



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 03:11 PM BST

PDB ID : 3J7P  
EMDB ID: : EMD-2646  
Title : Structure of the 80S mammalian ribosome bound to eEF2  
Authors : Voorhees, R.M.; Fernandez, I.S.; Scheres, S.H.W.; Hegde, R.S.  
Deposited on : 2014-08-01  
Resolution : 3.50 Å(reported)  
Based on PDB ID : 3J3B, 3J3A, 3J3F, 3J3D

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.  
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>

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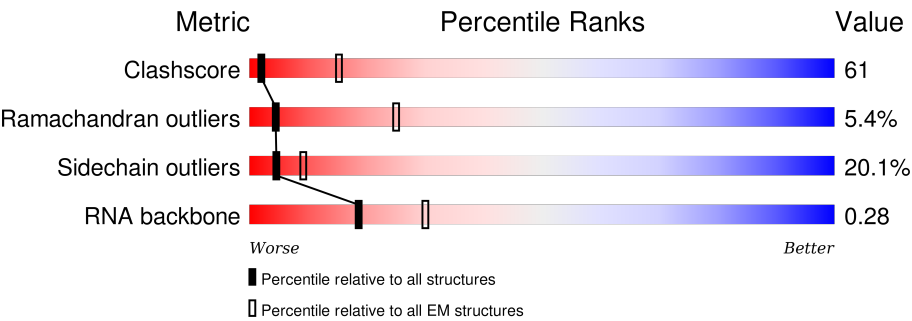
MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk27241

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.50 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	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	5	3664	<div><div>9%</div><div>44%</div><div>35%</div><div>12%</div></div>
2	7	120	<div><div>18%</div><div>56%</div><div>21%</div><div>5%</div></div>
3	8	156	<div><div>7%</div><div>53%</div><div>26%</div><div>13%</div></div>
4	A	257	<div><div>49%</div><div>28%</div><div>12%</div><div>6%</div><div>5%</div></div>
5	B	394	<div><div>48%</div><div>34%</div><div>14%</div><div>5%</div></div>
6	C	367	<div><div>55%</div><div>31%</div><div>11%</div><div>.</div></div>
7	D	297	<div><div>45%</div><div>35%</div><div>13%</div><div>5%</div><div>.</div></div>
8	E	236	<div><div>47%</div><div>27%</div><div>19%</div><div>6%</div></div>









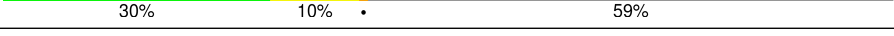

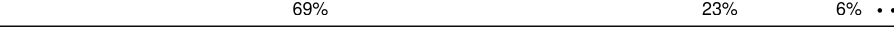
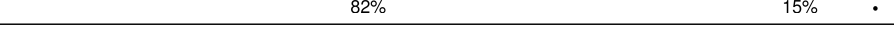

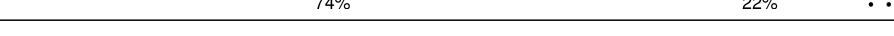
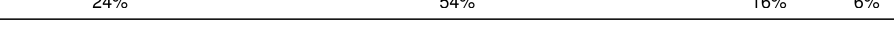

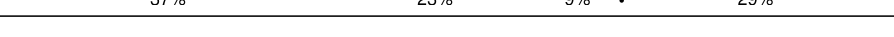

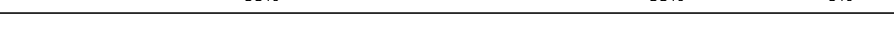




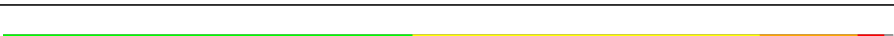

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Mol	Chain	Length	Quality of chain
9	F	225	
10	G	266	
11	H	192	
12	I	213	
13	J	178	
14	K	163	
15	L	211	
16	M	213	
17	N	204	
18	O	204	
19	P	153	
20	Q	188	
21	R	196	
22	S	224	
23	T	160	
24	U	128	
25	V	140	
26	W	157	
27	X	156	
28	Y	145	
29	Z	136	
30	a	148	
31	b	160	
32	c	115	
33	d	125	

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Mol	Chain	Length	Quality of chain
34	e	135	
35	f	110	
36	g	117	
37	h	123	
38	i	105	
39	j	86	
40	k	70	
41	l	51	
42	m	128	
43	n	25	
44	o	106	
45	p	91	
46	q	202	
47	r	125	
48	4	856	
49	S2	1742	
50	SA	295	
51	SB	264	
52	SC	218	
53	SD	243	
54	SE	263	
55	SF	204	
56	SG	249	
57	SH	194	
58	SI	208	

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Mol	Chain	Length	Quality of chain
59	SJ	194	
60	SK	165	
61	SL	158	
62	SM	124	
63	SN	151	
64	SO	151	
65	SP	145	
66	SQ	146	
67	SR	135	
68	SS	152	
69	ST	145	
70	SU	119	
71	SV	83	
72	SW	130	
73	SX	143	
74	SY	132	
75	SZ	125	
76	Sa	115	
77	Sb	84	
78	Sc	69	
79	Sd	56	
80	Se	133	
81	Sf	156	
82	Sg	317	

## 2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 221686 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 RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3662	Total	C	N	O	P	0	0
			78486	34947	14363	25515	3661		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called Ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 5 is a protein called Ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	394	Total	C	N	O	S	0	0
			3147	2005	591	538	13		

- Molecule 6 is a protein called Ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	367	Total	C	N	O	S	0	0
			2919	1836	582	486	15		

- Molecule 7 is a protein called Ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	292	Total	C	N	O	S	0	0
			2380	1508	434	426	12		

- Molecule 8 is a protein called Ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	236	Total	C	N	O	S	0	0
			1904	1219	364	316	5		

- Molecule 9 is a protein called Ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 10 is a protein called Ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	241	Total	C	N	O	S	0	0
			1934	1232	372	326	4		

- Molecule 11 is a protein called Ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called Ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	213	Total	C	N	O	S	0	0
			1713	1083	331	284	15		

- Molecule 13 is a protein called Ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	170	Total	C	N	O	S	0	0
			1359	856	256	241	6		

- Molecule 14 is a protein called Ribosomal protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	151	Total	C	N	O	S	0	0
			1140	708	215	213	4		

- Molecule 15 is a protein called Ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	210	Total	C	N	O	S	0	0
			1703	1064	354	280	5		

- Molecule 16 is a protein called Ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	138	Total	C	N	O	S	0	0
			1131	727	216	181	7		

- Molecule 17 is a protein called Ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 18 is a protein called Ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	201	Total	C	N	O	S	0	0
			1651	1063	323	260	5		

- Molecule 19 is a protein called Ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 20 is a protein called Ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 21 is a protein called Ribosomal protein eL19.



Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 22 is a protein called Ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 23 is a protein called Ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 24 is a protein called Ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 25 is a protein called Ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 26 is a protein called Ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 27 is a protein called Ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 28 is a protein called Ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 29 is a protein called Ribosomal protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 30 is a protein called Ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	147	Total	C	N	O	S	0	0
			1163	735	239	185	4		

- Molecule 31 is a protein called Ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 32 is a protein called Ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 33 is a protein called Ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 34 is a protein called Ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 35 is a protein called Ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	f	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 36 is a protein called Ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 37 is a protein called Ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	122	Total	C	N	O	S	0	0
			1015	642	205	167	1		

- Molecule 38 is a protein called Ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 39 is a protein called Ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	86	Total	C	N	O	S	0	0
			706	436	155	110	5		

- Molecule 40 is a protein called Ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 41 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 42 is a protein called Ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 43 is a protein called Ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 44 is a protein called Ribosomal protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 45 is a protein called Ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 46 is a protein called Ribosomal protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	202	Total	C	N	O	S	0	0
			1556	989	272	286	9		

- Molecule 47 is a protein called Ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	125	Total	C	N	O	S	0	0
			1001	622	206	168	5		

- Molecule 48 is a protein called Eukaryotic elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	4	856	Total	C	N	O	S	0	0
			6673	4234	1148	1247	44		

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S2	1742	Total	C	N	O	P	0	0
			36900	16458	6595	12106	1741		

- Molecule 50 is a protein called Ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SA	208	Total	C	N	O	S	0	0
			1642	1045	289	300	8		

- Molecule 51 is a protein called Ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SB	213	Total	C	N	O	S	0	0
			1725	1093	311	308	13		

- Molecule 52 is a protein called Ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SC	218	Total	C	N	O	S	0	0
			1690	1094	289	297	10		

- Molecule 53 is a protein called Ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 54 is a protein called Ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 55 is a protein called Ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SF	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 56 is a protein called Ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 57 is a protein called Ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SH	189	Total	C	N	O	S	0	0
			1521	969	280	271	1		

- Molecule 58 is a protein called Ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 59 is a protein called Ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 60 is a protein called Ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 61 is a protein called Ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SL	152	Total	C	N	O	S	0	0
			1238	788	232	212	6		

- Molecule 62 is a protein called Ribosomal protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SM	124	Total	C	N	O	S	0	0
			960	600	171	181	8		

- Molecule 63 is a protein called Ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 64 is a protein called Ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 65 is a protein called Ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SP	96	Total	C	N	O	S	0	0
			805	506	158	135	6		

- Molecule 66 is a protein called Ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SQ	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 67 is a protein called Ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SR	129	Total	C	N	O	S	0	0
			1047	658	193	191	5		

- Molecule 68 is a protein called Ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SS	137	Total	C	N	O	S	0	0
			1139	714	231	193	1		

- Molecule 69 is a protein called Ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	ST	141	Total	C	N	O	S	0	0
			1101	690	212	196	3		

- Molecule 70 is a protein called Ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SU	104	Total	C	N	O	S	0	0
			818	513	153	148	4		

- Molecule 71 is a protein called Ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SV	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 72 is a protein called Ribosomal protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 73 is a protein called Ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SX	141	Total	C	N	O	S	0	0
			1099	694	220	182	3		

- Molecule 74 is a protein called Ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SY	126	Total	C	N	O	S	0	0
			1023	646	200	172	5		

- Molecule 75 is a protein called Ribosomal protein es25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 76 is a protein called Ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sa	98	Total	C	N	O	S	0	0
			781	486	161	129	5		

- Molecule 77 is a protein called Ribosomal protein eS27.



Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 78 is a protein called Ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 79 is a protein called Ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sd	52	Total	C	N	O	S	0	0
			434	273	87	69	5		

- Molecule 80 is a protein called Ribosomal protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Se	57	Total	C	N	O	S	0	0
			452	279	99	73	1		

- Molecule 81 is a protein called Ribosomal protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sf	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 82 is a protein called Ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 83 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
83	o	1	Total	Zn	0
			1	1	
83	j	1	Total	Zn	0
			1	1	
83	Sa	1	Total	Zn	0
			1	1	

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms		AltConf
83	m	1	Total 1	Zn 1	0

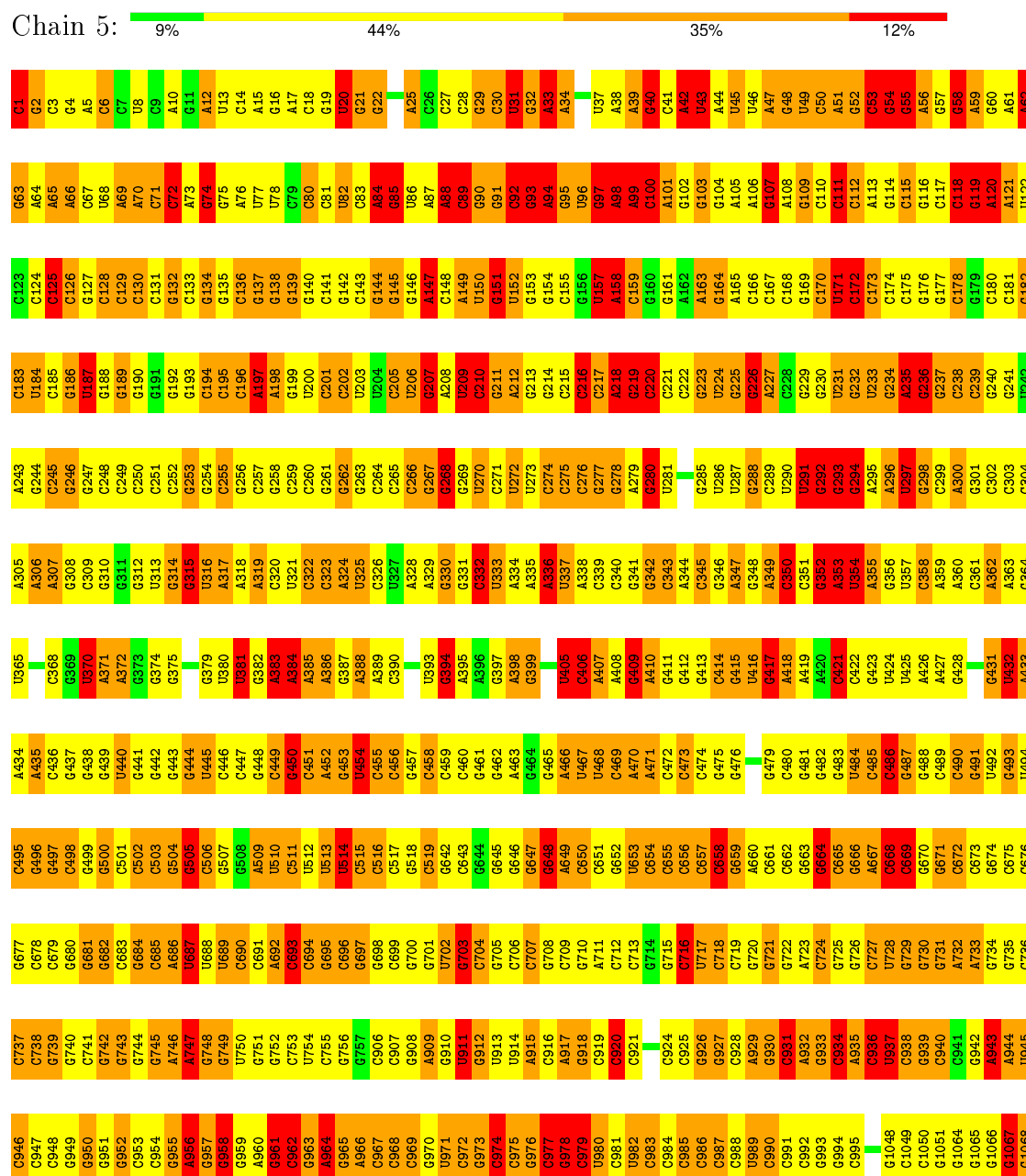
- Molecule 84 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
84	P	1	Total 1	Mg 1	0
84	S2	36	Total 36	Mg 36	0
84	V	1	Total 1	Mg 1	0
84	7	5	Total 5	Mg 5	0
84	4	1	Total 1	Mg 1	0
84	5	118	Total 118	Mg 118	0
84	8	4	Total 4	Mg 4	0

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: 28S ribosomal RNA



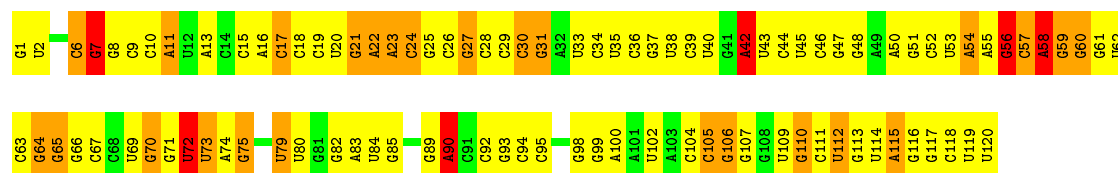



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C3854	C3794	A3733	C3673	U3613	U2874	A2807	A2744	A2679	G2557	G2496	U2436	U2371	G2310	C2250
C3855	A3795	G3734	G3674	G3614	C2875	C2808	A2745	G2682	G2558	C2497	C2437	U2372	C2311	C2251
C3856	U3796	G3735	G3675	G3615	C2876	G2811	A2746	C2683	G2559	C2498	A2438	C2373	U2312	G2252
C3857	C3797	U3736	G3676	U3616	G2877	A2812	U2747	C2684	C2560	G2439	U2439	A2376	A2313	A2253
C3858	U3798	A3737	G3677	G3617	G2878	C2813	C2748	C2685	C2561	U2440	U2440	C2377	G2314	G2254
G3859	A3799	G3738	G3678	C3618	A2879	A2814	G2751	C2686	G2562	C2441	C2442	C2378	G2315	C2255
A3860	A3800	G3739	U3679	G3619	U2880	C2815	U2752	U2687	G2563	G2502	G2443	G2379	G2316	G2256
A3861	G3740	G3740	U3680	G3620	G2884	C2816	G2753	G2688	G2564	C2503	G2444	G2380	C2317	G2257
A3862	U3802	C3741	G3681	A3621	G2885	C2817	G2754	C2689	A2565	C2504	G2445	A2382	G2318	C2258
C3863	C3803	G3742	A3682	C3622	G2886	C2818	G2755	G2690	A2566	C2505	C2446	C2383	C2319	C2259
C3864	G3804	G3743	C3683	C3623	G2887	C2819	A2756	C2691	G2567	A2507	U2447	U2384	G2320	C2260
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C3869	G3809	A3748	U3688	G3628	G2895	C2824	U2761	A2696	A2572	A2512	A2451	C2383	G2325	C2265
C3870	C3810	C3749	G3689	A3629	C2896	C2825	G2762	A2697	G2574	G2513	G2452	G2392	G2326	C2266
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C3872	C3812	G3751	A3692	U3631	C2898	C2827	U2764	G2699	G2576	G2515	U2454	C2394	G2328	A2268
G3873	A3813	C3752	G3693	C3632	G2899	C2828	A2765	G2700	A2577	G2516	G2455	C2395	U2329	C2269
G3874	U3814	G3753	U3694	G3633	C2900	C2829	U2766	U2701	G2578	A2517	G2456	A2395	G2330	C2270
G3875	G3815	G3754	G3695	A3634	U2900	C2830	U2767	G2702	G2640	G2518	G2457	A2396	G2331	C2271
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A3877	A3817	G3756	C3696	C3636	U2904	G2832	C2769	G2704	A2642	G2520	G2459	U2398	G2333	G2273
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G3879	G3819	U3758	G3698	G3638	G2906	C2834	C2770	G2706	G2644	G2522	G2461	G2400	C2335	G2275
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G3881	A3821	A3760	C3700	U3640	U2908	A2836	C2772	U2707	G2646	U2524	G2463	U2408	C2337	C2277
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C3883	G3823	U3762	A3702	A3642	G2910	U2837	C2774	C2709	G2648	C2526	C2465	A2404	G2339	A2279
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G3895	C3835	A3774	G3714	G3654	C3594	C2851	U2788	G2723	A2660	U2538	A2477	G2416	G2351	G2291
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G5041	C4980	C4918	C4859	C4714	G4652	U4688	G4528	A4467	U4404	C4342	A4281	G4216	C4155	G4095	U3914
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A5048	C4987	U4925	G4865	C4720	G4658	U4694	G4534	A4473	G4410	G4347	G4287	G4222	C4162	C4101	U3920
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A5060	U5000	C4937	G4877	C4734	C4671	A4607	A4546	C4485	U4423	U4361	U4299	A4234	U4174	U4113	C3935
C5061	C5001	A4938	C4878	A4735	G4672	G4608	C4547	A4486	U4424	A4362	U4300	G4235	C4175	G4115	A3936
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U5066	U5006	G4944	C4883	C4740	U4677	G4617	U4552	G4491	G4429	G4369	U4306	G4241	U4181	C4120	A3943
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A5011	U5011	U4949	C4887	G4745	U4683	A4622	U4557	U4498	U4434	A4374	A4311	G4246	A4186	C4125	U4066
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A5014	A5014	G4953	G4890	C4748	G4686	C4625	C4560	G4501	U4437	G4377	C4314	G4251	U4189	U4069	U4070
G5015	G5015	G4954	A4892	C4749	A4687	A4626	C4562	C4502	G4440	A4378	A4315	G4252	U4190	U4071	U4071
A5016	A5016	U4955	A4893	G4750	C4688	U4627	U4563	A4503	A441	A4379	G4316	G4253	G4191	C4130	C4072
G5017	G5017	C4956	A4894	G4751	U4689	U4628	A4564	C4504	U4442	A4380	A4317	G4254	A4192	G4131	C4073
C5018	C5018	C4957	G4895	U4752	G4690	U4629	A4565	C4505	C4443	A4381	C4318	G4256	U4193	C4132	C4074
A5019	A5019	C4958	G4896	U4753	A4691	G4630	U4566	C4506	C4444	G4382	C4319	G4257	U4194	C4133	U4075
C5020	G5020	U4959	G4897	G4754	A4692	U4631	A4567	A4507	C4447	U4383	G4320	C4258	G4195	G4134	G4076
C5021	C5021	G4960	G4898	G4755	C4693	U4632	A4568	C4508	U4448	U4384	U4321	C4259	G4196	G4135	G4077
U5022	U5022	G4961	G4899	C4756	G4694	G4633	U4569	U4509	G4449	A4385	G4322	U4260	G4197	G4136	G4078
C5023	C5023	C4962	C4900	C4757	C4695	U4634	G4570	A4510	U4450	C4386	A4323	C4261	C4198	C4137	A4077
C5024	C5024	G4963	G4901	U4758	C4696	A4635	A4571	A4511	U4451	C4387	A4324	C4262	C4199	C4138	C4078
C5025	C5025	C4964	C4902	C4759	U4697	U4636	U4572	A4512	U4452	C4388	A4325	U4265	G4200	C4139	C4079
U5026	U5026	U4965	G4903	G4760	C4698	G4637	G4573	U4513	U4453	C4389	G4326	G4266	G4201	C4140	C4080
C5027	C5027	A4966	G4904	C4761	U4699	U4638	U4574	G4514	C4453	A4390	C4327	G4267	U4202	G4141	G4081
G5028	G5028	A4967	C4905	A4762	A4700	G4639	G4575	G4515	G4454	G4391	G4328	A4268	A4203	C4142	G4082
C5029	C5029	U4968	C4906	U4763	A4701	C4640	U4576	G4516	G4455	G4392	G4329	G4269	C4204	G4143	U4083
U5030	U5030	G4969	G4907	A4764	G4702	U4641	U4577	A4517	C4456	G4393	G4330	C4270	A4205	C4144	G4084
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C5032	C5032	A4971	A4909	C4766	C4704	G4643	U4579	C4519	U4458	U4395	C4332	G4272	C4207	G4146	G4086
G5033	G5033	G4972	G4910	C4767	C4705	G4644	U4580	G4520	U4459	A4396	C4333	A4273	U4208	G4147	G4087
A5034	A5034	U4973	A4911	G4768	A4707	C4645	G4581	U4521	U4460	A4397	G4334	A4274	A4209	C4148	G4088
C5035	C5035	C4974	G4912	G4769	A4708	U4646	C4582	G4522	C4461	C4398	C4335	G4275	U4210	C4149	G4089
C5036	C5036	G4975	G4913	U4770	U4709	G4647	C4583	A4523	C4462	U4399	A4336	G4276	C4211	G4150	G4090
U5037	U5037	U4976	C4914	C4771	C4710	G4648	U4584	A4524	U4463	G4400	G4337	G4277	A4212	G4151	G4091
A5038	A5038	C4977	G4915	C4772	C4711	U4649	U4585	C4525	U4464	A4401	G4338	C4278	A4213	G4152	G4092
U5039	U5039	G4978	G4916	C4773	C4712	G4650	G4586	U4526	U4465	C4402	A4339	A4279	A4214	C4153	G4093

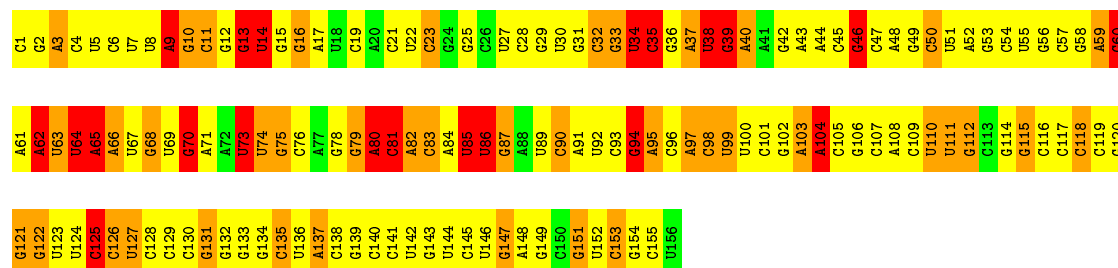
- Molecule 2: 5S ribosomal RNA

Chain 7:



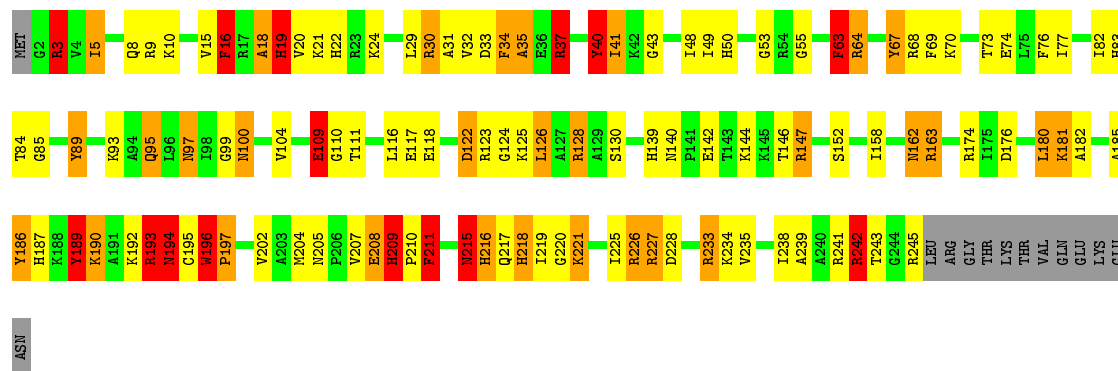
- Molecule 3: 5.8S ribosomal RNA

Chain 8:



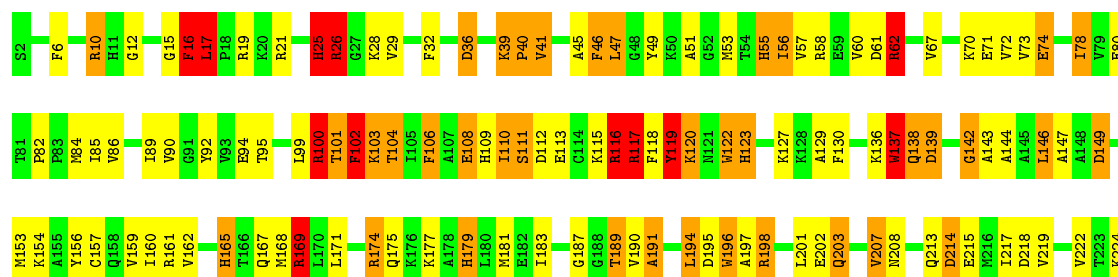
- Molecule 4: Ribosomal protein uL2

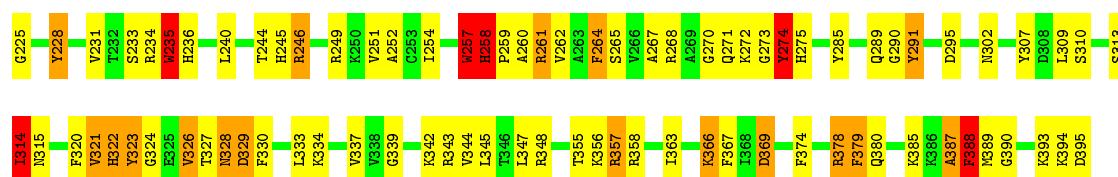
Chain A:



- Molecule 5: Ribosomal protein uL3

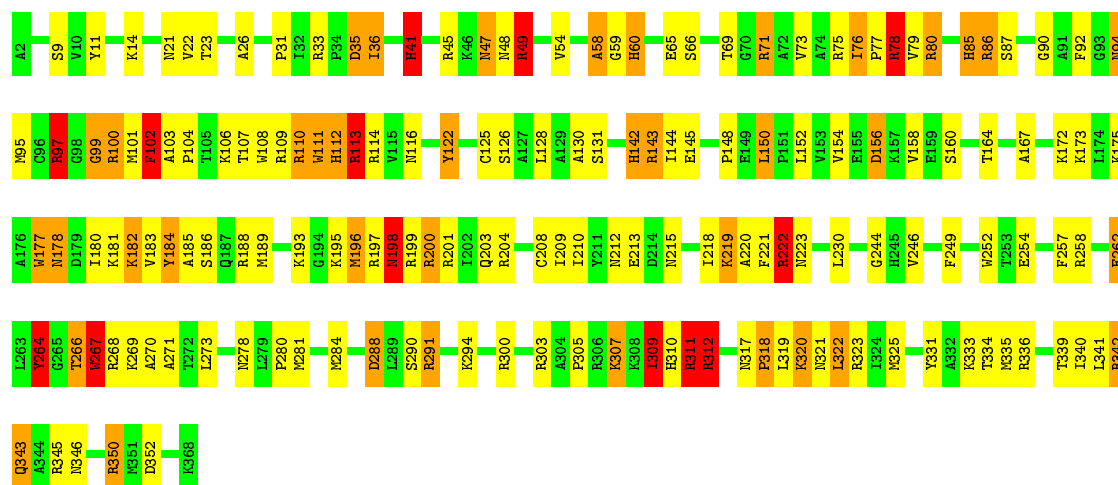
Chain B:





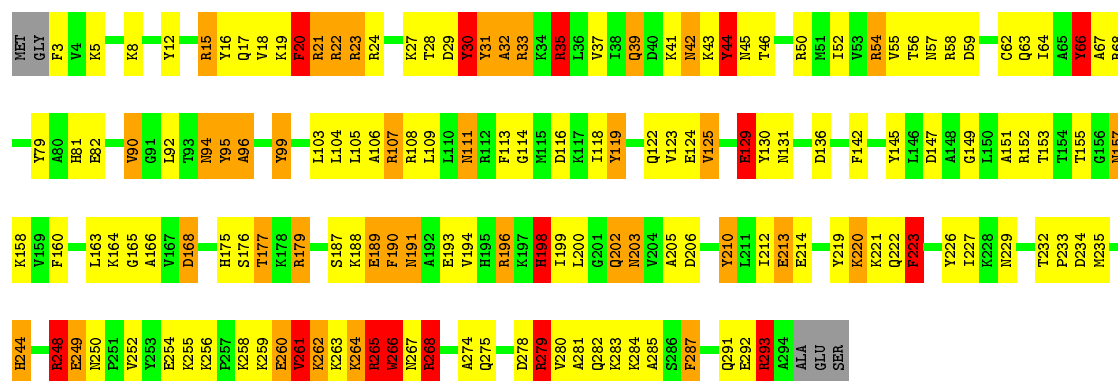
• Molecule 6: Ribosomal protein uL4

Chain C: 55% 31% 11%



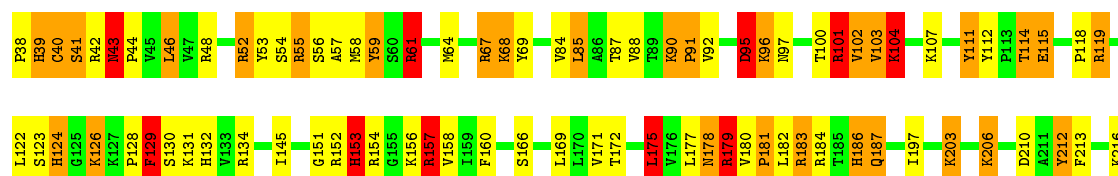
• Molecule 7: Ribosomal protein uL18

Chain D: 45% 35% 13% 5%



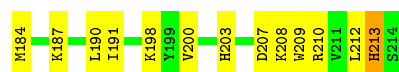
• Molecule 8: Ribosomal protein eL6

Chain E: 47% 27% 19% 6%

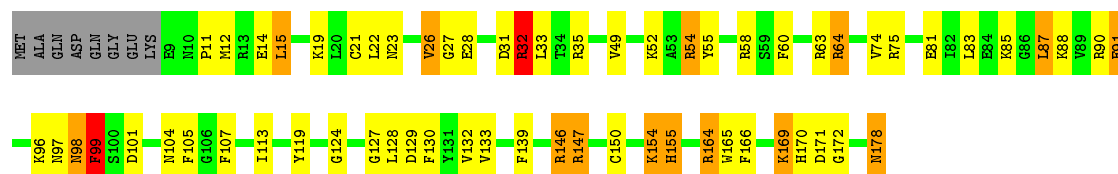




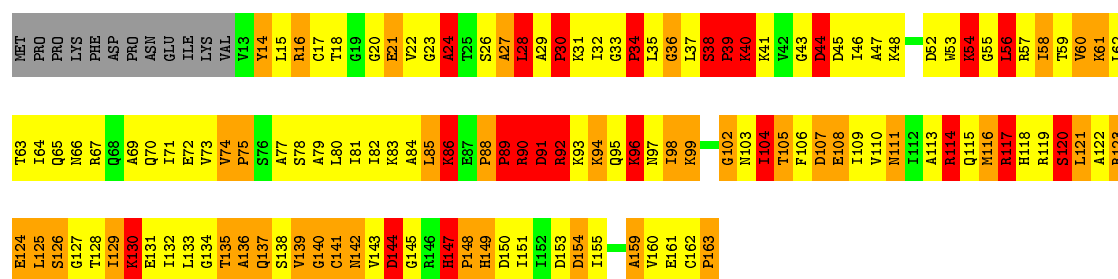




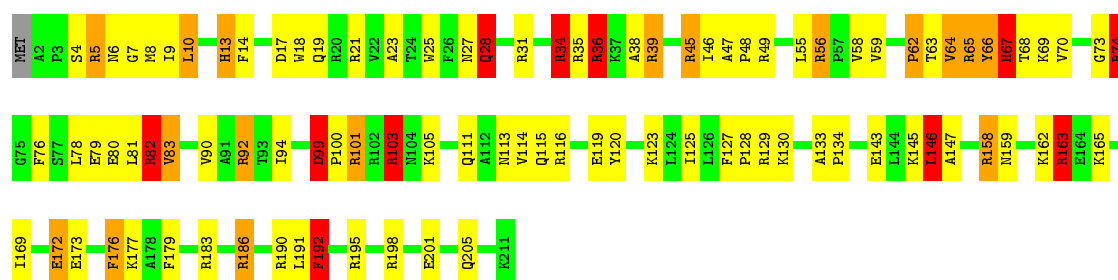
• Molecule 13: Ribosomal protein uL5



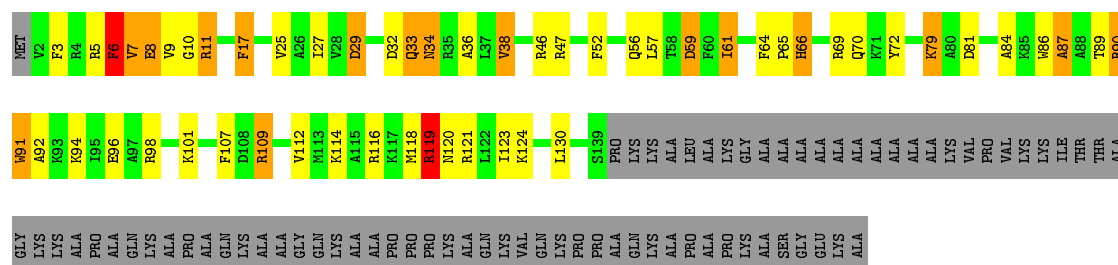
• Molecule 14: Ribosomal protein uL11



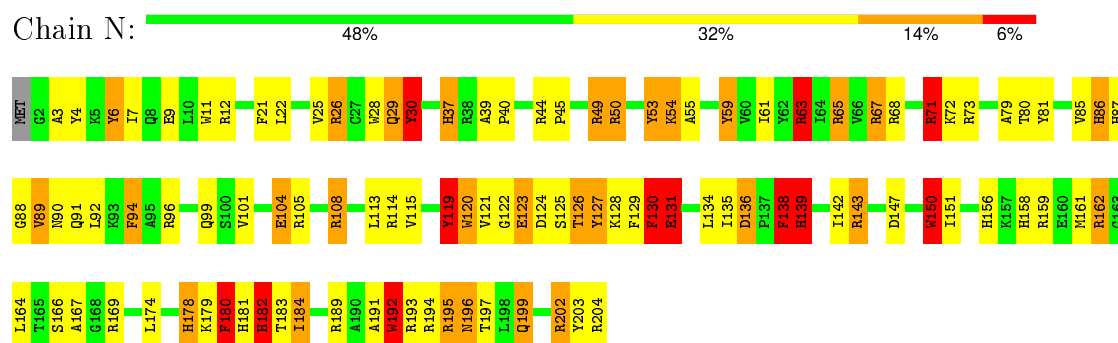
• Molecule 15: Ribosomal protein eL13



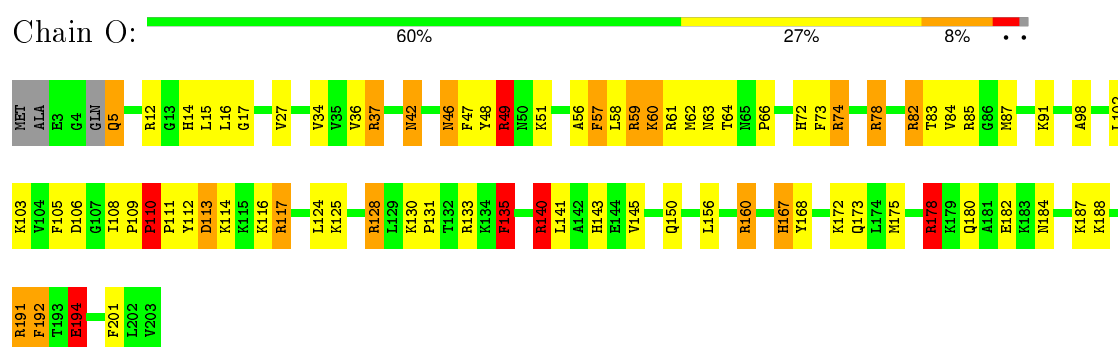
• Molecule 16: Ribosomal protein eL14



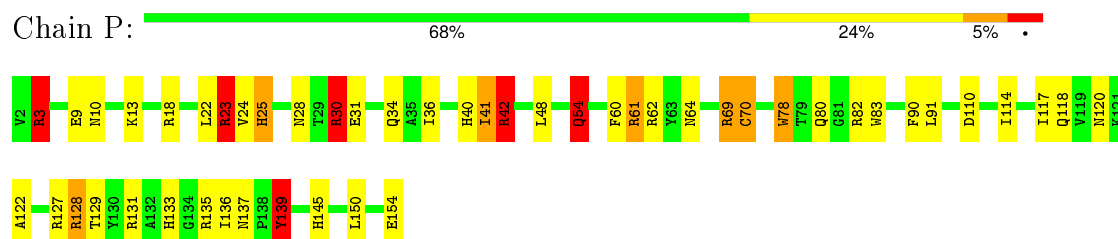
- Molecule 17: Ribosomal protein eL15



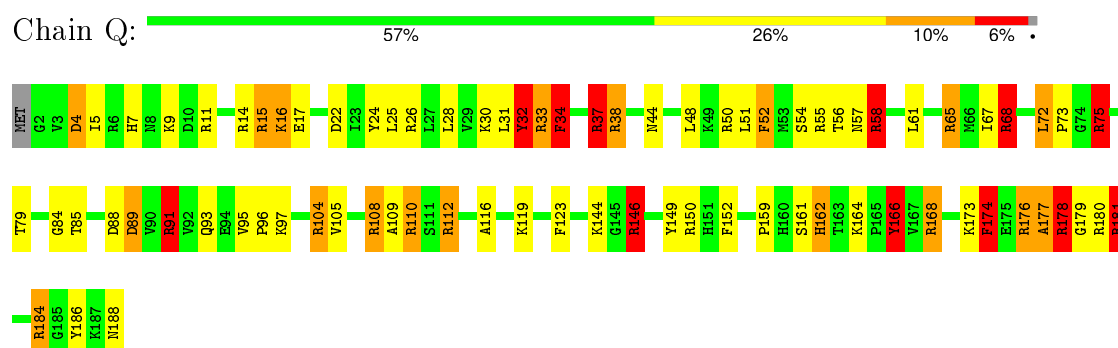
- Molecule 18: Ribosomal protein uL13



- Molecule 19: Ribosomal protein uL22

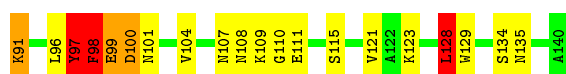


- Molecule 20: Ribosomal protein eL18



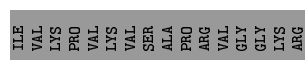
- Molecule 21: Ribosomal protein eL19





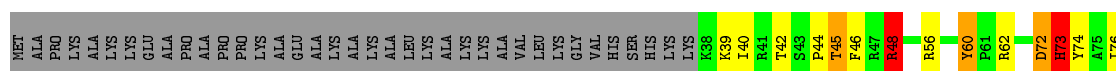
• Molecule 26: Ribosomal protein eL24

Chain W: 24% 10% 60%



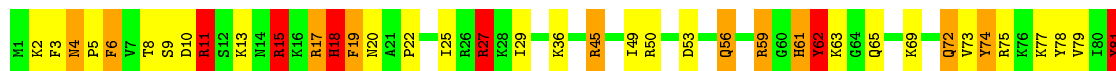
• Molecule 27: Ribosomal protein uL23

Chain X: 48% 20% 6% 24%



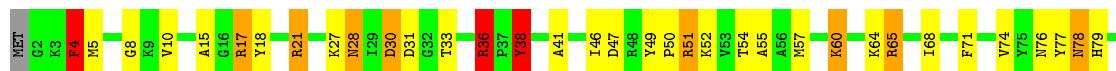
• Molecule 28: Ribosomal protein uL24

Chain Y: 52% 25% 10% 5% 8%



• Molecule 29: Ribosomal protein eL27

Chain Z: 55% 32% 10%

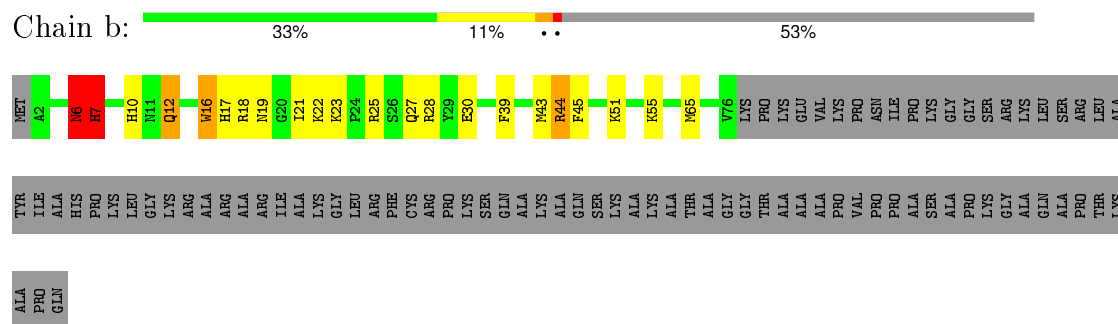


• Molecule 30: Ribosomal protein uL15

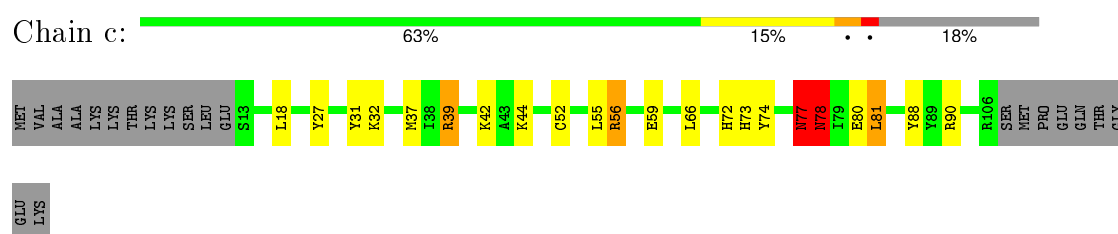
Chain a: 77% 17%



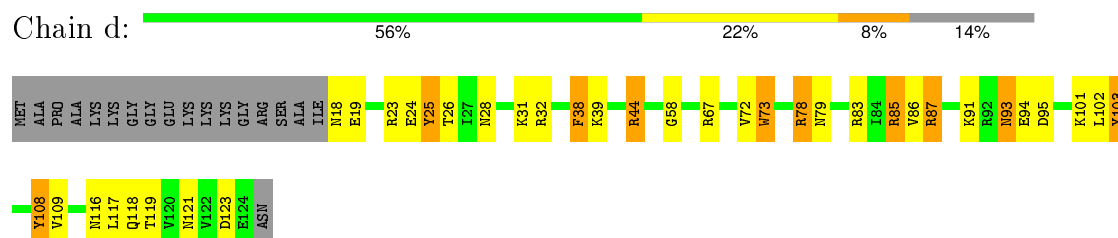
- Molecule 31: Ribosomal protein eL29



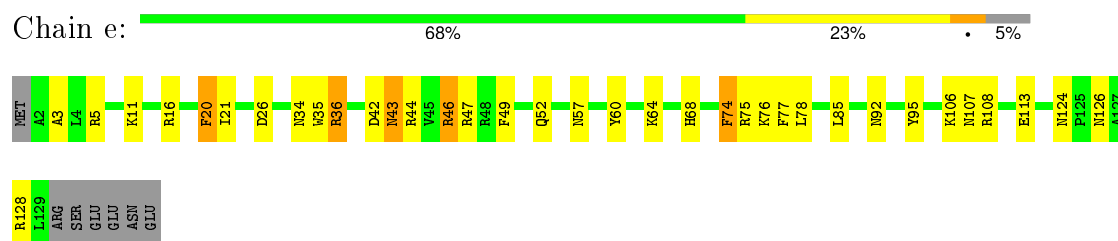
- Molecule 32: Ribosomal protein eL30



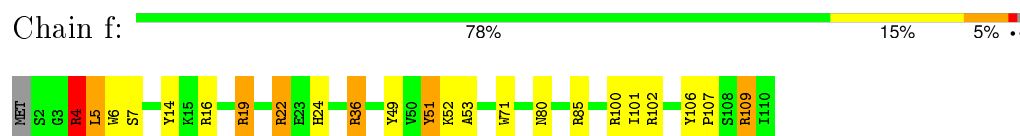
- Molecule 33: Ribosomal protein eL31




- Molecule 34: Ribosomal protein eL32



- Molecule 35: Ribosomal protein eL33




- Molecule 36: Ribosomal protein eL34

Chain g:  77% 19% ..



- Molecule 37: Ribosomal protein uL29

Chain h:  80% 12% 6% ..



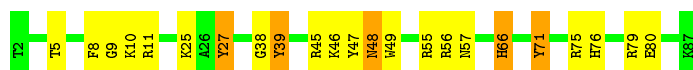
- Molecule 38: Ribosomal protein eL36

Chain i:  76% 17% ..



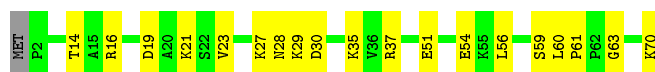
- Molecule 39: Ribosomal protein eL37

Chain j:  73% 21% 6% ..



- Molecule 40: Ribosomal protein eL38

Chain k:  71% 27% ..



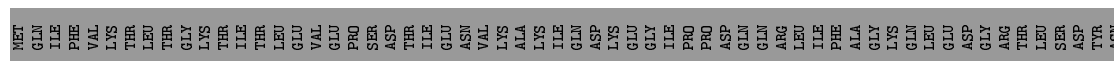
- Molecule 41: Ribosomal protein eL39

Chain l:  76% 18% ..



- Molecule 42: Ribosomal protein eL40

Chain m:  30% 10% 59%



- Molecule 43: Ribosomal protein eL41

Chain n: 




- Molecule 44: Ribosomal protein eL42

Chain o: 



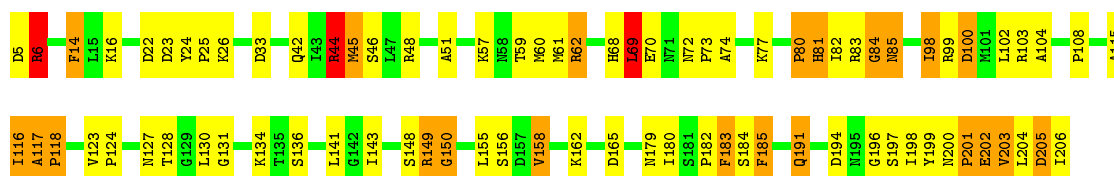
- Molecule 45: Ribosomal protein eL43

Chain p: 



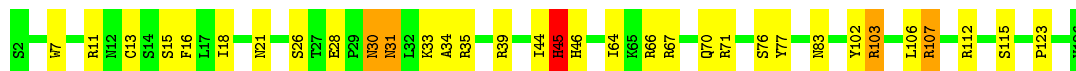
- Molecule 46: Ribosomal protein uL10

Chain q: 



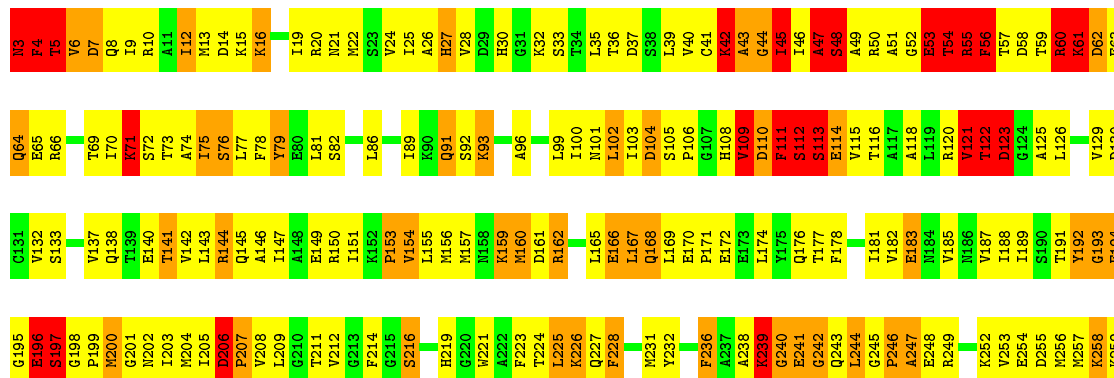
- Molecule 47: Ribosomal protein eL28

Chain r: 

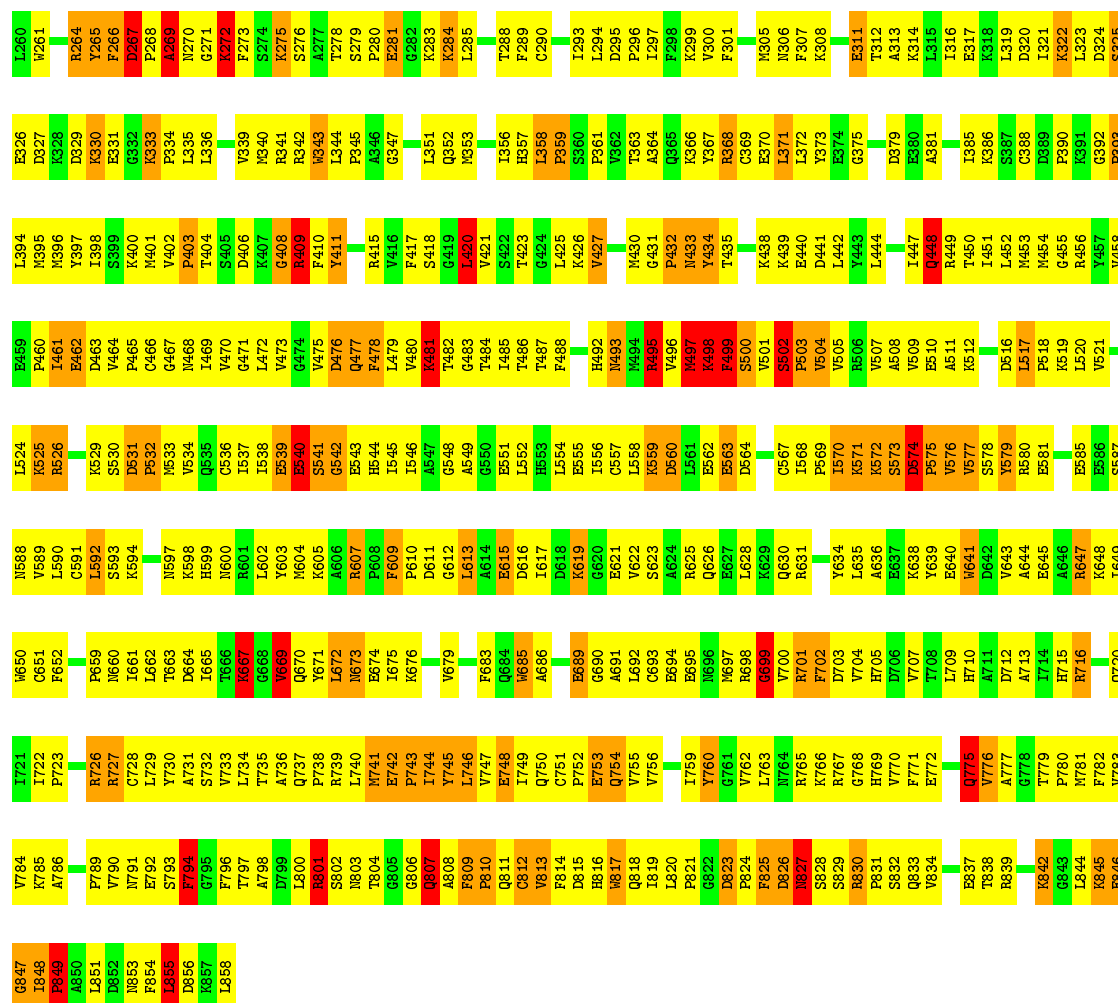


- Molecule 48: Eukaryotic elongation factor 2

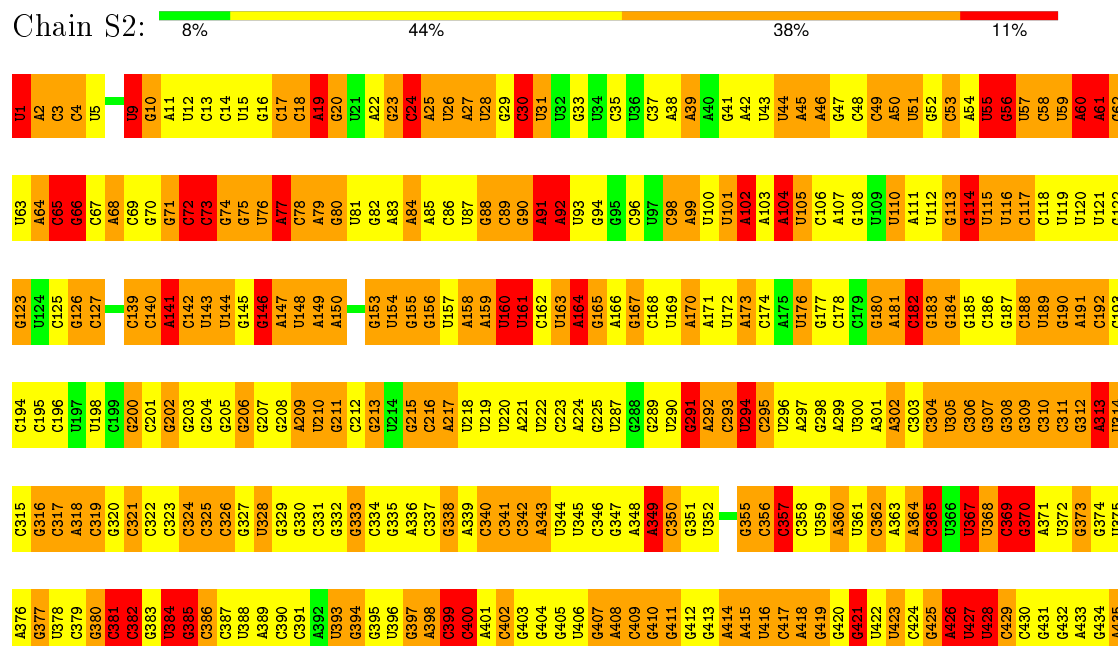
Chain 4: 



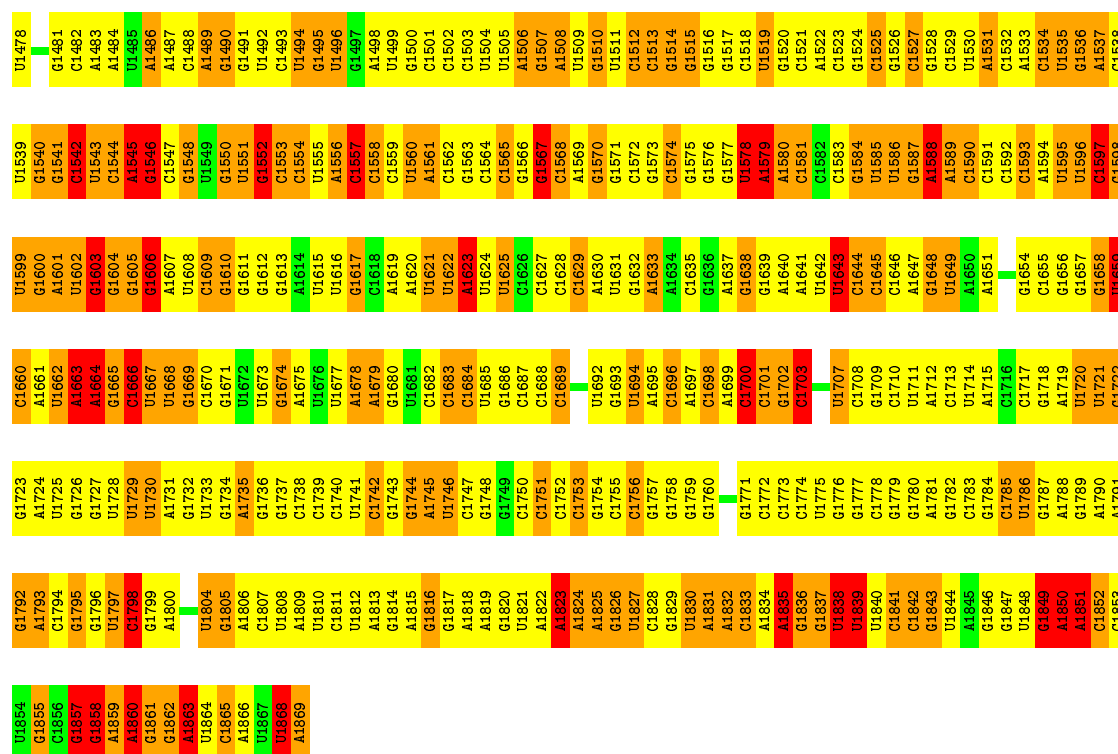




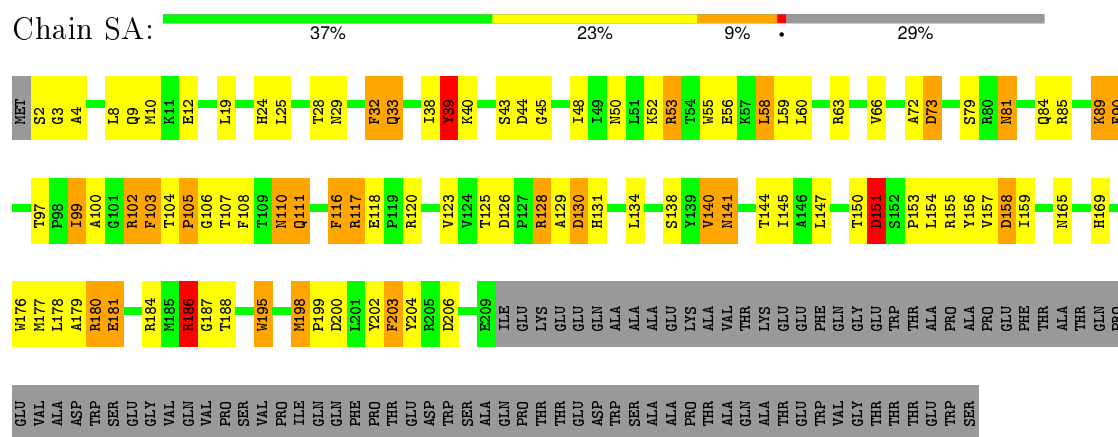
• Molecule 49: 18S ribosomal RNA



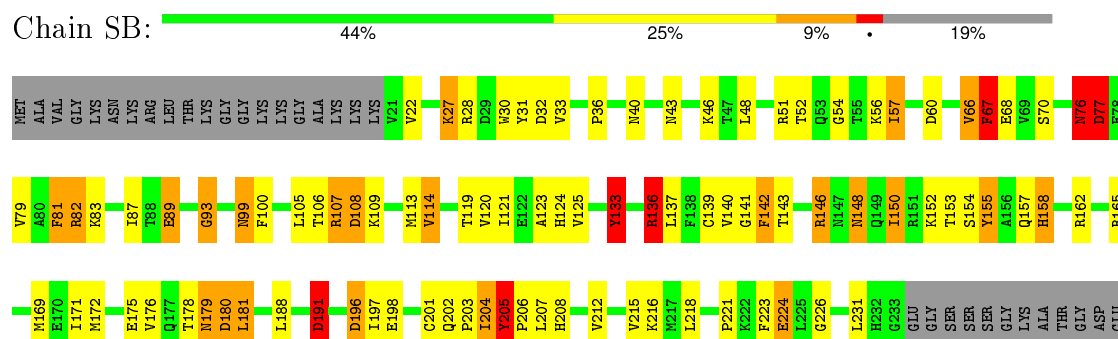


### • Molecule 50: Ribosomal protein uS2

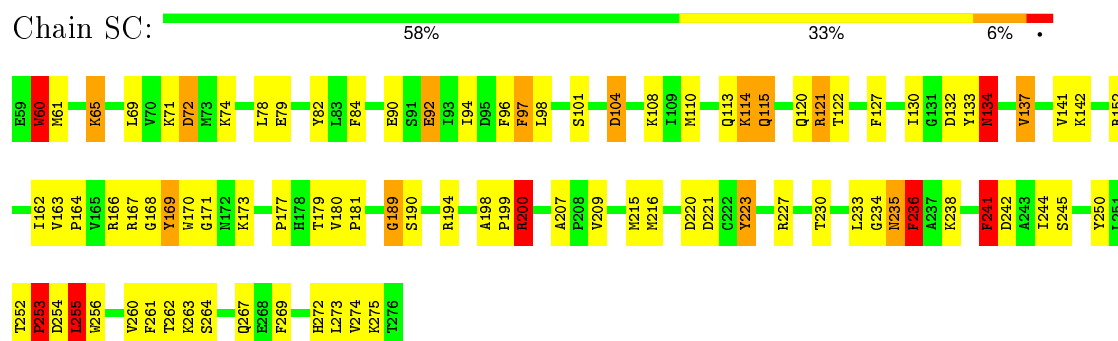


### • Molecule 51: Ribosomal protein eS1

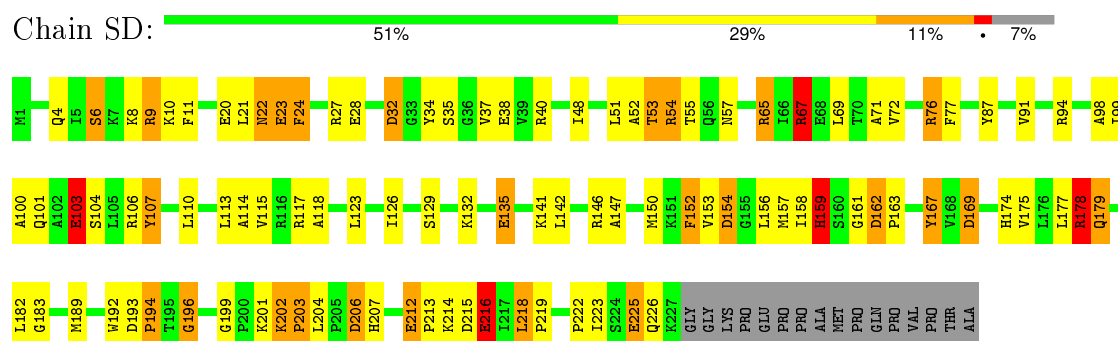


THR  
GLY  
ALA  
LYS  
VAL  
GLU  
ARG  
ALA  
ASP  
GLY  
TYR  
GLU  
PRO  
PRO  
VAL  
GLN  
GLU  
SER  
VAL

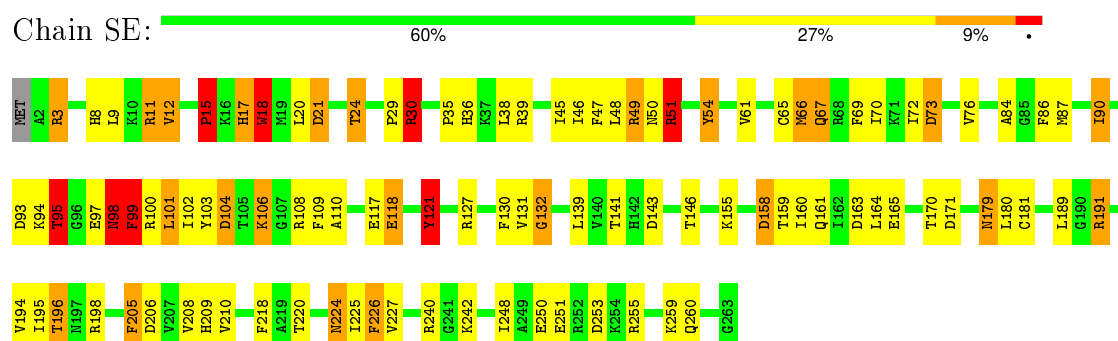
• Molecule 52: Ribosomal protein uS5



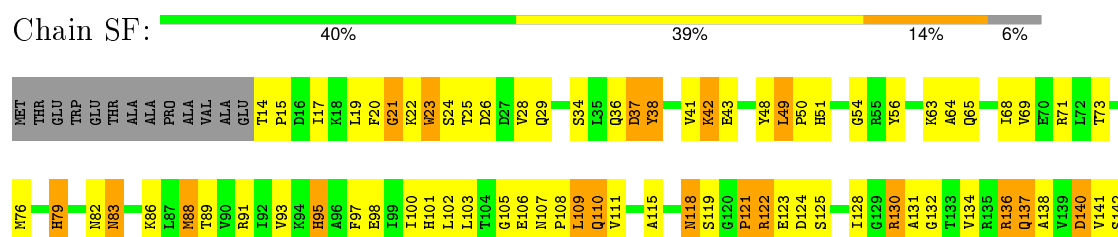
• Molecule 53: Ribosomal protein uS3



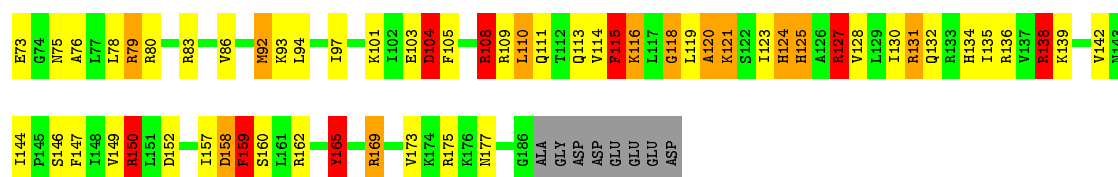
• Molecule 54: Ribosomal protein eS4



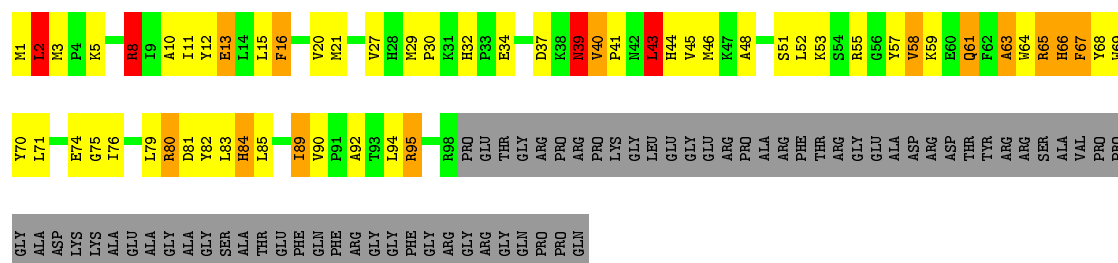
• Molecule 55: Ribosomal protein uS7



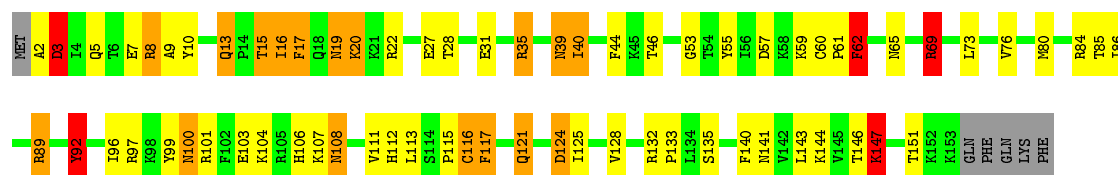




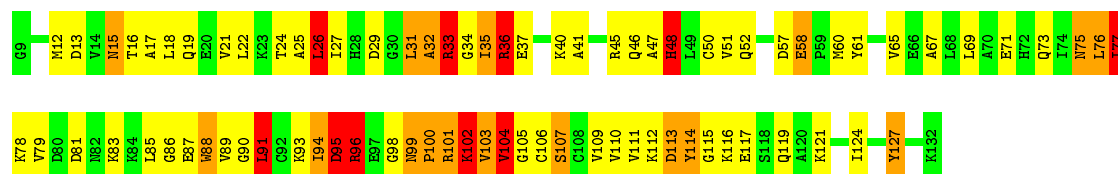
- Molecule 60: Ribosomal protein eS10



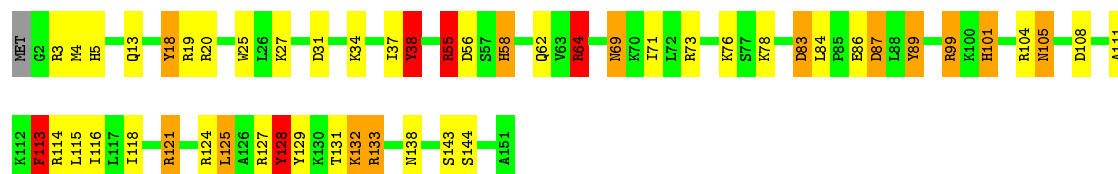
- Molecule 61: Ribosomal protein uS17



- Molecule 62: Ribosomal protein eS12

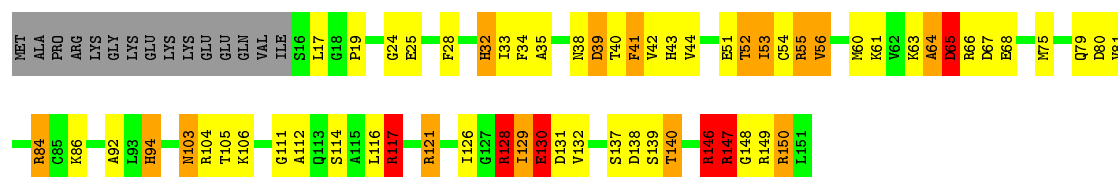


- Molecule 63: Ribosomal protein uS15

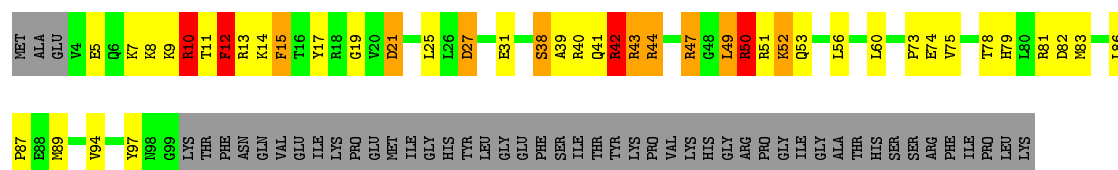


- Molecule 64: Ribosomal protein uS11

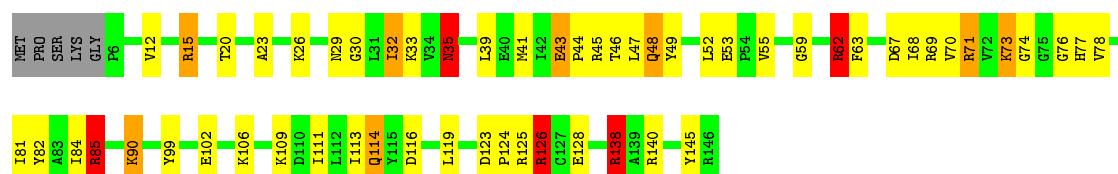




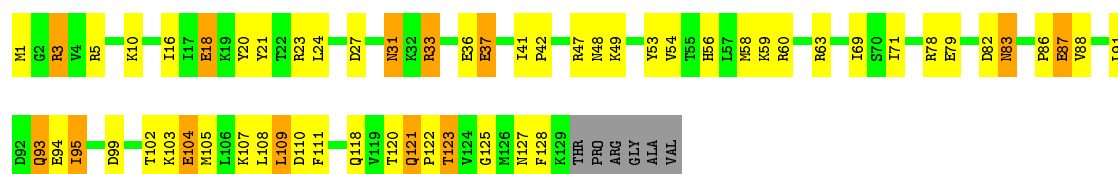
• Molecule 65: Ribosomal protein uS19



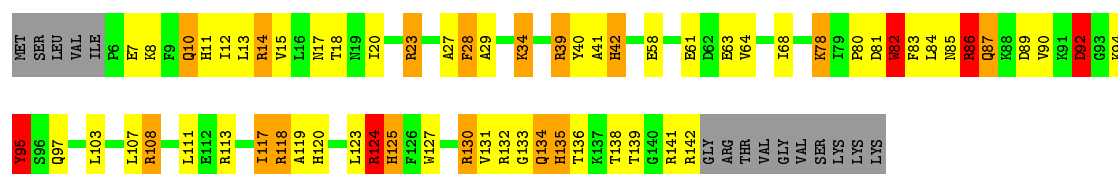
• Molecule 66: Ribosomal protein uS9



• Molecule 67: Ribosomal protein eS17

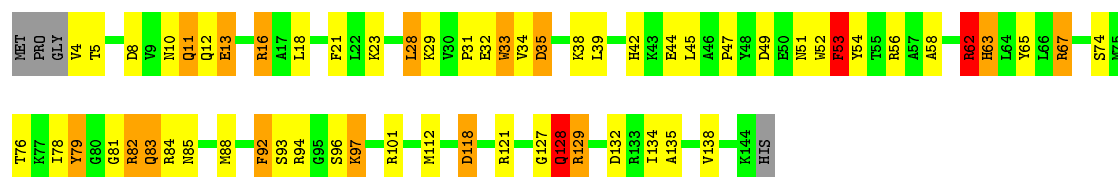


• Molecule 68: Ribosomal protein uS13

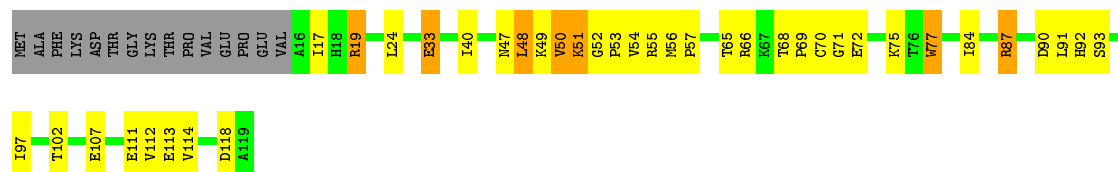


• Molecule 69: Ribosomal protein eS19

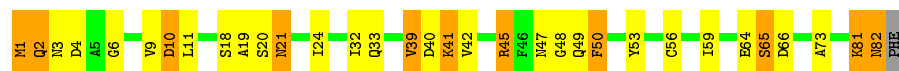




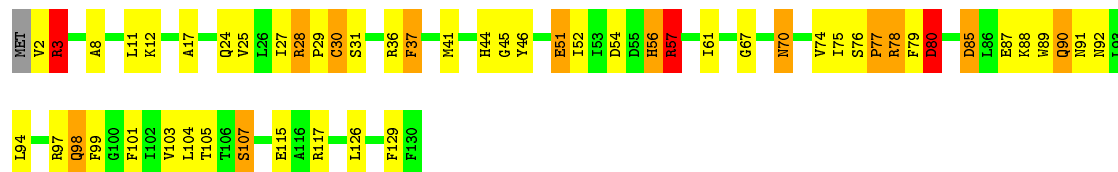
- Molecule 70: Ribosomal protein uS10



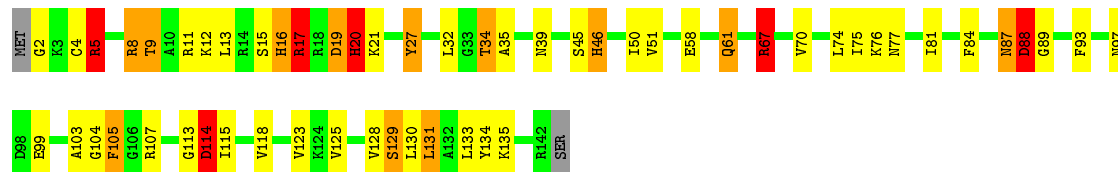
- Molecule 71: Ribosomal protein eS21



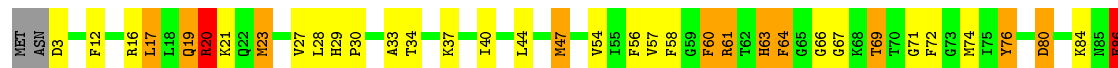
- Molecule 72: Ribosomal protein uS8



- Molecule 73: Ribosomal protein uS12



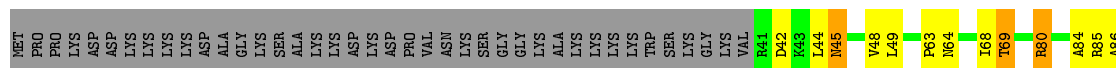
- Molecule 74: Ribosomal protein eS24



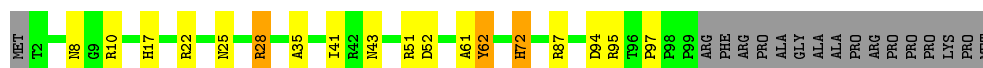




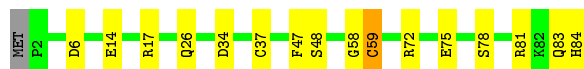
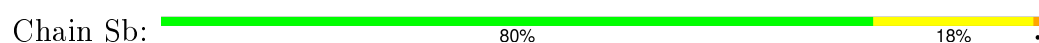
- Molecule 75: Ribosomal protein es25



- Molecule 76: Ribosomal protein eS26



- Molecule 77: Ribosomal protein eS27



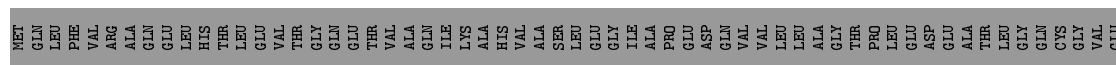
- Molecule 78: Ribosomal protein eS28



- Molecule 79: Ribosomal protein uS14



- Molecule 80: Ribosomal protein eS30



- Molecule 81: Ribosomal protein eS31



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	36667	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	27	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	5	0.64	75/87792 (0.1%)	1.12	729/136945 (0.5%)
10	G	0.76	4/1966 (0.2%)	1.09	14/2645 (0.5%)
11	H	0.77	3/1537 (0.2%)	1.17	10/2066 (0.5%)
12	I	0.66	1/1753 (0.1%)	1.11	12/2343 (0.5%)
13	J	0.63	1/1382 (0.1%)	1.04	12/1849 (0.6%)
14	K	1.04	11/1154 (1.0%)	1.78	54/1555 (3.5%)
15	L	0.70	2/1734 (0.1%)	1.12	15/2318 (0.6%)
16	M	0.76	2/1152 (0.2%)	1.11	5/1539 (0.3%)
17	N	0.84	4/1746 (0.2%)	1.33	23/2338 (1.0%)
18	O	0.72	3/1684 (0.2%)	1.10	12/2251 (0.5%)
19	P	0.74	2/1268 (0.2%)	1.10	9/1701 (0.5%)
2	7	0.54	1/2858 (0.0%)	0.96	9/4455 (0.2%)
20	Q	0.69	0/1530	1.35	31/2041 (1.5%)
21	R	0.79	3/1524 (0.2%)	1.27	20/2013 (1.0%)
22	S	0.95	8/1493 (0.5%)	1.30	19/2002 (0.9%)
23	T	0.67	1/1326 (0.1%)	1.04	7/1770 (0.4%)
24	U	0.63	1/822 (0.1%)	1.03	3/1103 (0.3%)
25	V	0.89	4/993 (0.4%)	1.11	7/1332 (0.5%)
26	W	0.71	0/541	1.23	5/720 (0.7%)
27	X	0.64	0/993	1.09	10/1334 (0.7%)
28	Y	0.72	0/1132	1.24	19/1504 (1.3%)
29	Z	0.63	0/1130	1.11	10/1507 (0.7%)
3	8	0.68	3/3701 (0.1%)	1.19	42/5766 (0.7%)
30	a	0.93	6/1192 (0.5%)	1.37	17/1591 (1.1%)
31	b	0.88	2/620 (0.3%)	1.17	5/819 (0.6%)
32	c	0.70	0/742	1.14	5/996 (0.5%)
33	d	0.84	3/903 (0.3%)	1.37	16/1216 (1.3%)
34	e	0.90	3/1071 (0.3%)	1.23	15/1429 (1.0%)
35	f	1.01	2/895 (0.2%)	1.34	17/1198 (1.4%)
36	g	0.65	0/916	1.08	5/1220 (0.4%)
37	h	0.63	0/1023	1.21	14/1350 (1.0%)
38	i	0.63	0/843	1.20	8/1115 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
39	j	0.97	1/721 (0.1%)	1.43	11/953 (1.2%)
4	A	0.80	3/1906 (0.2%)	1.26	21/2556 (0.8%)
40	k	0.59	0/575	0.97	1/761 (0.1%)
41	l	0.70	0/454	1.14	4/599 (0.7%)
42	m	0.55	0/435	0.95	1/575 (0.2%)
43	n	0.49	0/223	1.01	0/284
44	o	0.64	0/864	1.27	8/1140 (0.7%)
45	p	0.64	1/718 (0.1%)	1.01	3/953 (0.3%)
46	q	0.81	7/1580 (0.4%)	1.35	37/2133 (1.7%)
47	r	0.68	0/1017	1.12	8/1365 (0.6%)
48	4	0.99	20/6804 (0.3%)	1.41	93/9189 (1.0%)
49	S2	0.65	37/41243 (0.1%)	1.14	330/64257 (0.5%)
5	B	0.81	8/3214 (0.2%)	1.16	25/4308 (0.6%)
50	SA	0.94	4/1679 (0.2%)	1.06	6/2283 (0.3%)
51	SB	0.89	6/1753 (0.3%)	1.15	14/2350 (0.6%)
52	SC	0.99	8/1726 (0.5%)	1.11	9/2332 (0.4%)
53	SD	1.39	12/1793 (0.7%)	1.10	9/2414 (0.4%)
54	SE	0.83	8/2118 (0.4%)	0.98	7/2849 (0.2%)
55	SF	0.74	1/1531 (0.1%)	1.08	9/2059 (0.4%)
56	SG	0.97	9/1946 (0.5%)	1.03	9/2590 (0.3%)
57	SH	0.73	2/1544 (0.1%)	1.02	8/2068 (0.4%)
58	SI	0.97	8/1715 (0.5%)	1.12	12/2287 (0.5%)
59	SJ	1.07	12/1550 (0.8%)	1.28	16/2069 (0.8%)
6	C	0.73	3/2973 (0.1%)	1.12	18/3990 (0.5%)
60	SK	0.75	1/851 (0.1%)	1.00	3/1147 (0.3%)
61	SL	0.85	5/1259 (0.4%)	1.09	7/1684 (0.4%)
62	SM	2.22	2/970 (0.2%)	1.21	8/1300 (0.6%)
63	SN	0.82	4/1232 (0.3%)	1.15	10/1656 (0.6%)
64	SO	1.18	7/1029 (0.7%)	1.38	12/1380 (0.9%)
65	SP	1.52	6/816 (0.7%)	1.29	8/1084 (0.7%)
66	SQ	0.72	2/1142 (0.2%)	1.01	8/1528 (0.5%)
67	SR	0.81	5/1060 (0.5%)	1.02	2/1421 (0.1%)
68	SS	0.66	1/1157 (0.1%)	1.18	13/1548 (0.8%)
69	ST	0.67	2/1119 (0.2%)	1.08	7/1499 (0.5%)
7	D	0.73	2/2426 (0.1%)	1.23	26/3252 (0.8%)
70	SU	0.94	4/828 (0.5%)	0.96	1/1112 (0.1%)
71	SV	0.73	0/631	0.97	0/844
72	SW	1.06	6/1051 (0.6%)	1.22	5/1406 (0.4%)
73	SX	0.99	6/1118 (0.5%)	1.12	12/1493 (0.8%)
74	SY	1.63	5/1040 (0.5%)	1.11	9/1382 (0.7%)
75	SZ	0.56	0/604	0.87	0/810
76	Sa	0.81	1/794 (0.1%)	1.25	5/1065 (0.5%)
77	Sb	0.59	0/665	0.90	0/891

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
78	Sc	0.68	0/508	1.13	4/680 (0.6%)
79	Sd	0.79	0/445	1.12	1/589 (0.2%)
8	E	0.73	5/1941 (0.3%)	1.21	20/2601 (0.8%)
80	Se	0.72	1/458 (0.2%)	1.16	5/602 (0.8%)
81	Sf	1.08	6/593 (1.0%)	1.57	12/786 (1.5%)
82	Sg	0.80	11/2493 (0.4%)	0.89	8/3394 (0.2%)
9	F	0.80	2/1905 (0.1%)	1.27	27/2539 (1.1%)
All	All	0.75	379/237633 (0.2%)	1.15	2051/348088 (0.6%)

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
1	5	0	154
10	G	0	3
11	H	0	3
12	I	0	4
13	J	0	2
14	K	0	5
15	L	0	5
16	M	0	4
17	N	0	11
18	O	0	3
19	P	0	1
2	7	0	2
20	Q	0	5
21	R	0	6
22	S	0	11
23	T	0	2
24	U	0	2
25	V	0	3
26	W	0	1
27	X	0	1
28	Y	0	4
3	8	0	11
30	a	0	9
31	b	0	1
32	c	0	2
33	d	0	4
34	e	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
35	f	0	2
36	g	0	1
37	h	0	3
38	i	0	3
39	j	0	4
4	A	0	6
40	k	0	1
44	o	0	6
45	p	0	1
46	q	0	7
47	r	0	5
48	4	0	40
49	S2	1	66
5	B	0	13
50	SA	0	2
51	SB	0	4
52	SC	0	4
53	SD	0	3
54	SE	0	2
55	SF	0	1
57	SH	0	1
58	SI	0	6
59	SJ	0	2
6	C	0	5
60	SK	0	1
61	SL	0	4
62	SM	0	3
63	SN	0	1
64	SO	0	1
65	SP	0	1
66	SQ	0	1
67	SR	0	2
7	D	0	8
70	SU	0	1
71	SV	0	2
72	SW	0	2
73	SX	0	2
74	SY	0	1
75	SZ	0	1
76	Sa	0	1
77	Sb	0	1
79	Sd	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
8	E	0	12
81	Sf	0	4
9	F	0	5
All	All	1	507

The worst 5 of 379 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	SM	58	GLU	CD-OE1	64.43	1.96	1.25
53	SD	216	GLU	CD-OE1	43.67	1.73	1.25
1	5	1823	G	O3'-P	41.55	2.11	1.61
74	SY	86	GLU	CD-OE2	39.60	1.69	1.25
65	SP	21	ASP	CG-OD1	30.90	1.96	1.25

The worst 5 of 2051 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	4	699	GLY	CA-C-N	-32.10	46.58	117.20
48	4	699	GLY	C-N-CA	-28.33	50.88	121.70
48	4	768	GLY	O-C-N	21.39	156.93	122.70
72	SW	117	ARG	NE-CZ-NH2	-20.64	109.98	120.30
46	q	205	ASP	CA-C-N	-20.22	72.71	117.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
49	S2	1109	C	C1'

5 of 507 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	5	22	G	Sidechain
1	5	31	U	Sidechain
1	5	42	A	Sidechain
1	5	43	U	Sidechain
1	5	53	C	Sidechain

## 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	5	78486	0	39660	10326	0
2	7	2558	0	1296	309	0
3	8	3314	0	1683	481	0
4	A	1868	0	1959	159	0
5	B	3147	0	3280	216	0
6	C	2919	0	3100	160	0
7	D	2380	0	2412	174	0
8	E	1904	0	2055	132	0
9	F	1870	0	1996	174	0
10	G	1934	0	2086	132	0
11	H	1518	0	1601	87	0
12	I	1713	0	1752	106	0
13	J	1359	0	1389	73	0
14	K	1140	0	1189	583	0
15	L	1703	0	1818	75	0
16	M	1131	0	1209	68	0
17	N	1701	0	1749	118	0
18	O	1651	0	1786	87	0
19	P	1242	0	1269	54	0
20	Q	1506	0	1623	80	0
21	R	1508	0	1664	104	0
22	S	1454	0	1496	121	0
23	T	1298	0	1366	75	0
24	U	808	0	831	25	0
25	V	979	0	1039	53	0
26	W	528	0	541	52	0
27	X	976	0	1053	37	0
28	Y	1115	0	1205	62	0
29	Z	1107	0	1182	49	0
30	a	1163	0	1211	0	0
31	b	610	0	650	0	0
32	c	732	0	769	0	0
33	d	888	0	930	0	0
34	e	1053	0	1147	0	0
35	f	876	0	912	0	0
36	g	906	0	1002	0	0
37	h	1015	0	1149	0	0
38	i	832	0	917	0	0
39	j	706	0	743	0	0
40	k	569	0	637	0	0
41	l	444	0	483	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	m	429	0	466	0	0
43	n	222	0	261	0	0
44	o	851	0	922	0	0
45	p	708	0	760	0	0
46	q	1556	0	1604	0	0
47	r	1001	0	1062	0	0
48	4	6673	0	6737	2045	0
49	S2	36900	0	18598	5189	0
50	SA	1642	0	1646	99	0
51	SB	1725	0	1797	76	0
52	SC	1690	0	1777	66	0
53	SD	1765	0	1865	95	0
54	SE	2076	0	2177	74	0
55	SF	1509	0	1563	61	0
56	SG	1923	0	2089	97	0
57	SH	1521	0	1616	90	0
58	SI	1686	0	1772	102	0
59	SJ	1525	0	1640	95	0
60	SK	827	0	854	50	0
61	SL	1238	0	1315	57	0
62	SM	960	0	989	108	0
63	SN	1208	0	1294	55	0
64	SO	1016	0	1039	58	0
65	SP	805	0	861	25	0
66	SQ	1124	0	1193	47	0
67	SR	1047	0	1103	43	0
68	SS	1139	0	1191	76	0
69	ST	1101	0	1135	69	0
70	SU	818	0	883	25	0
71	SV	625	0	628	19	0
72	SW	1034	0	1080	48	0
73	SX	1099	0	1166	64	0
74	SY	1023	0	1090	54	0
75	SZ	598	0	656	16	0
76	Sa	781	0	830	0	0
77	Sb	651	0	672	0	0
78	Sc	506	0	536	0	0
79	Sd	434	0	427	0	0
80	Se	452	0	494	0	0
81	Sf	581	0	599	0	0
82	Sg	2436	0	2393	0	0
83	Sa	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	j	1	0	0	0	0
83	m	1	0	0	0	0
83	o	1	0	0	0	0
84	4	1	0	0	0	0
84	5	118	0	0	0	0
84	7	5	0	0	0	0
84	8	4	0	0	0	0
84	P	1	0	0	0	0
84	S2	36	0	0	0	0
84	V	1	0	0	0	0
All	All	221686	0	166619	21521	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 61.

The worst 5 of 21521 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)
48:4:753:GLU:HA	48:4:782:PHE:CE1	1.25	1.71
48:4:236:PHE:CE2	48:4:273:PHE:CZ	1.79	1.71
10:G:261:LEU:CD2	10:G:264:LYS:HE2	1.21	1.66
1:5:4413:C:H4'	12:I:157:PHE:CE2	1.13	1.65
48:4:751:CYS:CB	48:4:755:VAL:HB	1.23	1.64

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	
4	A	242/257 (94%)	203 (84%)	30 (12%)	9 (4%)	4	36
5	B	392/394 (100%)	319 (81%)	40 (10%)	33 (8%)	1	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	C	365/367 (100%)	304 (83%)	46 (13%)	15 (4%)	3	33
7	D	290/297 (98%)	235 (81%)	33 (11%)	22 (8%)	1	15
8	E	232/236 (98%)	150 (65%)	51 (22%)	31 (13%)	0	5
9	F	223/225 (99%)	190 (85%)	23 (10%)	10 (4%)	3	30
10	G	239/266 (90%)	200 (84%)	32 (13%)	7 (3%)	6	42
11	H	188/192 (98%)	164 (87%)	20 (11%)	4 (2%)	9	50
12	I	211/213 (99%)	166 (79%)	31 (15%)	14 (7%)	1	19
13	J	168/178 (94%)	137 (82%)	23 (14%)	8 (5%)	3	28
14	K	147/163 (90%)	83 (56%)	31 (21%)	33 (22%)	0	1
15	L	208/211 (99%)	172 (83%)	25 (12%)	11 (5%)	2	25
16	M	136/213 (64%)	118 (87%)	16 (12%)	2 (2%)	13	56
17	N	201/204 (98%)	172 (86%)	23 (11%)	6 (3%)	5	42
18	O	199/204 (98%)	182 (92%)	14 (7%)	3 (2%)	13	56
19	P	151/153 (99%)	140 (93%)	9 (6%)	2 (1%)	15	60
20	Q	185/188 (98%)	160 (86%)	20 (11%)	5 (3%)	6	44
21	R	178/196 (91%)	153 (86%)	21 (12%)	4 (2%)	8	49
22	S	173/224 (77%)	146 (84%)	24 (14%)	3 (2%)	11	54
23	T	157/160 (98%)	128 (82%)	26 (17%)	3 (2%)	10	51
24	U	97/128 (76%)	74 (76%)	21 (22%)	2 (2%)	9	50
25	V	129/140 (92%)	112 (87%)	14 (11%)	3 (2%)	8	48
26	W	61/157 (39%)	57 (93%)	3 (5%)	1 (2%)	12	55
27	X	117/156 (75%)	108 (92%)	7 (6%)	2 (2%)	11	54
28	Y	132/145 (91%)	112 (85%)	14 (11%)	6 (4%)	3	30
29	Z	133/136 (98%)	113 (85%)	15 (11%)	5 (4%)	4	35
30	a	145/148 (98%)	111 (77%)	26 (18%)	8 (6%)	2	24
31	b	73/160 (46%)	58 (80%)	11 (15%)	4 (6%)	2	24
32	c	92/115 (80%)	78 (85%)	10 (11%)	4 (4%)	3	31
33	d	105/125 (84%)	85 (81%)	16 (15%)	4 (4%)	4	35
34	e	126/135 (93%)	110 (87%)	15 (12%)	1 (1%)	24	70
35	f	107/110 (97%)	95 (89%)	7 (6%)	5 (5%)	3	29
36	g	112/117 (96%)	103 (92%)	7 (6%)	2 (2%)	11	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	h	120/123 (98%)	102 (85%)	15 (12%)	3 (2%)	7	46
38	i	100/105 (95%)	91 (91%)	7 (7%)	2 (2%)	9	51
39	j	84/86 (98%)	67 (80%)	13 (16%)	4 (5%)	3	28
40	k	67/70 (96%)	55 (82%)	7 (10%)	5 (8%)	1	15
41	l	48/51 (94%)	42 (88%)	4 (8%)	2 (4%)	3	32
42	m	50/128 (39%)	44 (88%)	6 (12%)	0	100	100
43	n	21/25 (84%)	21 (100%)	0	0	100	100
44	o	102/106 (96%)	85 (83%)	11 (11%)	6 (6%)	2	22
45	p	89/91 (98%)	79 (89%)	9 (10%)	1 (1%)	17	63
46	q	200/202 (99%)	133 (66%)	27 (14%)	40 (20%)	0	1
47	r	123/125 (98%)	97 (79%)	20 (16%)	6 (5%)	3	27
48	4	854/856 (100%)	754 (88%)	58 (7%)	42 (5%)	3	27
50	SA	206/295 (70%)	176 (85%)	24 (12%)	6 (3%)	6	42
51	SB	211/264 (80%)	170 (81%)	27 (13%)	14 (7%)	1	19
52	SC	216/218 (99%)	189 (88%)	19 (9%)	8 (4%)	4	36
53	SD	225/243 (93%)	170 (76%)	44 (20%)	11 (5%)	3	27
54	SE	260/263 (99%)	202 (78%)	41 (16%)	17 (6%)	1	20
55	SF	189/204 (93%)	160 (85%)	19 (10%)	10 (5%)	2	25
56	SG	235/249 (94%)	194 (83%)	35 (15%)	6 (3%)	7	45
57	SH	187/194 (96%)	143 (76%)	29 (16%)	15 (8%)	1	13
58	SI	204/208 (98%)	176 (86%)	21 (10%)	7 (3%)	5	39
59	SJ	183/194 (94%)	145 (79%)	24 (13%)	14 (8%)	1	14
60	SK	96/165 (58%)	60 (62%)	26 (27%)	10 (10%)	1	8
61	SL	150/158 (95%)	122 (81%)	21 (14%)	7 (5%)	3	29
62	SM	122/124 (98%)	77 (63%)	25 (20%)	20 (16%)	0	3
63	SN	148/151 (98%)	115 (78%)	28 (19%)	5 (3%)	5	39
64	SO	134/151 (89%)	102 (76%)	18 (13%)	14 (10%)	1	8
65	SP	94/145 (65%)	65 (69%)	18 (19%)	11 (12%)	0	7
66	SQ	139/146 (95%)	112 (81%)	21 (15%)	6 (4%)	3	31
67	SR	127/135 (94%)	95 (75%)	24 (19%)	8 (6%)	2	21
68	SS	135/152 (89%)	104 (77%)	23 (17%)	8 (6%)	2	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	ST	139/145 (96%)	116 (84%)	17 (12%)	6 (4%)	3	31
70	SU	102/119 (86%)	80 (78%)	18 (18%)	4 (4%)	4	34
71	SV	80/83 (96%)	63 (79%)	10 (12%)	7 (9%)	1	12
72	SW	127/130 (98%)	112 (88%)	11 (9%)	4 (3%)	5	41
73	SX	139/143 (97%)	116 (84%)	18 (13%)	5 (4%)	4	37
74	SY	124/132 (94%)	92 (74%)	23 (18%)	9 (7%)	1	16
75	SZ	73/125 (58%)	54 (74%)	13 (18%)	6 (8%)	1	13
76	Sa	96/115 (84%)	74 (77%)	15 (16%)	7 (7%)	1	16
77	Sb	81/84 (96%)	61 (75%)	15 (18%)	5 (6%)	2	21
78	Sc	62/69 (90%)	46 (74%)	16 (26%)	0	100	100
79	Sd	50/56 (89%)	38 (76%)	9 (18%)	3 (6%)	2	21
80	Se	55/133 (41%)	40 (73%)	14 (26%)	1 (2%)	11	53
81	Sf	69/156 (44%)	39 (56%)	21 (30%)	9 (13%)	0	5
82	Sg	311/317 (98%)	250 (80%)	45 (14%)	16 (5%)	2	26
All	All	12341/13747 (90%)	10066 (82%)	1613 (13%)	662 (5%)	4	25

5 of 662 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	19	HIS
4	A	197	PRO
5	B	16	PHE
5	B	40	PRO
5	B	108	GLU

### 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	
4	A	187/199 (94%)	139 (74%)	48 (26%)	0	4
5	B	335/335 (100%)	265 (79%)	70 (21%)	1	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	C	305/305 (100%)	239 (78%)	66 (22%)	1	7
7	D	246/250 (98%)	178 (72%)	68 (28%)	0	3
8	E	209/209 (100%)	158 (76%)	51 (24%)	1	5
9	F	194/194 (100%)	145 (75%)	49 (25%)	1	4
10	G	206/226 (91%)	158 (77%)	48 (23%)	1	5
11	H	169/171 (99%)	125 (74%)	44 (26%)	0	4
12	I	180/180 (100%)	135 (75%)	45 (25%)	1	4
13	J	143/149 (96%)	115 (80%)	28 (20%)	1	9
14	K	124/136 (91%)	98 (79%)	26 (21%)	1	8
15	L	176/177 (99%)	135 (77%)	41 (23%)	1	5
16	M	116/160 (72%)	95 (82%)	21 (18%)	2	12
17	N	171/172 (99%)	129 (75%)	42 (25%)	1	5
18	O	172/174 (99%)	146 (85%)	26 (15%)	3	21
19	P	134/134 (100%)	112 (84%)	22 (16%)	3	17
20	Q	163/164 (99%)	132 (81%)	31 (19%)	2	10
21	R	159/175 (91%)	120 (76%)	39 (24%)	1	5
22	S	156/192 (81%)	121 (78%)	35 (22%)	1	6
23	T	139/140 (99%)	112 (81%)	27 (19%)	2	10
24	U	89/114 (78%)	67 (75%)	22 (25%)	1	5
25	V	101/107 (94%)	77 (76%)	24 (24%)	1	5
26	W	55/126 (44%)	42 (76%)	13 (24%)	1	5
27	X	107/133 (80%)	89 (83%)	18 (17%)	2	15
28	Y	124/135 (92%)	96 (77%)	28 (23%)	1	6
29	Z	117/118 (99%)	94 (80%)	23 (20%)	1	9
30	a	119/120 (99%)	102 (86%)	17 (14%)	4	24
31	b	63/123 (51%)	45 (71%)	18 (29%)	0	3
32	c	79/97 (81%)	60 (76%)	19 (24%)	1	5
33	d	98/110 (89%)	66 (67%)	32 (33%)	0	2
34	e	114/121 (94%)	89 (78%)	25 (22%)	1	7
35	f	88/89 (99%)	73 (83%)	15 (17%)	2	15
36	g	98/100 (98%)	79 (81%)	19 (19%)	2	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	h	109/110 (99%)	92 (84%)	17 (16%)	3	20
38	i	86/89 (97%)	71 (83%)	15 (17%)	2	14
39	j	73/73 (100%)	60 (82%)	13 (18%)	2	13
40	k	64/65 (98%)	52 (81%)	12 (19%)	2	11
41	l	47/48 (98%)	39 (83%)	8 (17%)	2	15
42	m	48/116 (41%)	34 (71%)	14 (29%)	0	3
43	n	22/24 (92%)	17 (77%)	5 (23%)	1	6
44	o	92/94 (98%)	70 (76%)	22 (24%)	1	5
45	p	74/74 (100%)	61 (82%)	13 (18%)	2	13
46	q	170/170 (100%)	133 (78%)	37 (22%)	1	7
47	r	109/109 (100%)	86 (79%)	23 (21%)	1	8
48	4	728/728 (100%)	586 (80%)	142 (20%)	2	10
50	SA	174/245 (71%)	141 (81%)	33 (19%)	2	10
51	SB	194/231 (84%)	164 (84%)	30 (16%)	3	20
52	SC	184/184 (100%)	148 (80%)	36 (20%)	1	9
53	SD	190/202 (94%)	163 (86%)	27 (14%)	4	24
54	SE	224/225 (100%)	180 (80%)	44 (20%)	1	9
55	SF	161/170 (95%)	128 (80%)	33 (20%)	1	8
56	SG	207/218 (95%)	171 (83%)	36 (17%)	2	14
57	SH	169/174 (97%)	149 (88%)	20 (12%)	6	31
58	SI	178/180 (99%)	148 (83%)	30 (17%)	2	15
59	SJ	161/168 (96%)	128 (80%)	33 (20%)	1	8
60	SK	89/136 (65%)	68 (76%)	21 (24%)	1	5
61	SL	136/142 (96%)	116 (85%)	20 (15%)	4	22
62	SM	104/104 (100%)	76 (73%)	28 (27%)	0	4
63	SN	130/131 (99%)	101 (78%)	29 (22%)	1	6
64	SO	106/119 (89%)	83 (78%)	23 (22%)	1	7
65	SP	88/130 (68%)	73 (83%)	15 (17%)	2	15
66	SQ	117/121 (97%)	100 (86%)	17 (14%)	4	23
67	SR	117/121 (97%)	102 (87%)	15 (13%)	5	28
68	SS	119/132 (90%)	97 (82%)	22 (18%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	ST	112/115 (97%)	89 (80%)	23 (20%)	1	8
70	SU	94/107 (88%)	84 (89%)	10 (11%)	8	38
71	SV	66/67 (98%)	53 (80%)	13 (20%)	1	9
72	SW	112/113 (99%)	93 (83%)	19 (17%)	2	15
73	SX	113/115 (98%)	97 (86%)	16 (14%)	4	24
74	SY	108/114 (95%)	86 (80%)	22 (20%)	1	8
75	SZ	66/103 (64%)	55 (83%)	11 (17%)	3	16
76	Sa	85/98 (87%)	76 (89%)	9 (11%)	8	38
77	Sb	75/76 (99%)	64 (85%)	11 (15%)	4	22
78	Sc	57/62 (92%)	43 (75%)	14 (25%)	1	5
79	Sd	45/48 (94%)	35 (78%)	10 (22%)	1	6
80	Se	46/105 (44%)	35 (76%)	11 (24%)	1	5
81	Sf	64/140 (46%)	45 (70%)	19 (30%)	0	3
82	Sg	272/275 (99%)	242 (89%)	30 (11%)	8	36
All	All	10721/11706 (92%)	8570 (80%)	2151 (20%)	4	9

5 of 2151 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	b	7	HIS
44	o	99	ARG
72	SW	56	HIS
32	c	66	LEU
36	g	66	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 296 such sidechains are listed below:

Mol	Chain	Res	Type
30	a	66	ASN
42	m	109	ASN
72	SW	82	GLN
31	b	12	GLN
34	e	126	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3647/3664 (99%)	1616 (44%)	621 (17%)
2	7	119/120 (99%)	31 (26%)	9 (7%)
3	8	155/156 (99%)	61 (39%)	22 (14%)
49	S2	1717/1742 (98%)	745 (43%)	269 (15%)
All	All	5638/5682 (99%)	2453 (43%)	921 (16%)

5 of 2453 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	5	A
1	5	6	C
1	5	8	U
1	5	12	A

5 of 921 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	3593	C
1	5	4297	G
49	S2	1429	G
1	5	3667	C
1	5	4075	U

## 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](#)

Of 170 ligands modelled in this entry, 170 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.