



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:

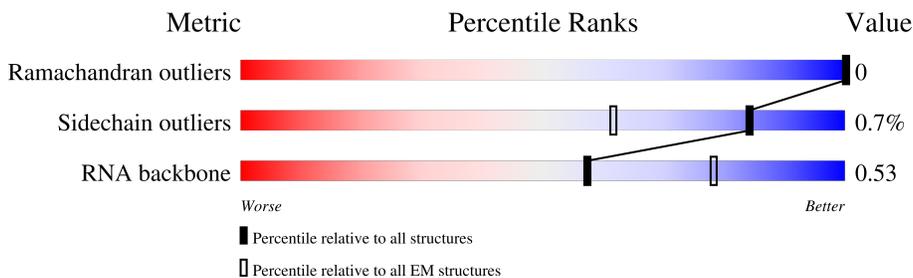
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)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

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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%
23	p	59	92%
24	q	49	98%
25	r	44	100%
26	s	66	97%
27	t	37	97%
28	u	62	94%
29	v	66	98%
30	w	59	98%

2 Entry composition [i](#)

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
			Total	C	N	O	S		
1	B	183	1425	887	269	266	3	0	0
1	A	69	548	343	108	95	2	0	0

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
			Total	C	N	O	P		
2	V	123	2628	1172	473	860	123	0	0

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

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

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

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

- 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 [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

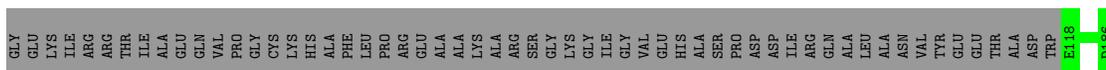
- Molecule 1: Ribonuclease M5

Chain B:  97%



- Molecule 1: Ribonuclease M5

Chain A:  37% 63%



ALA

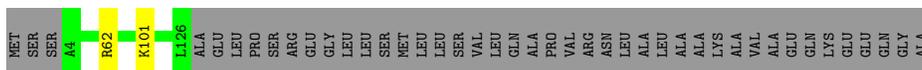
- Molecule 2: pre-5S rRNA

Chain V:  76% 24%



- Molecule 3: 50S ribosomal protein L10

Chain b:  73% 26%

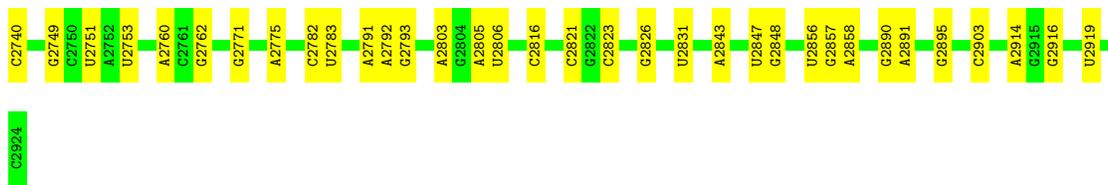


- Molecule 4: pre-23S rRNA

Chain U:  78% 22%



A205	A214	A217	A222	A223	A224	A226	A227	A228	G231	A328	G336	A341	A342	A343	A344	A351	A352	A353	G365	U370	A371	A372	G380	A387	A388	A389	C390	C265	A266	G267	A273	A279	G280	U284	G285	C286	C287	U288	C289	U296	U297	G298	U299	A300	U311	A312	C313	U319	C449	C450	A457	A323	A324	G325	C501	A502
A206	A215	A218	A221	A225	A227	A229	A230	A231	A232	A337	A338	A340	A343	A344	A352	A354	A355	A356	A357	U371	A373	A374	G381	A388	A389	A390	C391	C266	A267	A274	A280	G281	G282	G283	G284	G285	G286	G288	G289	U298	U299	G299	A301	U312	A313	U320	C449	C450	A457	A324	A325	G326	C502	A503		
A207	A216	A219	A220	A221	A222	A223	A224	A225	A226	A338	A339	A341	A342	A343	A344	A351	A352	A353	A354	U372	A374	A375	G382	A389	A390	C392	C267	A268	A275	A281	G282	G283	G284	G285	G286	G287	G289	U299	U300	G300	A302	U313	A314	U321	C450	C451	A458	A325	A326	G327	C503	A504				
A208	A217	A220	A221	A222	A223	A224	A225	A226	A227	A339	A340	A342	A343	A344	A351	A352	A353	A354	A355	U373	A375	A376	G383	A390	C393	C268	A269	A276	A282	G283	G284	G285	G286	G287	G288	G290	U301	U302	G301	A303	U314	A315	U322	C451	C452	A459	A326	A327	G328	C504	A505					
A209	A218	A221	A222	A223	A224	A225	A226	A227	A228	A340	A341	A343	A344	A351	A352	A353	A354	A355	A356	U374	A376	A377	G384	A391	C394	C269	A270	A277	A283	G284	G285	G286	G287	G288	G291	U303	U304	G302	A304	U315	A316	U323	C452	C453	A460	A327	A328	G329	C505	A506						
A210	A219	A222	A223	A224	A225	A226	A227	A228	A229	A341	A342	A344	A345	A351	A352	A353	A354	A355	A356	U375	A377	A378	G385	A392	C395	C270	A271	A278	A284	G285	G286	G287	G288	G292	U305	U306	G303	A305	U316	A317	U324	C453	C454	A461	A328	A329	G330	C506	A507							
A211	A220	A223	A224	A225	A226	A227	A228	A229	A230	A342	A343	A345	A346	A351	A352	A353	A354	A355	A356	U376	A378	A379	G386	A393	C396	C271	A272	A279	A285	G286	G287	G288	G293	U307	U308	G304	A306	U317	A318	U325	C454	C455	A462	A329	A330	G331	C507	A508								
A212	A221	A224	A225	A226	A227	A228	A229	A230	A231	A343	A344	A346	A347	A351	A352	A353	A354	A355	A356	U377	A379	A380	G387	A394	C397	C272	A273	A280	A286	G287	G288	G289	G294	U309	U310	G305	A307	U318	A319	U326	C455	C456	A463	A330	A331	G332	C508	A509								
A213	A222	A225	A226	A227	A228	A229	A230	A231	A232	A344	A345	A347	A348	A351	A352	A353	A354	A355	A356	U378	A380	A381	G388	A395	C398	C273	A274	A281	A287	G288	G289	G290	G295	U311	U312	G306	A308	U319	A320	U327	C456	C457	A464	A331	A332	G333	C509	A510								
A214	A223	A226	A227	A228	A229	A230	A231	A232	A233	A345	A346	A348	A349	A351	A352	A353	A354	A355	A356	U379	A381	A382	G389	A396	C399	C274	A275	A282	A288	G289	G290	G291	G296	U313	U314	G307	A309	U320	A321	U328	C457	C458	A465	A332	A333	G334	C510	A511								
A215	A224	A227	A228	A229	A230	A231	A232	A233	A234	A346	A347	A349	A350	A351	A352	A353	A354	A355	A356	U380	A382	A383	G390	A397	C400	C275	A276	A283	A289	G290	G291	G292	G297	U315	U316	G308	A310	U321	A322	U329	C458	C459	A466	A333	A334	G335	C511	A512								
A216	A225	A228	A229	A230	A231	A232	A233	A234	A235	A347	A348	A350	A351	A352	A353	A354	A355	A356	A357	U381	A383	A384	G391	A398	C401	C276	A277	A284	A290	G291	G292	G293	G298	U317	U318	G309	A311	U322	A323	U330	C459	C460	A467	A334	A335	G336	C512	A513								
A217	A226	A229	A230	A231	A232	A233	A234	A235	A236	A348	A349	A351	A352	A353	A354	A355	A356	A357	A358	U382	A384	A385	G392	A400	C402	C277	A278	A285	A291	G292	G293	G294	G299	U319	U320	G310	A312	U323	A324	U331	C460	C461	A468	A335	A336	G337	C513	A514								
A218	A227	A230	A231	A232	A233	A234	A235	A236	A237	A349	A350	A352	A353	A354	A355	A356	A357	A358	A359	U383	A385	A386	G393	A401	C403	C278	A279	A286	A292	G293	G294	G295	G300	U321	U322	G311	A313	U324	A325	U332	C461	C462	A469	A336	A337	G338	C514	A515								
A219	A228	A231	A232	A233	A234	A235	A236	A237	A238	A350	A351	A353	A354	A355	A356	A357	A358	A359	A360	U384	A386	A387	G394	A402	C404	C279	A280	A287	A293	G294	G295	G296	G301	U323	U324	G312	A314	U325	A326	U333	C462	C463	A470	A337	A338	G339	C515	A516								
A220	A229	A232	A233	A234	A235	A236	A237	A238	A239	A351	A352	A354	A355	A356	A357	A358	A359	A360	A361	U385	A387	A388	G395	A403	C405	C280	A281	A288	A294	G295	G296	G297	G302	U325	U326	G313	A315	U326	A327	U334	C463	C464	A471	A338	A339	G340	C516	A517								
A221	A230	A233	A234	A235	A236	A237	A238	A239	A240	A352	A353	A355	A356	A357	A358	A359	A360	A361	A362	U386	A388	A389	G396	A404	C406	C281	A282	A289	A295	G296	G297	G298	G303	U327	U328	G314	A316	U327	A328	U335	C464	C465	A472	A339	A340	G341	C517	A518								
A222	A231	A234	A235	A236	A237	A238	A239	A240	A241	A353	A354	A356	A357	A358	A359	A360	A361	A362	A363	U387	A389	A390	G397	A405	C407	C282	A283	A290	A296	G297	G298	G299	G304	U329	U330	G315	A317	U328	A329	U336	C465	C466	A473	A340	A341	G342	C518	A519								
A223	A232	A235	A236	A237	A238	A239	A240	A241	A242	A354	A355	A357	A358	A359	A360	A361	A362	A363	A364	U388	A390	A391	G398	A406	C408	C283	A284	A291	A297	G298	G299	G300	G305	U331	U332	G316	A318	U329	A330	U337	C466	C467	A474	A341	A342	G343	C519	A520								
A224	A233	A236	A237	A238	A239	A240	A241	A242	A243	A355	A356	A358	A359	A360	A361	A362	A363	A364	A365	U389	A391	A392	G399	A407	C409	C284	A285	A292	A298	G299	G300	G301	G306	U333	U334	G317	A319	U330	A331	U338	C467	C468	A475	A342	A343	G344	C520	A521								
A225	A234	A237	A238	A239	A240	A241	A242	A243	A244	A356	A357	A359	A360	A361	A362	A363	A364	A365	A366	U390	A392	A393	G400	A408	C410	C285	A286	A293	A299	G300	G301	G302	G307	U335	U336	G318	A320	U331	A332	U339	C468	C469	A476	A343	A344	G345	C521	A522								
A226	A235	A238	A239	A240	A241	A242	A243	A244	A245	A357	A358	A360	A361	A362	A363	A364	A365	A366	A367	U391	A393	A394	G401	A409	C411	C286	A287	A294	A300	G301	G302	G303	G308	U337	U338	G319	A321	U332	A333	U340	C469	C470	A477	A344	A345	G346	C522	A523								
A227	A236	A239	A240	A241	A242	A243	A244	A245	A246	A358	A359	A361	A362	A363	A364	A365	A366	A367	A368	U392	A394	A395	G402	A410	C412	C287	A288	A295	A301	G302	G303	G304	G309	U339	U340	G320	A322	U333	A334	U341	C470	C471	A478	A345	A346	G347	C523	A524								
A228	A237	A240	A241	A242	A243	A244	A245	A246	A247	A359	A360	A362	A363	A364	A365	A366	A367	A368	A369	U393	A395	A396	G403	A411	C413	C288	A289	A296	A302	G303	G304	G305	G310	U341	U342	G321	A323	U334	A335	U342	C471	C472	A479	A346	A347	G348	C524	A525								
A229	A238	A241	A242	A243	A244	A245	A246	A247	A248	A360	A361	A363	A364	A365	A366	A367	A368	A369	A370	U394	A396	A397	G404	A412	C414	C289	A290	A297	A303	G304	G305	G306	G311	U343	U344	G322	A324	U335	A336	U343	C472	C473	A480	A347	A348	G349	C525	A526								
A230	A239	A242	A243	A244	A245	A246	A247	A248	A249	A361	A362	A364	A365	A366	A367	A368	A369	A370	A371	U395	A397	A398	G405	A413	C415	C290	A291	A298	A304	G305	G306	G307	G312	U345	U346	G323	A325	U336	A337	U344	C473	C474	A481	A348	A349	G350	C526	A527								
A231	A240	A243	A244	A245	A246	A247	A248	A249	A250	A362	A363	A365	A366	A367	A368	A369	A370	A371	A372	U396	A398	A399	G406	A414	C416	C291	A292	A299	A305	G306	G307	G308	G313	U347	U348	G324	A326	U337	A338	U345	C474	C475	A482	A349	A350	G351	C527	A528								
A232	A241	A244	A245	A246	A247	A248	A249	A250	A251	A363	A364	A366	A367	A368	A369	A370	A371	A372	A373	U397	A399	A400	G407	A415	C417	C292	A293	A300	A306	G307	G308	G309	G314	U349	U350	G325	A327	U338	A339	U346	C475	C476	A483	A350	A351	G352	C528	A529								
A233	A242	A245	A246	A247	A248	A249	A250	A251	A252	A364	A365	A367	A368	A369	A370	A371	A372	A373	A374	U398	A400	A401	G408	A416	C418	C293	A294	A301	A307	G308	G309	G310	G315	U351	U352	G326	A328	U339	A340	U347	C476	C477	A484	A351	A352	G353	C529	A530								
A234	A243	A246	A247	A248	A249	A250	A251	A252	A253	A365	A366	A368	A369	A370	A371	A372	A373	A374	A375	U399	A401	A402	G409	A417	C419	C294	A295	A302	A308	G309	G310	G311	G316	U353	U354	G327	A329	U340	A341	U348	C477	C478	A485	A352	A35											



- Molecule 5: 50S ribosomal protein L2



- Molecule 6: 50S ribosomal protein L3



- Molecule 7: 50S ribosomal protein L4



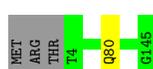
- Molecule 8: 50S ribosomal protein L5



- Molecule 9: 50S ribosomal protein L6



- Molecule 10: 50S ribosomal protein L13



- Molecule 11: 50S ribosomal protein L14

Chain d:  100%

There are no outlier residues recorded for this chain.

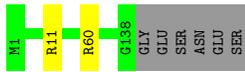
- Molecule 12: 50S ribosomal protein L15

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%



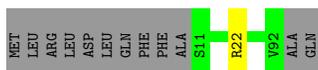
- Molecule 21: 50S ribosomal protein L24

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%

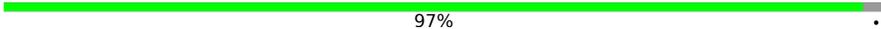


- Molecule 25: 50S ribosomal protein L34

Chain r: 100%

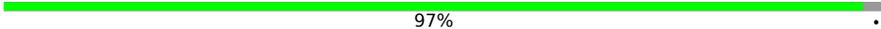
There are no outlier residues recorded for this chain.

- Molecule 26: 50S ribosomal protein L35

Chain s:  97%

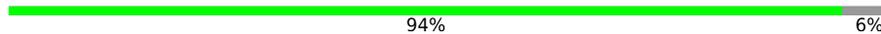


- Molecule 27: 50S ribosomal protein L36

Chain t:  97%

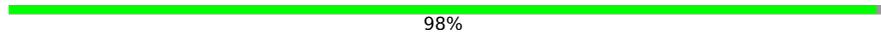


- Molecule 28: 50S ribosomal protein L28

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 i

5.1 Standard geometry i

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.30	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

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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 [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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.