



Full wwPDB EM Validation 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

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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

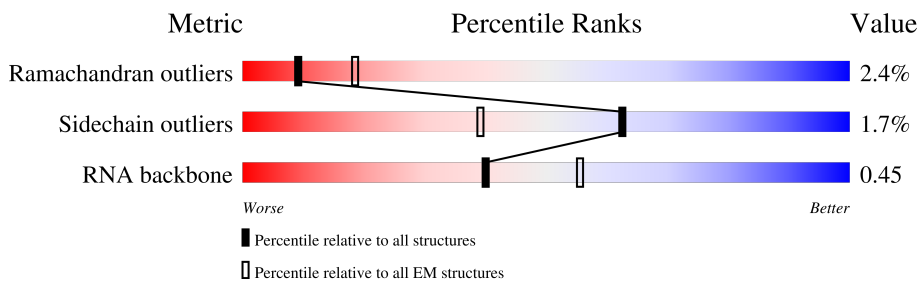
1 Overall quality at a glance i

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	1472	73% (Green), 27% (Yellow)
2	B	56	77% (Green), 23% (Yellow)
3	D	236	96% (Green), . (Grey)
4	E	304	95% (Green), .. (Grey)
5	F	250	96% (Green), .. (Grey)
6	H	95	96% (Green), . (Grey)
7	I	168	92% (Green), . 6% (Grey)
8	J	140	96% (Green), . (Grey)
9	K	177	95% (Green), 5% (Yellow)

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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%

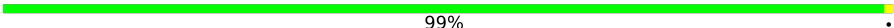

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Mol	Chain	Length	Quality of chain
60	AE	122	97%
61	AF	208	95%
62	AG	326	88%
63	AH	122	94%
64	AI	136	96%
65	AJ	108	95%
66	AK	101	92%
67	AL	164	99%
68	AM	116	97%
69	AN	107	93%
70	AO	185	94%
71	AP	96	98%
72	AQ	86	97%
73	AR	242	94%
74	AS	126	98%
75	AT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

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Mol	Chain	Length	Quality of chain
85	A3	69	 99%
86	A4	474	 86% 13%

2 Entry composition [i](#)

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	C	H	N	O	S	0	0
			2652	828	1369	235	210	10		

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	H	N	O	P		
56	AA	923	29552	8790	9946	3535	6358	923	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
69	AN	107	1754	549	908	153	141	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
87	A	97	Total	Mg	0
			97	97	
87	M	1	Total	Mg	0
			1	1	
87	g	1	Total	Mg	0
			1	1	
87	AA	28	Total	Mg	0
			28	28	

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

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

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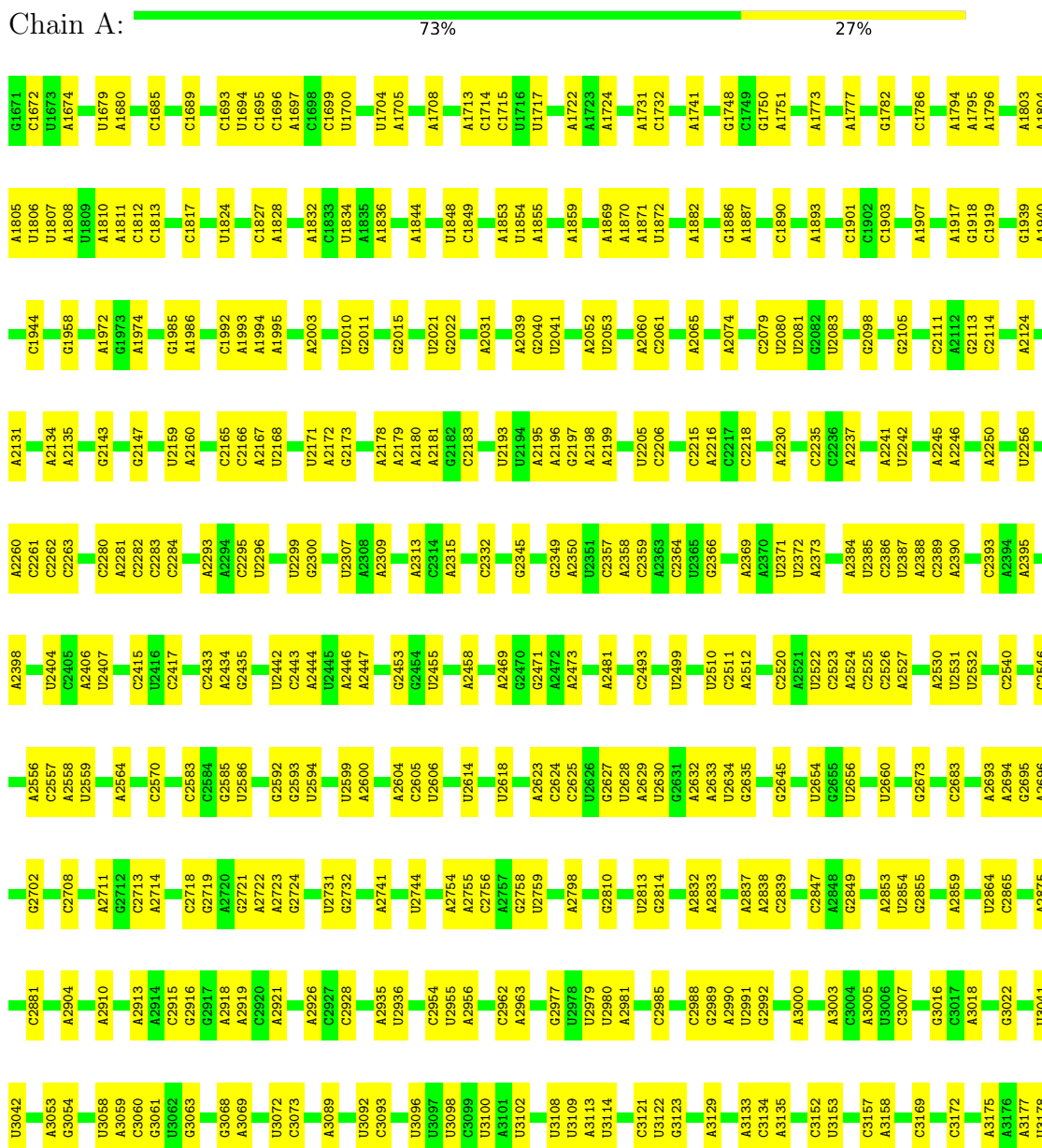
Continued from previous page...

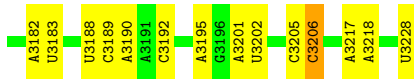
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
88	AT	1	1	1	0

3 Residue-property plots

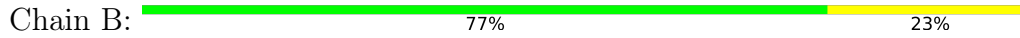
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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



- Molecule 3: 39S ribosomal protein L2, mitochondrial



- Molecule 4: 39S ribosomal protein L3, mitochondrial



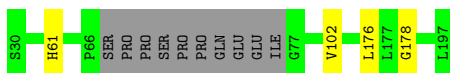
- Molecule 5: 39S ribosomal protein L4, mitochondrial



- Molecule 6: 39S ribosomal protein L9, mitochondrial



- Molecule 7: 39S ribosomal protein L10, mitochondrial



- Molecule 8: 39S ribosomal protein L11, mitochondrial

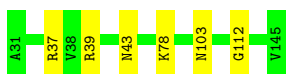




- Molecule 9: 39S ribosomal protein L13, mitochondrial



- Molecule 10: 39S ribosomal protein L14, mitochondrial



- Molecule 11: 39S ribosomal protein L15, mitochondrial



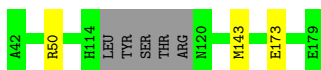
- Molecule 12: 39S ribosomal protein L16, mitochondrial



- Molecule 13: 39S ribosomal protein L17, mitochondrial



- Molecule 14: 39S ribosomal protein L18, mitochondrial



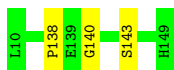
- Molecule 15: 39S ribosomal protein L19, mitochondrial





- Molecule 16: 39S ribosomal protein L20, mitochondrial

Chain R: 98%



- Molecule 17: 39S ribosomal protein L21, mitochondrial

Chain S: 97%



- Molecule 18: 39S ribosomal protein L22, mitochondrial

Chain T: 98%



- Molecule 19: 39S ribosomal protein L23, mitochondrial

Chain U: 96%



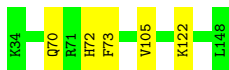
- Molecule 20: 39S ribosomal protein L24, mitochondrial

Chain V: 87% 6% 6%



- Molecule 21: 39S ribosomal protein L27, mitochondrial

Chain W: 96%



- Molecule 22: 39S ribosomal protein L28, mitochondrial

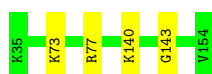
Chain X: 94% 6%



- Molecule 23: 39S ribosomal protein L47, mitochondrial



- Molecule 24: 39S ribosomal protein L30, mitochondrial



- Molecule 25: 39S ribosomal protein L32, mitochondrial



- Molecule 26: 39S ribosomal protein L33, mitochondrial



- Molecule 27: 39S ribosomal protein L34, mitochondrial



There are no outlier residues recorded for this chain.

- Molecule 28: 39S ribosomal protein L35, mitochondrial



- Molecule 29: 39S ribosomal protein L36, mitochondrial




There are no outlier residues recorded for this chain.

- Molecule 30: 39S ribosomal protein L37, mitochondrial

Chain 5:  92%




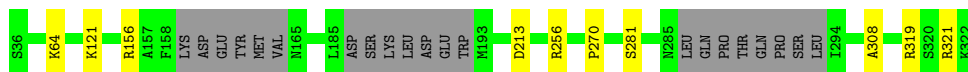
- Molecule 31: 39S ribosomal protein L38, mitochondrial

Chain 6:  88%



- Molecule 32: 39S ribosomal protein L39, mitochondrial

Chain 7:  89%




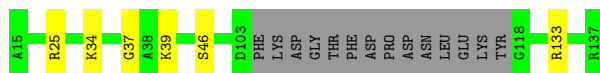
- Molecule 33: 39S ribosomal protein L40, mitochondrial

Chain 8:  97%



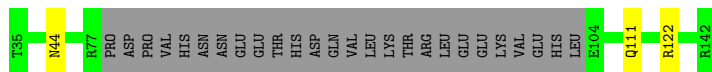
- Molecule 34: 39S ribosomal protein L41, mitochondrial

Chain 9:  84%



- Molecule 35: 39S ribosomal protein L42, mitochondrial

Chain a:  73%

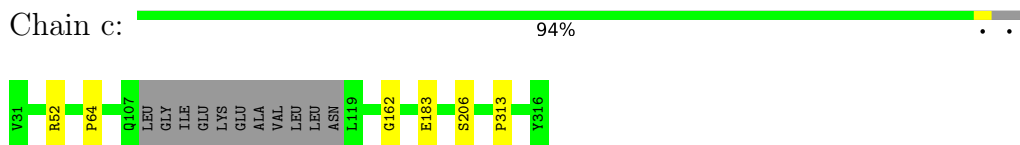


- Molecule 36: 39S ribosomal protein L43, mitochondrial

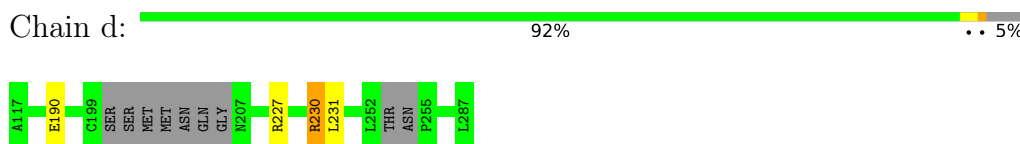
Chain b:  97%



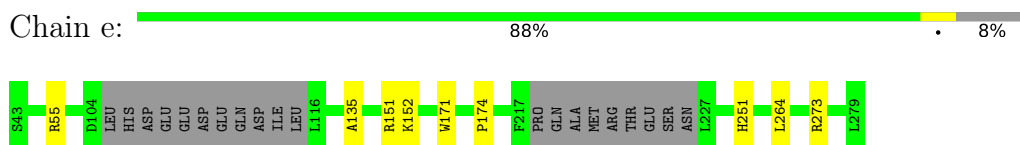
- Molecule 37: 39S ribosomal protein L44, mitochondrial



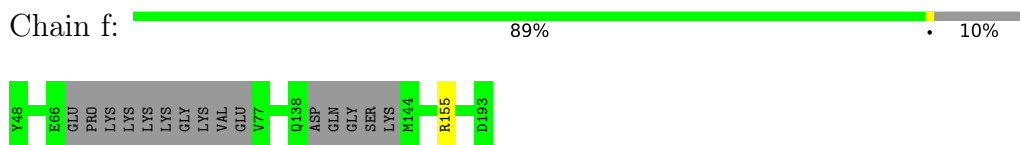
- Molecule 38: 39S ribosomal protein L45, mitochondrial



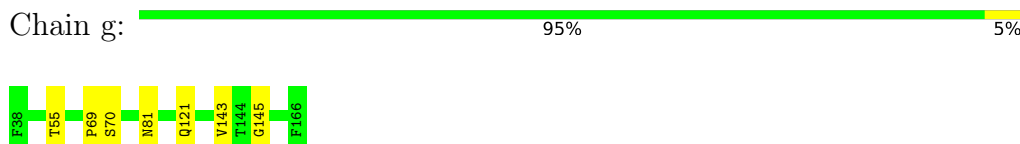
- Molecule 39: 39S ribosomal protein L46, mitochondrial



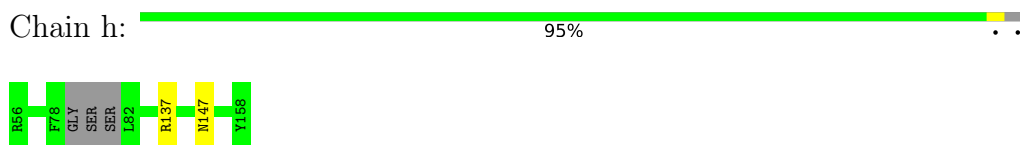
- Molecule 40: 39S ribosomal protein L48, mitochondrial



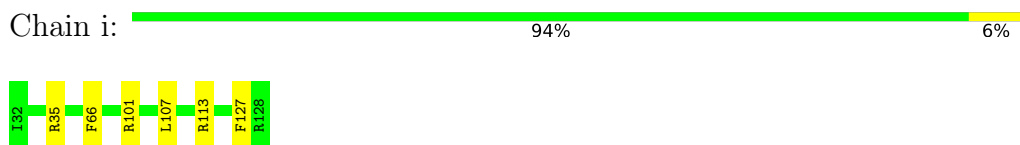
- Molecule 41: 39S ribosomal protein L49, mitochondrial



- Molecule 42: 39S ribosomal protein L50, mitochondrial



- Molecule 43: 39S ribosomal protein L51, mitochondrial



- Molecule 44: 39S ribosomal protein L52, mitochondrial

Chain j:  98%



- Molecule 45: 39S ribosomal protein L53, mitochondrial

Chain k:  93% 7%



- Molecule 46: 39S ribosomal protein L54, mitochondrial

Chain l:  100%

There are no outlier residues recorded for this chain.

- Molecule 47: 39S ribosomal protein L55, mitochondrial

Chain m:  93% 7%




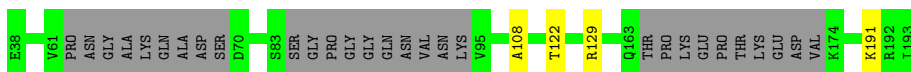
- Molecule 48: Ribosomal protein 63, mitochondrial

Chain o:  96%



- Molecule 49: Peptidyl-tRNA hydrolase ICT1, mitochondrial

Chain p:  79% 19%




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

Chain q:  96%



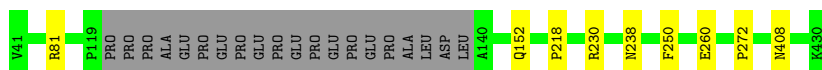
- Molecule 51: 39S ribosomal protein S18a, mitochondrial

Chain r:  86% 10%



- Molecule 52: 39S ribosomal protein S30, mitochondrial

Chain s: 93% • 5%



- Molecule 53: Unknown protein/protein extension

Chain t: 100%

There are no outlier residues recorded for this chain.

- Molecule 54: E-site tRNA

Chain u: 100%

There are no outlier residues recorded for this chain.

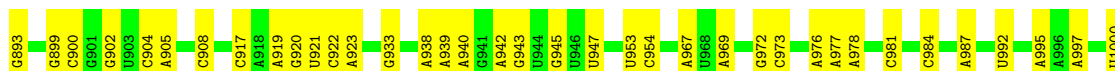
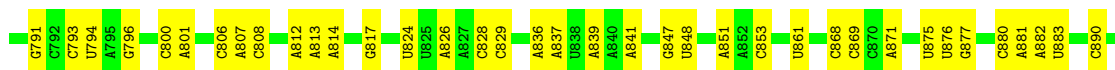
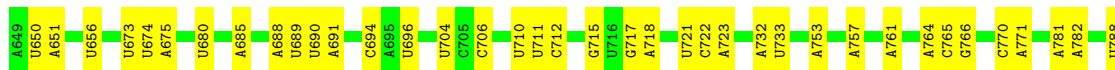
- Molecule 55: Ribosome-recycling factor, mitochondrial

Chain z: 97%



- Molecule 56: 12S rRNA

Chain AA: 66% 34%





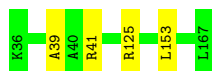
- Molecule 57: 28S ribosomal protein S2, mitochondrial

Chain AB: 99%



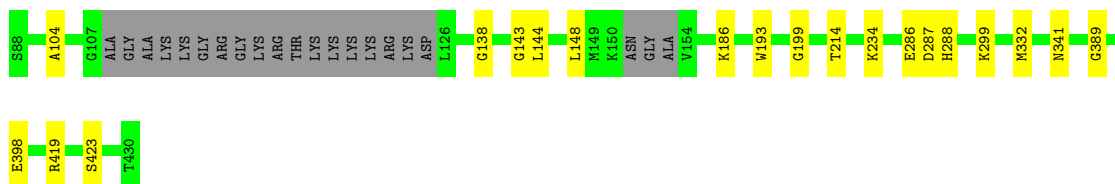
- Molecule 58: 28S ribosomal protein S24, mitochondrial

Chain AC: 97%



- Molecule 59: 28S ribosomal protein S5, mitochondrial

Chain AD: 88% 6% 6%



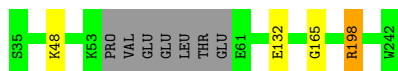
- Molecule 60: 28S ribosomal protein S6, mitochondrial

Chain AE: 97%



- Molecule 61: 28S ribosomal protein S7, mitochondrial

Chain AF: 95%



- Molecule 62: 28S ribosomal protein S9, mitochondrial

Chain AG: 88% 5% 6%



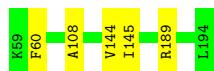
- Molecule 63: 28S ribosomal protein S10, mitochondrial

Chain AH: 94% 6%



- Molecule 64: 28S ribosomal protein S11, mitochondrial

Chain AI: 96% 4%



- Molecule 65: 28S ribosomal protein S12, mitochondrial

Chain AJ: 95% 5%



- Molecule 66: 28S ribosomal protein S14, mitochondrial

Chain AK: 92% 8%



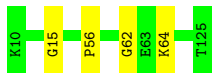
- Molecule 67: 28S ribosomal protein S15, mitochondrial

Chain AL: 99% 1%



- Molecule 68: 28S ribosomal protein S16, mitochondrial

Chain AM:  97%



- Molecule 69: 28S ribosomal protein S17, mitochondrial

Chain AN:  93% 7%



- Molecule 70: 28S ribosomal protein S18b, mitochondrial

Chain AO:  94% 6%



- Molecule 71: 28S ribosomal protein S18c, mitochondrial

Chain AP:  98%



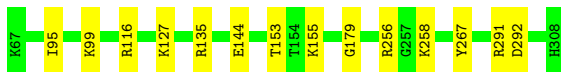
- Molecule 72: 28S ribosomal protein S21, mitochondrial

Chain AQ:  97%



- Molecule 73: 28S ribosomal protein S22, mitochondrial

Chain AR:  94% 6%



- Molecule 74: 28S ribosomal protein S23, mitochondrial

Chain AS:  98%



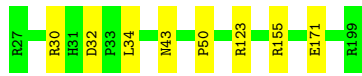
- Molecule 75: 28S ribosomal protein S25, mitochondrial

Chain AT: 98%



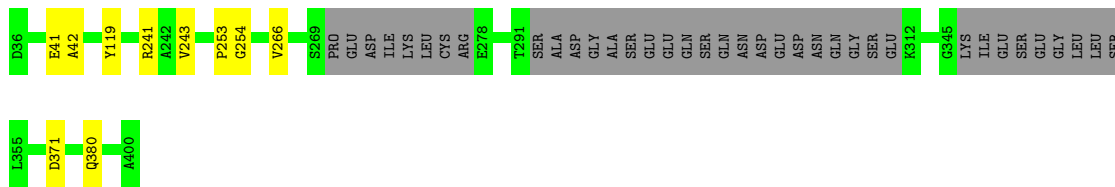
• Molecule 76: 28S ribosomal protein S26, mitochondrial

Chain AU: 95%



• Molecule 77: 28S ribosomal protein S27, mitochondrial

Chain AV: 87% 10%



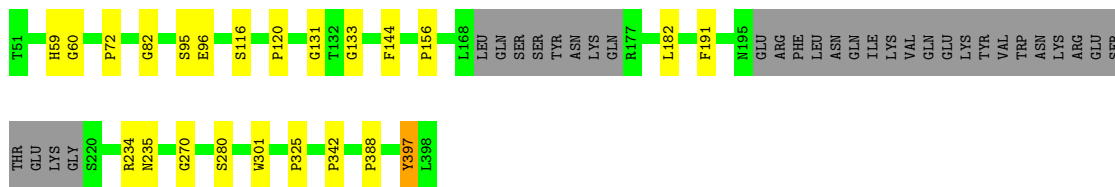
• Molecule 78: 28S ribosomal protein S28, mitochondrial

Chain AW: 97%



• Molecule 79: 28S ribosomal protein S29, mitochondrial

Chain AX: 84% 6% 9%



• Molecule 80: 28S ribosomal protein S31, mitochondrial

Chain AY: 95%

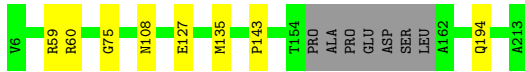


• Molecule 81: 28S ribosomal protein S33, mitochondrial

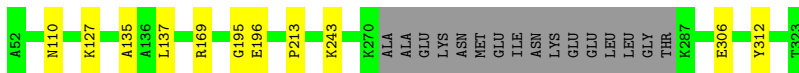
Chain AZ: 94%



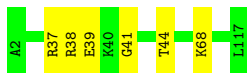
- Molecule 82: 28S ribosomal protein S34, mitochondrial



- Molecule 83: 28S ribosomal protein S35, mitochondrial



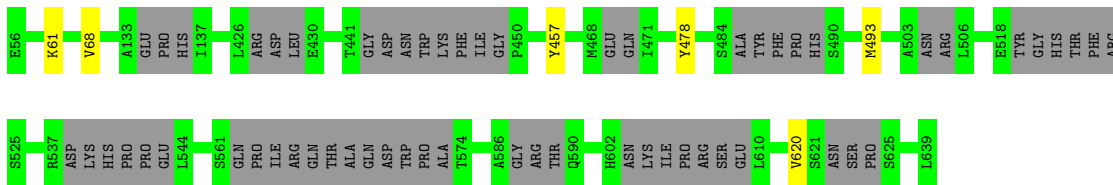
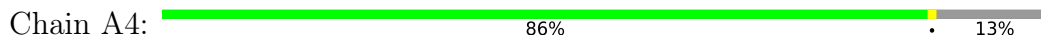
- Molecule 84: Coiled-coil-helix-coiled-coil-helix domain-containing protein 1



- Molecule 85: Aurora kinase A-interacting protein



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



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 ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

All (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
56	AA	1093	C	N3-C2-O2	-5.74	117.89	121.90
56	AA	1413	U	C2-N1-C1'	5.38	124.16	117.70
56	AA	984	C	N1-C2-O2	5.31	122.09	118.90
56	AA	1314	C	C2-N1-C1'	5.27	124.60	118.80
56	AA	1241	C	N3-C2-O2	-5.15	118.29	121.90
1	A	1786	C	N3-C2-O2	-5.11	118.33	121.90

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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

All (311) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	M	134	ARG
20	V	101	THR
20	V	177	THR

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Mol	Chain	Res	Type
30	5	381	LEU
30	5	383	TYR
32	7	308	ALA
36	b	116	ARG
38	d	230	ARG
38	d	231	LEU
58	AC	39	ALA
66	AK	63	LEU
66	AK	82	SER
73	AR	291	ARG
76	AU	34	LEU
77	AV	41	GLU
79	AX	96	GLU
79	AX	156	PRO
79	AX	234	ARG
79	AX	342	PRO
83	A1	243	LYS
4	E	126	ASP
4	E	241	GLY
4	E	317	PRO
5	F	128	TRP
8	J	29	ALA
8	J	125	ALA
10	L	112	GLY
11	M	280	LYS
15	Q	127	SER
16	R	140	GLY
17	S	138	ALA
20	V	99	GLY
20	V	151	GLY
21	W	72	HIS
22	X	18	GLU
22	X	220	GLU
25	0	116	LEU
31	6	189	CYS
32	7	321	ARG
34	9	34	LYS
34	9	37	GLY
34	9	133	ARG
37	c	183	GLU
37	c	206	SER
39	e	174	PRO

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Mol	Chain	Res	Type
41	g	55	THR
41	g	70	SER
41	g	81	ASN
41	g	143	VAL
41	g	145	GLY
42	h	137	ARG
42	h	147	ASN
45	k	36	THR
48	o	61	GLY
49	p	108	ALA
52	s	250	PHE
55	z	117	ASP
58	AC	125	ARG
59	AD	143	GLY
59	AD	148	LEU
59	AD	193	TRP
59	AD	199	GLY
59	AD	287	ASP
59	AD	299	LYS
59	AD	398	GLU
59	AD	423	SER
62	AG	210	VAL
62	AG	392	THR
64	AI	145	ILE
69	AN	97	GLY
70	AO	221	GLN
72	AQ	81	ALA
73	AR	292	ASP
75	AT	137	ARG
77	AV	119	TYR
77	AV	254	GLY
79	AX	60	GLY
79	AX	270	GLY
79	AX	325	PRO
83	A1	135	ALA
83	A1	196	GLU
3	D	67	LYS
3	D	167	ASN
3	D	177	ARG
3	D	221	ASN
4	E	215	PHE
4	E	325	GLU

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Mol	Chain	Res	Type
5	F	290	TYR
6	H	61	LYS
6	H	103	GLU
7	I	61	HIS
8	J	31	PRO
8	J	43	GLY
9	K	4	PHE
9	K	148	PRO
10	L	37	ARG
10	L	103	ASN
11	M	242	TYR
13	O	105	THR
15	Q	76	LEU
15	Q	183	LEU
20	V	125	PRO
21	W	73	PHE
22	X	175	GLN
22	X	221	LYS
23	Y	83	ALA
23	Y	162	ARG
24	Z	140	LYS
24	Z	143	GLY
25	0	163	GLU
26	1	60	LYS
30	5	70	LEU
30	5	297	ALA
30	5	348	ASP
31	6	50	LYS
31	6	69	HIS
31	6	378	GLY
32	7	121	LYS
34	9	46	SER
37	c	313	PRO
39	e	251	HIS
43	i	127	PHE
44	j	34	ALA
45	k	39	SER
48	o	15	ARG
50	q	42	PRO
50	q	52	LEU
52	s	152	GLN
52	s	272	PRO

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Mol	Chain	Res	Type
52	s	408	ASN
59	AD	286	GLU
59	AD	288	HIS
60	AE	116	LYS
61	AF	198	ARG
62	AG	154	GLY
63	AH	147	HIS
63	AH	179	GLN
65	AJ	136	GLN
66	AK	126	ALA
67	AL	194	LEU
68	AM	64	LYS
70	AO	128	CYS
71	AP	131	LYS
73	AR	127	LYS
73	AR	256	ARG
76	AU	30	ARG
76	AU	50	PRO
77	AV	371	ASP
78	AW	146	ASP
79	AX	72	PRO
79	AX	95	SER
79	AX	397	TYR
80	AY	339	GLU
82	A0	108	ASN
82	A0	127	GLU
83	A1	137	LEU
3	D	208	ARG
4	E	211	ILE
4	E	326	GLU
5	F	125	ARG
6	H	64	LEU
7	I	176	LEU
9	K	151	ILE
11	M	47	ARG
11	M	260	LYS
11	M	287	ASP
12	N	174	GLY
16	R	143	SER
18	T	79	GLN
18	T	158	TYR
19	U	34	ALA

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Mol	Chain	Res	Type
20	V	152	ARG
22	X	154	CYS
23	Y	183	GLN
28	3	95	THR
30	5	215	ARG
30	5	296	LYS
33	8	91	PRO
34	9	25	ARG
34	9	39	LYS
36	b	50	GLU
37	c	64	PRO
38	d	190	GLU
39	e	264	LEU
43	i	66	PHE
48	o	81	LYS
51	r	55	ALA
52	s	260	GLU
55	z	112	SER
59	AD	104	ALA
59	AD	138	GLY
60	AE	104	GLU
61	AF	132	GLU
62	AG	232	GLN
62	AG	234	GLY
62	AG	249	THR
62	AG	252	SER
62	AG	261	GLN
65	AJ	130	TYR
66	AK	30	VAL
66	AK	58	ARG
68	AM	15	GLY
69	AN	102	GLY
69	AN	109	PRO
70	AO	53	ASP
73	AR	155	LYS
73	AR	179	GLY
73	AR	267	TYR
75	AT	149	CYS
79	AX	59	HIS
79	AX	131	GLY
79	AX	182	LEU
79	AX	280	SER

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Mol	Chain	Res	Type
79	AX	301	TRP
82	A0	194	GLN
83	A1	195	GLY
84	A2	39	GLU
84	A2	41	GLY
84	A2	44	THR
86	A4	620	VAL
9	K	153	LYS
11	M	286	THR
14	P	173	GLU
15	Q	228	PRO
16	R	138	PRO
18	T	69	ARG
19	U	11	ARG
20	V	117	HIS
20	V	193	THR
21	W	122	LYS
22	X	68	PRO
22	X	155	SER
30	5	272	ASP
30	5	277	THR
30	5	286	PRO
31	6	225	LEU
31	6	359	HIS
37	c	52	ARG
39	e	135	ALA
45	k	58	ASP
45	k	62	PRO
47	m	70	GLU
49	p	122	THR
62	AG	291	GLY
63	AH	127	TYR
64	AI	60	PHE
64	AI	108	ALA
72	AQ	6	LYS
75	AT	132	ARG
76	AU	43	ASN
76	AU	171	GLU
77	AV	253	PRO
79	AX	82	GLY
79	AX	120	PRO
79	AX	133	GLY

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Mol	Chain	Res	Type
79	AX	388	PRO
80	AY	319	ALA
82	A0	75	GLY
83	A1	213	PRO
83	A1	306	GLU
85	A3	185	ALA
5	F	91	PRO
7	I	178	GLY
30	5	171	PRO
31	6	314	ALA
32	7	213	ASP
33	8	96	ASP
51	r	57	PRO
51	r	64	PRO
57	AB	139	LYS
59	AD	214	THR
59	AD	389	GLY
61	AF	165	GLY
62	AG	289	GLY
65	AJ	54	GLY
73	AR	95	ILE
73	AR	153	THR
77	AV	42	ALA
78	AW	97	ASP
78	AW	117	GLY
79	AX	116	SER
79	AX	235	ASN
4	E	79	PRO
15	Q	226	PRO
41	g	69	PRO
45	k	64	VAL
81	AZ	90	GLY
7	I	102	VAL
15	Q	242	GLY
31	6	351	HIS
32	7	270	PRO
37	c	162	GLY
64	AI	144	VAL
66	AK	123	ILE
68	AM	62	GLY
74	AS	54	GLY
74	AS	77	VAL

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Mol	Chain	Res	Type
77	AV	243	VAL
80	AY	293	PRO
80	AY	325	GLY
47	m	71	PRO
55	z	183	PRO
68	AM	56	PRO
86	A4	68	VAL
51	r	61	PRO
17	S	168	PRO
44	j	25	GLY
52	s	218	PRO
57	AB	243	PRO
82	A0	143	PRO
17	S	147	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	D	190/190 (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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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

All (191) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	92	ARG
3	D	113	ARG
3	D	147	ARG
3	D	232	ARG
3	D	274	ARG
4	E	154	ARG
4	E	324	ASP
5	F	108	ARG
5	F	125	ARG
5	F	131	LYS
5	F	147	ARG
5	F	170	ARG
5	F	221	LEU
5	F	290	TYR
6	H	75	ARG
8	J	50	CYS
9	K	95	LEU
9	K	145	LEU
9	K	154	ARG
9	K	168	ARG
10	L	39	ARG
10	L	43	ASN
10	L	78	LYS
11	M	41	ARG
11	M	44	ARG
11	M	109	ARG
11	M	134	ARG
11	M	160	SER
12	N	51	ARG

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Mol	Chain	Res	Type
12	N	105	MET
13	O	16	ARG
14	P	50	ARG
14	P	143	MET
15	Q	102	ARG
17	S	115	LEU
17	S	144	LEU
18	T	133	ASN
19	U	3	ARG
19	U	71	ARG
20	V	15	LEU
20	V	33	ARG
20	V	143	ARG
20	V	145	ARG
20	V	185	ARG
21	W	70	GLN
21	W	105	VAL
22	X	23	ARG
22	X	36	ARG
22	X	44	ARG
22	X	59	ARG
22	X	101	LEU
22	X	141	LEU
22	X	216	ARG
23	Y	198	ARG
24	Z	73	LYS
24	Z	77	ARG
25	0	84	ARG
25	0	179	ARG
26	1	34	ARG
26	1	38	ARG
28	3	167	LYS
30	5	229	ARG
30	5	294	LEU
30	5	373	LEU
30	5	415	LEU
31	6	159	ARG
31	6	173	LEU
31	6	277	GLN
31	6	334	LEU
32	7	64	LYS
32	7	156	ARG

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Mol	Chain	Res	Type
32	7	256	ARG
32	7	281	SER
32	7	319	ARG
33	8	101	ARG
35	a	44	ASN
35	a	111	GLN
35	a	122	ARG
36	b	15	LEU
36	b	74	ARG
36	b	144	ARG
38	d	227	ARG
38	d	230	ARG
39	e	55	ARG
39	e	151	ARG
39	e	152	LYS
39	e	171	TRP
39	e	273	ARG
40	f	155	ARG
41	g	121	GLN
43	i	35	ARG
43	i	101	ARG
43	i	107	LEU
43	i	113	ARG
45	k	46	ASN
47	m	42	ARG
48	o	9	ARG
49	p	129	ARG
49	p	191	LYS
50	q	28	ARG
50	q	78	SER
50	q	114	ARG
51	r	36	ARG
51	r	74	ARG
52	s	81	ARG
52	s	230	ARG
52	s	238	ASN
55	z	65	LYS
55	z	170	ASN
55	z	205	LYS
57	AB	169	ARG
58	AC	41	ARG
58	AC	153	LEU

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Mol	Chain	Res	Type
59	AD	144	LEU
59	AD	186	LYS
59	AD	234	LYS
59	AD	332	MET
59	AD	341	ASN
59	AD	419	ARG
60	AE	15	ARG
60	AE	105	CYS
61	AF	48	LYS
61	AF	198	ARG
62	AG	106	ARG
62	AG	111	LEU
62	AG	232	GLN
62	AG	243	ARG
62	AG	276	ARG
62	AG	301	GLN
62	AG	310	ARG
62	AG	312	GLN
62	AG	389	ARG
63	AH	92	GLU
63	AH	113	ARG
63	AH	136	MET
63	AH	170	MET
64	AI	189	ARG
65	AJ	43	LYS
65	AJ	129	LYS
66	AK	95	SER
66	AK	102	ARG
67	AL	145	LYS
69	AN	65	LEU
69	AN	73	ARG
69	AN	78	LYS
69	AN	100	CYS
70	AO	94	CYS
70	AO	96	ARG
70	AO	109	ARG
70	AO	136	TYR
70	AO	143	CYS
70	AO	148	LYS
70	AO	163	LEU
70	AO	173	ARG
71	AP	54	MET

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Mol	Chain	Res	Type
72	AQ	10	ARG
73	AR	99	LYS
73	AR	116	ARG
73	AR	135	ARG
73	AR	144	GLU
73	AR	258	LYS
74	AS	42	ARG
75	AT	66	MET
76	AU	32	ASP
76	AU	123	ARG
76	AU	155	ARG
77	AV	241	ARG
77	AV	266	VAL
77	AV	380	GLN
79	AX	144	PHE
79	AX	191	PHE
79	AX	397	TYR
80	AY	376	PHE
81	AZ	19	PHE
81	AZ	61	LEU
81	AZ	89	ARG
81	AZ	91	LYS
82	A0	59	ARG
82	A0	60	ARG
82	A0	135	MET
83	A1	110	ASN
83	A1	127	LYS
83	A1	169	ARG
83	A1	312	TYR
84	A2	37	ARG
84	A2	38	ARG
84	A2	68	LYS
86	A4	61	LYS
86	A4	457	TYR
86	A4	478	TYR
86	A4	493	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
3	D	205	GLN
3	D	235	GLN

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Mol	Chain	Res	Type
5	F	105	ASN
5	F	130	GLN
5	F	276	GLN
6	H	121	ASN
9	K	48	HIS
12	N	173	GLN
13	O	31	ASN
15	Q	158	GLN
16	R	12	ASN
16	R	89	ASN
18	T	133	ASN
23	Y	73	ASN
23	Y	76	GLN
23	Y	195	ASN
26	1	35	ASN
27	2	64	HIS
28	3	178	GLN
37	c	192	GLN
38	d	149	HIS
41	g	93	ASN
41	g	141	ASN
42	h	151	ASN
49	p	184	ASN
51	r	148	ASN
52	s	238	ASN
55	z	75	ASN
57	AB	226	ASN
59	AD	341	ASN
60	AE	100	GLN
61	AF	140	ASN
61	AF	147	GLN
64	AI	119	ASN
69	AN	56	GLN
72	AQ	53	GLN
73	AR	214	ASN
74	AS	91	ASN
77	AV	170	GLN
77	AV	224	GLN
79	AX	143	HIS
79	AX	363	ASN
79	AX	367	GLN

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%)

All (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
1	A	1689	C
1	A	1693	C
1	A	1694	U
1	A	1695	C
1	A	1696	C
1	A	1697	A
1	A	1699	C
1	A	1700	U
1	A	1704	U
1	A	1705	A
1	A	1708	A
1	A	1713	A
1	A	1714	C
1	A	1715	C
1	A	1717	U
1	A	1722	A
1	A	1724	A
1	A	1732	C
1	A	1741	A
1	A	1748	G
1	A	1750	G
1	A	1751	A
1	A	1773	A
1	A	1777	A
1	A	1782	G
1	A	1794	A
1	A	1795	A

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Mol	Chain	Res	Type
1	A	1796	A
1	A	1803	A
1	A	1804	A
1	A	1805	A
1	A	1806	U
1	A	1807	U
1	A	1808	A
1	A	1811	A
1	A	1812	C
1	A	1813	C
1	A	1817	C
1	A	1824	U
1	A	1827	C
1	A	1828	A
1	A	1832	A
1	A	1834	U
1	A	1836	A
1	A	1844	A
1	A	1849	C
1	A	1853	A
1	A	1854	U
1	A	1855	A
1	A	1859	A
1	A	1869	A
1	A	1870	A
1	A	1871	A
1	A	1872	U
1	A	1882	A
1	A	1886	G
1	A	1887	A
1	A	1893	A
1	A	1901	C
1	A	1903	C
1	A	1907	A
1	A	1917	A
1	A	1918	G
1	A	1919	C
1	A	1939	G
1	A	1940	A
1	A	1944	C
1	A	1958	G
1	A	1972	A

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Mol	Chain	Res	Type
1	A	1974	A
1	A	1985	G
1	A	1986	A
1	A	1992	C
1	A	1993	A
1	A	1994	A
1	A	1995	A
1	A	2003	A
1	A	2010	U
1	A	2011	G
1	A	2015	G
1	A	2021	U
1	A	2022	G
1	A	2031	A
1	A	2039	A
1	A	2041	U
1	A	2053	U
1	A	2060	A
1	A	2061	C
1	A	2065	A
1	A	2074	A
1	A	2079	C
1	A	2081	U
1	A	2083	U
1	A	2098	G
1	A	2105	G
1	A	2111	C
1	A	2113	G
1	A	2114	C
1	A	2124	A
1	A	2131	A
1	A	2134	A
1	A	2135	A
1	A	2143	G
1	A	2147	G
1	A	2159	U
1	A	2160	A
1	A	2165	C
1	A	2166	C
1	A	2167	A
1	A	2168	U
1	A	2171	U

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Mol	Chain	Res	Type
1	A	2172	A
1	A	2173	G
1	A	2178	A
1	A	2179	A
1	A	2180	A
1	A	2181	A
1	A	2183	C
1	A	2193	U
1	A	2195	A
1	A	2196	A
1	A	2197	G
1	A	2198	A
1	A	2199	A
1	A	2206	C
1	A	2215	C
1	A	2216	A
1	A	2218	C
1	A	2230	A
1	A	2235	C
1	A	2237	A
1	A	2241	A
1	A	2242	U
1	A	2245	A
1	A	2246	A
1	A	2250	A
1	A	2256	U
1	A	2260	A
1	A	2261	C
1	A	2262	C
1	A	2263	C
1	A	2280	C
1	A	2281	A
1	A	2282	C
1	A	2283	C
1	A	2284	C
1	A	2293	A
1	A	2295	C
1	A	2296	U
1	A	2299	U
1	A	2300	G
1	A	2307	U
1	A	2309	A

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Mol	Chain	Res	Type
1	A	2313	A
1	A	2315	A
1	A	2332	C
1	A	2345	G
1	A	2350	A
1	A	2358	A
1	A	2359	C
1	A	2364	C
1	A	2366	G
1	A	2369	A
1	A	2372	U
1	A	2373	A
1	A	2384	A
1	A	2385	U
1	A	2386	C
1	A	2387	U
1	A	2388	A
1	A	2389	C
1	A	2390	A
1	A	2393	C
1	A	2395	A
1	A	2398	A
1	A	2404	U
1	A	2406	A
1	A	2407	U
1	A	2415	C
1	A	2417	C
1	A	2433	C
1	A	2434	A
1	A	2435	G
1	A	2442	U
1	A	2443	C
1	A	2444	A
1	A	2446	A
1	A	2447	A
1	A	2453	G
1	A	2455	U
1	A	2458	A
1	A	2469	A
1	A	2471	G
1	A	2473	A
1	A	2481	A

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Mol	Chain	Res	Type
1	A	2493	C
1	A	2499	U
1	A	2511	C
1	A	2512	A
1	A	2520	C
1	A	2522	U
1	A	2523	C
1	A	2524	A
1	A	2525	C
1	A	2526	C
1	A	2527	A
1	A	2530	A
1	A	2531	U
1	A	2532	U
1	A	2540	C
1	A	2546	G
1	A	2556	A
1	A	2557	C
1	A	2558	A
1	A	2559	U
1	A	2564	A
1	A	2570	C
1	A	2583	C
1	A	2585	G
1	A	2586	U
1	A	2592	G
1	A	2593	G
1	A	2594	U
1	A	2599	U
1	A	2600	A
1	A	2604	A
1	A	2605	C
1	A	2606	U
1	A	2614	U
1	A	2618	U
1	A	2623	A
1	A	2624	C
1	A	2625	C
1	A	2627	G
1	A	2629	A
1	A	2630	U
1	A	2632	A

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Mol	Chain	Res	Type
1	A	2633	A
1	A	2634	U
1	A	2635	G
1	A	2645	G
1	A	2654	U
1	A	2656	U
1	A	2660	U
1	A	2673	G
1	A	2683	C
1	A	2693	A
1	A	2694	A
1	A	2695	G
1	A	2696	A
1	A	2702	G
1	A	2708	C
1	A	2711	A
1	A	2714	A
1	A	2718	C
1	A	2719	G
1	A	2721	G
1	A	2722	A
1	A	2723	A
1	A	2724	G
1	A	2731	U
1	A	2732	G
1	A	2741	A
1	A	2744	U
1	A	2755	A
1	A	2756	C
1	A	2758	G
1	A	2759	U
1	A	2798	A
1	A	2810	G
1	A	2813	U
1	A	2814	G
1	A	2832	A
1	A	2833	A
1	A	2837	A
1	A	2838	A
1	A	2839	C
1	A	2847	C
1	A	2849	G

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Mol	Chain	Res	Type
1	A	2853	A
1	A	2854	U
1	A	2855	G
1	A	2859	A
1	A	2864	U
1	A	2865	C
1	A	2875	A
1	A	2881	C
1	A	2904	A
1	A	2910	A
1	A	2913	A
1	A	2915	C
1	A	2916	G
1	A	2918	A
1	A	2919	A
1	A	2921	A
1	A	2926	A
1	A	2928	C
1	A	2935	A
1	A	2936	U
1	A	2954	C
1	A	2955	U
1	A	2956	A
1	A	2962	C
1	A	2963	A
1	A	2977	G
1	A	2980	U
1	A	2981	A
1	A	2985	C
1	A	2988	C
1	A	2989	G
1	A	2990	A
1	A	2991	U
1	A	2992	G
1	A	3000	A
1	A	3003	A
1	A	3005	A
1	A	3007	C
1	A	3016	G
1	A	3018	A
1	A	3022	G
1	A	3041	U

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Mol	Chain	Res	Type
1	A	3042	U
1	A	3053	A
1	A	3054	G
1	A	3059	A
1	A	3060	C
1	A	3061	G
1	A	3063	G
1	A	3068	G
1	A	3069	A
1	A	3072	U
1	A	3073	C
1	A	3089	A
1	A	3093	C
1	A	3096	U
1	A	3098	U
1	A	3100	U
1	A	3102	U
1	A	3108	U
1	A	3109	U
1	A	3114	U
1	A	3122	U
1	A	3123	G
1	A	3129	A
1	A	3133	A
1	A	3134	C
1	A	3135	A
1	A	3152	C
1	A	3153	U
1	A	3157	C
1	A	3158	A
1	A	3169	C
1	A	3172	C
1	A	3175	A
1	A	3177	A
1	A	3178	U
1	A	3182	A
1	A	3183	U
1	A	3188	U
1	A	3189	C
1	A	3190	A
1	A	3192	C
1	A	3195	A

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Mol	Chain	Res	Type
1	A	3202	U
1	A	3206	C
1	A	3217	A
1	A	3218	A
1	A	3228	U
2	B	1604	G
2	B	1609	U
2	B	1611	G
2	B	1631	C
2	B	1637	C
2	B	1638	U
2	B	1644	G
2	B	1645	A
2	B	1646	U
2	B	1651	A
2	B	1667	C
2	B	1670	A
56	AA	650	U
56	AA	651	A
56	AA	656	U
56	AA	673	U
56	AA	674	U
56	AA	675	A
56	AA	680	U
56	AA	685	A
56	AA	688	A
56	AA	689	U
56	AA	690	U
56	AA	691	A
56	AA	694	C
56	AA	696	U
56	AA	704	U
56	AA	706	C
56	AA	710	U
56	AA	711	U
56	AA	712	C
56	AA	715	G
56	AA	718	A
56	AA	721	U
56	AA	722	C
56	AA	723	A
56	AA	732	A

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Mol	Chain	Res	Type
56	AA	733	U
56	AA	753	A
56	AA	757	A
56	AA	761	A
56	AA	764	A
56	AA	766	G
56	AA	770	C
56	AA	771	A
56	AA	781	A
56	AA	782	A
56	AA	788	U
56	AA	791	G
56	AA	794	U
56	AA	796	G
56	AA	800	C
56	AA	801	A
56	AA	806	C
56	AA	807	A
56	AA	808	C
56	AA	812	A
56	AA	813	A
56	AA	814	A
56	AA	817	G
56	AA	824	U
56	AA	826	A
56	AA	828	C
56	AA	829	C
56	AA	836	A
56	AA	837	A
56	AA	839	A
56	AA	841	A
56	AA	847	G
56	AA	848	U
56	AA	851	A
56	AA	853	C
56	AA	861	U
56	AA	868	C
56	AA	869	C
56	AA	871	A
56	AA	875	U
56	AA	877	G
56	AA	880	C

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Mol	Chain	Res	Type
56	AA	881	A
56	AA	883	U
56	AA	890	C
56	AA	893	G
56	AA	899	G
56	AA	900	C
56	AA	902	G
56	AA	904	C
56	AA	905	A
56	AA	908	C
56	AA	917	C
56	AA	919	A
56	AA	920	G
56	AA	921	U
56	AA	922	C
56	AA	923	A
56	AA	933	G
56	AA	938	A
56	AA	939	A
56	AA	940	A
56	AA	942	A
56	AA	943	G
56	AA	945	G
56	AA	947	U
56	AA	954	C
56	AA	967	A
56	AA	969	A
56	AA	972	G
56	AA	973	C
56	AA	976	A
56	AA	977	A
56	AA	978	A
56	AA	981	C
56	AA	987	A
56	AA	992	U
56	AA	995	A
56	AA	997	A
56	AA	1000	U
56	AA	1007	G
56	AA	1010	A
56	AA	1012	A
56	AA	1013	A

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Mol	Chain	Res	Type
56	AA	1014	A
56	AA	1015	A
56	AA	1017	A
56	AA	1022	A
56	AA	1031	G
56	AA	1042	U
56	AA	1044	U
56	AA	1048	C
56	AA	1049	A
56	AA	1052	C
56	AA	1054	A
56	AA	1059	U
56	AA	1063	A
56	AA	1064	C
56	AA	1065	C
56	AA	1072	G
56	AA	1080	A
56	AA	1081	U
56	AA	1082	A
56	AA	1089	U
56	AA	1100	C
56	AA	1102	A
56	AA	1105	C
56	AA	1106	C
56	AA	1108	C
56	AA	1109	A
56	AA	1121	A
56	AA	1123	C
56	AA	1125	A
56	AA	1128	C
56	AA	1138	G
56	AA	1142	A
56	AA	1143	C
56	AA	1147	G
56	AA	1151	C
56	AA	1152	A
56	AA	1153	C
56	AA	1154	A
56	AA	1160	A
56	AA	1166	A
56	AA	1167	A
56	AA	1179	G

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Mol	Chain	Res	Type
56	AA	1180	U
56	AA	1187	U
56	AA	1188	A
56	AA	1189	U
56	AA	1190	C
56	AA	1191	C
56	AA	1195	U
56	AA	1200	G
56	AA	1202	G
56	AA	1203	C
56	AA	1206	G
56	AA	1211	G
56	AA	1213	A
56	AA	1214	A
56	AA	1215	U
56	AA	1216	C
56	AA	1217	G
56	AA	1219	U
56	AA	1220	A
56	AA	1223	C
56	AA	1225	C
56	AA	1226	C
56	AA	1227	G
56	AA	1228	A
56	AA	1229	U
56	AA	1230	C
56	AA	1231	A
56	AA	1232	A
56	AA	1234	C
56	AA	1235	U
56	AA	1236	C
56	AA	1237	A
56	AA	1245	U
56	AA	1247	G
56	AA	1248	C
56	AA	1250	C
56	AA	1251	A
56	AA	1253	C
56	AA	1257	U
56	AA	1258	A
56	AA	1269	U
56	AA	1270	U

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Mol	Chain	Res	Type
56	AA	1271	C
56	AA	1272	A
56	AA	1283	A
56	AA	1284	U
56	AA	1285	G
56	AA	1290	C
56	AA	1292	A
56	AA	1293	C
56	AA	1295	A
56	AA	1296	A
56	AA	1298	U
56	AA	1300	A
56	AA	1309	A
56	AA	1311	C
56	AA	1312	C
56	AA	1314	C
56	AA	1315	G
56	AA	1321	A
56	AA	1326	A
56	AA	1327	G
56	AA	1330	C
56	AA	1331	A
56	AA	1332	A
56	AA	1336	G
56	AA	1342	C
56	AA	1343	A
56	AA	1353	A
56	AA	1354	A
56	AA	1355	G
56	AA	1356	A
56	AA	1357	A
56	AA	1358	A
56	AA	1365	A
56	AA	1371	U
56	AA	1372	C
56	AA	1373	U
56	AA	1376	C
56	AA	1378	C
56	AA	1379	A
56	AA	1382	A
56	AA	1383	A
56	AA	1390	A

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Mol	Chain	Res	Type
56	AA	1393	G
56	AA	1397	U
56	AA	1398	U
56	AA	1399	A
56	AA	1400	U
56	AA	1401	G
56	AA	1402	A
56	AA	1408	A
56	AA	1409	A
56	AA	1410	G
56	AA	1412	G
56	AA	1415	G
56	AA	1416	A
56	AA	1418	G
56	AA	1420	U
56	AA	1422	G
56	AA	1429	C
56	AA	1430	A
56	AA	1431	G
56	AA	1442	G
56	AA	1444	A
56	AA	1446	A
56	AA	1447	G
56	AA	1448	U
56	AA	1451	U
56	AA	1454	G
56	AA	1461	A
56	AA	1466	C
56	AA	1478	A
56	AA	1481	C
56	AA	1482	A
56	AA	1491	C
56	AA	1493	C
56	AA	1495	C
56	AA	1503	G
56	AA	1512	A
56	AA	1516	G
56	AA	1523	A
56	AA	1525	C
56	AA	1526	U
56	AA	1527	A
56	AA	1528	A

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Mol	Chain	Res	Type
56	AA	1531	C
56	AA	1532	C
56	AA	1533	C
56	AA	1535	U
56	AA	1536	A
56	AA	1537	C
56	AA	1538	G
56	AA	1539	C
56	AA	1540	A
56	AA	1549	G
56	AA	1554	G
56	AA	1555	A
56	AA	1556	C
56	AA	1560	U
56	AA	1561	C
56	AA	1562	G
56	AA	1564	A
56	AA	1568	U
56	AA	1582	G
56	AA	1594	G
56	AA	1595	G
56	AA	1598	G
56	AA	1599	A
56	AA	1600	A

All (70) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1713	A
1	A	1731	A
1	A	1794	A
1	A	1795	A
1	A	1807	U
1	A	1810	A
1	A	1848	U
1	A	1870	A
1	A	1871	A
1	A	2040	G
1	A	2052	A
1	A	2080	U
1	A	2179	A
1	A	2205	U

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Mol	Chain	Res	Type
1	A	2245	A
1	A	2260	A
1	A	2280	C
1	A	2349	G
1	A	2357	C
1	A	2371	U
1	A	2384	A
1	A	2385	U
1	A	2386	C
1	A	2387	U
1	A	2442	U
1	A	2510	U
1	A	2511	C
1	A	2524	A
1	A	2530	A
1	A	2558	A
1	A	2628	U
1	A	2713	C
1	A	2721	G
1	A	2754	A
1	A	2758	G
1	A	2838	A
1	A	2979	U
1	A	3041	U
1	A	3058	U
1	A	3060	C
1	A	3092	U
1	A	3113	A
1	A	3121	C
1	A	3177	A
1	A	3201	A
1	A	3205	C
2	B	1603	A
2	B	1637	C
56	AA	688	A
56	AA	717	G
56	AA	793	C
56	AA	876	U
56	AA	882	A
56	AA	920	G
56	AA	953	U
56	AA	1012	A

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Mol	Chain	Res	Type
56	AA	1013	A
56	AA	1021	U
56	AA	1062	G
56	AA	1099	C
56	AA	1166	A
56	AA	1213	A
56	AA	1320	G
56	AA	1331	A
56	AA	1415	G
56	AA	1429	C
56	AA	1511	C
56	AA	1515	G
56	AA	1534	C
56	AA	1555	A

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues i

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	14
86	A4	13
56	AA	8
2	B	4

All 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
1	A4	380:ASP	C	386:UNK	N	24.84
1	A4	399:UNK	C	414:LYS	N	22.74
1	B	1651:A	O3'	1658:U	P	19.37
1	A	3207:A	O3'	3212:C	P	19.36
1	A4	345:UNK	C	353:UNK	N	18.19
1	A	2067:C	O3'	2072:A	P	17.99
1	AA	734:C	O3'	740:G	P	17.26
1	A	3196:G	O3'	3201:A	P	16.51
1	AA	1518:C	O3'	1521:U	P	16.45
1	A	2575:U	O3'	2580:U	P	15.23
1	A4	250:UNK	C	255:UNK	N	14.86
1	A	1732:C	O3'	1737:A	P	14.30
1	B	1616:A	O3'	1621:A	P	14.15
1	A4	326:UNK	C	331:UNK	N	13.54
1	A	2351:U	O3'	2357:C	P	13.47
1	AA	1383:A	O3'	1388:C	P	13.43
1	AA	1115:U	O3'	1120:C	P	12.89
1	A4	300:UNK	C	311:UNK	N	12.39
1	A	3109:U	O3'	3113:A	P	12.02
1	A	1935:A	O3'	1938:A	P	11.52
1	A4	362:UNK	C	368:SER	N	11.52
1	AA	1404:A	O3'	1407:U	P	11.35
1	A4	143:GLU	C	145:UNK	N	10.77
1	A4	173:UNK	C	220:UNK	N	10.76
1	AA	928:A	O3'	931:C	P	9.54
1	A4	269:UNK	C	272:UNK	N	8.06
1	A4	156:UNK	C	161:UNK	N	7.08

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	1556:C	O3'	1559:G	P	6.41
1	A4	285:UNK	C	290:UNK	N	6.07
1	A	1709:G	O3'	1711:C	P	5.88
1	A4	232:UNK	C	237:UNK	N	4.45
1	B	1661:A	O3'	1663:C	P	3.29
1	A	2359:C	O3'	2363:A	P	3.25
1	B	1646:U	O3'	1648:U	P	3.15

6 Map visualisation

This section contains visualisations of the EMDDB 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

This section was not generated.