

wwPDB EM Validation Summary Report (i)

Feb 27, 2024 – 01:00 AM EST

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PDB ID	:	
EMDB ID	:	EMD-21233
Title	:	Structure of the human mitochondrial ribosome-EF-G1 complex (ClassI)
Authors	:	Sharma, M.R.; Koripella, R.K.; Agrawal, R.K.
Deposited on	:	2020-01-27
Resolution	:	2.97 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org* A user guide is available at https://www.wwpdb.org/validation/2017/EMValidationReportHelp with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

EMDB validation analysis	:	0.0.1. dev 70
Mogul	:	1.8.5 (274361), 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	:	1.9.13
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 2.97 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)	${ m EM~structures}\ (\#{ m Entries})$		
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 $\leq=5\%$ The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain					
1	АА	954		21% •				
2	AB	296	^{6%}	26%				
3	AC	167	35%	• 21%				
4	AE	125	26%					
5	AI	194	68% •	30%				
6	AJ	138	8%	• 22%				
7	AK	128	19%	• 21%				
8	AM	137	9%83%	• 15%				



Mol	Chain	Length	Quality of chain	
0	A DT	120	—	
9	AN	130	81%	• 18%
10	AO	258	72%	• 26%
11	ΔP	149		220/
11	711	142	• 9%	32 %
12	AQ	87	99%	
13	AT	173	96%	
14	4337	107	10%	
14	AW	187	50% •	48%
15	AX	398	87%	• 11%
16	A2	118	47%	•••
1 17	A TT	201	34%	
1(AH	201	59% •	39%
18	AL	257	66% ·	32%
19	AR	360	81%	• 19%
20	AS	190	68%	29%
01	A T T	205	10%	
21	AU	205	86%	14%
22	AV	414	86%	• 11%
23	AY	395	30% 70%	
94	17	106	46%	
24	AL	100	93%	7%
25	A1	323	83%	• 15%
26	AO	218	95%	
	1.0	100		
27	A3	199	35% • 64%	
28	A4	689	78%	• 20%
29	AD	430	79%	• 20%
30	AF	242	43%	• 14%
31	AG	396	32%	20%
01		000	1 3 /0	20 /0
32	А	1559	75%	23% •
33	В	73	67% 10	% 23%

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Mol	Chain	Length	Quality of chain	
34	D	305	78% •	22%
35	F	311	79% •	20%
36	Н	267	3 6% • 63%	
37	К	178	96%	•••
38	L	145	• 78% •	21%
39	М	296	94%	
40	О	175	85%	• 13%
41	R	149	89%	• • 6%
42	S	205	73% •	24%
43	Т	212	75% •	22%
44	W	148	74%	25%
45	Х	256	91%	• 5%
46	Y	250	68% •	30%
47	Z	161	75%	25%
48	0	188	• 56% • 439	6
49	1	65	77% •	20%
50	2	92	49% • 50%	
51	3	188	50% · 49%	
52	4	103	37% 63%	
53	8	206	48% 52%	
54	b	155	94%	• 5%
55	e	279	10%	22%
56	Q,	166	75%	20%
57	i	128	75%	24%
58	j	123		24%

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Mol	Chain	Length	Quality of chain	
59	m	128	• 34% • 65%	
60	О	102	88%	• 8%
61	q	222	74%	• 24%
62	r	196	• 79%	• 17%
63	J	192	6% 87%	• 9%
64	Ι	261	9% 67% ·	31%
65	Ν	251	88%	12%
66	Р	179	77%	•• 20%
67	U	153	98%	<mark></mark>
68	V	216	• 95%	5%
69	Е	348	86%	• 12%
70	5	423	91%	• 7%
71	6	380	9 2%	• 7%
72	7	338	86%	• 12%
73	9	137	89%	• 9%
74	a	142	74%	• 24%
75	с	332	86%	• 13%
76	d	306	81%	• 16%
77	f	194	75%	• 25%
78	h	158	• 68% •	30%
79	k	112	85%	• 14%
80	1	138	51% ·	48%
81	р	206	۵% 72%	26%
82	s	439	87%	• 10%
83	Q	292	٥ %	• 18%

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Mol	Chain	Length		Quality of chain	
84	ТА	198	20%	77%	
84	TB	198	13%	86%	
84	TC	198	36% 35%	• 64%	
85	u	65	49%	100%	
86	V	751	10%	89%	6% 5%
87	A5	11		100% 100%	
88	A7	71		79% 87%	13%



2 Entry composition (i)

There are 92 unique types of molecules in this entry. The entry contains 174849 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

• Molecule 1 is a RNA chain called 12s rRNA.

Mol	Chain	Residues		A	AltConf	Trace			
1	AA	944	Total 20030	C 8980	N 3612	O 6494	Р 944	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	220	Total 1787	C 1141	N 324	0 312	S 10	0	0

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

Mol	Chain	Residues		At	oms	AltConf	Trace		
3	AC	132	Total 1082	C 699	N 195	0 184	$\begin{array}{c} \mathrm{S} \\ 4 \end{array}$	0	0

• Molecule 4 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
4	AE	122	Total 972	C 614	N 177	0 177	${f S}$ 4	0	0

• Molecule 5 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues		At	oms	AltConf	Trace		
5	AI	136	Total 1011	C 637	N 192	0 178	${S \atop 4}$	0	0

• Molecule 6 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues		At	\mathbf{oms}	AltConf	Trace		
6	AJ	108	Total 838	C 521	N 169	0 142	S 6	0	0



• Molecule 7 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
7	AK	101	Total 861	C 537	N 179	0 140	${ m S}{ m 5}$	0	0

• Molecule 8 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AM	116	Total 920	C 582	N 182	O 150	S 6	0	0

• Molecule 9 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues		At	oms	AltConf	Trace		
9	AN	107	Total 846	C 549	N 153	0 141	${ m S} { m 3}$	0	0

• Molecule 10 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
10	AO	190	Total 1570	C 998	N 291	0 274	S 7	0	0

• Molecule 11 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues		At	oms	AltConf	Trace		
11	AP	96	Total 774	C 498	N 133	0 135	S 8	0	0

• Molecule 12 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AQ	86	Total 740	C 458	N 150	0 124	S 8	0	0

There is a discrepancy between the modelled and reference sequences:

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

• Molecule 13 is a protein called 28S ribosomal protein S25, mitochondrial.



Mol	Chain	Residues		\mathbf{A}	toms			AltConf	Trace
13	AT	168	Total 1371	C 877	N 239	0 244	S 11	0	0

• Molecule 14 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AW	97	Total 766	C 486	N 137	O 139	$\frac{S}{4}$	0	0

• Molecule 15 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
15	AX	353	Total 2860	C 1828	N 503	0 518	S 11	0	0

• Molecule 16 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

Mol	Chain	Residues		At	oms		AltConf	Trace	
16	A2	116	Total 925	C 574	N 181	0 162	S 8	0	0

• Molecule 17 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues		At	oms	AltConf	Trace		
17	AH	122	Total 1014	C 656	N 172	0 183	${ m S} { m 3}$	0	0

• Molecule 18 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues		At	oms	AltConf	Trace		
18	AL	174	Total 1451	C 924	N 271	O 249	${f S}{7}$	0	0

• Molecule 19 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues		At		AltConf	Trace		
19	AR	292	Total 2388	C 1521	N 410	0 449	S 8	0	0

• Molecule 20 is a protein called 28S ribosomal protein S23, mitochondrial.



Mol	Chain	Residues		At	oms	AltConf	Trace		
20	AS	135	Total 1111	C 716	N 198	O 196	S 1	0	0

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

Mol	Chain	Residues		At	oms	AltConf	Trace		
21	AU	177	Total 1499	C 922	N 305	O 268	$\frac{S}{4}$	0	0

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

Mol	Chain	Residues		At	AltConf	Trace			
22	AV	367	Total 3009	C 1931	N 502	0 564	S 12	0	0

• Molecule 23 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
23	AY	120	Total 1016	C 657	N 167	O 190	${ m S} { m 2}$	0	0

• Molecule 24 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
24	AZ	99	Total 833	C 531	N 152	0 146	S 4	0	0

• Molecule 25 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues		At	AltConf	Trace			
25	A1	275	Total 2231	C 1414	N 380	0 426	S 11	0	0

• Molecule 26 is a protein called 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues		Ate	AltConf	Trace			
26	A0	214	Total 1781	C 1125	N 341	0 310	${f S}{5}$	0	0

• Molecule 27 is a protein called Aurora kinase A-interacting protein.



Mol	Chain	Residues		Ate	oms			AltConf	Trace
27	A3	72	Total 639	C 409	N 137	O 92	S 1	0	0

• Molecule 28 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues		At	AltConf	Trace			
28	A4	549	Total 3010	C 1841	N 573	O 593	${ m S} { m 3}$	0	0

• Molecule 29 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
29	AD	343	Total 2731	C 1713	N 518	0 487	S 13	0	0

• Molecule 30 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues		At	AltConf	Trace			
30	AF	208	Total 1724	C 1103	N 312	O 298	S 11	0	0

• Molecule 31 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
31	AG	315	Total 2587	C 1640	N 462	0 471	S 14	0	0

• Molecule 32 is a RNA chain called 16s rRNA.

Mol	Chain	Residues		1	AltConf	Trace			
32	А	1527	Total 32395	C 14536	N 5844	O 10488	Р 1527	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	3107	U	С	conflict	GB 1616239084

• Molecule 33 is a RNA chain called tRNAval.



Mol	Chain	Residues		\mathbf{A}	AltConf	Trace			
33	В	56	Total 1191	С 534	N 214	0 387	Р 56	0	0

• Molecule 34 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues		Ate	AltConf	Trace			
34	D	239	Total 1866	C 1162	N 377	0 318	S 9	0	0

• Molecule 35 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues		Ate	AltConf	Trace			
35	F	250	Total 2013	C 1294	N 365	0 348	S 6	0	0

• Molecule 36 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
36	Н	98	Total 806	C 510	N 156	O 140	0	0

• Molecule 37 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
37	K	177	Total 1451	C 934	N 259	0 251	S 7	0	0

• Molecule 38 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues		At	oms	AltConf	Trace		
38	L	115	Total 889	C 559	N 171	0 154	${f S}{5}$	0	0

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

Mol	Chain	Residues		Ate	AltConf	Trace			
39	М	287	Total 2305	C 1472	N 425	0 402	S 6	0	0

• Molecule 40 is a protein called 39S ribosomal protein L17, mitochondrial.



Mol	Chain	Residues		At	oms			AltConf	Trace
40	Ο	152	Total 1245	C 784	N 239	O 215	${ m S} 7$	0	0

• Molecule 41 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues		At	AltConf	Trace			
41	R	140	Total 1153	C 732	N 231	0 186	$\frac{S}{4}$	0	0

• Molecule 42 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues		At	AltConf	Trace			
42	S	156	Total 1251	C 806	N 222	0 219	${S \atop 4}$	0	0

• Molecule 43 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
43	Т	166	Total 1368	C 875	N 254	0 232	S 7	0	0

• Molecule 44 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
44	W	111	Total 871	C 558	N 164	0 146	${ m S} { m 3}$	0	0

• Molecule 45 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues		At	AltConf	Trace			
45	Х	243	Total 2027	C 1310	N 350	O 362	${ m S}{ m 5}$	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Х	148	ALA	THR	conflict	UNP Q13084
Х	149	SER	PRO	conflict	UNP Q13084
Х	150	GLY	LYS	conflict	UNP Q13084

• Molecule 46 is a protein called 39S ribosomal protein L47, mitochondrial.



Mol	Chain	Residues		At	oms			AltConf	Trace
46	Y	176	Total 1517	C 970	N 291	O 252	$\frac{S}{4}$	0	0

• Molecule 47 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues		At	AltConf	Trace			
47	Z	120	Total 978	C 626	N 183	0 166	${ m S} { m 3}$	0	0

• Molecule 48 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues		At	oms	AltConf	Trace		
48	0	108	Total 880	C 545	N 172	0 157	S 6	0	0

• Molecule 49 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues		Atc	\mathbf{ms}			AltConf	Trace
49	1	52	Total	С	Ν	Ο	\mathbf{S}	0	0
-10	T	02	433	278	83	70	2	0	0

• Molecule 50 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues		Ato	\mathbf{ms}	AltConf	Trace		
50	2	46	Total 376	C 233	N 83	O 59	S 1	0	0

• Molecule 51 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues		At	oms	AltConf	Trace		
51	3	95	Total 831	C 539	N 162	0 127	${ m S} { m 3}$	0	0

• Molecule 52 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues		Atc	\mathbf{ms}	AltConf	Trace		
52	4	38	Total 342	С 217	N 72	O 49	${f S}{4}$	0	0

• Molecule 53 is a protein called 39S ribosomal protein L40, mitochondrial.



Mol	Chain	Residues		At	oms			AltConf	Trace
53	8	99	Total 836	C 535	N 144	0 155	${ m S} { m 2}$	0	0

• Molecule 54 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues		At	oms	AltConf	Trace		
54	b	148	Total 1178	C 733	N 229	0 213	${ m S} { m 3}$	0	0

• Molecule 55 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues		Ate	AltConf	Trace			
55	е	217	Total 1762	C 1124	N 310	O 323	${S \atop 5}$	0	0

• Molecule 56 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues		At	oms		AltConf	Trace	
56	g	132	Total 1096	C 709	N 191	0 194	${ m S} { m 2}$	0	0

• Molecule 57 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
57	i	97	Total 827	C 532	N 165	0 126	S 4	0	0

• Molecule 58 is a protein called cDNA FLJ76418, highly similar to Homo sapiens mitochondrial ribosomal protein L52 (MRPL52), transcript variant 1, mRNA.

Mol	Chain	Residues		At	oms			AltConf	Trace
58	j	93	Total 740	C 460	N 143	0 135	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 59 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues		Atc	\mathbf{ms}	AltConf	Trace		
59	m	45	Total 372	C 232	N 76	O 62	${ m S} { m 2}$	0	0

• Molecule 60 is a protein called Ribosomal protein 63, mitochondrial.



Mol	Chain	Residues		At	oms	AltConf	Trace		
60	О	94	Total 797	$\begin{array}{c} \mathrm{C} \\ 501 \end{array}$	N 165	0 128	${ m S} { m 3}$	0	0

• Molecule 61 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues		At	oms			AltConf	Trace
61	q	168	Total 1294	C 801	N 255	O 233	${S \atop 5}$	0	0

• Molecule 62 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
62	r	162	Total 1322	C 839	N 252	0 223	S 8	0	0

• Molecule 63 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues		At	\mathbf{oms}			AltConf	Trace
63	J	175	Total 1330	C 847	N 237	0 244	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 64 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues		A	toms			AltConf	Trace
64	Ι	179	Total 1435	C 925	N 258	0 242	S 10	0	0

• Molecule 65 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
65	Ν	222	Total 1786	C 1143	N 326	O 307	S 10	0	0

• Molecule 66 is a protein called Mitochondrial ribosomal protein L18, isoform CRA_b.

Mol	Chain	Residues		At	oms	AltConf	Trace		
66	Р	143	Total 1165	C 729	N 223	O 208	${ m S}{ m 5}$	0	0

• Molecule 67 is a protein called 39S ribosomal protein L23, mitochondrial.



Mol	Chain	Residues		At	oms			AltConf	Trace
67	U	152	Total 1224	С 774	N 233	0 214	${ m S} { m 3}$	0	0

• Molecule 68 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues		Ate		AltConf	Trace		
68	V	206	Total 1682	C 1071	N 299	0 304	S 8	0	0

• Molecule 69 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues		At	AltConf	Trace			
69	Е	306	Total 2410	C 1547	N 419	0 433	S 11	0	0

• Molecule 70 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
70	5	394	Total 3210	C 2073	N 560	0 566	S 11	0	0

• Molecule 71 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
71	6	354	Total 2948	C 1881	N 525	O 533	S 9	0	0

• Molecule 72 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
72	7	297	Total 2410	C 1540	N 409	0 443	S 18	0	0

• Molecule 73 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
73	9	124	Total 997	C 644	N 170	0 181	${S \over 2}$	0	0

• Molecule 74 is a protein called 39S ribosomal protein L42, mitochondrial.



Mol	Chain	Residues		At	oms			AltConf	Trace
74	a	108	Total 896	$\begin{array}{c} \mathrm{C} \\ 560 \end{array}$	N 162	0 169	${ m S}{ m 5}$	0	0

• Molecule 75 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues		Ate	AltConf	Trace			
75	с	289	Total 2322	C 1483	N 400	O 430	S 9	0	0

• Molecule 76 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues		At	AltConf	Trace			
76	d	257	Total 2075	C 1326	N 363	0 372	S 14	0	0

• Molecule 77 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
77	f	146	Total 1126	С 714	N 186	O 222	$\frac{S}{4}$	0	0

• Molecule 78 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
78	h	110	Total 894	C 568	N 156	0 167	${ m S} { m 3}$	0	0

• Molecule 79 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
79	k	96	Total 743	C 462	N 143	0 133	${ m S}{ m 5}$	0	0

• Molecule 80 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues		At	oms			AltConf	Trace
80	1	72	Total 619	C 394	N 112	0 111	${ m S} { m 2}$	0	0

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



Mol	Chain	Residues		At	oms			AltConf	Trace
81	р	152	Total 1227	C 762	N 232	O 229	$\frac{S}{4}$	0	0

• Molecule 82 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues		At	AltConf	Trace			
82	s	393	Total 3178	C 2036	N 565	O 563	S 14	0	0

• Molecule 83 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues		Ate	AltConf	Trace			
83	Q	240	Total 1995	C 1280	N 354	0 352	S 9	0	0

• Molecule 84 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues		Aton	ıs		AltConf	Trace
8/	ТΔ	45	Total	С	Ν	0	0	0
04	111	40	345	222	54	69	0	0
81	TB	97	Total	С	Ν	0	0	0
04	ID	21	213	137	33	43	0	0
84	тС	71	Total	С	Ν	0	0	0
04	10	11	352	210	71	71	0	U

• Molecule 85 is a protein called P-site finger.

Mol	Chain	Residues	Atoms			AltConf	Trace	
85	u	65	Total 325	C 195	N 65	O 65	0	0

• Molecule 86 is a protein called Elongation factor G, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace	
86	v	712	Total 5546	C 3494	N 957	O 1062	S 33	0	0

• Molecule 87 is a DNA chain called mRNA.

Mol	Chain	Residues	Atoms				AltConf	Trace	
87	A5	11	Total 213	C 104	N 32	O 66	Р 11	0	0



• Molecule 88 is a DNA chain called E-tRNA.

Mol	Chain	Residues	Atoms			AltConf	Trace		
88	A7	62	Total 1197	C 586	N 180	O 370	Р 61	0	0

• Molecule 89 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
89	AA	26	TotalMg2626	0
89	A2	1	Total Mg 1 1	0
89	AH	1	Total Mg 1 1	0
89	А	97	Total Mg 97 97	0
89	D	1	Total Mg 1 1	0
89	W	1	Total Mg 1 1	0
89	g	1	Total Mg 1 1	0
89	Е	1	Total Mg 1 1	0
89	V	1	Total Mg 1 1	0

• Molecule 90 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
90	AB	1	Total Zn 1 1	0
90	AO	1	Total Zn 1 1	0
90	AP	1	Total Zn 1 1	0
90	AT	1	Total Zn 1 1	0
90	0	1	Total Zn 1 1	0
90	4	1	Total Zn 1 1	0
90	r	1	Total Zn 1 1	0



- Molecule 91 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms			AltConf		
01	٨v	1	Total	С	Ν	Ο	Р	0
91 AA		28	10	5	11	2	U	

• Molecule 92 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms			AltConf		
92	V	1	Total 32	C 11	N 5	O 13	Р 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 and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Chain AA: 78% 21% • Molecule 2: 28S ribosomal protein S2, mitochondrial Chain AB: 73% 26% 3LN CLYSS CL
- Molecule 1: 12s rRNA

• Molecule 3: 28S ribo	somal protein S24, mitoc	hondrial		
Chain AC:	5%			
Chain AC:	78%	•	21%	
MET ALA ALA SER SER VAL CYS SER CYS CYS CYS CYS PRO CICY VAL LEU VAL LEU VAL LEU VAL	SER ARG GLU CLU CLEU PRO CYS ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	K36 N37 R38 A39 A40 R41 V42 R43 V44 S45 S45 S45	G47 D48 K49 L69 S70 L71	D77 G78 A82 A83
E84 E88 E88 E92 H92 W97 W96 W96 W97 W96 M96 M101 C102 C102	D106 Q107 Q107 L108 V109 V109 M112 M112 Q114 Q116 Q116 Q115 Q115 Q115 Q115 Q115 Q115 Q115 Q115 Q115 Q115 Q115 Q115 Q115 Q107 Q108 Q107 Q109 Q107 Q109 Q107 Q109 Q107 Q109 Q107 Q109 Q107 Q109 Q107 Q109 Q107 Q107 Q109 Q107 Q109 Q107 Q109 Q107 Q109 Q107 Q109 Q115 Q15 Q15 Q15 Q15 Q15 Q15 Q15 Q15 Q15	L124 R125 S128 S128 Y132 Y132 Y133 S139 E140	T141 L142 L143 S144 Y145 F146 Y147	P150 V151 R152 L153 H154 L155 P159 S160 K161 V162
1167 ♦				
• Molecule 4: 28S ribo	somal protein S6, mitoch	ondrial		
26%	. ,			
Chain AE:	94%		• •	
MET P2 L10 H13 M13 M13 P16 F17 L22 L22 K23 K24	E27 830 831 831 832 833 63 833 63 833 65 71 172 871 172 876	H81 H84 B85 B85 C91 C109 C100	L102 K103 E104 C105 E106 G107 I108	P110 V111 P112 L113 A114 E115 K122 R122
SAT SAT				
• Molecule 5: 28S ribo	somal protein S11, mitoc	chondrial		
Chain AL				
Chain AI:	68%	• 30	0%	
MET GLN ALA VAL ARG ASN ARG ARG ARG PHE CLEU PHE TTRP SER TTRP TTRP	PRO GLN THR ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	GLY ALA ALA ALA GLN GLN ALA ALA ALA ALA CLN CLN CLN	VAL GLU GLU ALA ALA ALA PRO FRO SER HIS	F60
861 166 166 668 669 669 677 677 677 677 677 677 677	E82 S103 G113 G13 R138 A139 A139 A139 A139 C141 K142 C143 C143 V144	1145		
• Molecule 6: 28S ribo	somal protein S12, mitoc	chondrial		
Chain AJ:	77%	·	22%	
	••	• • • •	• • • •	
MET SERR SERR SER SER CLY CLY CLY CLY CLY CLY CLY CLY CLY CLY	ALA ALA ALA ALA VAL LEU VAL PRO ALA ALA ALA ALA ALA A1 A31 A31 A34 A44	R47 K48 L49 E53 F53 K71 K71 K72 K72 K72 K72	D13. 013. 0136 K13	
• Molecule 7: 28S ribo	somal protein S14, mitoc	chondrial		
Chain AK:	77%	·	21%	
MET ALA ALA ALA ALA ALA MET MET ELEU TLEU LLEU LLEU LLEU TLEU PHE CLN GLN	NAL PRO SER SER SER SER SER CLY VAL CLN VAL CLN VAL CLN VAL CLN VAL CLN VAL CLN VAL CLN VAL SER RAL ARG	K42 E46 D49 N55 € A L62 C61 L62	P64 K65 I66 D69 V70 A71	Dr ≤ E73 A77 L78
	W O R			
	PROTEI	N DATA BANK		





• Molecule 13: 28S ribosomal protein S25, mitochondrial



Chain AT:		96%			
MET P2 E1105 E1123 R132 E133 E138	E142 V143 E144 E144 A165 A165 A165 A165 A165 A169 A169 A169 A169 A169 A161 A	ASP ASP			
• Molecule 14: 28S r	ibosomal protein	S28, mitochond	rial		
Chain AW:	50%	·	48%		
MET ALA ALA ALA CYS CYS ALG ALG ALA ALA ALA ALA ALA ALA ALA	PHE LEU ARG VAL PHE PHE PHE PRO PRO PRO CLV	VAL CALY CLY CLY CLU CLU SER CLU SER CLU SER CLY SER CLY	ALA ALA LLYS GLU PRO LLYS THR ALA ALA GLY	GLY PHE ALA SER ALA LEU GLU GLU HIS SER SER	
HIS GLU HIS LEU LVS CLN LYS CLN LYS CLN CLV CLV CLN CLN CLN CLN CLN SER SER SER SER	V77 V77 E78 A95 X96 D97 B109 N110	R126 P127 E128 V129 R143 L144	L149 F153 V162 N166	V168 L169 L170 ⊕ 173 QLU SER ASP SER ANG SER	
• Molecule 15: 28S r	ibosomal protein	S29, mitochond	rial		
Chain AX:	54%	87%		• 11%	
MET MET LEEU LYS LYS LYS LEU THR NGR SER SER SER SER SER SER SER SER SER SE	LEU ASP ASP CIY AIC AIC AIC AIC AIC AIC AIC	ARC ARC SER ILE ALA ALA ALA ASN ASN CLN	PRU VAL GLU SER PRO A47 A47 S49	R50 T51 N52 E53 N64 P56 A57 K58	C 20 C 20 C 20 C 20 C 20 C 20 C 20 C 20
D61 q62 H63 Y68 Y68 N69 Y170 S71 P72 Q73 D74 L75	E76 177 777 779 779 780 181 181 183 183 183	R86 F87 V88 M89 Q90 K92 F94	S95 E96 A97 C98 V101 P104	L108 L109 Y1110 Y1111 K112 K113 K113 S116	A121 Y124 L126 H140 V141 H143 F144
C145 A146 K147 Q148 D149 H154 H155 P156 H155 A158 H155	W160 W161 V162 K163 N164 C165 R166 L165 L168	Q170 S171 S172 Y173 Y173 K175 K175 R175 F178 F179	q180 P181 L182 E183 A184 A184 T186 T186 W187	L188 K189 F191 F191 T193 T193 K193 E196 F196	F198 L199 N200 Q201 Y204 Y204 C205 K205 K205 K205
Y208 V209 W210 W211 W211 K212 R213 E214 S215 T216 E217 K218 C219	5220 F221 L222 C223 E224 V226 V226 E227 C226 E227	2229 1230 1231 1231 1231 1233 1235 1235 1237	230 239 231 234 241 242 245 K245 K245 K245	2252 1253 0254 M255 A261 V262 V262	N265 A267 A267 V269 V269 C270 R271 T272 T273 T273 K274 K275
R276 E277 D278 K279 K279 F281 F281 F281 F281 F285 F285 F285 F285 F285	A285 N292 4 R294 7 R294 7 N296 7 N296 7 N297 8 N299 8 N297 7 N298 7 N298 7 N298 7 N298 7 N298 7 N298 7 N297 7 N298 7 N297 7 N298 7 N200 N298 7 N298 7	A305 A305 S308 A309 L310 S311 F317 F317 K318	P319 R320 K321 K321 A322 V322 E327 L328 L329 L329	(1330 ♦ K331 € E332 6 (1333 6 F334 € D336 9 D336 9 P339 9 P339	P342 + 1343 + 12344 + V345 + N347 + K351 +
Q358 ← B363 ← N363 ← V365 ← C366 ← C366 ← C366 ← C366 ← C366 ← C367 ← C	P372 T373 E374 E375 E375 E379 L398				
• Molecule 16: Coilec	d-coil-helix-coiled	l-coil-helix doma	in-containing _l	protein 1	
Chain A2:	47%	95%			
MET A2 S5 L5 R7 G14 A30 A30 A30	R38 E39 G41 E42 A43 A43 A43 C45 C45 C45	S50 M53 A54 K57 R57 R57 R59 S60	F61 R62 D63 A65 C66 K67 K68	E69 F07 G71 A77 A78 A78 A80 A80 A80	E82 R84 K85 K85 K85 R87 S88 S88 C90 Q90





















• Molecule 32: 16s rRNA







• Molecule 37: 39S ribosomal protein L13, mitochondrial

Chain K:	96%	<mark>.</mark> .	
MET S2 S5 K24 V101 E143	1151 1158 1178 1178		
• Molecule 38:	39S ribosomal protein L14, mitochondrial		
Chain L:	78%	• 21%	
MET ALA PHE PHE THR GLY CLEU CLEU CLEU CLEU PHO	THR CYS VAL ARG ARG LEU LEU CYS SER HIS FIR FIR CYS SER CYS SER CYS SER THR THR THR THR THR THR THR THR THR TH		
• Molecule 39:	39S ribosomal protein L15, mitochondrial		
Chain M:	94%		
MET ALA GLY PRO LEU GLY GLY GLY A10	R64 R64 R64 R64 R134 R134 R242 R266 R266 R266 R266 R266 R266 R26		
• Molecule 40:	39S ribosomal protein L17, mitochondrial		
Chain O:	85%	• 13%	
MET ARG LEU SER VAL ALA ALA ALA ALA ALA	P111 P111 N128 1128 ALA SER ALA ALA ALA ALA ALA ALA ALA ALA ALA AL		
• Molecule 41:	39S ribosomal protein L20, mitochondrial		
Chain R:	89%	•• 6%	
MET VAL VAL LEU THR ALA GLN LIO LIO	V95 D134 G135 F137 F138 S143 S143 H149		
• Molecule 42:	39S ribosomal protein L21, mitochondrial		
Chain S:	73% .	24%	
MET ALA ALA ALA SER SER SER LEU THR THR LEU CLY	ARG LEU ALA SER ALA CALA CALA SER HITS SER HITS SER ALA ALA ALA ALA ALA ALA ALA SER ALA SER ALA SER SER SER CLY SER ALA SER SER SER SER SER SER SER SER SER SER	THR TYR TYR LEU PLO G49 0145 C145 C145 C145 C145	E165 N196



• Molecule 43: 39S ribosomal protein L22, mitochondrial



Chain T:	75%	• 22%	
MET ALA ALA ALA ALA ALA GLY GLN GLN GLN ALA	LEU TRP TIRP TIRP AHIS ANG ARG ARG ARG ARG ARG ARG CLY CLEU CLEU CLEU CLEU CLEU CLEU CLEU CLEU	ALA SER LEU ASP ASP ASP ASP 147 Y82 Y82 T94 T94	Y158 T211 L212
• Molecule 44:	39S ribosomal protein L27, mitochondrial		
Chain W:	74%	• 25%	
MET ALA SER VAL VAL LEU LEU LEU LEU THR ARG	THR ALA VAL SER SER SER LEU LEU THR PRO PRO PRO PRO PRO PRO PRO PRO PRO PR		
• Molecule 45:	39S ribosomal protein L28, mitochondrial		
Chain X:	91%	• 5%	I
MET P2 E18 K55 A92 A92 T124 V124	1126 F157 F157 F157 L176 E220 E221 C1243 E220 E221 C1243 C1244 <		
• Molecule 46:	39S ribosomal protein L47, mitochondrial		
Chain Y:	68%	30%	I
MET ALA ALA ALA GLY CEU LEU LEU LEU CYS ANG	ARG SER SER SER ALA LEU LEU LYS PRO PRO PRO PRO PRO PRO PRO PRO PRO PRO	THR PRO ASN VAL THR SER PHE HIS GLN TYR LEU LEU	HIS THR LEU SER
ARG LYS L63 L64 E65 E65 E65 S94 S94 R162	4183 1202 1202 1203 1203 1203 1203 1203 120		
• Molecule 47:	39S ribosomal protein L30, mitochondrial		
Chain Z:	75%	25%	
MET ALA GLY ILE LEU ARG LEU VAL CLN GLN	PRO PRO GLV GLV GLV CLU CLVS GLU CLVS GLU CLVS GLU CLVS CLV CLVS CLV CLVS CLV CLVS CLV CLVS CLV CLV CLV CLVS CLV CLV CLV CLV CLV CLV CLV CLV CLV CLV	SER	
• Molecule 48:	39S ribosomal protein L32, mitochondrial		
Chain 0:	56%	43%	
MET ALA LEU ALA MET LEU VAL VAL VAL VAL SER SER	PRO TRP SER ALA ALA ALA ALA ALA CLEU CLEU ARG ALEU ARG ALEU ARG ALEU ARG ALEU ARG ALEU ARG ALEU ARG ALEU ARG ARA ARA ARA ARA ARA ARA ARA ARA ARA	TRP GLY PRO LEU LEU ALA GLN GLN PRO PRO PRO PHE	THR GLU PRO ALA ASN
ASP THR SER GLY GLU GLU ASN SER SER SER	LEU ASP SER SER TILE TRP MET MET C113 E163 E163 E163 E163 E163 E163 E163 E		
• Molecule 49:	39S ribosomal protein L33, mitochondrial		
Chain 1:	77%	• 20%	

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• Molecule 50: 39S ribosomal protein L34, mitochondrial

Chain 2:	49%	50%					
MET ALA VAL LEU GLY SER LEU LEU GLY PRD	THR SER SER SER SER ALA ALA ALA ALA CLEU CLEU CLEU CLEU CLEU ALA ALC ALC CLEU CLEU CLEU CLEU CLEU CLEU CLEU CL	PHE PRO ASP ALA ALA CLY CLY CLY CLN CLN CLN CLN CLN CLN CLN CLN CLN CLN					
• Molecule 51:	39S ribosomal protein L35	, mitochondrial					
Chain 3:	50%	• 49%					
MET ALA ALA SER ALA ALA GLY ALA VAL	ALA ALA SER ALA SER CLY CLY CLEU LLEU LLEU LLEU LLEU LLEU LLEU ARG SER TYR TYR CYS	VAL LYS LYS ALA ALA ALA SER LEU LEU LEU SER ARG CLY ARG CLY THR THR THR CLY VAL CVAL	THR PRO ARG LEU				
THR THR SER SER GLU ARG ASN ASN LEU LEU THR CYS GLY	THR THR VAL TIR TIR THR ALC ANC ANC ANC ANC ANC ANC ANC ANC ANC AN	ARC ARC L944 V188 V188					
• Molecule 52:	39S ribosomal protein L36	, mitochondrial					
Chain 4:	37%	63%					
MET ALA ASN ASN LEU PHE ILE ASG LYS MET VAL	PRO LEU LEU TYR LEU TR LEU ALS PRO PRO ALA LUY SER ALA LEU SER THR LEU LEU	GLY SER ILE ARG GLY ALA PRO PRO CLU VAL ALA ALA ALA ALA ALA ALA ALA CLY PRO SER SER SER SER SER	LEU LEU LEU				
LEU PRO ALA LEU CLY F66 M103							
\bullet Molecule 53: 39S ribosomal protein L40, mitochondrial							
Chain 8:	48%	52%					
MET THR ALA SER VAL LEU LEU ARG SER ILE SER	ALA LEU PARG PARG PARG PARG PARG CLY CLEU CLEU CLAU CLAU CLAU CLAU CLAU CLAU CLAU CLA	GLN ARG ARG SER LEU LEU LEU SER PHE TILE TILE TILE PRO GLU LEU LEU ARG SER ARG SER ARG SLVS LVS LVS	VAL ASP PRO LYS LYS				
ASP GLN GLU CLU ALA ALA CLU CLU CLU LEU CLU CYS CVS	TILE ARG LIYS LIVS LIVS LEU LEU CLU CLU CLU CLU CLU CLU CLU CLU CLU CL	L95 D96 F169 F169 F169 P102 P102 P102 P115 T115 T115 T115 T115 T115 T115 T115	TLE THR LYS LYS TYR TYR GLN				
VAL GLU PHE LYS ARG							
• Molecule 54:	39S ribosomal protein L43	, mitochondrial					
Chain b:	94%	• 5%	I				
MET 12 1113 R116 Q149 Q149 PRD	ALA PRO GLN GLN						

• Molecule 55: 39S ribosomal protein L46, mitochondrial



Chain e:	779	6	22	%	
MET ALA ALA PRO PRO ARG ARG ARG ARG CLEU CLEU	VAL ALA ALA CLY CLY CLY ARG ARG ARG CLU CLU ARG CLU ARG CLU CLU CLU CLU SER ACA	LEU SER SER SER SER SER LEU LEU LLEU ALA ALA ALA ALA SER SER SER	GLY S43 E68 R90	E94 E94 R97 L98 A99 K100 K100 K100	TEU OF
HIS ASP GLU GLU GLU GLU GLN LLEU LLEU LLEU	F131 ◆ A140 ◆ N144 ◆ N199 ◆ M200 €201 ◆	E205 E205 P20 P217 P20 GLN ALA ALA ALA SER ASM ASW ASW	G241 D242 F243 S244 Q245 A246	K249 ◆ L260 K265 D278 L279	
• Molecule 56:	39S ribosomal prote	in L49, mitochondria	al		
Chain g:	75%		••	20%	
MET ALA ALA ALA THR MET PHE ALA ALA THR LEU ARG	GLY TRP ARG GLY GLY GLY GLY GLY GLY CVS GLY LEU LEU LEU	SER CLN THN CLN CLN CLN CLN CLN CLN PRO PRO PRO PSO PSO PSO PSO PSO PSO PSO PSO PSO PS	Y66 D77 P79 P79		
• Molecule 57:	39S ribosomal prote	in L51, mitochondria	al		
Chain i:	75%		• 249	%	
MET ALA GLY ASN LEU LEU LEU SER GLY ALA ALA ARG	ARG LEU TRP ASP ASP VAL PRO PRO ARA CYS SER SER SER SER LEU	GLY VAL PRO ARG LEU LEU LEU R128 R128			
• Molecule 58: L52 (MRPL52)	cDNA FLJ76418, hi , transcript variant	ghly similar to Hom 1, mRNA	o sapiens m	itochondrial rib	osomal protein
Chain j:	75%		• 249	%	
MET ALA ALA ALA LEU VAL THR VAL LEU PHE THR CLU	ARG ARG ARG ARG HIS CYS CYS CYS CYS ALA ALA ALA ALA ALA ALA ALA 740	K61 E106 B107 A108 A108 A108 CVS ERR PRD FRD FRD FRD FRD FRD	GLN		
• Molecule 59:	39S ribosomal prote	in L55, mitochondria	al		
Chain m:	34% ·	65%			
MET ALA ALA ALA CLY CLY CLY SER LEU CLU CLU CLY ARG CLY	ARG GLN SER THR THR LYS ALA ALA ALA ALA ARG ARG ARG ARG	HIS THR SER SER TRP ARG ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	P78 ILE ASP ASP ASP LEU LEU SSC	Frud GLU GLU GLU ARG ARG ARG LEU ARG CLYS GLU GLU	
ALA GLN LEU CLN GLN SER ARG LYS GLU GLU GLN	GLU SER SER ASP ASP ASP LEU HIEU HIEU ARG GLU ARG GLU GLN PHE	THR ARG THR LYS LYS			
• Molecule 60:	Ribosomal protein 6	53, mitochondrial			
Chain o:		88%		• 8%	
MET PHE LEU LEU LEU LEU TRP RIS	P52 061 093 81 02				

R L D W I D E PDB FEIN DATA BANK
\bullet Molecule 61:	Growth arrest and DNA damage-ind	ucible proteins-interac	ting protein 1
Chain q:	74%	• 24%	I
.		•••• •• ••• •	
MET ALA ALA SER VAL ARG GLN ALA SER SER LEU	LEU QLY VAL ALA ALA ALA ALA ALA PALA CLY GLY CLEU CLEU CLY CLEU CLY CLEU CLY CLEU CLY CLEU CLY CLEU CLA CLY CLEU CLEU CLEU CLEU CLEU CLEU CLEU CLEU	E159 A160 A160 E162 L164 L164 C165 C165 G165 Q166 Q169 D169 P170 R171	\$172 A173 R174 F175 Q176 E177 E177 L178 L178 Q180 Q180
*******	•••		
L182 E183 K184 K185 E186 E186 R187 K188 R189	L190 K191 LYS GUN CYS GUN CYS CIN CYS CIN CYS CIN ALA ALA ALA ALA ALA ALA ALA	SER ALA PRO SER SER	
• Molecule 62:	39S ribosomal protein S18a, mitocho	ndrial	
Chain r:	79%	• 17%	
_			
MET ALA ALA LYS LYS LYS ALA LEU VAL CYS CYS	CLY LEU LEU LEU LEU LEU LEU LEU LEU CLY CLY CLY CLY CLY CLY CLY CLY CLY CLY	P14 144 144 144 144 144 146 116	
• Molecule 63:	39S ribosomal protein L11, mitochon	ıdrial	
Chain J:	87%	• 9%	
MET SER LEV SER LEV GLY ALA ALA ARG GLY LEU	ARG LAS PAO CLU CLU CLU CLU CLU CLU CLU CLU	K157 2161 2161 2161 2162 K191 K191	
• Molecule 64:	39S ribosomal protein L10, mitochon	ıdrial	
Chain I:	67%	• 31%	I
MET ALA ALA ALA VAL ALA GLY ARG GLY GLY	CLY LEU PRO PRO PRO PRO CLN ALK CLEU CLEU PRO PRO CO CCO CCO CCO CCO CCO CCO CCO CCO CC	A97 A1043 E107 L110 L110 L112 L113 A E118 B118	R166
*****	****		
K196 L197 P198 S199 L200 P201 L202 V203	9204 6205 6205 6205 6206 627 627 627 718 718 718 718 718 718 718 718 718 71	THR THR LEU LEU LEU ASP GLN GLN GLN GLN GLN GLN CLV SER	VAL MET SER ALA ASN GLY PRO ASP
PRO ASP THR VAL PRO ASP SER			
• Molecule 65:	39S ribosomal protein L16, mitochon	ıdrial	
Chain N:	88%	12%	-
MET TRP TRP LEU LEU LEU ALA ALA SER SER PLA	LEU LEU ARG VAL ARG SER SER SER ALA ALA ALA ALA ALA ALA ALA CU E171 V261		

 \bullet Molecule 66: Mitochondrial ribosomal protein L18, isoform CRA_b



Chain P:	77%	•••	20%
MET LLEU LLEU ARG SER SER TLP PHE PHE SER VAL VAL ARC	ASN PRO GLY ANG ANG ANA ALA ALA ALA ALA ALA ALA ALA ALA ALA	P38 W68 F72 F73 S74 K75 S118 S118 V146	E180
• Molecule 67: 39S	ribosomal protein L23, mitocl	hondrial	
Chain U:	98%		
MET A2 F111 D115 S117 P118 F110 F118 G120 G120 S121	A122		
• Molecule 68: 39S	ribosomal protein L24, mitocl	hondrial	
Chain V:	95%		5%
MET ARG LEU ARG SER SER ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	K100 11 19 12 16 12 16		
• Molecule 69: 39S	ribosomal protein L3, mitocho	ondrial	
Chain E:	86%		• 12%
MET PRO GLY TRP CLEU TRP TRP TRP TRP TRP TRP TRP CLU	LEU GLY ARG CLU ARG CLU CLU CLU GLY ASP ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	PHE VAL ARG GLY LEU HIS D82 0125 0125	K303 P317 S344 A348
• Molecule 70: 39S	ribosomal protein L37, mitocl	hondrial	
Chain 5:	91%		• 7%
MET ALA ALA LEU LEU ALA ALA ARG ARG ARG ARG ARG ARG ARG ARG ARG AR	SER GLY GLY GLY GLY GLY GLY CLEU GLY A1A A1A A1A A1A A1A A1A A1A A1A A1A A1	R72 P73 L114 E148 Q165 P286	E368 D379 A423
• Molecule 71: 39S	ribosomal protein L38, mitocl	hondrial	
Chain 6:	92%		• 7%
MET ALA ALA ALA ALA PRO PRO PRO ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	ARG TRP ARG CLY PHE SER SER SER SER ALA ALA ALA ALA ALA ALA ALA CT CT CT CT CT CT CT CT CT CT CT CT CT	P84 D182 S288 P289 Y380	
• Molecule 72: 39S	ribosomal protein L39, mitocl	hondrial	
Chain 7:	86%		• 12%
MET OLU ALLA ALLA ALLA ALLA MET ALLA ALLA ALLA ALLA ALLA TRP	LEU VAL AAA AAA AAA GLY CLY CLY AAA AAA AAA AAA AAA AAA AAA AAA AAA A	v167 F230 P270 S281 Q287	U322 D322 SER ALA LYS LYS CUU GLU GLU GLU CYS SER THR THR
	VORLD PROTEIN D		

• Molecule 73:	39S ribosomal protein L41, mitochondrial		
Chain 9:	89%	• 9%	
MET GLY VAL LLEU ALA ALA ALA ALA ARG CYS	VAL ARG C14 R31 R137		
• Molecule 74:	39S ribosomal protein L42, mitochondrial		
Chain a:	74%	• 24%	1
MET ALA ALA ALA ALA ALA VAL VAL VAL MET SER	LYS ARG THR THR LEU LEU LEU LEU LEU CLN ALA ALA ALA ALA ALA ALA ALA ALA ALA A	H82 N83 N84 N84 N84 N84 N84 N84 N84 N84 N84 N84	кус 196 697 698 К99 К99 6104 8142
• Molecule 75:	39S ribosomal protein L44, mitochondrial		
Chain c:	86%	• 13%	1
MET ALA ALA GLY GLY VAL LEU CLN GLN	GLY HIS ARG CYS CYS CYS CYS CYS CYS ALA ALA ALA PRO PRO PRO PRO PRO PRO PRO PRO PRO PRO	E183 V186 S251 S251 CYS GLU THR THR LEU	ARG ALA GLU LYS SER THR THR
ALA SER			
• Molecule 76:	39S ribosomal protein L45, mitochondrial		
Chain d:	81%	• 16%	
MET ALA ALA PRO TILE PRO GLY PHE SER CYS	LEU SER SER ARG CLEU CLEU CLEU ARC ARA ARA ARA ALA ALA ALA ALA ALA ALA ALA	R61 K62 A63 G64 L65 L65 V66 K71	A82 A95 I97 S98 S99 L100
S101 K102 E103 G104 L105 E107 R108	1109 R111 R112 R112 R112 R112 R112 R112 R203 R204 R203 R204 R203 R204 R203 R204 R204 R204 R204 R204 <	GLN LEU ALA	
• Molecule 77:	39S ribosomal protein L48, mitochondrial		
Chain f:	75%	25%	
MET SER GLY THR LLEU CLY CLY LLV LLV LLU LEU CYS	ARG ASN ASN ASN ASN ASN ASN ASN ASN CLA CLA ASS ASR ASR ALA ARG ALA ARG ARG ARG ARG ARG CLY CLU CLY SER ARG CLY CLU SER ARG ASN ASN ASN ASN ASN ASN ASN ASN ASN ASN	ILE SER ARG PRO PRO FAS E65 E65 E65 E65 E66	K69 K71 K71 K72 G73 G73 K74 V75
E76 V77 L82 G83 G83 C83 C83 C83 C83 C122	K130 D139 C141 C141 C144 C144 C144 C145 D147 F166 D193 PHE		
• Molecule 78:	39S ribosomal protein L50, mitochondrial		
Chain h:	68% ·	30%	
	PROTEIN DATA BANK		

MET ALA ALA ARG SER VAL SER CLY THR THR ARG	ARG VAL PHE MET TRP TRP THR SER GLY ARC CYS ARG GLV CYS ARG GLV	PHE TRP SER ARG PHE ARG CLU CLYS GLU PRO	VAL VAL VAL CLU CLU CLU CLU CLU CLU CLU CLU	PR0 149 L50 V51 C52 C52 Y73	S81 S81 P83 P83
1158					
• Molecule 79:	39S ribosomal pro-	tein L53, mitoo	chondrial		
Chain k:		85%		• 14%	
MET A2 R11 E40 K41 S44	L47 G69 G69 A96 A18 A18 A14 A14 A14 A14 A14 C17 SER G17 SER G17	ASP LYS PRO GLY GLY ALA ASP GLY GLY ARG			
• Molecule 80:	39S ribosomal pro-	tein L54, mitoc	chondrial		
Chain l:	51%		48%		
MET ALA THR LVS LVS LEU PHE GLY ALA ARG	THR TRP ALLA GLY GLY TRP ALA ALA CLU LEU LEU PRO PRO	THR SER GLY GLY ARG ALA ARG ASP ASP	LYS LYS PRO PRO NET LYS GLY ALA LYS SER SER SER SER SER	LYS GLY ALA VAL THR SER GLU ALA	LEU LYS ASP PRO ASP
VAL CYS THR ASP PRO PRO 067 CL68 CC CL68 T69 T70	IT77 IT77				
• Molecule 81:	Peptidyl-tRNA hy	drolase ICT1,	mitochondrial		
Chain p:	729	%		26%	
MET ALA ALA ALA ARG CYS CYS CYS CYS CYS CYS CYS CYS CYS LEU CLZU	SER ARG ALA ALA CLY VAL TRP PRO PRO PRO PRO PRO ALA ALA CYS CYS	PRO ARG ALA ALA LEU LEU LYS GLN CYS CY	THR E38 G64 A65 K66 A68 A68 A68 A68	172 686 PR0 GLY GLY GLA	ASN VAL ASN K94 V95 T164
E167 P168 T169 K170 E171 D173	4190 1194 8195 8195 1198 1198 1198 1198 1199 1199	ASP			
• Molecule 82:	39S ribosomal pro-	tein S30, mitoc	chondrial		
Chain s:		87%		• 10%	
MET ALA ALA ALA ALA ARG CYS CYS TRP ARG PRO LEU LEU	ARG CLY PRO PRO LEU LEU LEU LEU LEU LEU ALA ALA ALA	ALA THR ALA ALA THR GLU THR THR CYS GLN ASP	ALA ALA ALA ALA P40 P123 E124 P125 E125 P127	E128 P129 P131 P131 E132 P133	R160 V163 R230 P272
D350 1404 E432 E432 LYS SER CLN LEU LEU	GLU ASN				
• Molecule 83:	39S ribosomal pro-	tein L19, mitoc	chondrial		
Chain Q:		79%	·	18%	I
		W O R L PROTEIN	D W I D E D B DATA BANK		

							•••		
MET ALA ALA ALA CYS CYS TLE ALA ALA ALA GLY	HIS TRP ALA ALA ALA MET GLY CLU CLU	ARG SER PHE GLN GLN ALA ALA ALA ARG THR THR TLEU	LEU PRO PRO PRO ALA SER ILE ALA	CYS ARG VAL HIS ALA ALA CLY VAL	ARG GLN GLN SER THR CLY PRO	SER GLU PRO GLY GLY F54	P55 P58 K59 P60	TOA	
162 V63 V65 H66 R67	P68 V69 E70 E72 E72 R73	V215 P226 K227 W229 V229 Y273	R291 S292						
• Molecule	84: 39S ril	posomal prot	tein L12, mi	itochondri	al				
Chain TA:	20% 23%	_		77%			_		
MET LEU PLO ALA ALA ALA ARG PRO	LEU GLY CYS LEU LEU LEU	ARG ALA ALA ALA PHE PHE LEU ARG ARG	ARG GLN VAL PRO CYS CYS CYS	VAL HIS MET ARG SER SER GIY	HIS GLN ARG CYS E46	451 P52 L53 D54 N55	A56 P57 K58 E59 Y60	P61 P62 K63	
164 Q65 Q66 L67 V68 Q69	D70 171 472 873 174 175	L76 L77 E78 E78 179 S80 S80 D81 L82 L82	N83 E84 L85 L85 L86 K87 K87 K88 K88 T89	L90 LYS LYS ILE GLN ASP VAL VAL GLY	LEU VAL PRO MET GLY GLY VAL	MET SER GLY ALA VAL PRO	ALA ALA ALA ALA GLU GLU	ALA VAL GLU GLU ASP ILE PRO TLE	
ALA LYS GLU GLU ARG THR HIS PHE THR	VAL ARG LEU THR GLU ALA LYS PRO	VAL ASP LYS VAL LYS LYS LEU LEU LIEU LYS GLU	ILE LYS ASN TYR ILE GLN GLY ILE	ASN LEU VAL GLN GLN LYS LYS LYS	VAL GLU SER LEU PRO GLN GLU	ILE LYS ALA ASN VAL ALA	LYS ALA GLU ALA GLU LYS		
ILE LYS ALA ALA LEU GLU ALA VAL	GLY GLY VAL VAL VAL LEU CLU GLU								
• Molecule	84: 39S ril	posomal prot	tein L12, mi	itochondri	al				
Chain TB:	13% 14%			86%			_		
MET LEU PRO ALA ALA ALA ARG PRO	LEU GLY PRO CYS LEU GLY LEU	ARG ALA ALA ALA PHE ARG ALA ARG ARG	ARG GLN VAL PRO CYS VAL CYS ALA	VAL ARG MET ARG SER SER GIY	HIS GLN ARG CYS GLU ALA LEU	ALA GLY ALA PRO LEU ASP	ASN ALA PRO LYS GLU TYR		
PR0 PR0 LYS 164 Q65 Q65 L67	V68 Q69 D70 A72 S73	L74 T75 L76 L77 E78 F79 S80	D81 L82 N83 E84 L85 K87	K88 1990 L90 L17 L15 L16 L18	VAL GLY LEU VAL PRO MET GLY	GLY VAL MET SER GLY AIA	VAL PRO ALA ALA ALA ALA	GLN GLU ALA ALA GLU GLU ASP	
ILE PRO ILE ALA LYS GLU ARG THR	HIS PHE VAL ARG LEU THR GLU	ALA LYS PRO VAL ASP LYS VAL LYS LEU	ILE LYS GLU GLU ILE LYS ASN TYR ILE	GLN GLY ASN LEU VAL GLN ATA	LYS LYS LEU VAL GLU SER LEU	PRO GLN GLU ILE LYS ALA	ASN VAL ALA LYS ALA ALA GLU		
ALA GLU CYS LYS LYS ALA ALA LEU	GLU ALA VAL GLY GLY THR VAL VAL	GLU							
• Molecule	84: 39S ril	oosomal prot	tein L12, mi	itochondri	al				
Chain TC:	:	36% 35%		6	4%		_		
MET LEU PRO ALA ALA ALA ALA ARG PRO	LEU TRP GLY PRO CYS CYS CLEU LLEU LLEU	ARG ALA ALA ALA PHE ARG ARG ARG ARG	ARG GLN VAL PRO CYS VAL CYS ALA	VAL ARG MET ARG SER SER CLY	HIS GLN ARG CYS GLU ALA LEU	ALA GLY ALA PRO LEU ASP	ASN ALA PRO LYS GLU TYR		
PRO PRO LYS ILE GLN GLN LEU VAL	GLN ASP ILE ALA SER LEU LEU	LEU GLU TLE SER ASP LEU ASN GLU LEU	LEU LYS LYS LYS THR LEU LYS ILE GLN	ASP VAL GLY LEU VAL PRO MET MET	GLY VAL MET SER GLY ALA VAL	PRO ALA ALA ALA ALA GLN	GLU ALA VAL GLU GLU ASP		
ILE PRO ILE ALA ALA CLU GLU ARG	H129 F130 T131 V132 R133 L134	T135 E136 A137 K138 P139 V140 V140	K142 V143 K144 L145 T146 K147	E148 1149 K150 N151 Y152 1153	Q154 G155 1156 N157 L158 V159	4160 4161 K162 K163	L164 V165 E166 S167 L168	P169 q170 E171 E172 K173 A174	N175 V176 A177 K178 A179 A179 E180



181 182 183 184 185 185 185 188 188 188 198 199 195 195 195 195 195 195		
• Molecule 85: P-site finger		
49%	100%	
X99 X100 X101 X102 X103 X105 X105 X105 X105 X105 X105 X105 X105	X399 X400 X401 X401 X403 X403 X403 X405 X405 X410 X411 X411 X411 X413 X413 X413 X413 X413	X10-01
• Molecule 86: Elongation factor C	G, mitochondrial	
Chain v:	89%	6% 5%
MET MET LEU LEU LEU LEU LEU ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	LYS CLN VALN VALN TRP LYS CYS CYS SER SER SER SER SER SER SER SER SER SE	K80 V85 1102 103 104 H124 H124
A141 L145 V148 V151 K163 K175 F200 F200 F211 L217 F211	E262 1264	T 335 X 340 X
D404 ♦ D424 ♦ A435 ♦ A435 ♦ A435 ♦ A435 ♦ A431 ♦ E442 ♦ R475 ♦ R475 ♦ R475 ♦ T491 ↓ V492 ↓ V492 ↓ V492 ↓ V493 ♦ D536 ♦	K640 K641 9542 S543 6544 6544 6544 7549 6547 7549 650 650 650 650 650 650 653 1563	S570 D571 E572 F574 F574 6575 S576 G575 F574 G575 F582 F582 D592 D592 C594 E595 K596
D613 6614 6614 M618 M618 M618 M619 C052 C0532 C0532 C0535 C0532 A631 L638 M640 M640 M640 M641	roos R7 04 A7 38 A7 38 A7 38 G7 40 G7 41 C7 43 V7 44 K7 46 G7 47 K7 46 G7 47 K7 46 M7 49 M7 49 M7 49 M7 49 M7 50	
• Molecule 87: mRNA		
Chain A5:	100% 100%	
YEP1 A2 YEP3 YEP4 A5 A6 YEP8 A9 YEP10 A11		
• Molecule 88: E-tRNA		
Chain A7:	79% 87%	13%
A1 A2 Y5P3 A5 A6 A6 A6 A7 Y5P8 Y5P8 Y5P12 Y5P12 Y5P12 Y5P13 A16 Y5P13 A16 Y5P13 A16 Y5P13 A16 Y5P13 A16 A18 A18 A18 A18 A18 A18 A18 A18 A18 A18	Y5P21 Y5P22 Y5P22 Y5P24 Y5P25 A27 A27 A27 Y5P Y5P Y5P Y5P Y5P37 Y5	A41 A42 A43 Y5544 Y5544 Y5547 A48 Y5551 A49 Y5551 A49 Y5553 A54 Y5553 A54 Y5553 Y5553 Y5553 Y5555 Y5555 Y5555 Y5555 Y5555 Y5556 Y5567 Y5677 Y5777 Y5777 Y5777 Y5777 Y5777 Y5777 Y5777 Y5777 Y5777 Y5777 Y5777 Y5777 Y5777 Y57777 Y57777 Y57777 Y577777 Y577777777
Y5P61 Y5P62 Y5P63 Y5P65 Y5P63 Y5P64 Y5P63 Y5P43		



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	99804	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	69.2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.725	Depositor
Minimum map value	-1.810	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.111	Depositor
Recommended contour level	0.267	Depositor
Map size (Å)	438.44, 438.44, 438.44	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0961, 1.0961, 1.0961	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: GCP, GDP, P5P, Y5P, 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).

Mal	Chain	Chain Bond lengths		Bond angles		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	AA	0.14	0/22406	0.73	11/34881~(0.0%)	
2	AB	0.23	0/1830	0.38	0/2477	
3	AC	0.23	0/1112	0.38	0/1505	
4	AE	0.23	0/989	0.43	0/1335	
5	AI	0.24	0/1031	0.45	0/1390	
6	AJ	0.23	0/854	0.41	0/1148	
7	AK	0.21	0/879	0.37	0/1182	
8	AM	0.23	0/941	0.39	0/1265	
9	AN	0.23	0/864	0.40	0/1169	
10	AO	0.23	0/1624	0.37	0/2209	
11	AP	0.23	0/791	0.36	0/1062	
12	AQ	0.22	0/752	0.36	0/1001	
13	AT	0.24	0/1402	0.39	0/1883	
14	AW	0.23	0/778	0.42	0/1048	
15	AX	0.23	0/2932	0.39	0/3968	
16	A2	0.23	0/939	0.38	0/1256	
17	AH	0.23	0/1037	0.40	0/1403	
18	AL	0.23	0/1475	0.34	0/1970	
19	AR	0.23	0/2435	0.37	0/3288	
20	AS	0.24	0/1138	0.37	0/1533	
21	AU	0.23	0/1521	0.34	0/2039	
22	AV	0.23	0/3071	0.36	0/4147	
23	AY	0.24	0/1046	0.40	0/1410	
24	AZ	0.24	0/851	0.37	0/1133	
25	A1	0.23	0/2277	0.36	0/3079	
26	A0	0.22	0/1827	0.38	0/2473	
27	A3	0.23	0/650	0.36	0/855	
28	A4	0.23	0/3028	0.36	0/4197	
29	AD	0.23	0/2783	0.39	0/3724	
30	AF	0.23	0/1765	0.38	0/2369	
31	AG	0.23	0/2642	0.39	0/3538	
32	A	0.14	$0/3\overline{6246}$	0.74	6/56422 $(0.0%)$	



Mal	Chain	Bond lengths		Bond angles		
	Unain	RMSZ	# Z > 5	RMSZ	# Z > 5	
33	В	0.13	0/1328	0.71	0/2056	
34	D	0.23	0/1904	0.41	0/2561	
35	F	0.23	0/2071	0.39	0/2817	
36	Н	0.22	0/820	0.41	0/1102	
37	Κ	0.23	0/1495	0.38	0/2029	
38	L	0.23	0/904	0.41	0/1218	
39	М	0.24	0/2359	0.38	0/3185	
40	0	0.23	0/1269	0.39	0/1708	
41	R	0.23	0/1174	0.42	1/1572~(0.1%)	
42	S	0.23	0/1276	0.47	2/1729~(0.1%)	
43	Т	0.23	0/1402	0.38	0/1886	
44	W	0.24	0/893	0.42	0/1204	
45	Х	0.23	0/2081	0.37	0/2812	
46	Y	0.23	0/1552	0.35	0/2079	
47	Ζ	0.23	0/1003	0.39	0/1354	
48	0	0.22	0/895	0.40	0/1201	
49	1	0.23	0/438	0.41	0/583	
50	2	0.22	0/382	0.38	0/507	
51	3	0.23	0/852	0.38	0/1136	
52	4	0.22	0/350	0.39	0/461	
53	8	0.23	0/855	0.38	0/1152	
54	b	0.23	0/1202	0.40	0/1626	
55	е	0.24	0/1797	0.40	0/2422	
56	g	0.25	0/1132	0.41	0/1543	
57	i	0.23	0/849	0.36	0/1135	
58	j	0.23	0/755	0.38	0/1016	
59	m	0.21	0/379	0.41	0/510	
60	0	0.22	0/818	0.36	0/1097	
61	q	0.23	0/1325	0.39	0/1799	
62	r	0.22	0/1362	0.37	0/1846	
63	J	0.30	0/1348	0.47	0/1813	
64	Ι	0.24	0/1467	0.42	0/1984	
65	N	0.24	0/1833	0.40	0/2468	
66	Р	0.25	0/1191	0.48	0/1611	
67	U	0.24	0/1254	0.39	0/1700	
68	V	0.23	0/1727	0.40	0/2341	
69	Е	0.24	0/2479	0.40	0/3360	
70	5	0.29	1/3305~(0.0%)	0.43	0/4502	
71	6	0.23	0/3043	0.39	0/4140	
72	7	0.23	0/2467	0.39	0/3337	
73	9	0.25	0/1025	0.39	0/1379	
74	a	0.22	0/923	0.39	0/1254	
75	с	0.24	0/2371	0.37	0/3205	



Mal	Chain	Bo	ond lengths	E	Bond angles
	Ullalli	RMSZ	# Z > 5	RMSZ	# Z > 5
76	d	0.24	0/2132	0.40	0/2887
77	f	0.23	0/1144	0.43	0/1551
78	h	0.23	0/917	0.38	0/1249
79	k	0.23	0/754	0.40	0/1017
80	1	0.23	0/636	0.37	0/860
81	р	0.22	0/1246	0.39	0/1675
82	s	0.24	0/3262	0.40	0/4435
83	Q	0.24	0/2044	0.39	0/2757
84	TA	0.23	0/349	0.41	0/475
84	TB	0.21	0/212	0.39	0/286
84	TC	0.24	0/351	0.41	0/488
86	V	0.25	0/5647	0.44	0/7623
All	All	0.21	1/181965~(0.0%)	0.54	$20/258102 \ (0.0\%)$

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
41	R	0	1
42	S	0	1
56	g	0	1
66	Р	0	1
82	s	0	1
86	V	0	1
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	$\operatorname{Ideal}(\operatorname{\AA})$
70	5	69	TRP	CD2-CE2	-6.57	1.33	1.41

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	AA	765	С	C2-N1-C1'	8.18	127.80	118.80
1	AA	1443	U	C2-N1-C1'	7.01	126.12	117.70
32	А	3169	С	C2-N1-C1'	6.91	126.40	118.80
1	AA	765	С	N1-C2-O2	6.87	123.02	118.90
32	А	3169	С	N1-C2-O2	6.45	122.77	118.90



There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
66	Р	72	PHE	Peptide
41	R	134	ASP	Peptide
42	S	144	LEU	Peptide
56	g	79	PRO	Peptide
82	s	160	ARG	Peptide

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 (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perc	entiles
2	AB	218/296~(74%)	187 (86%)	27~(12%)	4 (2%)	8	35
3	AC	130/167~(78%)	107 (82%)	22 (17%)	1 (1%)	19	55
4	AE	120/125~(96%)	98 (82%)	18 (15%)	4 (3%)	4	19
5	AI	134/194~(69%)	113 (84%)	18 (13%)	3 (2%)	6	29
6	AJ	106/138~(77%)	92 (87%)	12 (11%)	2 (2%)	8	33
7	AK	99/128~(77%)	88 (89%)	8 (8%)	3 (3%)	4	21
8	AM	114/137~(83%)	103 (90%)	10 (9%)	1 (1%)	17	53
9	AN	105/130~(81%)	85 (81%)	18 (17%)	2 (2%)	8	33
10	AO	188/258~(73%)	166 (88%)	18 (10%)	4 (2%)	7	30
11	AP	94/142~(66%)	82 (87%)	10 (11%)	2 (2%)	7	30
12	AQ	84/87~(97%)	71 (84%)	13 (16%)	0	100	100
13	AT	166/173~(96%)	149 (90%)	16 (10%)	1 (1%)	25	61
14	AW	95/187~(51%)	77 (81%)	15 (16%)	3 (3%)	4	20



<i>a i</i> :	1 C		
Continuea	l trom	previous	<i>paae</i>
0 0 1 0 0 0 0 0 0 0 0 0	<i>.</i>	proceed as	P ~ 9 ~

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
15	AX	351/398~(88%)	319 (91%)	28 (8%)	4 (1%)	14	47
16	A2	114/118~(97%)	96 (84%)	17~(15%)	1 (1%)	17	53
17	AH	120/201~(60%)	101 (84%)	16~(13%)	3 (2%)	5	26
18	AL	172/257~(67%)	154 (90%)	15 (9%)	3 (2%)	9	36
19	AR	290/360~(81%)	263 (91%)	26 (9%)	1 (0%)	41	74
20	AS	133/190~(70%)	119 (90%)	10 (8%)	4 (3%)	4	21
21	AU	175/205~(85%)	163 (93%)	12 (7%)	0	100	100
22	AV	363/414~(88%)	319 (88%)	36 (10%)	8 (2%)	6	29
23	AY	118/395~(30%)	107 (91%)	10 (8%)	1 (1%)	19	55
24	AZ	97/106~(92%)	82 (84%)	15 (16%)	0	100	100
25	A1	273/323 (84%)	242 (89%)	25 (9%)	6 (2%)	6	29
26	A0	212/218~(97%)	185 (87%)	22 (10%)	5 (2%)	6	27
27	A3	70/199~(35%)	64 (91%)	6 (9%)	0	100	100
28	A4	541/689~(78%)	465 (86%)	66 (12%)	10 (2%)	8	35
29	AD	341/430~(79%)	306 (90%)	31 (9%)	4 (1%)	13	45
30	AF	206/242~(85%)	180 (87%)	23 (11%)	3 (2%)	10	39
31	AG	311/396~(78%)	272 (88%)	37 (12%)	2 (1%)	25	61
34	D	237/305~(78%)	208 (88%)	27 (11%)	2 (1%)	19	55
35	F	248/311~(80%)	217 (88%)	27 (11%)	4 (2%)	9	38
36	Н	96/267~(36%)	84 (88%)	10 (10%)	2 (2%)	7	30
37	Κ	175/178~(98%)	153 (87%)	16 (9%)	6 (3%)	3	18
38	L	113/145~(78%)	102 (90%)	10 (9%)	1 (1%)	17	53
39	М	285/296~(96%)	252 (88%)	26 (9%)	7 (2%)	5	26
40	Ο	150/175~(86%)	128 (85%)	19 (13%)	3 (2%)	7	32
41	R	138/149~(93%)	123 (89%)	10 (7%)	5 (4%)	3	17
42	S	154/205~(75%)	135 (88%)	15 (10%)	4 (3%)	5	25
43	Т	$\overline{164/212}~(77\%)$	148 (90%)	13 (8%)	3 (2%)	8	35
44	W	109/148~(74%)	97~(89%)	11 (10%)	1 (1%)	17	53
45	Х	241/256~(94%)	212 (88%)	24 (10%)	5 (2%)	7	30
46	Y	174/250~(70%)	161 (92%)	7 (4%)	6 (3%)	3	18
47	Z	$118/16\overline{1}\ (73\%)$	106 (90%)	12 (10%)	0	100	100



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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
48	0	106/188~(56%)	93 (88%)	10 (9%)	3 (3%)	5	23
49	1	50/65~(77%)	42 (84%)	7 (14%)	1 (2%)	7	32
50	2	44/92~(48%)	41 (93%)	2~(4%)	1 (2%)	6	28
51	3	93/188~(50%)	84 (90%)	8 (9%)	1 (1%)	14	47
52	4	36/103~(35%)	34 (94%)	2~(6%)	0	100	100
53	8	97/206~(47%)	85 (88%)	12 (12%)	0	100	100
54	b	146/155~(94%)	129 (88%)	14 (10%)	3 (2%)	7	30
55	е	211/279~(76%)	188 (89%)	22 (10%)	1 (0%)	29	66
56	g	130/166~(78%)	109 (84%)	17 (13%)	4 (3%)	4	20
57	i	95/128~(74%)	75 (79%)	20 (21%)	0	100	100
58	j	91/123~(74%)	84 (92%)	6~(7%)	1 (1%)	14	47
59	m	43/128~(34%)	34 (79%)	8 (19%)	1 (2%)	6	28
60	О	92/102~(90%)	79~(86%)	10 (11%)	3 (3%)	4	19
61	q	166/222~(75%)	154 (93%)	10 (6%)	2 (1%)	13	45
62	r	160/196~(82%)	139 (87%)	16 (10%)	5 (3%)	4	20
63	J	173/192~(90%)	152 (88%)	15 (9%)	6 (4%)	3	18
64	Ι	177/261~(68%)	164 (93%)	12 (7%)	1 (1%)	25	61
65	Ν	220/251~(88%)	203 (92%)	16 (7%)	1 (0%)	29	66
66	Р	141/179~(79%)	123 (87%)	14 (10%)	4 (3%)	5	23
67	U	150/153~(98%)	122 (81%)	26~(17%)	2 (1%)	12	43
68	V	204/216~(94%)	179 (88%)	25~(12%)	0	100	100
69	Е	304/348~(87%)	268 (88%)	32 (10%)	4 (1%)	12	43
70	5	392/423~(93%)	347 (88%)	41 (10%)	4 (1%)	15	50
71	6	352/380~(93%)	302 (86%)	47 (13%)	3 (1%)	17	53
72	7	295/338~(87%)	260 (88%)	28~(10%)	7 (2%)	6	27
73	9	122/137~(89%)	106 (87%)	15~(12%)	1 (1%)	19	55
74	a	106/142~(75%)	95~(90%)	8 (8%)	3 (3%)	5	23
75	с	287/332 (86%)	265 (92%)	18 (6%)	4 (1%)	11	41
76	d	255/306~(83%)	216 (85%)	33~(13%)	6 (2%)	6	27
77	f	$144/\overline{194~(74\%)}$	121 (84%)	22(15%)	1 (1%)	22	58
78	h	108/158~(68%)	93 (86%)	13 (12%)	2 (2%)	8	33



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
79	k	94/112~(84%)	85~(90%)	9 (10%)	0	100	100
80	1	70/138~(51%)	62~(89%)	7 (10%)	1 (1%)	11	41
81	р	148/206~(72%)	130 (88%)	16 (11%)	2 (1%)	11	41
82	S	391/439~(89%)	342 (88%)	41 (10%)	8 (2%)	7	32
83	Q	238/292~(82%)	211 (89%)	20 (8%)	7 (3%)	4	22
84	ТА	43/198~(22%)	32~(74%)	11 (26%)	0	100	100
84	TB	25/198~(13%)	24 (96%)	1 (4%)	0	100	100
84	TC	69/198~(35%)	57~(83%)	11 (16%)	1 (1%)	11	41
86	v	710/751~(94%)	566 (80%)	117 (16%)	27 (4%)	3	16
All	All	14720/19244~(76%)	12876 (88%)	1589 (11%)	255 (2%)	13	36

5 of 255 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	AI	68	GLY
22	AV	35	VAL
28	A4	203	PRO
40	0	111	PRO
41	R	137	GLU

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	AB	193/249~(78%)	192 (100%)	1 (0%)	88 95
3	AC	115/143~(80%)	115 (100%)	0	100 100
4	AE	104/107~(97%)	103~(99%)	1 (1%)	76 91
5	AI	104/147~(71%)	103 (99%)	1 (1%)	76 91
6	AJ	93/118~(79%)	93~(100%)	0	100 100
7	AK	91/113~(80%)	91 (100%)	0	100 100
8	AM	95/113~(84%)	94 (99%)	1 (1%)	73 90



Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
9	AN	93/115~(81%)	93 (100%)	0	100	100
10	AO	171/230~(74%)	171 (100%)	0	100	100
11	AP	87/123 (71%)	85 (98%)	2 (2%)	50	79
12	AQ	78/79~(99%)	78 (100%)	0	100	100
13	AT	153/157~(98%)	152 (99%)	1 (1%)	84	93
14	AW	84/158~(53%)	84 (100%)	0	100	100
15	AX	312/351~(89%)	311 (100%)	1 (0%)	92	97
16	A2	99/101~(98%)	96 (97%)	3 (3%)	41	73
17	AH	112/180~(62%)	111 (99%)	1 (1%)	78	91
18	AL	157/226~(70%)	155 (99%)	2 (1%)	69	88
19	AR	262/318~(82%)	261 (100%)	1 (0%)	91	97
20	AS	116/164~(71%)	115 (99%)	1 (1%)	78	91
21	AU	153/174~(88%)	153 (100%)	0	100	100
22	AV	328/364~(90%)	323 (98%)	5 (2%)	65	86
23	AY	111/357~(31%)	111 (100%)	0	100	100
24	AZ	89/95~(94%)	89 (100%)	0	100	100
25	A1	253/291~(87%)	253 (100%)	0	100	100
26	A0	186/190~(98%)	184 (99%)	2 (1%)	73	90
27	A3	66/166~(40%)	63 (96%)	3 (4%)	27	62
28	A4	83/609 (14%)	83 (100%)	0	100	100
29	AD	286/357~(80%)	286 (100%)	0	100	100
30	AF	185/209~(88%)	178 (96%)	7 (4%)	33	67
31	AG	273/342~(80%)	272 (100%)	1 (0%)	91	97
34	D	193/245~(79%)	193 (100%)	0	100	100
35	F	217/262~(83%)	216 (100%)	1 (0%)	88	95
36	Н	88/228~(39%)	88 (100%)	0	100	100
37	K	155/156~(99%)	155 (100%)	0	100	100
38	L	98/124~(79%)	97 (99%)	1 (1%)	76	91
39	М	245/249~(98%)	242 (99%)	3 (1%)	71	89
40	0	133/150~(89%)	133 (100%)	0	100	100
41	R	118/126~(94%)	117 (99%)	1 (1%)	81	92



Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
42	S	141/180~(78%)	140 (99%)	1 (1%)	84	93
43	Т	146/182~(80%)	143 (98%)	3 (2%)	53	80
44	W	91/119~(76%)	91 (100%)	0	100	100
45	Х	217/227~(96%)	211 (97%)	6 (3%)	43	75
46	Y	159/223~(71%)	157 (99%)	2 (1%)	69	88
47	Ζ	111/147~(76%)	111 (100%)	0	100	100
48	0	97/164~(59%)	97 (100%)	0	100	100
49	1	49/60~(82%)	48 (98%)	1 (2%)	55	81
50	2	40/72~(56%)	40 (100%)	0	100	100
51	3	88/166~(53%)	88 (100%)	0	100	100
52	4	37/89~(42%)	37 (100%)	0	100	100
53	8	91/190~(48%)	91 (100%)	0	100	100
54	b	130/135~(96%)	130 (100%)	0	100	100
55	е	188/236~(80%)	186 (99%)	2 (1%)	73	90
56	g	122/148~(82%)	119 (98%)	3 (2%)	47	77
57	i	86/110 (78%)	85 (99%)	1 (1%)	71	89
58	j	74/97~(76%)	74 (100%)	0	100	100
59	m	40/113~(35%)	40 (100%)	0	100	100
60	О	80/87~(92%)	79~(99%)	1 (1%)	69	88
61	q	114/178~(64%)	113 (99%)	1 (1%)	78	91
62	r	147/169~(87%)	145 (99%)	2 (1%)	67	86
63	J	138/150~(92%)	136 (99%)	2 (1%)	67	86
64	Ι	164/232~(71%)	161 (98%)	3 (2%)	59	83
65	Ν	189/211~(90%)	189 (100%)	0	100	100
66	Р	125/154~(81%)	123 (98%)	2 (2%)	62	85
67	U	126/135~(93%)	126 (100%)	0	100	100
68	V	184/191~(96%)	183 (100%)	1 (0%)	88	95
69	Е	260/290~(90%)	259 (100%)	1 (0%)	91	97
70	5	353/368~(96%)	349 (99%)	4 (1%)	73	90
71	6	313/332~(94%)	312 (100%)	1 (0%)	92	97
72	7	272/303~(90%)	272 (100%)	0	100	100



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
73	9	104/112~(93%)	103~(99%)	1 (1%)	76	91	
74	a	101/133~(76%)	101 (100%)	0	100	100	
75	с	253/288~(88%)	253~(100%)	0	100	100	
76	d	224/274~(82%)	222~(99%)	2 (1%)	78	91	
77	f	122/173~(70%)	122 (100%)	0	100	100	
78	h	104/148~(70%)	103 (99%)	1 (1%)	76	91	
79	k	81/90~(90%)	80 (99%)	1 (1%)	71	89	
80	1	67/116~(58%)	66~(98%)	1 (2%)	65	86	
81	р	134/181~(74%)	132 (98%)	2 (2%)	65	86	
82	\mathbf{S}	336/381~(88%)	335~(100%)	1 (0%)	92	97	
83	Q	221/256~(86%)	219~(99%)	2 (1%)	78	91	
84	ТА	39/158~(25%)	39 (100%)	0	100	100	
84	TB	26/158~(16%)	26 (100%)	0	100	100	
86	v	598/630~(95%)	580(97%)	18 (3%)	41	73	
All	All	12561/16442~(76%)	12455 (99%)	106 (1%)	82	92	

 $5~{\rm of}~106$ residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
56	g	77	ASP
69	Е	303	LYS
86	V	393	VAL
60	0	93	ASP
64	Ι	34	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 200 such sidechains are listed below:

Mol	Chain	Res	Type
58	j	63	GLN
69	Е	313	ASN
86	V	678	GLN
61	q	81	GLN
64	Ι	91	GLN

5.3.3 RNA (i)



Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	940/954~(98%)	191 (20%)	7~(0%)
32	А	1523/1559~(97%)	347 (22%)	18 (1%)
33	В	51/73~(69%)	6 (11%)	1 (1%)
All	All	2514/2586~(97%)	544 (21%)	26 (1%)

5 of 544 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	650	U
1	AA	651	А
1	AA	674	U
1	AA	676	G
1	AA	680	U

5 of 26 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
32	А	2165	С
32	А	2457	А
32	А	3196	G
32	А	2245	А
32	А	2507	А

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

73 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).

Mal	Turne	Chain	Dec	Ros	Tinle	Bo	ond leng	ths	B	ond ang	les
IVIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2	
88	P5P	A7	1	88	16,20,24	1.44	1 (6%)	14,29,36	2.06	2 (14%)	
88	Y5P	A7	50	88	14,19,20	3.46	1 (7%)	18,26,29	0.99	1 (5%)	
88	P5P	A7	23	88	16,23,24	1.38	2 (12%)	14,33,36	1.99	2 (14%)	
88	Y5P	A7	17	88	14,19,20	<mark>3.53</mark>	1 (7%)	18,26,29	0.93	1 (5%)	
88	Y5P	A7	8	88	14,19,20	<mark>3.65</mark>	1 (7%)	18,26,29	0.96	2 (11%)	



Mal	Tune	Chain	Dec	Tink	Bond lengths		Bond angles			
	туре	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
88	P5P	A7	19	88	16,23,24	1.43	2 (12%)	14,33,36	<mark>2.19</mark>	3 (21%)
88	P5P	A7	4	88	16,23,24	1.36	2 (12%)	14,33,36	2.21	3 (21%)
88	Y5P	A7	37	88	14,19,20	3.44	1 (7%)	18,26,29	0.99	2 (11%)
88	Y5P	A7	69	88	14,19,20	3.50	1 (7%)	18,26,29	1.00	2 (11%)
87	P5P	A5	9	87	16,23,24	1.34	2 (12%)	14,33,36	2.00	2 (14%)
88	P5P	A7	43	88	16,23,24	1.54	3 (18%)	14,33,36	2.43	4 (28%)
88	Y5P	A7	46	88	14,19,20	<mark>3.59</mark>	1 (7%)	18,26,29	1.08	2 (11%)
88	Y5P	A7	58	88	14,19,20	3.61	1 (7%)	18,26,29	1.05	1 (5%)
87	P5P	A5	5	87	16,23,24	1.38	2 (12%)	14,33,36	2.07	2 (14%)
88	P5P	A7	48	88	16,23,24	1.35	2 (12%)	14,33,36	2.16	2 (14%)
88	Y5P	A7	62	88	14,19,20	3.49	1 (7%)	18,26,29	1.08	1 (5%)
88	P5P	A7	49	88	16,23,24	1.39	2 (12%)	14,33,36	2.13	2 (14%)
88	Y5P	A7	55	88	14,19,20	3.44	1 (7%)	18,26,29	1.10	1 (5%)
88	P5P	A7	40	88	16,23,24	1.36	2 (12%)	14,33,36	2.13	2 (14%)
87	Y5P	A5	7	87	14,19,20	3.57	1 (7%)	18,26,29	1.03	2 (11%)
88	Y5P	A7	3	88	14,19,20	3.58	1 (7%)	18,26,29	1.09	1 (5%)
88	P5P	A7	10	88	16,23,24	1.35	2 (12%)	14,33,36	2.10	2 (14%)
87	Y5P	A5	4	87	14,19,20	3.75	2 (14%)	18,26,29	1.53	3 (16%)
88	P5P	A7	41	88	16,23,24	1.41	2 (12%)	14,33,36	1.94	2 (14%)
88	P5P	A7	16	88	16,23,24	1.54	4 (25%)	14,33,36	2.29	3 (21%)
87	P5P	A5	2	87	16,23,24	1.50	2 (12%)	14,33,36	2.09	2 (14%)
88	Y5P	A7	21	88	14,19,20	3.50	1 (7%)	18,26,29	1.14	1 (5%)
88	Y5P	A7	67	88	14,19,20	3.75	1 (7%)	18,26,29	1.15	1 (5%)
88	P5P	A7	5	88	16,23,24	1.36	1 (6%)	14,33,36	2.14	2 (14%)
88	Y5P	A7	13	88	14,19,20	3.33	1 (7%)	18,26,29	0.85	1 (5%)
88	Y5P	A7	51	88	14,19,20	3.49	1 (7%)	18,26,29	1.04	2 (11%)
88	Y5P	A7	68	88	14,19,20	3.58	1 (7%)	18,26,29	1.30	3 (16%)
88	Y5P	A7	25	88	14,19,20	3.40	1 (7%)	18,26,29	0.96	1 (5%)
88	Y5P	A7	44	88	14,19,20	3.72	1 (7%)	18,26,29	0.94	1 (5%)
88	Y5P	A7	47	88	14,19,20	3.59	1 (7%)	18,26,29	1.12	1 (5%)
87	Y5P	A5	10	87	14,19,20	3.45	1 (7%)	18,26,29	0.99	1 (5%)
88	Y5P	A7	63	88	14,19,20	3.50	1 (7%)	18,26,29	1.08	2 (11%)
88	P5P	A7	2	88	16,23,24	1.54	3 (18%)	14,33,36	2.22	2 (14%)
88	P5P	A7	52	88	16,23,24	1.42	2 (12%)	14,33,36	2.16	3 (21%)
88	P5P	A7	54	88	16,23,24	1.40	2 (12%)	14,33,36	2.05	2 (14%)



Mal	Tuno	Chain	Dec	Tink	Bond lengths		Bond angles			
10101	туре	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
88	Y5P	A7	53	88	14,19,20	3.80	1 (7%)	18,26,29	1.18	2 (11%)
88	P5P	A7	26	88	16,23,24	1.38	2 (12%)	14,33,36	2.20	2 (14%)
88	P5P	A7	27	88	16,23,24	1.34	1 (6%)	14,33,36	2.20	2 (14%)
88	P5P	A7	39	88	16,23,24	1.35	2 (12%)	14,33,36	2.21	2 (14%)
88	Y5P	A7	24	88	14,19,20	<mark>3.35</mark>	1 (7%)	18,26,29	0.95	1 (5%)
88	Y5P	A7	9	88	14,19,20	<mark>3.65</mark>	1 (7%)	18,26,29	1.47	2 (11%)
88	P5P	A7	42	88	16,23,24	1.32	2 (12%)	14,33,36	2.16	2 (14%)
88	P5P	A7	15	88	16,23,24	1.54	4 (25%)	14,33,36	2.04	2 (14%)
88	Y5P	A7	60	88	14,19,20	<mark>3.59</mark>	1 (7%)	18,26,29	1.15	1 (5%)
87	P5P	A5	6	87	16,23,24	1.37	2 (12%)	14,33,36	2.17	3 (21%)
88	Y5P	A7	57	88	14,19,20	3.51	1 (7%)	18,26,29	1.02	1 (5%)
88	Y5P	A7	56	88	14,19,20	3.42	1 (7%)	18,26,29	1.08	1 (5%)
88	Y5P	A7	59	88	14,19,20	<mark>3.62</mark>	1 (7%)	18,26,29	1.02	1 (5%)
87	Y5P	A5	1	87	14,19,20	3.76	2 (14%)	18,26,29	1.55	2 (11%)
88	Y5P	A7	65	88	14,19,20	<mark>3.63</mark>	1 (7%)	18,26,29	1.04	1 (5%)
88	Y5P	A7	70	88	14,19,20	<mark>3.68</mark>	1 (7%)	18,26,29	0.93	2 (11%)
88	P5P	A7	6	88	16,23,24	1.34	1 (6%)	14,33,36	2.21	2 (14%)
88	Y5P	A7	61	88	14,19,20	3.44	1 (7%)	18,26,29	1.00	1 (5%)
87	Y5P	A5	3	87	14,19,20	3.47	1 (7%)	18,26,29	1.29	2 (11%)
87	P5P	A5	11	87	16,23,24	1.35	2 (12%)	14,33,36	2.01	2 (14%)
88	Y5P	A7	22	88	14,19,20	3.48	1 (7%)	18,26,29	1.02	1 (5%)
88	P5P	A7	18	88	16,23,24	1.43	3 (18%)	14,33,36	2.17	2 (14%)
88	Y5P	A7	38	88	14,19,20	<mark>3.49</mark>	1 (7%)	18,26,29	0.97	1 (5%)
87	Y5P	A5	8	87	14,19,20	<mark>3.51</mark>	1 (7%)	18,26,29	1.01	2 (11%)
88	P5P	A7	11	88	16,23,24	1.36	2 (12%)	14,33,36	2.18	2 (14%)
88	P5P	A7	45	88	16,23,24	1.34	2 (12%)	14,33,36	2.28	2 (14%)
88	P5P	A7	71	88,32	16,23,24	1.32	3 (18%)	14,33,36	1.99	2 (14%)
88	Y5P	A7	66	88	14,19,20	<mark>3.70</mark>	1 (7%)	18,26,29	1.02	1 (5%)
88	Y5P	A7	12	88	14,19,20	<mark>3.31</mark>	1 (7%)	18,26,29	1.00	1 (5%)
88	P5P	A7	20	88	16,23,24	1.37	1 (6%)	14,33,36	2.10	2 (14%)
88	P5P	A7	7	88	16,23,24	1.41	2 (12%)	14,33,36	2.23	2 (14%)
88	Y5P	A7	64	88	14,19,20	3.68	1 (7%)	18,26,29	0.95	1 (5%)
88	P5P	A7	14	88	16,23,24	1.41	3 (18%)	14,33,36	1.98	2(14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral



Y5P

Y5P

Y5P

Y5P

Y5P

Y5P

Y5P

A7

Α7

A7

A7

A7

A5

A7

51

68

25

44

47

10

63

88

88

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88

88

88

88

88

87

88

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
88	P5P	A7	1	88	-	0/2/22/26	0/3/3/3
88	Y5P	A7	50	88	-	4/7/33/34	0/2/2/2
88	P5P	A7	23	88	-	0/3/25/26	0/3/3/3
88	Y5P	A7	17	88	-	2/7/33/34	0/2/2/2
88	Y5P	A7	8	88	-	1/7/33/34	0/2/2/2
88	P5P	A7	19	88	-	0/3/25/26	0/3/3/3
88	P5P	A7	4	88	_	0/3/25/26	0/3/3/3
88	Y5P	A7	37	88	-	1/7/33/34	0/2/2/2
88	Y5P	A7	69	88	-	1/7/33/34	0/2/2/2
87	P5P	A5	9	87	-	0/3/25/26	0/3/3/3
88	P5P	A7	43	88	-	3/3/25/26	0/3/3/3
88	Y5P	A7	46	88	-	3/7/33/34	0/2/2/2
88	Y5P	A7	58	88	_	3/7/33/34	0/2/2/2
87	P5P	A5	5	87	-	2/3/25/26	0/3/3/3
88	P5P	A7	48	88	-	0/3/25/26	0/3/3/3
88	Y5P	A7	62	88	-	1/7/33/34	0/2/2/2
88	P5P	A7	49	88	-	0/3/25/26	0/3/3/3
88	Y5P	A7	55	88	-	1/7/33/34	0/2/2/2
88	P5P	A7	40	88	-	0/3/25/26	0/3/3/3
87	Y5P	A5	7	87	-	3/7/33/34	0/2/2/2
88	Y5P	A7	3	88	-	1/7/33/34	0/2/2/2
88	P5P	A7	10	88	-	0/3/25/26	0/3/3/3
87	Y5P	A5	4	87	-	7/7/33/34	0/2/2/2
88	P5P	A7	41	88	-	0/3/25/26	0/3/3/3
88	P5P	A7	16	88	_	2/3/25/26	0/3/3/3
87	P5P	A5	2	87	_	2/3/25/26	0/3/3/3
88	Y5P	A7	21	88	-	3/7/33/34	0/2/2/2
88	Y5P	A7	67	88	-	1/7/33/34	0/2/2/2
88	P5P	A7	5	88	_	2/3/25/26	0/3/3/3
88	Y5P	A7	13	88	_	1/7/33/34	0/2/2/2

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.

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2/7/33/34

1/7/33/34

1/7/33/34

3/7/33/34

1/7/33/34

1/7/33/34

1/7/33/34

0/2/2/2

0/2/2/2

0/2/2/2

0/2/2/2

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0/2/2/2

0/2/2/2



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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
88	P5P	A7	2	88	-	0/3/25/26	0/3/3/3
88	P5P	A7	52	88	-	3/3/25/26	0/3/3/3
88	P5P	A7	54	88	-	1/3/25/26	0/3/3/3
88	Y5P	A7	53	88	-	3/7/33/34	0/2/2/2
88	P5P	A7	26	88	-	0/3/25/26	0/3/3/3
88	P5P	A7	27	88	-	0/3/25/26	0/3/3/3
88	P5P	A7	39	88	-	0/3/25/26	0/3/3/3
88	Y5P	A7	24	88	-	1/7/33/34	0/2/2/2
88	Y5P	A7	9	88	-	3/7/33/34	0/2/2/2
88	P5P	A7	42	88	-	0/3/25/26	0/3/3/3
88	P5P	A7	15	88	-	0/3/25/26	0/3/3/3
88	Y5P	A7	60	88	-	1/7/33/34	0/2/2/2
87	P5P	A5	6	87	-	0/3/25/26	0/3/3/3
88	Y5P	A7	57	88	-	1/7/33/34	0/2/2/2
88	Y5P	A7	56	88	-	3/7/33/34	0/2/2/2
88	Y5P	A7	59	88	-	1/7/33/34	0/2/2/2
87	Y5P	A5	1	87	-	7/7/33/34	0/2/2/2
88	Y5P	A7	65	88	_	2/7/33/34	0/2/2/2
88	Y5P	A7	70	88	_	3/7/33/34	0/2/2/2
88	P5P	A7	6	88	-	3/3/25/26	0/3/3/3
88	Y5P	A7	61	88	-	1/7/33/34	0/2/2/2
87	Y5P	A5	3	87	-	4/7/33/34	0/2/2/2
87	P5P	A5	11	87	_	0/3/25/26	0/3/3/3
88	Y5P	A7	22	88	-	3/7/33/34	0/2/2/2
88	P5P	A7	18	88	-	1/3/25/26	0/3/3/3
88	Y5P	A7	38	88	-	2/7/33/34	0/2/2/2
87	Y5P	A5	8	87	-	3/7/33/34	0/2/2/2
88	P5P	A7	11	88	-	0/3/25/26	0/3/3/3
88	P5P	A7	45	88	-	2/3/25/26	0/3/3/3
88	P5P	A7	71	88,32	_	1/3/25/26	0/3/3/3
88	Y5P	A7	66	88	-	1/7/33/34	0/2/2/2
88	Y5P	A7	12	88	-	3/7/33/34	0/2/2/2
88	P5P	A7	20	88	-	0/3/25/26	0/3/3/3
88	P5P	A7	7	88	-	3/3/25/26	0/3/3/3
88	Y5P	A7	64	88	-	2/7/33/34	0/2/2/2
88	P5P	A7	14	88	_	2/3/25/26	0/3/3/3

The worst 5 of 112 bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	A7	53	Y5P	C4-N3	-13.91	1.33	1.46
88	A7	67	Y5P	C4-N3	-13.84	1.33	1.46
88	A7	44	Y5P	C4-N3	-13.71	1.33	1.46
87	A5	1	Y5P	C4-N3	-13.62	1.33	1.46
88	A7	66	Y5P	C4-N3	-13.62	1.33	1.46

The worst 5 of 130 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
88	A7	45	P5P	C6-N1-C2	7.22	126.18	115.84
88	A7	27	P5P	C6-N1-C2	7.10	126.02	115.84
88	A7	2	P5P	C6-N1-C2	7.06	125.95	115.84
88	A7	11	P5P	C6-N1-C2	7.04	125.93	115.84
88	A7	7	P5P	C6-N1-C2	6.99	125.85	115.84

There are no chirality outliers.

5 of 114 torsion outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Atoms
87	A5	1	Y5P	O4'-C4'-C5'-O5'
87	A5	1	Y5P	C3'-C4'-C5'-O5'
87	A5	2	P5P	O4'-C4'-C5'-O5'
87	A5	4	Y5P	O4'-C4'-C5'-O5'
87	A5	4	Y5P	C3'-C4'-C5'-O5'

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 139 ligands modelled in this entry, 137 are monoatomic - leaving 2 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



Mol Two		Chain	Chain	Chain	Dog	Link	Bo	ond leng	ths	B	ond ang	les
	Type	Ullalli	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2		
92	GCP	v	802	89	27,34,34	1.82	6 (22%)	$34,\!54,\!54$	2.36	8 (23%)		
91	GDP	AX	500	-	24,30,30	0.96	1 (4%)	30,47,47	1.30	4 (13%)		

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).

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
92	GCP	v	802	89	-	5/15/38/38	0/3/3/3
91	GDP	AX	500	-	-	1/12/32/32	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
92	V	802	GCP	PG-01G	5.34	1.61	1.50
92	V	802	GCP	C5-C6	4.49	1.49	1.41
92	V	802	GCP	PG-O3G	3.01	1.61	1.54
92	V	802	GCP	PG-O2G	-2.53	1.49	1.54
91	AX	500	GDP	C6-N1	-2.36	1.34	1.37

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
92	V	802	GCP	PB-O3A-PA	-6.13	113.13	132.56
92	V	802	GCP	C4-C5-C6	-5.86	115.20	120.80
92	V	802	GCP	C2-N1-C6	4.66	123.34	115.93
92	V	802	GCP	C2-N3-C4	4.59	120.60	115.36
92	V	802	GCP	N3-C2-N1	-4.02	121.86	127.22

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
92	V	802	GCP	PG-C3B-PB-O1B
92	V	802	GCP	PG-C3B-PB-O3A
92	V	802	GCP	O4'-C4'-C5'-O5'
92	V	802	GCP	C3'-C4'-C5'-O5'



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Mol	Chain	Res	Type	Atoms
92	V	802	GCP	PG-C3B-PB-O2B

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 then 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
85	u	4

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	u	414:UNK	С	601:UNK	Ν	48.04
1	u	106:UNK	С	301:UNK	Ν	30.89
1	u	315:UNK	С	399:UNK	Ν	19.09
1	u	615:UNK	С	700:UNK	Ν	18.25



6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-21233. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections (i)

6.1.1 Primary map



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

6.2 Central slices (i)

6.2.1 Primary map



X Index: 200



Y Index: 200



Z Index: 200 $\,$

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

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 205

Y Index: 172

Z Index: 243

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

6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map



The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.



6.5 Orthogonal surface views (i)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.267. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.6 Mask visualisation (i)

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



7 Map analysis (i)

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

7.1 Map-value distribution (i)



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



7.2 Volume estimate (i)



The volume at the recommended contour level is 1618 $\rm nm^3;$ this corresponds to an approximate mass of 1461 kDa.

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



7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.337 ${\rm \AA^{-1}}$



8 Fourier-Shell correlation (i)

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



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-21233 and PDB model 6VLZ. Per-residue inclusion information can be found in section 3 on page 22.

9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.267 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.



9.2 Q-score mapped to coordinate model (i)



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

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.267).



9.4 Atom inclusion (i)



At the recommended contour level, 82% of all backbone atoms, 75% of all non-hydrogen atoms, are inside the map.


1.0

0.0 <0.0

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.267) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	$\mathbf{Q} extsf{-score}$
All	0.7470	0.3170
0	0.8580	0.4350
1	0.8410	0.4250
2	0.9110	0.4820
3	0.8970	0.4990
4	0.8590	0.4400
5	0.8880	0.4360
6	0.8750	0.4050
7	0.8610	0.4030
8	0.7270	0.2300
9	0.8720	0.4070
А	0.8440	0.3320
A0	0.6790	0.2400
A1	0.3650	0.1370
A2	0.4450	0.2500
A3	0.7270	0.3760
A4	0.1020	0.1390
A5	0.0240	0.0310
A7	0.1290	0.0240
AA	0.8170	0.2590
AB	0.6750	0.2520
AC	0.4550	0.1700
AD	0.5850	0.2880
AE	0.5540	0.2510
AF	0.4060	0.2070
AG	0.5010	0.1720
AH	0.4080	0.1910
AI	0.6400	0.2880
AJ	0.6970	0.3530
AK	0.6190	0.1700
AL	0.6750	0.3090
AM	0.7240	0.2890
AN	0.7960	0.3620
AO	0.6780	0.2530
AP	0.6310	0.2770

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Chain	Atom inclusion	Q-score
AQ	0.7190	0.3230
AR	0.6150	0.2080
AS	0.5480	0.2090
AT	0.7510	0.3280
AU	0.6650	0.2020
AV	0.5190	0.1380
AW	0.6120	0.2510
AX	0.3530	0.0800
AY	0.3590	0.1320
AZ	0.4080	0.1530
В	0.9480	0.2870
D	0.8650	0.4350
Е	0.8820	0.4590
F	0.8880	0.4590
Н	0.8360	0.3920
Ι	0.6890	0.2600
J	0.7400	0.2690
K	0.9050	0.4740
L	0.8510	0.4540
М	0.8910	0.4500
N	0.8540	0.4300
0	0.8740	0.4370
Р	0.8810	0.4120
Q	0.8070	0.4040
R	0.8890	0.4660
S	0.9020	0.4580
Т	0.8910	0.4670
ТА	0.1310	0.0810
TB	0.1550	0.0700
TC	0.0340	0.1480
U	0.8680	0.4330
V	0.8590	0.4160
W	0.8830	0.4550
X	0.8800	0.4430
Y	0.8900	0.4430
Z	0.8800	0.4520
a	0.7980	0.3920
b	0.9000	0.4710
С	0.8610	0.4180
d	0.7530	0.3680
e	0.6990	0.1610
f	0.7010	0.2860

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Chain	Atom inclusion	Q-score
g	0.8720	0.4180
h	0.8210	0.3580
i	0.9010	0.4680
j	0.8450	0.4100
k	0.7430	0.2880
1	0.7680	0.2830
m	0.7420	0.2190
0	0.8580	0.4220
р	0.7950	0.3700
q	0.7480	0.3460
r	0.8750	0.4280
S	0.8800	0.4360
u	0.4740	0.1660
V	0.6950	0.2920

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