wwPDB EM Validation Summary Report ⓘ

Dec 17, 2022 – 10:10 am GMT

PDB ID	:	6YLY
EMDB ID	:	EMD-10842
Title	:	pre-60S State NE2 (TAP-Flag-Nop53)
Authors	:	Kater, L.; Beckmann, R.
Deposited on	:	2020-04-07
Resolution	:	3.80 Å(reported)
Based on initial models	:	3JCT, 6N8J

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

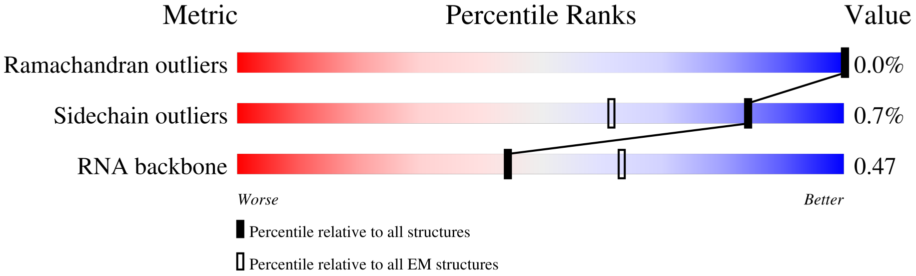
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance

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

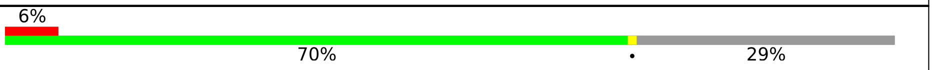
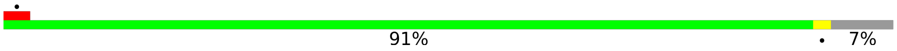
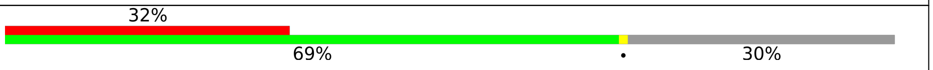
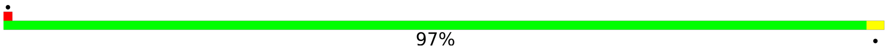
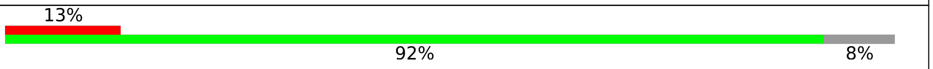
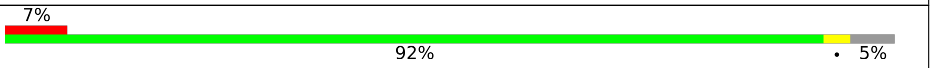
The reported resolution of this entry is 3.80 Å.

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	A	254	
2	a	149	
3	B	387	
4	b	647	
5	C	362	
6	c	105	
7	d	113	
8	E	176	

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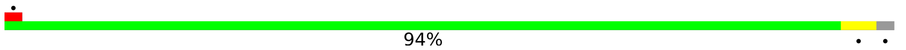
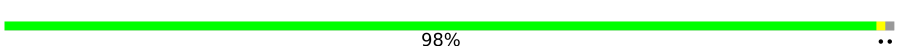
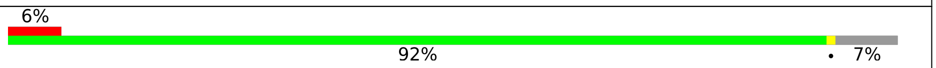
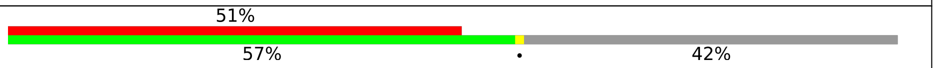
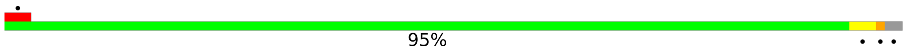
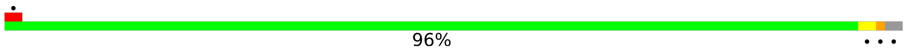
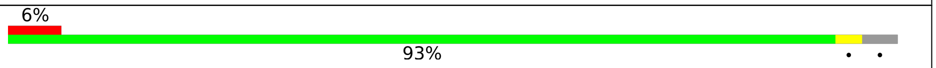
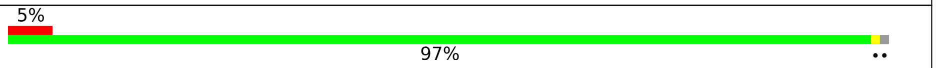
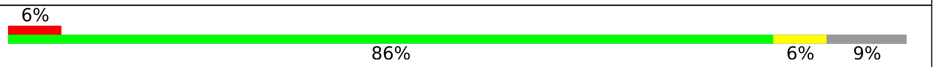
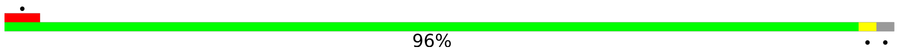
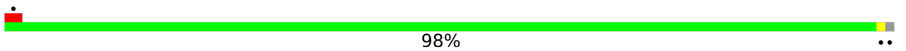
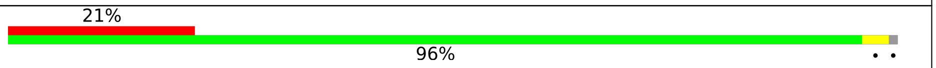
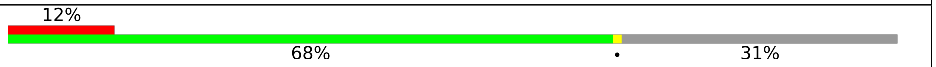
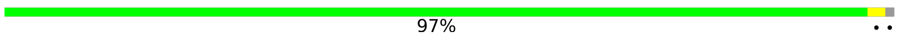
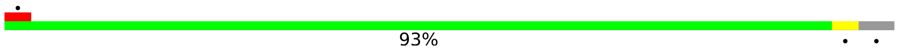
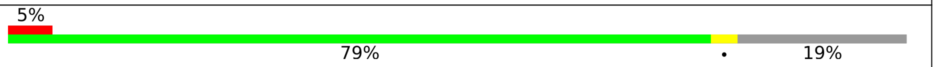
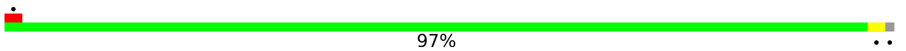
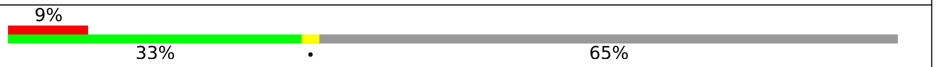
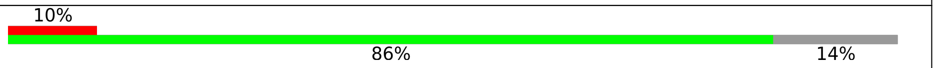
Mol	Chain	Length	Quality of chain
9	e	130	
10	F	244	
11	f	107	
12	G	256	
13	g	121	
14	I	166	
15	H	191	
16	h	120	
17	i	100	
18	j	88	
19	k	78	
20	L	199	
21	l	51	
22	M	138	
23	p	92	
24	N	204	
25	u	199	
26	O	199	
27	P	184	
28	Q	186	
29	R	189	
30	r	261	
31	S	172	
32	T	160	
33	U	121	

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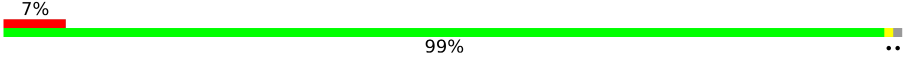
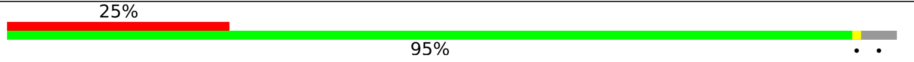
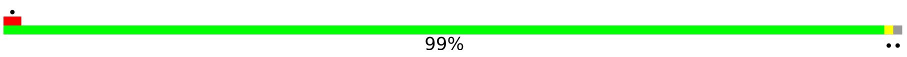
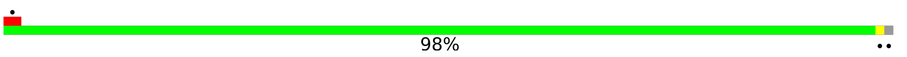
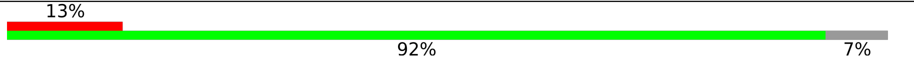
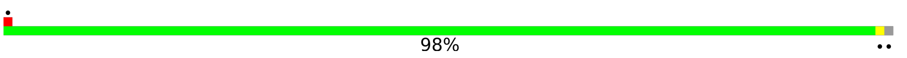
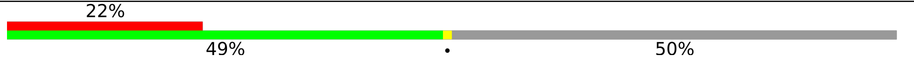
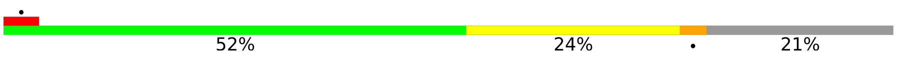
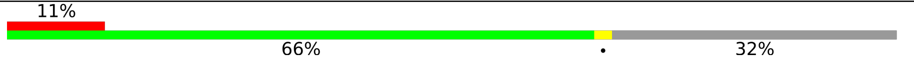
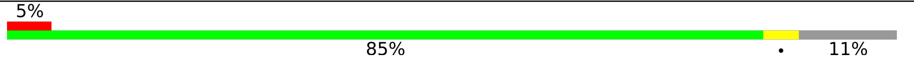
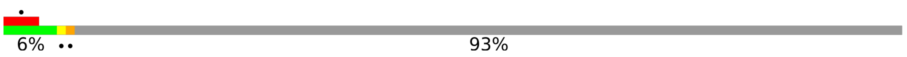
Mol	Chain	Length	Quality of chain
34	V	137	
35	W	236	
36	X	142	
37	Y	127	
38	y	245	
39	Z	136	
40	z	106	
41	1	3396	
42	3	158	
43	K	376	
44	n	605	
45	o	220	
46	q	455	
47	t	322	
48	6	232	
49	s	520	

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 120663 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 protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	A	180	1391	877	271	243	0	0

- Molecule 2 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	a	84	652	426	113	113	0	0

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	360	2866	1821	536	502	7	0	0

- Molecule 4 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	b	451	3651	2324	628	681	18	0	0

- Molecule 5 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	C	361	2749	1730	522	494	3	0	0

- Molecule 6 is a protein called 60S ribosomal protein L30.

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

- Molecule 7 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	d	107	Total	C	N	O	S	0	0
			873	553	165	154	1		

- Molecule 8 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 9 is a protein called 60S ribosomal protein L32.

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

- Molecule 10 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 11 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 12 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	230	Total	C	N	O	S	0	0
			1798	1149	323	323	3		

- Molecule 13 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 14 is a protein called Bud site selection protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	96	Total	C	N	O	S	0	0
			776	487	146	140	3		

- Molecule 15 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	188	Total	C	N	O	S	0	0
			1493	948	271	270	4		

- Molecule 16 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	h	118	Total	C	N	O	S	0	0
			964	612	185	166	1		

- Molecule 17 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	i	96	Total	C	N	O	S	0	0
			743	465	148	128	2		

- Molecule 18 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	j	81	Total	C	N	O	S	0	0
			646	394	141	106	5		

- Molecule 19 is a protein called 60S ribosomal protein L38.

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

- Molecule 20 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	L	182	Total	C	N	O	0	0
			1451	902	299	250		

- Molecule 21 is a protein called 60S ribosomal protein L39.

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

- Molecule 22 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	M	137	1059	678	200	179	2	0	0

- Molecule 23 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	N	187	1607	1005	341	260	1	0	0

- Molecule 25 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	u	137	1158	727	234	188	9	0	0

- Molecule 26 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 27 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
27	P	176	1393	865	278	250	0	0

- Molecule 28 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Q	134	Total 1035	C 659	N 196	O 179	S 1	0	0

- Molecule 29 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	R	154	Total 1241	C 772	N 262	O 207	0	0

- Molecule 30 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	r	67	Total 579	C 358	N 124	O 96	S 1	0	0

- Molecule 31 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	S	170	Total 1425	C 916	N 265	O 241	S 3	0	0

- Molecule 32 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	T	56	Total 434	C 268	N 86	O 79	S 1	0	0

- Molecule 33 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	U	104	Total 826	C 535	N 136	O 155	0	0

- Molecule 34 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 35 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	W	227	Total 1814	C 1149	N 310	O 350	S 5	0	0

- Molecule 36 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	X	141	Total 1100	C 705	N 196	O 197	S 2	0	0

- Molecule 37 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 38 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	y	227	Total 1712	C 1062	N 298	O 346	S 6	0	0

- Molecule 39 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 40 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	z	53	Total 430	C 264	N 85	O 81	0	0

- Molecule 41 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	1	2676	Total 57244	C 25566	N 10318	O 18684	P 2676	0	0

- Molecule 42 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
42	3	158	3353	1500	586	1109	158	0	0

- Molecule 43 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	K	256	2064	1332	342	387	3	0	0

- Molecule 44 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	n	371	3030	1963	523	534	10	0	0

- Molecule 45 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	o	125	1046	676	188	178	4	0	0

- Molecule 46 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	q	141	1178	743	208	226	1	0	0

- Molecule 47 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	t	287	2306	1459	427	417	3	0	0

- Molecule 48 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
48	6	65	1370	614	228	463	65	0	0

- Molecule 49 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	s	36	301	184	69	46	2	0	0

- Molecule 50 is ZINC ION (three-letter code: ZN) (formula: Zn).

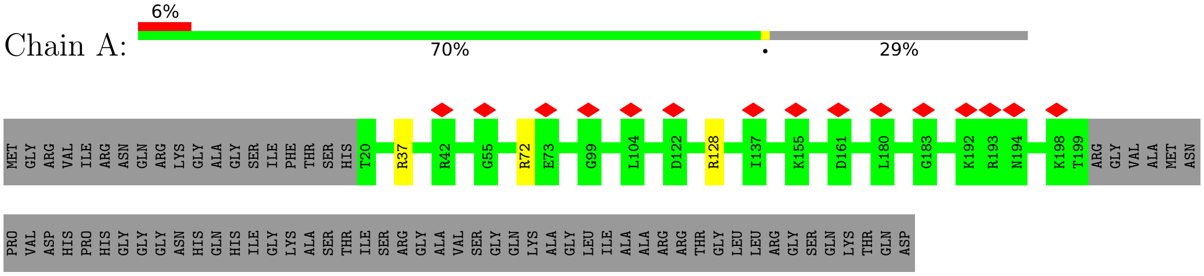
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
50	j	1	1	1	0
50	p	1	1	1	0
50	u	1	1	1	0

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.

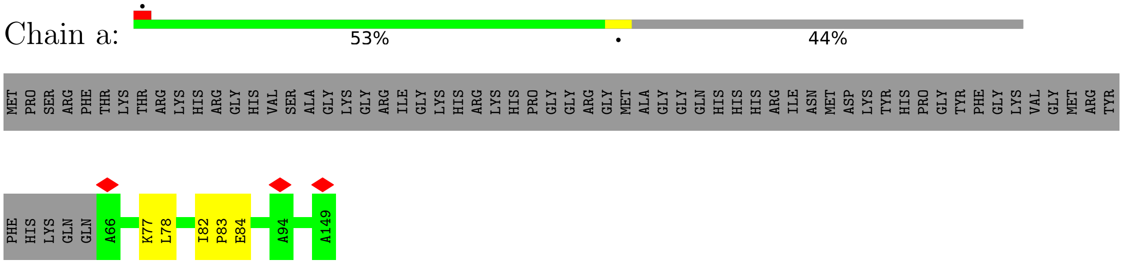
- Molecule 1: 60S ribosomal protein L2-A

Chain A:



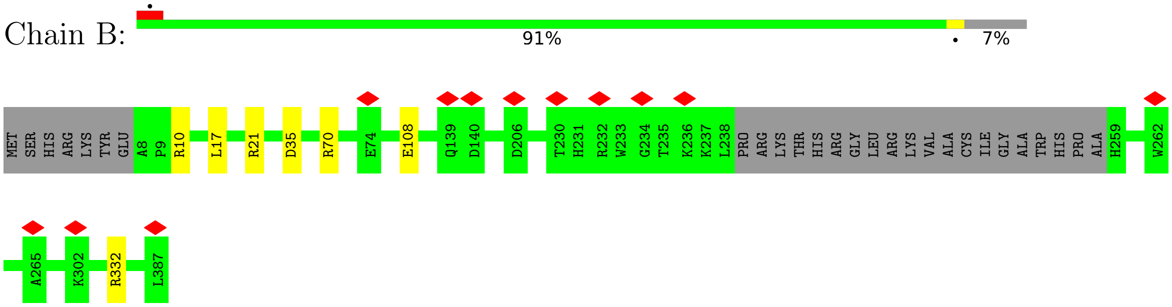
- Molecule 2: 60S ribosomal protein L28

Chain a:



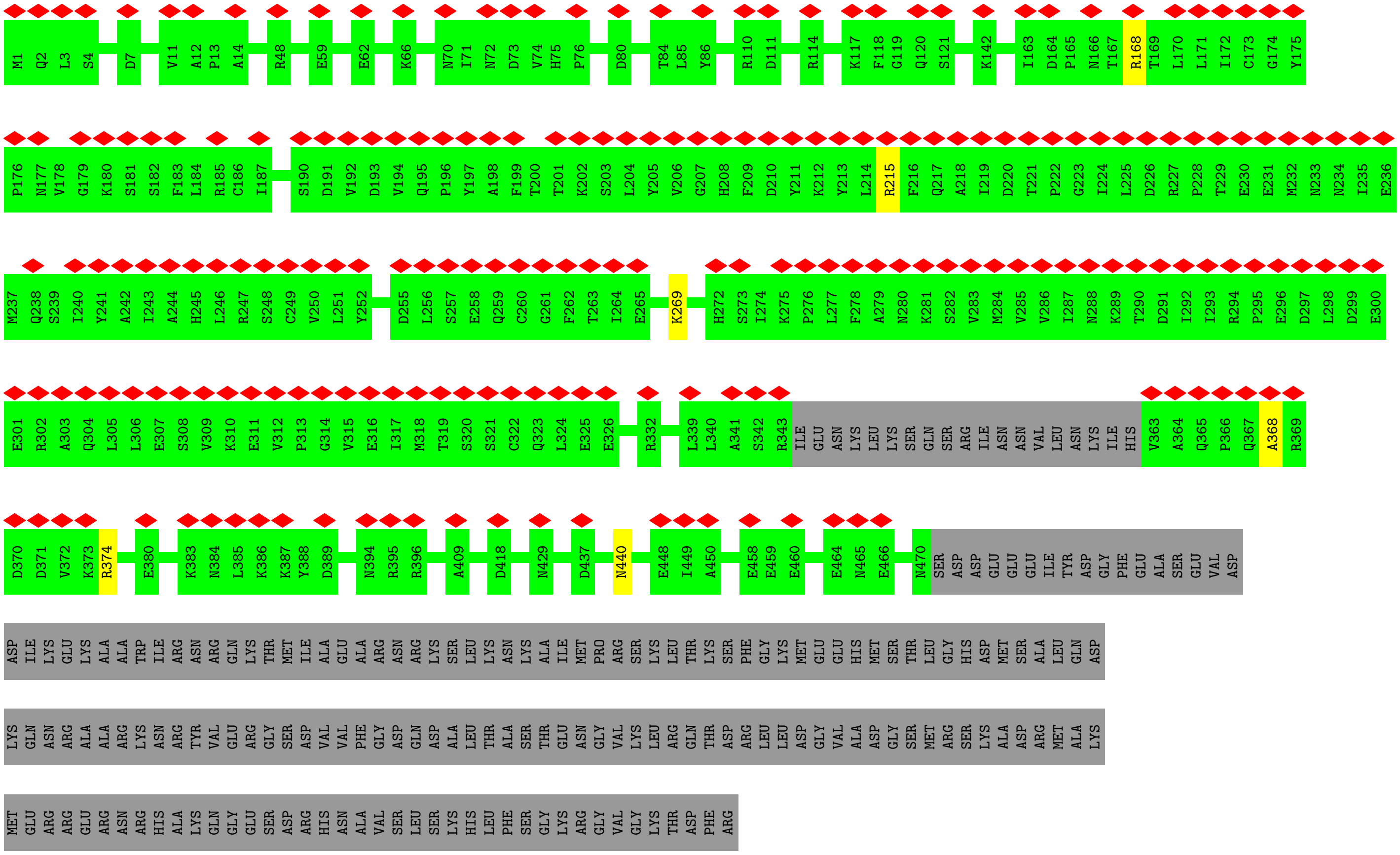
- Molecule 3: 60S ribosomal protein L3

Chain B:



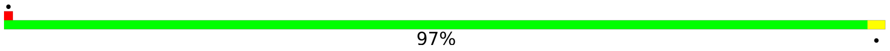
- Molecule 4: Nucleolar GTP-binding protein 1

Chain b:



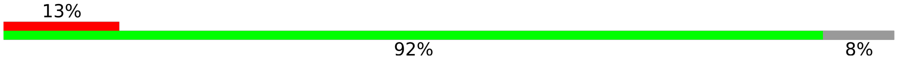
- Molecule 5: 60S ribosomal protein L4-A

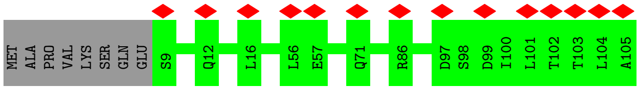
Chain C:



- Molecule 6: 60S ribosomal protein L30

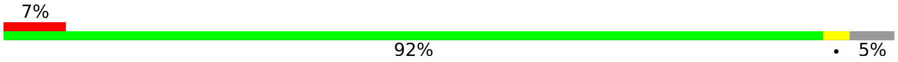
Chain c:

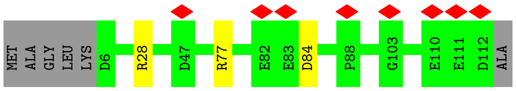




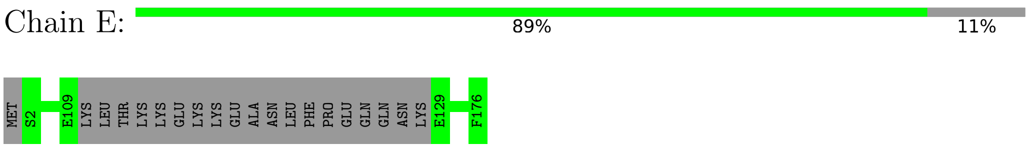
- Molecule 7: 60S ribosomal protein L31-A

Chain d:

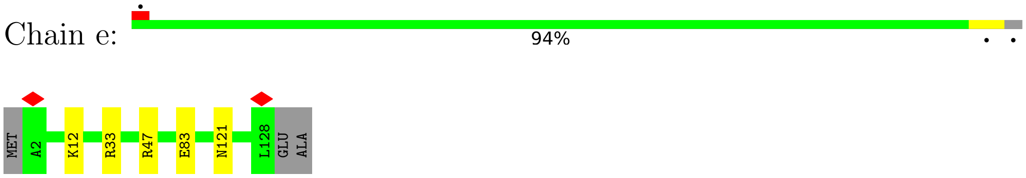




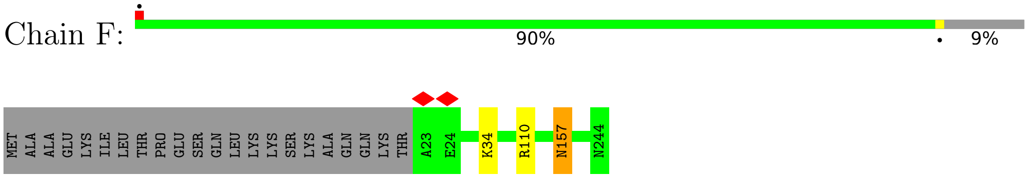
- Molecule 8: 60S ribosomal protein L6-A



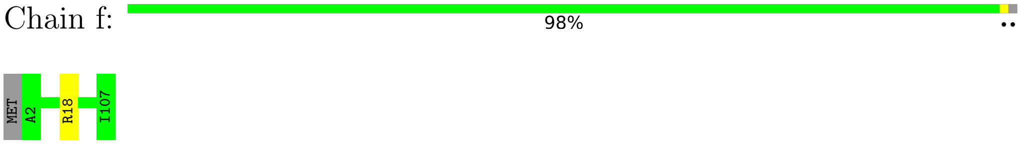
- Molecule 9: 60S ribosomal protein L32



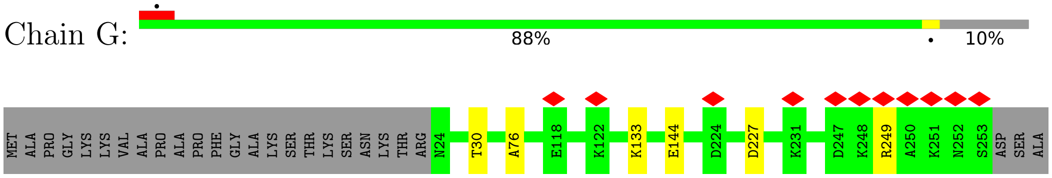
- Molecule 10: 60S ribosomal protein L7-A



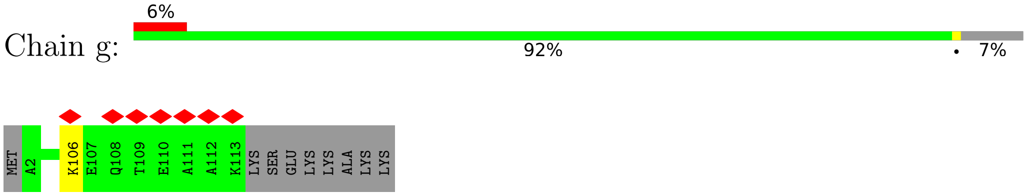
- Molecule 11: 60S ribosomal protein L33-A



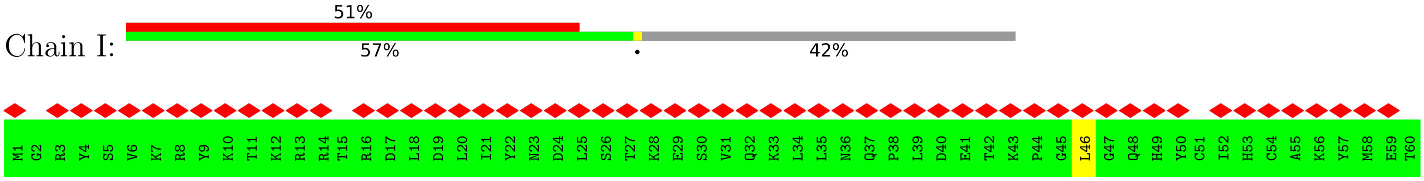
- Molecule 12: 60S ribosomal protein L8-A

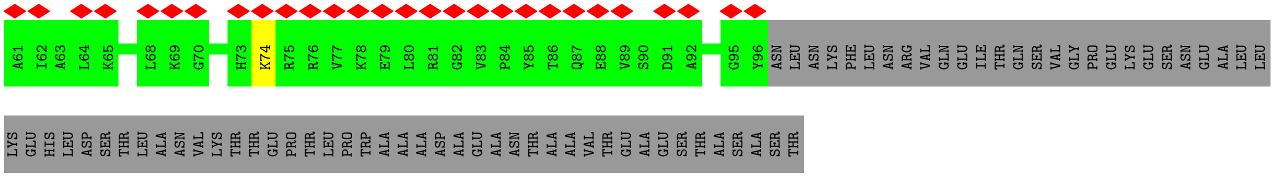


- Molecule 13: 60S ribosomal protein L34-A



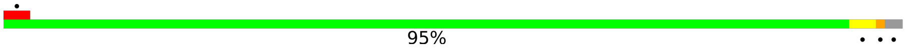
- Molecule 14: Bud site selection protein 20

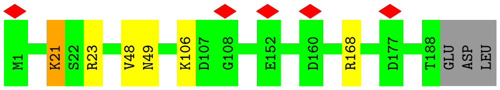




- Molecule 15: 60S ribosomal protein L9-A

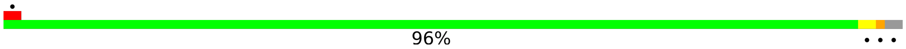
Chain H:

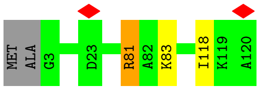




- Molecule 16: 60S ribosomal protein L35-A

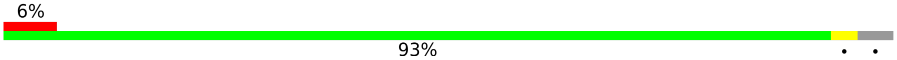
Chain h:

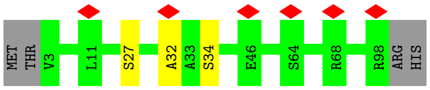




- Molecule 17: 60S ribosomal protein L36-A

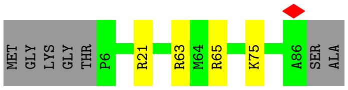
Chain i:





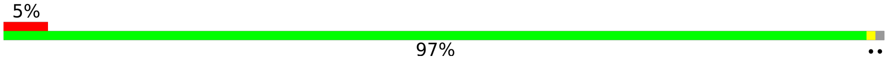
- Molecule 18: 60S ribosomal protein L37-A

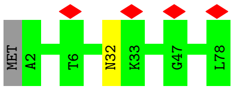
Chain j:



- Molecule 19: 60S ribosomal protein L38

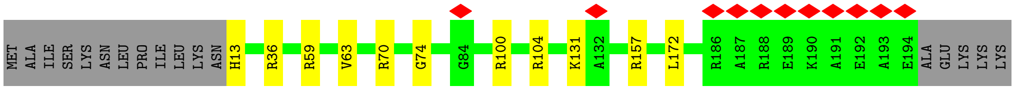
Chain k:





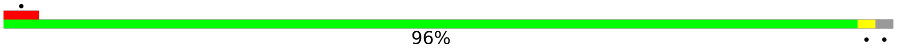
- Molecule 20: 60S ribosomal protein L13-A

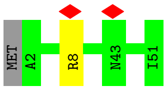
Chain L:



- Molecule 21: 60S ribosomal protein L39

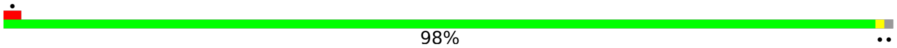
Chain l:

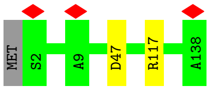




- Molecule 22: 60S ribosomal protein L14-A

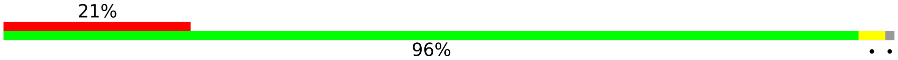
Chain M:

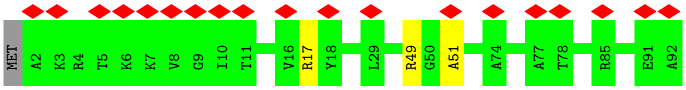




- Molecule 23: 60S ribosomal protein L43-A

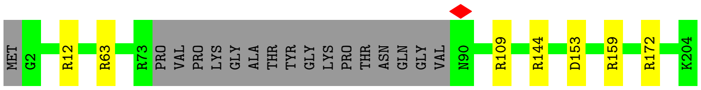
Chain p:





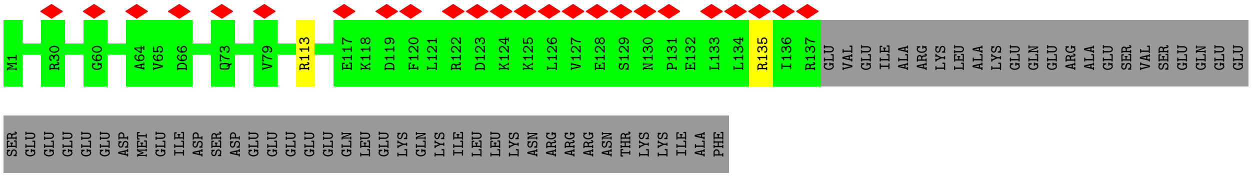
- Molecule 24: 60S ribosomal protein L15-A

Chain N:



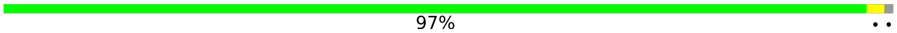
- Molecule 25: Ribosome biogenesis protein RLP24

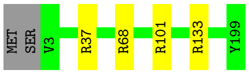
Chain u:



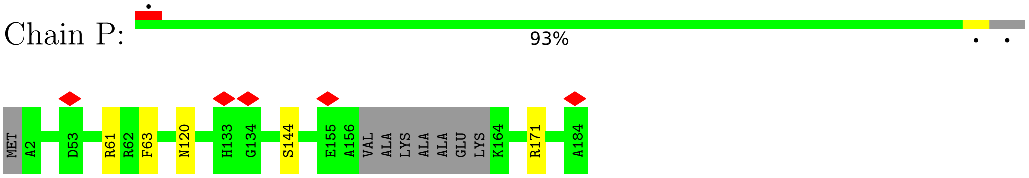
- Molecule 26: 60S ribosomal protein L16-A

Chain O:

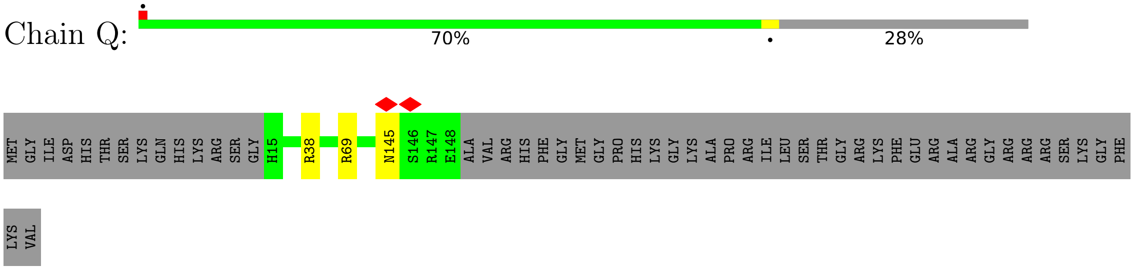




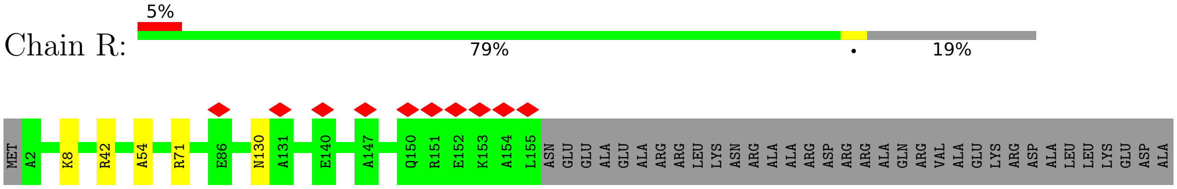
- Molecule 27: 60S ribosomal protein L17-A



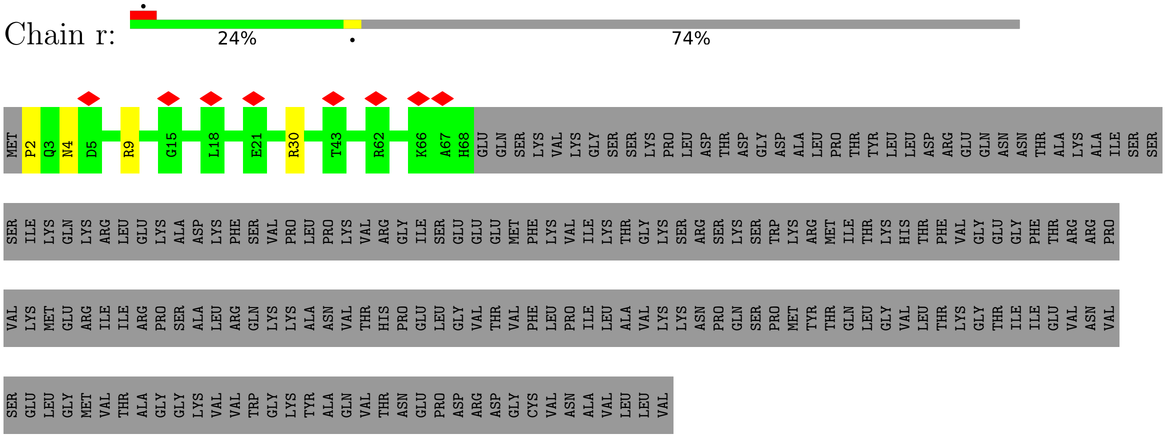
- Molecule 28: 60S ribosomal protein L18-A



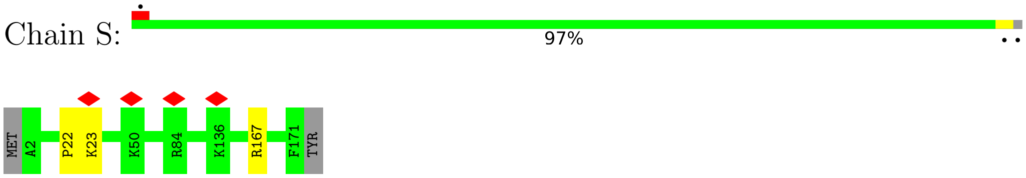
- Molecule 29: 60S ribosomal protein L19-A



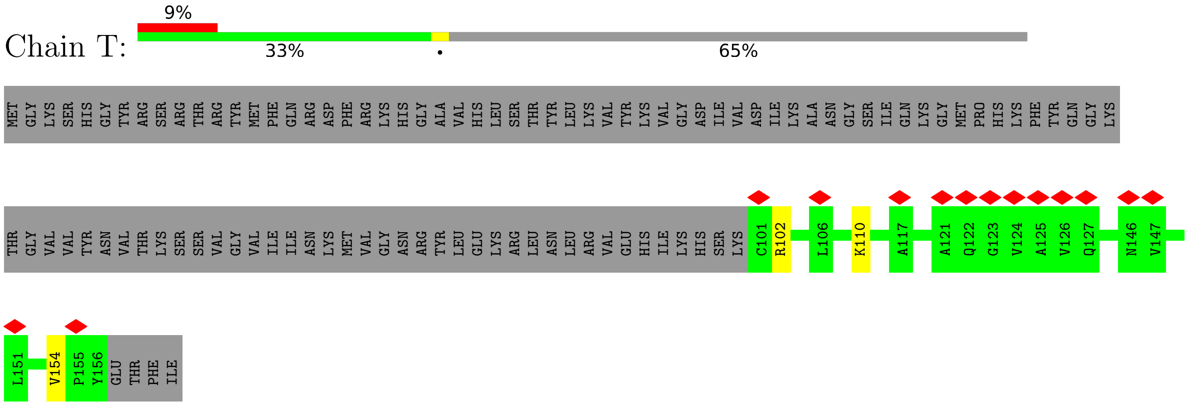
- Molecule 30: Ribosome biogenesis protein NSA2



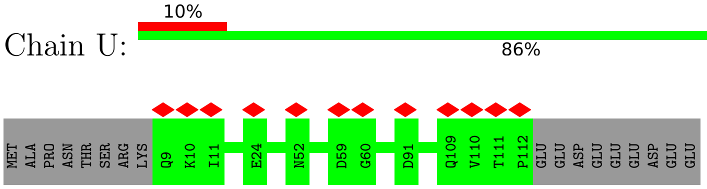
- Molecule 31: 60S ribosomal protein L20-A



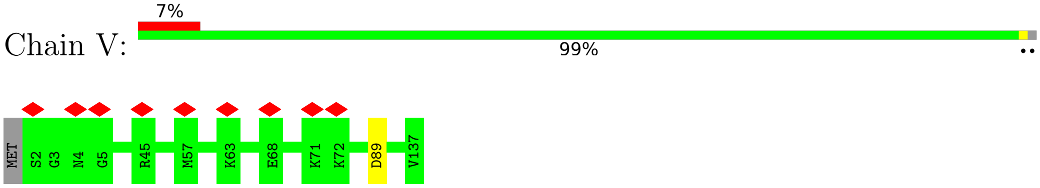
- Molecule 32: 60S ribosomal protein L21-A



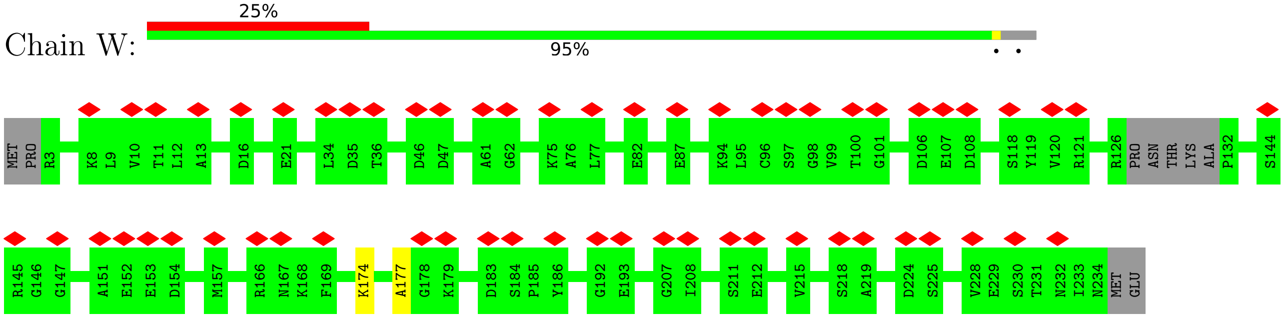
- Molecule 33: 60S ribosomal protein L22-A



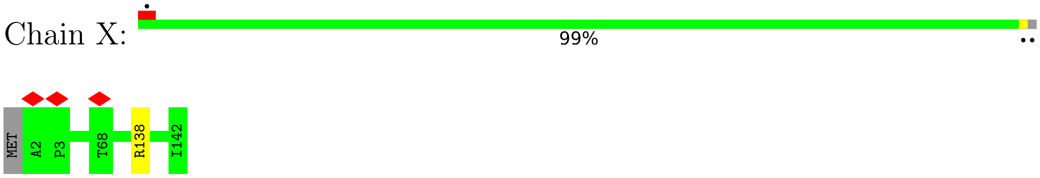
- Molecule 34: 60S ribosomal protein L23-A



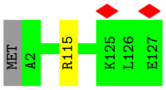
- Molecule 35: Ribosome assembly factor MRT4



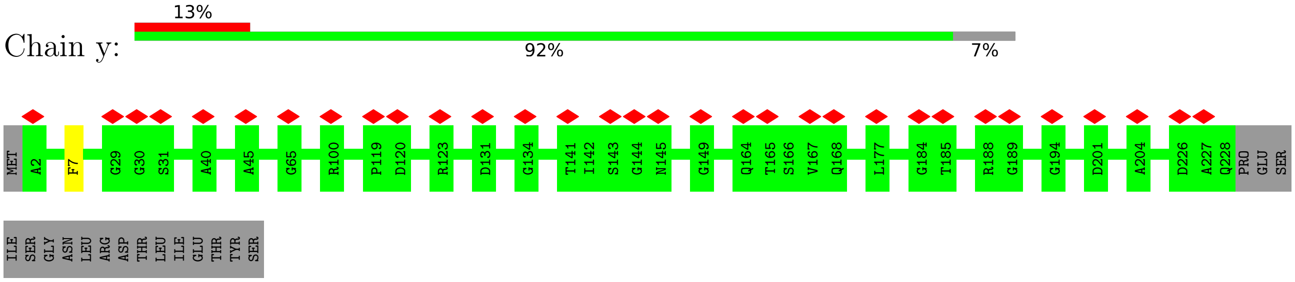
- Molecule 36: 60S ribosomal protein L25



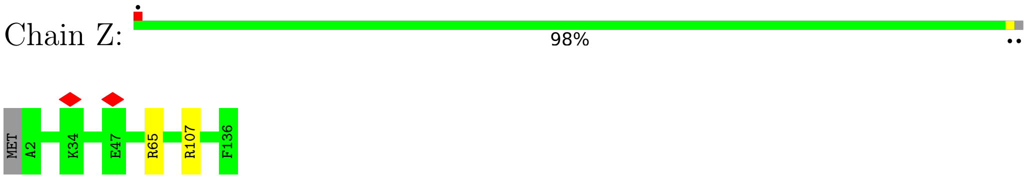
- Molecule 37: 60S ribosomal protein L26-A



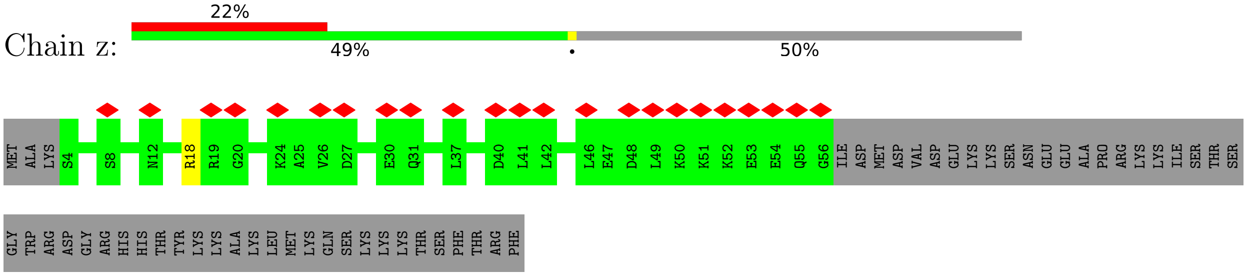
- Molecule 38: Eukaryotic translation initiation factor 6



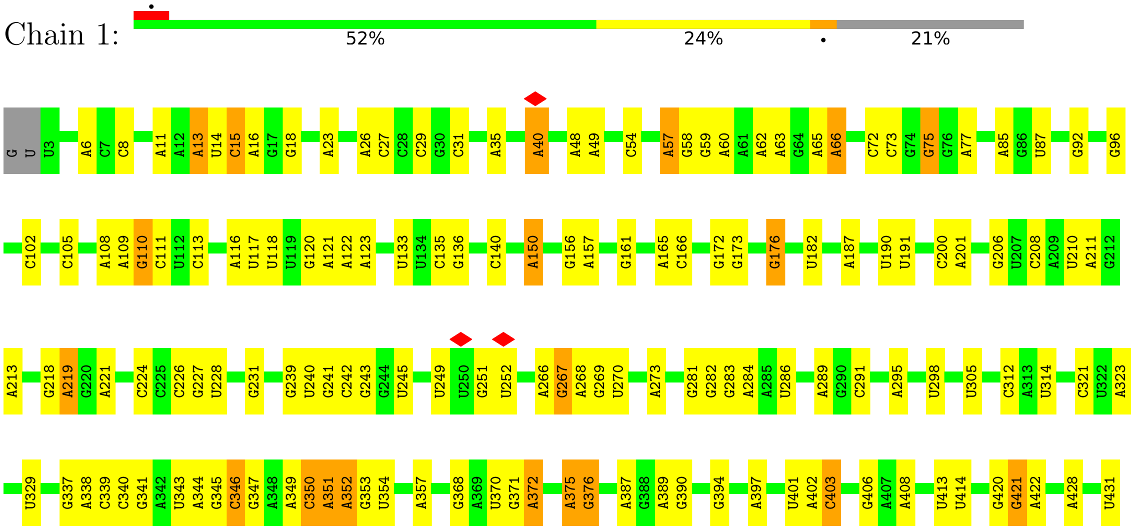
- Molecule 39: 60S ribosomal protein L27-A

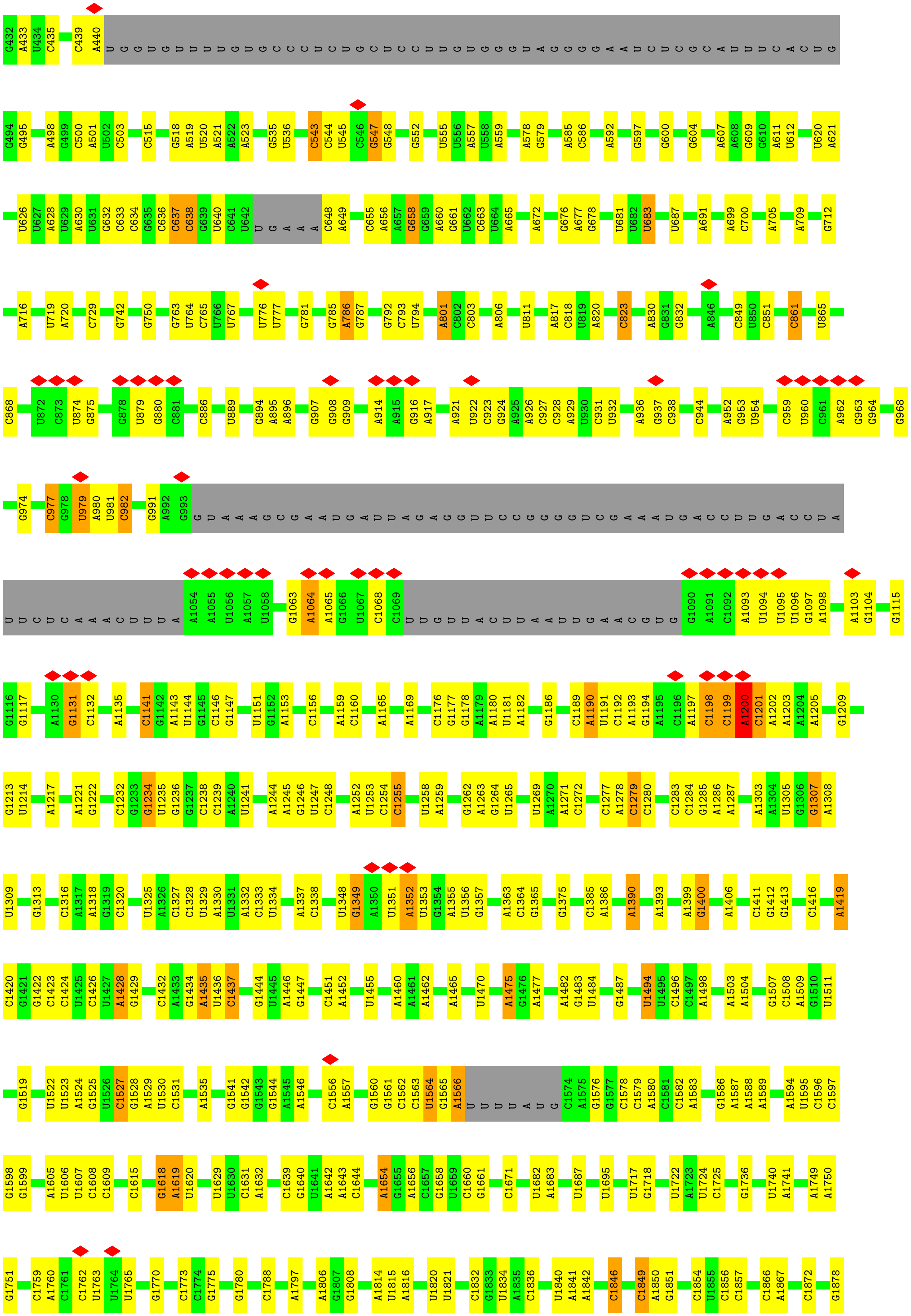


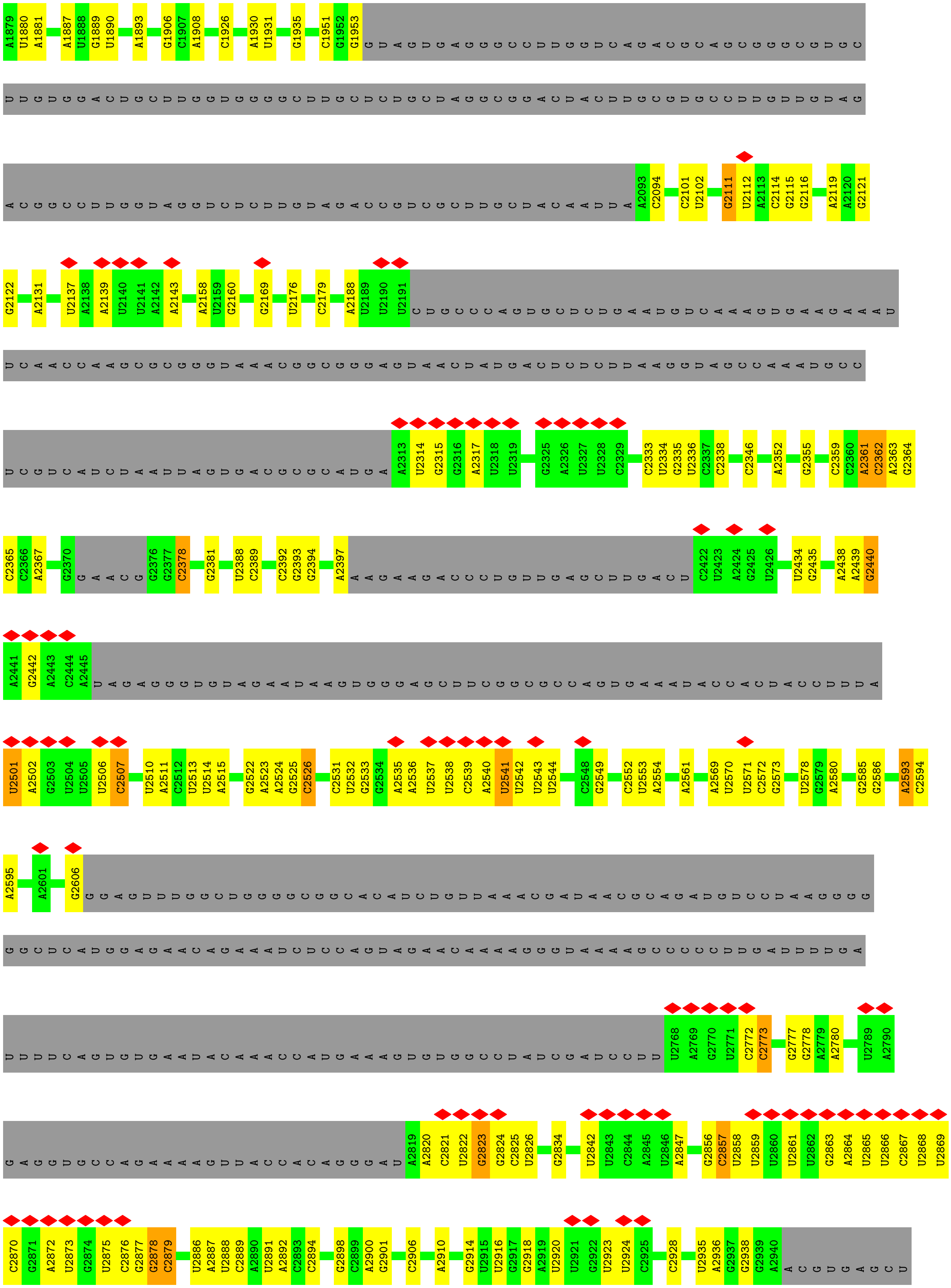
- Molecule 40: UPF0642 protein YBL028C

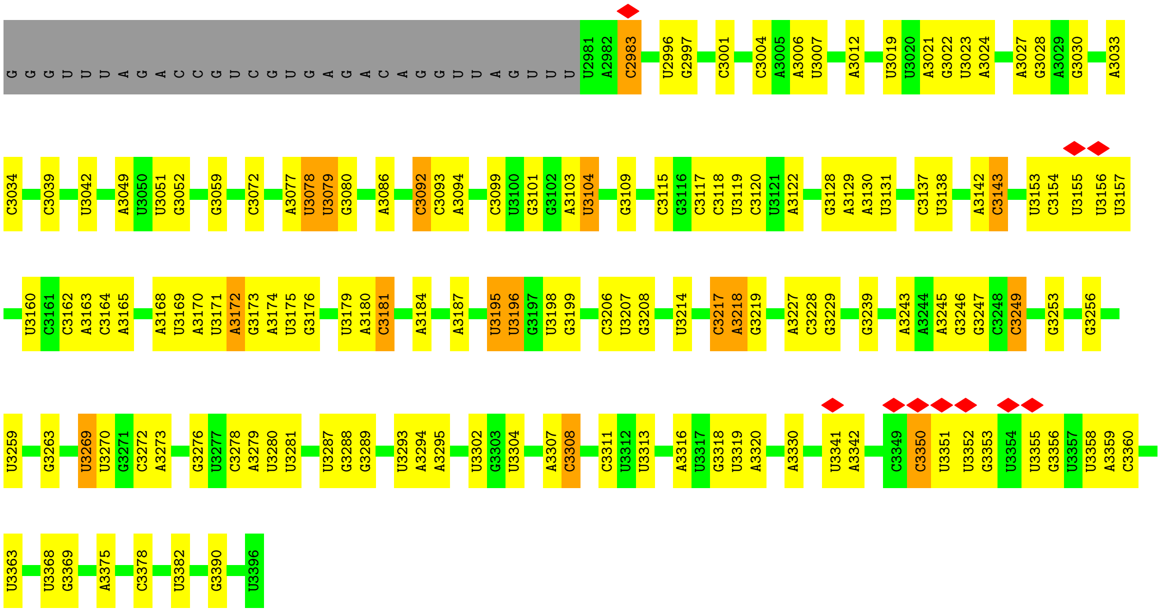


- Molecule 41: 25S rRNA



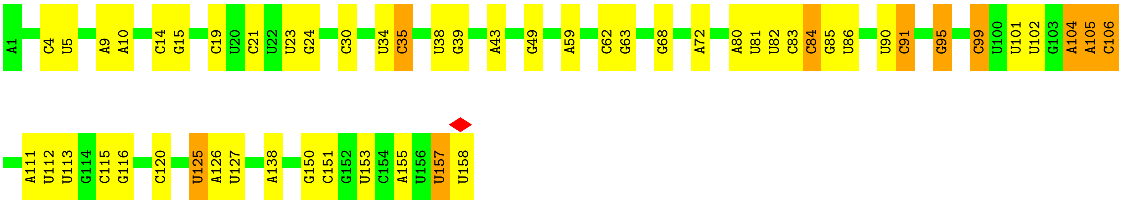

G432 A433 U434 C435 C439 A440 U G G U G U U U U G U G C C C U C U G C U C C C U U G U G G G G U A G G G G A A U C U C G G C A U U U C A C U G
G494 G495 A498 G499 C500 A501 U502 C503 C515 G518 A519 U520 A521 A522 A523 C535 U536 C543 C544 U545 C546 G547 G548 G552 U555 U556 A557 U558 A559 A578 G579 A585 C586 A592 G597 G600 G604 A607 A608 G609 G610 A611 U612 U620 A621
U626 U627 A628 U629 A630 U631 G632 C633 C634 G635 C636 C637 C638 G639 U640 C641 U642 U G A A A C648 A649 C655 A656 A657 G658 G659 A660 G661 U662 C663 U664 A665 A672 G676 A677 G678 U681 U682 U683 U687 A691 A699 C700 A705 A709 G712
A716 U719 A720 C729 G742 G750 G763 U764 C765 U766 U767 U776 U777 G781 G785 A786 G787 G792 C793 U794 A801 C802 C803 A806 U811 A817 C818 U819 A820 C823 A830 G831 G832 A846 C849 U850 C851 C861 U865
C868 U872 C873 U874 G875 G878 U879 G880 C881 C886 U889 G894 A895 A896 G907 G908 G909 A914 A915 G916 A917 A921 U922 C923 G924 A925 A926 C927 C928 A929 U930 C931 U932 A936 G937 C938 C944 A952 G953 U954 C959 U960 C961 A962 G963 G964 G968
G974 C977 G978 U979 A980 U981 C982 G991 A992 G993 G U A A A G C G A A U G A U U A G A G G U U C C G G G G U C G A A A U G A C C U U G A C C U A
U U C U C A A A C U U U A A1054 A1055 U1056 A1057 U1058 G1063 A1064 A1065 G1066 U1067 C1068 C1069 U U G U U A C U U A A U U G A A C G U G G1090 A1091 C1092 A1093 U1094 U1095 U1096 G1097 A1098 A1103 G1104 G1115
G1116 G1117 A1130 G1131 C1132 A1135 C1141 G1142 A1143 U1144 G1145 C1146 G1147 U1151 G1152 A1153 C1156 A1159 C1160 A1165 A1169 C1176 G1177 G1178 A1179 A1180 U1181 A1182 G1186 C1189 A1190 U1191 C1192 A1193 G1194 A1195 C1196 A1197 C1198 C1199 A1200 C1201 A1202 A1203 A1204 A1205 G1209
G1213 U1214 A1217 A1221 G1222 C1232 G1233 G1234 U1235 G1236 G1237 C1238 C1239 A1240 U1241 A1244 A1245 G1246 U1247 C1248 A1252 U1253 C1254 C1255 U1258 A1259 G1262 A1263 G1264 U1265 U1269 A1270 A1271 C1272 C1277 A1278 C1279 C1280 C1283 C1284 G1285 A1286 A1287 A1303 A1304 U1305 G1306 G1307 A1308
U1309 G1313 C1316 A1317 A1318 G1319 C1320 U1325 A1326 C1327 C1328 U1329 A1330 U1331 A1332 C1333 U1334 A1337 C1338 U1348 G1349 A1350 U1351 A1352 U1353 G1354 A1355 U1356 G1357 A1363 C1364 G1365 G1375 C1385 A1386 A1390 A1393 A1399 G1400 A1406 C1411 G1412 G1413 C1416 A1419
C1420 G1421 G1422 C1423 C1424 U1425 C1426 U1427 A1428 G1429 C1432 A1433 G1434 A1435 U1436 C1437 G1444 U1445 A1446 G1447 C1451 A1452 U1455 A1460 A1461 A1462 A1465 U1470 A1475 G1476 A1477 A1482 G1483 U1484 G1487 U1494 U1495 C1496 C1497 A1498 A1503 A1504 G1507 C1508 A1509 G1510 U1511
G1519 U1522 U1523 A1524 G1525 U1526 C1527 G1528 A1529 U1530 C1531 A1535 G1541 G1542 G1543 U1544 A1545 A1546 C1556 A1557 G1560 G1561 C1562 C1563 U1564 G1565 A1566 U U U U A U G C1574 A1575 G1576 G1577 C1578 C1579 A1580 C1581 C1582 A1583 G1586 A1587 A1588 A1589 A1594 U1595 C1596 C1597
G1598 G1599 A1605 U1606 U1607 C1608 C1609 C1615 G1618 A1619 U1620 U1629 U1630 C1631 A1632 C1639 G1640 U1641 A1642 A1643 C1644 A1654 G1655 A1656 C1657 G1658 U1659 C1660 G1661 C1671 U1682 A1683 U1687 U1695 U1717 G1718 U1722 A1723 U1724 C1725 G1736 U1740 A1741 A1749 A1750
G1751 C1759 A1760 C1761 C1762 U1763 U1764 U1765 G1770 C1773 C1774 G1775 G1780 C1788 A1797 A1806 G1807 G1808 A1814 U1815 A1816 U1820 U1821 C1832 G1833 U1834 A1835 C1836 U1840 A1841 A1842 C1846 C1849 A1850 G1851 C1854 U1855 C1856 C1857 C1866 A1867 C1872 G1878


A1879 U1880 A1881 A1887 U1888 G1889 U1890 A1893 G1906 C1907 A1908 C1926 A1930 U1931 G1935 C1951 G1952 G1953 G U A G U G A G G G C C U U G G G U C A G A C G C A G C G G G C C G U G C
U U G U G G A C U G C U U G G U G G G G C U U G C U C U G C U A G G C G G A C U A C U U G C G U G C C U U G U U G U A G
A C G G C C U U G G U A G G U C U C U U G G U A G G A C C G U C G C U U G C U A C A A U U A A2093 C2094 C2101 U2102 G2111 U2112 A2113 C2114 G2115 G2116 A2119 A2120 G2121
G2122 A2131 U2137 A2138 A2139 U2140 U2141 A2142 A2143 A2158 U2159 G2160 G2169 U2176 C2179 A2188 U2189 U2190 U2191 C U G C C C A G U G C U C U G A A U G U C A A A G U G A A G A A A U
U C A A C C A A G C G C G G G U A A A C G G C G G G A G U A A C U A U G A C U C U C U U A A G G U A G C C A A A U G C C
U C G U C A U C U A A U U A G U G A C G C G C A U G A A2313 U2314 G2315 G2316 A2317 U2318 U2319 G2325 A2326 U2327 U2328 C2329 C2333 U2334 G2335 U2336 C2337 C2338 C2346 A2352 G2355 C2359 C2360 A2361 C2362 A2363 G2364
C2365 C2366 A2367 G2370 G A A C G G2376 G2377 C2378 G2381 U2388 C2389 C2392 G2393 G2394 A2397 A A G A A G A C C C U G U U G A G C U U G A C U C2422 U2423 A2424 G2425 U2426 U2434 G2435 A2438 A2439 G2440
A2441 G2442 A2443 C2444 A2445 U A G A G G G U G U A G A A U A A G U G G G A G C U U C G G C G C C A G U G A A A U A C C A C U A C C U U U A
U2501 A2502 G2503 U2504 U2505 U2506 C2507 U2510 A2511 C2512 U2513 U2514 A2515 G2522 U2523 A2524 G2525 C2526 C2531 U2532 G2533 G2534 A2535 A2536 U2537 U2538 C2539 A2540 U2541 U2542 U2543 U2544 C2548 G2549 C2552 U2553 A2554 A2561 A2569 U2570 U2571 C2572 G2573 U2578 G2579 A2580 G2585 G2586 A2593 C2594
A2595 A2601 G2606 G G A G U U U G G C U G G G G C G G C A C A U C U G U U A A A C G G A U A A C G C A G A U G U C C U A A G G G G
G G C U C A U G G A G A A C A G A A A U C U C C A G U A G A A C A A A A G G G U A A A A G C C C C C U U G A U U U U G A
U U U U C A G U U G U G A A U A C A A A C C A U G A A A G U G U G G C C U A U C G A U C C U U U2768 A2769 G2770 U2771 C2772 C2773 G2777 G2778 A2779 A2780 U2789 A2790
G A G G U G C C A G A A A A G U U A C C A C A G G G A U A2819 A2820 C2821 U2822 G2823 G2824 C2825 U2826 G2834 U2842 U2843 C2844 A2845 U2846 A2847 G2856 C2857 U2858 U2859 U2860 U2861 U2862 G2863 A2864 U2865 U2866 C2867 U2868 U2869
C2870 G2871 A2872 U2873 G2874 U2875 C2876 G2877 G2878 C2879 U2886 A2887 U2888 C2889 A2890 U2891 A2892 C2893 C2894 G2898 C2899 A2900 G2901 C2906 A2910 G2914 U2915 G2916 G2917 G2918 A2919 U2920 U2921 G2922 U2923 U2924 C2925 C2928 U2935 A2936 G2937 G2938 G2939 A2940 A C G U G A G C U



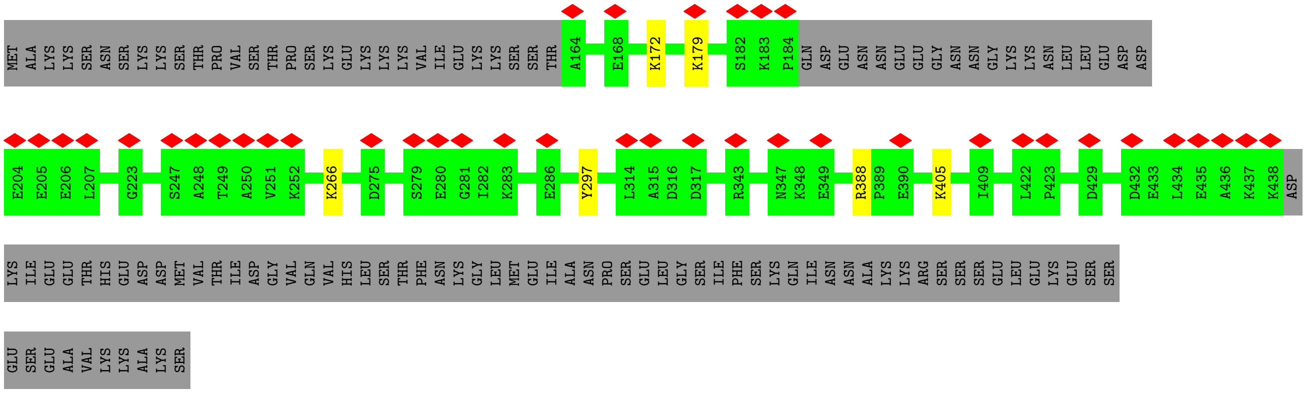
- Molecule 42: 5.8S rRNA

Chain 3:



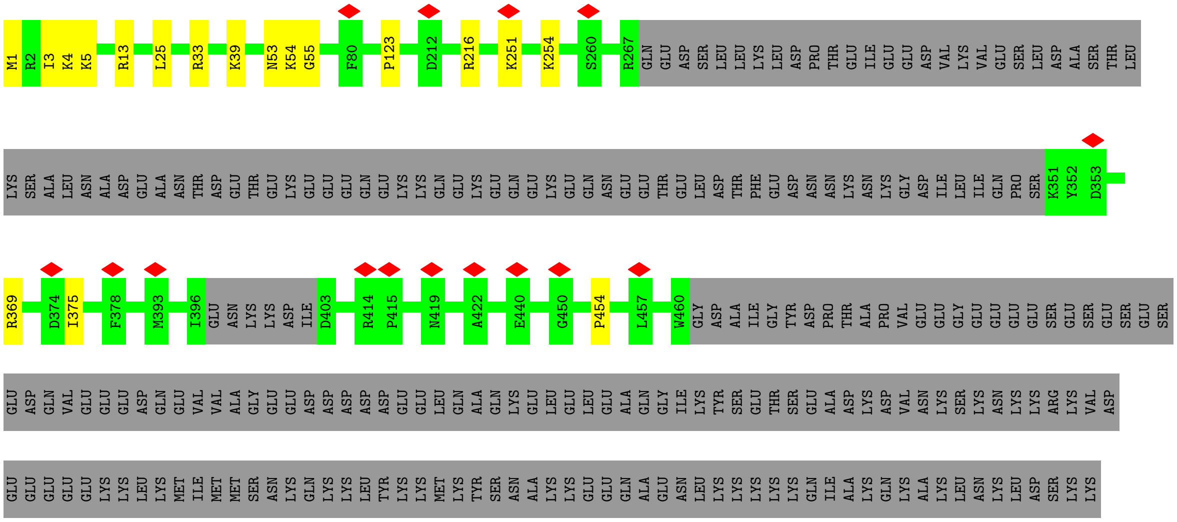
- Molecule 43: Proteasome-interacting protein CIC1

Chain K:

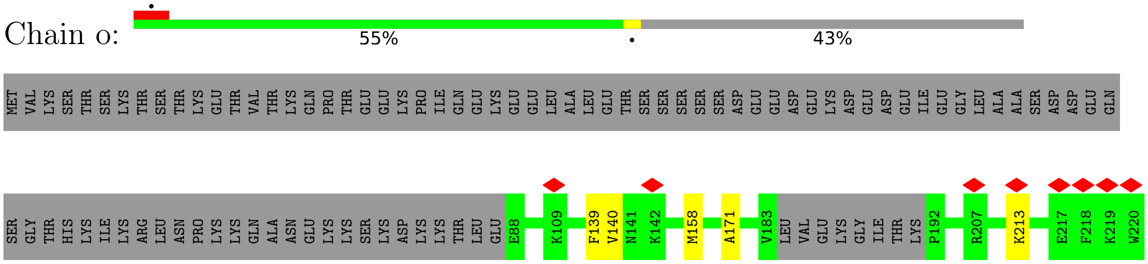


- Molecule 44: Pescadillo homolog

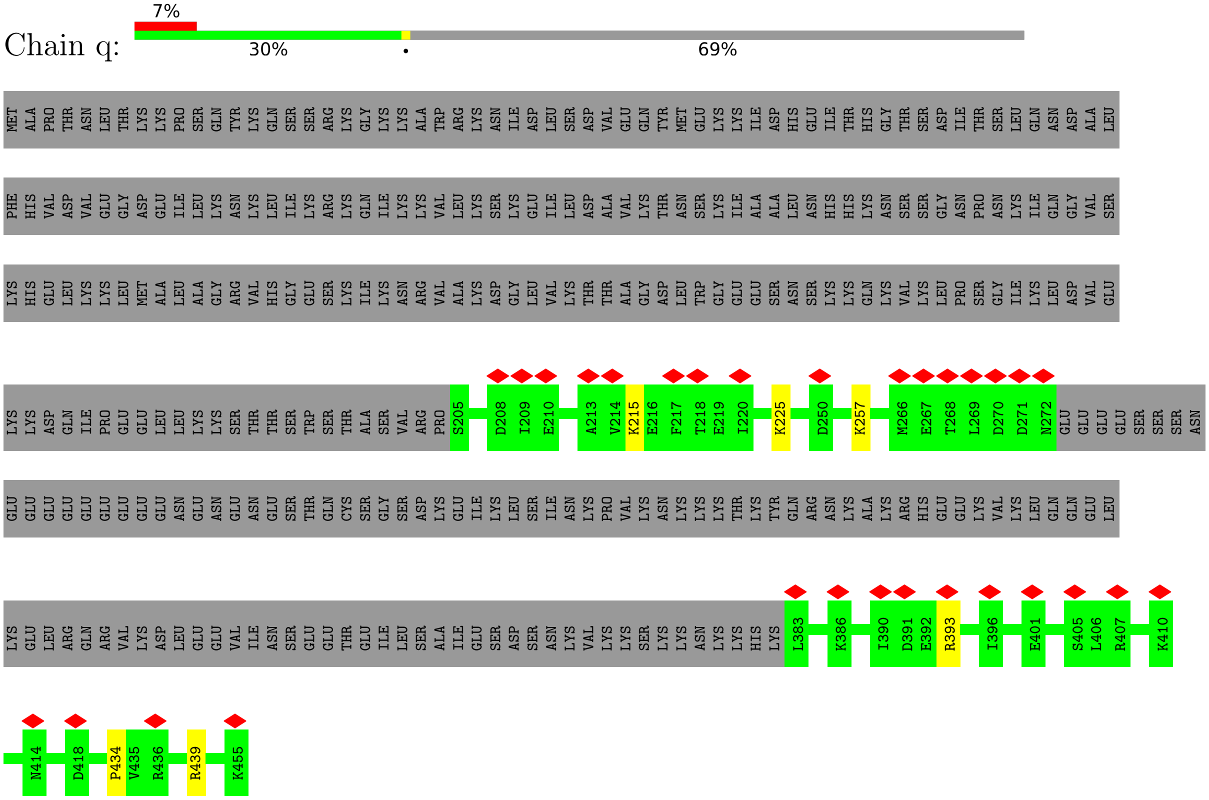
Chain n:



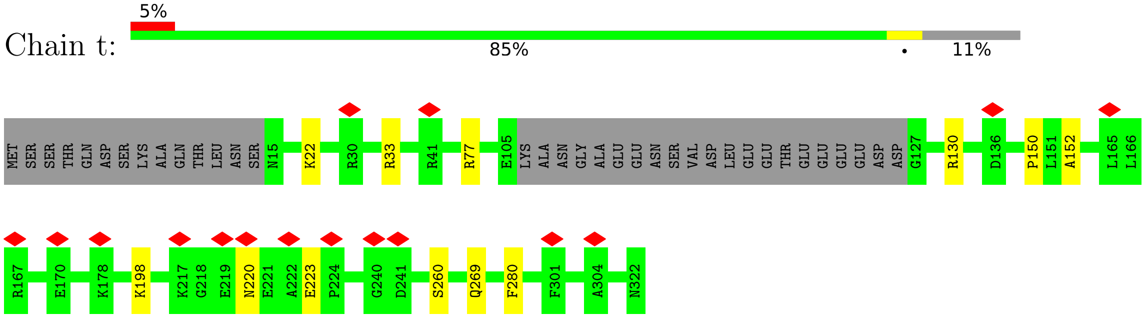
- Molecule 45: Ribosome biogenesis protein 15



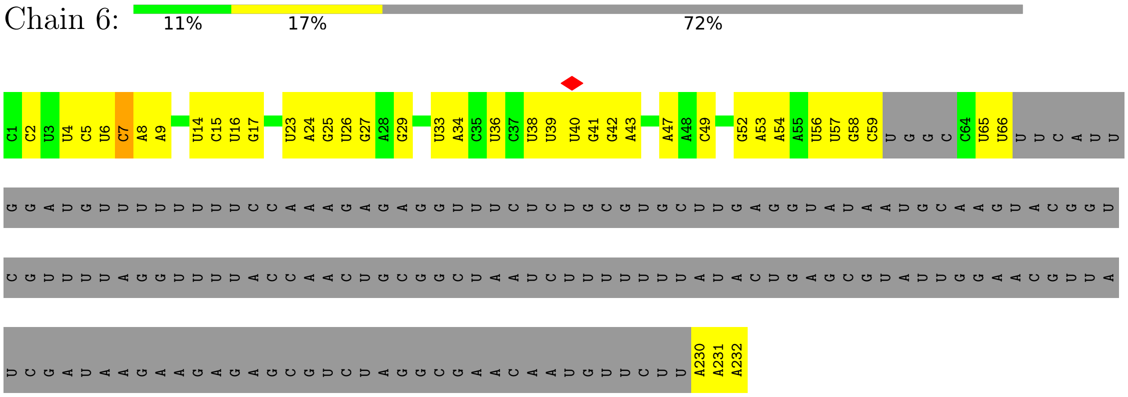
- Molecule 46: Ribosome biogenesis protein NOP53



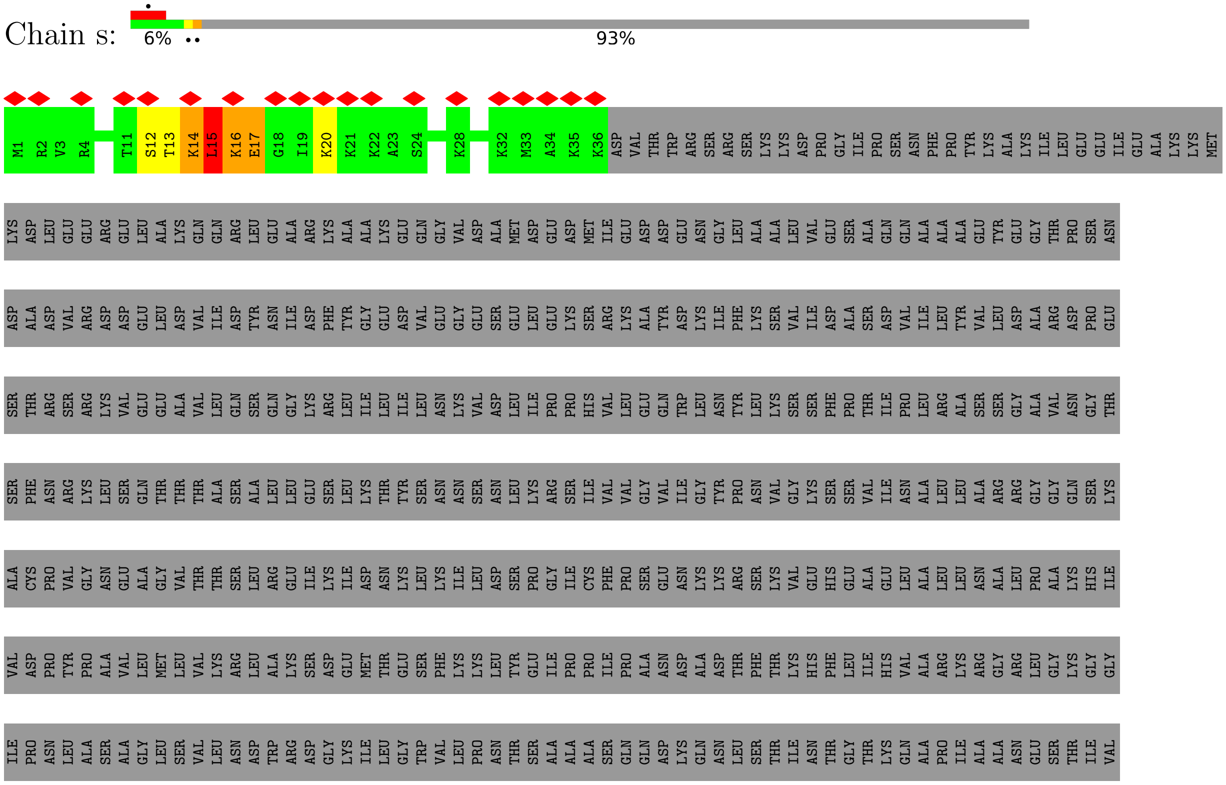
- Molecule 47: Ribosome biogenesis protein RLP7



- Molecule 48: ITS2



- Molecule 49: Nuclear GTP-binding protein NUG1




SER
GLU
TRP
SER
LYS
GLU
PHE
ASP
LEU
ASP
GLY
LEU
PHE
SER
SER
LEU
ASP
LYS
ALA
ILE
ASP
ALA
SER
LYS
ASP
GLN
ASP
THR
MET
MET
GLU

4 Experimental information ⓘ

Property	**Value**	**Source**
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	30364	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	24	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.575	Depositor
Minimum map value	-0.352	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	416.25598, 416.25598, 416.25598	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	A	0.42	0/1417	0.79	5/1907 (0.3%)
2	a	0.52	0/665	0.71	0/900
3	B	0.57	0/2928	0.82	4/3936 (0.1%)
4	b	0.35	0/3720	0.67	1/5021 (0.0%)
5	C	0.75	0/2801	0.81	2/3792 (0.1%)
6	c	0.37	0/751	0.65	0/1008
7	d	0.54	0/887	0.84	3/1191 (0.3%)
8	E	0.52	0/1260	0.72	0/1694
9	e	0.78	0/1041	0.81	2/1394 (0.1%)
10	F	0.69	0/1821	0.77	2/2451 (0.1%)
11	f	0.93	0/868	0.88	1/1168 (0.1%)
12	G	0.62	0/1830	0.73	1/2469 (0.0%)
13	g	0.55	0/891	0.84	0/1191
14	I	0.37	0/789	0.73	1/1058 (0.1%)
15	H	0.41	0/1514	0.73	0/2039
16	h	0.67	0/973	0.79	1/1294 (0.1%)
17	i	0.44	0/749	0.76	0/995
18	j	0.86	0/661	0.97	4/876 (0.5%)
19	k	0.39	0/618	0.69	0/826
20	L	0.64	0/1475	0.89	5/1982 (0.3%)
21	l	0.50	0/443	0.93	2/588 (0.3%)
22	M	0.50	0/1074	0.71	1/1446 (0.1%)
23	p	0.37	0/701	0.77	1/934 (0.1%)
24	N	0.92	0/1639	0.93	6/2190 (0.3%)
25	u	0.42	0/1180	0.76	0/1569
26	O	0.79	0/1585	0.81	4/2128 (0.2%)
27	P	0.74	0/1415	0.81	2/1900 (0.1%)
28	Q	0.67	0/1050	0.84	3/1419 (0.2%)
29	R	0.46	0/1258	0.79	1/1679 (0.1%)
30	r	0.38	0/589	0.78	2/773 (0.3%)
31	S	0.50	0/1460	0.73	0/1962
32	T	0.36	0/440	0.78	0/594

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	U	0.38	0/843	0.61	0/1143
34	V	0.40	0/1018	0.71	0/1369
35	W	0.32	0/1843	0.63	0/2483
36	X	0.71	0/1115	0.80	1/1500 (0.1%)
37	Y	0.67	0/1004	0.79	1/1341 (0.1%)
38	y	0.32	0/1733	0.66	0/2359
39	Z	0.39	0/1118	0.70	2/1497 (0.1%)
40	z	0.35	0/431	0.72	1/567 (0.2%)
41	1	1.73	75/64064 (0.1%)	1.38	559/99858 (0.6%)
42	3	1.35	9/3746 (0.2%)	1.49	50/5832 (0.9%)
43	K	0.36	0/2098	0.66	0/2830
44	n	0.48	0/3101	0.78	5/4187 (0.1%)
45	o	0.40	0/1067	0.73	0/1417
46	q	0.37	0/1197	0.73	2/1601 (0.1%)
47	t	0.39	0/2333	0.78	2/3128 (0.1%)
48	6	0.54	0/1527	1.17	7/2371 (0.3%)
49	s	2.83	10/301 (3.3%)	2.81	17/386 (4.4%)
All	All	1.30	94/129032 (0.1%)	1.17	701/188243 (0.4%)

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
2	a	0	4
3	B	1	1
4	b	0	2
5	C	0	4
7	d	0	1
9	e	0	3
10	F	0	1
12	G	0	4
15	H	0	3
16	h	0	2
17	i	0	3
19	k	0	1
20	L	0	2
22	M	0	1
23	p	0	1
27	P	0	2
28	Q	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
29	R	0	2
30	r	0	2
31	S	0	3
32	T	0	1
34	V	0	1
35	W	0	1
38	y	0	1
41	1	0	1
43	K	0	1
44	n	0	11
45	o	0	4
46	q	0	3
47	t	0	7
49	s	0	8
All	All	1	82

The worst 5 of 94 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	1	1200	A	N3-C4	213.88	2.63	1.34
41	1	1200	A	C2-N3	157.72	2.75	1.33
41	1	1200	A	C6-N1	137.77	2.31	1.35
41	1	1200	A	N1-C2	112.09	2.35	1.34
41	1	1200	A	C5-C4	88.28	2.00	1.38

The worst 5 of 701 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
41	1	1200	A	N1-C2-N3	-71.35	93.62	129.30
41	1	1200	A	C4-C5-N7	-48.99	86.20	110.70
41	1	1200	A	C8-N9-C4	-48.58	86.37	105.80
41	1	1200	A	N7-C8-N9	35.34	131.47	113.80
41	1	1200	A	C5-N7-C8	35.19	121.49	103.90

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	17	LEU	CA

5 of 82 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	35	ASP	Peptide
2	a	77	LYS	Peptide
2	a	82	ILE	Peptide
2	a	83	PRO	Peptide
2	a	84	GLU	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	
1	A	178/254 (70%)	178 (100%)	0	0	100	100
2	a	82/149 (55%)	78 (95%)	3 (4%)	1 (1%)	13	50
3	B	356/387 (92%)	344 (97%)	12 (3%)	0	100	100
4	b	447/647 (69%)	434 (97%)	13 (3%)	0	100	100
5	C	359/362 (99%)	347 (97%)	12 (3%)	0	100	100
6	c	95/105 (90%)	95 (100%)	0	0	100	100
7	d	105/113 (93%)	105 (100%)	0	0	100	100
8	E	152/176 (86%)	150 (99%)	2 (1%)	0	100	100
9	e	125/130 (96%)	124 (99%)	1 (1%)	0	100	100
10	F	220/244 (90%)	210 (96%)	10 (4%)	0	100	100
11	f	104/107 (97%)	104 (100%)	0	0	100	100
12	G	228/256 (89%)	228 (100%)	0	0	100	100
13	g	110/121 (91%)	110 (100%)	0	0	100	100
14	I	94/166 (57%)	92 (98%)	2 (2%)	0	100	100
15	H	186/191 (97%)	182 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	h	116/120 (97%)	116 (100%)	0	0	100	100
17	i	94/100 (94%)	90 (96%)	4 (4%)	0	100	100
18	j	79/88 (90%)	78 (99%)	1 (1%)	0	100	100
19	k	75/78 (96%)	75 (100%)	0	0	100	100
20	L	180/199 (90%)	172 (96%)	7 (4%)	1 (1%)	25	62
21	l	48/51 (94%)	48 (100%)	0	0	100	100
22	M	135/138 (98%)	134 (99%)	1 (1%)	0	100	100
23	p	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
24	N	183/204 (90%)	179 (98%)	4 (2%)	0	100	100
25	u	135/199 (68%)	133 (98%)	2 (2%)	0	100	100
26	O	195/199 (98%)	195 (100%)	0	0	100	100
27	P	172/184 (94%)	171 (99%)	1 (1%)	0	100	100
28	Q	132/186 (71%)	132 (100%)	0	0	100	100
29	R	152/189 (80%)	149 (98%)	3 (2%)	0	100	100
30	r	65/261 (25%)	57 (88%)	8 (12%)	0	100	100
31	S	168/172 (98%)	163 (97%)	5 (3%)	0	100	100
32	T	54/160 (34%)	50 (93%)	4 (7%)	0	100	100
33	U	102/121 (84%)	101 (99%)	1 (1%)	0	100	100
34	V	134/137 (98%)	133 (99%)	1 (1%)	0	100	100
35	W	223/236 (94%)	221 (99%)	2 (1%)	0	100	100
36	X	137/142 (96%)	136 (99%)	1 (1%)	0	100	100
37	Y	124/127 (98%)	124 (100%)	0	0	100	100
38	y	225/245 (92%)	223 (99%)	2 (1%)	0	100	100
39	Z	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
40	z	51/106 (48%)	51 (100%)	0	0	100	100
43	K	252/376 (67%)	245 (97%)	7 (3%)	0	100	100
44	n	365/605 (60%)	342 (94%)	23 (6%)	0	100	100
45	o	121/220 (55%)	117 (97%)	4 (3%)	0	100	100
46	q	137/455 (30%)	128 (93%)	9 (7%)	0	100	100
47	t	283/322 (88%)	264 (93%)	19 (7%)	0	100	100
49	s	34/520 (6%)	30 (88%)	4 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	7234/9776 (74%)	7056 (98%)	176 (2%)	2 (0%)	100 100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	a	78	LEU
20	L	63	VAL

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
1	A	142/196 (72%)	142 (100%)	0	100 100
2	a	68/119 (57%)	68 (100%)	0	100 100
3	B	301/323 (93%)	298 (99%)	3 (1%)	76 86
4	b	404/573 (70%)	401 (99%)	3 (1%)	84 91
5	C	288/289 (100%)	285 (99%)	3 (1%)	76 86
6	c	81/88 (92%)	81 (100%)	0	100 100
7	d	94/97 (97%)	94 (100%)	0	100 100
8	E	134/153 (88%)	134 (100%)	0	100 100
9	e	109/111 (98%)	109 (100%)	0	100 100
10	F	186/205 (91%)	185 (100%)	1 (0%)	88 94
11	f	90/91 (99%)	90 (100%)	0	100 100
12	G	189/208 (91%)	188 (100%)	1 (0%)	88 94
13	g	95/103 (92%)	94 (99%)	1 (1%)	73 85
14	I	83/141 (59%)	82 (99%)	1 (1%)	71 84
15	H	168/171 (98%)	164 (98%)	4 (2%)	49 71
16	h	104/105 (99%)	103 (99%)	1 (1%)	76 86
17	i	78/82 (95%)	78 (100%)	0	100 100
18	j	67/71 (94%)	66 (98%)	1 (2%)	65 81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	k	68/69 (99%)	68 (100%)	0	100	100
20	L	142/159 (89%)	139 (98%)	3 (2%)	53	74
21	l	45/46 (98%)	45 (100%)	0	100	100
22	M	108/109 (99%)	108 (100%)	0	100	100
23	p	71/72 (99%)	70 (99%)	1 (1%)	67	81
24	N	163/176 (93%)	162 (99%)	1 (1%)	86	92
25	u	122/180 (68%)	120 (98%)	2 (2%)	62	79
26	O	160/162 (99%)	160 (100%)	0	100	100
27	P	141/146 (97%)	140 (99%)	1 (1%)	84	91
28	Q	110/151 (73%)	110 (100%)	0	100	100
29	R	127/154 (82%)	125 (98%)	2 (2%)	62	79
30	r	59/229 (26%)	59 (100%)	0	100	100
31	S	154/156 (99%)	154 (100%)	0	100	100
32	T	45/137 (33%)	43 (96%)	2 (4%)	28	57
33	U	91/107 (85%)	91 (100%)	0	100	100
34	V	104/105 (99%)	104 (100%)	0	100	100
35	W	201/213 (94%)	200 (100%)	1 (0%)	88	94
36	X	117/118 (99%)	117 (100%)	0	100	100
37	Y	109/110 (99%)	109 (100%)	0	100	100
38	y	193/211 (92%)	193 (100%)	0	100	100
39	Z	115/116 (99%)	115 (100%)	0	100	100
40	z	47/95 (50%)	47 (100%)	0	100	100
43	K	236/346 (68%)	231 (98%)	5 (2%)	53	74
44	n	334/548 (61%)	331 (99%)	3 (1%)	78	88
45	o	111/199 (56%)	110 (99%)	1 (1%)	78	88
46	q	131/420 (31%)	130 (99%)	1 (1%)	81	89
47	t	256/287 (89%)	253 (99%)	3 (1%)	71	84
49	s	32/445 (7%)	31 (97%)	1 (3%)	40	65
All	All	6273/8392 (75%)	6227 (99%)	46 (1%)	84	91

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	R	71	ARG
43	K	388	ARG
32	T	102	ARG
43	K	172	LYS
44	n	13	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
45	o	154	ASN
45	o	163	GLN
47	t	265	ASN
15	H	163	GLN
15	H	156	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
41	1	2663/3396 (78%)	694 (26%)	43 (1%)
42	3	157/158 (99%)	36 (22%)	3 (1%)
48	6	63/232 (27%)	38 (60%)	0
All	All	2883/3786 (76%)	768 (26%)	46 (1%)

5 of 768 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
41	1	11	A
41	1	14	U
41	1	15	C
41	1	18	G
41	1	26	A

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
41	1	2541	U
41	1	3078	U
41	1	2593	A
41	1	2886	U
41	1	3218	A

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 ⓘ

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	X	1
41	1	1
49	s	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	X	23:ALA	C	24:LEU	N	5.12
1	1	1199:C	O3’	1200:A	P	1.89
1	s	13:THR	C	14:LYS	N	1.75

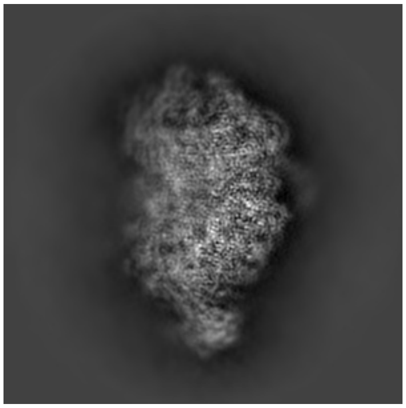
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-10842. These allow visual inspection of the internal detail of the map and identification of artifacts.

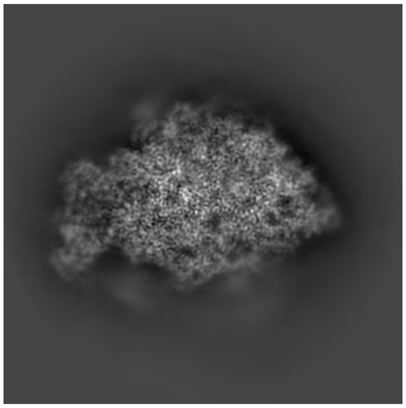
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

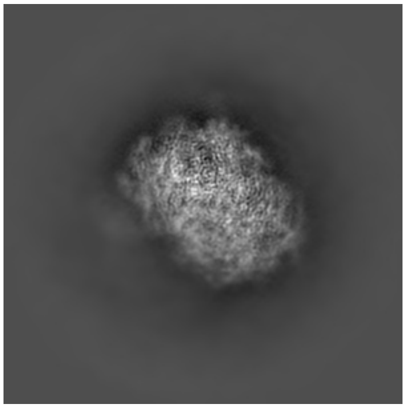
6.1.1 Primary map



X

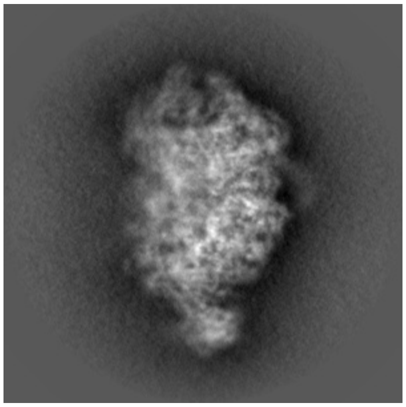


Y

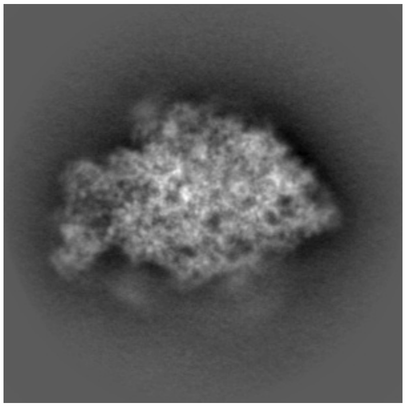


Z

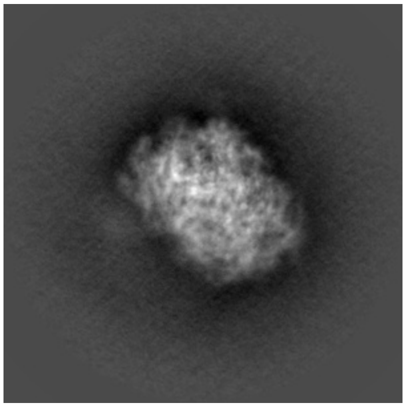
6.1.2 Raw map



X



Y

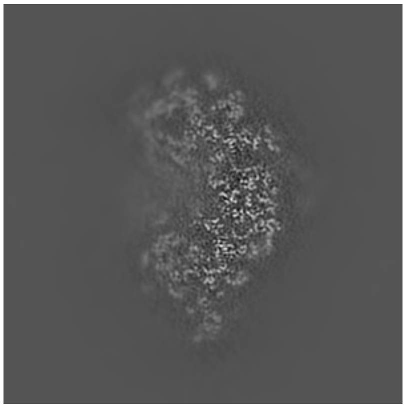


Z

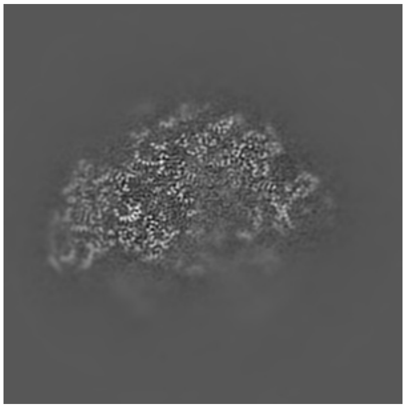
The images above show the map projected in three orthogonal directions.

6.2 Central slices

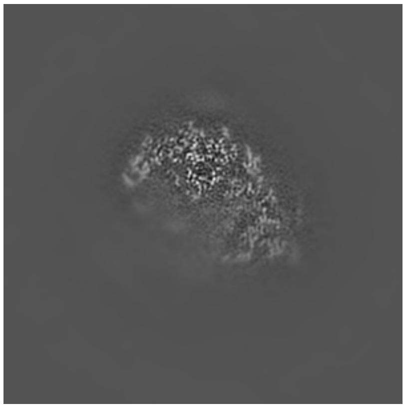
6.2.1 Primary map



X Index: 192

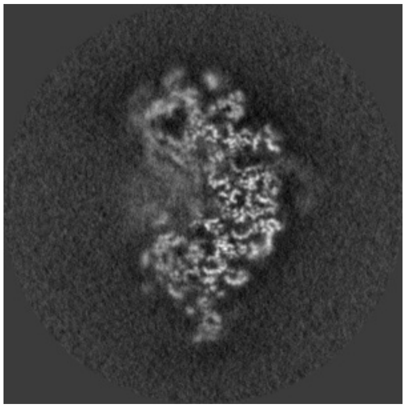


Y Index: 192

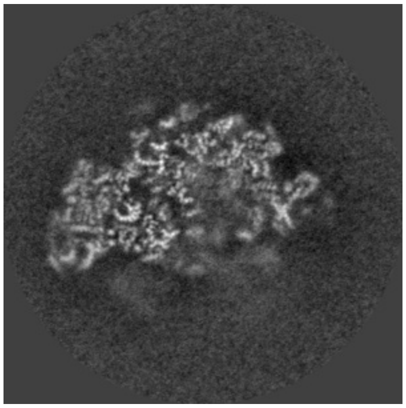


Z Index: 192

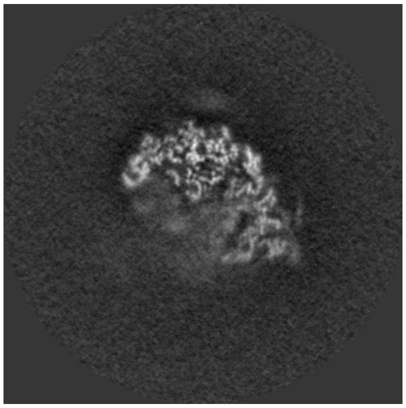
6.2.2 Raw map



X Index: 192



Y Index: 192

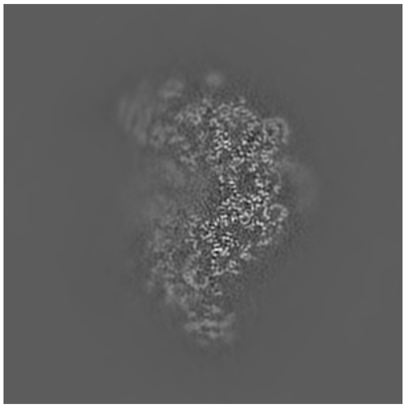


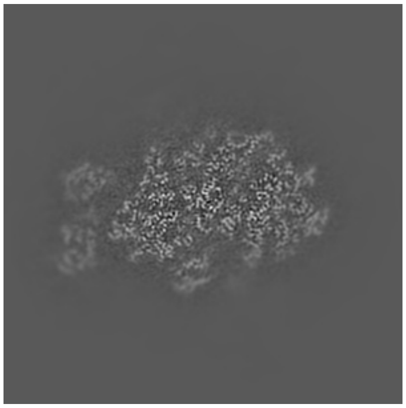
Z Index: 192

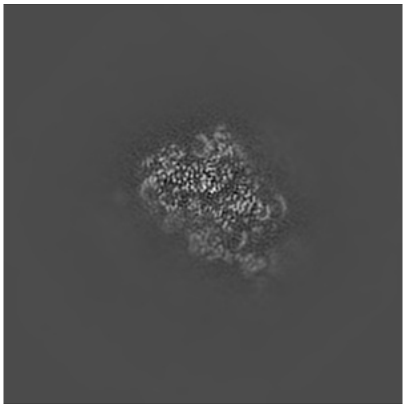
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices ⓘ

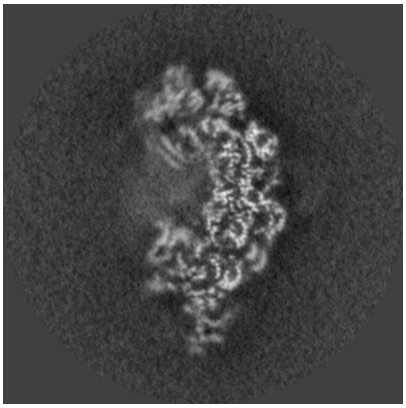
6.3.1 Primary map

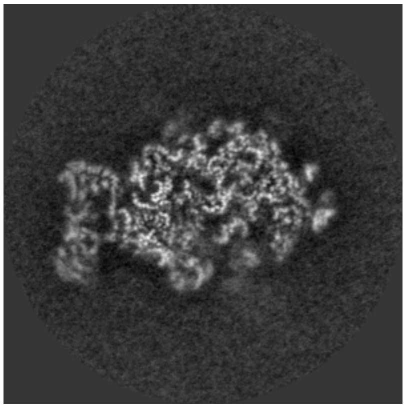

X Index: 201

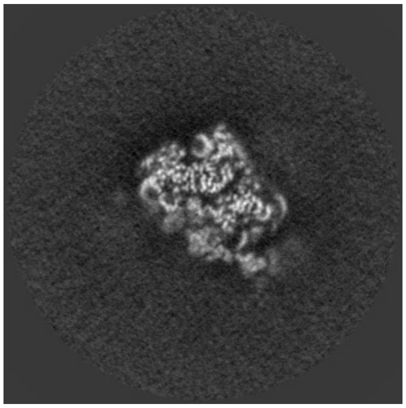

Y Index: 216


Z Index: 152

6.3.2 Raw map


X Index: 185


Y Index: 209


Z Index: 152

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 0.04. 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.

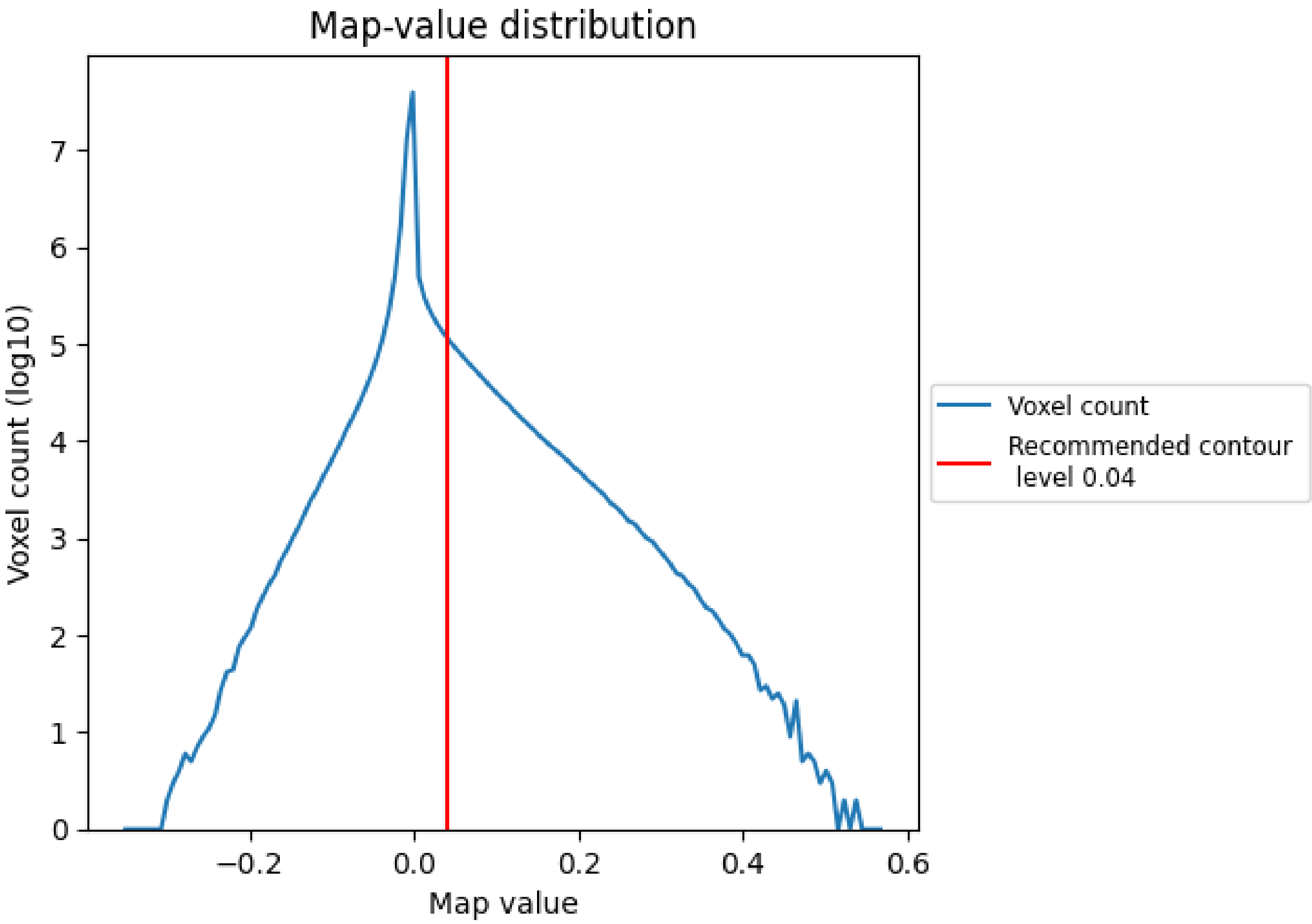
6.5 Mask visualisation ⓘ

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

7 Map analysis ⓘ

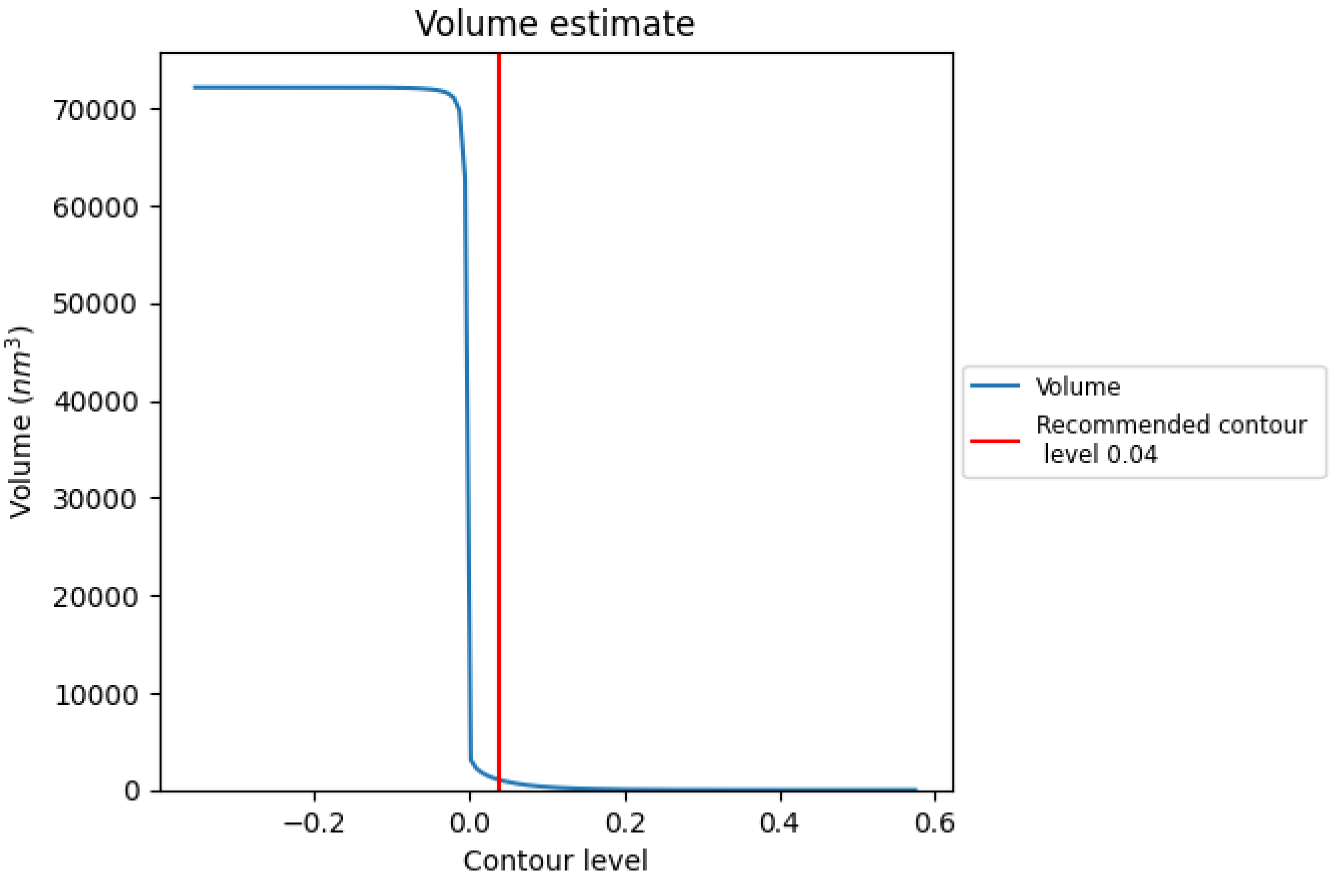
This section contains the results of statistical analysis of the map.

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.

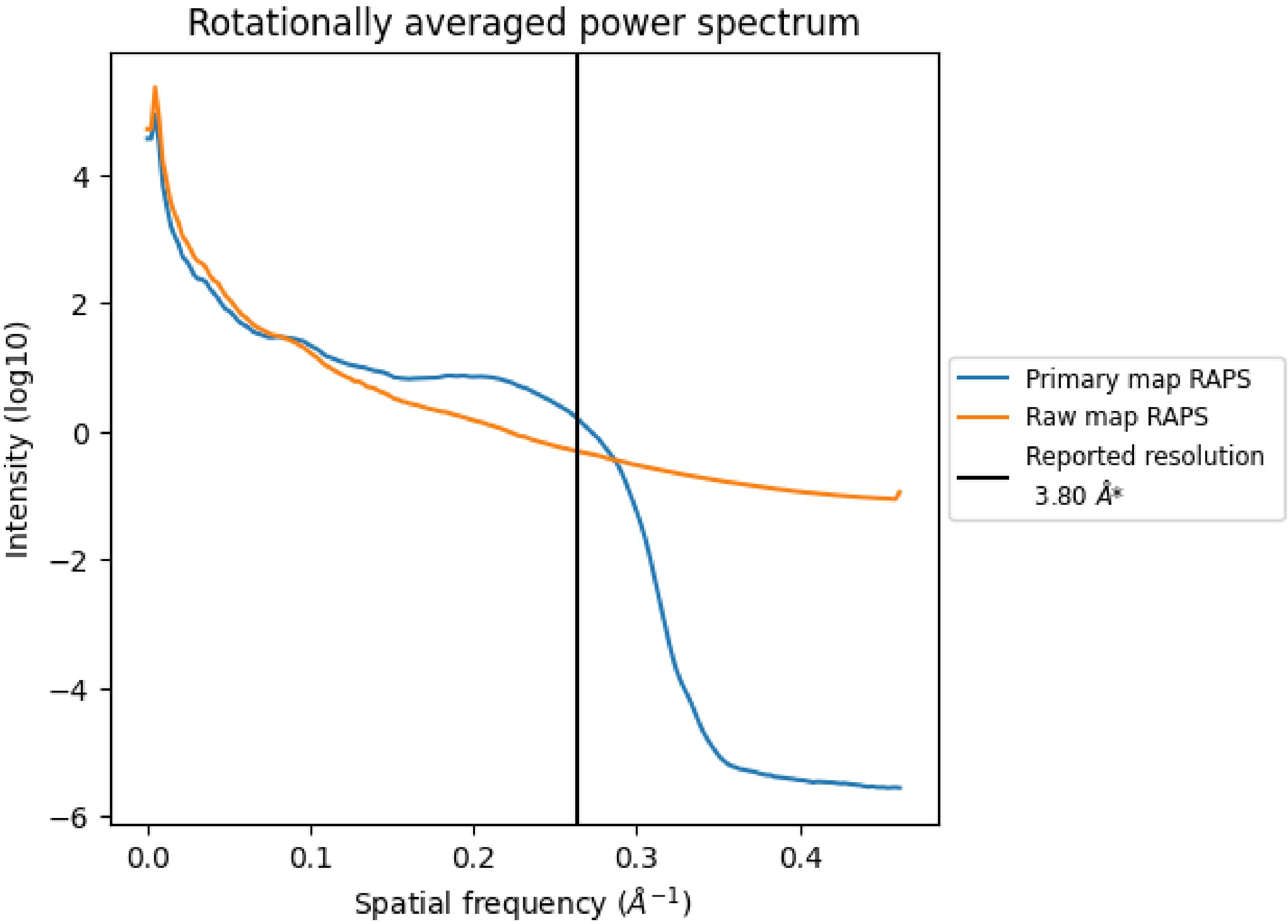
7.2 Volume estimate (i)



The volume at the recommended contour level is 1033 nm^3; this corresponds to an approximate mass of 934 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 ⓘ

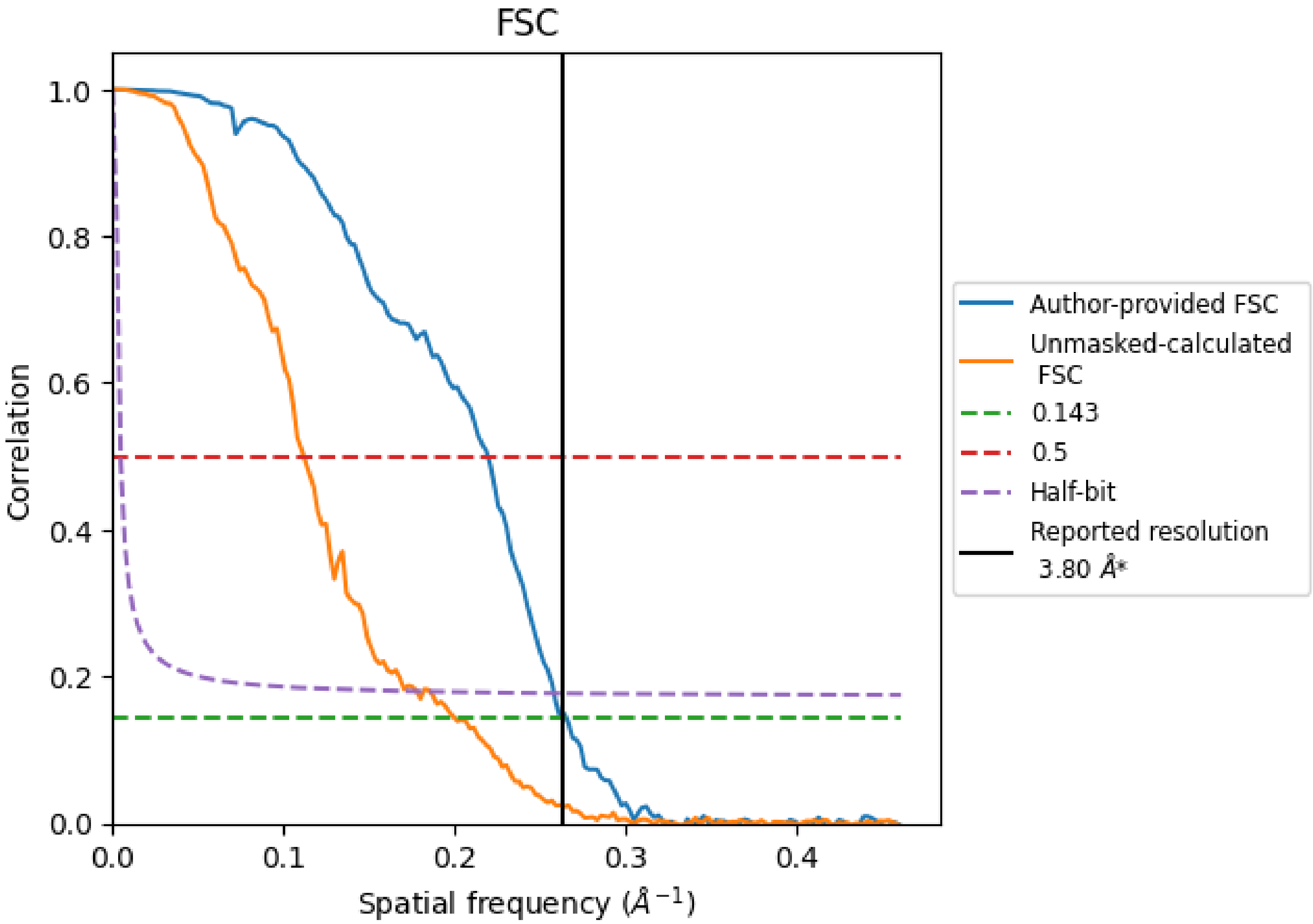


*Reported resolution corresponds to spatial frequency of 0.263 Å^{-1}

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 0.263 $Å^{-1}$

8.2 Resolution estimates ⓘ

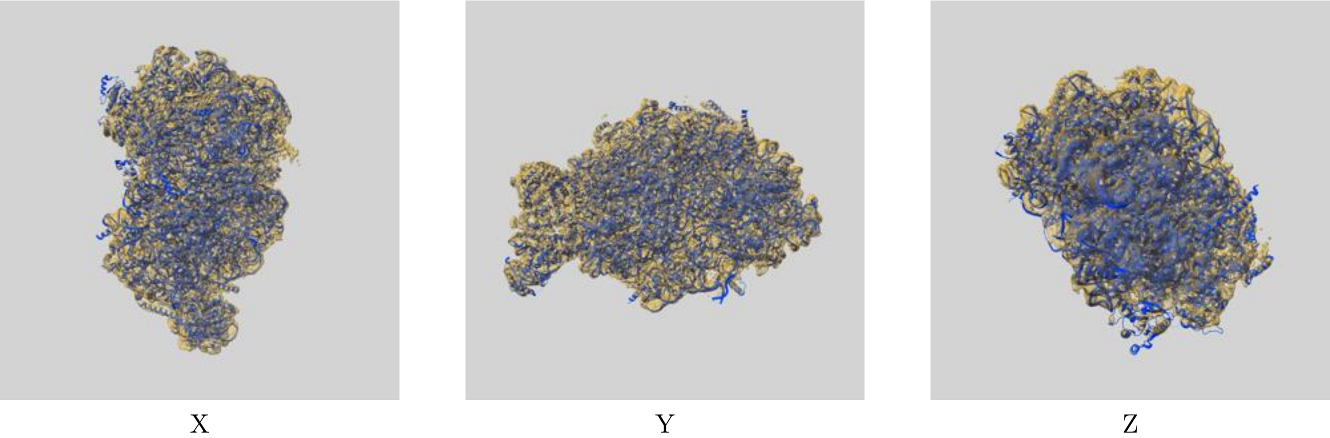
Resolution estimate (Å)	**Estimation criterion (FSC cut-off)**		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.77	4.55	3.87
Unmasked-calculated*	5.00	8.94	5.62

*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 5.00 differs from the reported value 3.8 by more than 10 %

9 Map-model fit ⓘ

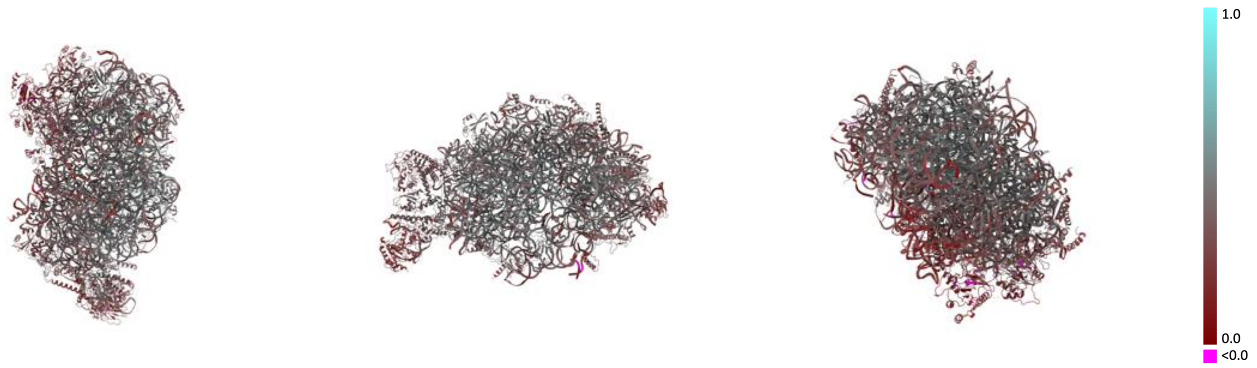
This section contains information regarding the fit between EMDB map EMD-10842 and PDB model 6YLY. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay ⓘ



The images above show the 3D surface view of the map at the recommended contour level 0.04 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.

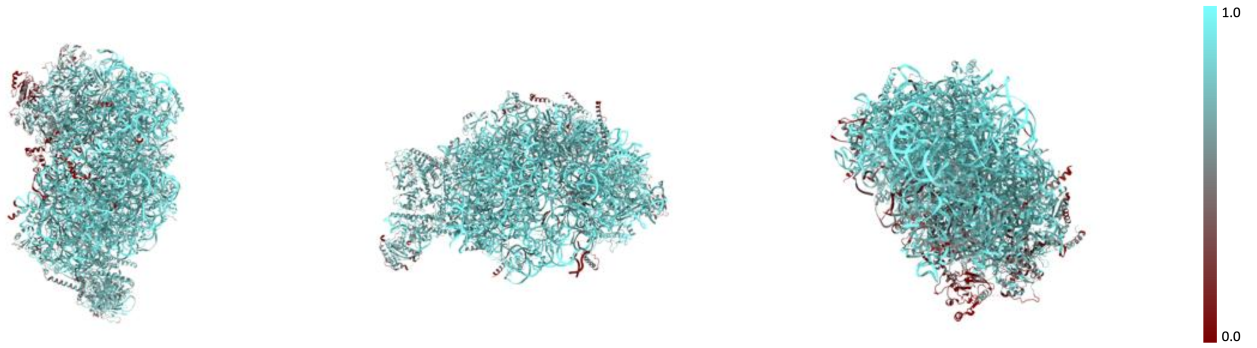
9.2 Q-score mapped to coordinate model



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.

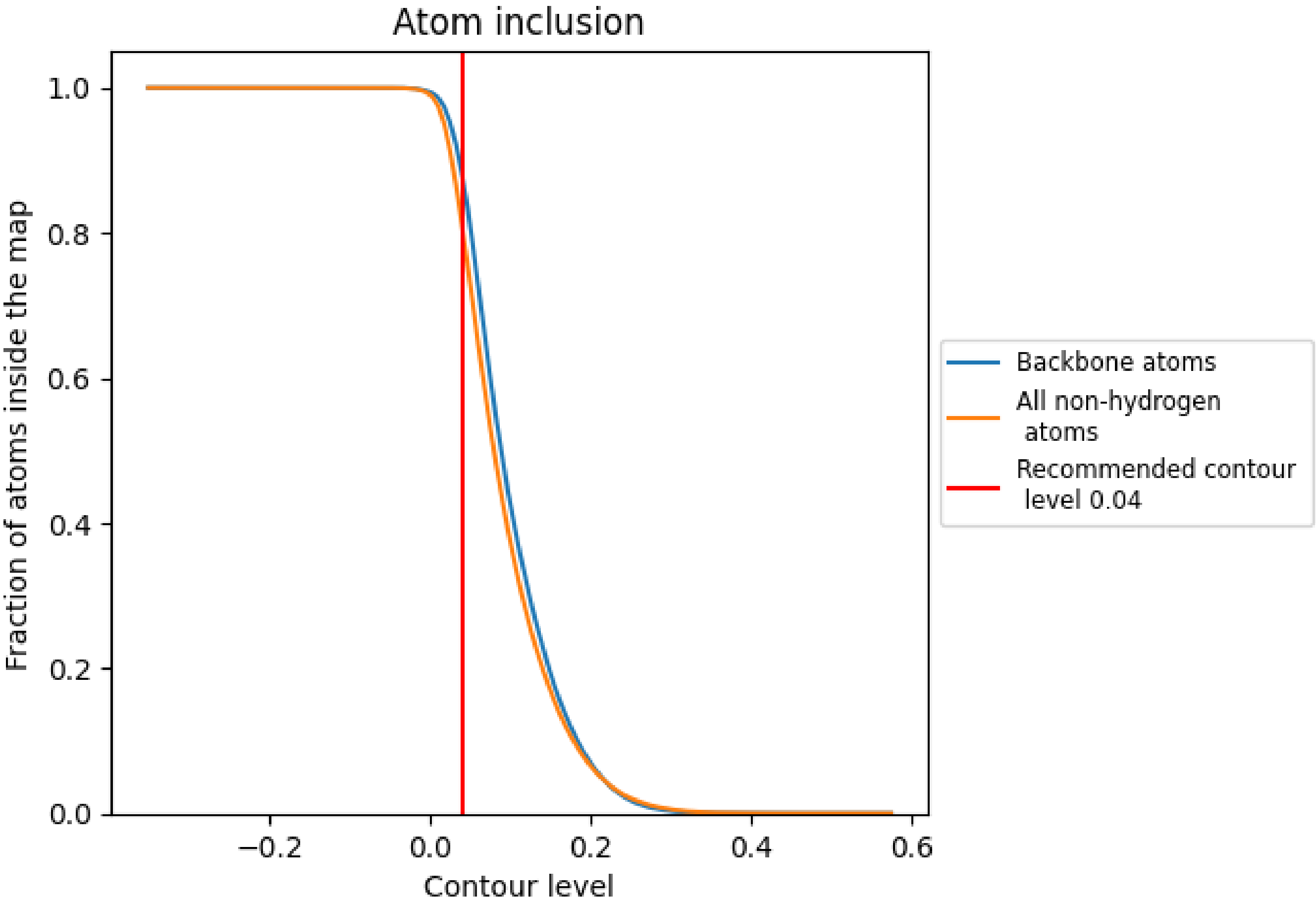
9.3 Atom inclusion mapped to coordinate model



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 (0.04).

9.4 Atom inclusion ⓘ



At the recommended contour level, 88% of all backbone atoms, 81% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8062	0.3920
1	0.8709	0.3950
3	0.9427	0.4660
6	0.8745	0.3270
A	0.7186	0.3890
B	0.8169	0.4290
C	0.8523	0.4680
E	0.8302	0.4200
F	0.8542	0.4290
G	0.7945	0.4100
H	0.7672	0.3790
I	0.1275	0.3230
K	0.6075	0.2480
L	0.8093	0.4350
M	0.8411	0.4230
N	0.8551	0.4960
O	0.8686	0.4670
P	0.8426	0.4560
Q	0.8560	0.4510
R	0.7582	0.3970
S	0.8308	0.4330
T	0.5629	0.3010
U	0.7217	0.3520
V	0.7140	0.4080
W	0.5474	0.2400
X	0.8571	0.4680
Y	0.8685	0.4720
Z	0.7740	0.3700
a	0.8406	0.4200
b	0.3954	0.2420
c	0.6566	0.3000
d	0.7993	0.4370
e	0.8451	0.5010
f	0.8879	0.5020
g	0.7688	0.4370

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Chain	Atom inclusion	Q-score
h	0.8689	0.4650
i	0.7955	0.3940
j	0.8551	0.5000
k	0.7295	0.3980
l	0.7181	0.4520
n	0.7579	0.3690
o	0.7002	0.3010
p	0.6045	0.3380
q	0.5957	0.3320
r	0.6810	0.3290
s	0.4118	0.2620
t	0.7131	0.3390
u	0.6439	0.3560
y	0.6684	0.2980
z	0.4810	0.3480