



wwPDB EM Validation Summary Report ⓘ

May 13, 2024 – 09:34 pm BST

PDB ID : 6TPQ
EMDB ID : EMD-10543
Title : RNase M5 bound to 50S ribosome with precursor 5S rRNA
Authors : Oerum, S.; Dendooven, T.; Gilet, L.; Catala, M.; Degut, C.; Trinquier, A.; Barraud, P.; Luisi, B.; Condon, C.; Tisne, C.
Deposited on : 2019-12-13
Resolution : 3.07 Å(reported)
Based on initial model : 3J3V

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

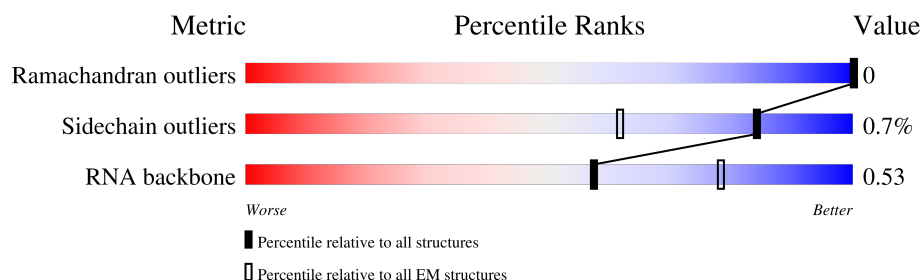
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

1 Overall quality at a glance

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

The reported resolution of this entry is 3.07 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.



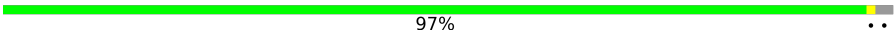
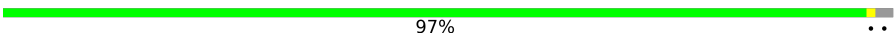
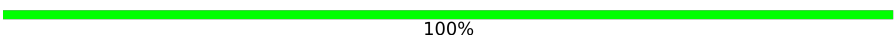
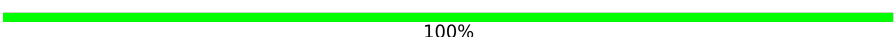

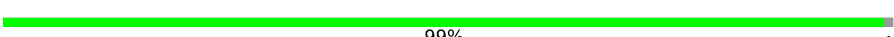
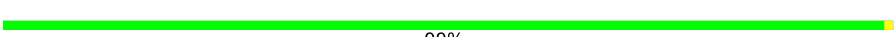



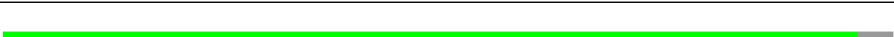


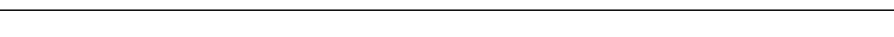
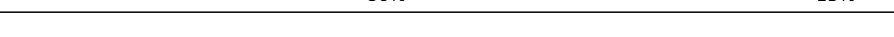
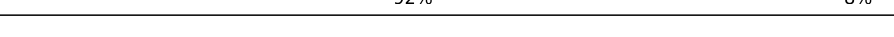
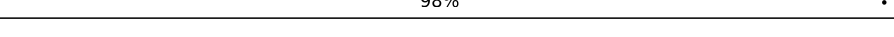
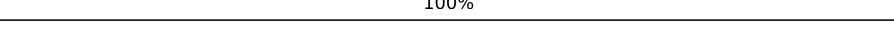
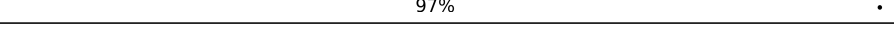
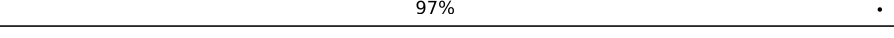
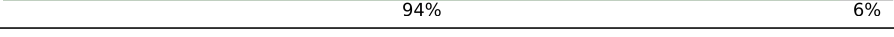
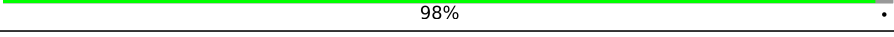
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	187	
1	B	187	
2	V	123	
3	b	166	
4	U	2924	
5	W	277	
6	X	209	
7	Y	207	
8	Z	179	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	a	179	 97% ..
10	c	145	 97% ..
11	d	122	 100%
12	e	146	 100%
13	f	144	 94% ..
14	g	120	 99% .
15	h	120	 99% .
16	i	115	 96% ..
17	j	119	 98% .
18	k	102	 98% ..
19	l	113	 96% .
20	m	95	 98% .
21	n	103	 98% .
22	o	94	 86% . 13%
23	p	59	 92% 8%
24	q	49	 98% .
25	r	44	 100%
26	s	66	 97% .
27	t	37	 97% .
28	u	62	 94% 6%
29	v	66	 98% .
30	w	59	 98% .

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 91728 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 protein called Ribonuclease M5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	183	Total	C	N	O	S	0	0
			1425	887	269	266	3		
1	A	69	Total	C	N	O	S	0	0
			548	343	108	95	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	58	ALA	ASP	engineered mutation	UNP A0A087LGV4
A	58	ALA	ASP	engineered mutation	UNP A0A087LGV4

- Molecule 2 is a RNA chain called pre-5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	V	123	Total	C	N	O	P	0	0
			2628	1172	473	860	123		

- Molecule 3 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	b	123	Total	C	N	O	S	0	0
			955	602	163	189	1		

- Molecule 4 is a RNA chain called pre-23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	U	2924	Total	C	N	O	P	0	0
			62790	28012	11594	20260	2924		

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	W	275	Total	C	N	O	S	0	0
			2111	1312	416	377	6		

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	X	207	Total	C	N	O	S	0	0
			1575	988	290	292	5		

- Molecule 7 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Y	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Z	178	Total	C	N	O	S	0	0
			1404	893	245	259	7		

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	c	142	Total	C	N	O	S	0	0
			1124	710	206	203	5		

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	d	122	Total	C	N	O	S	0	0
			921	571	173	173	4		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	e	146	Total	C	N	O	S	0	0
			1082	671	207	202	2		

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	f	138	Total	C	N	O	S	0	0
			1097	703	208	181	5		

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	g	119	Total	C	N	O	S	0	0
			954	583	186	181	4		

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	h	120	Total	C	N	O	S	0	0
			913	564	176	172	1		

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	i	114	Total	C	N	O	0	0
			937	595	184	158		

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	j	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	k	101	Total	C	N	O	0	0
			787	501	139	147		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	l	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	m	93	Total	C	N	O	S	0	0
			752	472	137	139	4		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	n	101	Total	C	N	O	S	0	0
			762	478	142	138	4		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	o	82	Total	C	N	O		0	0
			630	390	123	117			

- Molecule 23 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	p	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 24 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	q	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 25 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	r	44	Total	C	N	O	S	0	0
			368	222	89	55	2		

- Molecule 26 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	s	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 27 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	t	36	Total	C	N	O	S	0	0
			289	181	59	45	4		

- Molecule 28 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	u	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 29 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	v	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 30 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	w	58	Total	C	N	O	S	0	0
			456	281	89	85	1		

- Molecule 31 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
31	V	1	Total	Mg	0
			1	1	
31	U	214	Total	Mg	0
			214	214	
31	W	2	Total	Mg	0
			2	2	
31	e	1	Total	Mg	0
			1	1	
31	u	1	Total	Mg	0
			1	1	

- Molecule 32 is ZINC ION (three-letter code: ZN) (formula: Zn).

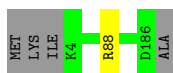
Mol	Chain	Residues	Atoms		AltConf
32	p	1	Total 1	Zn 1	0
32	q	1	Total 1	Zn 1	0
32	t	1	Total 1	Zn 1	0

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.

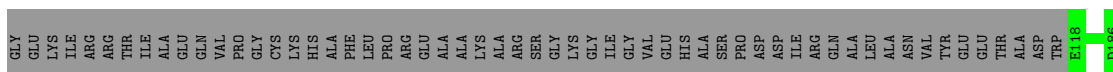
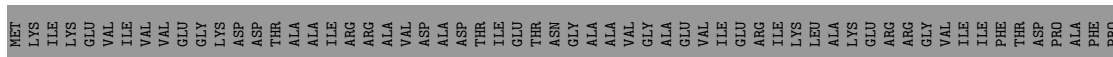
- Molecule 1: Ribonuclease M5

Chain B:  97%



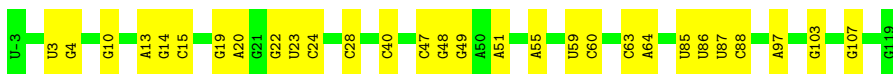
- Molecule 1: Ribonuclease M5

Chain A:  37% 63%



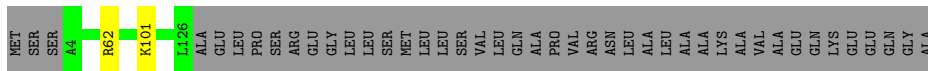
- Molecule 2: pre-5S rRNA

Chain V:  76% 24%




- Molecule 3: 50S ribosomal protein L10

Chain b:  73% 26%

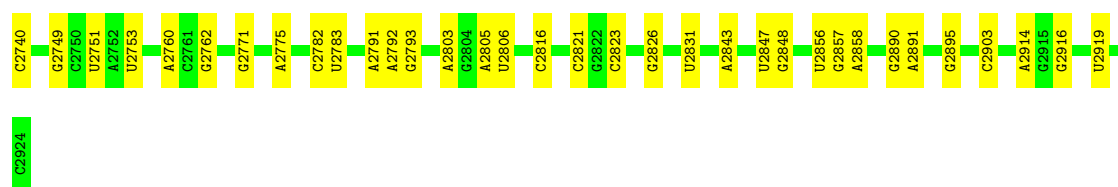


- Molecule 4: pre-23S rRNA

Chain U:  78% 22%

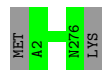


A2503	G2331	G2169	G2048	G1896	C1680	A1530	G1421	A1186	U1104	G936	A700	A328	A205
G2504	U2332	C2173	A2050	U1897	A1665	A1532	A1422	A1192	G1106	A941	G714	G336	A214
A2505	A2174	A2174		A1898	A1665	U1533	A1431	A1192	G1107	C942	A715	G526	A217
G2508	A2335	A2336	A2058	A1899	A1689	A1534	U1431	G1201	C1108	C943	U731	A341	A222
G2511	A2337	G2359	G2059	G1900	U1690	C1537	A1432	G1201	U1109	G944	U731	G342	A222
G2511	A2338	A2060	A2060	G1904	C1691	A1538	U1433	G1207	U1110	A945	A756	A343	A223
G2529	U2343	G2180	C2070	A1904	C1717	U1541	C1436	G1207	G1112	A1111	A756	A344	A224
G2532	G2181	G2181		G1910	C1718		U1437	U1215	G1113	A955	A760	A351	G225
G2532	G2345	A2185	A2078	A1911			U1437	U1216	A1114	A956	A760	A351	G226
A2540	G2346	A2185	G2079	A1916	A1743	C1550	C1447	C1217	G1115	C957	A763	A352	A227
A2540	A2347	G2186	A2186	A1917	A1744	A1551	C1448	G1218	C1116	C957	A763	A353	A227
A2545	G2348	G2187	C2082	G2187	A1744	U1552	C1448	A1219	A1117	C959	C775	A353	A228
A2545	A2349	G2188		A1904	C1691	A1538	U1433	A1220	G1118	C959	C775	G365	G231
G2556	A2355	C2188		G1920	G1755	C1555	A1454	A1220	C1119	A962	U791	U370	G231
G2561	A2360	C2191	G2087	A1926	U1756	A1554	U1455	G1243	C1120	A962	U791	U370	G231
G2562	C2361	G2192	G2088	A1927	A1772	G1555	U1456	G1244	A1121	U970	U792	A371	A234
A2362	A2362	U2194	G2096	A1928	A1772	C1557	U1457	G1245	C1122	A985	U792	A372	G243
A2569	G2372	G2195	U2119	G1933	G1775	U1558	G1458	G1248	C1123	A989	G820	G380	G249
U2579	A2373	G2196	G2120	G1933	A1776	G1559	U1463	G1276	U1125	A989	A827	A387	G250
U2582	C2374	U1942		U1942	C1778	A1560	U1464	G1276	U1126	G990	A828	A388	G251
U2583	C2377	A1943	U2123	A1943	C1779	G1564	U1471	A1291	U1127	A1003	U829	A389	G256
G2582	U2202	U1944	G2127	U1944	G1790	U1568	C1472	A1294	A1128	A1004	U829	A390	A256
A2593	G2208	A1945	G2128	A1945	G1791	G1569	C1472	G1294	G1131	U835	U835	G394	G265
G2594	G2209	C1951	U2129	G1957	G1791	C1570	U1486	C1295	A1132	A590	C836	A266	G266
	G2310	C2210	A2130	C1957	G1796	C1571	U1487	A1303	G1133	U837	G837	U398	G267
A2599	G2398	C2210	G2131	A1954			A1488	A1303	U1134	A1018			
G2605	A2404	U2215	A2132	A1955	A1800	A1577	C1493	G1309	G1137	A1027	A847	U403	A273
G2609	G2410	U2216	U2135	A1956	A1800	A1578	C1493	G1309	U1138	A1040	U604	G404	
G2610	G2411	G2217	U2136	G1957	G1803	A1579	G1494	A1310	U1138	G850	G605	G404	A279
G2611	G2412	A2218	G2137	A1963	G1808	U1580	G1495	A1311	A1139	G1041	G605	U407	G280
U2612	C2219	C2220	U2138	A1964	G1808	A1581	U1496	A1312	A1140	C857	G615	G408	
G2613	C2433	G2230	C2140	A1965	A1811	U1582	A1497	A1313	U1141	C857	G615	G409	U284
		G2230	A2141	U1966	A1812	A1583	U1498	A1337	C1144	A864	A616		G285
		G2231		U1967	A1818	U1585	G1500	A1338	U1145	U1048	A617		C286
U2636	C2449	U1982	A2144	U1982	A1818	U1593	A1502	U1339	C1146	A1057	G629	G417	C287
G2637	U2450	C2236	U2145	C1990	C1827	U1594	A1503	U1349	G1150	A1057	U890	C430	U288
U2640	A2452	G2243	A2146	G1991	G1828	C1605	A1504	C1351	G1151	U1066	A645	C430	U296
	G2456	G2244	G2147	G1992	A1829	A1612	U1505	C1362	C1153	G904	U649	U431	U297
A2656	A2457	G2250	G2148	C1993	U1835	A1615	U1511	C1362	G1154	A1070	A656	G433	G298
G2657		G2251	U2149	A1994	A1836	A1615	G1516	G1375	A1155	U1077	A677	A435	A300
A2666	A2466	A2252	G2151	A1997	A1837	A1615	C1517	G1375	U1157	U1077	A677	A436	
G2668	C2467	A2153	G2152	A1998	A1843	U1624	U1520	U1378	G1158	U1089	A923	A446	U311
G2673	G2468	G2265	G2154	G1999	G1844	G1628	U1521	C1382	A1171	A1090	G924	A681	C313
	A2475	G2266	C2155		A1844	A1629	A1522	A1386	A1172	G1091	G925	C449	
G2686				U2018	A1856	G1630	G1523	A1386	A1172	A1092	G926	A687	U319
	U2487	G2306	G2160	G2019	A1874	G1630	G1524	A1386	U1176	A1098	G927	A688	A322
U2716	G2497	C2310	A2161	U2020	A1874	G1649	C1525	U1389	U1177	G1099	C929	U689	A322
A2717			A2162		A1874	C1650	U1526	U1389	A1177	A1100	C929	A696	A323
				C2023	G1885	A1651	G1527	A1402	C1179	A1100	A933	A697	A324
G2729	C2501	A2314	G2167	A2024	G1885	A1651	G1528	A1402	C1179	A1100	A933	A697	A325
	G2502		G2168		A1893	A1652	G1529	A1402	C1179	A1100	A933	A697	A326
						A1652	G1529	A1402	C1179	A1100	A933	A697	A327



- Molecule 5: 50S ribosomal protein L2

Chain W: 99%



- Molecule 6: 50S ribosomal protein L3

Chain X: 99%



- Molecule 7: 50S ribosomal protein L4

Chain Y: 99%



- Molecule 8: 50S ribosomal protein L5

Chain Z: 98%



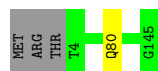
- Molecule 9: 50S ribosomal protein L6

Chain a: 97%



- Molecule 10: 50S ribosomal protein L13

Chain c: 97%



- Molecule 11: 50S ribosomal protein L14

Chain d:  100%

There are no outlier residues recorded for this chain.

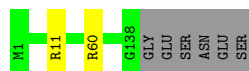
- Molecule 12: 50S ribosomal protein L15

Chain e:  100%

There are no outlier residues recorded for this chain.

- Molecule 13: 50S ribosomal protein L16

Chain f:  94%



- Molecule 14: 50S ribosomal protein L17

Chain g:  99%



- Molecule 15: 50S ribosomal protein L18

Chain h:  99%



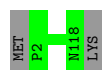
- Molecule 16: 50S ribosomal protein L19

Chain i:  96%



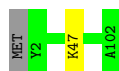
- Molecule 17: 50S ribosomal protein L20

Chain j:  98%



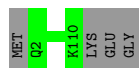
- Molecule 18: 50S ribosomal protein L21

Chain k:  98%



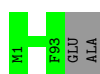
- Molecule 19: 50S ribosomal protein L22

Chain l: 96%



- Molecule 20: 50S ribosomal protein L23

Chain m: 98%



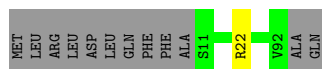
- Molecule 21: 50S ribosomal protein L24

Chain n: 98%



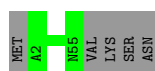
- Molecule 22: 50S ribosomal protein L27

Chain o: 86% 13%



- Molecule 23: 50S ribosomal protein L32

Chain p: 92% 8%



- Molecule 24: 50S ribosomal protein L33 1

Chain q: 98%



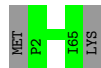
- Molecule 25: 50S ribosomal protein L34

Chain r: 100%

There are no outlier residues recorded for this chain.

- Molecule 26: 50S ribosomal protein L35

Chain s:  97% .



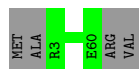
- Molecule 27: 50S ribosomal protein L36

Chain t:  97% .



- Molecule 28: 50S ribosomal protein L28

Chain u:  94% 6% .



- Molecule 29: 50S ribosomal protein L29

Chain v:  98% .



- Molecule 30: 50S ribosomal protein L30

Chain w:  98% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	92799	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	23.94	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.30	0/554	0.44	0/736
1	B	0.27	0/1444	0.44	0/1939
2	V	0.64	0/2938	0.84	0/4579
3	b	0.27	0/963	0.51	0/1298
4	U	0.90	0/70333	0.89	61/109728 (0.1%)
5	W	0.43	0/2148	0.51	0/2881
6	X	0.45	0/1597	0.49	0/2140
7	Y	0.43	0/1580	0.48	0/2132
8	Z	0.31	0/1423	0.50	0/1910
9	a	0.34	0/1360	0.47	0/1832
10	c	0.48	1/1147 (0.1%)	0.50	0/1542
11	d	0.42	0/928	0.51	0/1245
12	e	0.43	0/1094	0.52	0/1457
13	f	0.42	0/1120	0.47	0/1496
14	g	0.43	0/961	0.48	0/1284
15	h	0.33	0/922	0.46	0/1236
16	i	0.45	0/950	0.49	0/1269
17	j	0.53	0/952	0.50	0/1266
18	k	0.48	0/798	0.52	0/1070
19	l	0.44	0/851	0.46	0/1146
20	m	0.45	0/759	0.49	0/1011
21	n	0.40	0/772	0.49	0/1032
22	o	0.46	0/638	0.52	0/847
23	p	0.45	0/433	0.47	0/574
24	q	0.41	0/406	0.49	0/540
25	r	0.46	0/371	0.47	0/483
26	s	0.41	0/519	0.45	0/680
27	t	0.40	0/292	0.45	0/383
28	u	0.37	0/448	0.50	0/596
29	v	0.36	0/531	0.45	0/707
30	w	0.41	0/458	0.49	0/613
All	All	0.80	1/99690 (0.0%)	0.81	61/149652 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	c	80	GLN	C-N	-5.04	1.22	1.34

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	U	696	C	N1-C2-O2	9.20	124.42	118.90
4	U	1243	G	O4'-C1'-N9	9.03	115.43	108.20
4	U	1525	C	C2-N1-C1'	-8.69	109.25	118.80
4	U	696	C	C2-N1-C1'	8.28	127.91	118.80
4	U	696	C	N3-C2-O2	-7.78	116.46	121.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	67/187 (36%)	63 (94%)	4 (6%)	0	100	100
1	B	181/187 (97%)	169 (93%)	12 (7%)	0	100	100
3	b	121/166 (73%)	97 (80%)	24 (20%)	0	100	100
5	W	273/277 (99%)	242 (89%)	31 (11%)	0	100	100
6	X	205/209 (98%)	183 (89%)	22 (11%)	0	100	100
7	Y	203/207 (98%)	178 (88%)	25 (12%)	0	100	100
8	Z	176/179 (98%)	149 (85%)	27 (15%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	a	173/179 (97%)	151 (87%)	22 (13%)	0	100	100
10	c	140/145 (97%)	131 (94%)	9 (6%)	0	100	100
11	d	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
12	e	144/146 (99%)	129 (90%)	15 (10%)	0	100	100
13	f	136/144 (94%)	129 (95%)	7 (5%)	0	100	100
14	g	117/120 (98%)	105 (90%)	12 (10%)	0	100	100
15	h	118/120 (98%)	108 (92%)	10 (8%)	0	100	100
16	i	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
17	j	115/119 (97%)	109 (95%)	6 (5%)	0	100	100
18	k	99/102 (97%)	83 (84%)	16 (16%)	0	100	100
19	l	107/113 (95%)	105 (98%)	2 (2%)	0	100	100
20	m	91/95 (96%)	84 (92%)	7 (8%)	0	100	100
21	n	99/103 (96%)	90 (91%)	9 (9%)	0	100	100
22	o	80/94 (85%)	73 (91%)	7 (9%)	0	100	100
23	p	52/59 (88%)	47 (90%)	5 (10%)	0	100	100
24	q	46/49 (94%)	42 (91%)	4 (9%)	0	100	100
25	r	42/44 (96%)	40 (95%)	2 (5%)	0	100	100
26	s	62/66 (94%)	58 (94%)	4 (6%)	0	100	100
27	t	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
28	u	56/62 (90%)	50 (89%)	6 (11%)	0	100	100
29	v	63/66 (96%)	56 (89%)	7 (11%)	0	100	100
30	w	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
All	All	3288/3571 (92%)	2974 (90%)	314 (10%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	50/143 (35%)	50 (100%)	0	100	100
1	B	139/143 (97%)	138 (99%)	1 (1%)	84	92
3	b	105/138 (76%)	103 (98%)	2 (2%)	57	79
5	W	223/225 (99%)	223 (100%)	0	100	100
6	X	168/170 (99%)	167 (99%)	1 (1%)	86	93
7	Y	169/170 (99%)	168 (99%)	1 (1%)	86	93
8	Z	153/154 (99%)	151 (99%)	2 (1%)	69	86
9	a	148/151 (98%)	146 (99%)	2 (1%)	67	84
10	c	120/123 (98%)	120 (100%)	0	100	100
11	d	101/101 (100%)	101 (100%)	0	100	100
12	e	110/110 (100%)	110 (100%)	0	100	100
13	f	111/116 (96%)	109 (98%)	2 (2%)	59	80
14	g	99/100 (99%)	99 (100%)	0	100	100
15	h	93/93 (100%)	92 (99%)	1 (1%)	73	88
16	i	99/100 (99%)	95 (96%)	4 (4%)	31	63
17	j	96/98 (98%)	96 (100%)	0	100	100
18	k	83/84 (99%)	82 (99%)	1 (1%)	71	87
19	l	90/93 (97%)	90 (100%)	0	100	100
20	m	84/85 (99%)	84 (100%)	0	100	100
21	n	85/87 (98%)	85 (100%)	0	100	100
22	o	64/74 (86%)	63 (98%)	1 (2%)	62	83
23	p	48/53 (91%)	48 (100%)	0	100	100
24	q	46/47 (98%)	46 (100%)	0	100	100
25	r	39/39 (100%)	39 (100%)	0	100	100
26	s	54/56 (96%)	54 (100%)	0	100	100
27	t	34/35 (97%)	34 (100%)	0	100	100
28	u	47/50 (94%)	47 (100%)	0	100	100
29	v	56/57 (98%)	56 (100%)	0	100	100
30	w	52/53 (98%)	52 (100%)	0	100	100
All	All	2766/2948 (94%)	2748 (99%)	18 (1%)	84	92

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	i	54	ARG
22	o	22	ARG
18	k	47	LYS
9	a	165	TYR
16	i	40	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
17	j	72	ASN
21	n	64	HIS
17	j	91	ASN
19	l	97	ASN
24	q	16	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	V	122/123 (99%)	27 (22%)	4 (3%)
4	U	2923/2924 (99%)	607 (20%)	41 (1%)
All	All	3045/3047 (99%)	634 (20%)	45 (1%)

5 of 634 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	V	4	G
2	V	10	G
2	V	13	A
2	V	14	G
2	V	15	C

5 of 45 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	U	1337	A
4	U	1593	U
4	U	1349	U
4	U	1516	G
4	U	1689	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 222 ligands modelled in this entry, 222 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](#)

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-10543. 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 standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

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

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.