



wwPDB EM Validation Summary Report ⓘ

Sep 9, 2026 – 09:40 am BST

PDB ID : 7QI6 / pdb_00007qi6
EMDB ID : EMD-13982
Title : Human mitochondrial ribosome in complex with mRNA, A/P- and P/E-tRNAs at 2.98 Å resolution
Authors : Singh, V.; Itoh, Y.; Amunts, A.
Deposited on : 2021-12-14
Resolution : 2.98 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:

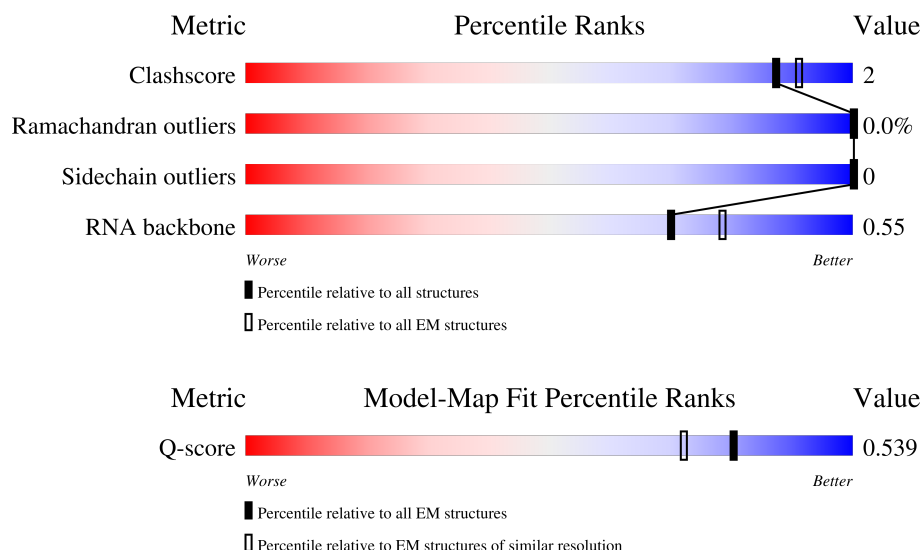
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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

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

The reported resolution of this entry is 2.98 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.



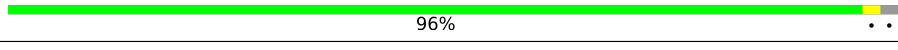
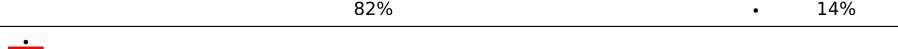
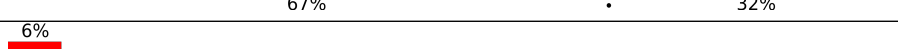
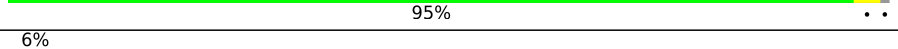
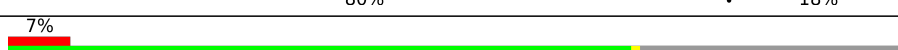
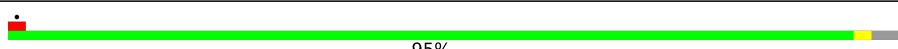
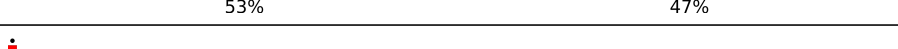
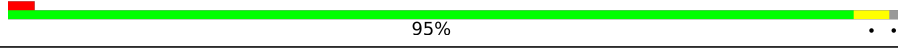
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13236 (2.48 - 3.48)

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	AA	954	
2	AB	296	
3	AC	167	

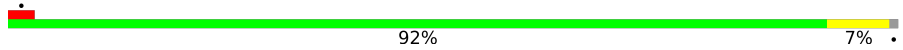
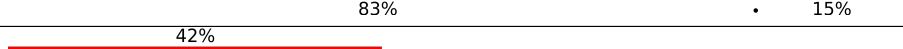
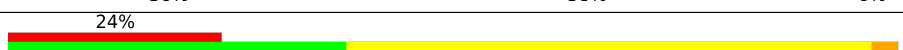
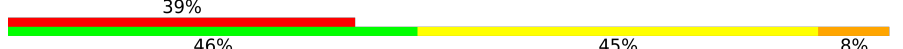
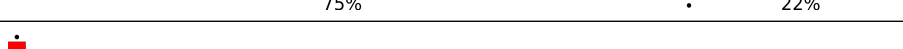
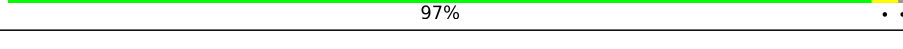
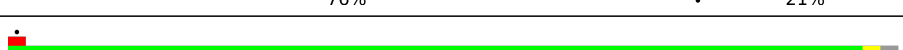
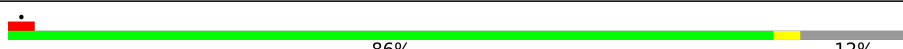
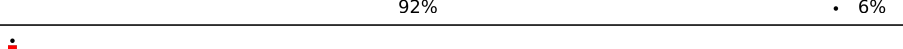
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Mol	Chain	Length	Quality of chain
4	AD	430	
5	AE	125	
6	AF	242	
7	AG	396	
8	AH	201	
9	AI	194	
10	AJ	138	
11	AK	128	
12	AL	257	
13	AM	137	
14	AN	130	
15	AO	258	
16	AP	142	
17	AQ	87	
18	AR	360	
19	AS	190	
20	AT	173	
21	AU	205	
22	AV	414	
23	AW	187	
24	AX	398	
25	AY	395	
26	AZ	106	
27	A0	217	
28	A1	323	

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Mol	Chain	Length	Quality of chain
29	A2	118	
30	A3	199	
31	A4	689	
32	Az	33	
33	Aw	68	
34	Ax	71	
35	A	1561	
36	B	72	
37	D	305	
38	E	348	
39	F	311	
40	I	261	
41	J	192	
42	K	178	
43	L	145	
44	M	296	
45	N	251	
46	O	175	
47	P	180	
48	R	149	
49	S	205	
50	T	206	
51	U	153	
52	V	216	
53	W	148	

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Mol	Chain	Length	Quality of chain
54	X	256	
55	Y	250	
56	Z	161	
57	0	188	
58	1	65	
59	2	92	
60	3	188	
61	4	103	
62	5	423	
63	6	380	
64	7	338	
65	8	206	
66	9	137	
67	a	142	
68	b	215	
69	c	332	
70	d	306	
71	e	279	
72	f	212	
73	g	166	
74	h	158	
75	i	128	
76	j	123	
77	k	112	
78	l	138	

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Mol	Chain	Length	Quality of chain
79	m	128	
80	o	102	
81	p	206	
82	q	222	
83	r	196	
84	s	439	
85	t	198	
85	u	198	
85	v	198	
85	w	198	
85	x	198	
85	y	198	
86	Q	292	
87	H	267	
88	z	325	

2 Entry composition

There are 100 unique types of molecules in this entry. The entry contains 336523 atoms, of which 153004 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 RNA chain called 12S mitochondrial rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	AA	954	Total	C	H	N	O	P	0	0
			30565	9088	10305	3647	6571	954		

- Molecule 2 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	AB	225	Total	C	H	N	O	S	0	0
			3644	1164	1816	331	323	10		

- Molecule 3 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	AC	132	Total	C	H	N	O	S	0	0
			2172	699	1089	195	185	4		

- Molecule 4 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	AD	339	Total	C	H	N	O	S	0	0
			5469	1695	2769	510	482	13		

- Molecule 5 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	AE	122	Total	C	H	N	O	S	0	0
			1972	614	1000	177	177	4		

- Molecule 6 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	AF	208	Total	C	H	N	O	S	0	0
			3495	1104	1770	312	298	11		

- Molecule 7 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	AG	328	Total	C	H	N	O	S	0	0
			5390	1714	2695	478	489	14		

- Molecule 8 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	AH	140	Total	C	H	N	O	S	0	0
			2336	745	1184	194	210	3		

- Molecule 9 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	AI	137	Total	C	H	N	O	S	0	0
			2081	642	1061	192	182	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AI	184	5F0	ASN	conflict	UNP P82912

- Molecule 10 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	AJ	108	Total	C	H	N	O	S	0	0
			1727	521	888	169	143	6		

- Molecule 11 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	AK	101	Total	C	H	N	O	S	0	0
			1748	537	886	179	141	5		

- Molecule 12 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AL	174	Total	C	H	N	O	S	0	0
			2994	925	1541	270	251	7		

- Molecule 13 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AM	119	Total	C	H	N	O	S	0	0
			1908	594	966	185	157	6		

- Molecule 14 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AN	110	Total	C	H	N	O	S	0	0
			1797	562	929	156	147	3		

- Molecule 15 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	AO	193	Total	C	H	N	O	S	0	0
			3153	1014	1561	294	277	7		

- Molecule 16 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	AP	97	Total	C	H	N	O	S	0	0
			1588	501	807	134	138	8		

- Molecule 17 is a protein called MRPS21 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	AQ	86	Total	C	H	N	O	S	0	0
			1501	460	757	150	126	8		

- Molecule 18 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	AR	295	Total	C	H	N	O	S	0	0
			4839	1533	2430	413	455	8		

- Molecule 19 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	AS	135	Total	C	H	N	O	S	0	0
			2227	716	1116	198	196	1		

- Molecule 20 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	AT	168	Total	C	H	N	O	S	0	0
			2764	877	1393	239	244	11		

- Molecule 21 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	AU	176	Total	C	H	N	O	S	0	0
			2989	916	1501	301	267	4		

- Molecule 22 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	AV	362	Total	C	H	N	O	S	0	0
			5933	1904	2964	495	558	12		

- Molecule 23 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	AW	100	Total	C	H	N	O	S	0	0
			1592	498	803	141	146	4		

- Molecule 24 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	AX	352	Total	C	H	N	O	S	0	0
			5694	1822	2845	499	517	11		

- Molecule 25 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	AY	149	Total	C	H	N	O	S	0	0
			2444	801	1198	207	234	4		

- Molecule 26 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	AZ	100	Total	C	H	N	O	S	0	0
			1698	534	859	153	148	4		

- Molecule 27 is a protein called 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	A0	215	Total	C	H	N	O	S	0	0
			3584	1130	1797	339	313	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
28	A1	279	Total	C	H	N	O	S	0	0
			4561	1435	2296	387	432	11		

- Molecule 29 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	A2	117	Total	C	H	N	O	S	0	0
			1905	579	970	182	166	8		

- Molecule 30 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	A3	70	Total	C	H	N	O	S	0	0
			1326	401	701	134	89	1		

- Molecule 31 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	A4	588	Total	C	H	N	O	S	0	0
			9538	3053	4770	808	879	28		

- Molecule 32 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	Az	33	Total	C	H	N	O	P	0	0
			1052	316	351	124	228	33		

- Molecule 33 is a RNA chain called A/P-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	Aw	68	Total	C	H	N	O	P	0	0
			2161	646	726	249	472	68		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Aw	35	A	C	conflict	GB 1896813690
Aw	36	C	G	conflict	GB 1896813690
Aw	44	C	A	conflict	GB 1896813690

- Molecule 34 is a RNA chain called P/E-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	Ax	71	Total	C	H	N	O	P	0	0
			2262	672	763	260	496	71		

- Molecule 35 is a RNA chain called 16S mitochondrial rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	A	1558	Total	C	H	N	O	P	0	0
			49872	14843	16802	5963	10706	1558		

- Molecule 36 is a RNA chain called mitochondrial tRNA^{Val}.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	B	72	Total	C	H	N	O	P	0	0
			2303	685	779	269	498	72		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	74	C	G	conflict	GB NC_012920.1
B	76	A	U	conflict	GB NC_012920.1

- Molecule 37 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	D	238	Total	C	H	N	O	S	0	0
			3780	1157	1921	376	317	9		

- Molecule 38 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	E	305	Total	C	H	N	O	S	0	0
			4822	1545	2416	418	432	11		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
39	F	252	Total	C	H	N	O	S	0	0
			4097	1305	2066	370	350	6		

- Molecule 40 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	I	212	Total	C	H	N	O	S	0	0
			3481	1088	1786	304	292	11		

- Molecule 41 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	J	175	Total	C	H	N	O	S	0	0
			2738	847	1408	237	244	2		

- Molecule 42 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	K	177	Total	C	H	N	O	S	0	0
			2906	936	1451	259	253	7		

- Molecule 43 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	L	115	Total	C	H	N	O	S	0	0
			1832	559	942	171	155	5		

- Molecule 44 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	M	291	Total	C	H	N	O	S	0	0
			4723	1483	2396	430	408	6		

- Molecule 45 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	N	222	Total	C	H	N	O	S	0	0
			3604	1143	1818	326	307	10		

- Molecule 46 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	O	154	Total	C	H	N	O	S	
			2554	792	1295	241	219	7	
								0	0

- Molecule 47 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	P	144	Total	C	H	N	O	S	
			2339	733	1166	224	211	5	
								0	0

- Molecule 48 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	R	140	Total	C	H	N	O	S	
			2369	732	1215	231	187	4	
								0	0

- Molecule 49 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S	161	Total	C	H	N	O	S	
			2659	835	1366	227	227	4	
								0	0

- Molecule 50 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	T	166	Total	C	H	N	O	S	
			2781	875	1412	254	233	7	
								0	0

- Molecule 51 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	U	152	Total	C	H	N	O	S	
			2482	788	1231	234	226	3	
								0	0

- Molecule 52 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	V	205	Total	C	H	N	O	S	
			3365	1068	1689	298	302	8	
								0	0

- Molecule 53 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	W	113	Total	C	H	N	O	S	0	0
			1785	562	905	166	149	3		

- Molecule 54 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	X	244	Total	C	H	N	O	S	0	0
			4105	1322	2061	352	365	5		

- Molecule 55 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	Y	181	Total	C	H	N	O	S	0	0
			3154	995	1598	298	259	4		

- Molecule 56 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	Z	122	Total	C	H	N	O	S	0	0
			2041	636	1045	186	171	3		

- Molecule 57 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	0	110	Total	C	H	N	O	S	0	0
			1815	554	917	176	162	6		

- Molecule 58 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	1	56	Total	C	H	N	O	S	0	0
			977	296	513	89	77	2		

- Molecule 59 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	2	46	Total	C	H	N	O	S	0	0
			784	233	407	83	60	1		

- Molecule 60 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	3	95	Total	C	H	N	O	S	0	0
			1716	539	884	162	128	3		

- Molecule 61 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	4	38	Total	C	H	N	O	S	0	0
			704	217	362	72	49	4		

- Molecule 62 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	5	393	Total	C	H	N	O	S	0	0
			6402	2067	3202	557	565	11		

- Molecule 63 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	6	354	Total	C	H	N	O	S	0	0
			5792	1881	2844	525	533	9		

- Molecule 64 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	7	294	Total	C	H	N	O	S	0	0
			4789	1529	2399	405	438	18		

- Molecule 65 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	8	150	Total	C	H	N	O	S	0	0
			2566	806	1297	224	237	2		

- Molecule 66 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
66	9	124	Total	C	H	N	O	S	0	0
			1985	644	988	170	181	2		

- Molecule 67 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
67	a	100	Total	C	H	N	O	S	0	0
			1652	529	812	152	154	5		

- Molecule 68 is a protein called Large ribosomal subunit protein mL43.

Mol	Chain	Residues	Atoms						AltConf	Trace
68	b	151	Total	C	H	N	O	S	0	0
			2391	744	1195	231	218	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	2	ACE	-	acetylation	UNP Q8N983

- Molecule 69 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
69	c	286	Total	C	H	N	O	S	0	0
			4621	1470	2322	397	423	9		

- Molecule 70 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	d	241	Total	C	H	N	O	S	0	0
			3965	1273	1980	340	359	13		

- Molecule 71 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
71	e	230	Total	C	H	N	O	S	0	0
			3736	1185	1870	329	346	6		

- Molecule 72 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
72	f	157	Total	C	H	N	O	S	0	0
			2523	799	1271	207	242	4		

- Molecule 73 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
73	g	134	Total	C	H	N	O	S	0	0
			2210	719	1097	193	199	2		

- Molecule 74 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	h	110	Total	C	H	N	O	S	0	0
			1777	568	882	156	168	3		

- Molecule 75 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
75	i	97	Total	C	H	N	O	S	0	0
			1687	532	859	165	127	4		

- Molecule 76 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
76	j	94	Total	C	H	N	O	S	0	0
			1492	463	747	144	136	2		

- Molecule 77 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	k	101	Total	C	H	N	O	S	0	0
			1558	479	784	148	142	5		

- Molecule 78 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
78	l	82	Total	C	H	N	O	S	0	0
			1363	437	675	120	128	3		

- Molecule 79 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
79	m	92	Total	C	H	N	O	S	0	0
			1552	488	761	159	142	2		

- Molecule 80 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
80	o	94	Total	C	H	N	O	S	0	0
			1604	501	806	165	129	3		

- Molecule 81 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
81	p	147	Total	C	H	N	O	S	0	0
			2431	748	1226	228	225	4		

- Molecule 82 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
82	q	166	Total	C	H	N	O	S	0	0
			2726	870	1328	272	251	5		

- Molecule 83 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
83	r	162	Total	C	H	N	O	S	0	0
			2671	839	1349	252	223	8		

- Molecule 84 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
84	s	386	Total	C	H	N	O	S	0	0
			6298	2023	3143	559	559	14		

- Molecule 85 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
85	t	46	Total	C	H	N	O		0	0
			732	228	378	56	70			
85	u	32	Total	C	H	N	O		0	0
			541	168	284	40	49			
85	v	32	Total	C	H	N	O		0	0
			541	168	284	40	49			
85	w	31	Total	C	H	N	O		0	0
			520	159	275	39	47			
85	x	31	Total	C	H	N	O		0	0
			520	159	275	39	47			
85	y	31	Total	C	H	N	O		0	0
			520	159	275	39	47			

- Molecule 86 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
86	Q	239	4021	1277	2031	353	351	9	0	0

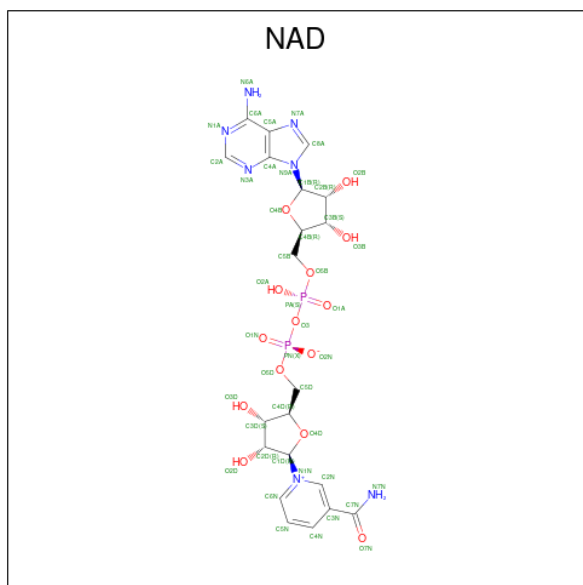
- Molecule 87 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
87	H	202	3398	1067	1737	304	286	4	0	0

- Molecule 88 is a protein called 39S ribosomal protein L1, mitochondrial.

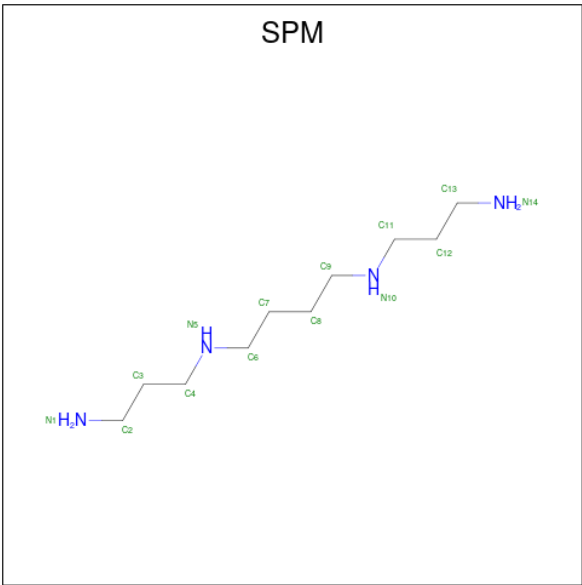
Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
88	z	252	4104	1304	2077	336	381	6	0	0

- Molecule 89 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



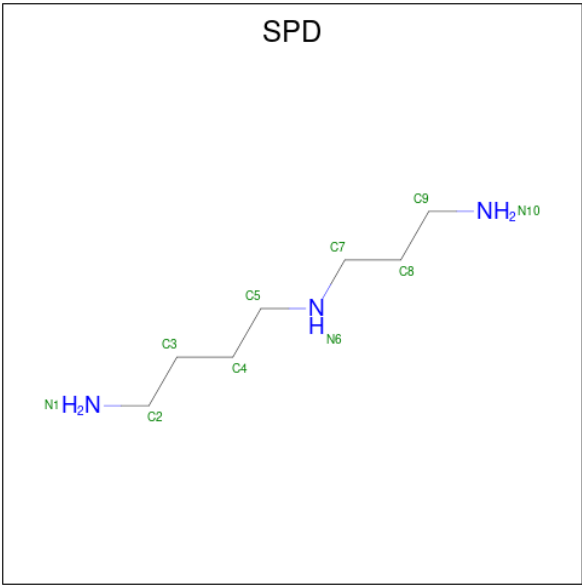
Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
89	AA	1	70	21	26	7	14	2	0

- Molecule 90 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	H	N	
90	AA	1	44	10	30	4	0

- Molecule 91 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	H	N	
91	AA	1	32	7	22	3	0
91	A	1	32	7	22	3	0
91	A	1	32	7	22	3	0

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Mol	Chain	Residues	Atoms				AltConf
91	A	1	Total	C	H	N	0
			32	7	22	3	

- Molecule 92 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
92	AA	20	Total	K	0
			20	20	
92	A	27	Total	K	0
			27	27	
92	D	1	Total	K	0
			1	1	
92	M	1	Total	K	0
			1	1	
92	N	1	Total	K	0
			1	1	
92	3	1	Total	K	0
			1	1	
92	6	1	Total	K	0
			1	1	
92	i	1	Total	K	0
			1	1	
92	o	1	Total	K	0
			1	1	

- Molecule 93 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
93	AA	57	Total	Mg	0
			57	57	
93	AB	1	Total	Mg	0
			1	1	
93	AX	1	Total	Mg	0
			1	1	
93	A3	1	Total	Mg	0
			1	1	
93	A	137	Total	Mg	0
			137	137	
93	D	2	Total	Mg	0
			2	2	
93	E	1	Total	Mg	0
			1	1	

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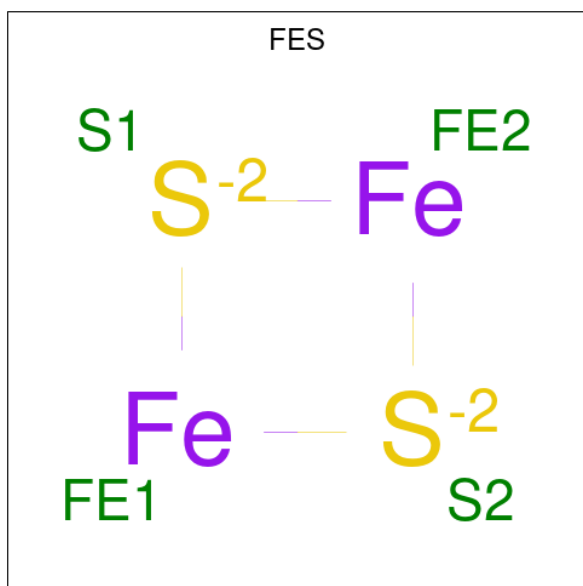
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Mol	Chain	Residues	Atoms		AltConf
93	8	1	Total	Mg	0
			1	1	
93	g	1	Total	Mg	0
			1	1	

- Molecule 94 is ZINC ION (CCD ID: ZN) (formula: Zn).

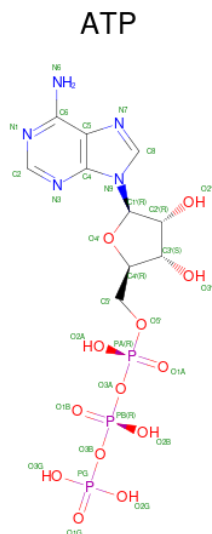
Mol	Chain	Residues	Atoms		AltConf
94	AO	1	Total	Zn	0
			1	1	
94	0	1	Total	Zn	0
			1	1	
94	4	1	Total	Zn	0
			1	1	

- Molecule 95 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



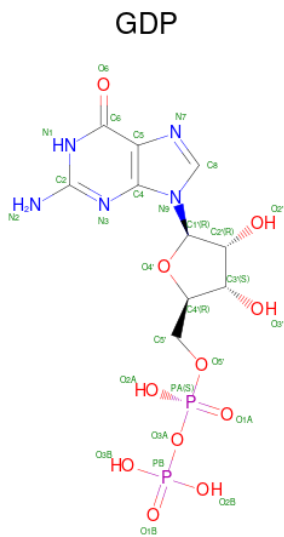
Mol	Chain	Residues	Atoms			AltConf
95	AP	1	Total	Fe	S	0
			4	2	2	
95	AT	1	Total	Fe	S	0
			4	2	2	
95	r	1	Total	Fe	S	0
			4	2	2	

- Molecule 96 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



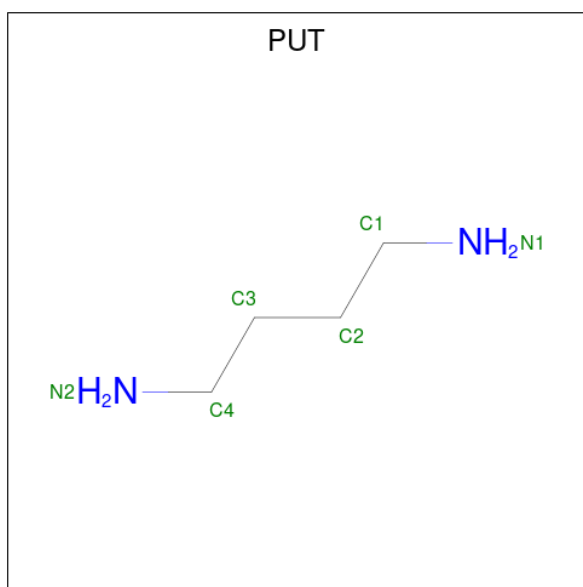
Mol	Chain	Residues	Atoms						AltConf
96	AX	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	

- Molecule 97 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{11}\text{P}_2$).



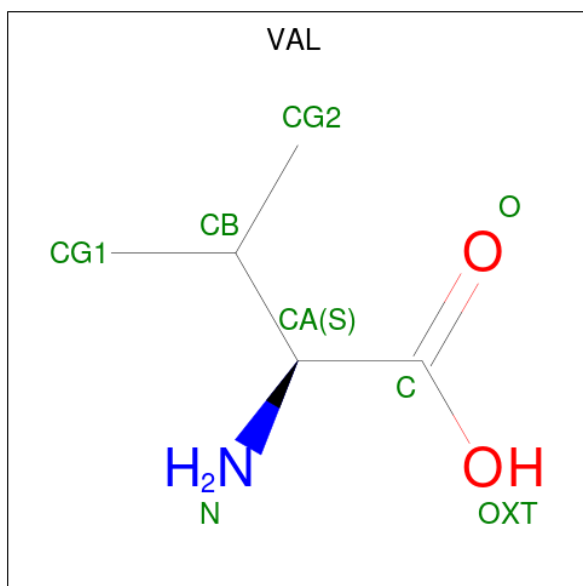
Mol	Chain	Residues	Atoms						AltConf
97	AX	1	Total	C	H	N	O	P	0
			40	10	12	5	11	2	

- Molecule 98 is 1,4-DIAMINOBUTANE (CCD ID: PUT) (formula: $\text{C}_4\text{H}_{12}\text{N}_2$).



Mol	Chain	Residues	Atoms				AltConf
98	A	1	Total	C	H	N	0
			20	4	14	2	

- Molecule 99 is VALINE (CCD ID: VAL) (formula: C₅H₁₁NO₂).



Mol	Chain	Residues	Atoms					AltConf
99	B	1	Total	C	H	N	O	0
			18	5	11	1	1	

- Molecule 100 is water.

Mol	Chain	Residues	Atoms		AltConf
100	AA	649	Total 649	O 649	0
100	AB	11	Total 11	O 11	0
100	AC	20	Total 20	O 20	0
100	AD	20	Total 20	O 20	0
100	AE	4	Total 4	O 4	0
100	AF	5	Total 5	O 5	0
100	AG	6	Total 6	O 6	0
100	AH	14	Total 14	O 14	0
100	AI	13	Total 13	O 13	0
100	AJ	11	Total 11	O 11	0
100	AK	11	Total 11	O 11	0
100	AL	15	Total 15	O 15	0
100	AM	1	Total 1	O 1	0
100	AN	6	Total 6	O 6	0
100	AO	4	Total 4	O 4	0
100	AP	9	Total 9	O 9	0
100	AQ	22	Total 22	O 22	0
100	AS	2	Total 2	O 2	0
100	AT	4	Total 4	O 4	0
100	AW	1	Total 1	O 1	0
100	AX	1	Total 1	O 1	0
100	AY	2	Total 2	O 2	0

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Mol	Chain	Residues	Atoms		AltConf
100	AZ	8	Total 8	O 8	0
100	A1	4	Total 4	O 4	0
100	A2	8	Total 8	O 8	0
100	A3	15	Total 15	O 15	0
100	Az	3	Total 3	O 3	0
100	Aw	2	Total 2	O 2	0
100	Ax	1	Total 1	O 1	0
100	A	1824	Total 1824	O 1824	0
100	B	3	Total 3	O 3	0
100	D	31	Total 31	O 31	0
100	E	33	Total 33	O 33	0
100	F	53	Total 53	O 53	0
100	I	7	Total 7	O 7	0
100	K	33	Total 33	O 33	0
100	L	7	Total 7	O 7	0
100	M	36	Total 36	O 36	0
100	N	18	Total 18	O 18	0
100	O	9	Total 9	O 9	0
100	P	12	Total 12	O 12	0
100	R	38	Total 38	O 38	0
100	S	29	Total 29	O 29	0

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Mol	Chain	Residues	Atoms		AltConf
100	T	22	Total 22	O 22	0
100	U	9	Total 9	O 9	0
100	V	3	Total 3	O 3	0
100	W	14	Total 14	O 14	0
100	X	1	Total 1	O 1	0
100	Y	12	Total 12	O 12	0
100	Z	18	Total 18	O 18	0
100	0	19	Total 19	O 19	0
100	2	26	Total 26	O 26	0
100	3	22	Total 22	O 22	0
100	4	1	Total 1	O 1	0
100	5	4	Total 4	O 4	0
100	6	11	Total 11	O 11	0
100	7	1	Total 1	O 1	0
100	9	11	Total 11	O 11	0
100	a	4	Total 4	O 4	0
100	b	21	Total 21	O 21	0
100	c	7	Total 7	O 7	0
100	f	1	Total 1	O 1	0
100	g	5	Total 5	O 5	0
100	i	27	Total 27	O 27	0

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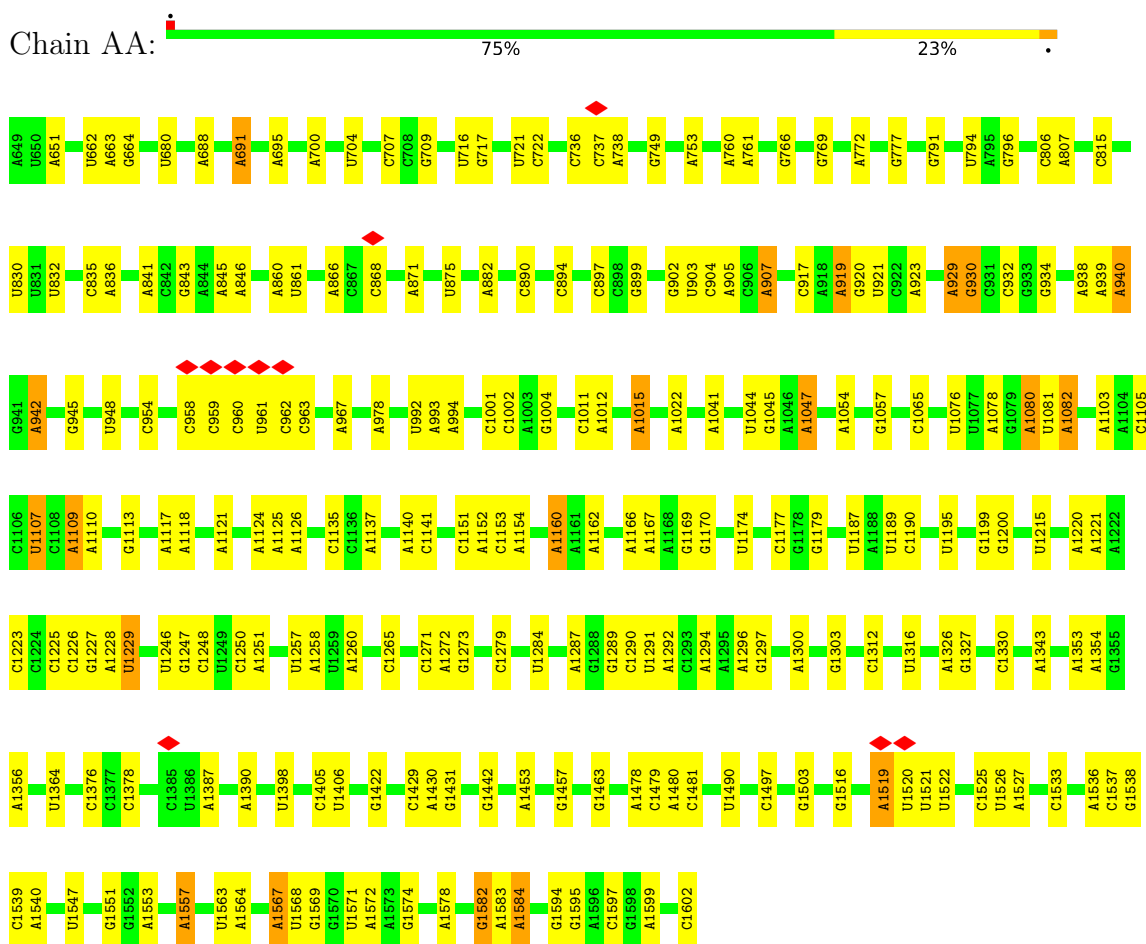
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Mol	Chain	Residues	Atoms		AltConf
100	j	6	Total 6	O 6	0
100	o	16	Total 16	O 16	0
100	p	1	Total 1	O 1	0
100	r	7	Total 7	O 7	0
100	s	18	Total 18	O 18	0
100	Q	6	Total 6	O 6	0
100	H	6	Total 6	O 6	0

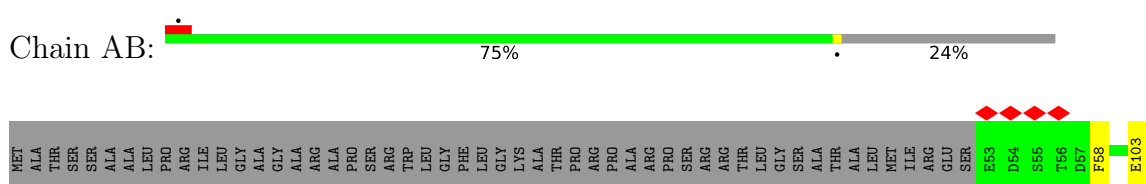
3 Residue-property plots

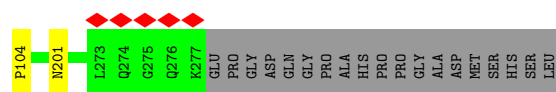
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 12S mitochondrial rRNA



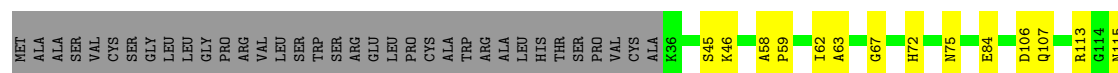
• Molecule 2: 28S ribosomal protein S2, mitochondrial





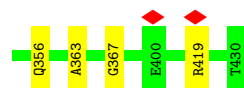
- Molecule 3: 28S ribosomal protein S24, mitochondrial

Chain AC: 71% 8% 21%



- Molecule 4: 28S ribosomal protein S5, mitochondrial

Chain AD: 76% 21%



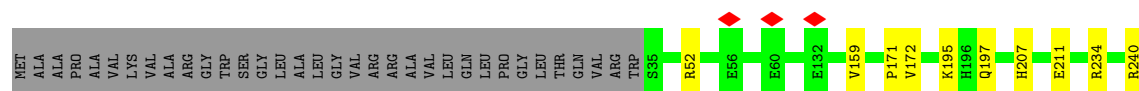
- Molecule 5: 28S ribosomal protein S6, mitochondrial

Chain AE: 96% ..



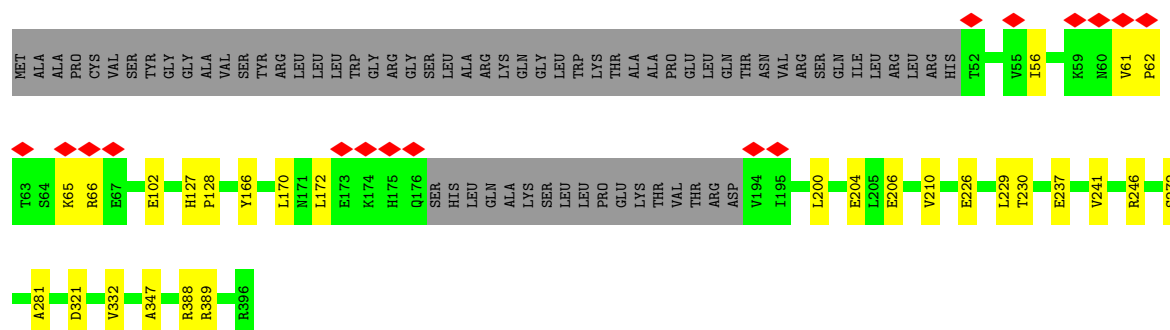
- Molecule 6: 28S ribosomal protein S7, mitochondrial

Chain AF: 82% 14%



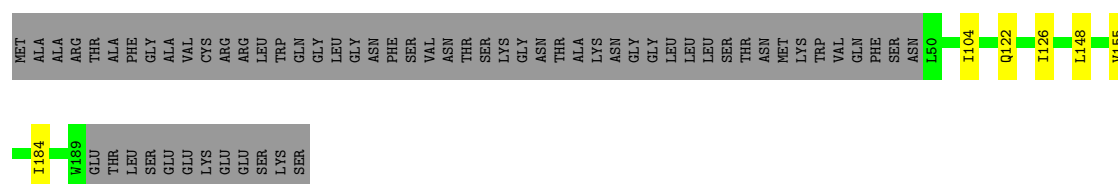
- Molecule 7: 28S ribosomal protein S9, mitochondrial

Chain AG: 76% 7% 17%



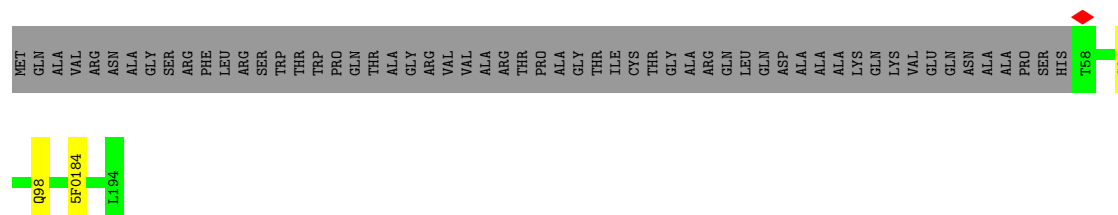
- Molecule 8: 28S ribosomal protein S10, mitochondrial

Chain AH: 67% 30%



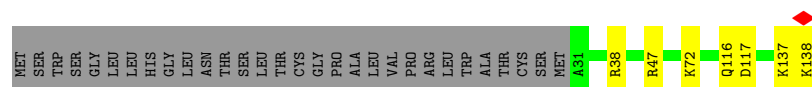
- Molecule 9: 28S ribosomal protein S11, mitochondrial

Chain AI: 69% 29%



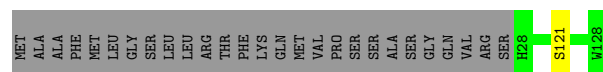
- Molecule 10: 28S ribosomal protein S12, mitochondrial

Chain AJ: 73% 5% 22%



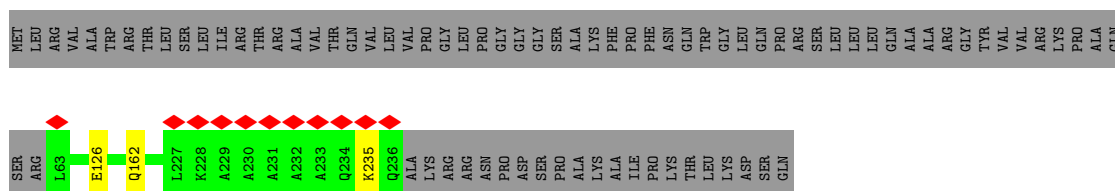
- Molecule 11: 28S ribosomal protein S14, mitochondrial

Chain AK: 78% 21%

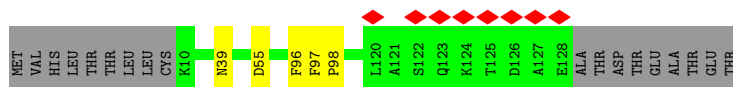
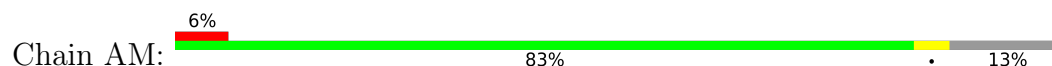


- Molecule 12: 28S ribosomal protein S15, mitochondrial

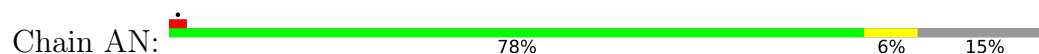
Chain AL: 67% 32%



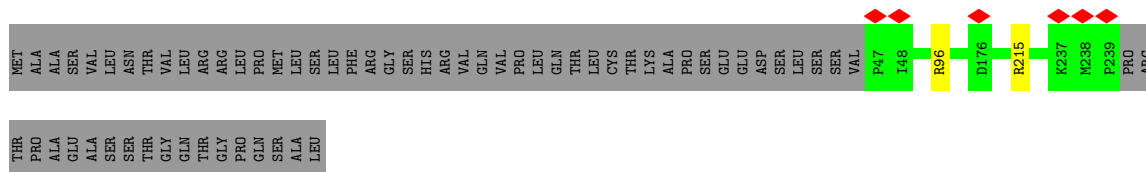
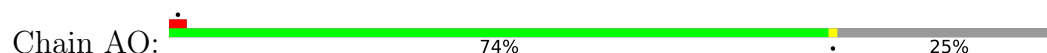
- Molecule 13: 28S ribosomal protein S16, mitochondrial



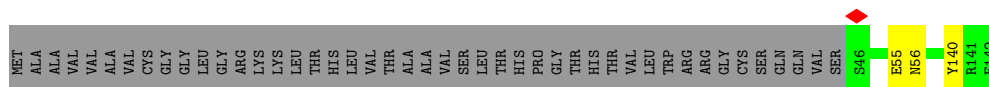
- Molecule 14: 28S ribosomal protein S17, mitochondrial



- Molecule 15: 28S ribosomal protein S18b, mitochondrial



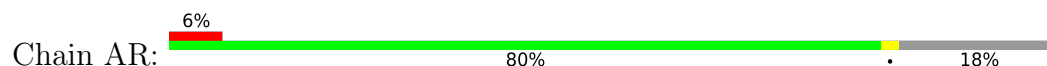
- Molecule 16: 28S ribosomal protein S18c, mitochondrial

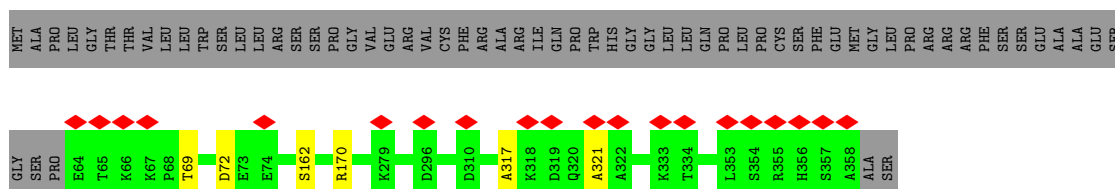


- Molecule 17: MRPS21 isoform 1

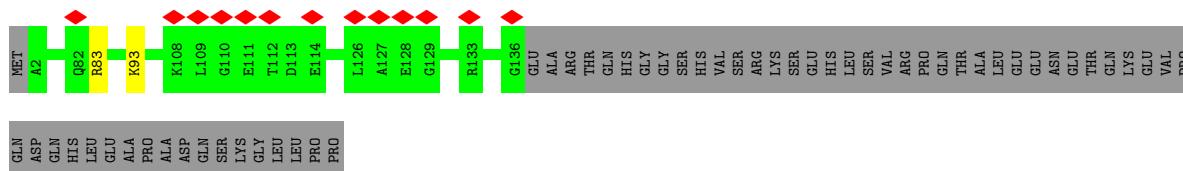


- Molecule 18: 28S ribosomal protein S22, mitochondrial

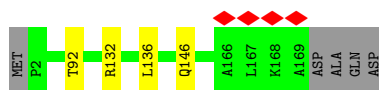




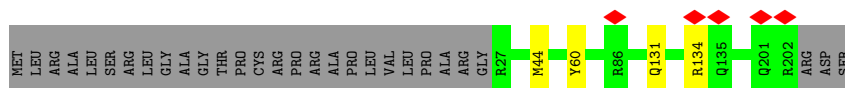
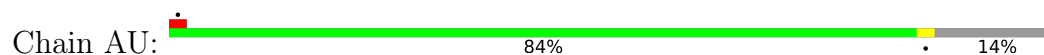
- Molecule 19: 28S ribosomal protein S23, mitochondrial



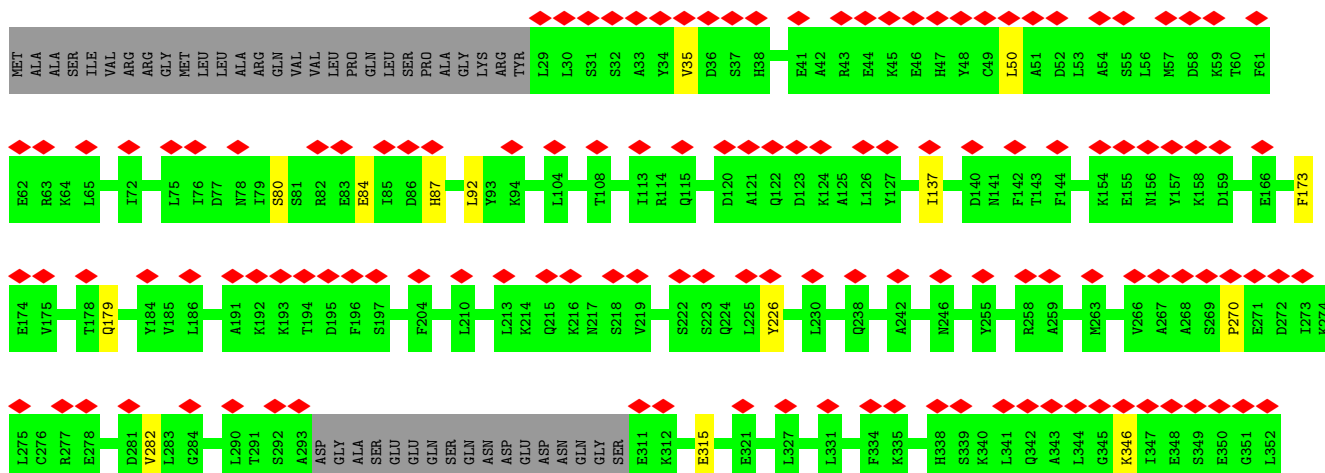
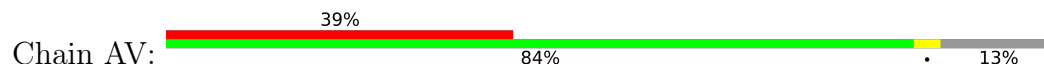
- Molecule 20: 28S ribosomal protein S25, mitochondrial

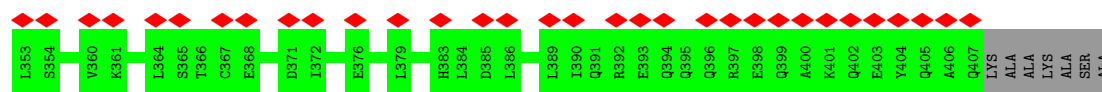


- Molecule 21: 28S ribosomal protein S26, mitochondrial



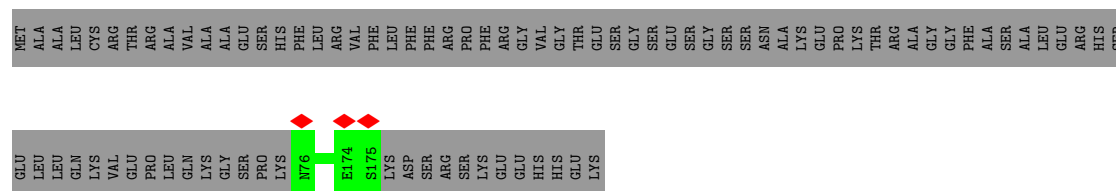
- Molecule 22: 28S ribosomal protein S27, mitochondrial





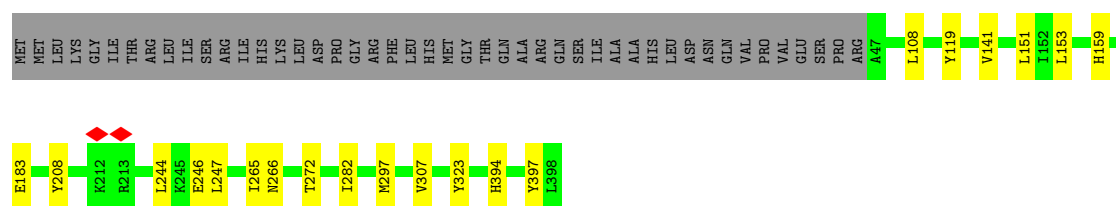
- Molecule 23: 28S ribosomal protein S28, mitochondrial

Chain AW: 53% 47%



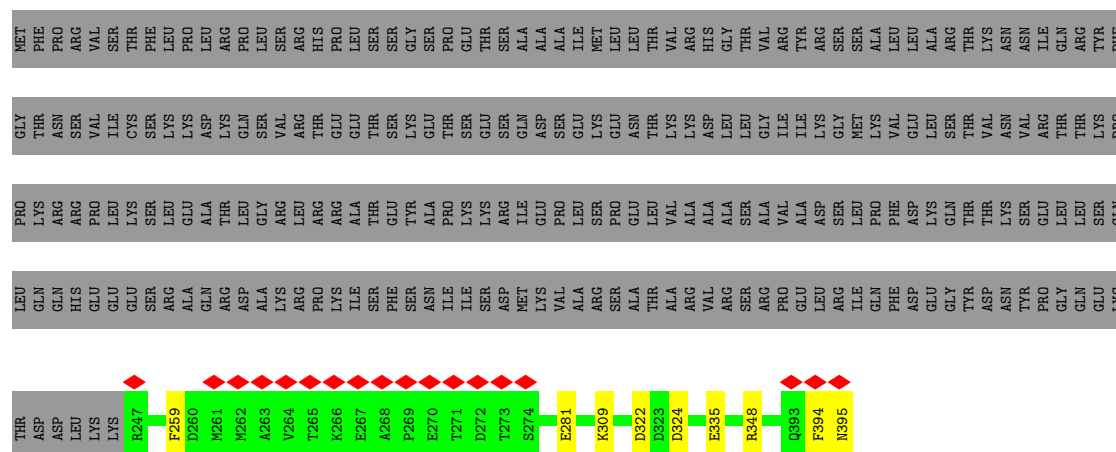
- Molecule 24: 28S ribosomal protein S29, mitochondrial

Chain AX: 83% 5% 12%



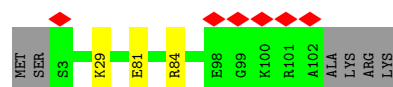
- Molecule 25: 28S ribosomal protein S31, mitochondrial

Chain AY: 5% 35% 62%

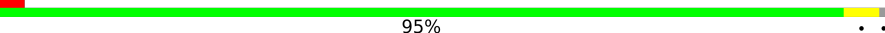


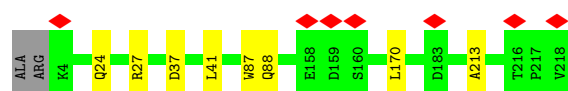
- Molecule 26: 28S ribosomal protein S33, mitochondrial

Chain AZ: 6% 92% 6%



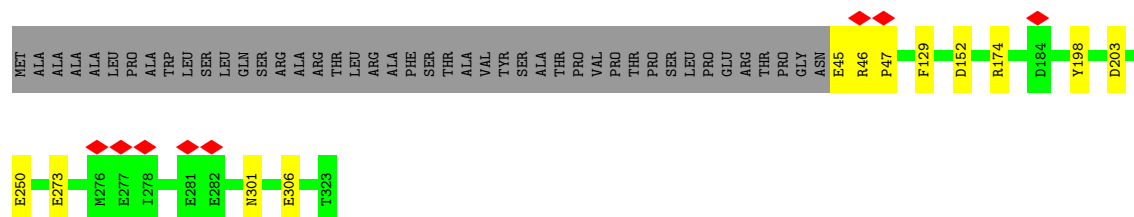
- Molecule 27: 28S ribosomal protein S34, mitochondrial

Chain A0:  95%



- Molecule 28: 28S ribosomal protein S35, mitochondrial

Chain A1:  83% 14%



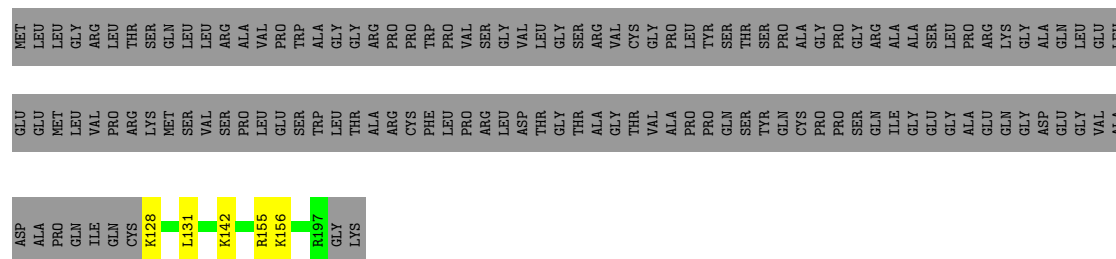
- Molecule 29: Coiled-coil-helix-coiled-coil-helix domain-containing protein 1

Chain A2:  92% 7%



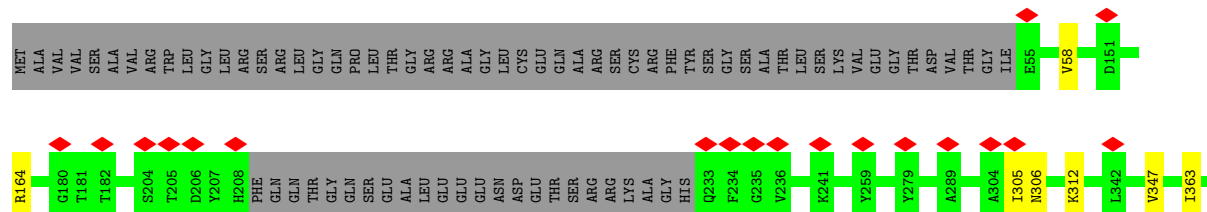
- Molecule 30: Aurora kinase A-interacting protein

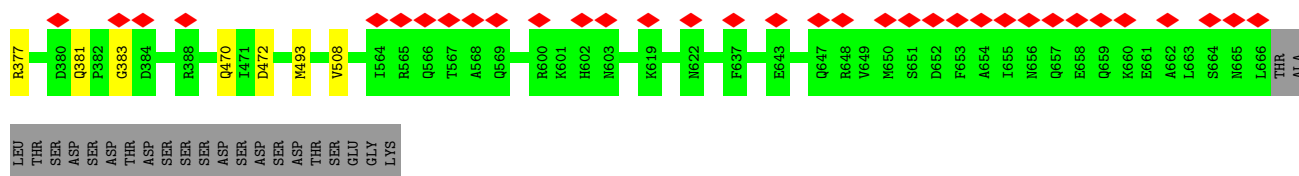
Chain A3:  33% 65%



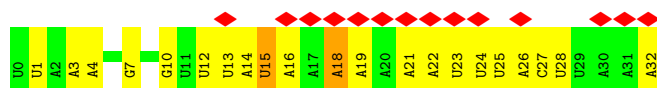
- Molecule 31: Pentatricopeptide repeat domain-containing protein 3, mitochondrial

Chain A4:  8% 83% 15%

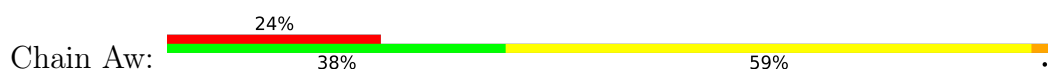




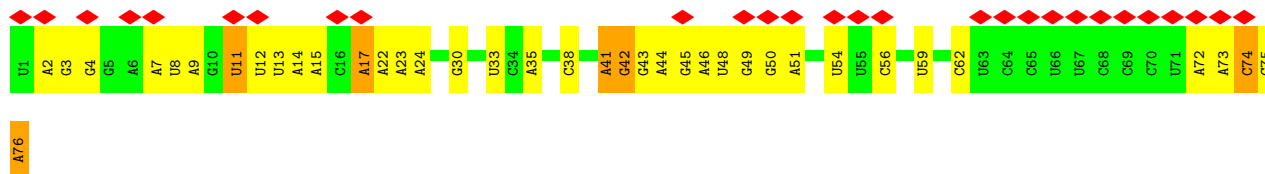
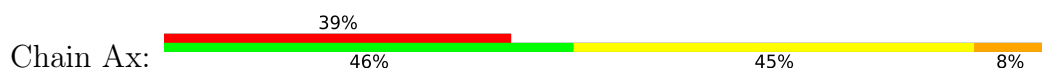
- Molecule 32: mRNA



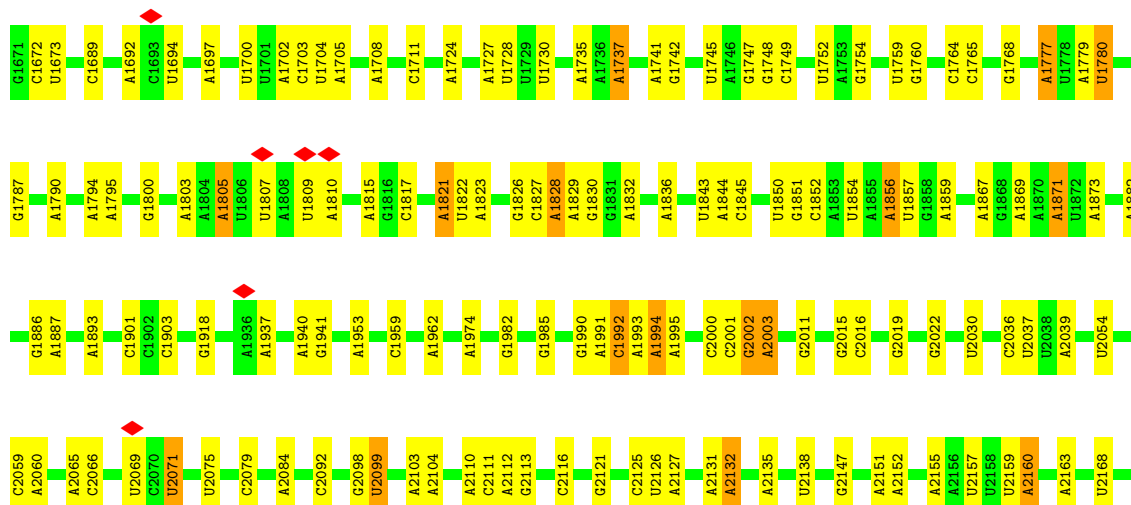
- Molecule 33: A/P-tRNA

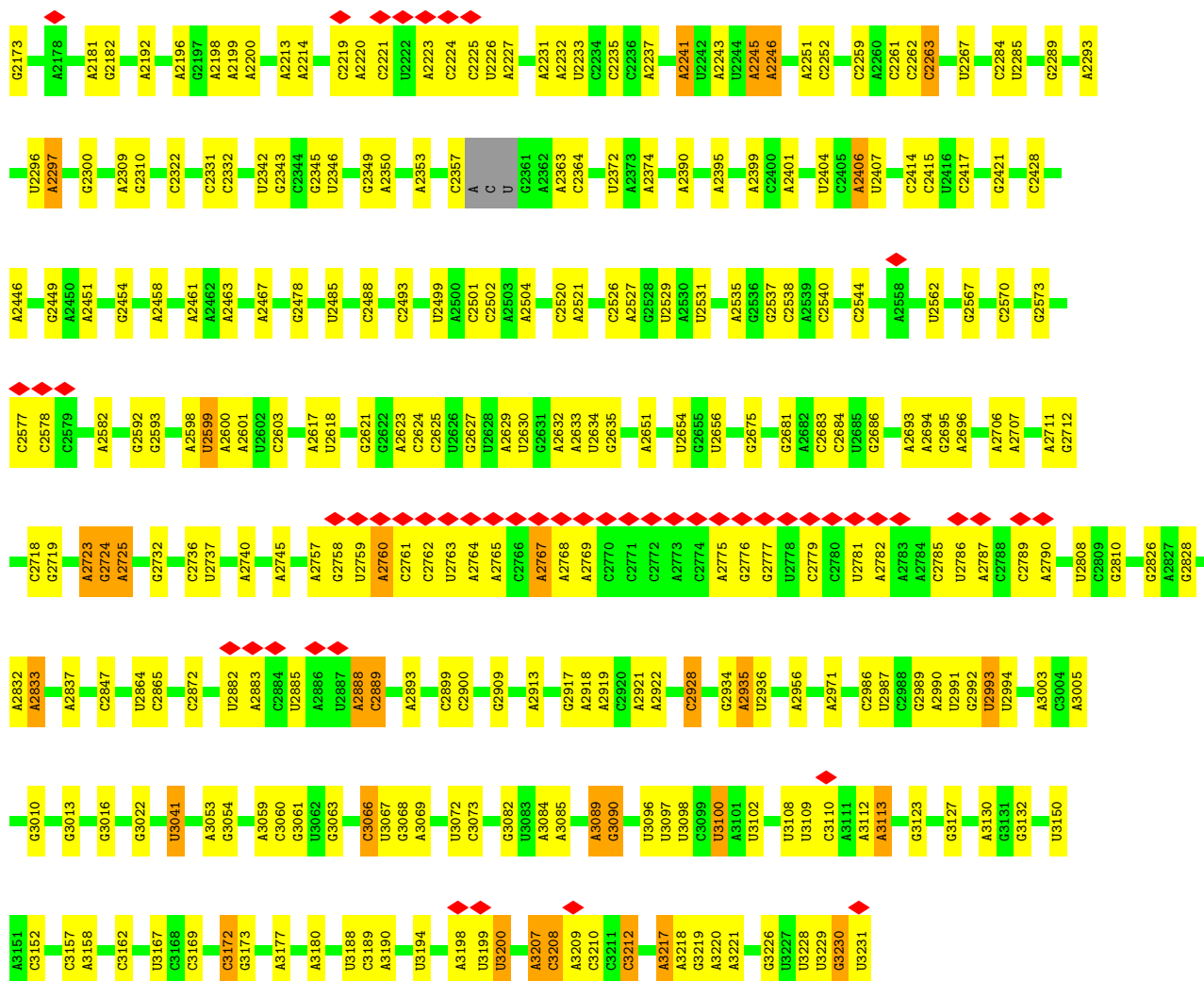


- Molecule 34: P/E-tRNA

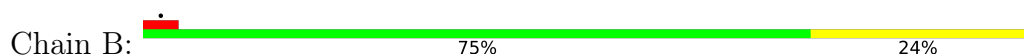


- Molecule 35: 16S mitochondrial rRNA

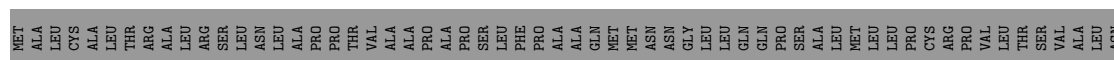
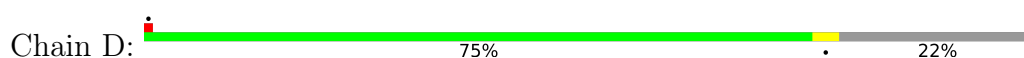




• Molecule 36: mitochondrial tRNA^{Val}



• Molecule 37: 39S ribosomal protein L2, mitochondrial



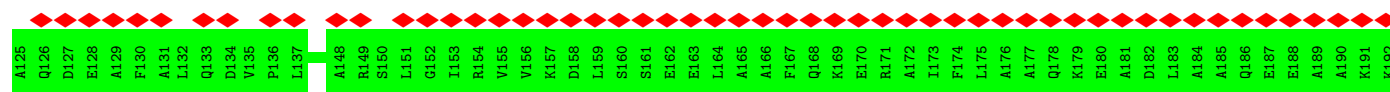
• Molecule 38: 39S ribosomal protein L3, mitochondrial

Sequence logo for the 10th position of the 1000bp upstream region. The y-axis represents information content in bits, ranging from 0 to 0.4. The x-axis shows the 1000bp upstream region with positions 1 to 1000. The logo shows a strong preference for 'G' at position 1000, with a peak of approximately 0.35 bits. Other positions show lower information content, with 'G' and 'A' being the most frequent bases. A red arrow points to the 'G' at position 1000.

-
- Sequence logo for the 100th position. The y-axis shows amino acid frequencies: S291 (0.01), D292 (0.01), R295 (0.01), and others. The x-axis shows amino acid frequencies: MET (0.01), LEU (0.01), GLN (0.01), PHE (0.01), VAL (0.01), ARG (0.01), ALA (0.01), GLY (0.01), HIS (0.01), THR (0.01), TRP (0.01), LEU (0.01), ARG (0.01), PRO (0.01), THR (0.01), GLY (0.01), SER (0.01), GLN (0.01), GLY (0.01), LEU (0.01), SER (0.01), SER (0.01), LEU (0.01), LEU (0.01), ALA (0.01), GLU (0.01), GLU (0.01), ALA (0.01), ALA (0.01), ARG (0.01), ALA (0.01), THR (0.01), ASN (0.01), PRO (0.01), GLU (0.01), GLN (0.01), VAL (0.01), ALA (0.01), SER (0.01), GLU (0.01), GLY (0.01), LEU (0.01). The logo shows a strong preference for P44 (0.01) and R70 (0.01) at the 100th position.

- [illegible]

- | | | | | | | | | | | | | | | | | | | | | | |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|
| E62 | E63 | E64 | E65 | E66 | E67 | E68 | E69 | I70 | I71 | V72 | K73 | P74 | D75 | R76 | T77 | F78 | E79 | I80 | K81 | I82 | G83 | Q84 | P85 | S88 | Y89 | F90 | L91 | K92 | A93 | A94 | A95 | I97 | E98 | K99 | G100 | A101 | R102 | K106 | E107 | V108 | A109 | G110 | L111 | V112 | T113 | L114 | K115 | H116 | V117 | Y118 | E119 | I120 | | | | |
| MET | SER | LYS | LEU | GLY | ARG | ALA | ARG | GLY | LEU | ARG | LYS | PRO | GLU | VAL | GLY | G18 | R21 | A22 | I23 | V24 | R25 | A26 | G27 | L28 | A29 | K30 | P31 | G32 | P33 | P34 | G36 | P37 | V38 | L39 | Q40 | Q41 | B42 | G43 | V44 | S45 | I46 | M47 | Q48 | F49 | C50 | K51 | E52 | F53 | N54 | E55 | R56 | T57 | K58 | D59 | I60 | V61 |



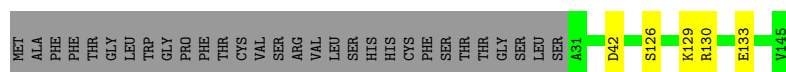
- Molecule 42: 39S ribosomal protein L13, mitochondrial

Chain K: 97%



- Molecule 43: 39S ribosomal protein L14, mitochondrial

Chain L: 76% 21%



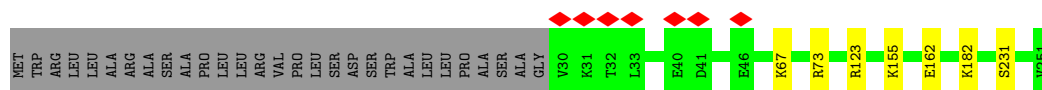
- Molecule 44: 39S ribosomal protein L15, mitochondrial

Chain M: 96%



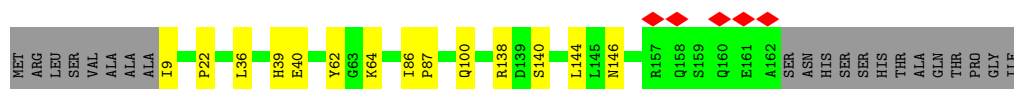
- Molecule 45: 39S ribosomal protein L16, mitochondrial

Chain N: 86% 12%



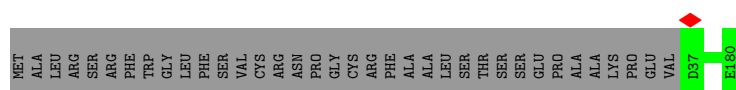
- Molecule 46: 39S ribosomal protein L17, mitochondrial

Chain O: 80% 8% 12%

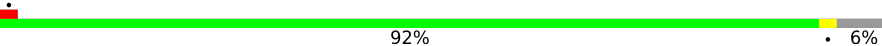


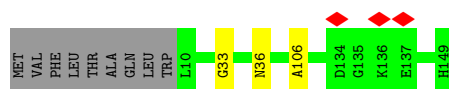
- Molecule 47: 39S ribosomal protein L18, mitochondrial

Chain P: 80% 20%



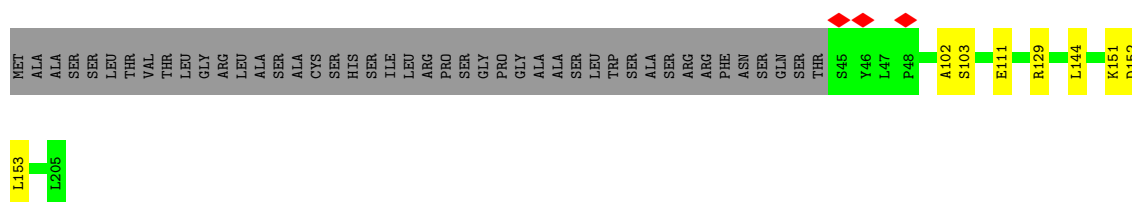
- Molecule 48: 39S ribosomal protein L20, mitochondrial

Chain R:  92% • 6%



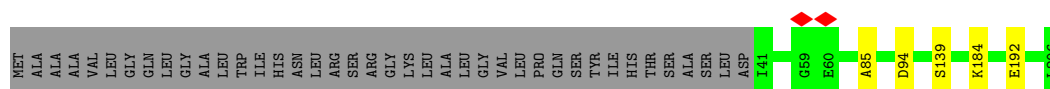
- Molecule 49: 39S ribosomal protein L21, mitochondrial

Chain S:  75% • 21%

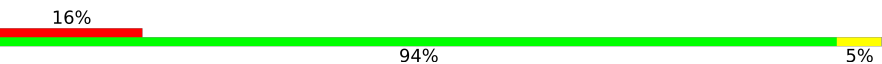


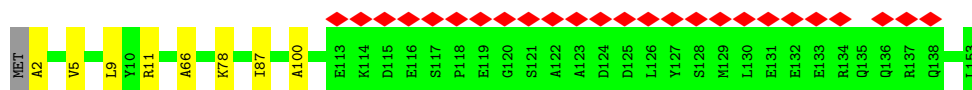
- Molecule 50: 39S ribosomal protein L22, mitochondrial

Chain T:  78% • 19%



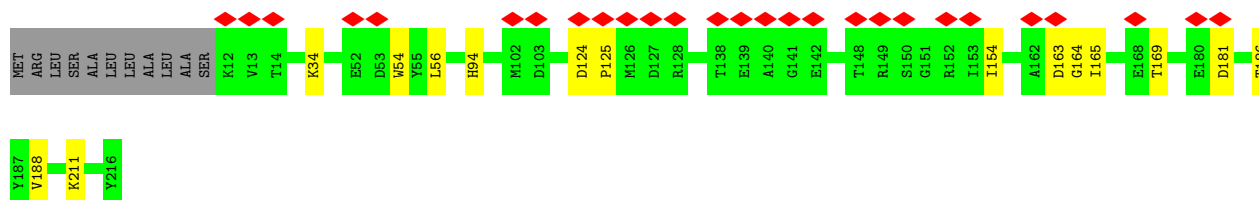
- Molecule 51: 39S ribosomal protein L23, mitochondrial

Chain U:  16% 94% 5% •



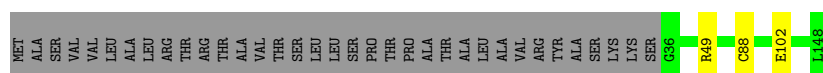
- Molecule 52: 39S ribosomal protein L24, mitochondrial

Chain V:  12% 88% 7% 5%

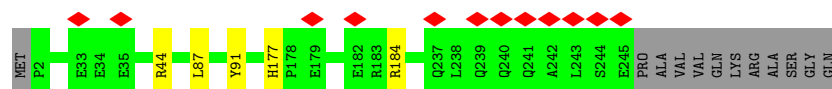


- Molecule 53: 39S ribosomal protein L27, mitochondrial

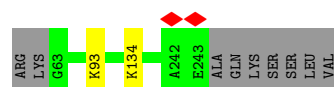
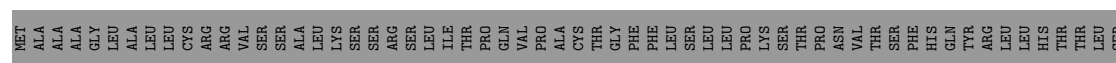
Chain W:  74% • 24%



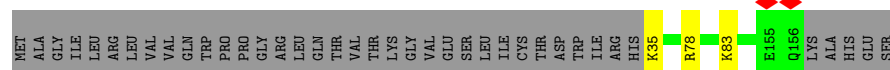
- Molecule 54: 39S ribosomal protein L28, mitochondrial



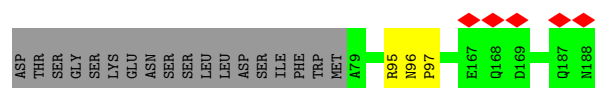
- Molecule 55: 39S ribosomal protein L47, mitochondrial



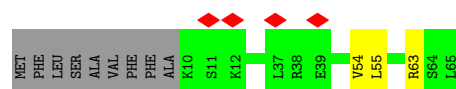
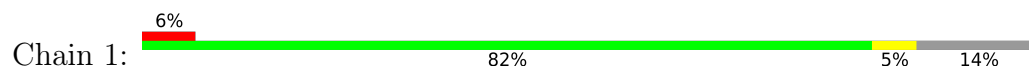
- Molecule 56: 39S ribosomal protein L30, mitochondrial



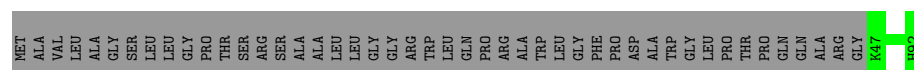
- Molecule 57: 39S ribosomal protein L32, mitochondrial



- Molecule 58: 39S ribosomal protein L33, mitochondrial

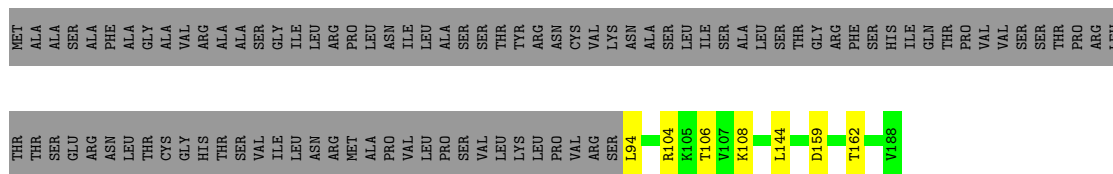


- Molecule 59: 39S ribosomal protein L34, mitochondrial



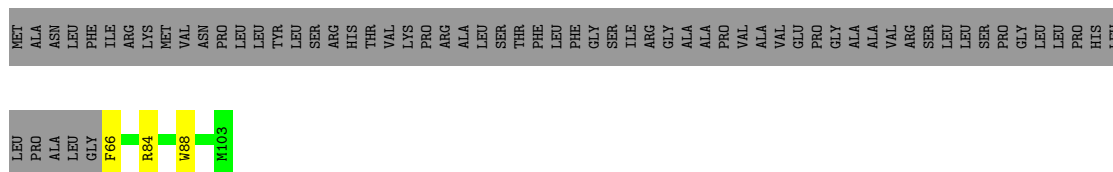
- Molecule 60: 39S ribosomal protein L35, mitochondrial

Chain 3:  47% . 49%



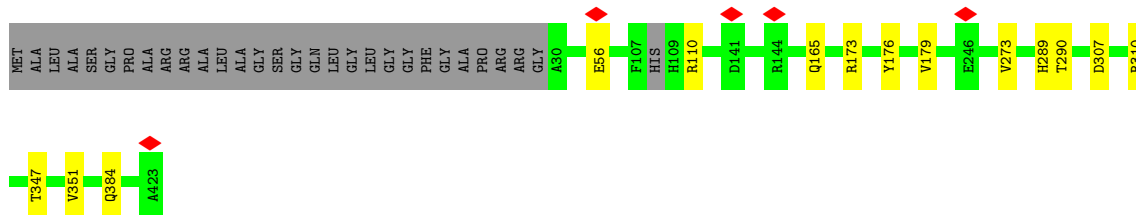
- Molecule 61: 39S ribosomal protein L36, mitochondrial

Chain 4:  34% . 63%



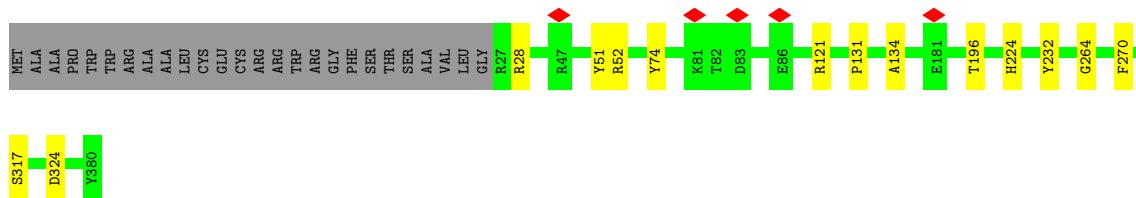
- Molecule 62: 39S ribosomal protein L37, mitochondrial

Chain 5:  90% . 7%



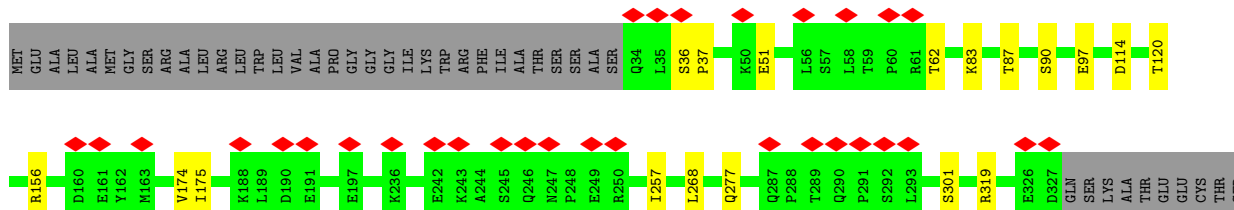
- Molecule 63: 39S ribosomal protein L38, mitochondrial

Chain 6:  89% . 7%



- Molecule 64: 39S ribosomal protein L39, mitochondrial

Chain 7:  9% 82% 5% 13%



THR

- Molecule 65: 39S ribosomal protein L40, mitochondrial

Chain 8: 17% 69% 27%

MET THR ALA SER VAL LEU ARG SER ILE LEU LEU ALA ARG PRO THR THR GLY LEU LEU GLY THR TRP GLN THR LEU ARG GLU THR HIS GLN ARG ALA SER LEU LEU SER TRP PHE GLU LEU ILE PRO MET ARG S47 F48 F49 L50 R51 K52 LYS LYS VAL ASP PRO LYS K60

D61 Q62 E63 A64 K65 F66 R67 L68 K69 R70 K71 I72 R73 K74 L75 E76 F77 A78 T79 L92 L95 D96 K97 A98 R101 E105 E112 E132 E153 Y199 T200 Q201 V202 E203 PHE LYS ARG

- Molecule 66: 39S ribosomal protein L41, mitochondrial

Chain 9: 9% 88% 9%

MET GLY VAL LEU ALA ALA ALA ALA CYS LEU VAL ARG G14 A15 D16 R25 Y76 E101 K102 D103 F104 K105 G107 T108 F109 D110 P111 D112 N113 K116 R137

- Molecule 67: 39S ribosomal protein L42, mitochondrial

Chain a: 8% 68% 30%

MET ALA VAL ALA ALA VAL LYS TRP MET LEU LYS ARG THR ILE LEU LYS HIS PHE PRO VAL ASN GLN ALA LEU TYR CYS VAL CYS HIS LYS SER T35 I58 R77 P78 D79 PRO VAL HIS ASN ASN GLU THR H88 D89 Q90 L96 E97 E98 K99 V100 E101

F117 G127 R142

- Molecule 68: Large ribosomal subunit protein mL43

Chain b: 66% 30%

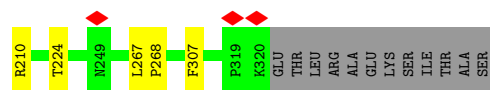
ACE2 T2A A3 S34 R35 D36 R41 R44 R85 A105 D106 Q107 Q149 D150 P151 PRO PRO ALA GLN ASP THR LEU ARG LEU SER ALA VAL PRO GLN ILE LEU PRO GLY TRP PRO ASP PRO PRO LEU PRO THR VAL ASP PRO ILE SER SER THR

SER ALA PRO GLY PRO MET LEU SER ALA VAL SER CYS LEU PRO ILE VAL PRO ALA THR THR VAL CYS SER ALA

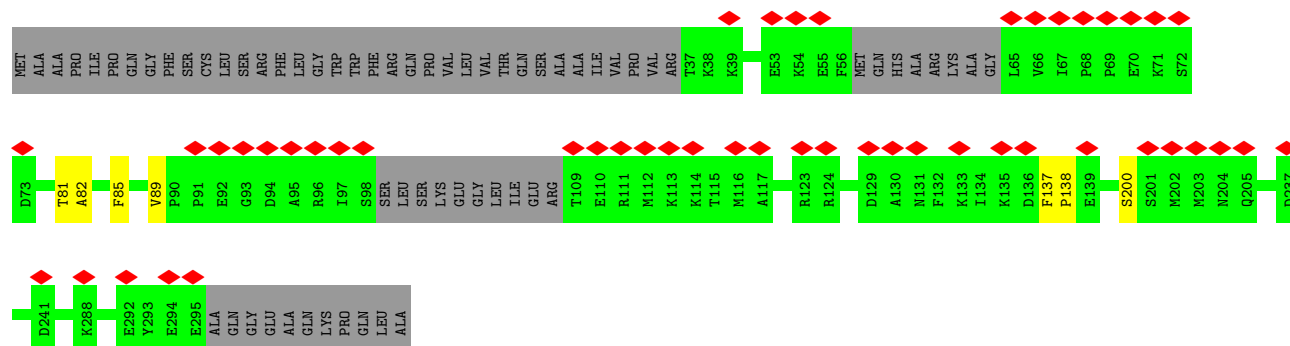
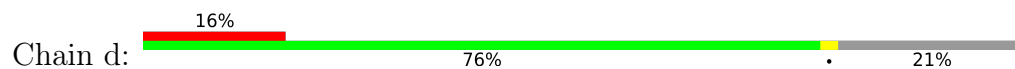
- Molecule 69: 39S ribosomal protein L44, mitochondrial

Chain c: 5% 83% 14%

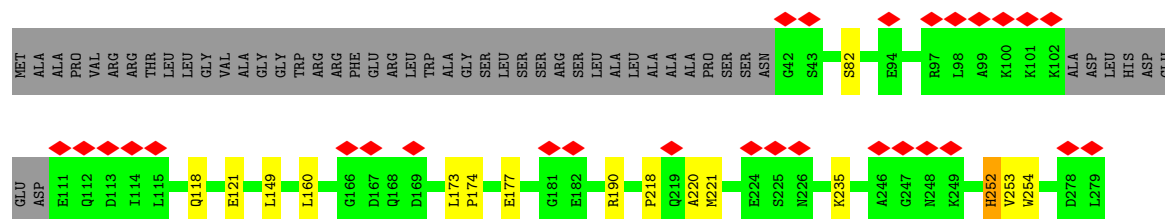
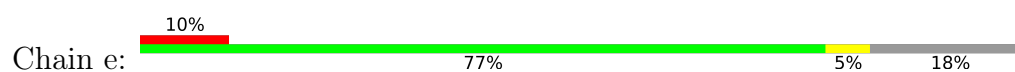
MET ALA SER LEU VAL ARG LEU LEU GLN GLN GLY HIS ARG CYS LEU LEU ALA PRO VAL ALA PRO LYS LEU VAL PRO VAL ARG GLY V31 R52 Q80 D86 R105 Q106 Q107 L108 G109 I110 GLU LYS GLU ALA V115 L116 L117 N118 Q139 D143 M148 P149



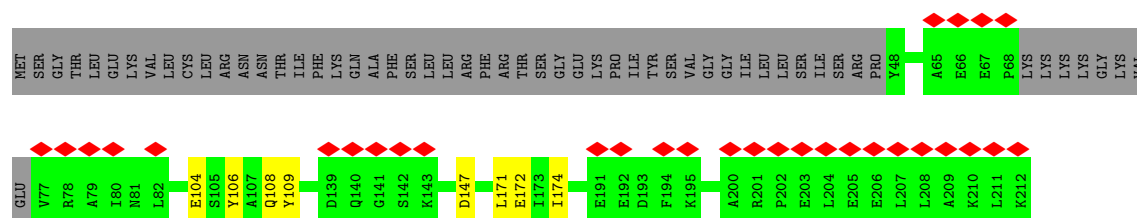
- Molecule 70: 39S ribosomal protein L45, mitochondrial



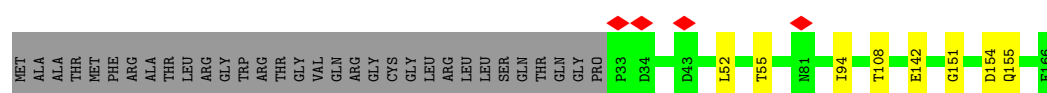
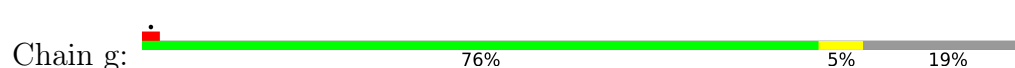
- Molecule 71: 39S ribosomal protein L46, mitochondrial



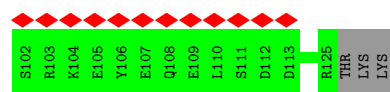
- Molecule 72: 39S ribosomal protein L48, mitochondrial



- Molecule 73: 39S ribosomal protein L49, mitochondrial

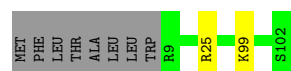


- Molecule 74: 39S ribosomal protein L50, mitochondrial



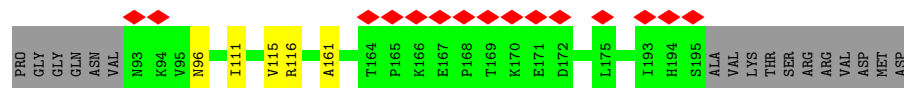
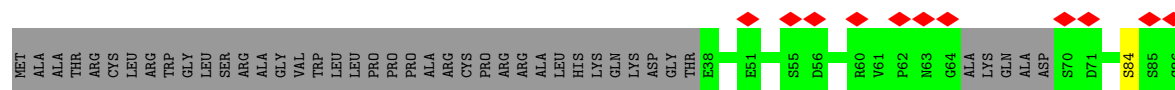
- Molecule 80: Ribosomal protein 63, mitochondrial

Chain o: 90% 8%



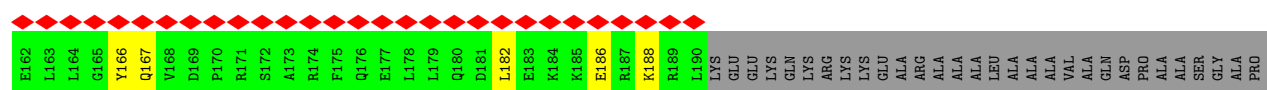
- Molecule 81: Peptidyl-tRNA hydrolase ICT1, mitochondrial

Chain p: 13% 68% 29%



- Molecule 82: Growth arrest and DNA damage-inducible proteins-interacting protein 1

Chain q: 23% 71% 25%



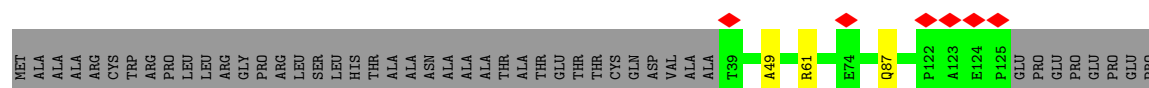
- Molecule 83: 39S ribosomal protein S18a, mitochondrial

Chain r: 81% 17%



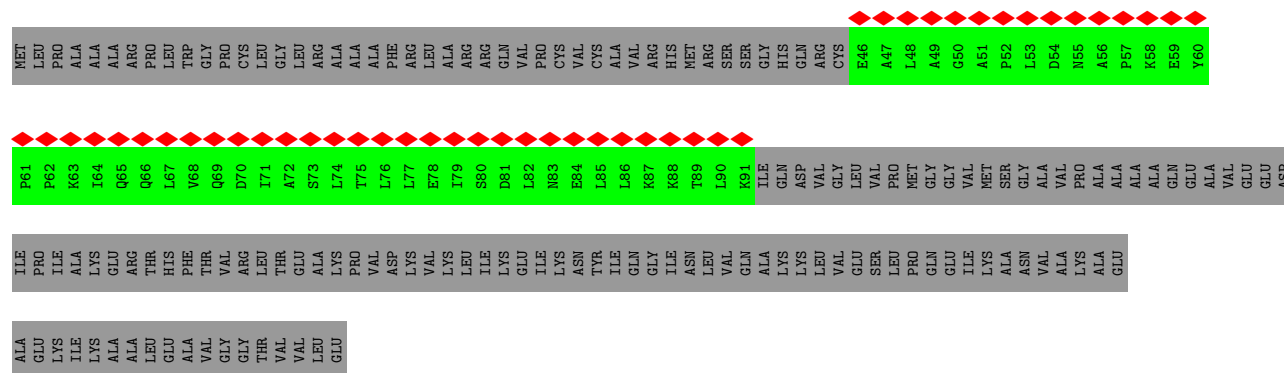
- Molecule 84: 39S ribosomal protein S30, mitochondrial

Chain s: 86% 12%

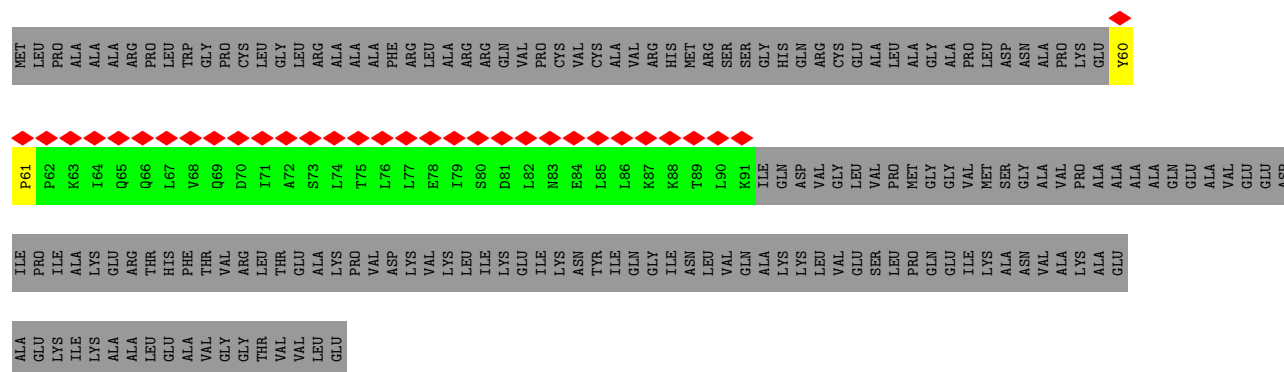




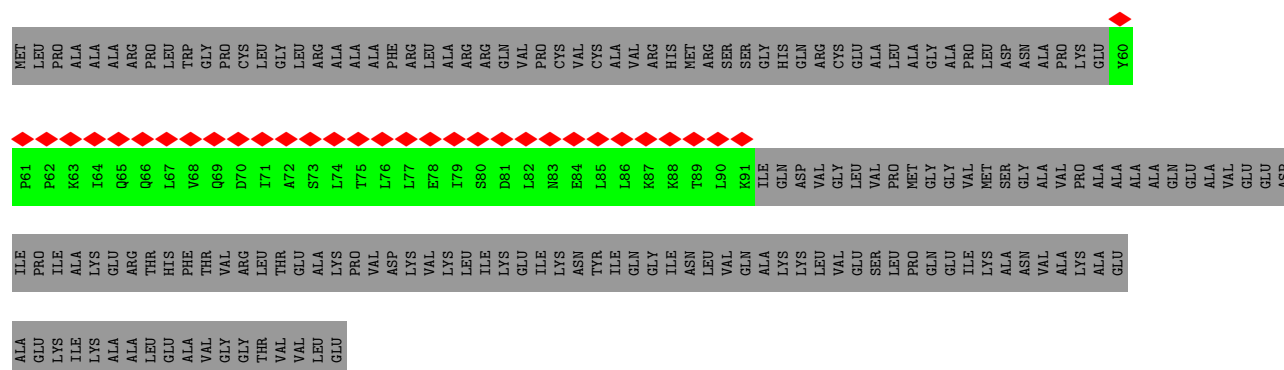
- Molecule 85: 39S ribosomal protein L12, mitochondrial



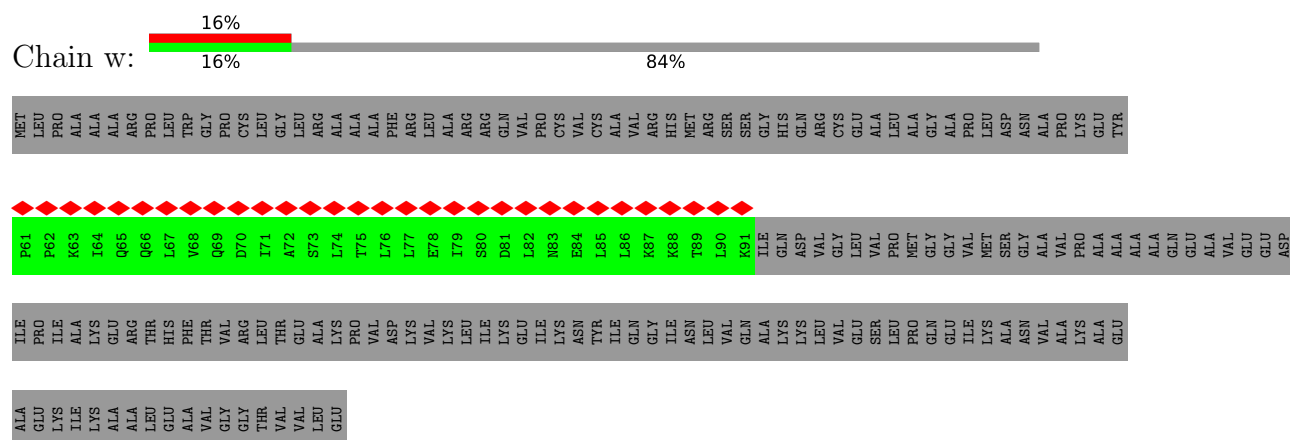
- Molecule 85: 39S ribosomal protein L12, mitochondrial



- Molecule 85: 39S ribosomal protein L12, mitochondrial



• Molecule 85: 39S ribosomal protein L12, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	20143	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	60.865	Depositor
Minimum map value	-27.488	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	1.287	Depositor
Recommended contour level	3.8	Depositor
Map size (Å)	448.19998, 448.19998, 448.19998	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SPD, PUT, OMG, ZN, 1MA, PSU, B8T, NAD, FES, AYA, SAC, SPM, GDP, 2MG, K, MG, 5F0, ATP, MA6, 5MC, ACE, OMU, 5MU

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	AA	0.10	0/22537	0.17	0/35085
2	AB	0.09	0/1871	0.23	0/2531
3	AC	0.11	0/1113	0.24	0/1505
4	AD	0.09	0/2751	0.22	0/3681
5	AE	0.08	0/989	0.22	0/1335
6	AF	0.09	0/1767	0.22	0/2373
7	AG	0.09	0/2753	0.24	0/3691
8	AH	0.11	0/1178	0.26	0/1598
9	AI	0.09	0/1030	0.22	0/1386
10	AJ	0.11	0/855	0.26	0/1148
11	AK	0.10	0/880	0.21	0/1182
12	AL	0.09	0/1477	0.22	0/1974
13	AM	0.10	0/963	0.25	0/1295
14	AN	0.09	0/886	0.24	0/1199
15	AO	0.09	0/1648	0.23	0/2243
16	AP	0.09	0/798	0.24	0/1070
17	AQ	0.09	0/748	0.22	0/994
18	AR	0.08	0/2456	0.20	0/3317
19	AS	0.08	0/1138	0.20	0/1533
20	AT	0.09	0/1402	0.23	0/1883
21	AU	0.07	0/1510	0.18	0/2025
22	AV	0.07	0/3030	0.20	0/4093
23	AW	0.10	0/801	0.23	0/1079
24	AX	0.10	0/2921	0.26	0/3954
25	AY	0.09	0/1280	0.22	0/1725
26	AZ	0.10	0/857	0.23	0/1141
27	A0	0.09	0/1834	0.24	0/2484
28	A1	0.09	0/2313	0.23	0/3129
29	A2	0.09	0/941	0.24	0/1257
30	A3	0.09	0/636	0.25	0/839
31	A4	0.09	0/4877	0.23	0/6598

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Az	0.11	0/785	0.22	0/1219
33	Aw	0.14	0/1604	0.28	0/2490
34	Ax	0.13	0/1673	0.26	0/2599
35	A	0.09	0/36876	0.19	0/57402
36	B	0.07	0/1627	0.15	0/2527
37	D	0.09	0/1896	0.25	0/2549
38	E	0.10	0/2475	0.26	0/3355
39	F	0.10	0/2090	0.27	0/2842
40	I	0.09	0/1731	0.27	0/2345
41	J	0.09	0/1348	0.24	0/1813
42	K	0.09	0/1490	0.24	0/2021
43	L	0.09	0/905	0.26	0/1218
44	M	0.09	0/2381	0.27	0/3212
45	N	0.08	0/1833	0.24	0/2468
46	O	0.08	0/1283	0.24	0/1727
47	P	0.11	0/1199	0.24	0/1623
48	R	0.09	0/1175	0.23	0/1572
49	S	0.09	0/1320	0.26	0/1789
50	T	0.09	0/1403	0.25	0/1886
51	U	0.10	0/1274	0.25	0/1723
52	V	0.09	0/1721	0.26	0/2333
53	W	0.10	0/902	0.24	0/1214
54	X	0.09	0/2099	0.22	0/2837
55	Y	0.08	0/1593	0.21	0/2136
56	Z	0.09	0/1021	0.26	0/1378
57	0	0.08	0/913	0.23	0/1224
58	1	0.09	0/469	0.27	0/621
59	2	0.10	0/383	0.25	0/507
60	3	0.10	0/853	0.26	0/1136
61	4	0.08	0/350	0.22	0/461
62	5	0.09	0/3293	0.25	0/4484
63	6	0.11	0/3043	0.26	0/4140
64	7	0.10	0/2447	0.25	0/3310
65	8	0.09	0/1294	0.24	0/1739
66	9	0.09	0/1025	0.25	0/1379
67	a	0.10	0/866	0.27	0/1174
68	b	0.10	0/1219	0.26	0/1651
69	c	0.09	0/2347	0.22	0/3171
70	d	0.09	0/2039	0.25	0/2759
71	e	0.08	0/1903	0.24	0/2565
72	f	0.08	0/1273	0.21	0/1716
73	g	0.11	0/1151	0.26	0/1569
74	h	0.08	0/918	0.22	0/1249

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	i	0.09	0/850	0.24	0/1135
76	j	0.11	0/760	0.25	0/1023
77	k	0.07	0/777	0.20	0/1048
78	l	0.07	0/707	0.25	0/960
79	m	0.08	0/805	0.22	0/1081
80	o	0.11	0/819	0.27	0/1097
81	p	0.08	0/1223	0.23	0/1641
82	q	0.08	0/1432	0.22	0/1931
83	r	0.10	0/1362	0.27	0/1846
84	s	0.09	0/3239	0.25	0/4400
85	t	0.06	0/358	0.18	0/486
85	u	0.08	0/259	0.20	0/350
85	v	0.07	0/259	0.16	0/350
85	w	0.08	0/246	0.19	0/331
85	x	0.07	0/246	0.16	0/331
85	y	0.07	0/246	0.17	0/331
86	Q	0.10	0/2039	0.27	0/2750
87	H	0.11	0/1698	0.30	0/2292
88	z	0.11	0/2067	0.34	0/2793
All	All	0.09	0/189122	0.22	0/268656

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [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	AA	20260	10305	10287	88	0
2	AB	1828	1816	1815	3	0
3	AC	1083	1089	1088	11	0
4	AD	2700	2769	2767	9	0
5	AE	972	1000	1000	2	0
6	AF	1725	1770	1769	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	AG	2695	2695	2694	18	0
8	AH	1152	1184	1183	4	0
9	AI	1020	1061	1053	2	0
10	AJ	839	888	887	6	0
11	AK	862	886	885	1	0
12	AL	1453	1541	1540	3	0
13	AM	942	966	965	4	0
14	AN	868	929	928	6	0
15	AO	1592	1561	1557	3	0
16	AP	781	807	806	2	0
17	AQ	744	757	758	3	0
18	AR	2409	2430	2428	4	0
19	AS	1111	1116	1115	1	0
20	AT	1371	1393	1393	3	0
21	AU	1488	1501	1499	3	0
22	AV	2969	2964	2961	9	0
23	AW	789	803	802	0	0
24	AX	2849	2845	2843	13	0
25	AY	1246	1198	1197	6	0
26	AZ	839	859	858	2	0
27	A0	1787	1797	1796	6	0
28	A1	2265	2296	2294	8	0
29	A2	935	970	971	6	0
30	A3	625	701	699	5	0
31	A4	4768	4770	4766	11	0
32	Az	701	351	351	4	0
33	Aw	1435	726	726	6	0
34	Ax	1499	763	763	9	0
35	A	33070	16802	16797	187	0
36	B	1524	779	779	4	0
37	D	1859	1921	1920	7	0
38	E	2406	2416	2415	6	0
39	F	2031	2066	2065	7	0
40	I	1695	1786	1785	6	0
41	J	1330	1408	1407	4	0
42	K	1455	1451	1452	3	0
43	L	890	942	941	3	0
44	M	2327	2396	2395	6	0
45	N	1786	1818	1817	5	0
46	O	1259	1295	1294	10	0
47	P	1173	1166	1165	0	0
48	R	1154	1215	1214	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	S	1293	1366	1365	5	0
50	T	1369	1412	1410	3	0
51	U	1251	1231	1232	6	0
52	V	1676	1689	1687	12	0
53	W	880	905	904	3	0
54	X	2044	2061	2060	4	0
55	Y	1556	1598	1597	2	0
56	Z	996	1045	1044	2	0
57	0	898	917	916	2	0
58	1	464	513	511	2	0
59	2	377	407	406	0	0
60	3	832	884	883	6	0
61	4	342	362	361	3	0
62	5	3200	3202	3198	10	0
63	6	2948	2844	2841	11	0
64	7	2390	2399	2397	12	0
65	8	1269	1297	1295	6	0
66	9	997	988	987	4	0
67	a	840	812	810	3	0
68	b	1196	1195	1195	7	0
69	c	2299	2322	2320	6	0
70	d	1985	1980	1976	5	0
71	e	1866	1870	1868	11	0
72	f	1252	1271	1269	7	0
73	g	1113	1097	1097	6	0
74	h	895	882	881	3	0
75	i	828	859	857	2	0
76	j	745	747	746	1	0
77	k	774	784	784	1	0
78	l	688	675	674	1	0
79	m	791	761	796	6	0
80	o	798	806	804	2	0
81	p	1205	1226	1223	3	0
82	q	1398	1328	1383	8	0
83	r	1322	1349	1348	3	0
84	s	3155	3143	3139	7	0
85	t	354	378	377	0	0
85	u	257	284	283	1	0
85	v	257	284	283	0	0
85	w	245	275	275	0	0
85	x	245	275	275	0	0
85	y	245	275	275	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	Q	1990	2031	2031	10	0
87	H	1661	1737	1734	20	0
88	z	2027	2077	2076	29	0
89	AA	44	26	26	0	0
90	AA	14	30	26	0	0
91	A	30	66	57	0	0
91	AA	10	22	19	0	0
92	3	1	0	0	0	0
92	6	1	0	0	0	0
92	A	27	0	0	0	0
92	AA	20	0	0	0	0
92	D	1	0	0	0	0
92	M	1	0	0	0	0
92	N	1	0	0	0	0
92	i	1	0	0	0	0
92	o	1	0	0	0	0
93	8	1	0	0	0	0
93	A	137	0	0	0	0
93	A3	1	0	0	0	0
93	AA	57	0	0	0	0
93	AB	1	0	0	0	0
93	AX	1	0	0	0	0
93	D	2	0	0	0	0
93	E	1	0	0	0	0
93	g	1	0	0	0	0
94	0	1	0	0	0	0
94	4	1	0	0	0	0
94	AO	1	0	0	0	0
95	AP	4	0	0	0	0
95	AT	4	0	0	0	0
95	r	4	0	0	0	0
96	AX	31	12	12	0	0
97	AX	28	12	12	0	0
98	A	6	14	12	0	0
99	B	7	11	8	2	0
100	0	19	0	0	0	0
100	2	26	0	0	0	0
100	3	22	0	0	2	0
100	4	1	0	0	0	0
100	5	4	0	0	0	0
100	6	11	0	0	1	0
100	7	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
100	9	11	0	0	0	0
100	A	1824	0	0	82	0
100	A1	4	0	0	0	0
100	A2	8	0	0	0	0
100	A3	15	0	0	2	0
100	AA	649	0	0	30	0
100	AB	11	0	0	0	0
100	AC	20	0	0	3	0
100	AD	20	0	0	0	0
100	AE	4	0	0	0	0
100	AF	5	0	0	0	0
100	AG	6	0	0	1	0
100	AH	14	0	0	0	0
100	AI	13	0	0	1	0
100	AJ	11	0	0	1	0
100	AK	11	0	0	0	0
100	AL	15	0	0	1	0
100	AM	1	0	0	0	0
100	AN	6	0	0	1	0
100	AO	4	0	0	0	0
100	AP	9	0	0	0	0
100	AQ	22	0	0	0	0
100	AS	2	0	0	0	0
100	AT	4	0	0	0	0
100	AW	1	0	0	0	0
100	AX	1	0	0	0	0
100	AY	2	0	0	0	0
100	AZ	8	0	0	0	0
100	Aw	2	0	0	0	0
100	Ax	1	0	0	0	0
100	Az	3	0	0	0	0
100	B	3	0	0	0	0
100	D	31	0	0	1	0
100	E	33	0	0	0	0
100	F	53	0	0	1	0
100	H	6	0	0	0	0
100	I	7	0	0	1	0
100	K	33	0	0	0	0
100	L	7	0	0	0	0
100	M	36	0	0	2	0
100	N	18	0	0	0	0
100	O	9	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
100	P	12	0	0	0	0
100	Q	6	0	0	1	0
100	R	38	0	0	1	0
100	S	29	0	0	0	0
100	T	22	0	0	0	0
100	U	9	0	0	1	0
100	V	3	0	0	0	0
100	W	14	0	0	0	0
100	X	1	0	0	0	0
100	Y	12	0	0	0	0
100	Z	18	0	0	0	0
100	a	4	0	0	0	0
100	b	21	0	0	4	0
100	c	7	0	0	0	0
100	f	1	0	0	0	0
100	g	5	0	0	1	0
100	i	27	0	0	0	0
100	j	6	0	0	0	0
100	o	16	0	0	0	0
100	p	1	0	0	0	0
100	r	7	0	0	0	0
100	s	18	0	0	1	0
All	All	183519	153004	152935	632	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 2.

The worst 5 of 632 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)
35:A:2779:C:OP1	88:z:115:THR:OG1	1.94	0.85
44:M:11:ARG:NH2	73:g:142:GLU:OE2	2.16	0.79
72:f:106:TYR:OH	72:f:174:ILE:O	2.01	0.79
1:AA:1574:G:OP2	100:AA:1802:HOH:O	1.99	0.78
24:AX:272:THR:OG1	24:AX:282:ILE:O	2.00	0.78

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	
2	AB	223/296 (75%)	221 (99%)	2 (1%)	0	100	100
3	AC	130/167 (78%)	124 (95%)	6 (5%)	0	100	100
4	AD	335/430 (78%)	326 (97%)	9 (3%)	0	100	100
5	AE	120/125 (96%)	119 (99%)	1 (1%)	0	100	100
6	AF	206/242 (85%)	205 (100%)	1 (0%)	0	100	100
7	AG	324/396 (82%)	317 (98%)	7 (2%)	0	100	100
8	AH	138/201 (69%)	136 (99%)	1 (1%)	1 (1%)	18	50
9	AI	134/194 (69%)	133 (99%)	1 (1%)	0	100	100
10	AJ	106/138 (77%)	103 (97%)	3 (3%)	0	100	100
11	AK	99/128 (77%)	99 (100%)	0	0	100	100
12	AL	172/257 (67%)	170 (99%)	2 (1%)	0	100	100
13	AM	117/137 (85%)	117 (100%)	0	0	100	100
14	AN	108/130 (83%)	106 (98%)	2 (2%)	0	100	100
15	AO	191/258 (74%)	186 (97%)	5 (3%)	0	100	100
16	AP	95/142 (67%)	94 (99%)	1 (1%)	0	100	100
17	AQ	84/87 (97%)	81 (96%)	3 (4%)	0	100	100
18	AR	293/360 (81%)	285 (97%)	8 (3%)	0	100	100
19	AS	133/190 (70%)	131 (98%)	2 (2%)	0	100	100
20	AT	166/173 (96%)	164 (99%)	2 (1%)	0	100	100
21	AU	174/205 (85%)	174 (100%)	0	0	100	100
22	AV	358/414 (86%)	352 (98%)	6 (2%)	0	100	100
23	AW	98/187 (52%)	95 (97%)	3 (3%)	0	100	100
24	AX	350/398 (88%)	343 (98%)	7 (2%)	0	100	100
25	AY	147/395 (37%)	145 (99%)	2 (1%)	0	100	100
26	AZ	98/106 (92%)	97 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	A0	213/217 (98%)	208 (98%)	5 (2%)	0	100	100
28	A1	277/323 (86%)	274 (99%)	3 (1%)	0	100	100
29	A2	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
30	A3	68/199 (34%)	67 (98%)	1 (2%)	0	100	100
31	A4	584/689 (85%)	579 (99%)	5 (1%)	0	100	100
37	D	236/305 (77%)	231 (98%)	5 (2%)	0	100	100
38	E	303/348 (87%)	298 (98%)	5 (2%)	0	100	100
39	F	250/311 (80%)	246 (98%)	4 (2%)	0	100	100
40	I	210/261 (80%)	203 (97%)	7 (3%)	0	100	100
41	J	173/192 (90%)	173 (100%)	0	0	100	100
42	K	175/178 (98%)	175 (100%)	0	0	100	100
43	L	113/145 (78%)	111 (98%)	2 (2%)	0	100	100
44	M	289/296 (98%)	284 (98%)	5 (2%)	0	100	100
45	N	220/251 (88%)	218 (99%)	2 (1%)	0	100	100
46	O	152/175 (87%)	149 (98%)	3 (2%)	0	100	100
47	P	142/180 (79%)	142 (100%)	0	0	100	100
48	R	138/149 (93%)	138 (100%)	0	0	100	100
49	S	159/205 (78%)	157 (99%)	2 (1%)	0	100	100
50	T	164/206 (80%)	162 (99%)	2 (1%)	0	100	100
51	U	150/153 (98%)	147 (98%)	3 (2%)	0	100	100
52	V	203/216 (94%)	197 (97%)	6 (3%)	0	100	100
53	W	111/148 (75%)	110 (99%)	1 (1%)	0	100	100
54	X	242/256 (94%)	241 (100%)	1 (0%)	0	100	100
55	Y	179/250 (72%)	177 (99%)	2 (1%)	0	100	100
56	Z	120/161 (74%)	120 (100%)	0	0	100	100
57	0	108/188 (57%)	108 (100%)	0	0	100	100
58	1	54/65 (83%)	54 (100%)	0	0	100	100
59	2	44/92 (48%)	43 (98%)	1 (2%)	0	100	100
60	3	93/188 (50%)	92 (99%)	1 (1%)	0	100	100
61	4	36/103 (35%)	36 (100%)	0	0	100	100
62	5	389/423 (92%)	380 (98%)	9 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	6	352/380 (93%)	343 (97%)	9 (3%)	0	100	100
64	7	292/338 (86%)	285 (98%)	7 (2%)	0	100	100
65	8	146/206 (71%)	143 (98%)	3 (2%)	0	100	100
66	9	122/137 (89%)	121 (99%)	1 (1%)	0	100	100
67	a	96/142 (68%)	96 (100%)	0	0	100	100
68	b	149/215 (69%)	147 (99%)	2 (1%)	0	100	100
69	c	282/332 (85%)	279 (99%)	3 (1%)	0	100	100
70	d	235/306 (77%)	230 (98%)	5 (2%)	0	100	100
71	e	226/279 (81%)	218 (96%)	7 (3%)	1 (0%)	30	62
72	f	153/212 (72%)	151 (99%)	2 (1%)	0	100	100
73	g	132/166 (80%)	129 (98%)	3 (2%)	0	100	100
74	h	108/158 (68%)	108 (100%)	0	0	100	100
75	i	95/128 (74%)	94 (99%)	1 (1%)	0	100	100
76	j	92/123 (75%)	90 (98%)	2 (2%)	0	100	100
77	k	99/112 (88%)	99 (100%)	0	0	100	100
78	l	80/138 (58%)	80 (100%)	0	0	100	100
79	m	90/128 (70%)	88 (98%)	2 (2%)	0	100	100
80	o	92/102 (90%)	92 (100%)	0	0	100	100
81	p	141/206 (68%)	141 (100%)	0	0	100	100
82	q	164/222 (74%)	163 (99%)	1 (1%)	0	100	100
83	r	160/196 (82%)	159 (99%)	1 (1%)	0	100	100
84	s	382/439 (87%)	374 (98%)	8 (2%)	0	100	100
85	t	44/198 (22%)	44 (100%)	0	0	100	100
85	u	30/198 (15%)	30 (100%)	0	0	100	100
85	v	30/198 (15%)	30 (100%)	0	0	100	100
85	w	29/198 (15%)	29 (100%)	0	0	100	100
85	x	29/198 (15%)	29 (100%)	0	0	100	100
85	y	29/198 (15%)	29 (100%)	0	0	100	100
86	Q	237/292 (81%)	235 (99%)	2 (1%)	0	100	100
87	H	200/267 (75%)	193 (96%)	7 (4%)	0	100	100
88	z	250/325 (77%)	237 (95%)	12 (5%)	1 (0%)	30	62

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	14675/19484 (75%)	14443 (98%)	229 (2%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	AH	126	ILE
71	e	252	HIS
88	z	128	ASP

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	198/249 (80%)	198 (100%)	0	100	100
3	AC	115/143 (80%)	115 (100%)	0	100	100
4	AD	283/357 (79%)	283 (100%)	0	100	100
5	AE	104/107 (97%)	104 (100%)	0	100	100
6	AF	185/209 (88%)	185 (100%)	0	100	100
7	AG	286/342 (84%)	286 (100%)	0	100	100
8	AH	130/180 (72%)	130 (100%)	0	100	100
9	AI	104/146 (71%)	104 (100%)	0	100	100
10	AJ	93/118 (79%)	93 (100%)	0	100	100
11	AK	91/113 (80%)	91 (100%)	0	100	100
12	AL	158/226 (70%)	158 (100%)	0	100	100
13	AM	97/113 (86%)	97 (100%)	0	100	100
14	AN	96/115 (84%)	96 (100%)	0	100	100
15	AO	174/230 (76%)	174 (100%)	0	100	100
16	AP	88/123 (72%)	88 (100%)	0	100	100
17	AQ	78/79 (99%)	78 (100%)	0	100	100
18	AR	264/318 (83%)	264 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	AS	116/164 (71%)	116 (100%)	0	100	100
20	AT	153/157 (98%)	153 (100%)	0	100	100
21	AU	152/174 (87%)	152 (100%)	0	100	100
22	AV	325/364 (89%)	325 (100%)	0	100	100
23	AW	87/158 (55%)	87 (100%)	0	100	100
24	AX	311/351 (89%)	311 (100%)	0	100	100
25	AY	137/357 (38%)	137 (100%)	0	100	100
26	AZ	90/95 (95%)	90 (100%)	0	100	100
27	A0	188/189 (100%)	188 (100%)	0	100	100
28	A1	257/291 (88%)	257 (100%)	0	100	100
29	A2	100/101 (99%)	100 (100%)	0	100	100
30	A3	65/166 (39%)	65 (100%)	0	100	100
31	A4	526/609 (86%)	526 (100%)	0	100	100
37	D	192/245 (78%)	192 (100%)	0	100	100
38	E	260/290 (90%)	260 (100%)	0	100	100
39	F	219/262 (84%)	219 (100%)	0	100	100
40	I	194/232 (84%)	194 (100%)	0	100	100
41	J	138/150 (92%)	138 (100%)	0	100	100
42	K	154/155 (99%)	154 (100%)	0	100	100
43	L	98/124 (79%)	98 (100%)	0	100	100
44	M	246/249 (99%)	246 (100%)	0	100	100
45	N	189/211 (90%)	189 (100%)	0	100	100
46	O	134/150 (89%)	134 (100%)	0	100	100
47	P	126/155 (81%)	126 (100%)	0	100	100
48	R	118/126 (94%)	118 (100%)	0	100	100
49	S	146/180 (81%)	146 (100%)	0	100	100
50	T	146/176 (83%)	146 (100%)	0	100	100
51	U	134/135 (99%)	134 (100%)	0	100	100
52	V	183/191 (96%)	183 (100%)	0	100	100
53	W	91/119 (76%)	91 (100%)	0	100	100
54	X	220/229 (96%)	220 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	Y	163/223 (73%)	163 (100%)	0	100	100
56	Z	113/147 (77%)	113 (100%)	0	100	100
57	0	99/164 (60%)	99 (100%)	0	100	100
58	1	53/60 (88%)	53 (100%)	0	100	100
59	2	40/72 (56%)	40 (100%)	0	100	100
60	3	88/166 (53%)	88 (100%)	0	100	100
61	4	37/89 (42%)	37 (100%)	0	100	100
62	5	352/368 (96%)	352 (100%)	0	100	100
63	6	313/332 (94%)	313 (100%)	0	100	100
64	7	270/303 (89%)	270 (100%)	0	100	100
65	8	139/190 (73%)	139 (100%)	0	100	100
66	9	104/112 (93%)	104 (100%)	0	100	100
67	a	96/133 (72%)	96 (100%)	0	100	100
68	b	132/185 (71%)	132 (100%)	0	100	100
69	c	251/288 (87%)	251 (100%)	0	100	100
70	d	223/274 (81%)	223 (100%)	0	100	100
71	e	200/236 (85%)	200 (100%)	0	100	100
72	f	139/188 (74%)	139 (100%)	0	100	100
73	g	124/148 (84%)	124 (100%)	0	100	100
74	h	104/148 (70%)	104 (100%)	0	100	100
75	i	86/110 (78%)	86 (100%)	0	100	100
76	j	74/97 (76%)	74 (100%)	0	100	100
77	k	83/90 (92%)	83 (100%)	0	100	100
78	l	76/116 (66%)	76 (100%)	0	100	100
79	m	85/113 (75%)	85 (100%)	0	100	100
80	o	80/87 (92%)	80 (100%)	0	100	100
81	p	135/181 (75%)	135 (100%)	0	100	100
82	q	143/178 (80%)	143 (100%)	0	100	100
83	r	147/169 (87%)	147 (100%)	0	100	100
84	s	340/381 (89%)	340 (100%)	0	100	100
85	t	40/158 (25%)	40 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
85	u	31/158 (20%)	31 (100%)	0	100	100
85	v	31/158 (20%)	31 (100%)	0	100	100
85	w	30/158 (19%)	30 (100%)	0	100	100
85	x	30/158 (19%)	30 (100%)	0	100	100
85	y	30/158 (19%)	30 (100%)	0	100	100
86	Q	221/256 (86%)	221 (100%)	0	100	100
87	H	182/228 (80%)	182 (100%)	0	100	100
88	z	226/287 (79%)	226 (100%)	0	100	100
All	All	13149/16790 (78%)	13149 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
31	A4	306	ASN
76	j	26	GLN
40	I	93	ASN
75	i	124	HIS
86	Q	66	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	953/954 (99%)	145 (15%)	1 (0%)
32	Az	32/33 (96%)	18 (56%)	0
33	Aw	67/68 (98%)	38 (56%)	0
34	Ax	70/71 (98%)	32 (45%)	0
35	A	1556/1561 (99%)	246 (15%)	2 (0%)
36	B	71/72 (98%)	12 (16%)	0
All	All	2749/2759 (99%)	491 (17%)	3 (0%)

5 of 491 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	651	A
1	AA	680	U
1	AA	688	A

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Mol	Chain	Res	Type
1	AA	691	A
1	AA	695	A

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	1539	C
35	A	2112	A
35	A	2296	U

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

19 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$
1	5MC	AA	1488	1	18,22,23	0.31	0	26,32,35	0.44	0
36	PSU	B	39	36	18,21,22	0.75	0	22,30,33	2.57	4 (18%)
1	5MU	AA	1076	1	19,22,23	0.64	0	28,32,35	1.21	3 (10%)
77	AYA	k	2	77	6,7,8	0.82	0	5,8,10	0.56	0
1	MA6	AA	1583	1	23,26,27	0.30	0	34,38,41	0.57	1 (2%)
1	MA6	AA	1584	1	23,26,27	0.30	0	34,38,41	0.58	1 (2%)
17	AYA	AQ	2	17	6,7,8	0.79	0	5,8,10	0.36	0
35	PSU	A	3067	35	18,21,22	0.79	0	22,30,33	2.57	5 (22%)
36	1MA	B	9	36	21,25,26	0.75	1 (4%)	31,37,40	0.65	1 (3%)
1	B8T	AA	1486	93,1	19,22,23	0.30	0	26,31,34	0.32	0
36	2MG	B	10	36	23,26,27	0.48	0	32,38,41	0.53	0
35	OMG	A	2815	35,33,92	23,26,27	0.29	0	33,38,41	0.38	0
9	5F0	AI	184	9	8,8,9	0.59	0	7,9,11	1.19	1 (14%)
29	AYA	A2	2	29	6,7,8	0.80	0	5,8,10	0.55	0
35	OMU	A	3039	35,92	19,22,23	0.27	0	26,31,34	0.43	0
35	1MA	A	2617	35	21,25,26	0.77	1 (4%)	31,37,40	0.67	1 (3%)
35	OMG	A	3040	35	23,26,27	0.27	0	33,38,41	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
42	SAC	K	2	42	7,8,9	0.24	0	8,9,11	0.55	0
51	AYA	U	2	51	6,7,8	0.80	0	5,8,10	0.45	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
1	5MC	AA	1488	1	-	0/7/25/26	0/2/2/2
36	PSU	B	39	36	-	1/7/25/26	0/2/2/2
1	5MU	AA	1076	1	-	0/7/25/26	0/2/2/2
77	AYA	k	2	77	-	0/4/6/8	-
1	MA6	AA	1583	1	-	0/11/29/30	0/3/3/3
1	MA6	AA	1584	1	-	2/11/29/30	0/3/3/3
17	AYA	AQ	2	17	-	1/4/6/8	-
35	PSU	A	3067	35	-	0/7/25/26	0/2/2/2
36	1MA	B	9	36	-	0/7/25/26	0/3/3/3
1	B8T	AA	1486	93,1	-	2/7/27/28	0/2/2/2
36	2MG	B	10	36	-	0/9/27/28	0/3/3/3
35	OMG	A	2815	35,33,92	-	0/9/27/28	0/3/3/3
9	5F0	AI	184	9	-	0/9/9/10	-
29	AYA	A2	2	29	-	0/4/6/8	-
35	OMU	A	3039	35,92	-	0/9/27/28	0/2/2/2
35	1MA	A	2617	35	-	0/7/25/26	0/3/3/3
35	OMG	A	3040	35	-	0/9/27/28	0/3/3/3
42	SAC	K	2	42	-	0/7/8/10	-
51	AYA	U	2	51	-	0/4/6/8	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	A	2617	1MA	C6-N6	3.04	1.35	1.28
36	B	9	1MA	C6-N6	3.03	1.35	1.28

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	B	39	PSU	N1-C2-N3	8.14	124.35	115.13
35	A	3067	PSU	N1-C2-N3	8.11	124.32	115.13
36	B	39	PSU	C4-N3-C2	-6.58	116.86	126.34
35	A	3067	PSU	C4-N3-C2	-6.56	116.89	126.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1076	5MU	C4-N3-C2	-4.80	121.13	127.35

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	AA	1584	MA6	C5-C6-N6-C9
1	AA	1486	B8T	O4'-C4'-C5'-O5'
17	AQ	2	AYA	C-CA-N-CT
1	AA	1584	MA6	C4'-C5'-O5'-P
36	B	39	PSU	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
51	U	2	AYA	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 272 ligands modelled in this entry, 259 are monoatomic - leaving 13 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	$\# Z > 2$
90	SPM	AA	1702	-	13,13,13	0.29	0	12,12,12	0.96	0
95	FES	AP	201	16,5	0,4,4	-	-	-		
96	ATP	AX	501	93	29,33,33	0.49	0	44,52,52	0.51	0
91	SPD	A	3302	-	9,9,9	0.30	0	8,8,8	1.17	0
95	FES	r	201	40,83	0,4,4	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
91	SPD	AA	1703	-	9,9,9	0.27	0	8,8,8	1.25	1 (12%)
91	SPD	A	3303	-	9,9,9	0.31	0	8,8,8	1.15	0
99	VAL	B	101	36	4,6,7	0.54	0	6,7,9	0.83	0
95	FES	AT	201	13,20	0,4,4	-	-	-	-	-
97	GDP	AX	503	-	28,30,30	0.42	0	44,47,47	0.43	0
98	PUT	A	3304	-	5,5,5	0.24	0	4,4,4	0.51	0
89	NAD	AA	1701	93	45,48,48	0.36	0	63,73,73	0.46	0
91	SPD	A	3301	-	9,9,9	0.29	0	8,8,8	1.20	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
90	SPM	AA	1702	-	-	1/11/11/11	-
95	FES	AP	201	16,5	-	-	0/1/1/1
96	ATP	AX	501	93	-	0/22/38/38	0/3/3/3
91	SPD	A	3302	-	-	0/7/7/7	-
95	FES	r	201	40,83	-	-	0/1/1/1
91	SPD	AA	1703	-	-	0/7/7/7	-
91	SPD	A	3303	-	-	2/7/7/7	-
99	VAL	B	101	36	-	0/5/6/8	-
95	FES	AT	201	13,20	-	-	0/1/1/1
97	GDP	AX	503	-	-	0/16/32/32	0/3/3/3
98	PUT	A	3304	-	-	0/3/3/3	-
89	NAD	AA	1701	93	-	5/30/62/62	0/5/5/5
91	SPD	A	3301	-	-	1/7/7/7	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
91	AA	1703	SPD	C4-C5-N6	-2.03	106.67	112.14

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
89	AA	1701	NAD	C3D-C4D-C5D-O5D
89	AA	1701	NAD	O4B-C4B-C5B-O5B

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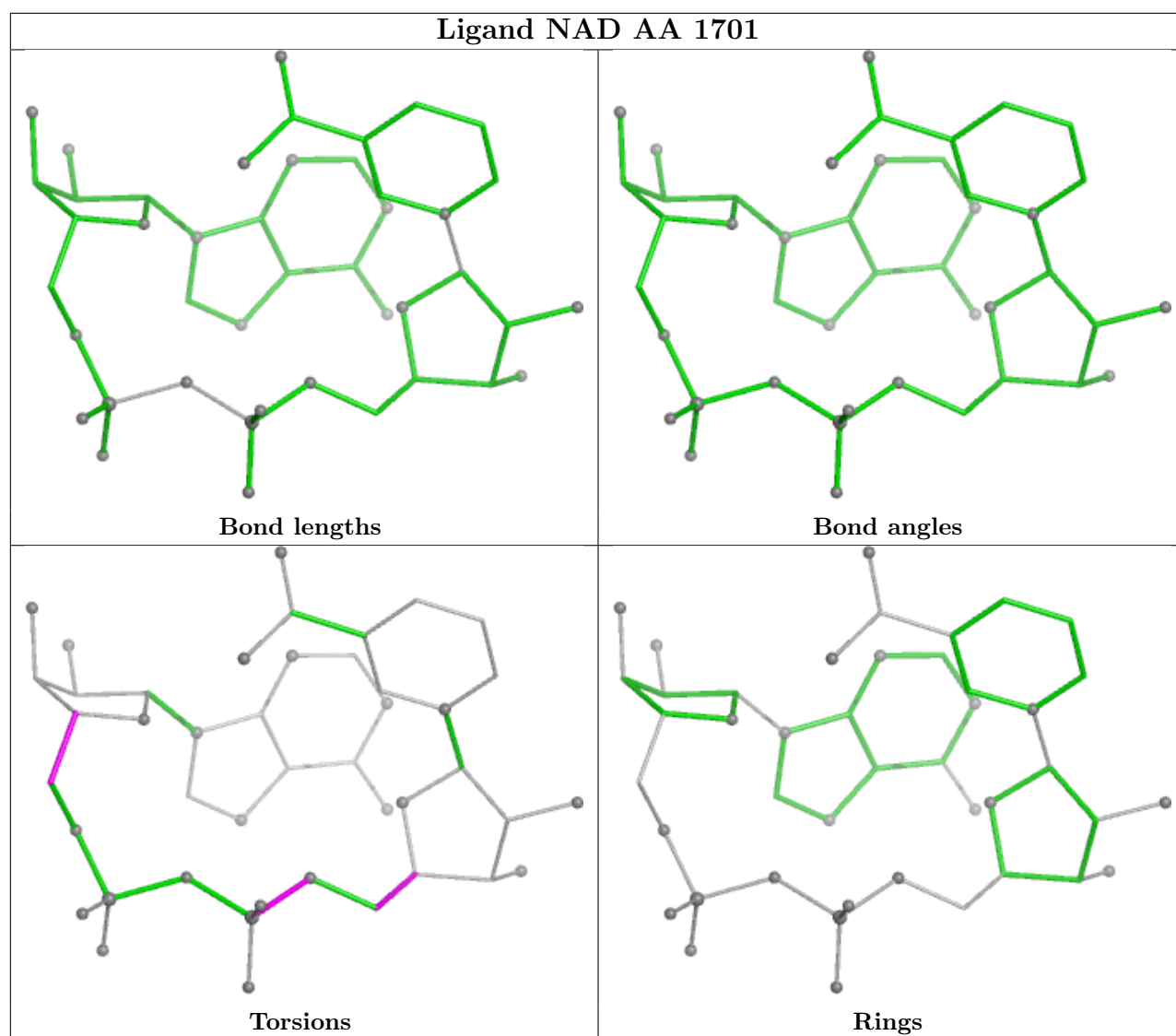
Mol	Chain	Res	Type	Atoms
91	A	3303	SPD	C4-C5-N6-C7
91	A	3301	SPD	N6-C7-C8-C9
90	AA	1702	SPM	N10-C11-C12-C13

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
99	B	101	VAL	2	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](#)

There are no chain breaks in this entry.

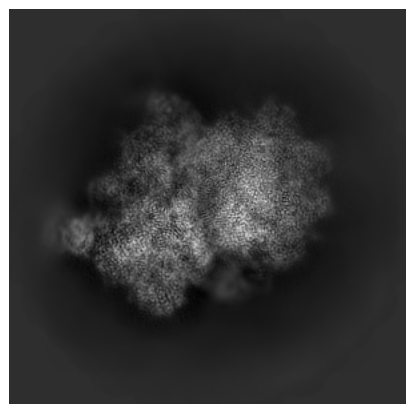
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13982. These allow visual inspection of the internal detail of the map and identification of artifacts.

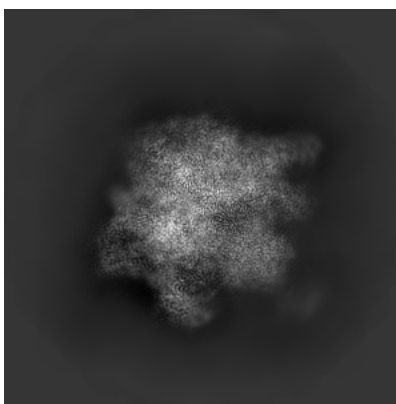
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

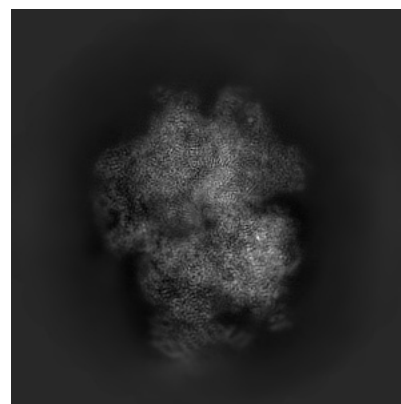
6.1.1 Primary map



X

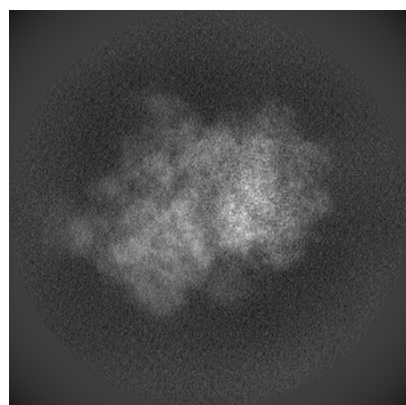


Y

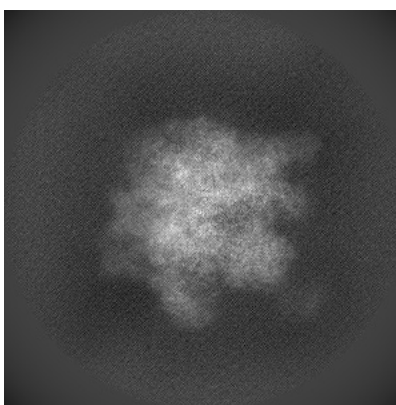


Z

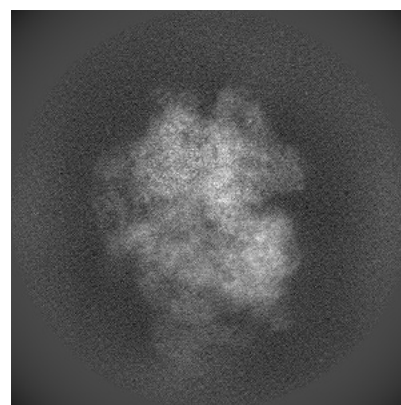
6.1.2 Raw map



X



Y

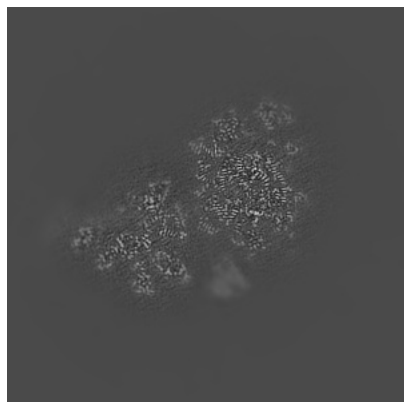


Z

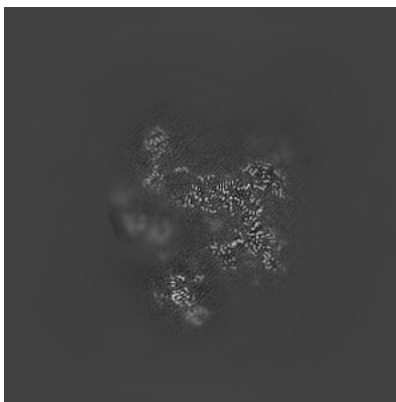
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

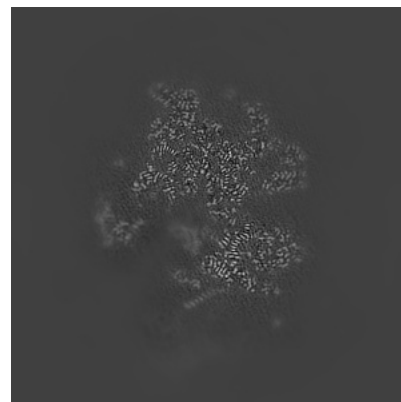
6.2.1 Primary map



X Index: 270

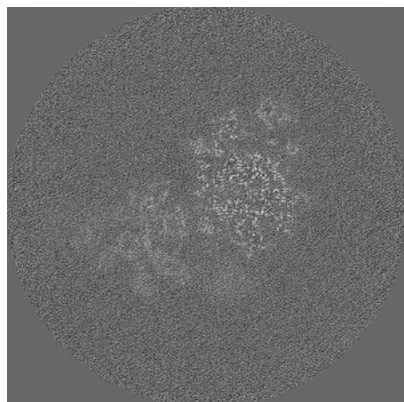


Y Index: 270

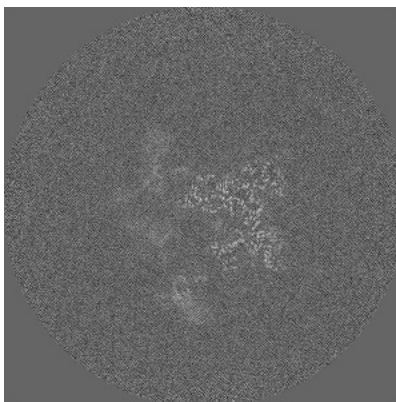


Z Index: 270

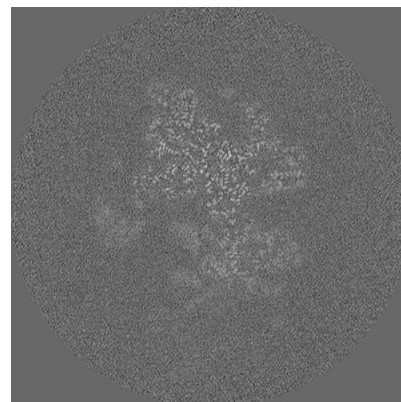
6.2.2 Raw map



X Index: 270



Y Index: 270

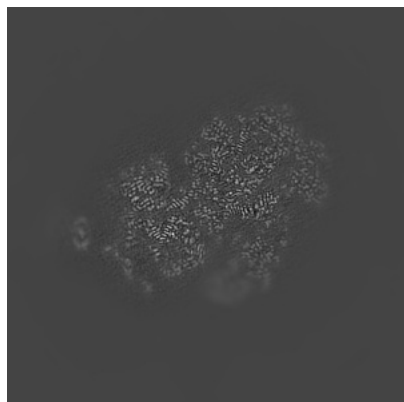


Z Index: 270

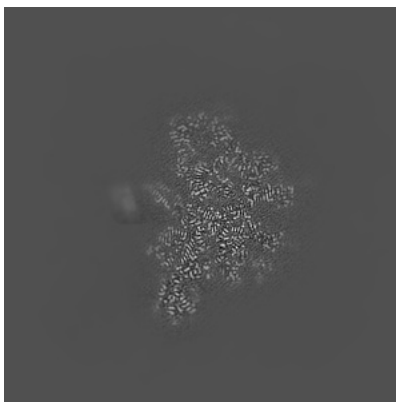
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

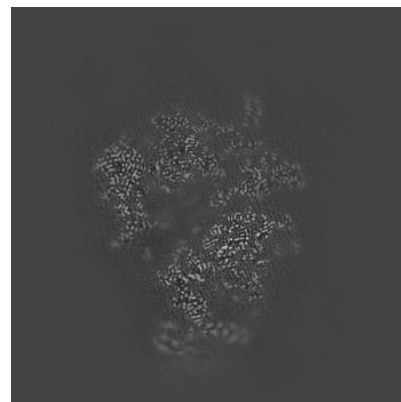
6.3.1 Primary map



X Index: 289

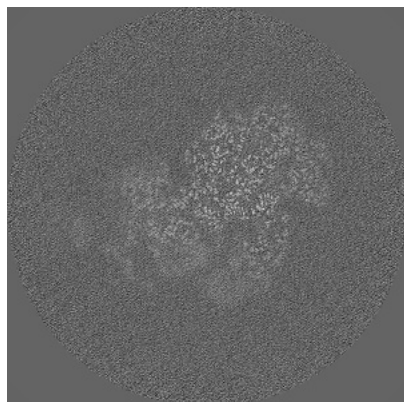


Y Index: 318

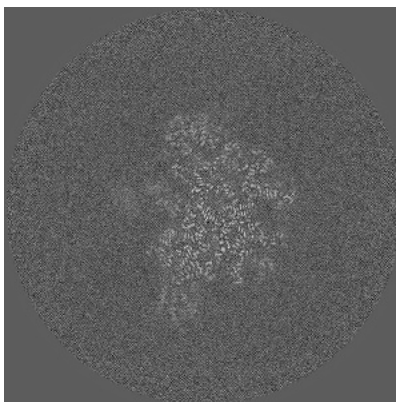


Z Index: 235

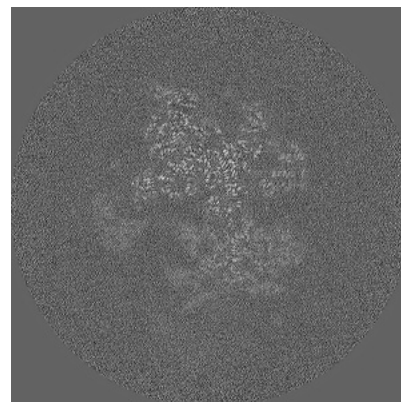
6.3.2 Raw map



X Index: 289



Y Index: 316

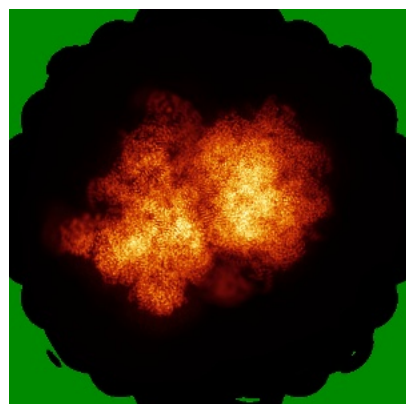


Z Index: 267

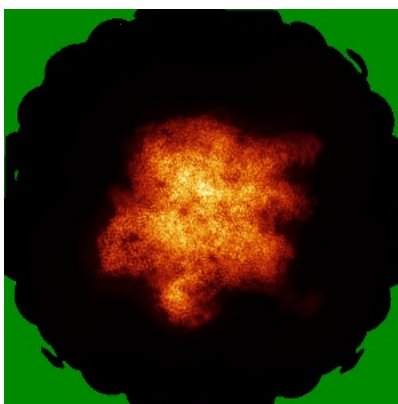
The images above show the largest variance slices of the map in three orthogonal directions.

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

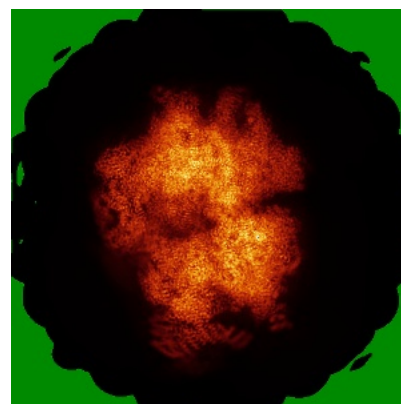
6.4.1 Primary map



X

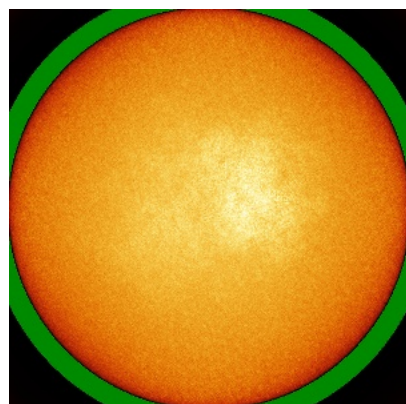


Y

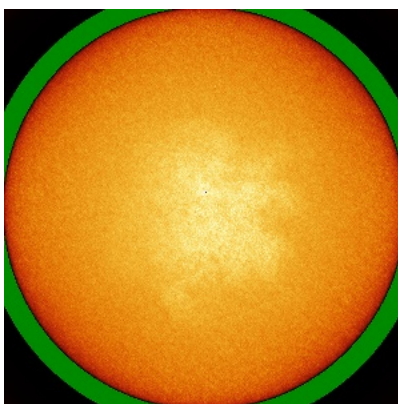


Z

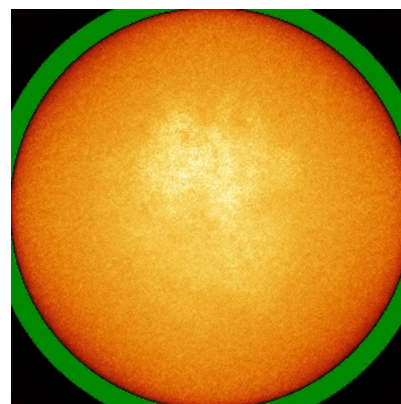
6.4.2 Raw map



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.

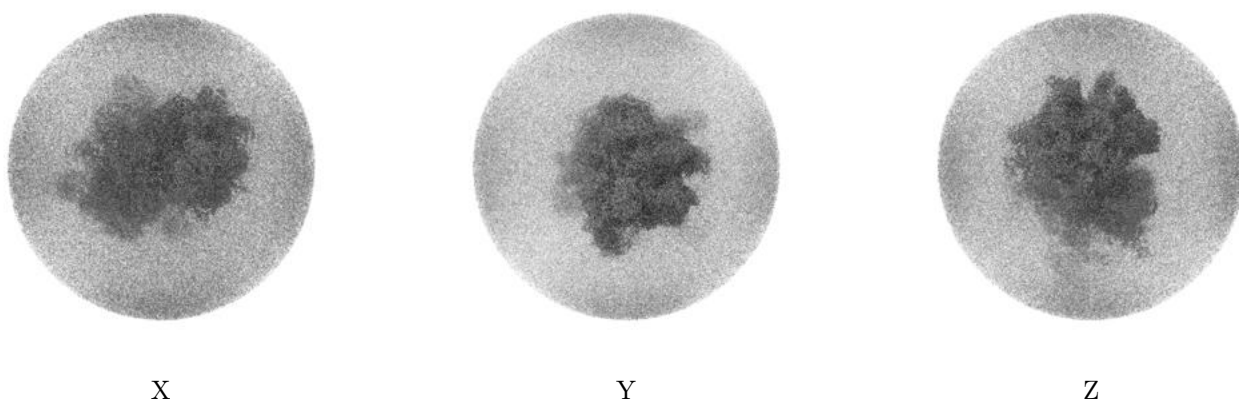
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.8. 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.

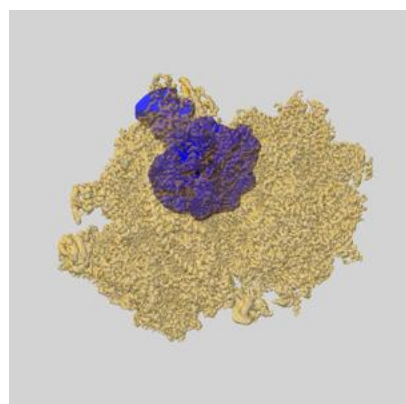
6.6 Mask visualisation [i](#)

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

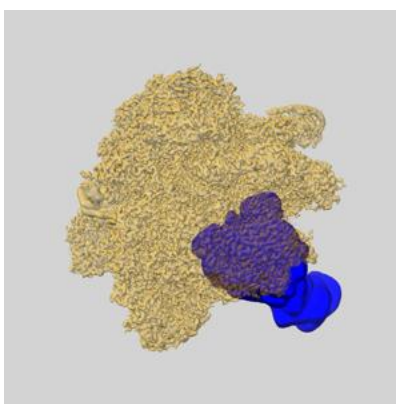
A mask typically either:

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

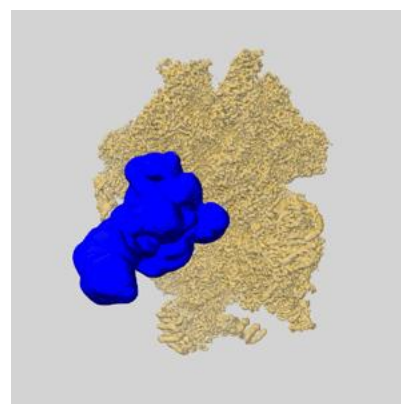
6.6.1 emd_13982_msk_1.map [i](#)



X

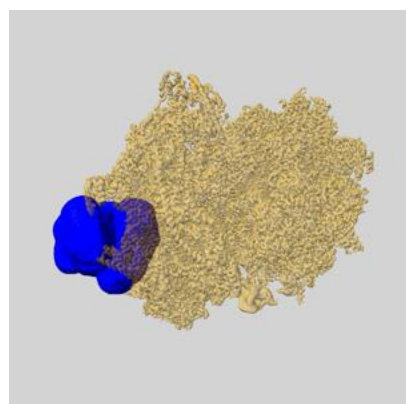


Y

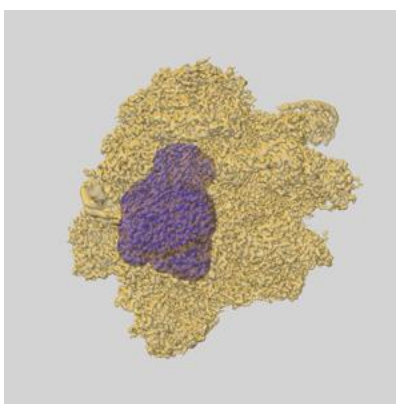


Z

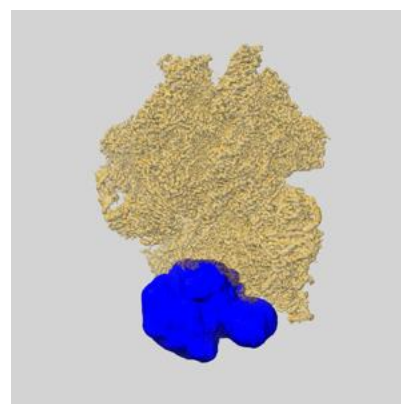
6.6.2 emd_13982_msk_2.map [i](#)



X

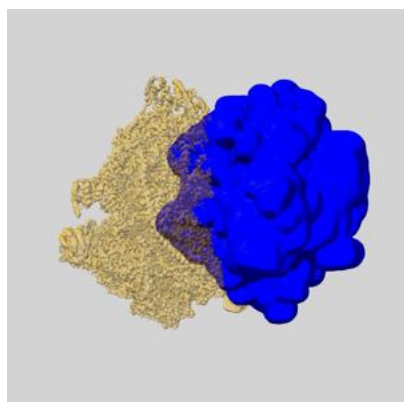


Y

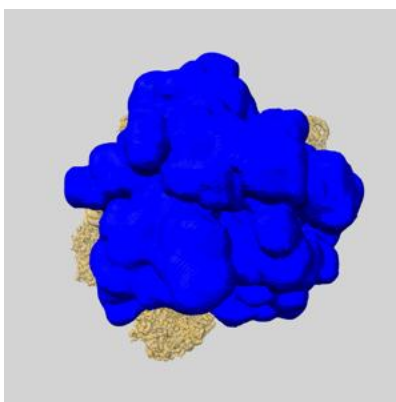


Z

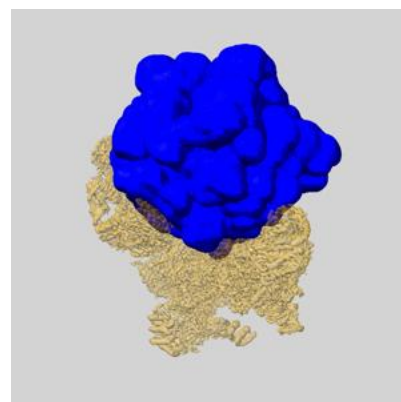
6.6.3 emd_13982_msk_3.map [i](#)



X

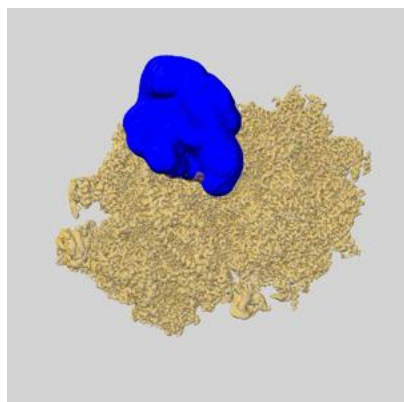


Y

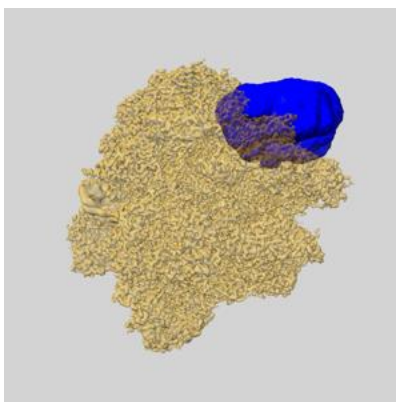


Z

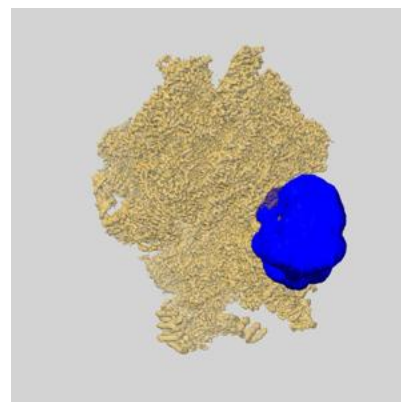
6.6.4 emd_13982_msk_4.map [i](#)



X

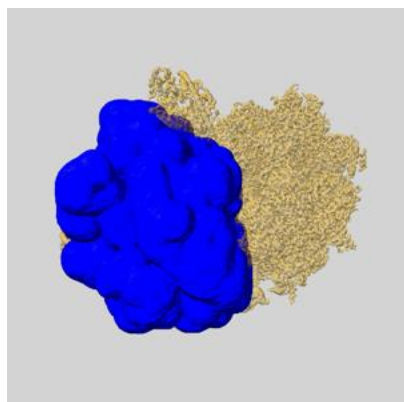


Y

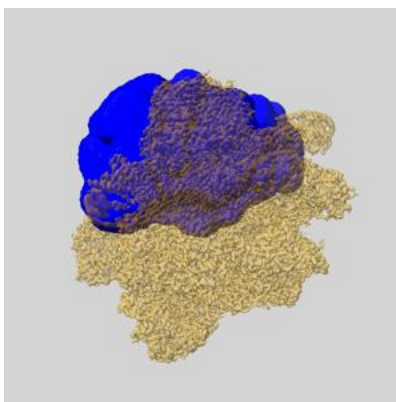


Z

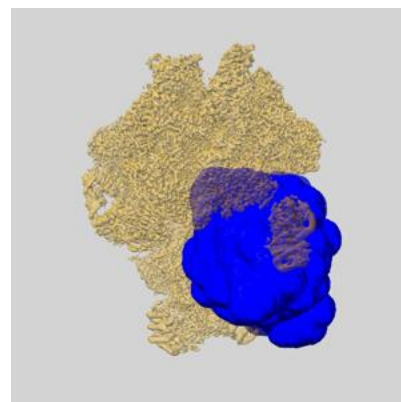
6.6.5 emd_13982_msk_5.map [i](#)



X

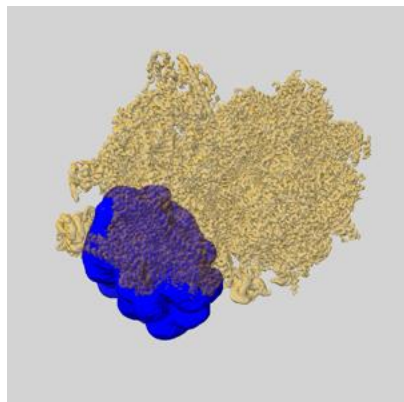


Y

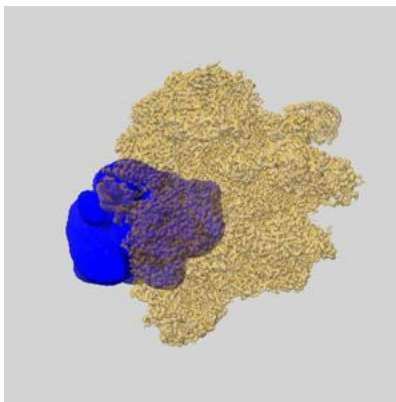


Z

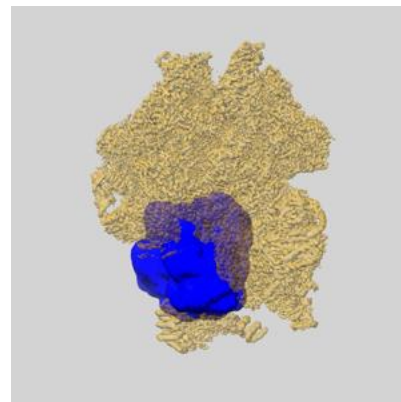
6.6.6 emd_13982_msk_6.map [i](#)



X



Y

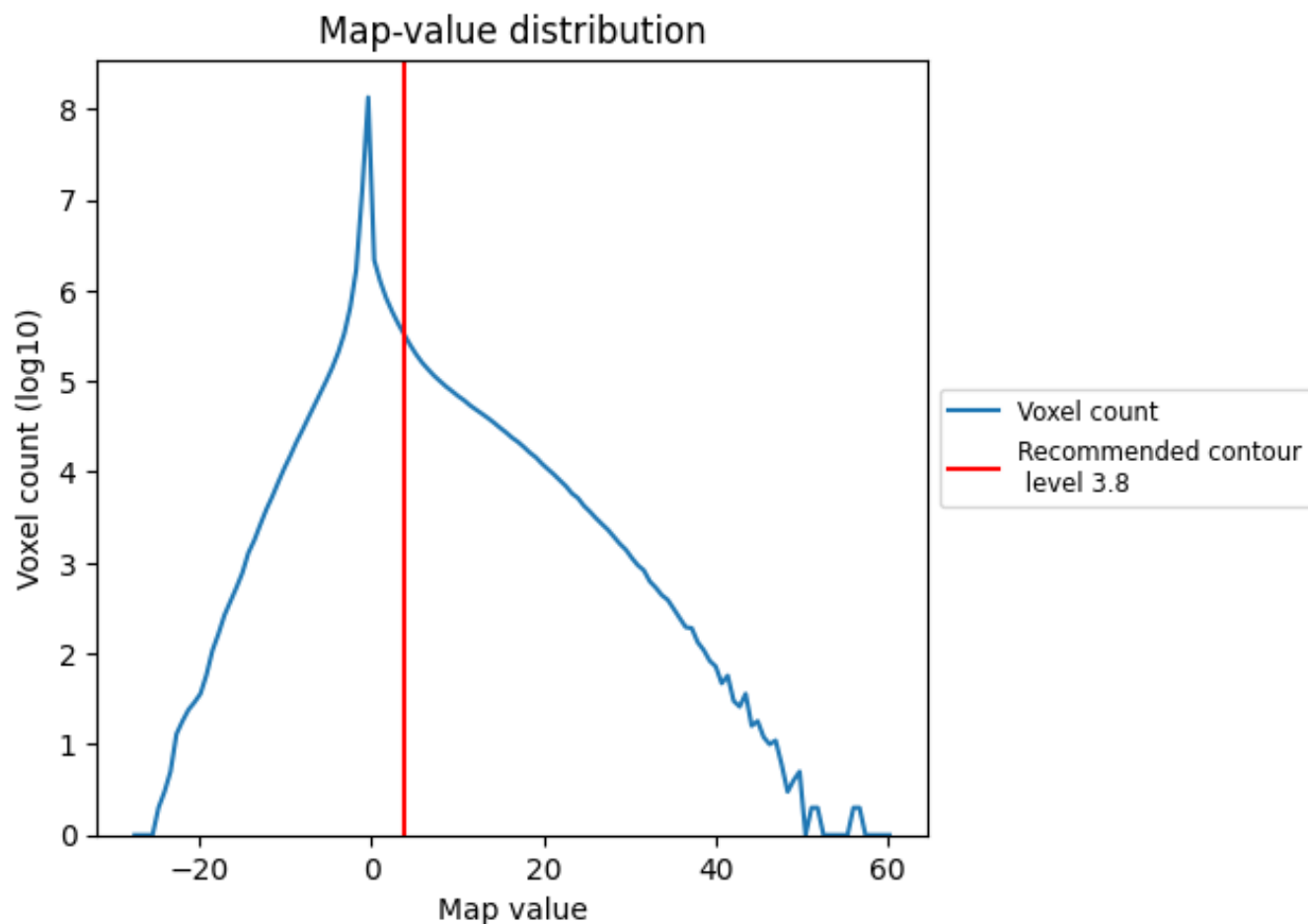


Z

7 Map analysis [i](#)

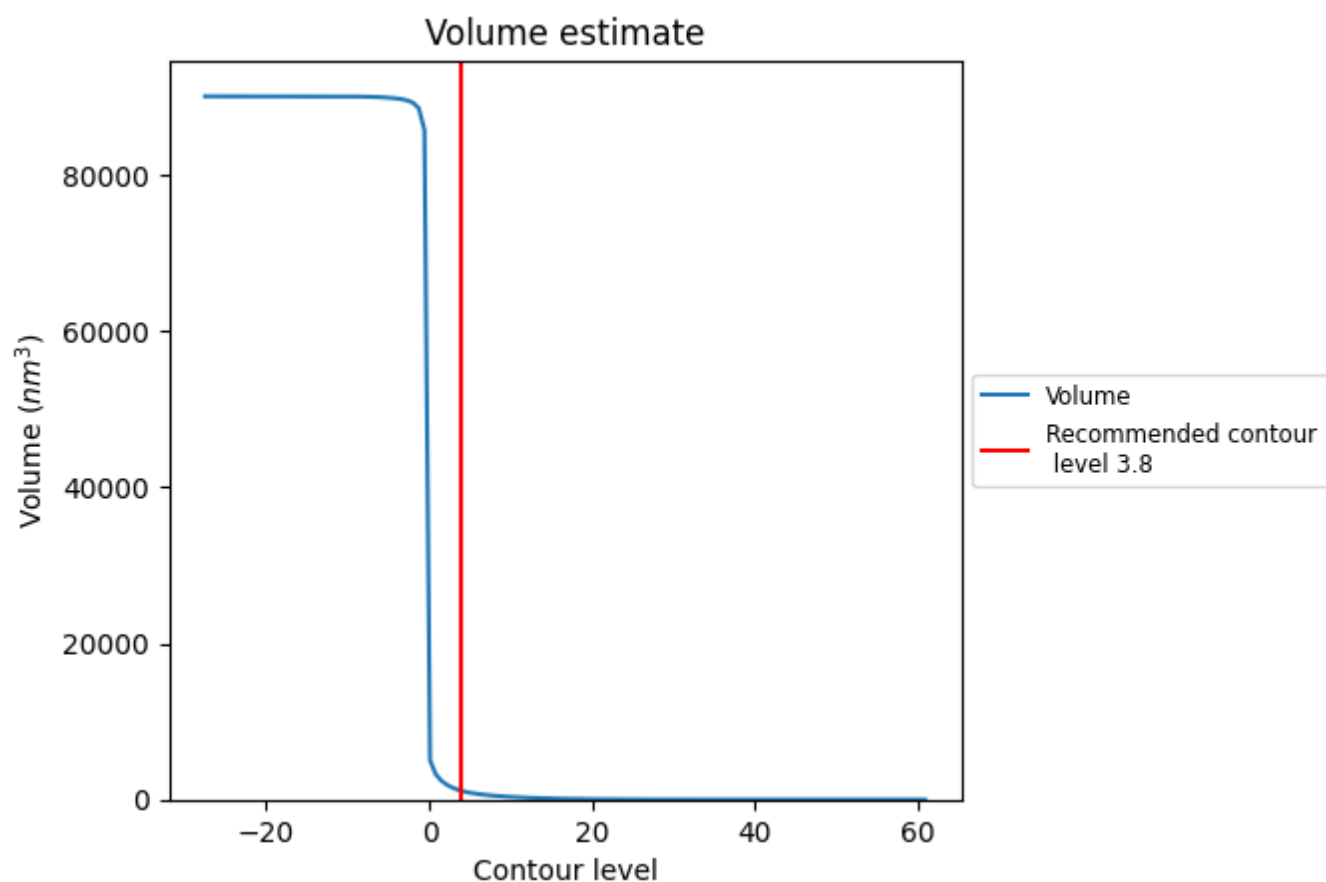
This section contains the results of statistical analysis of the map.

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.

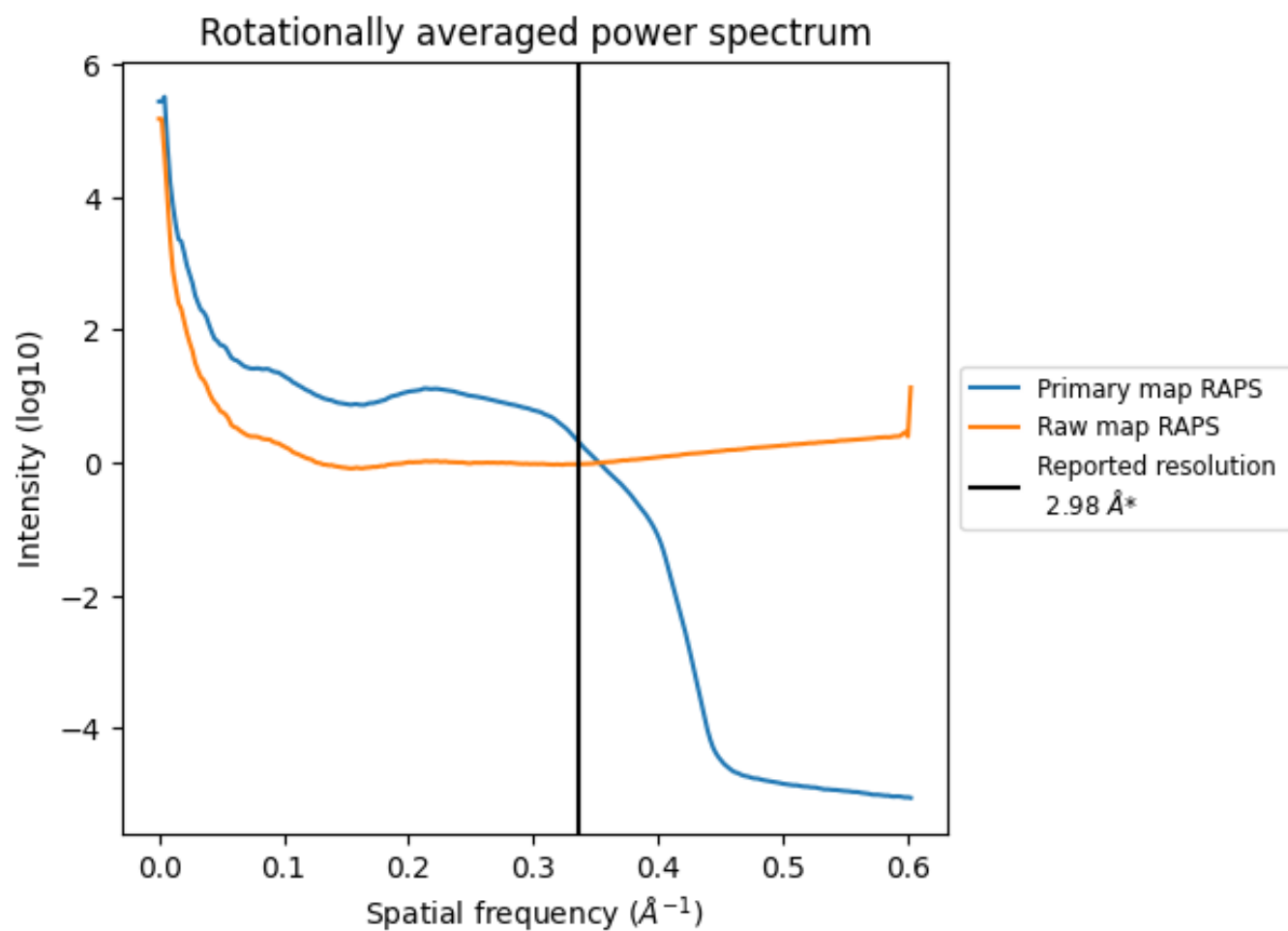
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1179 nm³; this corresponds to an approximate mass of 1065 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 ⓘ

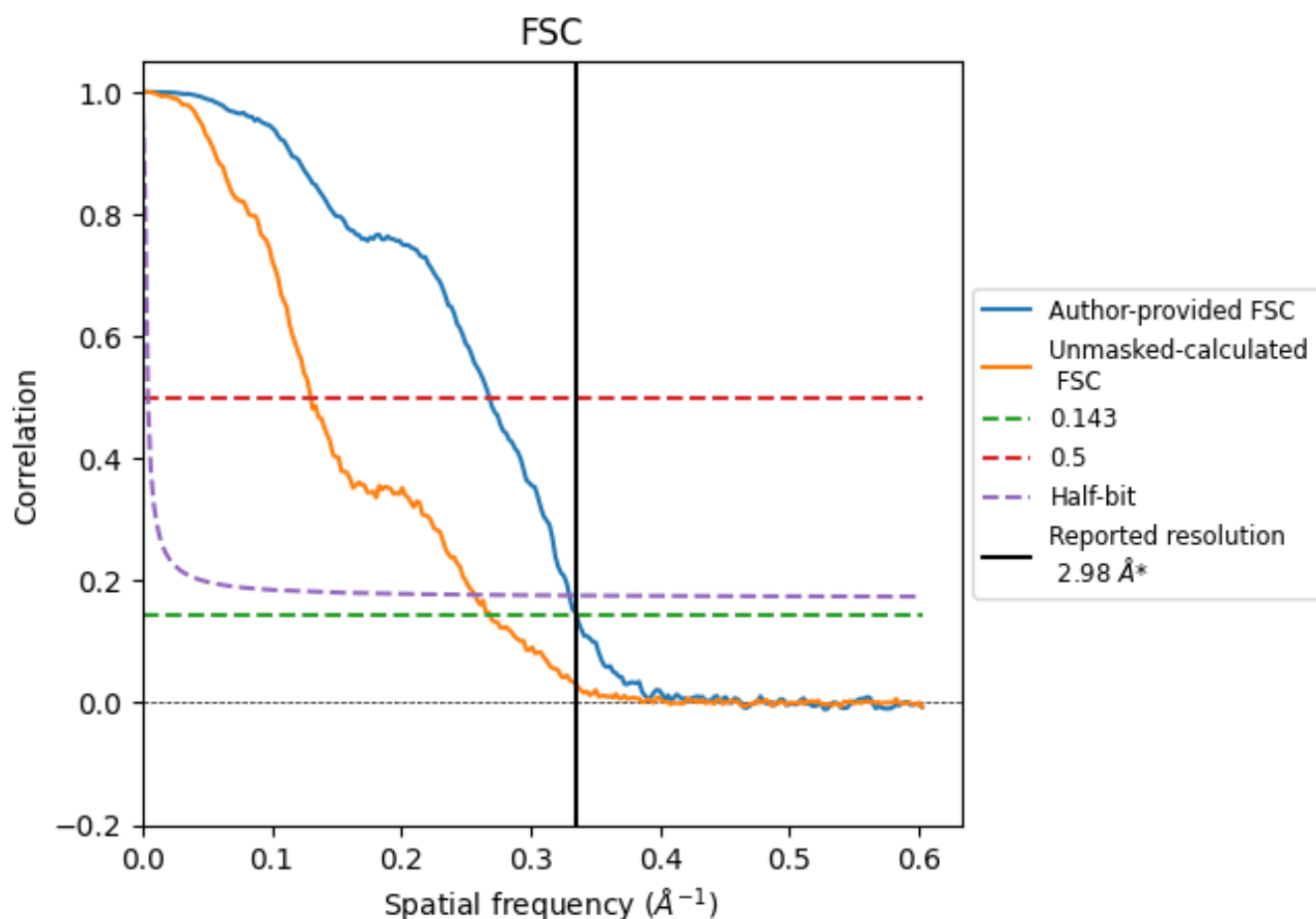


*Reported resolution corresponds to spatial frequency of 0.336 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.336 Å⁻¹

8.2 Resolution estimates [i](#)

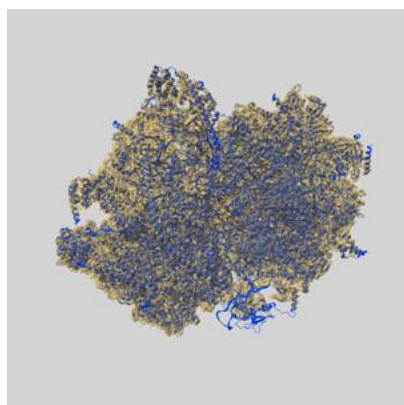
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.98	-	-
Author-provided FSC curve	2.98	3.73	3.03
Unmasked-calculated*	3.72	7.69	3.89

*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 3.72 differs from the reported value 2.98 by more than 10 %

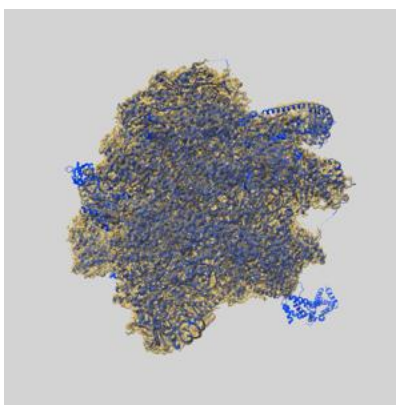
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13982 and PDB model 7QI6. Per-residue inclusion information can be found in section 3 on page 30.

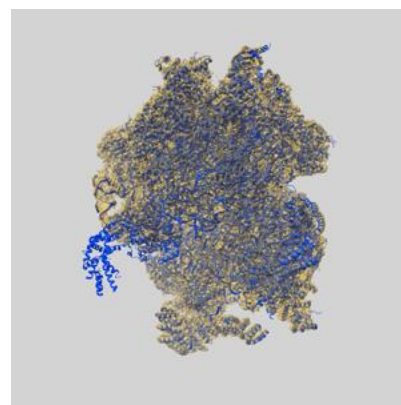
9.1 Map-model overlay [i](#)



X



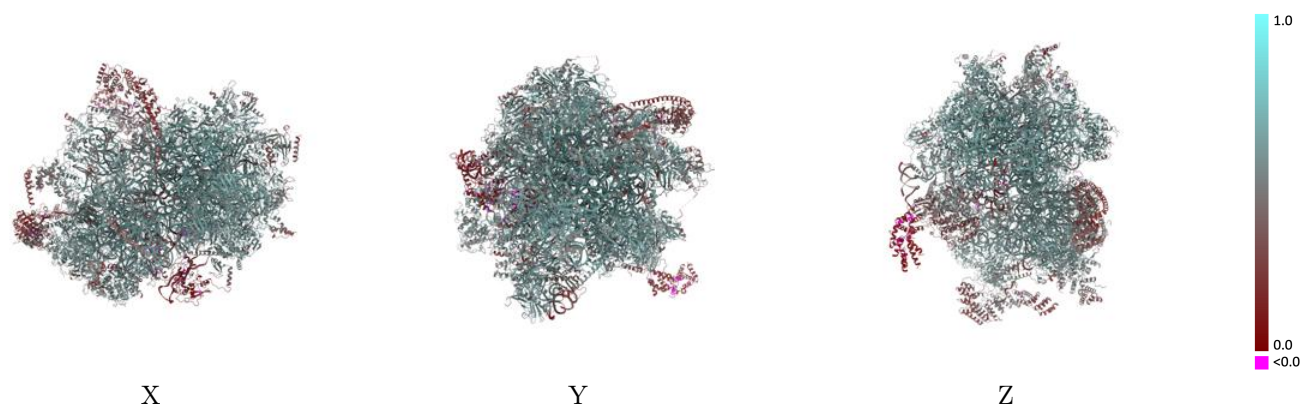
Y



Z

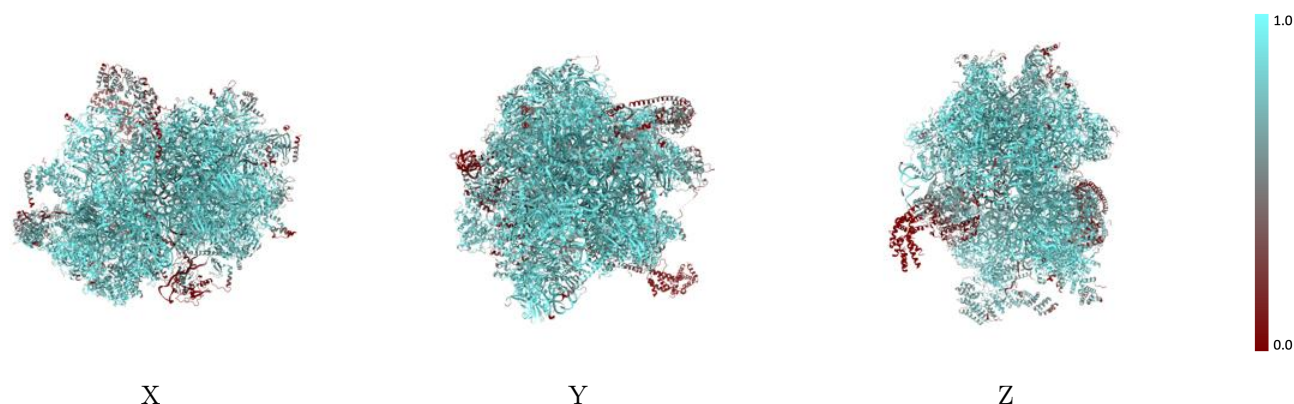
The images above show the 3D surface view of the map at the recommended contour level 3.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



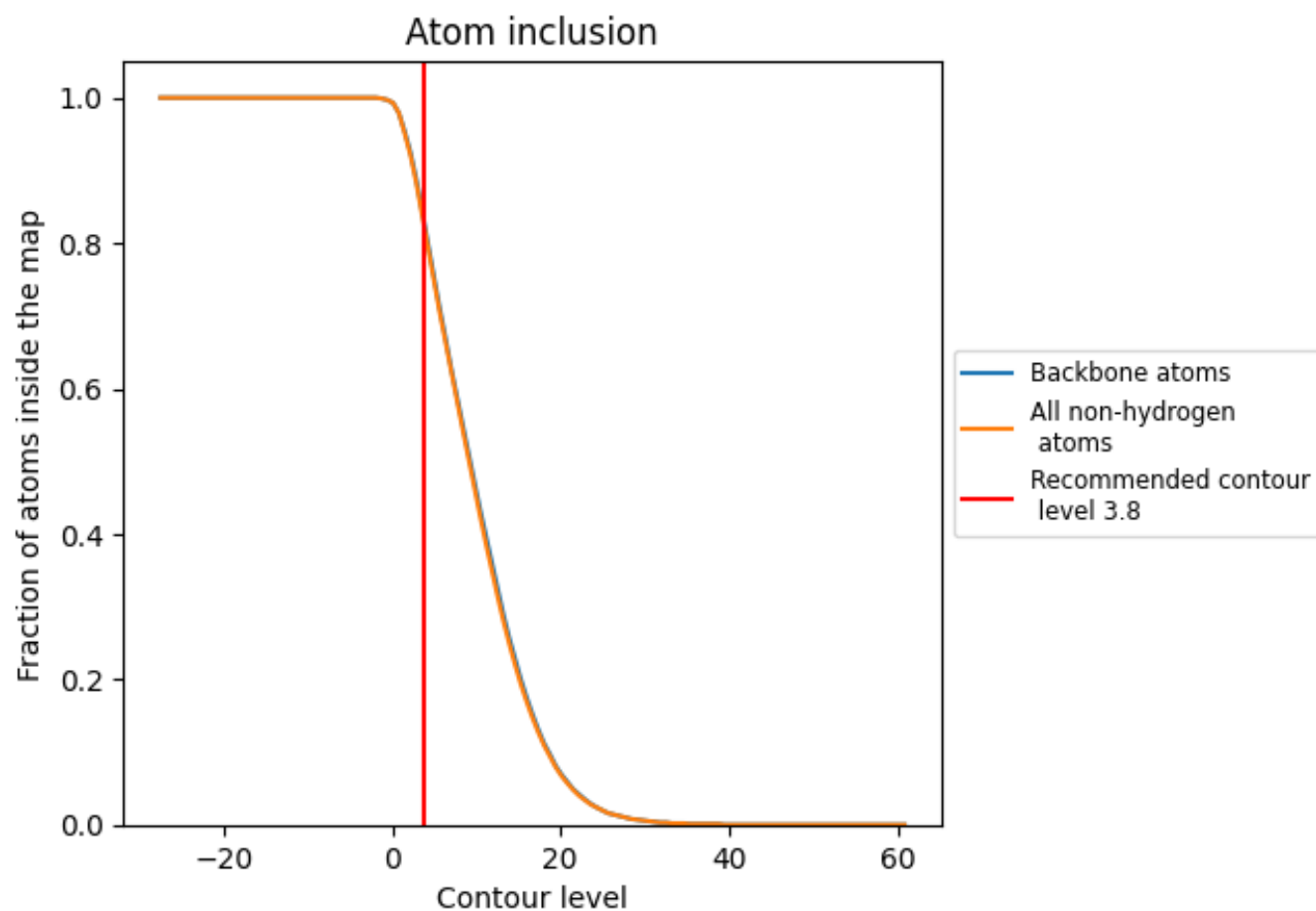
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 82% 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 (3.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8240	 0.5390
0	 0.8510	 0.5830
1	 0.8050	 0.5610
2	 0.9950	 0.6800
3	 0.9750	 0.6550
4	 0.9360	 0.6180
5	 0.8370	 0.5620
6	 0.9000	 0.5580
7	 0.7140	 0.5240
8	 0.6050	 0.3960
9	 0.7810	 0.5530
A	 0.9350	 0.6140
A0	 0.7740	 0.4760
A1	 0.8590	 0.5260
A2	 0.8240	 0.4980
A3	 0.9080	 0.5920
A4	 0.7100	 0.3630
AA	 0.9700	 0.6030
AB	 0.8920	 0.5590
AC	 0.9580	 0.6090
AD	 0.8690	 0.5460
AE	 0.9030	 0.5670
AF	 0.8980	 0.5480
AG	 0.8500	 0.5260
AH	 0.9120	 0.5640
AI	 0.9090	 0.5650
AJ	 0.8850	 0.5410
AK	 0.9570	 0.6120
AL	 0.8340	 0.5360
AM	 0.8720	 0.5490
AN	 0.9140	 0.5800
AO	 0.8670	 0.5360
AP	 0.9080	 0.5720
AQ	 0.9390	 0.5960
AR	 0.7610	 0.4710



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Chain	Atom inclusion	Q-score
AS	 0.7970	 0.4770
AT	 0.8860	 0.5490
AU	 0.7750	 0.4690
AV	 0.4290	 0.2850
AW	 0.8830	 0.5290
AX	 0.8950	 0.5400
AY	 0.7530	 0.4710
AZ	 0.8660	 0.5520
Aw	 0.6130	 0.3250
Ax	 0.5340	 0.2470
Az	 0.5350	 0.3310
B	 0.8800	 0.4590
D	 0.8990	 0.6120
E	 0.9120	 0.6160
F	 0.9210	 0.6240
H	 0.3620	 0.3170
I	 0.3780	 0.3770
J	 0.1870	 0.3140
K	 0.9360	 0.6280
L	 0.9140	 0.6100
M	 0.9100	 0.6130
N	 0.8680	 0.5850
O	 0.9090	 0.6100
P	 0.9410	 0.5920
Q	 0.7960	 0.5570
R	 0.9430	 0.6400
S	 0.9080	 0.6120
T	 0.9260	 0.6140
U	 0.8060	 0.5560
V	 0.7310	 0.5180
W	 0.9500	 0.6270
X	 0.8250	 0.5650
Y	 0.8900	 0.5950
Z	 0.9120	 0.6140
a	 0.7850	 0.5470
b	 0.9170	 0.6110
c	 0.8100	 0.5570
d	 0.6180	 0.4600
e	 0.7060	 0.4010
f	 0.6560	 0.4380
g	 0.8770	 0.5880
h	 0.6640	 0.5140

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Continued from previous page...

Chain	Atom inclusion	Q-score
i	 0.9560	 0.6530
j	 0.8260	 0.5510
k	 0.5090	 0.4460
l	 0.3110	 0.3750
m	 0.6270	 0.4050
o	 0.9530	 0.6340
p	 0.6670	 0.4820
q	 0.5520	 0.4300
r	 0.8470	 0.5760
s	 0.8680	 0.5840
t	 0.0060	 0.2170
u	 0.0000	 0.1720
v	 0.0000	 0.1070
w	 0.0000	 0.0340
x	 0.0000	 0.0660
y	 0.0000	 0.0730
z	 0.3880	 0.1360