



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 09:37 AM UTC

PDB ID : 7PIQ / pdb_00007piq
EMDB ID : EMD-13447
Title : 70S ribosome with A- and P-site tRNAs in pseudouridimycin-treated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-23
Resolution : 9.70 Å (reported)
Based on initial models : 7OOD, 7OOC, 4V7C

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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

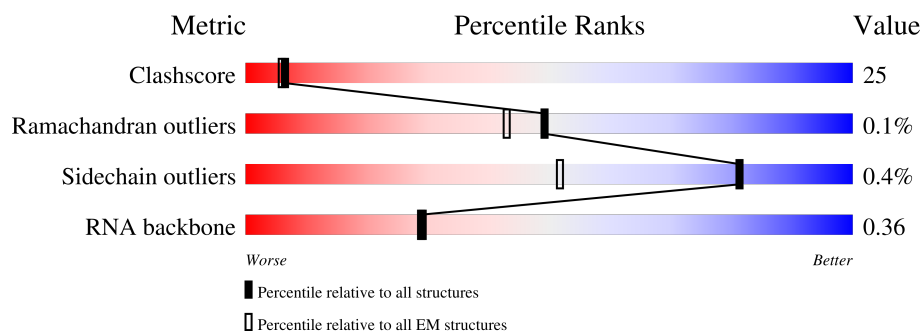
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.70 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.



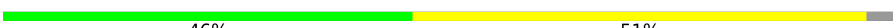
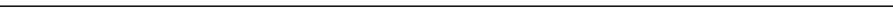
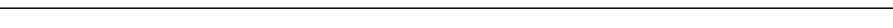
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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	0	48	
2	1	59	
3	2	37	
4	A	294	
5	B	273	
6	C	205	
7	D	219	

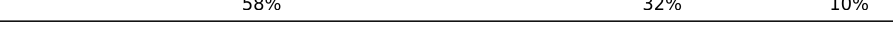
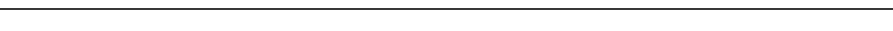
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Mol	Chain	Length	Quality of chain
8	E	215	
9	F	155	
10	G	142	
11	H	132	
12	I	108	
13	J	121	
14	K	139	
15	L	124	
16	M	61	
17	N	86	
18	O	94	
19	P	85	
20	Q	104	
21	R	87	
22	S	87	
23	T	60	
24	a	287	
25	b	287	
26	c	212	
27	d	180	
28	e	184	
29	f	149	
30	g	161	
31	h	137	
32	i	146	

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Mol	Chain	Length	Quality of chain
33	j	122	
34	k	151	
35	l	139	
36	m	124	
37	n	116	
38	o	119	
39	p	127	
40	q	100	
41	r	159	
42	s	237	
43	t	111	
44	u	104	
45	v	65	
46	w	111	
47	x	97	
48	y	57	
49	z	53	
50	3	2907	
51	4	108	
52	5	1520	
53	6	76	
53	7	76	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 146057 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 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	37	Total	C	N	O	S	0	0
			304	189	65	46	4		

- Molecule 4 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	240	Total	C	N	O	S	0	0
			1921	1226	334	352	9		

- Molecule 5 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	215	Total	C	N	O	S	0	0
			1698	1073	313	307	5		

- Molecule 6 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	203	Total	C	N	O	S	0	0
			1660	1051	314	290	5		

- Molecule 7 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	153	Total	C	N	O	S	0	0
			1173	742	226	202	3		

- Molecule 8 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	167	Total	C	N	O	S	0	0
			1362	857	240	263	2		

- Molecule 9 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	154	Total	C	N	O	S	0	0
			1246	785	239	216	6		

- Molecule 10 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	141	Total	C	N	O	S	0	0
			1110	723	193	192	2		

- Molecule 11 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	128	Total	C	N	O	S	0	0
			1028	655	191	181	1		

- Molecule 12 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	101	Total	C	N	O	S	0	0
			809	523	142	143	1		

- Molecule 13 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	114	Total	C	N	O	S	0	0
			829	514	153	156	6		

- Molecule 14 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	136	Total	C	N	O	S	0	0
			1076	680	213	181	2		

- Molecule 15 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	118	Total	C	N	O		0	0
			951	594	191	166			

- Molecule 16 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	60	Total	C	N	O	S	0	0
			474	302	96	72	4		

- Molecule 17 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	83	Total	C	N	O		0	0
			673	428	125	120			

- Molecule 18 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	80	Total	C	N	O	S	0	0
			646	414	119	111	2		

- Molecule 19 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	83	Total	C	N	O		0	0
			675	425	135	115			

- Molecule 20 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	65	Total	C	N	O	S	0	0
			535	342	103	86	4		

- Molecule 21 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	84	Total	C	N	O	S	0	0
			682	435	127	118	2		

- Molecule 22 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S	77	Total	C	N	O		0	0
			629	383	135	111			

- Molecule 23 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	53	Total	C	N	O	S	0	0
			471	295	103	72	1		

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

- Molecule 26 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

- Molecule 27 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	d	175	Total	C	N	O	S	0	0
			1388	893	245	246	4		

- Molecule 28 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	e	176	Total	C	N	O	0	0
			1396	899	247	250		

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	f	145	Total	C	N	O	S	0
			1160	746	204	207	3	0

- Molecule 30 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	g	121	Total	C	N	O	S	0
			910	580	158	169	3	0

- Molecule 31 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	h	128	Total	C	N	O	S	0
			959	616	160	177	6	0

- Molecule 32 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	i	144	Total	C	N	O	S	0
			1164	737	213	209	5	0

- Molecule 33 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	j	122	Total	C	N	O	S	0
			944	595	178	167	4	0

- Molecule 34 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	k	148	Total	C	N	O	0	0
			1153	731	226	196		

- Molecule 35 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	l	136	Total	C	N	O	S	0	0
			1079	694	196	182	7		

- Molecule 36 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	119	Total	C	N	O	S	0	0
			958	609	175	171	3		

- Molecule 37 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	n	112	Total	C	N	O	S	0	0
			889	557	175	155	2		

- Molecule 38 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	o	115	Total	C	N	O	S	0	0
			938	592	180	165	1		

- Molecule 39 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	p	112	Total	C	N	O	S	0	0
			934	594	186	152	2		

- Molecule 40 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	q	99	Total	C	N	O	S	0	0
			811	525	148	134	4		

- Molecule 41 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 42 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	s	92	Total	C	N	O	S	0	0
			720	475	122	122	1		

- Molecule 43 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	111	Total	C	N	O	S	0	0
			872	550	166	153	3		

- Molecule 44 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	86	Total	C	N	O	S	0	0
			657	409	130	117	1		

- Molecule 45 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	v	63	Total	C	N	O	S	0	0
			513	317	108	87	1		

- Molecule 46 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	w	100	Total	C	N	O	0	0
			818	517	153	148		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

- Molecule 49 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 50 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 51 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

- Molecule 53 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	6	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
53	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

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: 50S ribosomal protein L34

Chain 0: 



- Molecule 2: 50S ribosomal protein L35

Chain 1: 



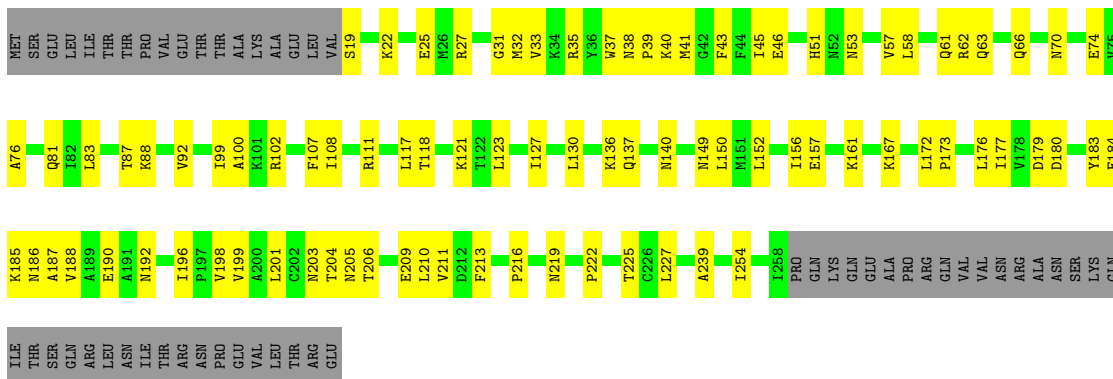
- Molecule 3: 50S ribosomal protein L36

Chain 2: 

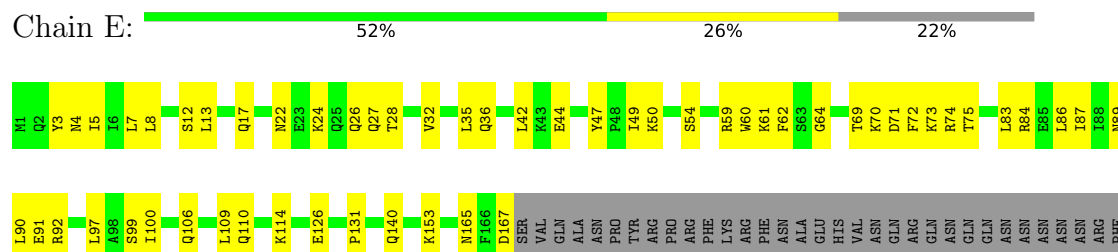


- Molecule 4: 30S ribosomal protein S2

Chain A: 



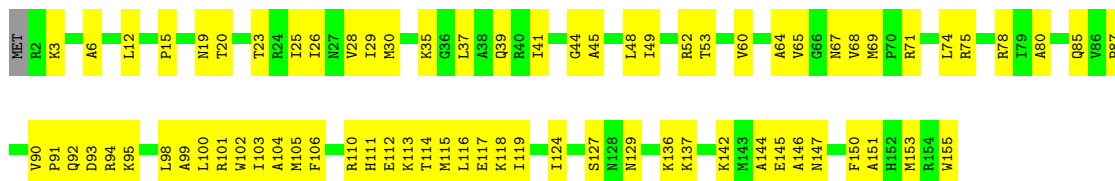
- Molecule 5: 30S ribosomal protein S3



ASP
ARG
ASN
ARG
ASN
ASN
GLN
HIS
ASN
ARG
PHE
LYS
ASP
LYS
GLN

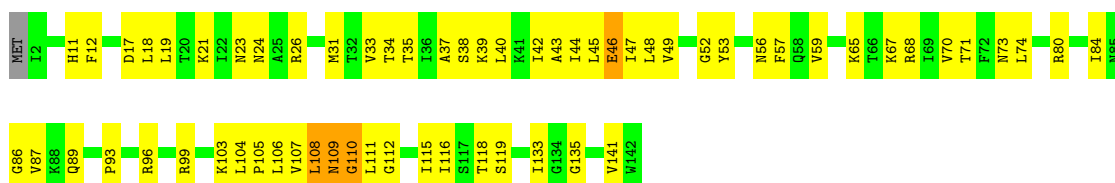
• Molecule 9: 30S ribosomal protein S7

Chain F:  52% 48%



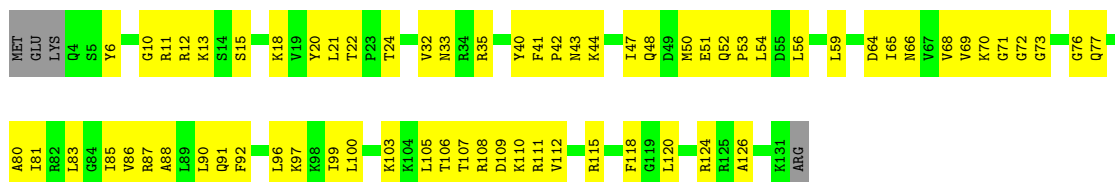
• Molecule 10: 30S ribosomal protein S8

Chain G:  56% 41%



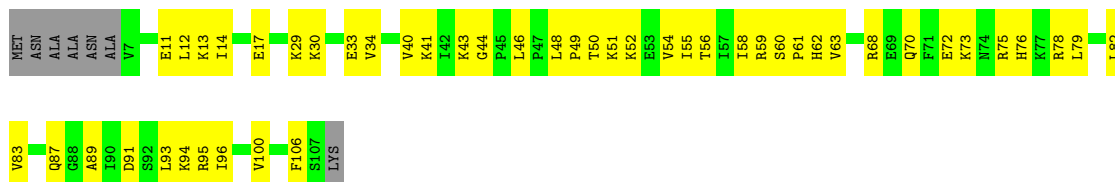
• Molecule 11: 30S ribosomal protein S9

Chain H:  46% 51%



• Molecule 12: 30S ribosomal protein S10

Chain I:  50% 44% 6%



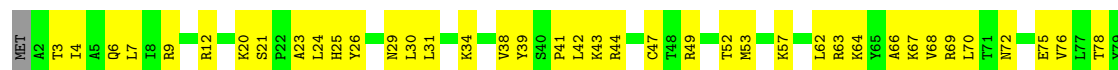
• Molecule 13: 30S ribosomal protein S11

Chain J:  52% 40% 6%





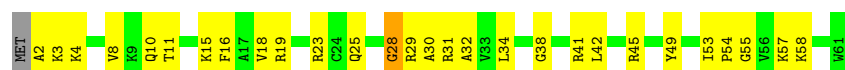
- Molecule 14: 30S ribosomal protein S12



- Molecule 15: 30S ribosomal protein S13



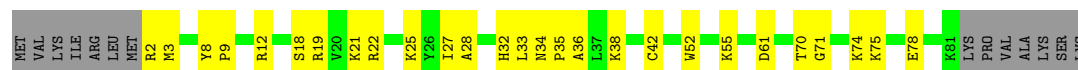
- Molecule 16: 30S ribosomal protein S14 type Z



- Molecule 17: 30S ribosomal protein S15

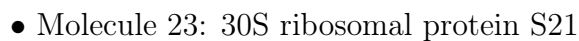
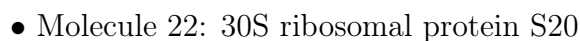
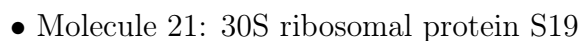
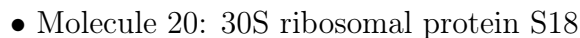


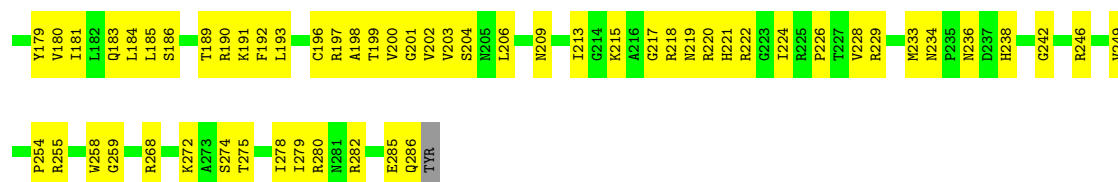
- Molecule 18: 30S ribosomal protein S16



- Molecule 19: 30S ribosomal protein S17

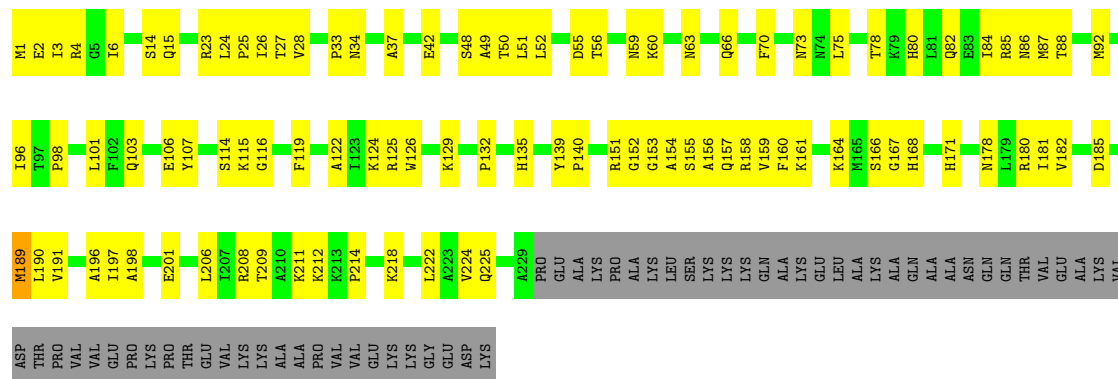






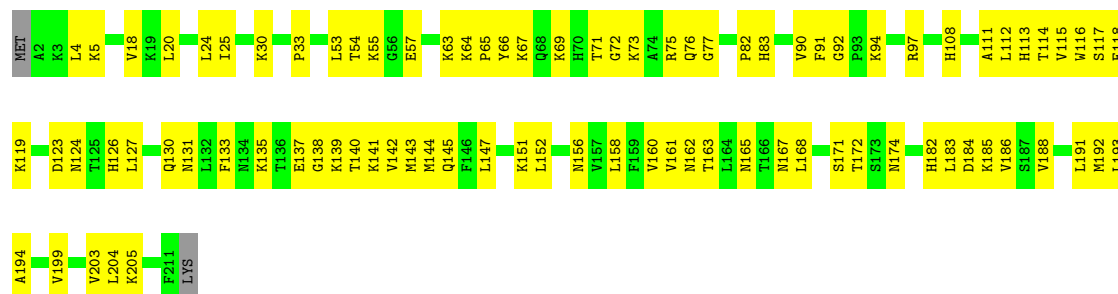
• Molecule 25: 50S ribosomal protein L3

Chain b: 46% 33% 20%



• Molecule 26: 50S ribosomal protein L4

Chain c: 58% 41%



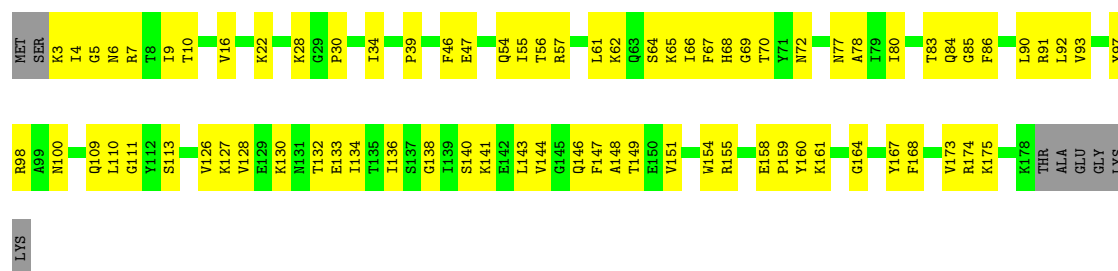
• Molecule 27: 50S ribosomal protein L5

Chain d: 52% 46%



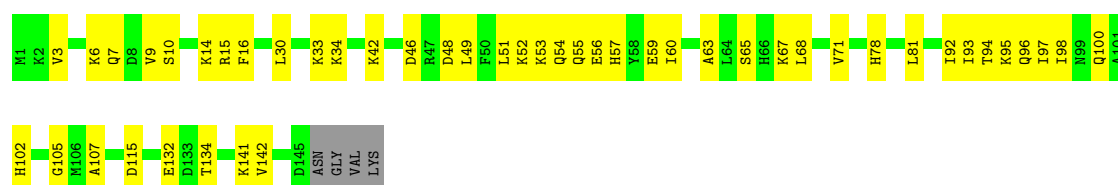
• Molecule 28: 50S ribosomal protein L6

Chain e:  54% 42% .



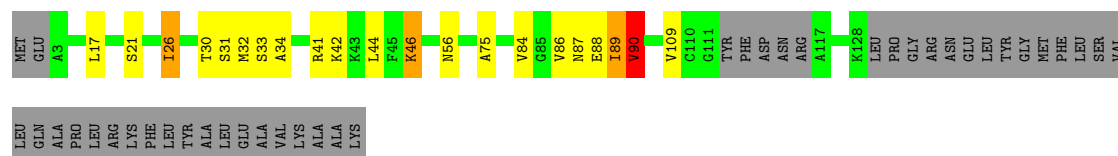
- Molecule 29: 50S ribosomal protein L9

Chain f:  66% 32% .



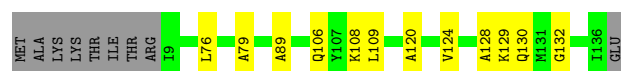
- Molecule 30: 50S ribosomal protein L10

Chain g:  62% 11% 25% ..



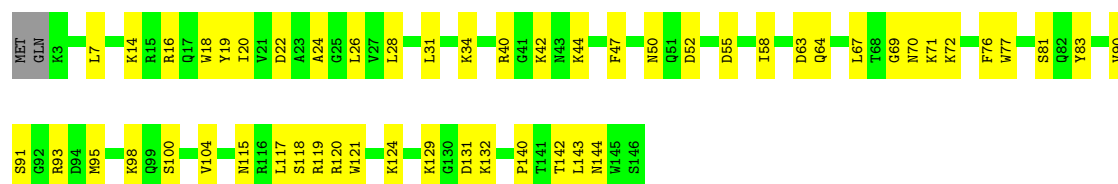
- Molecule 31: 50S ribosomal protein L11

Chain h:  85% 9% 7%



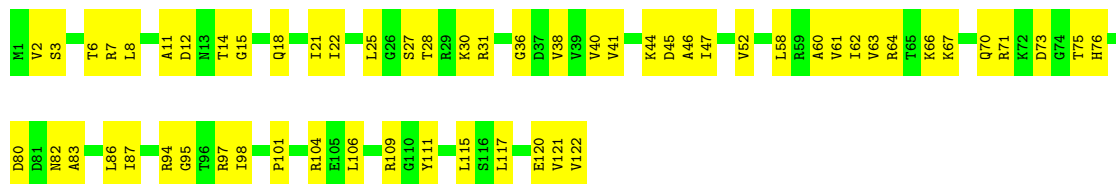
- Molecule 32: 50S ribosomal protein L13

Chain i:  63% 36% .



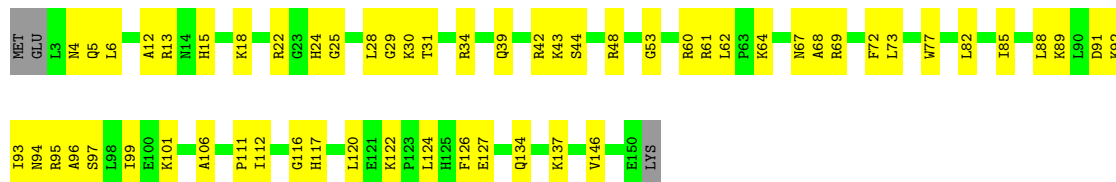
- Molecule 33: 50S ribosomal protein L14

Chain j:  52% 48%



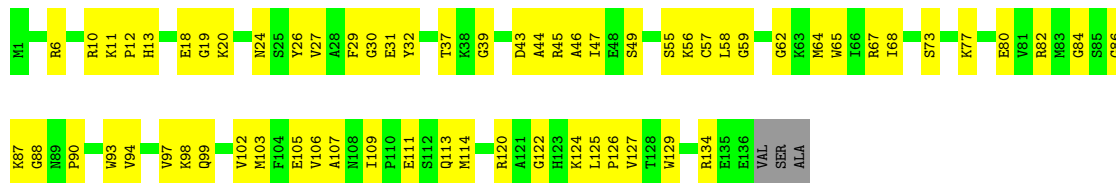
- Molecule 34: 50S ribosomal protein L15

Chain k:  60% 38%



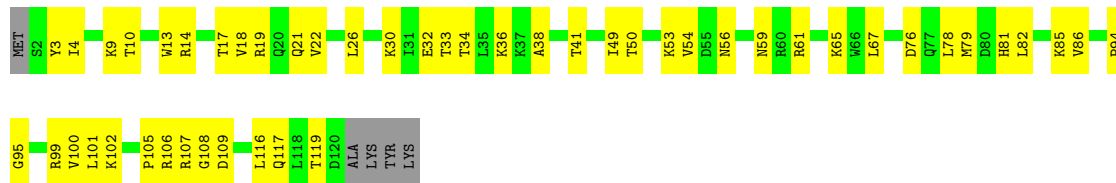
- Molecule 35: 50S ribosomal protein L16

Chain l:  52% 46%



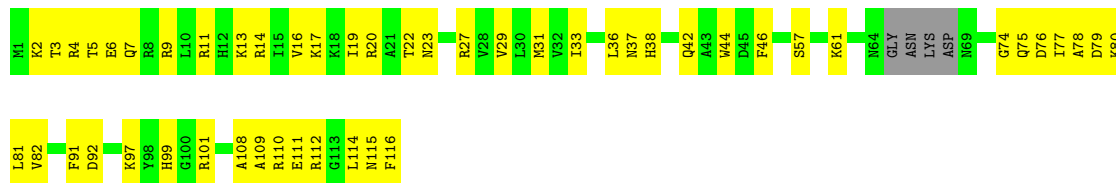
- Molecule 36: 50S ribosomal protein L17

Chain m:  56% 40%



- Molecule 37: 50S ribosomal protein L18

Chain n:  53% 43%



- Molecule 38: 50S ribosomal protein L19

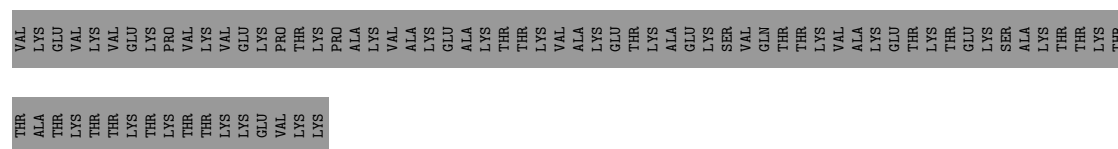
- Molecule 39: 50S ribosomal protein L20

- Molecule 40: 50S ribosomal protein L21

- Molecule 41: 50S ribosomal protein L22

- Molecule 42: 50S ribosomal protein L23

THR	ASP	LYS	PRO	ALA	ASP	LYS	THR	THR	LEU	GLY	GLU	SER	THR	VAL	LYS	ILE	LYS	ASP	THR	LYS	ASN	SER	PRO	GLU	ALA	ALA	VAL	VAL	LYS	THR	ALA	ALA	GLN	LEU	ILE	LYS	LYS	PRO	THR	THR	ALA	ALA	ALA	VAL	VAL	GLN	LEU	THR	THR	VAL	ALA	LYS	THR
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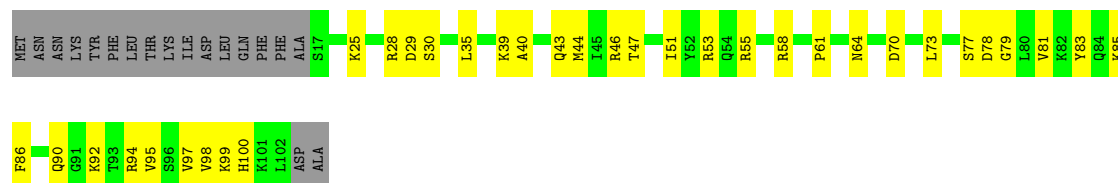
• Molecule 43: 50S ribosomal protein L24

Chain t: 64% 36%



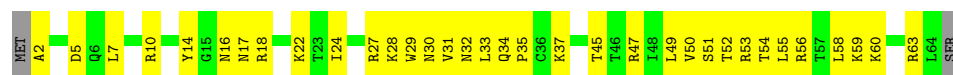
• Molecule 44: 50S ribosomal protein L27

Chain u: 50% 33% 17%



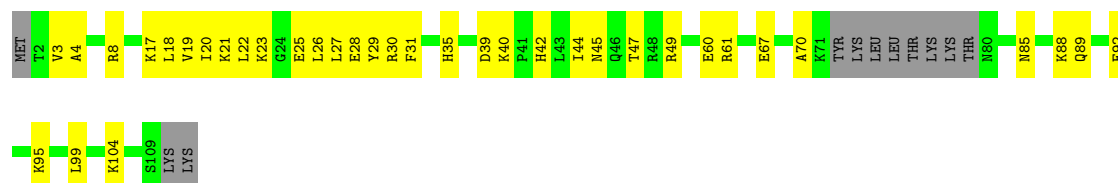
• Molecule 45: 50S ribosomal protein L28

Chain v: 45% 52%



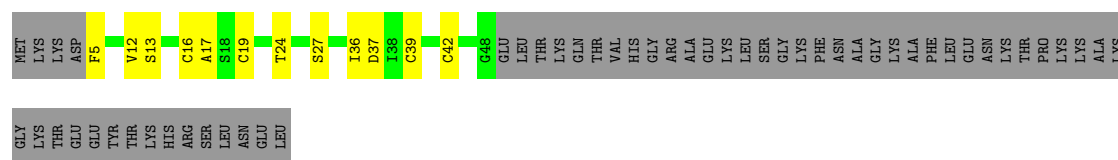
• Molecule 46: 50S ribosomal protein L29

Chain w: 58% 32% 10%



• Molecule 47: 50S ribosomal protein L31

Chain x: 33% 12% 55%



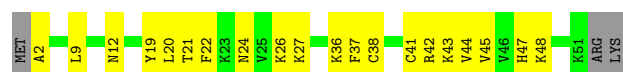
• Molecule 48: 50S ribosomal protein L32

Chain y: 

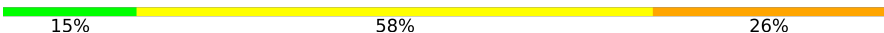


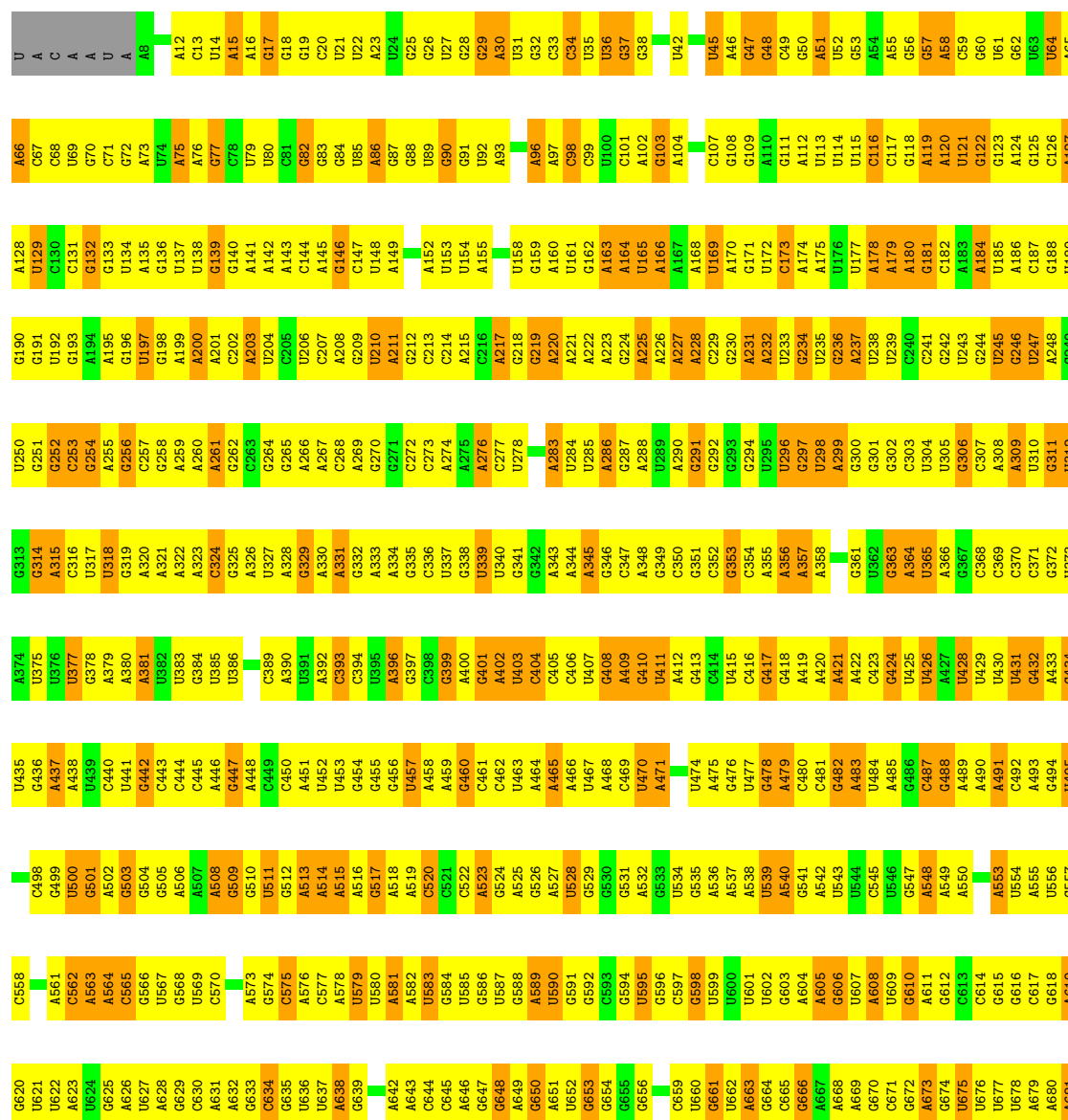
- Molecule 49: 50S ribosomal protein L33 1

Chain z: 



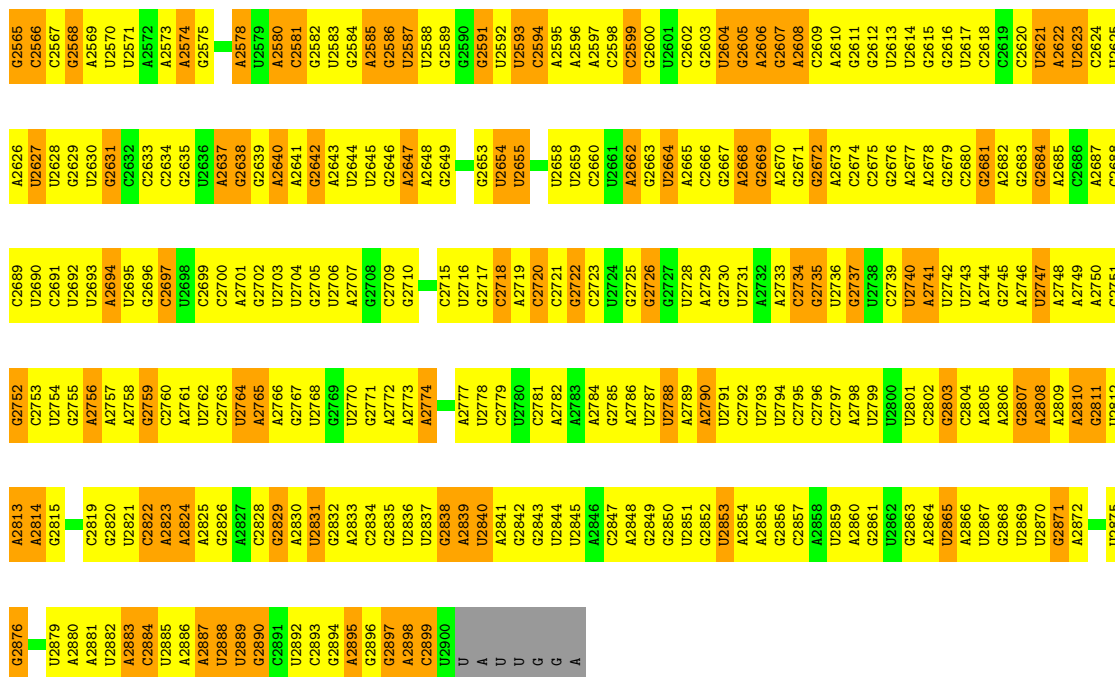
- Molecule 50: 23S ribosomal RNA

Chain 3: 

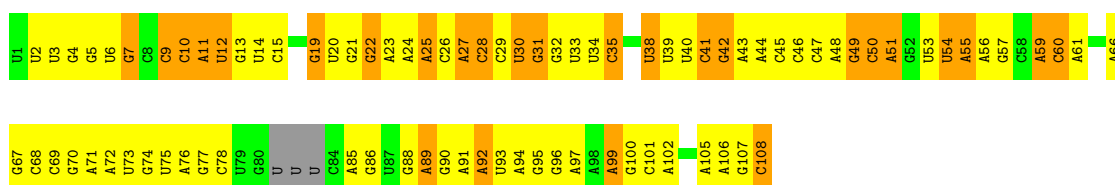
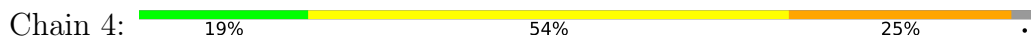


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A1553	G1491	G1429	U1388	A1308	C1247	U1184	A1123	A1062	U1000	U939	A870	U808	U744	A694
G1554	G1492	U1430	G1369	G1309	A1248	U1185	G1124	A1063	C1001	U939	G871	A809	U745	G685
U1555	A1493	A1431	A1370	G1310	A1249	A1186	U1125	A1064	A1002	A940	C872	G810	G746	G686
G1556	U1494	C1432	G1371	G1311	A1250	C1187	G1126	G1065	U1003	C941	G873	G811	A747	G687
G1557	A1495	U1433	U1372	A1312	G1251	C1188	C1127	G1066	U1004	A942	U874	G812	G748	U688
A1558	A1496	U1434	C1373	G1313	C1252	A1189	U1128	A1067	G1005	A943	G875	G813	U749	U689
A1559	A1497	A1435	U1374	G1314	G1253	C1190	U1129	U1068	U1006	U944	C880	A816	U754	U690
U	U1498	C1436	G1375	A1315	U1254	A1191	A1130	G1069	C1007	U945	A881	A817	U755	G691
G	A1499	A1437	G1376	G1316	U1255	U1192	A1131	U1070	A1008	A946	C882	A818	C755	U692
A	A1500	G1438	A1377	G1317	A1256	U1193	C1132	G1071	A1009	A947	C883	A819	A756	U693
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U	A1502	U1440	C1379	G1319	C1258	A1195	G1134	A1073	A1011	C949	A884	U820	G695	G695
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C	U1506	G1444	G1383	A1323	U1262	U1199	A1138	C1078	U953	G887	U890	A824	G763	U699
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U1519	A1396	A1336	C1275	A1336	C1275	U1214	U1151	G1090	A1029	U968	A903	U838	U776	C712
G1520	G1397	G1337	A1276	G1337	A1276	G1215	U1152	G1091	U1030	A969	C904	A839	C777	C713
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U1526	G1403	C1343	G1282	C1343	G1282	G1221	C1158	G1097	A1036	G975	U913	U845	G783	G719
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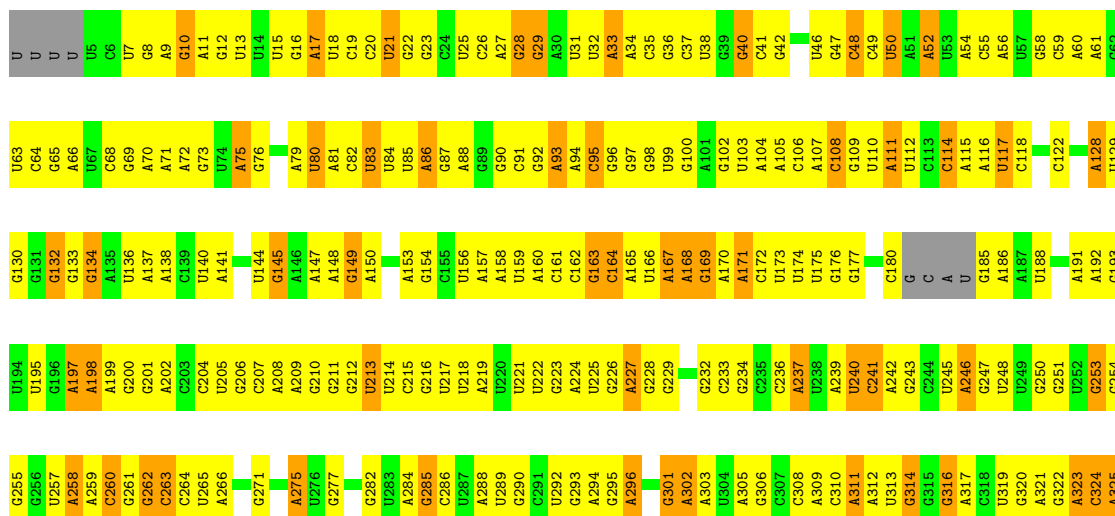
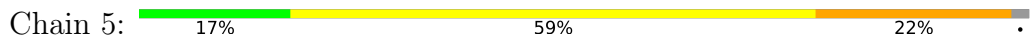
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A2438	G2378	G2378	G2378	G2315		G2190	G2122	C2062	U2000	U1933	G1866	U1805	U1743	G1681	U1617
U2439	G2379	G2316	U2380	G2316	G2254	G2191	A2123	G2063	C2001	A1934	G1867	G1806	U1744	G1681	U1618
C2504	U2381	A2317	A2374	A2317	A2255	U2192	A2124	G2064	U2002	A1935	G1868	C1807	U1745	G1682	A1619
A2442	G2381	A2318	G2381	A2318	C2256	U2193		G2065	C2003	A1936	A1868	C1808	U1746	G1683	U1621
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G2450	C2388	U2375	U2388	U2375	G2263	U2200	G2134	C2072	G2011	A1943	G1876	U1815	A1753	G1691	G1628
C2451	A2389	G2326	G2389	G2326	G2264	G2201	C2135	C2073	A2012	A1944	C1877	A1816	U1754	U1692	U1629
G2452	G2390	U2327	G2390	U2327	U2265	U2202	A2136	C2074		A1945	C1878	A1817	U1755	U1693	A1630
C2453	G2391	A2328	G2391	A2328	G2266	U2203	A2137	G2074	C2015	U1946	A1879	A1818	U1756	A1694	A1631
G2454	U2392	G2329	G2454	G2329	G2267	C2204	U2138	G2076	G2016	C1947	C1879	G1819	G1757	G1695	C1632
C2455	C2393	A2330	C2393	A2330	G2268	U2205	C2139	G2076	G2017	U1948	C1881	U1820	G1758		
A2517	U2394	U2332	U2394	U2332	G2269	A2206	G2140	A2078	U2018	C1949	G1882	G1821	C1759	A1698	G1635
U2457	U2395	U2332	U2395	U2332	U2270	A2207	A2141	G2079	C2019	U1950	A1883	A1822	G1760	U1636	U1637
A2458	A2396	G2333	G2397	G2333	C2271	U2208		C2080	A2020	A1951	A1884	U1823	C1761	G1700	U1638
C2460	U2397	U2334	U2397	U2334	C2272	U2209	C2144	U2081	A2021		G1885	G1824	A1762	G1701	C1638
U2460	C2398	A2335	A2405	A2335	U2273	G2210	A2145	U2082	A2022	C1954	G1886	U1825	G1763	A1702	C1639
U2524	A2461	A2336	G2405	A2336	A2274	G2211	A2146	U2083	U2023	G1955	C1896	A1826	U1764	A1703	G1640
C2462	A2400	U2337	G2406	U2337	A2275	U2212	G2147	U2084	C2024	G1956	U1888	U1827	A1770	C1704	A1641
G2463	U2401	G2338	G2407	G2338	A2276	A2213	U2148	C2085	C2095	G1957	U1889	A1828	A1766	U1705	G1642
	C2402	G2339	C2403	G2339	A2277	A2214	U2149	U2086	C2095	U1958	U1890	U1829	U1767	C1706	A1643
G2466	G2403	U2340	G2404	U2340	A2281	C2215	G2150	G2087	G2027	U1959	A1891	G1830	G1768	C1707	A1644
A2467	G2404	G2341	G2405	G2341	A2282	U2216	G2151	U2088	C2028	A1960	A1892	G1831	U1769	G1708	C1645
U2468	A2405	U2342	G2406	U2342	G2283	G2217	C2152	A2089	U2029	A1961		G1832	A1770	G1646	C1646
A2469	U2406	A2343	U2407	A2343	G2284	U2218	U2153	G2090	C2030	U1962	G1895	G1833	C1771	A1710	A1647
C2470	U2407	A2344	G2408	A2344	G2285	U2219	A2154	C2091	C2031	U1963	A1896	U1834	G1772	A1711	A1648
C2535	U2471	G2345	G2409	G2345	G2286	A2220	G2155	U2092	G2032	C1964	A1897	G1835	G1776	A1712	C1649
U2536	G2472	G2346	U2409	G2346	A2287	U2217	G2156	U2093	G2033	C1965		A1836	G1777	U1713	A1650
G2473	C2473	G2347	C2410	G2347	G2287	C2222	A2157	A2094	G2034			C1837	G1778	U1714	C1651
C2474	C2411	U2348	G2411	U2348	G2288	C2223	C2158	A2095	U2035	G1968	A1902	A1838	G1779	A1715	A1652
A2538	G2475	G2349	A2412	G2349	G2289	C2224	U2159	U2096	G2036	C1969	A1903	C1839	U1779	C1653	G1653
C2476	G2413		G2413		G2290	G2225	U2160	A2097	A2037	G1970	G1906	C1840	A1780	G1654	U1655
U2541	U2414	U2352	U2414	U2352	U2291	U2226	G2161	U2098	A2038	G1971	G1907	U1841	A1781	C1719	G1656
A2542	A2415	G2353	A2415	G2353	A2292	U2227	U2162	U2099	G2039	C1972	A1907	G1842	U1782	C1720	U1656
G2543	U2416	A2354	U2416	A2354	G2293	U2228	U2163	G2100	C2040	C1973	A1908	C1843	U1783	G1721	G1657
C2544	G2417	C2355	G2417	C2355	A2294	C2229	G2164	A2094	C2041	U1974	G1909	C1844	U1784	G1857	U1658
U2545	G2418	U2356	G2418	U2356	A2295	A2230	A2165	U2095	C2042	G1975	G1910	C1845	U1785	A1723	C1659
	A2419	G2357	A2419	G2357	A2296	A2231	U2166	C2103	C2043	A1976	G1911	A1846	U1786	G1724	
C2483	A2420	U2358	A2420	U2358	G2297	G2232	G2167	A2104	C2044	A1977	C1912	G1847	U1787	A1725	
A2484	U2421	G2359	G2421	G2359	A2298	A2233	C2168	G2105	C2045	U1978	G1913	U1848	A1788	U1726	G1663
U2485	G2422	A2360	G2422	A2360	U2299	G2234	G2169	G2106	G2046	U1979	G1913	U1849	C1789	U1727	A1664
U2487	G2423	G2361	G2423	G2361	A2300	A2235	A2170	A2107	U2047	G1980	G1914	U1850	U1790	A1728	A1666
C2488	G2424	A2362	G2424	A2362	C2301	G2236	A2171	C2108	U2048	U1981	U1918	G1852	U1791	G1729	A1667
G2489	C2425	C2363	C2425	C2363	C2302	U2237	A2172	A2109	A2049	C1982	A1919	G1853	A1792	C1730	G1668
C2490	A2426	A2364	A2426	A2364	U2303	G2238	G2173	U2110	G2050		A1920	A1854	A1793	G1731	G1669
C2491	U2427	U2365	U2427	U2365	U2304	C2242	U2174	U2111	C2051	U1989	A1921	A1855	A1794	A1732	U1670
G2492	A2428	A2366	G2428	A2366	A2305	G2243	U2175	A2112	C2052	C1990	U1922	G1856	C1795	G1733	C1671
G2493	G2429	C2367	G2429	C2367	A2306	G2244		U2113	G2053	U1991	A1923	G1857	A1796	A1734	C1672
C2494	U2430	U2368	C2430	U2368	G2307	U2245	A2179	C2114	C2054	C1992	U1924	U1858	C1797	U1673	U1673
A2505	U2431	C2369	U2431	C2369	U2308	G2246	A2180	A2115	C2055	U1993	A1925	U1859	C1798	A1729	A1674



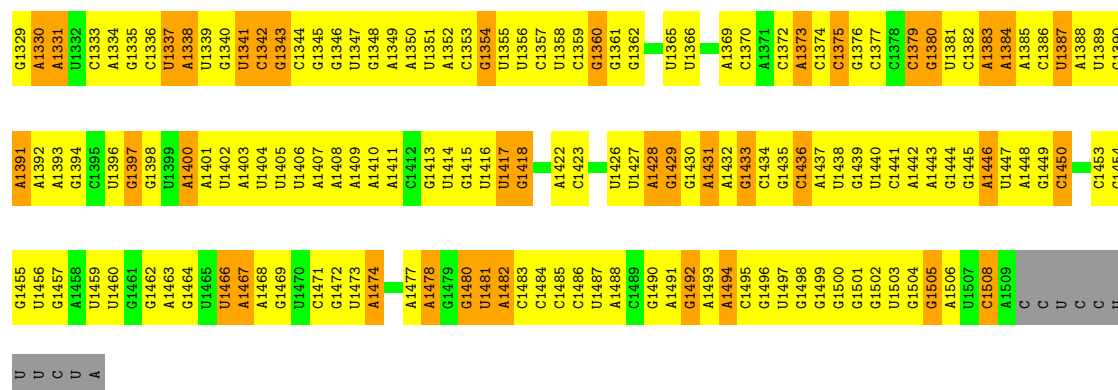
• Molecule 51: 5S ribosomal RNA



• Molecule 52: 16S ribosomal RNA

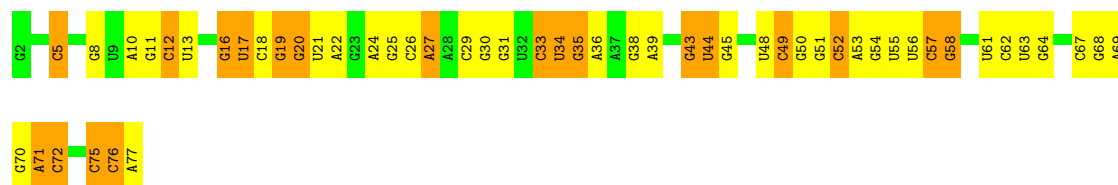


G1267	A1204	A1139	G1078	U1018	C957	G896	G832	A770	A705	A638	G577	U514	A452	G388	C326
G1268		U1140	G1079	G1019	G958	A897	G833	G770	U706	A639	C578	G515	C453	A389	G327
U1269	G1208	G1142	G1080	G	A959		G834	G771	G707	C640	G579	C516	U454	G390	G328
U1270	G1209	G1143	U1081	A	C960	G900	G835		A708	C580	C517	C517	U455	G391	C329
C1271	U1210	C1143	U1082	G	G961	A901	C836	A774	A709	A642	A581	A519	U456	U394	C330
C1272	A1211	A1144	A1083	G	G962	A902	C837	A775	G710	U643	G582	G518	A457	G395	C331
A1273	C1212	A1145	A1084	U	U963	A903	A838	C776	G711	U644	G583	C520	G458	A332	A330
U1274	A1213	A1146	G1085	U	A964	C904	U839	A777	A712	A645	C584	A521	C459	G396	U334
U1275	A1214	U1147	U1086	A	C965	U905	G940	A778	A713	A646	G585	G522	A460	G397	A334
U1276	G1215	U1148	C1087	A	A966	C906	C841	A779	C714	U647	G586	C523	G398	A335	C335
C1277	G1216	G1149	C1088		C967	A907	C842	U780	A715	G648	A587	C524	G461		
G1278	C1217	G1150	G1089	C1028	G968	A908	C843	A781	C716	U649	U588	G525	A464		
G1279	U1218	A1151	G1090	G1030	A969	A909	U844	G782	C717	A650	U589	C526	A465	U401	U339
A1280	C1219	G1152	C1091	U1031	A970	C910	C845	G783	A718	G651	G590	G527	A466	A340	U340
	A1220	G1153	A1092	G1032	A971	G911	G846	A784	G719	A652	A591	G528	U467	G402	C341
G1283	A1221	A1154	A1093	U1033	A972	G912	G847	U785	U720	A653	A592	G529	A403	A403	G342
A1284	U1222	A1155	C1094	G1034	A973	A913	U848	U786	G721	A530	A593	U528	A404	G343	G343
G1285	A1223	G1156	G1095	A1035	C974	A914	U849	A787	G722	A531	A594	A530	C405	C344	G344
G1286	C1224	G1157		C1036	C975	U915		G788	G723	U532	G595		A406	G345	A345
G1287	A1225	A1158		A1037	U976	U916	G852	A789	G724	A533		U533	A407	G346	G346
A1288	A1226	A1159	G1098	G1038	U977	G917	A853	U790	A725	C594	U598	C534	U408	G347	C347
A1289	A1227	G1160	C1100	G1039	A978	A918	A854	A791	A726	A535	G599	C535	A410	A349	A349
G1290	C1228	G1161	A1101	U1040	C979	C919	G855	C792	G727	U536	G600	U536	A411	G350	G350
C1291	A1229	G1162	A1102	G1041	C980	G920	U856	C793	G728	U601	A537	U475	U476	G412	C351
A1292	G1230	A1163	C1103	G1042	U981	G921	U857	C793	G729	A664	G602	G538	U477	A432	A352
A1293	U1231	U1164	C1104	U1043	A982	G922	A858	A796	G730	G665	U603	G539	G478	U414	G353
U1294	C1232	G1165	G1105	G1044	G983	G923	A859	G797	A731		U604			C415	U354
U1295	C1233	A1166	U1106	C1045	A984	A924		U798	A732	U668	A605	C543	U481	A355	A355
C1296	C1234		U1107	A1046	C985	C925	C862	A799	A733	U669	A544	A544	G482	U417	G356
G1297	A1235	A1171	A1108	U1047	U986	C926	A863	C800	A734	U670	A545	A607	U418	U418	G357
U1298	A1236	A1172	U1109	G1048	U987	C927	U864	U801	C735	G671	G546	G608	A484	A419	G358
C1299	C1237	A1173	C1110	U1049	G988	C928	U865	C802	U736	A672	C547	C547	C485	A420	A359
C1300	G1238	U1174	G1111	U1050	A989	C929	A866	C803	U737	U673	C486	C486	G421	G421	A360
U1301	U1239	C1175	U1112	U1051	C990	A930	A867	U674	A738	A611	U549	U549	A422	A422	U361
C1302	U1240	A1176	U1113	G1052	A991	C931	G868	U675	G739	U550	U488	U488	U423	U423	U362
A1303	G1241	U1177	A1114	U1053	U992	A932		C805	G740	C613	A551	U550	U424	U424	U363
U1304	U1242	C1178	G1115	C1054	C993	A933	C872		C741	U614	U552	U552	U490	G425	U364
A1243	A1243	A1179	U1116	G1055	C994	G934	U873		C742	G615	C553	C553	U491	U426	U365
A1246	A1246	U1180	U1117	U1056		U935	C874		A743	U616	C554	C554	G427	A428	C366
G1247	G1247	G1181	C1118	C1057	G997	G936	G875	A811	U744	U617	G555	G555	A493	A428	A367
U1248	U1248		C1119	A1058	G998	A937	C876	A812	U745	U618	G556	G556	A494	A429	C368
G1249		C1184	A1120	G1059	C999	U938	C877	A813	A746	U619	A557	A557	U495	G430	A369
			U1121	C1060	A1000	G939	U878	C814		G620	U558	U558	A496	U431	A370
		U1187	U1122	U1061	A1001	G940	G879	G815	G749	C621	U559	U559	A497	U432	U371
		A1188	G1123	C1062	A1002	A941	G880	A816	A750	A622	U560	U560	G498	G433	G372
C1252		U1189	U1124	G1063	A1003	G942	G881	U817	C751	G623	A561	A561	U499	U434	A373
A1253	A1253	G1190	C1125	U1064	U1004	C943	U882	A818	G752	U624	U562	U562	G500	U435	G374
A1254	U1191	U1191	U1126	G1065	A1005	A944	A883	G819	C753	U625	A501		A501		C375
A1255	C1192	A1254	A1127	U1066	A1006	U945	G884	A820	U754	G626	G565	G565	C502	G376	G376
U1256	U1193	U1193	G1128	C1067	U1007	G946	U885	U821	U755	U627	G566	G566	G503	A377	A377
C1257		A1194	C1129	G1068	G1008	U947	A886	A822	A756	A628	C567	C567	A504	G442	A378
U1258	U1310	G1195	G1130	U1069	G1009	U948	C887	C823	U760	U629	G568	G568	C505	G443	A379
G1259	A1131	G1196	G1070	A1010	A949	U948	A888	U824	G630	U569	U569	U569	U506	G444	G380
U1260	G1132	G1197	A1071	A1011	C950	C950	A889	A825	U761	A631	A570	A570	A445	A445	C381
A1261	A1133	C1198	G1072	A1012	U951	U951	U890	G826	G762	A632	A571	A571	A508	A446	U382
A1262	C1134	A1073	A1073	C1013	U952	U952	C891	C827	A763	U633	A572	A572	C509	G447	U383
A1263	U1135	U1074	U1074	A1014	A953	A953	G892	U828	A764	U634	G573	G573	U510	A448	G384
G1264	G1136	G1075	G1075	U1015	A954	A954	C893	G829	A765	G635	C574	C574	A511	A449	A385
U1265	C1137	U1076	U1076	A1016	U955	U955	A894	A703	G766	G636	A575	A575	U512	U460	U386
U1266		A1017	U1077	A1017	U956	U956	A895	C831	U767	U704	A576	A576	G513	G451	G387



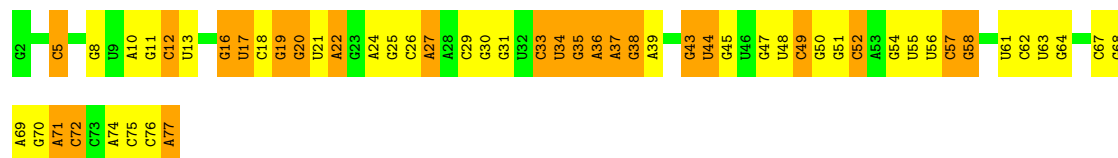
• Molecule 53: tRNA-Phe

Chain 6: 30% 43% 26%



• Molecule 53: tRNA-Phe

Chain 7: 28% 42% 30%



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	1534	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0	0.17	0/383	0.51	0/504
2	1	0.15	0/484	0.45	0/637
3	2	0.28	0/306	0.68	0/401
4	A	0.18	0/1954	0.48	0/2642
5	B	0.18	0/1721	0.54	1/2323 (0.0%)
6	C	0.21	0/1691	0.54	0/2267
7	D	0.22	0/1188	0.57	0/1593
8	E	0.30	1/1384 (0.1%)	0.53	0/1867
9	F	0.20	0/1266	0.64	0/1700
10	G	0.26	0/1126	0.59	2/1517 (0.1%)
11	H	0.17	0/1044	0.44	0/1395
12	I	0.19	0/820	0.54	0/1103
13	J	0.24	0/844	0.58	2/1136 (0.2%)
14	K	0.28	0/1094	0.58	0/1468
15	L	0.16	0/962	0.44	0/1289
16	M	0.15	0/483	0.49	1/643 (0.2%)
17	N	0.15	0/679	0.41	0/907
18	O	0.17	0/659	0.50	0/885
19	P	0.19	0/684	0.49	0/913
20	Q	0.15	0/545	0.45	0/730
21	R	0.19	0/698	0.56	0/936
22	S	0.15	0/631	0.44	0/838
23	T	0.22	0/475	0.64	0/621
24	a	0.17	0/2267	0.47	0/3044
25	b	0.27	0/1795	0.60	1/2412 (0.0%)
26	c	0.15	0/1671	0.49	0/2246
27	d	0.20	0/1409	0.55	0/1894
28	e	0.19	0/1420	0.54	2/1912 (0.1%)
29	f	0.19	0/1183	0.55	1/1587 (0.1%)
30	g	0.46	0/916	0.80	1/1222 (0.1%)
31	h	0.15	0/968	0.42	0/1298
32	i	0.20	0/1186	0.45	0/1592
33	j	0.23	0/953	0.57	0/1275
34	k	0.22	0/1170	0.46	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	l	0.17	0/1104	0.80	2/1481 (0.1%)
36	m	0.20	0/973	0.50	0/1309
37	n	0.17	0/897	0.50	0/1198
38	o	0.15	0/948	0.46	0/1262
39	p	2.05	7/947 (0.7%)	0.61	0/1257
40	q	0.18	0/828	0.50	0/1111
41	r	0.18	0/1077	0.48	0/1441
42	s	0.15	0/732	0.46	0/988
43	t	0.20	0/879	0.46	0/1165
44	u	0.23	0/665	0.57	0/884
45	v	0.15	0/519	0.43	0/695
46	w	0.20	0/826	0.55	0/1104
47	x	0.14	0/353	0.40	0/474
48	y	0.39	0/457	0.66	0/601
49	z	0.16	0/412	0.43	0/547
50	3	0.12	0/69073	0.29	0/107710
51	4	0.12	0/2505	0.31	0/3902
52	5	0.11	0/35768	0.28	0/55764
53	6	0.16	0/1808	0.47	0/2817
53	7	0.16	0/1808	0.47	0/2817
All	All	0.22	8/158638 (0.0%)	0.37	13/236883 (0.0%)

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	p	105	PHE	CD2-CE2	28.50	2.24	1.38
39	p	105	PHE	CD1-CE1	28.27	2.23	1.38
39	p	105	PHE	CE1-CZ	27.79	2.22	1.38
39	p	105	PHE	CE2-CZ	27.76	2.21	1.38
39	p	105	PHE	CG-CD2	19.73	1.80	1.38

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	l	88	GLY	CA-C-N	17.08	144.74	120.49
35	l	88	GLY	C-N-CA	17.08	144.74	120.49
30	g	46	LYS	N-CA-C	-8.16	102.88	113.17
28	e	113	SER	CA-C-N	6.67	133.62	120.94
28	e	113	SER	C-N-CA	6.67	133.62	120.94

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	380	0	429	27	0
2	1	477	0	530	22	0
3	2	304	0	350	14	0
4	A	1921	0	1973	61	0
5	B	1698	0	1768	70	0
6	C	1660	0	1719	87	0
7	D	1173	0	1267	51	0
8	E	1362	0	1377	46	0
9	F	1246	0	1308	67	0
10	G	1110	0	1226	56	0
11	H	1028	0	1094	76	0
12	I	809	0	894	41	0
13	J	829	0	855	48	0
14	K	1076	0	1170	63	0
15	L	951	0	1014	45	0
16	M	474	0	509	30	0
17	N	673	0	730	20	0
18	O	646	0	677	26	0
19	P	675	0	728	36	0
20	Q	535	0	562	25	0
21	R	682	0	691	33	0
22	S	629	0	681	35	0
23	T	471	0	522	26	0
24	a	2225	0	2301	129	0
25	b	1762	0	1808	90	0
26	c	1644	0	1731	86	0
27	d	1388	0	1469	72	0
28	e	1396	0	1481	65	0
29	f	1160	0	1172	41	0
30	g	910	0	972	7	0
31	h	959	0	1039	7	0
32	i	1164	0	1192	46	0
33	j	944	0	1019	47	0
34	k	1153	0	1256	60	0
35	l	1079	0	1134	61	0
36	m	958	0	1011	41	0
37	n	889	0	952	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	o	938	0	1008	39	0
39	p	934	0	1011	60	0
40	q	811	0	858	35	0
41	r	1068	0	1150	49	0
42	s	720	0	803	23	0
43	t	872	0	972	45	0
44	u	657	0	695	34	0
45	v	513	0	560	32	0
46	w	818	0	870	29	0
47	x	344	0	333	8	0
48	y	452	0	472	24	0
49	z	408	0	440	15	0
50	3	61664	0	30954	2692	0
51	4	2239	0	1137	99	0
52	5	31943	0	16058	1429	0
53	6	1618	0	821	40	0
53	7	1618	0	821	39	0
All	All	146057	0	99574	5768	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 25.

The worst 5 of 5768 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:p:105:PHE:CD2	39:p:105:PHE:CG	1.80	1.70
39:p:105:PHE:CG	39:p:105:PHE:CD1	1.79	1.67
39:p:105:PHE:CZ	39:p:105:PHE:CE2	2.21	1.28
39:p:105:PHE:CZ	39:p:105:PHE:CE1	2.22	1.28
39:p:105:PHE:CD2	39:p:105:PHE:CE2	2.24	1.26

There are no symmetry-related clashes.

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	0	45/48 (94%)	43 (96%)	2 (4%)	0	100	100
2	1	57/59 (97%)	52 (91%)	5 (9%)	0	100	100
3	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
4	A	238/294 (81%)	221 (93%)	17 (7%)	0	100	100
5	B	213/273 (78%)	200 (94%)	13 (6%)	0	100	100
6	C	201/205 (98%)	188 (94%)	13 (6%)	0	100	100
7	D	151/219 (69%)	139 (92%)	12 (8%)	0	100	100
8	E	165/215 (77%)	141 (86%)	24 (14%)	0	100	100
9	F	152/155 (98%)	130 (86%)	22 (14%)	0	100	100
10	G	139/142 (98%)	124 (89%)	14 (10%)	1 (1%)	18	56
11	H	126/132 (96%)	115 (91%)	11 (9%)	0	100	100
12	I	99/108 (92%)	87 (88%)	12 (12%)	0	100	100
13	J	112/121 (93%)	107 (96%)	4 (4%)	1 (1%)	14	51
14	K	134/139 (96%)	116 (87%)	18 (13%)	0	100	100
15	L	116/124 (94%)	109 (94%)	7 (6%)	0	100	100
16	M	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
17	N	81/86 (94%)	80 (99%)	1 (1%)	0	100	100
18	O	78/94 (83%)	75 (96%)	3 (4%)	0	100	100
19	P	81/85 (95%)	72 (89%)	9 (11%)	0	100	100
20	Q	63/104 (61%)	58 (92%)	5 (8%)	0	100	100
21	R	82/87 (94%)	74 (90%)	8 (10%)	0	100	100
22	S	75/87 (86%)	75 (100%)	0	0	100	100
23	T	51/60 (85%)	49 (96%)	2 (4%)	0	100	100
24	a	283/287 (99%)	261 (92%)	22 (8%)	0	100	100
25	b	227/287 (79%)	204 (90%)	23 (10%)	0	100	100
26	c	208/212 (98%)	199 (96%)	9 (4%)	0	100	100
27	d	173/180 (96%)	155 (90%)	18 (10%)	0	100	100
28	e	174/184 (95%)	164 (94%)	10 (6%)	0	100	100
29	f	143/149 (96%)	130 (91%)	13 (9%)	0	100	100
30	g	117/161 (73%)	108 (92%)	8 (7%)	1 (1%)	14	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	h	126/137 (92%)	114 (90%)	12 (10%)	0	100	100
32	i	142/146 (97%)	132 (93%)	10 (7%)	0	100	100
33	j	120/122 (98%)	111 (92%)	9 (8%)	0	100	100
34	k	146/151 (97%)	135 (92%)	11 (8%)	0	100	100
35	l	134/139 (96%)	125 (93%)	9 (7%)	0	100	100
36	m	117/124 (94%)	108 (92%)	9 (8%)	0	100	100
37	n	108/116 (93%)	96 (89%)	12 (11%)	0	100	100
38	o	113/119 (95%)	98 (87%)	15 (13%)	0	100	100
39	p	108/127 (85%)	100 (93%)	7 (6%)	1 (1%)	14	51
40	q	97/100 (97%)	82 (84%)	15 (16%)	0	100	100
41	r	137/159 (86%)	127 (93%)	10 (7%)	0	100	100
42	s	90/237 (38%)	81 (90%)	9 (10%)	0	100	100
43	t	109/111 (98%)	100 (92%)	9 (8%)	0	100	100
44	u	84/104 (81%)	77 (92%)	7 (8%)	0	100	100
45	v	61/65 (94%)	60 (98%)	1 (2%)	0	100	100
46	w	96/111 (86%)	90 (94%)	6 (6%)	0	100	100
47	x	42/97 (43%)	37 (88%)	5 (12%)	0	100	100
48	y	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
49	z	48/53 (91%)	46 (96%)	2 (4%)	0	100	100
All	All	5809/6670 (87%)	5335 (92%)	470 (8%)	4 (0%)	49	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	g	90	VAL
39	p	102	PRO
10	G	109	ASN
13	J	112	ASN

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	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	A	212/262 (81%)	212 (100%)	0	100	100
5	B	180/232 (78%)	180 (100%)	0	100	100
6	C	181/183 (99%)	181 (100%)	0	100	100
7	D	123/178 (69%)	123 (100%)	0	100	100
8	E	150/196 (76%)	150 (100%)	0	100	100
9	F	131/132 (99%)	131 (100%)	0	100	100
10	G	123/124 (99%)	122 (99%)	1 (1%)	73	80
11	H	111/115 (96%)	111 (100%)	0	100	100
12	I	95/99 (96%)	95 (100%)	0	100	100
13	J	91/97 (94%)	91 (100%)	0	100	100
14	K	117/120 (98%)	114 (97%)	3 (3%)	40	62
15	L	100/105 (95%)	100 (100%)	0	100	100
16	M	47/48 (98%)	47 (100%)	0	100	100
17	N	76/78 (97%)	76 (100%)	0	100	100
18	O	69/82 (84%)	69 (100%)	0	100	100
19	P	73/75 (97%)	73 (100%)	0	100	100
20	Q	56/94 (60%)	56 (100%)	0	100	100
21	R	74/77 (96%)	74 (100%)	0	100	100
22	S	70/77 (91%)	70 (100%)	0	100	100
23	T	49/56 (88%)	49 (100%)	0	100	100
24	a	241/243 (99%)	241 (100%)	0	100	100
25	b	186/233 (80%)	186 (100%)	0	100	100
26	c	182/184 (99%)	182 (100%)	0	100	100
27	d	150/154 (97%)	150 (100%)	0	100	100
28	e	153/159 (96%)	153 (100%)	0	100	100
29	f	123/134 (92%)	123 (100%)	0	100	100
30	g	96/129 (74%)	83 (86%)	13 (14%)	4	14
31	h	102/110 (93%)	102 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	i	126/128 (98%)	126 (100%)	0	100	100
33	j	103/103 (100%)	103 (100%)	0	100	100
34	k	123/126 (98%)	123 (100%)	0	100	100
35	l	113/115 (98%)	113 (100%)	0	100	100
36	m	105/109 (96%)	105 (100%)	0	100	100
37	n	96/99 (97%)	96 (100%)	0	100	100
38	o	101/105 (96%)	101 (100%)	0	100	100
39	p	99/108 (92%)	97 (98%)	2 (2%)	48	66
40	q	90/91 (99%)	90 (100%)	0	100	100
41	r	116/132 (88%)	116 (100%)	0	100	100
42	s	82/208 (39%)	82 (100%)	0	100	100
43	t	96/96 (100%)	96 (100%)	0	100	100
44	u	69/85 (81%)	69 (100%)	0	100	100
45	v	58/60 (97%)	58 (100%)	0	100	100
46	w	87/98 (89%)	87 (100%)	0	100	100
47	x	41/86 (48%)	41 (100%)	0	100	100
48	y	48/49 (98%)	47 (98%)	1 (2%)	47	65
49	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5087/5751 (88%)	5067 (100%)	20 (0%)	81	84

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	g	88	GLU
39	p	100	LYS
48	y	51	LEU
39	p	102	PRO
30	g	32	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76 such sidechains are listed below:

Mol	Chain	Res	Type
38	o	46	GLN
44	u	64	ASN
39	p	80	ASN

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Mol	Chain	Res	Type
41	r	120	GLN
48	y	40	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	975 (33%)	34 (1%)
51	4	103/108 (95%)	35 (33%)	3 (2%)
52	5	1490/1520 (98%)	440 (29%)	12 (0%)
53	6	75/76 (98%)	32 (42%)	6 (8%)
53	7	75/76 (98%)	33 (44%)	6 (8%)
All	All	4618/4687 (98%)	1515 (32%)	61 (1%)

5 of 1515 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	12	A
50	3	14	U
50	3	15	A
50	3	16	A
50	3	17	G

5 of 61 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	3	2506	C
53	7	16	G
51	4	54	U
53	6	76	C
53	7	71	A

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-13447. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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.