

wwPDB EM Validation Summary Report (i)

Nov 9, 2024 – 07:48 PM EST

PDB ID	:	6X6T
EMDB ID	:	EMD-22082
Title	:	Cryo-EM structure of an Escherichia coli coupled transcription-translati
		on complex B1 (TTC-B1) containing an mRNA with a 24 nt long spacer,
		transcription factors NusA and NusG, and fMet-tRNAs at P-site and E-site
Authors	:	Molodtsov, V.; Ebright, R.H.; Wang, C.; Su, M.
Deposited on	:	2020-05-29
Resolution	:	3.20 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 113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.20 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.



Motric	Whole archive	EM structures		
INTEGI IC	$(\# {\rm Entries})$	$(\# { m Entries})$		
Ramachandran outliers	207382	16835		
Sidechain outliers	206894	16415		
RNA backbone	6643	2191		

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 <=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						
	-			68%							
1	0	103		96%		•					
				79%							
2	1	110		92%							
				63%							
3	2	100		90%		• 6%					
			48%								
4	3	104	93%								
			5	9%							
5	4	94		97%							
				64%							
6	5	36	47%	17	7%	36%					
				75%							
7	6	36		64%	11%	25%					
				71%							
8	7	41	24%	41%	15%	20%					



Mol	Chain	Length	Quality of chain								
0	0	165	75%								
9	9	105	67%	22% • 10%							
10	А	76	46% 47%	7%							
10	В	76	38% 49%	13%							
11	AA	1342	99%	·							
12	AB	181	67%	18% • • 10%							
13	AC	329	91% 90%	• 9%							
13	AD	329	91% 91%	9%							
14	AE	1407	95% 89%	5% • 5%							
15	AF	91	90%	10%							
16	AG	495	69%	27% •							
17	С	75	40%	• 12%							
18	D	1542	27%	21% •							
19	Е	87	95%								
20	F	71	59%	•••							
21	G	241	39%	5% 7%							
22	Н	557	45% 42% • 54								
23	Ι	233	33%	• 11%							
24	J	206	52%								
25	K	167	58%	7% 7%							
26	L	135	52% 69% 8	% 23%							
27	M	179	18%	5% 16%							
28	N	130	63%								
20	0	130	30%	50/ -							
20	D	100	₩ 45%	•• •							
0U 01	Г	100	84% 29%	12% •							
51	Q	129	88%	• 9%							

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Mol	Chain	Length	Quality of chain	
			70%	
32	R	124	91% 45%	6% •
33	S	101	94%	5% •
34	Т	89	83%	16% •
35	U	82	94%	6%
36	V	84	49% 90%	5% 5%
37	W	92	55%	• 10%
38	X	118	59% 86%	12% •
39	Y	142	97% 84%	15% ••
40	Z	121	25% 17% 7% 75%	
41	a	2904	47%	20% ••
42	h	85	62%	11%
43	С С	78	58%	1170
44	d	120	37%	
44	u	120	85% 59%	15%
40	e	05	98% 63%	•
46	t	59	93% 73%	5% •
47	g	70	87% 66%	7% 6%
48	h	273	94% 67%	5% •
49	i	57	88%	11% •
50	j	209	95%	5%
51	k	55	91% 69%	• 5%
52	1	201	95%	5%
53	m	46	93%	7%
54	n	179	91%	8% •
55	0	65	63% 92%	5%••
56	р	177	95%	•••



Mol	Chain	Length	Quality of chain	
			79%	
57	q	38	95%	5%
			72%	
58	r	149	94%	6%
			71%	
59	\mathbf{S}	142	96%	•
			67%	
60	t	123	93%	7%
			62%	
61	u	144	95%	5%
			72%	
62	V	136	97%	•
			59%	
63	W	127	89%	5% 6%
			60%	
64	Х	117	95%	••
			62%	
65	У	115	96%	••
			63%	
66	Z	118	96%	• •

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2 Entry composition (i)

There are 68 unique types of molecules in this entry. The entry contains 291628 atoms, of which 109913 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 50S ribosomal protein L21.

Mol	Chain	Residues			AltConf	Trace				
1	0	103	Total 1655	C 516	H 839	N 153	0 145	${S \over 2}$	0	0

• Molecule 2 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	1	110	Total 1779	C 532	Н 922	N 166	O 156	${ m S} { m 3}$	0	0

• Molecule 3 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues			AltConf	Trace				
3	2	94	Total 1557	C 470	Н 811	N 140	0 134	${ m S} { m 2}$	0	0

• Molecule 4 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues		Α	AltConf	Trace			
4	3	103	Total 1632	C 498	Н 844	N 148	0 142	0	0

• Molecule 5 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues			AltConf	Trace				
5	4	94	Total 1533	C 479	Н 780	N 137	0 134	${ m S} { m 3}$	0	0

• Molecule 6 is a DNA chain called NT DNA.

Mol	Chain	Residues			AltConf	Trace				
6	5	23	Total 732	C 225	Н 260	N 87	0 137	Р 23	0	0



• Molecule 7 is a DNA chain called T DNA.

Mol	Chain	Residues			Atom	ıs			AltConf	Trace
7	6	27	Total 847	C 259	Н 305	N 89	0 167	Р 27	0	0

• Molecule 8 is a RNA chain called mRNA with 24 nt long spacer.

Mol	Chain	Residues		1	AltConf	Trace				
8	7	33	Total 784	C 307	Н 97	N 96	0 251	Р 33	0	0

• Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues		At	oms	AltConf	Trace		
9	9	148	Total 1117	C 705	N 196	O 209	S 7	0	0

• Molecule 10 is a RNA chain called E-site and P-site tRNA (fMet).

Mol	Chain	Residues			Ator		AltConf	Trace		
10	Λ	76	Total	С	Η	Ν	0	Р	0	0
10	Л	70	2446	723	826	295	527	75	0	0
10	В	76	Total	С	Η	Ν	0	Р	0	0
10	D	70	2433	723	813	295	527	75	0	0

• Molecule 11 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues		A	AltConf	Trace			
11	АА	1340	Total	С	Ν	0	\mathbf{S}	0	0
		1010	10567	6631	1841	2052	43		0

• Molecule 12 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues		ŀ	Ator	\mathbf{ms}			AltConf	Trace
12	AB	162	Total 1283	C 816	H 1	N 222	0 237	${f S}{7}$	0	0

• Molecule 13 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues		Ate	AltConf	Trace			
13	AC	301	Total 2094	C 1296	N 379	0 413	S 6	0	0



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Mol	Chain	Residues		At	oms			AltConf	Trace
13	AD	299	Total 2078	C 1287	N 378	O 407	S 6	0	0

• Molecule 14 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues			Atom	ıs			AltConf	Trace
14	AE	1335	Total 21000	C 6526	H 10612	N 1854	0 1958	S 50	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	1384	VAL	MET	conflict	UNP A0A4S1NBU2

• Molecule 15 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues		At	\mathbf{oms}			AltConf	Trace
15	AF	82	Total 650	C 396	N 122	0 131	S 1	0	0

• Molecule 16 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues		At	oms			AltConf	Trace
16	AG	495	Total 3852	C 2396	N 669	О 774	S 13	0	0

• Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues		_	Atom	s			AltConf	Trace
17	С	66	Total 1103	C 344	Н 559	N 102	O 97	S 1	0	0

• Molecule 18 is a RNA chain called 16S rRNA.

Mol	Chain	Residues			Ato	ms			AltConf	Trace
18	D	1524	Total 49126	C 14585	Н 16423	N 6003	O 10591	Р 1524	0	0

• Molecule 19 is a protein called 30S ribosomal protein S20.



Mol	Chain	Residues			Aton	ns			AltConf	Trace
19	Е	86	Total 1388	C 414	Н 719	N 138	0 114	${ m S} { m 3}$	0	0

• Molecule 20 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues			Atom	AltConf	Trace			
20	F	70	Total 1218	C 366	Н 629	N 125	O 97	S 1	0	0

• Molecule 21 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues			AltConf	Trace				
21	G	225	Total 3545	C 1113	Н 1785	N 316	O 323	S 8	0	0

• Molecule 22 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues			Atoms	5			AltConf	Trace
22	Н	259	Total 3184	C 1073	Н 1454	N 305	0 349	${ m S} { m 3}$	0	0

• Molecule 23 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues			Atoms	5			AltConf	Trace
23	Ι	208	Total 3346	C 1036	Н 1710	N 307	O 290	${ m S} { m 3}$	0	0

• Molecule 24 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues			Atom	5			AltConf	Trace
24	J	205	Total 3350	C 1026	Н 1707	N 315	O 298	$\frac{S}{4}$	0	0

• Molecule 25 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues			Atom	IS			AltConf	Trace
25	K	156	Total 2348	С 717	Н 1196	N 217	0 212	S 6	0	0

• Molecule 26 is a protein called 30S ribosomal protein S6.



Mol	Chain	Residues			Aton	ns			AltConf	Trace
26	L	104	Total 1694	$\begin{array}{c} \mathrm{C} \\ 536 \end{array}$	Н 846	N 153	O 152	${ m S} 7$	0	0

• Molecule 27 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues			Atoms						
27	М	151	Total 2416	C 735	Н 1235	N 227	O 215	$\frac{S}{4}$	0	0	

• Molecule 28 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues			Atom	S			AltConf	Trace
28	Ν	129	Total 2010	C 616	Н 1031	N 173	O 184	${ m S}{ m 6}$	0	0

• Molecule 29 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues			Atom	.s			AltConf	Trace
29	Ο	127	Total 2092	C 634	Н 1070	N 206	0 179	${ m S} { m 3}$	0	0

• Molecule 30 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues			Aton	ns			AltConf	Trace
30	Р	99	Total 1621	C 495	Н 831	N 151	0 143	S 1	0	0

• Molecule 31 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues			AltConf	Trace				
31	Q	117	Total 1764	С 540	Н 887	N 174	O 160	${ m S} { m 3}$	0	0

• Molecule 32 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues			AltConf	Trace				
32	R	121	Total 1940	C 580	Н 1001	N 194	0 161	$\begin{array}{c} \mathrm{S} \\ 4 \end{array}$	0	0

• Molecule 33 is a protein called 30S ribosomal protein S14.



Mol	Chain	Residues			Atom	ns			AltConf	Trace
33	S	100	Total 1649	C 499	Н 844	N 164	O 139	${ m S} { m 3}$	0	0

• Molecule 34 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues			Aton	ıs			AltConf	Trace
34	Т	88	Total 1448	C 439	Н 734	N 144	O 130	S 1	0	0

• Molecule 35 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues			Aton	ns			AltConf	Trace
35	U	82	Total 1315	C 406	Н 666	N 128	0 114	S 1	0	0

• Molecule 36 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues			Aton	ns			AltConf	Trace
36	V	80	Total 1339	C 411	Н 691	N 121	0 113	${ m S} { m 3}$	0	0

• Molecule 37 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues			Aton	ns			AltConf	Trace
37	W	83	Total 1351	C 424	H 688	N 126	0 111	$\frac{S}{2}$	0	0

• Molecule 38 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues			Atom	ns			AltConf	Trace
38	Х	116	Total 1864	C 558	Н 964	N 181	0 158	${ m S} { m 3}$	0	0

• Molecule 39 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues		At	oms	AltConf	Trace		
39	Y	141	Total 1032	C 651	N 179	0 196	S 6	0	0

• Molecule 40 is a protein called 50S ribosomal protein L7/L12.



Mol	Chain	Residues		Ato	\mathbf{ms}			AltConf	Trace
40	Z	30	Total 227	C 144	N 33	0 47	${ m S} { m 3}$	0	0

• Molecule 41 is a RNA chain called 23S rRNA.

Mol	Chain	Residues			Ato	ms			AltConf	Trace
41	a	2880	Total 92918	C 27587	Н 31077	N 11398	O 19976	Р 2880	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	887	А	U	conflict	GB 937521852

• Molecule 42 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues			Atom	ıs			AltConf	Trace
42	b	76	Total 1181	C 360	Н 599	N 117	0 104	S 1	0	0

• Molecule 43 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues			Atom	ıs			AltConf	Trace
43	с	77	Total 1277	C 388	Н 652	N 129	0 106	${ m S} { m 2}$	0	0

• Molecule 44 is a RNA chain called 5S rRNA.

Mol	Chain	Residues			Aton	ns			AltConf	Trace
4.4	d	120	Total	С	Η	Ν	0	Р	0	0
44	u	120	3870	1144	1301	468	837	120	0	0

• Molecule 45 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues		A	Atom	s			AltConf	Trace
45	е	62	Total 1032	C 308	Н 531	N 98	0 94	S 1	0	0

• Molecule 46 is a protein called 50S ribosomal protein L30.



Mol	Chain	Residues		A	Atom	s			AltConf	Trace
46	f	58	Total 936	C 281	H 488	N 87	0 78	${ m S} { m 2}$	0	0

• Molecule 47 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues		A	Atom	s			AltConf	Trace
47	g	66	Total 1042	C 323	Н 520	N 99	0 94	S 6	0	0

• Molecule 48 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues			AltConf	Trace				
48	h	271	Total 4236	C 1288	Н 2154	N 423	O 364	${f S}{7}$	0	0

• Molecule 49 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues		A	Atom	s			AltConf	Trace
49	i	56	Total 903	C 269	Н 459	N 94	O 80	S 1	0	0

• Molecule 50 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues			Atom	S			AltConf	Trace
50	j	209	Total 3182	C 979	Н 1617	N 288	O 294	$\frac{S}{4}$	0	0

• Molecule 51 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues		At	oms			AltConf	Trace
51	k	52	Total 890	C 275	Н 464	N 78	0 73	0	0

• Molecule 52 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues			Atom	.S			AltConf	Trace
52	1	201	Total 3171	C 974	H 1619	N 283	O 290	${S \atop 5}$	0	0

• Molecule 53 is a protein called 50S ribosomal protein L34.



Mol	Chain	Residues		A	Atoms	S			AltConf	Trace
53	m	46	Total 795	C 228	Н 418	N 90	O 57	${ m S} { m 2}$	0	0

• Molecule 54 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues			Atom	.s			AltConf	Trace
54	n	177	Total 2853	C 899	Н 1443	N 249	O 256	${ m S}{ m 6}$	0	0

• Molecule 55 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues			Atom	S			AltConf	Trace
55	О	64	Total 1076	C 323	Н 572	N 105	0 74	${S \over 2}$	0	0

• Molecule 56 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues			Atom	.s			AltConf	Trace
56	р	175	Total	С	Н	Ν	0	S	0	0
00	Р	110	2671	826	1358	241	244	2	Ŭ	Ŭ

• Molecule 57 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues		ŀ	Atom	S			AltConf	Trace
57	q	38	Total 645	C 185	Н 343	N 65	0 48	S 4	0	0

• Molecule 58 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues			Atom	IS			AltConf	Trace
58	r	149	Total 2259	C 699	Н 1148	N 197	0 214	S 1	0	0

• Molecule 59 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues			Atom	S			AltConf	Trace
59	s	142	Total 2291	С 714	Н 1162	N 212	O 199	${S \atop 4}$	0	0

• Molecule 60 is a protein called 50S ribosomal protein L14.



Mol	Chain	Residues			Atom	S			AltConf	Trace
60	t	123	Total 1969	C 593	Н 1023	N 181	O 166	S 6	0	0

• Molecule 61 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues			Atom	S			AltConf	Trace
61	u	144	Total 2182	$\begin{array}{c} \mathrm{C} \\ 654 \end{array}$	Н 1129	N 207	0 190	${ m S} { m 2}$	0	0

• Molecule 62 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues			Atom	.S			AltConf	Trace
62	v	136	Total 2231	C 686	H 1157	N 205	O 177	S 6	0	0

• Molecule 63 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues			Aton	ıs			AltConf	Trace
63	W	119	Total 1945	C 588	Н 994	N 195	0 163	${ m S}{ m 5}$	0	0

• Molecule 64 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues		Α	toms			AltConf	Trace
64	x	116	Total 1815	C 552	Н 923	N 178	O 162	0	0

• Molecule 65 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues			Aton	ns			AltConf	Trace
65	У	114	Total 1879	C 574	Н 962	N 179	0 163	S 1	0	0

• Molecule 66 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues		A	toms			AltConf	Trace
66	Z	117	Total 1967	C 604	Н 1020	N 192	O 151	0	0

• Molecule 67 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).



Mol	Chain	Residues	Atoms	AltConf
67	7	1	Total Mg 1 1	0

• Molecule 68 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
68	AA	2	Total Zn 2 2	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.

• Molecule 1: 50S ribosomal protein L21









••	•	•	••	•	••	••		••		•	••	••			••		•	•	••	••		•	•	••	•4	•	•	••	•	•	•4	•	••	•4	•	•	••	••	•	••	•4	••		••	•
Y301 T302	D303	E304	S305 T306	G307	E308	L309 I310	C311	A312	A313 N314	M315	E316	L317	5318 L319	D320	L321	L322	K324	L325	S326	q 327	S328	H330	K331	R332	I333 E334	T335	L336	F337 T330	1339 N339	D340	L341 D340	H343	G344	P345 V346	1347	S348	E349	T350	R352	V353	D354	гз56 Т356	N357	D358	L360
					•					•	•							•	•					•			•					•	•							•					
S361	L363	V364	Е365 ТЗ66	Y367	R368	M369 M370	R371	P372	G373 F374	P375	P376	T377	K378 E379	A380	A381	E382 e 2002	L384	F385	E386	N387	L388 F380	F 309	S391	E392	D393	Y 395	D396	L397	A399	V400	G401 B407	M403	K404	F405 MADE	R407	S408	L409	L410 R411	E412	E413	1414 7445	E415 G416	S417	G418 T410	L420
3421 (422	0423	0424	[425 гаре	0427	1428	1429 (430	(431	432	1433 1434	1435	1436	1437 1460	i438 (439	3440	544.1	1442 7113	0444	145	0446	1447	.448 1440	1450	1451	1452	С453 2 ЛЕ Л	3455	1456	1457 2452	1459 1459	1460	5461 1460	102 1463	464	1465 1466	1467	468	1469	8470 1471	5472	t473	1474 - 476	1415 (476	5477	1478 170	3480
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 | A784 M724 1564 M604 D785 M725 Q665 L605 T786 A726 E666 N606

 | A787 D727 Q667 T607 L788 \$3728 \$F668 \$C608 | K789 G729 Q669 Y609 T790 A730 S570 H610 | N/31 M/31 U0/1 L0/1 N/92 G732 L6/2 L6/2 S793 S733 VG73 G613

 | G794 ♦ A734 ♦ T674 ♦ L614 ♦ Y795 ♦ A735 ♦ A675 ♦ K615 ♦ | L796 Ф (336) G676 Ф (376) P616 Ф (377) T797 1737 Ф (377) Ф | | K799 ↓ 1739 ↑ 1619 ↓
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 | V803 ♦ M743 ♦ I683 ♦ Q623 ♦ A80.4 € F7.4 € F624 | A004 M.44 D004 1024 024 024 024 025 0 | D806 ♥ L746 ♥ W686 ♥ Y626 ♥
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 | T823 F763 T703 D643 | V825 E765 T705 V645 I 1826 G766 V706 1646 0 0
 | E827 	 I.767 	 I.707 	 F647 	 E48 	 E48 | C829 K109 K109 K649 | | K832 ♦ Y772 ♦ Q712 ♦ E652 ♦
E833 ♦ F773 ♦ E713 ♦ I653 ♦ | P834 I774 E714 I654 L835 S775 K715 S655 | R836 ↓ 1776 ↓ ↓ €656 ↓ D837 ↓ H777 ↓ V717 ▲ Å657 ↓ | R838 • G778 • S718 • E658 • 1839 • A779 • F719 • A659 | L940 ♥ R780 ♥ N720 ♥ E660 ♥
G941 ♥ K781 ♥ S721 ♥ V661 ♥ |
| G782 ♦ I722 ♦ A662 ♦ 8602 ♦ K603 ♦ K603 ♦
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 | ▲ A787 ◆ D727 ◆ q667 ◆ T607 ◆ T607 ◆ L788 ◆ S728 ◆ F568 ◆ C608 ◆ | K789 € G729 € q669 € Y609 € T790 € X730 € S670 € M610 € | N 791 N 701 4001 1011 N 792 0 732 1672 1612 S 793 5733 0733 6613

 | C794 ← A734 ← T674 ← L614 ← Y795 ← A735 ← A675 ← K615 ← | L796 T797 T797 E677 T617 T617 T617 | | K/99 q/39 Y679 1619 L800 L740 N680 F520 | V801 A741 K681 A621 A621 <th< td=""><td></td><td>0005 01745 010034 1024 025 01745 01685 01685 01625 01</td><td>● D806 ● L746 ● W686 ● Y626 ● L807 ● M747 ● A687 ● T627 ●</td><td>V808 A 748 A 688 G628 € V809 K 749 A 689 F 629 €</td><td>Lalo ← P750 ← N690 ← A630 ← Esti ← D751 ← D631 ← V631 ←</td><td>DB12 C75.2 R69.2 A632 DB13 C75.2 R69.2 A633 DB13 S75.3 V00.3 A633</td><td>C11 C11 C11 C11 C11 C11 C11 C11 C11 C11</td><td>T1816 E756 A886 G636 H817 A1757 M887 A657</td><td>E818 P758 M698 5638 6819 1759 D699 V639</td><td>1820 1760 1700 640 640 1701 1701 1701 1701</td><td>M822 M762 Q702 D642</td><td>Lag23</td><td>• U825 ◆ E765 ◆ 1705 ◆ 1705 ◆ 1646 ◆
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E333 ♦ F773 ♦ E713 ♦ I653 ♦</td><td>● P834 ■ 1774 ● E714 ● 1654 ● ● L835 ● 3775 ● K715 ● 5655 ●</td><td></td><td>● R838 ● G778 ● E658 ● V839 ● A779 ● F719 ▲ A659 ●</td><td>Contract → Contract → Contr</td></th<> | | 0005 01745 010034 1024 025 01745 01685 01685 01625 01 | ● D806 ● L746 ● W686 ● Y626 ● L807 ● M747 ● A687 ● T627 ● | V808 A 748 A 688 G628 € V809 K 749 A 689 F 629 €
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| R842 G782 I722 A662 S602 K603 K603 <th< th=""><th>T844 A784 M724 E654 M604 A845 D785 M725 Q665 L605 B846 T786 A726 E666 N606</th><th>D847 A787 D727 q667 T507 V848 L788 \$5728 \$668 \$608 \$</th><th>L849 • K789 • G729 • Q669 • Y609 • K600 • K6</th><th>Pool A/91 A/91 A/91 A/91 A/91 A/91 A/91 A/91</th><th>AB54
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Q867 ♦ L807 ♦ M747 ♦ A687 ♦ T627 ♦</th><th>W868 V 808 A 74.8 A 668 G628 G628 C C369 V 809 K 74.9 A 669 F 629 F<th>B870 ♦ T810 ♦ P750 ♦ N690 ♦ A630 ♦
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H897 ♦ D837 ♦ H777 ♦ V717 ♦ A657 ♦</th><th>C398 • R838 • G778 • S718 • E658 • Y899 • V839 • A779 • F719 • A659</th><th>G900 La40 R730 N720 E660 € R901 G341 K731 \$3721 ¥661 €</th></th>
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| R842 G782 I722 A662 S602 K603 K603 <th< td=""><td>● T344 ▲774 ■ 1664 ● M604 ▲845 ● D785 ● M725 ● 0665 ● 1665 ● B846 ■ T786 ▲726 ● E666 N606</td><td>D847 A787 D727 q667 T607 V848 L788 S728 F668 C608</td><td>K850 ↔ 1730 ↔ 0729 ↔ 0669 ↔ 7609 ↔ 1730 ↔ 173</td><td>• 001 • 001</td><td>♦ A854 ♦ G794 ♦ A734 ♦ T674 ♦ L614 ♦
D855 ♦ Y795 ♦ A735 ♦ A675 ♦ K615 ♦</td><td>the set of the s</td><td></td><td>P889 K799 U739 Y679 1519 P880 F520 F520</td><td></td><td>● L863 ● V803 ● M743 ● I683 ● G623 ● 1 8 6 4904 8 744 6 1633 ●</td><td>H865 Q805 G745 1685 M626</td><td>B866 ♥ D806 ♥ L746 ♥ W686 ♥ Y626 ♥ B87 ● L807 ● M47 ● A67 ● T627 ●</td><td>W868 V308 A748 A688 C628 <t< td=""><td>◆ D870 ◆ T810 ◆ P750 ◆ N890 ◆ A630 ◆
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c2004 ● 1864 ● 4804 ● 8744 ● 1884 ● 1694 ●</th><th>19.22 Loot Aout Arit Doot 10.24 Loot 10.24 L</th><th>P926 ♥ E866 ♥ D806 ♥ L746 ♥ W686 ♥ Y626 ♥
G927 ♦ Q867 ♦ L807 ♦ M747 ♦ A687 ● T627 ●</th><th>T928 W868 V808 A748 A688 C628 C629 <t< th=""><th>L930 D870 T810 P750 N690 A630 T331 F811 D751 D601 V631</th><th>1002 1 1012 1012 1012 1012 1012 1012 10</th><th>Maximum Maximum <t< th=""><th>HIS SS76 TELE 6 2755 6 A096 6 G556 1 G27 4 G27 4 G57 6 G556 6 G5566 6 G5566 6 G</th><th>GLY D878 E818 P758 M698 5638 4038
 4038 4038</th><th>ALM VESO 1820 TT60 17760 6640 ALA ALM ALM ALM ALM ALM ALM ALM ALM ALM</th><th>ALA V882 M822 M702 D642 D642 ALA</th><th>ALA R883 • T223 • F763 • T703 • D643 •
GLU S884 • P824 • R764 • E704 • M644 •</th><th>S948 V885 V825 E765 T705 V645 1 S949 V886 1826 0766 V706 1646 0</th><th>1950 ♦ 3887 ♦ E827 ♦ L767 ♦ 1707 ♦ P647 ♦
951 ♦ C888 ♦ G928 ♦ N768 ● N708 ● E648 ●</th><th>V952 C D889 C C829 V769 K709 K709 K649</th><th></th><th>K955 € F892 K832 ¥772 ¶ ¶ 12 € E652 € G956 • G893 • E833 • F773 • E713 • E652 •</th><th>8957 ♥ V894 ♥ P834 ♥ 1774 ♥ E714 ♥ 1654 ♥
1958 ♥ C395 ♥ L835 ♥ 3775 ♥ K715 ♥ 8655 ♥</th><th>K959 Ma96 R836 T776 Q716 E656 L960 H397 D837 H777 V117 A657 A6577 A65777 A65777 A65777 A65777 A65777 <th< th=""><th>S961 C398 R338 G778 S718 E658 4 Y899 V839 A779 F719 A659 A659 A</th><th>G900 ● L840 ● R780 ● N720 ● E660 ● R901 ● G841 ● K781 ● S721 ● V661 ●</th></th<></th></t<></th></t<></th></thl<></thl011<></thl> | A914 • A854 • 0794 • A734 • 1674 • 1614 • 1615 • 1615 • 1615 • 1616 | 0916 ◆ 1356 ◆ 1796 ◆ 1736 ◆ 6676 ◆ ▶ v917 ◆ 1857 ◆ 1737 ◆ £677 ◆ 1617 | | A919 P859 K799 U739 1679 1619 A920 A920 R860 E800 F620 | q921 ◆ N861 ◆ V801 ◆ A741 ◆ K681 ◆ A621 ◆ S922 ◆ T862 ◆ D802 ◆ G742 ◆ V682 ◆ D622 ◆
 | 1923 ♦ L863 ♦ V803 ♦ N743 ♦ L683 ♦ q623 ♦
c2004 ● 1864 ● 4804 ● 8744 ● 1884 ● 1694 ● | 19.22 Loot Aout Arit Doot 10.24 Loot 10.24 L | P926 ♥ E866 ♥ D806 ♥ L746 ♥ W686 ♥ Y626 ♥
G927 ♦ Q867 ♦ L807 ♦ M747 ♦ A687 ● T627 ● | T928 W868 V808 A748 A688 C628 C629 C629 <t< th=""><th>L930 D870 T810 P750 N690 A630 T331 F811 D751 D601 V631</th><th>1002 1 1012 1012 1012 1012 1012 1012 10</th><th>Maximum Maximum <t< th=""><th>HIS SS76 TELE 6 2755 6 A096 6 G556 1 G27 4 G27 4 G57 6 G556 6 G5566 6 G5566 6 G</th><th>GLY D878 E818 P758 M698 5638 4038</th><th>ALM VESO 1820 TT60 17760 6640 ALA ALM ALM ALM ALM ALM ALM ALM ALM ALM</th><th>ALA V882 M822 M702 D642 D642 ALA</th><th>ALA R883 • T223 • F763 • T703 • D643 •
GLU S884 • P824 • R764 • E704 • M644 •</th><th>S948 V885 V825 E765 T705 V645 1 S949 V886 1826 0766 V706 1646 0</th><th>1950 ♦ 3887 ♦ E827 ♦ L767 ♦ 1707 ♦ P647 ♦
951 ♦ C888 ♦ G928 ♦ N768 ● N708 ● E648 ●</th><th>V952 C D889 C C829 V769 K709 K709 K649</th><th></th><th>K955 € F892 K832 ¥772 ¶ ¶ 12 € E652 € G956 • G893 • E833 • F773 • E713 • E652 •</th><th>8957 ♥ V894 ♥ P834 ♥ 1774 ♥ E714 ♥ 1654 ♥
1958 ♥ C395 ♥ L835 ♥ 3775 ♥ K715 ♥ 8655 ♥</th><th>K959 Ma96 R836 T776 Q716 E656 L960 H397
 D837 H777 V117 A657 A6577 A65777 A65777 A65777 A65777 A65777 <th< th=""><th>S961 C398 R338 G778 S718 E658 4 Y899 V839 A779 F719 A659 A659 A</th><th>G900 ● L840 ● R780 ● N720 ● E660 ● R901 ● G841 ● K781 ● S721 ● V661 ●</th></th<></th></t<></th></t<> | L930 D870 T810 P750 N690 A630 T331 F811 D751 D601 V631 | 1002 1 1012 1012 1012 1012 1012 1012 10 | Maximum Maximum <t< th=""><th>HIS SS76 TELE 6 2755 6 A096 6 G556 1 G27 4 G27 4 G57 6 G556 6 G5566 6 G5566 6 G</th><th>GLY D878 E818 P758 M698 5638 4038</th><th>ALM VESO 1820 TT60 17760 6640 ALA ALM ALM ALM ALM ALM ALM ALM ALM ALM</th><th>ALA V882 M822 M702 D642 D642 ALA</th><th>ALA R883 • T223 • F763 • T703 • D643 •
GLU S884 • P824 • R764 • E704 • M644 •</th><th>S948 V885 V825 E765 T705 V645 1 S949 V886 1826 0766 V706 1646 0</th><th>1950 ♦ 3887 ♦ E827 ♦ L767 ♦ 1707 ♦ P647 ♦
951 ♦ C888 ♦ G928 ♦ N768 ● N708 ● E648 ●</th><th>V952 C D889 C C829 V769 K709 K709 K649</th><th></th><th>K955 € F892 K832 ¥772 ¶ ¶ 12 € E652 € G956 • G893 • E833 • F773 • E713 • E652 •</th><th>8957 ♥ V894 ♥ P834 ♥ 1774 ♥ E714 ♥ 1654 ♥
1958 ♥ C395 ♥ L835 ♥ 3775 ♥ K715 ♥ 8655 ♥</th><th>K959 Ma96 R836 T776 Q716 E656 L960 H397 D837 H777 V117 A657 A6577 A65777 A65777 A65777 A65777 A65777 <th< th=""><th>S961 C398 R338 G778 S718 E658 4 Y899 V839 A779 F719 A659 A659 A</th><th>G900 ● L840 ● R780 ● N720 ● E660 ● R901 ● G841 ● K781 ● S721 ● V661 ●</th></th<></th></t<> | HIS SS76 TELE 6 2755 6 A096 6 G556 1 G27 4 G27 4 G57 6 G556 6 G5566 6 G5566 6 G | GLY D878 E818 P758 M698 5638 4038 | ALM VESO 1820 TT60 17760 6640 ALA ALM ALM ALM ALM ALM ALM ALM ALM ALM | ALA V882 M822 M702 D642 D642 ALA
 | ALA R883 • T223 • F763 • T703 • D643 •
GLU S884 • P824 • R764 • E704 • M644 • | S948 V885 V825 E765 T705 V645 1 S949 V886 1826 0766 V706 1646 0
 | 1950 ♦ 3887 ♦ E827 ♦ L767 ♦ 1707 ♦ P647 ♦
951 ♦ C888 ♦ G928 ♦ N768 ● N708 ● E648 ● | V952 C D889 C C829 V769 K709 K709 K649 | | K955 € F892 K832 ¥772 ¶ ¶ 12 € E652 € G956 • G893 • E833 • F773 • E713 • E652 • | 8957 ♥ V894 ♥ P834 ♥ 1774 ♥ E714 ♥ 1654 ♥
1958 ♥ C395 ♥ L835 ♥ 3775 ♥ K715 ♥ 8655 ♥ | K959 Ma96 R836 T776 Q716 E656 L960 H397 D837 H777 V117 A657 A6577 A65777 A65777 A65777 A65777 A65777 <th< th=""><th>S961 C398 R338 G778 S718 E658 4 Y899 V839 A779 F719 A659 A659 A</th><th>G900 ● L840 ● R780 ● N720 ● E660 ● R901 ● G841 ● K781 ● S721 ● V661 ●</th></th<> | S961 C398 R338 G778 S718 E658 4 Y899 V839 A779 F719 A659 A659 A | G900 ● L840 ● R780 ● N720 ● E660 ● R901 ● G841 ● K781 ● S721 ● V661 ● |
| D902 R842 G782 I722 A662 S602 L903 V843 L783 Y723 E663 K603
 | ▲ 0.4 ■ 1844 ▲ 4784 ▲ 1784 ● 11724 ■ 1664 ● 1604 ● ▲ 1005 ▲ 845 ● 1785 ● 1725 ● 1665 ● 1605 ● 0555 ● 055

 | H907 D847 A787 D727 q667 T607 1908 V848 L788 \$728 F668 C608 | 1909 1249 K789 6729 9669 Y609 9 1010 K860 1790 5770 8610 9 | Nail Fool A/ai A/ai <th< th=""><th>♦ A914 ♦ A854 € G794 ♦ A734 € T674 € L614 € ● 1915 ● D855 ● Y795 ● A735 ● A675 ● K615 ● <</th><th></th><th></th><th>A319 P859 R799 779 1679 1619 1619 1619 1619 1619 16</th><th>Φ Q921 ■ N861 ■ V801 ● A741 ■ K681 ● A621 ● Φ S922 Φ T862 ■ D802 ● G742 ● V682 ● D622 ●</th><th>1923 1863 V803 M743 1633 0623 0 0024 1864 5804 1874 1724 1524
 1524 1524<</th><th>1924 A004 A044 L024 L024 1925 1885 0805 0745 1685 M625</th><th>← P926 ← E866 ← D806 ← L746 ← W686 ← Y626 ← ← 2627 ← M747 ← A687 ← T627 ←</th><th></th><th></th><th>N322 L872 Da1 C152 R002 A532 N332 L872 D812 C152 R692 A532 N332 E873 D812 C152 R692 A532 N332 E873 D812 C152 R692 A532</th><th>No.05 B0/15 D0/15 <thd0 15<="" th=""> <thd< th=""><th>HLS SB76 T816 E756 A886 G636 G10 G11E SB76 H817 T757 M837 A657 A557 A557 A557 A557 A557 A557 A55</th><th>GLY DB78 E818 P758 M698 5638 9 ALA ARF9 G819 1759 D699 V639 9</th><th>ALA NIA NIA</th></thd<></thd0></th></th<> <th>ALA V882 M822 M702 D642 D642 ALA</th> <th>ALA RB83 T823 F763 T703 D643 P643 <th< th=""><th>◆ S948 • V885 ◆ V825 ◆ E765 ◆ T705 ◆ V645 ◆ ◆ S949 ◆ V886 ◆ I326 ◆ G766 ♦ V645 ♦ 1646 ♦ <</th><th>● 1950 ● 8837 ● E827 ● L767 ● P647 ● ● 0951 ● 0828 ● 0828 ● 1767 ● P647 ●</th><th></th><th></th><th>♦ 1895 ♦ 1892 ♦ 1872 ♦ 1712 ♦ E652 ♦
0366 ♦ 0893 ♦ E833 ♦ 1773 ♦ E713 ♦ 1653 ♦</th><th>◆ 3957 ◆ 0894 ◆ P834 ◆ 1774 ◆ 5714 ◆ 1654 ◆ 1958 ◆ 1958 ◆ 2895 ◆ 1835 ◆ 3775 ◆ X715 ◆ 3655 ◆</th><th>♦ 1296 ♦ 1897 ♦ 1776 ♦ 1777 ♦ 267 ♦ 457 ♦ 1717 ♦ 4657 ♦</th><th>◆ S961 ◆ C898 ♦ R833 ♦ G778 ♦ E658 ♦ Y899 V839 A779 ♦ F719 ▲ A659 ♦</th><th>Contract Contract Contra</th></th<></th> | ♦ A914 ♦ A854 € G794 ♦ A734 € T674 € L614 € ● 1915 ● D855 ● Y795 ● A735 ● A675 ● K615 ● < | | | A319 P859 R799 779 1679 1619 1619 1619 1619 1619 16 | Φ Q921 ■ N861 ■ V801 ● A741 ■ K681 ● A621 ● Φ S922 Φ T862 ■ D802 ● G742 ● V682 ● D622 ●
 | 1923 1863 V803 M743 1633 0623 0 0024 1864 5804 1874 1724 1524< | 1924 A004 A044 L024 L024 1925 1885 0805 0745 1685 M625 | ← P926 ← E866 ← D806 ← L746 ← W686 ← Y626 ← ← 2627 ← M747 ← A687 ← T627 ← |
 | | N322 L872 Da1 C152 R002 A532 N332 L872 D812 C152 R692 A532 N332 E873
D812 C152 R692 A532 N332 E873 D812 C152 R692 A532 | No.05 B0/15 D0/15 D0/15 <thd0 15<="" th=""> <thd< th=""><th>HLS SB76 T816 E756 A886 G636 G10 G11E SB76 H817 T757 M837 A657 A557 A557 A557 A557 A557 A557 A55</th><th>GLY DB78 E818 P758 M698 5638 9 ALA ARF9 G819 1759 D699 V639 9</th><th>ALA NIA NIA</th></thd<></thd0> | HLS SB76 T816 E756 A886 G636 G10 G11E SB76 H817 T757 M837 A657 A557 A557 A557 A557 A557 A557 A55 | GLY DB78 E818 P758 M698 5638 9 ALA ARF9 G819 1759 D699 V639 | ALA NIA NIA | ALA V882 M822 M702 D642 D642 ALA
 | ALA RB83 T823 F763 T703 D643 P643 P643 <th< th=""><th>◆ S948 • V885 ◆ V825 ◆ E765 ◆ T705 ◆ V645 ◆ ◆ S949 ◆ V886 ◆ I326 ◆ G766 ♦ V645 ♦ 1646 ♦ <</th><th>● 1950 ● 8837 ● E827 ● L767 ● P647 ● ● 0951 ● 0828 ● 0828 ● 1767 ● P647 ●</th><th></th><th></th><th>♦ 1895 ♦ 1892 ♦ 1872 ♦ 1712 ♦ E652 ♦
0366 ♦ 0893 ♦ E833 ♦ 1773 ♦ E713 ♦ 1653 ♦</th><th>◆ 3957 ◆ 0894 ◆ P834 ◆ 1774 ◆ 5714 ◆ 1654 ◆ 1958 ◆ 1958 ◆ 2895 ◆ 1835 ◆ 3775 ◆ X715 ◆ 3655 ◆</th><th>♦ 1296 ♦ 1897 ♦ 1776 ♦ 1777 ♦ 267 ♦ 457 ♦ 1717 ♦ 4657 ♦</th><th>◆ S961 ◆ C898 ♦ R833 ♦ G778 ♦ E658 ♦ Y899 V839 A779 ♦ F719 ▲ A659 ♦</th><th>Contract Contract Contra</th></th<> | ◆ S948 • V885 ◆ V825 ◆ E765 ◆ T705 ◆ V645 ◆ ◆ S949 ◆ V886 ◆ I326 ◆ G766 ♦ V645 ♦ 1646 ♦ < | ● 1950 ● 8837 ● E827 ● L767 ● P647 ● ● 0951 ● 0828 ● 0828 ● 1767 ● P647 ● | | | ♦ 1895 ♦ 1892 ♦ 1872 ♦ 1712 ♦ E652 ♦
0366 ♦ 0893 ♦ E833 ♦ 1773 ♦ E713 ♦ 1653 ♦
 | ◆ 3957 ◆ 0894 ◆ P834 ◆ 1774 ◆ 5714 ◆ 1654 ◆ 1958 ◆ 1958 ◆ 2895 ◆ 1835 ◆ 3775 ◆ X715 ◆ 3655 ◆ | ♦ 1296 ♦ 1897 ♦ 1776 ♦ 1777 ♦ 267 ♦ 457 ♦ 1717 ♦ 4657 ♦ | ◆ S961 ◆ C898 ♦ R833 ♦ G778 ♦ E658 ♦ Y899 V839 A779 ♦ F719 ▲ A659 ♦ | Contract Contra |





















• Molecule 30: 30S ribosomal protein S10 45% Chain P: 84% 12% MET GLN ASN GLN R3 R4(R6: D6: Q6: D91 L92 A93 G95 G95 V96 D97 V98 Q99 I1000 S101 L102 889 R89 L90 L87 • Molecule 31: 30S ribosomal protein S11 29% Chain Q: 88% 9% MET ALA LYS ALA PRO PRO ALA ALA ALA ALA ARG ARG ARG F52 G54 R56 • Molecule 32: 30S ribosomal protein S12 70% Chain R: 6% • 91% T35 R36 V37 Y38 T39 T40 K44 P45 N46 S47 S47 A48 L49 L49 R50 R50 R51 V52 V52 C53 R31 K88 ASP LEU H96 T97 V98 R99 G10 P91 G92 • Molecule 33: 30S ribosomal protein S14 45% Chain S: 5% • 94% <mark>8555</mark> 856 957 858 R59 Q60 R61 N62 R63 P52 • Molecule 34: 30S ribosomal protein S15 66% Chain T: 83% 16%







WORLDWIDE PROTEIN DATA BANK





A1328 U1329	G1334 C1335	C1345 G1346 A1347	C1350	U1362	G1356 C1357 G1358	A1359 C1363	61364 A1365 A1366	A1367 G1368 G1369	C1370	G1377	U1379 G1380 G1381	G1382	C1386	G1388 G1389	01390 01391 A1392	A1395 U1396	C1399	G1407 G1408	U1409	G1416 C1417	
G1418 A1419 A1420	G1421 G1422 G1423	A1427 C1428 G1429	G1430 A1431 G1432	A1433 A1434 C1435	G1436	A1433 U1440 G1441	U1442 U1443 G1444	G1445	G1448 G1449 G1450	<mark>C1451</mark> G1452 A1453	C1454 G1455 C1456	U1460	C1463	G1465 U1466	01468	G1475 • G1478 •	G1479 G1482	G1483 U1484	U1485 U1486 111487	A1490	G1492
C1493 ♦ U1497	d1500 d1501 A1502	A1504 A1504 A1508	A1509 G1510	U1513 • G1514 A1515 •	C1518	C1526 G1527	A1528 G1529	G1530 C1531 A1532	C1533 U1534 A1535	C1536 C1536 G1537	G1538 U1539	A1545	C1550 A1551	A1553 A1553 U1554	G1555 ◆ C1558 ◆	U1559 G1560	U1563 0 C1564	C1565	G1568	41570	A LOL
A1580 G1581 C1582	A1583 A1586 A1586 G1587	G1588 U1589 A1590	A1591 C1592	C1595 A1596	C1600 G1601	C1607		C1612 G1613 A1614	C1615 A1616	C1617 A G1619	G1620	G1623 U1624 C1625	A1626	G1631	G1633 A1634 A1635	U1636	C1639 G1645	C1646 U1647 U1648	G1649 A1650	41652 61653	
C1656 U1657 C1658	G1659 ♦ G1660 ♦ A1664	A1665 G1666 G1667	C1670	A1672 G1673 G1674	C1675 A1676 A1677	A1678	A1689 A1690	C1691 U1692	G1697 A1698	A1701 G1702		C1706 G1707	U1709	A1713 U1714	01716	61719 A1722	u1729 C1730	61731 C1732	G1/33 G1734 A1735	G1738	C1741
U1742 G1743 A1744	A1745 A1746 U1747	G1750 G1750 H1751	A1754	G1756 A1757	U1758 A1759 C1760	C1761 A1762 G1763	C1764	01769 01769 G1770	C1771	C1774 U1775	A1780 U1781	U1782 A1783 A1784	A1785	A1791	C1795 U1796		A1801 A1802 A1803		C1806 G1807	A1808 4	C1816
G1817 U1818 A1819	U1820 G1824 U1825	G1826	C1833 U1834	c1836	G1839 G1840 U1841	A1847 A1848 A1848	G1850	A1858 U1859 G1860	G1861 G1862 G1863	01864 G1869	C1870 A1871	A1872 G1873 C1874	U1882	G1888	C1892 C1893	G1896 G1897	A1900	C1902	G1906 G1907	G1910	
U A1912 A1913	C1914 U U U U	A1918 A1919 C1920 G1921	01923 01923 01924 01925	A1928 61929	G1930 U1931	A1937 A1938	U1940 C1941	C1942 U1943	01944 G1945 U1946	C1947 G1948	G1949 G1950	U1955	C1958	C U1963 G1964	C1965 A1966 C1967	G1968 A1969		G1973 C1974	G1975 U1976 A1977	A1978 U1979 G1980	
A1981 U1982 G1983	G1984 ♦ C1985 C1986 A1987 ♦	G1988 G1989 C1990	U1991 G1992 U1993	C1994 U1995 C1996	C1997 A1998 C1999	C2000		C2008	G2010 U2011 G2012	A2013 A2014 A2015	U2016 U2017	A2020 C2021	U2022	U2026 G2027	U2028 G2029 A	A2031 G2032 A2033	U2034	A2042 C2043 C2044	C2045 G2046		A2052
G2053 A2054 C2055	G2056 G2057 A2058	A2060 G2061 A2062	C2063 C2064 C2065	C2066 G2067 U2068	G A2070 A2071	<mark>C2072</mark> C2073 U	U2075	C2078 C2078	U2092	C2096 A2097	G2 100	C2103 C2104	U2105 U2106	A2108 A2108 U2109	G2110 U2111 G2112	UZ113 A2114 G2115	42115 A2117 U2118	U2122	G2124 G2125	A2126 G2127 G2128	
U2131 U2132	G2133 A2134 U2139	C2145 C2146 A2147	A2154 G2157	A2158 G2159 C2160	C2161 G2162 A2163	C2164 C2165 U2166	U2167 G2168 A2169	<mark>A2170</mark> A2171 U2172	A2173	U2180 U2181 112182	A2183	62190 A2191	U2192 G2193 U2194	A2198 A2199	C2200 ◀ G2201 ◀ U2202 ♦	U2203 G2204 A2205	C2206	A2211	U2213 C2214		
G2218	G2223 G2224 A2225 C2226 A2227	G2228	U2233	G2237 G2238 G2239	U2240 A2241	U2243 U2244	02245 C2248	U2249 ♦ G2250 ♦ G	G2252 G2253 C2254	G2255 ↔ G2256	U2257	02259 C2260 C2261	U2262 C2263 ♦ C2264 ♦	U2265	A226 / A2268 G2269	A2270 G2271 U2272	A2273 A2274		G2279	G2283 C2283 G2286	
A2287 A2288 G2289	G2293 G2294 C77365	U2296	U2305 C2306 G2307	G2308 A2309 C2310	C2313	G2315 G2316	G2319	A2322 G2325	C2326 A2327 A2328	U2329	A2333 U2334 A2335	A2336 G2337	C2338 C2339 A2340	<mark>G2341</mark> ♦ C2342 ♦	<mark>G2345 A2346 C2347</mark>	C2350	G2355 U2356 G2357	A2358	G2361 G2365	A2366 G2367 C2368	













• Molecule 52: 50S ribosomal protein L4















• Molecule 64: 50S ribosomal protein L18







4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38957	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 $(e^-/\text{\AA}^2)$	45	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	0.065	Depositor
Minimum map value	-0.026	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.014	Depositor
Map size (Å)	532.48, 532.48, 532.48	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	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).

Mal	Chain	B	ond lengths	E	Bond angles
1VIOI	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5
1	0	0.61	0/829	0.54	0/1107
2	1	0.59	0/864	0.55	0/1156
3	2	0.55	0/752	0.52	0/1005
4	3	0.53	0/796	0.53	0/1062
5	4	0.51	0/766	0.49	0/1025
6	5	1.13	6/528~(1.1%)	0.97	1/810~(0.1%)
7	6	1.11	4/603~(0.7%)	0.96	0/926
8	7	0.72	1/761~(0.1%)	1.80	23/1178~(2.0%)
9	9	0.35	0/1131	0.60	0/1524
10	А	0.71	2/1810~(0.1%)	1.25	18/2821~(0.6%)
10	В	0.95	1/1810~(0.1%)	1.50	25/2821~(0.9%)
11	AA	0.44	1/10736~(0.0%)	0.61	2/14487~(0.0%)
12	AB	0.68	2/1310~(0.2%)	0.67	2/1766~(0.1%)
13	AC	0.38	0/2113	0.58	0/2877
13	AD	0.34	0/2096	0.59	0/2854
14	AE	0.52	4/10545~(0.0%)	0.66	6/14236~(0.0%)
15	AF	0.33	0/652	0.57	0/879
16	AG	0.64	1/3897~(0.0%)	0.89	30/5273~(0.6%)
17	С	0.61	1/553~(0.2%)	0.62	0/743
18	D	1.35	22/36610~(0.1%)	1.18	99/57091~(0.2%)
19	Ε	0.46	0/675	0.46	0/895
20	F	0.50	0/597	0.47	0/792
21	G	0.58	1/1791~(0.1%)	0.57	1/2413~(0.0%)
22	Н	0.31	0/1746	0.58	0/2382
23	Ι	0.53	0/1663	0.51	0/2241
24	J	0.53	0/1665	0.49	0/2227
25	Κ	0.60	0/1165	0.57	0/1568
26	L	0.54	0/867	0.49	0/1171
27	М	0.47	0/1195	0.53	0/1602
28	N	0.57	0/989	0.51	0/1326
29	0	0.51	0/1034	0.53	0/1375
30	Р	0.46	0/800	0.54	0/1082



Mal	Chain	B	ond lengths	I	Bond angles
	Unain	RMSZ	# Z > 5	RMSZ	# Z > 5
31	Q	0.52	0/893	0.50	0/1205
32	R	0.60	0/952	0.55	0/1274
33	S	0.53	0/817	0.50	0/1088
34	Т	0.52	0/722	0.51	0/964
35	U	0.54	0/659	0.52	0/884
36	V	0.55	0/657	0.51	0/881
37	W	0.47	0/680	0.51	0/915
38	Х	0.45	0/909	0.51	0/1215
39	Y	0.51	2/1046~(0.2%)	0.62	0/1410
40	Ζ	0.24	0/227	0.40	0/304
41	a	1.45	45/69247~(0.1%)	1.12	140/107985~(0.1%)
42	b	0.59	0/589	0.51	0/779
43	с	0.57	0/635	0.55	0/848
44	d	1.23	0/2872	1.00	0/4478
45	е	0.48	0/502	0.50	0/667
46	f	0.52	0/452	0.51	0/605
47	g	0.39	0/531	0.52	0/709
48	h	0.64	0/2121	0.54	0/2852
49	i	0.57	0/450	0.55	0/599
50	j	0.63	0/1586	0.55	0/2134
51	k	0.60	0/433	0.54	0/576
52	1	0.54	0/1571	0.52	0/2113
53	m	0.63	0/380	0.54	0/498
54	n	0.47	0/1434	0.52	0/1926
55	0	0.58	0/513	0.55	0/676
56	р	0.49	0/1333	0.52	0/1805
57	q	0.58	0/303	0.55	0/397
58	r	0.40	0/1122	0.50	0/1515
59	\mathbf{S}	0.64	0/1152	0.51	0/1551
60	\mathbf{t}	0.63	0/955	0.52	0/1279
61	u	0.55	0/1062	0.56	$0/1\overline{413}$
62	V	0.60	0/1093	0.53	0/1460
63	W	0.60	0/964	0.52	$0/1\overline{289}$
64	Х	0.49	0/902	0.49	0/1209
65	У	0.63	0/929	0.52	0/1242
66	Z	0.68	0/960	0.50	0/1278
All	All	1.12	93/195002~(0.0%)	0.97	$34\overline{7/286738}~(0.1\%)$

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
9	9	0	3
13	AC	0	3
13	AD	0	1
14	AE	0	5
16	AG	0	7
21	G	0	2
22	Н	0	5
29	0	0	1
54	n	0	1
55	0	0	1
All	All	0	29

The worst 5 of 93 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
12	AB	124	PRO	N-CA	13.13	1.69	1.47
21	G	157	LEU	C-N	10.81	1.54	1.34
14	AE	88	CYS	CB-SG	-10.21	1.64	1.82
41	a	74	А	C6-N1	-9.21	1.29	1.35
16	AG	429	LYS	C-N	8.82	1.51	1.34

The worst 5 of 347 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
18	D	37	U	C5-C4-O4	35.68	147.31	125.90
18	D	884	U	C5-C4-O4	35.09	146.95	125.90
41	а	1019	U	C5-C4-O4	34.63	146.68	125.90
18	D	827	U	C5-C4-O4	34.07	146.34	125.90
41	a	1141	U	C5-C4-O4	33.77	146.16	125.90

There are no chirality outliers.

5 of 29 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	9	107	GLU	Peptide
9	9	117	LEU	Peptide
9	9	49	GLY	Peptide
13	AC	192	VAL	Peptide
13	AC	319	GLU	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	Perce	ntiles
1	0	101/103~(98%)	92 (91%)	9~(9%)	0	100	100
2	1	108/110~(98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/100~(92%)	89 (97%)	3(3%)	0	100	100
4	3	101/104~(97%)	97~(96%)	4 (4%)	0	100	100
5	4	92/94~(98%)	89 (97%)	3~(3%)	0	100	100
9	9	146/165~(88%)	107 (73%)	37~(25%)	2(1%)	9	40
11	AA	1338/1342~(100%)	1206 (90%)	126 (9%)	6~(0%)	30	64
12	AB	158/181~(87%)	119 (75%)	26 (16%)	13 (8%)	1	4
13	AC	295/329~(90%)	274 (93%)	19 (6%)	2(1%)	19	54
13	AD	293/329~(89%)	269 (92%)	24 (8%)	0	100	100
14	AE	1329/1407~(94%)	1199 (90%)	121 (9%)	9 (1%)	19	54
15	AF	80/91~(88%)	77 (96%)	3 (4%)	0	100	100
16	AG	493/495~(100%)	377 (76%)	85 (17%)	31~(6%)	1	8
17	С	64/75~(85%)	61 (95%)	3~(5%)	0	100	100
19	Е	84/87~(97%)	82 (98%)	2(2%)	0	100	100
20	F	68/71~(96%)	67 (98%)	1 (2%)	0	100	100
21	G	223/241~(92%)	209 (94%)	13 (6%)	1 (0%)	30	64
22	Н	255/557~(46%)	201 (79%)	45 (18%)	9 (4%)	3	20
23	Ι	$\overline{206/233}~(88\%)$	200 (97%)	6 (3%)	0	100	100
24	J	$\overline{203/206}~(98\%)$	199 (98%)	4 (2%)	0	100	100
25	K	154/167~(92%)	146 (95%)	6 (4%)	2 (1%)	10	41



Conti	Continued from previous page								
Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles			
26	L	102/135~(76%)	97~(95%)	4 (4%)	1 (1%)	13 47			
27	М	149/179~(83%)	139 (93%)	9 (6%)	1 (1%)	19 54			
20	NT	107/100 (0007)	104 (0007)	ρ (ρ (τ))	0	100 100			

26	L	102/135~(76%)	97 (95%)	4 (4%)	1 (1%)	13	47
27	М	149/179~(83%)	139 (93%)	9~(6%)	1 (1%)	19	54
28	Ν	127/130~(98%)	124 (98%)	3~(2%)	0	100	100
29	Ο	125/130~(96%)	118 (94%)	6~(5%)	1 (1%)	16	51
30	Р	97/103~(94%)	88 (91%)	8 (8%)	1 (1%)	13	47
31	Q	115/129~(89%)	105 (91%)	10 (9%)	0	100	100
32	R	117/124~(94%)	112 (96%)	4 (3%)	1 (1%)	14	49
33	S	98/101~(97%)	96 (98%)	2(2%)	0	100	100
34	Т	86/89~(97%)	83 (96%)	3 (4%)	0	100	100
35	U	80/82~(98%)	77 (96%)	3 (4%)	0	100	100
36	V	78/84~(93%)	74 (95%)	4 (5%)	0	100	100
37	W	81/92~(88%)	78 (96%)	3 (4%)	0	100	100
38	Х	114/118~(97%)	104 (91%)	8 (7%)	2(2%)	7	35
39	Y	139/142~(98%)	113 (81%)	25 (18%)	1 (1%)	19	54
40	Z	28/121~(23%)	24 (86%)	4 (14%)	0	100	100
42	b	74/85~(87%)	70 (95%)	4(5%)	0	100	100
43	с	75/78~(96%)	72 (96%)	3 (4%)	0	100	100
45	е	60/63~(95%)	59 (98%)	1 (2%)	0	100	100
46	f	56/59~(95%)	53~(95%)	3~(5%)	0	100	100
47	g	64/70~(91%)	62 (97%)	2(3%)	0	100	100
48	h	269/273~(98%)	254 (94%)	15~(6%)	0	100	100
49	i	54/57~(95%)	48 (89%)	6 (11%)	0	100	100
50	j	207/209~(99%)	198 (96%)	9~(4%)	0	100	100
51	k	50/55~(91%)	49 (98%)	1 (2%)	0	100	100
52	1	199/201~(99%)	192 (96%)	7~(4%)	0	100	100
53	m	44/46~(96%)	42 (96%)	2~(4%)	0	100	100
54	n	175/179~(98%)	168 (96%)	6(3%)	1 (1%)	22	57
55	0	$62/65~(9\overline{5\%})$	56 (90%)	5(8%)	1 (2%)	8	37
56	р	173/177~(98%)	165 (95%)	7~(4%)	1 (1%)	22	57
57	q	$36/38\ (95\%)$	36 (100%)	0	0	100	100
58	r	147/149~(99%)	137 (93%)	10 (7%)	0	100	100



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
59	S	140/142~(99%)	137~(98%)	3~(2%)	0	100	100
60	t	121/123~(98%)	114 (94%)	7~(6%)	0	100	100
61	u	142/144~(99%)	133~(94%)	9~(6%)	0	100	100
62	v	134/136~(98%)	126 (94%)	8~(6%)	0	100	100
63	W	117/127~(92%)	111 (95%)	6 (5%)	0	100	100
64	х	114/117~(97%)	113 (99%)	1 (1%)	0	100	100
65	У	112/115~(97%)	109~(97%)	3~(3%)	0	100	100
66	Z	115/118~(98%)	110 (96%)	5 (4%)	0	100	100
All	All	10159/11072~(92%)	9310 (92%)	763 (8%)	86 (1%)	19	51

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5 of 86 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	79	PRO
11	AA	888	THR
12	AB	121	LYS
12	AB	122	PRO
12	AB	123	ARG

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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Perce	entiles
1	0	84/84~(100%)	80~(95%)	4 (5%)	21	55
2	1	93/93~(100%)	84 (90%)	9~(10%)	6	27
3	2	81/84~(96%)	77~(95%)	4 (5%)	21	54
4	3	84/85~(99%)	78~(93%)	6~(7%)	12	42
5	4	78/78~(100%)	75~(96%)	3~(4%)	28	60
9	9	112/123~(91%)	79~(70%)	33~(30%)	0	1
11	AA	1155/1157~(100%)	1142 (99%)	13 (1%)	70	86
12	AB	138/158~(87%)	$105 \ (76\%)$	33~(24%)	0	2



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Mol	Chain	Analysed	Rotameric	Outliers	Perce	entiles
13	AC	186/286~(65%)	186 (100%)	0	100	100
13	AD	185/286~(65%)	185 (100%)	0	100	100
14	AE	1120/1168~(96%)	1051 (94%)	69~(6%)	15	47
15	AF	70/75~(93%)	70~(100%)	0	100	100
16	AG	409/409~(100%)	296~(72%)	113~(28%)	0	1
17	\mathbf{C}	57/65~(88%)	55~(96%)	2 (4%)	31	63
19	Ε	65/66~(98%)	62~(95%)	3~(5%)	23	56
20	F	60/61~(98%)	57~(95%)	3~(5%)	20	54
21	G	187/199~(94%)	177~(95%)	10~(5%)	19	52
22	Н	137/461~(30%)	125~(91%)	12 (9%)	8	32
23	Ι	171/190~(90%)	162~(95%)	9~(5%)	19	52
24	J	172/173~(99%)	166 (96%)	6 (4%)	31	63
25	Κ	119/126~(94%)	110 (92%)	9~(8%)	11	39
26	L	91/116~(78%)	81 (89%)	10 (11%)	5	23
27	М	124/147~(84%)	116 (94%)	8~(6%)	14	45
28	Ν	104/105~(99%)	101~(97%)	3~(3%)	37	67
29	Ο	105/107~(98%)	98~(93%)	7~(7%)	13	44
30	Р	86/90~(96%)	75 (87%)	11 (13%)	3	17
31	Q	90/99~(91%)	87~(97%)	3~(3%)	33	64
32	R	101/104~(97%)	94~(93%)	7~(7%)	13	43
33	S	83/84~(99%)	78~(94%)	5~(6%)	16	48
34	Т	76/77~(99%)	62~(82%)	14 (18%)	1	7
35	U	65/65~(100%)	60~(92%)	5 (8%)	10	39
36	V	74/78~(95%)	70~(95%)	4(5%)	18	51
37	W	72/79~(91%)	68 (94%)	4 (6%)	17	50
38	Х	94/96~(98%)	82 (87%)	12 (13%)	3	17
39	Y	109/110~(99%)	89~(82%)	20 (18%)	1	7
40	Ζ	26/85~(31%)	17 (65%)	9(35%)	0	0
42	b	58/63~(92%)	58 (100%)	0	100	100
43	с	67/68~(98%)	64 (96%)	3 (4%)	23	56
45	е	54/55~(98%)	54 (100%)	0	100	100



Mol	Chain	Analysed	Rotameric	Outliers	Perce	entiles
46	f	48/49~(98%)	45 (94%)	3~(6%)	15	46
47	g	59/62~(95%)	54 (92%)	5~(8%)	8	34
48	h	216/218~(99%)	202~(94%)	14 (6%)	14	45
49	i	47/48~(98%)	41 (87%)	6~(13%)	3	17
50	j	164/164~(100%)	154 (94%)	10 (6%)	15	47
51	k	47/49~(96%)	45 (96%)	2 (4%)	25	57
52	1	165/165~(100%)	154 (93%)	11 (7%)	13	44
53	m	38/38~(100%)	35~(92%)	3 (8%)	10	38
54	n	148/150~(99%)	136~(92%)	12 (8%)	9	36
55	О	51/52~(98%)	48 (94%)	3~(6%)	16	48
56	р	136/138~(99%)	131 (96%)	5 (4%)	29	62
57	q	34/34~(100%)	32~(94%)	2~(6%)	16	48
58	r	114/114~(100%)	105~(92%)	9~(8%)	10	38
59	s	116/116~(100%)	111 (96%)	5 (4%)	25	57
60	t	104/104~(100%)	96~(92%)	8 (8%)	10	39
61	u	103/103~(100%)	96~(93%)	7 (7%)	13	43
62	V	109/109~(100%)	105~(96%)	4 (4%)	29	62
63	W	99/103~(96%)	93~(94%)	6 (6%)	15	47
64	х	86/87~(99%)	81 (94%)	5 (6%)	17	49
65	У	99/100~(99%)	95~(96%)	4 (4%)	27	59
66	Z	89/90~(99%)	85 (96%)	4 (4%)	23	56
All	All	8314/9148 (91%)	7720 (93%)	594 (7%)	15	42

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5 of 594 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	с	5	CYS
62	V	115	GLU
48	h	52	ARG
40	Ζ	30	PHE
54	n	6	ASP

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



Mol	Chain	Res	Type
21	G	18	HIS
27	М	148	ASN
21	G	39	HIS
26	L	63	ASN
31	Q	15	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	А	76/76~(100%)	33 (43%)	10 (13%)
10	В	75/76~(98%)	41 (54%)	8 (10%)
18	D	1513/1542~(98%)	282 (18%)	8~(0%)
41	a	2859/2904~(98%)	534 (18%)	0
44	d	119/120~(99%)	18 (15%)	0
8	7	32/41~(78%)	19~(59%)	4(12%)
All	All	4674/4759~(98%)	927 (19%)	30(0%)

5 of 927 RNA backbone outliers are listed below:

Mol	Chain	\mathbf{Res}	Type
8	7	-19	U
8	7	-17	U
8	7	-16	U
8	7	-15	U
8	7	-14	U

5 of 30 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	В	6	G
18	D	1145	А
10	В	21	А
18	D	1493	А
18	D	428	G

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 3 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 (i)

This section contains visualisations of the EMDB entry EMD-22082. 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: 256







Z Index: 256



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: 242

Y Index: 250

Z Index: 259

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 0.014. 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 $1238~{\rm nm^3};$ this corresponds to an approximate mass of 1118 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 0.312 ${\rm \AA^{-1}}$



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-22082 and PDB model 6X6T. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.014 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 (0.014).



9.4 Atom inclusion (i)



At the recommended contour level, 32% of all backbone atoms, 34% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3360	0.0150
0	0.2720	-0.0410
1	0.2300	-0.0340
2	0.2890	0.0050
3	0.4240	0.0080
4	0.3270	0.0250
5	0.0250	0.0380
6	0.0760	0.0390
7	0.1340	0.0770
9	0.1540	0.0020
А	0.4380	0.0920
AA	0.0070	0.0250
AB	0.1210	0.1110
AC	0.0010	0.0090
AD	0.0010	0.0120
AE	0.0030	0.0160
AF	0.0000	0.0220
AG	0.1970	0.1380
В	0.4330	0.0350
С	0.4020	0.0440
D	0.5580	0.0510
E	0.2630	-0.0470
F	0.3720	0.1300
G	0.4710	0.1440
Н	0.0300	0.0480
I	0.5160	0.2070
J	0.4130	0.0240
K	0.3480	0.0120
L	0.3170	-0.0540
M	0.5520	0.2370
N	0.2880	-0.0650
0	0.5360	0.1620
P	0.4380	0.1200
Q	0.5270	0.1840
R	0.2590	-0.0640



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Chain	Atom inclusion	Q-score
S	0.4380	0.1180
Т	0.3040	-0.0380
U	0.3090	-0.0520
V	0.3730	-0.0230
W	0.3460	-0.0050
Х	0.3550	0.0100
Y	0.0340	-0.0050
Z	0.0000	0.0130
a	0.4330	-0.0200
b	0.2620	-0.0670
С	0.3560	-0.0570
d	0.4860	-0.0050
е	0.3520	-0.0330
f	0.2960	0.0030
g	0.2430	0.0390
h	0.2920	-0.0770
i	0.3530	-0.0260
j	0.2900	-0.0160
k	0.3090	-0.0500
1	0.2990	-0.0110
m	0.3380	-0.0130
n	0.2830	-0.0430
0	0.3180	-0.0230
р	0.2090	-0.0260
q	0.2330	-0.0190
r	0.2470	0.0160
s	0.2660	-0.0210
t	0.2770	0.0020
u	0.3100	-0.0260
V	0.2800	-0.0150
W	0.3380	-0.0330
X	0.3560	-0.0420
У	0.3130	-0.0130
Z	0.3030	-0.0140

