



wwPDB EM Validation Summary Report ⓘ

Nov 2, 2024 – 07:26 PM EDT

PDB ID : 6P5I
EMDB ID : EMD-20255
Title : Structure of a mammalian 80S ribosome in complex with the Israeli Acute Paralysis Virus IRES (Class 1)
Authors : Acosta-Reyes, F.J.; Neupane, R.; Frank, J.; Fernandez, I.S.
Deposited on : 2019-05-30
Resolution : 3.10 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:

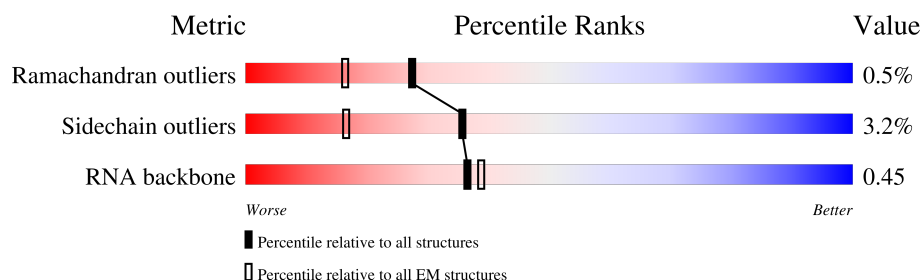
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

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 3.10 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	2	1869	<div> <div>11%</div> <div>67%</div> <div>23%</div> <div>9%</div> </div>
2	B	295	<div> <div>15%</div> <div>72%</div> <div>26%</div> </div>
3	C	264	<div> <div>9%</div> <div>78%</div> <div>19%</div> </div>
4	D	255	<div> <div>9%</div> <div>84%</div> <div>13%</div> </div>
5	E	281	<div> <div>42%</div> <div>78%</div> <div>19%</div> </div>
6	F	263	<div> <div>15%</div> <div>97%</div> </div>
7	G	204	<div> <div>26%</div> <div>88%</div> <div>9%</div> </div>
8	H	249	<div> <div>38%</div> <div>94%</div> <div>5%</div> </div>

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Mol	Chain	Length	Quality of chain
9	I	194	
10	J	207	
11	K	194	
12	L	149	
13	M	158	
14	N	132	
15	O	151	
16	P	151	
17	Q	145	
18	R	172	
19	S	135	
20	T	152	
21	U	145	
22	V	119	
23	W	83	
24	X	130	
25	Y	143	
26	Z	134	
27	a	125	
28	b	115	
29	c	84	
30	d	69	
31	e	56	
32	f	133	
33	g	156	





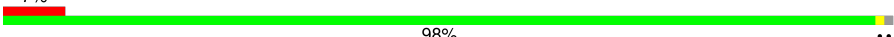
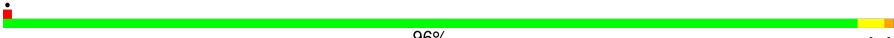




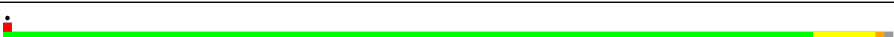


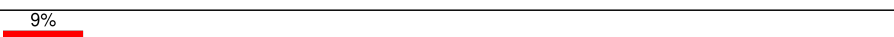
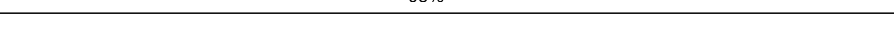
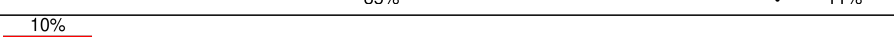
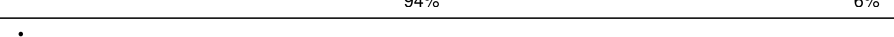
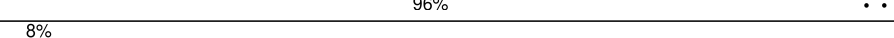
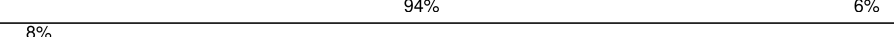
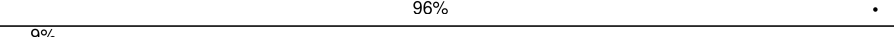
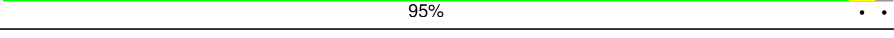
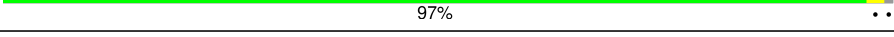

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Mol	Chain	Length	Quality of chain
34	h	317	
35	1	253	
36	5	3594	
37	7	119	
38	8	156	
39	AA	257	
40	AB	403	
41	AC	392	
42	AD	297	
43	AE	291	
44	AF	249	
45	AG	242	
46	AH	192	
47	AI	214	
48	AJ	178	
49	AL	211	
50	AM	198	
51	AN	204	
52	AO	203	
53	AP	184	
54	AQ	188	
55	AR	196	
56	AS	176	
57	AT	160	
58	AU	128	

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Mol	Chain	Length	Quality of chain
59	AV	140	
60	AW	157	
61	AX	156	
62	AY	145	
63	AZ	136	
64	Aa	148	
65	Ab	226	
66	Ac	115	
67	Ad	125	
68	Ae	135	
69	Af	110	
70	Ag	126	
71	Ah	123	
72	Ai	105	
73	Aj	97	
74	Ak	69	
75	Al	51	
76	Am	52	
77	An	25	
78	Ao	106	
79	Ap	92	
80	Ar	137	
81	AK	217	

2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 215974 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 2 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	217	Total	C	N	O	S	0	0
			1706	1085	295	317	9		

- Molecule 3 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 4 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	221	Total	C	N	O	S	0	0
			1712	1107	296	299	10		

- Molecule 5 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 6 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	262	Total	C	N	O	S	0	0
			2073	1323	384	357	9		

- Molecule 7 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 8 is a protein called eS6.

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

- Molecule 9 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 10 is a protein called eS8.

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

- Molecule 11 is a protein called uS4.

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

- Molecule 12 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 13 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 14 is a protein called eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 15 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 16 is a protein called uS11.

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

- Molecule 17 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	119	Total	C	N	O	S	0	0
			990	630	186	167	7		

- Molecule 18 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 19 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 20 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 21 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 22 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 23 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	83	Total	C	N	O	S	0	0
			630	387	118	120	5		

- Molecule 24 is a protein called uS8.

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

- Molecule 25 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 26 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 27 is a protein called eS25.

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

- Molecule 28 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	98	Total	C	N	O	S	0	0
			776	483	158	129	6		

- Molecule 29 is a protein called eS27.

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

- Molecule 30 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 31 is a protein called eS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 32 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	56	Total	C	N	O	S	0	0
			447	276	98	72	1		

- Molecule 33 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 34 is a protein called RACK1.

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

- Molecule 35 is a RNA chain called IAPV-IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	1	205	Total	C	N	O	P	0	0
			4366	1951	775	1435	205		

- Molecule 36 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	5	3594	Total	C	N	O	P	0	0
			77074	34325	14116	25039	3594		

- Molecule 37 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 38 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 39 is a protein called uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	AA	248	Total	C	N	O	S	0	0
			1895	1186	389	314	6		

- Molecule 40 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	AB	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 41 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AC	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 42 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AD	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 43 is a protein called eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AE	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 44 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AF	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 45 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AG	225	Total	C	N	O	S	0	0
			1819	1161	351	303	4		

- Molecule 46 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AH	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 47 is a protein called uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	AI	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 48 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AJ	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 49 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	AL	201	Total	C	N	O	S	0	0
			1627	1020	341	262	4		

- Molecule 50 is a protein called L14e.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	AM	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 51 is a protein called eL15.

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

- Molecule 52 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AO	199	Total	C	N	O	S	0	0
			1631	1052	319	255	5		

- Molecule 53 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	AP	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 54 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AQ	187	Total	C	N	O	S	0	0
			1526	964	306	252	4		

- Molecule 55 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AR	180	Total	C	N	O	S	0	0
			1503	931	324	238	10		

- Molecule 56 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AS	176	Total	C	N	O	S	0	0
			1457	928	283	235	11		

- Molecule 57 is a protein called eL21.

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

- Molecule 58 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AU	99	Total	C	N	O	S	0	0
			818	520	146	150	2		

- Molecule 59 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AV	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 60 is a protein called eL24.

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

- Molecule 61 is a protein called eL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AX	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 62 is a protein called uL24.

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

- Molecule 63 is a protein called eL27.

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

- Molecule 64 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Aa	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 65 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Ab	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 66 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Ac	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 67 is a protein called eL31.

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

- Molecule 68 is a protein called eL32.

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

- Molecule 69 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Af	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 70 is a protein called eL34.

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

- Molecule 71 is a protein called eL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Ah	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 72 is a protein called eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Ai	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 73 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Aj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 74 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Ak	69	Total	C	N	O	S	0	0
			569	366	101	99	3		

- Molecule 75 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Al	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 76 is a protein called eL40.

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

- Molecule 77 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	An	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 78 is a protein called eL42.

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

- Molecule 79 is a protein called eL43.

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

- Molecule 80 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Ar	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

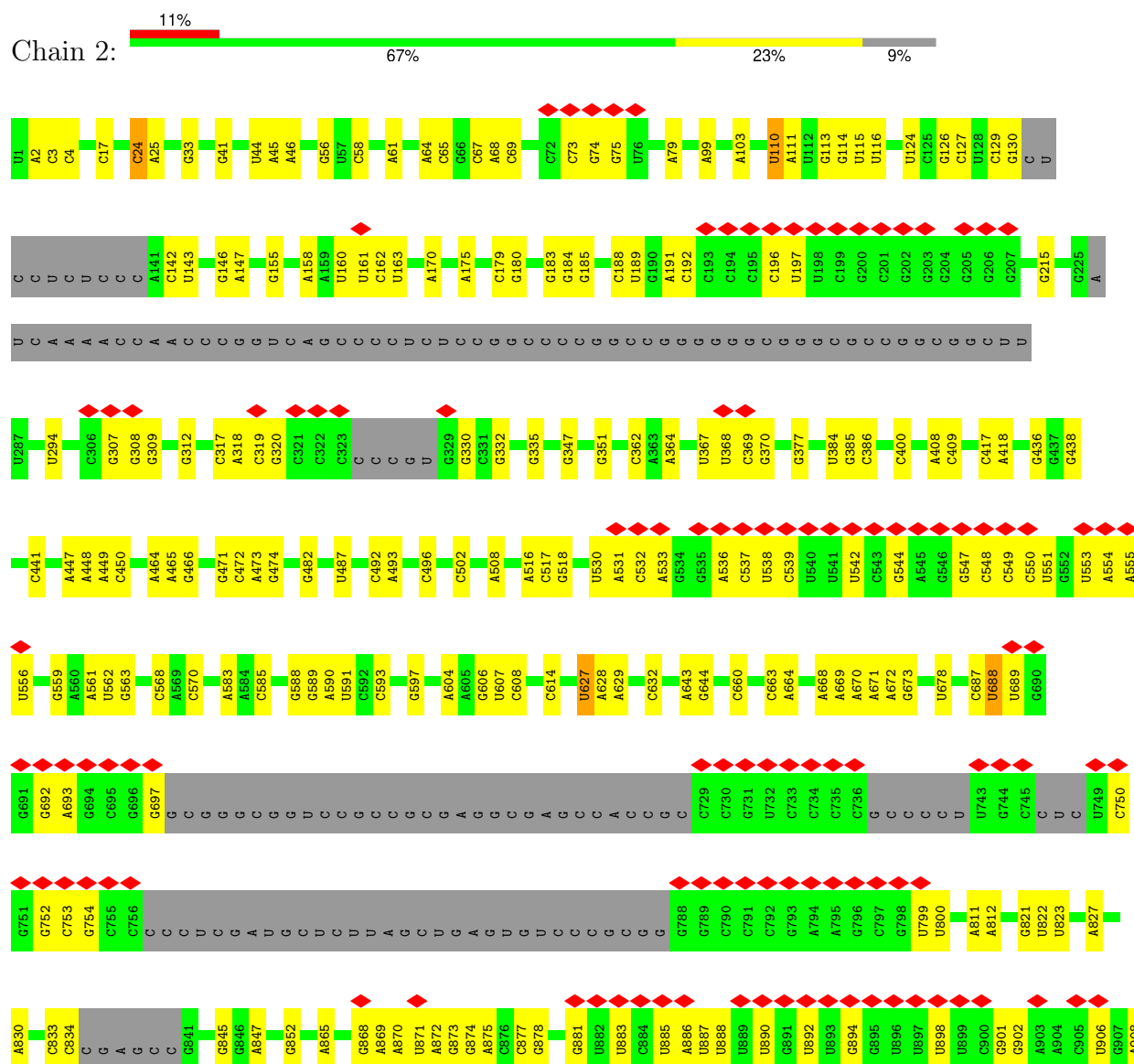
- Molecule 81 is a protein called uL1.

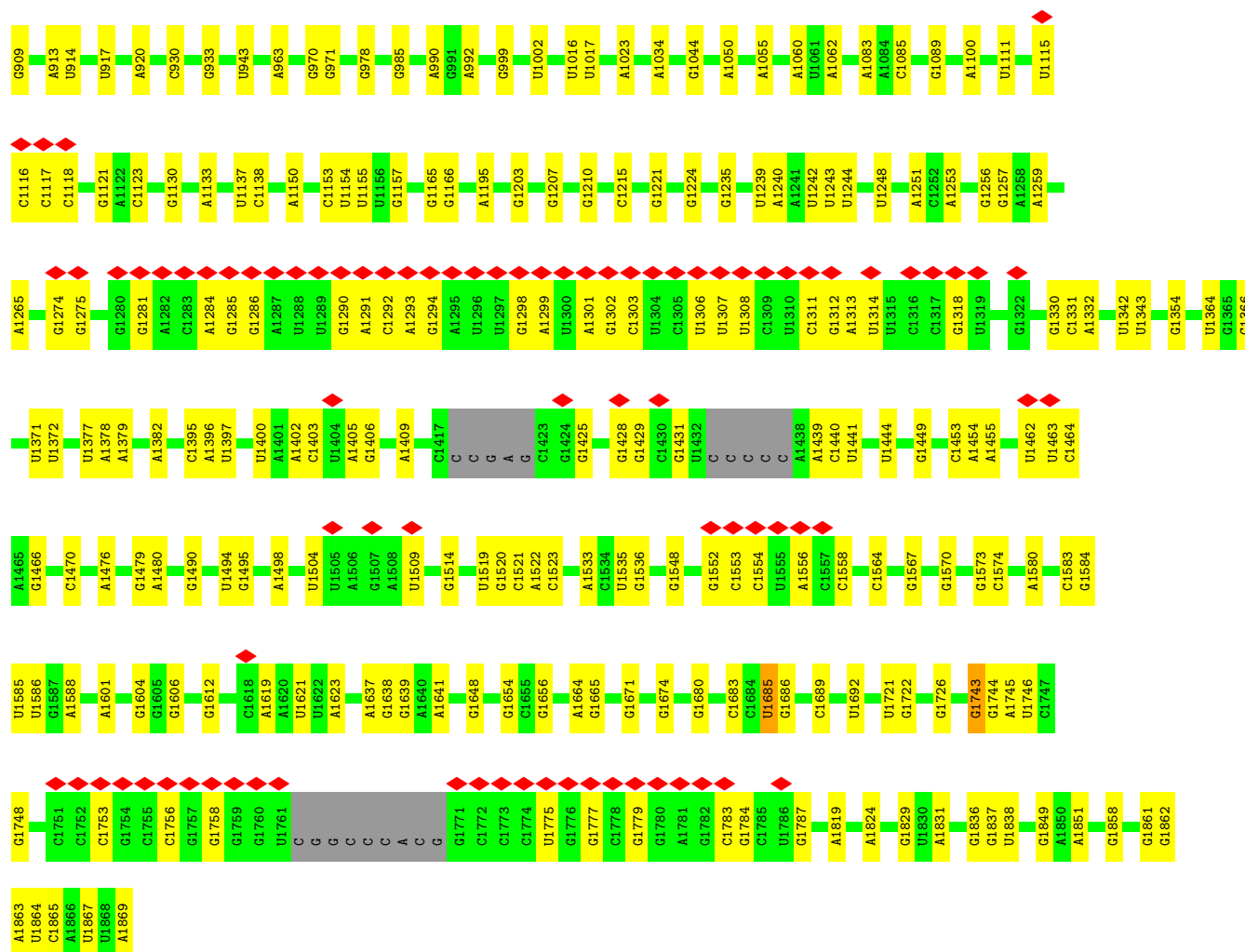
Mol	Chain	Residues	Atoms					AltConf	Trace
81	AK	212	Total	C	N	O	S	0	0
			1705	1091	306	300	8		

3 Residue-property plots

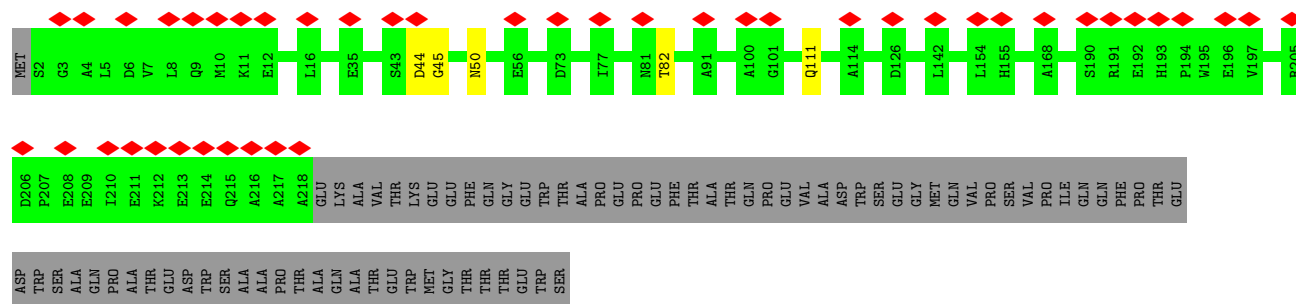
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 18S rRNA

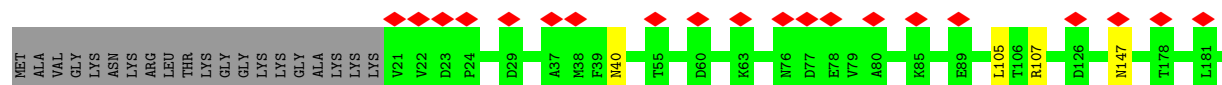
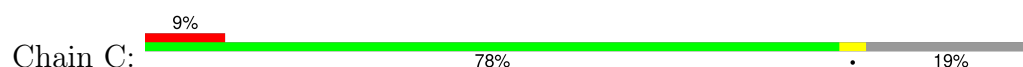


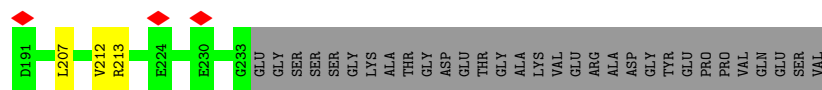


• Molecule 2: uS2

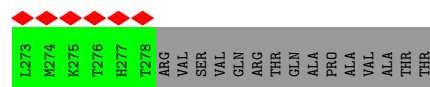
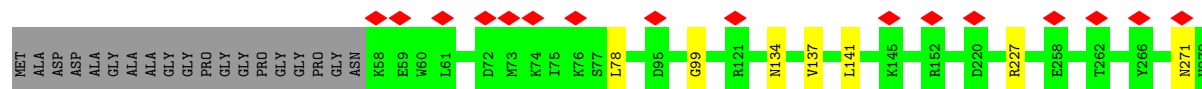
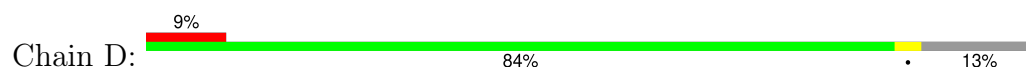


• Molecule 3: eS1

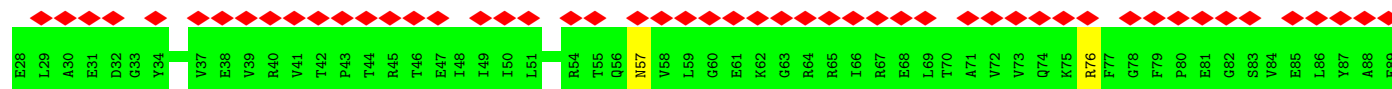
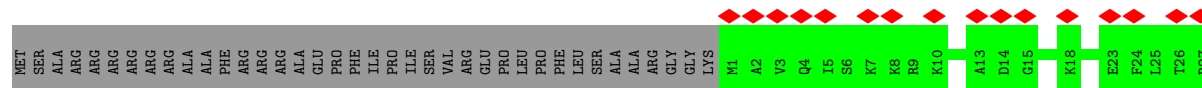
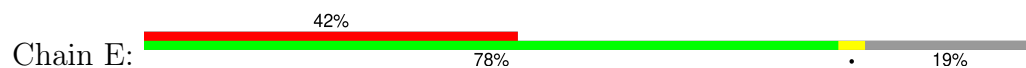




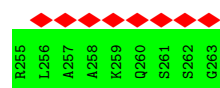
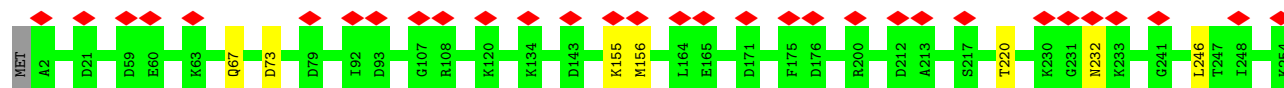
• Molecule 4: uS5



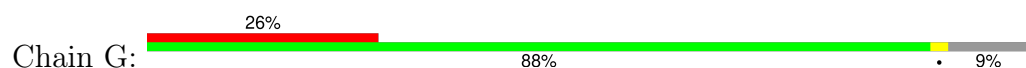
• Molecule 5: uS3

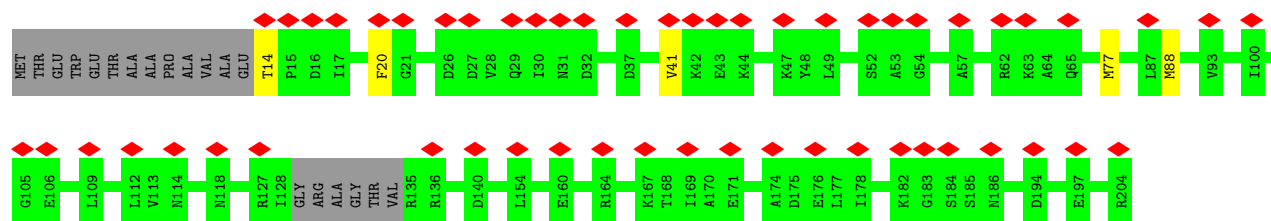


• Molecule 6: eS4

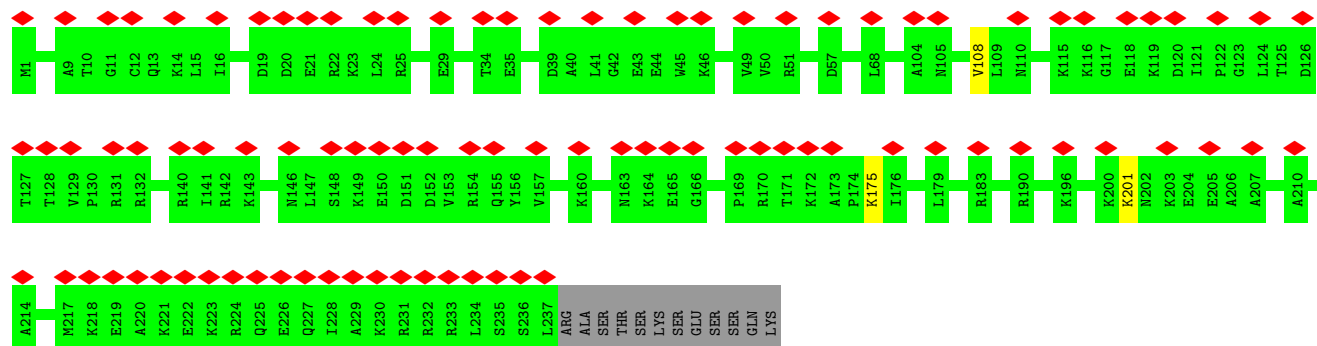
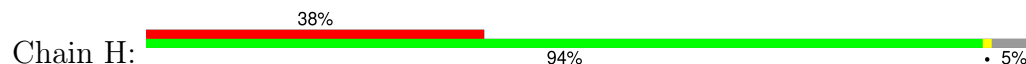


• Molecule 7: uS7

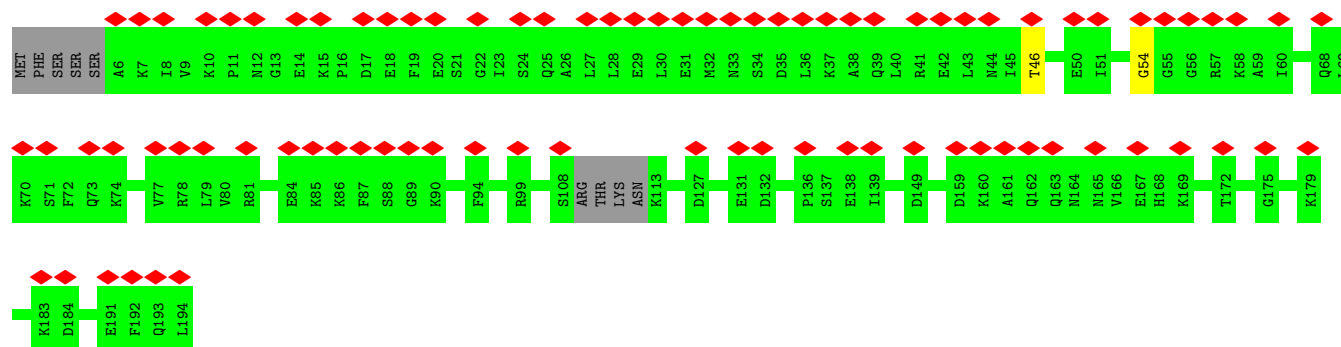
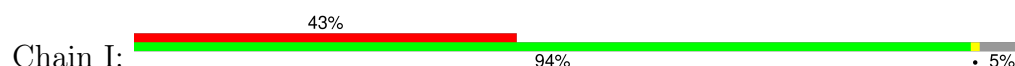




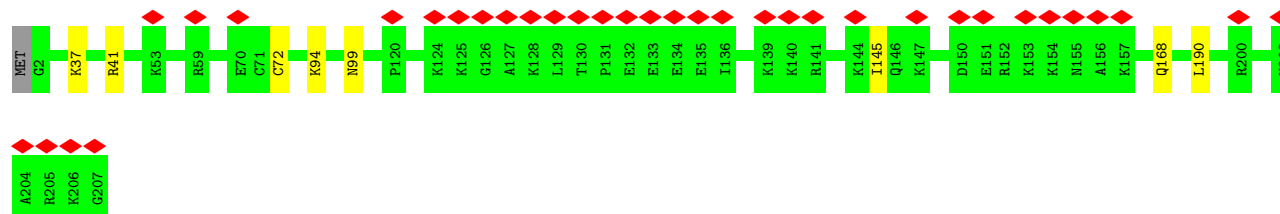
- Molecule 8: eS6



- Molecule 9: eS7

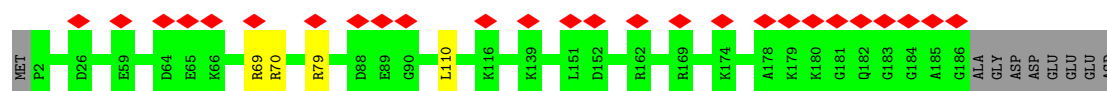


- Molecule 10: eS8



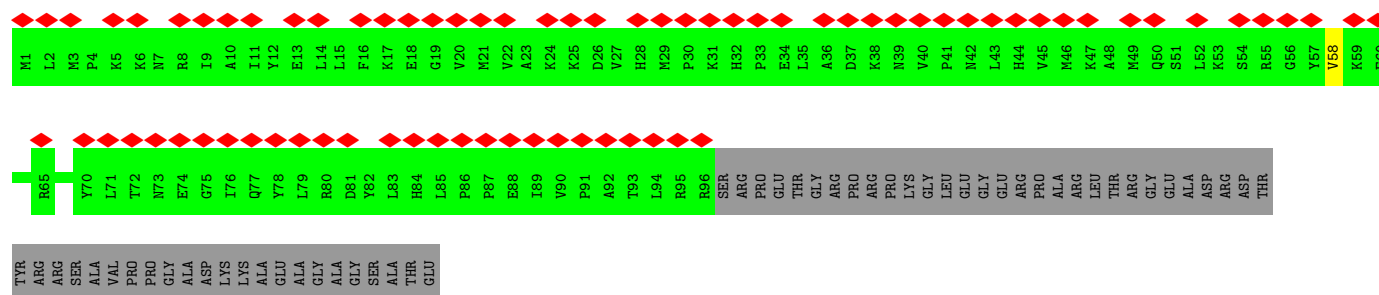
- Molecule 11: uS4

Chain K: 




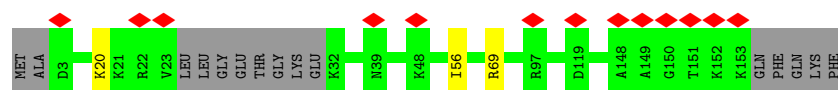
• Molecule 12: eS10

Chain L: 




• Molecule 13: uS17

Chain M: 



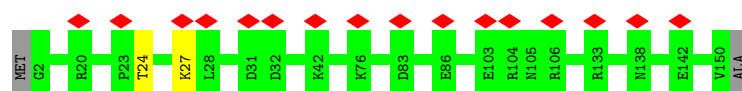
• Molecule 14: eS12

Chain N: 

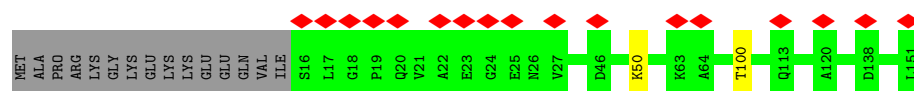
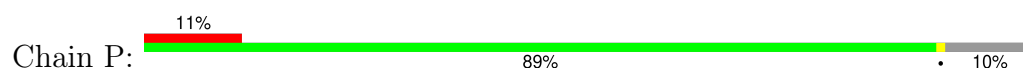


• Molecule 15: uS15

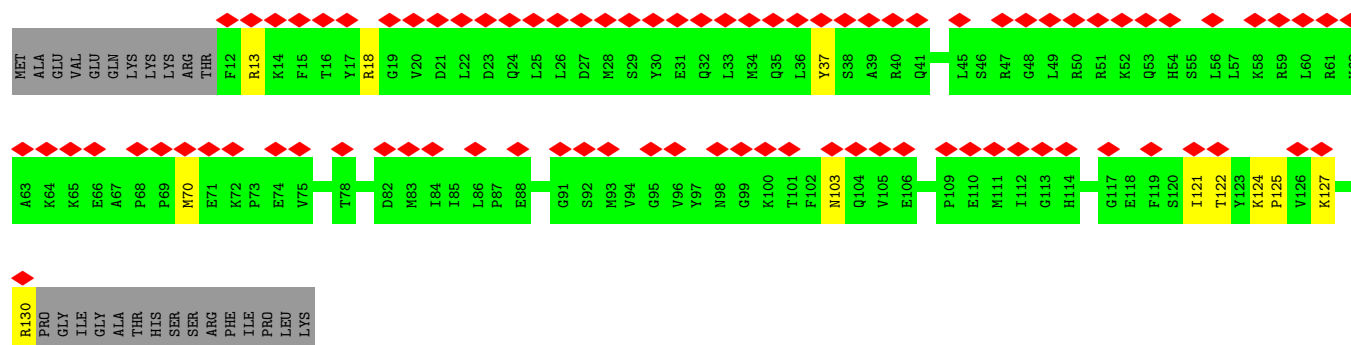
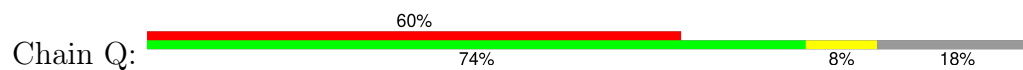
Chain O: 



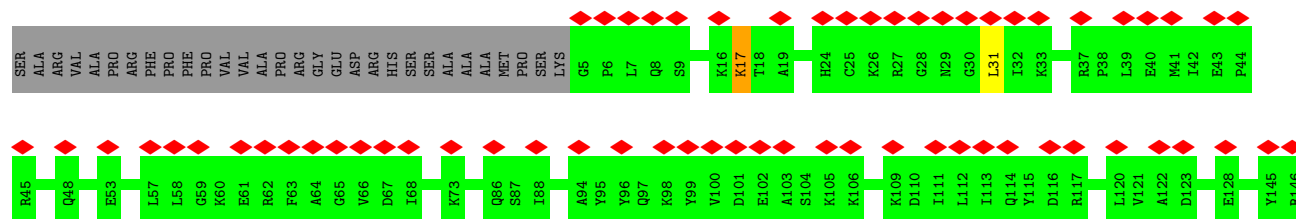
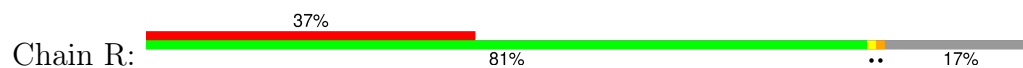
• Molecule 16: uS11



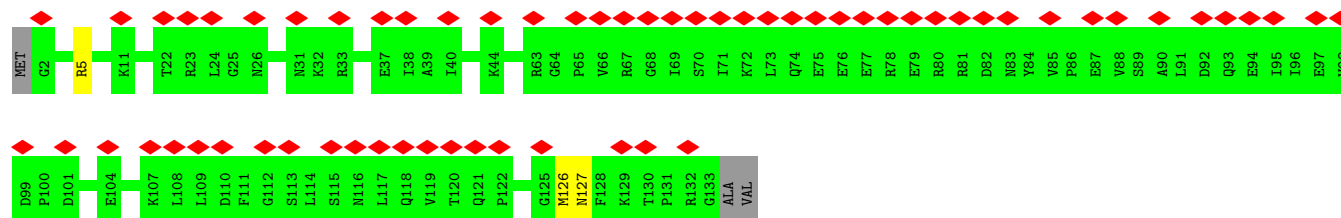
• Molecule 17: uS19



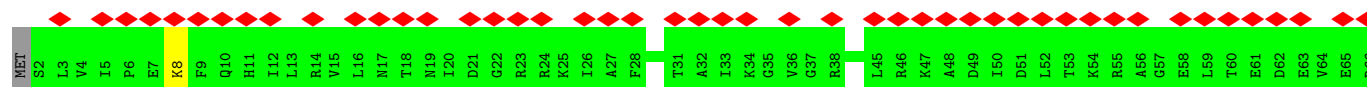
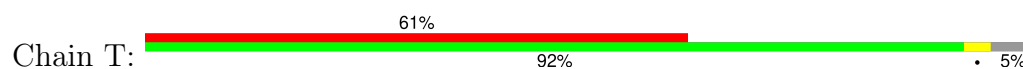
• Molecule 18: uS9

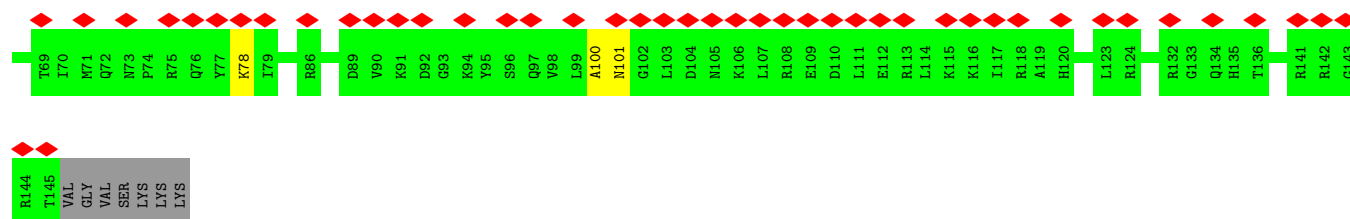


• Molecule 19: eS17

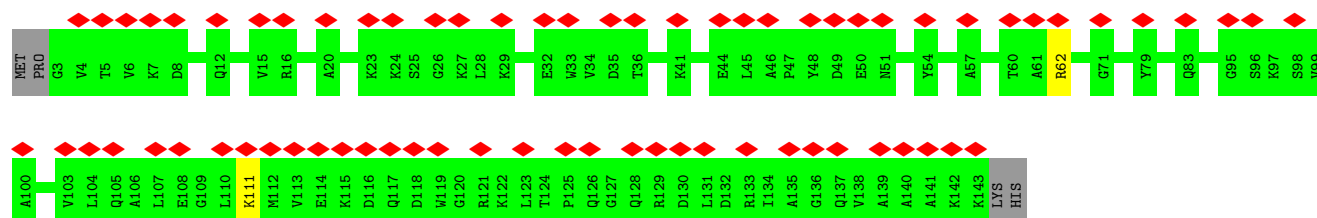


• Molecule 20: uS13

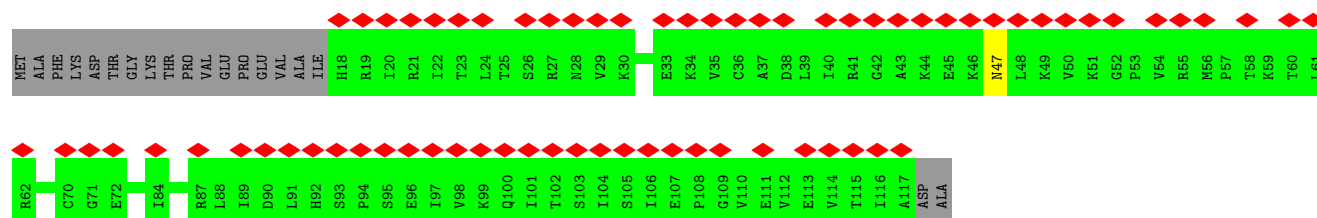
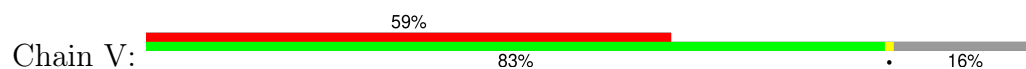




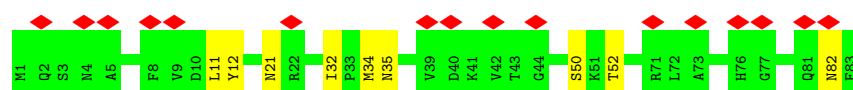
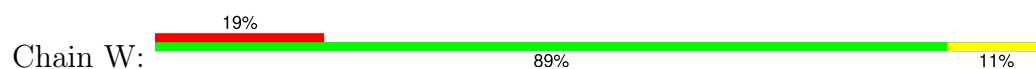
• Molecule 21: eS19



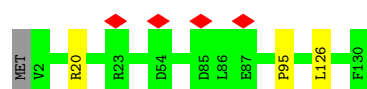
• Molecule 22: uS10



• Molecule 23: eS21



• Molecule 24: uS8

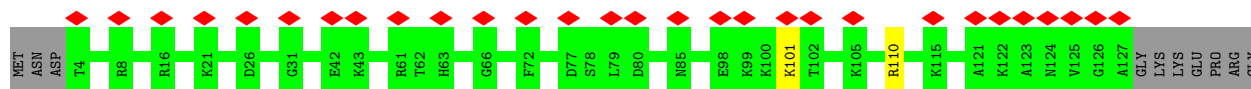


• Molecule 25: uS12

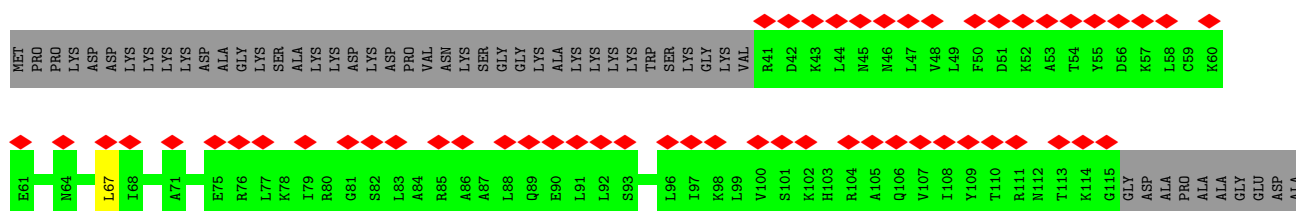




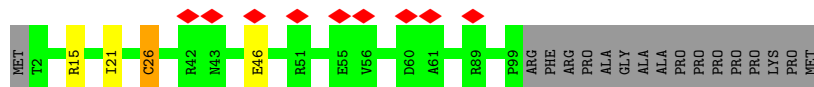
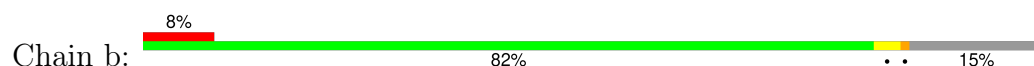
• Molecule 26: eS24



• Molecule 27: eS25



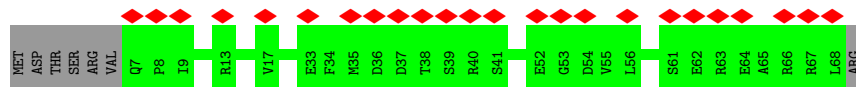
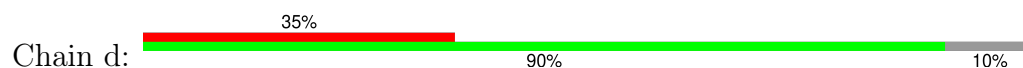
• Molecule 28: eS26



• Molecule 29: eS27

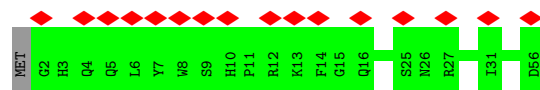


• Molecule 30: eS28

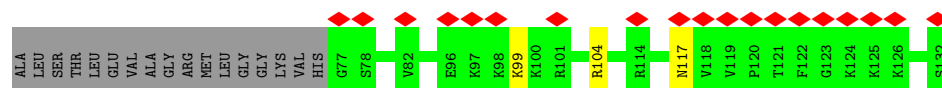
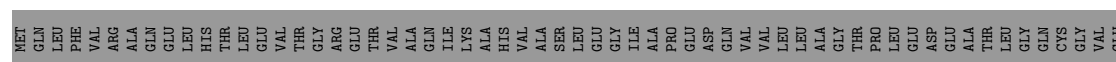


• Molecule 31: eS29

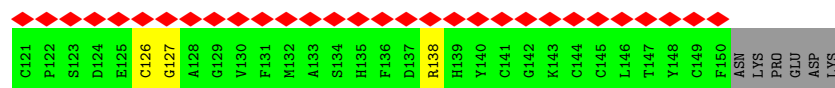
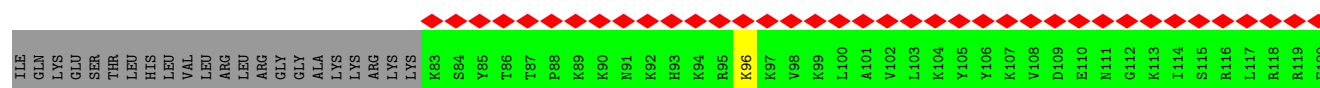
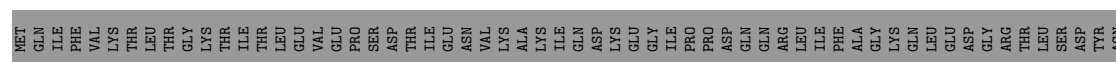




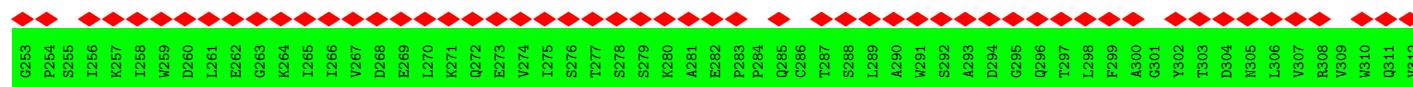
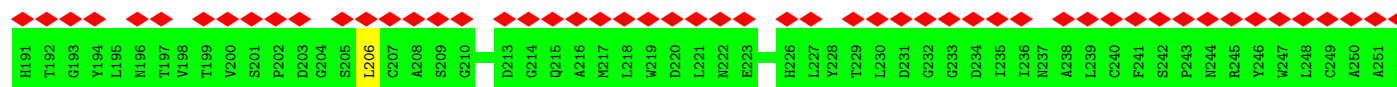
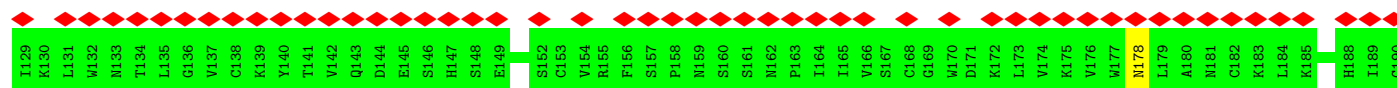
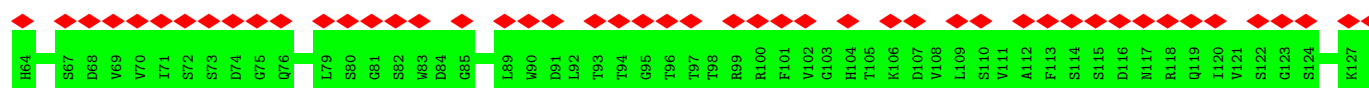
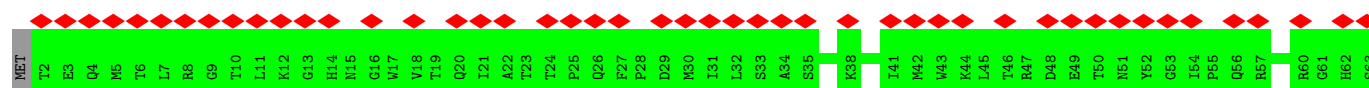
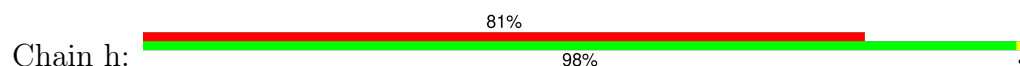
• Molecule 32: eS30



• Molecule 33: eS31

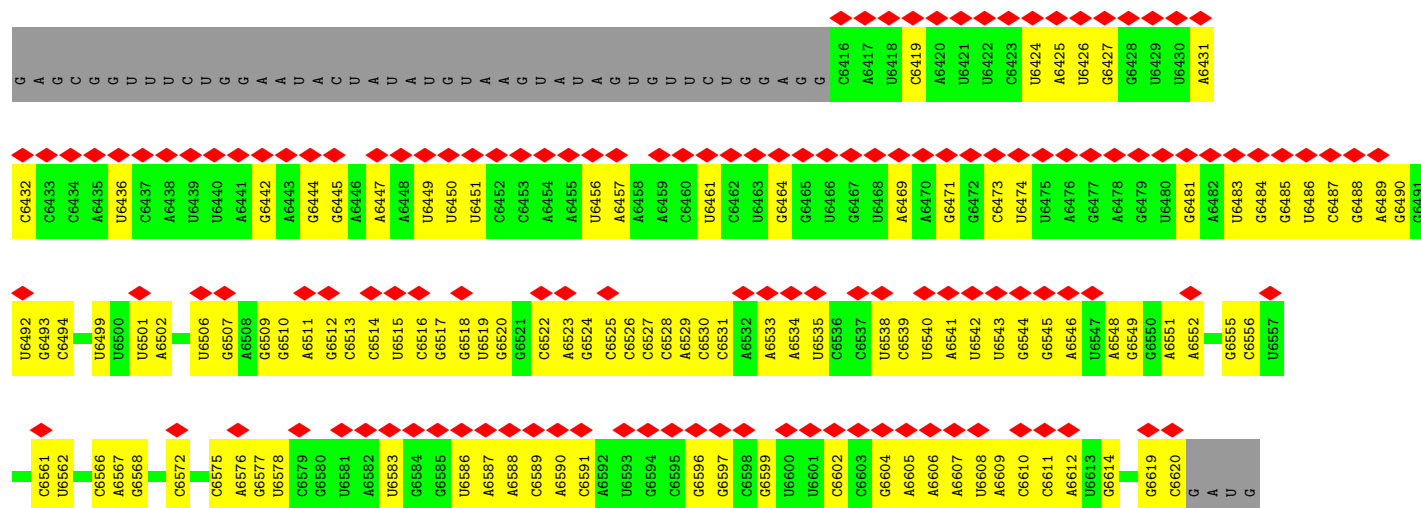


• Molecule 34: RACK1

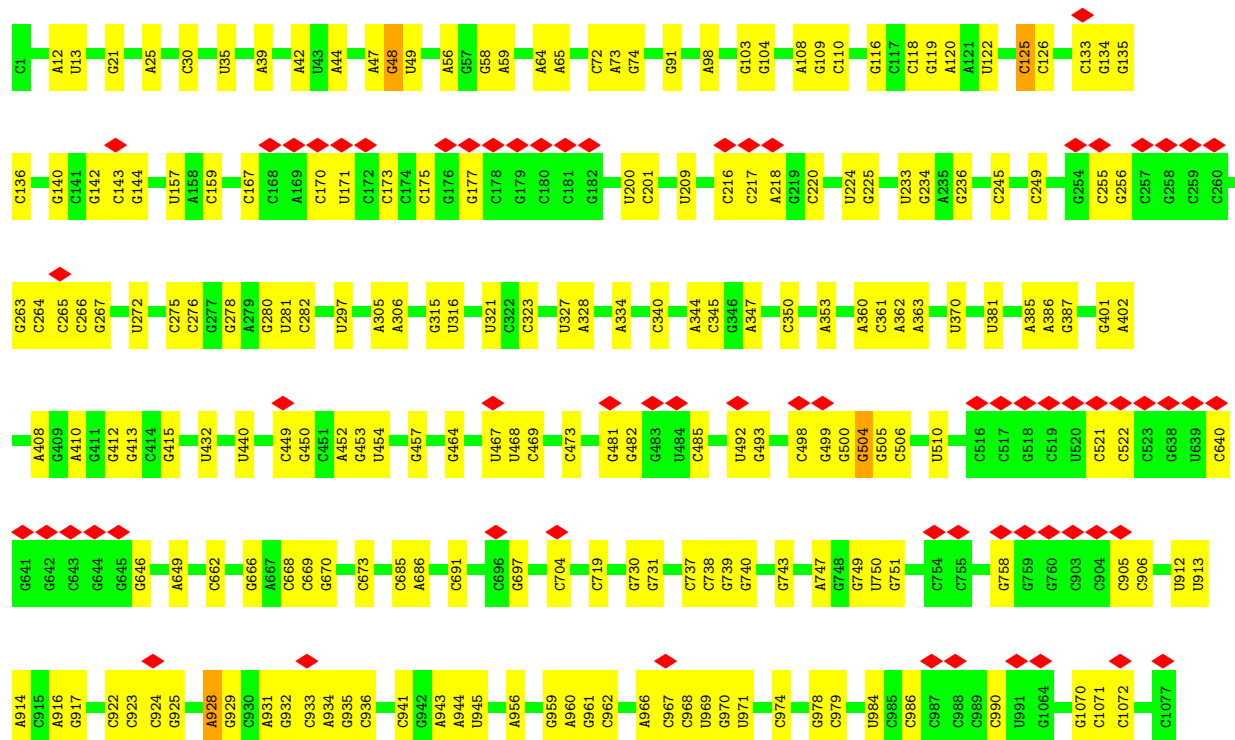
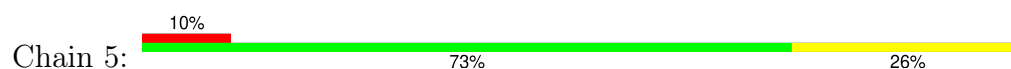




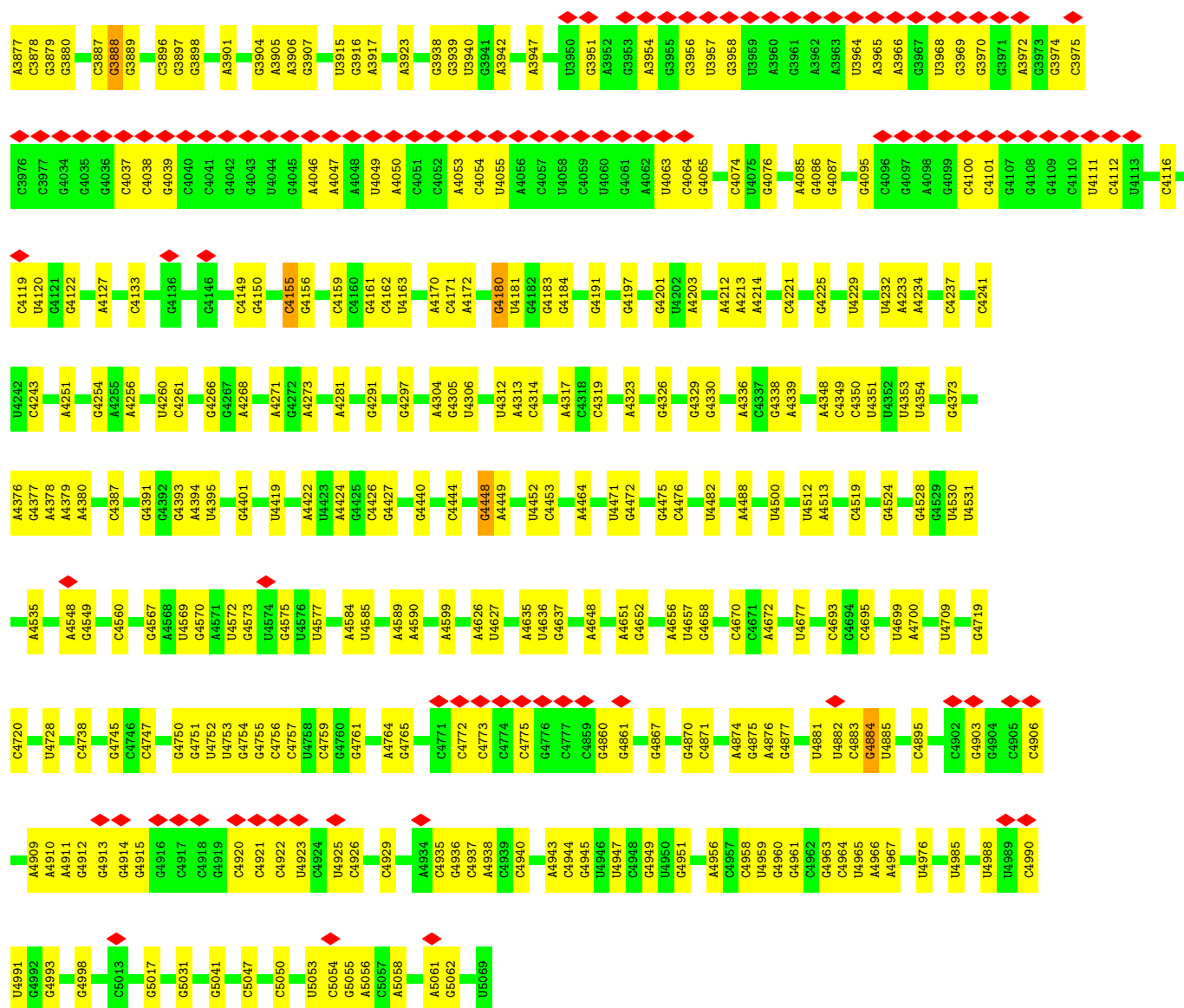
• Molecule 35: IAPV-IRES



• Molecule 36: 28S rRNA



A1078	C1079	C1080	C1097	G1098	G1099	U1100	C1180	C1183	A1184	C1192	C1193	G1194	G1195	G1196	C1197	G1198	G1199	G1200	U1201	C1202	U1209	C1210	C1211	G1212	G1213	C1214	C1215	G1234	G1235	C1236	C1237	A1238	C1239	G1244	C1245	G1246	U1247	C1248	C1249	C1251	C1252	G1271	C1272	G1273	A1274	G1275	C1276	C1277	C1278	A1279	C1280	G1281	G1282
G1283	G1284	G1287	G1288	C1289	C1292	G1296	U1297	C1301	U1302	A1326	A1337	G1354	G1358	G1359	G1370	A1371	G1377	G1380	U1381	A1387	G1394	A1397	A1398	G1399	G1400	C1401	C1402	G1403	G1404	C1405	G1409	C1410	C1411	G1412	C1413	C1414	G1415	G1416	C1417	G1418	A1419	A1420	G1421	G1426									
G1435	C1436	C1437	U1438	U1440	C1441	G1444	U1445	C1446	G1455	C1456	G1457	C1476	C1477	C1478	C1481	G1482	C1483	G1484	A1497	G1498	G1502	A1503	U1514	A1515	G1516	G1517	A1518	A1523	A1533	A1534	C1535	A1547	G1548	G1549	A1554	C1566	U1567	C1568	U1578	U1582	G1586	U1591											
U1596	A1601	G1612	A1613	G1617	G1618	G1624	G1625	A1631	A1632	G1633	A1634	A1637	C1640	G1641	A1642	G1651	G1654	U1660	C1661	C1676	U1677	A1684	C1694	U1695	C1696	C1720	U1726	G1733	G1734	C1740	G1741	A1742	A1746	G1750	A1751	U1754	C1755	U1756	U1757														
G1758	G1759	G1760	G1761	C1762	C1763	G1764	G1765	A1766	A1767	C1768	G1769	A1770	U1771	C1772	U1773	C1774	A1775	U1781	A1787	G1799	A1804	C1809	C1812	G1818	G1819	U1820	G1821	C1828	C1832	G1833	U1834	G1836	A1837	G1842	G1855	G1869	C1881	U1882	G1890	A1891	A1892	C1893	A1897										
G1910	G1916	U1917	U1918	G1919	C1920	G1921	G1922	G1925	U1930	C1931	C1935	G1940	G1945	G1948	G1951	U1957	A1958	U1959	A1960	G1961	A1962	C1963	A1964	G1965	C1966	A1967	G1968	G1969	A1970	U1971	G1972	G1973	U1974	G1975	G1976	C1977	C1978	A1979	U1980	G1981	G1982	A1983	A1984	G1985	U1986	C1987	G1988	G1989	A1990				
A1991	U1992	C1993	C1994	G1995	C1996	U1997	A1998	A1999	G2000	G2001	A2002	G2003	U2004	G2005	U2006	U2008	G2007	A2009	A2010	C2011	A2012	A2013	C2014	U2015	C2016	A2017	C2018	C2019	U2020	G2021	C2022	C2023	G2024	A2025	A2026	U2044	G2045	C2046	A2047	U2048	G2052	G2055	G2056	C2062	A2069	U2084	G2085	A2088	G2089	U2090	C2091	G2092	
G2093	C2094	A2095	G2096	A2097	C2098	C2099	G2100	A2101	G2102	A2107	G2108	A2109	G2110	U2111	G2112	G2259	C2260	U2267	A2268	G2275	A2276	C2277	C2289	G2294	A2300	G2301	A2313	G2314	C2325	G2333	C2338	G2348	C2351	A2360	G2364	A2369	A2395	A2404	U2409														
A2417	C2422	U2425	A2428	U2433	C2434	C2441	U2444	U2447	G2450	U2468	C2469	G2475	G2479	G2480	G2481	C2482	A2484	U2485	G2486	G2487	C2488	C2489	U2490	C2491	C2492	G2493	U2494	U2495	G2496	C2497	C2498	C2499	A2502	G2503	C2504	U2505	G2507	G2508	G2511	A2512	G2513	G2514	G2521	A2529									
U2530	A2536	A2537	G2544	U2545	G2546	G2547	A2553	U2554	G2555	G2556	G2559	C2560	C2561	G2562	C2563	G2564	A2565	G2566	C2567	C2568	G2569	C2572	A2573	G2574	U2575	G2576	C2583	A2587	C2588	A2601	G2617	C2627	G2638	U2639	C2653	C2654	C2655	U2656	G2657	G2658	U2661	G2662	C2669	A2676									
G2686	U2687	G2694	A2695	A2696	U2701	G2705	G2706	U2707	U2708	C2709	G2710	G2711	G2712	C2713	G2714	G2715	G2716	U2723	G2724	A2725	G2726	G2735	C2739	U2740	U2741	G2742	A2743	A2744	G2756	U2761	C2762	U2763	U2764	C2768	U2769	C2770	A2787	U2788	A2789	U2790	C2794	A2798	A2806	C2814									
A2815	U2826	G2827	U2828	U2829	G2830	A2835	A2836	U2837	G2838	G2842	U2843	A2844	A2845	G2855	C2856	G2862	U2874	C2875	G2884	G2898	G2901	C2907	C3598	A3599	C3602	G3603	A3604	C3605	U3606	C3610	G3811	C3812	C3813	U3814	A3817	U3818	G3819	U3822	G3839	U3840	U3851	A3862	A3863	C3673	C3674								
C3696	G3710	A3711	A3712	U3713	A3717	G3725	U3729	G3740	A3748	G3753	A3760	C3761	U3762	A3763	G3765	A3766	G3776	C3777	A3783	A3784	A3785	U3802	G3809	C3810	C3811	C3812	U3814	A3817	U3818	G3819	U3822	G3839	U3840	U3851	A3862	A3863	C3867	A3876															



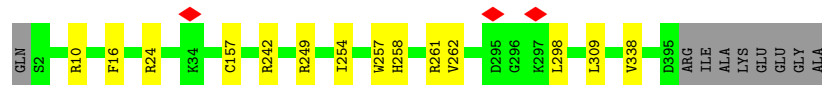
- Molecule 39: uL2

Chain AA:  89% 7%




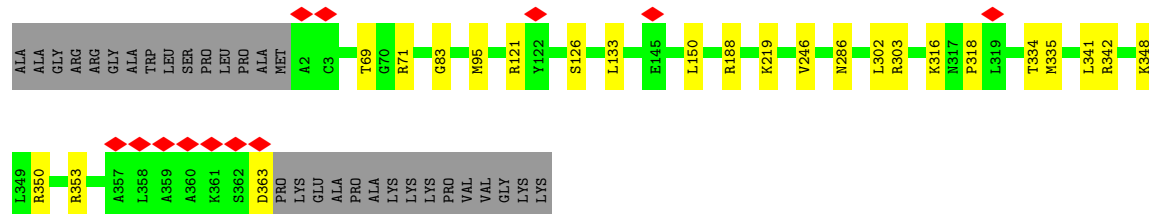
- Molecule 40: uL3

Chain AB:  94%



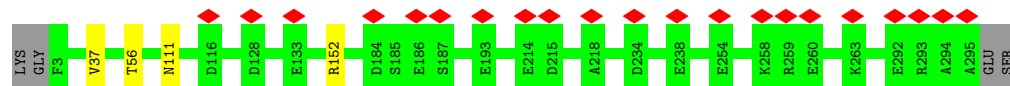
- Molecule 41: uL4

Chain AC:  86% 6% 8%



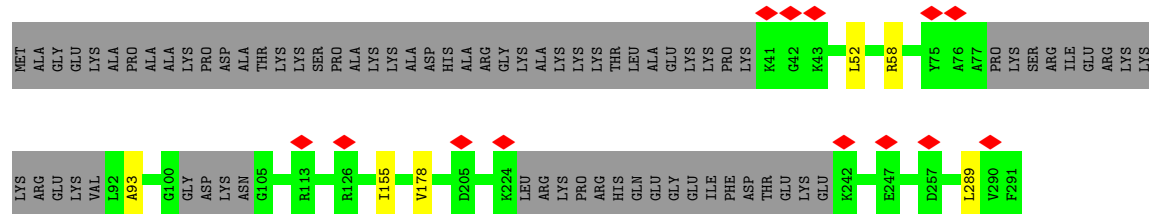
- Molecule 42: uL18

Chain AD:  7% 97%




- Molecule 43: eL6

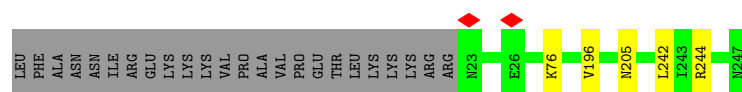
Chain AE:  72% 26%



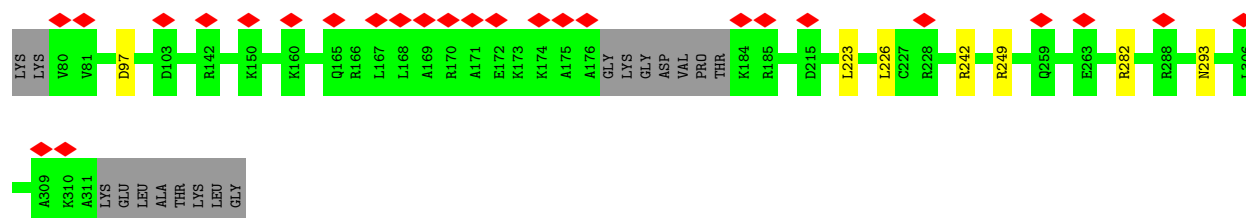
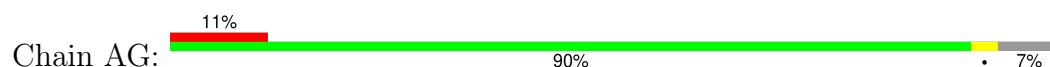
- Molecule 44: uL30

Chain AF:  88% 10%

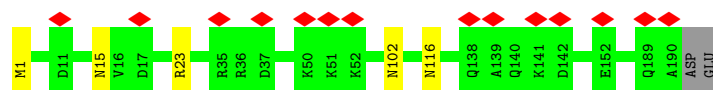




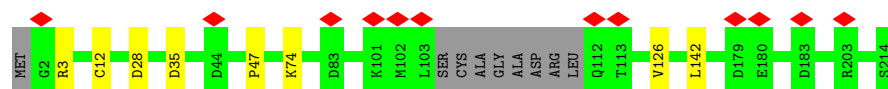
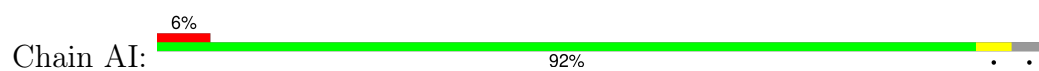
• Molecule 45: eL8



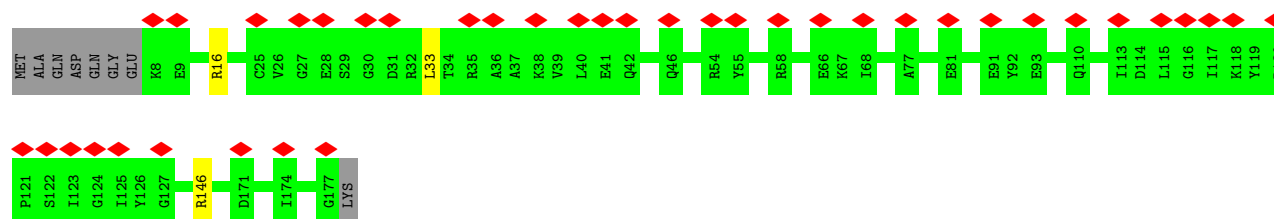
• Molecule 46: uL6



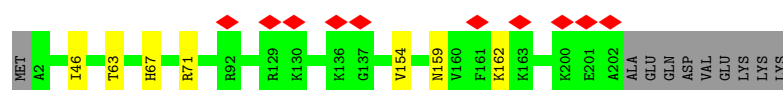
• Molecule 47: uL16



• Molecule 48: uL11

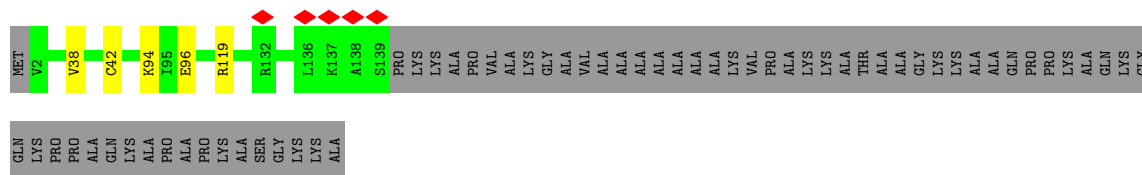


• Molecule 49: eL13



• Molecule 50: L14e

Chain AM:  67% 30%



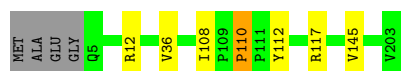
- Molecule 51: eL15

Chain AN:  96%




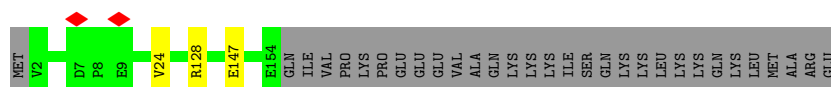
- Molecule 52: uL13

Chain AO:  95%



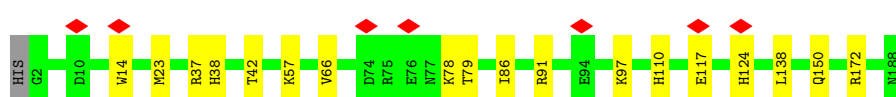
- Molecule 53: uL22

Chain AP:  82% 17%



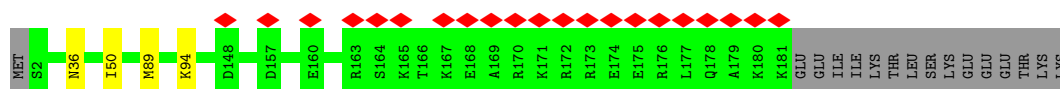
- Molecule 54: eL18

Chain AQ:  90% 10%



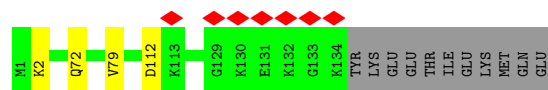
- Molecule 55: eL19

Chain AR:  11% 90% 8%

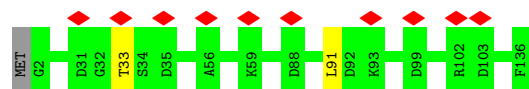


- Molecule 56: eL20

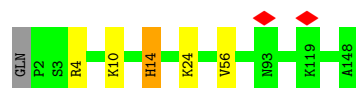
Chain AS:  90% 10%



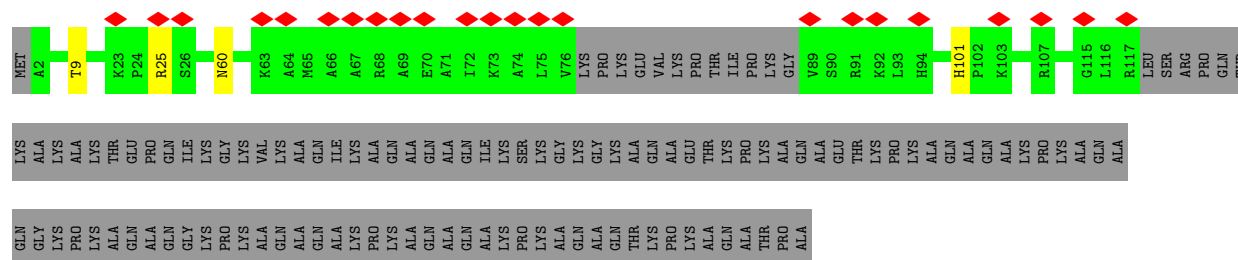
• Molecule 63: eL27



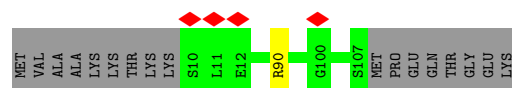
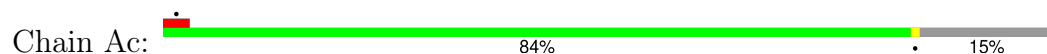
• Molecule 64: uL15



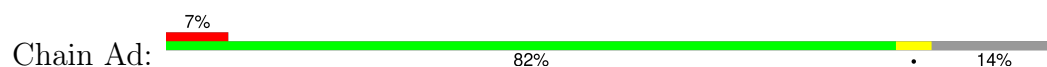
• Molecule 65: eL29



• Molecule 66: eL30

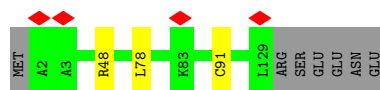


• Molecule 67: eL31

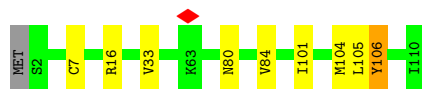
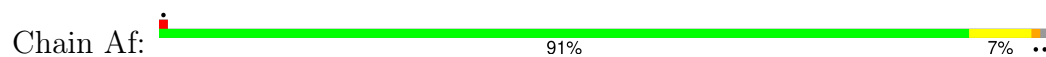


• Molecule 68: eL32

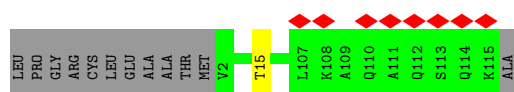
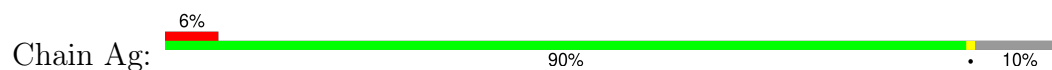




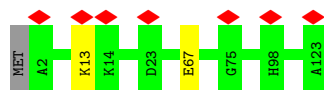
• Molecule 69: eL33



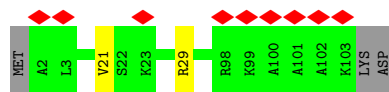
• Molecule 70: eL34



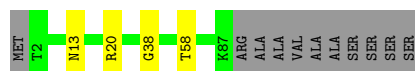
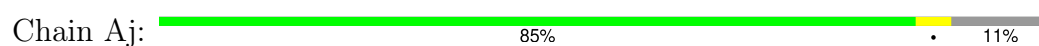
• Molecule 71: eL35



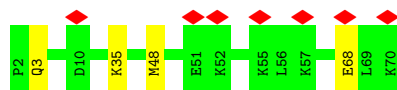
• Molecule 72: eL36



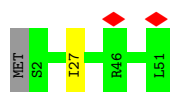
• Molecule 73: eL37



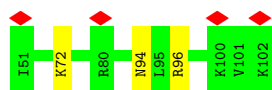
• Molecule 74: eL38



• Molecule 75: eL39



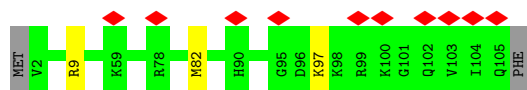
- Molecule 76: eL40



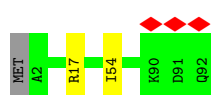
- Molecule 77: eL41



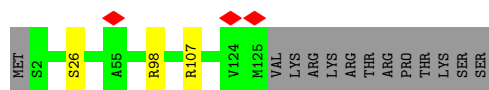
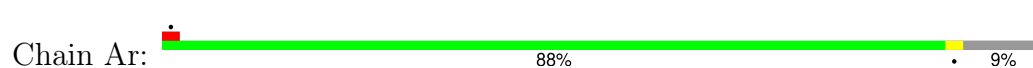
- Molecule 78: eL42



- Molecule 79: eL43



- Molecule 80: eL28



- Molecule 81: uL1



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	120176	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42.09	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	31000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.289	Depositor
Minimum map value	-0.163	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.032	Depositor
Map size (Å)	443.88, 443.88, 443.88	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.233, 1.233, 1.233	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	2	0.23	0/40509	0.69	6/63128 (0.0%)
2	B	0.66	0/1744	0.78	0/2371
3	C	0.66	0/1756	0.79	0/2350
4	D	0.66	0/1748	0.80	0/2362
5	E	0.69	0/1796	0.81	0/2417
6	F	0.66	0/2115	0.81	0/2843
7	G	0.68	0/1492	0.79	0/2005
8	H	0.67	0/1946	0.83	0/2590
9	I	0.68	0/1510	0.78	0/2022
10	J	0.65	0/1715	0.82	0/2287
11	K	0.67	0/1550	0.83	0/2069
12	L	0.66	0/834	0.78	0/1125
13	M	0.65	0/1195	0.81	0/1597
14	N	0.72	0/918	0.80	0/1233
15	O	0.67	0/1226	0.80	0/1649
16	P	0.67	0/1029	0.84	0/1380
17	Q	0.67	0/1009	0.80	0/1346
18	R	0.68	0/1146	0.81	0/1534
19	S	0.68	0/1082	0.79	0/1452
20	T	0.68	0/1208	0.81	0/1618
21	U	0.69	0/1115	0.81	0/1493
22	V	0.69	0/805	0.80	0/1081
23	W	0.69	0/638	0.83	0/855
24	X	0.66	0/1051	0.80	0/1406
25	Y	0.66	0/1116	0.83	0/1490
26	Z	0.67	0/1028	0.80	0/1366
27	a	0.69	0/604	0.80	0/810
28	b	0.65	0/789	0.81	0/1059
29	c	0.66	0/665	0.79	0/891
30	d	0.69	0/490	0.83	0/656
31	e	0.67	0/470	0.80	0/623
32	f	0.68	0/451	0.81	0/592
33	g	0.69	0/567	0.83	0/753
34	h	0.69	0/2493	0.80	0/3394

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	1	0.24	0/4881	0.72	0/7604
36	5	0.26	0/86215	0.70	15/134459 (0.0%)
37	7	0.23	0/2836	0.68	0/4421
38	8	0.26	0/3581	0.69	0/5577
39	AA	0.64	0/1933	0.87	0/2592
40	AB	0.63	0/3240	0.81	0/4339
41	AC	0.63	0/2937	0.79	0/3946
42	AD	0.65	0/2437	0.78	0/3264
43	AE	0.65	0/1762	0.82	0/2362
44	AF	0.63	0/1911	0.80	0/2549
45	AG	0.65	0/1850	0.82	0/2491
46	AH	0.66	0/1535	0.81	0/2063
47	AI	0.63	0/1702	0.80	0/2272
48	AJ	0.67	0/1385	0.80	0/1852
49	AL	0.64	0/1658	0.83	0/2219
50	AM	0.64	0/1158	0.80	0/1547
51	AN	0.61	0/1746	0.85	0/2338
52	AO	0.63	0/1663	0.82	0/2223
53	AP	0.62	0/1268	0.81	0/1700
54	AQ	0.63	0/1557	0.83	0/2086
55	AR	0.65	0/1519	0.82	0/2006
56	AS	0.62	0/1498	0.80	0/2012
57	AT	0.62	0/1326	0.79	0/1770
58	AU	0.66	0/832	0.78	0/1116
59	AV	0.66	0/983	0.82	0/1319
60	AW	0.63	0/541	0.81	0/720
61	AX	0.63	0/984	0.80	0/1323
62	AY	0.64	0/1132	0.80	0/1504
63	AZ	0.64	0/1130	0.82	0/1507
64	Aa	0.63	0/1191	0.83	1/1590 (0.1%)
65	Ab	0.65	0/861	0.81	0/1138
66	Ac	0.68	0/771	0.80	0/1034
67	Ad	0.63	0/903	0.83	0/1216
68	Ae	0.63	0/1071	0.83	0/1429
69	Af	0.62	0/895	0.89	1/1198 (0.1%)
70	Ag	0.66	0/916	0.87	0/1220
71	Ah	0.65	0/1021	0.82	0/1348
72	Ai	0.65	0/841	0.81	0/1112
73	Aj	0.62	0/720	0.89	0/952
74	Ak	0.65	0/575	0.80	0/759
75	Al	0.62	0/459	0.80	0/608
76	Am	0.64	0/435	0.81	0/575
77	An	0.60	0/240	0.84	0/305

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	Ao	0.63	0/864	0.82	0/1140
79	Ap	0.66	0/718	0.84	0/953
80	Ar	0.65	0/1010	0.84	0/1354
81	AK	0.69	0/1733	0.84	0/2324
All	All	0.46	0/232234	0.74	23/341283 (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
28	b	0	1
40	AB	0	2
All	All	0	3

There are no bond length outliers.

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
69	Af	106	TYR	CB-CA-C	9.14	128.67	110.40
36	5	4180	G	C2'-C3'-O3'	7.16	125.24	109.50
36	5	3625	G	C2'-C3'-O3'	6.05	123.39	113.70
1	2	1685	U	C2'-C3'-O3'	5.89	123.12	113.70
36	5	928	A	C2'-C3'-O3'	5.83	123.03	113.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
40	AB	257	TRP	Peptide
40	AB	258	HIS	Peptide
28	b	26	CYS	Peptide

5.2 Too-close contacts

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
2	B	215/295 (73%)	196 (91%)	17 (8%)	2 (1%)	14	45
3	C	211/264 (80%)	188 (89%)	23 (11%)	0	100	100
4	D	219/255 (86%)	199 (91%)	18 (8%)	2 (1%)	14	45
5	E	226/281 (80%)	209 (92%)	17 (8%)	0	100	100
6	F	260/263 (99%)	239 (92%)	20 (8%)	1 (0%)	30	63
7	G	181/204 (89%)	169 (93%)	10 (6%)	2 (1%)	12	39
8	H	235/249 (94%)	210 (89%)	25 (11%)	0	100	100
9	I	181/194 (93%)	169 (93%)	11 (6%)	1 (1%)	22	53
10	J	204/207 (99%)	187 (92%)	15 (7%)	2 (1%)	13	42
11	K	183/194 (94%)	167 (91%)	16 (9%)	0	100	100
12	L	94/149 (63%)	86 (92%)	8 (8%)	0	100	100
13	M	139/158 (88%)	124 (89%)	15 (11%)	0	100	100
14	N	115/132 (87%)	100 (87%)	15 (13%)	0	100	100
15	O	147/151 (97%)	139 (95%)	8 (5%)	0	100	100
16	P	134/151 (89%)	119 (89%)	15 (11%)	0	100	100
17	Q	117/145 (81%)	106 (91%)	8 (7%)	3 (3%)	4	21
18	R	140/172 (81%)	127 (91%)	12 (9%)	1 (1%)	19	51
19	S	130/135 (96%)	120 (92%)	9 (7%)	1 (1%)	16	48
20	T	142/152 (93%)	125 (88%)	15 (11%)	2 (1%)	9	34
21	U	139/145 (96%)	126 (91%)	12 (9%)	1 (1%)	19	51
22	V	98/119 (82%)	87 (89%)	11 (11%)	0	100	100
23	W	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
24	X	127/130 (98%)	119 (94%)	7 (6%)	1 (1%)	16	48
25	Y	139/143 (97%)	129 (93%)	10 (7%)	0	100	100
26	Z	122/134 (91%)	113 (93%)	9 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	a	73/125 (58%)	68 (93%)	5 (7%)	0	100	100
28	b	96/115 (84%)	83 (86%)	11 (12%)	2 (2%)	5	25
29	c	81/84 (96%)	71 (88%)	9 (11%)	1 (1%)	11	38
30	d	60/69 (87%)	59 (98%)	1 (2%)	0	100	100
31	e	53/56 (95%)	49 (92%)	4 (8%)	0	100	100
32	f	54/133 (41%)	48 (89%)	5 (9%)	1 (2%)	6	27
33	g	66/156 (42%)	58 (88%)	6 (9%)	2 (3%)	3	19
34	h	311/317 (98%)	268 (86%)	43 (14%)	0	100	100
39	AA	246/257 (96%)	230 (94%)	14 (6%)	2 (1%)	16	48
40	AB	392/403 (97%)	362 (92%)	30 (8%)	0	100	100
41	AC	360/392 (92%)	337 (94%)	20 (6%)	3 (1%)	16	48
42	AD	291/297 (98%)	270 (93%)	20 (7%)	1 (0%)	37	68
43	AE	208/291 (72%)	184 (88%)	23 (11%)	1 (0%)	25	58
44	AF	223/249 (90%)	211 (95%)	11 (5%)	1 (0%)	30	63
45	AG	221/242 (91%)	208 (94%)	13 (6%)	0	100	100
46	AH	188/192 (98%)	174 (93%)	14 (7%)	0	100	100
47	AI	201/214 (94%)	186 (92%)	13 (6%)	2 (1%)	13	42
48	AJ	168/178 (94%)	159 (95%)	8 (5%)	1 (1%)	22	53
49	AL	199/211 (94%)	191 (96%)	7 (4%)	1 (0%)	25	58
50	AM	136/198 (69%)	126 (93%)	10 (7%)	0	100	100
51	AN	201/204 (98%)	186 (92%)	15 (8%)	0	100	100
52	AO	197/203 (97%)	188 (95%)	8 (4%)	1 (0%)	25	58
53	AP	151/184 (82%)	145 (96%)	6 (4%)	0	100	100
54	AQ	185/188 (98%)	170 (92%)	15 (8%)	0	100	100
55	AR	178/196 (91%)	168 (94%)	10 (6%)	0	100	100
56	AS	174/176 (99%)	157 (90%)	14 (8%)	3 (2%)	7	30
57	AT	157/160 (98%)	143 (91%)	12 (8%)	2 (1%)	10	36
58	AU	97/128 (76%)	86 (89%)	10 (10%)	1 (1%)	13	42
59	AV	127/140 (91%)	120 (94%)	6 (5%)	1 (1%)	16	48
60	AW	61/157 (39%)	57 (93%)	4 (7%)	0	100	100
61	AX	116/156 (74%)	110 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	AY	132/145 (91%)	126 (96%)	6 (4%)	0	100	100
63	AZ	133/136 (98%)	124 (93%)	8 (6%)	1 (1%)	16	48
64	Aa	145/148 (98%)	132 (91%)	11 (8%)	2 (1%)	9	34
65	Ab	100/226 (44%)	94 (94%)	5 (5%)	1 (1%)	13	42
66	Ac	96/115 (84%)	91 (95%)	5 (5%)	0	100	100
67	Ad	105/125 (84%)	97 (92%)	7 (7%)	1 (1%)	13	42
68	Ae	126/135 (93%)	121 (96%)	5 (4%)	0	100	100
69	Af	107/110 (97%)	102 (95%)	5 (5%)	0	100	100
70	Ag	112/126 (89%)	110 (98%)	2 (2%)	0	100	100
71	Ah	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
72	Ai	100/105 (95%)	93 (93%)	7 (7%)	0	100	100
73	Aj	84/97 (87%)	78 (93%)	5 (6%)	1 (1%)	11	38
74	Ak	67/69 (97%)	63 (94%)	3 (4%)	1 (2%)	8	33
75	Al	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
76	Am	50/52 (96%)	49 (98%)	0	1 (2%)	6	26
77	An	23/25 (92%)	23 (100%)	0	0	100	100
78	Ao	102/106 (96%)	97 (95%)	5 (5%)	0	100	100
79	Ap	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
80	Ar	122/137 (89%)	112 (92%)	10 (8%)	0	100	100
81	AK	210/217 (97%)	155 (74%)	51 (24%)	4 (2%)	6	27
All	All	11321/12916 (88%)	10408 (92%)	856 (8%)	57 (0%)	27	58

5 of 57 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	45	GLY
17	Q	18	ARG
18	R	17	LYS
20	T	100	ALA
41	AC	126	SER

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	B	180/245 (74%)	177 (98%)	3 (2%)	56	78
3	C	194/231 (84%)	187 (96%)	7 (4%)	30	60
4	D	186/205 (91%)	181 (97%)	5 (3%)	40	67
5	E	190/232 (82%)	182 (96%)	8 (4%)	25	56
6	F	223/225 (99%)	217 (97%)	6 (3%)	40	67
7	G	158/170 (93%)	155 (98%)	3 (2%)	52	75
8	H	207/218 (95%)	204 (99%)	3 (1%)	62	81
9	I	165/174 (95%)	164 (99%)	1 (1%)	84	91
10	J	178/179 (99%)	172 (97%)	6 (3%)	32	62
11	K	161/168 (96%)	157 (98%)	4 (2%)	42	69
12	L	87/125 (70%)	86 (99%)	1 (1%)	70	84
13	M	130/142 (92%)	127 (98%)	3 (2%)	45	70
14	N	99/108 (92%)	98 (99%)	1 (1%)	73	86
15	O	130/131 (99%)	128 (98%)	2 (2%)	60	80
16	P	106/119 (89%)	104 (98%)	2 (2%)	52	75
17	Q	108/130 (83%)	100 (93%)	8 (7%)	11	36
18	R	117/140 (84%)	115 (98%)	2 (2%)	56	78
19	S	119/121 (98%)	117 (98%)	2 (2%)	56	78
20	T	125/132 (95%)	123 (98%)	2 (2%)	58	79
21	U	111/116 (96%)	110 (99%)	1 (1%)	75	88
22	V	92/107 (86%)	91 (99%)	1 (1%)	70	84
23	W	68/68 (100%)	59 (87%)	9 (13%)	3	14
24	X	112/113 (99%)	110 (98%)	2 (2%)	54	76
25	Y	113/114 (99%)	110 (97%)	3 (3%)	40	67
26	Z	107/115 (93%)	105 (98%)	2 (2%)	52	75
27	a	66/103 (64%)	65 (98%)	1 (2%)	60	80
28	b	85/99 (86%)	83 (98%)	2 (2%)	44	70
29	c	75/76 (99%)	75 (100%)	0	100	100
30	d	55/62 (89%)	55 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	e	48/49 (98%)	48 (100%)	0	100	100
32	f	46/106 (43%)	44 (96%)	2 (4%)	25	55
33	g	61/140 (44%)	59 (97%)	2 (3%)	33	62
34	h	272/275 (99%)	270 (99%)	2 (1%)	81	90
39	AA	189/199 (95%)	172 (91%)	17 (9%)	8	29
40	AB	342/348 (98%)	330 (96%)	12 (4%)	31	61
41	AC	302/323 (94%)	281 (93%)	21 (7%)	12	39
42	AD	247/250 (99%)	244 (99%)	3 (1%)	67	83
43	AE	190/251 (76%)	185 (97%)	5 (3%)	41	68
44	AF	196/218 (90%)	192 (98%)	4 (2%)	50	74
45	AG	194/208 (93%)	187 (96%)	7 (4%)	30	60
46	AH	169/171 (99%)	164 (97%)	5 (3%)	36	64
47	AI	175/181 (97%)	169 (97%)	6 (3%)	32	62
48	AJ	143/149 (96%)	141 (99%)	2 (1%)	62	81
49	AL	167/176 (95%)	161 (96%)	6 (4%)	30	60
50	AM	117/151 (78%)	112 (96%)	5 (4%)	25	55
51	AN	171/172 (99%)	163 (95%)	8 (5%)	22	52
52	AO	171/173 (99%)	164 (96%)	7 (4%)	26	57
53	AP	134/163 (82%)	131 (98%)	3 (2%)	47	71
54	AQ	166/167 (99%)	148 (89%)	18 (11%)	5	21
55	AR	159/175 (91%)	155 (98%)	4 (2%)	42	69
56	AS	155/155 (100%)	141 (91%)	14 (9%)	8	29
57	AT	139/140 (99%)	133 (96%)	6 (4%)	25	55
58	AU	91/116 (78%)	86 (94%)	5 (6%)	18	47
59	AV	100/107 (94%)	95 (95%)	5 (5%)	20	50
60	AW	55/126 (44%)	54 (98%)	1 (2%)	54	76
61	AX	106/134 (79%)	105 (99%)	1 (1%)	75	88
62	AY	124/135 (92%)	120 (97%)	4 (3%)	34	63
63	AZ	117/118 (99%)	116 (99%)	1 (1%)	75	88
64	Aa	119/120 (99%)	116 (98%)	3 (2%)	42	69
65	Ab	84/172 (49%)	81 (96%)	3 (4%)	30	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	Ac	84/98 (86%)	83 (99%)	1 (1%)	67	83
67	Ad	98/110 (89%)	94 (96%)	4 (4%)	26	57
68	Ae	114/121 (94%)	111 (97%)	3 (3%)	41	68
69	Af	88/89 (99%)	79 (90%)	9 (10%)	6	23
70	Ag	98/106 (92%)	97 (99%)	1 (1%)	73	86
71	Ah	109/110 (99%)	107 (98%)	2 (2%)	54	76
72	Ai	86/89 (97%)	84 (98%)	2 (2%)	45	70
73	Aj	73/80 (91%)	70 (96%)	3 (4%)	26	57
74	Ak	64/64 (100%)	61 (95%)	3 (5%)	22	52
75	Al	47/48 (98%)	46 (98%)	1 (2%)	48	72
76	Am	48/48 (100%)	46 (96%)	2 (4%)	25	56
77	An	24/24 (100%)	23 (96%)	1 (4%)	25	56
78	Ao	92/94 (98%)	89 (97%)	3 (3%)	33	62
79	Ap	74/75 (99%)	72 (97%)	2 (3%)	40	67
80	Ar	108/121 (89%)	105 (97%)	3 (3%)	38	66
81	AK	190/196 (97%)	181 (95%)	9 (5%)	22	52
All	All	9893/11009 (90%)	9572 (97%)	321 (3%)	36	63

5 of 321 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	AS	19	THR
69	Af	104	MET
56	AS	104	SER
61	AX	72	ASP
75	Al	27	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 90 such sidechains are listed below:

Mol	Chain	Res	Type
47	AI	123	GLN
56	AS	146	HIS
48	AJ	104	ASN
53	AP	75	GLN
60	AW	30	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1685/1869 (90%)	430 (25%)	35 (2%)
35	1	204/253 (80%)	109 (53%)	11 (5%)
36	5	3569/3594 (99%)	930 (26%)	88 (2%)
37	7	118/119 (99%)	11 (9%)	1 (0%)
38	8	149/156 (95%)	34 (22%)	3 (2%)
All	All	5725/5991 (95%)	1514 (26%)	138 (2%)

5 of 1514 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	C
1	2	4	C
1	2	17	C
1	2	25	A

5 of 138 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
36	5	4155	C
36	5	4232	U
36	5	4884	G
36	5	48	G
36	5	47	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no 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
36	5	25

The worst 5 of 25 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	41.19
1	5	1252:C	O3'	1271:G	P	35.34
1	5	1219:G	O3'	1233:G	P	21.81
1	5	1405:C	O3'	1409:G	P	18.37
1	5	4138:C	O3'	4146:G	P	18.26

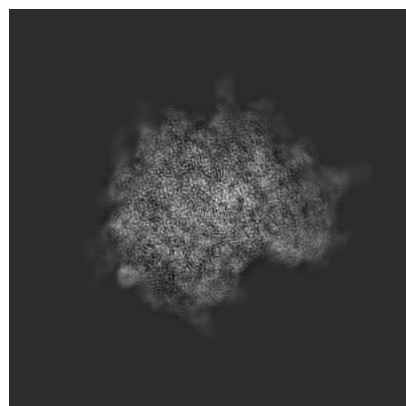
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20255. These allow visual inspection of the internal detail of the map and identification of artifacts.

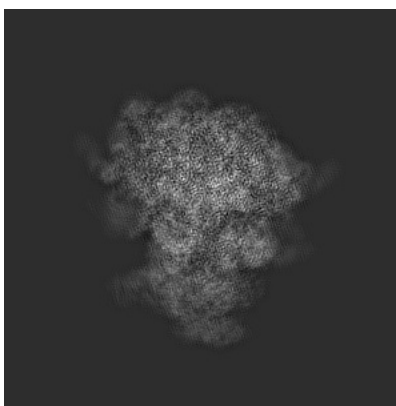
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

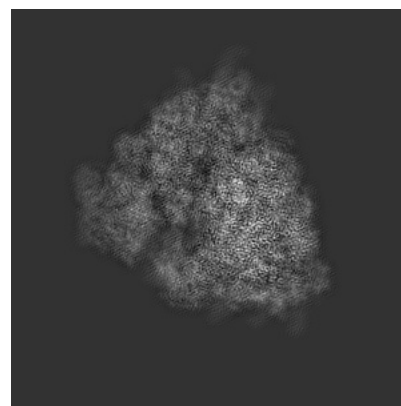
6.1.1 Primary map



X

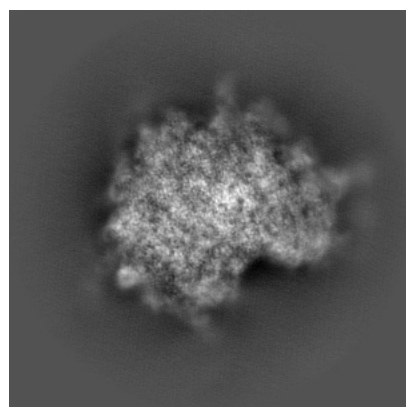


Y

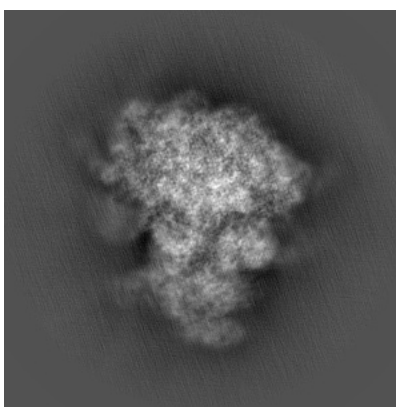


Z

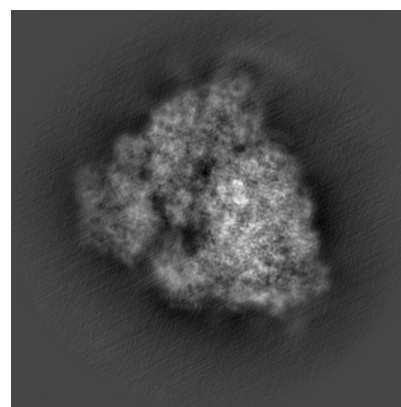
6.1.2 Raw map



X



Y

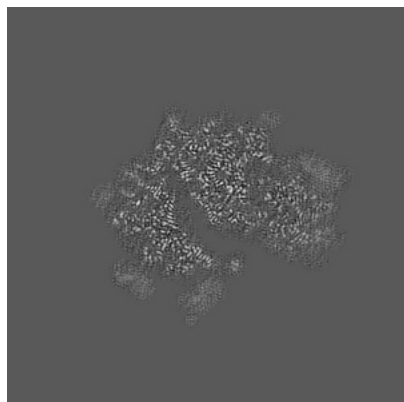


Z

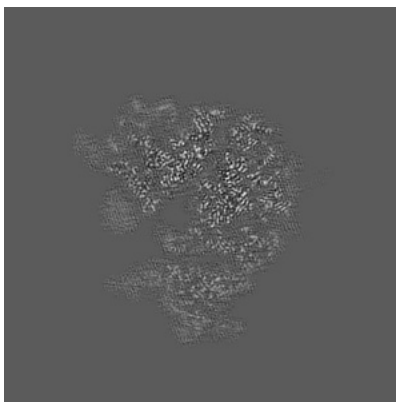
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

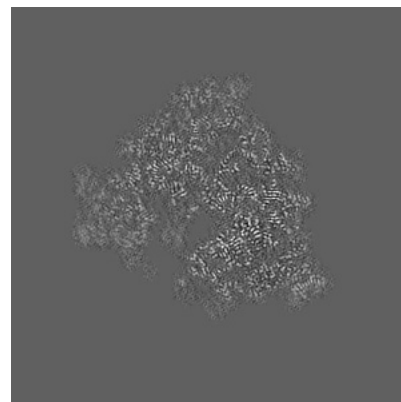
6.2.1 Primary map



X Index: 180

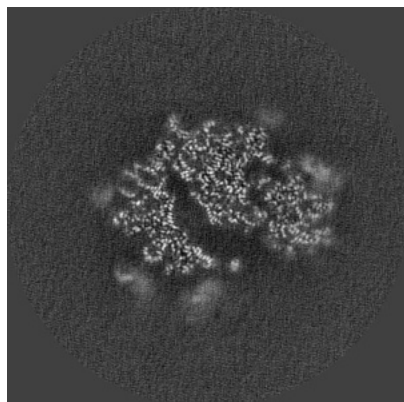


Y Index: 180

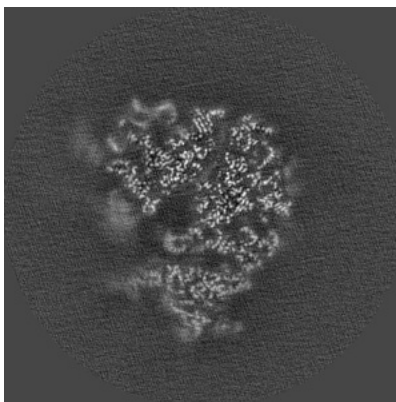


Z Index: 180

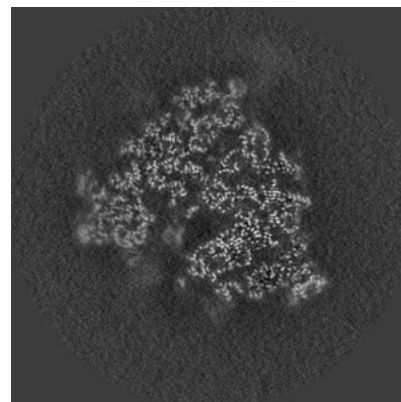
6.2.2 Raw map



X Index: 180



Y Index: 180

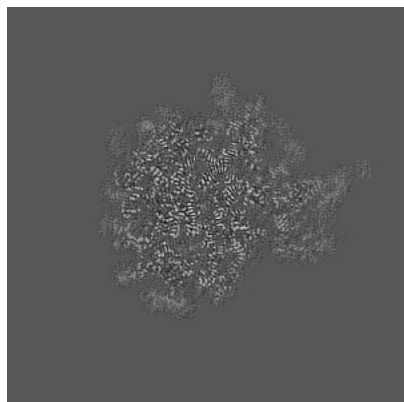


Z Index: 180

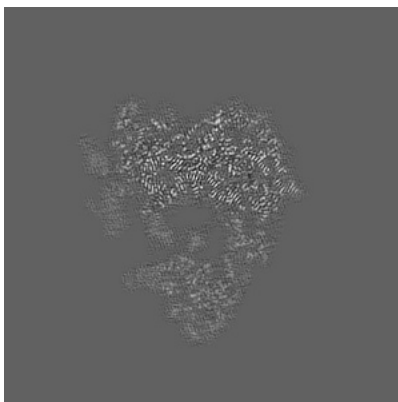
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

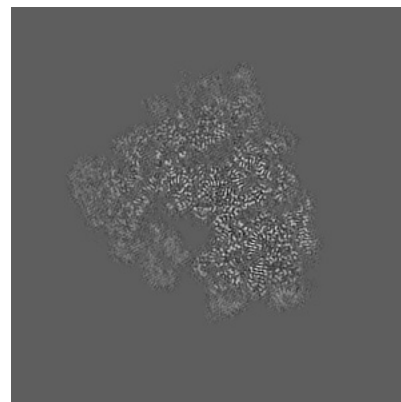
6.3.1 Primary map



X Index: 206

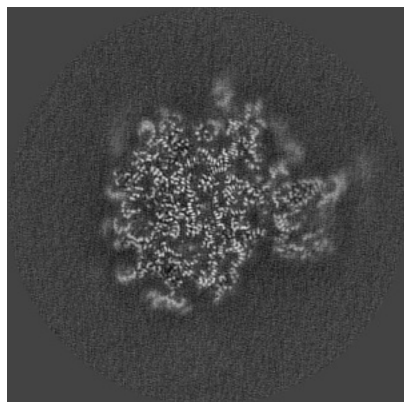


Y Index: 167

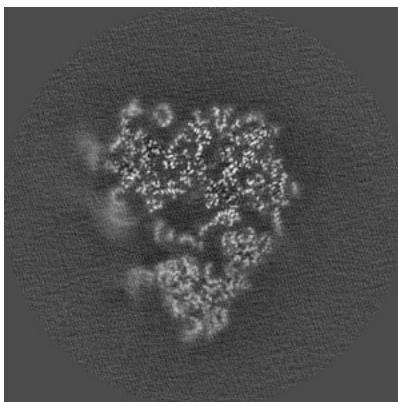


Z Index: 194

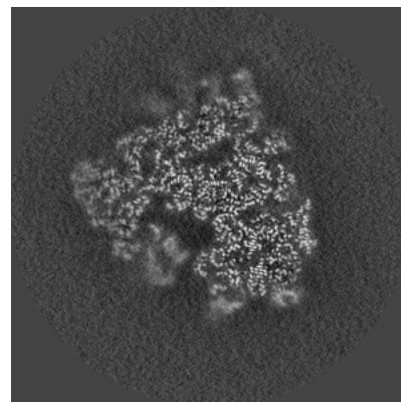
6.3.2 Raw map



X Index: 206



Y Index: 174

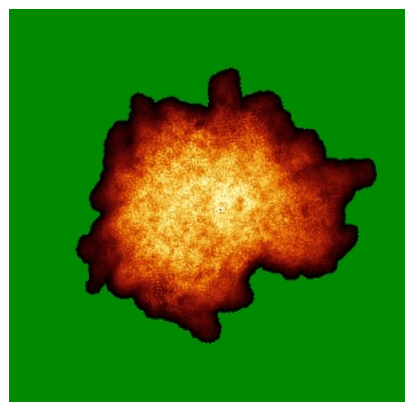


Z Index: 194

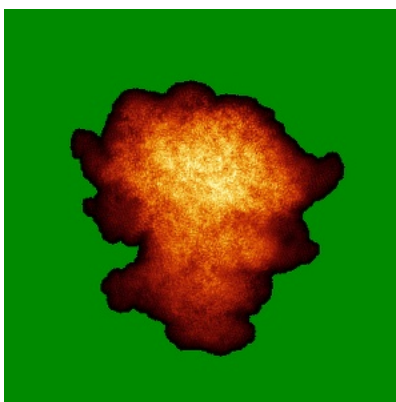
The images above show the largest variance slices of the map in three orthogonal directions.

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

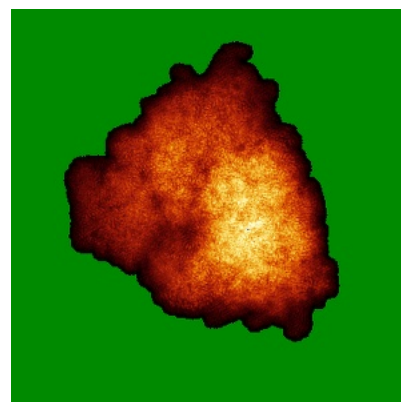
6.4.1 Primary map



X

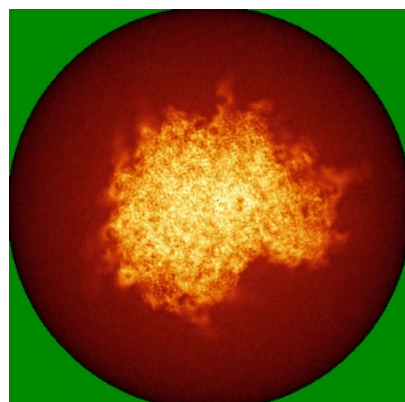


Y

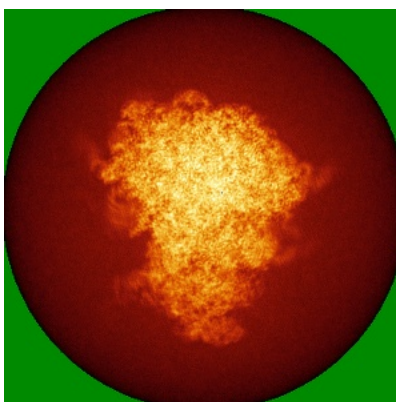


Z

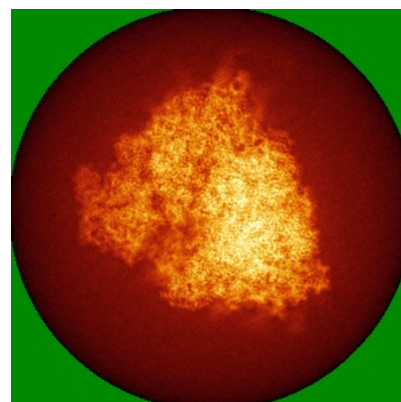
6.4.2 Raw map



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 0.032. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

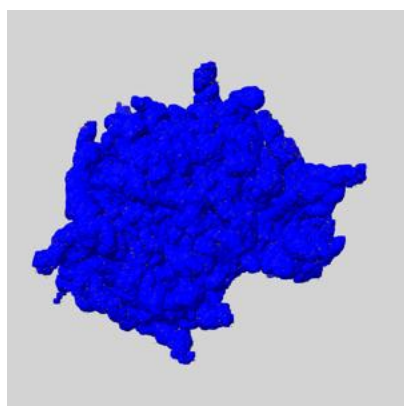
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

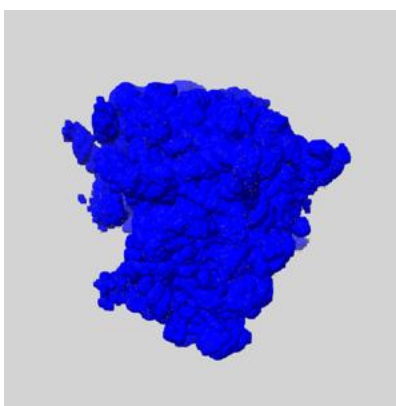
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

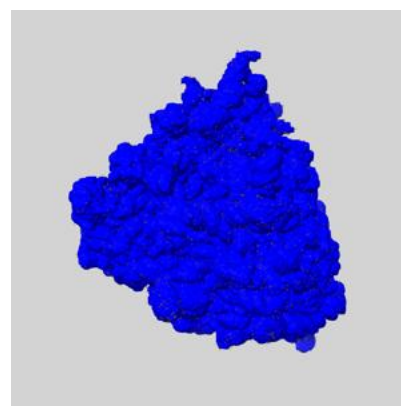
6.6.1 emd_20255_msk_1.map [i](#)



X



Y

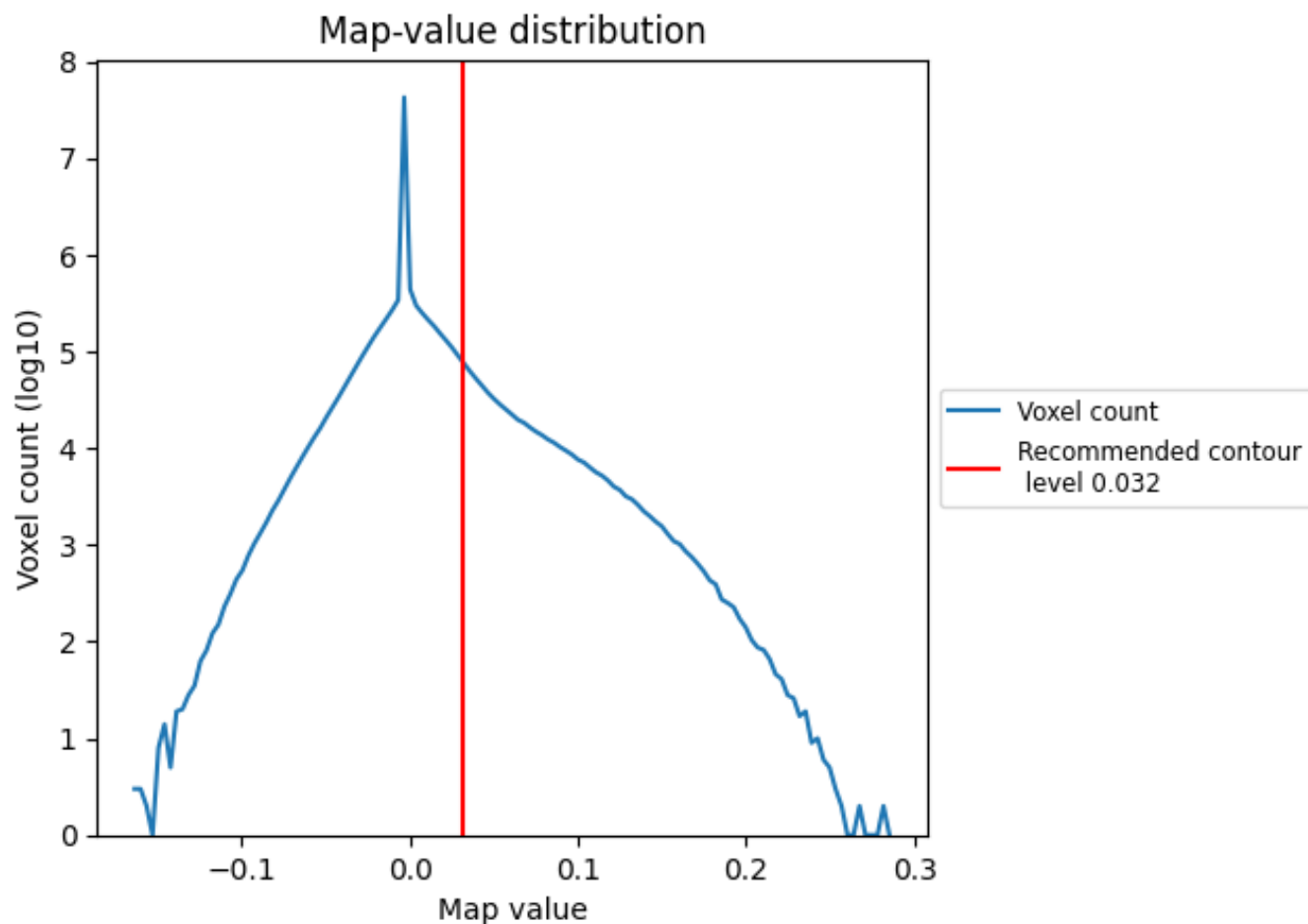


Z

7 Map analysis [i](#)

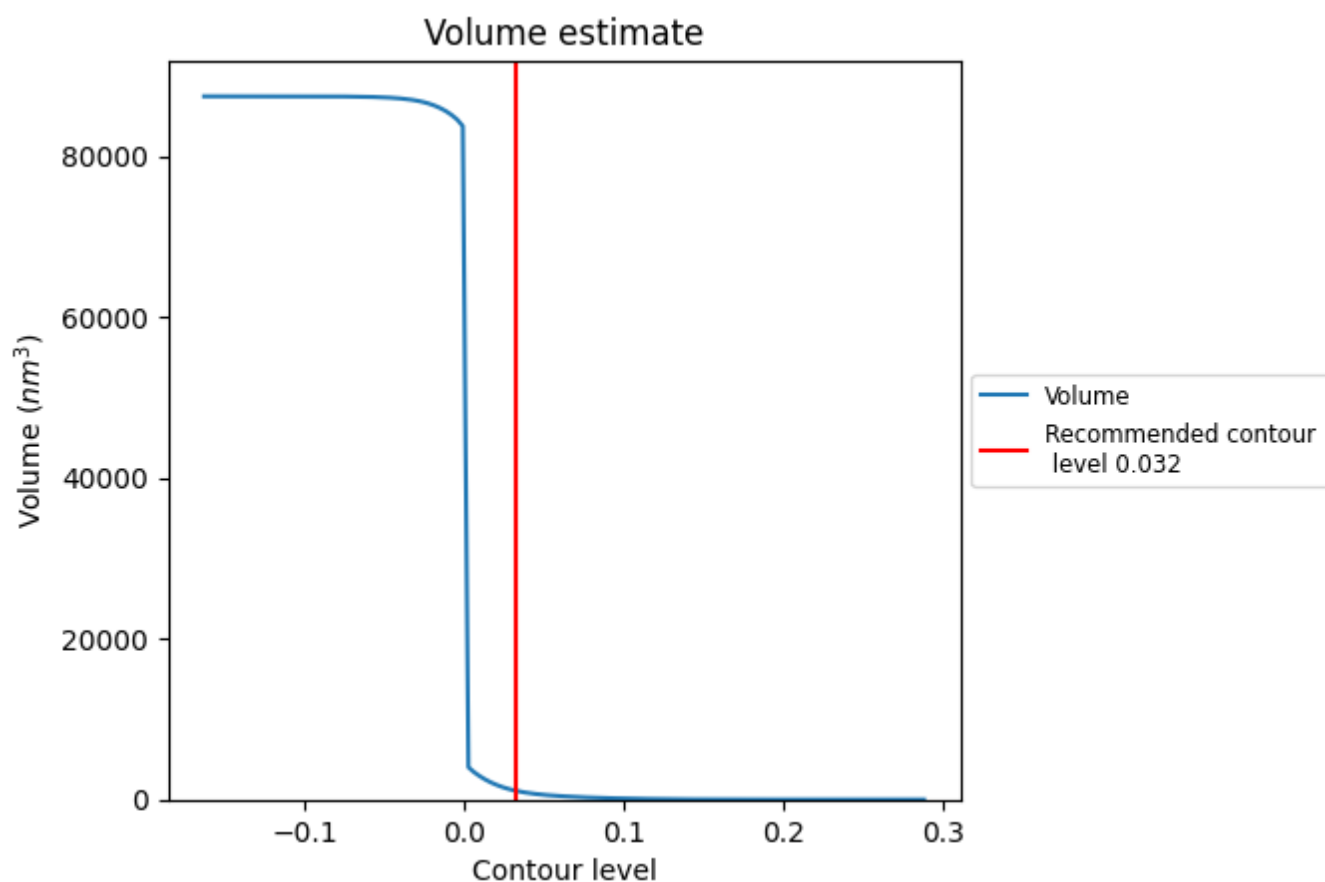
This section contains the results of statistical analysis of the map.

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.

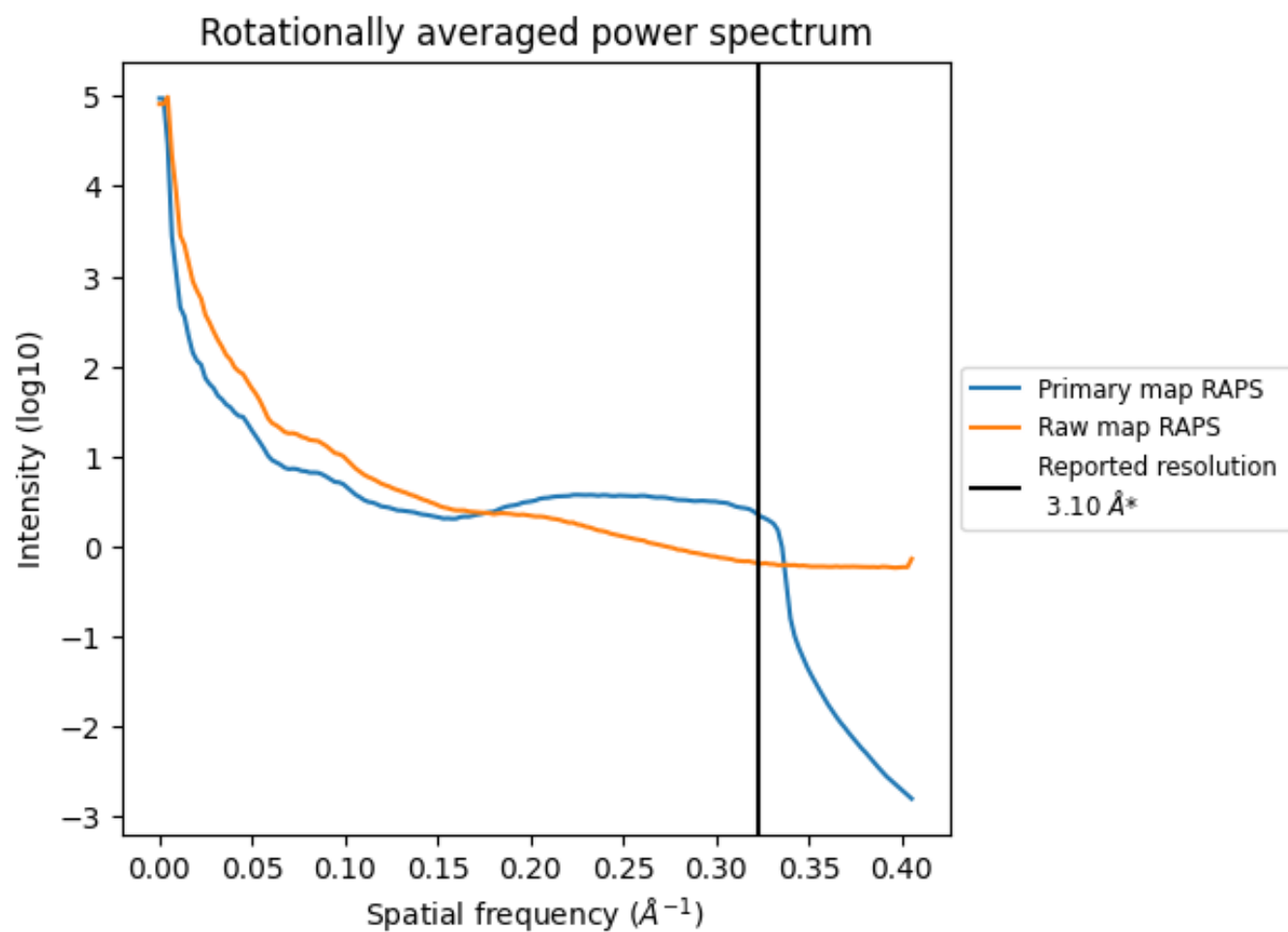
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1113 nm³; this corresponds to an approximate mass of 1005 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 ⓘ

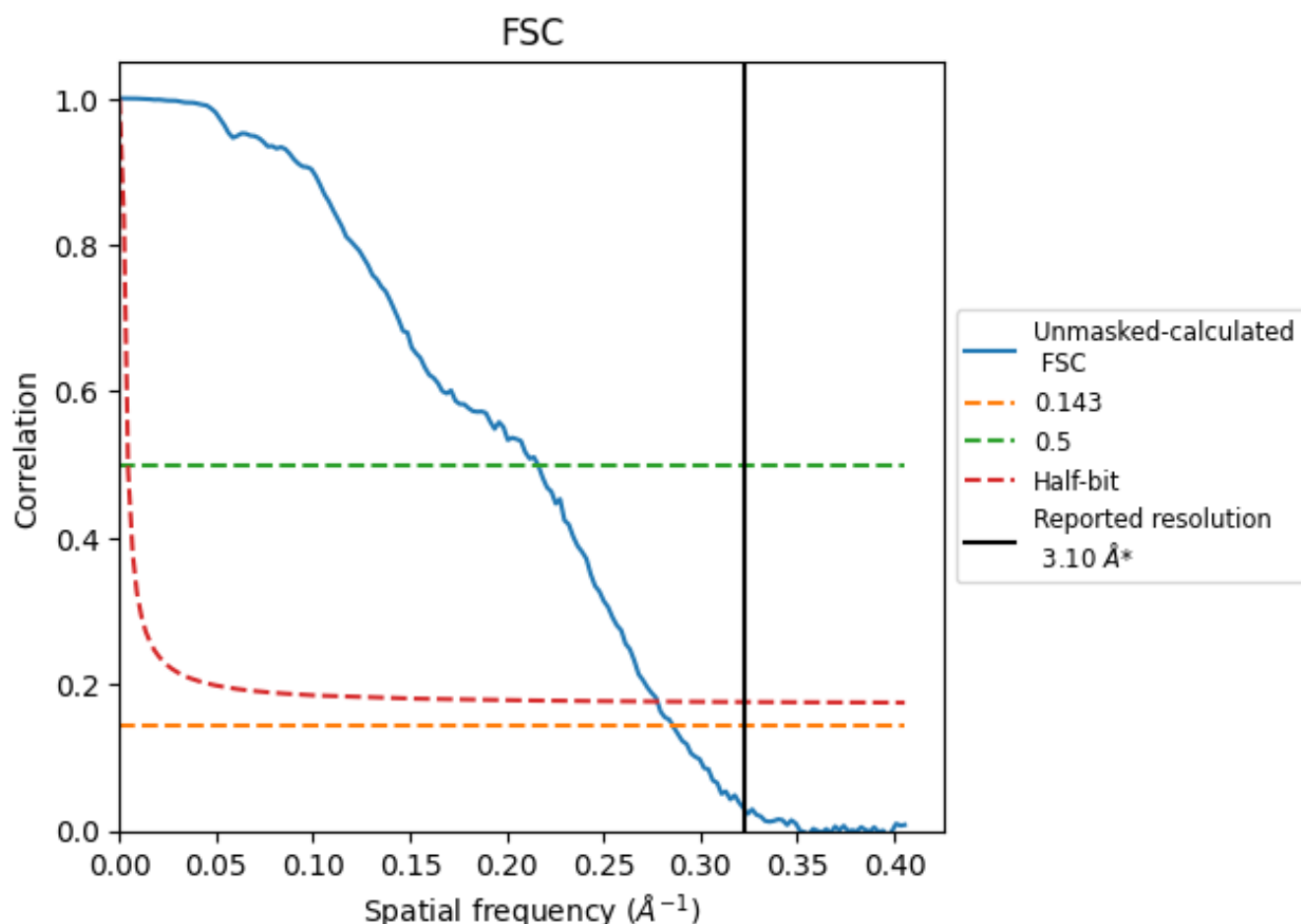


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

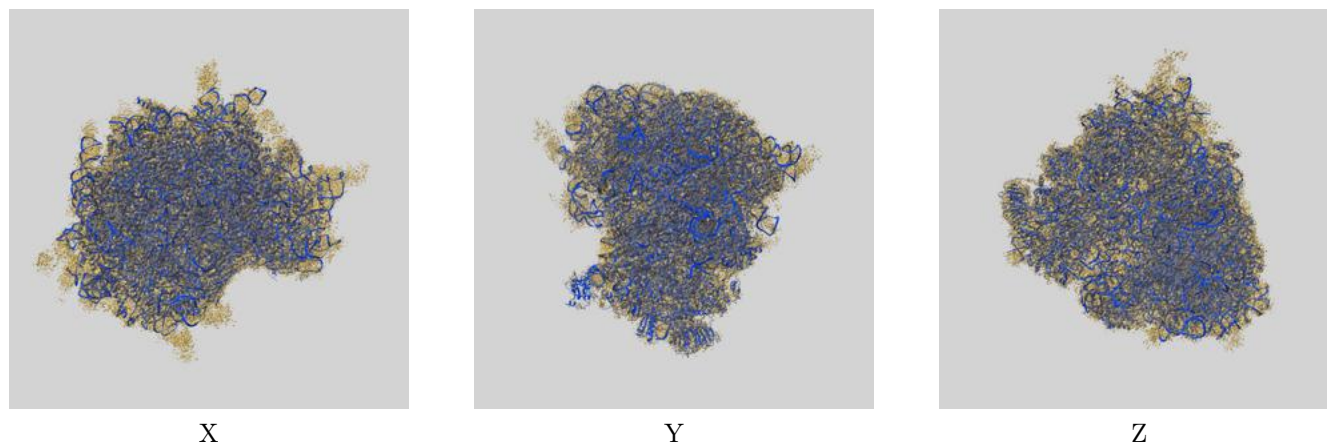
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.50	4.63	3.60

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.50 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

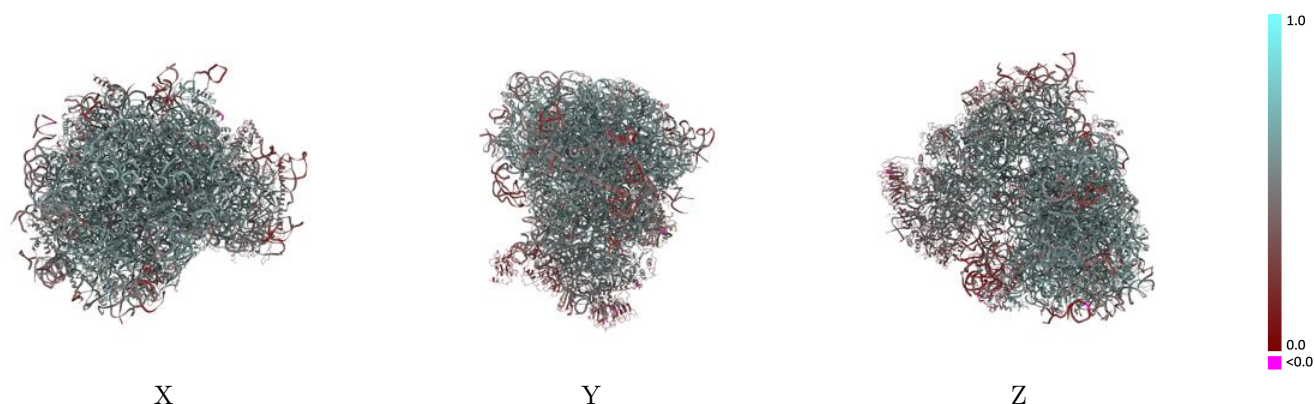
This section contains information regarding the fit between EMDB map EMD-20255 and PDB model 6P5I. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

9.1 Map-model overlay [i](#)



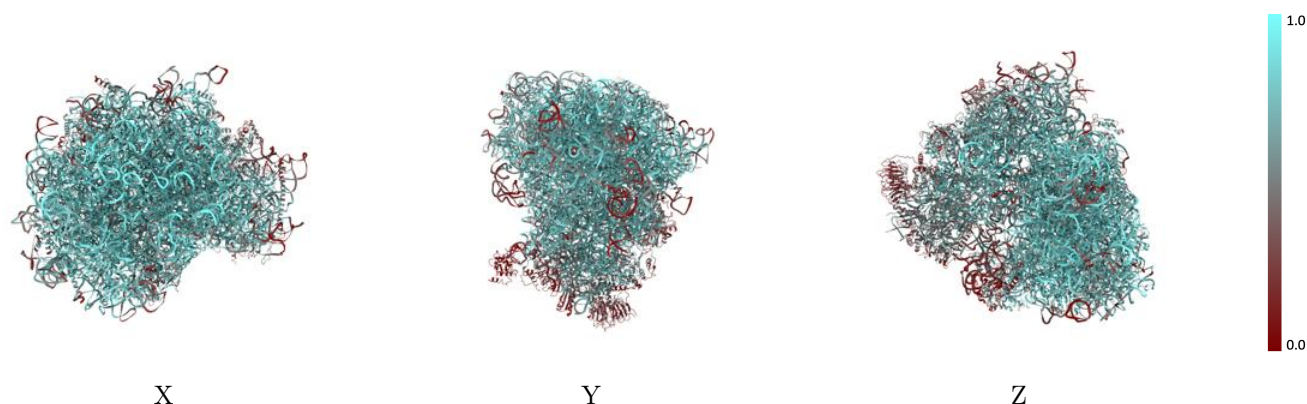
The images above show the 3D surface view of the map at the recommended contour level 0.032 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



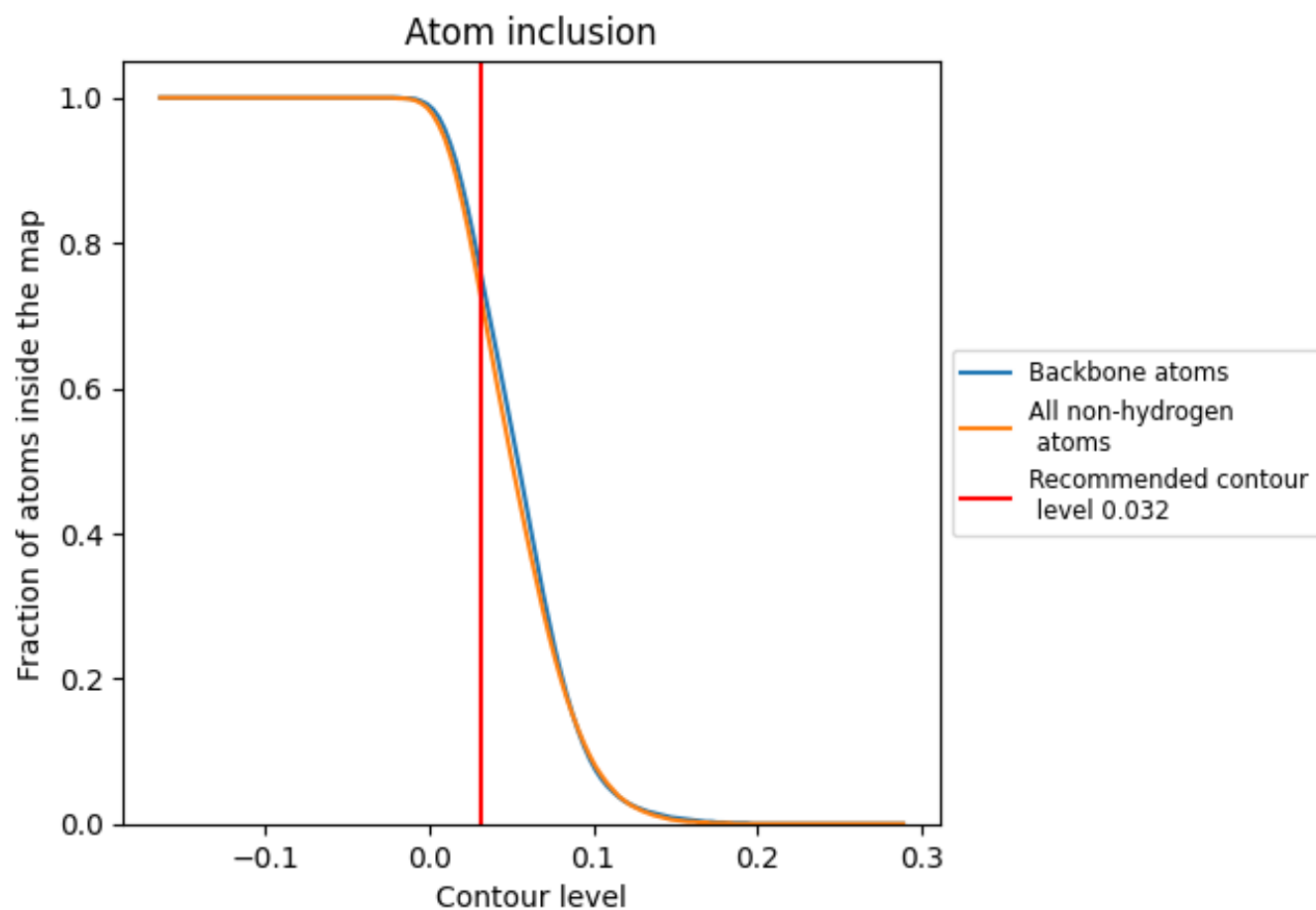
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.032).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 72% 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 (0.032) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7220	 0.5080
1	 0.3580	 0.3040
2	 0.7460	 0.5020
5	 0.8210	 0.5380
7	 0.9150	 0.5770
8	 0.8650	 0.5630
AA	 0.8030	 0.5750
AB	 0.7960	 0.5620
AC	 0.7950	 0.5520
AD	 0.7160	 0.5160
AE	 0.7300	 0.5190
AF	 0.8000	 0.5690
AG	 0.6800	 0.4990
AH	 0.7260	 0.5270
AI	 0.7620	 0.5500
AJ	 0.5530	 0.4670
AK	 0.0780	 0.2230
AL	 0.7430	 0.5270
AM	 0.7690	 0.5430
AN	 0.8420	 0.5810
AO	 0.7920	 0.5620
AP	 0.7980	 0.5670
AQ	 0.7810	 0.5540
AR	 0.6940	 0.5200
AS	 0.8080	 0.5650
AT	 0.7310	 0.5390
AU	 0.6020	 0.4610
AV	 0.7930	 0.5700
AW	 0.7210	 0.5530
AX	 0.7340	 0.5400
AY	 0.7720	 0.5540
AZ	 0.7320	 0.5180
Aa	 0.8410	 0.5800
Ab	 0.6380	 0.4940
Ac	 0.6950	 0.5280













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Chain	Atom inclusion	Q-score
Ad	 0.7110	 0.5310
Ae	 0.8060	 0.5760
Af	 0.8370	 0.5840
Ag	 0.7380	 0.5530
Ah	 0.7200	 0.5380
Ai	 0.6810	 0.5110
Aj	 0.8190	 0.5670
Ak	 0.6370	 0.4890
Al	 0.7660	 0.5590
Am	 0.7520	 0.5450
An	 0.7250	 0.5210
Ao	 0.7030	 0.5340
Ap	 0.7310	 0.5540
Ar	 0.7990	 0.5600
B	 0.5940	 0.4660
C	 0.6350	 0.4920
D	 0.6560	 0.5100
E	 0.3980	 0.3930
F	 0.6210	 0.4750
G	 0.5060	 0.4330
H	 0.4630	 0.4150
I	 0.4460	 0.4070
J	 0.6430	 0.4890
K	 0.6260	 0.4890
L	 0.2670	 0.3410
M	 0.7230	 0.5370
N	 0.0550	 0.2240
O	 0.6680	 0.5070
P	 0.6510	 0.5130
Q	 0.2790	 0.2930
R	 0.4690	 0.4380
S	 0.4050	 0.4050
T	 0.3350	 0.3520
U	 0.3890	 0.3820
V	 0.3090	 0.3640
W	 0.5710	 0.4680
X	 0.7100	 0.5270
Y	 0.7180	 0.5290
Z	 0.5540	 0.4510
a	 0.3210	 0.3490
b	 0.7130	 0.5300
c	 0.5620	 0.4750

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Chain	Atom inclusion	Q-score
d	 0.4530	 0.4200
e	 0.5310	 0.4440
f	 0.5090	 0.4330
g	 0.0430	 0.2010
h	 0.2450	 0.3190