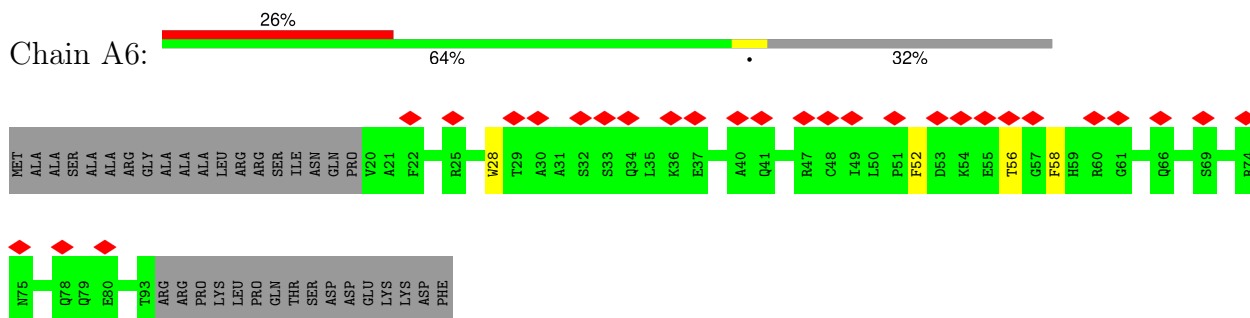
• Molecule 12: Small ribosomal subunit protein mS34



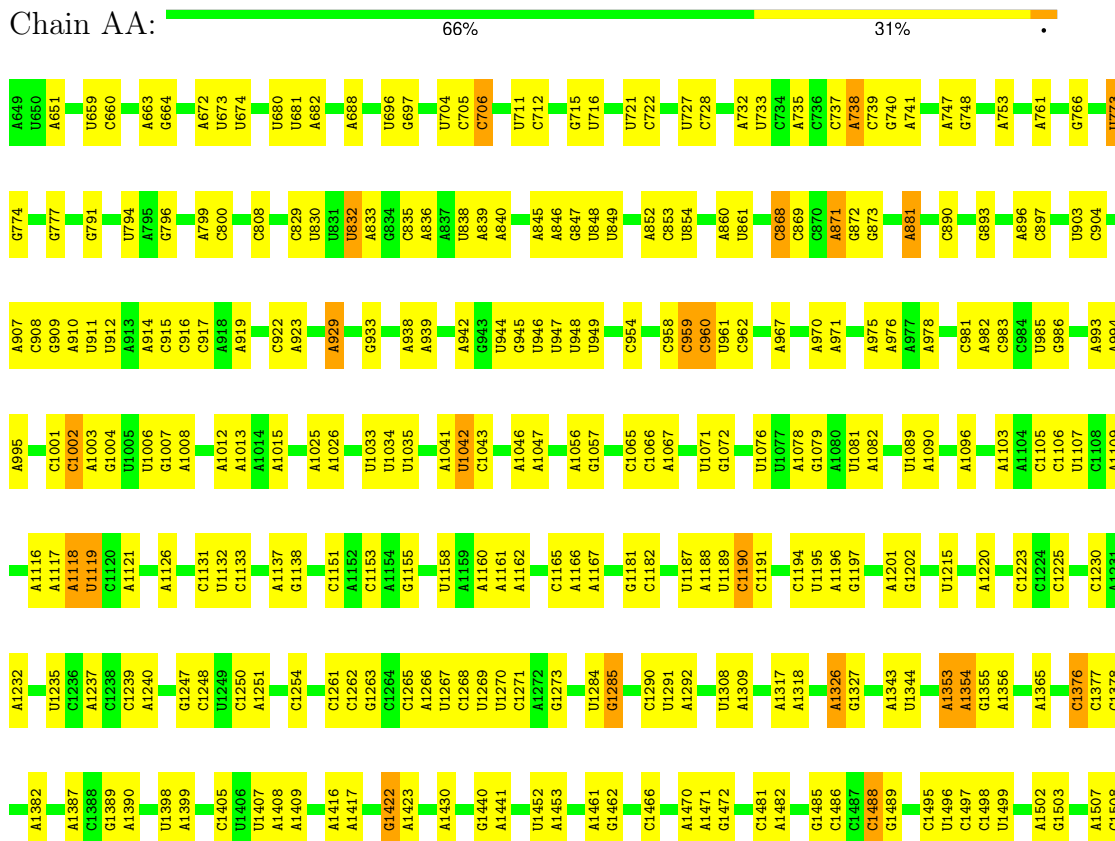
Chain A5:



- Molecule 18: SRA stem-loop-interacting RNA-binding protein, mitochondrial



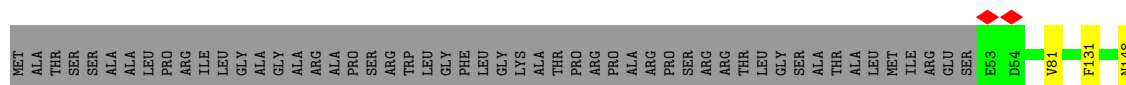
- Molecule 19: 12S mitochondrial rRNA





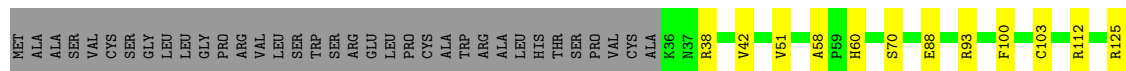
- Molecule 20: 28S ribosomal protein S2, mitochondrial

Chain AB: 72% 24%



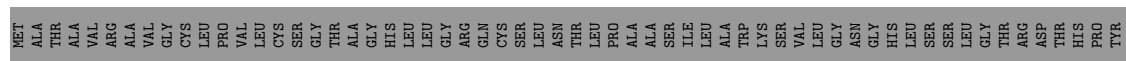
- Molecule 21: 28S ribosomal protein S24, mitochondrial

Chain AC: 69% 10% 21%



- Molecule 22: 28S ribosomal protein S5, mitochondrial

Chain AD: 75% 5% 20%



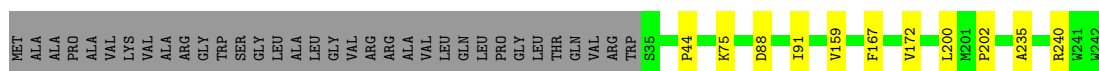
- Molecule 23: 28S ribosomal protein S6, mitochondrial

Chain AE: 91% 6%

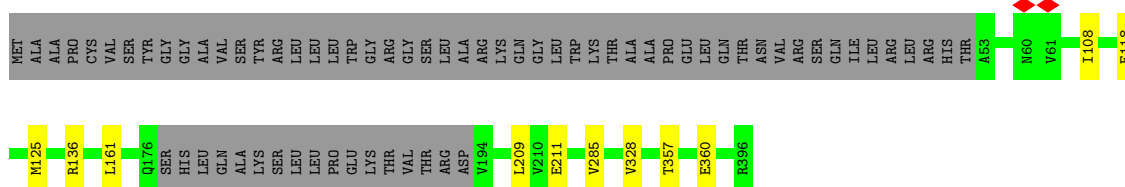
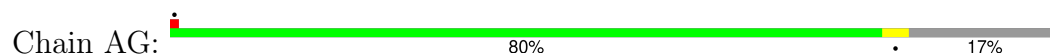


- Molecule 24: 28S ribosomal protein S7, mitochondrial

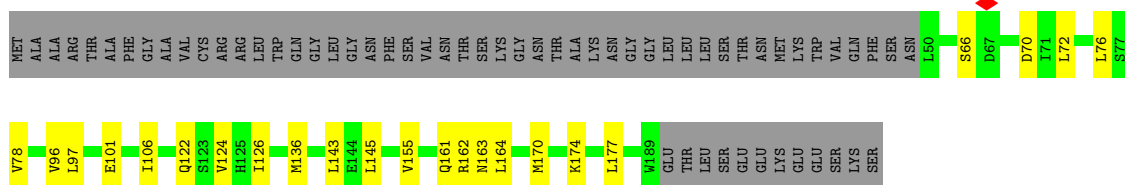
Chain AF: 81% 5% 14%



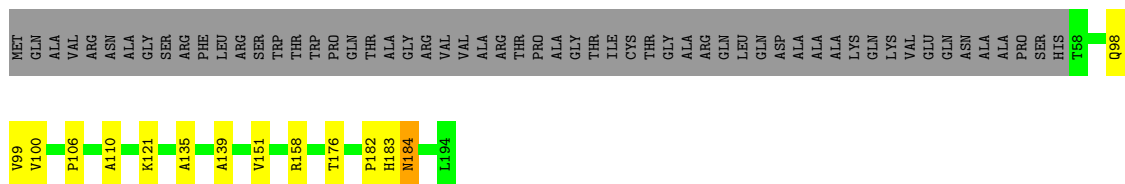
- Molecule 25: 28S ribosomal protein S9, mitochondrial



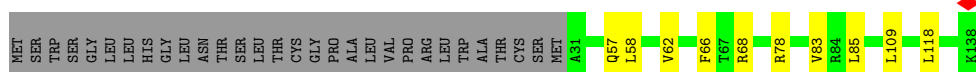
- Molecule 26: 28S ribosomal protein S10, mitochondrial



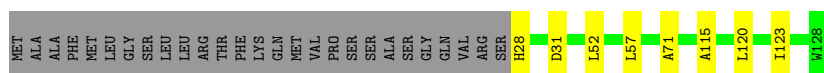
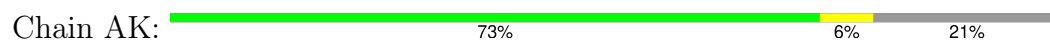
- Molecule 27: 28S ribosomal protein S11, mitochondrial



- Molecule 28: 28S ribosomal protein S12, mitochondrial



- Molecule 29: 28S ribosomal protein S14, mitochondrial



- Molecule 30: 28S ribosomal protein S15, mitochondrial

Chain AL:  65% 32%

MET LEU ARG VAL ALA TRP ARG THR LEU SER LEU ILE ARG THR ARG ALA VAL THR GLN VAL LEU VAL ARG PRO GLY LEU PRO PRO GLY GLY GLY SER SER ALA LYS PHE PHE ASN GLN TRP GLY LEU GLN PRO ARG SER LEU LEU LEU GLN ALA ALA ARG GLY TYR VAL VAL ARG LYS PRO ALA GLN

SER ARG L63 H97 L143 K153 K165 Y175 K206 L209 Q236 ALA LYS ARG ARG ASN PRO ASP SER PRO GLY ALA LYS ILE PHE PRO LYS THR LEU LYS ASP SER SER GLN

- Molecule 31: 28S ribosomal protein S16, mitochondrial

Chain AM:  75% 12% 13%

MET VAL HIS LEU THR THR LEU LEU CYS K10 R20 L21 R29 Y32 R33 I34 Y54 K64 L65 V66 I73 I77 M87 L93 R114 A115 R116 E117 V118 D126 A127 E128 ALA THR ASP THR GLU ALA THR GLU THR

- Molecule 32: 28S ribosomal protein S17, mitochondrial

Chain AN:  78% 6% 15%

MET SER VAL V4 R5 S6 I13 K21 Q57 L66 T84 Q89 Y95 T96 E113 THR THR GLN LEU SER LYS LEU LEU LEU GLU GLU LYS LEU LEU LEU ASN ILE SER SER ALA GLN

- Molecule 33: 28S ribosomal protein S18b, mitochondrial

Chain AO:  71% 25%

MET ALA ALA SER VAL LEU ASN THR VAL ARG LEU ARG ARG MET SER SER LEU PHE ARG GLY SER HIS ARG VAL GLN VAL VAL PRO LEU GLN THR LEU CYS LYS THR VAL TRP ARG ARG CYS ASP SER SER SER SER VAL P47 K62 C94 C105 C108 V142 A183

P208 L213 R217 P239 PRO ARG THR PRO PRO ALA GLU ALA SER SER THR GLY HIS LEU THR THR GLY GLN ALA LEU

- Molecule 34: 28S ribosomal protein S18c, mitochondrial

Chain AP:  65% 32%

MET ALA ALA VAL VAL ALA VAL CYS GLY GLY LEU LEU GLY ARG LYS LYS LEU THR HIS LEU VAL THR THR ALA PRO ALA VAL SER LEU THR THR HIS VAL TRP ARG ARG CYS SER GLN GLN VAL SER S46 M54 K63 K103 M117 Y124 E142

- Molecule 35: Small ribosomal subunit protein bS21m

Chain AQ:  94% 6%

ACE1 K6 A9 R10 T11 R42 C87

- Molecule 36: 28S ribosomal protein S22, mitochondrial

Chain AR:  77% 5% 18%

MET ALA PRO LEU GLY THR THR VAL LEU LEU TRP SER LEU ARG SER SER PRO GLY VAL GLU ARG VAL CYS PHE ARG ALA ARG ILE GLN LYS PRO TRP HIS GLY GLY LEU LEU GLN PRO CYS SER PHE GLU MET GLY LEU PRO ARG ARG ARG PHE SER SER SER GLU ALA ALA SER

GLY SER PRO E84 M62 M128 L142 K155 Y156 Y157 V174 P177 K183 Q194 K199 I204 P207 I208 I209 D254 F275 Q288 L300 A358 ALA SER

- Molecule 37: 28S ribosomal protein S23, mitochondrial

Chain AS:  67% 29%

MET A2 R48 V51 W64 L106 E120 R134 V135 G136 GLU ALA ARG THR GLN HIS GLY SER HIS VAL SER ARG LYS SER GLU HIS LEU SER VAL ARG PRO GLN THR ALA LEU GLU ASN GLU GLU THR GLN LYS VAL PRO GLN ASP ASP HIS LEU GLU ALA PRO

ALA ASP GLN SER LYS GLY LEU LEU PRO PRO

- Molecule 38: 28S ribosomal protein S25, mitochondrial

Chain AT:  93%

MET P2 L76 L80 E84 V88 I140 G161 K164 L167 K168 A169 ASP ALA GLN ASP

- Molecule 39: 28S ribosomal protein S26, mitochondrial

Chain AU:  84% 14%

MET LEU ARG ALA ALA SER ARG LEU GLY ALA ALA THR PRO CYS ARG PRO ARG ALA ALA LEU LEU PRO PRO ALA ARG ARG GLY E27 R64 V67 K183 F167 F202 ARG ASP SER

- Molecule 40: 28S ribosomal protein S27, mitochondrial

Chain AV:  79% 9% 13%

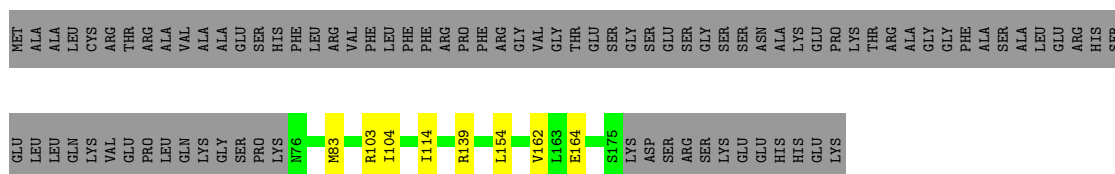
MET ALA ALA SER ILE VAL ARG ARG GLY MET LEU LEU ALA ALA ARG GLN VAL VAL LEU PRO GLN LEU LEU SER PRO PRO ALA ALA GLY LYS ARG TYR L29 P66 V67 S68 S69 L70 L76 R96 C101 V112 V113 R114 L117 D120 A121 Q122 M148 D149 I152 V163 V167

V175 P176 S177 V185 A206 Y228 A229 K233 K246 L249 A259 V262 M263 E264 K265 V286 A293 ASP GLY ALA SER V67 S68 S69 L70 L76 R96 C101 V112 V113 R114 L117 D120 A121 Q122 M148 D149 I152 V163 V167

LYS ALA ALA LYS LYS SER SER ALA

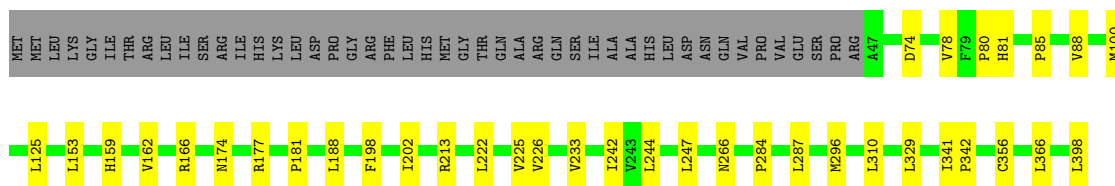
- Molecule 41: 28S ribosomal protein S28, mitochondrial

Chain AW:  49% 47%



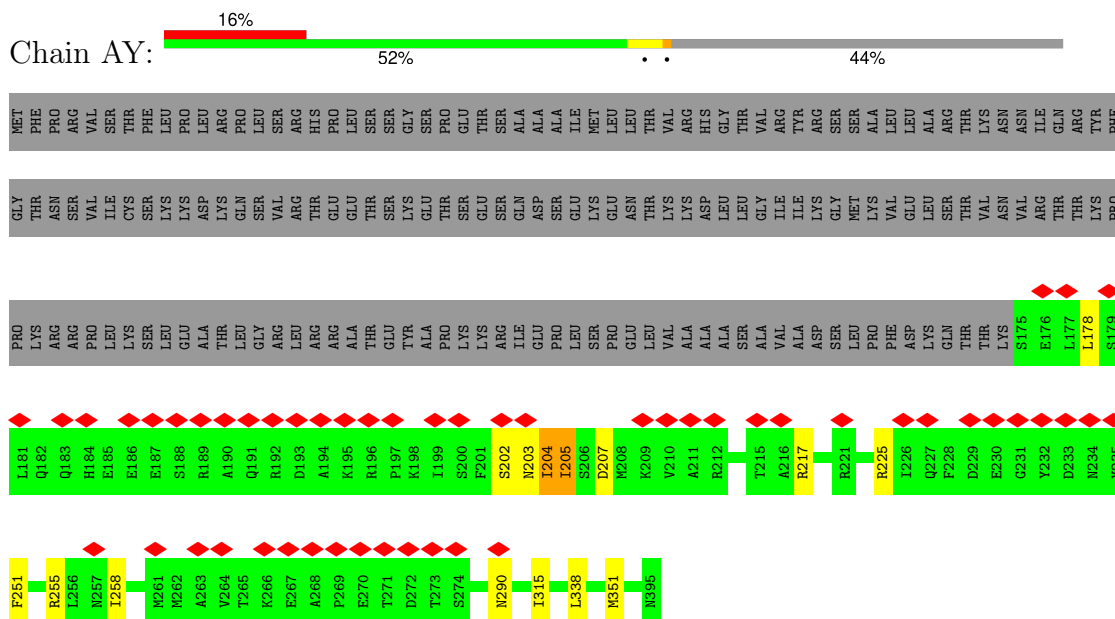
- Molecule 42: 28S ribosomal protein S29, mitochondrial

Chain AX:



- Molecule 43: 28S ribosomal protein S31, mitochondrial

Chain AY:



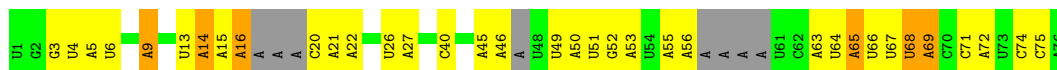
- Molecule 44: 28S ribosomal protein S33, mitochondrial

Chain AZ:



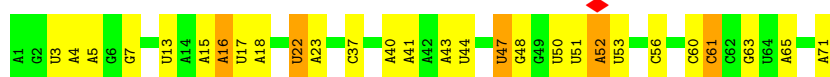
- Molecule 45: A/A-tRNA

Chain Aw:



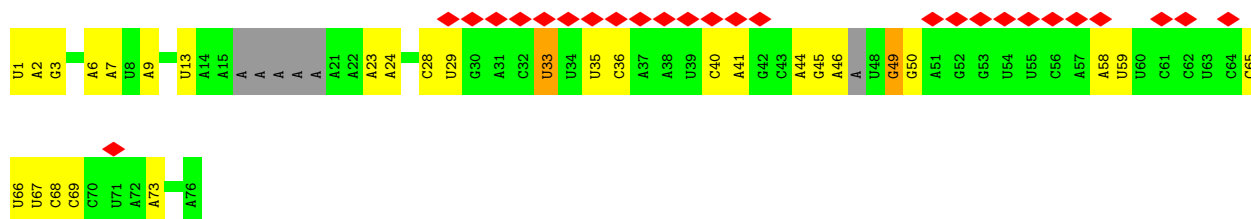
- Molecule 46: P/P-tRNA

Chain Ax: 



- Molecule 47: E/E-tRNA

Chain Ay: 



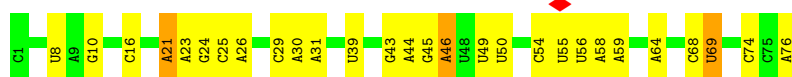
- Molecule 48: mRNA

Chain Az: 



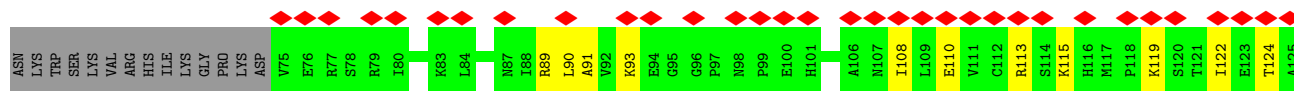
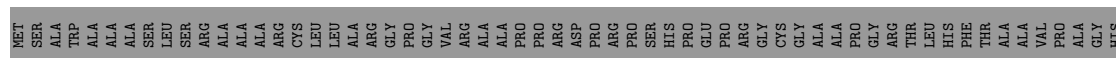
- Molecule 49: RNA (73-MER)mitochondrial tRNAVal

Chain B: 



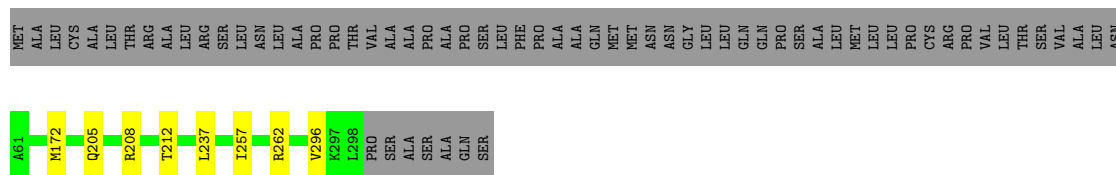
- Molecule 50: Translational activator of cytochrome c oxidase 1

Chain C: 



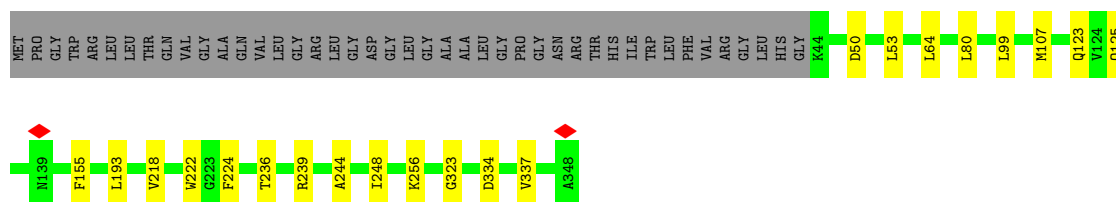
- Molecule 51: 39S ribosomal protein L2, mitochondrial

Chain D:  75% 22%



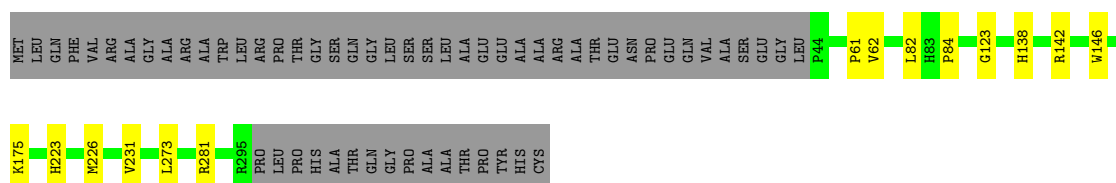
- Molecule 52: 39S ribosomal protein L3, mitochondrial

Chain E:  82% 6% 12%



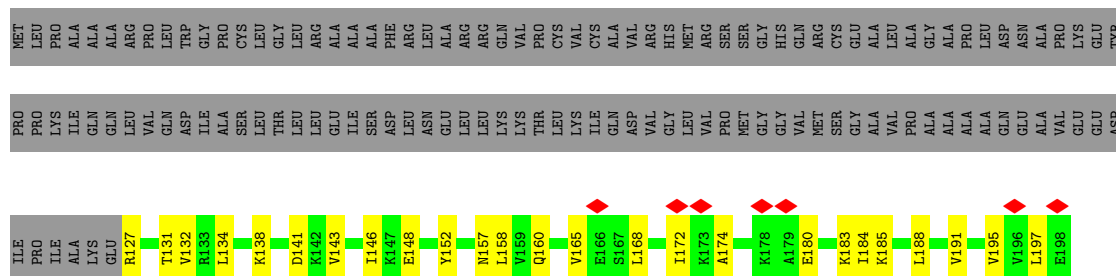
- Molecule 53: 39S ribosomal protein L4, mitochondrial

Chain F:  77% 5% 19%



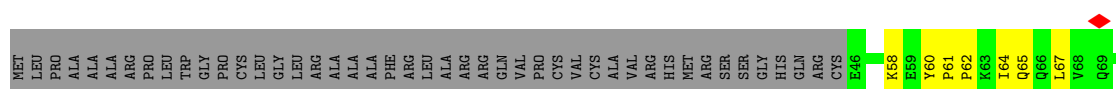
- Molecule 54: 39S ribosomal protein L12, mitochondrial

Chain G:  24% 13% 64%

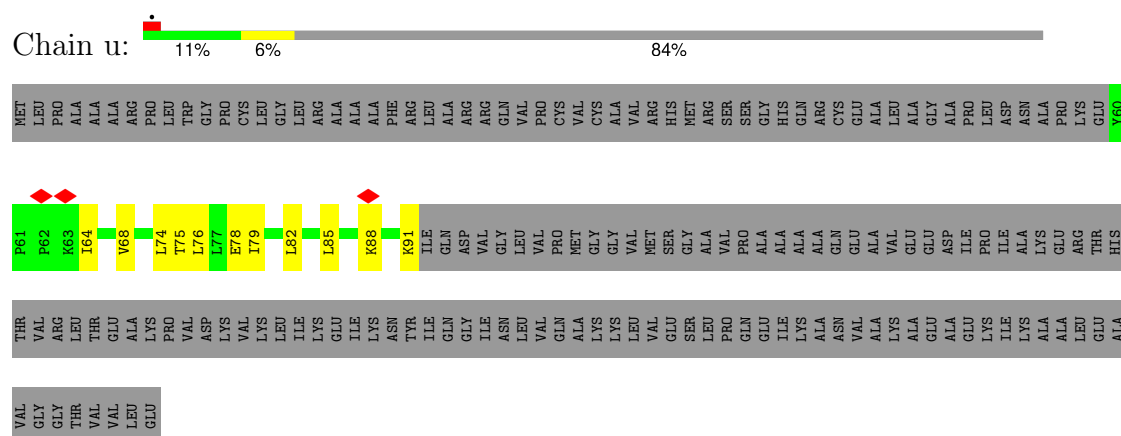


- Molecule 54: 39S ribosomal protein L12, mitochondrial

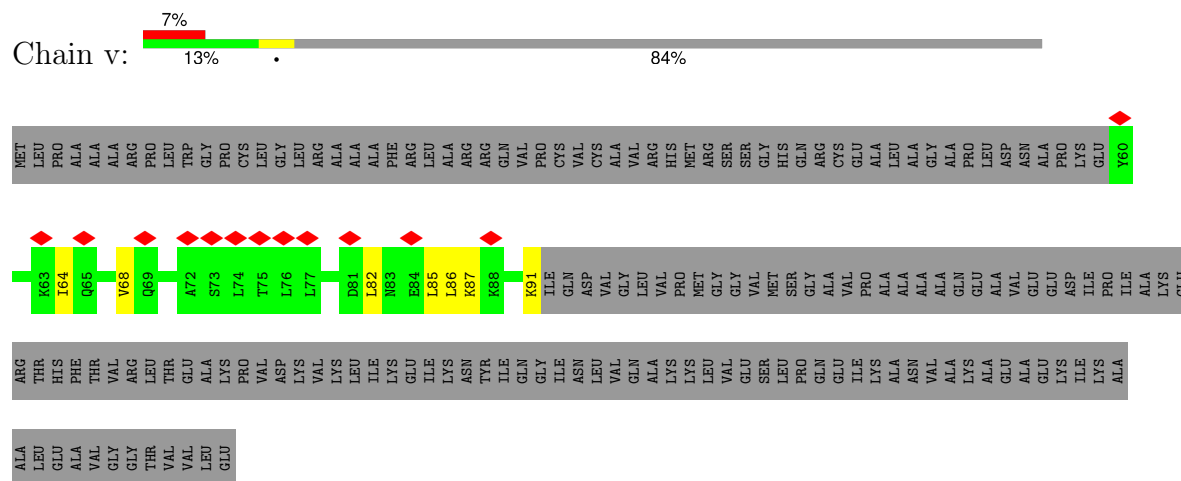
Chain t:  17% 7% 77%



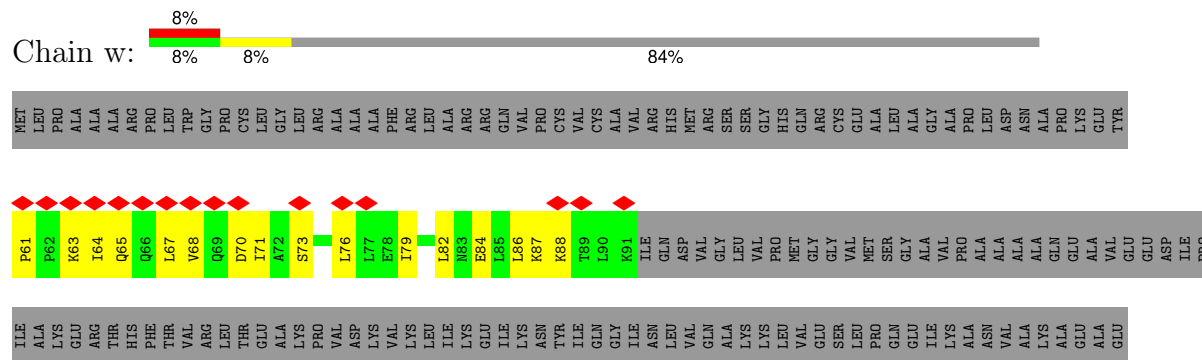
- Molecule 54: 39S ribosomal protein L12, mitochondrial



- Molecule 54: 39S ribosomal protein L12, mitochondrial



- Molecule 54: 39S ribosomal protein L12, mitochondrial

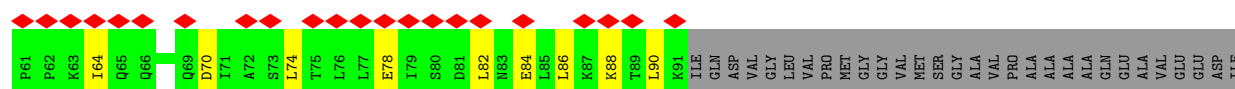


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- Molecule 54: 39S ribosomal protein L12, mitochondrial



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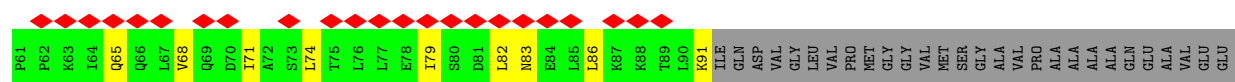
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- Molecule 54: 39S ribosomal protein L12, mitochondrial



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S73
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T89
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K91

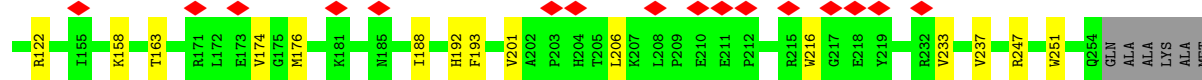
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- Molecule 55: 39S ribosomal protein L9, mitochondrial



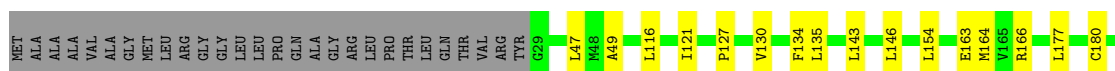
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GLY
T53
L98
V106
G106
L118


R122
I155
K158
T163
R171
L172
E173
V174
G175
M176
K181
N185
I188
H192
F193
V201
A202
P203
H204
T205
L206
K207
L208
P209
E210
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P212
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G217
E218
Y219
R232
V233
V237
R247
W251
Q254

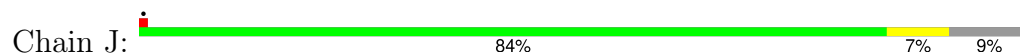
ALA
PRO
THR
SER
PRO
GLN
ILE

- Molecule 56: 39S ribosomal protein L10, mitochondrial

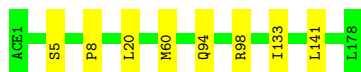




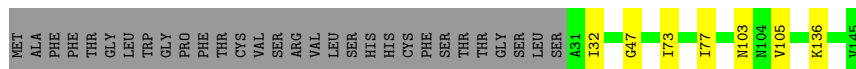
- Molecule 57: 39S ribosomal protein L11, mitochondrial



- Molecule 58: Large ribosomal subunit protein uL13m



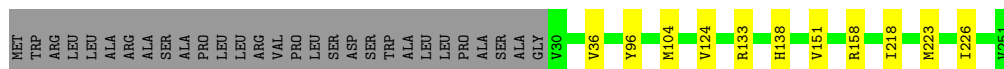
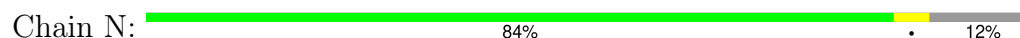
- Molecule 59: 39S ribosomal protein L14, mitochondrial



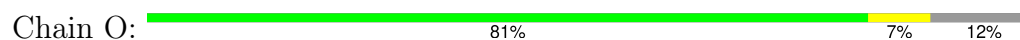
- Molecule 60: 39S ribosomal protein L15, mitochondrial



- Molecule 61: 39S ribosomal protein L16, mitochondrial

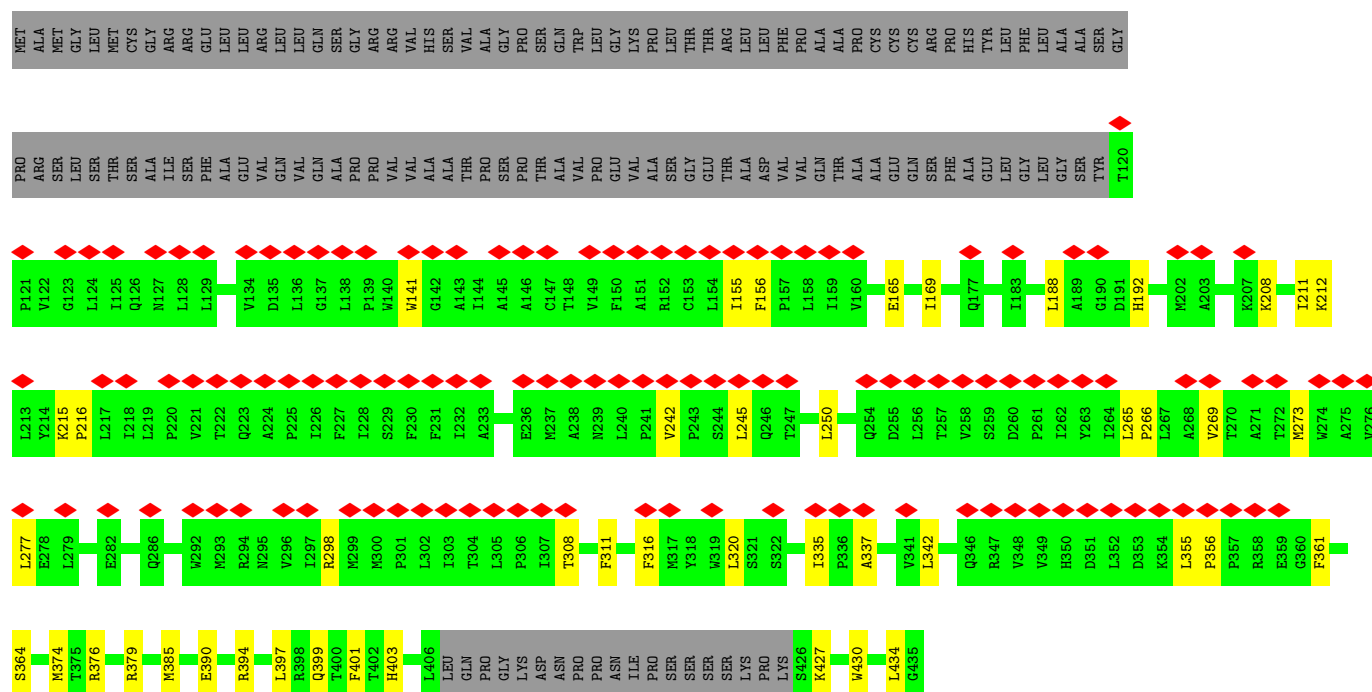


- Molecule 62: 39S ribosomal protein L17, mitochondrial



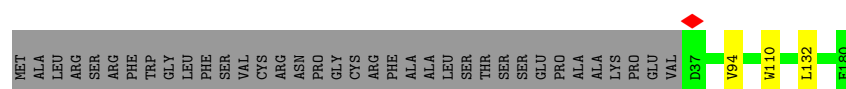
- Molecule 63: Mitochondrial inner membrane protein OXA1L

Chain OX: 



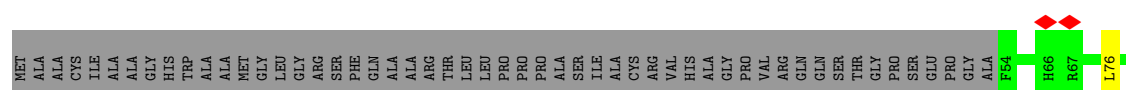
- Molecule 64: 39S ribosomal protein L18, mitochondrial

Chain P: 



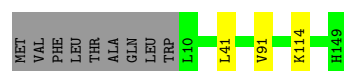
- Molecule 65: 39S ribosomal protein L19, mitochondrial

Chain Q: 



- Molecule 66: 39S ribosomal protein L20, mitochondrial

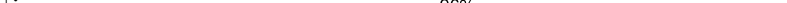
Chain R: 



- Molecule 67: 39S ribosomal protein L21, mitochondrial

[illegible]

- MET
 ALA
 ALA
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 SER
 TYR
 ILE
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 THR
 SER
 THR
 ALA
 SER
 SER
 LEU
 LEU
 ASP
 T41
 R62
 L206

- Chain U:  8% 96%

-
- | Amino Acid | Relative Abundance (%) |
|------------|------------------------|
| MET | 100 |
| ARG | ~95 |
| LEU | ~90 |
| SER | ~85 |
| ALA | ~80 |
| LEU | ~75 |
| LEU | ~70 |
| LEU | ~65 |
| ALA | ~60 |
| SER | ~55 |
| K12 | ~50 |
| P16 | ~45 |
| Y19 | ~40 |
| P43 | ~35 |
| V79 | ~30 |
| I80 | ~25 |
| W85 | ~20 |
| V86 | ~15 |
| R136 | ~10 |
| E168 | ~5 |
| T169 | ~5 |
| L191 | ~5 |
| Y216 | ~5 |

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|------|------|------|
| MET | ALA | SER | VAL | VAL | LEU | ALA | LEU | ARG | THR | ARG | THR | ALA | VAL | THR | SER | LEU | LEU | SER | PRO | THR | PRO | ALA | THR | ALA | LEU | ALA | VAL | ARG | TYR | ALA | SER | R33 | G36 | R74 | Y104 | K128 | L148 |
|------|------|------|

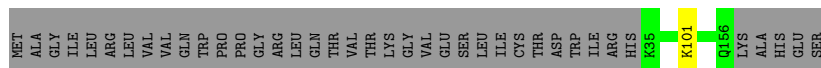
- | |
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| MET |
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| MET | ALA | ALA | ALA | GLY | LEU | LEU | ALA | LEU | CYS | ARG | ARG | VAL | SER | SER | ALA | ALA | LYS | LEU | LEU | THR | THR | GLN | PRO | VAL | PRO | ALA | CYS | THR | GLY | PHE | LEU | SER | LEU | LEU | PRO | LYS | SER | THR | PRO | ASN | VAL | THR | THR | HIS | GLN | TYR | ARG | LEU | LEU | HIS | THR | THR | LEU |
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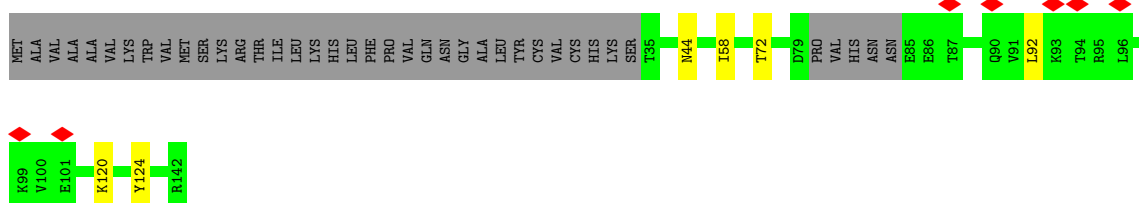
- Molecule 74: 39S ribosomal protein L30, mitochondrial

Chain Z: 75% 24%



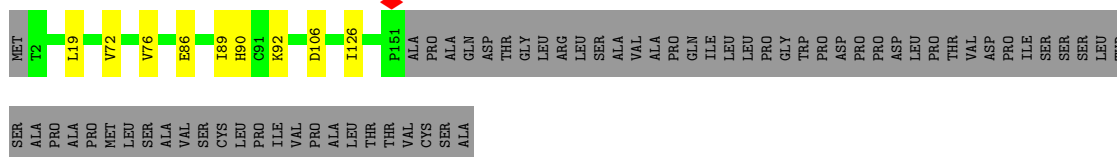
- Molecule 75: 39S ribosomal protein L42, mitochondrial

Chain a: 5% 68% 27%



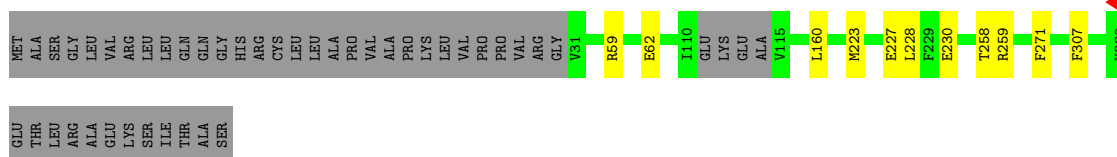
- Molecule 76: 39S ribosomal protein L43, mitochondrial

Chain b: 66% 30%



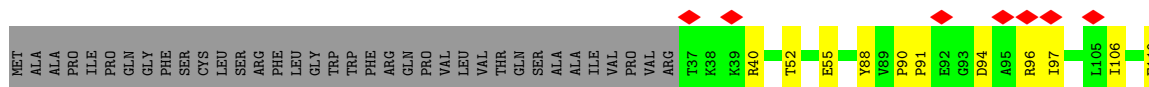
- Molecule 77: 39S ribosomal protein L44, mitochondrial

Chain c: 83% 14%



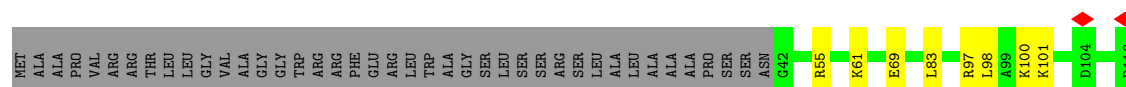
- Molecule 78: 39S ribosomal protein L45, mitochondrial

Chain d: 75% 10% 15%

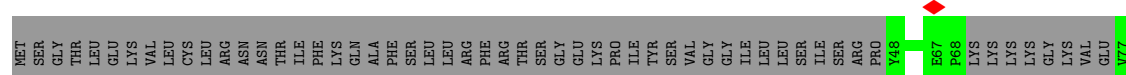




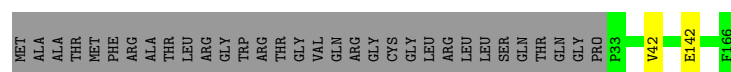
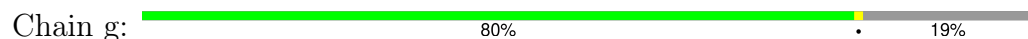
- Molecule 79: 39S ribosomal protein L46, mitochondrial



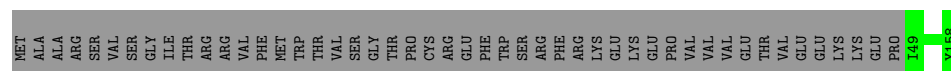
- Molecule 80: 39S ribosomal protein L48, mitochondrial



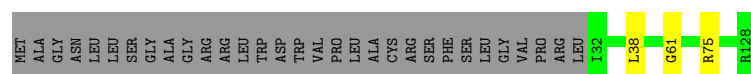
- Molecule 81: 39S ribosomal protein L49, mitochondrial



- Molecule 82: 39S ribosomal protein L50, mitochondrial

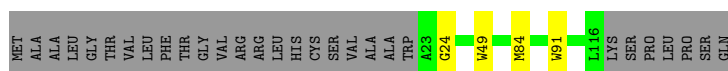


- Molecule 83: 39S ribosomal protein L51, mitochondrial

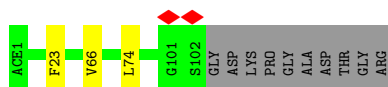
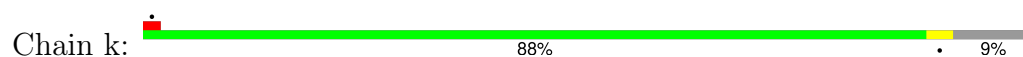


- Molecule 84: 39S ribosomal protein L52, mitochondrial

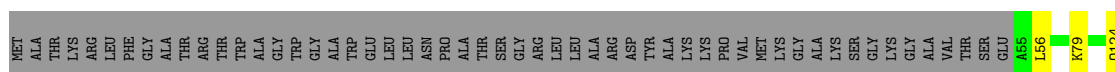




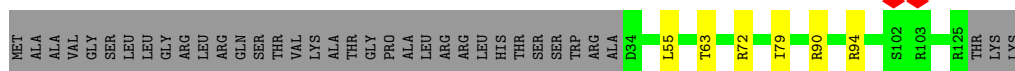
- Molecule 85: Large ribosomal subunit protein mL53



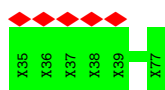
- Molecule 86: 39S ribosomal protein L54, mitochondrial



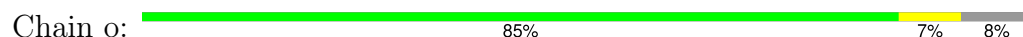
- Molecule 87: 39S ribosomal protein L55, mitochondrial



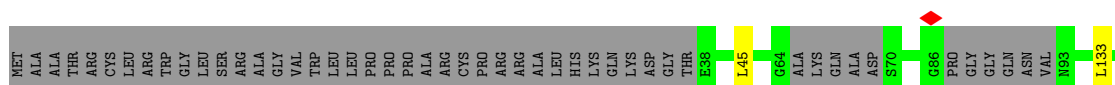
- Molecule 88: Nascent polypeptide

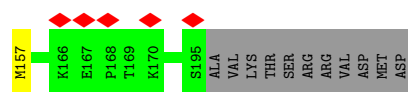


- Molecule 89: Ribosomal protein 63, mitochondrial



- Molecule 90: Peptidyl-tRNA hydrolase ICT1, mitochondrial





K306	I307	D308	P309	L310	L311	P312	LYS	GLU	VAL	LYS	ASN	GLU	SER	GLU	LYS	GLU	ASP	ALA
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	526704	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	55	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.651	Depositor
Minimum map value	-0.143	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	512.63995, 512.63995, 512.63995	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.068, 1.068, 1.068	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, PUT, GDP, B8T, 5MC, K, SPM, NAD, PSU, MG, ZN, 2MG, 1MA, OMG, SPD, OMU, 5MU, MA6, ACE, FES

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	0	0.24	0/913	0.24	0/1224
2	1	0.22	0/469	0.28	0/621
3	2	0.31	0/383	0.28	0/507
4	3	0.30	0/853	0.29	0/1136
5	4	0.29	0/350	0.27	0/461
6	5	0.22	0/3305	0.27	0/4502
7	6	0.18	0/3043	0.26	0/4140
8	7	0.18	0/2447	0.24	0/3310
9	8	0.13	0/1354	0.30	0/1819
10	9	0.22	0/1025	0.25	0/1379
11	A	0.31	0/36876	0.31	0/57402
12	A0	0.12	0/1834	0.27	0/2484
13	A1	0.17	0/2313	0.26	0/3129
14	A2	0.18	0/947	0.27	0/1266
15	A3	0.21	0/636	0.24	0/839
16	A4	0.13	0/4877	0.28	0/6598
17	A5	0.12	0/4737	0.33	0/6398
18	A6	0.11	0/619	0.30	0/835
19	AA	0.25	0/22537	0.27	0/35085
20	AB	0.21	0/1871	0.25	0/2531
21	AC	0.22	0/1113	0.29	0/1505
22	AD	0.19	0/2783	0.24	0/3724
23	AE	0.20	0/989	0.25	0/1335
24	AF	0.17	0/1767	0.23	0/2373
25	AG	0.18	0/2746	0.24	0/3681
26	AH	0.23	0/1178	0.30	0/1598
27	AI	0.21	0/1039	0.28	0/1400
28	AJ	0.20	0/855	0.27	0/1148
29	AK	0.22	0/880	0.23	0/1182
30	AL	0.20	0/1477	0.21	0/1974
31	AM	0.16	0/963	0.28	0/1295

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	AN	0.20	0/886	0.26	0/1199
33	AO	0.16	0/1648	0.27	0/2243
34	AP	0.22	0/798	0.25	0/1070
35	AQ	0.22	0/754	0.22	0/1003
36	AR	0.13	0/2456	0.24	0/3317
37	AS	0.15	0/1138	0.18	0/1533
38	AT	0.18	0/1402	0.26	0/1883
39	AU	0.12	0/1510	0.21	0/2025
40	AV	0.11	0/3030	0.29	0/4093
41	AW	0.18	0/801	0.25	0/1079
42	AX	0.15	0/2921	0.29	0/3954
43	AY	0.16	0/1877	0.33	0/2524
44	AZ	0.19	0/857	0.29	0/1141
45	Aw	0.14	0/1600	0.28	0/2476
46	Ax	0.18	0/1673	0.33	0/2602
47	Ay	0.12	0/1655	0.24	0/2567
48	Az	0.17	0/804	0.33	0/1248
49	B	0.17	0/1626	0.26	0/2523
50	C	0.12	0/1754	0.28	0/2357
51	D	0.24	0/1896	0.27	0/2549
52	E	0.25	0/2475	0.30	0/3355
53	F	0.26	0/2090	0.28	0/2842
54	G	0.16	0/562	0.48	0/754
54	t	0.20	0/358	0.44	0/486
54	u	0.21	0/259	0.39	0/350
54	v	0.17	0/259	0.33	0/350
54	w	0.22	0/246	0.51	0/331
54	x	0.15	0/246	0.34	0/331
54	y	0.18	0/246	0.42	0/331
55	H	0.15	0/1698	0.26	0/2292
56	I	0.20	0/1731	0.32	0/2345
57	J	0.12	0/1348	0.26	0/1813
58	K	0.27	0/1497	0.28	0/2031
59	L	0.23	0/905	0.28	0/1218
60	M	0.26	0/2381	0.28	0/3212
61	N	0.24	0/1833	0.27	0/2468
62	O	0.25	0/1283	0.27	0/1727
63	OX	0.15	0/2471	0.36	1/3360 (0.0%)
64	P	0.20	0/1199	0.25	0/1623
65	Q	0.23	0/2039	0.28	0/2750
66	R	0.28	0/1175	0.24	0/1572
67	S	0.27	0/1320	0.30	0/1789
68	T	0.26	0/1403	0.26	0/1886

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
69	U	0.25	0/1279	0.33	0/1730
70	V	0.21	0/1721	0.26	0/2333
71	W	0.27	0/926	0.26	0/1244
72	X	0.22	0/2099	0.24	0/2837
73	Y	0.25	0/1593	0.24	0/2136
74	Z	0.25	0/1021	0.29	0/1378
75	a	0.22	0/891	0.31	0/1208
76	b	0.25	0/1218	0.28	0/1649
77	c	0.21	0/2347	0.24	0/3171
78	d	0.17	0/2181	0.30	0/2949
79	e	0.11	0/1970	0.27	0/2658
80	f	0.15	0/1273	0.31	0/1716
81	g	0.24	0/1151	0.27	0/1569
82	h	0.17	0/918	0.22	0/1249
83	i	0.29	0/850	0.28	0/1135
84	j	0.22	0/760	0.23	0/1023
85	k	0.15	0/783	0.22	0/1057
86	l	0.12	0/707	0.25	0/960
87	m	0.11	0/805	0.29	0/1081
89	o	0.26	0/819	0.28	0/1097
90	p	0.17	0/1223	0.25	0/1641
91	q	0.16	0/1529	0.26	0/2055
92	r	0.23	0/1362	0.29	0/1846
93	s	0.24	0/3231	0.27	0/4389
94	z	0.13	0/2067	0.33	0/2793
All	All	0.23	0/202013	0.28	1/286387 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
63	OX	155	ILE	N-CA-C	-5.68	106.95	112.29

There are no chirality outliers.

There are no planarity outliers.

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	0	898	0	916	3	0
2	1	464	0	511	5	0
3	2	377	0	406	1	0
4	3	832	0	883	4	0
5	4	342	0	361	3	0
6	5	3210	0	3206	12	0
7	6	2948	0	2841	8	0
8	7	2390	0	2397	15	0
9	8	1327	0	1368	15	0
10	9	997	0	987	4	0
11	A	33070	0	16793	117	0
12	A0	1787	0	1796	10	0
13	A1	2265	0	2294	20	0
14	A2	935	0	971	3	0
15	A3	625	0	699	3	0
16	A4	4768	0	4766	56	0
17	A5	4646	0	4674	51	0
18	A6	603	0	588	3	0
19	AA	20260	0	10284	157	0
20	AB	1828	0	1815	7	0
21	AC	1083	0	1088	10	0
22	AD	2731	0	2804	15	0
23	AE	972	0	1000	6	0
24	AF	1725	0	1769	7	0
25	AG	2688	0	2687	6	0
26	AH	1152	0	1183	17	0
27	AI	1019	0	1059	10	0
28	AJ	839	0	887	5	0
29	AK	862	0	885	6	0
30	AL	1453	0	1540	6	0
31	AM	942	0	965	11	0
32	AN	868	0	928	5	0
33	AO	1592	0	1557	6	0
34	AP	781	0	806	5	0
35	AQ	744	0	758	6	0
36	AR	2409	0	2428	14	0
37	AS	1111	0	1115	5	0
38	AT	1371	0	1393	4	0
39	AU	1488	0	1499	3	0
40	AV	2969	0	2961	22	0
41	AW	789	0	802	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	AX	2849	0	2844	21	0
43	AY	1835	0	1780	18	0
44	AZ	839	0	858	6	0
45	Aw	1434	0	728	11	0
46	Ax	1498	0	766	9	0
47	Ay	1483	0	754	18	0
48	Az	719	0	359	2	0
49	B	1524	0	779	9	0
50	C	1732	0	1740	29	0
51	D	1859	0	1920	5	0
52	E	2406	0	2415	12	0
53	F	2031	0	2065	8	0
54	G	558	0	612	18	0
54	t	354	0	377	15	0
54	u	257	0	283	12	0
54	v	257	0	283	8	0
54	w	245	0	275	22	0
54	x	245	0	275	6	0
54	y	245	0	275	7	0
55	H	1661	0	1734	11	0
56	I	1695	0	1785	25	0
57	J	1330	0	1407	9	0
58	K	1455	0	1452	4	0
59	L	890	0	941	4	0
60	M	2327	0	2395	8	0
61	N	1786	0	1817	9	0
62	O	1259	0	1294	9	0
63	OX	2404	0	2464	30	0
64	P	1173	0	1165	2	0
65	Q	1990	0	2031	6	0
66	R	1154	0	1214	3	0
67	S	1293	0	1365	12	0
68	T	1369	0	1410	1	0
69	U	1248	0	1228	4	0
70	V	1676	0	1687	8	0
71	W	904	0	934	3	0
72	X	2044	0	2060	4	0
73	Y	1556	0	1597	5	0
74	Z	996	0	1044	1	0
75	a	865	0	829	5	0
76	b	1193	0	1191	6	0
77	c	2299	0	2320	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
78	d	2124	0	2125	19	0
79	e	1931	0	1916	26	0
80	f	1252	0	1269	15	0
81	g	1113	0	1097	2	0
82	h	895	0	881	0	0
83	i	828	0	857	3	0
84	j	745	0	746	4	0
85	k	774	0	784	2	0
86	l	688	0	673	3	0
87	m	791	0	796	5	0
88	n	215	0	54	0	0
89	o	798	0	804	6	0
90	p	1205	0	1223	2	0
91	q	1495	0	1492	10	0
92	r	1322	0	1348	3	0
93	s	3148	0	3131	14	0
94	z	2027	0	2076	30	0
95	0	1	0	0	0	0
95	4	1	0	0	0	0
95	AO	1	0	0	0	0
96	A	40	0	76	0	0
96	AA	20	0	38	1	0
96	O	10	0	19	0	0
97	A	137	0	0	0	0
97	A3	1	0	0	0	0
97	AA	60	0	0	0	0
97	AB	1	0	0	0	0
97	AX	1	0	0	0	0
97	Az	1	0	0	0	0
97	D	2	0	0	0	0
97	E	1	0	0	0	0
97	g	1	0	0	0	0
98	A	6	0	12	0	0
99	A	29	0	0	0	0
99	AA	18	0	0	0	0
99	D	1	0	0	0	0
99	M	2	0	0	0	0
99	N	1	0	0	0	0
99	P	1	0	0	0	0
99	W	1	0	0	0	0
99	o	1	0	0	0	0
100	AA	28	0	52	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
101	AA	44	0	26	1	0
102	AP	4	0	0	0	0
102	AT	4	0	0	0	0
102	r	4	0	0	1	0
103	AX	28	0	12	0	0
104	AX	31	0	12	0	0
105	B	7	0	8	2	0
All	All	192936	0	164949	1030	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 3.

The worst 5 of 1030 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)
56:I:220:SER:HA	56:I:223:GLN:HG2	1.61	0.81
17:A5:98:GLY:HA3	17:A5:336:PRO:HB3	1.64	0.78
50:C:268:LEU:HD23	50:C:272:ASP:HB3	1.66	0.78
79:e:219:GLN:HA	79:e:222:ARG:HB2	1.66	0.76
54:t:76:LEU:HB3	54:w:71:ILE:HG21	1.68	0.73

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	0	108/188 (57%)	108 (100%)	0	0	100	100
2	1	54/65 (83%)	54 (100%)	0	0	100	100
3	2	44/92 (48%)	43 (98%)	1 (2%)	0	100	100
4	3	93/188 (50%)	92 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	4	36/103 (35%)	36 (100%)	0	0	100	100
6	5	392/423 (93%)	389 (99%)	3 (1%)	0	100	100
7	6	352/380 (93%)	346 (98%)	6 (2%)	0	100	100
8	7	292/338 (86%)	283 (97%)	9 (3%)	0	100	100
9	8	155/206 (75%)	151 (97%)	4 (3%)	0	100	100
10	9	122/137 (89%)	120 (98%)	2 (2%)	0	100	100
12	A0	213/217 (98%)	209 (98%)	4 (2%)	0	100	100
13	A1	277/323 (86%)	270 (98%)	7 (2%)	0	100	100
14	A2	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
15	A3	68/199 (34%)	67 (98%)	1 (2%)	0	100	100
16	A4	584/689 (85%)	569 (97%)	15 (3%)	0	100	100
17	A5	579/1394 (42%)	550 (95%)	27 (5%)	2 (0%)	36	45
18	A6	72/109 (66%)	65 (90%)	7 (10%)	0	100	100
20	AB	223/296 (75%)	221 (99%)	2 (1%)	0	100	100
21	AC	130/167 (78%)	127 (98%)	3 (2%)	0	100	100
22	AD	341/430 (79%)	335 (98%)	6 (2%)	0	100	100
23	AE	120/125 (96%)	117 (98%)	3 (2%)	0	100	100
24	AF	206/242 (85%)	206 (100%)	0	0	100	100
25	AG	323/396 (82%)	317 (98%)	6 (2%)	0	100	100
26	AH	138/201 (69%)	132 (96%)	5 (4%)	1 (1%)	18	24
27	AI	135/194 (70%)	133 (98%)	1 (1%)	1 (1%)	18	24
28	AJ	106/138 (77%)	104 (98%)	2 (2%)	0	100	100
29	AK	99/128 (77%)	99 (100%)	0	0	100	100
30	AL	172/257 (67%)	171 (99%)	1 (1%)	0	100	100
31	AM	117/137 (85%)	116 (99%)	1 (1%)	0	100	100
32	AN	108/130 (83%)	108 (100%)	0	0	100	100
33	AO	191/258 (74%)	186 (97%)	5 (3%)	0	100	100
34	AP	95/142 (67%)	95 (100%)	0	0	100	100
35	AQ	85/87 (98%)	84 (99%)	1 (1%)	0	100	100
36	AR	293/360 (81%)	286 (98%)	7 (2%)	0	100	100
37	AS	133/190 (70%)	132 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	AT	166/173 (96%)	165 (99%)	1 (1%)	0	100	100
39	AU	174/205 (85%)	174 (100%)	0	0	100	100
40	AV	358/414 (86%)	348 (97%)	10 (3%)	0	100	100
41	AW	98/187 (52%)	97 (99%)	1 (1%)	0	100	100
42	AX	350/398 (88%)	342 (98%)	8 (2%)	0	100	100
43	AY	219/395 (55%)	198 (90%)	19 (9%)	2 (1%)	14	17
44	AZ	98/106 (92%)	96 (98%)	2 (2%)	0	100	100
50	C	221/297 (74%)	215 (97%)	6 (3%)	0	100	100
51	D	236/305 (77%)	232 (98%)	4 (2%)	0	100	100
52	E	303/348 (87%)	297 (98%)	6 (2%)	0	100	100
53	F	250/311 (80%)	247 (99%)	3 (1%)	0	100	100
54	G	70/198 (35%)	66 (94%)	4 (6%)	0	100	100
54	t	44/198 (22%)	43 (98%)	1 (2%)	0	100	100
54	u	30/198 (15%)	29 (97%)	1 (3%)	0	100	100
54	v	30/198 (15%)	29 (97%)	1 (3%)	0	100	100
54	w	29/198 (15%)	27 (93%)	2 (7%)	0	100	100
54	x	29/198 (15%)	26 (90%)	3 (10%)	0	100	100
54	y	29/198 (15%)	26 (90%)	3 (10%)	0	100	100
55	H	200/267 (75%)	193 (96%)	7 (4%)	0	100	100
56	I	210/261 (80%)	207 (99%)	3 (1%)	0	100	100
57	J	173/192 (90%)	172 (99%)	1 (1%)	0	100	100
58	K	176/178 (99%)	174 (99%)	2 (1%)	0	100	100
59	L	113/145 (78%)	112 (99%)	1 (1%)	0	100	100
60	M	289/296 (98%)	283 (98%)	6 (2%)	0	100	100
61	N	220/251 (88%)	220 (100%)	0	0	100	100
62	O	152/175 (87%)	148 (97%)	4 (3%)	0	100	100
63	OX	293/435 (67%)	279 (95%)	14 (5%)	0	100	100
64	P	142/180 (79%)	139 (98%)	3 (2%)	0	100	100
65	Q	237/292 (81%)	235 (99%)	2 (1%)	0	100	100
66	R	138/149 (93%)	137 (99%)	1 (1%)	0	100	100
67	S	159/205 (78%)	158 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	T	164/206 (80%)	163 (99%)	1 (1%)	0	100	100
69	U	150/153 (98%)	146 (97%)	4 (3%)	0	100	100
70	V	203/216 (94%)	201 (99%)	2 (1%)	0	100	100
71	W	114/148 (77%)	113 (99%)	1 (1%)	0	100	100
72	X	242/256 (94%)	240 (99%)	2 (1%)	0	100	100
73	Y	179/250 (72%)	176 (98%)	3 (2%)	0	100	100
74	Z	120/161 (74%)	119 (99%)	1 (1%)	0	100	100
75	a	99/142 (70%)	97 (98%)	2 (2%)	0	100	100
76	b	148/215 (69%)	142 (96%)	6 (4%)	0	100	100
77	c	282/332 (85%)	280 (99%)	2 (1%)	0	100	100
78	d	257/306 (84%)	242 (94%)	15 (6%)	0	100	100
79	e	236/279 (85%)	230 (98%)	6 (2%)	0	100	100
80	f	153/212 (72%)	148 (97%)	5 (3%)	0	100	100
81	g	132/166 (80%)	130 (98%)	2 (2%)	0	100	100
82	h	108/158 (68%)	106 (98%)	2 (2%)	0	100	100
83	i	95/128 (74%)	95 (100%)	0	0	100	100
84	j	92/123 (75%)	92 (100%)	0	0	100	100
85	k	100/112 (89%)	100 (100%)	0	0	100	100
86	l	80/138 (58%)	78 (98%)	2 (2%)	0	100	100
87	m	90/128 (70%)	89 (99%)	1 (1%)	0	100	100
89	o	92/102 (90%)	92 (100%)	0	0	100	100
90	p	141/206 (68%)	139 (99%)	2 (1%)	0	100	100
91	q	175/222 (79%)	175 (100%)	0	0	100	100
92	r	160/196 (82%)	159 (99%)	1 (1%)	0	100	100
93	s	381/439 (87%)	376 (99%)	5 (1%)	0	100	100
94	z	250/325 (77%)	235 (94%)	15 (6%)	0	100	100
All	All	16051/21917 (73%)	15711 (98%)	334 (2%)	6 (0%)	100	100

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	A5	283	ILE
26	AH	126	ILE

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Mol	Chain	Res	Type
43	AY	204	ILE
17	A5	257	VAL
27	AI	184	ASN

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	0	99/164 (60%)	99 (100%)	0	100	100
2	1	53/60 (88%)	53 (100%)	0	100	100
3	2	40/72 (56%)	40 (100%)	0	100	100
4	3	88/166 (53%)	88 (100%)	0	100	100
5	4	37/89 (42%)	37 (100%)	0	100	100
6	5	353/368 (96%)	353 (100%)	0	100	100
7	6	313/332 (94%)	313 (100%)	0	100	100
8	7	270/303 (89%)	270 (100%)	0	100	100
9	8	146/190 (77%)	146 (100%)	0	100	100
10	9	104/112 (93%)	104 (100%)	0	100	100
12	A0	188/189 (100%)	188 (100%)	0	100	100
13	A1	257/291 (88%)	256 (100%)	1 (0%)	84	89
14	A2	100/100 (100%)	100 (100%)	0	100	100
15	A3	65/166 (39%)	65 (100%)	0	100	100
16	A4	526/609 (86%)	526 (100%)	0	100	100
17	A5	515/1219 (42%)	515 (100%)	0	100	100
18	A6	63/90 (70%)	63 (100%)	0	100	100
20	AB	198/249 (80%)	198 (100%)	0	100	100
21	AC	115/143 (80%)	115 (100%)	0	100	100
22	AD	286/357 (80%)	286 (100%)	0	100	100
23	AE	104/107 (97%)	104 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	AF	185/209 (88%)	185 (100%)	0	100	100
25	AG	285/342 (83%)	285 (100%)	0	100	100
26	AH	130/180 (72%)	130 (100%)	0	100	100
27	AI	105/147 (71%)	105 (100%)	0	100	100
28	AJ	93/118 (79%)	93 (100%)	0	100	100
29	AK	91/113 (80%)	91 (100%)	0	100	100
30	AL	158/226 (70%)	158 (100%)	0	100	100
31	AM	97/113 (86%)	97 (100%)	0	100	100
32	AN	96/115 (84%)	96 (100%)	0	100	100
33	AO	174/230 (76%)	174 (100%)	0	100	100
34	AP	88/123 (72%)	88 (100%)	0	100	100
35	AQ	78/78 (100%)	78 (100%)	0	100	100
36	AR	264/318 (83%)	264 (100%)	0	100	100
37	AS	116/164 (71%)	116 (100%)	0	100	100
38	AT	153/157 (98%)	153 (100%)	0	100	100
39	AU	152/174 (87%)	152 (100%)	0	100	100
40	AV	325/364 (89%)	325 (100%)	0	100	100
41	AW	87/158 (55%)	87 (100%)	0	100	100
42	AX	311/351 (89%)	311 (100%)	0	100	100
43	AY	202/357 (57%)	202 (100%)	0	100	100
44	AZ	90/95 (95%)	90 (100%)	0	100	100
50	C	193/245 (79%)	193 (100%)	0	100	100
51	D	192/245 (78%)	192 (100%)	0	100	100
52	E	260/290 (90%)	260 (100%)	0	100	100
53	F	219/262 (84%)	219 (100%)	0	100	100
54	G	60/158 (38%)	60 (100%)	0	100	100
54	t	40/158 (25%)	40 (100%)	0	100	100
54	u	31/158 (20%)	31 (100%)	0	100	100
54	v	31/158 (20%)	31 (100%)	0	100	100
54	w	30/158 (19%)	30 (100%)	0	100	100
54	x	30/158 (19%)	30 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	y	30/158 (19%)	30 (100%)	0	100	100
55	H	182/228 (80%)	182 (100%)	0	100	100
56	I	194/232 (84%)	194 (100%)	0	100	100
57	J	138/150 (92%)	138 (100%)	0	100	100
58	K	155/155 (100%)	155 (100%)	0	100	100
59	L	98/124 (79%)	98 (100%)	0	100	100
60	M	246/249 (99%)	246 (100%)	0	100	100
61	N	189/211 (90%)	189 (100%)	0	100	100
62	O	134/150 (89%)	134 (100%)	0	100	100
63	OX	261/372 (70%)	261 (100%)	0	100	100
64	P	126/155 (81%)	126 (100%)	0	100	100
65	Q	221/256 (86%)	221 (100%)	0	100	100
66	R	118/126 (94%)	118 (100%)	0	100	100
67	S	146/180 (81%)	146 (100%)	0	100	100
68	T	146/176 (83%)	146 (100%)	0	100	100
69	U	134/135 (99%)	134 (100%)	0	100	100
70	V	183/191 (96%)	183 (100%)	0	100	100
71	W	94/119 (79%)	94 (100%)	0	100	100
72	X	220/229 (96%)	220 (100%)	0	100	100
73	Y	163/223 (73%)	163 (100%)	0	100	100
74	Z	113/147 (77%)	113 (100%)	0	100	100
75	a	99/133 (74%)	99 (100%)	0	100	100
76	b	132/186 (71%)	132 (100%)	0	100	100
77	c	251/288 (87%)	251 (100%)	0	100	100
78	d	237/274 (86%)	237 (100%)	0	100	100
79	e	207/236 (88%)	207 (100%)	0	100	100
80	f	139/188 (74%)	139 (100%)	0	100	100
81	g	124/148 (84%)	124 (100%)	0	100	100
82	h	104/148 (70%)	104 (100%)	0	100	100
83	i	86/110 (78%)	86 (100%)	0	100	100
84	j	74/97 (76%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
85	k	83/89 (93%)	83 (100%)	0	100	100
86	l	76/116 (66%)	76 (100%)	0	100	100
87	m	85/113 (75%)	85 (100%)	0	100	100
89	o	80/87 (92%)	80 (100%)	0	100	100
90	p	135/181 (75%)	135 (100%)	0	100	100
91	q	153/178 (86%)	153 (100%)	0	100	100
92	r	147/169 (87%)	147 (100%)	0	100	100
93	s	339/381 (89%)	339 (100%)	0	100	100
94	z	226/287 (79%)	226 (100%)	0	100	100
All	All	14354/18873 (76%)	14353 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	A1	268	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
56	I	119	HIS
69	U	77	ASN
57	J	84	GLN
64	P	142	ASN
74	Z	150	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	1556/1558 (99%)	252 (16%)	2 (0%)
19	AA	953/954 (99%)	139 (14%)	0
45	Aw	64/76 (84%)	22 (34%)	0
46	Ax	70/71 (98%)	17 (24%)	0
47	Ay	67/76 (88%)	12 (17%)	0
48	Az	33/34 (97%)	13 (39%)	0
49	B	70/72 (97%)	14 (20%)	0
All	All	2813/2841 (99%)	469 (16%)	2 (0%)

5 of 469 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A	1681	G
11	A	1689	C
11	A	1692	A
11	A	1699	C
11	A	1700	U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	A	2245	A
11	A	2484	C

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

13 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	$\# Z > 2$
11	OMU	A	3039	11,99	19,22,23	0.31	0	25,31,34	0.71	1 (4%)
19	MA6	AA	1584	19	23,26,27	0.32	0	33,38,41	0.75	1 (3%)
49	2MG	B	10	49	23,26,27	0.36	0	33,38,41	0.42	0
11	OMG	A	3040	45,11	23,26,27	0.35	0	32,38,41	0.39	0
19	B8T	AA	1486	97,19	19,22,23	0.41	0	25,31,34	0.33	0
49	1MA	B	9	49	21,25,26	0.39	0	30,37,40	0.67	0
19	MA6	AA	1583	19	23,26,27	0.35	0	33,38,41	0.76	1 (3%)
49	PSU	B	39	49	18,21,22	1.04	1 (5%)	21,30,33	0.71	0
11	PSU	A	3067	11	18,21,22	1.11	2 (11%)	21,30,33	0.86	1 (4%)
19	5MU	AA	1076	19	19,22,23	0.37	0	27,32,35	0.55	0
11	OMG	A	2815	11,46,99	23,26,27	0.36	0	32,38,41	0.41	0
11	1MA	A	2617	11	21,25,26	0.40	0	30,37,40	0.61	0
19	5MC	AA	1488	19	19,22,23	0.86	1 (5%)	26,32,35	0.51	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
11	OMU	A	3039	11,99	-	0/9/27/28	0/2/2/2
19	MA6	AA	1584	19	-	1/11/29/30	0/3/3/3
49	2MG	B	10	49	-	0/9/27/28	0/3/3/3
11	OMG	A	3040	45,11	-	2/9/27/28	0/3/3/3
19	B8T	AA	1486	97,19	-	1/7/27/28	0/2/2/2
49	1MA	B	9	49	-	0/7/25/26	0/3/3/3
19	MA6	AA	1583	19	-	0/11/29/30	0/3/3/3
49	PSU	B	39	49	-	0/7/25/26	0/2/2/2
11	PSU	A	3067	11	-	0/7/25/26	0/2/2/2
19	5MU	AA	1076	19	-	5/7/25/26	0/2/2/2
11	OMG	A	2815	11,46,99	-	1/9/27/28	0/3/3/3
11	1MA	A	2617	11	-	0/7/25/26	0/3/3/3
19	5MC	AA	1488	19	-	0/7/25/26	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	B	39	PSU	C6-C5	3.61	1.39	1.35
11	A	3067	PSU	C6-C5	3.45	1.39	1.35
19	AA	1488	5MC	C5-C4	-3.39	1.41	1.44
11	A	3067	PSU	O4'-C1'	-2.45	1.40	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	AA	1583	MA6	C2-N1-C6	2.95	119.04	111.83
19	AA	1584	MA6	C2-N1-C6	2.95	119.03	111.83
11	A	3039	OMU	C2'-C1'-N1	-2.78	108.97	114.24
11	A	3067	PSU	O4'-C1'-C2'	2.60	108.75	105.15

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	A	2815	OMG	C1'-C2'-O2'-CM2
19	AA	1076	5MU	O4'-C4'-C5'-O5'
19	AA	1076	5MU	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
11	A	3040	OMG	C3'-C4'-C5'-O5'
11	A	3040	OMG	O4'-C4'-C5'-O5'

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	AA	1486	B8T	1	0
19	AA	1583	MA6	1	0
11	A	2815	OMG	1	0
19	AA	1488	5MC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 279 ligands modelled in this entry, 262 are monoatomic - leaving 17 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
96	SPD	A	3301	-	9,9,9	0.18	0	8,8,8	0.22	0
96	SPD	AA	1712	-	9,9,9	0.15	0	8,8,8	0.21	0
102	FES	r	201	56,92	0,4,4	-	-	-	-	-
101	NAD	AA	1781	97	46,48,48	1.17	3 (6%)	64,73,73	0.84	2 (3%)
105	VAL	B	101	49	4,6,7	0.80	0	6,7,9	1.03	1 (16%)
96	SPD	A	3471	-	9,9,9	0.18	0	8,8,8	0.29	0
100	SPM	AA	1706	-	13,13,13	0.15	0	12,12,12	0.22	0
102	FES	AT	201	31,38	0,4,4	-	-	-	-	-
96	SPD	A	3470	-	9,9,9	0.14	0	8,8,8	0.26	0
96	SPD	O	301	-	9,9,9	0.16	0	8,8,8	0.24	0
96	SPD	AA	1779	-	9,9,9	0.16	0	8,8,8	0.25	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
98	PUT	A	3309	-	5,5,5	0.13	0	4,4,4	0.23	0
103	GDP	AX	401	-	29,30,30	1.17	3 (10%)	45,47,47	1.73	7 (15%)
102	FES	AP	201	34,23	0,4,4	-	-	-	-	-
104	ATP	AX	403	97	32,33,33	0.55	0	48,52,52	0.34	0
96	SPD	A	3302	-	9,9,9	0.14	0	8,8,8	0.21	0
100	SPM	AA	1780	-	13,13,13	0.18	0	12,12,12	0.21	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
96	SPD	A	3301	-	-	0/7/7/7	-
96	SPD	AA	1712	-	-	0/7/7/7	-
102	FES	r	201	56,92	-	-	0/1/1/1
101	NAD	AA	1781	97	-	2/30/62/62	0/5/5/5
105	VAL	B	101	49	-	0/5/6/8	-
96	SPD	A	3471	-	-	0/7/7/7	-
100	SPM	AA	1706	-	-	0/11/11/11	-
102	FES	AT	201	31,38	-	-	0/1/1/1
96	SPD	A	3470	-	-	1/7/7/7	-
96	SPD	O	301	-	-	1/7/7/7	-
96	SPD	AA	1779	-	-	0/7/7/7	-
98	PUT	A	3309	-	-	0/3/3/3	-
103	GDP	AX	401	-	-	0/16/32/32	0/3/3/3
102	FES	AP	201	34,23	-	-	0/1/1/1
104	ATP	AX	403	97	-	0/22/38/38	0/3/3/3
96	SPD	A	3302	-	-	1/7/7/7	-
100	SPM	AA	1780	-	-	0/11/11/11	-

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
101	AA	1781	NAD	PA-O3	4.55	1.64	1.59
103	AX	401	GDP	C5-C4	3.11	1.47	1.38
101	AA	1781	NAD	O4D-C1D	-2.81	1.37	1.40
101	AA	1781	NAD	PN-O3	2.70	1.62	1.59
103	AX	401	GDP	C6-N1	-2.57	1.34	1.38

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
103	AX	401	GDP	C5-C4-N3	-6.01	118.82	128.39
103	AX	401	GDP	C2-N3-C4	4.88	120.70	112.30
103	AX	401	GDP	N9-C4-N3	4.57	135.08	125.95
103	AX	401	GDP	C6-C5-N7	3.07	135.87	130.29
103	AX	401	GDP	C4-C5-N7	-2.42	106.84	110.67

There are no chirality outliers.

All (5) torsion outliers are listed below:

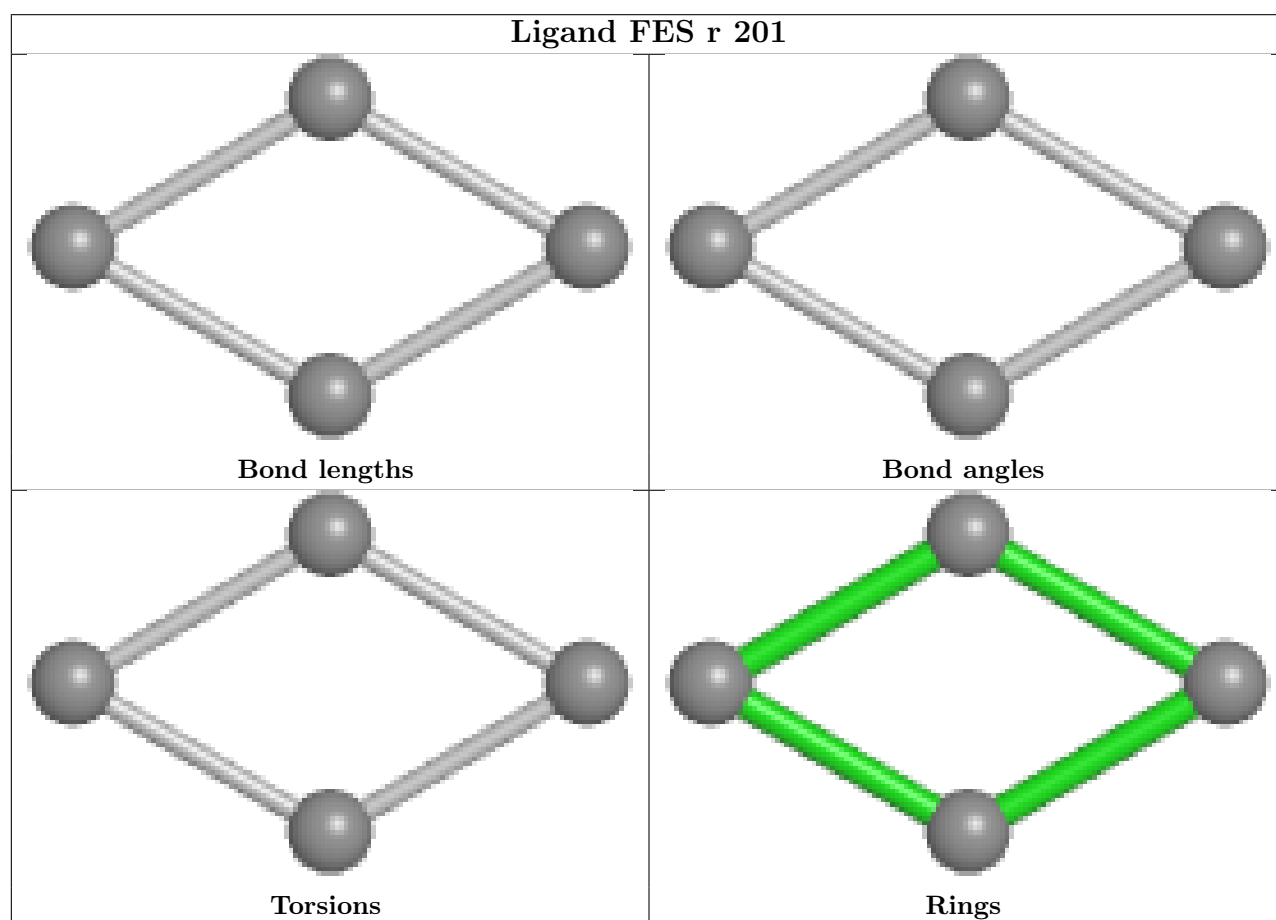
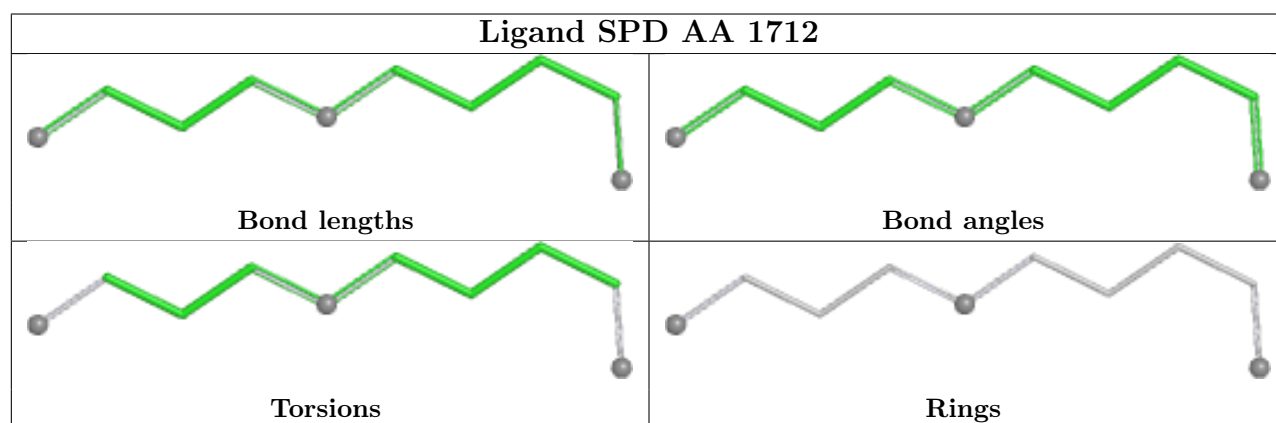
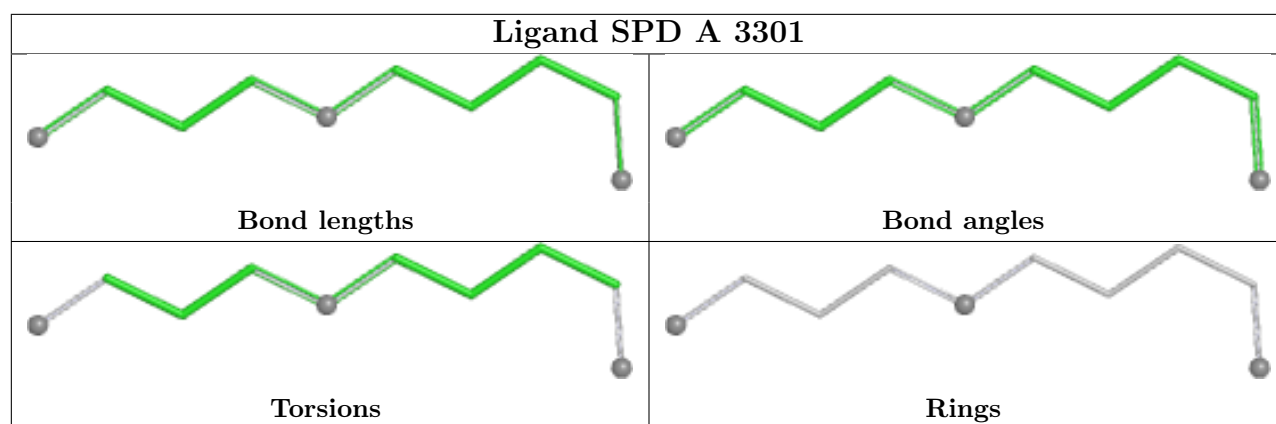
Mol	Chain	Res	Type	Atoms
101	AA	1781	NAD	C5D-O5D-PN-O1N
96	A	3302	SPD	N1-C2-C3-C4
96	A	3470	SPD	C2-C3-C4-C5
96	O	301	SPD	N6-C7-C8-C9
101	AA	1781	NAD	PA-O3-PN-O2N

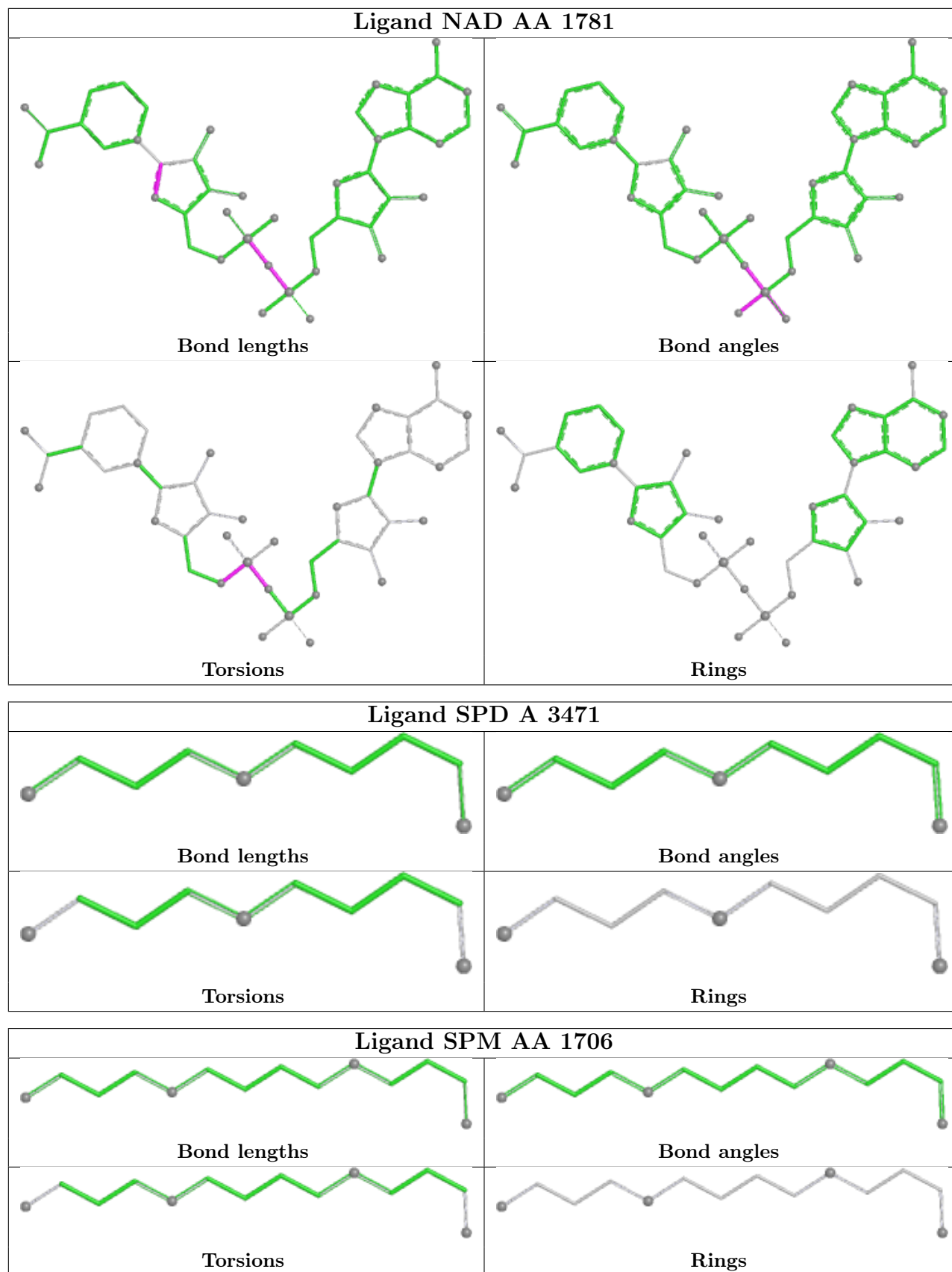
There are no ring outliers.

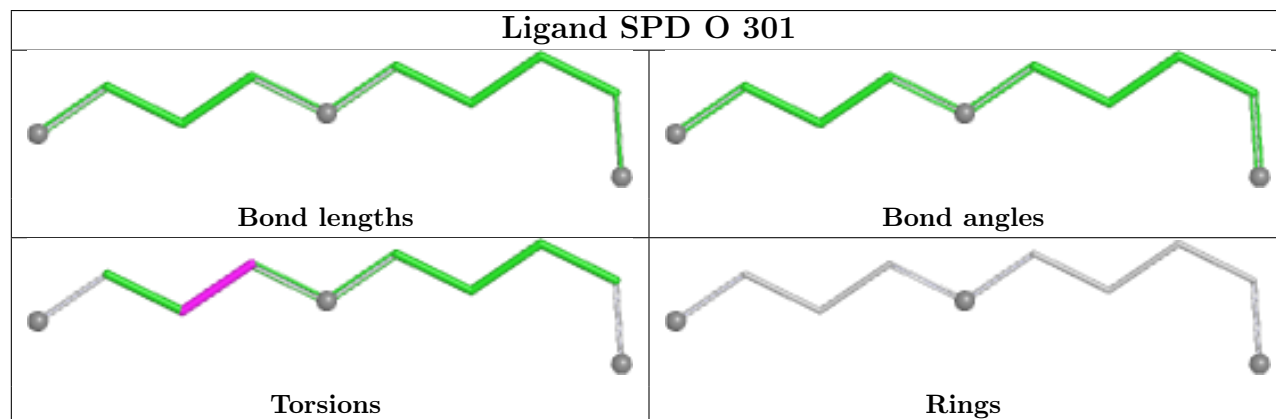
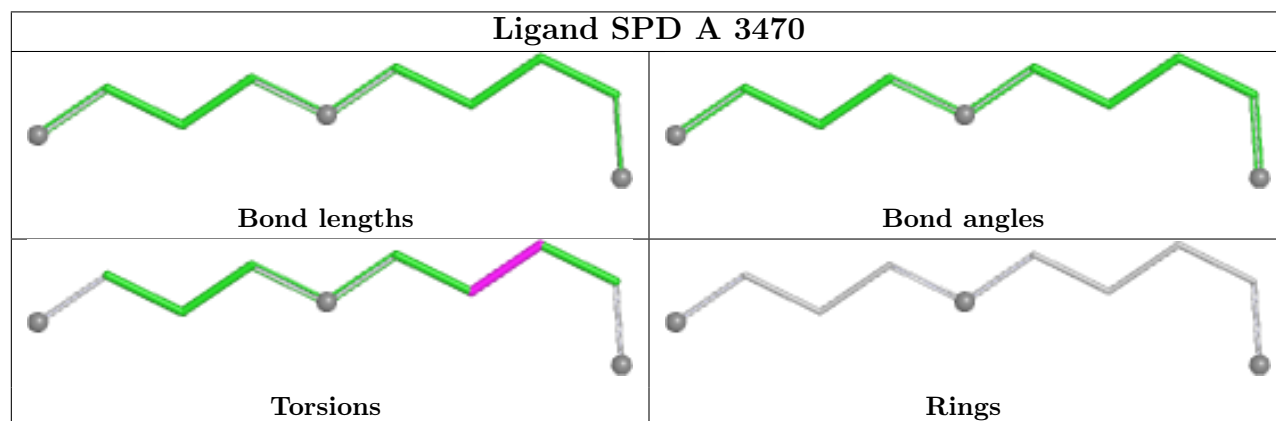
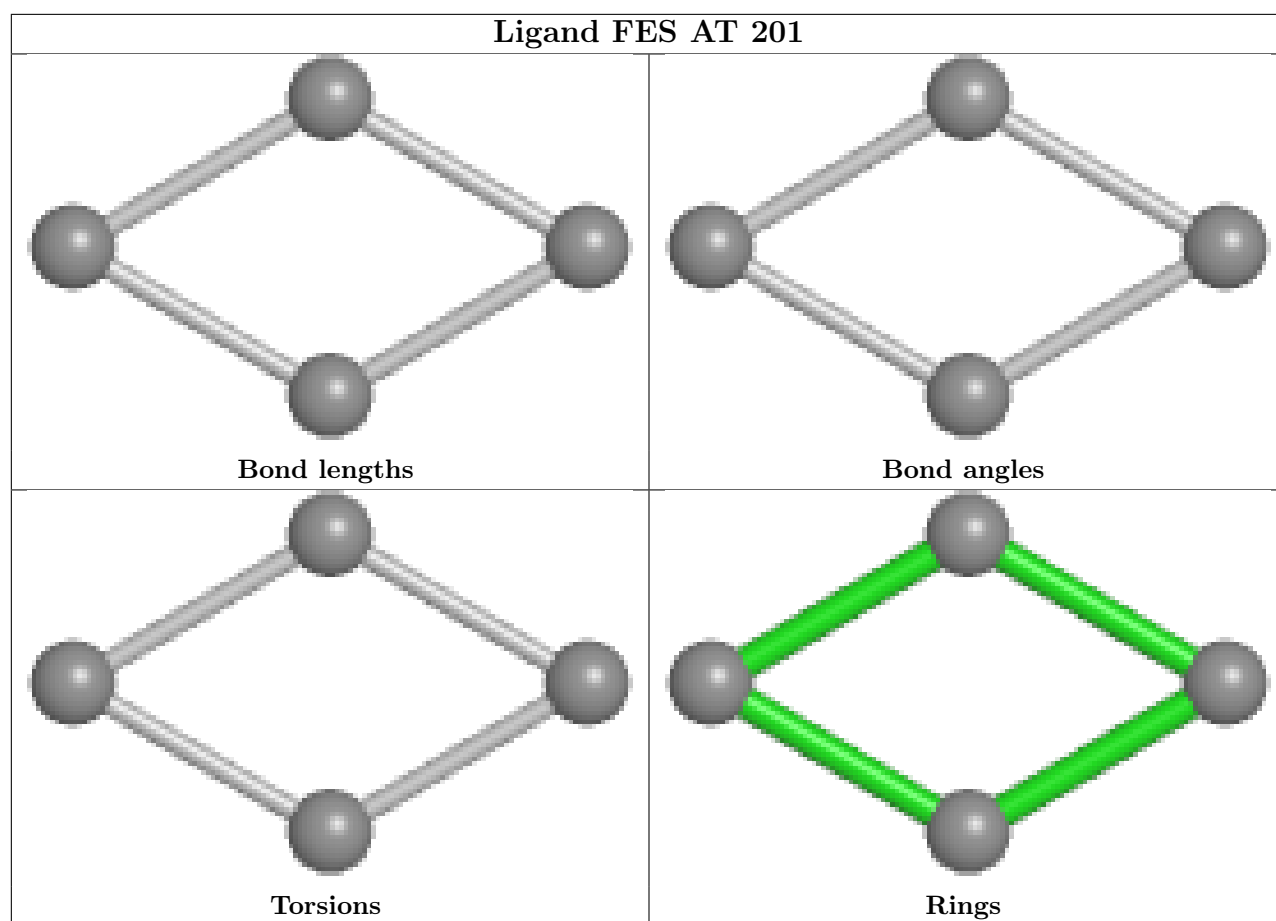
4 monomers are involved in 5 short contacts:

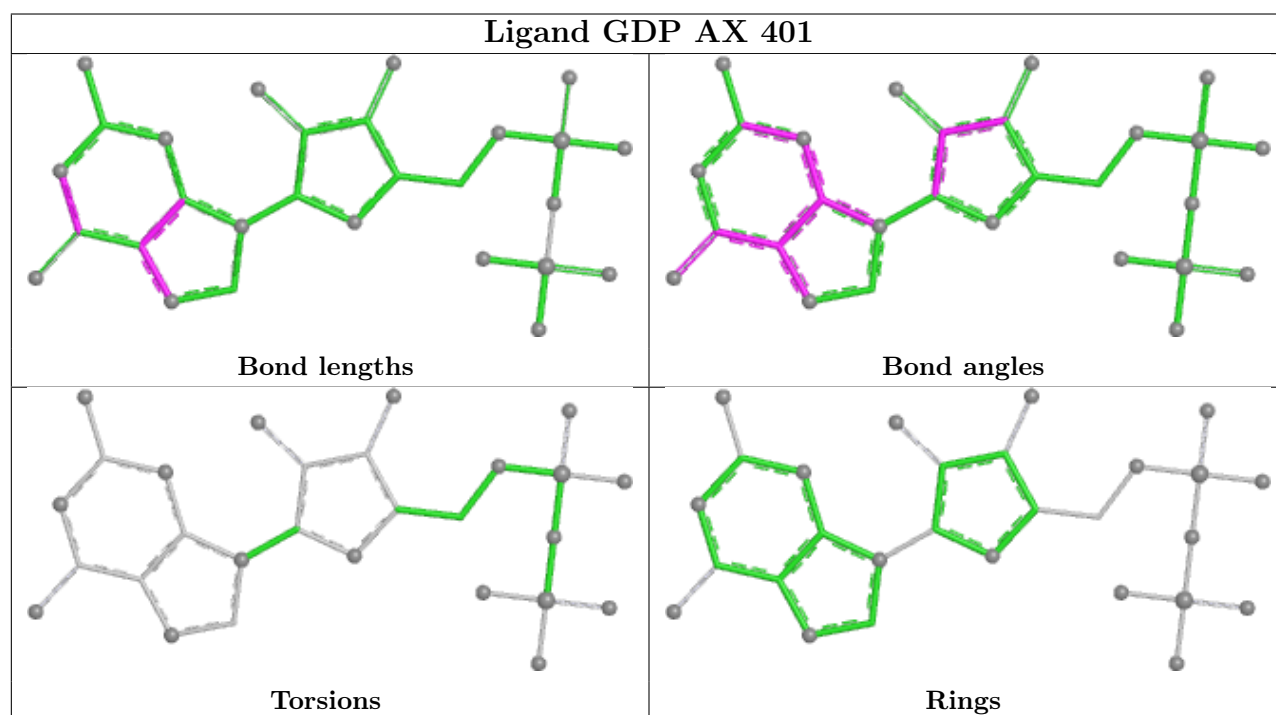
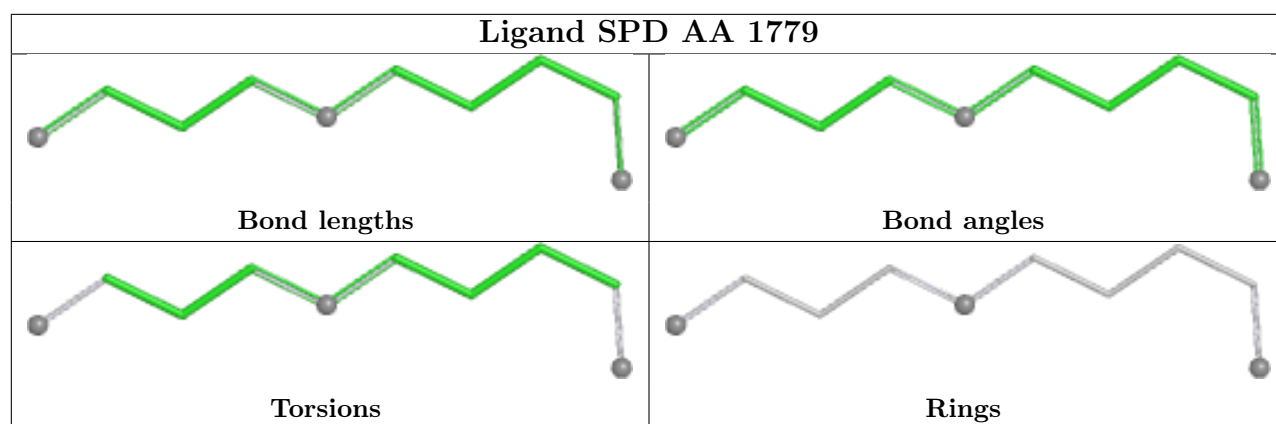
Mol	Chain	Res	Type	Clashes	Symm-Clashes
102	r	201	FES	1	0
101	AA	1781	NAD	1	0
105	B	101	VAL	2	0
96	AA	1779	SPD	1	0

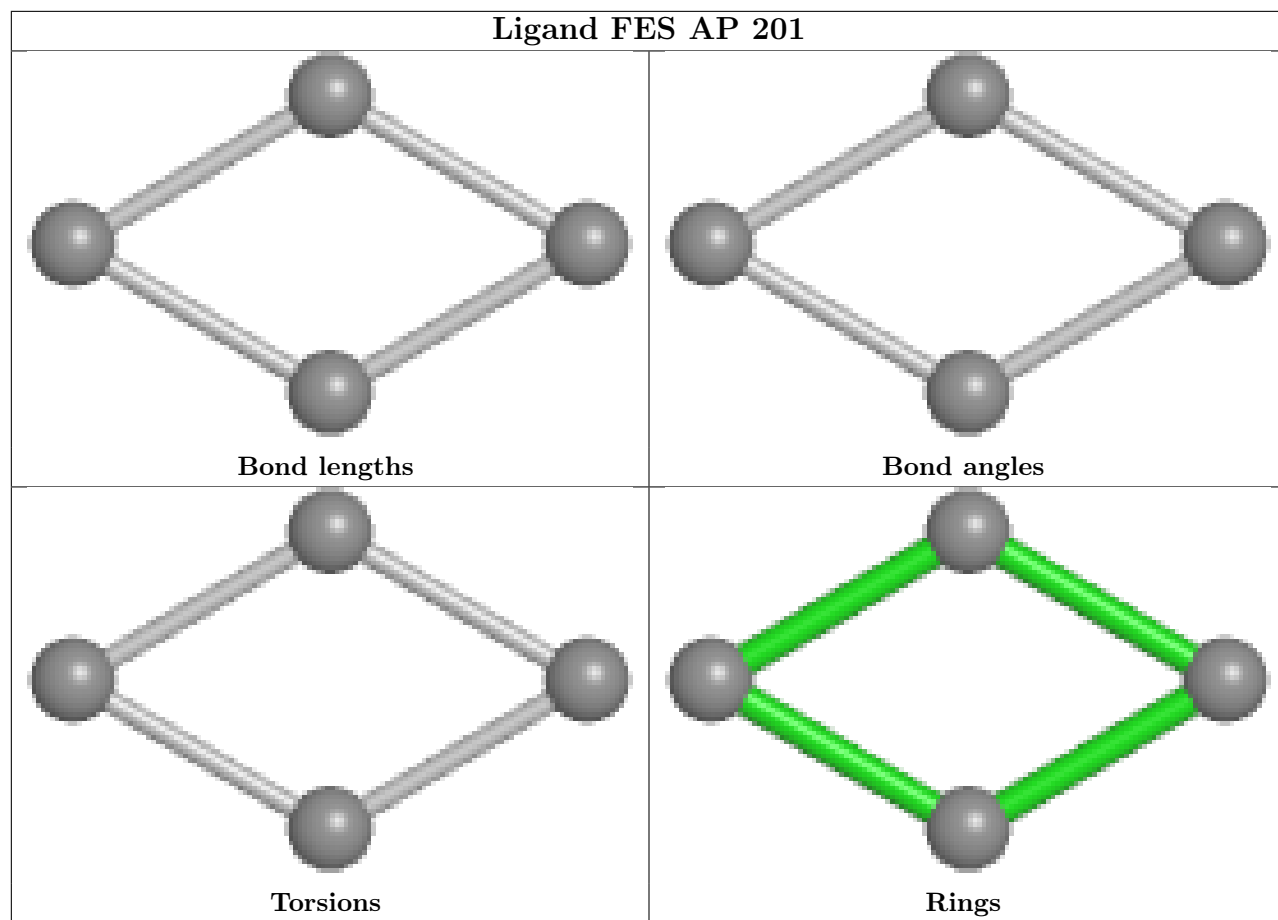
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

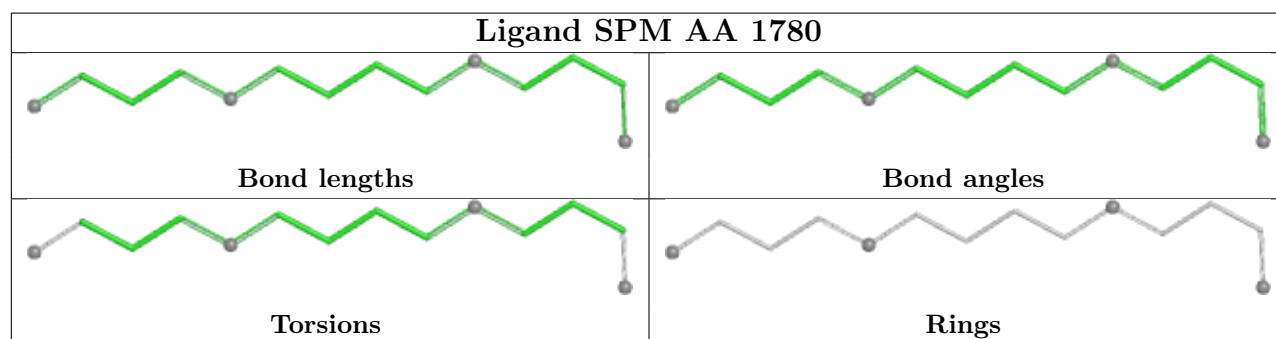
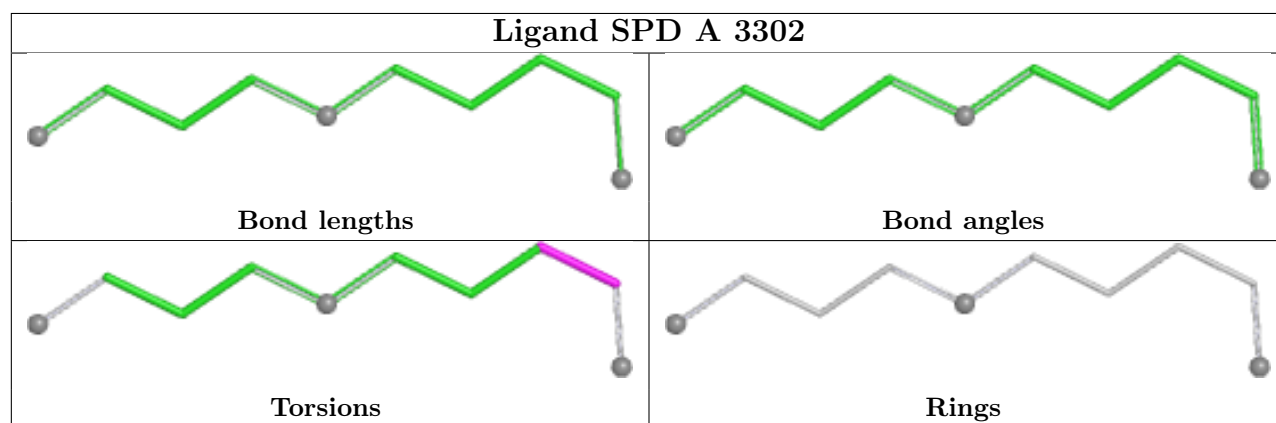
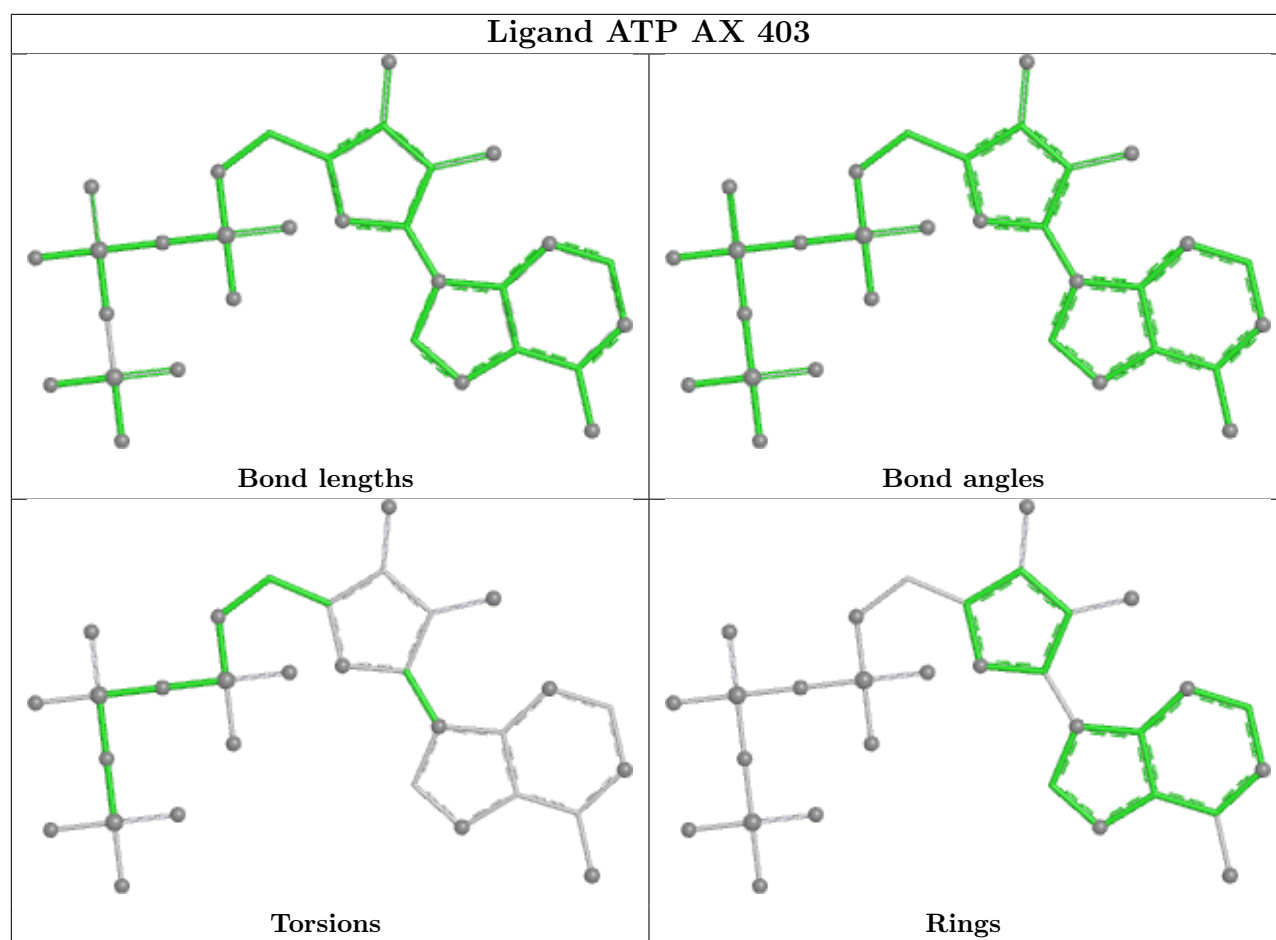












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
11	A	1
49	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2357:C	O3'	2361:G	P	9.25
1	B	46:A	O3'	48:U	P	4.54

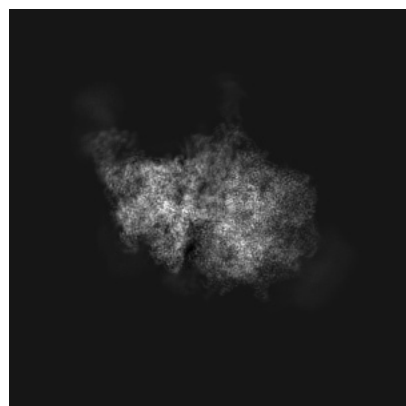
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70592. These allow visual inspection of the internal detail of the map and identification of artifacts.

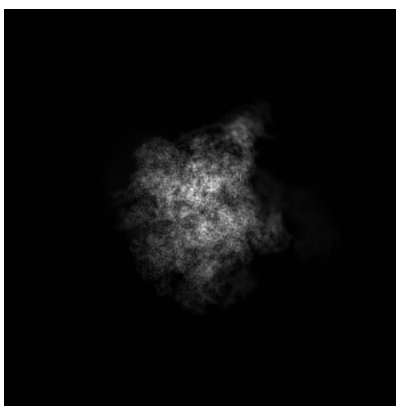
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

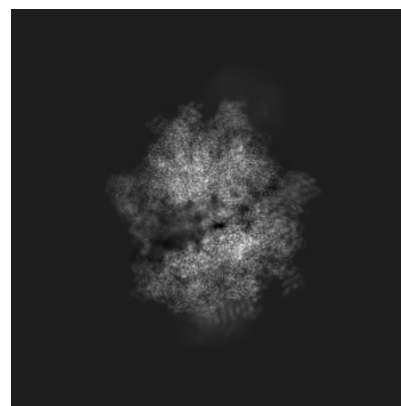
6.1.1 Primary map



X

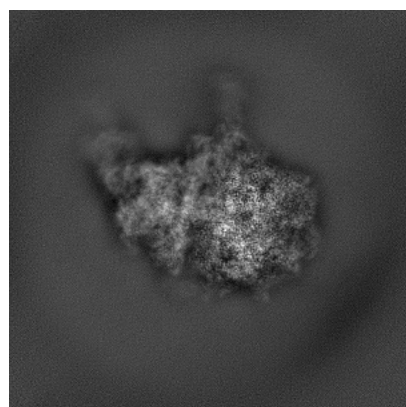


Y

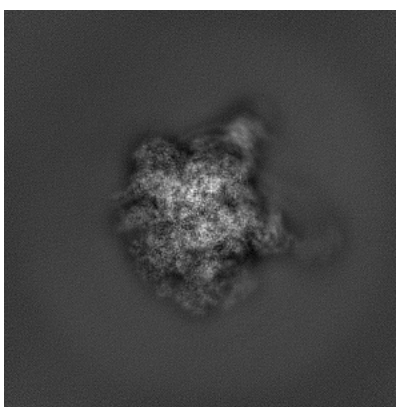


Z

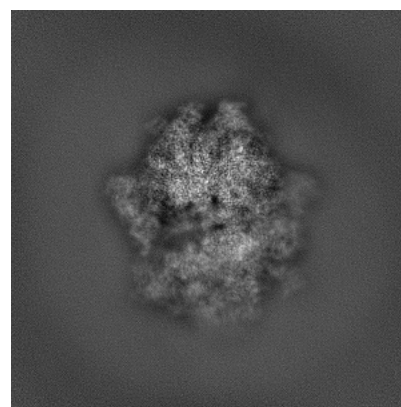
6.1.2 Raw map



X



Y



Z

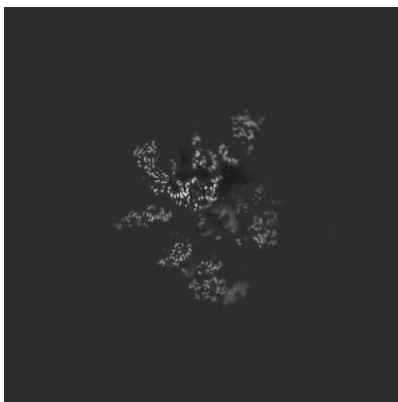
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

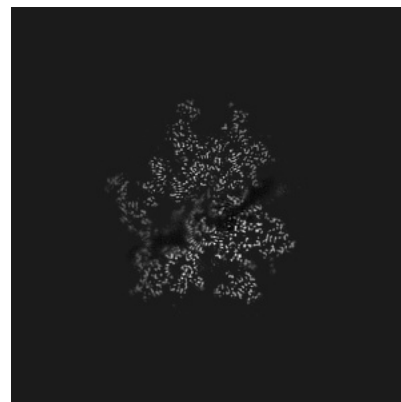
6.2.1 Primary map



X Index: 240

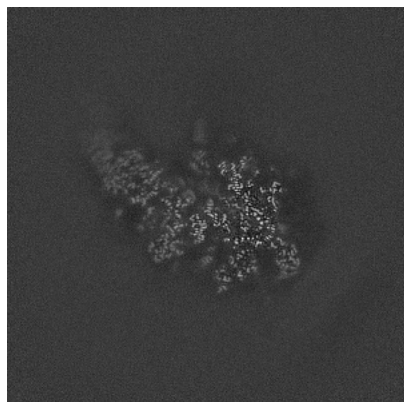


Y Index: 240

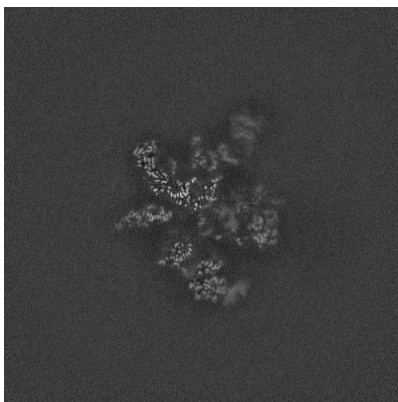


Z Index: 240

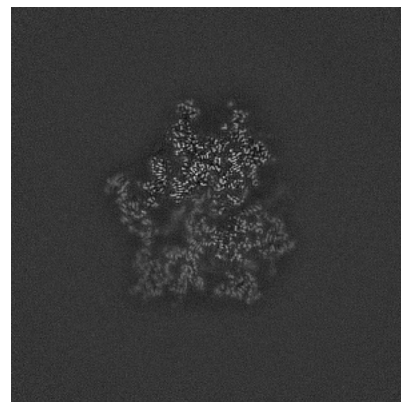
6.2.2 Raw map



X Index: 240



Y Index: 240

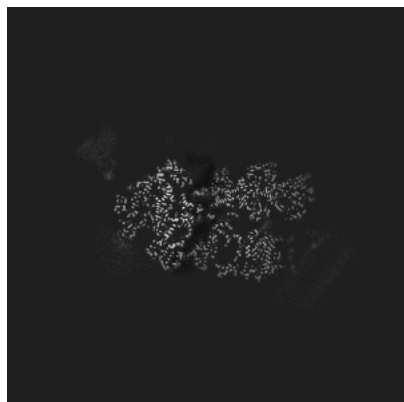


Z Index: 240

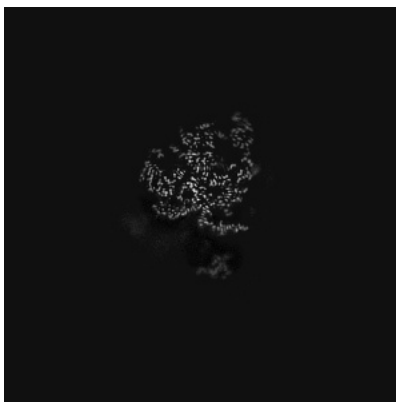
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

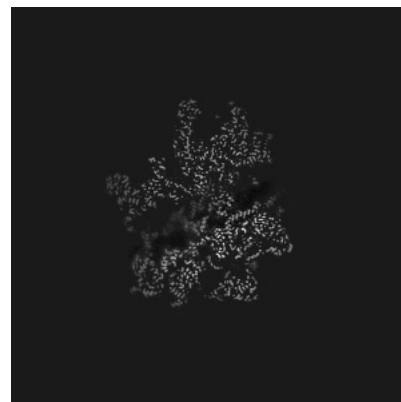
6.3.1 Primary map



X Index: 275

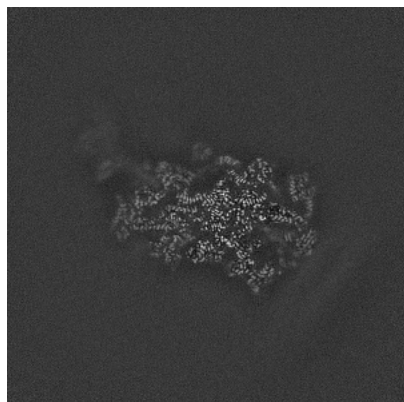


Y Index: 194

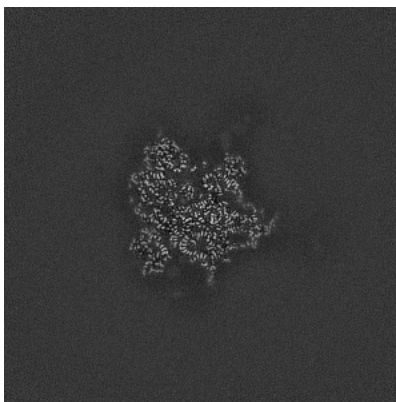


Z Index: 236

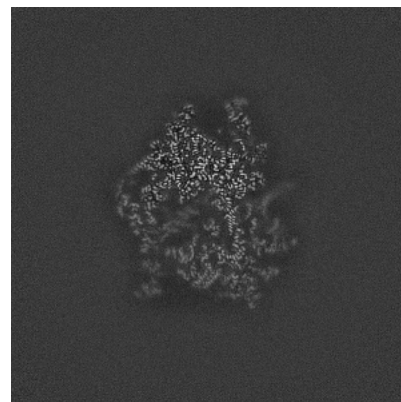
6.3.2 Raw map



X Index: 262



Y Index: 287

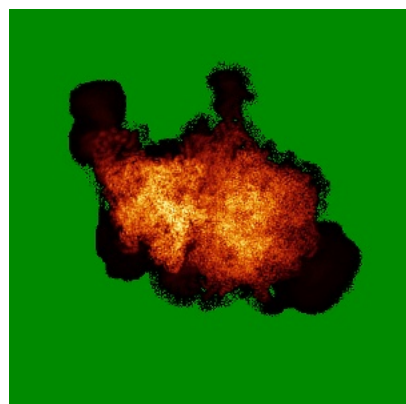


Z Index: 249

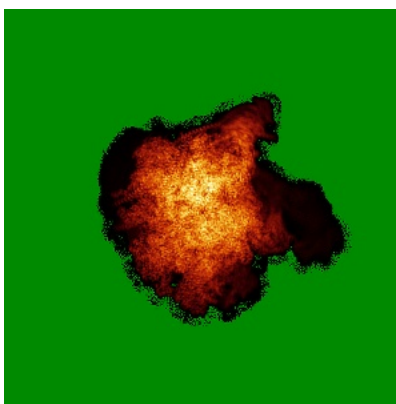
The images above show the largest variance slices of the map in three orthogonal directions.

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

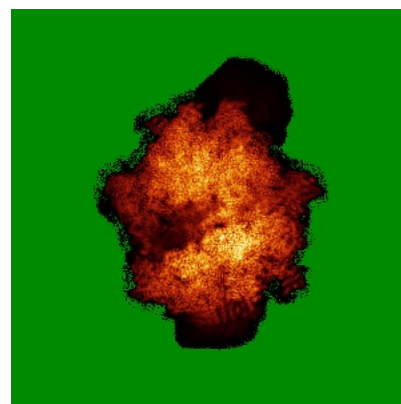
6.4.1 Primary map



X

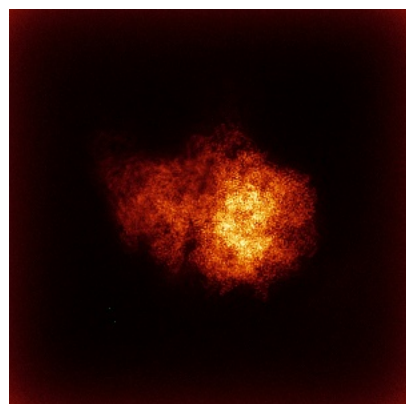


Y

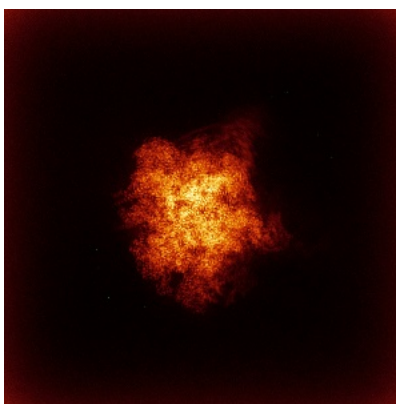


Z

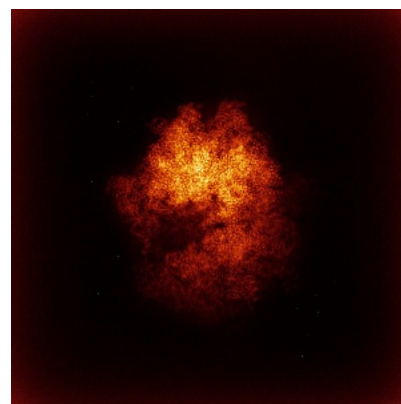
6.4.2 Raw map



X



Y

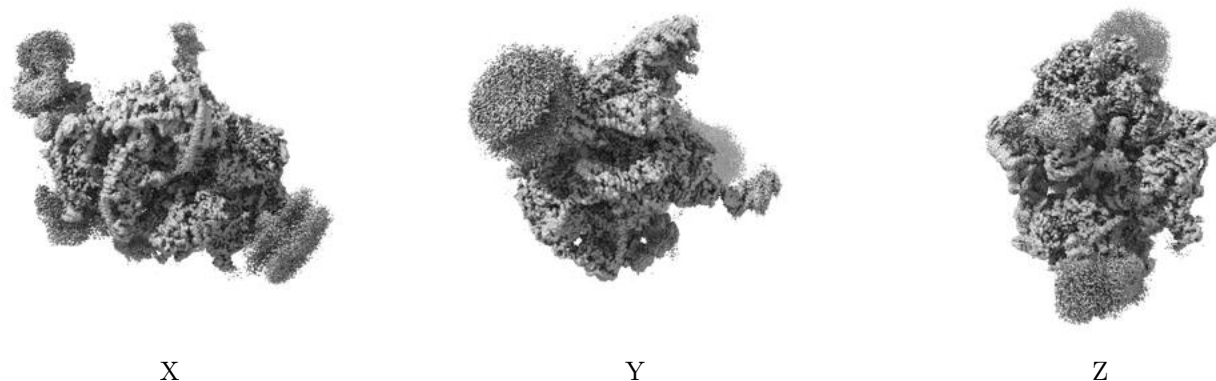


Z

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.

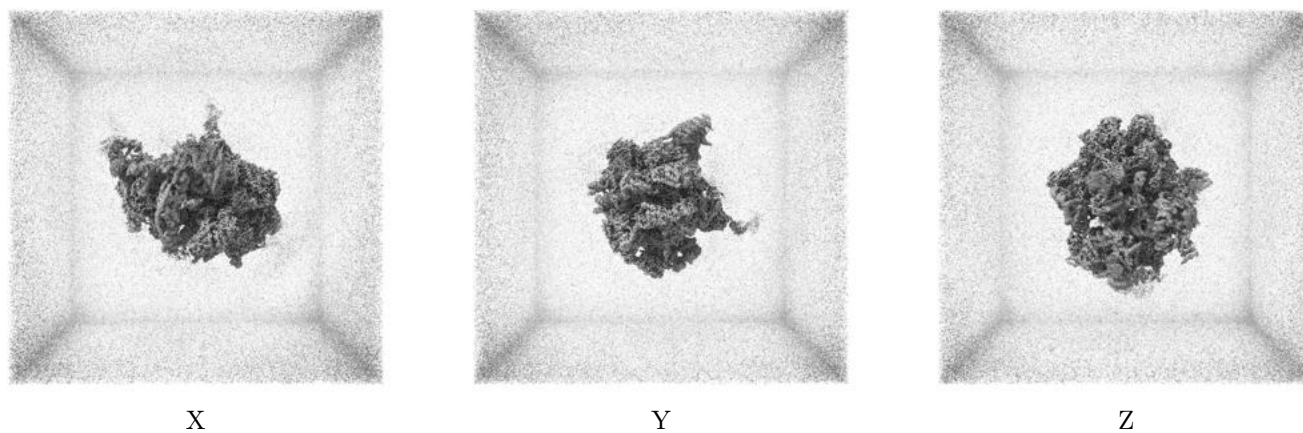
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.016. 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.

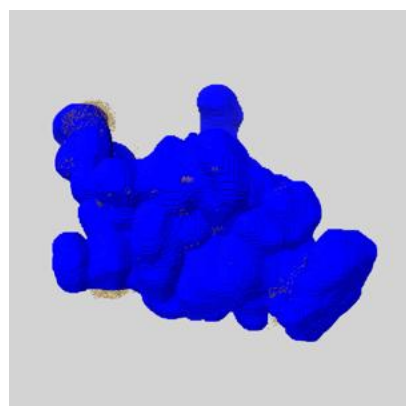
6.6 Mask visualisation [i](#)

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

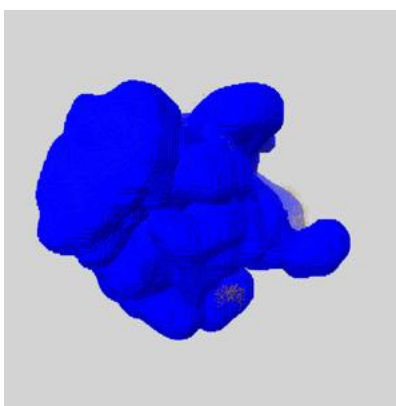
A mask typically either:

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

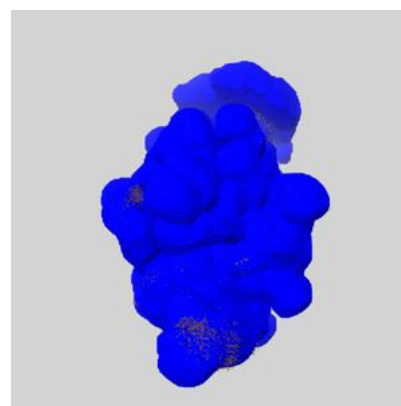
6.6.1 emd_70592_msk_1.map [i](#)



X



Y

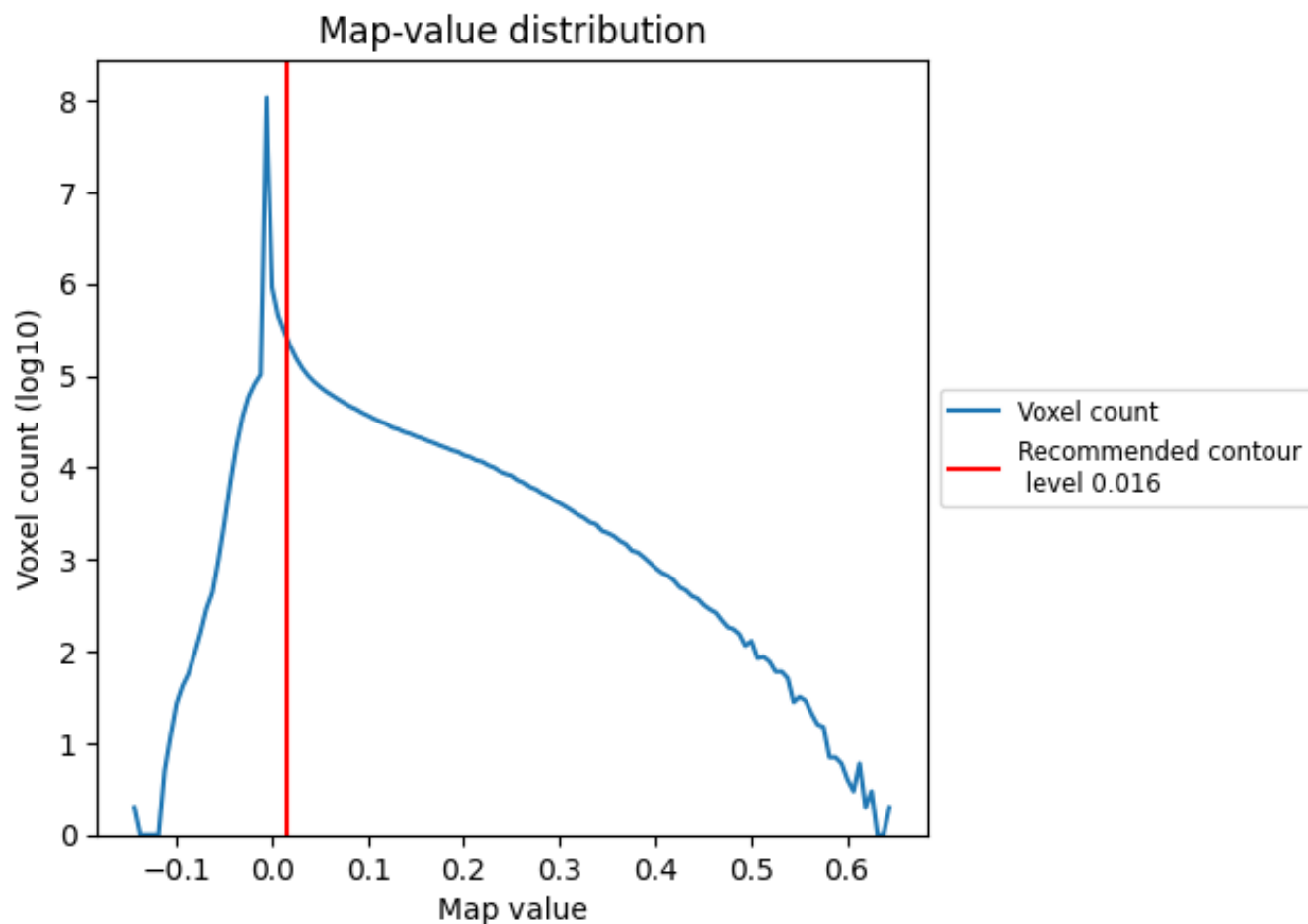


Z

7 Map analysis [i](#)

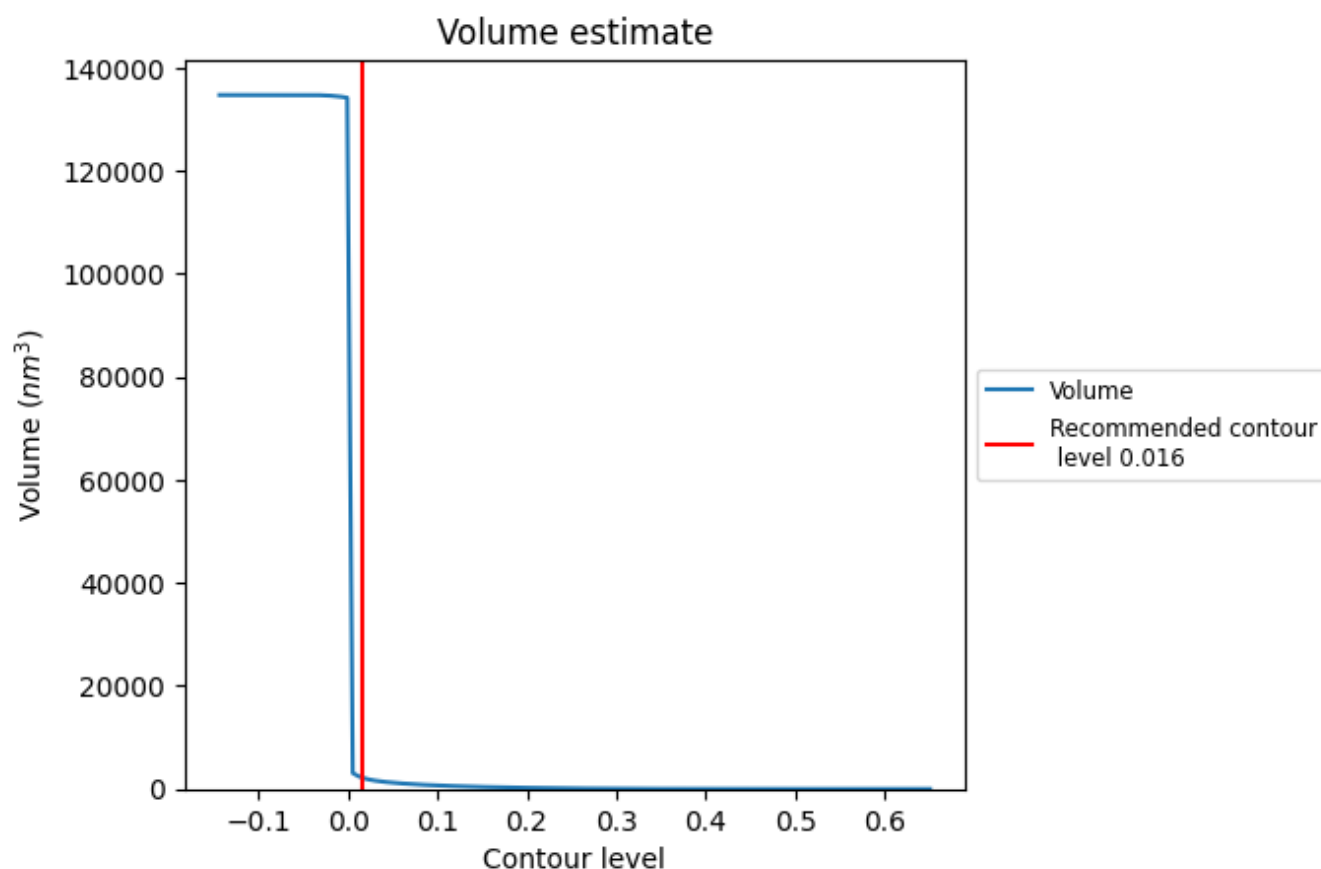
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

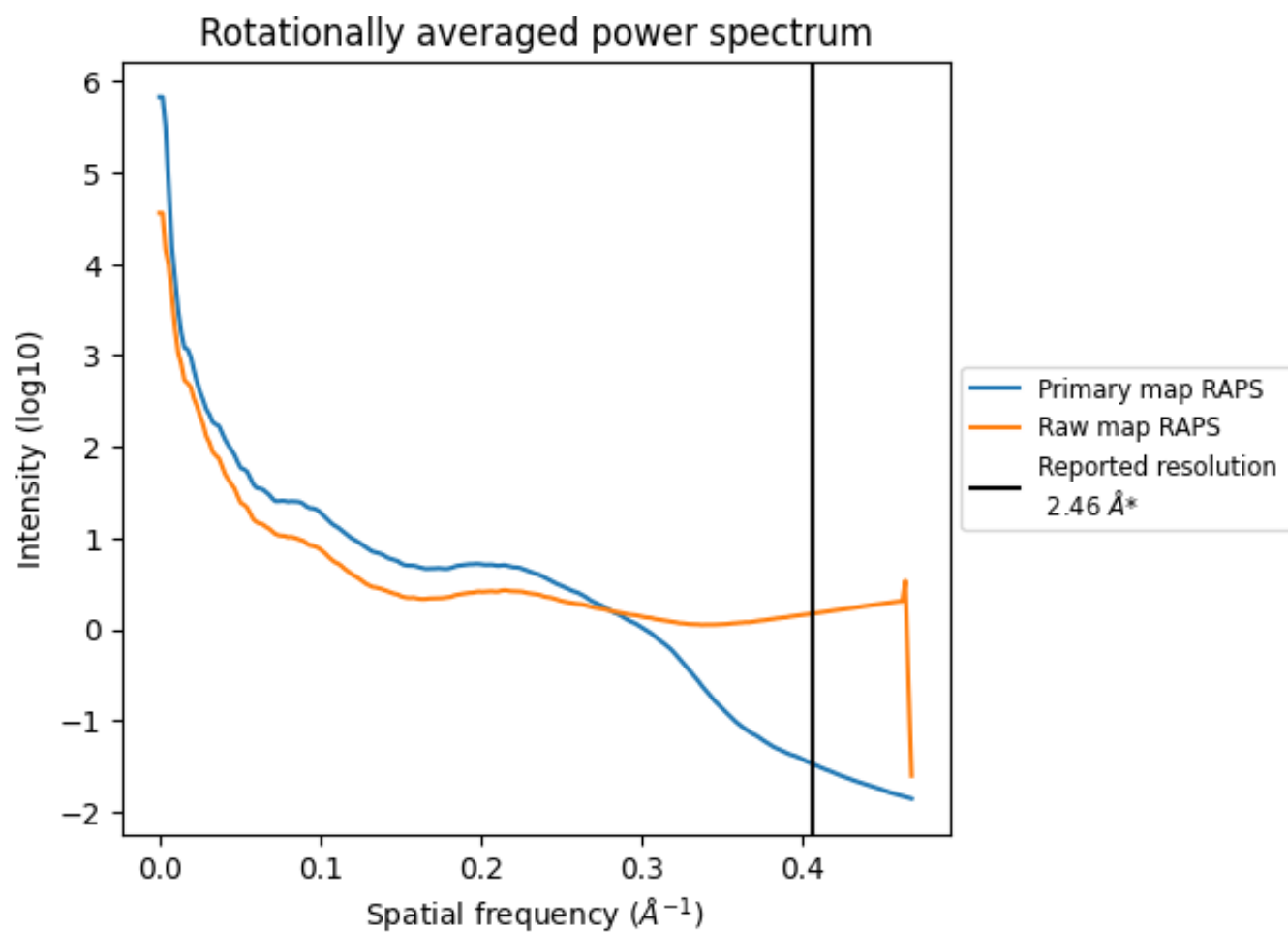
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2209 nm^3 ; this corresponds to an approximate mass of 1995 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 ⓘ

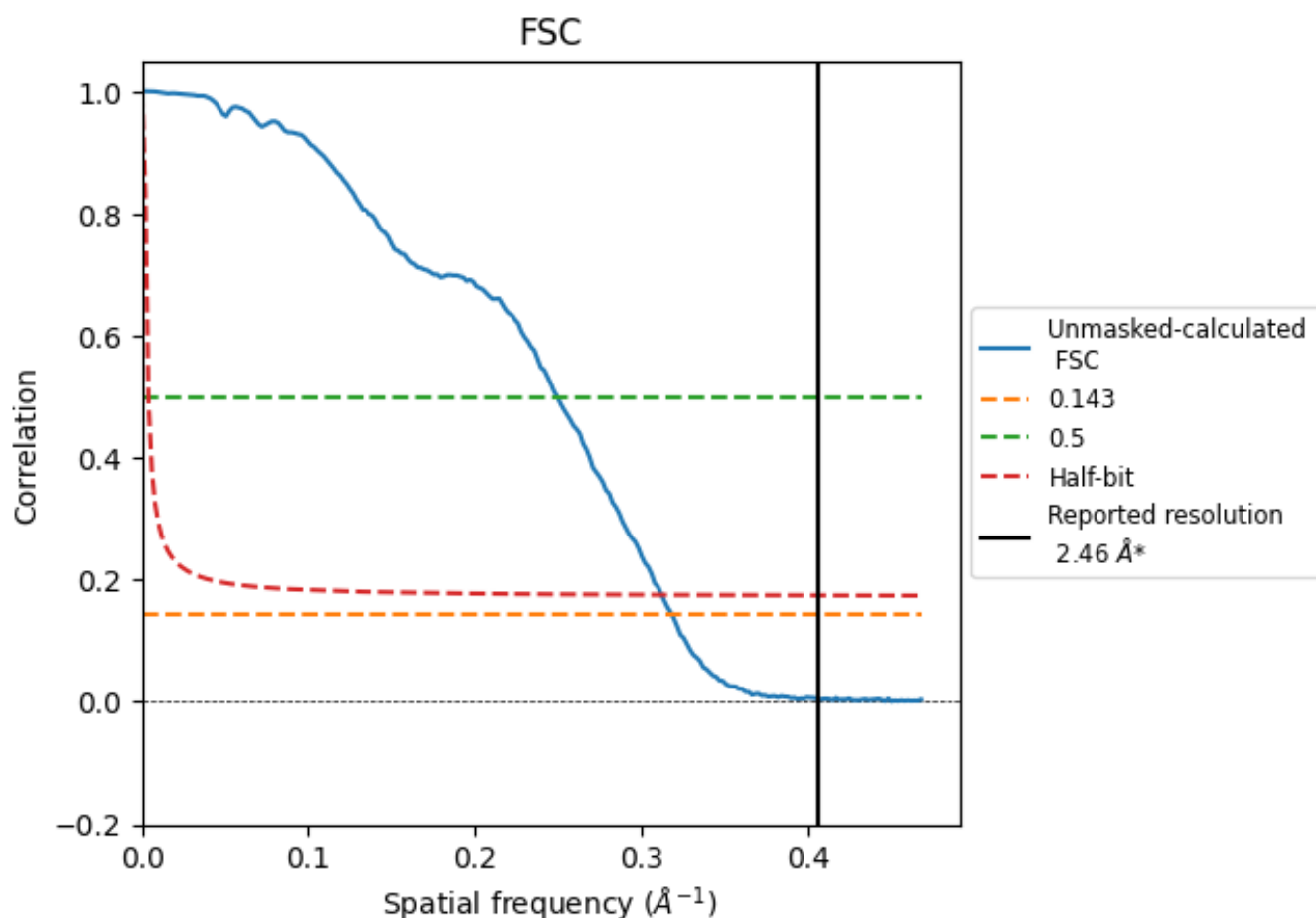


*Reported resolution corresponds to spatial frequency of 0.407 Å⁻¹

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 0.407 Å⁻¹

8.2 Resolution estimates [i](#)

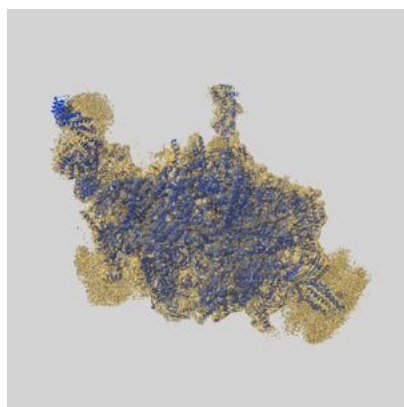
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.46	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.14	4.00	3.20

*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 3.14 differs from the reported value 2.46 by more than 10 %

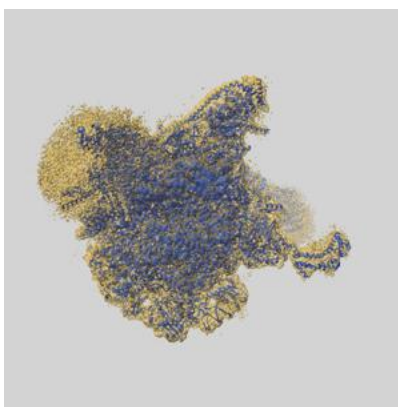
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-70592 and PDB model 9OLF. Per-residue inclusion information can be found in section [3](#) on page [28](#).

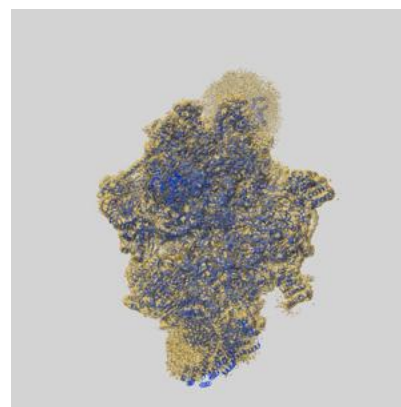
9.1 Map-model overlay [i](#)



X



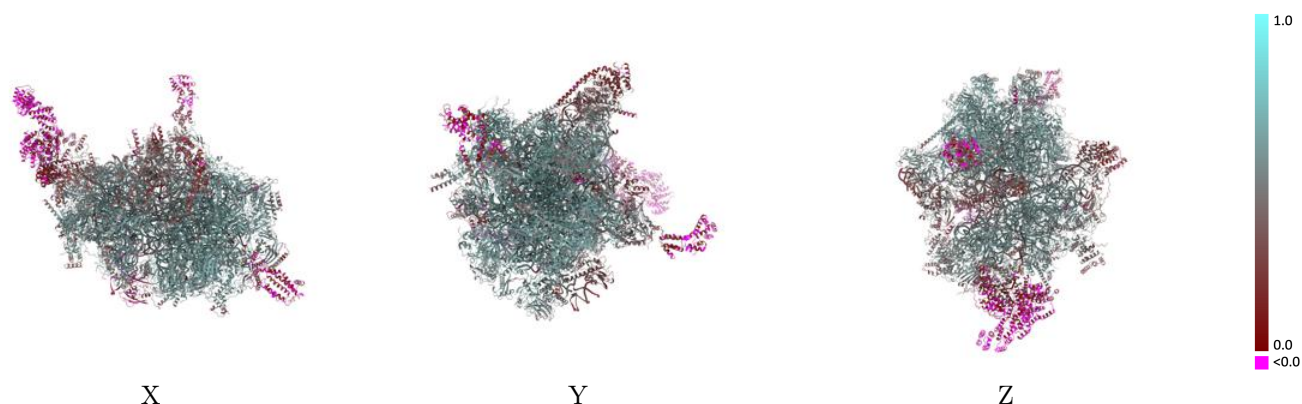
Y



Z

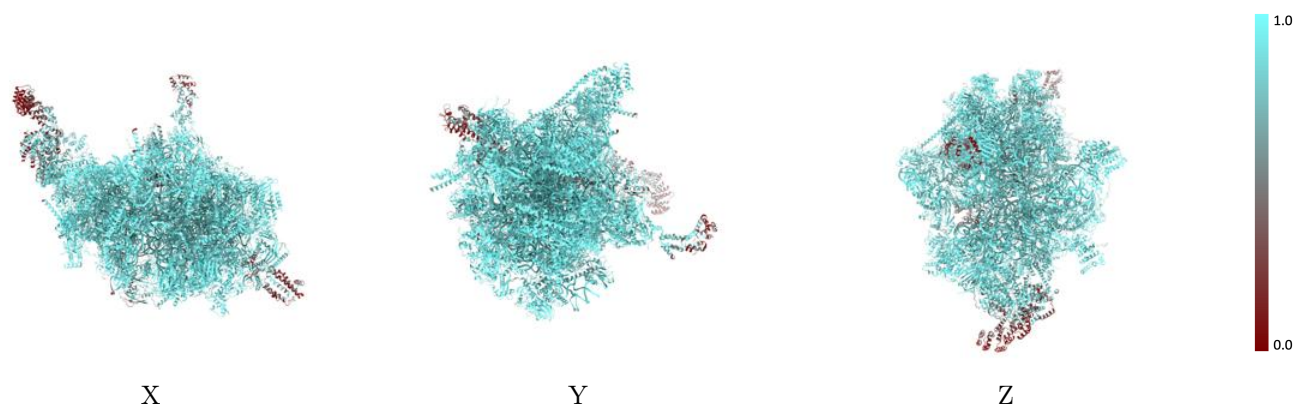
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



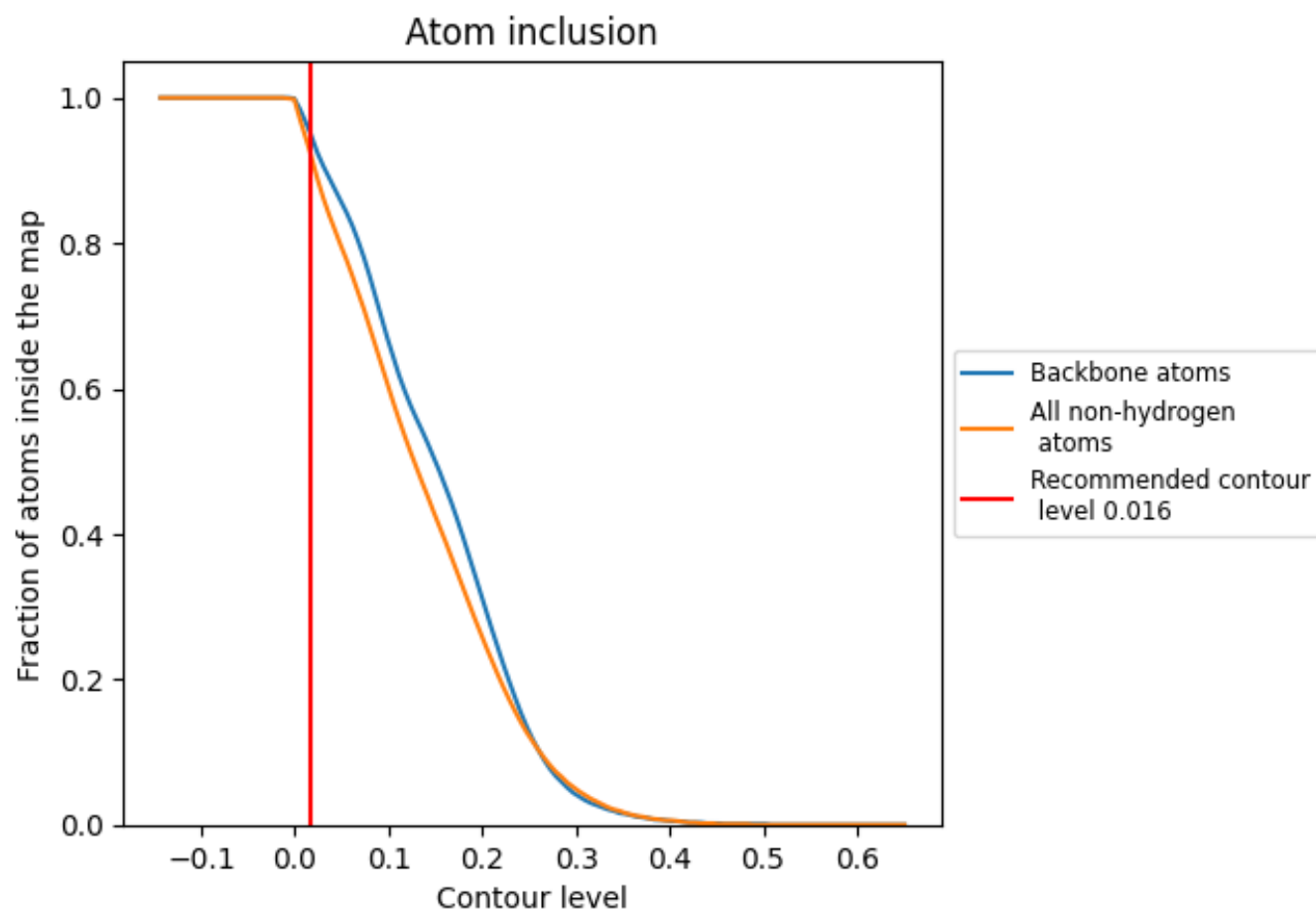
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.016).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9260	 0.4950
0	 0.9690	 0.5980
1	 0.9360	 0.5600
2	 0.9970	 0.6500
3	 0.9930	 0.6430
4	 0.9850	 0.6260
5	 0.9720	 0.5850
6	 0.9580	 0.5330
7	 0.9610	 0.5280
8	 0.8900	 0.3750
9	 0.9610	 0.5640
A	 0.9900	 0.5960
A0	 0.9420	 0.3940
A1	 0.9470	 0.4500
A2	 0.9340	 0.5120
A3	 0.9700	 0.5660
A4	 0.8700	 0.2200
A5	 0.4750	 0.0260
A6	 0.5020	 0.0080
AA	 0.9970	 0.5700
AB	 0.9700	 0.5530
AC	 0.9730	 0.5240
AD	 0.9530	 0.5160
AE	 0.9660	 0.5640
AF	 0.9690	 0.5310
AG	 0.9440	 0.5020
AH	 0.9400	 0.4930
AI	 0.9820	 0.5630
AJ	 0.9660	 0.5630
AK	 0.9820	 0.5850
AL	 0.9530	 0.5330
AM	 0.9450	 0.4670
AN	 0.9560	 0.5640
AO	 0.9630	 0.4830
AP	 0.9790	 0.5710



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Chain	Atom inclusion	Q-score
AQ	 0.9840	 0.5890
AR	 0.9440	 0.4250
AS	 0.9600	 0.4920
AT	 0.9500	 0.5300
AU	 0.9430	 0.4500
AV	 0.9250	 0.2610
AW	 0.9720	 0.5520
AX	 0.9760	 0.4870
AY	 0.6740	 0.2550
AZ	 0.9640	 0.5200
Aw	 0.9690	 0.3340
Ax	 0.9740	 0.4360
Ay	 0.5060	 0.1230
Az	 0.9680	 0.3060
B	 0.9700	 0.3840
C	 0.7170	 0.3440
D	 0.9880	 0.6020
E	 0.9720	 0.6090
F	 0.9890	 0.6210
G	 0.7180	 0.2300
H	 0.8230	 0.3300
I	 0.8830	 0.3920
J	 0.8960	 0.3720
K	 0.9860	 0.6240
L	 0.9840	 0.5950
M	 0.9790	 0.6150
N	 0.9740	 0.6070
O	 0.9820	 0.6110
OX	 0.4950	 0.1340
P	 0.9760	 0.5800
Q	 0.9480	 0.5580
R	 0.9790	 0.6230
S	 0.9760	 0.6100
T	 0.9840	 0.6250
U	 0.9040	 0.5410
V	 0.9560	 0.5430
W	 0.9820	 0.6260
X	 0.9610	 0.5820
Y	 0.9690	 0.5990
Z	 0.9710	 0.6110
a	 0.8880	 0.5060
b	 0.9740	 0.6140

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Chain	Atom inclusion	Q-score
c	 0.9610	 0.5720
d	 0.9140	 0.4860
e	 0.8980	 0.3270
f	 0.9000	 0.4280
g	 0.9730	 0.6000
h	 0.9660	 0.5360
i	 0.9930	 0.6380
j	 0.9540	 0.5590
k	 0.9300	 0.4750
l	 0.9120	 0.4190
m	 0.9280	 0.3680
n	 0.8840	 0.3450
o	 0.9860	 0.6330
p	 0.9150	 0.4960
q	 0.8410	 0.4090
r	 0.9790	 0.5940
s	 0.9730	 0.5950
t	 0.8190	 0.2170
u	 0.7230	 0.1420
v	 0.4650	 0.0500
w	 0.4610	 -0.0330
x	 0.2780	 0.0510
y	 0.1880	 0.0330
z	 0.4730	 0.0930