



wwPDB EM Validation Summary Report ⓘ

Mar 14, 2026 – 12:03 AM UTC

PDB ID : 6P5I / pdb_00006p5i
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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

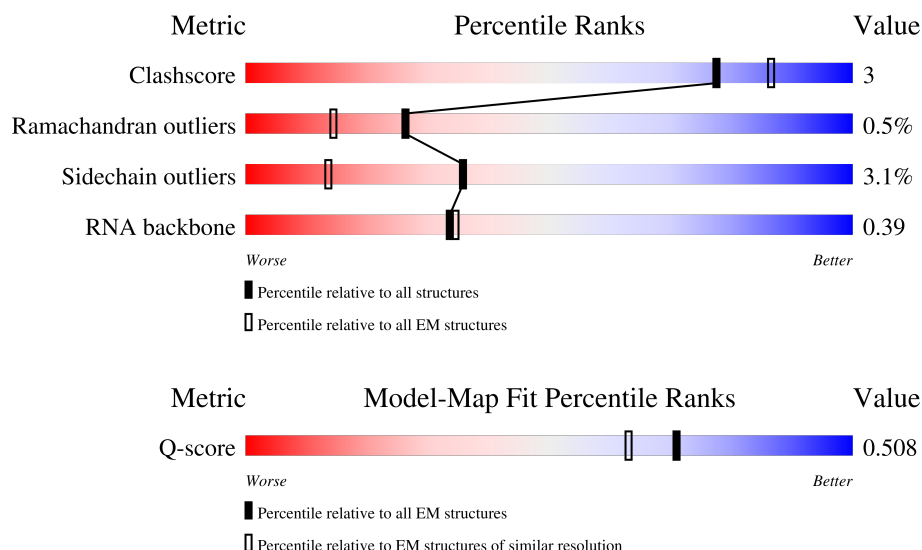
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	11% 62% 24% 9%
2	B	295	15% 65% 8% 26%
3	C	264	9% 75% 5% 19%

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Mol	Chain	Length	Quality of chain
4	D	255	
5	E	281	
6	F	263	
7	G	204	
8	H	249	
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	

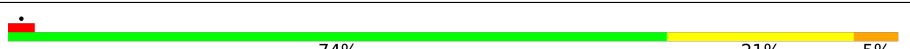
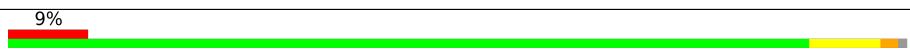
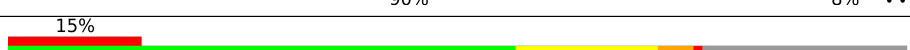
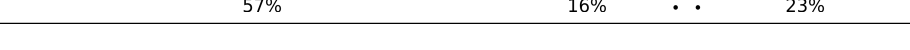
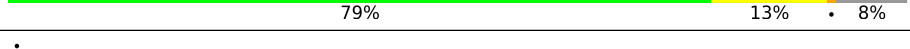
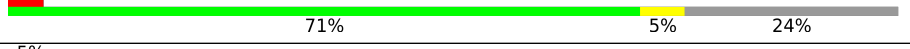
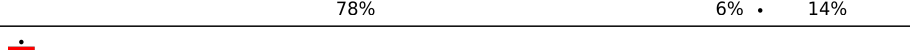
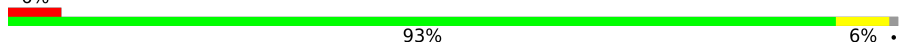
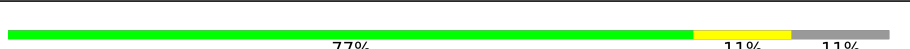
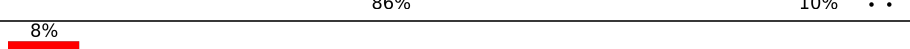
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Mol	Chain	Length	Quality of chain
29	c	84	
30	d	69	
31	e	56	
32	f	133	
33	g	156	
34	h	317	
35	1	253	
36	5	3594	
37	7	119	
38	8	156	
39	AA	257	
40	AB	403	
41	AC	392	
42	AD	297	
43	AE	291	
44	AF	249	
45	AG	242	
46	AH	192	
47	AI	214	
48	AJ	178	
49	AL	211	
50	AM	198	
51	AN	204	
52	AO	203	
53	AP	184	

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Mol	Chain	Length	Quality of chain
54	AQ	188	
55	AR	196	
56	AS	176	
57	AT	160	
58	AU	128	
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	

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Mol	Chain	Length	Quality of chain
79	Ap	92	 88% 10% ..
80	Ar	137	 77% 12% • 9%
81	AK	217	 96% 87% 9% • •

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		

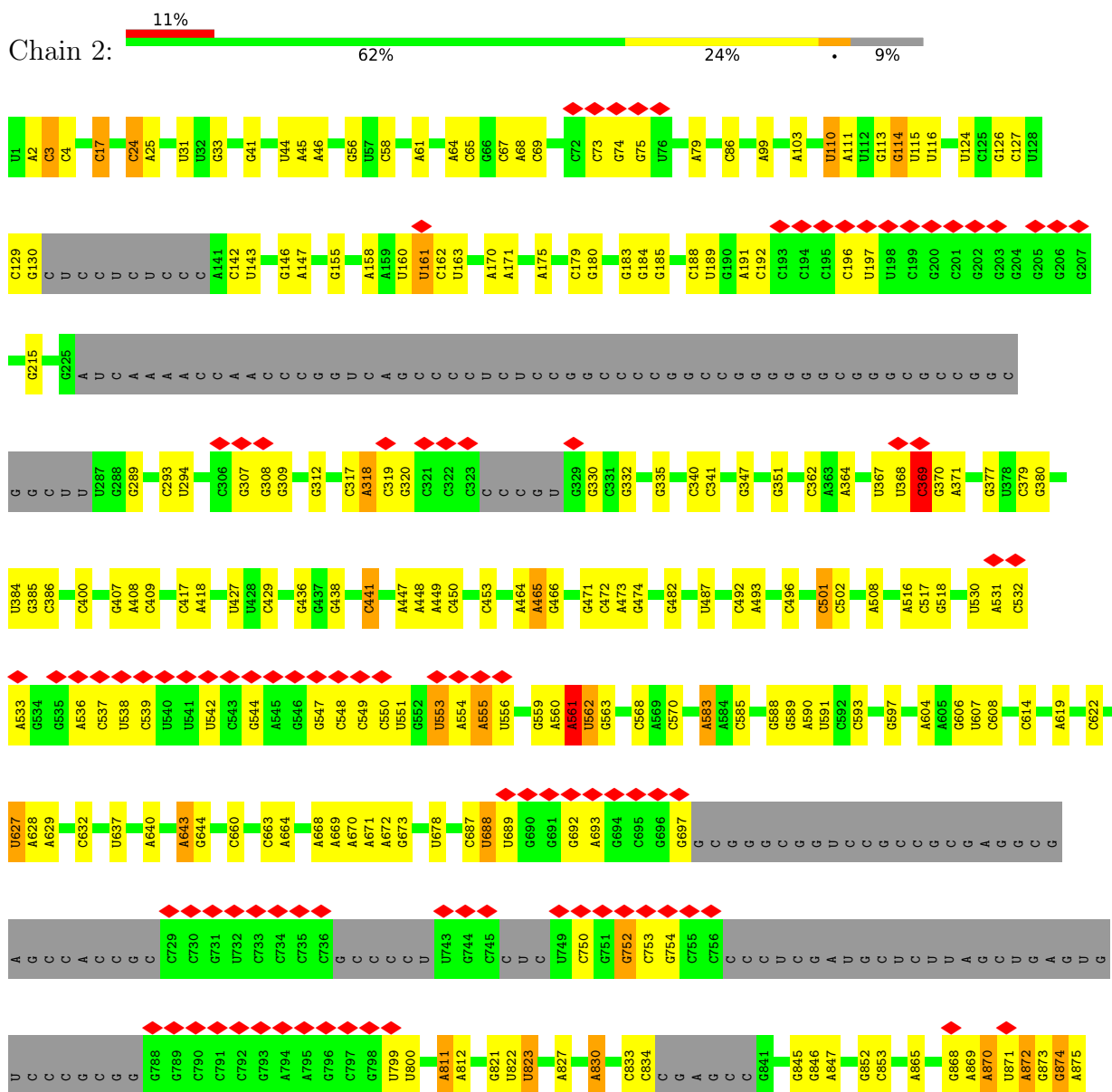
- Molecule 81 is a protein called uL1.

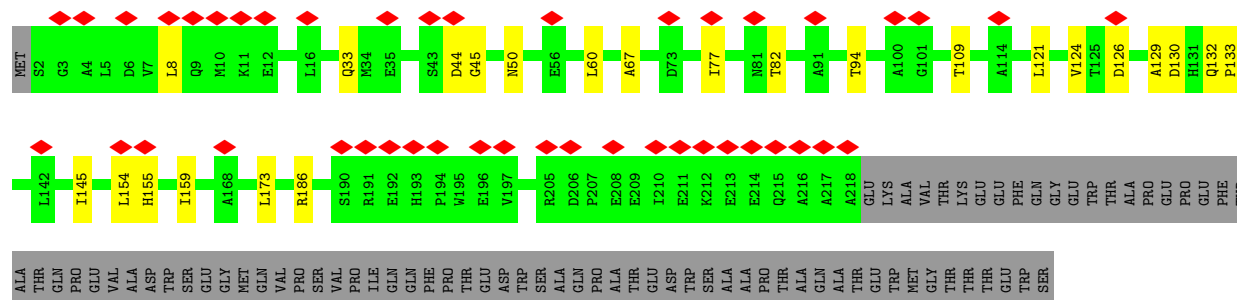
Mol	Chain	Residues	Atoms					AltConf	Trace
81	AK	212	Total	C	N	O	S	0	0
			1705	1091	306	300	8		

3 Residue-property plots

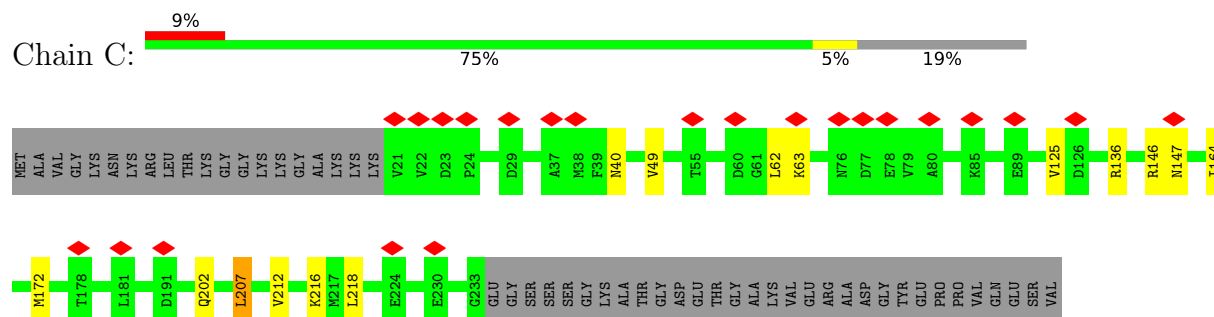
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

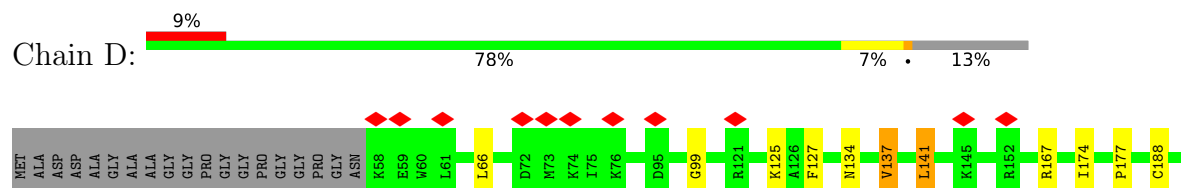




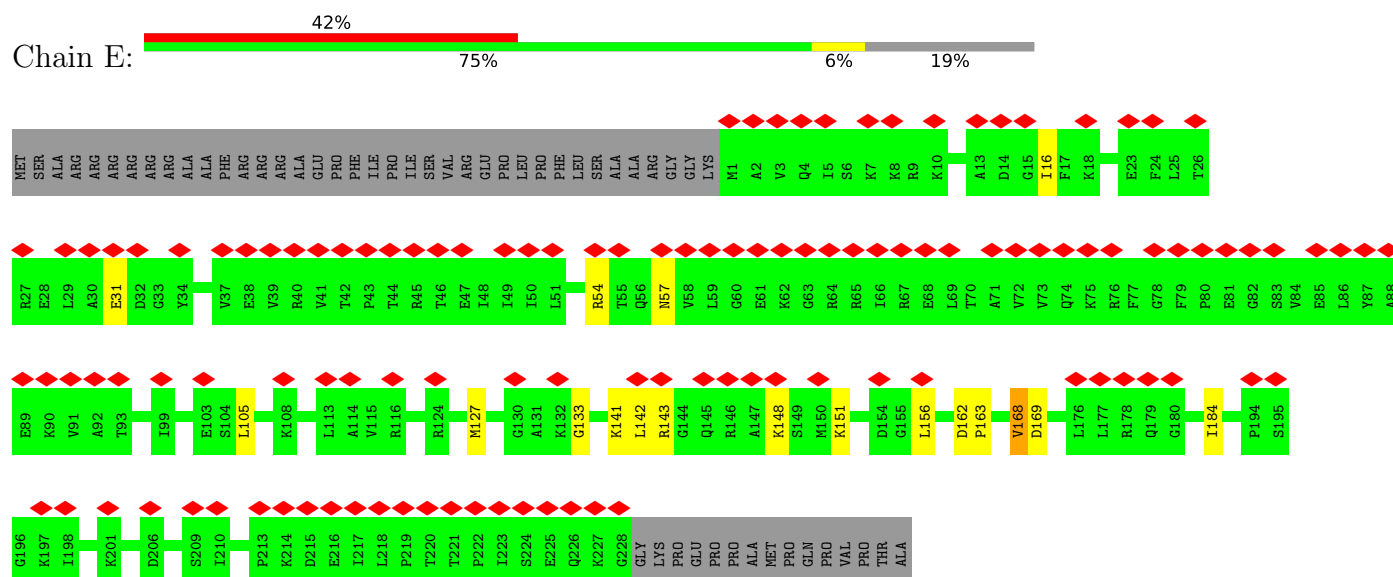
- Molecule 3: eS1



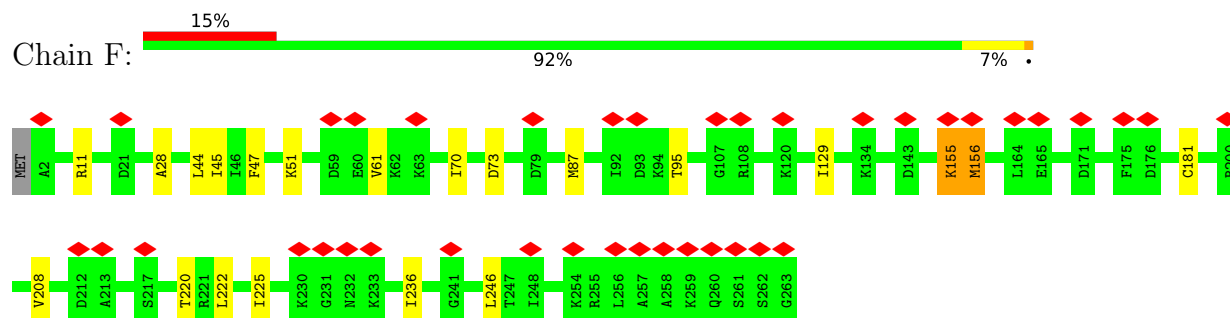
- Molecule 4: uS5



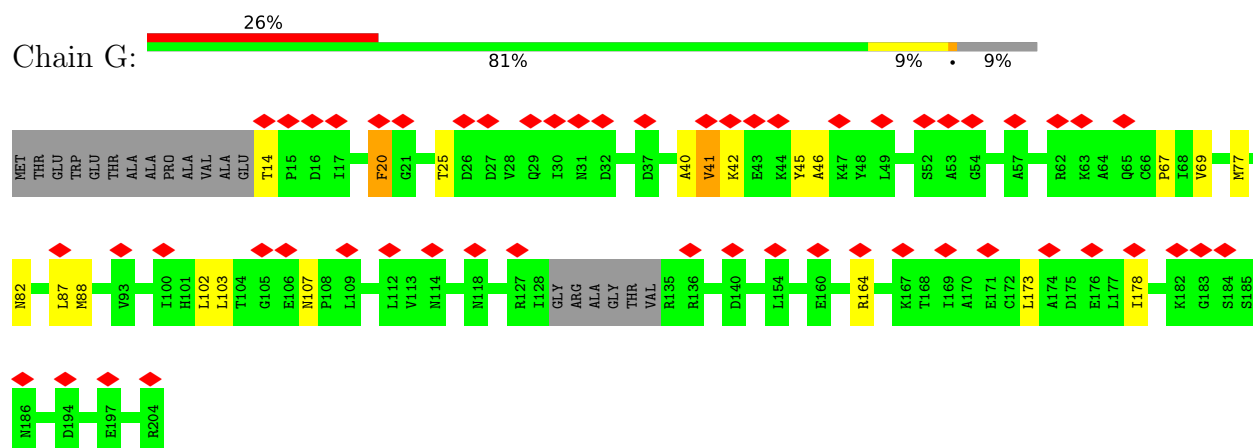
- Molecule 5: uS3



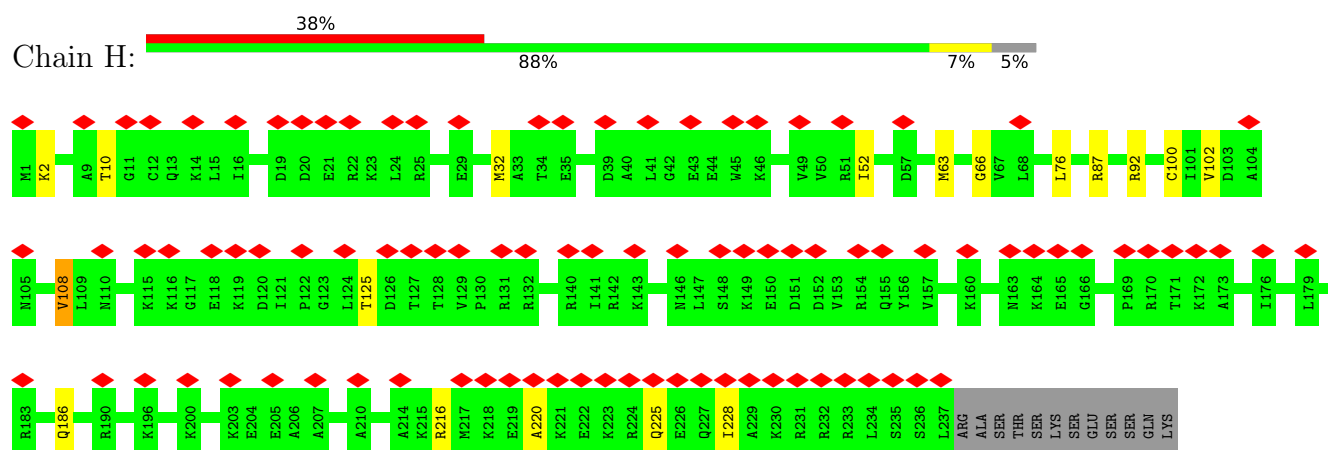
- Molecule 6: eS4



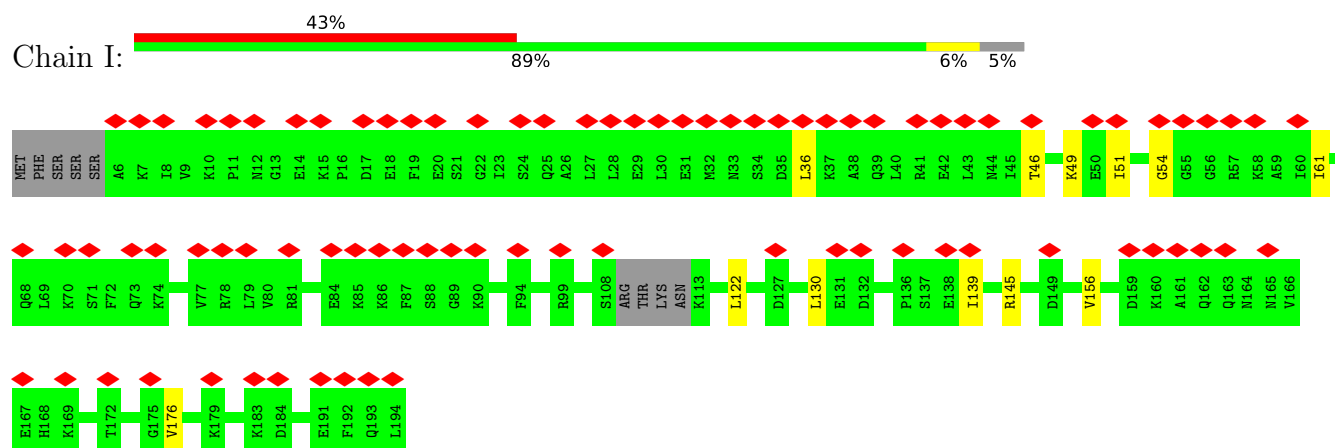
- Molecule 7: uS7



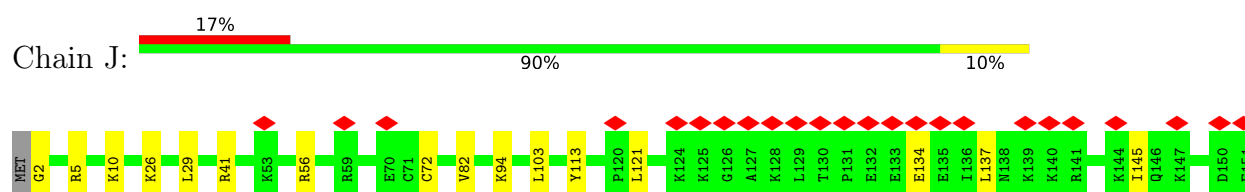
- Molecule 8: eS6

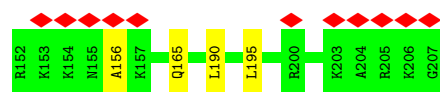


- Molecule 9: eS7

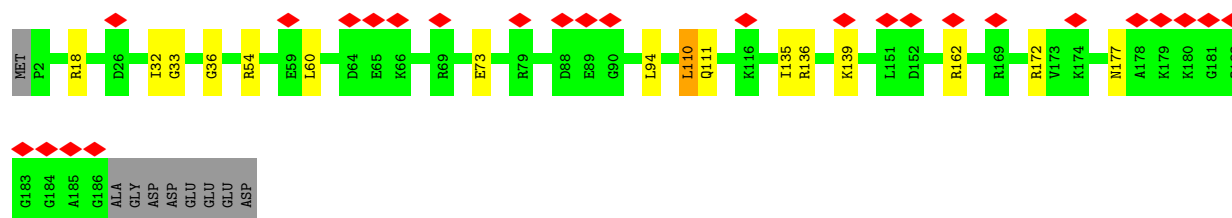
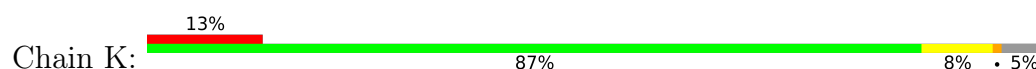


- Molecule 10: eS8

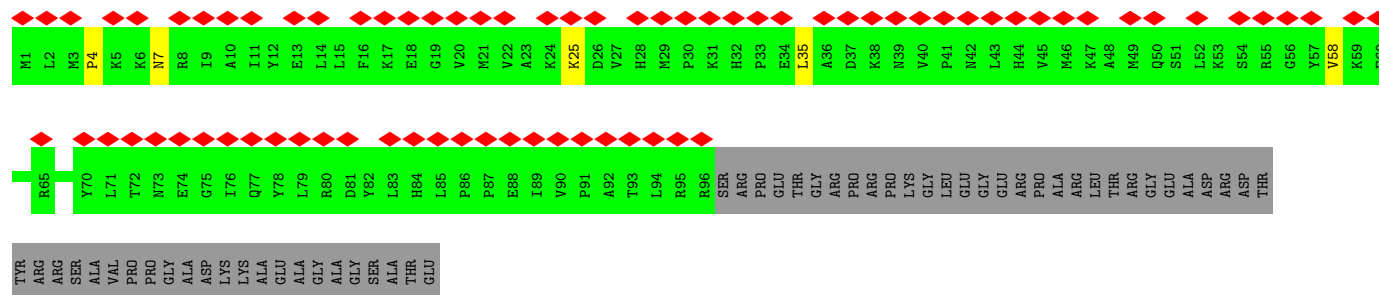




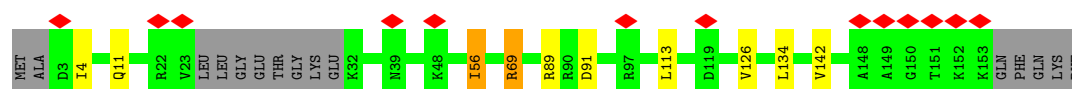
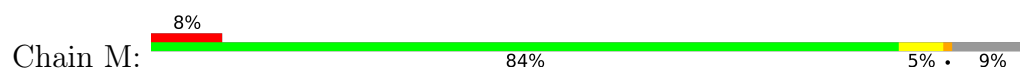
- Molecule 11: uS4



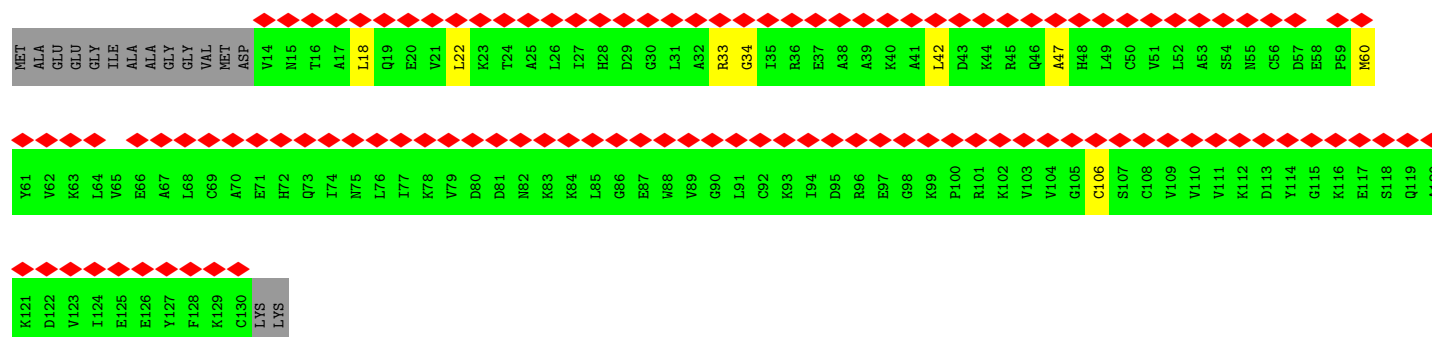
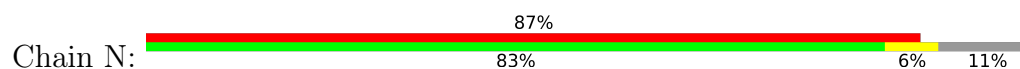
- Molecule 12: eS10



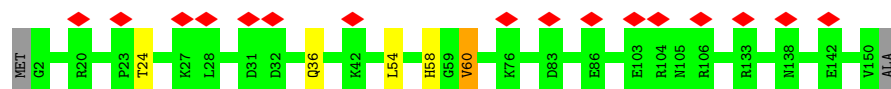
- Molecule 13: uS17



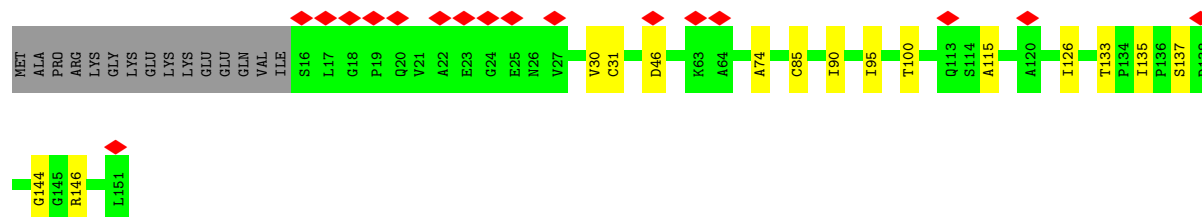
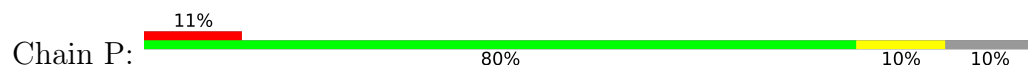
- Molecule 14: eS12



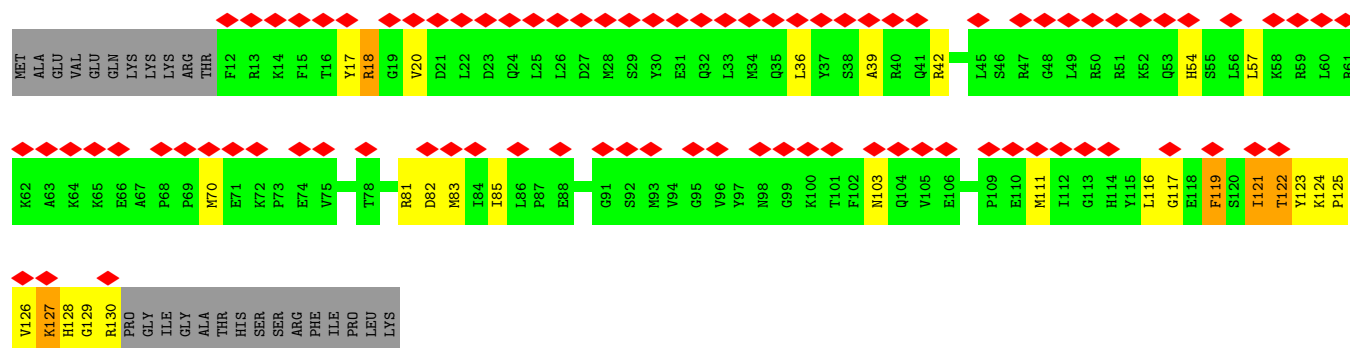
- Molecule 15: uS15



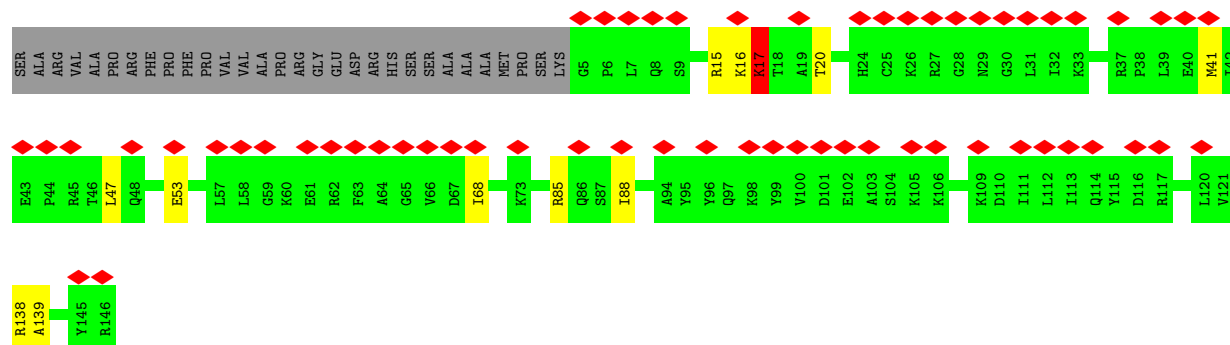
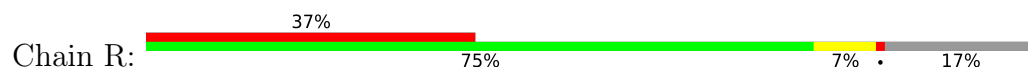
• Molecule 16: uS11



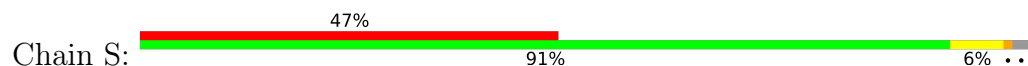
• Molecule 17: uS19

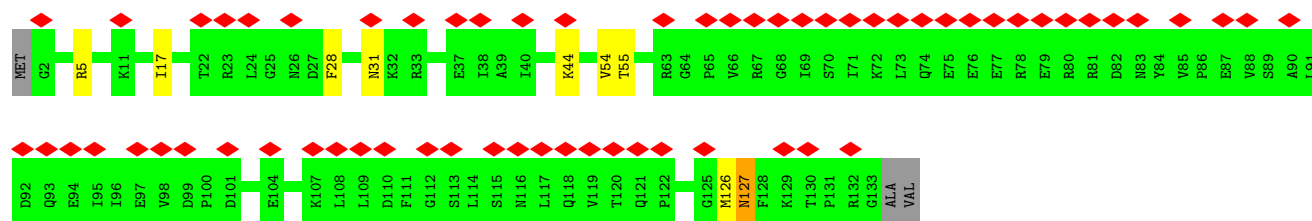


• Molecule 18: uS9

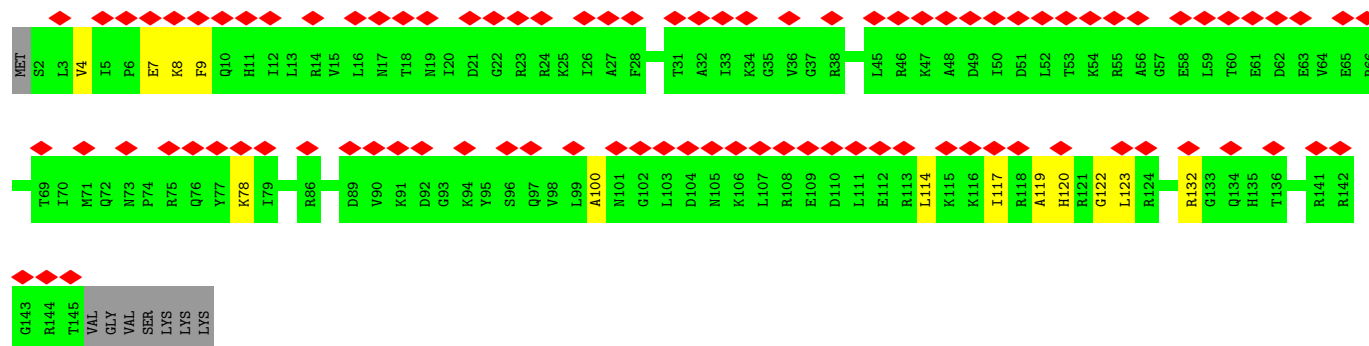
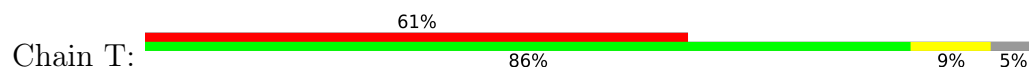


• Molecule 19: eS17

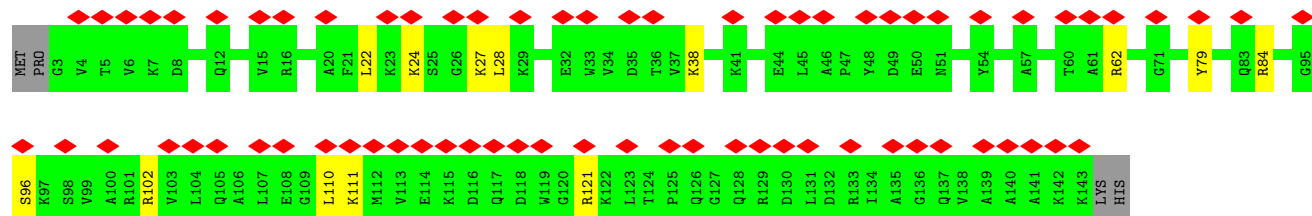
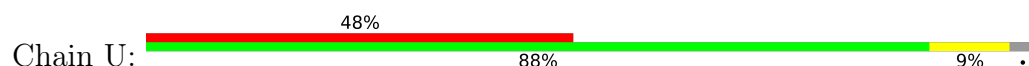




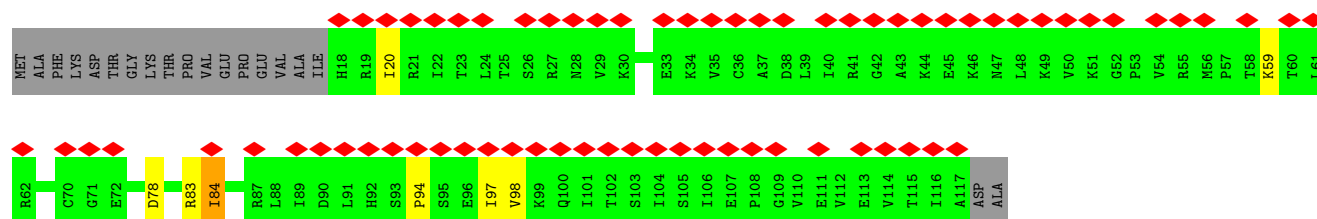
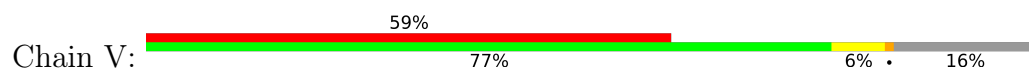
• Molecule 20: uS13



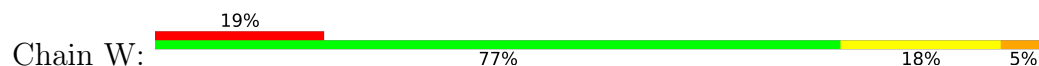
• Molecule 21: eS19

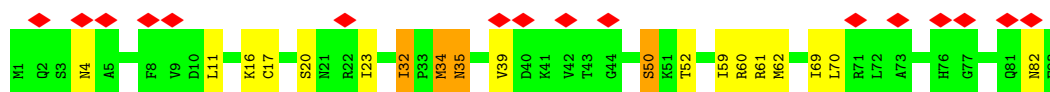


• Molecule 22: uS10

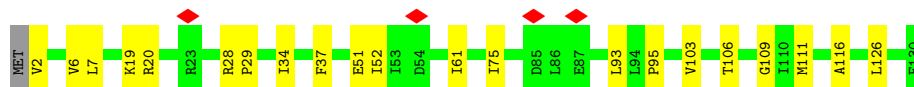
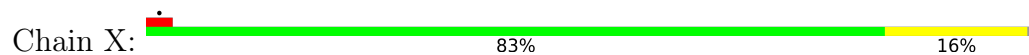


• Molecule 23: eS21

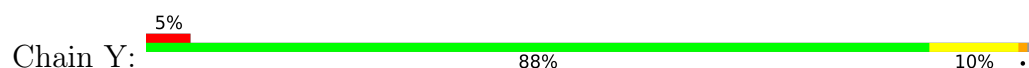




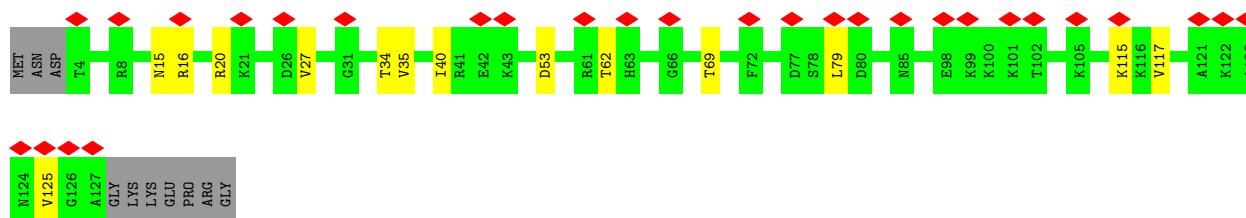
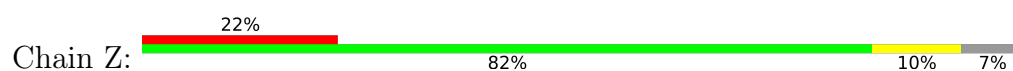
• Molecule 24: uS8



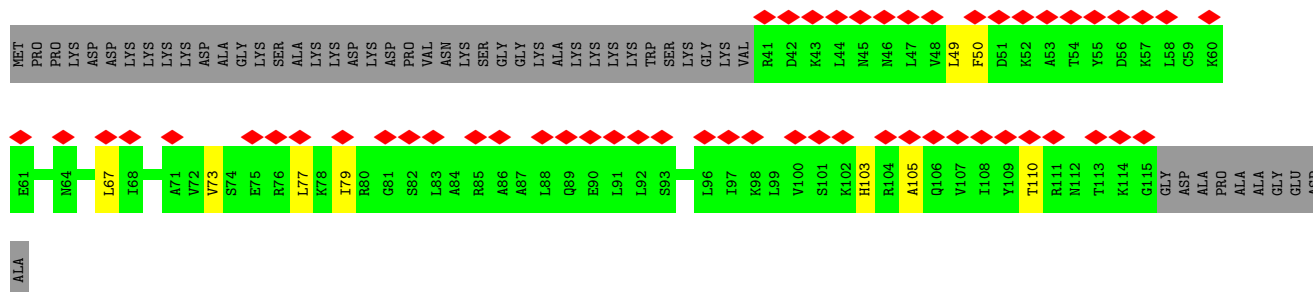
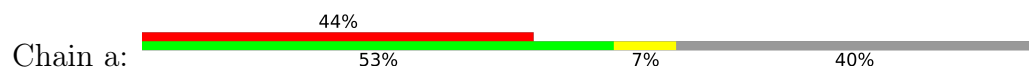
• Molecule 25: uS12



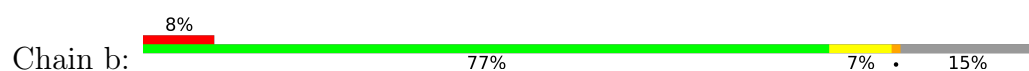
• Molecule 26: eS24



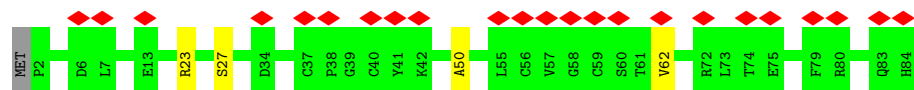
• Molecule 27: eS25



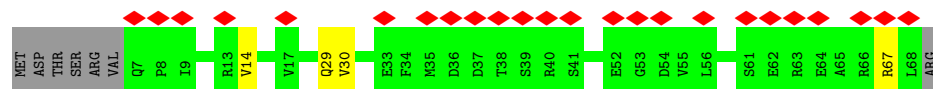
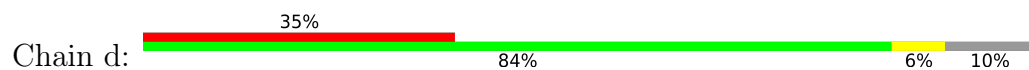
• Molecule 28: eS26



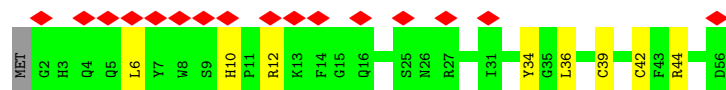
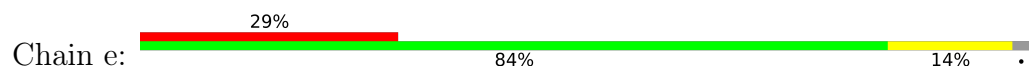
- Molecule 29: eS27



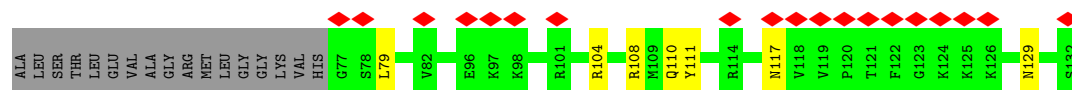
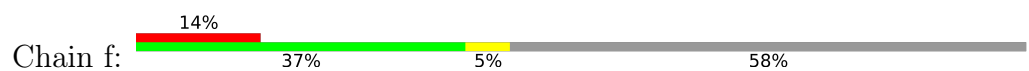
- Molecule 30: eS28



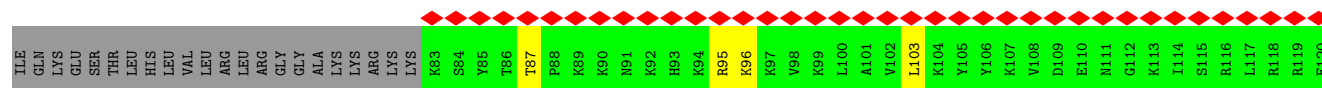
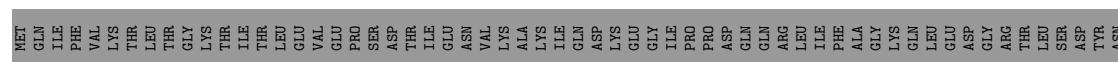
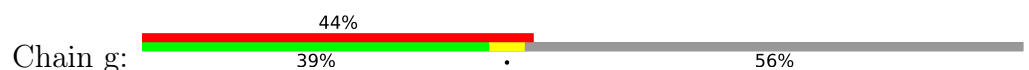
- Molecule 31: eS29



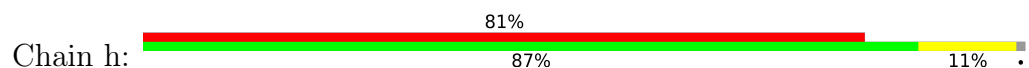
- Molecule 32: eS30

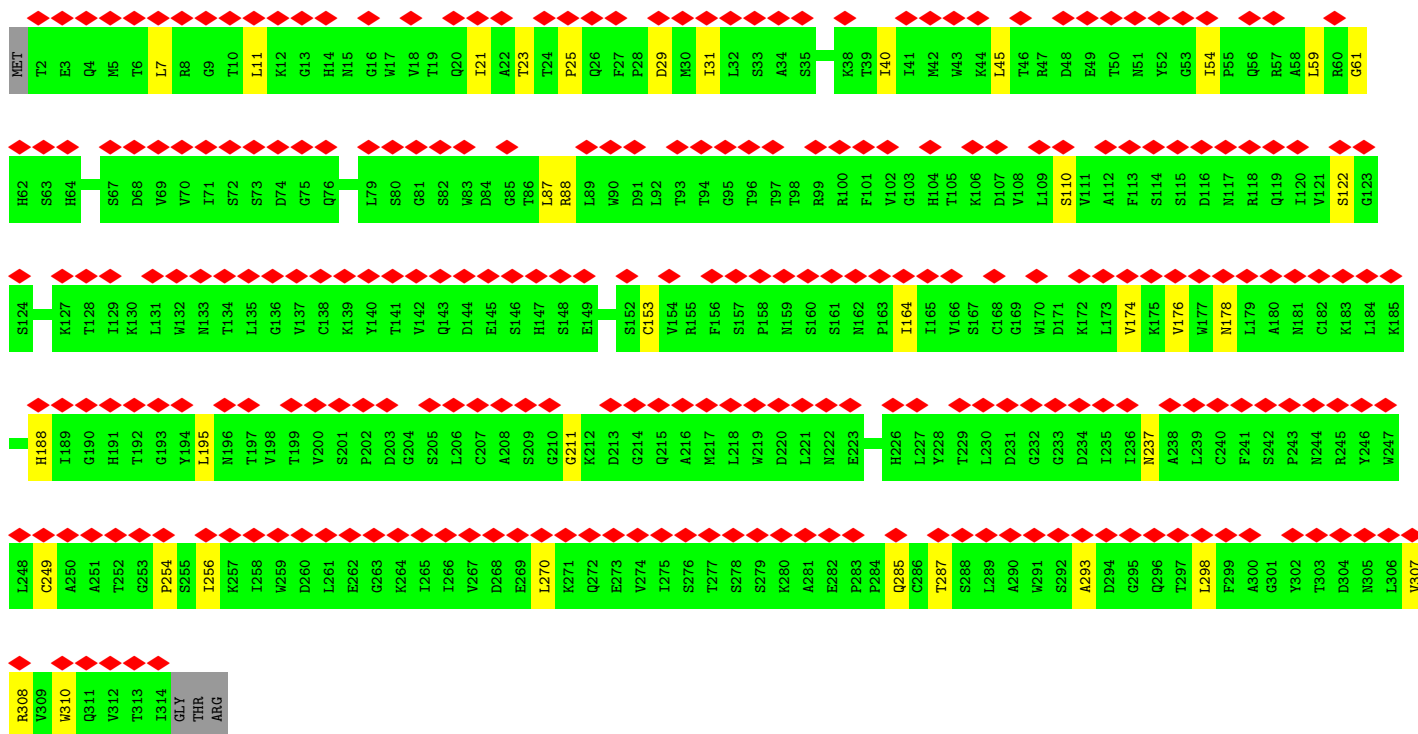


- Molecule 33: eS31

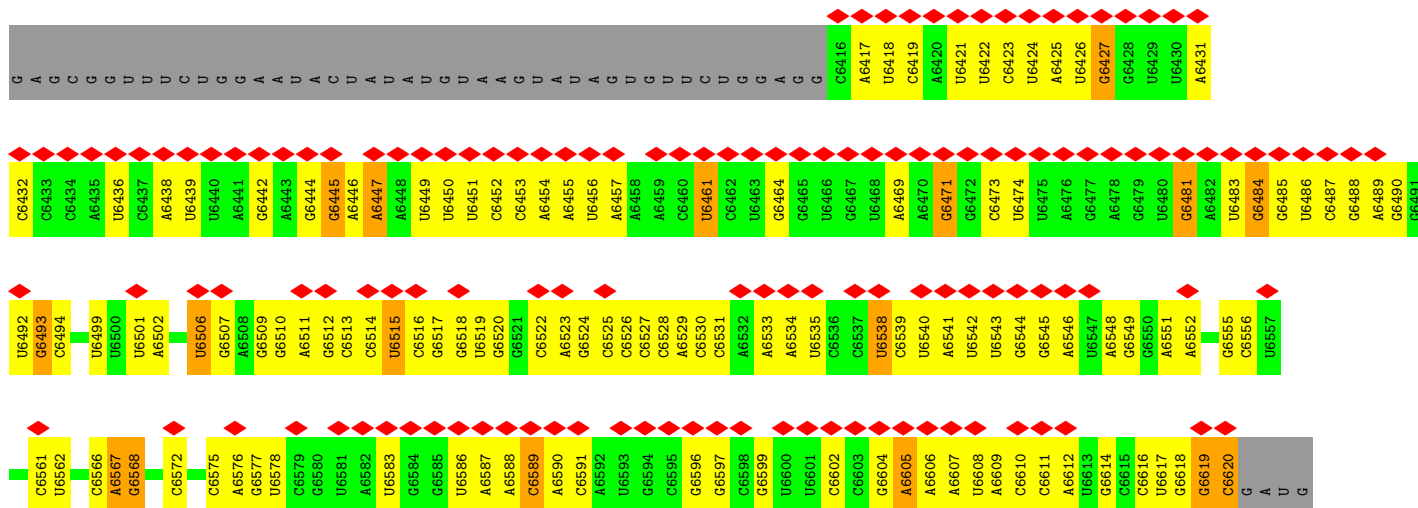


- Molecule 34: RACK1

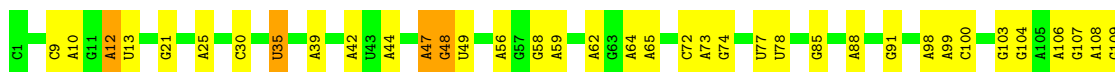




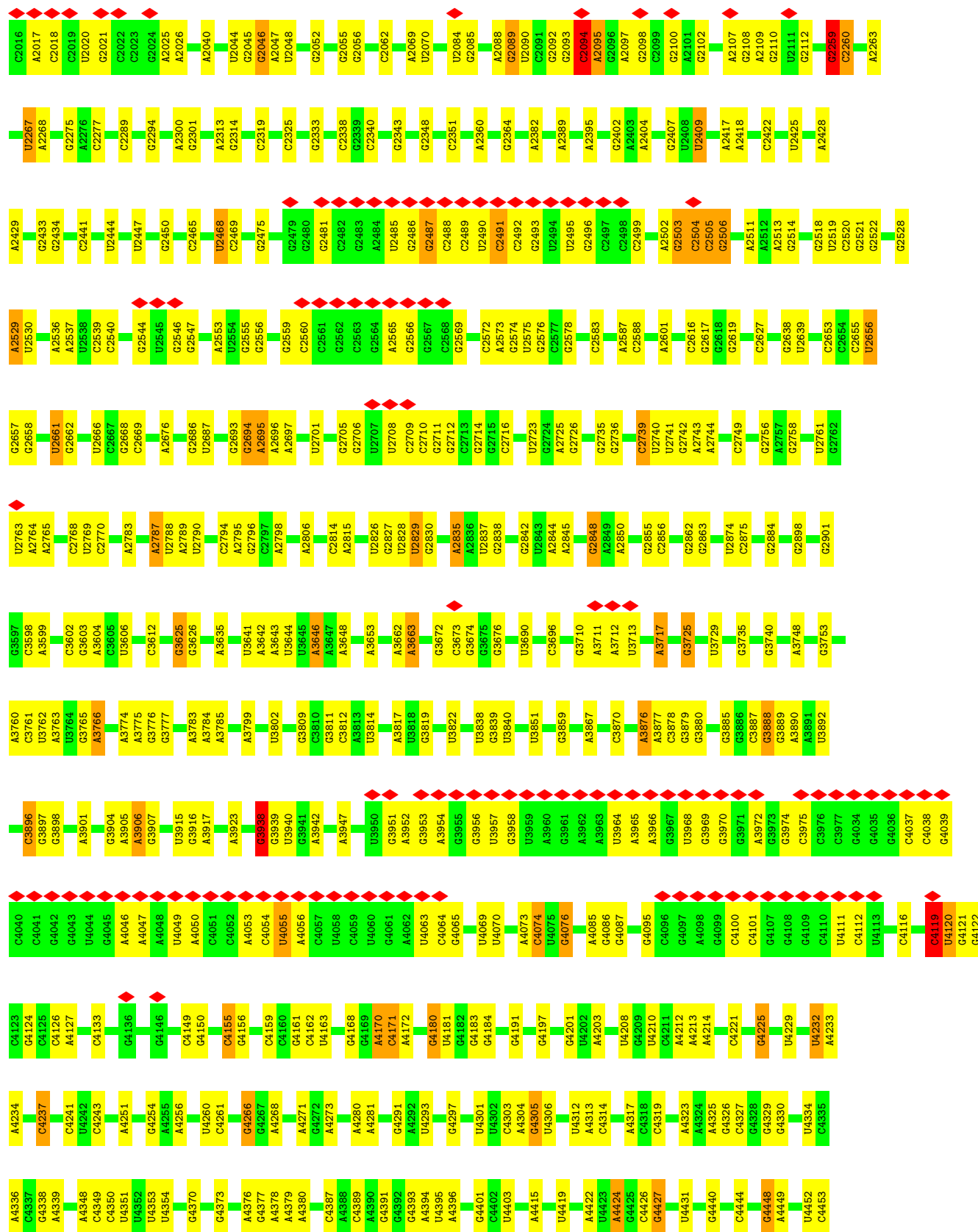
• Molecule 35: IAPV-IRES

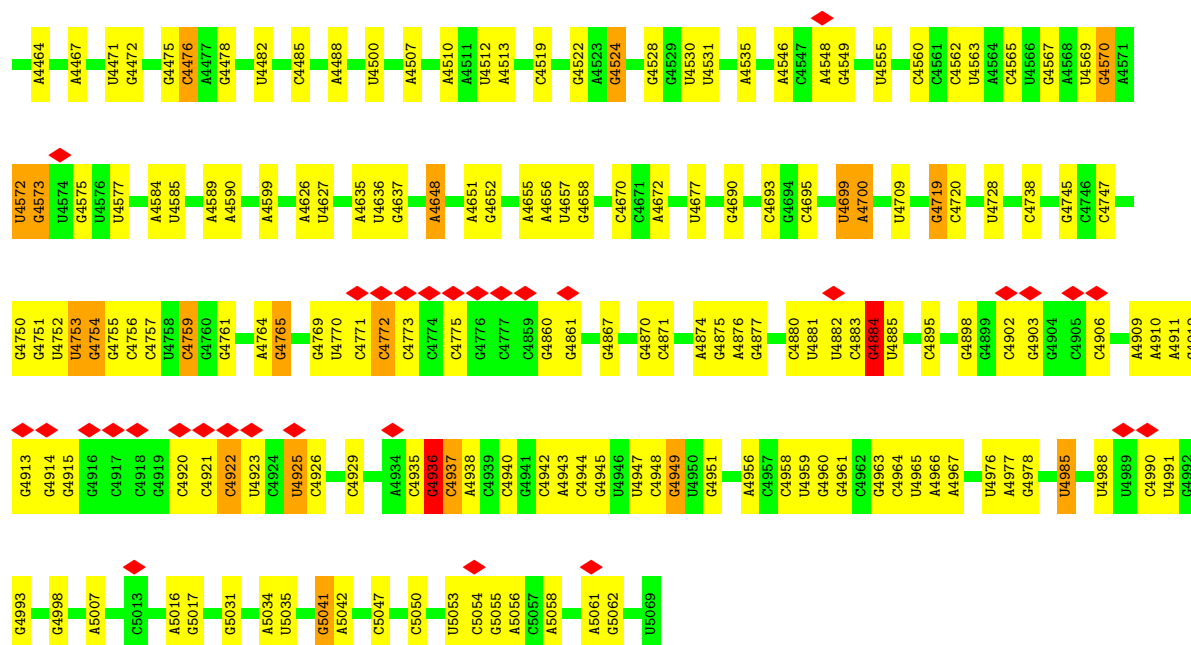


• Molecule 36: 28S rRNA

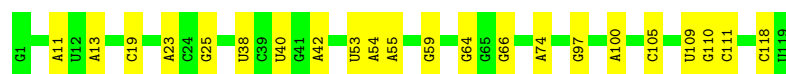






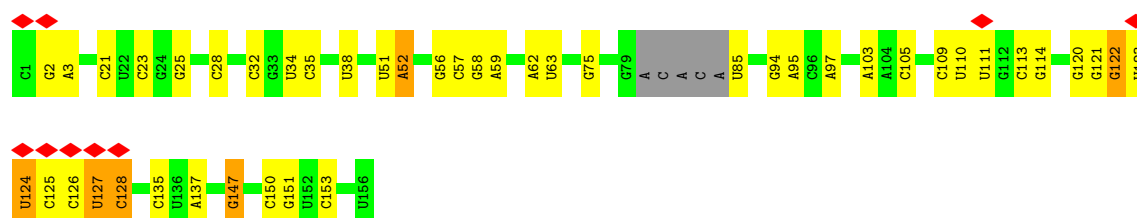


Chain 7: 82% 18%



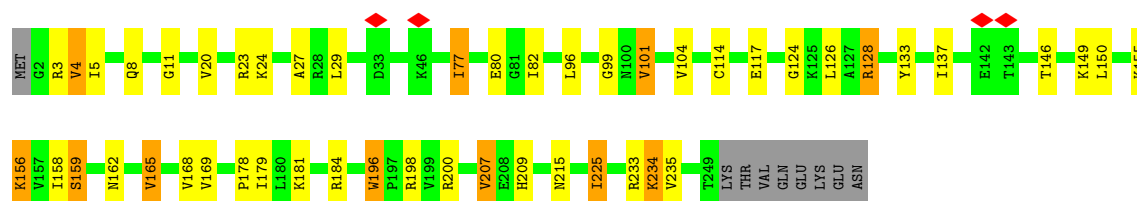
• Molecule 38: 5.8S rRNA

Chain 8: 6% 68% 25%



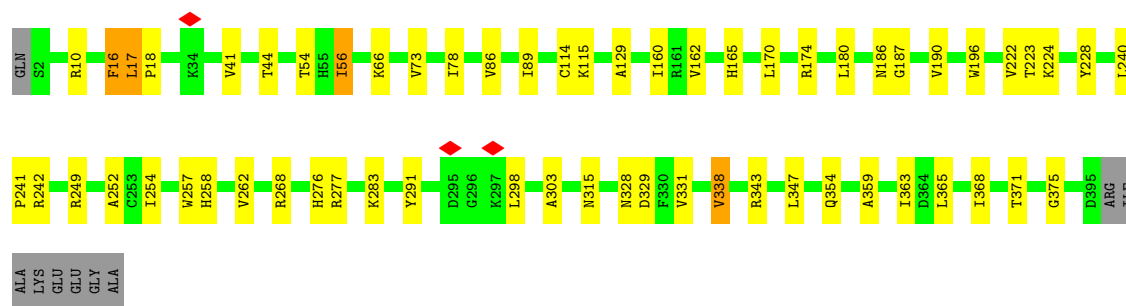
• Molecule 39: uL2

Chain AA: 77% 15%



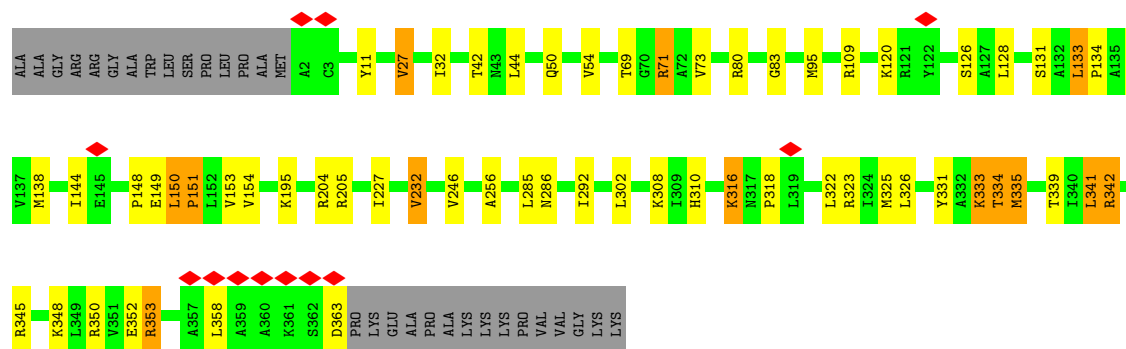
• Molecule 40: uL3

Chain AB:  83% 14% ..

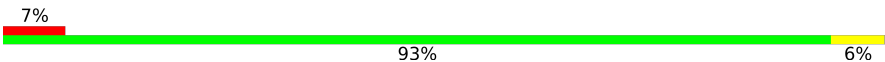


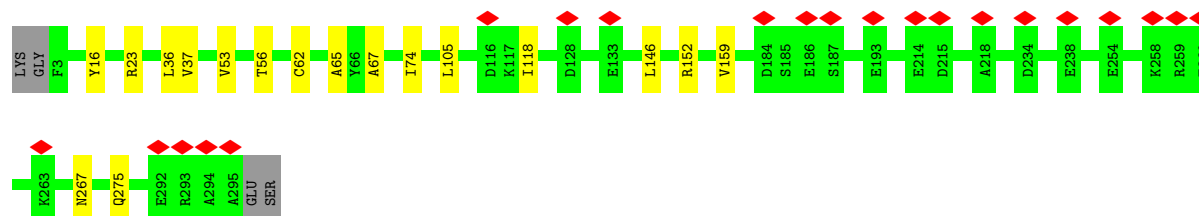
• Molecule 41: uL4

Chain AC:  77% 12% • 8%



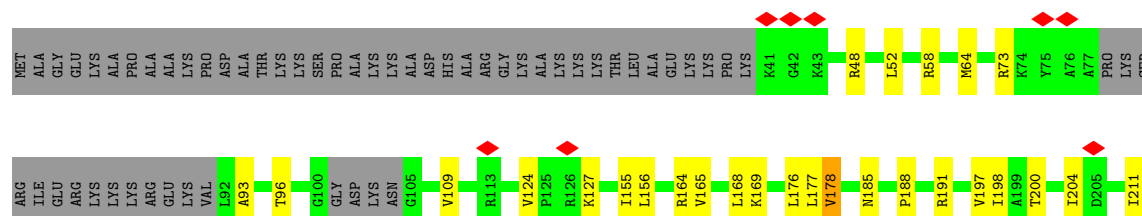
• Molecule 42: uL18

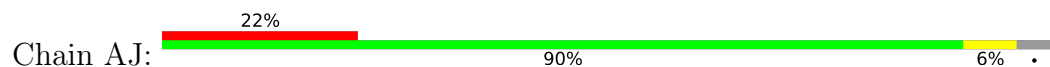
Chain AD:  7% 93% 6% •

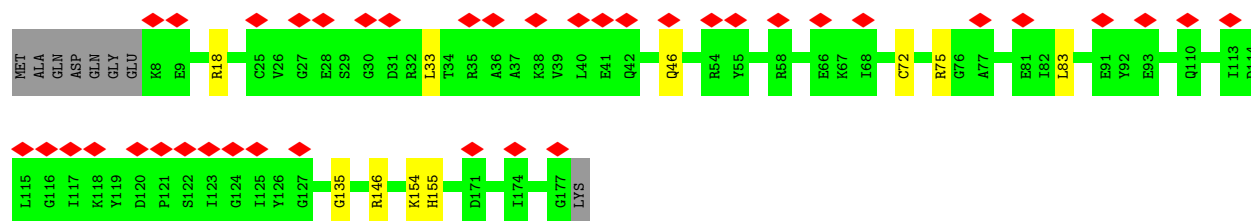


• Molecule 43: eL6

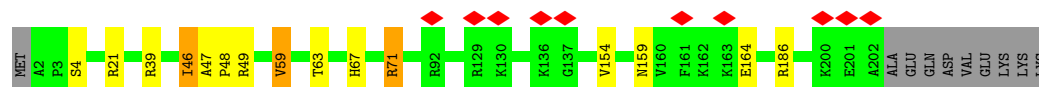
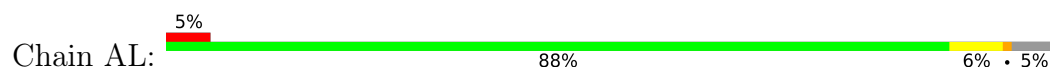
Chain AE:  62% 12% 26%



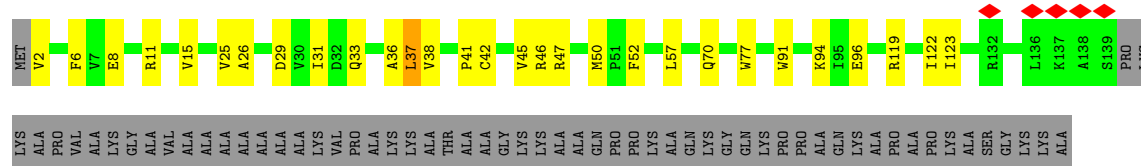




• Molecule 49: eL13



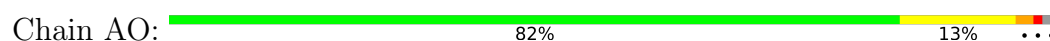
• Molecule 50: L14e



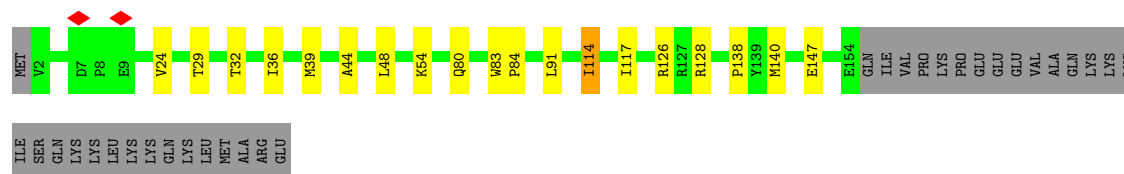
• Molecule 51: eL15



• Molecule 52: uL13

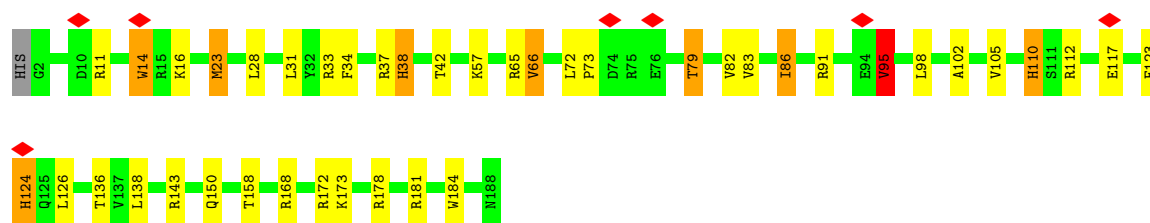


• Molecule 53: uL22



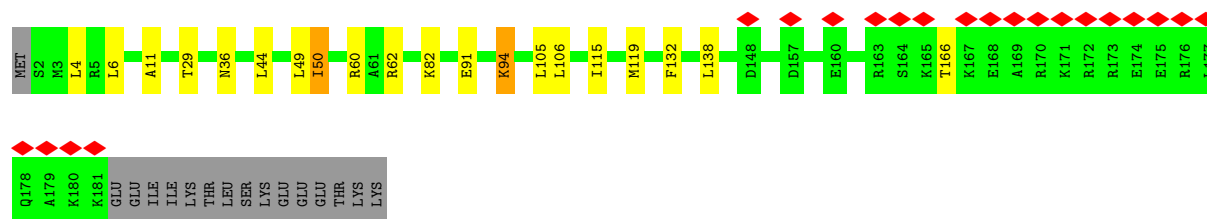
- Molecule 54: eL18

Chain AQ:  77% 18% . .



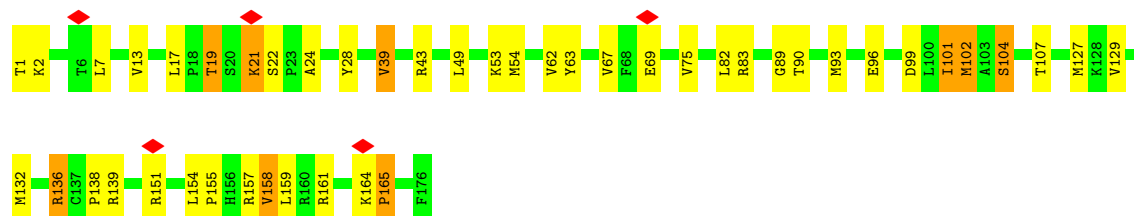
- Molecule 55: eL19

Chain AR:  11% 82% 9% 8% .



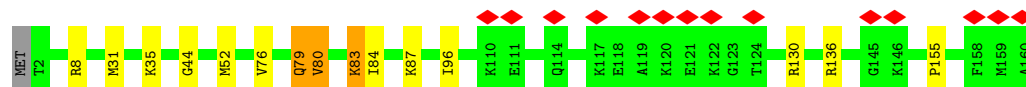
- Molecule 56: eL20

Chain AS:  74% 21% 5%



- Molecule 57: eL21

Chain AT:  9% 90% 8% . .



- Molecule 58: eL22

Chain AU:  15% 57% 16% 23% . .





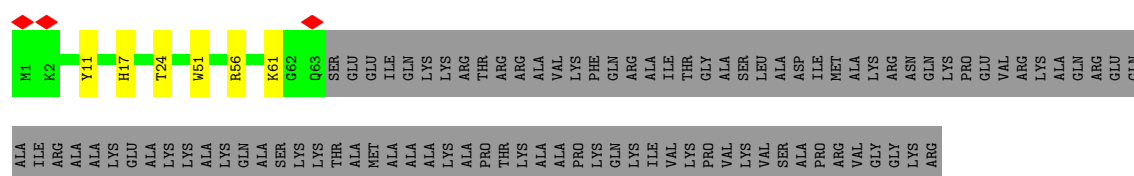
• Molecule 59: uL14

Chain AV: 79% 13% 8%



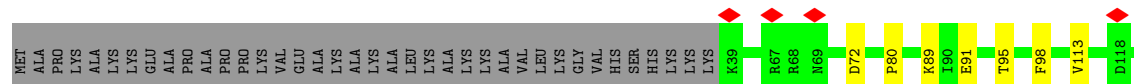
• Molecule 60: eL24

Chain AW: 36% 60%



• Molecule 61: eL23

Chain AX: 71% 5% 24%



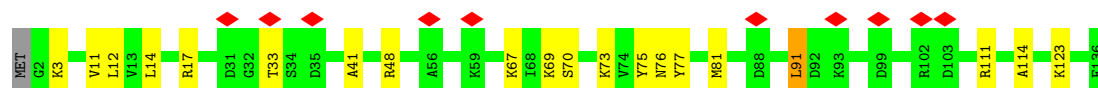
• Molecule 62: uL24

Chain AY: 5% 85% 6% 8%



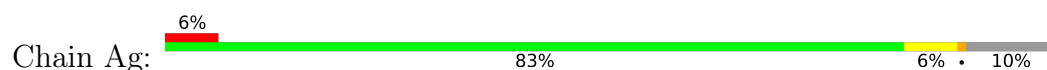
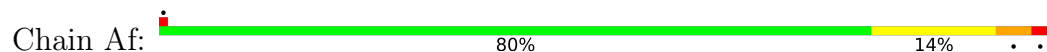
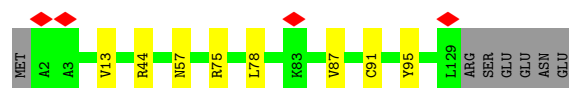
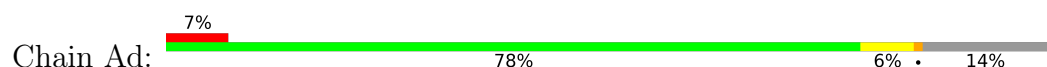
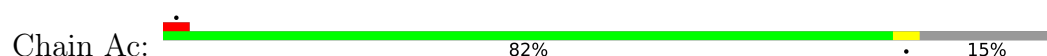
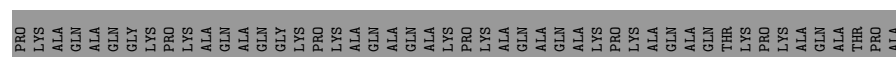
• Molecule 63: eL27

Chain AZ: 7% 85% 14% ..



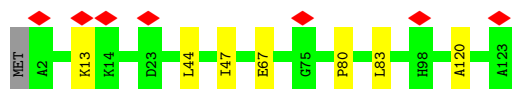
• Molecule 64: uL15

Chain Aa: 87% 11% ..

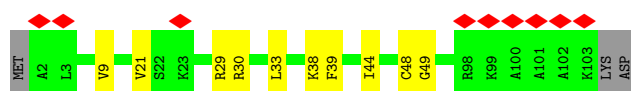
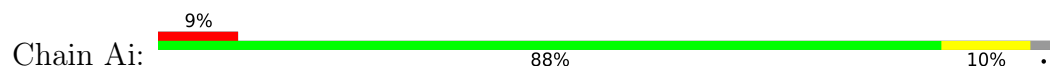




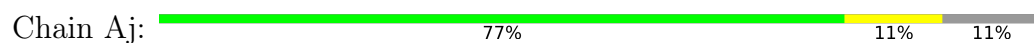
- Molecule 71: eL35



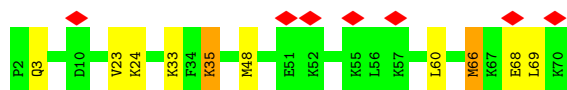
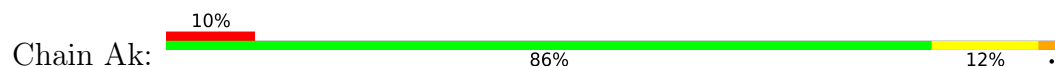
- Molecule 72: eL36



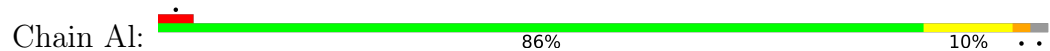
- Molecule 73: eL37



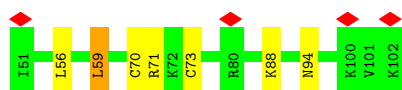
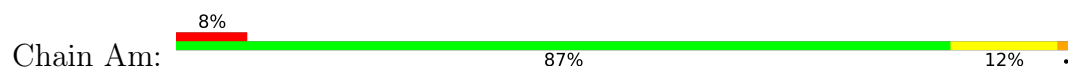
- Molecule 74: eL38



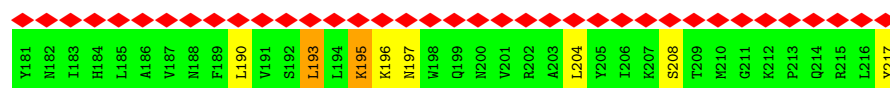
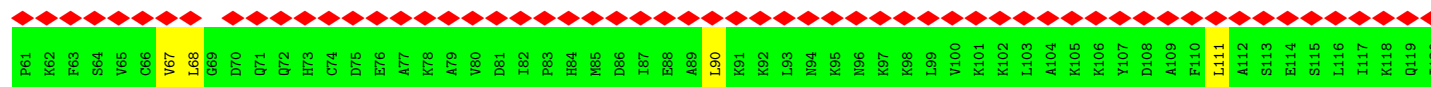
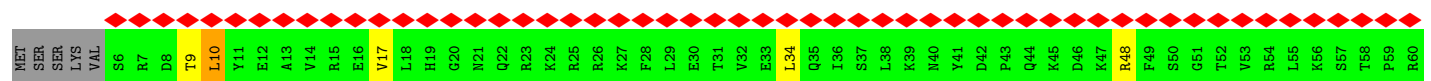
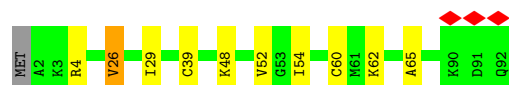
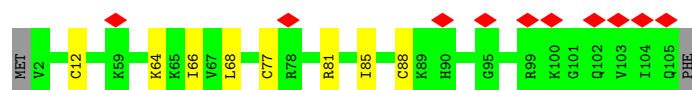
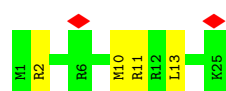
- Molecule 75: eL39



- Molecule 76: eL40



- Molecule 77: eL41



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	0.37	0/40509	0.71	22/63128 (0.0%)
2	B	1.03	0/1744	1.49	0/2371
3	C	1.02	0/1756	1.44	0/2350
4	D	1.03	0/1748	1.43	0/2362
5	E	1.05	0/1796	1.44	2/2417 (0.1%)
6	F	1.04	0/2115	1.40	0/2843
7	G	1.05	0/1492	1.56	2/2005 (0.1%)
8	H	1.05	0/1946	1.44	0/2590
9	I	1.07	0/1510	1.41	0/2022
10	J	1.00	0/1715	1.40	0/2287
11	K	1.01	0/1550	1.49	0/2069
12	L	1.04	0/834	1.40	0/1125
13	M	1.01	0/1195	1.33	0/1597
14	N	1.11	0/918	1.45	1/1233 (0.1%)
15	O	1.02	0/1226	1.52	0/1649
16	P	1.04	0/1029	1.49	1/1380 (0.1%)
17	Q	1.03	0/1009	1.38	1/1346 (0.1%)
18	R	1.04	0/1146	1.45	0/1534
19	S	1.05	0/1082	1.51	0/1452
20	T	1.05	0/1208	1.50	0/1618
21	U	1.04	0/1115	1.53	2/1493 (0.1%)
22	V	1.05	0/805	1.40	0/1081
23	W	1.07	0/638	1.47	0/855
24	X	1.02	0/1051	1.45	1/1406 (0.1%)
25	Y	1.02	0/1116	1.42	2/1490 (0.1%)
26	Z	1.03	0/1028	1.44	0/1366
27	a	1.06	0/604	1.49	0/810
28	b	1.03	0/789	1.40	0/1059
29	c	1.03	0/665	1.37	0/891
30	d	1.08	0/490	1.32	0/656
31	e	1.02	0/470	1.42	0/623
32	f	1.03	0/451	1.49	0/592
33	g	1.08	0/567	1.35	0/753
34	h	1.08	1/2493 (0.0%)	1.36	0/3394

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	1	0.39	0/4881	0.75	7/7604 (0.1%)
36	5	0.37	0/86215	0.75	50/134459 (0.0%)
37	7	0.37	0/2836	0.69	0/4421
38	8	0.36	0/3581	0.71	1/5577 (0.0%)
39	AA	1.01	0/1933	1.43	2/2592 (0.1%)
40	AB	0.98	0/3240	1.39	5/4339 (0.1%)
41	AC	0.97	0/2937	1.40	3/3946 (0.1%)
42	AD	1.00	0/2437	1.49	0/3264
43	AE	1.02	0/1762	1.39	0/2362
44	AF	0.96	0/1911	1.49	0/2549
45	AG	1.01	0/1850	1.50	0/2491
46	AH	1.02	0/1535	1.36	1/2063 (0.0%)
47	AI	0.98	0/1702	1.39	0/2272
48	AJ	1.02	0/1385	1.43	0/1852
49	AL	1.00	0/1658	1.53	0/2219
50	AM	0.99	0/1158	1.50	0/1547
51	AN	0.95	0/1746	1.42	0/2338
52	AO	0.97	0/1663	1.48	3/2223 (0.1%)
53	AP	0.97	0/1268	1.46	2/1700 (0.1%)
54	AQ	0.99	1/1557 (0.1%)	1.40	2/2086 (0.1%)
55	AR	1.00	0/1519	1.54	0/2006
56	AS	0.95	0/1498	1.36	8/2012 (0.4%)
57	AT	0.97	0/1326	1.36	0/1770
58	AU	1.00	0/832	1.37	0/1116
59	AV	1.04	0/983	1.39	0/1319
60	AW	0.95	0/541	1.40	0/720
61	AX	1.01	0/984	1.41	0/1323
62	AY	1.00	0/1132	1.47	0/1504
63	AZ	1.00	0/1130	1.45	0/1507
64	Aa	0.98	0/1191	1.45	6/1590 (0.4%)
65	Ab	0.99	0/861	1.52	0/1138
66	Ac	1.03	0/771	1.52	1/1034 (0.1%)
67	Ad	0.98	0/903	1.42	0/1216
68	Ae	0.97	0/1071	1.44	0/1429
69	Af	0.97	0/895	1.35	2/1198 (0.2%)
70	Ag	1.02	0/916	1.47	2/1220 (0.2%)
71	Ah	0.99	0/1021	1.55	0/1348
72	Ai	0.99	0/841	1.52	0/1112
73	Aj	0.93	0/720	1.44	0/952
74	Ak	1.00	0/575	1.40	0/759
75	Al	0.94	0/459	1.37	0/608
76	Am	1.01	0/435	1.43	0/575
77	An	0.88	0/240	1.52	0/305

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	Ao	0.98	0/864	1.41	0/1140
79	Ap	1.01	0/718	1.56	0/953
80	Ar	1.01	0/1010	1.48	2/1354 (0.1%)
81	AK	1.09	0/1733	1.39	3/2324 (0.1%)
All	All	0.71	2/232234 (0.0%)	1.05	134/341283 (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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	h	54	ILE	N-CA	5.41	1.50	1.45
54	AQ	95	VAL	N-CA	5.17	1.49	1.45

The worst 5 of 134 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
69	Af	106	TYR	CB-CA-C	9.16	128.67	111.64
1	2	870	A	C4'-C3'-O3'	8.96	122.84	109.40
36	5	47	A	C4'-C3'-O3'	8.92	122.78	109.40
1	2	688	U	C2'-C3'-O3'	8.87	122.80	109.50
36	5	2046	G	C2'-C3'-O3'	8.85	122.78	109.50

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 ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	36229	0	18300	132	0
2	B	1706	0	1697	11	0
3	C	1729	0	1803	7	0
4	D	1712	0	1808	15	0
5	E	1768	0	1866	9	0
6	F	2073	0	2173	16	0
7	G	1471	0	1522	10	0
8	H	1923	0	2089	13	0
9	I	1488	0	1582	7	0
10	J	1686	0	1772	9	0
11	K	1525	0	1640	12	0
12	L	810	0	836	2	0
13	M	1175	0	1249	5	0
14	N	908	0	939	3	0
15	O	1202	0	1289	2	0
16	P	1016	0	1039	8	0
17	Q	990	0	1038	25	0
18	R	1128	0	1195	10	0
19	S	1068	0	1121	5	0
20	T	1190	0	1249	11	0
21	U	1097	0	1130	9	0
22	V	795	0	862	5	0
23	W	630	0	631	11	0
24	X	1034	0	1080	10	0
25	Y	1098	0	1167	10	0
26	Z	1011	0	1083	9	0
27	a	598	0	656	6	0
28	b	776	0	821	5	0
29	c	651	0	672	1	0
30	d	488	0	514	2	0
31	e	459	0	452	7	0
32	f	447	0	495	5	0
33	g	555	0	567	4	0
34	h	2436	0	2393	21	0
35	1	4366	0	2204	21	0
36	5	77074	0	38936	247	0
37	7	2538	0	1286	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	8	3208	0	1629	15	0
39	AA	1895	0	1984	40	0
40	AB	3172	0	3310	34	0
41	AC	2883	0	3053	47	0
42	AD	2391	0	2424	11	0
43	AE	1729	0	1887	23	0
44	AF	1875	0	1995	19	0
45	AG	1819	0	1956	17	0
46	AH	1516	0	1597	17	0
47	AI	1664	0	1712	11	0
48	AJ	1362	0	1399	5	0
49	AL	1627	0	1743	12	0
50	AM	1137	0	1211	21	0
51	AN	1701	0	1749	15	0
52	AO	1631	0	1780	28	0
53	AP	1242	0	1274	10	0
54	AQ	1526	0	1623	38	0
55	AR	1503	0	1657	11	0
56	AS	1457	0	1490	28	0
57	AT	1298	0	1366	8	0
58	AU	818	0	838	24	0
59	AV	969	0	1031	10	0
60	AW	528	0	541	6	0
61	AX	967	0	1040	3	0
62	AY	1115	0	1205	6	0
63	AZ	1107	0	1182	12	0
64	Aa	1162	0	1209	9	0
65	Ab	848	0	920	3	0
66	Ac	761	0	794	1	0
67	Ad	888	0	930	3	0
68	Ae	1053	0	1147	3	0
69	Af	876	0	912	16	0
70	Ag	906	0	1002	7	0
71	Ah	1013	0	1147	3	0
72	Ai	830	0	916	7	0
73	Aj	705	0	741	6	0
74	Ak	569	0	634	5	0
75	Al	447	0	480	6	0
76	Am	429	0	469	6	0
77	An	239	0	289	4	0
78	Ao	851	0	924	5	0
79	Ap	708	0	760	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	Ar	994	0	1051	9	0
81	AK	1705	0	1810	12	0
All	All	215974	0	159967	1020	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 1020 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:1276:C:H2'	36:5:1277:G:H5''	1.46	0.98
58:AU:56:LEU:HB3	58:AU:61:VAL:HG13	1.57	0.86
52:AO:110:PRO:HB2	52:AO:111:PRO:HD3	1.56	0.86
52:AO:37:ARG:HG3	52:AO:108:ILE:HG13	1.58	0.86
58:AU:47:ILE:HG13	58:AU:63:ILE:HD11	1.60	0.83

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	215/295 (73%)	196 (91%)	17 (8%)	2 (1%)	14	44
3	C	211/264 (80%)	188 (89%)	23 (11%)	0	100	100
4	D	219/255 (86%)	199 (91%)	18 (8%)	2 (1%)	14	44
5	E	226/281 (80%)	209 (92%)	17 (8%)	0	100	100
6	F	260/263 (99%)	239 (92%)	20 (8%)	1 (0%)	30	61
7	G	181/204 (89%)	169 (93%)	10 (6%)	2 (1%)	11	39
8	H	235/249 (94%)	210 (89%)	25 (11%)	0	100	100
9	I	181/194 (93%)	169 (93%)	11 (6%)	1 (1%)	21	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	204/207 (99%)	187 (92%)	15 (7%)	2 (1%)	12	41
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%)	18	49
19	S	130/135 (96%)	120 (92%)	9 (7%)	1 (1%)	16	47
20	T	142/152 (93%)	125 (88%)	15 (11%)	2 (1%)	9	34
21	U	139/145 (96%)	126 (91%)	12 (9%)	1 (1%)	18	49
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	47
25	Y	139/143 (97%)	129 (93%)	10 (7%)	0	100	100
26	Z	122/134 (91%)	113 (93%)	9 (7%)	0	100	100
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%)	10	37
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	47
40	AB	392/403 (97%)	362 (92%)	30 (8%)	0	100	100
41	AC	360/392 (92%)	337 (94%)	20 (6%)	3 (1%)	16	47
42	AD	291/297 (98%)	270 (93%)	20 (7%)	1 (0%)	36	67
43	AE	208/291 (72%)	184 (88%)	23 (11%)	1 (0%)	24	57
44	AF	223/249 (90%)	211 (95%)	11 (5%)	1 (0%)	30	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	12	41
48	AJ	168/178 (94%)	159 (95%)	8 (5%)	1 (1%)	21	52
49	AL	199/211 (94%)	191 (96%)	7 (4%)	1 (0%)	24	57
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%)	24	57
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%)	9	35
58	AU	97/128 (76%)	86 (89%)	10 (10%)	1 (1%)	12	41
59	AV	127/140 (91%)	120 (94%)	6 (5%)	1 (1%)	16	47
60	AW	61/157 (39%)	57 (93%)	4 (7%)	0	100	100
61	AX	116/156 (74%)	110 (95%)	6 (5%)	0	100	100
62	AY	132/145 (91%)	126 (96%)	6 (4%)	0	100	100
63	AZ	133/136 (98%)	124 (93%)	8 (6%)	1 (1%)	16	47
64	Aa	145/148 (98%)	132 (91%)	11 (8%)	2 (1%)	9	34
65	Ab	100/226 (44%)	94 (94%)	5 (5%)	1 (1%)	12	41
66	Ac	96/115 (84%)	91 (95%)	5 (5%)	0	100	100
67	Ad	105/125 (84%)	97 (92%)	7 (7%)	1 (1%)	12	41
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%)	10	37
74	Ak	67/69 (97%)	63 (94%)	3 (4%)	1 (2%)	8	32
75	Al	48/51 (94%)	44 (92%)	4 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
76	Am	50/52 (96%)	49 (98%)	0	1 (2%)	6	25
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%)	26	57

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%)	176 (98%)	4 (2%)	45	71
3	C	194/231 (84%)	189 (97%)	5 (3%)	40	68
4	D	186/205 (91%)	182 (98%)	4 (2%)	45	71
5	E	190/232 (82%)	186 (98%)	4 (2%)	47	71
6	F	223/225 (99%)	219 (98%)	4 (2%)	51	73
7	G	158/170 (93%)	153 (97%)	5 (3%)	34	64
8	H	207/218 (95%)	206 (100%)	1 (0%)	81	85
9	I	165/174 (95%)	164 (99%)	1 (1%)	78	83
10	J	178/179 (99%)	174 (98%)	4 (2%)	45	71
11	K	161/168 (96%)	160 (99%)	1 (1%)	78	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	L	87/125 (70%)	85 (98%)	2 (2%)	44	70
13	M	130/142 (92%)	126 (97%)	4 (3%)	35	64
14	N	99/108 (92%)	97 (98%)	2 (2%)	48	72
15	O	130/131 (99%)	128 (98%)	2 (2%)	57	75
16	P	106/119 (89%)	105 (99%)	1 (1%)	70	80
17	Q	108/130 (83%)	104 (96%)	4 (4%)	30	61
18	R	117/140 (84%)	116 (99%)	1 (1%)	70	80
19	S	119/121 (98%)	117 (98%)	2 (2%)	53	74
20	T	125/132 (95%)	125 (100%)	0	100	100
21	U	111/116 (96%)	110 (99%)	1 (1%)	70	80
22	V	92/107 (86%)	91 (99%)	1 (1%)	65	78
23	W	68/68 (100%)	60 (88%)	8 (12%)	5	21
24	X	112/113 (99%)	109 (97%)	3 (3%)	39	67
25	Y	113/114 (99%)	110 (97%)	3 (3%)	39	67
26	Z	107/115 (93%)	106 (99%)	1 (1%)	70	80
27	a	66/103 (64%)	65 (98%)	1 (2%)	57	75
28	b	85/99 (86%)	84 (99%)	1 (1%)	63	78
29	c	75/76 (99%)	74 (99%)	1 (1%)	61	77
30	d	55/62 (89%)	55 (100%)	0	100	100
31	e	48/49 (98%)	47 (98%)	1 (2%)	47	71
32	f	46/106 (43%)	46 (100%)	0	100	100
33	g	61/140 (44%)	60 (98%)	1 (2%)	55	75
34	h	272/275 (99%)	271 (100%)	1 (0%)	84	86
39	AA	189/199 (95%)	176 (93%)	13 (7%)	14	41
40	AB	342/348 (98%)	330 (96%)	12 (4%)	32	62
41	AC	302/323 (94%)	279 (92%)	23 (8%)	12	39
42	AD	247/250 (99%)	244 (99%)	3 (1%)	63	78
43	AE	190/251 (76%)	184 (97%)	6 (3%)	34	64
44	AF	196/218 (90%)	190 (97%)	6 (3%)	35	64
45	AG	194/208 (93%)	188 (97%)	6 (3%)	35	64
46	AH	169/171 (99%)	163 (96%)	6 (4%)	31	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	AI	175/181 (97%)	169 (97%)	6 (3%)	32	63
48	AJ	143/149 (96%)	141 (99%)	2 (1%)	59	76
49	AL	167/176 (95%)	161 (96%)	6 (4%)	31	62
50	AM	117/151 (78%)	112 (96%)	5 (4%)	26	57
51	AN	171/172 (99%)	166 (97%)	5 (3%)	37	66
52	AO	171/173 (99%)	163 (95%)	8 (5%)	23	55
53	AP	134/163 (82%)	130 (97%)	4 (3%)	36	65
54	AQ	166/167 (99%)	148 (89%)	18 (11%)	6	25
55	AR	159/175 (91%)	154 (97%)	5 (3%)	35	64
56	AS	155/155 (100%)	140 (90%)	15 (10%)	8	30
57	AT	139/140 (99%)	133 (96%)	6 (4%)	26	57
58	AU	91/116 (78%)	83 (91%)	8 (9%)	9	33
59	AV	100/107 (94%)	96 (96%)	4 (4%)	28	60
60	AW	55/126 (44%)	55 (100%)	0	100	100
61	AX	106/134 (79%)	104 (98%)	2 (2%)	50	73
62	AY	124/135 (92%)	120 (97%)	4 (3%)	34	64
63	AZ	117/118 (99%)	114 (97%)	3 (3%)	40	68
64	Aa	119/120 (99%)	117 (98%)	2 (2%)	53	74
65	Ab	84/172 (49%)	81 (96%)	3 (4%)	31	62
66	Ac	84/98 (86%)	82 (98%)	2 (2%)	43	69
67	Ad	98/110 (89%)	95 (97%)	3 (3%)	35	64
68	Ae	114/121 (94%)	110 (96%)	4 (4%)	32	62
69	Af	88/89 (99%)	78 (89%)	10 (11%)	5	23
70	Ag	98/106 (92%)	97 (99%)	1 (1%)	68	79
71	Ah	109/110 (99%)	107 (98%)	2 (2%)	51	73
72	Ai	86/89 (97%)	84 (98%)	2 (2%)	44	70
73	Aj	73/80 (91%)	71 (97%)	2 (3%)	39	67
74	Ak	64/64 (100%)	58 (91%)	6 (9%)	8	31
75	Al	47/48 (98%)	46 (98%)	1 (2%)	47	71
76	Am	48/48 (100%)	47 (98%)	1 (2%)	47	71
77	An	24/24 (100%)	23 (96%)	1 (4%)	26	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
78	Ao	92/94 (98%)	92 (100%)	0	100	100
79	Ap	74/75 (99%)	71 (96%)	3 (4%)	27	59
80	Ar	108/121 (89%)	102 (94%)	6 (6%)	19	49
81	AK	190/196 (97%)	186 (98%)	4 (2%)	47	71
All	All	9893/11009 (90%)	9590 (97%)	303 (3%)	36	64

5 of 303 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
58	AU	33	ILE
74	Ak	69	LEU
59	AV	25	VAL
68	Ae	13	VAL
81	AK	10	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 168 such sidechains are listed below:

Mol	Chain	Res	Type
51	AN	15	GLN
64	Aa	44	ASN
52	AO	26	GLN
56	AS	125	GLN
67	Ad	79	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1685/1869 (90%)	434 (25%)	35 (2%)
35	1	204/253 (80%)	109 (53%)	11 (5%)
36	5	3570/3594 (99%)	943 (26%)	88 (2%)
37	7	118/119 (99%)	12 (10%)	1 (0%)
38	8	149/156 (95%)	36 (24%)	3 (2%)
All	All	5726/5991 (95%)	1534 (26%)	138 (2%)

5 of 1534 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A

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Mol	Chain	Res	Type
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

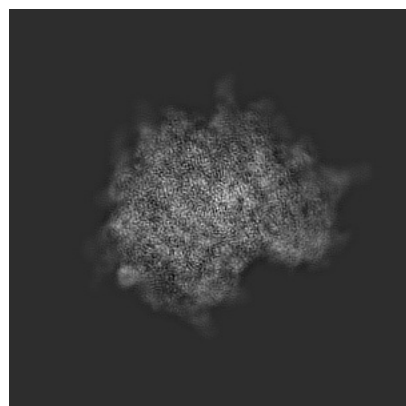
6 Map visualisation [i](#)

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.

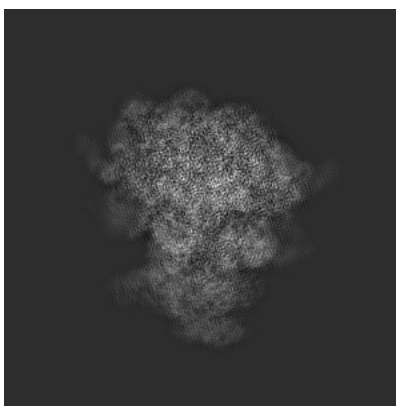
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

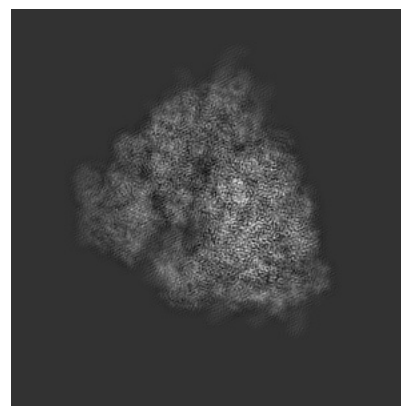
6.1.1 Primary map



X

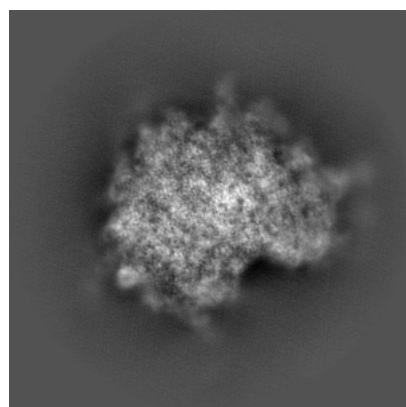


Y

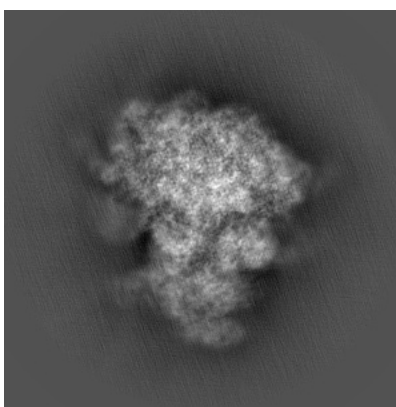


Z

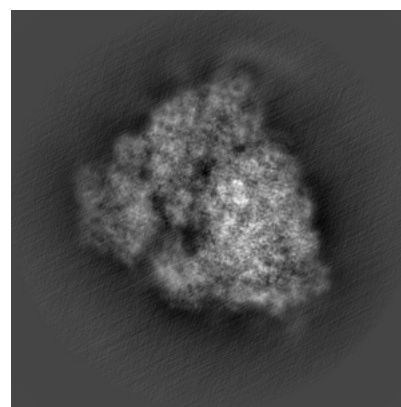
6.1.2 Raw map



X



Y

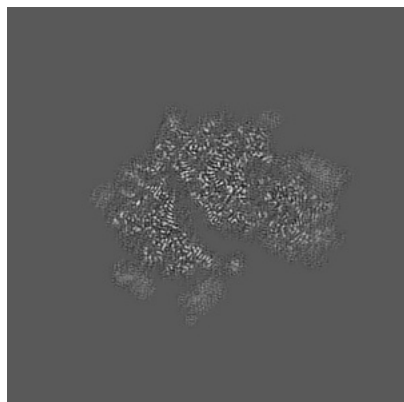


Z

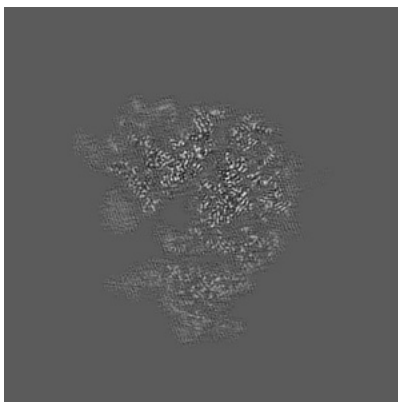
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

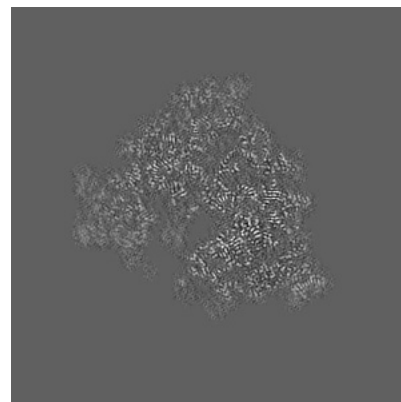
6.2.1 Primary map



X Index: 180

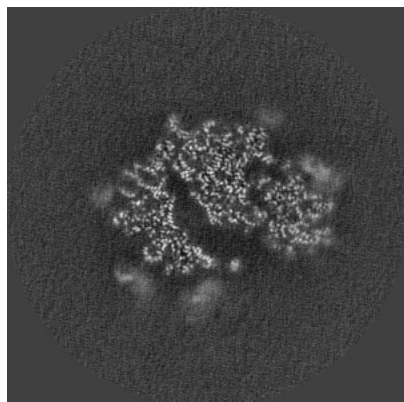


Y Index: 180

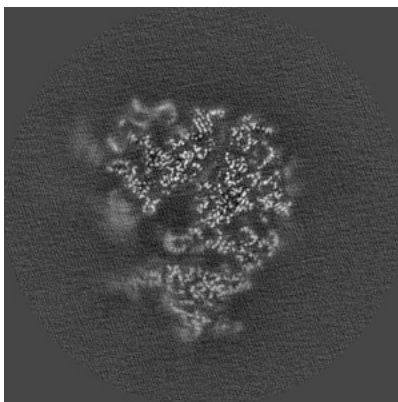


Z Index: 180

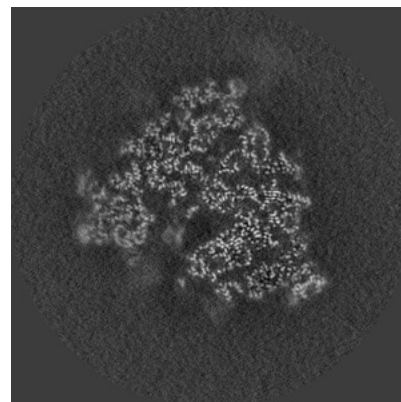
6.2.2 Raw map



X Index: 180



Y Index: 180

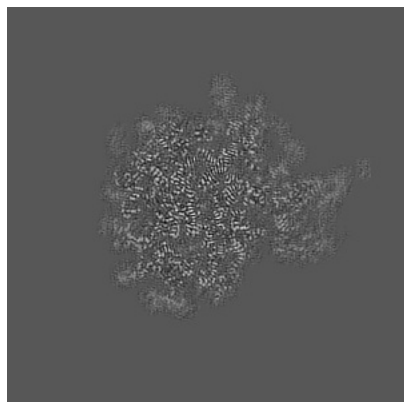


Z Index: 180

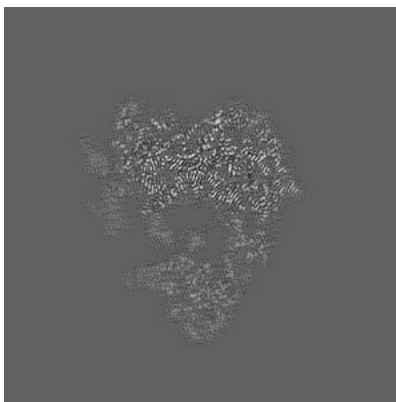
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

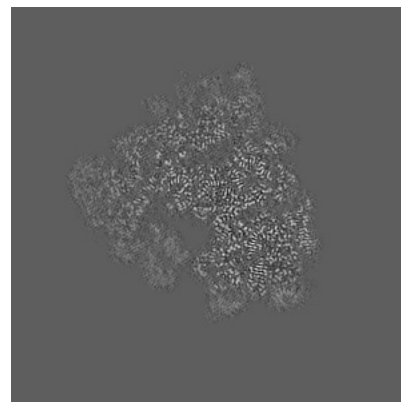
6.3.1 Primary map



X Index: 206

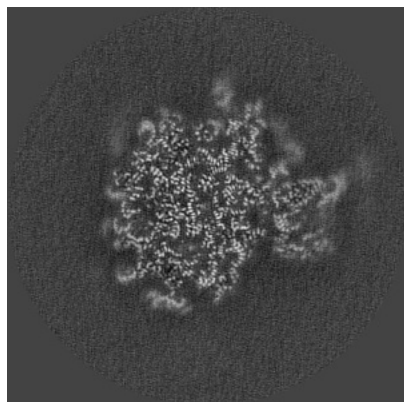


Y Index: 167

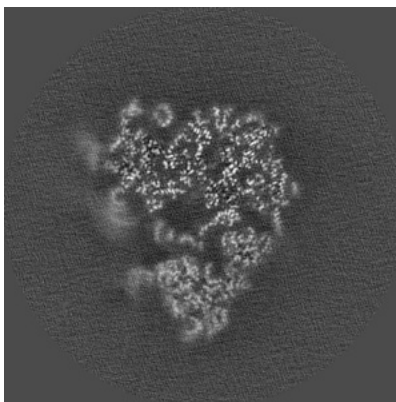


Z Index: 194

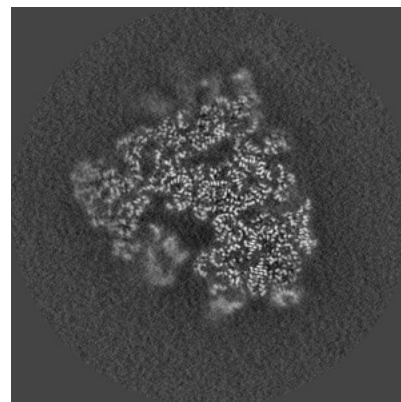
6.3.2 Raw map



X Index: 206



Y Index: 174

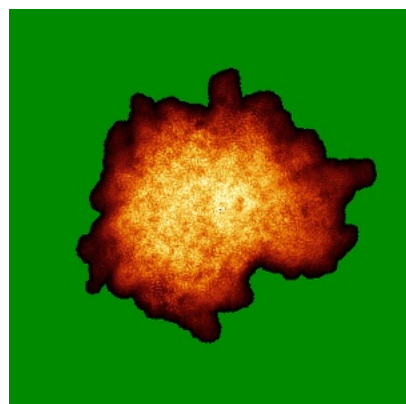


Z Index: 194

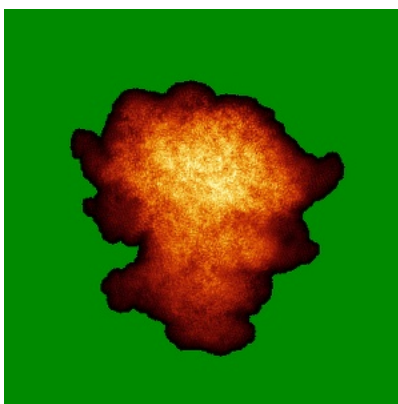
The images above show the largest variance slices of the map in three orthogonal directions.

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

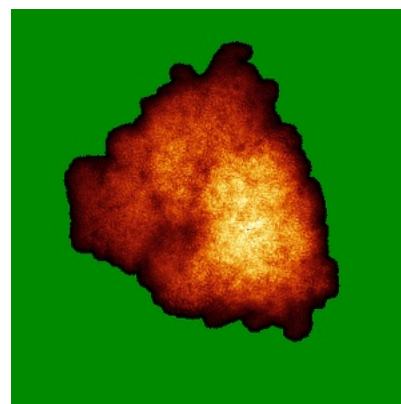
6.4.1 Primary map



X

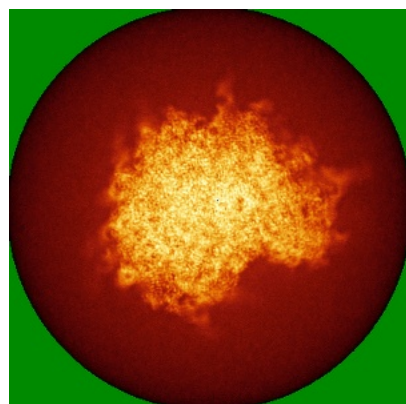


Y

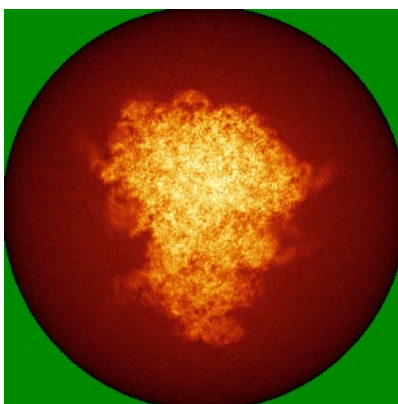


Z

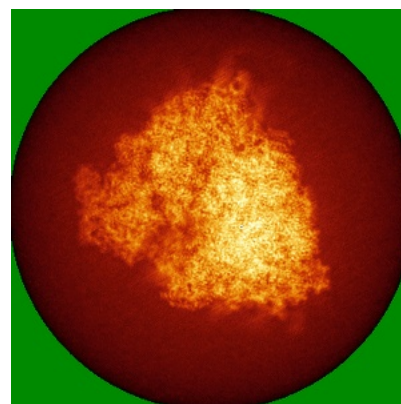
6.4.2 Raw map



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.

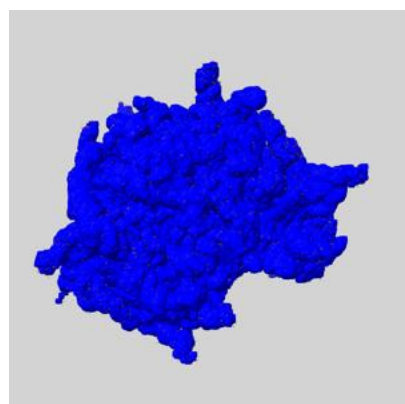
6.6 Mask visualisation [i](#)

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

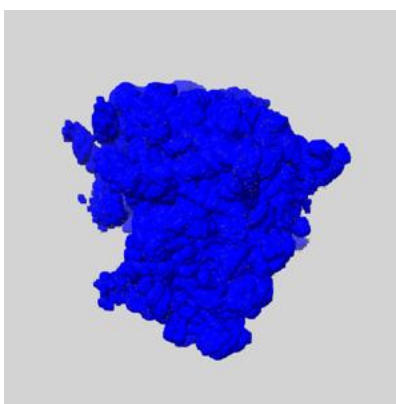
A mask typically either:

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

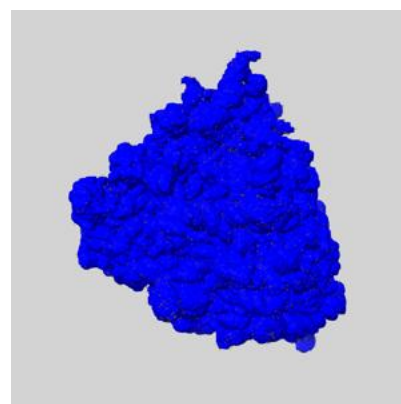
6.6.1 emd_20255_msk_1.map [i](#)



X



Y

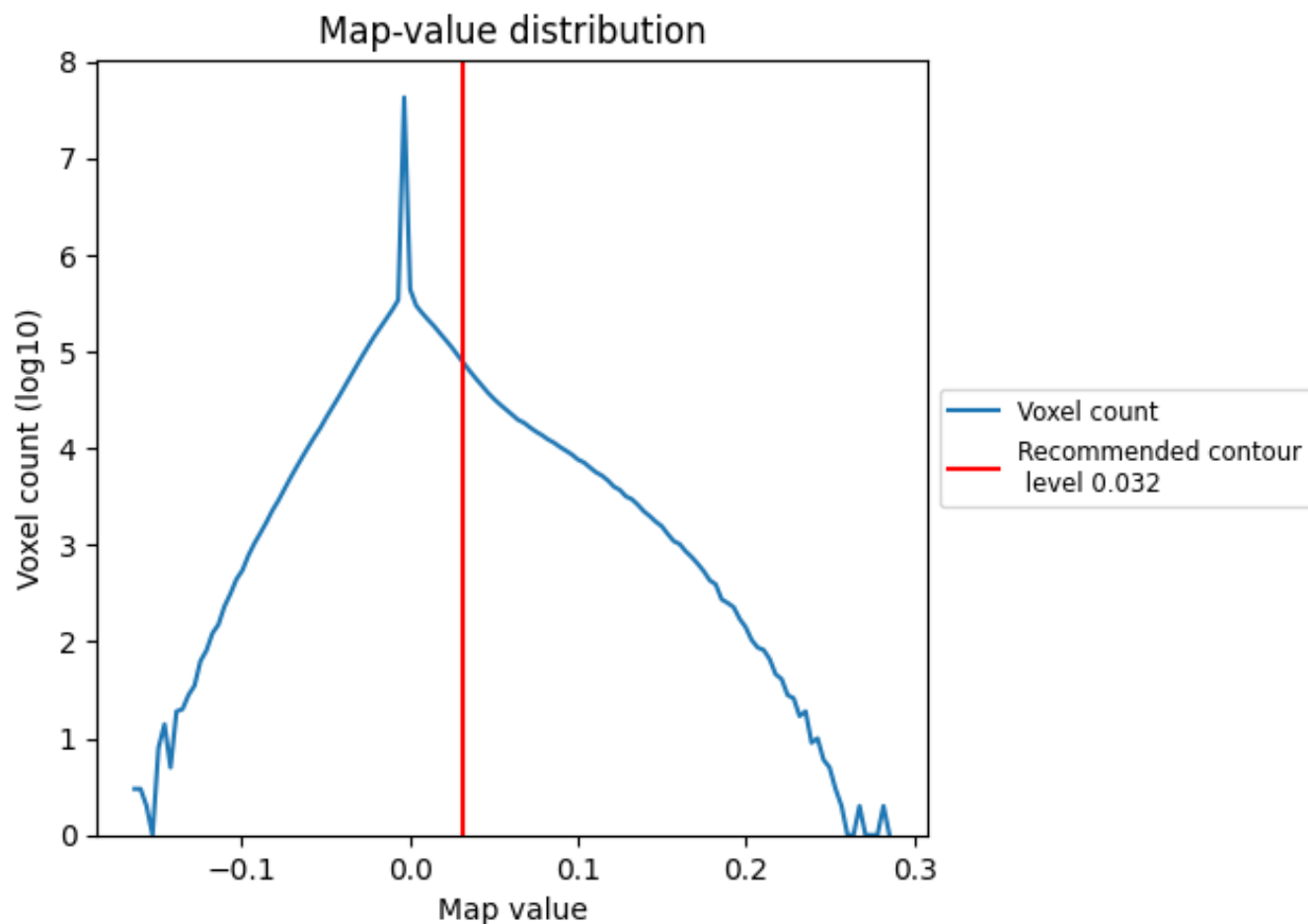


Z

7 Map analysis [i](#)

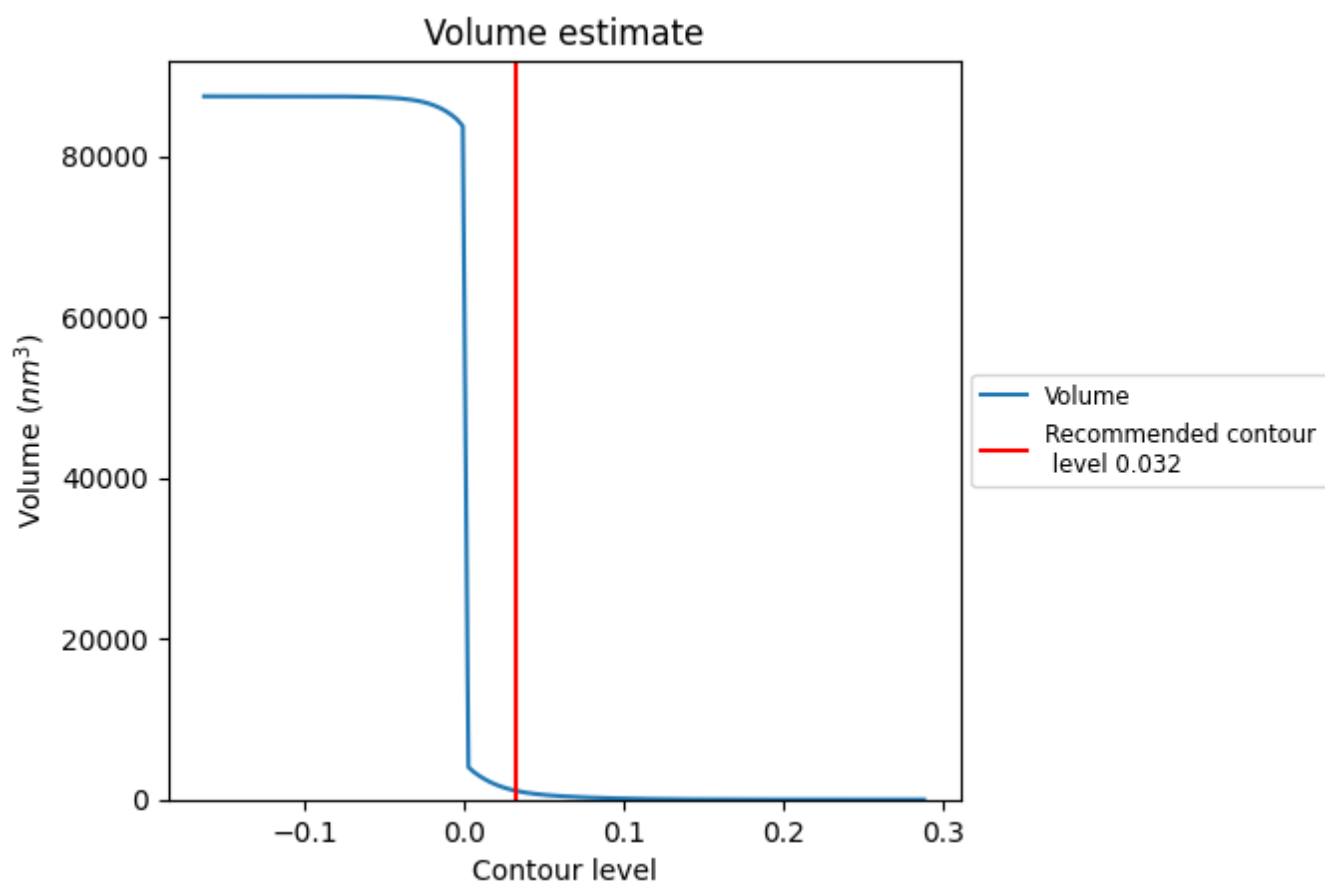
This section contains the results of statistical analysis of the map.

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.

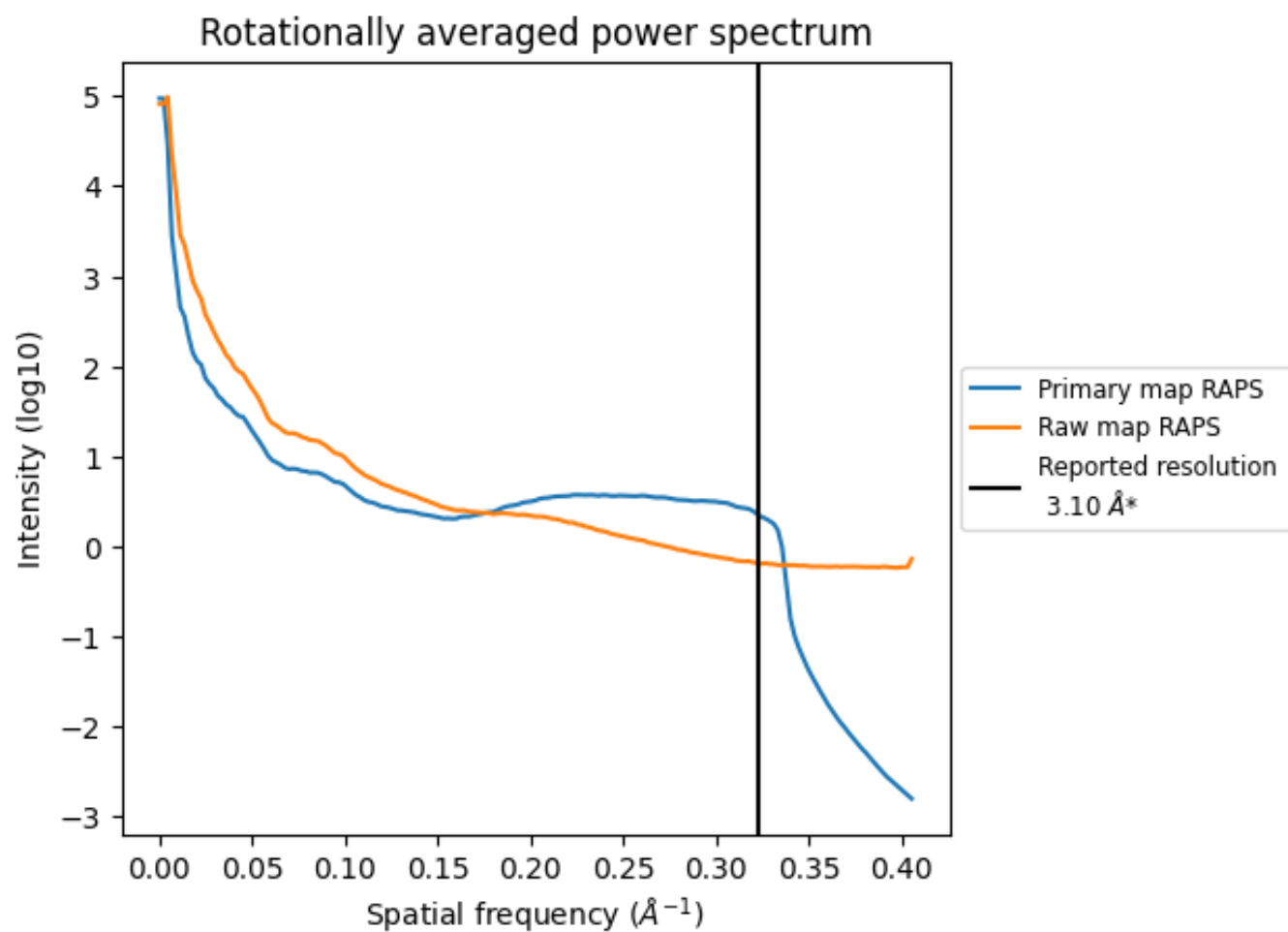
7.2 Volume estimate [i](#)



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 ⓘ

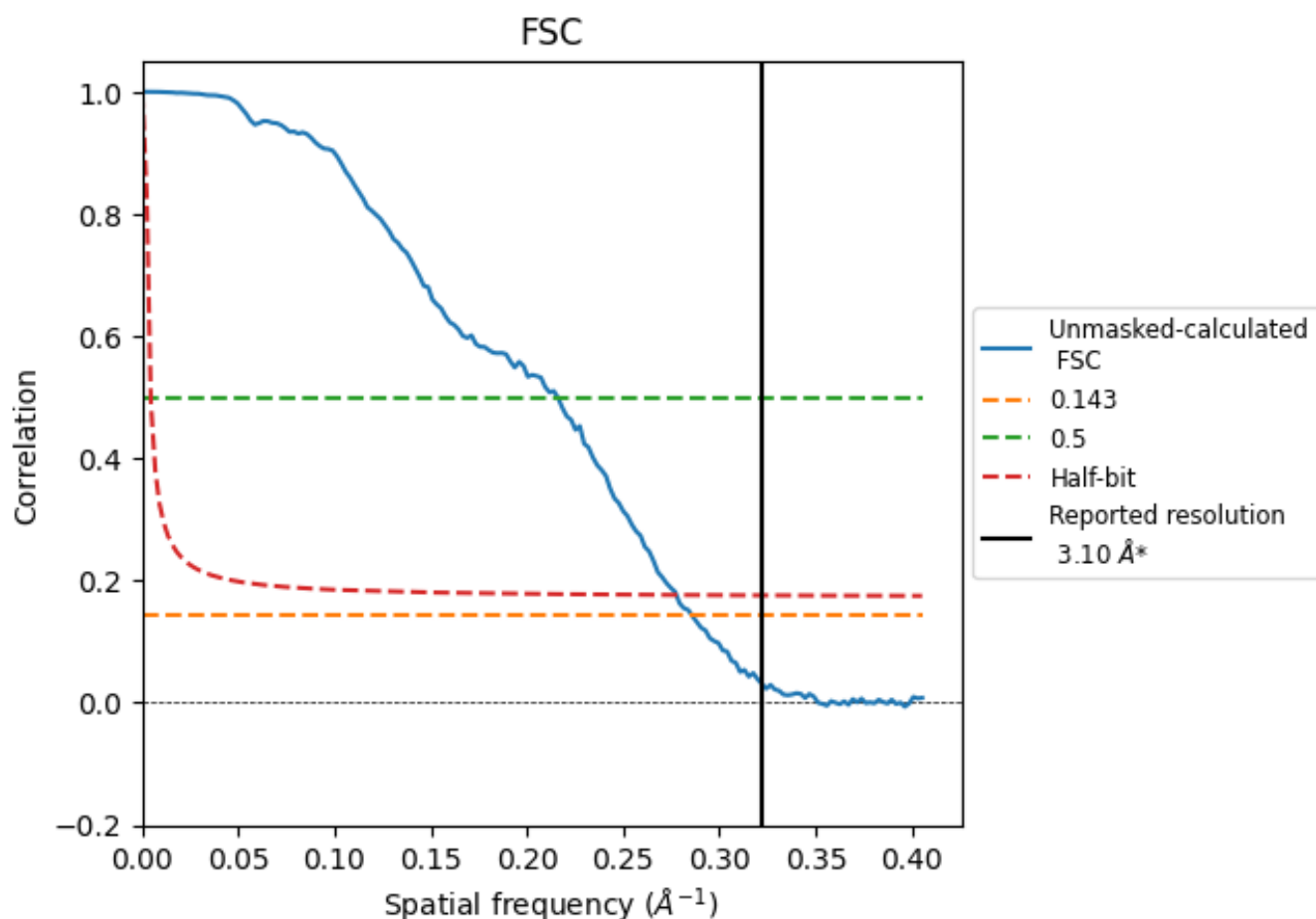


*Reported resolution corresponds to spatial frequency of $0.323 \text{ \AA}^{-1}$

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](#)

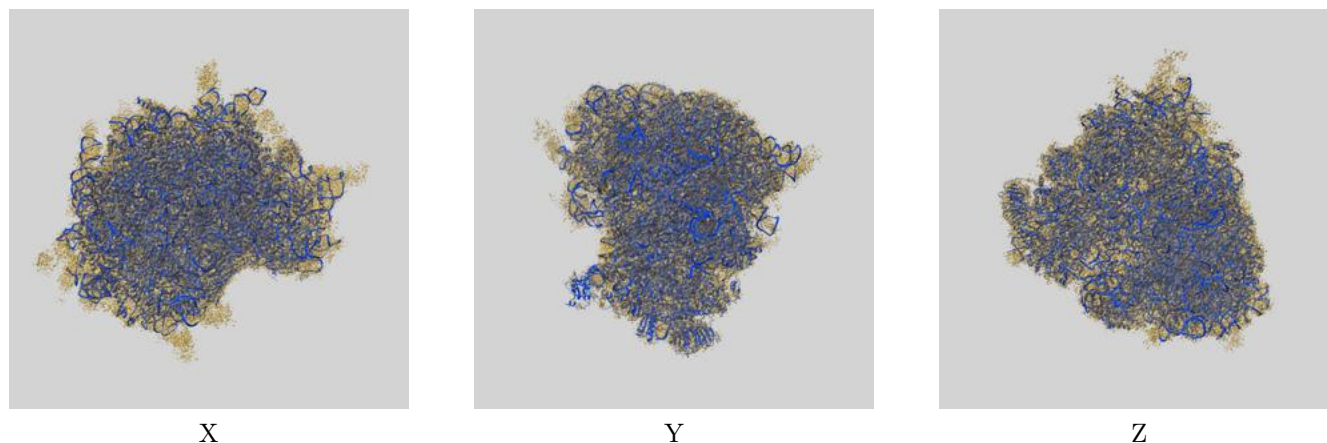
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.50	4.63	3.60

*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](#)

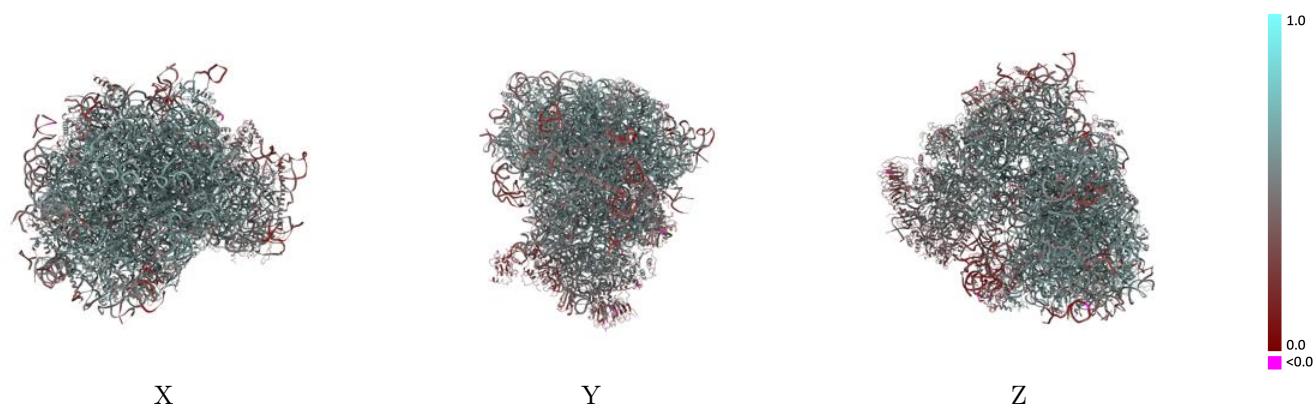
This section contains information regarding the fit between EMDB map EMD-20255 and PDB model 6P5I. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

9.1 Map-model overlay [i](#)



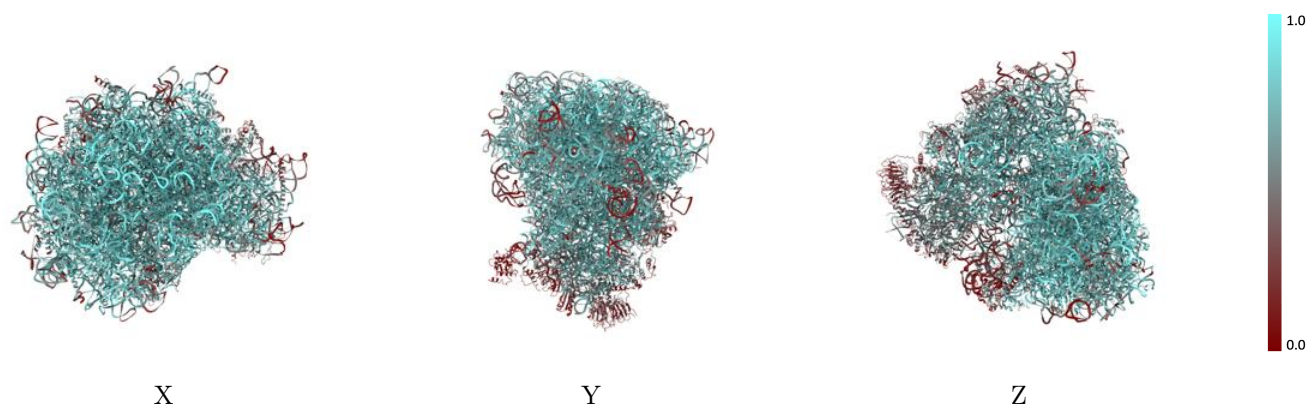
The images above show the 3D surface view of the map at the recommended contour level 0.032 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



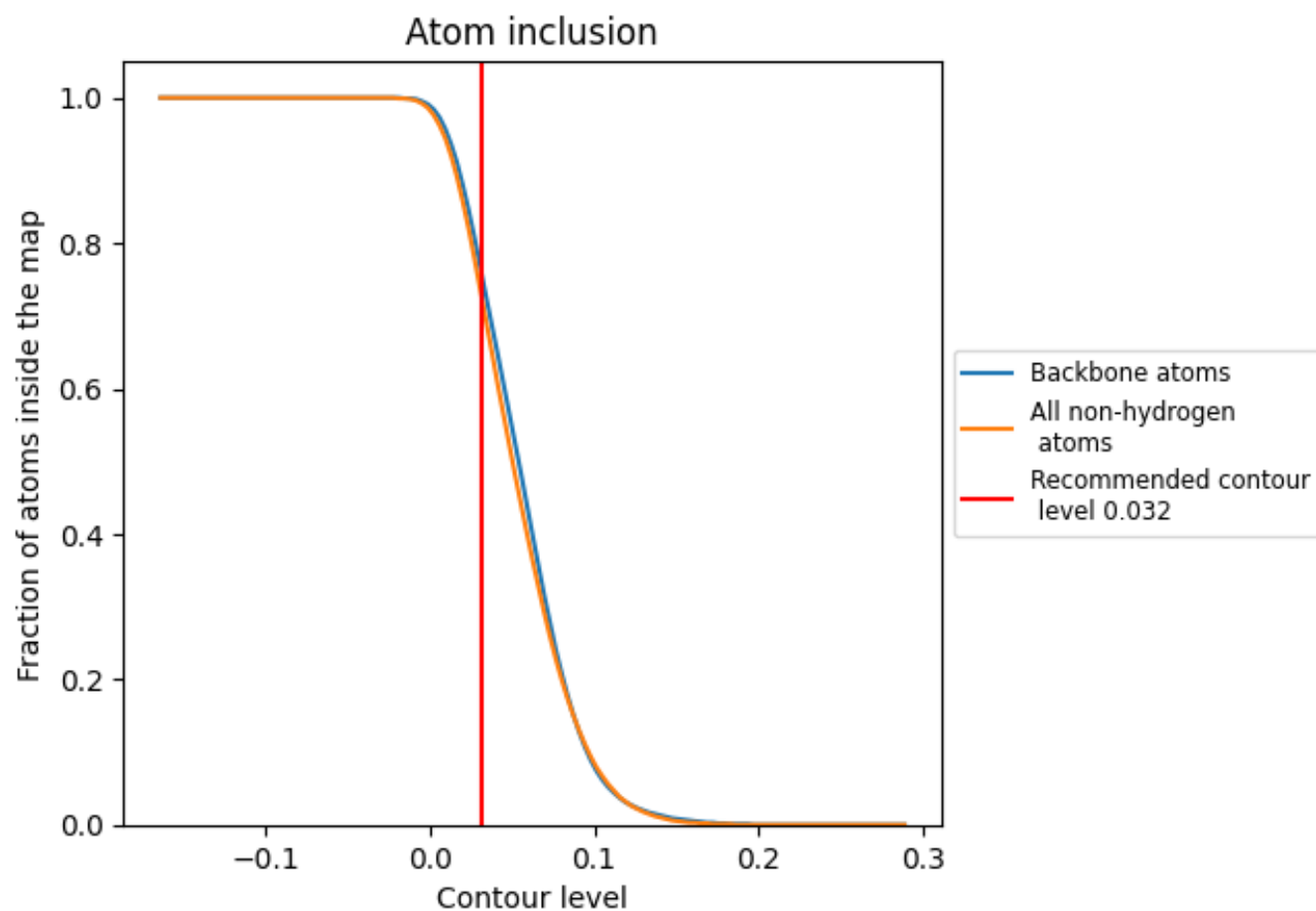
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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