



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 06:23 PM UTC

PDB ID : 7WOO / pdb_00007woo
EMDB ID : EMD-32653
Title : Cryo-EM structure of the inner ring protomer 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 : 3.71 Å(reported)

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

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A user guide is available at

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

The types of validation reports are described at

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

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

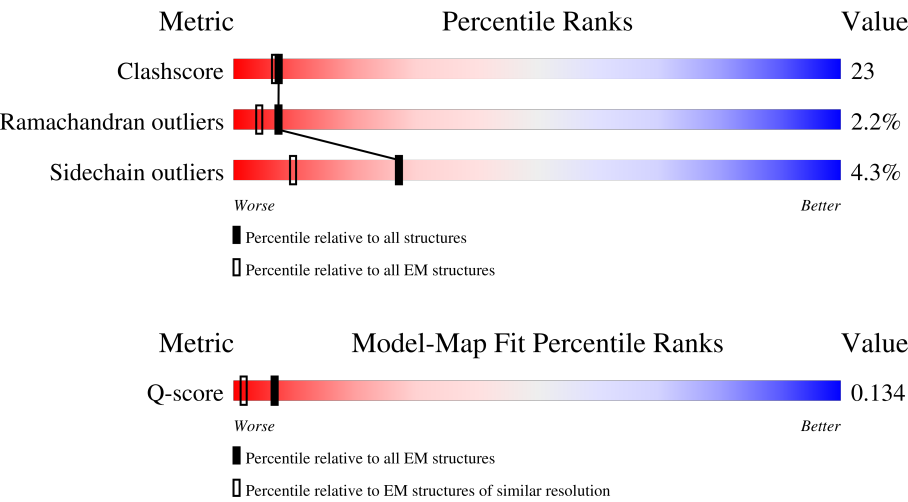
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.71 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10534 (3.21 - 4.21)

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	A	839	
1	Z	839	
2	C	1391	
3	D	1502	

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Mol	Chain	Length	Quality of chain
4	E	1655	
5	F	1683	
6	G	472	
6	J	472	
7	H	541	
7	K	541	
8	I	823	
8	L	823	

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 66949 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
1	A	732	Total	C	N	O	S	0	0
			5723	3631	975	1101	16		
1	Z	746	Total	C	N	O	S	0	0
			5776	3660	981	1120	15		

- Molecule 2 is a protein called Nucleoporin NUP157.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	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
3	D	1398	Total	C	N	O	S	0	0
			10976	7018	1811	2115	32		

- Molecule 4 is a protein called Nucleoporin NUP188.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	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
			12232	7805	2031	2365	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		

- 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		

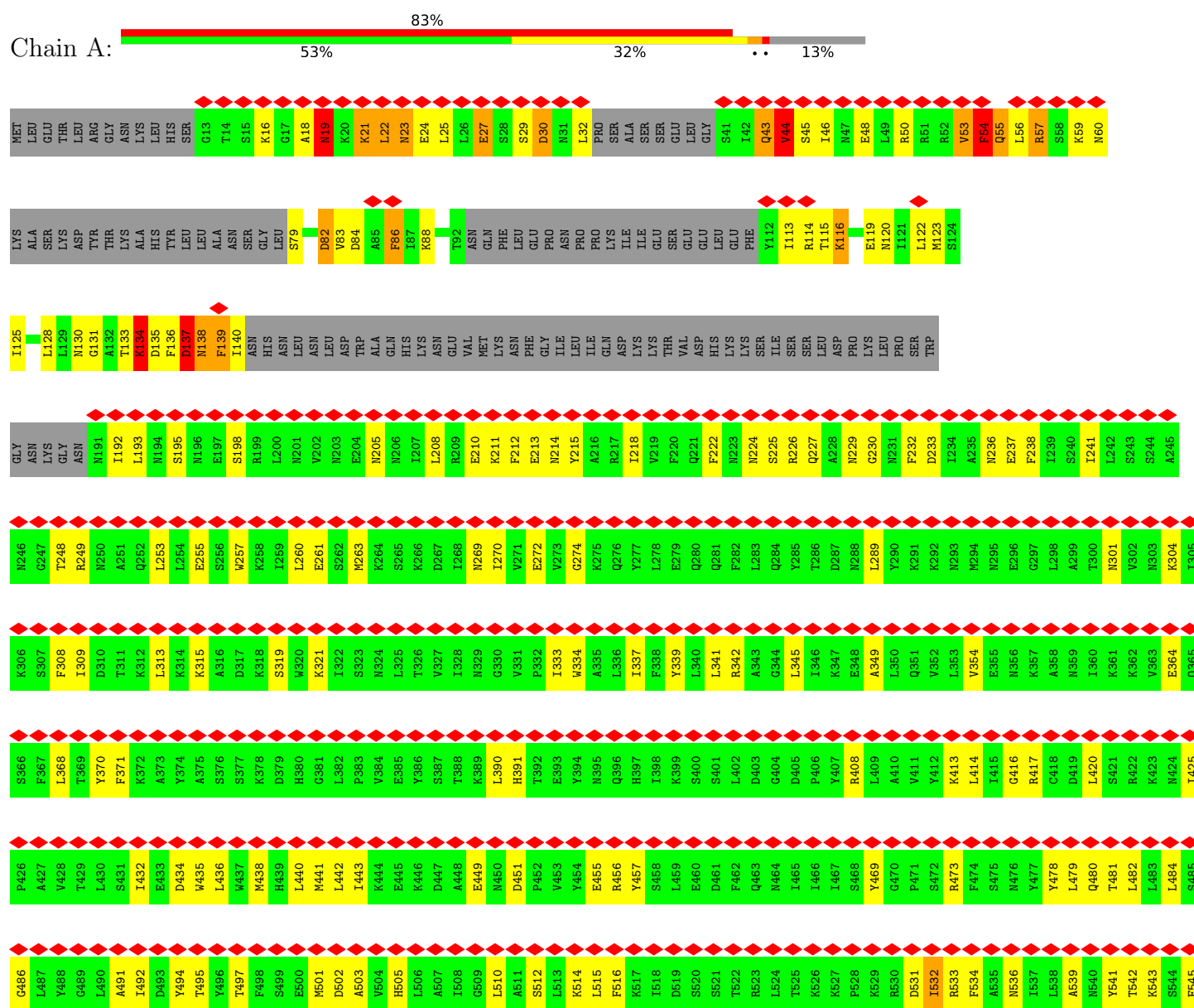
- Molecule 8 is a protein called Nucleoporin NSP1.

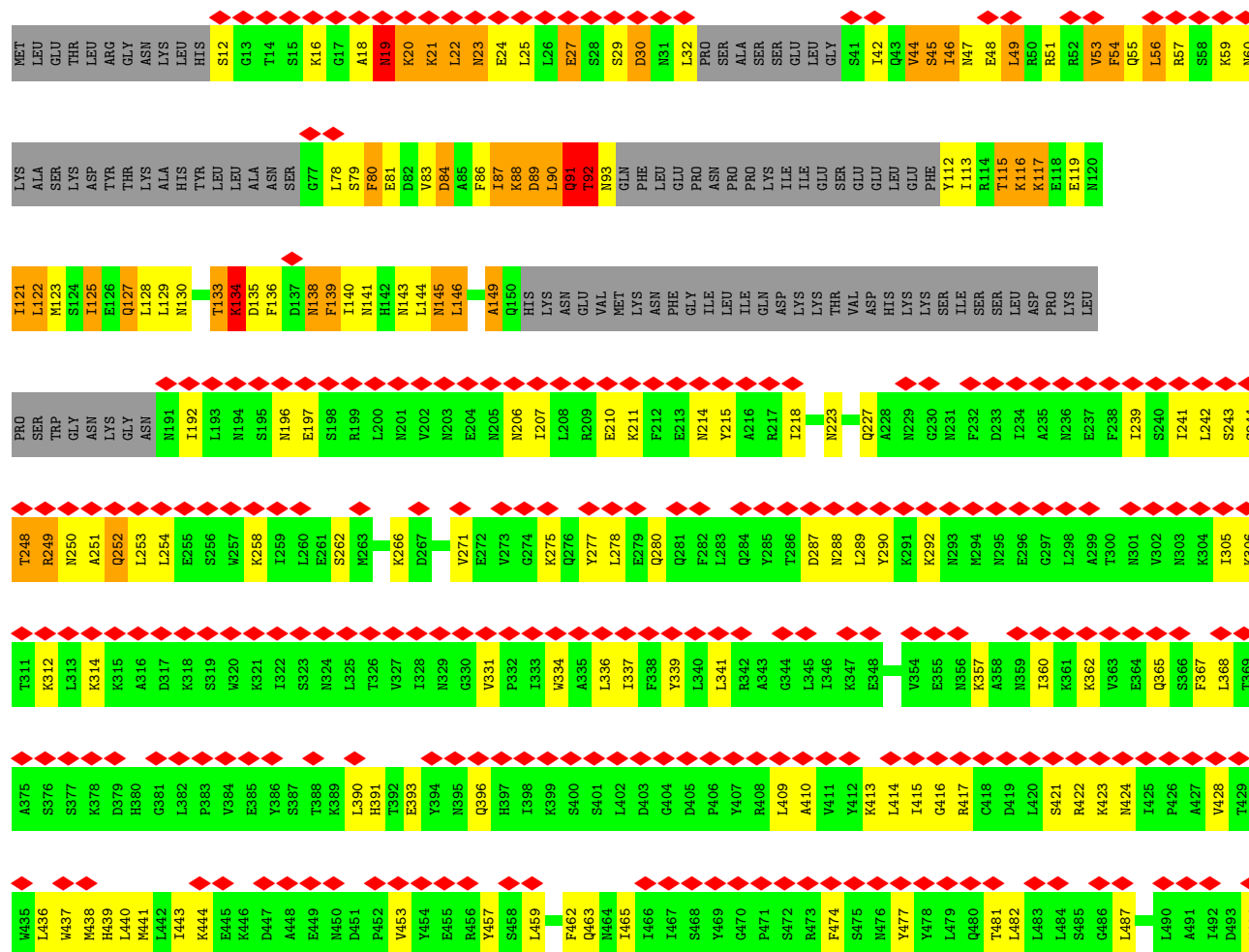
Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	187	Total	C	N	O	S	0	0
			1418	862	244	311	1		
8	L	187	Total	C	N	O	S	0	0
			1366	830	240	295	1		

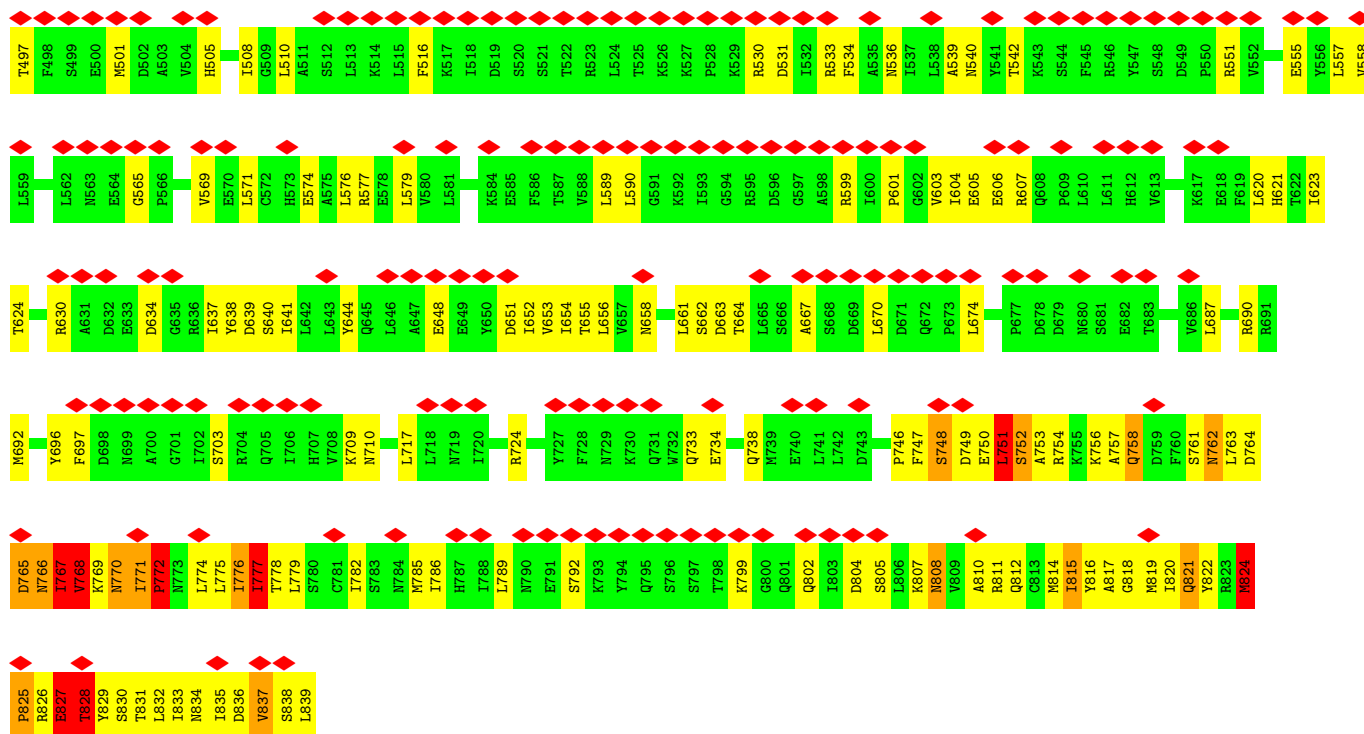
3 Residue-property plots

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.

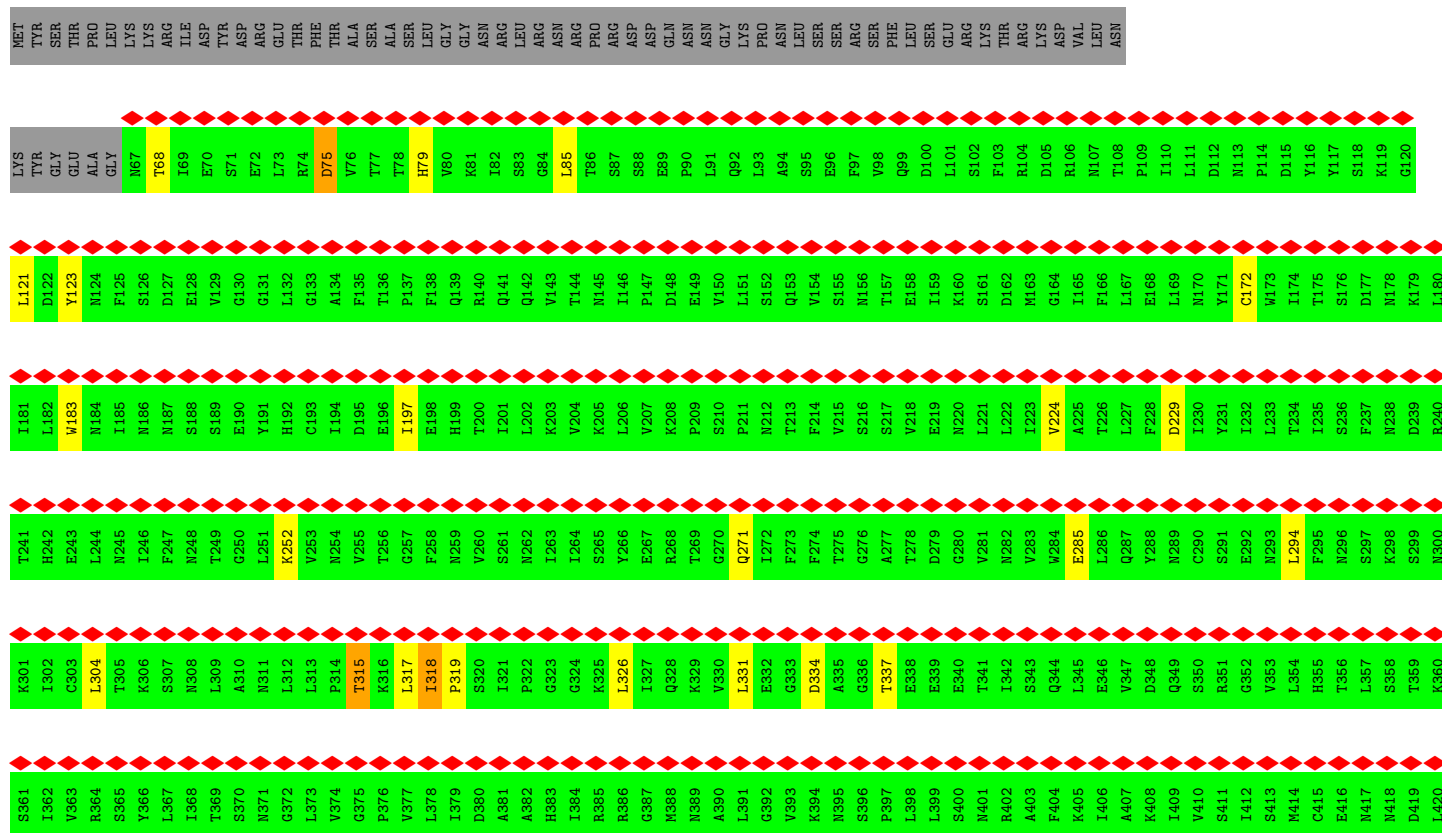
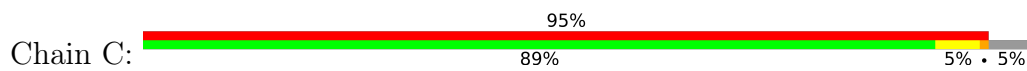
• Molecule 1: Nucleoporin NIC96





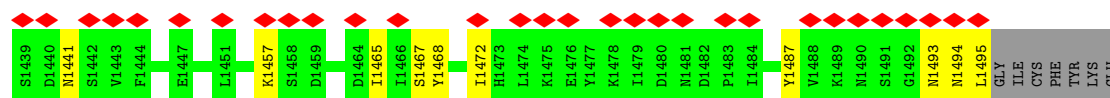


● Molecule 2: Nucleoporin NUP157

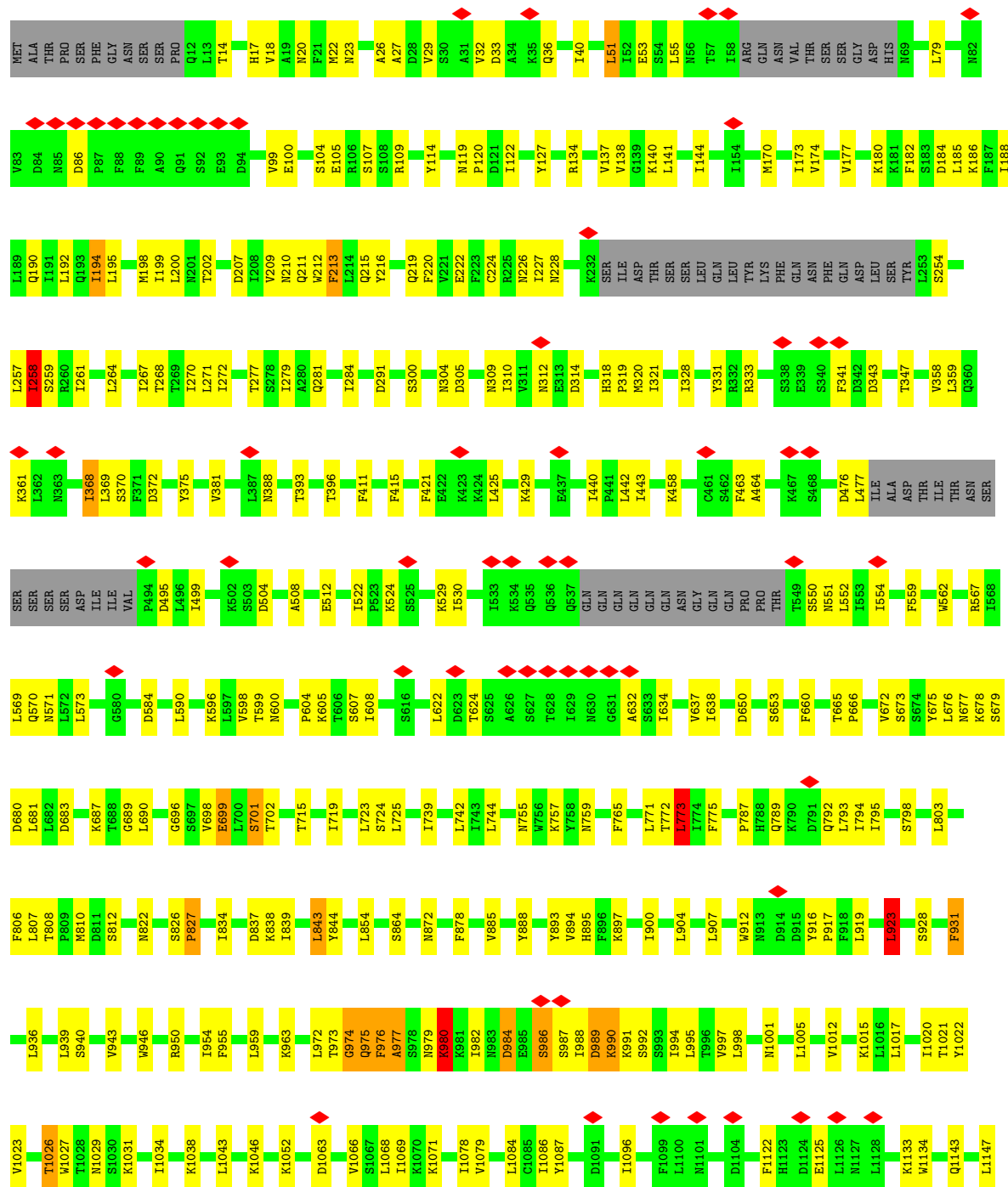


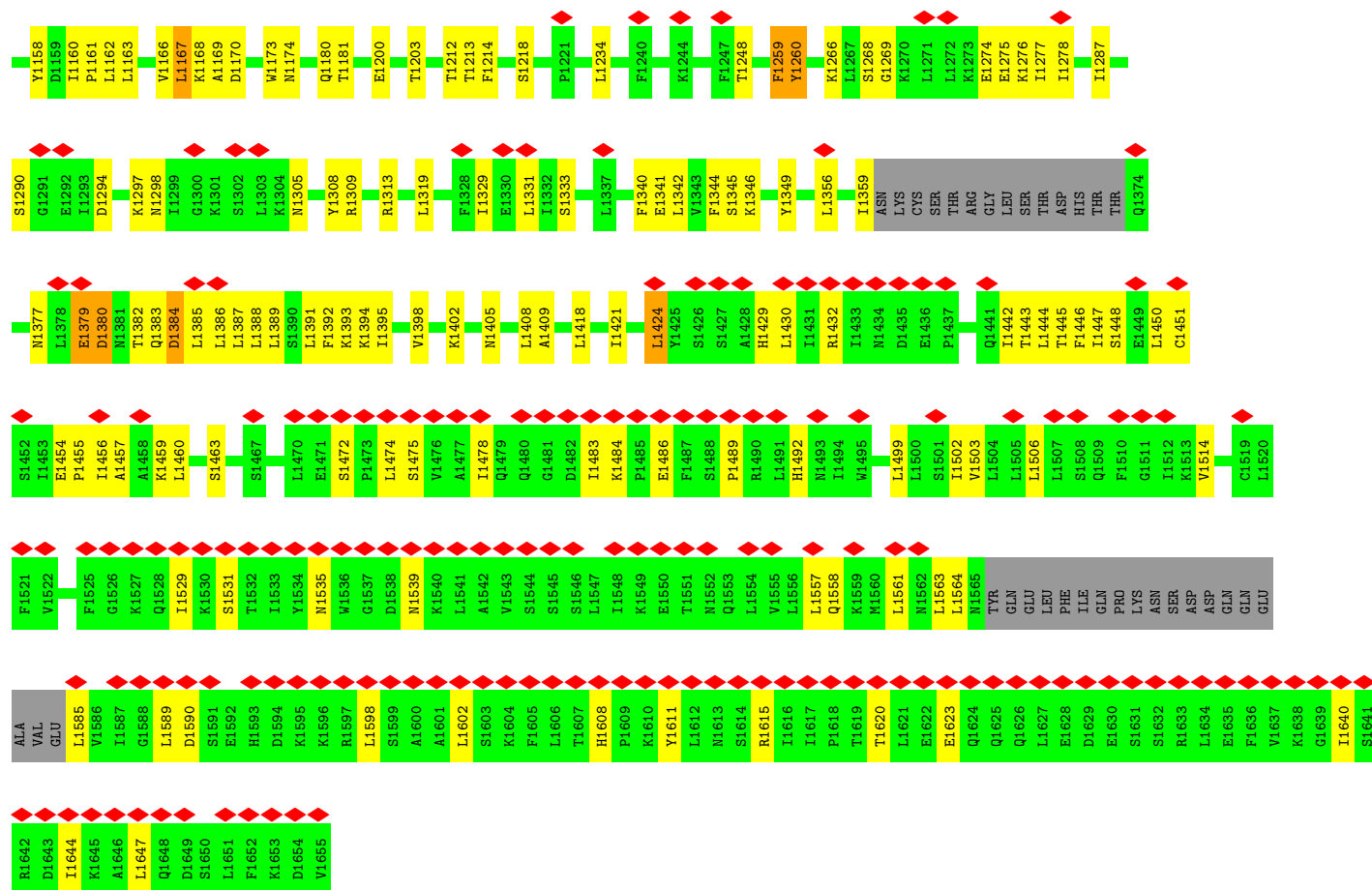
C1141	L1081	I1021	P961	I901	R841	G781	S721	A661	V601	S541	G481	F421
D1142	P1082	E1022	K962	L902	E842	S782	Q722	L662	A602	A542	P482	L422
S1143	Y1083	Q1023	T963	C903	Y843	J783	I723	A663	V603	P643	L483	A423
S1144	L1084	S1024	V964	Y904	F844	A784	W724	F664	L604	D544	S484	V424
T1145	K1085	P1025	G965	R905	F945	I785	E725	F665	T605	Y545	T485	I425
S1146	E1086	S1026	F966	A906	D846	T786	E726	S666	S606	G546	Q486	T426
F1147	R1087	S1027	L967	G907	L847	A787	R727	A667	N607	I547	K487	T427
L1148	A1088	A1028	L968	E908	K848	S788	W728	G668	A608	L548	A488	T428
Q1149	E1089	M1029	R969	H909	F949	D789	F729	I669	L609	K549	S489	G429
K1150	K1090	I1030	F970	L910	H850	A790	W730	P670	E610	N550	S490	V430
P1151	S1091	S1031	A971	E911	D851	E791	F731	G671	I611	Y551	T491	R431
A1152	L1092	D972	D972	A912	L852	S792	K732	V672	Y612	G552	Y492	L432
L1153	E1093	F1033	K973	A913	F953	I793	R733	G673	C613	K553	I493	Y433
V1154	I1094	S1034	I974	Q914	T854	A794	A734	E674	Y614	Y554	N494	F434
Q1155	D975	P1035	D975	K915	P855	M795	S735	I675	R615	V555	T495	K435
L1156	K976	A1036	K976	F916	N856	N796	K736	K676	T616	E556	T496	G436
S1157	G977	S1037	G977	E917	A857	A797	T737	P677	P617	N557	C497	S437
E1158	N978	S1038	N978	K918	K858	L798	E738	K678	D618	T558	A498	I438
M1159	Q979	L1039	Q979	I919	T859	I799	K739	S679	E619	A559	S499	S439
I1160	A980	K1040	Q981	D920	K860	L800	M740	S680	V620	L560	T500	R440
H1161	Y1101	K1041	Q981	S921	Q861	L801	D741	R681	F621	L561	I501	R441
E1162	L1102	R1042	E982	K922	L862	I802	A742	E682	E622	D562	I502	S442
L1163	F1103	V1043	Y983	I923	I863	N803	F743	S683	S623	T563	S503	I443
F1164	K1104	Y1044	S984	S924	K864	S804	G744	G684	L624	T564	P504	G444
L1165	E1105	S1045	S985	R925	E865	I805	I745	S685	I625	D565	G505	S445
E1166	N986	V1046	R986	N926	I866	K806	S746	V686	E626	E566	I506	L446
A1167	G987	I1047	G987	H927	L867	D807	I747	P687	N627	I567	Y507	K447
S1168	C988	M1048	C988	L928	T868	A808	T748	P688	P628	K568	F508	L448
L1169	N989	S1049	N989	D929	E869	L809	R749	I689	L629	E569	T509	D449
Q1170	E1110	S1050	V970	T930	V670	S810	P750	S690	P630	I570	C510	S450
D1171	A1111	M1051	V871	A931	V671	L811	Q751	Q891	F631	V571	V511	V451
L1172	D992	N1052	N872	I932	N872	I812	V752	N692	I632	P572	R512	K452
L1173	D1113	R1053	A873	D933	A873	N813	E753	L693	H633	L573	K513	F453
L1174	N1114	F1054	N874	L934	N874	V814	V754	F694	S634	T574	R514	P454
M1175	L1115	F1055	I875	Y835	I875	F815	V755	D895	Y635	R575	A515	P455
L1176	Y1116	H1056	A876	E936	A876	V816	L756	K696	G636	S576	N516	T456
F1177	A1117	Y1057	S977	R937	S977	E817	S757	S697	L637	F577	S517	S457
R1178	L1118	C1058	G978	C938	G978	D818	S758	G698	S638	N578	G518	I458
M1179	A1119	F1059	T879	A939	T879	I819	I759	E999	E639	Y579	E519	S459
E1180	S1120	Y1060	S880	E940	S880	D820	S760	C700	A640	T580	L520	S460
T1181	S1121	D1061	A881	N941	A881	A821	V761	D701	C641	S581	S521	S461
R1182	D1122	V1062	D882	I942	D882	F822	L762	G702	S642	T582	K522	L462
L1183	F1123	L1063	Y883	E943	Y883	K823	A763	I703	T643	P583	G523	E463
D1184	D1124	V1064	T884	L944	T884	S824	R764	W704	A644	Q584	I524	Q464
E1185	L1125	A1065	V885	C945	V885	L825	F765	L705	L645	G585	T525	N465
L1186	T1006	M1066	N886	E946	N886	L826	F766	S706	Y546	Y586	N526	K466
Y1187	L1007	K1067	V887	L947	V887	N827	N767	F707	L647	A587	K527	S467
R1188	I1008	R1068	L888	R948	L888	T828	I768	R708	A648	N588	A528	F468
K1189	F1009	Q1069	K889	R949	K889	L829	H769	F709	C649	V589	L529	I469
Q1190	E1010	S1070	E990	V950	E990	M830	R770	Y710	K650	F590	L530	I470
L1191	I1011	Y1071	R891	V951	R891	G831	F771	G711	F651	A591	E531	G471
T1192	V1012	L1072	F892	D952	F892	A832	S772	S712	N652	S592	N532	H472
L1193	C1133	L1073	G893	I953	G893	G833	F773	A713	K653	Q593	K533	H473
K1194	S1014	R1074	S894	N954	S894	G834	V774	L714	S654	Y594	E534	P474
L1195	V1015	L1075	F955	V955	F955	V835	S775	L715	E855	S595	E535	L475
M1196	D1016	D1076	C956	K956	C956	V836	F776	I716	H656	A596	H536	N476
K1197	D1017	S1077	H897	L957	H897	D837	T777	T717	I657	E597	K537	T477
R1198	N1018	Q1078	S898	N958	S898	S838	P778	R718	K658	E598	H478	H478
V1199	G1139	F1079	A899	Y959	A899	K639	P779	L719	S859	L599	Y539	D479
L1200	S1020	V1080	D900	Q960	D900	T840	K780	F720	S660	K600	V540	T480

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M1365	R1238	V1084	K1144	D1022	Y842	R782	V722	L662	A602	T642
L1366	G1241	A1085	S1145	S1023	L843	D783	S723	I663	G603	H543
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Q1379	V1246	E1090	L1150	L1028	L848	W789	L729	F669	P609	K548
D1380	S1247	N1091	K1151	M1029	L849	F790	S730	E670	P610	N550
S1381	P1248	D1092	Y1152	N1030	N850	N791	K731	L671	L611	S551
E1382	L1249	D1093	M1153	A1031	E851	T792	V732	N672	S612	S552
F1388	S1250	K1094	D1154	T1032	F852	F793	T733	Y673	G613	V553
E1389	Q1251	K1095	L1155	A1033	L854	T794	L734	G674	L614	T554
L1390	K1252	Q1096	L1156	L1034	T855	D795	S735	A675	F615	G555
F1391	Q1253	Y1097	F1157	L1035	T856	N796	T736	A676	N616	T556
I1392	R1254	Y1098	H1158	E1036	Y856	R797	T737	E677	A617	T557
I1393	I1255	D1099	Y1159	Q1037	G857	W798	A738	A678	T618	A558
I1394	V1256	K1100	H1160	I1038	D858	T799	T739	C679	T619	T559
C1395	R1261	R1101	M1161	V1039	S859	I860	N740	S680	K620	A560
F1397	Y1166	L1102	Y1162	D1040	I861	S861	L741	T681	P621	G561
F1398	T1281	L1103	L1163	D1041	I862	Q862	Q742	A682	Q622	S562
Y1399	D1282	Y1104	V1164	L1042	E863	F863	Q743	L683	G623	K563
R1284	I1283	D1106	M1169	S1043	S864	I864	S744	F684	F624	T564
I1285	R1170	L1107	R1170	I1044	A865	S865	I745	A685	A625	V665
D1286	E1171	F1108	E1171	E1045	P866	S866	T746	T686	N626	K566
S1287	E1172	F1109	E1172	K1046	Y867	S867	G747	C687	E627	Q567
K1290	K1173	D1110	L1047	L1047	V868	D868	F748	K688	F628	Q568
E1405	L1174	L1112	K1048	K1048	L869	P869	S749	S689	A629	P569
H1406	D1175	L1113	E1049	A1050	A870	I810	K750	N690	T630	V570
I1407	I1177	K1114	V1051	V1051	N871	T811	P751	K691	Q631	T571
V1408	E1178	V1115	S1052	S1052	N872	S812	S752	S692	Y632	L572
S1409	T1179	D1116	M1053	M1053	S873	S813	P753	E693	T633	Q573
G1410	F1180	E1117	L1054	L1054	N874	I814	A754	K694	S634	H574
S1411	F1181	L1118	L1055	L1055	G875	N815	N755	L695	E635	K575
I1412	I1182	A1119	S1056	S1056	R876	N816	K756	R696	T636	L576
V1413	L1183	K1121	V1057	V1057	V877	L817	E757	S697	L637	F577
T1418	I1199	K1122	M1058	M1058	I878	K818	D758	N698	K638	V578
A1419	L1200	Q1123	Y1059	Y1059	D879	S819	F759	A699	V639	S579
L1420	Q1345	S1124	Y1060	Y1060	K880	D820	D760	L700	A640	V580
V1421	S1346	S1125	P1061	P1061	T881	E821	L761	T701	P641	P581
S1422	Y1203	K1126	K1062	K1062	E882	I822	D762	F702	L642	D582
F1423	Y1204	T1127	S1063	S1063	E883	S823	D763	L703	T643	Y583
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K1430	S1207	Q1130	A1066	A1066	N886	G826	L766	G706	S646	L586
E1432	K1208	I1131	I1007	I1007	K887	N827	S767	I707	I647	K587
L1433	K1209	I1132	E1008	E1008	A888	I828	P768	P708	E648	T588
I1434	F1210	I1133	H1009	H1009	E889	I829	R769	G709	I649	H589
E1435	F1211	S1134	K1010	K1010	S890	S830	F770	V710	Y650	G590
T1436	E1212	N1135	R1011	R1011	I891	K831	Y771	V711	K651	K591
S1437	S1213	D1136	R1012	R1012	A892	V832	G772	D712	Y652	Y592
D1438	A1214	D1137	A1013	A1013	T893	S833	I773	I713	R653	V593
	E1215	E1138	K1014	K1014	N894	I834	A774	K714	T654	E594
	Y1218	Y1139	E1015	E1015	A895	S835	L775	P715	P655	N595
	I1227	K1140	I1016	I1016	N896	K836	L776	V716	D656	A596
		L1141	L1017	L1017	I897	D837	I777	T717	E657	T597
		R1142	A1080	A1080	K958	C838	T778	N718	I658	F598
			C1081	C1081	N899	I839	R779	R719	F659	L599
			Q1082	Q1082	V900	E840	L780	Y720	E660	E600

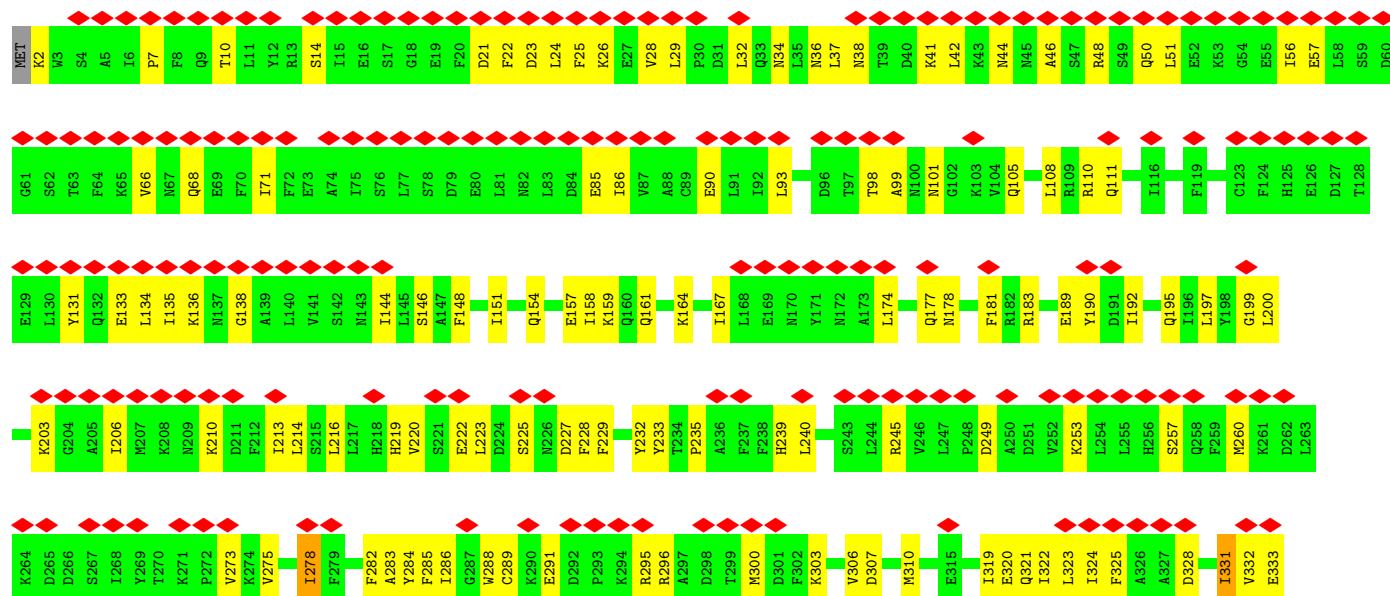


• Molecule 4: Nucleoporin NUP188

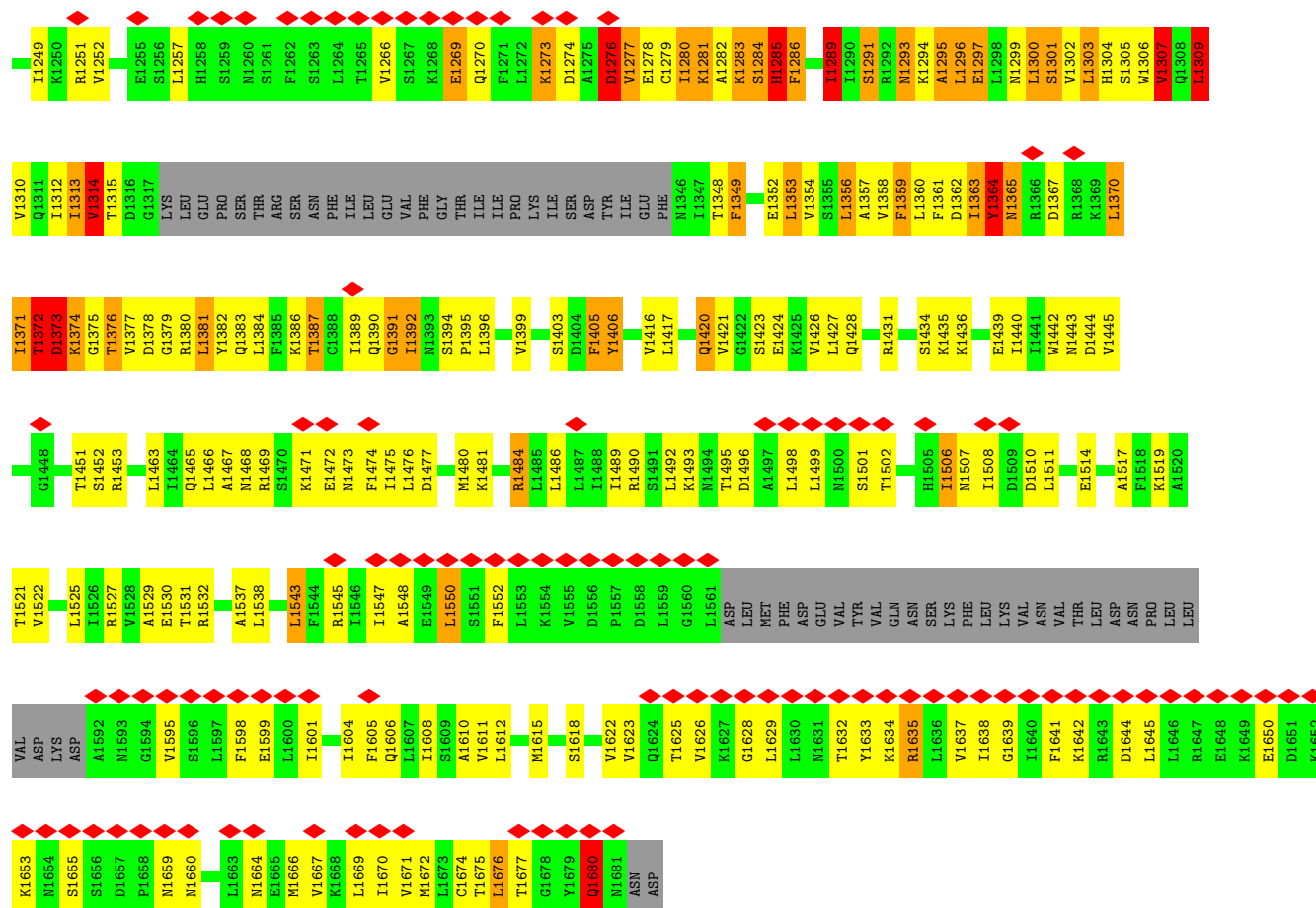




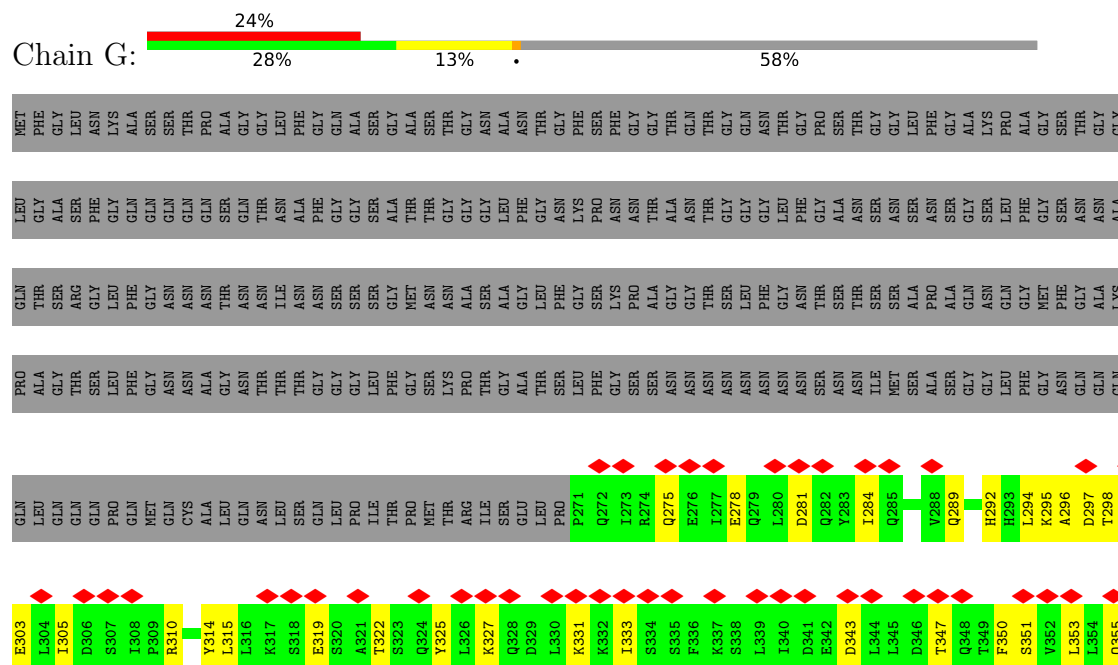
• Molecule 5: Nucleoporin NUP192

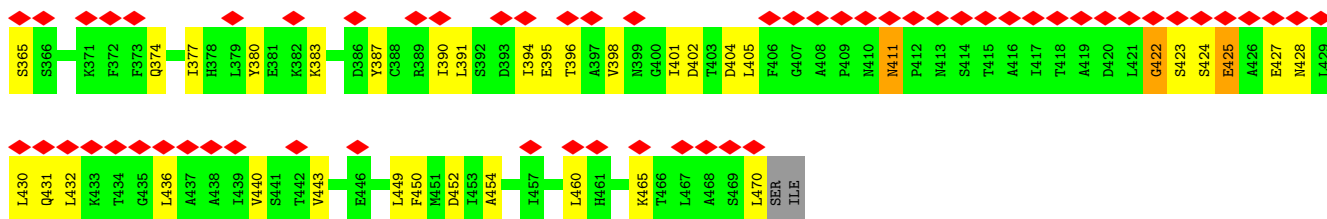




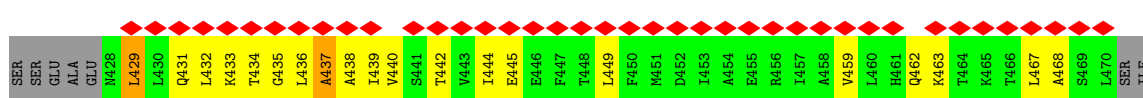
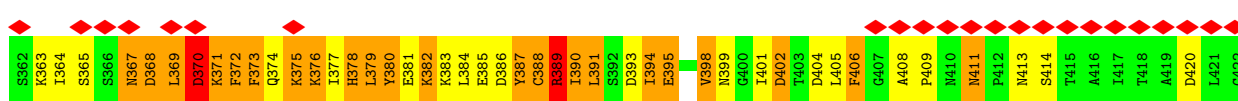
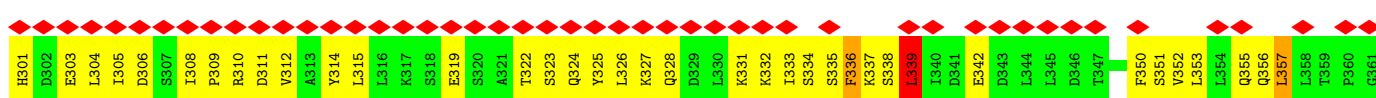
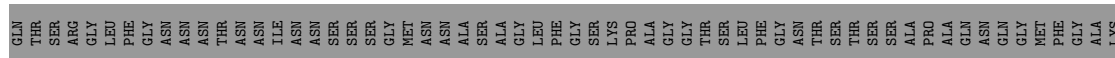
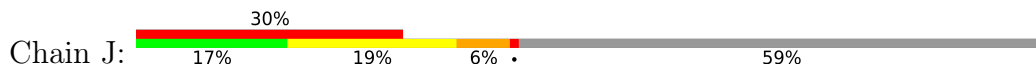


• Molecule 6: Nucleoporin NUP49/NSP49



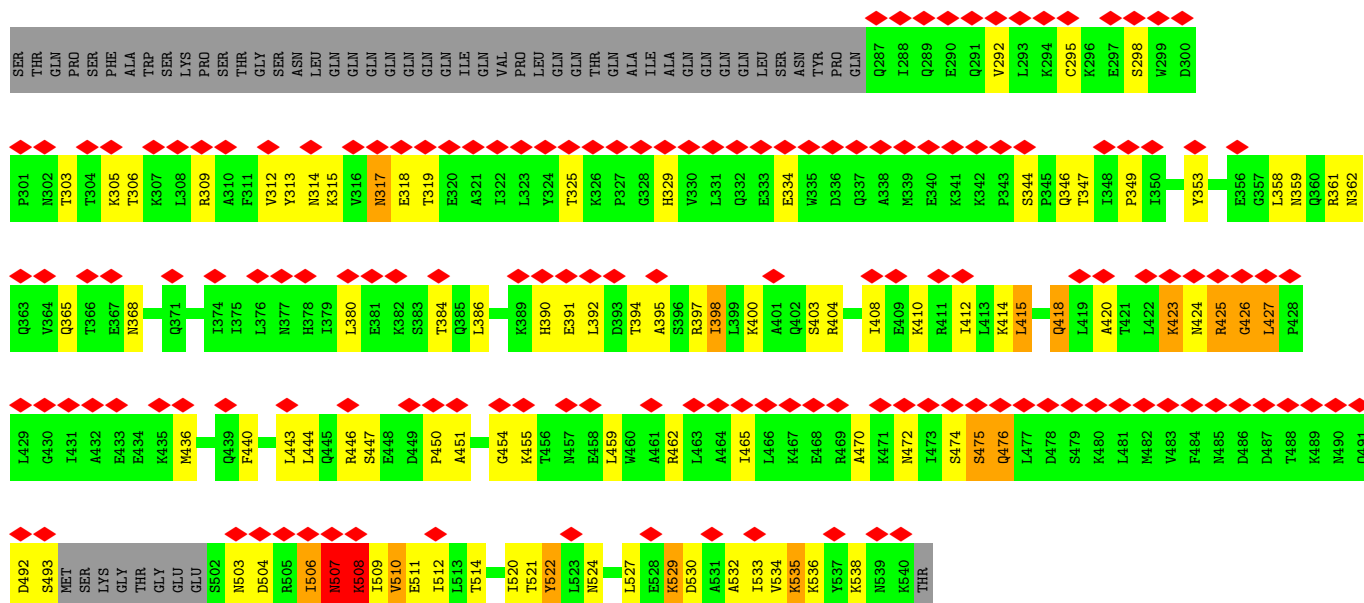


• Molecule 6: Nucleoporin NUP49/NSP49

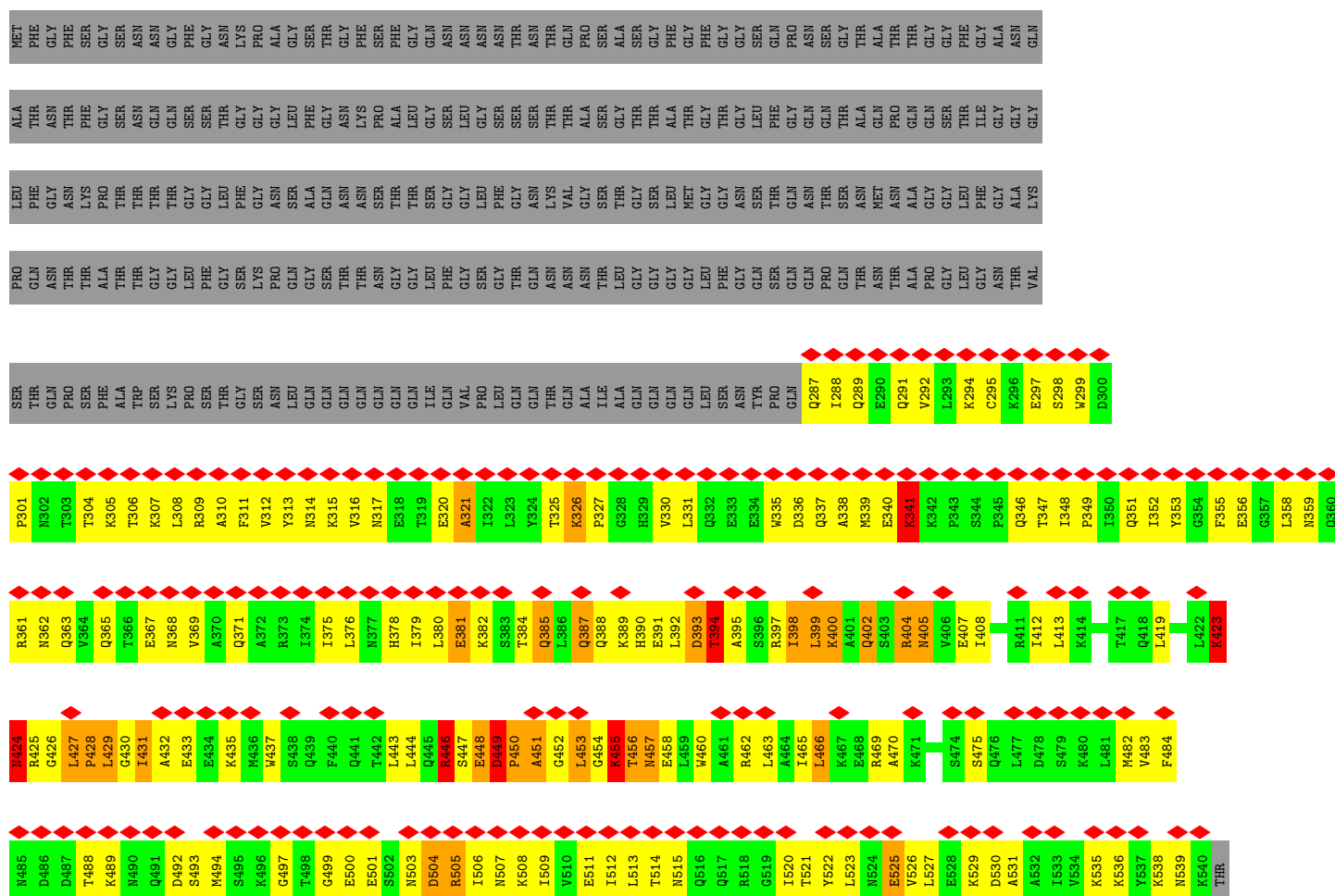
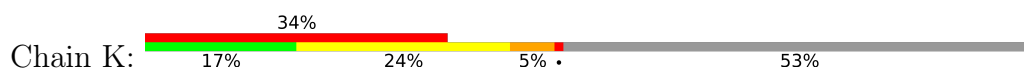


• Molecule 7: Nucleoporin NUP57

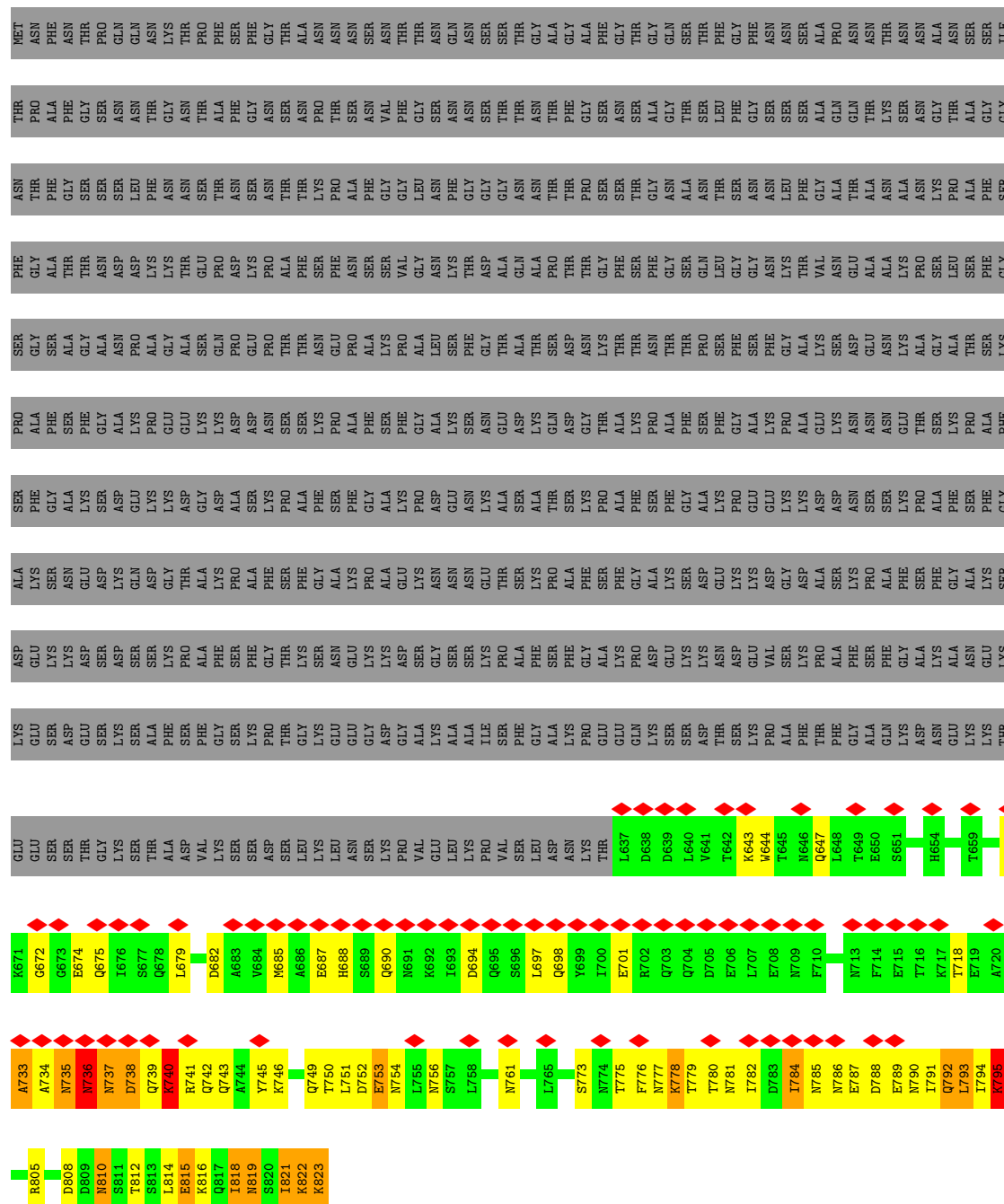




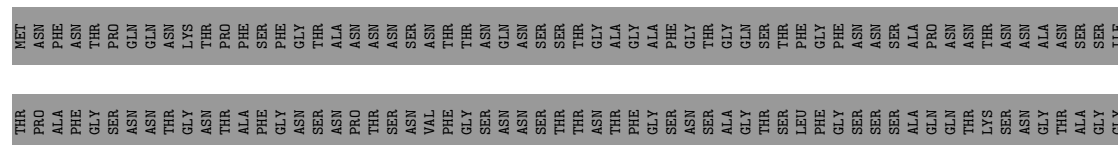
• Molecule 7: Nucleoporin NUP57



● Molecule 8: Nucleoporin NSP1



● Molecule 8: Nucleoporin NSP1



E789	L721	K661	GLU	LYS	ASP	ALA	SER	GLY	THR	PRO	SER	PHE	ASN
N790	L722	I662	GLU	SER	GLU	LYS	LYS	LYS	THR	ALA	GLY	GLY	THR
I791	S723	M663	SER	ASP	SER	ASN	ALA	GLY	THR	PHE	ALA	THR	SER
Q792	D724	M664	THR	THR	ASP	GLU	LYS	LYS	GLY	PHE	ALA	ASN	SER
L793	V725	M665	GLY	LYS	SER	SER	ASP	LYS	ASP	GLY	ALA	ASN	SER
I794	V726	D666	LYS	LYS	ASP	SER	GLN	GLU	GLY	ASN	PRO	ASP	SER
K795	S727	Q667	SER	ALA	SER	ALA	ASP	LYS	LYS	PRO	ALA	LEU	PHE
L796	T728	V668	THR	PHE	ALA	THR	GLY	GLY	GLY	GLY	ALA	THR	ASN
M798	S729	L669	VAL	PHE	ALA	ALA	THR	THR	ASP	GLY	LYS	GLU	SER
S799	V730	V670	LYS	GLY	PHE	LYS	LYS	LYS	ASP	LYS	LYS	GLN	THR
H800	G731	K671	SER	SER	SER	PRO	LYS	LYS	ASP	ALA	ASP	PRO	ASN
F801	A732	G672	ASP	LYS	THR	THR	GLY	THR	LYS	ASN	PRO	ALA	THR
D802	A733	G673	SER	GLY	LYS	GLY	LYS	LYS	PHE	ALA	SER	PHE	LYS
A803	N734	E674	LEU	LYS	SER	LYS	LYS	LYS	GLY	PHE	ALA	ASN	THR
R805	N735	Q675	LYS	LYS	ASN	GLU	GLY	GLY	ALA	SER	PRO	PHE	LYS
S806	N736	I676	ASN	GLY	GLY	GLY	GLY	LYS	PRO	PHE	ALA	ASN	PHE
L807	N737	S677	SER	GLY	ASP	LYS	LYS	LYS	ALA	SER	LYS	GLY	GLY
D808	D738	Q678	PRO	GLY	ASP	GLY	GLY	GLY	PHE	PHE	VAL	VAL	LEU
D809		L679	VAL	ALA	SER	LYS	LYS	LYS	LYS	ALA	GLY	GLY	LEU
T812	R741	Y680	GLU	LYS	GLY	ASN	ASN	ASN	ASP	ALA	LEU	ASN	ASN
K816	A744	S681	LEU	ALA	GLY	ALA	ALA	LYS	SER	LYS	LEU	PHE	PHE
Q817		D682	LYS	ALA	SER	ASN	ASN	LYS	PHE	GLY	THR	GLY	GLY
I818	T747	A683	PRO	ILE	LYS	ILE	GLY	GLY	ASN	ASN	GLY	GLY	GLY
N819	A748	V684	VAL	SER	PHE	SER	PHE	THR	ALA	GLY	THR	ALA	ASN
S820	Q749	M685	LEU	SER	ALA	PRO	ALA	GLY	SER	ASP	ALA	GLN	GLN
I821	T750	A686	ASP	GLY	PHE	GLY	PHE	LYS	THR	LYS	THR	ALA	ASN
K822	L751	E687	ASN	LYS	PHE	ALA	ALA	LYS	THR	GLY	PRO	PRO	THR
R823	D752	H688	LYS	GLY	GLY	GLY	GLY	LYS	THR	THR	LYS	THR	THR
	L755	S689	THR	GLU	LYS	ALA	LYS	LYS	ALA	ALA	ALA	PHE	GLY
	N756	Q690		GLN	PRO	GLY	GLY	GLY	PHE	LYS	THR	THR	THR
	S759	M691	D638	LYS	ASP	GLY	GLY	LYS	SER	PRO	ASN	PHE	GLY
		K692	D639	SER	GLU	SER	ALA	LYS	PHE	ALA	ASN	PHE	ASN
	L762	I693	L640	SER	LYS	LYS	SER	LYS	GLY	PHE	THR	GLY	ASN
		D694	V641	THR	ASN	LYS	ASP	GLY	ALA	SER	PRO	GLN	ASN
L765	L766	Q695		LYS	ASP	LYS	GLY	LYS	PHE	GLY	LYS	LEU	THR
V767	V768	S696	K643	SER	GLY	GLY	LYS	LYS	GLY	PHE	ALA	ASN	ASN
E768	I769	L697	V644	PRO	VAL	VAL	ASP	ASP	GLY	LYS	ALA	ASN	ASN
I769		Q698	T645	ALA	SER	ALA	LYS	LYS	GLY	PRO	GLY	VAL	GLY
		Y699	M646	THR	THR	THR	PRO	PRO	ALA	ASP	LYS	VAL	ALA
	V772	I700	Q647	PHE	ALA	PHE	ALA	ALA	SER	LYS	ASN	ASN	THR
S773	S773	E701	GLY	GLY	PHE	GLY	LYS	LYS	ASN	ASN	ASP	GLY	THR
N774	T774	R702	L648	ALA	SER	ALA	PRO	PRO	SER	ASN	GLY	ALA	ASN
T775		Q703	GLN	GLN	PHE	GLN	PHE	GLY	SER	ASN	GLY	ALA	ASN
F776	F776	Q704	E650	LYS	GLY	LYS	GLY	LYS	PRO	LYS	ALA	LYS	ASN
N777	N777	D705	S651	ASP	ALA	ASP	ALA	ALA	THR	THR	GLY	PRO	ASN
K778	K778	E706	A652	ASN	GLU	GLU	ALA	ALA	PHE	LYS	GLY	LEU	PRO
T779	T779	L707	M653	GLY	LYS	LYS	LYS	LYS	ALA	SER	PRO	SER	ALA
T780	T780	E708	H654	LYS	THR	LYS	LYS	LYS	ALA	PHE	ALA	PHE	PHE
N781		N709	F655	LYS	THR	LYS	LYS	LYS	ALA	GLY	GLY	GLY	GLY
I782	I782	F710	E656	LYS	THR	LYS	LYS	LYS	ALA	GLY	GLY	GLY	GLY
D783	D783	L711	Q657	ASP	ALA	ASP	ALA	ALA	THR	THR	ALA	GLY	GLY
I784	I784	D712	Y658	ASN	LYS	GLU	PHE	PHE	LYS	LYS	GLY	LEU	PRO
N785	N785	N713	T659	GLU	ALA	ALA	ALA	ALA	PHE	LYS	PRO	LEU	PRO
N786	N786	F714	T659	ASN	ALA	ASN	ALA	ALA	SER	LYS	PRO	SER	ALA
E787	E787	E715	K660	LYS	GLU	LYS	LYS	LYS	PHE	ALA	ALA	PHE	PHE
D788	D788	A720		THR	LYS	LYS	THR	THR	GLY	PHE	PHE	GLY	SER

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1266268	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	2.677	Depositor
Minimum map value	-1.782	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.043	Depositor
Recommended contour level	0.24	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

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	A	0.44	1/5813 (0.0%)	0.79	23/7867 (0.3%)
1	Z	0.57	0/5862	1.08	25/7942 (0.3%)
2	C	0.74	0/10658	1.19	11/14443 (0.1%)
3	D	0.48	0/11192	0.83	9/15173 (0.1%)
4	E	0.43	1/12583 (0.0%)	0.79	19/17054 (0.1%)
5	F	0.77	18/12435 (0.1%)	1.57	241/16887 (1.4%)
6	G	0.38	0/1553	0.83	6/2104 (0.3%)
6	J	0.68	0/1509	1.42	29/2042 (1.4%)
7	H	0.95	5/1832 (0.3%)	1.35	27/2482 (1.1%)
7	K	0.79	2/1829 (0.1%)	1.52	33/2485 (1.3%)
8	I	0.83	7/1431 (0.5%)	1.36	24/1940 (1.2%)
8	L	0.48	0/1378	1.02	5/1873 (0.3%)
All	All	0.62	34/68075 (0.0%)	1.13	452/92292 (0.5%)

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	Z	0	1
5	F	0	3
6	G	0	1
7	H	0	1
7	K	0	2
All	All	0	8

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	H	427	LEU	C-N	23.13	1.53	1.33
5	F	1235	ASN	C-N	14.77	1.53	1.33
7	K	326	LYS	C-N	13.71	1.50	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	H	425	ARG	C-N	10.73	1.49	1.33
5	F	1312	ILE	C-O	-9.57	1.14	1.24

The worst 5 of 452 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	1090	PRO	CA-N-CD	-38.16	58.58	112.00
5	F	356	ILE	CA-C-N	19.99	144.83	119.84
5	F	356	ILE	C-N-CA	19.99	144.83	119.84
7	K	326	LYS	CA-C-N	17.29	136.80	120.21
7	K	326	LYS	C-N-CA	17.29	136.80	120.21

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	F	1188	THR	Mainchain
5	F	360	LEU	Mainchain
5	F	813	GLU	Mainchain
6	G	422	GLY	Mainchain
7	H	509	ILE	Mainchain

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	A	5723	0	5587	299	0
1	Z	5776	0	5607	427	0
2	C	10452	0	10392	49	0
3	D	10976	0	10827	413	0
4	E	12362	0	12566	355	0
5	F	12232	0	11559	848	0
6	G	1533	0	1515	120	0
6	J	1492	0	1465	280	0
7	H	1811	0	1697	148	0
7	K	1808	0	1614	313	0
8	I	1418	0	1293	171	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	L	1366	0	1211	166	0
All	All	66949	0	65333	3074	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 23.

The worst 5 of 3074 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:Z:810:ALA:CB	1:Z:836:ASP:HA	1.26	1.59
3:D:955:PRO:CB	3:D:994:SER:CB	1.78	1.59
7:H:522:TYR:CB	1:Z:54:PHE:CB	1.82	1.56
5:F:841:PHE:CD2	5:F:918:PHE:HE1	1.21	1.55
5:F:1357:ALA:HB2	5:F:1381:LEU:CB	1.19	1.53

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%)	700 (97%)	20 (3%)	2 (0%)	36	65
1	Z	736/839 (88%)	675 (92%)	39 (5%)	22 (3%)	3	26
2	C	1323/1391 (95%)	1269 (96%)	41 (3%)	13 (1%)	12	43
3	D	1396/1502 (93%)	1275 (91%)	113 (8%)	8 (1%)	21	52
4	E	1538/1655 (93%)	1376 (90%)	149 (10%)	13 (1%)	16	47
5	F	1616/1683 (96%)	1203 (74%)	317 (20%)	96 (6%)	1	15
6	G	198/472 (42%)	188 (95%)	9 (4%)	1 (0%)	24	56
6	J	191/472 (40%)	175 (92%)	13 (7%)	3 (2%)	7	35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	H	242/541 (45%)	202 (84%)	36 (15%)	4 (2%)	7	34
7	K	252/541 (47%)	209 (83%)	32 (13%)	11 (4%)	2	19
8	I	185/823 (22%)	158 (85%)	16 (9%)	11 (6%)	1	15
8	L	185/823 (22%)	164 (89%)	15 (8%)	6 (3%)	3	25
All	All	8584/11581 (74%)	7594 (88%)	800 (9%)	190 (2%)	7	30

5 of 190 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 ⓘ

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	609/762 (80%)	586 (96%)	23 (4%)	29	53
1	Z	611/762 (80%)	559 (92%)	52 (8%)	10	34
2	C	1177/1250 (94%)	1149 (98%)	28 (2%)	43	62
3	D	1215/1353 (90%)	1201 (99%)	14 (1%)	63	72
4	E	1421/1557 (91%)	1389 (98%)	32 (2%)	44	62
5	F	1260/1538 (82%)	1166 (92%)	94 (8%)	12	39
6	G	167/377 (44%)	162 (97%)	5 (3%)	36	57
6	J	162/377 (43%)	146 (90%)	16 (10%)	7	30
7	H	171/439 (39%)	163 (95%)	8 (5%)	23	48
7	K	153/439 (35%)	130 (85%)	23 (15%)	3	16
8	I	152/674 (23%)	136 (90%)	16 (10%)	6	28
8	L	138/674 (20%)	136 (99%)	2 (1%)	59	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	7236/10202 (71%)	6923 (96%)	313 (4%)	27	50

5 of 313 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	J	398	VAL
1	Z	125	ILE
7	K	384	THR
8	L	703	GLN
1	Z	766	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 159 such sidechains are listed below:

Mol	Chain	Res	Type
7	K	329	HIS
1	Z	214	ASN
7	K	365	GLN
8	L	704	GLN
1	Z	464	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

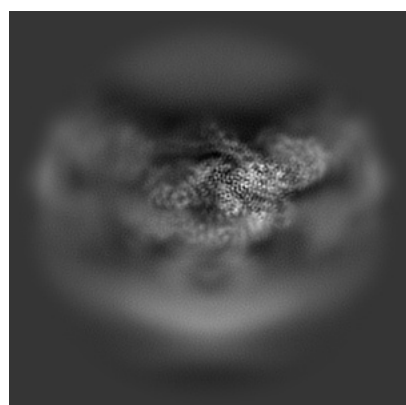
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32653. These allow visual inspection of the internal detail of the map and identification of artifacts.

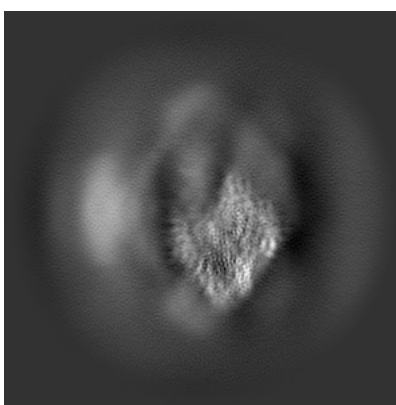
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

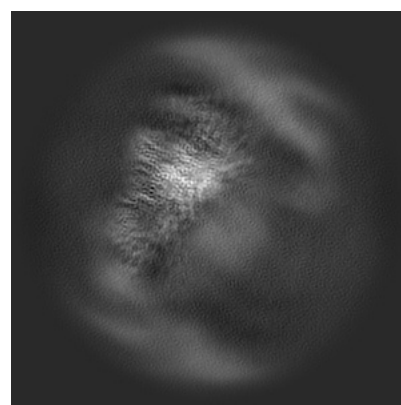
6.1.1 Primary map



X



Y

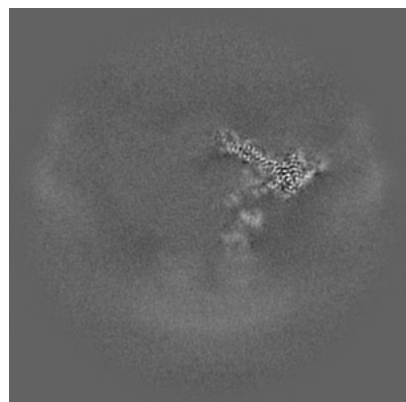


Z

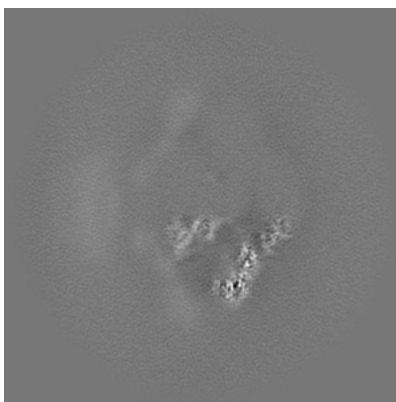
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

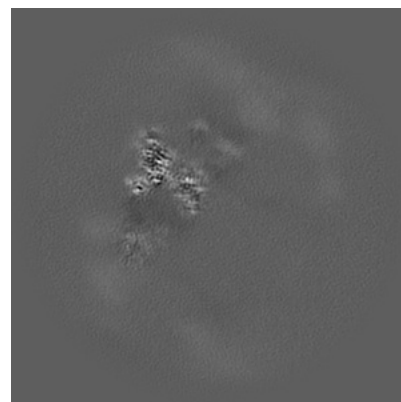
6.2.1 Primary map



X Index: 175



Y Index: 175

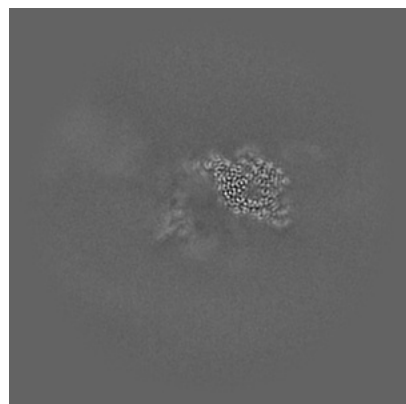


Z Index: 175

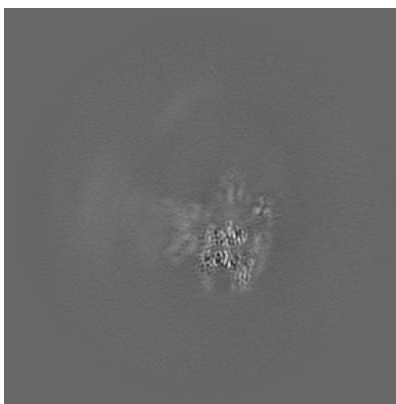
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

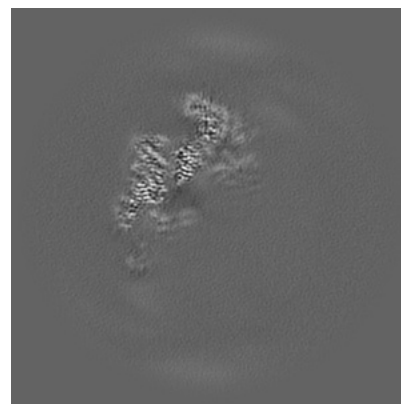
6.3.1 Primary map



X Index: 124



Y Index: 203

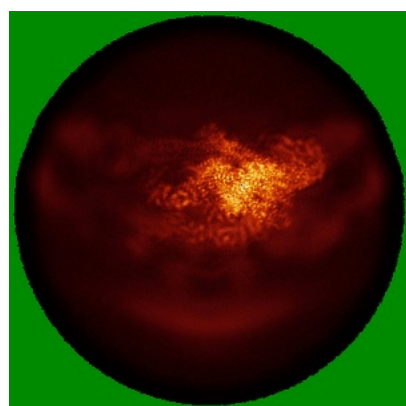


Z Index: 204

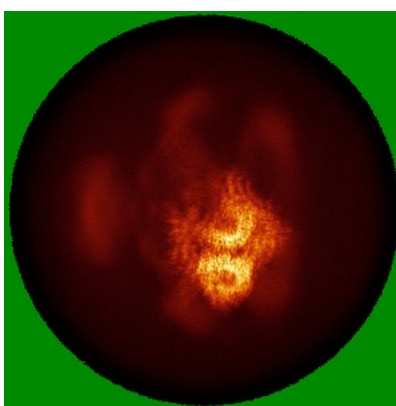
The images above show the largest variance slices of the map in three orthogonal directions.

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

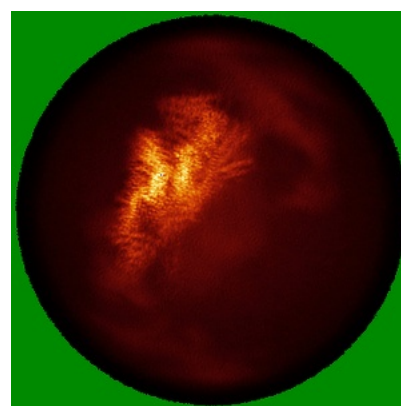
6.4.1 Primary map



X



Y

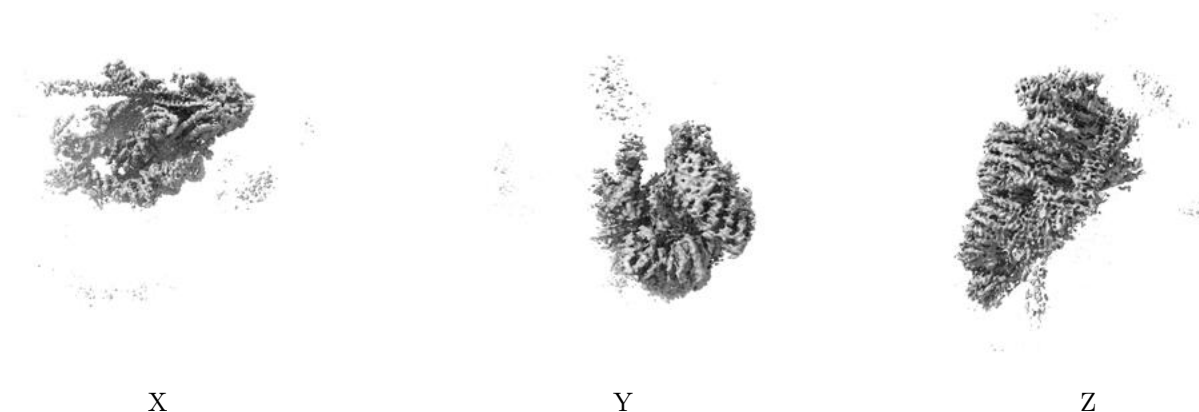


Z

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

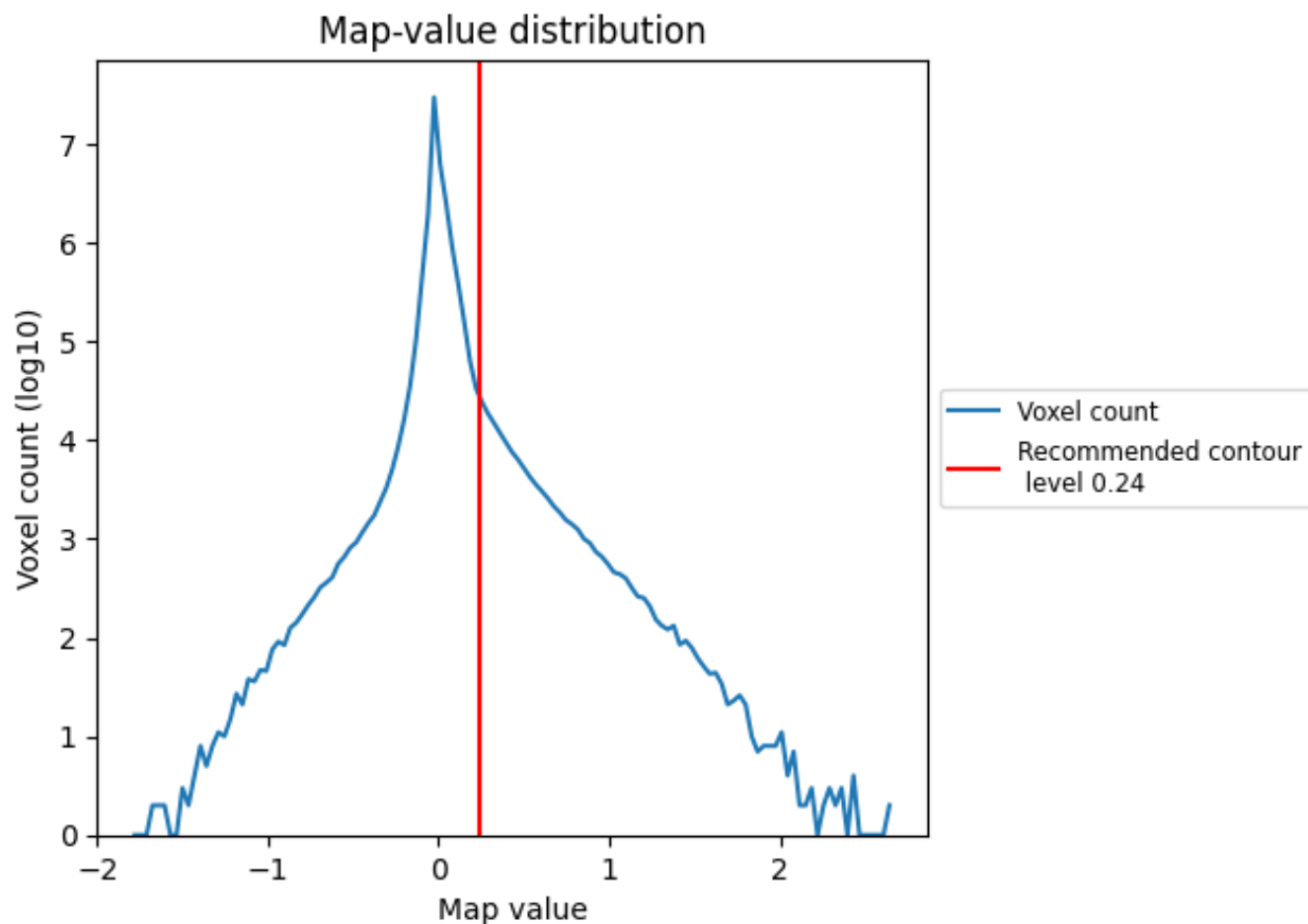
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

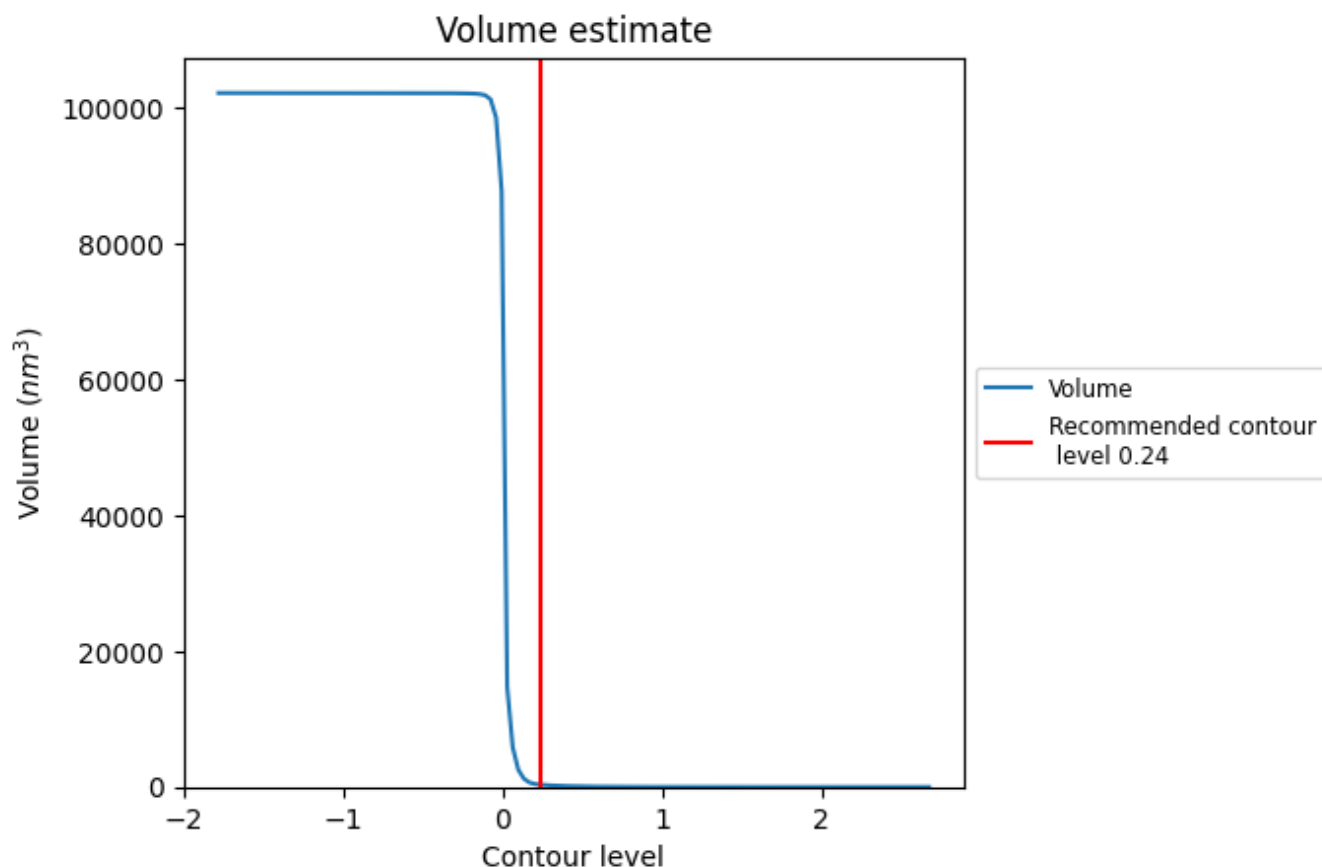
This section contains the results of statistical analysis of the map.

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.

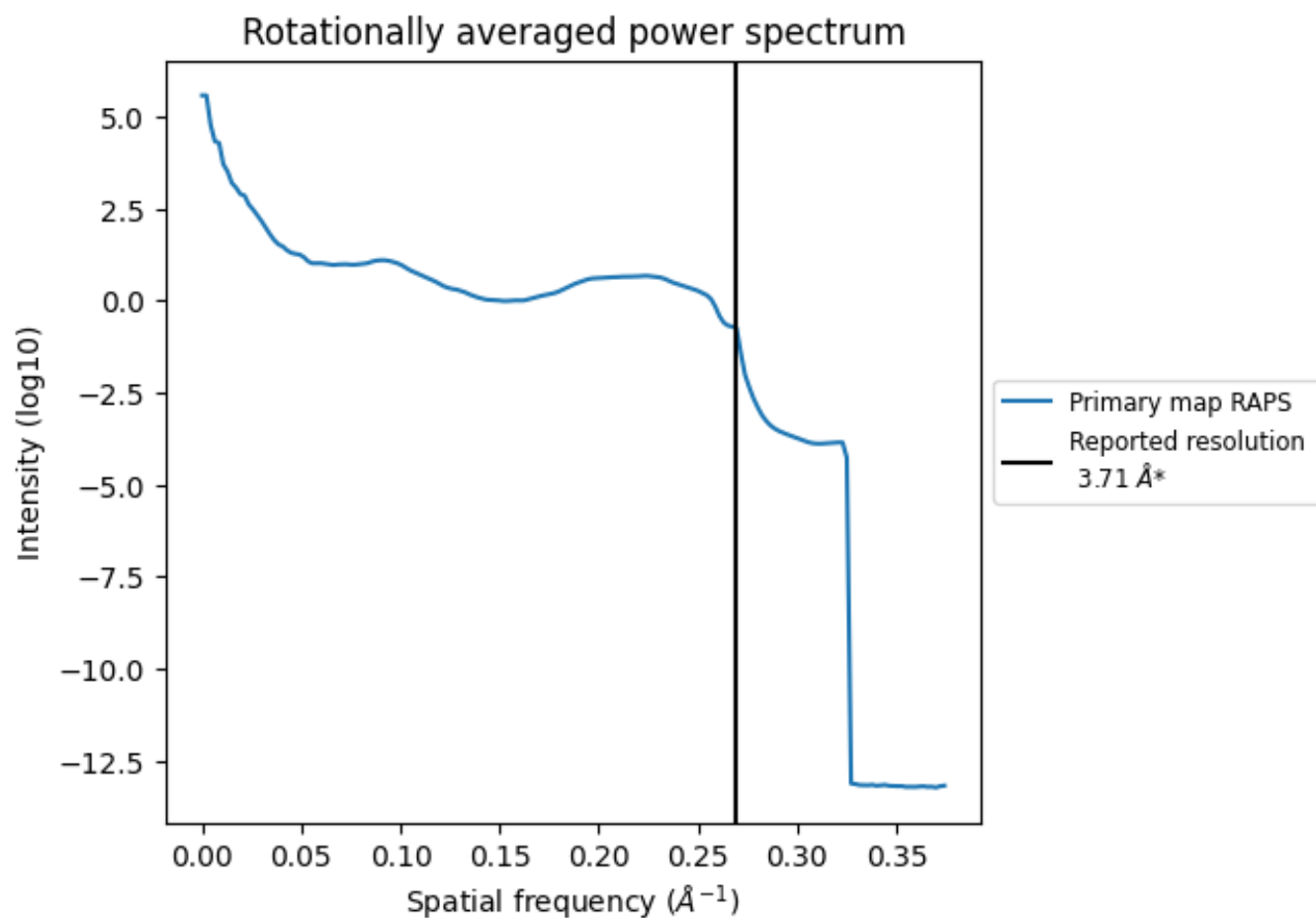
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 332 nm³; this corresponds to an approximate mass of 300 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 0.270 Å⁻¹

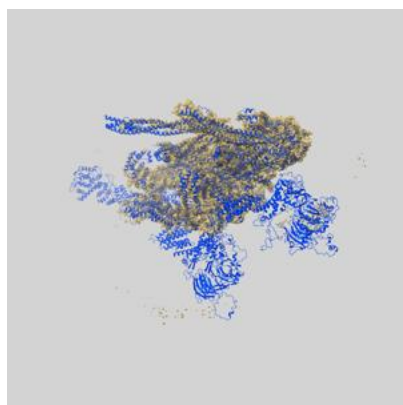
8 Fourier-Shell correlation

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

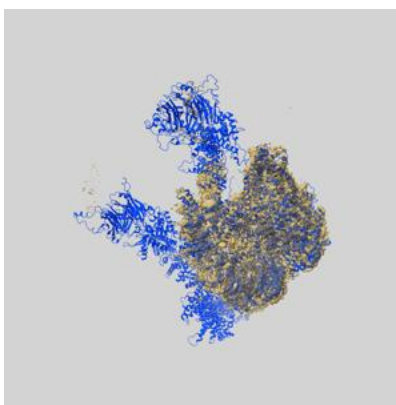
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32653 and PDB model 7WOO. Per-residue inclusion information can be found in section 3 on page 6.

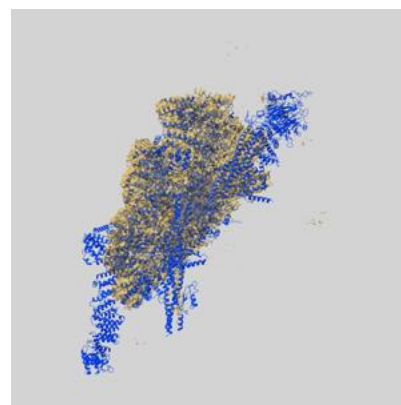
9.1 Map-model overlay [i](#)



X



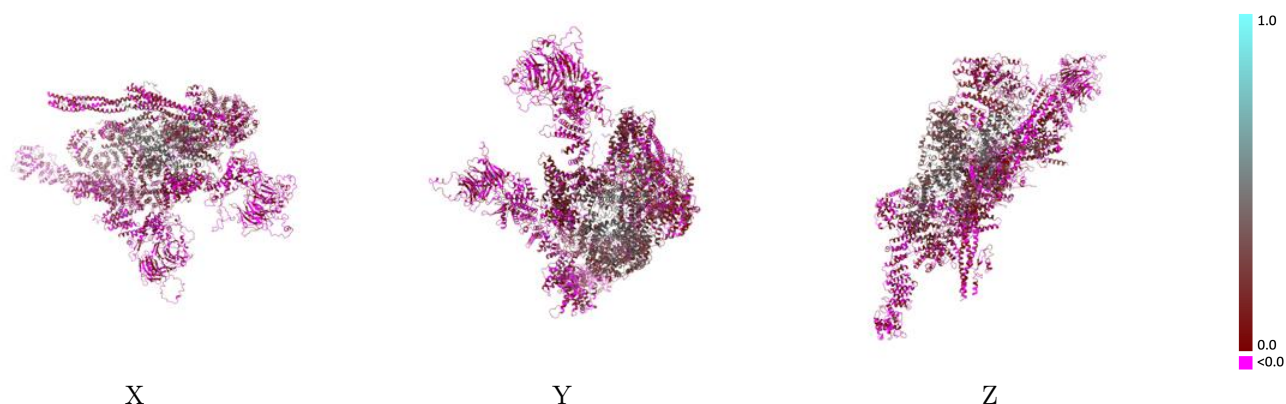
Y



Z

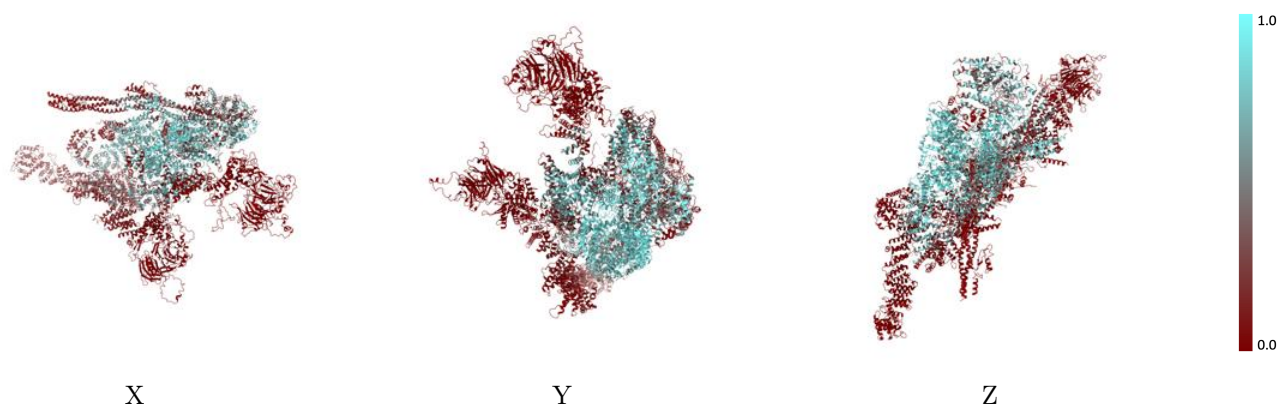
The images above show the 3D surface view of the map at the recommended contour level 0.24 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



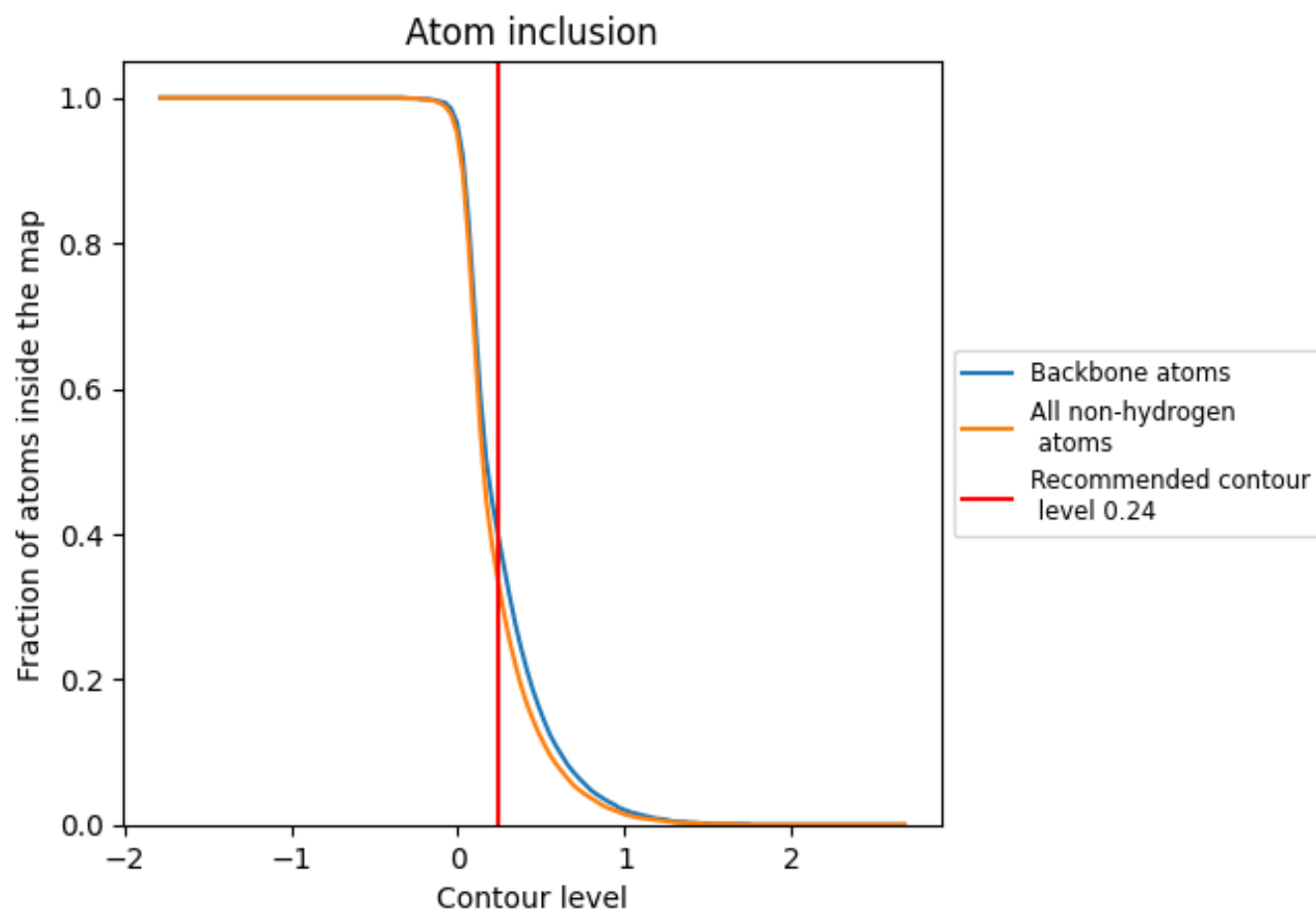
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.24).

9.4 Atom inclusion [i](#)



At the recommended contour level, 40% of all backbone atoms, 34% 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 (0.24) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3370	0.1340
A	0.0350	0.0150
C	0.0010	0.0220
D	0.1240	0.0320
E	0.7100	0.3120
F	0.5690	0.2180
G	0.3910	0.0730
H	0.3420	0.0980
I	0.4900	0.1220
J	0.2860	0.1480
K	0.2420	0.1210
L	0.3040	0.0820
Z	0.3470	0.1290

1.0

0.0

<0.0