



## wwPDB EM Validation Summary Report ⓘ

Nov 11, 2023 – 03:11 pm GMT

PDB ID : 6ZM5  
EMDB ID : EMD-11278  
Title : Human mitochondrial ribosome in complex with OXA1L, mRNA, A/A tRNA,  
P/P tRNA and nascent polypeptide  
Authors : Itoh, Y.; Andrell, J.; Amunts, A.  
Deposited on : 2020-07-01  
Resolution : 2.89 Å (reported)  
Based on initial models : 3J9M, 6RW4, 5OOL

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev70  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

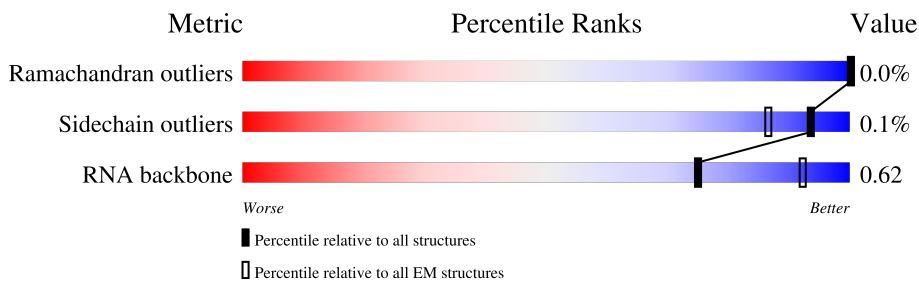
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.89 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.




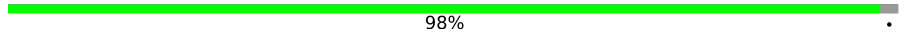




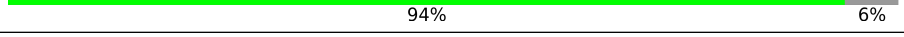

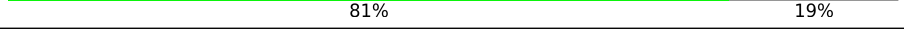

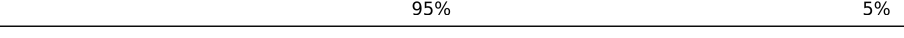
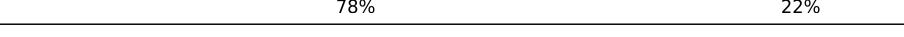
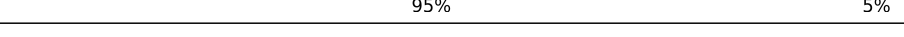
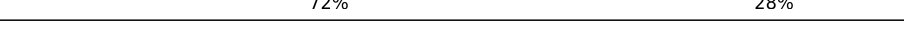


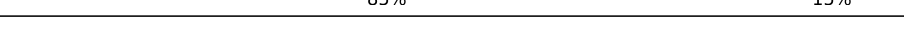

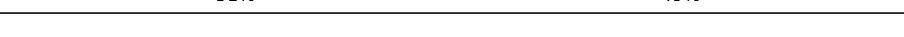






Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	1561	84% 14% .
2	B	72	81% 19%
3	D	305	78% 22%
4	E	348	88% 12%
5	F	311	81% 19%
6	H	267	36% 64%
7	I	261	81% 19%
8	J	192	91% 9%
9	K	177	100%

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Mol	Chain	Length	Quality of chain
10	L	145	 79% 21%
11	M	296	 98%
12	N	251	 88% 12%
13	O	175	 88% 12%
14	P	180	 80% 20%
15	Q	292	 82% 18%
16	R	149	 94% 6%
17	S	205	 79% 21%
18	T	206	 81% 19%
19	U	152	 88% 12%
20	V	216	 95% 5%
21	W	148	 78% 22%
22	X	256	 95% 5%
23	Y	250	 72% 28%
24	Z	161	 76% 24%
25	0	188	 58% 41%
26	1	65	 85% 15%
27	2	92	 50% 50%
28	3	188	 51% 49%
29	4	103	 37% 63%
30	5	423	 93% 7%
31	6	380	 93% 7%
32	7	338	 87% 13%
33	8	206	 76% 24%
34	9	137	 91% 9%

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Mol	Chain	Length	Quality of chain	
35	a	142	70%	30%
36	b	214	70%	30%
37	c	332	86%	14%
38	d	306	79%	21%
39	e	279	82%	18%
40	f	212	74%	26%
41	g	166	81%	19%
42	h	158	70%	30%
43	i	128	76%	24%
44	j	123	76%	24%
45	k	111	91%	9%
46	l	138	59%	41%
47	m	128	68%	32%
48	o	102	92%	8%
49	p	206	71%	29%
50	q	222	73%	27%
51	r	196	82%	17%
52	s	439	88%	12%
53	t1	198	23%	77%
53	t2	198	16%	84%
53	t3	198	16%	84%
53	t4	198	16%	84%
53	t5	198	16%	84%
53	t6	198	16%	84%
54	AA	954	87%	13%

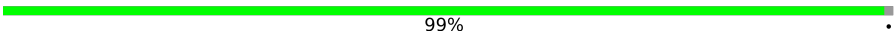

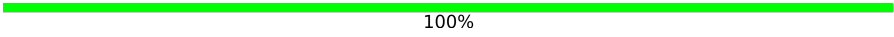



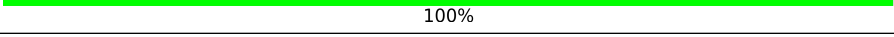

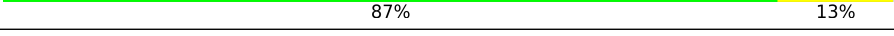
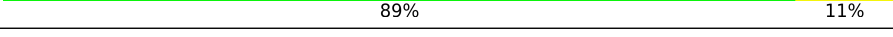
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Mol	Chain	Length	Quality of chain	
55	AB	296	76%	24%
56	AC	167	79%	21%
57	AD	430	80%	20%
58	AE	125	98%	.
59	AF	242	86%	14%
60	AG	396	79%	21%
61	AH	201	69%	30%
62	AI	194	70%	29%
63	AJ	138	78%	22%
64	AK	128	79%	21%
65	AL	257	68%	32%
66	AM	137	87%	13%
67	AN	130	85%	15%
68	AO	258	75%	25%
69	AP	142	68%	32%
70	AQ	86	100%	
71	AR	360	82%	18%
72	AS	190	71%	29%
73	AT	173	97%	.
74	AU	205	86%	14%
75	AV	414	87%	13%
76	AW	187	53%	47%
77	AX	398	88%	12%
78	AY	395	38%	62%
79	AZ	106	94%	6%

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Mol	Chain	Length	Quality of chain
80	A0	218	 99%
81	A1	323	 85% 15%
82	A2	117	 100%
83	A3	199	 35% 65%
84	A4	689	 85% 15%
85	u	435	 12% 88%
86	v	32	 100%
87	w	68	 75% 25%
88	x	70	 87% 13%
89	y	19	 89% 11%

## 2 Entry composition [i](#)

There are 97 unique types of molecules in this entry. The entry contains 326964 atoms, of which 149830 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 mitochondrial rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
1	A	1534	49092	14611	16532	5870	10545	1534	0	0

- Molecule 2 is a RNA chain called mitochondrial tRNAVal.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
2	B	72	2298	683	776	269	498	72	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	238	3780	1157	1921	376	317	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	305	4823	1545	2417	418	432	11	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	252	4097	1305	2066	370	350	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	97	1649	508	847	155	139	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	212	3481	1088	1786	304	292	11	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	175	2739	847	1409	237	244	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	2909	936	1454	259	253	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	1832	559	942	171	155	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	291	4723	1483	2396	430	408	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	222	3605	1143	1819	326	307	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	154	2554	792	1295	241	219	7	0	0

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



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

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
15	Q	238	Total	C	H	N	O	S	0	0
			4002	1268	2023	352	350	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
			2369	732	1215	231	187	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
17	S	161	Total	C	H	N	O	S	0	0
			2659	835	1366	227	227	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
			2780	875	1411	254	233	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
19	U	133	Total	C	H	N	O	S	0	0
			2215	702	1108	214	189	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
20	V	205	Total	C	H	N	O	S	0	0
			3364	1068	1688	298	302	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	116	1841	577	937	171	153	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	244	4105	1322	2061	352	365	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	181	3154	995	1598	298	259	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	122	2041	636	1045	186	171	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	110	1815	554	917	176	162	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	55	954	290	499	87	76	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	784	233	407	83	60	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	1716	539	884	162	128	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	38	704	217	362	72	49	4	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	394	6418	2073	3208	560	566	11	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	354	5792	1881	2844	525	533	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	294	4789	1529	2399	405	438	18	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	157	2696	844	1369	235	246	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	124	1985	644	988	170	181	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	100	1652	529	812	152	154	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	150	2392	744	1196	231	218	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	286	4621	1470	2322	397	423	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	242	3970	1275	1982	343	358	12	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	228	3699	1174	1851	326	342	6	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	157	2523	799	1271	207	242	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	134	2210	719	1097	193	199	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	110	1777	568	882	156	168	3	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	1687	532	859	165	127	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	94	1492	463	747	144	136	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	101	1558	479	784	148	142	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			S
46	l	82	1363	437	675	120	128	3	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	87	1515	466	761	152	134	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	1605	501	807	165	129	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	147	2431	748	1226	228	225	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	161	2678	841	1328	260	244	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	162	2671	839	1349	252	223	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	386	6298	2023	3143	559	559	14	0	0

- Molecule 53 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
53	t1	46	732	228	378	56	70	0	0
53	t2	32	541	168	284	40	49	0	0
53	t3	32	541	168	284	40	49	0	0
53	t4	31	520	159	275	39	47	0	0
53	t5	31	520	159	275	39	47	0	0
53	t6	31	520	159	275	39	47	0	0

- Molecule 54 is a RNA chain called 12S mitochondrial rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
54	AA	954	30542	9081	10289	3647	6571	954	0	0

- Molecule 55 is a protein called 28S ribosomal protein S2, mitochondrial.

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

- Molecule 56 is a protein called 28S ribosomal protein S24, mitochondrial.

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

- Molecule 57 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
57	AD	343	5536	1713	2805	518	487	13	0	0

- Molecule 58 is a protein called 28S ribosomal protein S6, mitochondrial.

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

- Molecule 59 is a protein called 28S ribosomal protein S7, mitochondrial.

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

- Molecule 60 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
60	AG	312	5126	1632	2558	455	467	14	0	0

- Molecule 61 is a protein called 28S ribosomal protein S10, mitochondrial.

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

- Molecule 62 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
62	AI	137	2076	641	1058	192	181	4	0	0

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 63 is a protein called 28S ribosomal protein S12, mitochondrial.

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

- Molecule 64 is a protein called 28S ribosomal protein S14, mitochondrial.

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

- Molecule 65 is a protein called 28S ribosomal protein S15, mitochondrial.

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

- Molecule 66 is a protein called 28S ribosomal protein S16, mitochondrial.

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

- Molecule 67 is a protein called 28S ribosomal protein S17, mitochondrial.

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

- Molecule 68 is a protein called 28S ribosomal protein S18b, mitochondrial.



Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
68	AO	193	3149	1014	1557	294	277	7	0	0

- Molecule 69 is a protein called 28S ribosomal protein S18c, mitochondrial.

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

- Molecule 70 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
70	AQ	86	1502	460	758	150	126	8	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AQ	50	ARG	CYS	variant	UNP P82921

- Molecule 71 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
71	AR	295	4838	1533	2429	413	455	8	0	0

- Molecule 72 is a protein called 28S ribosomal protein S23, mitochondrial.

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

- Molecule 73 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
73	AT	168	2765	877	1394	239	244	11	0	0

- Molecule 74 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
74	AU	176	2988	916	1500	301	267	4	0	0

- Molecule 75 is a protein called 28S ribosomal protein S27, mitochondrial.

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

- Molecule 76 is a protein called 28S ribosomal protein S28, mitochondrial.

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

- Molecule 77 is a protein called 28S ribosomal protein S29, mitochondrial.

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

- Molecule 78 is a protein called 28S ribosomal protein S31, mitochondrial.

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

- Molecule 79 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
79	AZ	100	1699	534	860	153	148	4	0	0

- Molecule 80 is a protein called 28S ribosomal protein S34, mitochondrial.

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

- Molecule 81 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
81	A1	276	4507	1419	2269	381	427	11	0	0

- Molecule 82 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
82	A2	117	1904	579	969	182	166	8	0	0

- Molecule 83 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
83	A3	70	1325	401	700	134	89	1	0	0

- Molecule 84 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
84	A4	588	9536	3053	4768	808	879	28	0	0

- Molecule 85 is a protein called Mitochondrial inner membrane protein OXA1L.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
85	u	51	863	265	432	87	77	2	0	0

- Molecule 86 is a protein called Nascent polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
86	v	32	320	96	160	32	32	0	0

- Molecule 87 is a RNA chain called A-site tRNA with aminoacylation.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
87	w	68	2163	647	725	251	472	68	0	0

- Molecule 88 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
88	x	70	2234	665	751	261	487	70	0	0

- Molecule 89 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
89	y	19	598	179	199	63	138	19	0	0

- Molecule 90 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
90	A	128	Total	Mg	0
			128	128	
90	D	3	Total	Mg	0
			3	3	
90	E	1	Total	Mg	0
			1	1	
90	g	1	Total	Mg	0
			1	1	
90	AA	53	Total	Mg	0
			53	53	
90	AB	1	Total	Mg	0
			1	1	
90	AX	1	Total	Mg	0
			1	1	
90	A3	1	Total	Mg	0
			1	1	

- Molecule 91 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
91	A	30	Total	K	0
			30	30	
91	M	1	Total	K	0
			1	1	
91	N	1	Total	K	0
			1	1	
91	P	1	Total	K	0
			1	1	
91	i	1	Total	K	0
			1	1	

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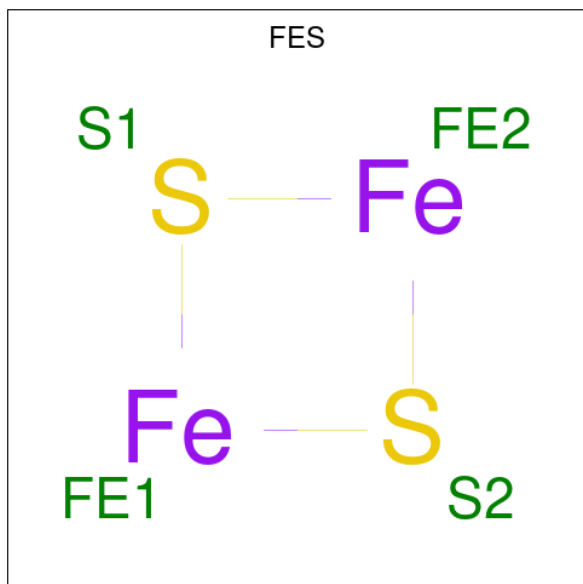
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Mol	Chain	Residues	Atoms	AltConf
91	o	1	Total K 1 1	0
91	AA	9	Total K 9 9	0

- Molecule 92 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
92	0	1	Total Zn 1 1	0
92	4	1	Total Zn 1 1	0
92	AO	1	Total Zn 1 1	0

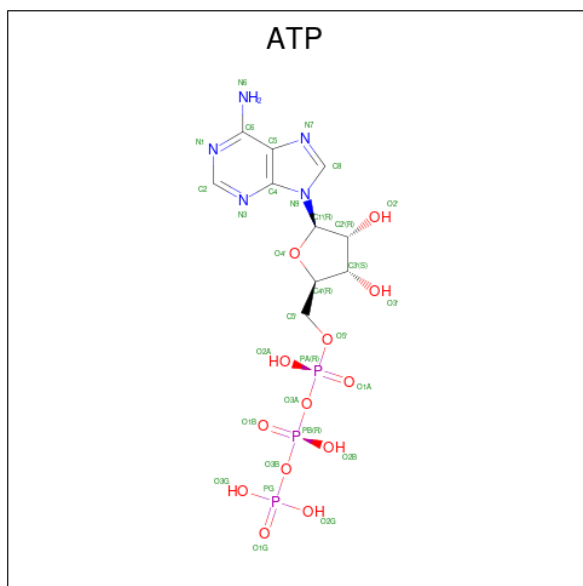
- Molecule 93 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe<sub>2</sub>S<sub>2</sub>).



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

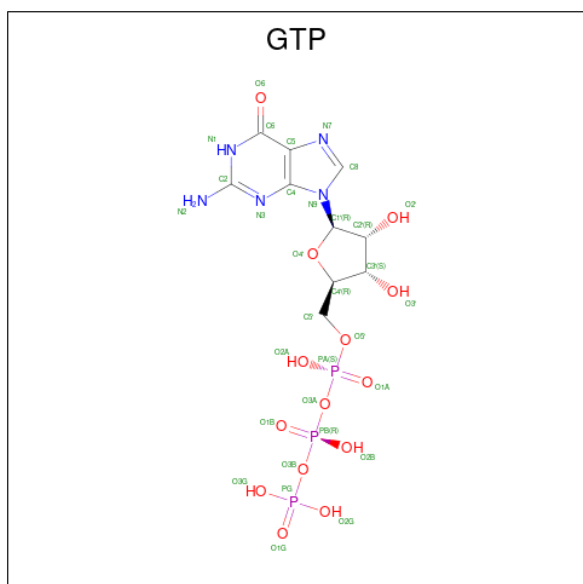
- Molecule 94 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula:

$C_{10}H_{16}N_5O_{13}P_3$ ).



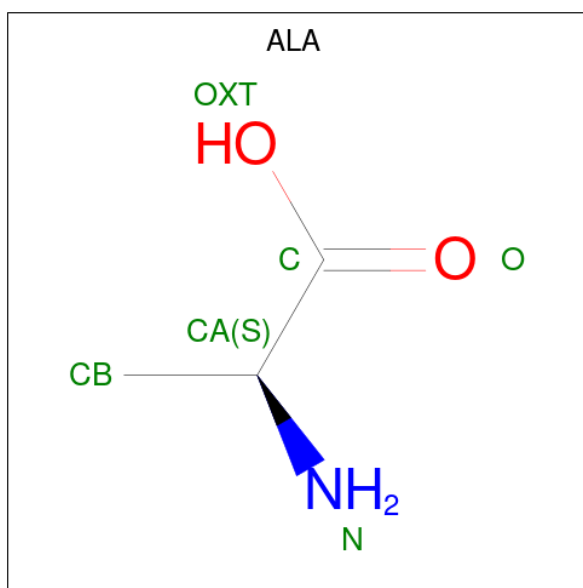
Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
94	AX	1	43	10	12	5	13	3	0

- Molecule 95 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ).



Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
95	AX	1	44	10	12	5	14	3	0

- Molecule 96 is ALANINE (three-letter code: ALA) (formula: C<sub>3</sub>H<sub>7</sub>NO<sub>2</sub>).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	N	O	
96	w	1	12	3	7	1	1	0

- Molecule 97 is water.

Mol	Chain	Residues	Atoms		AltConf
			Total	O	
97	A	340	340	340	0
97	B	1	1	1	0
97	D	5	5	5	0
97	E	4	4	4	0
97	F	6	6	6	0
97	K	3	3	3	0
97	L	1	1	1	0
97	M	7	7	7	0
97	N	1	1	1	0
97	O	2	2	2	0

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Mol	Chain	Residues	Atoms		AltConf
97	Q	1	Total 1	O 1	0
97	R	3	Total 3	O 3	0
97	S	1	Total 1	O 1	0
97	T	1	Total 1	O 1	0
97	U	1	Total 1	O 1	0
97	W	2	Total 2	O 2	0
97	6	1	Total 1	O 1	0
97	c	1	Total 1	O 1	0
97	f	1	Total 1	O 1	0
97	i	1	Total 1	O 1	0
97	o	2	Total 2	O 2	0
97	r	1	Total 1	O 1	0
97	s	2	Total 2	O 2	0
97	AA	69	Total 69	O 69	0
97	AC	1	Total 1	O 1	0
97	AG	1	Total 1	O 1	0
97	AH	3	Total 3	O 3	0
97	AK	2	Total 2	O 2	0
97	AX	2	Total 2	O 2	0
97	A0	1	Total 1	O 1	0
97	A3	3	Total 3	O 3	0

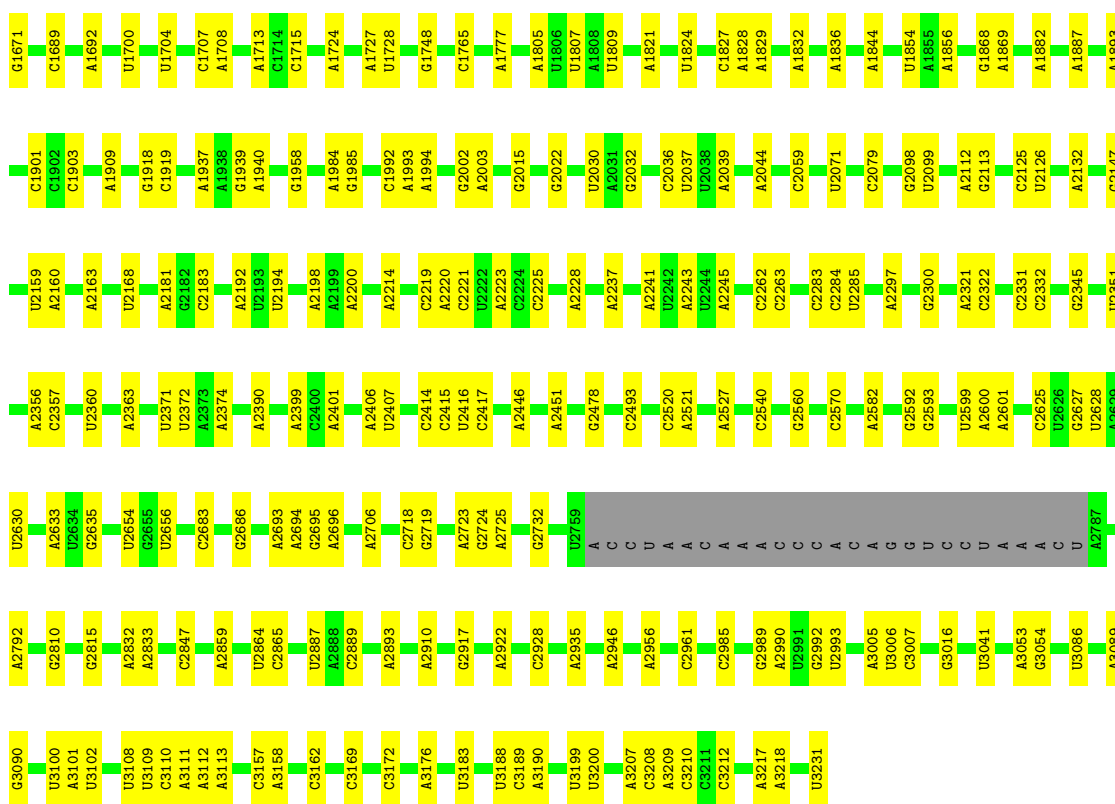


### 3 Residue-property plots [i](#)


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

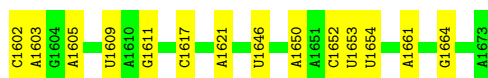
- Molecule 1: 16S mitochondrial rRNA

Chain A:  84% 14%




- Molecule 2: mitochondrial tRNA<sup>Val</sup>

Chain B:  81% 19%



- Molecule 3: 39S ribosomal protein L2, mitochondrial


Chain D:  78% 22%

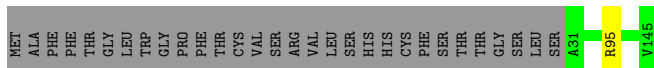


Chain K:  100%

There are no outlier residues recorded for this chain.

- Molecule 10: 39S ribosomal protein L14, mitochondrial

Chain L:  79% 21%




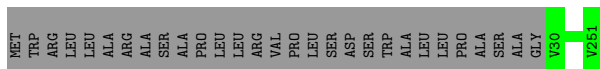
- Molecule 11: 39S ribosomal protein L15, mitochondrial

Chain M:  98%




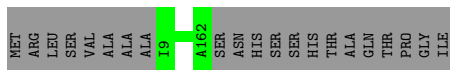
- Molecule 12: 39S ribosomal protein L16, mitochondrial

Chain N:  88% 12%




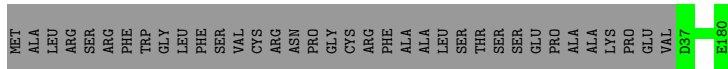
- Molecule 13: 39S ribosomal protein L17, mitochondrial

Chain O:  88% 12%




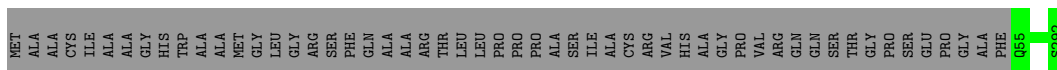
- Molecule 14: 39S ribosomal protein L18, mitochondrial

Chain P:  80% 20%



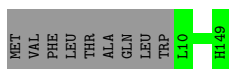
- Molecule 15: 39S ribosomal protein L19, mitochondrial

Chain Q:  82% 18%

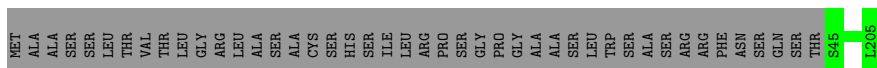
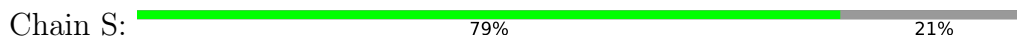


- Molecule 16: 39S ribosomal protein L20, mitochondrial

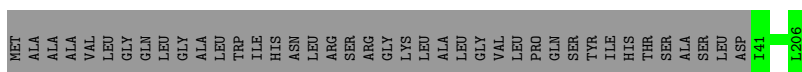
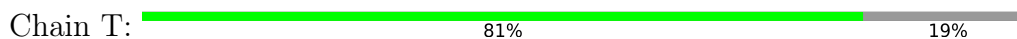
Chain R:  94% 6%



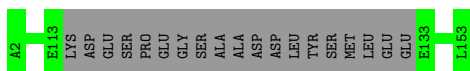
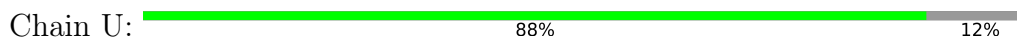
- Molecule 17: 39S ribosomal protein L21, mitochondrial



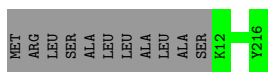
- Molecule 18: 39S ribosomal protein L22, mitochondrial



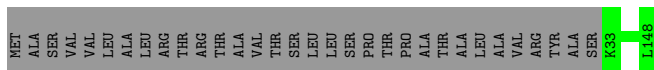
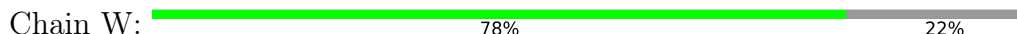
- Molecule 19: 39S ribosomal protein L23, mitochondrial



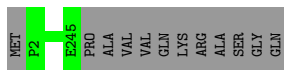
- Molecule 20: 39S ribosomal protein L24, mitochondrial



- Molecule 21: 39S ribosomal protein L27, mitochondrial



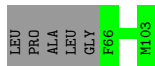
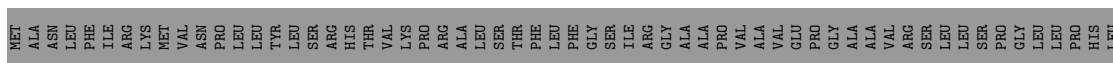
- Molecule 22: 39S ribosomal protein L28, mitochondrial



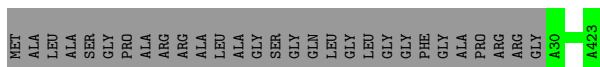
- Molecule 23: 39S ribosomal protein L47, mitochondrial



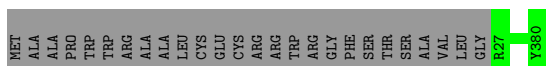




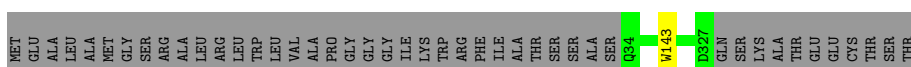
- Molecule 30: 39S ribosomal protein L37, mitochondrial



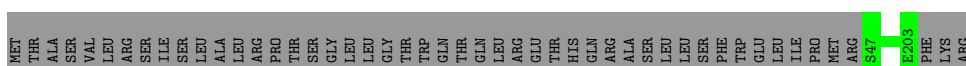
- Molecule 31: 39S ribosomal protein L38, mitochondrial



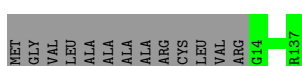
- Molecule 32: 39S ribosomal protein L39, mitochondrial



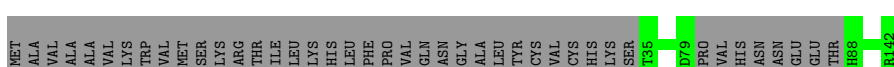
- Molecule 33: 39S ribosomal protein L40, mitochondrial



- Molecule 34: 39S ribosomal protein L41, mitochondrial



- Molecule 35: 39S ribosomal protein L42, mitochondrial



- Molecule 36: 39S ribosomal protein L43, mitochondrial



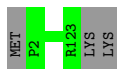




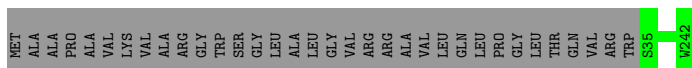
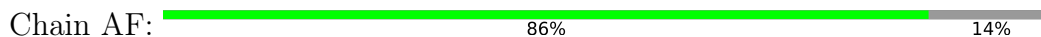




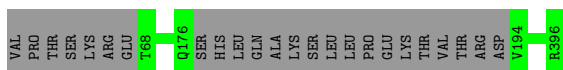
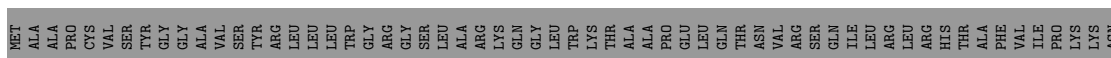
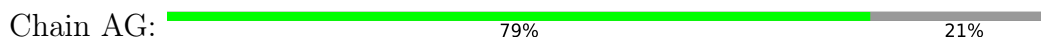




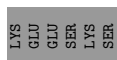
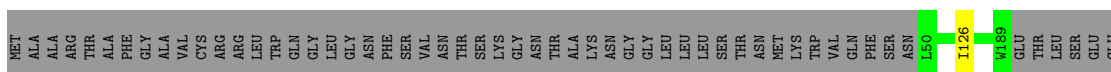
- Molecule 59: 28S ribosomal protein S7, mitochondrial



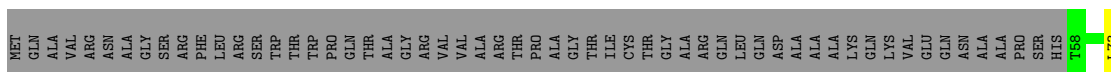
- Molecule 60: 28S ribosomal protein S9, mitochondrial



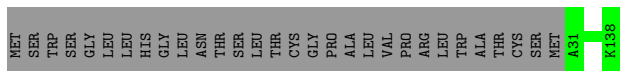
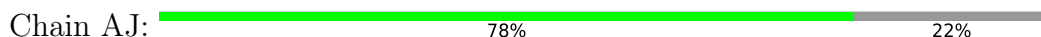
- Molecule 61: 28S ribosomal protein S10, mitochondrial



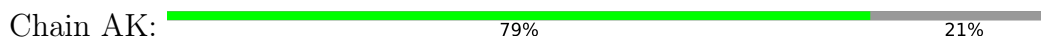
- Molecule 62: 28S ribosomal protein S11, mitochondrial



- Molecule 63: 28S ribosomal protein S12, mitochondrial



- Molecule 64: 28S ribosomal protein S14, mitochondrial



MET ALA ALA PHE MET MET LEU LEU LEU LEU ARG ARG THR PHE LYS GLN MET MET VAL PRO SER SER ALA ALA SER GLY GLN VAL ARG SER H28 W128

- Molecule 65: 28S ribosomal protein S15, mitochondrial

Chain AL: 68% 32%

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

SER ARG L63 Q236 ALA LYS ARG ARG ASN PRO ASP SER SER PRO ALA LYS ALA ILE PRO LYS THR THR LYS ASP SER SER GLN

- Molecule 66: 28S ribosomal protein S16, mitochondrial

Chain AM: 87% 13%

MET VAL HIS LEU THR THR LEU LEU CYS K10 E128 ALA THR ASP THR GLU ALA THR GLU THR

- Molecule 67: 28S ribosomal protein S17, mitochondrial

Chain AN: 85% 15%

MET SER VAL V4 E113 THR THR GLN LEU SER LYS ASN LEU MET LEU SER LEU LEU ILE SER SER SER ALA GLN

- Molecule 68: 28S ribosomal protein S18b, mitochondrial

Chain AO: 75% 25%

MET ALA ALA SER VAL ASN THR VAL ARG ARG LEU PRO MET LEU SER PHE ARG GLY HIS VAL GLN VAL PRO LEU GLN THR LEU THR CYS THR LYS ALA PRO SER GLY ASP SER LEU SER SER VAL P47 P239 PRO ARG THR PRO ALA ALA ALA SER SER THR GLY

GLN THR GLY PRO GLN SER ALA LEU

- Molecule 69: 28S ribosomal protein S18c, mitochondrial

Chain AP: 68% 32%


MET ALA VAL VAL ALA VAL CYS GLY LEU LEU ARG LYS LEU THR HIS VAL THR ALA VAL SER LEU HIS HIS THR VAL TRP ARG ARG GLY CYS SER GLN GLN VAL S46 E142

- Molecule 70: 28S ribosomal protein S21, mitochondrial

Chain AQ: 100%

There are no outlier residues recorded for this chain.

- Molecule 71: 28S ribosomal protein S22, mitochondrial

Chain AR:  82% 18%

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

GLY SER PRO E64 A358 ALA SER

- Molecule 72: 28S ribosomal protein S23, mitochondrial

Chain AS:  71% 29%


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

- Molecule 73: 28S ribosomal protein S25, mitochondrial

Chain AT:  97%


MET LEU ASP A169 ALA GLN ASP P2

- Molecule 74: 28S ribosomal protein S26, mitochondrial

Chain AU:  86% 14%

MET LEU ARG ALA LEU SER ARG LEU GLY ALA MET LEU LEU ARG ARG VAL VAL PRO ALA LEU PRO GLN LEU VAL LEU PRO PRO ALA ALA GLY ARG R27 R202 ARG ASP SER

- Molecule 75: 28S ribosomal protein S27, mitochondrial

Chain AV:  87% 13%

MET ALA ALA LEU CYS VAL ARG ARG GLY MET LEU LEU ARG ARG VAL VAL PRO GLN LEU LEU SER PRO PRO GLY LYS ARG TYR L29 Y226 A295 ASP GLY ALA SER SER GLU GLN SER SER ASN LYS ASP GLU ASP ASN GLN GLY SER E311 Q407 LYS ALA ALA LYS ALA


- Molecule 76: 28S ribosomal protein S28, mitochondrial

Chain AW:  53% 47%

MET ALA ALA LEU CYS THR ARG ALA VAL ALA ALA GLU SER HIS PHE ARG VAL PHE LEU PHE ARG ARG PRO PHE ARG VAL THR GLU SER GLY SER GLU SER SER ASN LYS GLU PRO LYS THR LYS ARG ALA GLY GLE PHE ALA SER SER ALA LEU GLU ARG HIS SER

GLU LEU GLN LYS VAL GLU PRO GLN LYS GLY SER PRO LYS N76 S175 LYS ASP SER ARG SER LYS GLU GLU HIS HIS LYS

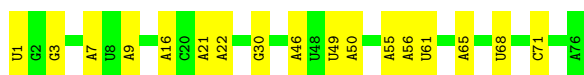
- Molecule 77: 28S ribosomal protein S29, mitochondrial

Chain AX:  88% 12%

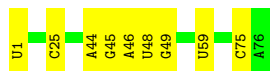
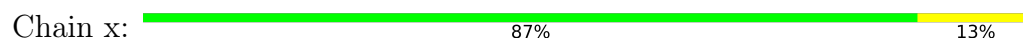




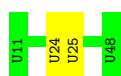
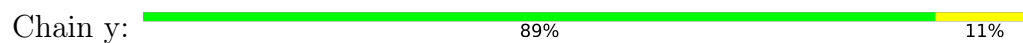




- Molecule 88: P-site tRNA



- Molecule 89: mRNA



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	30744	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	3600	Depositor
Magnification	165000	Depositor
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: ATP, IAS, THC, GTP, AYA, SAC, ZN, MG, K, FES

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.30	1/36431 (0.0%)	0.69	0/56711
2	B	0.36	1/1700 (0.1%)	0.67	0/2641
3	D	0.27	0/1896	0.44	0/2549
4	E	0.27	0/2475	0.42	0/3355
5	F	0.27	0/2090	0.41	0/2842
6	H	0.26	0/816	0.41	0/1097
7	I	0.28	0/1731	0.41	0/2345
8	J	0.28	0/1348	0.39	0/1813
9	K	0.29	0/1490	0.40	0/2021
10	L	0.27	0/905	0.45	0/1218
11	M	0.28	0/2381	0.43	0/3212
12	N	0.29	0/1833	0.43	0/2468
13	O	0.26	0/1283	0.40	0/1727
14	P	0.32	0/1199	0.42	0/1623
15	Q	0.26	0/2027	0.41	0/2734
16	R	0.28	0/1175	0.40	0/1572
17	S	0.27	0/1320	0.45	0/1789
18	T	0.29	0/1403	0.41	0/1886
19	U	0.28	0/1127	0.42	0/1523
20	V	0.25	0/1721	0.41	0/2333
21	W	0.36	0/926	0.44	0/1244
22	X	0.26	0/2099	0.38	0/2837
23	Y	0.26	0/1593	0.38	0/2136
24	Z	0.26	0/1021	0.42	0/1378
25	0	0.27	0/913	0.41	0/1224
26	1	0.26	0/460	0.45	0/610
27	2	0.27	0/383	0.41	0/507
28	3	0.29	0/853	0.43	0/1136
29	4	0.31	0/350	0.44	0/461
30	5	0.26	0/3305	0.41	0/4502
31	6	0.32	0/3043	0.43	0/4140
32	7	0.25	0/2447	0.38	0/3310

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	8	0.27	0/1354	0.37	0/1819
34	9	0.28	0/1025	0.40	0/1379
35	a	0.26	0/866	0.43	0/1174
36	b	0.28	0/1211	0.43	0/1639
37	c	0.26	0/2347	0.39	0/3171
38	d	0.25	0/2043	0.40	0/2764
39	e	0.26	0/1885	0.40	0/2542
40	f	0.32	0/1273	0.42	0/1716
41	g	0.28	0/1151	0.42	0/1569
42	h	0.24	0/918	0.37	0/1249
43	i	0.28	0/850	0.39	0/1135
44	j	0.26	0/760	0.38	0/1023
45	k	0.27	0/777	0.41	0/1048
46	l	0.26	0/707	0.39	0/960
47	m	0.26	0/767	0.41	0/1028
48	o	0.27	0/819	0.41	0/1097
49	p	0.24	0/1223	0.39	0/1641
50	q	0.24	0/1384	0.34	0/1869
51	r	0.30	0/1362	0.43	0/1846
52	s	0.27	0/3239	0.42	0/4400
53	t1	0.23	0/358	0.34	0/486
53	t2	0.22	0/259	0.33	0/350
53	t3	0.22	0/259	0.33	0/350
53	t4	0.21	0/246	0.34	0/331
53	t5	0.21	0/246	0.33	0/331
53	t6	0.22	0/246	0.34	0/331
54	AA	0.26	0/22655	0.67	0/35273
55	AB	0.27	0/1871	0.40	0/2531
56	AC	0.32	0/1113	0.42	0/1505
57	AD	0.27	0/2783	0.43	0/3724
58	AE	0.25	0/989	0.42	0/1335
59	AF	0.25	0/1767	0.38	0/2373
60	AG	0.27	0/2623	0.40	0/3515
61	AH	0.31	0/1178	0.44	0/1598
62	AI	0.26	0/1030	0.43	0/1386
63	AJ	0.26	0/855	0.45	0/1148
64	AK	0.28	0/880	0.42	0/1182
65	AL	0.25	0/1477	0.36	0/1974
66	AM	0.27	0/963	0.43	0/1295
67	AN	0.27	0/886	0.42	0/1199
68	AO	0.27	0/1648	0.40	0/2243
69	AP	0.27	0/798	0.40	0/1070
70	AQ	0.27	0/748	0.40	0/994

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
71	AR	0.26	0/2456	0.39	0/3317
72	AS	0.27	0/1138	0.40	0/1533
73	AT	0.27	0/1402	0.40	0/1883
74	AU	0.24	0/1510	0.38	0/2025
75	AV	0.24	0/3030	0.36	0/4093
76	AW	0.27	0/801	0.44	0/1079
77	AX	0.24	0/2921	0.38	0/3954
78	AY	0.27	0/1280	0.36	0/1725
79	AZ	0.28	0/857	0.39	0/1141
80	A0	0.25	0/1834	0.41	0/2484
81	A1	0.28	0/2285	0.39	0/3090
82	A2	0.24	0/941	0.39	0/1257
83	A3	0.26	0/636	0.42	0/839
84	A4	0.25	0/4877	0.36	0/6598
85	u	0.22	0/439	0.37	0/586
86	v	0.30	0/159	0.56	0/221
87	w	0.30	1/1608 (0.1%)	0.65	0/2497
88	x	0.30	1/1656 (0.1%)	0.66	0/2571
89	y	0.20	0/443	0.67	0/684
All	All	0.28	4/185856 (0.0%)	0.53	0/264114

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1671	G	OP3-P	-10.65	1.48	1.61
2	B	1602	C	OP3-P	-10.65	1.48	1.61
88	x	1	U	OP3-P	-10.58	1.48	1.61
87	w	1	U	OP3-P	-10.57	1.48	1.61

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

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

## 5.3 Torsion angles

### 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	236/305 (77%)	233 (99%)	3 (1%)	0	100	100
4	E	303/348 (87%)	296 (98%)	7 (2%)	0	100	100
5	F	250/311 (80%)	248 (99%)	2 (1%)	0	100	100
6	H	95/267 (36%)	94 (99%)	1 (1%)	0	100	100
7	I	210/261 (80%)	205 (98%)	5 (2%)	0	100	100
8	J	173/192 (90%)	173 (100%)	0	0	100	100
9	K	175/177 (99%)	173 (99%)	2 (1%)	0	100	100
10	L	113/145 (78%)	111 (98%)	2 (2%)	0	100	100
11	M	289/296 (98%)	287 (99%)	2 (1%)	0	100	100
12	N	220/251 (88%)	218 (99%)	2 (1%)	0	100	100
13	O	152/175 (87%)	152 (100%)	0	0	100	100
14	P	142/180 (79%)	141 (99%)	1 (1%)	0	100	100
15	Q	236/292 (81%)	234 (99%)	2 (1%)	0	100	100
16	R	138/149 (93%)	137 (99%)	1 (1%)	0	100	100
17	S	159/205 (78%)	156 (98%)	3 (2%)	0	100	100
18	T	164/206 (80%)	164 (100%)	0	0	100	100
19	U	129/152 (85%)	128 (99%)	1 (1%)	0	100	100
20	V	203/216 (94%)	203 (100%)	0	0	100	100
21	W	114/148 (77%)	114 (100%)	0	0	100	100
22	X	242/256 (94%)	241 (100%)	1 (0%)	0	100	100
23	Y	179/250 (72%)	178 (99%)	1 (1%)	0	100	100
24	Z	120/161 (74%)	117 (98%)	3 (2%)	0	100	100
25	0	108/188 (57%)	108 (100%)	0	0	100	100
26	1	53/65 (82%)	53 (100%)	0	0	100	100
27	2	44/92 (48%)	43 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	3	93/188 (50%)	92 (99%)	1 (1%)	0	100	100
29	4	36/103 (35%)	36 (100%)	0	0	100	100
30	5	392/423 (93%)	388 (99%)	4 (1%)	0	100	100
31	6	352/380 (93%)	338 (96%)	14 (4%)	0	100	100
32	7	292/338 (86%)	287 (98%)	5 (2%)	0	100	100
33	8	155/206 (75%)	154 (99%)	1 (1%)	0	100	100
34	9	122/137 (89%)	121 (99%)	1 (1%)	0	100	100
35	a	96/142 (68%)	94 (98%)	2 (2%)	0	100	100
36	b	148/214 (69%)	143 (97%)	5 (3%)	0	100	100
37	c	282/332 (85%)	277 (98%)	5 (2%)	0	100	100
38	d	236/306 (77%)	232 (98%)	4 (2%)	0	100	100
39	e	224/279 (80%)	219 (98%)	5 (2%)	0	100	100
40	f	153/212 (72%)	151 (99%)	2 (1%)	0	100	100
41	g	132/166 (80%)	129 (98%)	3 (2%)	0	100	100
42	h	108/158 (68%)	105 (97%)	3 (3%)	0	100	100
43	i	95/128 (74%)	94 (99%)	1 (1%)	0	100	100
44	j	92/123 (75%)	91 (99%)	1 (1%)	0	100	100
45	k	99/111 (89%)	99 (100%)	0	0	100	100
46	l	80/138 (58%)	80 (100%)	0	0	100	100
47	m	83/128 (65%)	81 (98%)	2 (2%)	0	100	100
48	o	92/102 (90%)	92 (100%)	0	0	100	100
49	p	141/206 (68%)	140 (99%)	1 (1%)	0	100	100
50	q	159/222 (72%)	159 (100%)	0	0	100	100
51	r	160/196 (82%)	158 (99%)	2 (1%)	0	100	100
52	s	382/439 (87%)	378 (99%)	4 (1%)	0	100	100
53	t1	44/198 (22%)	43 (98%)	1 (2%)	0	100	100
53	t2	30/198 (15%)	30 (100%)	0	0	100	100
53	t3	30/198 (15%)	30 (100%)	0	0	100	100
53	t4	29/198 (15%)	29 (100%)	0	0	100	100
53	t5	29/198 (15%)	29 (100%)	0	0	100	100
53	t6	29/198 (15%)	29 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	AB	223/296 (75%)	221 (99%)	2 (1%)	0	100	100
56	AC	130/167 (78%)	128 (98%)	2 (2%)	0	100	100
57	AD	341/430 (79%)	335 (98%)	6 (2%)	0	100	100
58	AE	120/125 (96%)	118 (98%)	2 (2%)	0	100	100
59	AF	206/242 (85%)	206 (100%)	0	0	100	100
60	AG	308/396 (78%)	305 (99%)	3 (1%)	0	100	100
61	AH	138/201 (69%)	134 (97%)	3 (2%)	1 (1%)	22	54
62	AI	133/194 (69%)	130 (98%)	3 (2%)	0	100	100
63	AJ	106/138 (77%)	104 (98%)	2 (2%)	0	100	100
64	AK	99/128 (77%)	98 (99%)	1 (1%)	0	100	100
65	AL	172/257 (67%)	171 (99%)	1 (1%)	0	100	100
66	AM	117/137 (85%)	117 (100%)	0	0	100	100
67	AN	108/130 (83%)	107 (99%)	1 (1%)	0	100	100
68	AO	191/258 (74%)	187 (98%)	4 (2%)	0	100	100
69	AP	95/142 (67%)	95 (100%)	0	0	100	100
70	AQ	84/86 (98%)	84 (100%)	0	0	100	100
71	AR	293/360 (81%)	291 (99%)	2 (1%)	0	100	100
72	AS	133/190 (70%)	133 (100%)	0	0	100	100
73	AT	166/173 (96%)	166 (100%)	0	0	100	100
74	AU	174/205 (85%)	172 (99%)	2 (1%)	0	100	100
75	AV	358/414 (86%)	357 (100%)	1 (0%)	0	100	100
76	AW	98/187 (52%)	97 (99%)	1 (1%)	0	100	100
77	AX	350/398 (88%)	346 (99%)	4 (1%)	0	100	100
78	AY	147/395 (37%)	146 (99%)	1 (1%)	0	100	100
79	AZ	98/106 (92%)	98 (100%)	0	0	100	100
80	A0	213/218 (98%)	210 (99%)	3 (1%)	0	100	100
81	A1	274/323 (85%)	269 (98%)	5 (2%)	0	100	100
82	A2	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
83	A3	68/199 (34%)	67 (98%)	1 (2%)	0	100	100
84	A4	584/689 (85%)	575 (98%)	9 (2%)	0	100	100
85	u	47/435 (11%)	47 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
86	v	30/32 (94%)	30 (100%)	0	0	100	100
All	All	14361/19621 (73%)	14193 (99%)	167 (1%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
61	AH	126	ILE

### 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	192/245 (78%)	192 (100%)	0	100	100
4	E	260/290 (90%)	260 (100%)	0	100	100
5	F	219/262 (84%)	219 (100%)	0	100	100
6	H	88/228 (39%)	88 (100%)	0	100	100
7	I	194/232 (84%)	194 (100%)	0	100	100
8	J	138/150 (92%)	138 (100%)	0	100	100
9	K	154/154 (100%)	154 (100%)	0	100	100
10	L	98/124 (79%)	97 (99%)	1 (1%)	76	92
11	M	246/249 (99%)	245 (100%)	1 (0%)	91	97
12	N	189/211 (90%)	189 (100%)	0	100	100
13	O	134/150 (89%)	134 (100%)	0	100	100
14	P	126/155 (81%)	126 (100%)	0	100	100
15	Q	220/256 (86%)	220 (100%)	0	100	100
16	R	118/126 (94%)	118 (100%)	0	100	100
17	S	146/180 (81%)	146 (100%)	0	100	100
18	T	146/176 (83%)	146 (100%)	0	100	100
19	U	118/134 (88%)	118 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	V	183/191 (96%)	183 (100%)	0	100	100
21	W	94/119 (79%)	94 (100%)	0	100	100
22	X	220/229 (96%)	220 (100%)	0	100	100
23	Y	163/223 (73%)	163 (100%)	0	100	100
24	Z	113/147 (77%)	113 (100%)	0	100	100
25	0	99/164 (60%)	98 (99%)	1 (1%)	76	92
26	1	52/60 (87%)	52 (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	37/89 (42%)	37 (100%)	0	100	100
30	5	353/368 (96%)	353 (100%)	0	100	100
31	6	313/332 (94%)	313 (100%)	0	100	100
32	7	270/303 (89%)	269 (100%)	1 (0%)	91	97
33	8	146/190 (77%)	146 (100%)	0	100	100
34	9	104/112 (93%)	104 (100%)	0	100	100
35	a	96/133 (72%)	96 (100%)	0	100	100
36	b	131/184 (71%)	131 (100%)	0	100	100
37	c	251/288 (87%)	251 (100%)	0	100	100
38	d	221/274 (81%)	220 (100%)	1 (0%)	88	96
39	e	198/236 (84%)	198 (100%)	0	100	100
40	f	139/188 (74%)	139 (100%)	0	100	100
41	g	124/148 (84%)	124 (100%)	0	100	100
42	h	104/148 (70%)	104 (100%)	0	100	100
43	i	86/110 (78%)	86 (100%)	0	100	100
44	j	74/97 (76%)	74 (100%)	0	100	100
45	k	83/89 (93%)	83 (100%)	0	100	100
46	l	76/116 (66%)	76 (100%)	0	100	100
47	m	81/113 (72%)	81 (100%)	0	100	100
48	o	80/87 (92%)	80 (100%)	0	100	100
49	p	135/181 (75%)	135 (100%)	0	100	100
50	q	138/178 (78%)	138 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	r	147/169 (87%)	146 (99%)	1 (1%)	84	95
52	s	340/381 (89%)	340 (100%)	0	100	100
53	t1	40/158 (25%)	40 (100%)	0	100	100
53	t2	31/158 (20%)	31 (100%)	0	100	100
53	t3	31/158 (20%)	31 (100%)	0	100	100
53	t4	30/158 (19%)	30 (100%)	0	100	100
53	t5	30/158 (19%)	30 (100%)	0	100	100
53	t6	30/158 (19%)	30 (100%)	0	100	100
55	AB	198/249 (80%)	198 (100%)	0	100	100
56	AC	115/143 (80%)	115 (100%)	0	100	100
57	AD	286/357 (80%)	286 (100%)	0	100	100
58	AE	104/107 (97%)	104 (100%)	0	100	100
59	AF	185/209 (88%)	185 (100%)	0	100	100
60	AG	271/342 (79%)	271 (100%)	0	100	100
61	AH	130/180 (72%)	130 (100%)	0	100	100
62	AI	104/146 (71%)	103 (99%)	1 (1%)	76	92
63	AJ	93/118 (79%)	93 (100%)	0	100	100
64	AK	91/113 (80%)	91 (100%)	0	100	100
65	AL	158/226 (70%)	158 (100%)	0	100	100
66	AM	97/113 (86%)	97 (100%)	0	100	100
67	AN	96/115 (84%)	96 (100%)	0	100	100
68	AO	174/230 (76%)	174 (100%)	0	100	100
69	AP	88/123 (72%)	88 (100%)	0	100	100
70	AQ	78/78 (100%)	78 (100%)	0	100	100
71	AR	264/318 (83%)	264 (100%)	0	100	100
72	AS	116/164 (71%)	116 (100%)	0	100	100
73	AT	153/157 (98%)	153 (100%)	0	100	100
74	AU	152/174 (87%)	152 (100%)	0	100	100
75	AV	325/364 (89%)	324 (100%)	1 (0%)	92	98
76	AW	87/158 (55%)	87 (100%)	0	100	100
77	AX	311/351 (89%)	310 (100%)	1 (0%)	92	98

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
78	AY	137/357 (38%)	137 (100%)	0	100	100
79	AZ	90/95 (95%)	90 (100%)	0	100	100
80	A0	188/190 (99%)	188 (100%)	0	100	100
81	A1	254/291 (87%)	254 (100%)	0	100	100
82	A2	100/100 (100%)	100 (100%)	0	100	100
83	A3	65/166 (39%)	65 (100%)	0	100	100
84	A4	526/609 (86%)	525 (100%)	1 (0%)	93	98
85	u	46/373 (12%)	46 (100%)	0	100	100
All	All	12839/16871 (76%)	12829 (100%)	10 (0%)	93	98

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
75	AV	226	TYR
77	AX	81	HIS
84	A4	486	TYR
32	7	143	TRP
38	d	280	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
78	AY	290	ASN
79	AZ	56	HIS
35	a	46	ASN
32	7	255	HIS
80	A0	111	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1532/1561 (98%)	217 (14%)	1 (0%)
2	B	71/72 (98%)	13 (18%)	0
54	AA	953/954 (99%)	125 (13%)	0
87	w	67/68 (98%)	16 (23%)	0
88	x	68/70 (97%)	8 (11%)	0
89	y	17/19 (89%)	2 (11%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	2708/2744 (98%)	381 (14%)	1 (0%)

5 of 381 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	1689	C
1	A	1692	A
1	A	1700	U
1	A	1704	U
1	A	1707	C

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2112	A

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

7 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
62	IAS	AI	184	62	5,6,8	0.79	0	3,6,10	1.21	0
36	THC	b	2	36	8,9,10	0.77	0	9,11,13	0.63	0
45	AYA	k	2	45	6,7,8	0.79	0	5,8,10	0.73	0
82	AYA	A2	2	82	6,7,8	0.80	0	5,8,10	0.68	0
9	SAC	K	2	9	7,8,9	0.88	0	8,9,11	0.52	0
70	AYA	AQ	2	70	6,7,8	0.78	0	5,8,10	0.57	0
19	AYA	U	2	19	6,7,8	0.78	0	5,8,10	0.52	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
62	IAS	AI	184	62	-	1/3/5/8	-
36	THC	b	2	36	-	0/8/10/12	-
45	AYA	k	2	45	-	0/4/6/8	-
82	AYA	A2	2	82	-	0/4/6/8	-
9	SAC	K	2	9	-	0/7/8/10	-
70	AYA	AQ	2	70	-	0/4/6/8	-
19	AYA	U	2	19	-	1/4/6/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
62	AI	184	IAS	O-C-CA-CB
19	U	2	AYA	C-CA-N-CT

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 242 ligands modelled in this entry, 236 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
93	FES	AT	201	66,73	0,4,4	-	-	-		
94	ATP	AX	501	90	26,33,33	0.76	0	31,52,52	0.94	0
93	FES	r	201	51,7	0,4,4	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
93	FES	AP	201	69,58	0,4,4	-	-	-		
95	GTP	AX	503	-	26,34,34	1.27	3 (11%)	32,54,54	1.52	4 (12%)
96	ALA	w	101	87	3,4,5	0.69	0	2,4,6	0.88	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
93	FES	AT	201	66,73	-	-	0/1/1/1
94	ATP	AX	501	90	-	0/18/38/38	0/3/3/3
93	FES	r	201	51,7	-	-	0/1/1/1
93	FES	AP	201	69,58	-	-	0/1/1/1
95	GTP	AX	503	-	-	0/18/38/38	0/3/3/3
96	ALA	w	101	87	-	0/0/2/4	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
95	AX	503	GTP	C5-C6	-4.03	1.39	1.47
95	AX	503	GTP	C6-N1	-2.93	1.33	1.37
95	AX	503	GTP	C2-N3	2.25	1.38	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
95	AX	503	GTP	C2-N1-C6	-4.84	116.19	125.10
95	AX	503	GTP	C5-C6-N1	4.52	121.92	113.95
95	AX	503	GTP	C8-N7-C5	3.02	108.74	102.99
95	AX	503	GTP	O6-C6-C5	-2.83	118.84	124.37

There are no chirality outliers.

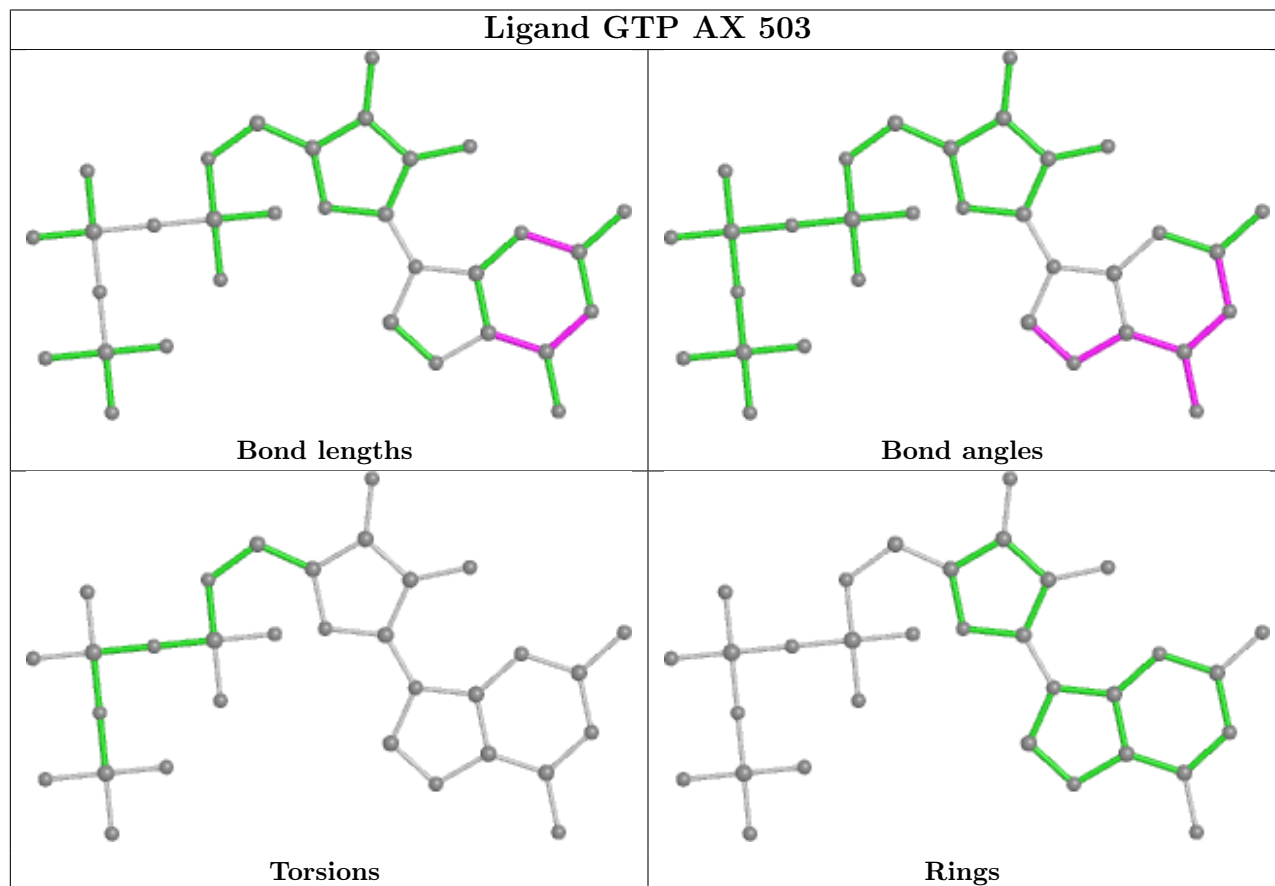
There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
89	y	1
88	x	1



All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	y	26:A	O3'	46:U	P	66.64
1	x	15:A	O3'	21:A	P	9.86

## 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-11278. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

### 6.1 Orthogonal projections

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 standard-deviation projections (False-color)

This section was not generated.

### 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

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

This section was not generated.