wwPDB EM Validation Summary Report ⓘ

Nov 6, 2022 – 11:04 PM EST

PDB ID	:	6NU2
EMDB ID	:	EMD-0514
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	:	3.90 Å(reported)
Based on initial model	:	3JD5

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

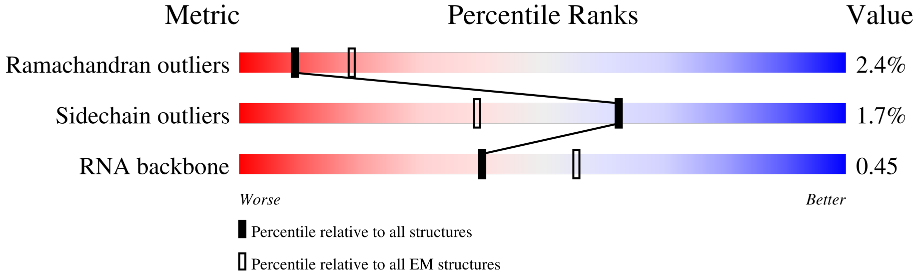
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

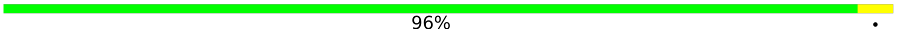
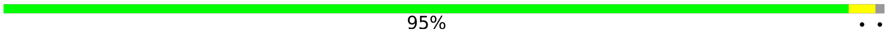
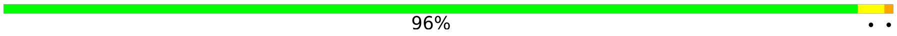
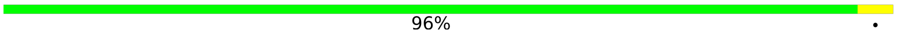
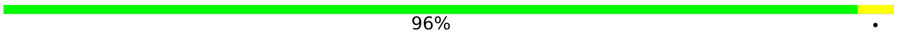
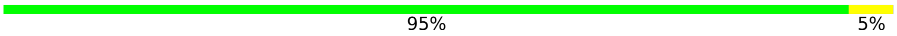
The reported resolution of this entry is 3.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	A	1472	
2	B	56	
3	D	236	
4	E	304	
5	F	250	
6	H	95	
7	I	168	
8	J	140	
9	K	177	

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Mol	Chain	Length	Quality of chain
10	L	115	95% 5%
11	M	287	96% •
12	N	205	99% •
13	O	152	99% •
14	P	138	94% • •
15	Q	219	97% •
16	R	140	98% •
17	S	156	97% •
18	T	166	98% •
19	U	111	96% •
20	V	202	87% 6% 6%
21	W	115	96% •
22	X	243	94% 6%
23	Y	176	98% •
24	Z	120	97% •
25	0	108	96% •
26	1	52	94% 6%
27	2	46	100%
28	3	95	98% •
29	4	36	100%
30	5	392	92% • •
31	6	354	88% • 8%
32	7	287	89% • 7%
33	8	99	97% •
34	9	123	84% 5% 11%

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Mol	Chain	Length	Quality of chain
35	a	108	73% • 24%
36	b	148	97% •
37	c	286	94% • •
38	d	171	92% • • 5%
39	e	237	88% • 8%
40	f	146	89% • 10%
41	g	129	95% 5%
42	h	103	95% • •
43	i	97	94% 6%
44	j	85	98% •
45	k	84	93% 7%
46	l	23	100%
47	m	45	93% 7%
48	o	94	96% •
49	p	156	79% • 19%
50	q	128	96% •
51	r	162	86% • 10%
52	s	390	93% • 5%
53	t	28	100%
54	u	2	100%
55	z	204	97% •
56	AA	923	66% 34%
57	AB	217	99% •
58	AC	132	97% •
59	AD	343	88% 6% 6%

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Mol	Chain	Length	Quality of chain
60	AE	122	97% •
61	AF	208	95% • •
62	AG	326	88% 5% 6%
63	AH	122	94% 6%
64	AI	136	96% •
65	AJ	108	95% 5%
66	AK	101	92% 8%
67	AL	164	99% •
68	AM	116	97% •
69	AN	107	93% 7%
70	AO	185	94% 6%
71	AP	96	98% •
72	AQ	86	97% •
73	AR	242	94% 6%
74	AS	126	98% •
75	AT	162	98% •
76	AU	173	95% 5%
77	AV	365	87% • 10%
78	AW	97	97% •
79	AX	348	84% 6% 9%
80	AY	108	95% 5%
81	AZ	87	94% 6%
82	A0	208	93% • •
83	A1	272	90% • 6%
84	A2	116	95% 5%

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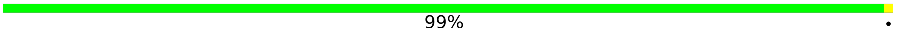
Mol	Chain	Length	Quality of chain
85	A3	69	
86	A4	474	

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 294948 atoms, of which 134991 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	47118	14025	15857	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
7	I	158	Total 2652	C 828	H 1369	N 235	O 210	S 10	0	0

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
12	N	205	Total 3334	C 1056	H 1680	N 308	O 280	S 10	0	0

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

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
14	P	133	2162	677	1082	209	189	5	0	0

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

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

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

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

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

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

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

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

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

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

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

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

- 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	115	1816	571	922	169	151	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	4089	1317	2054	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	1782	545	902	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	666	203	344	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	5087	1692	2451	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 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	2423	764	1220	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 protein called Ribosome-recycling factor, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
55	z	204	3240	974	1665	285	308	8	0	0

- Molecule 56 is a RNA chain called 12S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	AA	923	Total	C	H	N	O	P	0	0
			29552	8790	9946	3535	6358	923		

- Molecule 57 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	AB	217	Total	C	H	N	O	S	0	0
			3533	1131	1765	321	306	10		

- Molecule 58 is a protein called 28S ribosomal protein S24, mitochondrial.

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

- Molecule 59 is a protein called 28S ribosomal protein S5, mitochondrial.

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

- Molecule 60 is a protein called 28S ribosomal protein S6, mitochondrial.

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

- Molecule 61 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	AF	201	Total	C	H	N	O	S	0	0
			3385	1069	1717	305	283	11		

- Molecule 62 is a protein called 28S ribosomal protein S9, mitochondrial.

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

- Molecule 63 is a protein called 28S ribosomal protein S10, mitochondrial.

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

- Molecule 64 is a protein called 28S ribosomal protein S11, mitochondrial.

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

- Molecule 65 is a protein called 28S ribosomal protein S12, mitochondrial.

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

- Molecule 66 is a protein called 28S ribosomal protein S14, mitochondrial.

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

- Molecule 67 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
67	AL	164	Total 2855	C 883	H 1473	N 257	O 235	S 7	0	0

- Molecule 68 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
68	AM	116	Total 1870	C 582	H 950	N 182	O 150	S 6	0	0

- Molecule 69 is a protein called 28S ribosomal protein S17, mitochondrial.

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

- Molecule 70 is a protein called 28S ribosomal protein S18b, mitochondrial.

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

- Molecule 71 is a protein called 28S ribosomal protein S18c, mitochondrial.

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

- Molecule 72 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
72	AQ	86	1481	455	746	147	124	9	0	0

- Molecule 73 is a protein called 28S ribosomal protein S22, mitochondrial.

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

- Molecule 74 is a protein called 28S ribosomal protein S23, mitochondrial.

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

- Molecule 75 is a protein called 28S ribosomal protein S25, mitochondrial.

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

- Molecule 76 is a protein called 28S ribosomal protein S26, mitochondrial.

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

- Molecule 77 is a protein called 28S ribosomal protein S27, mitochondrial.

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

- Molecule 78 is a protein called 28S ribosomal protein S28, mitochondrial.

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

- Molecule 79 is a protein called 28S ribosomal protein S29, mitochondrial.

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

- Molecule 80 is a protein called 28S ribosomal protein S31, mitochondrial.

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

- Molecule 81 is a protein called 28S ribosomal protein S33, mitochondrial.

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

- Molecule 82 is a protein called 28S ribosomal protein S34, mitochondrial.

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

- Molecule 83 is a protein called 28S ribosomal protein S35, mitochondrial.

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

- Molecule 84 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		
84	A2	116	1887	574	962	181	162	8	0	0

- Molecule 85 is a protein called Aurora kinase A-interacting protein.

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

- Molecule 86 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
86	A4	414	5103	1805	2265	490	529	14	0	0

- Molecule 87 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 88 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
88	0	1	1	1	0
88	4	1	1	1	0
88	r	1	1	1	0
88	AB	1	1	1	0
88	AO	1	1	1	0
88	AP	1	1	1	0

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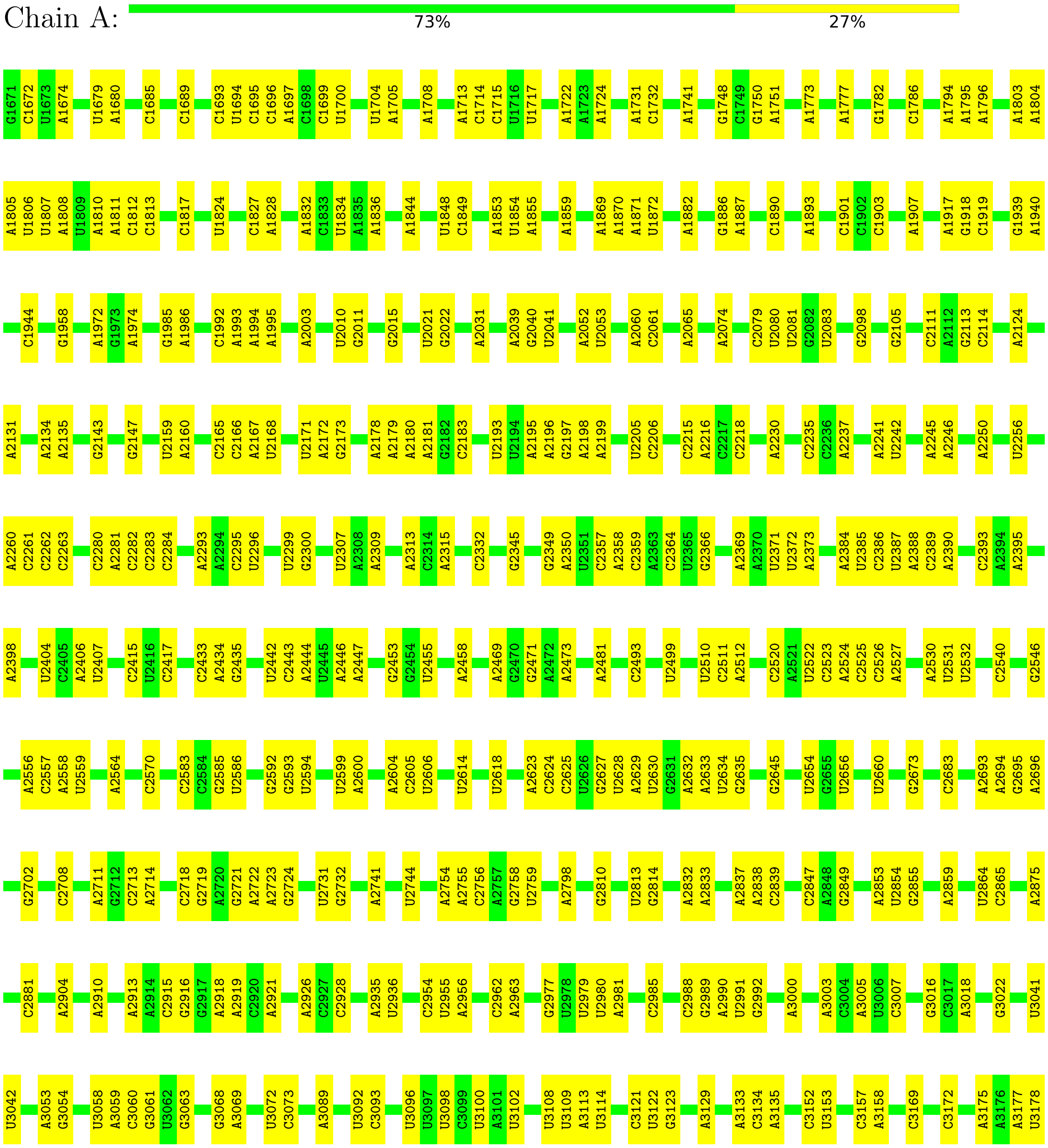
Mol	Chain	Residues	Atoms	AltConf
88	AT	1	Total Zn 1 1	0

3 Residue-property plots ⓘ

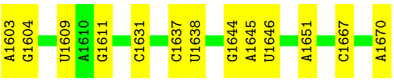
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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



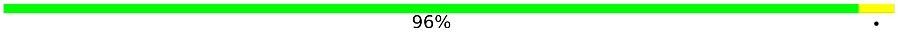
- Molecule 2: mt-tRNAVal

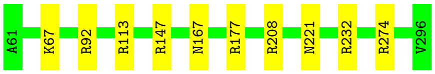
Chain B:



- Molecule 3: 39S ribosomal protein L2, mitochondrial

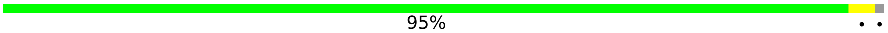
Chain D:

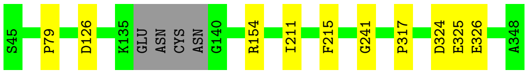




- Molecule 4: 39S ribosomal protein L3, mitochondrial

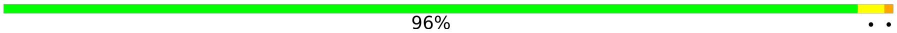
Chain E:

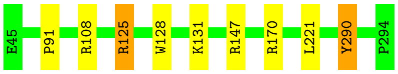




- Molecule 5: 39S ribosomal protein L4, mitochondrial

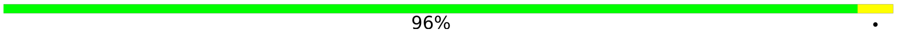
Chain F:

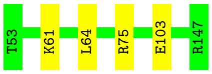




- Molecule 6: 39S ribosomal protein L9, mitochondrial

Chain H:



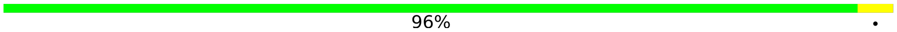


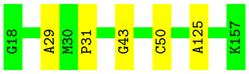
- Molecule 7: 39S ribosomal protein L10, mitochondrial

Chain I:

- Molecule 8: 39S ribosomal protein L11, mitochondrial

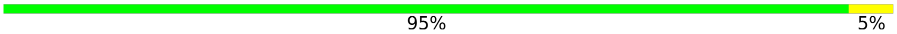
Chain J:

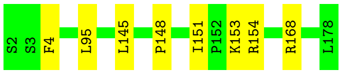




- Molecule 9: 39S ribosomal protein L13, mitochondrial

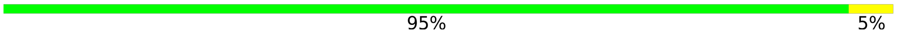
Chain K:

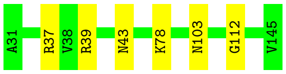




- Molecule 10: 39S ribosomal protein L14, mitochondrial

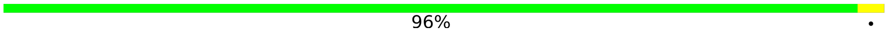
Chain L:

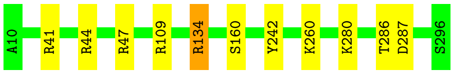




- Molecule 11: 39S ribosomal protein L15, mitochondrial

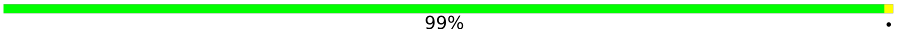
Chain M:

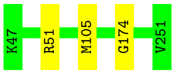




- Molecule 12: 39S ribosomal protein L16, mitochondrial

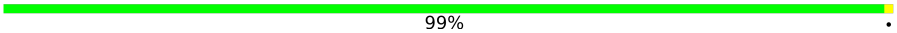
Chain N:

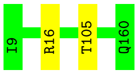




- Molecule 13: 39S ribosomal protein L17, mitochondrial

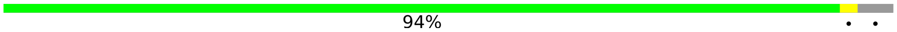
Chain O:

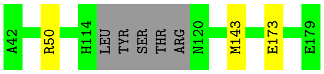




- Molecule 14: 39S ribosomal protein L18, mitochondrial

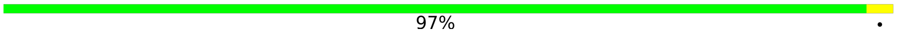
Chain P:

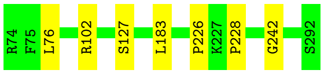




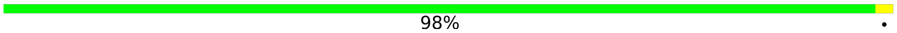
- Molecule 15: 39S ribosomal protein L19, mitochondrial

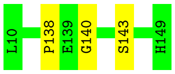
Chain Q:



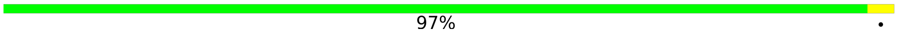


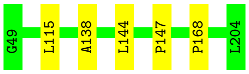
- Molecule 16: 39S ribosomal protein L20, mitochondrial

Chain R:


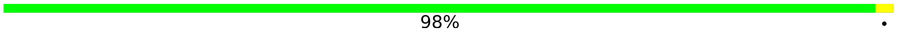


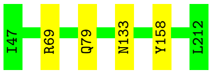
- Molecule 17: 39S ribosomal protein L21, mitochondrial

Chain S:


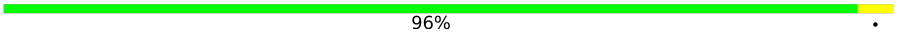


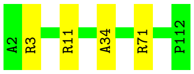
- Molecule 18: 39S ribosomal protein L22, mitochondrial

Chain T:




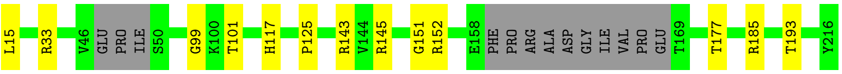
- Molecule 19: 39S ribosomal protein L23, mitochondrial

Chain U:


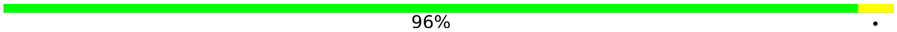


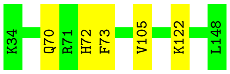
- Molecule 20: 39S ribosomal protein L24, mitochondrial

Chain V:

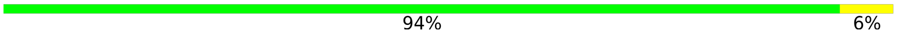



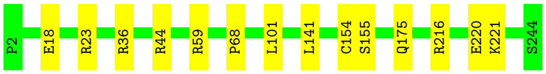
- Molecule 21: 39S ribosomal protein L27, mitochondrial

Chain W:


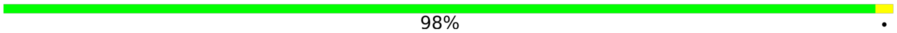


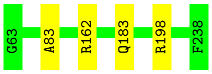
- Molecule 22: 39S ribosomal protein L28, mitochondrial

Chain X:


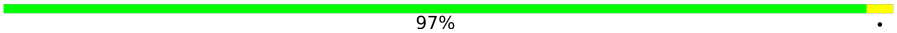


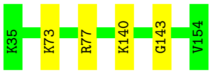
- Molecule 23: 39S ribosomal protein L47, mitochondrial

Chain Y:


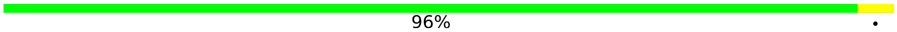


- Molecule 24: 39S ribosomal protein L30, mitochondrial

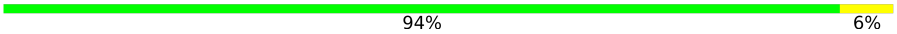
Chain Z:


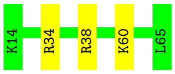


- Molecule 25: 39S ribosomal protein L32, mitochondrial

Chain 0:


- Molecule 26: 39S ribosomal protein L33, mitochondrial

Chain 1:


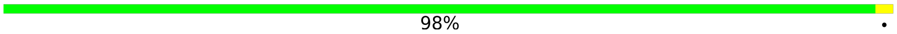


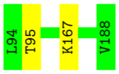
- Molecule 27: 39S ribosomal protein L34, mitochondrial

Chain 2:


There are no outlier residues recorded for this chain.

- Molecule 28: 39S ribosomal protein L35, mitochondrial

Chain 3:




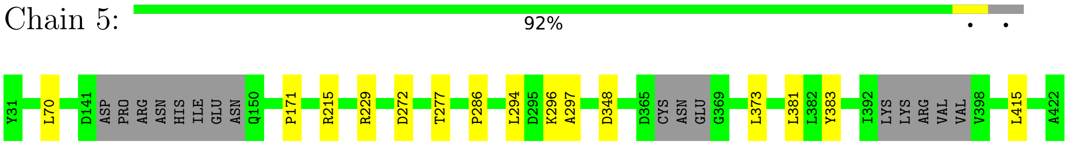
- Molecule 29: 39S ribosomal protein L36, mitochondrial

Chain 4:


There are no outlier residues recorded for this chain.

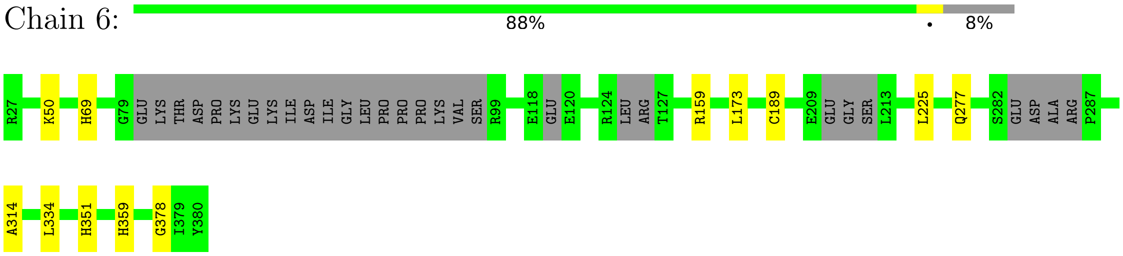
- Molecule 30: 39S ribosomal protein L37, mitochondrial

Chain 5:



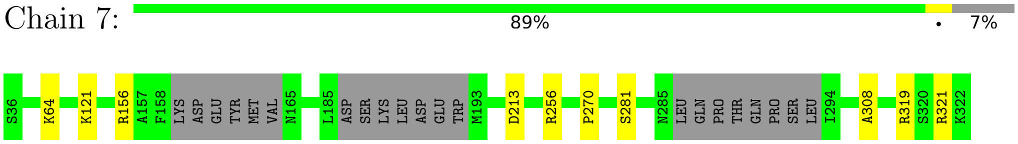
- Molecule 31: 39S ribosomal protein L38, mitochondrial

Chain 6:



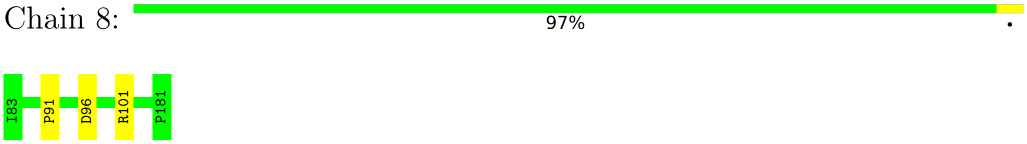
- Molecule 32: 39S ribosomal protein L39, mitochondrial

Chain 7:



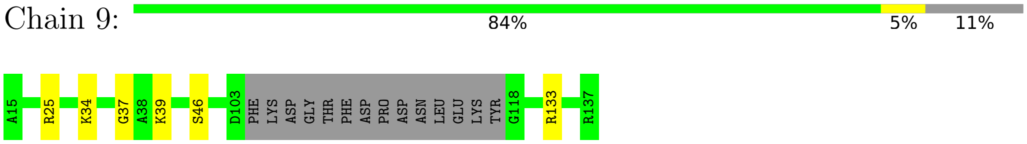
- Molecule 33: 39S ribosomal protein L40, mitochondrial

Chain 8:



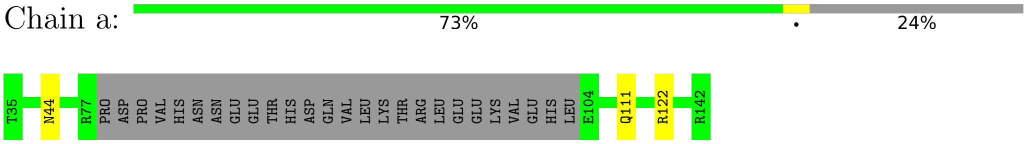
- Molecule 34: 39S ribosomal protein L41, mitochondrial

Chain 9:



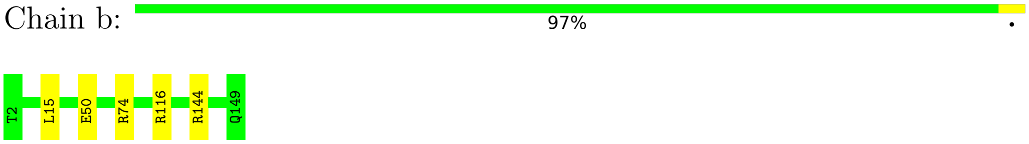
- Molecule 35: 39S ribosomal protein L42, mitochondrial

Chain a:



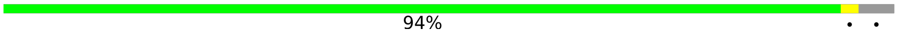
- Molecule 36: 39S ribosomal protein L43, mitochondrial

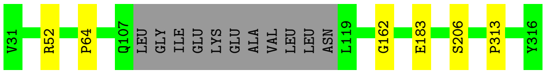
Chain b:



- Molecule 37: 39S ribosomal protein L44, mitochondrial

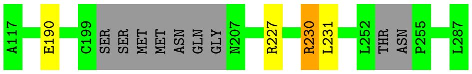
Chain c:





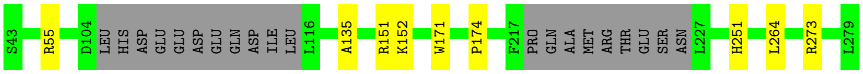
- Molecule 38: 39S ribosomal protein L45, mitochondrial

Chain d:



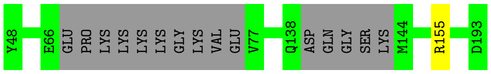
- Molecule 39: 39S ribosomal protein L46, mitochondrial

Chain e:



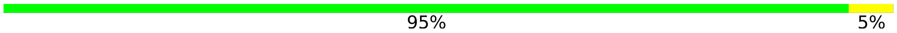
- Molecule 40: 39S ribosomal protein L48, mitochondrial

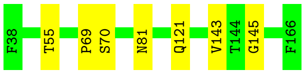
Chain f:



- Molecule 41: 39S ribosomal protein L49, mitochondrial

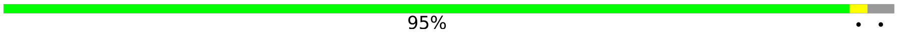
Chain g:

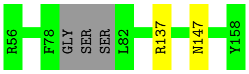




- Molecule 42: 39S ribosomal protein L50, mitochondrial

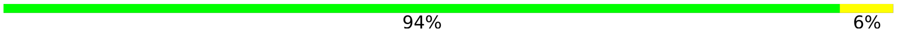
Chain h:

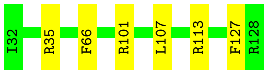




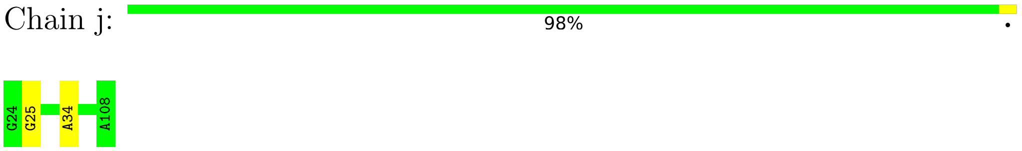
- Molecule 43: 39S ribosomal protein L51, mitochondrial

Chain i:

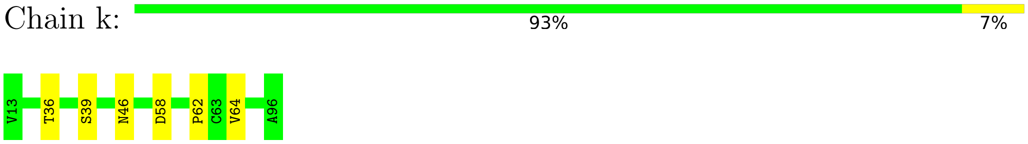




- Molecule 44: 39S ribosomal protein L52, mitochondrial



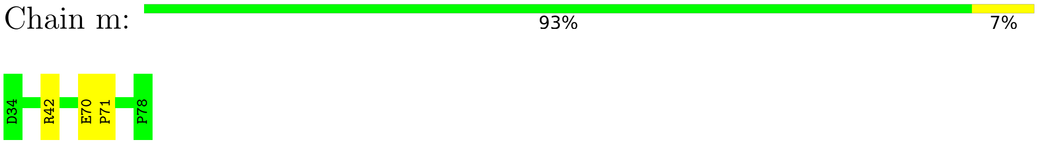
- Molecule 45: 39S ribosomal protein L53, mitochondrial



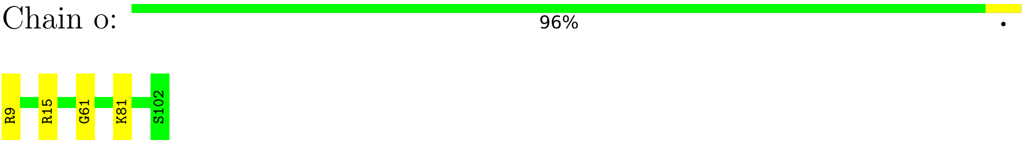
- Molecule 46: 39S ribosomal protein L54, mitochondrial

There are no outlier residues recorded for this chain.

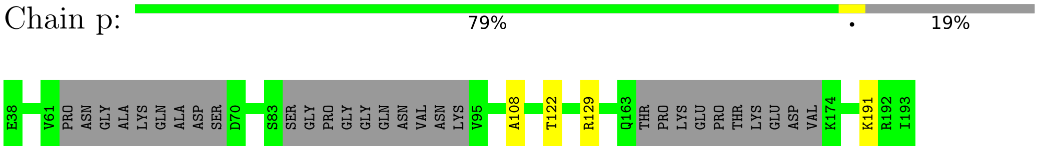
- Molecule 47: 39S ribosomal protein L55, mitochondrial



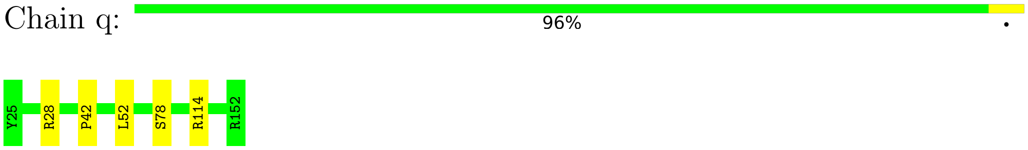
- Molecule 48: Ribosomal protein 63, mitochondrial



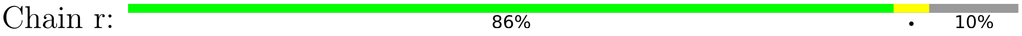
- Molecule 49: Peptidyl-tRNA hydrolase ICT1, mitochondrial

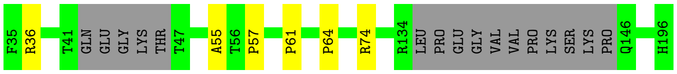


- Molecule 50: Growth arrest and DNA damage-inducible proteins-interacting protein 1

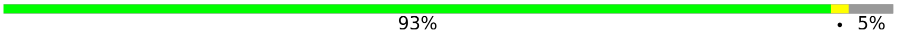


- Molecule 51: 39S ribosomal protein S18a, mitochondrial

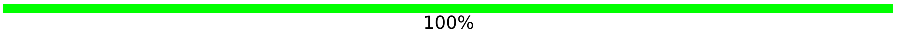




- Molecule 52: 39S ribosomal protein S30, mitochondrial

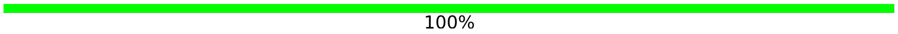
Chain s:


- Molecule 53: Unknown protein/protein extension

Chain t:


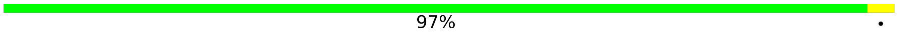
There are no outlier residues recorded for this chain.

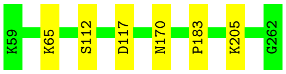
- Molecule 54: E-site tRNA

Chain u:


There are no outlier residues recorded for this chain.

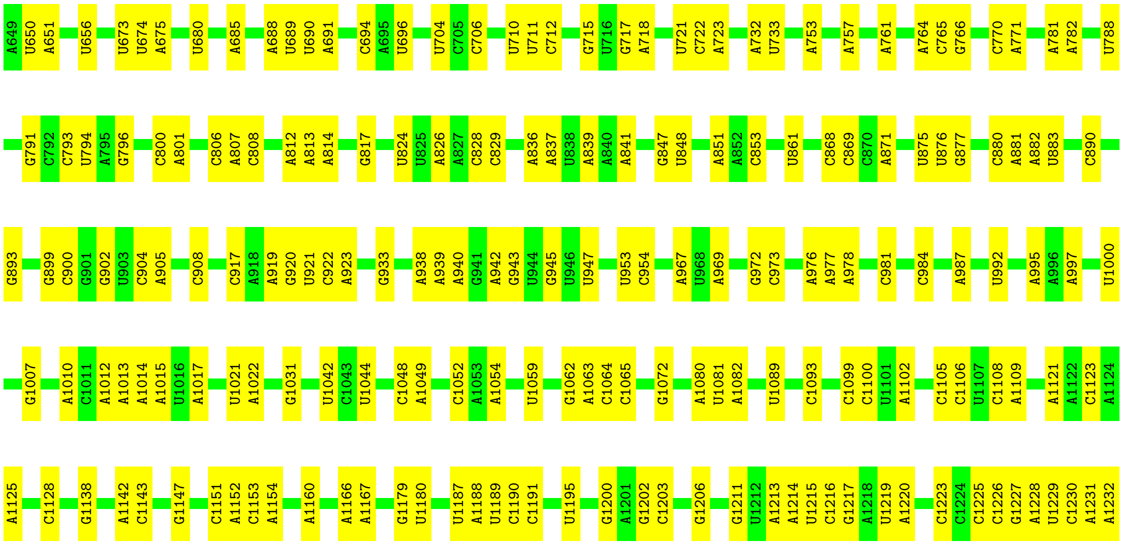
- Molecule 55: Ribosome-recycling factor, mitochondrial

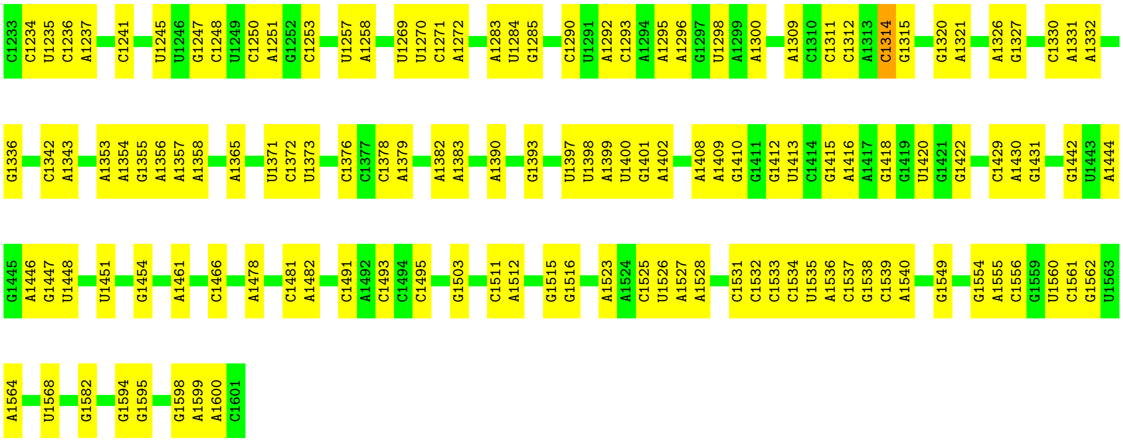
Chain z:




- Molecule 56: 12S rRNA

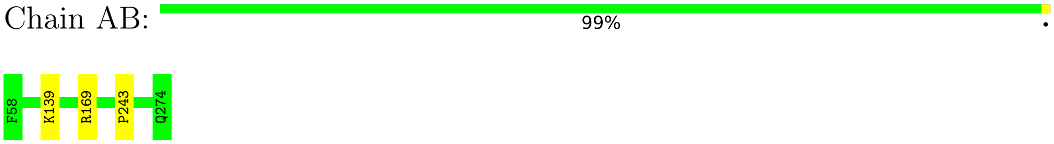
Chain AA:



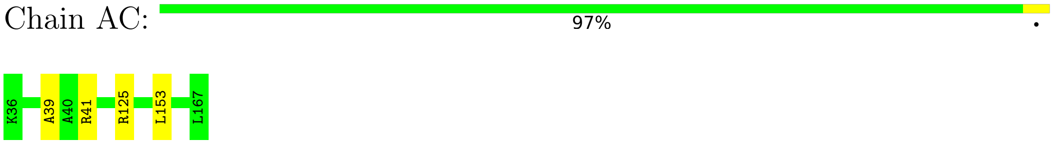
- Molecule 57: 28S ribosomal protein S2, mitochondrial

Chain AB:



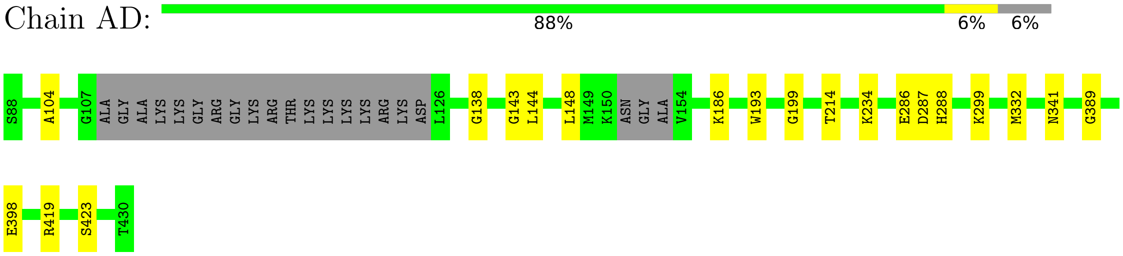
- Molecule 58: 28S ribosomal protein S24, mitochondrial

Chain AC:



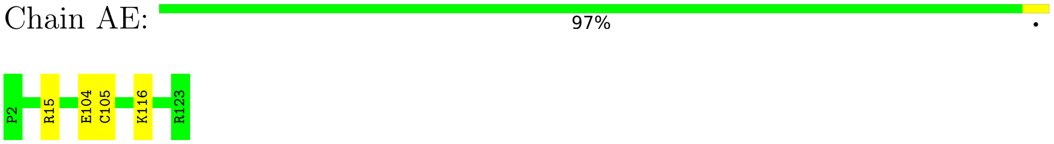
- Molecule 59: 28S ribosomal protein S5, mitochondrial

Chain AD:



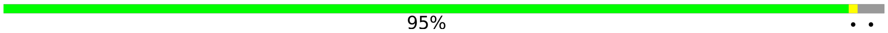
- Molecule 60: 28S ribosomal protein S6, mitochondrial

Chain AE:



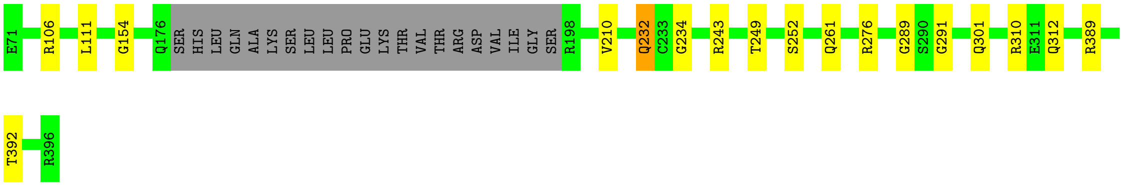
- Molecule 61: 28S ribosomal protein S7, mitochondrial

Chain AF:



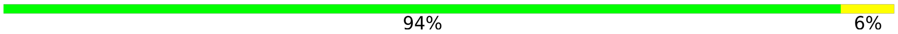
- Molecule 62: 28S ribosomal protein S9, mitochondrial

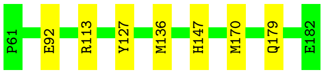
Chain AG:



- Molecule 63: 28S ribosomal protein S10, mitochondrial

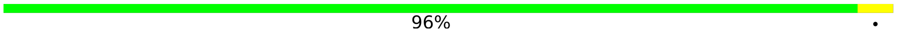
Chain AH:

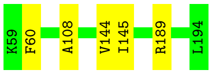




- Molecule 64: 28S ribosomal protein S11, mitochondrial

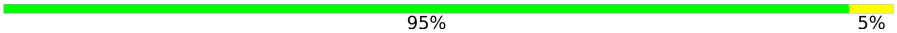
Chain AI:

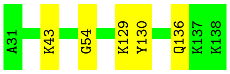




- Molecule 65: 28S ribosomal protein S12, mitochondrial

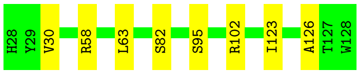
Chain AJ:





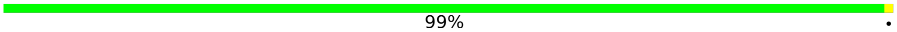
- Molecule 66: 28S ribosomal protein S14, mitochondrial

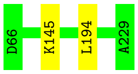
Chain AK:



- Molecule 67: 28S ribosomal protein S15, mitochondrial

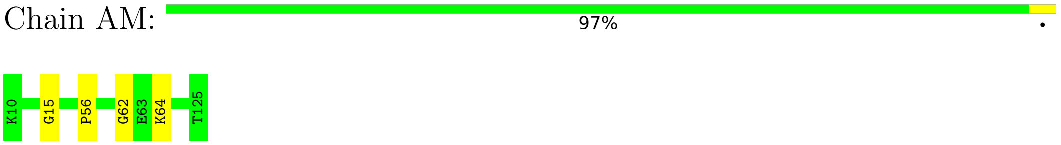
Chain AL:





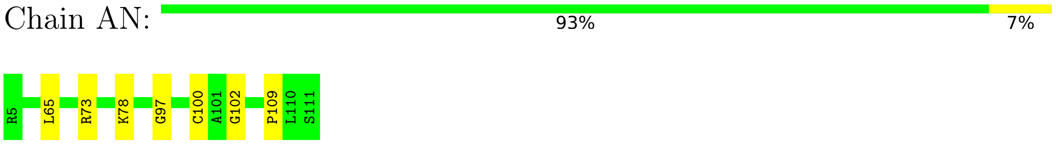
- Molecule 68: 28S ribosomal protein S16, mitochondrial

Chain AM:



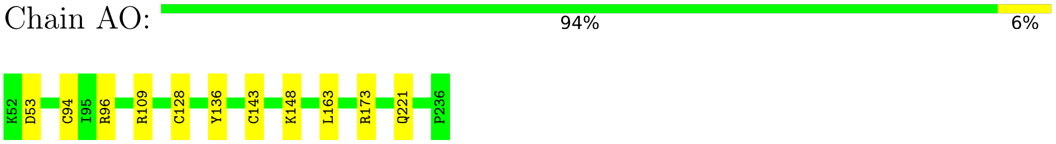
- Molecule 69: 28S ribosomal protein S17, mitochondrial

Chain AN:



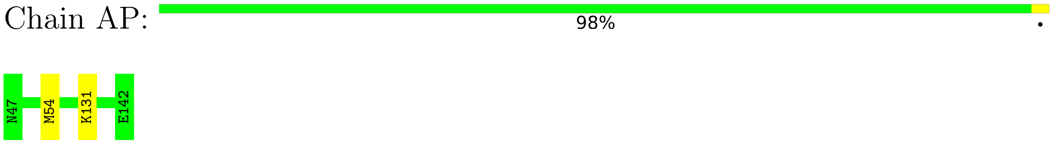
- Molecule 70: 28S ribosomal protein S18b, mitochondrial

Chain AO:



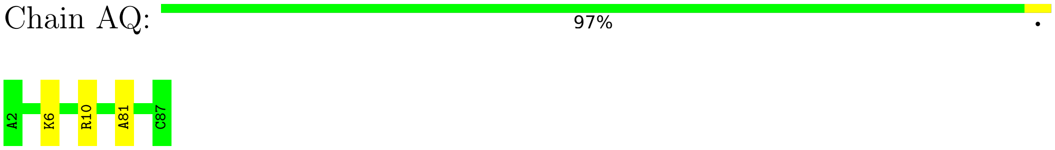
- Molecule 71: 28S ribosomal protein S18c, mitochondrial

Chain AP:



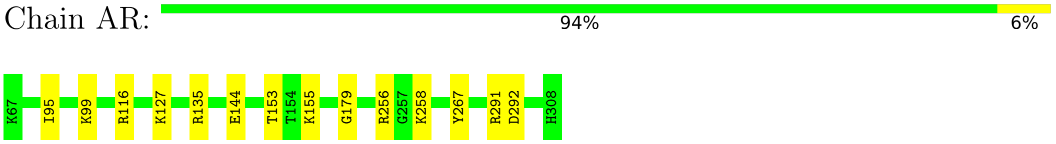
- Molecule 72: 28S ribosomal protein S21, mitochondrial

Chain AQ:



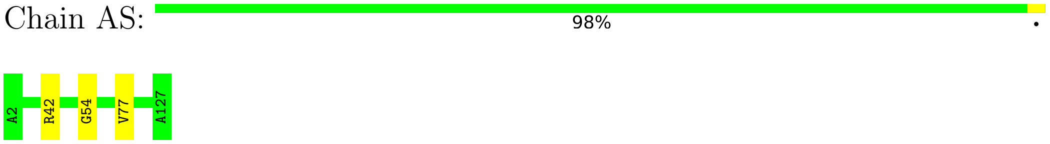
- Molecule 73: 28S ribosomal protein S22, mitochondrial

Chain AR:



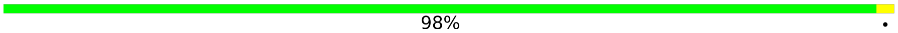
- Molecule 74: 28S ribosomal protein S23, mitochondrial

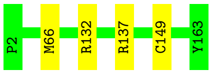
Chain AS:



- Molecule 75: 28S ribosomal protein S25, mitochondrial

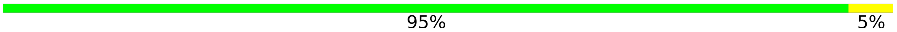
Chain AT:

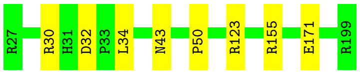




- Molecule 76: 28S ribosomal protein S26, mitochondrial

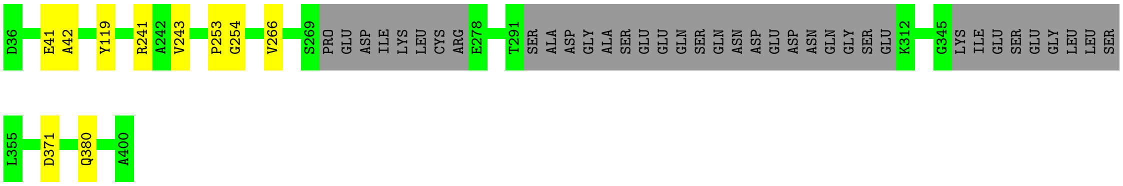
Chain AU:





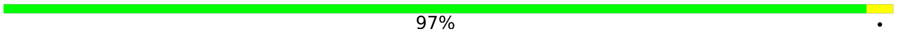
- Molecule 77: 28S ribosomal protein S27, mitochondrial

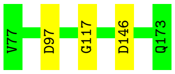
Chain AV:



- Molecule 78: 28S ribosomal protein S28, mitochondrial

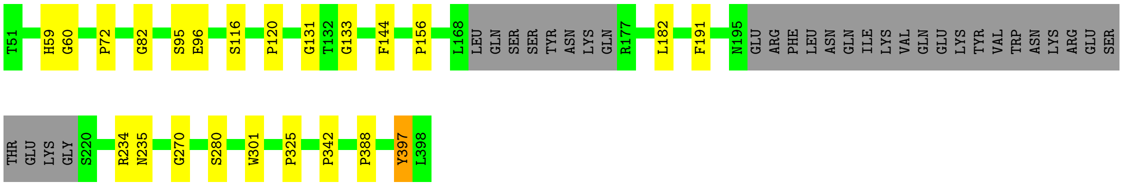
Chain AW:





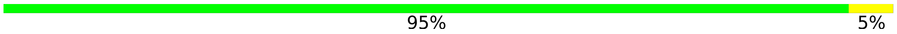
- Molecule 79: 28S ribosomal protein S29, mitochondrial

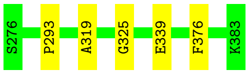
Chain AX:



- Molecule 80: 28S ribosomal protein S31, mitochondrial

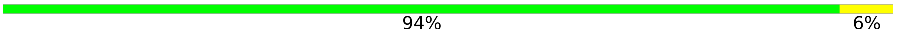
Chain AY:

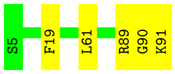




- Molecule 81: 28S ribosomal protein S33, mitochondrial

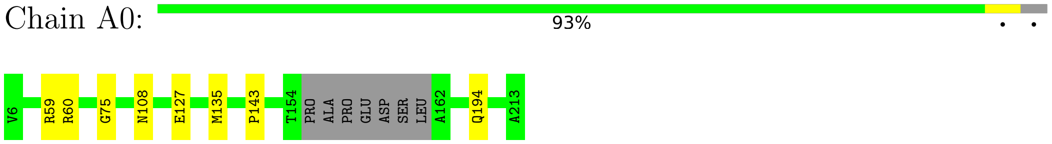
Chain AZ:





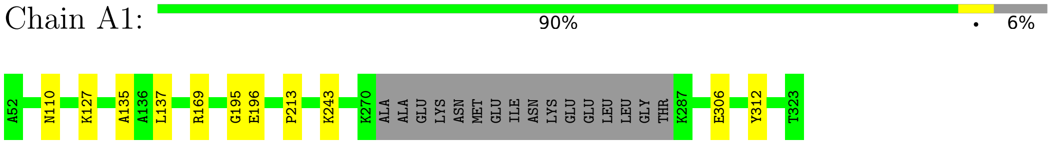
- Molecule 82: 28S ribosomal protein S34, mitochondrial

Chain A0:



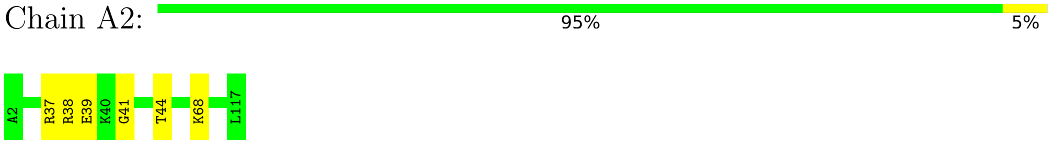
- Molecule 83: 28S ribosomal protein S35, mitochondrial

Chain A1:



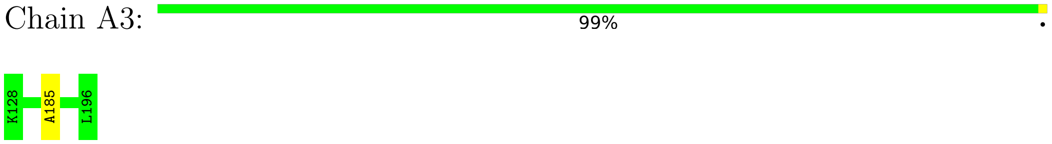
- Molecule 84: Coiled-coil-helix-coiled-coil-helix domain-containing protein 1

Chain A2:



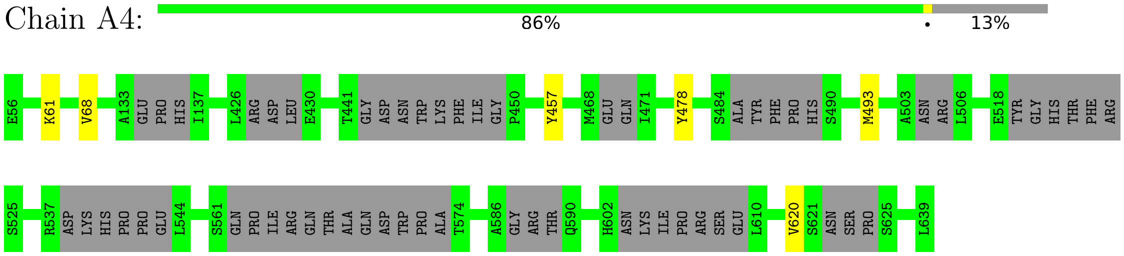
- Molecule 85: Aurora kinase A-interacting protein

Chain A3:



- Molecule 86: Pentatricopeptide repeat domain-containing protein 3, mitochondrial

Chain A4:



4 Experimental information ⓘ

Property	**Value**	**Source**
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	67116	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 $(e^-/\text{Å}^2)$	70	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

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	0.14	0/34967	0.71	4/54407 (0.0%)
2	B	0.13	0/1328	0.69	0/2056
3	D	0.23	0/1879	0.40	0/2527
4	E	0.23	0/2433	0.39	0/3299
5	F	0.23	0/2071	0.37	0/2817
6	H	0.22	0/798	0.40	0/1073
7	I	0.23	0/1308	0.37	0/1761
8	J	0.23	0/1077	0.38	0/1452
9	K	0.23	0/1495	0.36	0/2029
10	L	0.22	0/904	0.40	0/1218
11	M	0.24	0/2359	0.38	0/3185
12	N	0.23	0/1697	0.38	0/2281
13	O	0.22	0/1269	0.36	0/1708
14	P	0.23	0/1103	0.38	0/1491
15	Q	0.23	0/1863	0.38	0/2509
16	R	0.23	0/1174	0.35	0/1572
17	S	0.23	0/1276	0.40	0/1729
18	T	0.23	0/1402	0.36	0/1886
19	U	0.24	0/946	0.39	0/1283
20	V	0.22	0/1590	0.39	0/2151
21	W	0.23	0/916	0.39	0/1233
22	X	0.23	0/2090	0.35	0/2825
23	Y	0.23	0/1552	0.34	0/2079
24	Z	0.22	0/1003	0.38	0/1354
25	0	0.23	0/895	0.39	0/1201
26	1	0.23	0/438	0.41	0/583
27	2	0.23	0/382	0.40	0/507
28	3	0.23	0/852	0.38	0/1136
29	4	0.21	0/329	0.40	0/435
30	5	0.23	0/3154	0.39	0/4295
31	6	0.23	0/2722	0.37	0/3709
32	7	0.23	0/2207	0.36	0/2978

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
33	8	0.23	0/855	0.36	0/1152
34	9	0.24	0/896	0.37	0/1205
35	a	0.22	0/709	0.37	0/963
36	b	0.23	0/1202	0.39	0/1626
37	c	0.24	0/2264	0.35	0/3059
38	d	0.22	0/1385	0.38	0/1877
39	e	0.23	0/1797	0.37	0/2422
40	f	0.23	0/1055	0.39	0/1427
41	g	0.24	0/1102	0.38	0/1503
42	h	0.23	0/847	0.35	0/1150
43	i	0.23	0/849	0.35	0/1135
44	j	0.23	0/698	0.33	0/940
45	k	0.22	0/665	0.38	0/897
46	l	0.20	0/226	0.29	0/299
47	m	0.22	0/379	0.40	0/510
48	o	0.22	0/818	0.35	0/1097
49	p	0.22	0/1071	0.37	0/1433
50	q	0.23	0/1107	0.33	0/1498
51	r	0.22	0/1238	0.36	0/1676
52	s	0.23	0/3114	0.38	0/4225
54	u	0.06	0/46	0.62	0/69
55	z	0.23	0/1584	0.37	0/2126
56	AA	0.15	0/21926	0.74	7/34121 (0.0%)
57	AB	0.24	0/1811	0.37	0/2451
58	AC	0.23	0/1112	0.37	0/1505
59	AD	0.23	0/2607	0.38	0/3498
60	AE	0.23	0/989	0.39	0/1335
61	AF	0.23	0/1708	0.36	0/2291
62	AG	0.23	0/2570	0.37	0/3443
63	AH	0.22	0/1019	0.38	0/1379
64	AI	0.23	0/1031	0.40	0/1390
65	AJ	0.23	0/854	0.41	0/1148
66	AK	0.21	0/879	0.36	0/1182
67	AL	0.23	0/1406	0.34	0/1878
68	AM	0.23	0/941	0.37	0/1265
69	AN	0.23	0/864	0.40	0/1169
70	AO	0.23	0/1580	0.38	0/2150
71	AP	0.23	0/791	0.38	0/1062
72	AQ	0.22	0/747	0.37	0/995
73	AR	0.23	0/2050	0.36	0/2770
74	AS	0.23	0/1069	0.35	0/1441
75	AT	0.24	0/1361	0.38	0/1829
76	AU	0.23	0/1482	0.34	0/1987

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
77	AV	0.23	0/2758	0.34	0/3724
78	AW	0.23	0/778	0.40	0/1048
79	AX	0.23	0/2596	0.37	0/3519
80	AY	0.23	0/943	0.32	0/1274
81	AZ	0.23	0/757	0.36	0/1011
82	A0	0.22	0/1727	0.38	0/2338
83	A1	0.23	0/2121	0.37	0/2873
84	A2	0.23	0/939	0.37	0/1256
85	A3	0.22	0/621	0.35	0/820
86	A4	0.23	0/2137	0.31	0/2872
All	All	0.20	0/167560	0.53	11/238082 (0.0%)

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3206	C	C2-N1-C1'	6.09	125.50	118.80
1	A	1890	C	N3-C2-O2	-6.02	117.68	121.90
56	AA	984	C	N3-C2-O2	-5.93	117.75	121.90
56	AA	765	C	C2-N1-C1'	5.86	125.24	118.80
1	A	1786	C	N1-C2-O2	5.79	122.37	118.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

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	
3	D	234/236 (99%)	200 (86%)	29 (12%)	5 (2%)	7	39
4	E	296/304 (97%)	245 (83%)	43 (14%)	8 (3%)	5	35
5	F	248/250 (99%)	206 (83%)	38 (15%)	4 (2%)	9	44
6	H	93/95 (98%)	79 (85%)	11 (12%)	3 (3%)	4	32
7	I	154/168 (92%)	133 (86%)	17 (11%)	4 (3%)	5	35
8	J	138/140 (99%)	115 (83%)	19 (14%)	4 (3%)	4	33
9	K	175/177 (99%)	155 (89%)	16 (9%)	4 (2%)	6	38
10	L	113/115 (98%)	93 (82%)	17 (15%)	3 (3%)	5	35
11	M	285/287 (99%)	238 (84%)	40 (14%)	7 (2%)	5	36
12	N	203/205 (99%)	177 (87%)	25 (12%)	1 (0%)	29	67
13	O	150/152 (99%)	133 (89%)	16 (11%)	1 (1%)	22	60
14	P	129/138 (94%)	114 (88%)	14 (11%)	1 (1%)	19	57
15	Q	217/219 (99%)	180 (83%)	31 (14%)	6 (3%)	5	34
16	R	138/140 (99%)	124 (90%)	11 (8%)	3 (2%)	6	38
17	S	154/156 (99%)	134 (87%)	17 (11%)	3 (2%)	8	41
18	T	164/166 (99%)	145 (88%)	16 (10%)	3 (2%)	8	42
19	U	109/111 (98%)	90 (83%)	17 (16%)	2 (2%)	8	42
20	V	183/202 (91%)	151 (82%)	24 (13%)	8 (4%)	2	25
21	W	113/115 (98%)	97 (86%)	13 (12%)	3 (3%)	5	35
22	X	241/243 (99%)	207 (86%)	27 (11%)	7 (3%)	4	33
23	Y	174/176 (99%)	154 (88%)	17 (10%)	3 (2%)	9	43
24	Z	118/120 (98%)	106 (90%)	10 (8%)	2 (2%)	9	43
25	0	106/108 (98%)	91 (86%)	13 (12%)	2 (2%)	8	41
26	1	50/52 (96%)	41 (82%)	8 (16%)	1 (2%)	7	40
27	2	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
28	3	93/95 (98%)	85 (91%)	7 (8%)	1 (1%)	14	51
29	4	34/36 (94%)	29 (85%)	5 (15%)	0	100	100
30	5	368/392 (94%)	308 (84%)	49 (13%)	11 (3%)	4	33
31	6	313/354 (88%)	266 (85%)	39 (12%)	8 (3%)	5	35
32	7	258/287 (90%)	227 (88%)	26 (10%)	5 (2%)	8	41
33	8	97/99 (98%)	88 (91%)	7 (7%)	2 (2%)	7	39
34	9	105/123 (85%)	89 (85%)	10 (10%)	6 (6%)	1	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	a	78/108 (72%)	75 (96%)	3 (4%)	0	100	100
36	b	146/148 (99%)	126 (86%)	18 (12%)	2 (1%)	11	46
37	c	271/286 (95%)	240 (89%)	25 (9%)	6 (2%)	6	38
38	d	156/171 (91%)	127 (81%)	26 (17%)	3 (2%)	8	41
39	e	211/237 (89%)	177 (84%)	30 (14%)	4 (2%)	8	41
40	f	125/146 (86%)	106 (85%)	19 (15%)	0	100	100
41	g	127/129 (98%)	109 (86%)	12 (9%)	6 (5%)	2	24
42	h	96/103 (93%)	78 (81%)	16 (17%)	2 (2%)	7	39
43	i	95/97 (98%)	84 (88%)	9 (10%)	2 (2%)	7	39
44	j	83/85 (98%)	77 (93%)	4 (5%)	2 (2%)	6	37
45	k	82/84 (98%)	62 (76%)	15 (18%)	5 (6%)	1	20
46	l	21/23 (91%)	20 (95%)	1 (5%)	0	100	100
47	m	43/45 (96%)	33 (77%)	8 (19%)	2 (5%)	2	24
48	o	92/94 (98%)	80 (87%)	9 (10%)	3 (3%)	4	31
49	p	119/156 (76%)	109 (92%)	8 (7%)	2 (2%)	9	43
50	q	126/128 (98%)	120 (95%)	4 (3%)	2 (2%)	9	44
51	r	140/162 (86%)	119 (85%)	17 (12%)	4 (3%)	4	33
52	s	366/390 (94%)	318 (87%)	42 (12%)	6 (2%)	9	44
55	z	202/204 (99%)	176 (87%)	23 (11%)	3 (2%)	10	45
57	AB	215/217 (99%)	186 (86%)	27 (13%)	2 (1%)	17	54
58	AC	130/132 (98%)	101 (78%)	27 (21%)	2 (2%)	10	45
59	AD	316/343 (92%)	261 (83%)	41 (13%)	14 (4%)	2	25
60	AE	120/122 (98%)	96 (80%)	22 (18%)	2 (2%)	9	43
61	AF	197/208 (95%)	168 (85%)	26 (13%)	3 (2%)	10	45
62	AG	301/326 (92%)	248 (82%)	43 (14%)	10 (3%)	4	31
63	AH	120/122 (98%)	97 (81%)	20 (17%)	3 (2%)	5	36
64	AI	134/136 (98%)	102 (76%)	28 (21%)	4 (3%)	4	33
65	AJ	106/108 (98%)	88 (83%)	15 (14%)	3 (3%)	5	34
66	AK	99/101 (98%)	73 (74%)	20 (20%)	6 (6%)	1	20
67	AL	162/164 (99%)	146 (90%)	15 (9%)	1 (1%)	25	63
68	AM	114/116 (98%)	100 (88%)	10 (9%)	4 (4%)	3	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	AN	105/107 (98%)	89 (85%)	13 (12%)	3 (3%)	4	33
70	AO	183/185 (99%)	153 (84%)	27 (15%)	3 (2%)	9	44
71	AP	94/96 (98%)	77 (82%)	16 (17%)	1 (1%)	14	51
72	AQ	84/86 (98%)	72 (86%)	10 (12%)	2 (2%)	6	37
73	AR	240/242 (99%)	204 (85%)	27 (11%)	9 (4%)	3	28
74	AS	124/126 (98%)	105 (85%)	17 (14%)	2 (2%)	9	44
75	AT	160/162 (99%)	136 (85%)	21 (13%)	3 (2%)	8	41
76	AU	171/173 (99%)	154 (90%)	12 (7%)	5 (3%)	4	33
77	AV	320/365 (88%)	273 (85%)	40 (12%)	7 (2%)	6	38
78	AW	95/97 (98%)	76 (80%)	16 (17%)	3 (3%)	4	32
79	AX	310/348 (89%)	233 (75%)	56 (18%)	21 (7%)	1	18
80	AY	106/108 (98%)	92 (87%)	10 (9%)	4 (4%)	3	28
81	AZ	85/87 (98%)	75 (88%)	9 (11%)	1 (1%)	13	49
82	A0	197/208 (95%)	162 (82%)	30 (15%)	5 (2%)	5	36
83	A1	252/272 (93%)	197 (78%)	48 (19%)	7 (3%)	5	34
84	A2	114/116 (98%)	95 (83%)	16 (14%)	3 (3%)	5	35
85	A3	67/69 (97%)	61 (91%)	5 (8%)	1 (2%)	10	45
86	A4	237/474 (50%)	215 (91%)	20 (8%)	2 (1%)	19	57
All	All	12834/13719 (94%)	10913 (85%)	1610 (12%)	311 (2%)	9	37

5 of 311 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	M	134	ARG
20	V	101	THR
20	V	177	THR
30	5	381	LEU
30	5	383	TYR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	D	190/190 (100%)	185 (97%)	5 (3%)	46	68
4	E	255/259 (98%)	253 (99%)	2 (1%)	81	89
5	F	217/217 (100%)	210 (97%)	7 (3%)	39	63
6	H	86/86 (100%)	85 (99%)	1 (1%)	71	83
7	I	145/155 (94%)	145 (100%)	0	100	100
8	J	113/113 (100%)	112 (99%)	1 (1%)	78	87
9	K	155/155 (100%)	151 (97%)	4 (3%)	46	68
10	L	98/98 (100%)	95 (97%)	3 (3%)	40	64
11	M	245/245 (100%)	240 (98%)	5 (2%)	55	74
12	N	172/172 (100%)	170 (99%)	2 (1%)	71	83
13	O	133/133 (100%)	132 (99%)	1 (1%)	81	89
14	P	115/120 (96%)	113 (98%)	2 (2%)	60	78
15	Q	201/201 (100%)	200 (100%)	1 (0%)	88	93
16	R	118/118 (100%)	118 (100%)	0	100	100
17	S	141/141 (100%)	139 (99%)	2 (1%)	67	81
18	T	146/146 (100%)	145 (99%)	1 (1%)	84	90
19	U	99/99 (100%)	97 (98%)	2 (2%)	55	74
20	V	169/180 (94%)	164 (97%)	5 (3%)	41	64
21	W	93/93 (100%)	91 (98%)	2 (2%)	52	71
22	X	219/219 (100%)	212 (97%)	7 (3%)	39	63
23	Y	159/159 (100%)	158 (99%)	1 (1%)	86	91
24	Z	111/111 (100%)	109 (98%)	2 (2%)	59	77
25	0	97/97 (100%)	95 (98%)	2 (2%)	53	73
26	1	49/49 (100%)	47 (96%)	2 (4%)	30	58
27	2	40/40 (100%)	40 (100%)	0	100	100
28	3	88/88 (100%)	87 (99%)	1 (1%)	73	84
29	4	35/35 (100%)	35 (100%)	0	100	100
30	5	337/353 (96%)	333 (99%)	4 (1%)	71	83
31	6	266/313 (85%)	262 (98%)	4 (2%)	65	80
32	7	242/263 (92%)	237 (98%)	5 (2%)	53	73
33	8	91/91 (100%)	90 (99%)	1 (1%)	73	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	9	91/104 (88%)	91 (100%)	0	100	100
35	a	78/104 (75%)	75 (96%)	3 (4%)	33	59
36	b	130/130 (100%)	127 (98%)	3 (2%)	50	71
37	c	241/250 (96%)	241 (100%)	0	100	100
38	d	151/159 (95%)	149 (99%)	2 (1%)	69	82
39	e	188/207 (91%)	183 (97%)	5 (3%)	44	67
40	f	117/130 (90%)	116 (99%)	1 (1%)	78	87
41	g	119/119 (100%)	118 (99%)	1 (1%)	81	89
42	h	95/97 (98%)	95 (100%)	0	100	100
43	i	86/86 (100%)	82 (95%)	4 (5%)	26	55
44	j	68/68 (100%)	68 (100%)	0	100	100
45	k	74/74 (100%)	73 (99%)	1 (1%)	67	81
46	l	23/23 (100%)	23 (100%)	0	100	100
47	m	40/40 (100%)	39 (98%)	1 (2%)	47	69
48	o	80/80 (100%)	79 (99%)	1 (1%)	69	82
49	p	117/140 (84%)	115 (98%)	2 (2%)	60	78
50	q	110/110 (100%)	107 (97%)	3 (3%)	44	67
51	r	133/147 (90%)	131 (98%)	2 (2%)	65	80
52	s	326/344 (95%)	323 (99%)	3 (1%)	78	87
55	z	179/179 (100%)	176 (98%)	3 (2%)	60	78
57	AB	191/191 (100%)	190 (100%)	1 (0%)	88	93
58	AC	115/115 (100%)	113 (98%)	2 (2%)	60	78
59	AD	269/286 (94%)	263 (98%)	6 (2%)	52	71
60	AE	104/104 (100%)	102 (98%)	2 (2%)	57	75
61	AF	178/185 (96%)	176 (99%)	2 (1%)	73	84
62	AG	265/284 (93%)	256 (97%)	9 (3%)	37	62
63	AH	112/112 (100%)	108 (96%)	4 (4%)	35	61
64	AI	104/104 (100%)	103 (99%)	1 (1%)	76	86
65	AJ	93/93 (100%)	91 (98%)	2 (2%)	52	71
66	AK	91/91 (100%)	89 (98%)	2 (2%)	52	71
67	AL	152/152 (100%)	151 (99%)	1 (1%)	84	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	AM	95/95 (100%)	95 (100%)	0	100	100
69	AN	93/93 (100%)	89 (96%)	4 (4%)	29	57
70	AO	166/166 (100%)	158 (95%)	8 (5%)	25	54
71	AP	87/87 (100%)	86 (99%)	1 (1%)	73	84
72	AQ	78/78 (100%)	77 (99%)	1 (1%)	69	82
73	AR	224/224 (100%)	219 (98%)	5 (2%)	52	71
74	AS	109/109 (100%)	108 (99%)	1 (1%)	78	87
75	AT	150/150 (100%)	149 (99%)	1 (1%)	84	90
76	AU	149/149 (100%)	146 (98%)	3 (2%)	55	74
77	AV	295/327 (90%)	292 (99%)	3 (1%)	76	86
78	AW	84/84 (100%)	84 (100%)	0	100	100
79	AX	275/308 (89%)	272 (99%)	3 (1%)	73	84
80	AY	99/99 (100%)	98 (99%)	1 (1%)	76	86
81	AZ	80/80 (100%)	76 (95%)	4 (5%)	24	53
82	A0	176/182 (97%)	173 (98%)	3 (2%)	60	78
83	A1	237/250 (95%)	233 (98%)	4 (2%)	60	78
84	A2	99/99 (100%)	96 (97%)	3 (3%)	41	64
85	A3	63/64 (98%)	63 (100%)	0	100	100
86	A4	226/291 (78%)	222 (98%)	4 (2%)	59	77
All	All	11530/11982 (96%)	11339 (98%)	191 (2%)	62	78

5 of 191 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
59	AD	234	LYS
69	AN	73	ARG
60	AE	15	ARG
62	AG	312	GLN
70	AO	143	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
57	AB	226	ASN

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Mol	Chain	Res	Type
72	AQ	53	GLN
59	AD	341	ASN
61	AF	147	GLN
74	AS	91	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1460/1472 (99%)	373 (25%)	46 (3%)
2	B	52/56 (92%)	12 (23%)	2 (3%)
54	u	1/2 (50%)	0	0
56	AA	914/923 (99%)	301 (32%)	22 (2%)
All	All	2427/2453 (98%)	686 (28%)	70 (2%)

5 of 686 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	1672	C
1	A	1674	A
1	A	1679	U
1	A	1680	A
1	A	1685	C

5 of 70 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
56	AA	1021	U
56	AA	1099	C
56	AA	1429	C
1	A	2442	U
1	A	2387	U

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

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 ⓘ

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
86	A4	13
56	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	35.95
1	AA	955:A	O3'	965:C	P	34.65
1	A	2760:A	O3'	2792:A	P	26.71
1	A	2881:C	O3'	2889:C	P	26.07
1	A	1760:G	O3'	1766:U	P	25.62

6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-0514. 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 ⓘ

This section was not generated.

6.2 Central slices ⓘ

This section was not generated.

6.3 Largest variance slices ⓘ

This section was not generated.

6.4 Orthogonal surface views ⓘ

This section was not generated.

6.5 Mask visualisation ⓘ

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit (i)

This section was not generated.