



wwPDB EM Validation Summary Report ⓘ

Nov 24, 2025 – 08:54 pm GMT

PDB ID : 9SOB / pdb_00009sob
EMDB ID : EMD-54657
Title : Structural Model of the Nuclear Pore Complex in Arabidopsis thaliana
Authors : Obarska-Kosinska, A.; Sanchez Carrillo, I.B.; Hoffmann, P.C.; Fourcassie, V.; Beck, M.; Germain, H.
Deposited on : 2025-09-12
Resolution : 35.00 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:

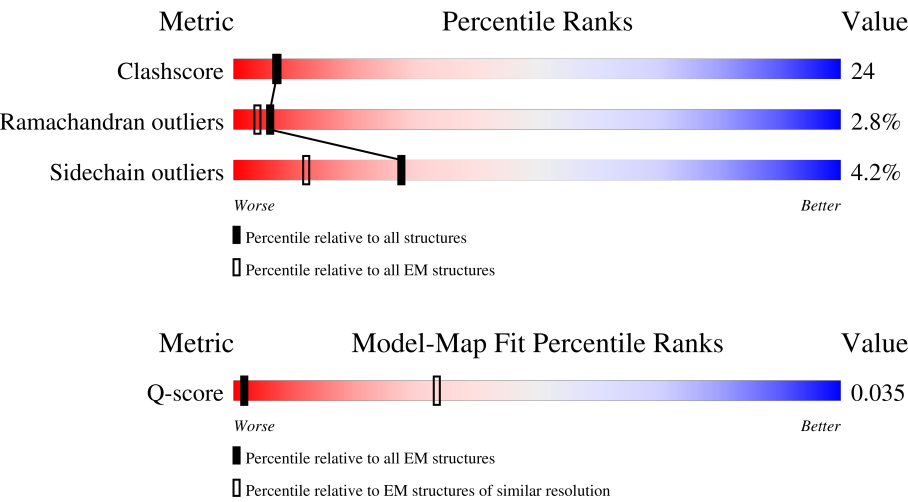
EMDB validation analysis : 0.0.1.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

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 35.00 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	3 (33.00 - 33.00)

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	R	1495	
1	R16	1495	
1	R8	1495	
2	M	704	

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Mol	Chain	Length	Quality of chain
2	M16	704	
2	M8	704	
3	N	302	
3	N16	302	
3	N8	302	
4	T	684	
4	T16	684	
4	T8	684	
5	P	716	
5	P16	716	
5	P8	716	
6	O	326	
6	O16	326	
6	O8	326	
7	Q	361	
7	Q16	361	
7	Q8	361	
8	L	977	
8	L16	977	
8	L8	977	
9	K	709	
9	K16	709	
9	K8	709	
10	C	1838	
10	C16	1838	

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Mol	Chain	Length	Quality of chain
10	C24	1838	
10	C32	1838	
10	C8	1838	
11	A16	860	
11	A24	860	
11	A32	860	
11	A40	860	
12	A	763	
12	A48	763	
13	V	196	
14	W	810	
15	J	185	
16	A8	63	
17	F	28	
17	F16	28	
17	F24	28	
17	F8	28	
18	B	1965	
18	B8	1965	
19	4	447	
19	48	447	
20	E	519	
20	E8	519	
21	H	254	
21	H16	254	

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Mol	Chain	Length	Quality of chain
21	H24	254	
21	H8	254	
22	I	237	
22	I16	237	
22	I24	237	
22	I8	237	
23	J16	197	
23	J24	197	
23	J32	197	
23	J8	197	
24	D	1464	
24	D16	1464	
24	D24	1464	
24	D32	1464	
24	D40	1464	
24	D8	1464	

2 Entry composition

There are 24 unique types of molecules in this entry. The entry contains 402561 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 Nuclear pore complex protein NUP160.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	1464	Total	C	N	O	S	0	0
			11593	7388	1952	2188	65		
1	R8	1464	Total	C	N	O	S	0	0
			11593	7388	1952	2188	65		
1	R16	1464	Total	C	N	O	S	0	0
			11593	7388	1952	2188	65		

- Molecule 2 is a protein called Nuclear pore complex protein NUP96.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	M	696	Total	C	N	O	S	0	0
			5598	3577	939	1054	28		
2	M8	696	Total	C	N	O	S	0	0
			5598	3577	939	1054	28		
2	M16	696	Total	C	N	O	S	0	0
			5598	3577	939	1054	28		

- Molecule 3 is a protein called Protein transport protein SEC13 homolog B.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	N	302	Total	C	N	O	S	0	0
			2302	1451	398	444	9		
3	N8	302	Total	C	N	O	S	0	0
			2302	1451	398	444	9		
3	N16	302	Total	C	N	O	S	0	0
			2302	1451	398	444	9		

- Molecule 4 is a protein called E3 ubiquitin-protein ligase HOS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	T	684	Total	C	N	O	S	0	0
			5498	3453	960	1049	36		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	T8	684	Total	C	N	O	S	0	0
			5498	3453	960	1049	36		
4	T16	684	Total	C	N	O	S	0	0
			5498	3453	960	1049	36		

- Molecule 5 is a protein called Nuclear pore complex protein NUP85.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	P	708	Total	C	N	O	S	0	0
			5620	3572	974	1041	33		
5	P8	708	Total	C	N	O	S	0	0
			5620	3572	974	1041	33		
5	P16	708	Total	C	N	O	S	0	0
			5620	3572	974	1041	33		

- Molecule 6 is a protein called Protein SEH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	O	303	Total	C	N	O	S	0	0
			2336	1467	387	468	14		
6	O8	303	Total	C	N	O	S	0	0
			2336	1467	387	468	14		
6	O16	303	Total	C	N	O	S	0	0
			2336	1467	387	468	14		

- Molecule 7 is a protein called Nuclear pore complex protein NUP43.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Q	361	Total	C	N	O	S	0	0
			2770	1732	480	546	12		
7	Q8	361	Total	C	N	O	S	0	0
			2770	1732	480	546	12		
7	Q16	361	Total	C	N	O	S	0	0
			2770	1732	480	546	12		

- Molecule 8 is a protein called Nuclear pore complex protein NUP107.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	974	Total	C	N	O	S	0	0
			7770	4912	1322	1481	55		
8	L8	974	Total	C	N	O	S	0	0
			7770	4912	1322	1481	55		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	L16	974	Total	C	N	O	S	0	0
			7770	4912	1322	1481	55		

- Molecule 9 is a protein called Nuclear pore complex protein NUP133.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	705	Total	C	N	O	S	0	0
			5695	3569	992	1104	30		
9	K8	705	Total	C	N	O	S	0	0
			5695	3569	992	1104	30		
9	K16	705	Total	C	N	O	S	0	0
			5696	3569	992	1105	30		

- Molecule 10 is a protein called Nuclear pore complex protein NUP205.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C16	1838	Total	C	N	O	S	0	0
			14529	9239	2457	2763	70		
10	C24	1838	Total	C	N	O	S	0	0
			14529	9239	2457	2763	70		
10	C	1824	Total	C	N	O	S	0	0
			14402	9155	2437	2740	70		
10	C8	1793	Total	C	N	O	S	0	0
			14177	9023	2397	2687	70		
10	C32	1838	Total	C	N	O	S	0	0
			14529	9239	2457	2763	70		

- Molecule 11 is a protein called Nuclear pore complex protein NUP93A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A24	818	Total	C	N	O	S	0	0
			6472	4058	1154	1227	33		
11	A40	818	Total	C	N	O	S	0	0
			6472	4058	1154	1227	33		
11	A16	818	Total	C	N	O	S	0	0
			6472	4058	1154	1227	33		
11	A32	818	Total	C	N	O	S	0	0
			6472	4058	1154	1227	33		

- Molecule 12 is a protein called Nuclear pore complex protein NUP93A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	A	723	Total	C	N	O	S	0	0
			5726	3594	1023	1078	31		
12	A48	726	Total	C	N	O	S	0	0
			5752	3612	1026	1083	31		

- Molecule 13 is a protein called Nuclear pore complex protein NUP214.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	V	196	Total	C	N	O	S	0	0
			1590	987	289	304	10		

- Molecule 14 is a protein called Nuclear pore complex protein NUP88.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	W	787	Total	C	N	O	S	0	0
			6141	3886	1047	1185	23		

- Molecule 15 is a protein called Nuclear pore complex protein NUP62.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	185	Total	C	N	O	S	0	0
			1504	923	266	310	5		

- Molecule 16 is a protein called Nuclear pore complex protein NUP93A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	A8	63	Total	C	N	O	S	0	0
			523	326	90	102	5		

- Molecule 17 is a protein called Nuclear pore complex protein NUP35.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	F8	28	Total	C	N	O	S	0	0
			213	133	31	48	1		
17	F	28	Total	C	N	O	S	0	0
			213	133	31	48	1		
17	F24	28	Total	C	N	O	S	0	0
			213	133	31	48	1		
17	F16	28	Total	C	N	O	S	0	0
			213	133	31	48	1		

- Molecule 18 is a protein called Nucleoporin (DUF3414).

Mol	Chain	Residues	Atoms					AltConf	Trace
18	B	1965	Total	C	N	O	S	0	0
			15417	9887	2528	2913	89		
18	B8	1965	Total	C	N	O	S	0	0
			15417	9887	2528	2913	89		

- Molecule 19 is a protein called Aladin.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	4	447	Total	C	N	O	S	0	0
			3413	2155	583	659	16		
19	48	447	Total	C	N	O	S	0	0
			3413	2155	583	659	16		

- Molecule 20 is a protein called Nucleoporin protein Ndc1-Nup protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	E	519	Total	C	N	O	S	0	0
			4057	2648	667	727	15		
20	E8	519	Total	C	N	O	S	0	0
			4057	2648	667	727	15		

- Molecule 21 is a protein called Nuclear pore complex protein NUP54.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	H	254	Total	C	N	O	S	0	0
			2023	1254	366	392	11		
21	H8	254	Total	C	N	O	S	0	0
			2023	1254	366	392	11		
21	H24	254	Total	C	N	O	S	0	0
			2023	1254	366	392	11		
21	H16	254	Total	C	N	O	S	0	0
			2023	1254	366	392	11		

- Molecule 22 is a protein called NUP58.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	I	237	Total	C	N	O	S	0	0
			1939	1219	351	359	10		
22	I8	237	Total	C	N	O	S	0	0
			1939	1219	351	359	10		
22	I24	237	Total	C	N	O	S	0	0
			1939	1219	351	359	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
22	I16	237	Total	C	N	O	S	0	0
			1939	1219	351	359	10		

- Molecule 23 is a protein called Nuclear pore complex protein NUP62.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	J32	197	Total	C	N	O	S	0	0
			1601	983	284	327	7		
23	J8	197	Total	C	N	O	S	0	0
			1601	983	284	327	7		
23	J24	197	Total	C	N	O	S	0	0
			1601	983	284	327	7		
23	J16	197	Total	C	N	O	S	0	0
			1601	983	284	327	7		

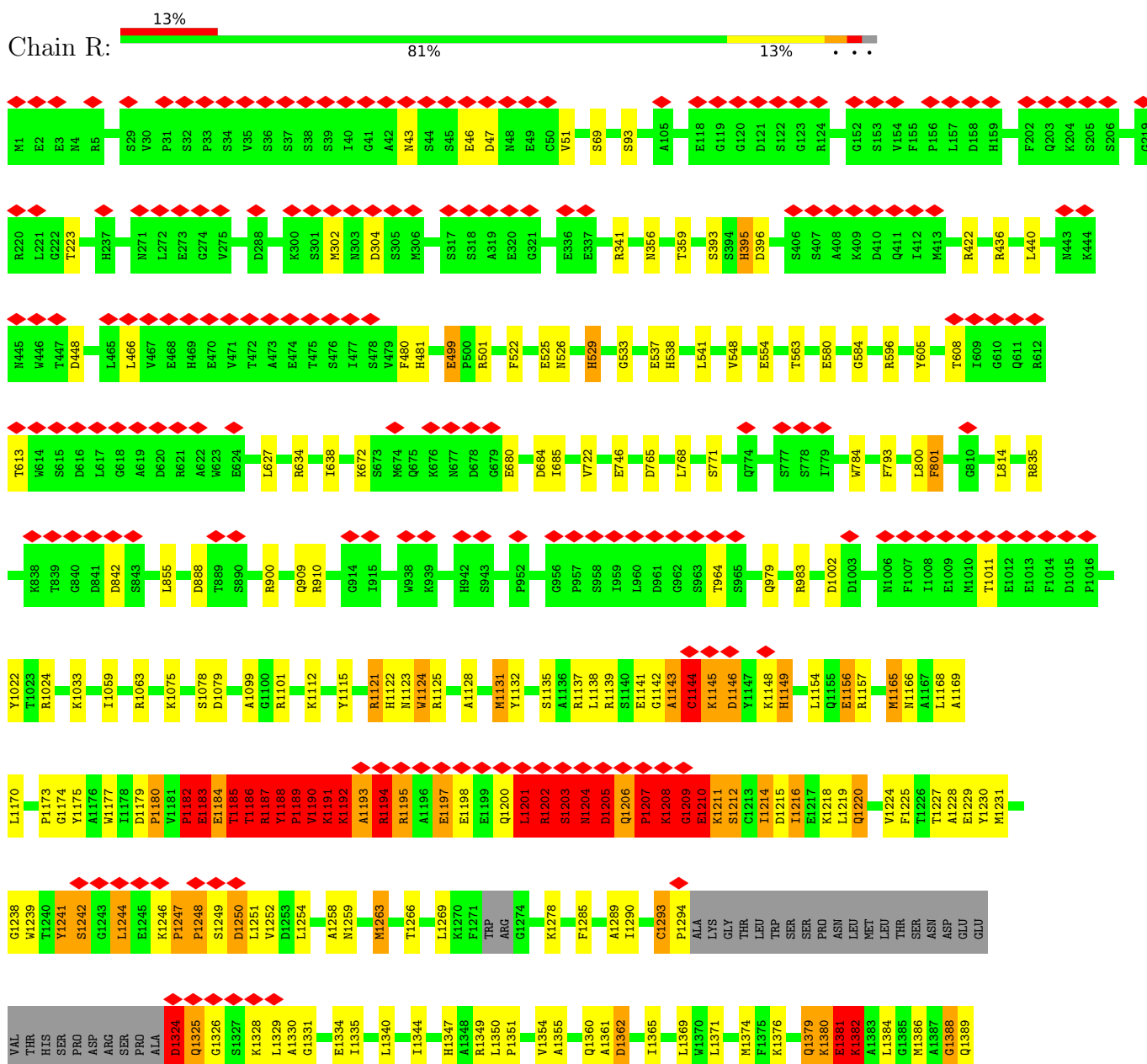
- Molecule 24 is a protein called Nuclear pore complex protein NUP155.

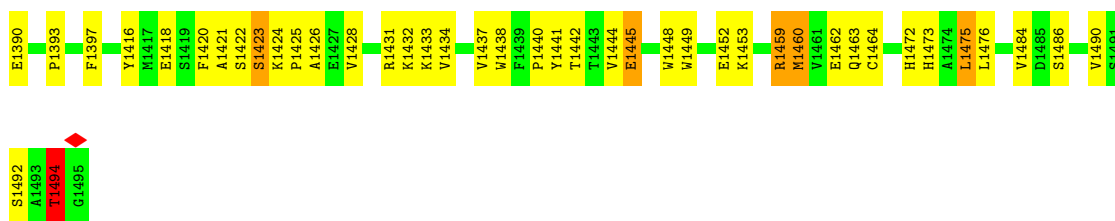
Mol	Chain	Residues	Atoms					AltConf	Trace
24	D	1453	Total	C	N	O	S	0	0
			11141	6950	1960	2168	63		
24	D8	1453	Total	C	N	O	S	0	0
			11141	6950	1960	2168	63		
24	D16	1453	Total	C	N	O	S	0	0
			11141	6950	1960	2168	63		
24	D24	1453	Total	C	N	O	S	0	0
			11141	6950	1960	2168	63		
24	D32	1453	Total	C	N	O	S	0	0
			11141	6950	1960	2168	63		
24	D40	1453	Total	C	N	O	S	0	0
			11141	6950	1960	2168	63		

3 Residue-property plots

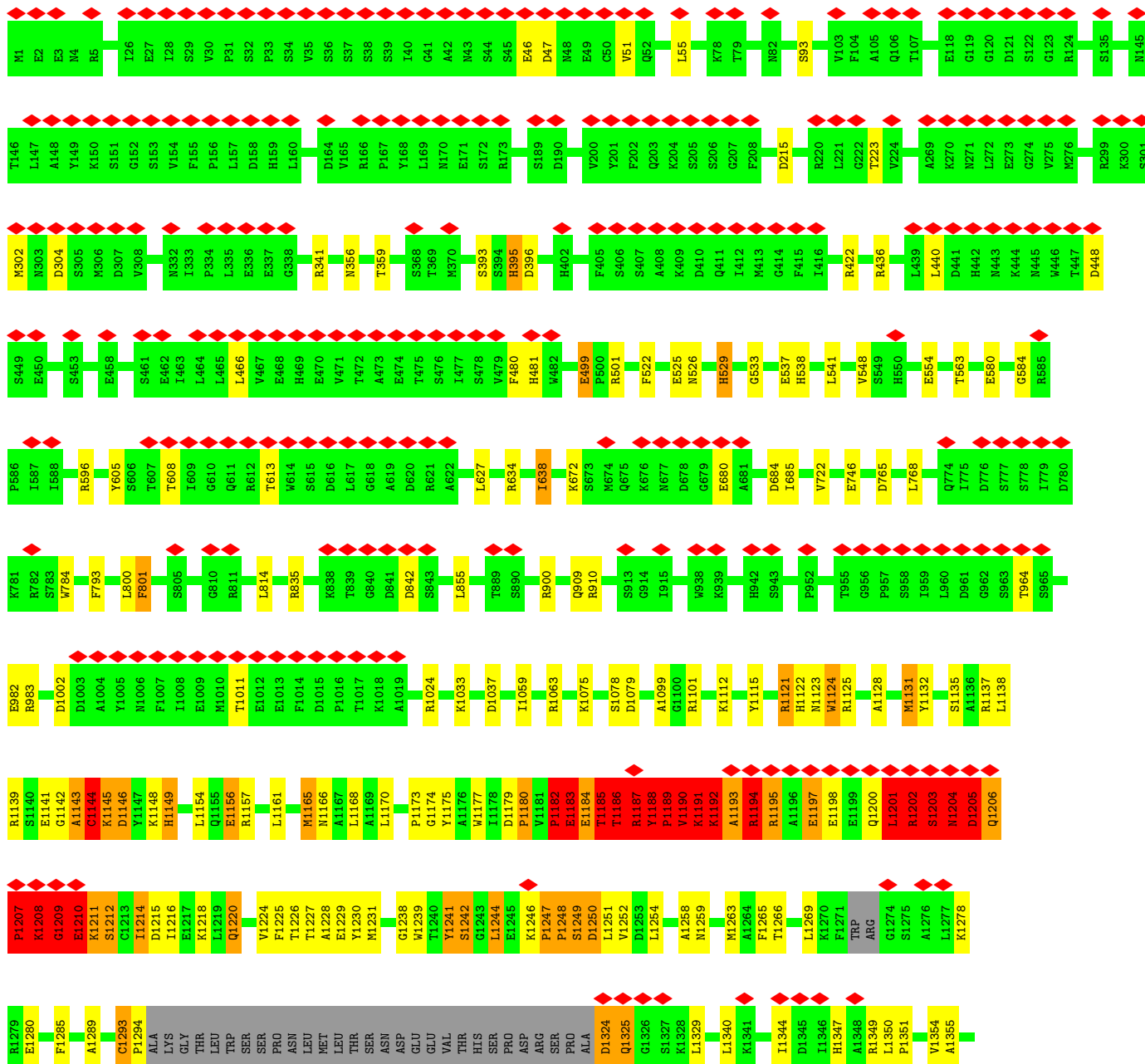
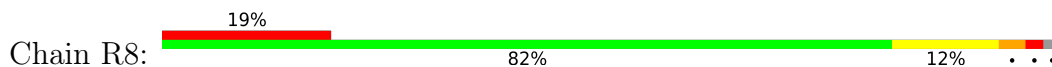
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

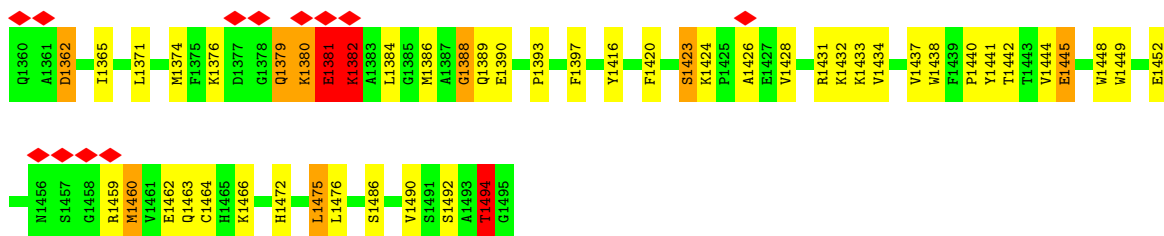
- Molecule 1: Nuclear pore complex protein NUP160



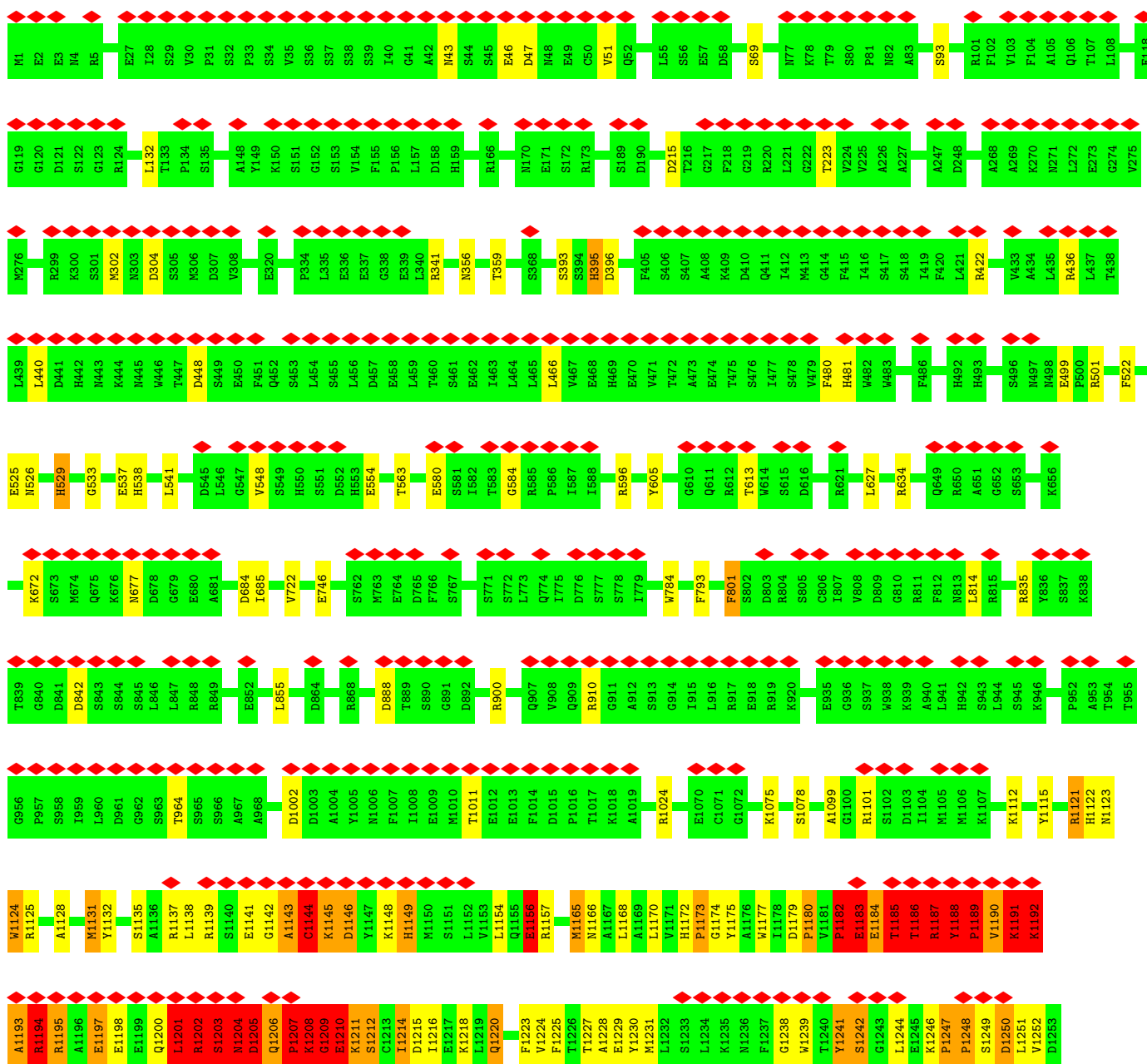
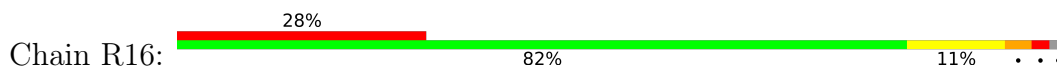


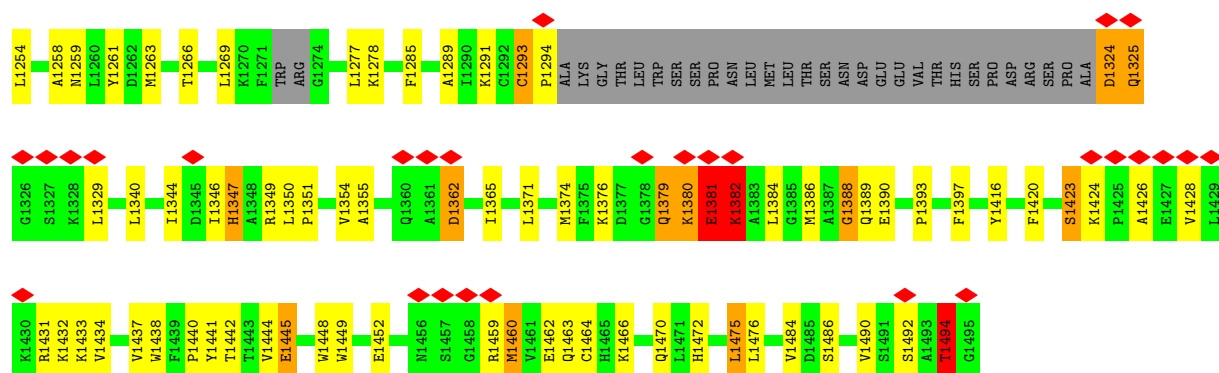
• Molecule 1: Nuclear pore complex protein NUP160



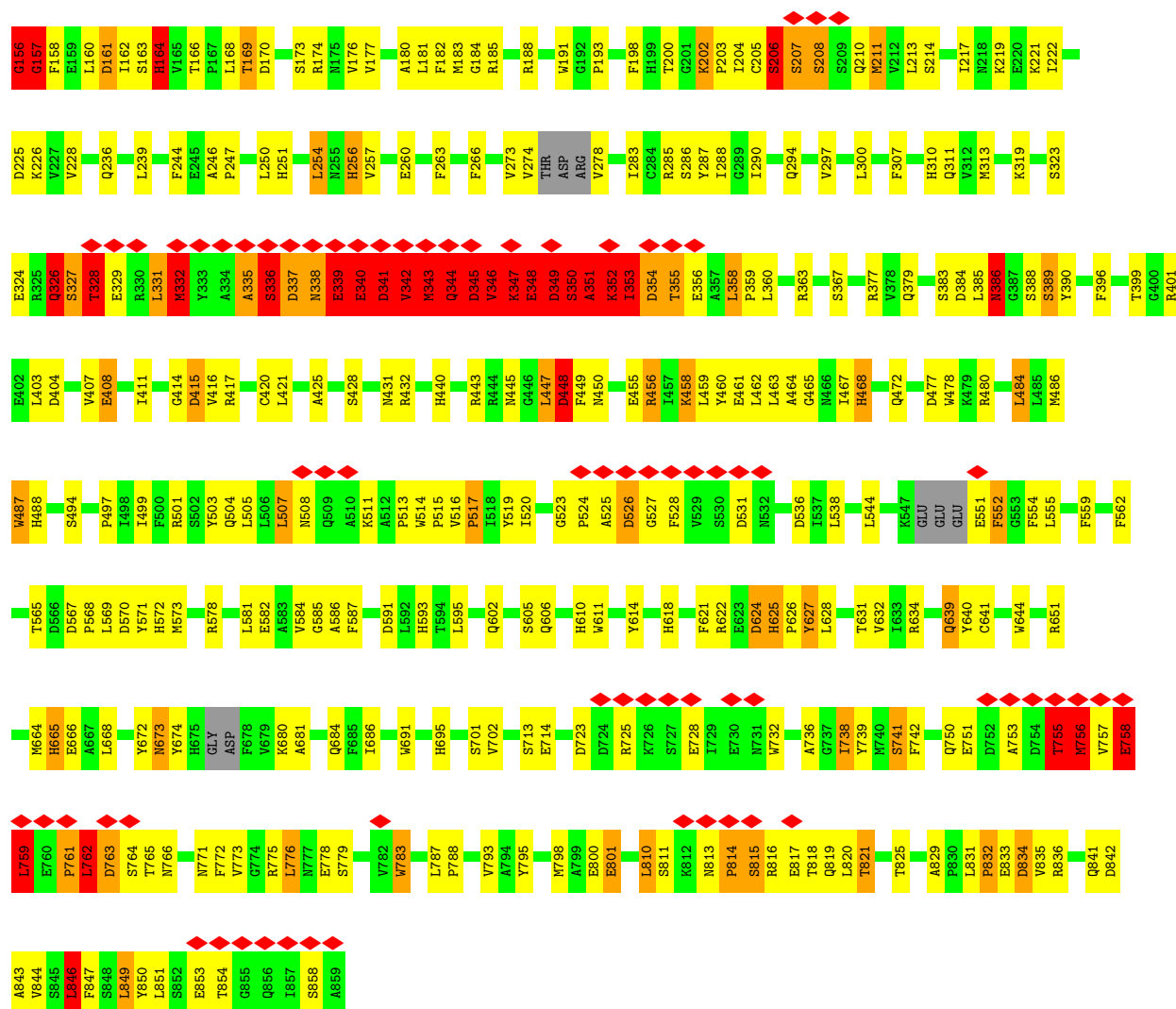


• Molecule 1: Nuclear pore complex protein NUP160



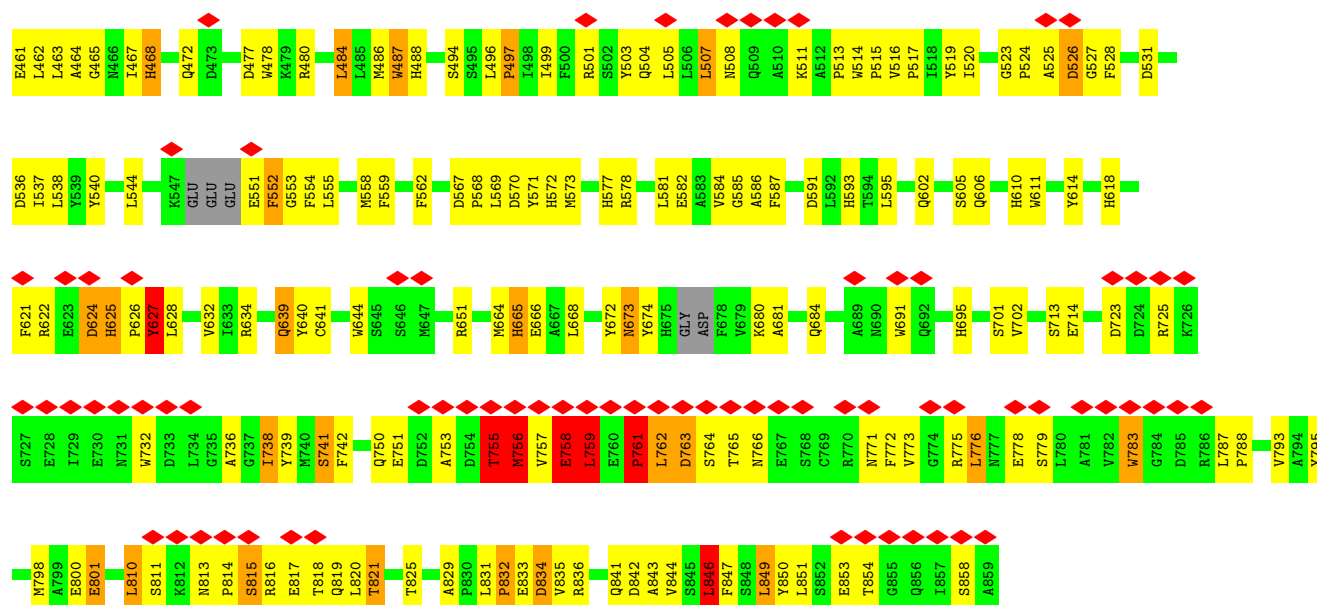


• Molecule 2: Nuclear pore complex protein NUP96



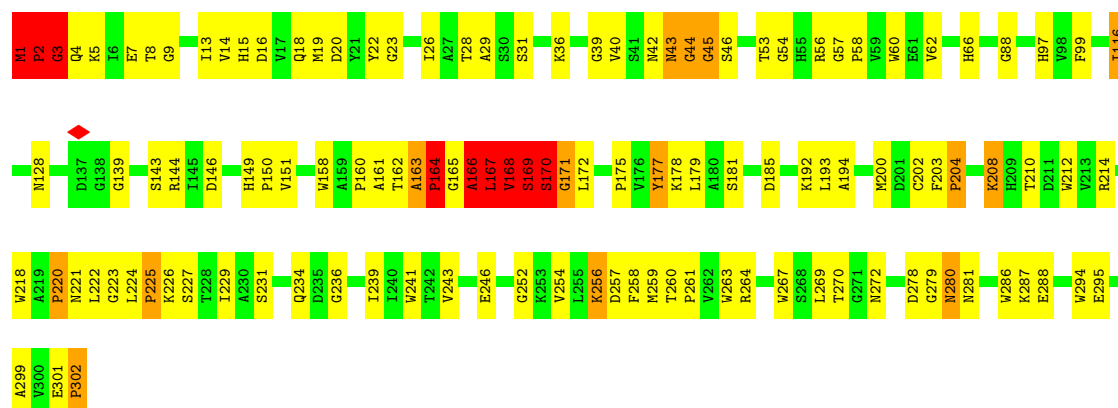
• Molecule 2: Nuclear pore complex protein NUP96





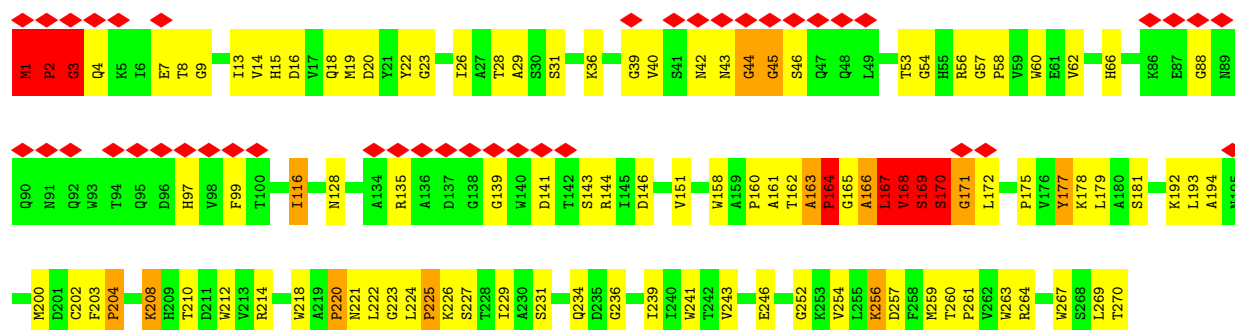
• Molecule 3: Protein transport protein SEC13 homolog B

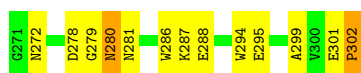
Chain N: 59% 33% 5% .



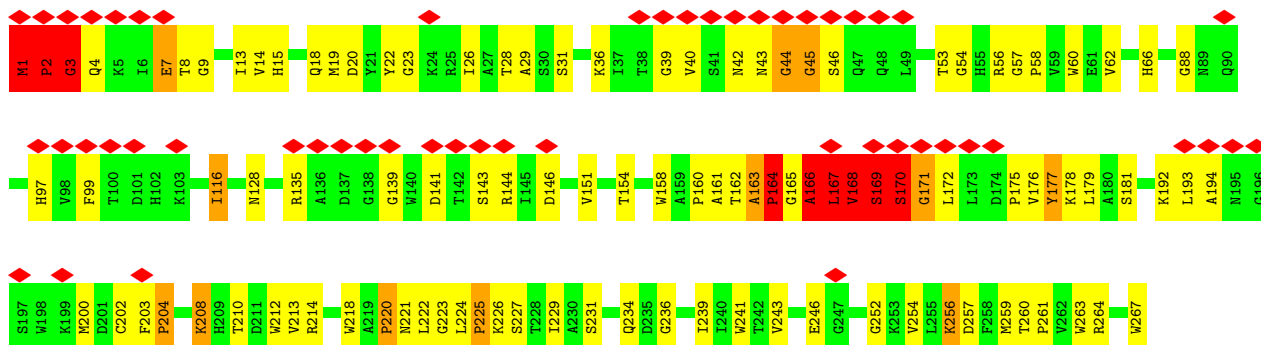
• Molecule 3: Protein transport protein SEC13 homolog B

Chain N8: 14% 60% 32% 5% .

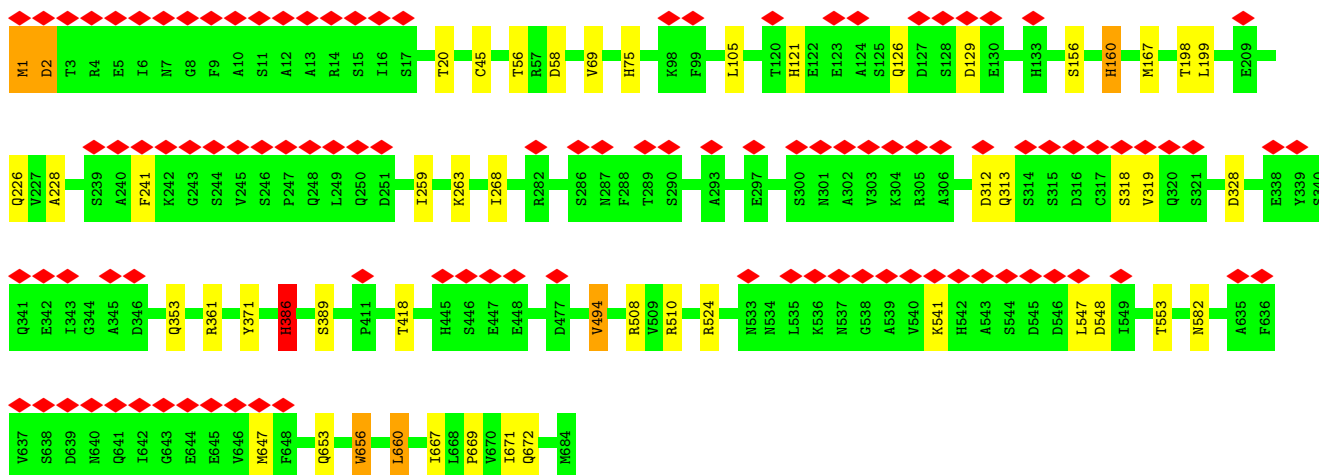




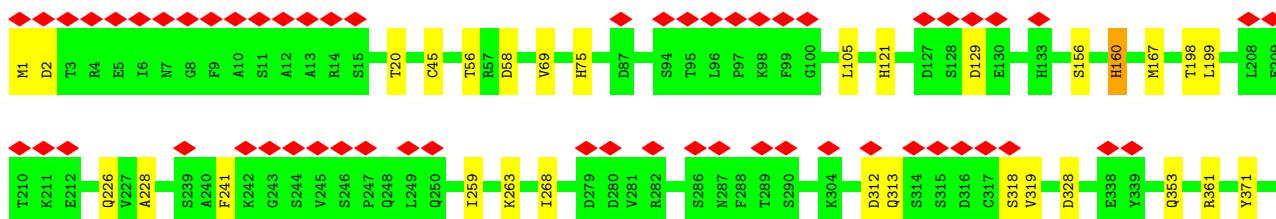
• Molecule 3: Protein transport protein SEC13 homolog B

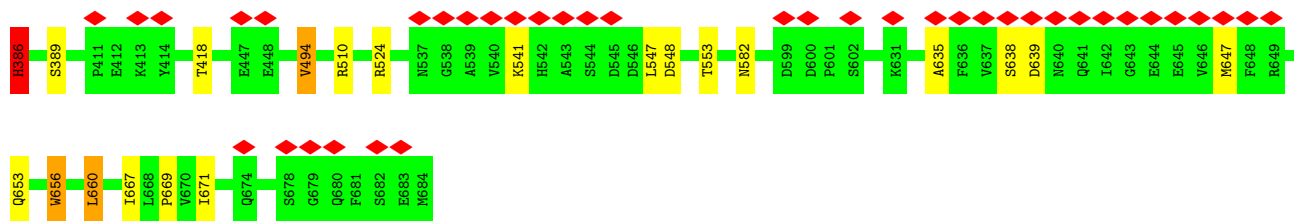


• Molecule 4: E3 ubiquitin-protein ligase HOS1

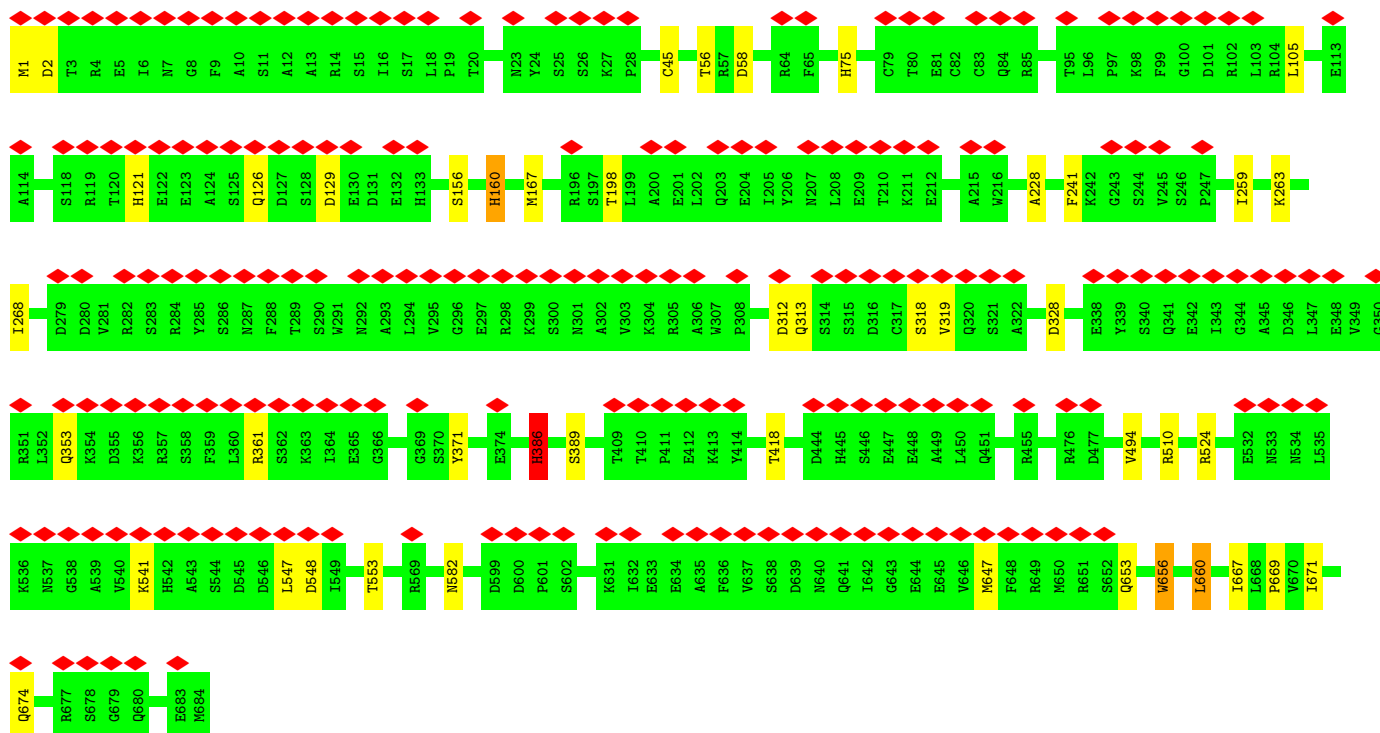


• Molecule 4: E3 ubiquitin-protein ligase HOS1

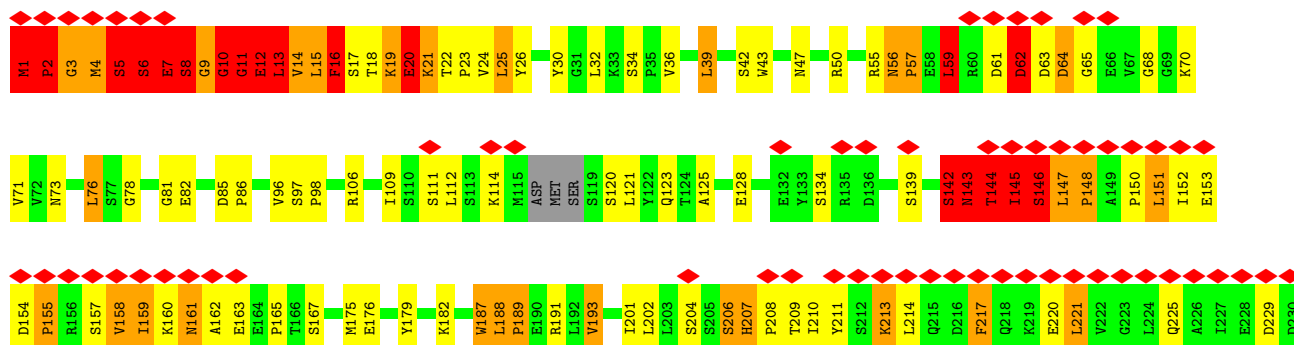


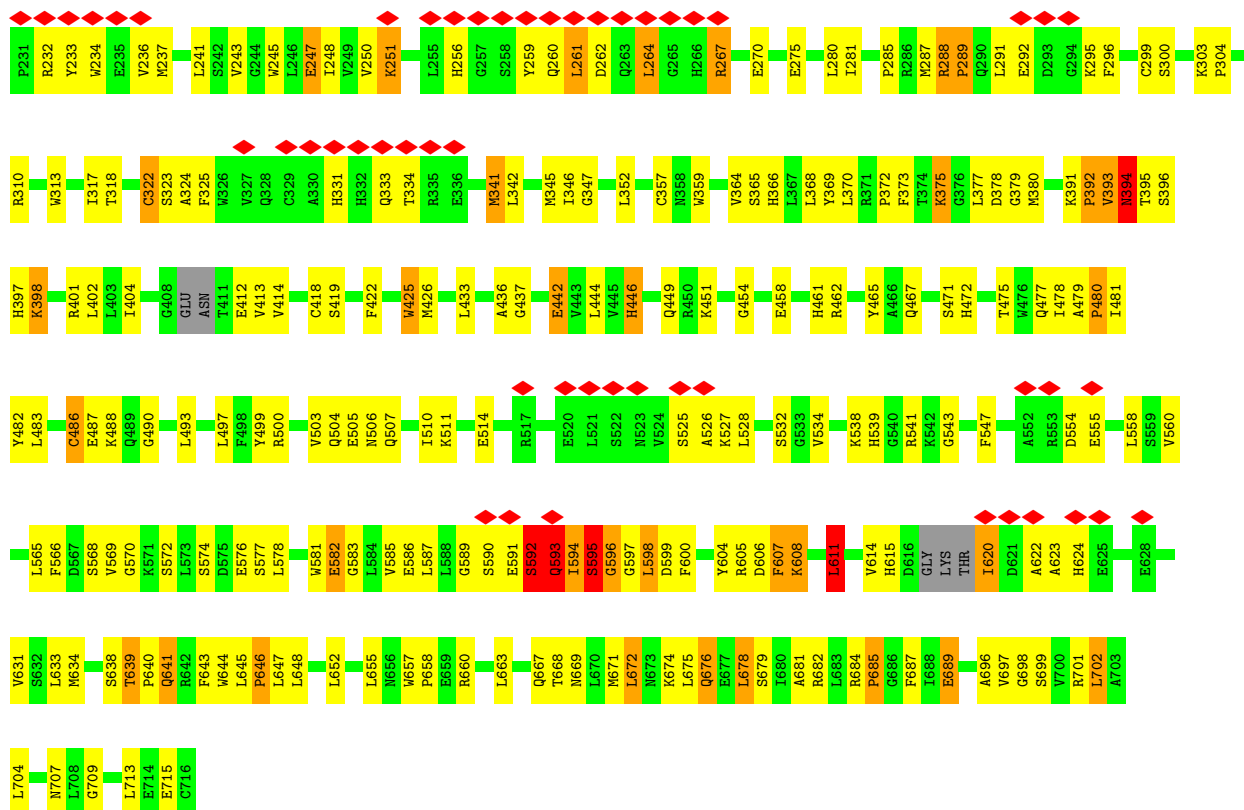


• Molecule 4: E3 ubiquitin-protein ligase HOS1

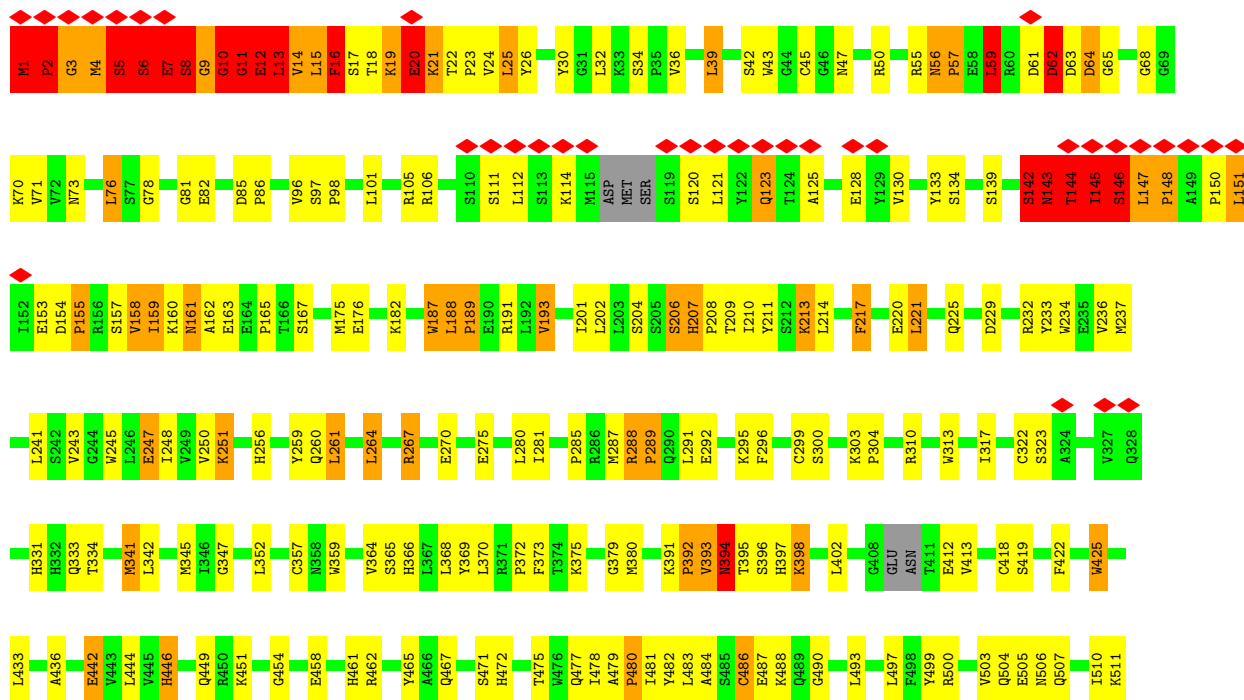


• Molecule 5: Nuclear pore complex protein NUP85





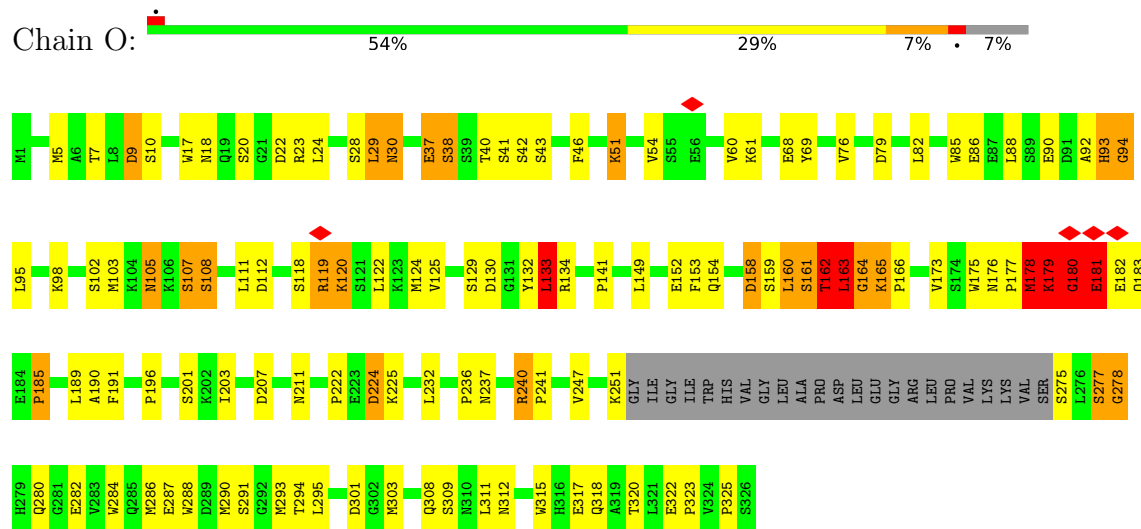
• Molecule 5: Nuclear pore complex protein NUP85



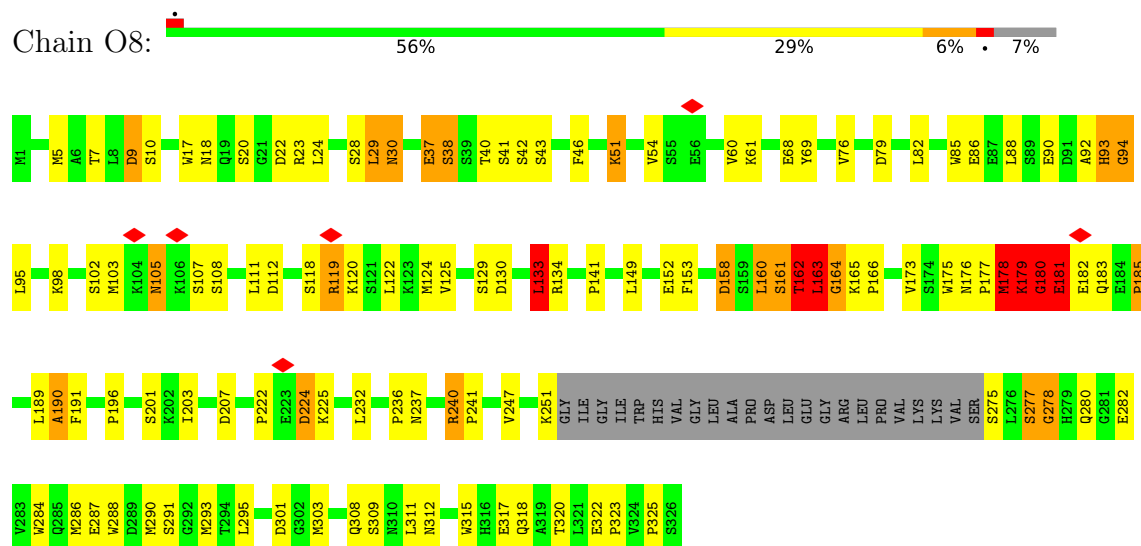


Chain P16: 

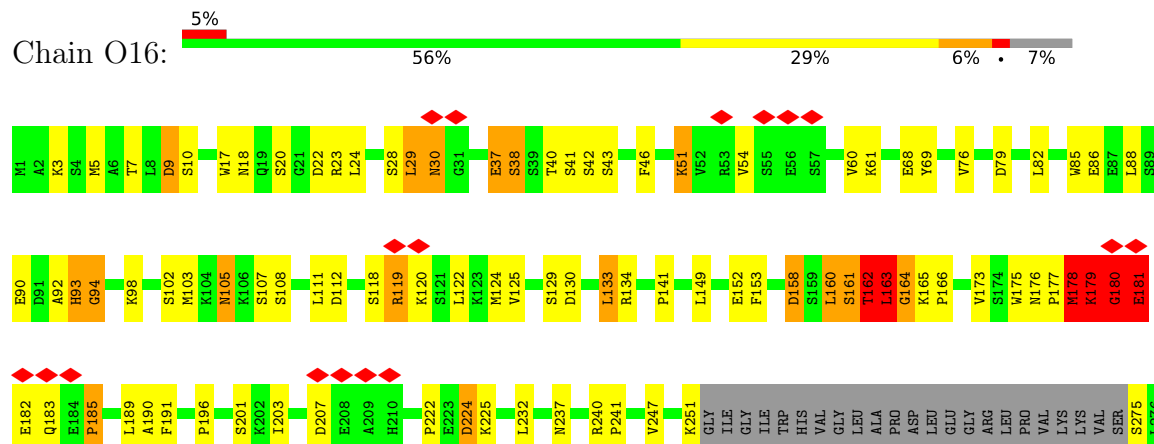
• Molecule 6: Protein SEH1

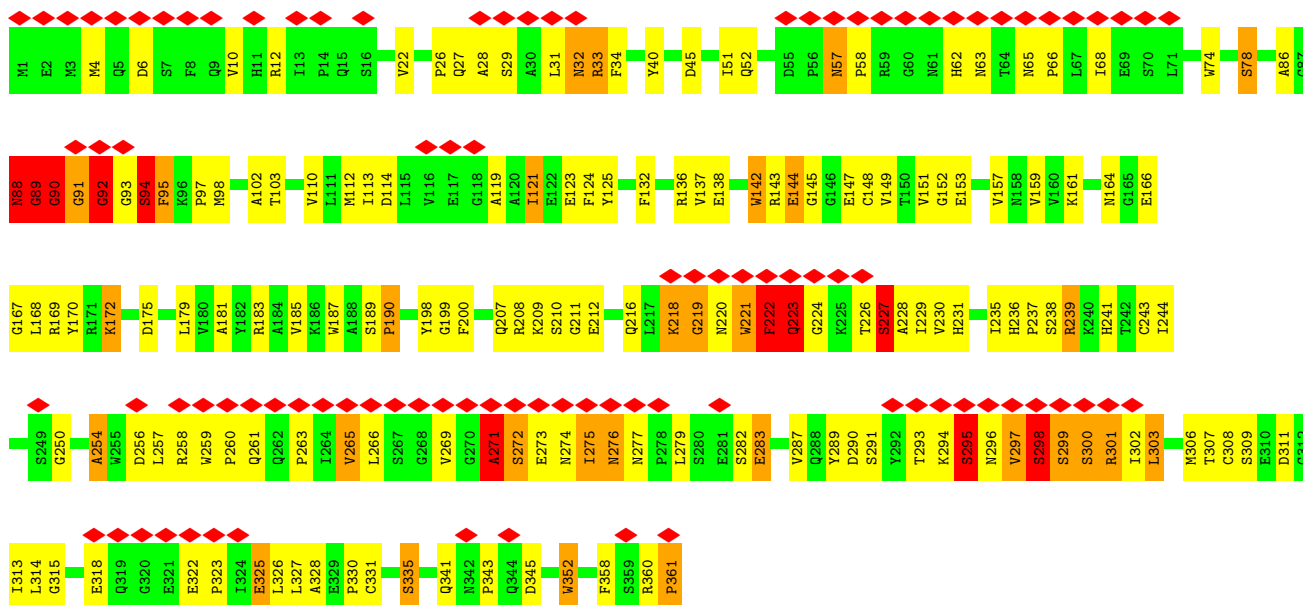


• Molecule 6: Protein SEH1

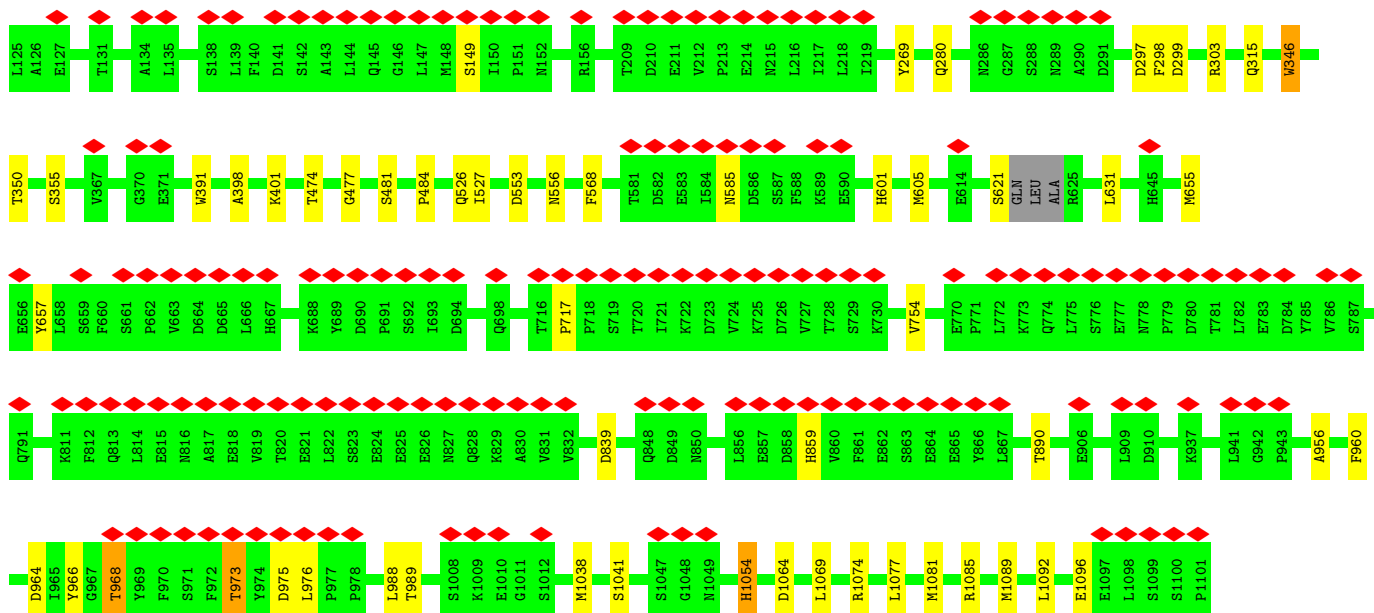


• Molecule 6: Protein SEH1

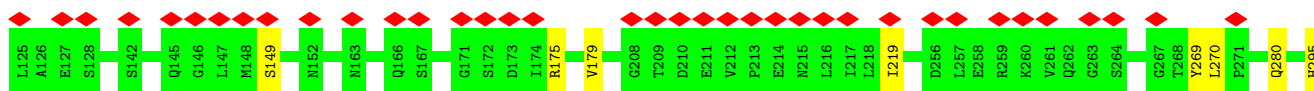
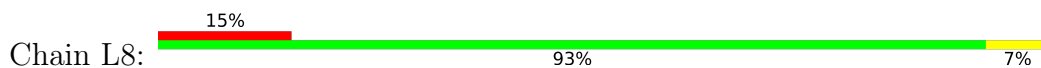


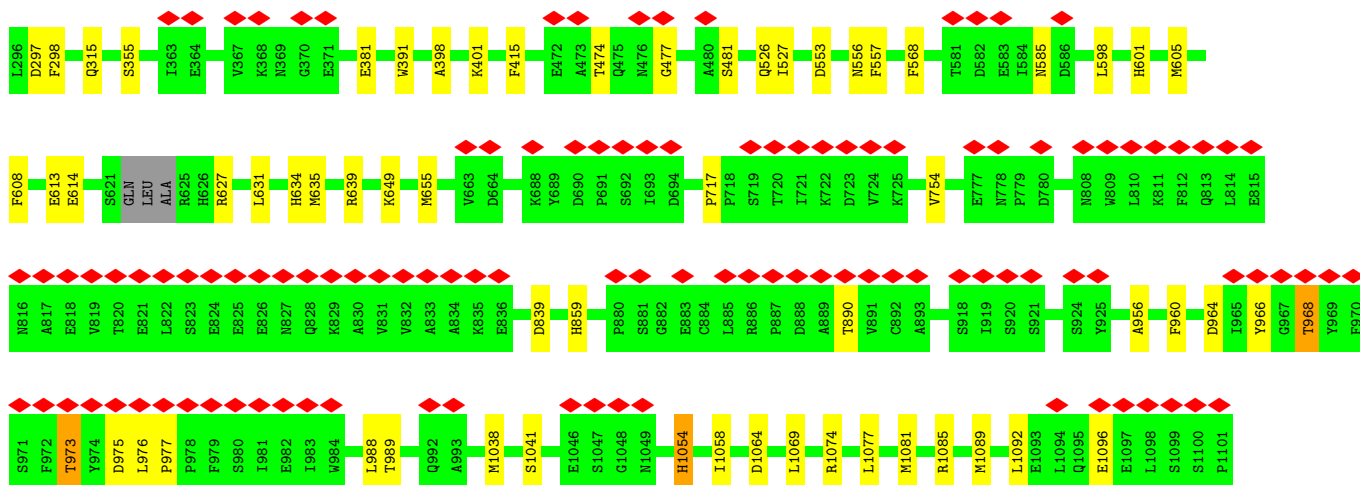


• Molecule 8: Nuclear pore complex protein NUP107

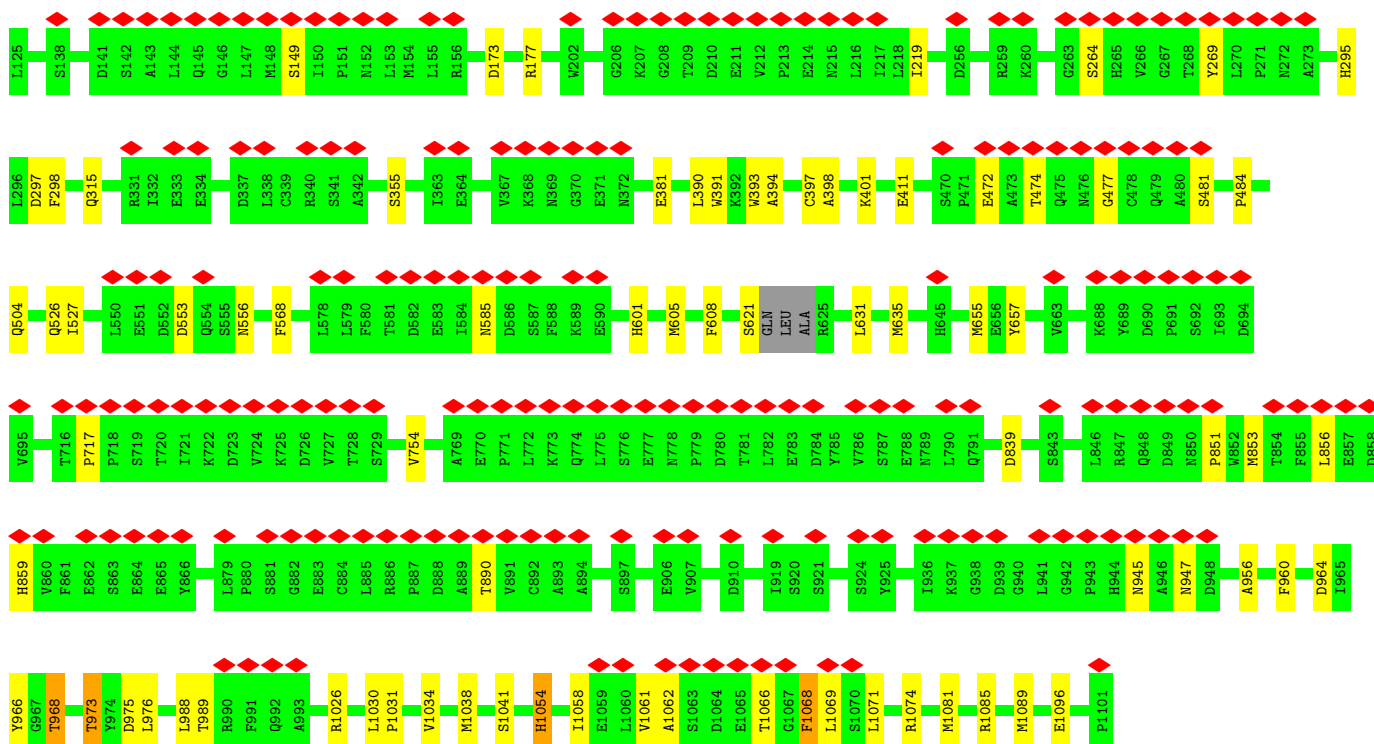


• Molecule 8: Nuclear pore complex protein NUP107

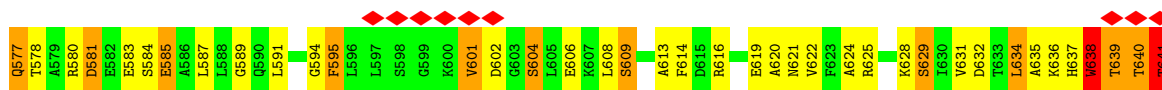


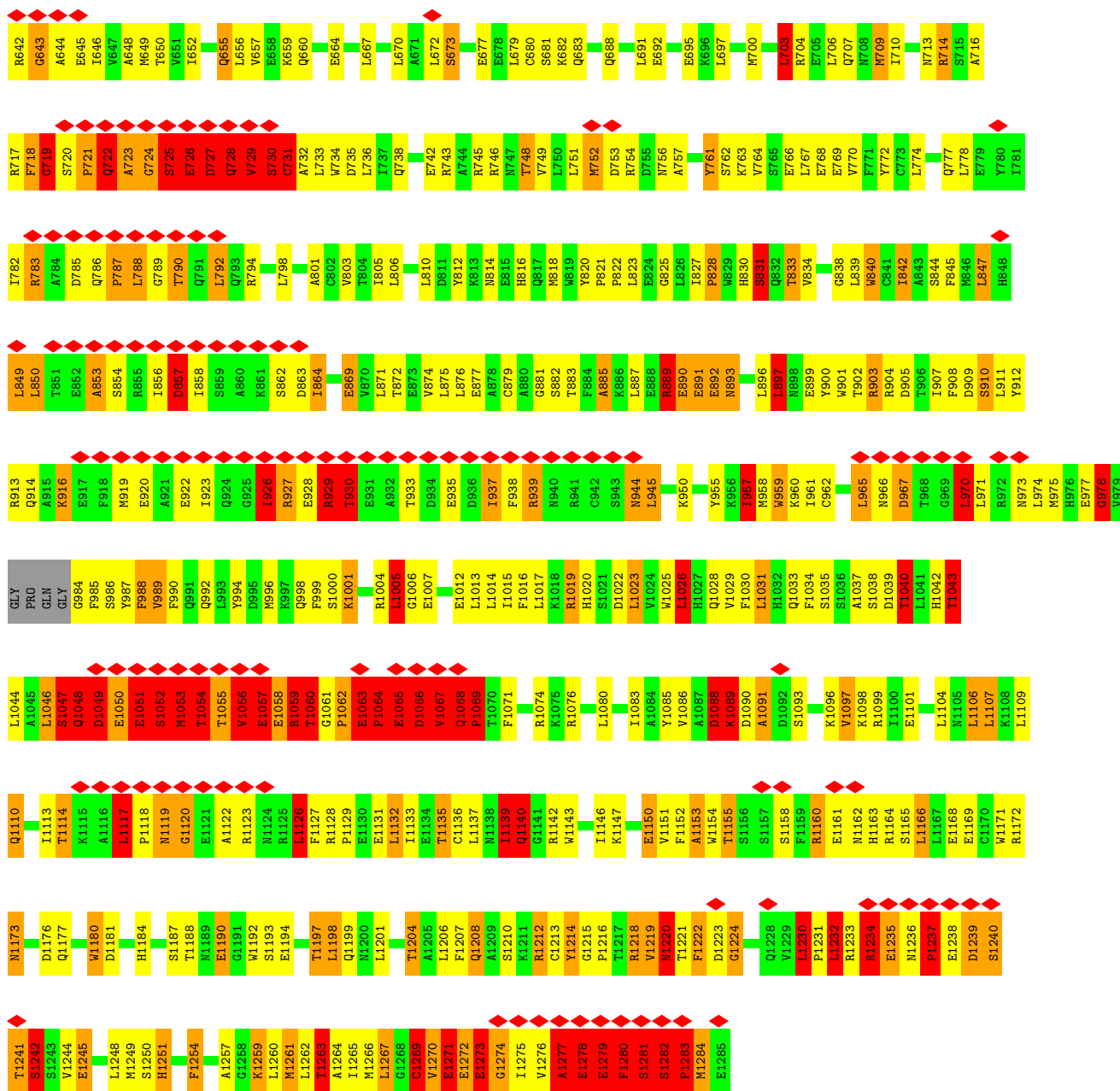


• Molecule 8: Nuclear pore complex protein NUP107



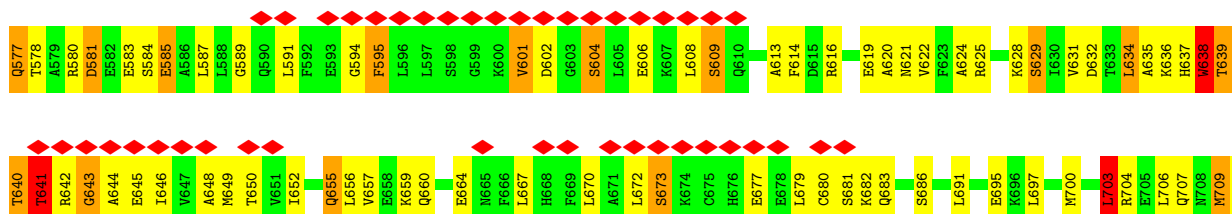
• Molecule 9: Nuclear pore complex protein NUP133

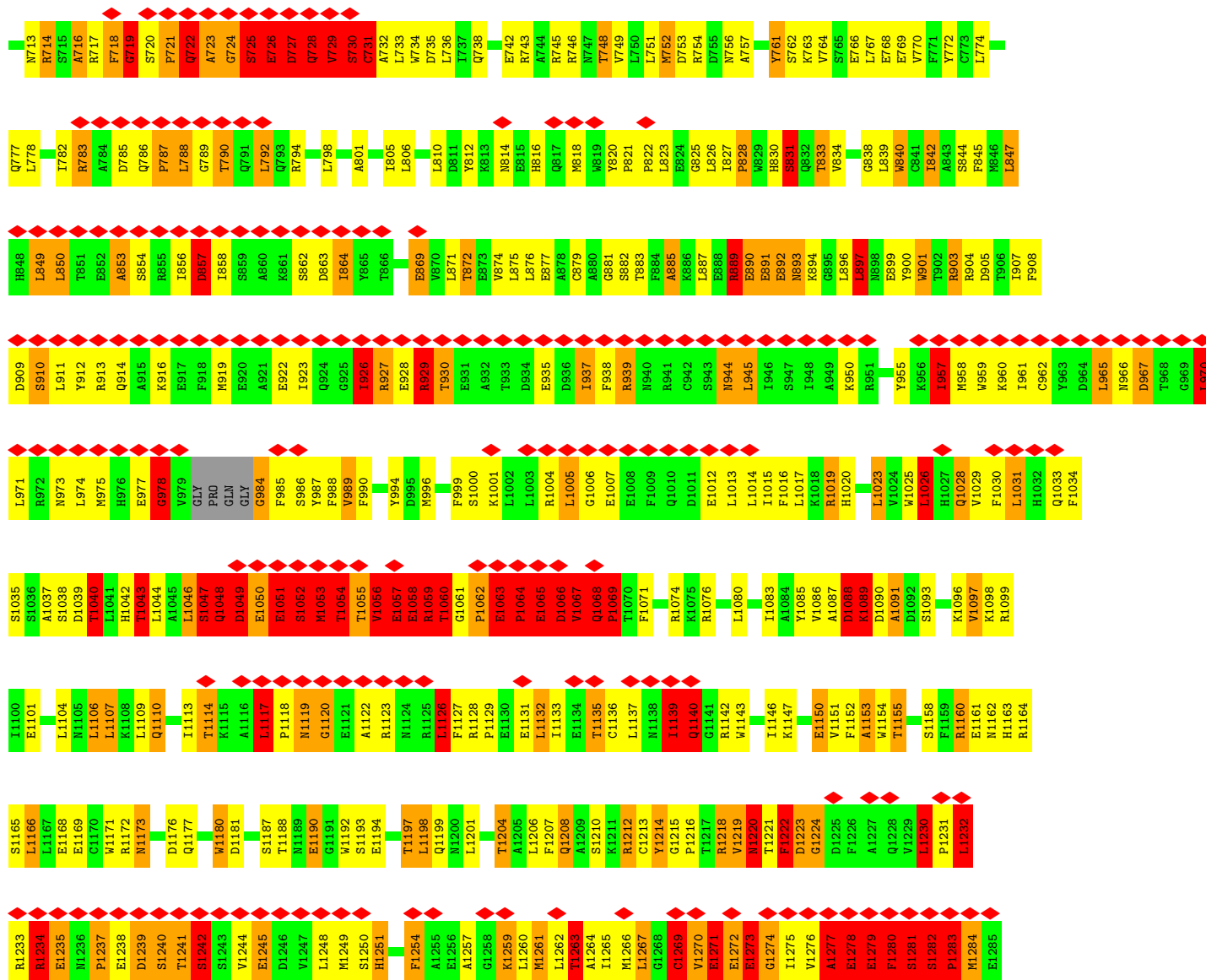


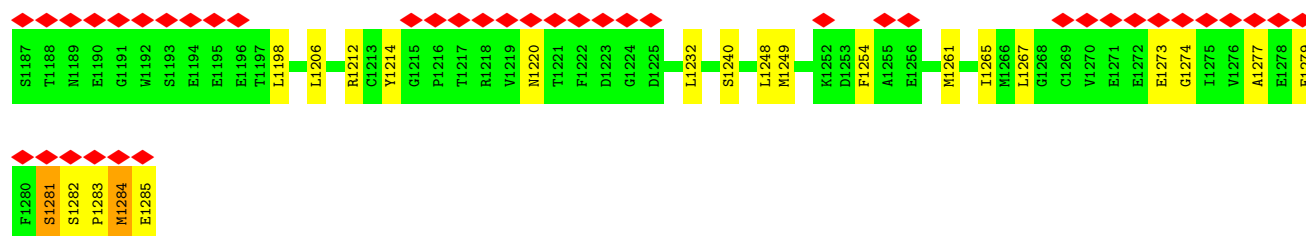


• Molecule 9: Nuclear pore complex protein NUP133

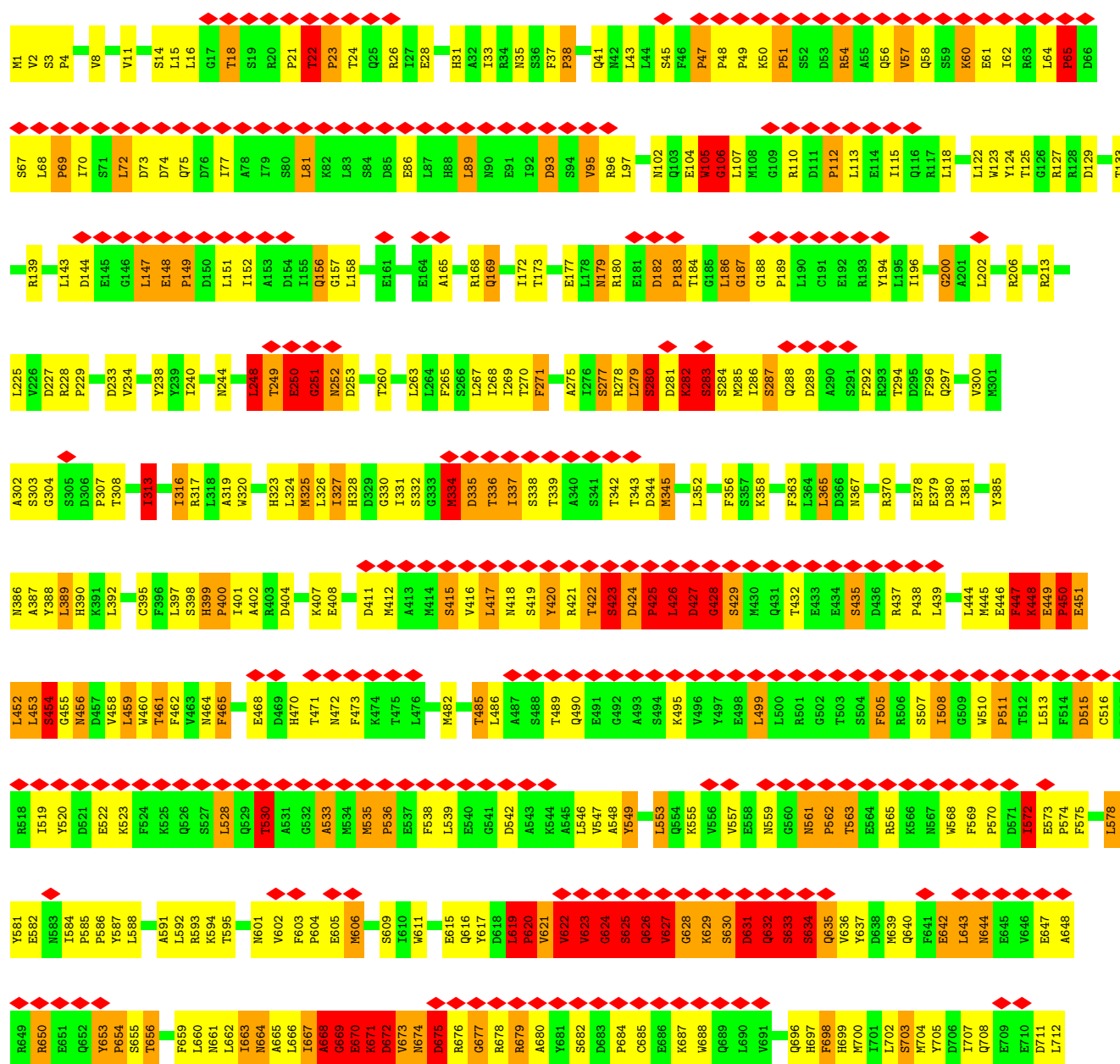
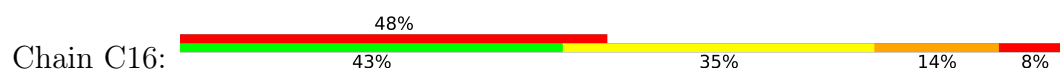
Chain K8: 36% 36% 38% 16% 9%.



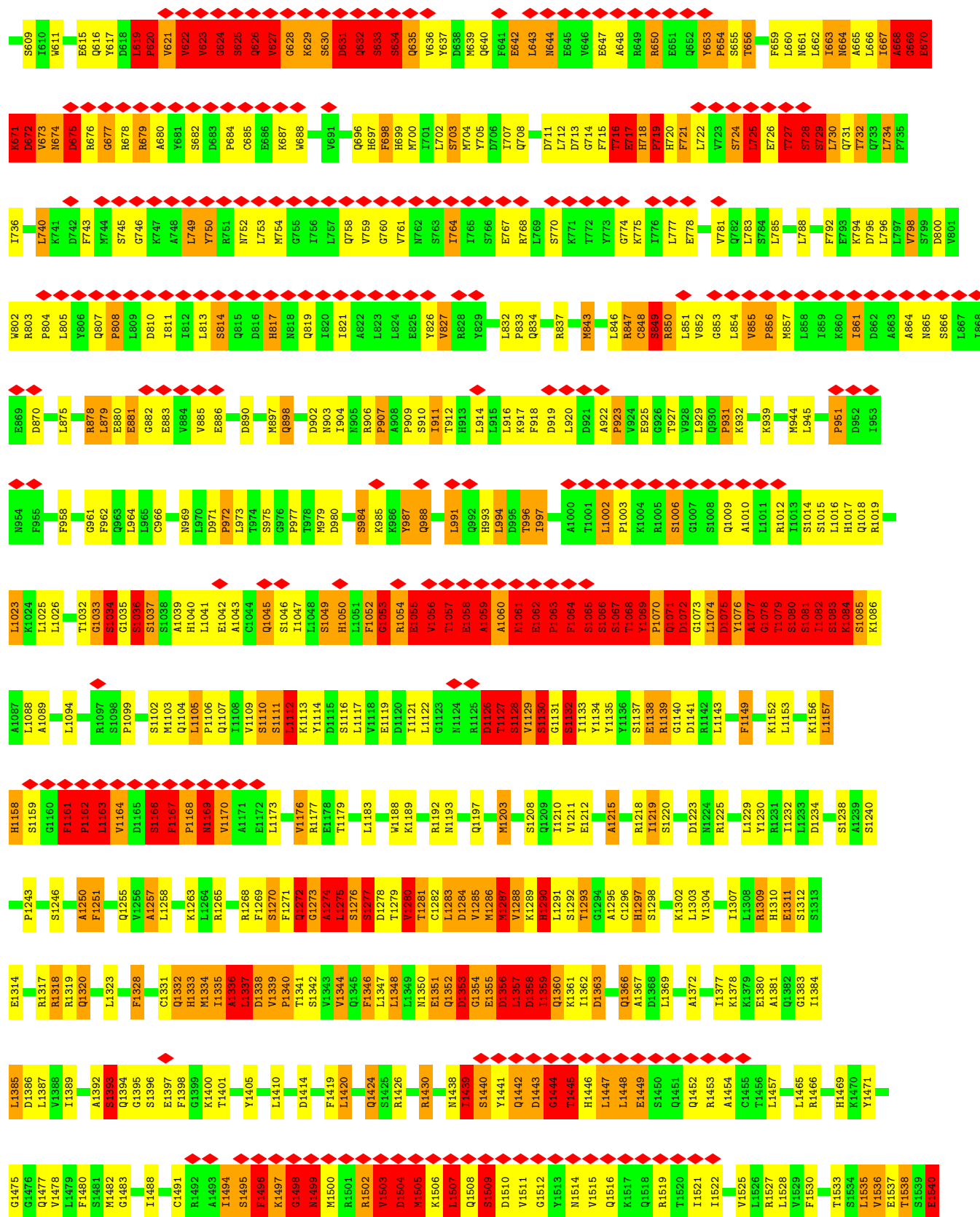




• Molecule 10: Nuclear pore complex protein NUP205



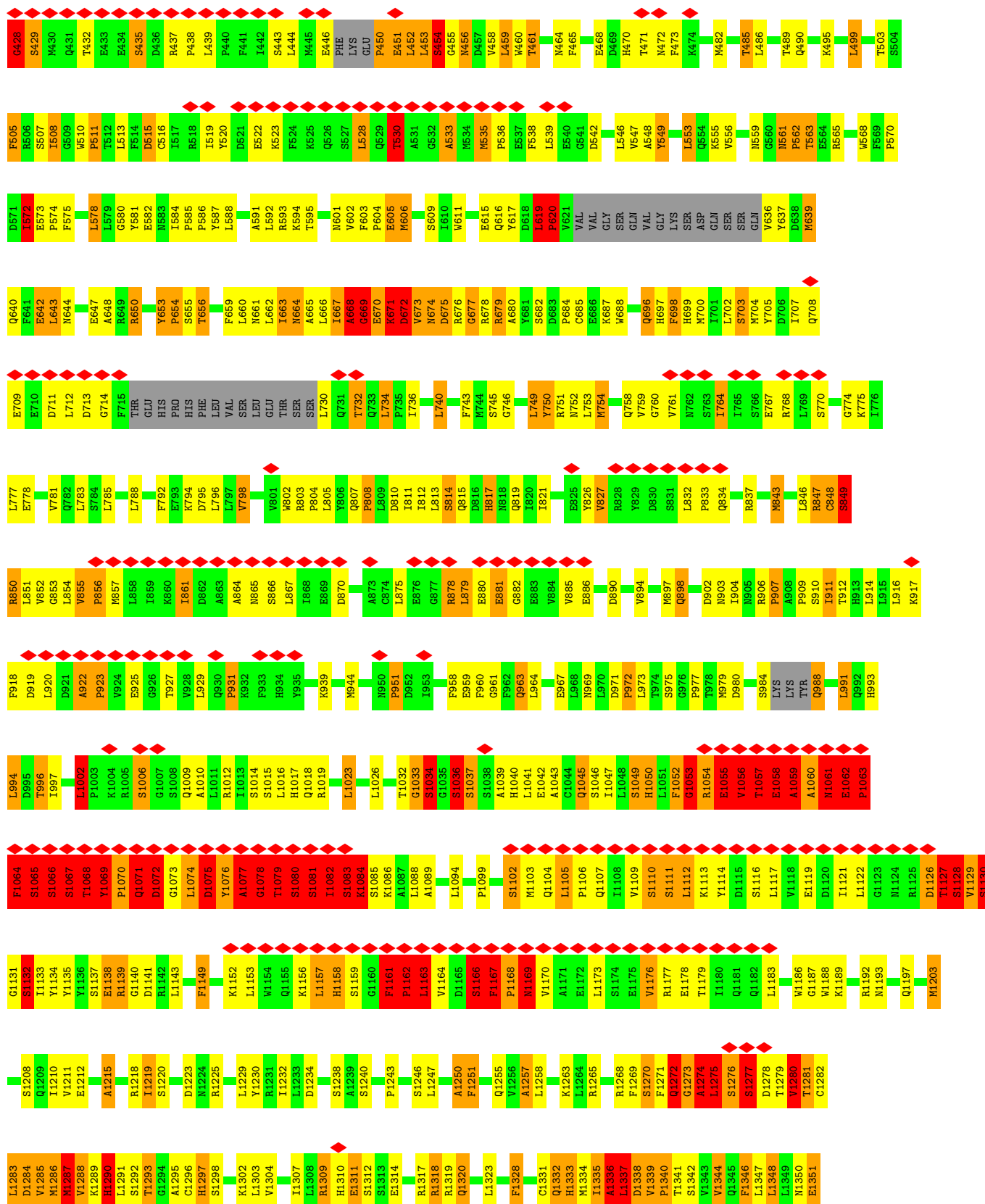
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T1456	L1457	E1458	A1459	E1460	L1461	A1462	L1465	R1466	H1469	K1470	Y1471	G1475	G1476	Q1477	V1478	L1479	F1480	N1481	M1482	G1483	I1488	C1491	R1492	A1493	I1494	S1495	F1496	K1497	G1498	Q1499	M1500	R1501	R1502	V1503	D1504	M1505	K1506	L1507	L1507	Q1508	S1509	D1510	V1511	V1511	G1512	Y1513	N1514	V1515	Q1516	K1517	Q1518	R1519	T1520	I1521	I1522	T1523
K1378	K1379	E1380	A1381	Q1382	G1383	I1384	D1385	D1386	L1387	V1388	I1389	D1391	A1392	S1393	Q1394	G1395	S1396	E1397	F1398	G1399	K1400	T1401	I1402	S1403	L1404	Y1405	L1410	D1414	F1419	L1420	Q1424	S1425	R1426	R1430	M1438	I1439	S1440	Y1441	Q1442	D1443	G1444	T1445	H1446	L1447	L1448	E1449	Q1451	Q1452	R1453	A1454	G1455					
L1308	R1309	H1310	E1311	S1312	S1313	E1314	S1315	L1316	R1317	R1318	R1319	Q1320	L1323	F1328	C1331	Q1332	R1333	M1334	I1335	A1336	L1337	D1338	V1339	T1341	S1342	V1343	V1344	Q1345	F1346	L1347	L1348	L1349	N1350	E1351	Q1352	G1354	E1355	D1356	L1357	I1358	Q1360	K1361	T1362	D1363	Q1366	A1367	D1368	L1369	A1372	I1377						
D1234	S1238	A1239	S1240	P1243	D1244	C1245	S1246	A1250	F1251	Q1255	V1256	L1258	K1263	L1264	R1265	R1268	F1269	S1270	T1271	L1272	Q1273	A1274	L1275	S1276	S1277	D1278	T1279	V1280	T1281	C1282	L1283	D1284	V1285	M1286	M1287	V1288	K1289	L1291	S1292	T1293	G1294	A1295	C1296	H1297	S1298	Q1366	A1367	D1368	L1369	A1372	I1377					
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D1234	S1238	A1239	S1240	P1243	D1244	C1245	S1246	A1250	F1251	Q1255	V1256	L1258	K1263	L1264	R1265	R1268	F1269	S1270	T1271	L1272	Q1273	A1274	L1275	S1276	S1277	D1278	T1279	V1280	T1281	C1282	L1283	D1284	V1285	M1286	M1287	V1288	K1289	L1291	S1292	T1293	G1294	A1295	C1296	H1297	S1298	Q1366	A1367	D1368	L1369	A1372	I1377					
L1308	R1309	H1310	E1311	S1312	S1313	E1314	S1315	L1316	R1317	R1318	R1319	Q1320	L1323	F1328	C1331	Q1332	R1333	M1334	I1335	A1336	L1337	D1338	V1339	T1341	S1342	V1343	V1344	Q1345	F1346	L1347	L1348	L1349	N1350	E1351	Q1352	G1354	E1355	D1356	L1357	I1358	Q1360	K1361	T1362	D1363	Q1366	A1367	D1368	L1369	A1372	I1377						
K1378	K1379	E1380	A1381	Q1382	G1383	I1384	D1385	D1386	L1387	V1388	I1389	D1391	A1392	S1393	Q1394	G1395	S1396	E1397	F1398	G1399	K1400	T1401	I1402	S1403	L1404	Y1405	L1410	D1414	F1419	L1420	Q1424	S1425	R1426	R1430	M1438	I1439	S1440	Y1441	Q1442	D1443	G1444	T1445	H1446	L1447	L1448	E1449	Q1451	Q1452	R1453	A1454	G1455					
T1456	L1457	E1458	A1459	E1460	L1461	A1462	L1465	R1466	H1469	K1470	Y1471	G1475	G1476	Q1477	V1478	L1479	F1480	N1481	M1482	G1483	I1488	C1491	R1492	A1493	I1494	S1495	F1496	K1497	G1498	Q1499	M1500	R1501	R1502	V1503	D1504	M1505	K1506	L1507	L1507	Q1508	S1509	D1510	V1511	V1511	G1512	Y1513	N1514	V1515	Q1516	K1517	Q1518	R1519	T1520	I1521	I1522	T1523
A1524	V1525	L1526	R1527	L1528	V1529	F1530	T1533	S1534	L1535	V1536	E1537	T1538	S1539	F1540	F1541	F1542	E1543	G1544	N1545	N1546	K1547	M1548	V1549	V1553	I1556	H1559	Q1560	S1561	F1562	D1564	Q1565	L1566	L1567	R1568	E1569	D1570	F1571	T1572	Q1573	A1574	D1575	D1576	L1577	L1578	M1579	E1580	Q1581	I1582	L1583	L1584	A1585	V1586	K1591			

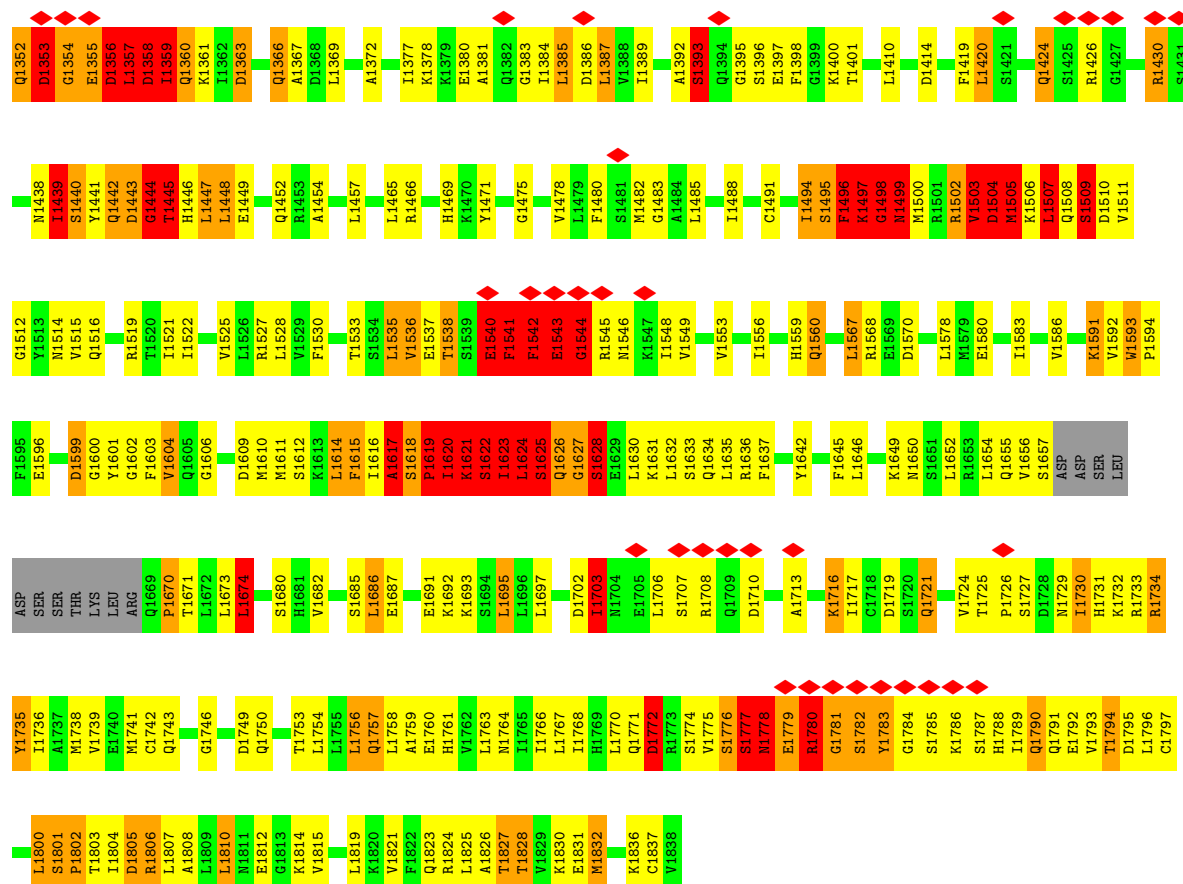




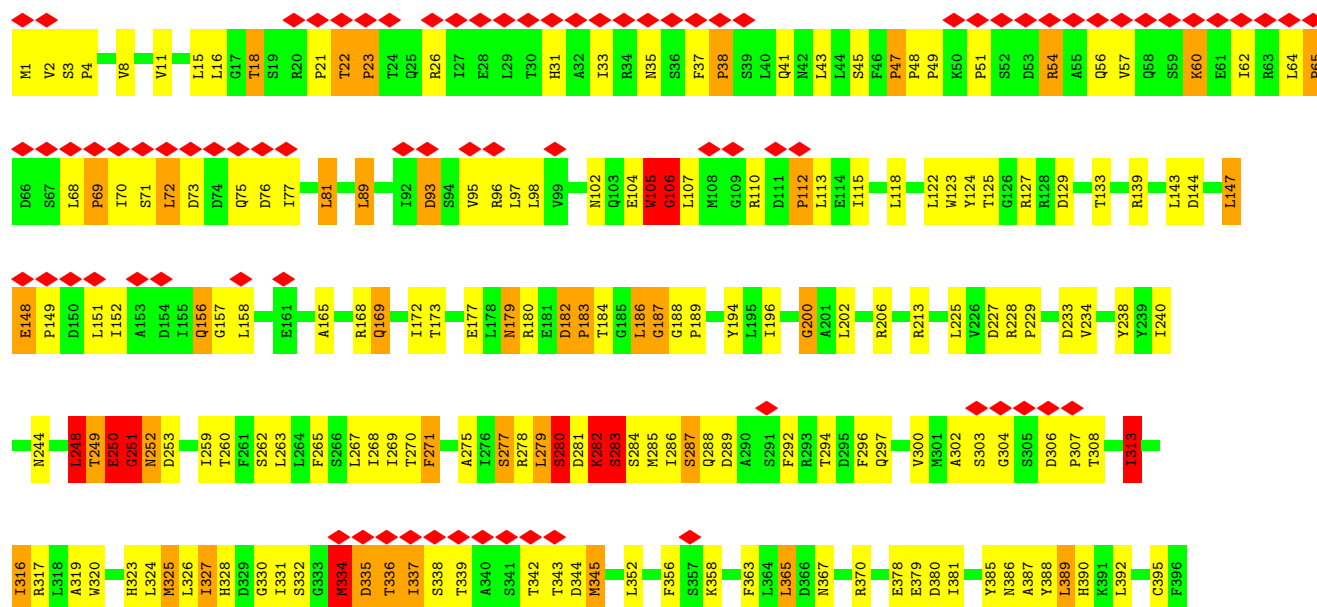
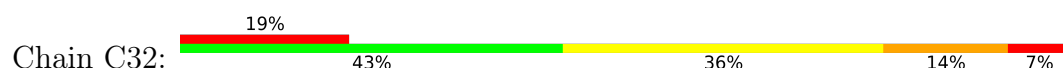




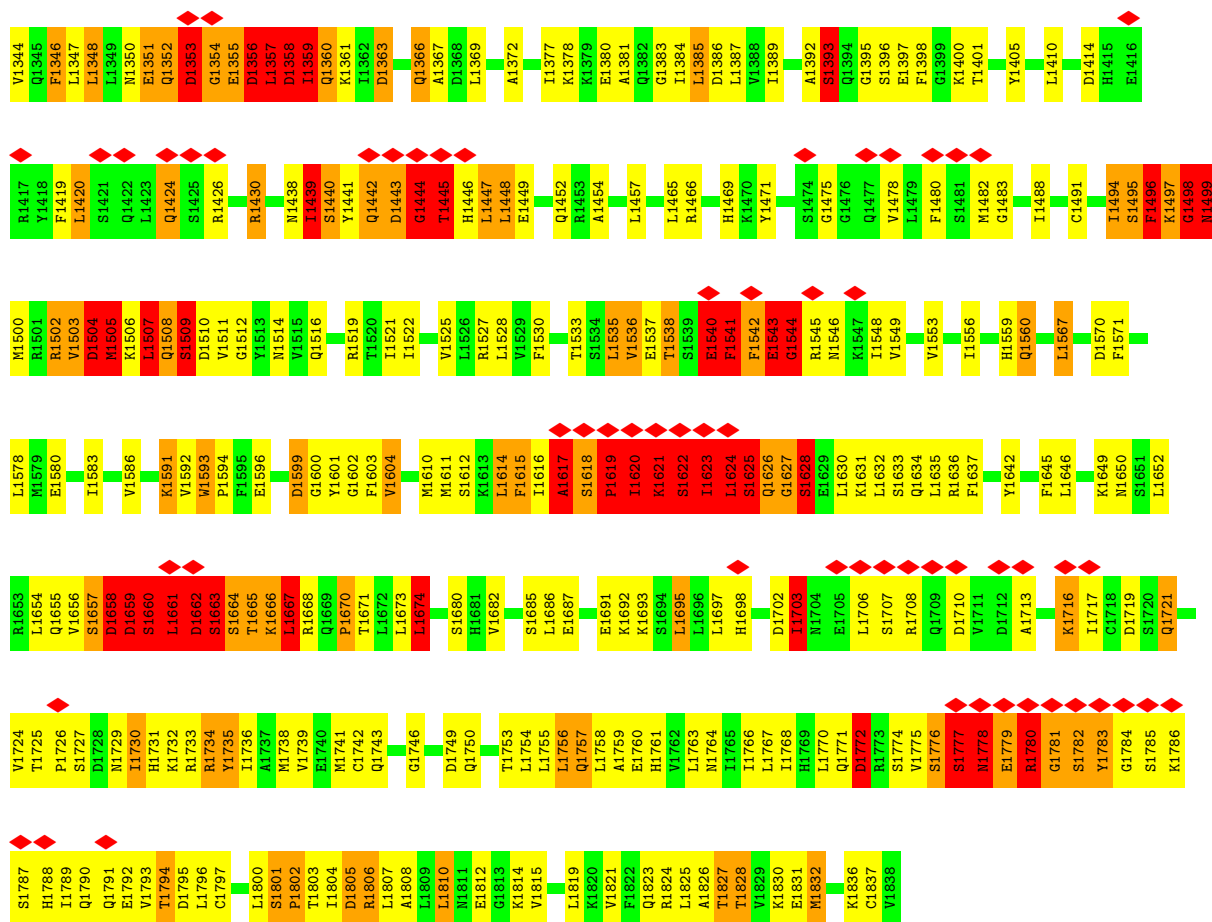




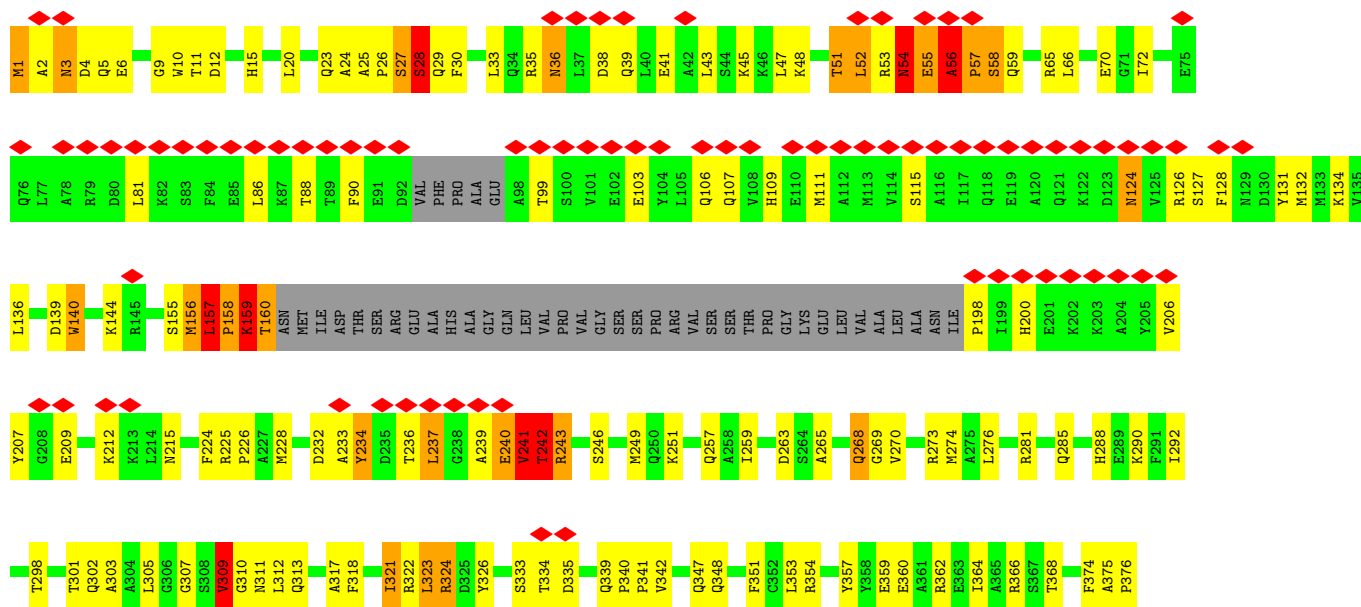
● Molecule 10: Nuclear pore complex protein NUP205

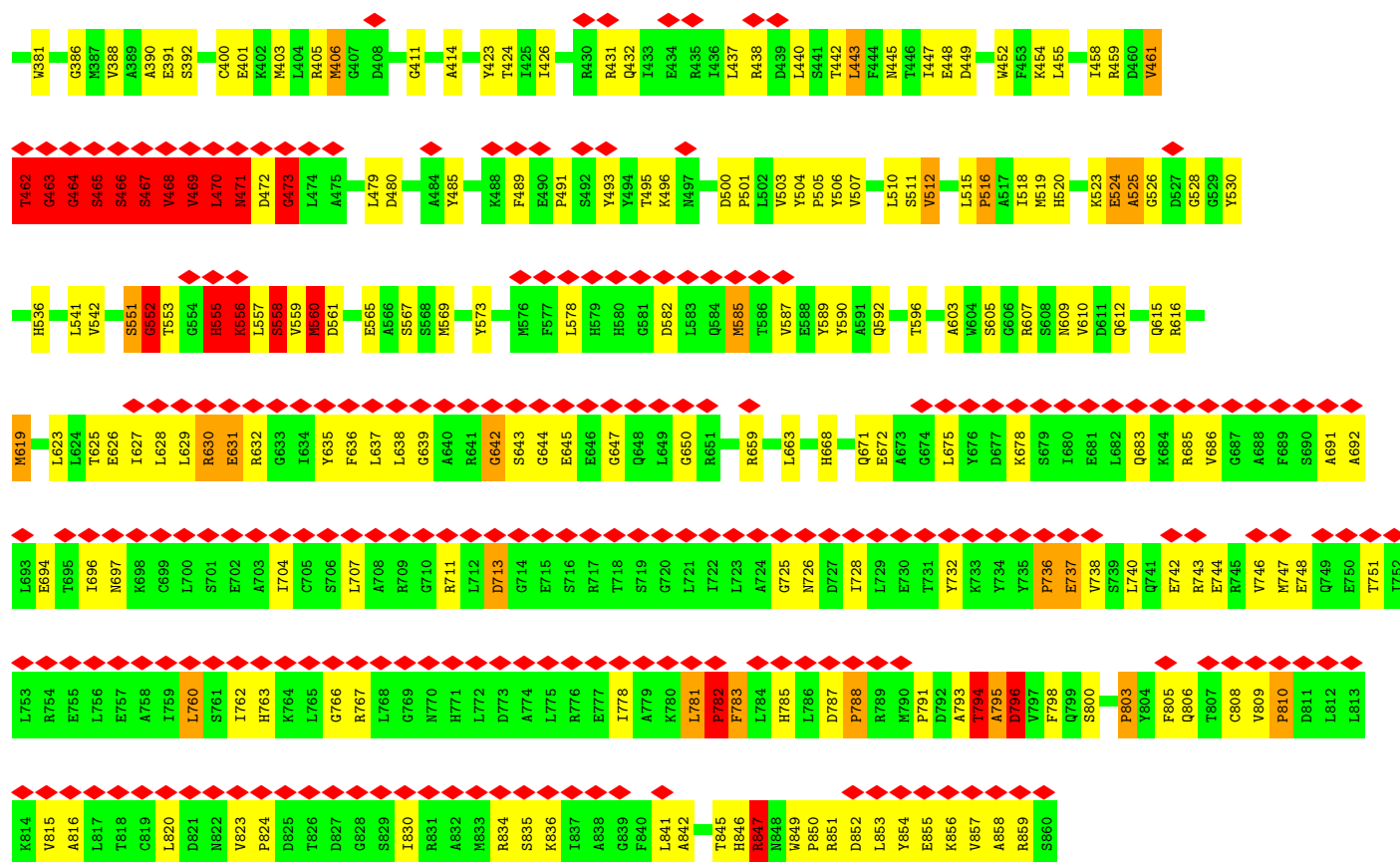




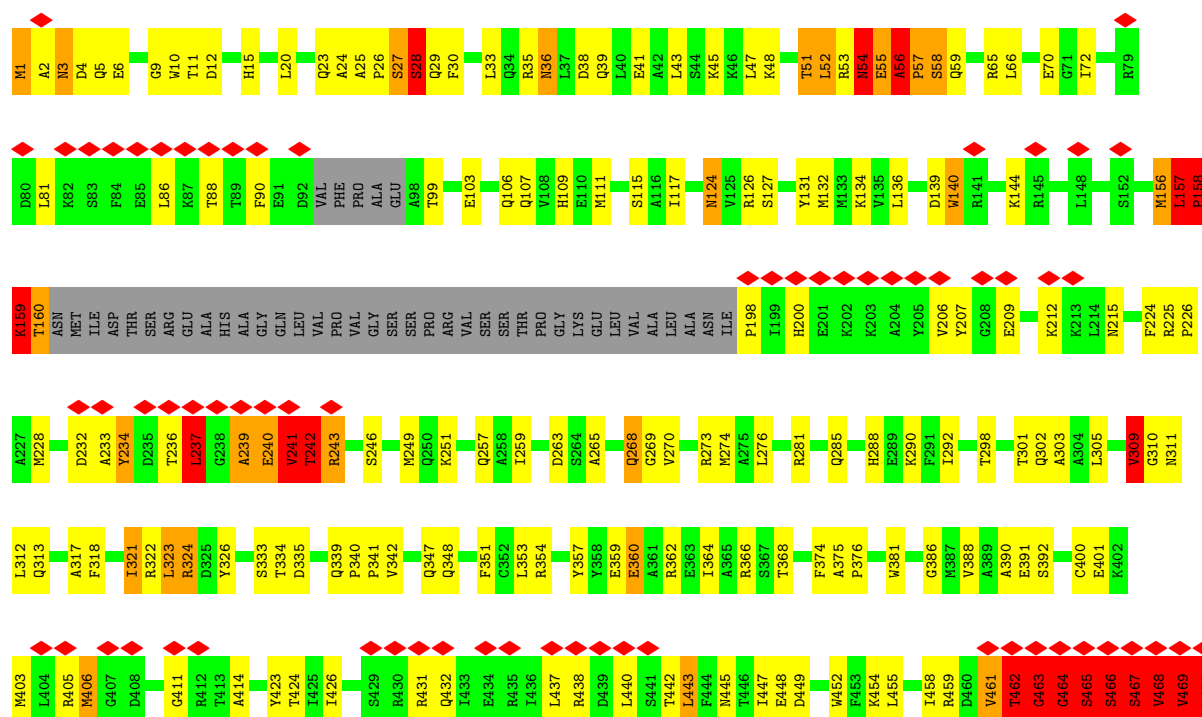


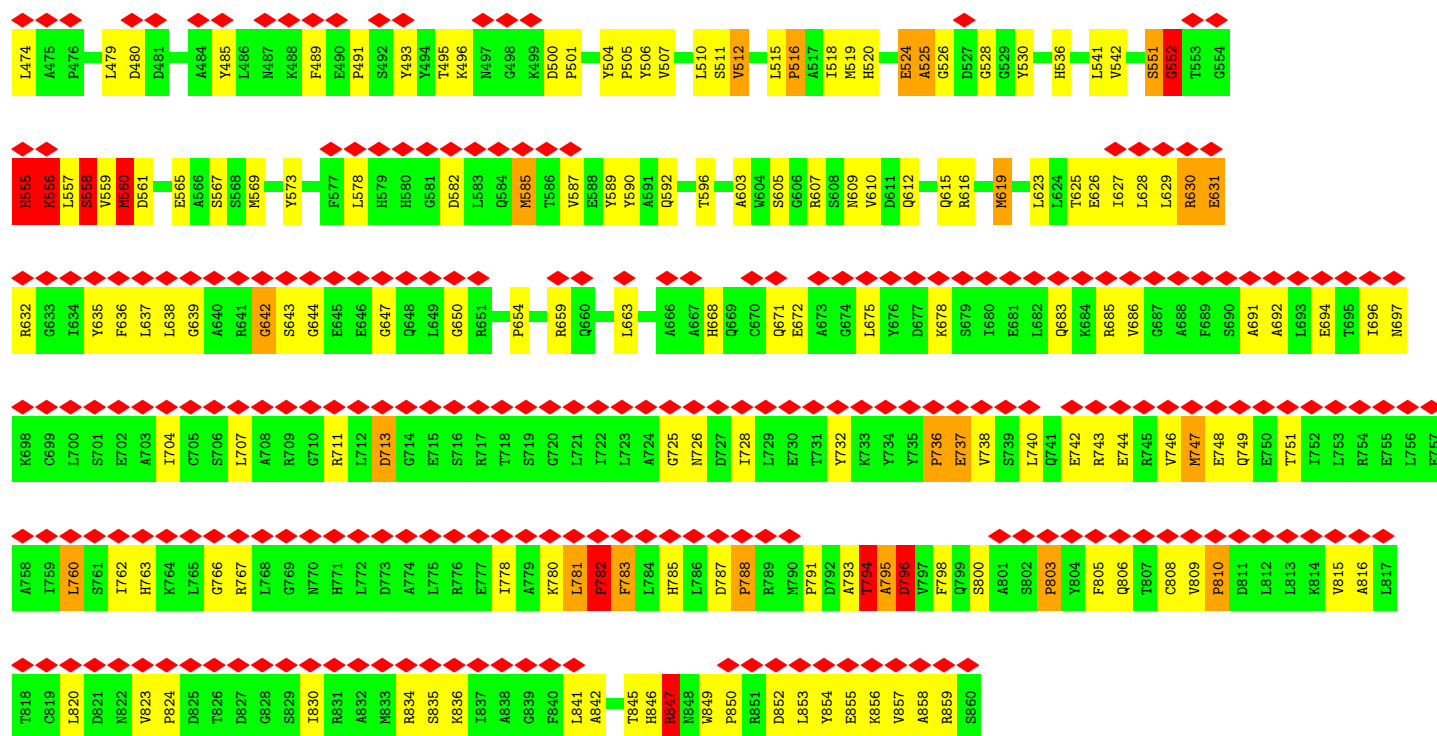
• Molecule 11: Nuclear pore complex protein NUP93A



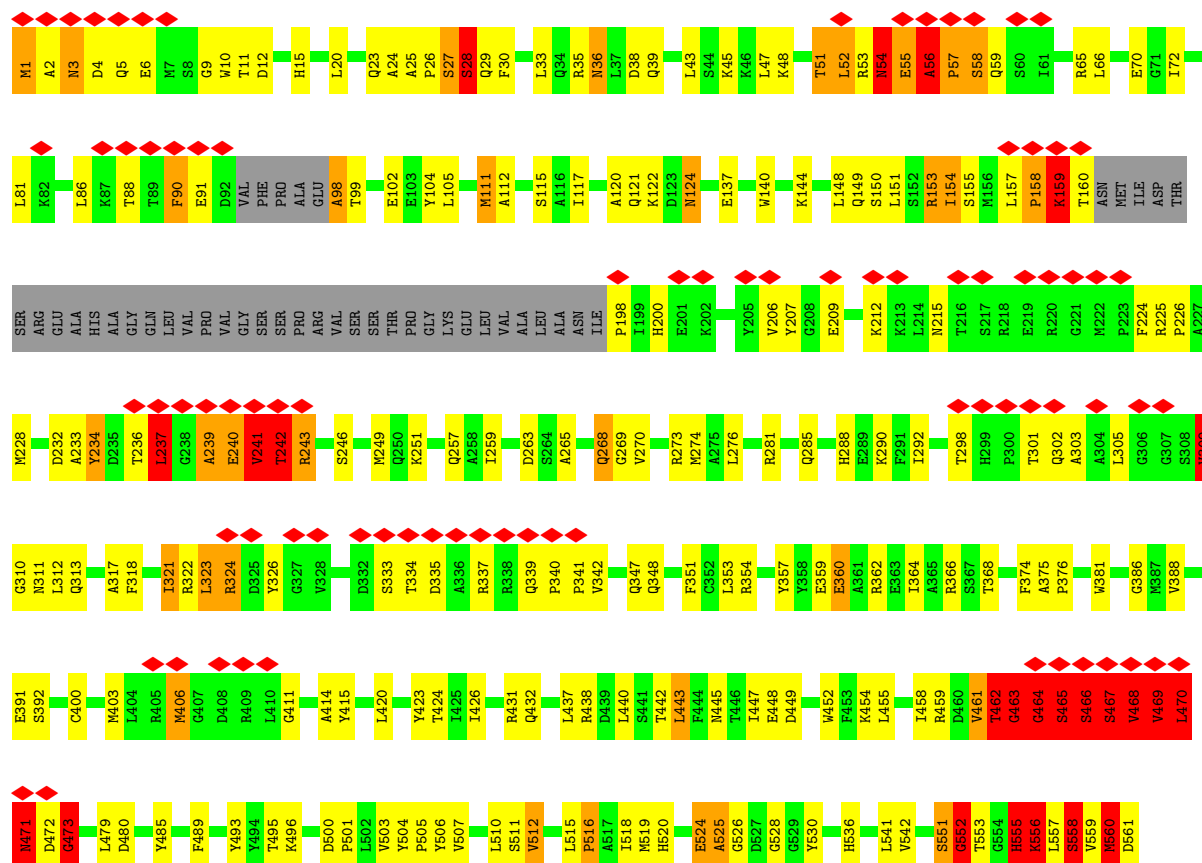


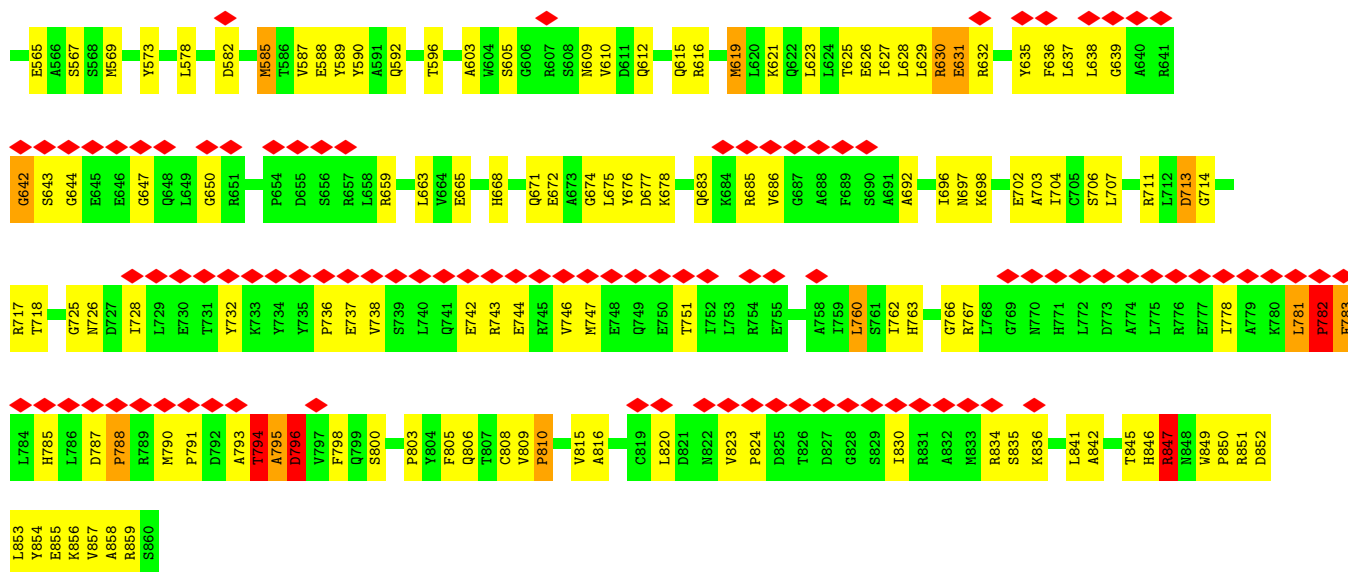
• Molecule 11: Nuclear pore complex protein NUP93A



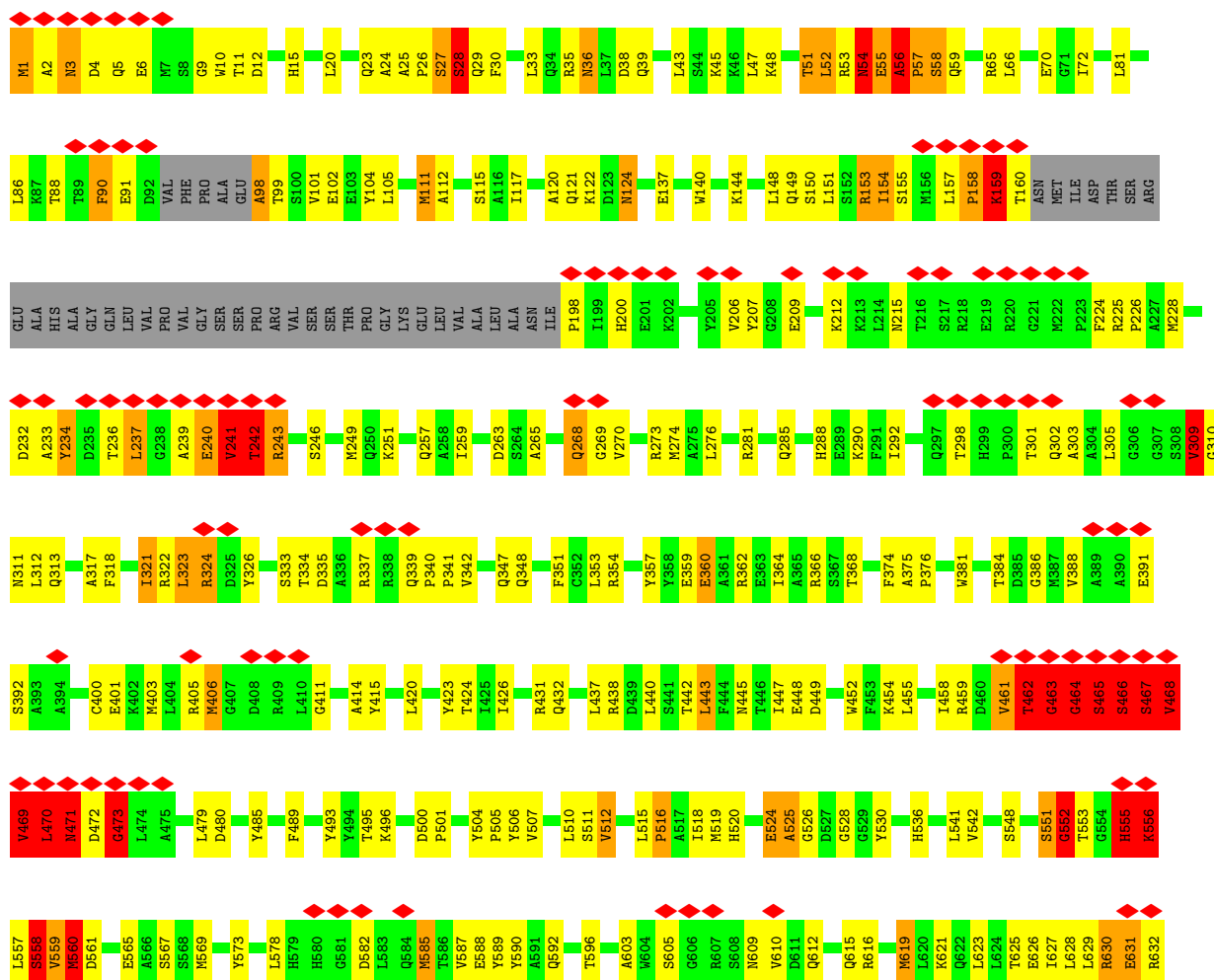


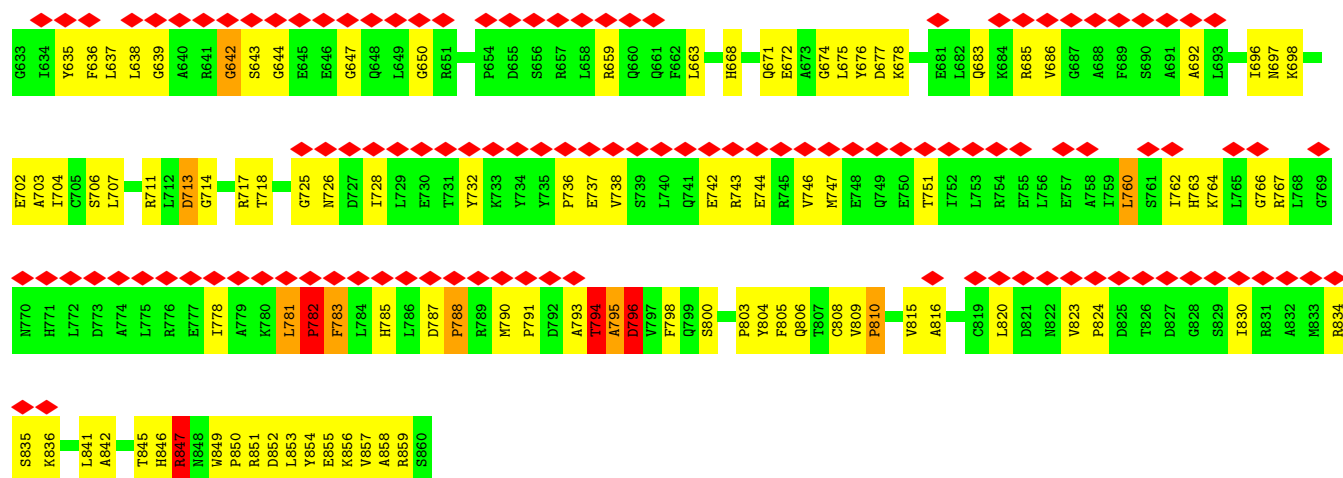
• Molecule 11: Nuclear pore complex protein NUP93A



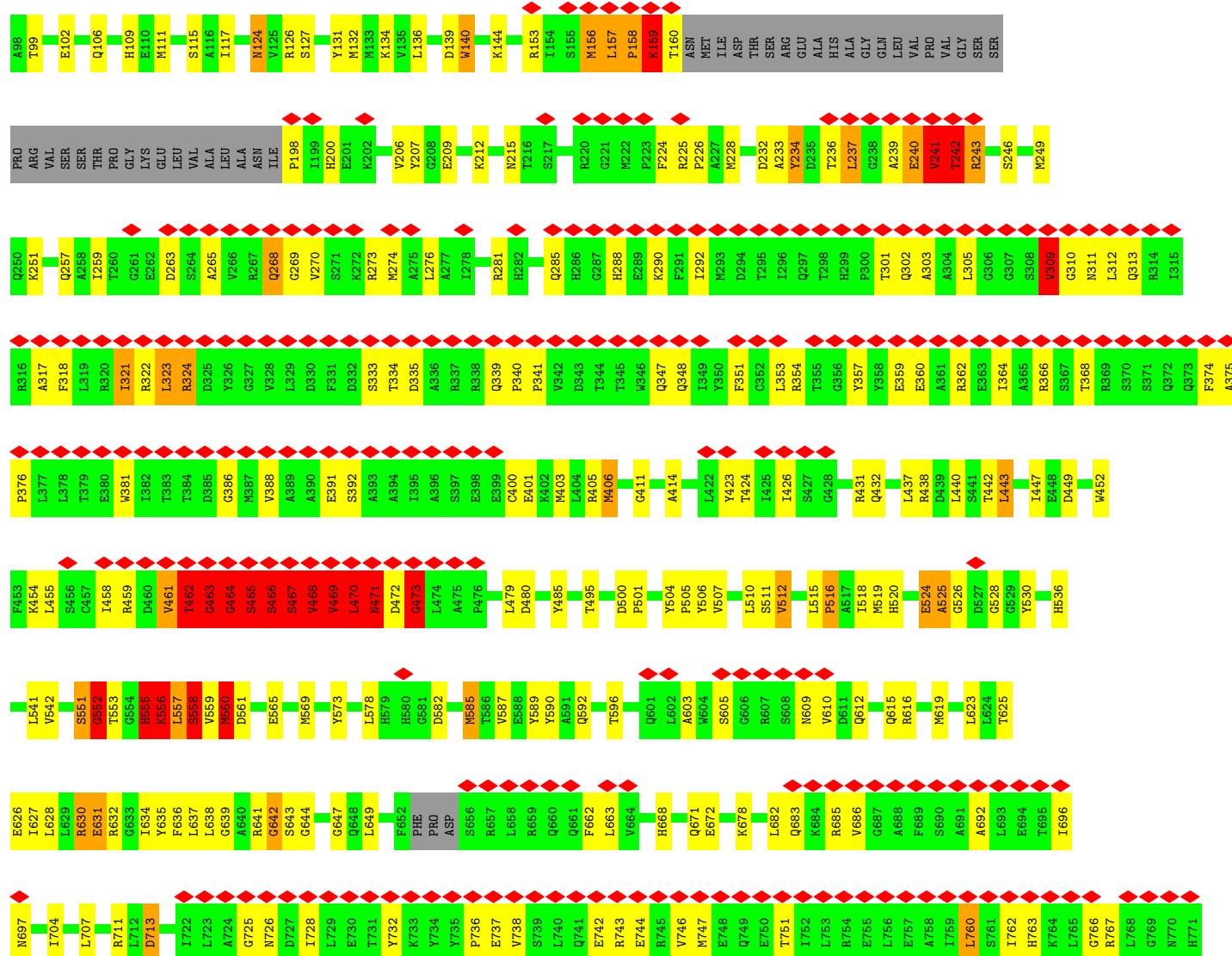


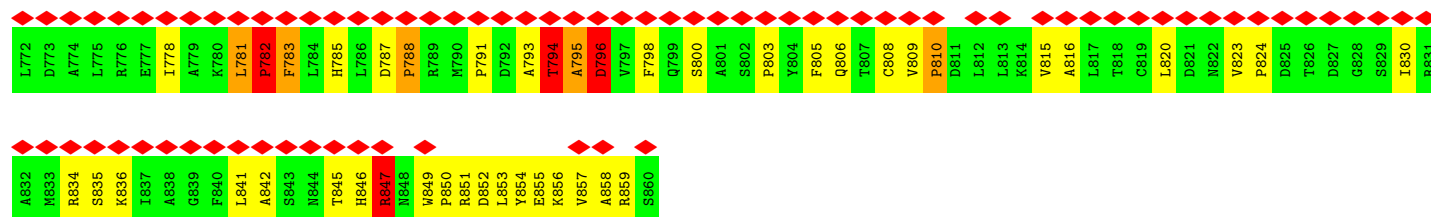
• Molecule 11: Nuclear pore complex protein NUP93A





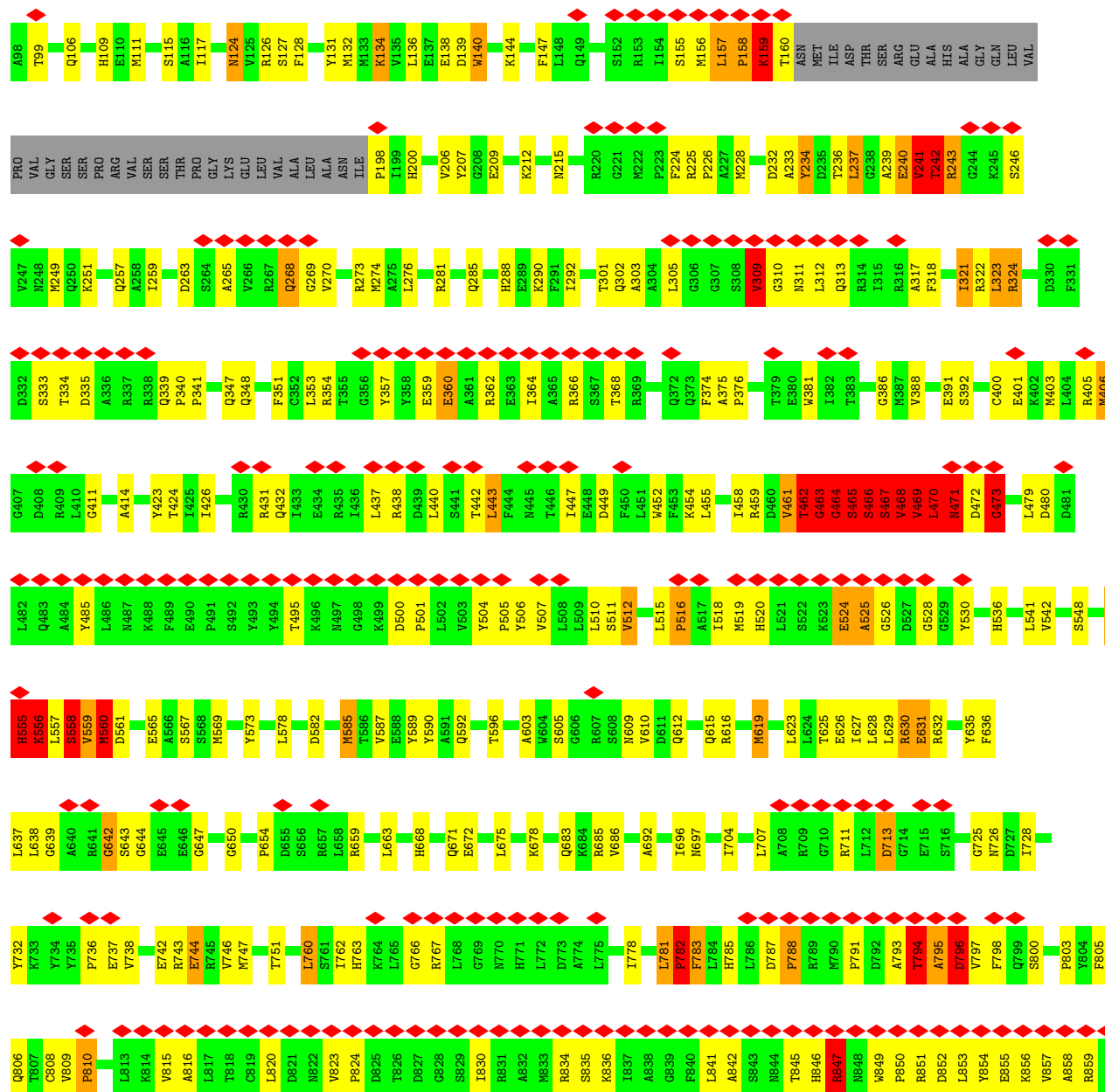
• Molecule 12: Nuclear pore complex protein NUP93A



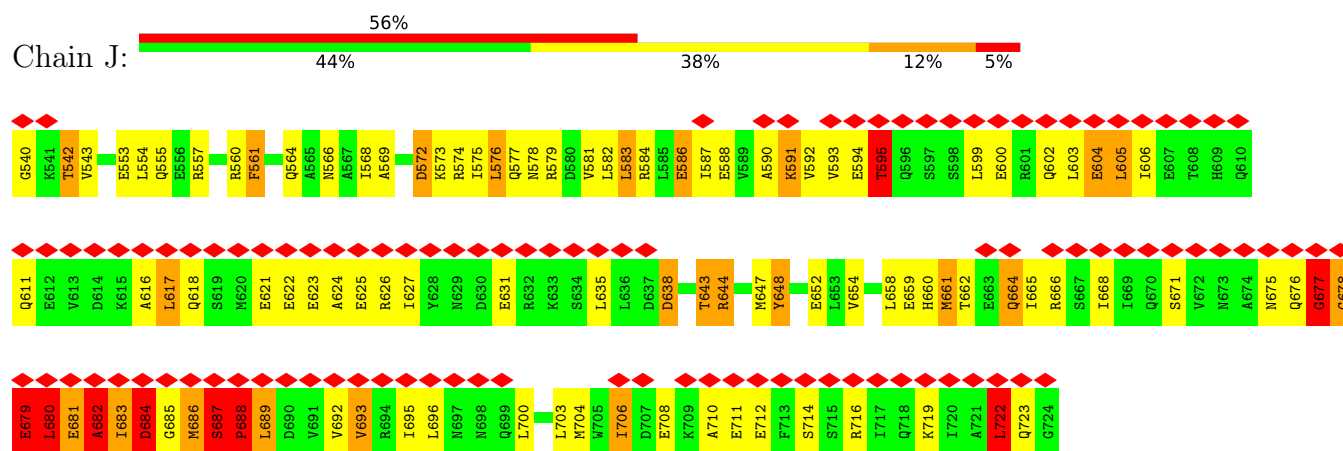


• Molecule 12: Nuclear pore complex protein NUP93A

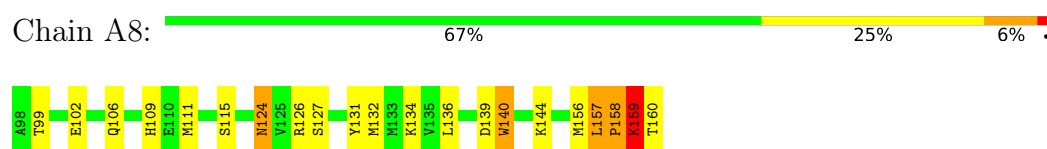
Chain A48: 28% 56% 31% 5% 5%



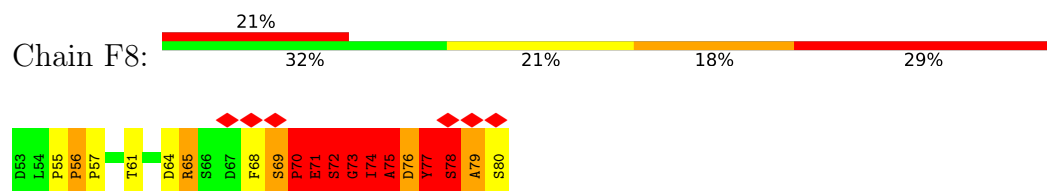
- Molecule 15: Nuclear pore complex protein NUP62



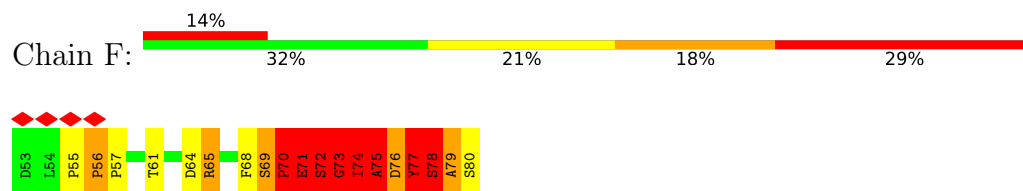
- Molecule 16: Nuclear pore complex protein NUP93A



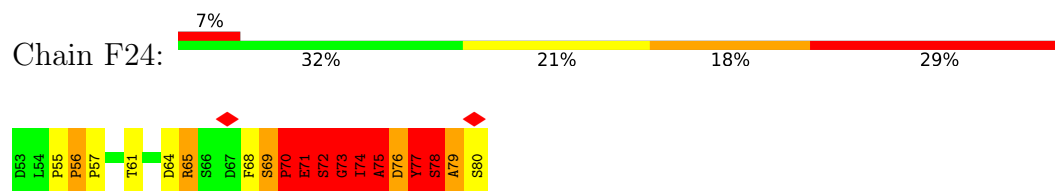
- Molecule 17: Nuclear pore complex protein NUP35



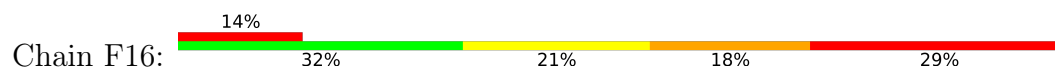
- Molecule 17: Nuclear pore complex protein NUP35

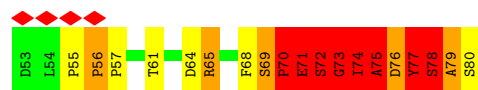


- Molecule 17: Nuclear pore complex protein NUP35

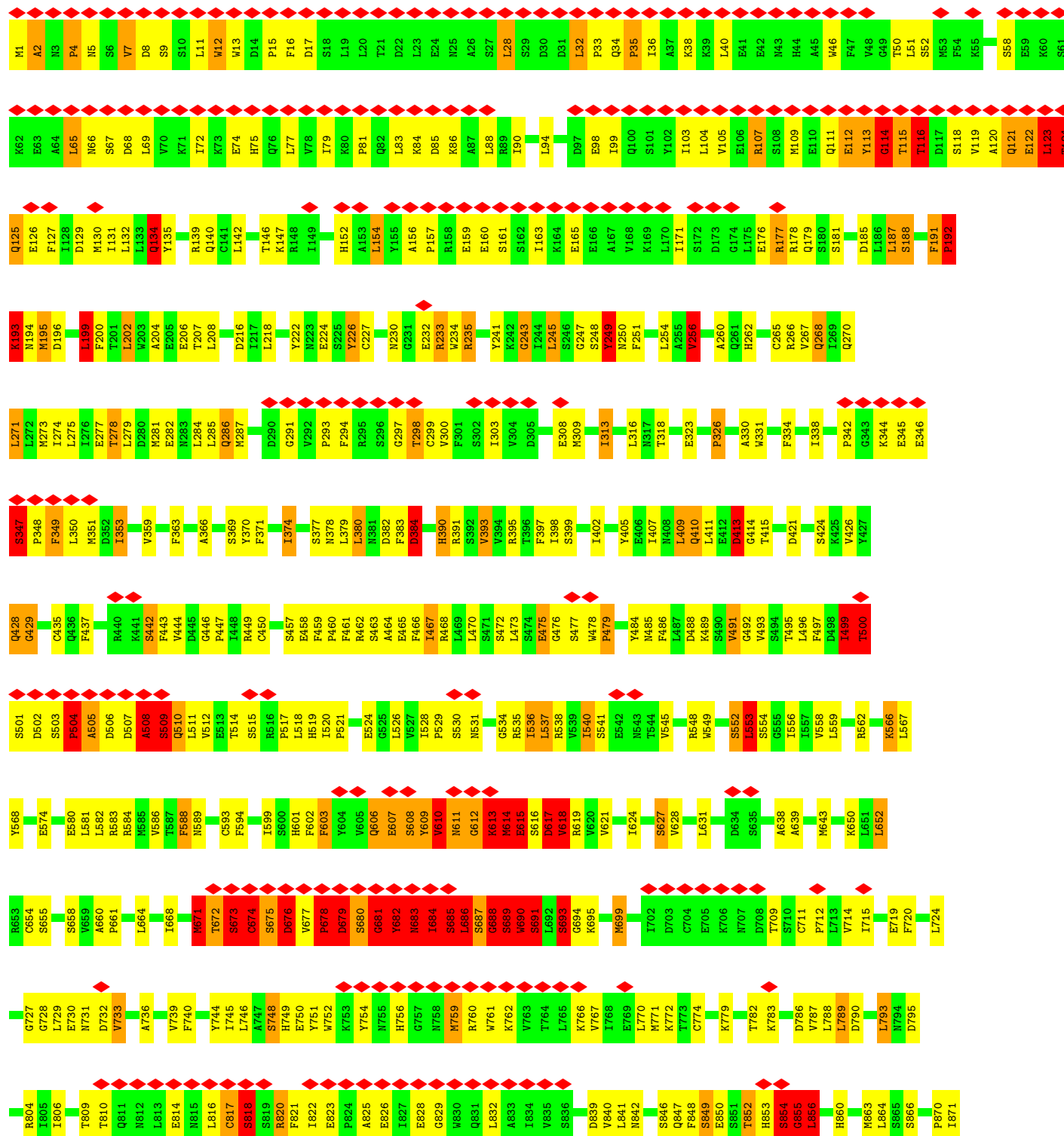


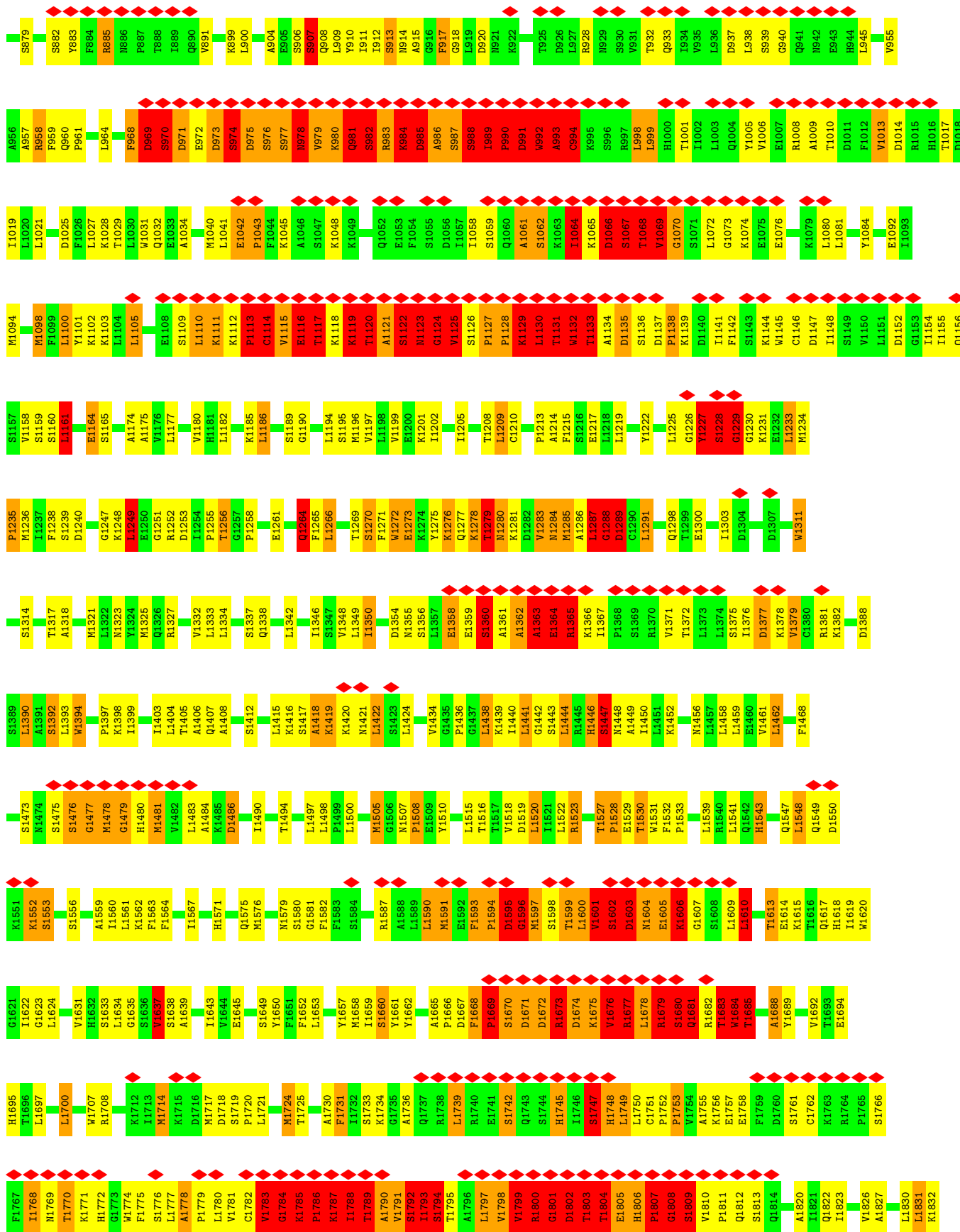
- Molecule 17: Nuclear pore complex protein NUP35

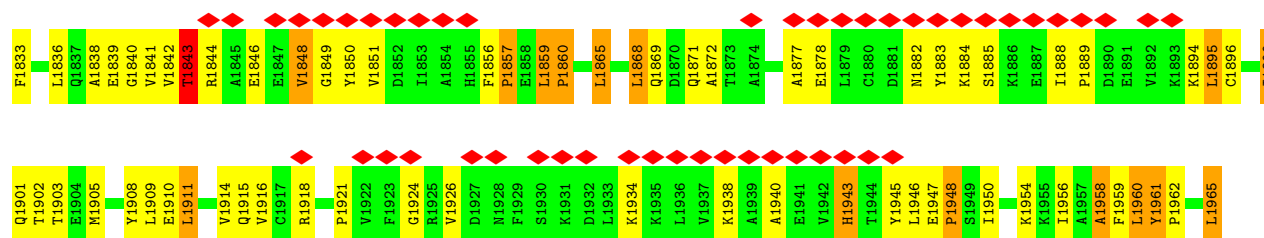




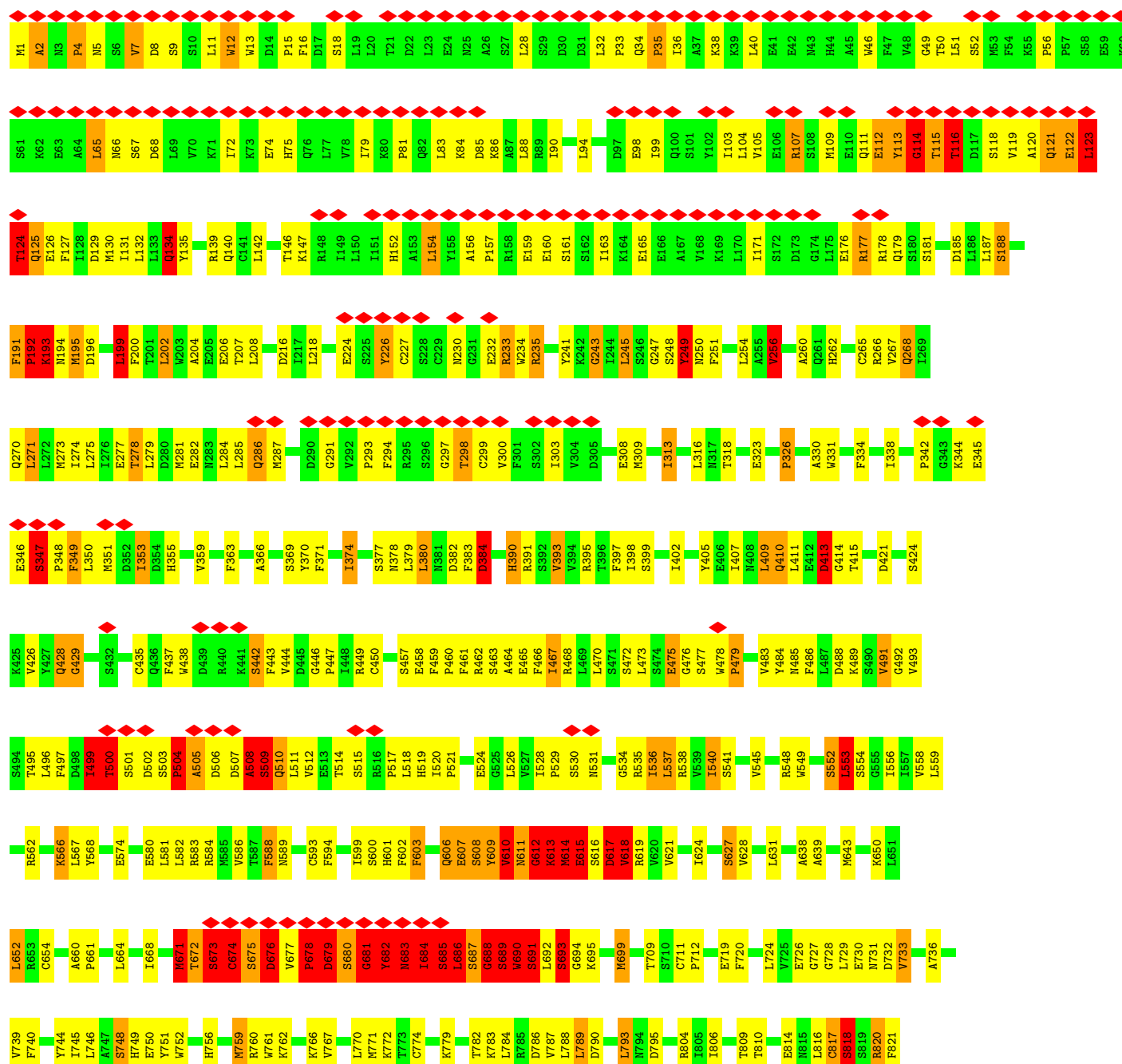
• Molecule 18: Nucleoporin (DUF3414)



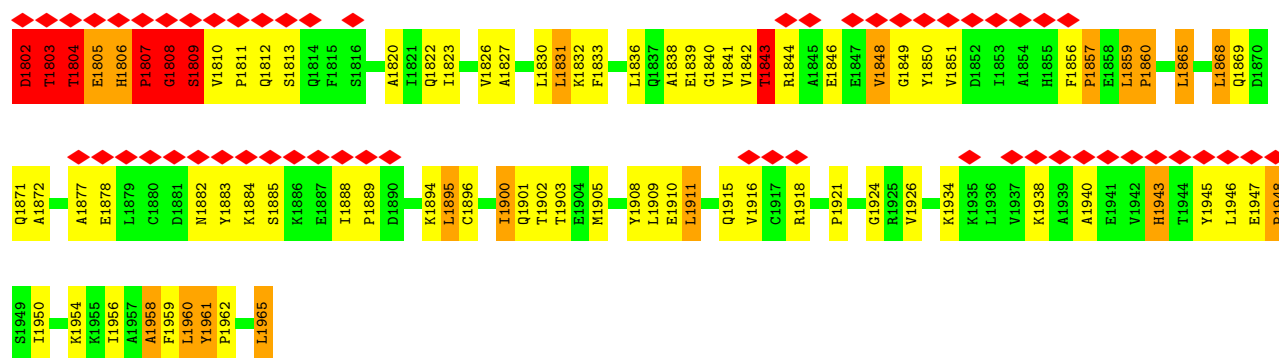




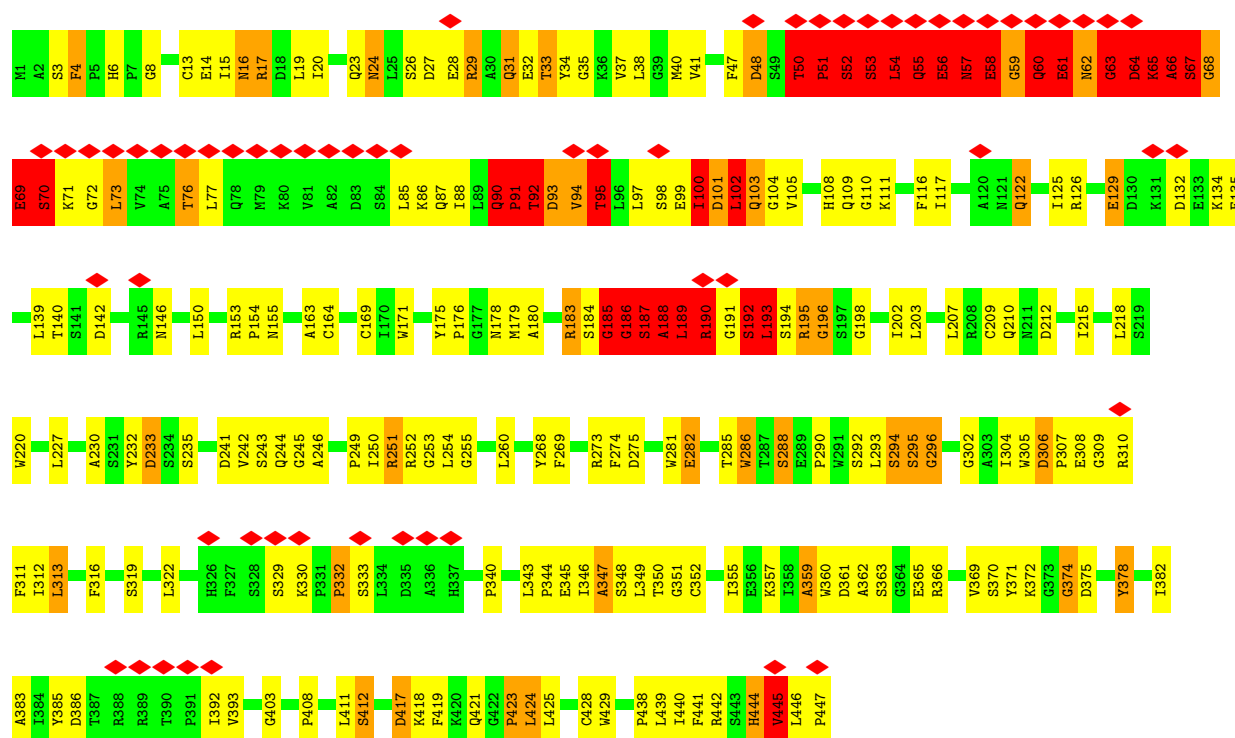
• Molecule 18: Nucleoporin (DUF3414)



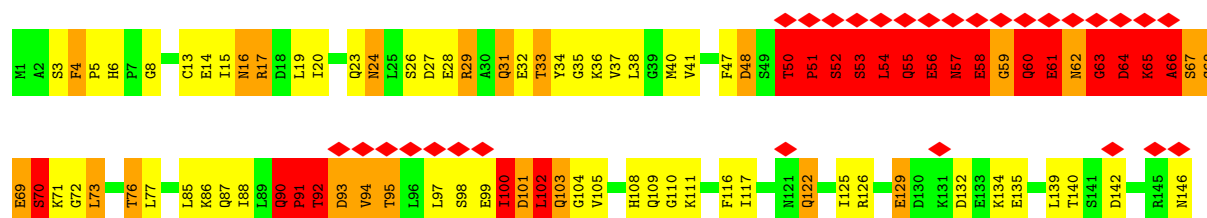
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S1744	P1669	D1595	P1436	E1357	K1273	V1199	S1126	D1056	D991	S913	S824
H1745	S1670	G1596	G1437	E1358	K1275	K1201	P1127	I1058	W992	N914	A825
L1746	D1671	M1597	L1438	S1359	K1276	I1202	P1128	S1059	A993	A915	E826
S1747	D1672	S1598	L1439	E1360	Q1277	L1205	K1129	Q1060	C994	G916	I827
H1748	D1673	T1599	I1440	A1361	K1278	T1205	L1129	Q1060	K995	F917	E828
L1749	R1673	L1600	G1442	A1362	T1279	T1208	L1130	A1061	K995	G918	G829
L1750	D1674	V1601	G1443	A1363	K1281	L1209	W1132	S1062	S996	L919	L832
K1675	S1675	S1602	S1444	E1364	K1282	C1210	T1133	K1064	R997	D920	
V1676	P1676	T1527	R1445	R1365	V1283	P1213	A1134	I1064	L998	R928	
R1677	E1629	W1528	H1446	K1366	M1284	F1213	D1135	K1065	L999		D839
L1678	E1605	T1530	S1447	L1367	M1285	A1214	A1134	K1065	H1000		V840
A1679	K1606	F1531	A1448	P1368	A1286	E1215	S1136	S1067	T1001		N842
S1680	G1607	F1532	A1449	S1369	L1287	S1216	D1137	S1067	I934		S846
Q1681	S1608	P1533	I1450	R1370	G1288	E1217	P1138	V1068	T1002		Q847
F1759	L1609	L1539	K1452	V1371	D1289	L1218	K1139	V1069	L1003		F848
D1760	R1682	R1540	L1452	T1372	L1291	L1219	D1140	G1070	Q1004		S849
S1761	T1613	R1541	M1456	L1373	L1291	Y1222	I1141	S1071	Y1005		E850
C1762	E1614	H1543	L1457	L1374	Q1298	S1223	F1142	L1072	V1006		S851
A1763	K1615	H1543	L1458	S1375	T1299	K1224	S1143	G1073	E1007		T852
R1764	T1616	L1546	F1460	D1377	E1300	L1225	K1144	K1074	R1008		H853
Y1689	Q1617	Q1547	V1461	K1378	I1303	G1226	W1145	E1075	A1009		S854
V1692	L1619	L1548	L1462	V1379	W1311	Y1227	C1146	E1076	T1010		C855
T1693	W1620	Q1549	F1468	K1380	S1314	G1229	D1147	S1078	T1010		L856
E1694	G1621	D1550	S1473	R1381	S1314	G1230	I1148	K1079	F1012		H860
H1695	G1623	K1551	S1475	K1382	T1317	E1232	S1149	L1080	V1013		M863
T1696	L1624	S1552	G1476	L1390	A1318	K1231	V1150	L1081	D1014		L864
L1697	V1631	S1553	G1477	I1399	M1321	L1233	L1151	V1082	R1015		S865
L1700	H1632	S1556	M1478	S1399	L1322	P1235	D1152	K1083	H016		S866
W1707	S1633	A1559	L1634	A1391	N1323	M1236	G1153	Y1084	T1017		P870
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D1716	A1639	F1564	L1483	K1398	K1327	S1249	V1158	L1021	L1021		
M1717	T1643	I1567	A1484	I1399	V1332	G1247	S1159				
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P1720	E1645	M1576	T1494	T1405	Q1338	G1251	E1164	S970	S970		
L1721	S1649	M1576	T1494	A1406	Q1338	R1252	S1165	D971	D971		
M1724	F1651	S1580	G1496	Q1407	L1342	D1253	E1164	K1103	T1029		
T1725	L1495	G1581	L1497	A1408	L1342	T1254	A1174	W1031	E972		
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R1732	T1732	R1587	M1576	L1415	S1347	G1257	V1176	E1033	S974		
L1733	K1658	A1588	K1505	K1416	V1348	P1258	V1180	S1109	D975		
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R1739	K1734	T1589	N1507	E1418	L1350	L1182	L1112	S977	L900		
A1736	G1735	P1589	M1507	K1419	E1265	L1182	E1042	R978	A904		
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R1738	Y1662	E1509	P1508	K1420	D1354	L1269	C1114	K980	S907		
L1739	A1665	M1591	Y1510	N1421	L1422	S1270	V1115	Q981	Q908		
A1796	T1795	E1592		L1423	L1424		A1046	S982	L909		
L1797	V1798	E1741					S1047	R983	Y910		
V1799							K1048	R984			
R1800							K1118	D985			
G1801							L1194	S986			
							M1196	A986			
								S987			
							Q1052	S988			
							E1053				

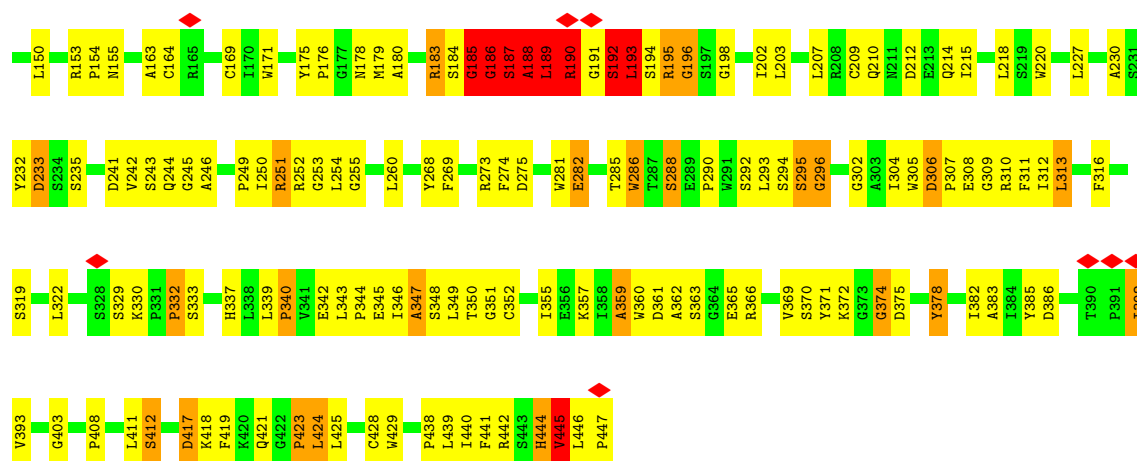


• Molecule 19: Aladin

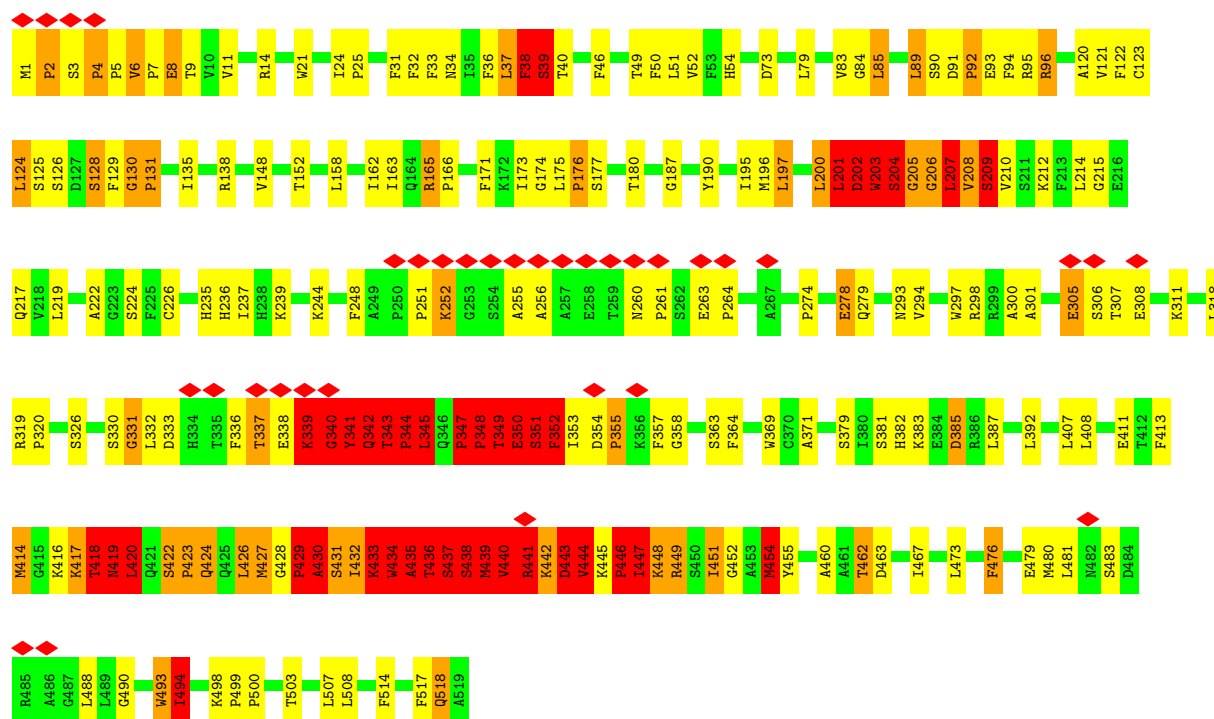


• Molecule 19: Aladin

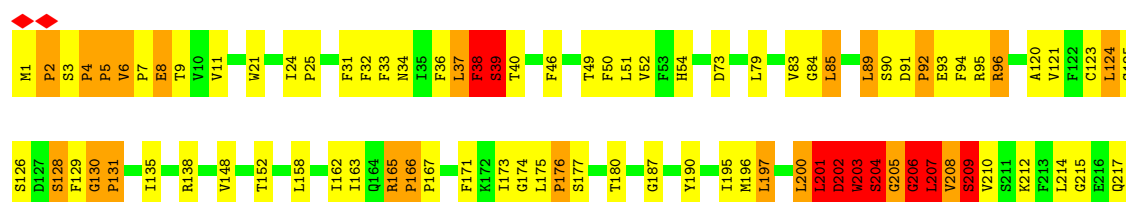


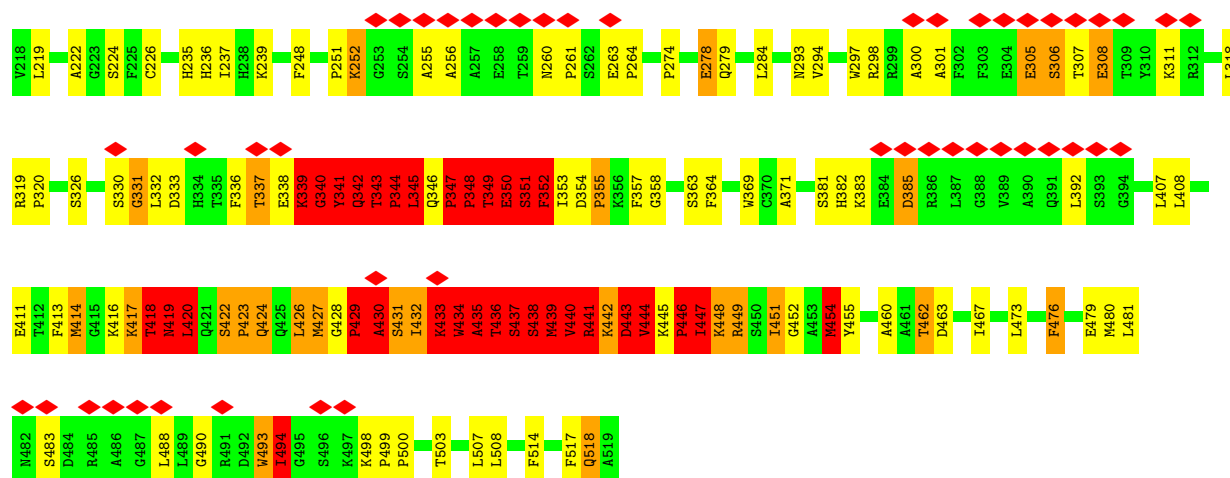


• Molecule 20: Nucleoporin protein Ndc1-Nup protein

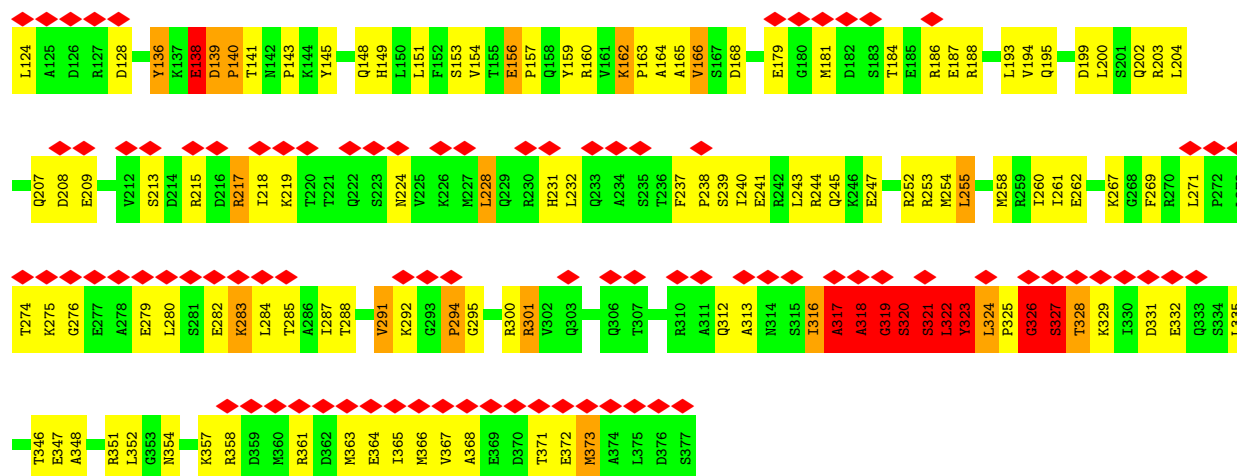


• Molecule 20: Nucleoporin protein Ndc1-Nup protein

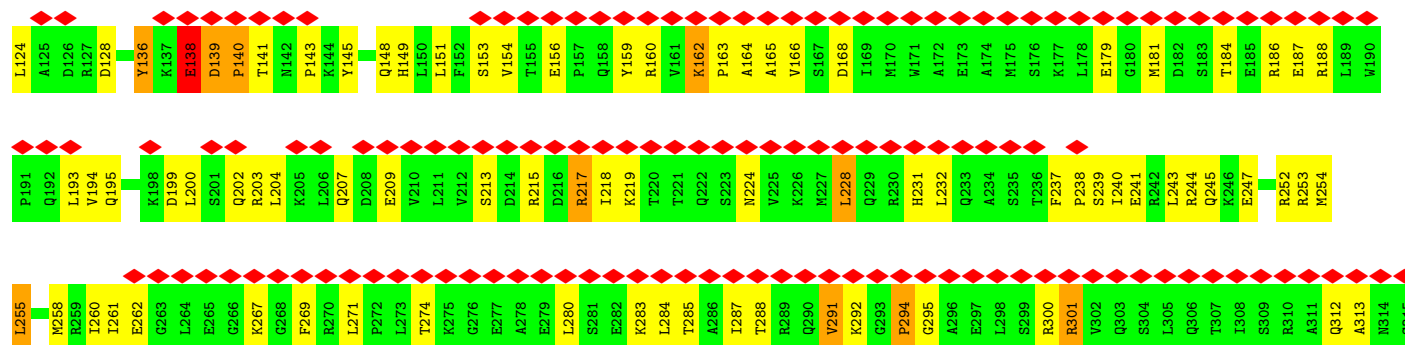


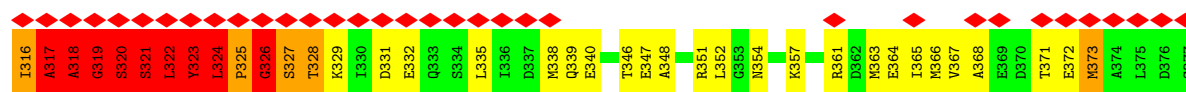


• Molecule 21: Nuclear pore complex protein NUP54

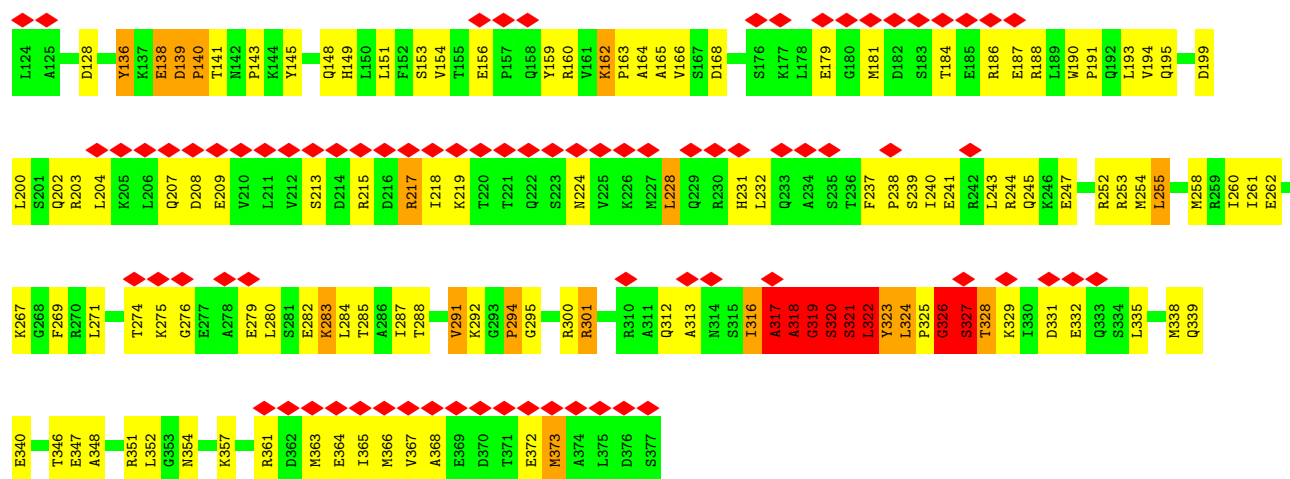


• Molecule 21: Nuclear pore complex protein NUP54

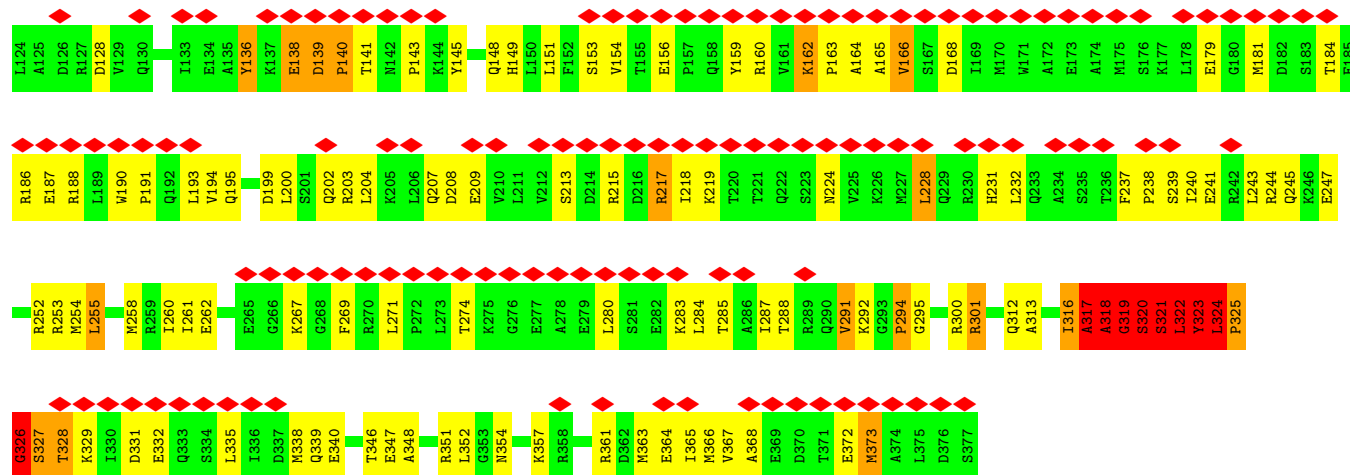




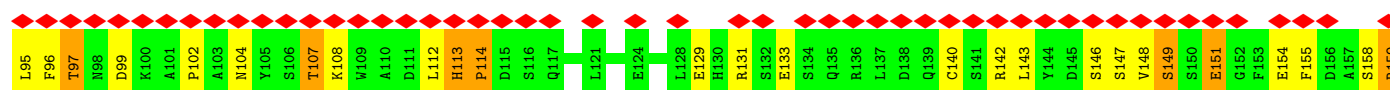
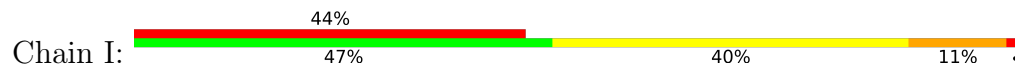
• Molecule 21: Nuclear pore complex protein NUP54

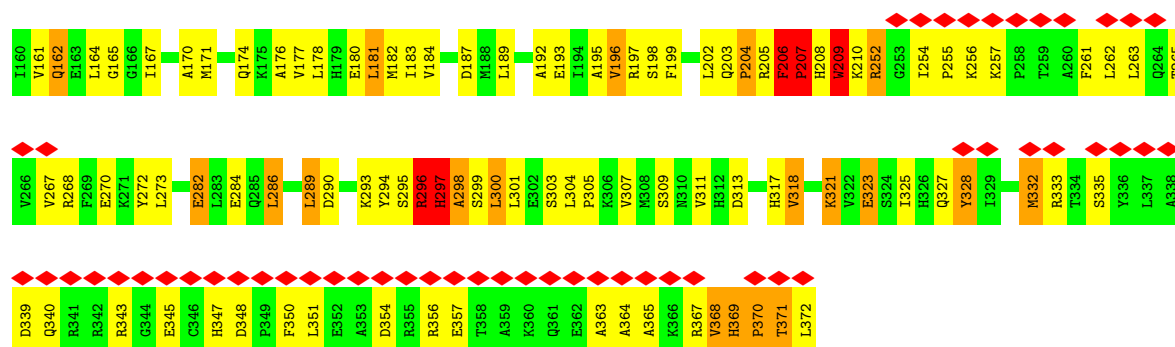


• Molecule 21: Nuclear pore complex protein NUP54

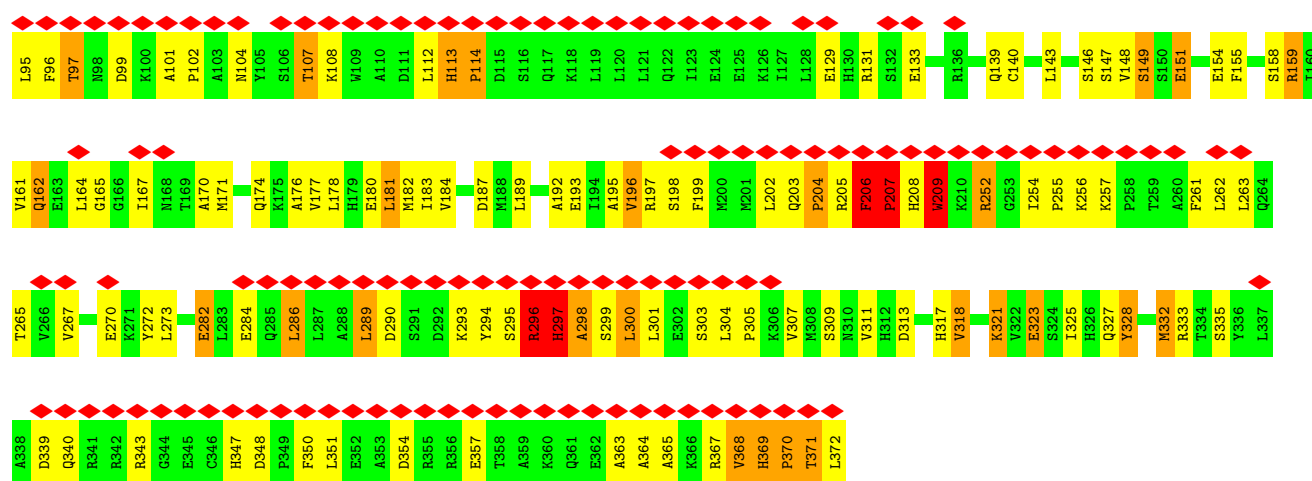


• Molecule 22: NUP58

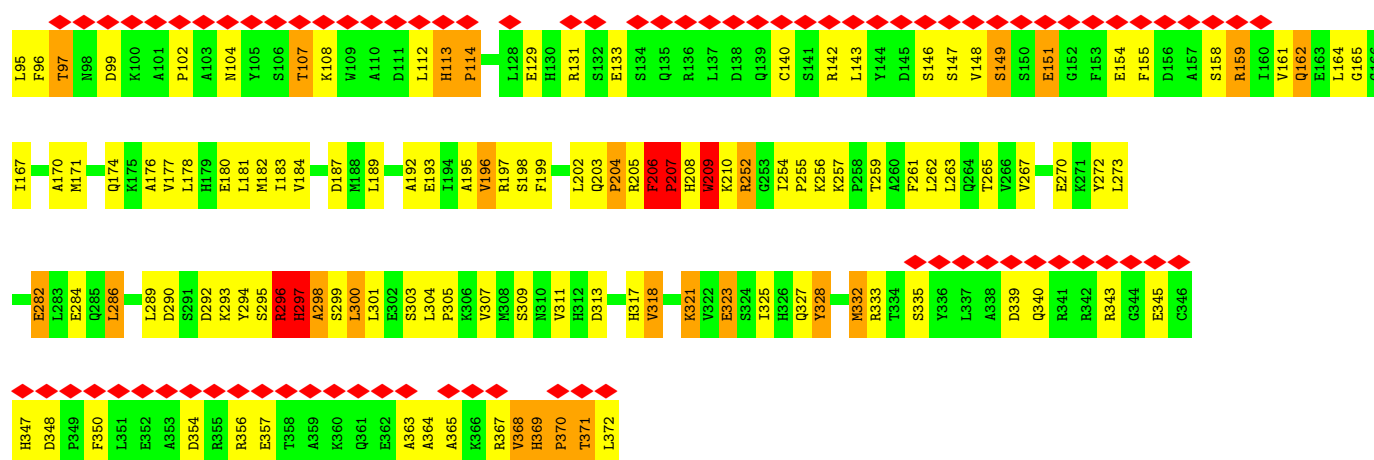




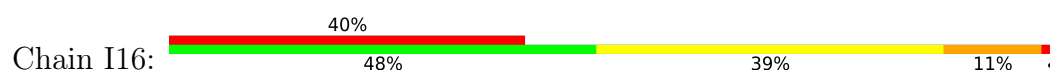
• Molecule 22: NUP58

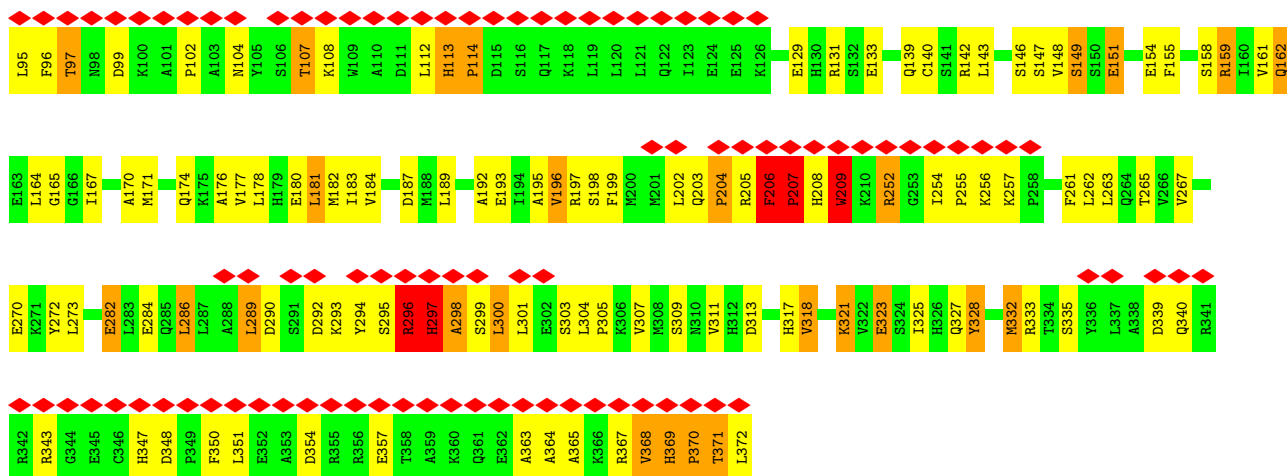


• Molecule 22: NUP58

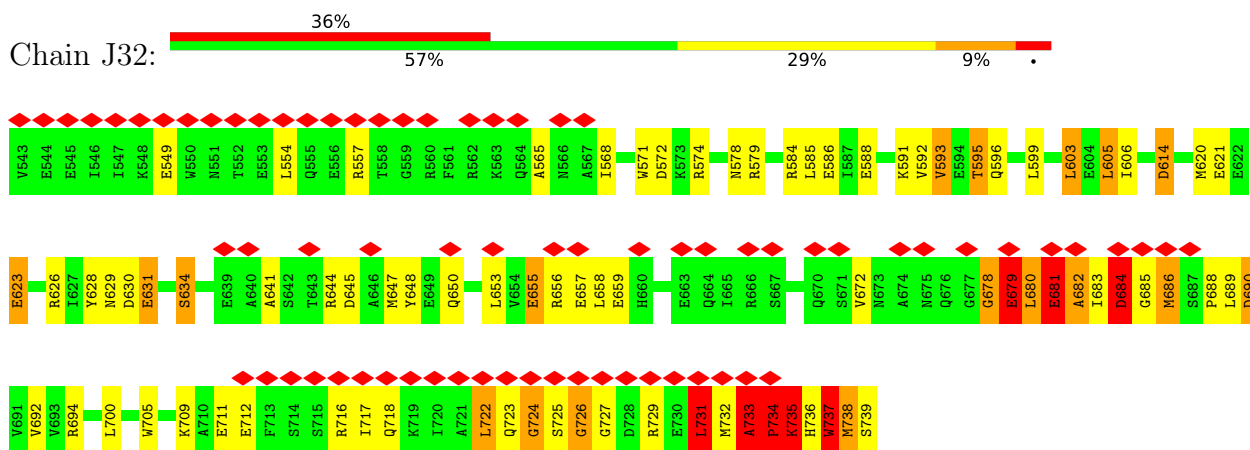


• Molecule 22: NUP58

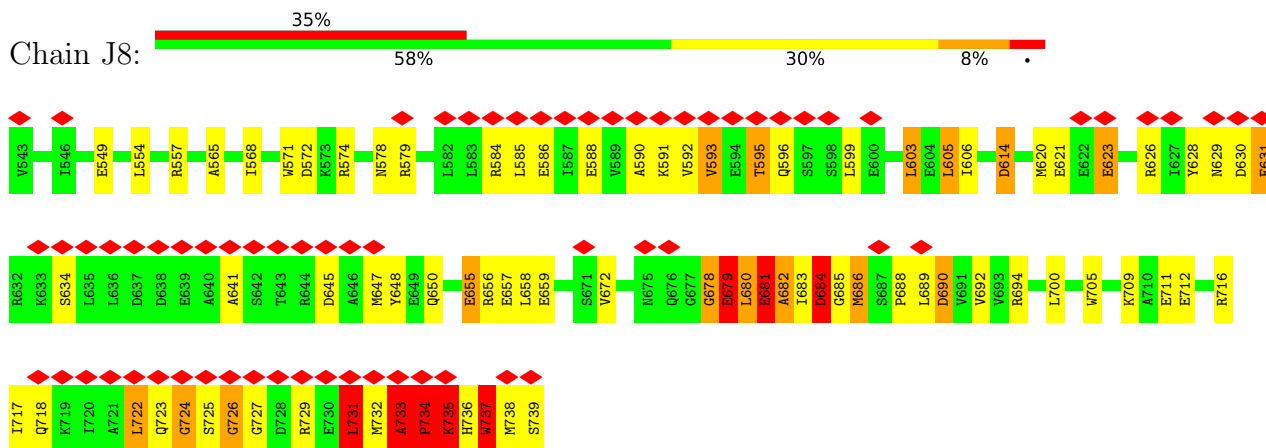




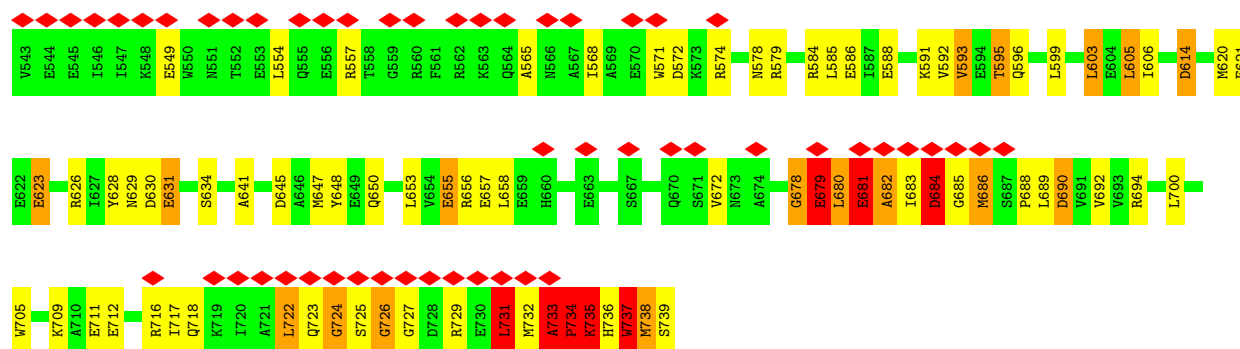
• Molecule 23: Nuclear pore complex protein NUP62



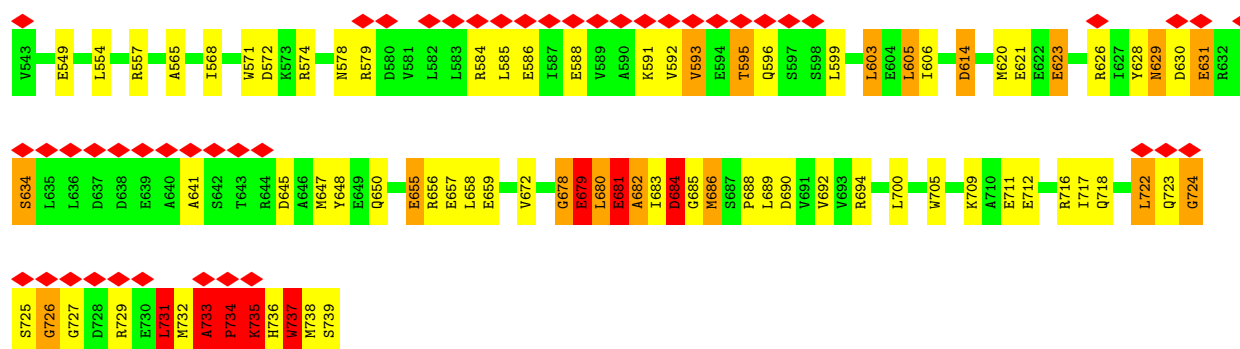
• Molecule 23: Nuclear pore complex protein NUP62



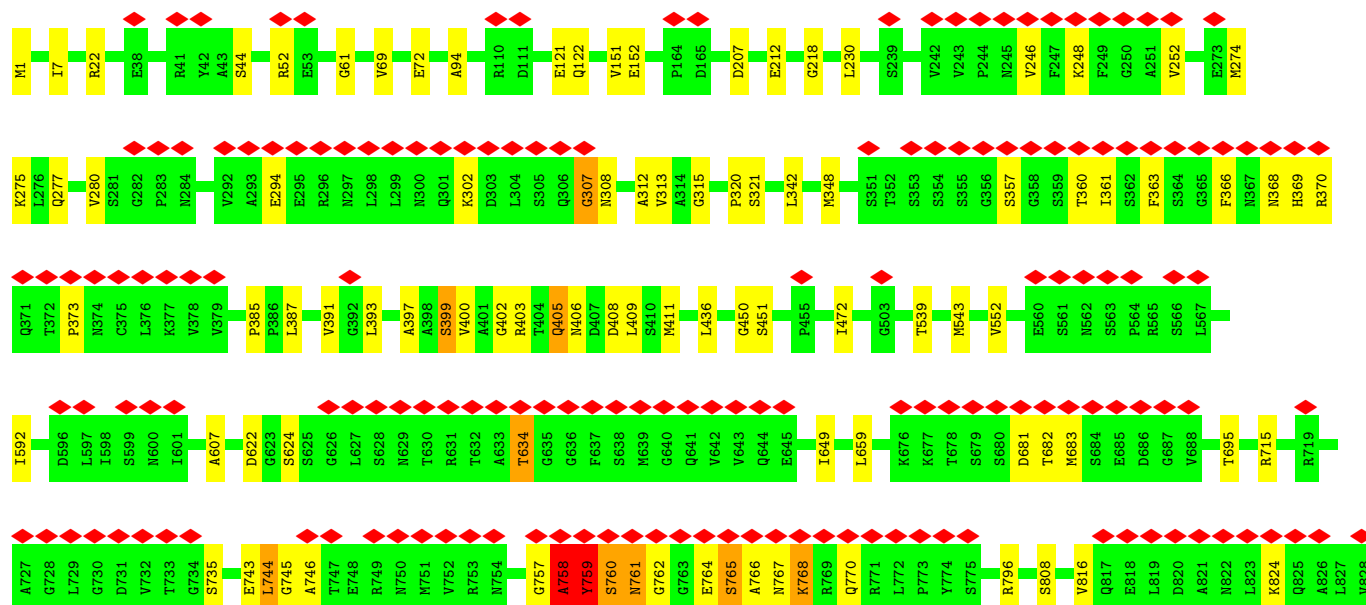
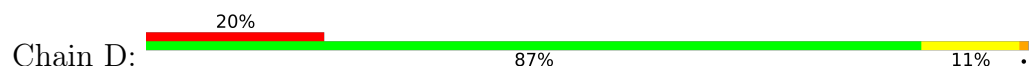
• Molecule 23: Nuclear pore complex protein NUP62

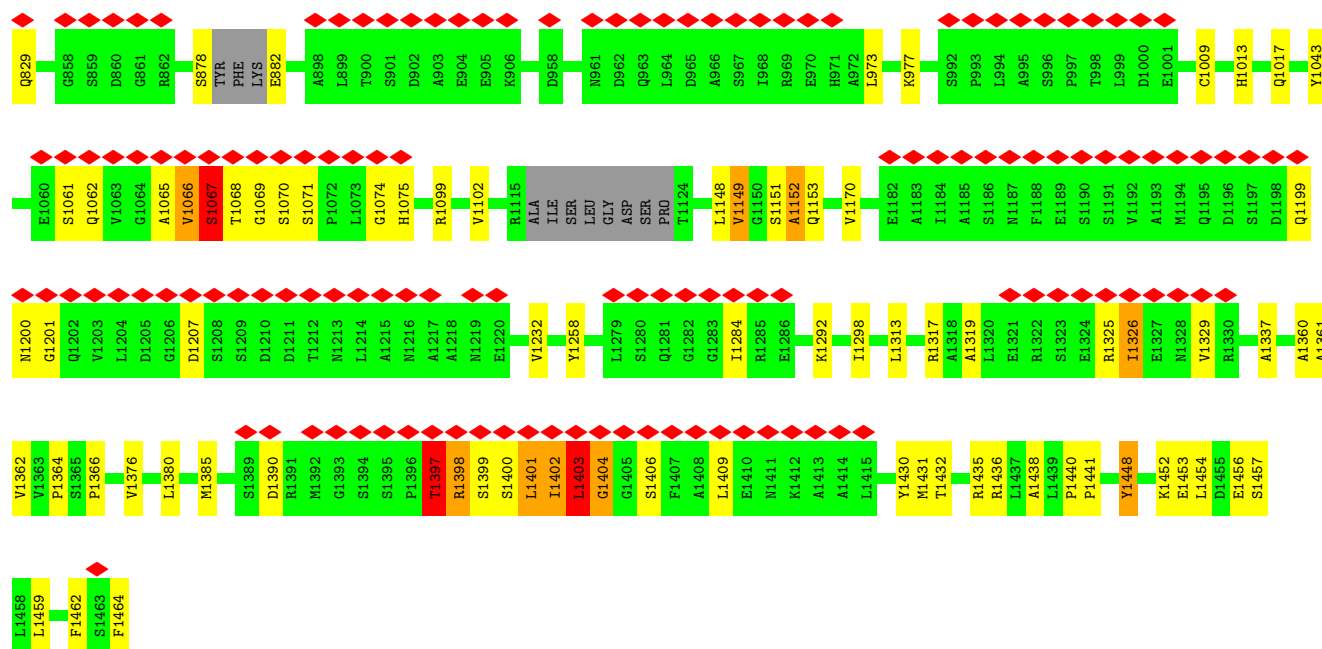


• Molecule 23: Nuclear pore complex protein NUP62

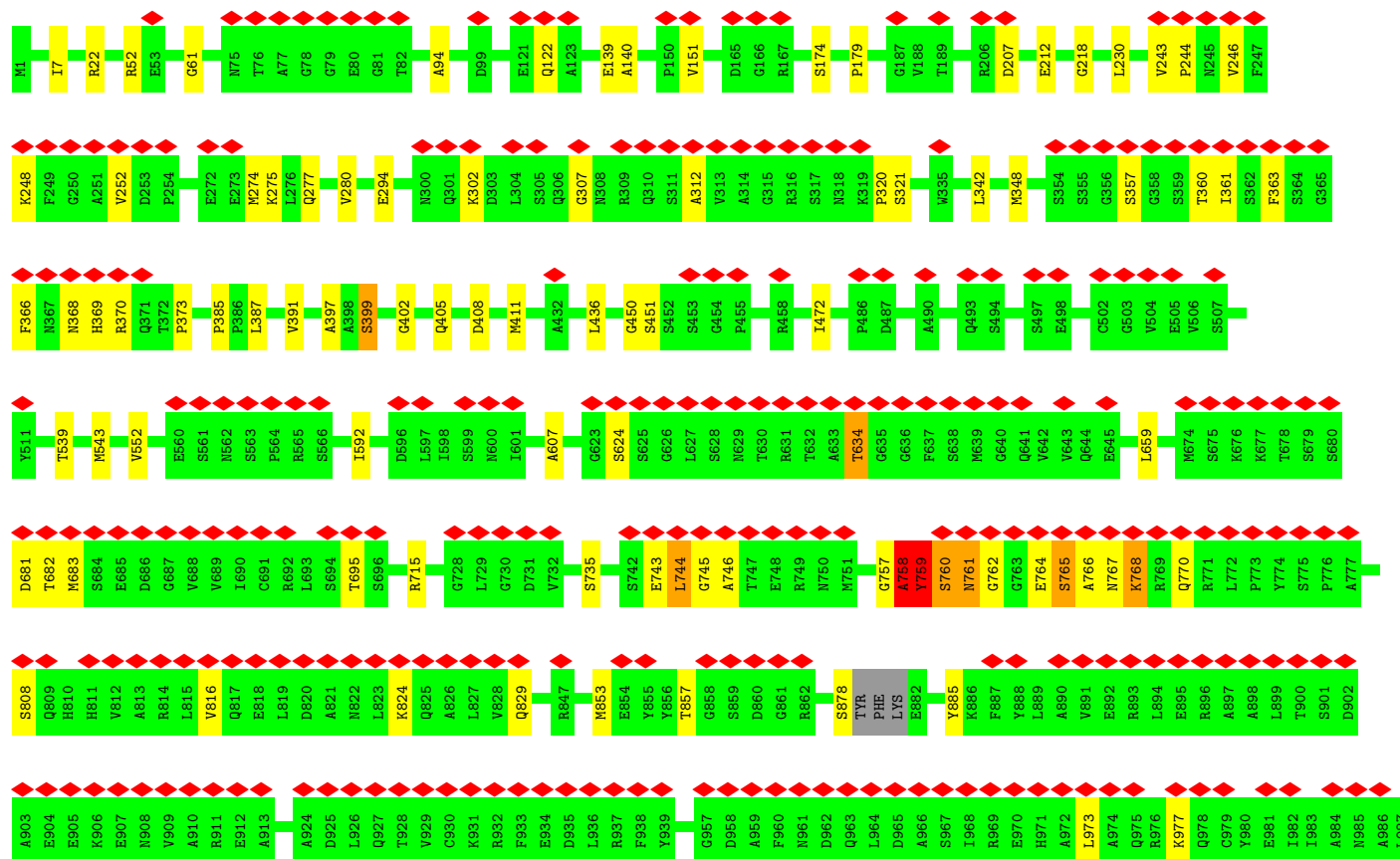
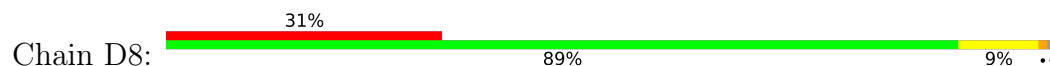


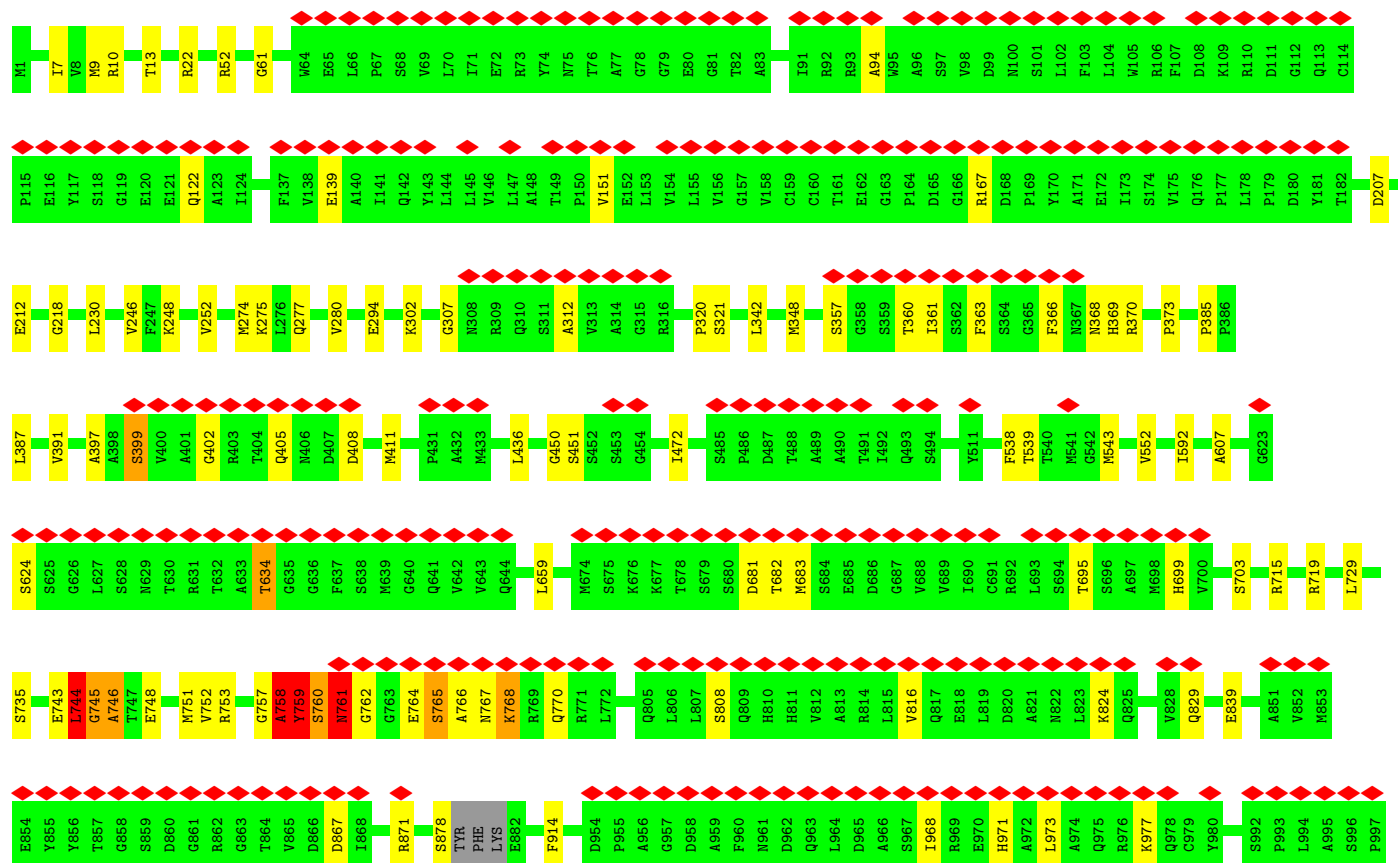
• Molecule 24: Nuclear pore complex protein NUP155



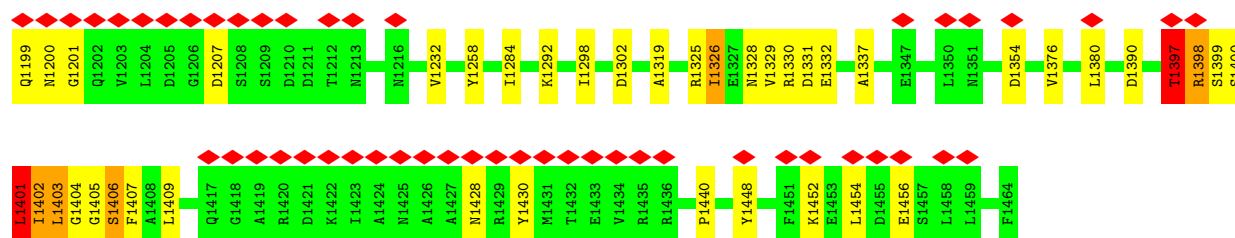


● Molecule 24: Nuclear pore complex protein NUP155

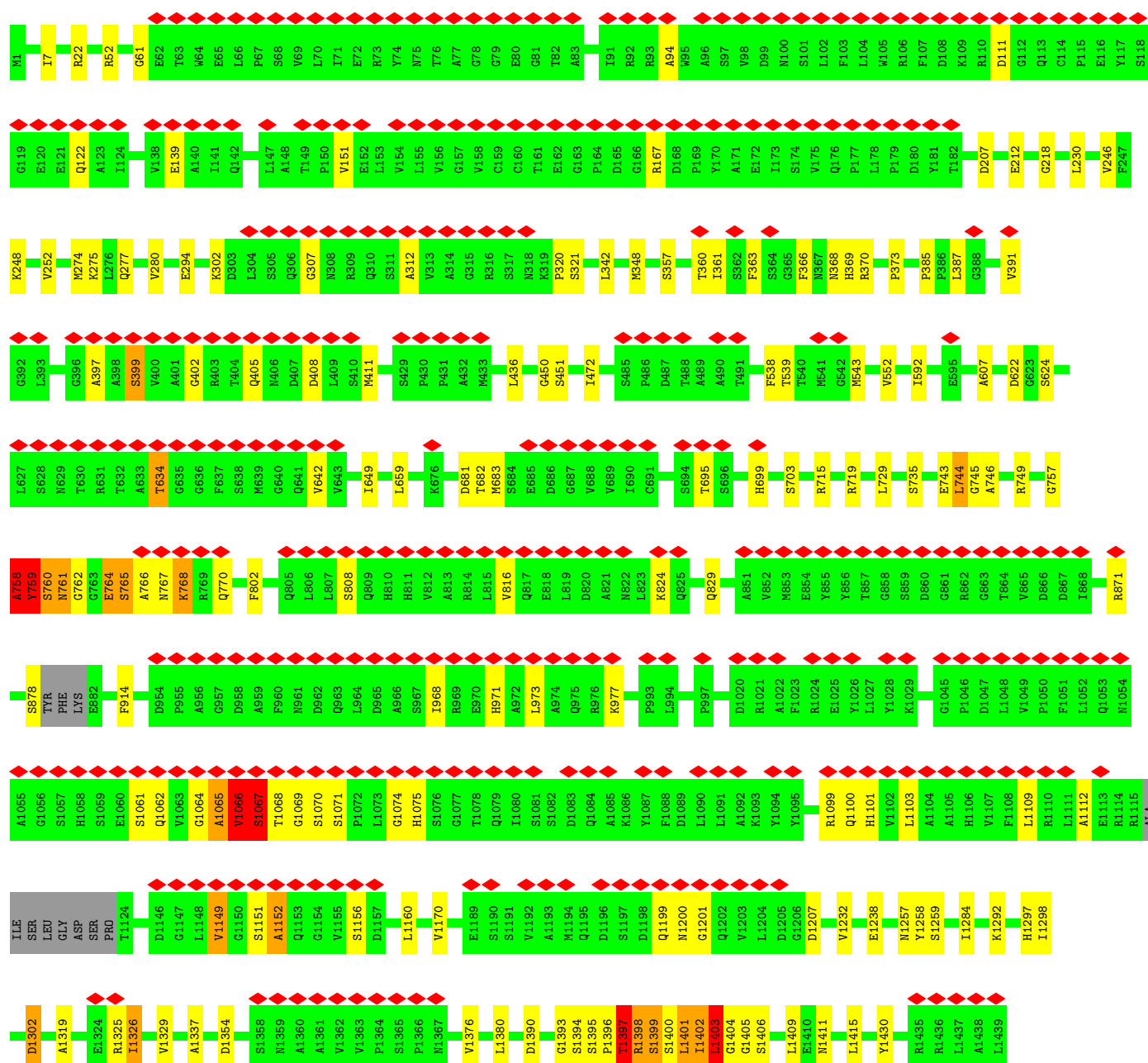
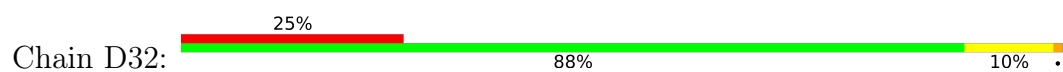


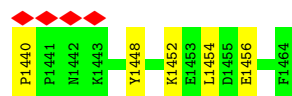




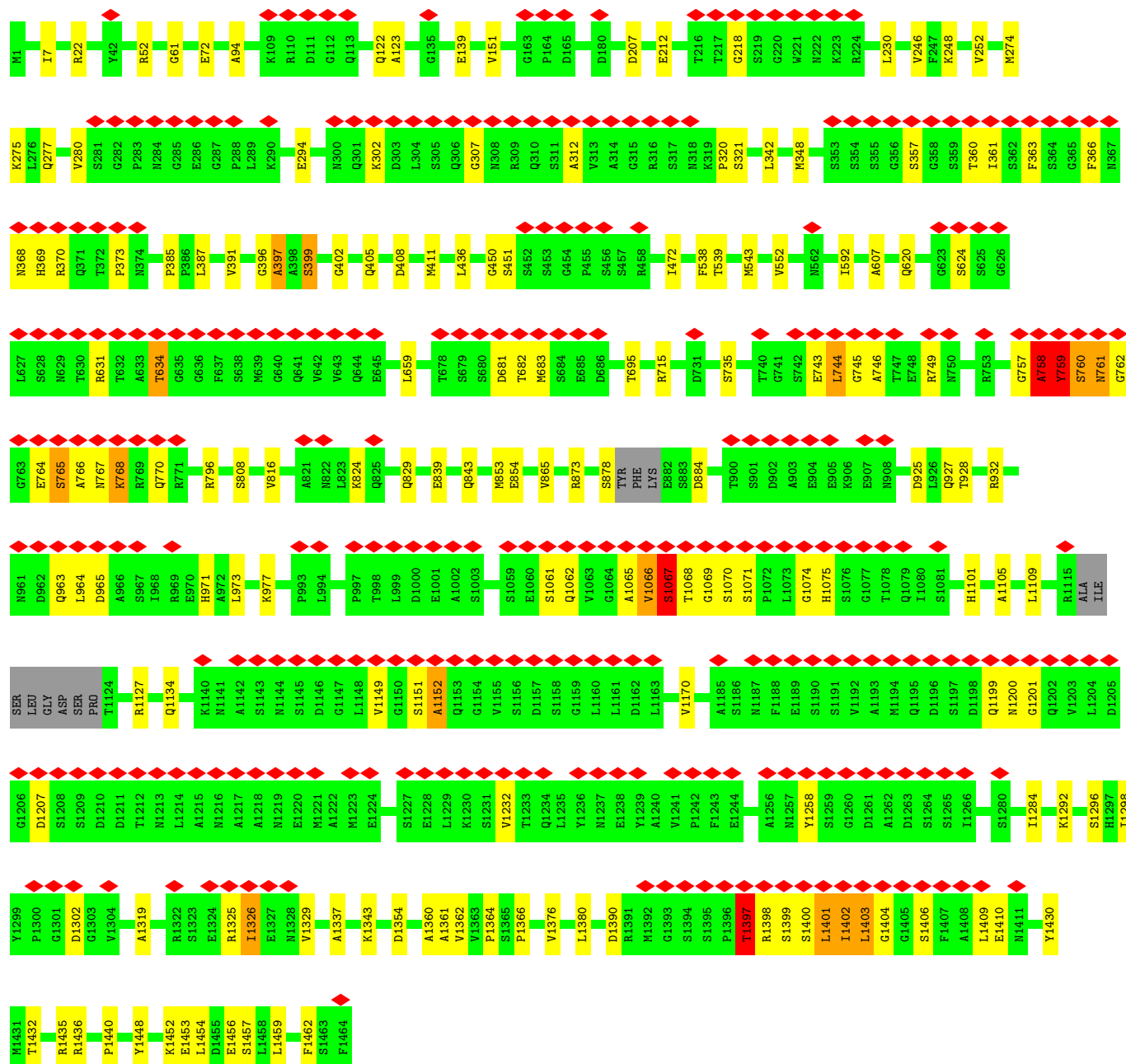
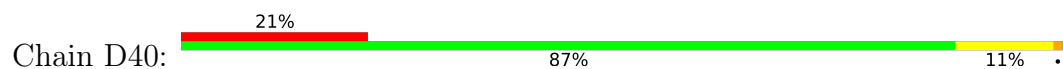


• Molecule 24: Nuclear pore complex protein NUP155





● Molecule 24: Nuclear pore complex protein NUP155



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C8	Depositor
Number of subtomograms used	75	Depositor
Resolution determination method	OTHER	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)	2500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.380	Depositor
Minimum map value	-0.333	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.07	Depositor
Map size (\AA)	1740.8, 1740.8, 1740.8	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	8.704, 8.704, 8.704	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	R	2.22	73/11843 (0.6%)	1.56	85/16033 (0.5%)
1	R16	2.21	73/11843 (0.6%)	1.56	84/16033 (0.5%)
1	R8	2.22	73/11843 (0.6%)	1.56	81/16033 (0.5%)
2	M	1.26	111/5730 (1.9%)	1.42	99/7766 (1.3%)
2	M16	1.26	114/5730 (2.0%)	1.42	97/7766 (1.2%)
2	M8	1.26	111/5730 (1.9%)	1.42	97/7766 (1.2%)
3	N	1.24	41/2366 (1.7%)	1.32	25/3234 (0.8%)
3	N16	1.24	39/2366 (1.6%)	1.32	25/3234 (0.8%)
3	N8	1.24	40/2366 (1.7%)	1.32	25/3234 (0.8%)
4	T	3.67	6/5605 (0.1%)	1.68	19/7591 (0.3%)
4	T16	3.67	6/5605 (0.1%)	1.68	17/7591 (0.2%)
4	T8	3.67	6/5605 (0.1%)	1.68	17/7591 (0.2%)
5	P	1.26	106/5736 (1.8%)	1.29	85/7754 (1.1%)
5	P16	1.26	105/5736 (1.8%)	1.29	85/7754 (1.1%)
5	P8	1.26	107/5736 (1.9%)	1.29	85/7754 (1.1%)
6	O	1.17	33/2391 (1.4%)	1.30	34/3246 (1.0%)
6	O16	1.16	33/2391 (1.4%)	1.30	34/3246 (1.0%)
6	O8	1.17	33/2391 (1.4%)	1.30	34/3246 (1.0%)
7	Q	1.29	51/2834 (1.8%)	1.48	53/3849 (1.4%)
7	Q16	1.29	51/2834 (1.8%)	1.48	53/3849 (1.4%)
7	Q8	1.28	48/2834 (1.7%)	1.48	53/3849 (1.4%)
8	L	2.52	4/7942 (0.1%)	1.52	13/10761 (0.1%)
8	L16	2.52	3/7942 (0.0%)	1.52	13/10761 (0.1%)
8	L8	2.52	3/7942 (0.0%)	1.52	13/10761 (0.1%)
9	K	1.77	213/5800 (3.7%)	1.91	212/7828 (2.7%)
9	K16	0.77	0/5801	1.25	6/7828 (0.1%)
9	K8	1.77	215/5800 (3.7%)	1.91	211/7828 (2.7%)
10	C	1.59	399/14649 (2.7%)	1.80	503/19823 (2.5%)
10	C16	1.59	409/14783 (2.8%)	1.82	520/20005 (2.6%)
10	C24	1.59	410/14783 (2.8%)	1.82	526/20005 (2.6%)
10	C32	1.59	413/14783 (2.8%)	1.82	525/20005 (2.6%)
10	C8	1.58	381/14420 (2.6%)	1.73	454/19508 (2.3%)
11	A16	1.24	107/6584 (1.6%)	1.21	61/8878 (0.7%)
11	A24	1.24	99/6584 (1.5%)	1.23	68/8878 (0.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
11	A32	1.24	108/6584 (1.6%)	1.21	61/8878 (0.7%)
11	A40	1.24	99/6584 (1.5%)	1.23	68/8878 (0.8%)
12	A	1.23	84/5826 (1.4%)	1.21	58/7855 (0.7%)
12	A48	1.23	86/5855 (1.5%)	1.21	58/7897 (0.7%)
13	V	1.78	67/1617 (4.1%)	1.71	42/2175 (1.9%)
14	W	1.13	65/6274 (1.0%)	1.36	70/8517 (0.8%)
15	J	1.49	50/1516 (3.3%)	1.41	26/2038 (1.3%)
16	A8	1.16	5/530 (0.9%)	1.38	10/709 (1.4%)
17	F	1.44	6/220 (2.7%)	2.85	17/302 (5.6%)
17	F16	1.45	6/220 (2.7%)	2.88	17/302 (5.6%)
17	F24	1.45	6/220 (2.7%)	2.88	17/302 (5.6%)
17	F8	1.44	6/220 (2.7%)	2.87	17/302 (5.6%)
18	B	1.42	356/15710 (2.3%)	1.68	461/21300 (2.2%)
18	B8	1.42	356/15710 (2.3%)	1.68	467/21300 (2.2%)
19	4	1.53	98/3497 (2.8%)	1.74	92/4746 (1.9%)
19	48	1.53	98/3497 (2.8%)	1.74	89/4746 (1.9%)
20	E	1.51	95/4165 (2.3%)	1.56	92/5657 (1.6%)
20	E8	1.51	95/4165 (2.3%)	1.56	91/5657 (1.6%)
21	H	1.31	46/2046 (2.2%)	1.31	24/2749 (0.9%)
21	H16	1.32	45/2046 (2.2%)	1.31	24/2749 (0.9%)
21	H24	1.31	45/2046 (2.2%)	1.31	24/2749 (0.9%)
21	H8	1.31	45/2046 (2.2%)	1.31	24/2749 (0.9%)
22	I	1.45	50/1978 (2.5%)	1.35	33/2664 (1.2%)
22	I16	1.45	50/1978 (2.5%)	1.34	32/2664 (1.2%)
22	I24	1.45	48/1978 (2.4%)	1.34	33/2664 (1.2%)
22	I8	1.45	51/1978 (2.6%)	1.34	31/2664 (1.2%)
23	J16	1.30	30/1617 (1.9%)	1.42	39/2174 (1.8%)
23	J24	1.30	29/1617 (1.8%)	1.42	39/2174 (1.8%)
23	J32	1.30	31/1617 (1.9%)	1.41	39/2174 (1.8%)
23	J8	1.30	31/1617 (1.9%)	1.42	39/2174 (1.8%)
24	D	0.76	2/11328 (0.0%)	1.25	27/15333 (0.2%)
24	D16	0.76	2/11328 (0.0%)	1.25	26/15333 (0.2%)
24	D24	0.76	2/11328 (0.0%)	1.25	24/15333 (0.2%)
24	D32	0.76	2/11328 (0.0%)	1.25	26/15333 (0.2%)
24	D40	0.76	2/11328 (0.0%)	1.25	27/15333 (0.2%)
24	D8	0.76	2/11328 (0.0%)	1.25	26/15333 (0.2%)
All	All	1.65	6115/410270 (1.5%)	1.52	6602/555195 (1.2%)

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	R	0	45
1	R16	0	45
1	R8	0	45
2	M	0	33
2	M16	0	34
2	M8	0	33
3	N	0	14
3	N16	0	14
3	N8	0	14
4	T	0	7
4	T16	0	7
4	T8	0	7
5	P	0	33
5	P16	0	33
5	P8	0	33
6	O	0	9
6	O16	0	9
6	O8	0	9
7	Q	0	17
7	Q16	0	17
7	Q8	0	17
8	L	0	3
8	L16	0	3
8	L8	0	3
9	K	0	84
9	K16	0	6
9	K8	0	84
10	C	0	171
10	C16	0	178
10	C24	0	178
10	C32	0	178
10	C8	0	146
11	A16	0	38
11	A24	0	40
11	A32	0	38
11	A40	0	40
12	A	0	36
12	A48	0	36
13	V	0	24
14	W	0	22
15	J	0	7
16	A8	0	3
17	F	0	10

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Mol	Chain	#Chirality outliers	#Planarity outliers
17	F16	0	10
17	F24	0	10
17	F8	0	10
18	B	0	196
18	B8	0	198
19	4	0	43
19	48	0	43
20	E	0	51
20	E8	0	51
21	H	0	8
21	H16	0	8
21	H24	0	8
21	H8	0	8
22	I	0	12
22	I16	0	12
22	I24	0	12
22	I8	0	12
23	J16	0	9
23	J24	0	9
23	J32	0	9
23	J8	0	9
24	D	0	29
24	D16	0	29
24	D24	0	29
24	D32	0	29
24	D40	0	29
24	D8	0	29
All	All	0	2705

The worst 5 of 6115 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	R	529	HIS	CD2-NE2	170.27	3.25	1.37
1	R8	529	HIS	CD2-NE2	170.21	3.25	1.37
1	R16	529	HIS	CD2-NE2	170.14	3.25	1.37
4	T	160	HIS	CD2-NE2	169.95	3.24	1.37
4	T8	160	HIS	CD2-NE2	169.94	3.24	1.37

The worst 5 of 6602 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	L8	1054	HIS	ND1-CE1-NE2	-53.29	55.11	108.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	L	1054	HIS	ND1-CE1-NE2	-53.27	55.12	108.40
8	L16	1054	HIS	ND1-CE1-NE2	-53.26	55.14	108.40
1	R16	529	HIS	ND1-CE1-NE2	-52.76	55.64	108.40
1	R	529	HIS	ND1-CE1-NE2	-52.75	55.65	108.40

There are no chirality outliers.

5 of 2705 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	R	436	ARG	Sidechain
1	R	47	ASP	Peptide
1	R	480	PHE	Sidechain
1	R	501	ARG	Sidechain
1	R	596	ARG	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	R	11593	0	11503	425	0
1	R16	11593	0	11502	207	0
1	R8	11593	0	11503	298	0
2	M	5598	0	5453	470	0
2	M16	5598	0	5451	523	0
2	M8	5598	0	5449	487	0
3	N	2302	0	2202	186	0
3	N16	2302	0	2202	192	0
3	N8	2302	0	2202	185	0
4	T	5498	0	5401	66	0
4	T16	5498	0	5401	68	0
4	T8	5498	0	5401	68	0
5	P	5620	0	5646	488	0
5	P16	5620	0	5647	375	0
5	P8	5620	0	5647	389	0
6	O	2336	0	2241	218	0
6	O16	2336	0	2243	164	0
6	O8	2336	0	2243	181	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	Q	2770	0	2651	175	0
7	Q16	2770	0	2651	163	0
7	Q8	2770	0	2651	167	0
8	L	7770	0	7584	103	0
8	L16	7770	0	7579	207	0
8	L8	7770	0	7583	161	0
9	K	5695	0	5537	500	0
9	K16	5696	0	5544	128	0
9	K8	5695	0	5537	493	0
10	C	14402	0	14575	1157	0
10	C16	14529	0	14695	1187	0
10	C24	14529	0	14696	1208	0
10	C32	14529	0	14697	1031	0
10	C8	14177	0	14346	1063	0
11	A16	6472	0	6473	547	0
11	A24	6472	0	6474	496	0
11	A32	6472	0	6472	530	0
11	A40	6472	0	6474	503	0
12	A	5726	0	5723	313	0
12	A48	5752	0	5745	317	0
13	V	1590	0	1576	201	0
14	W	6141	0	6109	391	0
15	J	1504	0	1487	188	0
16	A8	523	0	517	33	0
17	F	213	0	187	41	0
17	F16	213	0	187	40	0
17	F24	213	0	187	39	0
17	F8	213	0	187	40	0
18	B	15417	0	15672	1142	0
18	B8	15417	0	15674	1132	0
19	4	3413	0	3328	200	0
19	48	3413	0	3328	214	0
20	E	4057	0	4120	256	0
20	E8	4057	0	4120	272	0
21	H	2023	0	2068	226	0
21	H16	2023	0	2066	194	0
21	H24	2023	0	2066	231	0
21	H8	2023	0	2066	189	0
22	I	1939	0	1924	202	0
22	I16	1939	0	1924	206	0
22	I24	1939	0	1924	200	0
22	I8	1939	0	1923	189	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	J16	1601	0	1575	175	0
23	J24	1601	0	1575	203	0
23	J32	1601	0	1575	201	0
23	J8	1601	0	1575	173	0
24	D	11141	0	11068	316	0
24	D16	11141	0	11074	343	0
24	D24	11141	0	11072	147	0
24	D32	11141	0	11074	263	0
24	D40	11141	0	11072	230	0
24	D8	11141	0	11075	152	0
All	All	402561	0	400399	18966	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 24.

The worst 5 of 18966 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)
18:B8:1210:CYS:SG	18:B8:1234:MET:HE1	1.23	1.74
2:M:847:PHE:HB2	4:T:656:TRP:CZ3	1.17	1.70
9:K8:1085:TYR:CE1	9:K8:1093:SER:HB2	1.24	1.68
10:C:345:MET:HE1	10:C:401:ILE:CD1	1.19	1.67
18:B:1210:CYS:SG	18:B:1234:MET:HE1	1.23	1.67

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	R	1458/1495 (98%)	1379 (95%)	60 (4%)	19 (1%)	10	43
1	R16	1458/1495 (98%)	1379 (95%)	59 (4%)	20 (1%)	9	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R8	1458/1495 (98%)	1379 (95%)	59 (4%)	20 (1%)	9	41
2	M	688/704 (98%)	650 (94%)	19 (3%)	19 (3%)	4	24
2	M16	688/704 (98%)	650 (94%)	19 (3%)	19 (3%)	4	24
2	M8	688/704 (98%)	650 (94%)	19 (3%)	19 (3%)	4	24
3	N	300/302 (99%)	285 (95%)	12 (4%)	3 (1%)	13	49
3	N16	300/302 (99%)	285 (95%)	12 (4%)	3 (1%)	13	49
3	N8	300/302 (99%)	285 (95%)	12 (4%)	3 (1%)	13	49
4	T	682/684 (100%)	647 (95%)	29 (4%)	6 (1%)	14	52
4	T16	682/684 (100%)	647 (95%)	29 (4%)	6 (1%)	14	52
4	T8	682/684 (100%)	647 (95%)	29 (4%)	6 (1%)	14	52
5	P	700/716 (98%)	668 (95%)	15 (2%)	17 (2%)	5	27
5	P16	700/716 (98%)	668 (95%)	16 (2%)	16 (2%)	5	28
5	P8	700/716 (98%)	668 (95%)	16 (2%)	16 (2%)	5	28
6	O	299/326 (92%)	286 (96%)	5 (2%)	8 (3%)	4	25
6	O16	299/326 (92%)	287 (96%)	4 (1%)	8 (3%)	4	25
6	O8	299/326 (92%)	286 (96%)	5 (2%)	8 (3%)	4	25
7	Q	359/361 (99%)	335 (93%)	15 (4%)	9 (2%)	4	26
7	Q16	359/361 (99%)	335 (93%)	15 (4%)	9 (2%)	4	26
7	Q8	359/361 (99%)	335 (93%)	15 (4%)	9 (2%)	4	26
8	L	970/977 (99%)	925 (95%)	34 (4%)	11 (1%)	12	47
8	L16	970/977 (99%)	925 (95%)	34 (4%)	11 (1%)	12	47
8	L8	970/977 (99%)	925 (95%)	34 (4%)	11 (1%)	12	47
9	K	701/709 (99%)	638 (91%)	29 (4%)	34 (5%)	2	16
9	K16	701/709 (99%)	663 (95%)	24 (3%)	14 (2%)	6	32
9	K8	701/709 (99%)	638 (91%)	29 (4%)	34 (5%)	2	16
10	C	1816/1838 (99%)	1681 (93%)	64 (4%)	71 (4%)	2	19
10	C16	1836/1838 (100%)	1693 (92%)	69 (4%)	74 (4%)	2	18
10	C24	1836/1838 (100%)	1693 (92%)	69 (4%)	74 (4%)	2	18
10	C32	1836/1838 (100%)	1693 (92%)	68 (4%)	75 (4%)	2	18
10	C8	1781/1838 (97%)	1667 (94%)	56 (3%)	58 (3%)	3	21
11	A16	812/860 (94%)	779 (96%)	17 (2%)	16 (2%)	6	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	A24	812/860 (94%)	778 (96%)	17 (2%)	17 (2%)	5	30
11	A32	812/860 (94%)	779 (96%)	17 (2%)	16 (2%)	6	32
11	A40	812/860 (94%)	778 (96%)	17 (2%)	17 (2%)	5	30
12	A	717/763 (94%)	688 (96%)	15 (2%)	14 (2%)	6	32
12	A48	722/763 (95%)	693 (96%)	15 (2%)	14 (2%)	6	32
13	V	194/196 (99%)	175 (90%)	8 (4%)	11 (6%)	1	14
14	W	783/810 (97%)	737 (94%)	30 (4%)	16 (2%)	6	32
15	J	183/185 (99%)	175 (96%)	3 (2%)	5 (3%)	4	25
16	A8	61/63 (97%)	60 (98%)	0	1 (2%)	8	38
17	F	26/28 (93%)	18 (69%)	3 (12%)	5 (19%)	0	2
17	F16	26/28 (93%)	18 (69%)	3 (12%)	5 (19%)	0	2
17	F24	26/28 (93%)	18 (69%)	3 (12%)	5 (19%)	0	2
17	F8	26/28 (93%)	18 (69%)	3 (12%)	5 (19%)	0	2
18	B	1963/1965 (100%)	1806 (92%)	79 (4%)	78 (4%)	2	18
18	B8	1963/1965 (100%)	1807 (92%)	78 (4%)	78 (4%)	2	18
19	4	445/447 (100%)	403 (91%)	16 (4%)	26 (6%)	1	14
19	48	445/447 (100%)	403 (91%)	16 (4%)	26 (6%)	1	14
20	E	517/519 (100%)	471 (91%)	19 (4%)	27 (5%)	1	15
20	E8	517/519 (100%)	471 (91%)	18 (4%)	28 (5%)	1	15
21	H	252/254 (99%)	245 (97%)	1 (0%)	6 (2%)	5	27
21	H16	252/254 (99%)	245 (97%)	1 (0%)	6 (2%)	5	27
21	H24	252/254 (99%)	245 (97%)	1 (0%)	6 (2%)	5	27
21	H8	252/254 (99%)	245 (97%)	1 (0%)	6 (2%)	5	27
22	I	233/237 (98%)	224 (96%)	7 (3%)	2 (1%)	14	52
22	I16	233/237 (98%)	224 (96%)	7 (3%)	2 (1%)	14	52
22	I24	233/237 (98%)	224 (96%)	7 (3%)	2 (1%)	14	52
22	I8	233/237 (98%)	224 (96%)	7 (3%)	2 (1%)	14	52
23	J16	195/197 (99%)	188 (96%)	5 (3%)	2 (1%)	13	49
23	J24	195/197 (99%)	188 (96%)	5 (3%)	2 (1%)	13	49
23	J32	195/197 (99%)	188 (96%)	5 (3%)	2 (1%)	13	49
23	J8	195/197 (99%)	188 (96%)	5 (3%)	2 (1%)	13	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	D	1447/1464 (99%)	1335 (92%)	70 (5%)	42 (3%)	3	23
24	D16	1447/1464 (99%)	1336 (92%)	69 (5%)	42 (3%)	3	23
24	D24	1447/1464 (99%)	1334 (92%)	71 (5%)	42 (3%)	3	23
24	D32	1447/1464 (99%)	1334 (92%)	71 (5%)	42 (3%)	3	23
24	D40	1447/1464 (99%)	1336 (92%)	69 (5%)	42 (3%)	3	23
24	D8	1447/1464 (99%)	1336 (92%)	69 (5%)	42 (3%)	3	23
All	All	50840/51742 (98%)	47606 (94%)	1822 (4%)	1412 (3%)	6	24

5 of 1412 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	R	302	MET
1	R	1183	GLU
1	R	1185	THR
1	R	1186	THR
1	R	1192	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	R	1286/1314 (98%)	1245 (97%)	41 (3%)	34	53
1	R16	1286/1314 (98%)	1247 (97%)	39 (3%)	36	55
1	R8	1286/1314 (98%)	1246 (97%)	40 (3%)	35	54
2	M	619/626 (99%)	598 (97%)	21 (3%)	32	51
2	M16	619/626 (99%)	599 (97%)	20 (3%)	34	53
2	M8	619/626 (99%)	597 (96%)	22 (4%)	30	50
3	N	246/246 (100%)	243 (99%)	3 (1%)	67	78
3	N16	246/246 (100%)	242 (98%)	4 (2%)	58	73
3	N8	246/246 (100%)	244 (99%)	2 (1%)	79	85
4	T	611/611 (100%)	590 (97%)	21 (3%)	32	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	T16	611/611 (100%)	596 (98%)	15 (2%)	42	61
4	T8	611/611 (100%)	592 (97%)	19 (3%)	35	54
5	P	622/629 (99%)	603 (97%)	19 (3%)	35	54
5	P16	622/629 (99%)	606 (97%)	16 (3%)	41	59
5	P8	622/629 (99%)	604 (97%)	18 (3%)	37	56
6	O	262/280 (94%)	257 (98%)	5 (2%)	52	69
6	O16	262/280 (94%)	257 (98%)	5 (2%)	52	69
6	O8	262/280 (94%)	257 (98%)	5 (2%)	52	69
7	Q	302/302 (100%)	297 (98%)	5 (2%)	56	72
7	Q16	302/302 (100%)	298 (99%)	4 (1%)	65	77
7	Q8	302/302 (100%)	299 (99%)	3 (1%)	73	82
8	L	859/861 (100%)	853 (99%)	6 (1%)	81	87
8	L16	859/861 (100%)	851 (99%)	8 (1%)	75	83
8	L8	859/861 (100%)	853 (99%)	6 (1%)	81	87
9	K	621/623 (100%)	569 (92%)	52 (8%)	9	27
9	K16	621/623 (100%)	616 (99%)	5 (1%)	79	85
9	K8	621/623 (100%)	570 (92%)	51 (8%)	9	28
10	C	1628/1641 (99%)	1473 (90%)	155 (10%)	7	22
10	C16	1641/1641 (100%)	1488 (91%)	153 (9%)	7	23
10	C24	1641/1641 (100%)	1498 (91%)	143 (9%)	8	25
10	C32	1641/1641 (100%)	1499 (91%)	142 (9%)	8	25
10	C8	1598/1641 (97%)	1451 (91%)	147 (9%)	7	23
11	A16	696/730 (95%)	676 (97%)	20 (3%)	37	56
11	A24	696/730 (95%)	678 (97%)	18 (3%)	41	59
11	A32	696/730 (95%)	676 (97%)	20 (3%)	37	56
11	A40	696/730 (95%)	678 (97%)	18 (3%)	41	59
12	A	614/647 (95%)	597 (97%)	17 (3%)	38	57
12	A48	617/647 (95%)	602 (98%)	15 (2%)	44	62
13	V	175/175 (100%)	154 (88%)	21 (12%)	4	16
14	W	693/715 (97%)	665 (96%)	28 (4%)	27	47
15	J	166/166 (100%)	156 (94%)	10 (6%)	16	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	A8	59/59 (100%)	55 (93%)	4 (7%)	13	34
17	F	25/25 (100%)	22 (88%)	3 (12%)	4	16
17	F16	25/25 (100%)	22 (88%)	3 (12%)	4	16
17	F24	25/25 (100%)	22 (88%)	3 (12%)	4	16
17	F8	25/25 (100%)	22 (88%)	3 (12%)	4	16
18	B	1759/1759 (100%)	1652 (94%)	107 (6%)	15	37
18	B8	1759/1759 (100%)	1654 (94%)	105 (6%)	16	37
19	4	374/374 (100%)	356 (95%)	18 (5%)	21	43
19	48	374/374 (100%)	355 (95%)	19 (5%)	20	41
20	E	450/450 (100%)	425 (94%)	25 (6%)	17	38
20	E8	450/450 (100%)	423 (94%)	27 (6%)	16	37
21	H	223/223 (100%)	217 (97%)	6 (3%)	40	58
21	H16	223/223 (100%)	220 (99%)	3 (1%)	65	77
21	H24	223/223 (100%)	220 (99%)	3 (1%)	65	77
21	H8	223/223 (100%)	217 (97%)	6 (3%)	40	58
22	I	212/212 (100%)	204 (96%)	8 (4%)	28	49
22	I16	212/212 (100%)	202 (95%)	10 (5%)	22	44
22	I24	212/212 (100%)	202 (95%)	10 (5%)	22	44
22	I8	212/212 (100%)	203 (96%)	9 (4%)	25	46
23	J16	176/176 (100%)	168 (96%)	8 (4%)	23	45
23	J24	176/176 (100%)	168 (96%)	8 (4%)	23	45
23	J32	176/176 (100%)	168 (96%)	8 (4%)	23	45
23	J8	176/176 (100%)	168 (96%)	8 (4%)	23	45
24	D	1214/1223 (99%)	1201 (99%)	13 (1%)	70	80
24	D16	1214/1223 (99%)	1197 (99%)	17 (1%)	62	75
24	D24	1214/1223 (99%)	1196 (98%)	18 (2%)	60	75
24	D32	1214/1223 (99%)	1197 (99%)	17 (1%)	62	75
24	D40	1214/1223 (99%)	1197 (99%)	17 (1%)	62	75
24	D8	1214/1223 (99%)	1201 (99%)	13 (1%)	70	80
All	All	44535/45058 (99%)	42674 (96%)	1861 (4%)	27	46

5 of 1861 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	C	718	HIS
10	C32	805	LEU
10	C8	1614	LEU
10	C32	634	SER
22	I16	371	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 312 such sidechains are listed below:

Mol	Chain	Res	Type
18	B	1032	GLN
21	H8	312	GLN
18	B	1745	HIS
18	B8	1748	HIS
24	D	654	HIS

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
10	C16	17
10	C24	17
10	C	17
10	C32	17
10	C8	15
9	K	9
9	K8	9
18	B8	7
18	B	6
11	A24	5
11	A40	5
11	A16	5
11	A32	5
19	4	5
19	48	5
1	R	4
1	R8	4
1	R16	4
14	W	4
12	A	4
12	A48	4
20	E	3
20	E8	3
5	P	3
5	P8	3
5	P16	3
13	V	3
22	I	2
22	I8	2
22	I24	2
22	I16	2
7	Q	2
7	Q8	2
7	Q16	2
3	N	2
3	N8	2
3	N16	2
15	J	1
23	J32	1
23	J8	1
23	J24	1
23	J16	1

The worst 5 of 211 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	210:LYS	C	252:ARG	N	22.49
1	I8	210:LYS	C	252:ARG	N	22.49
1	I24	210:LYS	C	252:ARG	N	22.49
1	I16	210:LYS	C	252:ARG	N	22.49
1	R	1121:ARG	C	1122:HIS	N	1.87

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-54657. These allow visual inspection of the internal detail of the map and identification of artifacts.

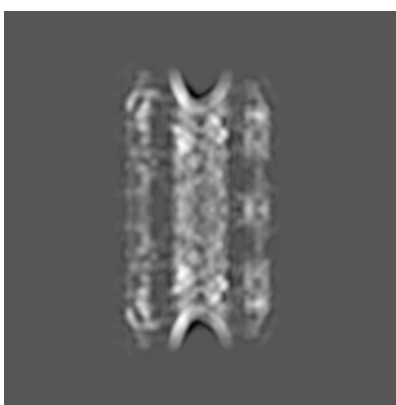
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

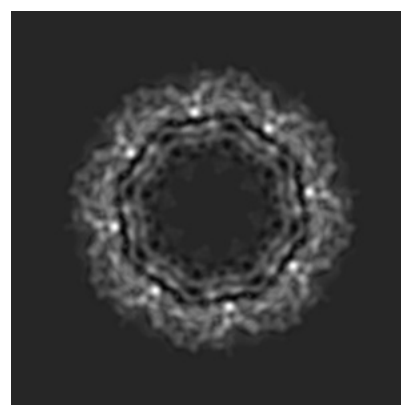
6.1.1 Primary map



X



Y



Z

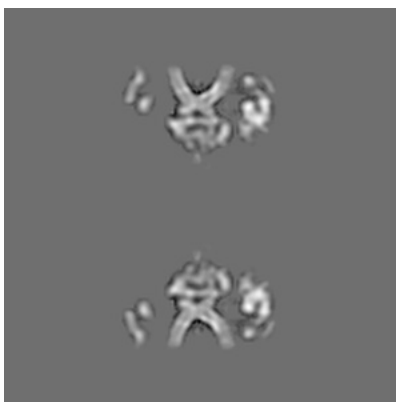
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

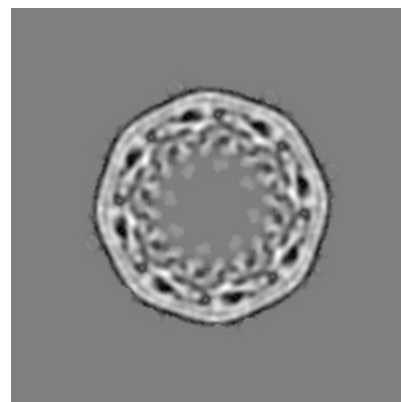
6.2.1 Primary map



X Index: 100



Y Index: 100



Z Index: 100

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

6.3 Largest variance slices [i](#)

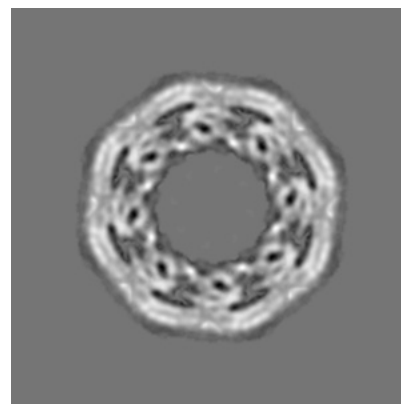
6.3.1 Primary map



X Index: 140



Y Index: 140

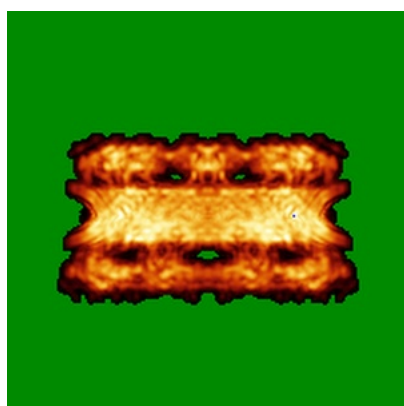


Z Index: 90

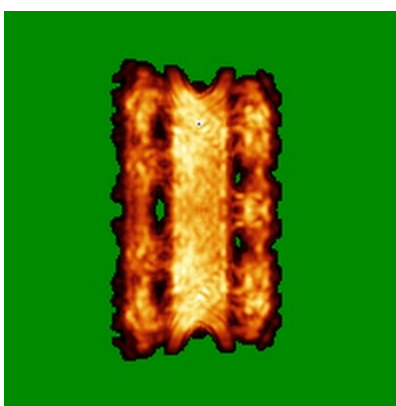
The images above show the largest variance slices of the map in three orthogonal directions.

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

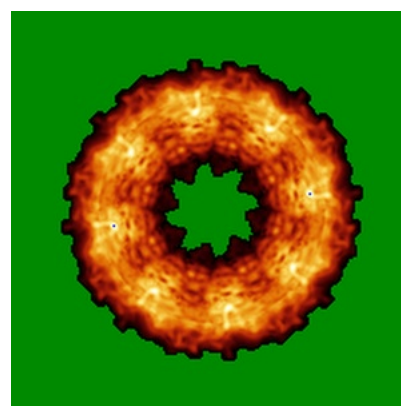
6.4.1 Primary map



X



Y

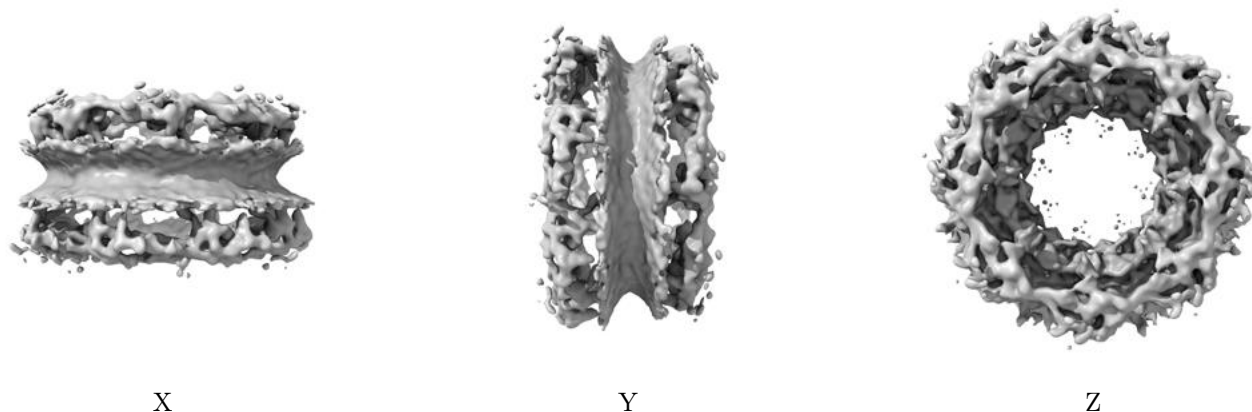


Z

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 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

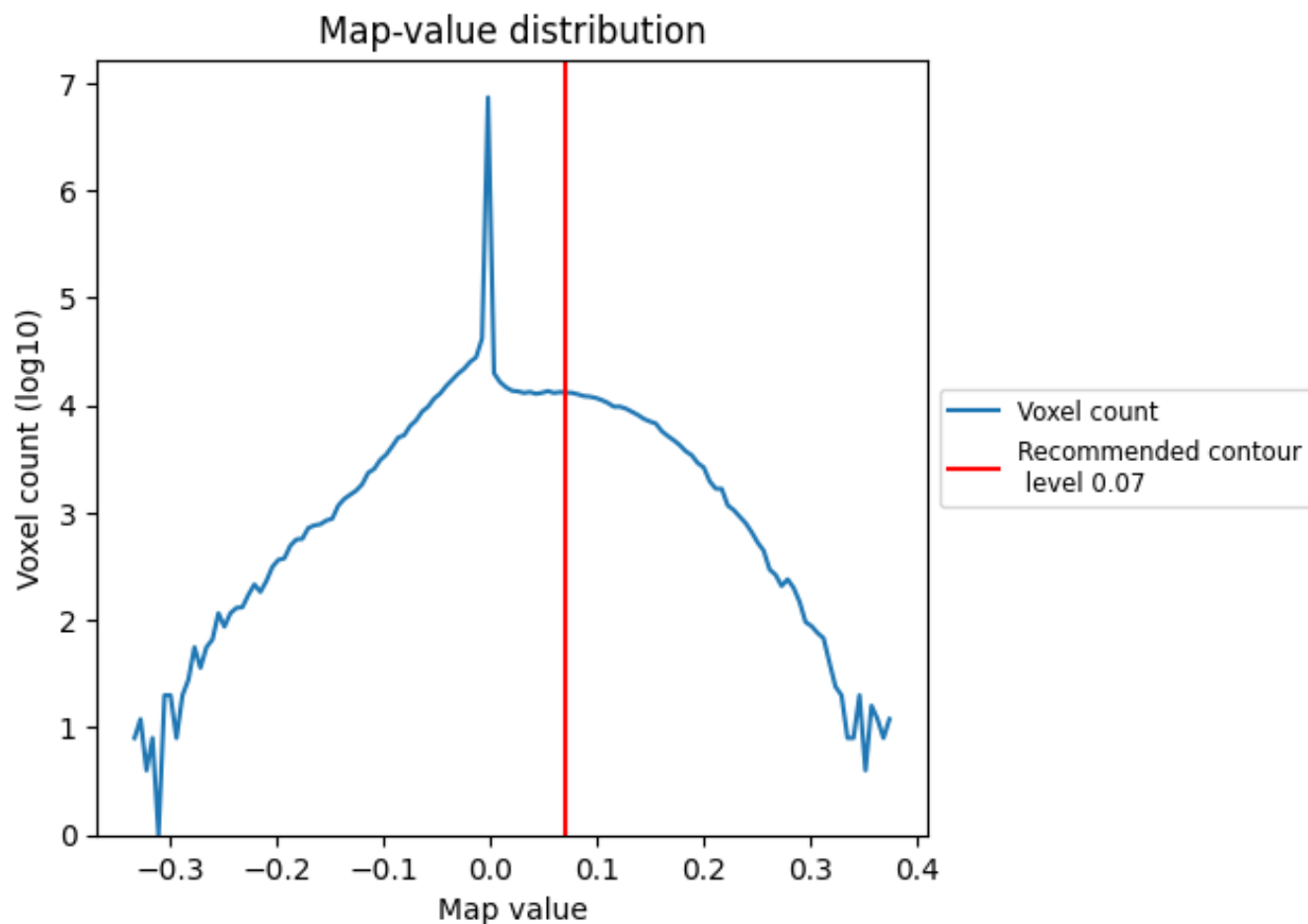
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

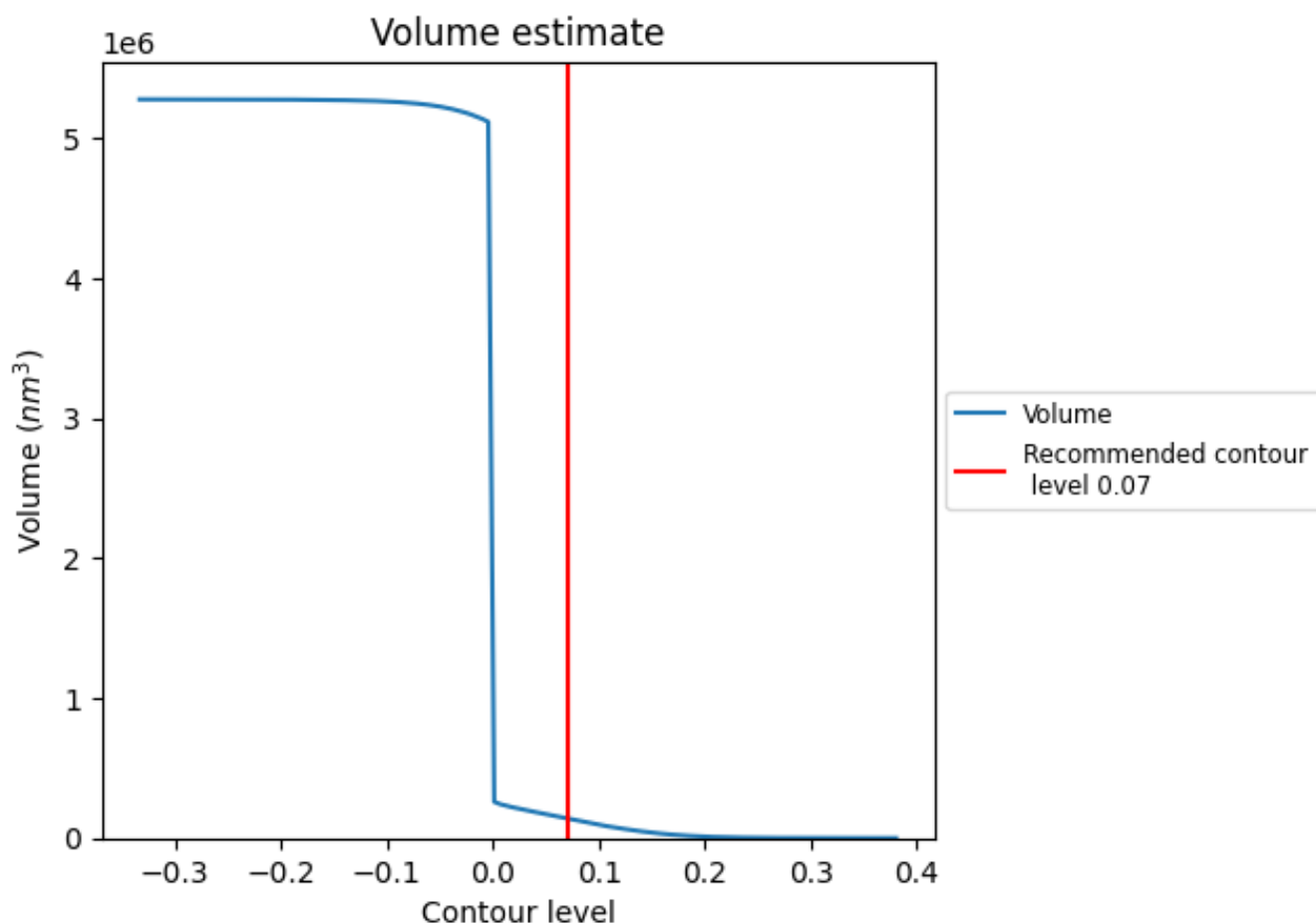
This section contains the results of statistical analysis of the map.

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.

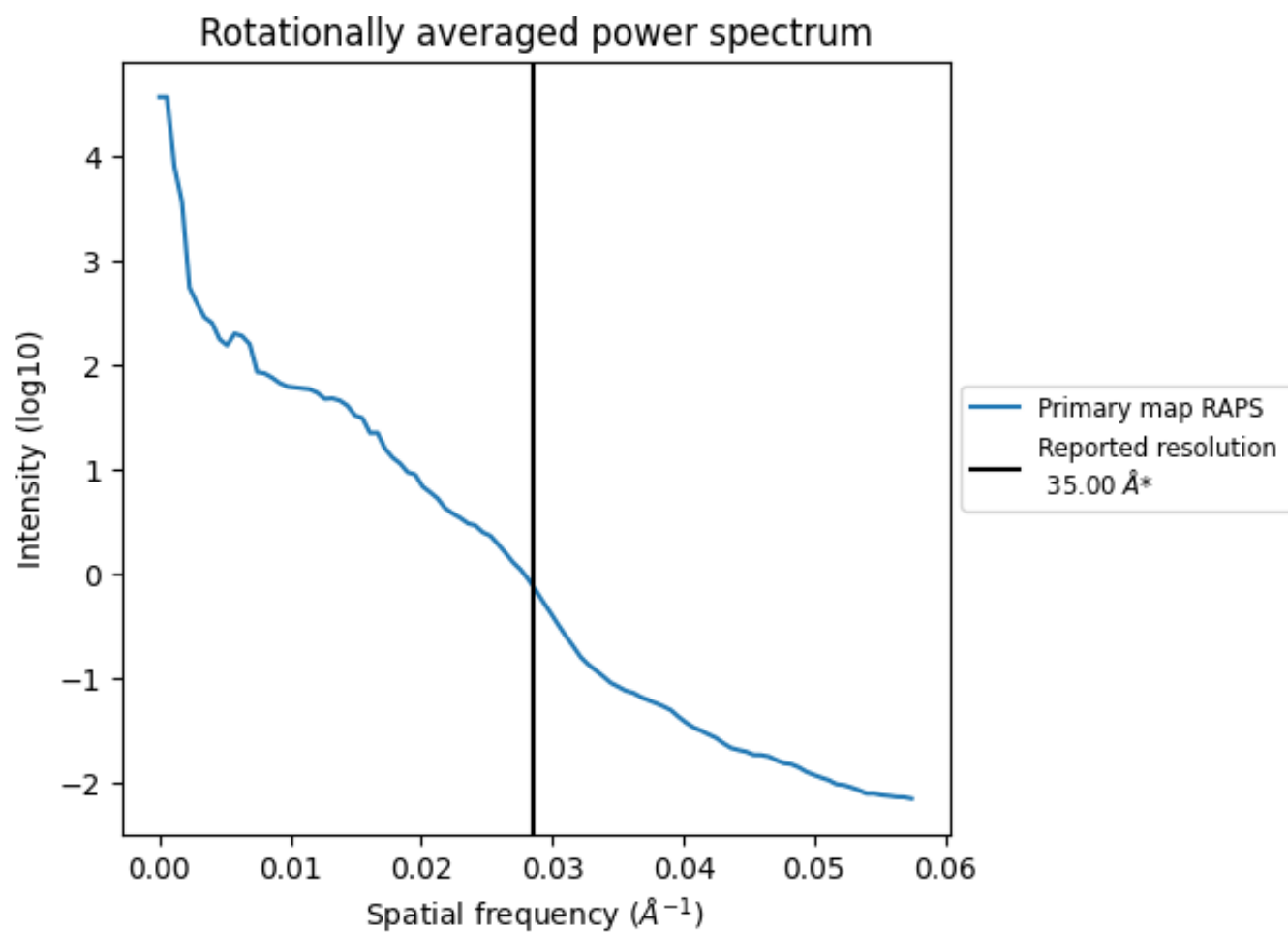
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 139608 nm^3 ; this corresponds to an approximate mass of 126112 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 0.029 Å⁻¹

8 Fourier-Shell correlation

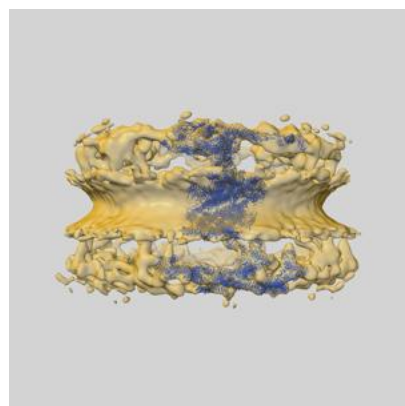
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit ⓘ

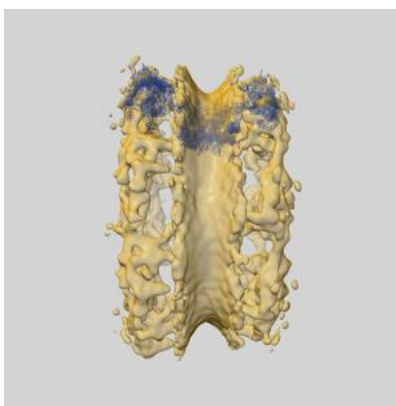
This section contains information regarding the fit between EMDB map EMD-54657 and PDB model 9SOB. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlays

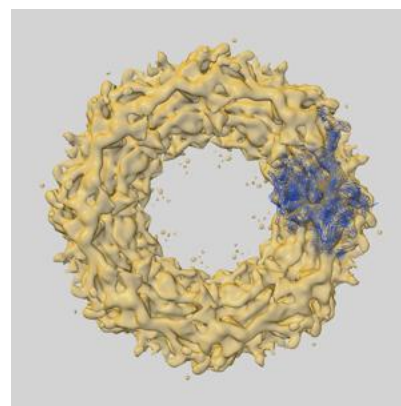
9.1.1 Map-model overlay ⓘ



X

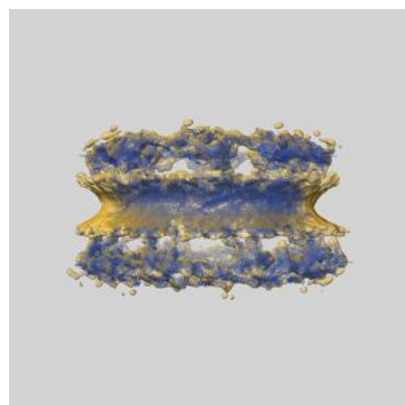


Y

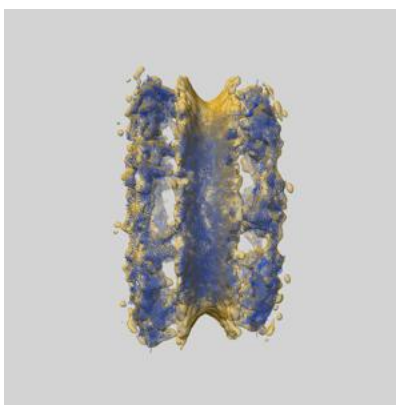


Z

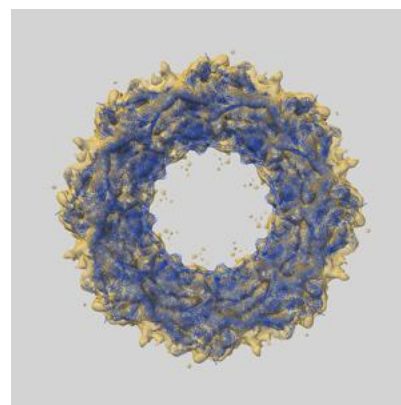
9.1.2 Map-model assembly overlay ⓘ



X



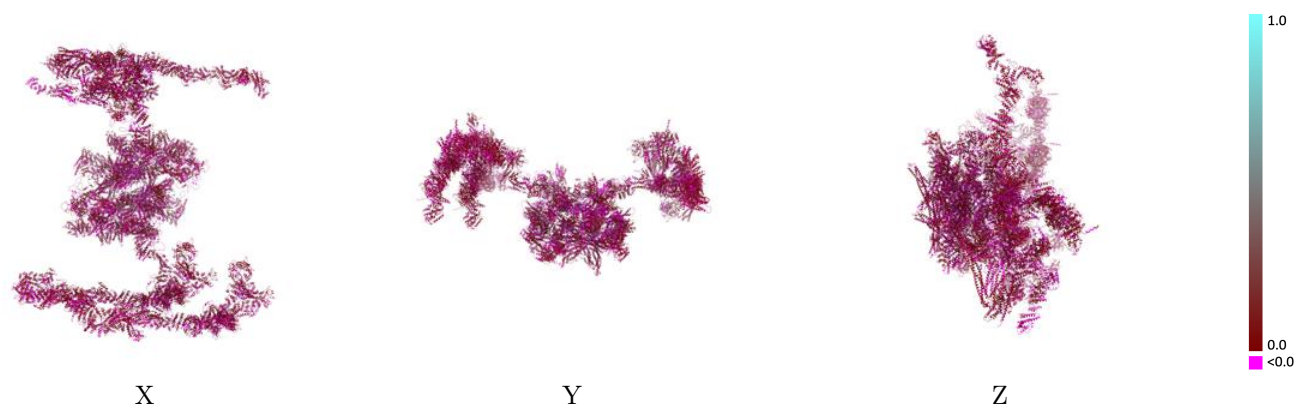
Y



Z

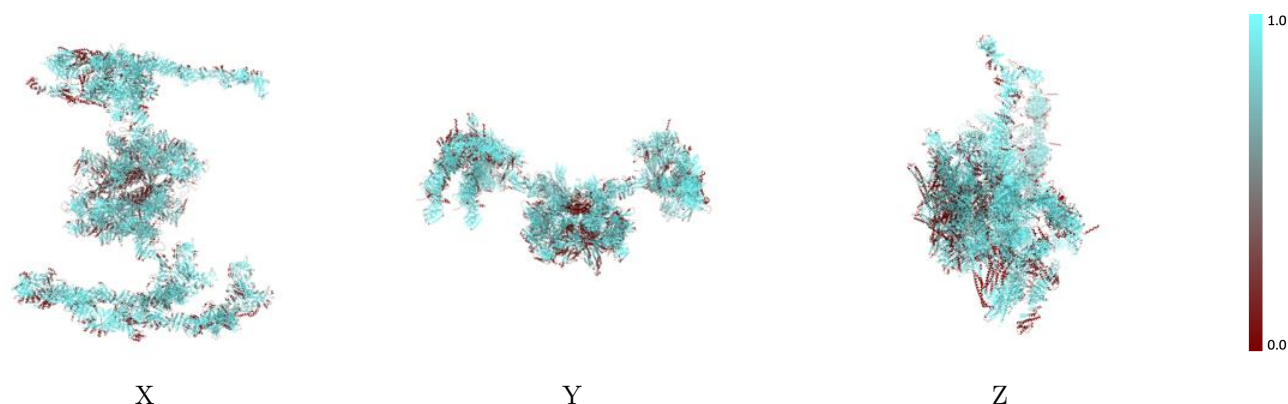
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



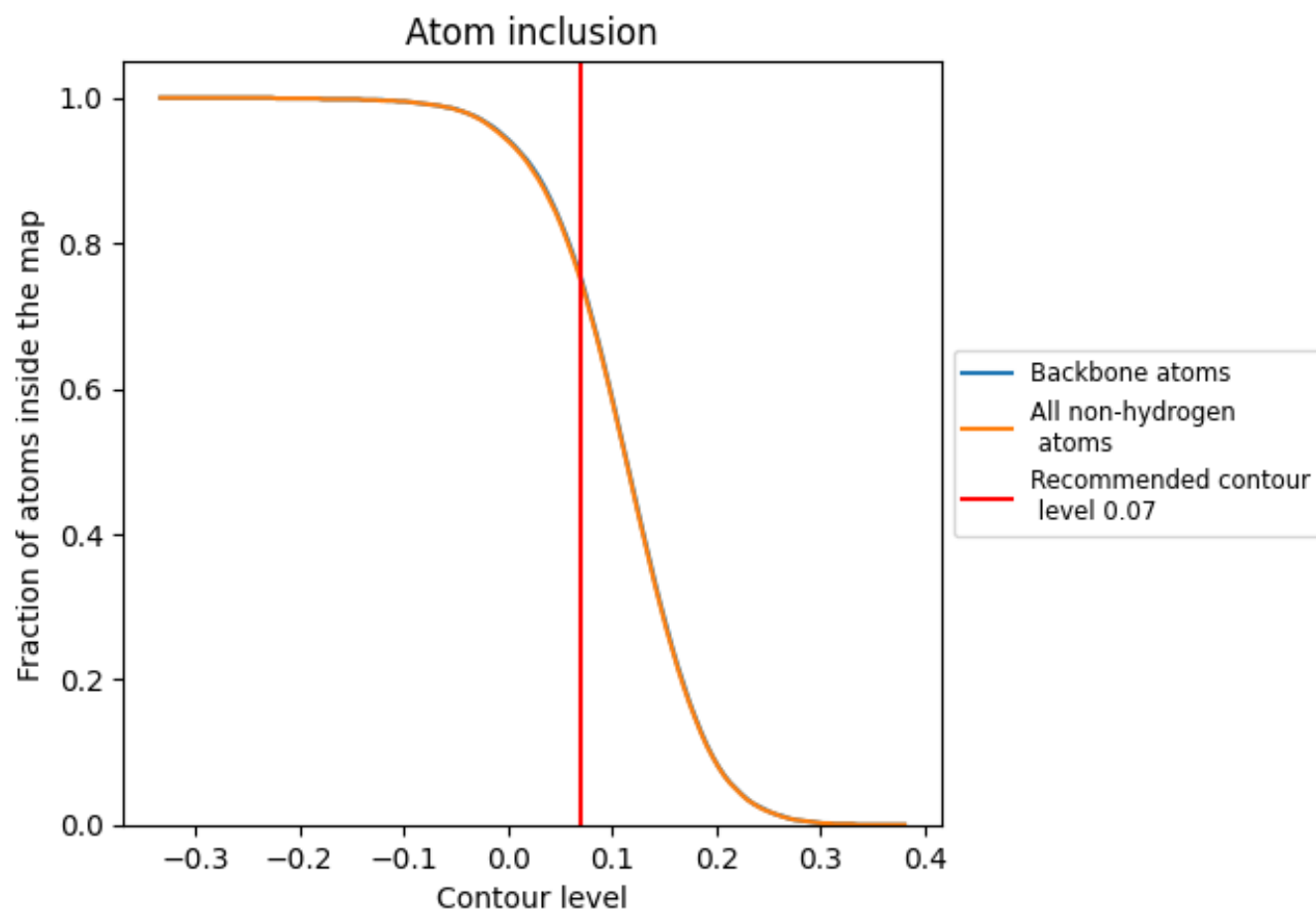
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 75% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7480	 0.0350
4	 0.8420	 0.0370
48	 0.8910	 0.0380
A	 0.5230	 0.0170
A16	 0.7680	 0.0370
A24	 0.6180	 0.0180
A32	 0.7450	 0.0350
A40	 0.6230	 0.0290
A48	 0.6960	 0.0400
A8	 0.9810	 0.0440
B	 0.6910	 0.0340
B8	 0.7400	 0.0350
C	 0.8060	 0.0340
C16	 0.5100	 0.0280
C24	 0.6970	 0.0300
C32	 0.8040	 0.0420
C8	 0.7490	 0.0370
D	 0.7880	 0.0320
D16	 0.7260	 0.0290
D24	 0.7400	 0.0260
D32	 0.7440	 0.0330
D40	 0.7880	 0.0360
D8	 0.6770	 0.0310
E	 0.9250	 0.0420
E8	 0.8990	 0.0270
F	 0.8570	 0.0250
F16	 0.8330	 0.0500
F24	 0.9230	 0.0260
F8	 0.8090	 -0.0060
H	 0.6330	 0.0390
H16	 0.4710	 0.0260
H24	 0.6750	 0.0350
H8	 0.3240	 0.0310
I	 0.5440	 0.0370
I16	 0.5770	 0.0310



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Chain	Atom inclusion	Q-score
I24	 0.6450	 0.0470
I8	 0.4490	 0.0230
J	 0.4350	 0.0320
J16	 0.7560	 0.0700
J24	 0.7140	 0.0420
J32	 0.6230	 0.0560
J8	 0.6470	 0.0580
K	 0.7940	 0.0400
K16	 0.8170	 0.0520
K8	 0.6200	 0.0310
L	 0.8160	 0.0450
L16	 0.7840	 0.0370
L8	 0.8380	 0.0370
M	 0.8920	 0.0450
M16	 0.7960	 0.0360
M8	 0.7930	 0.0400
N	 0.9880	 0.0350
N16	 0.8080	 0.0320
N8	 0.8520	 0.0260
O	 0.9760	 0.0380
O16	 0.9240	 0.0440
O8	 0.9770	 0.0460
P	 0.8200	 0.0350
P16	 0.8000	 0.0420
P8	 0.8740	 0.0440
Q	 0.8400	 0.0300
Q16	 0.7150	 0.0420
Q8	 0.8080	 0.0380
R	 0.8590	 0.0300
R16	 0.7130	 0.0360
R8	 0.8030	 0.0380
T	 0.8390	 0.0470
T16	 0.6860	 0.0300
T8	 0.8460	 0.0400
V	 0.5360	 0.0550
W	 0.7110	 0.0310