



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 06:24 AM UTC

PDB ID : 7R5J / pdb_00007r5j
EMDB ID : EMD-14321
Title : Human nuclear pore complex (dilated)
Authors : Mosalaganti, S.; Obarska-Kosinska, A.; Siggel, M.; Taniguchi, R.; Turonova, B.; Zimmerli, C.E.; Buczak, K.; Schmidt, F.H.; Margiotta, E.; Mackmull, M.T.; Hagen, W.J.H.; Hummer, G.; Kosinski, J.; Beck, M.
Deposited on : 2022-02-10
Resolution : 50.00 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

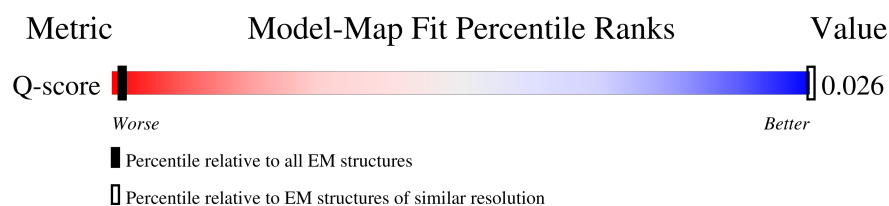
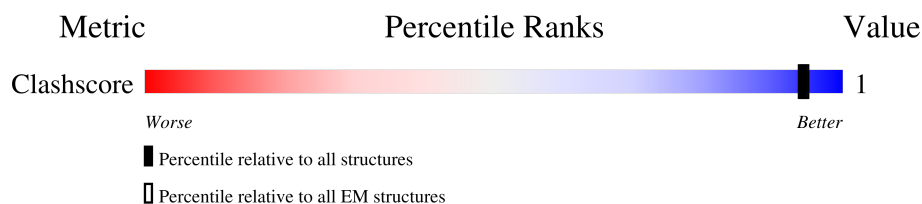
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

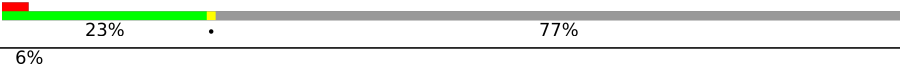
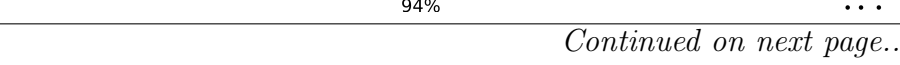
The reported resolution of this entry is 50.00 Å.

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	-
Q-score	-	25397	1 (50.00 - 50.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	00	3224	
1	01	3224	
1	02	3224	
1	03	3224	
1	04	3224	
2	10	1887	

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Mol	Chain	Length	Quality of chain
2	11	1887	49% 95% ..
2	12	1887	31% 95% ..
2	13	1887	40% 96% ..
2	14	1887	68% 94% ..
2	15	1887	27% 94% ..
2	16	1887	25% 94% ..
2	17	1887	39% 94% ..
3	40	546	67% 30%
3	41	546	67% 30%
4	A0	819	7% 94% 6%
4	A1	819	14% 95% .
4	A2	819	9% 93% 6%
4	A3	819	12% 95% .
4	A4	819	14% 84% 11%
4	A5	819	20% 85% 11%
4	A6	819	8% 85% 11%
5	B0	1749	15% 97% .
5	B1	1749	14% 96% .
6	C0	2012	18% 96% .
6	C1	2012	15% 97% .
6	C2	2012	16% 95% .
6	C3	2012	14% 96% .
6	C4	2012	17% 96% .
7	D0	1391	13% 91% 6%
7	D1	1391	18% 89% 5% 6%

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Mol	Chain	Length	Quality of chain
7	D2	1391	
7	D3	1391	
7	D4	1391	
7	D5	1391	
8	E0	674	
8	E1	674	
9	F0	326	
9	F1	326	
9	F2	326	
9	F3	326	
10	H0	507	
10	H1	507	
10	H2	507	
10	H3	507	
11	I0	599	
11	I1	599	
11	I2	599	
11	I3	599	
12	J0	522	
12	J1	522	
12	J2	522	
12	J3	522	
12	J4	522	
13	K0	1156	
13	K1	1156	

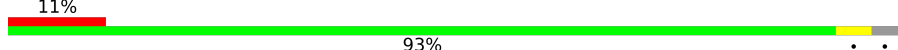
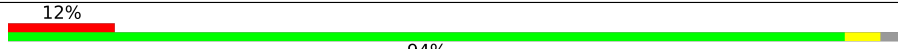
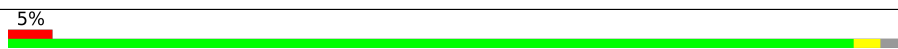
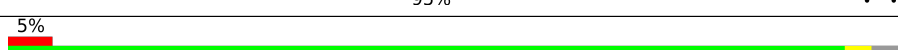
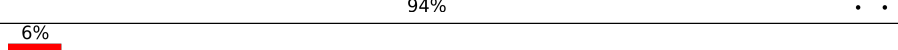
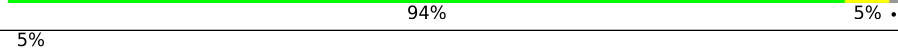
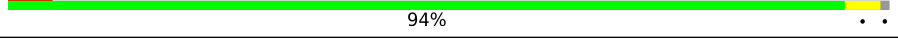
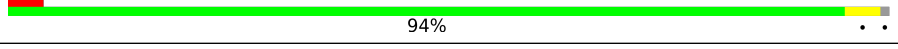
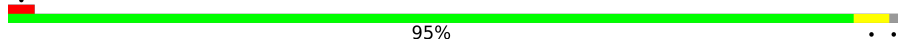
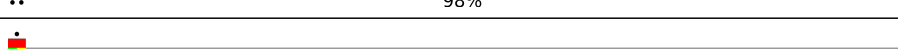
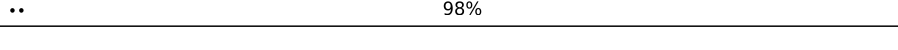
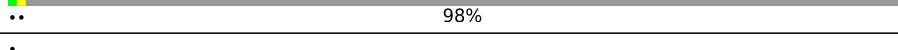
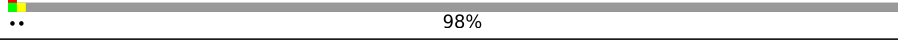
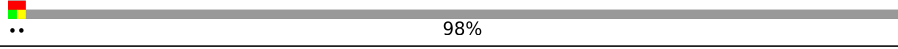
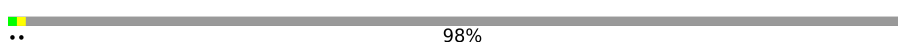
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Mol	Chain	Length	Quality of chain
13	K2	1156	
13	K3	1156	
14	L0	925	
14	L1	925	
14	L2	925	
14	L3	925	
15	M0	937	
15	M1	937	
15	M2	937	
15	M3	937	
16	N0	322	
16	N1	322	
16	N2	322	
16	N3	322	
17	O0	360	
17	O1	360	
17	O2	360	
17	O3	360	
18	P0	656	
18	P1	656	
18	P2	656	
18	P3	656	
19	Q0	380	
19	Q1	380	
19	Q2	380	

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Mol	Chain	Length	Quality of chain
19	Q3	380	
20	R0	1436	
20	R1	1436	
20	R2	1436	
20	R3	1436	
21	S0	326	
21	S1	326	
21	S2	326	
21	S3	326	
22	T0	2266	
22	T1	2266	
23	U0	880	
23	U1	880	
23	U2	880	
23	U3	880	
23	U4	880	
23	U5	880	
23	U6	880	
24	V0	2090	
25	W0	741	

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 617133 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 E3 SUMO-protein ligase RanBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	00	756	Total	C	N	O	S	0	0
			6085	3866	1045	1147	27		
1	01	756	Total	C	N	O	S	0	0
			6085	3866	1045	1147	27		
1	02	756	Total	C	N	O	S	0	0
			6085	3866	1045	1147	27		
1	03	756	Total	C	N	O	S	0	0
			6085	3866	1045	1147	27		
1	04	756	Total	C	N	O	S	0	0
			6085	3866	1045	1147	27		

- Molecule 2 is a protein called Nuclear pore membrane glycoprotein 210.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	10	1831	Total	C	N	O	S	0	0
			14046	8947	2406	2644	49		
2	11	1831	Total	C	N	O	S	0	0
			14046	8947	2406	2644	49		
2	12	1831	Total	C	N	O	S	0	0
			14046	8947	2406	2644	49		
2	13	1831	Total	C	N	O	S	0	0
			14046	8947	2406	2644	49		
2	14	1831	Total	C	N	O	S	0	0
			14046	8947	2406	2644	49		
2	15	1831	Total	C	N	O	S	0	0
			14046	8947	2406	2644	49		
2	16	1831	Total	C	N	O	S	0	0
			14046	8947	2406	2644	49		
2	17	1831	Total	C	N	O	S	0	0
			14046	8947	2406	2644	49		

- Molecule 3 is a protein called Aladin.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	40	383	Total	C	N	O	S	0	0
			2922	1864	509	533	16		
3	41	383	Total	C	N	O	S	0	0
			2922	1864	509	533	16		

- Molecule 4 is a protein called Nuclear pore complex protein Nup93.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A0	818	Total	C	N	O	S	0	0
			6568	4136	1145	1259	28		
4	A1	818	Total	C	N	O	S	0	0
			6568	4136	1145	1259	28		
4	A2	818	Total	C	N	O	S	0	0
			6568	4136	1145	1259	28		
4	A3	818	Total	C	N	O	S	0	0
			6568	4136	1145	1259	28		
4	A4	726	Total	C	N	O	S	0	0
			5860	3705	1018	1109	28		
4	A5	726	Total	C	N	O	S	0	0
			5860	3705	1018	1109	28		
4	A6	726	Total	C	N	O	S	0	0
			5860	3705	1018	1109	28		

- Molecule 5 is a protein called Nucleoporin NUP188 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B0	1748	Total	C	N	O	S	0	0
			13746	8743	2353	2559	91		
5	B1	1748	Total	C	N	O	S	0	0
			13746	8743	2353	2559	91		

- Molecule 6 is a protein called Nuclear pore complex protein Nup205.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C0	2011	Total	C	N	O	S	0	0
			16013	10208	2753	2965	87		
6	C1	2011	Total	C	N	O	S	0	0
			16013	10208	2753	2965	87		
6	C2	2011	Total	C	N	O	S	0	0
			16013	10208	2753	2965	87		
6	C3	2011	Total	C	N	O	S	0	0
			16013	10208	2753	2965	87		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	C4	2011	Total	C	N	O	S	0	0
			16013	10208	2753	2965	87		

- Molecule 7 is a protein called Nuclear pore complex protein Nup155.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D0	1312	Total	C	N	O	S	0	0
			10363	6569	1786	1949	59		
7	D1	1312	Total	C	N	O	S	0	0
			10363	6569	1786	1949	59		
7	D2	1312	Total	C	N	O	S	0	0
			10363	6569	1786	1949	59		
7	D3	1312	Total	C	N	O	S	0	0
			10363	6569	1786	1949	59		
7	D4	1312	Total	C	N	O	S	0	0
			10363	6569	1786	1949	59		
7	D5	1312	Total	C	N	O	S	0	0
			10363	6569	1786	1949	59		

- Molecule 8 is a protein called Nucleoporin NDC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E0	548	Total	C	N	O	S	0	0
			4432	2923	729	758	22		
8	E1	548	Total	C	N	O	S	0	0
			4432	2923	729	758	22		

- Molecule 9 is a protein called Nucleoporin NUP35.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F0	241	Total	C	N	O	S	0	0
			1837	1154	313	359	11		
9	F1	241	Total	C	N	O	S	0	0
			1837	1154	313	359	11		
9	F2	241	Total	C	N	O	S	0	0
			1837	1154	313	359	11		
9	F3	241	Total	C	N	O	S	0	0
			1837	1154	313	359	11		

- Molecule 10 is a protein called Nucleoporin p54.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H0	383	Total	C	N	O	S	0	0
			3066	1921	544	592	9		
10	H1	383	Total	C	N	O	S	0	0
			3066	1921	544	592	9		
10	H2	383	Total	C	N	O	S	0	0
			3066	1921	544	592	9		
10	H3	383	Total	C	N	O	S	0	0
			3066	1921	544	592	9		

- Molecule 11 is a protein called Nucleoporin p58/p45.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I0	173	Total	C	N	O	S	0	0
			1398	881	245	267	5		
11	I1	173	Total	C	N	O	S	0	0
			1398	881	245	267	5		
11	I2	173	Total	C	N	O	S	0	0
			1398	881	245	267	5		
11	I3	173	Total	C	N	O	S	0	0
			1398	881	245	267	5		

- Molecule 12 is a protein called Nuclear pore glycoprotein p62.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J0	171	Total	C	N	O	S	0	0
			1403	872	243	285	3		
12	J1	171	Total	C	N	O	S	0	0
			1403	872	243	285	3		
12	J2	171	Total	C	N	O	S	0	0
			1403	872	243	285	3		
12	J3	171	Total	C	N	O	S	0	0
			1403	872	243	285	3		
12	J4	171	Total	C	N	O	S	0	0
			1403	872	243	285	3		

- Molecule 13 is a protein called Nuclear pore complex protein Nup133.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K0	1086	Total	C	N	O	S	0	0
			8574	5420	1425	1692	37		
13	K1	1086	Total	C	N	O	S	0	0
			8574	5420	1425	1692	37		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	K2	1086	Total	C	N	O	S	0	0
			8574	5420	1425	1692	37		
13	K3	1086	Total	C	N	O	S	0	0
			8574	5420	1425	1692	37		

- Molecule 14 is a protein called Nuclear pore complex protein Nup107.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L0	782	Total	C	N	O	S	0	0
			6383	4064	1079	1208	32		
14	L1	782	Total	C	N	O	S	0	0
			6383	4064	1079	1208	32		
14	L2	782	Total	C	N	O	S	0	0
			6383	4064	1079	1208	32		
14	L3	782	Total	C	N	O	S	0	0
			6383	4064	1079	1208	32		

- Molecule 15 is a protein called Nuclear pore complex protein Nup96.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M0	673	Total	C	N	O	S	0	0
			5461	3467	964	1004	26		
15	M1	673	Total	C	N	O	S	0	0
			5461	3467	964	1004	26		
15	M2	673	Total	C	N	O	S	0	0
			5461	3467	964	1004	26		
15	M3	673	Total	C	N	O	S	0	0
			5461	3467	964	1004	26		

- Molecule 16 is a protein called Protein SEC13 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N0	301	Total	C	N	O	S	0	0
			2352	1479	409	452	12		
16	N1	301	Total	C	N	O	S	0	0
			2352	1479	409	452	12		
16	N2	301	Total	C	N	O	S	0	0
			2352	1479	409	452	12		
16	N3	301	Total	C	N	O	S	0	0
			2352	1479	409	452	12		

- Molecule 17 is a protein called Nucleoporin SEH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O0	323	Total	C	N	O	S	0	0
			2528	1584	452	475	17		
17	O1	323	Total	C	N	O	S	0	0
			2528	1584	452	475	17		
17	O2	323	Total	C	N	O	S	0	0
			2528	1584	452	475	17		
17	O3	323	Total	C	N	O	S	0	0
			2528	1584	452	475	17		

- Molecule 18 is a protein called Nuclear pore complex protein Nup85.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P0	655	Total	C	N	O	S	0	0
			5257	3341	898	982	36		
18	P1	655	Total	C	N	O	S	0	0
			5257	3341	898	982	36		
18	P2	655	Total	C	N	O	S	0	0
			5257	3341	898	982	36		
18	P3	655	Total	C	N	O	S	0	0
			5257	3341	898	982	36		

- Molecule 19 is a protein called Nucleoporin Nup43.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q0	345	Total	C	N	O	S	0	0
			2703	1690	474	527	12		
19	Q1	345	Total	C	N	O	S	0	0
			2703	1690	474	527	12		
19	Q2	345	Total	C	N	O	S	0	0
			2703	1690	474	527	12		
19	Q3	345	Total	C	N	O	S	0	0
			2703	1690	474	527	12		

- Molecule 20 is a protein called Nuclear pore complex protein Nup160.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R0	1399	Total	C	N	O	S	0	0
			11132	7093	1878	2088	73		
20	R1	1399	Total	C	N	O	S	0	0
			11132	7093	1878	2088	73		
20	R2	1399	Total	C	N	O	S	0	0
			11132	7093	1878	2088	73		

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Mol	Chain	Residues	Atoms					AltConf	Trace
20	R3	1399	Total	C	N	O	S	0	0
			11132	7093	1878	2088	73		

- Molecule 21 is a protein called Nucleoporin Nup37.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S0	322	Total	C	N	O	S	0	0
			2552	1626	436	475	15		
21	S1	322	Total	C	N	O	S	0	0
			2552	1626	436	475	15		
21	S2	322	Total	C	N	O	S	0	0
			2552	1626	436	475	15		
21	S3	322	Total	C	N	O	S	0	0
			2552	1626	436	475	15		

- Molecule 22 is a protein called Protein ELYS.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T0	1004	Total	C	N	O	S	0	0
			7960	5069	1359	1490	42		
22	T1	1004	Total	C	N	O	S	0	0
			7960	5069	1359	1490	42		

- Molecule 23 is a protein called Nuclear pore complex protein Nup98.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U0	150	Total	C	N	O	S	0	0
			1193	756	205	229	3		
23	U1	19	Total	C	N	O		0	0
			151	98	27	26			
23	U2	19	Total	C	N	O		0	0
			151	98	27	26			
23	U3	19	Total	C	N	O		0	0
			151	98	27	26			
23	U4	19	Total	C	N	O		0	0
			151	98	27	26			
23	U5	19	Total	C	N	O		0	0
			151	98	27	26			
23	U6	19	Total	C	N	O		0	0
			151	98	27	26			

- Molecule 24 is a protein called Nuclear pore complex protein Nup214.

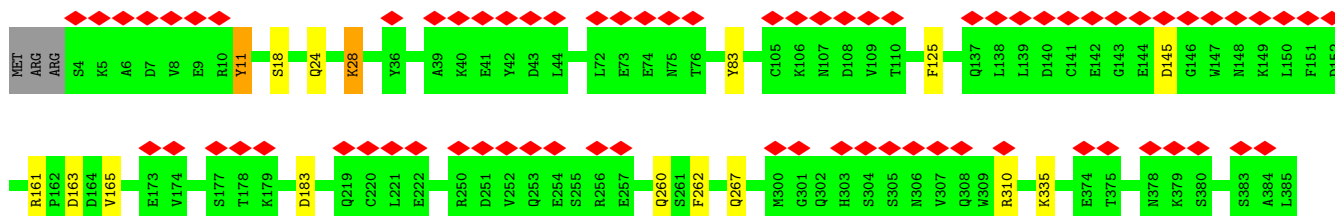
Mol	Chain	Residues	Atoms					AltConf	Trace
24	V0	273	Total	C	N	O	S	0	0
			2203	1376	398	423	6		

- Molecule 25 is a protein called Nuclear pore complex protein Nup88.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W0	735	Total	C	N	O	S	0	0
			5836	3714	988	1103	31		



- Molecule 1: E3 SUMO-protein ligase RanBP2







LYS
ILE
GLU
SER
PHE
GLY
SER
PRO
LYS
GLY
SER
VAL
CYS
ARG
ARG
ILE
THR
ILE
THR
GLU
CYS
GLY
GLN
ILE

Chain 02: 23% 77%









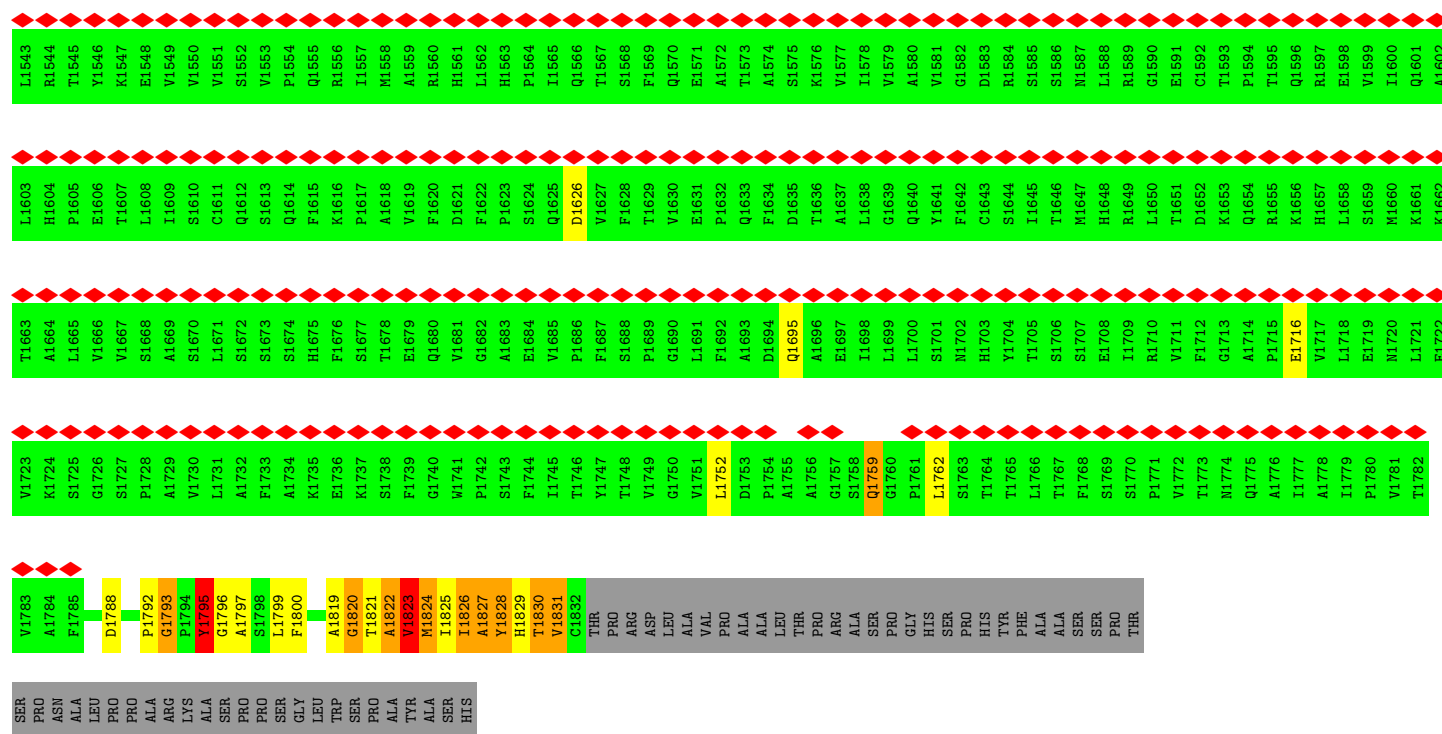


Chain 04:

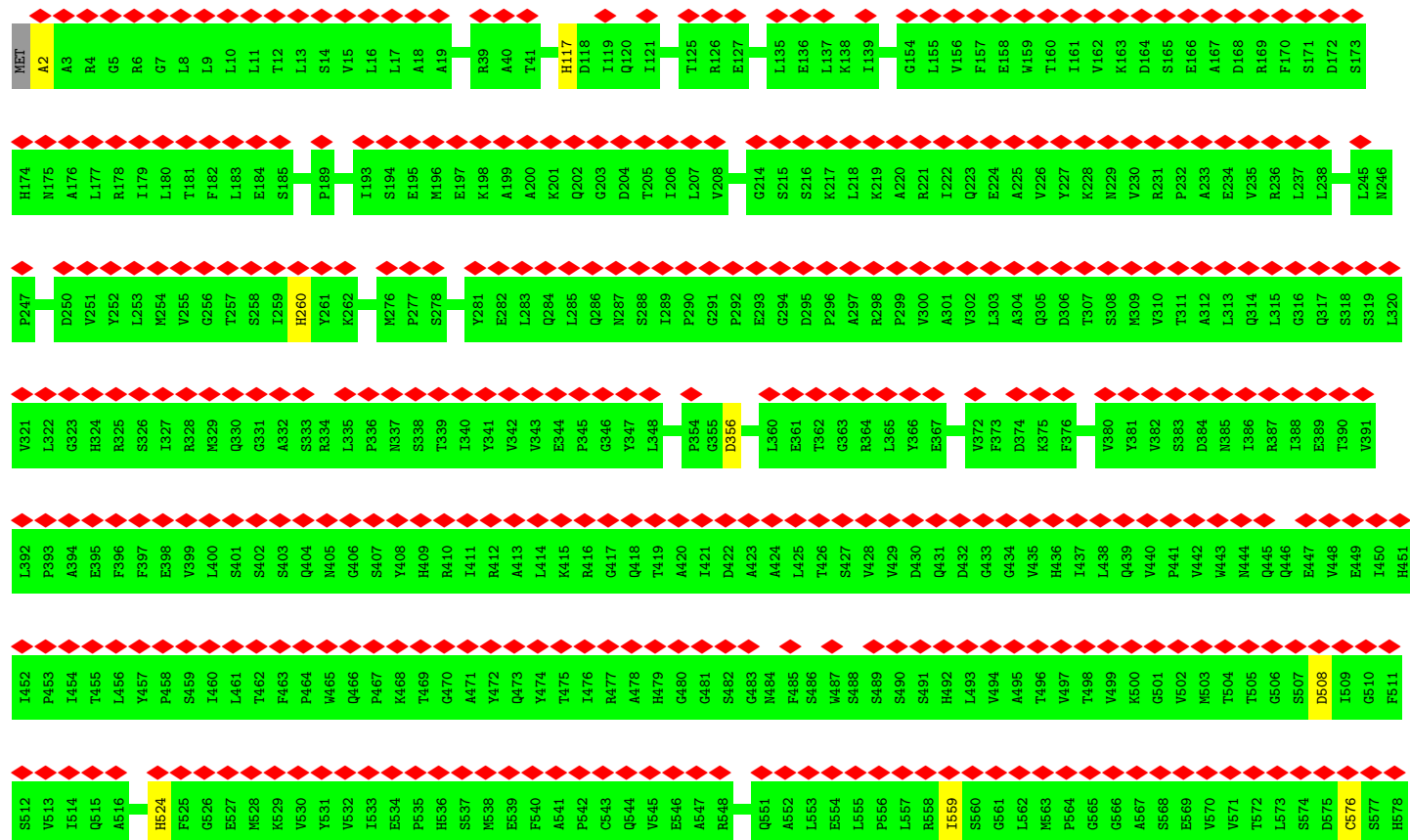


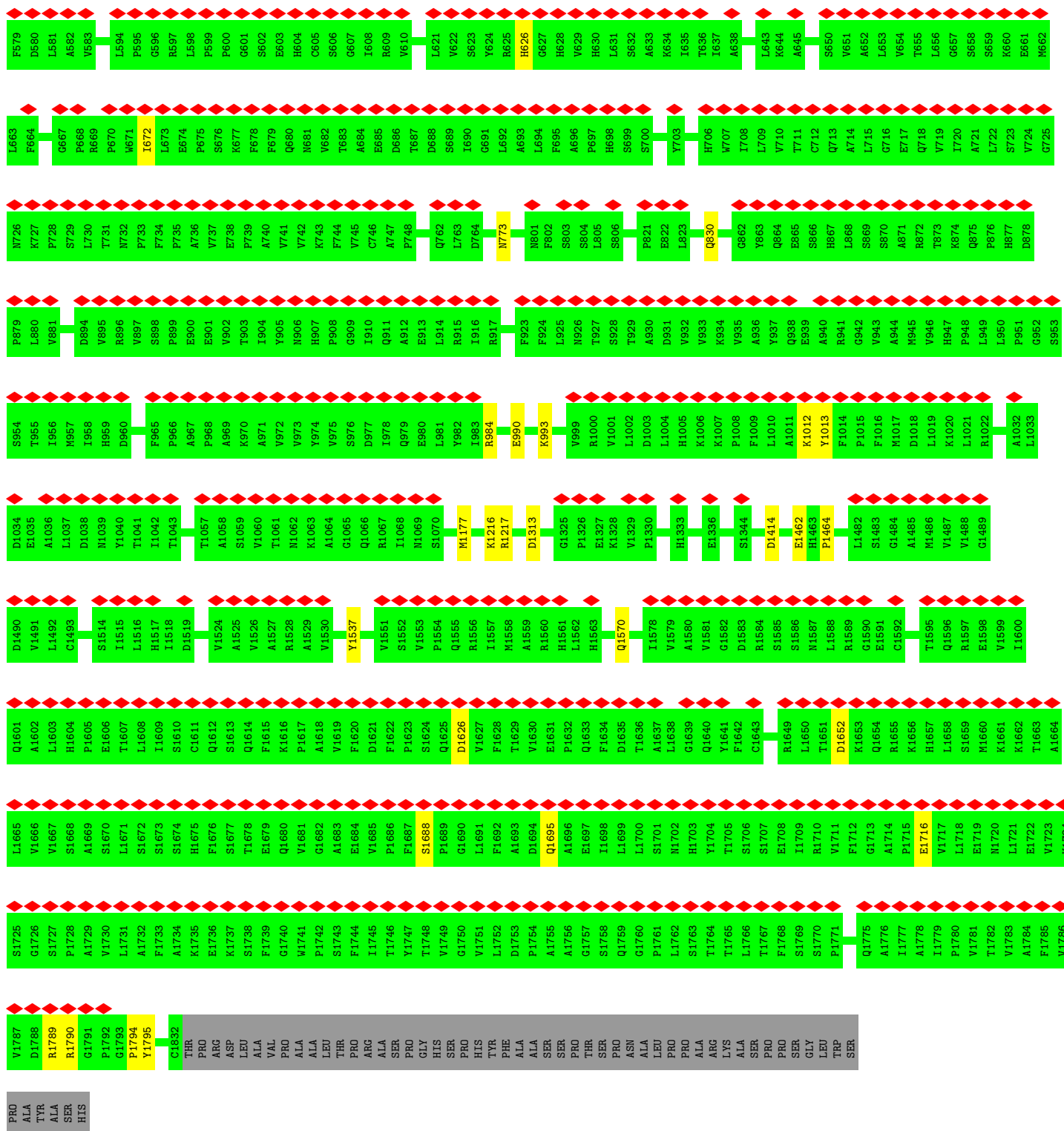


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S1382	P1383	V1384	L1385	H1386	T1387	Q1388	N1389	K1390	E1391	A1392	L1393	V1394	A1395	V1396	P1397	L1398	G1399	M1400	T1401	V1402	T1403	D1414		D1430	D1431	F1432	V1433	Q1434	I1435	G1436	K1437	G1438	P1439	T1440	N1441	N1442	T1443	C1444	V1445	V1446	R1447	T1448	V1449	S1450	V1451	G1452	L1472		P1473	V1474	L1475	Q1476	A1477	T1478	S1479	P1480	E1481	L1482		
Y1305	I1306	K1307	L1308	Q1309	T1310	N1311	R1312	D1313	G1314	A1315	A1316	S1317	L1318	S1319	Y1320	R1321	V1322	L1323	D1324	G1325	P1326	E1327	K1328	V1329	P1330	V1331	V1332	H1333	V1334	D1335	E1336	K1337	G1338	F1339	L1340	A1341	S1342	G1343	S1344	M1345	S1349		T1350	I1351	E1352	V1353	F1359	G1360	A1361	N1362	Q1363	T1364	I1365							
A1058	S1059	V1060	T1061	M1062	K1063	A1064	G1065	Q1066	R1067	I1068	N1069	A1070	S1071	P1072	Q1073	Q1074	I1075	E1076	V1077	Q1105		P1106	Q1107	S1108	N1109	A1124		D1146	T1149		G1150	K1151	V1152	V1205		P1206	G1207	R1217		A1229	S1230	P1234	S1235	Q1236	A1259		V1260	D1261	P1262	T1263	S1264	R1272		N1303	S1304					
Y998	V999	R1000	V1001	L1002	D1003	L1004	H1005	K1006	K1007	P1008	F1009	L1010	A1011	K1012	Y1013	F1014	P1015	F1016	M1017	D1018	L1019	K1020	L1021	R1022	A1023	A1024	S1025	P1026	I1027	I1028	T1029	L1030	V1031	A1032	L1033	D1034	E1035	A1036	L1037	D1038	N1039	Y1040	T1041	I1042	T1043	F1044	L1045	I1046	R1047	G1048	V1049	A1050	I1051	K1052	Q1053	T1054	S1055	L1056	T1057	
V933	K934	V935	A936	Y937	G942		V943	A944	Y945	V946	H947	P948	L949	L950	P951	G952	S953	S954	T955	I956	V957	I958	H959	D960	L961	C962	L963	V964	F965	P966	T967	P968	A969	K970	A971	V972	V973	Y974	V975	S976	D977	I978	Q979	E980	L981	Y982	I983	Y984		V985	Y986	E990		I991	G992	K993	T994	V995	K996	A997
T873	K874	Q875	P876	H877	D878	P879	L880	V881	P882	L883	S884	A885	S886	L887	E888	L889	T890	L891	V892	E893	D894	V895	R896	V897	S898	P899	E900	E901	V902	T903	I904	Y905	N906	H907	P908	G909	I910	Q911	A912	E913	L914	R915	I916	R917	E918	G919	S920	G921	Y922	P923	F924	L925	N926	T927	S928	T929	D930	V931		
R813	P814	V815	L816	A817	S818	I819	E820	P821	E822	L823	P824	M825	Q826	L827	V828	S829	Q830	D831	D832	E833	S834	Q835	Q836	K837	K838	L839	H840	G841	L842	Q843	A844	I845	L846	V847	H848	E849	A850	S851	G852	T853	T854	A855	I856	T857	A858	T859	A860	T861	G862	Y863	Q864	E865	S866	H867	L868	S869	S870	A871	R872	
L752	T753	L754	A755	P756	V757	Y758	T759	S760	P761	Q762	L763	D764	M765	S766	C767	F768	L769	L770	M773		K774	Q775	V776	V777	P778	V779	S780	H781	H782	R783	M784	P785	R786	L787	D788	L789	A790	A791	Y792	D793	Q794	E795	G796	R797	R798	V799	D800	N801	F802	S803	S804	L805	S806	T807	Q808	N809	E810	S811	T812	
I690	G691	A693	F695	A696	P697	H698	S699	S700	R701	N702	V703	Q704	Q705	H706	V707	I708	L709	V710	T711	C712	Q713	Q714	L715	G716	E717	Q718	L722		S723	V724	G725	N726	P727	L728	S729	L730	T731	N732	P733	F734	P735	A736	V737	E738	P739	A740	V741	V742	K743	F744	V745	C746	A747	P748	P749	S750	R751			
Y624	R625	H626	S632		A633	K634	I635	T636	I637	A638	A639	Y640	L641	P642	L643	K644	A645	V646	P647	P648	S649	S650	V651	A652	L653	V654	T655	L656	G657	S658	P659	K660	E661	M662	L663	F664	E665	Q666	G667	V671	I672	L673	E674	P675	S676	K677	F678	F679	Q680	A684		E685	D686	T687	D688	S689				
P564	G565	G566	A567	S568	E569	V570	V571	T572	L573	S574	D575	C576	S577	H578	F579	D580	L581	A582	V583	E584	V585	E586	N587	Q588	G589	V590	F591	Q592	P593	L594	P595	G596	R597	L598	E599	P600	G601	S602	E603	H604	C605	S606	G607	I608	R609	V610	K611	A612	E613	A614	Q615	G616	S617	T618	T619	L620	L621	V622	S623	
M503	T504	T505	G506	S507	D508	I509	G510	F511	S512	V513	I514	Q515	A516	H517	D518	N521		P522	L523	H524	F525	G526	E527	M528	K529	V530	Y531	V532	I533	E534	P535	H536	S537	M538	E539	F540	A541	P542	C543	Q544	V545	E546	A547	R548	V549	G550	Q551	A552	L553	E554	L555	P556	L557	R558	I559	S560	G561	L562	M563	



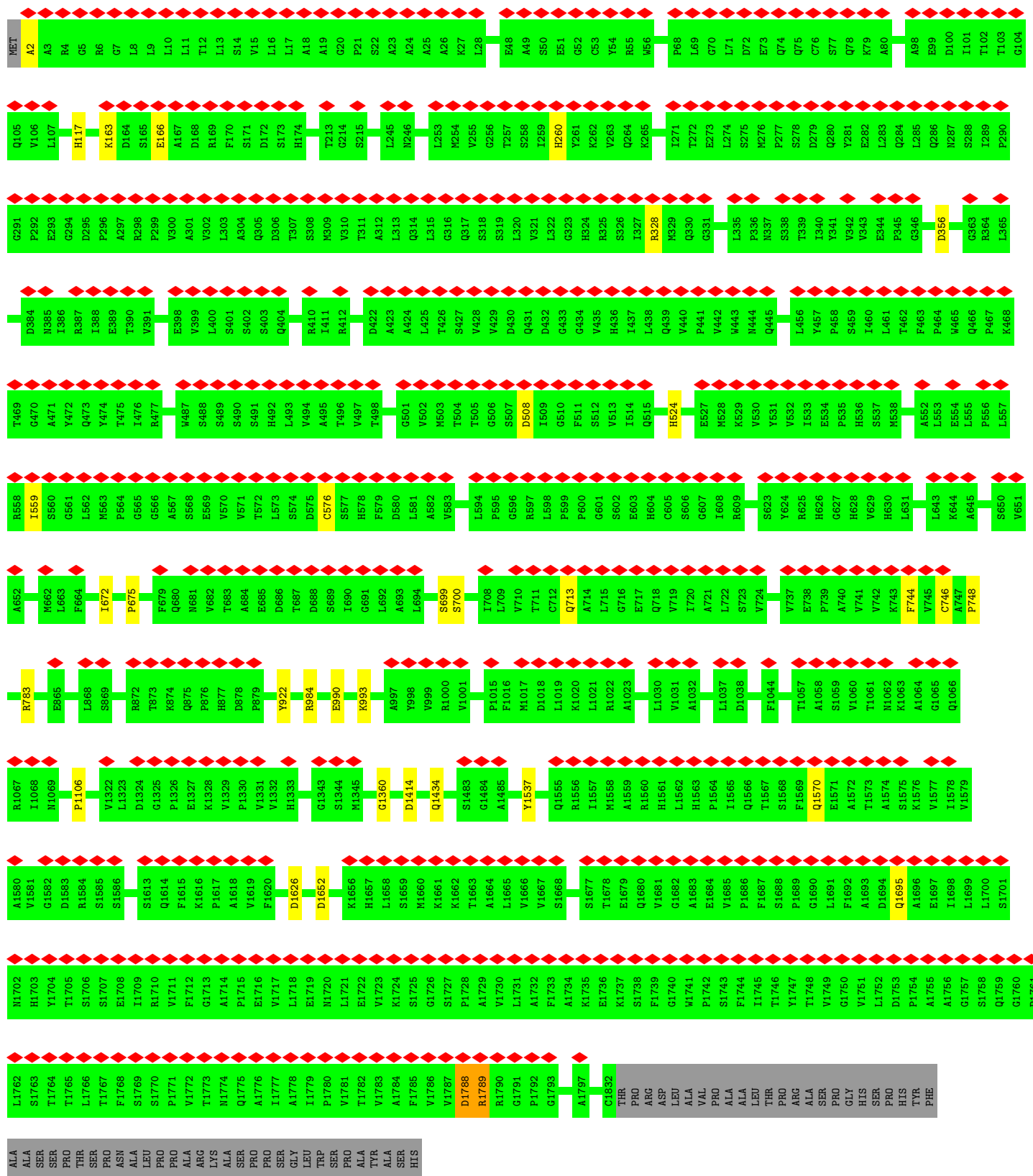
• Molecule 2: Nuclear pore membrane glycoprotein 210





- Molecule 2: Nuclear pore membrane glycoprotein 210

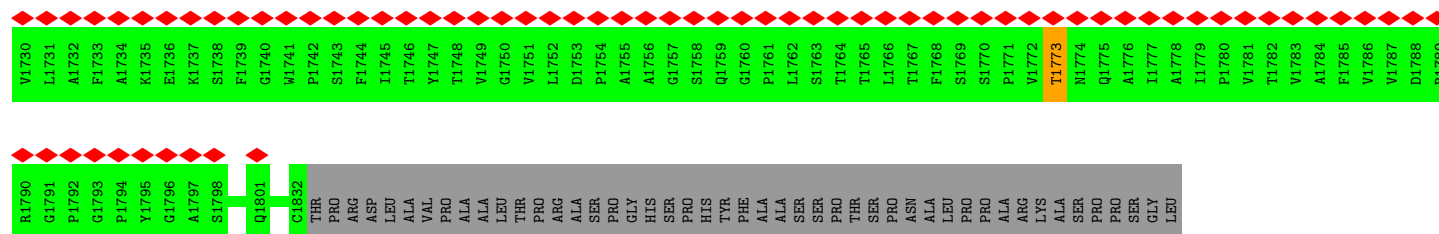




• Molecule 2: Nuclear pore membrane glycoprotein 210

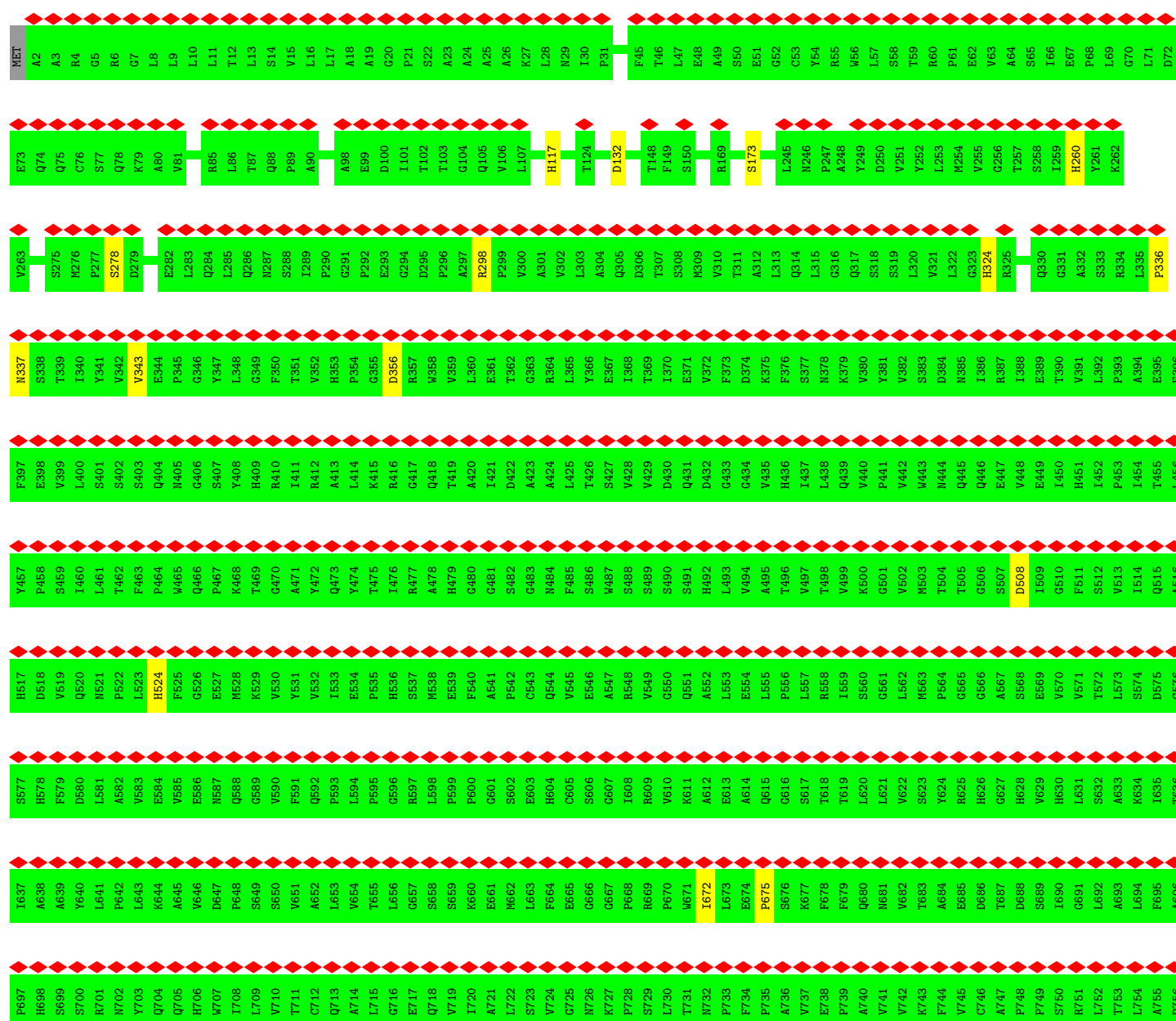
Chain 13: 40% 96%





TRP
SER
PRO
ALA
TYR
ALA
SER
HIS

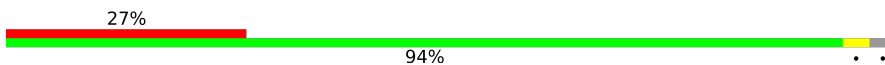
• Molecule 2: Nuclear pore membrane glycoprotein 210

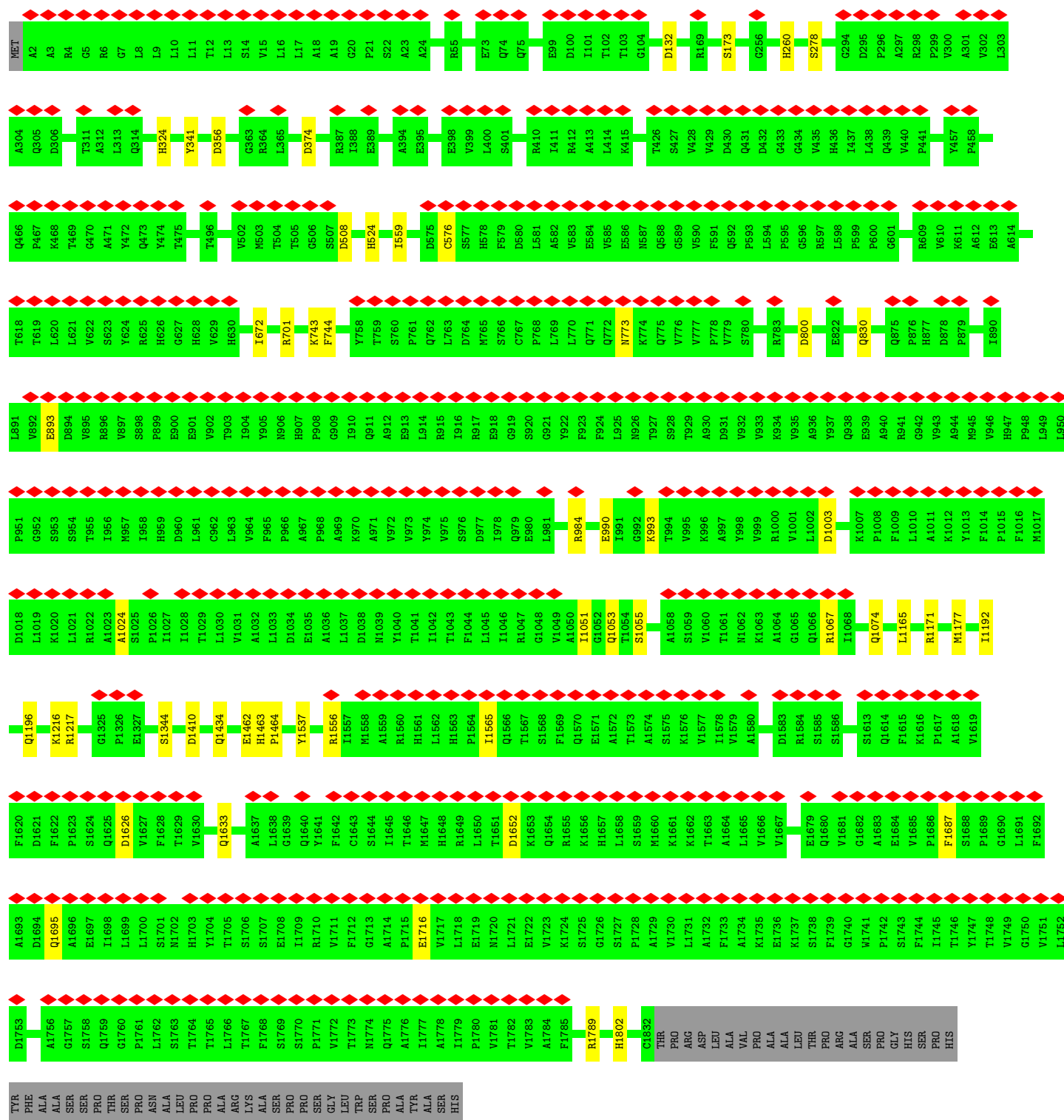


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F1615	K1616	P1617	A1618	V1619	F1620	D1621	F1622	P1623	S1624	Q1625	D1626	V1627	F1628	T1629	V1630	E1631	P1632	Q1633	F1634	D1635	T1636	A1637	L1638	G1639	Q1640	Y1641	F1642	C1643	S1644	I1645	T1646	H1647	R1648	A1649	L1650	T1651	D1652	K1653	Q1654	L1655	K1656	H1657	L1658	S1659	M1660	K1661	K1662	T1663	A1664	L1665	V1666	V1667	S1668	A1669	S1670	L1671	S1672	S1673	S1674	
Q1555	R1556	I1557	M1558	A1559	R1560	H1561	L1562	H1563	P1564	I1565	Q1566	T1567	S1568	F1569	Q1570	E1571	A1572	T1573	A1574	S1575	K1576	V1577	I1578	V1579	A1580	V1581	F1582	D1583	R1584	S1585	S1586	N1587	L1588	R1589	G1590	E1591	C1592	T1593	P1594	T1595	Q1596	R1597	E1598	V1599	I1600	Q1601	A1602	L1603	H1604	P1605	E1606	T1607	L1608	S1609	S1610	C1611	Q1612	S1613	Q1614	
M1411	D1414	Q1434	E1462	A1477	I1478	S1479	P1480	L1481	L1482	S1483	G1484	A1485	M1486	V1487	V1488	D1489	D1490	V1491	L1492	C1493	L1494	A1495	T1496	V1497	L1498	T1499	S1500	L1501	E1502	G1503	L1504	S1505	G1506	T1507	W1508	H1517	I1518	D1519	P1520	K1521	T1522	G1523	V1524	A1525	V1526	A1527	R1528	Y1537	E1538	V1539	A1540	P1554								
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Y937	Q938	E939	A940	R941	G942	Y943	A944	H945	Y946	H947	P948	L949	L950	P951	G952	S953	S954	T955	I956	P957	S958	H959	D960	L961	G962	L963	V964	P965	P966	A967	P968	A969	K970	A971	V972	V973	Y974	V975	S976	D977	I983	R984	V985	V986	V989	E990	I991	G992	K993	T994	V995	K996	A997	V999	R1000	V1001				
A817	S818	P879	I819	E820	P821	E822	L823	P824	M825	Q826	L827	V828	S829	Q830	D831	D832	E833	S834	G835	Q836	K837	K838	L839	H840	G841	L842	Q843	A844	I845	L846	V847	H848	E849	A850	Q851	G852	E853	L854	A855	I856	T857	E858	T859	A860	T861	Y862	F863	Y864	E865	S866	H867	Q868	W869	E870	A871	R872	T873	K874	Q875	P876
W757	Y758	T759	S760	P761	Q762	L763	D764	M765	S766	C767	P768	L769	L770	Q771	Q772	N773	K774	Q775	V776	V777	P778	V779	S780	S781	H782	R783	N784	P785	R786	L787	D788	L789	A790	A791	Y792	D793	Q794	E795	G796	R797	R798	F799	D800	N801	F802	S803	S804	L805	S806	I807	Q808	W809	E810	S811	T812	R813	P814	V815	L816	

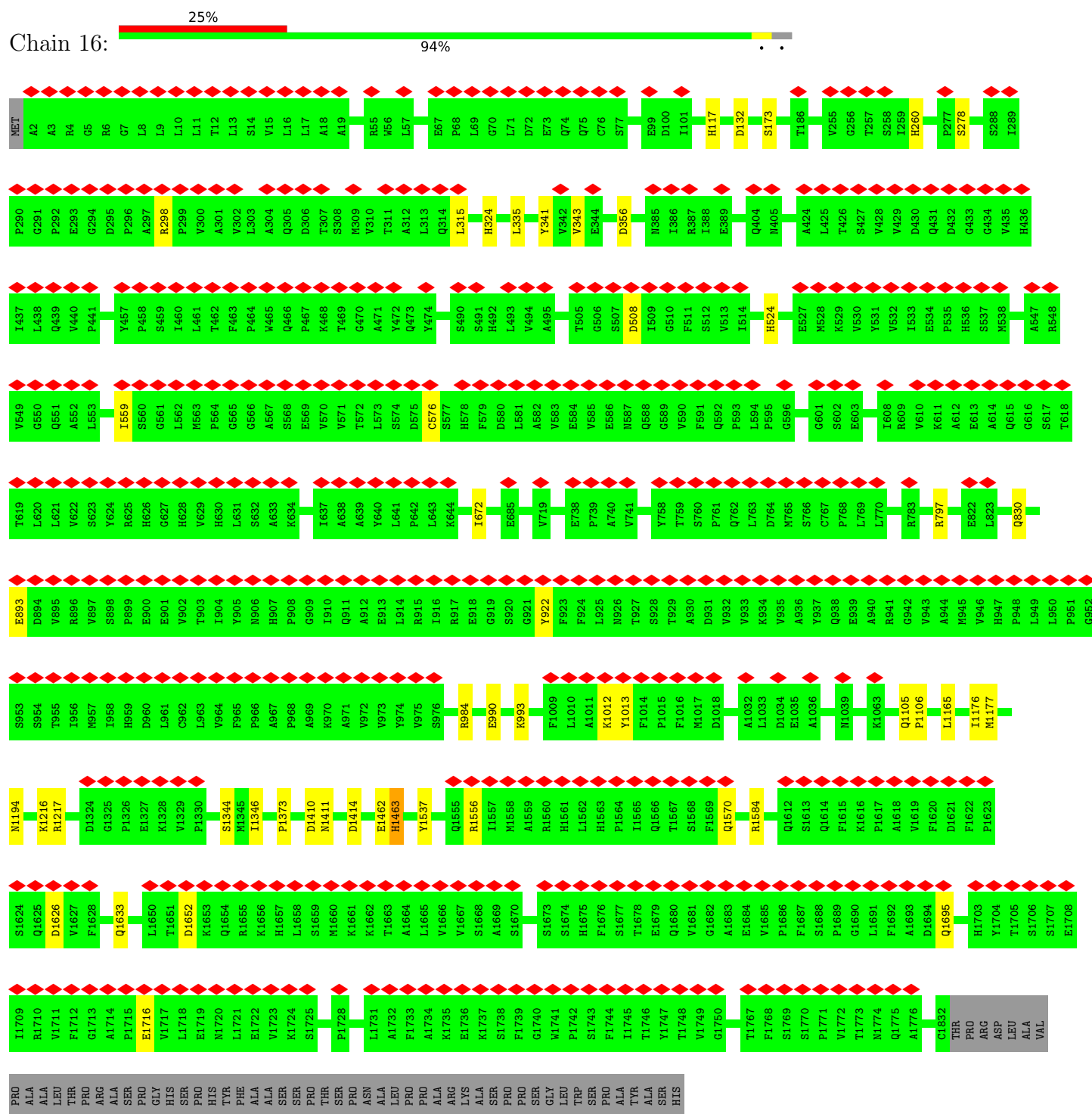
ALA
LEU
THR
PRO
ARG
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SER
PRO
GLY
HIS
SER
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TYR
PHE
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ALA
SER
SER
PRO
THR
SER
PRO
ASN
ALA
LEU
PRO
PRO
S22
ALA
ARG
LVS
ALA
SER
SER
PRO
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TRP
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PRO
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TYR
ALA
SER
HIS

• Molecule 2: Nuclear pore membrane glycoprotein 210

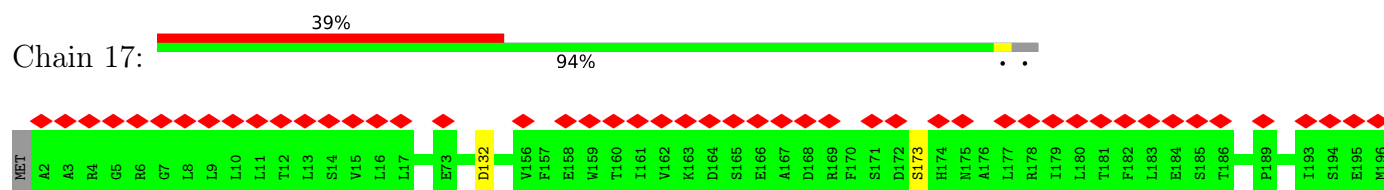
Chain 15:  27% 94%

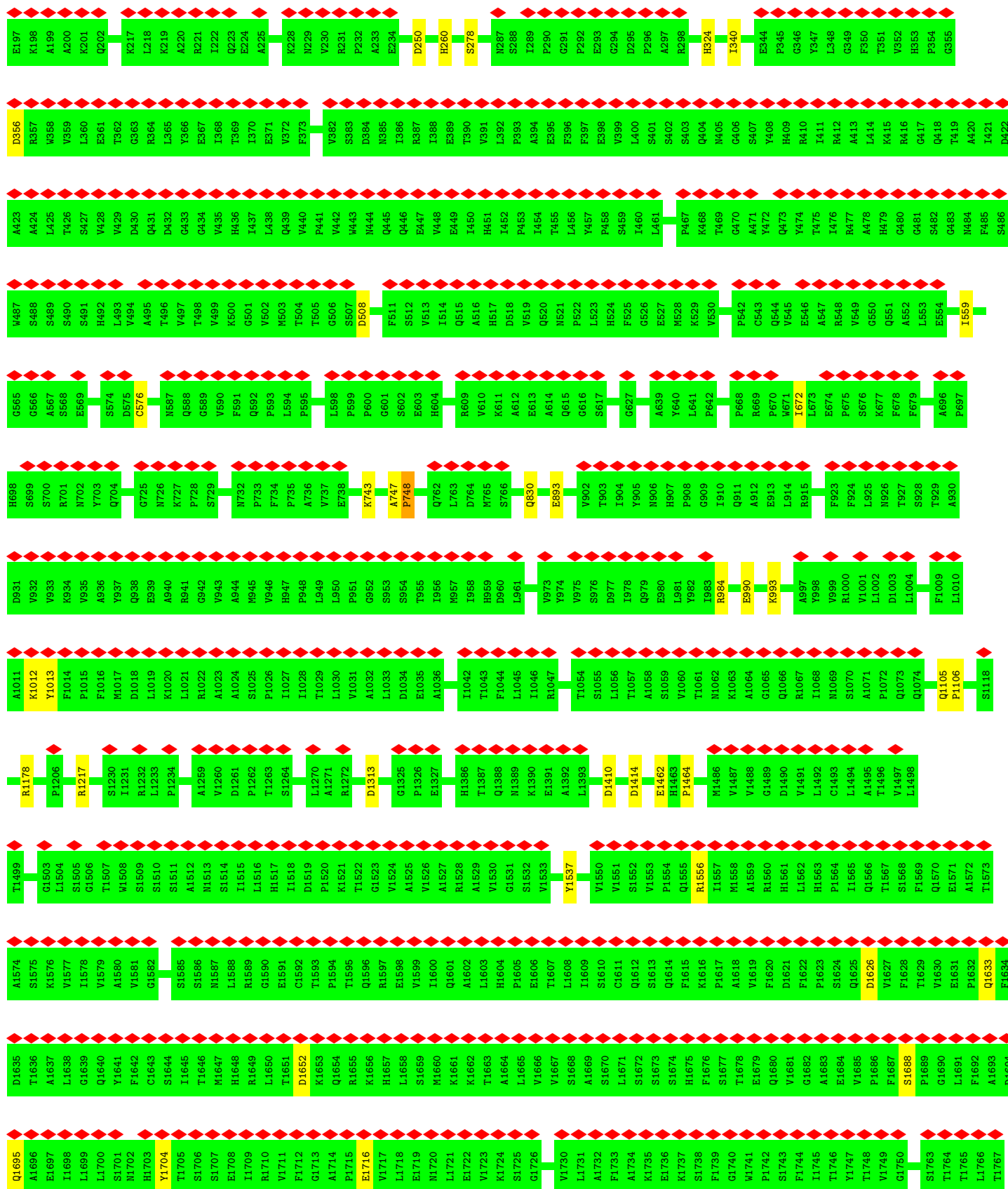


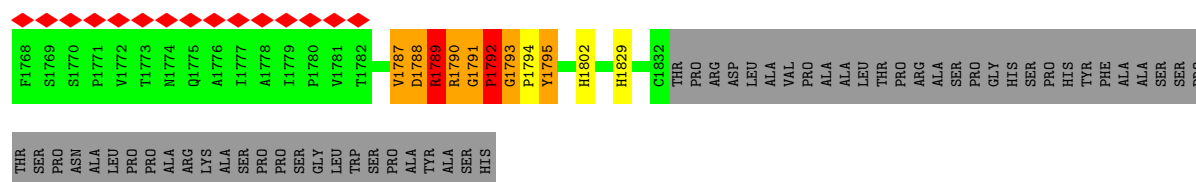
• Molecule 2: Nuclear pore membrane glycoprotein 210



• Molecule 2: Nuclear pore membrane glycoprotein 210

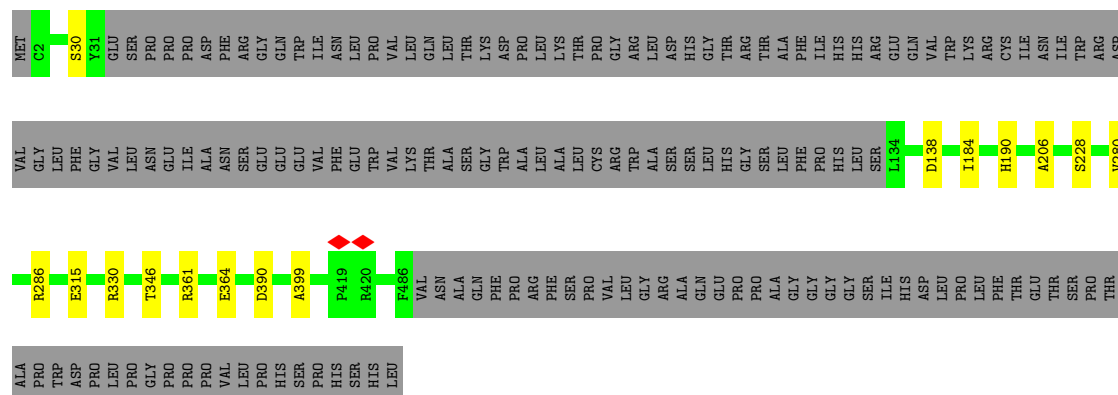






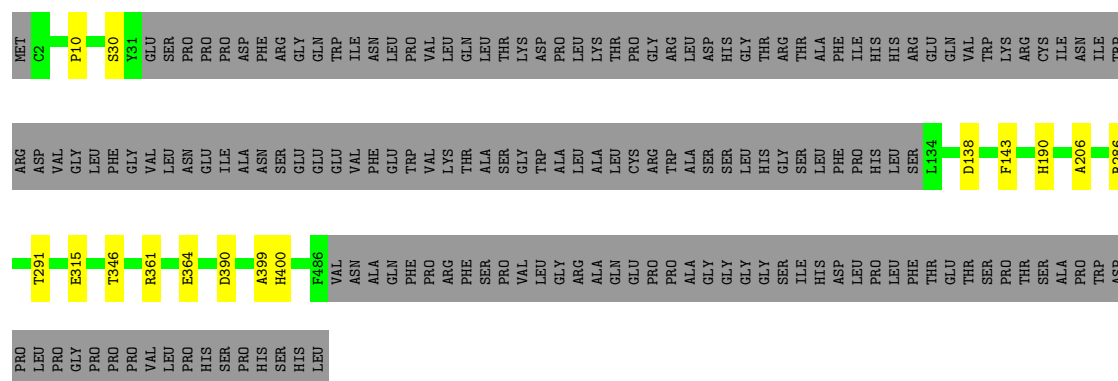
• Molecule 3: Aladin

Chain 40: 67% 30%



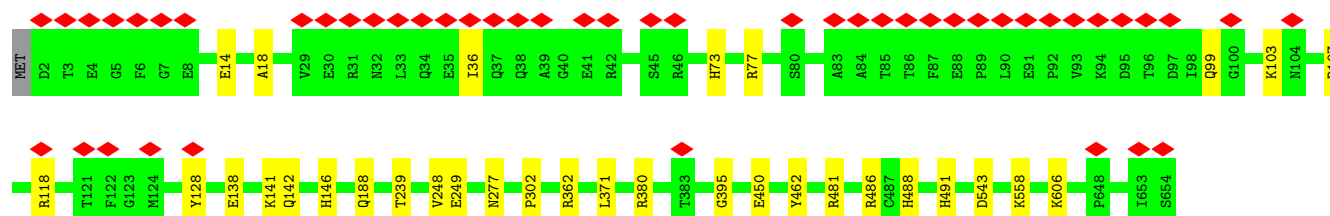
• Molecule 3: Aladin

Chain 41: 67% 30%



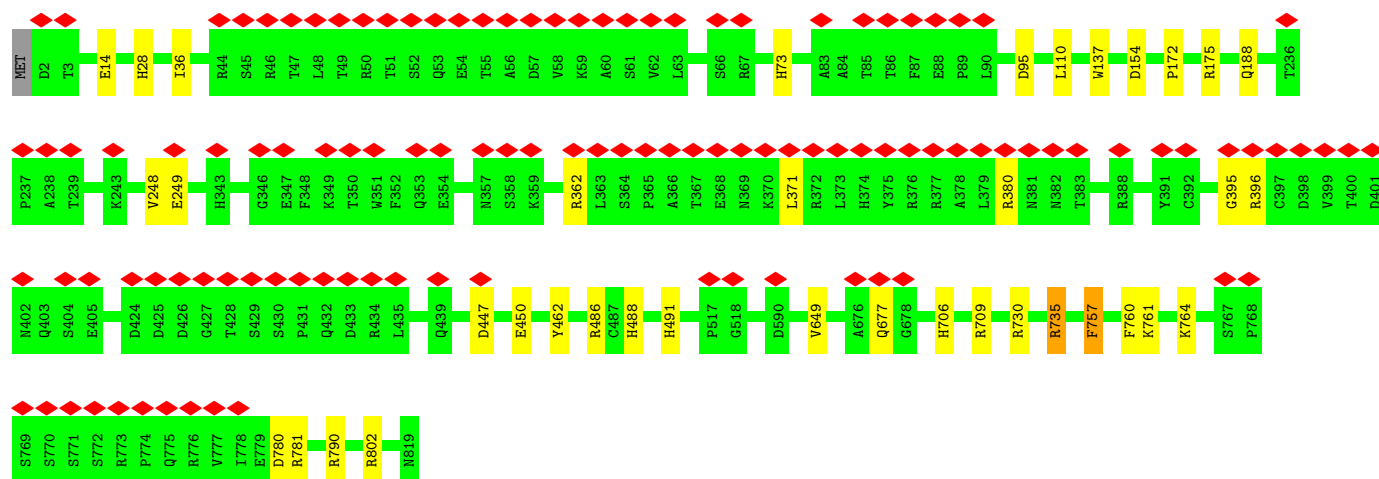
• Molecule 4: Nuclear pore complex protein Nup93

Chain A0: 7% 94% 6%

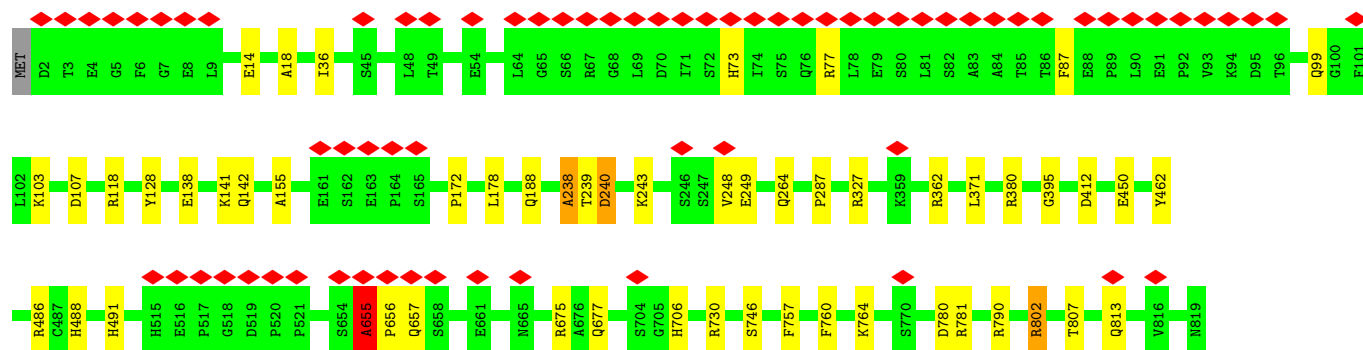




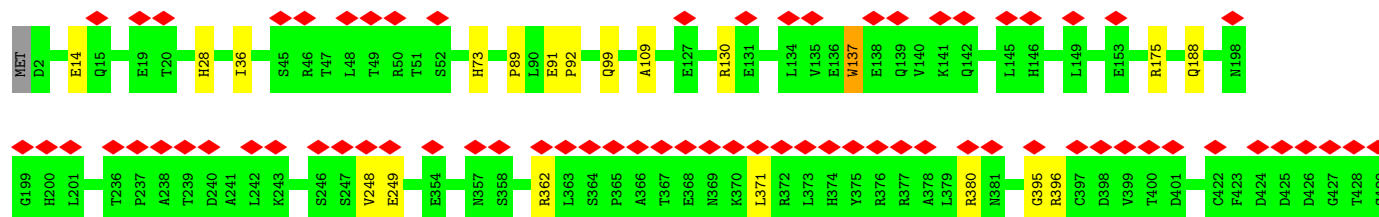
• Molecule 4: Nuclear pore complex protein Nup93

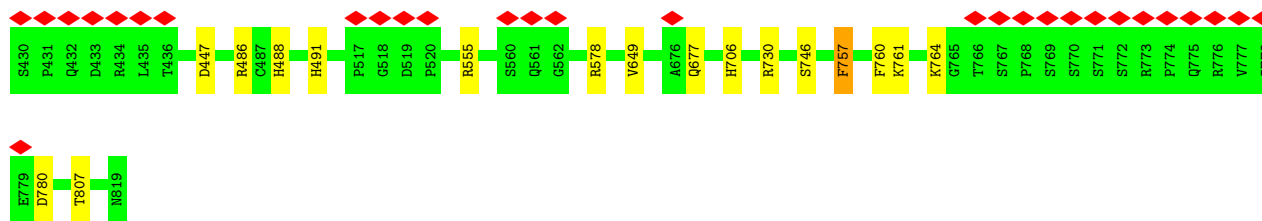


• Molecule 4: Nuclear pore complex protein Nup93

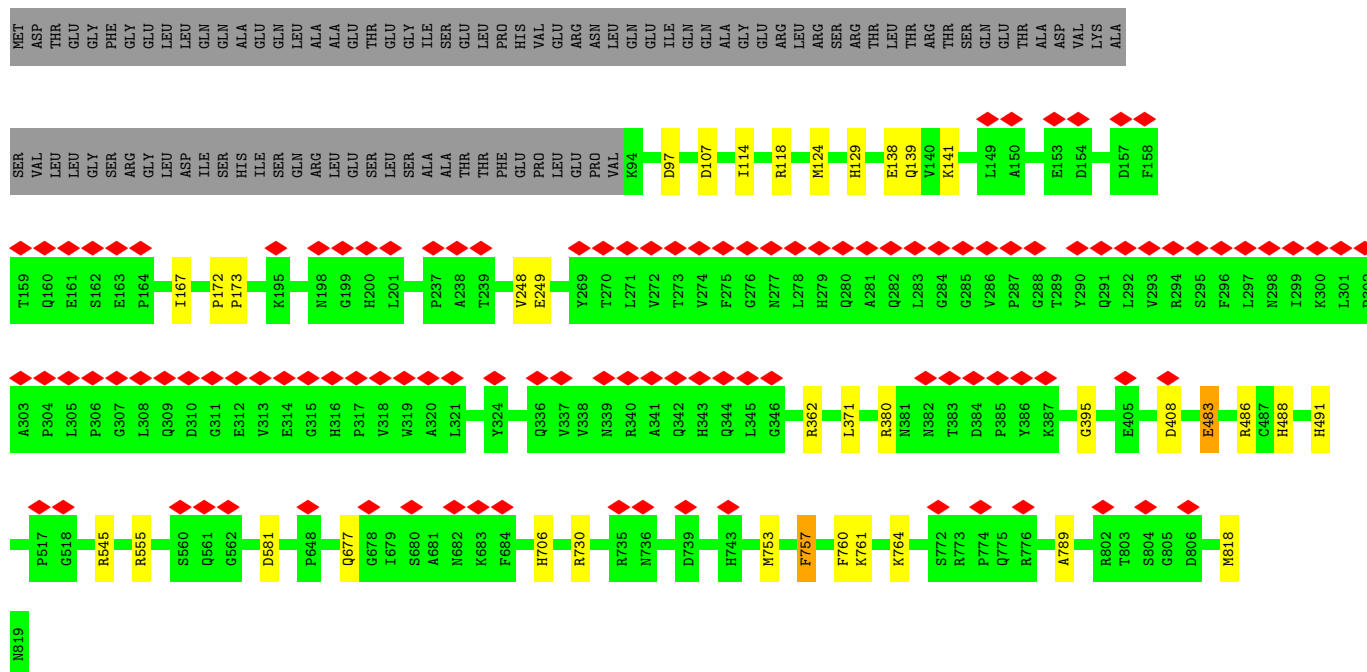
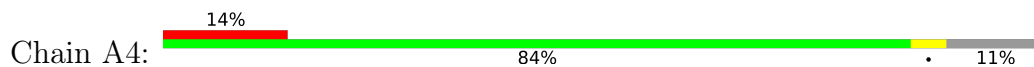


• Molecule 4: Nuclear pore complex protein Nup93

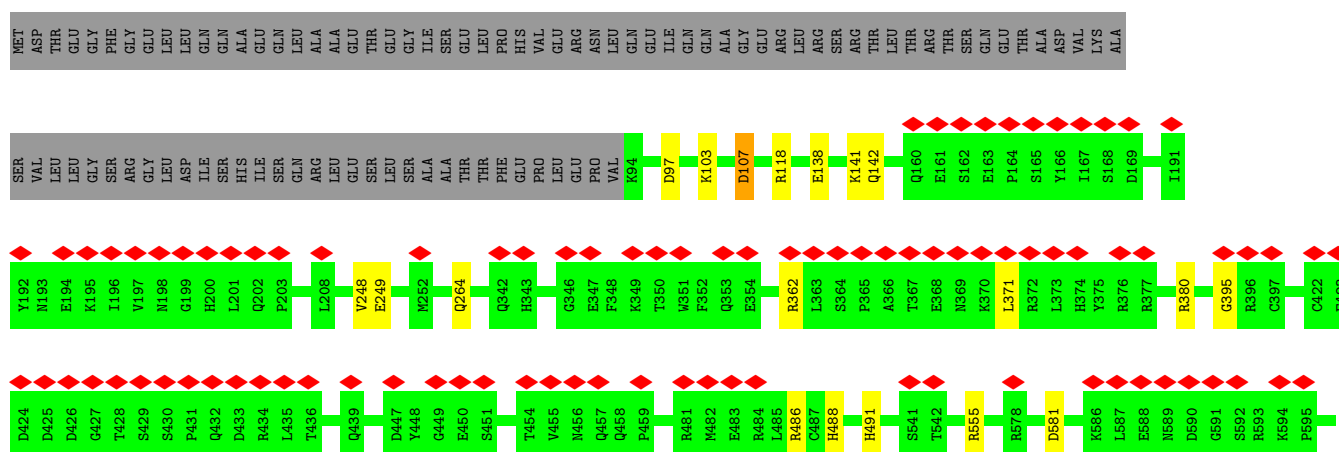
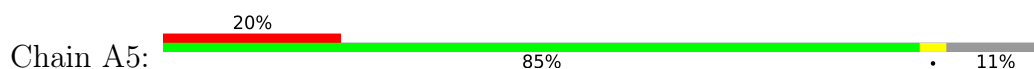


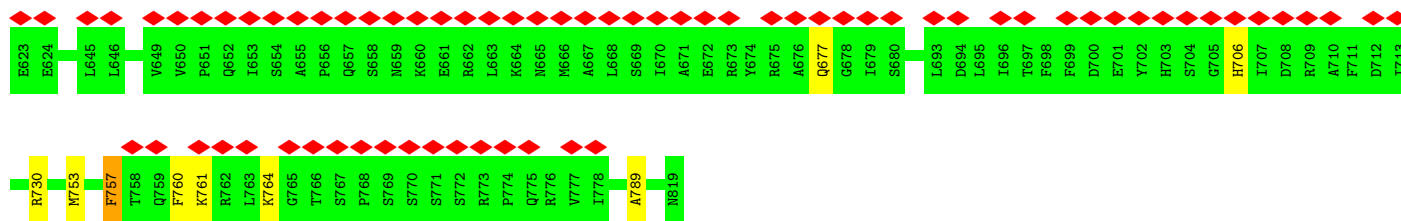


• Molecule 4: Nuclear pore complex protein Nup93



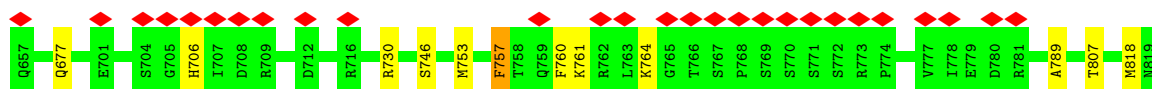
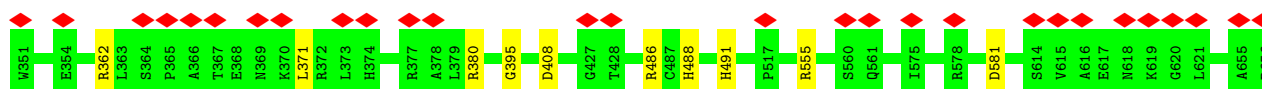
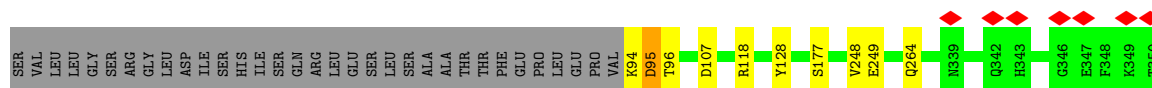
• Molecule 4: Nuclear pore complex protein Nup93





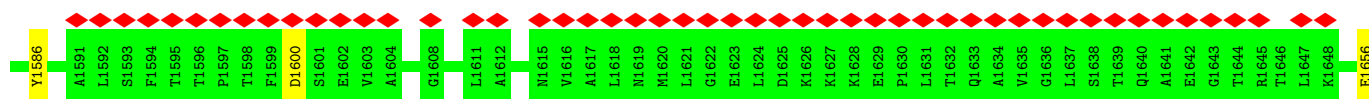
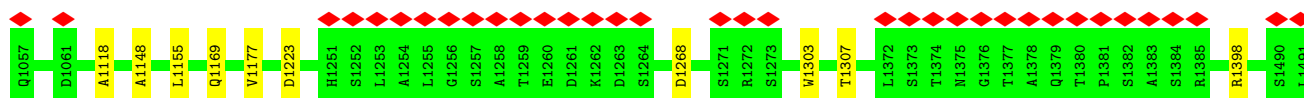
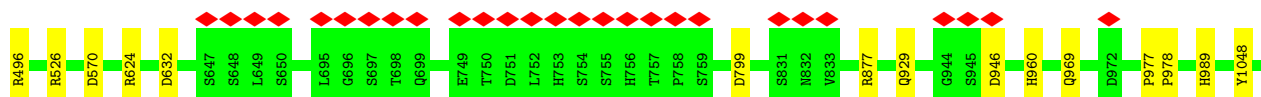
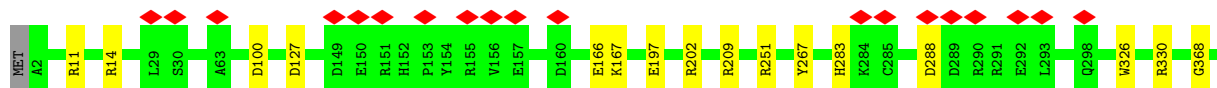
• Molecule 4: Nuclear pore complex protein Nup93

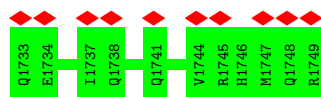
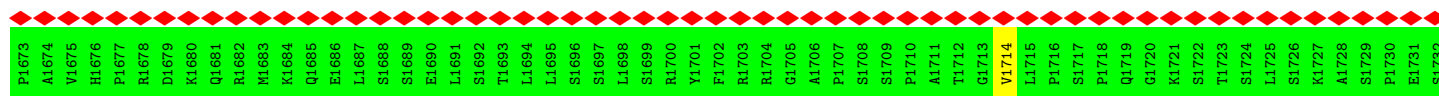
Chain A6: 8% 85% 11%



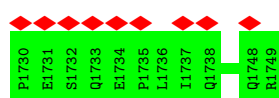
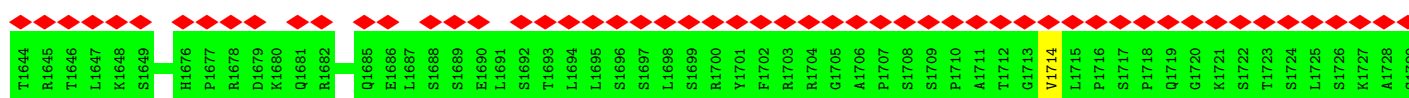
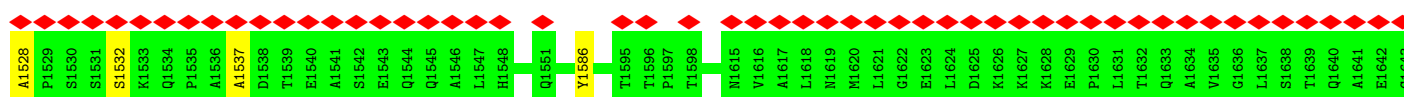
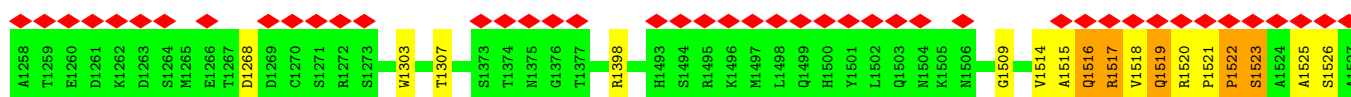
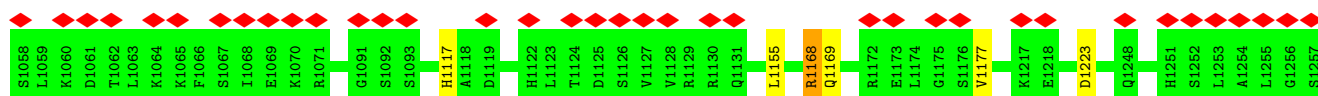
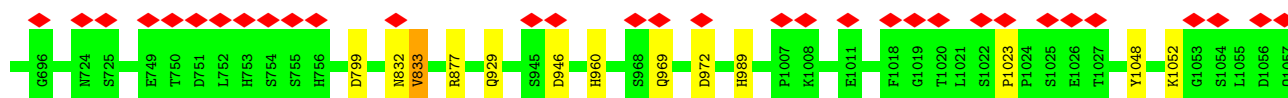
• Molecule 5: Nucleoporin NUP188 homolog

Chain B0: 15% 97%

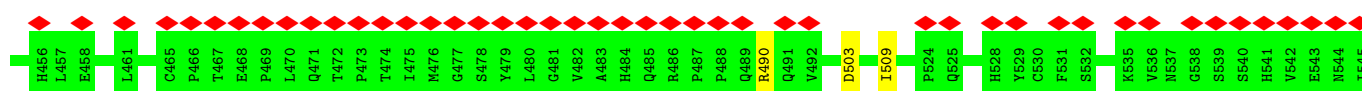
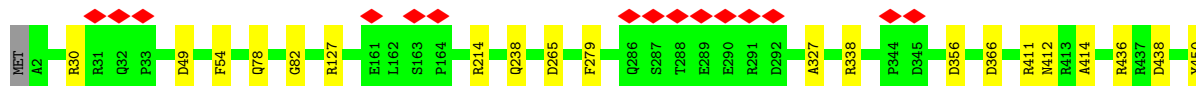


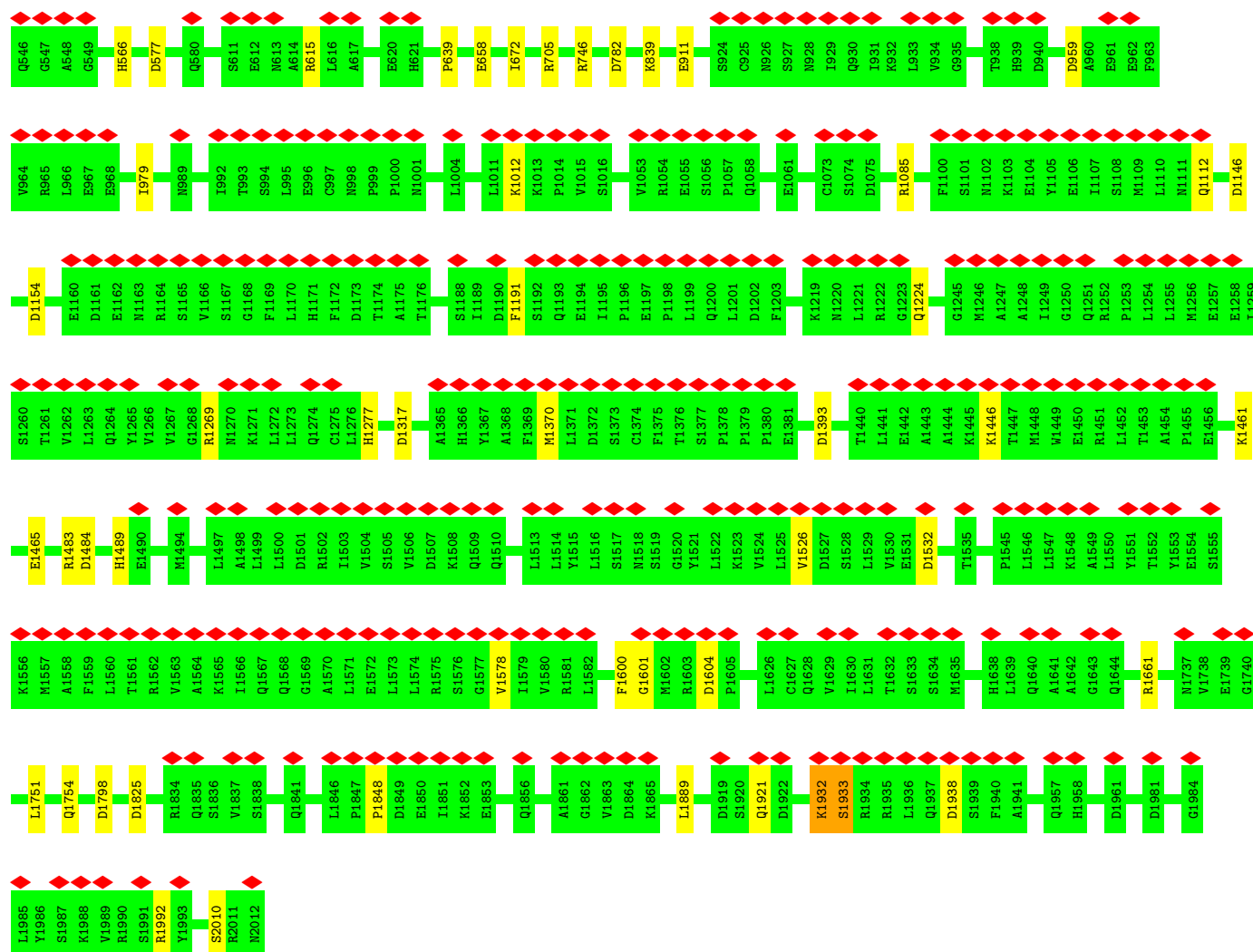


• Molecule 5: Nucleoporin NUP188 homolog

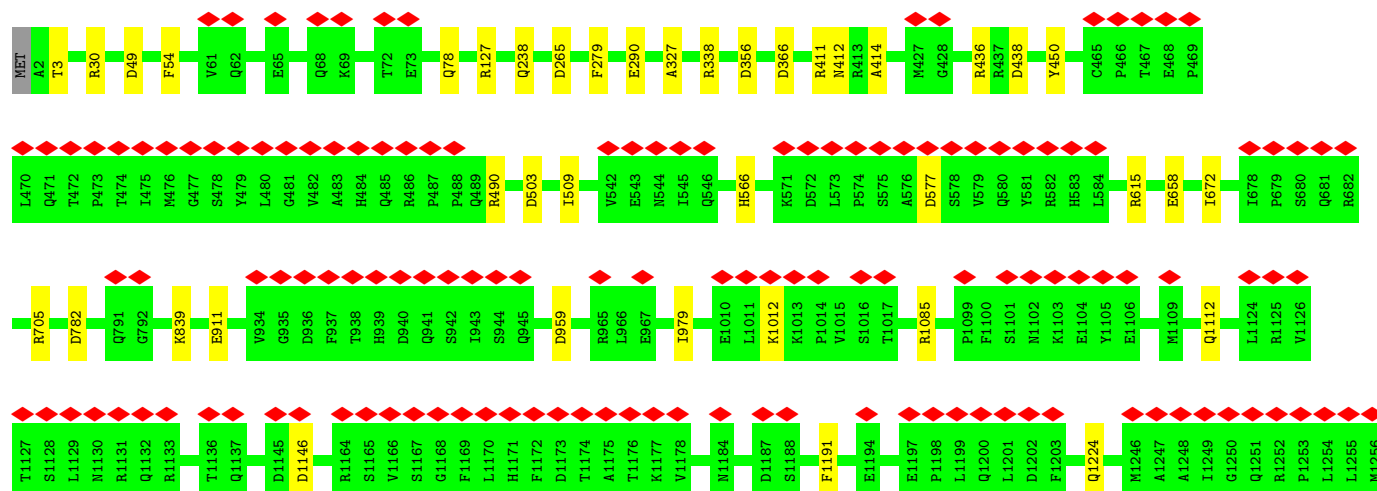


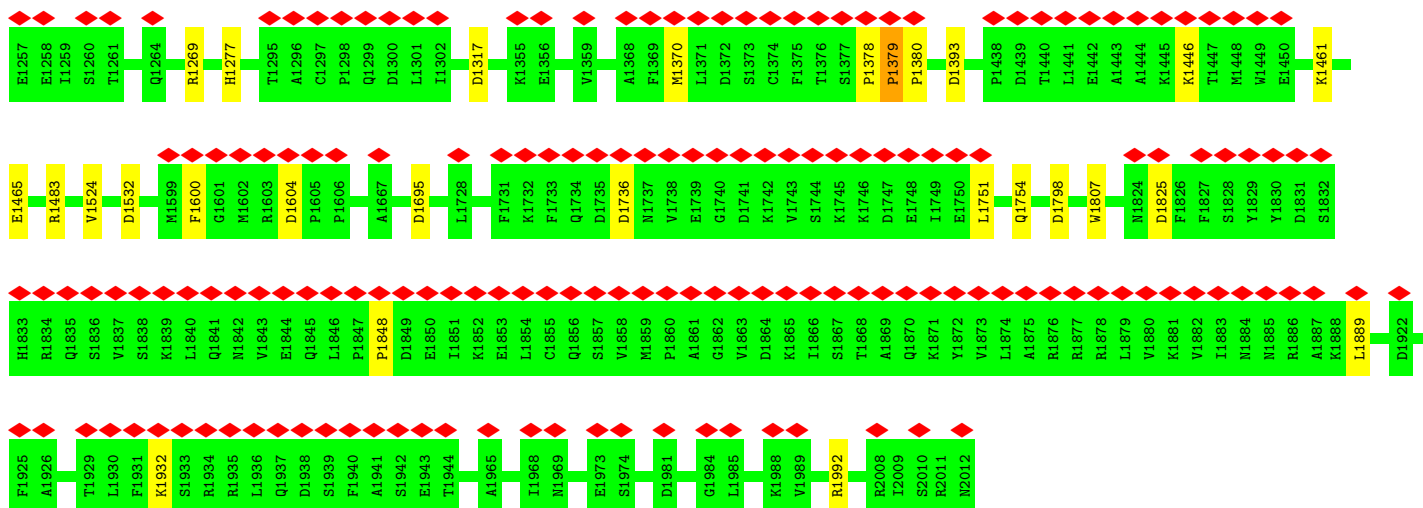
• Molecule 6: Nuclear pore complex protein Nup205



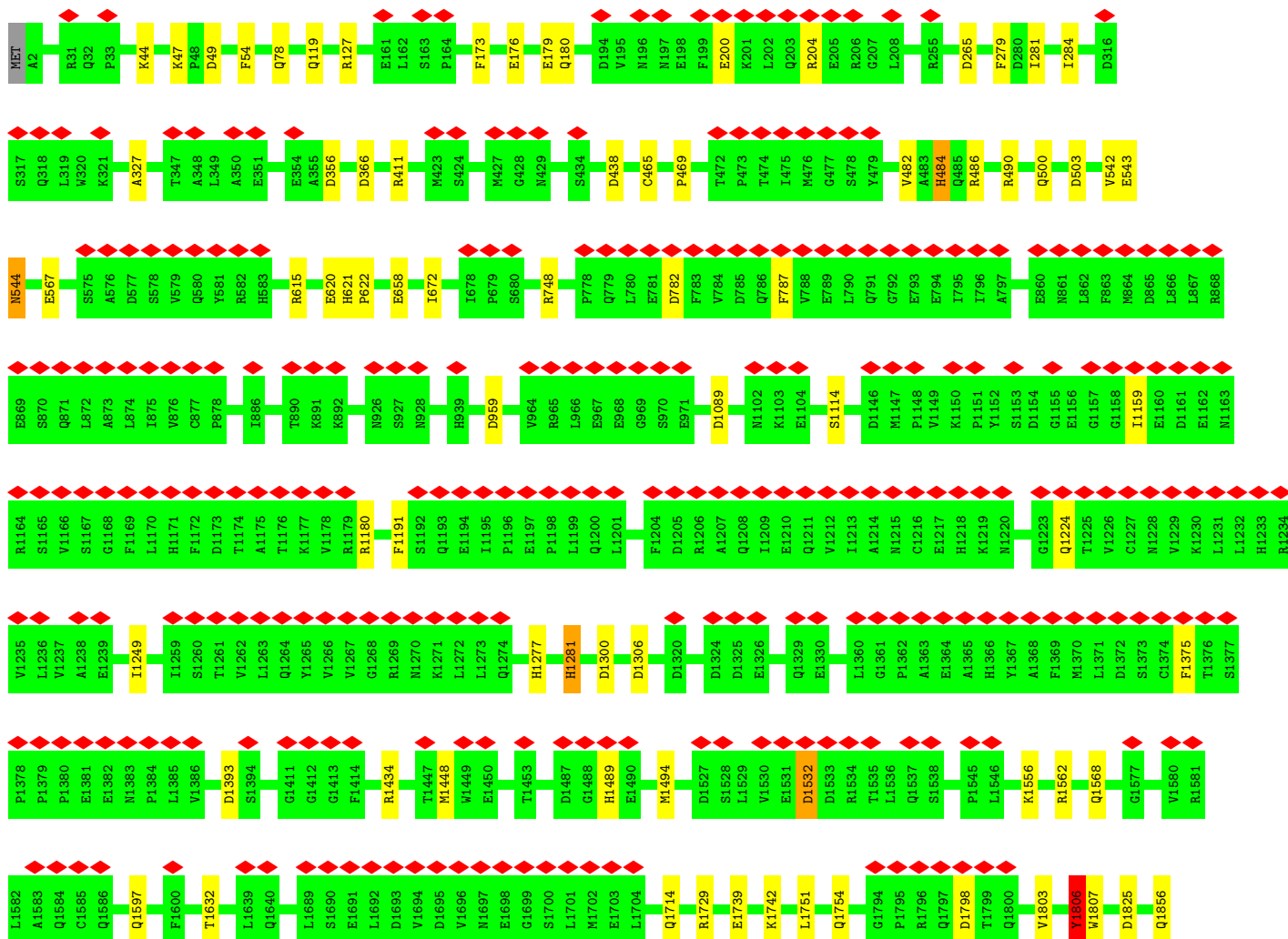


• Molecule 6: Nuclear pore complex protein Nup205





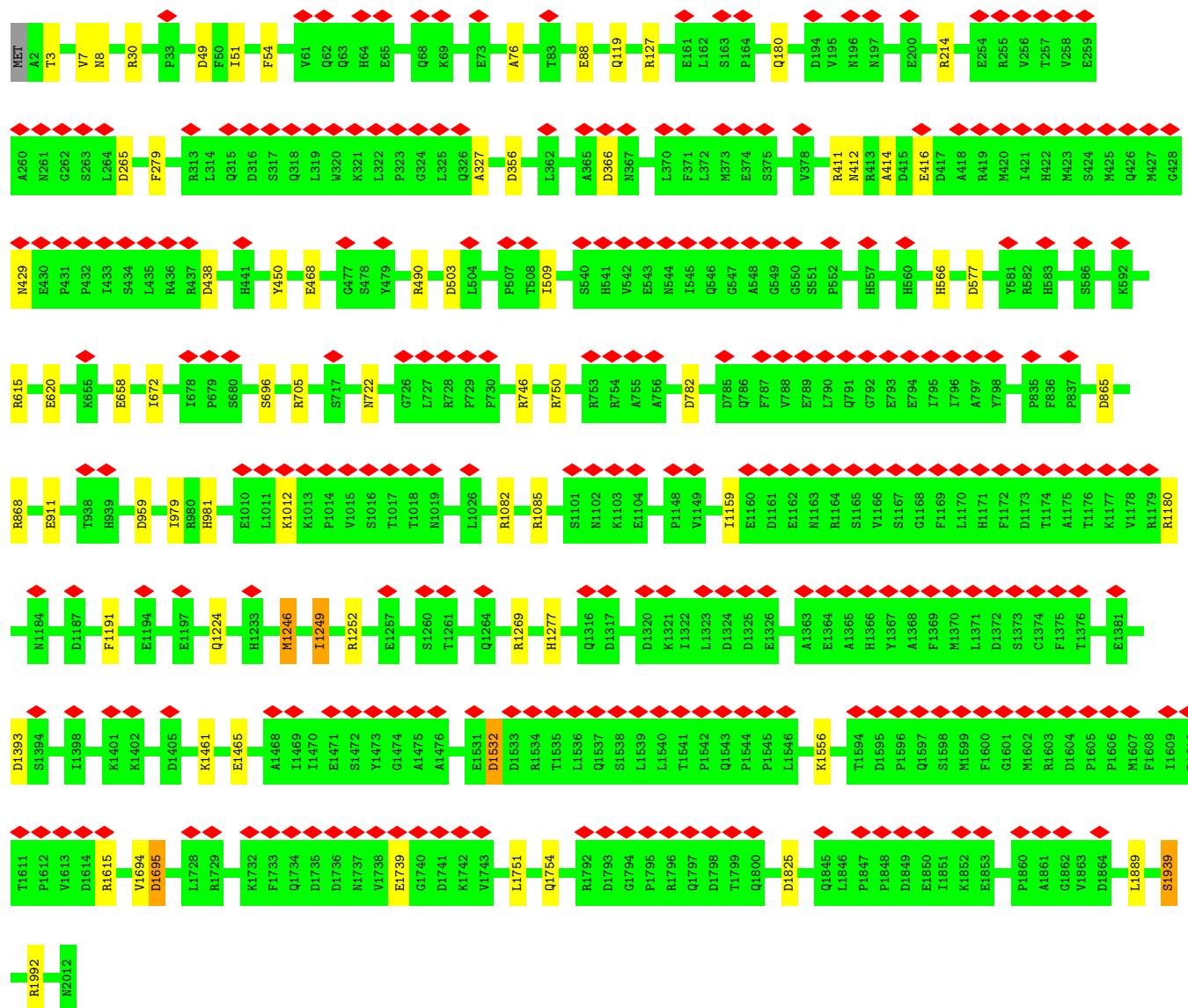
• Molecule 6: Nuclear pore complex protein Nup205





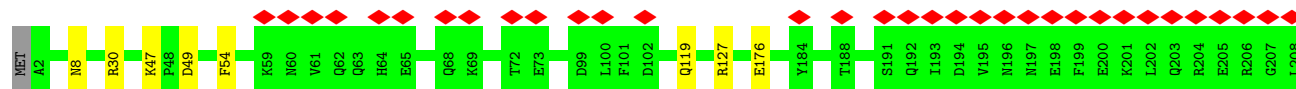
• Molecule 6: Nuclear pore complex protein Nup205

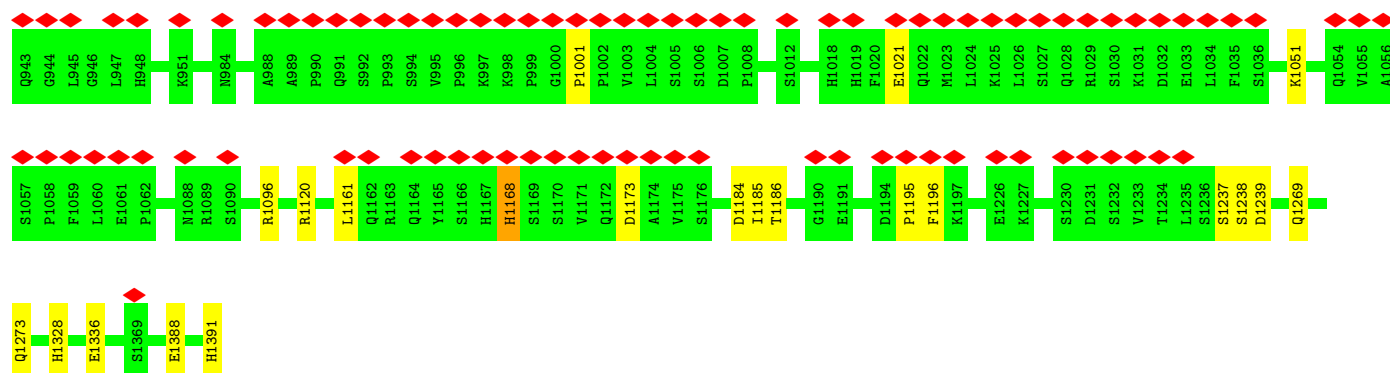
Chain C3: 14% 96%



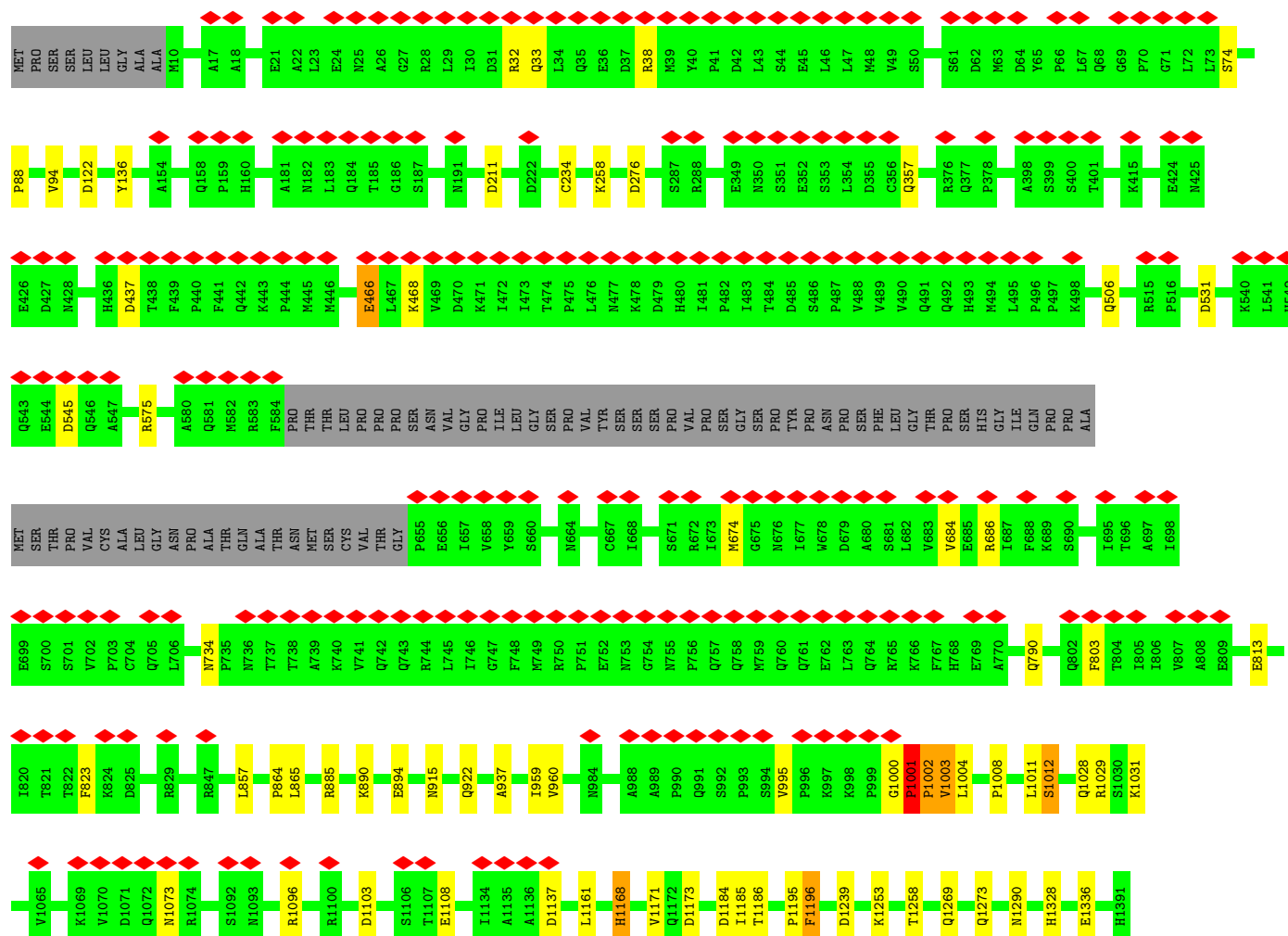
• Molecule 6: Nuclear pore complex protein Nup205

Chain C4: 17% 96%



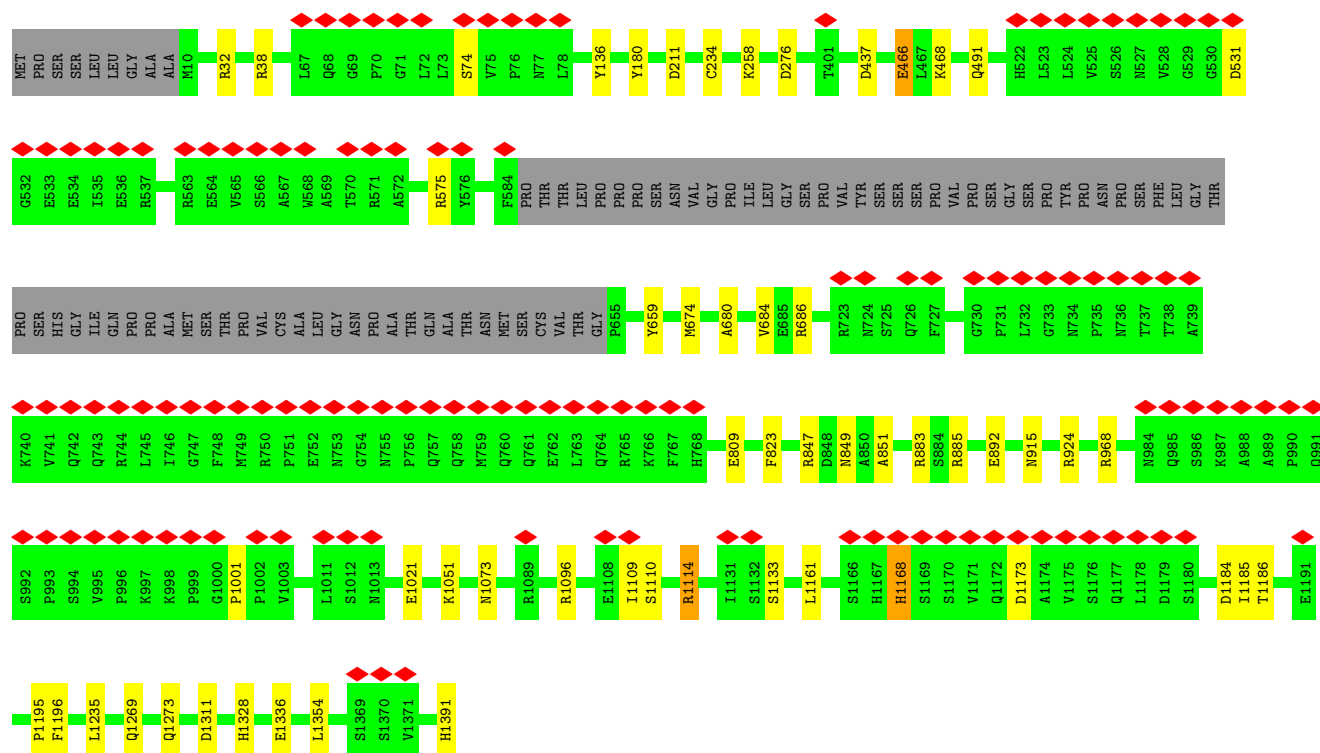


• Molecule 7: Nuclear pore complex protein Nup155

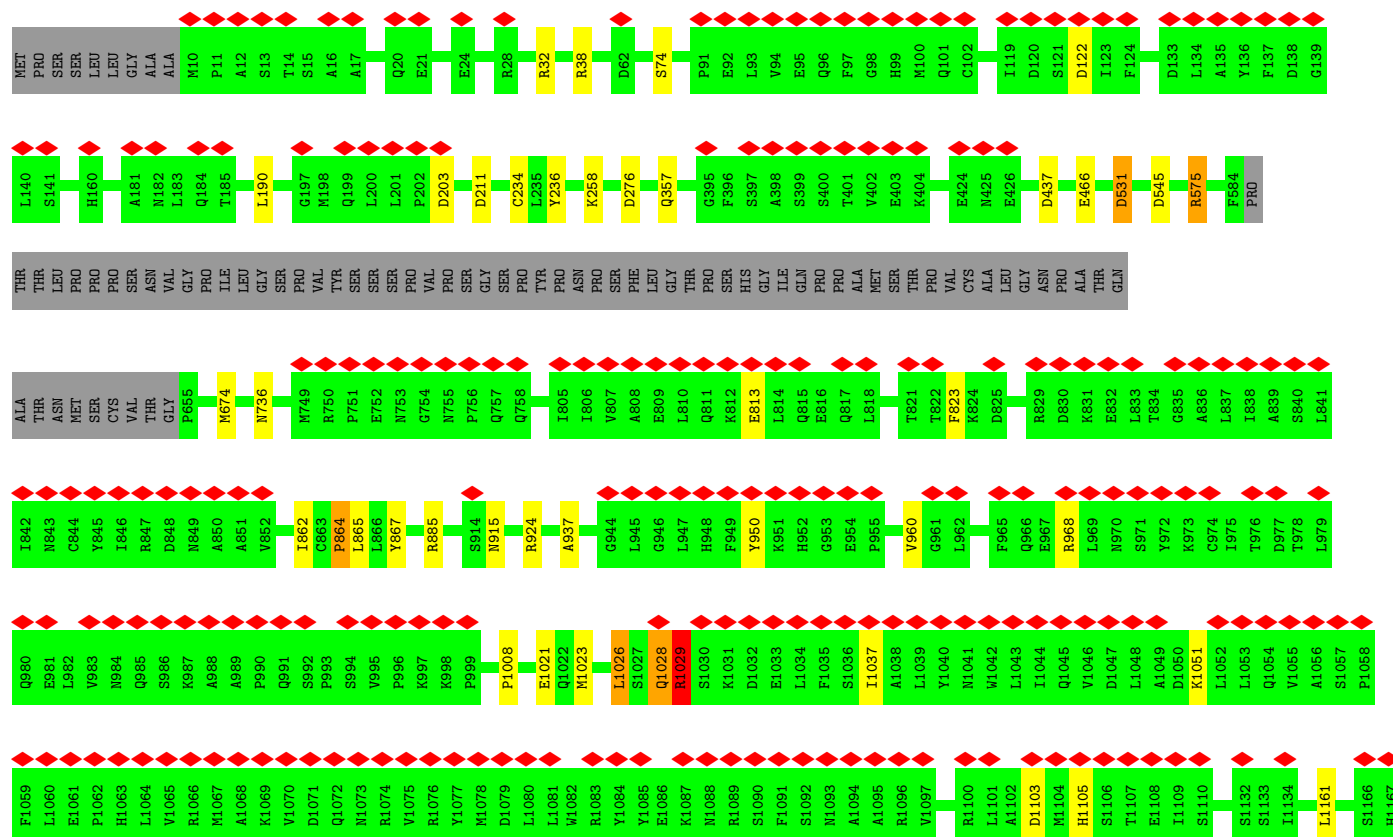
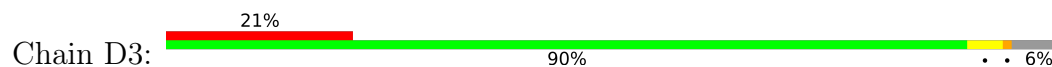


• Molecule 7: Nuclear pore complex protein Nup155

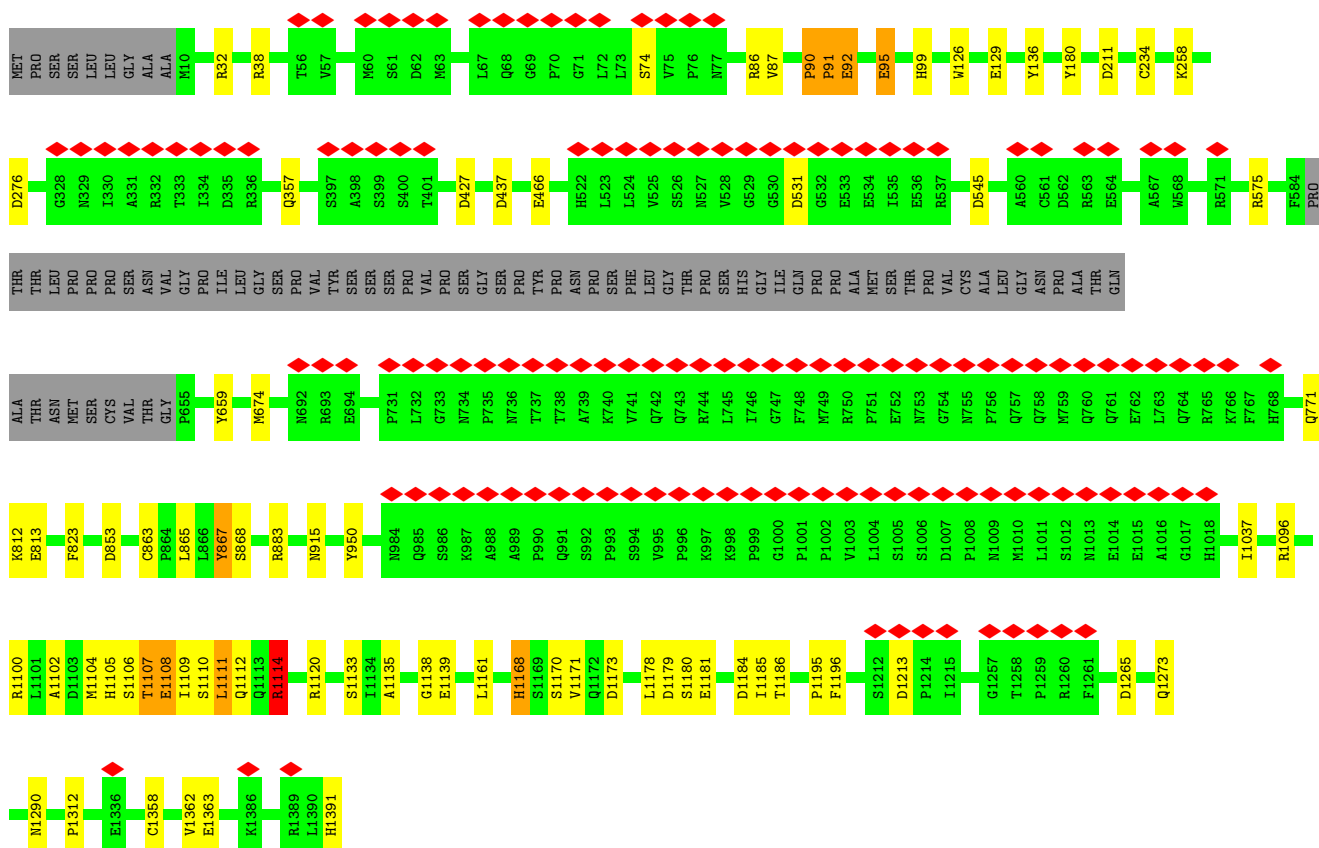
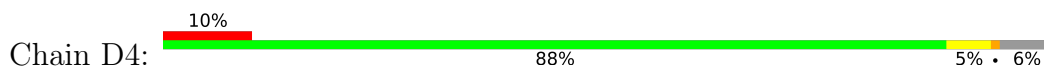




- Molecule 7: Nuclear pore complex protein Nup155



- Molecule 7: Nuclear pore complex protein Nup155

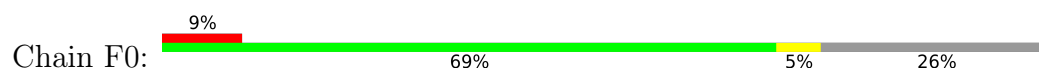


- Molecule 7: Nuclear pore complex protein Nup155





● Molecule 9: Nucleoporin NUP35



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

VAL MET MET MET ARG SER PRO LEU LEU ALA GLY ALA LEU SER PRO PRO GLN VAL VAL PRO ALA HIS LYS ASP LYS S86 D96 S105 T106 P107 L108 T109 T110 R111 R112 Q113 P114 N115 I116 M119 Q120 S121 P122 L123 V124 G125 V126 G131 T132 G133 Q134 S135 D163 D172

D173 K218 E234 K241 R254 K269 T270 P274 T275 Q301 V302 I303 Q307 T308 P309 K310 W326

● Molecule 9: Nucleoporin NUP35



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

VAL MET MET MET ARG SER PRO LEU LEU ALA GLY ALA LEU SER PRO PRO GLN VAL VAL PRO PRO ALA HIS LYS ASP LYS S86 D96 S109 L103 L108 T109 T110 R111 R112 Q113 P114 M115 I116 S117 V118 M119 Q120 S121 V124 G131 L165 T166 S167 E168 D169 H170 P182

Q183 A184 S185 A186 S187 Y196 M206 T207 K218 L219 R222 E234 S235 L257 S258 S259 P260 S261 L262 A263 F264 T265 P266 P267 I268 K269 T270 L271 Q272 T273 T274 T275 Q276 P277 G278 S279 T280 S284 T285 Y293 K294 A295 S296 Y300 S304 D305 R306 Q307 T308 P309

K310 K311 W326

● Molecule 9: Nucleoporin NUP35

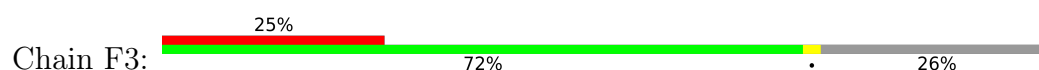


MET ALA ALA PHE MET ARG VAL GLU PRO GLN GLY PRO GLY ALA LEU GLY SER PRO MET MET LEU MET GLY LYS PRO THR SER PRO LYS PRO GLY VAL ASN ALA GLN PHE LEU PRO GLY PHE LEU MET GLY ASP LEU PRO ALA VAL THR PRO GLN ARG PRO ILE SER GLY PRO SER VAL GLY

VAL MET MET ARG SER PRO LEU LEU ALA GLY ALA LEU SER PRO PRO GLN VAL VAL PRO PRO ALA HIS LYS ASP LYS S86 G87 A88 D96 G102 L103 G104 S105 T106 P107 L108 T109 S110 R111 R112 Q113 P114 M115 I116 S117 V118 M119 Q120 S121 L123 V124 F137 S138 P139 A140

R146 K147 T148 T149 L150 S151 P152 Q154 L155 D156 D163 S164 L165 T166 S167 E168 D169 H170 D173 Q183 A184 Y196 N206 T207 R230 Q233 E234 K241 K246 E250 R254 T297 S304 T308 W326

● Molecule 9: Nucleoporin NUP35



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



Chain H2:

- Molecule 10: Nucleoporin p54

Chain H3:

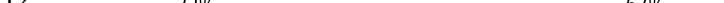
- Molecule 11: Nucleoporin p58/p45

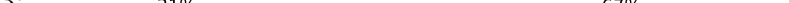
Chain I0:



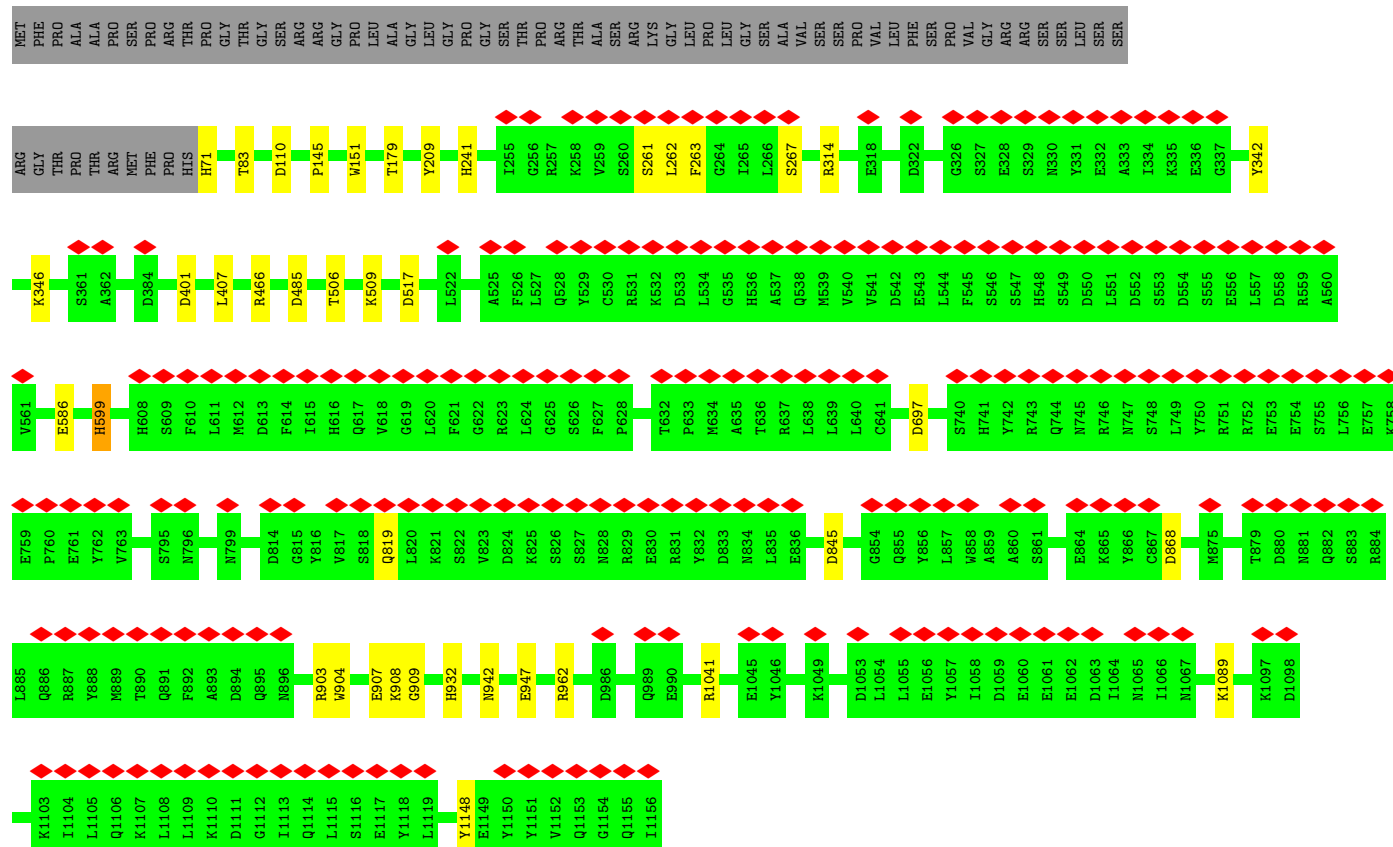
Chain J0:



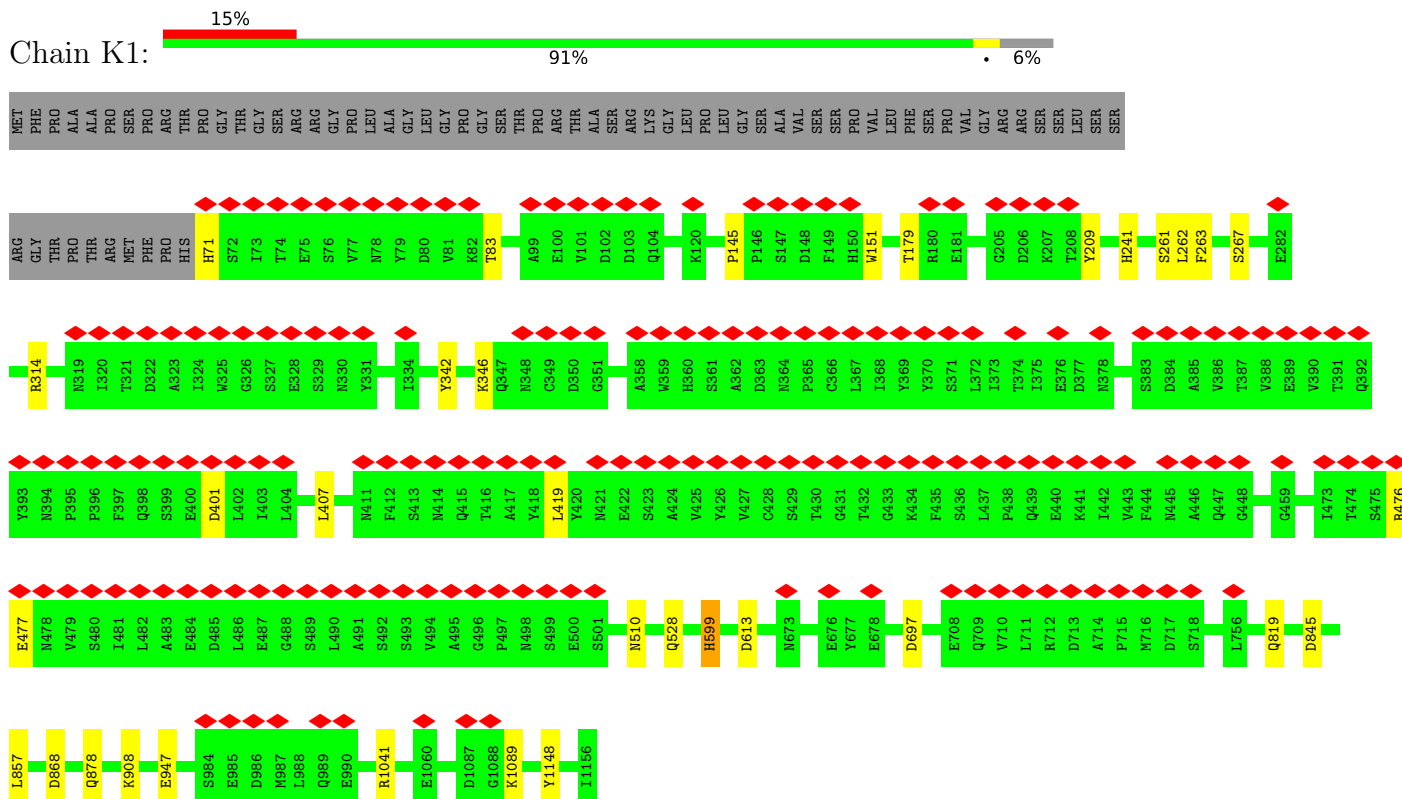
Chain J2: 

Chain J3: 

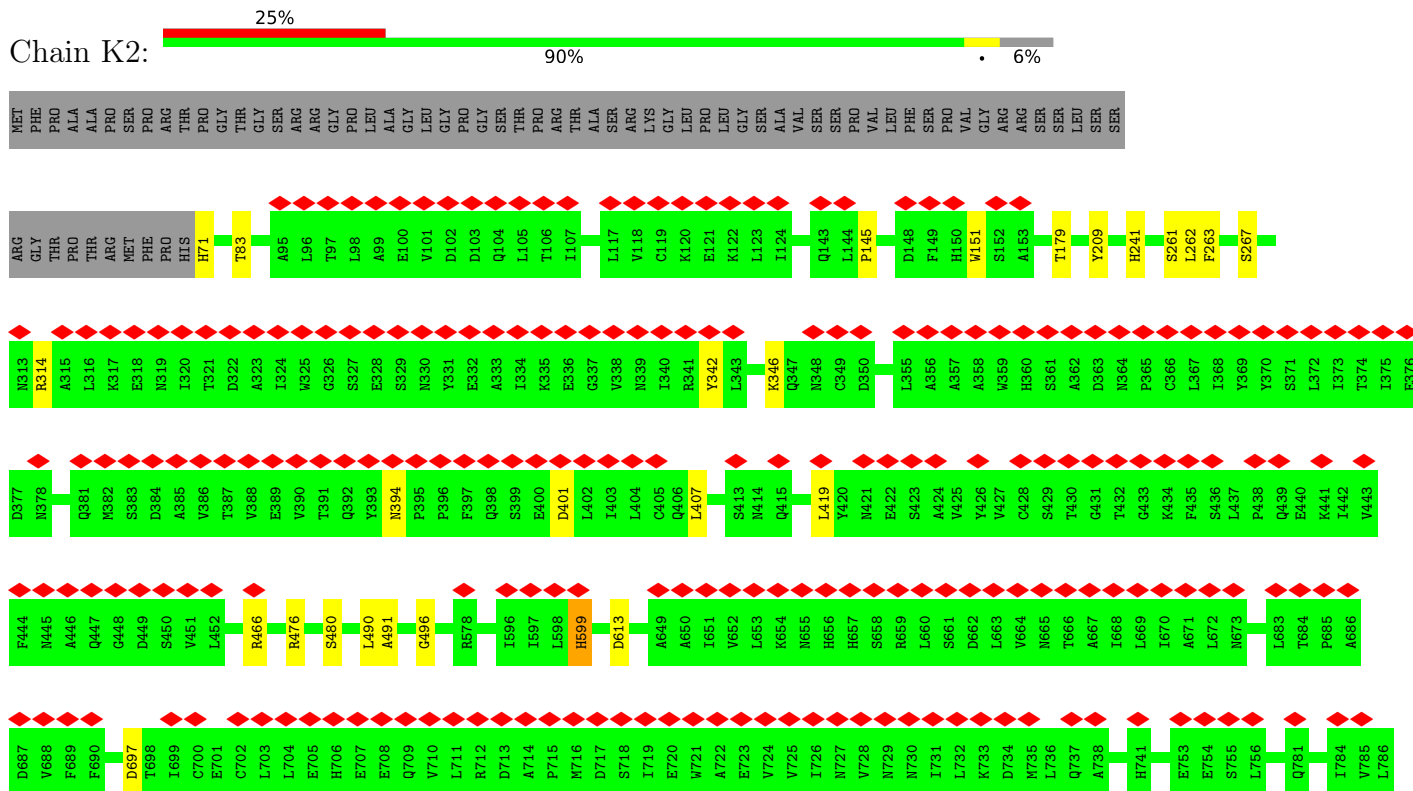
- Molecule 12: Nuclear pore glycoprotein p62

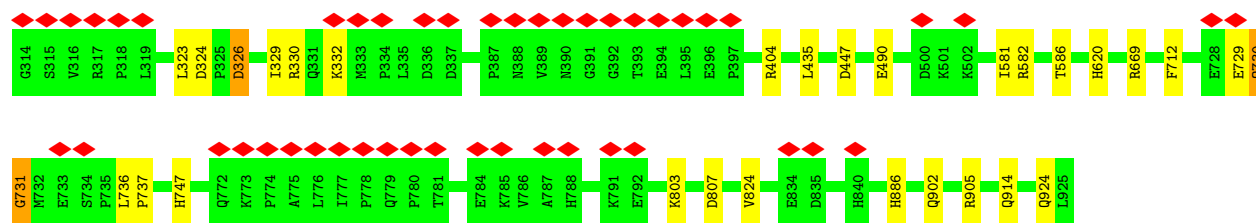


Chain K1:



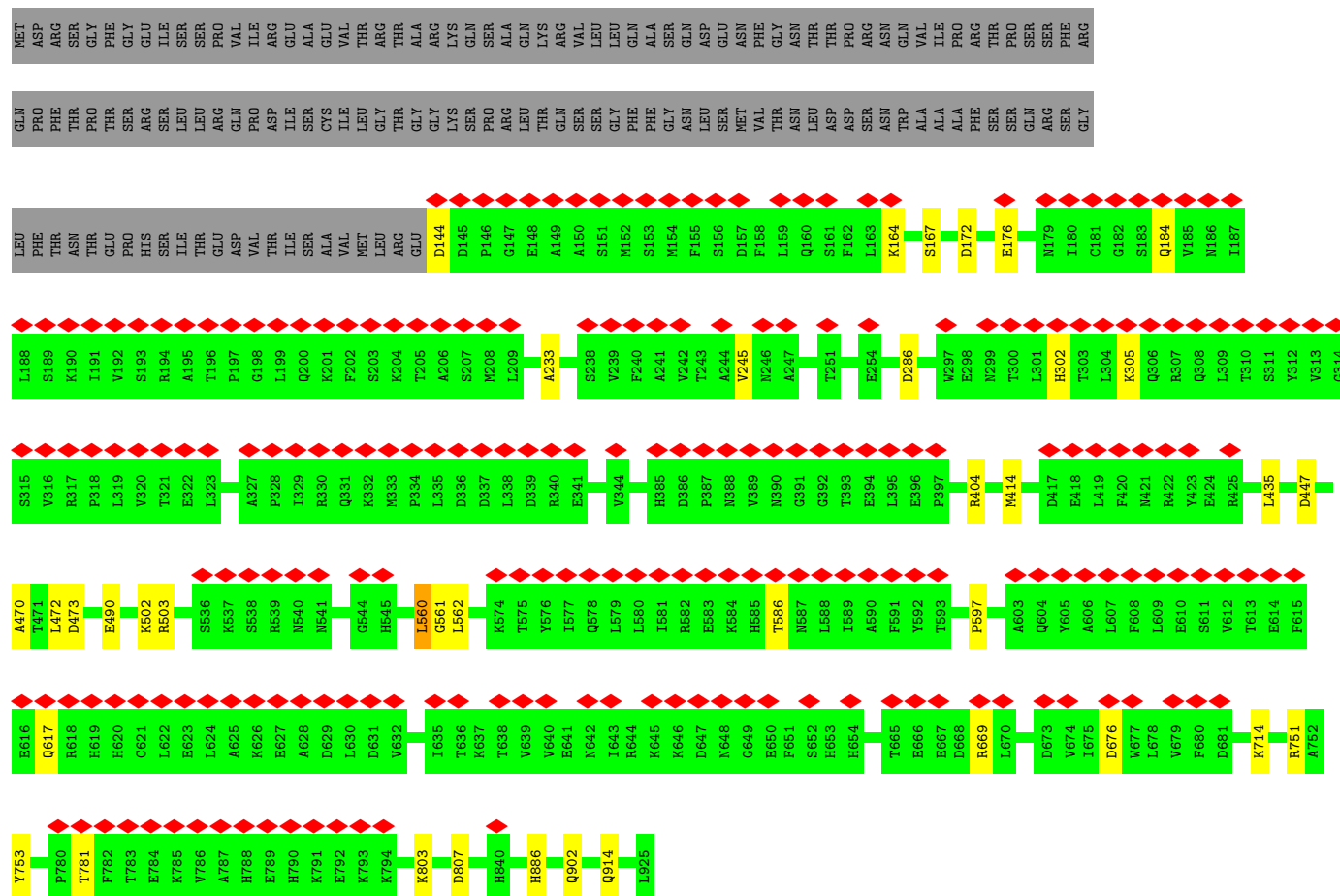
Chain K2:





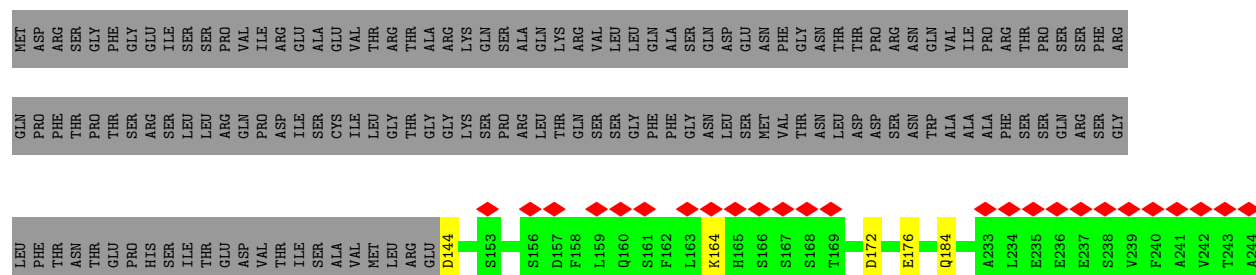
• Molecule 14: Nuclear pore complex protein Nup107

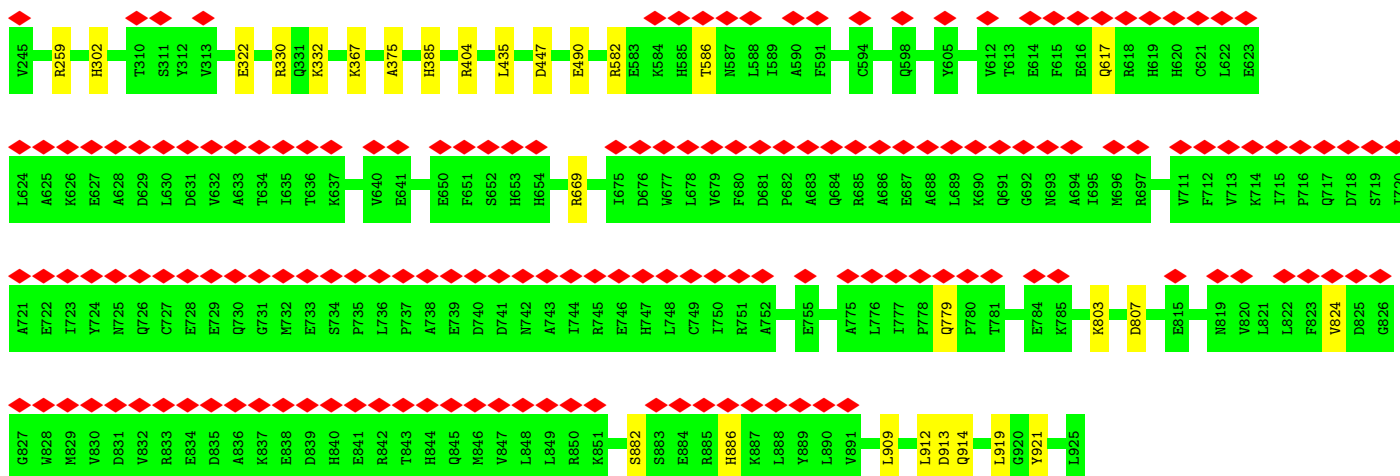
Chain L1: 24% 80% 15%



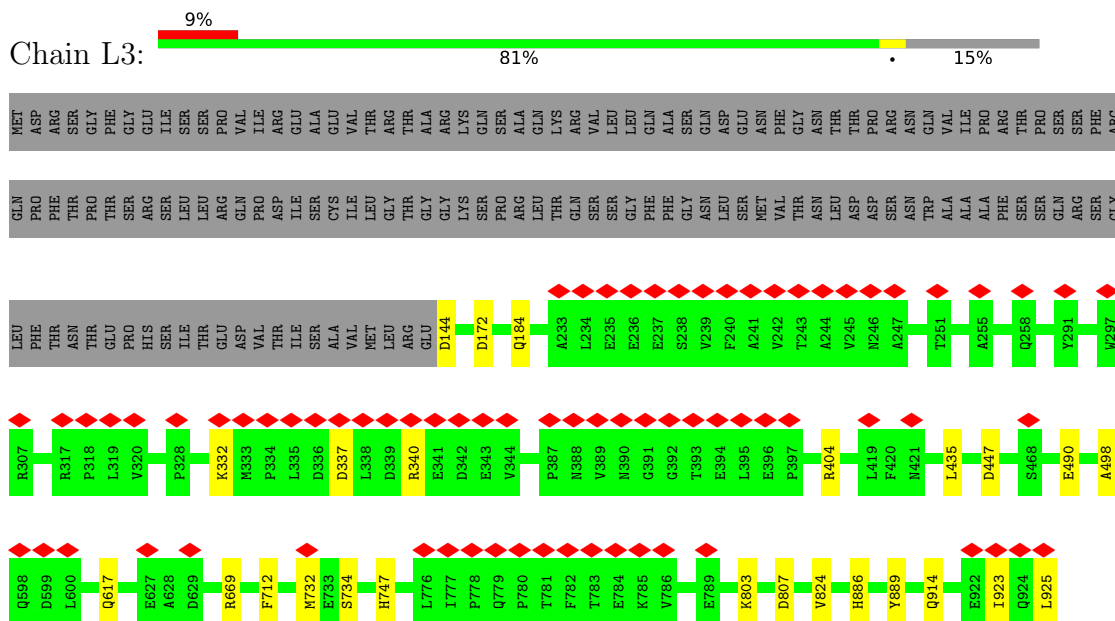
• Molecule 14: Nuclear pore complex protein Nup107

Chain L2: 20% 81% 15%



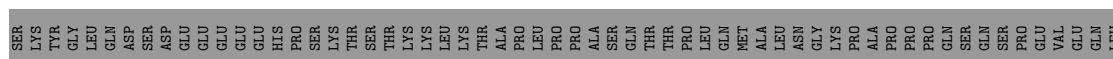


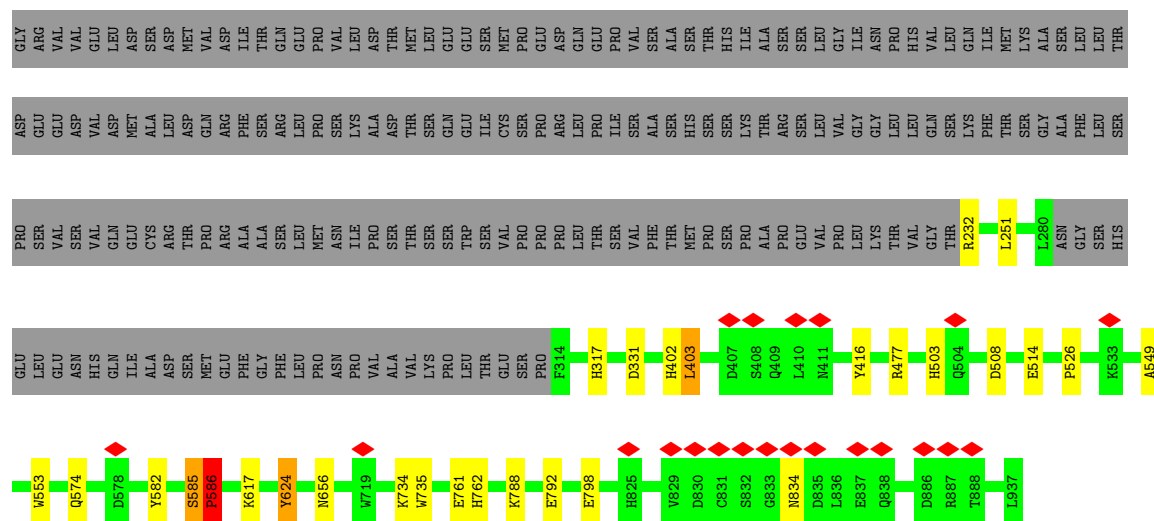
• Molecule 14: Nuclear pore complex protein Nup107



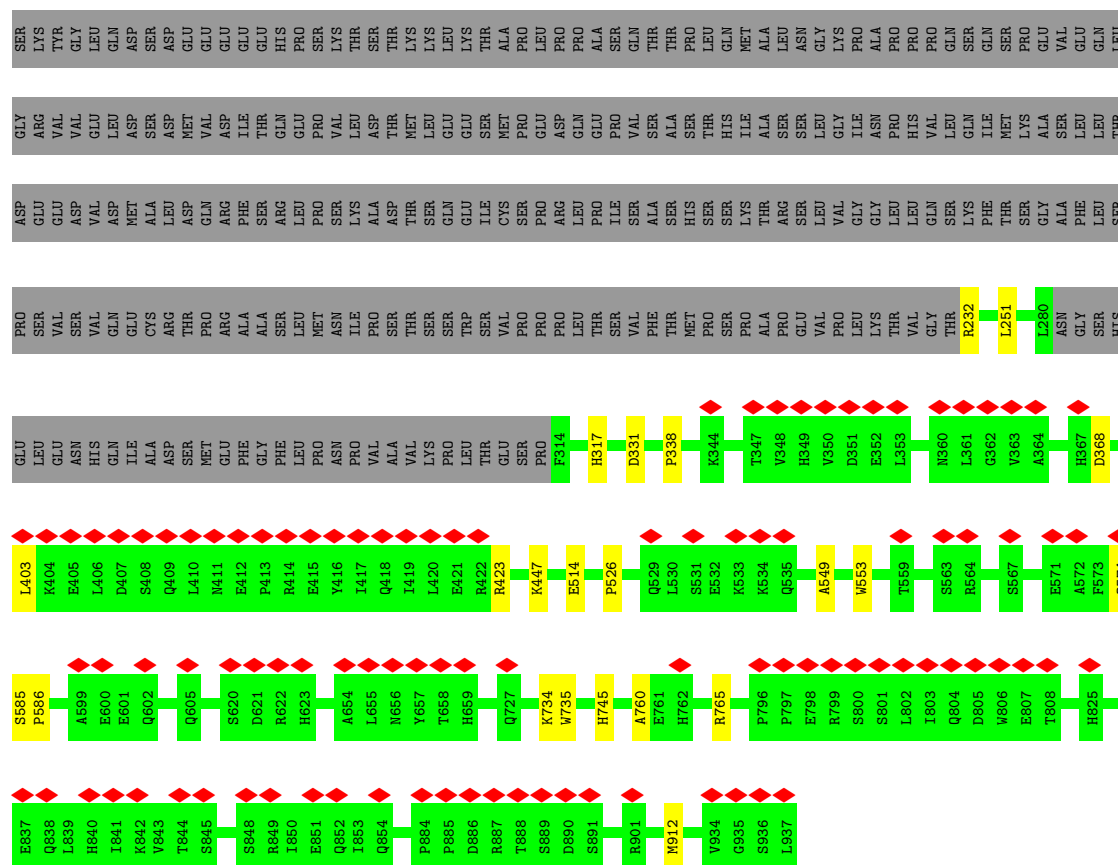
• Molecule 15: Nuclear pore complex protein Nup96



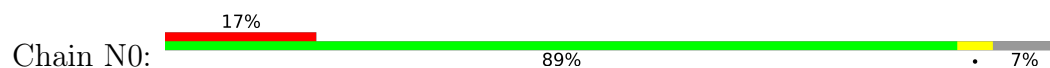


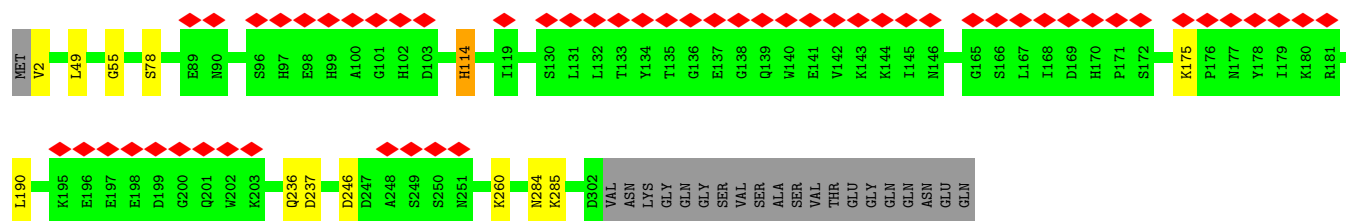


• Molecule 15: Nuclear pore complex protein Nup96

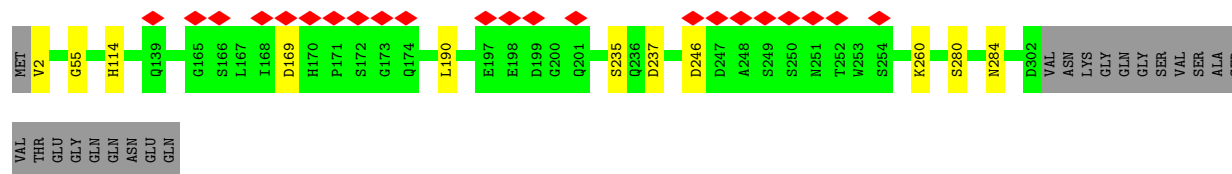
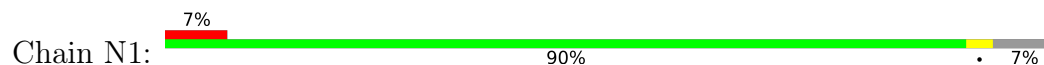


• Molecule 16: Protein SEC13 homolog

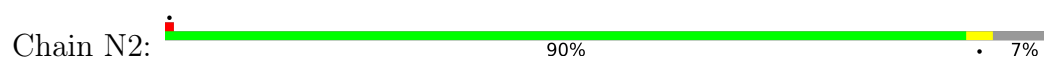




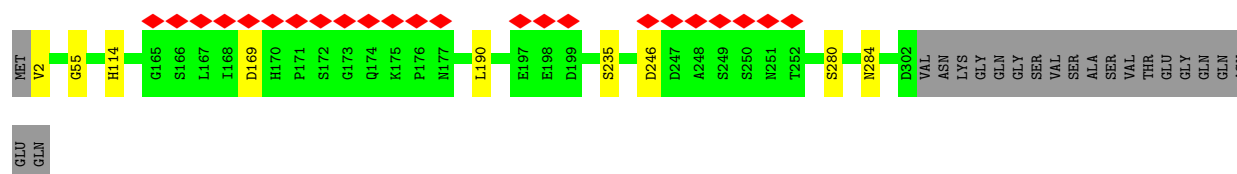
- Molecule 16: Protein SEC13 homolog



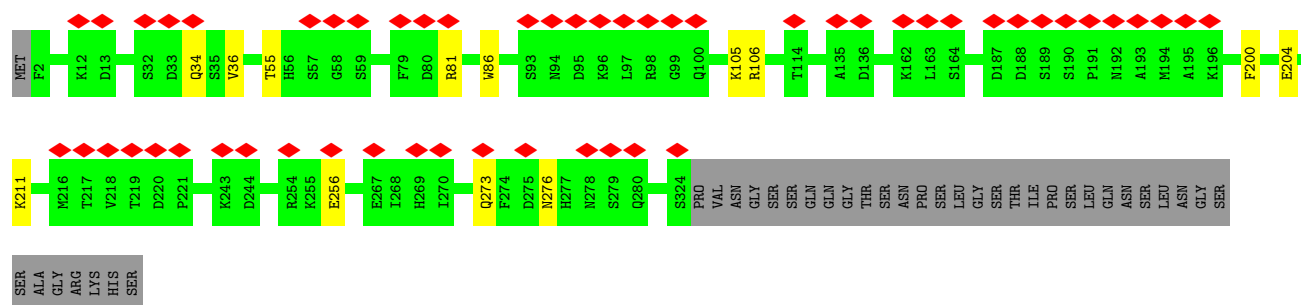
- Molecule 16: Protein SEC13 homolog



- Molecule 16: Protein SEC13 homolog

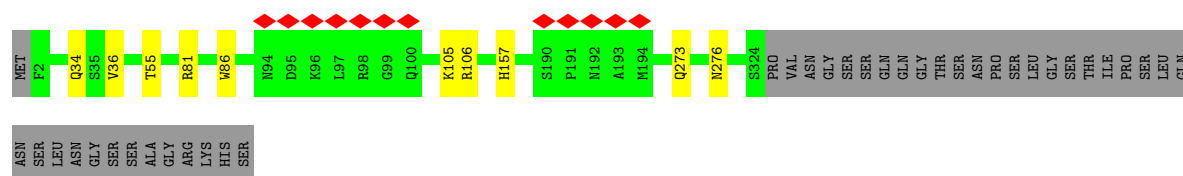


- Molecule 17: Nucleoporin SEH1



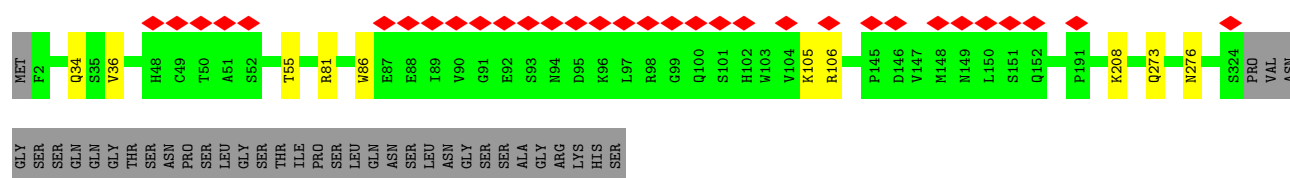
- Molecule 17: Nucleoporin SEH1

Chain O1:  87% 10%



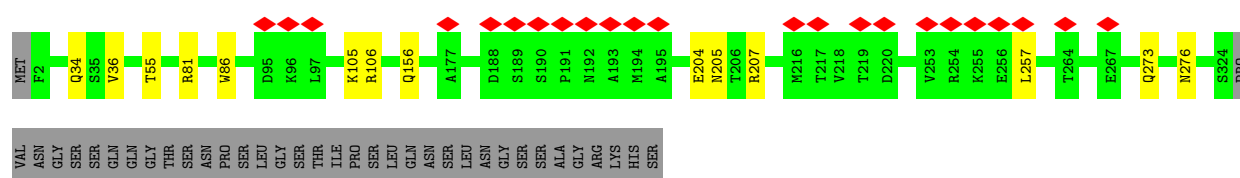
• Molecule 17: Nucleoporin SEH1

Chain O2:  9% 87% 10%



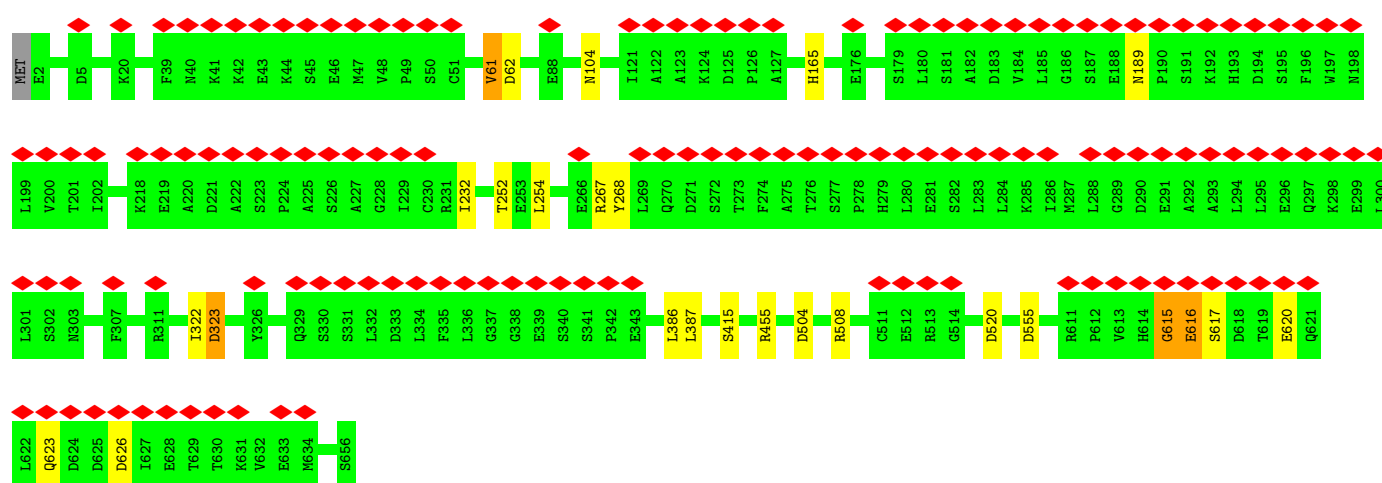
• Molecule 17: Nucleoporin SEH1

Chain O3:  6% 86% 10%



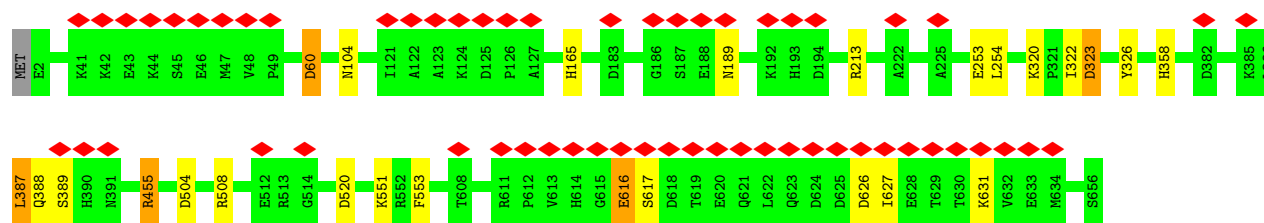
• Molecule 18: Nuclear pore complex protein Nup85

Chain P0:  21% 96% 2%

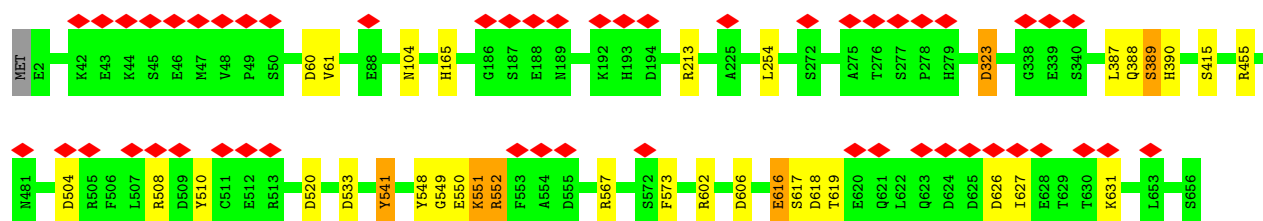


• Molecule 18: Nuclear pore complex protein Nup85

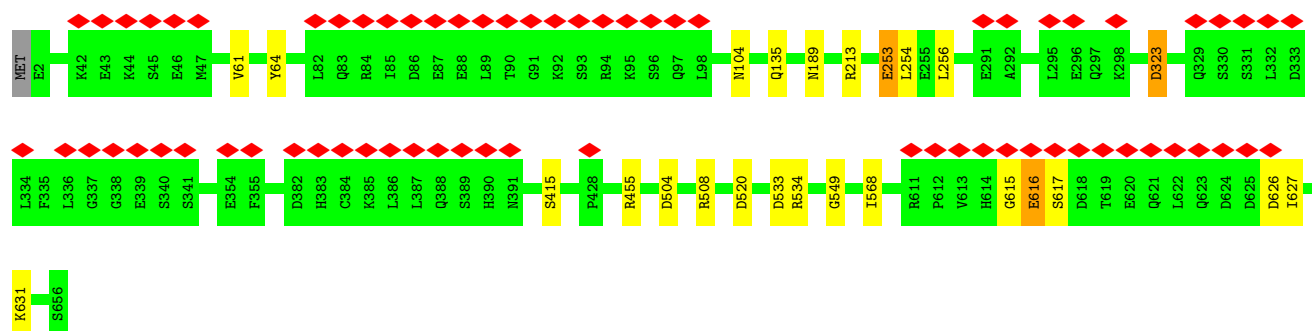
Chain P1:  9% 96% 2%



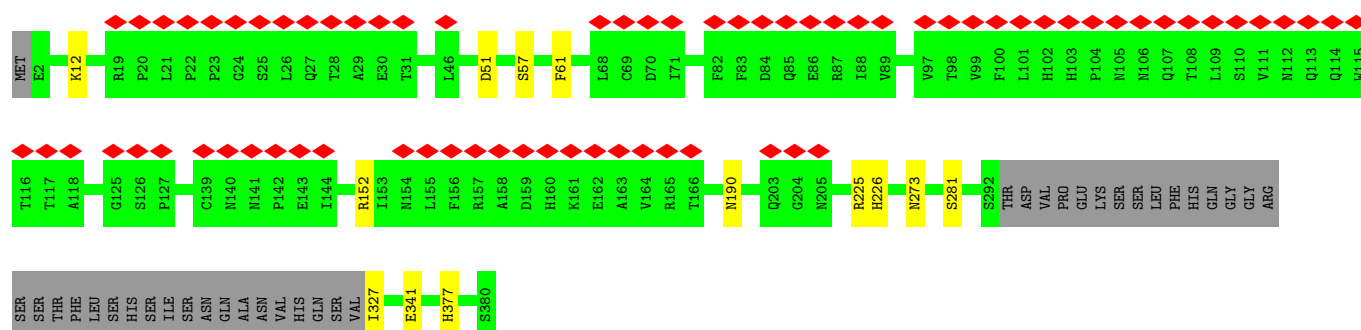
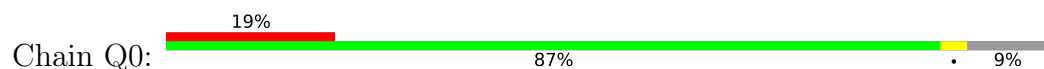
• Molecule 18: Nuclear pore complex protein Nup85



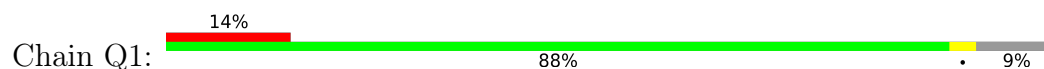
• Molecule 18: Nuclear pore complex protein Nup85

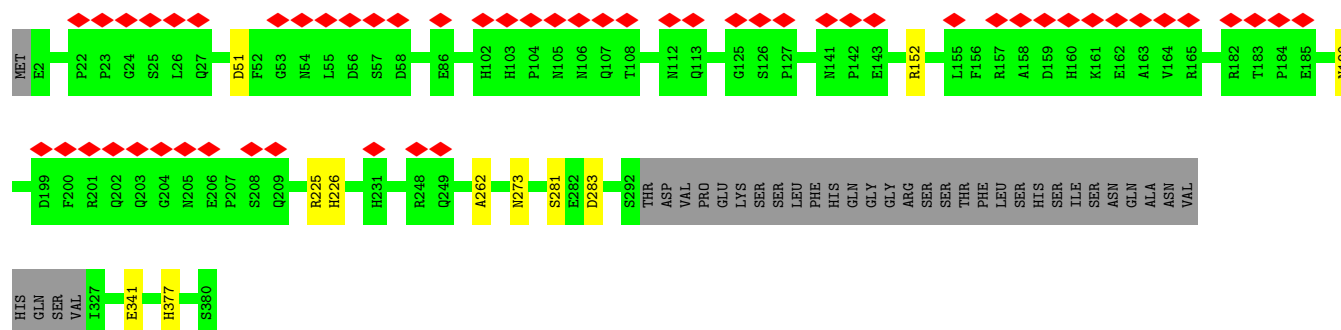


• Molecule 19: Nucleoporin Nup43

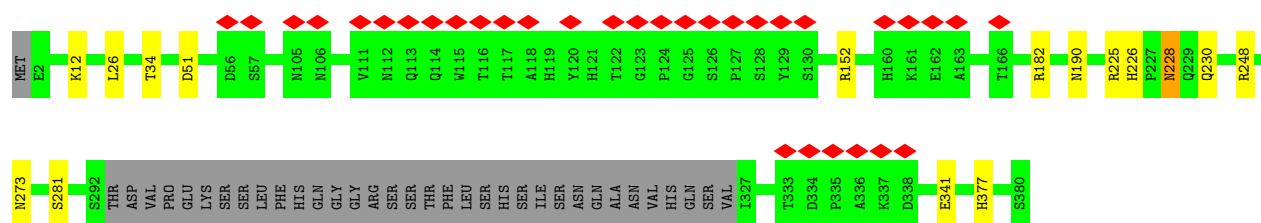
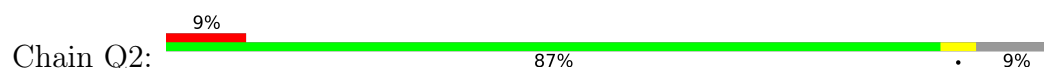


• Molecule 19: Nucleoporin Nup43

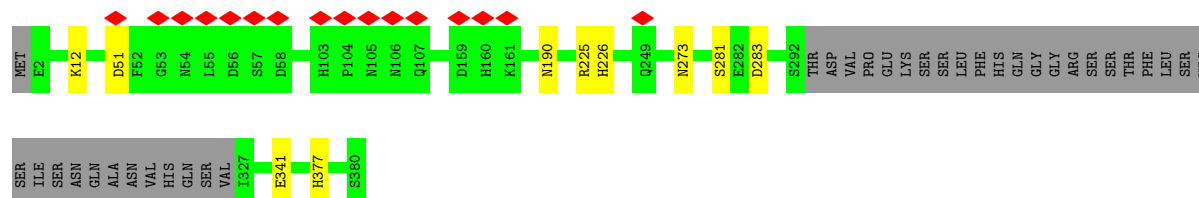
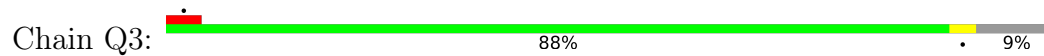




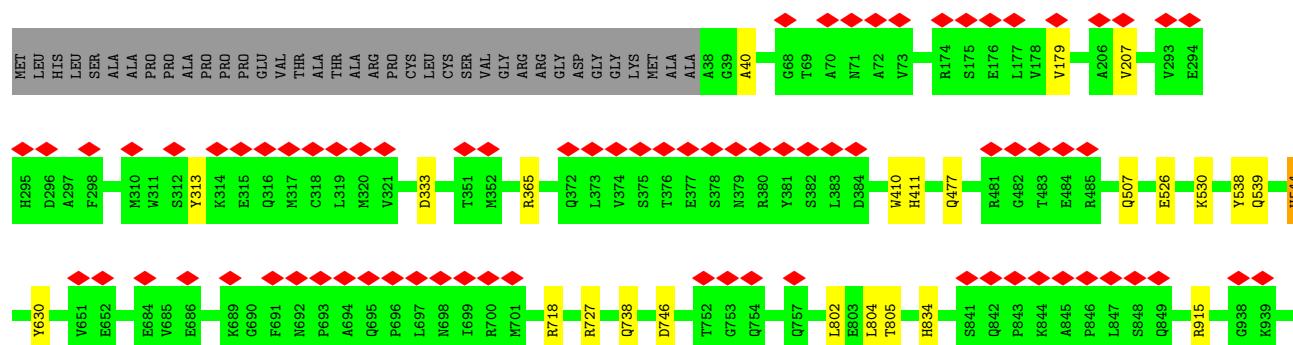
• Molecule 19: Nucleoporin Nup43

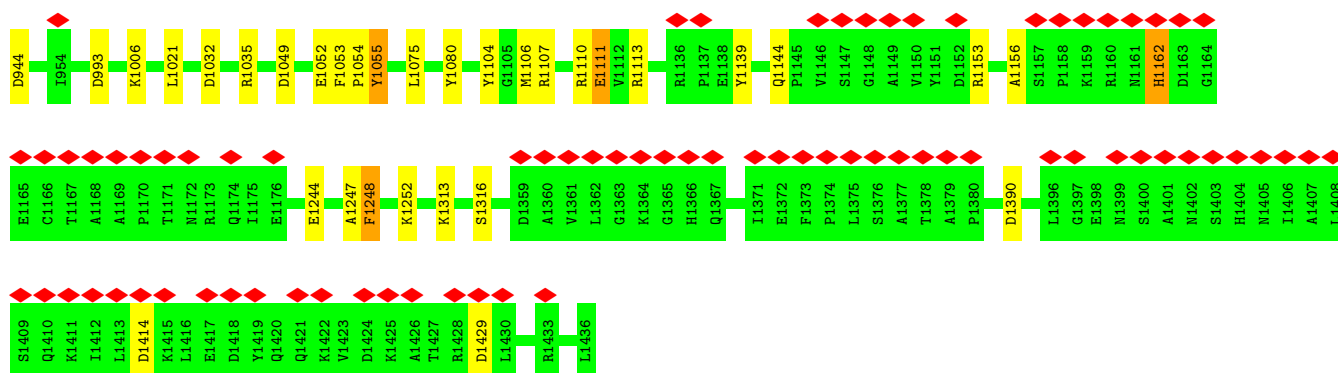


• Molecule 19: Nucleoporin Nup43

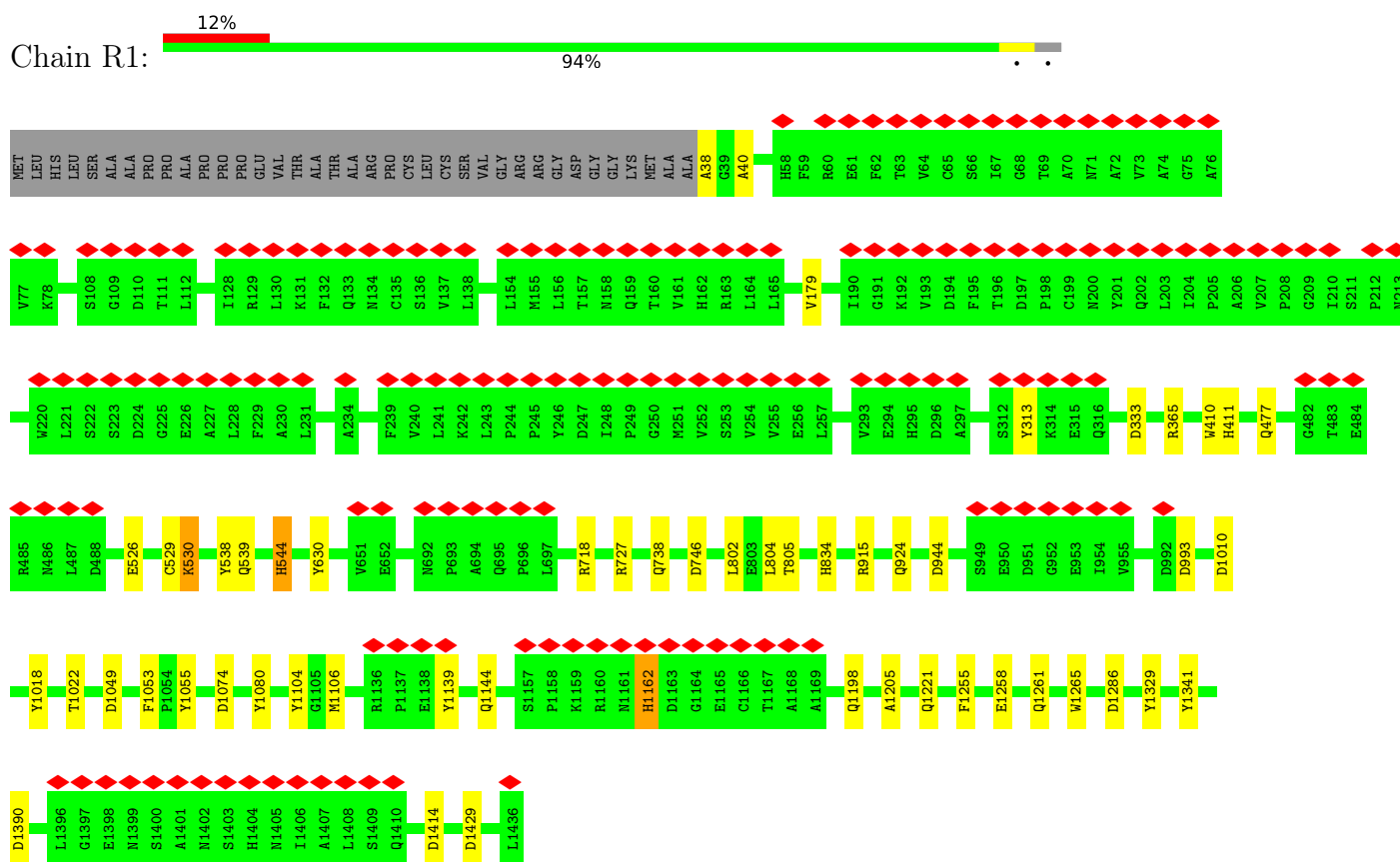


• Molecule 20: Nuclear pore complex protein Nup160

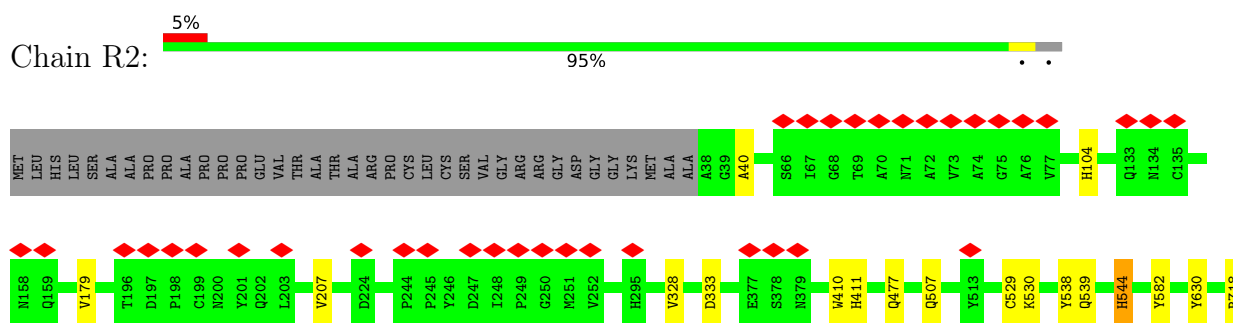


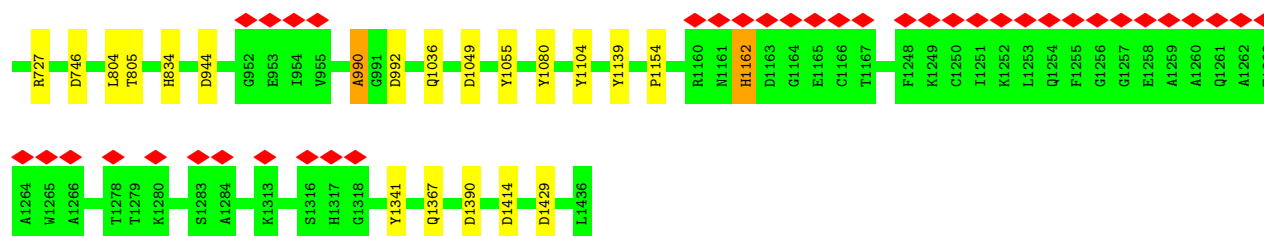


• Molecule 20: Nuclear pore complex protein Nup160

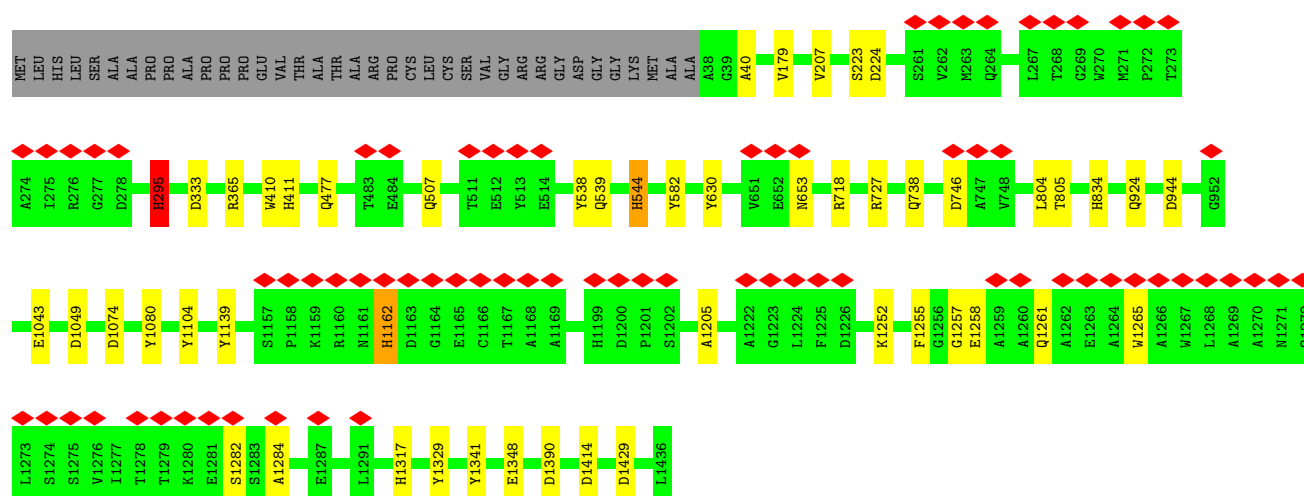


• Molecule 20: Nuclear pore complex protein Nup160

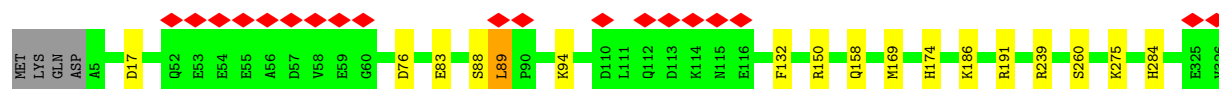




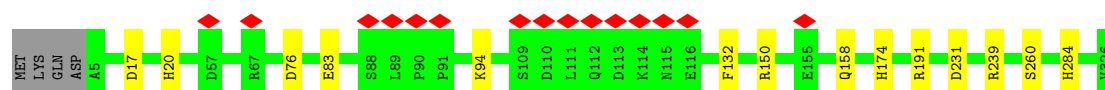
• Molecule 20: Nuclear pore complex protein Nup160



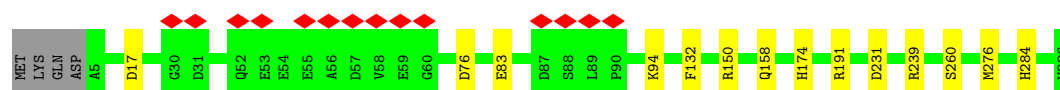
• Molecule 21: Nucleoporin Nup37



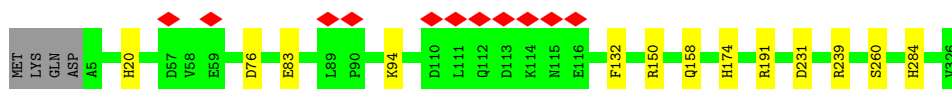
• Molecule 21: Nucleoporin Nup37



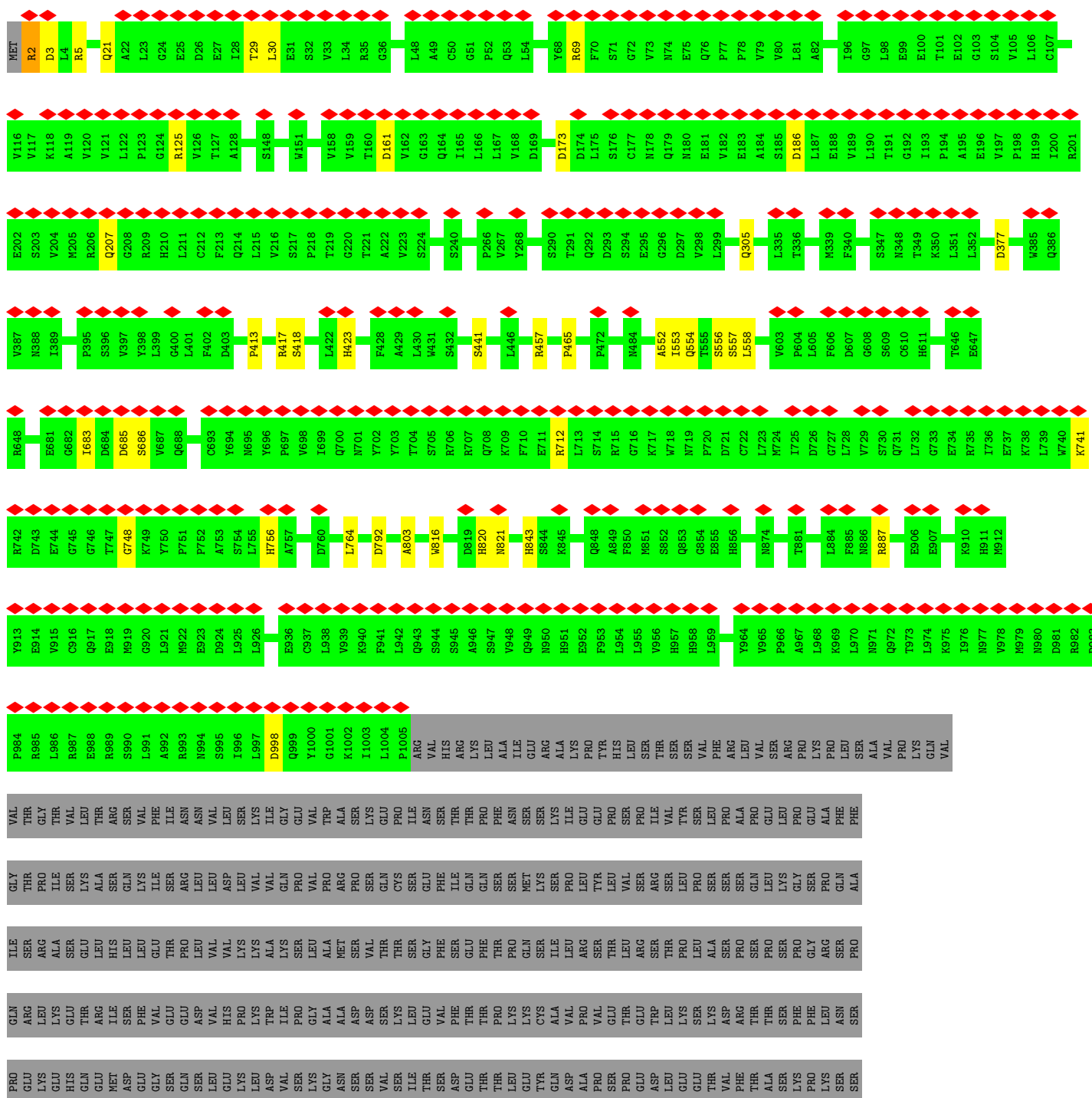
• Molecule 21: Nucleoporin Nup37



• Molecule 21: Nucleoporin Nup37



Chain T0:





LEU
SER
SER
TYR
PRO
LYS
GLN
ILE
LEU
ARG
ARG
LYS
MET
LEU

- 

[illegible]

- Molecule 23: Nuclear pore complex protein Nup98

Chain U3: 98%

[illegible]

[illegible]

- Molecule 23: Nuclear pore complex protein Nup98

Chain U5:  98%

[illegible]

- Molecule 23: Nuclear pore complex protein Nup98

98%

[illegible]

- Molecule 24: Nuclear pore complex protein Nup214

12%

[illegible]



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, Not provided	
Number of subtomograms used	150	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	130	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.878	Depositor
Minimum map value	-0.768	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.063	Depositor
Recommended contour level	0.0891	Depositor
Map size ($\text{\AA}$)	1987.2001, 1987.2001, 1987.2001	wwPDB
Map dimensions	144, 144, 144	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	13.8, 13.8, 13.8	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	00	0.84	0/6212	1.41	17/8405 (0.2%)
1	01	0.83	0/6212	1.40	17/8405 (0.2%)
1	02	0.84	0/6212	1.41	17/8405 (0.2%)
1	03	0.83	0/6212	1.40	11/8405 (0.1%)
1	04	0.84	0/6212	1.40	17/8405 (0.2%)
2	10	1.44	7/14350 (0.0%)	1.32	42/19560 (0.2%)
2	11	0.80	0/14350	1.28	18/19560 (0.1%)
2	12	0.80	1/14350 (0.0%)	1.29	19/19560 (0.1%)
2	13	0.80	0/14350	1.29	20/19560 (0.1%)
2	14	0.81	0/14350	1.31	33/19560 (0.2%)
2	15	0.80	0/14350	1.30	26/19560 (0.1%)
2	16	0.80	0/14350	1.30	29/19560 (0.1%)
2	17	0.85	8/14350 (0.1%)	1.36	51/19560 (0.3%)
3	40	0.85	0/3007	1.30	3/4114 (0.1%)
3	41	0.85	1/3007 (0.0%)	1.30	4/4114 (0.1%)
4	A0	0.84	0/6687	1.39	16/9036 (0.2%)
4	A1	0.83	0/6687	1.39	19/9036 (0.2%)
4	A2	0.84	1/6687 (0.0%)	1.41	28/9036 (0.3%)
4	A3	0.83	0/6687	1.38	20/9036 (0.2%)
4	A4	0.83	0/5972	1.37	13/8068 (0.2%)
4	A5	0.84	0/5972	1.36	13/8068 (0.2%)
4	A6	0.83	0/5972	1.38	14/8068 (0.2%)
5	B0	0.85	1/14018 (0.0%)	1.40	43/19022 (0.2%)
5	B1	0.85	3/14018 (0.0%)	1.40	39/19022 (0.2%)
6	C0	0.85	1/16330 (0.0%)	1.40	39/22131 (0.2%)
6	C1	0.85	1/16330 (0.0%)	1.40	39/22131 (0.2%)
6	C2	1.51	5/16330 (0.0%)	1.38	48/22131 (0.2%)
6	C3	0.85	0/16330	1.39	37/22131 (0.2%)
6	C4	0.85	1/16330 (0.0%)	1.39	36/22131 (0.2%)
7	D0	0.82	0/10568	1.40	22/14320 (0.2%)
7	D1	1.30	5/10568 (0.0%)	1.45	50/14320 (0.3%)
7	D2	0.82	0/10568	1.40	25/14320 (0.2%)
7	D3	0.83	0/10568	1.40	28/14320 (0.2%)
7	D4	1.04	6/10568 (0.1%)	1.42	44/14320 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
7	D5	0.81	0/10568	1.38	27/14320 (0.2%)
8	E0	1.23	14/4563 (0.3%)	1.48	44/6214 (0.7%)
8	E1	0.97	11/4563 (0.2%)	1.48	27/6214 (0.4%)
9	F0	0.88	0/1882	1.47	13/2556 (0.5%)
9	F1	0.89	0/1882	1.44	7/2556 (0.3%)
9	F2	0.90	0/1882	1.50	14/2556 (0.5%)
9	F3	0.93	0/1882	1.49	5/2556 (0.2%)
10	H0	0.80	1/3114 (0.0%)	1.37	7/4211 (0.2%)
10	H1	0.80	0/3114	1.39	10/4211 (0.2%)
10	H2	0.80	0/3114	1.38	8/4211 (0.2%)
10	H3	0.80	0/3114	1.38	6/4211 (0.1%)
11	I0	0.80	0/1416	1.39	2/1911 (0.1%)
11	I1	0.81	0/1416	1.41	2/1911 (0.1%)
11	I2	0.80	0/1416	1.40	2/1911 (0.1%)
11	I3	0.80	0/1416	1.41	2/1911 (0.1%)
12	J0	0.81	0/1420	1.38	3/1915 (0.2%)
12	J1	0.81	0/1420	1.40	5/1915 (0.3%)
12	J2	0.81	0/1420	1.40	5/1915 (0.3%)
12	J3	0.81	0/1420	1.39	5/1915 (0.3%)
12	J4	0.80	0/1420	1.44	4/1915 (0.2%)
13	K0	0.83	0/8740	1.37	19/11848 (0.2%)
13	K1	0.82	0/8740	1.36	17/11848 (0.1%)
13	K2	0.82	0/8740	1.36	19/11848 (0.2%)
13	K3	0.82	0/8740	1.36	16/11848 (0.1%)
14	L0	0.86	1/6518 (0.0%)	1.42	23/8819 (0.3%)
14	L1	0.84	0/6518	1.39	13/8819 (0.1%)
14	L2	0.85	0/6518	1.39	12/8819 (0.1%)
14	L3	0.85	0/6518	1.39	14/8819 (0.2%)
15	M0	0.86	0/5588	1.42	22/7581 (0.3%)
15	M1	0.87	0/5588	1.41	15/7581 (0.2%)
15	M2	0.86	0/5588	1.41	14/7581 (0.2%)
15	M3	0.86	0/5588	1.40	11/7581 (0.1%)
16	N0	0.85	0/2419	1.37	6/3301 (0.2%)
16	N1	0.85	0/2419	1.37	9/3301 (0.3%)
16	N2	0.85	0/2419	1.37	8/3301 (0.2%)
16	N3	0.85	0/2419	1.37	9/3301 (0.3%)
17	O0	0.84	0/2593	1.35	4/3520 (0.1%)
17	O1	0.85	0/2593	1.35	4/3520 (0.1%)
17	O2	0.84	0/2593	1.35	4/3520 (0.1%)
17	O3	0.85	0/2593	1.36	7/3520 (0.2%)
18	P0	0.85	0/5365	1.40	17/7257 (0.2%)
18	P1	0.85	0/5365	1.38	17/7257 (0.2%)
18	P2	0.85	0/5365	1.42	28/7257 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
18	P3	0.85	0/5365	1.37	13/7257 (0.2%)
19	Q0	0.87	0/2775	1.38	6/3786 (0.2%)
19	Q1	0.87	0/2775	1.38	7/3786 (0.2%)
19	Q2	0.87	0/2775	1.40	11/3786 (0.3%)
19	Q3	0.87	0/2775	1.37	7/3786 (0.2%)
20	R0	0.98	2/11371 (0.0%)	1.39	37/15446 (0.2%)
20	R1	0.84	0/11371	1.37	31/15446 (0.2%)
20	R2	0.84	0/11371	1.37	30/15446 (0.2%)
20	R3	0.84	0/11371	1.37	28/15446 (0.2%)
21	S0	0.85	0/2623	1.34	9/3568 (0.3%)
21	S1	0.85	0/2623	1.33	7/3568 (0.2%)
21	S2	0.85	0/2623	1.33	7/3568 (0.2%)
21	S3	0.85	0/2623	1.33	6/3568 (0.2%)
22	T0	0.84	0/8141	1.38	27/11065 (0.2%)
22	T1	0.84	0/8141	1.38	27/11065 (0.2%)
23	U0	0.85	0/1217	1.35	4/1644 (0.2%)
23	U1	1.41	1/152 (0.7%)	2.13	6/204 (2.9%)
23	U2	1.33	0/152	1.92	4/204 (2.0%)
23	U3	1.38	0/152	2.11	7/204 (3.4%)
23	U4	1.48	1/152 (0.7%)	1.91	3/204 (1.5%)
23	U5	1.41	0/152	2.13	6/204 (2.9%)
23	U6	1.30	0/152	1.90	7/204 (3.4%)
24	V0	0.86	0/2240	1.44	7/3019 (0.2%)
25	W0	0.86	1/5972 (0.0%)	1.37	20/8105 (0.2%)
All	All	0.90	73/630097 (0.0%)	1.38	1720/855041 (0.2%)

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	00	0	4
1	01	0	4
1	02	0	3
1	03	0	3
1	04	0	1
2	10	1	9
2	11	0	3
2	12	1	7
2	13	1	3
2	14	0	8

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	15	0	7
2	16	0	7
2	17	0	8
3	40	0	5
3	41	0	4
4	A0	0	11
4	A1	0	12
4	A2	0	12
4	A3	0	9
4	A4	0	7
4	A5	0	6
4	A6	1	9
5	B0	0	22
5	B1	0	26
6	C0	1	17
6	C1	1	13
6	C2	1	17
6	C3	1	15
6	C4	1	15
7	D0	0	16
7	D1	0	13
7	D2	0	18
7	D3	0	14
7	D4	1	19
7	D5	0	15
8	E0	0	5
8	E1	0	2
9	F0	0	3
9	F1	0	2
9	F2	0	3
9	F3	0	1
10	H0	0	5
10	H1	0	1
10	H2	0	2
10	H3	0	2
12	J0	0	1
12	J1	0	1
12	J2	0	1
12	J3	0	1
13	K0	0	10
13	K1	0	9
13	K2	0	12

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Mol	Chain	#Chirality outliers	#Planarity outliers
13	K3	0	8
14	L0	0	8
14	L1	0	5
14	L2	0	6
14	L3	0	6
15	M0	0	7
15	M1	0	5
15	M2	0	9
15	M3	1	6
16	N0	0	4
16	N1	0	2
16	N2	0	2
16	N3	0	2
17	O0	0	1
17	O1	0	2
17	O2	0	2
17	O3	0	2
18	P0	0	9
18	P1	0	10
18	P2	1	17
18	P3	0	10
19	Q0	0	3
19	Q1	0	3
19	Q2	0	3
19	Q3	0	2
20	R0	0	15
20	R1	0	16
20	R2	0	15
20	R3	0	15
21	S0	0	4
21	S1	0	5
21	S2	0	5
21	S3	0	5
22	T0	2	13
22	T1	2	14
24	V0	0	5
25	W0	0	7
All	All	16	676

The worst 5 of 73 bond length outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	10	1824	MET	N-CA	140.20	3.27	1.46
7	D1	1002	PRO	CA-C	103.26	2.99	1.52
6	C2	484	HIS	CD2-NE2	83.30	2.29	1.37
6	C2	484	HIS	CG-ND1	74.67	2.20	1.38
6	C2	484	HIS	ND1-CE1	69.44	2.02	1.32

The worst 5 of 1720 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	E1	243	SER	CA-C-O	-25.86	93.01	120.42
6	C1	1379	PRO	O-C-N	-24.31	110.13	121.31
2	17	1788	ASP	CA-C-N	21.79	163.16	121.54
2	17	1788	ASP	C-N-CA	21.79	163.16	121.54
7	D1	1000	GLY	CA-C-N	16.46	137.34	120.38

5 of 16 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	10	167	ALA	CA
2	12	167	ALA	CA
2	13	1773	THR	CA
4	A6	96	THR	CA
6	C0	174	THR	CB

5 of 676 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	00	132	TYR	Sidechain
1	00	161	ARG	Peptide
1	00	175	TYR	Sidechain
1	00	193	ARG	Sidechain
1	01	11	TYR	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	00	6085	0	6080	35	0
1	01	6085	0	6080	37	0
1	02	6085	0	6080	8	0
1	03	6085	0	6080	10	0
1	04	6085	0	6080	9	0
2	10	14046	0	14194	136	0
2	11	14046	0	14194	24	0
2	12	14046	0	14194	19	0
2	13	14046	0	14194	10	0
2	14	14046	0	14194	28	0
2	15	14046	0	14194	62	0
2	16	14046	0	14194	50	0
2	17	14046	0	14194	84	0
3	40	2922	0	2899	5	0
3	41	2922	0	2899	3	0
4	A0	6568	0	6527	41	0
4	A1	6568	0	6527	9	0
4	A2	6568	0	6527	34	0
4	A3	6568	0	6527	9	0
4	A4	5860	0	5828	30	0
4	A5	5860	0	5828	9	0
4	A6	5860	0	5828	9	0
5	B0	13746	0	13949	14	0
5	B1	13746	0	13949	17	0
6	C0	16013	0	16224	20	0
6	C1	16013	0	16224	27	0
6	C2	16013	0	16224	73	0
6	C3	16013	0	16224	46	0
6	C4	16013	0	16224	41	0
7	D0	10363	0	10400	65	0
7	D1	10363	0	10400	135	0
7	D2	10363	0	10400	57	0
7	D3	10363	0	10400	84	0
7	D4	10363	0	10400	134	0
7	D5	10363	0	10400	53	0
8	E0	4432	0	4472	140	0
8	E1	4432	0	4472	70	0
9	F0	1837	0	1825	2	0
9	F1	1837	0	1825	15	0
9	F2	1837	0	1825	0	0
9	F3	1837	0	1825	1	0
10	H0	3066	0	3103	5	0
10	H1	3066	0	3103	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	H2	3066	0	3103	5	0
10	H3	3066	0	3103	2	0
11	I0	1398	0	1431	5	0
11	I1	1398	0	1431	2	0
11	I2	1398	0	1431	5	0
11	I3	1398	0	1431	2	0
12	J0	1403	0	1391	2	0
12	J1	1403	0	1391	2	0
12	J2	1403	0	1391	1	0
12	J3	1403	0	1391	1	0
12	J4	1403	0	1391	2	0
13	K0	8574	0	8438	10	0
13	K1	8574	0	8438	7	0
13	K2	8574	0	8438	49	0
13	K3	8574	0	8438	31	0
14	L0	6383	0	6313	32	0
14	L1	6383	0	6313	63	0
14	L2	6383	0	6313	25	0
14	L3	6383	0	6313	12	0
15	M0	5461	0	5443	11	0
15	M1	5461	0	5443	15	0
15	M2	5461	0	5443	10	0
15	M3	5461	0	5443	7	0
16	N0	2352	0	2220	20	0
16	N1	2352	0	2220	1	0
16	N2	2352	0	2220	2	0
16	N3	2352	0	2220	0	0
17	O0	2528	0	2444	7	0
17	O1	2528	0	2444	2	0
17	O2	2528	0	2444	2	0
17	O3	2528	0	2444	5	0
18	P0	5257	0	5249	14	0
18	P1	5257	0	5249	10	0
18	P2	5257	0	5249	5	0
18	P3	5257	0	5249	6	0
19	Q0	2703	0	2555	12	0
19	Q1	2703	0	2555	1	0
19	Q2	2703	0	2555	14	0
19	Q3	2703	0	2555	1	0
20	R0	11132	0	11066	44	0
20	R1	11132	0	11066	17	0
20	R2	11132	0	11066	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	R3	11132	0	11066	28	0
21	S0	2552	0	2452	5	0
21	S1	2552	0	2452	2	0
21	S2	2552	0	2452	4	0
21	S3	2552	0	2452	2	0
22	T0	7960	0	7896	13	0
22	T1	7960	0	7896	1	0
23	U0	1193	0	1188	4	0
23	U1	151	0	167	61	0
23	U2	151	0	167	36	0
23	U3	151	0	167	48	0
23	U4	151	0	167	38	0
23	U5	151	0	167	48	0
23	U6	151	0	167	37	0
24	V0	2203	0	2226	14	0
25	W0	5836	0	5850	20	0
All	All	617133	0	616873	1526	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 1.

The worst 5 of 1526 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)
8:E0:18:TRP:CD2	8:E0:18:TRP:CG	1.82	1.64
2:10:1824:MET:C	2:10:1824:MET:CA	1.75	1.59
2:17:1788:ASP:C	2:17:1788:ASP:CA	1.75	1.54
8:E1:244:THR:N	8:E1:244:THR:CA	1.69	1.52
8:E0:18:TRP:NE1	8:E0:18:TRP:CE2	1.80	1.49

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14321. 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](#)

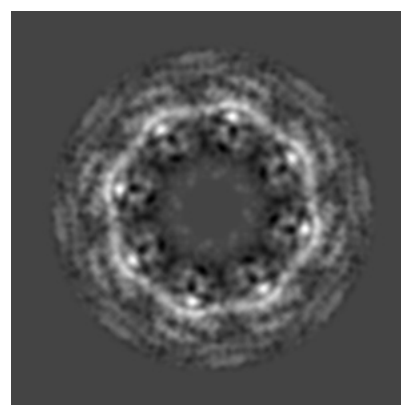
6.1.1 Primary map



X



Y



Z

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

6.2 Central slices [i](#)

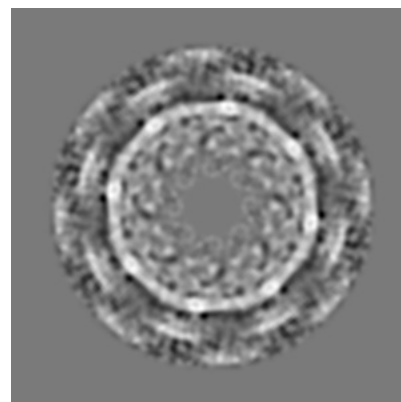
6.2.1 Primary map



X Index: 72



Y Index: 72



Z Index: 72

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

6.3 Largest variance slices [i](#)

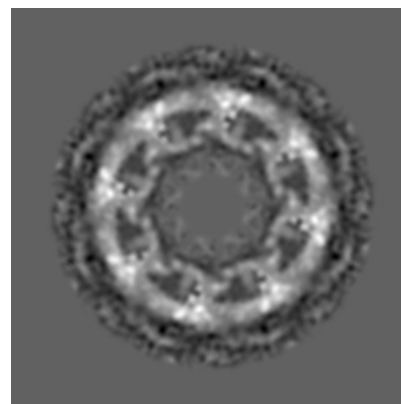
6.3.1 Primary map



X Index: 36



Y Index: 36

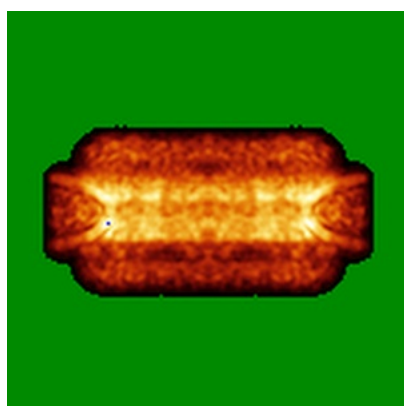


Z Index: 77

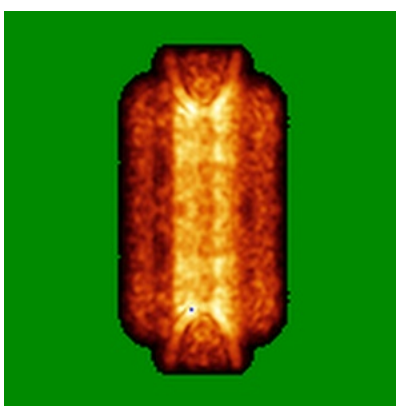
The images above show the largest variance slices of the map in three orthogonal directions.

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

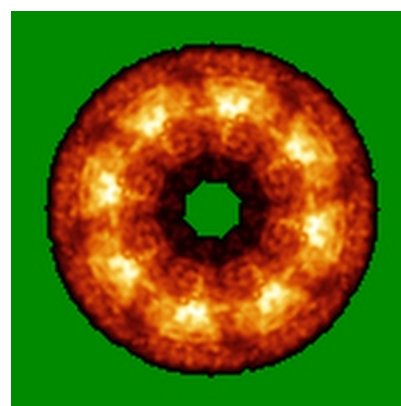
6.4.1 Primary map



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



The images above show the 3D surface view of the map at the recommended contour level 0.0891. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

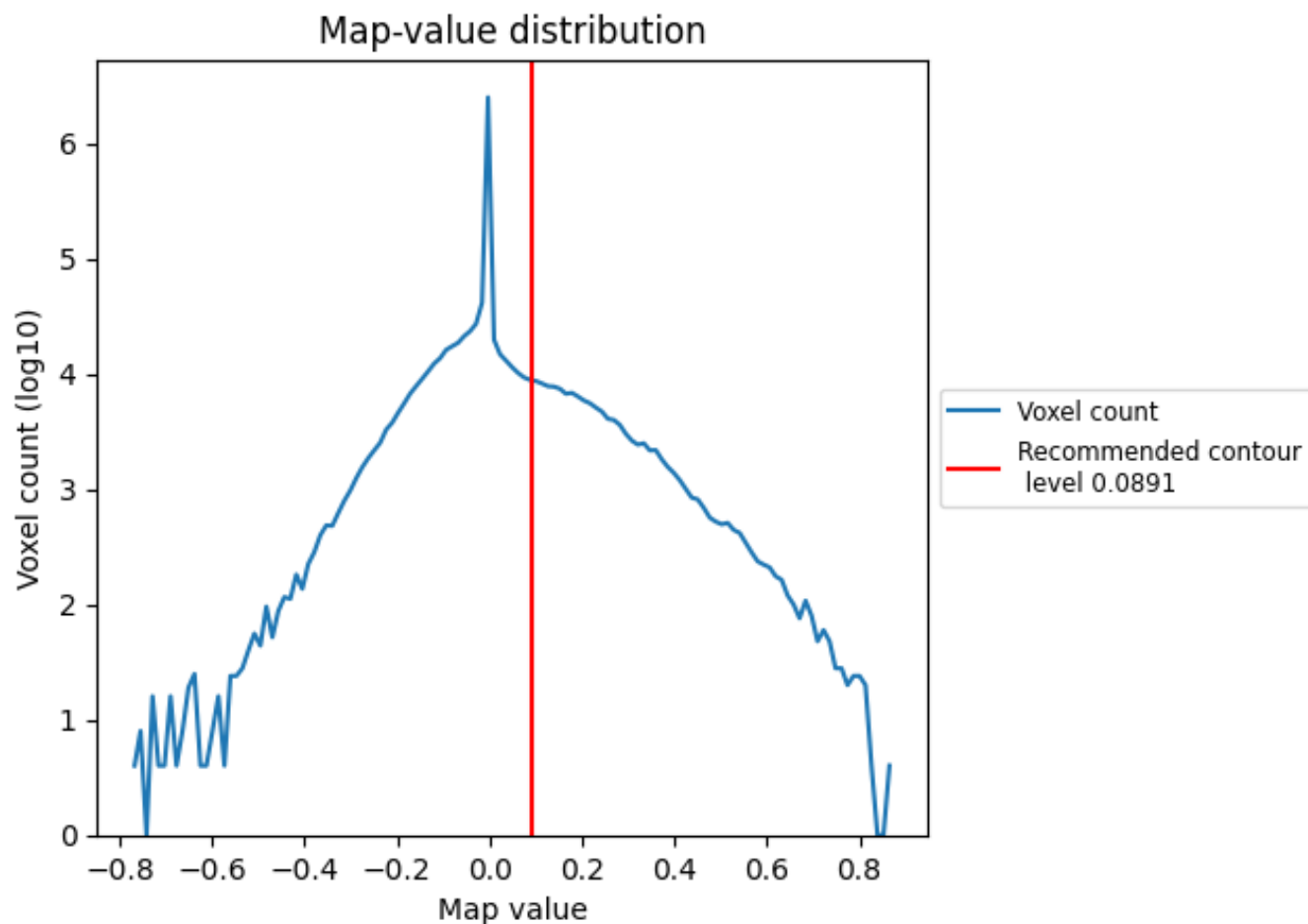
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

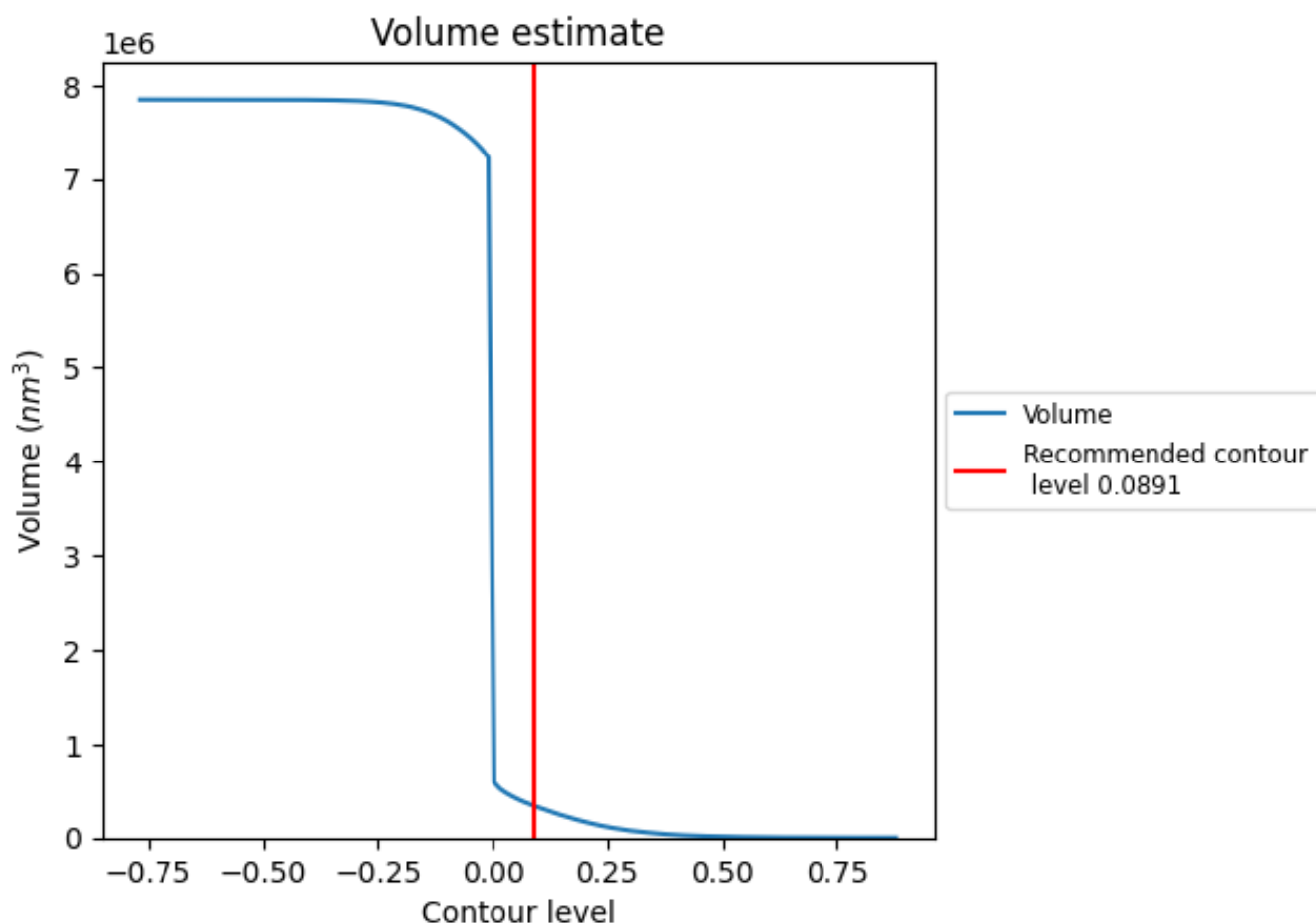
This section contains the results of statistical analysis of the map.

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.

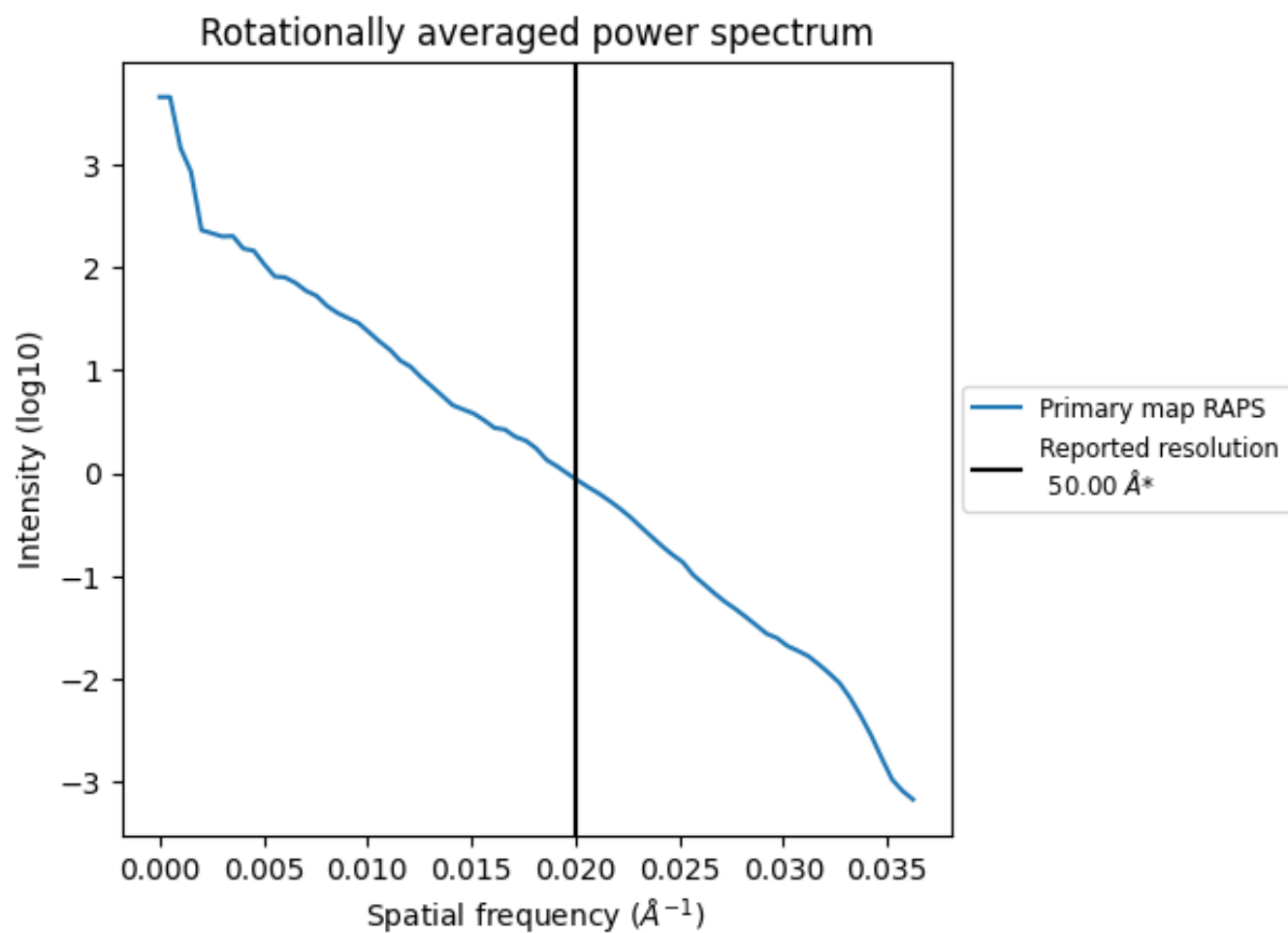
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 342613 nm^3 ; this corresponds to an approximate mass of 309491 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.020 Å⁻¹

8 Fourier-Shell correlation

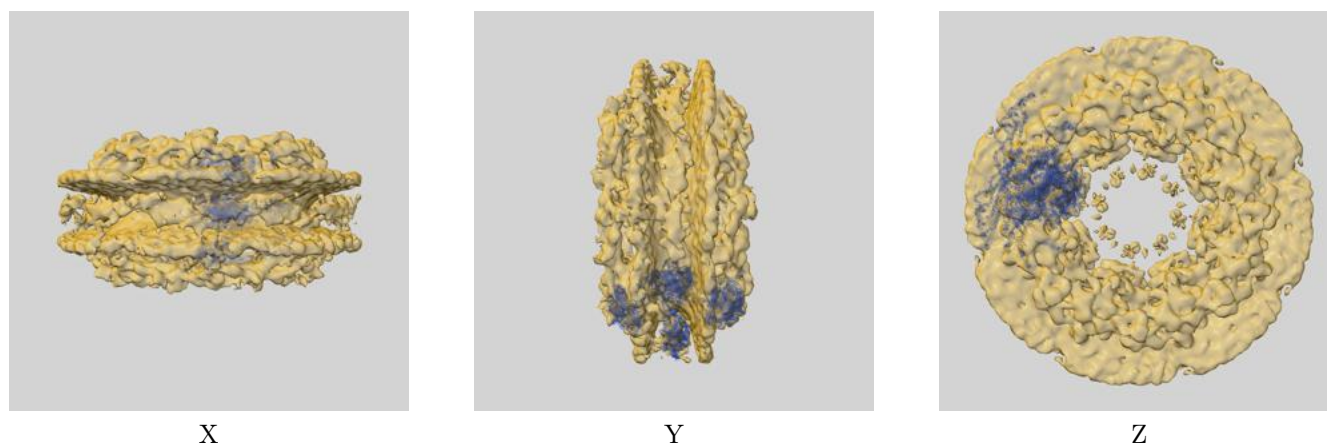
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

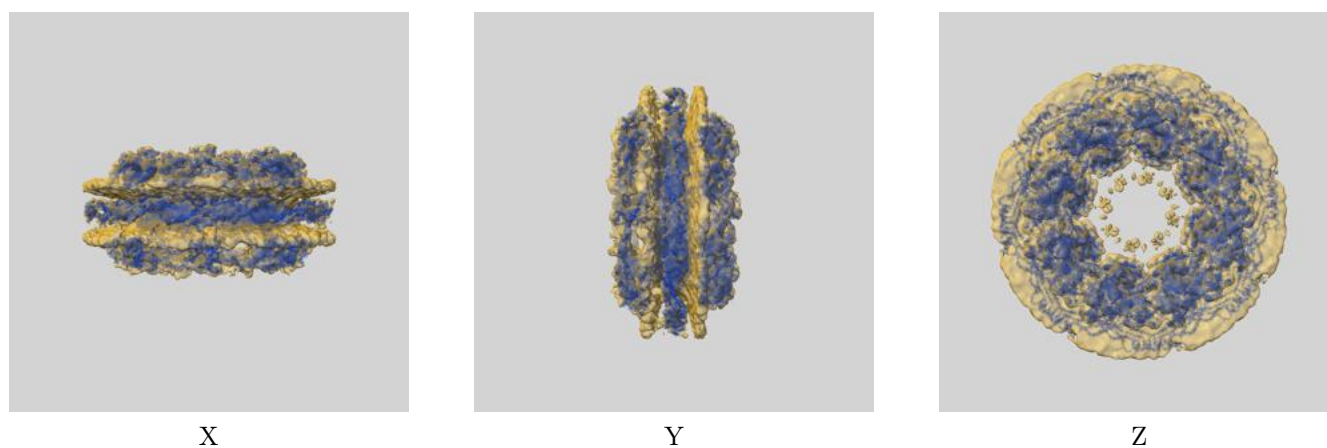
This section contains information regarding the fit between EMDB map EMD-14321 and PDB model 7R5J. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

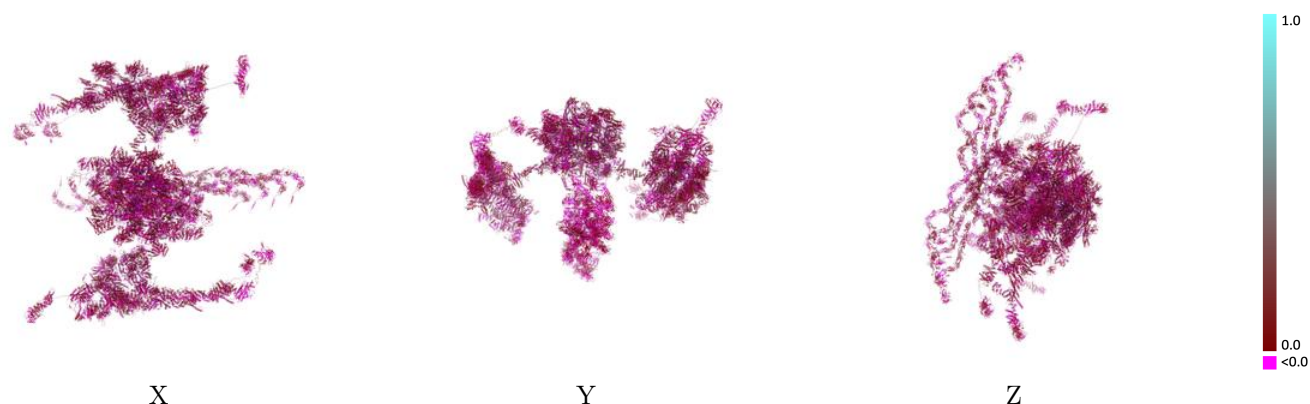


9.1.2 Map-model assembly overlay [i](#)



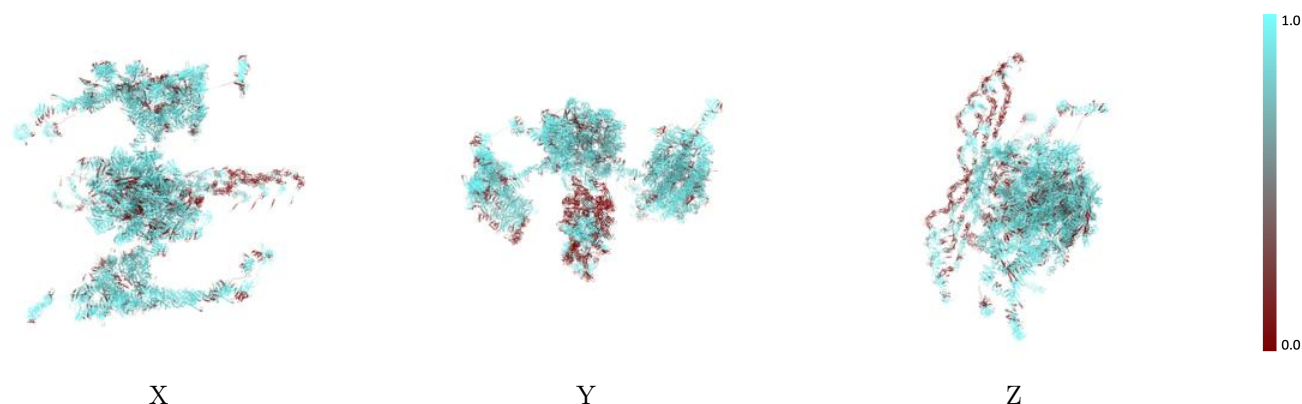
The images above show the 3D surface view of the map at the recommended contour level 0.0891 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



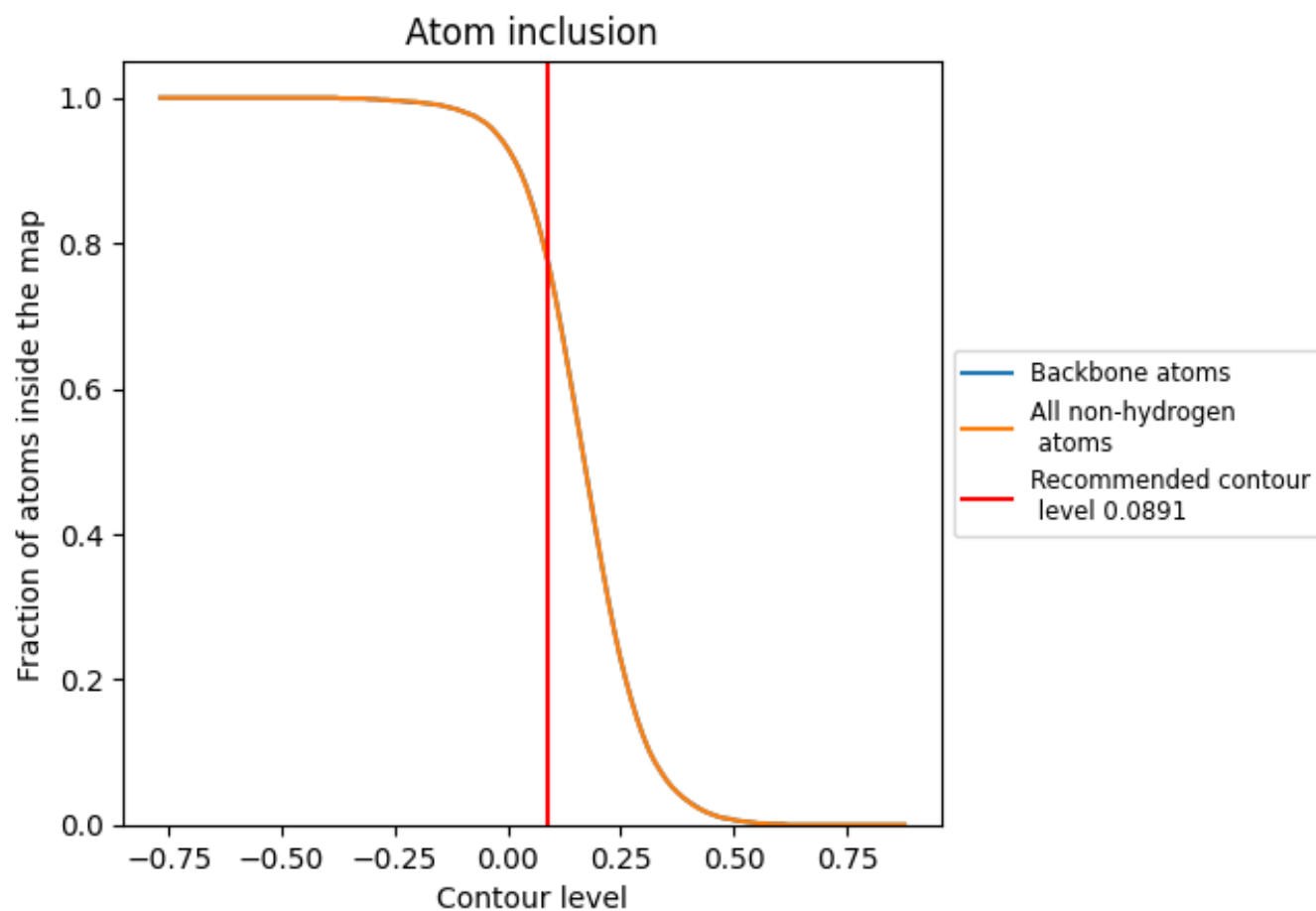
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0891).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0891) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7740	 0.0260
00	 0.6940	 0.0260
01	 0.8320	 0.0420
02	 0.8560	 0.0400
03	 0.7250	 0.0330
04	 0.8890	 0.0470
10	 0.2440	 0.0150
11	 0.4850	 0.0150
12	 0.6710	 0.0220
13	 0.5790	 0.0240
14	 0.2910	 0.0000
15	 0.7150	 0.0220
16	 0.7300	 0.0210
17	 0.5870	 0.0250
40	 0.9960	 0.0240
41	 0.9990	 0.0270
A0	 0.9250	 0.0230
A1	 0.8520	 0.0330
A2	 0.9070	 0.0210
A3	 0.8760	 0.0420
A4	 0.8380	 0.0390
A5	 0.7590	 0.0160
A6	 0.9110	 0.0340
B0	 0.8480	 0.0340
B1	 0.8550	 0.0320
C0	 0.8060	 0.0240
C1	 0.8360	 0.0180
C2	 0.8300	 0.0340
C3	 0.8520	 0.0170
C4	 0.8220	 0.0280
D0	 0.8470	 0.0270
D1	 0.8020	 0.0260
D2	 0.8970	 0.0310
D3	 0.7720	 0.0200
D4	 0.8920	 0.0340



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Chain	Atom inclusion	Q-score
D5	 0.8260	 0.0310
E0	 0.9900	 0.0160
E1	 0.9800	 0.0070
F0	 0.8740	 0.0280
F1	 0.7040	 0.0170
F2	 0.7790	 0.0280
F3	 0.6710	 0.0170
H0	 0.7580	 0.0260
H1	 0.7630	 0.0350
H2	 0.7230	 0.0180
H3	 0.8260	 0.0390
I0	 0.5810	 0.0190
I1	 0.6700	 0.0260
I2	 0.7210	 0.0430
I3	 0.6500	 0.0200
J0	 0.6840	 0.0250
J1	 0.5620	 0.0110
J2	 0.7980	 0.0440
J3	 0.5780	 0.0030
J4	 0.8320	 0.0220
K0	 0.7780	 0.0190
K1	 0.8210	 0.0400
K2	 0.7120	 0.0140
K3	 0.7450	 0.0420
L0	 0.9130	 0.0390
L1	 0.7030	 0.0100
L2	 0.7540	 0.0260
L3	 0.8890	 0.0300
M0	 0.9300	 0.0410
M1	 0.7500	 0.0420
M2	 0.9600	 0.0380
M3	 0.8000	 0.0360
N0	 0.7930	 0.0160
N1	 0.9130	 0.0390
N2	 0.9890	 0.0250
N3	 0.9200	 0.0370
O0	 0.8330	 0.0330
O1	 0.9650	 0.0360
O2	 0.8840	 0.0290
O3	 0.9170	 0.0230
P0	 0.7830	 0.0380
P1	 0.9050	 0.0250

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Chain	Atom inclusion	Q-score
P2	 0.9040	 0.0330
P3	 0.8850	 0.0300
Q0	 0.7680	 0.0330
Q1	 0.8240	 0.0380
Q2	 0.8960	 0.0260
Q3	 0.9450	 0.0330
R0	 0.8850	 0.0290
R1	 0.8770	 0.0250
R2	 0.9450	 0.0280
R3	 0.9440	 0.0240
S0	 0.9310	 0.0410
S1	 0.9470	 0.0360
S2	 0.9460	 0.0200
S3	 0.9570	 0.0410
T0	 0.6370	 -0.0040
T1	 0.1820	 -0.0130
U0	 0.4430	 0.0070
U1	 0.5560	 0.0070
U2	 0.2650	 0.0290
U3	 0.9200	 0.0140
U4	 0.3840	 0.0040
U5	 0.1990	 0.0090
U6	 0.7880	 0.0380
V0	 0.7210	 0.0220
W0	 0.8030	 0.0250