



wwPDB EM Validation Summary Report ⓘ

Nov 9, 2022 – 04:44 PM EST

PDB ID : 6P5J
EMDB ID : EMD-20256
Title : Structure of a mammalian 80S ribosome in complex with the Israeli Acute Paralysis Virus IRES (Class 2)
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:

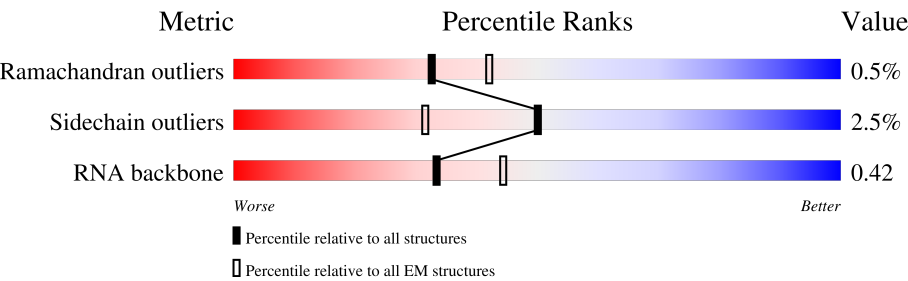
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.10 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	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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>22%</div><div>61%</div><div>30%</div><div>9%</div></div>
2	B	295	<div><div>37%</div><div>73%</div><div>26%</div></div>
3	C	264	<div><div>50%</div><div>78%</div><div>19%</div></div>
4	D	255	<div><div>32%</div><div>85%</div><div>13%</div></div>
5	E	281	<div><div>64%</div><div>78%</div><div>19%</div></div>
6	F	263	<div><div>81%</div><div>97%</div><div>2%</div></div>
7	G	204	<div><div>53%</div><div>89%</div><div>9%</div></div>
8	H	249	<div><div>71%</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	402	
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	70	
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 215969 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
			778	485	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	137	Total	C	N	O	S	0	0
			1130	722	220	181	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		

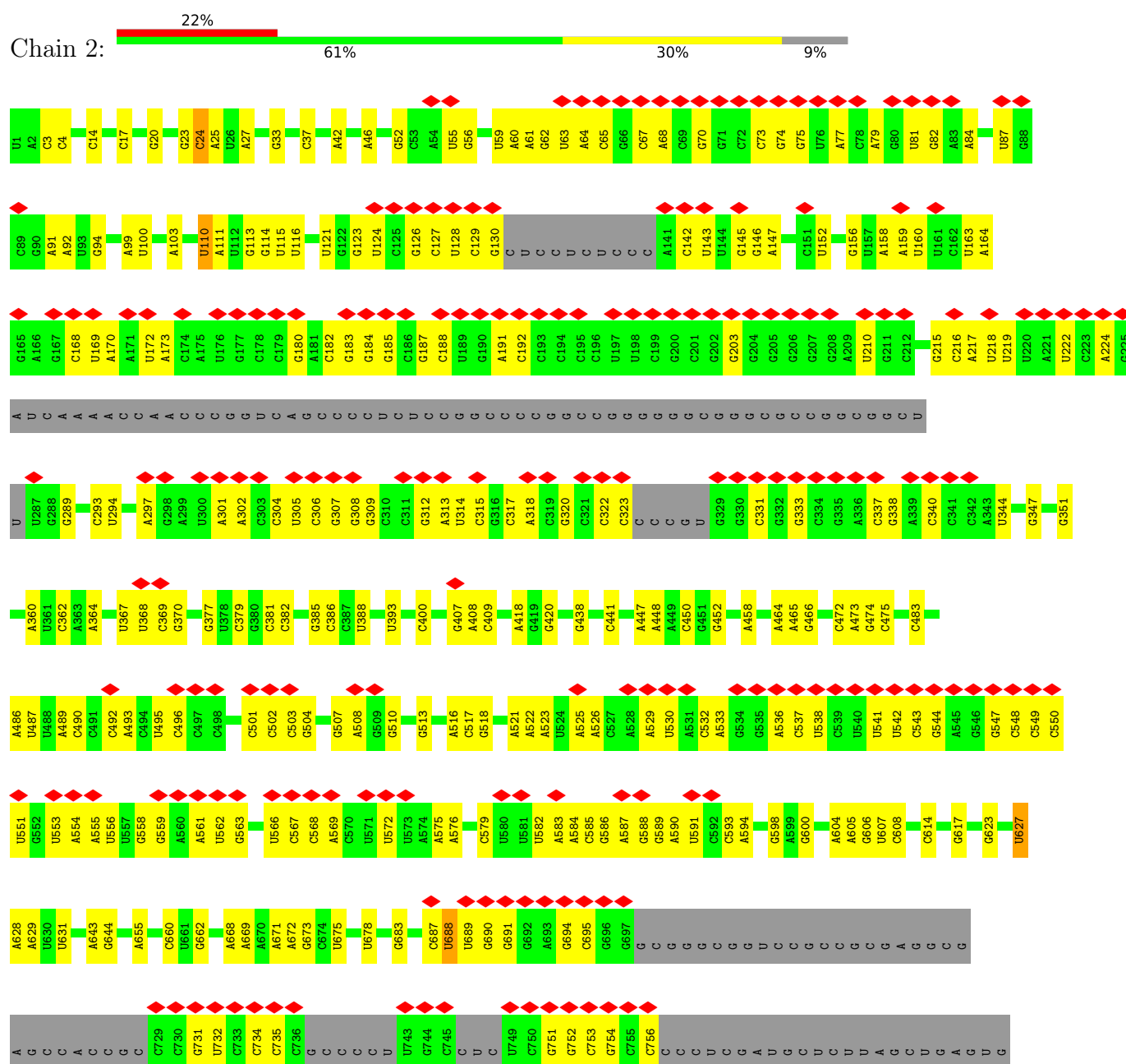
- Molecule 81 is a protein called uL1.

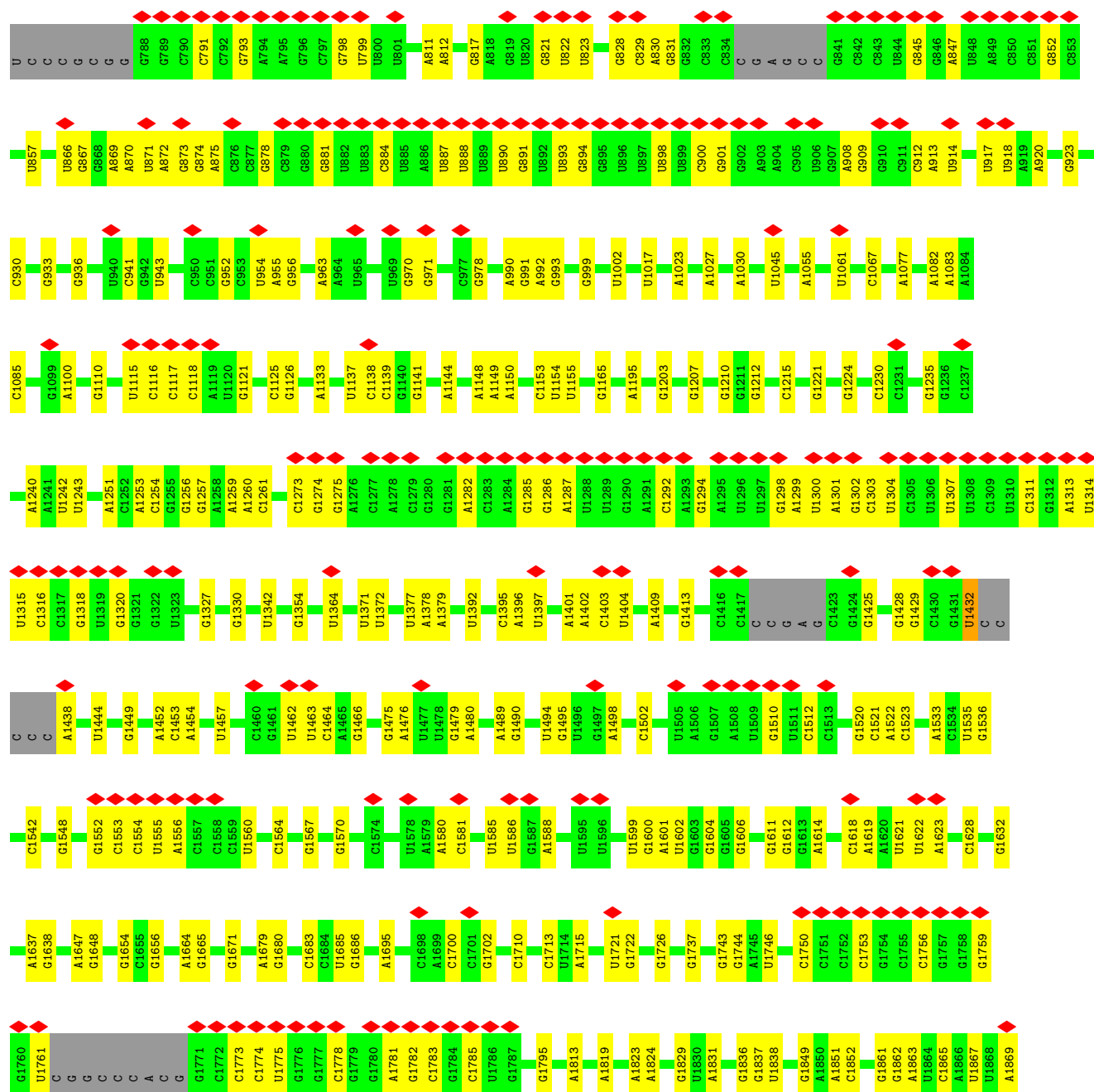
Mol	Chain	Residues	Atoms					AltConf	Trace
81	AK	212	Total	C	N	O	S	0	0
			1705	1091	306	300	8		

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.

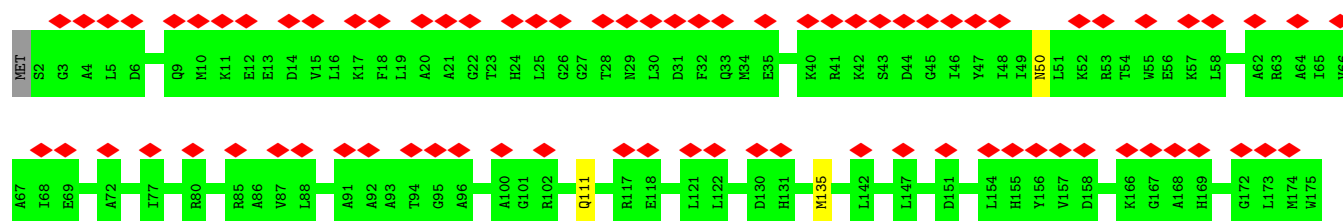
• Molecule 1: 18S rRNA

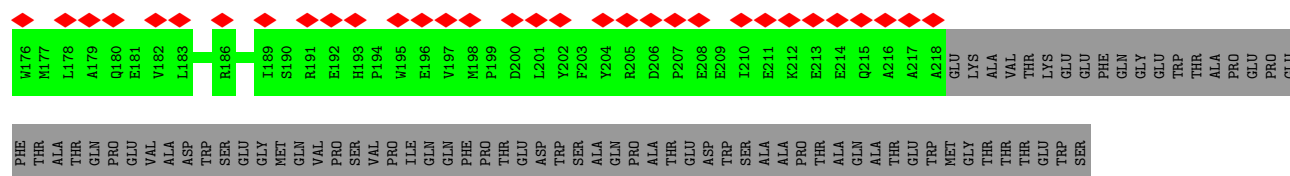




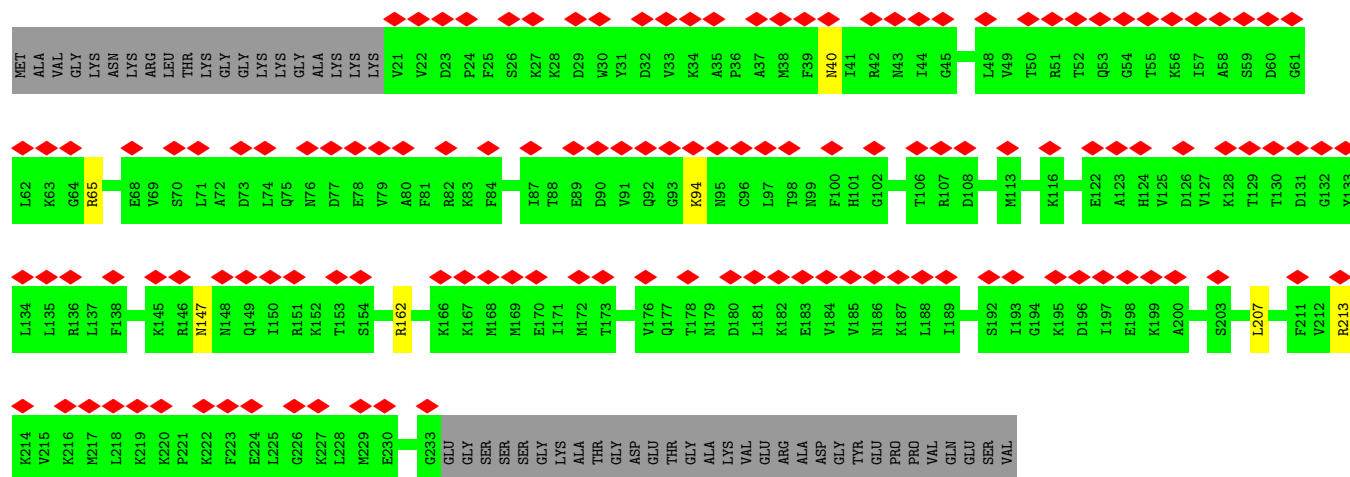
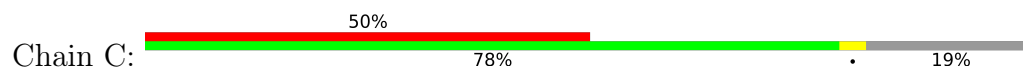
• Molecule 2: uS2

Chain B:

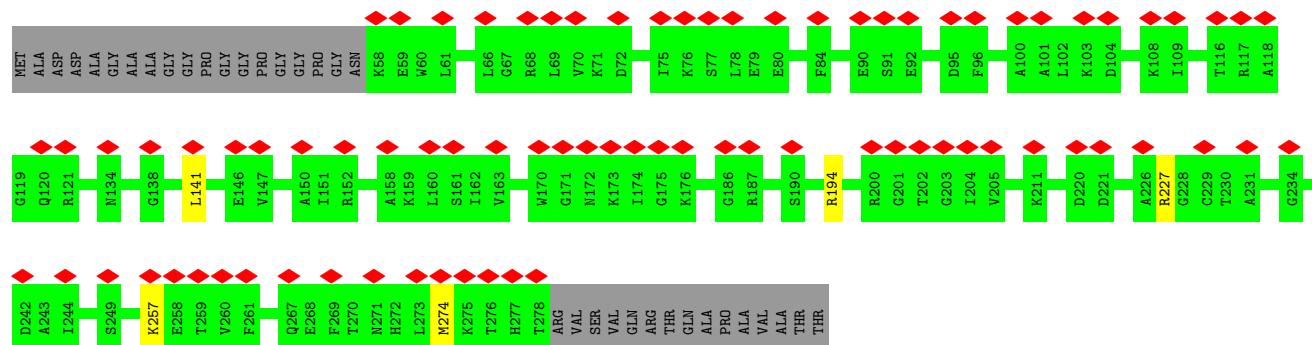
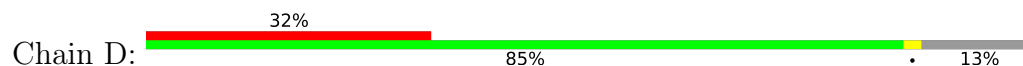




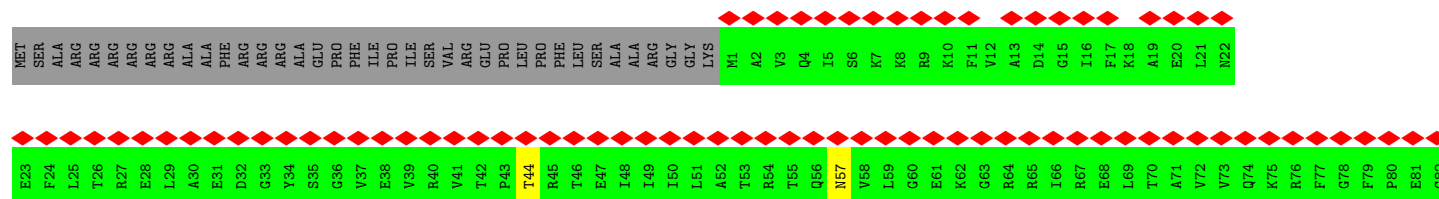
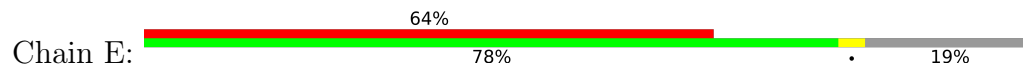
• Molecule 3: eS1

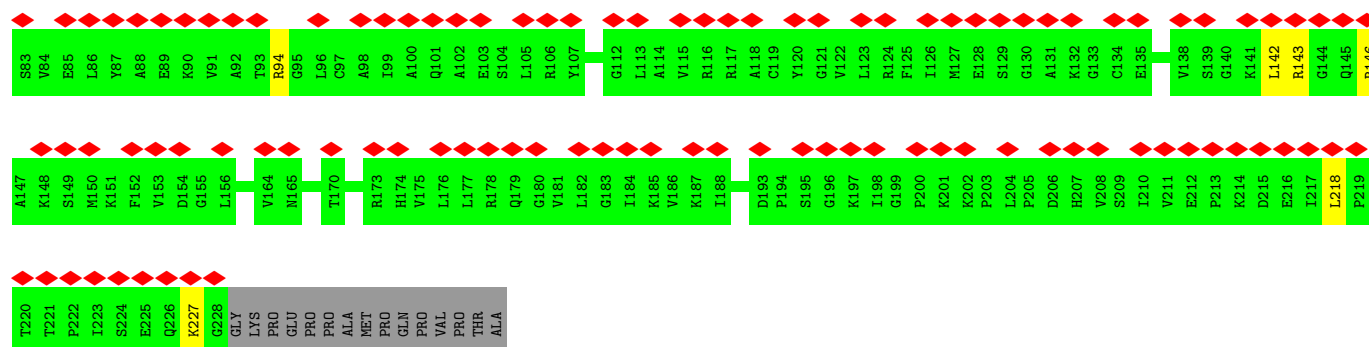


• Molecule 4: uS5

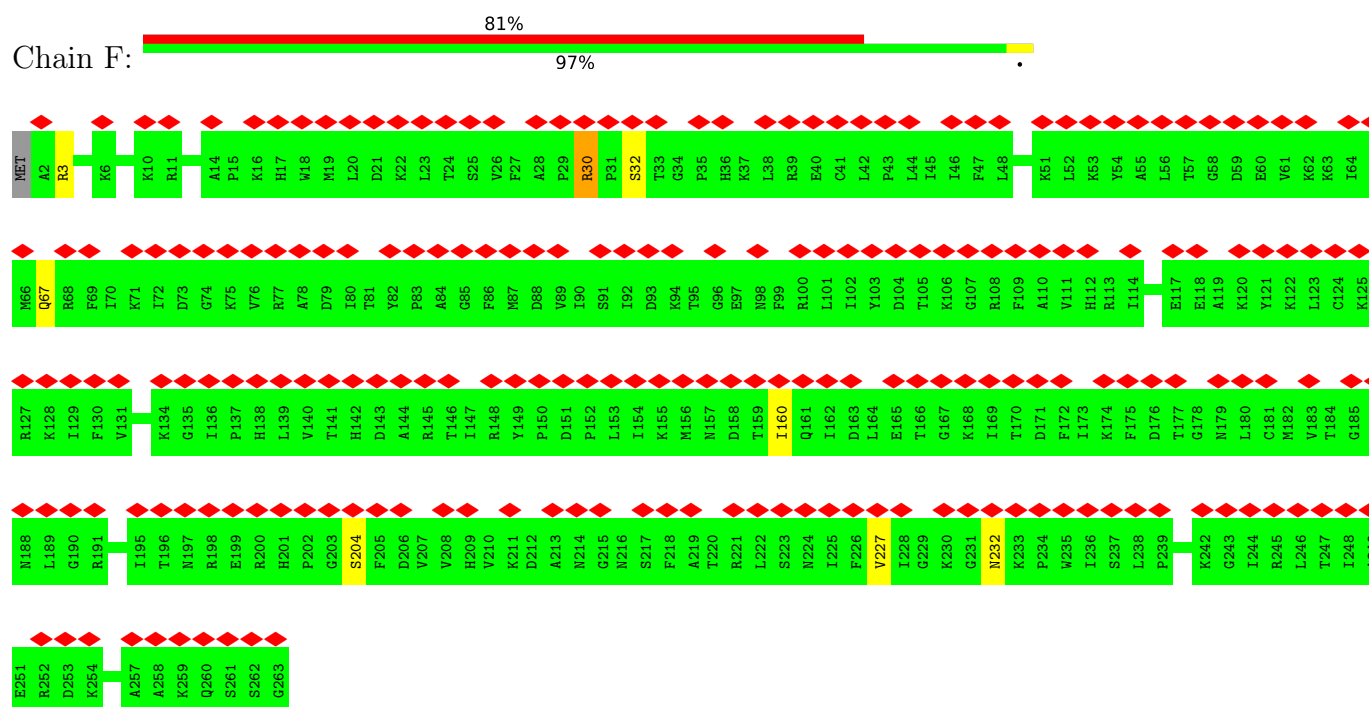


• Molecule 5: uS3

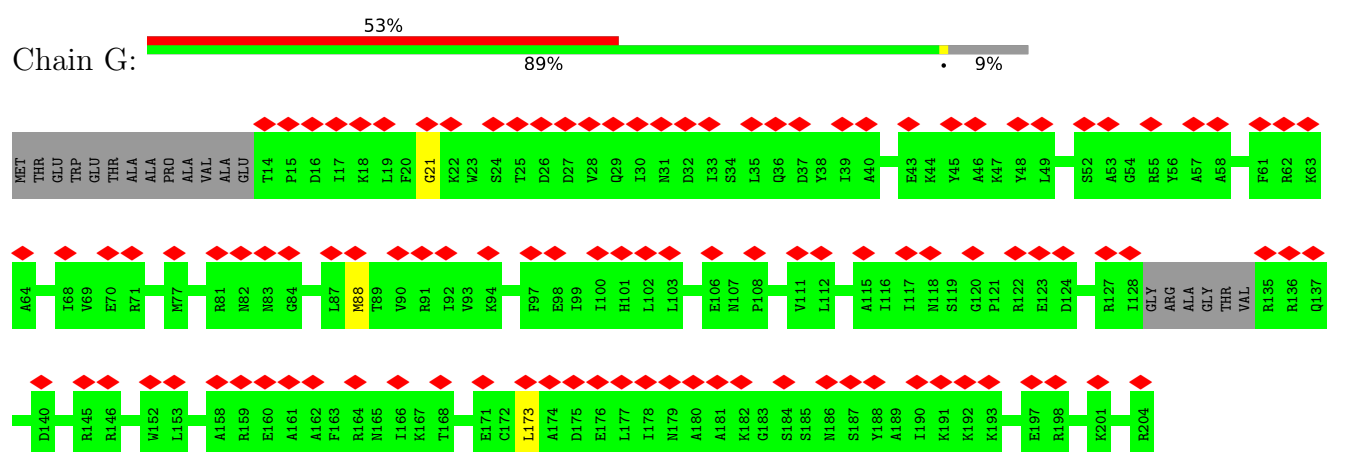




• Molecule 6: eS4

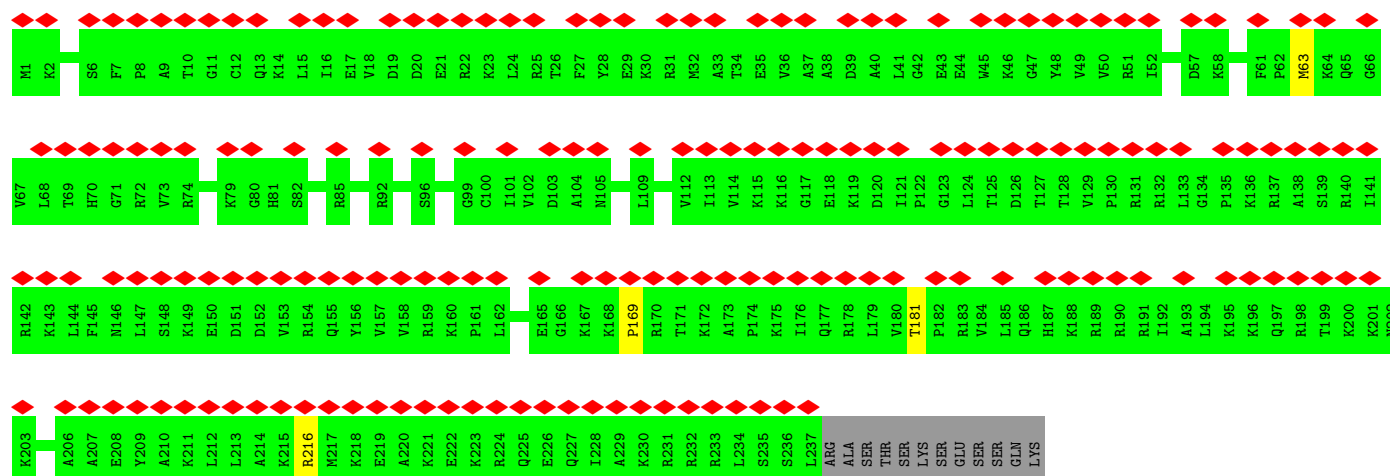


• Molecule 7: uS7

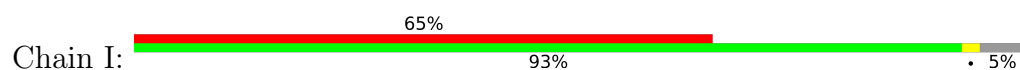


• Molecule 8: eS6

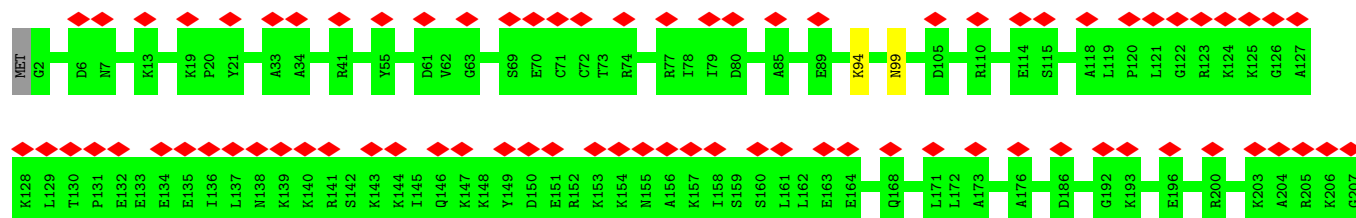




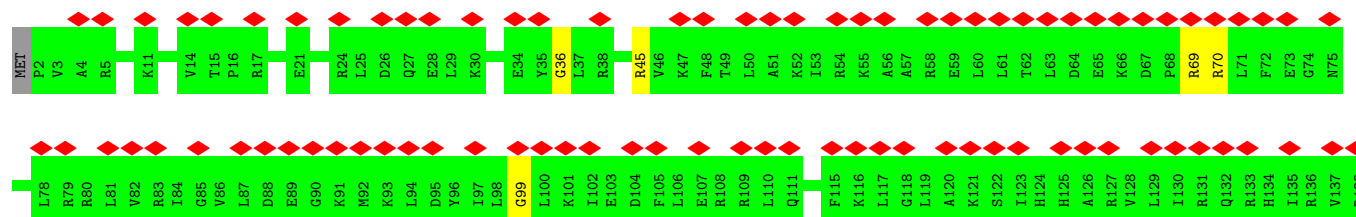
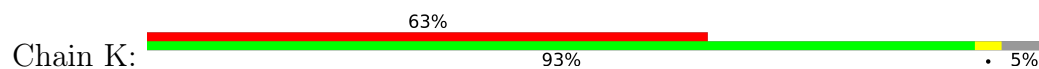
• Molecule 9: eS7

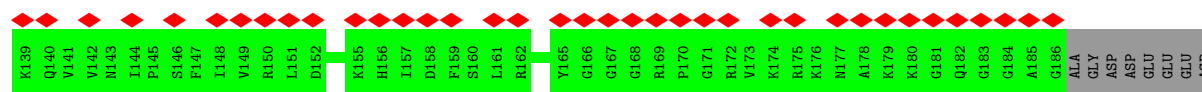


• Molecule 10: eS8

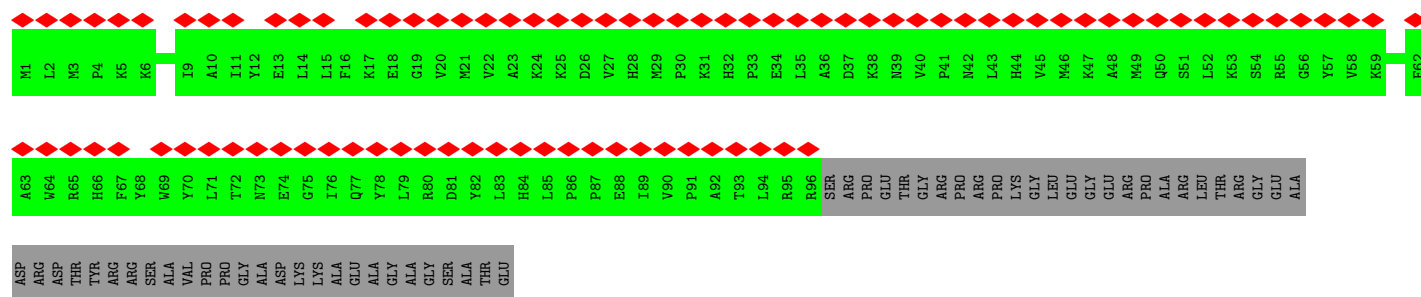


• Molecule 11: uS4

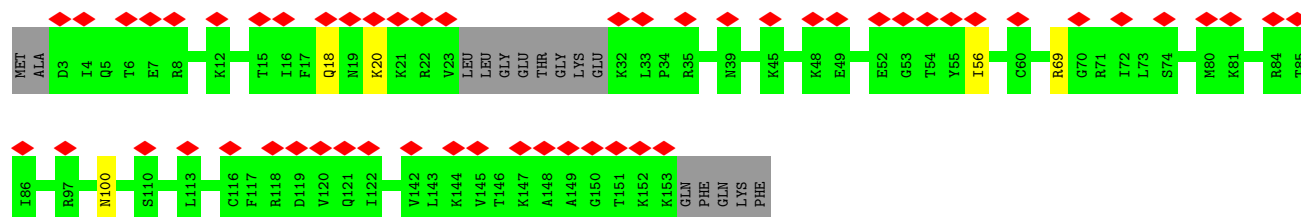




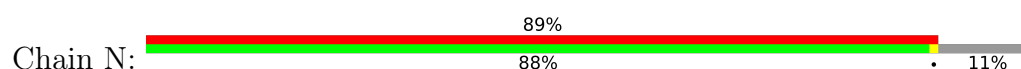
• Molecule 12: eS10



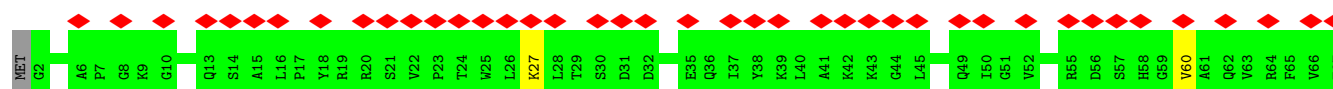
• Molecule 13: uS17



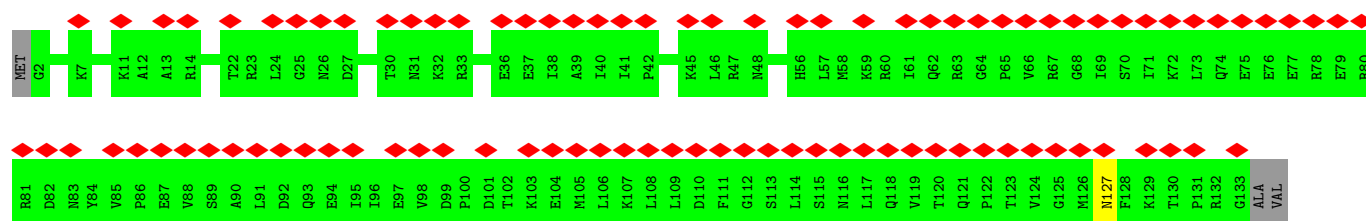
• Molecule 14: eS12



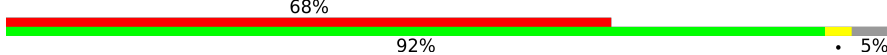
• Molecule 15: uS15



Chain S: 

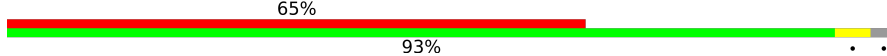


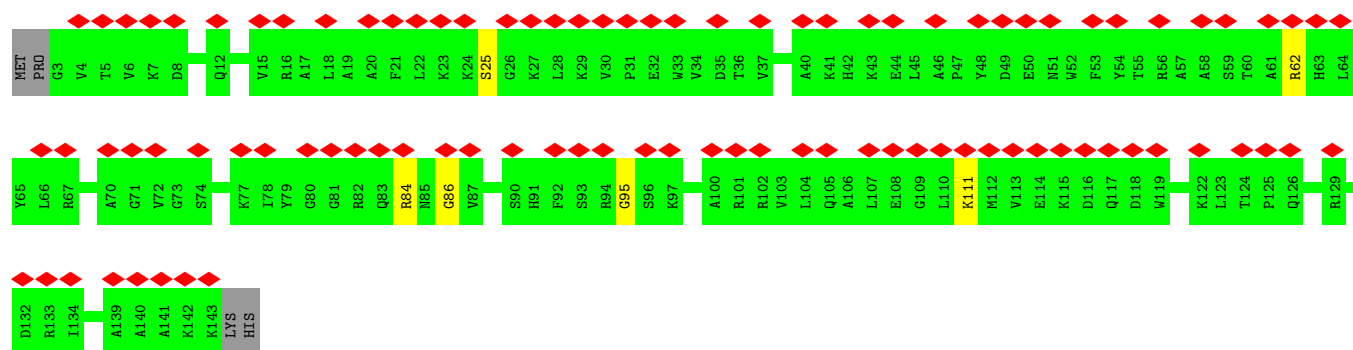
• Molecule 20: uS13

Chain T: 




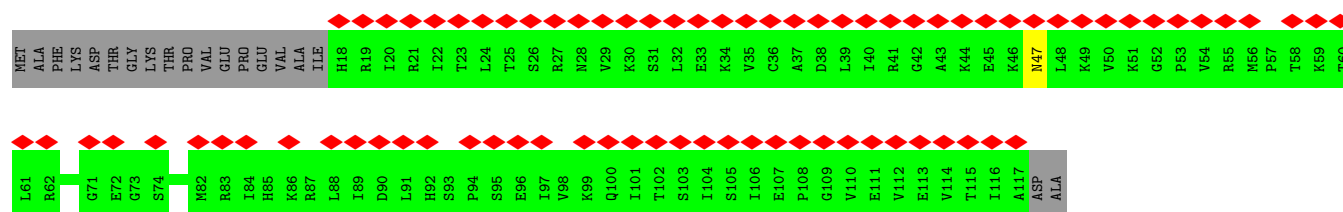
• Molecule 21: eS19

Chain U: 

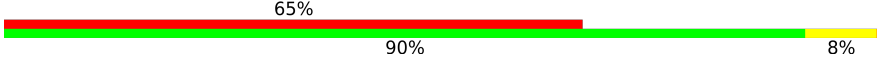


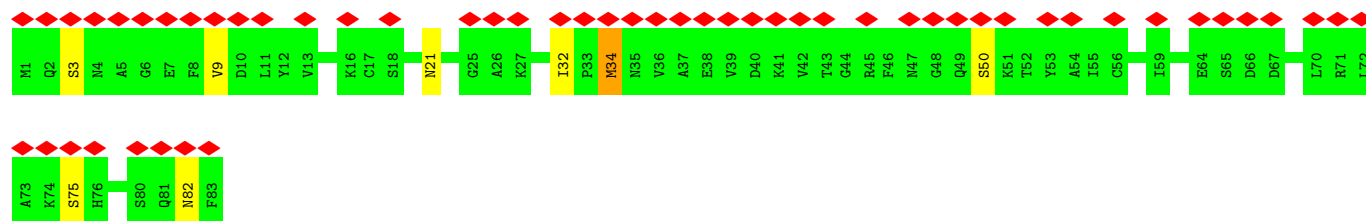
• Molecule 22: uS10

Chain V: 



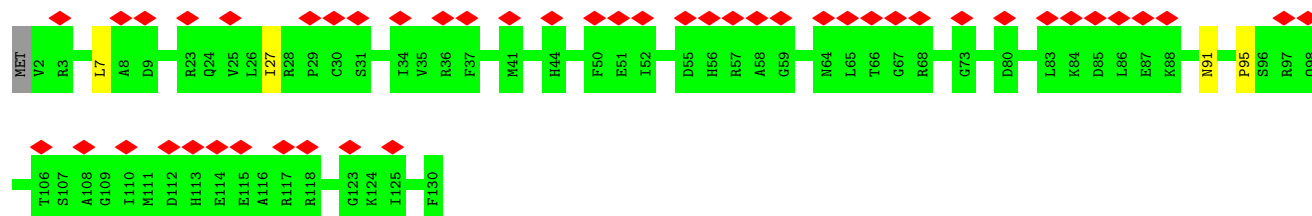
• Molecule 23: eS21

Chain W: 



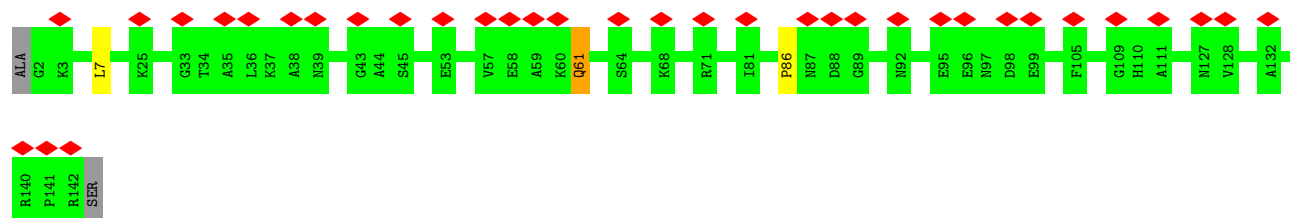
• Molecule 24: uS8

Chain X: 

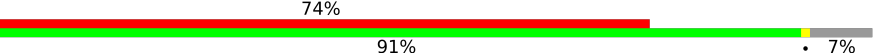


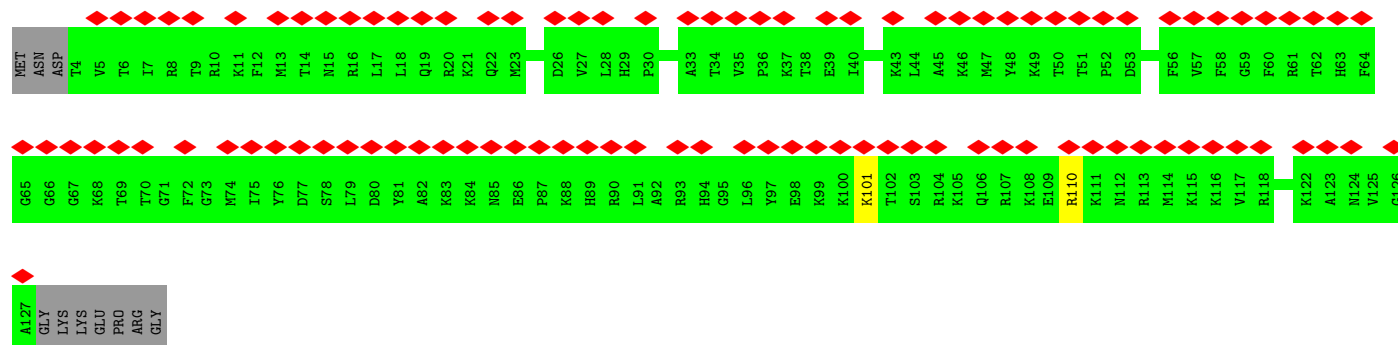
• Molecule 25: uS12

Chain Y: 



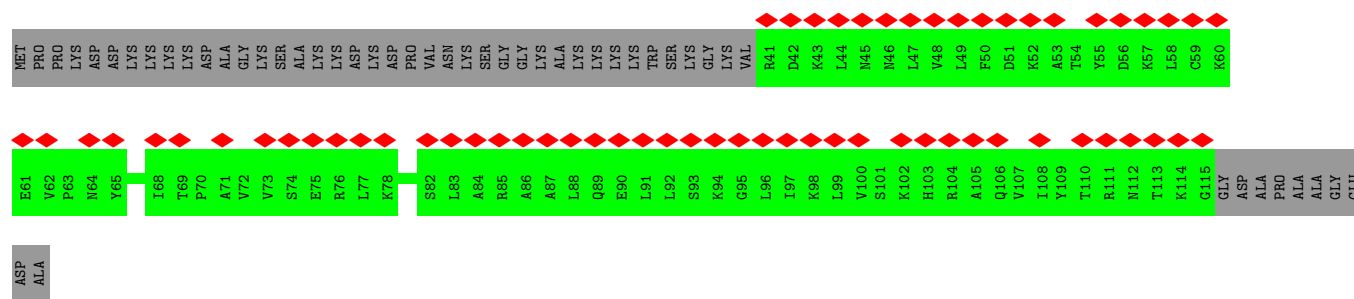
• Molecule 26: eS24

Chain Z: 

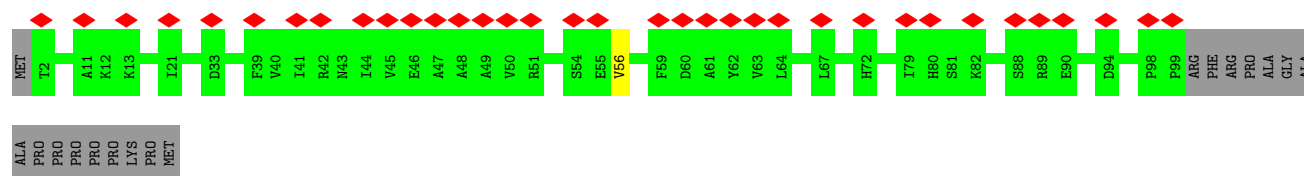
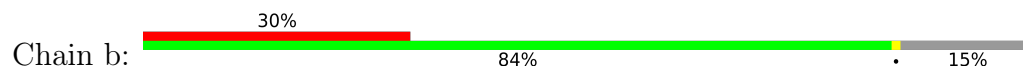


• Molecule 27: eS25

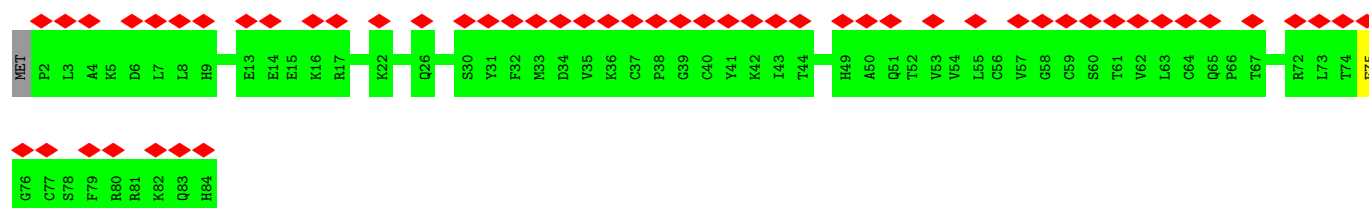
Chain a: 



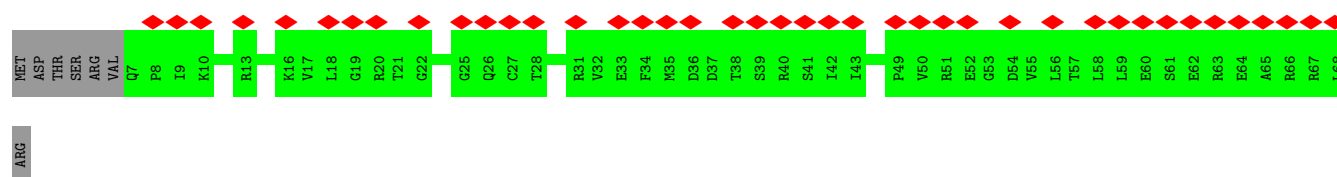
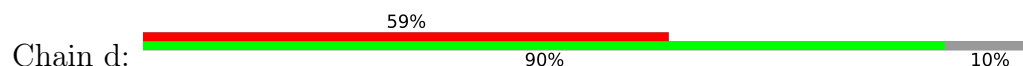
• Molecule 28: eS26



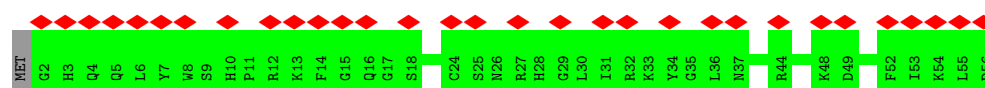
• Molecule 29: eS27



• Molecule 30: eS28

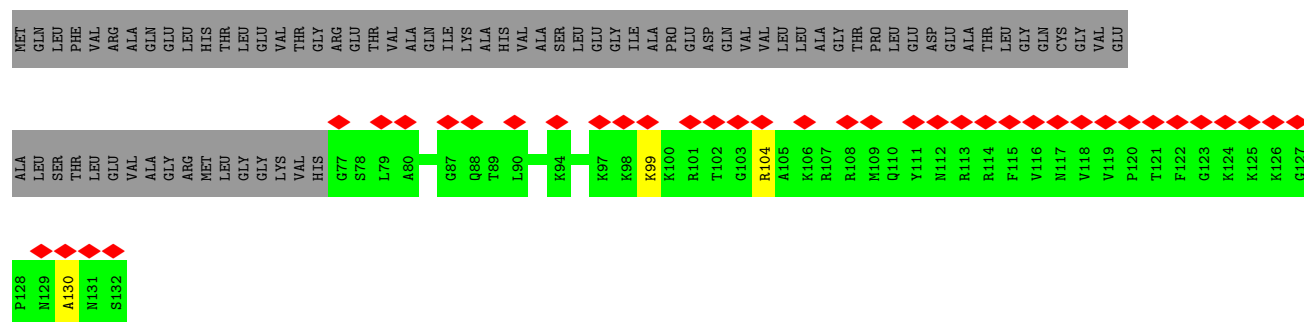


• Molecule 31: eS29

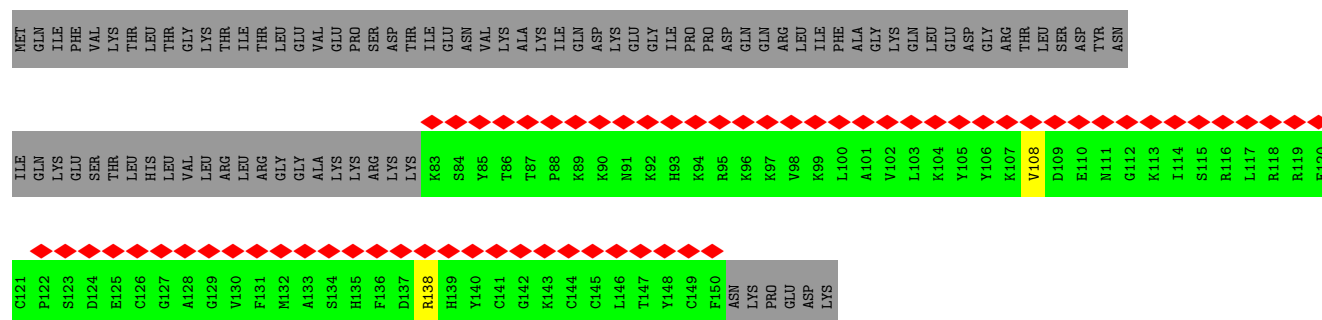
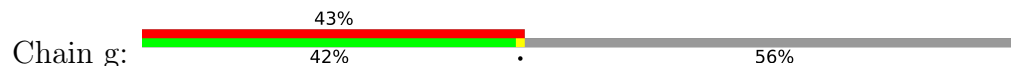


• Molecule 32: eS30

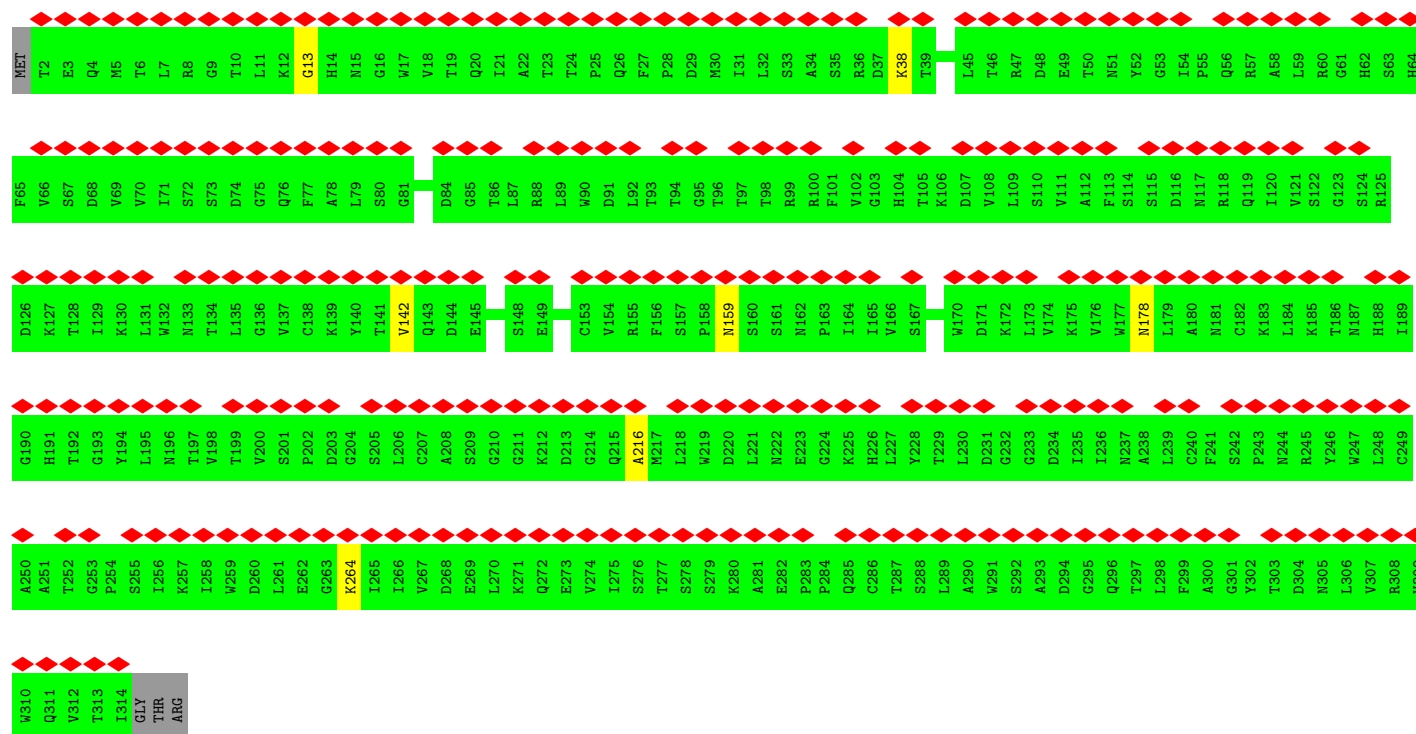
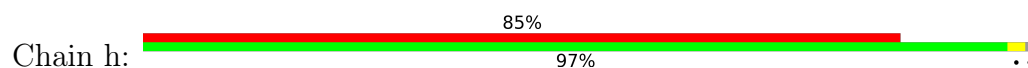




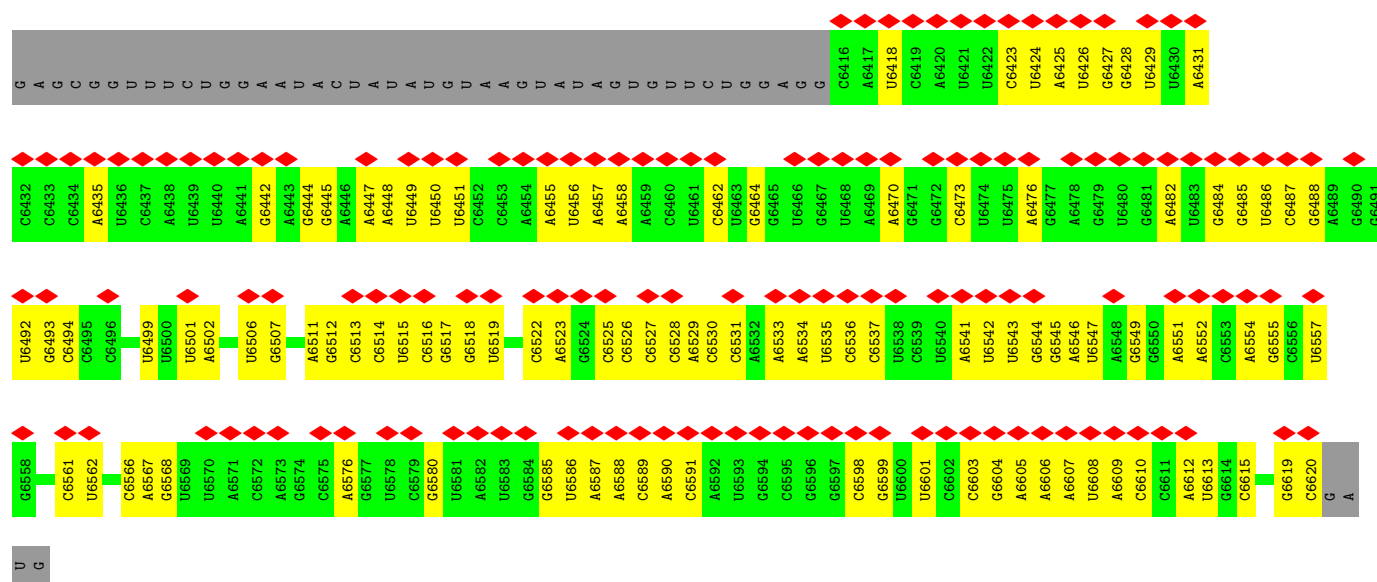
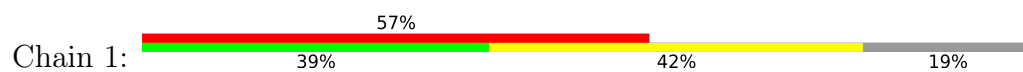
• Molecule 33: eS31



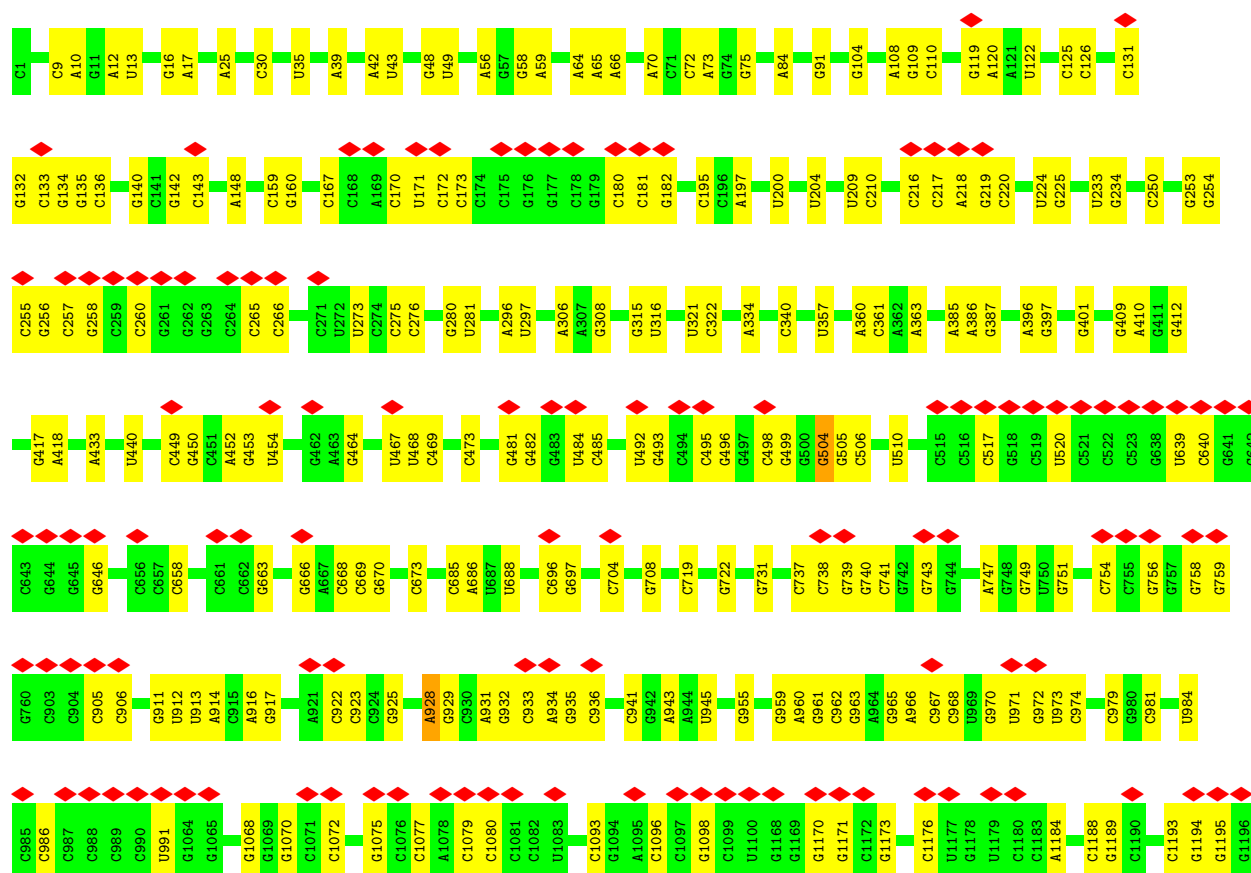
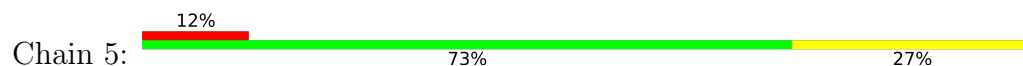
• Molecule 34: RACK1

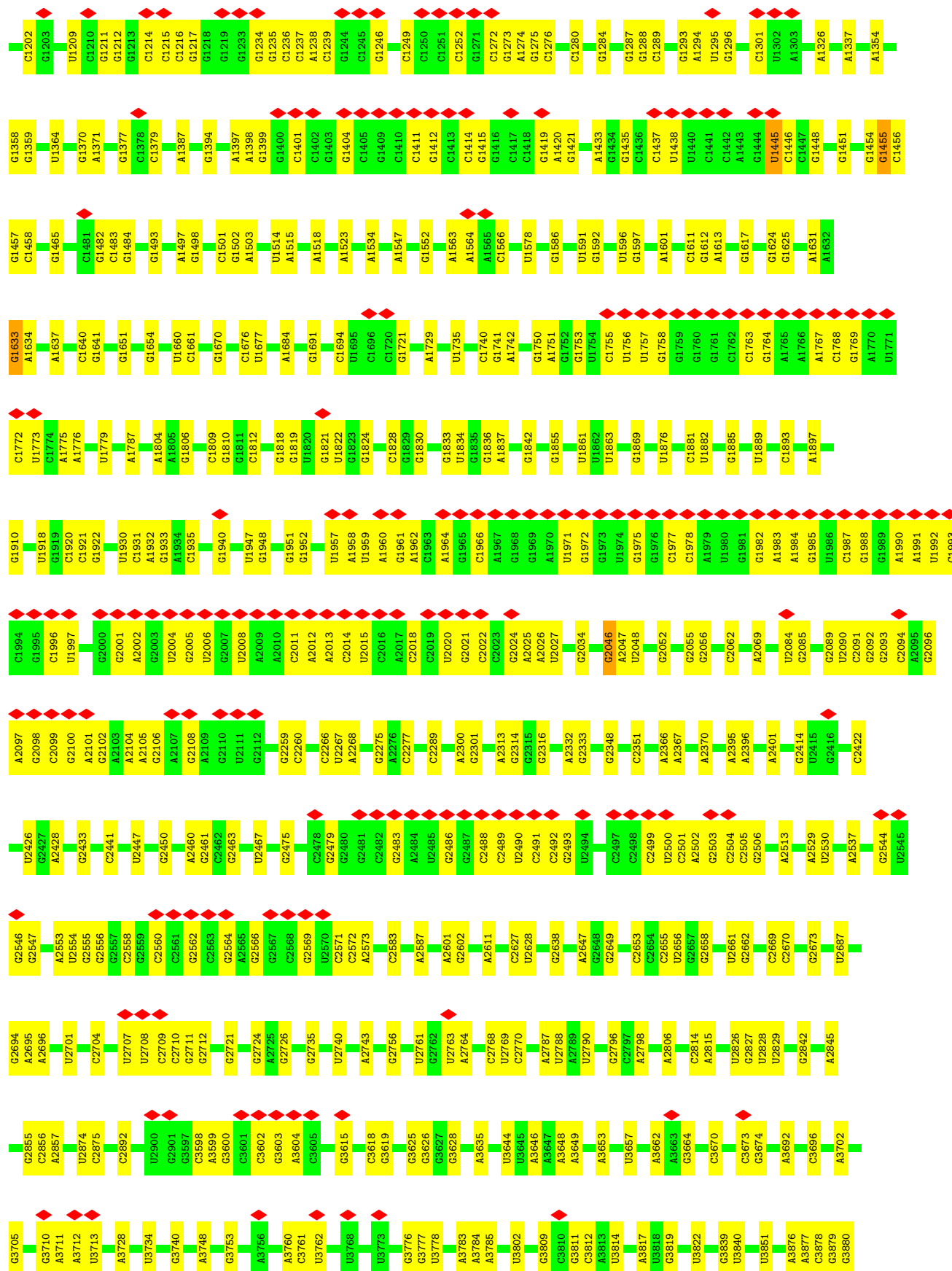


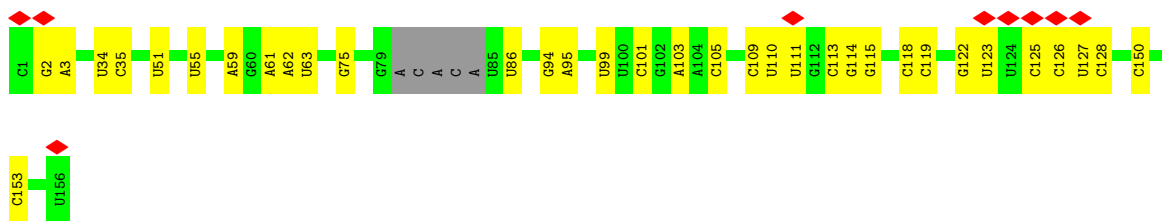
• Molecule 35: IAPV-IRES



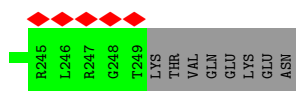
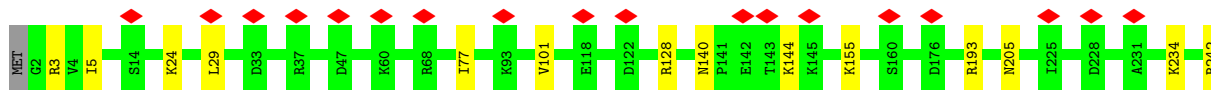
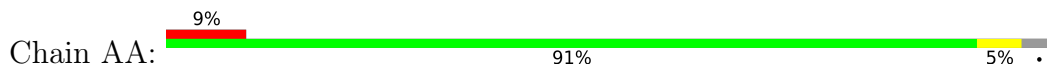
• Molecule 36: 28S rRNA



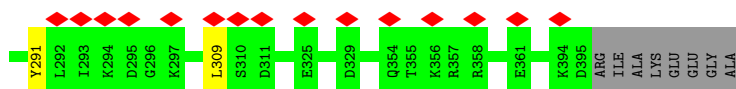




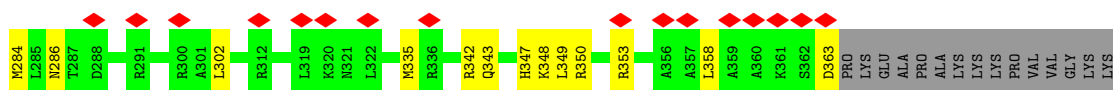
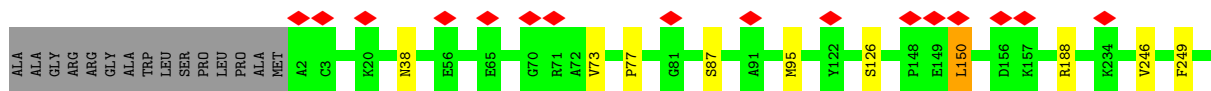
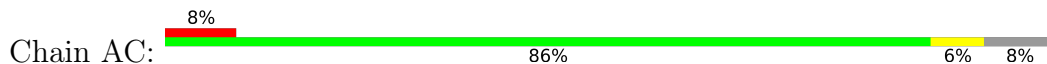
• Molecule 39: uL2



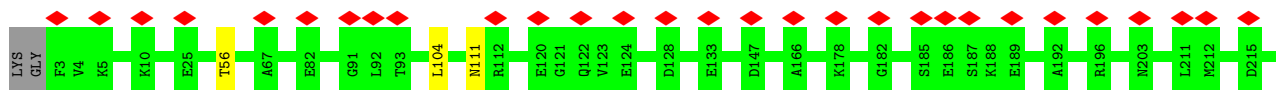
• Molecule 40: uL3

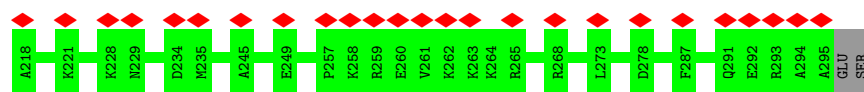


• Molecule 41: uL4

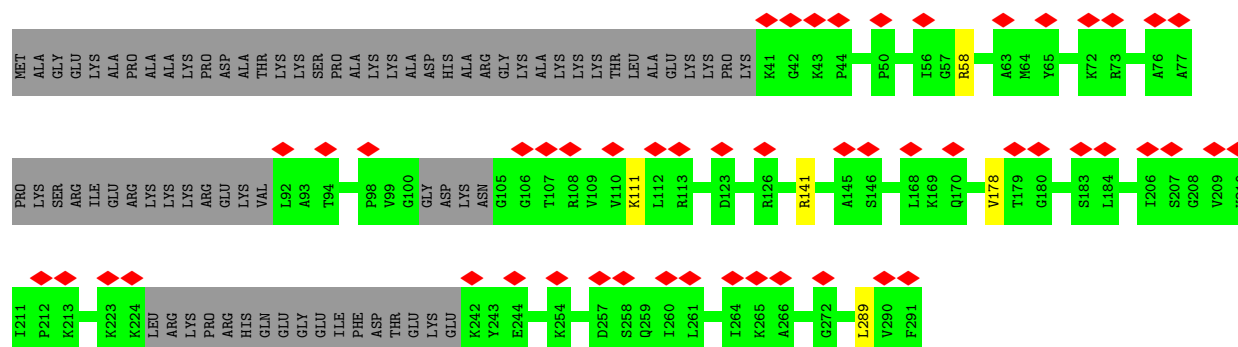
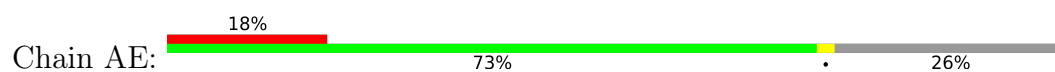


• Molecule 42: uL18

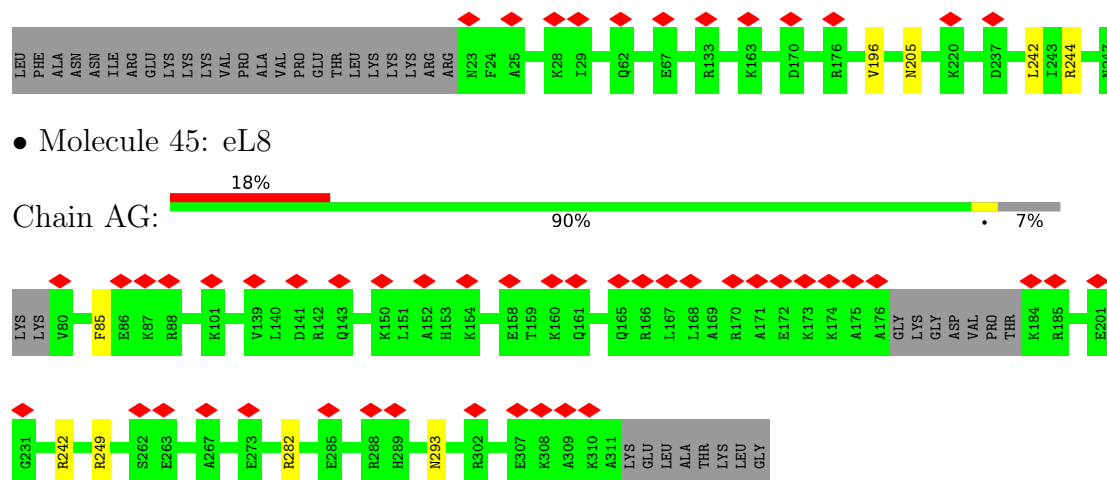
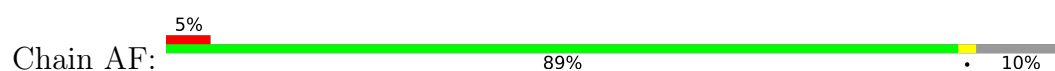




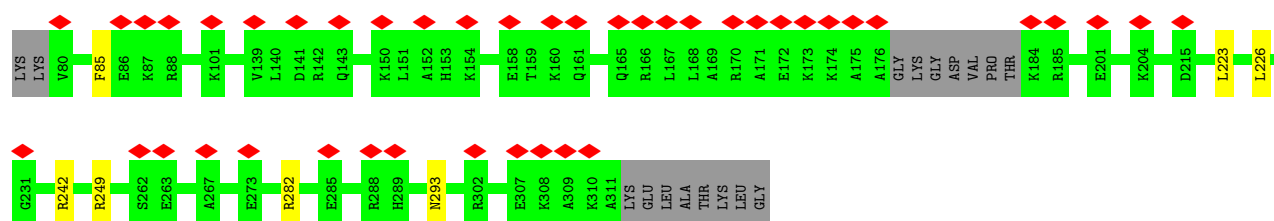
• Molecule 43: eL6



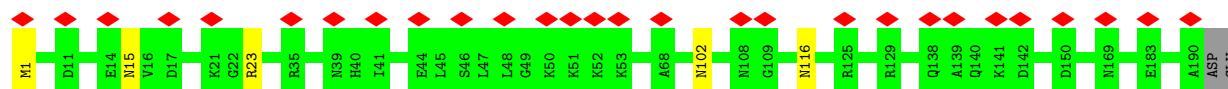
• Molecule 44: uL30



• Molecule 45: eL8

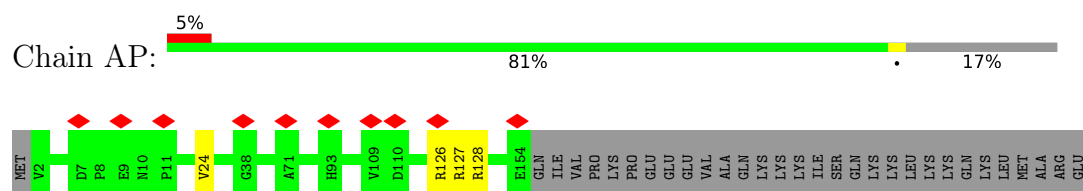


• Molecule 46: uL6

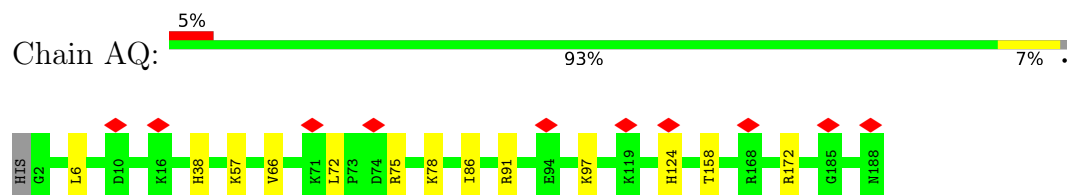


• Molecule 47: uL16

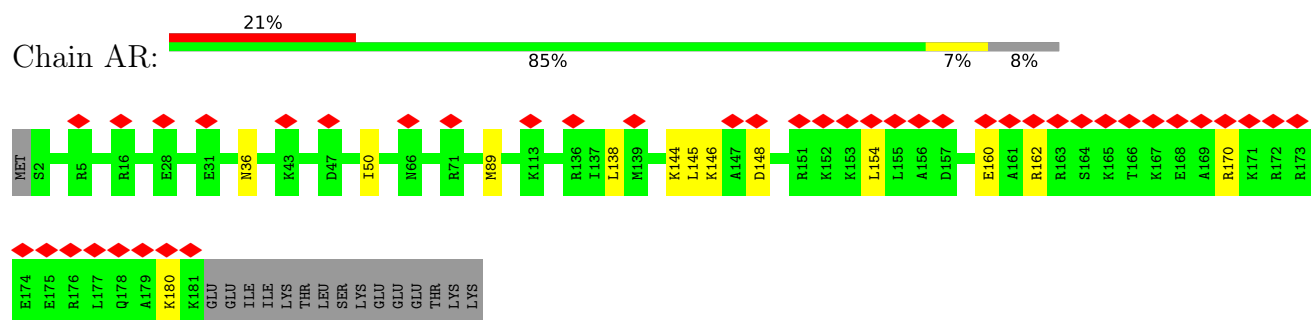




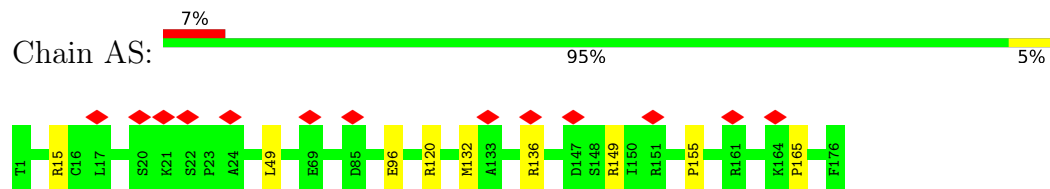
• Molecule 54: eL18



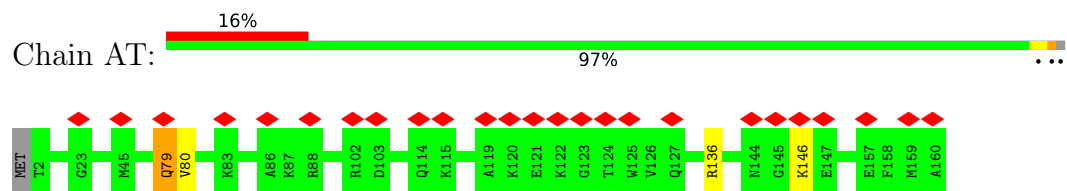
• Molecule 55: eL19



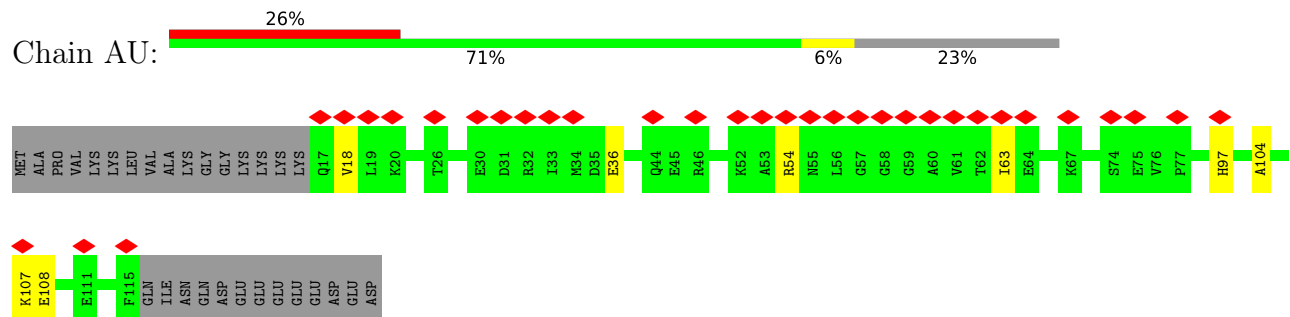
• Molecule 56: eL20

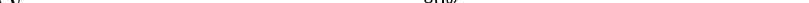


• Molecule 57: eL21




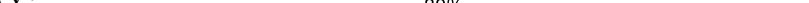
• Molecule 58: eL22



Chain AV:  7% 89% 8%

Chain AW: 


Chain AX: 


Chain AY:  8% 89% 8%

Chain AZ:  22% 99%

Chain Aa: 97%

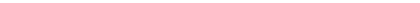
Chain Ab: 

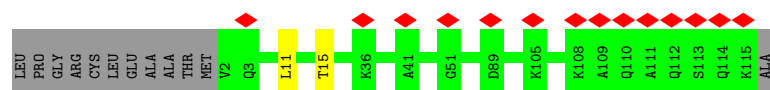
Chain Ac: 

Chain Ad: 

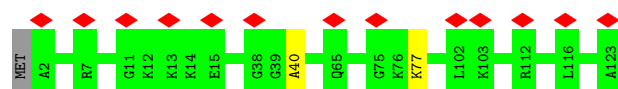
Chain Ae:  93% 6% 5%

Chain Af:  8% 94% 5%

Chain Ag:  89% 11% 10%



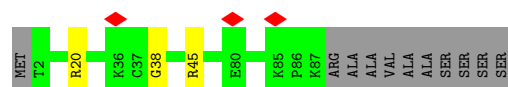
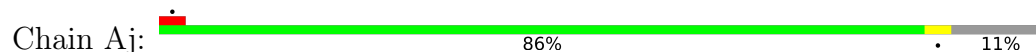
• Molecule 71: eL35



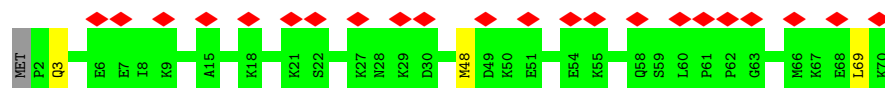
• Molecule 72: eL36



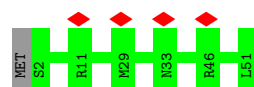
• Molecule 73: eL37



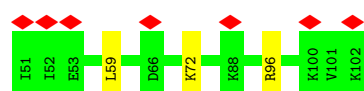
• Molecule 74: eL38



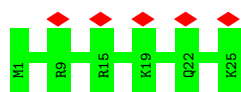
• Molecule 75: eL39



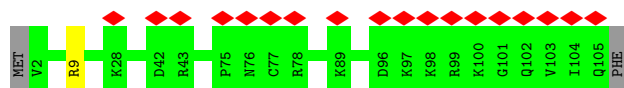
• Molecule 76: eL40



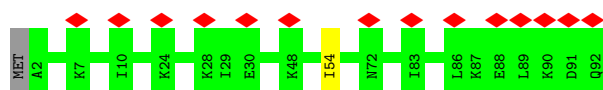
• Molecule 77: eL41



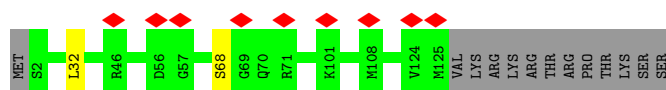
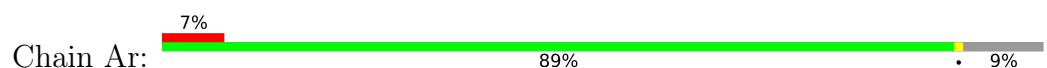
- Molecule 78: eL42



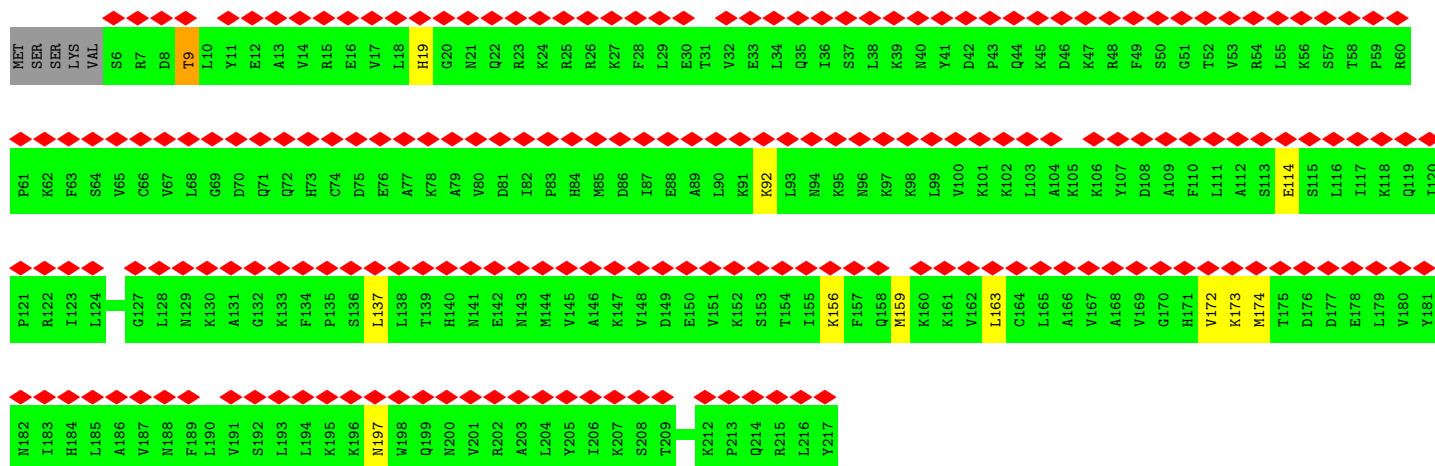
- Molecule 79: eL43



- Molecule 80: eL28



- Molecule 81: uL1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	40701	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	0.207	Depositor
Minimum map value	-0.124	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	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	0.21	0/40510	0.69	6/63132 (0.0%)
2	B	0.67	0/1744	0.77	0/2371
3	C	0.68	0/1756	0.80	0/2350
4	D	0.68	0/1748	0.80	0/2362
5	E	0.69	0/1796	0.80	0/2417
6	F	0.68	0/2115	0.82	0/2843
7	G	0.69	0/1492	0.79	0/2005
8	H	0.68	0/1946	0.85	0/2590
9	I	0.69	0/1510	0.78	0/2022
10	J	0.67	0/1715	0.80	0/2287
11	K	0.68	0/1550	0.82	0/2069
12	L	0.66	0/834	0.77	0/1125
13	M	0.67	0/1195	0.81	0/1597
14	N	0.71	0/918	0.79	0/1233
15	O	0.68	0/1226	0.78	0/1649
16	P	0.70	0/1029	0.83	0/1380
17	Q	0.67	0/1009	0.82	1/1346 (0.1%)
18	R	0.69	0/1146	0.82	0/1534
19	S	0.69	0/1082	0.78	0/1452
20	T	0.68	0/1208	0.81	0/1618
21	U	0.70	0/1115	0.80	0/1493
22	V	0.69	0/805	0.79	0/1081
23	W	0.71	0/638	0.81	0/855
24	X	0.68	0/1051	0.80	0/1406
25	Y	0.69	0/1116	0.83	0/1490
26	Z	0.68	0/1028	0.82	0/1366
27	a	0.69	0/604	0.81	0/810
28	b	0.67	0/791	0.81	0/1062
29	c	0.68	0/665	0.79	0/891
30	d	0.69	0/490	0.82	0/656
31	e	0.68	0/470	0.82	0/623
32	f	0.69	0/451	0.85	0/592
33	g	0.68	0/567	0.80	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	0.23	0/4881	0.71	0/7604
36	5	0.21	1/86215 (0.0%)	0.68	9/134459 (0.0%)
37	7	0.20	0/2836	0.66	0/4421
38	8	0.20	0/3581	0.68	0/5577
39	AA	0.67	0/1933	0.84	0/2592
40	AB	0.66	0/3240	0.80	0/4339
41	AC	0.66	0/2937	0.79	0/3946
42	AD	0.67	0/2437	0.79	0/3264
43	AE	0.67	0/1762	0.81	0/2362
44	AF	0.66	0/1911	0.78	0/2549
45	AG	0.67	0/1850	0.80	0/2491
46	AH	0.69	0/1535	0.82	0/2063
47	AI	0.66	0/1702	0.79	0/2272
48	AJ	0.68	0/1385	0.80	0/1852
49	AL	0.66	0/1658	0.84	0/2219
50	AM	0.66	0/1150	0.80	0/1534
51	AN	0.65	0/1746	0.82	0/2338
52	AO	0.66	0/1663	0.80	0/2223
53	AP	0.66	0/1268	0.79	0/1700
54	AQ	0.66	0/1557	0.80	0/2086
55	AR	0.67	0/1519	0.84	0/2006
56	AS	0.65	0/1498	0.79	0/2012
57	AT	0.65	0/1326	0.80	0/1770
58	AU	0.67	0/832	0.76	0/1116
59	AV	0.69	0/983	0.81	0/1319
60	AW	0.66	0/541	0.79	0/720
61	AX	0.66	0/984	0.77	0/1323
62	AY	0.67	0/1132	0.82	0/1504
63	AZ	0.66	0/1130	0.80	0/1507
64	Aa	0.66	0/1191	0.81	0/1590
65	Ab	0.67	0/861	0.81	0/1138
66	Ac	0.70	0/771	0.77	0/1034
67	Ad	0.66	0/903	0.82	0/1216
68	Ae	0.66	0/1071	0.80	0/1429
69	Af	0.65	0/895	0.81	0/1198
70	Ag	0.68	0/916	0.84	0/1220
71	Ah	0.68	0/1021	0.80	0/1348
72	Ai	0.67	0/841	0.81	0/1112
73	Aj	0.65	0/720	0.85	0/952
74	Ak	0.67	0/575	0.78	0/759
75	Al	0.64	0/459	0.81	0/608
76	Am	0.65	0/435	0.80	0/575
77	An	0.64	0/240	0.86	0/305

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	Ao	0.66	0/864	0.81	0/1140
79	Ap	0.69	0/718	0.83	0/953
80	Ar	0.68	0/1010	0.83	0/1354
81	AK	0.69	0/1733	0.82	0/2324
All	All	0.46	1/232229 (0.0%)	0.73	16/341277 (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
5	E	0	1
6	F	0	2
17	Q	0	1
24	X	0	1
25	Y	0	1
40	AB	0	4
41	AC	0	2
49	AL	0	1
53	AP	0	1
55	AR	0	1
57	AT	0	1
60	AW	0	1
69	Af	0	1
80	Ar	0	1
81	AK	0	2
All	All	0	21

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	5	5019	A	O3'-P	-5.11	1.55	1.61

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1432	U	C2'-C3'-O3'	6.29	123.77	113.70
17	Q	119	PHE	CB-CA-C	5.79	121.98	110.40
36	5	4180	G	C2'-C3'-O3'	5.73	122.86	113.70
1	2	55	U	N1-C1'-C2'	5.71	121.43	114.00
36	5	2046	G	C2'-C3'-O3'	5.68	122.78	113.70

There are no chirality outliers.

5 of 21 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	E	142	LEU	Peptide
6	F	30	ARG	Peptide
6	F	32	SER	Peptide
17	Q	111	MET	Peptide
24	X	27	ILE	Peptide

5.2 Too-close contacts [i](#)

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

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	B	215/295 (73%)	194 (90%)	21 (10%)	0	100	100
3	C	211/264 (80%)	180 (85%)	31 (15%)	0	100	100
4	D	219/255 (86%)	197 (90%)	21 (10%)	1 (0%)	29	64
5	E	226/281 (80%)	201 (89%)	24 (11%)	1 (0%)	34	69
6	F	260/263 (99%)	224 (86%)	34 (13%)	2 (1%)	19	54
7	G	181/204 (89%)	163 (90%)	17 (9%)	1 (1%)	25	59
8	H	235/249 (94%)	207 (88%)	27 (12%)	1 (0%)	34	69
9	I	181/194 (93%)	156 (86%)	22 (12%)	3 (2%)	9	36
10	J	204/207 (99%)	182 (89%)	21 (10%)	1 (0%)	29	64
11	K	183/194 (94%)	159 (87%)	22 (12%)	2 (1%)	14	46
12	L	94/149 (63%)	84 (89%)	10 (11%)	0	100	100
13	M	139/158 (88%)	118 (85%)	19 (14%)	2 (1%)	11	40
14	N	115/132 (87%)	94 (82%)	21 (18%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	O	147/151 (97%)	134 (91%)	13 (9%)	0	100	100
16	P	134/151 (89%)	121 (90%)	13 (10%)	0	100	100
17	Q	117/145 (81%)	100 (86%)	16 (14%)	1 (1%)	17	52
18	R	140/172 (81%)	123 (88%)	17 (12%)	0	100	100
19	S	130/135 (96%)	111 (85%)	19 (15%)	0	100	100
20	T	142/152 (93%)	132 (93%)	10 (7%)	0	100	100
21	U	139/145 (96%)	121 (87%)	13 (9%)	5 (4%)	3	20
22	V	98/119 (82%)	91 (93%)	7 (7%)	0	100	100
23	W	81/83 (98%)	76 (94%)	4 (5%)	1 (1%)	13	44
24	X	127/130 (98%)	117 (92%)	9 (7%)	1 (1%)	19	54
25	Y	139/143 (97%)	129 (93%)	8 (6%)	2 (1%)	11	40
26	Z	122/134 (91%)	101 (83%)	21 (17%)	0	100	100
27	a	73/125 (58%)	64 (88%)	9 (12%)	0	100	100
28	b	96/115 (84%)	88 (92%)	8 (8%)	0	100	100
29	c	81/84 (96%)	71 (88%)	9 (11%)	1 (1%)	13	44
30	d	60/69 (87%)	56 (93%)	4 (7%)	0	100	100
31	e	53/56 (95%)	48 (91%)	5 (9%)	0	100	100
32	f	54/133 (41%)	43 (80%)	10 (18%)	1 (2%)	8	33
33	g	66/156 (42%)	60 (91%)	6 (9%)	0	100	100
34	h	311/317 (98%)	256 (82%)	52 (17%)	3 (1%)	15	49
39	AA	246/257 (96%)	223 (91%)	22 (9%)	1 (0%)	34	69
40	AB	392/402 (98%)	356 (91%)	34 (9%)	2 (0%)	29	64
41	AC	360/392 (92%)	334 (93%)	21 (6%)	5 (1%)	11	40
42	AD	291/297 (98%)	273 (94%)	18 (6%)	0	100	100
43	AE	208/291 (72%)	186 (89%)	22 (11%)	0	100	100
44	AF	223/249 (90%)	210 (94%)	12 (5%)	1 (0%)	34	69
45	AG	221/242 (91%)	204 (92%)	16 (7%)	1 (0%)	29	64
46	AH	188/192 (98%)	173 (92%)	15 (8%)	0	100	100
47	AI	201/214 (94%)	184 (92%)	17 (8%)	0	100	100
48	AJ	168/178 (94%)	156 (93%)	11 (6%)	1 (1%)	25	59
49	AL	199/211 (94%)	187 (94%)	11 (6%)	1 (0%)	29	64

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	AM	133/198 (67%)	118 (89%)	14 (10%)	1 (1%)	19	54
51	AN	201/204 (98%)	186 (92%)	15 (8%)	0	100	100
52	AO	197/203 (97%)	188 (95%)	8 (4%)	1 (0%)	29	64
53	AP	151/184 (82%)	138 (91%)	13 (9%)	0	100	100
54	AQ	185/188 (98%)	173 (94%)	12 (6%)	0	100	100
55	AR	178/196 (91%)	170 (96%)	8 (4%)	0	100	100
56	AS	174/176 (99%)	159 (91%)	13 (8%)	2 (1%)	14	46
57	AT	157/160 (98%)	134 (85%)	21 (13%)	2 (1%)	12	42
58	AU	97/128 (76%)	78 (80%)	18 (19%)	1 (1%)	15	49
59	AV	127/140 (91%)	114 (90%)	12 (9%)	1 (1%)	19	54
60	AW	61/157 (39%)	57 (93%)	4 (7%)	0	100	100
61	AX	116/156 (74%)	114 (98%)	2 (2%)	0	100	100
62	AY	132/145 (91%)	122 (92%)	10 (8%)	0	100	100
63	AZ	133/136 (98%)	120 (90%)	12 (9%)	1 (1%)	19	54
64	Aa	145/148 (98%)	133 (92%)	12 (8%)	0	100	100
65	Ab	100/226 (44%)	88 (88%)	10 (10%)	2 (2%)	7	31
66	Ac	96/115 (84%)	89 (93%)	7 (7%)	0	100	100
67	Ad	105/125 (84%)	93 (89%)	10 (10%)	2 (2%)	8	33
68	Ae	126/135 (93%)	118 (94%)	7 (6%)	1 (1%)	19	54
69	Af	107/110 (97%)	98 (92%)	8 (8%)	1 (1%)	17	52
70	Ag	112/126 (89%)	107 (96%)	5 (4%)	0	100	100
71	Ah	120/123 (98%)	118 (98%)	1 (1%)	1 (1%)	19	54
72	Ai	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
73	Aj	84/97 (87%)	75 (89%)	8 (10%)	1 (1%)	13	44
74	Ak	67/70 (96%)	61 (91%)	6 (9%)	0	100	100
75	Al	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
76	Am	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
77	An	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
78	Ao	102/106 (96%)	97 (95%)	5 (5%)	0	100	100
79	Ap	89/92 (97%)	79 (89%)	10 (11%)	0	100	100
80	Ar	122/137 (89%)	109 (89%)	12 (10%)	1 (1%)	19	54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
81	AK	210/217 (97%)	160 (76%)	48 (23%)	2 (1%)	15	49
All	All	11318/12916 (88%)	10190 (90%)	1067 (9%)	61 (0%)	32	64

5 of 61 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	E	143	ARG
10	J	94	LYS
25	Y	61	GLN
41	AC	150	LEU
49	AL	63	THR

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%)	60	83
3	C	194/231 (84%)	187 (96%)	7 (4%)	35	67
4	D	186/205 (91%)	182 (98%)	4 (2%)	52	78
5	E	190/232 (82%)	184 (97%)	6 (3%)	39	69
6	F	223/225 (99%)	218 (98%)	5 (2%)	52	78
7	G	158/170 (93%)	156 (99%)	2 (1%)	69	87
8	H	207/218 (95%)	204 (99%)	3 (1%)	67	86
9	I	165/174 (95%)	164 (99%)	1 (1%)	86	94
10	J	178/179 (99%)	177 (99%)	1 (1%)	86	94
11	K	161/168 (96%)	158 (98%)	3 (2%)	57	81
12	L	87/125 (70%)	87 (100%)	0	100	100
13	M	130/142 (92%)	127 (98%)	3 (2%)	50	77
14	N	99/108 (92%)	98 (99%)	1 (1%)	76	90
15	O	130/131 (99%)	127 (98%)	3 (2%)	50	77
16	P	106/119 (89%)	105 (99%)	1 (1%)	78	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	Q	108/130 (83%)	103 (95%)	5 (5%)	27	59
18	R	117/140 (84%)	113 (97%)	4 (3%)	37	69
19	S	119/121 (98%)	118 (99%)	1 (1%)	81	92
20	T	125/132 (95%)	121 (97%)	4 (3%)	39	69
21	U	111/116 (96%)	110 (99%)	1 (1%)	78	91
22	V	92/107 (86%)	91 (99%)	1 (1%)	73	89
23	W	68/68 (100%)	60 (88%)	8 (12%)	5	21
24	X	112/113 (99%)	110 (98%)	2 (2%)	59	82
25	Y	113/114 (99%)	112 (99%)	1 (1%)	78	91
26	Z	107/115 (93%)	105 (98%)	2 (2%)	57	81
27	a	66/103 (64%)	66 (100%)	0	100	100
28	b	86/99 (87%)	85 (99%)	1 (1%)	71	88
29	c	75/76 (99%)	75 (100%)	0	100	100
30	d	55/62 (89%)	55 (100%)	0	100	100
31	e	48/49 (98%)	48 (100%)	0	100	100
32	f	46/106 (43%)	44 (96%)	2 (4%)	29	62
33	g	61/140 (44%)	59 (97%)	2 (3%)	38	69
34	h	272/275 (99%)	268 (98%)	4 (2%)	65	85
39	AA	189/199 (95%)	176 (93%)	13 (7%)	15	45
40	AB	342/347 (99%)	334 (98%)	8 (2%)	50	77
41	AC	302/323 (94%)	285 (94%)	17 (6%)	21	52
42	AD	247/250 (99%)	244 (99%)	3 (1%)	71	88
43	AE	190/251 (76%)	185 (97%)	5 (3%)	46	74
44	AF	196/218 (90%)	193 (98%)	3 (2%)	65	85
45	AG	194/208 (93%)	188 (97%)	6 (3%)	40	70
46	AH	169/171 (99%)	164 (97%)	5 (3%)	41	71
47	AI	175/181 (97%)	172 (98%)	3 (2%)	60	83
48	AJ	143/149 (96%)	141 (99%)	2 (1%)	67	86
49	AL	167/176 (95%)	164 (98%)	3 (2%)	59	82
50	AM	116/151 (77%)	116 (100%)	0	100	100
51	AN	171/172 (99%)	168 (98%)	3 (2%)	59	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	AO	171/173 (99%)	167 (98%)	4 (2%)	50	77
53	AP	134/163 (82%)	131 (98%)	3 (2%)	52	78
54	AQ	166/167 (99%)	153 (92%)	13 (8%)	12	40
55	AR	159/175 (91%)	147 (92%)	12 (8%)	13	42
56	AS	155/155 (100%)	148 (96%)	7 (4%)	27	60
57	AT	139/140 (99%)	137 (99%)	2 (1%)	67	86
58	AU	91/116 (78%)	84 (92%)	7 (8%)	13	41
59	AV	100/107 (94%)	97 (97%)	3 (3%)	41	71
60	AW	55/126 (44%)	55 (100%)	0	100	100
61	AX	106/134 (79%)	106 (100%)	0	100	100
62	AY	124/135 (92%)	119 (96%)	5 (4%)	31	65
63	AZ	117/118 (99%)	117 (100%)	0	100	100
64	Aa	119/120 (99%)	115 (97%)	4 (3%)	37	69
65	Ab	84/172 (49%)	81 (96%)	3 (4%)	35	67
66	Ac	84/98 (86%)	83 (99%)	1 (1%)	71	88
67	Ad	98/110 (89%)	94 (96%)	4 (4%)	30	64
68	Ae	114/121 (94%)	113 (99%)	1 (1%)	78	91
69	Af	88/89 (99%)	83 (94%)	5 (6%)	20	52
70	Ag	98/106 (92%)	96 (98%)	2 (2%)	55	80
71	Ah	109/110 (99%)	108 (99%)	1 (1%)	78	91
72	Ai	86/89 (97%)	82 (95%)	4 (5%)	26	59
73	Aj	73/80 (91%)	71 (97%)	2 (3%)	44	74
74	Ak	64/65 (98%)	61 (95%)	3 (5%)	26	59
75	Al	47/48 (98%)	47 (100%)	0	100	100
76	Am	48/48 (100%)	45 (94%)	3 (6%)	18	48
77	An	24/24 (100%)	24 (100%)	0	100	100
78	Ao	92/94 (98%)	91 (99%)	1 (1%)	73	89
79	Ap	74/75 (99%)	73 (99%)	1 (1%)	67	86
80	Ar	108/121 (89%)	108 (100%)	0	100	100
81	AK	190/196 (97%)	181 (95%)	9 (5%)	26	59
All	All	9893/11009 (90%)	9641 (98%)	252 (2%)	50	75

5 of 252 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	AC	350	ARG
69	Af	16	ARG
47	AI	100	ASN
67	Ad	83	ARG
74	Ak	48	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 99 such sidechains are listed below:

Mol	Chain	Res	Type
42	AD	282	GLN
49	AL	19	GLN
44	AF	79	ASN
46	AH	78	GLN
51	AN	87	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1686/1869 (90%)	547 (32%)	37 (2%)
35	1	204/253 (80%)	105 (51%)	10 (4%)
36	5	3569/3594 (99%)	959 (26%)	64 (1%)
37	7	118/119 (99%)	16 (13%)	0
38	8	149/156 (95%)	33 (22%)	3 (2%)
All	All	5726/5991 (95%)	1660 (28%)	114 (1%)

5 of 1660 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	3	C
1	2	4	C
1	2	14	C
1	2	17	C
1	2	20	G

5 of 114 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
36	5	385	A
36	5	4936	G

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Mol	Chain	Res	Type
36	5	1445	U
36	5	4925	U
36	5	4170	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 monosaccharides 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	41.95
1	5	1252:C	O3'	1271:G	P	38.04
1	5	1405:C	O3'	1409:G	P	20.69
1	5	4138:C	O3'	4146:G	P	19.42
1	5	1219:G	O3'	1233:G	P	19.04

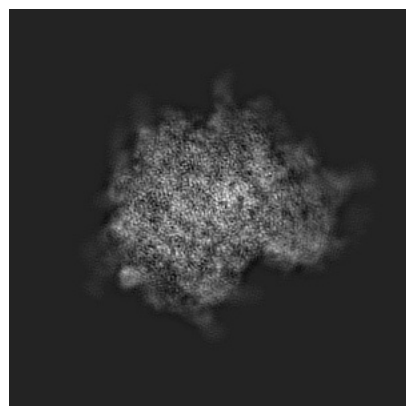
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20256. These allow visual inspection of the internal detail of the map and identification of artifacts.

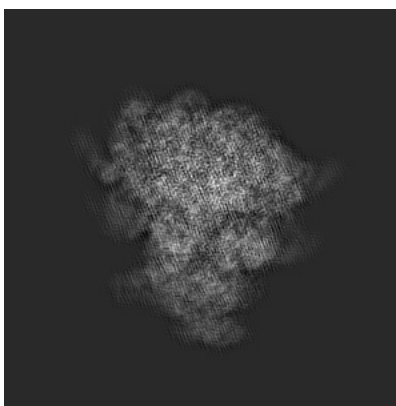
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

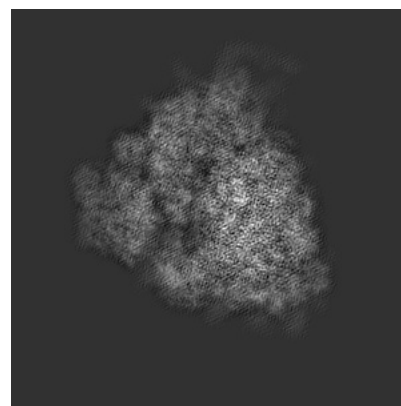
6.1.1 Primary map



X

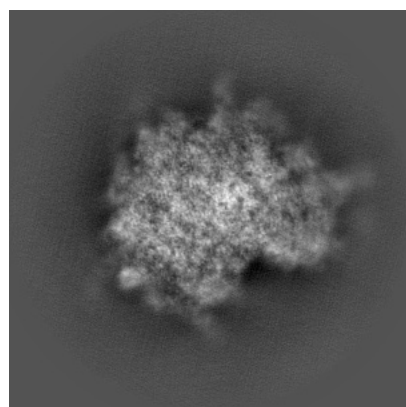


Y

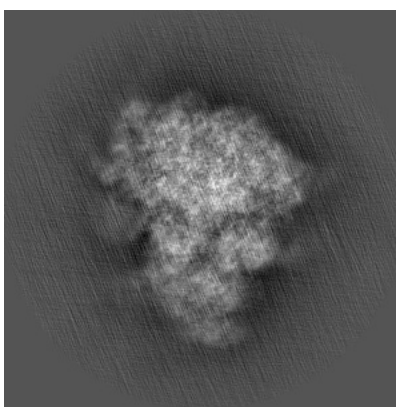


Z

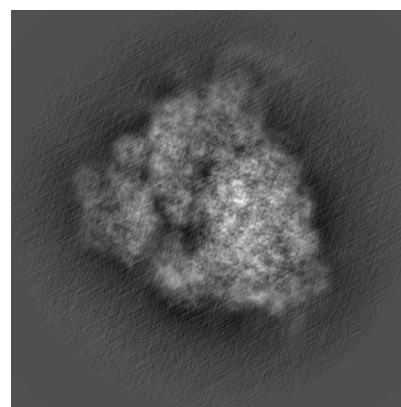
6.1.2 Raw map



X



Y

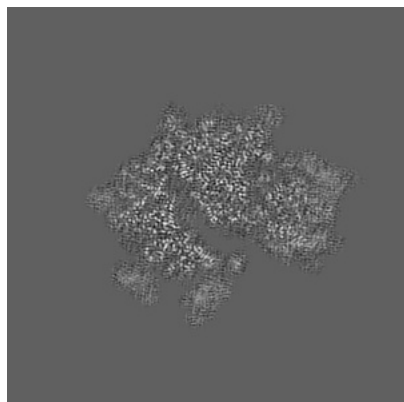


Z

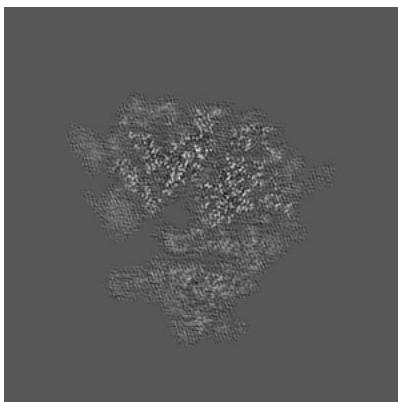
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

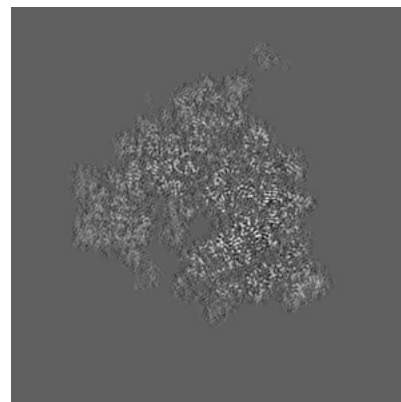
6.2.1 Primary map



X Index: 180

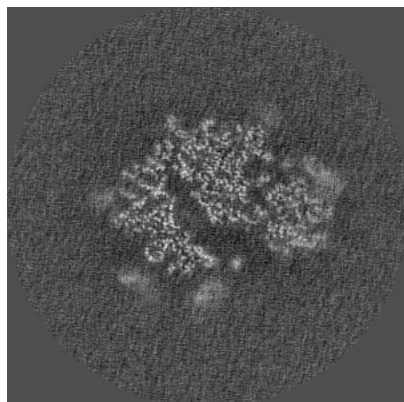


Y Index: 180

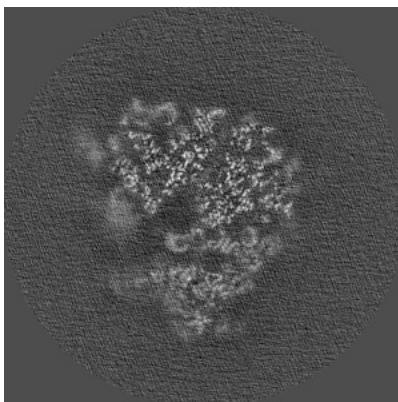


Z Index: 180

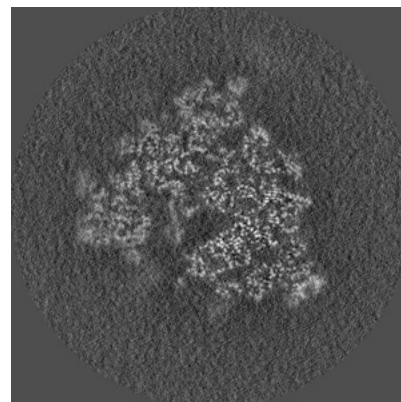
6.2.2 Raw map



X Index: 180



Y Index: 180

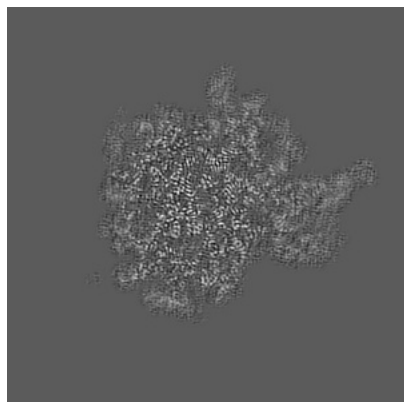


Z Index: 180

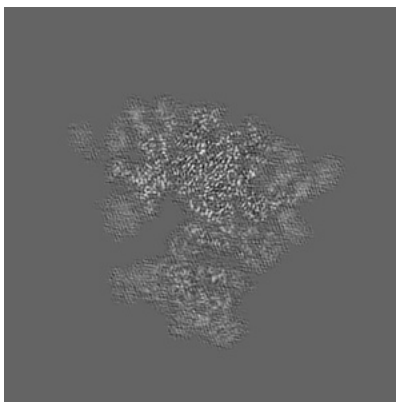
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

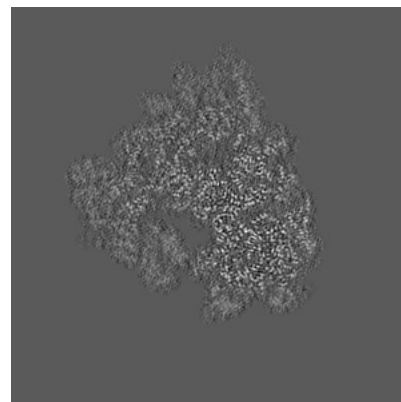
6.3.1 Primary map



X Index: 206

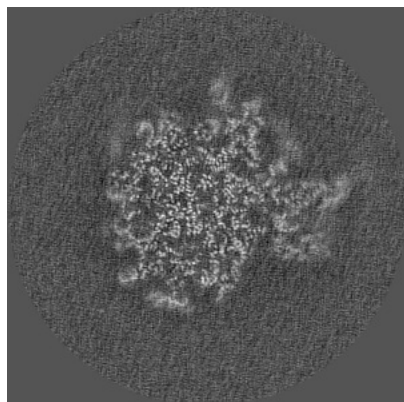


Y Index: 188

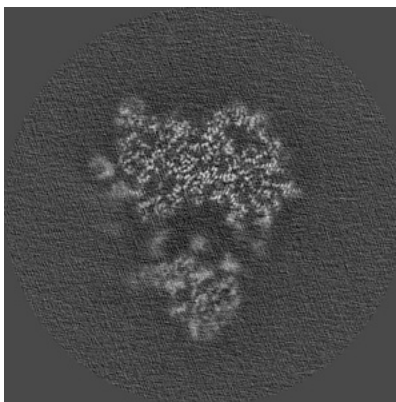


Z Index: 195

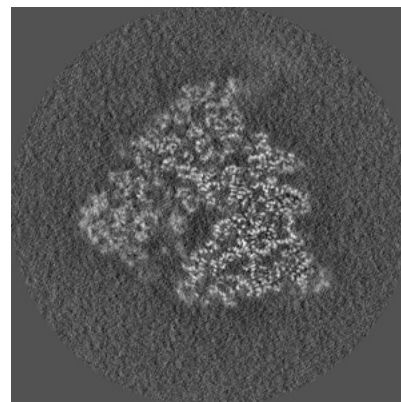
6.3.2 Raw map



X Index: 206



Y Index: 163

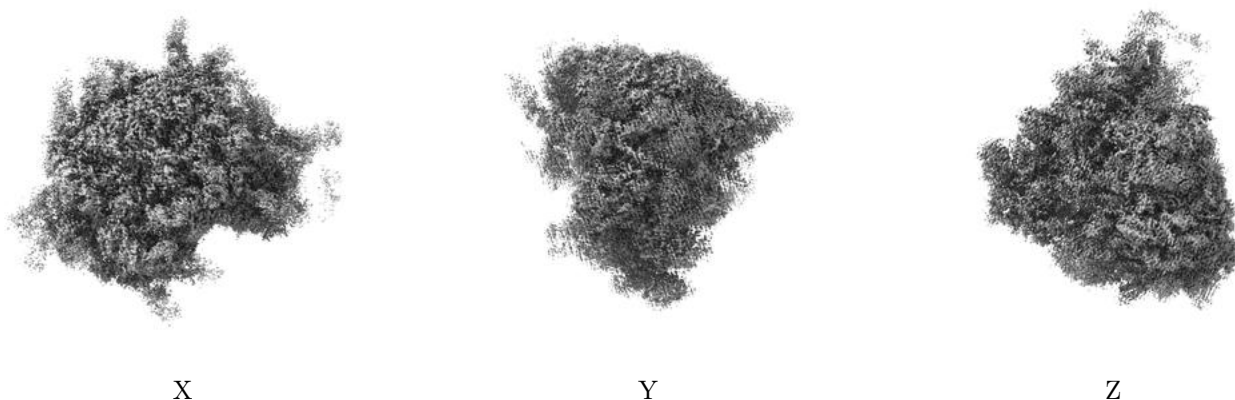


Z Index: 173

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

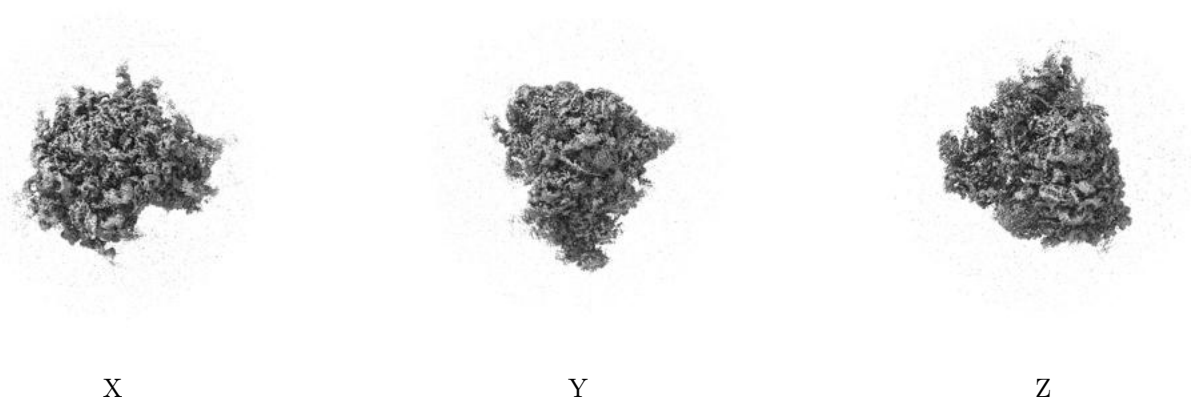
6.4 Orthogonal surface views [i](#)

6.4.1 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.

6.4.2 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.

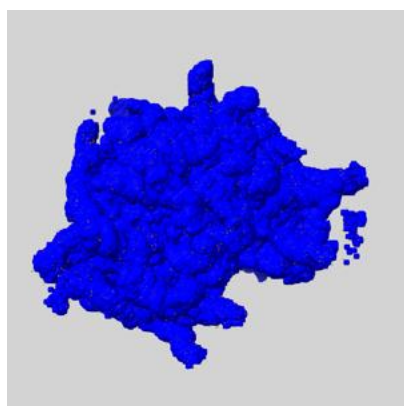
6.5 Mask visualisation [i](#)

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

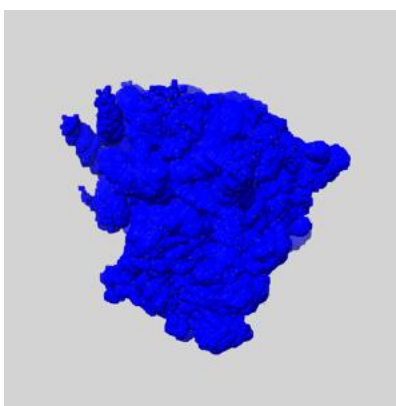
A mask typically either:

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

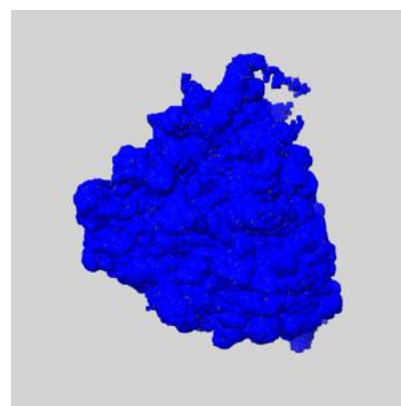
6.5.1 emd_20256_msk_1.map [i](#)



X



Y

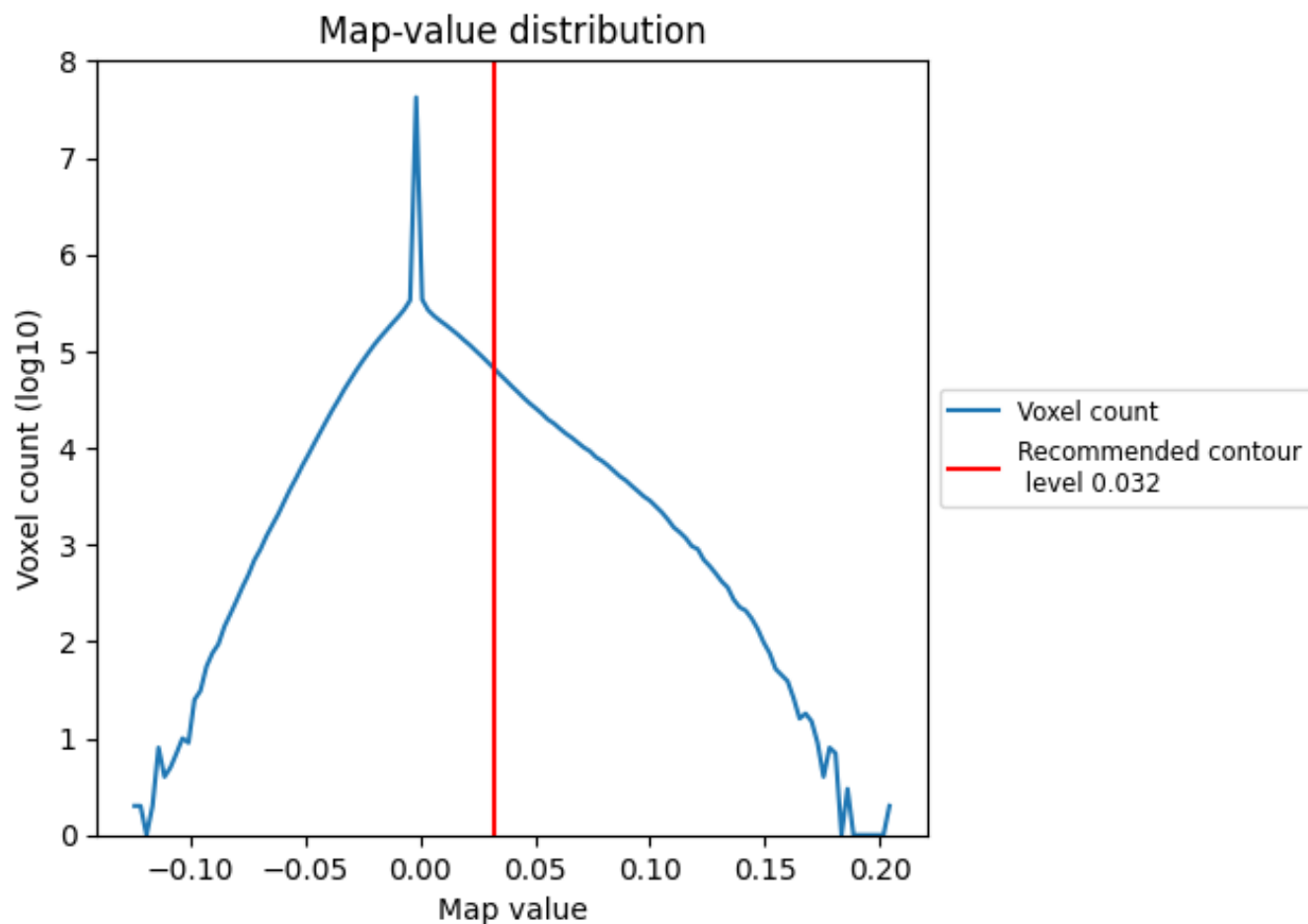


Z

7 Map analysis [i](#)

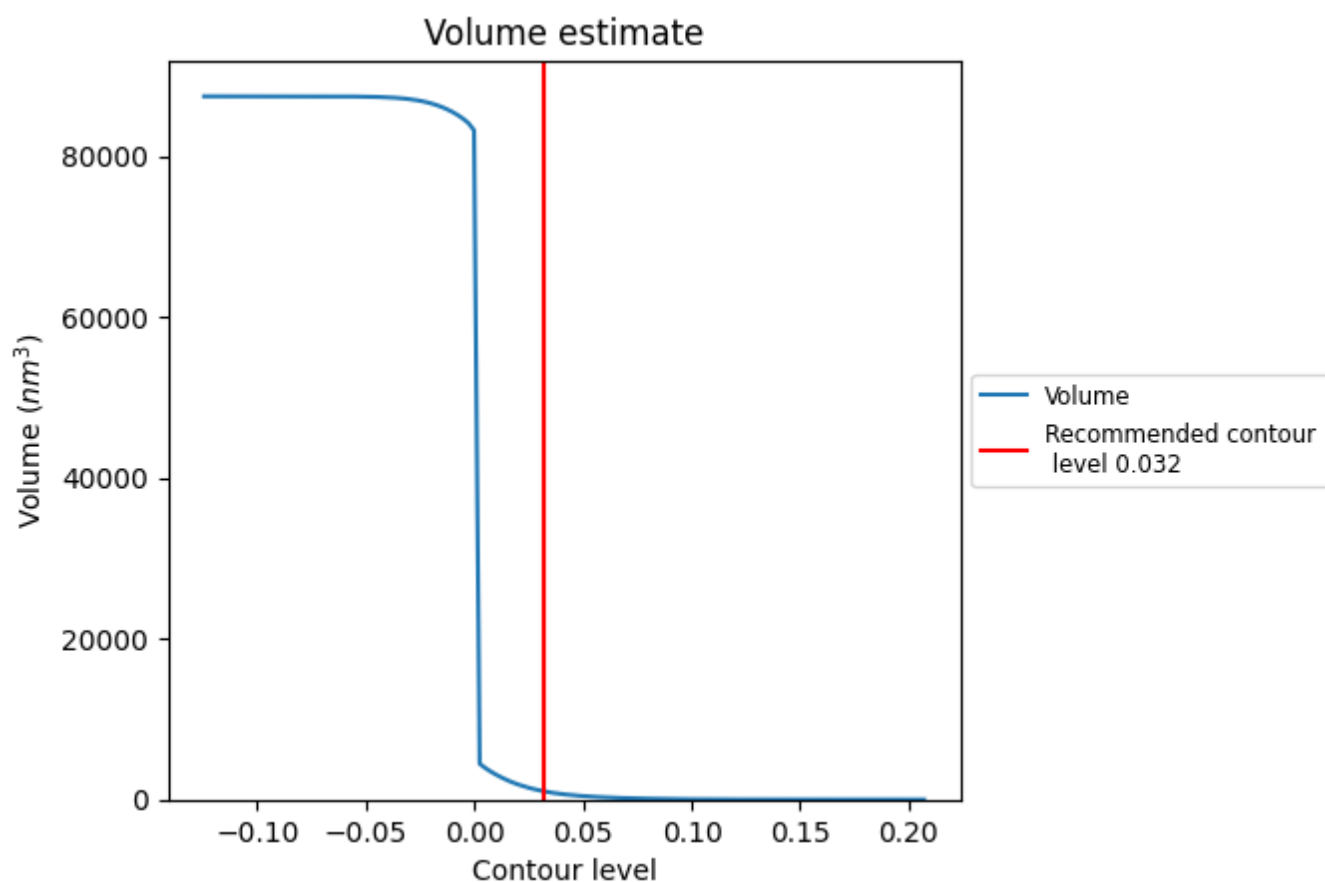
This section contains the results of statistical analysis of the map.

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.

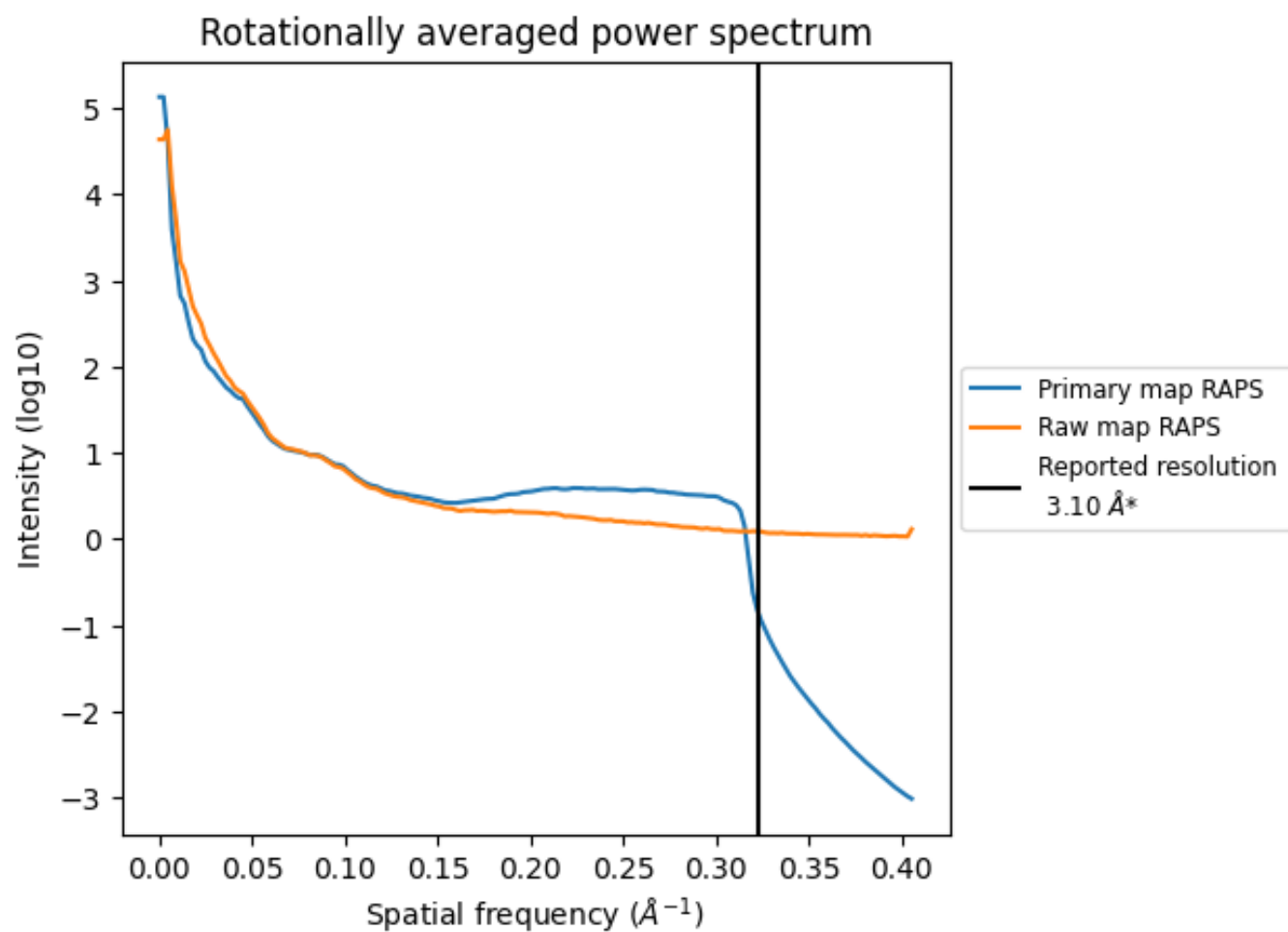
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1031 nm³; this corresponds to an approximate mass of 931 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 ⓘ

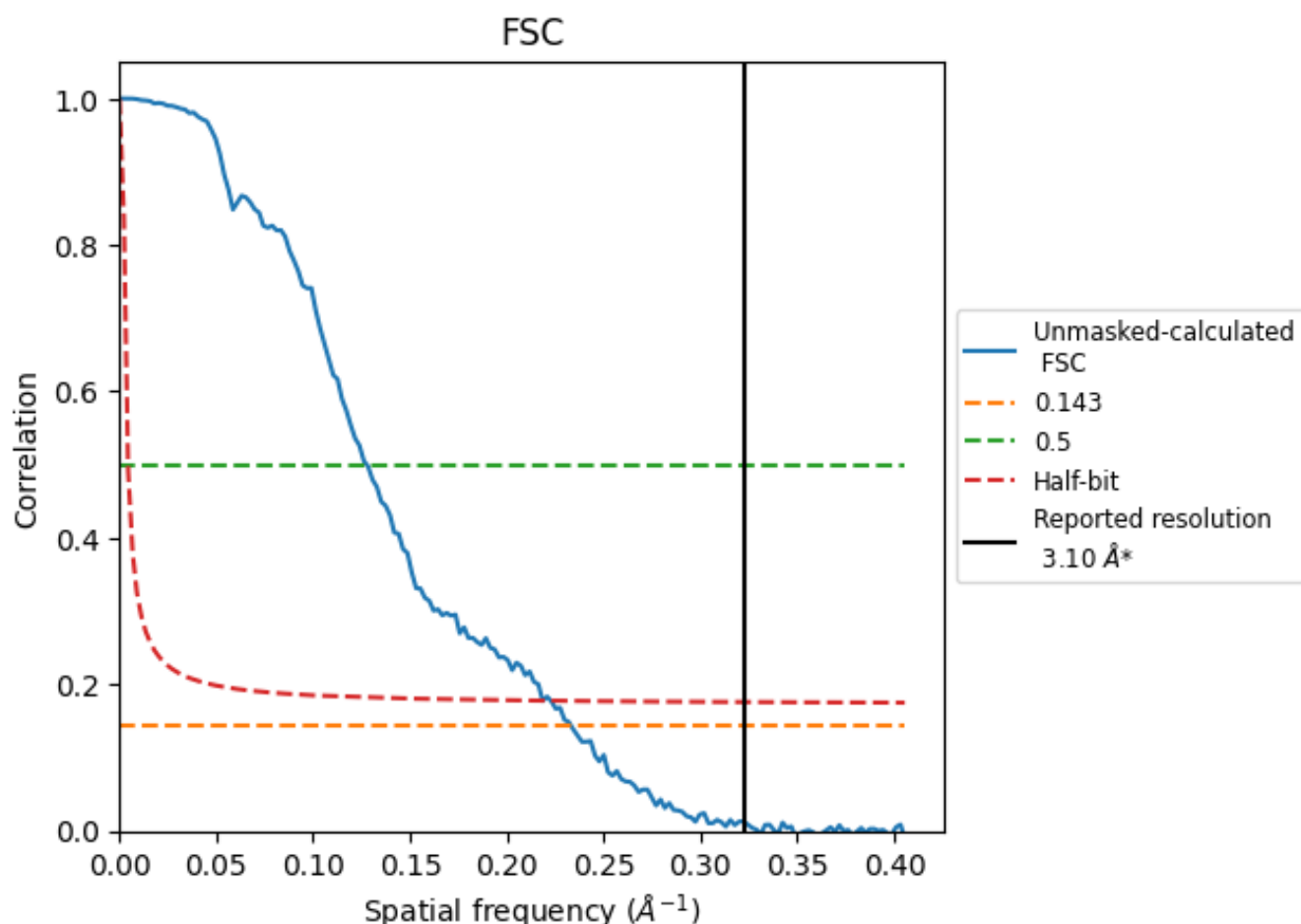


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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](#)

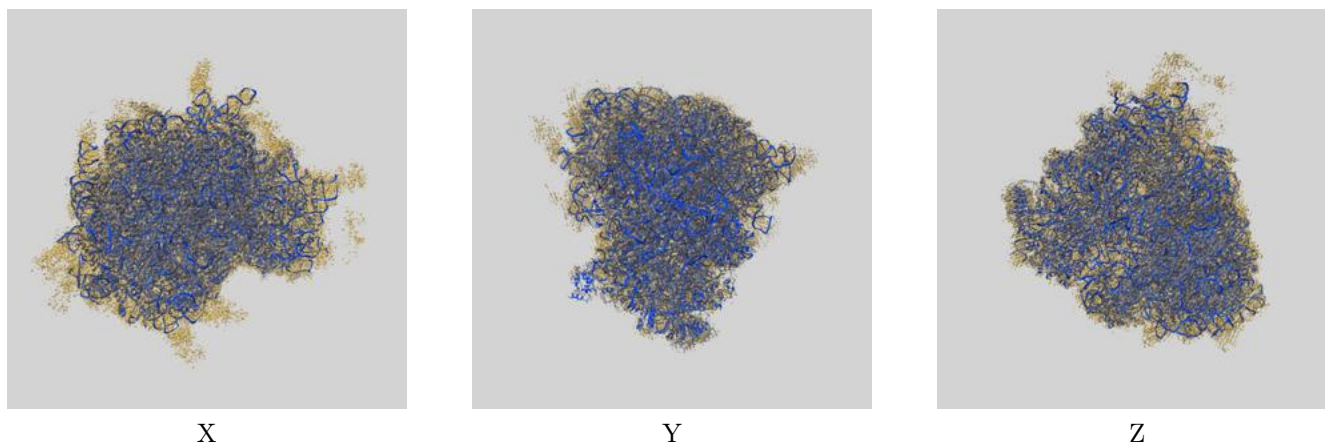
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.29	7.84	4.58

*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 4.29 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

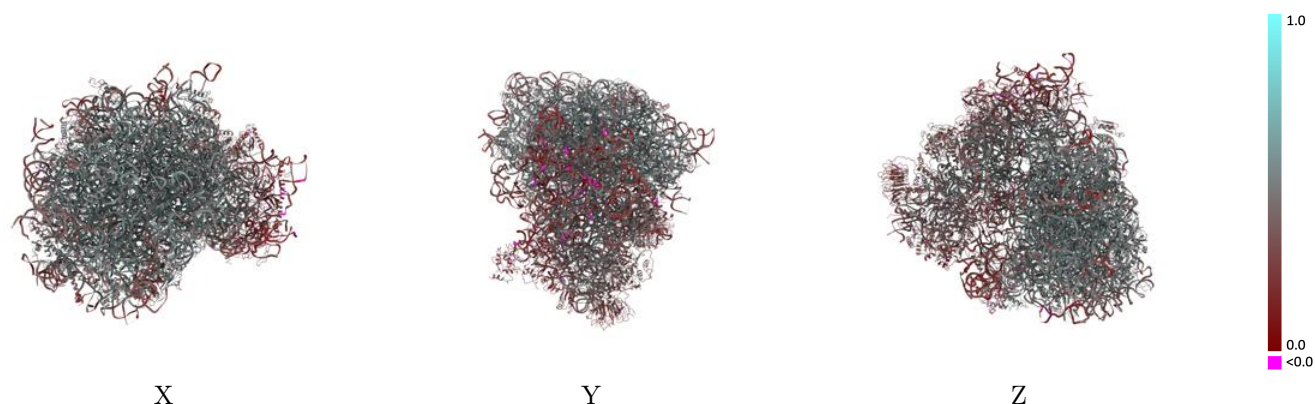
This section contains information regarding the fit between EMDB map EMD-20256 and PDB model 6P5J. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

9.1 Map-model overlay [i](#)



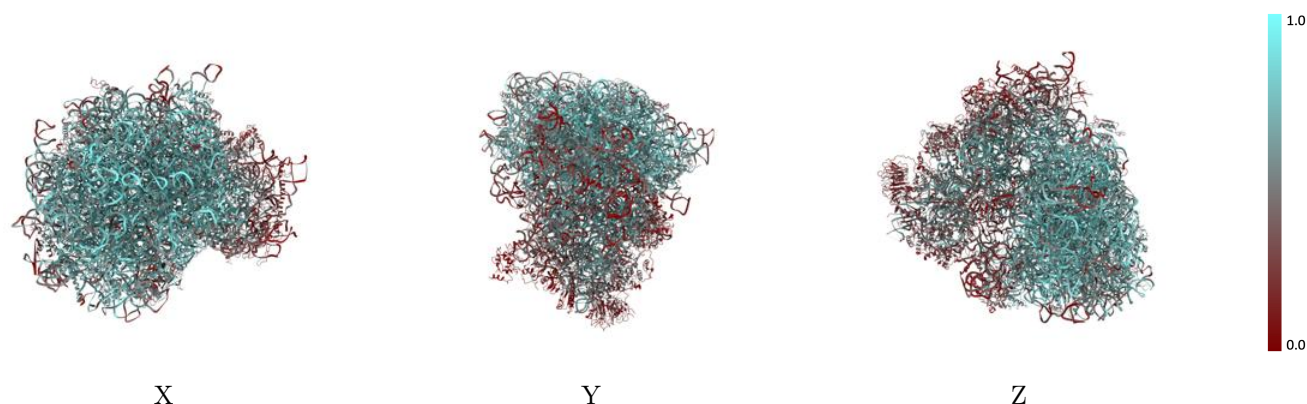
The images above show the 3D surface view of the map at the recommended contour level 0.032 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



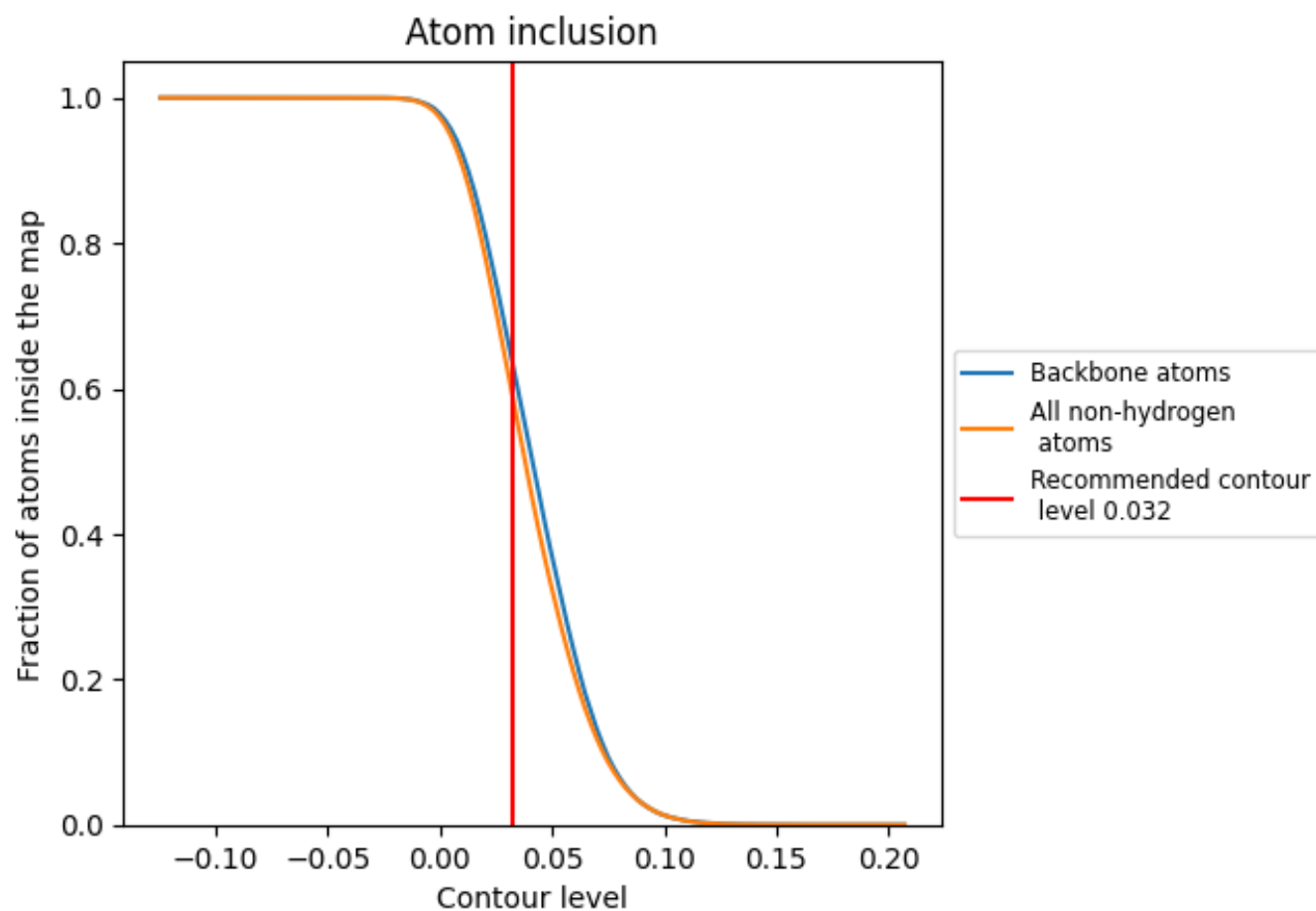
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 64% of all backbone atoms, 60% 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	 0.5950	 0.4340
1	 0.3204	 0.2790
2	 0.5762	 0.3940
5	 0.7268	 0.4780
7	 0.8128	 0.5090
8	 0.7746	 0.5070
AA	 0.6763	 0.5120
AB	 0.6589	 0.4990
AC	 0.6760	 0.4980
AD	 0.5834	 0.4520
AE	 0.5742	 0.4540
AF	 0.6830	 0.5120
AG	 0.5745	 0.4490
AH	 0.6123	 0.4660
AI	 0.6351	 0.4980
AJ	 0.4315	 0.3980
AK	 0.1275	 0.2260
AL	 0.6350	 0.4770
AM	 0.6447	 0.4850
AN	 0.7352	 0.5230
AO	 0.6806	 0.5150
AP	 0.6816	 0.5130
AQ	 0.6832	 0.4980
AR	 0.5771	 0.4480
AS	 0.6800	 0.5000
AT	 0.6144	 0.4800
AU	 0.4825	 0.3780
AV	 0.6367	 0.5120
AW	 0.5914	 0.4970
AX	 0.6213	 0.4760
AY	 0.6549	 0.4970
AZ	 0.5676	 0.4550
Aa	 0.7154	 0.5190
Ab	 0.4798	 0.4490
Ac	 0.5618	 0.4460













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Chain	Atom inclusion	Q-score
Ad	 0.6138	 0.4680
Ae	 0.7070	 0.5280
Af	 0.7019	 0.5300
Ag	 0.6053	 0.4840
Ah	 0.6078	 0.4770
Ai	 0.5817	 0.4400
Aj	 0.7247	 0.5190
Ak	 0.5045	 0.4230
Al	 0.6581	 0.4950
Am	 0.6434	 0.4940
An	 0.5917	 0.4770
Ao	 0.5915	 0.4930
Ap	 0.6221	 0.4880
Ar	 0.6635	 0.4910
B	 0.4028	 0.3790
C	 0.3314	 0.3420
D	 0.4661	 0.4040
E	 0.2475	 0.3120
F	 0.2223	 0.2170
G	 0.3771	 0.3620
H	 0.2690	 0.2690
I	 0.2676	 0.3310
J	 0.4370	 0.3880
K	 0.3133	 0.2830
L	 0.1848	 0.2700
M	 0.4667	 0.4090
N	 0.0391	 0.2190
O	 0.4022	 0.3920
P	 0.3414	 0.3570
Q	 0.2610	 0.2740
R	 0.3645	 0.3700
S	 0.2909	 0.3460
T	 0.2672	 0.3060
U	 0.3346	 0.3300
V	 0.2274	 0.3290
W	 0.3653	 0.3800
X	 0.4861	 0.4330
Y	 0.5341	 0.4510
Z	 0.2345	 0.2400
a	 0.2539	 0.2700
b	 0.4740	 0.4380
c	 0.3380	 0.3720

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Chain	Atom inclusion	Q-score
d	 0.3085	 0.3610
e	 0.3628	 0.3520
f	 0.3070	 0.3100
g	 0.0426	 0.2350
h	 0.2079	 0.2770