Full wwPDB EM Validation Report ⓘ

Nov 9, 2022 – 02:05 PM EST

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

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

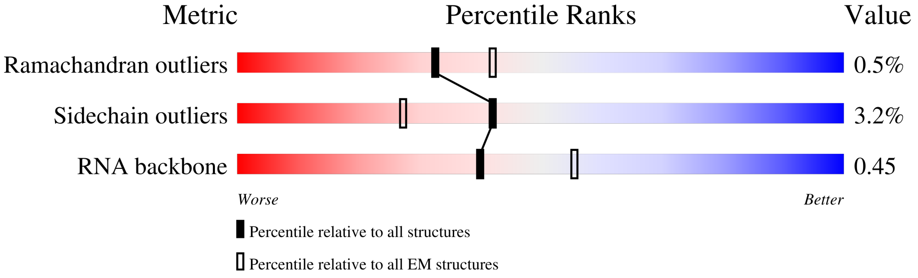
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance ⓘ

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

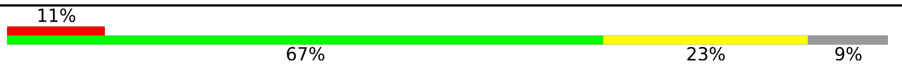
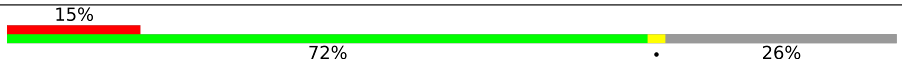
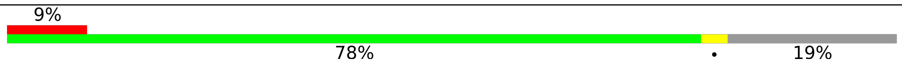
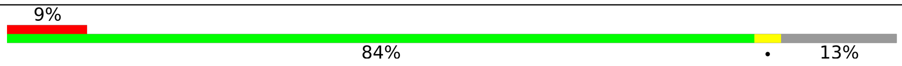
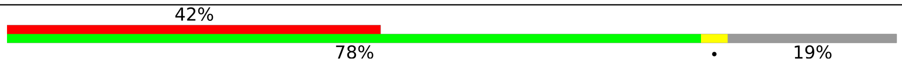
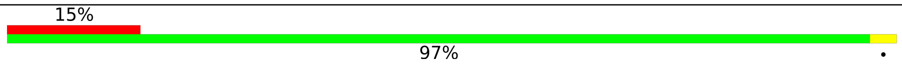
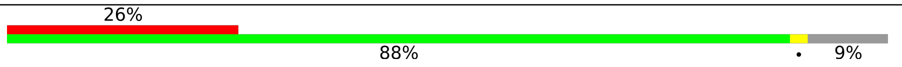
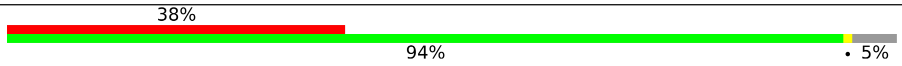
The reported resolution of this entry is 3.10 Å.

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

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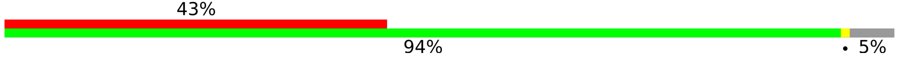
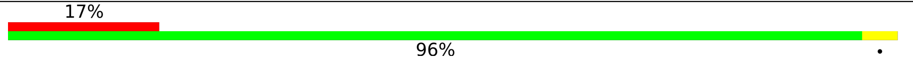
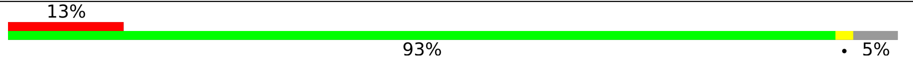
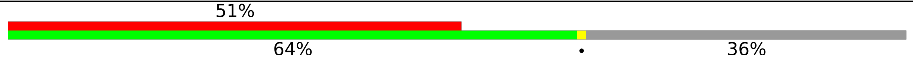
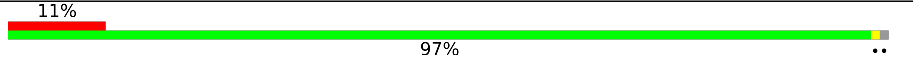
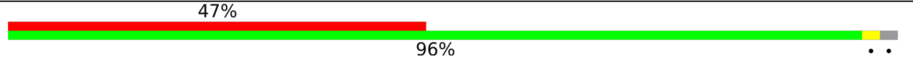
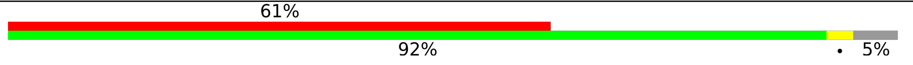
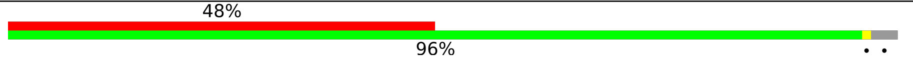
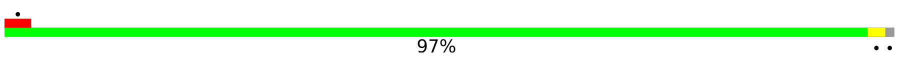
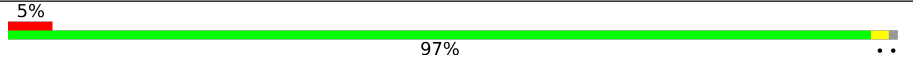
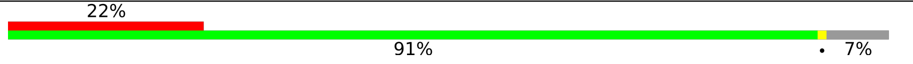
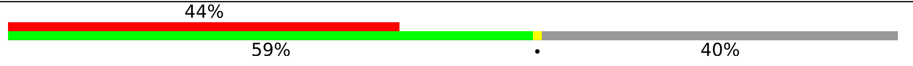
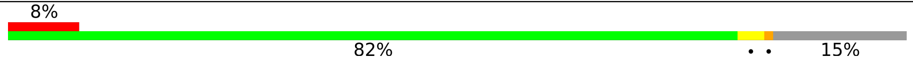
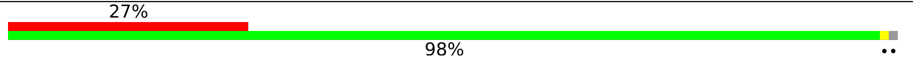
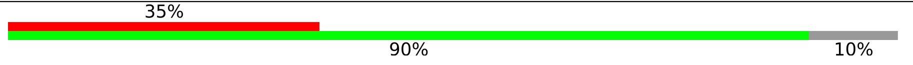
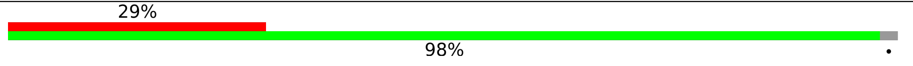
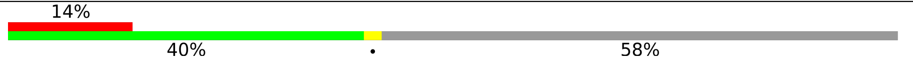
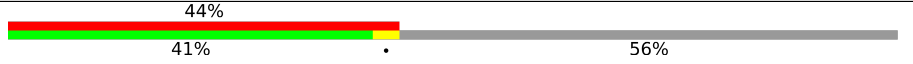
Mol	Chain	Length	Quality of chain
9	I	194	
10	J	207	
11	K	194	
12	L	149	
13	M	158	
14	N	132	
15	O	151	
16	P	151	
17	Q	145	
18	R	172	
19	S	135	
20	T	152	
21	U	145	
22	V	119	
23	W	83	
24	X	130	
25	Y	143	
26	Z	134	
27	a	125	
28	b	115	
29	c	84	
30	d	69	
31	e	56	
32	f	133	
33	g	156	

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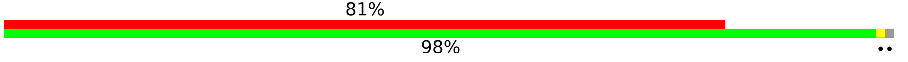
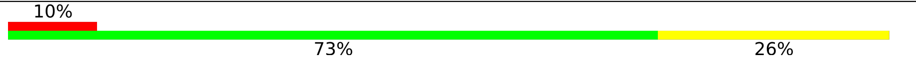
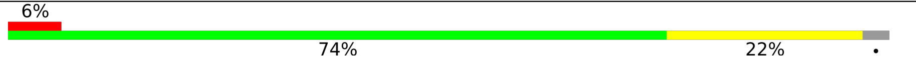
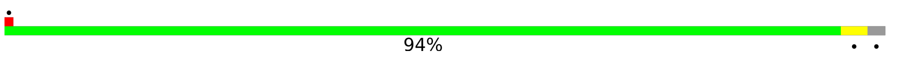
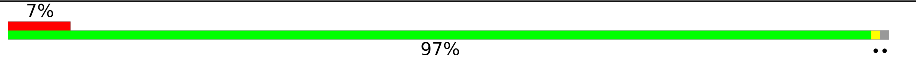
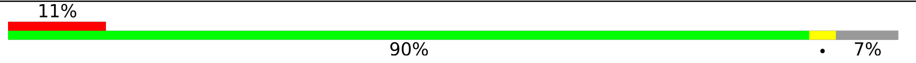
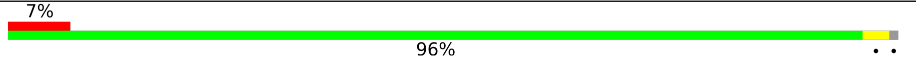
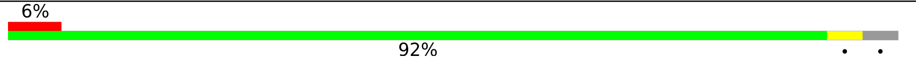
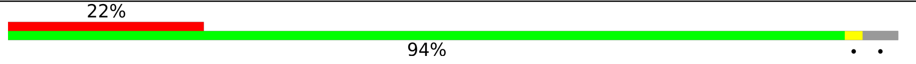
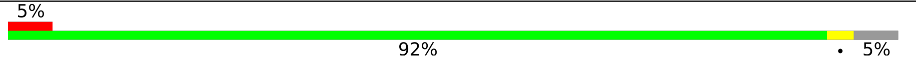
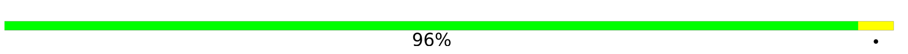
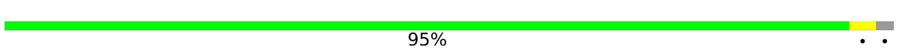
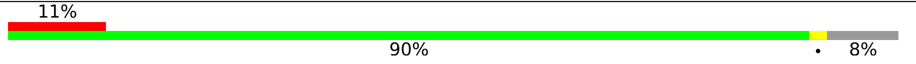
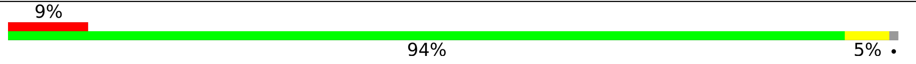
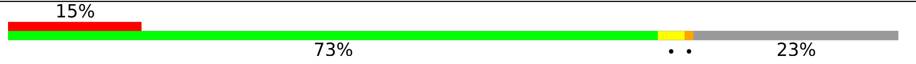
Mol	Chain	Length	Quality of chain
34	h	317	
35	1	253	
36	5	3594	
37	7	119	
38	8	156	
39	AA	257	
40	AB	403	
41	AC	392	
42	AD	297	
43	AE	291	
44	AF	249	
45	AG	242	
46	AH	192	
47	AI	214	
48	AJ	178	
49	AL	211	
50	AM	198	
51	AN	204	
52	AO	203	
53	AP	184	
54	AQ	188	
55	AR	196	
56	AS	176	
57	AT	160	
58	AU	128	

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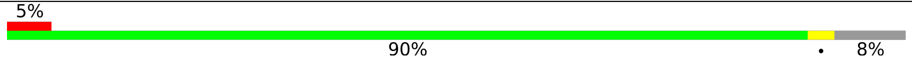
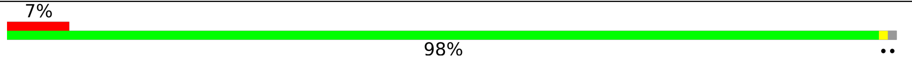
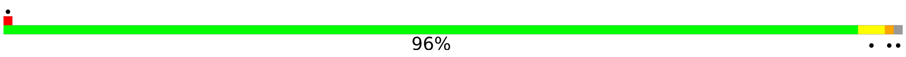
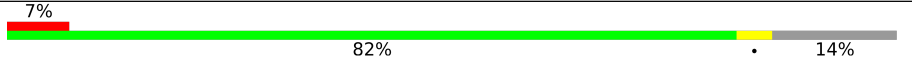
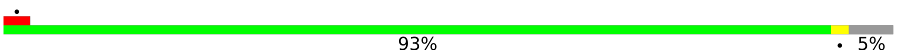
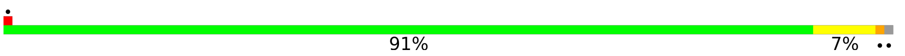
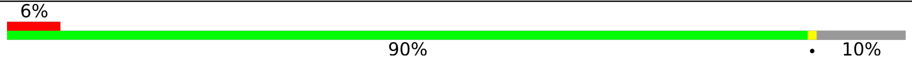
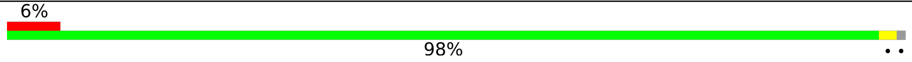
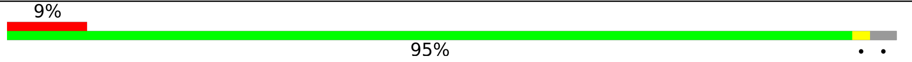
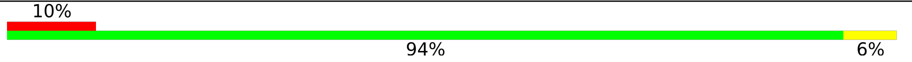
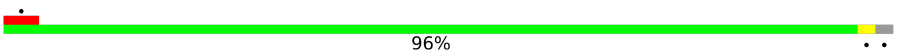
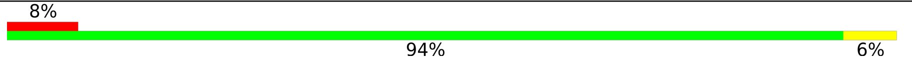
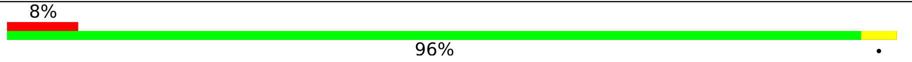
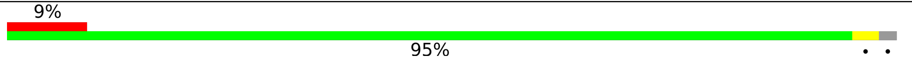
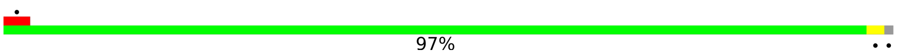
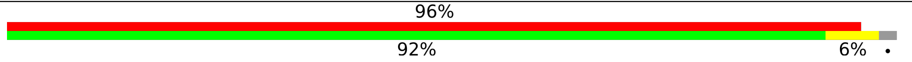
Mol	Chain	Length	Quality of chain
59	AV	140	
60	AW	157	
61	AX	156	
62	AY	145	
63	AZ	136	
64	Aa	148	
65	Ab	226	
66	Ac	115	
67	Ad	125	
68	Ae	135	
69	Af	110	
70	Ag	126	
71	Ah	123	
72	Ai	105	
73	Aj	97	
74	Ak	69	
75	Al	51	
76	Am	52	
77	An	25	
78	Ao	106	
79	Ap	92	
80	Ar	137	
81	AK	217	

2 Entry composition ⓘ

There are 81 unique types of molecules in this entry. The entry contains 215974 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 18S rRNA.

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

- Molecule 2 is a protein called uS2.

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

- Molecule 3 is a protein called eS1.

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

- Molecule 4 is a protein called uS5.

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

- Molecule 5 is a protein called uS3.

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

- Molecule 6 is a protein called eS4.

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

- Molecule 7 is a protein called uS7.

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

- Molecule 8 is a protein called eS6.

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

- Molecule 9 is a protein called eS7.

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

- Molecule 10 is a protein called eS8.

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

- Molecule 11 is a protein called uS4.

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

- Molecule 12 is a protein called eS10.

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

- Molecule 13 is a protein called uS17.

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

- Molecule 14 is a protein called eS12.

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

- Molecule 15 is a protein called uS15.

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

- Molecule 16 is a protein called uS11.

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

- Molecule 17 is a protein called uS19.

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

- Molecule 18 is a protein called uS9.

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

- Molecule 19 is a protein called eS17.

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

- Molecule 20 is a protein called uS13.

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

- Molecule 21 is a protein called eS19.

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

- Molecule 22 is a protein called uS10.

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

- Molecule 23 is a protein called eS21.

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

- Molecule 24 is a protein called uS8.

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

- Molecule 25 is a protein called uS12.

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

- Molecule 26 is a protein called eS24.

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

- Molecule 27 is a protein called eS25.

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

- 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 4366	C 1951	N 775	O 1435	P 205	0	0

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

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

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

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

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

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

- Molecule 39 is a protein called uL2.

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

- Molecule 40 is a protein called uL3.

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

- Molecule 41 is a protein called uL4.

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

- Molecule 42 is a protein called uL18.

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

- Molecule 43 is a protein called eL6.

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

- Molecule 44 is a protein called uL30.

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

- Molecule 45 is a protein called eL8.

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

- Molecule 46 is a protein called uL6.

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

- Molecule 47 is a protein called uL16.

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

- Molecule 48 is a protein called uL11.

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

- Molecule 49 is a protein called eL13.

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

- Molecule 50 is a protein called L14e.

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

- Molecule 51 is a protein called eL15.

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

- Molecule 52 is a protein called uL13.

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

- Molecule 53 is a protein called uL22.

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

- Molecule 54 is a protein called eL18.

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

- Molecule 55 is a protein called eL19.

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

- Molecule 56 is a protein called eL20.

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

- Molecule 57 is a protein called eL21.

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

- Molecule 58 is a protein called eL22.

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

- Molecule 59 is a protein called uL14.

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

- Molecule 60 is a protein called eL24.

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

- Molecule 61 is a protein called eL23.

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

- Molecule 62 is a protein called uL24.

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

- 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
			Total	C	N	O	S		
70	Ag	114	906	566	187	147	6	0	0

- Molecule 71 is a protein called eL35.

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

- Molecule 72 is a protein called eL36.

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

- Molecule 73 is a protein called eL37.

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

- Molecule 74 is a protein called eL38.

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

- Molecule 75 is a protein called eL39.

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

- Molecule 76 is a protein called eL40.

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

- Molecule 77 is a protein called eL41.

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

- Molecule 78 is a protein called eL42.

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

- Molecule 79 is a protein called eL43.

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

- Molecule 80 is a protein called eL28.

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

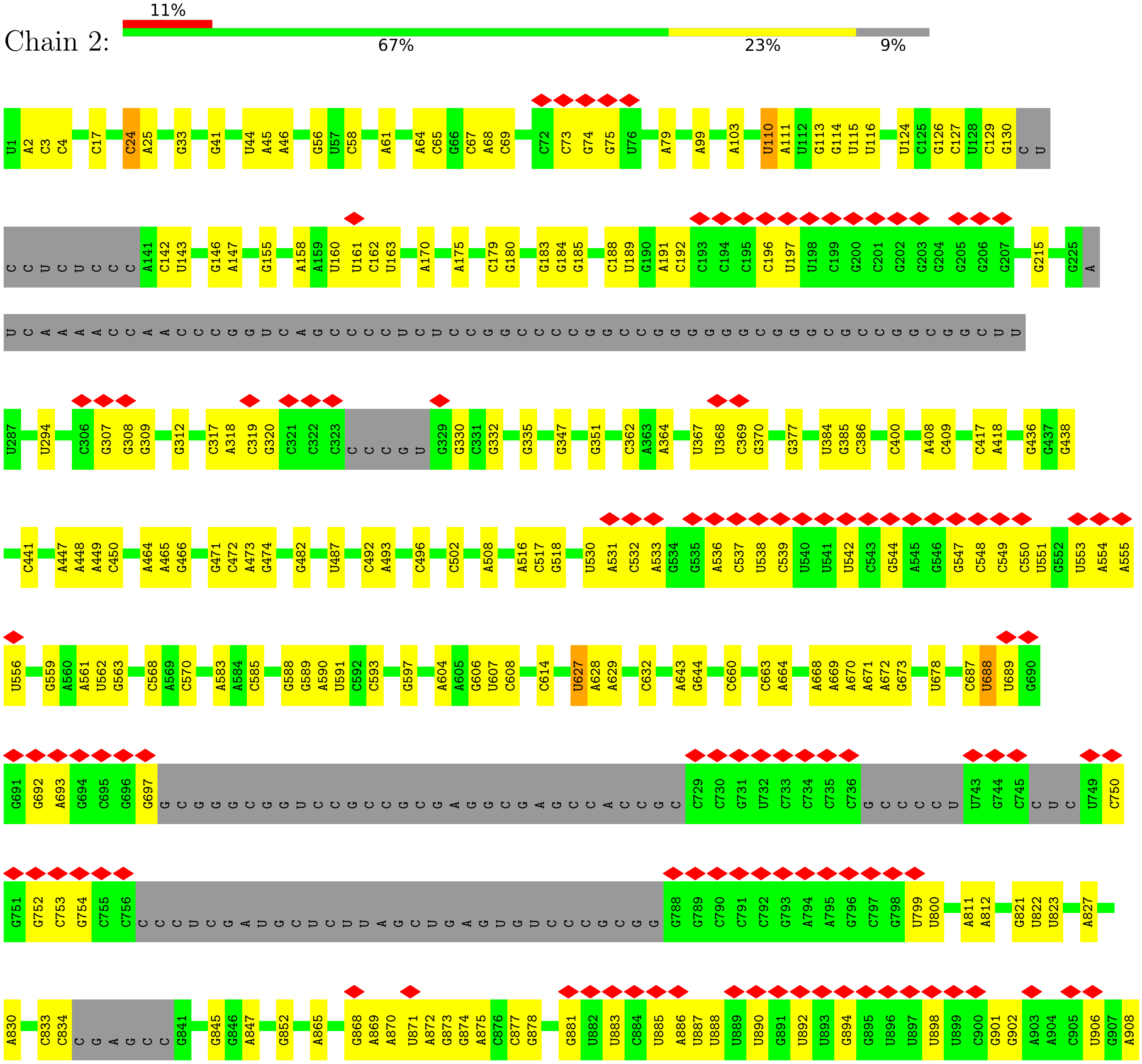
- Molecule 81 is a protein called uL1.

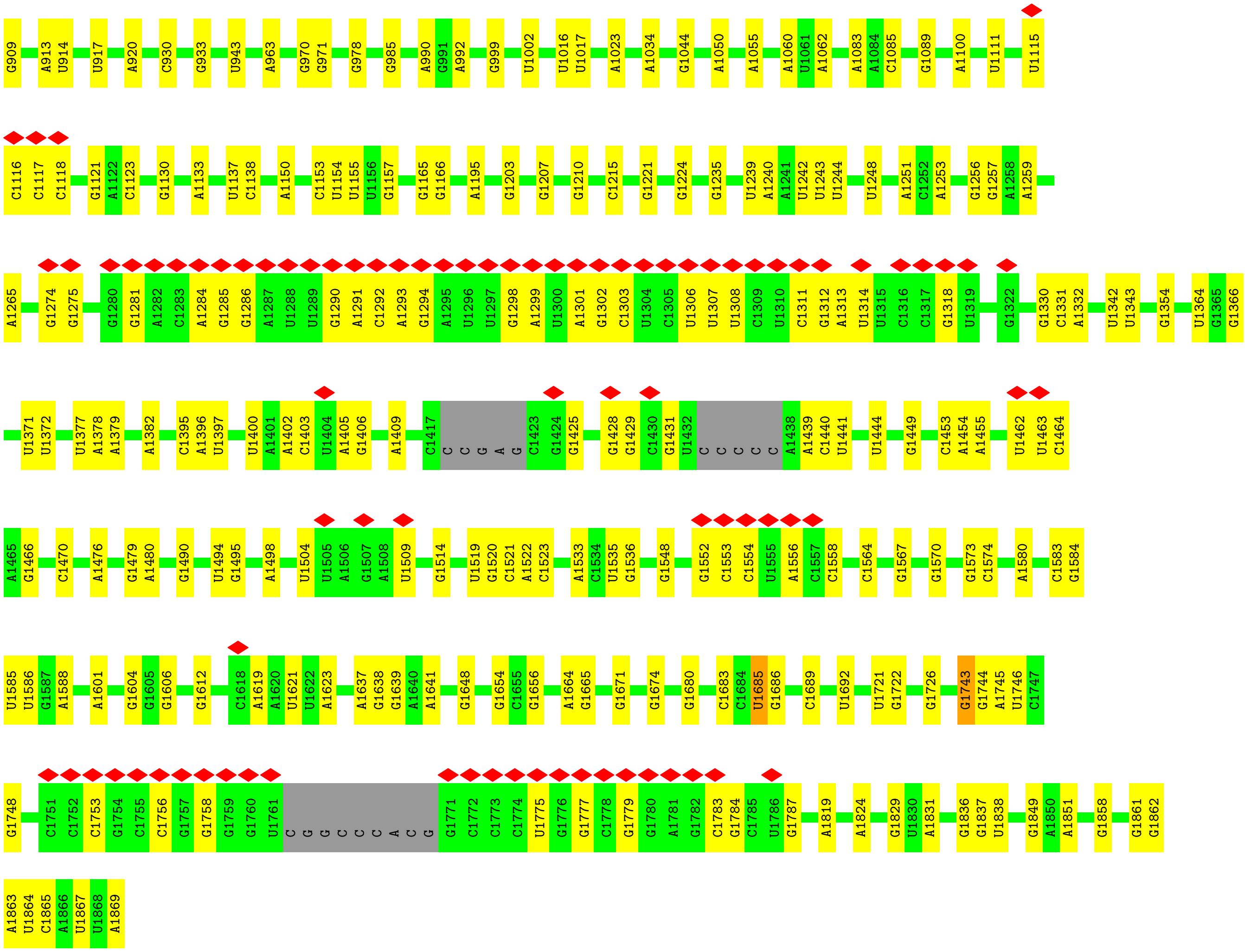
Mol	Chain	Residues	Atoms					AltConf	Trace
81	AK	212	Total 1705	C 1091	N 306	O 300	S 8	0	0

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.

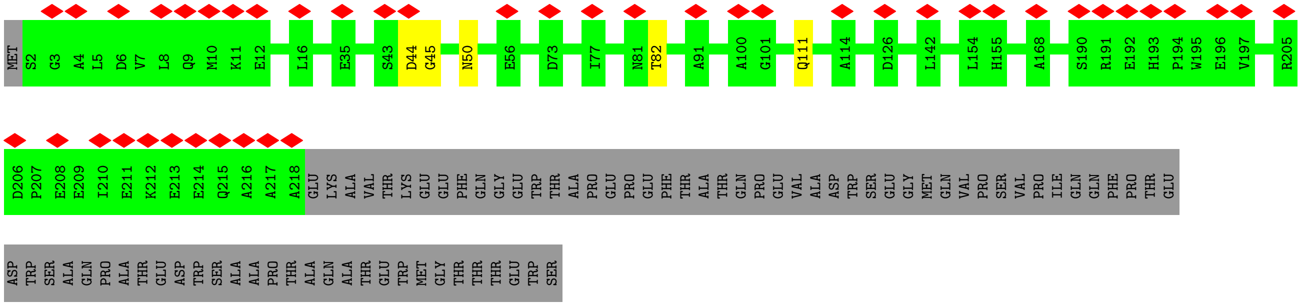
- Molecule 1: 18S rRNA





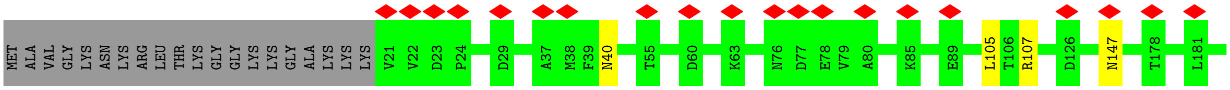
- Molecule 2: uS2

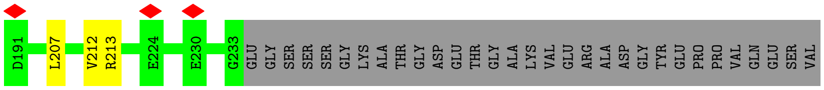
Chain B:



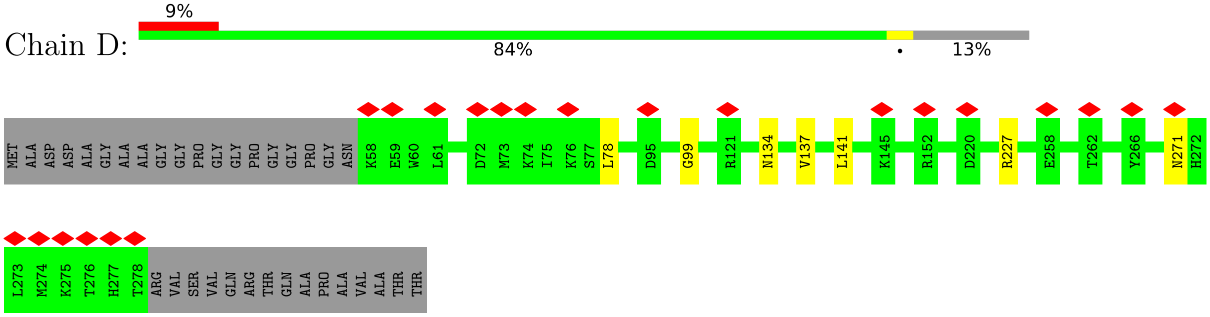
- Molecule 3: eS1

Chain C:

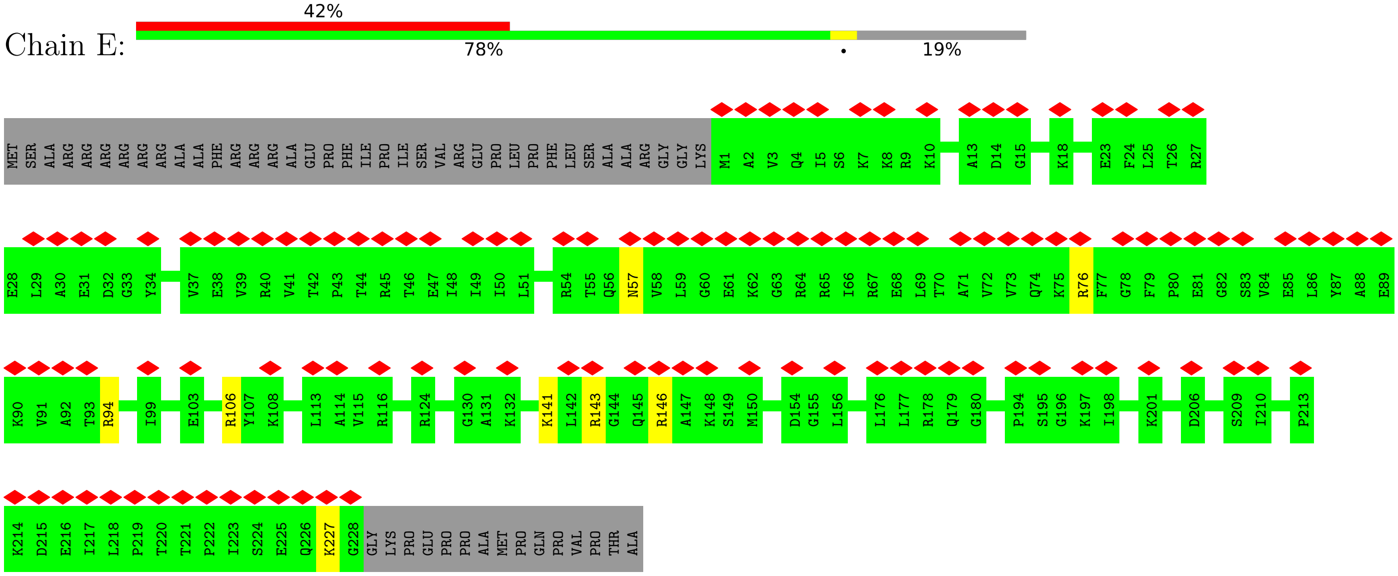




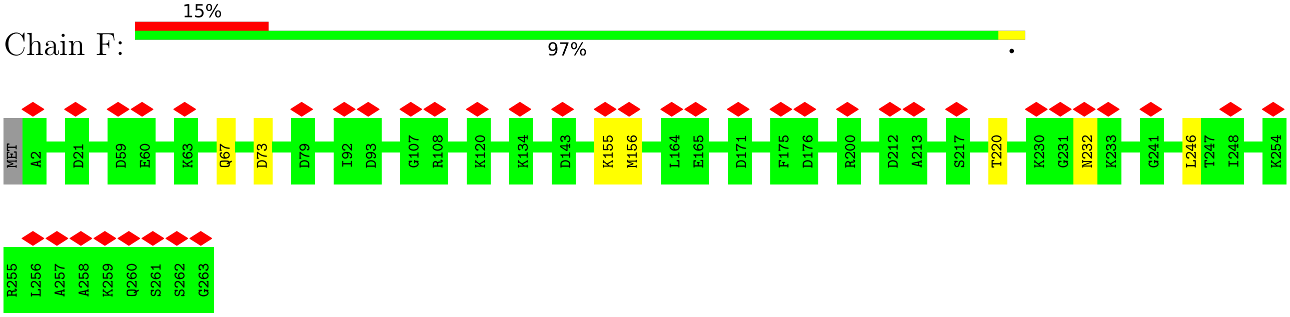
- Molecule 4: uS5



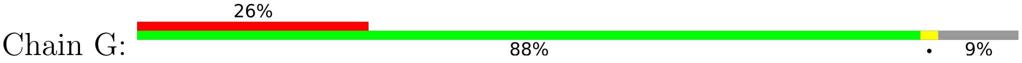
- Molecule 5: uS3

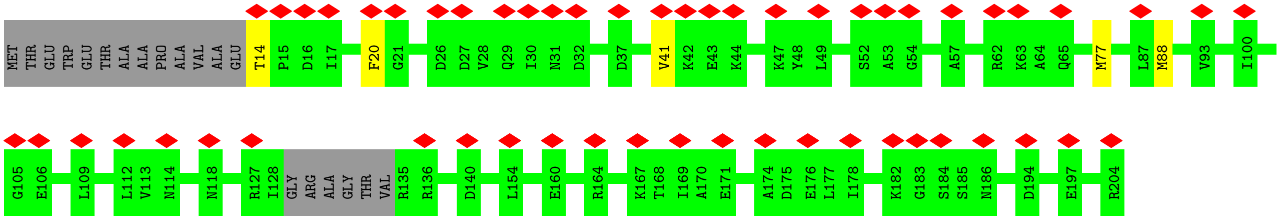


- Molecule 6: eS4



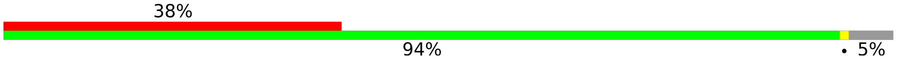
- Molecule 7: uS7

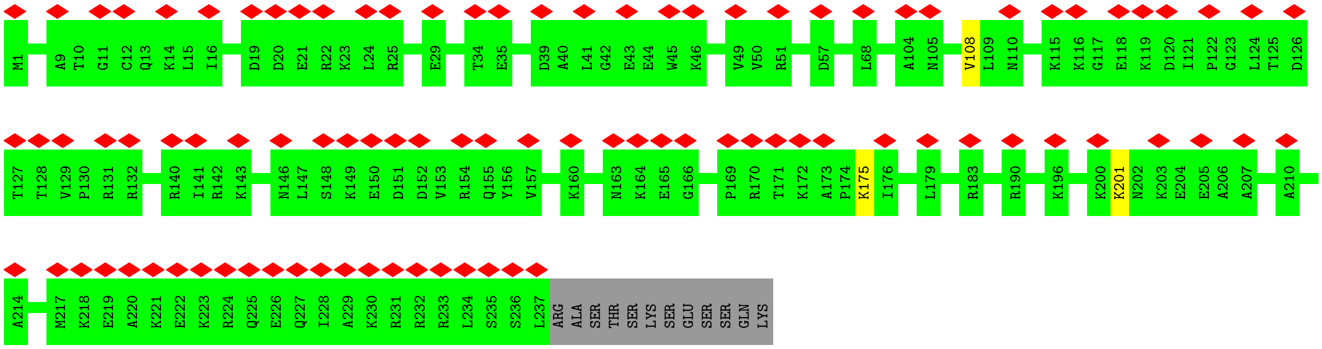




- Molecule 8: eS6

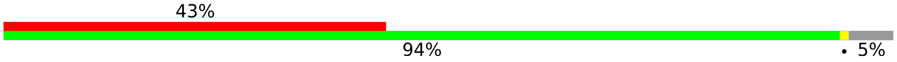
Chain H:

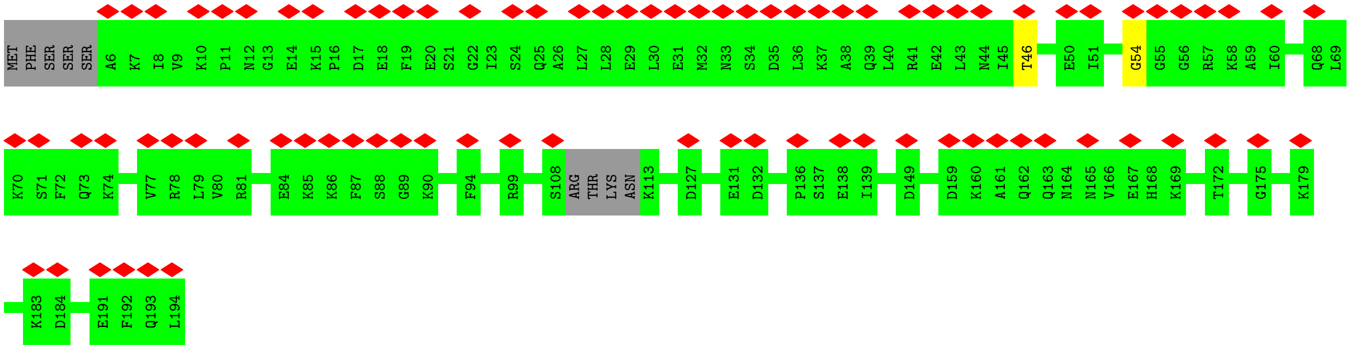




- Molecule 9: eS7

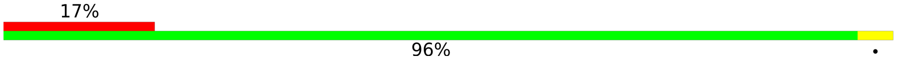
Chain I:

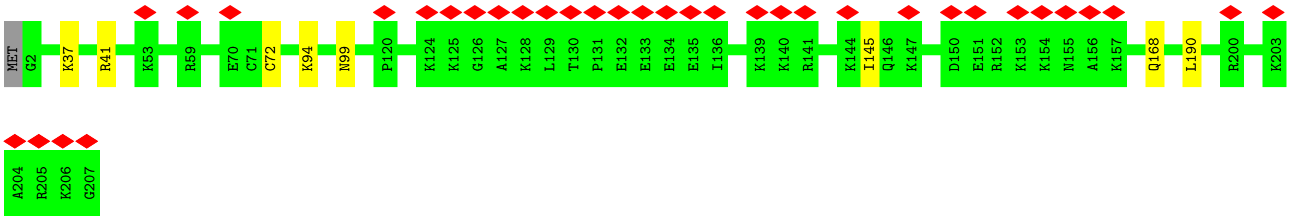




- Molecule 10: eS8

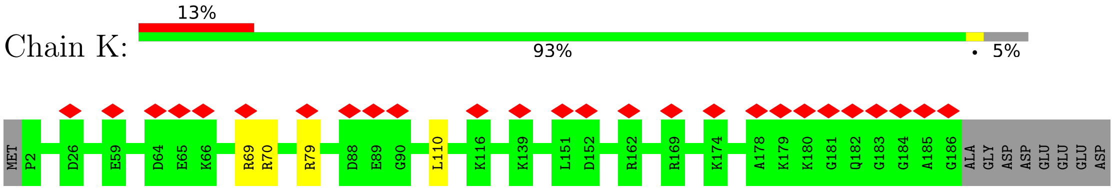
Chain J:





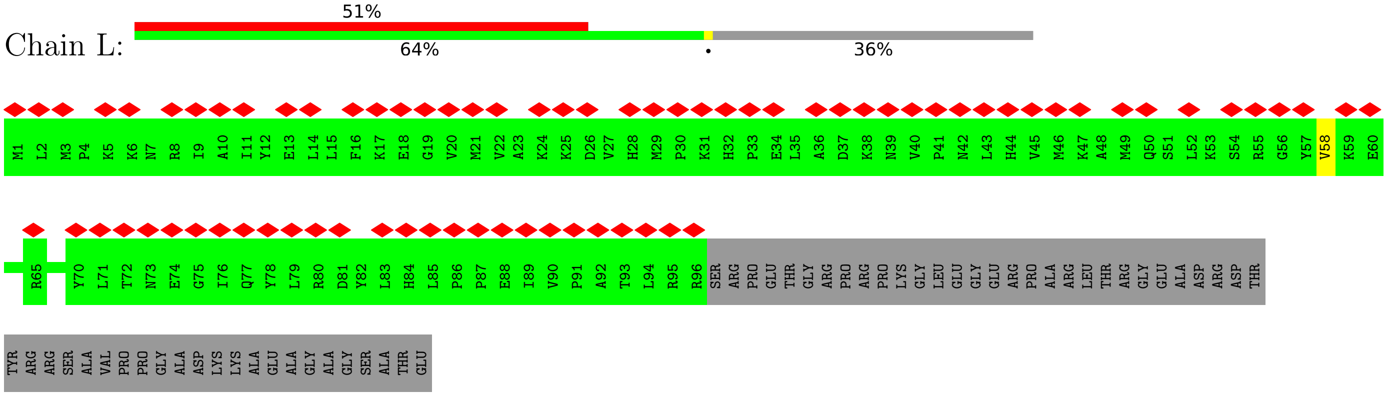
- Molecule 11: uS4

Chain K:



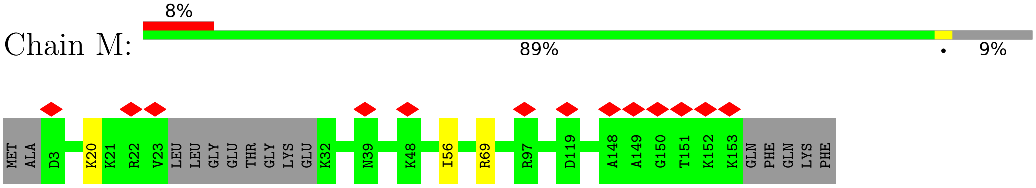
- Molecule 12: eS10

Chain L:



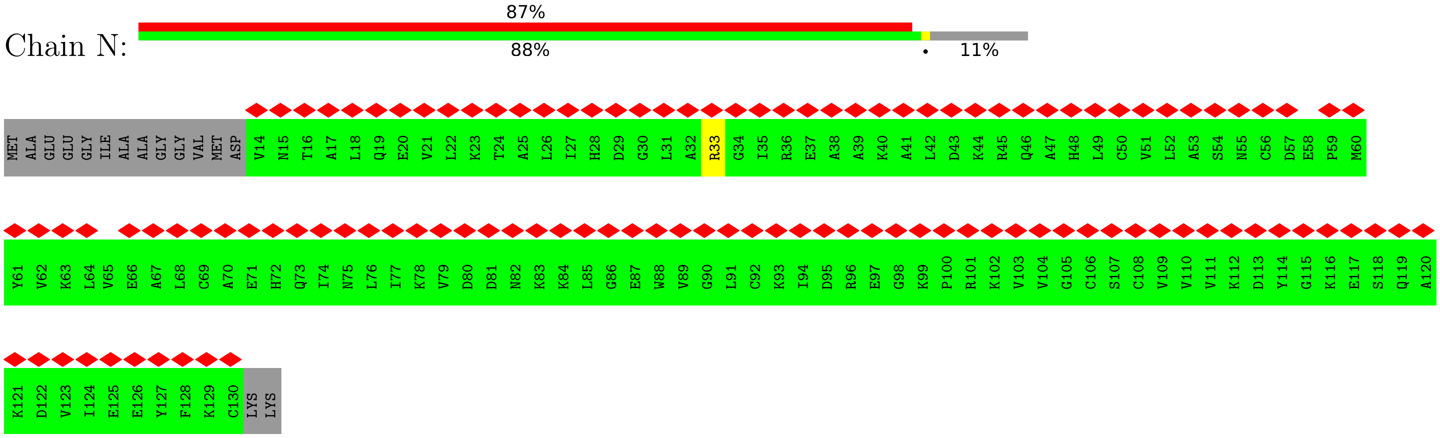
- Molecule 13: uS17

Chain M:



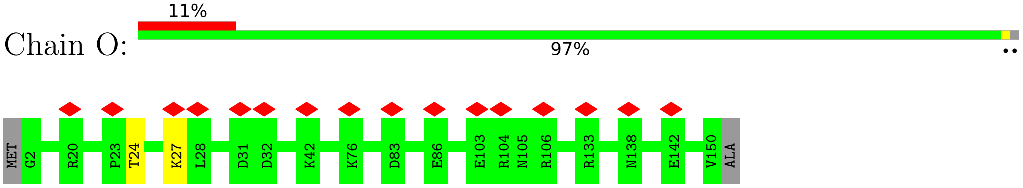
- Molecule 14: eS12

Chain N:



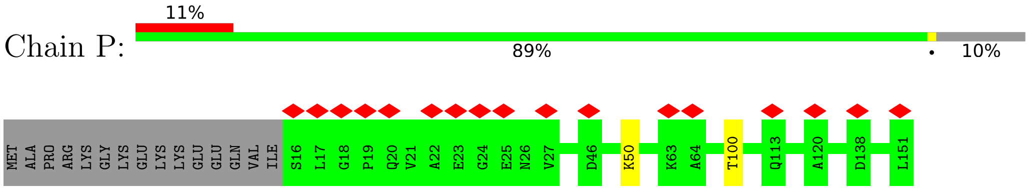
- Molecule 15: uS15

Chain O:



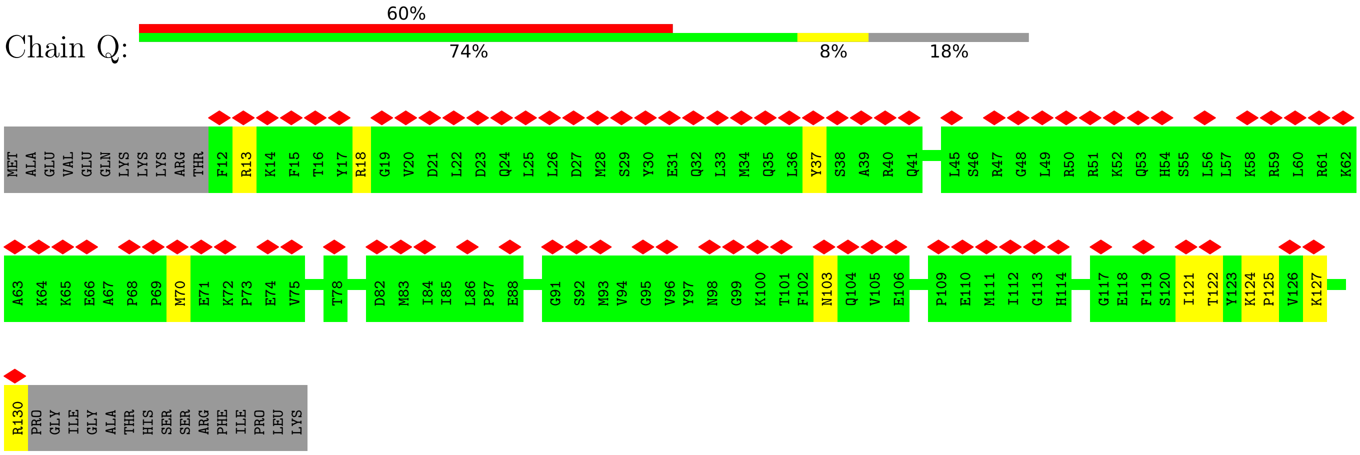
- Molecule 16: uS11

Chain P:



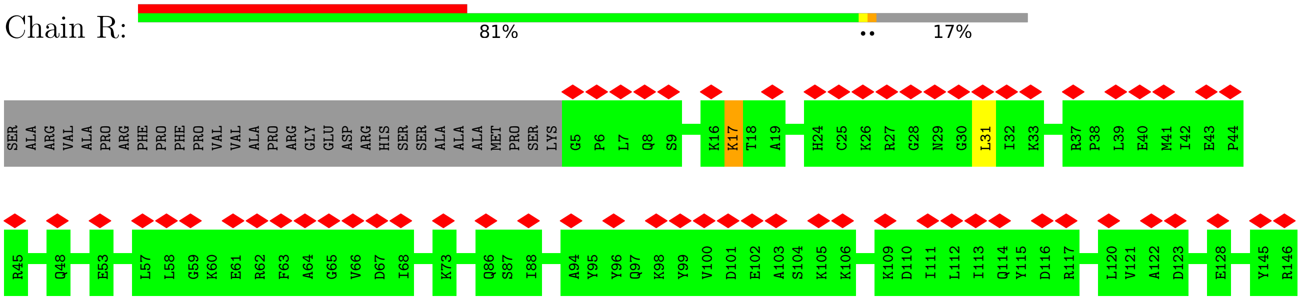
- Molecule 17: uS19

Chain Q:



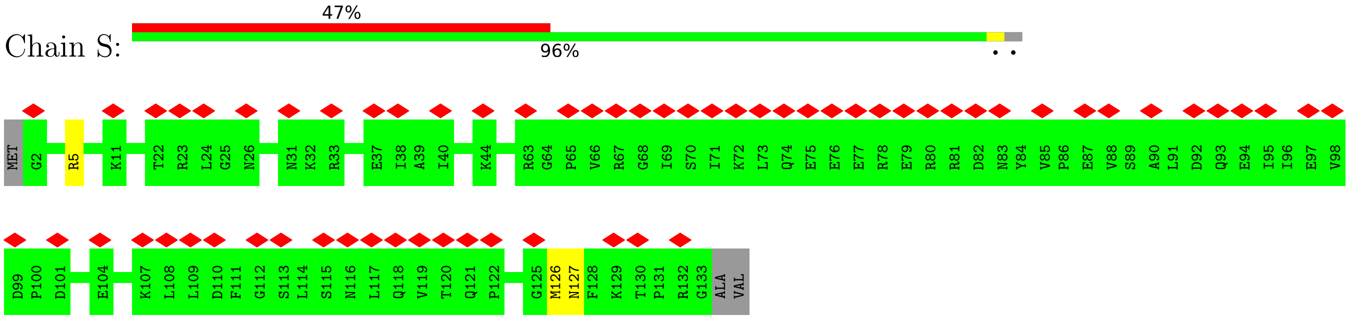
- Molecule 18: uS9

Chain R:



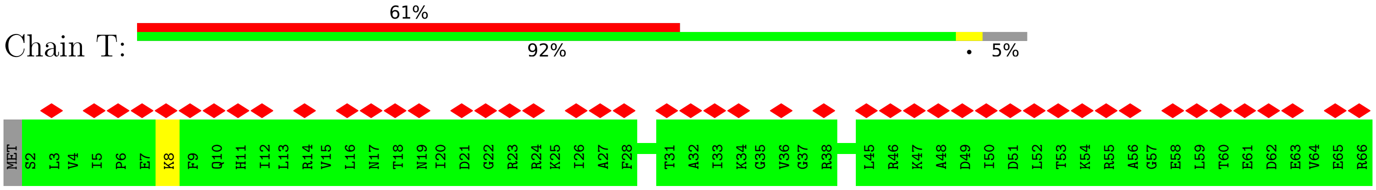
- Molecule 19: eS17

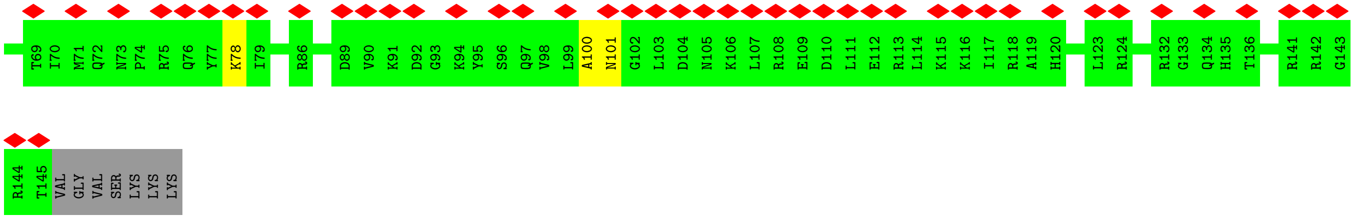
Chain S:



- Molecule 20: uS13

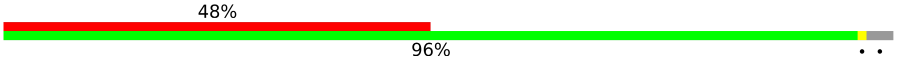
Chain T:

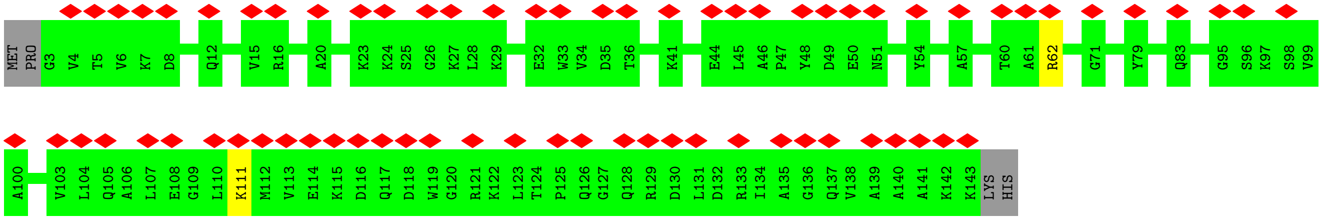




- Molecule 21: eS19

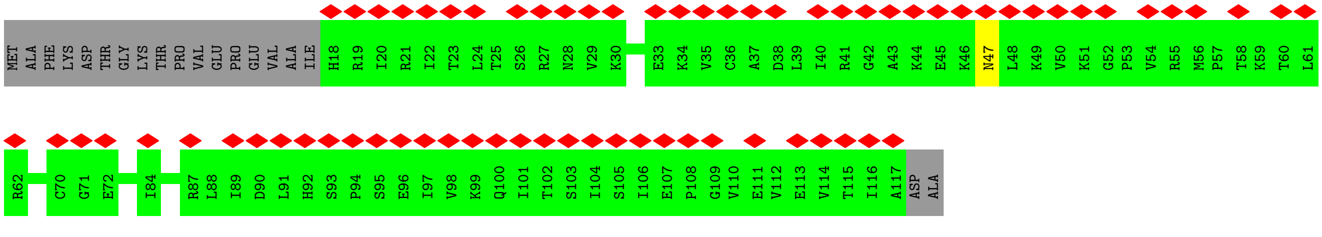
Chain U:





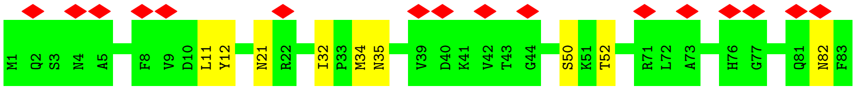
- Molecule 22: uS10

Chain V:



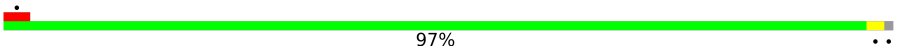
- Molecule 23: eS21

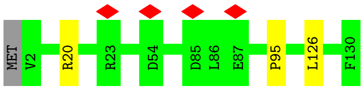
Chain W:



- Molecule 24: uS8

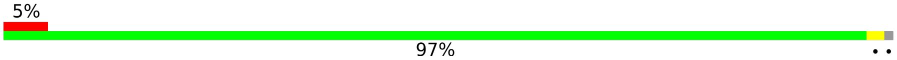
Chain X:

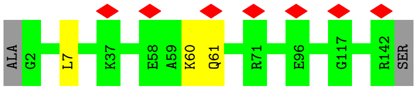




- Molecule 25: uS12

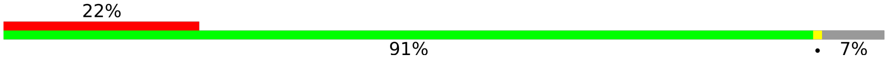
Chain Y:

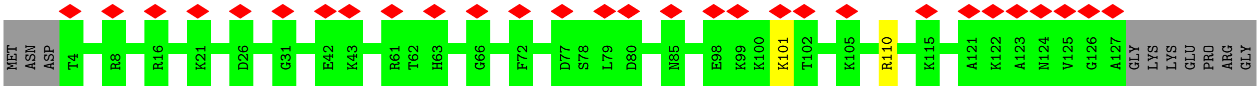




- Molecule 26: eS24

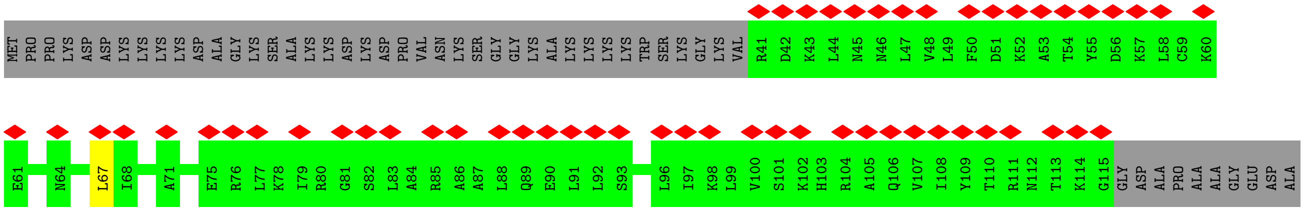
Chain Z:





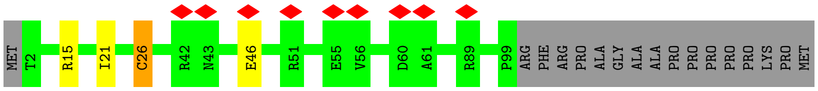
- Molecule 27: eS25

Chain a:



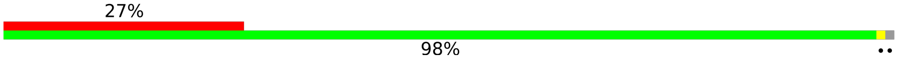
- Molecule 28: eS26

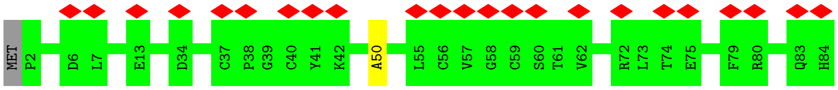
Chain b:



- Molecule 29: eS27

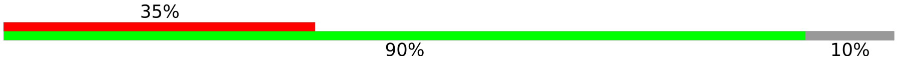
Chain c:

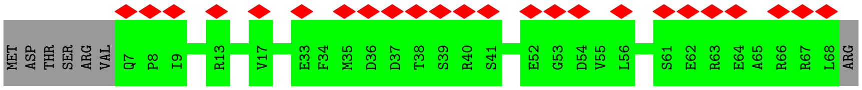




- Molecule 30: eS28

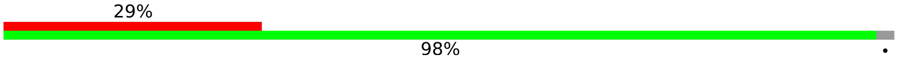
Chain d:

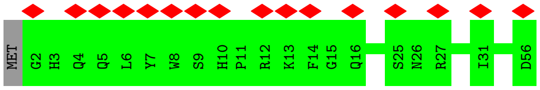




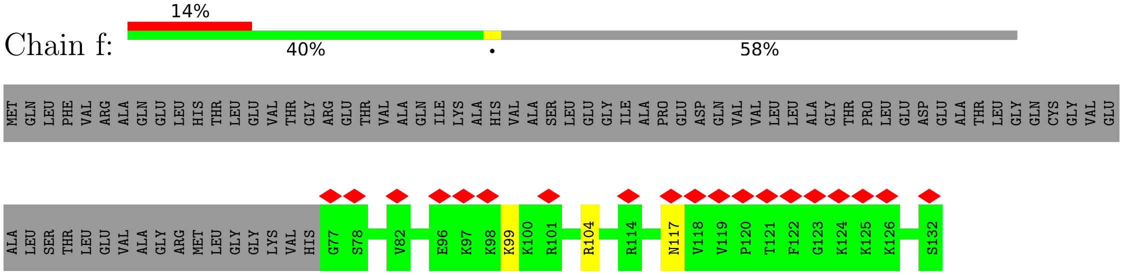
- Molecule 31: eS29

Chain e:

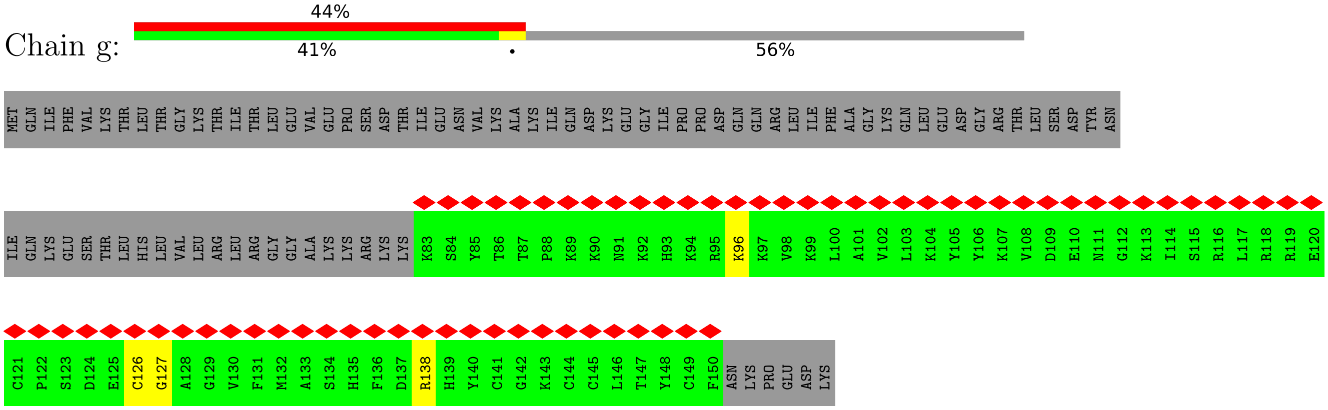




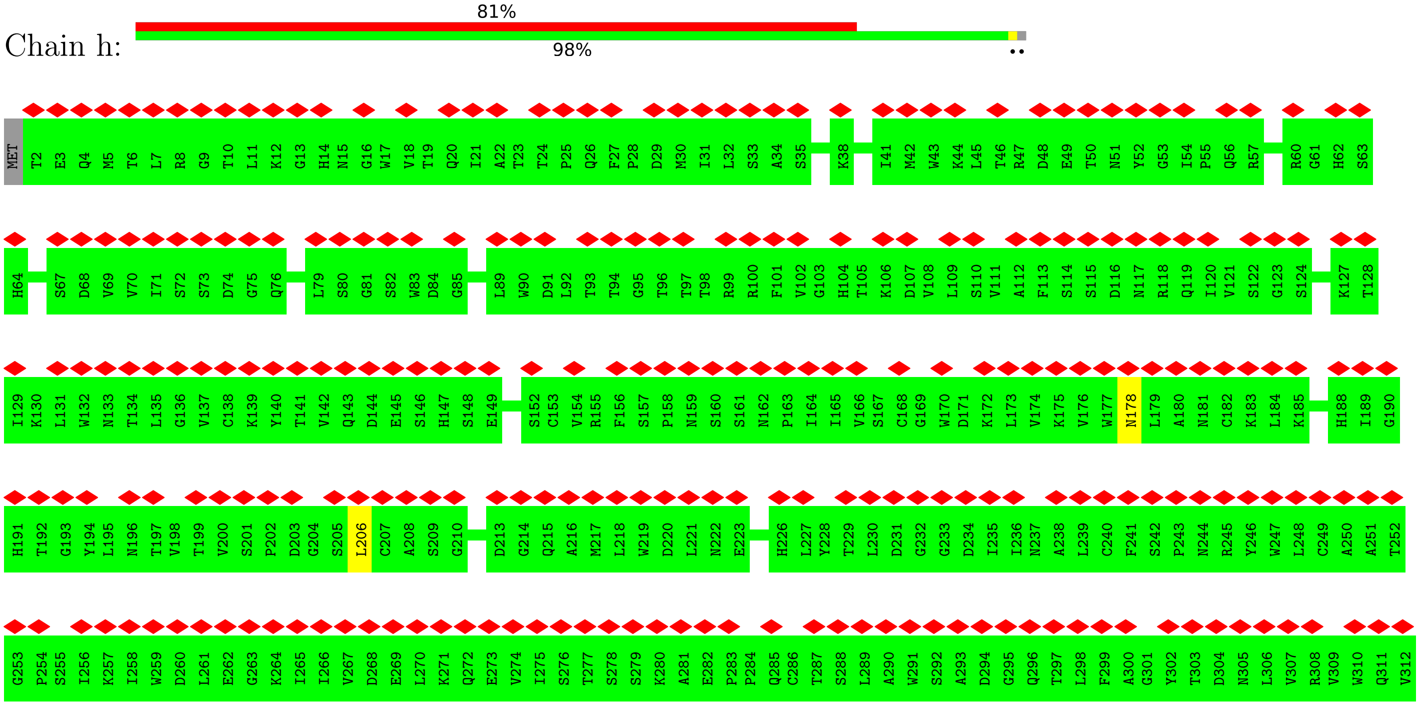
- Molecule 32: eS30

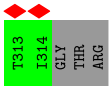


- Molecule 33: eS31



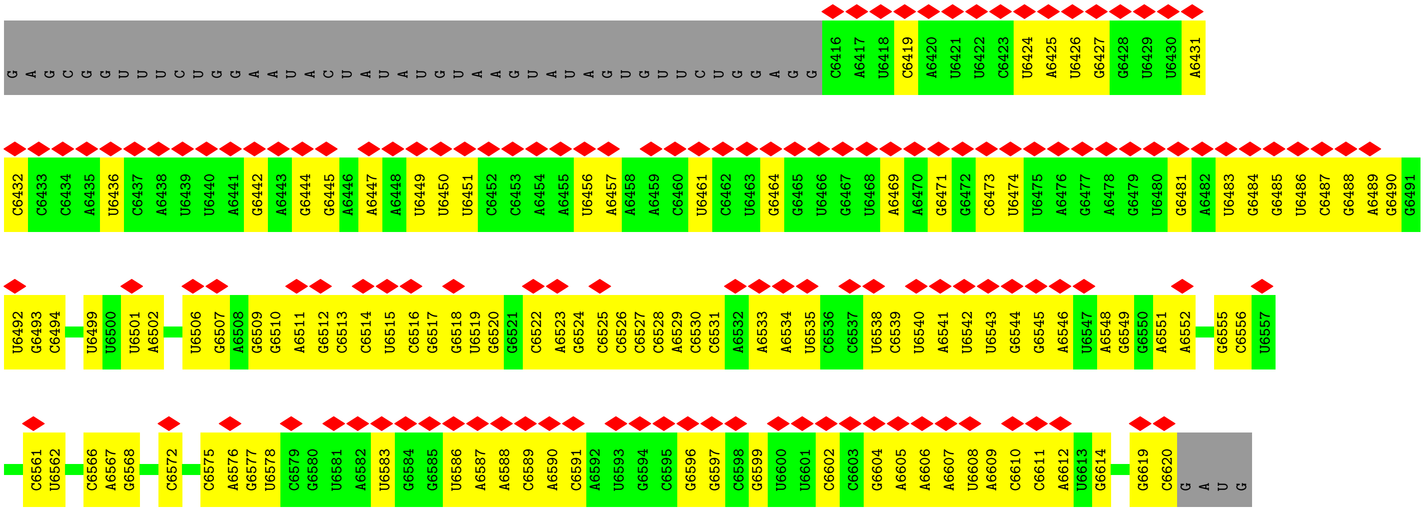
- Molecule 34: RACK1





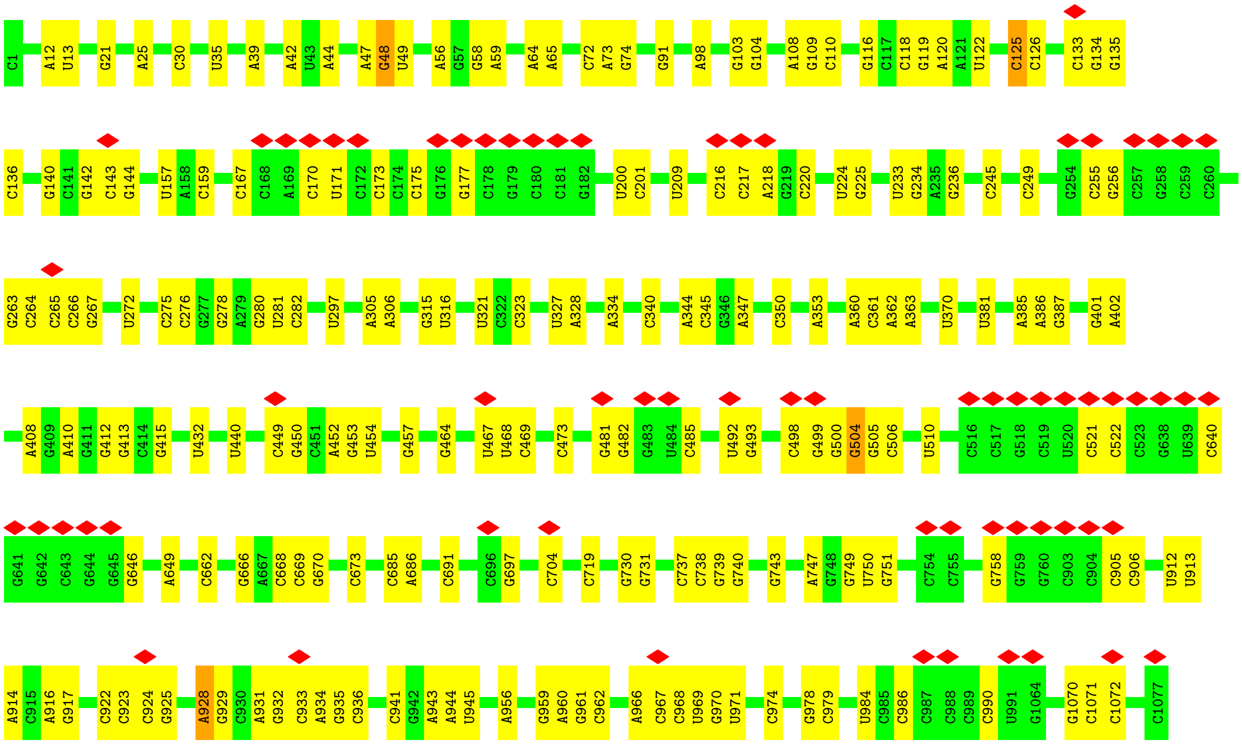
- Molecule 35: IAPV-IRES

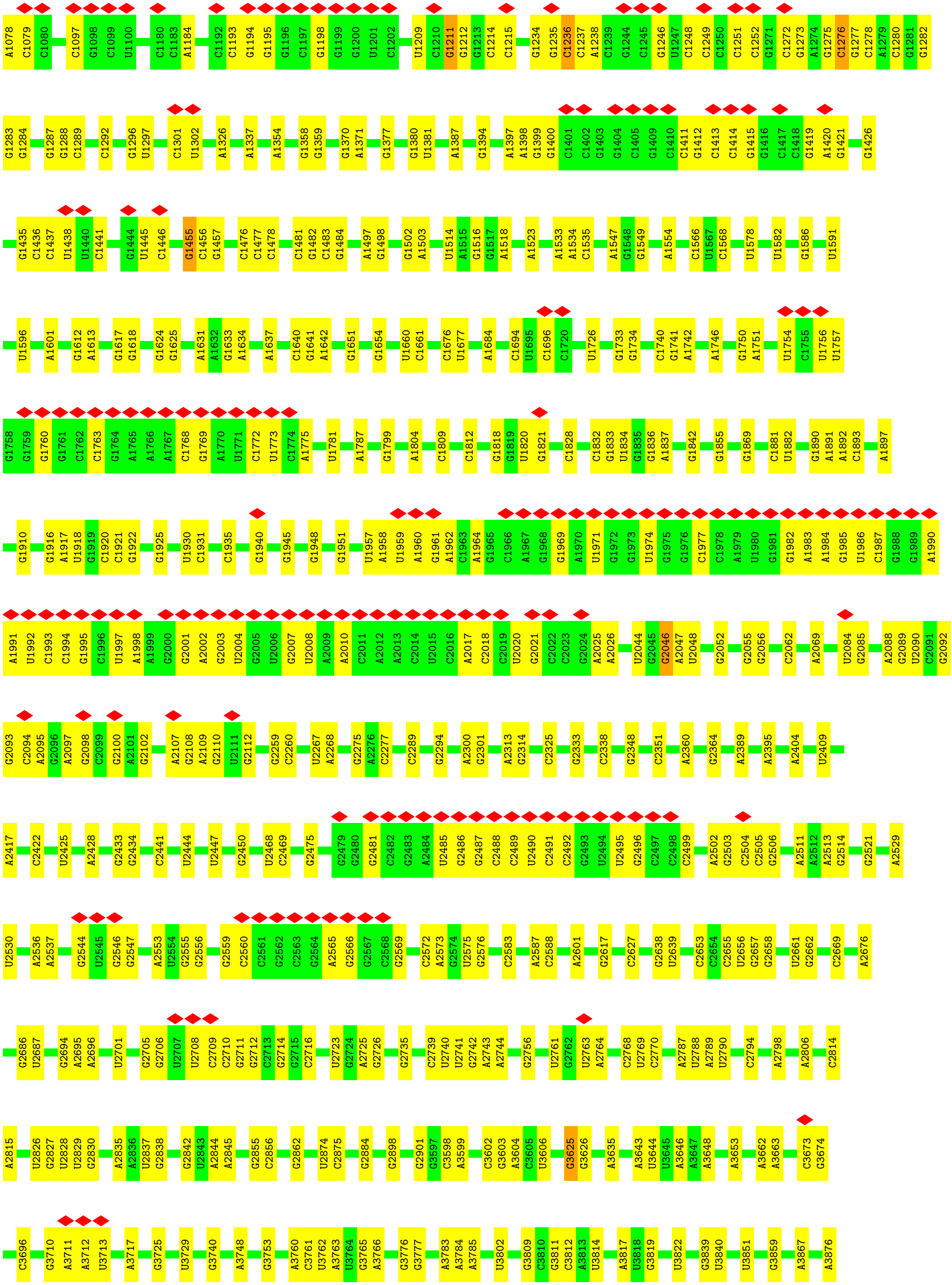
Chain 1:

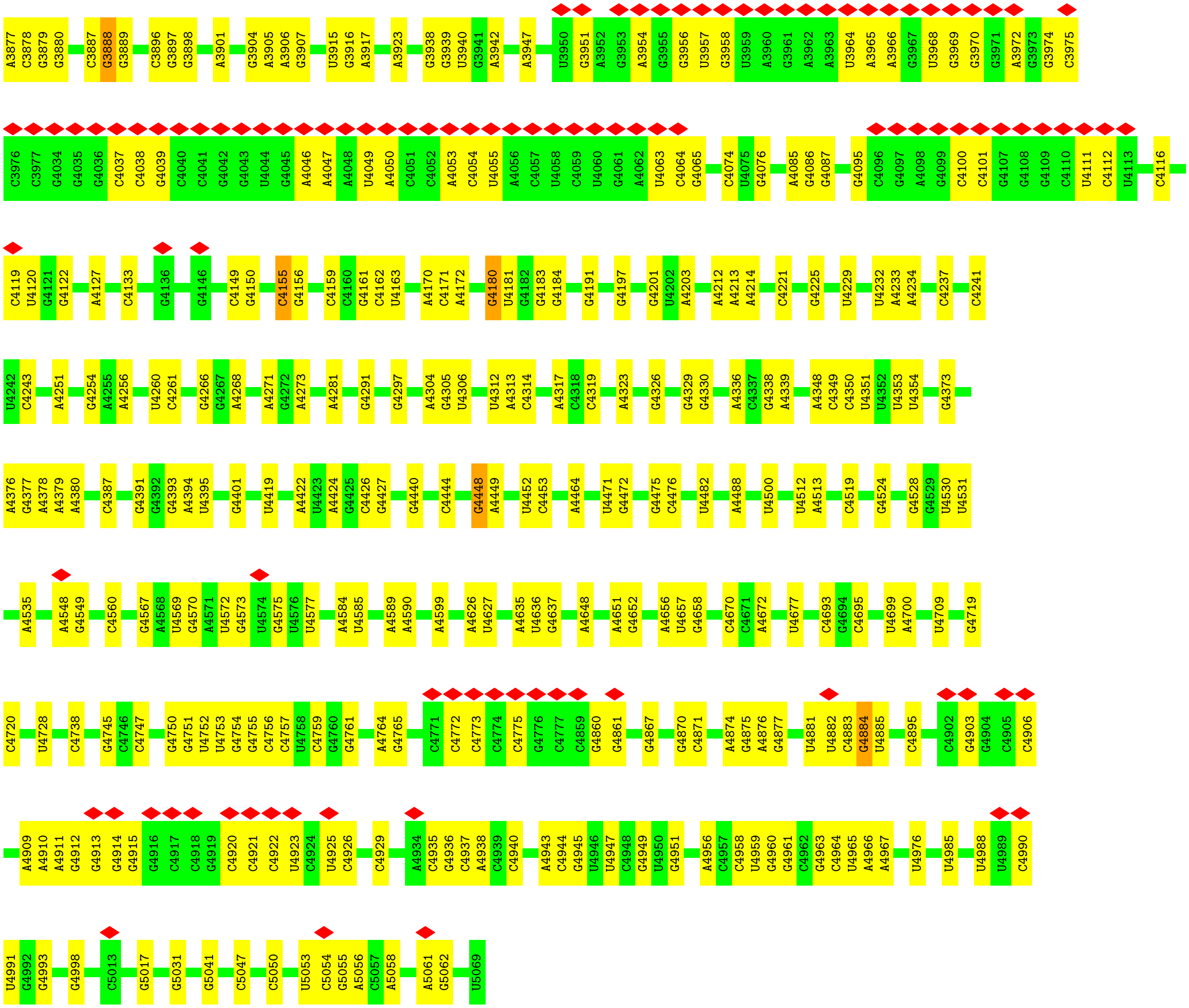


- Molecule 36: 28S rRNA

Chain 5:

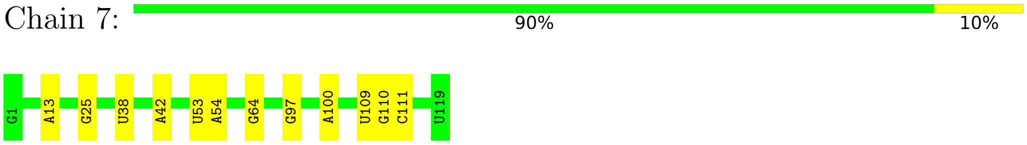



A1078 C1079 C1080 C1097 G1098 C1099 U1100 C1180 C1183 A1184 C1192 C1193 G1194 G1195 G1196 C1197 G1198 G1199 G1200 U1201 C1202 U1209 C1210 G1211 G1212 G1213 C1214 C1215 G1234 G1235 C1236 C1237 A1238 C1239 G1244 C1245 G1246 U1247 C1248 C1249 C1250 C1251 C1252 G1271 C1272 G1273 A1274 G1275 C1276 G1277 C1278 A1279 C1280 G1281 G1282
G1283 G1284 G1287 G1288 C1289 C1292 G1296 U1297 C1301 U1302 A1326 A1337 A1354 G1358 G1359 G1370 A1371 G1377 G1380 U1381 A1387 G1394 A1397 A1398 G1399 G1400 C1401 C1402 G1403 G1404 C1405 G1409 C1410 C1411 G1412 C1413 C1414 G1415 G1416 C1417 C1418 G1419 A1420 G1421 G1426
G1435 C1436 C1437 U1438 U1440 C1441 G1444 U1445 C1446 G1455 C1456 G1457 C1476 C1477 C1478 C1481 G1482 C1483 G1484 A1497 G1498 G1502 A1503 U1514 A1515 G1516 G1517 A1518 A1523 A1533 A1534 C1535 A1547 G1548 G1549 A1554 C1566 U1567 C1568 U1578 U1582 G1586 U1591
U1596 A1601 G1612 A1613 G1617 G1618 G1624 G1625 A1631 A1632 G1633 A1634 A1637 C1640 G1641 A1642 G1651 G1654 U1660 C1661 C1676 U1677 A1684 C1694 U1695 C1696 C1720 U1726 G1733 G1734 C1740 G1741 A1742 A1746 G1750 A1751 U1754 C1755 U1756 U1757
G1758 G1759 G1760 G1761 C1762 C1763 G1764 A1765 A1766 A1767 C1768 G1769 A1770 U1771 C1772 U1773 C1774 A1775 U1781 A1787 G1799 A1804 C1809 C1812 G1818 G1819 U1820 G1821 C1828 C1832 G1833 U1834 G1835 G1836 A1837 G1842 G1855 G1869 C1881 U1882 G1890 A1891 A1892 C1893 A1897
G1910 G1916 A1917 U1918 G1919 C1920 C1921 G1922 G1925 U1930 C1931 C1935 G1940 G1945 G1948 G1951 U1957 A1958 U1959 A1960 G1961 A1962 C1963 A1964 G1965 C1966 A1967 G1968 G1969 A1970 U1971 G1972 G1973 U1974 G1975 G1976 C1977 C1978 A1979 U1980 G1981 G1982 A1983 A1984 G1985 U1986 C1987 G1988 G1989 A1990
A1991 U1992 C1993 C1994 G1995 C1996 U1997 A1998 A1999 G2000 G2001 A2002 G2003 U2004 G2005 U2006 G2007 U2008 A2009 A2010 C2011 A2012 A2013 C2014 U2015 C2016 A2017 C2018 C2019 U2020 G2021 C2022 C2023 G2024 A2025 A2026 U2044 G2045 G2046 A2047 U2048 G2052 G2055 G2056 C2062 A2069 U2084 G2085 A2088 G2089 U2090 C2091 G2092
G2093 C2094 A2095 G2096 A2097 G2098 G2099 G2100 A2101 G2102 A2107 G2108 A2109 G2110 U2111 G2112 G2259 C2260 U2267 A2268 G2275 A2276 C2277 C2289 G2294 A2300 G2301 A2313 G2314 C2325 G2333 C2338 G2348 C2351 A2360 G2364 A2389 A2395 A2404 U2409
A2417 C2422 U2425 A2428 G2433 G2434 C2441 U2444 U2447 G2450 U2468 C2469 G2475 G2479 G2480 G2481 C2482 G2483 A2484 U2485 G2486 G2487 C2488 C2489 U2490 C2491 C2492 G2493 U2494 U2495 G2496 C2497 C2498 C2499 A2502 G2503 C2504 C2505 G2506 A2511 A2512 A2513 G2514 G2521 A2529
U2530 A2536 A2537 G2544 U2545 G2546 G2547 A2553 U2554 G2555 G2556 G2559 C2560 C2561 G2562 C2563 G2564 A2565 C2566 G2567 C2568 G2569 C2572 A2573 G2574 U2575 G2576 C2583 A2587 C2588 A2601 G2617 C2627 G2638 U2639 C2653 C2654 C2655 U2656 G2657 G2658 U2661 G2662 C2669 A2676
G2686 U2687 G2694 A2695 A2696 U2701 G2705 G2706 U2707 U2708 C2709 C2710 G2711 G2712 C2713 G2714 G2715 C2716 U2723 G2724 A2725 G2726 G2735 C2739 U2740 U2741 G2742 A2743 A2744 G2756 U2761 G2762 U2763 A2764 C2768 U2769 C2770 A2787 U2788 A2789 U2790 C2794 A2798 A2806 C2814
A2815 U2826 G2827 U2828 U2829 G2830 A2835 A2836 U2837 G2838 G2842 U2843 A2844 A2845 G2855 C2856 G2862 U2874 C2875 G2884 G2898 G2901 G3597 C3598 A3599 C3602 G3603 A3604 C3605 U3606 G3625 G3626 A3635 A3643 U3644 U3645 A3646 A3647 A3648 A3653 A3662 A3663 C3673 G3674
C3696 G3710 A3711 A3712 U3713 A3717 G3725 U3729 G3740 A3748 G3753 A3760 C3761 U3762 A3763 U3764 G3765 A3766 G3776 G3777 A3783 A3784 A3785 U3802 G3809 C3810 C3811 C3812 A3813 U3814 A3817 U3818 G3819 U3822 G3839 U3840 U3851 G3859 A3867 A3876



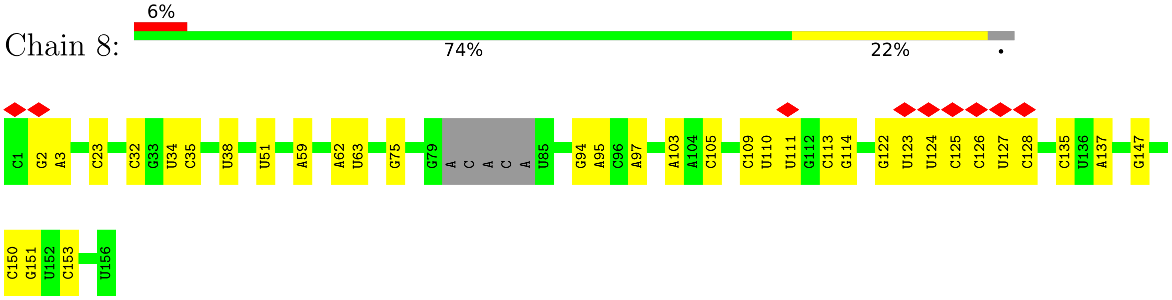
- Molecule 37: 5S rRNA

Chain 7:



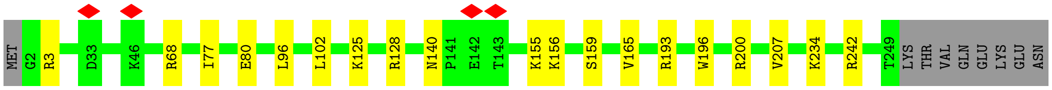
- Molecule 38: 5.8S rRNA

Chain 8:



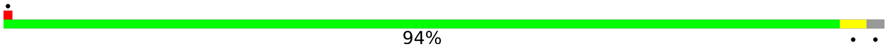
- Molecule 39: uL2

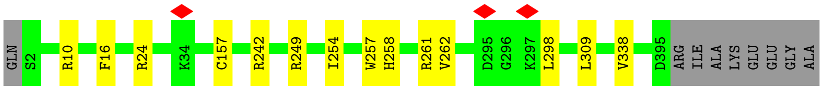
Chain AA:



- Molecule 40: uL3

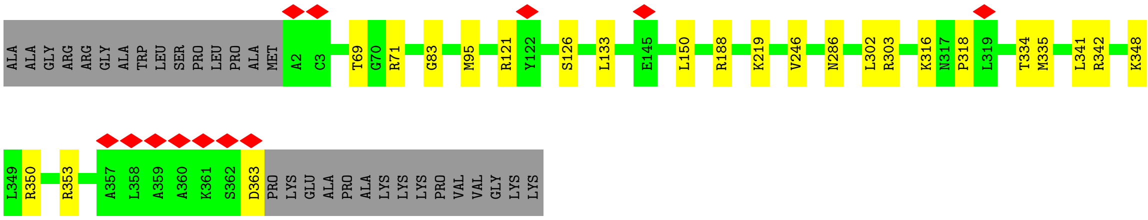
Chain AB:





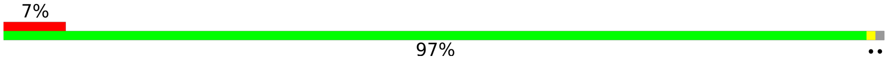
- Molecule 41: uL4

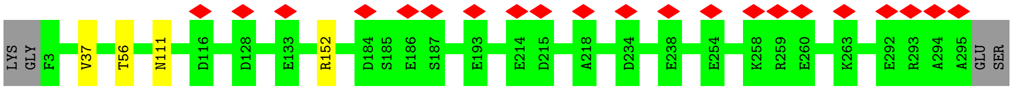
Chain AC:



- Molecule 42: uL18

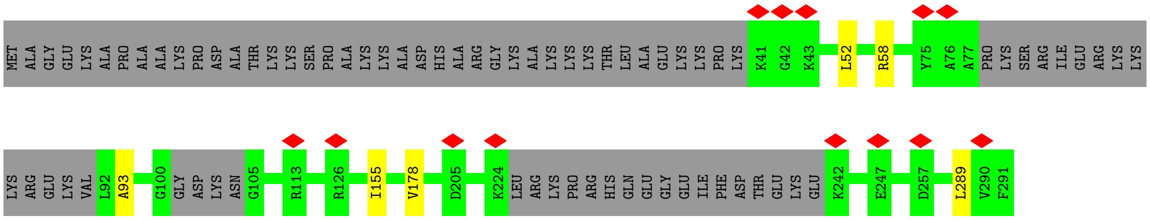
Chain AD:





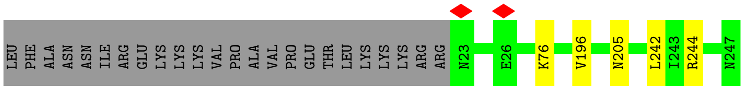
- Molecule 43: eL6

Chain AE:



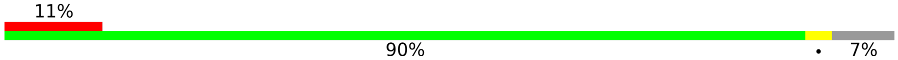
- Molecule 44: uL30

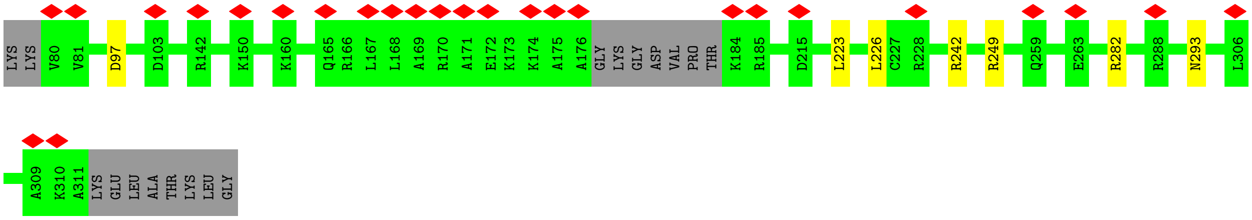
Chain AF:



- Molecule 45: eL8

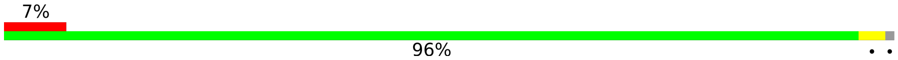
Chain AG:

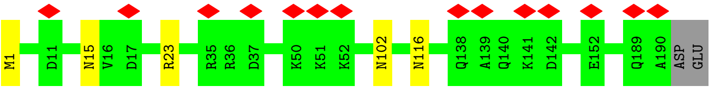




- Molecule 46: uL6

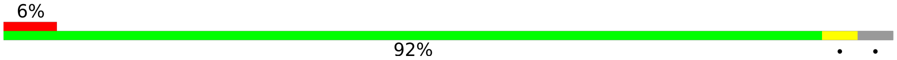
Chain AH:

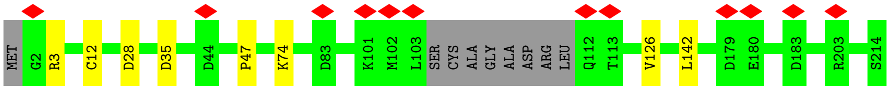




- Molecule 47: uL16

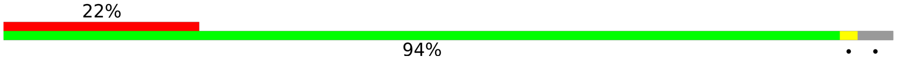
Chain AI:

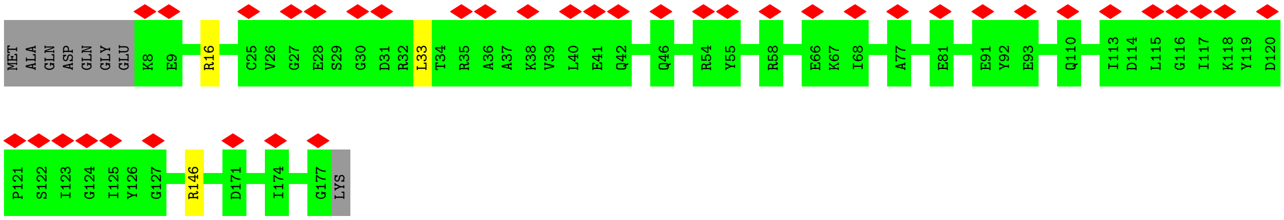




- Molecule 48: uL11

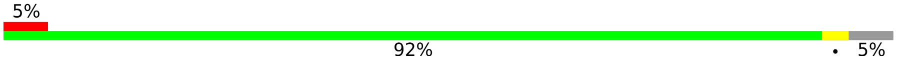
Chain AJ:

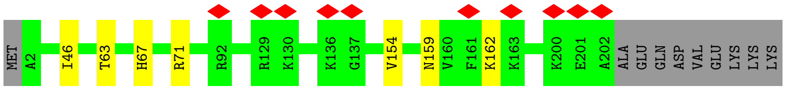




- Molecule 49: eL13

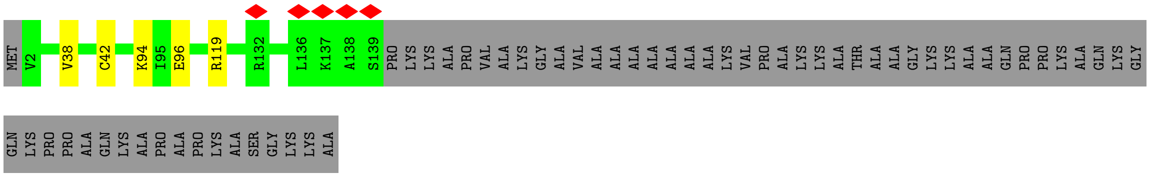
Chain AL:





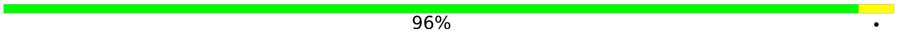
- Molecule 50: L14e

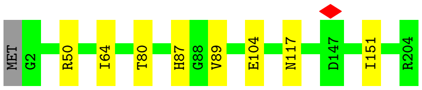
Chain AM:



- Molecule 51: eL15

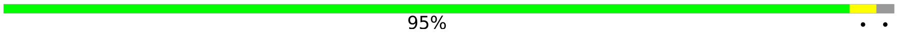
Chain AN:

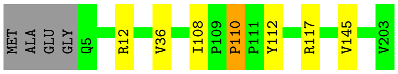




- Molecule 52: uL13

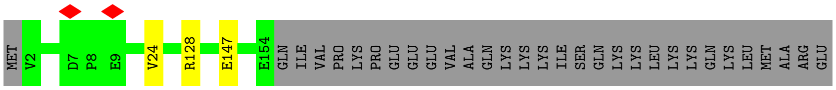
Chain AO:





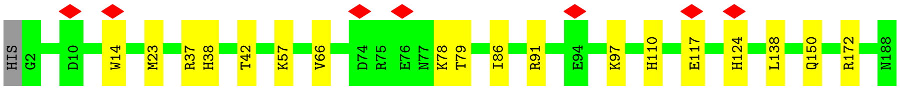
- Molecule 53: uL22

Chain AP:



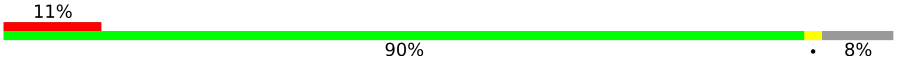
- Molecule 54: eL18

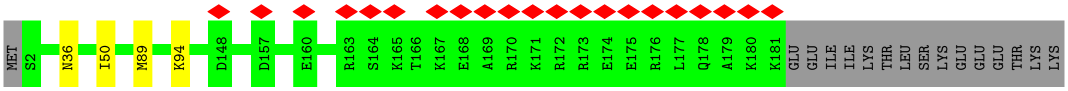
Chain AQ:



- Molecule 55: eL19

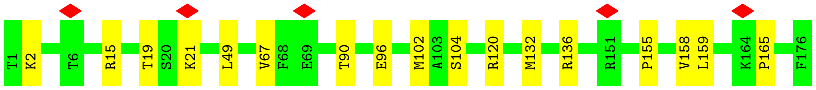
Chain AR:





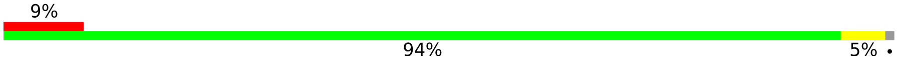
- Molecule 56: eL20

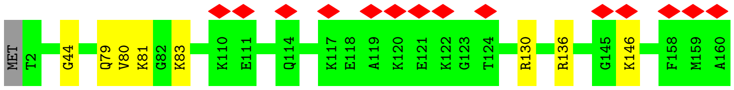
Chain AS:



- Molecule 57: eL21

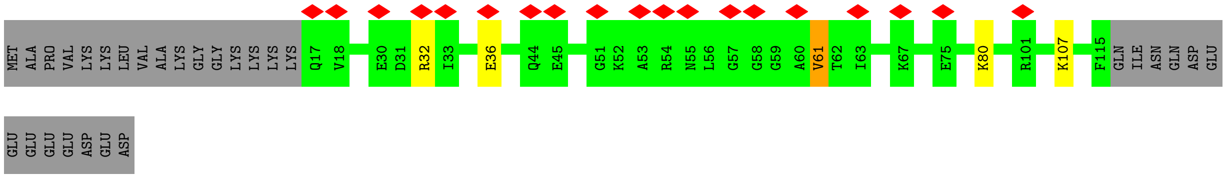
Chain AT:





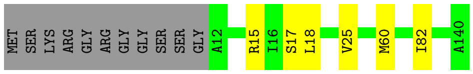
- Molecule 58: eL22

Chain AU:



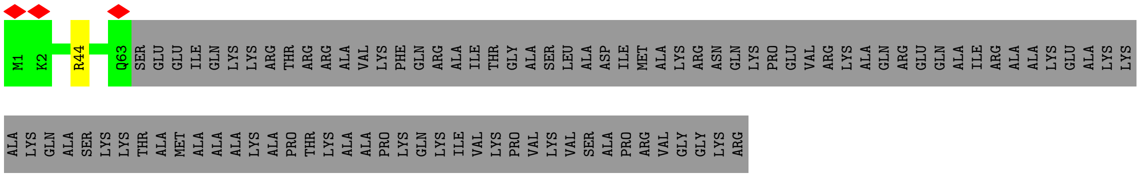
- Molecule 59: uL14

Chain AV:



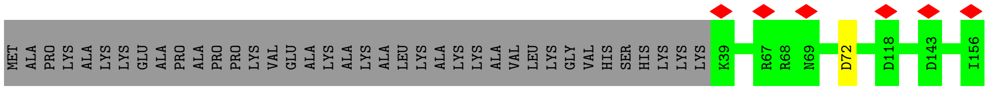
- Molecule 60: eL24

Chain AW:



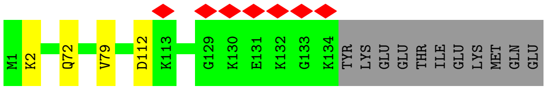
- Molecule 61: eL23

Chain AX:



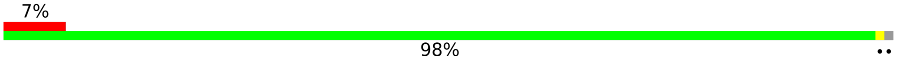
- Molecule 62: uL24

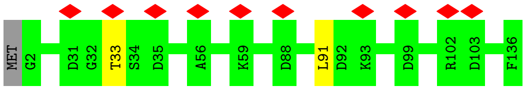
Chain AY:



- Molecule 63: eL27

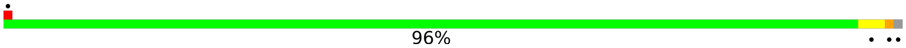
Chain AZ:

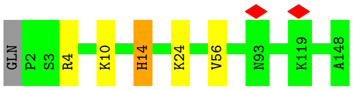




- Molecule 64: uL15

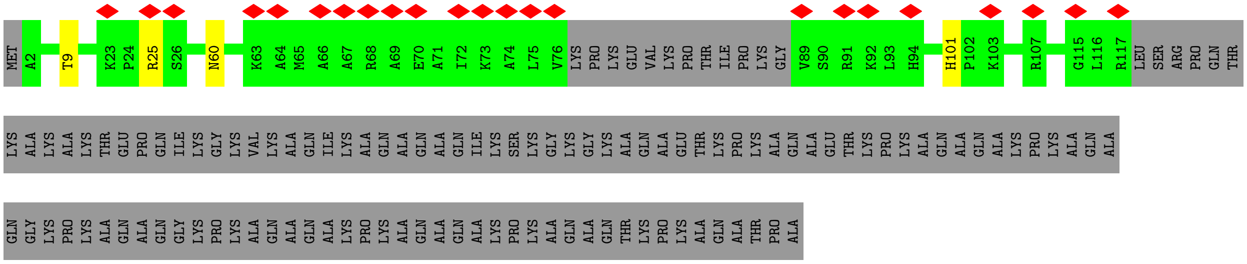
Chain Aa:





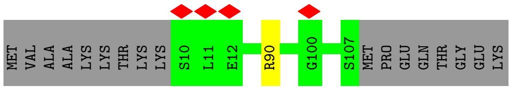
- Molecule 65: eL29

Chain Ab:



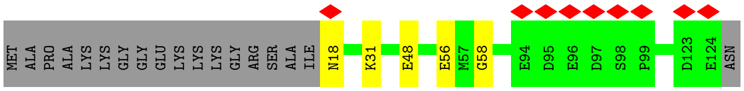
- Molecule 66: eL30

Chain Ac:



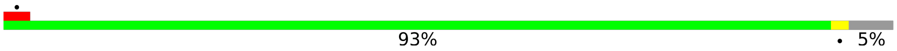
- Molecule 67: eL31

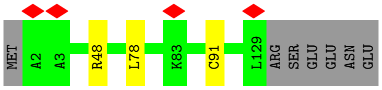
Chain Ad:



- Molecule 68: eL32

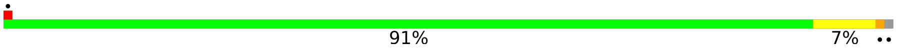
Chain Ae:

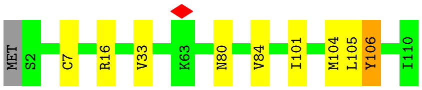




- Molecule 69: eL33

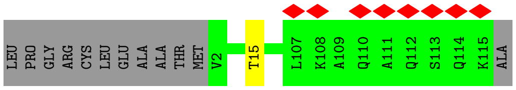
Chain Af:





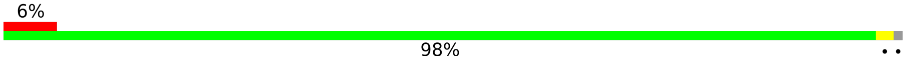
- Molecule 70: eL34

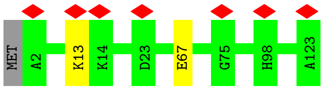
Chain Ag:



- Molecule 71: eL35

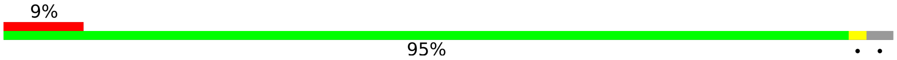
Chain Ah:

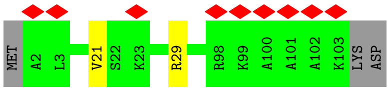




- Molecule 72: eL36

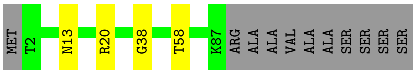
Chain Ai:





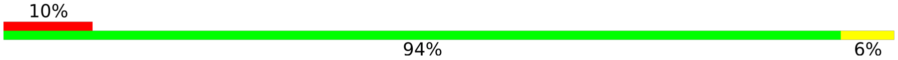
- Molecule 73: eL37

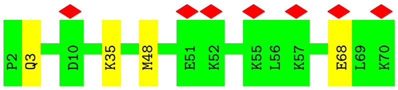
Chain Aj:



- Molecule 74: eL38

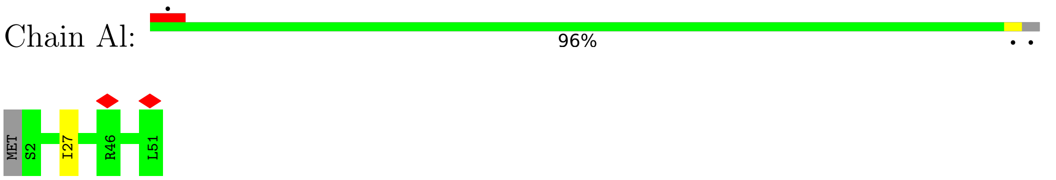
Chain Ak:





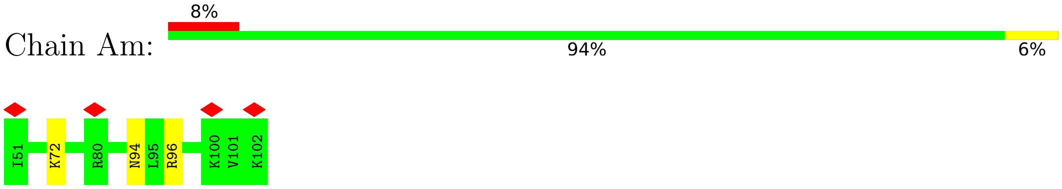
- Molecule 75: eL39

Chain Al:



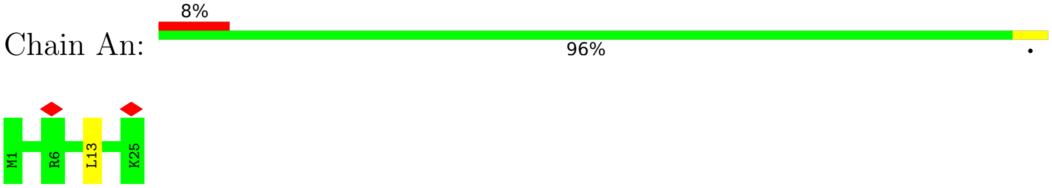
- Molecule 76: eL40

Chain Am:



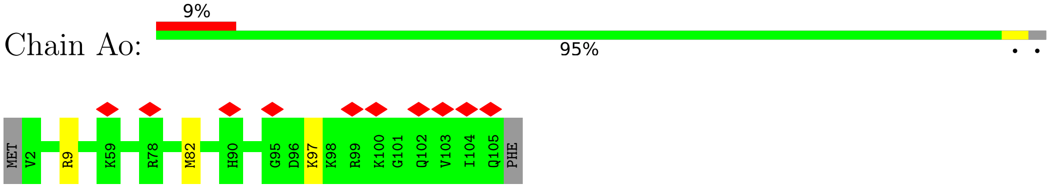
- Molecule 77: eL41

Chain An:



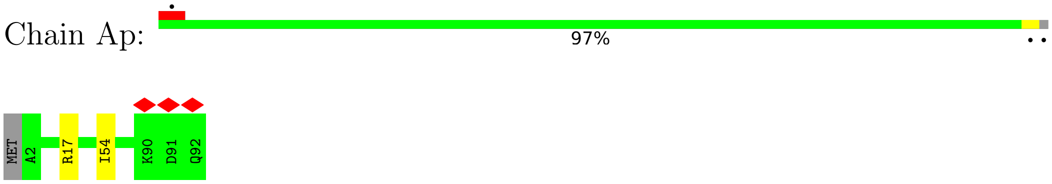
- Molecule 78: eL42

Chain Ao:



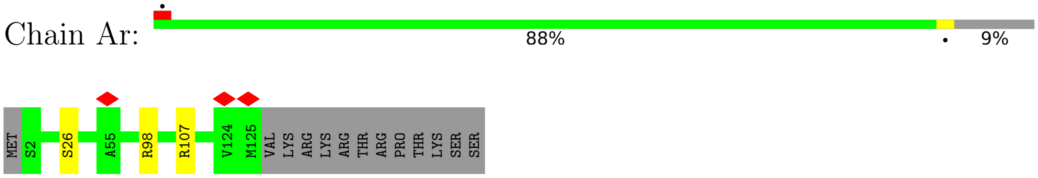
- Molecule 79: eL43

Chain Ap:



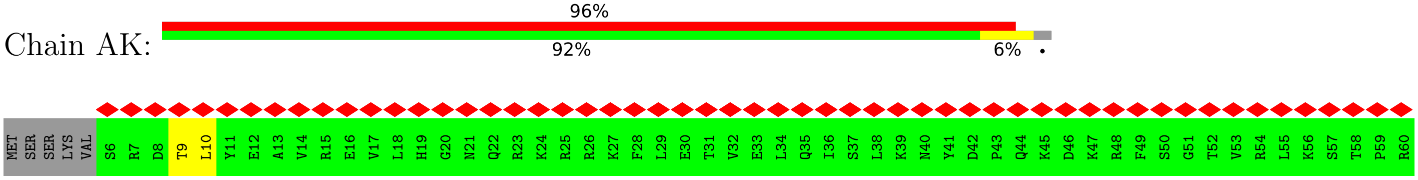
- Molecule 80: eL28

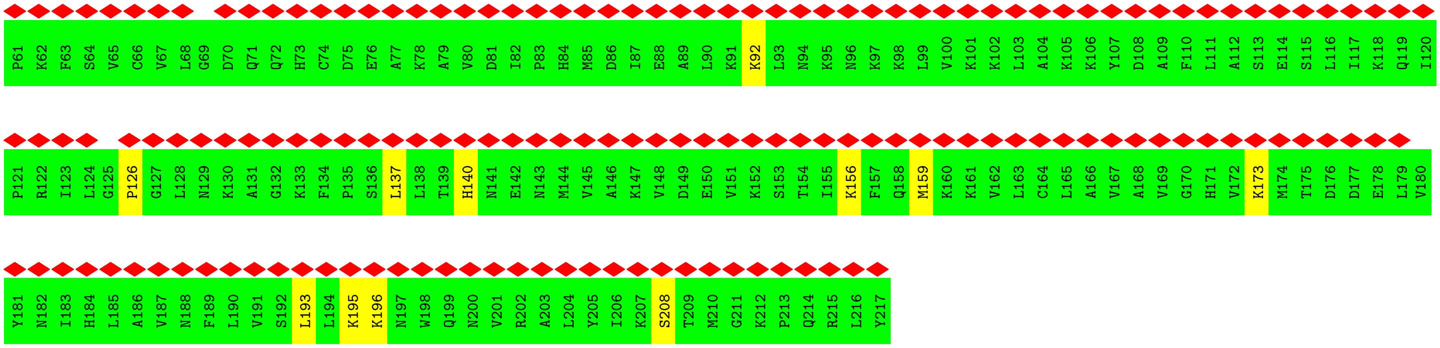
Chain Ar:



- Molecule 81: uL1

Chain AK:




P61 K62 F63 S64 V65 C66 V67 L68 G69 D70 Q71 Q72 H73 C74 D75 E76 A77 K78 A79 V80 D81 I82 P83 H84 M85 D86 I87 E88 A89 L90 K91 K92 L93 N94 K95 N96 K97 K98 L99 V100 K101 K102 L103 A104 K105 K106 Y107 D108 A109 F110 L111 A112 S113 E114 S115 L116 I117 K118 Q119 I120
P121 R122 I123 L124 G125 P126 G127 L128 N129 K130 A131 G132 K133 F134 P135 S136 L137 L138 T139 H140 N141 E142 N143 M144 V145 A146 K147 V148 D149 E150 V151 K152 S153 T154 I155 K156 F157 Q158 M159 K160 K161 V162 L163 C164 L165 A166 V167 A168 V169 G170 H171 V172 K173 M174 T175 D176 D177 E178 L179 V180
Y181 N182 I183 H184 L185 A186 V187 N188 F189 L190 V191 S192 L193 L194 K195 K196 N197 W198 Q199 N200 V201 R202 A203 L204 Y205 I206 K207 S208 T209 M210 G211 K212 P213 Q214 R215 L216 Y217

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 ($e^-/\text{Å}^2$)	42.09	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	31000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.289	Depositor
Minimum map value	-0.163	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.032	Depositor
Map size (Å)	443.88, 443.88, 443.88	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.233, 1.233, 1.233	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	2	0.23	0/40509	0.69	6/63128 (0.0%)
2	B	0.66	0/1744	0.78	0/2371
3	C	0.66	0/1756	0.79	0/2350
4	D	0.66	0/1748	0.80	0/2362
5	E	0.69	0/1796	0.81	0/2417
6	F	0.66	0/2115	0.81	0/2843
7	G	0.68	0/1492	0.79	0/2005
8	H	0.67	0/1946	0.83	0/2590
9	I	0.68	0/1510	0.78	0/2022
10	J	0.65	0/1715	0.82	0/2287
11	K	0.67	0/1550	0.83	0/2069
12	L	0.66	0/834	0.78	0/1125
13	M	0.65	0/1195	0.81	0/1597
14	N	0.72	0/918	0.80	0/1233
15	O	0.67	0/1226	0.80	0/1649
16	P	0.67	0/1029	0.84	0/1380
17	Q	0.67	0/1009	0.80	0/1346
18	R	0.68	0/1146	0.81	0/1534
19	S	0.68	0/1082	0.79	0/1452
20	T	0.68	0/1208	0.81	0/1618
21	U	0.69	0/1115	0.81	0/1493
22	V	0.69	0/805	0.80	0/1081
23	W	0.69	0/638	0.83	0/855
24	X	0.66	0/1051	0.80	0/1406
25	Y	0.66	0/1116	0.83	0/1490
26	Z	0.67	0/1028	0.80	0/1366
27	a	0.69	0/604	0.80	0/810
28	b	0.65	0/789	0.81	0/1059
29	c	0.66	0/665	0.79	0/891
30	d	0.69	0/490	0.83	0/656
31	e	0.67	0/470	0.80	0/623
32	f	0.68	0/451	0.81	0/592
33	g	0.69	0/567	0.83	0/753
34	h	0.69	0/2493	0.80	0/3394

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
78	Ao	0.63	0/864	0.82	0/1140
79	Ap	0.66	0/718	0.84	0/953
80	Ar	0.65	0/1010	0.84	0/1354
81	AK	0.69	0/1733	0.84	0/2324
All	All	0.46	0/232234	0.74	23/341283 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
28	b	0	1
40	AB	0	2
All	All	0	3

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^o^)	Ideal(^o^)
69	Af	106	TYR	CB-CA-C	9.14	128.67	110.40
36	5	4180	G	C2'-C3'-O3'	7.16	125.24	109.50
36	5	3625	G	C2'-C3'-O3'	6.05	123.39	113.70
1	2	1685	U	C2'-C3'-O3'	5.89	123.12	113.70
36	5	928	A	C2'-C3'-O3'	5.83	123.03	113.70
1	2	110	U	C2'-C3'-O3'	5.70	122.82	113.70
36	5	4884	G	C2'-C3'-O3'	5.70	122.81	113.70
1	2	688	U	C2'-C3'-O3'	5.69	122.80	113.70
1	2	24	C	C2'-C3'-O3'	5.68	122.79	113.70
36	5	4155	C	C2'-C3'-O3'	5.67	122.78	113.70
36	5	2046	G	C2'-C3'-O3'	5.67	122.78	113.70
36	5	125	C	C2'-C3'-O3'	5.63	122.71	113.70
36	5	1211	G	C2'-C3'-O3'	5.60	122.67	113.70
36	5	1276	C	P-O3'-C3'	5.33	126.10	119.70
36	5	4448	G	C4'-C3'-O3'	5.32	123.63	113.00
1	2	1743	G	C2'-C3'-O3'	5.29	122.17	113.70
36	5	504	G	C2'-C3'-O3'	5.26	122.11	113.70
36	5	1455	G	C2'-C3'-O3'	5.23	122.07	113.70
64	Aa	14	HIS	CB-CA-C	5.20	120.81	110.40
36	5	1236	C	C4'-C3'-O3'	5.19	123.37	113.00
36	5	48	G	C2'-C3'-O3'	5.14	121.93	113.70
36	5	3888	G	C2'-C3'-O3'	5.13	121.91	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2	627	U	C2'-C3'-O3'	5.04	121.76	113.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

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

5.2 Too-close contacts ⓘ

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

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	215/295 (73%)	196 (91%)	17 (8%)	2 (1%)	17	52
3	C	211/264 (80%)	188 (89%)	23 (11%)	0	100	100
4	D	219/255 (86%)	199 (91%)	18 (8%)	2 (1%)	17	52
5	E	226/281 (80%)	209 (92%)	17 (8%)	0	100	100
6	F	260/263 (99%)	239 (92%)	20 (8%)	1 (0%)	34	69
7	G	181/204 (89%)	169 (93%)	10 (6%)	2 (1%)	14	46
8	H	235/249 (94%)	210 (89%)	25 (11%)	0	100	100
9	I	181/194 (93%)	169 (93%)	11 (6%)	1 (1%)	25	59
10	J	204/207 (99%)	187 (92%)	15 (7%)	2 (1%)	15	49
11	K	183/194 (94%)	167 (91%)	16 (9%)	0	100	100
12	L	94/149 (63%)	86 (92%)	8 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	5	26
18	R	140/172 (81%)	127 (91%)	12 (9%)	1 (1%)	22	57
19	S	130/135 (96%)	120 (92%)	9 (7%)	1 (1%)	19	54
20	T	142/152 (93%)	125 (88%)	15 (11%)	2 (1%)	11	40
21	U	139/145 (96%)	126 (91%)	12 (9%)	1 (1%)	22	57
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%)	19	54
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%)	7	30
29	c	81/84 (96%)	71 (88%)	9 (11%)	1 (1%)	13	44
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%)	8	33
33	g	66/156 (42%)	58 (88%)	6 (9%)	2 (3%)	4	23
34	h	311/317 (98%)	268 (86%)	43 (14%)	0	100	100
39	AA	246/257 (96%)	230 (94%)	14 (6%)	2 (1%)	19	54
40	AB	392/403 (97%)	362 (92%)	30 (8%)	0	100	100
41	AC	360/392 (92%)	337 (94%)	20 (6%)	3 (1%)	19	54
42	AD	291/297 (98%)	270 (93%)	20 (7%)	1 (0%)	41	73
43	AE	208/291 (72%)	184 (88%)	23 (11%)	1 (0%)	29	64
44	AF	223/249 (90%)	211 (95%)	11 (5%)	1 (0%)	34	69
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%)	15	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	AJ	168/178 (94%)	159 (95%)	8 (5%)	1 (1%)	25	59
49	AL	199/211 (94%)	191 (96%)	7 (4%)	1 (0%)	29	64
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%)	29	64
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%)	9	36
57	AT	157/160 (98%)	143 (91%)	12 (8%)	2 (1%)	12	42
58	AU	97/128 (76%)	86 (89%)	10 (10%)	1 (1%)	15	49
59	AV	127/140 (91%)	120 (94%)	6 (5%)	1 (1%)	19	54
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%)	19	54
64	Aa	145/148 (98%)	132 (91%)	11 (8%)	2 (1%)	11	40
65	Ab	100/226 (44%)	94 (94%)	5 (5%)	1 (1%)	15	49
66	Ac	96/115 (84%)	91 (95%)	5 (5%)	0	100	100
67	Ad	105/125 (84%)	97 (92%)	7 (7%)	1 (1%)	15	49
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%)	13	44
74	Ak	67/69 (97%)	63 (94%)	3 (4%)	1 (2%)	10	39
75	Al	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
76	Am	50/52 (96%)	49 (98%)	0	1 (2%)	7	31
77	An	23/25 (92%)	23 (100%)	0	0	100	100
78	Ao	102/106 (96%)	97 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	8	33
All	All	11321/12916 (88%)	10408 (92%)	856 (8%)	57 (0%)	32	64

All (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
49	AL	63	THR
52	AO	110	PRO
58	AU	61	VAL
76	Am	94	ASN
81	AK	140	HIS
2	B	44	ASP
7	G	20	PHE
17	Q	70	MET
21	U	111	LYS
44	AF	196	VAL
48	AJ	146	ARG
65	Ab	25	ARG
67	Ad	58	GLY
73	Aj	38	GLY
7	G	77	MET
10	J	41	ARG
10	J	94	LYS
20	T	78	LYS
39	AA	234	LYS
41	AC	83	GLY
42	AD	152	ARG
43	AE	93	ALA
47	AI	12	CYS
57	AT	44	GLY
64	Aa	14	HIS
74	Ak	68	GLU
81	AK	126	PRO
81	AK	208	SER

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Mol	Chain	Res	Type
6	F	73	ASP
28	b	26	CYS
29	c	50	ALA
56	AS	158	VAL
63	AZ	91	LEU
64	Aa	24	LYS
81	AK	193	LEU
4	D	134	ASN
17	Q	125	PRO
28	b	46	GLU
33	g	96	LYS
39	AA	196	TRP
41	AC	318	PRO
59	AV	17	SER
4	D	99	GLY
19	S	126	MET
32	f	117	ASN
57	AT	130	ARG
9	I	54	GLY
56	AS	155	PRO
24	X	95	PRO
56	AS	165	PRO
33	g	127	GLY
47	AI	47	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	181 (97%)	5 (3%)	44	74
5	E	190/232 (82%)	182 (96%)	8 (4%)	30	62
6	F	223/225 (99%)	217 (97%)	6 (3%)	44	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G	158/170 (93%)	155 (98%)	3 (2%)	57	81
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%)	172 (97%)	6 (3%)	37	69
11	K	161/168 (96%)	157 (98%)	4 (2%)	47	75
12	L	87/125 (70%)	86 (99%)	1 (1%)	73	89
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%)	128 (98%)	2 (2%)	65	85
16	P	106/119 (89%)	104 (98%)	2 (2%)	57	81
17	Q	108/130 (83%)	100 (93%)	8 (7%)	13	42
18	R	117/140 (84%)	115 (98%)	2 (2%)	60	83
19	S	119/121 (98%)	117 (98%)	2 (2%)	60	83
20	T	125/132 (95%)	123 (98%)	2 (2%)	62	84
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%)	59 (87%)	9 (13%)	4	17
24	X	112/113 (99%)	110 (98%)	2 (2%)	59	82
25	Y	113/114 (99%)	110 (97%)	3 (3%)	44	74
26	Z	107/115 (93%)	105 (98%)	2 (2%)	57	81
27	a	66/103 (64%)	65 (98%)	1 (2%)	65	85
28	b	85/99 (86%)	83 (98%)	2 (2%)	49	76
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%)	270 (99%)	2 (1%)	84	93
39	AA	189/199 (95%)	172 (91%)	17 (9%)	9	34
40	AB	342/348 (98%)	330 (96%)	12 (4%)	36	68
41	AC	302/323 (94%)	281 (93%)	21 (7%)	15	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	192 (98%)	4 (2%)	55	80
45	AG	194/208 (93%)	187 (96%)	7 (4%)	35	67
46	AH	169/171 (99%)	164 (97%)	5 (3%)	41	71
47	AI	175/181 (97%)	169 (97%)	6 (3%)	37	69
48	AJ	143/149 (96%)	141 (99%)	2 (1%)	67	86
49	AL	167/176 (95%)	161 (96%)	6 (4%)	35	67
50	AM	117/151 (78%)	112 (96%)	5 (4%)	29	62
51	AN	171/172 (99%)	163 (95%)	8 (5%)	26	59
52	AO	171/173 (99%)	164 (96%)	7 (4%)	30	64
53	AP	134/163 (82%)	131 (98%)	3 (2%)	52	78
54	AQ	166/167 (99%)	148 (89%)	18 (11%)	6	25
55	AR	159/175 (91%)	155 (98%)	4 (2%)	47	75
56	AS	155/155 (100%)	141 (91%)	14 (9%)	9	34
57	AT	139/140 (99%)	133 (96%)	6 (4%)	29	62
58	AU	91/116 (78%)	86 (94%)	5 (6%)	21	53
59	AV	100/107 (94%)	95 (95%)	5 (5%)	24	57
60	AW	55/126 (44%)	54 (98%)	1 (2%)	59	82
61	AX	106/134 (79%)	105 (99%)	1 (1%)	78	91
62	AY	124/135 (92%)	120 (97%)	4 (3%)	39	69
63	AZ	117/118 (99%)	116 (99%)	1 (1%)	78	91
64	Aa	119/120 (99%)	116 (98%)	3 (2%)	47	75
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%)	111 (97%)	3 (3%)	46	74
69	Af	88/89 (99%)	79 (90%)	9 (10%)	7	27
70	Ag	98/106 (92%)	97 (99%)	1 (1%)	76	90
71	Ah	109/110 (99%)	107 (98%)	2 (2%)	59	82
72	Ai	86/89 (97%)	84 (98%)	2 (2%)	50	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	Aj	73/80 (91%)	70 (96%)	3 (4%)	30	64
74	Ak	64/64 (100%)	61 (95%)	3 (5%)	26	59
75	Al	47/48 (98%)	46 (98%)	1 (2%)	53	79
76	Am	48/48 (100%)	46 (96%)	2 (4%)	30	62
77	An	24/24 (100%)	23 (96%)	1 (4%)	30	62
78	Ao	92/94 (98%)	89 (97%)	3 (3%)	38	69
79	Ap	74/75 (99%)	72 (97%)	2 (3%)	44	74
80	Ar	108/121 (89%)	105 (97%)	3 (3%)	43	73
81	AK	190/196 (97%)	181 (95%)	9 (5%)	26	59
All	All	9893/11009 (90%)	9572 (97%)	321 (3%)	42	69

All (321) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	50	ASN
2	B	82	THR
2	B	111	GLN
3	C	40	ASN
3	C	105	LEU
3	C	107	ARG
3	C	147	ASN
3	C	207	LEU
3	C	212	VAL
3	C	213	ARG
4	D	78	LEU
4	D	137	VAL
4	D	141	LEU
4	D	227	ARG
4	D	271	ASN
5	E	57	ASN
5	E	76	ARG
5	E	94	ARG
5	E	106	ARG
5	E	141	LYS
5	E	143	ARG
5	E	146	ARG
5	E	227	LYS
6	F	67	GLN
6	F	155	LYS

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Mol	Chain	Res	Type
6	F	156	MET
6	F	220	THR
6	F	232	ASN
6	F	246	LEU
7	G	14	THR
7	G	41	VAL
7	G	88	MET
8	H	108	VAL
8	H	175	LYS
8	H	201	LYS
9	I	46	THR
10	J	37	LYS
10	J	72	CYS
10	J	99	ASN
10	J	145	ILE
10	J	168	GLN
10	J	190	LEU
11	K	69	ARG
11	K	70	ARG
11	K	79	ARG
11	K	110	LEU
12	L	58	VAL
13	M	20	LYS
13	M	56	ILE
13	M	69	ARG
14	N	33	ARG
15	O	24	THR
15	O	27	LYS
16	P	50	LYS
16	P	100	THR
17	Q	13	ARG
17	Q	37	TYR
17	Q	103	ASN
17	Q	121	ILE
17	Q	122	THR
17	Q	124	LYS
17	Q	127	LYS
17	Q	130	ARG
18	R	17	LYS
18	R	31	LEU
19	S	5	ARG
19	S	127	ASN

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Mol	Chain	Res	Type
20	T	8	LYS
20	T	101	ASN
21	U	62	ARG
22	V	47	ASN
23	W	11	LEU
23	W	12	TYR
23	W	21	ASN
23	W	32	ILE
23	W	34	MET
23	W	35	ASN
23	W	50	SER
23	W	52	THR
23	W	82	ASN
24	X	20	ARG
24	X	126	LEU
25	Y	7	LEU
25	Y	60	LYS
25	Y	61	GLN
26	Z	101	LYS
26	Z	110	ARG
27	a	67	LEU
28	b	15	ARG
28	b	21	ILE
32	f	99	LYS
32	f	104	ARG
33	g	126	CYS
33	g	138	ARG
34	h	178	ASN
34	h	206	LEU
39	AA	3	ARG
39	AA	68	ARG
39	AA	77	ILE
39	AA	80	GLU
39	AA	96	LEU
39	AA	102	LEU
39	AA	125	LYS
39	AA	128	ARG
39	AA	140	ASN
39	AA	155	LYS
39	AA	156	LYS
39	AA	159	SER
39	AA	165	VAL

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Mol	Chain	Res	Type
39	AA	193	ARG
39	AA	200	ARG
39	AA	207	VAL
39	AA	242	ARG
40	AB	10	ARG
40	AB	16	PHE
40	AB	24	ARG
40	AB	157	CYS
40	AB	242	ARG
40	AB	249	ARG
40	AB	254	ILE
40	AB	261	ARG
40	AB	262	VAL
40	AB	298	LEU
40	AB	309	LEU
40	AB	338	VAL
41	AC	69	THR
41	AC	71	ARG
41	AC	95	MET
41	AC	121	ARG
41	AC	133	LEU
41	AC	150	LEU
41	AC	188	ARG
41	AC	219	LYS
41	AC	246	VAL
41	AC	286	ASN
41	AC	302	LEU
41	AC	303	ARG
41	AC	316	LYS
41	AC	334	THR
41	AC	335	MET
41	AC	341	LEU
41	AC	342	ARG
41	AC	348	LYS
41	AC	350	ARG
41	AC	353	ARG
41	AC	363	ASP
42	AD	37	VAL
42	AD	56	THR
42	AD	111	ASN
43	AE	52	LEU
43	AE	58	ARG

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Mol	Chain	Res	Type
43	AE	155	ILE
43	AE	178	VAL
43	AE	289	LEU
44	AF	76	LYS
44	AF	205	ASN
44	AF	242	LEU
44	AF	244	ARG
45	AG	97	ASP
45	AG	223	LEU
45	AG	226	LEU
45	AG	242	ARG
45	AG	249	ARG
45	AG	282	ARG
45	AG	293	ASN
46	AH	1	MET
46	AH	15	ASN
46	AH	23	ARG
46	AH	102	ASN
46	AH	116	ASN
47	AI	3	ARG
47	AI	28	ASP
47	AI	35	ASP
47	AI	74	LYS
47	AI	126	VAL
47	AI	142	LEU
48	AJ	16	ARG
48	AJ	33	LEU
49	AL	46	ILE
49	AL	67	HIS
49	AL	71	ARG
49	AL	154	VAL
49	AL	159	ASN
49	AL	162	LYS
50	AM	38	VAL
50	AM	42	CYS
50	AM	94	LYS
50	AM	96	GLU
50	AM	119	ARG
51	AN	50	ARG
51	AN	64	ILE
51	AN	80	THR
51	AN	87	HIS

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Mol	Chain	Res	Type
51	AN	89	VAL
51	AN	104	GLU
51	AN	117	ASN
51	AN	151	ILE
52	AO	12	ARG
52	AO	36	VAL
52	AO	108	ILE
52	AO	110	PRO
52	AO	112	TYR
52	AO	117	ARG
52	AO	145	VAL
53	AP	24	VAL
53	AP	128	ARG
53	AP	147	GLU
54	AQ	14	TRP
54	AQ	23	MET
54	AQ	37	ARG
54	AQ	38	HIS
54	AQ	42	THR
54	AQ	57	LYS
54	AQ	66	VAL
54	AQ	78	LYS
54	AQ	79	THR
54	AQ	86	ILE
54	AQ	91	ARG
54	AQ	97	LYS
54	AQ	110	HIS
54	AQ	117	GLU
54	AQ	124	HIS
54	AQ	138	LEU
54	AQ	150	GLN
54	AQ	172	ARG
55	AR	36	ASN
55	AR	50	ILE
55	AR	89	MET
55	AR	94	LYS
56	AS	2	LYS
56	AS	15	ARG
56	AS	19	THR
56	AS	21	LYS
56	AS	49	LEU
56	AS	67	VAL

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Mol	Chain	Res	Type
56	AS	90	THR
56	AS	96	GLU
56	AS	102	MET
56	AS	104	SER
56	AS	120	ARG
56	AS	132	MET
56	AS	136	ARG
56	AS	159	LEU
57	AT	79	GLN
57	AT	80	VAL
57	AT	81	LYS
57	AT	83	LYS
57	AT	136	ARG
57	AT	146	LYS
58	AU	32	ARG
58	AU	36	GLU
58	AU	61	VAL
58	AU	80	LYS
58	AU	107	LYS
59	AV	15	ARG
59	AV	18	LEU
59	AV	25	VAL
59	AV	60	MET
59	AV	82	ILE
60	AW	44	ARG
61	AX	72	ASP
62	AY	2	LYS
62	AY	72	GLN
62	AY	79	VAL
62	AY	112	ASP
63	AZ	33	THR
64	Aa	4	ARG
64	Aa	10	LYS
64	Aa	56	VAL
65	Ab	9	THR
65	Ab	60	ASN
65	Ab	101	HIS
66	Ac	90	ARG
67	Ad	18	ASN
67	Ad	31	LYS
67	Ad	48	GLU
67	Ad	56	GLU

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Mol	Chain	Res	Type
68	Ae	48	ARG
68	Ae	78	LEU
68	Ae	91	CYS
69	Af	7	CYS
69	Af	16	ARG
69	Af	33	VAL
69	Af	80	ASN
69	Af	84	VAL
69	Af	101	ILE
69	Af	104	MET
69	Af	105	LEU
69	Af	106	TYR
70	Ag	15	THR
71	Ah	13	LYS
71	Ah	67	GLU
72	Ai	21	VAL
72	Ai	29	ARG
73	Aj	13	ASN
73	Aj	20	ARG
73	Aj	58	THR
74	Ak	3	GLN
74	Ak	35	LYS
74	Ak	48	MET
75	Al	27	ILE
76	Am	72	LYS
76	Am	96	ARG
77	An	13	LEU
78	Ao	9	ARG
78	Ao	82	MET
78	Ao	97	LYS
79	Ap	17	ARG
79	Ap	54	ILE
80	Ar	26	SER
80	Ar	98	ARG
80	Ar	107	ARG
81	AK	9	THR
81	AK	10	LEU
81	AK	92	LYS
81	AK	137	LEU
81	AK	156	LYS
81	AK	159	MET
81	AK	173	LYS

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Mol	Chain	Res	Type
81	AK	195	LYS
81	AK	196	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (90) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	147	ASN
4	D	271	ASN
6	F	232	ASN
7	G	118	ASN
8	H	186	GLN
8	H	202	ASN
10	J	99	ASN
10	J	165	GLN
10	J	168	GLN
11	K	177	ASN
12	L	7	ASN
13	M	18	GLN
13	M	19	ASN
13	M	83	GLN
15	O	36	GLN
15	O	105	ASN
15	O	123	HIS
17	Q	41	GLN
17	Q	103	ASN
17	Q	128	HIS
19	S	62	GLN
19	S	127	ASN
20	T	76	GLN
20	T	101	ASN
22	V	47	ASN
23	W	21	ASN
23	W	47	ASN
23	W	81	GLN
24	X	16	ASN
24	X	64	ASN
24	X	91	ASN
29	c	26	GLN
30	d	26	GLN
30	d	29	GLN
32	f	88	GLN
34	h	159	ASN

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Mol	Chain	Res	Type
34	h	178	ASN
39	AA	140	ASN
39	AA	205	ASN
39	AA	217	GLN
40	AB	271	GLN
41	AC	50	GLN
41	AC	286	ASN
41	AC	310	HIS
41	AC	329	ASN
41	AC	338	ASN
42	AD	275	GLN
43	AE	253	GLN
44	AF	130	ASN
45	AG	96	GLN
45	AG	99	GLN
45	AG	117	GLN
46	AH	8	GLN
46	AH	42	ASN
46	AH	102	ASN
46	AH	156	ASN
47	AI	95	HIS
47	AI	123	GLN
47	AI	163	GLN
48	AJ	104	ASN
49	AL	104	ASN
49	AL	188	ASN
51	AN	15	GLN
51	AN	32	GLN
52	AO	5	GLN
53	AP	75	GLN
53	AP	80	GLN
54	AQ	38	HIS
54	AQ	124	HIS
54	AQ	188	ASN
55	AR	36	ASN
56	AS	146	HIS
57	AT	49	GLN
59	AV	27	ASN
59	AV	36	ASN
60	AW	30	GLN
60	AW	50	ASN
61	AX	93	ASN

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Mol	Chain	Res	Type
61	AX	105	ASN
62	AY	14	ASN
64	Aa	34	ASN
64	Aa	44	ASN
65	Ab	50	ASN
66	Ac	19	GLN
67	Ad	79	ASN
73	Aj	30	GLN
73	Aj	57	ASN
78	Ao	45	GLN
80	Ar	21	ASN
80	Ar	45	HIS

5.3.3 RNA ⓘ

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

All (1514) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	C
1	2	4	C
1	2	17	C
1	2	25	A
1	2	33	G
1	2	41	G
1	2	44	U
1	2	45	A
1	2	46	A
1	2	56	G
1	2	58	C
1	2	61	A
1	2	64	A
1	2	65	C

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Mol	Chain	Res	Type
1	2	67	C
1	2	68	A
1	2	69	C
1	2	73	C
1	2	74	G
1	2	75	G
1	2	79	A
1	2	99	A
1	2	103	A
1	2	111	A
1	2	113	G
1	2	114	G
1	2	115	U
1	2	116	U
1	2	124	U
1	2	126	G
1	2	127	C
1	2	129	C
1	2	130	G
1	2	142	C
1	2	143	U
1	2	146	G
1	2	147	A
1	2	155	G
1	2	158	A
1	2	160	U
1	2	161	U
1	2	162	C
1	2	163	U
1	2	170	A
1	2	175	A
1	2	179	C
1	2	180	G
1	2	183	G
1	2	184	G
1	2	185	G
1	2	188	C
1	2	189	U
1	2	191	A
1	2	192	C
1	2	196	C
1	2	197	U

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Mol	Chain	Res	Type
1	2	215	G
1	2	294	U
1	2	307	G
1	2	308	G
1	2	309	G
1	2	312	G
1	2	317	C
1	2	318	A
1	2	319	C
1	2	320	G
1	2	330	G
1	2	332	G
1	2	335	G
1	2	347	G
1	2	351	G
1	2	362	C
1	2	364	A
1	2	367	U
1	2	368	U
1	2	369	C
1	2	370	G
1	2	377	G
1	2	384	U
1	2	385	G
1	2	386	C
1	2	400	C
1	2	408	A
1	2	409	C
1	2	417	C
1	2	418	A
1	2	436	G
1	2	438	G
1	2	441	C
1	2	447	A
1	2	448	A
1	2	449	A
1	2	450	C
1	2	464	A
1	2	465	A
1	2	466	G
1	2	471	G
1	2	472	C

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Mol	Chain	Res	Type
1	2	473	A
1	2	474	G
1	2	482	G
1	2	487	U
1	2	492	C
1	2	493	A
1	2	496	C
1	2	502	C
1	2	508	A
1	2	516	A
1	2	517	C
1	2	518	G
1	2	530	U
1	2	531	A
1	2	532	C
1	2	533	A
1	2	536	A
1	2	537	C
1	2	538	U
1	2	539	C
1	2	542	U
1	2	544	G
1	2	547	G
1	2	548	C
1	2	549	C
1	2	550	C
1	2	551	U
1	2	554	A
1	2	555	A
1	2	556	U
1	2	559	G
1	2	561	A
1	2	562	U
1	2	563	G
1	2	568	C
1	2	570	C
1	2	583	A
1	2	585	C
1	2	588	G
1	2	589	G
1	2	590	A
1	2	591	U

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Mol	Chain	Res	Type
1	2	593	C
1	2	597	G
1	2	604	A
1	2	606	G
1	2	607	U
1	2	608	C
1	2	614	C
1	2	627	U
1	2	628	A
1	2	629	A
1	2	632	C
1	2	643	A
1	2	644	G
1	2	660	C
1	2	663	C
1	2	664	A
1	2	668	A
1	2	669	A
1	2	671	A
1	2	672	A
1	2	673	G
1	2	678	U
1	2	687	C
1	2	688	U
1	2	689	U
1	2	692	G
1	2	693	A
1	2	697	G
1	2	750	C
1	2	752	G
1	2	753	C
1	2	754	G
1	2	799	U
1	2	800	U
1	2	811	A
1	2	812	A
1	2	821	G
1	2	822	U
1	2	823	U
1	2	827	A
1	2	830	A
1	2	833	C

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Mol	Chain	Res	Type
1	2	834	C
1	2	845	G
1	2	847	A
1	2	852	G
1	2	865	A
1	2	868	G
1	2	870	A
1	2	871	U
1	2	872	A
1	2	873	G
1	2	874	G
1	2	875	A
1	2	877	C
1	2	878	G
1	2	881	G
1	2	883	U
1	2	885	U
1	2	886	A
1	2	887	U
1	2	888	U
1	2	890	U
1	2	892	U
1	2	894	G
1	2	898	U
1	2	901	G
1	2	902	G
1	2	906	U
1	2	908	A
1	2	909	G
1	2	913	A
1	2	914	U
1	2	917	U
1	2	920	A
1	2	930	C
1	2	933	G
1	2	943	U
1	2	963	A
1	2	970	G
1	2	971	G
1	2	978	G
1	2	985	G
1	2	990	A

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Mol	Chain	Res	Type
1	2	992	A
1	2	999	G
1	2	1002	U
1	2	1017	U
1	2	1023	A
1	2	1034	A
1	2	1044	G
1	2	1050	A
1	2	1055	A
1	2	1060	A
1	2	1062	A
1	2	1083	A
1	2	1085	C
1	2	1089	G
1	2	1100	A
1	2	1111	U
1	2	1115	U
1	2	1116	C
1	2	1117	C
1	2	1118	C
1	2	1121	G
1	2	1123	C
1	2	1130	G
1	2	1133	A
1	2	1137	U
1	2	1138	C
1	2	1150	A
1	2	1153	C
1	2	1154	U
1	2	1155	U
1	2	1157	G
1	2	1166	G
1	2	1195	A
1	2	1203	G
1	2	1207	G
1	2	1210	G
1	2	1215	C
1	2	1221	G
1	2	1224	G
1	2	1235	G
1	2	1239	U
1	2	1240	A

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Mol	Chain	Res	Type
1	2	1242	U
1	2	1243	U
1	2	1244	U
1	2	1248	U
1	2	1251	A
1	2	1253	A
1	2	1256	G
1	2	1257	G
1	2	1259	A
1	2	1265	A
1	2	1274	G
1	2	1275	G
1	2	1281	G
1	2	1284	A
1	2	1285	G
1	2	1286	G
1	2	1290	G
1	2	1291	A
1	2	1292	C
1	2	1293	A
1	2	1294	G
1	2	1298	G
1	2	1299	A
1	2	1301	A
1	2	1302	G
1	2	1303	C
1	2	1306	U
1	2	1307	U
1	2	1308	U
1	2	1311	C
1	2	1314	U
1	2	1318	G
1	2	1330	G
1	2	1331	C
1	2	1332	A
1	2	1342	U
1	2	1343	U
1	2	1354	G
1	2	1364	U
1	2	1366	G
1	2	1371	U
1	2	1372	U

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Mol	Chain	Res	Type
1	2	1377	U
1	2	1378	A
1	2	1379	A
1	2	1382	A
1	2	1396	A
1	2	1397	U
1	2	1400	U
1	2	1402	A
1	2	1403	C
1	2	1405	A
1	2	1406	G
1	2	1409	A
1	2	1425	G
1	2	1428	G
1	2	1429	G
1	2	1431	G
1	2	1439	A
1	2	1440	C
1	2	1441	U
1	2	1444	U
1	2	1449	G
1	2	1453	C
1	2	1454	A
1	2	1455	A
1	2	1462	U
1	2	1463	U
1	2	1464	C
1	2	1466	G
1	2	1470	C
1	2	1476	A
1	2	1479	G
1	2	1480	A
1	2	1490	G
1	2	1494	U
1	2	1495	G
1	2	1498	A
1	2	1504	U
1	2	1509	U
1	2	1514	G
1	2	1519	U
1	2	1520	G
1	2	1521	C

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Mol	Chain	Res	Type
1	2	1522	A
1	2	1523	C
1	2	1533	A
1	2	1535	U
1	2	1536	G
1	2	1548	G
1	2	1552	G
1	2	1553	C
1	2	1554	C
1	2	1556	A
1	2	1558	C
1	2	1564	C
1	2	1567	G
1	2	1570	G
1	2	1573	G
1	2	1574	C
1	2	1580	A
1	2	1583	C
1	2	1584	G
1	2	1585	U
1	2	1586	U
1	2	1588	A
1	2	1601	A
1	2	1604	G
1	2	1606	G
1	2	1612	G
1	2	1619	A
1	2	1621	U
1	2	1623	A
1	2	1637	A
1	2	1638	G
1	2	1639	G
1	2	1641	A
1	2	1648	G
1	2	1654	G
1	2	1656	G
1	2	1664	A
1	2	1665	G
1	2	1671	G
1	2	1674	G
1	2	1680	G
1	2	1683	C

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Mol	Chain	Res	Type
1	2	1686	G
1	2	1689	C
1	2	1692	U
1	2	1721	U
1	2	1722	G
1	2	1726	G
1	2	1743	G
1	2	1744	G
1	2	1745	A
1	2	1746	U
1	2	1748	G
1	2	1753	C
1	2	1756	C
1	2	1758	G
1	2	1775	U
1	2	1777	G
1	2	1779	G
1	2	1783	C
1	2	1784	G
1	2	1787	G
1	2	1819	A
1	2	1824	A
1	2	1829	G
1	2	1831	A
1	2	1836	G
1	2	1837	G
1	2	1838	U
1	2	1849	G
1	2	1851	A
1	2	1858	G
1	2	1861	G
1	2	1862	G
1	2	1863	A
1	2	1864	U
1	2	1865	C
1	2	1867	U
1	2	1869	A
35	1	6419	C
35	1	6424	U
35	1	6425	A
35	1	6426	U
35	1	6427	G

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Mol	Chain	Res	Type
35	1	6431	A
35	1	6432	C
35	1	6436	U
35	1	6442	G
35	1	6444	G
35	1	6445	G
35	1	6447	A
35	1	6449	U
35	1	6450	U
35	1	6451	U
35	1	6457	A
35	1	6461	U
35	1	6464	G
35	1	6469	A
35	1	6471	G
35	1	6473	C
35	1	6474	U
35	1	6481	G
35	1	6483	U
35	1	6484	G
35	1	6485	G
35	1	6486	U
35	1	6487	C
35	1	6488	G
35	1	6489	A
35	1	6490	G
35	1	6492	U
35	1	6493	G
35	1	6494	C
35	1	6499	U
35	1	6501	U
35	1	6502	A
35	1	6506	U
35	1	6507	G
35	1	6509	G
35	1	6510	G
35	1	6511	A
35	1	6512	G
35	1	6513	C
35	1	6514	C
35	1	6515	U
35	1	6516	C

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Mol	Chain	Res	Type
35	1	6517	G
35	1	6518	G
35	1	6519	U
35	1	6520	G
35	1	6522	C
35	1	6523	A
35	1	6524	G
35	1	6525	C
35	1	6526	C
35	1	6527	C
35	1	6528	C
35	1	6529	A
35	1	6530	C
35	1	6531	C
35	1	6533	A
35	1	6534	A
35	1	6535	U
35	1	6539	C
35	1	6540	U
35	1	6541	A
35	1	6542	U
35	1	6544	G
35	1	6545	G
35	1	6546	A
35	1	6548	A
35	1	6549	G
35	1	6552	A
35	1	6555	G
35	1	6556	C
35	1	6561	C
35	1	6562	U
35	1	6566	C
35	1	6567	A
35	1	6568	G
35	1	6572	C
35	1	6575	C
35	1	6576	A
35	1	6577	G
35	1	6578	U
35	1	6583	U
35	1	6586	U
35	1	6587	A

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Mol	Chain	Res	Type
35	1	6588	A
35	1	6589	C
35	1	6590	A
35	1	6591	C
35	1	6596	G
35	1	6597	G
35	1	6599	G
35	1	6602	C
35	1	6604	G
35	1	6605	A
35	1	6606	A
35	1	6607	A
35	1	6608	U
35	1	6609	A
35	1	6610	C
35	1	6611	C
35	1	6612	A
35	1	6614	G
35	1	6619	G
35	1	6620	C
36	5	12	A
36	5	13	U
36	5	21	G
36	5	25	A
36	5	30	C
36	5	35	U
36	5	39	A
36	5	42	A
36	5	44	A
36	5	48	G
36	5	49	U
36	5	56	A
36	5	58	G
36	5	59	A
36	5	64	A
36	5	65	A
36	5	72	C
36	5	73	A
36	5	74	G
36	5	91	G
36	5	98	A
36	5	103	G

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Mol	Chain	Res	Type
36	5	104	G
36	5	108	A
36	5	109	G
36	5	110	C
36	5	116	G
36	5	118	C
36	5	119	G
36	5	120	A
36	5	122	U
36	5	126	C
36	5	133	C
36	5	134	G
36	5	135	G
36	5	136	C
36	5	140	G
36	5	142	G
36	5	143	C
36	5	144	G
36	5	157	U
36	5	159	C
36	5	167	C
36	5	171	U
36	5	173	C
36	5	175	C
36	5	177	G
36	5	200	U
36	5	201	C
36	5	209	U
36	5	216	C
36	5	217	C
36	5	218	A
36	5	220	C
36	5	224	U
36	5	225	G
36	5	233	U
36	5	234	G
36	5	236	G
36	5	245	C
36	5	249	C
36	5	255	C
36	5	256	G
36	5	263	G

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Mol	Chain	Res	Type
36	5	264	C
36	5	265	C
36	5	266	C
36	5	267	G
36	5	272	U
36	5	275	C
36	5	276	C
36	5	278	G
36	5	280	G
36	5	281	U
36	5	282	C
36	5	297	U
36	5	305	A
36	5	306	A
36	5	315	G
36	5	316	U
36	5	321	U
36	5	323	C
36	5	327	U
36	5	328	A
36	5	334	A
36	5	340	C
36	5	344	A
36	5	345	C
36	5	347	A
36	5	350	C
36	5	353	A
36	5	360	A
36	5	361	C
36	5	362	A
36	5	363	A
36	5	370	U
36	5	381	U
36	5	386	A
36	5	387	G
36	5	401	G
36	5	402	A
36	5	410	A
36	5	412	G
36	5	413	G
36	5	415	G
36	5	432	U

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Mol	Chain	Res	Type
36	5	440	U
36	5	449	C
36	5	450	G
36	5	452	A
36	5	453	G
36	5	454	U
36	5	457	G
36	5	464	G
36	5	467	U
36	5	468	U
36	5	469	C
36	5	473	C
36	5	481	G
36	5	482	G
36	5	485	C
36	5	492	U
36	5	493	G
36	5	498	C
36	5	499	G
36	5	500	G
36	5	505	G
36	5	506	C
36	5	510	U
36	5	521	C
36	5	522	C
36	5	640	C
36	5	646	G
36	5	649	A
36	5	662	C
36	5	666	G
36	5	668	C
36	5	669	C
36	5	670	G
36	5	673	C
36	5	685	C
36	5	686	A
36	5	691	C
36	5	697	G
36	5	704	C
36	5	719	C
36	5	730	G
36	5	731	G

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Mol	Chain	Res	Type
36	5	737	C
36	5	738	C
36	5	739	G
36	5	740	G
36	5	743	G
36	5	747	A
36	5	749	G
36	5	750	U
36	5	751	G
36	5	758	G
36	5	905	C
36	5	906	C
36	5	912	U
36	5	913	U
36	5	914	A
36	5	916	A
36	5	917	G
36	5	922	C
36	5	923	C
36	5	924	C
36	5	925	G
36	5	928	A
36	5	929	G
36	5	931	A
36	5	932	G
36	5	933	C
36	5	934	A
36	5	935	G
36	5	936	C
36	5	941	C
36	5	943	A
36	5	944	A
36	5	945	U
36	5	956	A
36	5	959	G
36	5	960	A
36	5	961	G
36	5	962	C
36	5	966	A
36	5	967	C
36	5	968	C
36	5	969	U

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Mol	Chain	Res	Type
36	5	970	G
36	5	971	U
36	5	974	C
36	5	978	G
36	5	979	C
36	5	984	U
36	5	986	C
36	5	990	C
36	5	1070	G
36	5	1071	C
36	5	1072	C
36	5	1078	A
36	5	1079	C
36	5	1097	C
36	5	1184	A
36	5	1193	C
36	5	1194	G
36	5	1195	G
36	5	1198	G
36	5	1209	U
36	5	1211	G
36	5	1212	G
36	5	1214	C
36	5	1215	C
36	5	1234	G
36	5	1235	G
36	5	1236	C
36	5	1237	C
36	5	1238	A
36	5	1246	G
36	5	1248	C
36	5	1249	C
36	5	1251	C
36	5	1252	C
36	5	1272	C
36	5	1273	G
36	5	1275	G
36	5	1276	C
36	5	1277	G
36	5	1278	C
36	5	1280	C
36	5	1282	G

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Mol	Chain	Res	Type
36	5	1283	G
36	5	1284	G
36	5	1287	G
36	5	1288	G
36	5	1289	C
36	5	1292	C
36	5	1296	G
36	5	1297	U
36	5	1301	C
36	5	1302	U
36	5	1326	A
36	5	1337	A
36	5	1354	A
36	5	1358	G
36	5	1359	G
36	5	1370	G
36	5	1371	A
36	5	1377	G
36	5	1380	G
36	5	1381	U
36	5	1387	A
36	5	1394	G
36	5	1397	A
36	5	1398	A
36	5	1399	G
36	5	1400	G
36	5	1411	C
36	5	1412	G
36	5	1413	C
36	5	1414	C
36	5	1415	G
36	5	1419	G
36	5	1420	A
36	5	1421	G
36	5	1426	G
36	5	1435	G
36	5	1436	C
36	5	1437	C
36	5	1438	U
36	5	1441	C
36	5	1445	U
36	5	1446	C

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Mol	Chain	Res	Type
36	5	1455	G
36	5	1456	C
36	5	1457	G
36	5	1476	C
36	5	1478	C
36	5	1481	C
36	5	1482	G
36	5	1483	C
36	5	1484	G
36	5	1497	A
36	5	1498	G
36	5	1502	G
36	5	1503	A
36	5	1514	U
36	5	1516	G
36	5	1518	A
36	5	1523	A
36	5	1534	A
36	5	1535	C
36	5	1547	A
36	5	1549	G
36	5	1554	A
36	5	1566	C
36	5	1568	C
36	5	1578	U
36	5	1582	U
36	5	1586	G
36	5	1591	U
36	5	1596	U
36	5	1601	A
36	5	1612	G
36	5	1613	A
36	5	1617	G
36	5	1618	G
36	5	1624	G
36	5	1625	G
36	5	1631	A
36	5	1633	G
36	5	1634	A
36	5	1637	A
36	5	1640	C
36	5	1641	G

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Mol	Chain	Res	Type
36	5	1642	A
36	5	1651	G
36	5	1654	G
36	5	1660	U
36	5	1661	C
36	5	1676	C
36	5	1677	U
36	5	1684	A
36	5	1694	C
36	5	1696	C
36	5	1726	U
36	5	1734	G
36	5	1740	C
36	5	1741	G
36	5	1742	A
36	5	1746	A
36	5	1750	G
36	5	1751	A
36	5	1754	U
36	5	1756	U
36	5	1757	U
36	5	1760	G
36	5	1763	C
36	5	1768	C
36	5	1769	G
36	5	1772	C
36	5	1773	U
36	5	1775	A
36	5	1781	U
36	5	1787	A
36	5	1799	G
36	5	1804	A
36	5	1809	C
36	5	1812	C
36	5	1818	G
36	5	1820	U
36	5	1821	G
36	5	1828	C
36	5	1832	C
36	5	1833	G
36	5	1834	U
36	5	1836	G

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Mol	Chain	Res	Type
36	5	1837	A
36	5	1842	G
36	5	1855	G
36	5	1869	G
36	5	1881	C
36	5	1882	U
36	5	1890	G
36	5	1891	A
36	5	1893	C
36	5	1897	A
36	5	1910	G
36	5	1916	G
36	5	1917	A
36	5	1918	U
36	5	1920	C
36	5	1921	C
36	5	1922	G
36	5	1925	G
36	5	1930	U
36	5	1931	C
36	5	1935	C
36	5	1940	G
36	5	1945	G
36	5	1948	G
36	5	1951	G
36	5	1957	U
36	5	1958	A
36	5	1959	U
36	5	1960	A
36	5	1961	G
36	5	1962	A
36	5	1964	A
36	5	1969	G
36	5	1971	U
36	5	1974	U
36	5	1977	C
36	5	1982	G
36	5	1983	A
36	5	1984	A
36	5	1985	G
36	5	1986	U
36	5	1987	C

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Mol	Chain	Res	Type
36	5	1990	A
36	5	1991	A
36	5	1992	U
36	5	1993	C
36	5	1994	C
36	5	1995	G
36	5	1997	U
36	5	1998	A
36	5	2001	G
36	5	2002	A
36	5	2003	G
36	5	2004	U
36	5	2007	G
36	5	2008	U
36	5	2010	A
36	5	2017	A
36	5	2018	C
36	5	2020	U
36	5	2021	G
36	5	2025	A
36	5	2026	A
36	5	2044	U
36	5	2046	G
36	5	2047	A
36	5	2048	U
36	5	2052	G
36	5	2055	G
36	5	2056	G
36	5	2062	C
36	5	2069	A
36	5	2084	U
36	5	2085	G
36	5	2088	A
36	5	2089	G
36	5	2090	U
36	5	2092	G
36	5	2093	G
36	5	2094	C
36	5	2095	A
36	5	2097	A
36	5	2098	G
36	5	2100	G

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Mol	Chain	Res	Type
36	5	2102	G
36	5	2107	A
36	5	2108	G
36	5	2109	A
36	5	2110	G
36	5	2112	G
36	5	2259	G
36	5	2260	C
36	5	2267	U
36	5	2268	A
36	5	2275	G
36	5	2277	C
36	5	2289	C
36	5	2294	G
36	5	2300	A
36	5	2301	G
36	5	2313	A
36	5	2314	G
36	5	2325	C
36	5	2333	G
36	5	2338	C
36	5	2348	G
36	5	2351	C
36	5	2360	A
36	5	2364	G
36	5	2389	A
36	5	2395	A
36	5	2404	A
36	5	2409	U
36	5	2417	A
36	5	2422	C
36	5	2425	U
36	5	2433	G
36	5	2434	G
36	5	2441	C
36	5	2444	U
36	5	2447	U
36	5	2450	G
36	5	2469	C
36	5	2475	G
36	5	2481	G
36	5	2485	U

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Mol	Chain	Res	Type
36	5	2486	G
36	5	2487	G
36	5	2488	C
36	5	2489	C
36	5	2490	U
36	5	2491	C
36	5	2492	C
36	5	2495	U
36	5	2496	G
36	5	2499	C
36	5	2503	G
36	5	2504	C
36	5	2505	C
36	5	2506	G
36	5	2511	A
36	5	2513	A
36	5	2514	G
36	5	2521	G
36	5	2530	U
36	5	2536	A
36	5	2537	A
36	5	2544	G
36	5	2546	G
36	5	2547	G
36	5	2553	A
36	5	2555	G
36	5	2556	G
36	5	2559	G
36	5	2560	C
36	5	2565	A
36	5	2566	G
36	5	2569	G
36	5	2572	C
36	5	2573	A
36	5	2575	U
36	5	2576	G
36	5	2583	C
36	5	2587	A
36	5	2588	C
36	5	2601	A
36	5	2617	G
36	5	2627	C

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Mol	Chain	Res	Type
36	5	2638	G
36	5	2639	U
36	5	2653	C
36	5	2655	C
36	5	2656	U
36	5	2657	G
36	5	2658	G
36	5	2661	U
36	5	2662	G
36	5	2669	C
36	5	2676	A
36	5	2686	G
36	5	2687	U
36	5	2694	G
36	5	2695	A
36	5	2696	A
36	5	2701	U
36	5	2705	G
36	5	2706	G
36	5	2708	U
36	5	2709	C
36	5	2710	C
36	5	2711	G
36	5	2712	G
36	5	2714	G
36	5	2716	C
36	5	2723	U
36	5	2725	A
36	5	2726	G
36	5	2735	G
36	5	2740	U
36	5	2741	U
36	5	2742	G
36	5	2743	A
36	5	2744	A
36	5	2756	G
36	5	2761	U
36	5	2763	U
36	5	2764	A
36	5	2768	C
36	5	2769	U
36	5	2770	C

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Mol	Chain	Res	Type
36	5	2787	A
36	5	2788	U
36	5	2789	A
36	5	2790	U
36	5	2798	A
36	5	2806	A
36	5	2814	C
36	5	2815	A
36	5	2826	U
36	5	2827	G
36	5	2828	U
36	5	2829	U
36	5	2830	G
36	5	2835	A
36	5	2837	U
36	5	2838	G
36	5	2842	G
36	5	2844	A
36	5	2845	A
36	5	2855	G
36	5	2856	C
36	5	2862	G
36	5	2874	U
36	5	2875	C
36	5	2884	G
36	5	2898	G
36	5	2901	G
36	5	3598	C
36	5	3599	A
36	5	3602	C
36	5	3603	G
36	5	3604	A
36	5	3606	U
36	5	3625	G
36	5	3626	G
36	5	3635	A
36	5	3643	A
36	5	3644	U
36	5	3646	A
36	5	3648	A
36	5	3653	A
36	5	3662	A

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Mol	Chain	Res	Type
36	5	3663	A
36	5	3673	C
36	5	3674	G
36	5	3696	C
36	5	3710	G
36	5	3711	A
36	5	3712	A
36	5	3713	U
36	5	3717	A
36	5	3725	G
36	5	3729	U
36	5	3740	G
36	5	3748	A
36	5	3753	G
36	5	3760	A
36	5	3761	C
36	5	3762	U
36	5	3763	A
36	5	3765	G
36	5	3766	A
36	5	3776	G
36	5	3777	G
36	5	3783	A
36	5	3784	A
36	5	3802	U
36	5	3809	G
36	5	3811	G
36	5	3812	C
36	5	3814	U
36	5	3817	A
36	5	3819	G
36	5	3822	U
36	5	3839	G
36	5	3840	U
36	5	3851	U
36	5	3859	G
36	5	3867	A
36	5	3877	A
36	5	3878	C
36	5	3879	G
36	5	3880	G
36	5	3887	C

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Mol	Chain	Res	Type
36	5	3888	G
36	5	3889	G
36	5	3896	C
36	5	3897	G
36	5	3898	G
36	5	3901	A
36	5	3905	A
36	5	3906	A
36	5	3907	G
36	5	3915	U
36	5	3916	G
36	5	3917	A
36	5	3923	A
36	5	3938	G
36	5	3939	G
36	5	3940	U
36	5	3942	A
36	5	3947	A
36	5	3951	G
36	5	3954	A
36	5	3956	G
36	5	3957	U
36	5	3958	G
36	5	3964	U
36	5	3965	A
36	5	3966	A
36	5	3968	U
36	5	3969	G
36	5	3970	G
36	5	3972	A
36	5	3974	G
36	5	3975	C
36	5	4037	C
36	5	4038	C
36	5	4039	G
36	5	4046	A
36	5	4047	A
36	5	4049	U
36	5	4050	A
36	5	4053	A
36	5	4054	C
36	5	4055	U

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Mol	Chain	Res	Type
36	5	4063	U
36	5	4064	C
36	5	4065	G
36	5	4074	C
36	5	4076	G
36	5	4085	A
36	5	4086	G
36	5	4087	G
36	5	4095	G
36	5	4100	C
36	5	4101	C
36	5	4111	U
36	5	4112	C
36	5	4116	C
36	5	4119	C
36	5	4120	U
36	5	4122	G
36	5	4127	A
36	5	4133	C
36	5	4149	C
36	5	4150	G
36	5	4156	G
36	5	4159	C
36	5	4161	G
36	5	4162	C
36	5	4163	U
36	5	4170	A
36	5	4171	C
36	5	4172	A
36	5	4181	U
36	5	4183	G
36	5	4184	G
36	5	4191	G
36	5	4197	G
36	5	4201	G
36	5	4203	A
36	5	4212	A
36	5	4213	A
36	5	4214	A
36	5	4225	G
36	5	4229	U
36	5	4233	A

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Mol	Chain	Res	Type
36	5	4234	A
36	5	4237	C
36	5	4241	C
36	5	4243	C
36	5	4251	A
36	5	4254	G
36	5	4256	A
36	5	4260	U
36	5	4261	C
36	5	4266	G
36	5	4268	A
36	5	4271	A
36	5	4273	A
36	5	4281	A
36	5	4291	G
36	5	4297	G
36	5	4304	A
36	5	4305	G
36	5	4306	U
36	5	4312	U
36	5	4313	A
36	5	4314	C
36	5	4317	A
36	5	4319	C
36	5	4323	A
36	5	4326	G
36	5	4329	G
36	5	4330	G
36	5	4336	A
36	5	4338	G
36	5	4339	A
36	5	4348	A
36	5	4349	C
36	5	4350	C
36	5	4351	U
36	5	4353	U
36	5	4354	U
36	5	4373	G
36	5	4376	A
36	5	4377	G
36	5	4378	A
36	5	4379	A

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Mol	Chain	Res	Type
36	5	4387	C
36	5	4391	G
36	5	4393	G
36	5	4394	A
36	5	4395	U
36	5	4401	G
36	5	4419	U
36	5	4422	A
36	5	4424	A
36	5	4426	C
36	5	4427	G
36	5	4440	G
36	5	4444	C
36	5	4448	G
36	5	4449	A
36	5	4452	U
36	5	4453	C
36	5	4464	A
36	5	4471	U
36	5	4472	G
36	5	4475	G
36	5	4476	C
36	5	4482	U
36	5	4488	A
36	5	4500	U
36	5	4512	U
36	5	4513	A
36	5	4519	C
36	5	4524	G
36	5	4528	G
36	5	4530	U
36	5	4531	U
36	5	4535	A
36	5	4548	A
36	5	4549	G
36	5	4560	C
36	5	4567	G
36	5	4569	U
36	5	4570	G
36	5	4573	G
36	5	4575	G
36	5	4577	U

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Mol	Chain	Res	Type
36	5	4584	A
36	5	4585	U
36	5	4589	A
36	5	4590	A
36	5	4599	A
36	5	4627	U
36	5	4635	A
36	5	4636	U
36	5	4637	G
36	5	4648	A
36	5	4651	A
36	5	4652	G
36	5	4656	A
36	5	4657	U
36	5	4658	G
36	5	4670	C
36	5	4672	A
36	5	4677	U
36	5	4693	C
36	5	4695	C
36	5	4700	A
36	5	4709	U
36	5	4720	C
36	5	4728	U
36	5	4738	C
36	5	4745	G
36	5	4747	C
36	5	4750	G
36	5	4751	G
36	5	4752	U
36	5	4754	G
36	5	4755	G
36	5	4756	C
36	5	4757	C
36	5	4759	C
36	5	4761	G
36	5	4764	A
36	5	4765	G
36	5	4772	C
36	5	4773	C
36	5	4775	C
36	5	4860	G

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Mol	Chain	Res	Type
36	5	4861	G
36	5	4867	G
36	5	4870	G
36	5	4871	C
36	5	4874	A
36	5	4875	G
36	5	4876	A
36	5	4877	G
36	5	4881	U
36	5	4882	U
36	5	4883	C
36	5	4885	U
36	5	4895	C
36	5	4903	G
36	5	4906	C
36	5	4909	A
36	5	4910	A
36	5	4911	A
36	5	4912	G
36	5	4913	G
36	5	4914	G
36	5	4915	G
36	5	4920	C
36	5	4921	C
36	5	4922	C
36	5	4923	U
36	5	4925	U
36	5	4926	C
36	5	4929	C
36	5	4935	C
36	5	4937	C
36	5	4938	A
36	5	4940	C
36	5	4943	A
36	5	4944	C
36	5	4945	G
36	5	4947	U
36	5	4949	G
36	5	4951	G
36	5	4956	A
36	5	4958	C
36	5	4959	U

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Mol	Chain	Res	Type
36	5	4960	G
36	5	4961	G
36	5	4963	G
36	5	4964	C
36	5	4965	U
36	5	4966	A
36	5	4967	A
36	5	4976	U
36	5	4985	U
36	5	4988	U
36	5	4990	C
36	5	4991	U
36	5	4993	G
36	5	4998	G
36	5	5017	G
36	5	5031	G
36	5	5041	G
36	5	5047	C
36	5	5050	C
36	5	5053	U
36	5	5054	C
36	5	5055	G
36	5	5056	A
36	5	5058	A
36	5	5061	A
36	5	5062	G
37	7	13	A
37	7	25	G
37	7	38	U
37	7	42	A
37	7	53	U
37	7	54	A
37	7	64	G
37	7	97	G
37	7	100	A
37	7	110	G
37	7	111	C
38	8	2	G
38	8	3	A
38	8	23	C
38	8	32	C
38	8	34	U

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Mol	Chain	Res	Type
38	8	35	C
38	8	38	U
38	8	59	A
38	8	62	A
38	8	63	U
38	8	75	G
38	8	94	G
38	8	95	A
38	8	97	A
38	8	103	A
38	8	105	C
38	8	109	C
38	8	110	U
38	8	111	U
38	8	113	C
38	8	114	G
38	8	122	G
38	8	123	U
38	8	124	U
38	8	125	C
38	8	126	C
38	8	127	U
38	8	128	C
38	8	135	C
38	8	137	A
38	8	147	G
38	8	150	C
38	8	151	G
38	8	153	C

All (138) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	24	C
1	2	110	U
1	2	127	C
1	2	448	A
1	2	465	A
1	2	532	C
1	2	553	U
1	2	555	A
1	2	561	A

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Mol	Chain	Res	Type
1	2	627	U
1	2	670	A
1	2	688	U
1	2	752	G
1	2	869	A
1	2	870	A
1	2	874	G
1	2	886	A
1	2	908	A
1	2	1016	U
1	2	1115	U
1	2	1130	G
1	2	1137	U
1	2	1165	G
1	2	1312	G
1	2	1313	A
1	2	1377	U
1	2	1395	C
1	2	1441	U
1	2	1637	A
1	2	1664	A
1	2	1665	G
1	2	1685	U
1	2	1743	G
1	2	1744	G
1	2	1837	G
35	1	6456	U
35	1	6484	G
35	1	6493	G
35	1	6506	U
35	1	6515	U
35	1	6538	U
35	1	6543	U
35	1	6551	A
35	1	6589	C
35	1	6605	A
35	1	6609	A
36	5	12	A
36	5	47	A
36	5	48	G
36	5	125	C
36	5	170	C

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Mol	Chain	Res	Type
36	5	217	C
36	5	265	C
36	5	266	C
36	5	275	C
36	5	361	C
36	5	385	A
36	5	408	A
36	5	449	C
36	5	453	G
36	5	504	G
36	5	737	C
36	5	928	A
36	5	933	C
36	5	934	A
36	5	961	G
36	5	1071	C
36	5	1211	G
36	5	1236	C
36	5	1237	C
36	5	1276	C
36	5	1287	G
36	5	1370	G
36	5	1411	C
36	5	1445	U
36	5	1455	G
36	5	1477	C
36	5	1503	A
36	5	1533	A
36	5	1625	G
36	5	1633	G
36	5	1654	G
36	5	1676	C
36	5	1733	G
36	5	1740	C
36	5	1892	A
36	5	1957	U
36	5	1990	A
36	5	2046	G
36	5	2089	G
36	5	2259	G
36	5	2260	C
36	5	2428	A

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Mol	Chain	Res	Type
36	5	2468	U
36	5	2502	A
36	5	2505	C
36	5	2513	A
36	5	2529	A
36	5	2587	A
36	5	2661	U
36	5	2695	A
36	5	2739	C
36	5	2787	A
36	5	2794	C
36	5	2806	A
36	5	3603	G
36	5	3625	G
36	5	3784	A
36	5	3785	A
36	5	3876	A
36	5	3888	G
36	5	3904	G
36	5	3938	G
36	5	4054	C
36	5	4119	C
36	5	4155	C
36	5	4170	A
36	5	4180	G
36	5	4221	C
36	5	4232	U
36	5	4291	G
36	5	4380	A
36	5	4395	U
36	5	4448	G
36	5	4572	U
36	5	4626	A
36	5	4635	A
36	5	4699	U
36	5	4719	G
36	5	4753	U
36	5	4884	G
36	5	4909	A
36	5	4925	U
36	5	4936	G
37	7	109	U

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Mol	Chain	Res	Type
38	8	51	U
38	8	94	G
38	8	124	U

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
36	5	25

All 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
1	5	1696:C	O3'	1720:C	P	17.92
1	5	523:C	O3'	638:G	P	17.19
1	5	3977:C	O3'	4034:G	P	16.38
1	5	760:G	O3'	903:C	P	15.99

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	4101:C	O3’	4107:G	P	15.68
1	5	991:U	O3’	1064:G	P	15.35
1	5	4777:C	O3’	4859:C	P	14.27
1	5	5022:U	O3’	5028:G	P	13.88
1	5	1364:U	O3’	1368:A	P	13.60
1	5	2901:G	O3’	3597:G	P	12.71
1	5	1180:C	O3’	1183:C	P	10.07
1	5	512:U	O3’	515:C	P	9.73
1	5	182:G	O3’	189:G	P	8.37
1	5	4729:A	O3’	4735:G	P	7.75
1	5	500:G	O3’	504:G	P	6.89
1	5	4740:G	O3’	4743:G	P	5.83
1	5	1100:U	O3’	1168:G	P	4.95
1	5	1438:U	O3’	1440:U	P	4.68
1	5	1239:C	O3’	1244:G	P	3.65
1	5	4899:G	O3’	4902:C	P	3.46

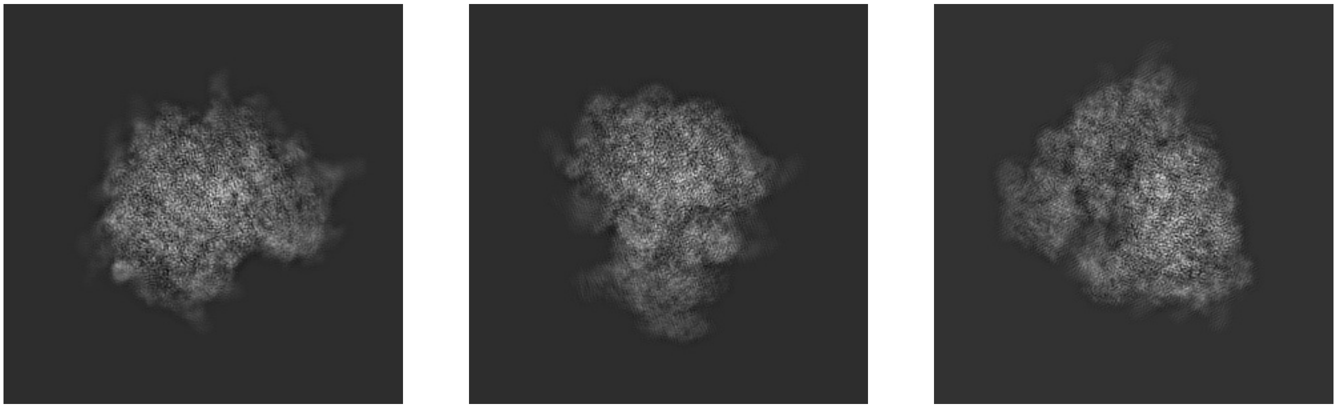
6 Map visualisation

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.

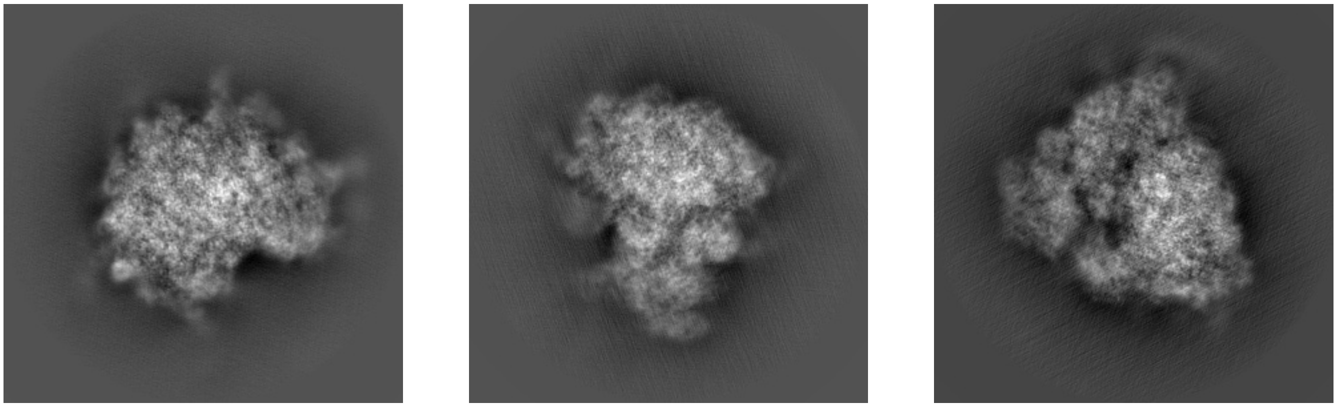
6.1 Orthogonal projections

6.1.1 Primary map



X Y Z

6.1.2 Raw map

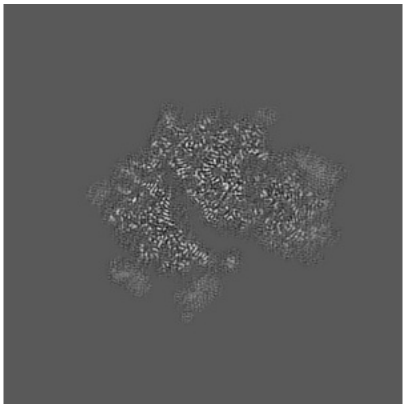


X Y Z

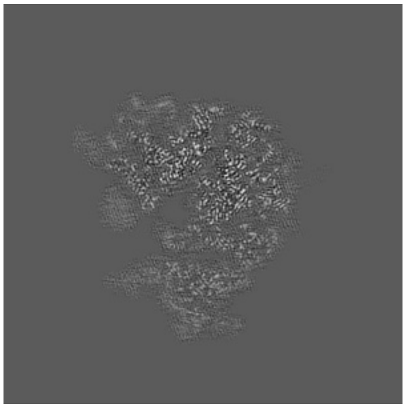
The images above show the map projected in three orthogonal directions.

6.2 Central slices ⓘ

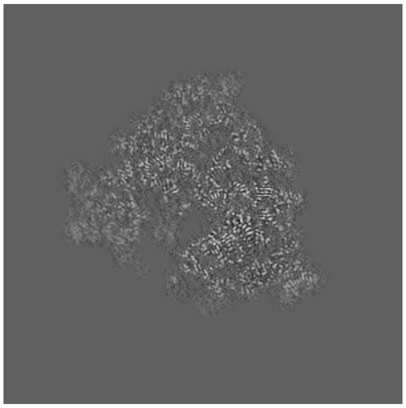
6.2.1 Primary map



X Index: 180

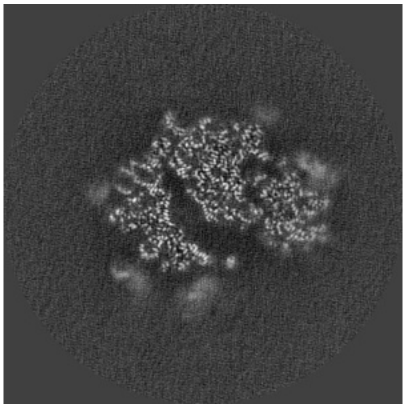


Y Index: 180

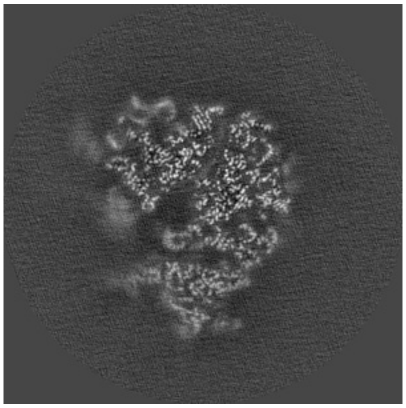


Z Index: 180

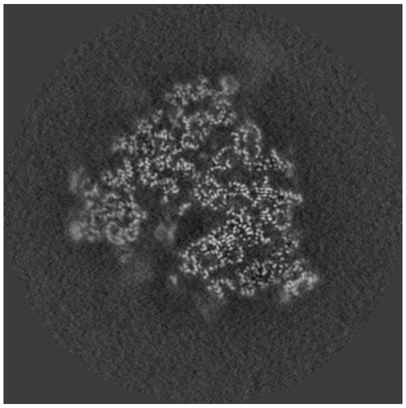
6.2.2 Raw map



X Index: 180



Y Index: 180

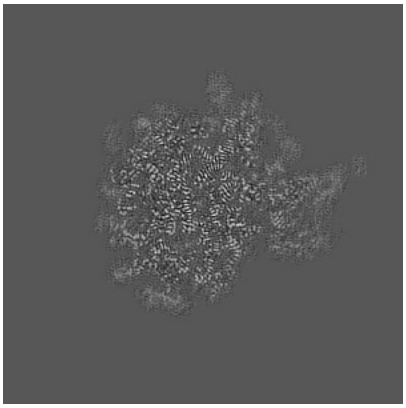


Z Index: 180

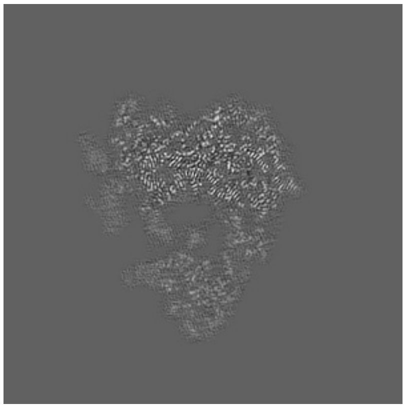
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices

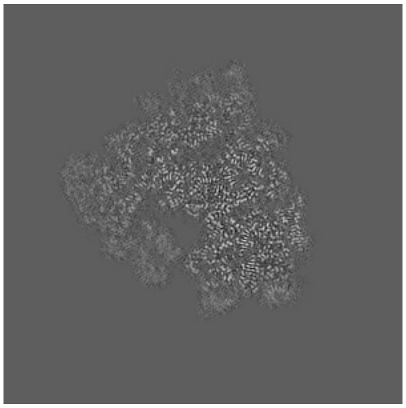
6.3.1 Primary map



X Index: 206

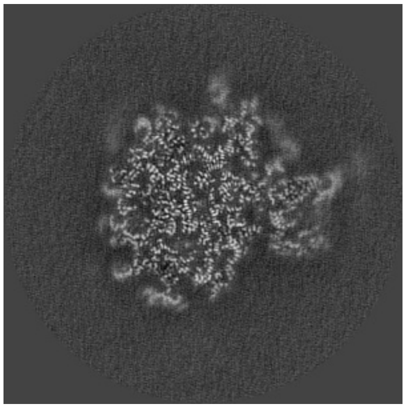


Y Index: 167

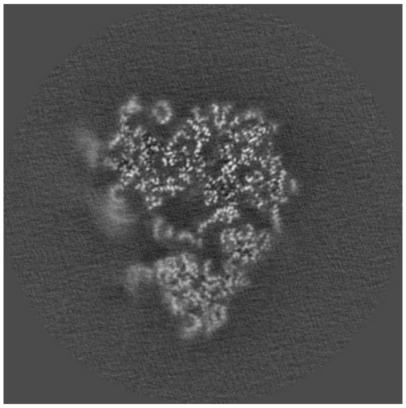


Z Index: 194

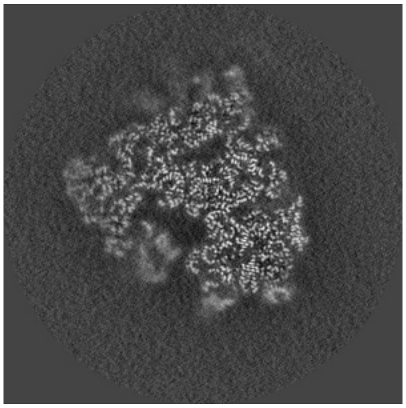
6.3.2 Raw map



X Index: 206



Y Index: 174

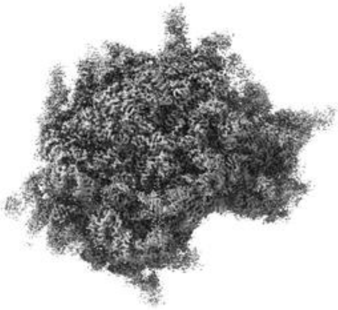


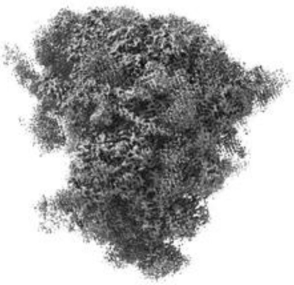
Z Index: 194

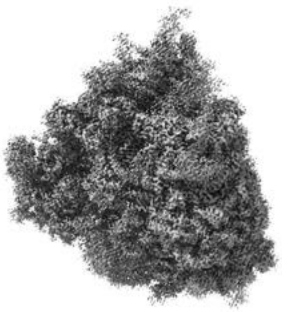
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views ⓘ

6.4.1 Primary map

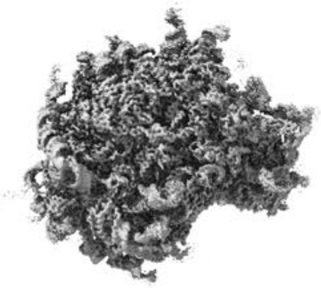

X


Y


Z

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


X


Y


Z

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.

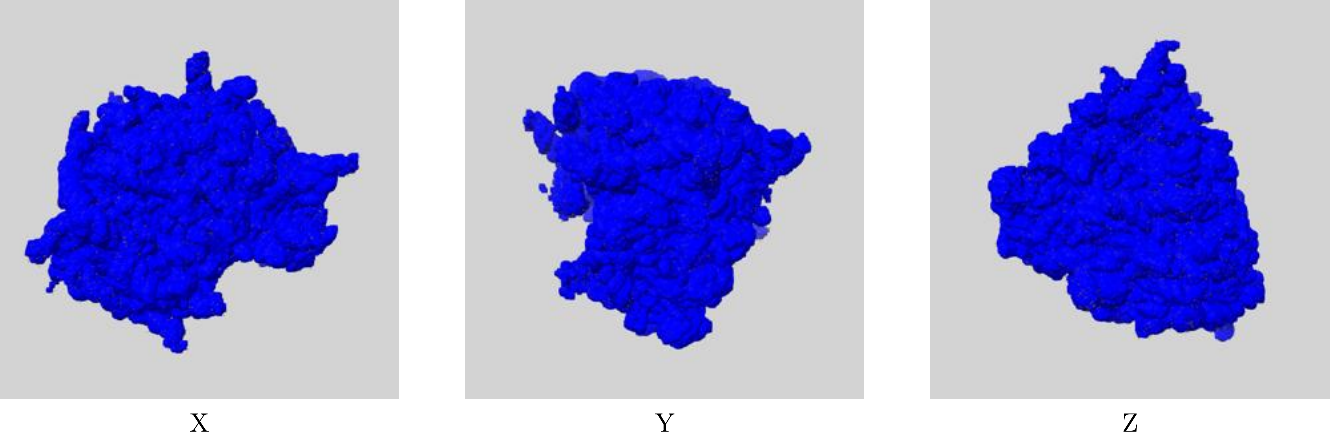
6.5 Mask visualisation ⓘ

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

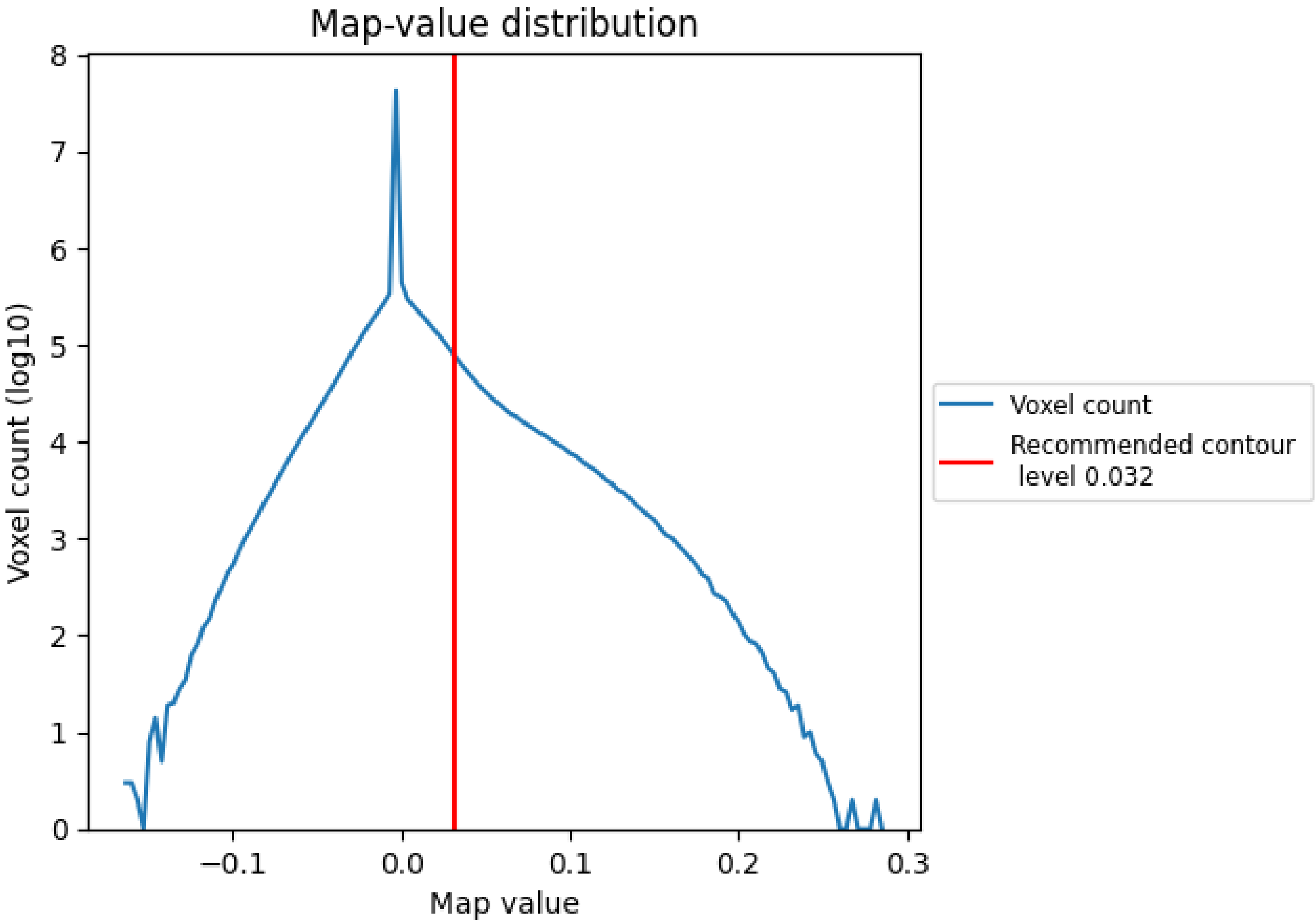
6.5.1 emd_20255_msk_1.map ⓘ



7 Map analysis ⓘ

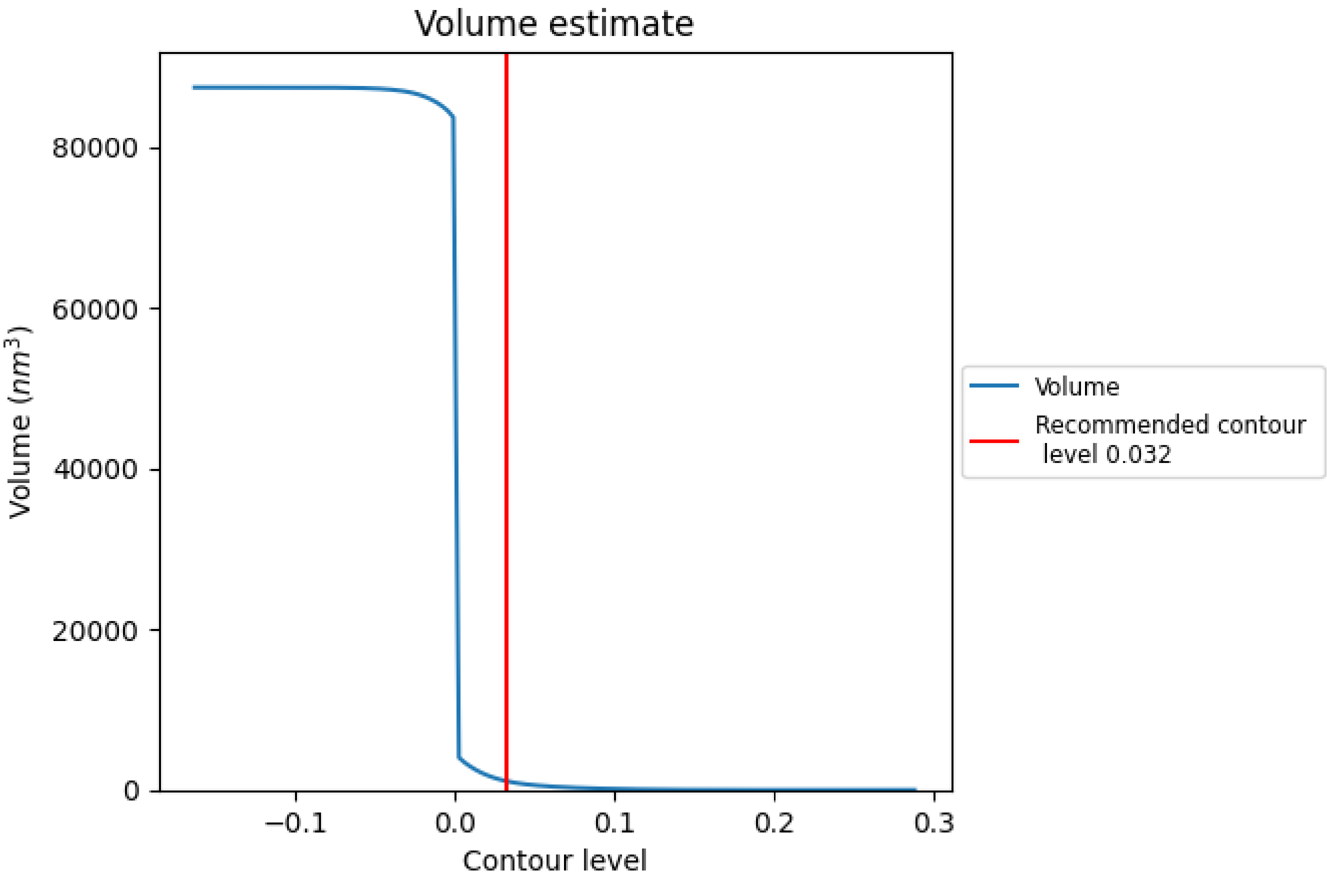
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

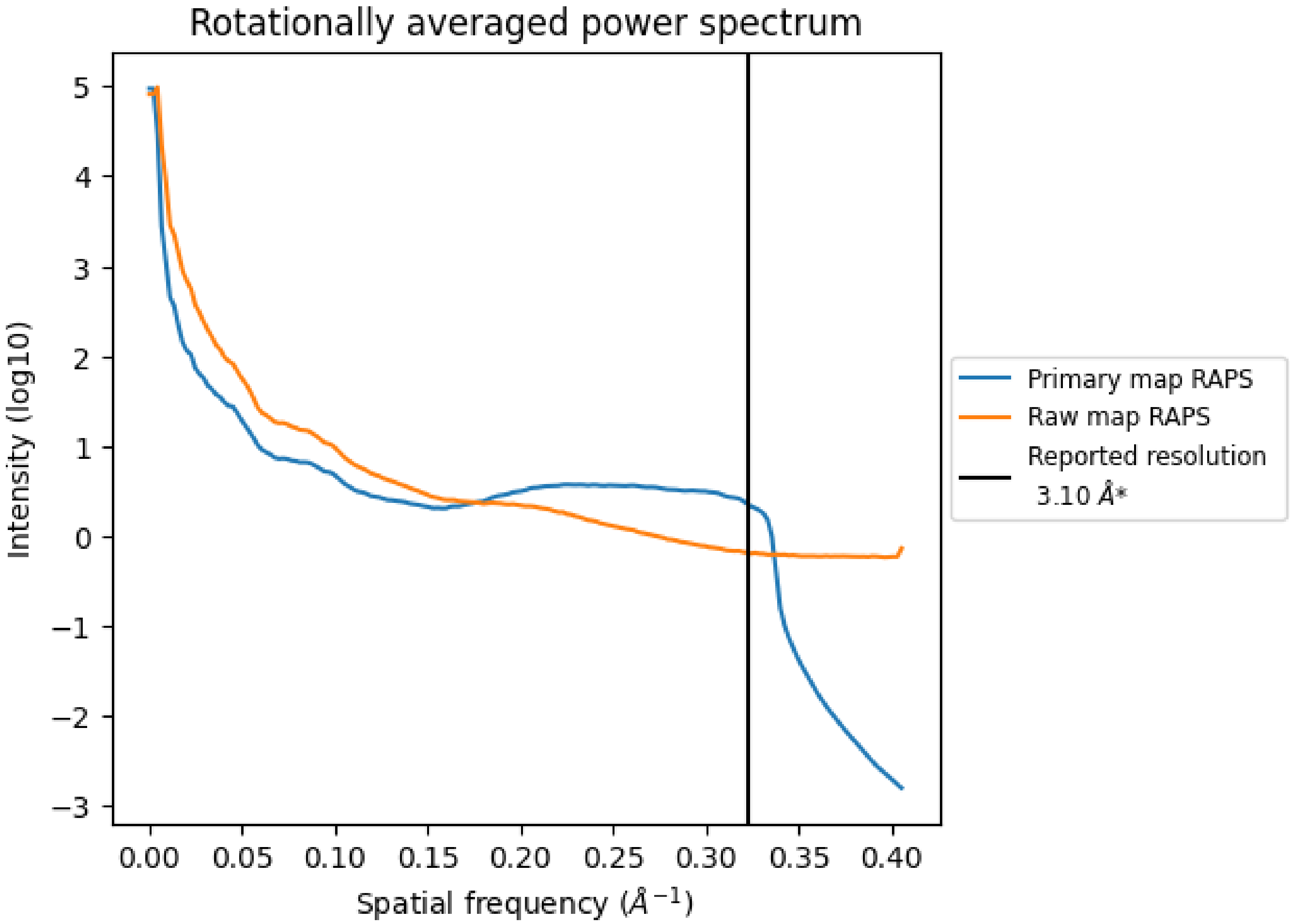
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 1113 nm^3; this corresponds to an approximate mass of 1005 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

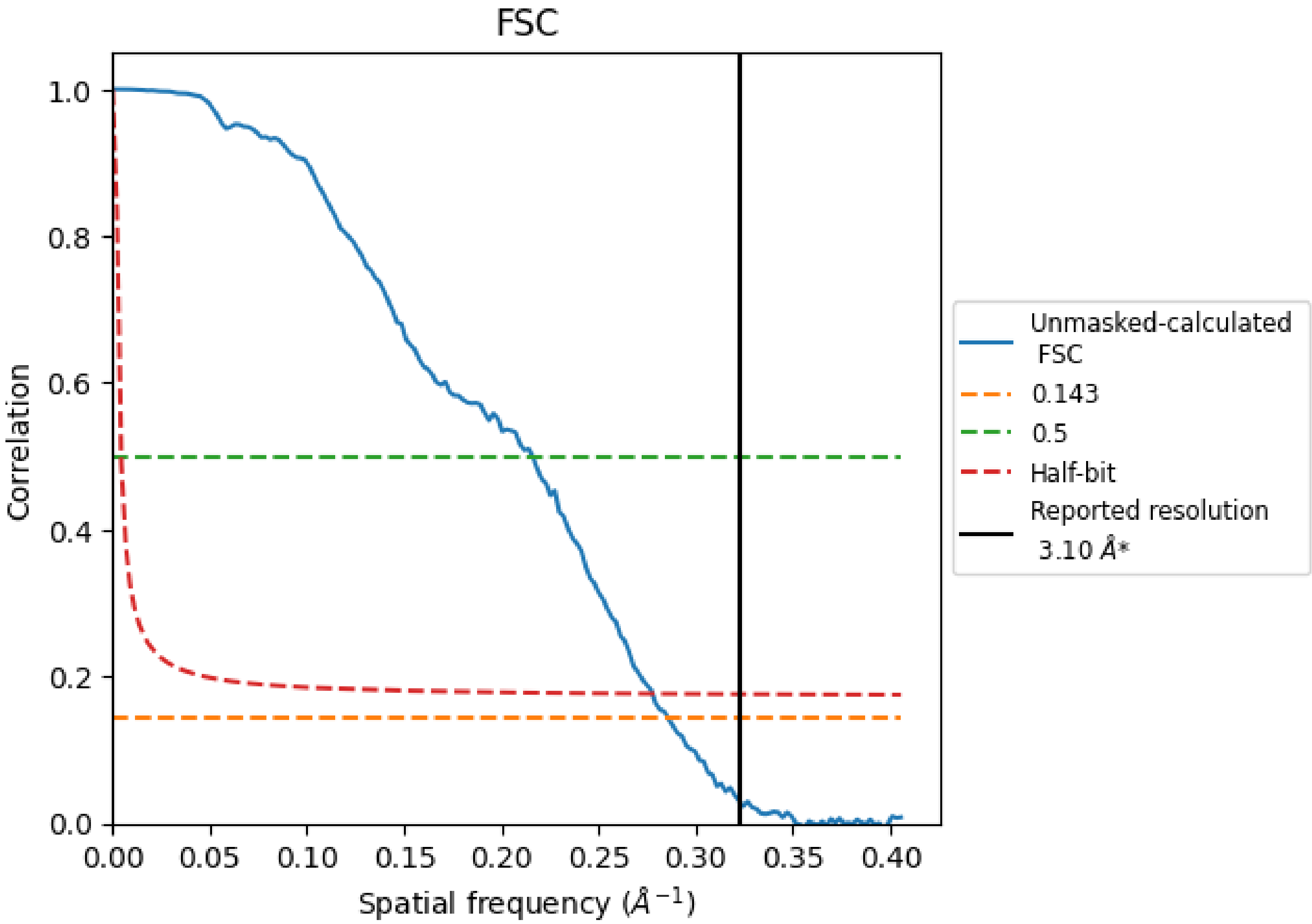


*Reported resolution corresponds to spatial frequency of 0.323 Å^{-1}

8 Fourier-Shell correlation ⓘ

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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.323 $Å^{-1}$

8.2 Resolution estimates ⓘ

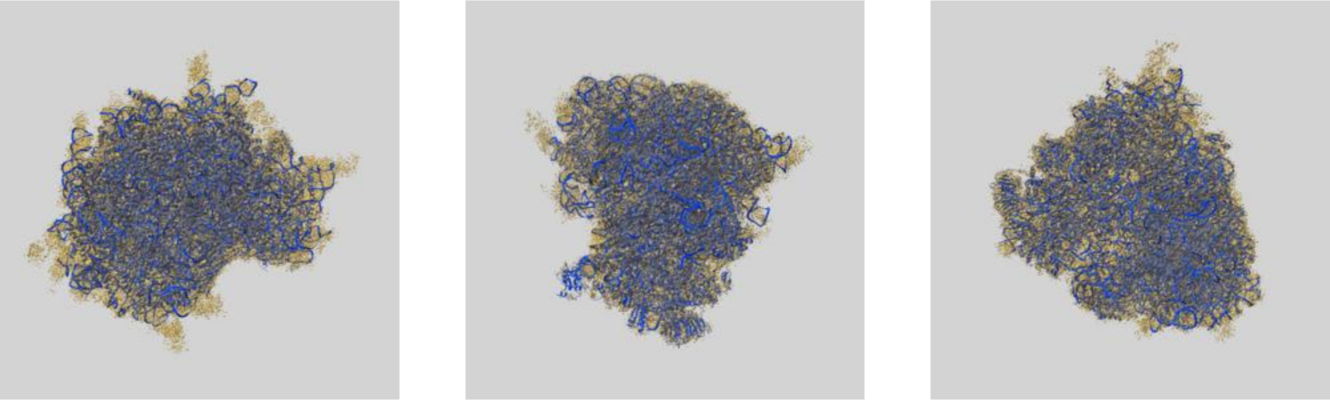
Resolution estimate (Å)	**Estimation criterion (FSC cut-off)**		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.50	4.63	3.60

*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 ⓘ

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

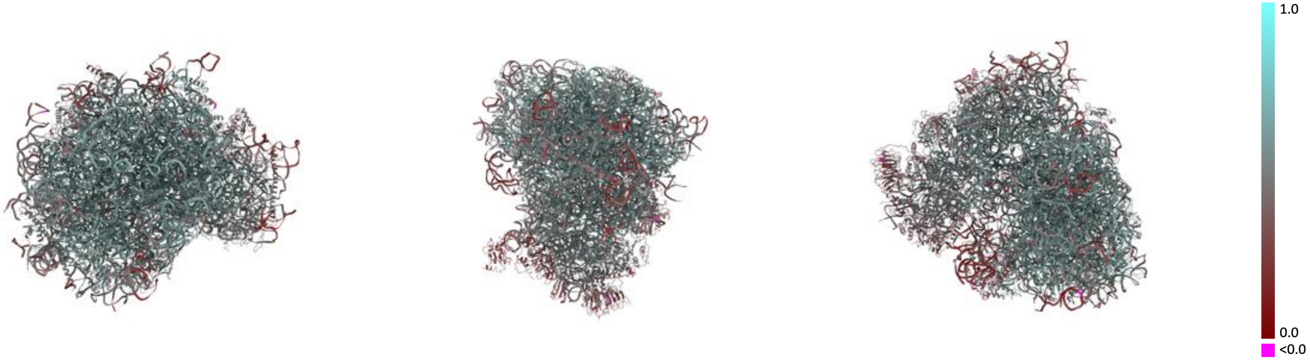
9.1 Map-model overlay ⓘ



X Y Z

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.

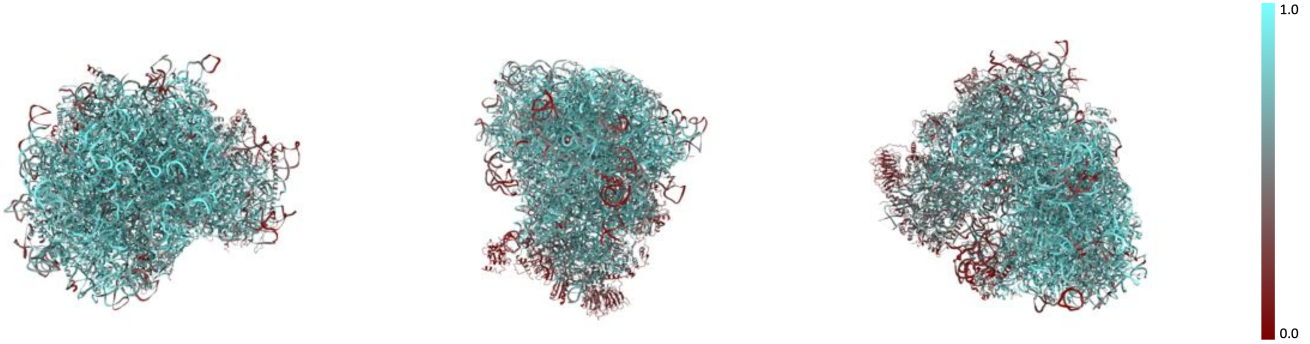
9.2 Q-score mapped to coordinate model ⓘ



X Y Z

The images above show the model with each residue coloured according 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.

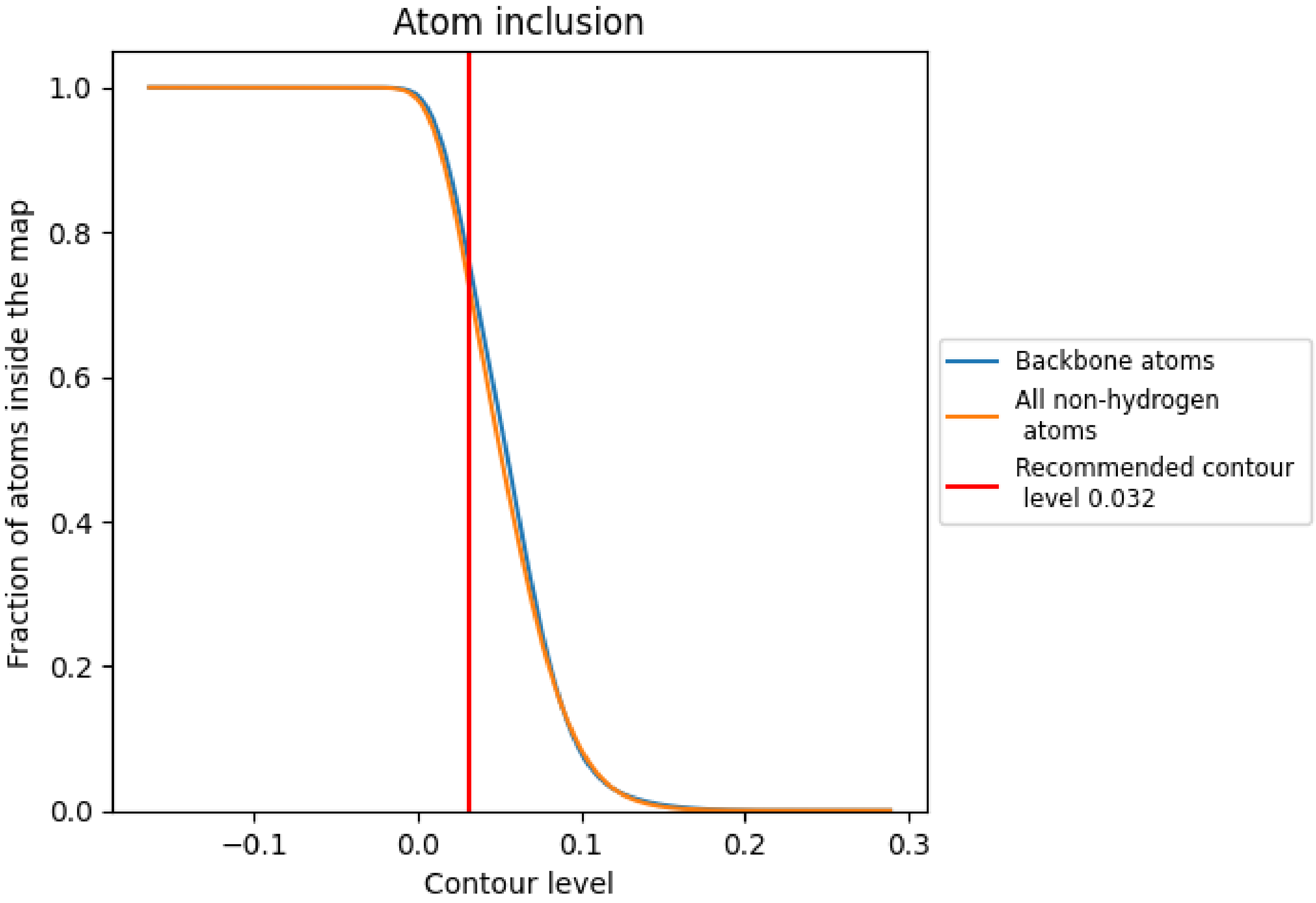
9.3 Atom inclusion mapped to coordinate model ⓘ



X Y Z

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 ⓘ



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	▬ 0.7216	▬ 0.5080
1	▬ 0.3585	▬ 0.3040
2	▬ 0.7461	▬ 0.5020
5	▬ 0.8208	▬ 0.5380
7	▬ 0.9149	▬ 0.5770
8	▬ 0.8653	▬ 0.5630
AA	▬ 0.8029	▬ 0.5750
AB	▬ 0.7962	▬ 0.5620
AC	▬ 0.7953	▬ 0.5520
AD	▬ 0.7163	▬ 0.5160
AE	▬ 0.7302	▬ 0.5190
AF	▬ 0.7999	▬ 0.5690
AG	▬ 0.6799	▬ 0.4990
AH	▬ 0.7260	▬ 0.5270
AI	▬ 0.7621	▬ 0.5500
AJ	▬ 0.5534	▬ 0.4670
AK	▬ 0.0781	▬ 0.2230
AL	▬ 0.7434	▬ 0.5270
AM	▬ 0.7689	▬ 0.5430
AN	▬ 0.8420	▬ 0.5810
AO	▬ 0.7921	▬ 0.5620
AP	▬ 0.7977	▬ 0.5670
AQ	▬ 0.7811	▬ 0.5540
AR	▬ 0.6937	▬ 0.5200
AS	▬ 0.8076	▬ 0.5650
AT	▬ 0.7308	▬ 0.5390
AU	▬ 0.6015	▬ 0.4610
AV	▬ 0.7930	▬ 0.5700
AW	▬ 0.7210	▬ 0.5530
AX	▬ 0.7340	▬ 0.5400
AY	▬ 0.7718	▬ 0.5540
AZ	▬ 0.7316	▬ 0.5180
Aa	▬ 0.8413	▬ 0.5800
Ab	▬ 0.6380	▬ 0.4940
Ac	▬ 0.6949	▬ 0.5280

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Chain	Atom inclusion	Q-score
Ad	0.7106	0.5310
Ae	0.8063	0.5760
Af	0.8373	0.5840
Ag	0.7376	0.5530
Ah	0.7201	0.5380
Ai	0.6809	0.5110
Aj	0.8185	0.5670
Ak	0.6369	0.4890
Al	0.7658	0.5590
Am	0.7518	0.5450
An	0.7248	0.5210
Ao	0.7030	0.5340
Ap	0.7311	0.5540
Ar	0.7994	0.5600
B	0.5937	0.4660
C	0.6351	0.4920
D	0.6560	0.5100
E	0.3983	0.3930
F	0.6206	0.4750
G	0.5056	0.4330
H	0.4625	0.4150
I	0.4463	0.4070
J	0.6435	0.4890
K	0.6259	0.4890
L	0.2671	0.3410
M	0.7228	0.5370
N	0.0548	0.2240
O	0.6681	0.5070
P	0.6515	0.5130
Q	0.2787	0.2930
R	0.4689	0.4380
S	0.4046	0.4050
T	0.3354	0.3520
U	0.3889	0.3820
V	0.3088	0.3640
W	0.5714	0.4680
X	0.7099	0.5270
Y	0.7180	0.5290
Z	0.5545	0.4510
a	0.3208	0.3490
b	0.7130	0.5300
c	0.5618	0.4750

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Chain	Atom inclusion	Q-score
d	■ 0.4532	■ 0.4200
e	■ 0.5306	■ 0.4440
f	■ 0.5093	■ 0.4330
g	■ 0.0426	■ 0.2010
h	■ 0.2447	■ 0.3190