



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:53 PM UTC

PDB ID : 5GAK / pdb_00005gak
EMDB ID : EMD-3227
Title : Yeast 60S ribosomal subunit with A-site tRNA, P-site tRNA and eIF-5A
Authors : Schmidt, C.; Becker, T.
Deposited on : 2015-12-09
Resolution : 3.88 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

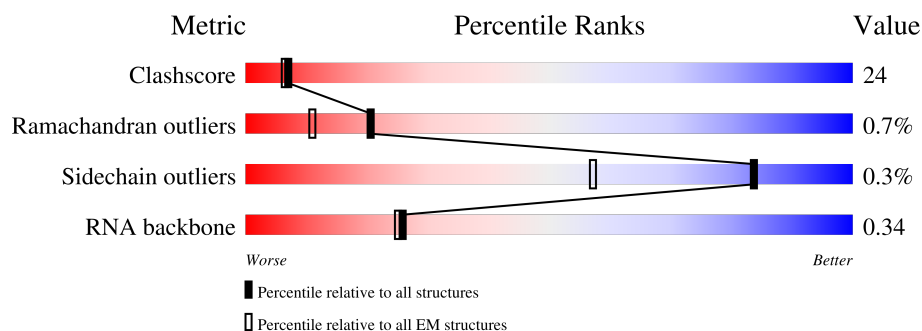
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.88 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	1	3396	
2	X	137	
3	3	121	
4	Y	155	
5	4	158	
6	Z	142	
7	A	76	

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Mol	Chain	Length	Quality of chain
8	a	127	
9	B	77	
10	b	136	
11	C	106	
12	c	149	
13	D	92	
14	d	59	
15	E	254	
16	e	105	
17	F	387	
18	f	109	
19	G	362	
20	g	130	
21	H	297	
22	h	107	
23	I	176	
24	i	121	
25	J	244	
26	j	120	
27	K	256	
28	k	100	
29	L	191	
30	l	88	
31	M	174	
32	m	78	

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Mol	Chain	Length	Quality of chain
33	N	199	
34	n	51	
35	O	138	
36	o	128	
37	P	204	
38	p	25	
39	Q	199	
40	q	157	
41	R	184	
42	r	210	
43	S	186	
44	s	221	
45	T	189	
46	U	172	
47	V	160	
48	W	121	
49	z	23	

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 128975 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 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3165	Total	C	N	O	P	0	0
			67695	30238	12201	22091	3165		

- Molecule 2 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 4 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Y	98	Total	C	N	O	S	0	0
			699	443	137	118	1		

- Molecule 5 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 6 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Z	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 7 is a RNA chain called The A-site tRNA was modeled based on an E. coli tRNA-Lys.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	76	Total	C	N	O	P	0	0
			1611	721	281	534	75		

- Molecule 8 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	a	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 9 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	77	Total	C	N	O	P	0	0
			1644	731	290	546	77		

- Molecule 10 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	b	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 11 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 12 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	c	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 13 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 14 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	d	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 15 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	E	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 16 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	e	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 17 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	F	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 18 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	f	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 19 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	G	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 20 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	g	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 21 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	H	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 22 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	h	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 23 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	I	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 24 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	i	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 25 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	J	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 26 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	j	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 27 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	K	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 28 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	k	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 29 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 30 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	l	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 31 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	M	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 32 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	m	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 33 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	N	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 34 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	n	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 35 is a protein called 60S ribosomal protein L14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	O	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 36 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	o	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 37 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	P	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 38 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	p	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 39 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Q	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 40 is a protein called Eukaryotic translation initiation factor 5A-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	q	154	Total	C	N	O	S	0	0
			1143	709	195	230	9		

- Molecule 41 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	R	183	Total	C	N	O		0	0
			1420	882	281	257			

- Molecule 42 is a protein called ribosomal protein RPL1.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	r	210	Total	C	N	O	0	0
			1050	630	210	210		

- Molecule 43 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	S	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 44 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	s	220	Total	C	N	O	S	0	0
			1770	1121	335	307	7		

- Molecule 45 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	T	188	Total	C	N	O	0	0
			1521	935	326	260		

- Molecule 46 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	U	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 47 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	V	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

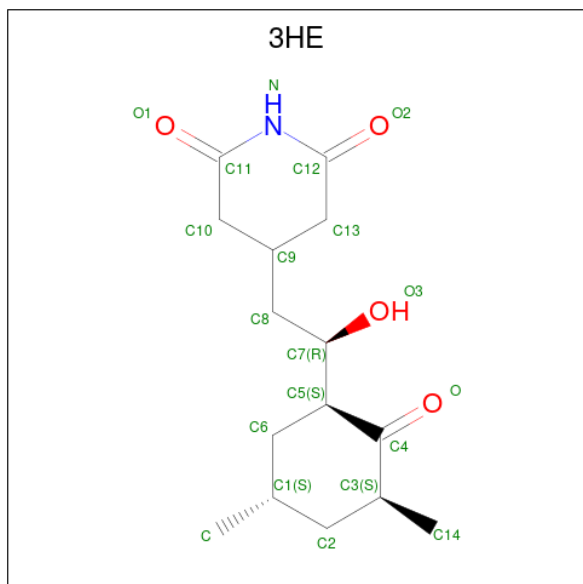
- Molecule 48 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	W	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 49 is a protein called nascent polypeptide chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	z	23	Total	C	N	O	0	0
			115	69	23	23		

- Molecule 50 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (CCD ID: 3HE) (formula: C₁₅H₂₃NO₄).

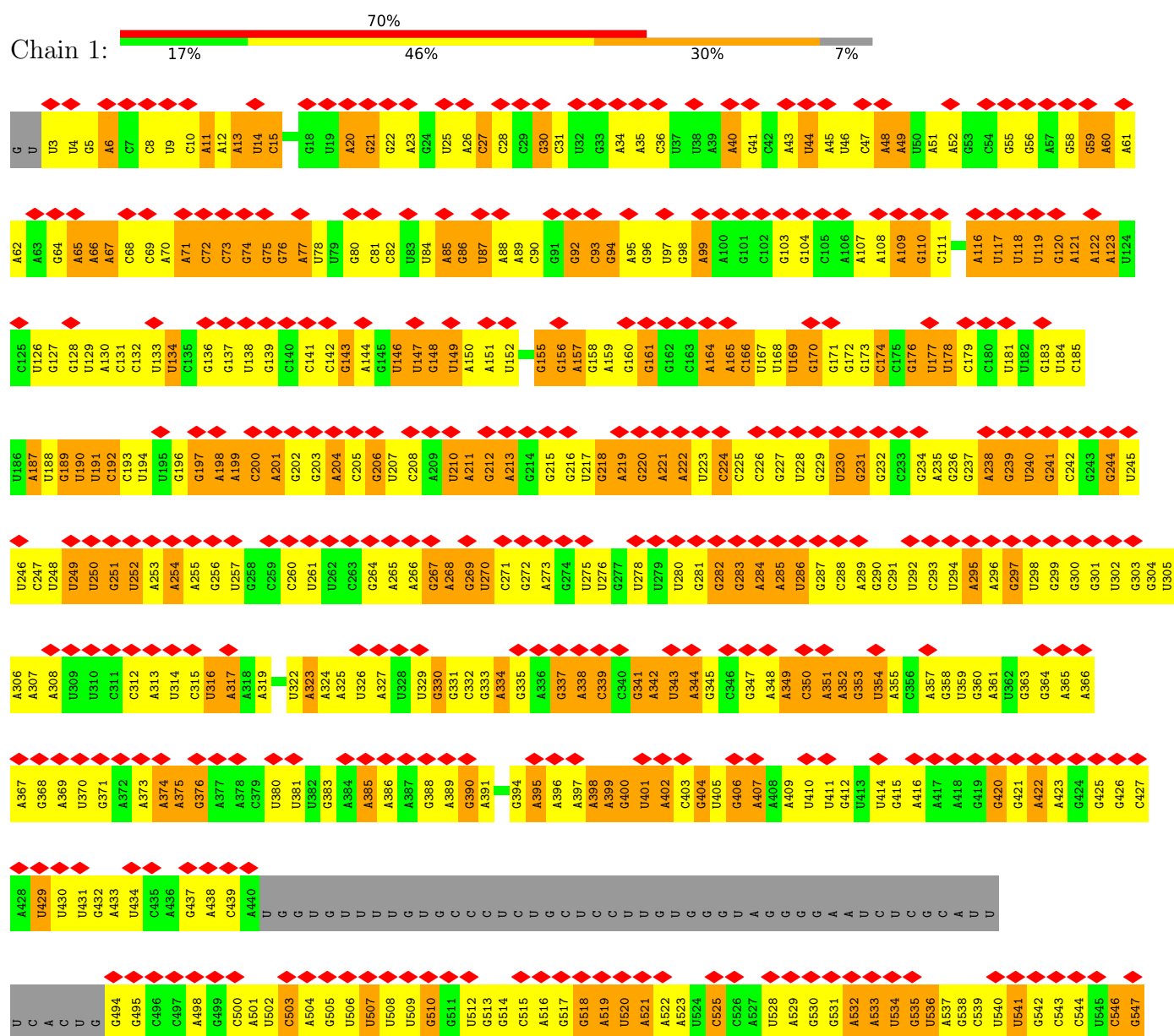


Mol	Chain	Residues	Atoms				AltConf
50	1	1	Total	C	N	O	0
			20	15	1	4	

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.

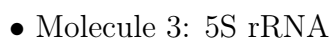
• Molecule 1: 25S rRNA

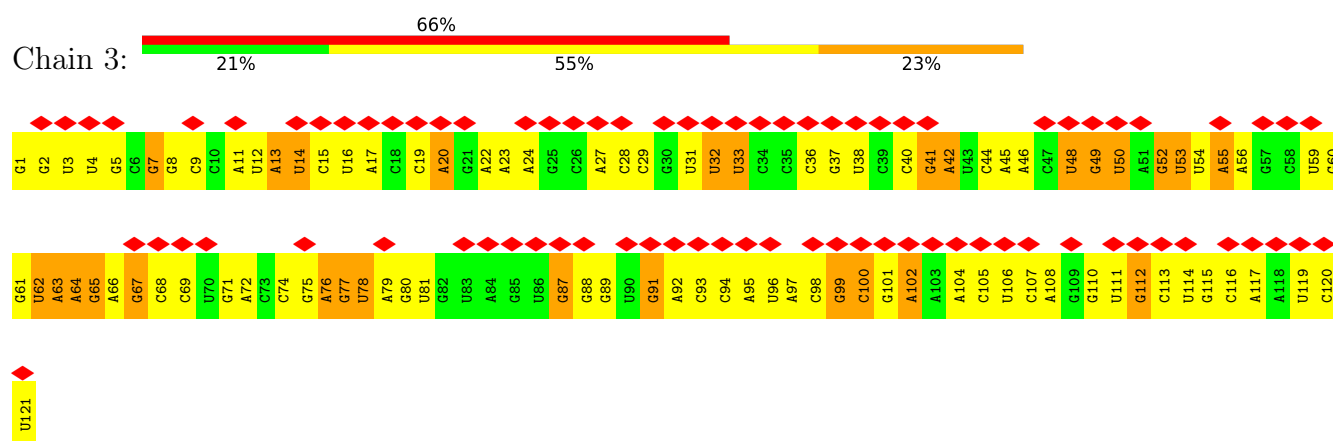


A1270	A1271	C1272	A1273	A1274	C1275	U1276	C1277	A1278	C1279	C1280	G1281	G1282	C1283	C1284	C1285	A1286	A1287	U1288	G1289	A1290	A1291	C1292	U1293	A1294	G1295	C1296	C1297	C1298	U1299	G1300	A1301	A1302	A1303	A1304	U1305	G1306	G1307	A1308	U1309	G1310	G1311	C1312	G1313	C1314	U1315	C1316	A1317	A1318	G1319	C1320	G1321	U1322	G1323	U1324	A1325	A1326	C1327	U1328	U1329	
U1210	U1211	A1212	G1213	U1214	U1215	C1216	A1217	U1218	C1219	U1220	A1221	G1222	A1223	C1224	A1225	G1226	C1227	U1228	C1229	U1230	A1231	C1232	G1233	G1234	U1235	G1236	G1237	C1238	C1239	A1240	U1241	G1242	G1243	A1244	A1245	G1246	U1247	C1248	G1249	G1250	A1251	A1252	G1253	C1254	C1255	G1256	C1257	U1258	U1259	A1260	C1261	G1262	A1263	U1264	U1265	G1266	U1267	U1268	U1269	
A1150	U1151	G1152	A1153	A1154	C1155	C1156	G1157	A1158	A1159	C1160	G1161	U1162	A1163	G1164	A1165	G1166	U1167	U1168	A1169	A1170	G1171	G1172	U1173	G1174	C1175	C1176	G1177	G1178	A1179	A1180	U1181	A1182	C1183	A1184	C1185	G1186	C1187	U1188	C1189	A1190	U1191	C1192	A1193	G1194	A1195	C1196	A1197	C1198	C1199	A1200	C1201	A1202	A1203	A1204	A1205	G1206	G1207	U1208	G1209	
G1090	A1091	C1092	A1093	U1094	U1095	U1096	G1097	A1098	A1099	U1100	G1101	A1102	A1103	G1104	A1105	G1106	U1107	U1108	U1109	U1110	U1111	A1112	G1113	U1114	G1115	G1116	G1117	C1118	C1119	A1120	U1121	U1122	U1123	U1124	U1125	G1126	G1127	U1128	A1129	A1130	G1131	C1132	A1133	G1134	A1135	A1136	C1137	U1138	G1139	G1140	C1141	G1142	A1143	U1144	G1145	C1146	G1147	G1148	G1149	
A1030	C1031	C1032	U1033	U1034	G1035	A1036	C1037	C1038	U1039	A1040	U1041	U1042	C1043	U1044	C1045	A1046	A1047	A1048	C1049	U1050	U1051	U1052	A1053	A1054	A1055	U1056	A1057	U1058	G1059	U1060	A1061	A1062	G1063	A1064	A1065	G1066	U1067	C1068	C1069	U1070	U1071	G1072	U1073	U1074	A1075	C1076	U1077	U1078	A1079	A1080	U1081	U1082	G1083	A1084	A1085	C1086	G1087	U1088	G1089	
G970	G971	A972	A973	G974	C975	U976	C977	G978	U979	A980	U981	C982	A983	U984	G984	U985	U986	U987	U988	A989	U990	G991	A992	G993	G994	U995	A996	A997	A998	G999	C1000	G1001	A1002	A1003	U1004	G1005	A1006	U1007	U1008	A1009	G1010	U1011	G1012	G1013	U1014	U1015	C1016	C1017	U1018	G1019	A1020	G1021	U1022	C1023	G1024	A1025	A1026	A1027	U1028	G1029
U850	C851	U852	G853	G854	U855	G856	G857	A858	G859	G860	C861	U862	C863	G864	U865	A866	G867	C868	G869	G870	U871	U872	C873	U874	G875	A876	C877	G878	U879	U880	C881	A882	C883	A884	U885	C886	G887	A888	U889	C890	G891	U892	C893	G894	A895	A896	U897	U898	U899	G900	G901	G902	U903	A904	U905	A906	G907	G908	G909	
A789	U790	A791	G792	C793	U794	G795	U796	U797	G798	G799	G800	A801	C802	C803	C804	G805	A806	A807	A808	G809	A810	U811	G812	G813	U814	G815	A816	A817	C818	U819	A820	U821	G822	C823	C824	U825	G826	A827	U828	U829	A830	G831	G832	C833	U834	G835	A836	U837	G838	C839	C840	A841	G842	G845	A846	A847	A848	C849		
C729	C730	U731	C732	C733	C734	A735	A736	G737	A738	G739	G740	U741	G742	C743	A744	C745	A746	U747	U748	C749	G750	A751	C752	C753	G754	A755	U756	C757	C758	U759	G760	A761	U762	G763	U764	C765	U766	U767	C768	G769	A770	U771	G772	G773	G774	A775	U776	U777	U778	G779	A780	G781	U782	A783	A784	G785	A786	G787	C788	
G668	U669	C670	U671	A672	U673	U674	C675	G676	A677	G678	U679	G680	U681	U682	U683	G684	G685	G686	U687	A688	A689	A690	A691	A692	C693	C694	C695	A696	U697	U698	A699	C700	G701	C702	G703	U704	A705	U706	U707	G708	A709	A710	A711	U712	U713	G714	A715	A716	C717	G718	U719	A720	G721	G722	U723	U724	G725	G726	G727	G728
A608	G609	G610	A611	U612	G613	C614	U615	G616	G617	C618	A619	U620	A621	A622	U623	G624	G625	U626	U627	A628	U629	A630	U631	G632	C633	C634	G635	C636	C637	C638	G639	U640	C641	U642	U643	G644	A645	A646	A647	C648	A649	C650	G651	G652	A653	C654	G655	U656	A657	G658	C659	U660	G661	U662	C663	U664	A665	A666	C667	
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C	A1933	U1873	A1813	G1753	U1692	A1632	U1572	U1512	A1452	C1391	A1330
C	G1934	A1874	A1814	G1754	C1693	C1633	G1573	G1513	A1453	G1392	U1331
U	A1936	G1875	U1815	C1755	U1694	G1634	C1574	A1514	A1454	A1393	A1332
G	U1937	U1876	A1816	G1756	U1695	U1635	A1575	A1515	U1455	G1395	C1333
G	U1938	U1817	G1817	A1757	A1696	U1636	A1576	C1516	U1456	C1396	U1334
U	G1939	G1878	U1818	G1758	A1697	A1637	G1577	G1517	U1457	C1397	C1335
A	G1940	A1879	U1819	A1760	C1698	A1638	C1578	U1518	U1458	U1398	U1336
G	U1941	U1880	U1820	C1761	A1699	C1639	C1579	G1519	A1337	A1399	A1337
G	U1942	U1881	U1821	C1762	G1700	G1640	A1580	G1520	A1460	G1400	C1338
U	C1943	U1882	U1822	U1763	G1701	U1641	C1581	G1521	A1461	A1401	C1339
G	U1944	G1882	A1823	U1764	U1702	A1642	C1582	U1522	A1462	C1402	G1340
C	A1945	U1765	U1703	U1765	U1703	A1643	A1583	U1523	U1463	G1403	U1341
U	A1946	G1766	U1704	G1766	U1704	C1644	A1584	A1524	G1464	G1404	U1342
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G	U1888	G1829	A1829	G1769	U1707	A1648	A1588	G1528	A1468	G1408	G1346
C	G1889	G1830	G1830	G1770	C1708	U1649	A1589	U1529	C1469	G1409	U1347
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C	G1892	A1833	C1833	C1773	C1711	G1652	G1592	C1532	U1472	G1412	A1350
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C	U1931	U1871	U1871	A1752	A1752	U1691			U1511		A1390
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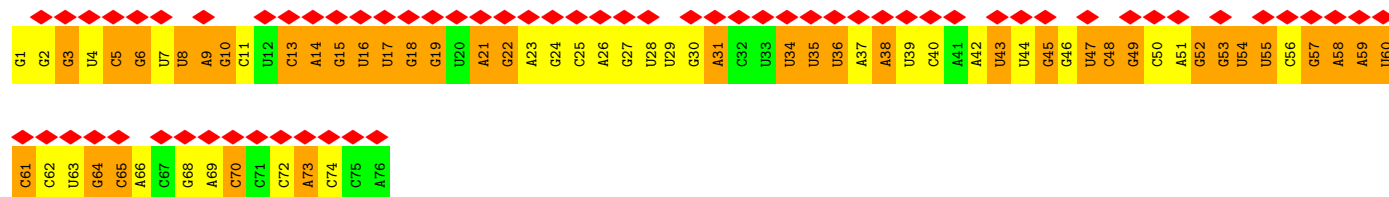
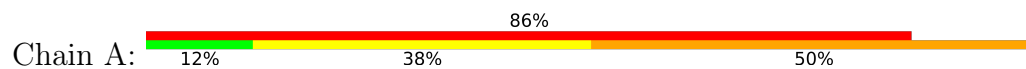




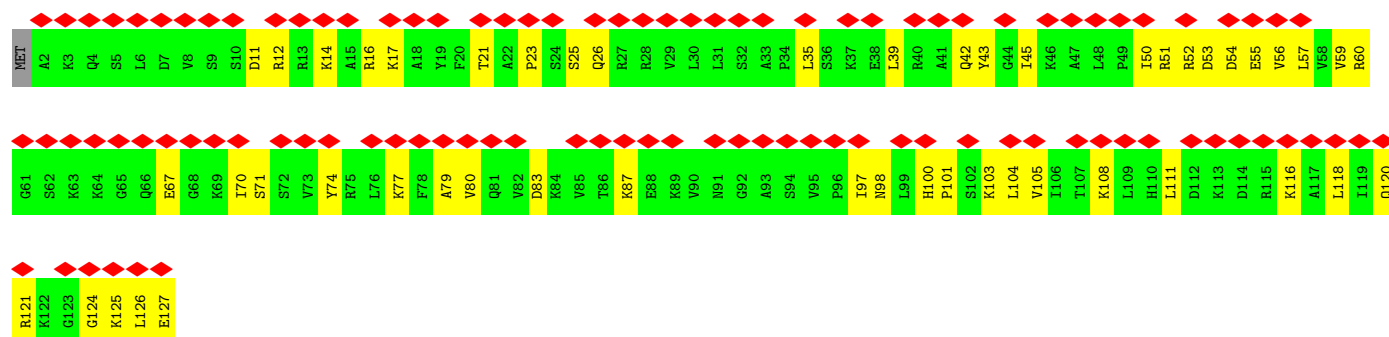
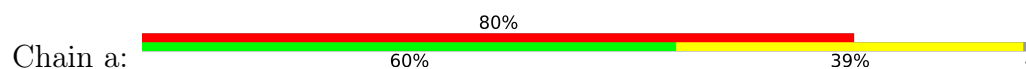




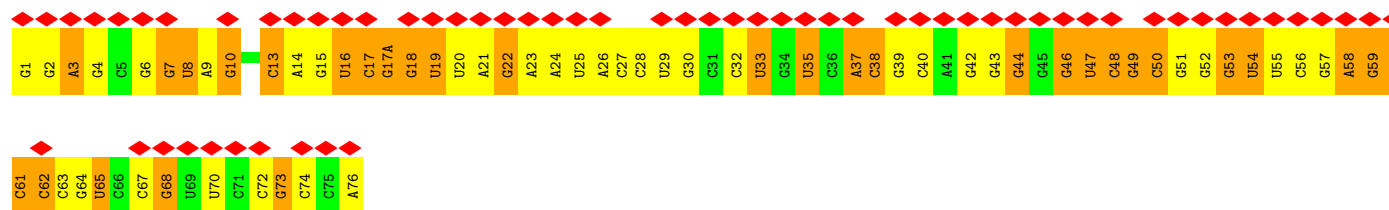
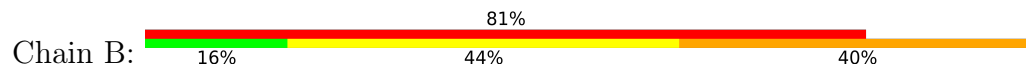
- Molecule 7: The A-site tRNA was modeled based on an *E. coli* tRNA-Lys



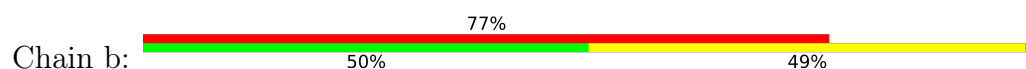
- Molecule 8: 60S ribosomal protein L26-A

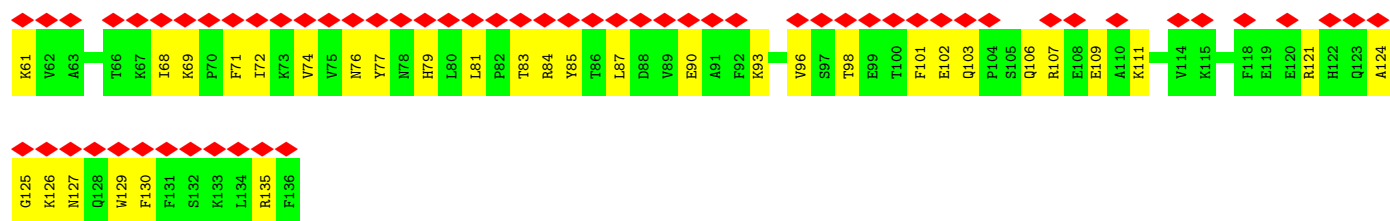


- Molecule 9: P-site tRNA

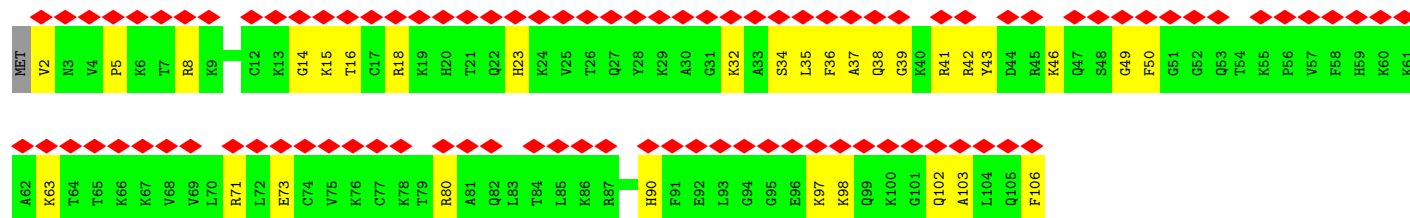
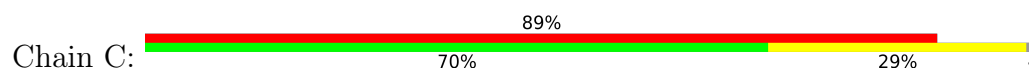


- Molecule 10: 60S ribosomal protein L27-A

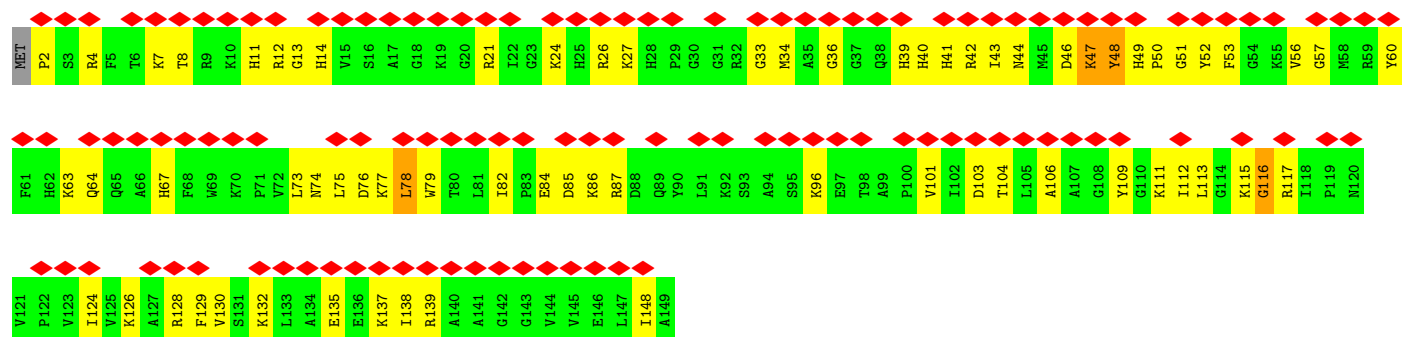
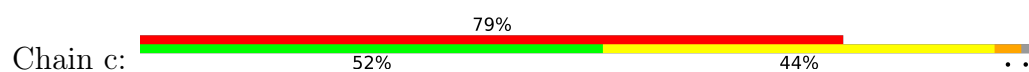




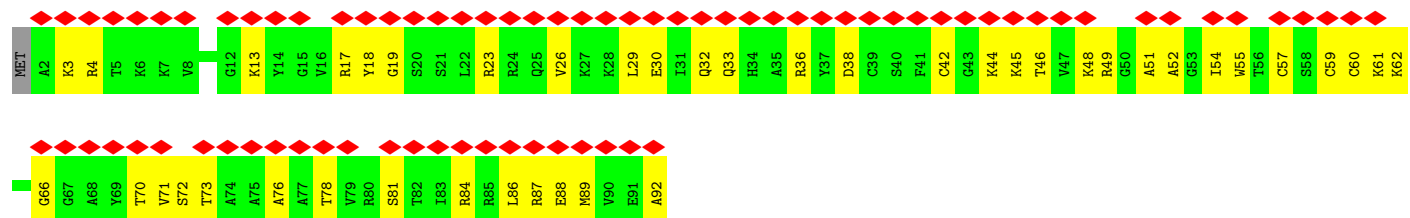
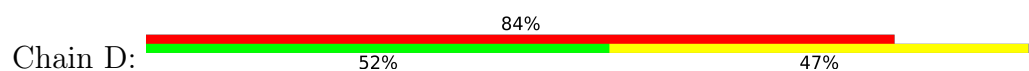
• Molecule 11: 60S ribosomal protein L42-A



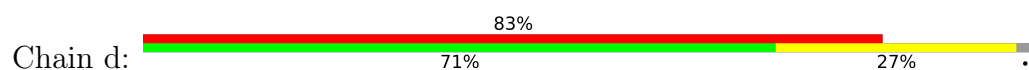
• Molecule 12: 60S ribosomal protein L28



• Molecule 13: 60S ribosomal protein L43-A

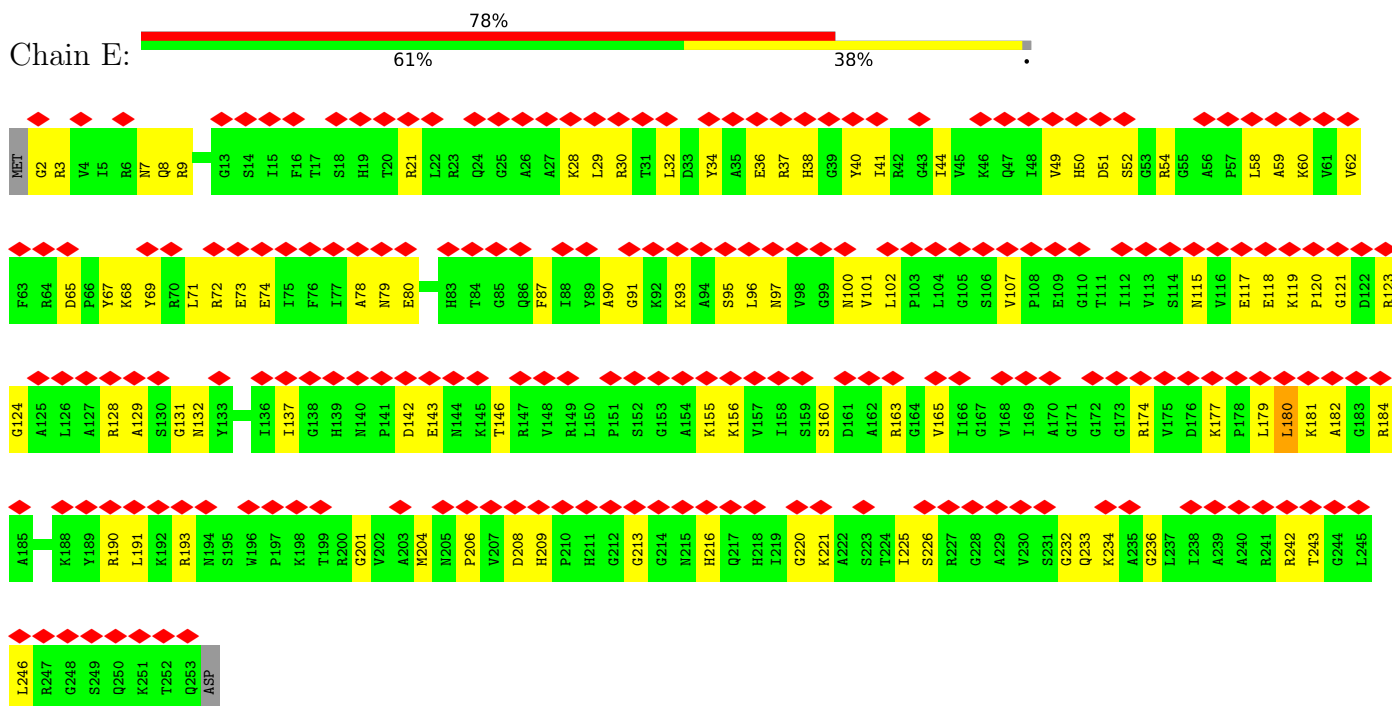


• Molecule 14: 60S ribosomal protein L29

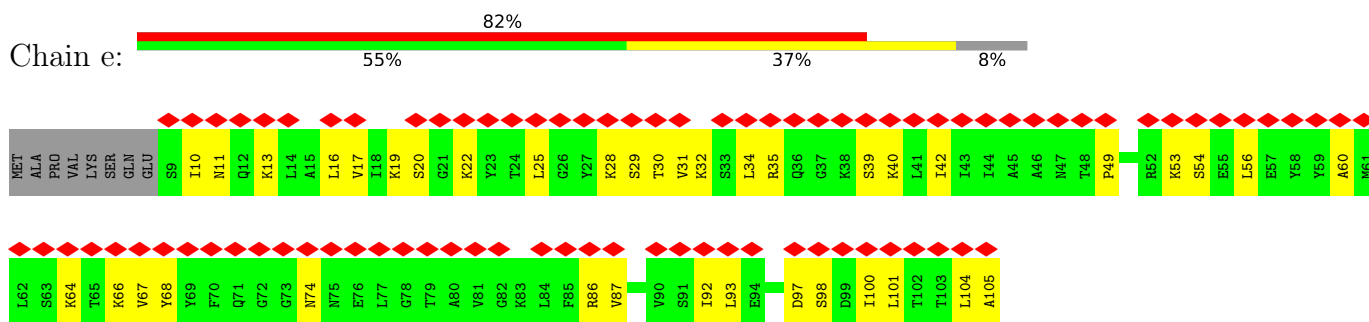




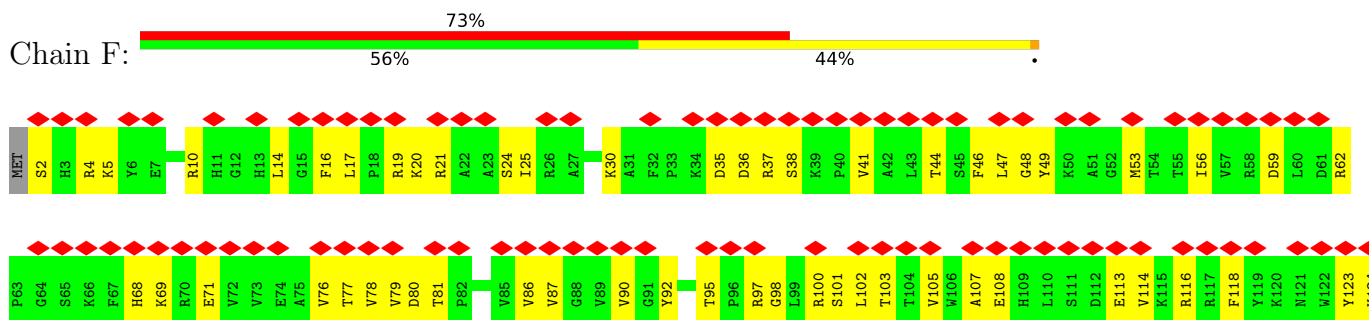
• Molecule 15: 60S ribosomal protein L2-A

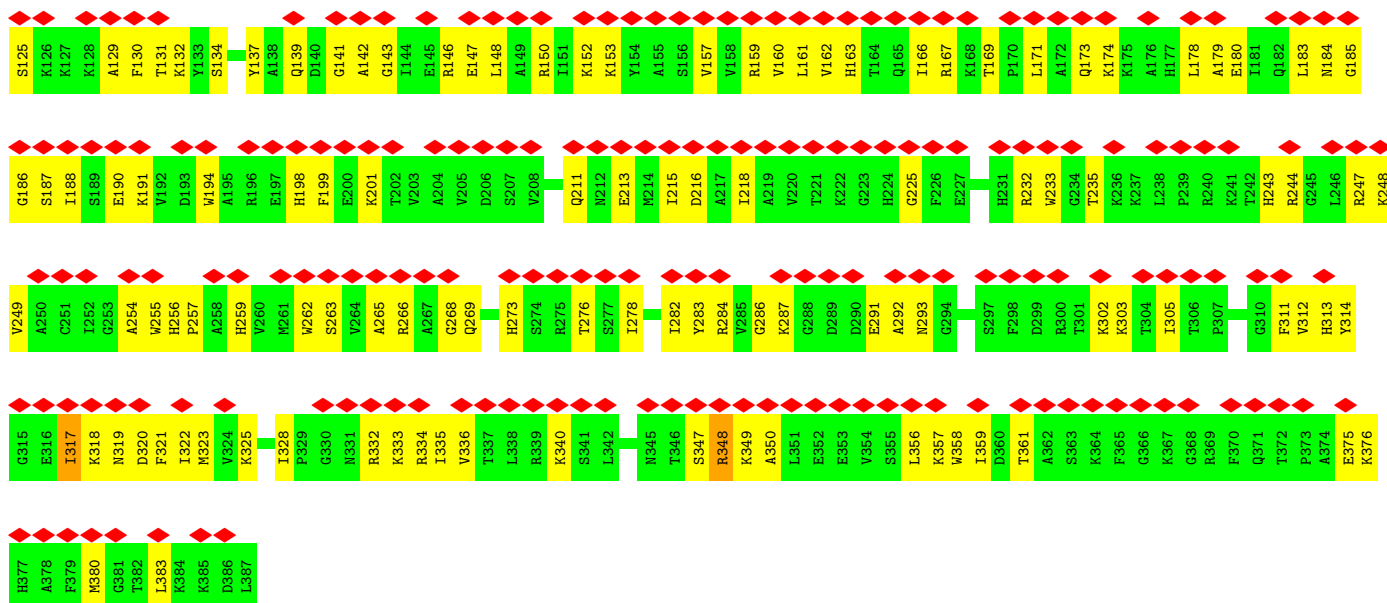


• Molecule 16: 60S ribosomal protein L30

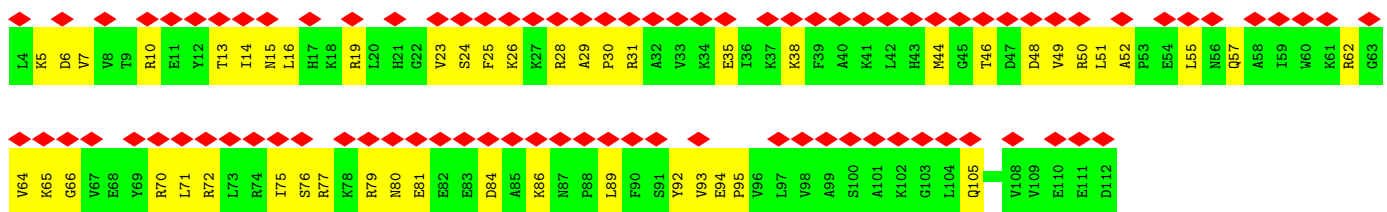
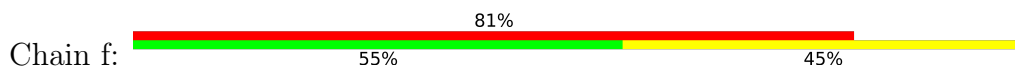


• Molecule 17: 60S ribosomal protein L3

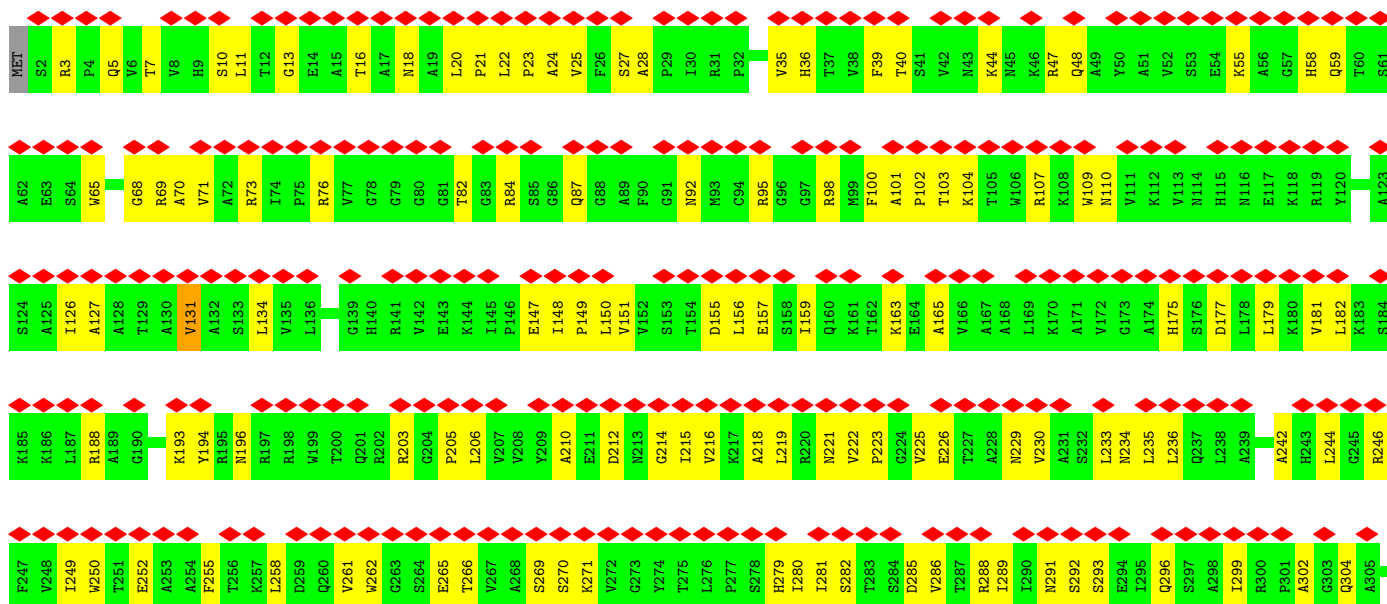
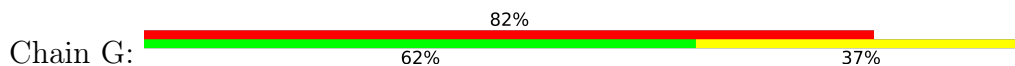




• Molecule 18: 60S ribosomal protein L31-A

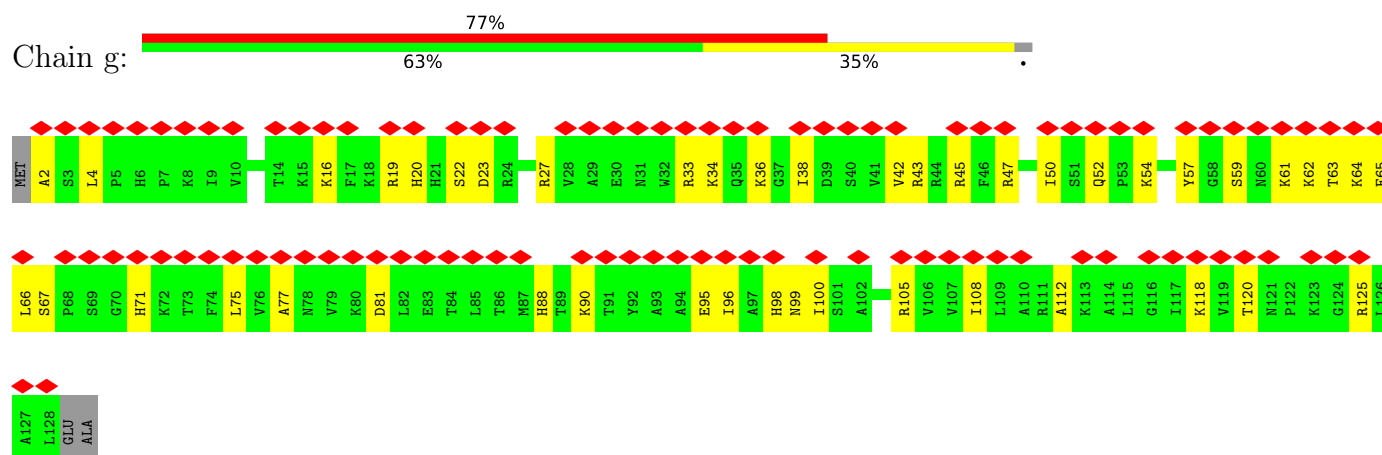


• Molecule 19: 60S ribosomal protein L4-A

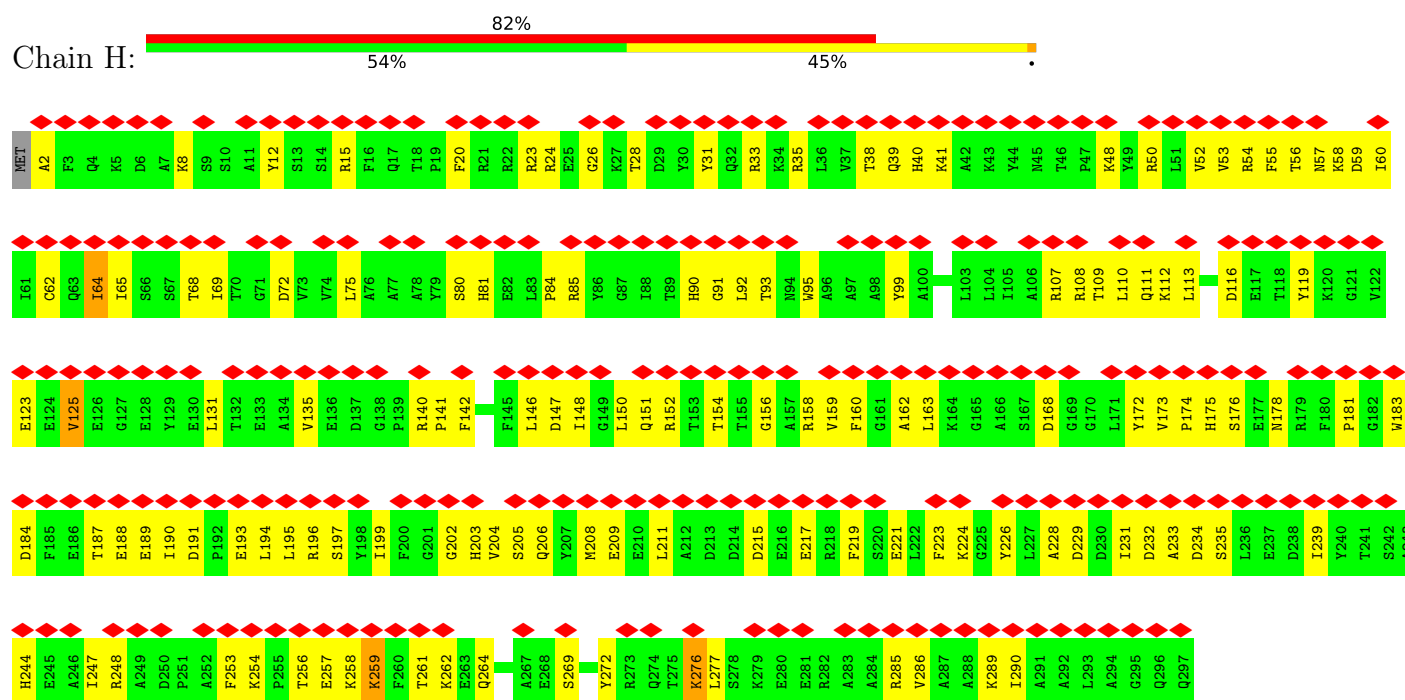




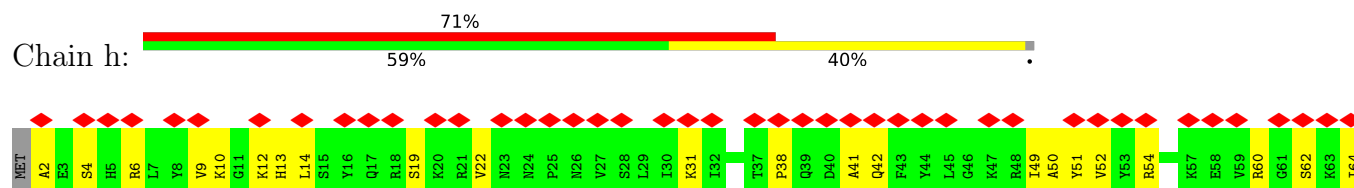
• Molecule 20: 60S ribosomal protein L32



• Molecule 21: 60S ribosomal protein L5

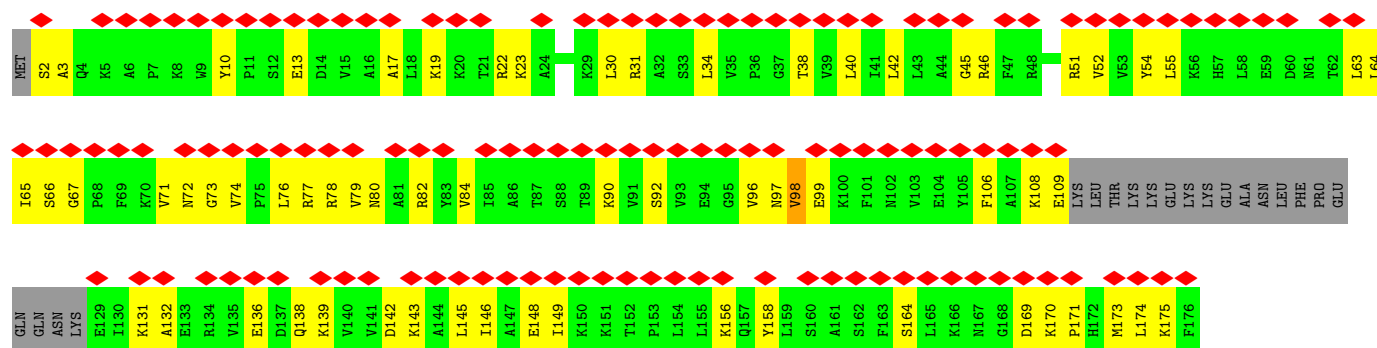
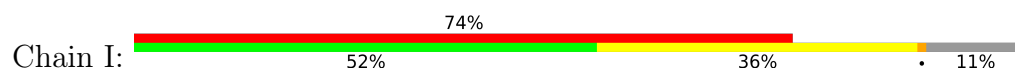


• Molecule 22: 60S ribosomal protein L33-A

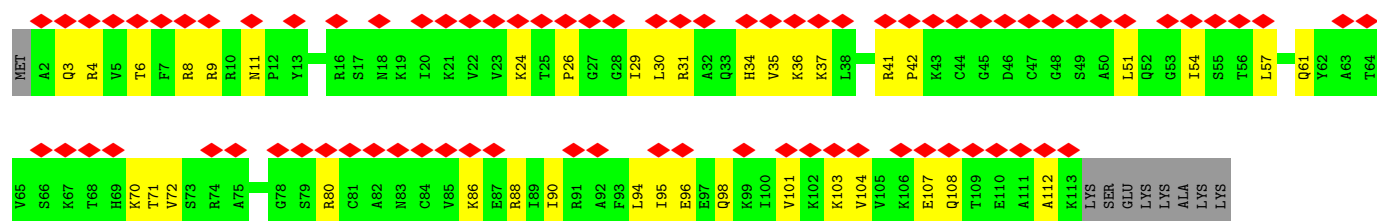




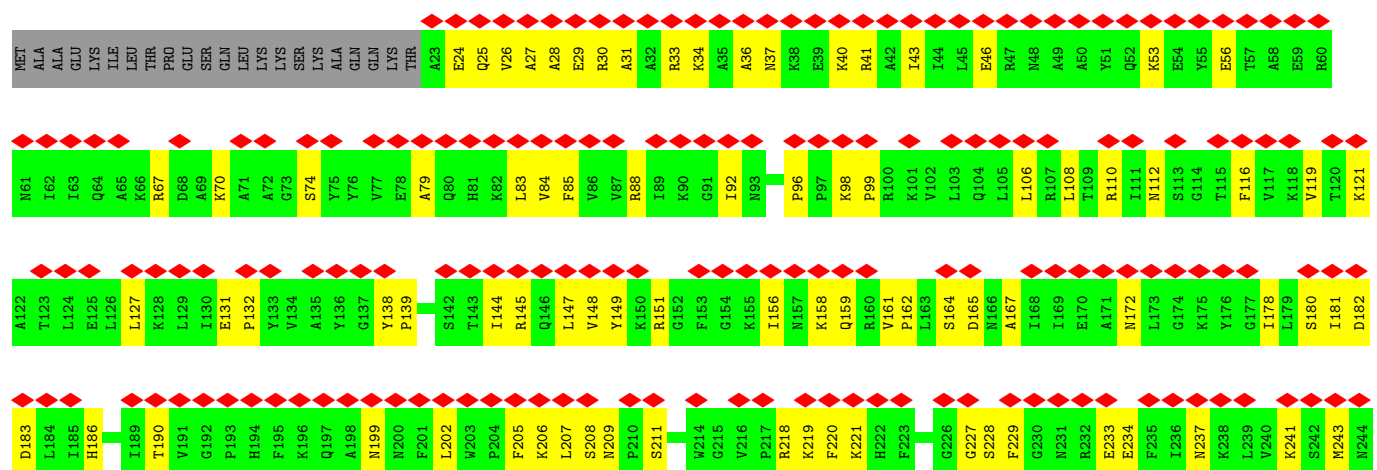
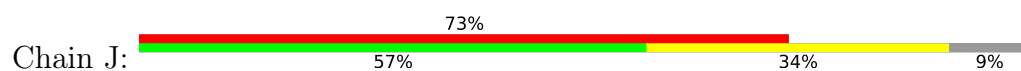
• Molecule 23: 60S ribosomal protein L6-A



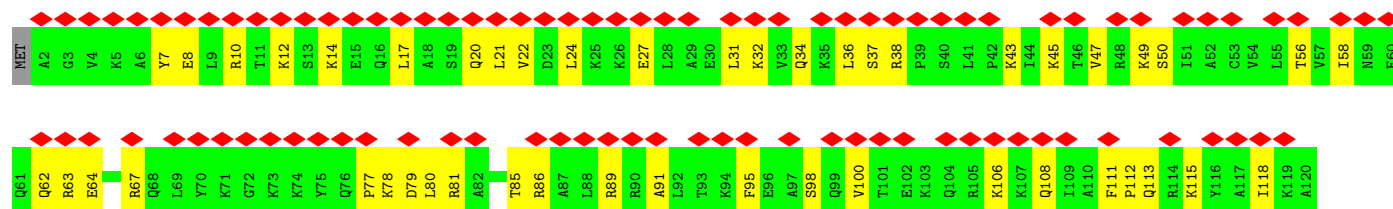
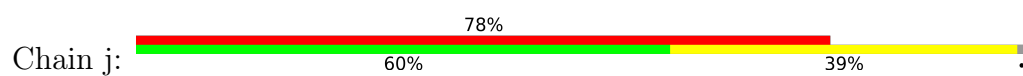
• Molecule 24: 60S ribosomal protein L34-A



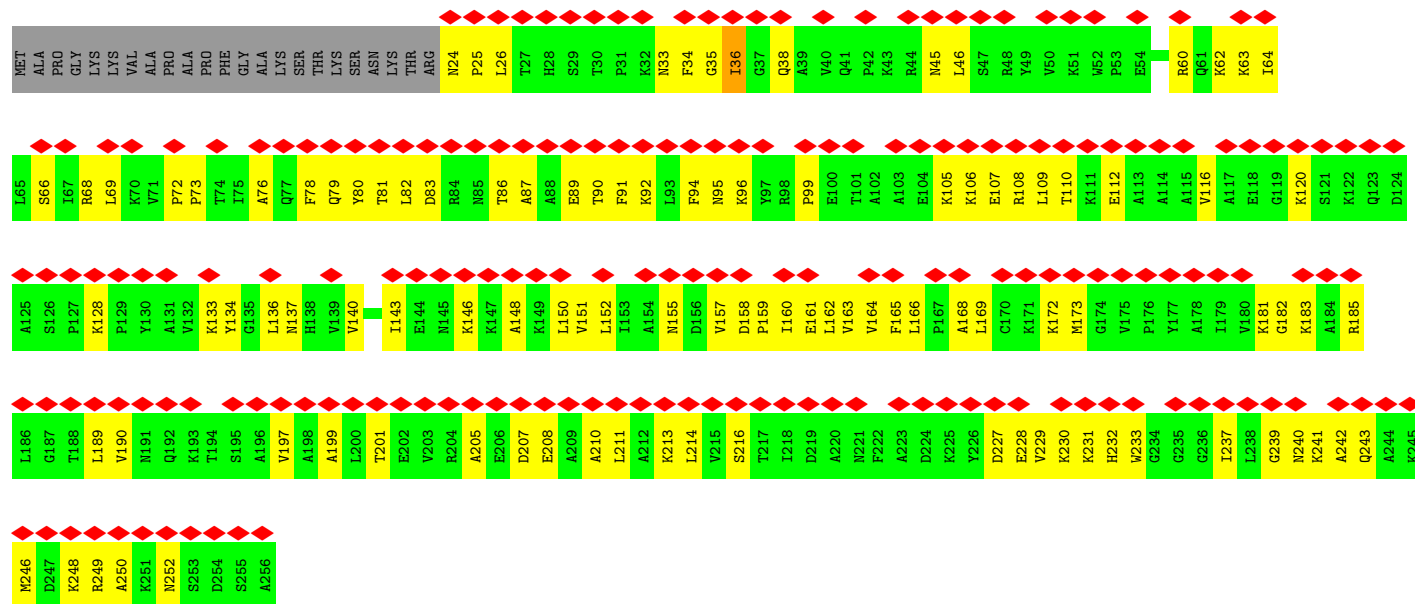
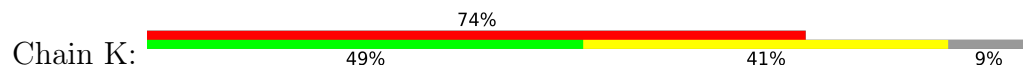
• Molecule 25: 60S ribosomal protein L7-A



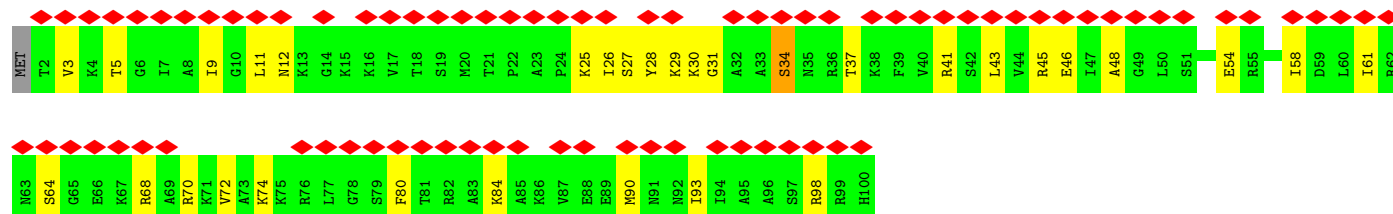
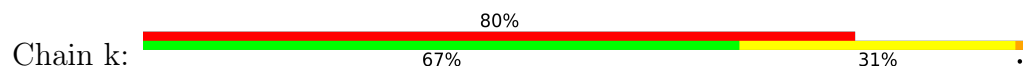
• Molecule 26: 60S ribosomal protein L35-A



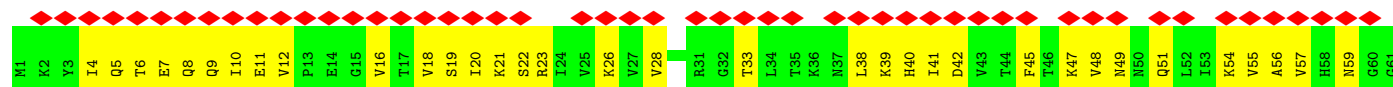
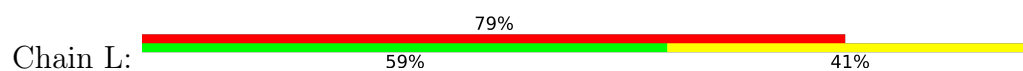
• Molecule 27: 60S ribosomal protein L8-A

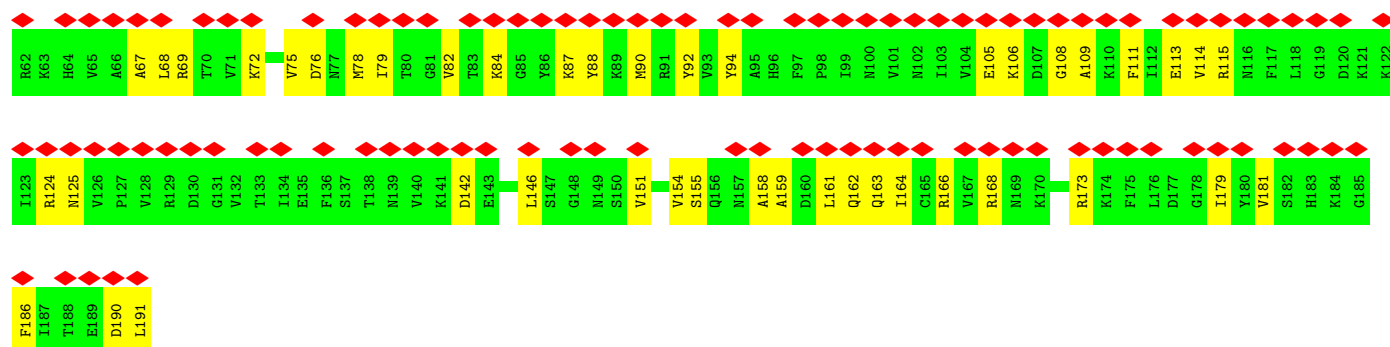


• Molecule 28: 60S ribosomal protein L36-A



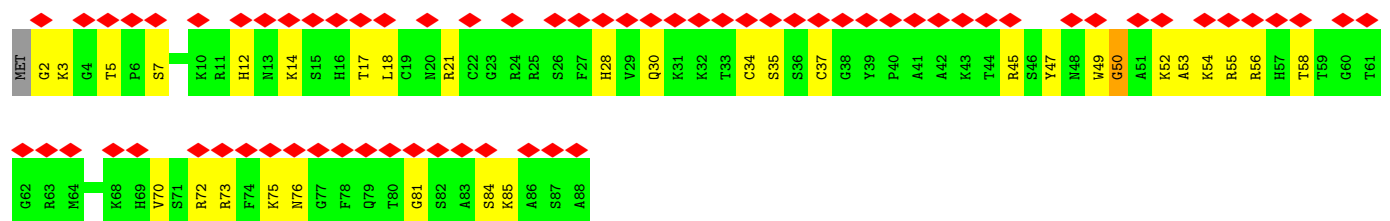
• Molecule 29: 60S ribosomal protein L9-A





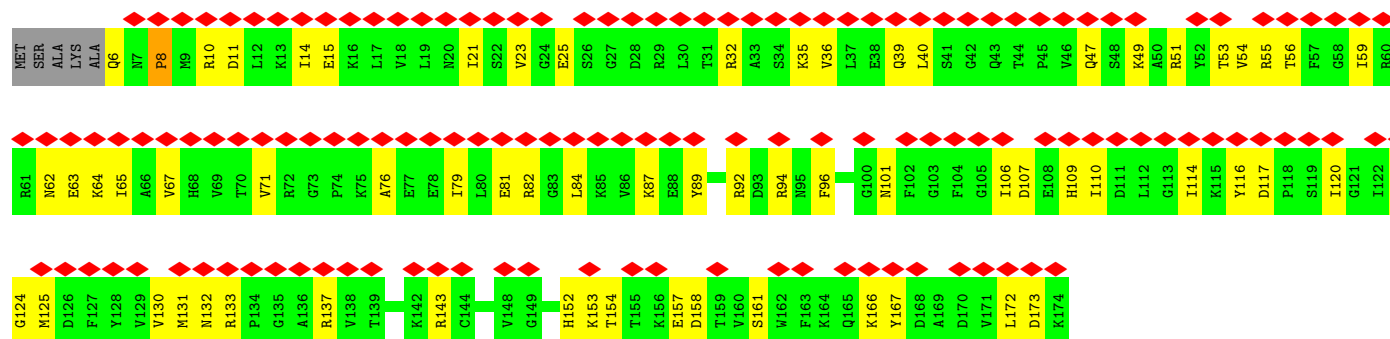
• Molecule 30: 60S ribosomal protein L37-A

Chain I:



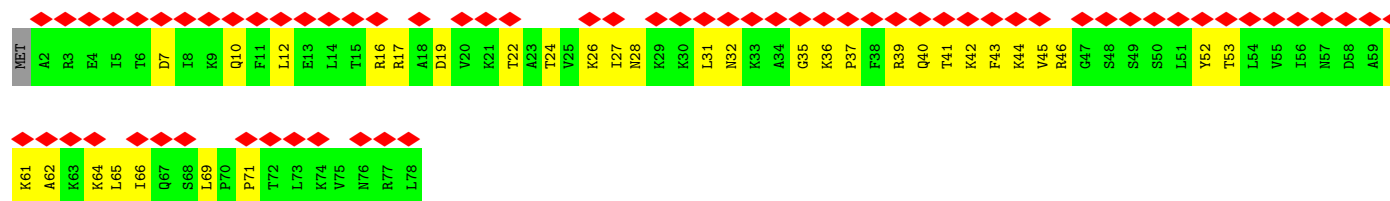
• Molecule 31: 60S ribosomal protein L11-A

Chain M:

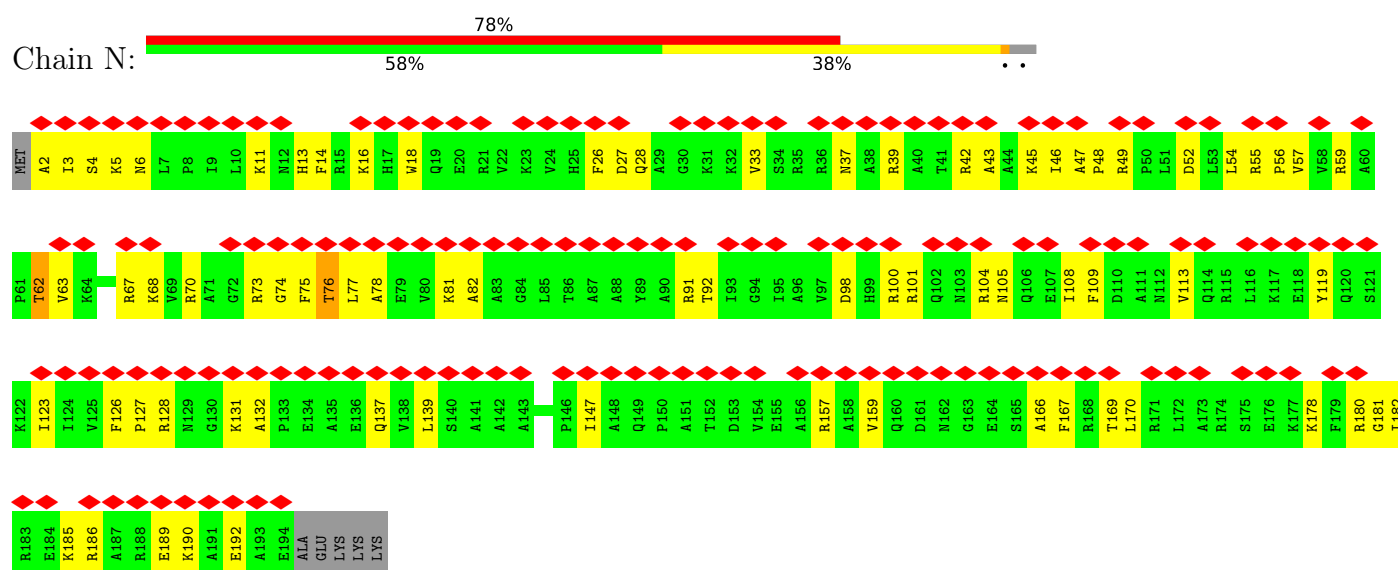


• Molecule 32: 60S ribosomal protein L38

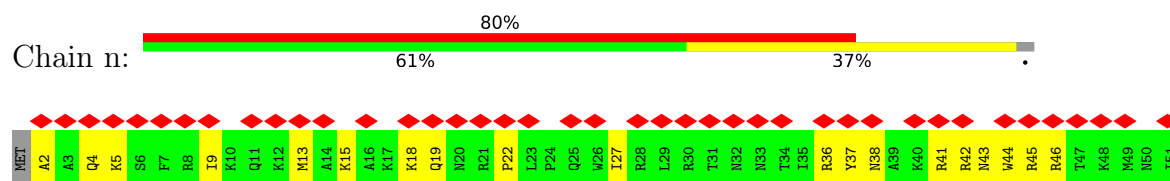
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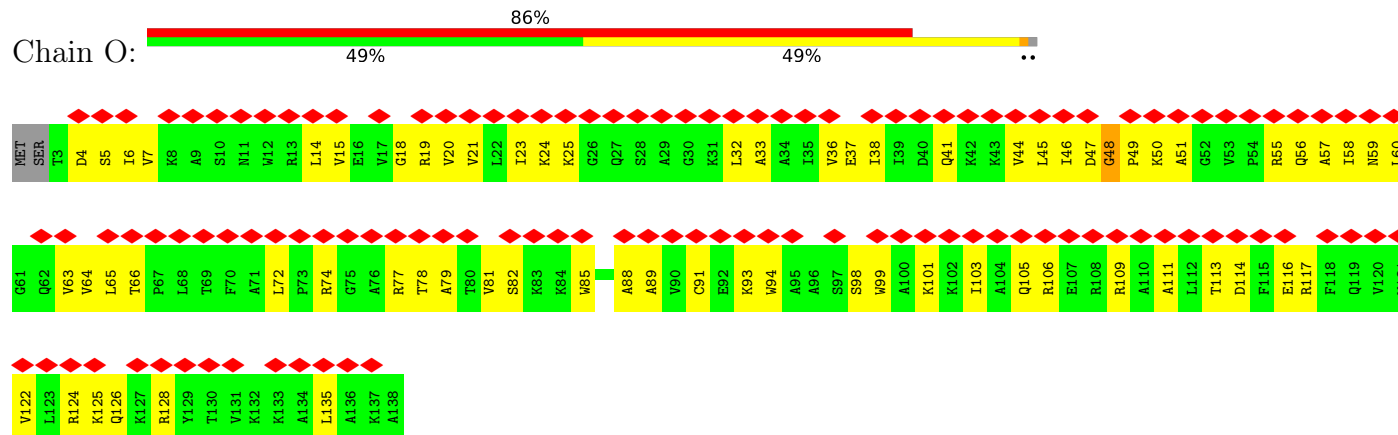
• Molecule 33: 60S ribosomal protein L13-A



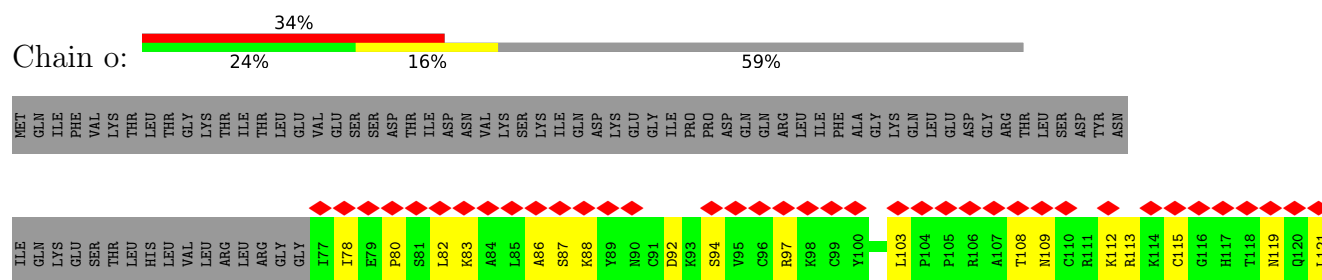
- Molecule 34: 60S ribosomal protein L39



- Molecule 35: 60S ribosomal protein L14-B

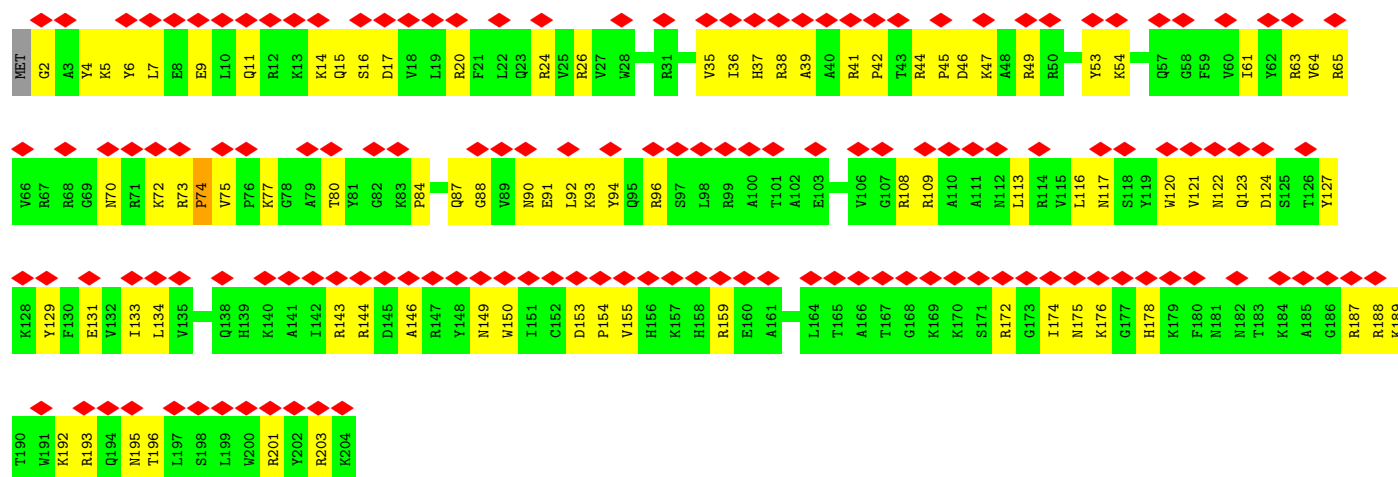


- Molecule 36: Ubiquitin-60S ribosomal protein L40

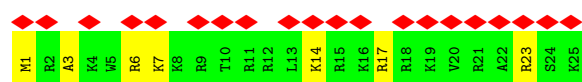
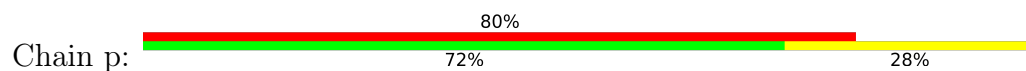




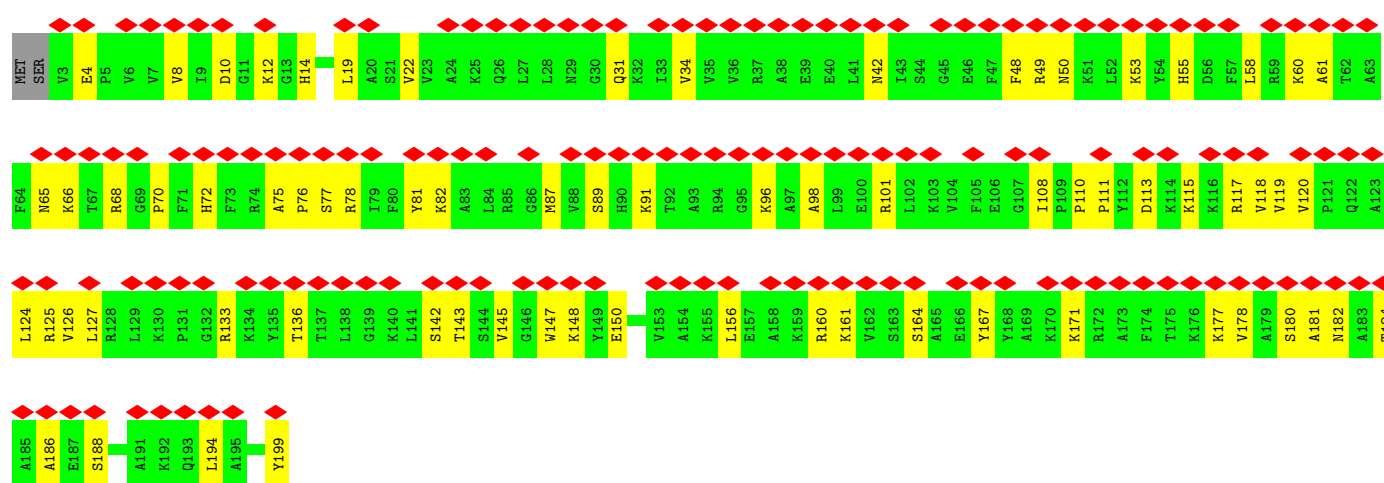
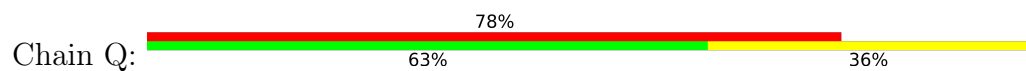
• Molecule 37: 60S ribosomal protein L15-A



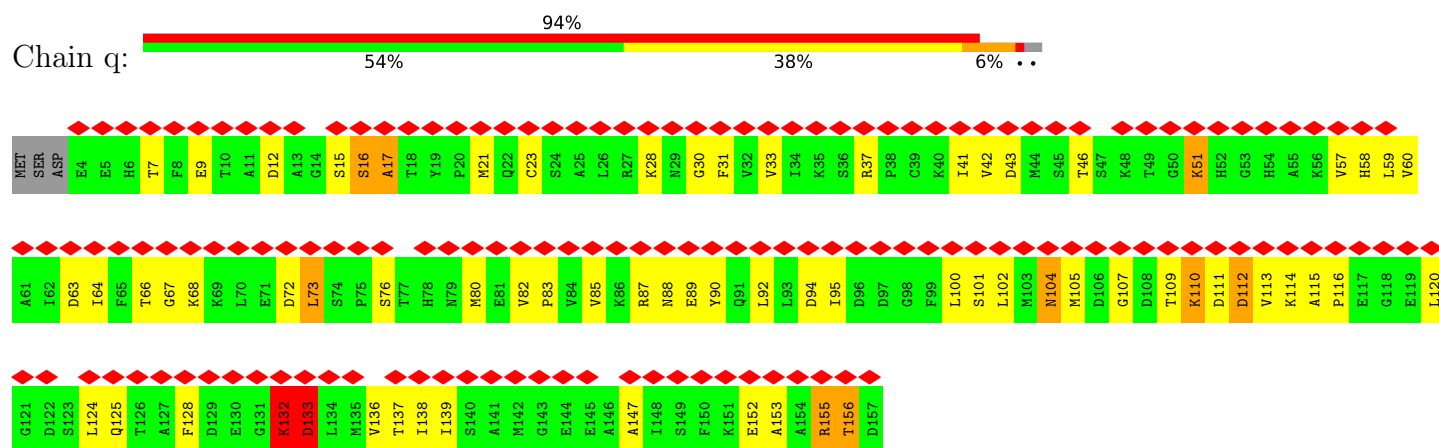
• Molecule 38: 60S ribosomal protein L41-A



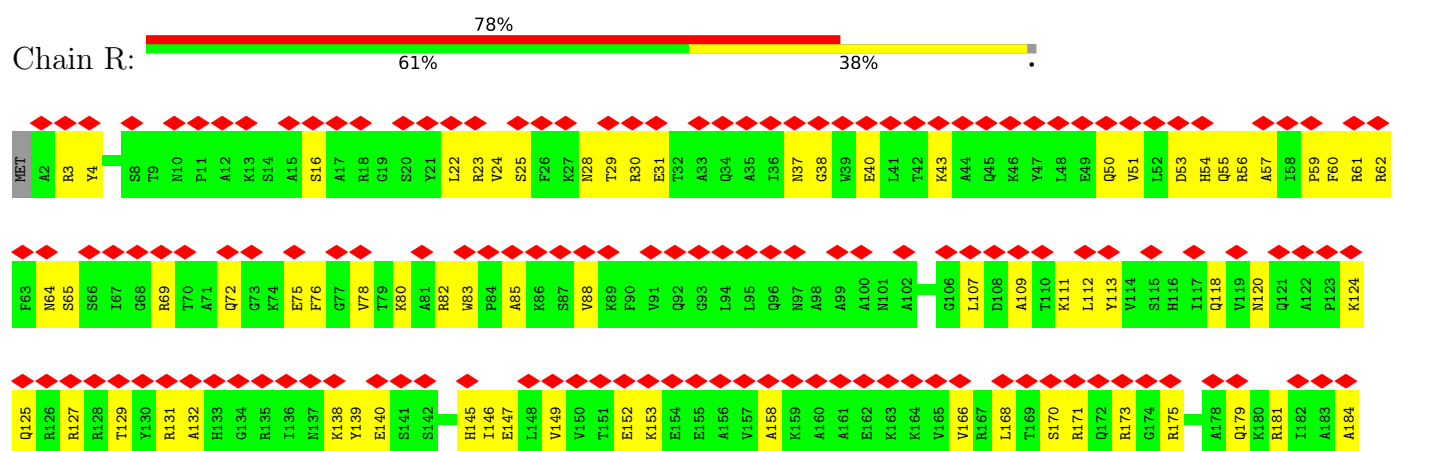
• Molecule 39: 60S ribosomal protein L16-A



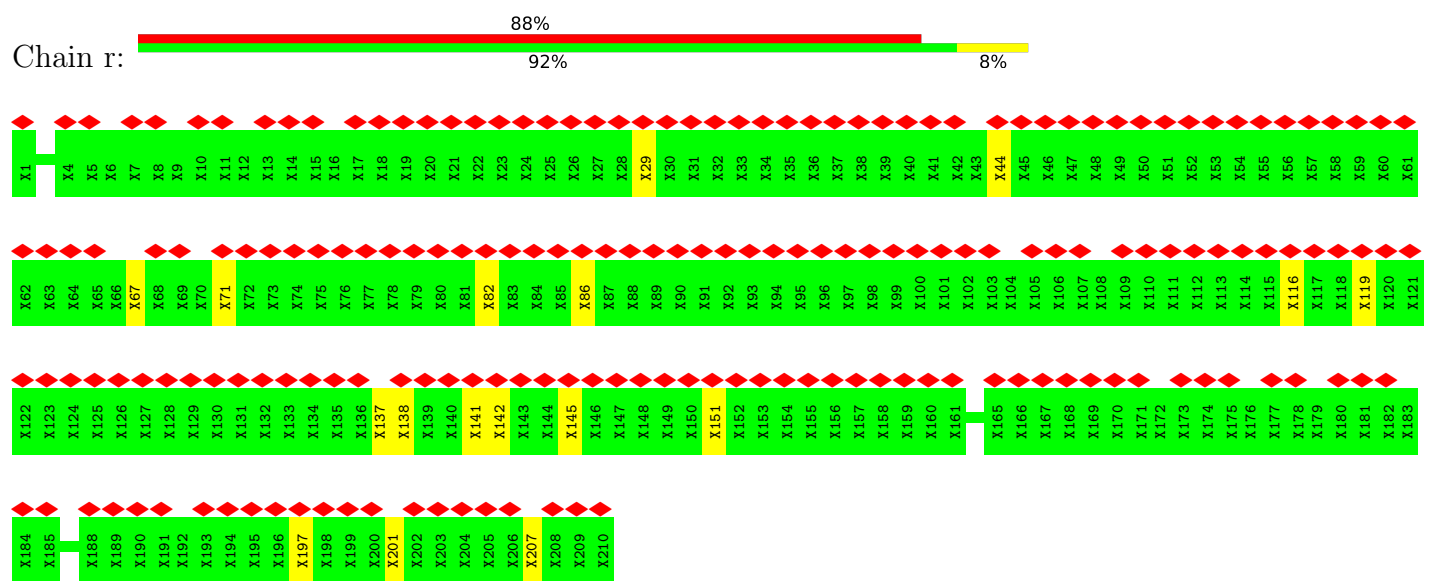
• Molecule 40: Eukaryotic translation initiation factor 5A-1



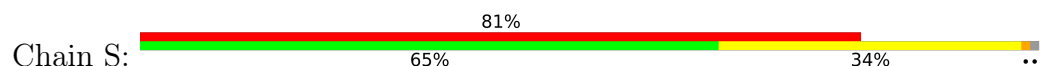
• Molecule 41: 60S ribosomal protein L17-A



• Molecule 42: ribosomal protein RPL1

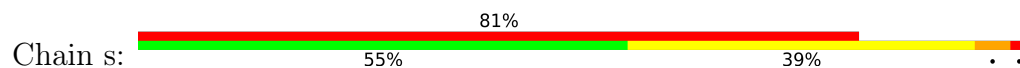


• Molecule 43: 60S ribosomal protein L18-A

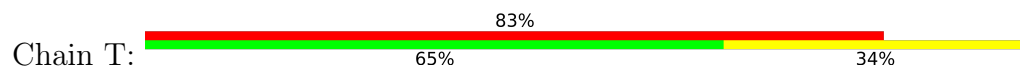




• Molecule 44: 60S ribosomal protein L10



• Molecule 45: 60S ribosomal protein L19-A



Chain z:

Color	Percentage
Red	96%
Green	74%
Yellow	26%

Below the chart, a sequence of 24 colored diamonds is shown, each labeled with a variable name (x2 to x24) in a small box. The colors of the diamonds correspond to the segments in the bar chart above: red for x2-x17, green for x18-x23, and yellow for x24.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	62532	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY; Each Particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.404	Depositor
Minimum map value	-0.244	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.06	Depositor
Map size ($\text{\AA}$)	401.08, 401.08, 401.08	wwPDB
Map dimensions	370, 370, 370	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 3HE, 5CT

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	1	0.33	0/75774	0.50	2/118137 (0.0%)
2	X	0.32	0/1018	0.58	1/1369 (0.1%)
3	3	0.28	0/2883	0.43	0/4491
4	Y	0.27	0/712	0.61	0/958
5	4	0.33	0/3746	0.49	0/5832
6	Z	0.32	0/979	0.59	0/1321
7	A	0.24	0/1799	0.44	0/2801
8	a	0.31	0/1004	0.62	0/1341
9	B	0.24	0/1835	0.43	0/2858
10	b	0.28	0/1118	0.59	0/1497
11	C	0.31	0/860	0.59	0/1136
12	c	0.36	0/1204	0.66	1/1612 (0.1%)
13	D	0.34	0/701	0.67	0/934
14	d	0.37	0/473	0.50	0/629
15	E	0.36	0/1948	0.65	2/2617 (0.1%)
16	e	0.26	0/751	0.46	0/1008
17	F	0.34	0/3146	0.65	2/4228 (0.0%)
18	f	0.36	0/890	0.60	0/1196
19	G	0.33	0/2800	0.58	0/3790
20	g	0.33	0/1041	0.59	0/1394
21	H	0.26	0/2425	0.53	0/3271
22	h	0.38	0/868	0.58	0/1168
23	I	0.27	0/1260	0.51	0/1694
24	i	0.33	0/890	0.56	0/1189
25	J	0.33	0/1821	0.52	0/2451
26	j	0.28	0/978	0.57	0/1301
27	K	0.28	0/1836	0.59	0/2481
28	k	0.27	0/778	0.61	2/1034 (0.2%)
29	L	0.30	0/1539	0.64	0/2073
30	l	0.40	0/696	0.66	0/923
31	M	0.26	0/1374	0.57	1/1842 (0.1%)
32	m	0.25	0/618	0.63	0/826

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	N	0.31	0/1568	0.67	4/2106 (0.2%)
34	n	0.33	0/443	0.59	0/588
35	O	0.27	0/1068	0.58	0/1438
36	o	0.28	0/423	0.60	0/562
37	P	0.39	0/1757	0.68	2/2354 (0.1%)
38	p	0.28	0/234	0.68	0/300
39	Q	0.34	0/1585	0.59	0/2128
40	q	0.30	0/1142	0.75	1/1537 (0.1%)
41	R	0.35	0/1443	0.66	1/1944 (0.1%)
43	S	0.32	0/1465	0.57	0/1965
44	s	0.34	1/1807 (0.1%)	0.64	1/2425 (0.0%)
45	T	0.29	0/1538	0.58	0/2050
46	U	0.34	0/1481	0.66	2/1990 (0.1%)
47	V	0.32	0/1300	0.62	0/1743
48	W	0.26	0/812	0.65	0/1099
All	All	0.32	1/137831 (0.0%)	0.54	22/203631 (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
17	F	0	1
25	J	0	1
27	K	0	1
30	l	0	1
35	O	0	1
39	Q	0	1
40	q	0	1
43	S	0	1
44	s	0	2
All	All	0	10

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	s	112	GLN	CD-OE1	5.11	1.33	1.23

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	N	62	THR	CB-CA-C	-7.23	106.34	115.89
46	U	13	ARG	CB-CA-C	-7.02	106.62	115.89
44	s	135	PHE	CB-CA-C	-6.91	107.57	115.79
46	U	24	LEU	CB-CA-C	-6.62	107.16	115.89
17	F	38	SER	CA-C-N	6.57	131.38	120.86

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	F	348	ARG	Peptide
25	J	108	LEU	Peptide
27	K	76	ALA	Peptide
35	O	48	GLY	Peptide
30	l	50	GLY	Peptide

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	1	67695	0	34019	3120	0
2	X	1003	0	1048	44	0
3	3	2579	0	1304	114	0
4	Y	699	0	640	26	0
5	4	3353	0	1695	157	0
6	Z	964	0	1025	44	0
7	A	1611	0	816	91	0
8	a	993	0	1081	41	0
9	B	1644	0	831	76	0
10	b	1092	0	1155	64	0
11	C	847	0	918	43	0
12	c	1173	0	1215	82	0
13	D	694	0	738	44	0
14	d	462	0	491	19	0
15	E	1914	0	1981	95	0
16	e	743	0	797	33	0
17	F	3075	0	3142	154	0
18	f	876	0	912	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	G	2748	0	2859	126	0
20	g	1020	0	1090	50	0
21	H	2375	0	2325	150	0
22	h	850	0	880	41	0
23	I	1239	0	1326	72	0
24	i	880	0	945	37	0
25	J	1784	0	1862	72	0
26	j	969	0	1078	47	0
27	K	1804	0	1877	96	0
28	k	771	0	849	31	0
29	L	1518	0	1587	67	0
30	l	681	0	687	30	0
31	M	1353	0	1383	55	0
32	m	612	0	682	30	0
33	N	1543	0	1608	85	0
34	n	436	0	475	27	0
35	O	1053	0	1149	77	0
36	o	417	0	459	20	0
37	P	1720	0	1779	109	0
38	p	233	0	284	8	0
39	Q	1555	0	1659	56	0
40	q	1143	0	1108	62	0
41	R	1420	0	1437	68	0
42	r	1050	0	222	11	0
43	S	1441	0	1543	76	0
44	s	1770	0	1808	102	0
45	T	1521	0	1617	71	0
46	U	1445	0	1487	70	0
47	V	1276	0	1323	54	0
48	W	796	0	812	25	0
49	z	115	0	37	9	0
50	1	20	0	23	2	0
All	All	128975	0	92068	5238	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 24.

The worst 5 of 5238 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)
1:1:2978:U:C4	49:z:17:UNK:CB	2.02	1.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1135:A:OP2	14:d:5:LYS:NZ	1.66	1.28
40:q:132:LYS:HB3	40:q:152:GLU:OE2	1.14	1.24
1:1:520:U:OP2	25:J:70:LYS:NZ	1.71	1.24
1:1:208:C:OP2	19:G:163:LYS:NZ	1.75	1.20

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	
2	X	134/137 (98%)	130 (97%)	4 (3%)	0	100	100
4	Y	96/155 (62%)	86 (90%)	10 (10%)	0	100	100
6	Z	119/142 (84%)	111 (93%)	7 (6%)	1 (1%)	16	50
8	a	124/127 (98%)	109 (88%)	15 (12%)	0	100	100
10	b	133/136 (98%)	120 (90%)	12 (9%)	1 (1%)	16	50
11	C	103/106 (97%)	88 (85%)	15 (15%)	0	100	100
12	c	146/149 (98%)	128 (88%)	15 (10%)	3 (2%)	5	32
13	D	89/92 (97%)	79 (89%)	10 (11%)	0	100	100
14	d	56/59 (95%)	48 (86%)	7 (12%)	1 (2%)	6	34
15	E	250/254 (98%)	230 (92%)	20 (8%)	0	100	100
16	e	95/105 (90%)	88 (93%)	7 (7%)	0	100	100
17	F	384/387 (99%)	358 (93%)	25 (6%)	1 (0%)	36	69
18	f	107/109 (98%)	99 (92%)	8 (8%)	0	100	100
19	G	359/362 (99%)	319 (89%)	38 (11%)	2 (1%)	21	55
20	g	125/130 (96%)	115 (92%)	10 (8%)	0	100	100
21	H	294/297 (99%)	260 (88%)	31 (10%)	3 (1%)	12	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	h	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
23	I	152/176 (86%)	145 (95%)	6 (4%)	1 (1%)	18	52
24	i	110/121 (91%)	106 (96%)	4 (4%)	0	100	100
25	J	220/244 (90%)	202 (92%)	18 (8%)	0	100	100
26	j	117/120 (98%)	103 (88%)	14 (12%)	0	100	100
27	K	231/256 (90%)	205 (89%)	23 (10%)	3 (1%)	9	40
28	k	97/100 (97%)	80 (82%)	16 (16%)	1 (1%)	12	45
29	L	189/191 (99%)	169 (89%)	20 (11%)	0	100	100
30	l	85/88 (97%)	74 (87%)	11 (13%)	0	100	100
31	M	167/174 (96%)	145 (87%)	20 (12%)	2 (1%)	10	41
32	m	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
33	N	191/199 (96%)	171 (90%)	20 (10%)	0	100	100
34	n	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
35	O	134/138 (97%)	119 (89%)	15 (11%)	0	100	100
36	o	50/128 (39%)	46 (92%)	4 (8%)	0	100	100
37	P	201/204 (98%)	176 (88%)	25 (12%)	0	100	100
38	p	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
39	Q	195/199 (98%)	179 (92%)	16 (8%)	0	100	100
40	q	151/157 (96%)	127 (84%)	14 (9%)	10 (7%)	1	15
41	R	181/184 (98%)	166 (92%)	15 (8%)	0	100	100
43	S	183/186 (98%)	169 (92%)	14 (8%)	0	100	100
44	s	218/221 (99%)	180 (83%)	29 (13%)	9 (4%)	2	21
45	T	186/189 (98%)	169 (91%)	16 (9%)	1 (0%)	24	59
46	U	170/172 (99%)	151 (89%)	18 (11%)	1 (1%)	21	55
47	V	157/160 (98%)	150 (96%)	6 (4%)	1 (1%)	21	55
48	W	98/121 (81%)	86 (88%)	11 (11%)	1 (1%)	12	45
All	All	6347/6736 (94%)	5722 (90%)	583 (9%)	42 (1%)	20	52

5 of 42 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	c	48	TYR
23	I	98	VAL

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Mol	Chain	Res	Type
40	q	110	LYS
40	q	112	ASP
40	q	133	ASP

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	
2	X	104/105 (99%)	104 (100%)	0	100	100
4	Y	57/129 (44%)	57 (100%)	0	100	100
6	Z	104/118 (88%)	104 (100%)	0	100	100
8	a	109/110 (99%)	109 (100%)	0	100	100
10	b	115/116 (99%)	115 (100%)	0	100	100
11	C	90/91 (99%)	90 (100%)	0	100	100
12	c	118/119 (99%)	118 (100%)	0	100	100
13	D	71/72 (99%)	71 (100%)	0	100	100
14	d	46/47 (98%)	46 (100%)	0	100	100
15	E	193/196 (98%)	192 (100%)	1 (0%)	81	81
16	e	81/88 (92%)	81 (100%)	0	100	100
17	F	320/323 (99%)	319 (100%)	1 (0%)	86	85
18	f	92/96 (96%)	92 (100%)	0	100	100
19	G	288/289 (100%)	288 (100%)	0	100	100
20	g	109/111 (98%)	109 (100%)	0	100	100
21	H	244/245 (100%)	243 (100%)	1 (0%)	84	83
22	h	90/91 (99%)	90 (100%)	0	100	100
23	I	134/153 (88%)	134 (100%)	0	100	100
24	i	95/103 (92%)	95 (100%)	0	100	100
25	J	186/205 (91%)	186 (100%)	0	100	100
26	j	104/105 (99%)	104 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	K	187/208 (90%)	187 (100%)	0	100	100
28	k	81/82 (99%)	81 (100%)	0	100	100
29	L	171/171 (100%)	171 (100%)	0	100	100
30	l	70/71 (99%)	70 (100%)	0	100	100
31	M	147/150 (98%)	147 (100%)	0	100	100
32	m	68/69 (99%)	68 (100%)	0	100	100
33	N	154/159 (97%)	154 (100%)	0	100	100
34	n	45/46 (98%)	45 (100%)	0	100	100
35	O	107/109 (98%)	107 (100%)	0	100	100
36	o	47/116 (40%)	47 (100%)	0	100	100
37	P	175/176 (99%)	175 (100%)	0	100	100
38	p	23/23 (100%)	23 (100%)	0	100	100
39	Q	160/162 (99%)	160 (100%)	0	100	100
40	q	118/132 (89%)	113 (96%)	5 (4%)	26	50
41	R	140/146 (96%)	140 (100%)	0	100	100
43	S	150/151 (99%)	150 (100%)	0	100	100
44	s	184/187 (98%)	178 (97%)	6 (3%)	33	56
45	T	153/154 (99%)	153 (100%)	0	100	100
46	U	156/156 (100%)	156 (100%)	0	100	100
47	V	136/137 (99%)	136 (100%)	0	100	100
48	W	87/107 (81%)	87 (100%)	0	100	100
All	All	5309/5624 (94%)	5295 (100%)	14 (0%)	84	85

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	q	155	ARG
44	s	102	LEU
44	s	110	LEU
44	s	108	ASP
44	s	109	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 113 such sidechains are listed below:

Mol	Chain	Res	Type
21	H	57	ASN
47	V	131	GLN
31	M	39	GLN
47	V	5	HIS
44	s	112	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3162/3396 (93%)	1117 (35%)	336 (10%)
3	3	120/121 (99%)	30 (25%)	7 (5%)
5	4	157/158 (99%)	58 (36%)	20 (12%)
7	A	75/76 (98%)	40 (53%)	7 (9%)
9	B	76/77 (98%)	35 (46%)	6 (7%)
All	All	3590/3828 (93%)	1280 (35%)	376 (10%)

5 of 1280 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	6	A
1	1	11	A
1	1	13	A
1	1	14	U
1	1	15	C

5 of 376 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2403	G
1	1	2850	G
1	1	2500	A
1	1	2635	A
1	1	3115	C

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
40	5CT	q	51	40	13,14,15	0.33	0	8,15,17	1.21	2 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
40	5CT	q	51	40	-	7/13/14/16	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	q	51	5CT	C1-NZ-CE	-2.36	108.23	113.38
40	q	51	5CT	C4-C3-C2	-2.05	109.16	113.47

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
40	q	51	5CT	O-C-CA-CB
40	q	51	5CT	C2-C1-NZ-CE
40	q	51	5CT	C2-C3-C4-N1
40	q	51	5CT	CD-CE-NZ-C1
40	q	51	5CT	C-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
40	q	51	5CT	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
50	3HE	1	3401	-	21,21,21	0.90	1 (4%)	23,30,30	0.75	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	3HE	1	3401	-	-	3/8/36/36	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	1	3401	3HE	C5-C7	3.43	1.58	1.53

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

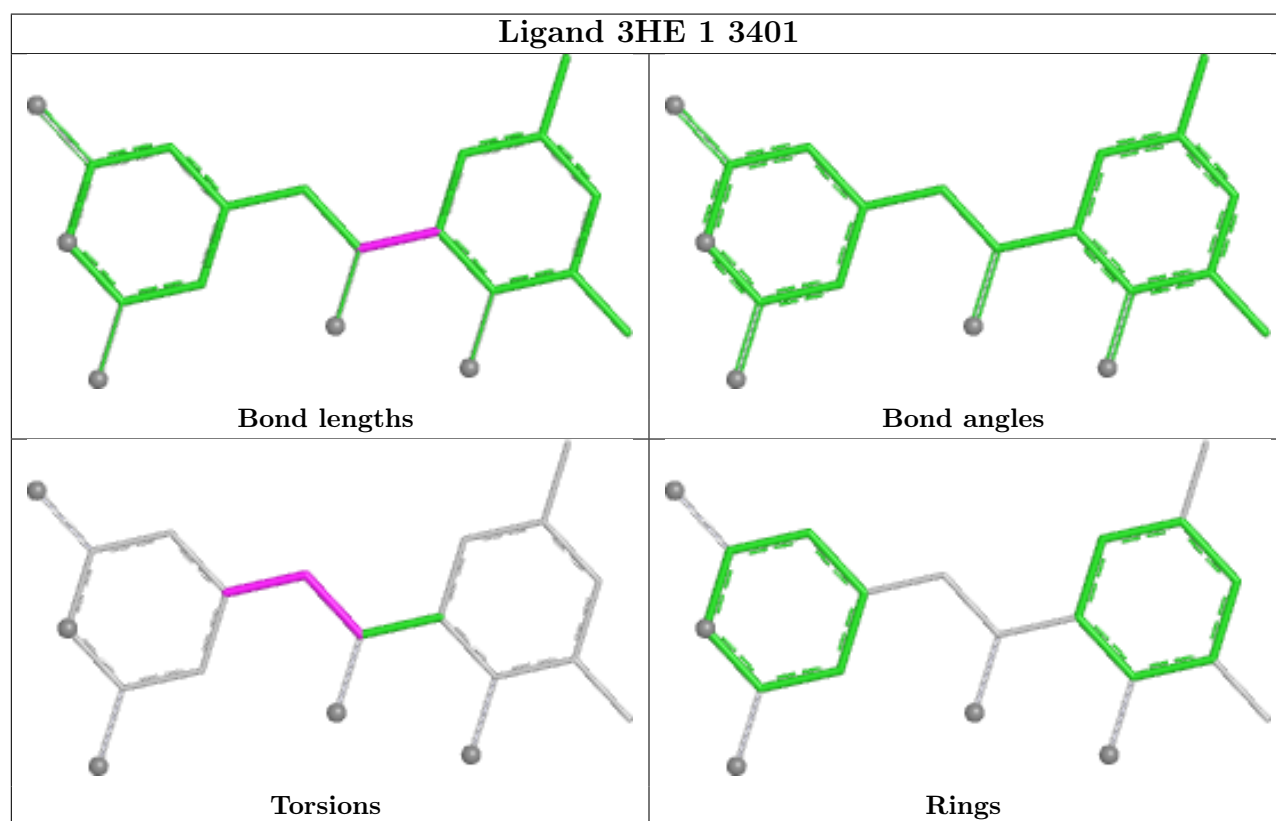
Mol	Chain	Res	Type	Atoms
50	1	3401	3HE	C7-C8-C9-C13
50	1	3401	3HE	C7-C8-C9-C10
50	1	3401	3HE	O3-C7-C8-C9

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
50	1	3401	3HE	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

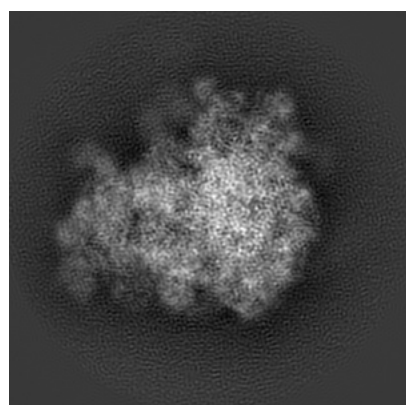
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3227. These allow visual inspection of the internal detail of the map and identification of artifacts.

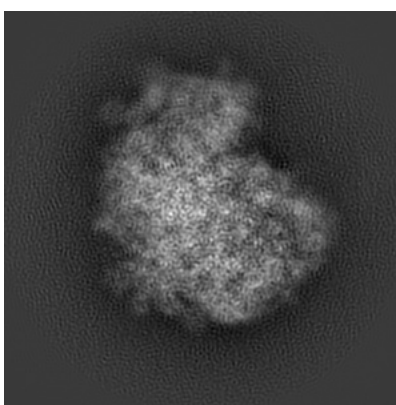
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

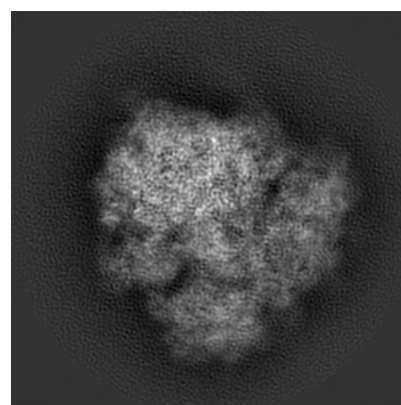
6.1.1 Primary map



X



Y

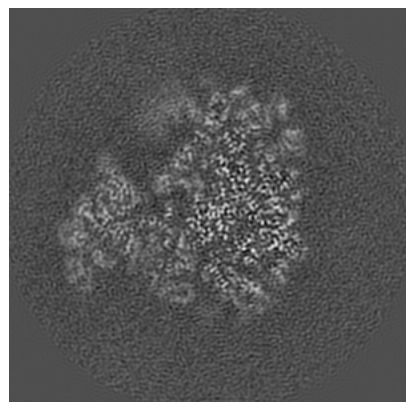


Z

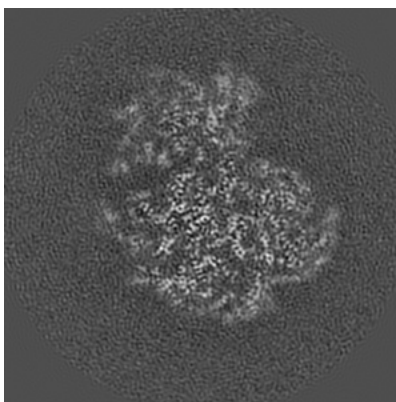
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

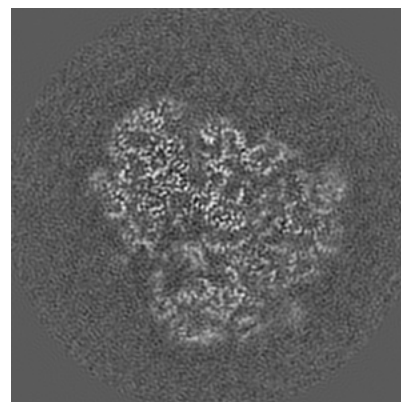
6.2.1 Primary map



X Index: 185



Y Index: 185

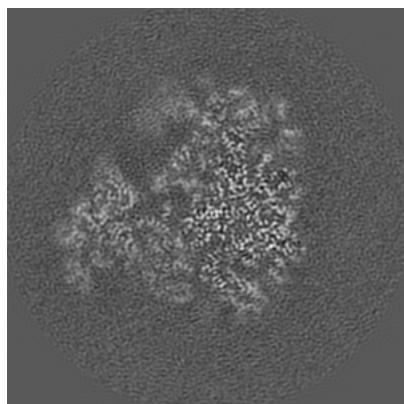


Z Index: 185

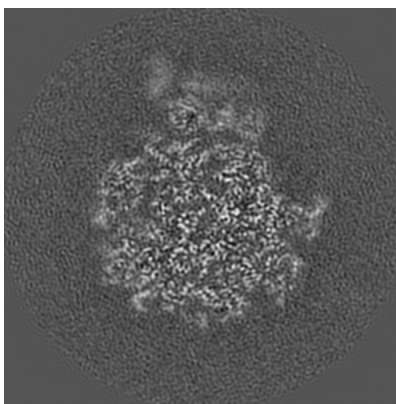
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

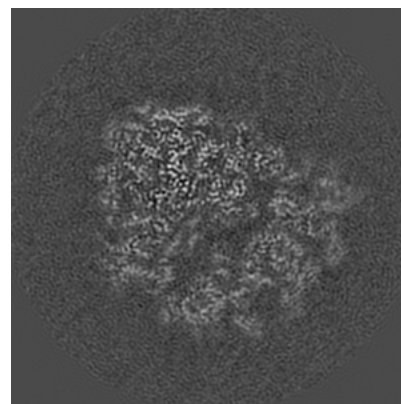
6.3.1 Primary map



X Index: 184



Y Index: 216

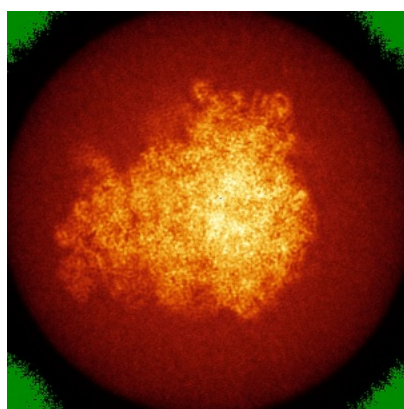


Z Index: 198

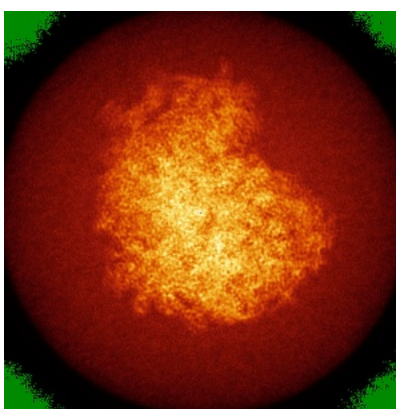
The images above show the largest variance slices of the map in three orthogonal directions.

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

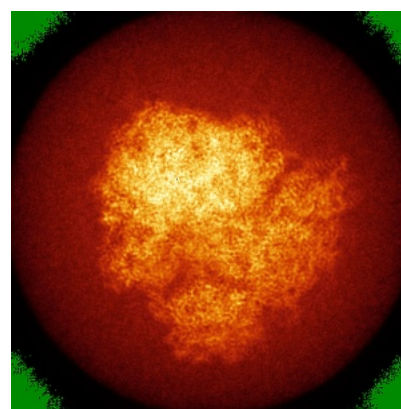
6.4.1 Primary map



X



Y

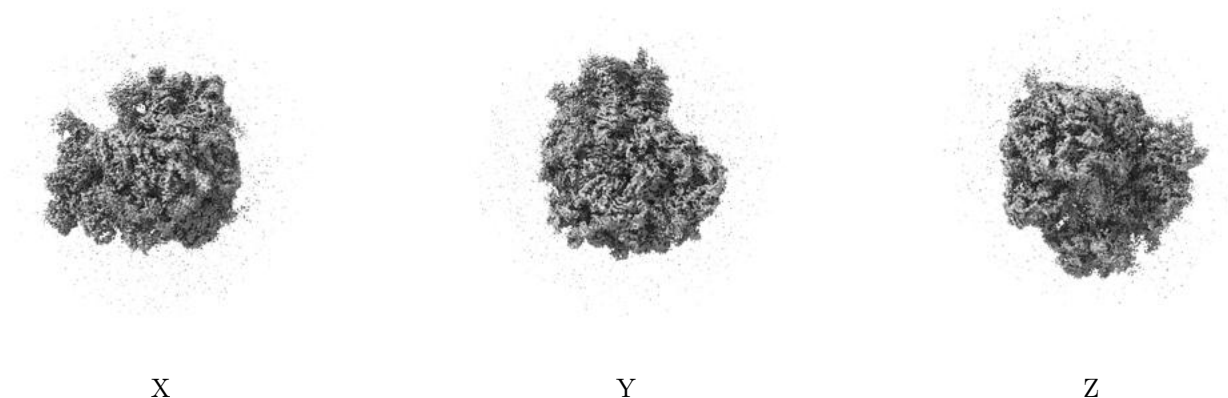


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

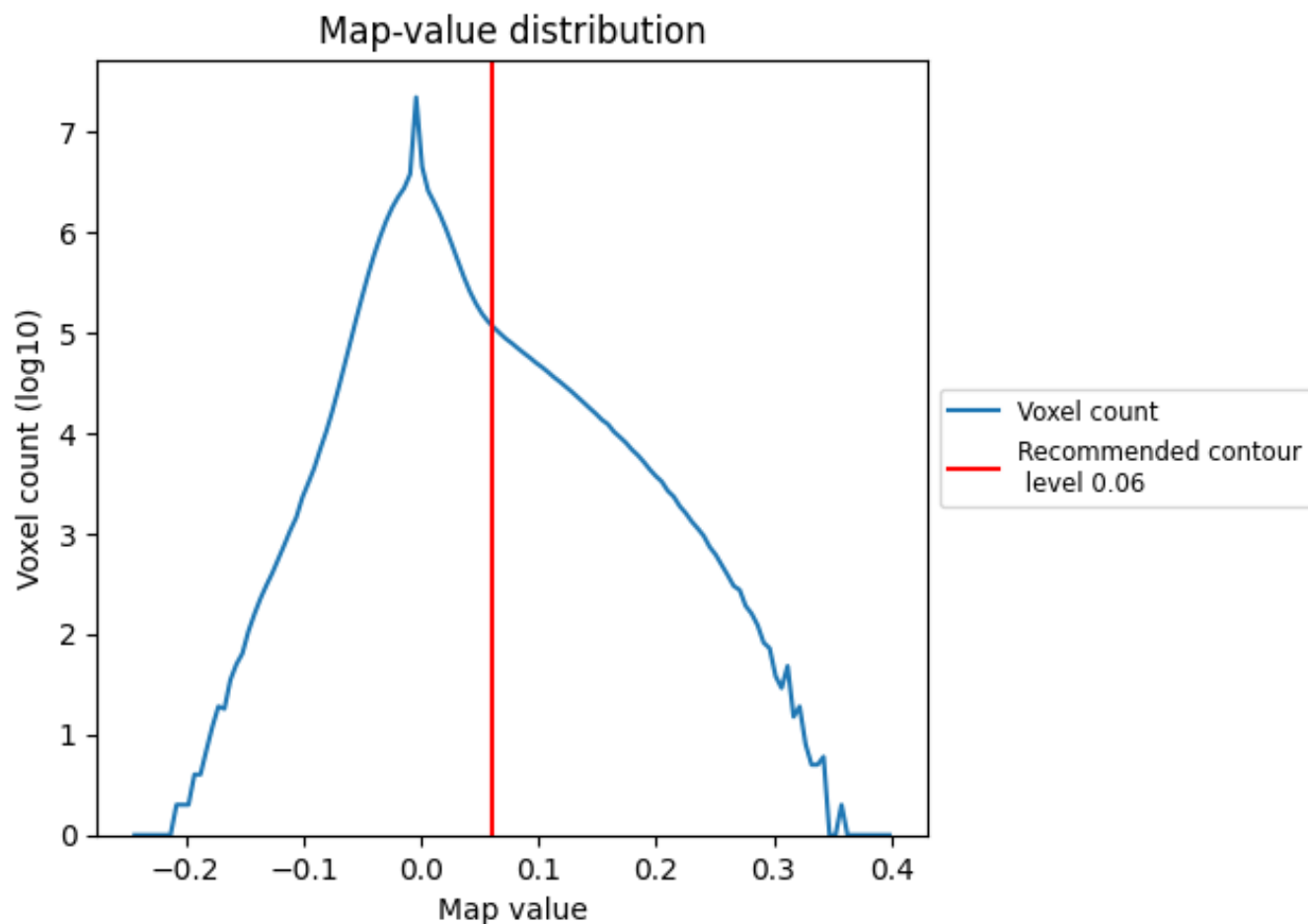
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

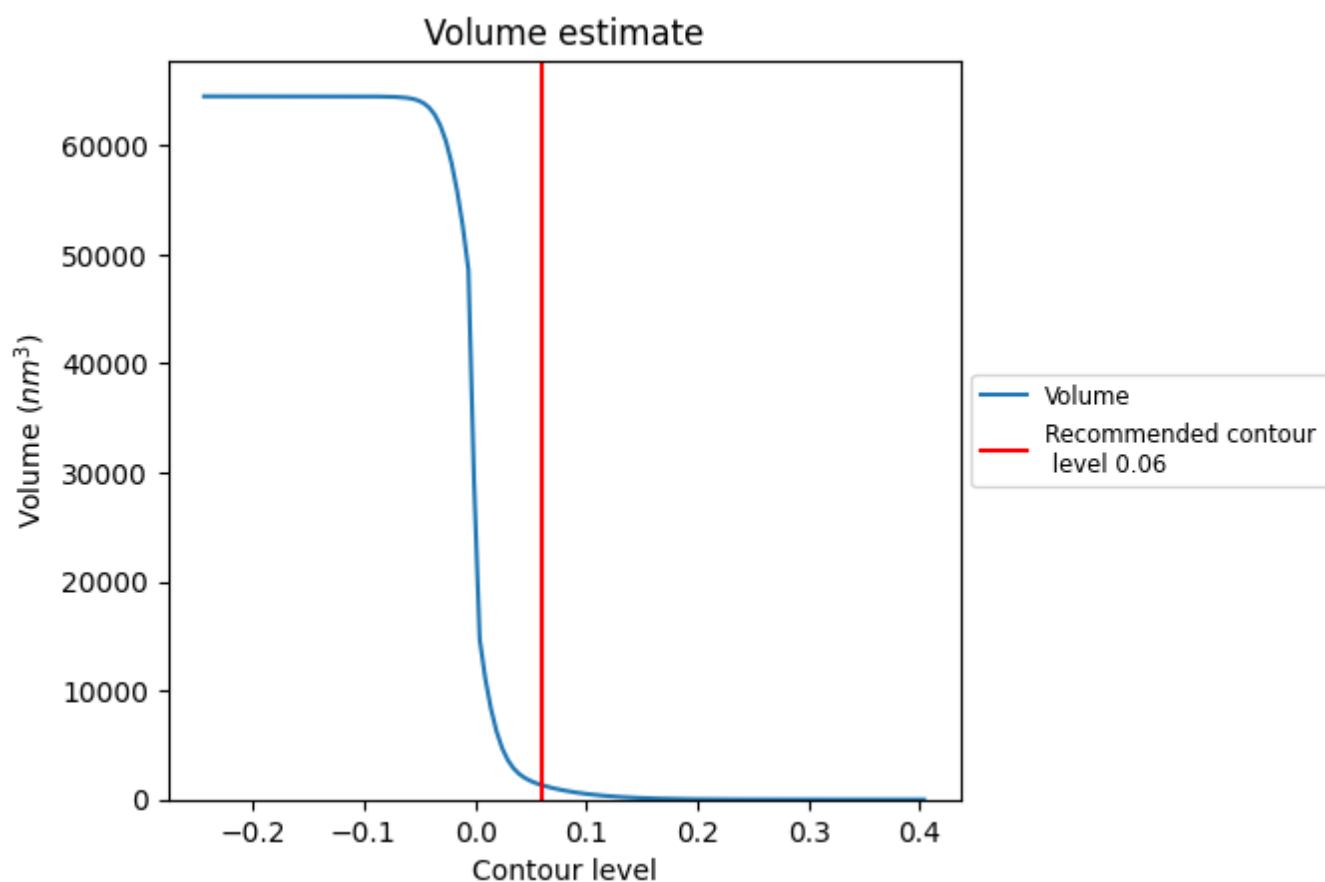
This section contains the results of statistical analysis of the map.

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.

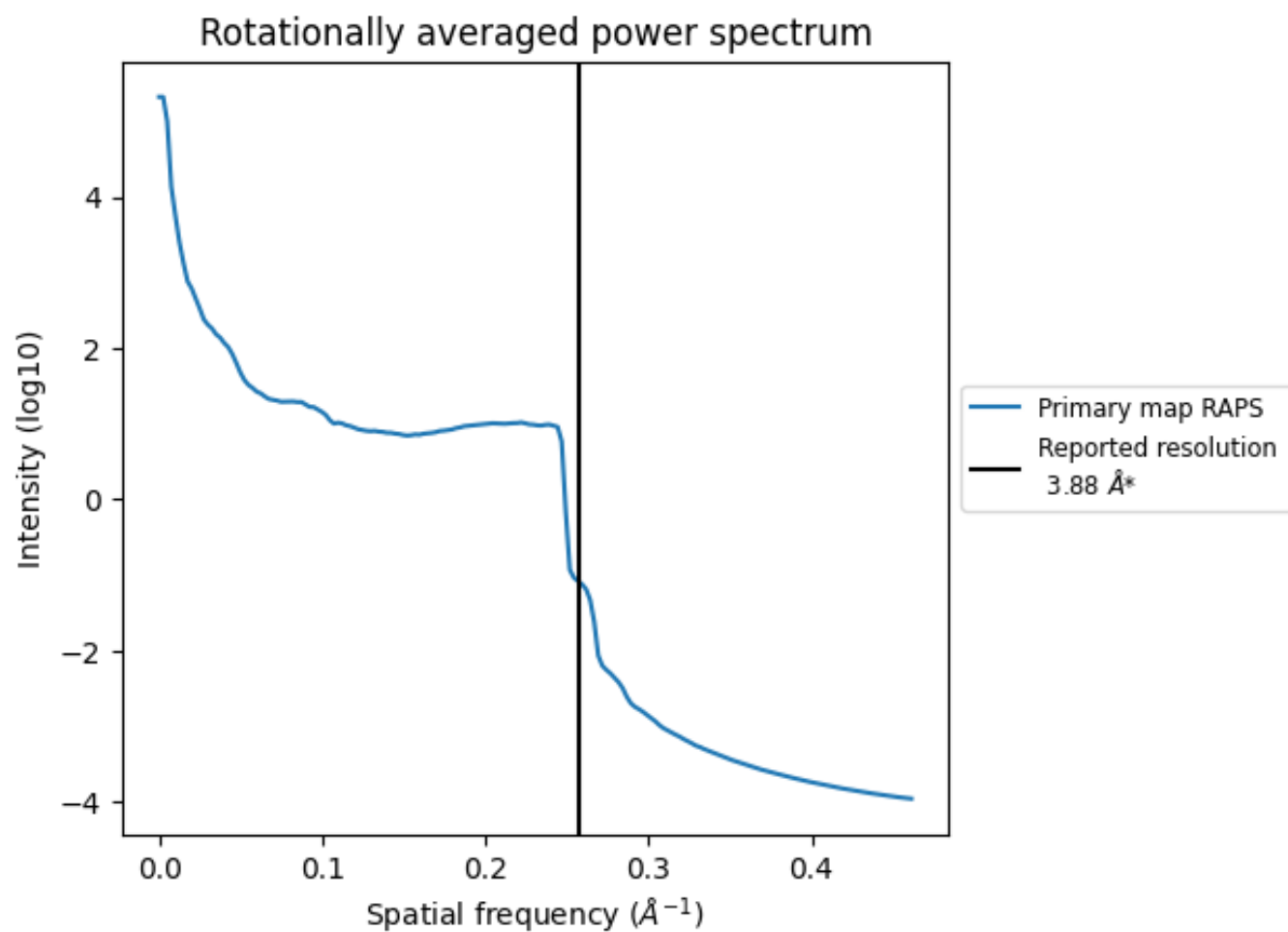
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1328 nm³; this corresponds to an approximate mass of 1199 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 0.258 Å⁻¹

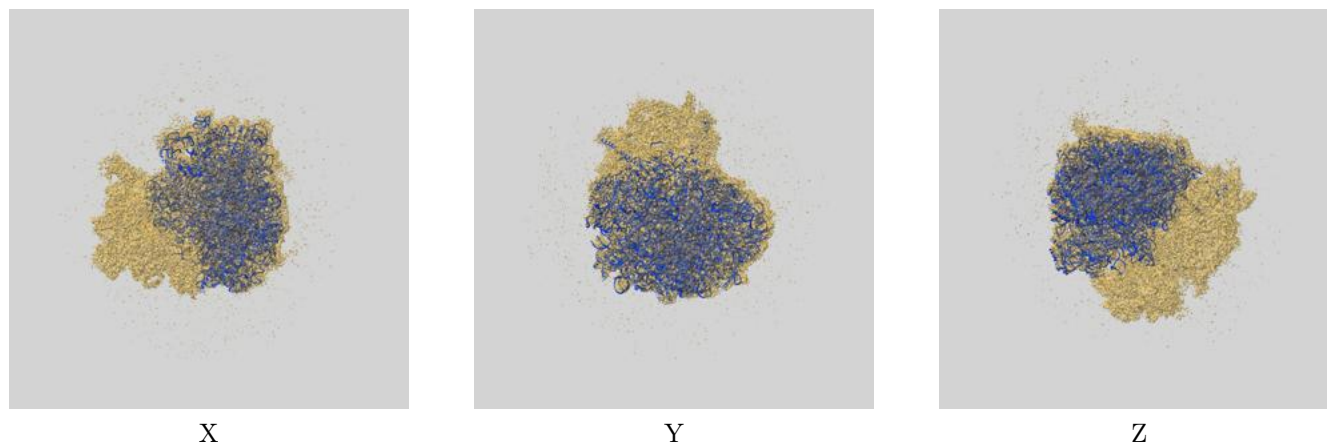
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

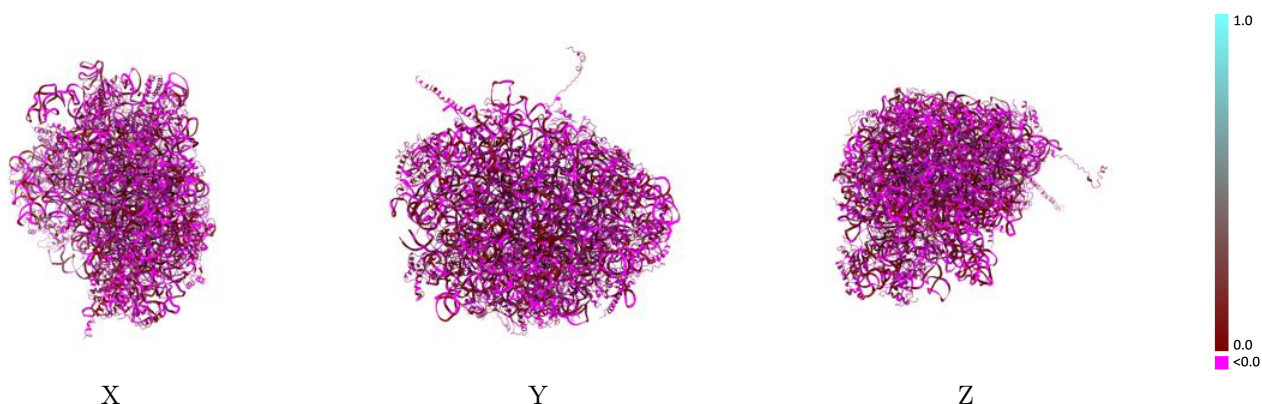
This section contains information regarding the fit between EMDB map EMD-3227 and PDB model 5GAK. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



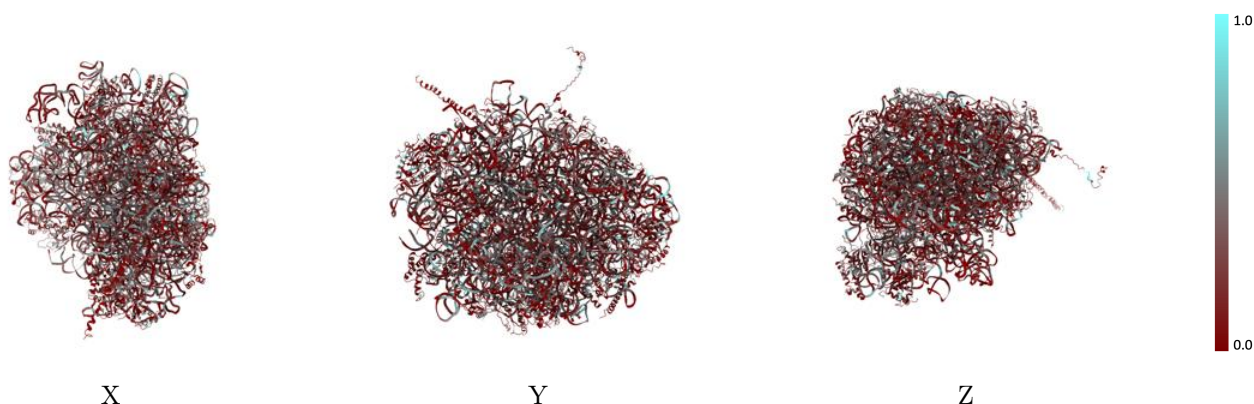
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



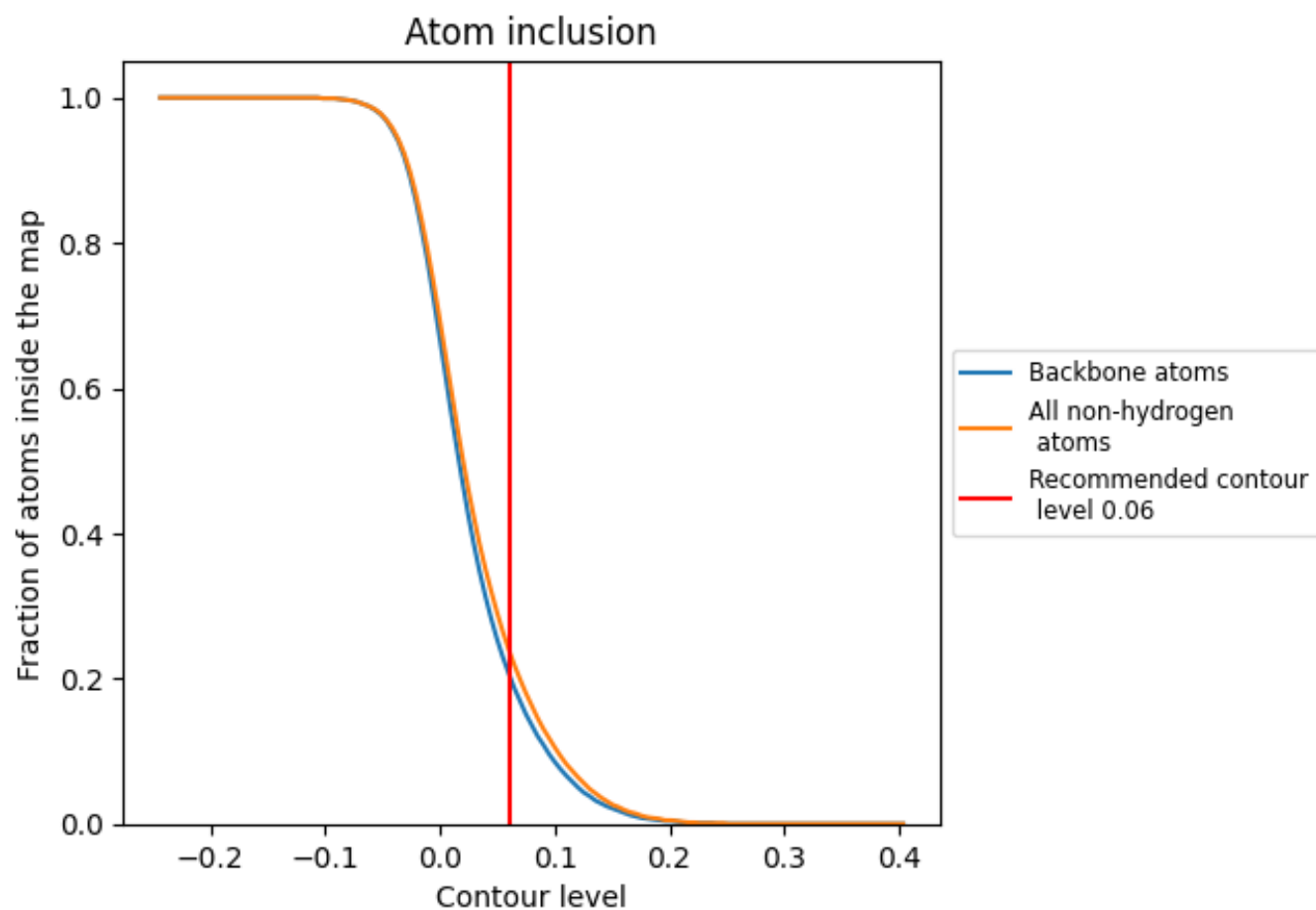
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 21% of all backbone atoms, 24% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.2400	-0.0120
1	0.2670	-0.0130
3	0.3180	-0.0210
4	0.2430	-0.0250
A	0.1680	-0.0150
B	0.2310	0.0010
C	0.1280	-0.0020
D	0.1460	-0.0120
E	0.2090	0.0100
F	0.2590	-0.0090
G	0.2020	-0.0280
H	0.2010	0.0080
I	0.1980	-0.0340
J	0.1910	-0.0280
K	0.1750	0.0320
L	0.2110	-0.0230
M	0.1910	0.0130
N	0.2140	0.0110
O	0.1550	-0.0430
P	0.2680	0.0110
Q	0.2360	-0.0320
R	0.2340	-0.0260
S	0.2140	-0.0210
T	0.1870	-0.0350
U	0.1950	-0.0200
V	0.1790	-0.0200
W	0.2200	-0.0260
X	0.1650	-0.0310
Y	0.1980	0.0080
Z	0.2210	-0.0080
a	0.2010	-0.0390
b	0.2180	0.0030
c	0.2090	-0.0130
d	0.1640	-0.0330
e	0.1350	-0.0040



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Chain	Atom inclusion	Q-score
f	 0.2130	 -0.0140
g	 0.2300	 -0.0230
h	 0.2750	 -0.0160
i	 0.2640	 0.0200
j	 0.2110	 0.0010
k	 0.1680	 0.0600
l	 0.2180	 -0.0270
m	 0.1520	 -0.0310
n	 0.1900	 -0.0230
o	 0.1840	 0.0130
p	 0.1930	 -0.0010
q	 0.1040	 0.0100
r	 0.1510	 -0.0060
s	 0.1900	 -0.0110
z	 0.0700	 -0.0450