



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 02:53 AM UTC

PDB ID : 6S13 / pdb_00006s13
EMDB ID : EMD-10079
Title : Erythromycin Resistant Staphylococcus aureus 70S ribosome (delta R88 A89 uL22).
Authors : Halfon, Y.; Matozv, D.; Eyal, Z.; Bashan, A.; Zimmerman, E.; Kjeldgaard, J.; Ingmer, H.; Yonath, A.
Deposited on : 2019-06-18
Resolution : 3.58 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

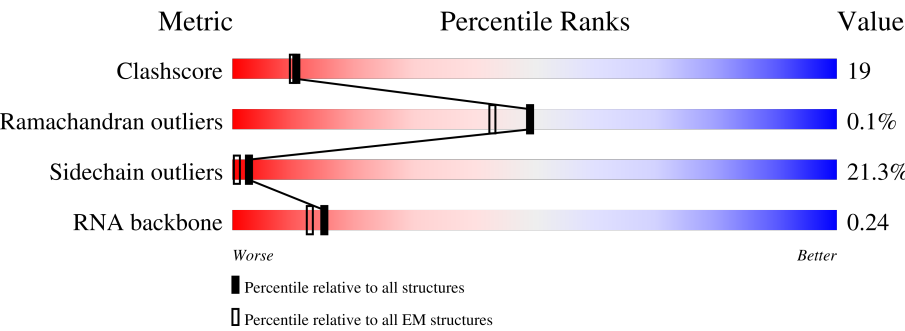
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.58 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2905	35% 35%42%23%
2	B	115	18% 37%42%22%
3	C	274	65% 49%40%11%
4	D	215	55% 60%33%7%
5	E	206	64% 49%42%9%
6	F	175	88% 45%46%9%
7	G	175	93% 62%31%7%

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Mol	Chain	Length	Quality of chain
8	H	145	
9	I	122	
10	J	146	
11	K	137	
12	L	120	
13	M	119	
14	N	114	
15	O	116	
16	P	102	
17	Q	110	
18	R	89	
19	S	103	
20	T	94	
21	U	82	
22	V	58	
23	W	67	
24	X	58	
25	Y	59	
26	Z	48	
27	1	47	
28	2	43	
29	3	64	
30	4	37	
31	a	1539	
32	b	226	

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Mol	Chain	Length	Quality of chain
33	c	202	
34	d	198	
35	e	156	
36	f	95	
37	g	152	
38	h	131	
39	i	127	
40	j	97	
41	k	114	
42	l	135	
43	m	104	
44	n	60	
45	o	88	
46	p	89	
47	q	80	
48	r	54	
49	s	80	
50	t	81	
51	u	52	
52	v	162	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 233957 atoms, of which 93218 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 23S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	2905	Total	C	H	N	O	P	0	0
			93564	27803	31287	11387	20182	2905		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	115	Total	C	H	N	O	P	0	0
			3685	1094	1240	436	801	114		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	274	Total	C	H	N	O	S	0	0
			4291	1301	2201	415	369	5		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	215	Total	C	H	N	O	S	0	0
			3294	1018	1667	299	305	5		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	206	Total	C	H	N	O	S	0	0
			3192	986	1620	288	296	2		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	175	Total	C	H	N	O	S	0	0
			2667	837	1342	227	255	6		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	175	Total	C	H	N	O	S	0	0
			2488	790	1225	239	231	3		

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	145	Total	C	H	N	O	S	0	0
			2277	714	1134	208	218	3		

- Molecule 9 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	122	Total	C	H	N	O	S	0	0
			1899	572	981	174	168	4		

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	146	Total	C	H	N	O	S	0	0
			2211	674	1125	214	197	1		

- Molecule 11 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	K	137	Total	C	H	N	O	S	0	0
			2194	689	1123	203	175	4		

- Molecule 12 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	L	120	Total	C	H	N	O	S	0	0
			1915	576	983	182	173	1		

- Molecule 13 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	M	119	Total	C	H	N	O	S	0	0
			1816	557	925	174	159	1		

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	114	Total	C	H	N	O	0	0
			1826	563	937	175	151		

- Molecule 15 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	O	116	Total	C	H	N	O	S	0	0
			1956	593	1014	189	156	4		

- Molecule 16 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	P	102	Total	C	H	N	O	S	0	0
			1620	503	830	142	144	1		

- Molecule 17 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	Q	110	Total	C	H	N	O	S	0	0
			1724	523	887	158	153	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	?	-	ARG	deletion	UNP A0A077UKF9
Q	?	-	ALA	deletion	UNP A0A077UKF9

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	R	89	Total	C	H	N	O	S	0	0
			1463	453	748	127	131	4		

- Molecule 19 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	S	103	Total	C	H	N	O	S	0	0
			1579	486	809	142	141	1		

- Molecule 20 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	94	Total	C	H	N	O	0	0
			1488	463	766	130	129		

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	82	Total	C	H	N	O	0	0
			1265	385	643	122	115		

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	58	Total	C	H	N	O	0	0
			911	277	466	96	72		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	67	Total	C	H	N	O	0	0
			1104	333	563	102	106		

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	58	Total	C	H	N	O	0	0
			940	280	491	85	84		

- Molecule 25 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace	
25	Y	59	Total	C	H	N	O	S	0	0
			613	225	243	68	76	1		

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace	
26	Z	48	Total	C	H	N	O	S	0	0
			718	222	358	77	59	2		

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	1	47	Total	C	H	N	O	S	0	0
			784	238	394	78	70	4		

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	2	43	Total	C	H	N	O	S	0	0
			782	225	415	89	52	1		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	3	64	Total	C	H	N	O	S	0	0
			1107	324	586	113	82	2		

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	4	37	Total	C	H	N	O	S	0	0
			635	186	340	60	44	5		

- Molecule 31 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	a	1539	Total	C	H	N	O	P	0	0
			49563	14719	16594	6017	10694	1539		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	b	226	Total	C	H	N	O	S	0	0
			3705	1159	1886	317	335	8		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	c	202	Total	C	H	N	O	S	0	0
			2965	945	1464	284	271	1		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	d	198	Total	C	H	N	O	S	0	0
			2946	952	1449	275	268	2		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	e	156	Total	C	H	N	O	S	0	0
			2347	723	1202	211	209	2		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	f	95	Total	C	H	N	O	S	0	0
			1553	493	775	138	145	2		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	g	152	Total	C	H	N	O	S	0	0
			2326	722	1165	218	217	4		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	h	131	Total	C	H	N	O	S	0	0
			2103	650	1077	183	189	4		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	i	127	Total	C	H	N	O	S	0	0
			1812	576	890	179	166	1		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	j	97	Total	C	H	N	O	S	0	0
			1527	475	775	140	136	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	k	114	Total	C	H	N	O	S	0	0
			1594	498	784	151	159	2		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	l	135	Total	C	H	N	O	S	0	0
			2128	646	1091	211	178	2		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	m	104	Total	C	H	N	O	S	0	0
			1401	453	674	139	135			

- Molecule 44 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	n	60	Total	C	H	N	O	S	0	0
			979	307	492	98	77	5		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	o	88	Total	C	H	N	O	S	0	0
			1475	448	752	150	124	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	p	89	Total	C	H	N	O	S	0	0
			1403	436	709	128	129	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	q	80	Total	C	H	N	O	S	0	0
			1237	392	616	112	117			

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	r	54	Total	C	H	N	O	S	0	0
			927	284	482	86	73	2		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	s	80	Total	C	H	N	O	S	0	0
			1262	410	626	113	111	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	t	81	Total	C	H	N	O	S	0	0
			1207	358	616	117	115	1		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	52	Total	C	H	N	O		
			807	249	407	79	72	0	0

- Molecule 52 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	v	162	Total	C	H	N	O	S	0	0
			2682	835	1349	242	254	2		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	?	-	GLU	deletion	UNP W8USK0
v	?	-	VAL	deletion	UNP W8USK0
v	?	-	PHE	deletion	UNP W8USK0
v	?	-	VAL	deletion	UNP W8USK0
v	?	-	ALA	deletion	UNP W8USK0
v	?	-	GLU	deletion	UNP W8USK0
v	?	-	LEU	deletion	UNP W8USK0
v	?	-	GLN	deletion	UNP W8USK0
v	?	-	GLU	deletion	UNP W8USK0
v	?	-	MET	deletion	UNP W8USK0
v	?	-	GLN	deletion	UNP W8USK0
v	?	-	GLU	deletion	UNP W8USK0

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Chain	Residue	Modelled	Actual	Comment	Reference
v	?	-	THR	deletion	UNP W8USK0
v	?	-	GLN	deletion	UNP W8USK0
v	?	-	VAL	deletion	UNP W8USK0
v	?	-	ASP	deletion	UNP W8USK0
v	?	-	ASN	deletion	UNP W8USK0
v	?	-	ASP	deletion	UNP W8USK0
v	?	-	ALA	deletion	UNP W8USK0
v	?	-	TYR	deletion	UNP W8USK0
v	?	-	ASP	deletion	UNP W8USK0
v	?	-	ASP	deletion	UNP W8USK0
v	?	-	ASN	deletion	UNP W8USK0
v	?	-	GLU	deletion	UNP W8USK0

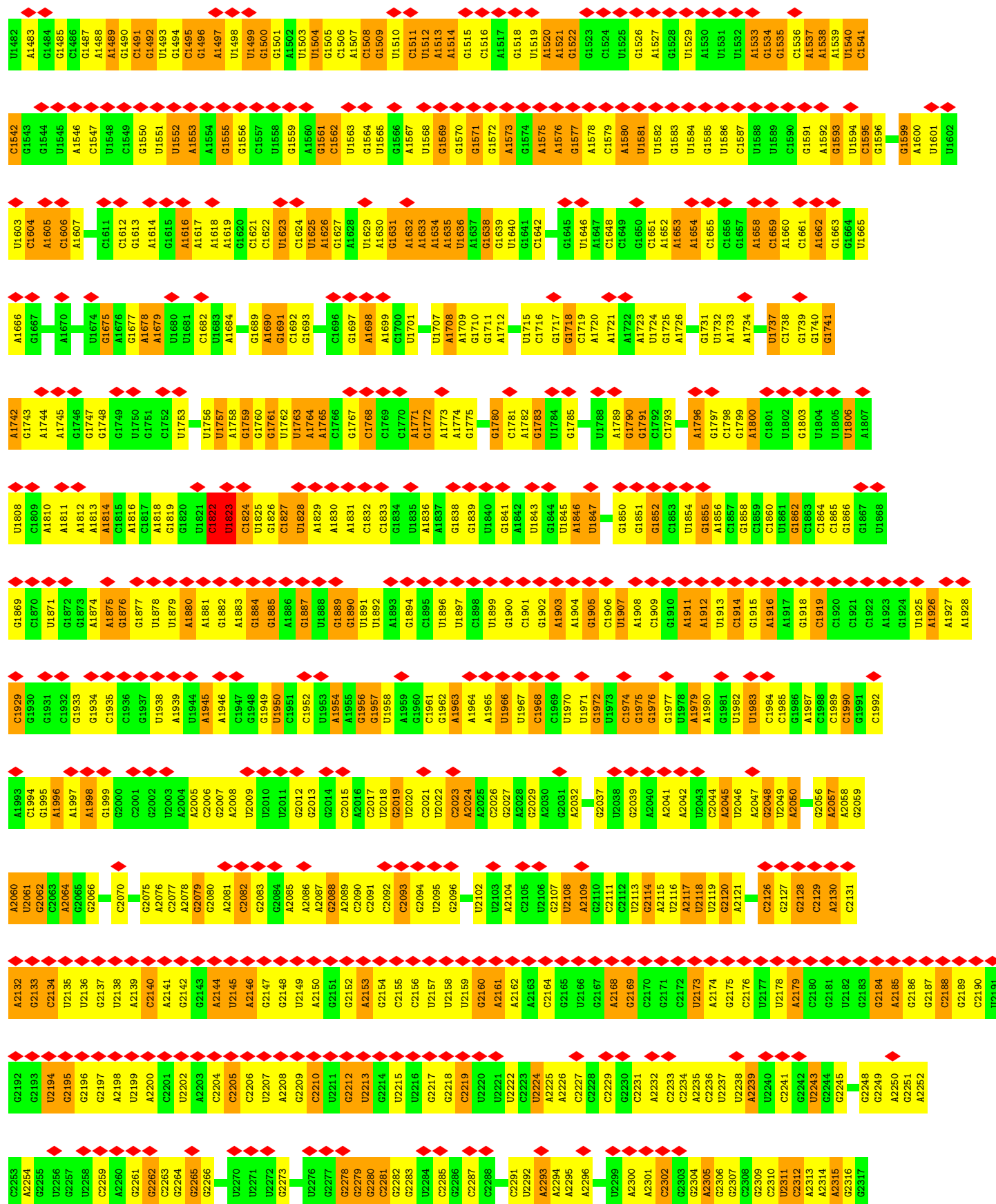
3 Residue-property plots

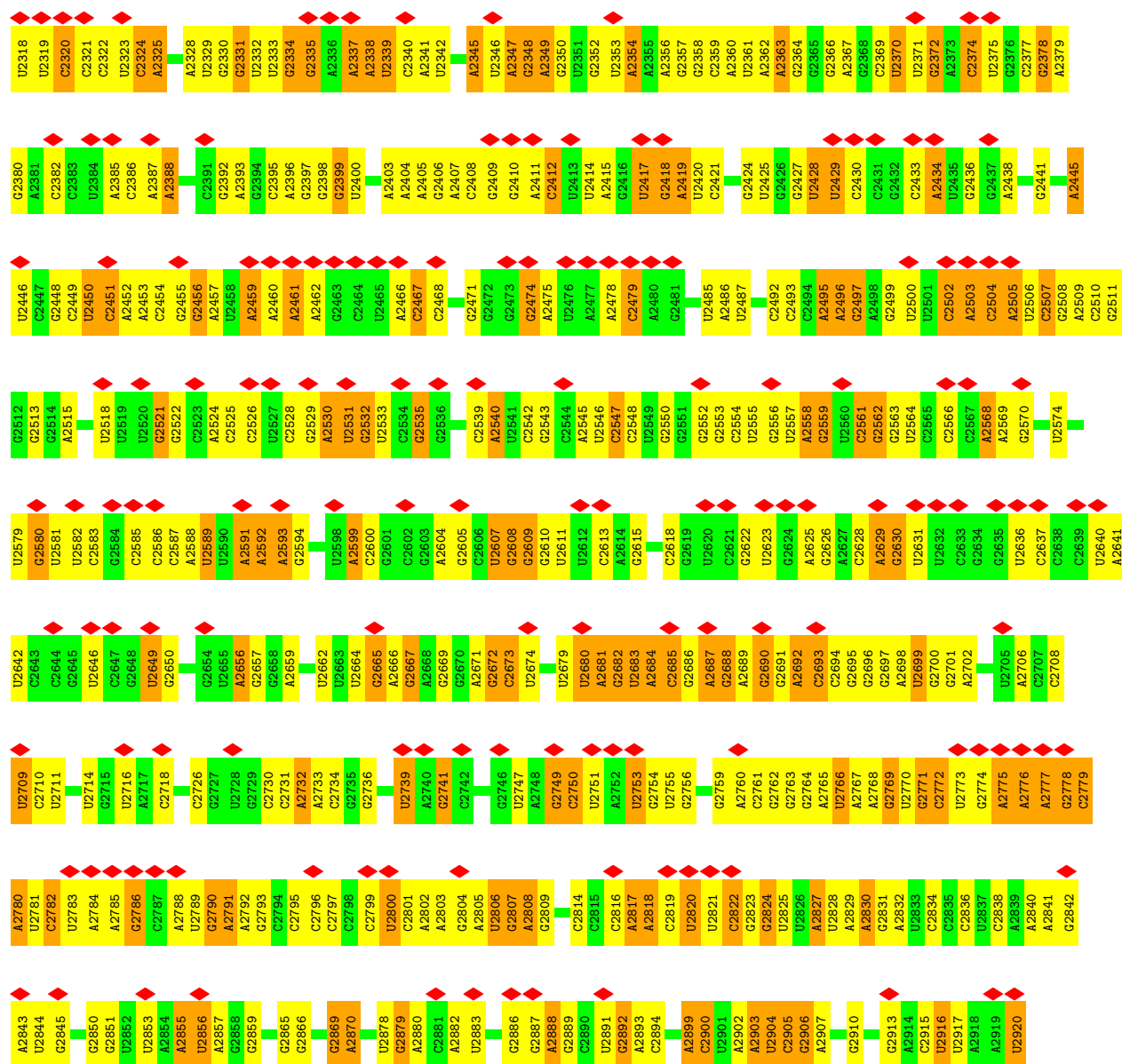
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 23S ribosomal RNA

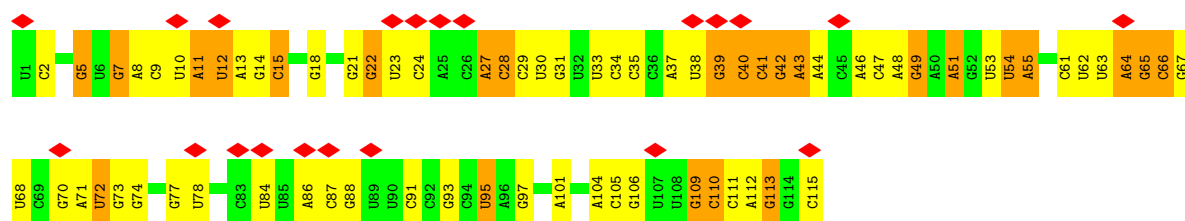


U1416	U1417	G1418	A1419	U1420	A1421	A1422	C1423	A1424	G1425	G1426	U1427	U1428	G1429	A1430	U1431	A1432	U1433	U1434	C1435	U1439	A1440	C1441	U1445	U1446	A1447	U1448	A1449	A1450	U1451	C1452	G1453	U1454	U1455	U1456	U1457	A1458	A1459	U1460	C1461	G1462	A1463	U1464	G1465	G1466	G1467	G1468	G1469	G1470	A1471	C1472	A1475	A1476	G1479	G1480	A1481			
U1350	C1351	C1352	A1353	G1354	A1355	G1356	C1357	A1358	A1359	G1360	G1361	C1362	U1363	U1366	G1369	C1370	U1371	C1372	G1375	G1376	U1377	U1378	A1379	G1380	U1381	C1382	G1383	A1384	G1385	U1386	C1387	C1388	U1389	A1390	A1391	G1392	C1393	U1394	G1395	A1396	C1400	G1401	A1402	C1403	A1404	G1405	G1406	C1407	U1408	U1409	G1412	G1413	G1414	A1415				
A1285	G1286	U1287	G1288	A1289	G1290	A1291	A1292	U1293	G1294	G1298	U1299	G1300	U1301	G1302	A1303	G1304	U1305	A1306	G1307	C1308	G1309	A1310	A1311	A1312	A1313	A1314	C1315	U1316	U1319	G1320	A1321	G1322	A1323	A1324	U1325	C1326	U1330	C1331	C1332	A1333	C1334	C1335	G1336	A1337	U1338	U1339	G1340	A1341	C1342	U1343	A1344	A1345	G1346	U1347	U1348	U1349		
U1212	C1213	C1214	U1215	U1216	U1217	G1218	G1219	A1220	C1221	A1222	A1223	U1224	G1225	U1226	U1227	A1228	G1229	U1230	G1234	C1235	G1236	U1237	U1238	C1239	U1240	A1241	A1242	G1243	G1244	G1245	U1248	U1249	G1250	G1253	A1258	G1261	U1262	A1263	A1264	G1265	A1267	U1270	G1271	G1274	A1275	G1276	C1277	A1282	A1284									
U1145	C1146	A1147	C1148	U1149	A1150	G1151	U1152	C1153	G1154	A1155	G1156	U1157	G1158	A1159	C1160	A1161	U1163	G1164	C1165	G1166	C1167	C1168	G1169	A1170	A1171	A1172	A1173	U1174	G1175	U1176	C1177	C1178	C1179	G1180	G1181	G1182	G1183	C1184	U1185	A1186	A1187	A1188	A1189	A1190	U1191	A1192	A1195	G1198	A1199	A1200	G1201	A1208	U1209	U1210	G1211			
U1085	G1086	C1087	C1088	C1089	A1090	G1091	A1092	C1093	A1094	A1095	C1096	U1097	A1098	G1099	G1100	A1101	U1102	G1103	U1105	G1106	G1107	C1108	U1109	U1110	A1111	G1112	A1113	A1114	G1115	C1116	A1117	G1118	C1119	A1120	A1121	U1122	C1123	U1125	U1126	U1127	A1128	A1129	A1130	G1131	A1132	G1133	U1134	G1135	C1136	G1137	U1138	A1139	U1140	U1141	A1142	G1143	C1144	
G1016	A1017	A1018	A1019	G1022	A1023	A1024	A1025	C1026	A1027	G1028	C1029	C1030	A1031	A1032	G1033	A1034	C1035	C1036	A1037	C1038	C1039	A1040	U1043	A1044	A1045	G1046	G1047	U1048	A1053	A1054	A1055	U1056	A1057	U1058	A1059	U1060	G1061	G1068	G1069	A1070	A1071	A1072	A1073	G1074	G1075	A1076	U1077	G1078	U1079	G1080	G1081	C1082	G1083	U1084				
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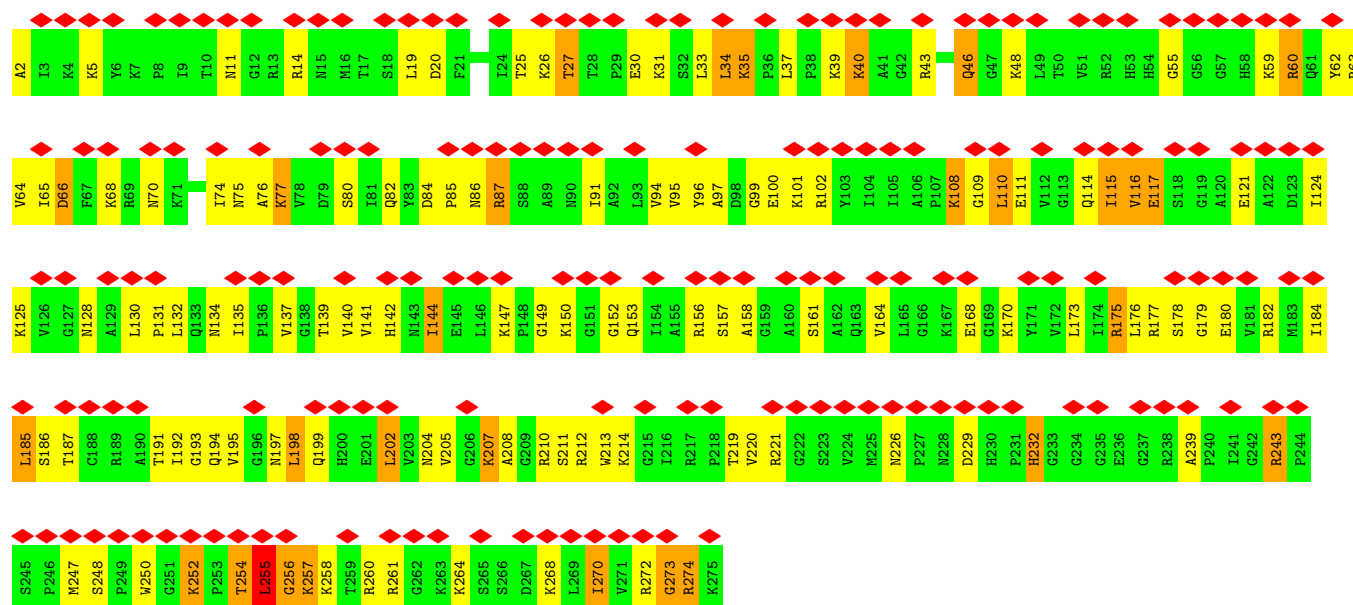


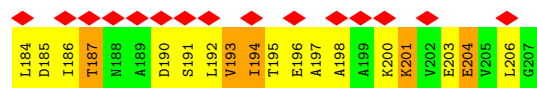
• Molecule 2: 5S ribosomal RNA



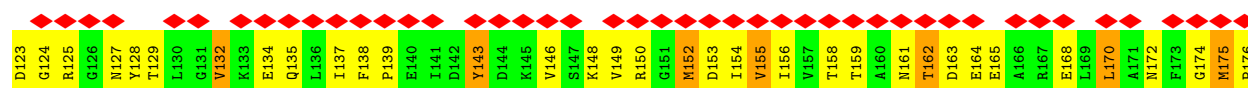
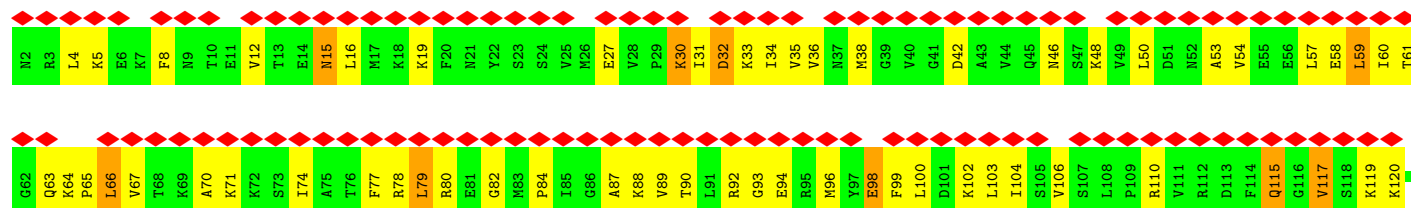
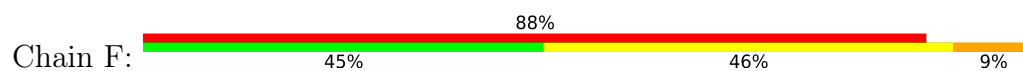
• Molecule 3: 50S ribosomal protein L2



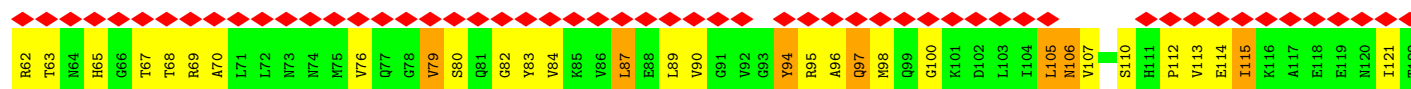




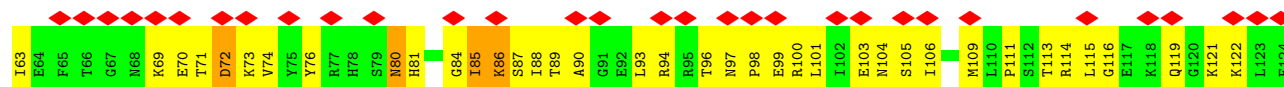
• Molecule 6: 50S ribosomal protein L5



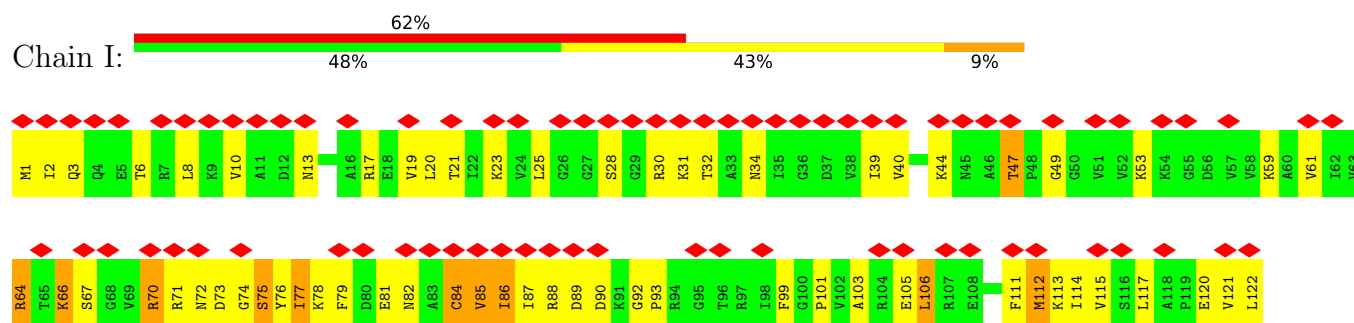
• Molecule 7: 50S ribosomal protein L6



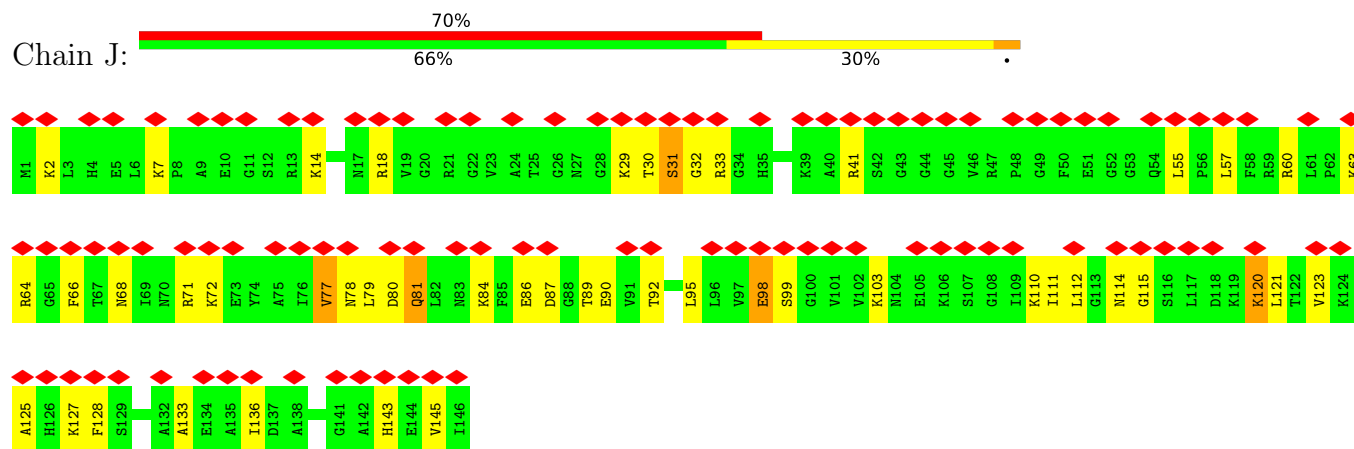
• Molecule 8: 50S ribosomal protein L13



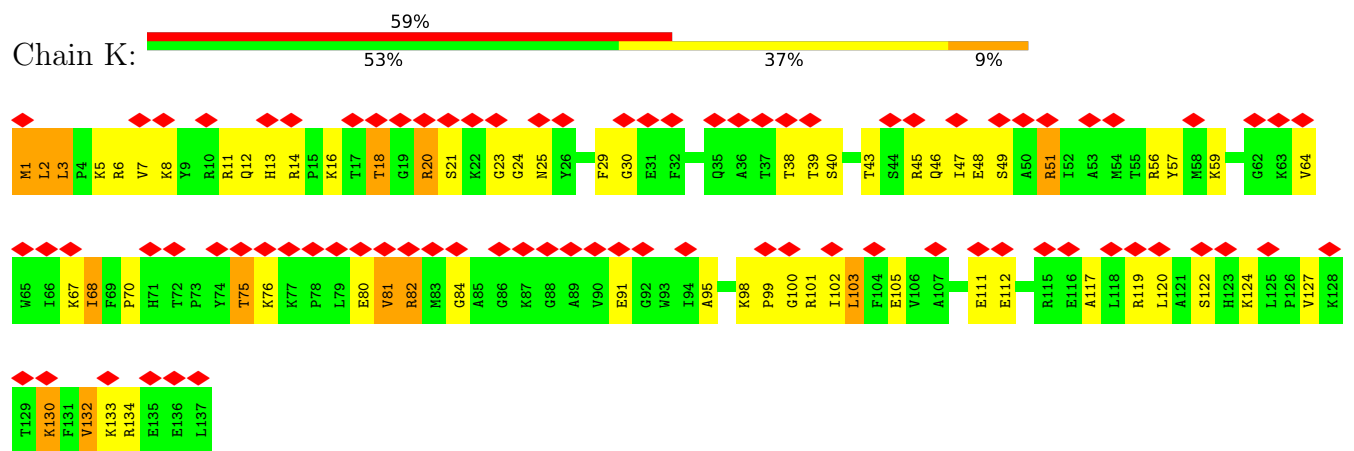
• Molecule 9: 50S ribosomal protein L14



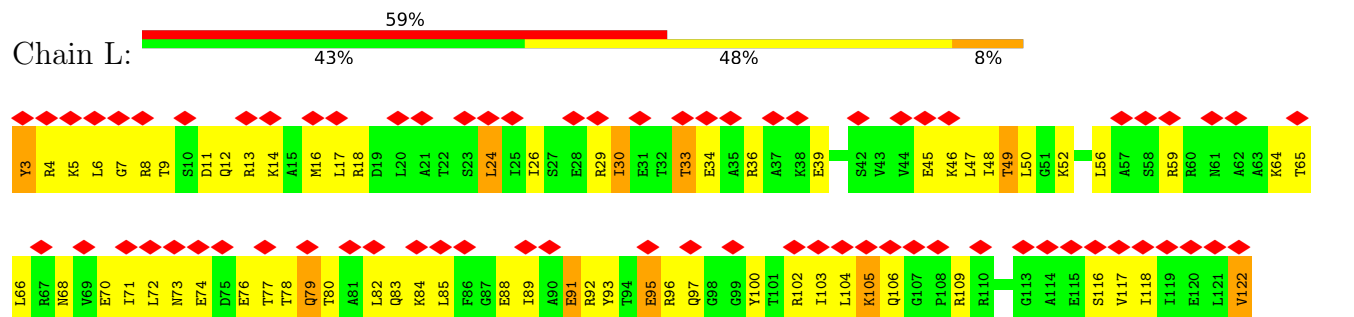
• Molecule 10: 50S ribosomal protein L15



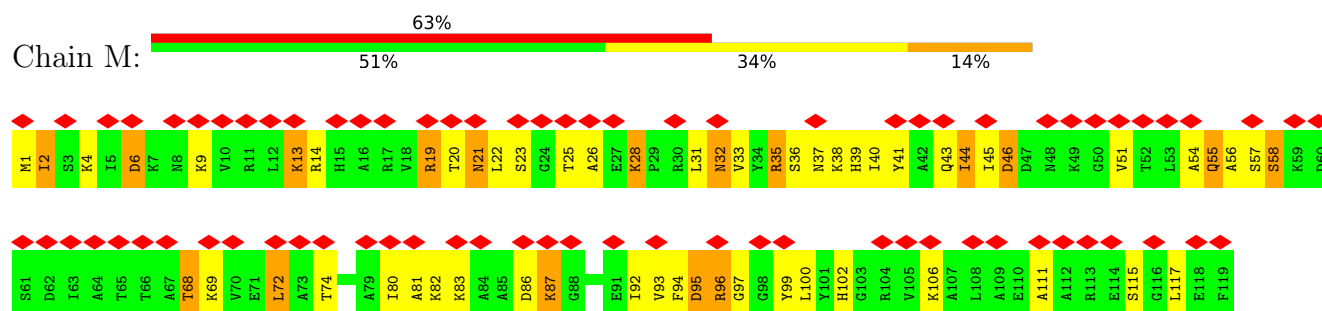
• Molecule 11: 50S ribosomal protein L16



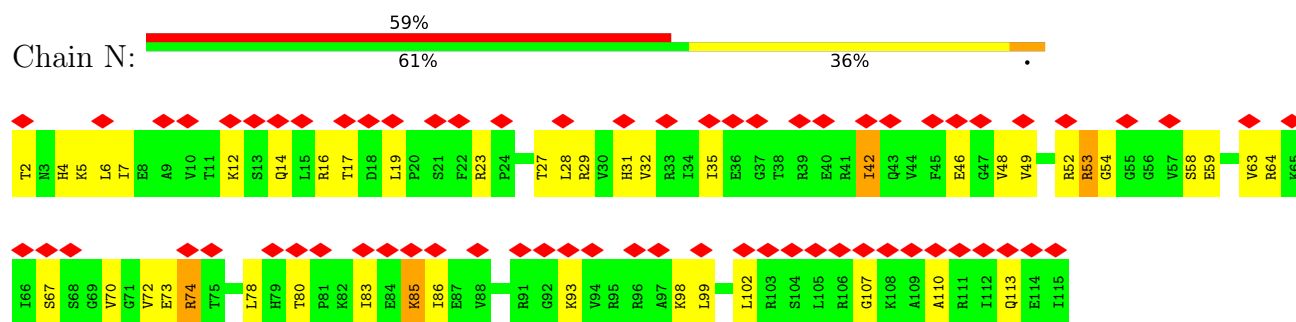
• Molecule 12: 50S ribosomal protein L17



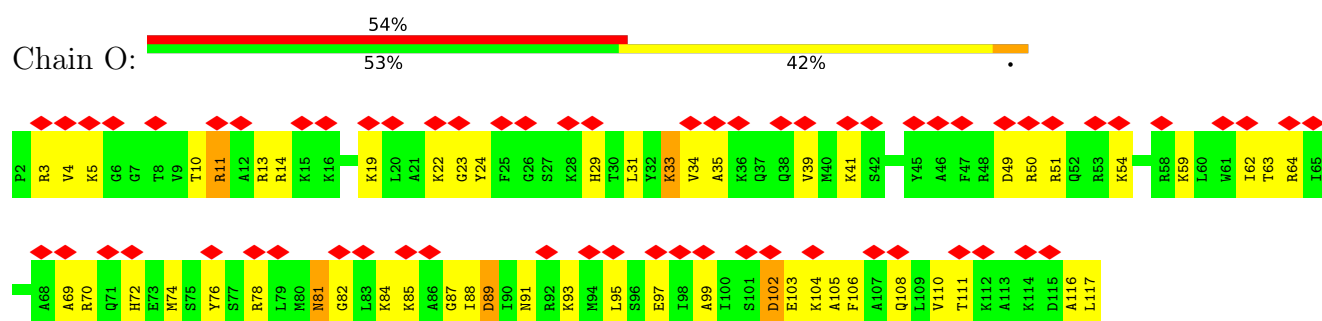
- Molecule 13: 50S ribosomal protein L18



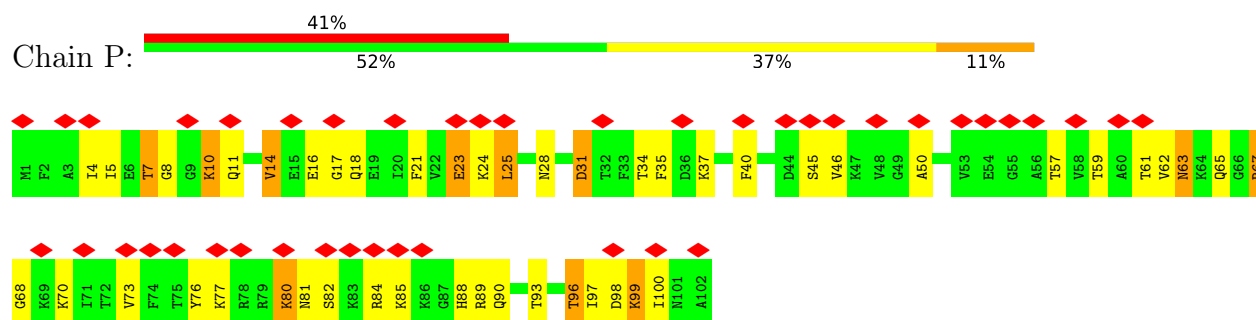
- Molecule 14: 50S ribosomal protein L19



- Molecule 15: 50S ribosomal protein L20

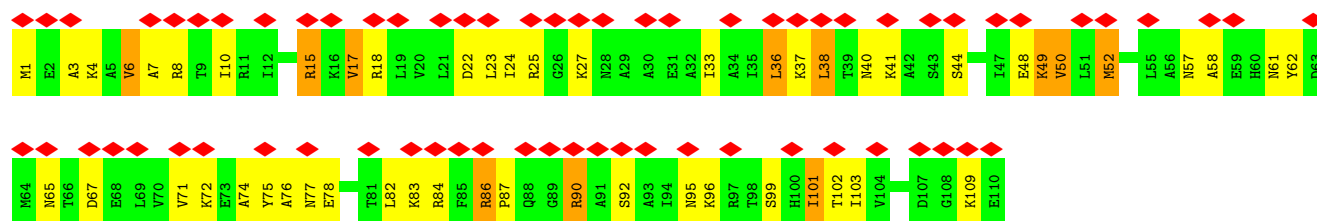


- Molecule 16: 50S ribosomal protein L21

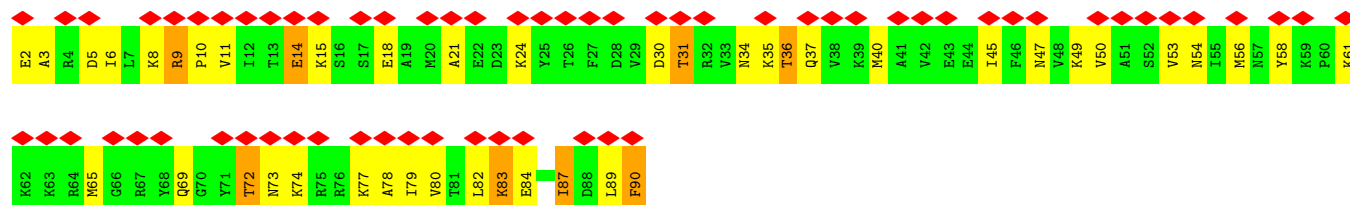


- Molecule 17: 50S ribosomal protein L22

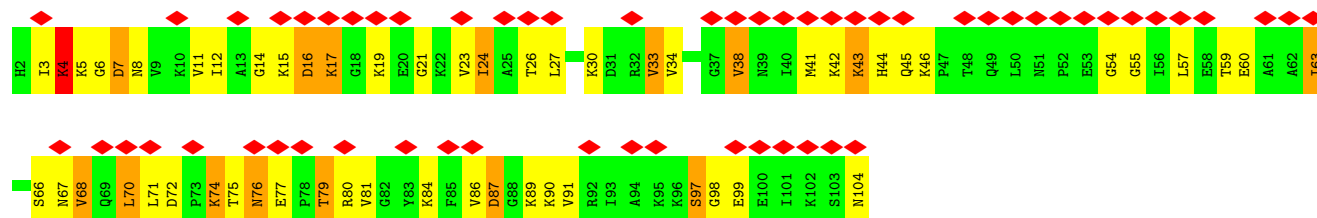




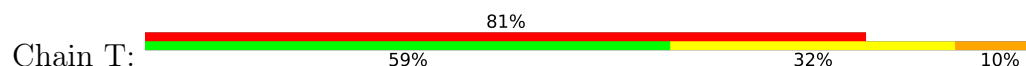
• Molecule 18: 50S ribosomal protein L23



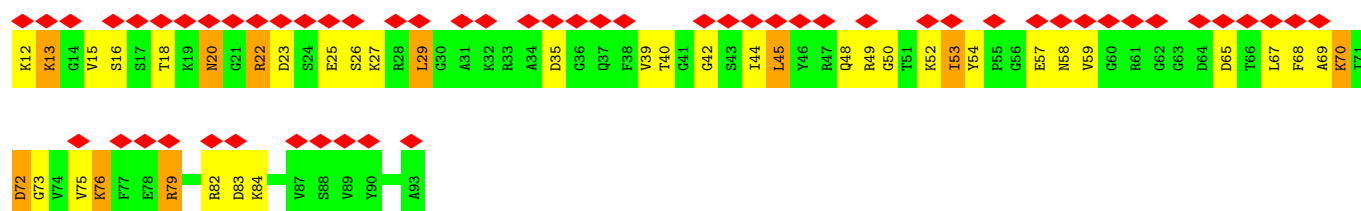
• Molecule 19: 50S ribosomal protein L24



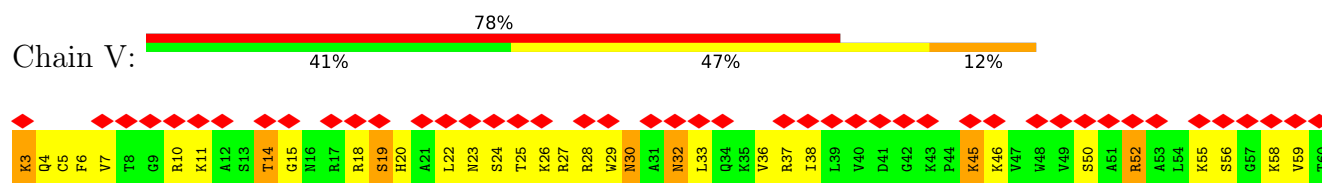
• Molecule 20: 50S ribosomal protein L25



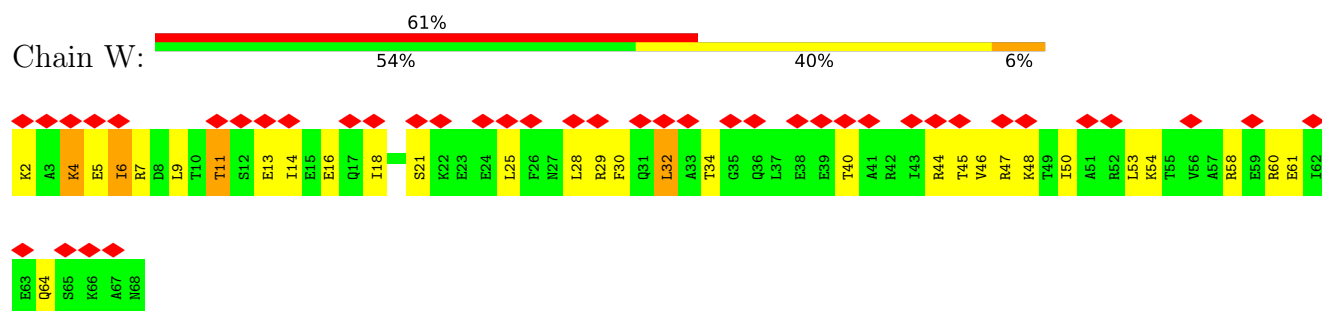
• Molecule 21: 50S ribosomal protein L27



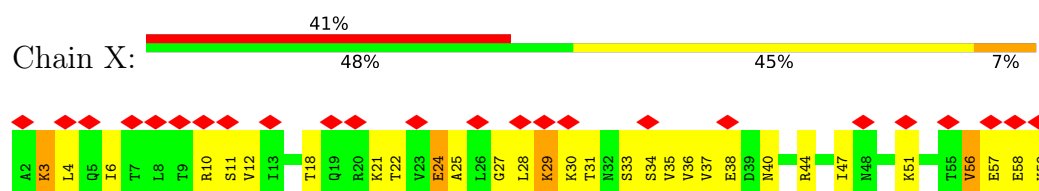
- Molecule 22: 50S ribosomal protein L28



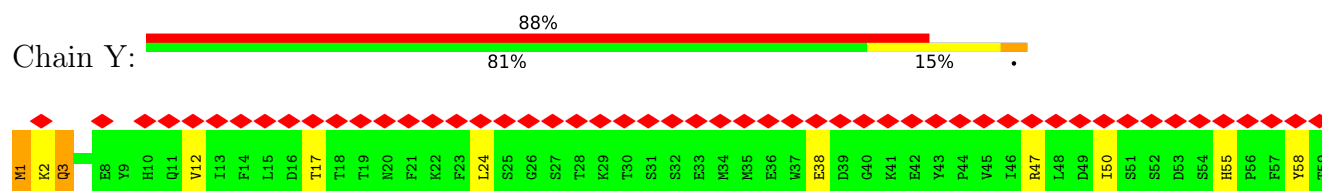
- Molecule 23: 50S ribosomal protein L29



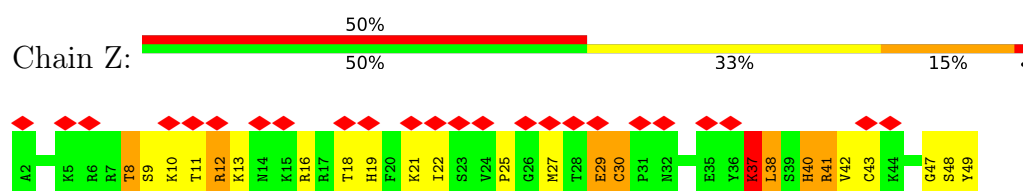
- Molecule 24: 50S ribosomal protein L30



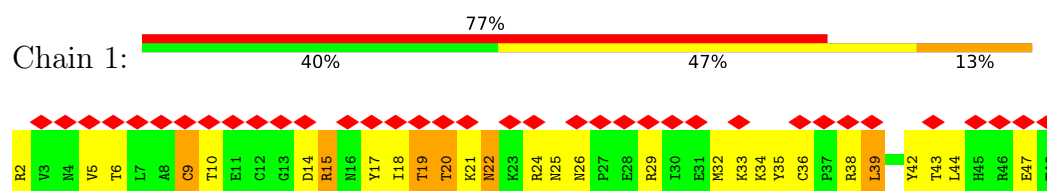
- Molecule 25: 50S ribosomal protein L31 type B



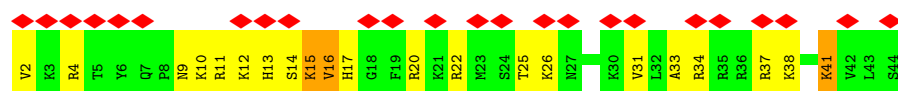
- Molecule 26: 50S ribosomal protein L32



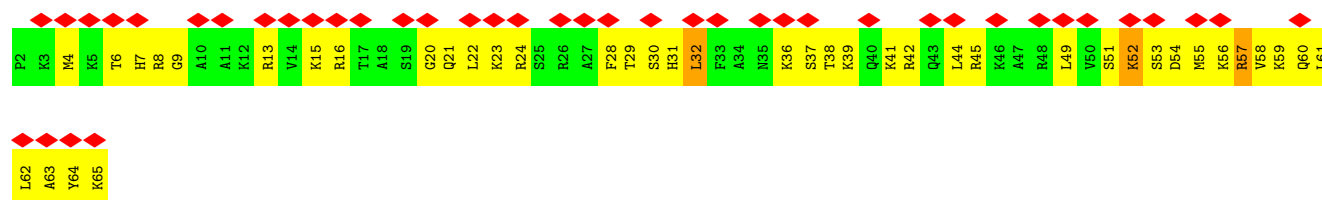
- Molecule 27: 50S ribosomal protein L33



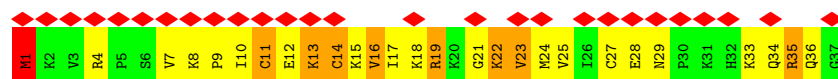
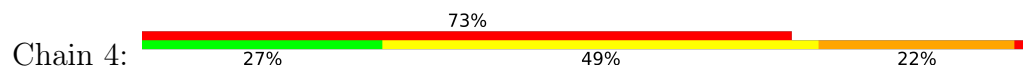
- Molecule 28: 50S ribosomal protein L34



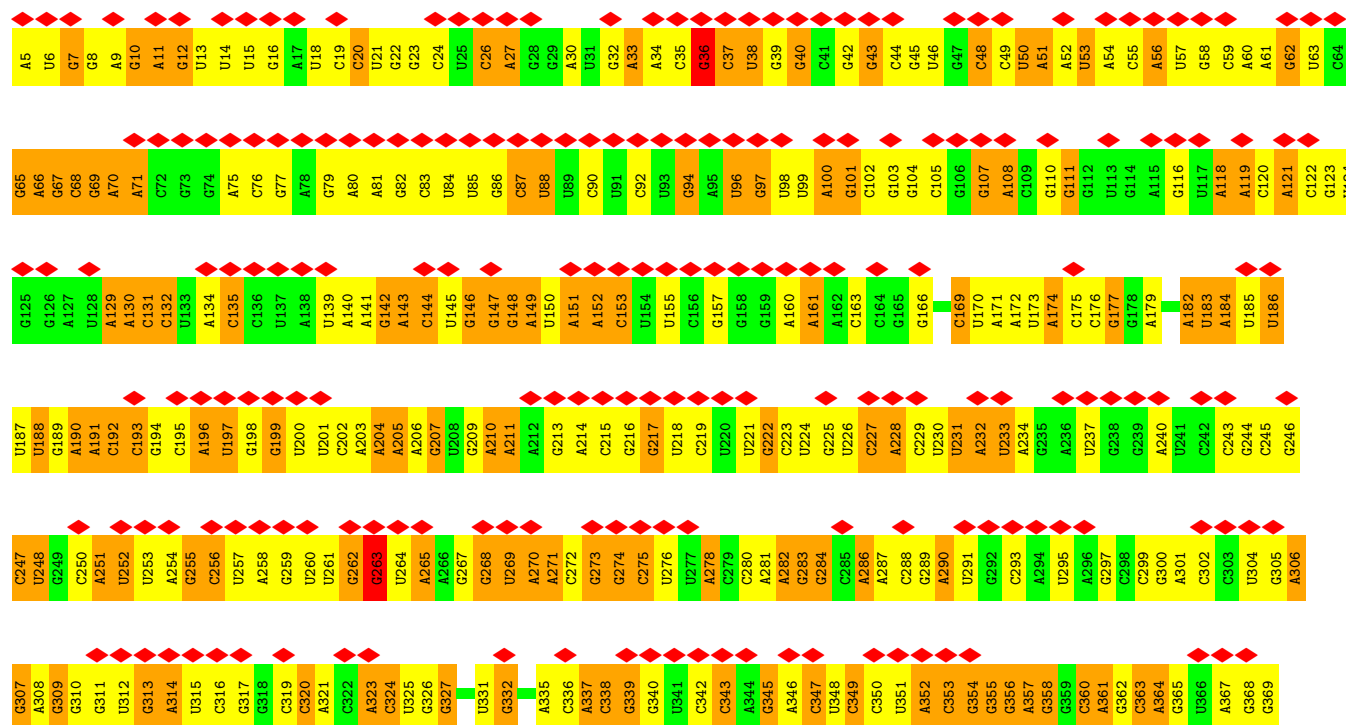
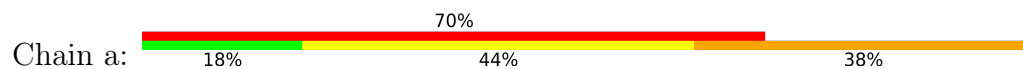
• Molecule 29: 50S ribosomal protein L35



• Molecule 30: 50S ribosomal protein L36



• Molecule 31: 16S ribosomal RNA

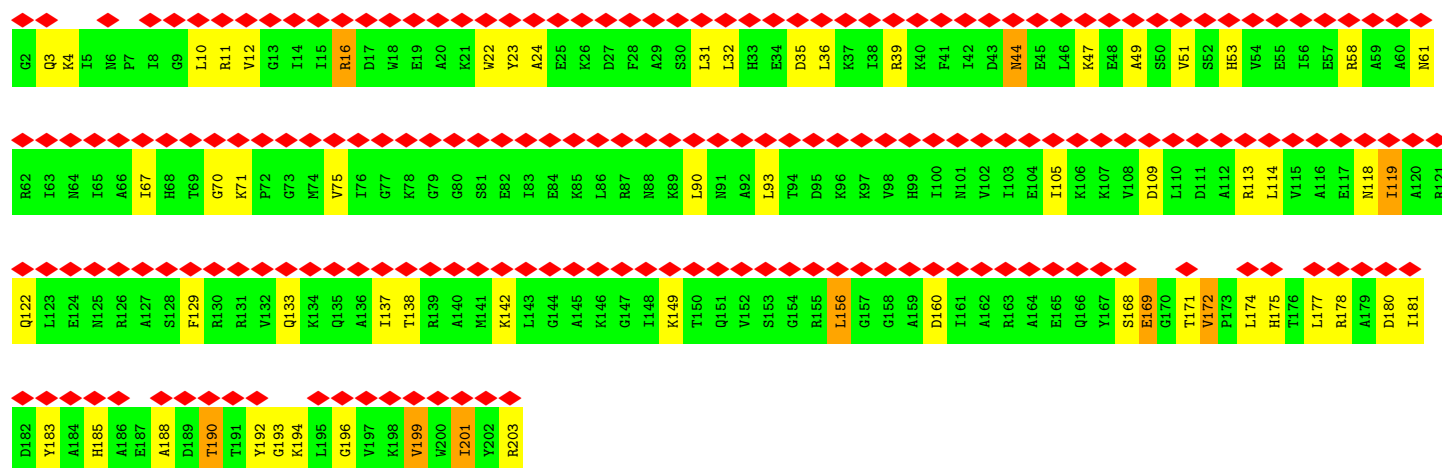


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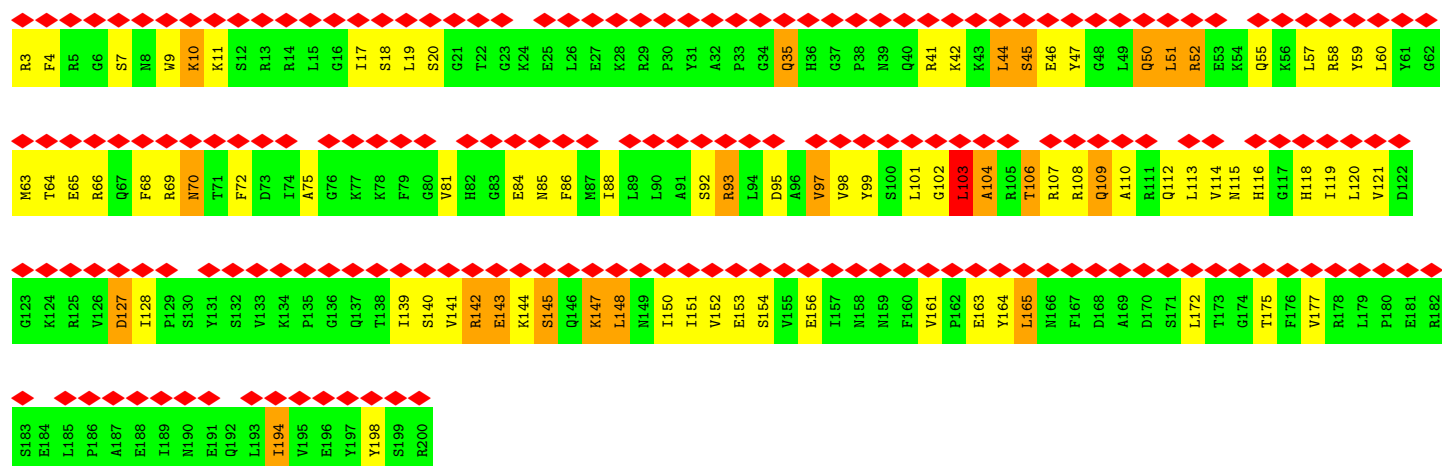


• Molecule 33: 30S ribosomal protein S3





• Molecule 34: 30S ribosomal protein S4

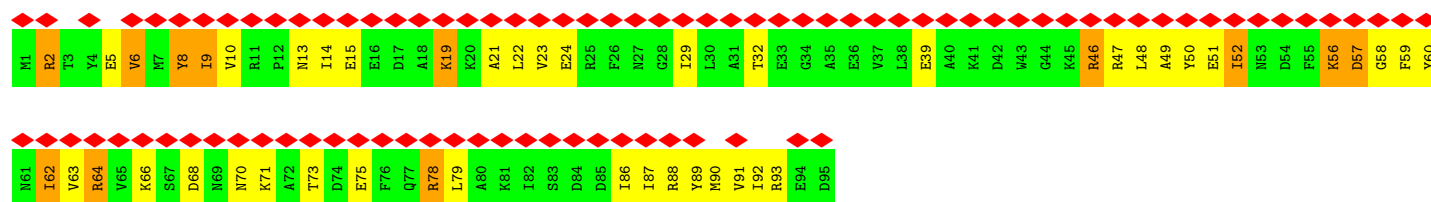


• Molecule 35: 30S ribosomal protein S5

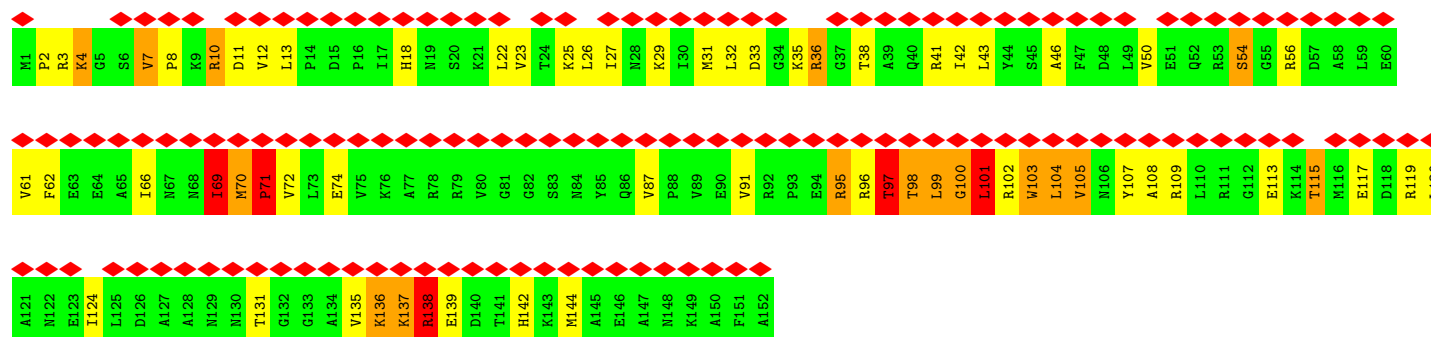
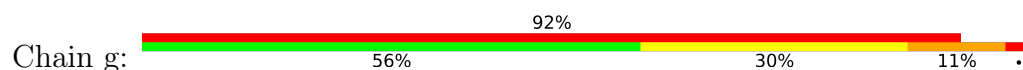


• Molecule 36: 30S ribosomal protein S6

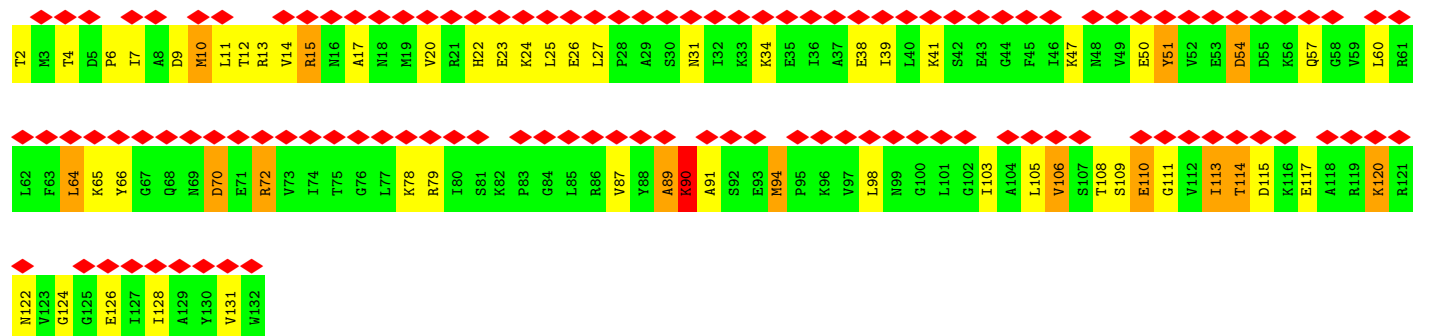
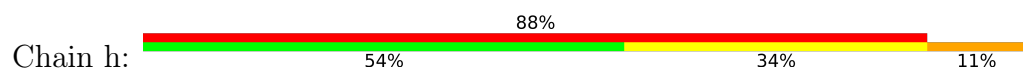




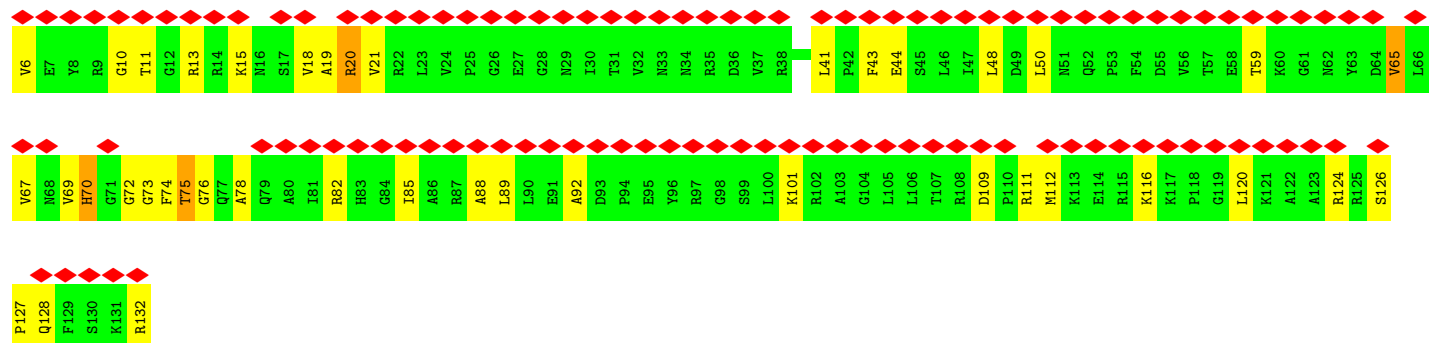
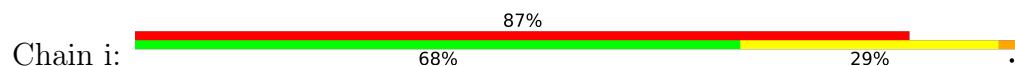
• Molecule 37: 30S ribosomal protein S7



• Molecule 38: 30S ribosomal protein S8



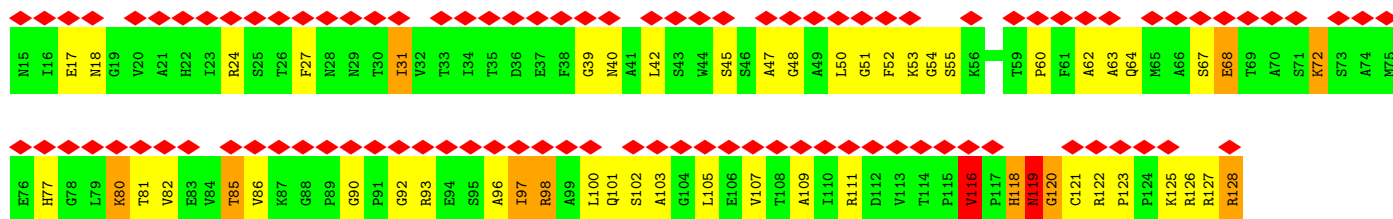
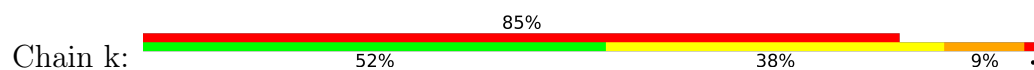
• Molecule 39: 30S ribosomal protein S9



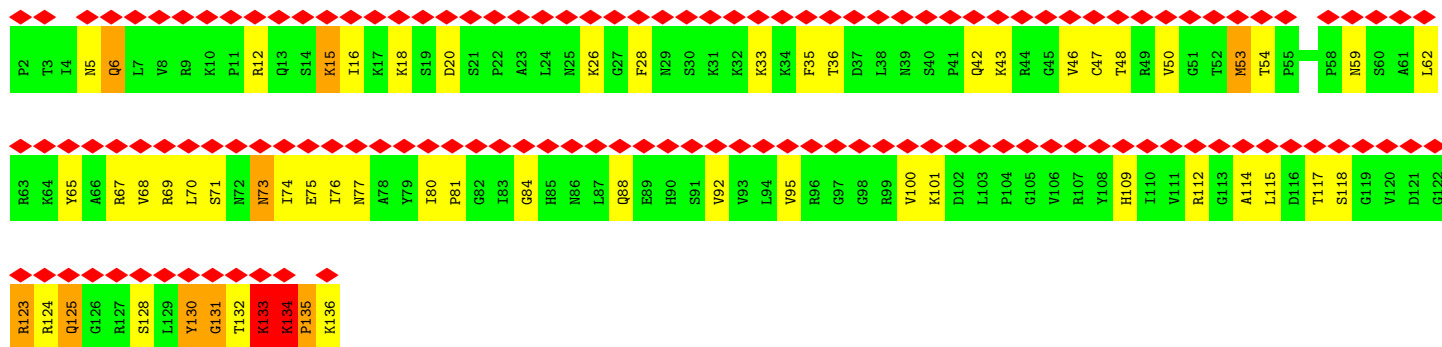
- Molecule 40: 30S ribosomal protein S10



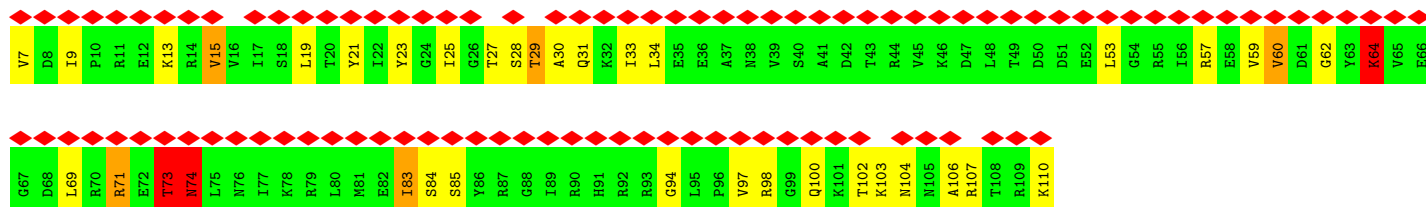
- Molecule 41: 30S ribosomal protein S11



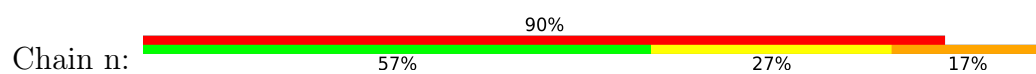
- Molecule 42: 30S ribosomal protein S12



- Molecule 43: 30S ribosomal protein S13



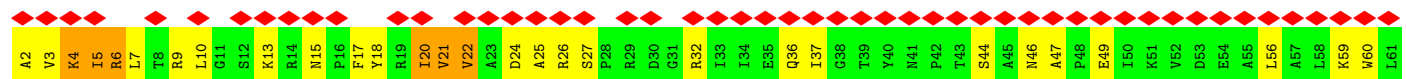
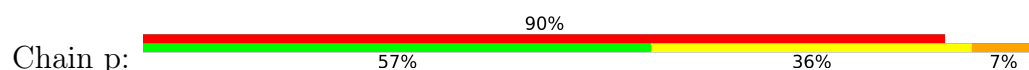
- Molecule 44: 30S ribosomal protein S14 type Z



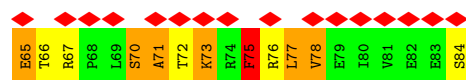
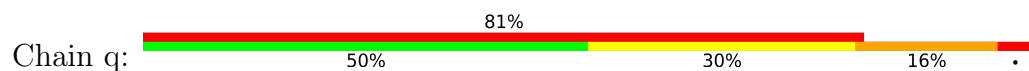
- Molecule 45: 30S ribosomal protein S15



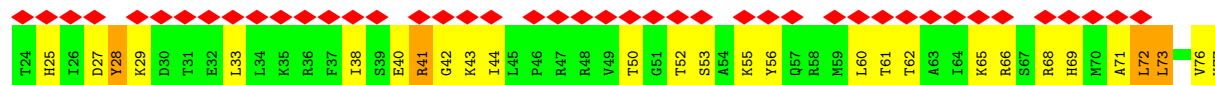
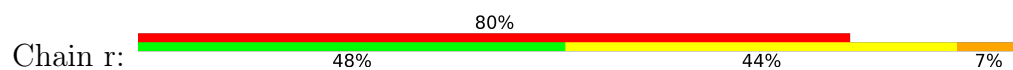
- Molecule 46: 30S ribosomal protein S16



- Molecule 47: 30S ribosomal protein S17



- Molecule 48: 30S ribosomal protein S18

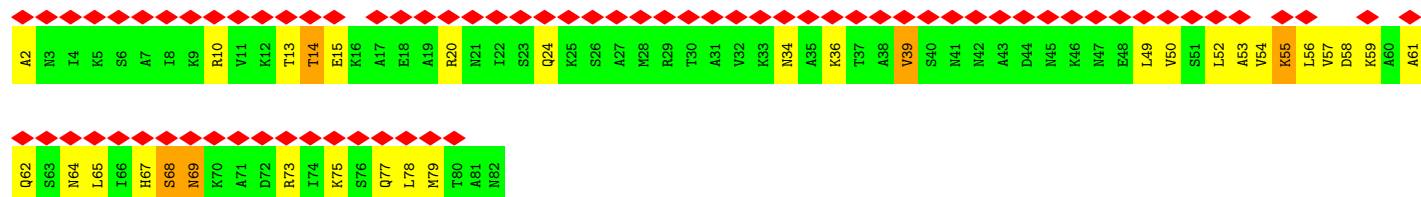


- Molecule 49: 30S ribosomal protein S19

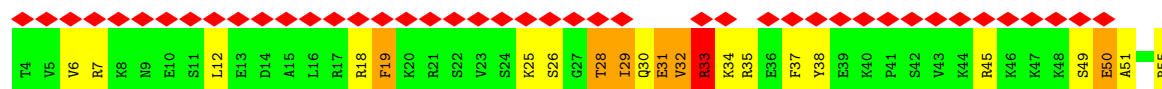
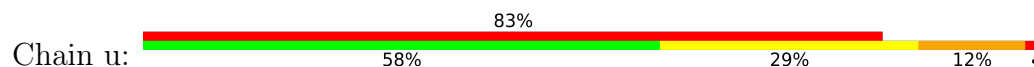




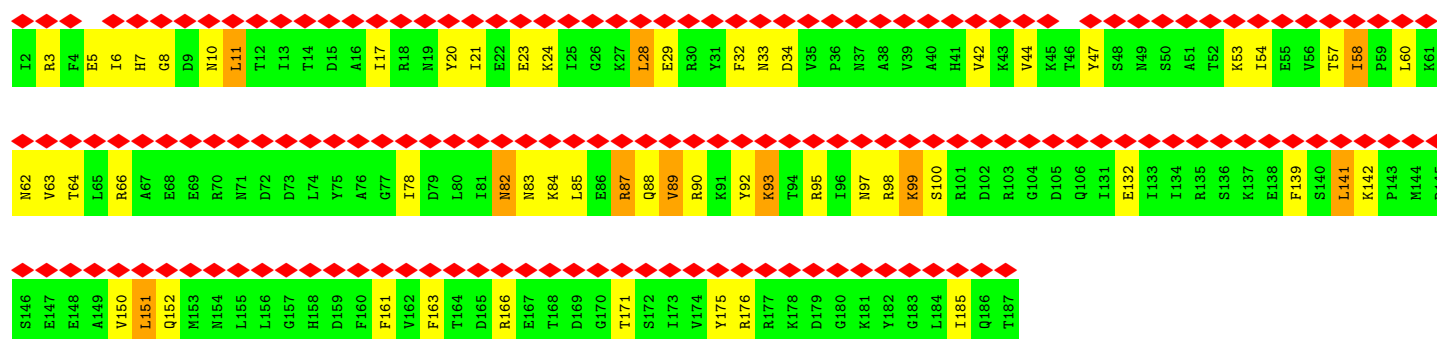
• Molecule 50: 30S ribosomal protein S20



• Molecule 51: 30S ribosomal protein S21



• Molecule 52: Ribosome hibernation promoting factor



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	145897	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.076	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.223	Depositor
Minimum map value	-0.111	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.024	Depositor
Map size ($\text{\AA}$)	430.4, 430.4, 430.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.076, 1.076, 1.076	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.76	16/69739 (0.0%)	0.60	19/108751 (0.0%)
2	B	0.48	0/2733	0.53	0/4257
3	C	0.65	0/2125	0.83	3/2853 (0.1%)
4	D	0.69	0/1651	0.63	0/2215
5	E	0.74	1/1595 (0.1%)	0.74	0/2154
6	F	0.33	0/1339	0.68	1/1805 (0.1%)
7	G	0.35	0/1281	0.64	0/1736
8	H	0.66	0/1165	0.69	0/1570
9	I	0.66	0/925	0.75	0/1242
10	J	0.64	0/1100	0.69	0/1467
11	K	2.72	1/1095 (0.1%)	0.72	2/1472 (0.1%)
12	L	0.67	0/936	0.74	0/1253
13	M	0.45	0/900	0.72	0/1205
14	N	0.64	0/901	0.71	0/1209
15	O	0.78	0/954	0.70	0/1264
16	P	0.68	0/800	0.70	0/1070
17	Q	0.67	0/845	0.79	1/1140 (0.1%)
18	R	0.59	0/723	0.68	0/966
19	S	0.45	0/779	0.65	0/1043
20	T	0.36	0/730	0.62	0/981
21	U	0.64	0/628	0.77	0/833
22	V	0.50	0/451	0.75	0/603
23	W	0.49	0/542	0.73	0/722
24	X	0.70	0/451	0.70	0/606
25	Y	0.28	0/378	0.55	0/521
26	Z	0.61	0/366	0.80	0/489
27	1	0.39	0/395	0.68	0/530
28	2	0.77	0/371	0.74	0/484
29	3	0.60	0/526	0.70	0/690
30	4	0.53	0/298	0.81	0/392
31	a	0.97	31/36913 (0.1%)	0.61	17/57564 (0.0%)
32	b	1.92	1/1846 (0.1%)	0.61	0/2477
33	c	0.28	0/1523	0.61	0/2062
34	d	0.28	0/1526	0.69	1/2063 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	e	0.27	0/1159	0.58	1/1566 (0.1%)
36	f	0.31	0/789	0.61	0/1060
37	g	0.46	0/1175	0.98	7/1584 (0.4%)
38	h	2.23	5/1037 (0.5%)	1.13	8/1392 (0.6%)
39	i	0.32	0/937	0.69	0/1269
40	j	0.39	0/764	0.82	0/1034
41	k	0.32	0/824	0.81	2/1119 (0.2%)
42	l	4.25	7/1054 (0.7%)	0.77	2/1415 (0.1%)
43	m	0.31	0/732	0.74	1/991 (0.1%)
44	n	4.34	2/497 (0.4%)	0.96	2/662 (0.3%)
45	o	0.31	0/732	0.71	0/979
46	p	0.29	0/705	0.63	0/952
47	q	0.40	0/629	0.93	1/849 (0.1%)
48	r	0.33	0/452	0.67	0/604
49	s	4.53	8/654 (1.2%)	1.34	9/879 (1.0%)
50	t	0.35	0/591	0.74	0/793
51	u	0.42	0/403	0.80	2/535 (0.4%)
52	v	0.30	0/1350	0.63	0/1812
All	All	0.98	72/153014 (0.0%)	0.64	79/229184 (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
3	C	0	5
5	E	0	1
6	F	0	2
7	G	0	1
8	H	0	4
11	K	0	3
12	L	0	1
13	M	0	1
16	P	0	2
19	S	0	1
26	Z	0	2
30	4	0	2
31	a	0	2
32	b	0	4
33	c	0	1
34	d	0	7

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Mol	Chain	#Chirality outliers	#Planarity outliers
37	g	0	10
39	i	0	1
40	j	0	4
41	k	0	5
42	l	0	2
43	m	0	5
44	n	0	4
45	o	0	4
47	q	0	5
49	s	0	3
50	t	0	1
51	u	0	3
52	v	0	3
All	All	0	89

The worst 5 of 72 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	l	134	LYS	CD-CE	99.60	4.51	1.52
44	n	16	TYR	CB-CG	95.89	3.62	1.51
11	K	2	LEU	CG-CD1	88.26	4.43	1.52
32	b	107	ILE	CG1-CD1	81.59	4.70	1.51
1	A	393	G	C1'-N9	67.45	2.49	1.48

The worst 5 of 79 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	a	36	G	P-O3'-C3'	27.64	161.66	120.20
38	h	90	LYS	O-C-N	-21.44	98.22	123.31
49	s	36	ARG	N-CA-CB	-17.58	84.61	110.80
38	h	90	LYS	N-CA-C	15.65	135.21	108.76
49	s	36	ARG	O-C-N	-15.36	104.08	122.20

There are no chirality outliers.

5 of 89 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	173	LEU	Peptide
3	C	255	LEU	Peptide
3	C	257	LYS	Peptide
3	C	273	GLY	Peptide

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Mol	Chain	Res	Type	Group
3	C	40	LYS	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	A	62277	31287	31296	1437	0
2	B	2445	1240	1240	64	0
3	C	2090	2201	2201	104	0
4	D	1627	1667	1667	60	0
5	E	1572	1620	1619	66	0
6	F	1325	1342	1342	74	0
7	G	1263	1225	1225	49	0
8	H	1143	1134	1134	62	0
9	I	918	981	981	50	0
10	J	1086	1125	1125	43	0
11	K	1071	1123	1123	64	0
12	L	932	983	983	53	0
13	M	891	925	925	44	0
14	N	889	937	937	24	0
15	O	942	1014	1014	41	0
16	P	790	830	830	26	0
17	Q	837	887	887	37	0
18	R	715	748	748	28	0
19	S	770	809	809	42	0
20	T	722	766	766	23	0
21	U	622	643	643	36	0
22	V	445	466	466	25	0
23	W	541	563	563	27	0
24	X	449	491	491	19	0
25	Y	370	243	243	8	0
26	Z	360	358	358	21	0
27	1	390	394	394	28	0
28	2	367	415	415	18	0
29	3	521	586	586	32	0
30	4	295	340	340	34	0
31	a	32969	16594	16595	1154	0
32	b	1819	1886	1886	92	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	c	1501	1464	1464	42	0
34	d	1497	1449	1449	50	0
35	e	1145	1202	1202	33	0
36	f	778	775	775	39	0
37	g	1161	1165	1165	49	0
38	h	1026	1077	1077	103	0
39	i	922	890	890	29	0
40	j	752	775	775	25	0
41	k	810	784	784	36	0
42	l	1037	1091	1091	71	0
43	m	727	674	674	28	0
44	n	487	492	492	34	0
45	o	723	752	752	27	0
46	p	694	709	709	22	0
47	q	621	616	615	32	0
48	r	445	482	482	25	0
49	s	636	626	626	49	0
50	t	591	616	616	23	0
51	u	400	407	407	27	0
52	v	1333	1349	1349	41	0
All	All	140739	93218	93226	3886	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 19.

The worst 5 of 3886 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)
31:a:989:C:C6	31:a:989:C:C5	1.82	1.61
31:a:989:C:C5	31:a:989:C:C4	1.92	1.58
31:a:405:A:N9	31:a:405:A:C8	1.69	1.54
49:s:74:PHE:CD2	49:s:74:PHE:CG	2.01	1.49
42:l:130:TYR:CG	42:l:130:TYR:CD2	2.03	1.47

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	
3	C	272/274 (99%)	215 (79%)	57 (21%)	0	100	100
4	D	213/215 (99%)	166 (78%)	47 (22%)	0	100	100
5	E	204/206 (99%)	175 (86%)	29 (14%)	0	100	100
6	F	173/175 (99%)	141 (82%)	32 (18%)	0	100	100
7	G	173/175 (99%)	140 (81%)	33 (19%)	0	100	100
8	H	143/145 (99%)	118 (82%)	25 (18%)	0	100	100
9	I	120/122 (98%)	104 (87%)	16 (13%)	0	100	100
10	J	144/146 (99%)	124 (86%)	20 (14%)	0	100	100
11	K	135/137 (98%)	113 (84%)	22 (16%)	0	100	100
12	L	118/120 (98%)	101 (86%)	17 (14%)	0	100	100
13	M	117/119 (98%)	98 (84%)	19 (16%)	0	100	100
14	N	112/114 (98%)	94 (84%)	18 (16%)	0	100	100
15	O	114/116 (98%)	105 (92%)	9 (8%)	0	100	100
16	P	100/102 (98%)	85 (85%)	15 (15%)	0	100	100
17	Q	108/110 (98%)	90 (83%)	17 (16%)	1 (1%)	14	46
18	R	87/89 (98%)	70 (80%)	17 (20%)	0	100	100
19	S	101/103 (98%)	82 (81%)	19 (19%)	0	100	100
20	T	92/94 (98%)	82 (89%)	10 (11%)	0	100	100
21	U	80/82 (98%)	70 (88%)	10 (12%)	0	100	100
22	V	56/58 (97%)	46 (82%)	10 (18%)	0	100	100
23	W	65/67 (97%)	58 (89%)	7 (11%)	0	100	100
24	X	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
25	Y	57/59 (97%)	48 (84%)	9 (16%)	0	100	100
26	Z	46/48 (96%)	29 (63%)	17 (37%)	0	100	100
27	1	45/47 (96%)	37 (82%)	8 (18%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	2	41/43 (95%)	38 (93%)	3 (7%)	0	100	100
29	3	62/64 (97%)	50 (81%)	12 (19%)	0	100	100
30	4	35/37 (95%)	21 (60%)	14 (40%)	0	100	100
32	b	224/226 (99%)	193 (86%)	31 (14%)	0	100	100
33	c	200/202 (99%)	161 (80%)	39 (20%)	0	100	100
34	d	196/198 (99%)	136 (69%)	59 (30%)	1 (0%)	24	57
35	e	154/156 (99%)	133 (86%)	21 (14%)	0	100	100
36	f	93/95 (98%)	75 (81%)	18 (19%)	0	100	100
37	g	149/152 (98%)	99 (66%)	50 (34%)	0	100	100
38	h	127/131 (97%)	98 (77%)	29 (23%)	0	100	100
39	i	125/127 (98%)	86 (69%)	39 (31%)	0	100	100
40	j	95/97 (98%)	59 (62%)	35 (37%)	1 (1%)	11	43
41	k	112/114 (98%)	81 (72%)	31 (28%)	0	100	100
42	l	133/135 (98%)	102 (77%)	29 (22%)	2 (2%)	8	37
43	m	100/104 (96%)	62 (62%)	38 (38%)	0	100	100
44	n	58/60 (97%)	36 (62%)	22 (38%)	0	100	100
45	o	86/88 (98%)	71 (83%)	15 (17%)	0	100	100
46	p	87/89 (98%)	68 (78%)	19 (22%)	0	100	100
47	q	78/80 (98%)	51 (65%)	27 (35%)	0	100	100
48	r	52/54 (96%)	43 (83%)	9 (17%)	0	100	100
49	s	78/80 (98%)	58 (74%)	20 (26%)	0	100	100
50	t	79/81 (98%)	59 (75%)	20 (25%)	0	100	100
51	u	50/52 (96%)	32 (64%)	18 (36%)	0	100	100
52	v	158/162 (98%)	117 (74%)	41 (26%)	0	100	100
All	All	5503/5608 (98%)	4369 (79%)	1129 (20%)	5 (0%)	49	79

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
42	l	131	GLY
34	d	110	ALA
40	j	7	ARG
17	Q	87	PRO
42	l	135	PRO

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	
3	C	220/221 (100%)	173 (79%)	47 (21%)	1	7
4	D	173/173 (100%)	143 (83%)	30 (17%)	2	12
5	E	168/168 (100%)	121 (72%)	47 (28%)	0	3
6	F	141/154 (92%)	113 (80%)	28 (20%)	1	8
7	G	124/153 (81%)	99 (80%)	25 (20%)	1	8
8	H	122/123 (99%)	95 (78%)	27 (22%)	1	7
9	I	100/100 (100%)	76 (76%)	24 (24%)	1	5
10	J	109/112 (97%)	94 (86%)	15 (14%)	3	20
11	K	108/114 (95%)	90 (83%)	18 (17%)	2	14
12	L	96/101 (95%)	80 (83%)	16 (17%)	2	14
13	M	86/95 (90%)	61 (71%)	25 (29%)	0	3
14	N	93/100 (93%)	76 (82%)	17 (18%)	2	11
15	O	96/96 (100%)	83 (86%)	13 (14%)	4	21
16	P	84/86 (98%)	62 (74%)	22 (26%)	0	4
17	Q	88/90 (98%)	65 (74%)	23 (26%)	0	4
18	R	78/80 (98%)	62 (80%)	16 (20%)	1	8
19	S	81/88 (92%)	56 (69%)	25 (31%)	0	2
20	T	78/82 (95%)	58 (74%)	20 (26%)	0	4
21	U	63/64 (98%)	44 (70%)	19 (30%)	0	2
22	V	44/49 (90%)	30 (68%)	14 (32%)	0	2
23	W	58/60 (97%)	48 (83%)	10 (17%)	2	12
24	X	52/52 (100%)	43 (83%)	9 (17%)	2	12
25	Y	23/56 (41%)	21 (91%)	2 (9%)	9	34
26	Z	35/44 (80%)	24 (69%)	11 (31%)	0	2
27	1	44/45 (98%)	32 (73%)	12 (27%)	0	3
28	2	39/39 (100%)	35 (90%)	4 (10%)	7	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	3	55/55 (100%)	47 (86%)	8 (14%)	3	18
30	4	35/35 (100%)	27 (77%)	8 (23%)	1	6
32	b	196/196 (100%)	160 (82%)	36 (18%)	1	10
33	c	138/164 (84%)	113 (82%)	25 (18%)	2	11
34	d	147/174 (84%)	111 (76%)	36 (24%)	1	5
35	e	118/122 (97%)	98 (83%)	20 (17%)	2	13
36	f	80/83 (96%)	61 (76%)	19 (24%)	1	5
37	g	118/128 (92%)	87 (74%)	31 (26%)	0	4
38	h	111/112 (99%)	88 (79%)	23 (21%)	1	7
39	i	86/105 (82%)	72 (84%)	14 (16%)	2	14
40	j	81/87 (93%)	66 (82%)	15 (18%)	1	10
41	k	82/90 (91%)	59 (72%)	23 (28%)	0	3
42	l	111/117 (95%)	84 (76%)	27 (24%)	1	5
43	m	62/92 (67%)	49 (79%)	13 (21%)	1	7
44	n	48/52 (92%)	35 (73%)	13 (27%)	0	3
45	o	77/80 (96%)	61 (79%)	16 (21%)	1	7
46	p	73/75 (97%)	59 (81%)	14 (19%)	1	9
47	q	65/75 (87%)	46 (71%)	19 (29%)	0	2
48	r	48/49 (98%)	41 (85%)	7 (15%)	3	17
49	s	67/70 (96%)	50 (75%)	17 (25%)	0	4
50	t	61/67 (91%)	51 (84%)	10 (16%)	2	14
51	u	40/48 (83%)	32 (80%)	8 (20%)	1	8
52	v	147/147 (100%)	120 (82%)	27 (18%)	1	10
All	All	4449/4768 (93%)	3501 (79%)	948 (21%)	3	7

5 of 948 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	V	29	TRP
49	s	6	LYS
33	c	16	ARG
47	q	77	LEU
52	v	151	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
41	k	40	ASN
52	v	71	ASN
42	l	86	ASN
45	o	68	ASN
10	J	68	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2896/2905 (99%)	1224 (42%)	55 (1%)
2	B	114/115 (99%)	44 (38%)	0
31	a	1537/1539 (99%)	918 (59%)	0
All	All	4547/4559 (99%)	2186 (48%)	55 (1%)

5 of 2186 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	5	A
1	A	6	A
1	A	15	G
1	A	28	A
1	A	34	U

5 of 55 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1108	C
1	A	1520	A
1	A	2816	C
1	A	2450	U
1	A	1190	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	8
31	a	2
52	v	1
43	m	1
37	g	1
38	h	1
5	E	1

The worst 5 of 15 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	v	106:GLN	C	131:ILE	N	30.98
1	A	2207:U	O3'	2208:A	P	12.82
1	A	1939:A	O3'	1944:U	P	12.52
1	a	465:U	O3'	466:G	P	11.00
1	A	929:C	O3'	937:G	P	9.63

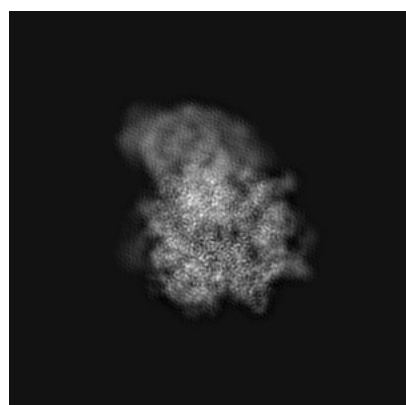
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10079. These allow visual inspection of the internal detail of the map and identification of artifacts.

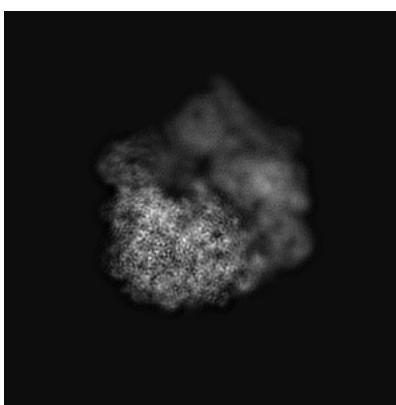
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

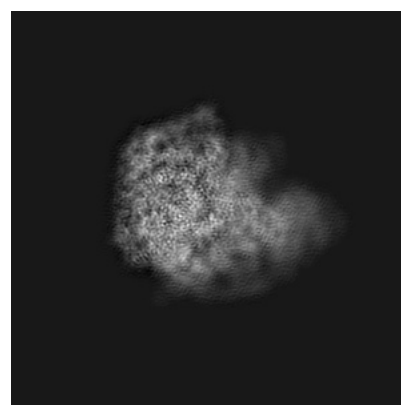
6.1.1 Primary map



X



Y

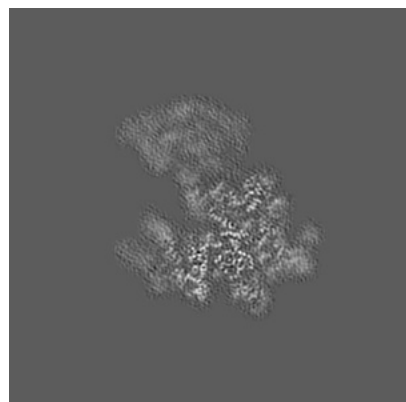


Z

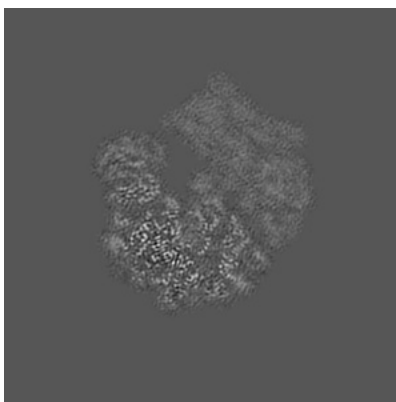
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

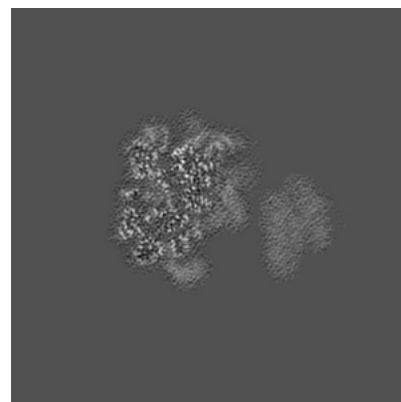
6.2.1 Primary map



X Index: 200



Y Index: 200

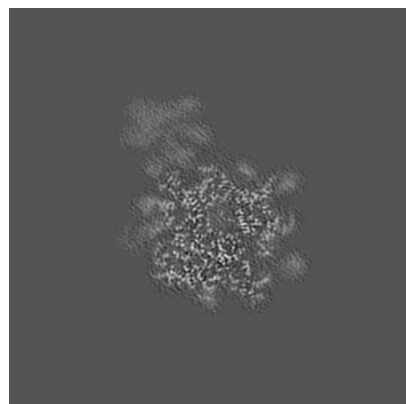


Z Index: 200

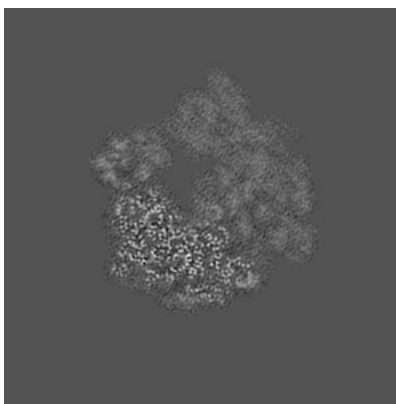
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

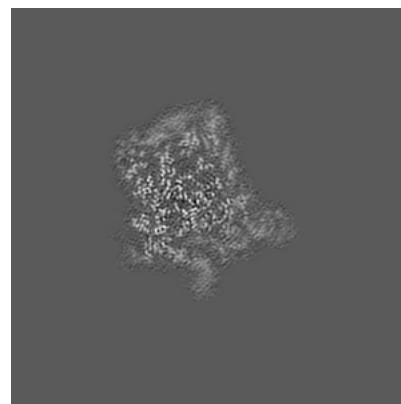
6.3.1 Primary map



X Index: 163



Y Index: 184

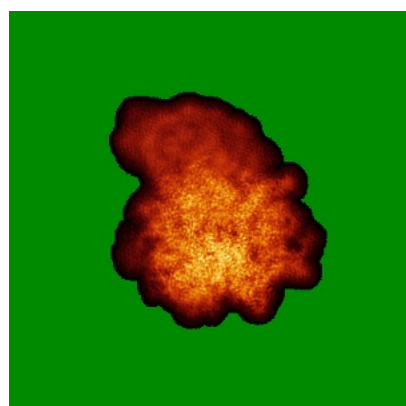


Z Index: 145

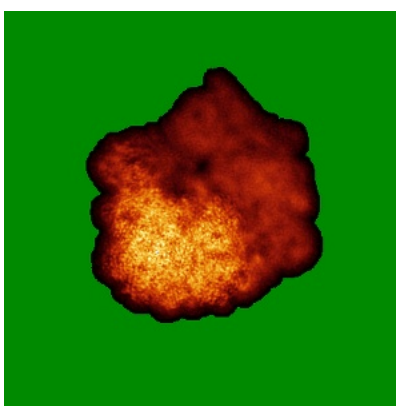
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

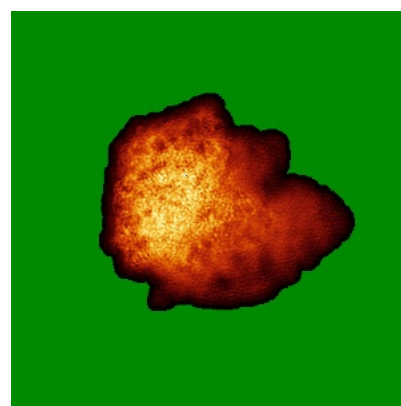
6.4.1 Primary map



X



Y

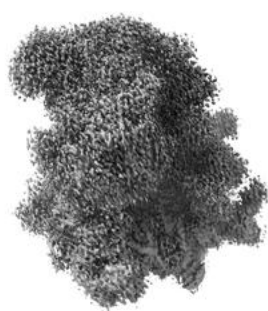


Z

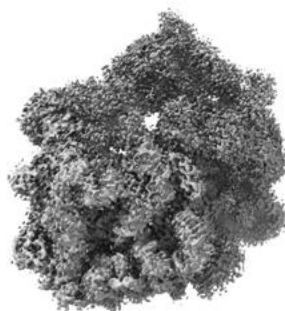
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.024. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

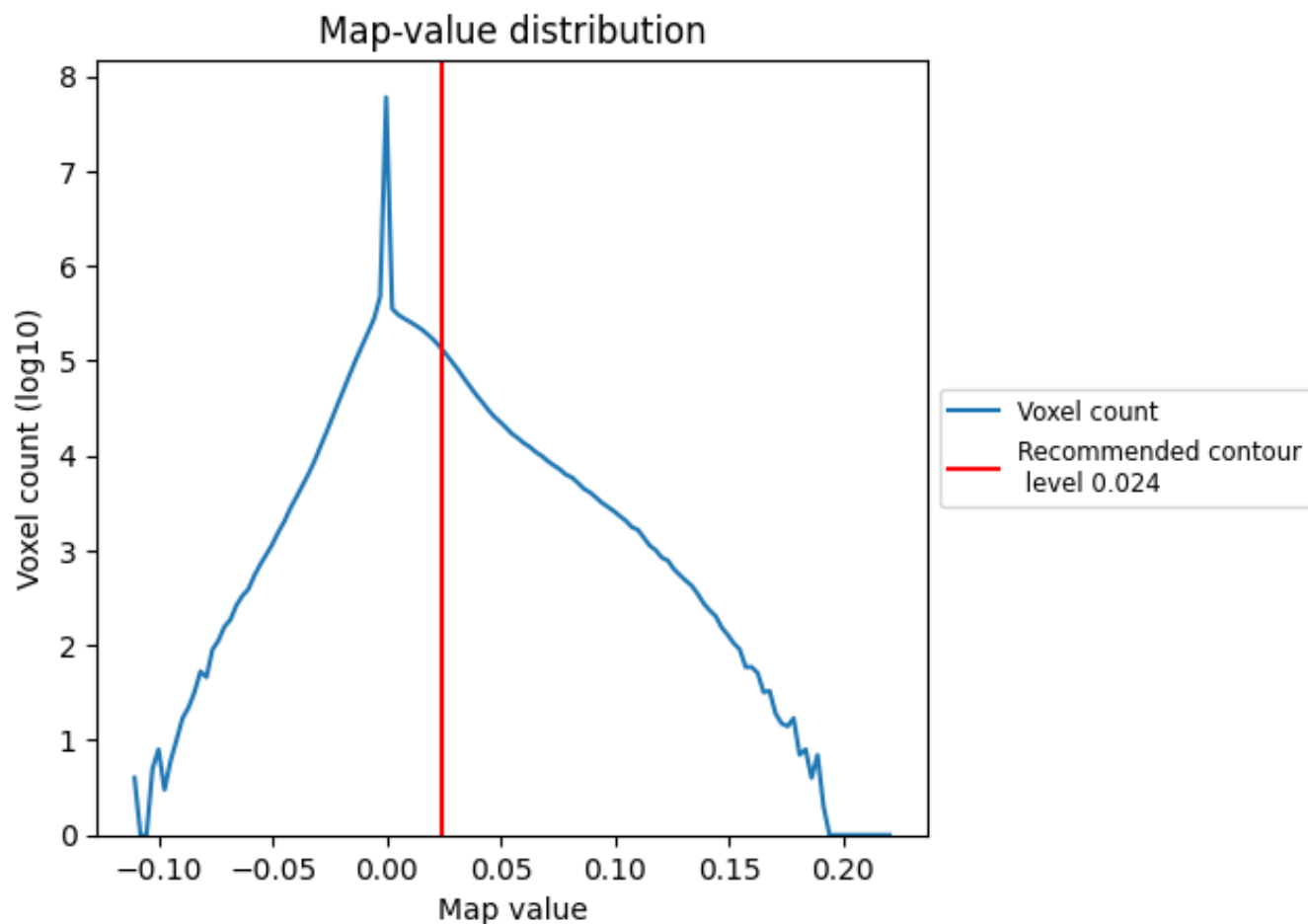
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

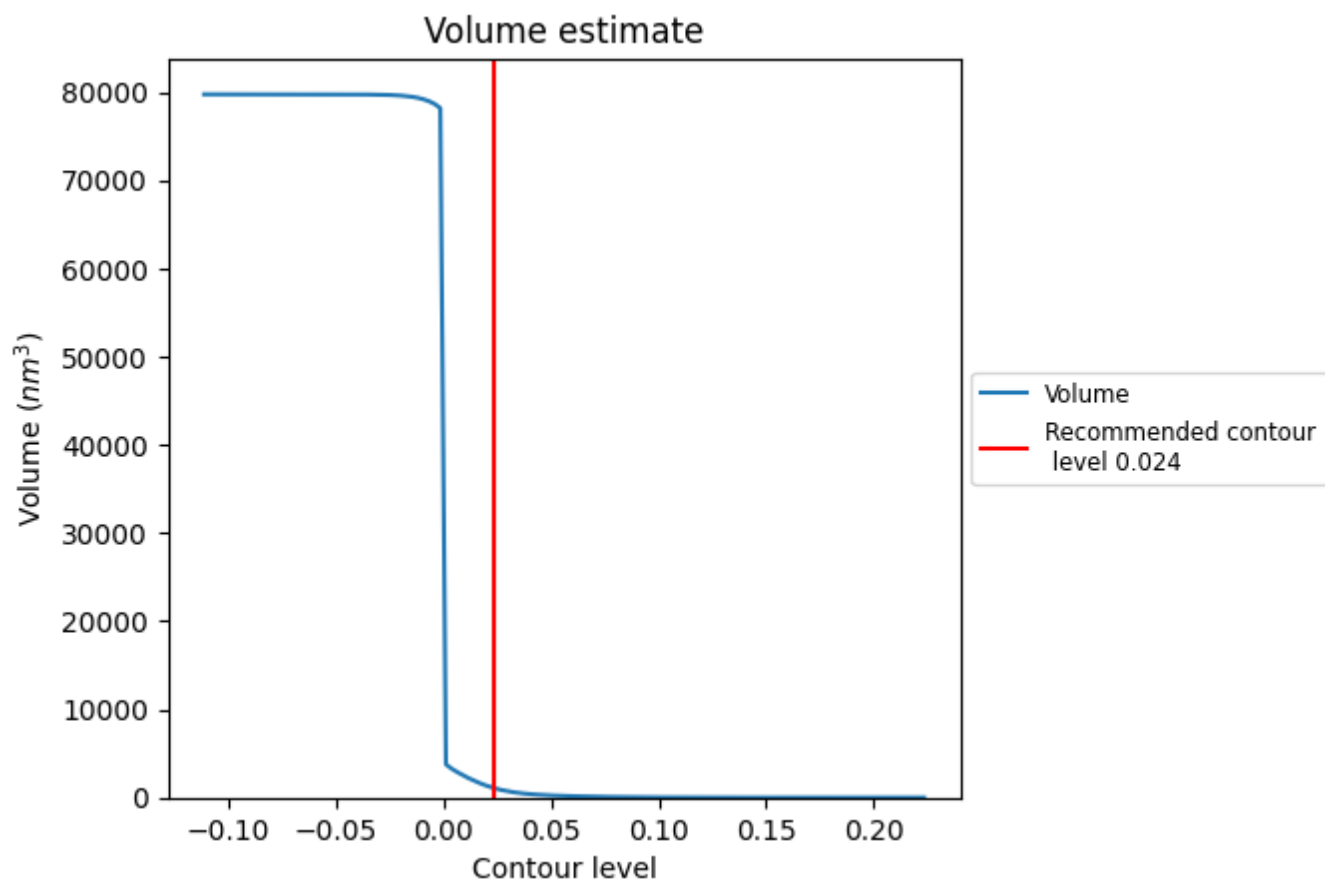
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

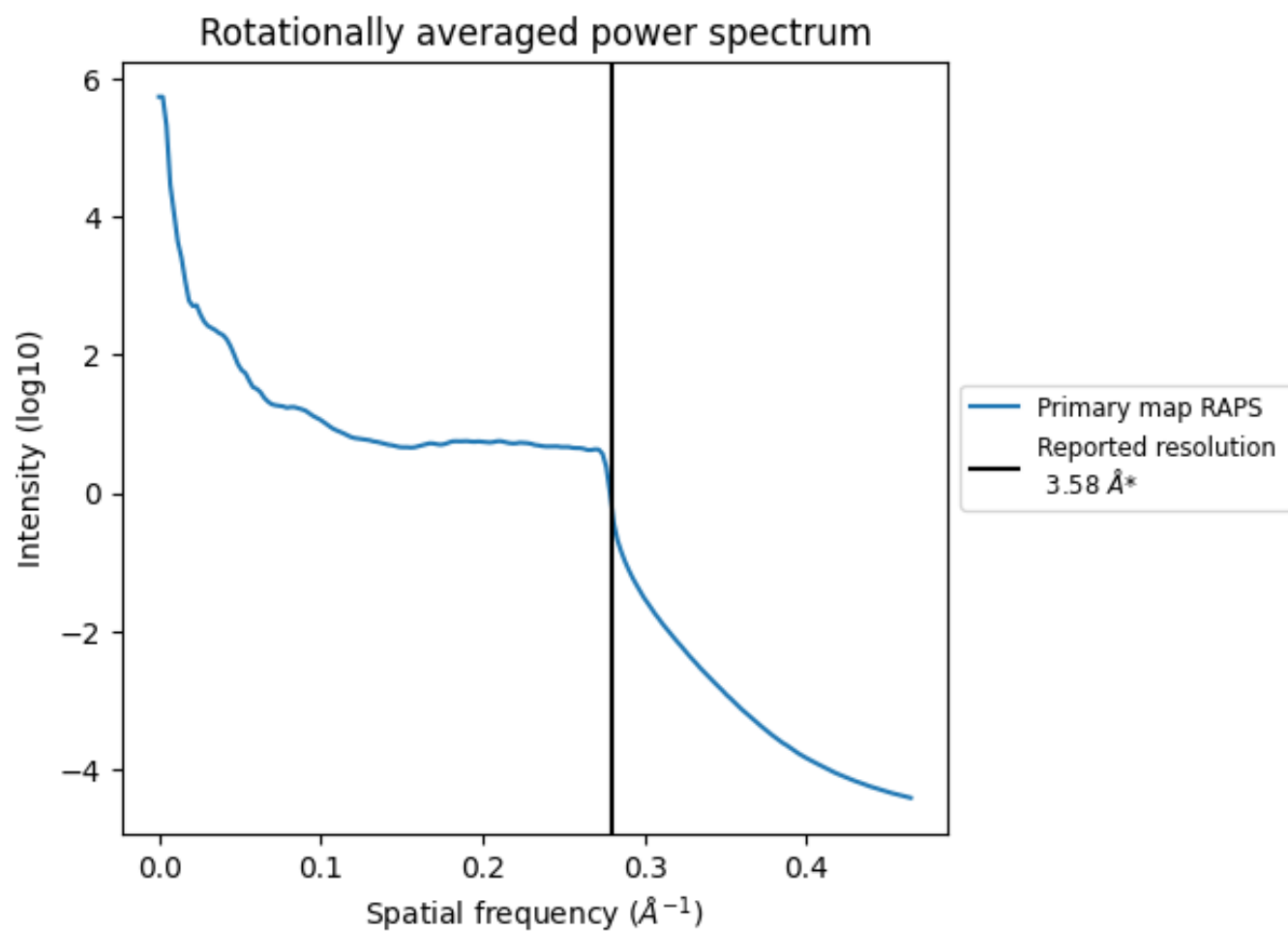
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1057 nm³; this corresponds to an approximate mass of 955 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.279 $\text{\AA}^{-1}$

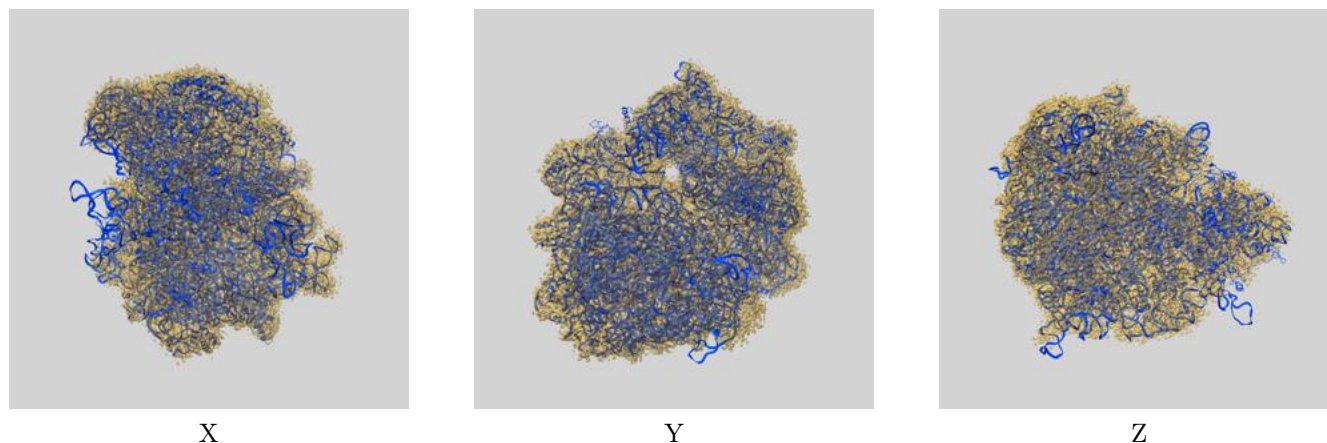
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

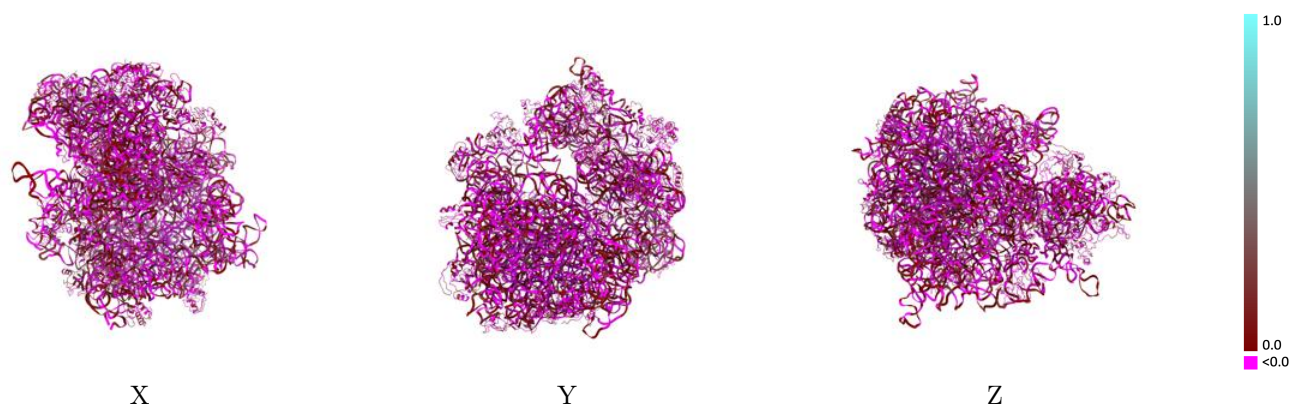
This section contains information regarding the fit between EMDB map EMD-10079 and PDB model 6S13. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



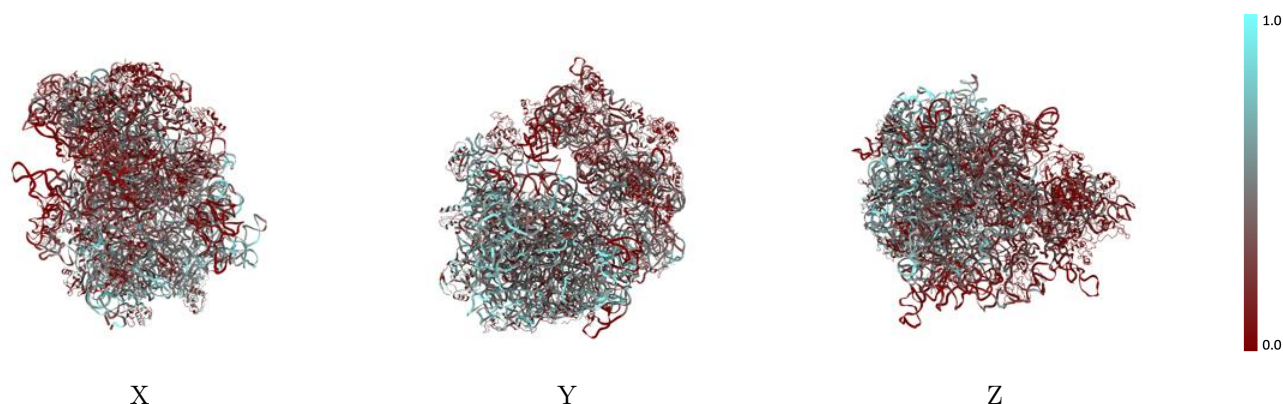
The images above show the 3D surface view of the map at the recommended contour level 0.024 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



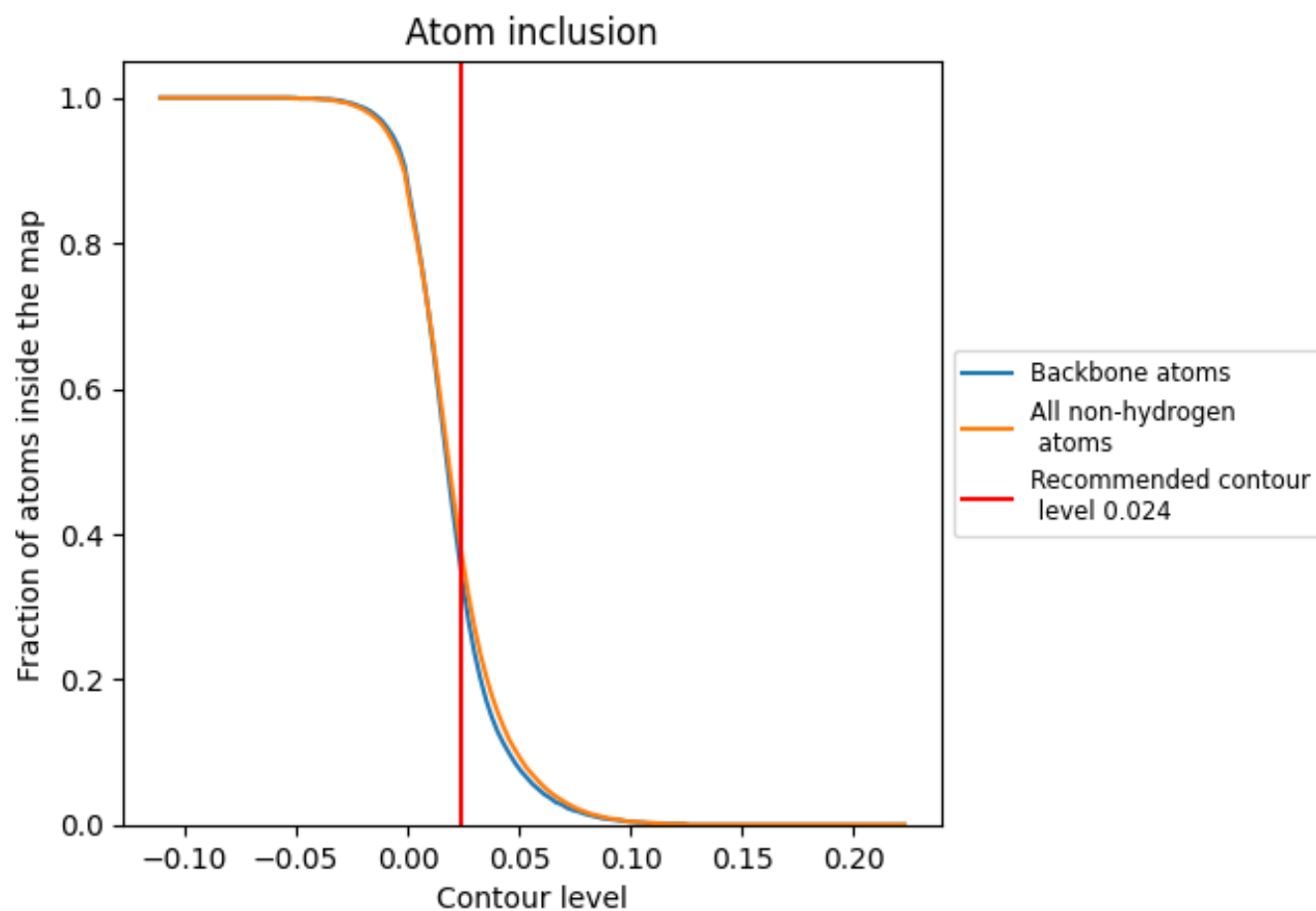
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.024).

9.4 Atom inclusion [i](#)



At the recommended contour level, 35% of all backbone atoms, 38% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.024) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3780	 0.0000
1	 0.2290	 -0.0040
2	 0.3500	 -0.0540
3	 0.3130	 -0.0380
4	 0.2980	 -0.0180
A	 0.4740	 -0.0050
B	 0.5730	 0.0480
C	 0.2990	 -0.0630
D	 0.3770	 -0.0010
E	 0.3470	 -0.0200
F	 0.1910	 0.0070
G	 0.0870	 0.0210
H	 0.4270	 0.0400
I	 0.3460	 -0.0150
J	 0.2960	 -0.0570
K	 0.3750	 0.0320
L	 0.3730	 -0.0090
M	 0.3260	 0.0230
N	 0.3690	 0.0090
O	 0.4070	 -0.0140
P	 0.4680	 0.0640
Q	 0.3610	 0.0150
R	 0.3150	 -0.0280
S	 0.3780	 0.0320
T	 0.2120	 0.0450
U	 0.2740	 -0.0630
V	 0.2560	 -0.0090
W	 0.3750	 0.0050
X	 0.4440	 0.0470
Y	 0.1300	 0.0460
Z	 0.4470	 0.0150
a	 0.3060	 0.0100
b	 0.0940	 -0.0110
c	 0.0960	 0.0130
d	 0.1580	 0.0010



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Chain	Atom inclusion	Q-score
e	 0.1370	 -0.0050
f	 0.1000	 -0.0310
g	 0.1180	 0.0080
h	 0.1730	 0.0040
i	 0.1860	 0.0240
j	 0.0680	 -0.0030
k	 0.1960	 -0.0190
l	 0.0590	 0.0220
m	 0.1020	 -0.0340
n	 0.1540	 -0.0110
o	 0.1240	 -0.0240
p	 0.1850	 0.0060
q	 0.2290	 -0.0070
r	 0.2200	 -0.0020
s	 0.1340	 -0.0130
t	 0.1200	 -0.0030
u	 0.1830	 0.0260
v	 0.0600	 0.0240