



## wwPDB EM Validation Summary Report ⓘ

Nov 29, 2022 – 05:29 PM JST

PDB ID : 7WOT  
EMDB ID : EMD-32658  
Title : Cryo-EM structure of the inner ring monomer of the *Saccharomyces cerevisiae* nuclear pore complex  
Authors : Li, Z.Q.; Chen, S.J.B.; Zhao, L.; Sui, S.F.  
Deposited on : 2022-01-22  
Resolution : 3.73 Å(reported)

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We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

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

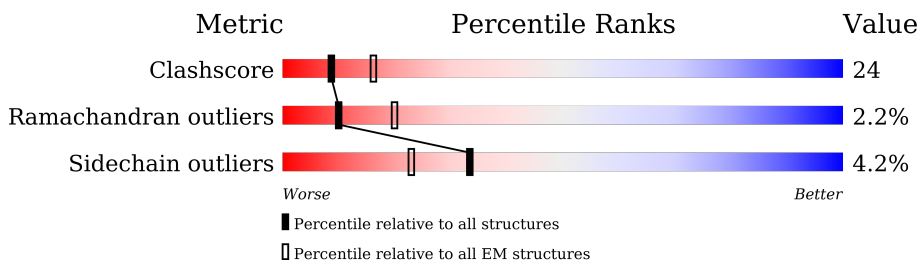
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.73 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	A	839	
1	M	839	
1	N	839	
1	Z	839	
2	C	1391	
2	O	1391	
3	D	1502	
3	P	1502	

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Mol	Chain	Length	Quality of chain
4	E	1655	
4	Q	1655	
5	F	1683	
5	R	1683	
6	G	472	
6	J	472	
6	S	472	
6	V	472	
7	H	541	
7	K	541	
7	T	541	
7	W	541	
8	I	823	
8	L	823	
8	U	823	
8	X	823	

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 133827 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 Nucleoporin NIC96.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	732	Total	C	N	O	S	0	0
			5720	3628	975	1101	16		
1	M	729	Total	C	N	O	S	0	0
			5697	3616	972	1093	16		
1	N	746	Total	C	N	O	S	0	0
			5766	3656	976	1119	15		
1	Z	746	Total	C	N	O	S	0	0
			5767	3658	976	1118	15		

- Molecule 2 is a protein called Nucleoporin NUP157.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	1325	Total	C	N	O	S	0	0
			10452	6664	1736	2018	34		
2	O	1325	Total	C	N	O	S	0	0
			10452	6664	1736	2018	34		

- Molecule 3 is a protein called Nucleoporin NUP170.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	1398	Total	C	N	O	S	0	0
			10966	7012	1811	2111	32		
3	P	1398	Total	C	N	O	S	0	0
			10956	7005	1811	2108	32		

- Molecule 4 is a protein called Nucleoporin NUP188.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	1552	Total	C	N	O	S	0	0
			12362	8017	1981	2337	27		
4	Q	1552	Total	C	N	O	S	0	0
			12362	8017	1981	2337	27		

- Molecule 5 is a protein called Nucleoporin NUP192.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	1622	Total	C	N	O	S	0	0
			12239	7813	2031	2364	31		
5	R	1622	Total	C	N	O	S	0	0
			12239	7813	2031	2364	31		

- Molecule 6 is a protein called Nucleoporin NUP49/NSP49.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	200	Total	C	N	O	S	0	0
			1533	973	251	307	2		
6	J	195	Total	C	N	O	S	0	0
			1492	938	251	302	1		
6	S	200	Total	C	N	O	S	0	0
			1529	970	250	307	2		
6	V	195	Total	C	N	O	S	0	0
			1492	938	251	302	1		

- Molecule 7 is a protein called Nucleoporin NUP57.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	246	Total	C	N	O	S	0	0
			1811	1128	332	348	3		
7	K	254	Total	C	N	O	S	0	0
			1808	1126	334	345	3		
7	T	246	Total	C	N	O	S	0	0
			1811	1128	332	348	3		
7	W	254	Total	C	N	O	S	0	0
			1805	1123	334	345	3		

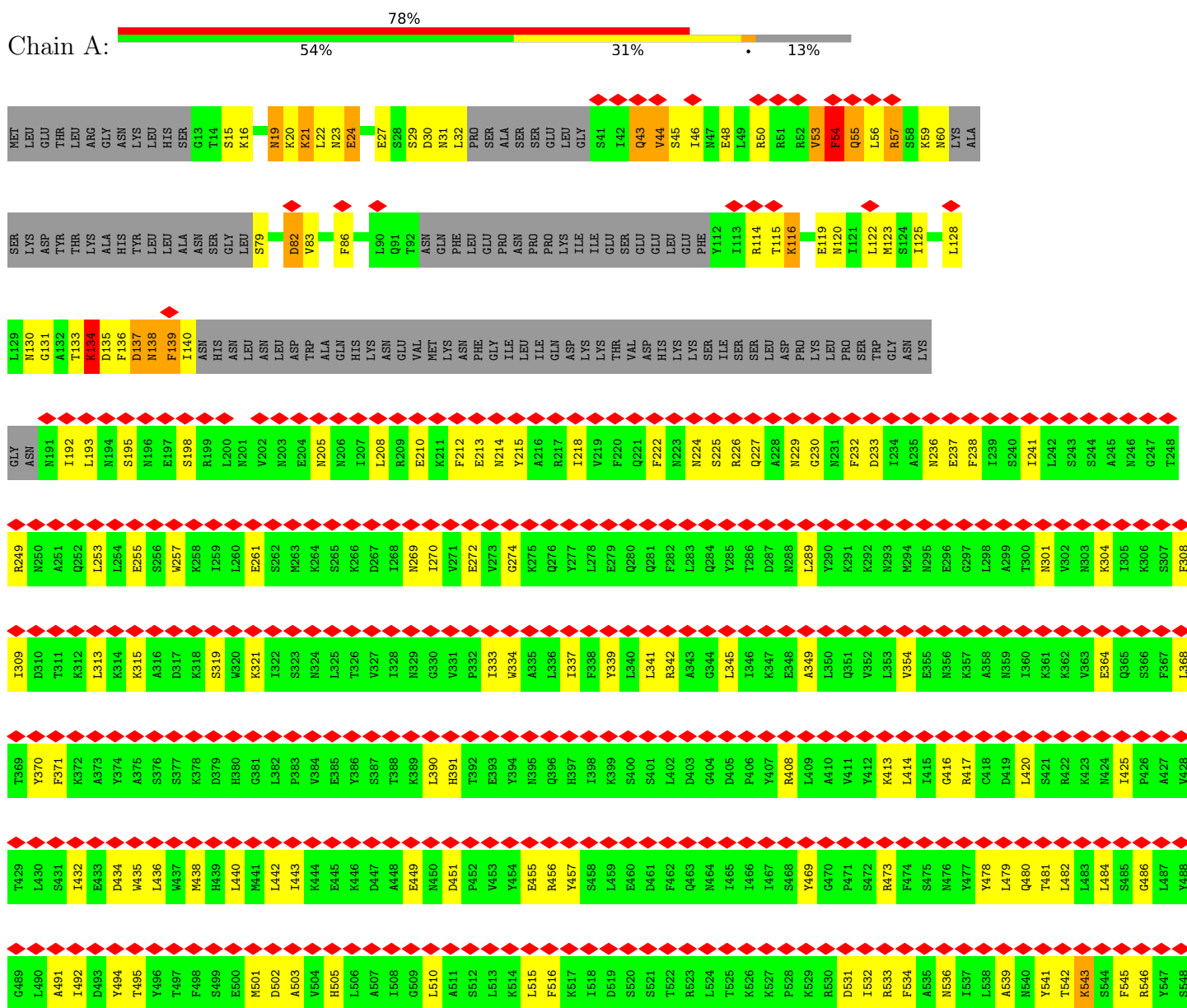
- Molecule 8 is a protein called Nucleoporin NSP1.

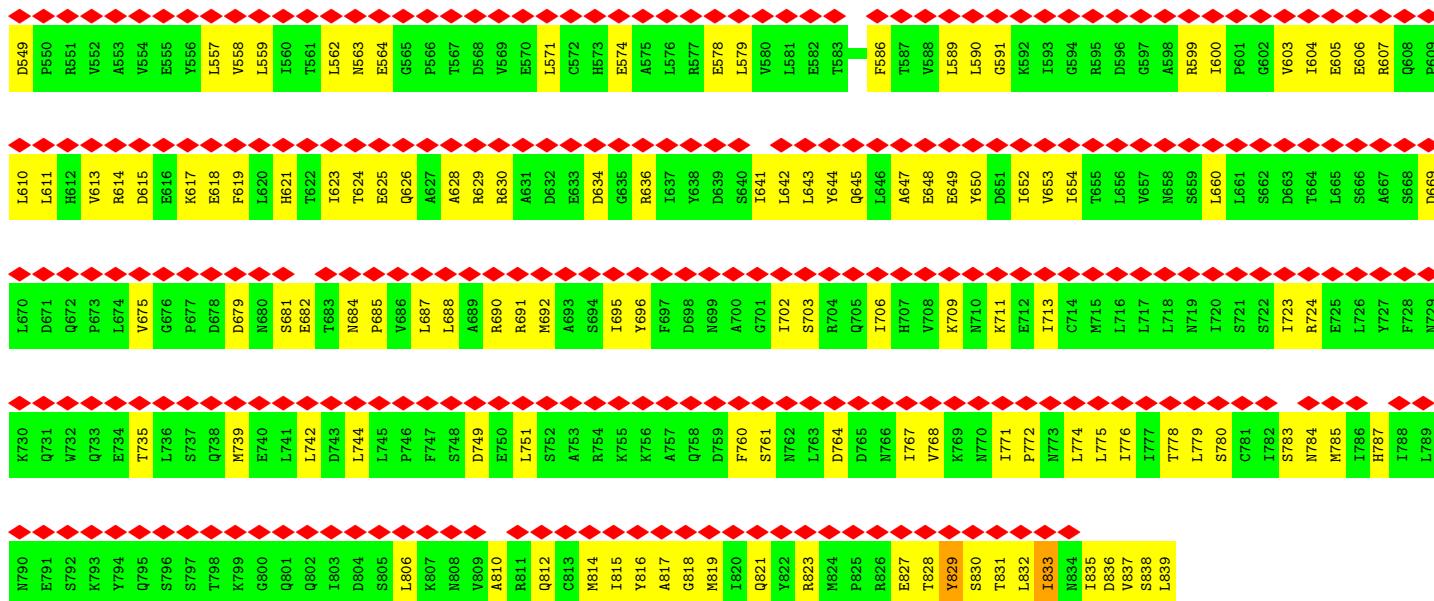
Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	187	Total	C	N	O	S	0	0
			1418	862	244	311	1		
8	L	187	Total	C	N	O	S	0	0
			1366	830	240	295	1		
8	U	187	Total	C	N	O	S	0	0
			1418	862	244	311	1		
8	X	187	Total	C	N	O	S	0	0
			1366	830	240	295	1		

### 3 Residue-property plots [i](#)

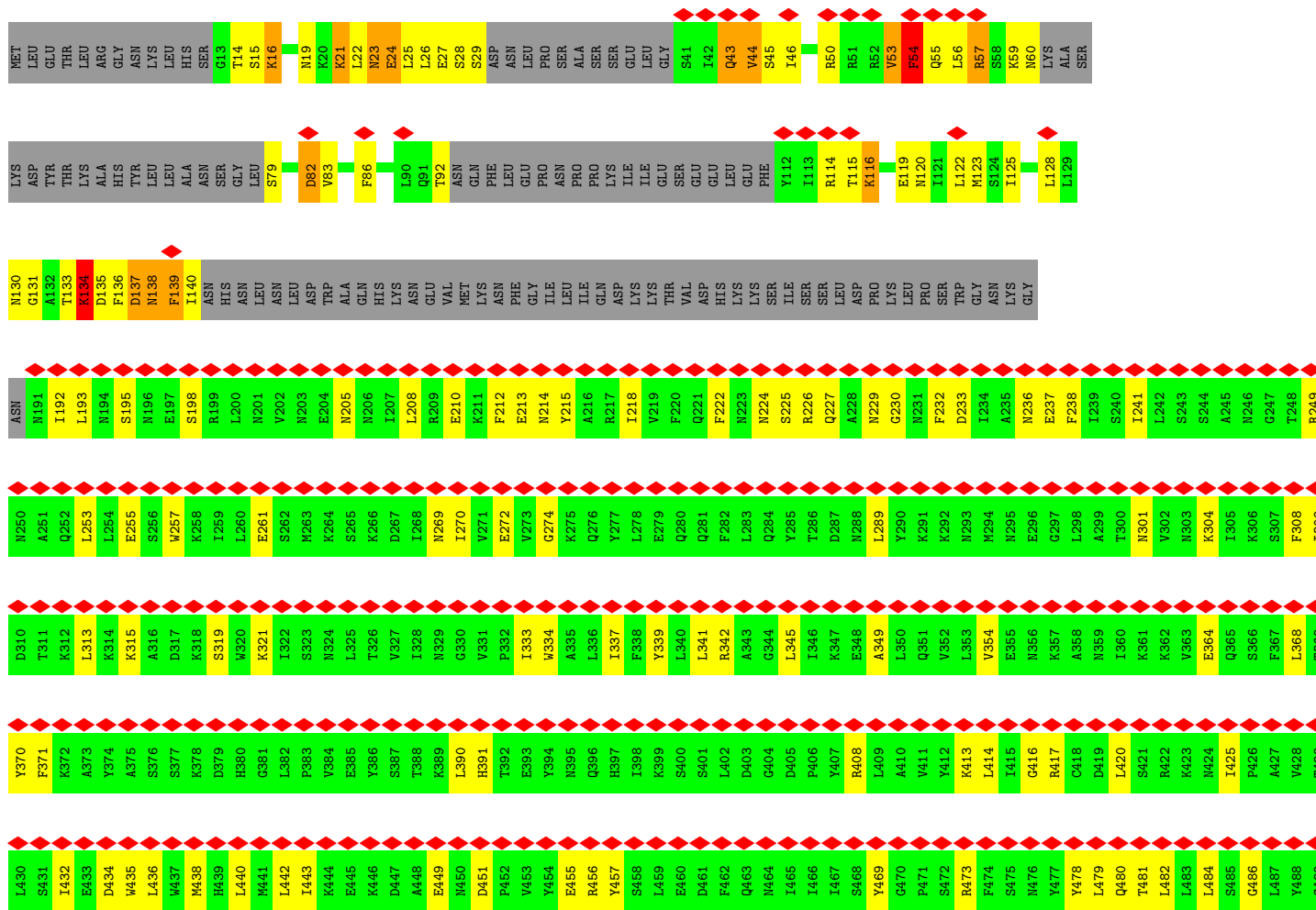
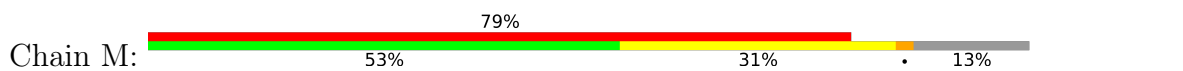
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

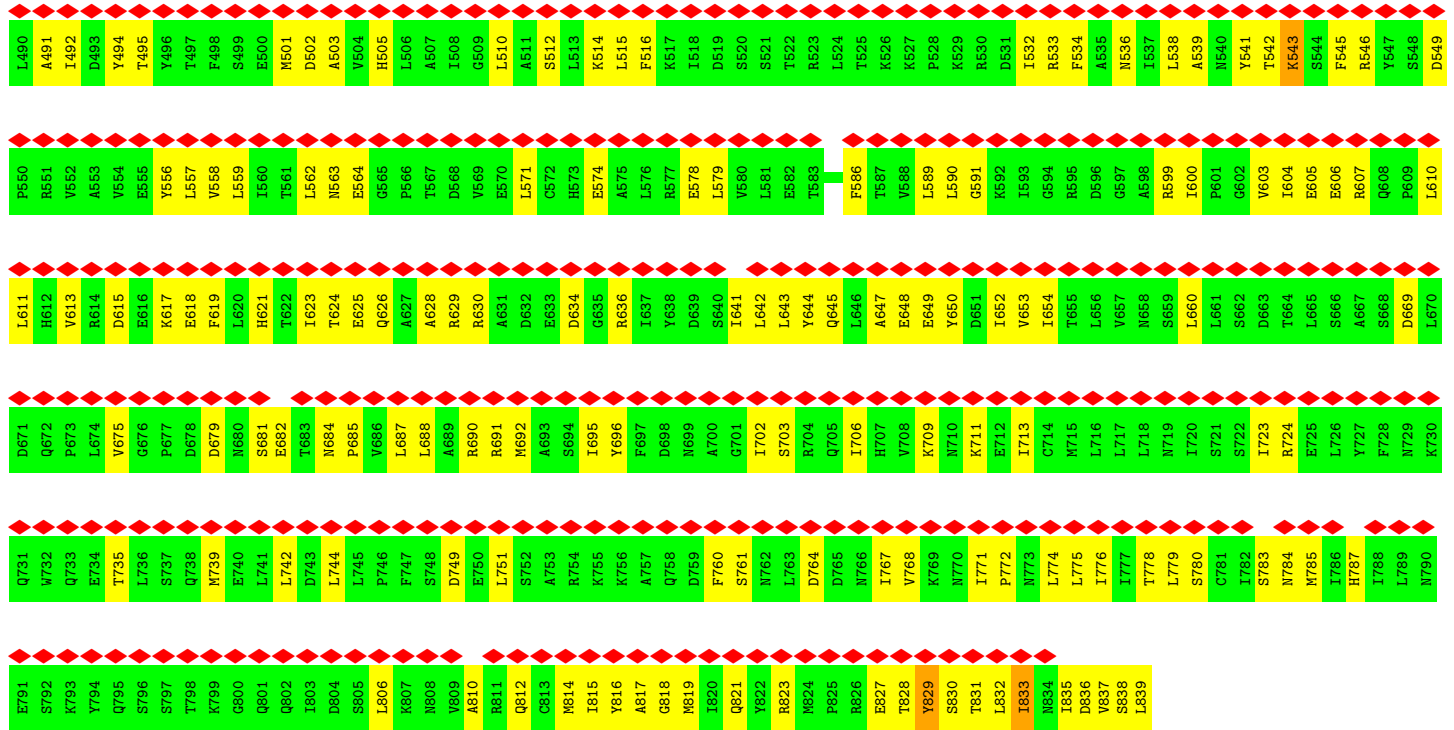
- Molecule 1: Nucleoporin NIC96



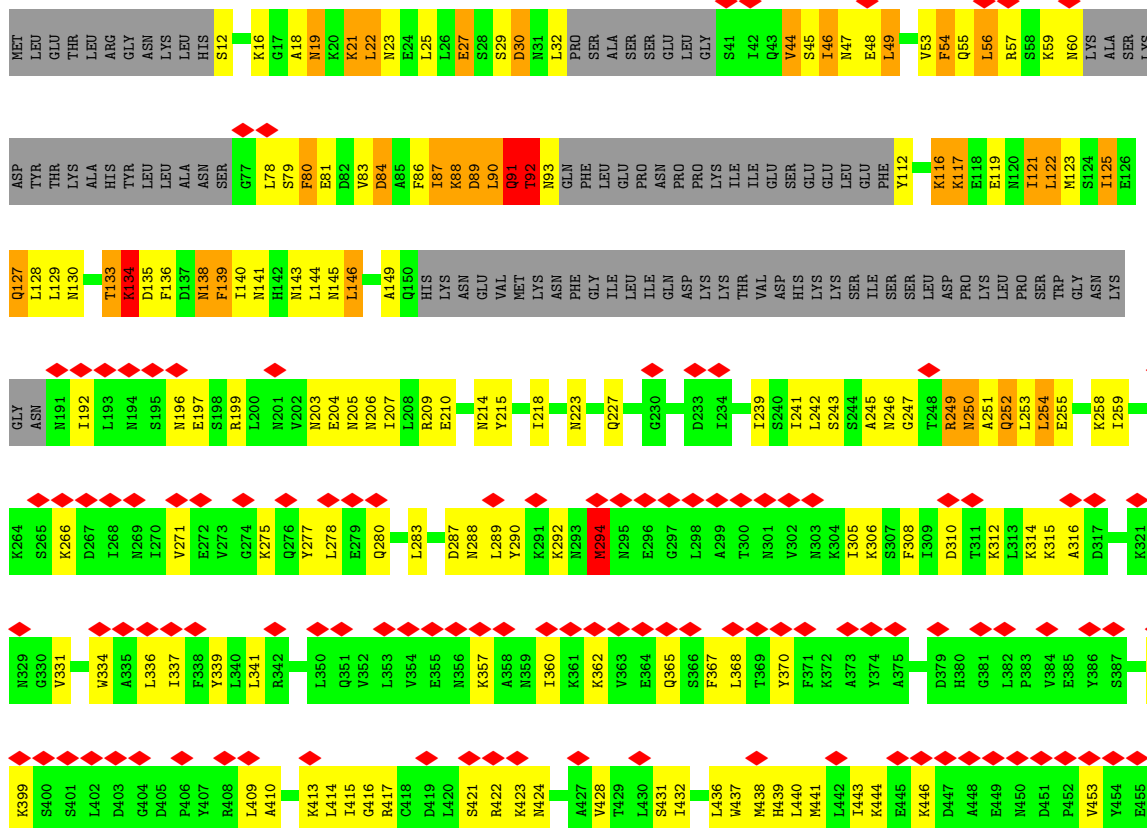


• Molecule 1: Nucleoporin NIC96

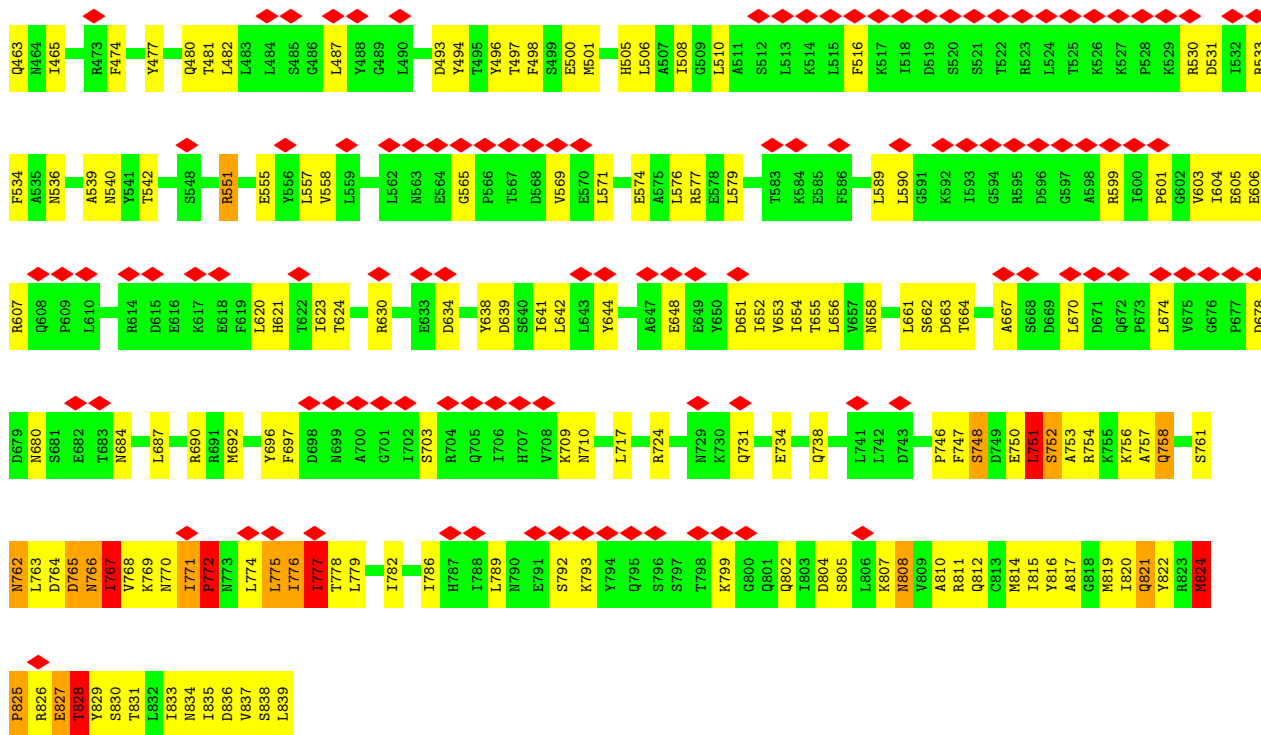




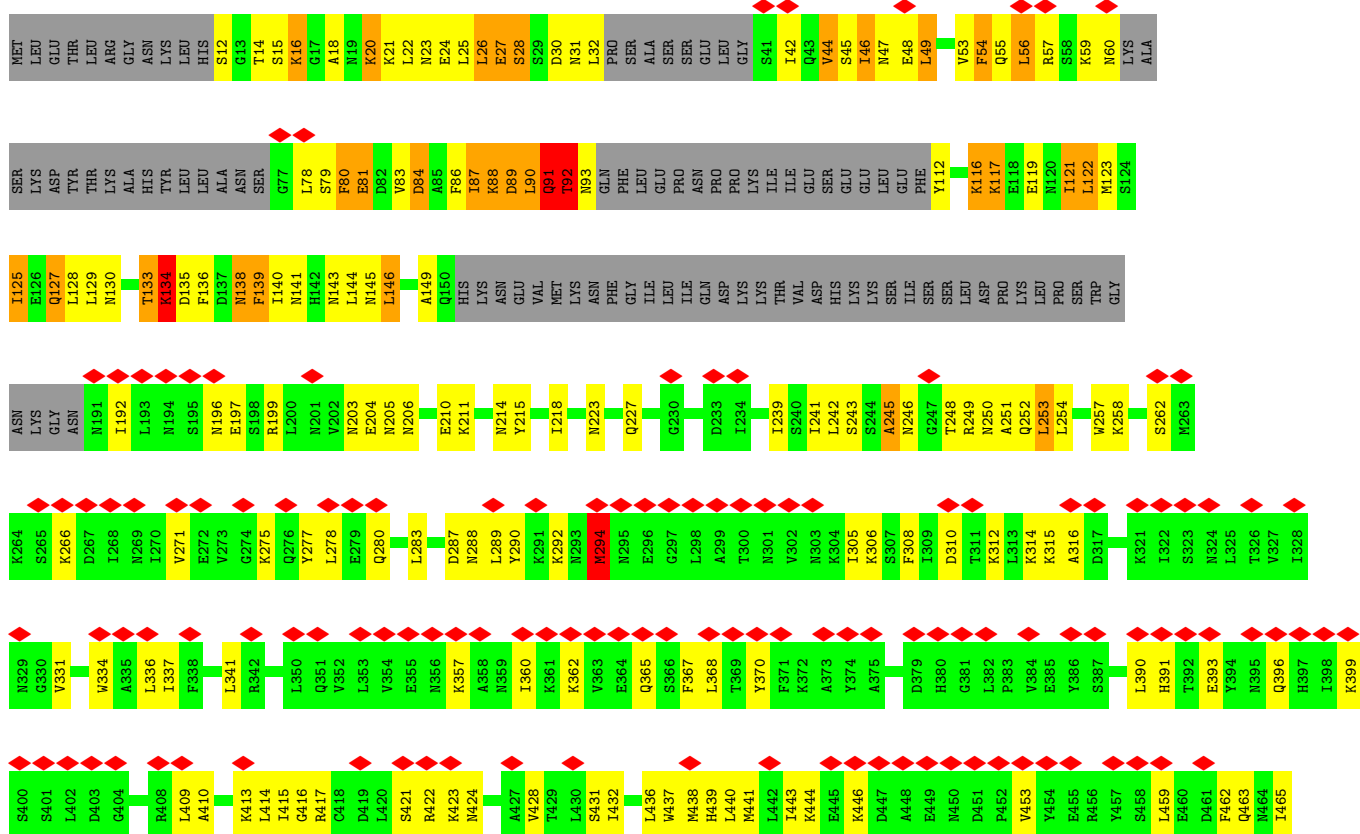
● Molecule 1: Nucleoporin NIC96

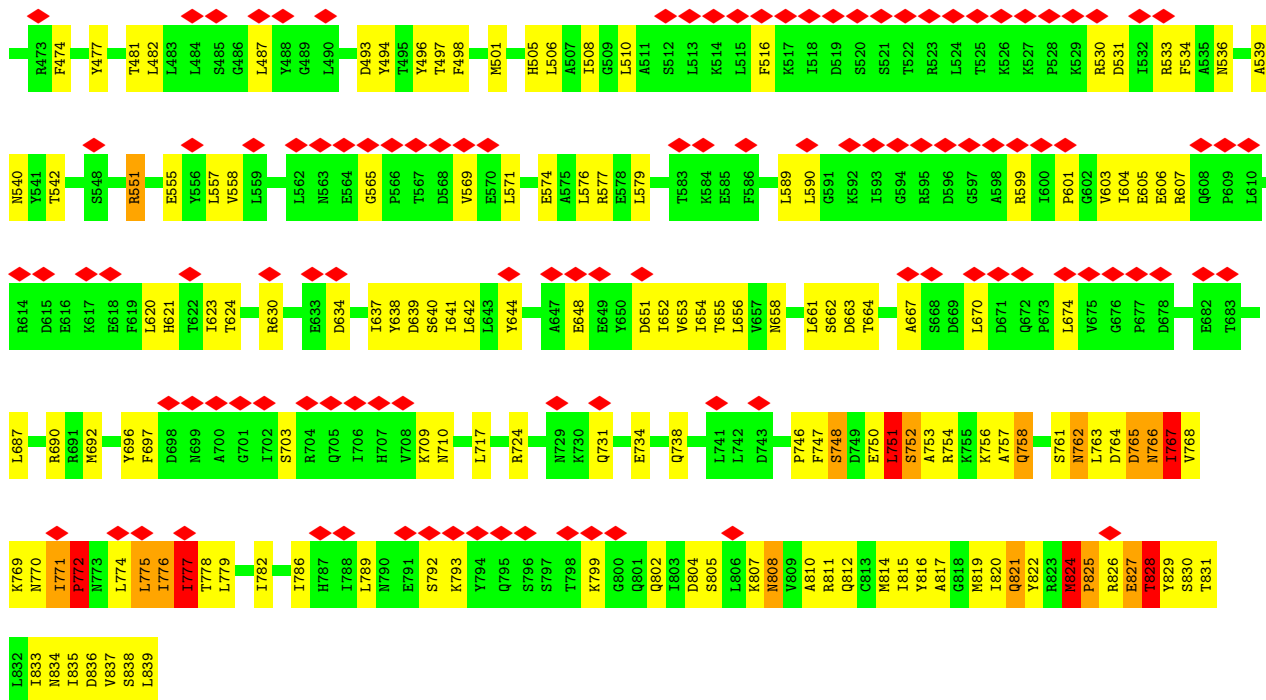




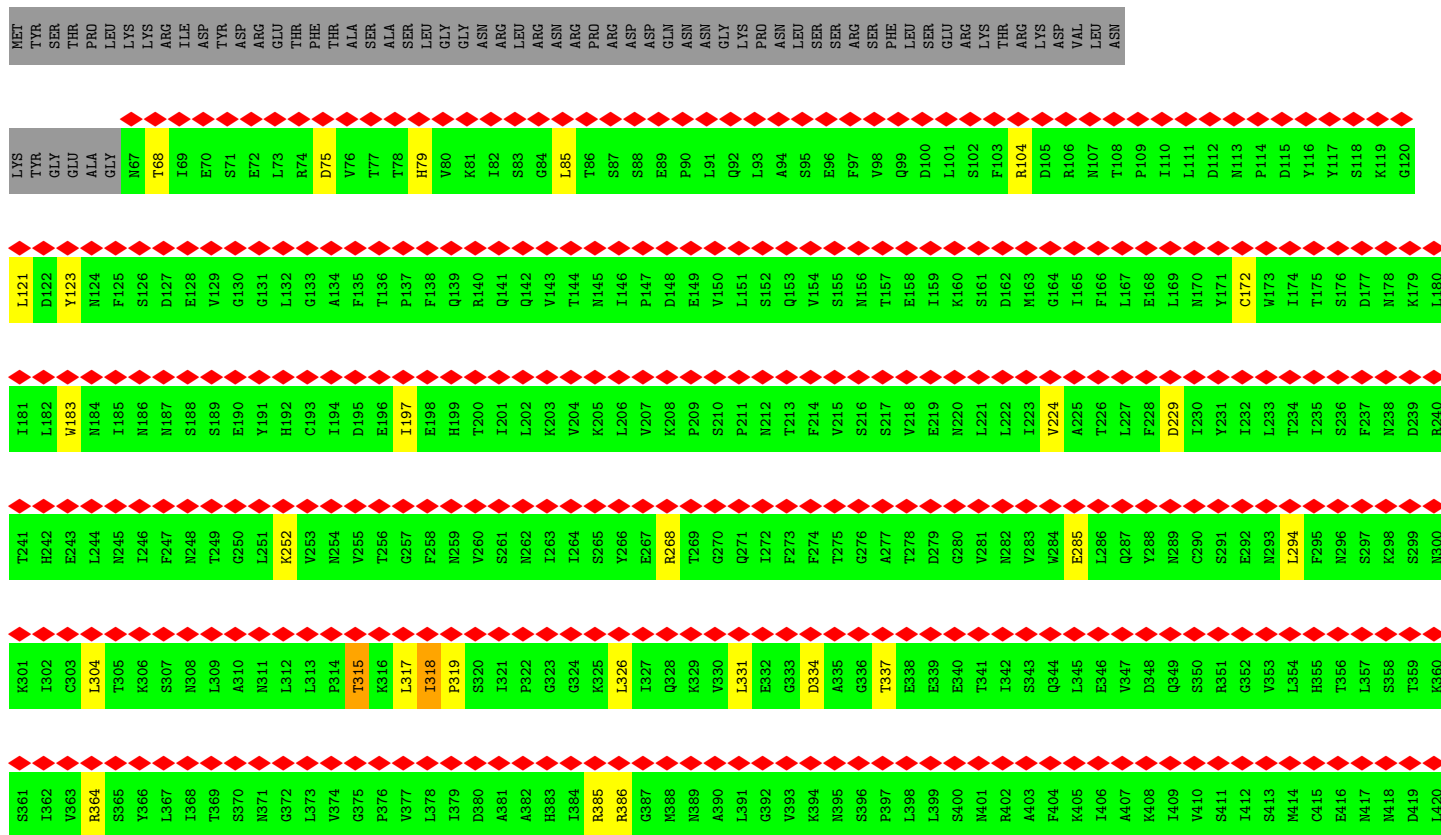
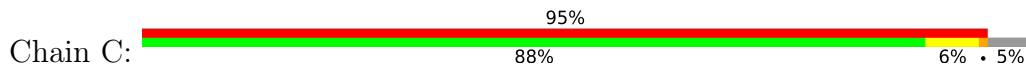


• Molecule 1: Nucleoporin NIC96

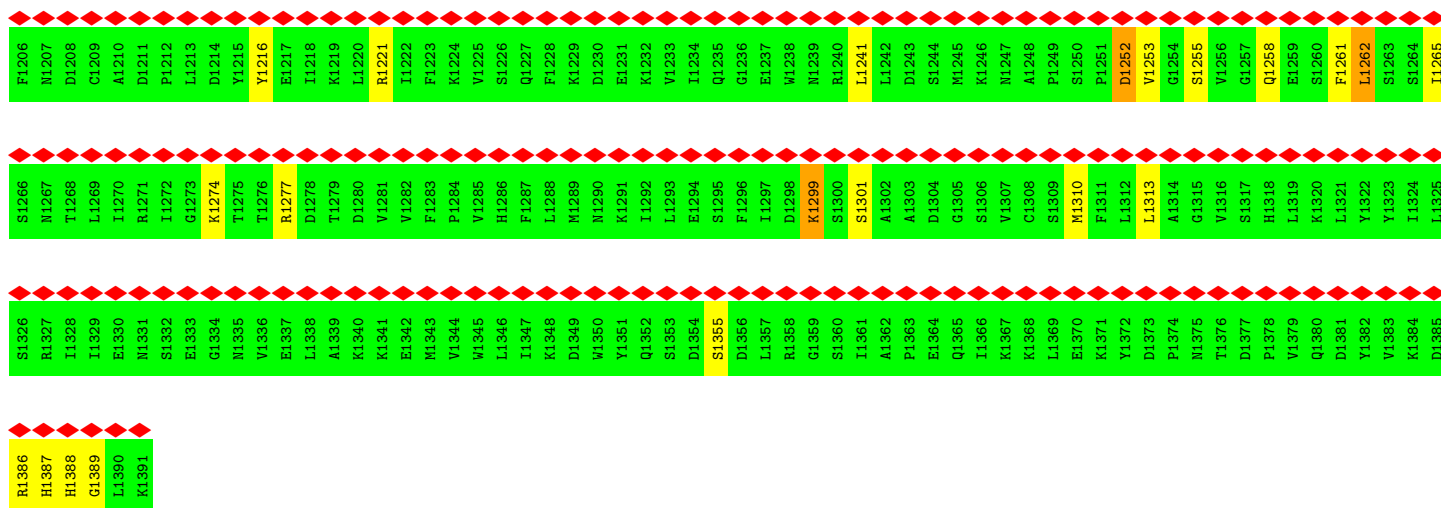




• Molecule 2: Nucleoporin NUP157

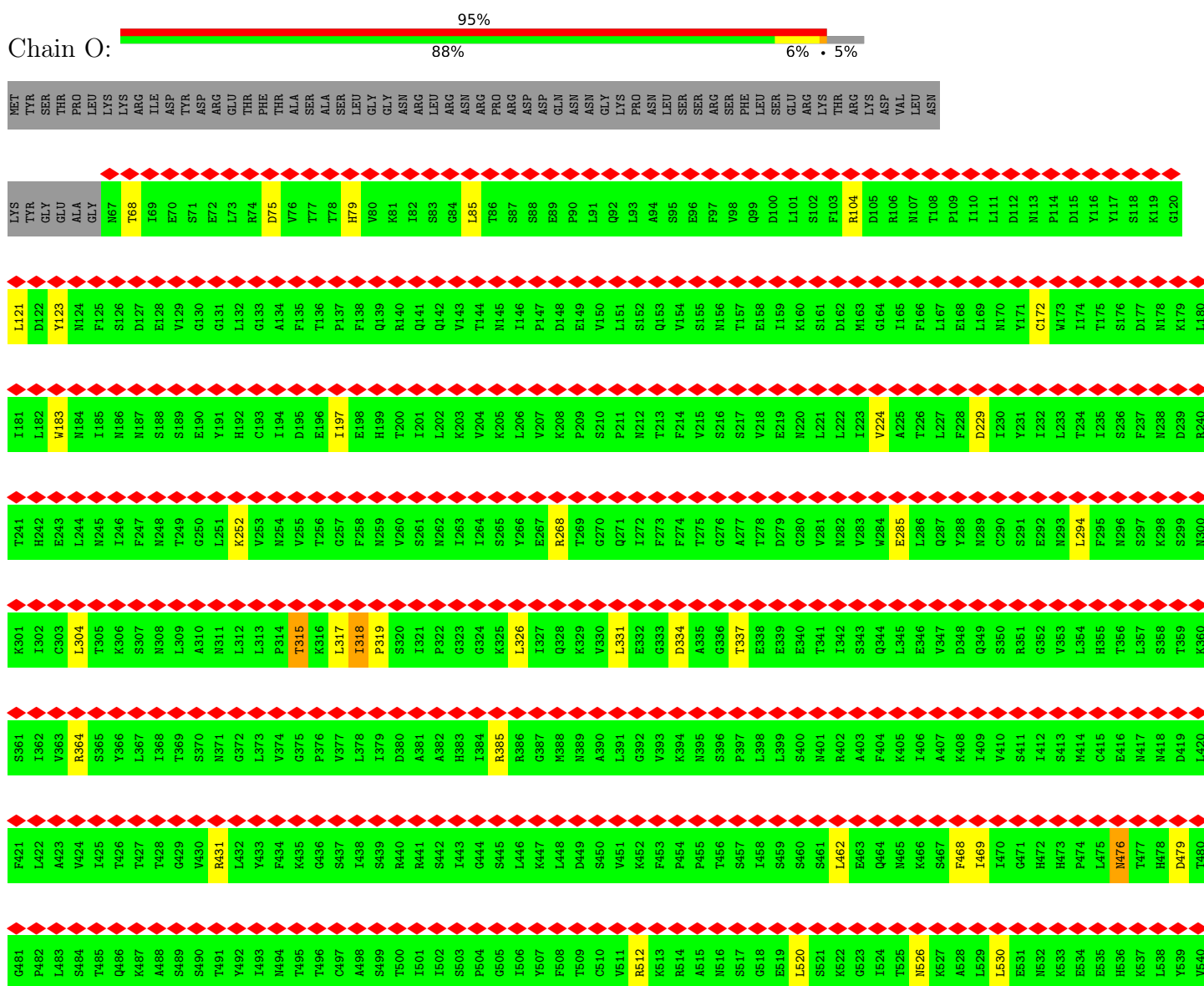






### Molecule 2: Nucleoporin NUP157

#### Chain O:



I1265	L1205	T1145	L1081	I1021	P961	1901	R841	G781	S721	A661	V601	S641
S1266	F1206	S1146	P1082	E1022	K962	L902	E942	S782	Q722	L662	A602	A642
M1267	N1207	F1147	Y1083	Q1023	T963	C903	Y943	M783	I723	A663	V603	P643
T1268	D1208	D1148	L1084	S1024	V964	Y904	F944	A784	M724	F664	L604	D644
L1269	C1209	Q1149	K1085	P1025	G965	R905	F945	I785	E725	T665	T605	Y645
I1270	A1210	K1150	E1086	S1026	F966	A906	D946	T786	ET26	S666	S606	G646
R1271	D1211	P1151	R1087	I1027	L967	G907	L947	A787	R727	A667	N607	I647
I1272	P1212	A1152	A1088	A1028	R968	E908	K948	S788	V728	G668	A608	L648
K1273	L1213	L1153	E1089	M1029	F969	H909	F949	D789	F729	I669	L609	K649
T1274	D1214	V1154	K1090	I1030	H850	L910	H850	A790	V730	P670	E610	N650
T1275	Y1215	Q1155	S1091	S1031	D851	E911	D851	E791	F731	G671	I611	Y651
T1276	Y1216	L1156	L1092	I1032	D972	A912	L852	S792	K732	V672	E612	G652
R1277	E1217	S1157	E1093	F1033	K973	A913	F853	I793	R733	V673	C813	K653
D1278	I1218	E1158	I1094	S1034	I974	A914	T854	A794	A734	E674	E614	Y654
T1279	K1219	M1159	S1095	P1035	D975	K915	P855	M795	S735	I675	R615	V655
D1280	L1220	I1160	N1096	A1036	K976	F916	N856	M796	K736	K676	T616	E656
V1281	R1221	H1161	L1097	S1037	G977	E917	A857	A797	T737	P677	P617	N657
F1283	F1223	L1163	L1098	S1038	N978	M918	K858	L798	E738	K678	D618	T658
P1284	K1224	F1164	F1100	S1039	Q979	I919	T859	I799	K739	S679	E619	A659
V1285	V1225	D1165	Y1101	K1040	A980	D920	K860	L800	M740	S680	V620	L660
H1286	S1226	I1166	L1102	R1042	Q821	S821	Q861	L801	D741	R681	F621	L661
F1287	Q1227	A1167	F1103	V1043	K922	K922	L862	I802	A742	E682	E622	D662
L1288	F1228	S1168	K1104	Y1044	V984	S924	K864	S804	F743	S683	S623	T663
M1289	K1229	I1169	E1105	S1045	S985	R925	E865	I805	G744	G684	L624	T664
K1291	D1230	Q1170	E1106	S1046	S986	N926	I866	K806	I746	S686	I626	D666
I1292	K1232	D1171	H1107	I1047	G987	H927	L867	D807	I747	P687	N627	I667
L1293	V1233	L1173	F1109	M1048	C988	L928	I868	A808	T748	P688	P628	K668
I1294	I1234	L1174	E1110	S1050	T989	D929	E869	L809	R749	I689	L629	E669
S1295	Q1235	M1175	A1111	M1051	T990	T930	V870	S810	Q750	S690	P630	I670
F1296	G1236	L1176	A1112	N1052	D992	A931	N872	I812	Q751	Q691	F631	V671
I1297	E1237	V1177	D1113	F1053	P983	D933	A873	N813	V752	N692	I632	P672
D1298	V1238	R1178	V1114	F1054	R994	L934	N874	V814	E753	L693	H633	L673
K1299	M1239	M1179	L1115	F1055	K985	Y935	I875	F815	Y754	D695	G634	T674
S1300	R1240	E1180	Y1116	V996	V996	E936	A876	Y816	L756	K696	G636	R675
S1301	L1241	T1181	A1117	Y1057	F987	R937	S877	E917	S757	S697	L637	S676
A1302	L1242	R1182	L1118	C1058	G988	C938	S878	D818	S758	G698	S638	N678
A1303	D1243	I1183	A1119	F1059	D989	C939	T879	I819	I759	E699	E639	Y679
D1304	S1244	D1184	S1120	Y1060	K1000	E940	S880	D820	S760	C700	A640	T680
S1305	M1245	E1185	S1121	D1061	A881	N941	A821	A821	V761	D701	C641	S681
S1306	K1246	D1186	D1122	W1062	I1002	I942	I882	F922	L762	G702	S642	T682
V1307	N1247	Y1187	F1123	L1063	M1003	E943	Y883	K823	A763	I703	T643	P683
C1308	A1248	R1188	D1124	V1064	V1004	L944	I884	S824	D764	V704	A644	Q684
S1309	P1249	K1189	L1125	A1065	Y1005	C945	V885	L825	F765	L705	L645	G685
M1310	S1250	Q1190	K1126	M1066	E946	E946	N886	L826	F766	S706	L646	G686
F1311	P1251	L1191	L1127	L1067	E947	L947	V887	L827	M767	P707	L647	A687
L1312	D1252	T1192	R1068	K1067	I1007	R948	L888	T828	I768	R708	A648	N688
L1313	V1253	E1129	F1069	Q1069	F1009	R949	K889	T829	H769	F709	C649	E689
A1314	G1254	E1129	D1070	D1070	E1010	V950	R889	M830	R770	Y710	K650	F690
G1315	S1255	I1131	E1010	Y1071	I1011	V951	R891	G831	P771	G711	F651	A691
V1316	V1256	M1196	L1072	L1072	V1012	D952	F922	A832	S772	S712	N652	S692
S1317	G1257	G1197	L1073	L1073	K1013	I953	G893	G833	F773	A713	K653	Q693
H1318	Q1258	R1198	R1074	R1074	S1014	N954	S894	G834	V774	L714	G654	Y694
L1319	E1259	V1199	L1075	L1075	V1015	V955	F895	V835	S775	L715	E655	S695
K1320	S1260	L1200	D1076	D1076	D1016	K956	C996	Y836	V776	I716	H656	A696
L1321	F1261	P1201	D1078	S1077	I1017	L957	H897	D837	V777	T717	I657	E697
Y1322	L1262	L1202	Q1078	Q1078	D1018	L958	S898	S838	V778	R718	H658	P698
Y1323	S1263	S1203	T1019	F1079	T1019	Y959	A899	K839	P779	L719	S659	L699
I1324	S1264	D1204	S1020	V1080	S1020	Q960	D900	T840	K780	F720	S660	K600

L1325	PHE
S1326	GLN
R1327	ASN
I1328	PRO
I1329	PHE
E1330	HIS
M1331	ASN
S1332	GLY
E1333	PRO
G1334	ALA
M1335	ALA
V1336	GLY
E1337	THR
L1338	PHE
A1339	SER
K1340	ASP
K1341	SER
E1342	ARG
M1343	TYR
V1344	PRO
M1345	LEU
L1346	THR
L1347	ASN
K1348	HIS
D1349	GLN
W1350	VAL
Y1351	PRO
Q1352	GLY
S1353	ASN
D1354	LEU
S1355	LEU
D1356	ALA
L1357	ALA
R1358	SER
G1359	ALA
S1360	ALA
I1361	ALA
A1362	GLN
P1363	GLN
E1364	PRO
Q1365	THR
I1366	HIS
K1367	ILE
K1368	LEU
L1369	ASN
E1370	SER
K1371	TYR
Y1372	ILE
D1373	PRO
P1374	PRO
M1375	PRO
T1376	PRO
D1377	PRO
V1378	PRO
V1379	PRO
Q1380	PRO
D1381	PRO
Y1382	PRO
V1383	PRO
K1384	PRO

● Molecule 3: Nucleoporin NUP170



MET	THR
PHE	GLY
GLN	SER
ASN	ASN
SER	PRO
PHE	LEU
HIS	MET
ASN	ARG
ASN	ALA
GLY	ALA
PRO	GLY
SER	THR
PHE	GLY
SER	SER
A1339	ILE
ASP	ASN
SER	PRO
ARG	ASN
TYR	MET
PRO	SER
LEU	ASN
THR	THR
ASN	GLN
HIS	HIS
GLN	ILE
VAL	ARG
PRO	VAL
GLY	SER
ASN	GLY
LEU	MET
ASN	THR
GLU	S98
LEU	K99
ALA	P100
SER	L101
SER	D102
ALA	L103
THR	L104
LYS	A104
ALA	G105
GLN	P157
GLN	K106
GLN	Y107
PRO	I108
THR	D109
HIS	K220
ILE	H110
LEU	L111
ASN	Q112
SER	S165
TYR	K113
PRO	K114
PRO	L115
PRO	D115
PRO	Q168
PRO	M116
PRO	N117
PRO	T118
PRO	P119
PRO	V120
PRO	L121
PRO	D122
PRO	E123
PRO	R124
PRO	S125
PRO	Y126
PRO	Y127
PRO	M128
PRO	S129
PRO	L130
PRO	Y131
PRO	D132
PRO	Y133
PRO	M134
PRO	F135
PRO	S136
PRO	R137
PRO	E138
PRO	K139
PRO	M140
PRO	G141
PRO	L142
PRO	G143
PRO	A144
PRO	F145
PRO	V146
PRO	P147
PRO	F148
PRO	E149
PRO	K150
PRO	Q151
PRO	D152
PRO	V153
PRO	F154
PRO	M155
PRO	I156
PRO	L216
PRO	V217
PRO	R218
PRO	P219
PRO	K220
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PRO	N222
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PRO	Y201
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PRO	V270
PRO	I271
PRO	D272
PRO	I273
PRO	V274
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PRO	N294
PRO	E295
PRO	L296
PRO	H297
PRO	Y298
PRO	S299
PRO	G300
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PRO	D302
PRO	D303
PRO	W304
PRO	F305
PRO	N306
PRO	S307
PRO	K308
PRO	C309
PRO	E430
PRO	S310
PRO	K311
PRO	V312
PRO	C313
PRO	L314
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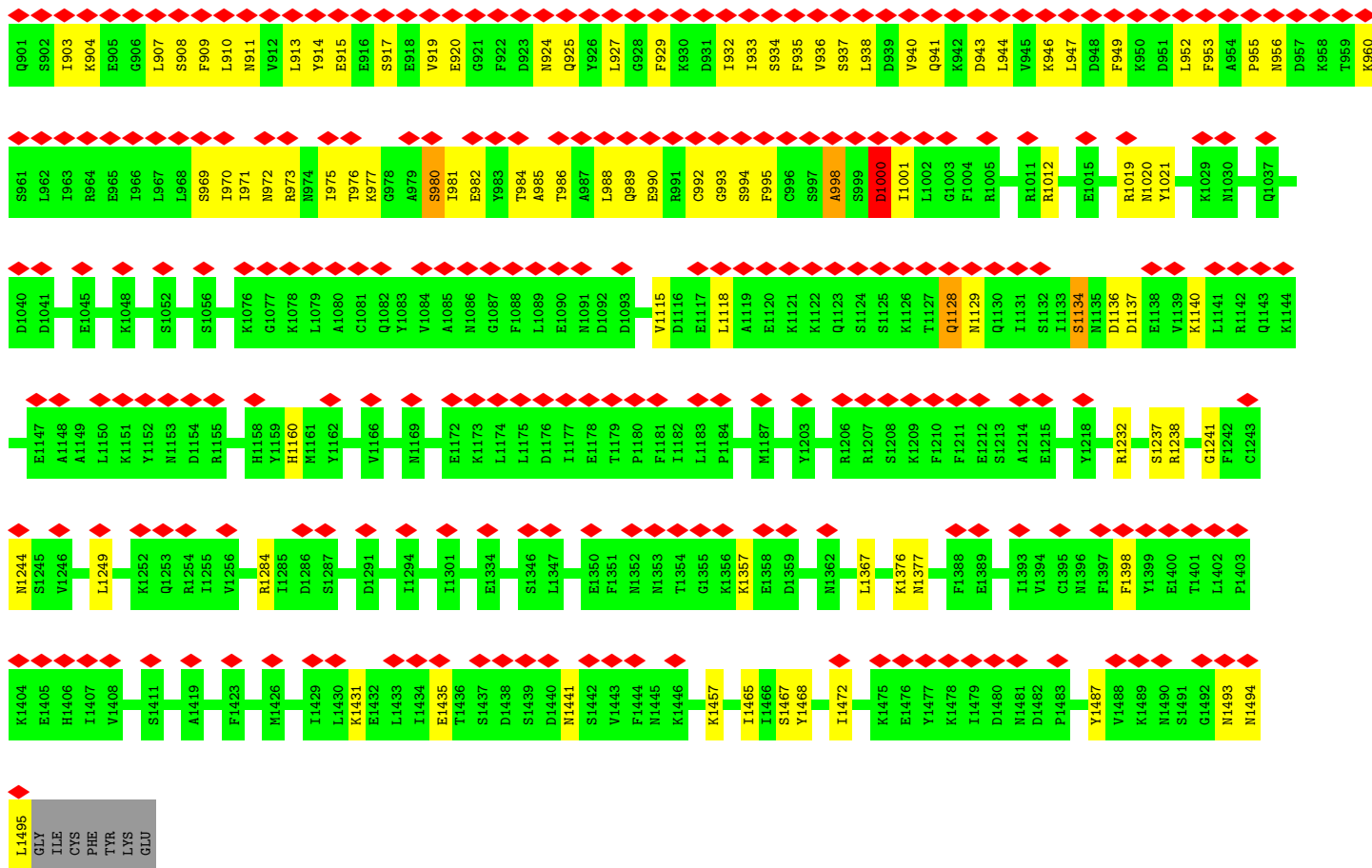
• Molecule 3: Nucleoporin NUP170



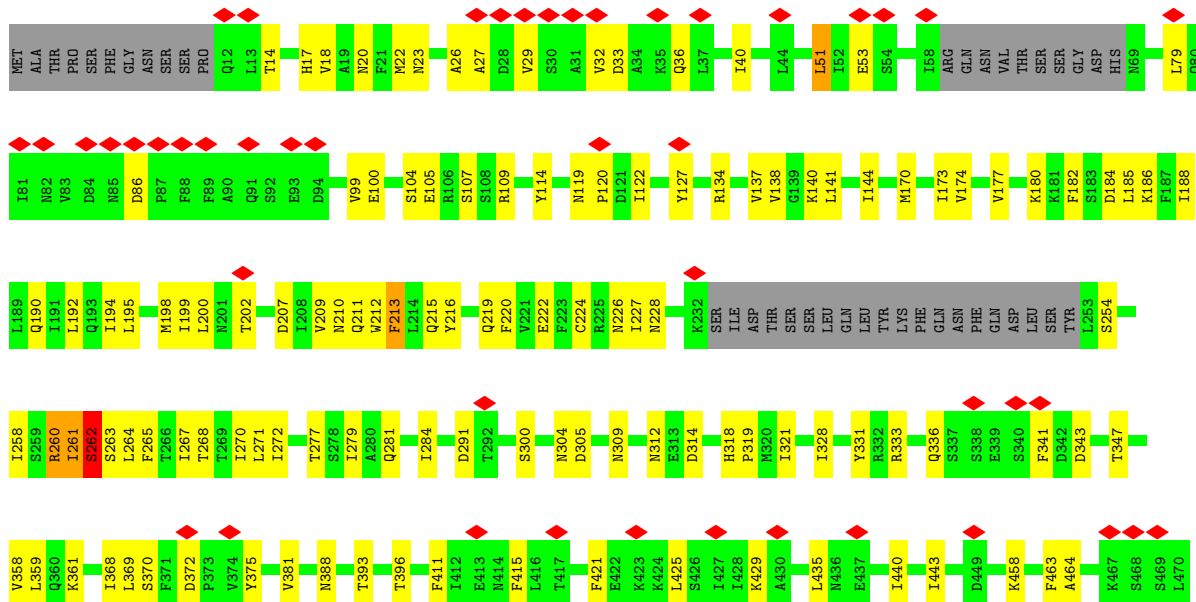
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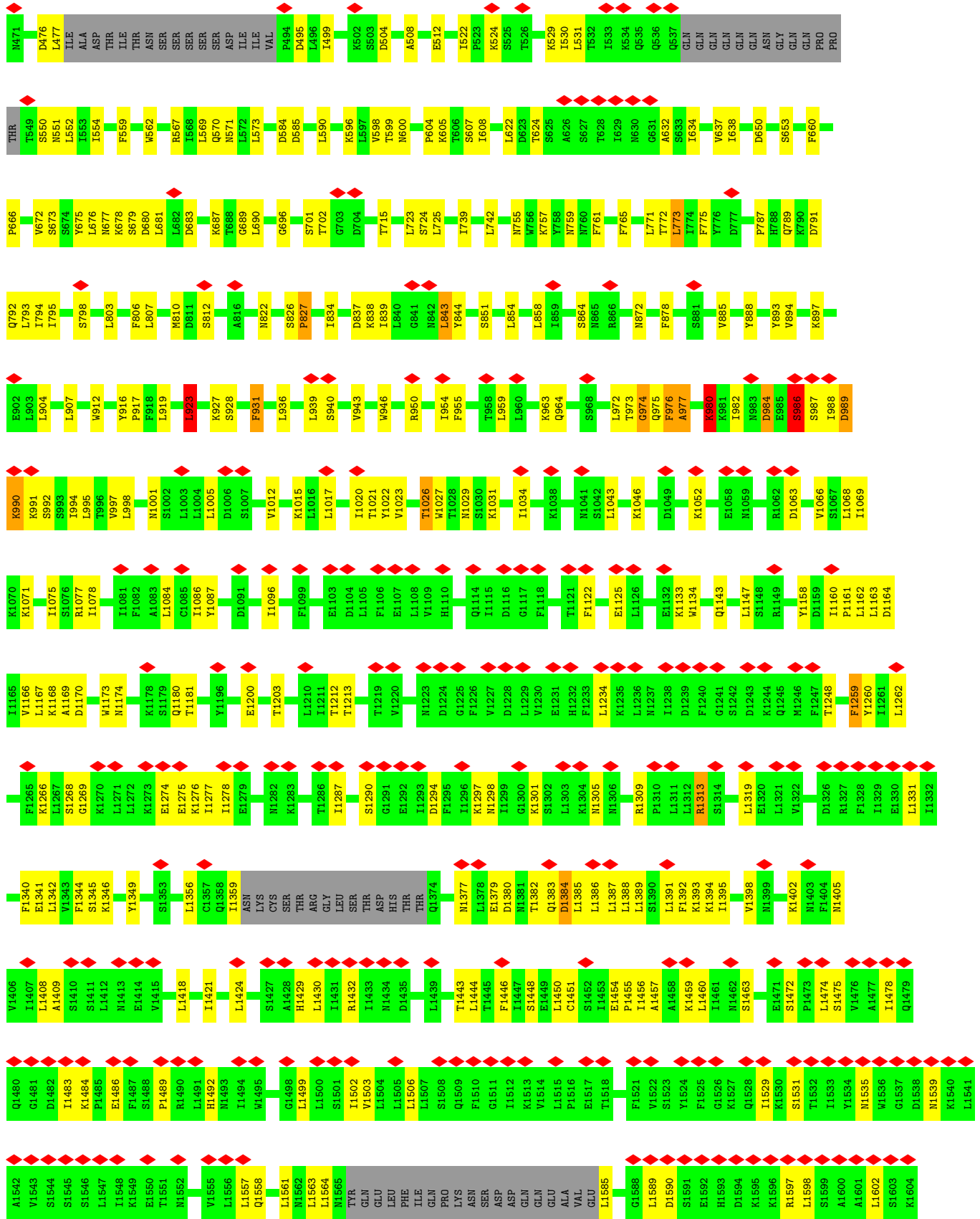
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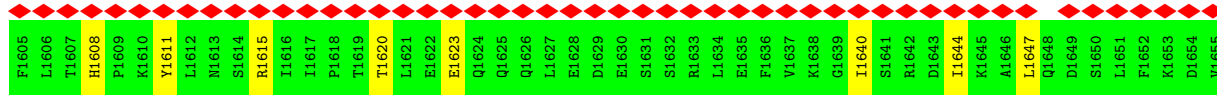




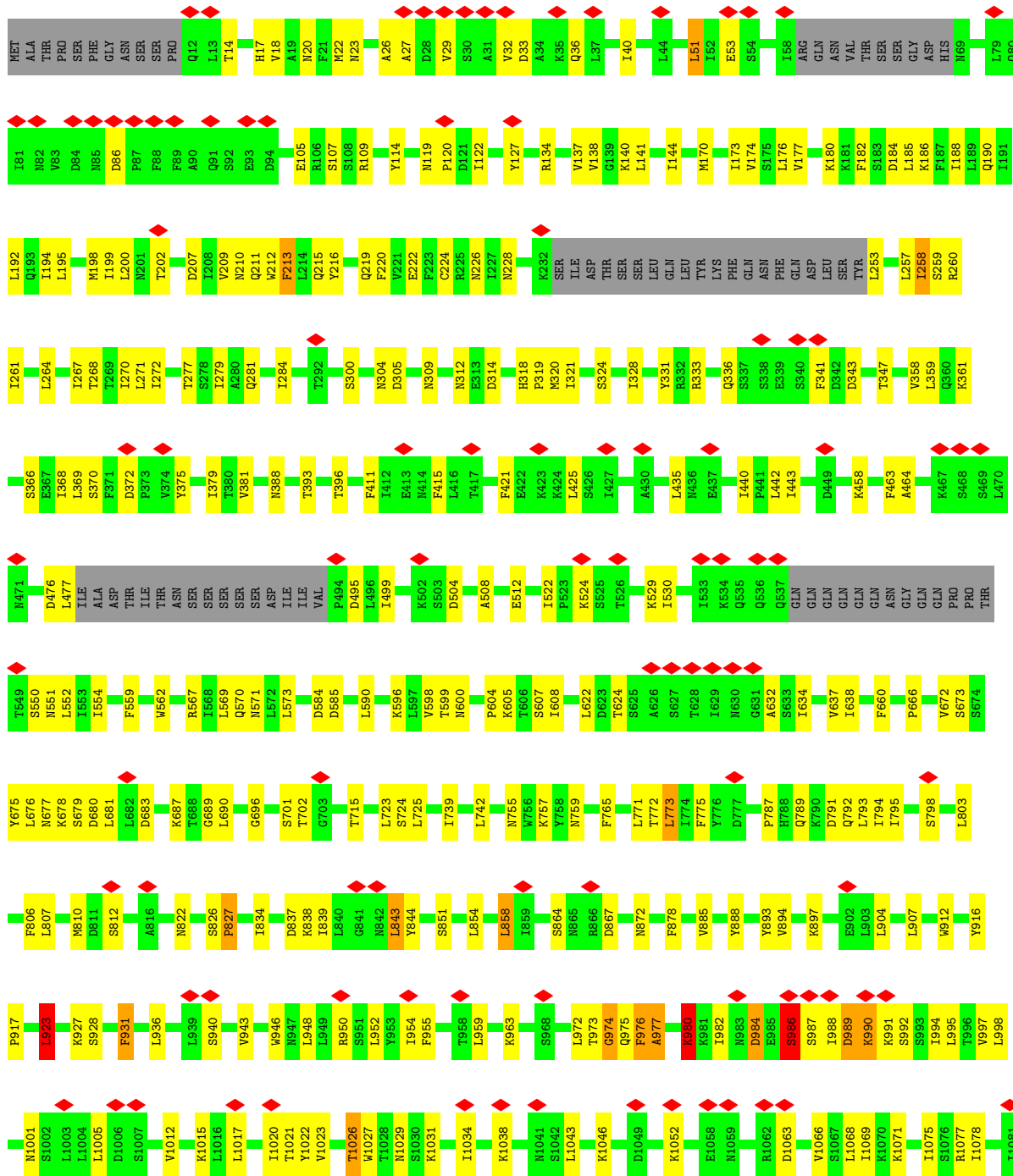
• Molecule 4: Nucleoporin NUP188

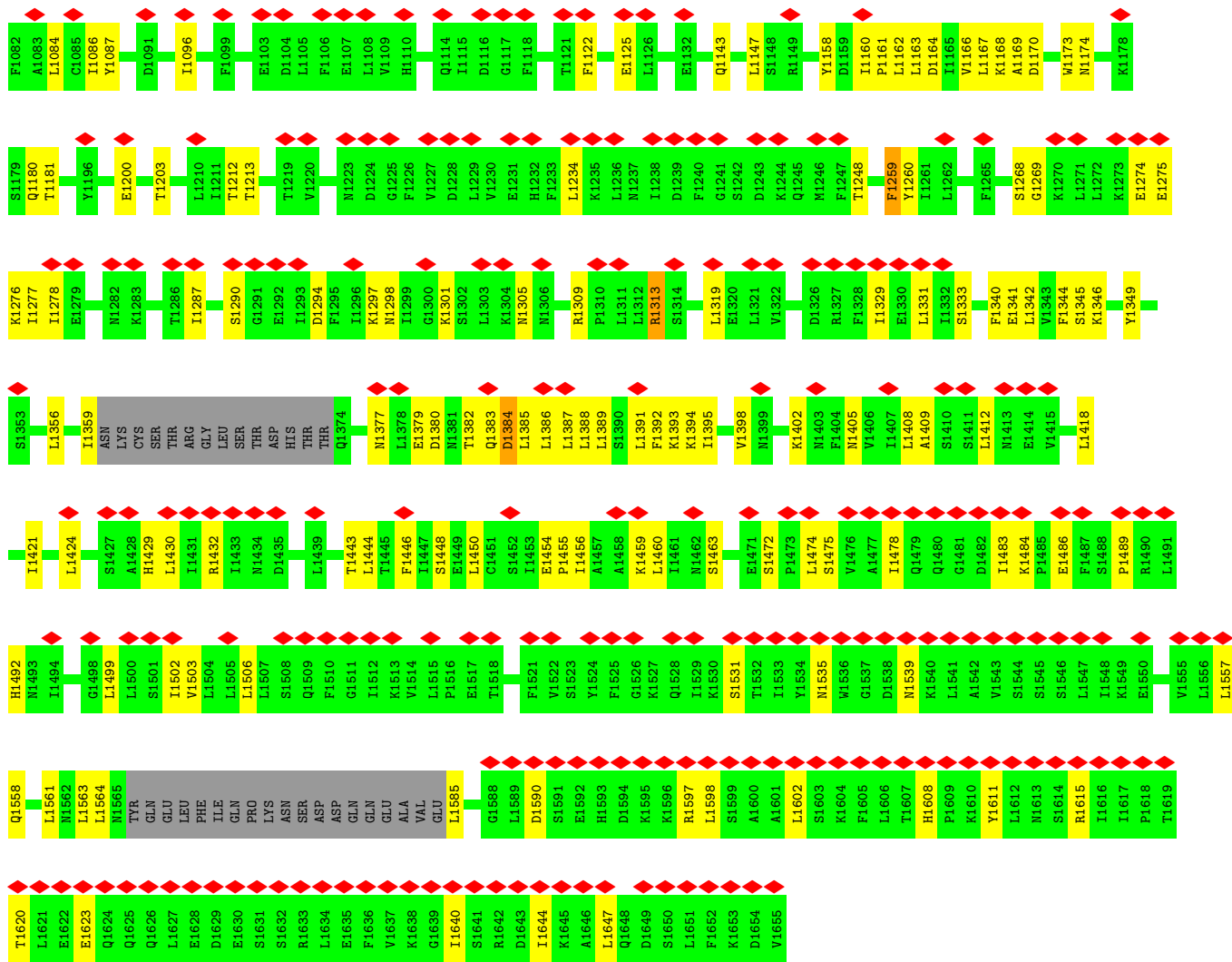




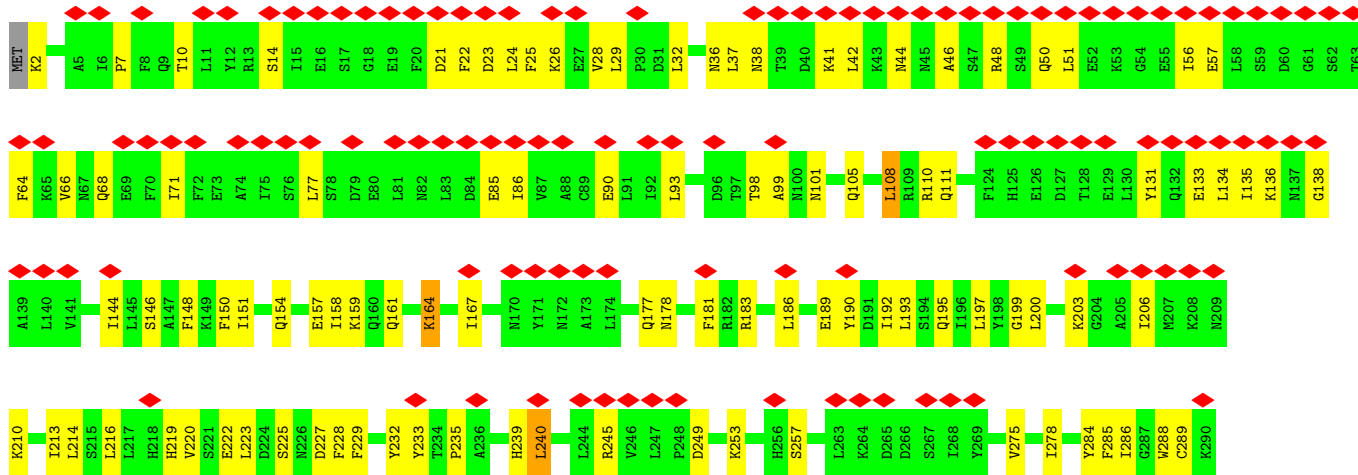


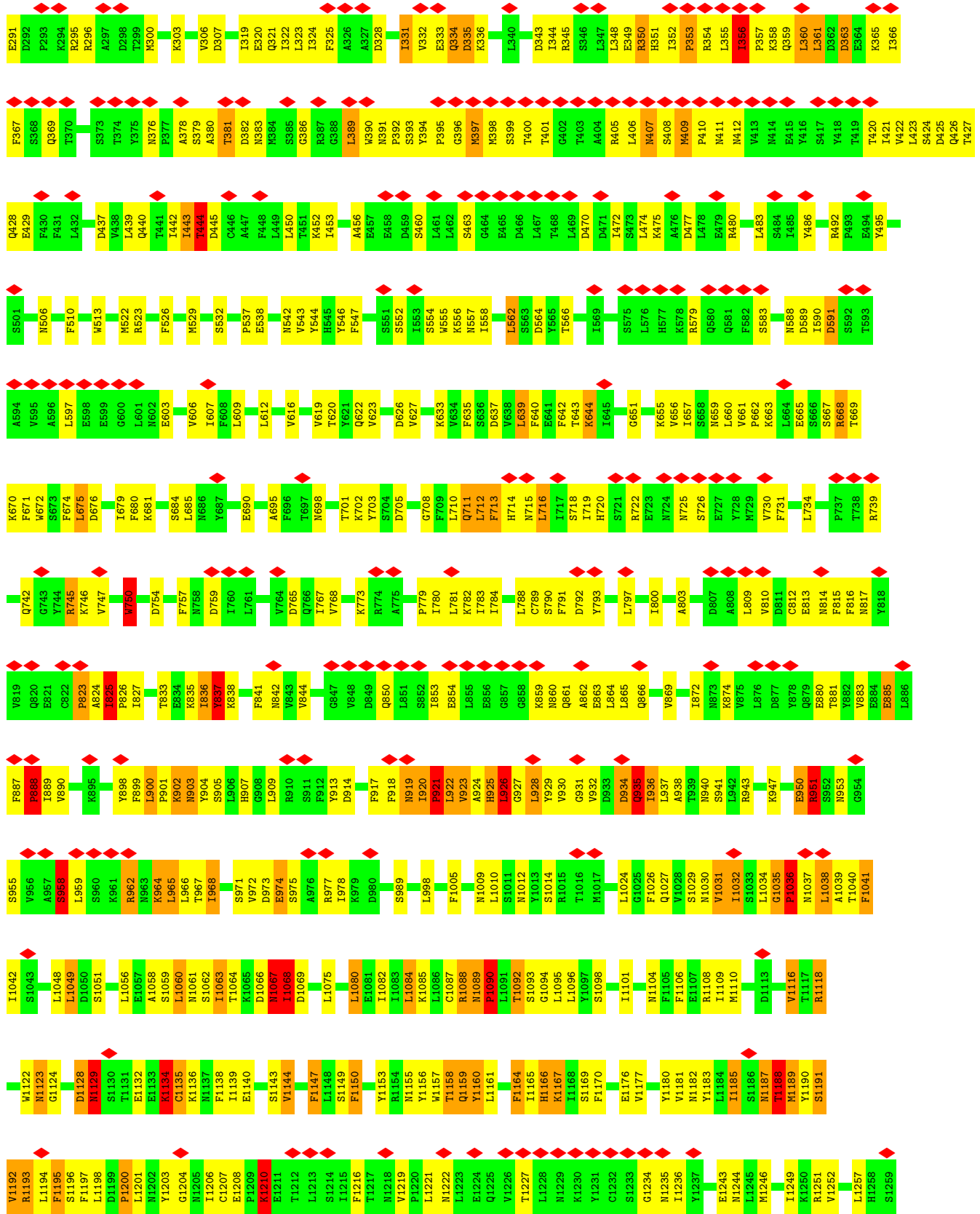
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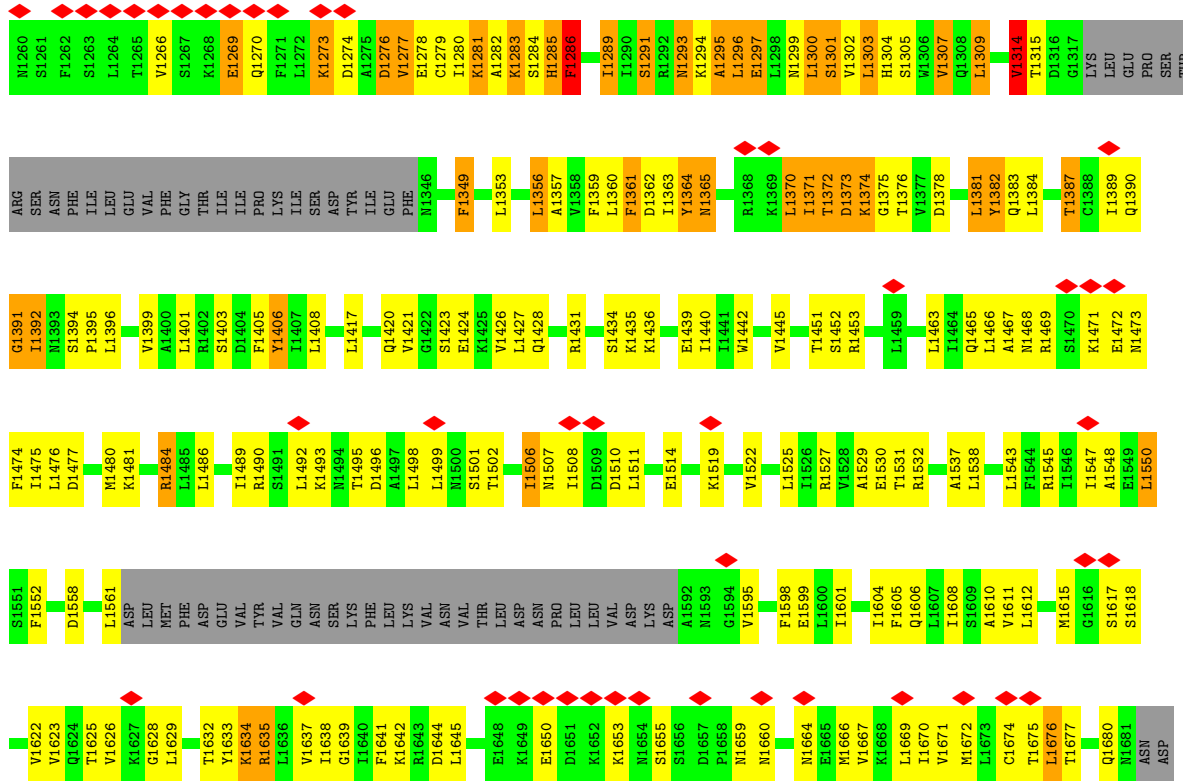




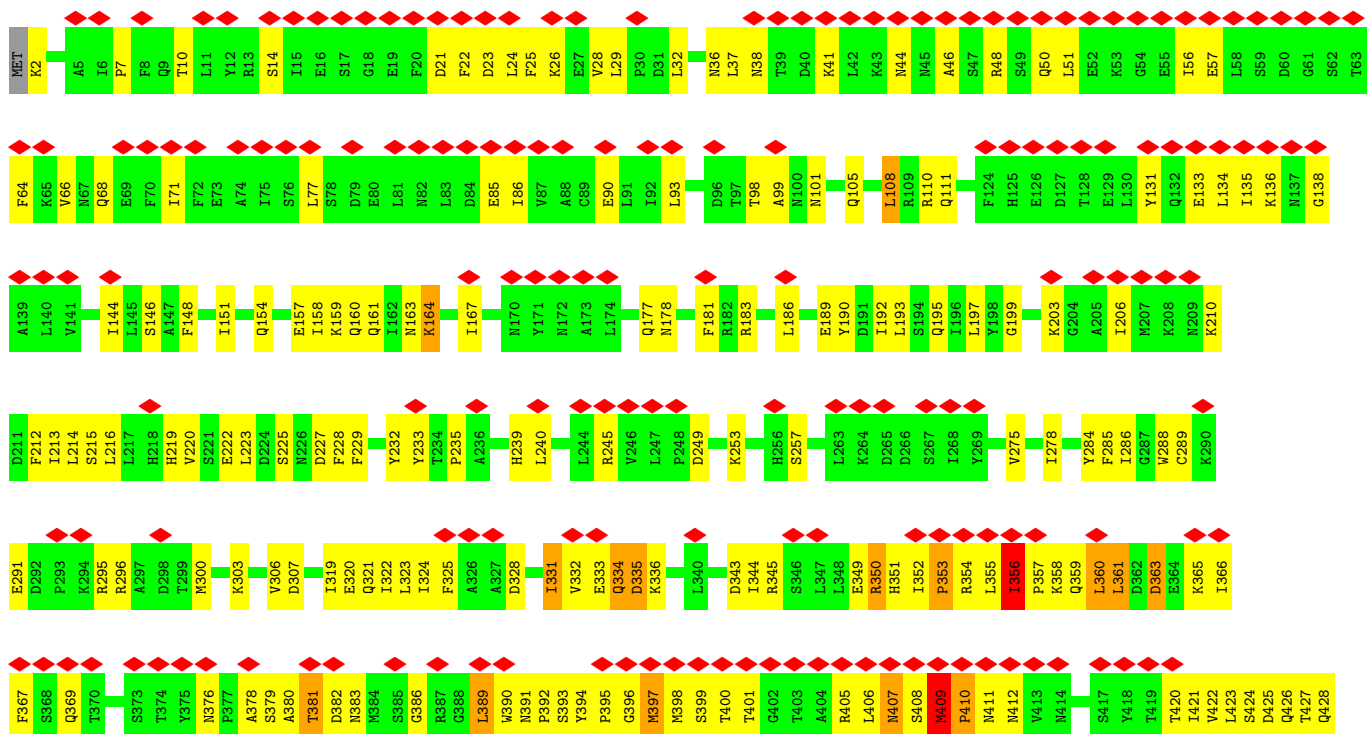
• Molecule 5: Nucleoporin NUP192

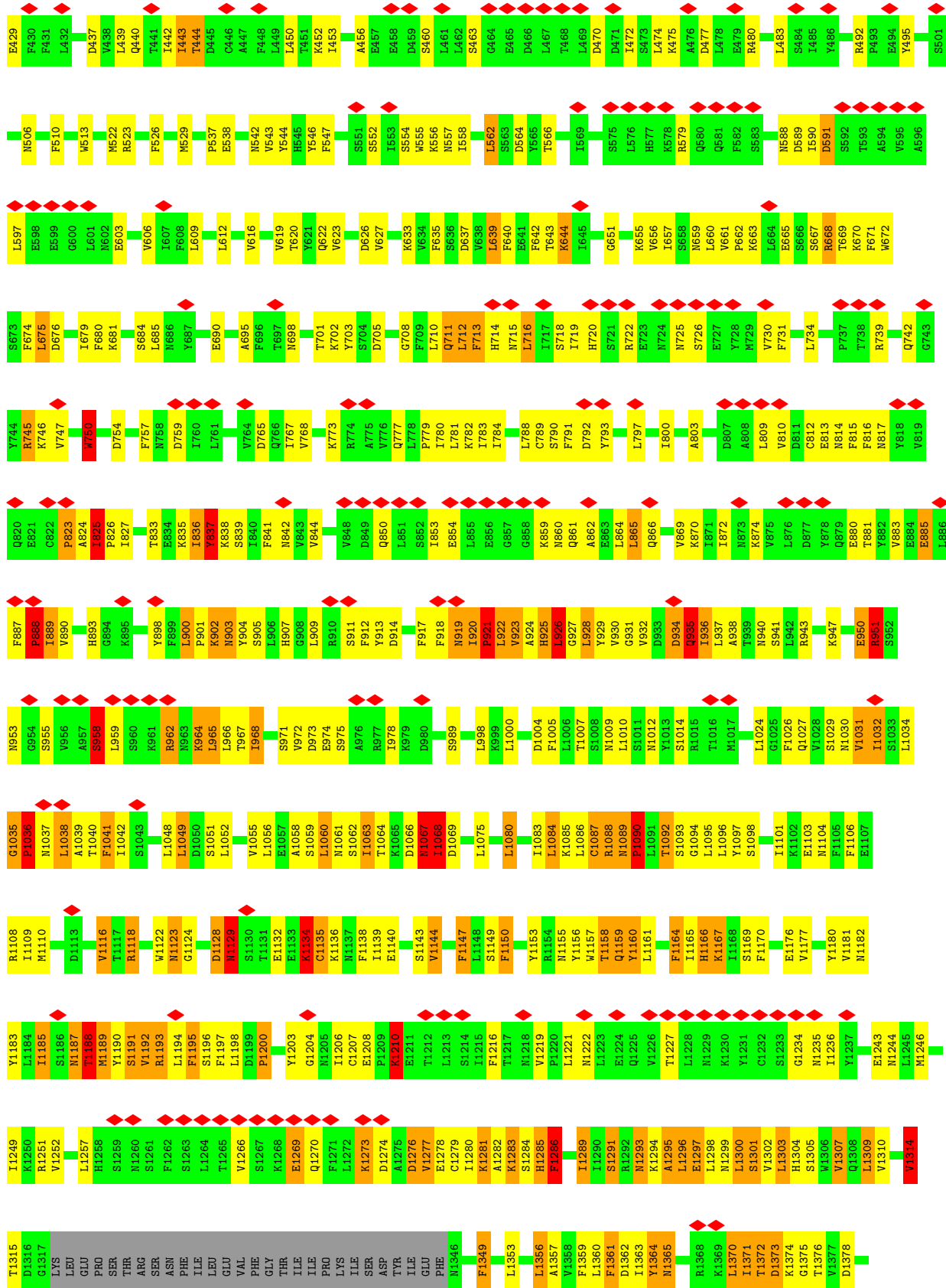


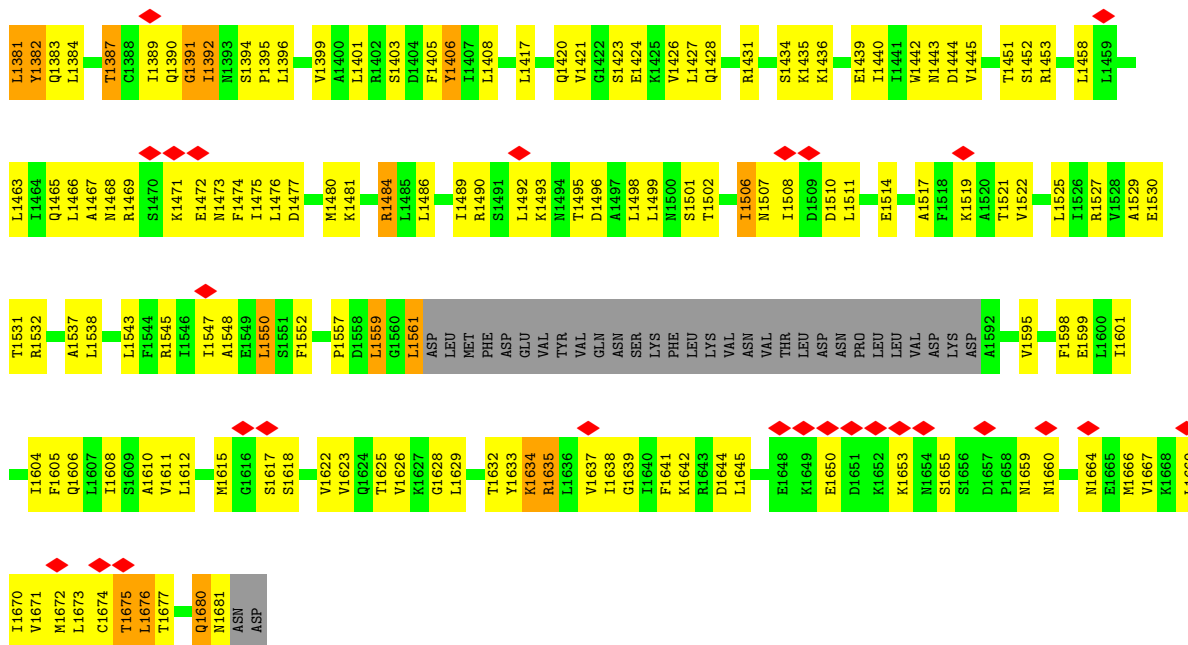




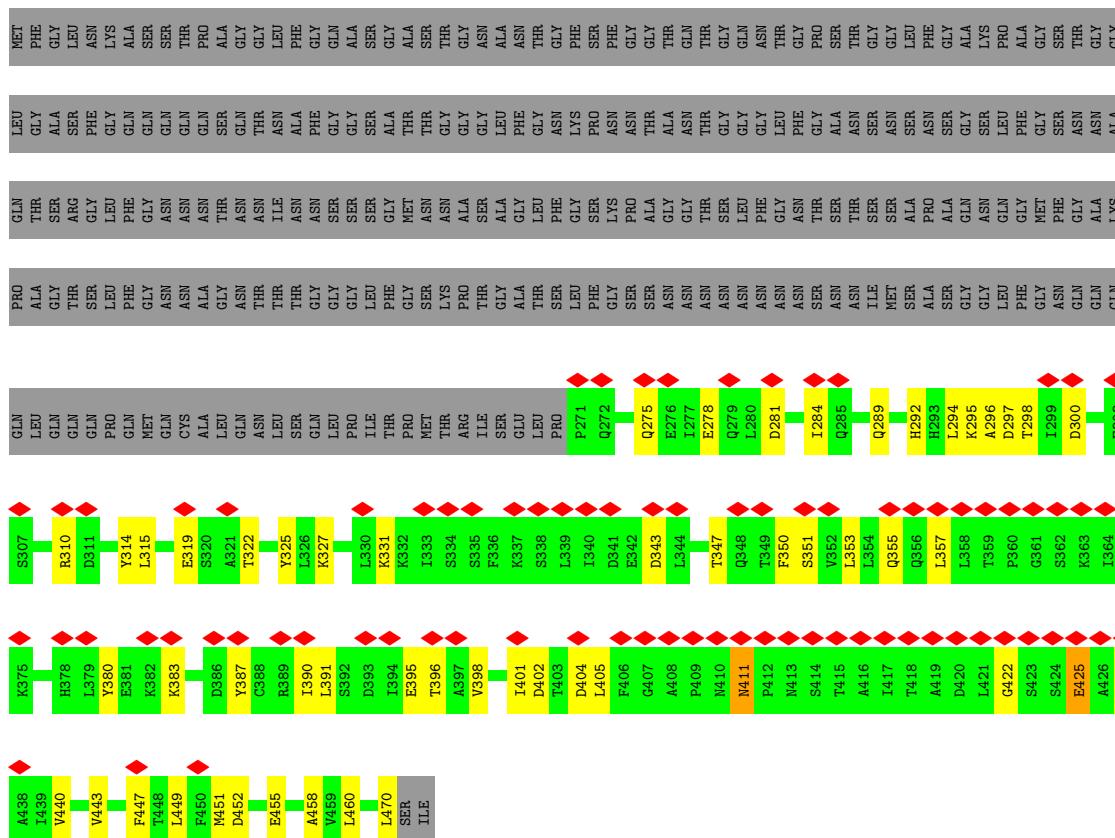
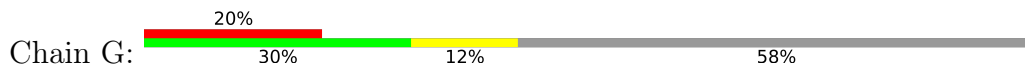
• Molecule 5: Nucleoporin NUP192





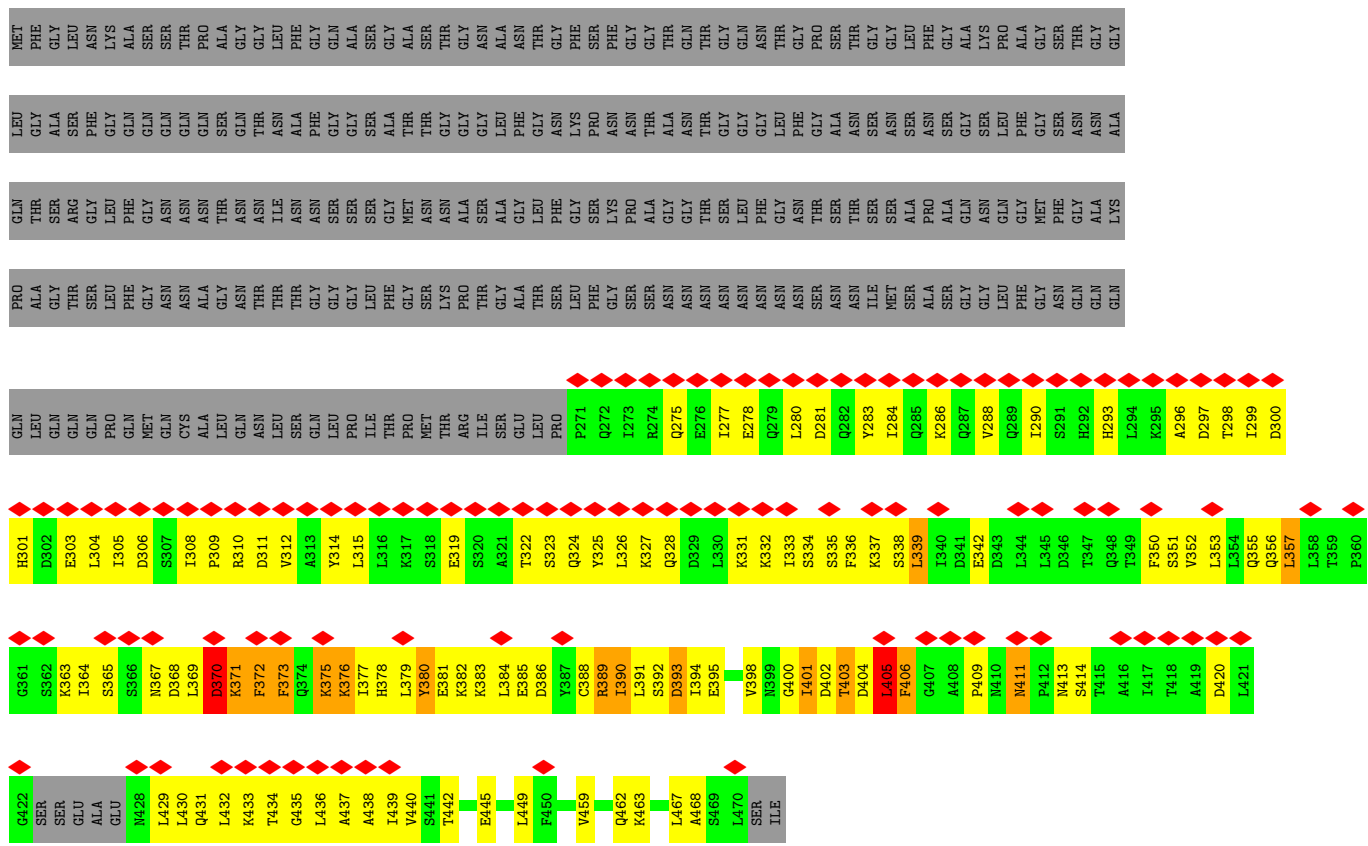


● Molecule 6: Nucleoporin NUP49/NSP49

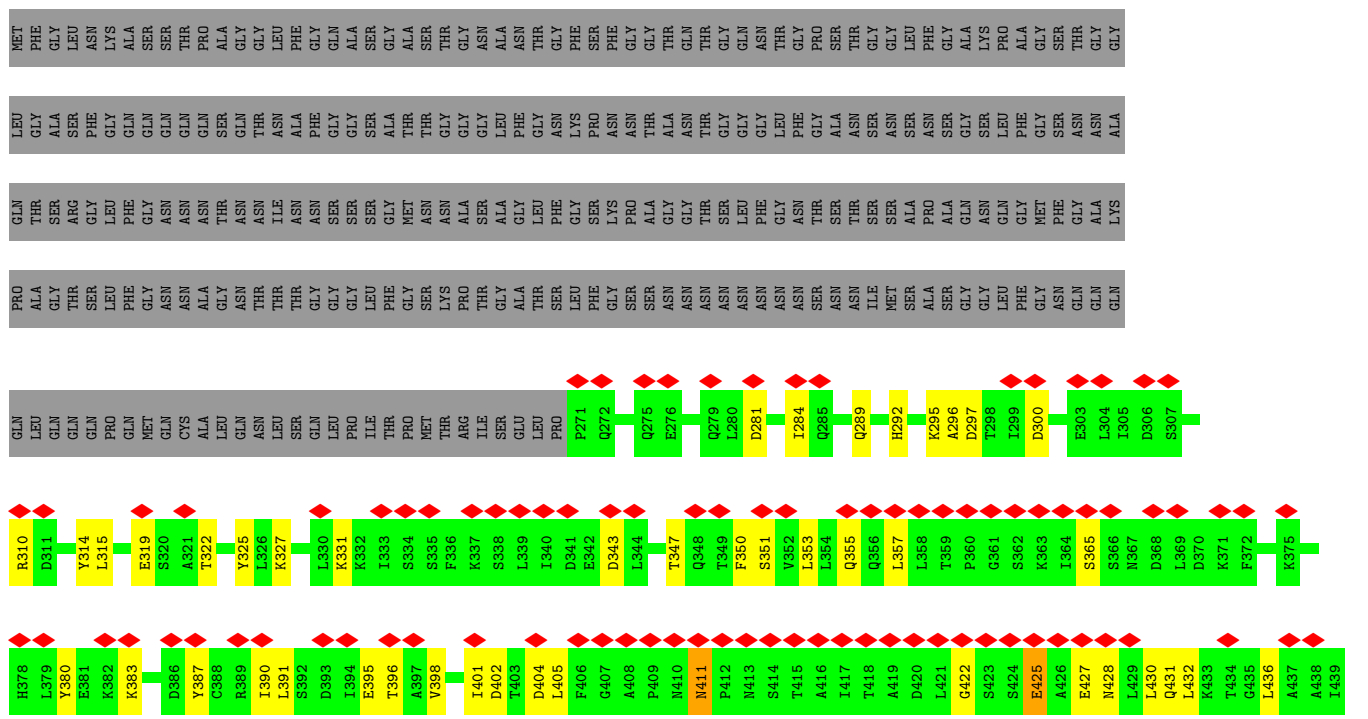
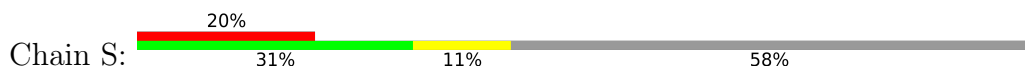


● Molecule 6: Nucleoporin NUP49/NSP49



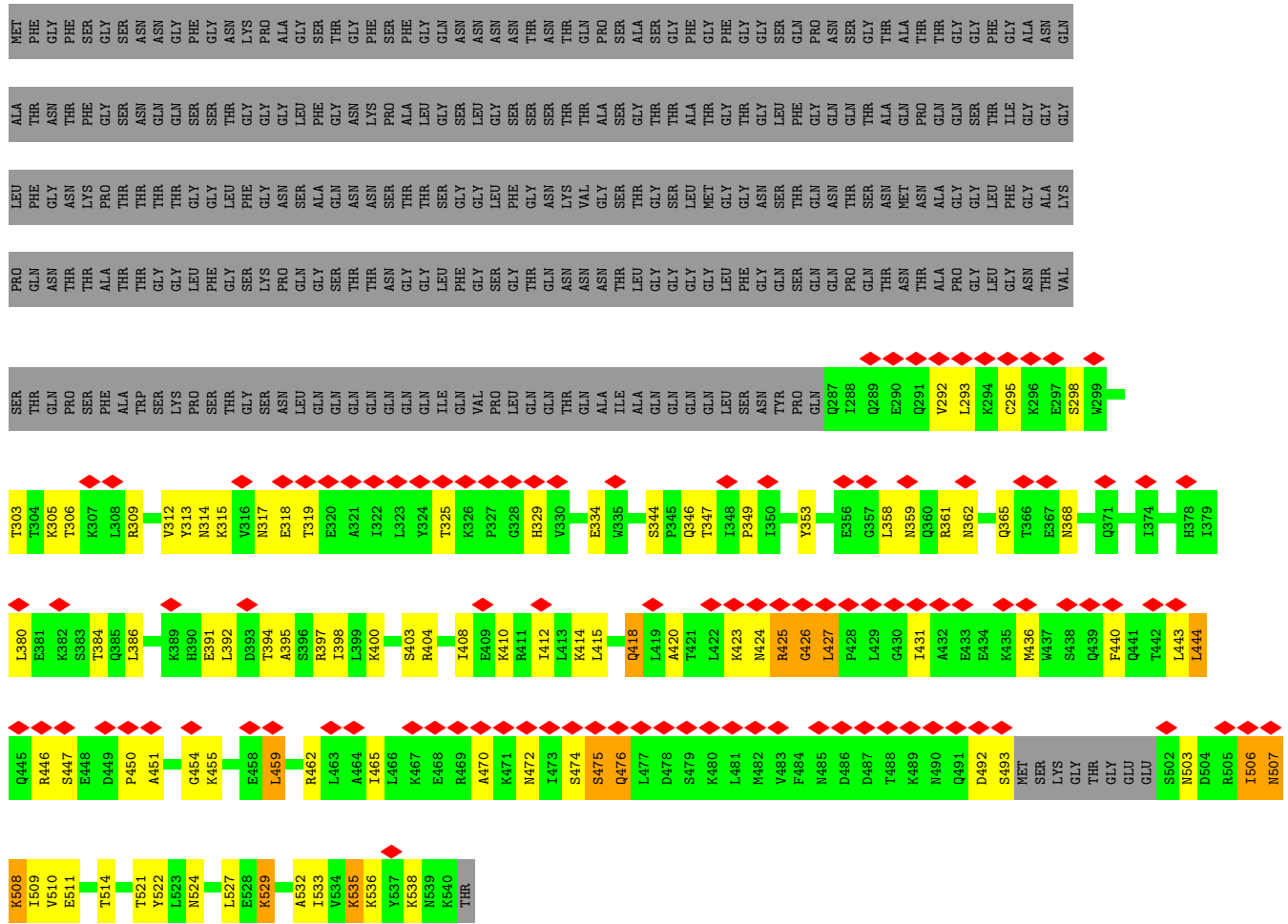


● Molecule 6: Nucleoporin NUP49/NSP49

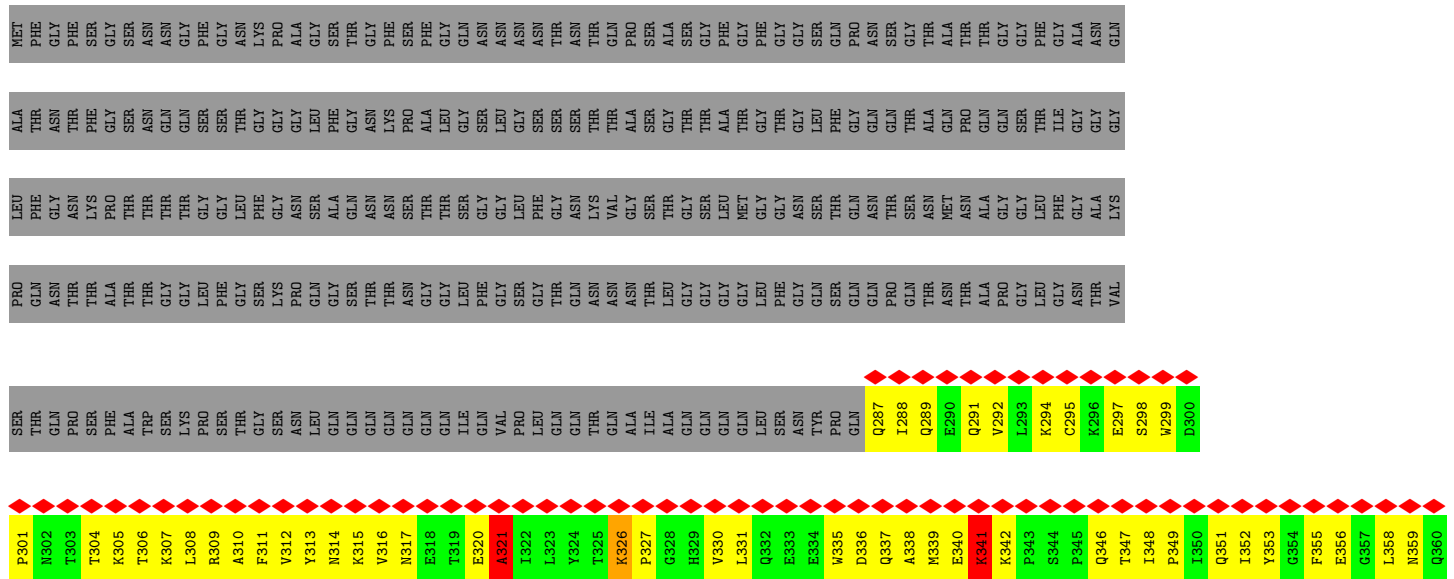








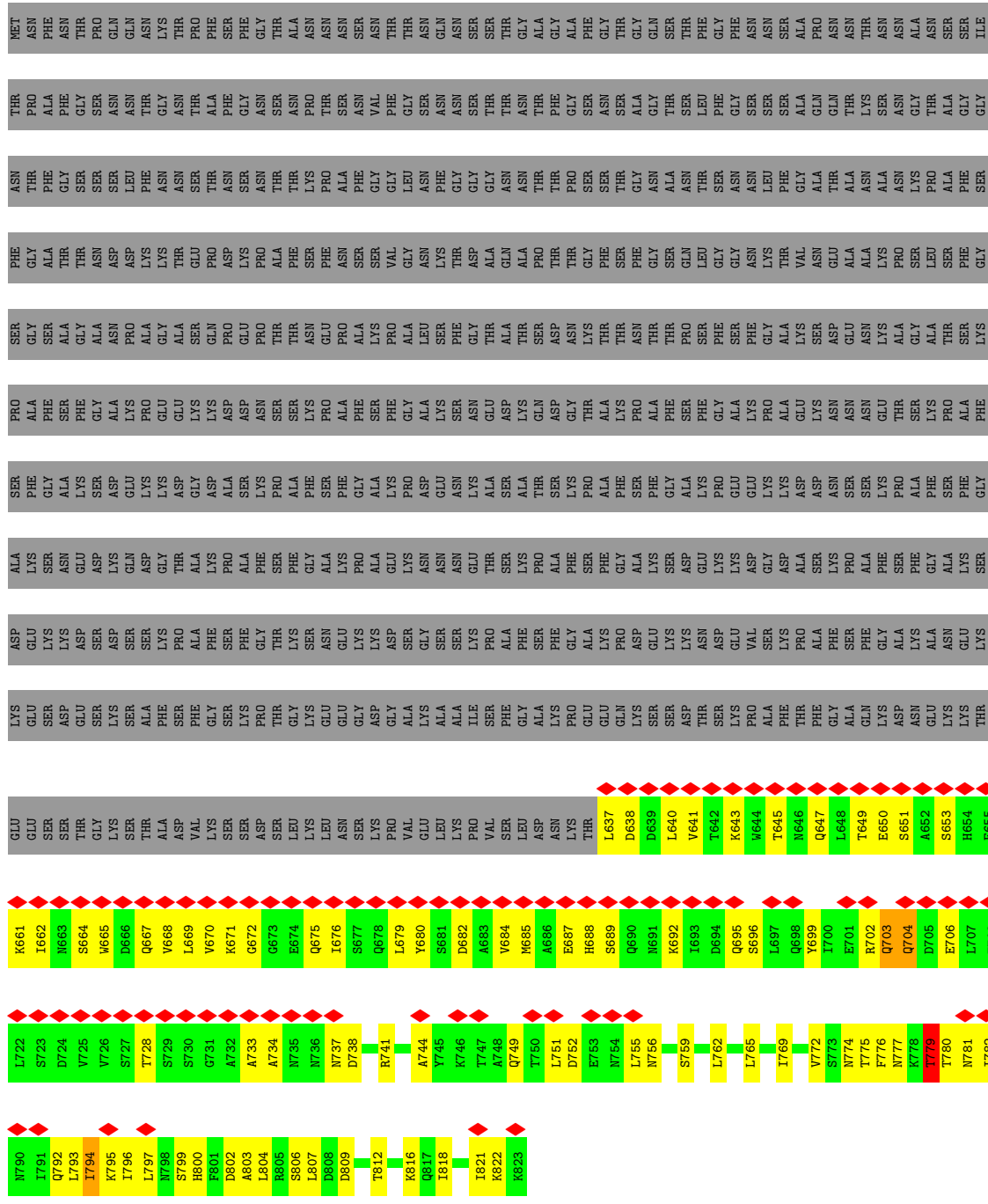
• Molecule 7: Nucleoporin NUP57





K822  
K823

Molecule 8: Nucleoporin NSP1



Molecule 8: Nucleoporin NSP1









## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	633134	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.483	Depositor
Minimum map value	-1.449	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.18	Depositor
Map size ( $\text{\AA}$ )	467.59998, 467.59998, 467.59998	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.336, 1.336, 1.336	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.37	0/5810	0.59	6/7863 (0.1%)
1	M	0.36	0/5787	0.58	5/7832 (0.1%)
1	N	0.46	0/5852	0.82	9/7931 (0.1%)
1	Z	0.46	0/5853	0.84	11/7931 (0.1%)
2	C	0.66	0/10658	0.90	22/14443 (0.2%)
2	O	0.66	0/10658	0.90	23/14443 (0.2%)
3	D	0.46	0/11182	0.63	5/15160 (0.0%)
3	P	0.46	0/11171	0.63	5/15145 (0.0%)
4	E	0.43	0/12583	0.68	9/17054 (0.1%)
4	Q	0.43	0/12583	0.68	8/17054 (0.0%)
5	F	0.63	5/12443 (0.0%)	1.18	91/16898 (0.5%)
5	R	0.63	5/12443 (0.0%)	1.18	90/16898 (0.5%)
6	G	0.35	0/1553	0.62	0/2104
6	J	0.50	0/1509	1.00	11/2042 (0.5%)
6	S	0.35	0/1549	0.62	0/2100
6	V	0.50	0/1509	1.02	11/2042 (0.5%)
7	H	0.61	2/1832 (0.1%)	0.88	10/2482 (0.4%)
7	K	0.56	1/1829 (0.1%)	0.96	12/2485 (0.5%)
7	T	0.61	2/1832 (0.1%)	0.88	11/2482 (0.4%)
7	W	0.61	1/1826 (0.1%)	1.03	15/2481 (0.6%)
8	I	0.59	0/1431	0.93	4/1940 (0.2%)
8	L	0.40	0/1378	0.74	1/1873 (0.1%)
8	U	0.59	0/1431	0.93	4/1940 (0.2%)
8	X	0.40	0/1378	0.74	1/1873 (0.1%)
All	All	0.53	16/136080 (0.0%)	0.85	364/184496 (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	N	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	Z	0	1
5	F	0	4
5	R	0	4
6	G	0	1
6	S	0	1
7	H	0	1
7	K	0	2
7	T	0	1
7	W	0	2
All	All	0	19

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	750	TRP	C-N	10.13	1.53	1.34
5	R	750	TRP	C-N	10.13	1.53	1.34
7	H	427	LEU	C-N	10.05	1.53	1.34
7	T	427	LEU	C-N	10.01	1.53	1.34
7	T	425	ARG	C-N	9.00	1.49	1.33

The worst 5 of 364 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	1090	PRO	CA-N-CD	-37.79	58.60	111.50
5	R	1090	PRO	CA-N-CD	-37.74	58.66	111.50
7	T	425	ARG	C-N-CA	-13.43	94.11	122.30
7	H	425	ARG	C-N-CA	-13.39	94.18	122.30
6	V	388	CYS	CB-CA-C	-12.61	85.19	110.40

There are no chirality outliers.

5 of 19 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	F	1185	ILE	Mainchain
5	F	1188	THR	Mainchain
5	F	360	LEU	Mainchain
5	F	814	ASN	Mainchain
6	G	422	GLY	Mainchain

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5720	0	5578	305	0
1	M	5697	0	5563	302	0
1	N	5766	0	5590	494	0
1	Z	5767	0	5596	531	0
2	C	10452	0	10392	51	0
2	O	10452	0	10392	50	0
3	D	10966	0	10812	459	0
3	P	10956	0	10803	473	0
4	E	12362	0	12566	356	0
4	Q	12362	0	12566	336	0
5	F	12239	0	11567	842	0
5	R	12239	0	11568	850	0
6	G	1533	0	1515	124	0
6	J	1492	0	1465	287	0
6	S	1529	0	1504	112	0
6	V	1492	0	1465	323	0
7	H	1811	0	1697	146	0
7	K	1808	0	1614	306	0
7	T	1811	0	1697	152	0
7	W	1805	0	1605	321	0
8	I	1418	0	1293	168	0
8	L	1366	0	1211	160	0
8	U	1418	0	1293	168	0
8	X	1366	0	1211	145	0
All	All	133827	0	130563	6256	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 6256 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)
1:N:810:ALA:CB	1:N:836:ASP:HA	1.26	1.63
6:G:451:MET:CE	1:M:14:THR:HG21	1.19	1.62
1:A:15:SER:HB2	6:S:447:PHE:CZ	1.35	1.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:955:PRO:CB	3:D:994:SER:CB	1.78	1.61
5:R:1357:ALA:HB2	5:R:1381:LEU:CB	1.19	1.60

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	722/839 (86%)	702 (97%)	18 (2%)	2 (0%)	41	74
1	M	719/839 (86%)	699 (97%)	18 (2%)	2 (0%)	41	74
1	N	736/839 (88%)	680 (92%)	39 (5%)	17 (2%)	6	38
1	Z	736/839 (88%)	681 (92%)	38 (5%)	17 (2%)	6	38
2	C	1323/1391 (95%)	1269 (96%)	41 (3%)	13 (1%)	15	51
2	O	1323/1391 (95%)	1270 (96%)	40 (3%)	13 (1%)	15	51
3	D	1396/1502 (93%)	1275 (91%)	113 (8%)	8 (1%)	25	61
3	P	1396/1502 (93%)	1275 (91%)	113 (8%)	8 (1%)	25	61
4	E	1538/1655 (93%)	1374 (89%)	150 (10%)	14 (1%)	17	53
4	Q	1538/1655 (93%)	1376 (90%)	149 (10%)	13 (1%)	19	56
5	F	1616/1683 (96%)	1200 (74%)	321 (20%)	95 (6%)	1	20
5	R	1616/1683 (96%)	1196 (74%)	324 (20%)	96 (6%)	1	20
6	G	198/472 (42%)	188 (95%)	9 (4%)	1 (0%)	29	65
6	J	191/472 (40%)	172 (90%)	15 (8%)	4 (2%)	7	40
6	S	198/472 (42%)	188 (95%)	9 (4%)	1 (0%)	29	65
6	V	191/472 (40%)	171 (90%)	16 (8%)	4 (2%)	7	40
7	H	242/541 (45%)	202 (84%)	36 (15%)	4 (2%)	9	43
7	K	252/541 (47%)	208 (82%)	33 (13%)	11 (4%)	2	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	T	242/541 (45%)	202 (84%)	36 (15%)	4 (2%)	9	43
7	W	252/541 (47%)	209 (83%)	32 (13%)	11 (4%)	2	25
8	I	185/823 (22%)	158 (85%)	16 (9%)	11 (6%)	1	20
8	L	185/823 (22%)	164 (89%)	15 (8%)	6 (3%)	4	32
8	U	185/823 (22%)	158 (85%)	16 (9%)	11 (6%)	1	20
8	X	185/823 (22%)	164 (89%)	15 (8%)	6 (3%)	4	32
All	All	17165/23162 (74%)	15181 (88%)	1612 (9%)	372 (2%)	10	39

5 of 372 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	44	VAL
2	C	319	PRO
2	C	468	PHE
2	C	476	ASN
2	C	694	PHE

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	608/762 (80%)	583 (96%)	25 (4%)	30	59
1	M	605/762 (79%)	578 (96%)	27 (4%)	27	57
1	N	609/762 (80%)	554 (91%)	55 (9%)	9	37
1	Z	609/762 (80%)	554 (91%)	55 (9%)	9	37
2	C	1177/1250 (94%)	1152 (98%)	25 (2%)	53	74
2	O	1177/1250 (94%)	1152 (98%)	25 (2%)	53	74
3	D	1212/1353 (90%)	1199 (99%)	13 (1%)	73	85
3	P	1210/1353 (89%)	1197 (99%)	13 (1%)	73	85
4	E	1421/1557 (91%)	1397 (98%)	24 (2%)	60	79
4	Q	1421/1557 (91%)	1397 (98%)	24 (2%)	60	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	F	1261/1538 (82%)	1165 (92%)	96 (8%)	13	43
5	R	1261/1538 (82%)	1163 (92%)	98 (8%)	12	43
6	G	167/377 (44%)	165 (99%)	2 (1%)	71	84
6	J	162/377 (43%)	145 (90%)	17 (10%)	7	31
6	S	166/377 (44%)	164 (99%)	2 (1%)	71	84
6	V	162/377 (43%)	148 (91%)	14 (9%)	10	40
7	H	171/439 (39%)	166 (97%)	5 (3%)	42	66
7	K	153/439 (35%)	134 (88%)	19 (12%)	4	24
7	T	171/439 (39%)	166 (97%)	5 (3%)	42	66
7	W	152/439 (35%)	128 (84%)	24 (16%)	2	17
8	I	152/674 (23%)	135 (89%)	17 (11%)	6	29
8	L	138/674 (20%)	137 (99%)	1 (1%)	84	91
8	U	152/674 (23%)	135 (89%)	17 (11%)	6	29
8	X	138/674 (20%)	137 (99%)	1 (1%)	84	91
All	All	14455/20404 (71%)	13851 (96%)	604 (4%)	33	58

5 of 604 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	R	1301	SER
1	Z	125	ILE
5	R	1382	TYR
5	R	1300	LEU
6	V	401	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 229 such sidechains are listed below:

Mol	Chain	Res	Type
1	N	738	GLN
1	Z	464	ASN
4	Q	770	HIS
1	Z	396	GLN
7	W	402	GLN

### 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 monosaccharides 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.



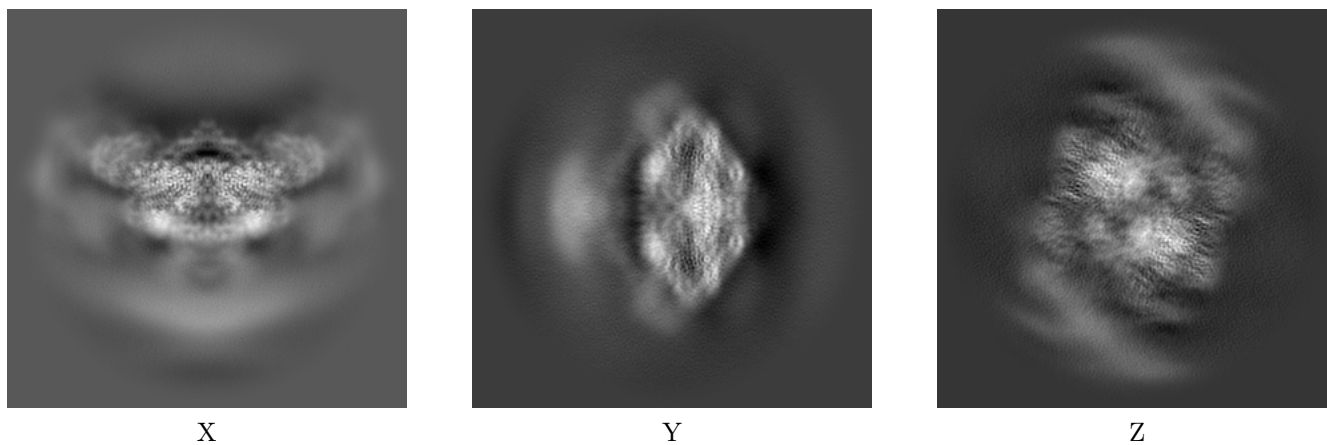
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32658. 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](#)

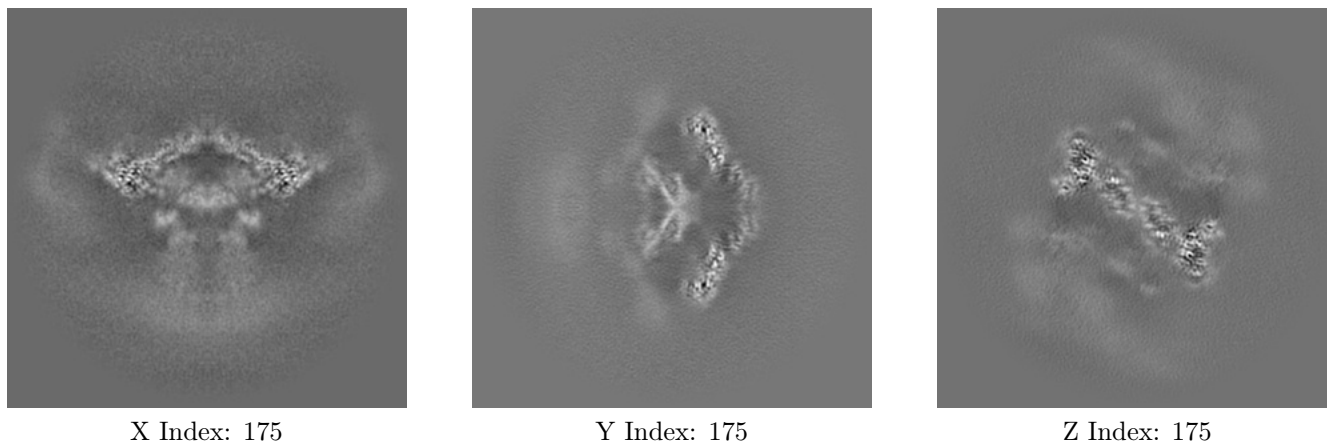
#### 6.1.1 Primary map



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

### 6.2 Central slices [i](#)

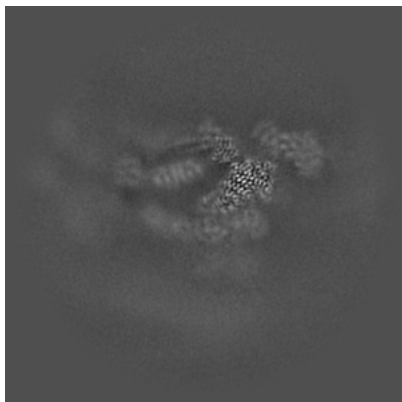
#### 6.2.1 Primary map



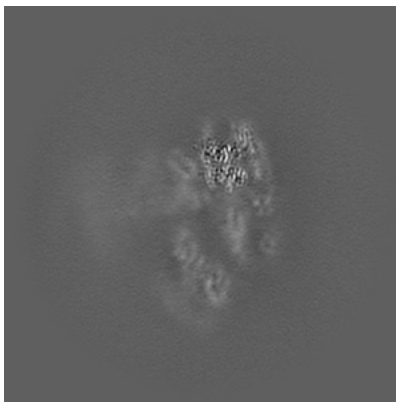
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

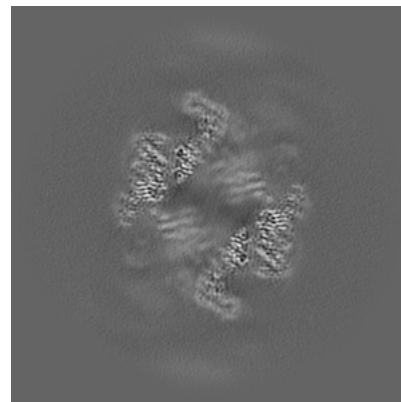
### 6.3.1 Primary map



X Index: 150



Y Index: 147



Z Index: 204

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

## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.18. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

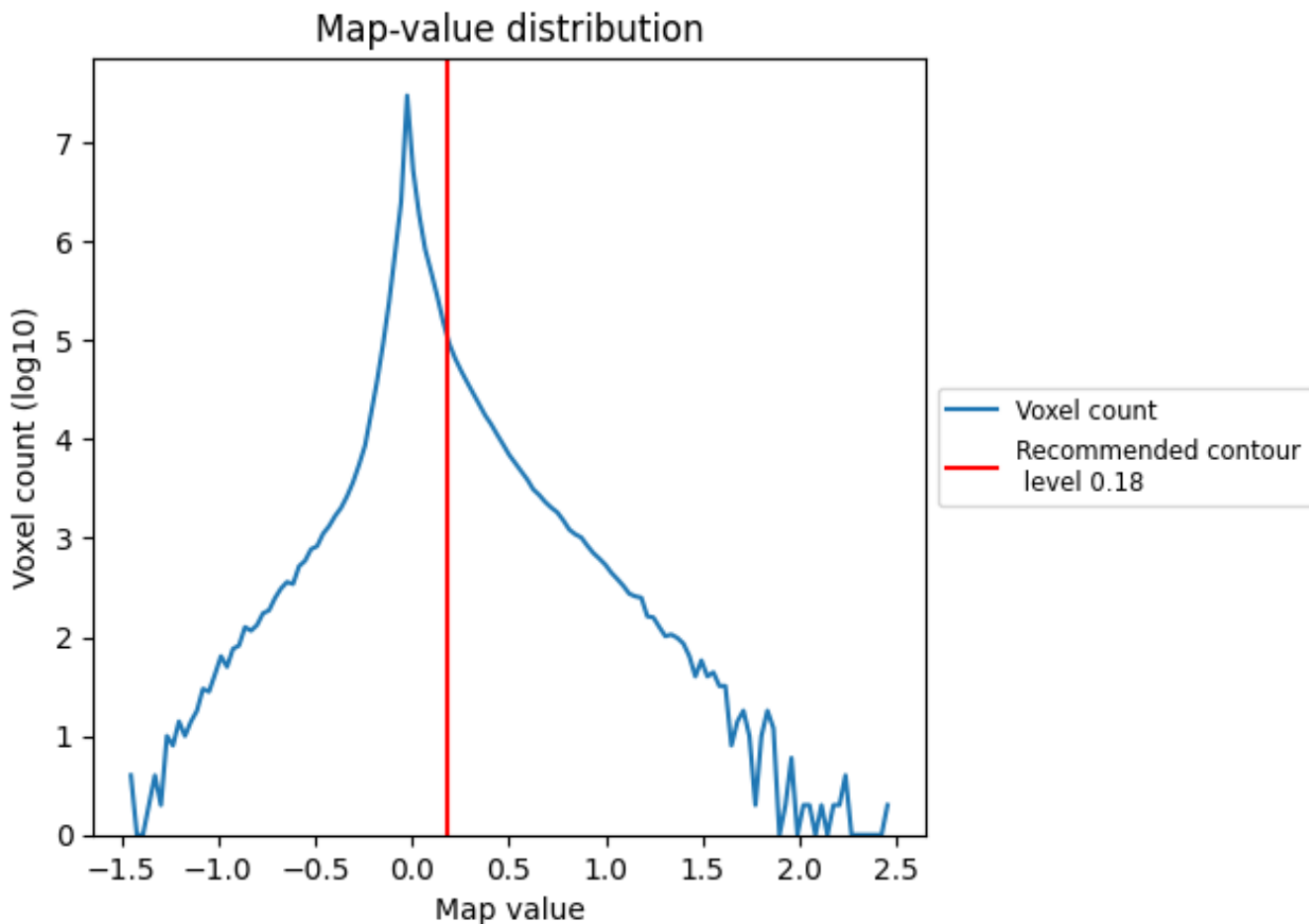
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

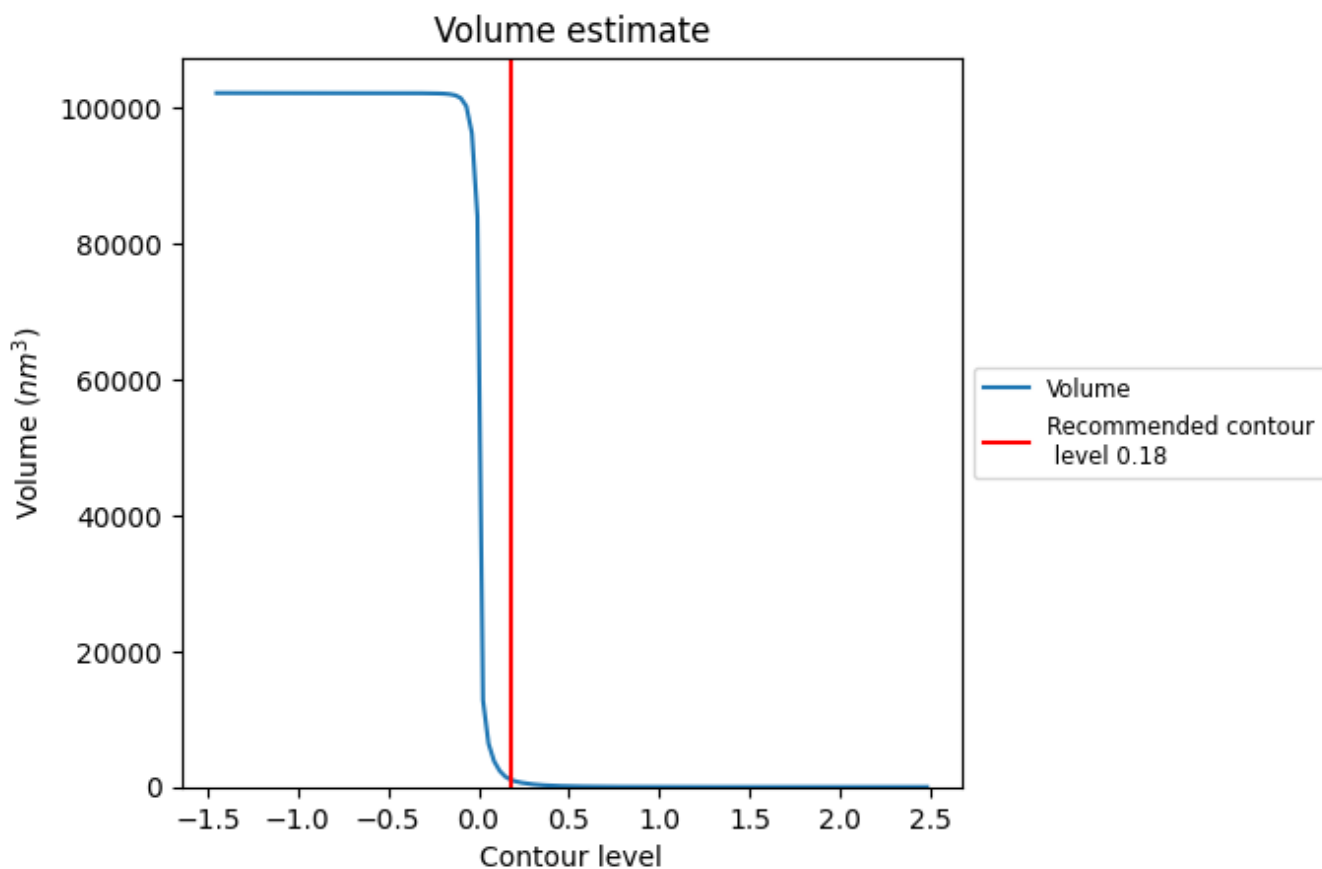
This section contains the results of statistical analysis of the map.

### 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.

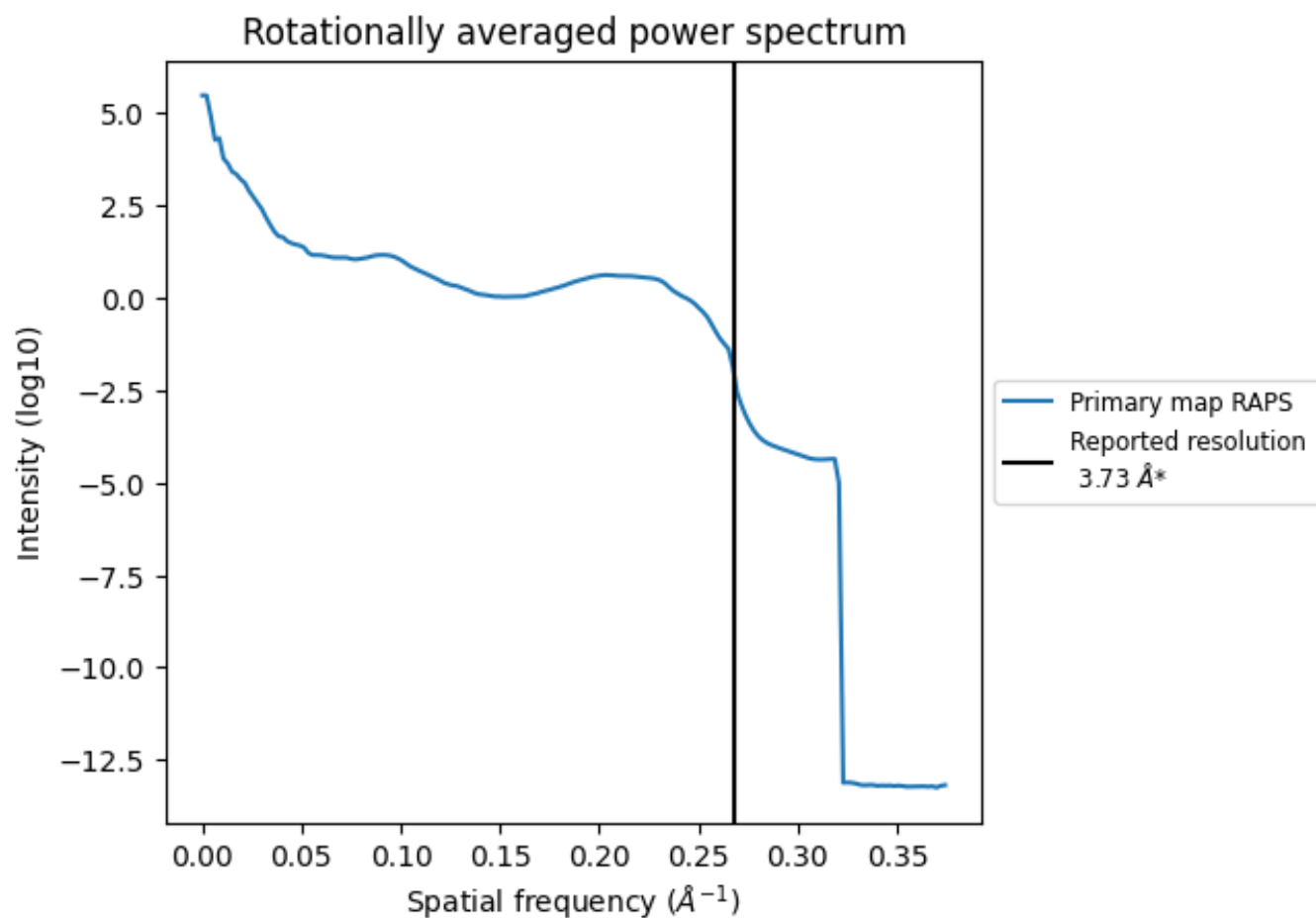
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1052 nm<sup>3</sup>; this corresponds to an approximate mass of 950 kDa.

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

### 7.3 Rotationally averaged power spectrum [i](#)



\*Reported resolution corresponds to spatial frequency of 0.268 Å<sup>-1</sup>

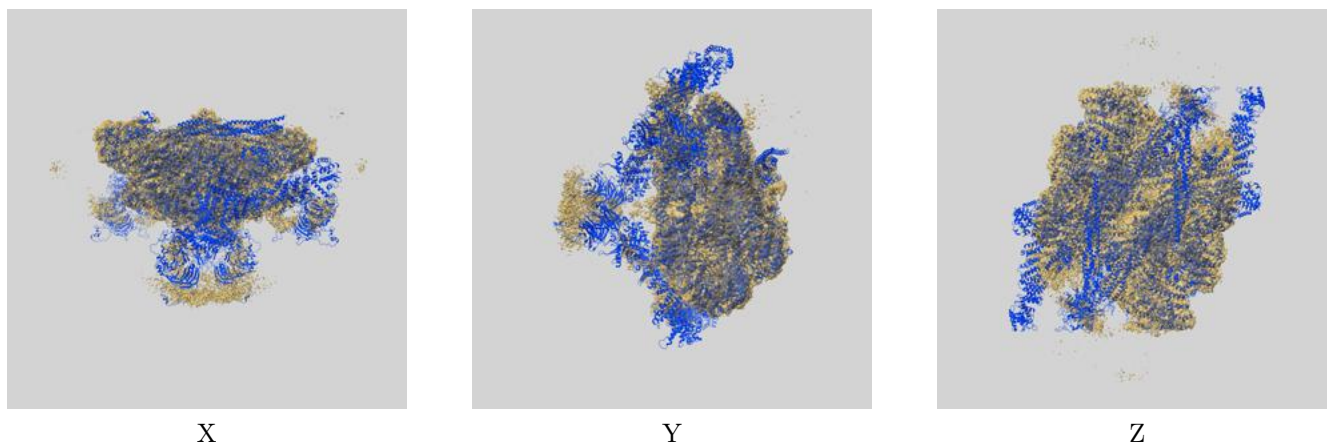
## 8 Fourier-Shell correlation

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-32658 and PDB model 7WOT. Per-residue inclusion information can be found in section 3 on page 6.

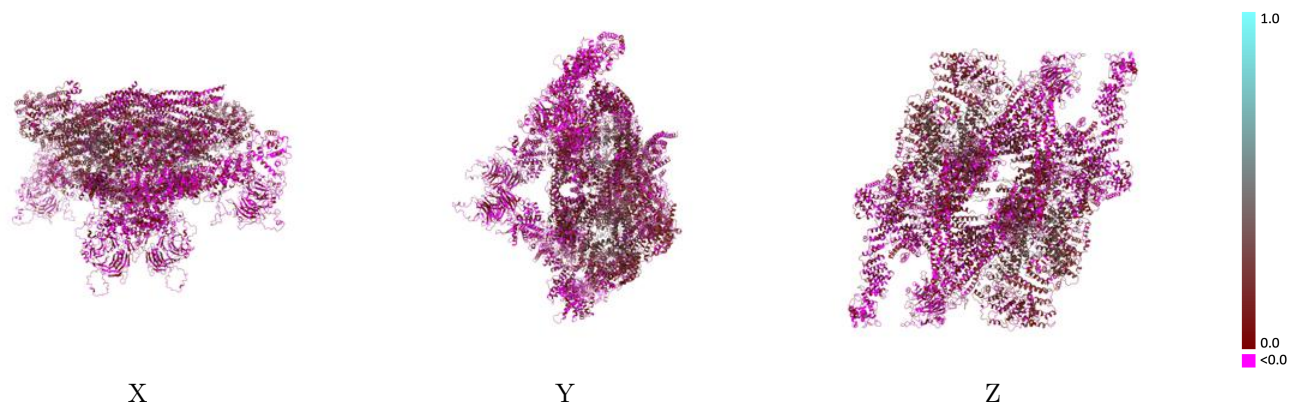
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.18 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.

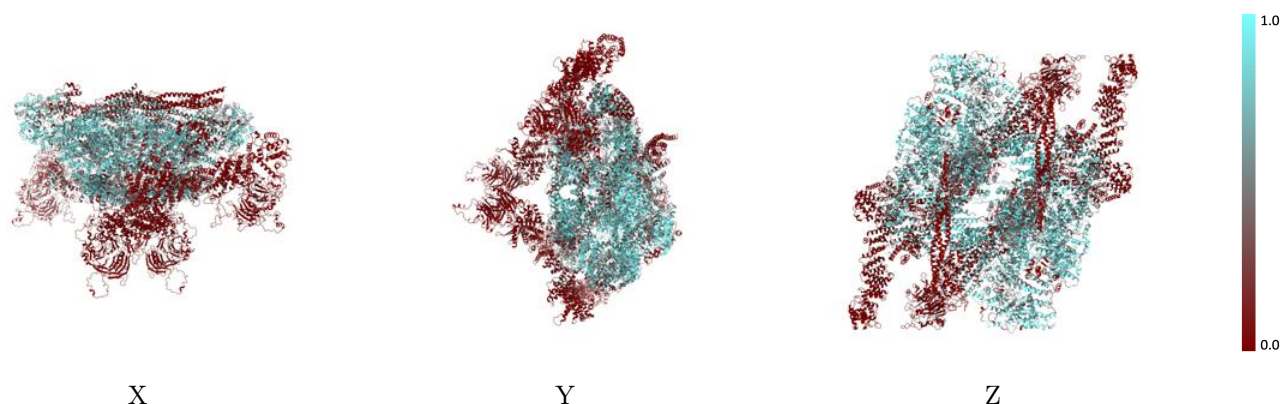


## 9.2 Q-score mapped to coordinate model [i](#)



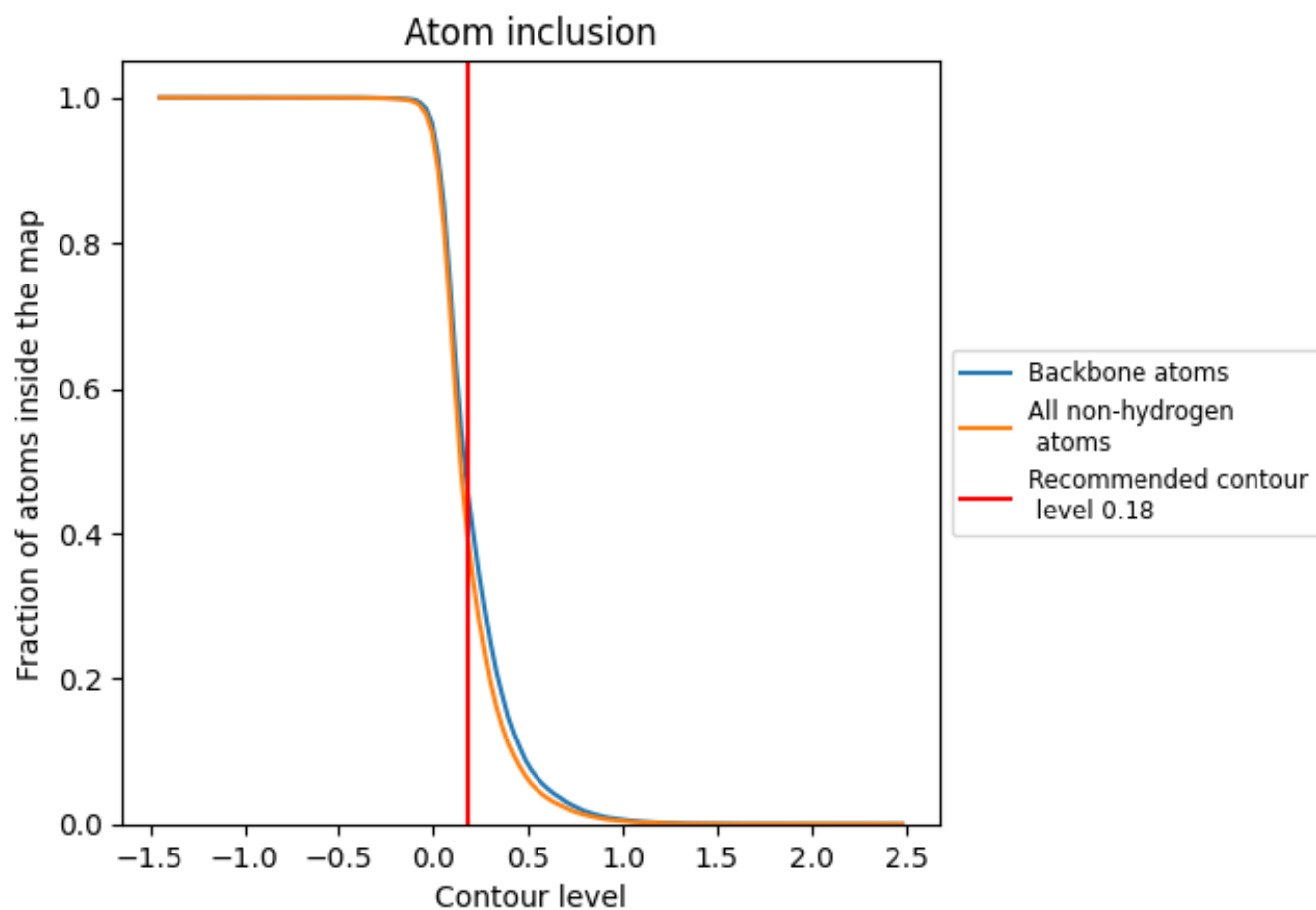
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.18).



















































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 46% of all backbone atoms, 40% 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 (0.18) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3966	 0.0910
A	 0.0875	 -0.0000
C	 0.0192	 0.0100
D	 0.2236	 0.0340
E	 0.6414	 0.1690
F	 0.6672	 0.1830
G	 0.4671	 0.0620
H	 0.4603	 0.0580
I	 0.5908	 0.1040
J	 0.3608	 0.0640
K	 0.2654	 0.0540
L	 0.3355	 0.0640
M	 0.0836	 0.0000
N	 0.5807	 0.1030
O	 0.0192	 0.0090
P	 0.2228	 0.0340
Q	 0.6449	 0.1740
R	 0.6700	 0.1830
S	 0.4671	 0.0620
T	 0.4609	 0.0570
U	 0.5936	 0.1070
V	 0.3642	 0.0620
W	 0.3035	 0.0730
X	 0.3333	 0.0650
Z	 0.5768	 0.1050

