wwPDB EM Validation Summary Report (i)

Mar 30, 2026 – 12:09 PM UTC

PDB ID	:	5Z56 / pdb_00005z56
EMDB ID	:	EMD-6889
Title	:	cryo-EM structure of a human activated spliceosome (mature Bact) at 5.1 angstrom.
Authors	:	Zhang, X.; Yan, C.; Zhan, X.; Li, L.; Lei, J.; Shi, Y.
Deposited on	:	2018-01-17
Resolution	:	5.10 Å(reported)

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

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

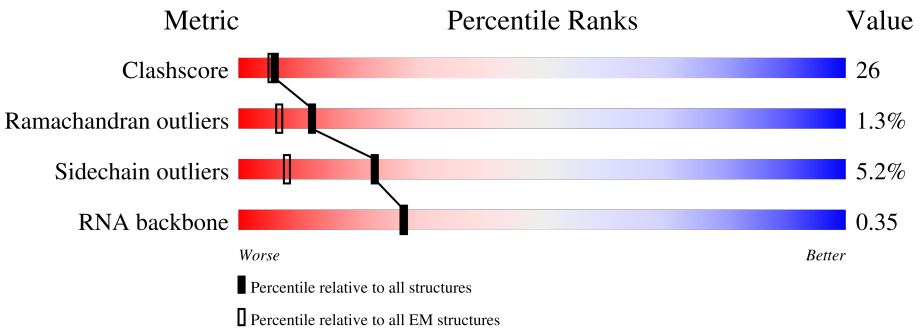
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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

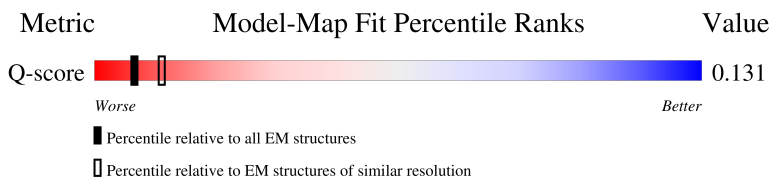
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 5.10 Å.

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





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	844 (4.60 - 5.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	21% 53% 37% 5% •
2	B	117	18% 30% 24% 15% • 28%
3	C	972	10% 46% 34% 8% • 12%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	2136	75% 78% • 19%
5	E	357	26% 57% 23% • 16%
6	a	126	62% 64% 36%
6	h	126	63% 63% 37%
7	b	231	33% 35% 65%
7	i	231	37% 34% • 63%
8	c	119	58% 69% 31%
8	j	119	68% 69% 31%
9	d	118	71% 78% • 18%
9	k	118	71% 67% 5% 28%
10	f	86	73% 85% • 14%
10	m	86	86% 85% • 14%
11	e	92	75% 82% • 14%
11	l	92	86% 85% • 14%
12	g	76	87% 95% • •
12	n	76	88% 86% • 11%
13	F	107	11% 26% 30% 28% • 13%
14	G	274	6% • 14% 13% 72%
15	H	188	43% 13% 40% 19% • 28%
16	o	255	64% 51% 11% • 36%
17	p	225	72% 53% 15% • 27%
18	w	501	71% 74% 12% • 13%
19	u	793	13% 13% • 87%
20	v	464	23% 24% 9% • 64%
21	1	1304	9% 50% 29% • 20%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
22	2	895	7% 14% 6% 80%
23	3	1217	19% 49% 47%
24	4	424	14% 9% 9% 82%
25	5	125	15% 56% 30% 14%
26	6	110	9% 51% 26% 23%
27	7	86	7% 45% 30% 23%
28	J	848	45% 54% 6% 38%
29	L	802	29% 34% 8% 57%
30	q	504	26% 24% 74%
30	r	504	26% 24% 74%
30	s	504	13% 13% 87%
30	t	504	13% 13% 87%
31	K	225	63% 52% 13% 32%
32	I	855	65% 60% 6% 34%
33	Q	1485	88% 88% 11%
34	M	343	8% 6% 90%
35	N	144	12% 58% 36% 6%
36	O	420	30% 31% 33% 32%
37	P	229	27% 18% 18% 5% 58%
38	R	540	20% 27% 19% 9% 43%
39	S	166	60% 58% 31% 6%
40	T	514	7% 31% 23% 6% 39%
41	U	2752	99%
42	V	908	30% 44% 5% 50%
43	W	579	70% 61% 19% 17%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
44	X	396	11% 31% 9% 60%
45	Y	322	16% 17% 67%
46	Z	619	9% 6% 82%
47	z	472	32% 28% 9% 62%
48	x	1041	56% 52% 44%
49	y	301	74% 76% 23%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
50	IHP	A	3000	-	-	X	-
51	GTP	C	1500	-	-	X	-

2 Entry composition (i)

There are 53 unique types of molecules in this entry. The entry contains 117278 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	2232	18450	11885	3217	3269	79	0	0

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	84	1768	792	295	597	84	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	6716	4294	1120	1270	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 protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	a	81	399	237	81	81	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	h	80	393	233	80	80	0	0

- Molecule 7 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	b	82	405	241	82	82	0	0
7	i	86	422	250	86	86	0	0

- Molecule 8 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	c	82	406	242	82	82	0	0
8	j	82	406	242	82	82	0	0

- Molecule 9 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	d	97	480	286	97	97	0	0
9	k	85	422	252	85	85	0	0

- Molecule 10 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	f	74	361	213	74	74	0	0
10	m	74	361	213	74	74	0	0

- Molecule 11 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	e	79	391	233	79	79	0	0
11	l	79	391	233	79	79	0	0

- Molecule 12 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	g	74	363	215	74	74	0	0
12	n	68	334	198	68	68	0	0

- Molecule 13 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
13	F	93	1988	889	363	643	93	0	0

- Molecule 14 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
14	G	77	1545	689	240	539	77	0	0

- Molecule 15 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
15	H	136	2886	1289	499	962	136	0	0

- Molecule 16 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	o	162	804	480	162	162	0	0

- Molecule 17 is a protein called U2 small nuclear ribonucleoprotein B".

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	p	165	813	483	165	165	0	0

- Molecule 18 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	w	437	2369	1448	460	458	3	0	0

- Molecule 19 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
19	u	106	530	318	106	106	0	0

- Molecule 20 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	v	167	946	571	193	180	2	0	0

- Molecule 21 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	1	1038	7702	4900	1347	1415	40	0	0

- Molecule 22 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	2	183	1252	809	213	226	4	0	0

- Molecule 23 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	3	1177	9220	5854	1566	1755	45	0	0

- Molecule 24 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
24	4	78	527	345	83	99	0	0

- Molecule 25 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	5	108	807	512	142	150	3	0	0

- Molecule 26 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	6	85	645	396	114	122	13	0	0

- Molecule 27 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	7	66	540	343	94	98	5	0	0

- Molecule 28 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	J	522	3463	2156	653	648	6	0	0

- Molecule 29 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	L	342	2260	1430	406	420	4	0	0

- Molecule 30 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
30	q	132	659	395	132	132	0	0
30	r	131	654	392	131	131	0	0
30	s	67	335	201	67	67	0	0
30	t	67	335	201	67	67	0	0

- Molecule 31 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	K	152	979	611	177	189	2	0	0

- Molecule 32 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
32	I	564	2778	1650	564	564	0	0

- Molecule 33 is a protein called Intron-binding protein aquarius.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
33	Q	1317	6528	3894	1317	1317	0	0

- Molecule 34 is a protein called RING finger protein 113A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	M	36	267	167	45	52	3	0	0

- Molecule 35 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	N	143	1184	746	217	209	12	0	0

- Molecule 36 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	O	285	2273	1428	401	424	20	0	0

- Molecule 37 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	P	96	829	508	162	157	2	0	0

- Molecule 38 is a protein called Skip.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	R	309	2316	1456	413	435	12	0	0

- Molecule 39 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	S	159	1236	787	215	227	7	0	0

- Molecule 40 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	T	313	2457	1552	447	450	8	0	0

- Molecule 41 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	U	26	193	120	36	36	1	0	0

- Molecule 42 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
42	V	452	2243	1339	452	452	0	0

- Molecule 43 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
43	W	481	2374	1412	481	481	0	0

- Molecule 44 is a protein called Smad nuclear-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	X	159	1021	649	173	198	1	0	0

- Molecule 45 is a protein called RNA-binding motif protein, X-linked 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	Y	105	743	470	127	144	2	0	0

- Molecule 46 is a protein called BUD13 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
46	Z	113	755	474	147	134	0	0

- Molecule 47 is a protein called Peptidyl-prolyl cis-trans isomerase CWC27 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	z	177	1381	869	241	266	5	1	0

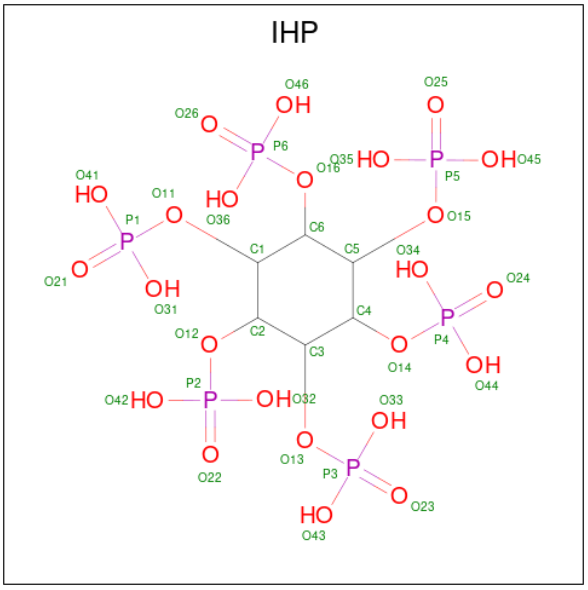
- Molecule 48 is a protein called Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
48	x	584	2887	1718	584	585	0	0

- Molecule 49 is a protein called Peptidyl-prolyl cis-trans isomerase E.

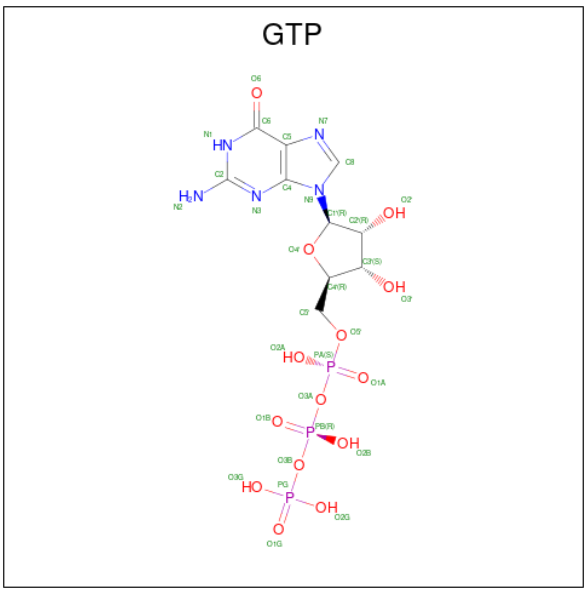
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
49	y	232	1133	669	232	232	0	0

- Molecule 50 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$).



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

- Molecule 51 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 52 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
52	C	1	1	1	0
52	F	5	5	5	0

- Molecule 53 is ZINC ION (CCD ID: ZN) (formula: Zn).

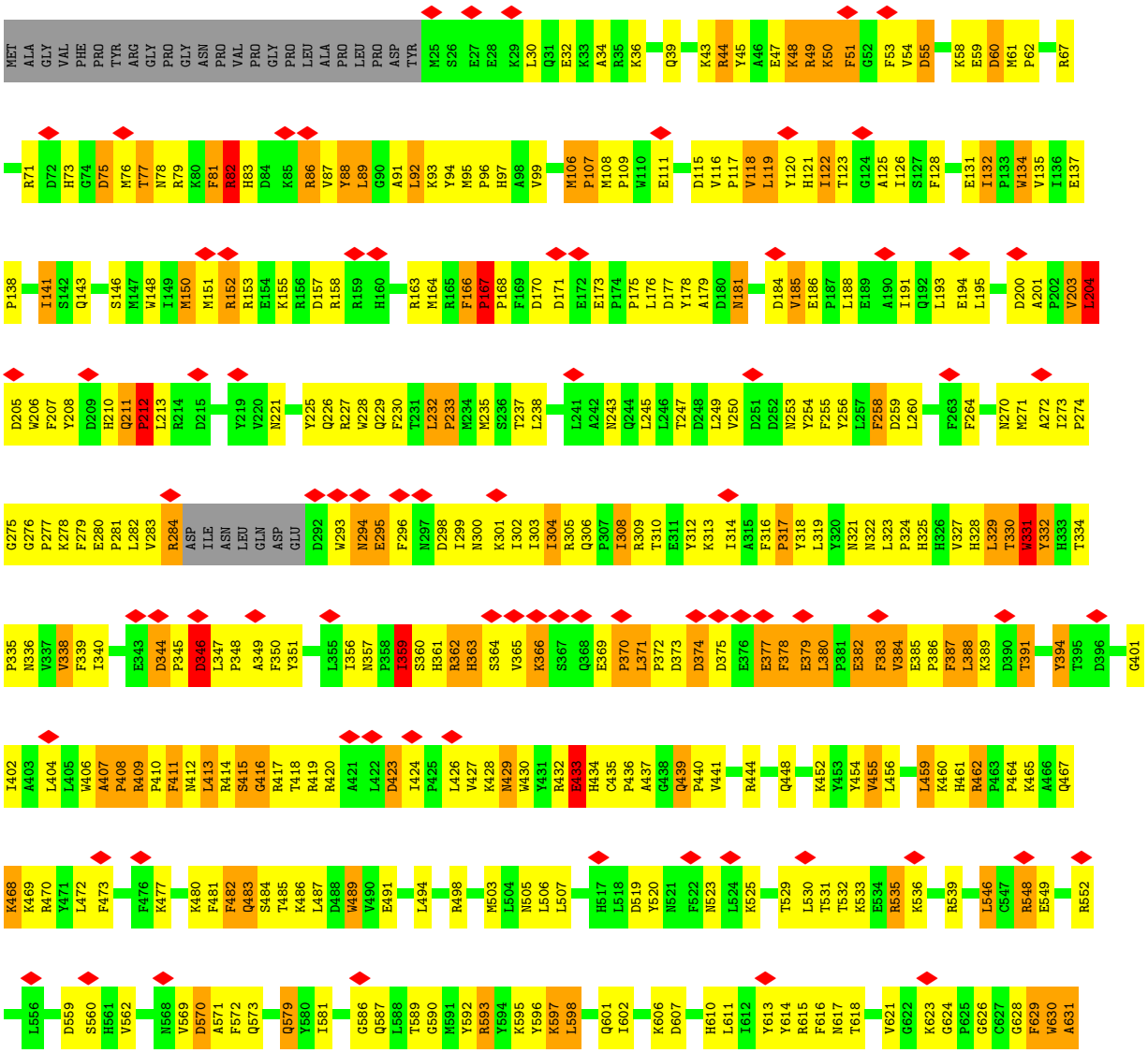
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
53	v	1	1	1	0
53	6	3	3	3	0
53	M	1	1	1	0
53	N	3	3	3	0
53	O	3	3	3	0
53	W	2	2	2	0

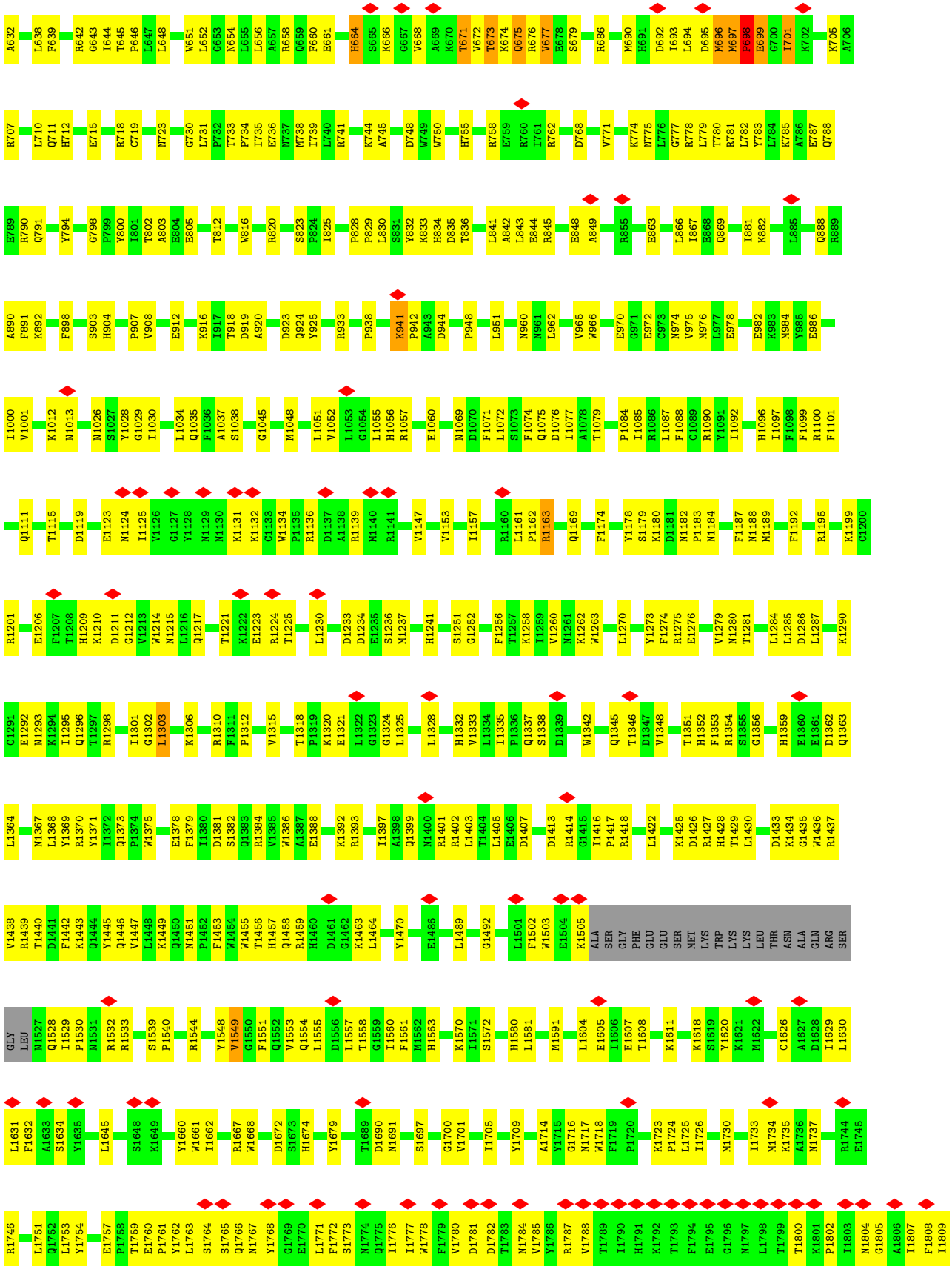
3 Residue-property plots (i)

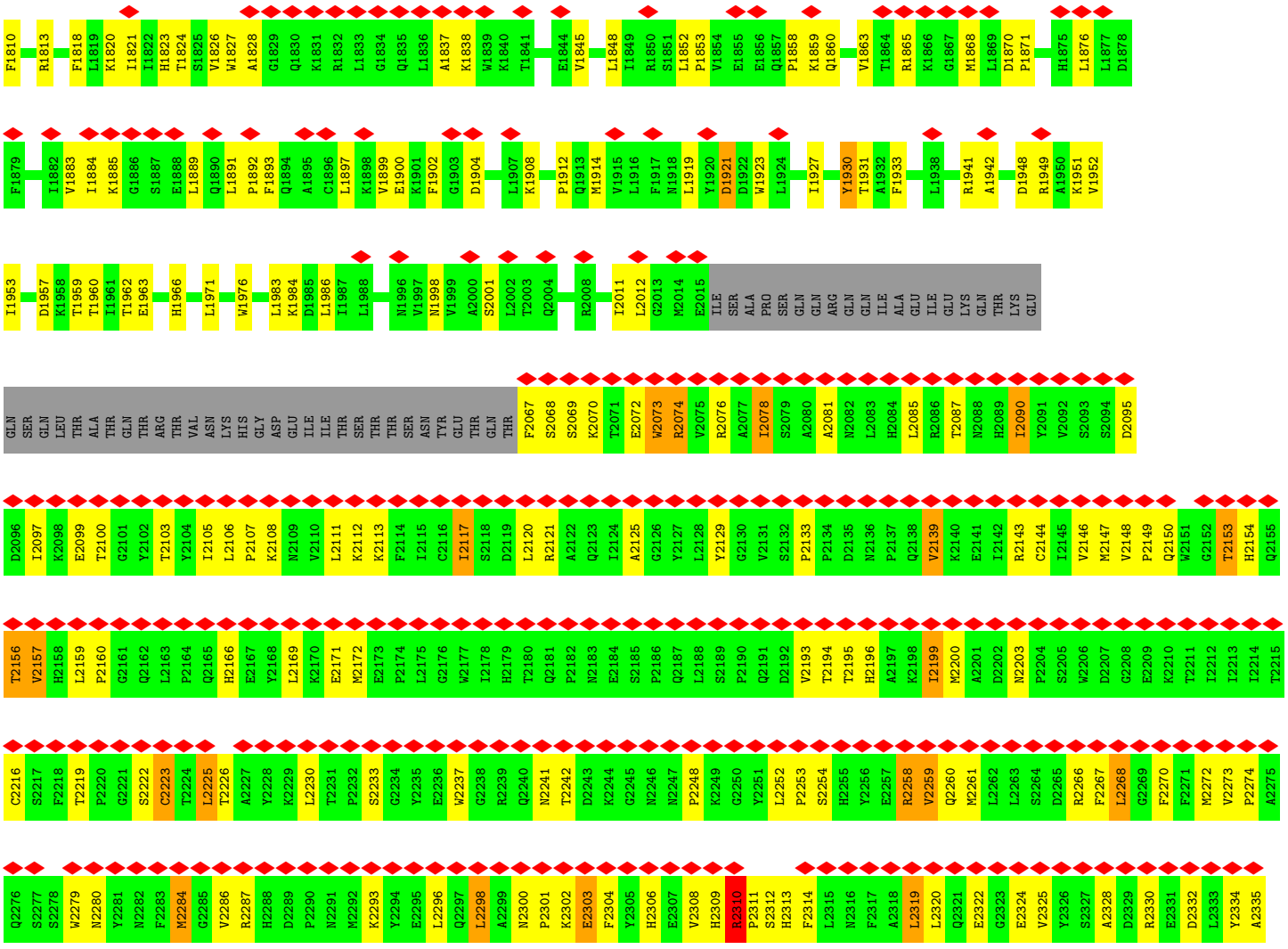
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

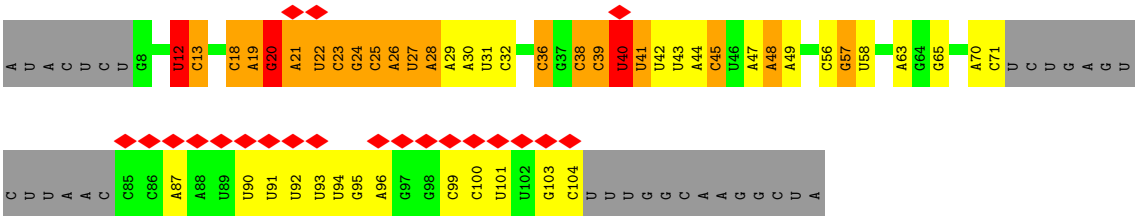



A632 L638 F639 R642 G643 I644 T645 P646 L647 L648 W651 L652 G653 N654 L655 L656 A657 R658 Q659 F660 E661 H664 S665 K666 G667 V668 A669 K670 T671 V672 T673 K674 Q675 R676 V677 E678 S679 R686 M690 H691 D692 I693 L694 D695 M696 M697 P698 E699 G700 I701 K702 K705 A706
R707 L710 Q711 H712 E715 R718 C719 N723 G730 L731 P732 T733 P734 I735 E736 N737 M738 I739 L740 R741 K744 A745 D748 W749 W750 H755 R758 E759 R760 I761 R762 D768 V771 K774 N775 L776 G777 R778 L779 T780 R781 L782 Y783 L784 K785 A786 E787 Q788
E789 R790 Q791 Y794 G798 P799 Y800 I801 T802 A803 E804 E805 T812 W816 R820 S823 P824 I825 P828 P829 L830 S831 Y832 K833 H834 D835 T836 L841 A842 L843 E844 R845 E848 A849 R855 E863 L866 I867 E868 Q869 I881 K882 L885 Q888 R889
A890 F891 K892 F898 S903 H904 P907 V908 E912 K916 I917 T918 D919 A920 D923 Q924 Y925 R933 P938 K941 P942 A943 D944 P948 L951 N960 N961 L962 V965 W966 E970 G971 E972 C973 N974 V975 M976 L977 E978 E982 K983 M984 Y985 E986
I1000 V1001 K1012 N1013 N1026 S1027 Y1028 G1029 I1030 L1034 Q1035 F1036 A1037 S1038 G1045 M1048 L1051 V1052 L1053 G1054 L1055 H1056 R1057 E1060 N1069 D1070 F1071 L1072 S1073 F1074 Q1075 D1076 I1077 A1078 T1079 P1084 I1085 R1086 L1087 F1088 C1089 R1090 Y1091 I1092 H1096 I1097 F1098 F1099 R1100 F1101
Q1111 T1115 D1119 E1123 N1124 I1125 V1126 G1127 Y1128 N1129 N1130 K1131 K1132 C1133 W1134 P1135 R1136 D1137 A1138 R1139 M1140 R1141 V1147 V1153 I1157 R1160 L1161 P1162 R1163 Q1169 F1174 Y1178 S1179 K1180 D1181 N1182 P1183 N1184 F1187 N1188 M1189 F1192 R1195 K1199 C1200
R1201 E1206 F1207 T1208 H1209 K1210 D1211 G1212 V1213 W1214 N1215 L1216 Q1217 T1221 K1222 E1223 R1224 T1225 L1230 D1233 D1234 E1235 S1236 M1237 H1241 S1251 G1252 F1256 T1257 K1258 I1259 V1260 N1261 K1262 W1263 L1270 Y1273 F1274 R1275 E1276 V1279 N1280 T1281 L1284 L1285 D1286 L1287 K1290
C1291 E1292 N1293 K1294 I1295 Q1296 T1297 R1298 I1301 G1302 L1303 K1306 R1310 F1311 P1312 V1315 T1318 P1319 K1320 E1321 L1322 G1323 G1324 L1325 L1328 H1332 V1333 L1334 I1335 P1336 Q1337 S1338 D1339 W1342 Q1345 T1346 D1347 V1348 T1351 H1352 F1353 R1354 S1355 G1356 H1359 E1360 E1361 D1362 Q1363
L1364 N1367 L1368 Y1369 R1370 Y1371 I1372 Q1373 P1374 W1375 E1378 F1379 I1380 D1381 S1382 Q1383 R1384 V1385 W1386 A1387 E1388 K1392 R1393 I1397 A1398 Q1399 N1400 R1401 R1402 L1403 T1404 L1405 E1406 D1407 D1413 R1414 G1415 I1416 P1417 R1418 L1422 K1425 D1426 R1427 H1428 T1429 L1430 D1433 K1434 G1435 W1436 R1437
V1438 R1439 T1440 D1441 F1442 K1443 Q1444 Y1445 Q1446 V1447 L1448 K1449 Q1450 N1451 P1452 F1453 W1454 W1455 T1456 H1457 Q1458 R1459 H1460 D1461 G1462 K1463 L1464 Y1470 E1486 L1489 G1492 L1501 F1502 W1503 E1504 K1505 ALA SER GLY PHE GLU GLU SER MET LYS TRP LYS LYS LEU THR ASN ALA GLN ARG SER
GLY LEU N1527 Q1528 I1529 P1530 N1531 R1532 R1533 S1539 P1540 R1544 Y1548 Y1549 G1550 F1551 Q1552 V1553 Q1554 L1555 D1556 L1557 T1558 G1559 I1560 F1561 M1562 H1563 K1570 I1571 S1572 H1580 L1581 M1591 L1604 E1605 I1606 E1607 T1608 K1611 K1618 S1619 Y1620 K1621 M1622 C1626 A1627 D1628 I1629 L1630
L1631 F1632 A1633 S1634 Y1635 L1645 S1648 K1649 Y1660 W1661 I1662 R1667 W1668 D1672 S1673 H1674 Y1679 T1689 D1690 N1691 S1697 G1700 V1701 I1705 Y1709 A1714 Y1715 G1716 N1717 W1718 F1719 P1720 K1723 P1724 L1725 I1726 M1730 I1733 M1734 K1735 A1736 N1737 R1744 E1745
R1746 L1751 Q1752 L1753 Y1754 E1757 P1758 T1759 E1760 P1761 Y1762 L1763 S1764 S1765 Q1766 N1767 Y1768 G1769 E1770 L1771 F1772 S1773 N1774 Q1775 I1776 I1777 W1778 F1779 V1780 D1781 D1782 T1783 N1784 V1785 Y1786 R1787 V1788 T1789 I1790 H1791 K1792 T1793 F1794 E1795 G1796 N1797 L1798 T1799 T1800 K1801 P1802 I1803 N1804 G1805 A1806 I1807 F1808 I1809



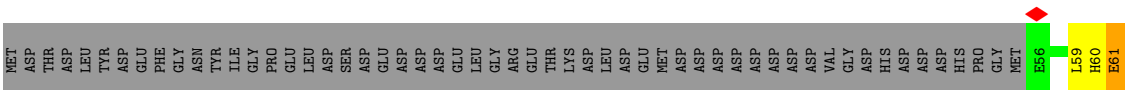
- Molecule 2: U5 snRNA

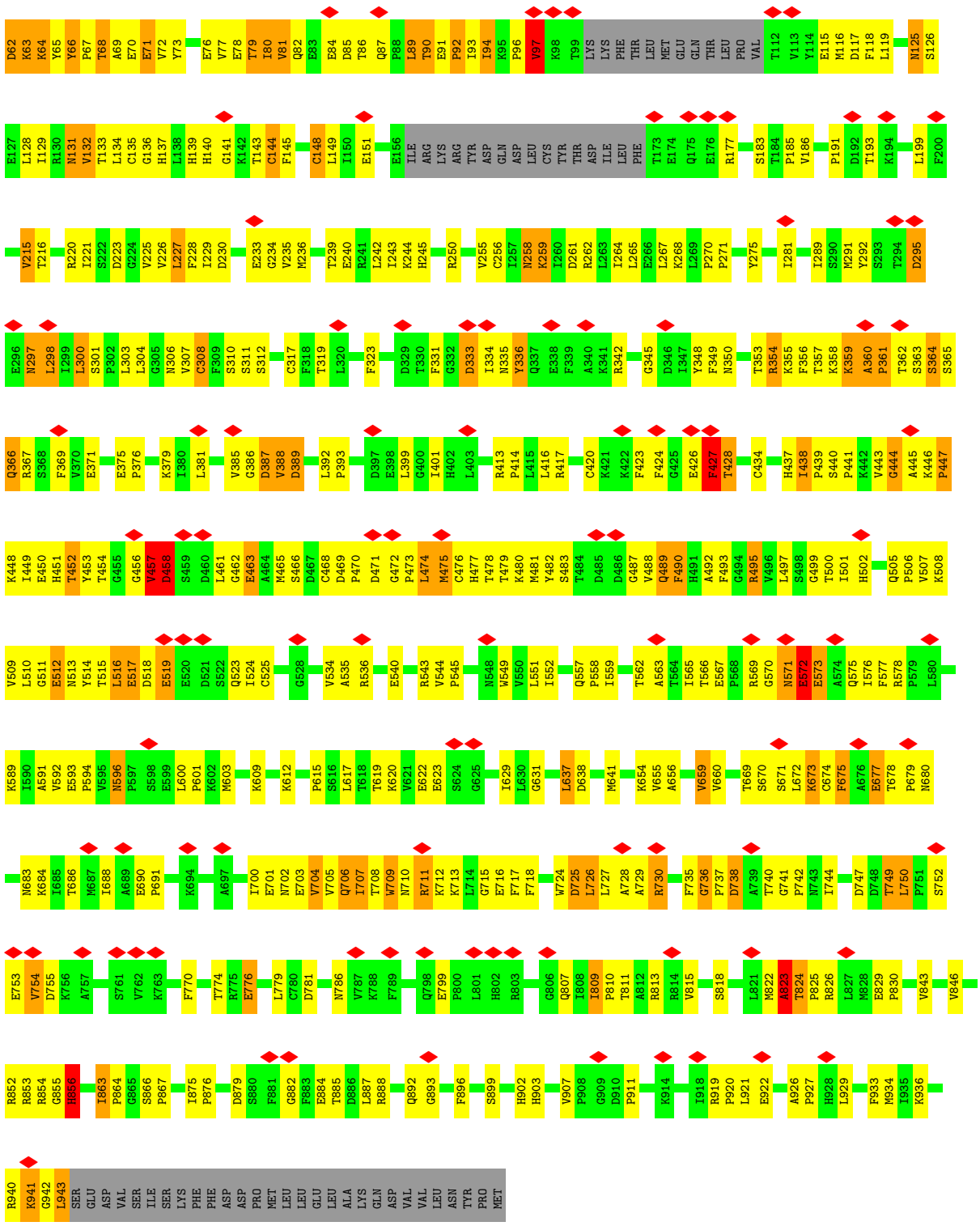
Chain B:



- Molecule 3: 116 kDa U5 small nuclear ribonucleoprotein component

Chain C:





- Molecule 4: U5 small nuclear ribonucleoprotein 200 kDa helicase

Chain D:

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

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

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

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

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

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

H421 F422 M423 A424 N425 K426 R427 C428 Q429 L430 P431 D432 G433 S434 F435 R436 R437 K440 G441 Y442 E443 E444 V445 H446 V447 P448 A449 L450 K451 P452 K453 P454 F455 G456 S457 E458 E459 Q460 L461 L462 P463 V464 E465 K466 L467 P468 K469 Y470 A471 Q472 A473 G474 F475 E476 G477 F478 K479 T480 L481

N482 R483 I484 Q485 L488 Y489 R490 A491 A492 L493 E494 T495 D496 E497 N498 L499 L500 L501 C502 A503 P504 T505 G506 A507 G508 K509 T510 N511 V512 A513 L514 M515 C516 M517 L518 R519 E520 I521 G522 K523 H524 I525 N526 M527 D528 G529 T530 I531 N532 V533 D534 D535 F536 K537 I538 I539 Y540 I541 A542

P543 M544 R545 S546 Q549 E550 M551 V552 G553 S554 F555 G556 K557 R558 L559 A560 T561 Y562 G563 I564 T565 V566 A567 E568 L569 T570 G571 D572 H573 Q574 L575 C576 K577 E578 E579 I580 S581 A582 T583 Q584 I585 I586 V587 C588 T589 P590 E591 K592 W593 D594 I595 I596 T597 R598 K599 G600 G601 E602 R603

T604 Y605 T606 Q607 L608 V609 R610 L611 I612 I613 L614 D615 E616 L620 H621 D622 D623 R624 G625 P626 V627 L628 E629 A630 L631 V632 A633 R634 A635 I636 R637 N638 I639 E640 M641 T642 Q643 E644 D645 V646 R647 L648 I649 G650 L651 S652 A653 T654 L655 P656 N657 Y658 E659 D660 V661 A662 T663 F664 L665

R666 V667 D668 P669 A670 K671 G672 L673 F674 Y675 F676 D677 N678 S679 F680 R681 P682 V683 P684 L685 E686 Q687 T688 Y689 Y690 G691 I692 T693 E694 K695 K696 A697 I698 K699 R700 I703 M704 N705 E706 I707 E710 M713 E714 H715 A716 G717 K718 N719 Q720 V721 L722 V723 F724 V725 H726 K729

E730 T731 G732 K733 T734 A735 I738 R739 D740 L743 E744 K745 D746 T747 L748 G749 L750 F751 L752 R753 E754 G755 S756 A757 S758 T759 E760 V761 L762 E765 N771 L772 E773 L774 K775 D776 L777 L778 P779 Y780 G781 F782 A783 I784 H785 H786 A787 G788 N789 D793 R794 T795 L796 V797 E798

D799 L800 F801 A802 D803 K804 H805 I806 Q807 V808 L809 V810 S811 T812 A813 T814 L815 A816 W817 G818 V819 N820 L821 P822 A823 H824 T825 V826 I827 I828 K829 G830 T831 Q832 V833 Y834 S835 P836 E837 K838 G839 R840 W841 T842 E843 L844 G845 A846 Q851 M852 L853 G854 R855 A856 G857 R858 P859 Q860

T863 K864 G865 E866 G867 I868 L869 I870 T871 S872 L876 Y879 L880 S881 L882 L883 N884 Q885 Q886 L887 P888 I889 E890 S891 Q892 M893 V894 S895 K896 L897 P898 D899 M900 L901 N902 A903 E904 I905 V906 L907 G908 N909 V910 Q911 N912 A913 K914 D915 A916 V917 N918 W919 L920 G921 Y922 A923 Y924 L925

Y926 I927 R928 M929 L930 R931 S932 P933 T934 L935 Y936 G937 I938 S939 H940 D941 D942 L943 K944 G945 D946 P947 L948 L949 D950 Q951 R952 R953 L954 D955 L956 V957 H958 T959 A960 A961 L962 M963 L964 D965 K966 N967 N968 L969 V970 K971 Y972 D973 K974 K975 T976 G977 N978 F979 Q980 V981 T982 E983 L984 G985

R986 I987 A988 S989 H990 I993 T994 N995 D996 T997 V998 Q999 T1000 Y1001 N1002 Q1003 L1004 L1005 K1006 P1007 T1008 L1009 S1010 E1011 I1012 E1013 L1014 F1015 R1016 V1017 F1018 S1019 L1020 S1021 S1022 E1023 F1024 K1025 N1026 I1027 T1028 V1029 R1030 E1031 E1032 E1033 K1034 L1035 E1036 L1037 Q1038 K1039 L1040 L1041 E1042 R1043 V1044 P1045 I1046

P1047 V1048 K1049 E1050 S1051 I1052 E1053 S1056 A1057 K1058 I1059 N1060 V1061 L1062 L1063 Q1064 A1065 F1066 I1067 S1068 Q1069 L1070 K1071 L1072 E1073 G1074 F1075 A1076 L1077 M1078 A1079 D1080 M1081 V1082 Y1083 V1084 T1085 Q1086 S1087 A1088 G1089 R1090 L1091 M1092 R1093 A1094 I1095 F1096 E1097 I1098 V1099 R1102 G1103 W1104 A1105 Q1106 L1107

K1110 T1111 L1112 N1113 L1114 C1115 K1116 M1117 I1118 D1119 K1120 R1121 M1122 W1123 Q1124 S1125 M1126 C1127 P1128 L1129 R1130 Q1131 F1132 R1133 K1134 L1135 P1136 E1137 E1138 V1139 V1140 K1141 E1144 K1145 K1146 N1147 F1148 P1149 F1150 E1151 R1152 L1153 Y1154 D1155 L1156 N1157 H1158 N1159 E1160 I1161 G1162 E1163 L1164 I1165 R1166 M1167 P1168 K1169 M1170

G1171 K1172 T1173 I1174 H1175 K1176 Y1177 V1178 H1179 L1180 F1181 P1182 K1183 L1184 E1185 L1186 S1187 V1188 H1189 L1190 Q1191 P1192 I1193 T1194 R1195 S1196 T1197 L1198 K1199 V1200 E1201 L1202 T1203 I1204 T1205 P1206 D1207 F1208 Q1209 W1210 D1211 E1212 K1213 V1214 H1215 G1216 S1217 S1218 E1219 A1220 F1221 W1222 I1223 L1224 V1225 E1226 D1227 V1228 D1229 S1230

E1231 V1232 I1233 L1234 H1235 H1236 E1237 Y1238 F1239 L1240 L1241 K1242 A1243 K1244 Y1245 A1246 Q1247 D1248 E1249 H1250 L1251 I1252 T1253 F1254 F1255 V1256 P1257 V1258 F1259 E1260 P1261 L1262 P1263 P1264 Q1265 Y1266 F1267 I1268 R1269 V1270 V1271 S1272 D1273 R1274 W1275 L1276 S1277 C1278 E1279 T1280 Q1281 L1282 P1283 V1284 S1285 F1286 R1287 H1288 L1289 I1290

L1291 P1292 E1293 K1294 Y1295 P1296 P1297 P1298 T1299 E1300 L1301 L1302 D1303 L1304 Q1305 P1306 L1307 P1308 V1309 S1310 A1311 L1312 R1313 N1314 S1315 A1316 F1317 E1318 S1319 L1320 Y1321 Q1322 D1323 K1324 F1325 P1326 F1327 F1328 N1329 P1330 I1331 Q1332 T1333 Q1334 V1335 F1336 N1337 T1338 V1339 Y1340 N1341 S1342 D1343 D1344 N1345 V1346 F1347 V1348 G1349 A1350

P1351 T1352 G1353 S1354 G1355 K1356 T1357 I1358 C1359 A1360 E1361 F1362 A1363 I1364 L1365 R1366 M1367 L1368 L1369 Q1370 S1371 S1372 E1373 G1374 R1375 C1376 V1377 Y1378 I1379 T1380 P1381 M1382 E1383 A1384 L1385 A1386 E1387 Q1388 V1389 Y1390 M1391 D1392 W1393 Y1394 E1395 K1396 F1397 Q1398 D1399 R1400 L1401 N1402 K1403 K1404 V1405 V1406 L1407 L1408 T1409 G1410

E1411 T1412 S1413 T1414 D1415 L1416 K1417 L1418 L1419 G1420 K1421 G1422 N1423 I1424 I1425 I1426 S1427 T1428 P1429 E1430 K1431 W1432 D1433 I1434 L1435 S1436 R1437 R1438 W1439 K1440 Q1441 R1442 K1443 N1444 V1445 Q1446 N1447 I1448 N1449 L1450 F1451 V1452 V1453 D1454 E1455 V1456 H1457 L1458 I1459 G1460 G1461 E1462 N1463 G1464 P1465 V1466 L1467 E1468 V1469 I1470

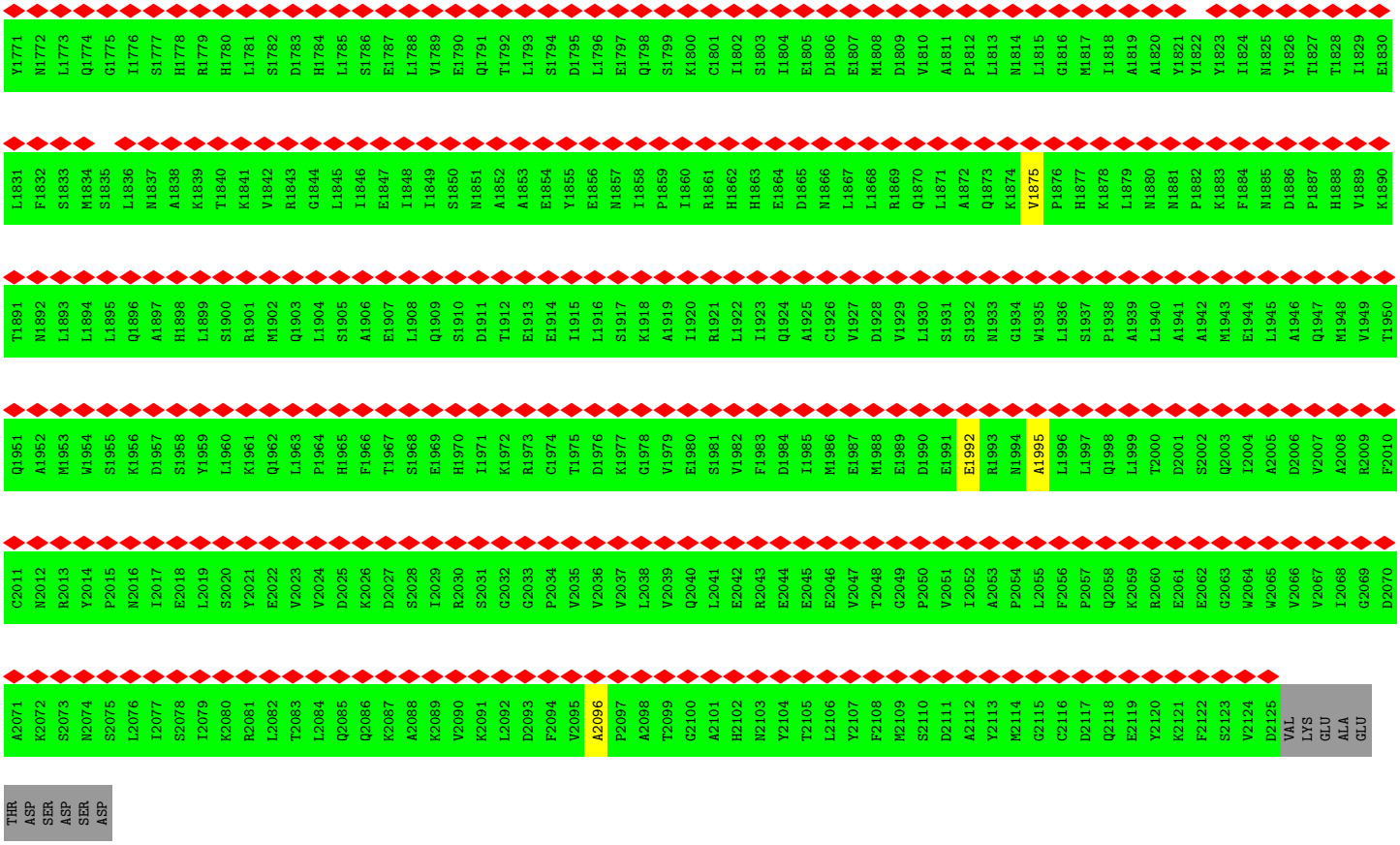
C1471 S1472 R1473 M1474 R1475 Y1476 I1477 S1478 S1479 Q1480 I1481 E1482 R1483 P1484 I1485 R1486 I1487 V1488 A1489 L1490 S1491 S1492 S1493 L1494 S1495 N1496 A1497 K1498 D1499 V1500 A1501 H1502 W1503 L1504 G1505 C1506 S1507 A1508 T1509 S1510 T1511 F1512 N1513 F1514 H1515 P1516 N1517 V1518 R1519 P1520 V1521 P1522 L1523 E1524 L1525 H1526 I1527 Q1528 G1529 F1530

N1531 I1532 S1533 H1534 T1535 Q1536 T1537 R1538 L1539 L1540 S1541 M1542 A1543 K1544 P1545 V1546 Y1547 H1548 A1549 I1550 T1551 K1552 H1553 S1554 P1555 K1556 K1557 P1558 V1559 I1560 V1561 F1562 V1563 P1564 S1565 R1566 K1567 Q1568 T1569 R1570 L1571 T1572 A1573 I1574 D1575 I1576 L1577 T1578 T1579 C1580 A1581 A1582 D1583 I1584 Q1585 R1586 Q1587 R1588 F1589 L1590

H1591 C1592 T1593 E1594 K1595 D1596 L1597 I1598 P1599 Y1600 L1601 E1602 K1603 L1604 S1605 D1606 S1607 T1608 L1609 K1610 E1611 T1612 L1613 L1614 N1615 G1616 V1617 G1618 Y1619 L1620 H1621 E1622 G1623 L1624 S1625 P1626 M1627 E1628 R1629 R1630 L1631 V1632 E1633 Q1634 L1635 F1636 S1637 S1638 G1639 A1640 I1641 Q1642 V1643 V1644 V1645 A1646 S1647 R1648 S1649 L1650

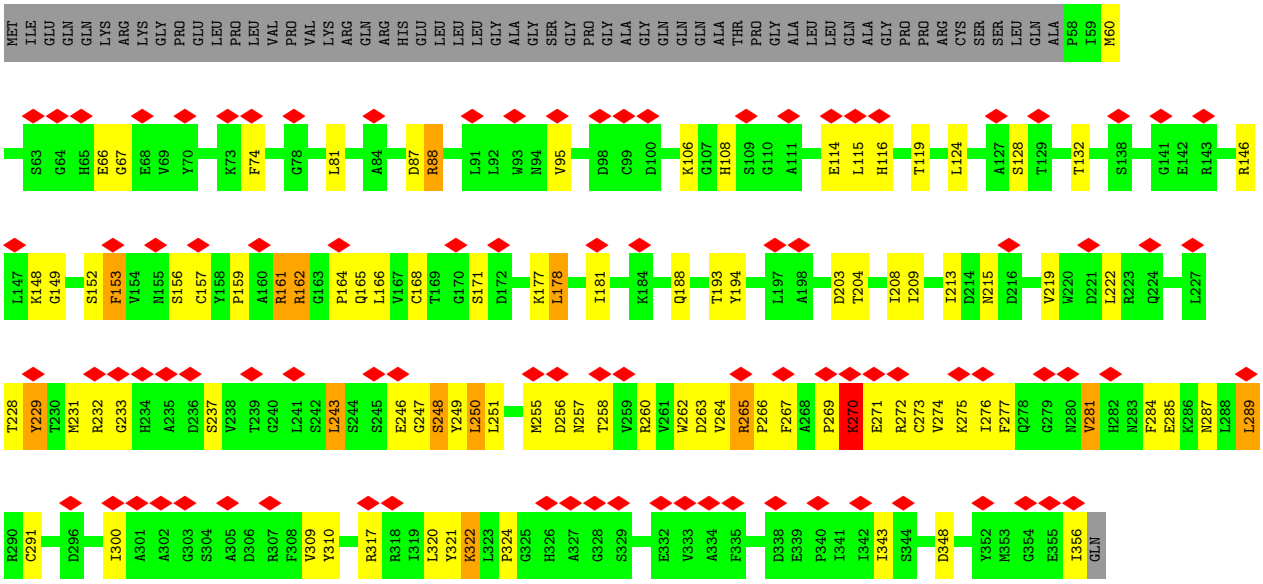
C1651 W1652 G1653 M1654 N1655 V1656 A1657 A1658 H1659 L1660 V1661 I1662 I1663 M1664 D1665 T1666 Q1667 Y1668 Y1669 N1670 G1671 K1672 I1673 H1674 A1675 Y1676 V1677 D1678 Y1679 P1680 I1681 Y1682 D1683 V1684 L1685 Q1686 M1687 V1688 G1689 H1690 A1691 N1692 R1693 P1694 L1695 Q1696 D1697 D1698 E1699 G1700 R1701 C1702 V1703 I1704 M1705 C1706 Q1707 G1708 S1709 K1710

K1711 D1712 F1713 F1714 K1715 K1716 F1717 L1718 Y1719 E1720 P1721 L1722 P1723 V1724 E1725 S1726 H1727 L1728 D1729 H1730 C1731 M1732 H1733 D1734 H1735 F1736 N1737 A1738 E1739 I1740 V1741 T1742 K1743 T1744 I1745 E1746 N1747 K1748 Q1749 D1750 A1751 V1752 D1753 Y1754 L1755 T1756 W1757 T1758 F1759 L1760 Y1761 R1762 R1763 M1764 T1765 Q1766 N1767 P1768 N1769 Y1770



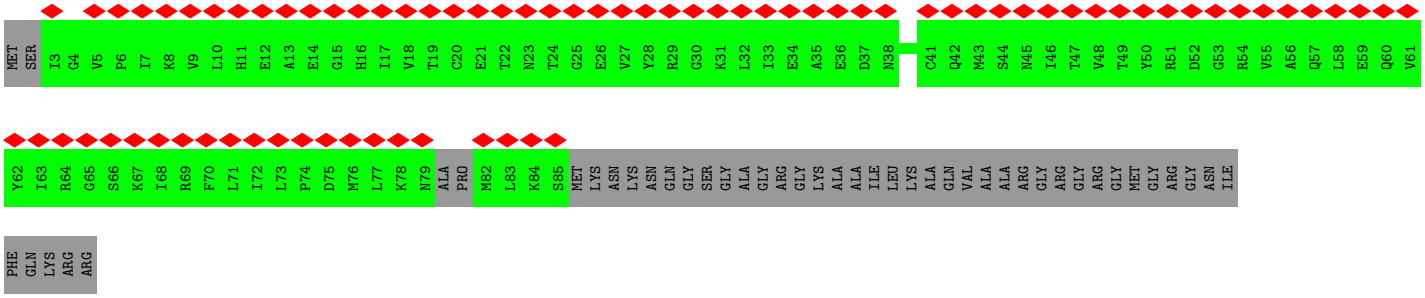
- Molecule 5: U5 small nuclear ribonucleoprotein 40 kDa protein

Chain E:



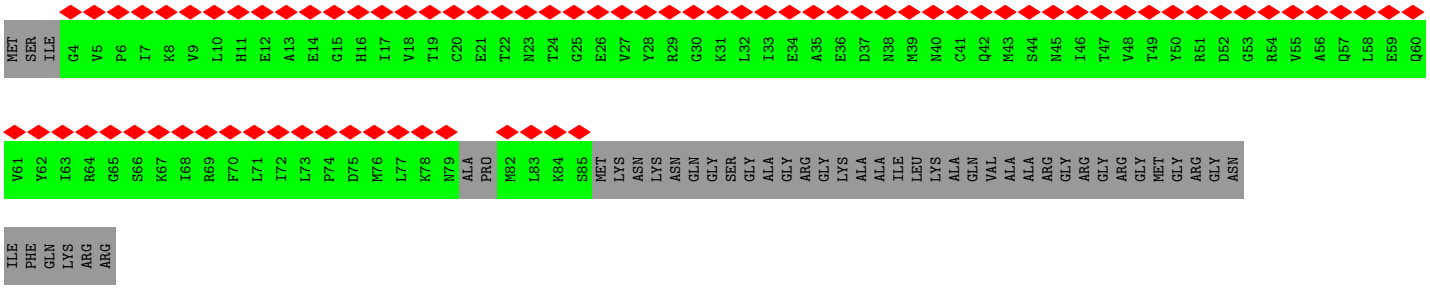
- Molecule 6: Small nuclear ribonucleoprotein Sm D3

Chain a:



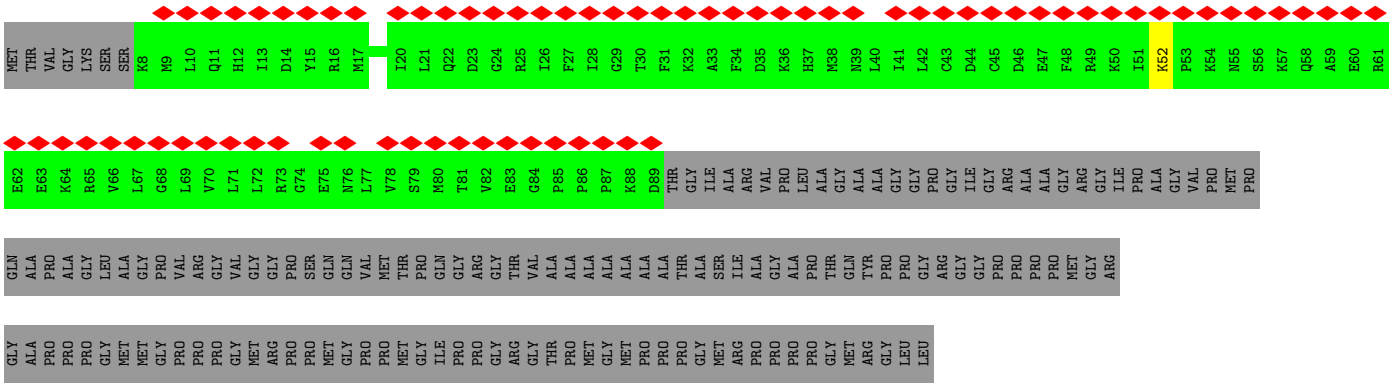
• Molecule 6: Small nuclear ribonucleoprotein Sm D3

Chain h:



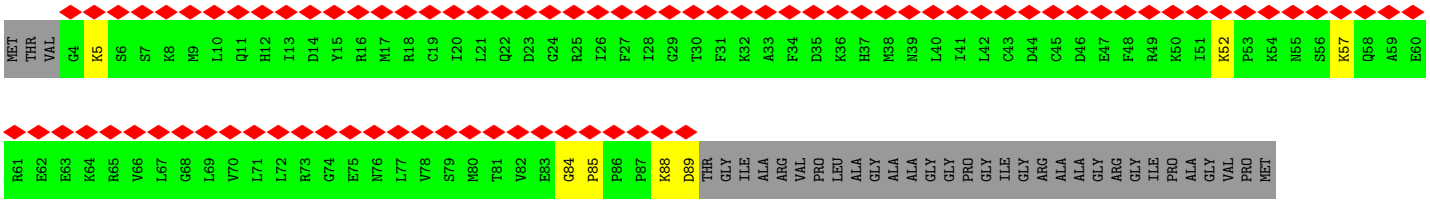
• Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'

Chain b:



• Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'

Chain i:



PRO GLN ALA PRO ALA GLY LEU ALA GLY PRO VAL ARG GLY VAL GLY GLY PRO SER GLN GLN VAL MET THR PRO GLN GLY ARG GLY THR VAL ALA ALA ALA ALA ALA ALA ALA ALA THR ALA SER ILE ALA GLY ALA PRO THR GLN TYR PRO PRO GLY ARG GLY GLY PRO PRO PRO PRO MET GLY

ARG GLY ALA PRO PRO PRO GLY MET MET MET GLY PRO PRO PRO PRO GLY MET ARG PRO PRO MET GLY PRO PRO MET GLY ILE PRO PRO GLY ARG GLY THR PRO MET GLY MET PRO PRO PRO GLY MET ARG PRO PRO PRO PRO GLY MET ARG GLY LEU LEU

- Molecule 8: Small nuclear ribonucleoprotein Sm D1

Chain c: 58% 69% 31%

M1 K2 L3 V4 R5 F6 L7 M8 K9 T14 V15 E18 L19 K20 N21 G22 T23 Q24 V25 H26 G27 T28 I29 T30 G31 V32 D33 V34 S35 M36 N37 T38 H39 L40 K41 A42 V43 K44 M45 T46 L47 K48 N49 R50 E51 P52 V53 Q54 L55 E56 T57 L58 S59 I60 R61 I65 R66

Y67 F68 I69 L70 P71 D72 S73 L74 P75 L76 D77 T78 L79 L80 V81 D82 VAL GLU PRO LYS VAL LYS SER LYS LYS LYS ARG GLU ALA VAL ALA GLY ARG GLY ARG GLY GLY ARG GLY ARG GLY ARG GLY ARG GLY ARG GLY ARG GLY ARG GLY GLY GLY PRO ARG ARG

- Molecule 8: Small nuclear ribonucleoprotein Sm D1

Chain j: 68% 69% 31%

M1 K2 L3 V4 R5 F6 L7 M8 K9 L10 S11 H12 E13 T14 V15 T16 I17 E18 L19 K20 N21 G22 T23 Q24 V25 H26 G27 T28 I29 T30 G31 V32 D33 V34 S35 M36 N37 T38 H39 L40 K41 A42 V43 K44 M45 T46 L47 K48 N49 R50 E51 P52 V53 Q54 L55 E56 T57 L58 S59 I60

R61 G62 N63 N64 I65 R66 Y67 F68 I69 L70 P71 D72 S73 L74 P75 L76 D77 T78 L79 L80 V81 D82 VAL GLU PRO LYS VAL LYS SER LYS LYS ARG GLU ALA VAL ALA GLY ARG GLY ARG GLY ARG GLY ARG GLY ARG GLY ARG GLY ARG GLY ARG GLY ARG GLY GLY GLY PRO ARG ARG

- Molecule 9: Small nuclear ribonucleoprotein Sm D2

Chain d: 71% 78% • 18%

MET SER LEU LEU ASN LYS PRO LYS SER GLU MET THR PRO GLU GLU GLU LEU GLN LYS ARG E20 E21 E22 E23 F24 N25 T26 G27 P28 L29 S30 V31 L32 T33 Q34 S35 V36 K37 N38 N39 T40 Q41 V42 L43 I44 N45 N49 K50 K51 L52 L53 G54 R55 A58 F59 D60 R61 H62 C63

N64 M65 V66 L67 E68 N69 V70 K71 E72 M73 W74 T75 E76 V77 P78 K79 S80 G81 K82 G83 K84 K85 K86 S87 K88 P89 V90 N91 K92 D93 R94 Y95 I96 S97 K98 M99 F100 L101 R102 G103 D104 I107 V108 V109 L110 R111 N112 P113 L114 I115 A116 GLY LYS

- Molecule 9: Small nuclear ribonucleoprotein Sm D2

Chain k: 71% 67% 5% 28%

MET SER LEU LEU ASN LYS PRO LYS SER GLU MET THR PRO GLU GLU GLU LEU GLN LYS ARG E20 E21 E22 E23 F24 N25 T26 G27 P28 L29 S30 V31 L32 T33 Q34 S35 V36 K37 N38 N39 T40 Q41 V42 L43 I44 N45 C46 R47 N48 N49 K50 K51 L52 L53 G54 R55 V56 K57 A58 F59 D60

R61 H62 C63 N64 M65 V66 L67 E68 N69 V70 K71 E72 M73 W74 T75 E76 VAL PRO LYS SER GLY LYS GLY LYS LYS LYS SER LYS P89 V90 N91 K92 D93 R94 Y95 I96 S97 K98 M99 F100 L101 R102 G103 D104 S105 V106 I107 V108 V109 L110 R111 N112 P113 L114 I115 A116 GLY LYS

- Molecule 10: Small nuclear ribonucleoprotein F

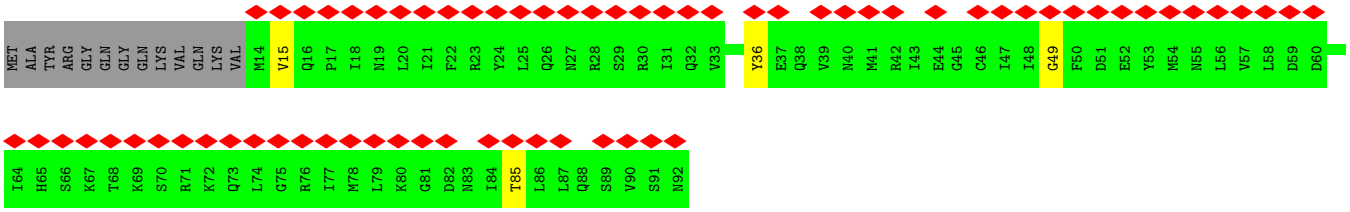
Chain f:

- Molecule 10: Small nuclear ribonucleoprotein F

Chain m:

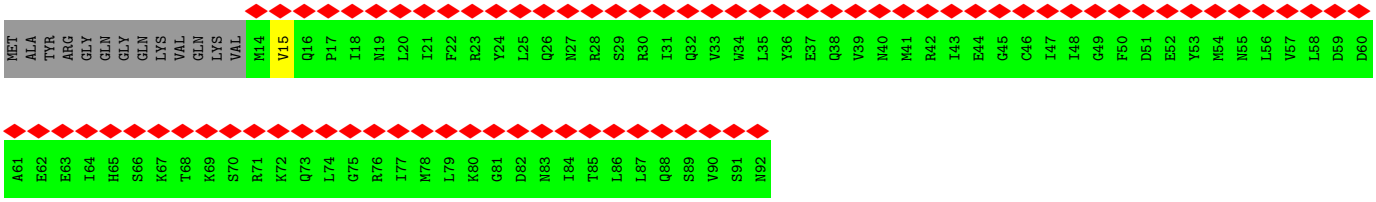
- Molecule 11: Small nuclear ribonucleoprotein E

Chain e:



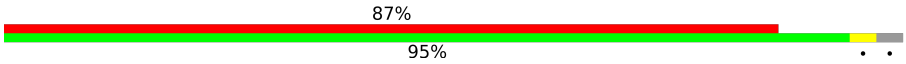
- Molecule 11: Small nuclear ribonucleoprotein E

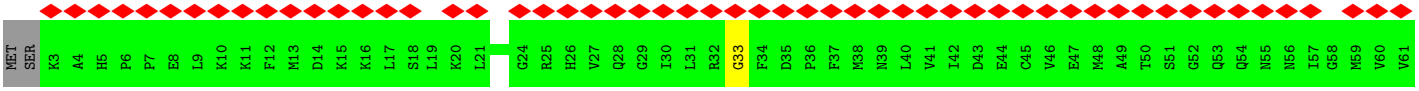
Chain l:

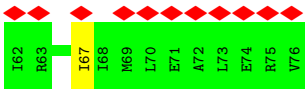


- Molecule 12: Small nuclear ribonucleoprotein G

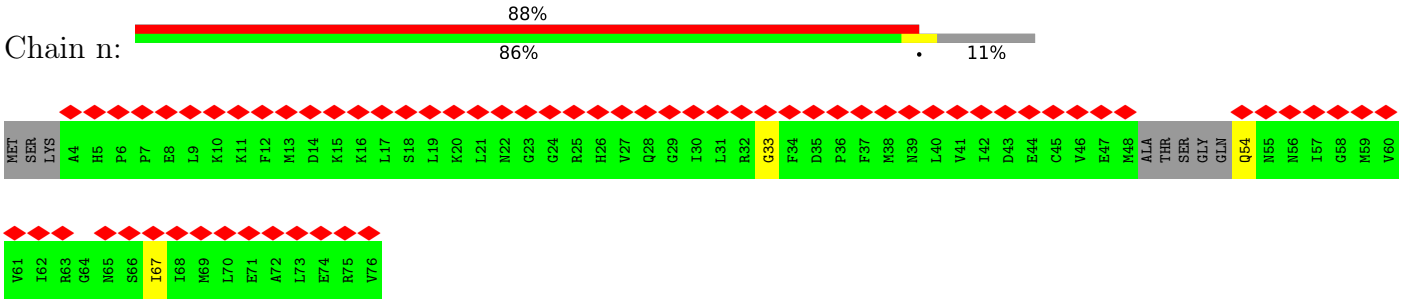
Chain g:



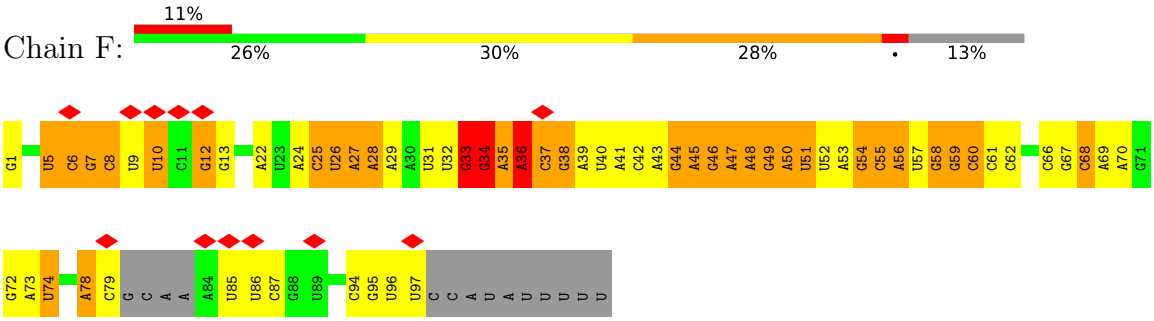




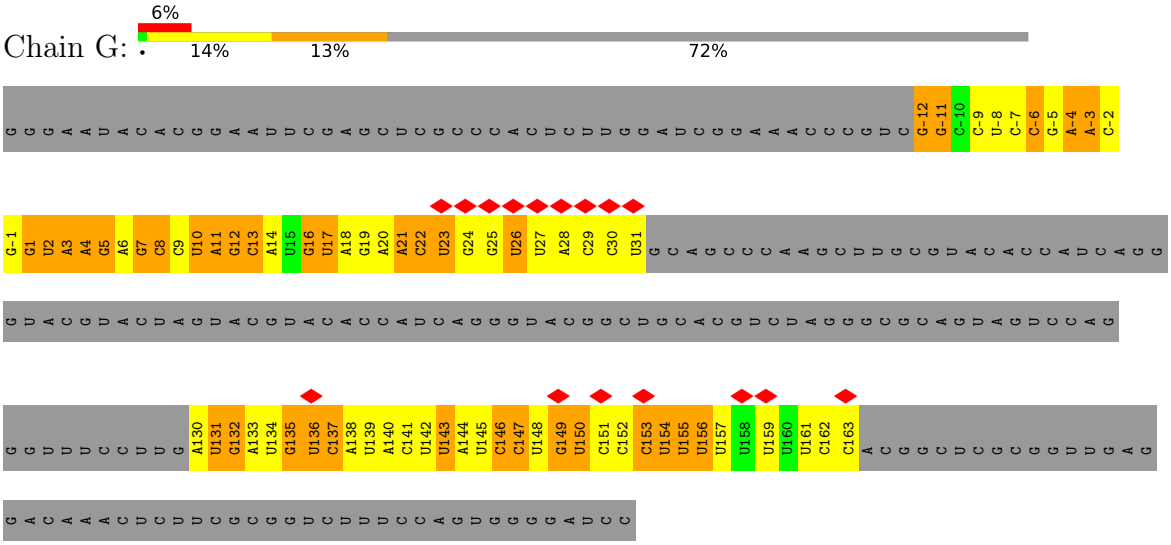
• Molecule 12: Small nuclear ribonucleoprotein G



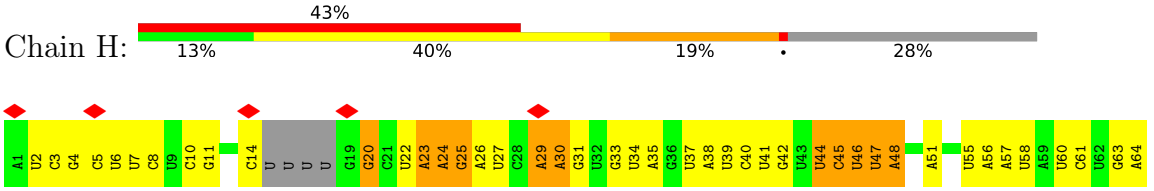
• Molecule 13: U6 snRNA

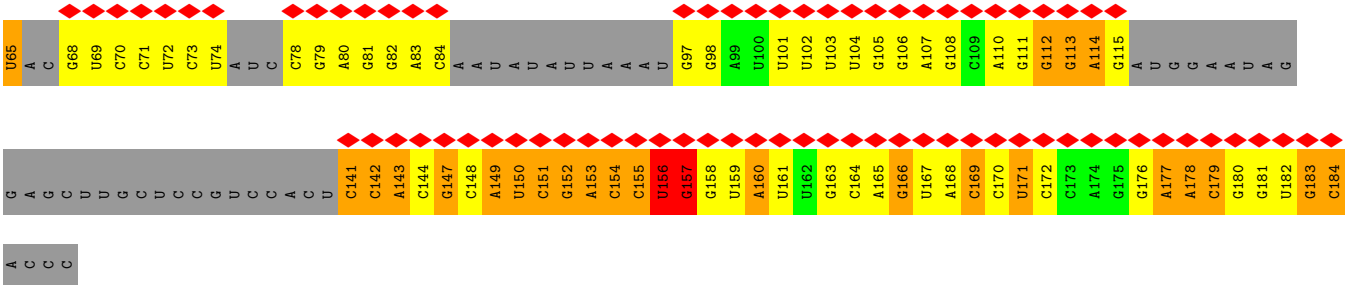


• Molecule 14: pre-mRNA



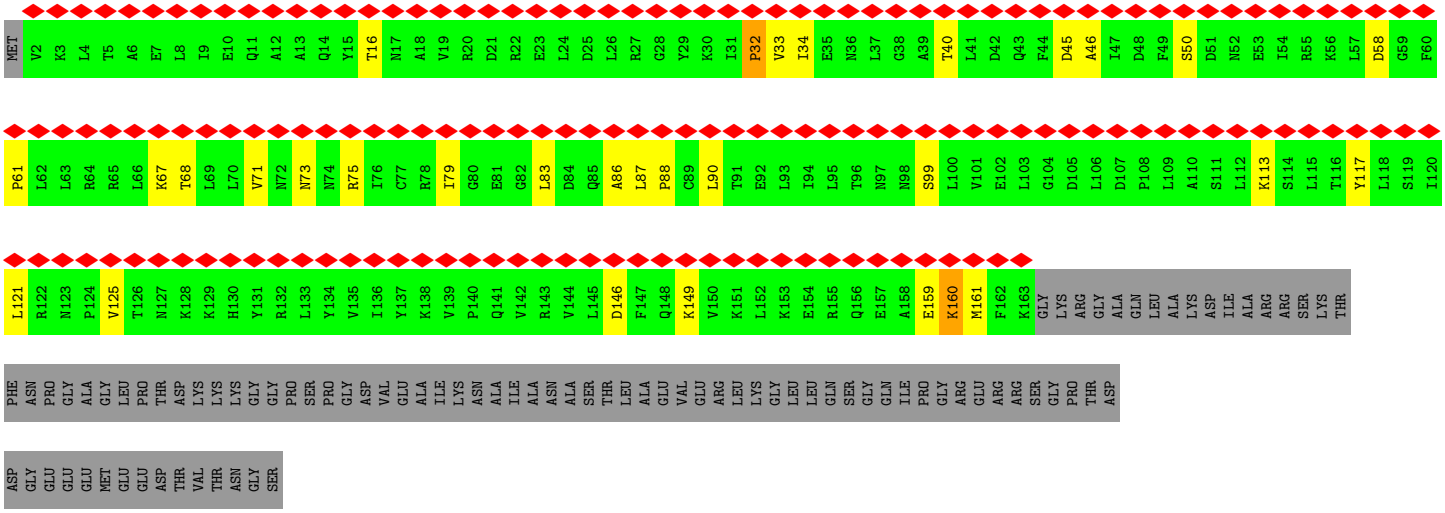
• Molecule 15: U2 snRNA





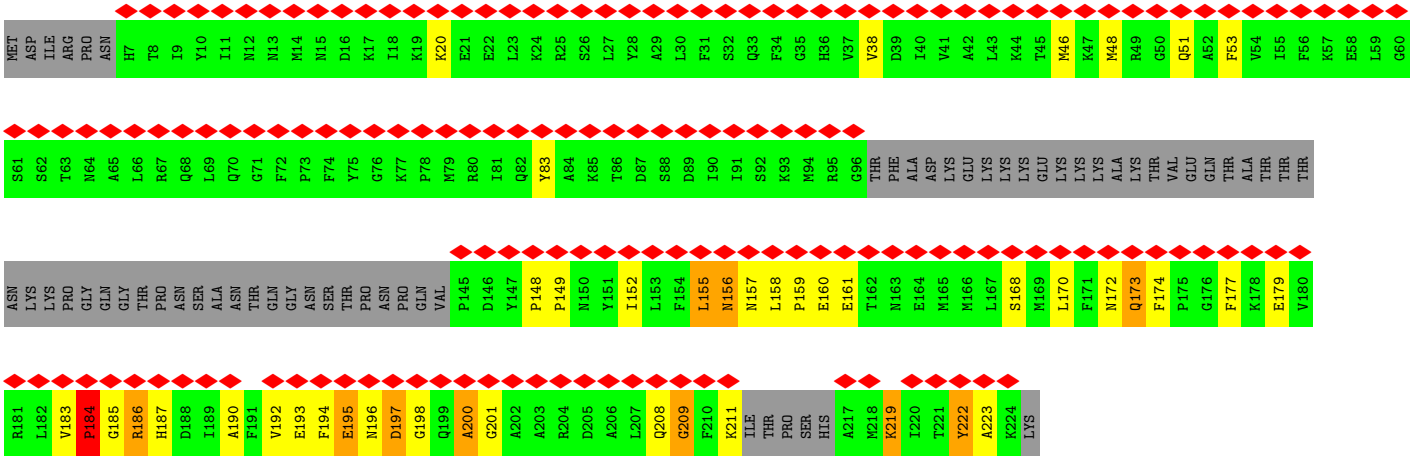
• Molecule 16: U2 small nuclear ribonucleoprotein A'

Chain o:



• Molecule 17: U2 small nuclear ribonucleoprotein B"

Chain p:



• Molecule 18: Splicing factor 3A subunit 3

Chain w:

MET E2 T3 I4 L5 E6 Q7 Q8 R9 R10 Y11 H12 E13 E14 K15 E16 R17 L18 M19 D20 V21 M22 A23 K24 E25 M26 L27 T28 K29 K30 S31 T32 L33 R34 D35 Q36 I37 N38 S39 D40 H41 R42 T43 R44 A45 M46 Q47 D48 R49 Y50 M51 E52 V53 S54 G55 N56 L57 R58 D59 L60

Y61 D62 D63 K64 D65 G66 L67 R68 LYS GLU GLU LEU ASN ALA ILE SER GLY PRO ASN GLU PHE A82 E83 F84 Y85 N86 R87 L88 K89 Q90 I91 K92 E93 F94 H95 R96 K97 H98 P99 N100 E101 I102 C103 V104 P105 M106 S107 VAL GLU PHE GLU GLU LEU L114 K115 A116 R117 E118 N119 P120

S121 E122 E123 A124 Q125 N126 L127 V128 E129 F130 T131 D132 E133 E134 G135 Y136 G137 R138 Y139 L140 D141 L142 H143 D144 CYS TYR LEU LYS Y149 I150 N151 L152 K153 A154 S155 E156 K157 L158 D159 Y160 I161 T162 Y163 L164 S165 I166 F167 D168 Q169 L170 F171 D172 I173 P174 K175 E176 R177 K178 N179 A180

E181 Y182 K183 R184 Y185 L186 E187 M188 L189 L190 E191 Y192 L193 Q194 D195 Y196 T197 D198 R199 V200 K201 P202 L203 Q204 D205 Q206 N207 E208 L209 F210 GLY LYS ILE GLN ALA GLU F217 E218 K219 K220 W221 E222 N223 G224 T225 F226 P227 G228 W229 P230 K231 E232 T233 S234 S235 A236 L237 T238 H239 A240

G241 A242 H243 L244 D245 L246 S247 A248 F249 S250 S251 W252 E253 E254 L255 A256 S257 L258 G259 L260 D261 R262 L263 K264 S265 A266 L267 I268 A269 L270 G271 L272 LYS CYS GLY G276 T277 L278 E279 E280 R281 A282 Q283 R284 L285 F286 S287 T288 LYS GLY K291 S292 L293 E294 S295 L296 D297 T298 S299 L300

F301 A302 K303 N304 P305 K306 S307 K308 G309 T310 K311 R312 D313 T314 E315 R316 N317 K318 D319 I320 A321 F322 L323 E324 A325 Q326 I327 Y328 E329 Y330 V331 E332 I333 L334 G335 E336 Q337 R338 H339 L340 T341 H342 E343 N344 V345 Q346 R347 K348 Q349 A350 R351 T352 G353 E354 E355 R356 E357 E358 E359 E360

E361 E362 Q363 I364 S365 E366 S367 E368 S369 E370 D371 E372 E373 N374 GLU ILE ILE TYR ASN PRO LYS ASN LEU PRO LEU GLY TRP ASP GLY LYS PRO I392 P393 Y394 W395 L396 Y397 K398 L399 H400 N403 I404 I410 C411 G412 N413 Y414 T415 Y416 R417 G418 P419 K420 A421 F422 Q423 R424 R425

F426 A427 E428 H431 G434 M435 R436 C437 L438 G439 I440 P441 N442 T443 A444 H445 F446 A447 N448 V449 T450 Q451 I452 S457 L462 K463 LEU GLN LYS ALA SER GLU ARG TRP GLN PRO D474 T475 E476 E477 E478 Y479 E480 D481 S482 S483 G484 N485 V486 T491 R497 Q498 G499 LEU

LEU

• Molecule 19: Splicing factor 3A subunit 1

Chain u: 13% 13% 87%

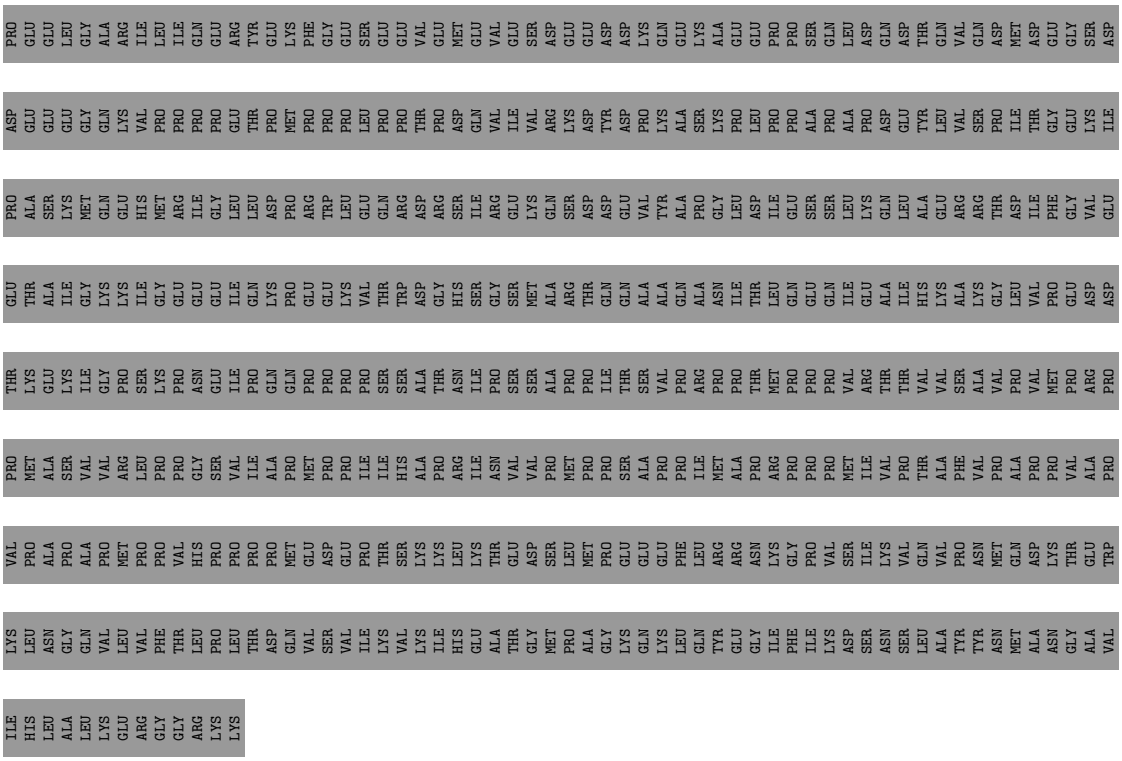
MET PRO ALA GLY PRO VAL GLN ALA VAL PRO PRO PRO PRO PRO VAL PRO THR GLU PRO LYS GLN PRO THR GLU GLU GLU ALA SER SER LYS GLU ASP SER ALA PRO SER LYS PRO VAL VAL GLY ILE ILE TYR PRO PRO PRO GLU VAL ARG ASN ILE VAL ASP LYS THR ALA SER PHE VAL

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

GLN GLN THR THR GLN GLN GLN LEU PRO GLN LYS VAL GLN ALA GLN VAL ILE ILE GLN GLU THR ILE VAL PRO LYS GLU PRO PRO PRO GLU PHE GLU PHE ILE ALA ASP PRO PRO SER ILE S160 A161 F162 D163 L164 D165 V166 V167 K168 L169 T170 A171 Q172 F173 V174 A175 R176 ASN GLY R179 Q180

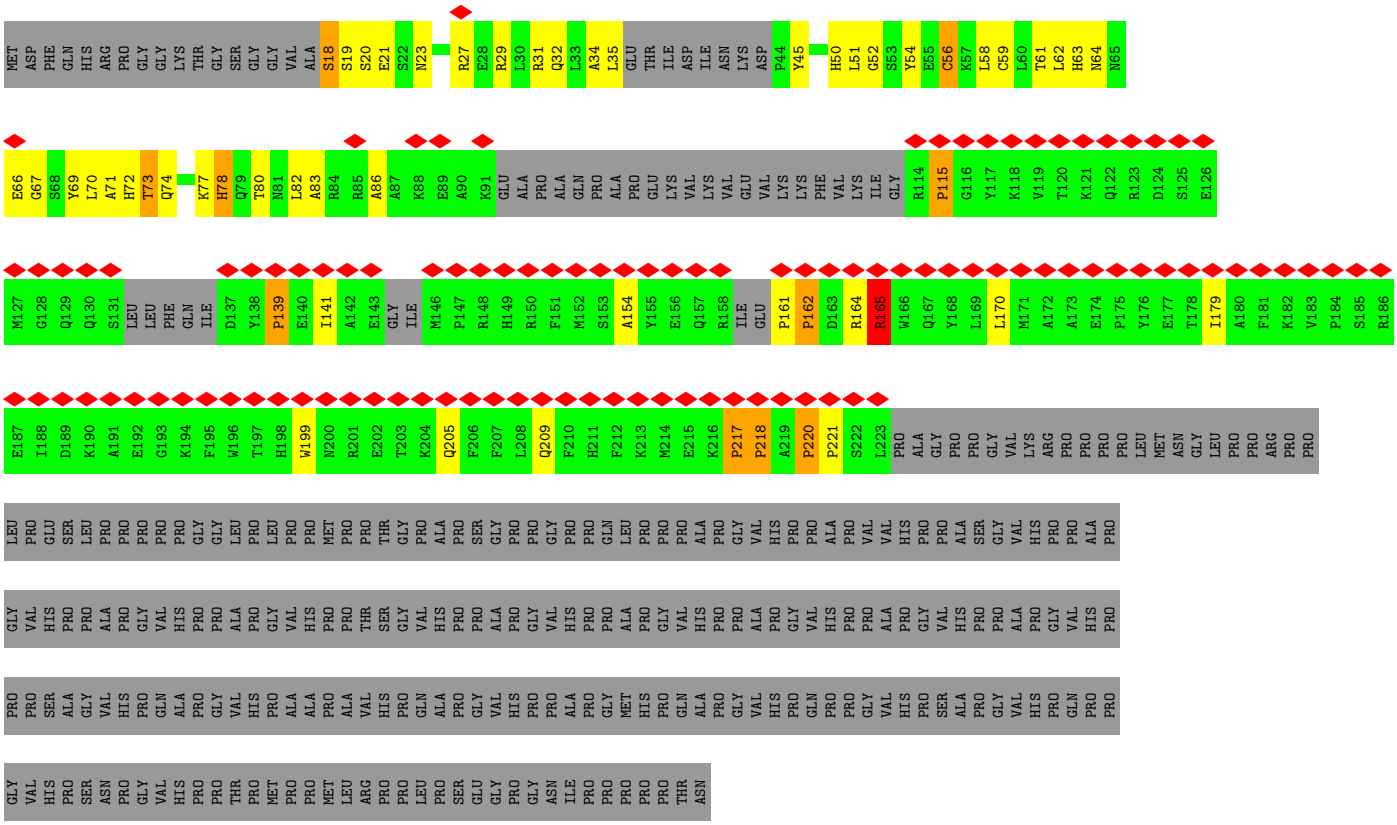
F181 L182 T183 Q184 L185 M186 Q187 K188 E189 GLN ARG N192 Y193 Q194 F195 D196 F197 L198 R199 P200 Q201 H202 S203 L204 F205 N206 Y207 F208 T209 K210 L211 V212 E213 Q214 Y215 T216 K217 I218 L219 I220 P221 P222 LYS GLY LEU PHE S227 K228 L229 K230 K231 GLU ALA GLU ASN PRO R237 E238 V239 L240

D241 Q242 V243 C244 Y245 R246 V247 E248 W249 ALA LYS PHE GLN GLU ARG GLU R257 K258 K259 E260 E261 E262 E263 K264 E265 K266 E267 R268 V269 A270 V271 A272 Q273 I274 D275 W276 H277 D278 F279 V280 V281 V282 E283 T284 V285 ASP PHE GLN PRO ASN GLU GLN GLY ASN PHE PRO PRO PRO THR THR



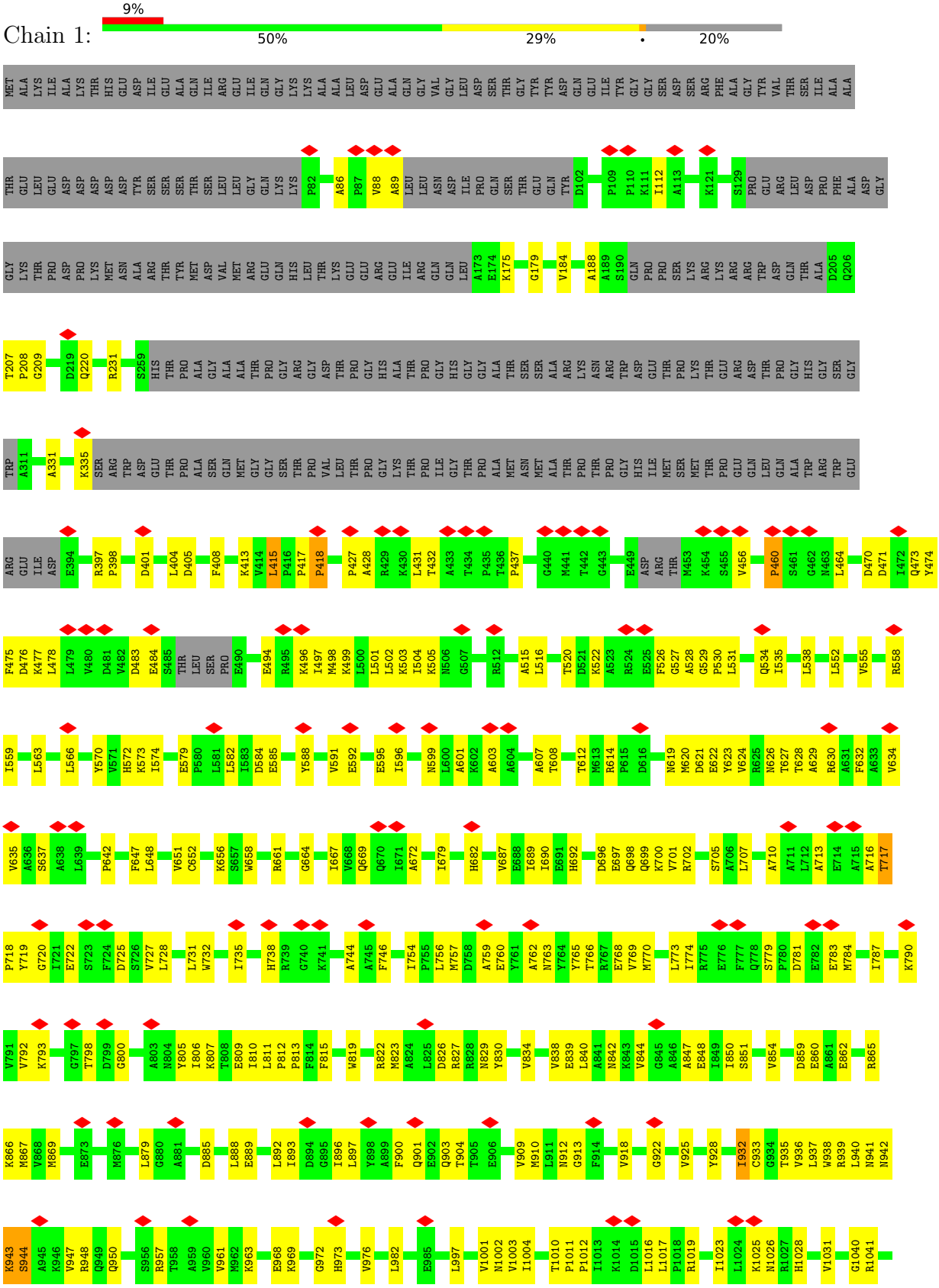
- Molecule 20: Splicing factor 3A subunit 2

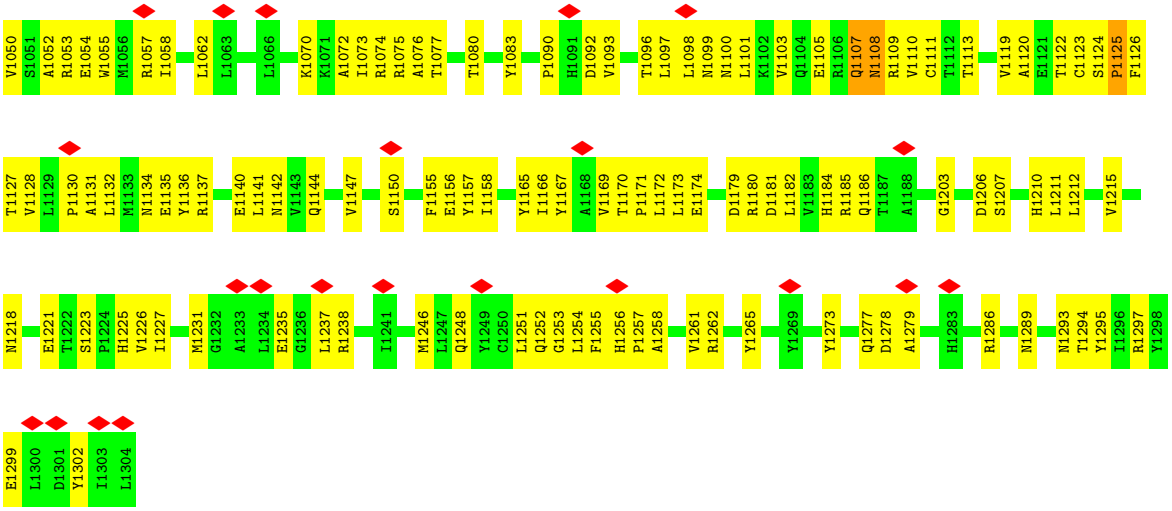
Chain v:



- Molecule 21: Splicing factor 3B subunit 1

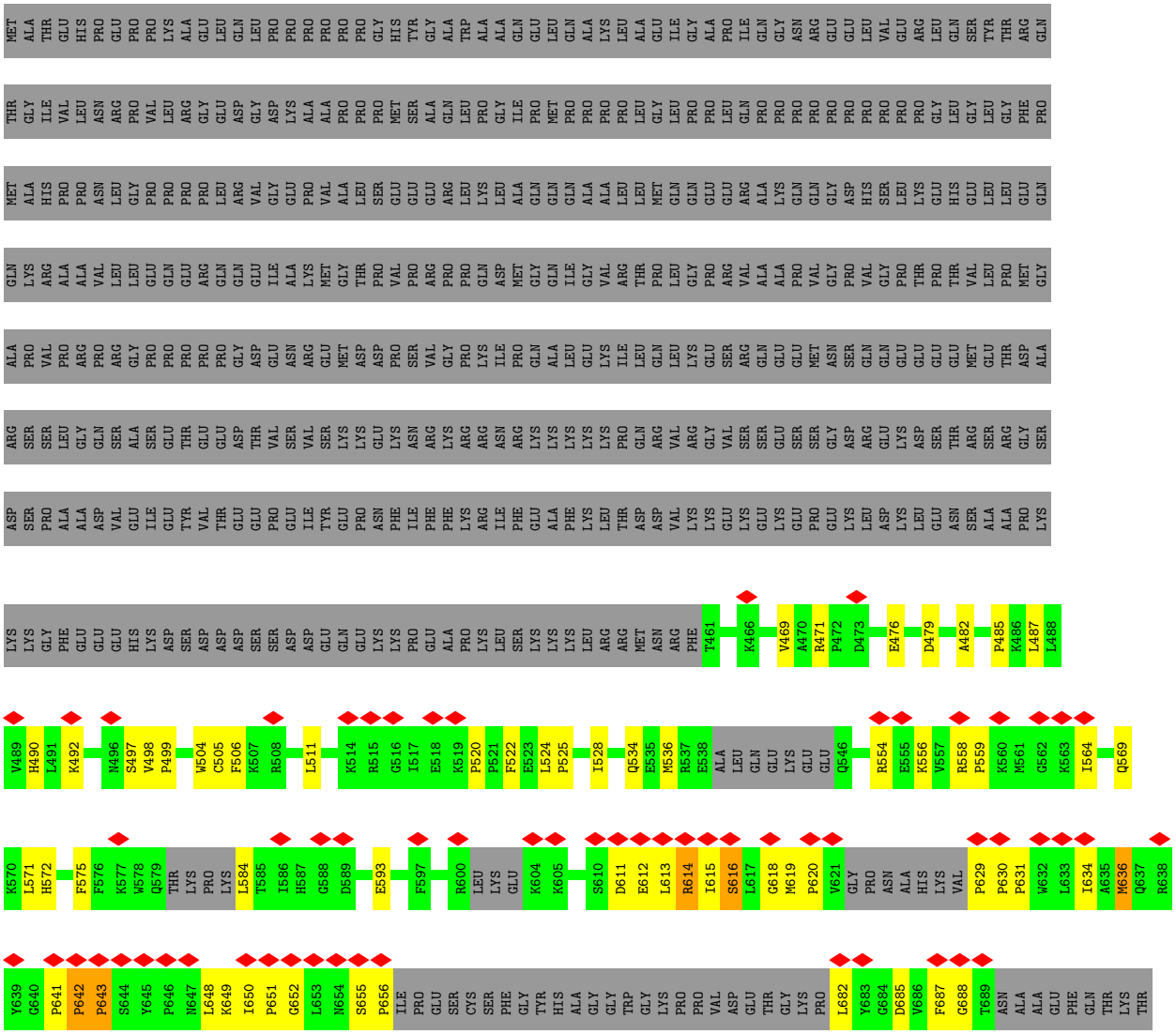
Chain 1:





- Molecule 22: Splicing factor 3B subunit 2

Chain 2:



GLU GLU GLU GLU ILE ASP ARG THR PRO TRP GLY GLU LEU GLU PRO SER ASP GLU GLU SER SER GLU GLU GLU GLU GLU GLU SER ASP GLU ASP LYS PRO ASP GLU THR GLY PHE ILE THR PRO ALA ASP SER GLY ILE LEU ILE THR PRO GLY GLY PHE SER SER VAL PRO ALA GLY MET

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

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

GLN PRO GLN ASP SER ARG GLY GLY SER LYS LYS TYR LYS GLU PHE LYS PHE

- Molecule 23: Splicing factor 3B subunit 3

Chain 3: 19% 49% 47%

M1 F2 L3 Y4 N5 L6 T7 L8 A11 T12 I18 N21 F22 S23 Q27 Q28 E29 I30 V31 V32 S33 R34 G35 K36 I37 L38 E39 L40 L41 R42 T47 G48 K49 L53 L54 V58 F59 G60 V61 I62 R63 S64 L65 M66 A67 F68 R69 L70 T71 G72 I78 V79

V80 D83 R86 I87 V88 P94 M98 F99 E100 K101 I102 H103 Q104 E105 G108 K109 S110 G111 C112 R113 R114 I115 V116 P117 G118 Q119 F120 K126 G127 R128 S133 E136 K137 Q138 K139 L140 V141 Y142 I143 L144 N145 R146 D147 A150 R151 L152 T153 P157 L158 E159

A160 H161 N164 T165 L166 V167 Y168 H169 V170 D174 V175 G176 F177 E178 N179 P180 M181 F182 A183 C184 L185 E186 M187 D188 Y189 A192 D193 N194 D195 P196 T197 G198 E199 A200 N203 T204 Q205 Q206 T209 F210 Y211 E212 L213 D214 L215 G216 L217 N218 R222 K223 Y224 S225 E226 P227

L228 G232 N233 F234 L235 I236 T237 V238 P239 G240 S246 G247 V248 L249 I250 C251 S252 E253 N254 T257 Y258 K259 N260 F261 Q264 P265 D266 I267 R268 R273 R274 R275 L278 D279 D280 R283 G284 M285 I286 F287 V288 C289 K294 T295 K296 S297 F300 F301 L302 A303 Q304

T305 E306 Q307 G308 D309 I310 F311 K312 I313 T314 L315 E316 T317 D318 E319 D320 M321 V322 I325 R326 L327 K328 Y329 F330 D331 T332 V335 A336 A337 A338 K343 V349 A350 S351 E352 F353 G354 N355 H356 A362 G365 D366 E369 E370 P371 E372 F373 S374 S375 A376 M377 P378 L379

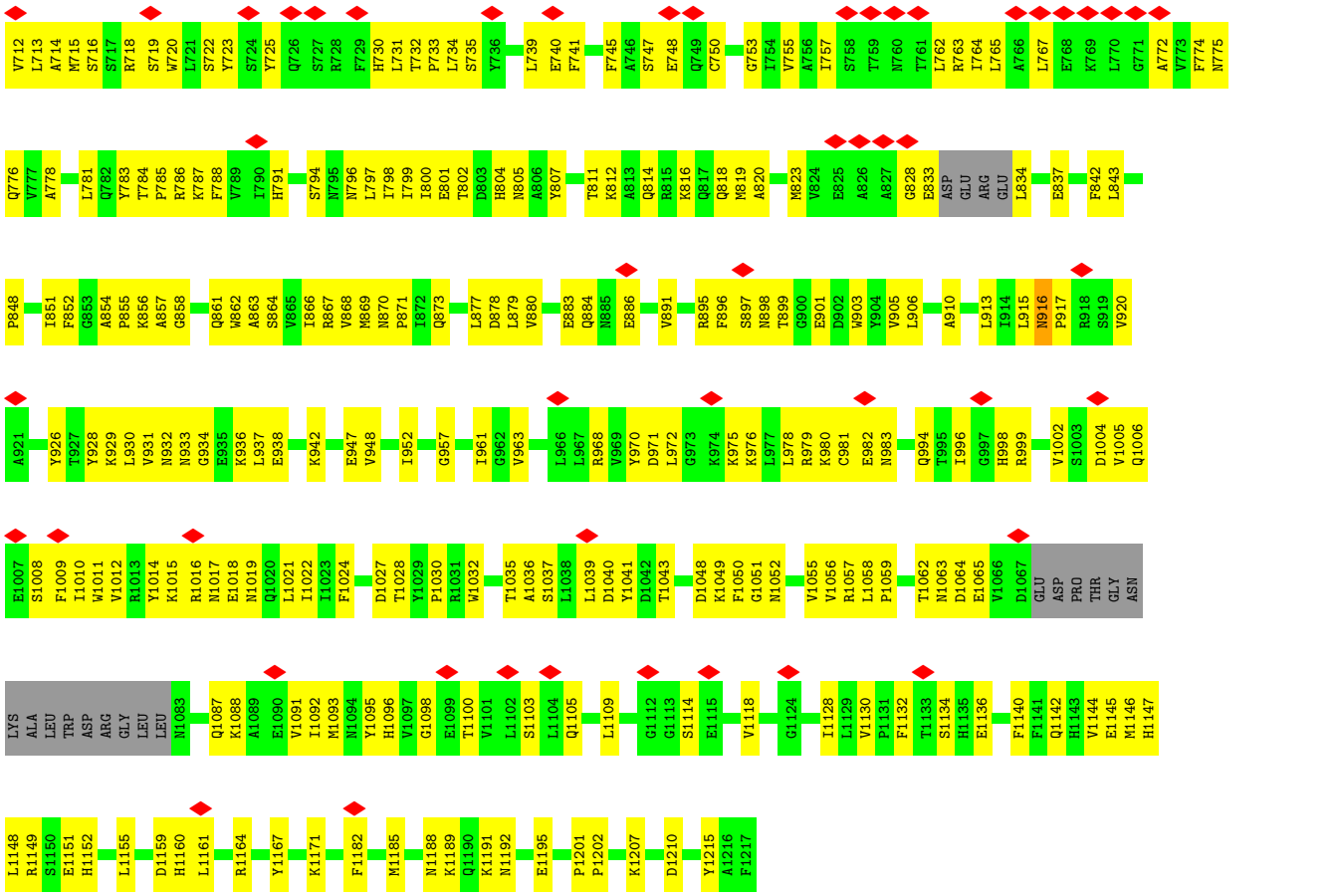
E380 GLU GLY D383 T384 F385 F386 F387 Q388 P389 N394 D399 E400 L401 L404 S405 P406 I407 L408 F409 C410 Q411 I412 N417 E418 L423 Y424 V425 G428 R429 R432 S433 S434 L435 R436 V437 L438 R439 H440 G441 L442 E443 V444 S445 E446 M447 A448 V449 S450 E451 L452 P453 G454

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 G488 E489 T490 V491 E492 E493 V494 T495 D496 S497 G498 F499 L500 G501 T502 T503 P504 T505 L506 S507 C508 S509 L510 L511 D514 A515 L516

V517 Q518 V519 Y520 P521 D522 G523 I524 R525 H526 I527 R528 A529 D530 K531 R532 V533 N534 V535 W536 K537 T538 P539 G540 K541 K542 T543 I544 V545 K546 C547 A548 V549 N550 Q551 R552 Q553 V554 V555 I556 A557 L558 T559 G560 G561 E562 L563 V564 Y565 F566 E567 M568 S571 G572 Y577 T578 E579 R580

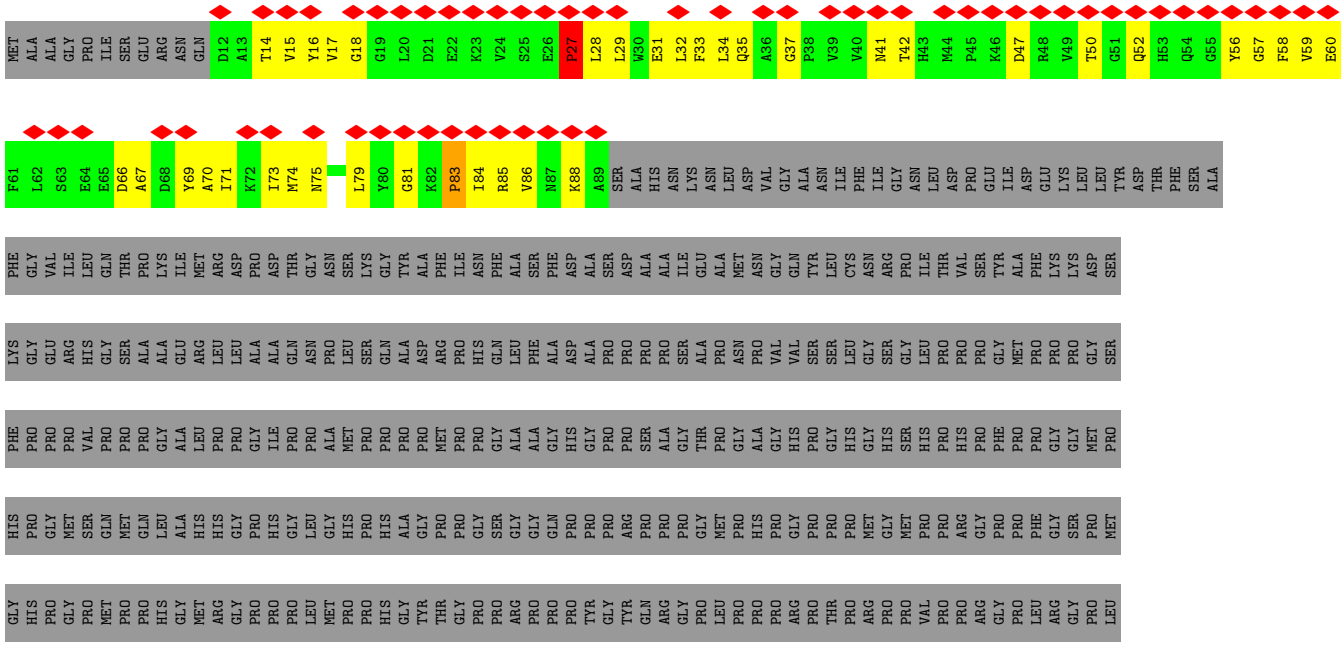
K581 E582 M583 S584 A585 D586 V587 V588 C589 M590 S591 L592 A593 N594 V595 P596 P597 Q600 R601 S602 R603 F604 L605 A606 V607 G608 L609 V610 D611 N612 T613 V614 R615 I616 I617 S618 L619 D620 P621 S622 D623 C624 L625 Q626 P627 L628 Q631 A632 L633 P634 A635 Q636 P637 E638 S639 L640 C641 I642

V643 E644 M645 GLY GLY THR GLU LYS GLN ASP GLU LEU GLY GLU ARG GLY SER ILE GLY F662 L663 Y664 I667 G668 L669 Q670 N671 G672 V673 L674 L675 L679 D680 G684 D685 L686 R690 T691 ARG TYR LEU G695 S696 R697 P698 V699 K700 L701 F702 R703 Q707 G708 Q709 E710 A711



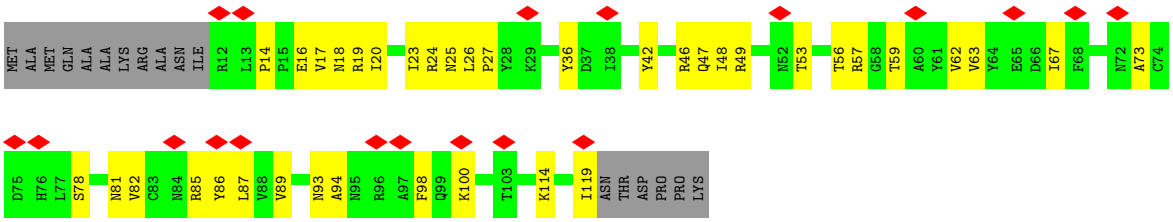
• Molecule 24: Splicing factor 3B subunit 4

Chain 4:



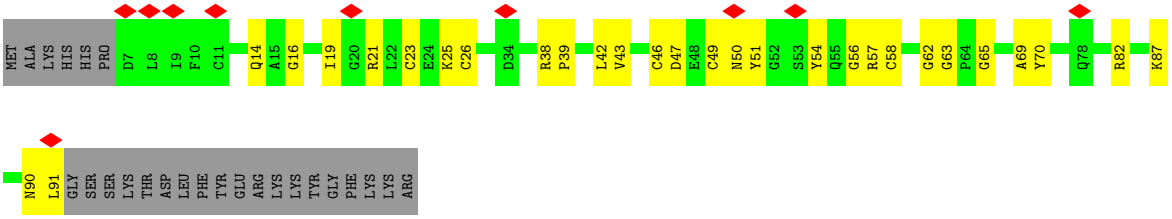
• Molecule 25: Splicing factor 3B subunit 6

Chain 5:



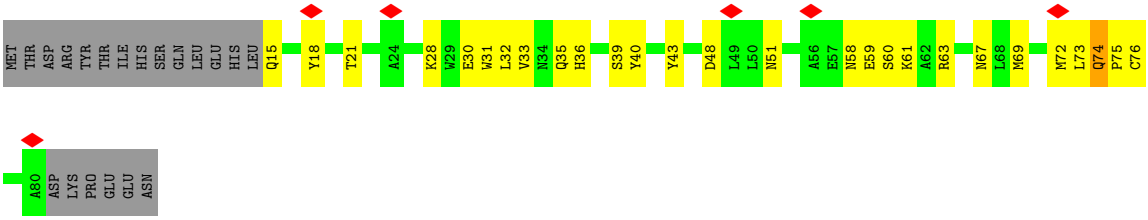
• Molecule 26: PHD finger-like domain-containing protein 5A

Chain 6:



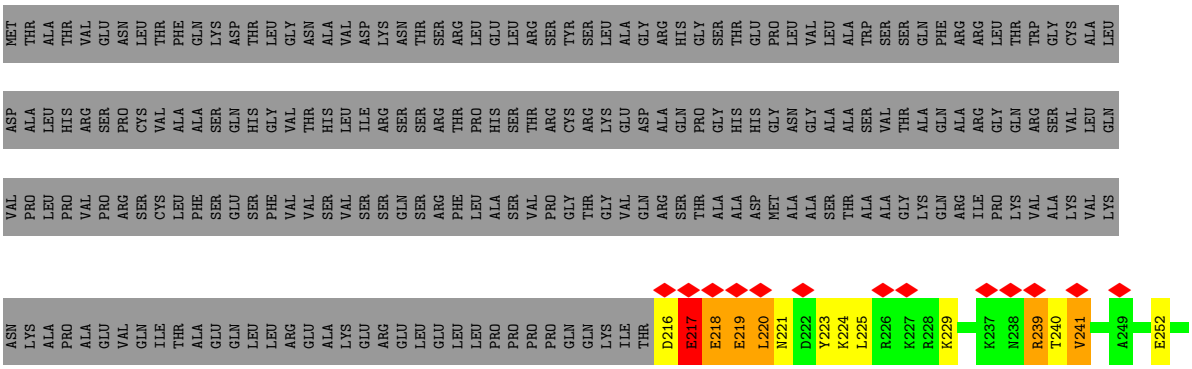
• Molecule 27: Splicing factor 3B subunit 5

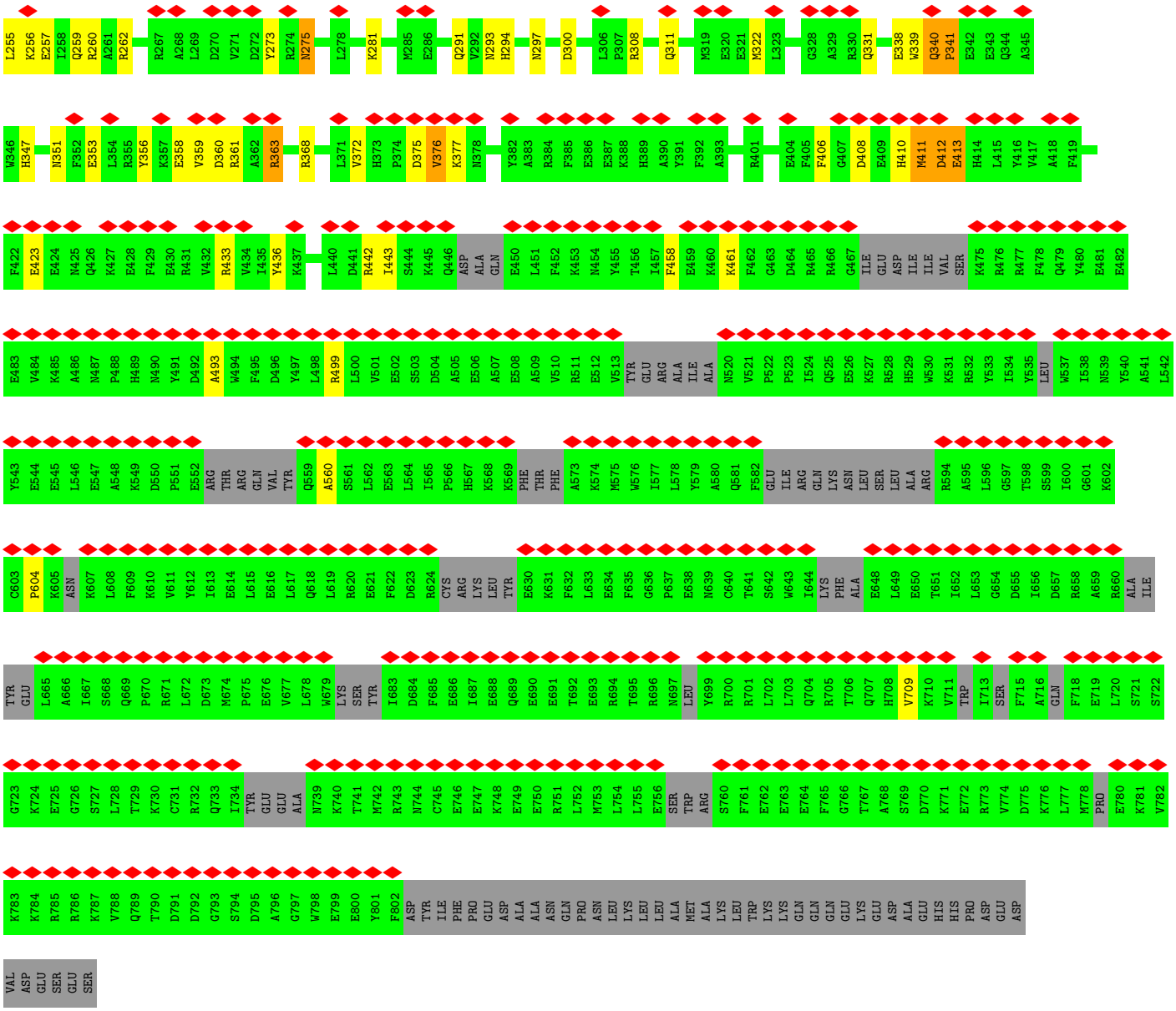
Chain 7:



• Molecule 28: Crooked neck-like protein 1

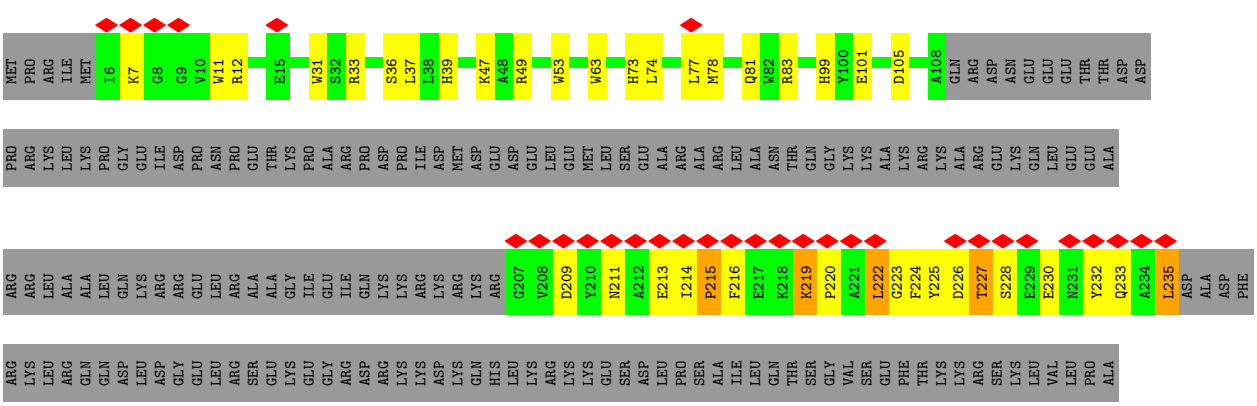
Chain J:





- Molecule 29: Cell division cycle 5-like protein

Chain L:



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

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

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

LEU LEU GLY LEU PRO ALA PRO LYS ASN ASP PHE GLU ILE VAL LEU PRO GLU ASN ALA GLU LYS GLU L502 E503 E504 R505 E506 I507 D508 D509 T510 Y511 I512 E513 D514 A515 A516 D517 V518 D519 A520 R521 K522 Q523 A524 I525 R526 D527 A528 E529 R530 V531 K532 E533 M534 K535 ARG MET HIS LYS

A540 V541 Q542 K543 D544 L545 P546 R547 P548 S549 E550 V551 N552 GLU THR ILE L556 R557 P558 L559 N560 V561 E562 P563 P564 L565 T566 D567 L568 Q569 K570 S571 GLU GLU LEU ILE LYS LYS GLU MET ILE T581 M582 L583 H584 Y585 D586 L587 L588 H589 HIS PRO TYR E593 P594 S595 G596 N597 K598 K599

G600 K601 T602 V603 G604 F605 G606 T607 N608 ASN SER GLU HIS ILE T614 Y615 L616 E617 H618 N619 P620 Y621 E622 K623 F624 S625 K626 E627 E628 L629 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 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 LYS LYS ASP ARG ILE E690 S691 L692 E693 K694 R695 L696 E697 I698 N699 R700 G701 H702 N703 T704 T705 E706 A707 K708 R709 A710 A711 K712 M713 E714 K715 K716 N717 K718 I719

L720 L721 G722 G723 Y724 Q725 S726 R727 A728 M729 G730 L731 M732 K733 Q734 L735 N736 D737 L738 W739 D740 Q741 I742 E743 Q744 A745 H746 L747 E748 L749 R750 T751 F752 E753 E754 L755 K756 K757 H758 E759 D760 S761 A762 I763 P764 R765 R766 L767 E768 C769 L770 K771 E772 D773 V774 Q775 R776 Q777 Q778 E779

R780 E781 Q785 H786 R787 Y788 A789 D790 L791 L792 L793 E794 K795 GLU THR LEU LYS SER LYS PHE

- Molecule 30: Pre-mRNA-processing factor 19

Chain q: 26% 24% •• 74%

MET SER L3 I4 C5 S6 I7 S8 N9 E10 V11 P12 E13 H14 P15 C16 V17 S18 P19 V20 S21 N22 H23 V24 Y25 E26 R27 R28 L29 I30 E31 K32 Y33 I34 A35 E36 N37 G38 T39 D40 P41 I42 N43 N44 Q45 P46 L47 S48 E49 E50 Q51 L52 I53 D54 I55 K56 V57 A58 H59 P60

I61 R62 P63 K64 P65 P66 S67 A68 T69 S70 I71 P72 A73 I74 L75 K76 A77 L78 Q79 D80 E81 W82 D83 A84 V85 M86 L87 H88 S89 F90 T91 L92 R93 Q94 Q95 L96 Q97 T98 T99 R100 Q101 E102 L103 S104 H105 A106 L107 Y108 Q109 H110 D111 A112 A113 C114 R115 V116 I117 A118 R119 L120

T121 K122 E123 V124 T125 A126 A127 R128 E129 A130 L131 A132 T133 L134 LYS PRO GLN ALA GLY LEU ILE VAL PRO GLN ALA VAL PRO SER SER GLN PRO SER VAL VAL GLY ALA GLY GLU PRO MET ASP LEU GLY GLU LEU VAL GLY MET THR PRO GLU ILE ILE GLN LYS LEU GLN ASP LYS ALA

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

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

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

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

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

VAL ALA PHE GLY HIS HIS ALA LYS PHE ILE ALA SER THR GLY MET ASP ARG SER LEU LYS PHE TYR SER LEU

- Molecule 30: Pre-mRNA-processing factor 19

Chain r: 26% 24% 74%

MET SER L3 I4 C5 S6 I7 S8 N9 E10 V11 P12 E13 H14 P15 C16 V17 S18 P19 V20 S21 N22 H23 V24 Y25 E26 R27 R28 L29 I30 E31 K32 Y33 I34 A35 E36 N37 G38 T39 D40 P41 I42 N43 N44 Q45 P46 L47 S48 E49 E50 Q51 L52 I53 D54 I55 K56 V57 A58 H59 P60

I61 R62 P63 K64 P65 P66 S67 A68 T69 S70 I71 P72 A73 I74 L75 K76 A77 L78 Q79 D80 E81 W82 D83 A84 V85 M86 L87 H88 S89 F90 T91 L92 R93 Q94 Q95 L96 Q97 T98 T99 R100 Q101 E102 L103 S104 H105 A106 L107 Y108 Q109 H110 D111 A112 A113 C114 R115 V116 I117 A118 R119 L120

T121 K122 E123 V124 T125 A126 A127 R128 E129 A130 L131 A132 T133 LEU LYS PRO GLN ALA GLY LEU ILE VAL PRO GLN ALA VAL PRO SER SER GLN PRO SER VAL VAL GLY ALA GLY GLU PRO MET ASP LEU GLY GLU LEU VAL GLY MET THR PRO GLU ILE ILE GLN LYS LEU GLN ASP LYS ALA

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

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

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

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

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

VAL ALA PHE GLY HIS HIS ALA LYS PHE ILE ALA SER THR GLY MET ASP ARG SER LEU LYS PHE TYR SER LEU

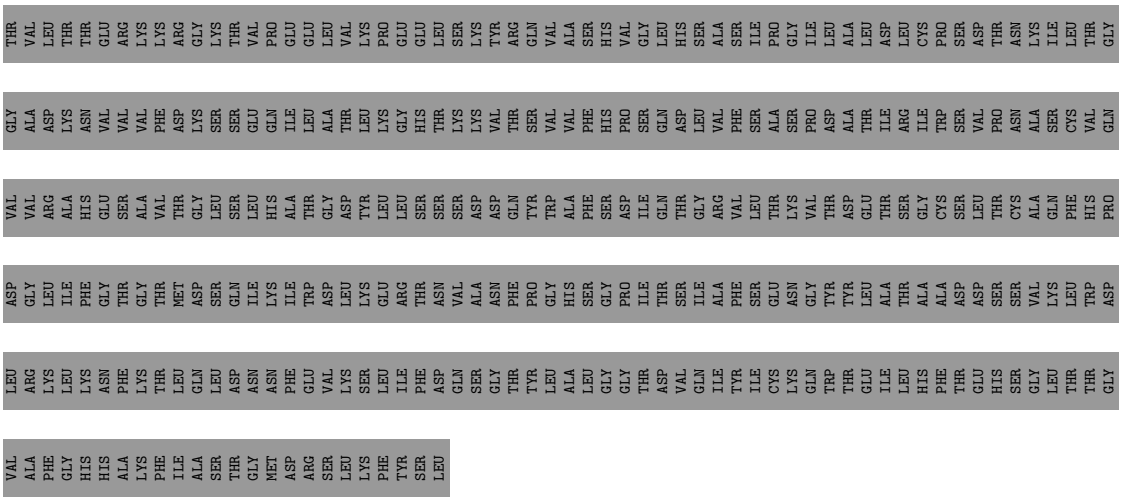
- Molecule 30: Pre-mRNA-processing factor 19

Chain s: 13% 13% 87%

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

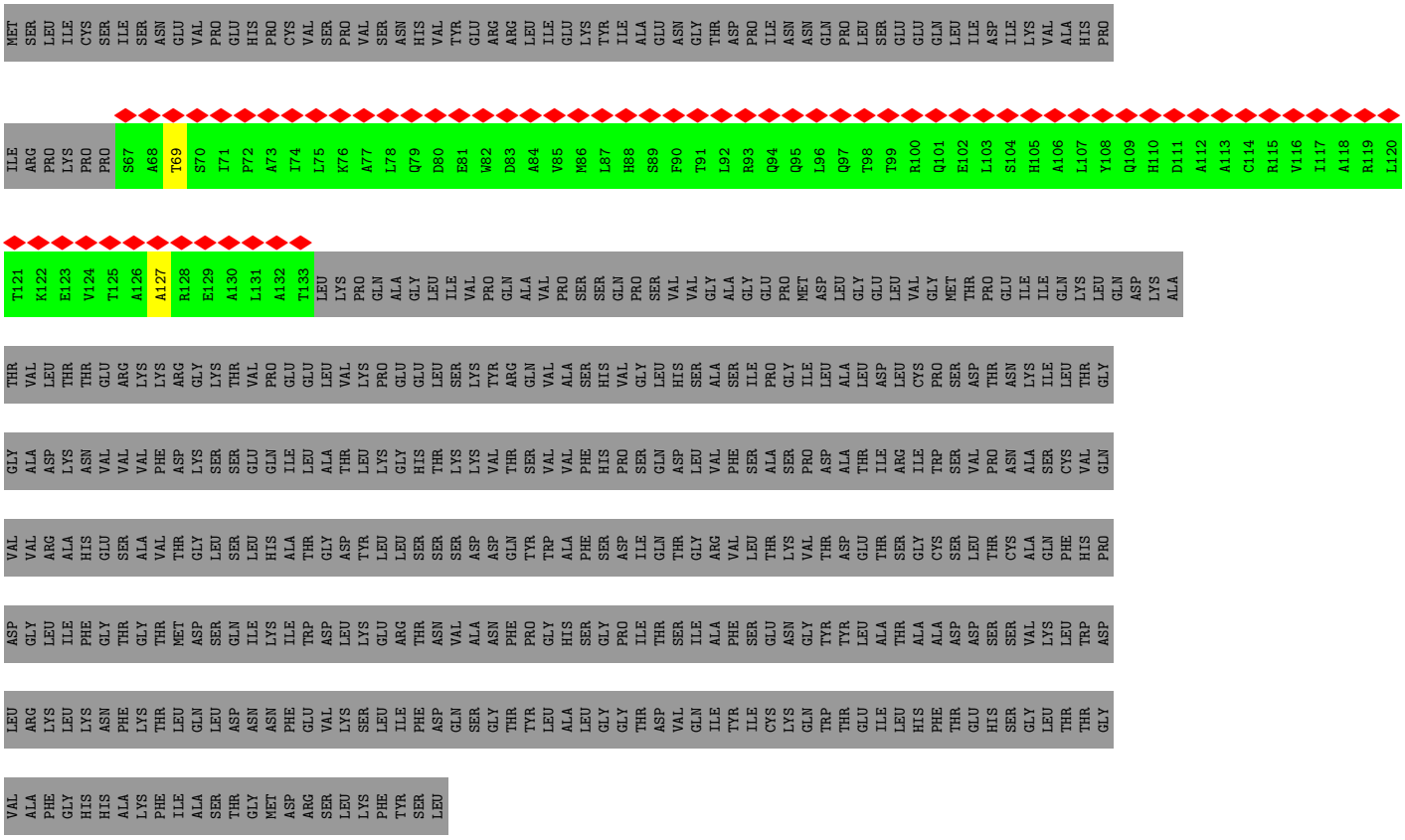
ILE ARG PRO LYS PRO PRO SER A68 T69 S70 I71 P72 A73 I74 L75 K76 A77 L78 Q79 D80 E81 W82 D83 A84 V85 M86 L87 H88 S89 F90 T91 L92 R93 Q94 Q95 L96 Q97 T98 T99 R100 Q101 E102 L103 S104 H105 A106 L107 Y108 Q109 H110 D111 A112 A113 C114 R115 V116 I117 A118 R119 L120

T121 K122 E123 V124 T125 A126 A127 R128 E129 A130 L131 A132 T133 L134 LYS PRO GLN ALA GLY LEU ILE VAL PRO GLN ALA VAL PRO SER SER GLN PRO SER VAL VAL GLY ALA GLY GLU PRO MET ASP LEU GLY GLU LEU VAL GLY MET THR PRO GLU ILE ILE GLN LYS LEU GLN ASP LYS ALA



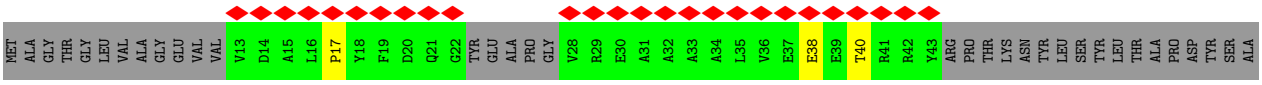
• Molecule 30: Pre-mRNA-processing factor 19

Chain t:



• Molecule 31: Pre-mRNA-splicing factor SPF27

Chain K:



PHE GLU T63 D64 I65 M66 R67 N68 E69 F70 E71 R72 L73 A74 A75 R76 Q77 P78 I79 E80 L81 L82 S83 M84 K85 R86 Y87 E88 L89 P90 A91 P92 S93 SER GLY GLN LYS ASN ASP ILE THR ALA TRP GLN E105 C106 V107 N108 N109 S110 M111 A112 Q113 L114 E115 H116 Q117 A118 V119 R120

I121 E122 N123 L124 E125 L126 M127 S128 Q129 H130 G131 C132 N133 A134 W135 K136 V137 Y138 N139 E140 N141 L142 S143 H144 M145 I146 E147 H148 A149 Q150 K151 E152 L153 Q154 K155 L156 R157 K158 H159 I160 Q161 D162 L163 N164 W165 Q166 R167 K168 N169 M170 Q171 L172 T173 A174 G175 S176 K177 L178 R179 E180

S183 N184 W185 V186 S187 L188 V189 S190 K191 E194 I195 E196 R197 T198 I199 VAL GLN LEU GLU ASN GLU ILE TYR GLN ILE LYS GLN GLN HIS GLY GLU ALA ASN LYS GLU ASN ILE ARG GLN ASP PHE

- Molecule 32: Pre-mRNA-splicing factor SYF1

Chain I: 65% 60% 6% 34%

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

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

MET ASP GLN GLY ARG VAL THR HIS THR ARG ARG THR PHE ASP ARG ALA LEU ARG ALA LEU PRO ILE THR GLN HIS SER ARG ILE TRP PRO LEU TYR LEU ARG PHE L156 R157 S158 H159 P160 L161 P162 E163 T164 A165 V166 ARG GLY TYR ARG ARG F172 L173 K174 L175 S176 P177 E178 S179 A180

E181 E182 Y183 ILE GLU Y186 L187 K188 S189 S190 D191 R192 L193 D194 E195 A196 A197 Q198 R199 L200 A201 T202 VAL V204 N205 D206 E207 R208 F209 V210 S211 K212 A213 G214 K215 S216 N217 Y218 GLN LEU TRP H222 E223 L224 C225 D226 L227 I228 S229 Q230 N231 P232 D233 K234 VAL Q236 S237 L238 N239 V240

D241 A242 I243 I244 R245 G246 G247 L248 T249 R250 F251 T252 ASP Q254 L255 G256 K257 L258 W259 C260 S261 L262 A263 D264 Y265 Y266 I267 ARG S269 G270 H271 F272 E273 K274 A275 R276 D277 V278 Y279 E280 E281 A282 I283 ARG THR V286 M287 T288 V289 R290 D291 F292 T293 Q294 V295 F296 D297 S298 Y299 ALA

GLN PHE E303 E304 S305 M306 I307 A308 A309 K310 M311 E312 T313 A314 S315 E316 LEU GLY ARG E320 E321 E322 D323 D324 V325 D326 L327 E328 L329 R330 L331 A332 R333 F334 E335 GLN L337 I338 S339 R340 R341 P342 L343 L344 L345 N346 S347 V348 L349 L350 R351 Q352 N353 PRO H355 H356 V357 H358 E359 W360

H361 K362 R363 V364 A365 L366 HIS GLN G369 R370 P371 R372 E373 I374 I375 N376 T377 Y378 T379 E380 A381 V382 Q383 THR VAL ASP P387 F388 K389 A390 T391 G392 K393 P394 H395 T396 L397 W398 VAL ALA PHE ALA LYS F404 Y405 E406 D407 N408 G409 Q410 L411 D412 D413 A414 R415 V416 I417 LEU GLU LYS

A421 T422 K423 V424 N425 F426 K427 Q428 V429 D430 D431 L432 A433 S434 V435 W436 C437 GLN C439 G440 E441 L442 E443 L444 R445 H446 E447 N448 Y449 D450 E451 A452 L453 R454 L455 L456 R457 K458 A459 T460 ALA L462 P463 A464 R465 R466 A467 E468 Y469 F470 D471 G472 S473 E474 P475 V476 Q477 N478 R479 V480

Y481 K482 S483 L484 K485 VAL W487 S488 M489 L490 A491 D492 E495 S496 L497 G498 T499 F500 Q501 S502 THR LYS ALA VAL Y507 D508 R509 I510 L511 D512 L513 R514 I515 A516 T517 P518 Q519 I520 V521 I522 N523 Y524 A525 MET F527 L528 E529 E530 H531 K532 Y533 F534 E535 E536 S537 F538 K539 A540 Y541

E542 ARG GLY ILE S546 L547 F548 K549 W550 P551 N552 V553 S554 D555 I556 W557 S558 T559 Y560 L561 THR LYS PHE ILE ALA ARG TYR G569 G570 R571 K572 L573 E574 R575 A576 R577 D578 L579 F580 GLU GLN ALA L584 D585 G586 C587 P588 P589 K590 Y591 A592 K593 T594 L595 Y596 L597 L598 Y599 A600 Q601

L602 E603 E604 E605 W606 G607 L608 A609 R610 H611 A612 M613 A614 V615 Y616 E617 R618 A619 T620 R621 E624 P625 A626 Q627 Q628 Y629 D630 M631 F632 N633 I634 Y635 I636 LYS ARG ALA A640 E641 I642 Y643 G644 V645 T646 H647 T648 R649 G650 I651 Y652 Q653 LYS ALA ILE GLU VAL LEU SER ASP GLU

H663 A664 R665 E666 M667 G668 L669 R670 F671 A672 D673 M674 E675 G676 LYS LEU G679 E680 I681 D682 R683 A684 R685 A686 I687 Y688 S689 PHE CYS SER GLN ILE CYS ASP PRO ARG THR THR GLY ALA PHE TRP GLN T706 W707 K708 D709 F710 E711 V712 R713 H714 G715 N716 E717 D718 T719 I720 K721 E722

M723 L724 R725 I726 R727 R728 S729 V730 Q731 A732 T733 Y734 ASN THR GLN VAL ASN F740 M741 A742 S743 Q744 M745 L746 K747 V748 S749 G750 S751 A752 T753 G754 T755 V756 SER ASP LEU A760 P761 G762 Q763 S764 G765 M766 D767 D768 M769 K770 L771 L772 E773 Q774 R775 ALA GLU GLN L779 A780 A781 E782

A783 E784 R785 D786 Q787 P788 L789 R790 A791 Q792 S793 K794 ILE L796 F797 V798 R799 S800 D801 A802 S803 R804 E805 E806 L807 A808 E809 L810 A811 Q812 Q813 V814 N815 P816 E817 E818 I819 GLN LEU GLY GLU ASP GLU ASP GLU ASP GLU ASP GLU MET ASP LEU GLU PRO ASN GLU VAL ARG LEU GLU GLN GLN

SER VAL PRO ALA ALA VAL PHE GLY SER LEU LYS GLU ASP

- Molecule 33: Intron-binding protein aquarius

Chain Q:

MET ALA ALA PRO ALA GLN PRO LYS LYS ILE VAL ALA PRO THR VAL SER GLN ILE ASN ALA 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 L67 E68 F69 S70 Q71 Y72 L73 E74 N75 Y76 L77 W78 M79 N80 Y81 S82 P83 E84 V85 S86 S87 K88 A89 Y90 L91 M92 S93 I94 C95 C96 M97 V98 N99 E100 K101 F102 R103 E104 N105 V106 P107 A108 W109 E110 I111 F112 K113 K114 K115 P116 D117 H118 F119 P120

F121 F122 F123 K124 H125 I126 L127 K128 A129 A130 L131 A132 E133 T134 D135 G136 E137 F138 S139 L140 H141 E142 Q143 T144 V145 L146 L147 L148 F149 L150 D151 H152 C153 F154 N155 S156 L157 E158 V159 D160 L161 I162 R163 S164 Q165 V166 Q167 Q168 L169 I170 S171 L172 P173 M174 W175 M176 G177 L178 Q179 L180

A181 R182 L183 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 Q227 K228 F229 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 L260 E261 A262 L263 L264 P265 T266 R267 R268 W269 F270 N271 T272 I273 L274 D275 D276 S277 H278 L279 L280 V281 H282 C283 Y284 L285 S286 N287 L288 V289 R290 R291 E292 E293 D294 G295 H296 L297 F298 S299 Q300

L301 L302 D303 M304 L305 K306 F307 Y308 T309 G310 F311 E312 I313 N314 D315 Q316 T317 L318 N319 A320 L321 T322 E323 N324 E325 M326 T327 T328 I329 H330 Y331 D332 R333 I334 T335 S336 L337 Q338 R339 A340 A341 F342 A343 H344 F345 PRO GLU L348 Y349 D350 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 L384 C385 L386 L387 P388 T389 L390 P391 K392 N393 E394 D395 T396 T397 F398 D399 K400 E401 F402 L403 L404 E405 L406 L407 V408 S409 R410 H411 E412 R413 R414 I415 S416 Q417 I418 Q419 Q420

L421 N422 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 K454 L455 N456 L457 Q458 F459 L460 T461 L462 H463 D464 Y465 L466 L467 R468 N469 F470 N471 L472 F473 R474 L475 E476 S477 T478 Y479 E480

I481 R482 Q483 D484 I485 E486 D487 S488 V489 S490 R491 M492 K493 P494 W495 Q496 S497 GLU TYR G500 G501 V502 V503 F504 G505 G506 W507 A508 R509 M510 A511 Q512 P513 I514 V515 A516 F517 T518 V519 V520 E521 V522 A523 K524 P525 N526 I527 G528 E529 N530 W531 P532 T533 R534 V535 R536 A537 D538 V539 T540

I541 N542 L543 N544 V545 R546 D547 H548 I549 K550 D551 E552 W553 E554 G555 L556 R557 K558 H559 D560 V561 C562 F563 L564 I565 T566 V567 R568 P569 T570 K571 P572 Y573 G574 T575 K576 F577 D578 R579 R580 R581 P582 F583 I584 E585 Q586 V587 G588 L589 V590 Y591 V592 R593 G594 C595 E596 I597 Q598 G599 M600

L601 D602 D603 K604 G605 R606 V607 I608 GLU ASP GLY PRO GLU P614 R615 P616 M617 L618 R619 G620 E621 S622 R623 T624 F625 R626 V627 F628 L629 D630 P631 M632 Q633 Y634 Q635 Q636 D637 M638 T639 N640 T641 I642 Q643 N644 G645 A646 E647 D648 V649 Y650 E651 T652 F653 N654 I655 I656 M657 R658 R659 K660

P661 K662 E663 N664 M665 F666 K667 A668 V669 L670 E671 T672 I673 R674 N675 L676 M677 N678 T679 D680 C681 V682 V683 P684 D685 W686 L687 H688 D689 I690 I691 L692 G693 Y694 G695 D696 P697 S698 S699 A700 H701 Y702 S703 K704 M705 P706 N707 Q708 I709 A710 T711 L712 D713 F714 N715 D716 T717 F718 L719 S720

I721 E722 H723 L724 K725 A726 S727 F728 P729 G730 H731 N732 V733 K734 V735 T736 V737 E738 D739 P740 A741 L742 Q743 ILE PRO P746 F747 R748 I749 T750 F751 P752 V753 ARG SER GLY LYS GLY LYS LYS ARG LYS ASP ALA ASP VAL GLU ASP GLU ASP THR GLU GLU A774 K775 T776 L777 I778 V779 E780

P781 H782 V783 I784 P785 N786 R787 G788 P789 Y790 P791 Y792 N793 Q794 P795 K796 R797 N798 T799 I800 Q801 F802 T803 H804 T805 Q806 I807 E808 A809 I810 R811 A812 G813 M814 Q815 P816 G817 L818 T819 M820 V821 V822 G823 P824 P825 G826 T827 G828 K829 T830 D831 V832 A833 V834 Q835 I836 I837 S838 N839 I840

Y841 H842 N843 F844 P845 E846 Q847 R848 T849 L850 I851 V852 T853 H854 S855 N856 Q857 A858 L859 N860 Q861 L862 F863 E864 K865 I866 M867 A868 L869 D870 I871 D872 E873 R874 H875 L876 L877 R878 L879 G880 H881 GLY GLU E884 E885 L886 E887 T888 E889 K890 D891 F892 S893 R894 Y895 G896 R897 V898 N899 Y900

V901 L902 A903 R904 R905 I906 E907 L908 L909 E910 E911 V912 K913 R914 L915 Q916 K917 S918 L919 G920 V921 P922 G923 D924 A925 S926 Y927 T928 C929 E930 T931 A932 G933 Y934 F935 F936 L937 Y938 Q939 V940 M941 S942 R943 W944 E945 E946 Y947 I948 S949 K950 V951 K952 N953 LYS GLY SER THR LEU P959 D960

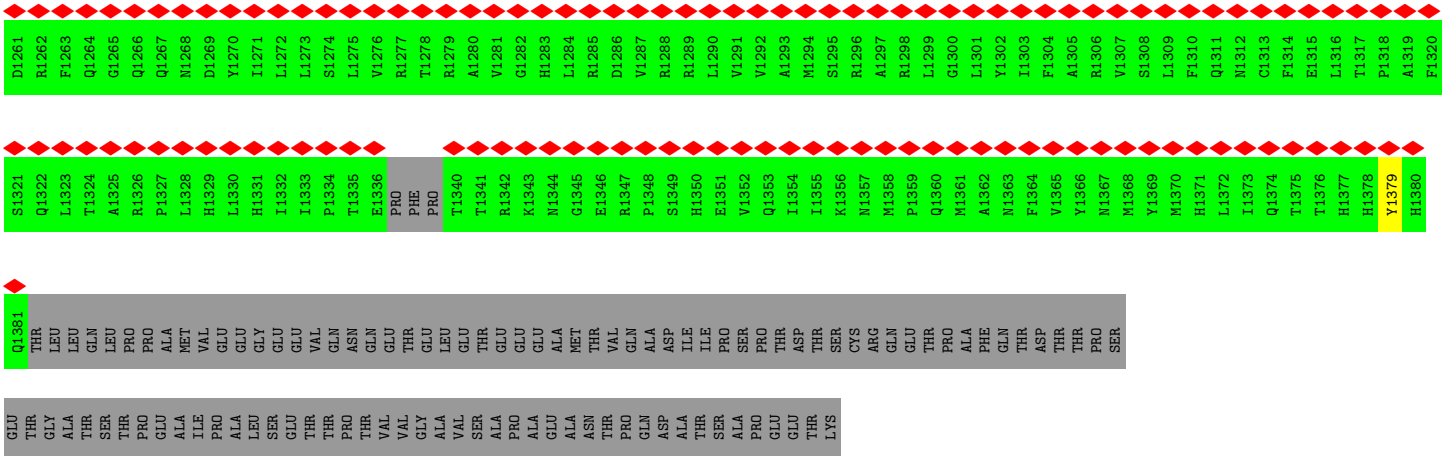
V961 T962 E963 V964 S965 T966 F967 F968 P969 F970 H971 E972 Y973 F974 A975 N976 A977 PRO GLN PRO I981 F982 K983 G984 R985 S986 Y987 E988 E989 D990 M991 E992 I993 A994 E995 G996 C997 F998 R999 H1000 T1001 K1002 K1003 I1004 F1005 T1006 Q1007 L1008 E1009 E1010 F1011 R1012 A1013 S1014 E1015 L1016 L1017 R1018 S1019 G1020

L1021 D1022 R1023 S1024 K1025 Y1026 L1027 L1028 V1029 K1030 E1031 A1032 K1033 I1034 I1035 A1036 M1037 T1038 C1039 T1040 H1041 A1042 A1043 L1044 K1045 R1046 H1047 D1048 L1049 V1050 K1051 L1052 G1053 F1054 K1055 Y1056 D1057 N1058 I1059 L1060 M1061 E1062 E1063 A1064 A1065 Q1066 I1067 L1068 E1069 I1070 E1071 T1072 F1073 I1074 P1075 L1076 L1077 L1078 Q1079 N1080

P1081 Q1082 D1083 G1084 F1085 S1086 R1087 L1088 K1089 R1090 W1091 I1092 M1093 I1094 G1095 D1096 H1097 H1098 Q1099 L1100 P1101 P1102 V1103 I1104 K1105 N1106 M1107 A1108 F1109 Q1110 K1111 Y1112 S1113 N1114 M1115 E1116 Q1117 S1118 L1119 F1120 T1121 R1122 F1123 V1124 R1125 V1126 G1127 V1128 P1129 T1130 V1131 D1132 L1133 D1134 A1135 Q1136 G1137 R1138 A1139 R1140

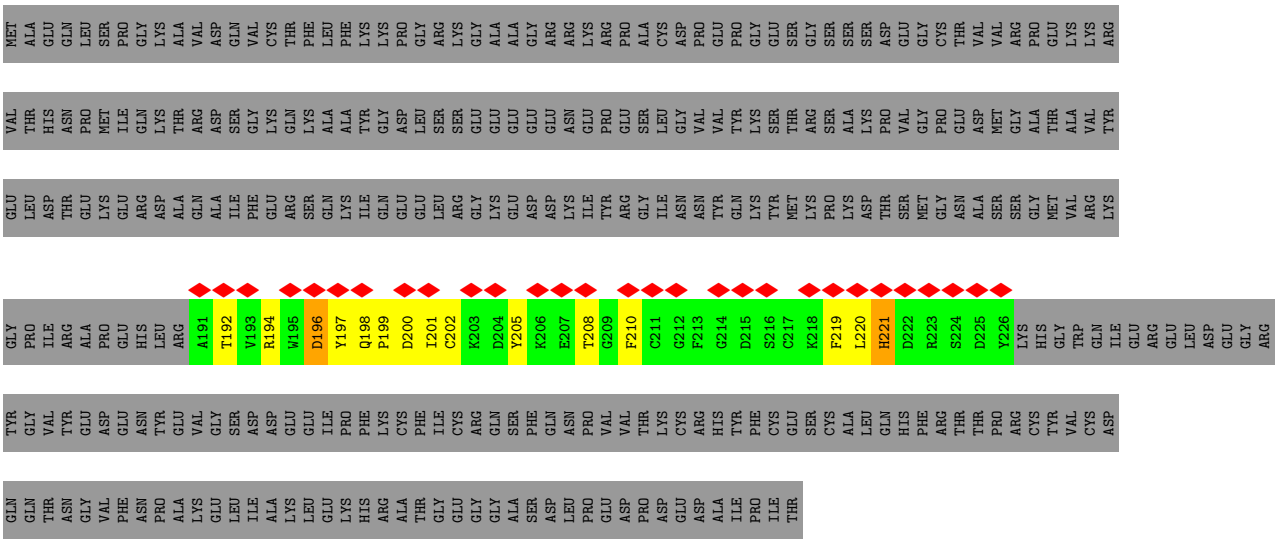
A1141 S1142 L1143 C1144 N1145 L1146 Y1147 N1148 W1149 R1150 Y1151 K1152 N1153 L1154 G1155 N1156 L1157 P1158 H1159 V1160 Q1161 L1162 L1163 P1164 E1165 F1166 S1167 T1168 A1169 N1170 A1171 G1172 L1173 L1174 Y1175 D1176 F1177 Q1178 L1179 I1180 N1181 V1182 E1183 D1184 F1185 Q1186 G1187 V1188 G1189 E1190 S1191 E1192 P1193 N1194 P1195 Y1196 F1197 Y1198 Q1199 N1200

L1201 G1202 E1203 A1204 E1205 Y1206 V1207 V1208 A1209 L1210 F1211 M1212 Y1213 M1214 C1215 L1216 L1217 G1218 Y1219 P1220 A1221 D1222 K1223 I1224 S1225 I1226 L1227 T1228 T1229 Y1230 N1231 G1232 Q1233 K1234 H1235 L1236 I1237 R1238 D1239 I1240 I1241 N1242 R1243 R1244 C1245 G1246 N1247 N1248 P1249 L1250 I1251 G1252 R1253 P1254 N1255 K1256 V1257 T1258 T1259 V1260



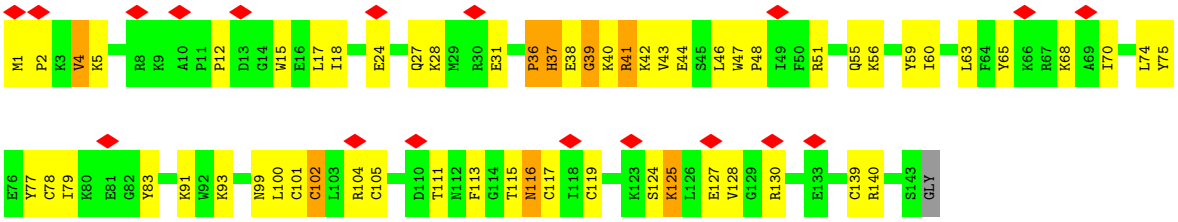
• Molecule 34: RING finger protein 113A

Chain M:



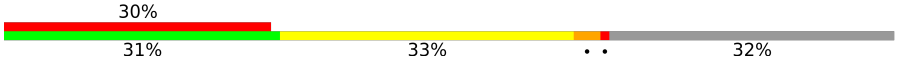
• Molecule 35: Protein BUD31 homolog

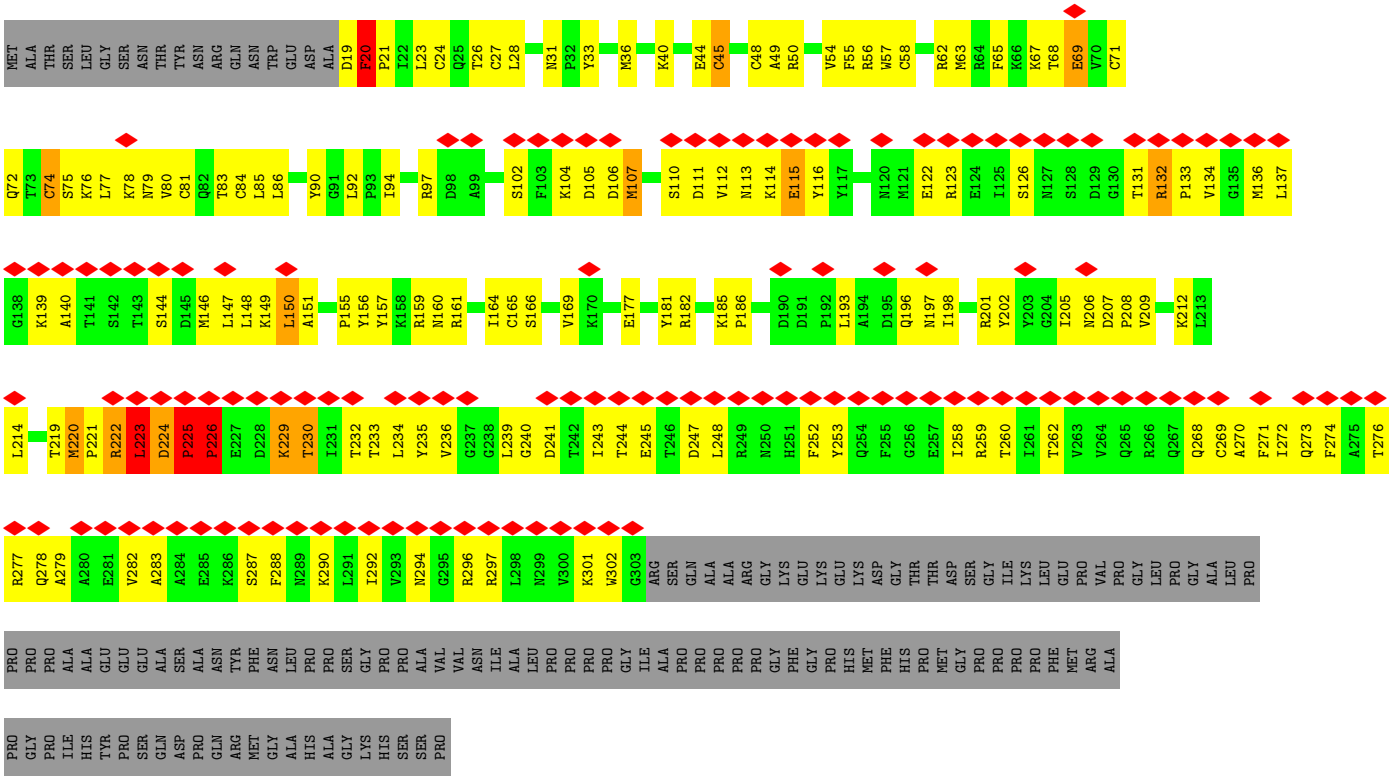
Chain N:



• Molecule 36: Pre-mRNA-splicing factor RBM22

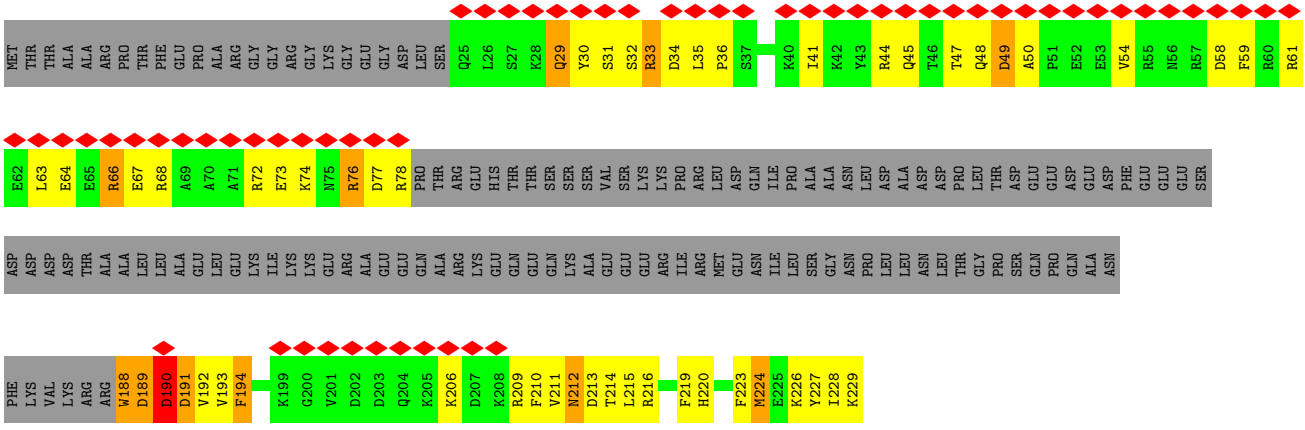
Chain O:





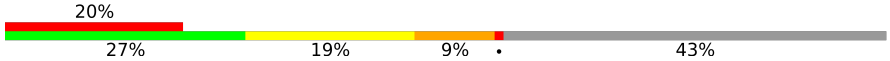
- Molecule 37: Spliceosome-associated protein CWC15 homolog

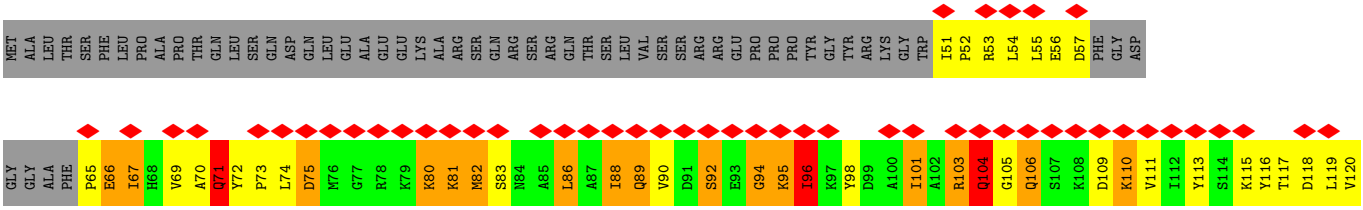
Chain P:

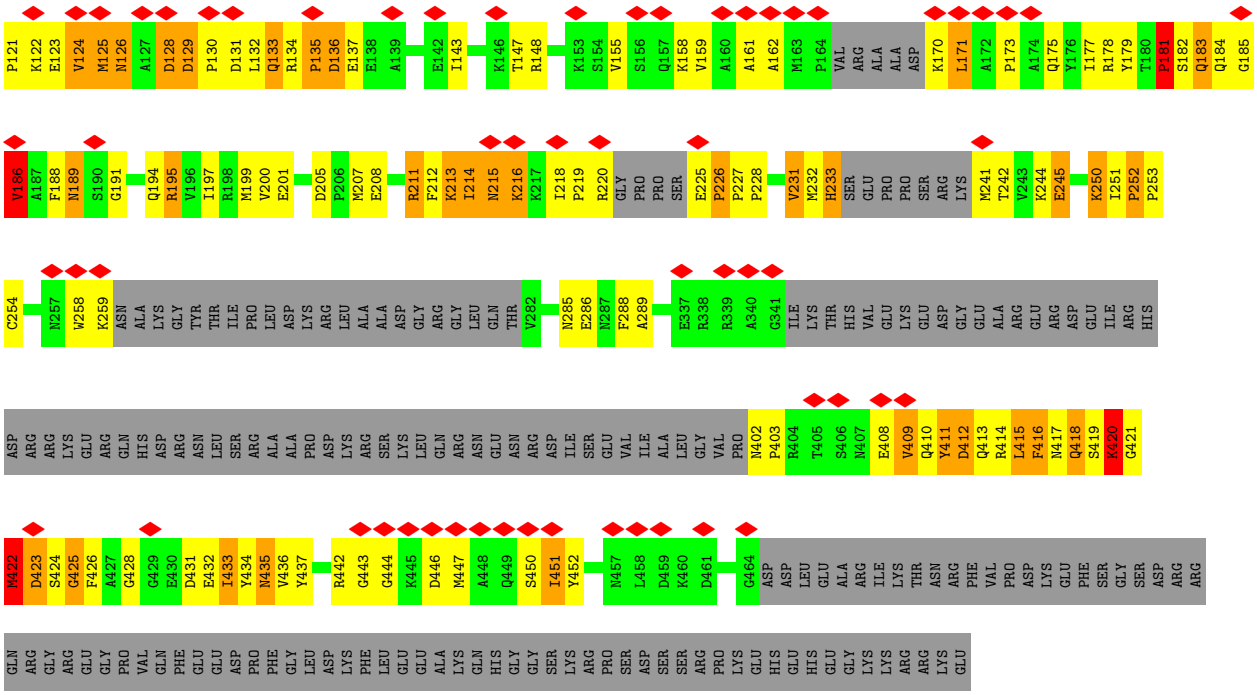


- Molecule 38: Skip

Chain R:

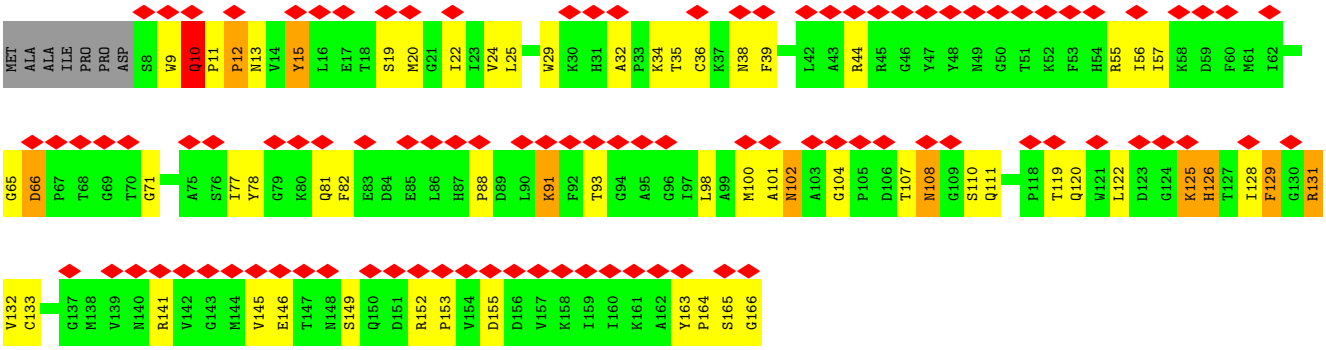






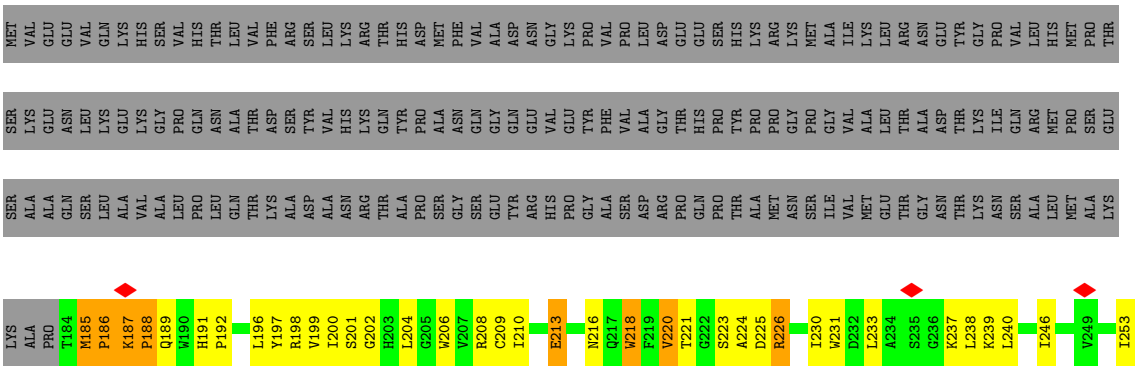
- Molecule 39: Peptidyl-prolyl cis-trans isomerase-like 1

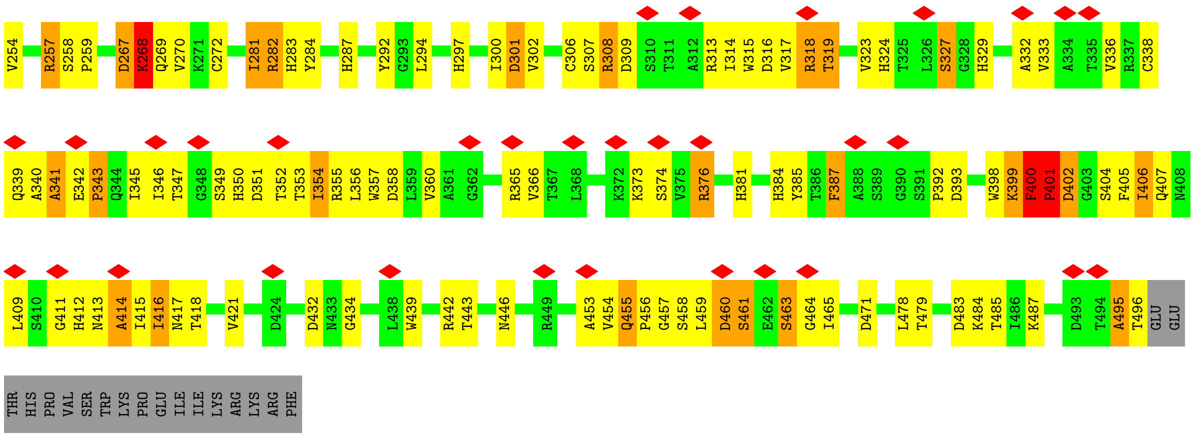
Chain S:



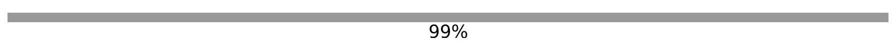
- Molecule 40: Pleiotropic regulator 1

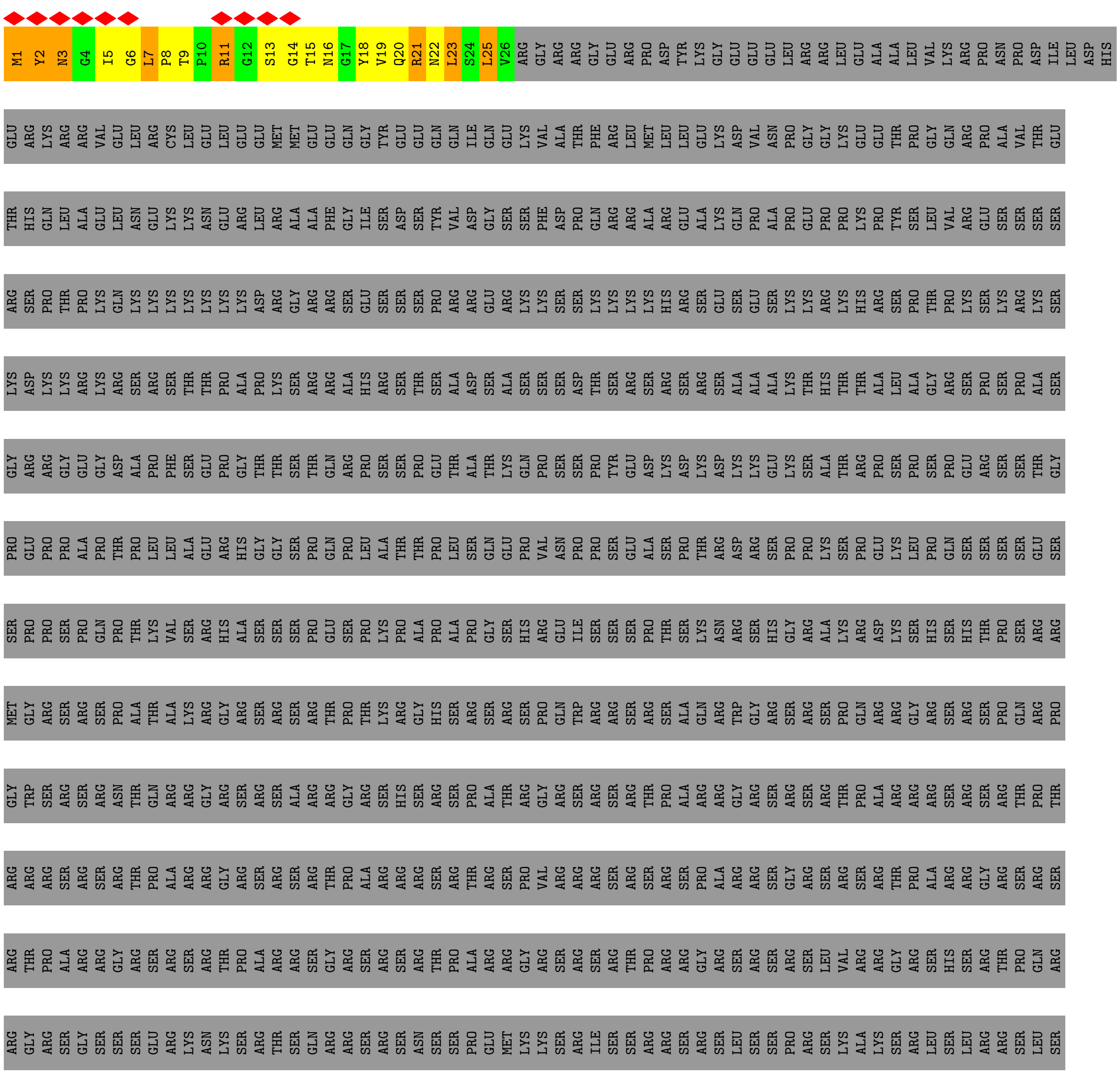
Chain T:





- Molecule 41: Serine/arginine repetitive matrix protein 2

Chain U:




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 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 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 PRO ARG THR PRO SER ARG GLU ARG SER SER SER ALA SER SER PRO GLU MET LYS ASP GLY LEU PRO ARG THR PRO SER ARG ARG SER ARG

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

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

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

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

ARG GLN ARG SER ARG SER ARG SER ARG VAL THR ARG ARG ARG GLY GLY SER GLY TYR HIS SER ARG SER PRO ALA ARG GLN GLU SER SER ARG THR SER SER ARG ARG ARG ARG GLY ARG SER ARG THR PRO PRO THR SER ARG LYS ARG SER ARG SER 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 ARG THR SER PRO VAL SER ARG ARG ARG SER ARG SER ARG THR SER VAL THR ARG ARG ARG SER ARG SER ARG ALA SER PRO VAL SER ARG

ARG ARG SER ARG SER ARG THR PRO PRO VAL THR ARG ARG ARG SER ARG SER ARG THR PRO THR THR ARG ARG ARG SER ARG SER ARG THR PRO PRO VAL THR ARG ARG ARG SER ARG SER ARG THR PRO PRO VAL THR ARG ARG ARG SER ARG SER ARG THR SER PRO ILE THR ARG ARG

ARG SER ARG SER ARG THR SER PRO VAL THR ARG ARG ARG SER ARG SER ARG THR SER PRO VAL THR ARG ARG ARG SER ARG SER ARG THR SER PRO VAL THR ARG ARG ARG SER ARG SER ARG THR PRO PRO ALA ILE ARG ARG ARG SER ARG SER ARG THR PRO LEU LEU PRO ARG LYS

ARG SER ARG SER ARG SER PRO LEU ALA ILE ARG ARG ARG SER ARG SER ARG THR PRO ARG THR ALA ARG GLY LYS ARG SER LEU THR ARG SER PRO PRO ALA ILE ARG ARG ARG SER ALA SER GLY SER SER SER ASP ARG SER ARG SER ALA THR PRO PRO ALA THR ARG ASN HIS SER

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

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

ARG THR ALA PRO ALA ALA ASN LEU ALA SER ARG ILE PRO ALA ALA SER ALA ALA ALA MET ASN LEU ALA SER ALA ARG THR PRO ALA ILE PRO THR ALA VAL ASN LEU ALA ASP SER ARG THR PRO ALA ALA ALA ALA ALA MET ASN LEU ALA SER PRO ARG THR ALA VAL ALA PRO SER

ALA VAL ASN LEU ALA ASP PRO ARG THR PRO THR ALA PRO ALA VAL ASN LEU ALA GLY ALA ARG THR PRO ALA ALA LEU ALA ALA LEU SER LEU THR GLY SER GLY THR PRO PRO THR ALA ALA ASN TYR PRO SER SER SER ARG THR PRO GLN ALA PRO ALA SER ALA ASN LEU VAL GLY

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

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

CYS LEU ILE ALA GLN THR THR PRO VAL ALA GLY SER GLN SER LEU SER SER GLY ALA VAL ALA THR THR THR SER SER ALA GLY ASP HIS ASN GLY MET LEU SER VAL PRO ALA PRO GLY VAL PRO HIS SER ASP VAL GLY GLU PRO PRO ALA SER THR GLY ALA GLN GLN PRO SER ALA

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

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

SER SER SER SER SER SER SER SER PRO SER PRO ALA LYS PRO GLY PRO GLN ALA LEU PRO LYS PRO ALA SER PRO LYS LYS PRO PRO PRO GLY GLU ARG ARG SER ARG SER PRO ARG LYS PRO ILE ASP SER LEU ARG ASP SER ARG SER LEU SER TYR SER PRO VAL GLU ARG ARG ARG

PRO SER PRO GLN PRO SER PRO ARG ASP GLN GLN SER SER SER SER GLU ARG GLY SER ARG ARG GLY GLN ARG GLY ASP SER ARG SER PRO SER HIS LYS ARG ARG ARG GLU THR PRO SER PRO ARG PRO MET ARG HIS ARG SER SER ARG SER PRO

- Molecule 42: Pre-mRNA-splicing factor CWC22 homolog

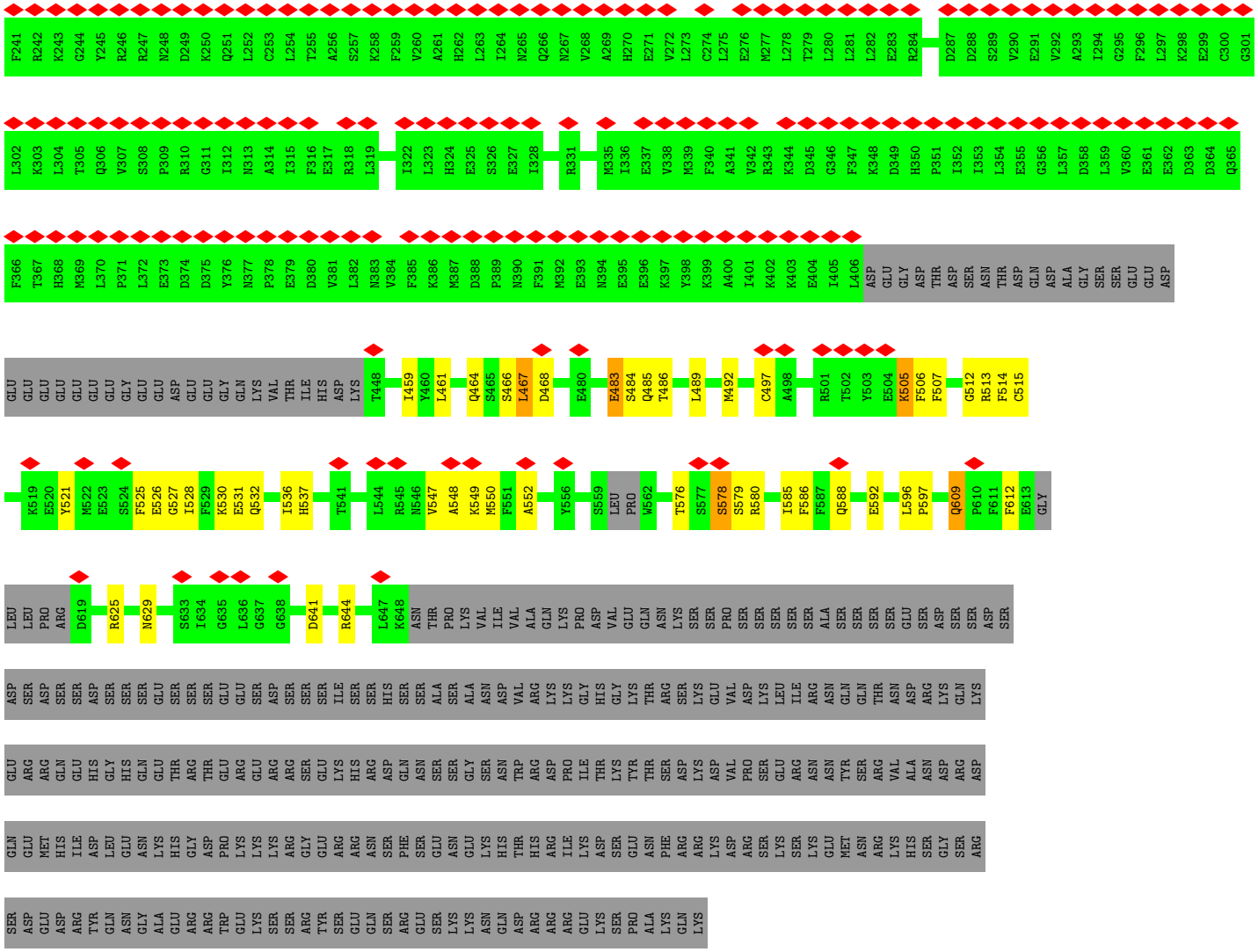
Chain V: 30% 44% 5% • 50%

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

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

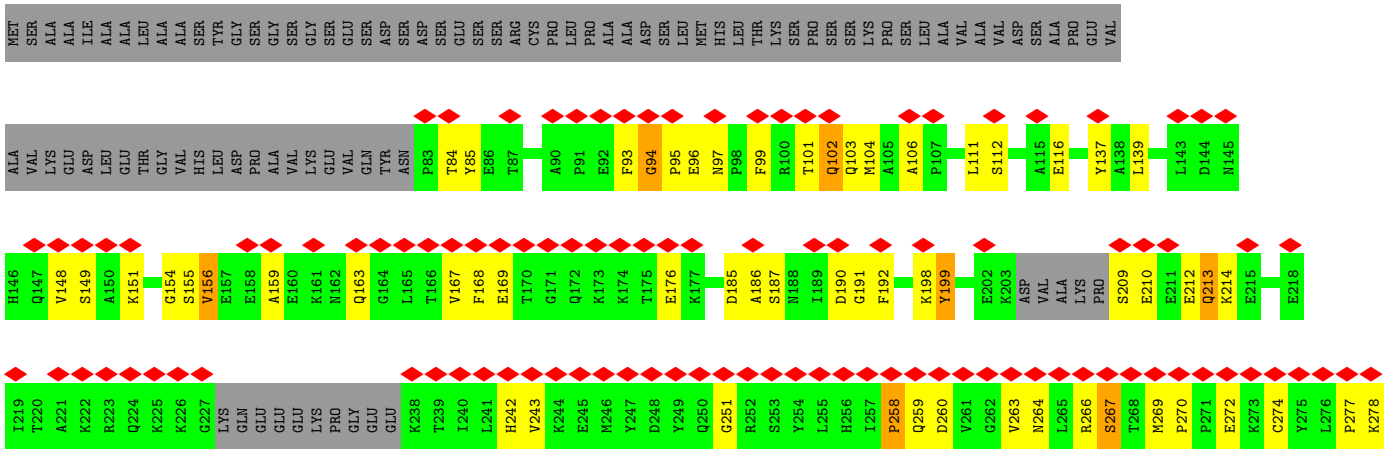
GLU LEU ASP PRO LEU LEU THR ARG THR GLY GLY ALA TYR ILE PRO PRO ALA LYS LEU ARG MET MET GLN GLU GLN ILE THR ASP K149 N150 S151 L152 A153 Y154 Q155 R156 M157 S158 W159 E160 A161 L162 K163 K164 S165 I166 N167 G168 L169 I170 N171 K172 V173 N174 I175 S176 N177 I178 S179 I180

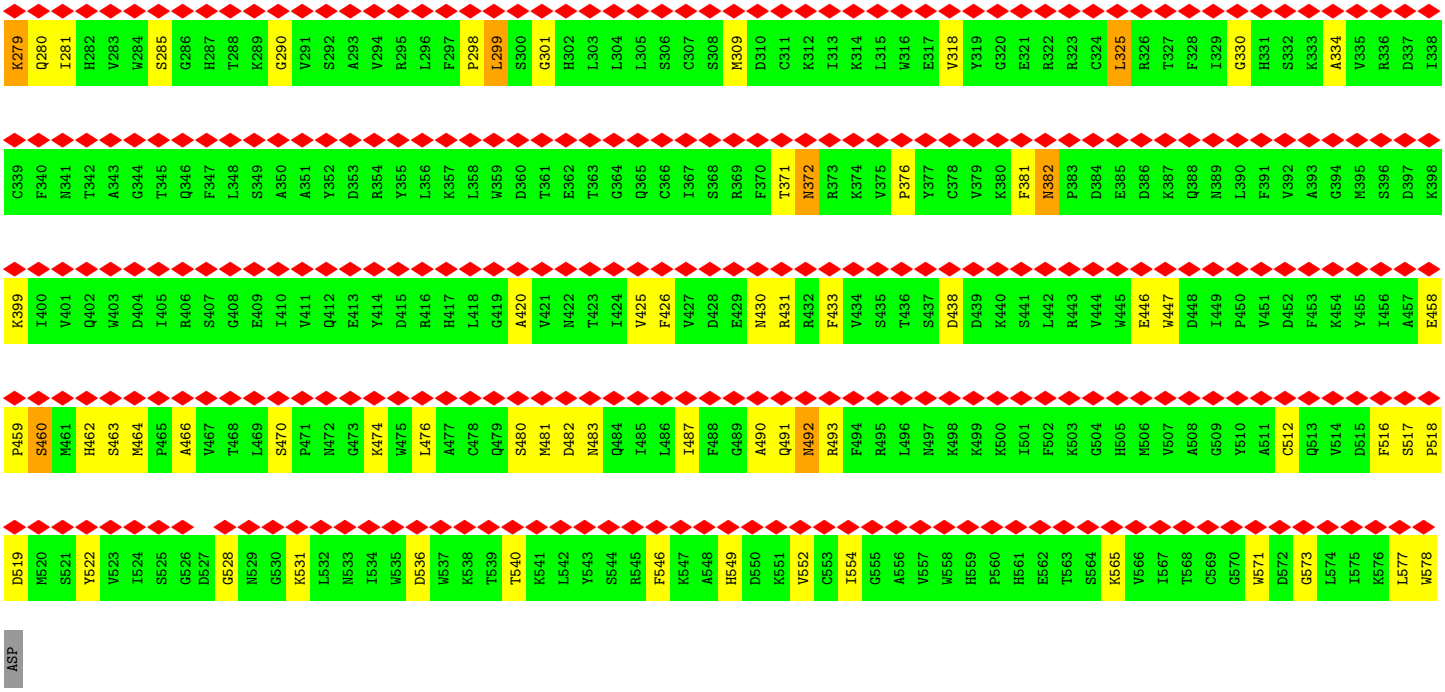
I181 I182 Q183 E184 L185 L186 Q187 E188 N189 I190 V191 R192 G193 R194 G195 L196 L197 S198 R199 S200 V201 L202 Q203 A204 Q205 S206 A207 S208 P209 I210 F211 T212 H213 V214 Y215 A216 A217 L218 V219 A220 I221 I222 N223 S224 K225 F226 P227 Q228 I229 G230 E231 L232 I233 L234 K235 R236 L237 I238 L239 N240



• Molecule 43: Pre-mRNA-processing factor 17

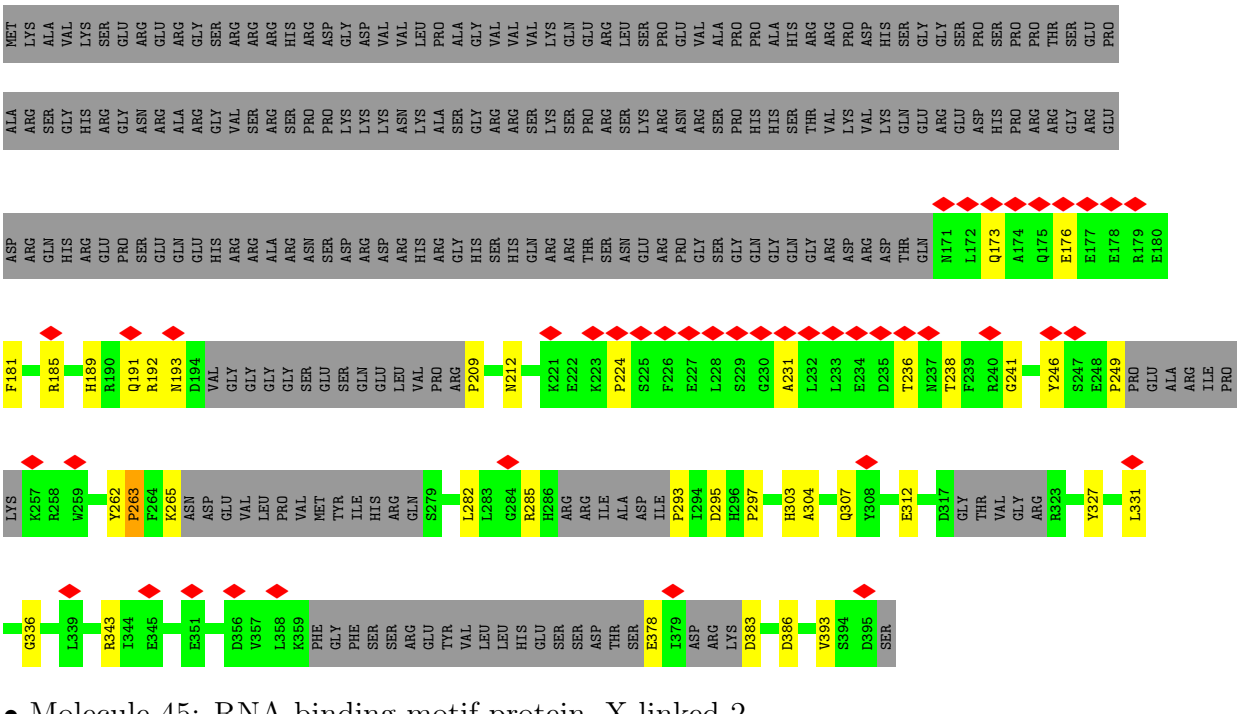
Chain W:





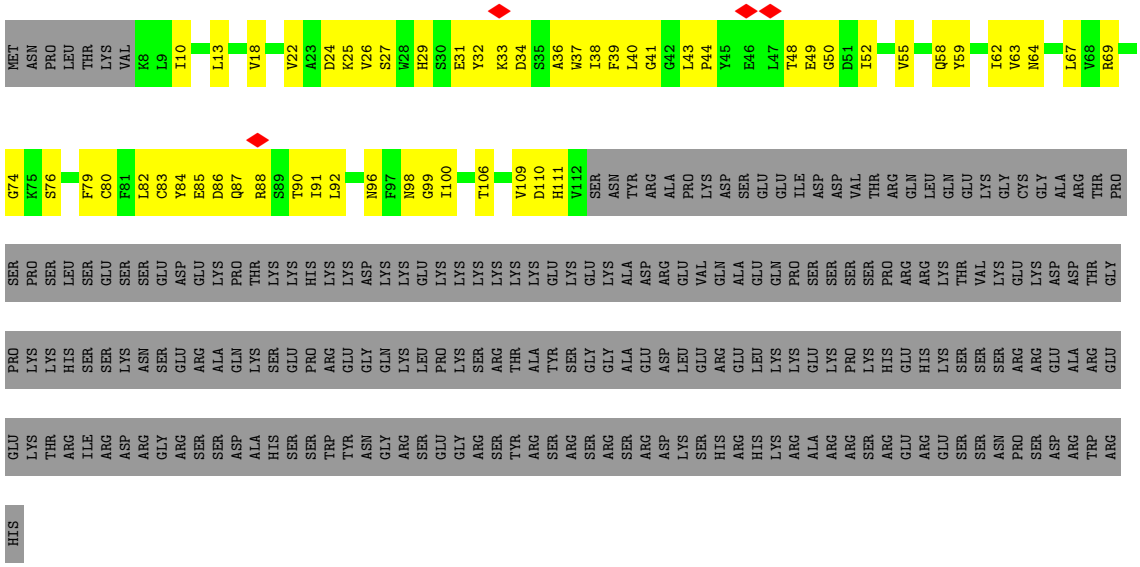
• Molecule 44: Smad nuclear-interacting protein 1

Chain X:



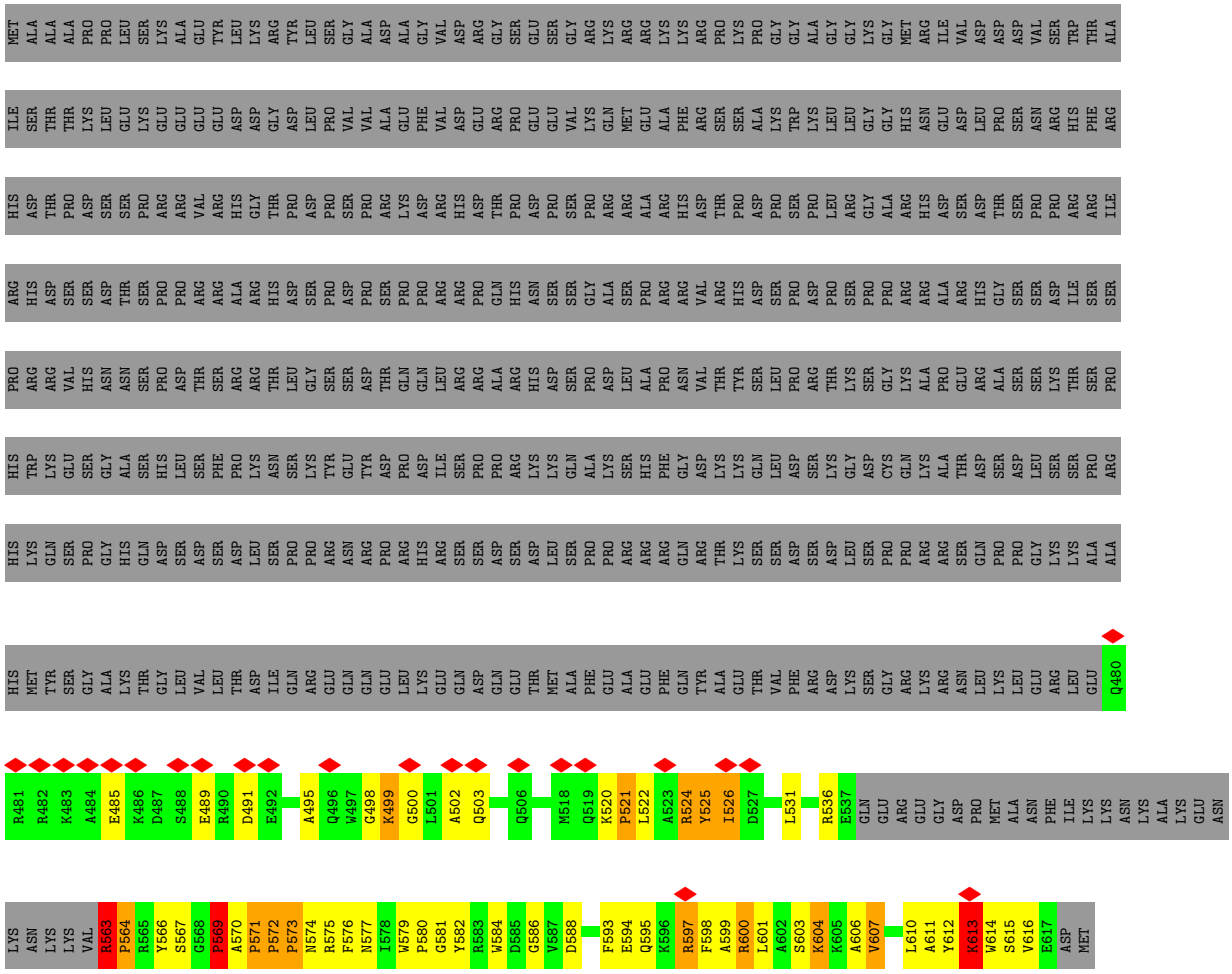
• Molecule 45: RNA-binding motif protein, X-linked 2

Chain Y:



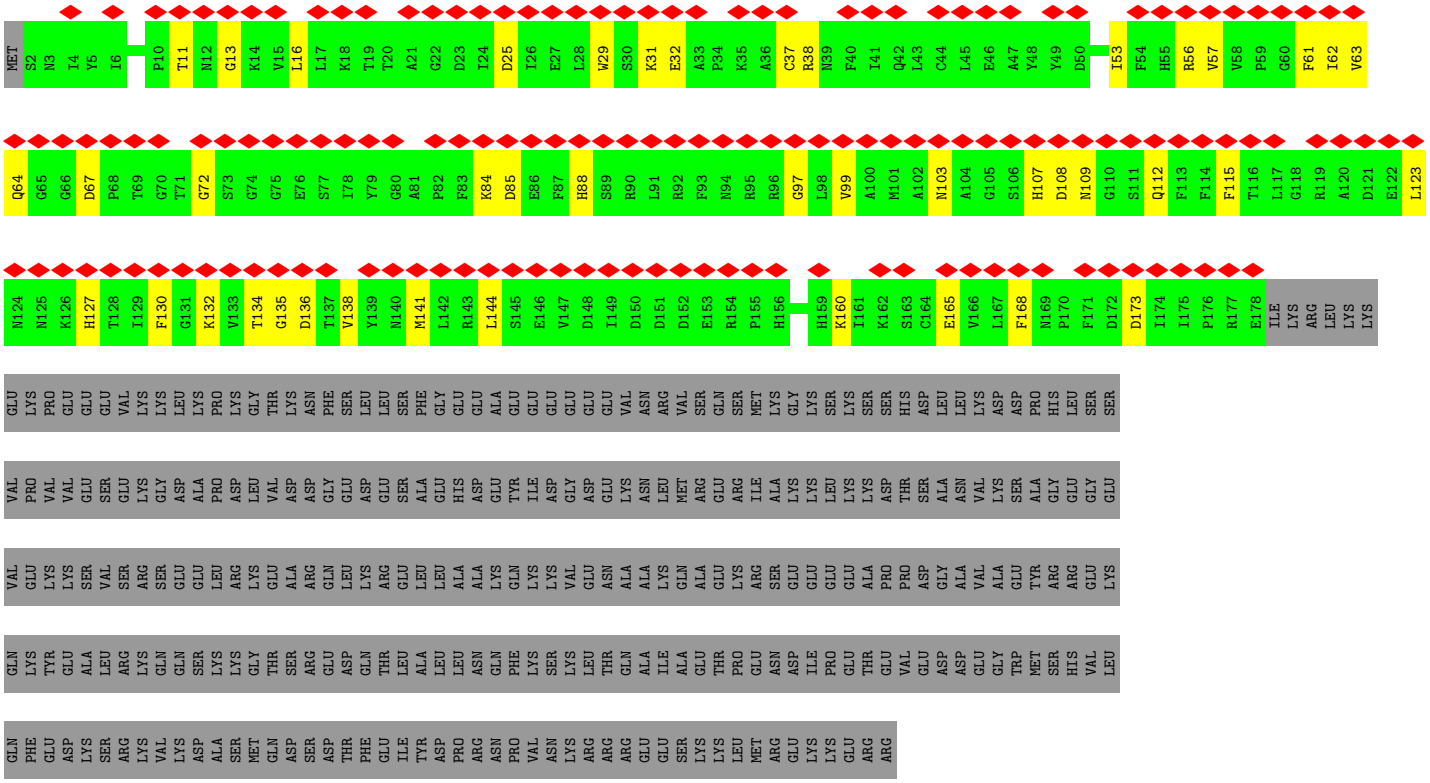
- Molecule 46: BUD13 homolog

Chain Z:



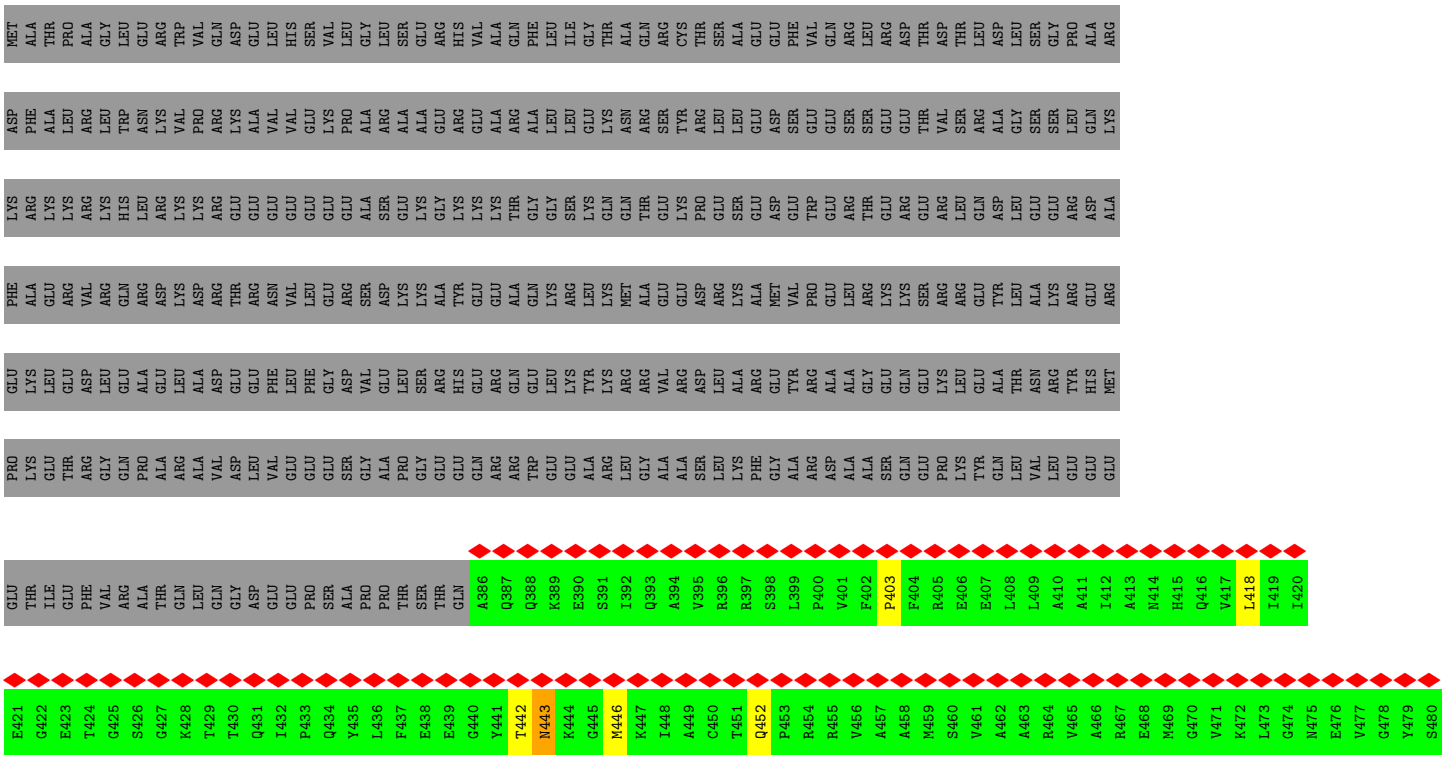
- Molecule 47: Peptidyl-prolyl cis-trans isomerase CWC27 homolog

Chain z:



• Molecule 48: Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16

Chain x:



I481 R482 F483 E484 D485 C486 T487 SER GLU ARG T491 V492 L493 R494 Y495 M496 T497 D498 G499 M500 L501 L502 R503 E504 F505 L506 S507 E508 P509 D510 L511 A512 S513 Y514 S515 V516 V517 M518 V519 D520 E521 A522 H523 E524 R525 T526 L527 H528 T529 D530 I531 L532 F533 G534 L535 I536 K537 D538 V539 A540

R541 F542 R543 P544 E545 L546 K547 V548 L549 V550 A551 S552 A553 T554 M555 D556 T557 A558 R559 F560 S561 T562 F563 F564 D565 D566 A567 P568 V569 F570 R571 I572 P573 G574 R575 R576 F577 P578 V579 D580 I581 F582 Y583 T584 K585 A586 P587 E588 A589 D590 Y591 L592 E593 A594 G595 V596 V597 S598 V599 L600

Q601 I602 H603 V604 T605 Q606 PRO PRO G609 D610 I611 L612 V613 F614 L615 T616 G617 Q618 E619 E620 I621 E622 A623 A624 C625 E626 M627 L628 Q629 D630 R631 C632 R633 R634 L635 G636 SER LYS I639 R640 E641 L642 L643 V644 L645 P646 I647 Y648 A649 N650 L651 P652 S653 D654 M655 Q656 A657 R658 I659 F660

Q661 P662 T663 P664 PRO GLY A667 R668 K669 V670 V671 V672 A673 T674 N675 I676 A677 E678 T679 S680 L681 T682 I683 E684 G685 I686 I687 Y688 V689 L690 D691 P692 G693 F694 C695 K696 Q697 K698 S699 Y700 N701 P702 R703 T704 G705 M706 E707 S708 L709 T710 V711 T712 P713 C714 S715 K716 A717 S718 A719 N720

Q721 R722 A723 G724 R725 A726 G727 R728 V729 A730 A731 G732 K733 C734 F735 R736 L737 Y738 T739 A740 W741 A742 Y743 Q744 H745 E746 L747 E748 E749 T750 T751 V752 P753 E754 I755 Q756 R757 T758 S759 L760 G761 N762 V763 V764 L765 L766 L767 K768 S769 L770 G771 I772 H773 D774 L775 M776 H777 F778 D779 F780

L781 D782 P783 P784 P785 V786 E787 T788 L789 L790 L791 A792 L793 E794 Q795 L796 Y797 A798 L799 G800 A801 L802 N803 H804 L805 G806 E807 L808 T809 T810 S811 G812 R813 K814 M815 A816 E817 L818 P819 V820 D821 P822 M823 L824 S825 K826 M827 I828 L829 A830 S831 E832 LYS TYR SER C836 S837 E838 E839 I840

L841 T842 V843 A844 A845 M846 L847 S848 VAL ASN ASN SER ILE PHE TYR ARG PRO LYS ASP LYS VAL VAL HIS ALA D865 N866 A867 R868 V869 N870 F871 F872 L873 P874 G875 G876 D877 H878 L879 V880 L881 L882 N883 V884 Y885 T886 Q887 W888 A889 E890 SER GLY TYR SER SER GLN TRP C898 Y899 E900

N901 F902 V903 Q904 F905 R906 S907 M908 R909 R910 A911 R912 D913 V914 R915 E916 Q917 L918 E919 G920 L921 L922 E923 R924 V925 E926 V927 G928 L929 S930 S931 C932 Q933 G934 D935 Y936 I937 R938 V939 R940 K941 A942 I943 T944 A945 G946 Y947 F948 Y949 H950 T951 A952 R953 LEU THR ARG SER G958 Y959 R960

T961 V962 LYS GLN GLN GLN THR V968 F969 I970 H971 P972 N973 S974 SER LEU PHE GLU Q979 Q980 P981 R982 W983 L984 L985 Y986 H987 E988 L989 V990 L991 T992 T993 K994 E995 F996 M997 R998 Q999 V1000 L1001 E1002 I1003 E1004 S1005 S1006 W1007 L1008 L1009 E1010 V1011 A1012 P1013 H1014 Y1015 Y1016 K1017 ALA LYS GLU

LEU GLU ASP PRO HIS ALA LYS LYS MET PRO LYS LYS ILE GLY LYS THR ARG GLU GLU LEU GLY

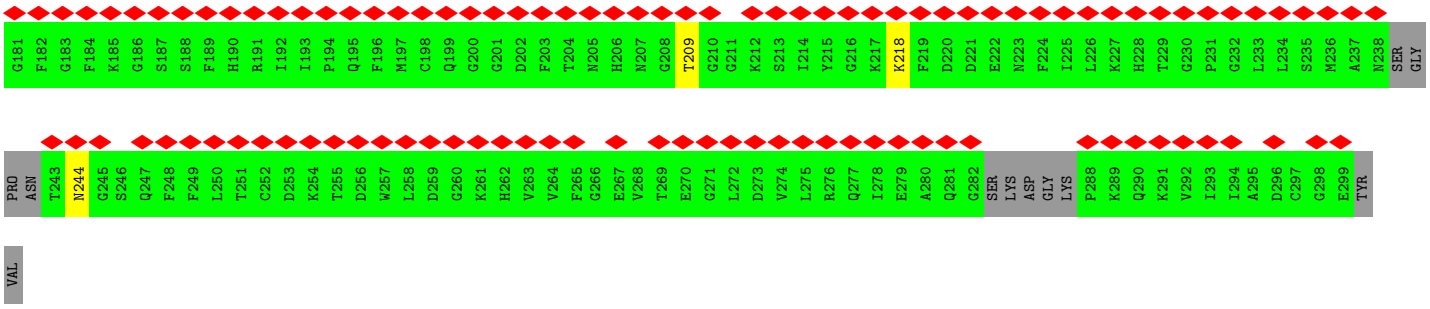
- Molecule 49: Peptidyl-prolyl cis-trans isomerase E

Chain y:

MET ALA THR THR K5 R6 V7 L8 Y9 V10 G11 G12 L13 A14 E15 E16 V17 D18 D19 K20 V21 L22 H23 A24 A25 F26 I27 P28 F29 G30 D31 I32 T33 D34 I35 Q36 I37 P38 L39 D40 Y41 E42 T43 E44 K45 H46 R47 G48 F49 A50 F51 V52 E53 F54 E55 L56 A57 E58 D59 A60

A61 A62 A63 I64 D65 N66 M67 N68 E69 S70 E71 L72 F73 G74 R75 T76 I77 R78 V79 N80 L81 A82 K83 PRO MET ARG ILE LYS GLU GLY SER SER ARG PRO VAL TRP SER ASP ASP ASP TRP LEU LYS LYS PHE SER GLY LYS THR LEU GLU GLU GLU ASN LYS GLU GLU GLU GLY SER GLU

PRO PRO LYS ALA GLU THR GLN GLU GLY GLU PRO ILE ALA LYS LYS ALA ARG S138 N139 P140 Q141 V142 Y143 M144 D145 I146 K147 I148 G149 N150 K151 P152 A153 G154 R155 I156 Q157 M158 L159 L160 R161 S162 D163 V164 V165 P166 M167 T168 A169 E170 N171 F172 R173 C174 L175 C176 T177 H178 E179 K180


G181 F182 G183 F184 K185 G186 S187 S188 F189 H190 R191 I192 I193 P194 Q195 F196 M197 C198 Q199 G200 G201 D202 F203 T204 N205 H206 N207 G208 T209 G210 G211 K212 S213 I214 Y215 G216 K217 K218 F219 D220 D221 E222 N223 F224 I225 L226 K227 H228 T229 G230 P231 G232 L233 L234 S235 M236 A237 N238 SER GLY
PRO ASN T243 N244 G245 S246 Q247 F248 F249 L250 T251 C252 D253 K254 T255 D256 W257 L258 D259 G260 K261 H262 V263 V264 F265 G266 E267 V268 T269 E270 G271 L272 D273 V274 L275 R276 Q277 I278 E279 A280 Q281 G282 SER LYS ASP GLY LYS P288 K289 Q290 K291 V292 I293 I294 A295 D296 C297 G298 E299 TYR
VAL

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	27405	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 ($e^-/Å^2$)	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.168	Depositor
Minimum map value	-0.080	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0374	Depositor
Map size (Å)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.338, 1.338, 1.338	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: ZN, IHP, MG, GTP

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	0.83	38/18964 (0.2%)	0.95	50/25741 (0.2%)
2	B	0.67	1/1970 (0.1%)	0.95	7/3060 (0.2%)
3	C	1.08	13/6864 (0.2%)	1.27	40/9334 (0.4%)
4	D	0.55	0/8527	1.11	27/11887 (0.2%)
5	E	0.87	0/2392	1.00	6/3242 (0.2%)
6	a	0.77	0/397	0.99	0/549
6	h	0.77	0/391	0.99	0/540
7	b	0.83	0/404	1.12	2/561 (0.4%)
7	i	0.84	0/421	1.15	3/583 (0.5%)
8	c	0.88	0/405	1.11	0/563
8	j	0.87	0/405	1.11	0/563
9	d	1.12	0/479	1.25	1/666 (0.2%)
9	k	1.14	0/420	1.23	1/583 (0.2%)
10	f	1.20	0/360	1.25	0/497
10	m	1.21	1/360 (0.3%)	1.25	0/497
11	e	1.03	0/390	1.24	1/542 (0.2%)
11	l	1.02	0/390	1.23	0/542
12	g	0.86	0/362	1.08	1/501 (0.2%)
12	n	0.85	0/332	1.08	1/458 (0.2%)
13	F	0.35	0/2224	0.66	5/3462 (0.1%)
14	G	0.25	0/1717	0.54	0/2664
15	H	0.51	7/3217 (0.2%)	0.77	8/4997 (0.2%)
16	o	0.93	0/803	2.15	35/1119 (3.1%)
17	p	1.60	3/810 (0.4%)	2.10	25/1122 (2.2%)
18	w	0.62	6/2376 (0.3%)	0.99	14/3269 (0.4%)
19	u	0.36	0/524	0.94	3/724 (0.4%)
20	v	0.87	4/945 (0.4%)	1.10	11/1280 (0.9%)
21	1	0.27	0/7826	0.61	3/10617 (0.0%)
22	2	0.59	4/1277 (0.3%)	0.92	9/1724 (0.5%)
23	3	0.23	0/9408	0.57	6/12767 (0.0%)
24	4	1.08	2/535 (0.4%)	1.28	5/724 (0.7%)
25	5	0.20	0/823	0.53	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
26	6	0.19	0/653	0.53	0/877
27	7	0.22	0/556	0.49	0/751
28	J	0.80	1/3500 (0.0%)	1.13	3/4750 (0.1%)
29	L	0.58	4/2283 (0.2%)	0.88	8/3088 (0.3%)
30	q	0.62	0/658	0.97	3/919 (0.3%)
30	r	0.58	0/653	0.99	3/912 (0.3%)
30	s	0.49	0/334	0.91	0/466
30	t	0.56	0/334	0.82	0/466
31	K	0.98	11/981 (1.1%)	1.03	6/1317 (0.5%)
32	I	0.54	0/2745	0.91	18/3765 (0.5%)
33	Q	0.37	0/6518	0.85	3/9075 (0.0%)
34	M	0.20	0/272	0.56	0/363
35	N	1.15	1/1210 (0.1%)	1.17	4/1622 (0.2%)
36	O	1.05	5/2321 (0.2%)	1.11	10/3135 (0.3%)
37	P	0.98	0/841	1.27	4/1117 (0.4%)
38	R	0.85	7/2353 (0.3%)	1.17	13/3167 (0.4%)
39	S	0.81	0/1268	1.14	9/1714 (0.5%)
40	T	1.44	13/2522 (0.5%)	1.42	26/3438 (0.8%)
41	U	1.44	2/196 (1.0%)	1.54	4/265 (1.5%)
42	V	0.89	1/2239 (0.0%)	1.17	3/3118 (0.1%)
43	W	0.88	2/2371 (0.1%)	1.33	27/3296 (0.8%)
44	X	0.21	0/1020	0.56	0/1360
45	Y	0.24	0/753	0.58	0/1014
46	Z	0.65	6/772 (0.8%)	1.11	9/1056 (0.9%)
47	z	0.21	0/1414	0.54	0/1916
48	x	0.59	1/2876 (0.0%)	0.82	11/3988 (0.3%)
49	y	0.55	0/1129	0.91	0/1558
All	All	0.73	133/119490 (0.1%)	0.99	428/165014 (0.3%)

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	6
3	C	0	3
4	D	0	1
9	d	0	1
9	k	0	1
21	1	0	9
22	2	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
23	3	0	4
27	7	0	1
34	M	0	1
35	N	0	1
38	R	0	1
40	T	0	2
44	X	0	1
All	All	0	33

The worst 5 of 133 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	K	106	CYS	CB-SG	-11.61	1.43	1.81
31	K	132	CYS	CB-SG	-8.70	1.52	1.81
3	C	387	ASP	CA-C	-8.61	1.48	1.52
17	p	156	ASN	C-N	-8.31	1.22	1.33
1	A	316	PHE	C-N	-8.15	1.25	1.34

The worst 5 of 428 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
40	T	187	LYS	CA-C-N	13.13	132.89	119.76
40	T	187	LYS	C-N-CA	13.13	132.89	119.76
24	4	83	PRO	CA-CB-CG	10.35	124.17	104.50
36	O	225	PRO	N-CA-C	10.32	123.29	110.70
43	W	278	LYS	CB-CA-C	-9.96	95.82	111.17

There are no chirality outliers.

5 of 33 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	166	PHE	Peptide
1	A	346	ASP	Peptide
1	A	408	PRO	Peptide
1	A	433	GLU	Peptide
1	A	697	MET	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	18450	0	18276	1529	0
2	B	1768	0	897	120	0
3	C	6716	0	6691	916	0
4	D	8528	0	3745	72	0
5	E	2338	0	2272	156	0
6	a	399	0	173	0	0
6	h	393	0	170	0	0
7	b	405	0	170	0	0
7	i	422	0	177	10	0
8	c	406	0	170	0	0
8	j	406	0	170	0	0
9	d	480	0	200	2	0
9	k	422	0	175	2	0
10	f	361	0	158	1	0
10	m	361	0	158	0	0
11	e	391	0	163	3	0
11	l	391	0	163	1	0
12	g	363	0	160	1	0
12	n	334	0	143	3	0
13	F	1988	0	1005	185	0
14	G	1545	0	786	202	0
15	H	2886	0	1463	277	0
16	o	804	0	350	9	0
17	p	813	0	366	14	0
18	w	2369	0	1298	96	0
19	u	530	0	218	1	0
20	v	946	0	594	82	0
21	1	7702	0	7389	319	0
22	2	1252	0	1040	61	0
23	3	9220	0	9139	520	0
24	4	527	0	438	41	0
25	5	807	0	729	28	0
26	6	645	0	628	21	0
27	7	540	0	509	24	0
28	J	3463	0	2544	110	0
29	L	2260	0	1776	100	0
30	q	659	0	296	7	0
30	r	654	0	294	6	0
30	s	335	0	168	0	0
30	t	335	0	168	1	0
31	K	979	0	739	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	I	2778	0	1238	22	0
33	Q	6528	0	2814	6	0
34	M	267	0	225	30	0
35	N	1184	0	1190	78	0
36	O	2273	0	2244	236	0
37	P	829	0	814	200	0
38	R	2316	0	2189	430	0
39	S	1236	0	1210	140	0
40	T	2457	0	2416	253	0
41	U	193	0	196	44	0
42	V	2243	0	971	50	0
43	W	2374	0	1051	115	0
44	X	1021	0	738	19	0
45	Y	743	0	613	67	0
46	Z	755	0	591	155	0
47	z	1381	0	1298	33	0
48	x	2887	0	1310	23	0
49	y	1133	0	519	2	0
50	A	36	0	6	10	0
51	C	32	0	12	11	0
52	C	1	0	0	0	0
52	F	5	0	0	0	0
53	6	3	0	0	0	0
53	M	1	0	0	0	0
53	N	3	0	0	0	0
53	O	3	0	0	2	0
53	W	2	0	0	0	0
53	v	1	0	0	0	0
All	All	117278	0	87813	5419	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 26.

The worst 5 of 5419 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)
45:Y:37:TRP:CH2	46:Z:498:GLY:HA2	1.23	1.65
1:A:2270:PHE:HB3	4:D:1264:PRO:CB	1.34	1.57
1:A:2270:PHE:CG	4:D:1264:PRO:CB	1.89	1.56
3:C:149:LEU:HD13	3:C:427:PHE:CD2	1.38	1.54
3:C:77:VAL:HG11	40:T:196:LEU:CG	1.39	1.52

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	2224/2335 (95%)	2081 (94%)	115 (5%)	28 (1%)	9 40
3	C	854/972 (88%)	777 (91%)	57 (7%)	20 (2%)	5 27
4	D	1720/2136 (80%)	1632 (95%)	85 (5%)	3 (0%)	43 78
5	E	297/357 (83%)	272 (92%)	16 (5%)	9 (3%)	3 22
6	a	77/126 (61%)	76 (99%)	1 (1%)	0	100 100
6	h	76/126 (60%)	75 (99%)	1 (1%)	0	100 100
7	b	80/231 (35%)	78 (98%)	2 (2%)	0	100 100
7	i	84/231 (36%)	82 (98%)	2 (2%)	0	100 100
8	c	80/119 (67%)	77 (96%)	3 (4%)	0	100 100
8	j	80/119 (67%)	77 (96%)	3 (4%)	0	100 100
9	d	95/118 (80%)	91 (96%)	4 (4%)	0	100 100
9	k	81/118 (69%)	78 (96%)	3 (4%)	0	100 100
10	f	72/86 (84%)	69 (96%)	3 (4%)	0	100 100
10	m	72/86 (84%)	68 (94%)	4 (6%)	0	100 100
11	e	77/92 (84%)	76 (99%)	1 (1%)	0	100 100
11	l	77/92 (84%)	76 (99%)	1 (1%)	0	100 100
12	g	72/76 (95%)	70 (97%)	2 (3%)	0	100 100
12	n	64/76 (84%)	62 (97%)	2 (3%)	0	100 100
16	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	9 40
17	p	159/225 (71%)	138 (87%)	9 (6%)	12 (8%)	1 9
18	w	419/501 (84%)	378 (90%)	38 (9%)	3 (1%)	18 55
19	u	94/793 (12%)	87 (93%)	5 (5%)	2 (2%)	5 29

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	v	155/464 (33%)	125 (81%)	22 (14%)	8 (5%)	1	14
21	1	1022/1304 (78%)	897 (88%)	119 (12%)	6 (1%)	21	58
22	2	171/895 (19%)	154 (90%)	17 (10%)	0	100	100
23	3	1165/1217 (96%)	1086 (93%)	78 (7%)	1 (0%)	48	83
24	4	76/424 (18%)	69 (91%)	6 (8%)	1 (1%)	9	40
25	5	106/125 (85%)	90 (85%)	16 (15%)	0	100	100
26	6	83/110 (76%)	76 (92%)	7 (8%)	0	100	100
27	7	64/86 (74%)	55 (86%)	9 (14%)	0	100	100
28	J	483/848 (57%)	452 (94%)	24 (5%)	7 (1%)	9	38
29	L	324/802 (40%)	304 (94%)	18 (6%)	2 (1%)	21	58
30	q	130/504 (26%)	119 (92%)	7 (5%)	4 (3%)	3	21
30	r	129/504 (26%)	118 (92%)	9 (7%)	2 (2%)	7	36
30	s	65/504 (13%)	62 (95%)	2 (3%)	1 (2%)	8	38
30	t	65/504 (13%)	64 (98%)	0	1 (2%)	8	38
31	K	144/225 (64%)	134 (93%)	6 (4%)	4 (3%)	4	24
32	I	498/855 (58%)	479 (96%)	11 (2%)	8 (2%)	7	36
33	Q	1297/1485 (87%)	1271 (98%)	26 (2%)	0	100	100
34	M	34/343 (10%)	30 (88%)	3 (9%)	1 (3%)	3	23
35	N	141/144 (98%)	126 (89%)	12 (8%)	3 (2%)	5	29
36	O	283/420 (67%)	247 (87%)	26 (9%)	10 (4%)	3	20
37	P	92/229 (40%)	82 (89%)	8 (9%)	2 (2%)	5	28
38	R	295/540 (55%)	249 (84%)	31 (10%)	15 (5%)	1	15
39	S	157/166 (95%)	144 (92%)	10 (6%)	3 (2%)	6	31
40	T	311/514 (60%)	282 (91%)	17 (6%)	12 (4%)	2	18
41	U	24/2752 (1%)	20 (83%)	3 (12%)	1 (4%)	2	17
42	V	444/908 (49%)	412 (93%)	27 (6%)	5 (1%)	11	45
43	W	475/579 (82%)	419 (88%)	32 (7%)	24 (5%)	1	15
44	X	143/396 (36%)	133 (93%)	10 (7%)	0	100	100
45	Y	103/322 (32%)	92 (89%)	11 (11%)	0	100	100
46	Z	109/619 (18%)	93 (85%)	10 (9%)	6 (6%)	1	14
47	z	176/472 (37%)	170 (97%)	6 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	x	562/1041 (54%)	537 (96%)	20 (4%)	5 (1%)	14	50
49	y	224/301 (74%)	217 (97%)	7 (3%)	0	100	100
All	All	16564/29872 (55%)	15374 (93%)	979 (6%)	211 (1%)	12	40

5 of 211 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	ARG
1	A	92	LEU
1	A	167	PRO
1	A	188	LEU
1	A	331	TRP

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	2001/2108 (95%)	1888 (94%)	113 (6%)	19	40
3	C	745/866 (86%)	676 (91%)	69 (9%)	8	26
5	E	256/300 (85%)	244 (95%)	12 (5%)	23	45
18	w	49/446 (11%)	47 (96%)	2 (4%)	27	48
20	v	30/382 (8%)	28 (93%)	2 (7%)	15	36
21	1	735/1104 (67%)	735 (100%)	0	100	100
22	2	94/776 (12%)	90 (96%)	4 (4%)	26	47
23	3	1018/1051 (97%)	1017 (100%)	1 (0%)	88	88
24	4	39/336 (12%)	37 (95%)	2 (5%)	21	42
25	5	74/109 (68%)	74 (100%)	0	100	100
26	6	73/95 (77%)	73 (100%)	0	100	100
27	7	57/77 (74%)	57 (100%)	0	100	100
28	J	205/751 (27%)	193 (94%)	12 (6%)	18	39
29	L	131/709 (18%)	123 (94%)	8 (6%)	17	38

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	K	54/196 (28%)	46 (85%)	8 (15%)	3	13
34	M	25/294 (8%)	24 (96%)	1 (4%)	28	49
35	N	130/130 (100%)	124 (95%)	6 (5%)	24	45
36	O	250/361 (69%)	240 (96%)	10 (4%)	28	49
37	P	90/203 (44%)	78 (87%)	12 (13%)	4	15
38	R	220/463 (48%)	166 (76%)	54 (24%)	1	5
39	S	129/134 (96%)	121 (94%)	8 (6%)	16	38
40	T	268/441 (61%)	251 (94%)	17 (6%)	16	37
41	U	21/2432 (1%)	16 (76%)	5 (24%)	1	5
44	X	52/349 (15%)	46 (88%)	6 (12%)	5	19
45	Y	57/291 (20%)	56 (98%)	1 (2%)	51	67
46	Z	47/545 (9%)	38 (81%)	9 (19%)	1	9
47	z	146/416 (35%)	146 (100%)	0	100	100
48	x	1/897 (0%)	1 (100%)	0	100	100
All	All	6997/16262 (43%)	6635 (95%)	362 (5%)	22	42

5 of 362 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	K	171	GLN
38	R	133	GLN
35	N	116	ASN
37	P	212	ASN
38	R	214	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 142 such sidechains are listed below:

Mol	Chain	Res	Type
38	R	189	ASN
38	R	418	GLN
40	T	417	ASN
3	C	248	GLN
3	C	245	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	F	91/107 (85%)	38 (41%)	12 (13%)
14	G	76/274 (27%)	48 (63%)	9 (11%)
15	H	130/188 (69%)	33 (25%)	4 (3%)
2	B	82/117 (70%)	19 (23%)	10 (12%)
All	All	379/686 (55%)	138 (36%)	35 (9%)

5 of 138 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	12	U
2	B	13	C
2	B	19	A
2	B	20	G
2	B	21	A

5 of 35 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
14	G	151	C
14	G	153	C
15	H	46	U
13	F	25	C
13	F	7	G

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 21 ligands modelled in this entry, 19 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	$\#\|Z\| > 2$
50	IHP	A	3000	-	36,36,36	1.04	2 (5%)	60,60,60	1.74	15 (25%)
51	GTP	C	1500	52	33,34,34	1.45	5 (15%)	50,54,54	2.04	10 (20%)

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
50	IHP	A	3000	-	-	6/30/54/54	0/1/1/1
51	GTP	C	1500	52	-	8/22/38/38	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	C	1500	GTP	C5-N7	-3.76	1.31	1.39
51	C	1500	GTP	C6-N1	-3.32	1.32	1.38
51	C	1500	GTP	PA-O3A	3.16	1.62	1.59
50	A	3000	IHP	P5-O45	-2.95	1.43	1.54
50	A	3000	IHP	P2-O12	2.73	1.64	1.59

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
51	C	1500	GTP	C5-C4-N3	-7.07	117.14	128.39
51	C	1500	GTP	C2-N3-C4	5.94	122.54	112.30
51	C	1500	GTP	N9-C4-N3	5.74	137.44	125.95
50	A	3000	IHP	O35-P5-O15	-4.53	88.19	105.85
50	A	3000	IHP	O45-P5-O35	4.13	123.30	107.80

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
50	A	3000	IHP	C4-C5-O15-P5
50	A	3000	IHP	C6-C5-O15-P5
51	C	1500	GTP	PB-O3B-PG-O3G
51	C	1500	GTP	C5'-O5'-PA-O1A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
51	C	1500	GTP	C5'-O5'-PA-O2A

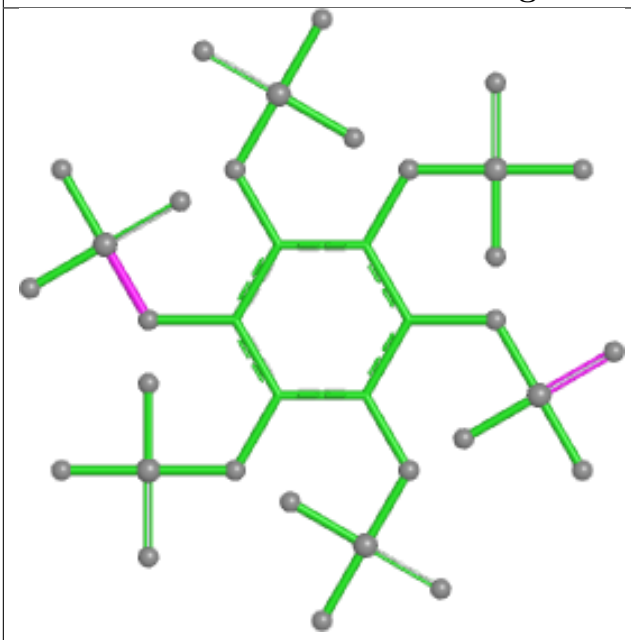
There are no ring outliers.

2 monomers are involved in 21 short contacts:

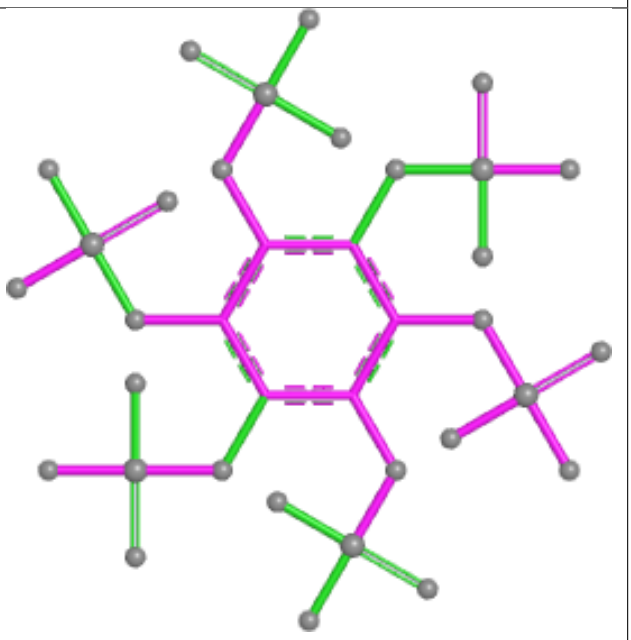
Mol	Chain	Res	Type	Clashes	Symm-Clashes
50	A	3000	IHP	10	0
51	C	1500	GTP	11	0

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.

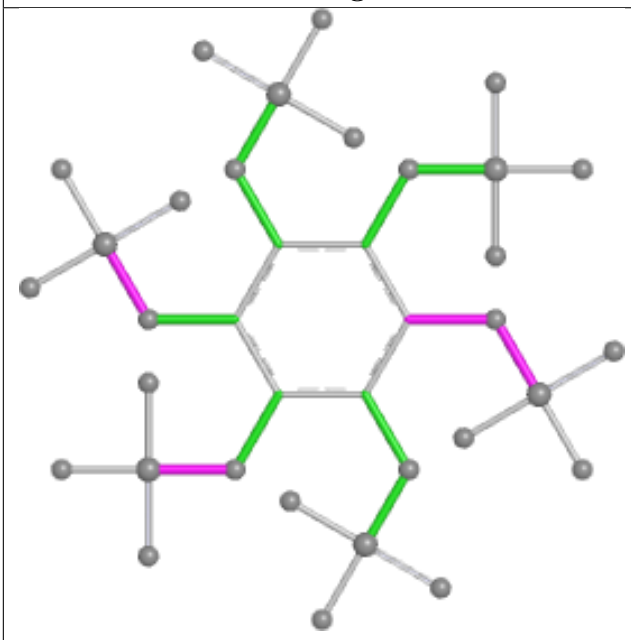
Ligand IHP A 3000



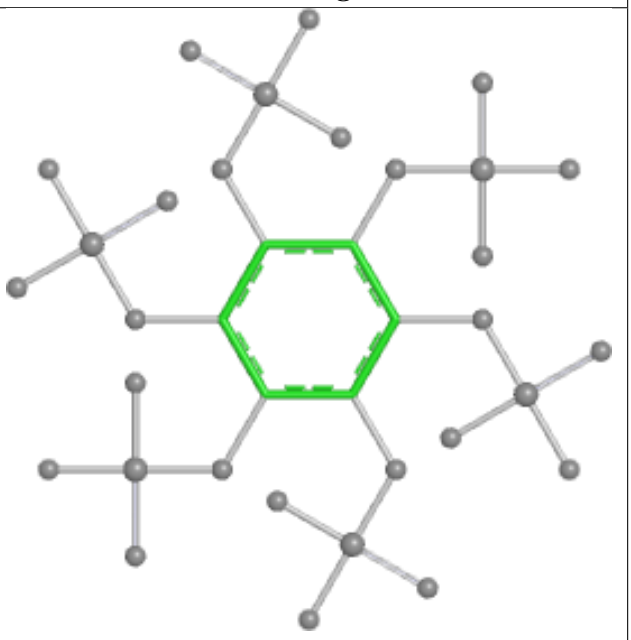
Bond lengths



Bond angles

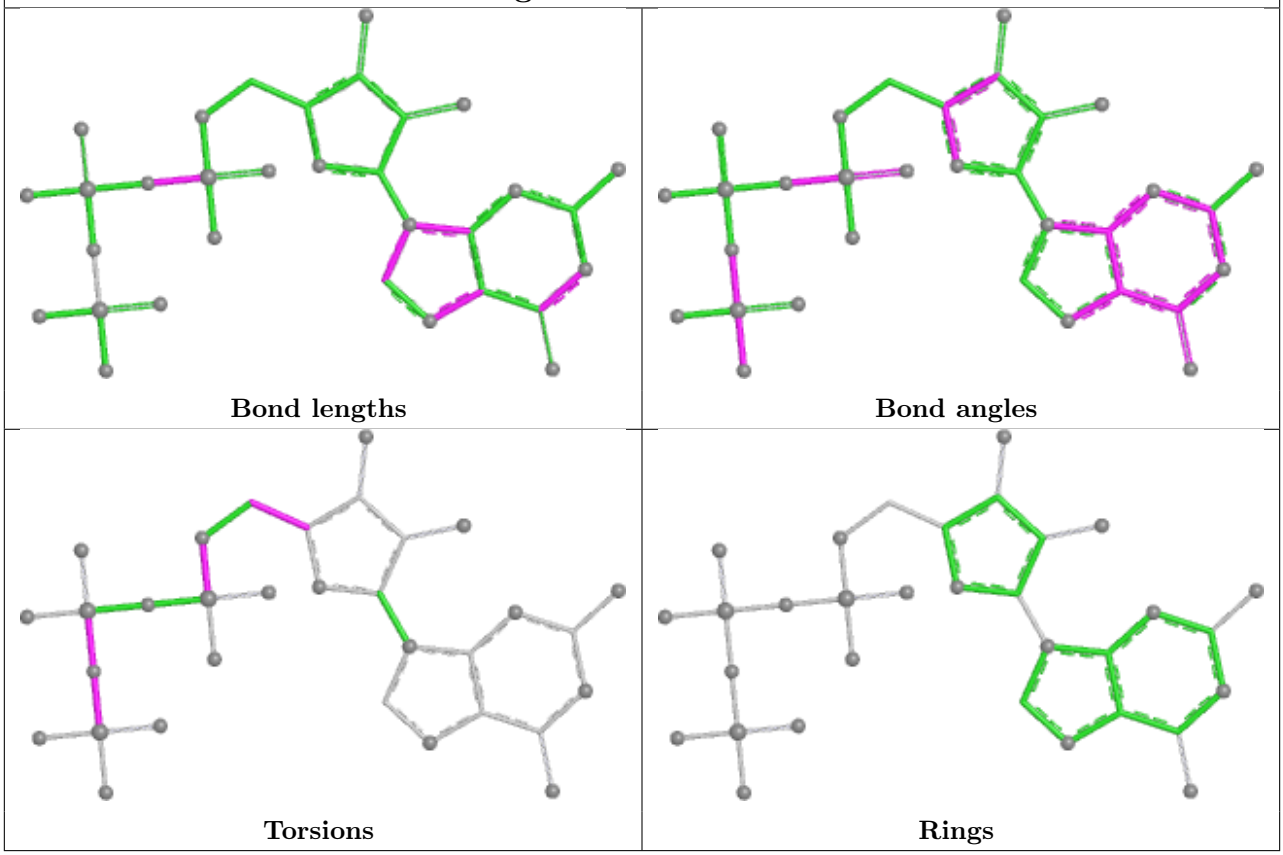


Torsions



Rings

Ligand GTP C 1500



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.

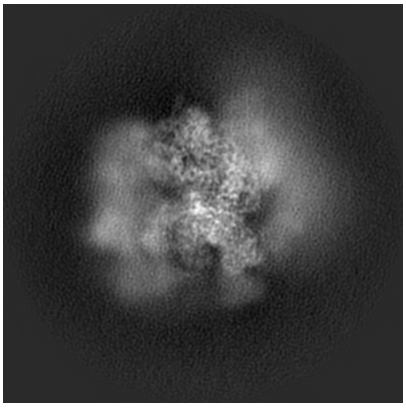
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-6889. These allow visual inspection of the internal detail of the map and identification of artifacts.

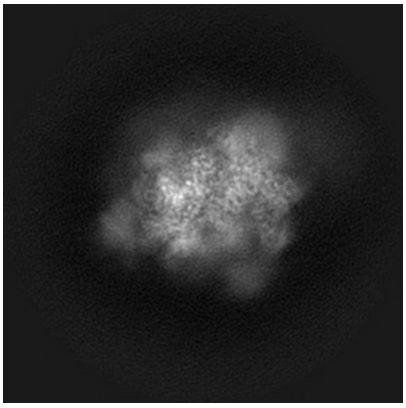
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

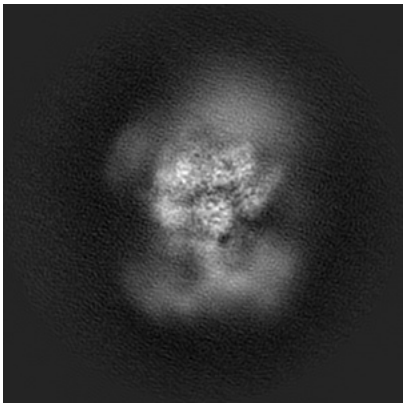
6.1.1 Primary map



X



Y

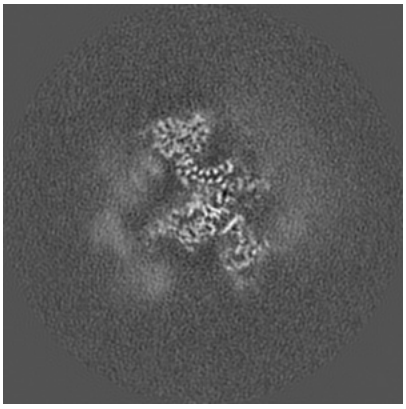


Z

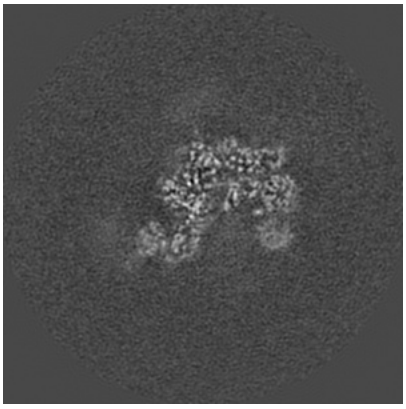
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

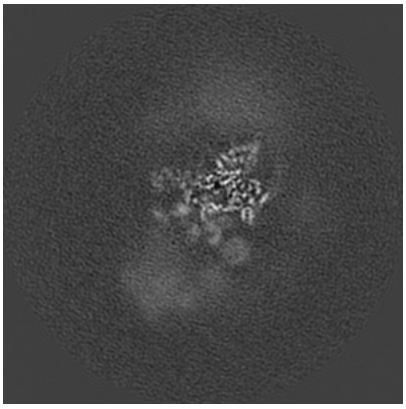
6.2.1 Primary map



X Index: 200



Y Index: 200

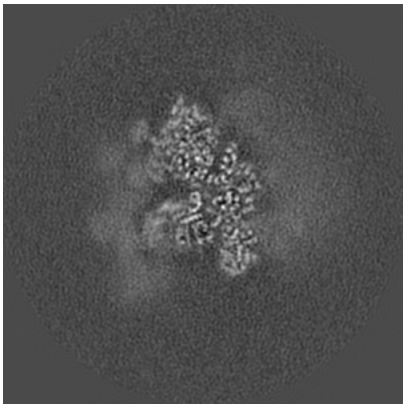


Z Index: 200

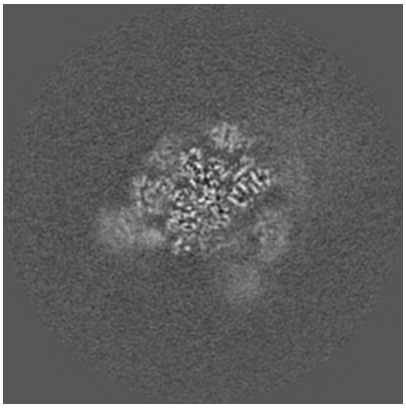
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

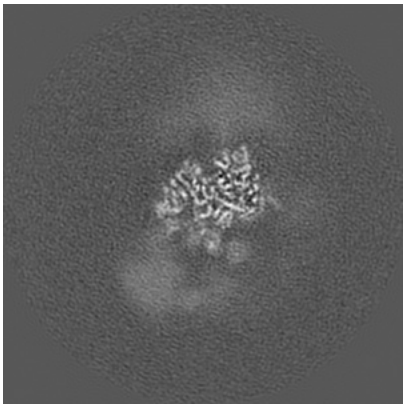
6.3.1 Primary map



X Index: 212



Y Index: 225

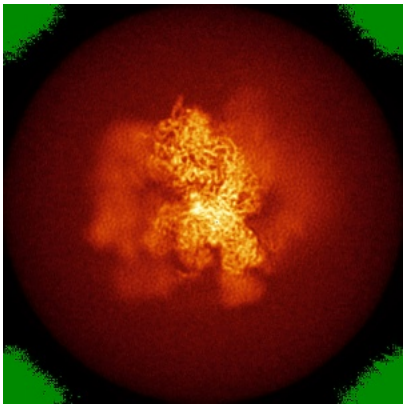


Z Index: 192

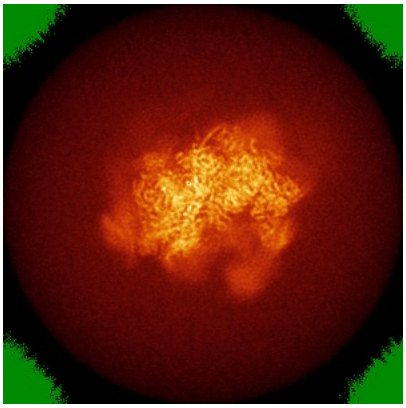
The images above show the largest variance slices of the map in three orthogonal directions.

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

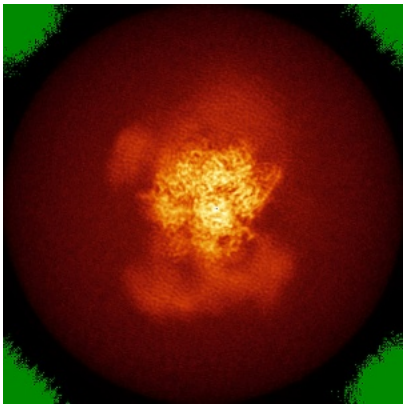
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0374. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

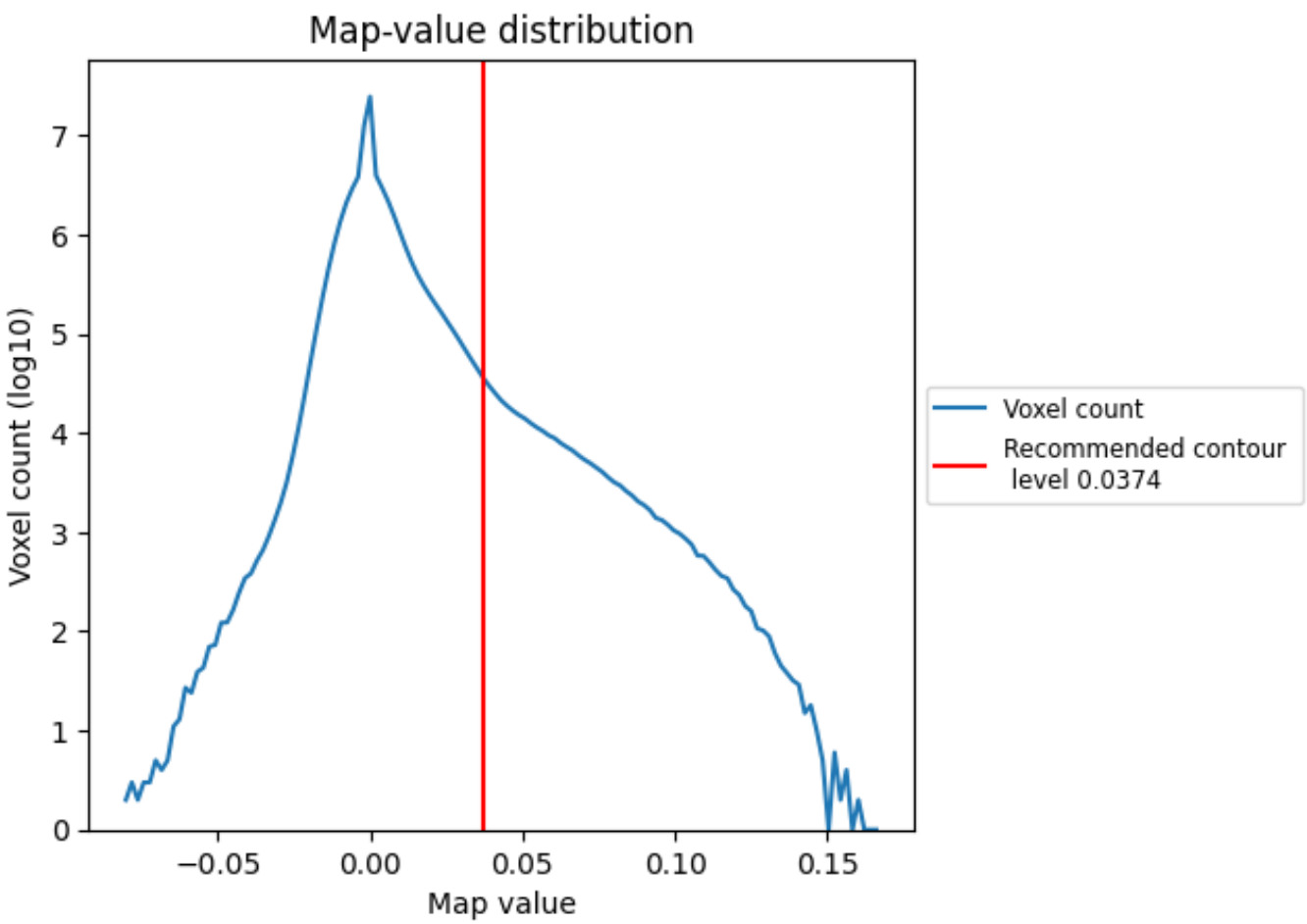
6.6 Mask visualisation (i)

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

7 Map analysis (i)

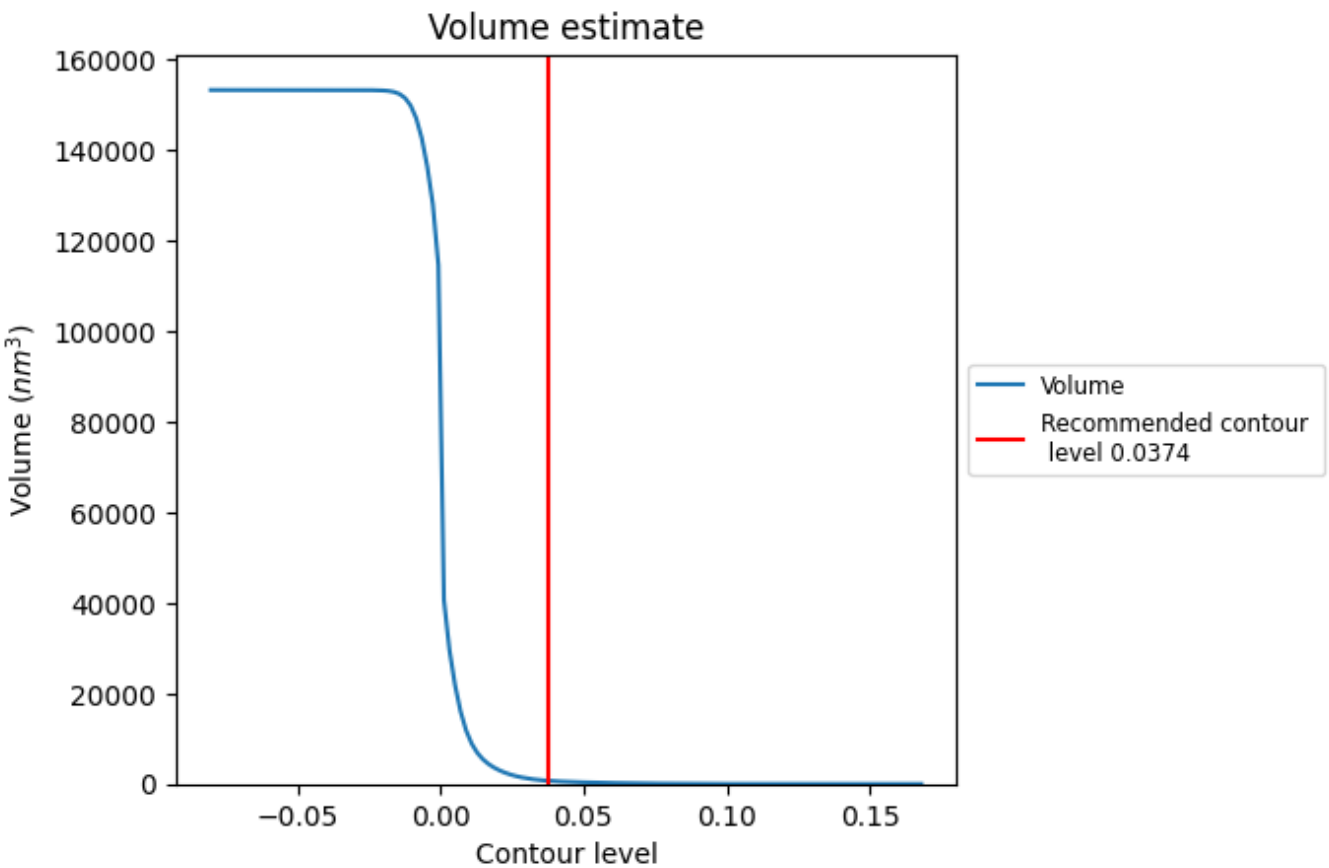
This section contains the results of statistical analysis of the map.

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.

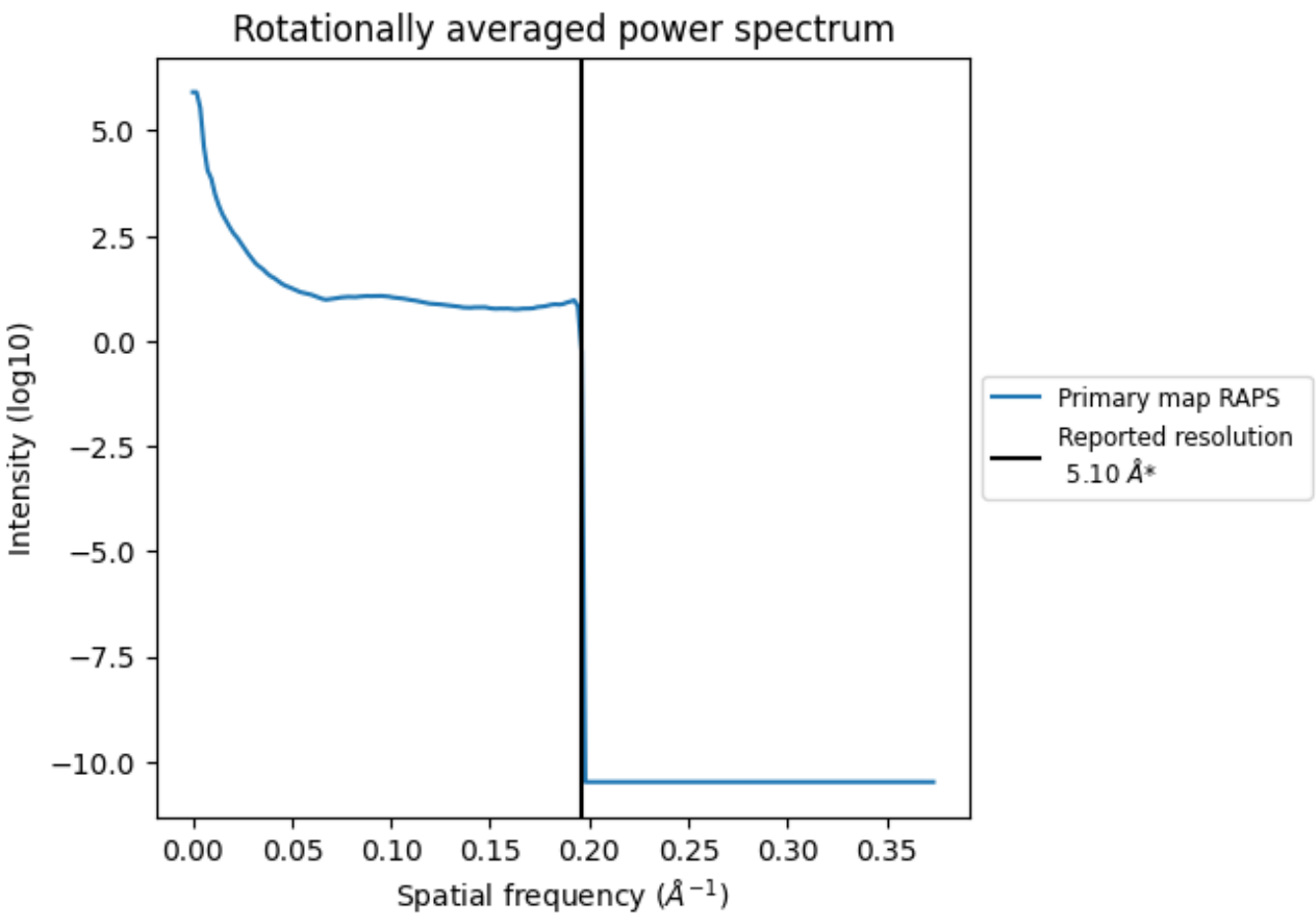
7.2 Volume estimate (i)



The volume at the recommended contour level is 725 nm^3; this corresponds to an approximate mass of 654 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 0.196 Å^{-1}

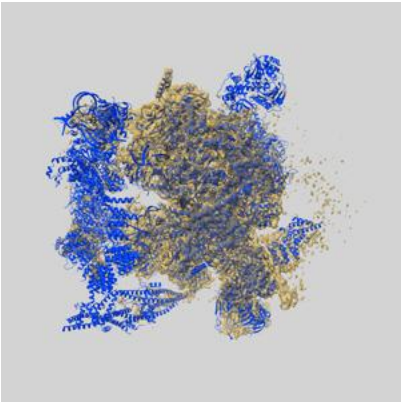
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

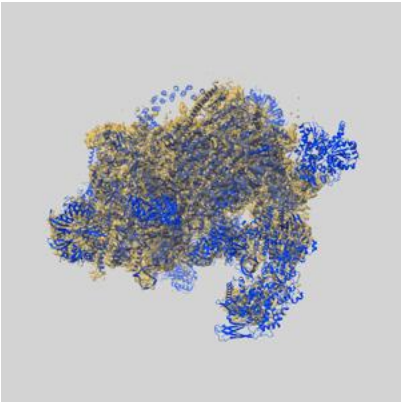
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-6889 and PDB model 5Z56. Per-residue inclusion information can be found in section 3 on page 15.

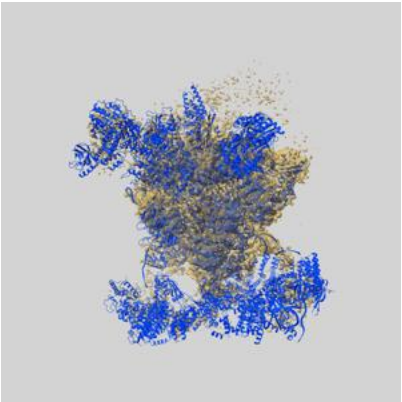
9.1 Map-model overlay (i)



X



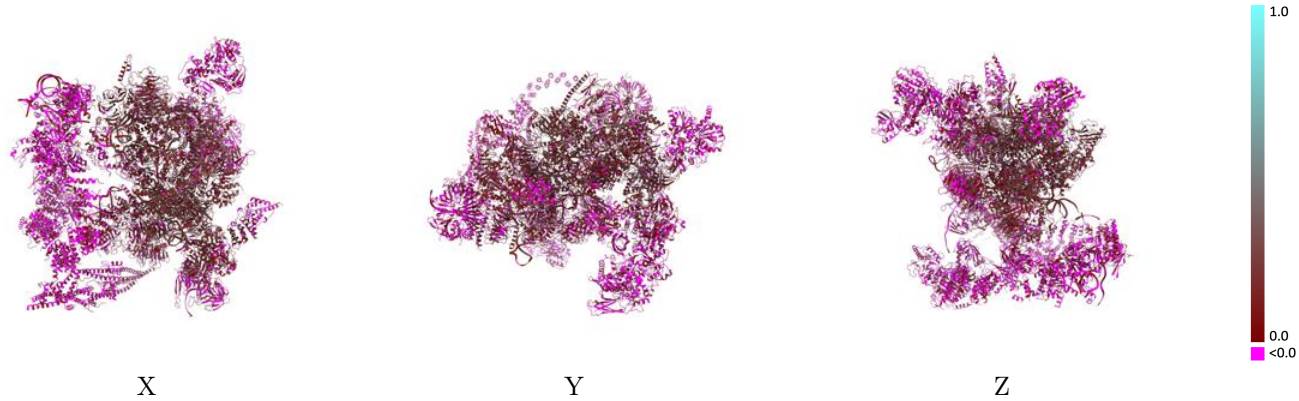
Y



Z

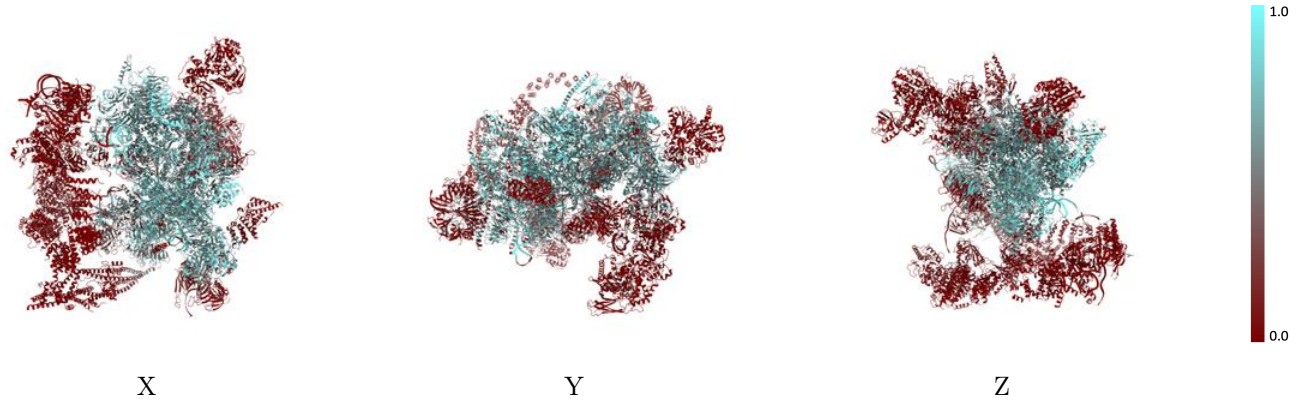
The images above show the 3D surface view of the map at the recommended contour level 0.0374 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



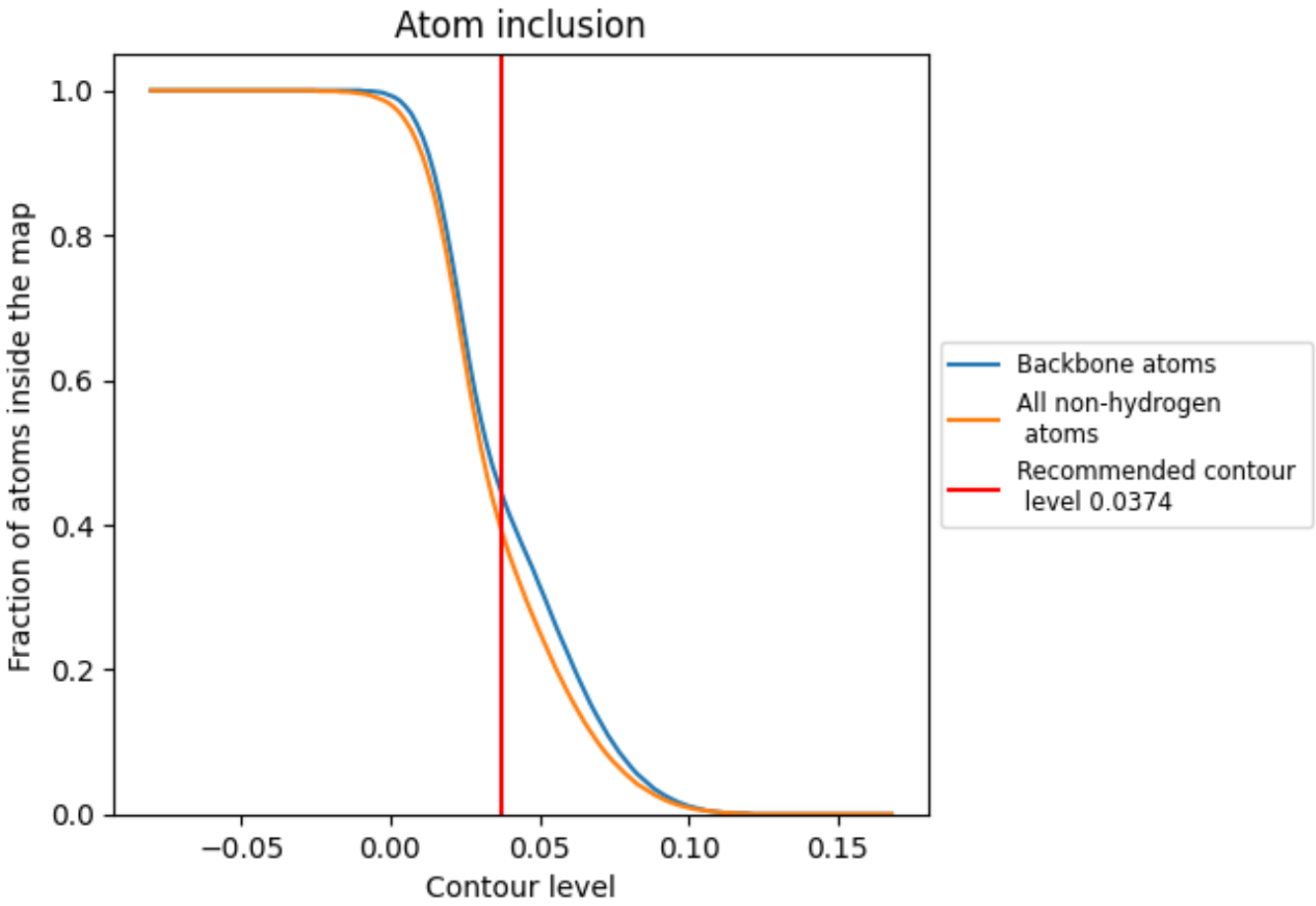
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0374).

9.4 Atom inclusion (i)



At the recommended contour level, 44% of all backbone atoms, 39% 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 (0.0374) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3900	0.1310
1	0.6320	0.2170
2	0.5230	0.1780
3	0.6060	0.1710
4	0.2310	0.0610
5	0.6450	0.2070
6	0.6670	0.2070
7	0.6700	0.2160
A	0.5630	0.2060
B	0.7040	0.1870
C	0.6430	0.1910
D	0.1000	0.0630
E	0.5400	0.1430
F	0.7610	0.2100
G	0.7270	0.2080
H	0.3810	0.1180
I	0.0210	0.0120
J	0.2700	0.0700
K	0.0710	0.0420
L	0.2920	0.1050
M	0.2260	0.1790
N	0.6190	0.1720
O	0.4390	0.1590
P	0.2840	0.1630
Q	0.0090	-0.0050
R	0.4890	0.2030
S	0.3280	0.0920
T	0.6900	0.1960
U	0.4870	0.2470
V	0.3750	0.1280
W	0.1590	0.0700
X	0.6110	0.1900
Y	0.7010	0.2550
Z	0.6410	0.2540
a	0.0550	0.0050

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
b	0.0960	0.0920
c	0.1870	-0.0010
d	0.1830	0.0510
e	0.1690	0.0540
f	0.1690	-0.0090
g	0.1180	0.0210
h	0.0280	0.0350
i	0.0090	0.0050
j	0.0370	-0.0030
k	0.0240	0.0350
l	0.0050	-0.0000
m	0.0220	0.0220
n	0.0270	0.0070
o	0.0110	0.0180
p	0.0320	0.0150
q	0.0020	-0.0120
r	0.0120	0.0120
s	0.0480	0.0470
t	0.0030	-0.0040
u	0.0020	0.0250
v	0.3360	0.1070
w	0.1970	0.0420
x	0.0010	-0.0010
y	0.0470	0.0010
z	0.1700	0.1660