wwPDB EM Validation Summary Report (i)

Mar 5, 2026 – 09:57 PM UTC

PDB ID	:	8I0S / pdb_00008i0s
EMDB ID	:	EMD-35108
Title	:	The cryo-EM structure of human Bact-II complex
Authors	:	Zhan, X.; Lu, Y.; Shi, Y.
Deposited on	:	2023-01-11
Resolution	:	4.20 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

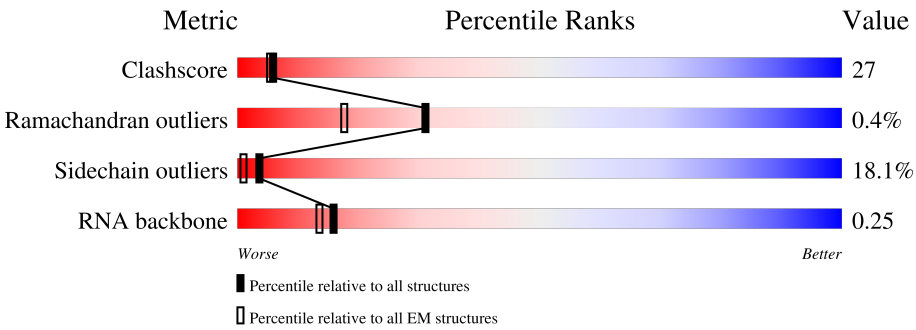
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

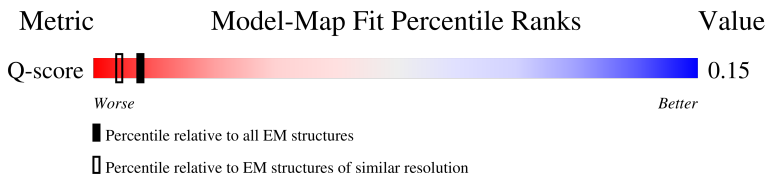
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5410 (3.70 - 4.70)

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	2335	16% 53% 34% 8% • •
2	B	117	6% 24% 42% 18% 16%
3	C	972	35% 44% 10% 12%

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Mol	Chain	Length	Quality of chain
4	D	2136	72% 74% 6% 19%
5	E	357	36% 29% 46% 9% 16%
6	F	107	7% 20% 36% 36% 9%
7	G	220	• • 13% 15% 67%
8	H	188	20% 17% 51% 20% • 11%
9	I	855	19% 62% • 33%
10	J	848	• 13% 14% • 71%
11	K	343	• 6% 6% • 87%
12	L	802	• 10% 10% • 79%
13	N	144	12% 47% 42% 9% ••
14	O	420	13% 59% 9% 32%
15	P	229	• 20% 21% • 56%
16	Q	1485	59% 82% 7% 11%
17	R	536	9% 35% 27% 5% 33%
18	S	166	27% 83% 13% 5%
19	T	514	31% 24% 7% 38%
20	U	2752	• 97%
21	V	908	17% 36% 13% • 49%
22	X	1041	• 29% 40% 7% 24%
23	Y	492	• 22% 35% 8% 35%
24	1	1304	• 26% 30% 7% 37%
25	3	1217	9% 35% 50% 11% •
26	p	225	28% 66% 8% 26%
27	w	501	48% 71% 14% • 13%
28	2	895	• 16% 10% • 72%

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Mol	Chain	Length	Quality of chain
29	4	424	6% 34% 62%
30	7	110	24% 40% 10% 26%
31	5	86	7% 35% 38% 16% 10%
32	y	301	9% 23% 74%
33	v	464	14% 23% 10% 66%
34	u	793	12% 23% 76%
35	9	520	11% 38% 23% 35%
36	a	240	9% 35% 64%
36	m	240	12% 29% 5% 66%
37	b	119	8% 67% 31%
37	n	119	23% 55% 12% 33%
38	c	118	18% 77% 5% 18%
38	h	118	27% 64% 17% 19%
39	d	86	12% 81% 5% 14%
39	i	86	28% 57% 27% 16%
40	e	92	9% 82% 14%
40	j	92	33% 74% 14% 12%
41	f	76	26% 95%
41	k	76	45% 76% 20%
42	g	126	63% 36%
42	l	126	26% 48% 18% 34%
43	o	255	40% 56% 7% 36%

2 Entry composition (i)

There are 47 unique types of molecules in this entry. The entry contains 112874 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 Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	2230	17607	11288	3122	3129	68	0	0

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	98	2066	925	347	696	98	0	0

- Molecule 3 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	860	6724	4298	1122	1272	32	0	0

- Molecule 4 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	D	1722	8528	5084	1722	1722	0	0

- Molecule 5 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	299	2338	1470	410	445	13	0	0

- Molecule 6 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	F	97	2075	928	381	669	97	0	0

- Molecule 7 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	G	72	1503	673	248	510	72	0	0

- Molecule 8 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	H	167	3539	1581	607	1184	167	0	0

- Molecule 9 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	I	571	2880	1738	571	571	0	0

- Molecule 10 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	249	2116	1355	380	375	6	0	0

- Molecule 11 is a protein called RING finger protein 113A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	46	392	246	67	76	3	0	0

- Molecule 12 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	169	1403	890	262	247	4	0	0

- Molecule 13 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	N	143	1174	740	213	209	12	0	0

- Molecule 14 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	O	287	1432	853	289	290	0	0

- Molecule 15 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	P	101	876	537	175	162	2	0	0

- Molecule 16 is a protein called RNA helicase aquarius.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	Q	1329	6730	4072	1329	1329	0	0

- Molecule 17 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	N	O	P	S		
17	R	361	2760	1694	524	529	1	12	0	0

- Molecule 18 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	S	158	770	454	158	158	0	0

- Molecule 19 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	T	320	2507	1582	456	462	7	0	0

- Molecule 20 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	U	72	422	257	82	82	1	0	0

- Molecule 21 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	V	462	2959	1842	537	567	13	0	0

- Molecule 22 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	X	786	6357	4010	1133	1184	30	0	0

- Molecule 23 is a protein called Peptidyl-prolyl cis-trans isomerase-like 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	Y	320	2556	1616	420	508	12	0	0

- Molecule 24 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	1	816	6468	4154	1110	1165	39	0	0

- Molecule 25 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	3	1177	9210	5849	1563	1753	45	0	0

- Molecule 26 is a protein called U2 small nuclear ribonucleoprotein B".

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
26	p	167	841	507	167	167	0	0

- Molecule 27 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	w	434	2275	1287	491	493	4	0	0

- Molecule 28 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	2	250	1803	1132	340	324	7	0	0

- Molecule 29 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
29	4	161	792	470	161	161	0	0

- Molecule 30 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	7	81	613	376	109	115	13	0	0

- Molecule 31 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	5	77	635	403	110	117	5	0	0

- Molecule 32 is a protein called Peptidyl-prolyl cis-trans isomerase E.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
32	y	79	390	232	79	79	0	0

- Molecule 33 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	v	158	964	558	203	200	3	0	0

- Molecule 34 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
34	u	187	834	460	187	187	0	0

- Molecule 35 is a protein called RING-type E3 ubiquitin-protein ligase PPIL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	9	338	2307	1429	420	450	8	0	0

- Molecule 36 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
36	a	86	344	172	86	86	0	0
36	m	82	413	249	82	82	0	0

- Molecule 37 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
37	b	82	328	164	82	82	0	0
37	n	80	402	242	80	80	0	0

- Molecule 38 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
38	c	97	388	194	97	97	0	0
38	h	95	482	292	95	95	0	0

- Molecule 39 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
39	d	74	296	148	74	74	0	0
39	i	72	359	215	72	72	0	0

- Molecule 40 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
40	e	79	316	158	79	79	0	0
40	j	81	403	241	81	81	0	0

- Molecule 41 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
41	f	74	296	148	74	74	0	0
41	k	73	364	218	73	73	0	0

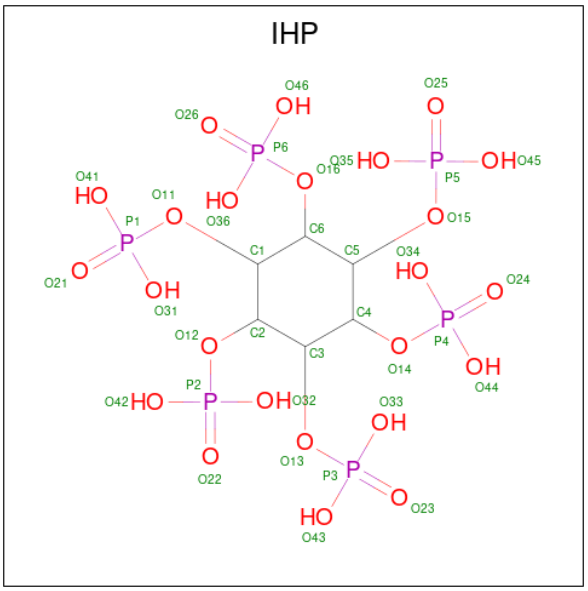
- Molecule 42 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
42	g	81	324	162	81	81	0	0
42	l	83	415	249	83	83	0	0

- Molecule 43 is a protein called U2 small nuclear ribonucleoprotein A'.

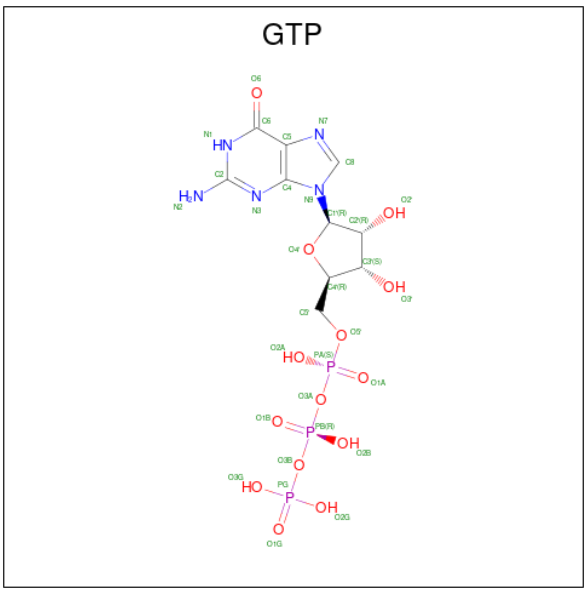
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
43	o	162	816	492	162	162	0	0

- Molecule 44 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
44	A	1	36	6	24	6	0

- Molecule 45 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
45	C	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 46 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
46	C	1	Total	Mg	0
			1	1	
46	F	6	Total	Mg	0
			6	6	

- Molecule 47 is ZINC ION (CCD ID: ZN) (formula: Zn).

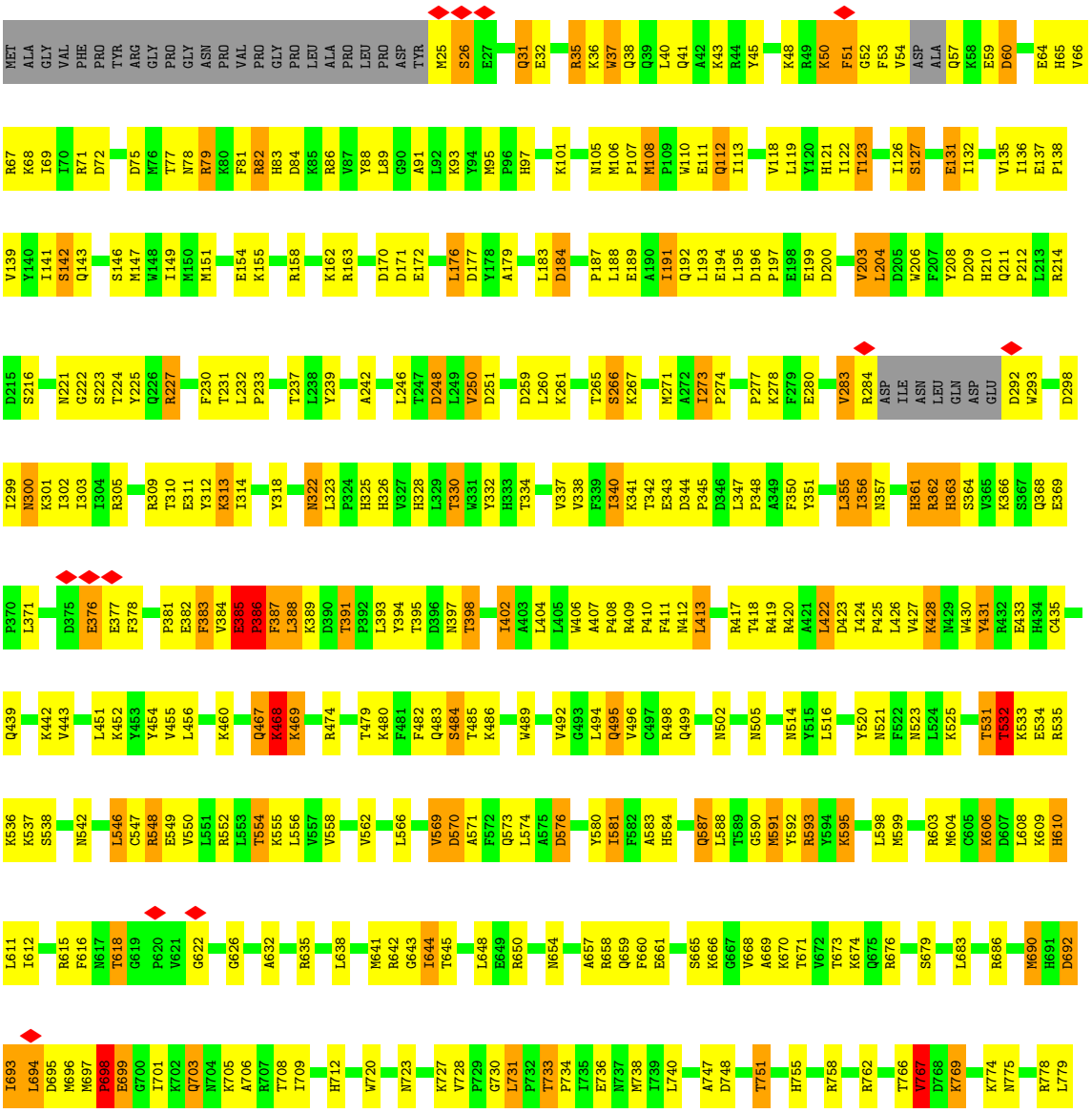
Mol	Chain	Residues	Atoms		AltConf
47	K	1	Total	Zn	0
			1	1	
47	N	3	Total	Zn	0
			3	3	
47	7	3	Total	Zn	0
			3	3	

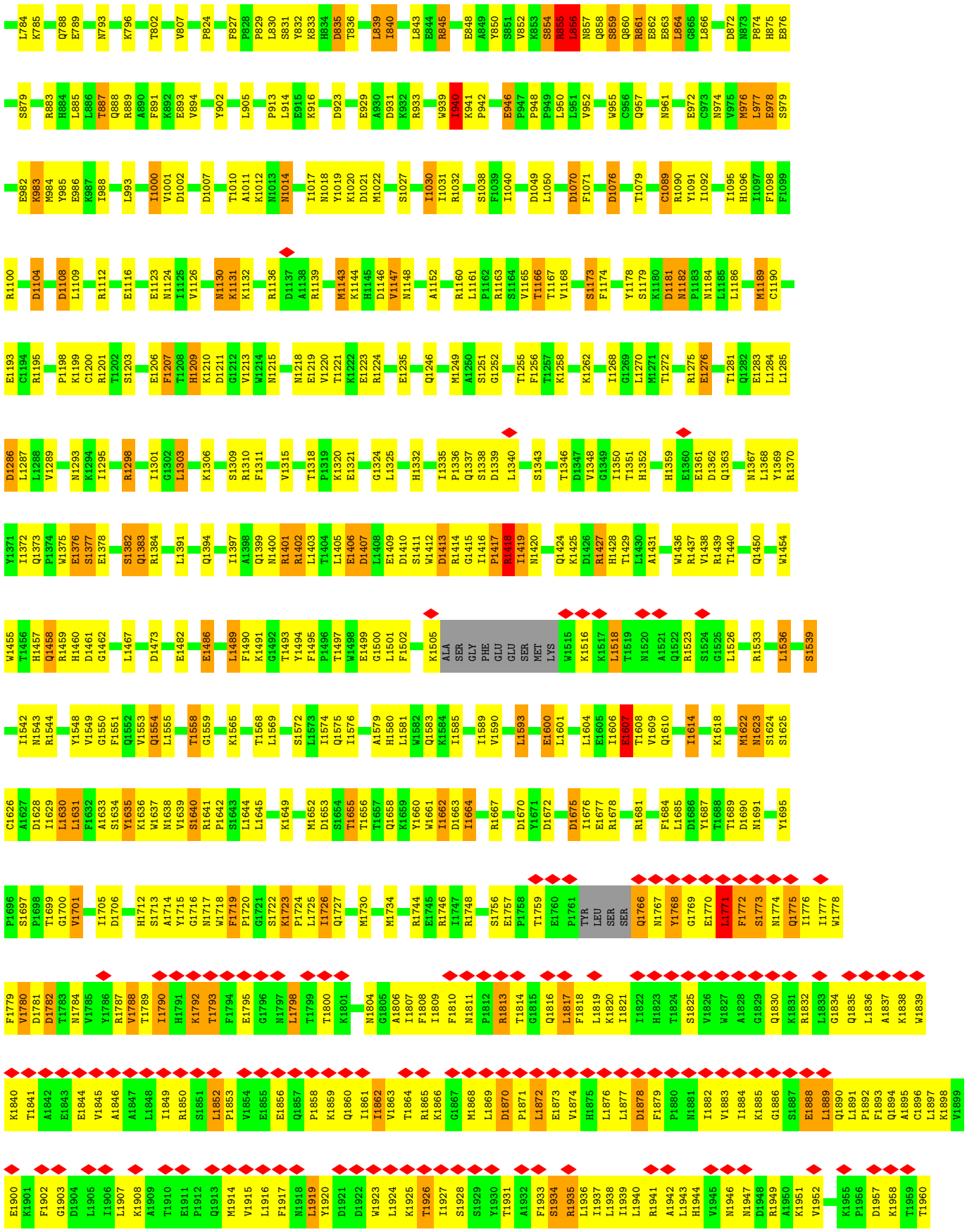
3 Residue-property plots (i)

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: Pre-mRNA-processing-splicing factor 8

Chain A:




L784 K785 Q788 E789 N793 K796 T802 V807 P824 F827 P828 P829 L830 S831 V832 K833 H834 D835 T836 L839 I840 L843 E844 R845 E848 A849 Y850 S851 V852 K853 S854 R855 L856 N857 Q858 S859 Q860 R861 E862 E863 L864 G865 L866 D872 N873 P874 H875 E876
S879 R883 H884 L885 L886 T887 Q888 R889 A890 F891 K892 E893 V894 Y902 L905 P913 L914 E915 K916 D923 E929 A930 D931 K932 R933 W939 I940 K941 P942 E946 P947 P948 P949 L950 L951 V952 W955 C956 Q957 N961 E972 C973 N974 V975 M976 L977 E978 S979
E982 K983 M984 Y985 E986 K987 I988 L993 I1000 V1001 D1002 D1007 T1010 A1011 K1012 N1013 N1014 I1017 N1018 Y1019 K1020 D1021 M1022 S1027 I1030 I1031 R1032 S1038 F1039 I1040 D1049 L1050 D1070 F1071 D1076 T1079 C1089 R1090 Y1091 I1092 I1095 H1096 I1097 F1098 F1099
R1100 D1104 D1108 L1109 R1112 E1116 E1123 N1124 I1125 V1126 N1130 K1131 K1132 R1136 D1137 A1138 R1139 M1143 K1144 H1145 D1146 V1147 N1148 A1152 R1160 L1161 P1162 R1163 S1164 V1165 T1166 T1167 V1168 S1173 F1174 Y1178 S1179 K1180 D1181 N1182 P1183 N1184 L1185 L1186 M1189 C1190
E1193 C1194 R1195 P1198 K1199 C1200 R1201 T1202 S1203 E1206 F1207 T1208 H1209 K1210 D1211 G1212 V1213 W1214 N1215 N1218 E1219 V1220 T1221 K1222 E1223 R1224 E1235 Q1246 M1249 A1250 S1251 G1252 T1255 F1256 T1257 K1258 K1262 I1268 G1269 L1270 M1271 T1272 R1275 E1276 T1281 Q1282 E1283 L1284 L1285
D1286 L1287 L1288 V1289 N1293 K1294 I1295 R1298 I1301 G1302 L1303 K1306 S1309 R1310 F1311 V1315 T1318 P1319 K1320 E1321 G1324 L1325 H1332 I1335 P1336 Q1337 S1338 D1339 L1340 S1343 T1346 D1347 V1348 G1349 I1350 T1351 H1352 H1359 E1360 E1361 D1362 Q1363 N1367 L1368 Y1369 R1370
Y1371 I1372 Q1373 P1374 W1375 E1376 S1377 E1378 S1382 Q1383 R1384 L1391 Q1394 I1397 A1398 Q1399 N1400 R1401 R1402 L1403 T1404 L1405 E1406 D1407 L1408 E1409 D1410 S1411 W1412 D1413 R1414 G1415 I1416 P1417 R1418 I1419 N1420 Q1424 K1425 D1426 R1427 H1428 T1429 L1430 A1431 W1436 R1437 V1438 R1439 T1440 Q1450 W1454
W1455 T1456 H1457 Q1458 R1459 H1460 D1461 G1462 L1467 D1473 E1482 E1486 L1489 F1490 K1491 G1492 T1493 Y1494 F1495 P1496 T1497 W1498 E1499 G1500 L1501 F1502 K1505 ALA SER GLY PHE GLU GLU SER MET LYS W1515 K1516 K1517 L1518 T1519 N1520 A1521 Q1522 R1523 S1524 G1525 L1526 R1533 L1536 S1539
I1542 N1543 R1544 Y1548 V1549 G1550 F1551 Q1552 V1553 Q1554 L1555 T1558 G1559 K1565 T1568 L1569 S1572 L1573 I1574 Q1575 I1576 A1579 H1580 L1581 W1582 Q1583 K1584 I1585 I1589 V1590 L1593 E1600 L1601 L1604 E1605 I1606 E1607 T1608 V1609 Q1610 I1614 K1618 M1622 N1623 S1624 S1625
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P1696 S1697 P1698 T1699 G1700 V1701 I1705 D1706 H1712 S1713 A1714 Y1715 G1716 N1717 W1718 F1719 P1720 G1721 S1722 K1723 P1724 L1725 I1726 Q1727 M1730 M1734 R1744 E1745 R1746 I1747 R1748 S1756 E1757 P1758 T1759 E1760 P1761 TYR LEU SER SER Q1766 N1767 Y1768 G1769 E1770 L1771 F1772 S1773 N1774 Q1775 I1776 I1777 W1778
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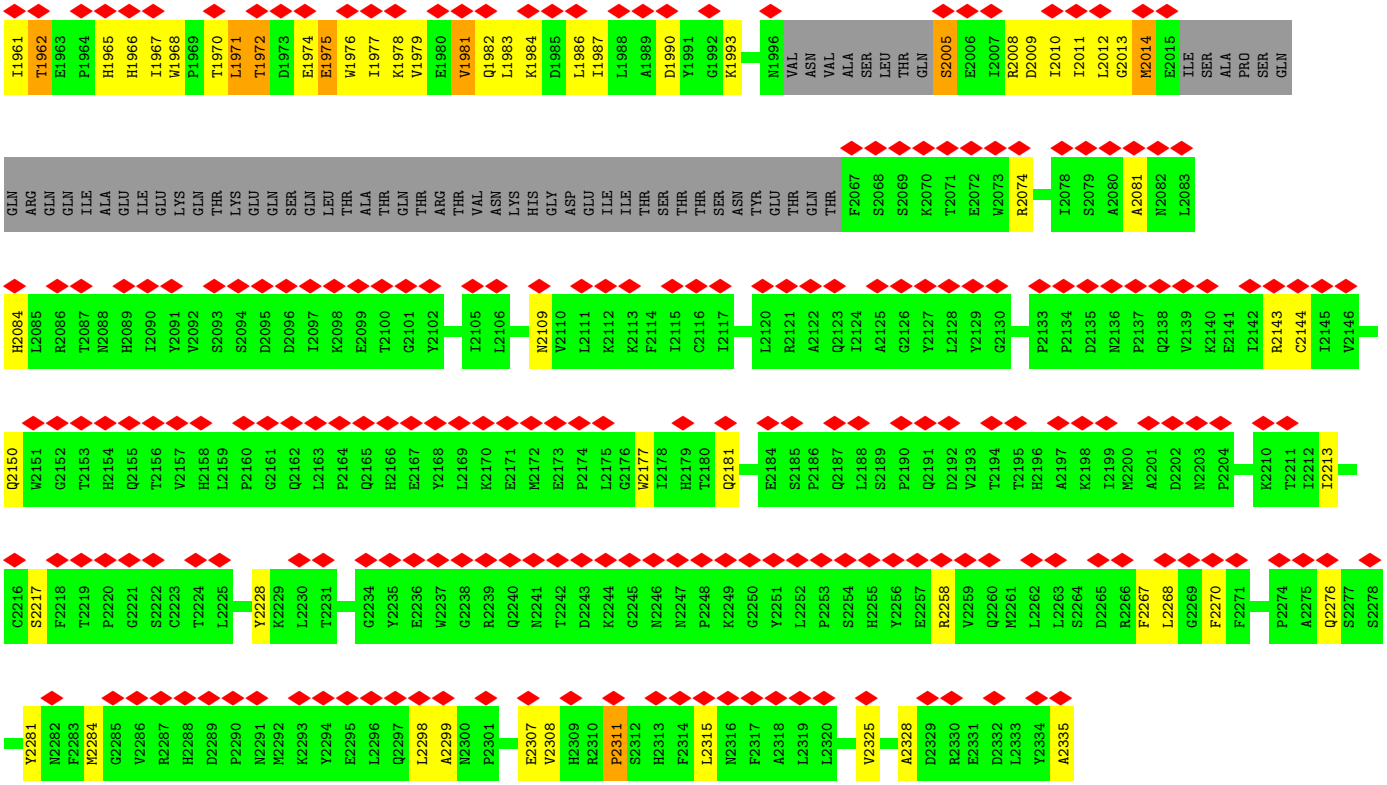

- Molecule 2: U5 snRNA

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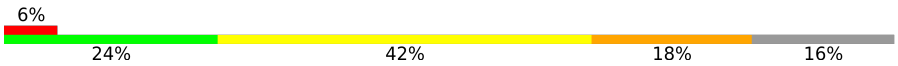

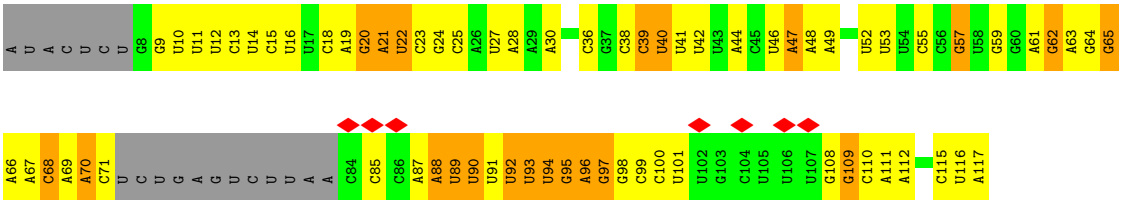

- Molecule 3: 116 kDa U5 small nuclear ribonucleoprotein component

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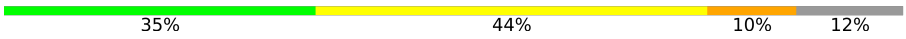
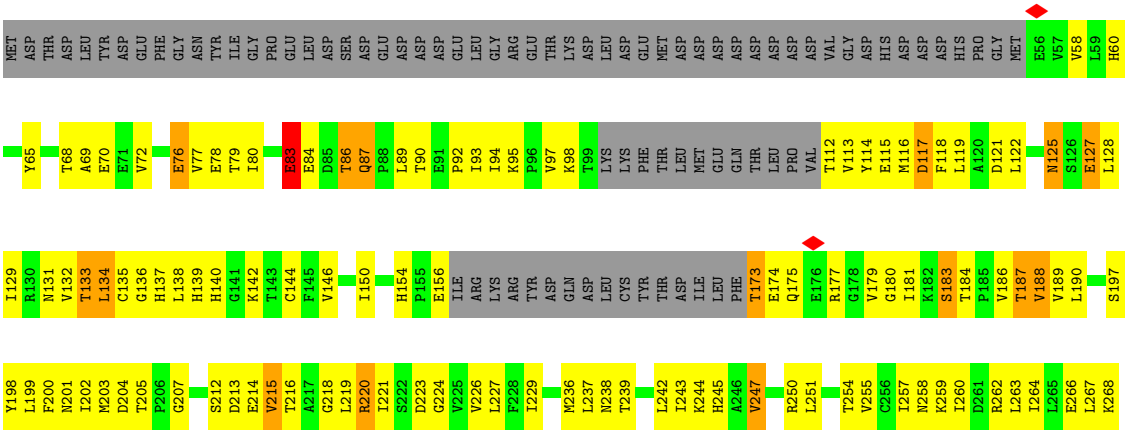
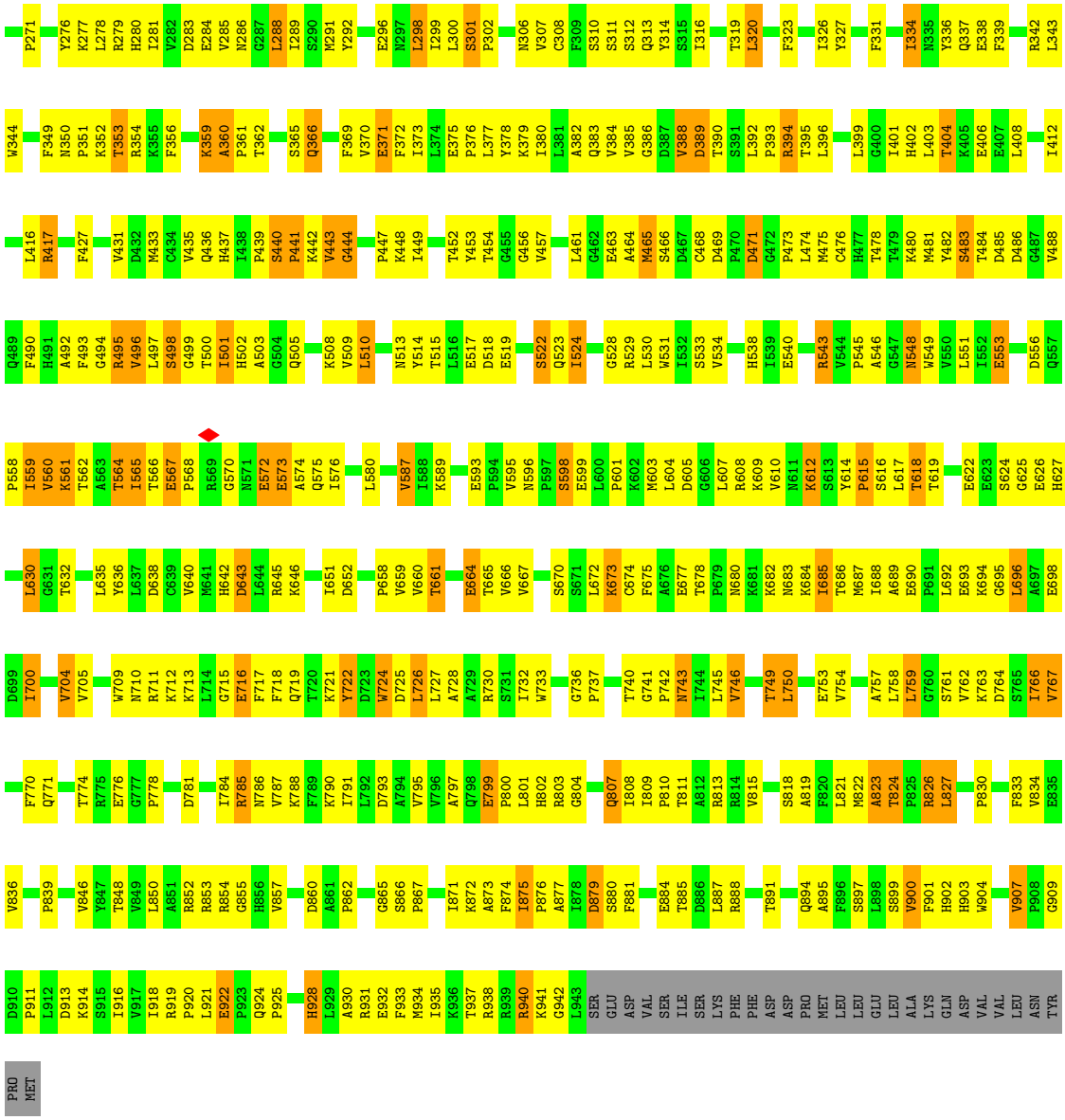
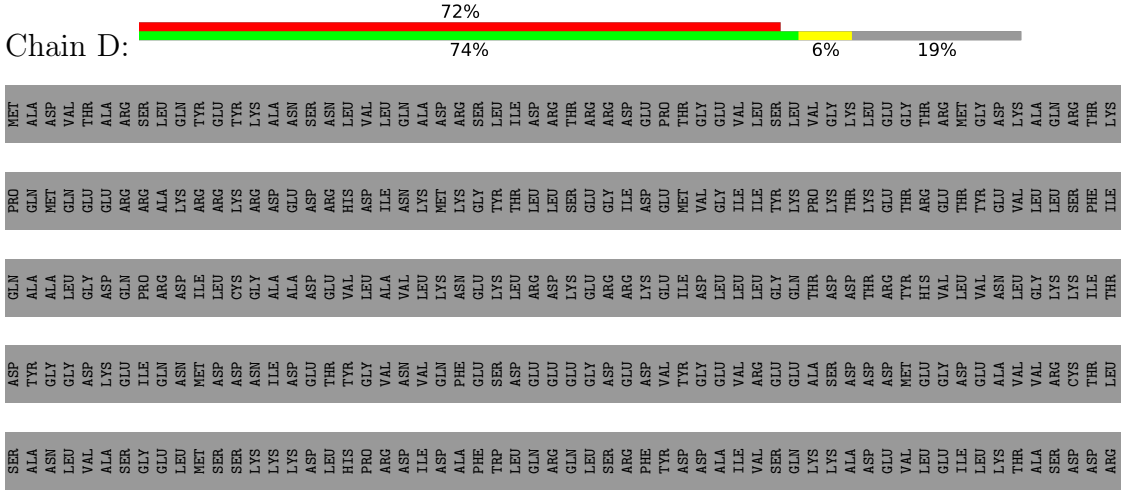






- Molecule 4: U5 small nuclear ribonucleoprotein 200 kDa helicase



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TYR GLN LEU HIS GLU THR GLU LYS GLU ASP LEU ILE ARG GLU GLU ARG SER ARG ARG GLU ARG VAL ARG GLN SER ARG MET ASP THR ASP LEU GLU THR MET ASP LEU ASP GLN GLY GLY GLU ALA LEU A404 P405 R406 Q407 V408 L409 D410 L411 E412 D413 L414 V415 F416 T417 Q418 G419 S420

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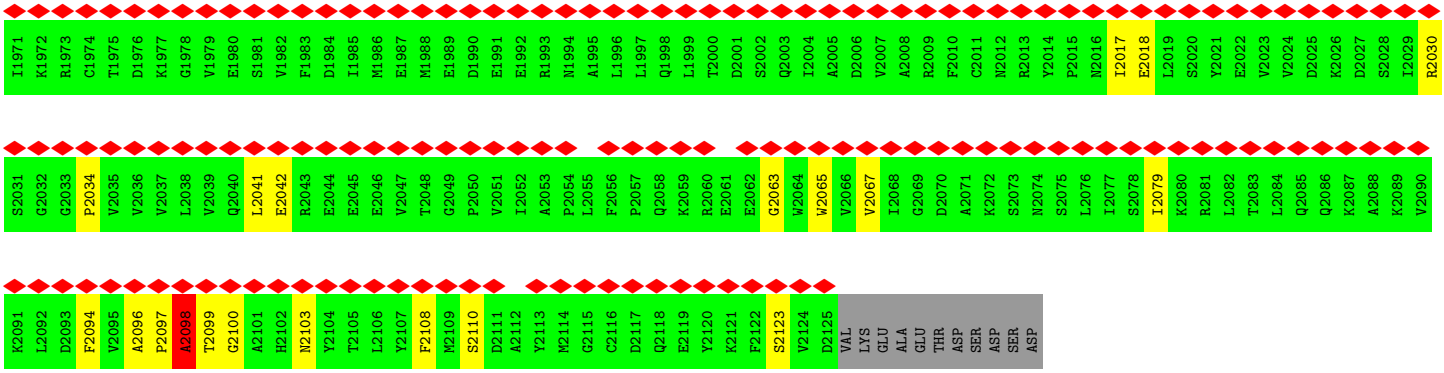
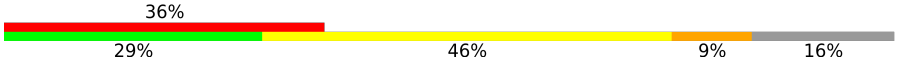
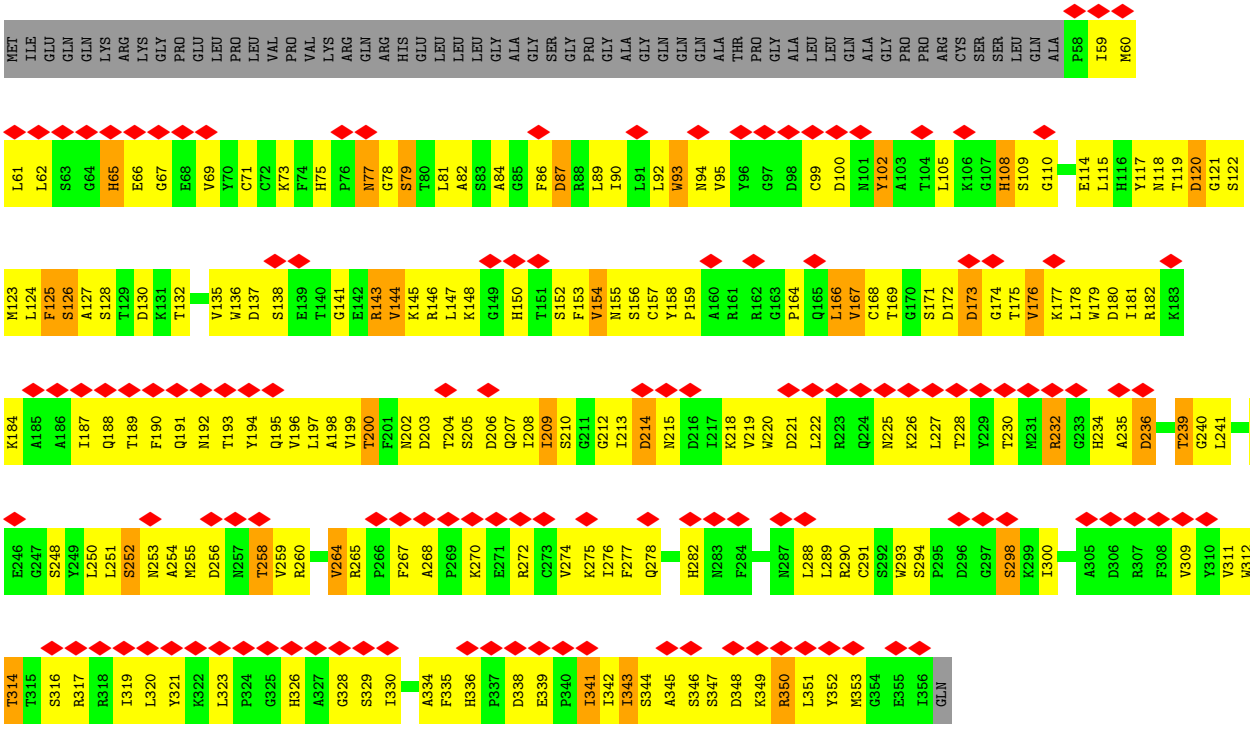


- Molecule 5: U5 small nuclear ribonucleoprotein 40 kDa protein

Chain E:





- Molecule 6: U6 snRNA

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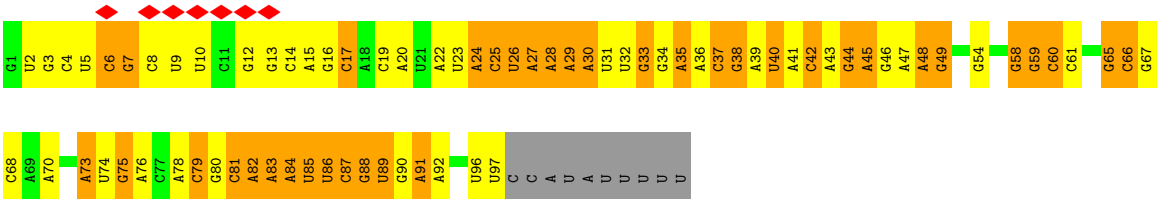
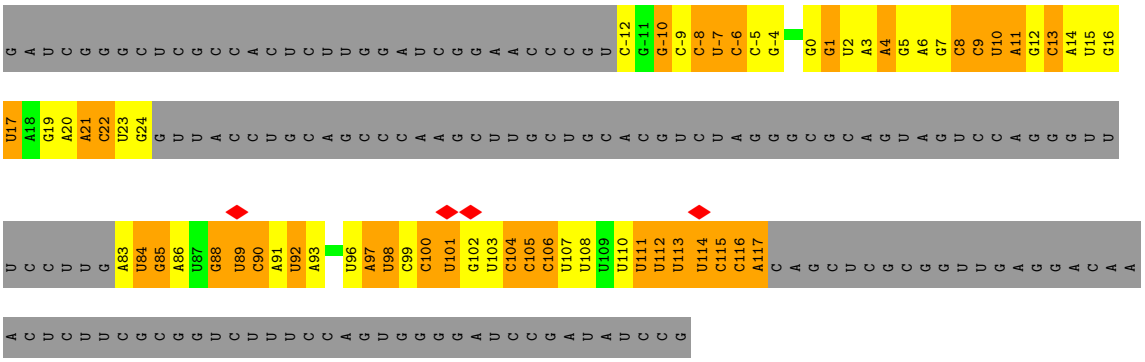


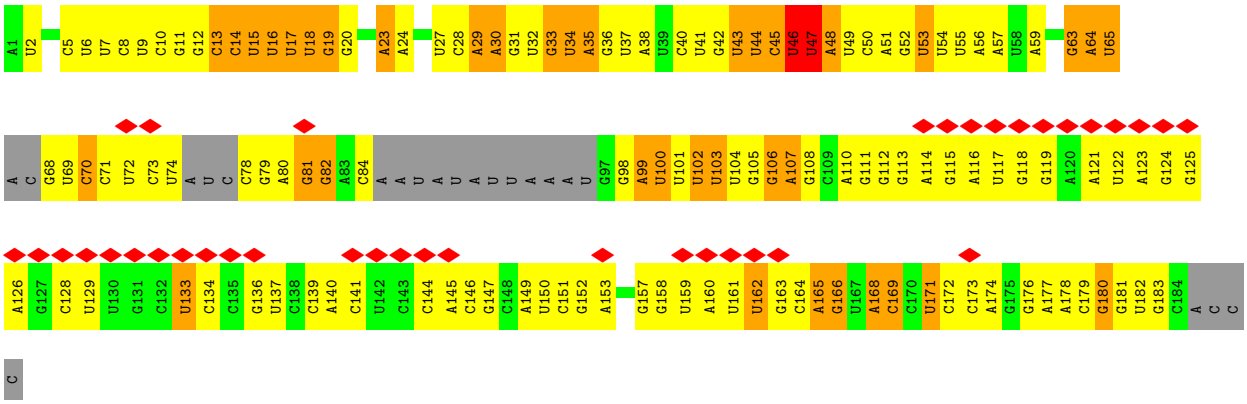
- Molecule 7: pre-mRNA

Chain G: 13% 15% 67%



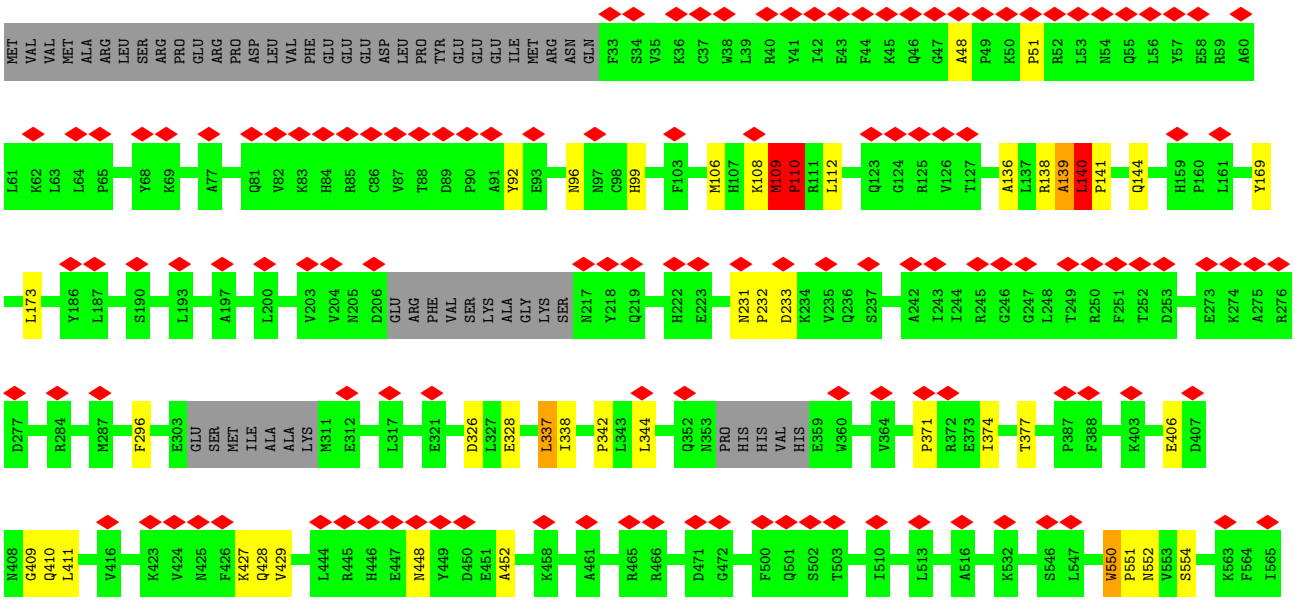
• Molecule 8: U2 snRNA

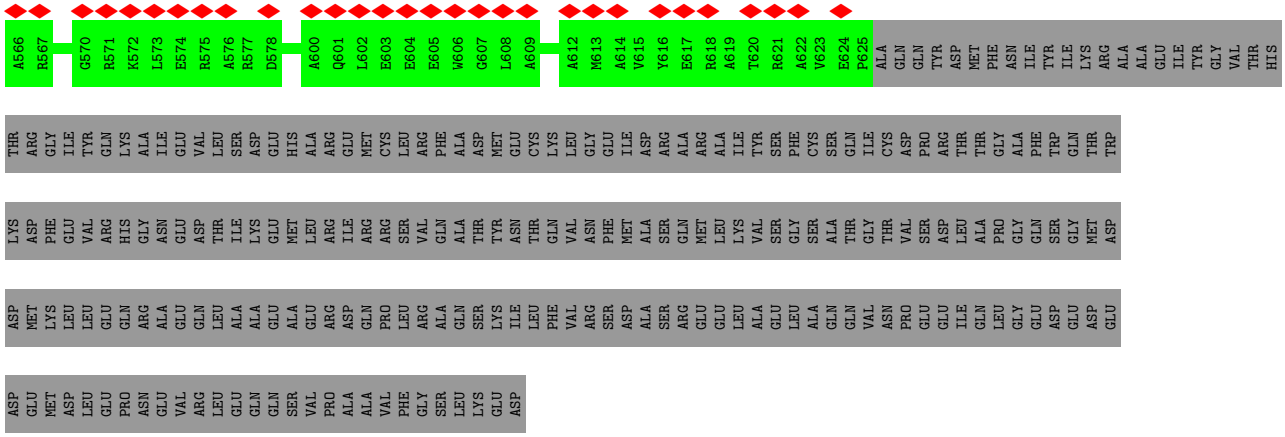
Chain H: 20% 17% 51% 20% 11%



• Molecule 9: Pre-mRNA-splicing factor SYF1

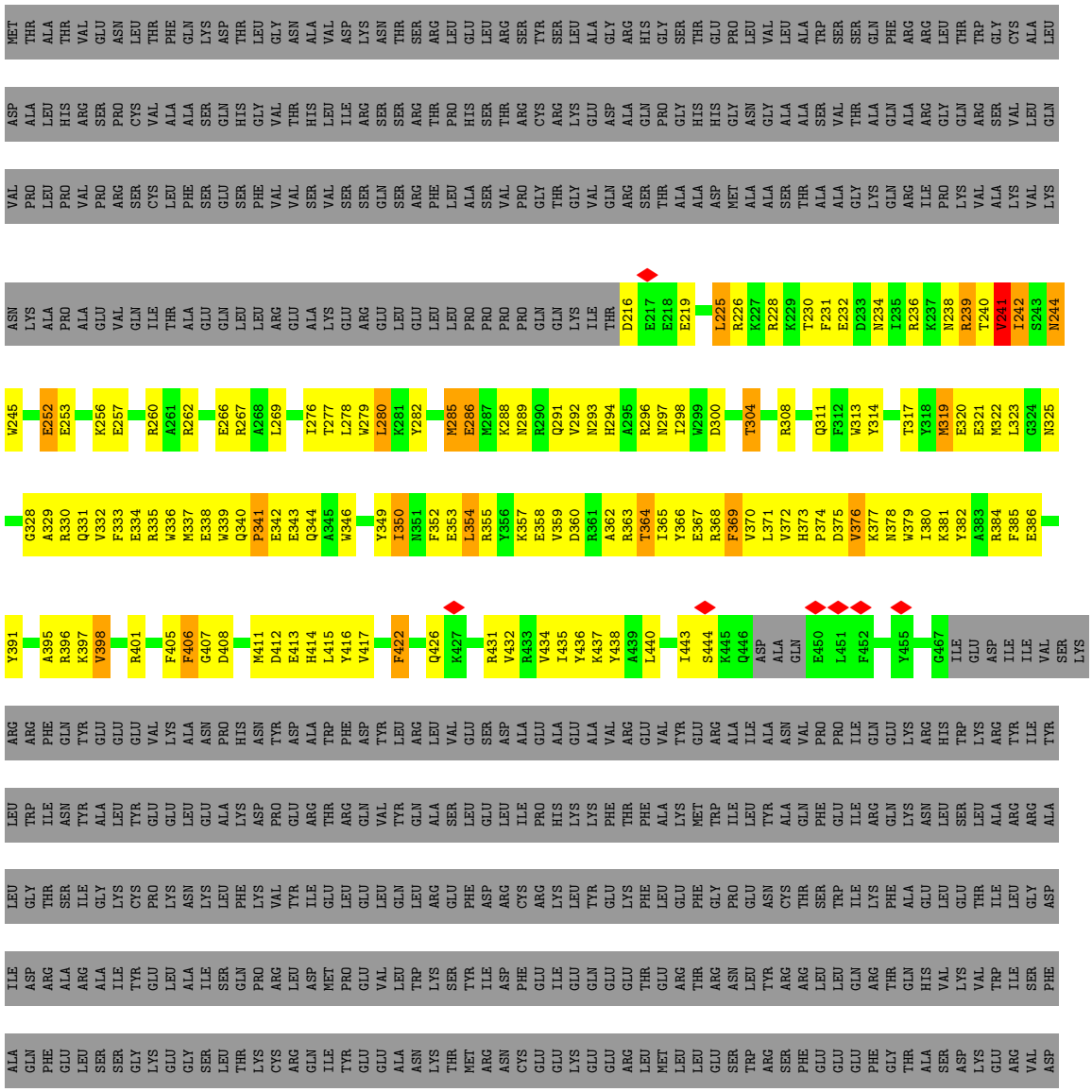
Chain I: 19% 62% 33%

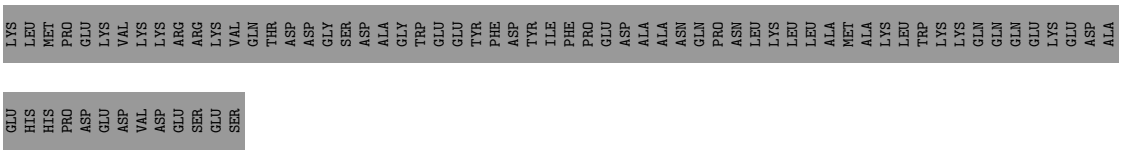




- Molecule 10: Crooked neck-like protein 1

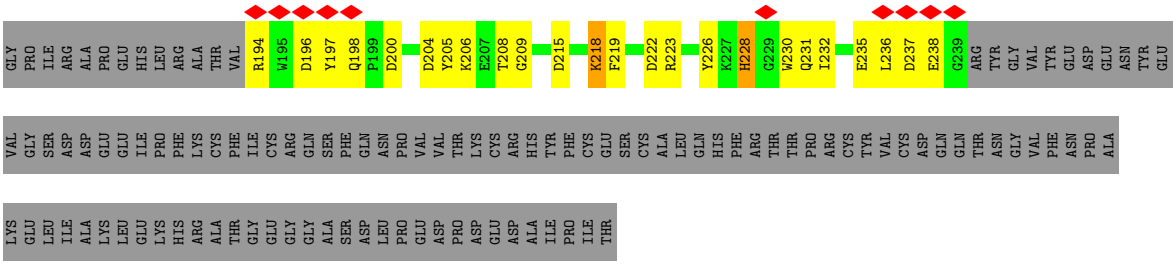
Chain J: 13% 14% 71%





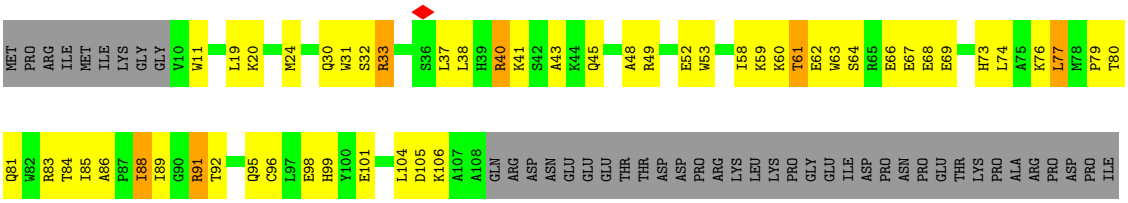
• Molecule 11: RING finger protein 113A

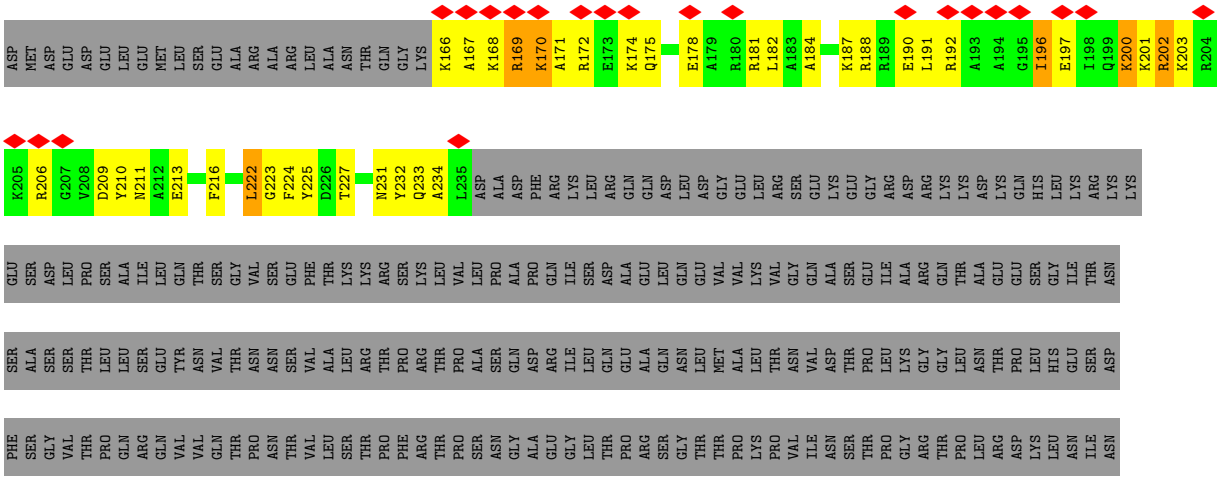
Chain K:



• Molecule 12: Cell division cycle 5-like protein

Chain L:





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ILE GLU ASP ALA ALA ASP VAL ASP ALA ARG LYS GLN LYS ALA ILE ARG ASP ALA GLU ARG VAL LYS GLU MET LYS ARG MET HIS LYS ALA VAL GLN LYS ASP LEU PRO ARG PRO SER GLU VAL ASN GLU THR ILE LEU ARG PRO LEU ASN VAL GLU PRO PRO LEU THR ASP LEU GLN LYS SER

GLU GLU LEU ILE LYS LYS GLU MET ILE THR MET LEU HIS TYR ASP LEU LEU HIS HIS PRO TYR GLU PRO SER GLY ASN LYS LYS GLY LYS THR VAL GLY PHE GLY THR ASN ASN SER GLU HIS ILE THR TYR LEU GLU HIS ASN PRO TYR GLU LYS PHE SER LYS GLU GLU LEU LYS LYS

ALA GLN ASP VAL LEU VAL GLN GLU MET GLU VAL VAL LYS GLN GLY MET SER HIS GLY GLU LEU SER SER GLU ALA TYR ASN LYS GLN VAL TRP GLU GLU CYS TYR SER GLN VAL LEU TYR LEU PRO GLY GLN SER ARG TYR THR ARG ALA ASN LEU ALA SER SER LYS LYS ASP ARG ILE ILE GLU SER

LEU GLU LYS ARG LEU GLU ILE ASN ARG GLY HIS MET THR THR GLU ALA LYS ARG ALA ALA LYS MET GLU LYS LYS MET LYS ILE LEU LEU GLY GLY GLY TYR GLN SER ARG ALA MET GLY LEU MET LYS GLN LEU ASN ASP LEU TRP ASP GLN ILE GLU GLN ALA HIS LEU GLU GLU LEU ARG THR

PHE GLU GLU LEU LYS LYS HIS GLU ASP SER ALA ILE PRO ARG ARG LEU GLU CYS LEU LYS GLU ASP VAL GLN ARG GLN GLN GLU ARG GLU LYS GLU LEU GLN HIS ARG TYR ALA ASP LEU LEU LEU GLU LYS GLU THR LEU LYS SER LYS PHE

- Molecule 13: Protein BUD31 homolog

Chain N: 12% 47% 42% 9%

M1 P2 K3 V4 K5 R6 S7 R8 K9 A10 P11 P12 D13 G14 W15 E16 L17 I18 E19 P20 T21 L22 D23 E24 L25 D26 Q27 K28 M29 A32 E33 T34 E35 P36 H37 E38 G39 K40 R41 K42 V43 E44 S45 L46 W47 P48 I49 F50 R51 I52 H53 K56 T57 R58 Y59 I60 L63

F64 A69 I70 S71 R72 E73 L74 Y75 E76 I79 Y83 K86 N87 L88 K91 W92 Y97 E98 C102 L103 R104 C105 I106 Q107 T108 R109 D110 T111 N112 F113 G114 T115 N116 C117 I118 C119 R120 V121 P122 K125 L126 E127 V128 C134 T135 H136 C137 G138 C139 R140 G141

C142 S143 GLY

- Molecule 14: Pre-mRNA-splicing factor RBM22

Chain O: 13% 59% 9% 32%

MET ALA THR SER LEU GLY SER ASN THR TYR ASN ARG GLN ASN TRP GLU ASP A18 I22 L23 C24 Q25 L28 M36 T37 K38 R56 Q82 F103 D106 M107 P108 Y116 N120 S128 D129 G130 T131 R132 G135 M136 L137 G138 K139 A140 T141 P162 H163

I164 C165 W168 E172 C173 K174 Y181 R182 T187 D188 P189 D195 P225 P226 E227 D228 K229 T230 I231 T232 T233 L234 Y235 V236 G240 D241 T242 I243 T244 E245 T246 D247 L248 R249 N250 H251 F252 Y253 Q254 F255 G256 R259 T260 I261 T262 V263 V264 Q265 R266 Q267 A270

F271 I272 Q273 F274 A275 T276 R277 Q278 A279 A280 E281 V282 A283 K290 L291 I292 V293 N294 G295 R296 N299 V300 K301 W302 G303 R304 SER GLN ALA ALA ARG GLY LYS GLU LYS GLU LYS ASP GLY THR THR ASP SER GLY ILE LYS LEU GLU PRO VAL PRO GLY LEU PRO GLY ALA LEU PRO

PRO PRO PRO ALA ALA GLU GLU GLU ALA SER ALA ASN TYR PHE ASN LEU PRO PRO SER GLY PRO PRO ALA VAL VAL ASN ILE ALA LEU PRO PRO PRO PRO GLY ILE ALA PRO PRO PRO PRO GLY PHE GLY PRO HIS MET PHE HIS PRO MET GLY PRO PRO PRO PRO PHE MET ARG ALA

PRO GLY PRO ILE HIS TYR PRO SER GLN ASP PRO GLN ARG MET GLY ALA HIS ALA GLY LYS HIS SER SER PRO

- Molecule 15: Spliceosome-associated protein CWC15 homolog

Chain P: 20% 21% 56%

MET THR THR ALA ALA ARG PRO THR PHE GLU PRO ALA ARG GLY GLY ARG GLY LYS GLY GLU GLY ASP LEU SER Q25 L26 S27 K28 Q29 Y30 S31 S32 T39 K40 I41 K42 Y43 R44 Q45 Q48 D49 A50 P51 E52 E53 V54 R55 N56 E67 R68 A69 R72 E73 K74 N75 R76

D77 R78 PRO THR ARG GLU HIS THR THR SER SER SER VAL SER LYS LYS PRO ARG LEU ASP GLN ILE PRO ALA ALA ASN LEU ASP ALA ASP ASP LEU THR ASP GLU GLU ASP GLU ASP PHE GLU GLU GLU SER ASP ASP ASP ASP THR ALA ALA LEU LEU ALA GLU LEU GLU LYS ILE

LYS LYS GLU ARG ALA GLU GLU GLN ALA ARG LYS GLU GLN GLU GLN LYS ALA GLU GLU GLU ARG ILE ARG MET GLU ASN ILE LEU SER GLY ASN PRO LEU LEU ASN LEU THR GLY PRO SER GLN PRO GLN ALA ASN PHE K183 V184 K185 R186 R187 W188 D189 D190 D191 V192 V193 F194 K195 N196

G200 V201 D202 D203 Q204 K205 K206 D207 K208 N212 D213 T214 L215 R216 S217 E218 F219 H220 M224 E225 K226 Y227 I228 K229

- Molecule 16: RNA helicase aquarius

Chain Q: 59% 82% 7% 11%

MET ALA ALA PRO ALA GLN PRO LYS LYS ILE VAL ALA PRO THR VAL SER GLN ILE N19 A20 E21 F22 V23 T24 Q25 L26 A27 C28 K29 Y30 W31 A32 P33 H34 I35 K36 K37 K38 S39 P40 F41 D42 I43 K44 V45 I46 E47 D48 I49 Y50 E51 K52 E53 I54 V55 K56 S57 R58 F59 A60

I61 R62 K63 I64 M65 L66 Q71 Y72 L73 E74 L77 W78 M79 N80 Y81 S82 P83 E84 V85 S86 S87 K88 A89 Y90 L91 C96 M97 V98 N99 E100 K101 F102 R103 E104 N105 E110 I111 F112 K113 K114 K115 P116 D117 H118 F119 P120 F121 K124 K128 A129 A130 L131 A132 E133

T134 D135 G136 E137 F138 S139 L140 H141 E142 Q143 T144 V145 L146 L147 L148 D151 L161 I162 R163 S164 Q165 V166 Q167 Q168 L169 I170 S171 L172 P173 M174 W175 M176 G177 L178 Q179 L180 A181 E184 L185 E186 L187 K188 K189 T190 P191 K192 L193 R194 K195 F196 W197 N198 L199 I200 K201 K202 N203

D204 E205 K206 M207 D208 P209 E210 A211 R212 E213 Q214 A215 Y216 Q217 E218 R219 R220 F221 L222 S223 Q224 L225 I226 I230 S231 V232 L233 K234 S235 V236 P237 L238 S239 E240 P241 V242 T243 M244 D245 K246 V247 H248 Y249 C250 E251 R252 F253 I254 E255 L256 M257 I258 D259 A262 L263 L264 R267

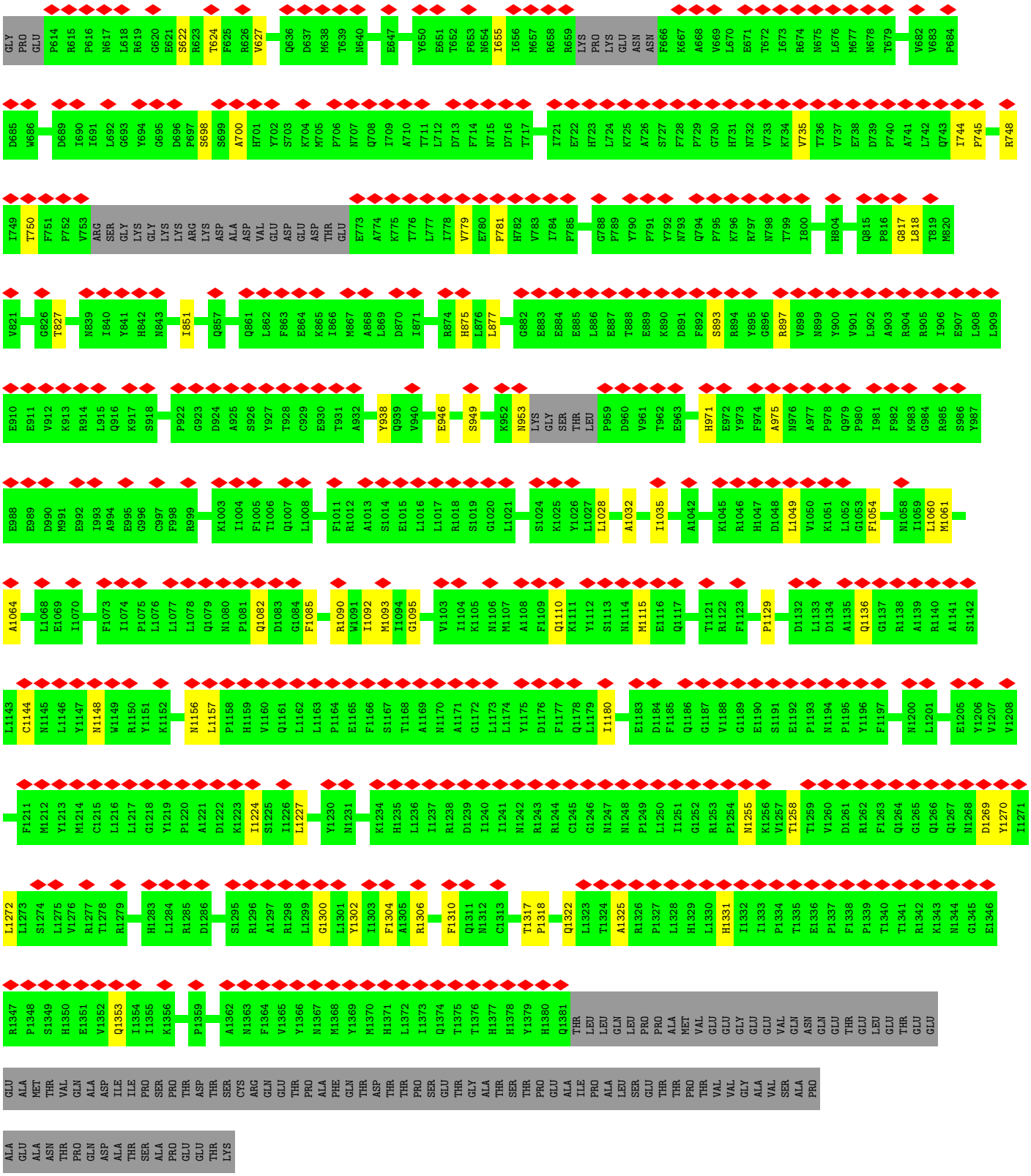
R268 W269 F270 N271 T272 I273 D276 S277 H278 L279 C283 S286 N287 L288 V289 R290 R291 E292 E293 D294 G295 H296 L297 F298 S299 Q300 D303 M304 L305 K306 F307 Y308 I313 N314 D315 Q316 T317 G318 N319 A320 L321 T322 E323 N324 E325 M326 T327 T328 I329 H330 Y331 D332 T335 S336

R339 A340 A341 F342 A343 H344 F345 F351 A352 L353 S354 N355 V356 A357 E358 V359 D360 T361 R362 E363 S364 L365 V366 K367 F368 F369 G370 P371 L372 S373 S374 N375 T376 L377 H378 Q379 V380 A381 S382 Y383 L386 L387 P388 T389 L390 P391 K392 N393 E394 D395 T396 T397 F398 D399 K400 E401 F402

L403 L406 L407 R410 H411 E412 R413 R414 I415 S416 Q417 I418 Q419 Q420 L421 M422 Q423 M424 P425 L426 Y427 P428 T429 E430 K431 I432 I433 W434 D435 E436 N437 I438 V439 P440 T441 E442 Y443 Y444 S445 G446 E447 G448 C449 L450 A451 L452 P453 N456 L457 Q458 F459 L460 T461 L462 H463 D464 Y465

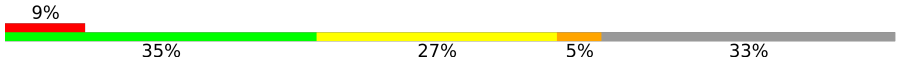
L466 L467 R468 F473 R474 L475 E476 S477 T478 Y479 E480 I481 R482 Q483 D484 I485 S488 V489 S490 R491 M492 K493 P494 W495 Q496 S497 E498 Y499 G500 G501 V502 V503 F504 G505 G506 W507 A508 R509 M510 I514 V515 A516 F517 T518 V519 P525 N526 I527 G528 E529 N530 W531 R536 A537 D538

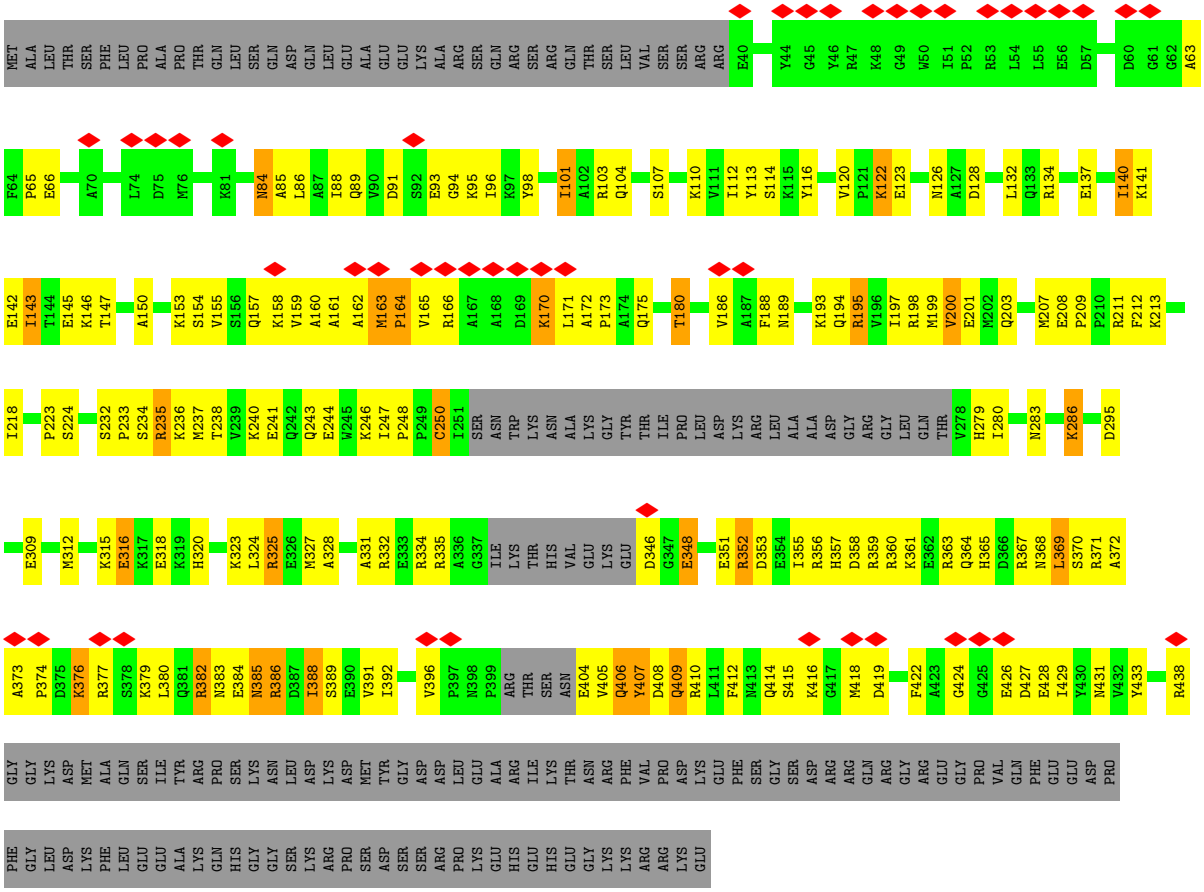
V539 T540 I541 N542 V545 R546 D547 H548 E552 L556 R557 K558 H559 C562 F563 L564 R568 P569 T570 K571 P572 Y573 G574 T575 K576 F577 D578 R579 R580 R581 P582 F583 I584 E585 Q586 V587 G588 L589 V592 I597 Q598 G599 M600 L601 D602 D603 K604 G605 R606 V607 I608 E609 ASP



- Molecule 17: SNW domain-containing protein 1

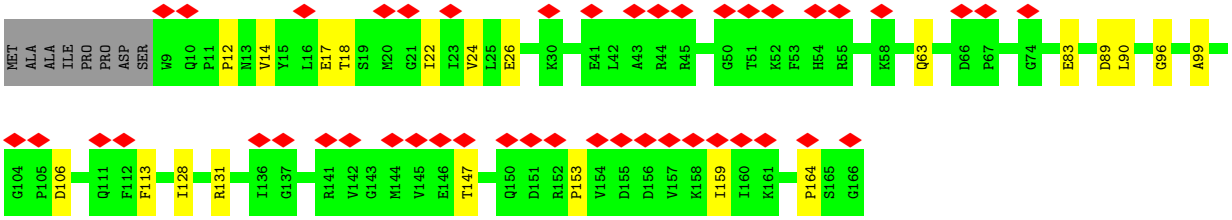
Chain R:





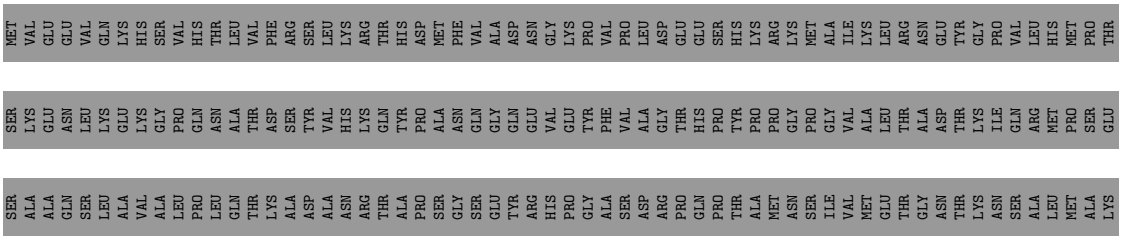
- Molecule 18: Peptidyl-prolyl cis-trans isomerase-like 1

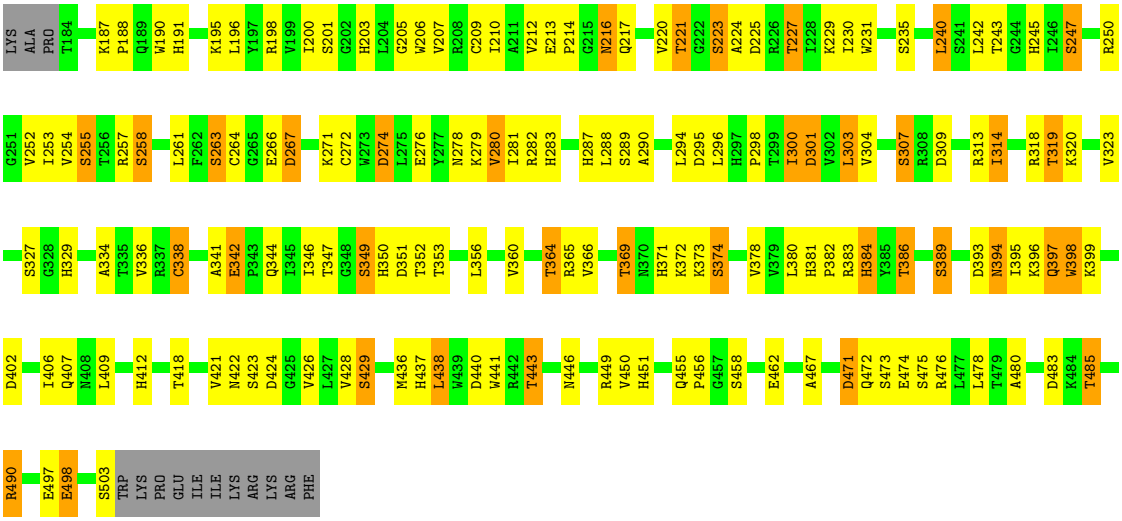
Chain S:



- Molecule 19: Pleiotropic regulator 1

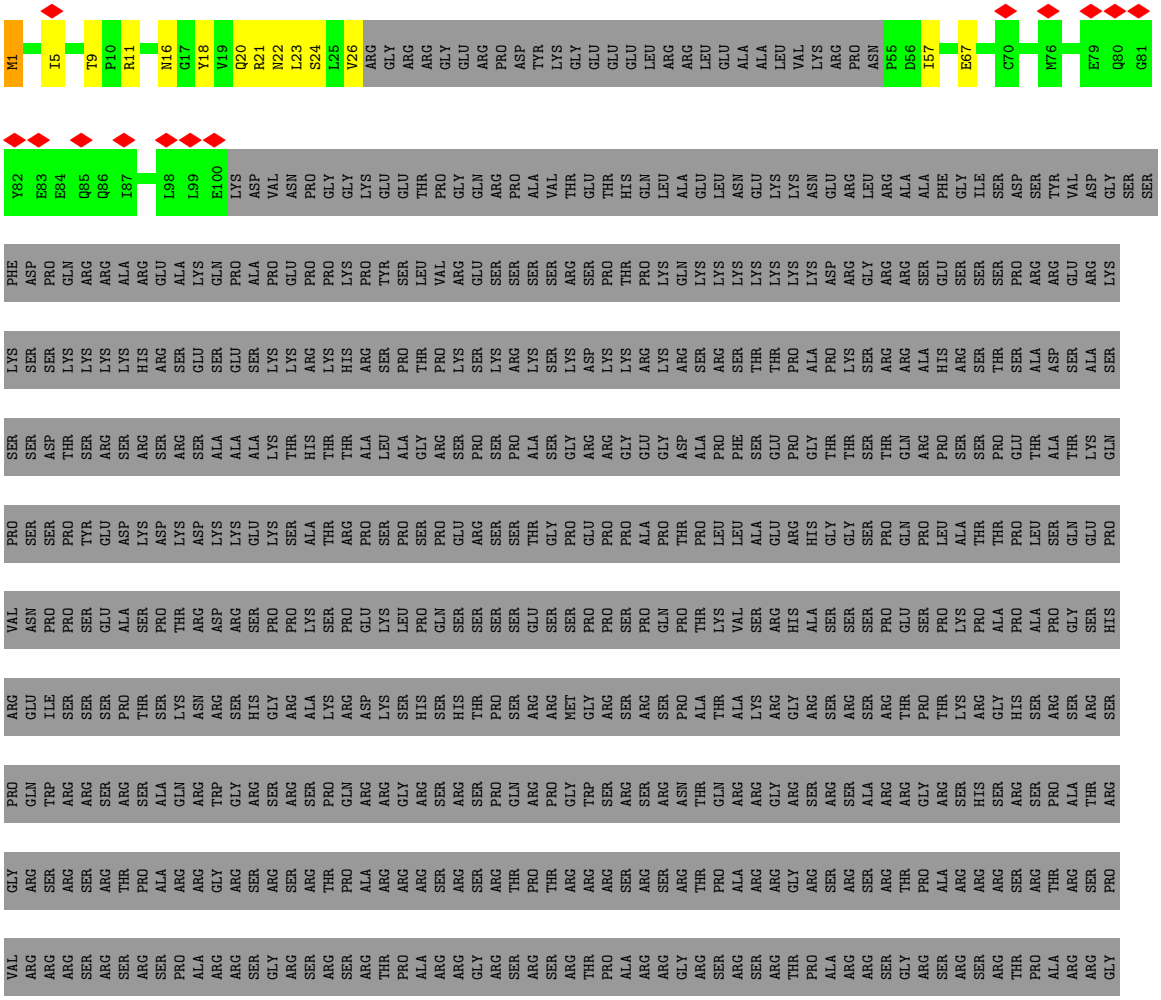
Chain T:





• Molecule 20: Serine/arginine repetitive matrix protein 2

Chain U: 97%



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LYS SER ARG ILE SER SER ARG ARG SER ARG SER LEU SER SER PRO ARG SER LYS ALA LYS SER ARG LEU SER LEU ARG ARG SER LEU SER GLY SER SER PRO CYS PRO LYS GLN LYS SER GLN THR PRO PRO ARG ARG SER ARG SER GLY SER SER GLN PRO LYS ALA LYS SER ARG THR

PRO PRO ARG ARG SER ARG SER SER SER SER PRO PRO PRO LYS GLN LYS SER LYS THR PRO SER ARG GLN SER HIS SER SER SER SER PRO HIS PRO LYS VAL LYS SER GLY THR PRO PRO ARG GLN GLY SER ILE THR SER PRO GLN ALA ASN GLU GLN SER VAL THR PRO GLN ARG ARG

SER CYS PHE GLU SER SER PRO ASP PRO GLU LEU LYS SER ARG THR PRO SER ARG HIS SER CYS SER GLY SER SER PRO PRO ARG VAL LYS SER SER THR PRO PRO ARG GLN SER PRO SER ARG SER SER SER PRO GLN PRO LYS VAL LYS ALA ILE ILE SER PRO ARG GLN ARG SER HIS

SER GLY SER SER SER PRO SER PRO SER ARG VAL THR SER ARG THR THR PRO ARG ARG SER ARG SER VAL SER PRO CYS SER ASN VAL GLU SER ARG LEU LEU PRO ARG TYR SER HIS SER GLY SER SER SER PRO ASP THR LYS VAL LYS PRO GLU THR PRO PRO ARG GLN SER HIS SER

GLY SER ILE SER PRO TYR PRO LYS VAL LYS ALA GLN THR PRO PRO GLY PRO SER LEU SER GLY SER LYS SER PRO CYS PRO GLN GLU LYS SER LYS ASP SER LEU VAL GLN SER CYS PRO GLY SER LEU SER LEU CYS ALA GLY VAL LYS SER SER THR PRO PRO GLY GLU SER TYR PHE

GLY VAL SER SER LEU GLN LEU LYS GLY GLN SER GLN THR SER PRO ASP HIS ARG SER ASP THR SER SER PRO GLU VAL ARG GLN SER HIS SER GLU SER PRO SER LEU GLN SER LYS SER GLN THR SER PRO LYS GLY GLY ARG SER ARG SER SER SER PRO VAL THR GLU LEU ALA SER

ARG SER PRO ILE ARG GLN ASP ARG GLY GLU PHE SER ALA SER PRO MET LEU LYS SER GLY MET SER PRO GLU GLN SER ARG PHE GLN SER ASP SER SER SER TYR PRO THR VAL ASP SER ASN SER LEU LEU GLY GLN SER ARG LEU GLU THR ALA GLU SER LYS GLU LYS MET ALA LEU

PRO PRO GLN GLU ASP ALA THR ALA SER PRO PRO ARG GLN LYS ASP LYS PHE SER PRO PHE PRO VAL GLN ASP ARG PRO GLU SER SER LEU VAL PHE LYS ASP THR LEU ARG THR PRO PRO ARG GLU ARG SER GLY ALA GLY SER SER PRO GLU THR LYS GLU GLN ASN SER ALA LEU PRO

THR SER SER GLN ASP GLU GLU LEU MET GLU VAL VAL GLU LYS SER GLU GLU PRO ALA GLY GLN ILE LEU SER HIS LEU SER SER GLU LEU LYS GLU MET SER THR SER ASN PHE GLU SER SER PRO GLU VAL GLU GLU ARG PRO ALA VAL SER LEU THR LEU ASP GLN SER GLN SER GLN

ALA SER LEU GLU ALA VAL GLU VAL PRO SER MET ALA SER SER TRP GLY GLY PRO HIS PHE SER PRO GLU HIS LYS GLU LEU SER ASN SER PRO LEU ARG GLU ASN SER PHE GLY SER PRO LEU GLU PHE ARG ASN SER GLY PRO LEU GLY THR GLU MET ASN THR GLY PHE SER SER GLU

VAL LYS GLU ASP LEU ASN GLY PRO PHE LEU ASN GLN LEU GLU THR ASP PRO SER LEU ASP MET LYS GLU GLN SER THR ARG SER SER GLY HIS SER SER SER GLU LEU SER PRO ASP ALA VAL GLU LYS ALA GLY MET SER SER ASN GLN SER ILE SER SER PRO VAL LEU ASP ALA VAL

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GLY SER SER SER THR GLU SER SER PRO GLU HIS PRO PRO LYS SER ARG THR ALA ARG ARG GLY SER ARG SER SER PRO GLU PRO LYS THR LYS SER ARG THR PRO PRO ARG ARG ARG SER SER ARG SER SER PRO GLU LEU THR ARG LYS ALA ARG LEU SER ARG ARG SER ARG SER ALA

SER SER SER PRO GLU THR ARG SER ARG THR PRO PRO ARG HIS ARG ARG SER PRO SER VAL SER SER PRO GLU PRO ALA GLU LYS SER ARG SER SER ARG ARG ARG ARG SER ALA SER SER PRO ARG THR LYS THR THR SER ARG ARG GLY ARG SER PRO SER PRO LYS PRO ARG GLY LEU

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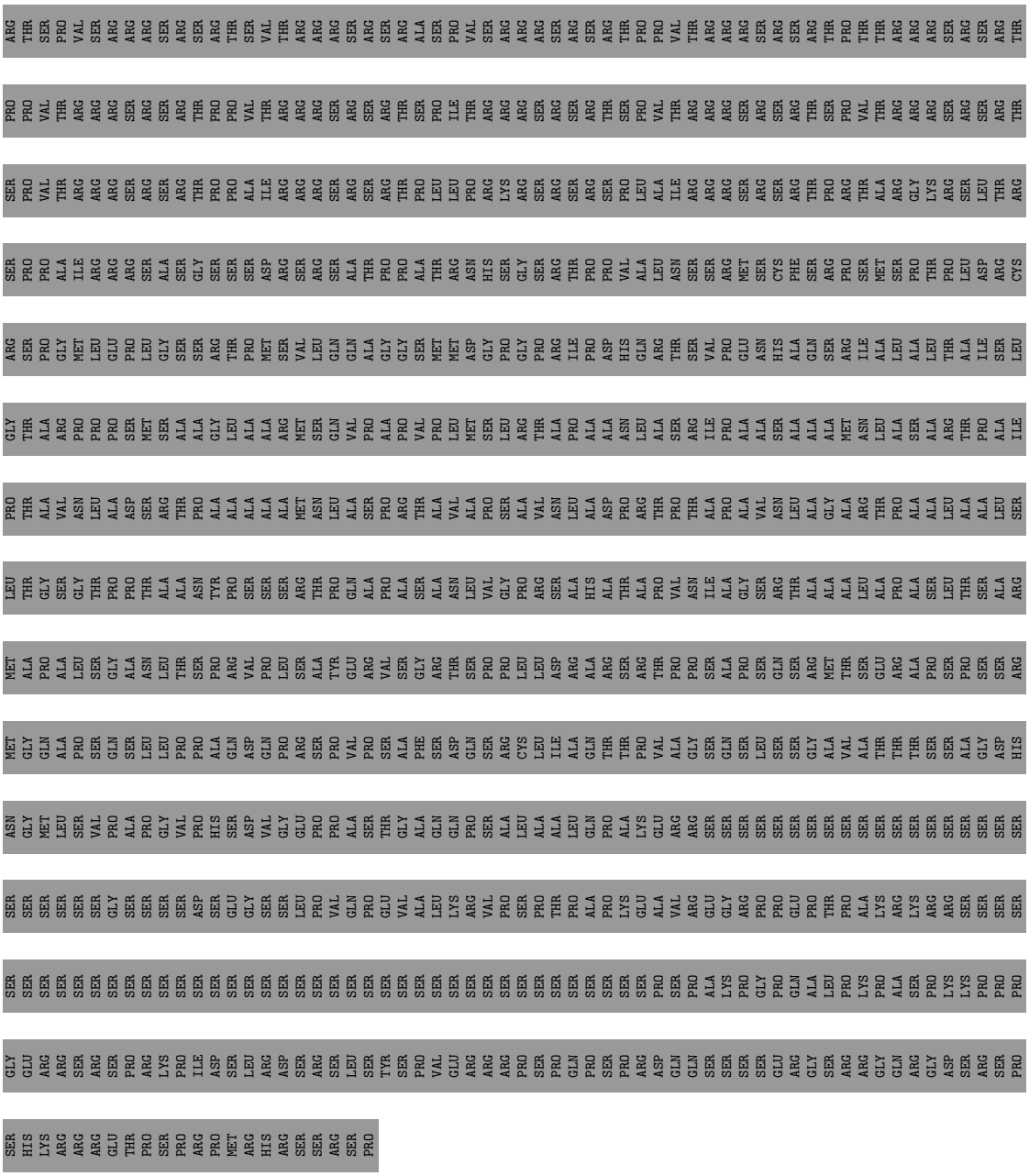
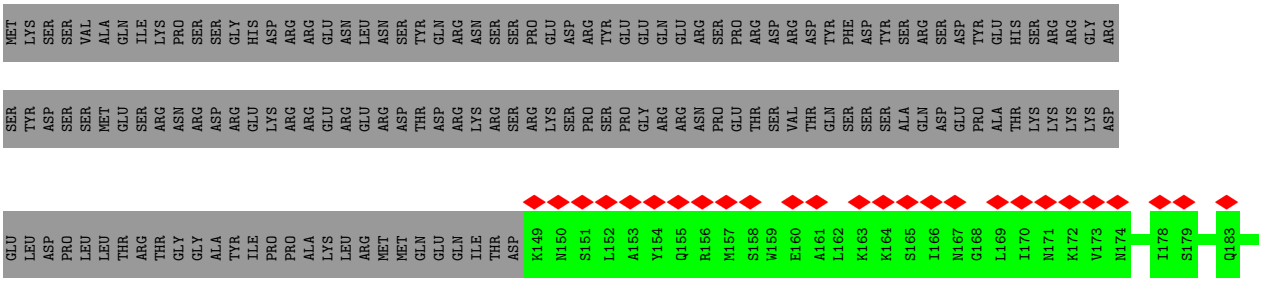
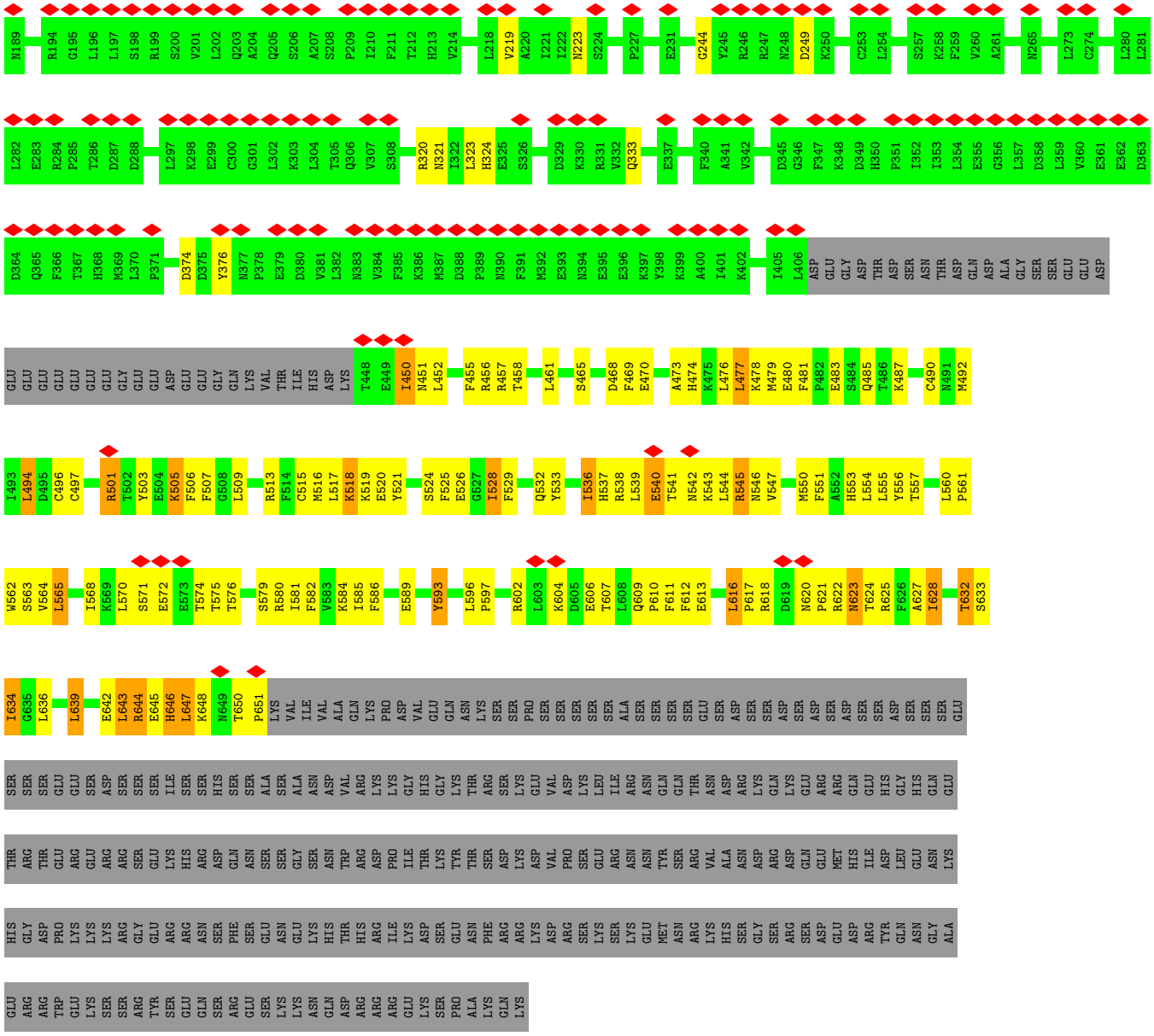
SER ARG THR SER SER ARG ARG ARG GLY ARG SER ARG THR PRO PRO THR SER ARG LYS ARG SER ARG SER ARG THR SER PRO ALA PRO TRP LYS ARG SER ARG SER ARG ALA SER PRO ALA THR HIS ARG ARG SER ARG SER ARG THR PRO LEU ILE SER ARG ARG ARG SER ARG SER



- Molecule 21: Pre-mRNA-splicing factor CWC22 homolog

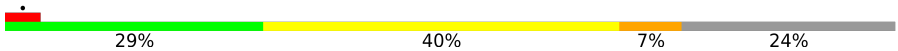
Chain V:

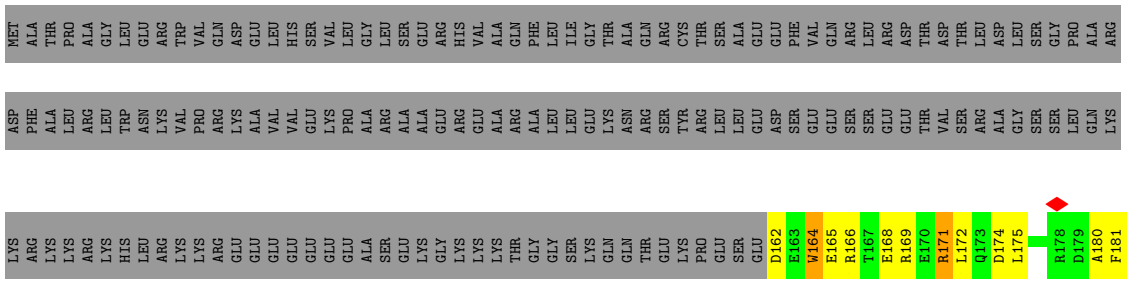


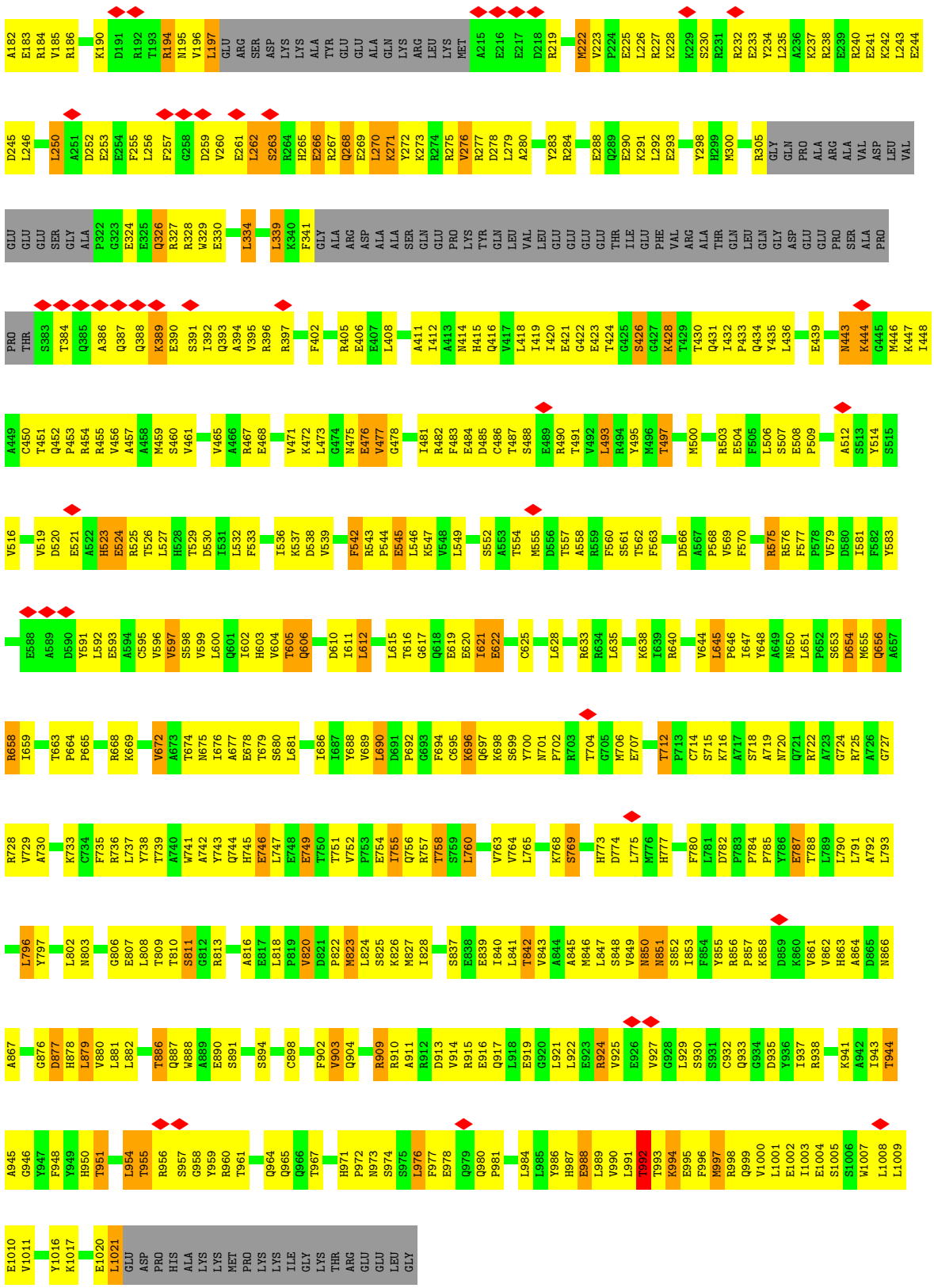


• Molecule 22: Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16

Chain X:

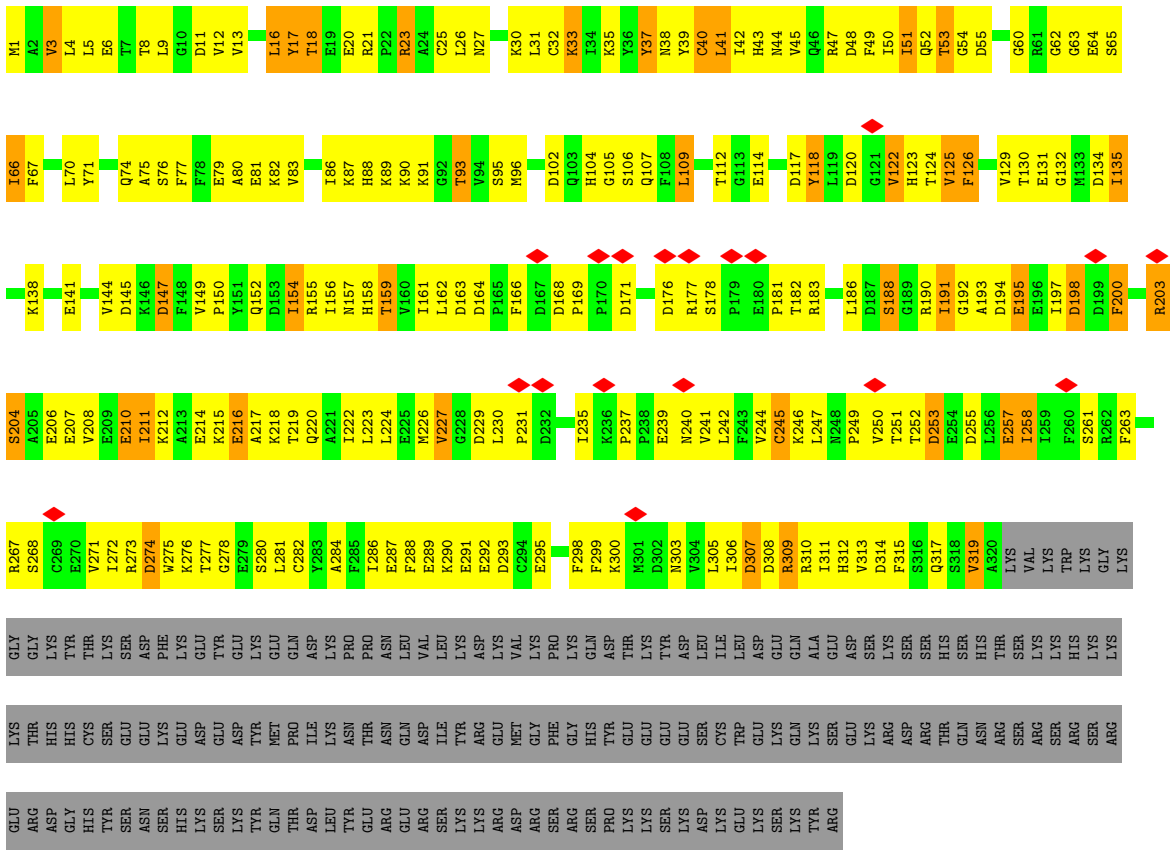






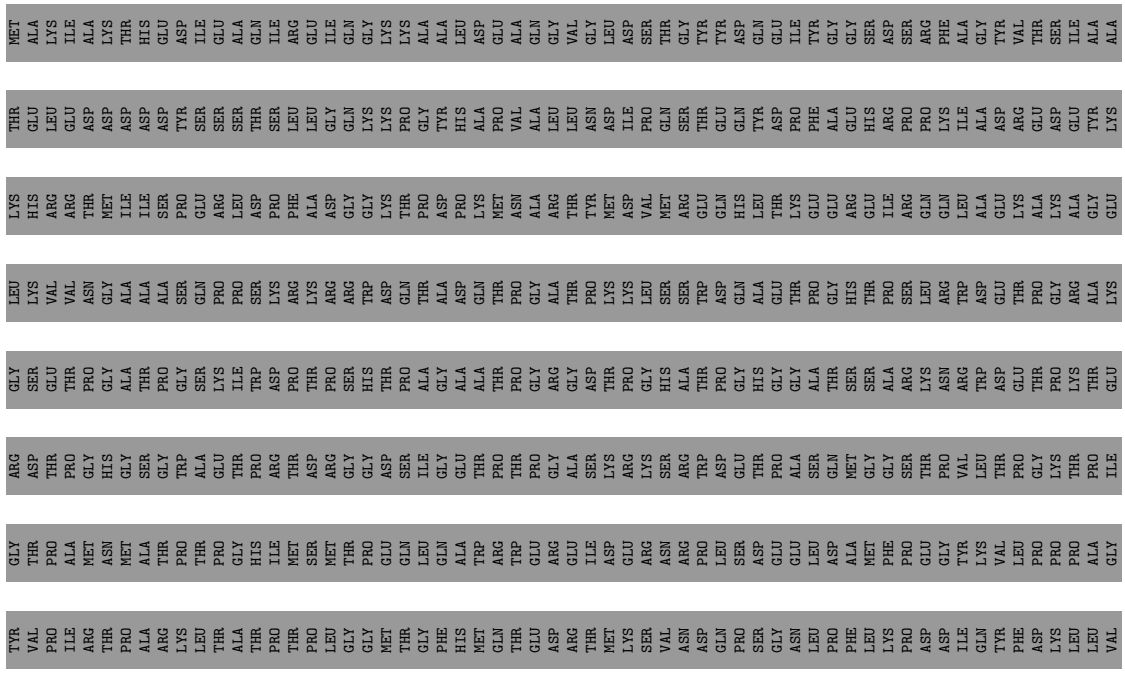
• Molecule 23: Peptidyl-prolyl cis-trans isomerase-like 4

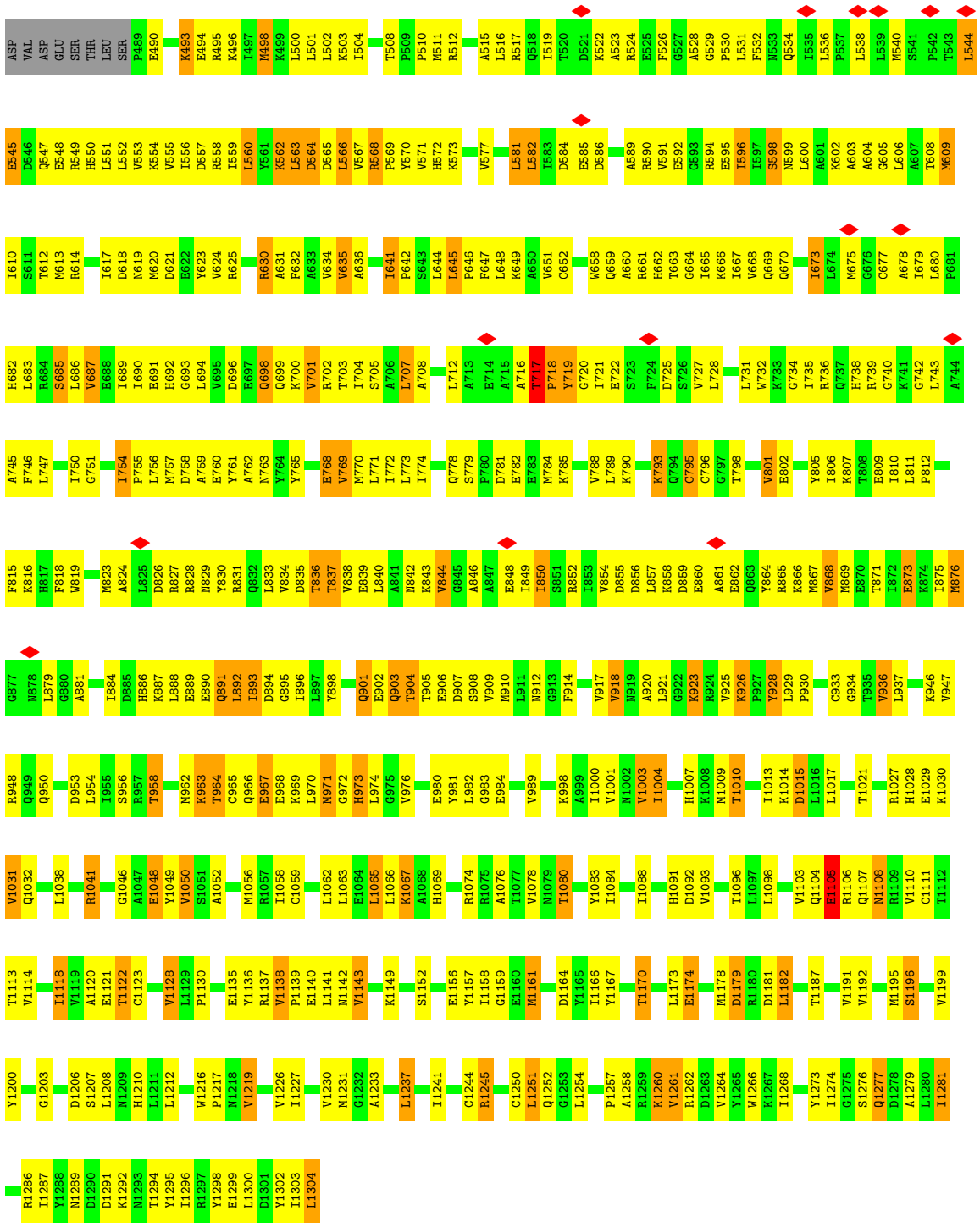
Chain Y: 22% 35% 8% 35%



• Molecule 24: Splicing factor 3B subunit 1

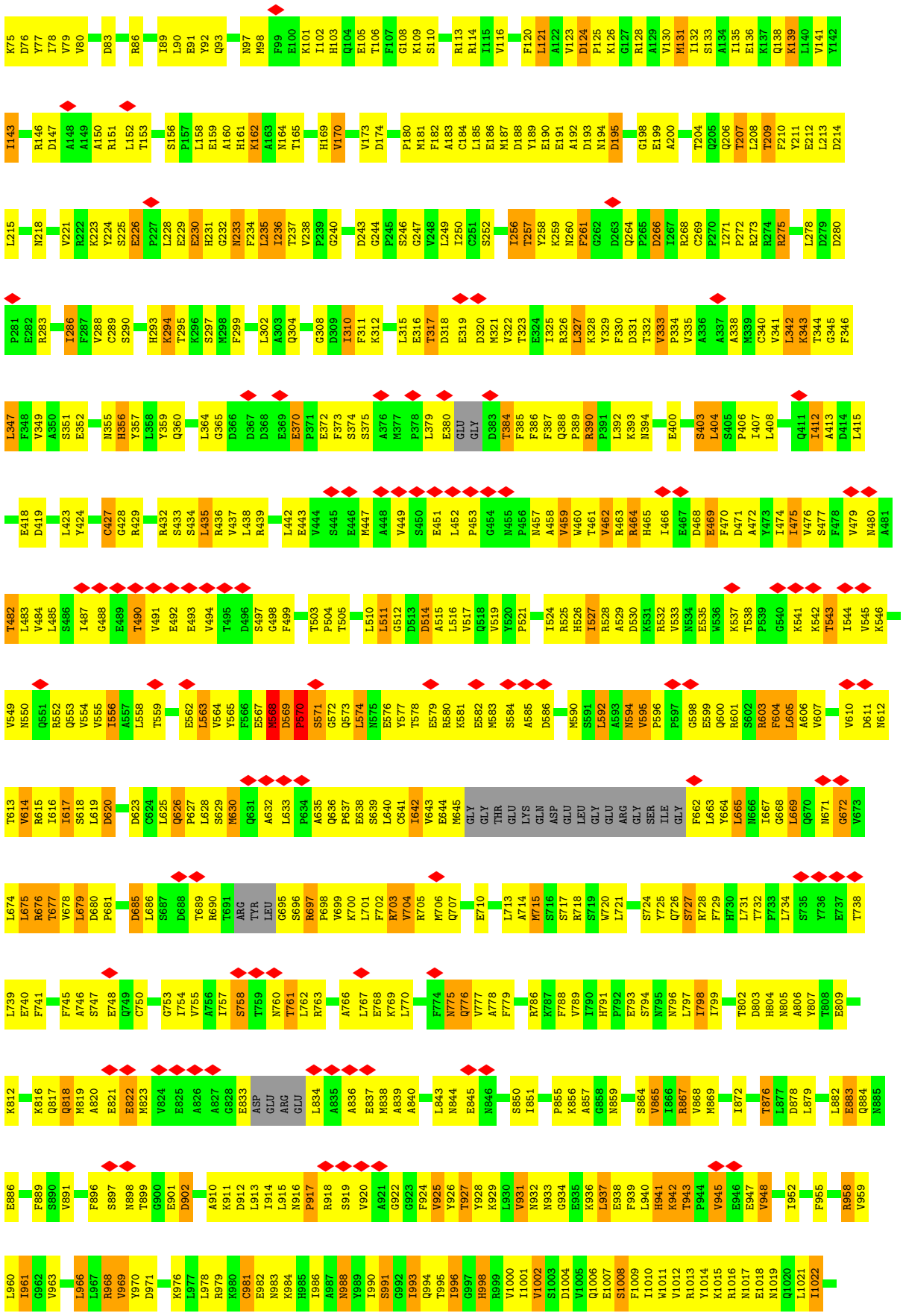
Chain 1:





• Molecule 25: Splicing factor 3B subunit 3

Chain 3: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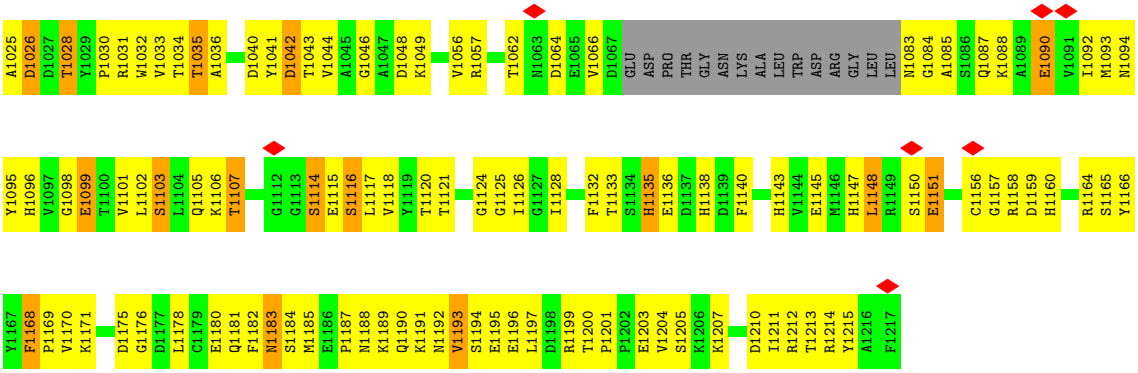
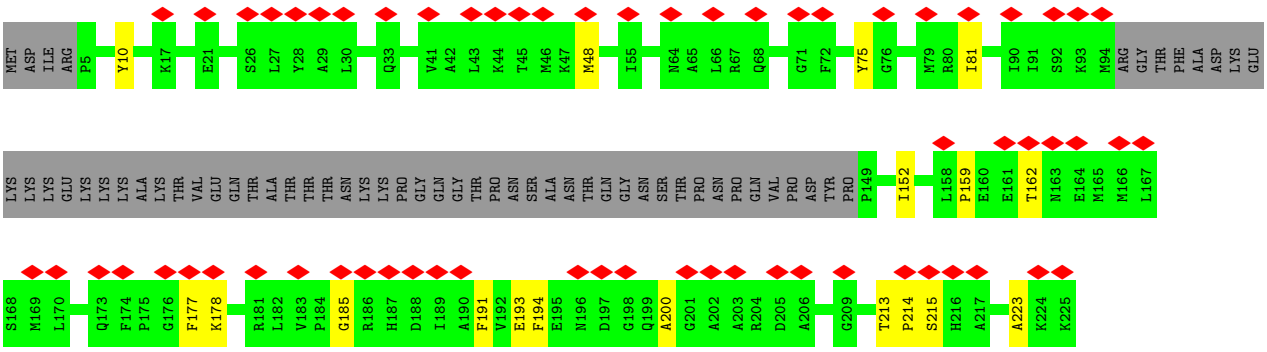
L347 F348 V349 A350 S351 E352 N355 H356 Y357 L358 Y359 Q360 L364 G365 D366 D367 D368 E369 E370 P371 E372 F373 S374 S375 A376 M377 P378 L379 E380 GLU GLY D383 T384 F385 F386 F387 Q388 P389 R390 P391 L392 K393 N394 E400 S403 L404 S405 P406 I407 L408 Q411 I412 A413 D414 L415
E418 D419 L423 Y424 C427 G428 R429 R432 S433 S434 L435 R436 V437 L438 R439 L442 E443 V444 S445 E446 M447 A448 V449 S450 E451 L452 P453 G454 N455 P456 N457 A458 V459 W460 T461 V462 R463 R464 H465 I466 E467 D468 E469 F470 D471 A472 Y473 I474 I475 V476 S477 F478 V479 N480 A481
T482 L483 V484 L485 S486 I487 G488 E489 T490 V491 E492 E493 V494 T495 D496 S497 G498 F499 T503 P504 T505 L510 L511 G512 D513 D514 A515 L516 V517 Q518 V519 Y520 P521 I524 R525 H526 T527 R528 A529 D530 K531 R532 V533 N534 E535 W536 K537 T538 P539 G540 K541 K542 T543 I544 V545 K546
V549 N550 Q551 R552 Q553 V554 V555 I556 A557 L558 T559 E562 L563 V564 Y565 F566 E567 M568 D569 P570 S571 G572 Q573 L574 N575 E576 Y577 T578 E579 R580 K581 E582 M583 S584 A585 D586 M590 S591 L592 A593 N594 V595 P596 P597 G598 E599 Q600 R601 S602 R603 F604 L605 A606 V607 V610 D611 N612
T613 V614 R615 I616 I617 S618 L619 D620 D623 C624 L625 Q626 P627 L628 S629 M630 Q631 A632 L633 P634 A635 Q636 P637 E638 S639 L640 C641 I642 V643 E644 M645 GLY GLY THR GLU LYS GLN ASP GLU LEU GLY GLU ARG GLY SER ILE GLY F662 L663 Y664 L665 N666 I667 G668 L669 Q670 N671 G672 V673
L674 L675 R676 T677 V678 L679 D680 P681 D685 L686 S687 D688 T689 R690 T691 ARG TYR LEU G695 S696 R697 P698 A699 K700 L701 F702 R703 V704 R705 M706 Q707 E710 L713 A714 M715 S716 S717 R718 S719 W720 L721 S724 Y725 Q726 S727 R728 F729 H730 L731 T732 P733 L734 S735 Y736 E737 T738
L739 E740 F741 F745 A746 S747 E748 Q749 C750 G753 I754 V755 A756 I757 S758 T759 N760 T761 L762 R763 A766 L767 E768 K769 L770 F774 N775 Q776 V777 A778 F779 R786 K787 F788 V789 T790 H791 P792 E793 S794 N795 N796 L797 T798 I799 T802 D803 H804 N805 A806 Y807 T808 E809
K812 K816 Q817 Q818 M819 A820 E821 E822 M823 V824 E825 A826 A827 G828 E833 ASP GLU ARG GLU L834 A835 A836 E837 M838 A839 A840 L843 N844 E845 N846 S850 I851 P855 K856 A857 G858 N859 S864 V865 I866 R867 V868 M869 I872 T876 L877 D878 L879 L882 E883 Q884 N885
E886 F889 S890 V891 F896 S897 N898 T899 G900 E901 D902 A910 K911 D912 L913 I914 L915 N916 P917 R918 S919 V920 A921 G922 G923 F924 V925 Y926 T927 Y928 K929 L930 V931 N932 N933 G934 E935 K936 L937 E938 F939 L940 H941 K942 T943 P944 V945 E946 E947 V948 I952 F955 R958 V959
L960 I961 G962 V963 L966 L967 R968 V969 Y970 D971 K976 L977 L978 R979 K980 C981 E982 N983 K984 H985 I986 A987 N988 Y989 I990 S991 G992 I993 Q994 T995 I996 G997 H998 R999 V1000 I1001 V1002 S1003 D1004 V1005 Q1006 E1007 S1008 F1009 I1010 W1011 V1012 R1013 Y1014 K1015 R1016 N1017 E1018 N1019 Q1020 L1021 I1022



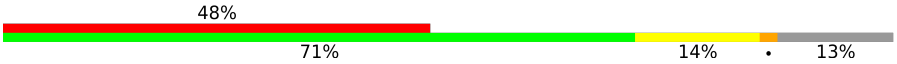
• Molecule 26: U2 small nuclear ribonucleoprotein B”

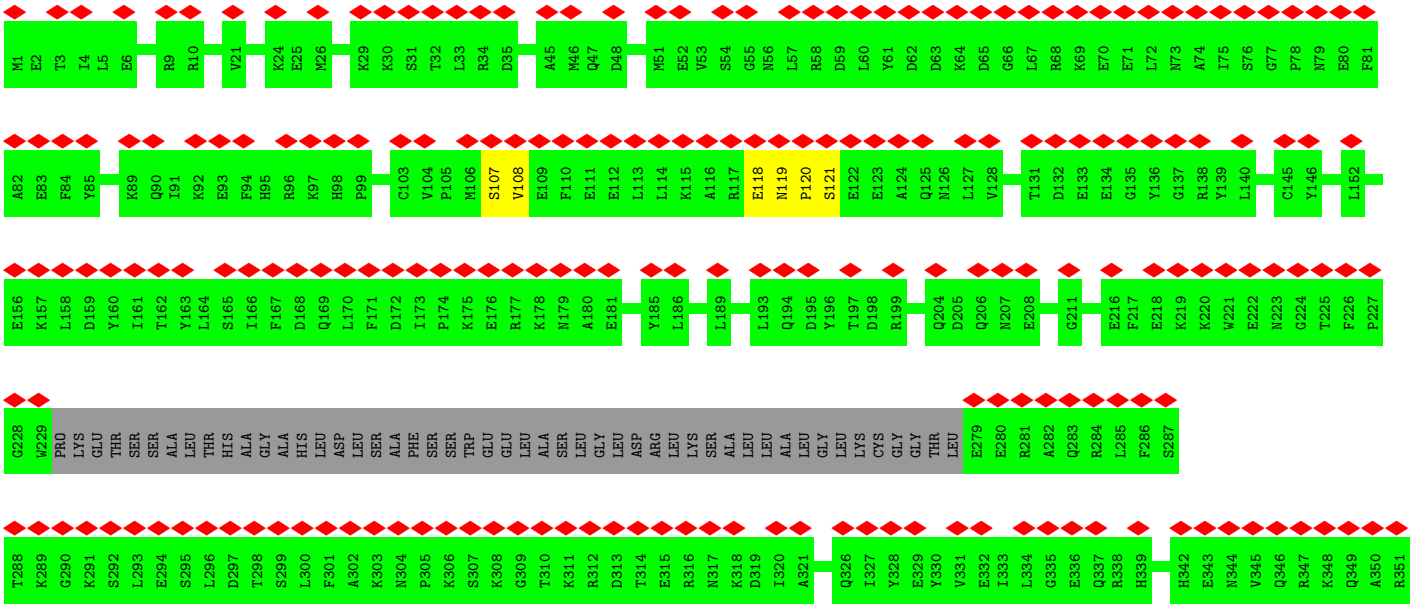
Chain p:

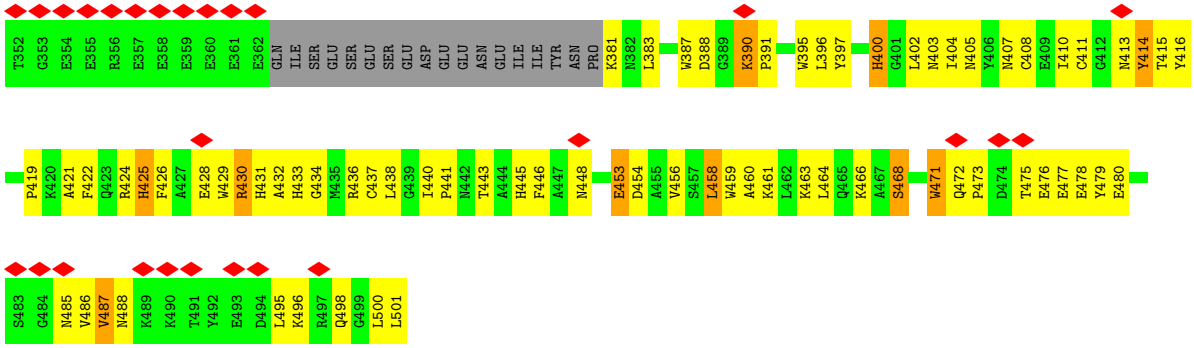


• Molecule 27: Splicing factor 3A subunit 3

Chain w:

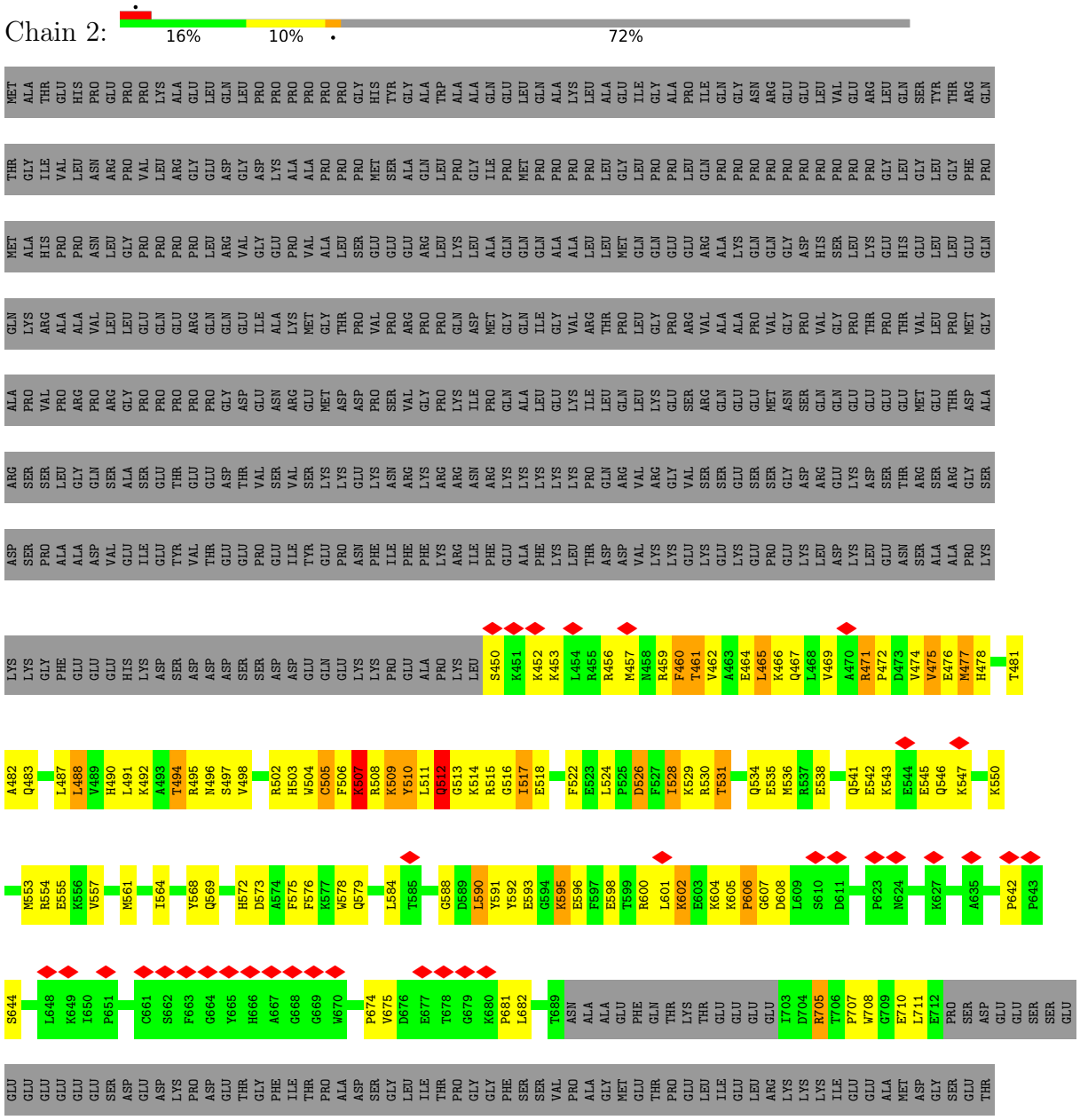


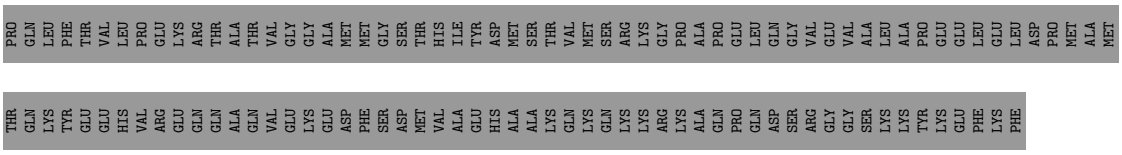




- Molecule 28: Splicing factor 3B subunit 2

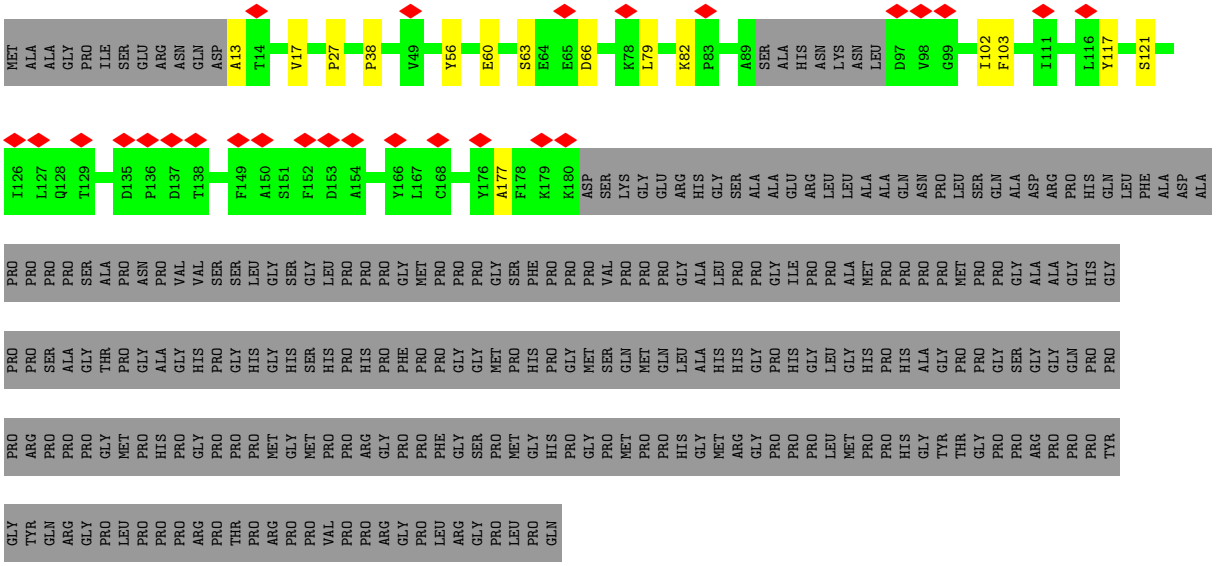
Chain 2:





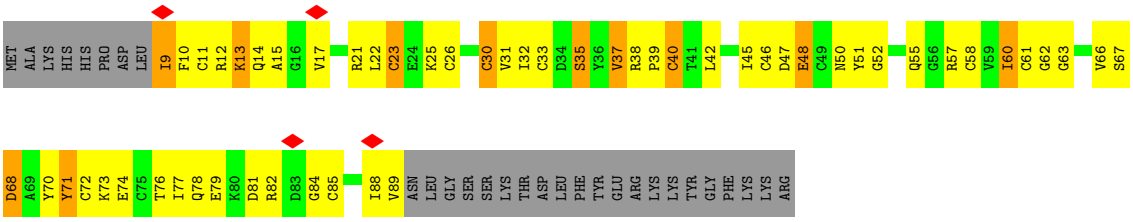
- Molecule 29: Splicing factor 3B subunit 4

Chain 4:



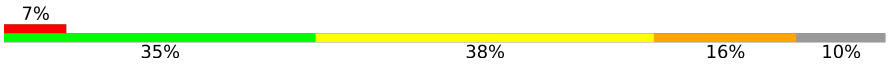
- Molecule 30: PHD finger-like domain-containing protein 5A

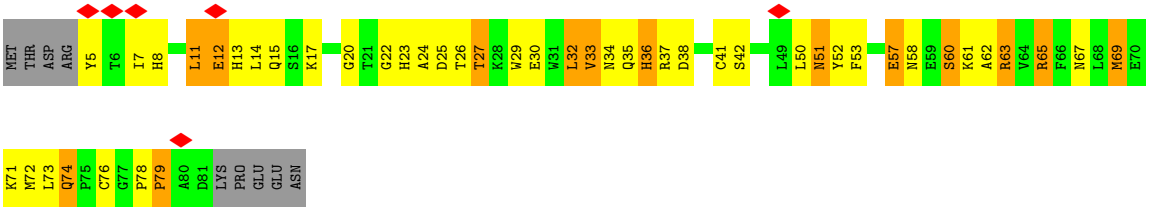
Chain 7:



- Molecule 31: Splicing factor 3B subunit 5

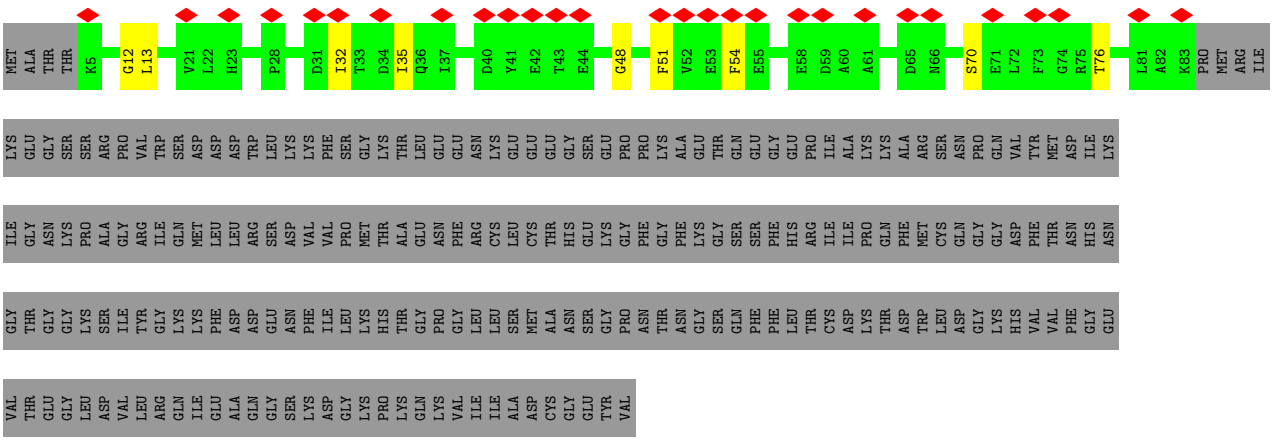
Chain 5:





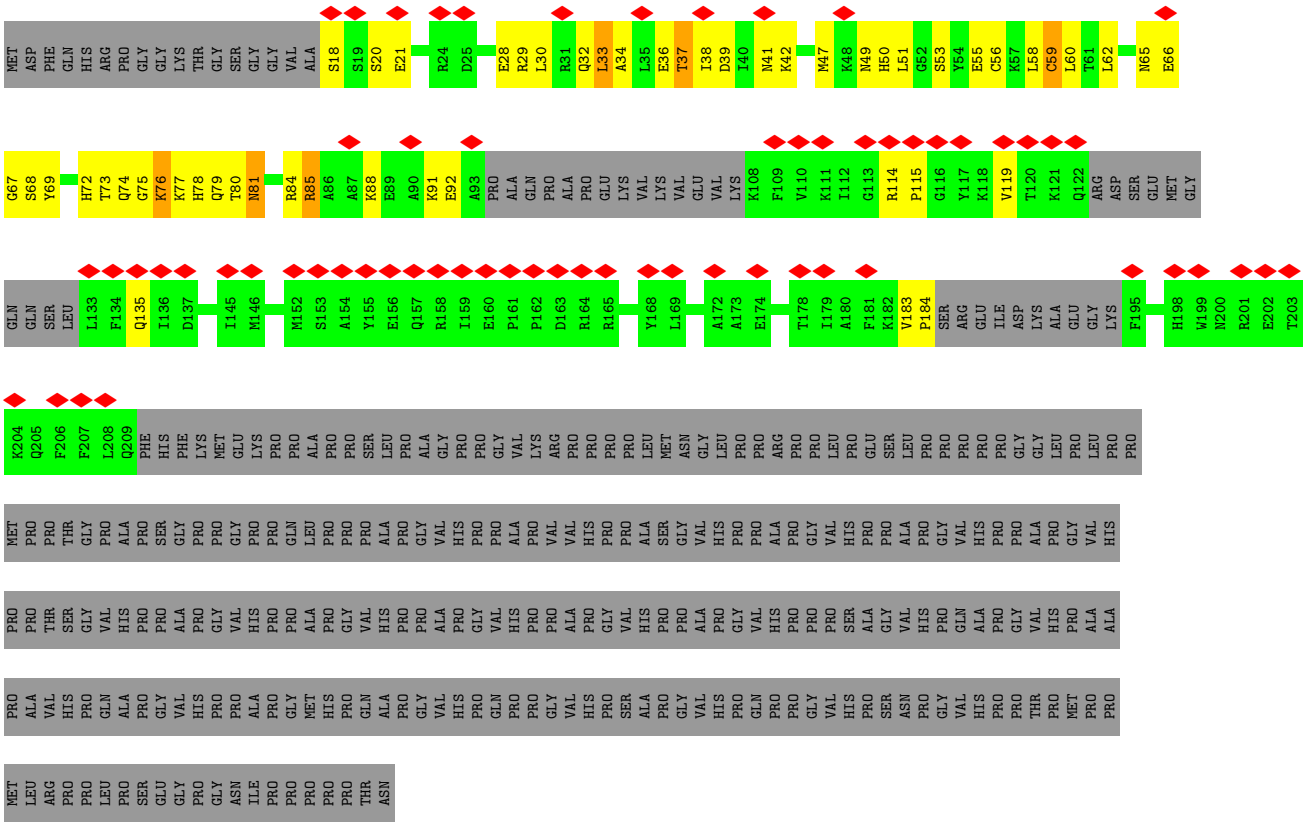
- Molecule 32: Peptidyl-prolyl cis-trans isomerase E

Chain y:



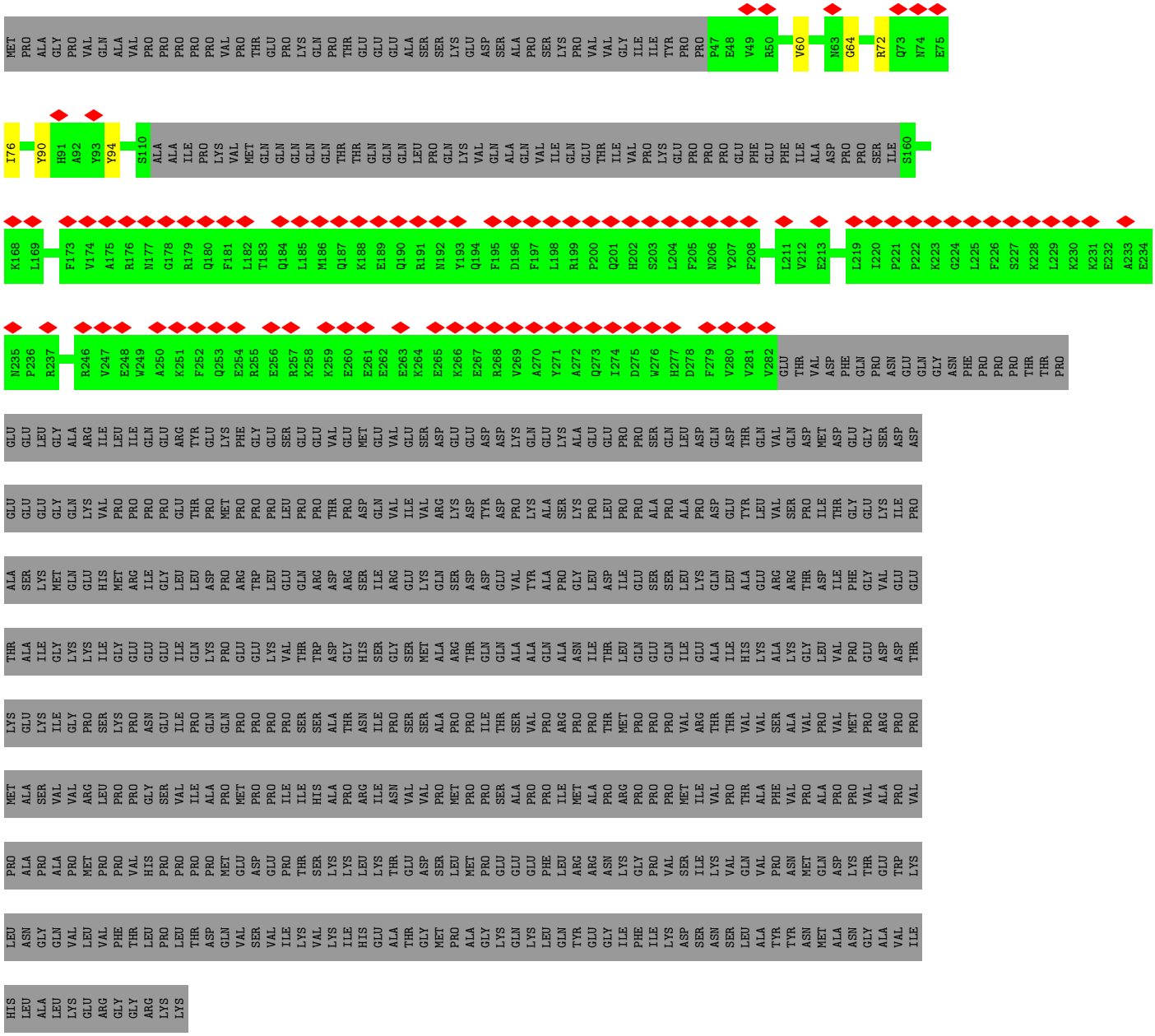
- Molecule 33: Splicing factor 3A subunit 2

Chain v:



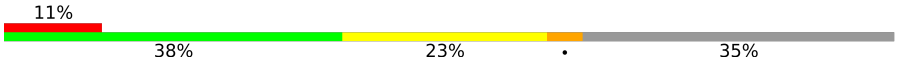
- Molecule 34: Splicing factor 3A subunit 1

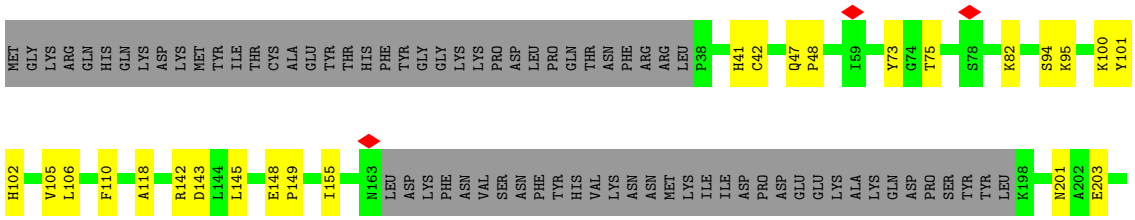
Chain u:

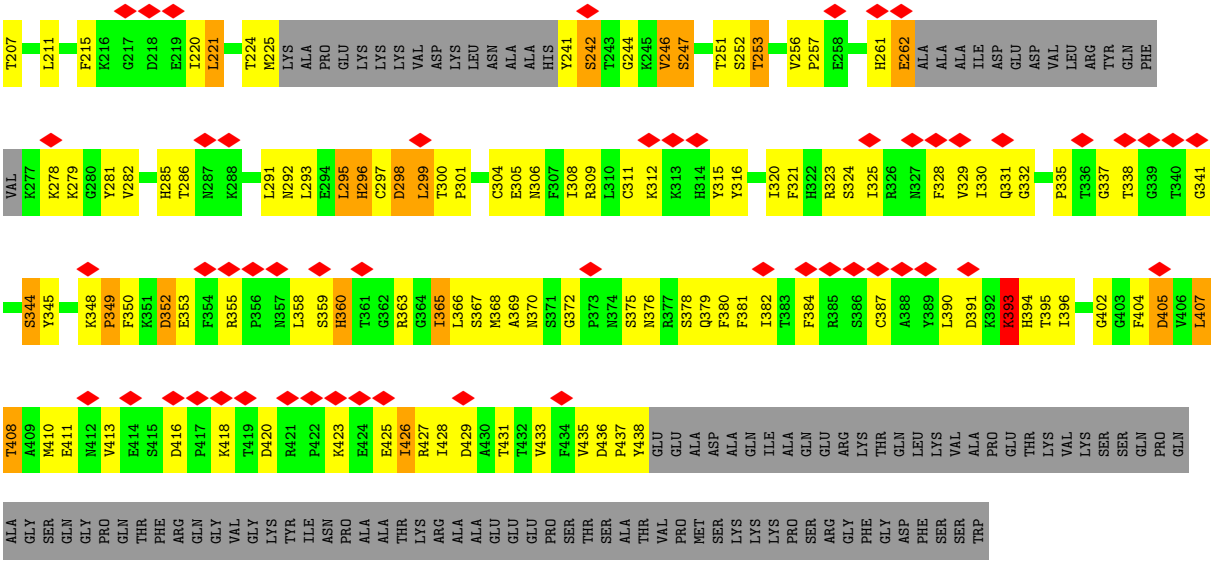


• Molecule 35: RING-type E3 ubiquitin-protein ligase PPIL2

Chain 9:

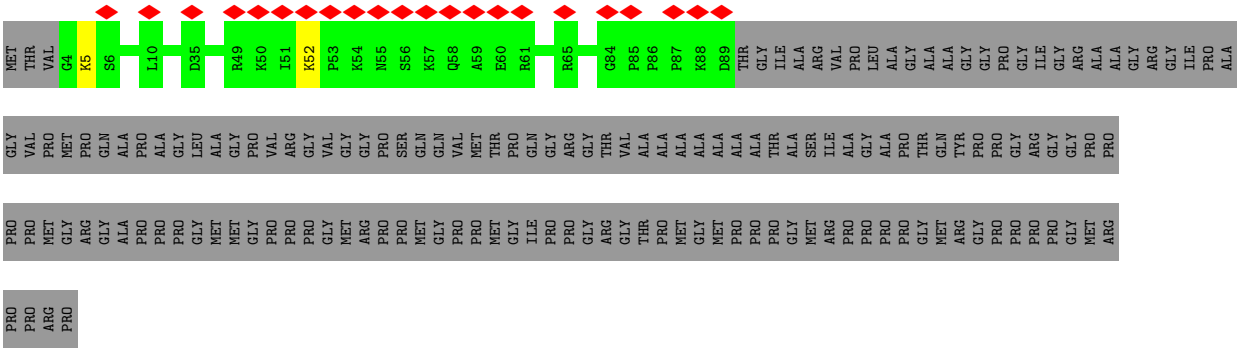






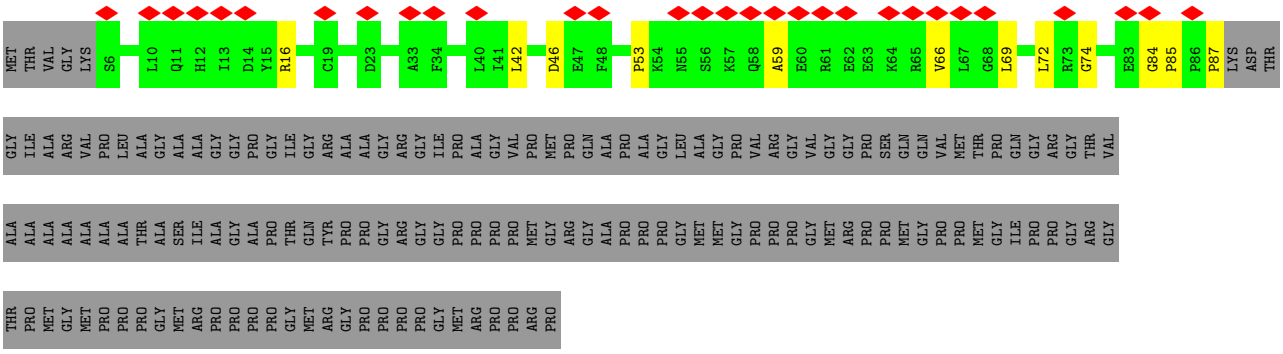
- Molecule 36: Small nuclear ribonucleoprotein-associated proteins B and B'

Chain a:



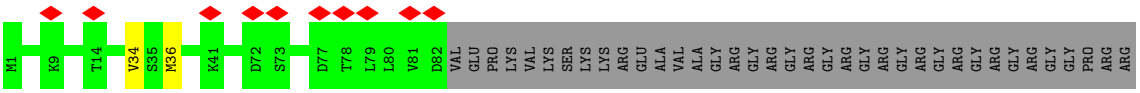
- Molecule 36: Small nuclear ribonucleoprotein-associated proteins B and B'

Chain m:



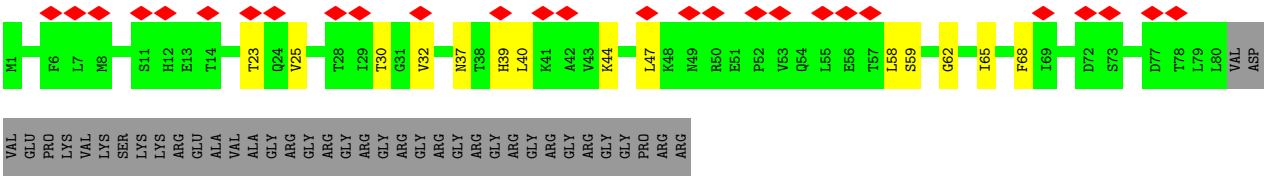
- Molecule 37: Small nuclear ribonucleoprotein Sm D1

Chain b:



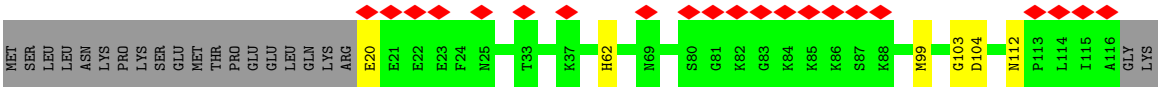
• Molecule 37: Small nuclear ribonucleoprotein Sm D1

Chain n:



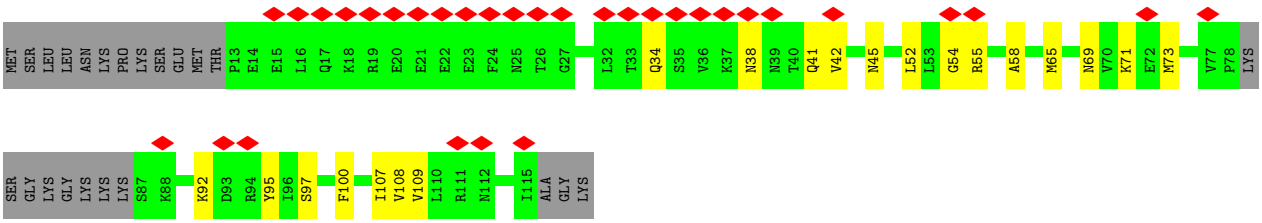
• Molecule 38: Small nuclear ribonucleoprotein Sm D2

Chain c:



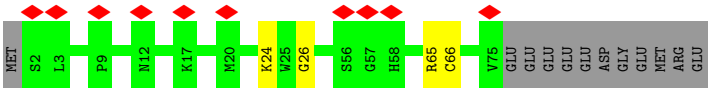
• Molecule 38: Small nuclear ribonucleoprotein Sm D2

Chain h:



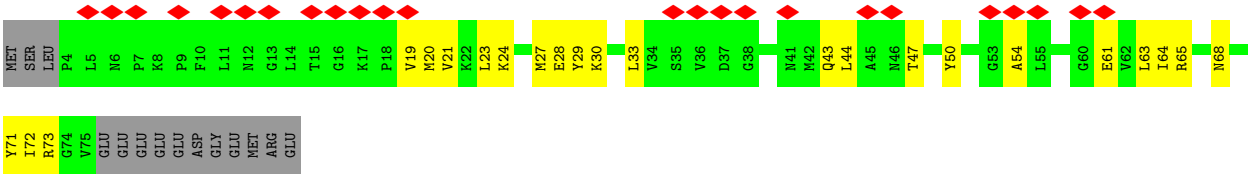
• Molecule 39: Small nuclear ribonucleoprotein F

Chain d:



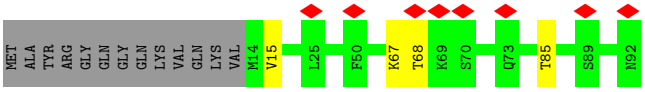
• Molecule 39: Small nuclear ribonucleoprotein F

Chain i:



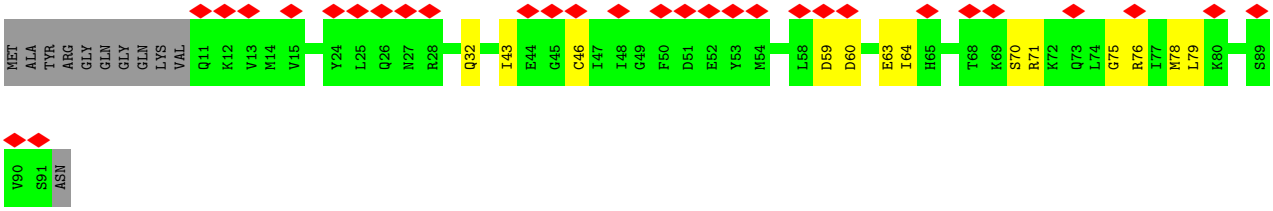
- Molecule 40: Small nuclear ribonucleoprotein E

Chain e:



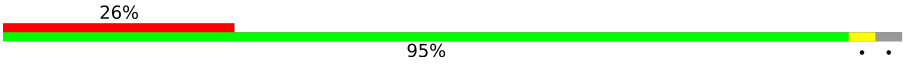
- Molecule 40: Small nuclear ribonucleoprotein E

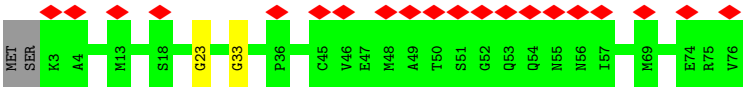
Chain j:



- Molecule 41: Small nuclear ribonucleoprotein G

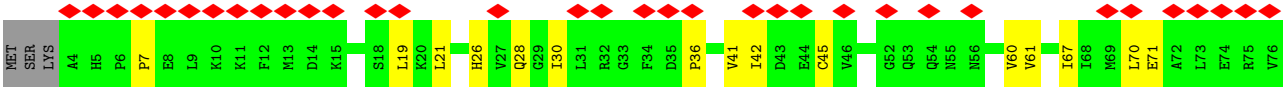
Chain f:





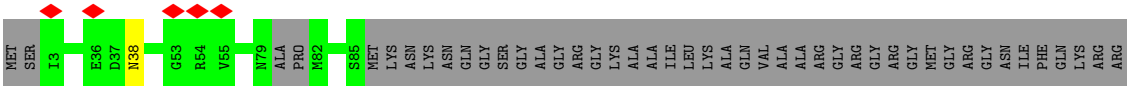
- Molecule 41: Small nuclear ribonucleoprotein G

Chain k:



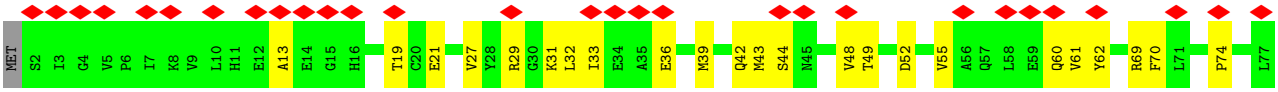
- Molecule 42: Small nuclear ribonucleoprotein Sm D3

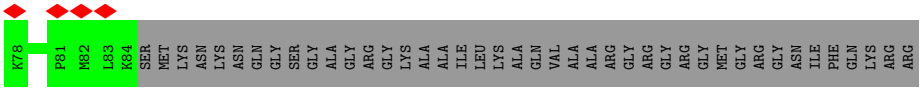
Chain g:



- Molecule 42: Small nuclear ribonucleoprotein Sm D3

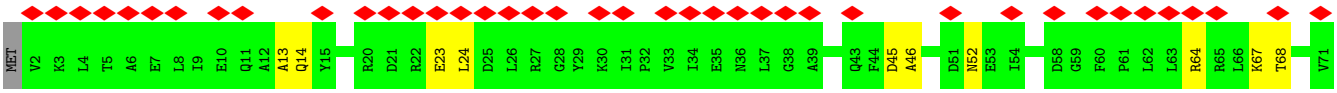
Chain l:

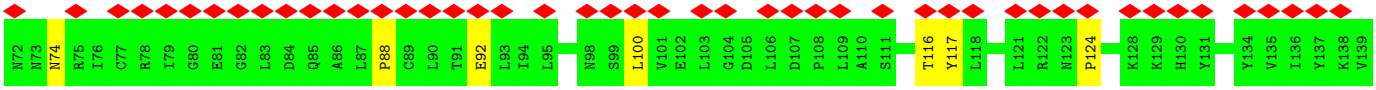


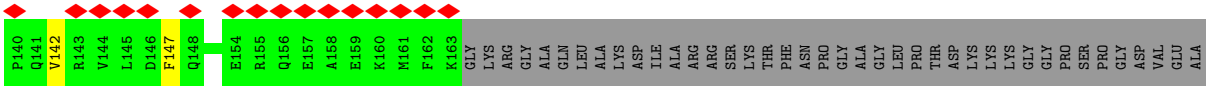


• Molecule 43: U2 small nuclear ribonucleoprotein A'

Chain o:







4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	13372	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.423	Depositor
Minimum map value	-0.641	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.057	Depositor
Recommended contour level	0.23	Depositor
Map size (Å)	516.96, 516.96, 516.96	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.077, 1.077, 1.077	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: IHP, GTP, ZN, MG, SEP

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	0.87	3/18048 (0.0%)	0.84	26/24520 (0.1%)
2	B	0.56	0/2303	0.49	0/3579
3	C	0.33	0/6873	0.65	3/9346 (0.0%)
4	D	0.24	0/8527	0.56	0/11887
5	E	0.27	0/2392	0.63	0/3242
6	F	0.72	0/2323	0.58	0/3619
7	G	0.49	0/1673	0.64	0/2597
8	H	0.42	0/3947	0.60	9/6138 (0.1%)
9	I	0.49	3/2898 (0.1%)	0.83	7/4057 (0.2%)
10	J	0.36	0/2171	0.63	0/2929
11	K	0.52	0/404	0.68	0/541
12	L	0.57	1/1430 (0.1%)	0.66	0/1915
13	N	0.76	2/1200 (0.2%)	1.04	4/1611 (0.2%)
14	O	0.27	0/1432	0.59	0/1992
15	P	0.68	0/888	0.76	0/1177
16	Q	0.22	0/6796	0.50	2/9527 (0.0%)
17	R	0.46	0/2789	0.66	0/3747
18	S	0.22	0/769	0.57	0/1063
19	T	0.81	0/2574	0.74	0/3511
20	U	0.47	0/424	0.63	0/582
21	V	0.39	1/2993 (0.0%)	0.61	0/4088
22	X	0.38	1/6479 (0.0%)	0.66	0/8747
23	Y	0.33	0/2605	0.66	2/3522 (0.1%)
24	1	0.56	0/6591	0.74	2/8926 (0.0%)
25	3	0.51	4/9398 (0.0%)	0.80	15/12755 (0.1%)
26	p	0.22	0/847	0.49	0/1181
27	w	0.25	0/2311	0.54	0/3008
28	2	0.51	0/1833	0.78	1/2468 (0.0%)
29	4	0.22	0/790	0.54	0/1095
30	7	0.46	0/621	0.74	0/833
31	5	0.65	0/654	0.78	0/885
32	y	0.24	0/389	0.52	0/540

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	v	0.37	0/976	0.62	0/1282
34	u	0.22	0/842	0.43	0/1110
35	9	0.27	0/2342	0.61	2/3182 (0.1%)
36	a	0.87	0/343	1.20	3/427 (0.7%)
36	m	0.23	0/416	0.58	0/581
37	b	0.89	0/327	1.11	0/407
37	n	0.24	0/404	0.57	0/564
38	c	1.15	0/387	1.22	1/482 (0.2%)
38	h	0.21	0/485	0.46	0/677
39	d	1.23	0/295	1.26	0/367
39	i	0.23	0/362	0.52	0/502
40	e	1.03	0/315	1.27	1/392 (0.3%)
40	j	0.22	0/403	0.49	0/561
41	f	0.87	0/295	1.05	0/367
41	k	0.24	0/366	0.54	0/509
42	g	0.80	0/322	1.01	0/399
42	l	0.23	0/417	0.55	0/581
43	o	0.21	0/821	0.55	0/1149
All	All	0.54	15/115490 (0.0%)	0.70	78/159167 (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
1	A	0	15
3	C	0	6
4	D	0	2
9	I	0	4
10	J	0	3
11	K	0	1
12	L	0	2
13	N	0	1
15	P	0	2
16	Q	0	2
17	R	0	1
18	S	0	1
22	X	0	1
23	Y	0	3
24	1	0	3
25	3	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
28	2	0	1
30	7	0	1
31	5	0	1
35	9	0	2
38	c	0	1
All	All	0	58

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	N	36	PRO	N-CA	19.82	1.71	1.47
9	I	110	PRO	N-CA	17.78	1.70	1.47
25	3	570	PRO	N-CA	13.77	1.65	1.47
13	N	35	GLU	C-N	9.45	1.45	1.33
1	A	385	GLU	C-N	7.47	1.51	1.33

The worst 5 of 78 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	N	35	GLU	CA-C-N	18.64	138.96	119.76
13	N	35	GLU	C-N-CA	18.64	138.96	119.76
9	I	109	MET	CA-C-N	17.98	142.32	119.84
9	I	109	MET	C-N-CA	17.98	142.32	119.84
25	3	569	ASP	CA-C-N	16.69	140.70	119.84

There are no chirality outliers.

5 of 58 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	MET	Peptide
1	A	187	PRO	Peptide
1	A	203	VAL	Peptide
1	A	376	GLU	Peptide
1	A	467	GLN	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	17607	0	16789	953	0
2	B	2066	0	1047	106	0
3	C	6724	0	6697	506	0
4	D	8528	0	3745	125	0
5	E	2338	0	2275	174	0
6	F	2075	0	1048	133	0
7	G	1503	0	766	165	0
8	H	3539	0	1791	180	0
9	I	2880	0	1411	41	0
10	J	2116	0	1977	123	0
11	K	392	0	343	49	0
12	L	1403	0	1431	98	0
13	N	1174	0	1168	103	0
14	O	1432	0	632	26	0
15	P	876	0	875	60	0
16	Q	6730	0	3268	69	0
17	R	2760	0	2639	298	0
18	S	770	0	356	20	0
19	T	2507	0	2451	118	0
20	U	422	0	291	31	0
21	V	2959	0	2237	131	0
22	X	6357	0	6349	581	0
23	Y	2556	0	2492	269	0
24	1	6468	0	6657	433	0
25	3	9210	0	9124	705	0
26	p	841	0	420	24	0
27	w	2275	0	1347	136	0
28	2	1803	0	1618	228	0
29	4	792	0	367	15	0
30	7	613	0	597	52	0
31	5	635	0	595	52	0
32	y	390	0	190	5	0
33	v	964	0	735	100	0
34	u	834	0	325	3	0
35	9	2307	0	1898	146	0
36	a	344	0	93	0	0
36	m	413	0	194	7	0
37	b	328	0	89	5	0
37	n	402	0	184	8	0
38	c	388	0	102	7	0
38	h	482	0	220	13	0
39	d	296	0	87	10	0
39	i	359	0	179	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	e	316	0	85	4	0
40	j	403	0	173	8	0
41	f	296	0	84	5	0
41	k	364	0	176	11	0
42	g	324	0	89	4	0
42	l	415	0	198	15	0
43	o	816	0	386	11	0
44	A	36	0	6	8	0
45	C	32	0	12	8	0
46	C	1	0	0	0	0
46	F	6	0	0	0	0
47	7	3	0	0	0	0
47	K	1	0	0	0	0
47	N	3	0	0	0	0
All	All	112874	0	88308	5357	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 27.

The worst 5 of 5357 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:w:387:TRP:CH2	33:v:84:ARG:HB2	1.26	1.61
1:A:2084:HIS:CB	4:D:1008:THR:CB	1.79	1.56
13:N:37:HIS:HB2	13:N:41:ARG:CB	1.10	1.52
1:A:2335:ALA:HA	4:D:592:LYS:CB	1.44	1.45
1:A:1889:LEU:HD12	1:A:2014:MET:N	1.21	1.44

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2216/2335 (95%)	1957 (88%)	246 (11%)	13 (1%)	21	58
3	C	854/972 (88%)	737 (86%)	110 (13%)	7 (1%)	16	52
4	D	1720/2136 (80%)	1585 (92%)	124 (7%)	11 (1%)	21	58
5	E	297/357 (83%)	271 (91%)	26 (9%)	0	100	100
9	I	563/855 (66%)	479 (85%)	79 (14%)	5 (1%)	14	49
10	J	245/848 (29%)	214 (87%)	28 (11%)	3 (1%)	10	42
11	K	44/343 (13%)	39 (89%)	5 (11%)	0	100	100
12	L	165/802 (21%)	142 (86%)	23 (14%)	0	100	100
13	N	141/144 (98%)	124 (88%)	17 (12%)	0	100	100
14	O	285/420 (68%)	239 (84%)	46 (16%)	0	100	100
15	P	97/229 (42%)	86 (89%)	9 (9%)	2 (2%)	5	30
16	Q	1319/1485 (89%)	1208 (92%)	111 (8%)	0	100	100
17	R	352/536 (66%)	314 (89%)	36 (10%)	2 (1%)	21	58
18	S	156/166 (94%)	147 (94%)	9 (6%)	0	100	100
19	T	318/514 (62%)	289 (91%)	29 (9%)	0	100	100
20	U	68/2752 (2%)	62 (91%)	6 (9%)	0	100	100
21	V	458/908 (50%)	430 (94%)	28 (6%)	0	100	100
22	X	778/1041 (75%)	692 (89%)	82 (10%)	4 (0%)	24	62
23	Y	318/492 (65%)	277 (87%)	41 (13%)	0	100	100
24	1	814/1304 (62%)	706 (87%)	104 (13%)	4 (0%)	24	62
25	3	1165/1217 (96%)	991 (85%)	172 (15%)	2 (0%)	43	77
26	p	163/225 (72%)	147 (90%)	15 (9%)	1 (1%)	21	58
27	w	428/501 (85%)	381 (89%)	47 (11%)	0	100	100
28	2	246/895 (28%)	210 (85%)	31 (13%)	5 (2%)	6	32
29	4	157/424 (37%)	138 (88%)	19 (12%)	0	100	100
30	7	79/110 (72%)	65 (82%)	14 (18%)	0	100	100
31	5	75/86 (87%)	64 (85%)	11 (15%)	0	100	100
32	y	77/301 (26%)	64 (83%)	13 (17%)	0	100	100
33	v	150/464 (32%)	134 (89%)	16 (11%)	0	100	100
34	u	183/793 (23%)	170 (93%)	13 (7%)	0	100	100
35	9	330/520 (64%)	292 (88%)	38 (12%)	0	100	100
36	a	84/240 (35%)	82 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	m	80/240 (33%)	72 (90%)	8 (10%)	0	100	100
37	b	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
37	n	78/119 (66%)	67 (86%)	11 (14%)	0	100	100
38	c	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
38	h	91/118 (77%)	82 (90%)	9 (10%)	0	100	100
39	d	72/86 (84%)	69 (96%)	3 (4%)	0	100	100
39	i	70/86 (81%)	64 (91%)	6 (9%)	0	100	100
40	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
40	j	79/92 (86%)	73 (92%)	6 (8%)	0	100	100
41	f	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
41	k	71/76 (93%)	63 (89%)	8 (11%)	0	100	100
42	g	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
42	l	81/126 (64%)	70 (86%)	11 (14%)	0	100	100
43	o	160/255 (63%)	136 (85%)	24 (15%)	0	100	100
All	All	15528/26144 (59%)	13822 (89%)	1647 (11%)	59 (0%)	31	66

5 of 59 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	1258	VAL
9	I	139	ALA
17	R	164	PRO
17	R	223	PRO
24	1	1106	ARG

5.3.2 Protein sidechains (i)

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	1762/2108 (84%)	1441 (82%)	321 (18%)	2	11
3	C	747/866 (86%)	614 (82%)	133 (18%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	256/300 (85%)	212 (83%)	44 (17%)	2	12
9	I	22/749 (3%)	22 (100%)	0	100	100
10	J	205/751 (27%)	175 (85%)	30 (15%)	3	15
11	K	41/294 (14%)	36 (88%)	5 (12%)	5	19
12	L	141/709 (20%)	118 (84%)	23 (16%)	2	13
13	N	128/130 (98%)	108 (84%)	20 (16%)	2	14
14	O	3/361 (1%)	3 (100%)	0	100	100
15	P	95/203 (47%)	77 (81%)	18 (19%)	1	10
16	Q	71/1336 (5%)	71 (100%)	0	100	100
17	R	268/458 (58%)	213 (80%)	55 (20%)	1	8
19	T	273/441 (62%)	216 (79%)	57 (21%)	1	7
20	U	21/2432 (1%)	18 (86%)	3 (14%)	3	16
21	V	188/838 (22%)	150 (80%)	38 (20%)	1	9
22	X	682/897 (76%)	573 (84%)	109 (16%)	2	13
23	Y	286/451 (63%)	235 (82%)	51 (18%)	2	11
24	1	697/1104 (63%)	572 (82%)	125 (18%)	2	11
25	3	1016/1051 (97%)	789 (78%)	227 (22%)	1	6
26	p	8/195 (4%)	8 (100%)	0	100	100
27	w	112/446 (25%)	95 (85%)	17 (15%)	3	14
28	2	151/776 (20%)	123 (82%)	28 (18%)	1	10
30	7	69/95 (73%)	53 (77%)	16 (23%)	1	5
31	5	68/77 (88%)	48 (71%)	20 (29%)	0	2
33	v	73/382 (19%)	64 (88%)	9 (12%)	4	19
34	u	10/709 (1%)	10 (100%)	0	100	100
35	9	185/456 (41%)	159 (86%)	26 (14%)	3	16
36	m	4/177 (2%)	4 (100%)	0	100	100
37	n	3/101 (3%)	3 (100%)	0	100	100
38	h	5/110 (4%)	5 (100%)	0	100	100
39	i	4/74 (5%)	4 (100%)	0	100	100
40	j	1/84 (1%)	1 (100%)	0	100	100
41	k	3/66 (4%)	3 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	l	3/101 (3%)	3 (100%)	0	100	100
43	o	6/218 (3%)	6 (100%)	0	100	100
All	All	7607/19546 (39%)	6232 (82%)	1375 (18%)	3	11

5 of 1375 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	1	630	ARG
25	3	584	SER
24	1	844	VAL
24	1	610	ILE
25	3	52	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 192 such sidechains are listed below:

Mol	Chain	Res	Type
22	X	720	ASN
25	3	5	ASN
22	X	904	GLN
24	1	682	HIS
25	3	205	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	96/117 (82%)	29 (30%)	3 (3%)
6	F	96/107 (89%)	48 (50%)	4 (4%)
7	G	71/220 (32%)	44 (61%)	9 (12%)
8	H	163/188 (86%)	73 (44%)	6 (3%)
All	All	426/632 (67%)	194 (45%)	22 (5%)

5 of 194 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	9	G
2	B	10	U
2	B	20	G
2	B	21	A
2	B	22	U

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	G	111	U
8	H	18	U
8	H	13	C
8	H	43	U
6	F	58	G

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
17	SEP	R	224	17	8,9,10	1.47	1 (12%)	7,12,14	1.48	1 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
17	SEP	R	224	17	-	0/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	R	224	SEP	P-O1P	3.24	1.60	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
17	R	224	SEP	OG-CB-CA	3.45	111.50	108.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 16 ligands modelled in this entry, 14 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
45	GTP	C	1500	46	33,34,34	0.83	0	50,54,54	1.65	9 (18%)
44	IHP	A	3000	-	36,36,36	0.95	0	60,60,60	1.71	15 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
45	GTP	C	1500	46	-	4/22/38/38	0/3/3/3
44	IHP	A	3000	-	-	7/30/54/54	0/1/1/1

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
45	C	1500	GTP	C5-C4-N3	-5.47	119.69	128.39
45	C	1500	GTP	C2-N3-C4	4.97	120.86	112.30
44	A	3000	IHP	P4-O14-C4	-4.00	112.74	123.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
44	A	3000	IHP	C6-C5-C4	3.75	118.65	110.43
44	A	3000	IHP	C5-C4-C3	3.69	118.52	110.43

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
44	A	3000	IHP	C2-C1-O11-P1
44	A	3000	IHP	C4-C5-O15-P5
44	A	3000	IHP	C6-C5-O15-P5
45	C	1500	GTP	C4'-C5'-O5'-PA
45	C	1500	GTP	C3'-C4'-C5'-O5'

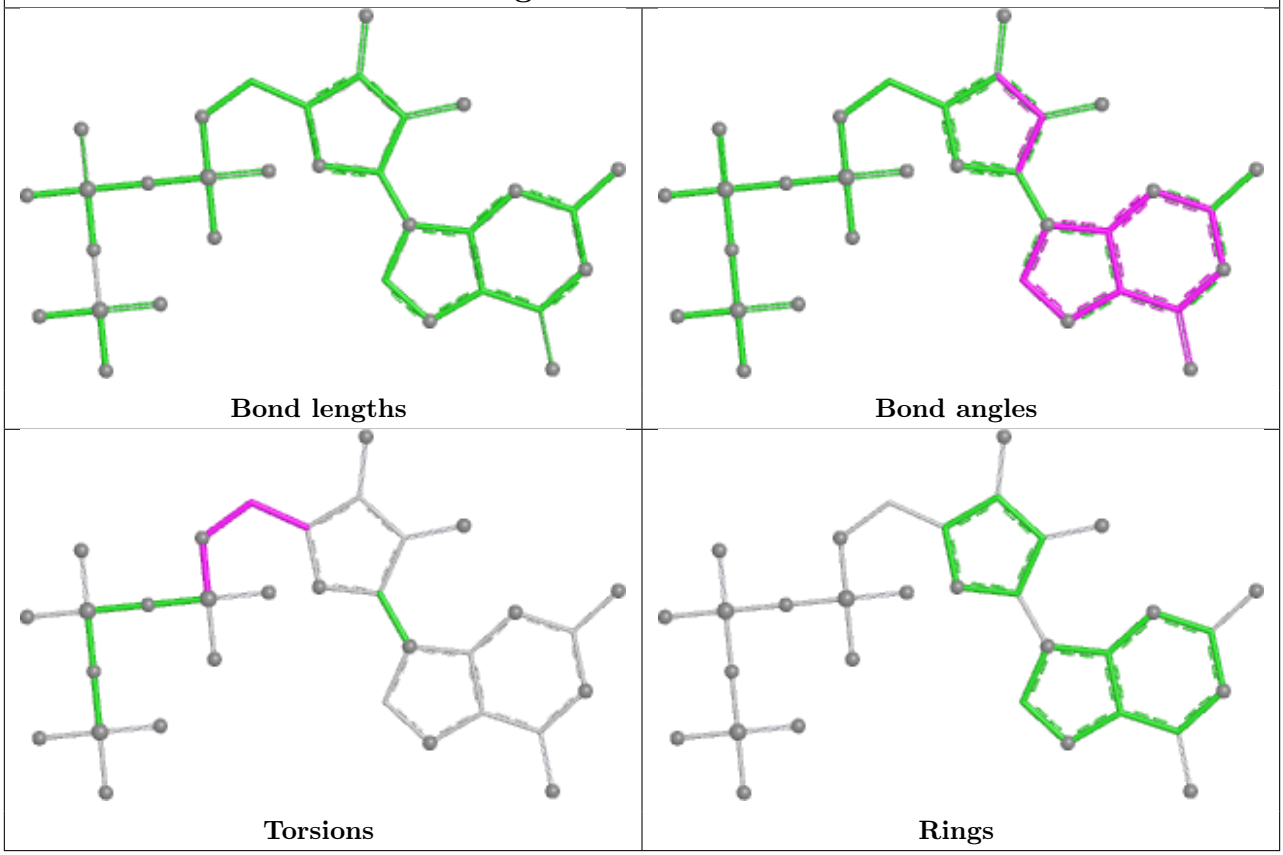
There are no ring outliers.

2 monomers are involved in 16 short contacts:

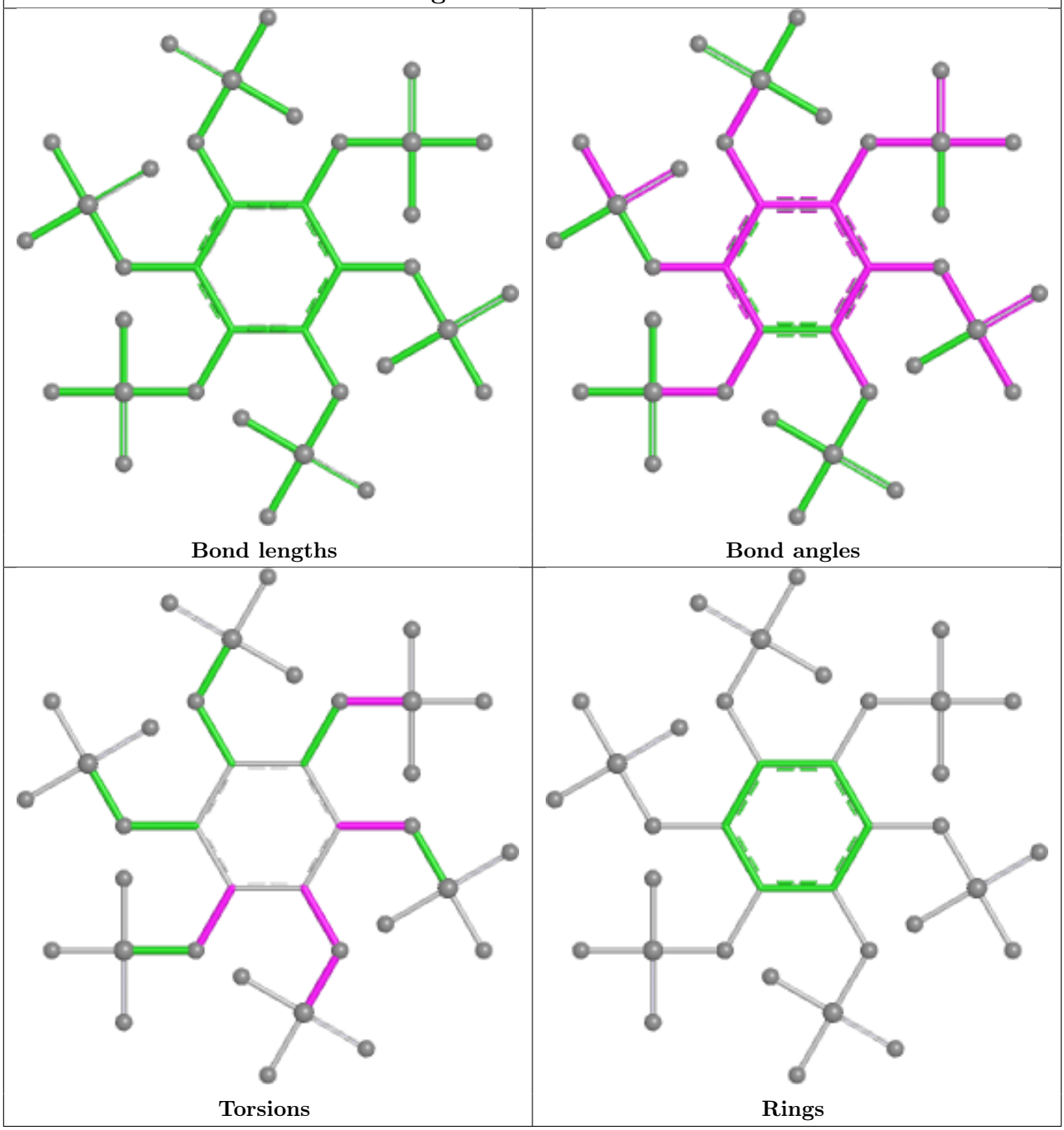
Mol	Chain	Res	Type	Clashes	Symm-Clashes
45	C	1500	GTP	8	0
44	A	3000	IHP	8	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand GTP C 1500



Ligand IHP A 3000



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

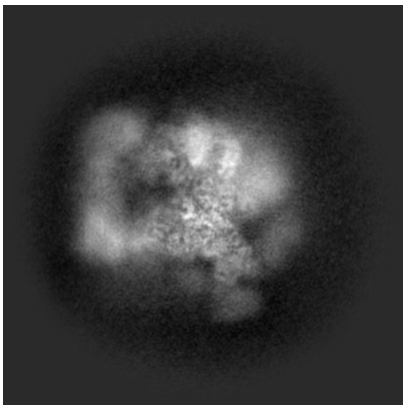
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-35108. These allow visual inspection of the internal detail of the map and identification of artifacts.

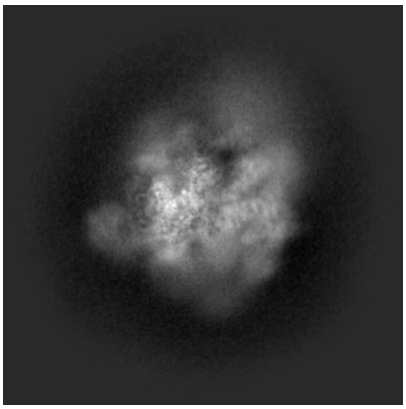
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

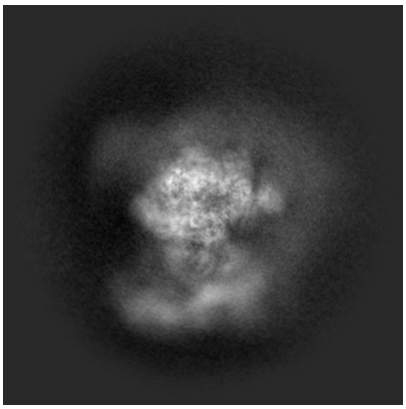
6.1.1 Primary map



X

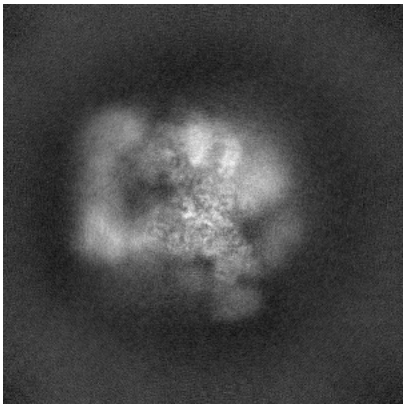


Y

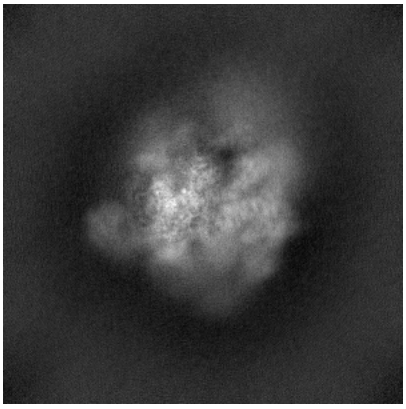


Z

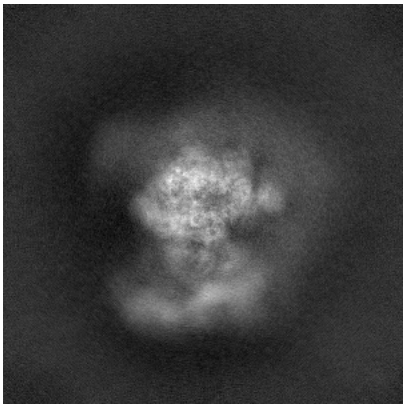
6.1.2 Raw map



X



Y

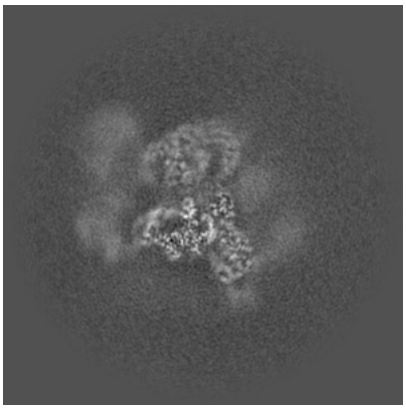


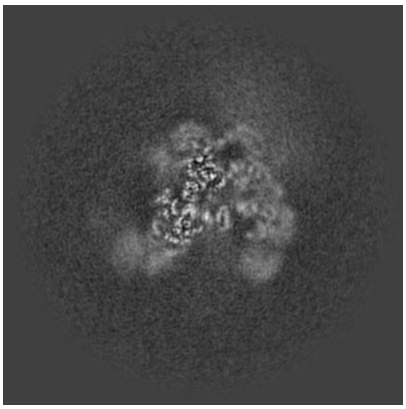
Z

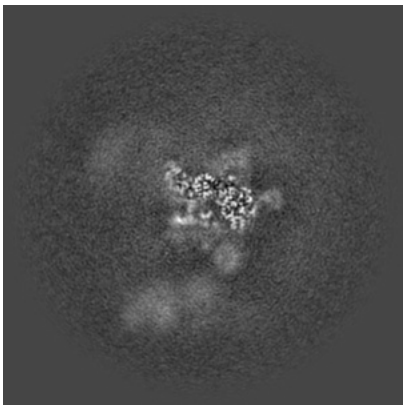
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

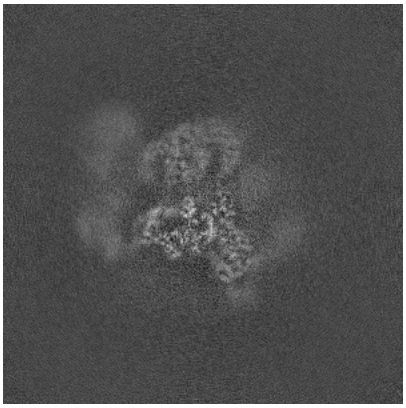
6.2.1 Primary map

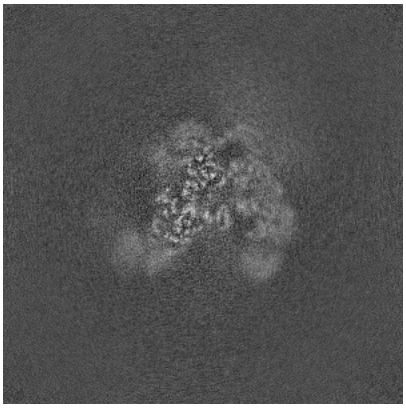

X Index: 240

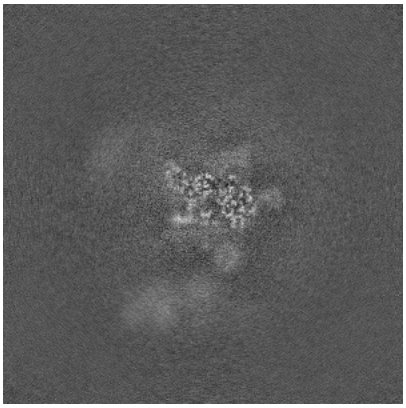

Y Index: 240


Z Index: 240

6.2.2 Raw map


X Index: 240

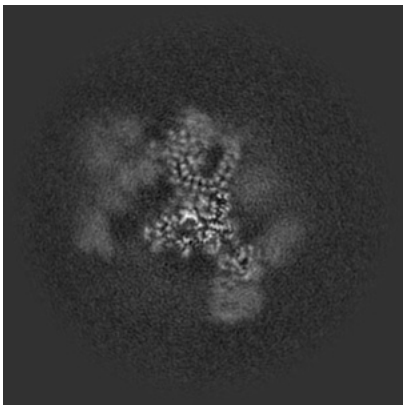

Y Index: 240


Z Index: 240

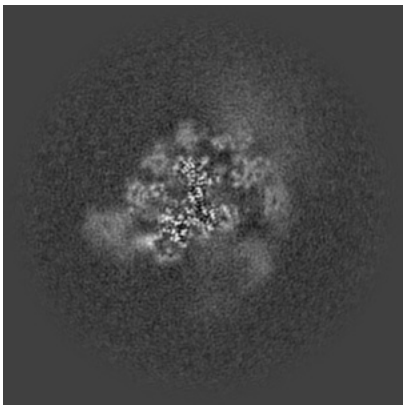
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

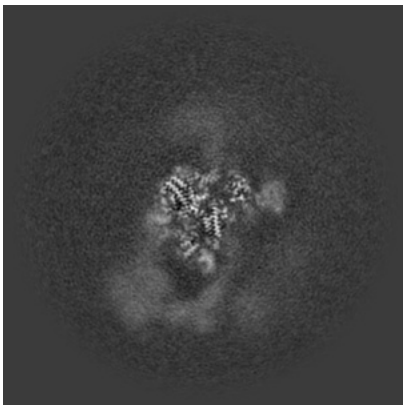
6.3.1 Primary map



X Index: 226

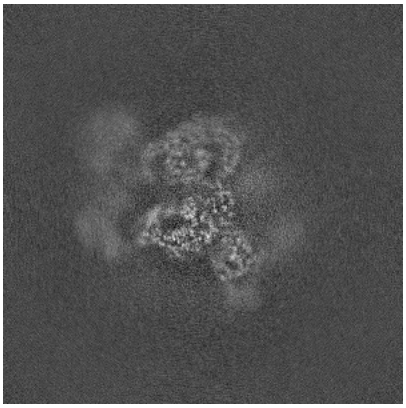


Y Index: 258

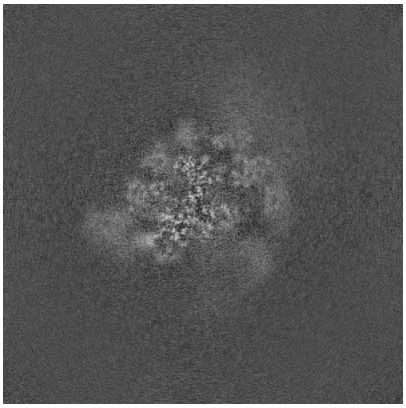


Z Index: 216

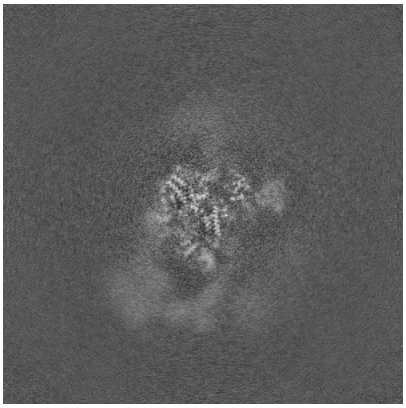
6.3.2 Raw map



X Index: 238



Y Index: 258

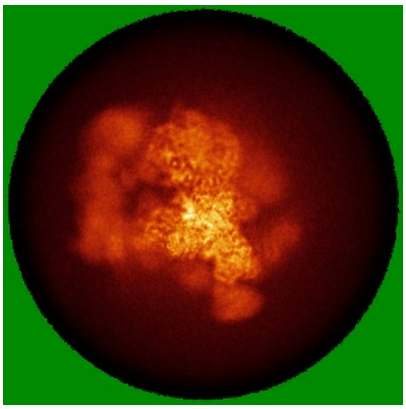


Z Index: 216

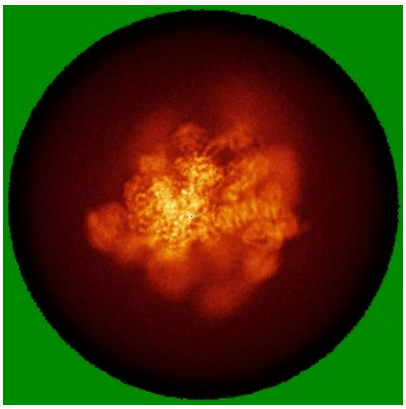
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

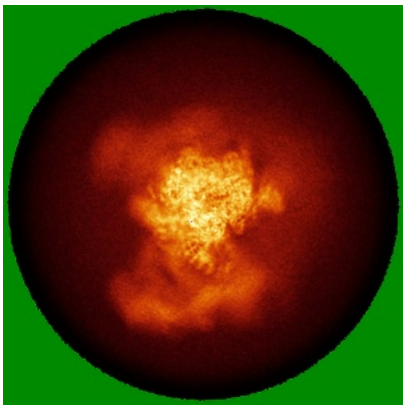
6.4.1 Primary map



X

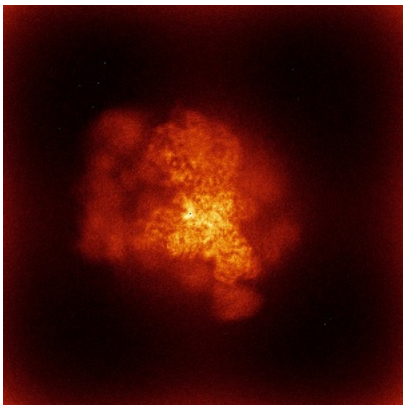


Y

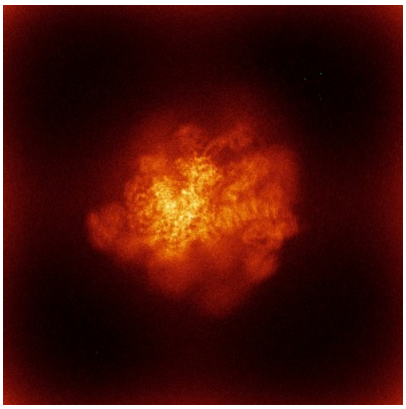


Z

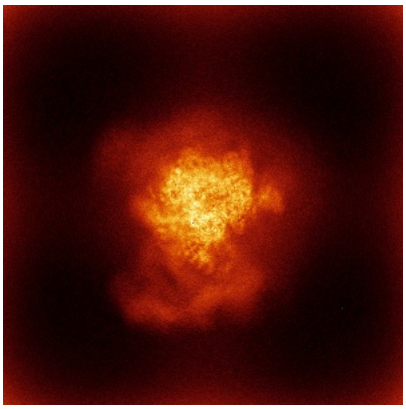
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

This section was not generated.

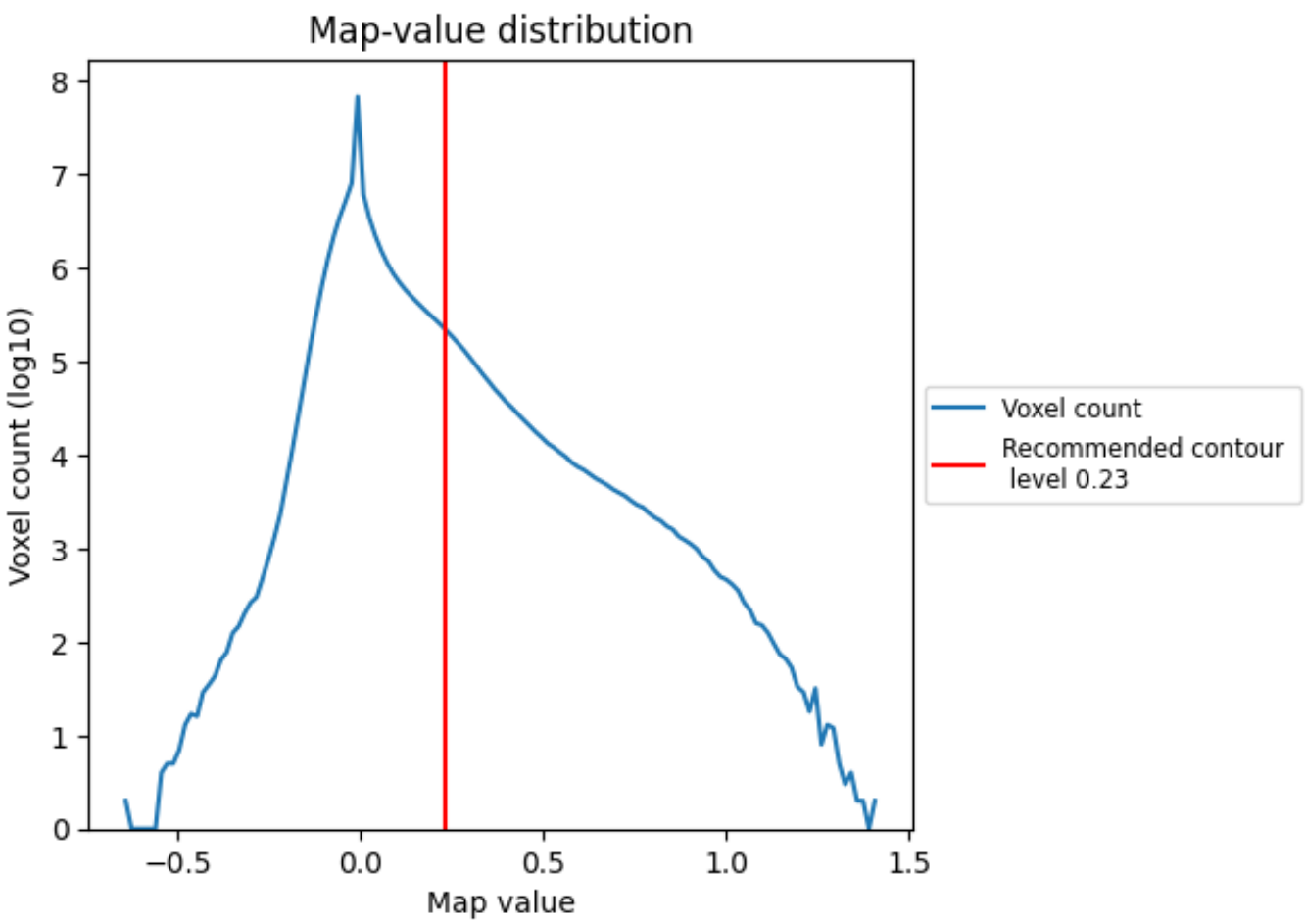
6.6 Mask visualisation (i)

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

7 Map analysis (i)

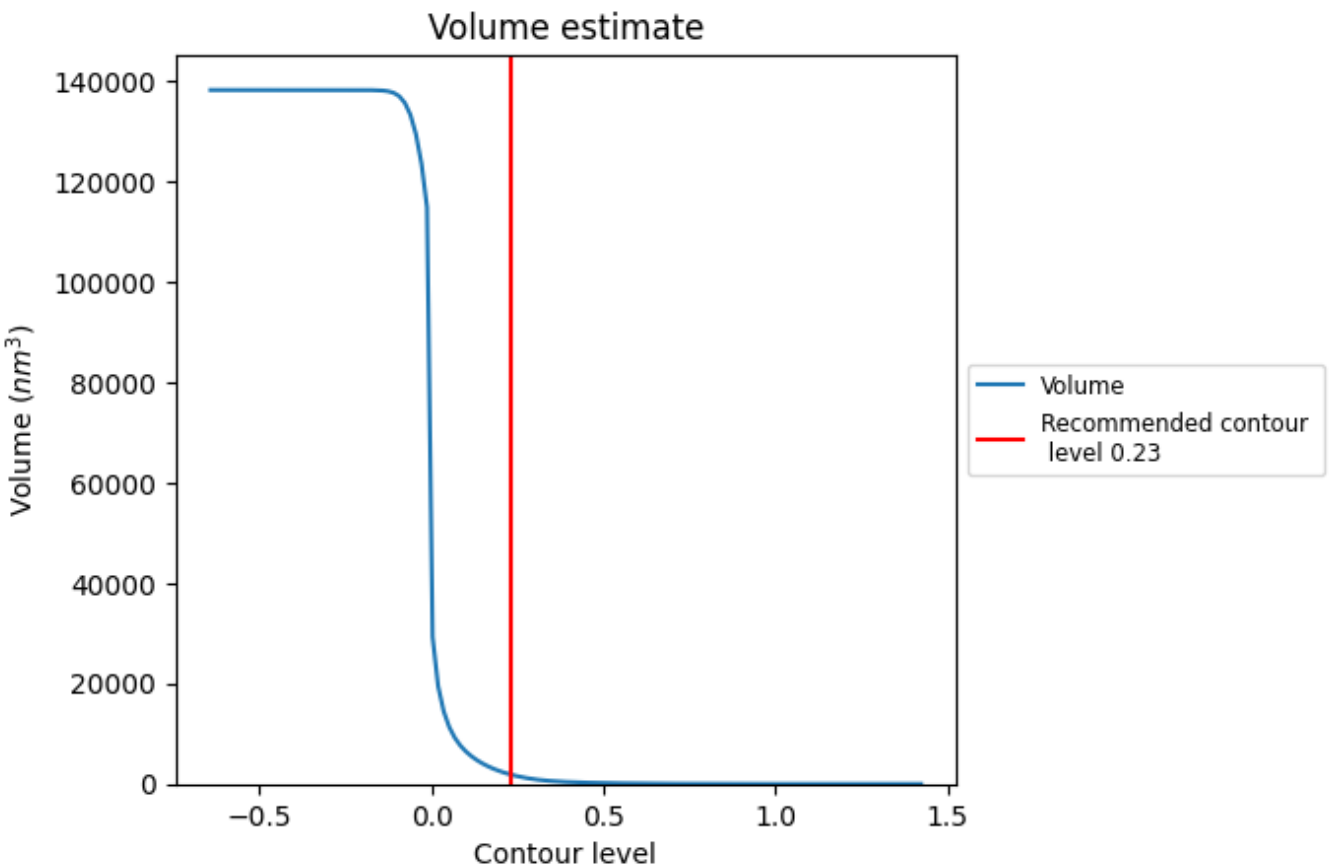
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

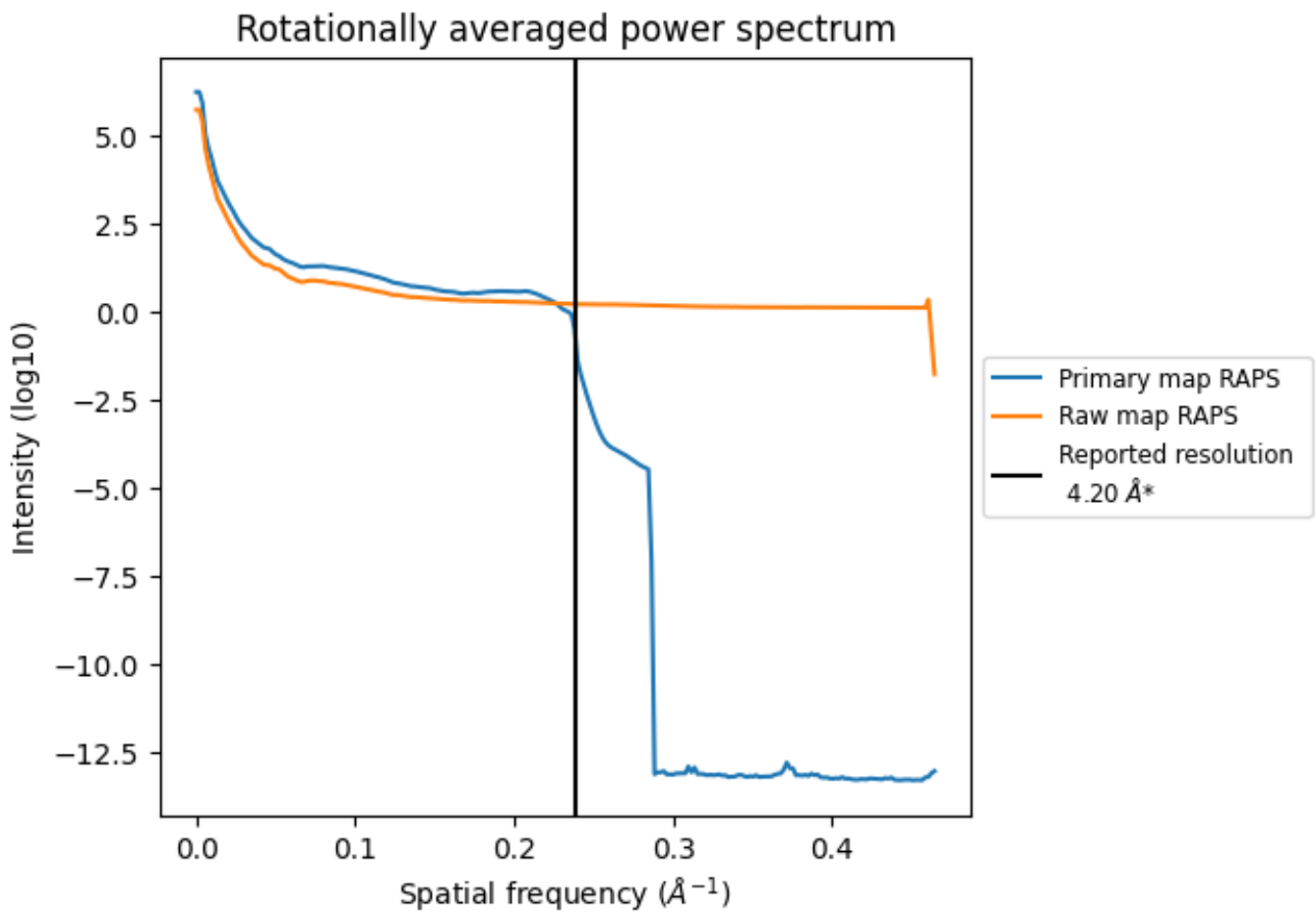
7.2 Volume estimate (i)



The volume at the recommended contour level is 1882 nm^3; this corresponds to an approximate mass of 1700 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 (i)

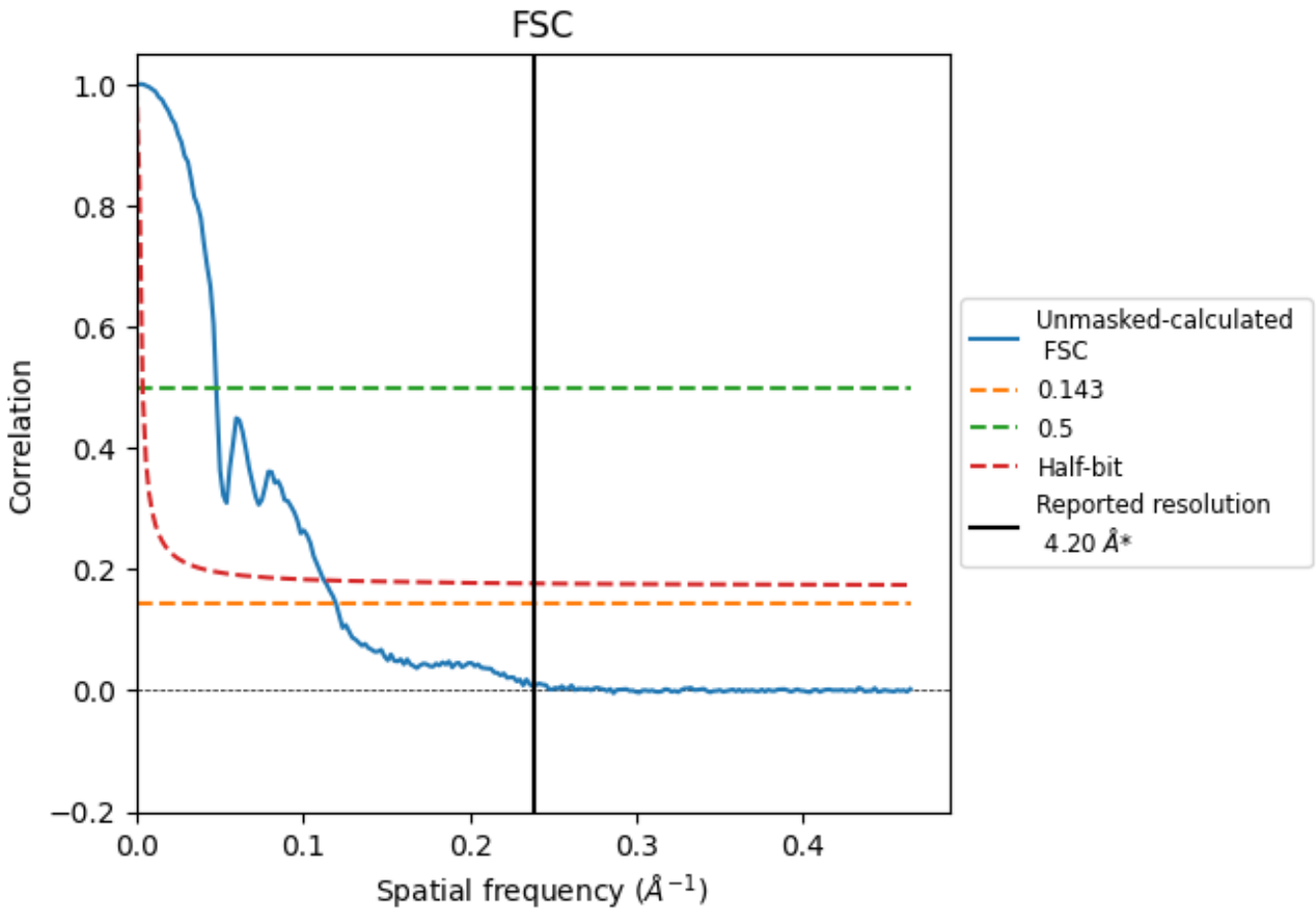


*Reported resolution corresponds to spatial frequency of 0.238 Å^{-1}

8 Fourier-Shell correlation (i)

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

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.238 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.35	20.83	8.88

*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 8.35 differs from the reported value 4.2 by more than 10 %

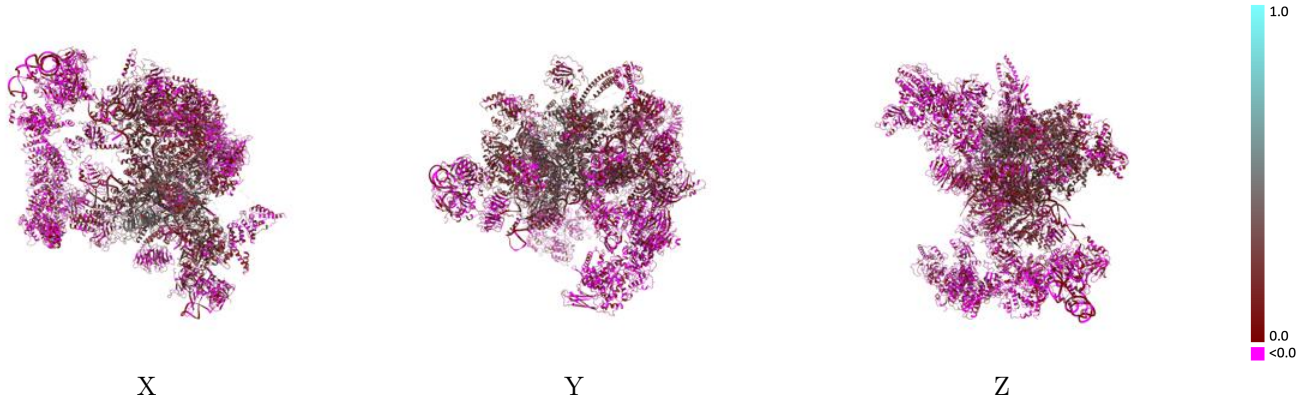
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-35108 and PDB model 8I0S. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay (i)

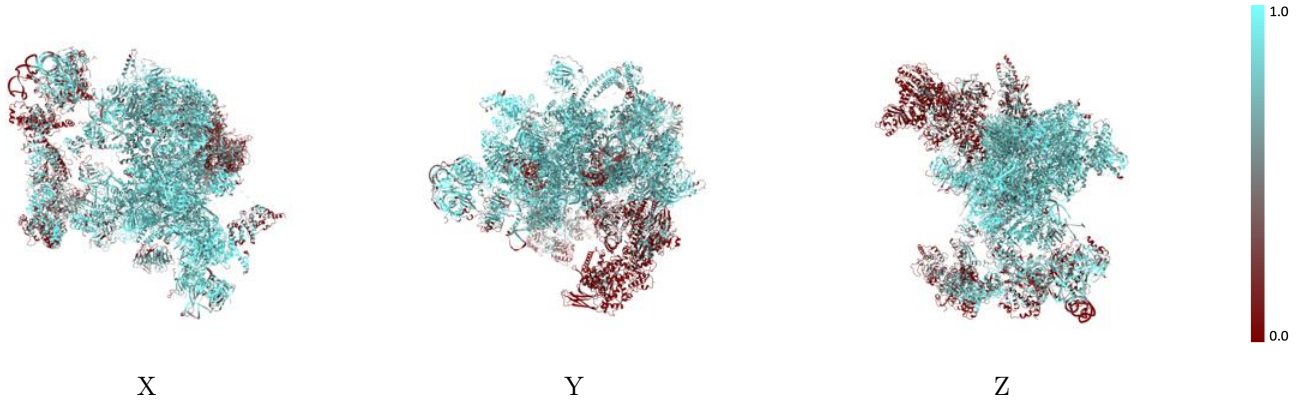
This section was not generated.

9.2 Q-score mapped to coordinate model (i)



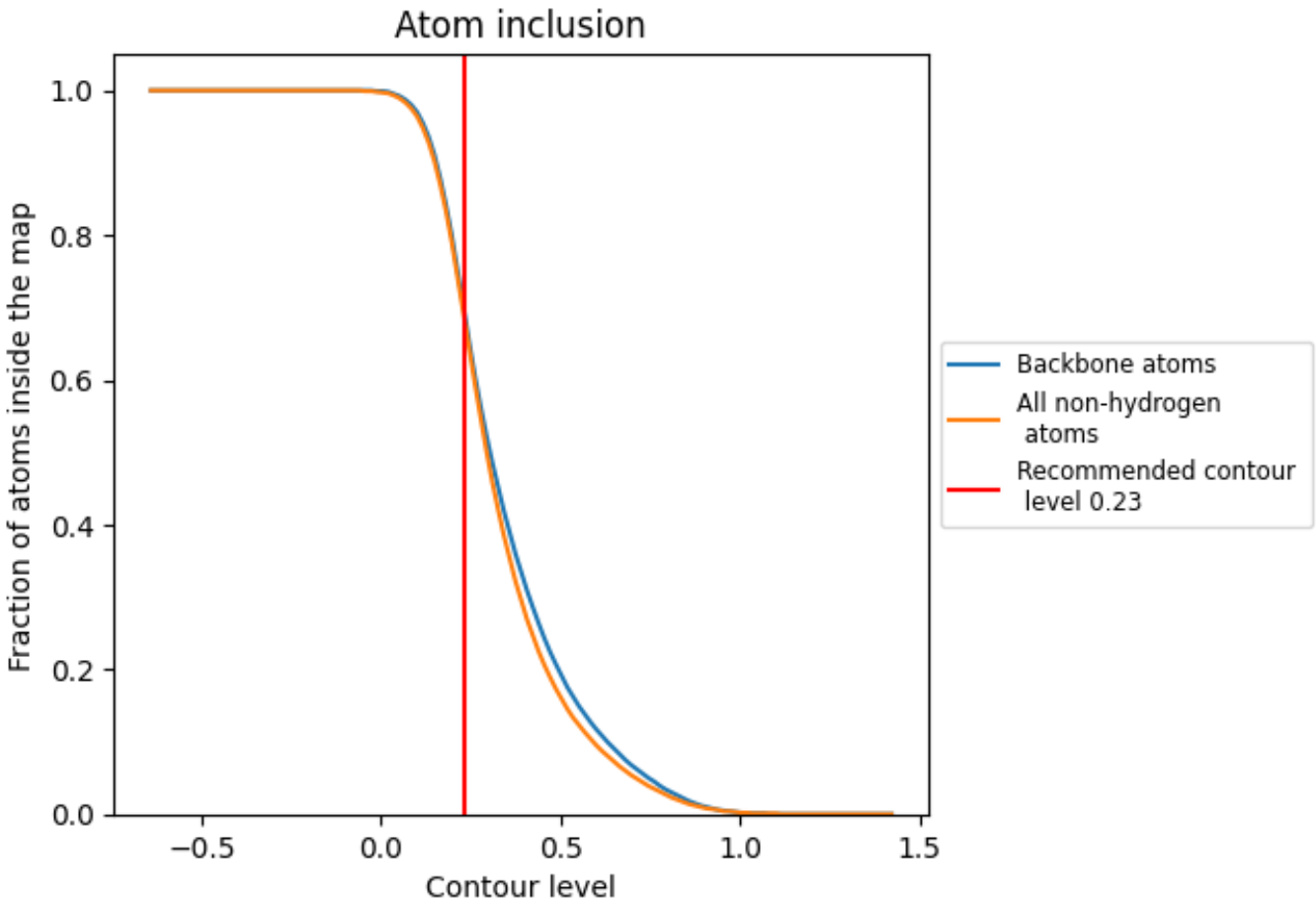
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.23).

9.4 Atom inclusion (i)



At the recommended contour level, 70% of all backbone atoms, 69% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.23) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6910	0.1500
1	0.8260	0.1670
2	0.7660	0.1690
3	0.8130	0.1010
4	0.7950	0.1090
5	0.7970	0.1510
7	0.8350	0.1360
9	0.7080	0.1070
A	0.7710	0.2800
B	0.8870	0.2130
C	0.8870	0.2460
D	0.1440	0.0090
E	0.5050	0.0060
F	0.8820	0.2120
G	0.8800	0.1740
H	0.6840	0.0940
I	0.6980	0.0410
J	0.8680	0.2330
K	0.7200	0.1860
L	0.7620	0.2020
N	0.7390	0.1910
O	0.7870	0.1710
P	0.8120	0.2930
Q	0.3560	0.0320
R	0.7710	0.2270
S	0.6420	0.0810
T	0.9300	0.4050
U	0.7620	0.2050
V	0.6430	0.1150
X	0.8030	0.1600
Y	0.8260	0.1320
a	0.7090	0.0930
b	0.8480	0.0790
c	0.7290	0.0670
d	0.7740	0.0580

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Chain	Atom inclusion	Q-score
e	0.8290	0.0740
f	0.6990	0.0610
g	0.8270	0.0670
h	0.6390	0.0150
i	0.6320	0.0050
j	0.6280	0.0460
k	0.5190	0.0200
l	0.5660	0.0070
m	0.5810	0.0300
n	0.6140	-0.0020
o	0.3680	0.0010
p	0.5760	0.0540
u	0.4830	0.0420
v	0.5610	0.1100
w	0.4710	0.0410
y	0.6460	0.0790