



## wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 12:22 pm GMT

PDB ID : 3JCD  
EMDB ID: : EMD-6549  
Title : Structure of Escherichia coli EF4 in posttranslocational ribosomes (Post EF4)  
Authors : Zhang, D.; Yan, K.; Liu, G.; Song, G.; Luo, J.; Shi, Y.; Cheng, E.; Wu, S.;  
Jiang, T.; Low, J.; Gao, N.; Qin, Y.  
Deposited on : 2015-12-01  
Resolution : 3.70 Å(reported)

This is a wwPDB/EMDatabank EM Map/Model Validation Summary Report  
for a publicly released PDB/EMDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc29047

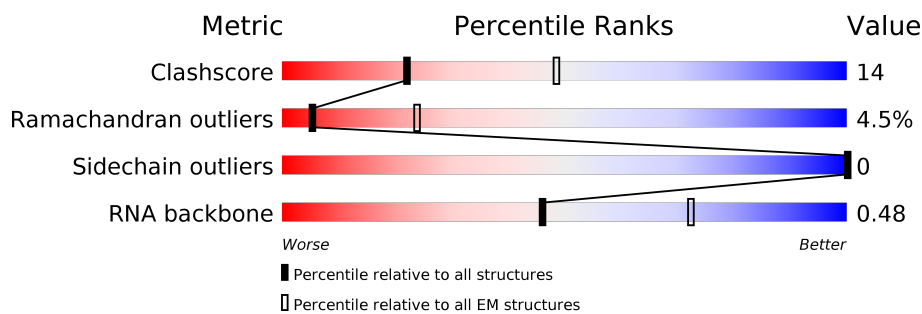
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.70 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.





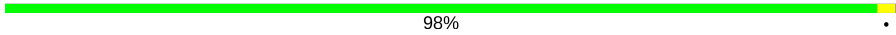
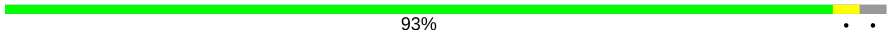

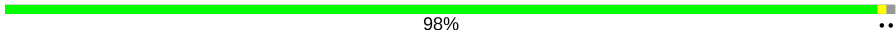
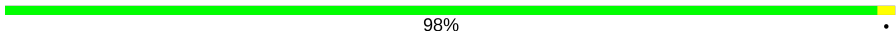



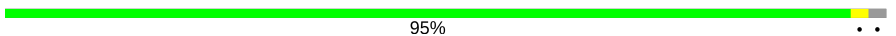














Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	b	241	
2	c	233	
3	d	206	
4	e	167	
5	f	135	
6	g	179	
7	h	130	
8	i	130	


















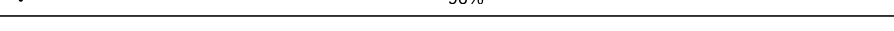
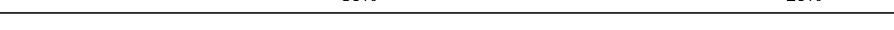

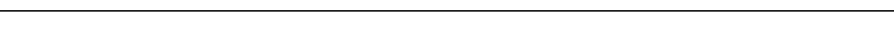
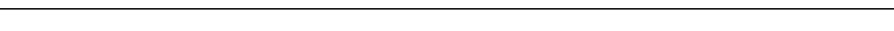

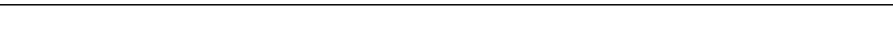
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Mol	Chain	Length	Quality of chain
9	j	103	
10	k	129	
11	l	124	
12	m	118	
13	n	101	
14	o	89	
15	p	82	
16	q	84	
17	r	75	
18	s	92	
19	t	87	
20	u	71	
21	0	57	
22	1	55	
23	2	46	
24	3	64	
25	4	38	
26	5	234	
27	C	273	
28	D	209	
29	E	201	
30	F	179	
31	G	177	
32	H	149	
33	I	142	

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Mol	Chain	Length	Quality of chain
34	J	142	
35	K	123	
36	L	144	
37	M	136	
38	N	127	
39	O	117	
40	P	115	
41	Q	118	
42	R	103	
43	S	110	
44	T	100	
45	U	104	
46	V	94	
47	W	85	
48	X	78	
49	Y	63	
50	Z	59	
51	x	599	
52	a	1533	
53	A	2904	
54	B	120	
55	7	15	
56	8	76	
56	9	76	

## 2 Entry composition [i](#)

There are 56 unique types of molecules in this entry. The entry contains 147815 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 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 3 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	102	Total	C	N	O	S	0	0
			832	525	150	150	7		

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	j	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	m	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 13 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	o	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	p	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
17	r	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	s	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	t	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	u	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

- Molecule 21 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 22 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1	50	Total	C	N	O	S	0	0
			409	263	75	71			

- Molecule 23 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 24 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 25 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 26 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	5	234	Total	C	N	O	S	0	0
			1733	1081	315	330	7		

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	C	270	Total	C	N	O	S	0	0
			2076	1285	422	362	7		

- Molecule 28 is a protein called 50S ribosomal protein L3.



Mol	Chain	Residues	Atoms					AltConf	Trace
28	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 29 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 30 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	F	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 31 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 32 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	H	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 33 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 34 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 35 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 36 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 37 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 38 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 39 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 40 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 41 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 42 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 43 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 44 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 45 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	U	102	Total	C	N	O		0	0
			779	492	146	141			

- Molecule 46 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 47 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W	79	Total	C	N	O	S	0	0
			596	367	120	108	1		

- Molecule 48 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 49 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 51 is a protein called Elongation factor 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	26	Total	C	N	O	S	0	0
			214	134	43	35	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
52	a	1533	Total	C	N	O	P	0	0
			32895	14671	6036	10655	1533		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	A	2903	Total	C	N	O	P	0	0
			62320	27801	11467	20149	2903		

- Molecule 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	B	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 55 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	7	9	Total	C	N	O	P	0	0
			191	86	34	62	9		

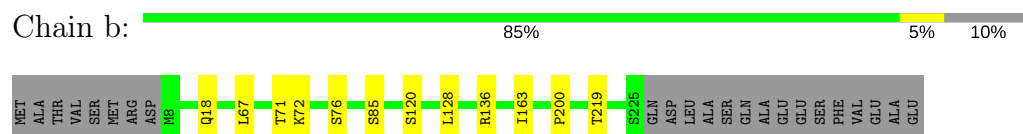
- Molecule 56 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	8	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		
56	9	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

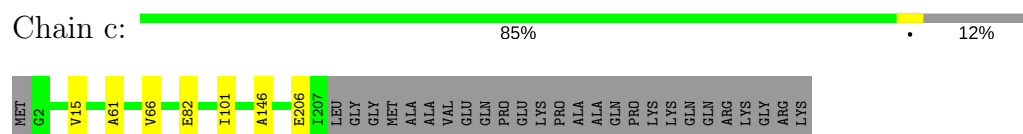
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

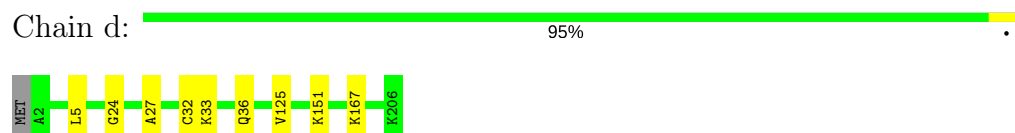
- Molecule 1: 30S ribosomal protein S2



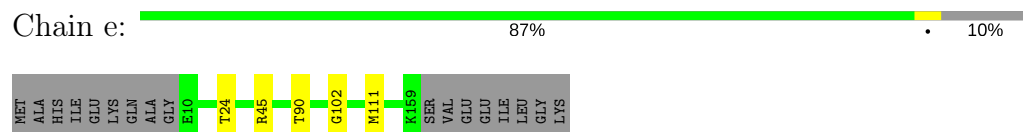
- Molecule 2: 30S ribosomal protein S3



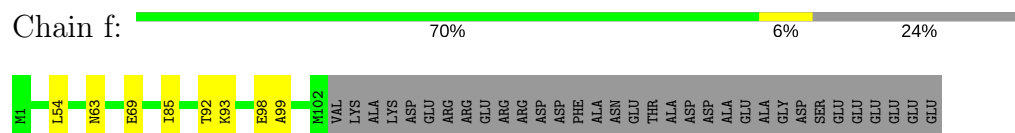
- Molecule 3: 30S ribosomal protein S4



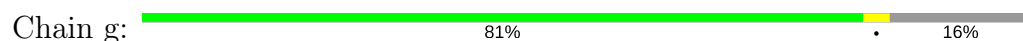
- Molecule 4: 30S ribosomal protein S5

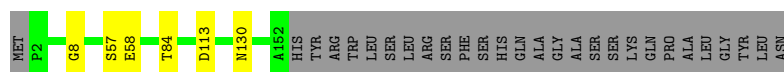


- Molecule 5: 30S ribosomal protein S6



- Molecule 6: 30S ribosomal protein S7





- Molecule 7: 30S ribosomal protein S8

Chain h: 98%



- Molecule 8: 30S ribosomal protein S9

Chain i: 95%



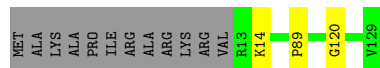
- Molecule 9: 30S ribosomal protein S10

Chain j: 90% 5% 5%



- Molecule 10: 30S ribosomal protein S11

Chain k: 88% 9%



- Molecule 11: 30S ribosomal protein S12

Chain l: 98%



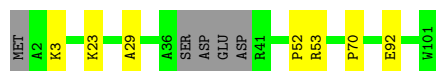
- Molecule 12: 30S ribosomal protein S13

Chain m: 93%



- Molecule 13: 30S ribosomal protein S14

Chain n: 88% 7% 5%



- Molecule 14: 30S ribosomal protein S15

Chain o:  98% ..




- Molecule 15: 30S ribosomal protein S16

Chain p:  98% .



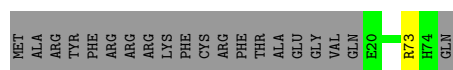
- Molecule 16: 30S ribosomal protein S17

Chain q:  89% 6% 5%




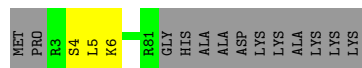
- Molecule 17: 30S ribosomal protein S18

Chain r:  72% 27%



- Molecule 18: 30S ribosomal protein S19

Chain s:  83% 14%



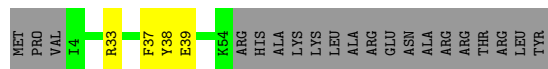
- Molecule 19: 30S ribosomal protein S20

Chain t:  95% ..




- Molecule 20: 30S ribosomal protein S21

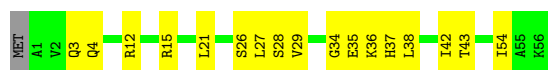
Chain u:  66% 6% 28%



- Molecule 21: 50S ribosomal protein L32



Chain 0: 



- Molecule 22: 50S ribosomal protein L33

Chain 1: 



- Molecule 23: 50S ribosomal protein L34

Chain 2: 



- Molecule 24: 50S ribosomal protein L35

Chain 3: 



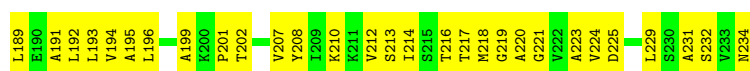
- Molecule 25: 50S ribosomal protein L36

Chain 4: 



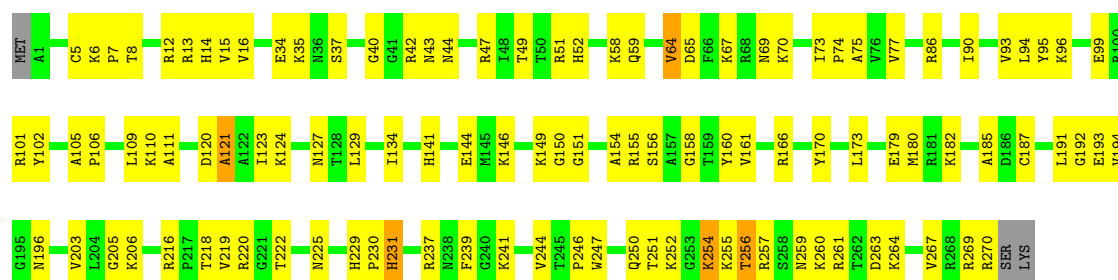
- Molecule 26: 50S ribosomal protein L1

Chain 5: 



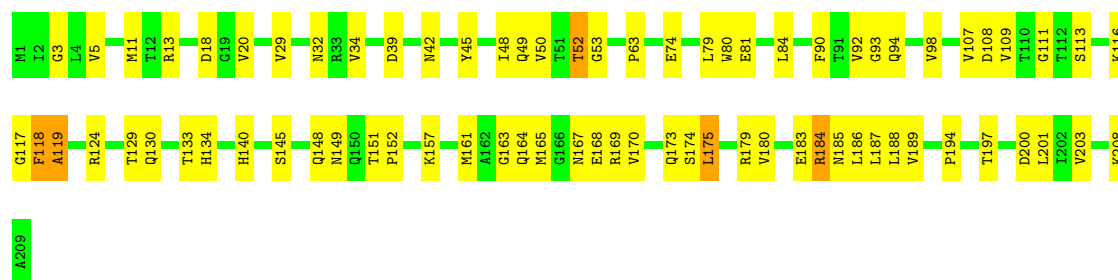
- Molecule 27: 50S ribosomal protein L2

Chain C: 



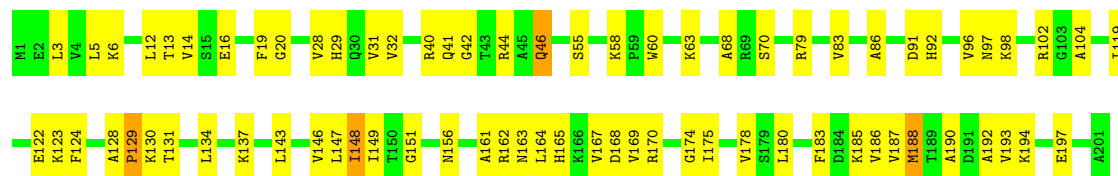
• Molecule 28: 50S ribosomal protein L3

Chain D: 64% 33%



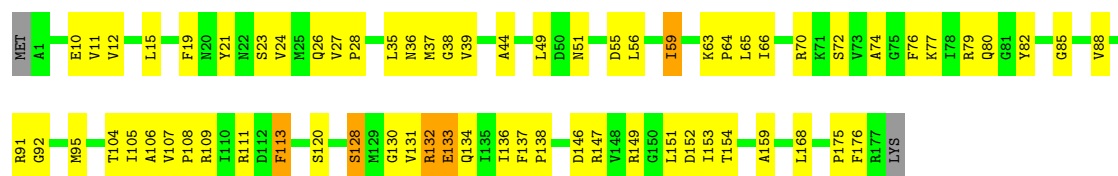
• Molecule 29: 50S ribosomal protein L4

Chain E: 63% 35%



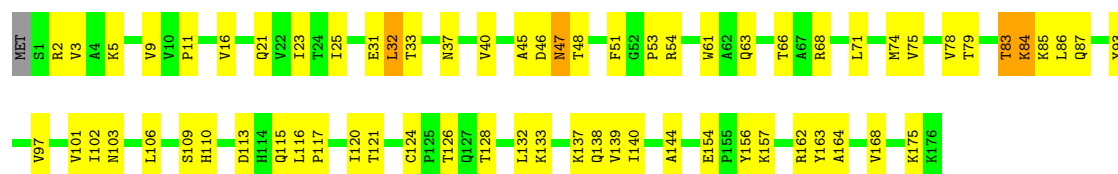
• Molecule 30: 50S ribosomal protein L5

Chain F: 61% 35%



• Molecule 31: 50S ribosomal protein L6

Chain G: 62% 36%



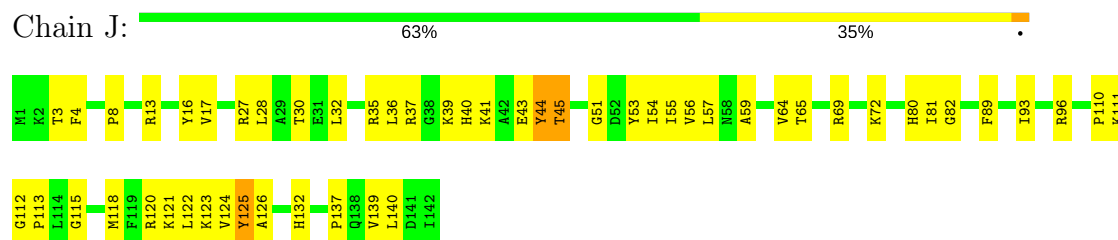
- Molecule 32: 50S ribosomal protein L9



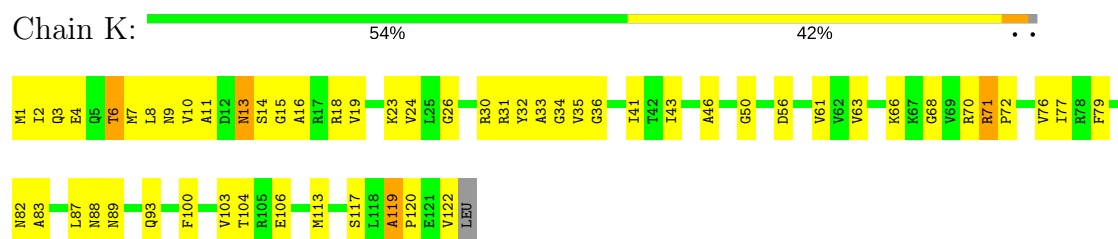
- Molecule 33: 50S ribosomal protein L11



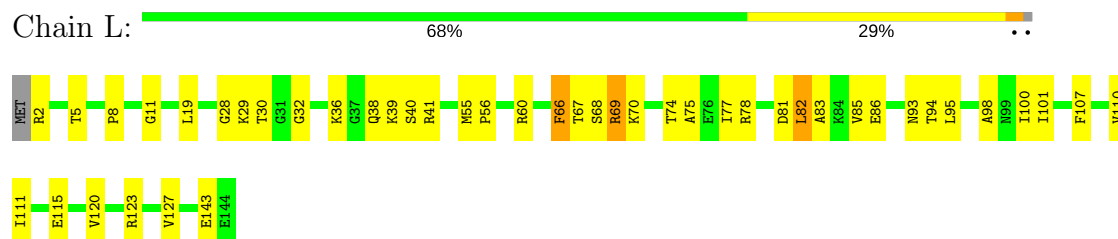
- Molecule 34: 50S ribosomal protein L13



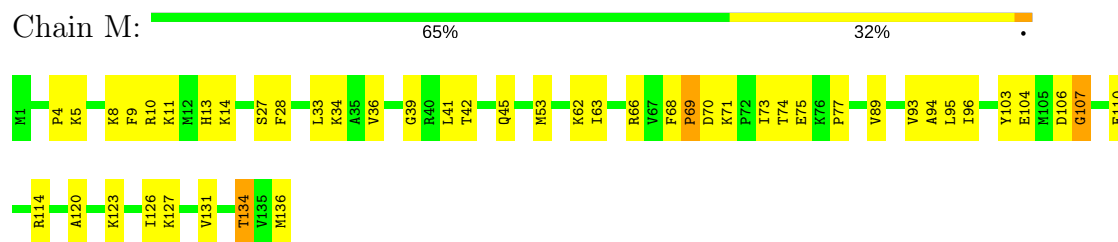
- Molecule 35: 50S ribosomal protein L14



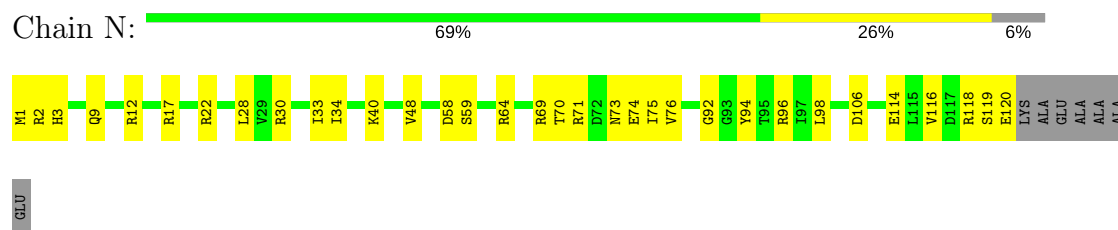
- Molecule 36: 50S ribosomal protein L15



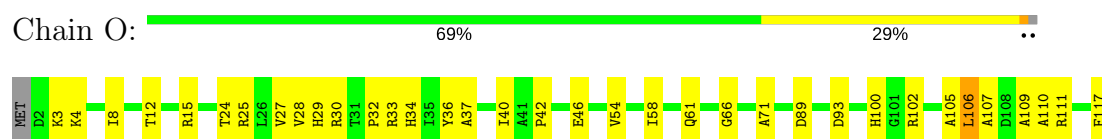
- Molecule 37: 50S ribosomal protein L16



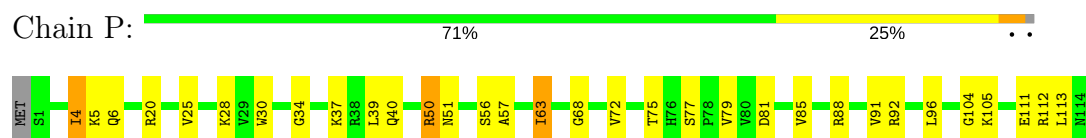
- Molecule 38: 50S ribosomal protein L17



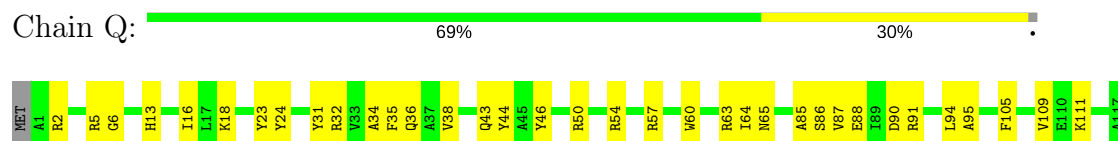
- Molecule 39: 50S ribosomal protein L18



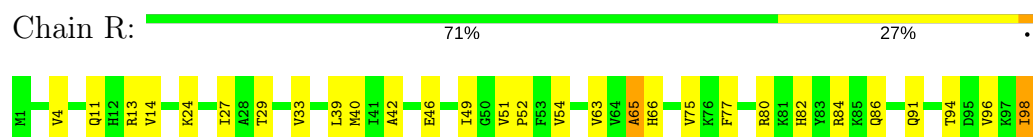
- Molecule 40: 50S ribosomal protein L19



- Molecule 41: 50S ribosomal protein L20



- Molecule 42: 50S ribosomal protein L21

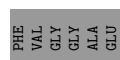
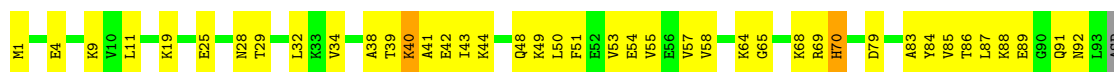


- Molecule 43: 50S ribosomal protein L22

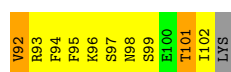
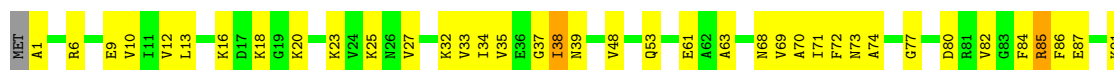




• Molecule 44: 50S ribosomal protein L23



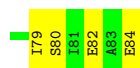
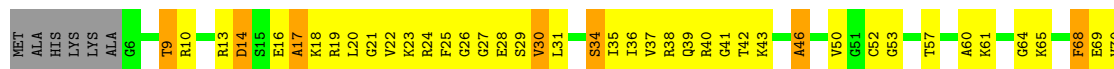
• Molecule 45: 50S ribosomal protein L24



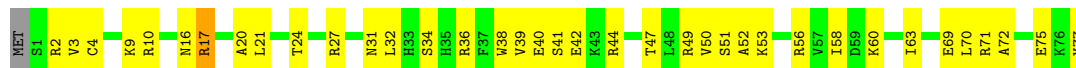
• Molecule 46: 50S ribosomal protein L25



• Molecule 47: 50S ribosomal protein L27



• Molecule 48: 50S ribosomal protein L28



• Molecule 49: 50S ribosomal protein L29





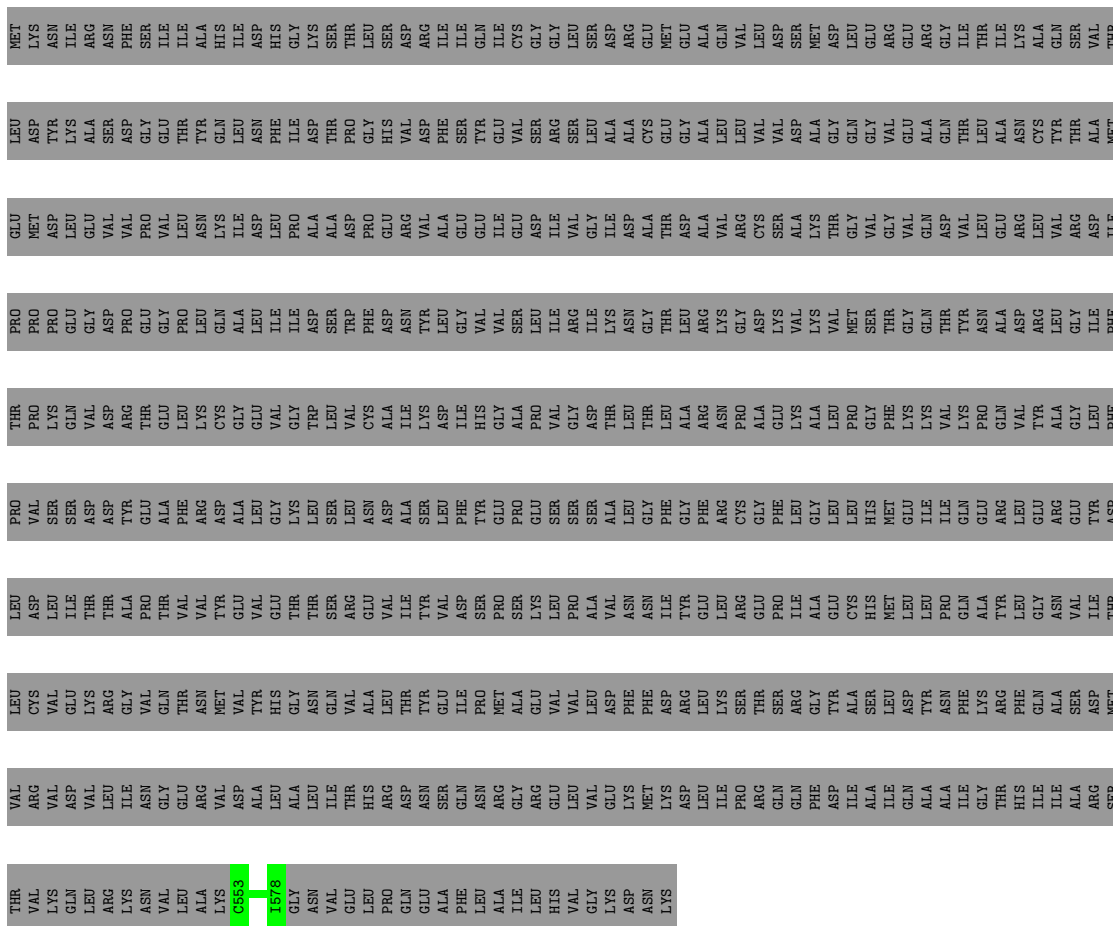
- Molecule 50: 50S ribosomal protein L30

Chain Z:  54% 41% •



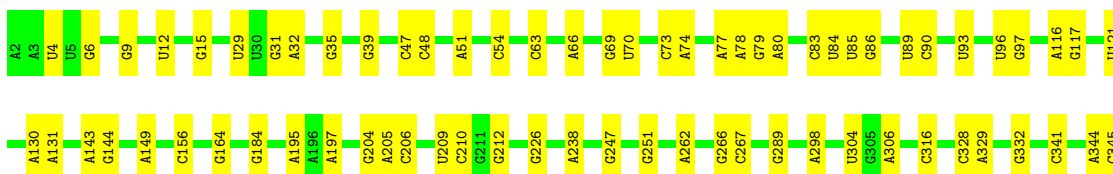
- Molecule 51: Elongation factor 4

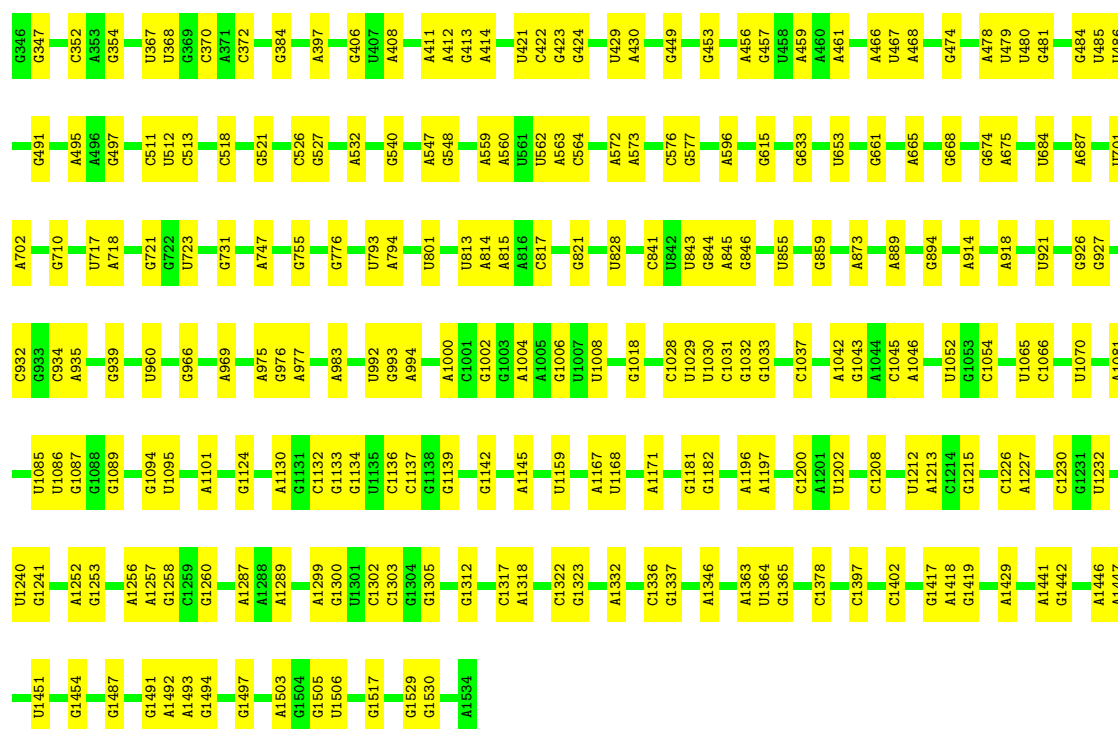
Chain x:  96%



- Molecule 52: 16S ribosomal RNA

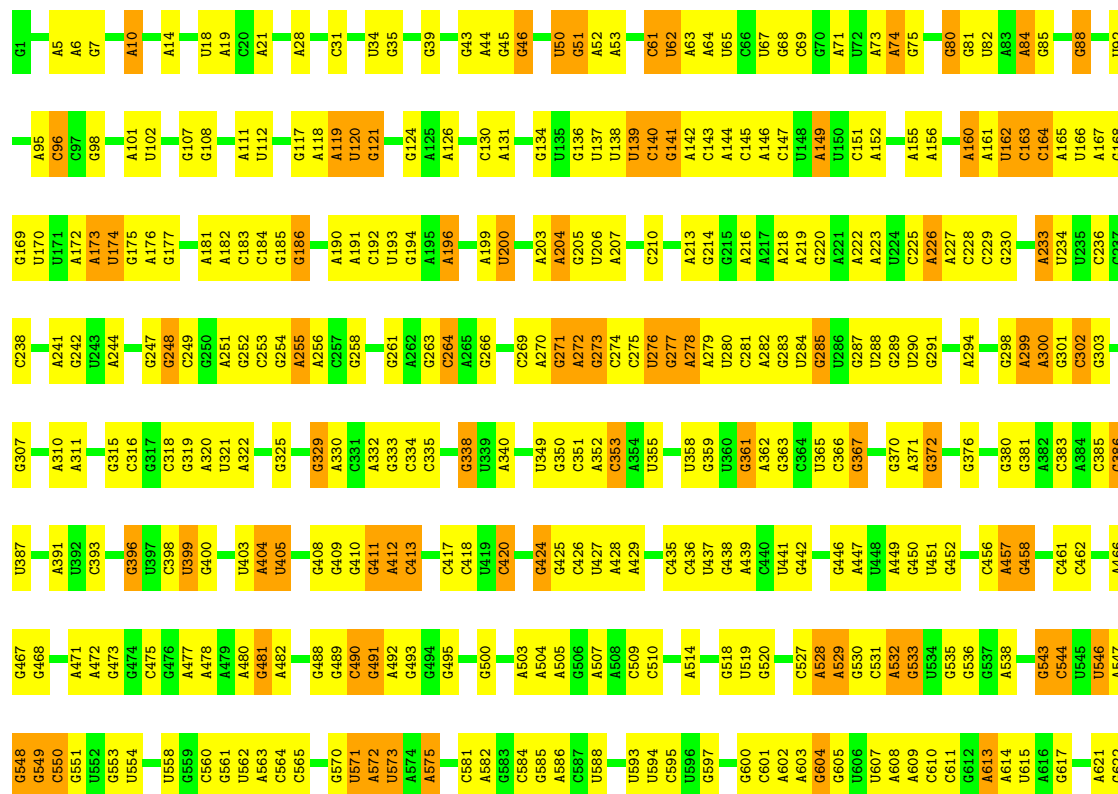
Chain a:  80% 20%





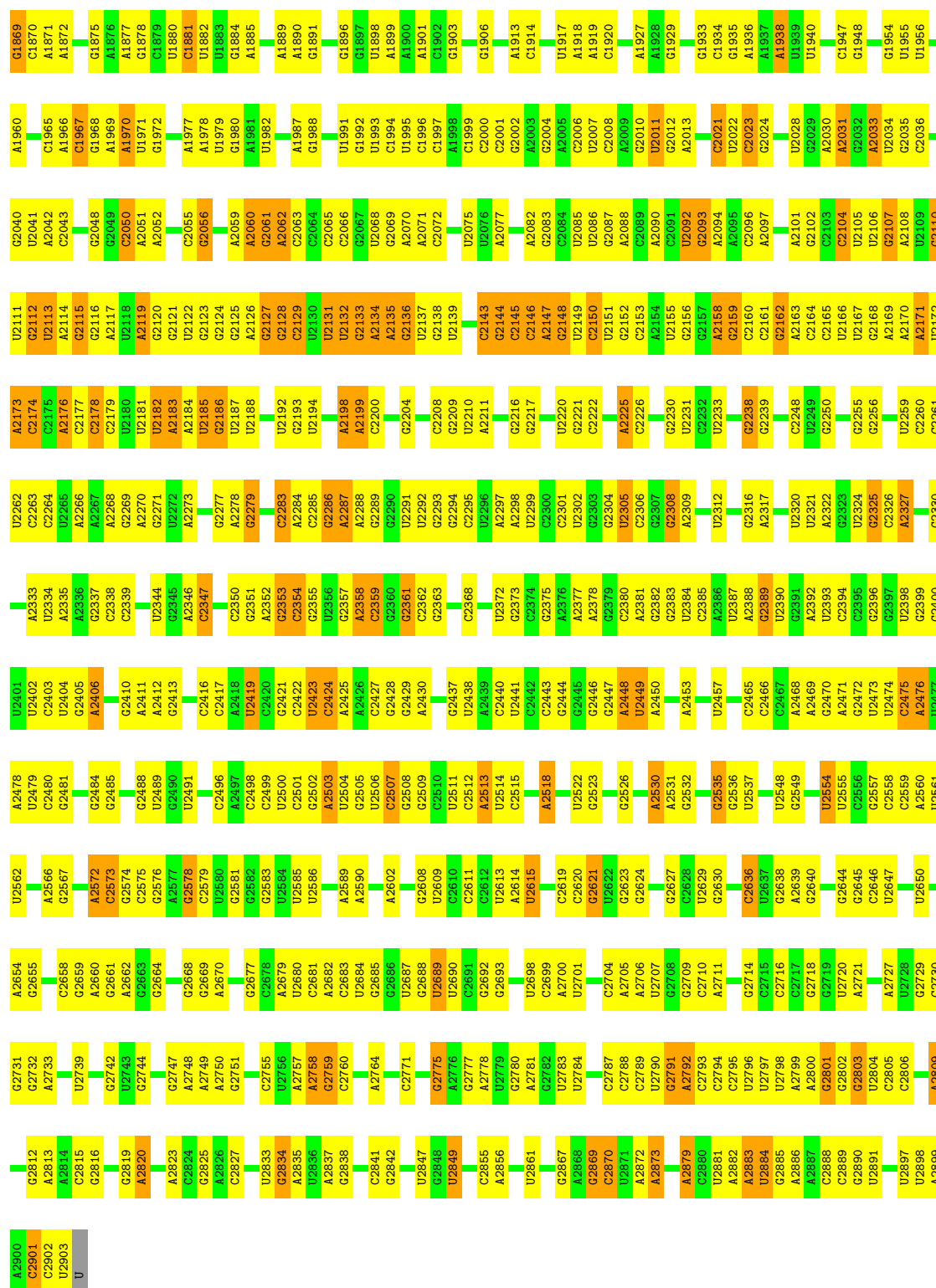
- Molecule 53: 23S ribosomal RNA

Chain A:  43% 46% 11%



A1791	G1704	G1620	C1541	U1467	A1393	G1232	C1150	C1076	C1013	G940	G869	G713	C623
A1794	A1705	U1621	U1542	U1468	U1394	G1236	C1151	A1077	A1014	A941	U870	U714	C624
C1795	A1713	G1622	G1543	A1469	U1396	A1237	A1152	U1078	U1015	G942	U871	A715	G625
G1796	G1714	G1623	G1546	A1470	U1397	G1238	C1153	A1080	U1018	A943	U872	A716	A626
G1797	G1715	A1626	C1547	C1471	C1398	G1239	G1154	U1081	U1019	C944	C873	C717	A627
U1798	U1716	A1548	A1548	C1472	C1399	U1240	G1155	U1082	A1020	C945	G874	A718	G628
G1799	A1717	A1549	A1549	C1473	U1400	A1241	A1156	U1083	A1021	C946	A877	C719	G629
C1800	G1718	C1550	U1550	U1474	G1401	G1325	G1157	U1084	G1022	A947	A878	U720	G630
A1801	U1636	A1553	A1553	A1477	U1402	A1244	G1160	A1085	U1023	G953	G879	A721	A631
A1802	A1637	U1554	G1554	G1478	G1407	G1245	G1161	A1086	G1026	G954	G880	U724	G636
G1807	G1723	G1638	G1555	G1479	U1408	A1246	C1164	A1087	U1027	G955	G881	G725	A637
A1808	G1724	C1639	G1556	G1482	U1409	G1248	A1165	A1088	A1028	G956	G882	G726	G638
A1809					G1410	U1249	C1166	A1089	A1029	C957	G883		U639
A1810		G1645	G1560	C1488	A1413	G1250	C1167	A1090	G1030	U958	U884	G729	C640
U1811	U1729	C1646	C1561	C1489	A1414	G1251	G1168	U1093	A1032	A960	U885	C736	C645
G1812	U1730	U1647	U1562	C1490	C1415	G1252	A1169	U1094	G1031	A959	U886	C737	U646
U1813	G1732	G1649	U1563	A1494	U1416	A1253	C1170	U1095	U1033	C961	U887	A742	U652
		A1650	A1566	A1495	U1417	G1256	G1171	A1096	G1034	G962		U828	U653
C1816	U1736	G1651	G1567	A1496	C1417	U1267	G1172	U1097	U1035	U963	G891	C738	A654
G1817	G1737	A1652	G1568	U1497	G1418	A1262	U1173	A1098	G1036	C964	A892	A739	A655
U1818	G1738	G1653	A1569	C1498	A1419	U1263	U1174	G1099	C1043	A975	C898	U745	G656
G1819	A1739	A1654	A1570	U1499	A1420	A1264	C1175	U1100	A1044		C899	U747	C650
U1820	G1740	A1655	A1571	G1500	G1421	A1265	U1176	C1101	G1045	G978	U894	G748	U657
A1821	C1741	U1657	C1577	G1501	G1425	U1266	G1177	U1101	A1040	A972	U895	A749	U658
C1822	G1742	C1658	U1578	A1504	C1428	G1267	U1180	C1104	G1041	A973	A896	U750	A661
G1823	G1743	A1659	A1579	U1508	A1429	A1268	U1181	U1105	G1042	G974	C898	A755	U665
U1825	A1745	G1660	A1580	A1509	G1430	A1269	G1182	G1106	C1043	A975	C899	U756	A666
G1826	U1746	A1661	C1581	G1510	A1431	G1270	U1183	G1110	G1046	G978	C901	G757	A668
U1827	A1747	A1665	C1582	G1511	G1432	G1271	U1184	A1111	U1047	A979	C902		
G1828	C1748	U1666	U1583	A1512	A1433	A1272	U1185	C903	A980	A981	G904	U758	U665
A1829	A1749	G1667	U1584	C1513	A1434	U1273	G1186	U1113	A1048	C982	U755	C771	A676
C1830	G1750	A1668	C1585	U1514	G1435	A1274	U1187	C1114	C1049	A983	U756	C772	A677
G1831	U1751	U1669	A1586	A1515	G1436	A1275	G1190	G1115	A1050	A984	G907	U773	C678
C1832	G1752	G1674	G1587	U1516	C1437	G1278	U1199	C1117	G1051	C985	A910	G774	C679
U1833	A1753	C1675	U1588	G1519	U1438	G1279	U1200	C1118	A1054	G989	A911	G775	C680
C1837	G1756	A1676	A1590	U1520	A1439	G1283	U1201	U1119	G1055	A990	C915	G776	U683
A1847	A1762	A1679	A1591	G1521	U1442	G1284	A1205	G1120	G1056	A990	G916	G777	U686
A1848	G1763	U1680	C1592	U1522	U1443	A1285	G1206	G1124	A1057	C995	C922	C778	A677
U1851	C1764	G1681	U1593	U1523	G1444	A1286	C1207	A1125	U1058	A996	G923	U779	C678
U1852	U1765		C1595	A1525	G1445	A1287	G1207	A1126	U1060	C997	G924	G775	C679
A1853	G1766	C1684	G1601	C1526	C1446	G1288	G1212	A1127	U1061	C998	G925	G776	C680
A1854		C1685	U1602	G1527	C1447	U1294	G1215	G1128	G1062	U999	A926	G777	
G1857	A1773	A1686	A1603	A1528	G1452	C1295	G1219	U1130	U1063	A1000	G927	G780	U683
U1858	U1779	A1688	C1605	U1530	A1453	G1296	U1219	G1131	U1065	A1001	A928	A781	U686
A1859	U1780	A1689	C1608	C1531	G1456	C1297	G1223	U1132	U1066	G1002		G782	G690
G1860	U1781	C1694	A1609	U1533	U1457	G1300	U1224	A1133	A1067	U1004	U931	A783	C691
A1861	A1783	G1695	U1610	U1534	U1458	A1301	G1225	A1134	G1068	C1005	U932	G784	C692
G1862	U1784	G1696	A1611	A1535	U1459	A1302	A1226	C1135	A1069	C1006	A933	G785	A693
G1863	A1785	G1697	C1611	U1536	U1460	A1306	G1227	G1139	A1070	C1007	U934	G862	
U1864	A1786	A1698	U1617	G1537	G1464	G1306	G1228	A1142	A1071	A1008	C935	A788	G700
U1865		G1699	C1618	U1538	G1465	G1309	C1229	A1143	C1072	A1009	A936	A789	G701
A1866	U1789	G1703	A1619	G1540	U1466	G1310	U1231	A1144	A1073	A1010	C937	U790	A705





Chain B:

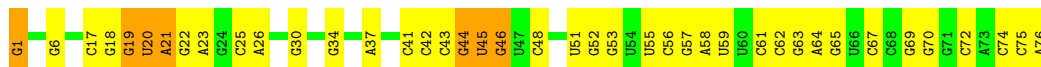




• Molecule 55: tRNA



• Molecule 56: tRNA



• Molecule 56: tRNA



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	18772	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	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	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	b	0.30	0/1735	0.55	0/2338
10	k	0.35	0/893	0.52	0/1205
11	l	0.35	0/969	0.54	0/1300
12	m	0.32	0/892	0.56	0/1193
13	n	0.33	0/785	0.52	0/1043
14	o	0.35	0/722	0.51	0/964
15	p	0.34	0/659	0.48	0/884
16	q	0.33	0/657	0.55	0/881
17	r	0.36	0/462	0.48	0/621
18	s	0.30	0/652	0.50	0/877
19	t	0.36	0/671	0.51	0/888
2	c	0.34	0/1651	0.50	0/2225
20	u	0.34	0/430	0.56	0/570
21	0	0.36	0/450	0.52	0/599
22	1	0.36	0/416	0.58	0/554
23	2	0.36	0/380	0.52	0/498
24	3	0.38	0/513	0.56	0/676
25	4	0.32	0/303	0.54	0/397
26	5	0.27	0/1748	0.60	0/2355
27	C	0.39	0/2115	0.58	1/2844 (0.0%)
28	D	0.37	0/1586	0.57	0/2134
29	E	0.34	0/1571	0.54	0/2113
3	d	0.32	0/1665	0.52	0/2227
30	F	0.32	0/1434	0.53	0/1926
31	G	0.31	0/1343	0.53	0/1816
32	H	0.30	0/1122	0.59	0/1515
33	I	0.26	0/1046	0.54	0/1410
34	J	0.39	0/1152	0.56	0/1551
35	K	0.40	0/947	0.57	0/1268
36	L	0.33	0/1054	0.56	0/1403
37	M	0.36	0/1093	0.57	0/1460
38	N	0.38	0/973	0.55	0/1301
39	O	0.31	0/902	0.51	1/1209 (0.1%)
4	e	0.35	0/1118	0.54	0/1504

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  > 2	RMSZ	# Z  > 2
40	P	0.37	0/929	0.56	0/1242
41	Q	0.43	0/960	0.51	0/1278
42	R	0.35	0/829	0.53	0/1107
43	S	0.37	0/864	0.55	0/1156
44	T	0.36	0/744	0.61	0/994
45	U	0.33	0/787	0.57	0/1051
46	V	0.33	0/766	0.50	0/1025
47	W	0.35	0/603	0.64	0/797
48	X	0.37	0/635	0.56	0/848
49	Y	0.32	0/510	0.51	0/677
5	f	0.33	0/851	0.56	0/1150
50	Z	0.32	0/453	0.57	0/605
51	x	0.31	0/214	0.54	0/275
52	a	0.52	0/36834	0.77	0/57462
53	A	0.58	0/69799	0.81	6/108892 (0.0%)
54	B	0.46	0/2828	0.77	0/4410
55	7	0.48	0/213	0.91	0/329
56	8	0.51	1/1813 (0.1%)	0.79	0/2823
56	9	0.39	1/1813 (0.1%)	0.83	3/2823 (0.1%)
6	g	0.32	0/1195	0.50	0/1602
7	h	0.36	0/989	0.53	0/1326
8	i	0.32	0/1034	0.52	0/1375
9	j	0.31	0/796	0.57	0/1077
All	All	0.50	2/160568 (0.0%)	0.74	11/240073 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
20	u	0	1
31	G	0	1
35	K	0	1
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	9	1	G	OP3-P	-10.74	1.48	1.61
56	8	1	G	OP3-P	-10.71	1.48	1.61

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
56	9	39	U	C2-N1-C1'	7.25	126.40	117.70
56	9	39	U	N1-C2-O2	7.22	127.85	122.80
56	9	39	U	N3-C2-O2	-6.07	117.95	122.20
53	A	1415	U	C2-N1-C1'	6.02	124.92	117.70
39	O	106	LEU	CA-CB-CG	5.67	128.34	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
31	G	83	THR	Peptide
35	K	71	ARG	Peptide
20	u	39	GLU	Peptide

## 5.2 Too-close contacts [i](#)

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	b	1704	0	1732	0	0
2	c	1624	0	1696	0	0
3	d	1643	0	1707	0	0
4	e	1105	0	1148	0	0
5	f	832	0	824	0	0
6	g	1181	0	1238	0	0
7	h	979	0	1031	0	0
8	i	1022	0	1070	0	0
9	j	786	0	828	0	0
10	k	877	0	887	0	0
11	l	955	0	1016	0	0
12	m	883	0	941	0	0
13	n	774	0	824	0	0
14	o	714	0	734	0	0
15	p	649	0	666	0	0
16	q	648	0	691	0	0
17	r	455	0	478	0	0
18	s	637	0	665	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	t	665	0	714	0	0
20	u	425	0	449	0	0
21	0	444	0	461	12	0
22	1	409	0	440	19	0
23	2	377	0	418	6	0
24	3	504	0	574	14	0
25	4	302	0	340	16	0
26	5	1733	0	1824	98	0
27	C	2076	0	2152	68	0
28	D	1565	0	1616	51	0
29	E	1552	0	1619	49	0
30	F	1410	0	1447	51	0
31	G	1323	0	1374	48	0
32	H	1111	0	1148	49	0
33	I	1032	0	1088	50	0
34	J	1129	0	1162	45	0
35	K	938	0	1012	37	0
36	L	1045	0	1117	25	0
37	M	1074	0	1157	31	0
38	N	960	0	1000	25	0
39	O	892	0	923	28	0
40	P	917	0	965	23	0
41	Q	947	0	1022	36	0
42	R	816	0	839	21	0
43	S	857	0	922	23	0
44	T	738	0	807	27	0
45	U	779	0	834	31	0
46	V	753	0	780	21	0
47	W	596	0	610	51	0
48	X	625	0	655	32	0
49	Y	509	0	543	10	0
50	Z	449	0	491	20	0
51	x	214	0	244	0	0
52	a	32895	0	16553	0	0
53	A	62320	0	31343	1212	0
54	B	2529	0	1281	51	0
55	7	191	0	97	3	0
56	8	1623	0	821	46	0
56	9	1623	0	821	94	0
All	All	147815	0	99839	2145	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 14.

The worst 5 of 2145 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)
53:A:271:G:C5	53:A:367:G:C2	1.87	1.62
53:A:271:G:C8	53:A:367:G:N2	1.70	1.54
53:A:271:G:N7	53:A:367:G:C2	1.77	1.45
53:A:271:G:N7	53:A:367:G:N1	1.67	1.40
53:A:272:A:C2	53:A:273:G:C5	2.10	1.39

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	b	216/241 (90%)	181 (84%)	23 (11%)	12 (6%)	2	25
2	c	204/233 (88%)	190 (93%)	7 (3%)	7 (3%)	4	39
3	d	203/206 (98%)	179 (88%)	15 (7%)	9 (4%)	3	31
4	e	148/167 (89%)	128 (86%)	15 (10%)	5 (3%)	4	39
5	f	100/135 (74%)	79 (79%)	13 (13%)	8 (8%)	1	16
6	g	149/179 (83%)	125 (84%)	18 (12%)	6 (4%)	3	34
7	h	127/130 (98%)	115 (91%)	11 (9%)	1 (1%)	22	66
8	i	125/130 (96%)	109 (87%)	12 (10%)	4 (3%)	5	40
9	j	96/103 (93%)	78 (81%)	13 (14%)	5 (5%)	2	27
10	k	115/129 (89%)	104 (90%)	8 (7%)	3 (3%)	6	44
11	l	121/124 (98%)	105 (87%)	14 (12%)	2 (2%)	11	53
12	m	112/118 (95%)	103 (92%)	5 (4%)	4 (4%)	4	37
13	n	92/101 (91%)	77 (84%)	8 (9%)	7 (8%)	1	17
14	o	86/89 (97%)	78 (91%)	7 (8%)	1 (1%)	15	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	p	80/82 (98%)	70 (88%)	8 (10%)	2 (2%)	6	45
16	q	78/84 (93%)	65 (83%)	8 (10%)	5 (6%)	1	23
17	r	53/75 (71%)	51 (96%)	1 (2%)	1 (2%)	9	51
18	s	77/92 (84%)	68 (88%)	6 (8%)	3 (4%)	3	34
19	t	83/87 (95%)	80 (96%)	1 (1%)	2 (2%)	7	46
20	u	49/71 (69%)	36 (74%)	10 (20%)	3 (6%)	2	23
21	0	54/57 (95%)	49 (91%)	2 (4%)	3 (6%)	2	25
22	1	48/55 (87%)	43 (90%)	3 (6%)	2 (4%)	3	32
23	2	44/46 (96%)	39 (89%)	3 (7%)	2 (4%)	3	31
24	3	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	11	54
25	4	36/38 (95%)	29 (81%)	2 (6%)	5 (14%)	0	5
26	5	232/234 (99%)	198 (85%)	32 (14%)	2 (1%)	20	64
27	C	268/273 (98%)	233 (87%)	20 (8%)	15 (6%)	2	25
28	D	207/209 (99%)	168 (81%)	28 (14%)	11 (5%)	2	26
29	E	199/201 (99%)	170 (85%)	18 (9%)	11 (6%)	2	26
30	F	175/179 (98%)	153 (87%)	13 (7%)	9 (5%)	2	28
31	G	174/177 (98%)	142 (82%)	24 (14%)	8 (5%)	3	30
32	H	147/149 (99%)	114 (78%)	22 (15%)	11 (8%)	1	18
33	I	139/142 (98%)	121 (87%)	13 (9%)	5 (4%)	4	37
34	J	140/142 (99%)	120 (86%)	13 (9%)	7 (5%)	2	28
35	K	120/123 (98%)	96 (80%)	17 (14%)	7 (6%)	2	24
36	L	141/144 (98%)	115 (82%)	14 (10%)	12 (8%)	1	14
37	M	134/136 (98%)	114 (85%)	13 (10%)	7 (5%)	2	27
38	N	118/127 (93%)	105 (89%)	10 (8%)	3 (2%)	6	45
39	O	114/117 (97%)	105 (92%)	7 (6%)	2 (2%)	10	52
40	P	112/115 (97%)	98 (88%)	8 (7%)	6 (5%)	2	26
41	Q	115/118 (98%)	109 (95%)	5 (4%)	1 (1%)	20	64
42	R	101/103 (98%)	86 (85%)	11 (11%)	4 (4%)	3	34
43	S	108/110 (98%)	93 (86%)	9 (8%)	6 (6%)	2	25
44	T	91/100 (91%)	65 (71%)	17 (19%)	9 (10%)	1	11
45	U	100/104 (96%)	79 (79%)	13 (13%)	8 (8%)	1	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	V	92/94 (98%)	84 (91%)	6 (6%)	2 (2%)	8	48
47	W	77/85 (91%)	55 (71%)	13 (17%)	9 (12%)	0	7
48	X	75/78 (96%)	65 (87%)	7 (9%)	3 (4%)	3	34
49	Y	61/63 (97%)	51 (84%)	7 (12%)	3 (5%)	2	28
50	Z	56/59 (95%)	48 (86%)	6 (11%)	2 (4%)	4	37
51	x	24/599 (4%)	23 (96%)	1 (4%)	0	100	100
All	All	5878/6817 (86%)	5045 (86%)	567 (10%)	266 (4%)	5	31

5 of 266 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	72	LYS
1	b	163	ILE
3	d	151	LYS
5	f	63	ASN
5	f	93	LYS

### 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	b	180/199 (90%)	180 (100%)	0	100	100
2	c	170/190 (90%)	170 (100%)	0	100	100
3	d	172/173 (99%)	172 (100%)	0	100	100
4	e	113/126 (90%)	113 (100%)	0	100	100
5	f	89/116 (77%)	89 (100%)	0	100	100
6	g	124/147 (84%)	124 (100%)	0	100	100
7	h	104/105 (99%)	104 (100%)	0	100	100
8	i	105/107 (98%)	105 (100%)	0	100	100
9	j	86/90 (96%)	86 (100%)	0	100	100
10	k	90/99 (91%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	l	103/104 (99%)	103 (100%)	0	100	100
12	m	92/96 (96%)	92 (100%)	0	100	100
13	n	79/84 (94%)	79 (100%)	0	100	100
14	o	76/77 (99%)	76 (100%)	0	100	100
15	p	65/65 (100%)	65 (100%)	0	100	100
16	q	74/78 (95%)	74 (100%)	0	100	100
17	r	48/65 (74%)	48 (100%)	0	100	100
18	s	70/79 (89%)	70 (100%)	0	100	100
19	t	65/66 (98%)	65 (100%)	0	100	100
20	u	44/61 (72%)	44 (100%)	0	100	100
21	0	47/48 (98%)	47 (100%)	0	100	100
22	1	45/49 (92%)	45 (100%)	0	100	100
23	2	38/38 (100%)	38 (100%)	0	100	100
24	3	51/51 (100%)	51 (100%)	0	100	100
25	4	34/34 (100%)	34 (100%)	0	100	100
26	5	181/181 (100%)	181 (100%)	0	100	100
27	C	215/218 (99%)	215 (100%)	0	100	100
28	D	164/164 (100%)	164 (100%)	0	100	100
29	E	165/165 (100%)	165 (100%)	0	100	100
30	F	148/150 (99%)	148 (100%)	0	100	100
31	G	137/138 (99%)	137 (100%)	0	100	100
32	H	114/114 (100%)	114 (100%)	0	100	100
33	I	109/110 (99%)	109 (100%)	0	100	100
34	J	116/116 (100%)	116 (100%)	0	100	100
35	K	103/104 (99%)	103 (100%)	0	100	100
36	L	102/103 (99%)	102 (100%)	0	100	100
37	M	109/109 (100%)	109 (100%)	0	100	100
38	N	100/103 (97%)	100 (100%)	0	100	100
39	O	86/87 (99%)	86 (100%)	0	100	100
40	P	99/100 (99%)	99 (100%)	0	100	100
41	Q	89/90 (99%)	89 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	R	84/84 (100%)	84 (100%)	0	100	100
43	S	93/93 (100%)	93 (100%)	0	100	100
44	T	80/84 (95%)	80 (100%)	0	100	100
45	U	83/85 (98%)	83 (100%)	0	100	100
46	V	78/78 (100%)	78 (100%)	0	100	100
47	W	59/63 (94%)	59 (100%)	0	100	100
48	X	67/68 (98%)	67 (100%)	0	100	100
49	Y	55/55 (100%)	55 (100%)	0	100	100
50	Z	48/49 (98%)	48 (100%)	0	100	100
51	x	23/511 (4%)	23 (100%)	0	100	100
All	All	4871/5569 (88%)	4871 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
26	5	234	ASN
28	D	49	GLN
44	T	70	HIS
27	C	52	HIS
27	C	199	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	a	1532/1533 (99%)	301 (19%)	0
53	A	2902/2904 (99%)	597 (20%)	0
54	B	117/120 (97%)	21 (17%)	0
55	7	8/15 (53%)	4 (50%)	0
56	8	75/76 (98%)	8 (10%)	0
56	9	75/76 (98%)	33 (44%)	0
All	All	4709/4724 (99%)	964 (20%)	0

5 of 964 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	a	4	U
52	a	6	G
52	a	9	G
52	a	12	U
52	a	15	G

There are no RNA pucker outliers to report.

#### 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 carbohydrates in this entry.

#### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

#### 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.