



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 07:01 AM UTC

PDB ID : 6NU3 / pdb_00006nu3
EMDB ID : EMD-0515
Title : Structural insights into unique features of the human mitochondrial ribosome recycling
Authors : Sharma, M.R.; Koripella, R.K.; Agrawal, R.K.
Deposited on : 2019-01-30
Resolution : 4.40 Å(reported)
Based on initial model : 3J9M

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

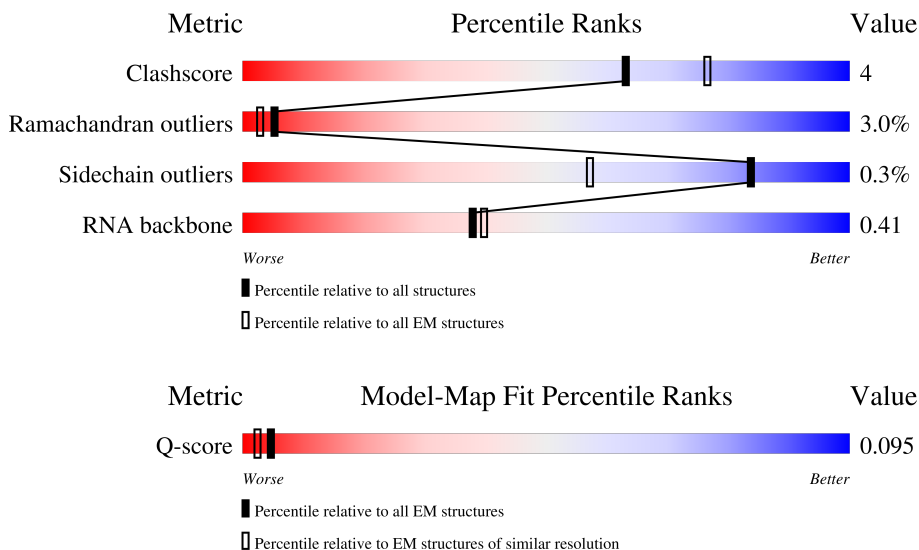
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.40 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	3132 (3.91 - 4.90)

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	A	1472	
2	B	56	
3	D	305	


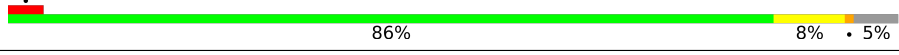

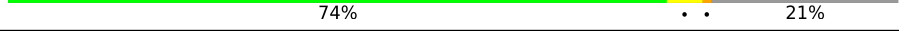
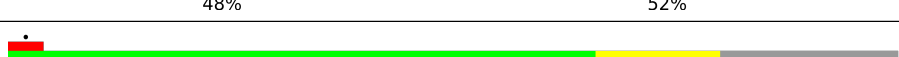
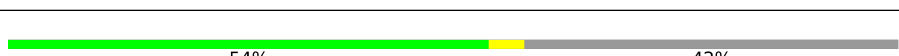


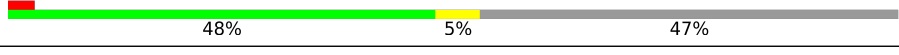









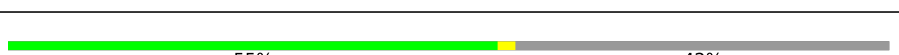
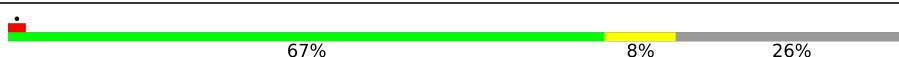

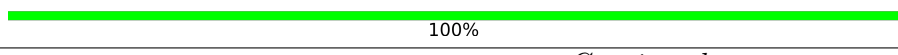



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Mol	Chain	Length	Quality of chain
4	E	348	78% 9% 14%
5	F	311	68% 12% 20%
6	H	267	32% 64%
7	I	261	54% 7% 39%
8	J	192	70% 27%
9	K	178	93% 6%
10	L	145	68% 10% 21%
11	M	296	83% 13%
12	N	251	72% 10% 18%
13	O	175	77% 9% 13%
14	P	180	68% 6% 26%
15	Q	219	95% 5%
16	R	149	85% 8% 6%
17	S	205	71% 24%
18	T	206	5% 73% 8% 19%
19	U	153	63% 8% 27%
20	V	216	81% 6% 12%
21	W	148	70% 5% 25%
22	X	243	91% 9%
23	Y	250	64% 6% 30%
24	Z	161	66% 7% 25%
25	0	188	50% 6% 43%
26	1	65	71% 8% 20%
27	2	92	42% 8% 50%
28	3	188	47% 49%

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Mol	Chain	Length	Quality of chain
29	4	103	
30	5	394	
31	6	380	
32	7	338	
33	8	206	
34	9	137	
35	a	142	
36	b	215	
37	c	332	
38	d	306	
39	e	279	
40	f	212	
41	g	166	
42	h	158	
43	i	128	
44	j	123	
45	k	112	
46	l	138	
47	m	128	
48	o	102	
49	p	206	
50	q	222	
51	r	196	
52	s	439	
53	t	28	








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Mol	Chain	Length	Quality of chain
54	u	2	
55	AA	923	
56	AB	296	
57	AC	167	
58	AD	430	
59	AE	125	
60	AF	242	
61	AG	396	
62	AH	201	
63	AI	194	
64	AJ	138	
65	AK	128	
66	AL	257	
67	AM	137	
68	AN	130	
69	AO	185	
70	AP	142	
71	AQ	86	
72	AR	360	
73	AS	190	
74	AT	173	
75	AU	205	
76	AV	414	
77	AW	187	
78	AX	398	

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Mol	Chain	Length	Quality of chain
79	AY	395	
80	AZ	106	
81	A0	225	
82	A1	323	
83	A2	118	
84	A3	199	
85	A4	474	

2 Entry composition [i](#)

There are 87 unique types of molecules in this entry. The entry contains 291640 atoms, of which 133281 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 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
1	A	1472	47126	14025	15865	5642	10122	1472	0	0

- Molecule 2 is a RNA chain called mt-tRNAVal.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
2	B	56	1794	534	603	214	387	56	0	0

- Molecule 3 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	D	236	3738	1145	1896	373	315	9	0	0

- Molecule 4 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	E	300	4743	1523	2378	410	422	10	0	0

- Molecule 5 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	F	250	4058	1294	2045	365	348	6	0	0

- Molecule 6 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
6	H	95	1616	498	832	152	134	0	0

- Molecule 7 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
7	I	158	2652	828	1369	235	210	10	0	0

- Molecule 8 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
8	J	140	2202	680	1141	192	187	2	0	0

- Molecule 9 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
9	K	177	2899	934	1448	259	251	7	0	0

- Molecule 10 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
10	L	115	1830	559	941	171	154	5	0	0

- Molecule 11 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
11	M	287	4683	1472	2378	425	402	6	0	0

- Molecule 12 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
12	N	205	3335	1056	1681	308	280	10	0	0

- Molecule 13 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
13	O	152	2528	784	1283	239	215	7	0	0

- Molecule 14 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
14	P	133	Total	C	H	N	O	S	0	0
			2161	677	1081	209	189	5		

- Molecule 15 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
15	Q	219	Total	C	H	N	O	S	0	0
			3681	1168	1859	322	323	9		

- Molecule 16 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
16	R	140	Total	C	H	N	O	S	0	0
			2367	732	1214	231	186	4		

- Molecule 17 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
17	S	156	Total	C	H	N	O	S	0	0
			2573	806	1322	222	219	4		

- Molecule 18 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
18	T	166	Total	C	H	N	O	S	0	0
			2778	875	1410	254	232	7		

- Molecule 19 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
19	U	111	Total	C	H	N	O	S	0	0
			1857	591	935	176	153	2		

- Molecule 20 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
20	V	189	Total	C	H	N	O	S	0	0
			3109	987	1558	278	278	8		

- Molecule 21 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
21	W	111	1769	558	898	164	146	3	0	0

- Molecule 22 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
22	X	243	4062	1317	2027	351	362	5	0	0

- Molecule 23 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
23	Y	176	3078	970	1561	291	252	4	0	0

- Molecule 24 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
24	Z	120	2008	626	1030	183	166	3	0	0

- Molecule 25 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
25	0	108	1784	545	904	172	157	6	0	0

- Molecule 26 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
26	1	52	908	278	475	83	70	2	0	0

- Molecule 27 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
27	2	46	782	233	406	83	59	1	0	0

- Molecule 28 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
28	3	95	1714	539	883	162	127	3	0	0

- Molecule 29 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
29	4	36	667	203	345	70	46	3	0	0

- Molecule 30 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
30	5	376	6123	1987	3059	529	538	10	0	0

- Molecule 31 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
31	6	325	5086	1692	2450	465	470	9	0	0

- Molecule 32 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
32	7	266	4331	1383	2173	371	388	16	0	0

- Molecule 33 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
33	8	99	1680	535	844	144	155	2	0	0

- Molecule 34 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
34	9	109	1751	565	878	152	154	2	0	0

- Molecule 35 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
35	a	82	1344	434	658	124	123	5	0	0

- Molecule 36 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
36	b	148	2358	733	1180	229	213	3	0	0

- Molecule 37 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
37	c	275	4437	1415	2220	383	410	9	0	0

- Molecule 38 is a protein called cDNA FLJ61100, highly similar to 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
38	d	162	2690	870	1343	234	235	8	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
39	e	217	3529	1124	1767	310	323	5	0	0

- Molecule 40 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
40	f	131	2083	663	1044	169	203	4	0	0

- Molecule 41 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
41	g	129	2123	690	1056	185	190	2	0	0

- Molecule 42 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
42	h	100	1633	524	806	146	155	2	0	0

- Molecule 43 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
43	i	97	1684	532	857	165	126	4	0	0

- Molecule 44 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
44	j	85	1357	423	673	133	126	2	0	0

- Molecule 45 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
45	k	84	1311	407	656	122	121	5	0	0

- Molecule 46 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
46	l	23	448	137	227	52	32	0	0

- Molecule 47 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
47	m	45	759	232	387	76	62	2	0	0

- Molecule 48 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
48	o	94	1601	501	804	165	128	3	0	0

- Molecule 49 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
49	p	127	2141	661	1083	201	192	4	0	0

- Molecule 50 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
50	q	128	2125	671	1049	208	192	5	0	0

- Molecule 51 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
51	r	146	2424	764	1221	232	199	8	0	0

- Molecule 52 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
52	s	370	6058	1946	3022	542	534	14	0	0

- Molecule 53 is a protein called Unknown protein/protein extension.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
53	t	28	170	84	30	28	28	0	0

- Molecule 54 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
54	u	2	65	19	23	8	13	2	0	0

- Molecule 55 is a RNA chain called 12S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
55	AA	923	29558	8790	9952	3535	6358	923	0	0

- Molecule 56 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
56	AB	217	3534	1131	1766	321	306	10	0	0

- Molecule 57 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
57	AC	132	2170	699	1088	195	184	4	0	0

- Molecule 58 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
58	AD	322	5153	1611	2596	476	457	13	0	0

- Molecule 59 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
59	AE	122	1973	614	1001	177	177	4	0	0

- Molecule 60 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
60	AF	201	3384	1069	1716	305	283	11	0	0

- Molecule 61 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
61	AG	305	5019	1599	2503	448	455	14	0	0

- Molecule 62 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
62	AH	122	2023	643	1024	168	185	3	0	0

- Molecule 63 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
63	AI	136	2063	637	1052	192	178	4	0	0

- Molecule 64 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
64	AJ	108	1725	521	887	169	142	6	0	0

- Molecule 65 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
65	AK	101	1746	537	885	179	140	5	0	0

- Molecule 66 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
66	AL	164	2854	883	1472	257	235	7	0	0

- Molecule 67 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
67	AM	116	1871	582	951	182	150	6	0	0

- Molecule 68 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
68	AN	107	1754	549	908	153	141	3	0	0

- Molecule 69 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
69	AO	185	3016	970	1488	285	267	6	0	0

- Molecule 70 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
70	AP	96	1578	498	804	133	135	8	0	0

- Molecule 71 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
71	AQ	86	1476	455	741	147	124	9	0	0

- Molecule 72 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
72	AR	242	4039	1285	2031	343	372	8	0	0

- Molecule 73 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
73	AS	126	2079	673	1037	183	185	1	0	0

- Molecule 74 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
74	AT	162	2674	850	1344	231	238	11	0	0

- Molecule 75 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
75	AU	173	2932	900	1471	294	263	4	0	0

- Molecule 76 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
76	AV	328	5392	1737	2690	452	502	11	0	0

- Molecule 77 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
77	AW	97	1551	486	785	137	139	4	0	0

- Molecule 78 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
78	AX	316	5051	1625	2520	440	455	11	0	0

- Molecule 79 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
79	AY	108	1773	593	859	150	169	2	0	0

- Molecule 80 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
80	AZ	87	1487	473	747	133	130	4	0	0

- Molecule 81 is a protein called 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
81	A0	201	3369	1065	1685	322	292	5	0	0

- Molecule 82 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
82	A1	256	4173	1321	2097	350	395	10	0	0

- Molecule 83 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
83	A2	116	1887	574	962	181	162	8	0	0

- Molecule 84 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
84	A3	69	1292	393	682	130	86	1	0	0

- Molecule 85 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial,mS39.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
85	A4	414	5097	1805	2259	490	529	14	0	0

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	A	97	Total	Mg	0
			97	97	
86	M	1	Total	Mg	0
			1	1	
86	g	1	Total	Mg	0
			1	1	
86	AA	28	Total	Mg	0
			28	28	

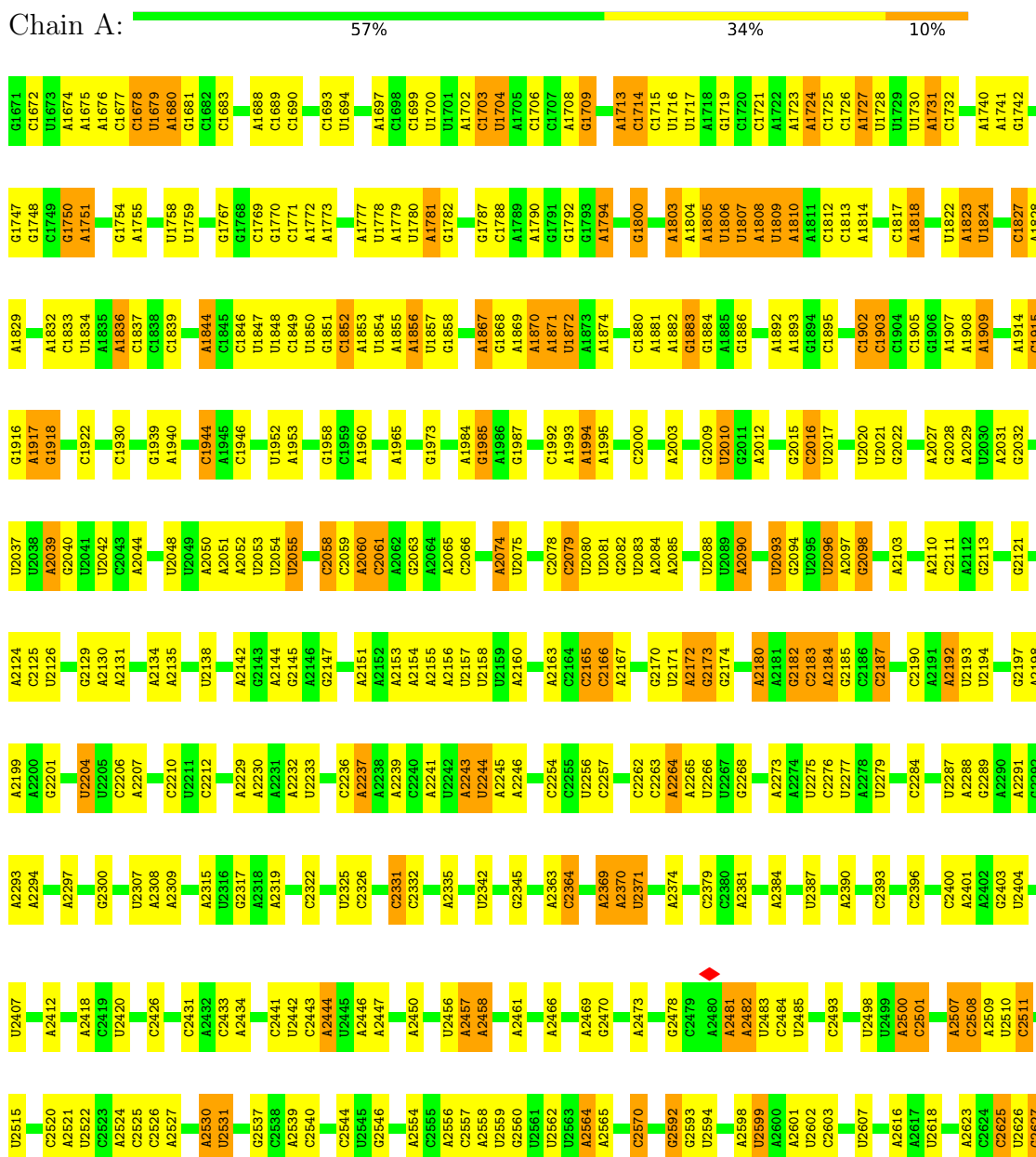
- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

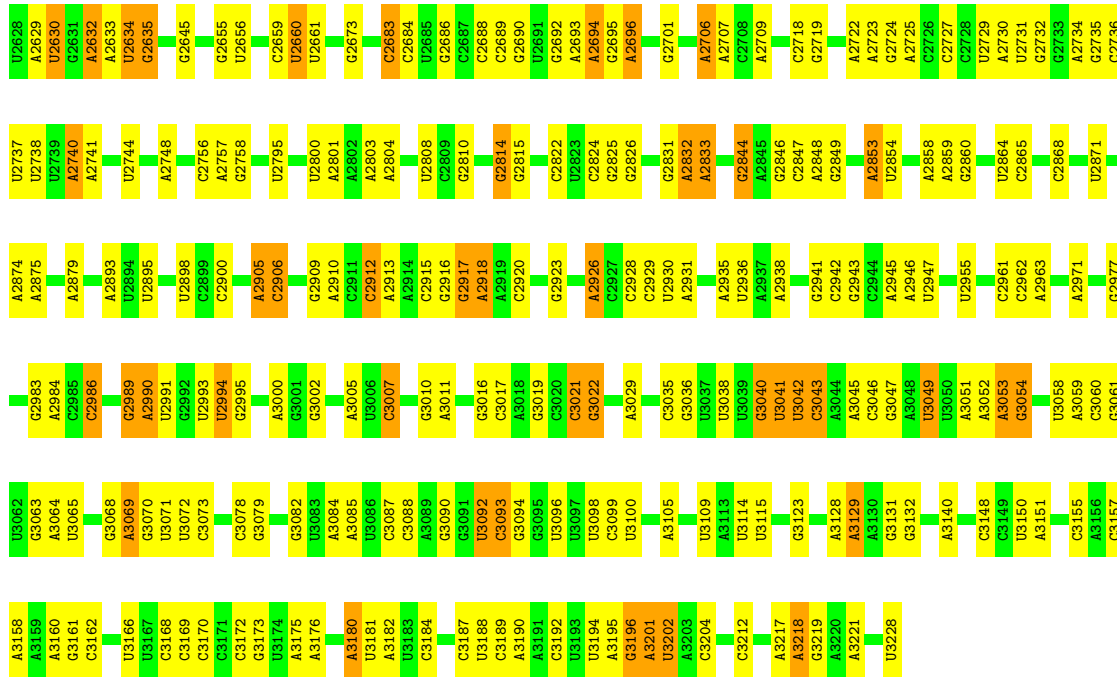
Mol	Chain	Residues	Atoms		AltConf
87	0	1	Total	Zn	0
			1	1	
87	4	1	Total	Zn	0
			1	1	
87	r	1	Total	Zn	0
			1	1	
87	AB	1	Total	Zn	0
			1	1	
87	AO	1	Total	Zn	0
			1	1	
87	AP	1	Total	Zn	0
			1	1	
87	AT	1	Total	Zn	0
			1	1	

3 Residue-property plots

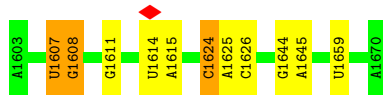
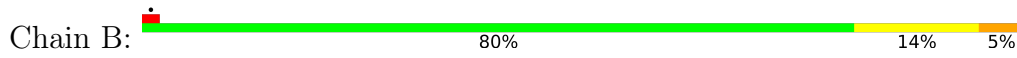
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S rRNA

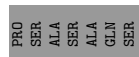
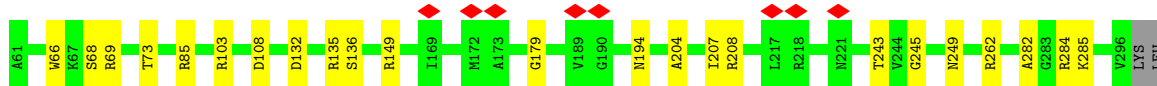
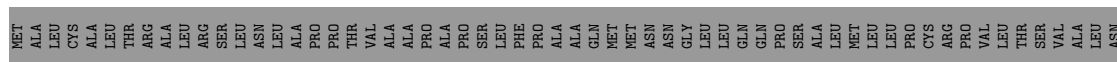




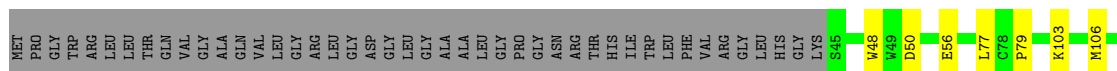
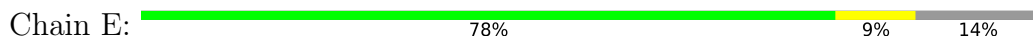
• Molecule 2: mt-tRNAVal



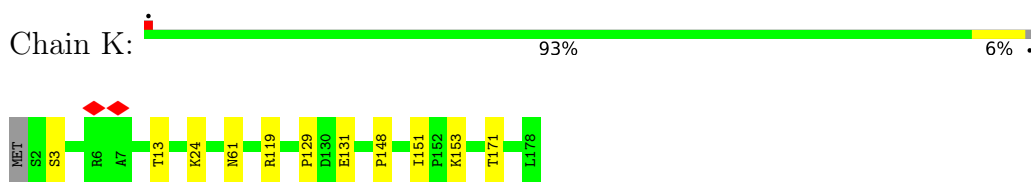
• Molecule 3: 39S ribosomal protein L2, mitochondrial



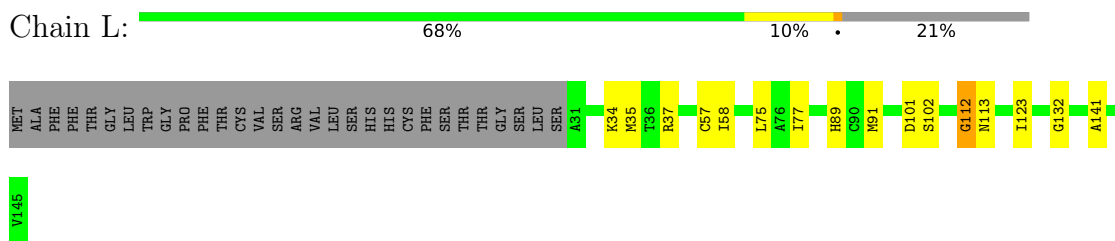
• Molecule 4: 39S ribosomal protein L3, mitochondrial



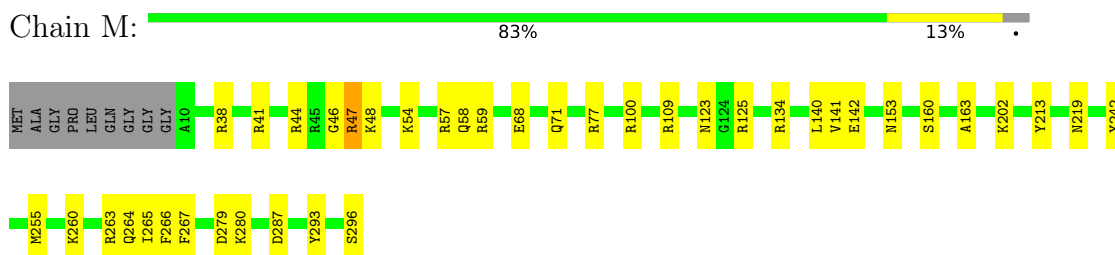
- Molecule 9: 39S ribosomal protein L13, mitochondrial



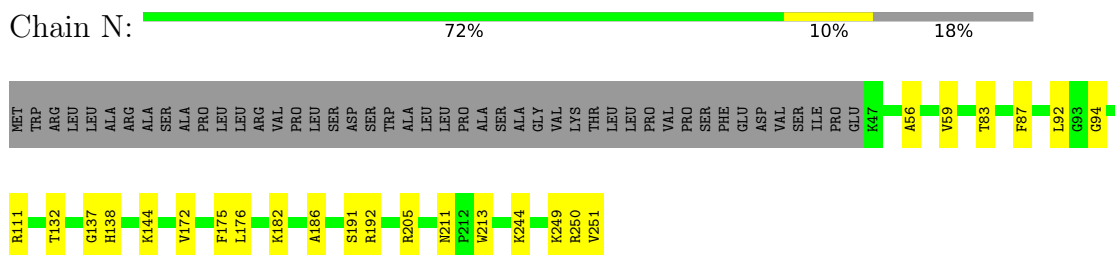
- Molecule 10: 39S ribosomal protein L14, mitochondrial



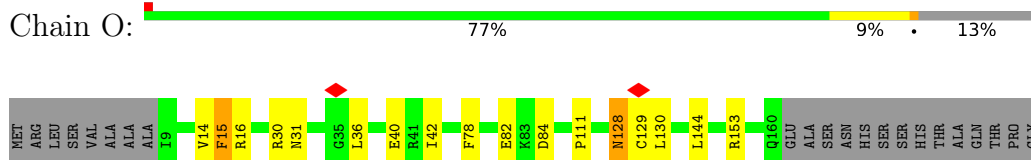
- Molecule 11: 39S ribosomal protein L15, mitochondrial



- Molecule 12: 39S ribosomal protein L16, mitochondrial

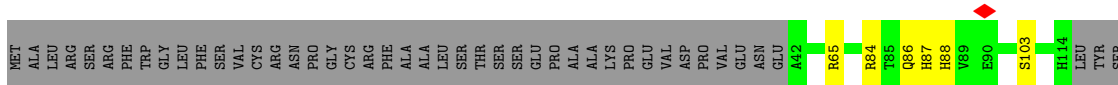


- Molecule 13: 39S ribosomal protein L17, mitochondrial



- Molecule 14: 39S ribosomal protein L18, mitochondrial

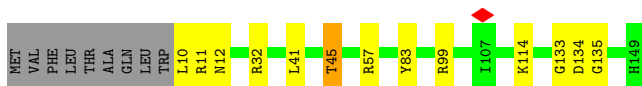
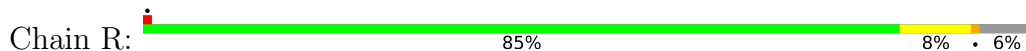




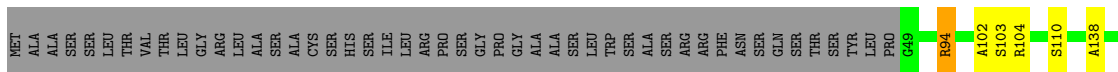
- Molecule 15: 39S ribosomal protein L19, mitochondrial



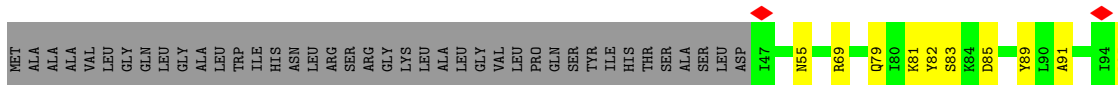
- Molecule 16: 39S ribosomal protein L20, mitochondrial



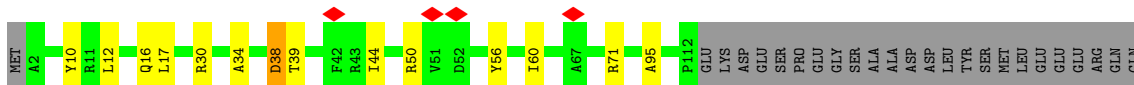
- Molecule 17: 39S ribosomal protein L21, mitochondrial

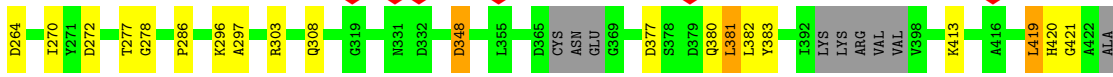
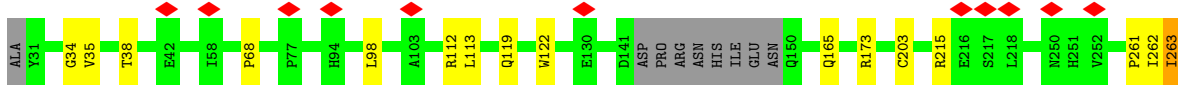


- Molecule 18: 39S ribosomal protein L22, mitochondrial

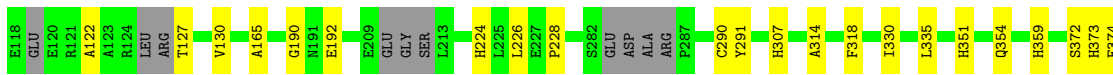
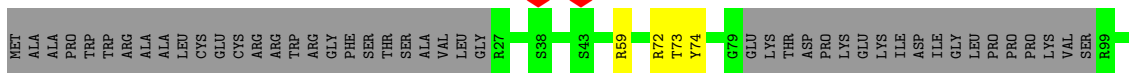
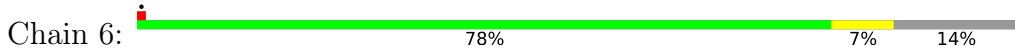


- Molecule 19: 39S ribosomal protein L23, mitochondrial

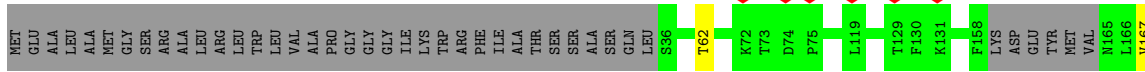




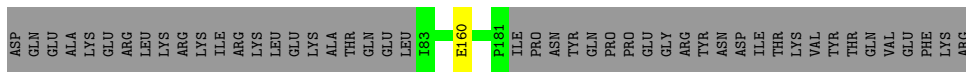
• Molecule 31: 39S ribosomal protein L38, mitochondrial



• Molecule 32: 39S ribosomal protein L39, mitochondrial

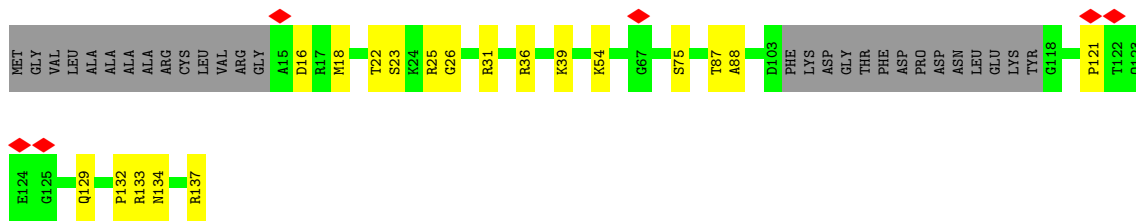


• Molecule 33: 39S ribosomal protein L40, mitochondrial

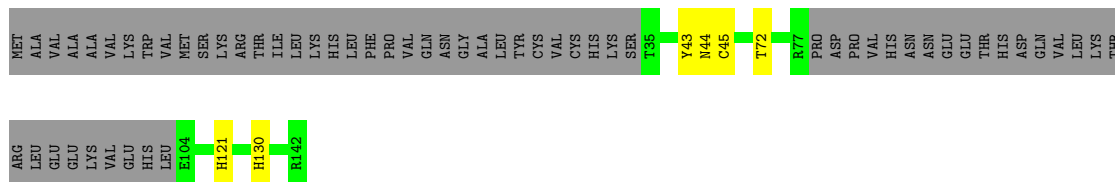


• Molecule 34: 39S ribosomal protein L41, mitochondrial

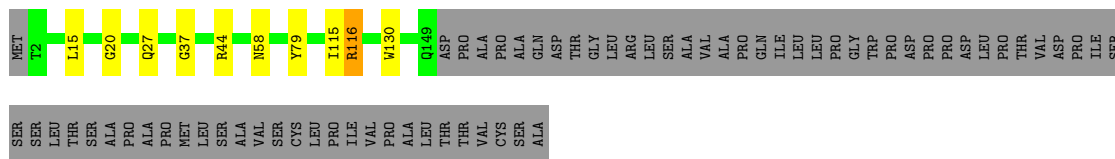




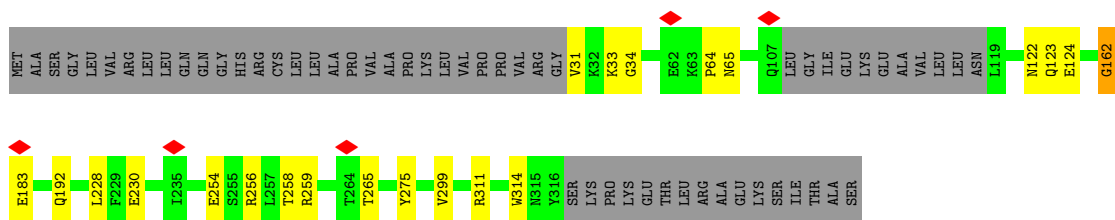
• Molecule 35: 39S ribosomal protein L42, mitochondrial



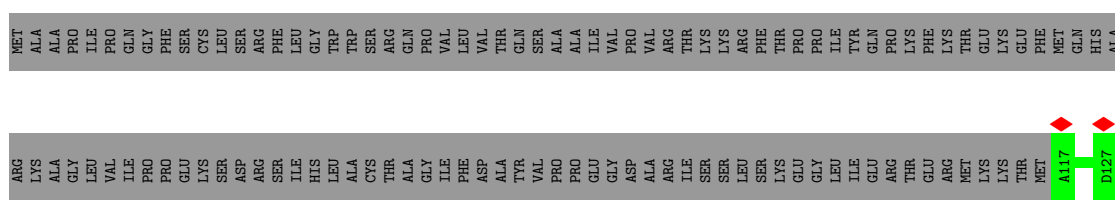
• Molecule 36: 39S ribosomal protein L43, mitochondrial

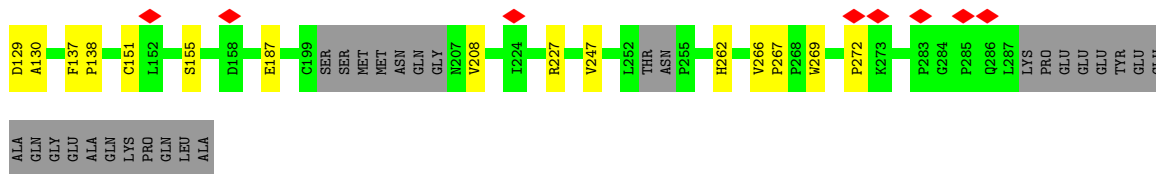


• Molecule 37: 39S ribosomal protein L44, mitochondrial



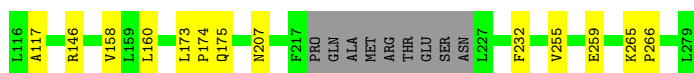
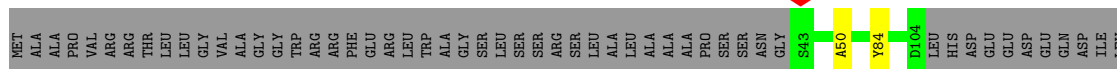
• Molecule 38: cDNA FLJ61100, highly similar to 39S ribosomal protein L45, mitochondrial





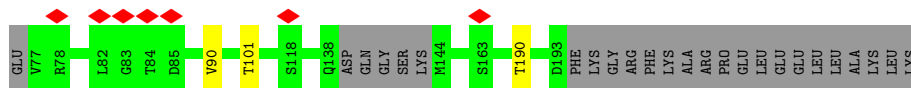
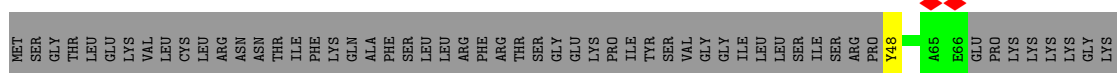
- Molecule 39: 39S ribosomal protein L46, mitochondrial

Chain e: 72% 5% 22%



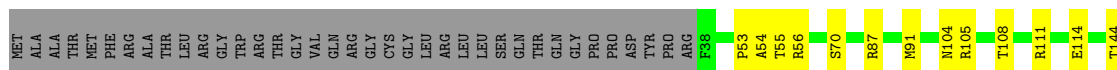
- Molecule 40: 39S ribosomal protein L48, mitochondrial

Chain f: 60% 38%



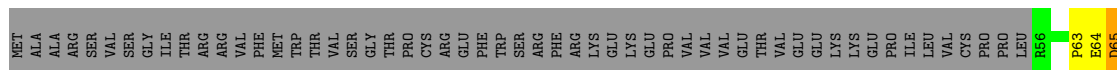
- Molecule 41: 39S ribosomal protein L49, mitochondrial

Chain g: 68% 10% 22%

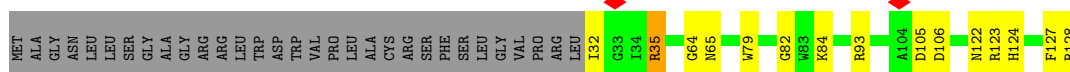


- Molecule 42: 39S ribosomal protein L50, mitochondrial

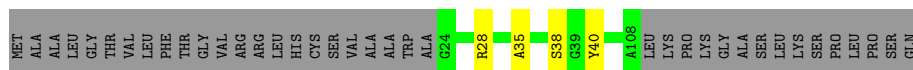
Chain h: 53% 9% 37%



- Molecule 43: 39S ribosomal protein L51, mitochondrial



- Molecule 44: 39S ribosomal protein L52, mitochondrial

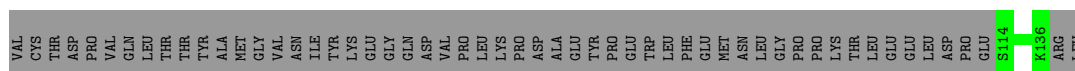


- Molecule 45: 39S ribosomal protein L53, mitochondrial

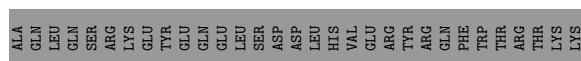
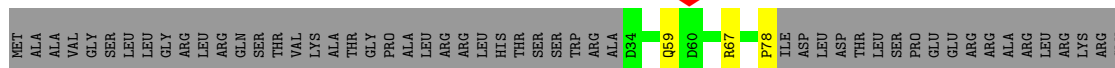


ARG

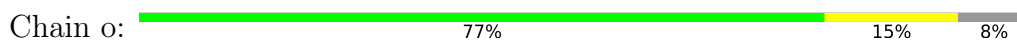
- Molecule 46: 39S ribosomal protein L54, mitochondrial



- Molecule 47: 39S ribosomal protein L55, mitochondrial



- Molecule 48: Ribosomal protein 63, mitochondrial

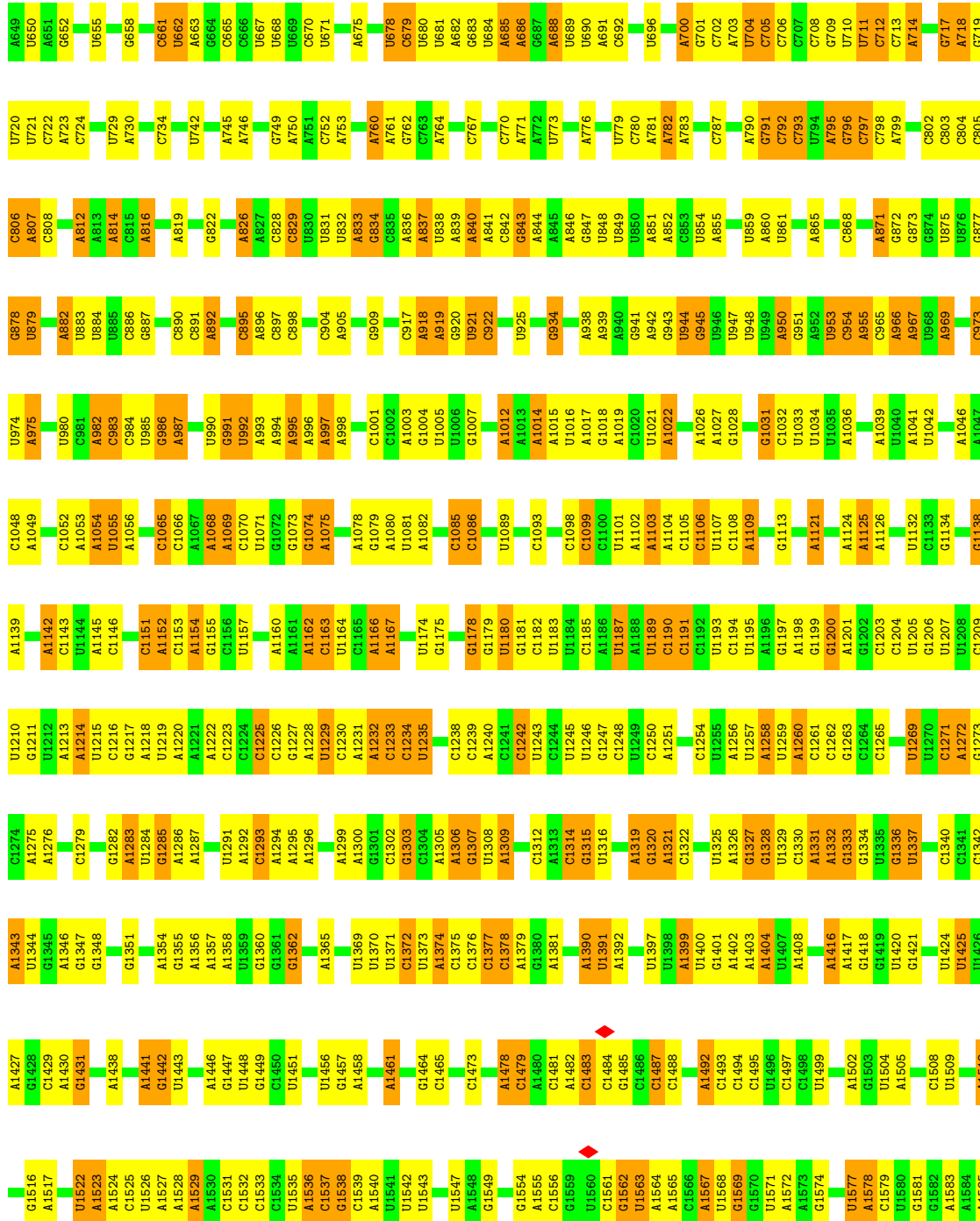


- Molecule 49: Peptidyl-tRNA hydrolase ICT1, mitochondrial



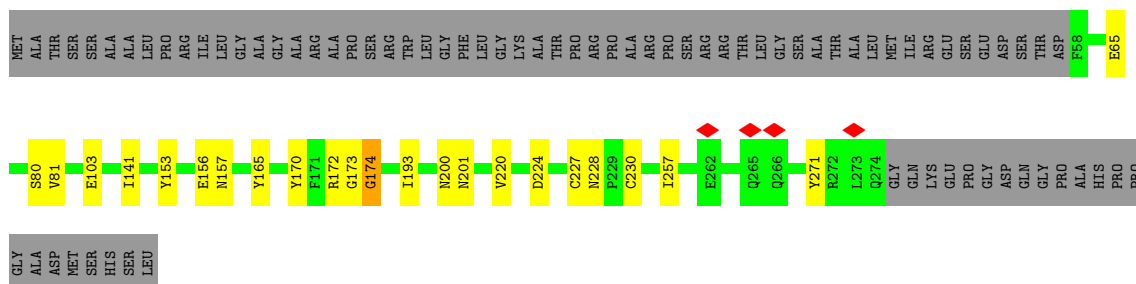
C1
A2

● Molecule 55: 12S rRNA

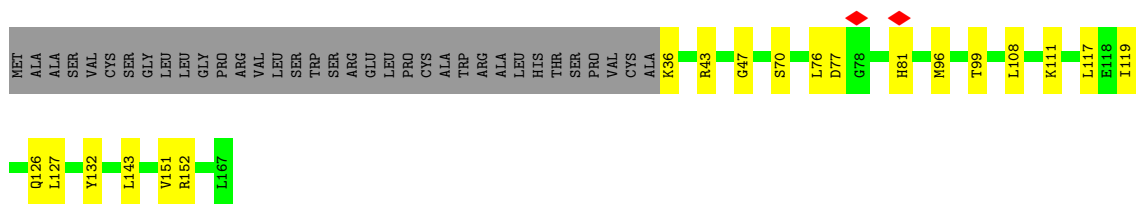




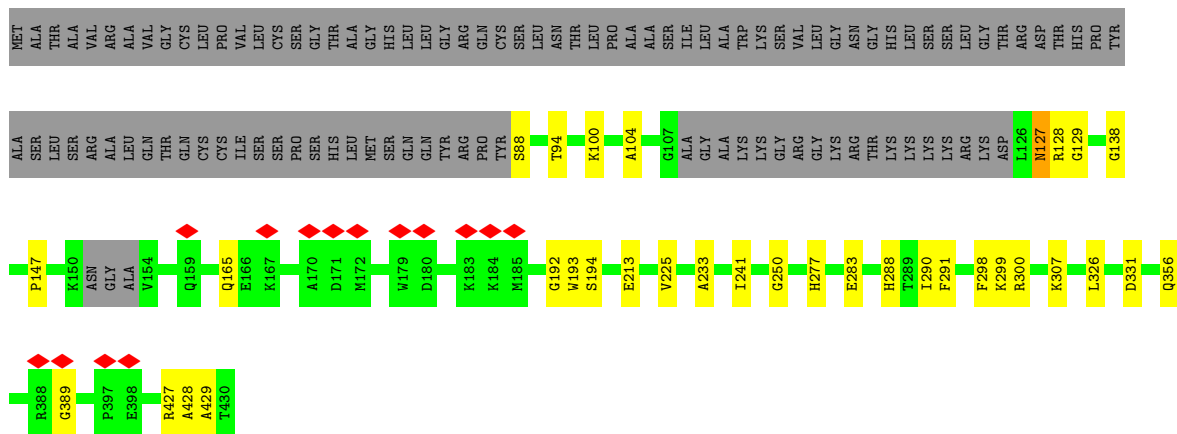
• Molecule 56: 28S ribosomal protein S2, mitochondrial



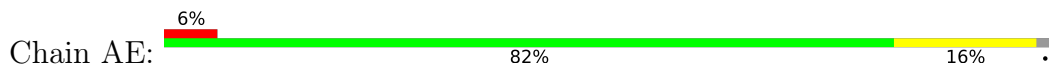
• Molecule 57: 28S ribosomal protein S24, mitochondrial



• Molecule 58: 28S ribosomal protein S5, mitochondrial

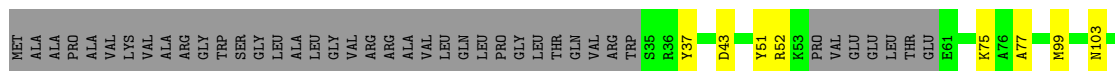
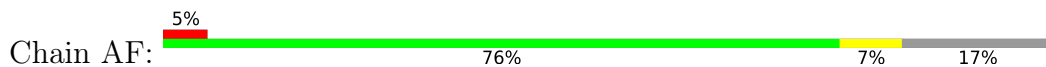


• Molecule 59: 28S ribosomal protein S6, mitochondrial

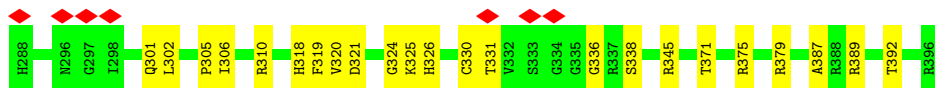
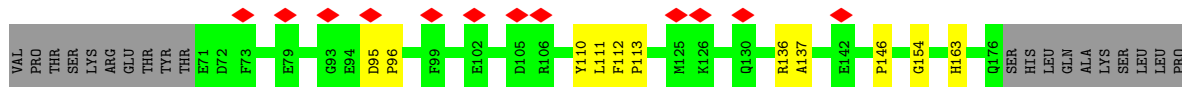
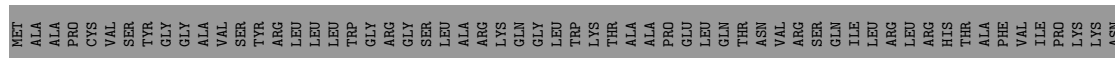




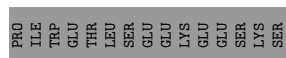
- Molecule 60: 28S ribosomal protein S7, mitochondrial



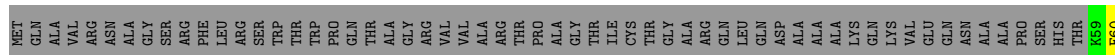
- Molecule 61: 28S ribosomal protein S9, mitochondrial

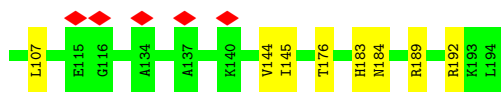


- Molecule 62: 28S ribosomal protein S10, mitochondrial

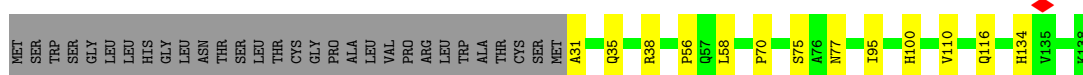


- Molecule 63: 28S ribosomal protein S11, mitochondrial





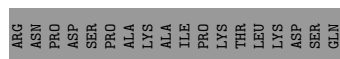
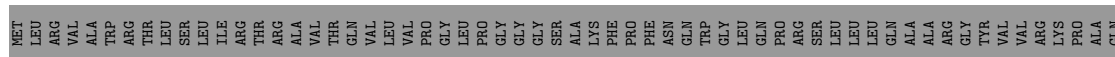
- Molecule 64: 28S ribosomal protein S12, mitochondrial



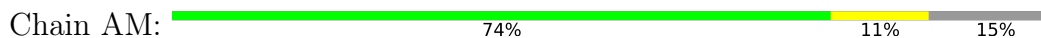
- Molecule 65: 28S ribosomal protein S14, mitochondrial



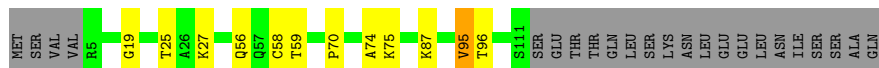
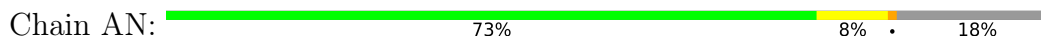
- Molecule 66: 28S ribosomal protein S15, mitochondrial



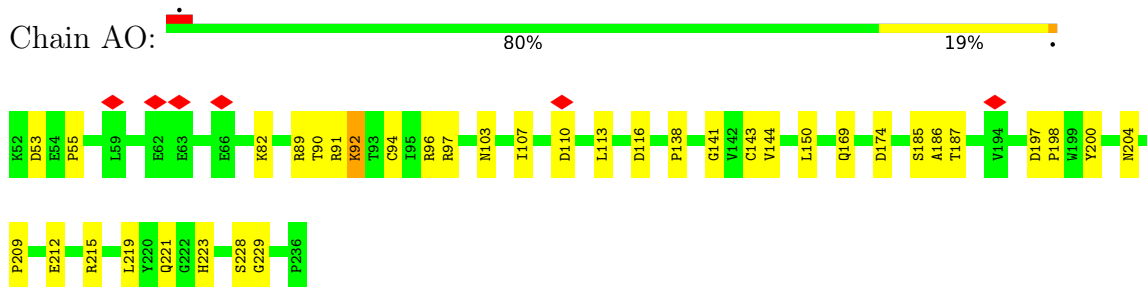
- Molecule 67: 28S ribosomal protein S16, mitochondrial



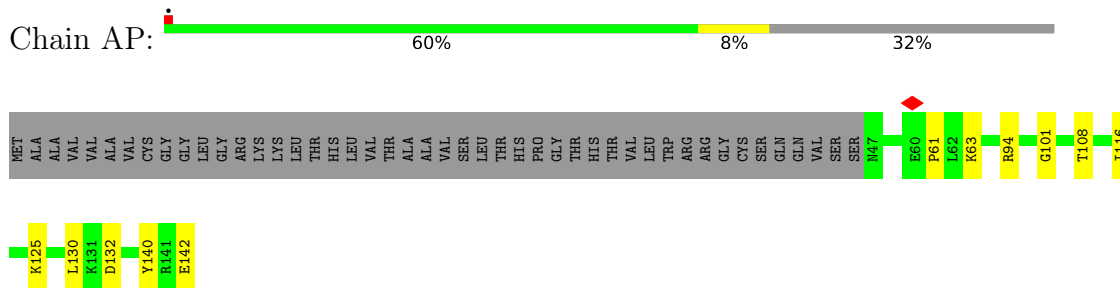
- Molecule 68: 28S ribosomal protein S17, mitochondrial



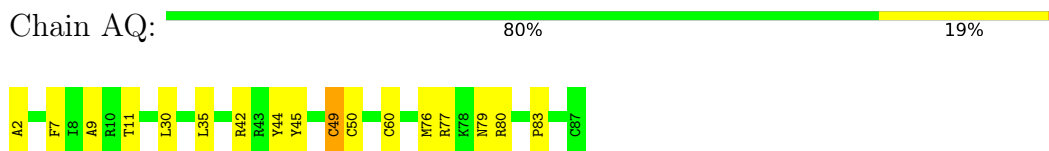
- Molecule 69: 28S ribosomal protein S18b, mitochondrial



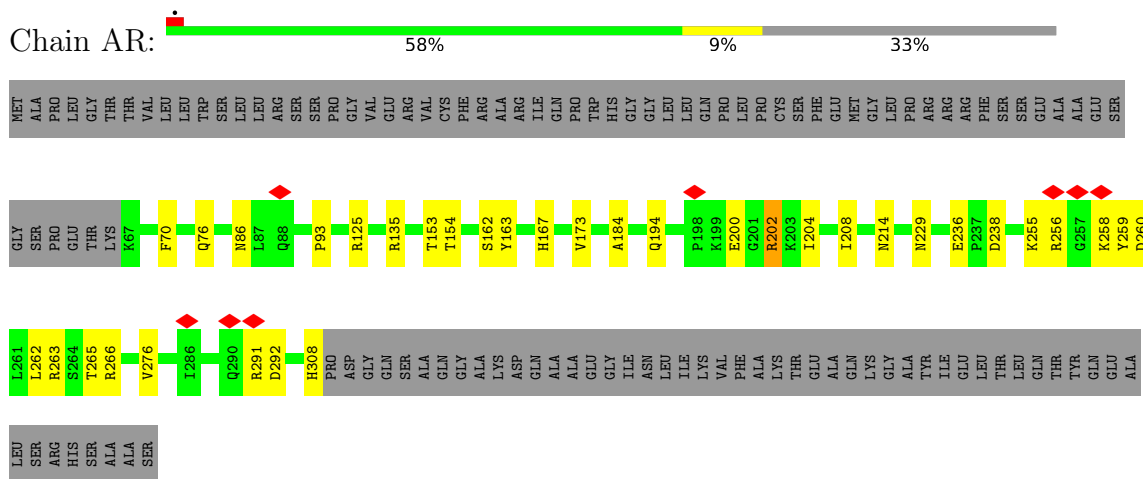
- Molecule 70: 28S ribosomal protein S18c, mitochondrial



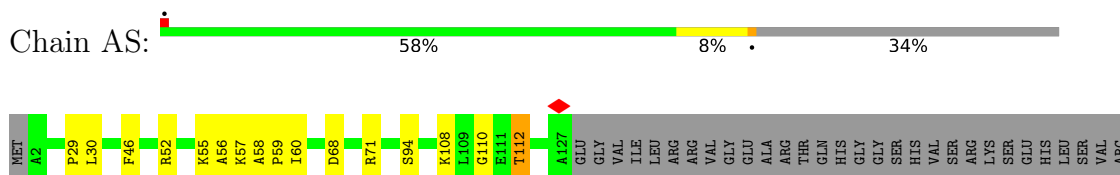
- Molecule 71: 28S ribosomal protein S21, mitochondrial



- Molecule 72: 28S ribosomal protein S22, mitochondrial

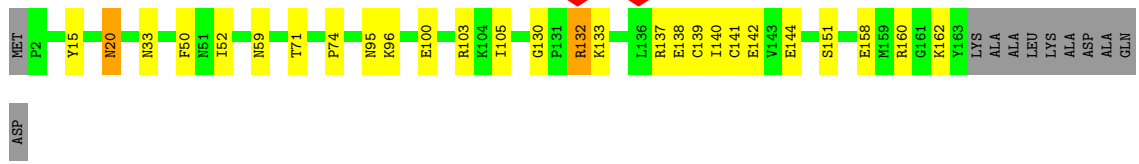
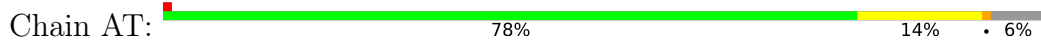


- Molecule 73: 28S ribosomal protein S23, mitochondrial

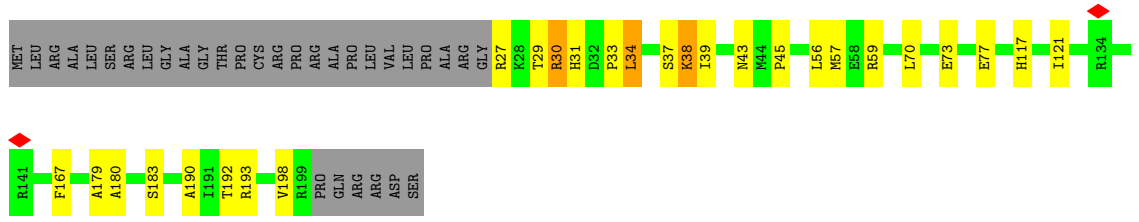


PRO GLN THR ALA LEU LEU LEU LEU ASN GLU THR GLN LYS VAL PRO GLN ASP HIS LEU ALA PRO ALA ASP GLN SER LYS GLY LEU LEU LEU PRO PRO

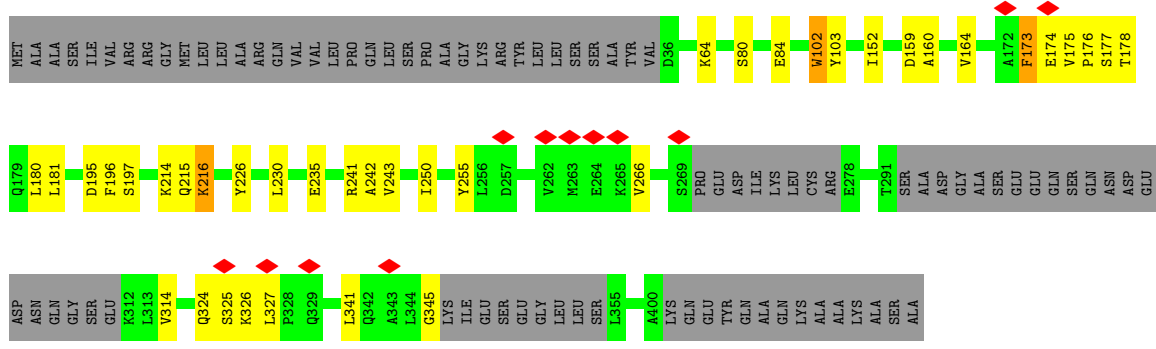
- Molecule 74: 28S ribosomal protein S25, mitochondrial



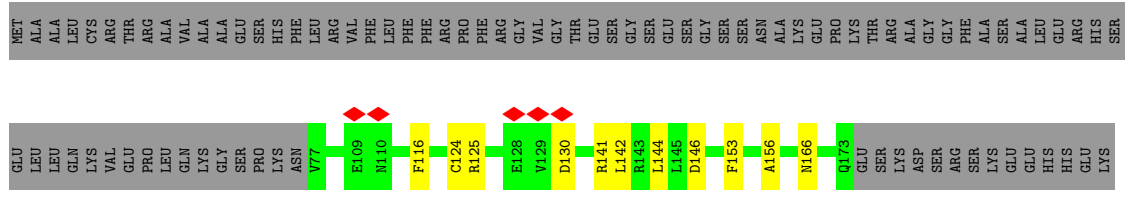
- Molecule 75: 28S ribosomal protein S26, mitochondrial



- Molecule 76: 28S ribosomal protein S27, mitochondrial



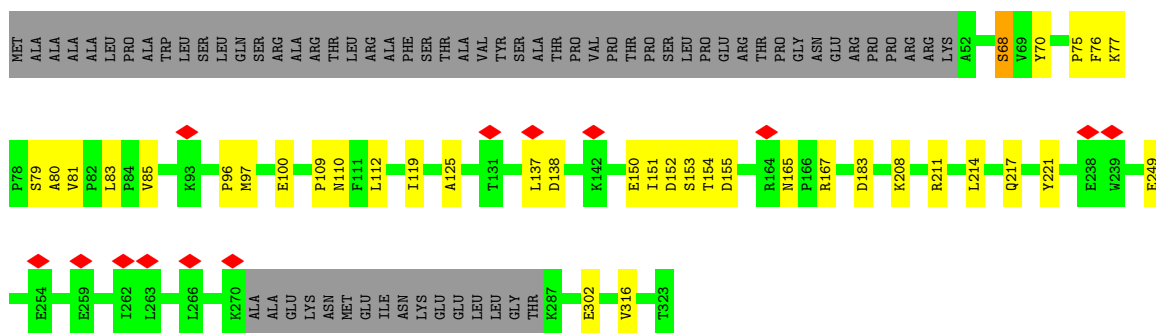
- Molecule 77: 28S ribosomal protein S28, mitochondrial



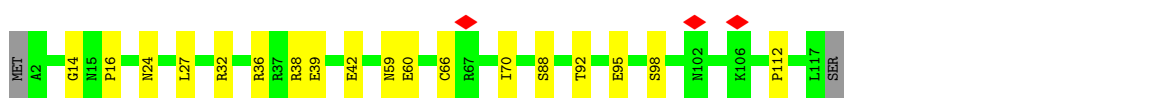
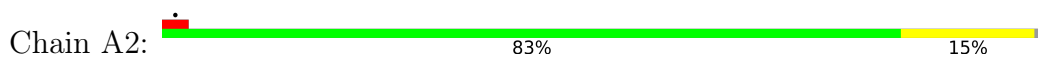
- Molecule 78: 28S ribosomal protein S29, mitochondrial



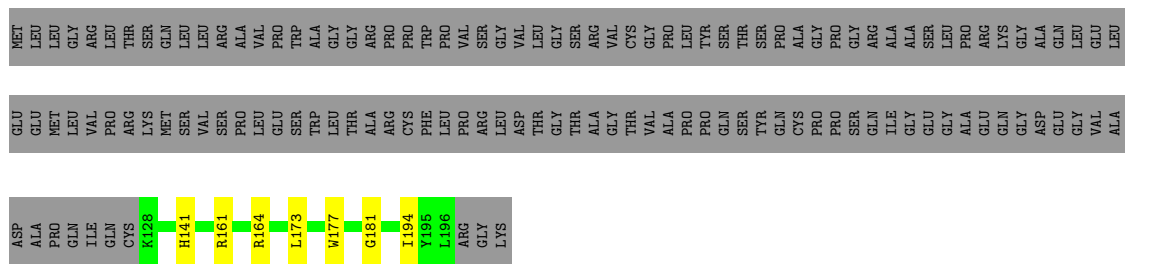
• Molecule 82: 28S ribosomal protein S35, mitochondrial



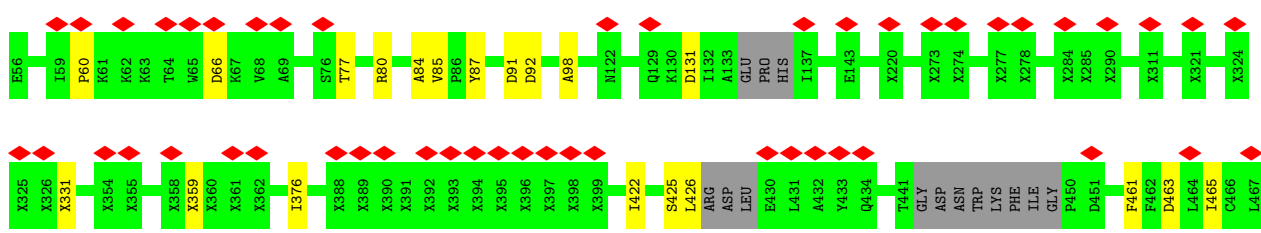
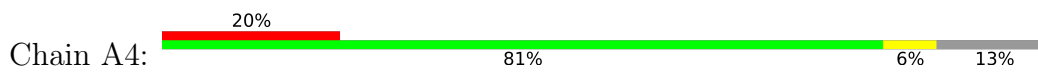
• Molecule 83: Coiled-coil-helix-coiled-coil-helix domain-containing protein 1

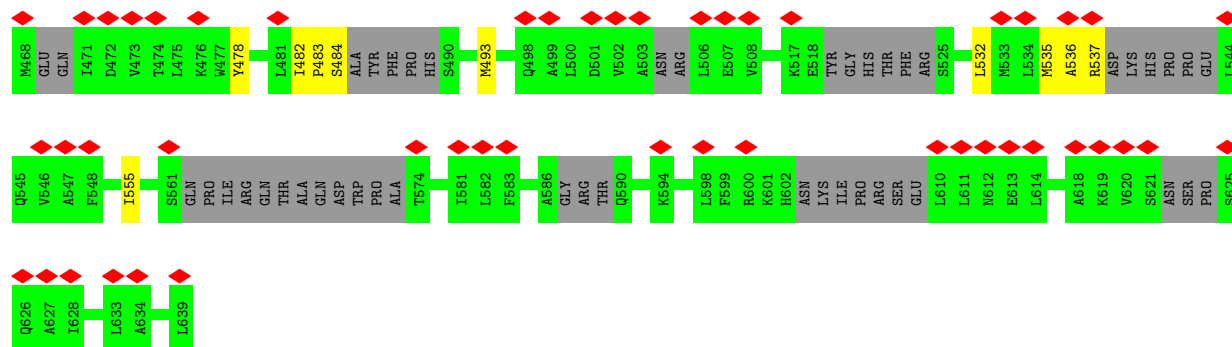


• Molecule 84: Aurora kinase A-interacting protein



• Molecule 85: Pentatricopeptide repeat domain-containing protein 3, mitochondrial, mS39





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	26195	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.462	Depositor
Minimum map value	-0.346	Depositor
Average map value	0.022	Depositor
Map value standard deviation	0.095	Depositor
Recommended contour level	0.165	Depositor
Map size (\AA)	414.2, 414.2, 414.2	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.09, 1.09, 1.09	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	A	0.07	0/34967	0.19	0/54407
2	B	0.06	0/1328	0.17	0/2056
3	D	0.09	0/1879	0.24	0/2527
4	E	0.07	0/2433	0.21	0/3299
5	F	0.09	0/2071	0.23	0/2817
6	H	0.09	0/798	0.22	0/1073
7	I	0.08	0/1308	0.21	0/1761
8	J	0.09	0/1077	0.22	0/1452
9	K	0.08	0/1495	0.21	0/2029
10	L	0.08	0/904	0.23	0/1218
11	M	0.09	0/2359	0.24	0/3185
12	N	0.08	0/1697	0.21	0/2281
13	O	0.10	0/1269	0.25	0/1708
14	P	0.09	0/1103	0.24	0/1491
15	Q	0.08	0/1863	0.20	0/2509
16	R	0.09	0/1174	0.26	0/1572
17	S	0.07	0/1276	0.21	0/1729
18	T	0.08	0/1402	0.22	0/1886
19	U	0.09	0/946	0.24	0/1283
20	V	0.08	0/1590	0.22	0/2151
21	W	0.08	0/893	0.20	0/1204
22	X	0.08	0/2090	0.22	0/2825
23	Y	0.09	0/1552	0.22	0/2079
24	Z	0.07	0/1003	0.21	0/1354
25	0	0.11	0/895	0.23	0/1201
26	1	0.08	0/438	0.24	0/583
27	2	0.09	0/382	0.24	0/507
28	3	0.08	0/852	0.22	0/1136
29	4	0.09	0/329	0.21	0/435
30	5	0.08	0/3154	0.23	0/4295
31	6	0.08	0/2722	0.23	0/3709
32	7	0.08	0/2207	0.20	0/2978

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	8	0.08	0/855	0.20	0/1152
34	9	0.08	0/896	0.22	0/1205
35	a	0.07	0/709	0.22	0/963
36	b	0.09	0/1202	0.25	0/1626
37	c	0.08	0/2264	0.21	0/3059
38	d	0.09	0/1385	0.23	0/1877
39	e	0.07	0/1797	0.19	0/2422
40	f	0.06	0/1055	0.17	0/1427
41	g	0.09	0/1102	0.23	0/1503
42	h	0.10	0/847	0.31	0/1150
43	i	0.09	0/849	0.23	0/1135
44	j	0.08	0/698	0.25	0/940
45	k	0.08	0/665	0.22	0/897
46	l	0.10	0/226	0.29	0/299
47	m	0.11	0/379	0.24	0/510
48	o	0.10	0/818	0.24	0/1097
49	p	0.08	0/1071	0.20	0/1433
50	q	0.09	0/1107	0.24	0/1498
51	r	0.09	0/1238	0.24	0/1676
52	s	0.08	0/3114	0.23	0/4225
54	u	0.03	0/46	0.11	0/69
55	AA	0.08	0/21926	0.21	0/34121
56	AB	0.09	0/1811	0.23	0/2451
57	AC	0.08	0/1112	0.22	0/1505
58	AD	0.08	0/2607	0.21	0/3498
59	AE	0.10	0/989	0.28	0/1335
60	AF	0.08	0/1708	0.22	0/2291
61	AG	0.09	0/2570	0.23	0/3443
62	AH	0.08	0/1019	0.21	0/1379
63	AI	0.09	0/1031	0.24	0/1390
64	AJ	0.09	0/854	0.24	0/1148
65	AK	0.11	0/879	0.28	0/1182
66	AL	0.09	0/1406	0.23	0/1878
67	AM	0.09	0/941	0.26	0/1265
68	AN	0.08	0/864	0.21	0/1169
69	AO	0.11	0/1580	0.27	0/2150
70	AP	0.07	0/791	0.19	0/1062
71	AQ	0.10	0/747	0.26	0/995
72	AR	0.09	0/2050	0.23	0/2770
73	AS	0.09	0/1069	0.23	0/1441
74	AT	0.09	0/1361	0.23	0/1829
75	AU	0.11	0/1482	0.28	0/1987
76	AV	0.08	0/2758	0.20	0/3724

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
77	AW	0.09	0/778	0.21	0/1048
78	AX	0.07	0/2596	0.21	0/3519
79	AY	0.07	0/943	0.20	0/1274
80	AZ	0.09	0/757	0.24	0/1011
81	A0	0.10	0/1727	0.27	0/2338
82	A1	0.09	0/2121	0.23	0/2873
83	A2	0.11	0/939	0.27	0/1256
84	A3	0.10	0/621	0.25	0/820
85	A4	0.07	0/2137	0.20	0/2872
All	All	0.08	0/165953	0.22	0/235927

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	A	31261	15865	15878	363	0
2	B	1191	603	607	5	0
3	D	1842	1896	1896	15	0
4	E	2365	2378	2378	17	0
5	F	2013	2045	2044	27	0
6	H	784	832	832	6	0
7	I	1283	1369	1370	10	0
8	J	1061	1141	1141	3	0
9	K	1451	1448	1448	5	0
10	L	889	941	941	9	0
11	M	2305	2378	2378	26	0
12	N	1654	1681	1681	12	0
13	O	1245	1283	1283	10	0
14	P	1080	1081	1081	7	0
15	Q	1822	1859	1859	4	0
16	R	1153	1214	1214	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	S	1251	1322	1322	5	0
18	T	1368	1410	1410	10	0
19	U	922	935	935	8	0
20	V	1551	1558	1558	6	0
21	W	871	898	898	5	0
22	X	2035	2027	2054	8	0
23	Y	1517	1561	1561	14	0
24	Z	978	1030	1030	7	0
25	0	880	904	904	11	0
26	1	433	475	475	4	0
27	2	376	406	406	6	0
28	3	831	883	883	6	0
29	4	322	345	344	1	0
30	5	3064	3059	3059	15	0
31	6	2636	2450	2450	10	0
32	7	2158	2173	2173	6	0
33	8	836	844	844	2	0
34	9	873	878	878	13	0
35	a	686	658	658	5	0
36	b	1178	1180	1180	9	0
37	c	2217	2220	2220	11	0
38	d	1347	1343	1343	7	0
39	e	1762	1767	1767	8	0
40	f	1039	1044	1044	3	0
41	g	1067	1056	1056	11	0
42	h	827	806	806	10	0
43	i	827	857	857	8	0
44	j	684	673	673	2	0
45	k	655	656	656	7	0
46	l	221	227	227	0	0
47	m	372	387	387	2	0
48	o	797	804	804	9	0
49	p	1058	1083	1083	0	0
50	q	1076	1049	1049	3	0
51	r	1203	1221	1221	7	0
52	s	3036	3022	3022	25	0
53	t	140	30	30	0	0
54	u	42	23	23	1	0
55	AA	19606	9952	9960	272	0
56	AB	1768	1766	1765	13	0
57	AC	1082	1088	1088	15	0
58	AD	2557	2596	2596	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	AE	972	1001	1001	10	0
60	AF	1668	1716	1716	13	0
61	AG	2516	2503	2503	28	0
62	AH	999	1024	1024	15	0
63	AI	1011	1052	1052	6	0
64	AJ	838	887	887	9	0
65	AK	861	885	885	22	0
66	AL	1382	1472	1472	17	0
67	AM	920	951	951	11	0
68	AN	846	908	908	4	0
69	AO	1528	1488	1488	18	0
70	AP	774	804	804	5	0
71	AQ	735	741	746	12	0
72	AR	2008	2031	2031	13	0
73	AS	1042	1037	1037	5	0
74	AT	1330	1344	1344	12	0
75	AU	1461	1471	1471	23	0
76	AV	2702	2690	2690	17	0
77	AW	766	785	785	2	0
78	AX	2531	2520	2520	23	0
79	AY	914	859	859	6	0
80	AZ	740	747	747	8	0
81	A0	1684	1685	1685	21	0
82	A1	2076	2097	2097	24	0
83	A2	925	962	962	9	0
84	A3	610	682	682	7	0
85	A4	2838	2259	2274	18	0
86	A	97	0	0	0	0
86	AA	28	0	0	0	0
86	M	1	0	0	0	0
86	g	1	0	0	0	0
87	0	1	0	0	0	0
87	4	1	0	0	0	0
87	AB	1	0	0	0	0
87	AO	1	0	0	0	0
87	AP	1	0	0	0	0
87	AT	1	0	0	0	0
87	r	1	0	0	0	0
All	All	158359	133281	133351	1175	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 4.

The worst 5 of 1175 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)
55:AA:1162:A:O2'	55:AA:1163:C:OP1	1.84	0.95
55:AA:1465:C:OP1	83:A2:38:ARG:NH2	2.02	0.93
55:AA:953:U:O2'	55:AA:954:C:OP2	1.88	0.92
55:AA:1372:C:O2'	55:AA:1373:U:O4'	1.87	0.91
55:AA:1027:A:O3'	55:AA:1054:A:O2'	1.90	0.89

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	D	234/305 (77%)	197 (84%)	35 (15%)	2 (1%)	14	49
4	E	296/348 (85%)	253 (86%)	34 (12%)	9 (3%)	3	22
5	F	248/311 (80%)	209 (84%)	30 (12%)	9 (4%)	2	20
6	H	93/267 (35%)	85 (91%)	7 (8%)	1 (1%)	11	45
7	I	154/261 (59%)	140 (91%)	12 (8%)	2 (1%)	9	41
8	J	138/192 (72%)	119 (86%)	16 (12%)	3 (2%)	5	29
9	K	175/178 (98%)	152 (87%)	18 (10%)	5 (3%)	3	23
10	L	113/145 (78%)	93 (82%)	17 (15%)	3 (3%)	4	25
11	M	285/296 (96%)	240 (84%)	36 (13%)	9 (3%)	3	21
12	N	203/251 (81%)	181 (89%)	20 (10%)	2 (1%)	12	47
13	O	150/175 (86%)	132 (88%)	15 (10%)	3 (2%)	6	31
14	P	129/180 (72%)	114 (88%)	12 (9%)	3 (2%)	5	28
15	Q	217/219 (99%)	180 (83%)	29 (13%)	8 (4%)	2	19
16	R	138/149 (93%)	125 (91%)	12 (9%)	1 (1%)	18	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	S	154/205 (75%)	132 (86%)	19 (12%)	3 (2%)	6	32
18	T	164/206 (80%)	148 (90%)	12 (7%)	4 (2%)	4	27
19	U	109/153 (71%)	92 (84%)	15 (14%)	2 (2%)	6	33
20	V	183/216 (85%)	151 (82%)	24 (13%)	8 (4%)	2	17
21	W	109/148 (74%)	94 (86%)	12 (11%)	3 (3%)	4	24
22	X	241/243 (99%)	201 (83%)	32 (13%)	8 (3%)	3	21
23	Y	174/250 (70%)	157 (90%)	14 (8%)	3 (2%)	7	35
24	Z	118/161 (73%)	100 (85%)	14 (12%)	4 (3%)	3	20
25	0	106/188 (56%)	89 (84%)	14 (13%)	3 (3%)	4	24
26	1	50/65 (77%)	43 (86%)	4 (8%)	3 (6%)	1	13
27	2	44/92 (48%)	40 (91%)	4 (9%)	0	100	100
28	3	93/188 (50%)	86 (92%)	7 (8%)	0	100	100
29	4	34/103 (33%)	33 (97%)	1 (3%)	0	100	100
30	5	368/394 (93%)	308 (84%)	47 (13%)	13 (4%)	3	20
31	6	313/380 (82%)	258 (82%)	45 (14%)	10 (3%)	3	21
32	7	258/338 (76%)	217 (84%)	36 (14%)	5 (2%)	6	32
33	8	97/206 (47%)	88 (91%)	9 (9%)	0	100	100
34	9	105/137 (77%)	90 (86%)	12 (11%)	3 (3%)	3	23
35	a	78/142 (55%)	72 (92%)	5 (6%)	1 (1%)	9	41
36	b	146/215 (68%)	128 (88%)	16 (11%)	2 (1%)	9	39
37	c	271/332 (82%)	233 (86%)	31 (11%)	7 (3%)	4	25
38	d	156/306 (51%)	132 (85%)	20 (13%)	4 (3%)	4	25
39	e	211/279 (76%)	188 (89%)	20 (10%)	3 (1%)	9	39
40	f	125/212 (59%)	106 (85%)	17 (14%)	2 (2%)	7	36
41	g	127/166 (76%)	106 (84%)	18 (14%)	3 (2%)	4	27
42	h	96/158 (61%)	80 (83%)	11 (12%)	5 (5%)	1	15
43	i	95/128 (74%)	76 (80%)	16 (17%)	3 (3%)	3	21
44	j	83/123 (68%)	77 (93%)	5 (6%)	1 (1%)	10	42
45	k	82/112 (73%)	62 (76%)	12 (15%)	8 (10%)	0	7
46	l	21/138 (15%)	21 (100%)	0	0	100	100
47	m	43/128 (34%)	38 (88%)	5 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	o	92/102 (90%)	80 (87%)	8 (9%)	4 (4%)	2	17
49	p	119/206 (58%)	109 (92%)	10 (8%)	0	100	100
50	q	126/222 (57%)	118 (94%)	8 (6%)	0	100	100
51	r	140/196 (71%)	121 (86%)	13 (9%)	6 (4%)	2	17
52	s	366/439 (83%)	315 (86%)	44 (12%)	7 (2%)	6	32
56	AB	215/296 (73%)	186 (86%)	27 (13%)	2 (1%)	14	49
57	AC	130/167 (78%)	97 (75%)	31 (24%)	2 (2%)	8	38
58	AD	316/430 (74%)	255 (81%)	46 (15%)	15 (5%)	2	16
59	AE	120/125 (96%)	87 (72%)	25 (21%)	8 (7%)	1	12
60	AF	197/242 (81%)	168 (85%)	25 (13%)	4 (2%)	6	31
61	AG	301/396 (76%)	245 (81%)	45 (15%)	11 (4%)	2	19
62	AH	120/201 (60%)	93 (78%)	24 (20%)	3 (2%)	4	26
63	AI	134/194 (69%)	106 (79%)	24 (18%)	4 (3%)	3	22
64	AJ	106/138 (77%)	83 (78%)	20 (19%)	3 (3%)	4	24
65	AK	99/128 (77%)	86 (87%)	7 (7%)	6 (6%)	1	13
66	AL	162/257 (63%)	137 (85%)	19 (12%)	6 (4%)	2	19
67	AM	114/137 (83%)	93 (82%)	17 (15%)	4 (4%)	3	20
68	AN	105/130 (81%)	82 (78%)	19 (18%)	4 (4%)	2	19
69	AO	183/185 (99%)	141 (77%)	33 (18%)	9 (5%)	1	16
70	AP	94/142 (66%)	73 (78%)	18 (19%)	3 (3%)	3	21
71	AQ	84/86 (98%)	77 (92%)	6 (7%)	1 (1%)	10	42
72	AR	240/360 (67%)	171 (71%)	55 (23%)	14 (6%)	1	14
73	AS	124/190 (65%)	102 (82%)	14 (11%)	8 (6%)	1	13
74	AT	160/173 (92%)	130 (81%)	21 (13%)	9 (6%)	1	14
75	AU	171/205 (83%)	152 (89%)	13 (8%)	6 (4%)	3	20
76	AV	320/414 (77%)	267 (83%)	43 (13%)	10 (3%)	3	22
77	AW	95/187 (51%)	65 (68%)	23 (24%)	7 (7%)	1	10
78	AX	310/398 (78%)	253 (82%)	46 (15%)	11 (4%)	3	20
79	AY	106/395 (27%)	86 (81%)	14 (13%)	6 (6%)	1	14
80	AZ	85/106 (80%)	74 (87%)	9 (11%)	2 (2%)	4	27
81	A0	197/225 (88%)	152 (77%)	29 (15%)	16 (8%)	1	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
82	A1	252/323 (78%)	198 (79%)	45 (18%)	9 (4%)	2	20
83	A2	114/118 (97%)	89 (78%)	20 (18%)	5 (4%)	2	17
84	A3	67/199 (34%)	58 (87%)	8 (12%)	1 (2%)	8	38
85	A4	237/474 (50%)	222 (94%)	12 (5%)	3 (1%)	9	41
All	All	12628/17575 (72%)	10637 (84%)	1611 (13%)	380 (3%)	5	22

5 of 380 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	W	73	PHE
22	X	69	ILE
22	X	149	PRO
30	5	263	ILE
30	5	296	LYS

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	
3	D	190/245 (78%)	190 (100%)	0	100	100
4	E	255/290 (88%)	255 (100%)	0	100	100
5	F	217/262 (83%)	217 (100%)	0	100	100
6	H	86/228 (38%)	84 (98%)	2 (2%)	44	63
7	I	145/232 (62%)	145 (100%)	0	100	100
8	J	113/150 (75%)	113 (100%)	0	100	100
9	K	155/156 (99%)	155 (100%)	0	100	100
10	L	98/124 (79%)	98 (100%)	0	100	100
11	M	245/249 (98%)	245 (100%)	0	100	100
12	N	172/211 (82%)	170 (99%)	2 (1%)	63	73
13	O	133/150 (89%)	132 (99%)	1 (1%)	73	77
14	P	115/155 (74%)	115 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	Q	201/201 (100%)	201 (100%)	0	100	100
16	R	118/126 (94%)	117 (99%)	1 (1%)	73	77
17	S	141/180 (78%)	140 (99%)	1 (1%)	76	79
18	T	146/176 (83%)	146 (100%)	0	100	100
19	U	99/135 (73%)	98 (99%)	1 (1%)	68	76
20	V	169/191 (88%)	169 (100%)	0	100	100
21	W	91/119 (76%)	91 (100%)	0	100	100
22	X	219/219 (100%)	219 (100%)	0	100	100
23	Y	159/223 (71%)	159 (100%)	0	100	100
24	Z	111/147 (76%)	111 (100%)	0	100	100
25	0	97/164 (59%)	97 (100%)	0	100	100
26	1	49/60 (82%)	49 (100%)	0	100	100
27	2	40/72 (56%)	40 (100%)	0	100	100
28	3	88/166 (53%)	88 (100%)	0	100	100
29	4	35/89 (39%)	35 (100%)	0	100	100
30	5	337/353 (96%)	335 (99%)	2 (1%)	78	80
31	6	266/332 (80%)	266 (100%)	0	100	100
32	7	242/303 (80%)	241 (100%)	1 (0%)	84	82
33	8	91/190 (48%)	91 (100%)	0	100	100
34	9	91/112 (81%)	91 (100%)	0	100	100
35	a	78/133 (59%)	78 (100%)	0	100	100
36	b	130/186 (70%)	130 (100%)	0	100	100
37	c	241/288 (84%)	241 (100%)	0	100	100
38	d	151/274 (55%)	151 (100%)	0	100	100
39	e	188/236 (80%)	188 (100%)	0	100	100
40	f	117/188 (62%)	117 (100%)	0	100	100
41	g	119/148 (80%)	118 (99%)	1 (1%)	73	77
42	h	95/148 (64%)	95 (100%)	0	100	100
43	i	86/110 (78%)	85 (99%)	1 (1%)	63	73
44	j	68/97 (70%)	68 (100%)	0	100	100
45	k	74/90 (82%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	l	23/116 (20%)	23 (100%)	0	100	100
47	m	40/113 (35%)	40 (100%)	0	100	100
48	o	80/87 (92%)	79 (99%)	1 (1%)	61	72
49	p	117/181 (65%)	117 (100%)	0	100	100
50	q	110/178 (62%)	110 (100%)	0	100	100
51	r	133/169 (79%)	133 (100%)	0	100	100
52	s	326/381 (86%)	326 (100%)	0	100	100
56	AB	191/249 (77%)	190 (100%)	1 (0%)	81	81
57	AC	115/143 (80%)	115 (100%)	0	100	100
58	AD	269/357 (75%)	269 (100%)	0	100	100
59	AE	104/107 (97%)	104 (100%)	0	100	100
60	AF	178/209 (85%)	178 (100%)	0	100	100
61	AG	265/342 (78%)	265 (100%)	0	100	100
62	AH	112/180 (62%)	112 (100%)	0	100	100
63	AI	104/147 (71%)	104 (100%)	0	100	100
64	AJ	93/118 (79%)	93 (100%)	0	100	100
65	AK	91/113 (80%)	90 (99%)	1 (1%)	65	74
66	AL	152/226 (67%)	151 (99%)	1 (1%)	76	79
67	AM	95/113 (84%)	95 (100%)	0	100	100
68	AN	93/115 (81%)	91 (98%)	2 (2%)	45	64
69	AO	166/166 (100%)	164 (99%)	2 (1%)	63	73
70	AP	87/123 (71%)	87 (100%)	0	100	100
71	AQ	78/78 (100%)	77 (99%)	1 (1%)	61	72
72	AR	224/318 (70%)	224 (100%)	0	100	100
73	AS	109/164 (66%)	109 (100%)	0	100	100
74	AT	150/157 (96%)	149 (99%)	1 (1%)	76	79
75	AU	149/174 (86%)	149 (100%)	0	100	100
76	AV	295/364 (81%)	294 (100%)	1 (0%)	86	84
77	AW	84/158 (53%)	84 (100%)	0	100	100
78	AX	275/351 (78%)	275 (100%)	0	100	100
79	AY	99/357 (28%)	99 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
80	AZ	80/95 (84%)	80 (100%)	0	100	100
81	A0	176/196 (90%)	175 (99%)	1 (1%)	78	80
82	A1	237/291 (81%)	236 (100%)	1 (0%)	84	82
83	A2	99/101 (98%)	98 (99%)	1 (1%)	68	76
84	A3	63/166 (38%)	62 (98%)	1 (2%)	55	69
85	A4	226/291 (78%)	225 (100%)	1 (0%)	84	82
All	All	11349/15102 (75%)	11320 (100%)	29 (0%)	84	84

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

Mol	Chain	Res	Type
56	AB	257	ILE
84	A3	194	ILE
68	AN	25	THR
81	A0	64	LEU
66	AL	185	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 80 such sidechains are listed below:

Mol	Chain	Res	Type
61	AG	261	GLN
78	AX	349	ASN
63	AI	163	HIS
74	AT	51	ASN
82	A1	217	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1458/1472 (99%)	332 (22%)	23 (1%)
2	B	51/56 (91%)	9 (17%)	1 (1%)
54	u	1/2 (50%)	0	0
55	AA	914/923 (99%)	366 (40%)	24 (2%)
All	All	2424/2453 (98%)	707 (29%)	48 (1%)

5 of 707 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	1672	C
1	A	1676	A
1	A	1677	C
1	A	1678	C
1	A	1679	U

5 of 48 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
55	AA	833	A
55	AA	982	A
55	AA	878	G
55	AA	943	G
55	AA	1102	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 134 ligands modelled in this entry, 134 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	14
85	A4	13
55	AA	8
2	B	4

The worst 5 of 39 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2218:C	O3'	2228:A	P	41.52
1	A4	399:UNK	C	414:LYS	N	32.07
1	A	2760:A	O3'	2792:A	P	25.98
1	A	1760:G	O3'	1766:U	P	24.98
1	AA	955:A	O3'	965:C	P	24.64

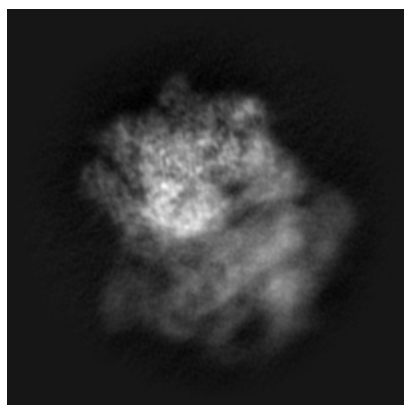
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0515. These allow visual inspection of the internal detail of the map and identification of artifacts.

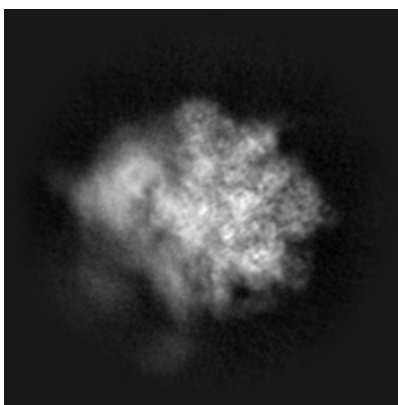
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

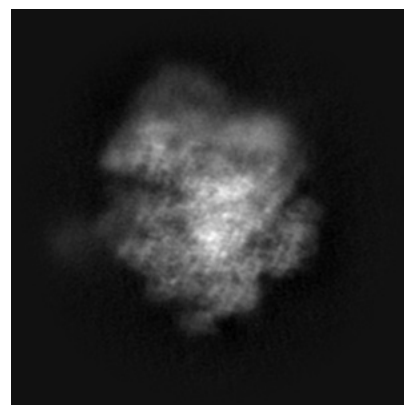
6.1.1 Primary map



X



Y

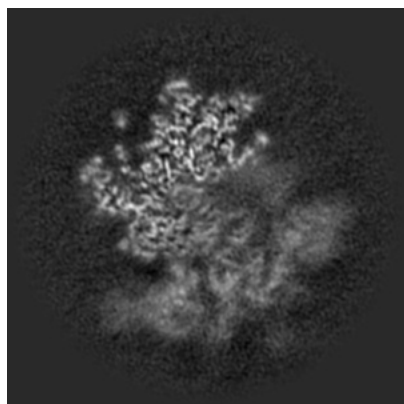


Z

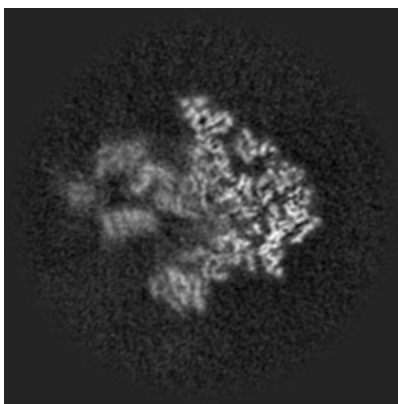
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

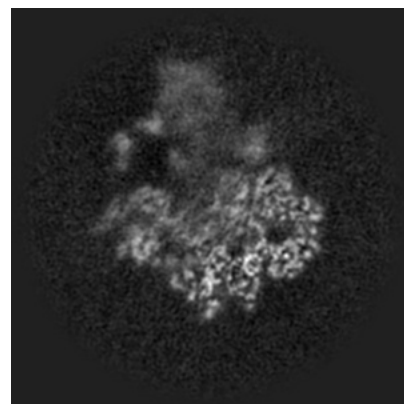
6.2.1 Primary map



X Index: 190



Y Index: 190

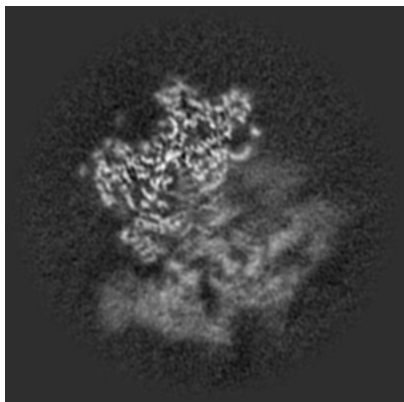


Z Index: 190

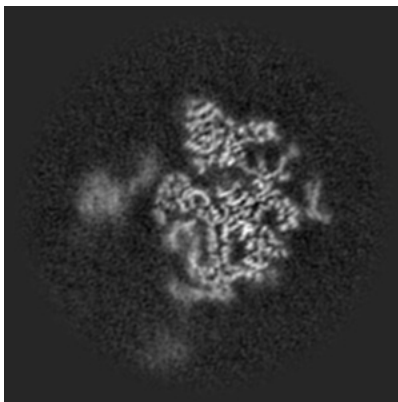
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

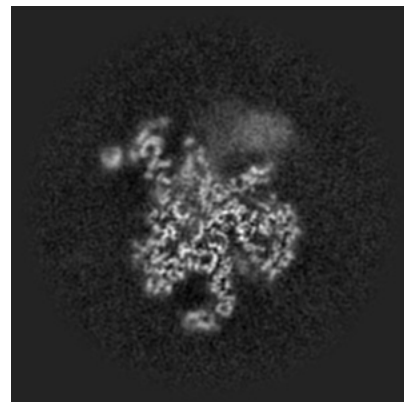
6.3.1 Primary map



X Index: 197



Y Index: 147

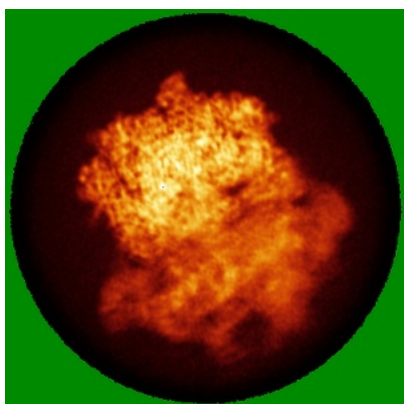


Z Index: 228

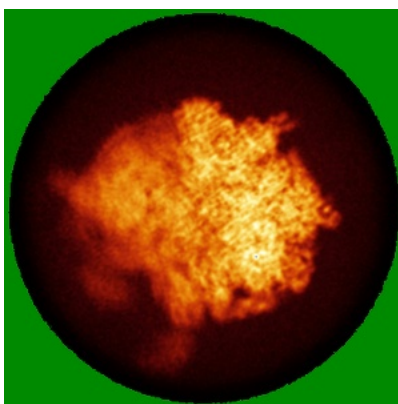
The images above show the largest variance slices of the map in three orthogonal directions.

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

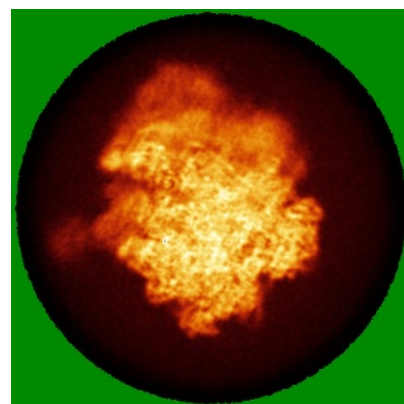
6.4.1 Primary map



X



Y



Z

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

This section was not generated.

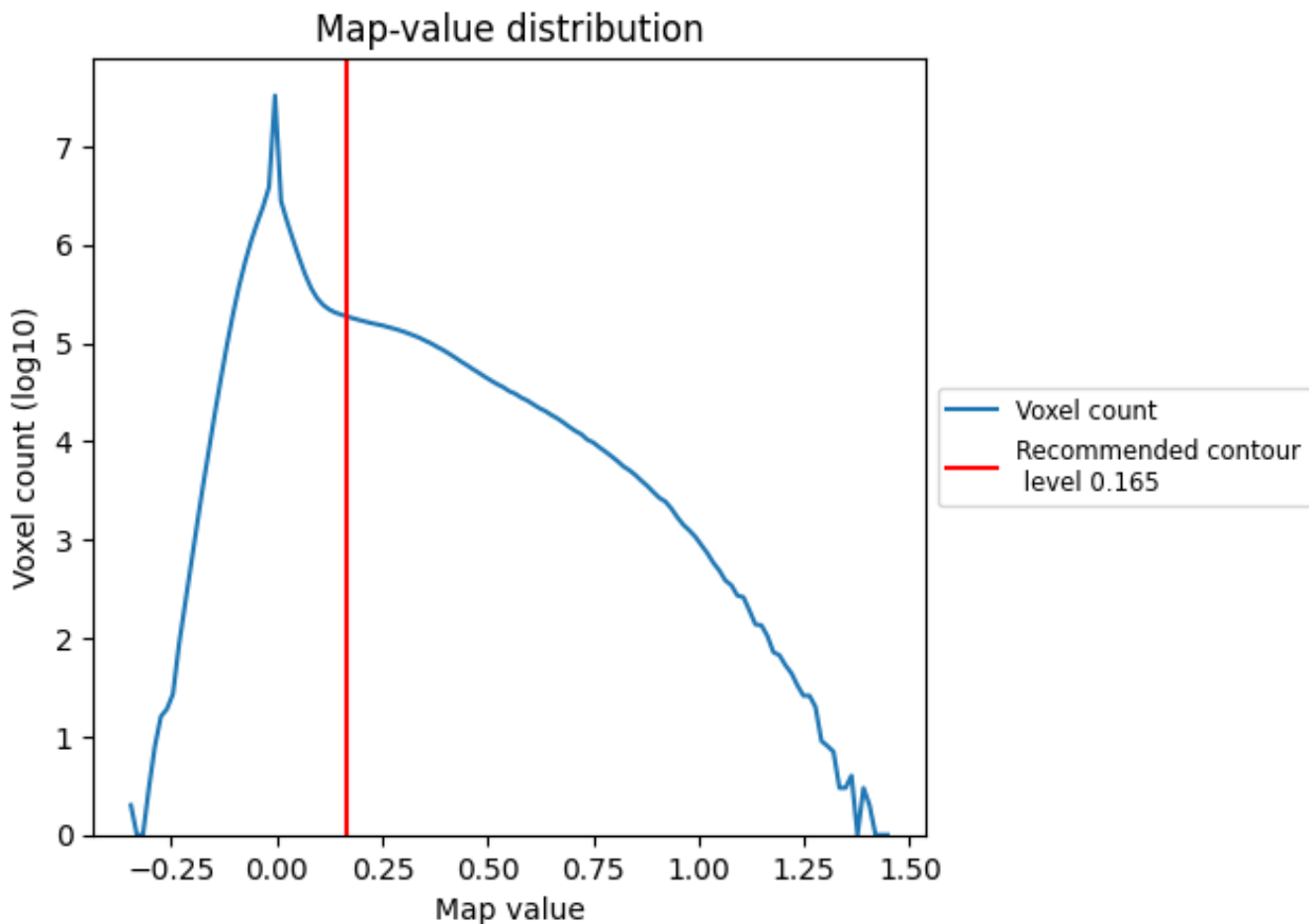
6.6 Mask visualisation

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

7 Map analysis [i](#)

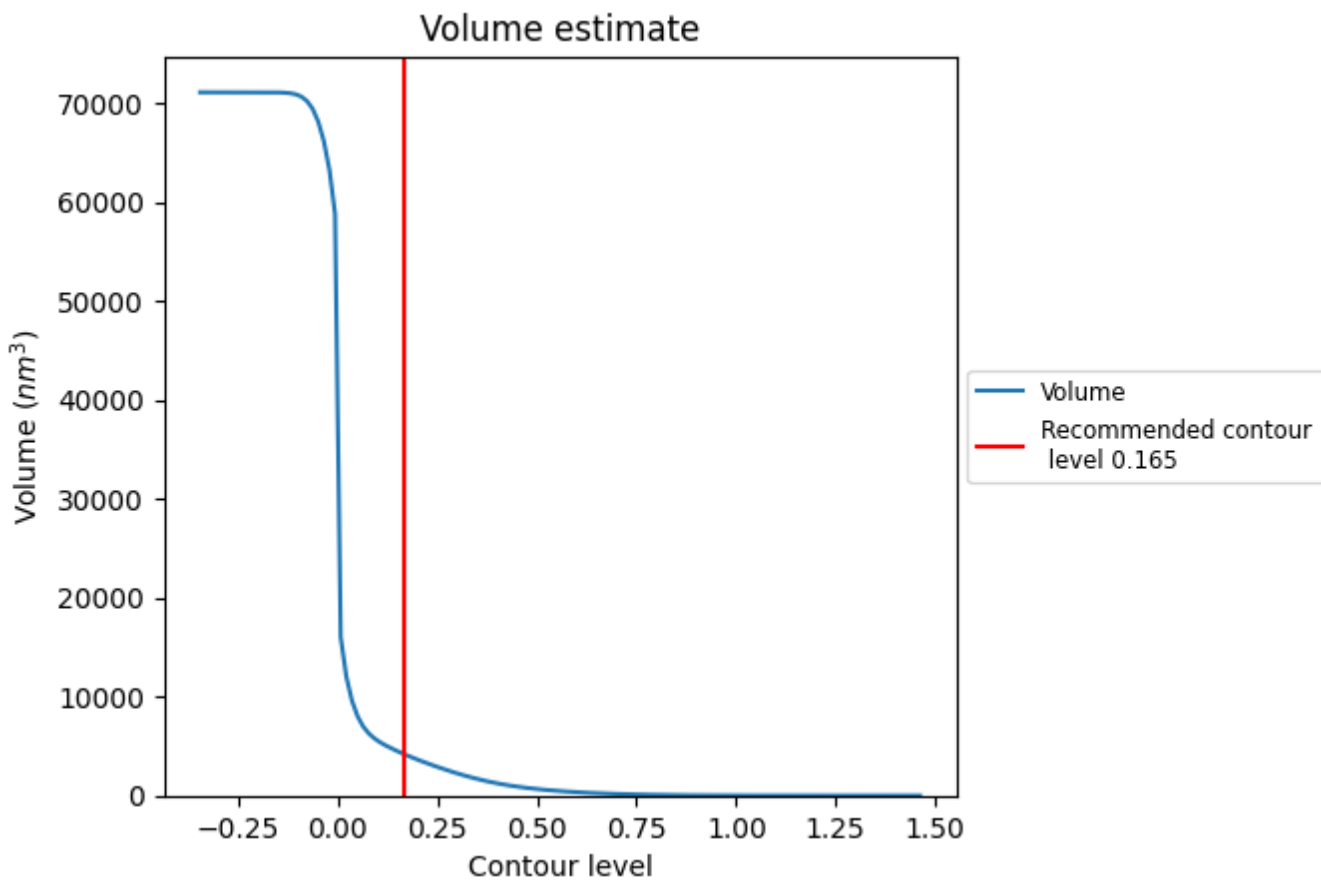
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

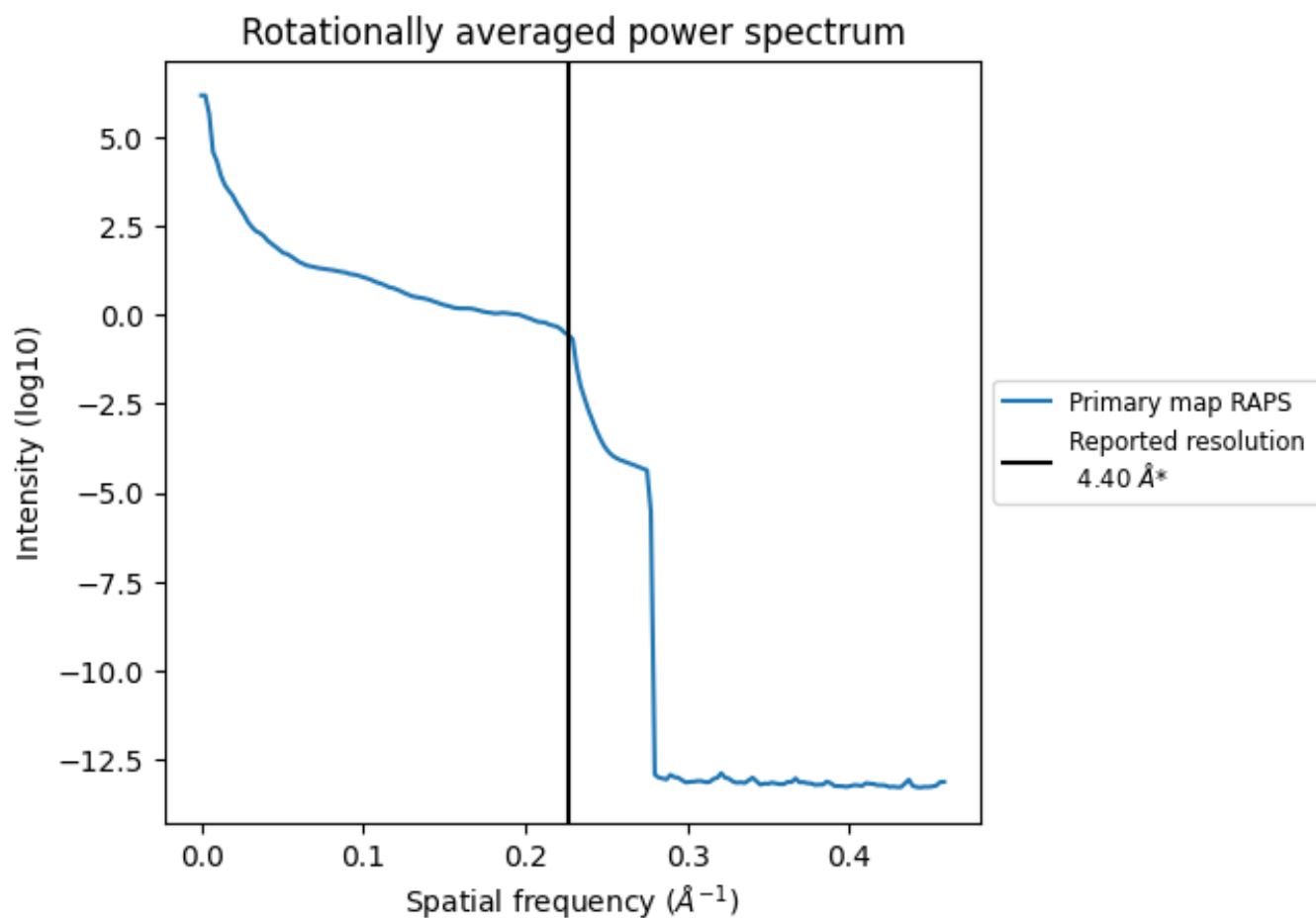
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4210 nm³; this corresponds to an approximate mass of 3803 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

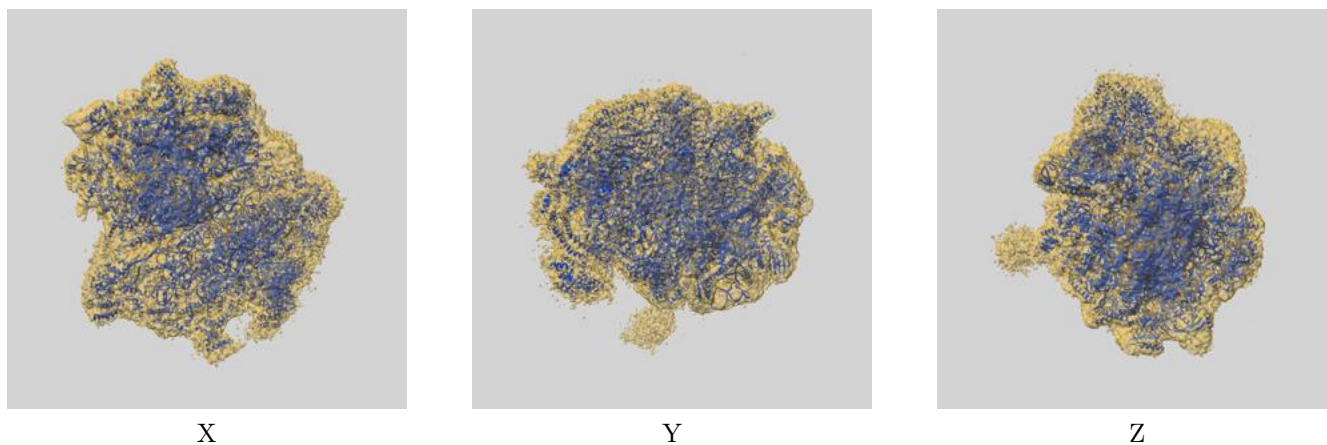
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

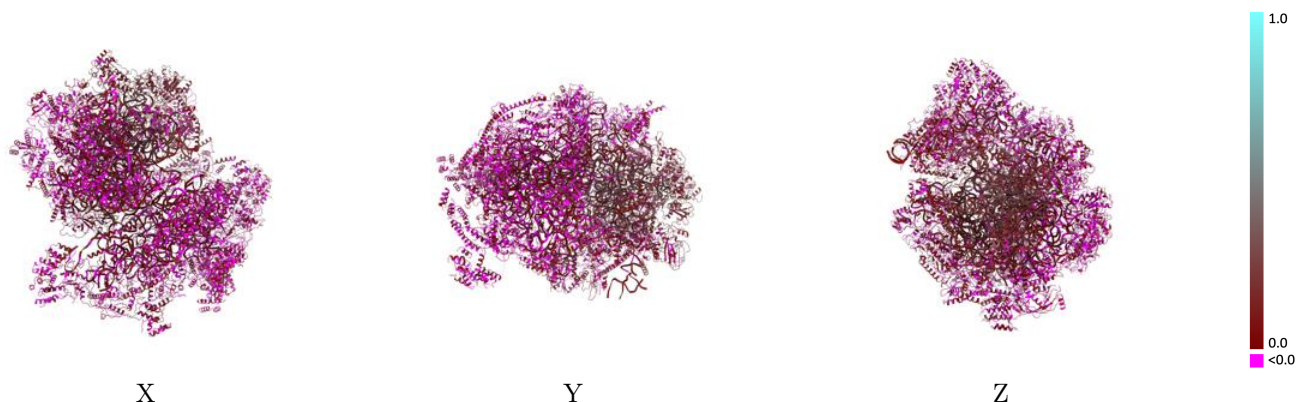
This section contains information regarding the fit between EMDB map EMD-0515 and PDB model 6NU3. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay [i](#)



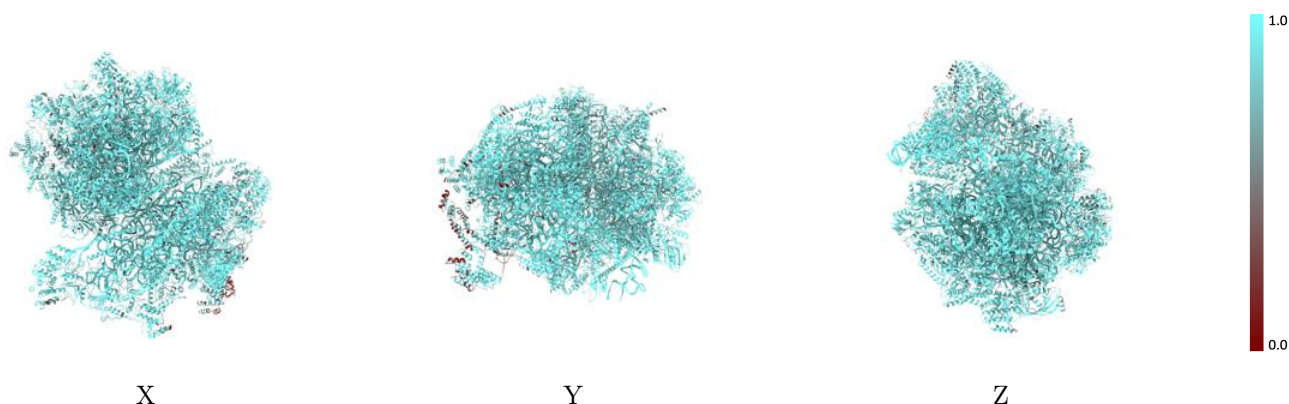
The images above show the 3D surface view of the map at the recommended contour level 0.165 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



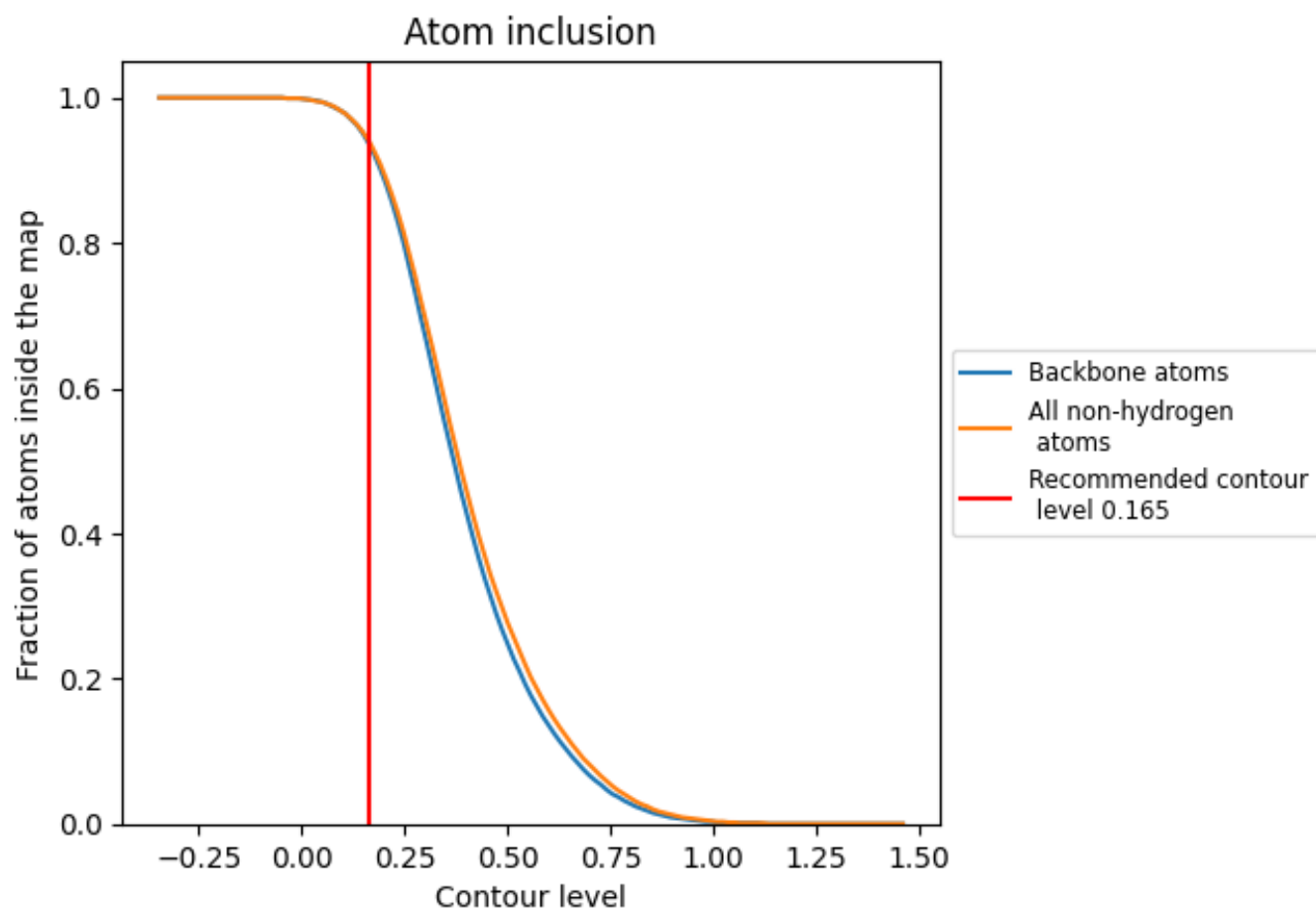
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.165).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.165) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9390	 0.0950
0	 0.8660	 0.0450
1	 0.9810	 0.1250
2	 0.8690	 0.0330
3	 0.9500	 0.2510
4	 0.9410	 0.1000
5	 0.9100	 0.0200
6	 0.9570	 0.1670
7	 0.8850	 0.0280
8	 0.9240	 0.0990
9	 0.9060	 0.0340
A	 0.9780	 0.1740
A0	 0.9520	 0.0590
A1	 0.8970	 0.0470
A2	 0.9270	 0.0240
A3	 0.9570	 0.0840
A4	 0.7080	 0.0270
AA	 0.9850	 0.0790
AB	 0.9610	 0.0160
AC	 0.9530	 0.0000
AD	 0.9070	 0.0320
AE	 0.9040	 -0.0190
AF	 0.9200	 0.0140
AG	 0.8240	 0.0350
AH	 0.8380	 0.0050
AI	 0.9470	 0.0130
AJ	 0.9460	 0.1030
AK	 0.9460	 0.0230
AL	 0.9670	 0.0120
AM	 0.9720	 0.0370
AN	 0.9920	 0.0210
AO	 0.9260	 0.0690
AP	 0.9660	 0.0040
AQ	 0.9520	 0.0530
AR	 0.8990	 0.0570





















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Chain	Atom inclusion	Q-score
AS	 0.9610	 0.0230
AT	 0.9560	 0.0710
AU	 0.9500	 0.0690
AV	 0.9300	 0.0550
AW	 0.9320	 -0.0190
AX	 0.8930	 0.0250
AY	 0.8230	 0.0330
AZ	 0.9650	 0.0100
B	 0.9740	 0.1320
D	 0.9090	 0.0250
E	 0.9580	 0.1030
F	 0.9260	 0.1950
H	 0.9040	 0.1250
I	 0.9470	 0.0830
J	 0.9460	 0.0510
K	 0.9300	 0.1070
L	 0.8850	 0.1580
M	 0.9590	 0.2250
N	 0.9480	 0.1690
O	 0.8850	 0.0200
P	 0.9370	 0.1170
Q	 0.9210	 0.1340
R	 0.9210	 0.1100
S	 0.9190	 0.1070
T	 0.8280	 0.0650
U	 0.8770	 -0.0080
V	 0.8630	 0.0610
W	 0.9280	 0.1280
X	 0.9050	 0.1050
Y	 0.9160	 0.0380
Z	 0.9330	 0.1410
a	 0.9430	 0.0870
b	 0.8960	 0.0910
c	 0.8840	 0.0590
d	 0.8810	 0.0520
e	 0.9700	 0.1010
f	 0.8940	 0.1190
g	 0.9690	 0.2690
h	 0.9440	 0.1650
i	 0.9080	 0.1780
j	 0.9210	 0.1190
k	 0.9240	 0.0440

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Chain	Atom inclusion	Q-score
l	 0.9900	 0.1070
m	 0.9210	 0.0360
o	 0.9630	 0.1550
p	 0.9650	 0.1770
q	 0.9390	 0.1990
r	 0.9600	 0.1020
s	 0.8940	 -0.0050
t	 0.9790	 0.1730
u	 1.0000	 0.0970