



wwPDB EM Validation Summary Report ⓘ

Jun 20, 2024 – 03:29 AM JST

PDB ID : 7WOO
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.

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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

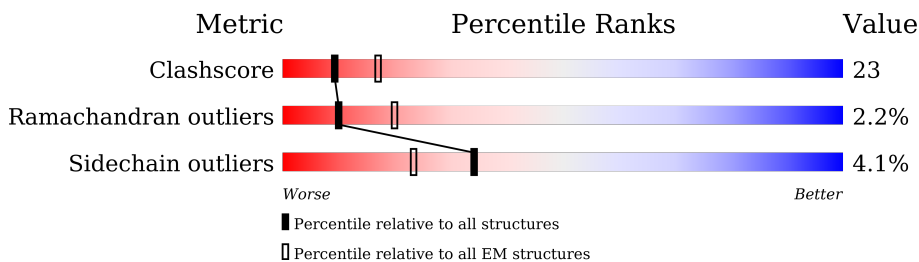
1 Overall quality at a glance i

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.



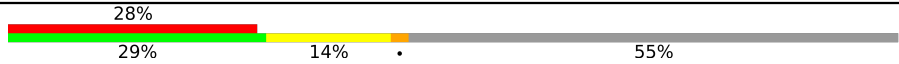



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 ≥ 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	83% 54% 31% 13%
1	Z	839	53% 52% 30% 5% 11%
2	C	1391	95% 88% 6% 5%
3	D	1502	80% 67% 26% 7%
4	E	1655	14% 68% 25% 6%
5	F	1683	33% 52% 36% 7%
6	G	472	24% 30% 12% 58%
6	J	472	30% 17% 21% 59%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
5	F	1622	Total	C	N	O	S	0	0
			12232	7805	2031	2365	31		

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

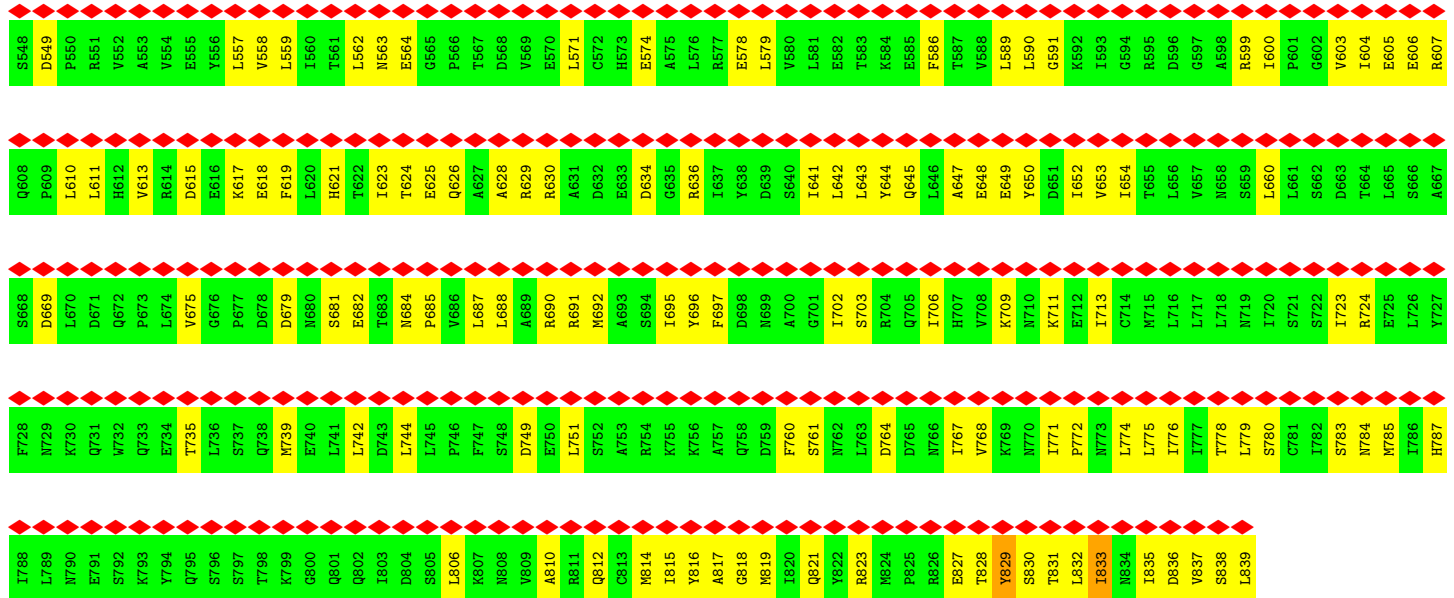
Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	200	Total	C	N	O	S	0	0
			1533	973	251	307	2		
6	J	195	Total	C	N	O	S	0	0
			1492	938	251	302	1		

- Molecule 7 is a protein called Nucleoporin NUP57.

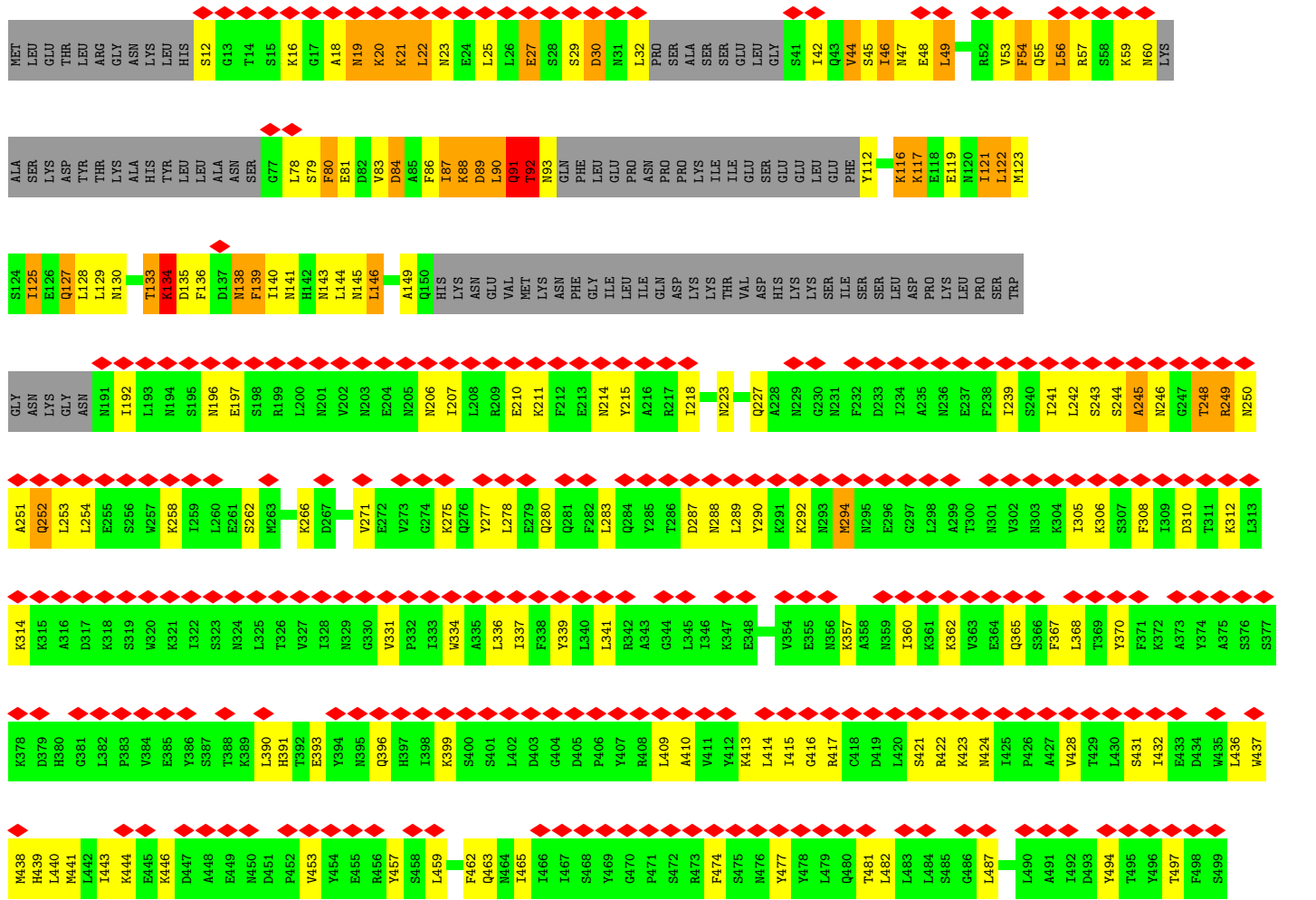
Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	246	Total	C	N	O	S	0	0
			1811	1128	332	348	3		
7	K	254	Total	C	N	O	S	0	0
			1808	1126	334	345	3		

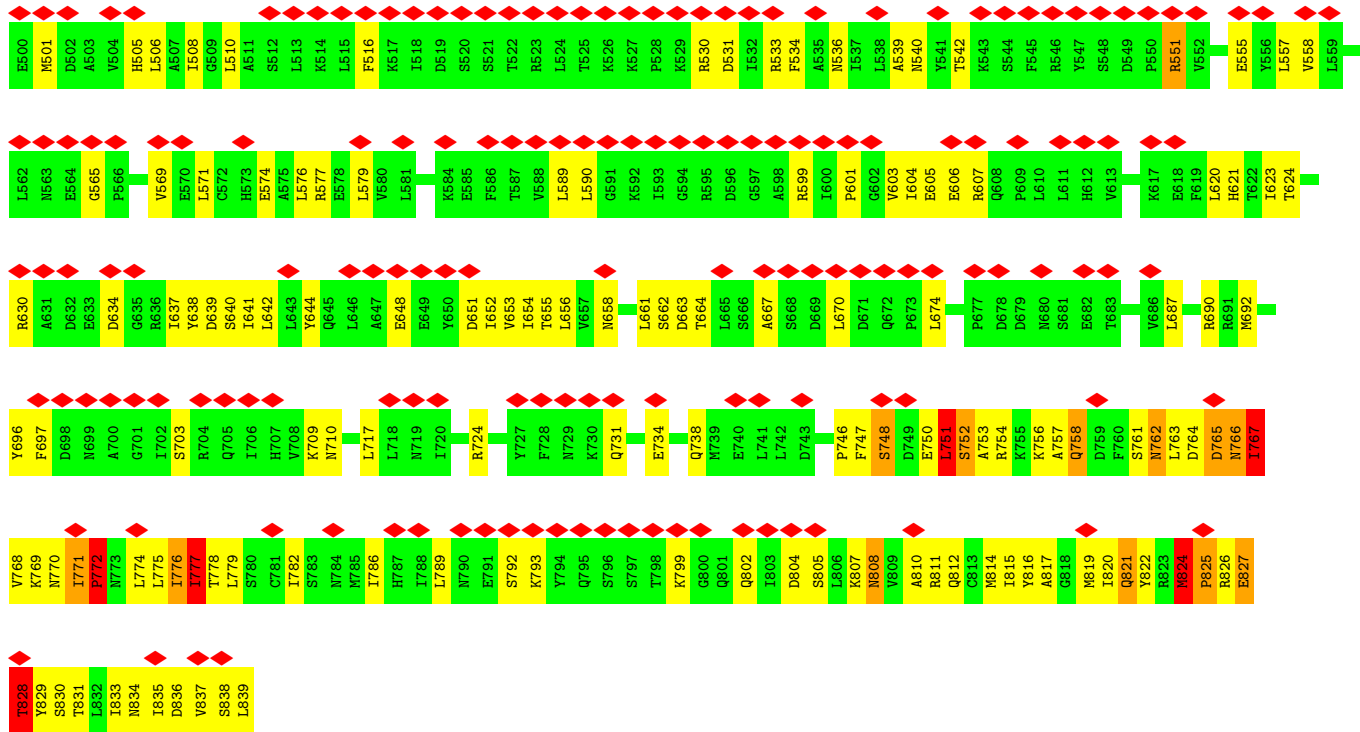
- Molecule 8 is a protein called Nucleoporin NSP1.

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		

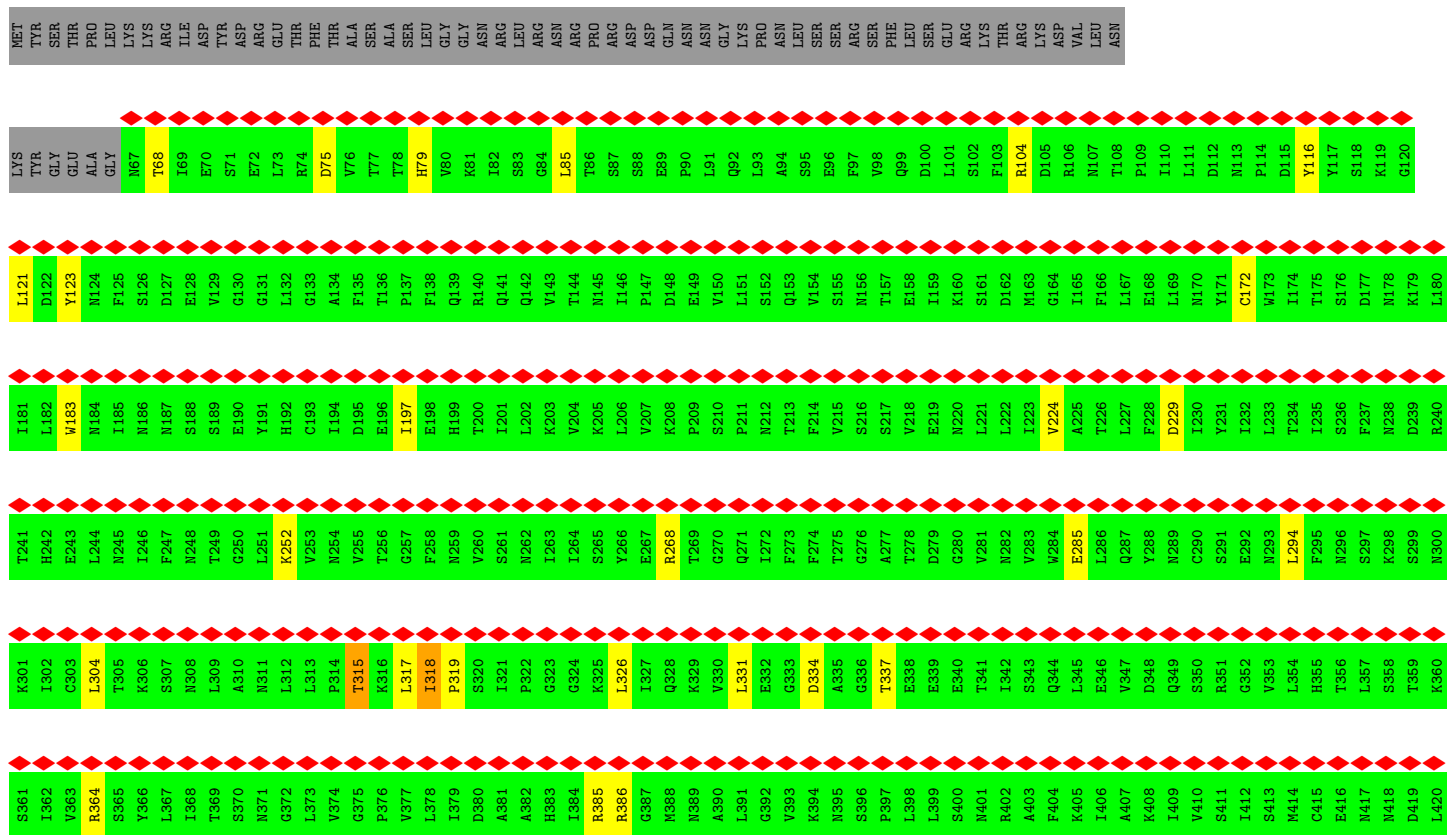
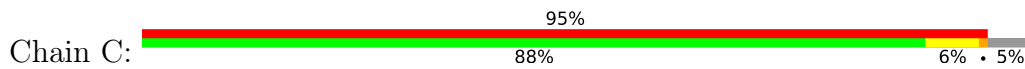


● Molecule 1: Nucleoporin NIC96





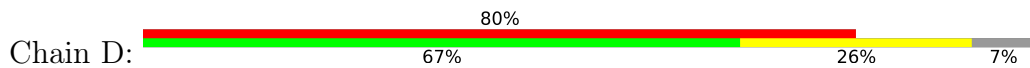
• Molecule 2: Nucleoporin NUP157



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	M783	I723	A663	V603	P443	L483	A423
S1144	L1084	S1024	V964	Y904	F844	A784	M724	F664	L604	D544	S484	V424
T1145	K1085	P1025	G965	R905	F845	I785	E725	F665	T605	Y545	T485	I425
S1146	E1086	S1026	F966	A906	D846	T786	E726	S666	S606	G546	Q486	T426
F1147	R1087	L967	L967	G907	L847	A787	R727	A667	M607	I547	K487	T427
A1088	A1088	A1028	R868	E908	K848	S788	V728	G668	A608	L548	A488	T428
E1089	E1089	M1029	R969	H909	F849	D789	V729	I669	L609	K549	S489	G429
K1150	K1090	F970	F970	L910	H850	A790	F730	P670	E610	N550	S490	V430
P1151	S1091	A971	A971	E911	D851	E791	F731	G671	I611	Y551	T491	R431
A1152	L1092	D972	D972	A912	L852	S792	K732	V672	B612	G552	Y492	L432
L1153	E1093	K973	K973	A913	F853	I793	A733	E673	C613	K553	I493	Y433
V1154	I1094	S1034	I974	Q914	T854	A794	R734	B674	B614	K554	I494	F434
Q1155	S1095	P1035	D975	K915	P855	M795	S735	I675	R615	V555	T495	K435
L1156	N1096	A1036	K976	F916	N856	M796	K736	K676	T616	E556	T496	G436
S1157	L1097	S1037	G977	E917	A857	A797	T737	P677	P617	N557	C497	S437
E1158	N1098	S1038	N878	M918	K858	L798	E738	K678	D618	T558	A498	I438
M1159	W1099	L1039	Q979	I919	T859	I799	K739	S679	E619	A559	S499	S439
I1160	F1100	K1040	A980	D920	K860	L800	M740	S680	V620	L560	T500	R440
H1161	Y1101	K1041	Q981	S921	L861	L801	D741	R681	F621	I561	I501	R441
E1162	L1102	E982	E982	K922	L862	I802	A742	E682	E622	I502	I502	I442
L1163	F1103	Y983	Y983	I923	L863	M803	F743	S883	S623	S503	S503	I443
F1164	K1104	Y1044	V984	S924	K864	S804	G744	G684	L624	T564	P504	G444
L1165	E1105	S1045	S985	R925	E865	I805	I745	S885	I625	D565	G505	S445
I1166	N1106	V1046	R986	N926	L866	K806	S746	V686	E626	E566	I506	L446
A1167	H1107	I1047	G987	H927	L867	D807	I747	P687	M627	I567	Y507	K447
S1168	F1108	M1048	C988	L928	L868	A808	T748	P688	P628	F508	F508	L448
L1169	L1109	M1049	N989	D929	E869	L809	R749	I689	L629	E569	T509	D449
Q1170	E1110	S1050	T990	T930	V670	S810	P750	S690	P630	I570	C510	S450
D1171	A1111	M1051	A991	A931	V671	L811	Q751	Q891	F631	V571	V511	V451
D1172	A1112	N1052	D992	I932	N872	I812	V752	N692	I632	P572	R512	K452
L1173	D1113	R1053	P993	D933	A873	M813	E753	L693	H633	L573	K513	F453
L1174	V1114	F1054	R994	L934	N874	B614	V754	F694	S634	T574	R514	P454
M1175	L1115	F1055	K995	Y935	L875	F615	Y755	D895	Y635	R575	A515	P455
L1176	Y1116	V1056	V996	E936	A876	B616	L756	K696	G636	S576	N516	T456
F1177	A1117	Y1057	F997	R937	S877	E617	S757	S697	L637	F577	S457	S457
R1178	L1118	C1058	C998	C938	G878	D818	S758	E698	S638	N578	G518	I458
M1179	A1119	F1059	D999	A939	T879	I619	I759	E699	E639	Y579	E519	S459
E1180	S1120	Y1060	K1000	E940	S880	D820	S760	C700	A640	T580	L520	S460
T1181	S1121	D1061	R1001	N941	A881	A621	V761	D701	C641	S521	S461	S461
R1182	I1122	W1062	I1002	I942	D882	F822	L762	G702	S642	S522	L462	L462
I1183	F1123	L1063	M1003	E943	Y883	K623	A763	I703	T643	P683	G523	E463
D1184	D1124	V1064	V1004	L944	L884	S824	D764	V704	A644	Q584	I524	Q464
E1185	L1125	A1065	Y1005	C945	V885	L825	F765	L705	L645	G585	T525	N465
L1186	K1126	T1006	T1006	E946	N886	L826	F766	S706	E646	N526	N526	K466
Y1187	L1127	K1067	L1007	L947	V887	N827	M767	F707	L647	A67	K527	S467
R1188	S1128	R1068	I1008	R948	L888	T828	I768	R708	A648	N588	A528	F468
K1189	F1069	Q1069	F1009	R949	K889	L829	H769	F709	C649	V589	L529	I469
Q1190	E1070	D1070	E1010	V950	E990	M830	R770	Y709	K650	F590	L530	L470
L1191	I1131	Y1071	I1011	Y951	R891	G631	F771	G711	F651	A591	E531	G471
T1192	E1132	L1072	V1012	D952	F892	A832	S772	S712	N652	S192	N532	H472
L1193	C1133	L1073	K1013	I953	G893	G633	F773	A713	K653	Q593	K533	H473
K1194	S1014	R1074	S1014	N954	S894	G634	V774	L714	S654	Y594	E534	P474
L1195	A1135	L1075	V1015	Y955	F895	B635	S775	L715	E555	S595	E535	L475
M1196	R1136	D1076	D1016	K956	C956	B636	F776	I716	H656	A596	H536	L476
G1197	A1137	S1077	L1017	L957	H897	D637	V777	T717	I657	E597	K537	M476
R1198	N1138	Q1078	Y1018	N958	S898	S638	P778	R718	K658	E598	F538	T477
V1199	G1139	F1079	T1019	Y959	A899	K639	F779	L719	S659	L599	Y539	D479
L1200	L1140	V1080	S1020	Q960	D900	T640	K780	F720	S660	K600	V540	T480

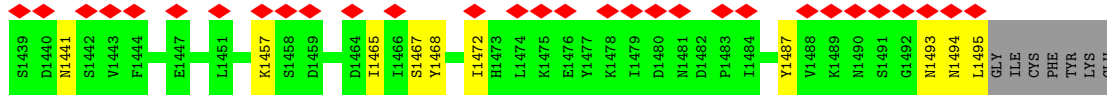
P1201	F1261	L1521	D1381
L1202	L1262	Y1322	Y1382
S1203	S1263	Y1323	Y1383
D1204	S1264	I1324	K1384
L1205	I1265	L1325	R1385
F1206	S1266	S1326	D1386
N1207	N1267	N1327	H1387
D1208	T1268	I1328	H1388
C1209	L1269	I1329	G1389
A1210	I1270	E1330	L1390
D1211	R1271	M1331	K1391
P1212	I1272	S1332	
L1213	G1273	E1333	
D1214	K1274	G1334	
Y1215	T1275	M1335	
Y1216	T1276	V1336	
E1217	T1277	E1337	
I1218	D1278	L1338	
K1219	T1279	L1339	
L1220	D1280	K1340	
I1221	V1281	L1341	
I1222	V1282	E1342	
F1223	F1283	M1343	
K1224	P1284	V1344	
V1225	V1285	V1345	
S1226	H1286	L1346	
Q1227	F1287	I1347	
F1228	L1288	K1348	
K1229	M1289	L1349	
D1230	N1290	W1350	
E1231	K1291	Y1351	
K1232	I1292	Q1352	
V1233	L1293	S1353	
I1234	E1294	D1354	
Q1235	S1295	S1355	
G1236	F1296	D1356	
E1237	L1297	L1357	
W1238	I1298	L1358	
N1239	K1299	G1359	
R1240	S1300	S1360	
L1241	I1301	I1361	
L1242	A1302	A1362	
D1243	A1303	P1363	
S1244	D1304	E1364	
M1245	G1305	Q1365	
K1246	S1306	I1366	
N1247	V1307	K1367	
A1248	C1308	L1368	
P1249	S1309	L1369	
S1250	M1310	E1370	
P1251	F1311	K1371	
D1252	L1312	Y1372	
G1253	L1313	D1373	
Y1254	A1314	P1374	
S1255	G1315	M1375	
V1256	V1316	T1376	
G1257	S1317	D1377	
E1258	H1318	P1378	
E1259	L1319	V1379	
S1260	K1320	Q1380	

● Molecule 3: Nucleoporin NUP170

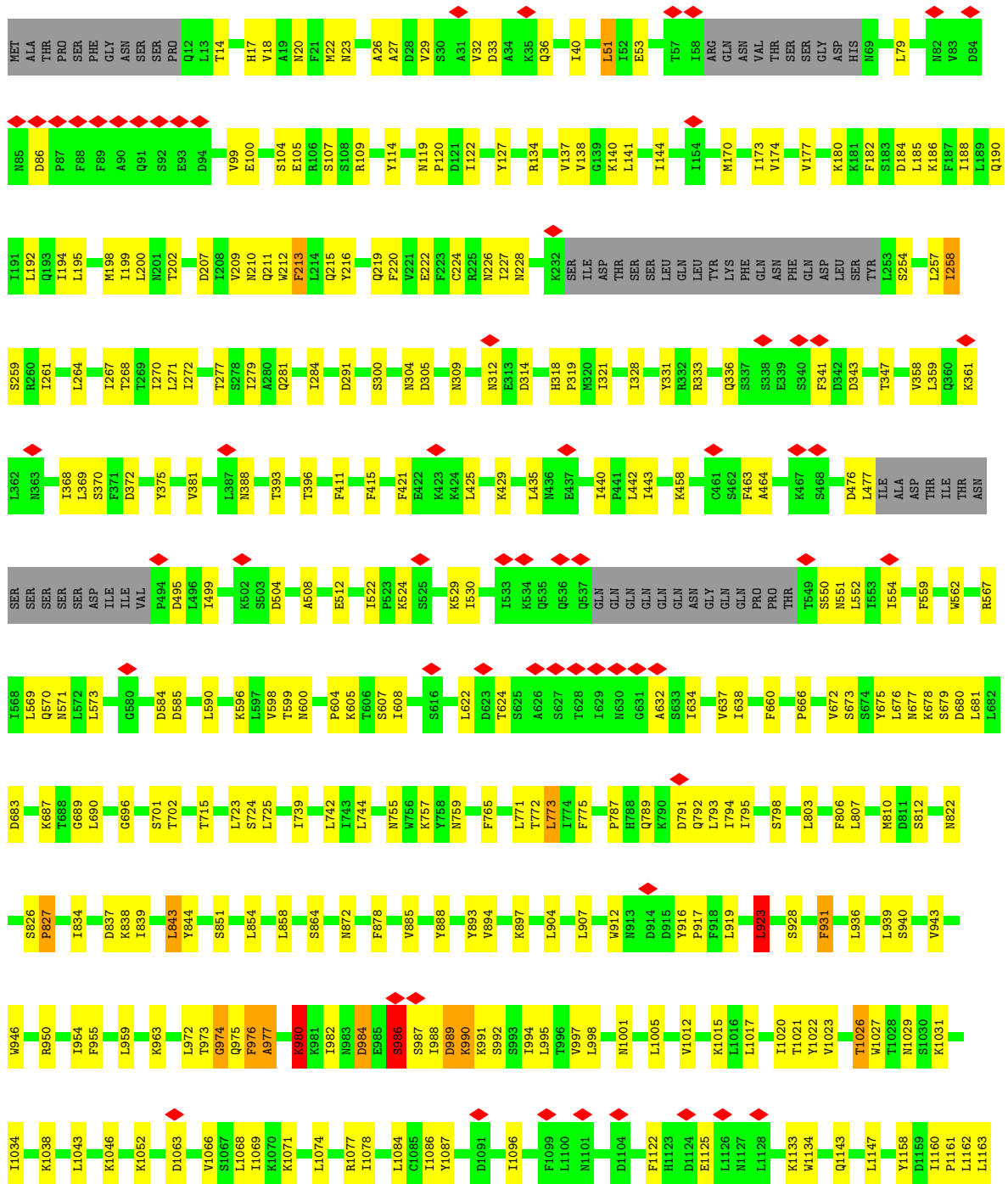


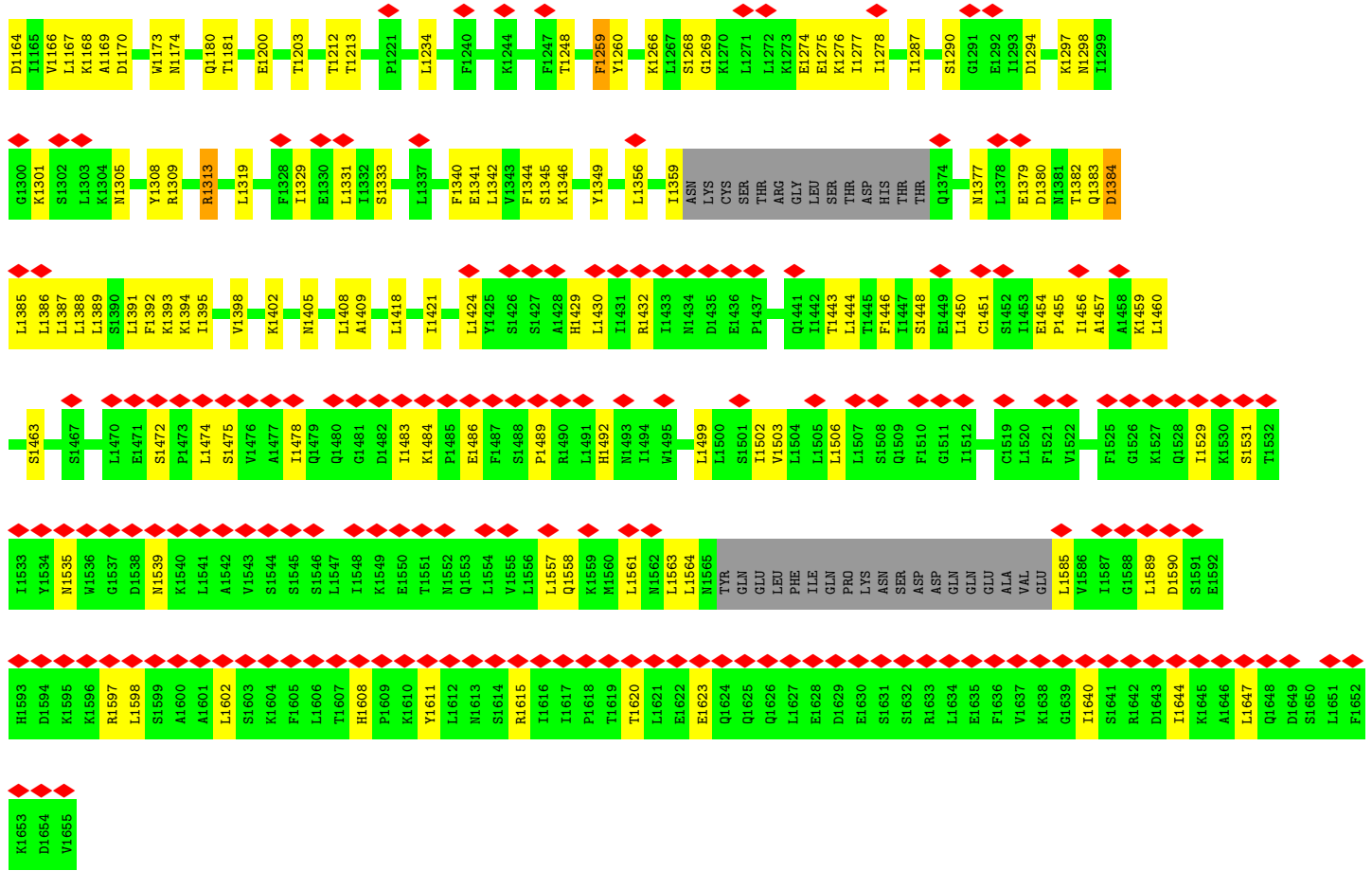
MET	THR	L121	R181	F241	S301	I361	V421	L481
PHE	GLY	D122	C182	N242	D302	D362	K422	I482
GLN	SER	E123	W183	F243	D303	Q363	I423	H483
SER	ASN	R124	I184	A244	W304	Q364	S424	Q484
PRO	LEU	S125	T185	I245	F305	R365	S425	Q485
PHE	MET	Y126	I186	S246	N306	G366	V426	Q486
HIS	ARG	Y127	D187	L247	S307	I367	A427	E487
ASN	ALA	N128	N188	D248	K308	I368	P428	Q488
ASN	GLY	N129	K189	K249	C309	Y369	E429	A489
PRO	ALA	G130	L190	A250	S310	S370	E430	K490
ALA	GLY	V131	I191	T251	K311	L371	M431	R491
ALA	THR	D132	L192	N252	V312	S372	M432	S492
GLY	GLU	Y133	W193	E253	C313	S373	M433	F493
THR	GLY	N134	N194	L254	L314	K374	L434	P494
PHE	SER	F135	I195	S255	T315	S375	F435	P495
SER	ASP	S136	N196	V256	K316	T376	L436	F496
ASP	PRO	R137	N197	F257	S317	I377	V437	S497
SER	SER	E138	D198	N258	A318	R378	A438	M498
TYR	TYR	K139	N199	T259	L319	A379	L439	L499
PRO	PRO	N140	E200	H260	L320	Y380	T440	M500
LEU	LEU	G141	Y201	L261	S321	V381	V441	S501
THR	ASN	L142	Q202	S262	L322	I382	G442	S502
ASN	GLU	G143	W203	V263	L323	T383	G443	E503
HIS	HIS	A144	V204	P264	P324	E384	V444	P504
GLN	GLU	F145	D205	V265	T325	K385	R445	V505
VAL	VAL	T146	D206	Q266	N326	S386	L446	V506
GLU	PRO	P147	M207	G267	M327	L387	Y447	L507
ARG	ARG	F148	K208	I268	L328	E388	F448	K508
GLY	GLY	E149	H209	D269	S329	G389	M449	P509
LEU	LEU	K150	T210	V270	Q330	P390	G450	P510
LEU	GLU	Q151	I211	I271	I331	M391	S451	K511
ALA	ALA	D152	Q212	L272	P332	S392	M452	K512
ALA	SER	V153	R213	I273	G333	I393	G453	S513
ALA	SER	F154	V214	V274	V334	E394	R454	S514
THR	THR	M155	A215	S275	D335	P395	P455	V515
LYS	LYS	I156	L216	H276	F336	A396	M456	L516
ALA	ALA	P157	W217	E277	I337	Y397	L457	L517
GLN	GLN	D158	R218	R278	Q338	I398	E458	E518
GLN	GLN	E159	P219	S279	A339	S399	A459	T519
PRO	PRO	I160	K220	G280	L340	R400	L460	T520
THR	THR	L161	F221	R281	F341	I401	R461	K521
HIS	HIS	H162	N222	I282	E342	L402	L462	A522
LEU	LEU	E163	T223	F283	D343	G403	E463	S523
ASN	ASN	F164	F224	F284	N344	T404	S464	T524
SER	SER	S165	V225	A285	S345	T405	I465	I525
TYR	TYR	T166	P226	G286	N346	T406	K466	I526
PRO	PRO	S167	A227	Q287	G347	A407	P467	S527
ILE	ILE	Q168	V228	A288	N348	R408	P468	P528
		I169	K229	S289	G349	A409	P469	G529
		K170	H230	G290	G350	A410	S470	I530
		T171	L231	L291	F351	P411	S471	F531
		D172	L232	N292	S352	I412	V472	F532
		M173	L233	I293	Q353	L413	T473	S533
		G174	L234	W294	E354	G414	P474	A534
		I175	S235	E295	T355	P415	E475	V535
		F176	T236	L296	I356	K416	V476	I536
		P177	T237	H297	F357	Y417	I477	K537
		L178	M238	E298	Q358	L418	Q478	S538
		L179	E239	S299	L359	K419	Q479	S539
		N180	L240	G300	T360	I420	E480	Q540

S1360	M1361	M1362	R1232	Q1143	Y1083	Y1021	S961	Q901	Y841	G721	D661	T601	Q541
M1365	L1366	L1367	S1237	K1144	V1084	D1022	L962	S902	Y842	S722	L662	A602	T642
L1376	L1377	K1376	R1238	S1145	A1085	S1023	I963	I903	L843	S723	I663	G603	H543
V1378	Q1379	Q1380	G1241	Y1146	M1086	L1024	R964	K904	S844	T724	D664	P604	Q644
S1381	E1382	S1249	F1242	E1147	G1087	M1025	R965	E905	S845	V725	N665	V605	Q545
F1388	E1389	L1390	C1243	A1148	F1088	H1026	I966	G906	I846	S726	P666	Q606	E646
F1397	F1398	F1399	A1149	L1150	L1089	H1027	L967	L907	N847	L728	P668	I608	K648
E1400	T1401	L1402	S1245	K1151	M1091	L1028	S969	S908	L848	L729	P669	I609	E549
L1403	L1404	L1405	V1246	Y1152	D1092	M1030	I970	F909	L849	S730	V670	P610	N650
E1405	H1406	I1407	K1154	M1153	D1093	A1031	I971	N911	N850	K731	L671	L611	S651
I1408	S1409	G1410	D1154	R1094	R1084	T1032	I972	V912	F852	P732	N672	S612	S652
S1411	T1418	A1419	L1249	L1155	K1095	A1033	R973	L913	F853	L733	G673	G613	V653
A1420	V1421	S1422	S1248	Q1096	Q1096	L1034	N974	Y914	I854	T734	G674	L614	V654
F1423	M1426	I1429	A1148	Y1097	Y1098	L1035	I975	E915	T855	S735	A675	F615	G655
T1418	A1419	G1420	E1147	Y1098	Y1099	E1036	T976	E916	Y856	T736	A676	M616	G656
A1420	V1421	S1422	H1160	K1100	K1037	Q1037	K977	S917	G857	A737	E677	A617	T657
F1423	M1426	I1429	M1161	R1101	I1038	I1038	G978	E918	D858	T738	A678	T618	A658
T1418	A1419	G1420	Y1162	I1102	V1039	V1039	A979	V919	S859	T739	C679	T619	T659
A1420	V1421	S1422	V1166	I1103	D1040	D1040	S980	E920	I860	N740	S680	K620	A660
F1423	M1426	I1429	M1169	L1104	D1041	D1041	I981	G921	S861	L741	T681	P621	G661
T1418	A1419	G1420	R1170	Y1105	L1042	L1042	E982	F922	Q862	Q742	A682	G622	S662
F1423	M1426	I1429	R1171	D1106	S1043	S1043	Y983	D923	I863	Q743	L683	G623	K663
T1418	A1419	G1420	E1171	L1107	I1044	I1044	T984	N924	S864	S744	F684	F624	T664
F1423	M1426	I1429	E1172	V1108	E1045	E1045	A985	Q925	A865	I745	V685	A625	V665
T1418	A1419	G1420	K1173	F1109	K1046	K1046	T986	Y926	P866	T746	T686	M626	V666
A1420	V1421	S1422	L1111	D1110	L1047	L1047	A987	L927	Y867	G747	C687	E627	Q667
F1423	M1426	I1429	L1112	T1111	K1048	K1048	L988	G928	V668	F748	K688	F628	Q668
T1418	A1419	G1420	L1113	L1112	E1049	E1049	Q989	F929	L869	S749	S689	A629	P669
F1423	M1426	I1429	V1114	I1113	A1050	A1050	E990	K930	A870	K750	N690	T630	V670
T1418	A1419	G1420	V1115	K1114	V1051	V1051	R991	D931	N871	P751	K691	Q631	T671
A1420	V1421	S1422	D1116	Y1115	S1052	S1052	C992	I932	N872	S752	S692	Y632	L672
F1423	M1426	I1429	E1117	D1117	M1053	M1053	G993	I933	S873	P753	K693	T633	Q673
T1418	A1419	G1420	L1118	E1118	M1054	M1054	S994	S934	N874	A754	E694	S634	H574
F1423	M1426	I1429	A1119	L1119	L1055	L1055	F995	F935	G875	N755	L695	E635	K575
T1418	A1419	G1420	E1120	E1120	S1056	S1056	C996	V936	R876	K756	R696	T636	L576
A1420	V1421	S1422	K1121	K1121	V1057	V1057	S997	S937	V877	E757	S697	L637	F577
F1423	M1426	I1429	L1122	L1122	M1058	M1058	A998	L938	I878	D758	N698	K638	V578
T1418	A1419	G1420	K1123	K1123	Y1059	Y1059	S999	D939	D879	F759	A699	V639	S579
A1420	V1421	S1422	S1124	S1124	Y1060	Y1060	D1000	V940	K880	D760	L700	A640	V680
F1423	M1426	I1429	S1125	S1125	P1061	P1061	I1001	Q941	T881	L761	T701	V641	P681
T1418	A1419	G1420	Y1203	Y1203	K1062	K1062	L1002	K942	E882	D621	F702	L642	D682
A1420	V1421	S1422	Y1204	Y1204	S1063	S1063	G1003	D943	E883	D763	L703	T643	Y683
F1423	M1426	I1429	S1205	S1205	I1064	I1064	F1004	L944	V884	V764	T704	S644	G684
T1418	A1419	G1420	R1206	R1206	E1065	E1065	R1005	V945	A885	I765	M705	T645	I685
A1420	V1421	S1422	R1207	R1207	F1066	F1066	A1006	K946	N886	L766	G706	S646	L686
F1423	M1426	I1429	S1208	S1208	M1069	M1069	I1007	L947	Q887	S767	I707	I647	K687
T1418	A1419	G1420	K1209	K1209	E1069	E1069	E1008	D948	A888	P768	P708	E648	T688
A1420	V1421	S1422	F1210	F1210	H1069	H1069	H1009	F949	S889	R769	G709	I649	H689
F1423	M1426	I1429	F1211	F1211	M1071	M1071	M1011	Q951	E890	F770	V710	Y650	G690
T1418	A1419	G1420	E1212	E1212	R1012	R1012	R1012	D952	A892	D772	D712	K651	K691
A1420	V1421	S1422	S1213	S1213	A1013	A1013	A1013	F953	I893	I773	I713	R653	Y693
F1423	M1426	I1429	A1214	A1214	K1014	K1014	K1014	A954	N894	A774	K714	T654	E594
T1418	A1419	G1420	E1215	E1215	E1015	E1015	E1015	P955	A895	L775	P715	P655	N695
A1420	V1421	S1422	Y1218	Y1218	I1016	I1016	I1016	N956	N896	L776	V716	D656	A596
F1423	M1426	I1429	I1227	I1227	G1017	G1017	G1017	D957	I897	T777	Y717	E657	T697
T1418	A1419	G1420	Q1082	Q1082	L1018	L1018	L1018	K958	K898	T778	N718	F658	F598
A1420	V1421	S1422	M1081	M1081	L1019	L1019	L1019	N959	M899	R779	R719	F659	L699
F1423	M1426	I1429	N1020	N1020	Y900	Y900	Y900	K960	M900	L780	Y720	E660	E600

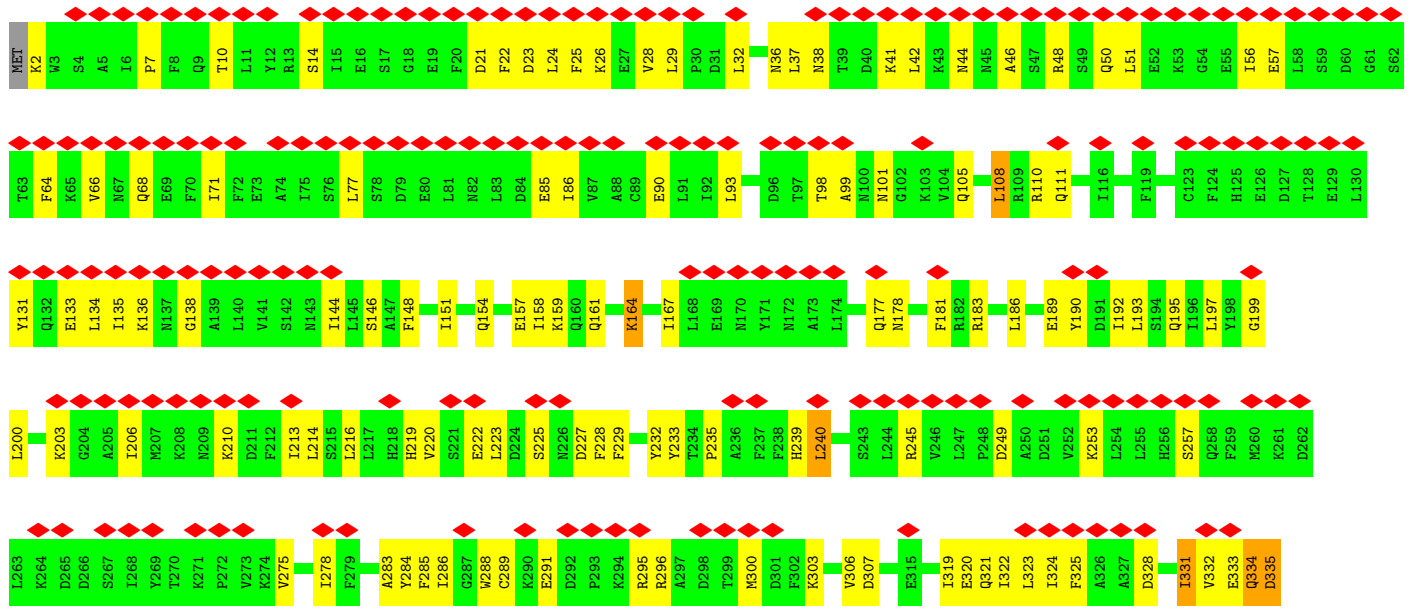


● Molecule 4: Nucleoporin NUP188

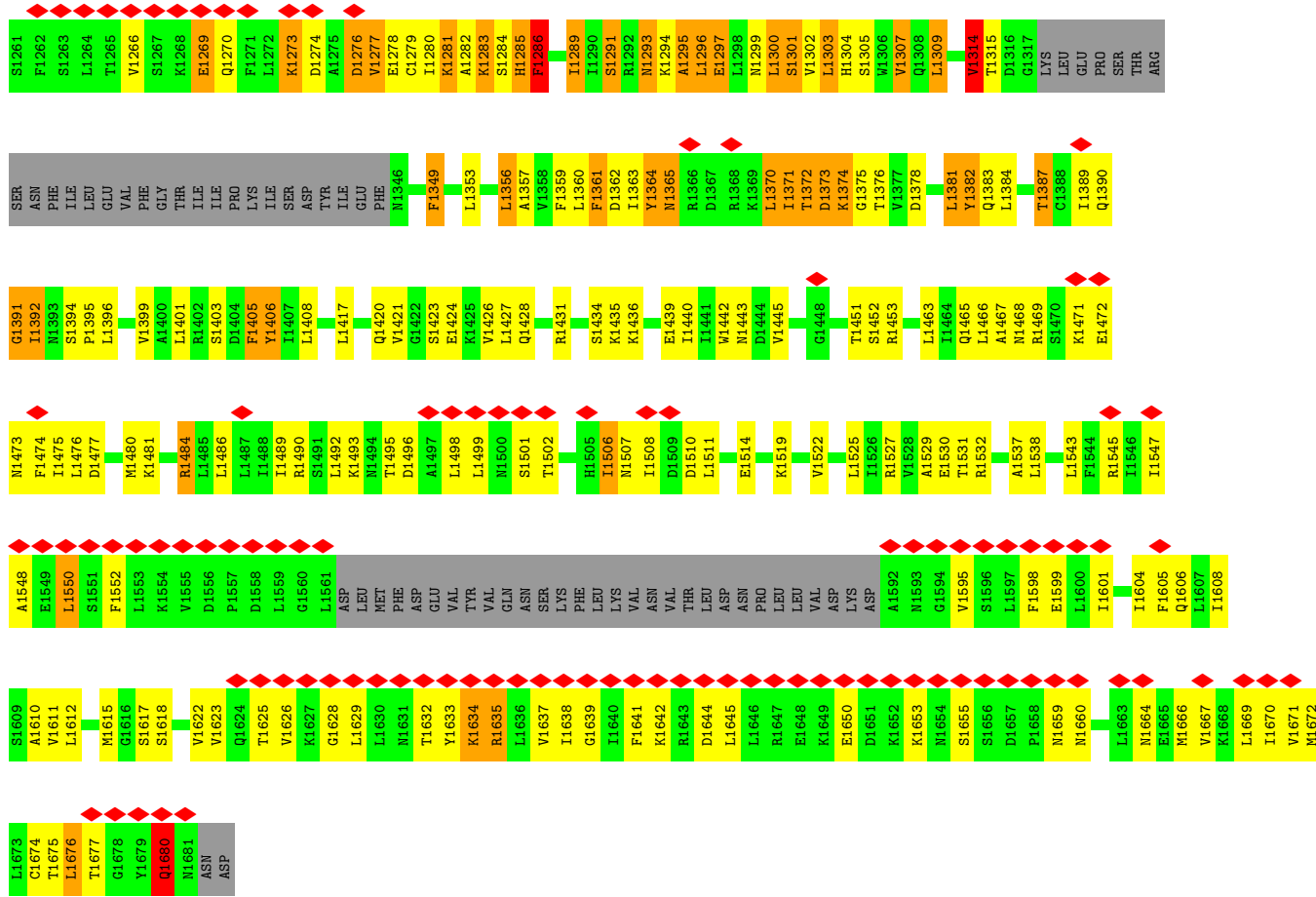




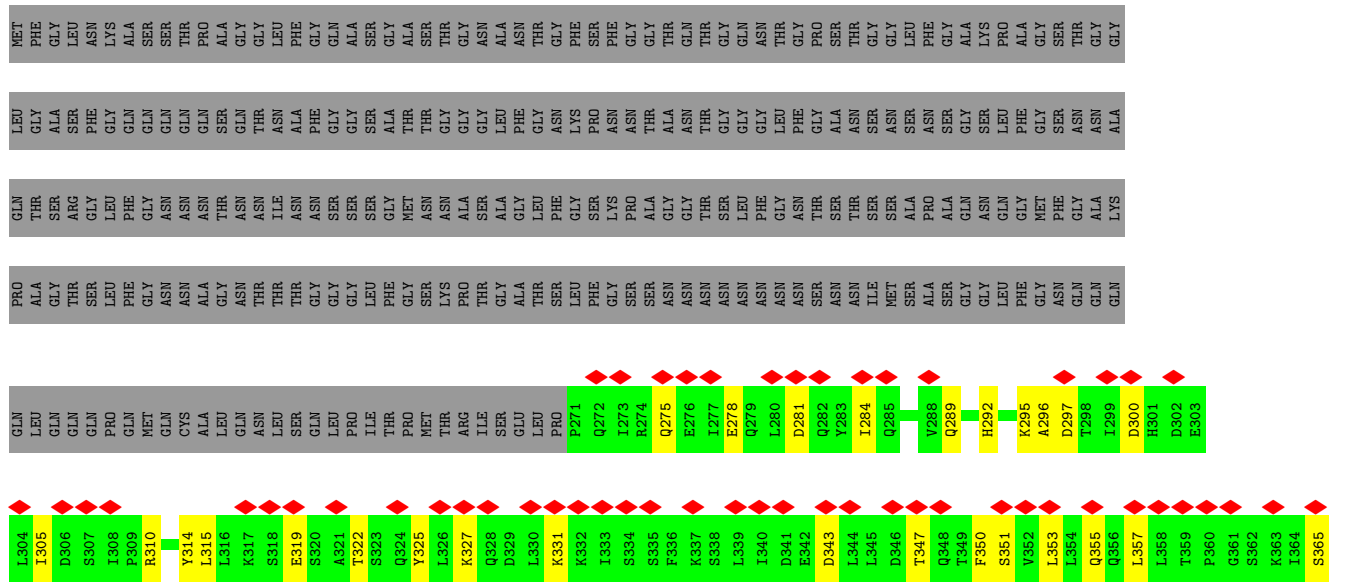
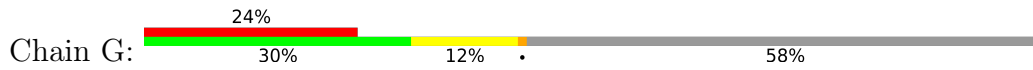
• Molecule 5: Nucleoporin NUP192

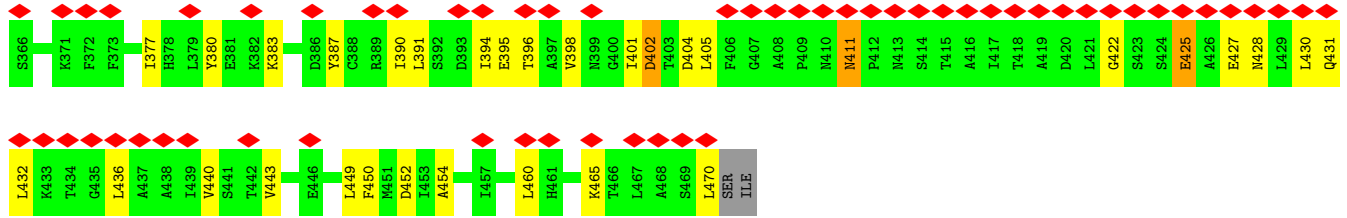




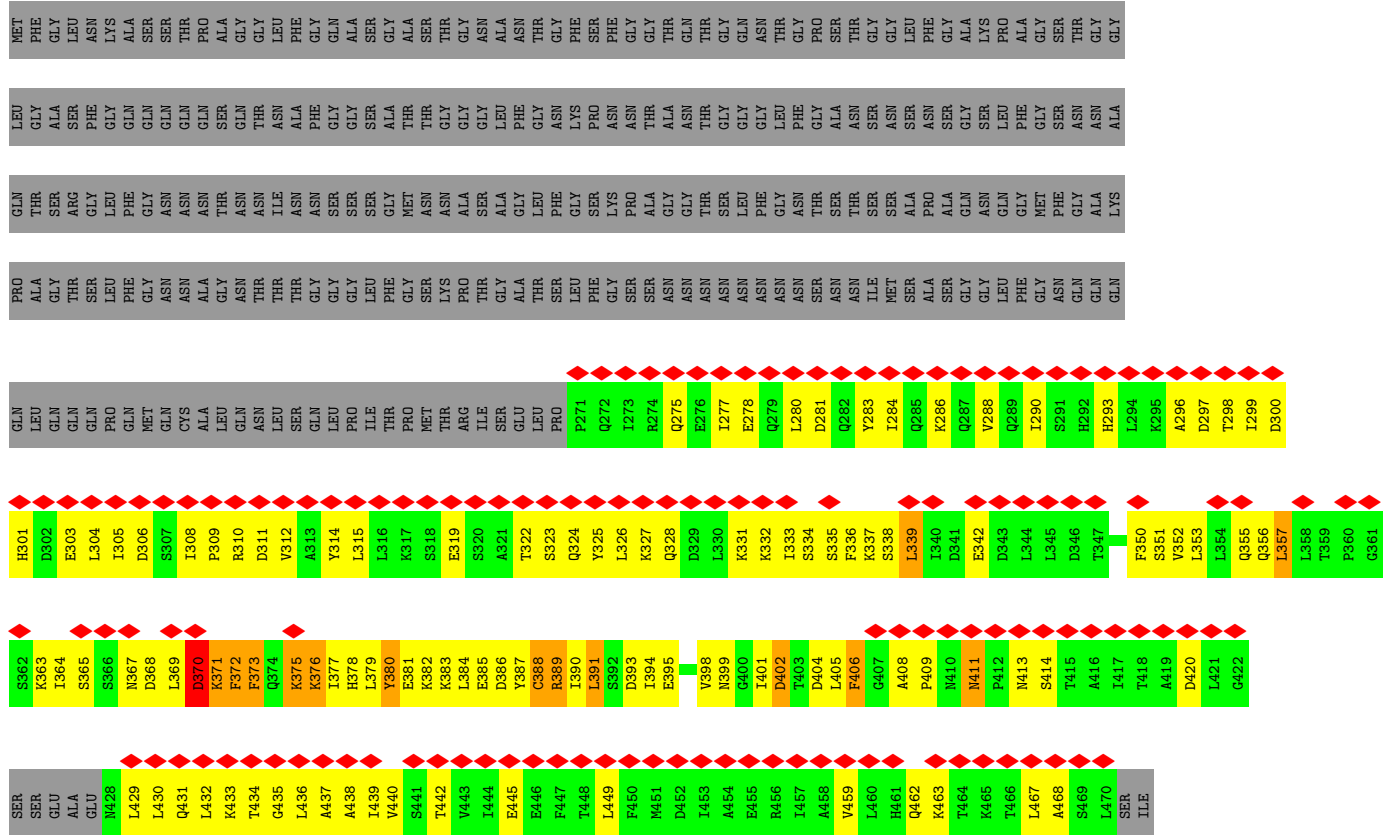


● Molecule 6: Nucleoporin NUP49/NSP49

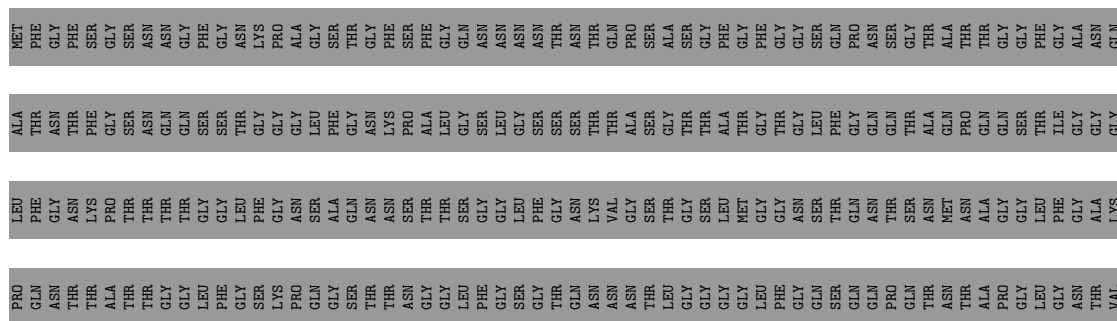
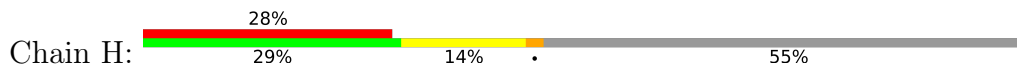


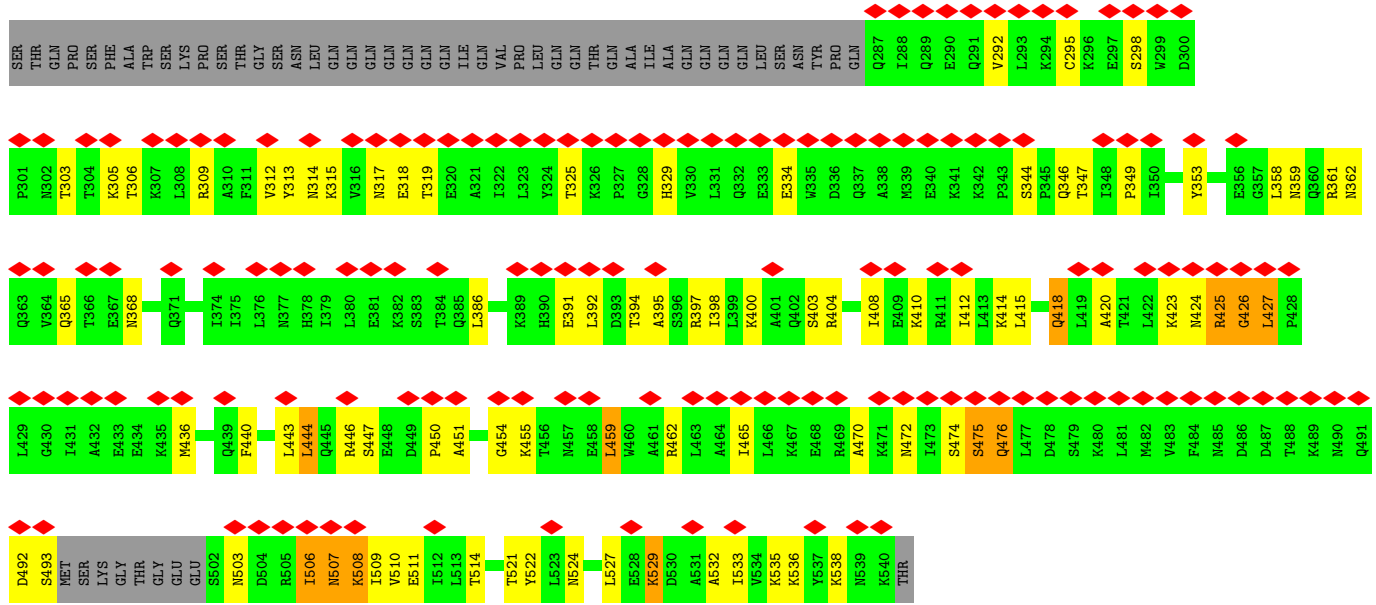


• Molecule 6: Nucleoporin NUP49/NSP49

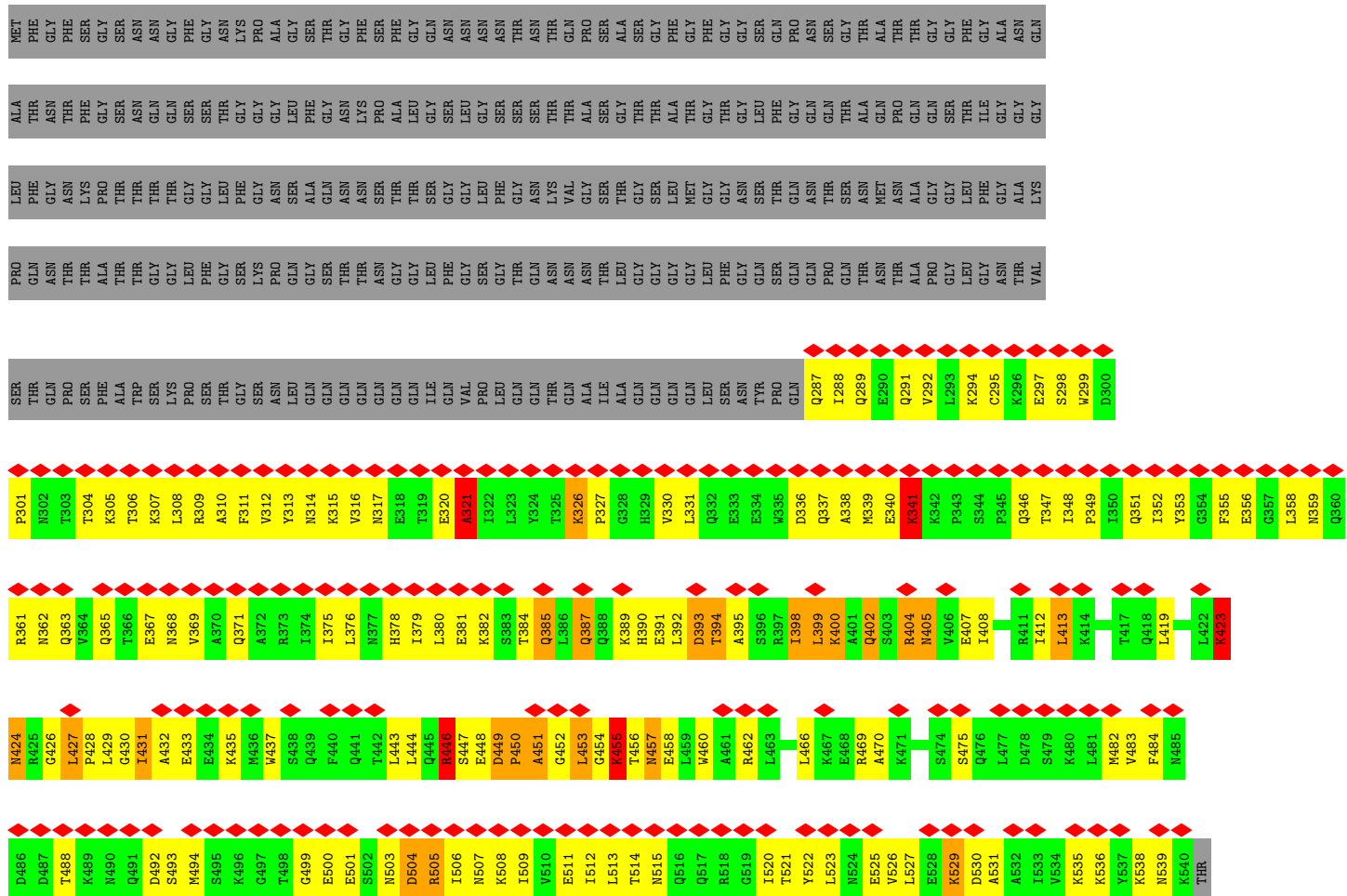


• Molecule 7: Nucleoporin NUP57





• Molecule 7: Nucleoporin NUP57



E789	L721	K661	GLU	LYS	ASP	ALA	SER	SER	SER	ALA	GLY	THR	ASN
M790	L722	I662	SER	GLY	LYS	PHE	SER	LYS	GLY	ALA	PHE	THR	THR
I791	S723	M663	SER	ASP	LYS	ASN	ALA	GLY	THR	THR	GLY	ALA	GLY
O792	D724	S664	THR	GLU	ASP	GLY	THR	GLY	GLY	PHE	THR	THR	THR
L793	V725	S665	GLY	SER	SER	ASP	GLY	THR	GLY	ALA	ASP	THR	ASN
I794	V726	D666	LYS	SER	SER	ASP	GLY	THR	GLY	ALA	ASP	THR	ASN
K795	S727	Q667	SER	SER	SER	ASP	GLY	THR	GLY	ALA	ASP	THR	ASN
I796	T728	V668	THR	ALA	ALA	PHE	THR	THR	GLY	ALA	ASP	THR	ASN
L797	S729	L669	ASP	SER	PRO	THR	THR	THR	THR	THR	THR	THR	THR
S798	S730	V670	VAL	PHE	ALA	ALA	ALA	LYS	LYS	LYS	GLY	GLY	GLY
H800	G731	K671	SER	SER	SER	THR	THR	THR	THR	THR	THR	THR	THR
D802	A732	G672	SER	LYS	PHE	ALA	ALA	LYS	LYS	LYS	ASP	PRO	ASN
A803	A733	G673	ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
L804	A734	E674	LEU	GLY	GLY	THR	THR	THR	THR	THR	THR	THR	THR
R805	N735	Q675	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
S806	N736	I676	LEU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
L807	N737	S677	ASN	SER	GLY	ASP	LYS	LYS	LYS	LYS	LYS	LYS	LYS
D808	D738	Q678	SER	LYS	LYS	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
D809	D738	L679	PRO	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
T812	R741	L679	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
R816	A744	Y680	GLU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
Q817	A744	S681	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
I818	T747	D682	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
N819	A748	A683	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
S820	Q749	V684	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
I821	T750	M685	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
K822	L751	A686	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
K823	D752	E687	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	L755	H688	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
	N756	H688	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	S759	S689	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
	L762	Q690	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	L765	D638	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
	I766	D639	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
	V767	L640	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	E768	V641	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	I769	T642	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
	V772	K643	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
	S773	M644	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	M774	T645	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	T775	N646	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
	F776	Y699	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	N777	I700	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	K778	E701	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
	I779	R702	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	T780	R703	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	N781	Q704	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	I782	T705	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
	D783	D705	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	I784	L706	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
	N785	L707	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
	M786	L707	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
	E787	T780	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
	D788	E708	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
		N709	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
		F710	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
		L711	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
		D712	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
		I784	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
		N713	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
		F714	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
		E715	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
		T716	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
		K717	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
		T718	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
		E719	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
		A720	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY

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 (\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 (\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	0.36	0/5813	0.58	5/7867 (0.1%)
1	Z	0.46	0/5862	0.82	9/7942 (0.1%)
2	C	0.66	0/10658	0.90	24/14443 (0.2%)
3	D	0.46	0/11192	0.63	5/15173 (0.0%)
4	E	0.43	0/12583	0.68	8/17054 (0.0%)
5	F	0.63	6/12435 (0.0%)	1.18	93/16887 (0.6%)
6	G	0.35	0/1553	0.62	1/2104 (0.0%)
6	J	0.49	0/1509	1.01	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%)
8	I	0.59	0/1431	0.93	4/1940 (0.2%)
8	L	0.40	0/1378	0.74	1/1873 (0.1%)
All	All	0.53	9/68075 (0.0%)	0.85	183/92292 (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	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 9 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
7	H	427	LEU	C-N	9.99	1.53	1.34
7	H	425	ARG	C-N	8.96	1.49	1.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	K	326	LYS	C-N	8.60	1.50	1.34
5	F	1235	ASN	C-N	8.56	1.53	1.34

The worst 5 of 183 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	1090	PRO	CA-N-CD	-37.80	58.58	111.50
7	H	425	ARG	C-N-CA	-13.39	94.18	122.30
6	J	388	CYS	CB-CA-C	-12.59	85.22	110.40
5	F	1036	PRO	N-CA-CB	10.85	116.32	103.30
5	F	1089	ASN	C-N-CD	10.13	149.68	128.40

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 [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	5723	0	5587	285	0
1	Z	5776	0	5607	420	0
2	C	10452	0	10392	49	0
3	D	10976	0	10827	406	0
4	E	12362	0	12566	349	0
5	F	12232	0	11559	829	0
6	G	1533	0	1515	118	0
6	J	1492	0	1465	274	0
7	H	1811	0	1697	146	0
7	K	1808	0	1614	305	0
8	I	1418	0	1293	170	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	L	1366	0	1211	166	0
All	All	66949	0	65333	3007	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 3007 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%)	41	74
1	Z	736/839 (88%)	675 (92%)	39 (5%)	22 (3%)	4	32
2	C	1323/1391 (95%)	1269 (96%)	41 (3%)	13 (1%)	15	51
3	D	1396/1502 (93%)	1275 (91%)	113 (8%)	8 (1%)	25	61
4	E	1538/1655 (93%)	1376 (90%)	149 (10%)	13 (1%)	19	56
5	F	1616/1683 (96%)	1203 (74%)	317 (20%)	96 (6%)	1	19
6	G	198/472 (42%)	188 (95%)	9 (4%)	1 (0%)	29	65
6	J	191/472 (40%)	175 (92%)	13 (7%)	3 (2%)	9	43

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	H	242/541 (45%)	202 (84%)	36 (15%)	4 (2%)	9	42
7	K	252/541 (47%)	209 (83%)	32 (13%)	11 (4%)	2	24
8	I	185/823 (22%)	158 (85%)	16 (9%)	11 (6%)	1	19
8	L	185/823 (22%)	164 (89%)	15 (8%)	6 (3%)	4	31
All	All	8584/11581 (74%)	7594 (88%)	800 (9%)	190 (2%)	10	38

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 [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	609/762 (80%)	583 (96%)	26 (4%)	29	58
1	Z	611/762 (80%)	556 (91%)	55 (9%)	9	37
2	C	1177/1250 (94%)	1152 (98%)	25 (2%)	53	74
3	D	1215/1353 (90%)	1202 (99%)	13 (1%)	73	85
4	E	1421/1557 (91%)	1396 (98%)	25 (2%)	59	77
5	F	1260/1538 (82%)	1164 (92%)	96 (8%)	13	43
6	G	167/377 (44%)	165 (99%)	2 (1%)	71	84
6	J	162/377 (43%)	147 (91%)	15 (9%)	9	35
7	H	171/439 (39%)	166 (97%)	5 (3%)	42	66
7	K	153/439 (35%)	134 (88%)	19 (12%)	4	24
8	I	152/674 (23%)	135 (89%)	17 (11%)	6	28
8	L	138/674 (20%)	137 (99%)	1 (1%)	84	91

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	7236/10202 (71%)	6937 (96%)	299 (4%)	34 59

5 of 299 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	K	398	ILE
1	Z	765	ASP
7	K	446	ARG
1	Z	89	ASP
5	F	407	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 115 such sidechains are listed below:

Mol	Chain	Res	Type
7	H	365	GLN
1	Z	738	GLN
6	J	324	GLN
1	Z	658	ASN
1	Z	127	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.

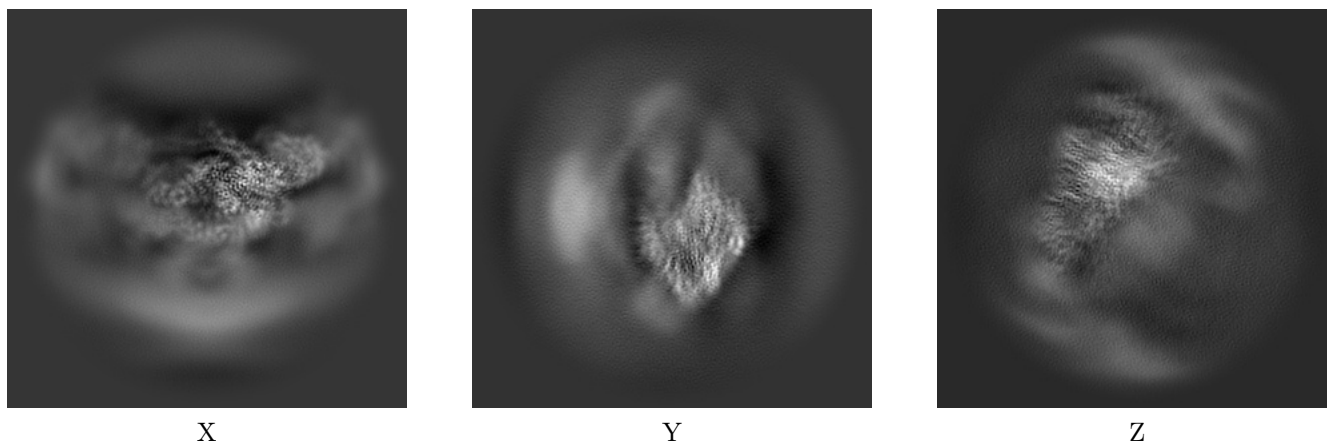
6 Map visualisation [i](#)

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

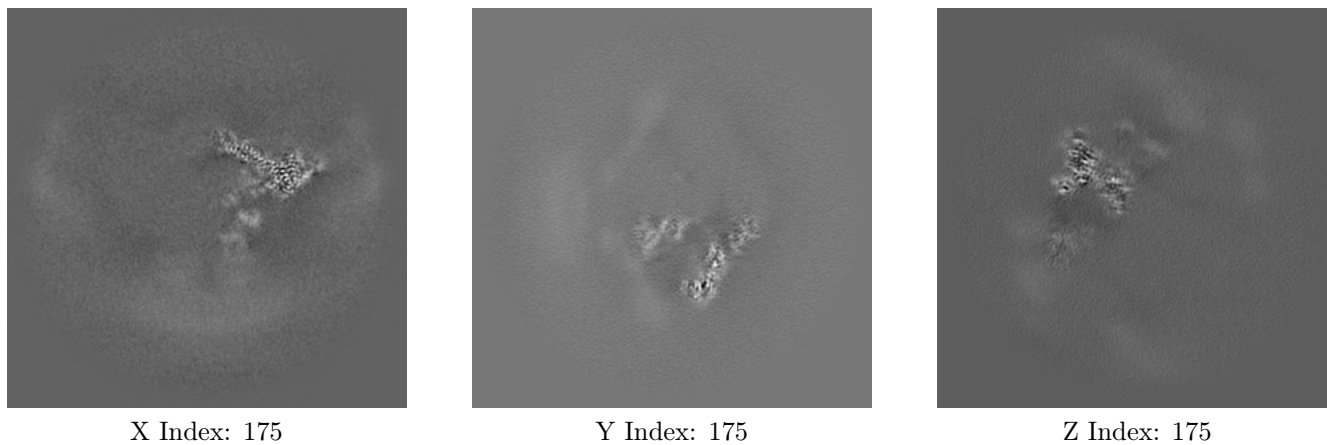
6.1.1 Primary map



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

6.2 Central slices [i](#)

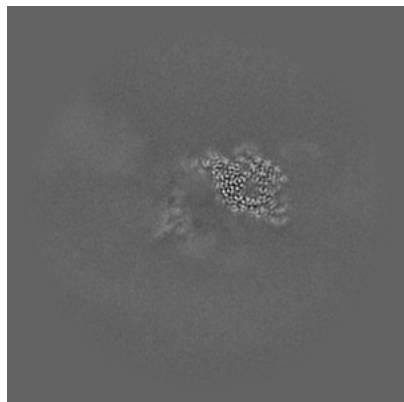
6.2.1 Primary map



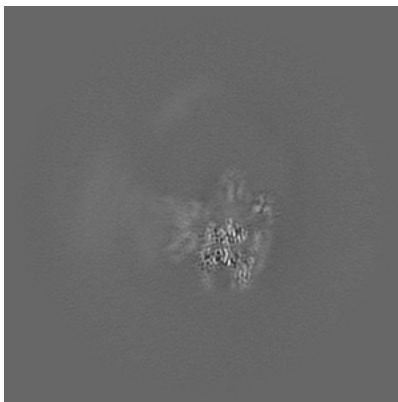
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

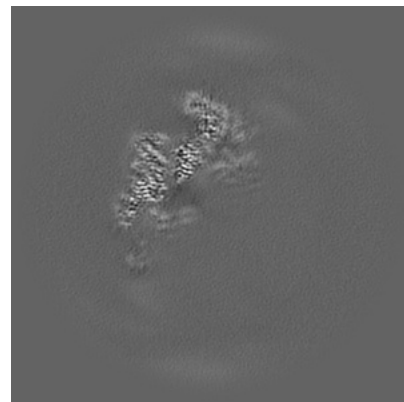
6.3.1 Primary map



X Index: 124



Y Index: 203

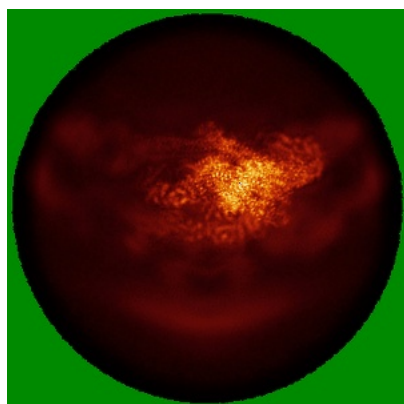


Z Index: 204

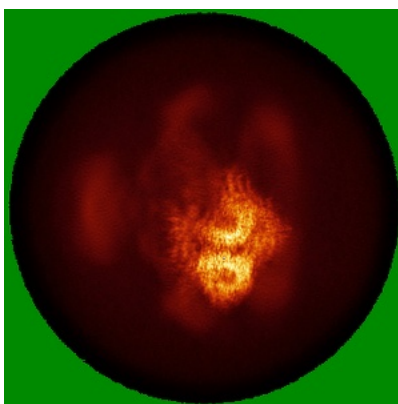
The images above show the largest variance slices of the map in three orthogonal directions.

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

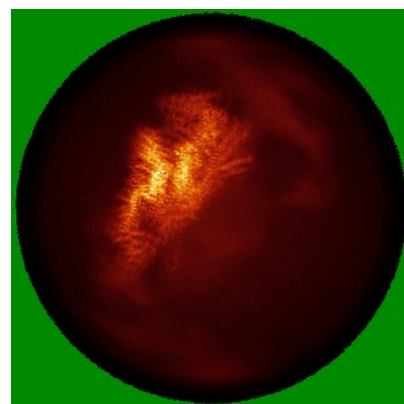
6.4.1 Primary map



X



Y

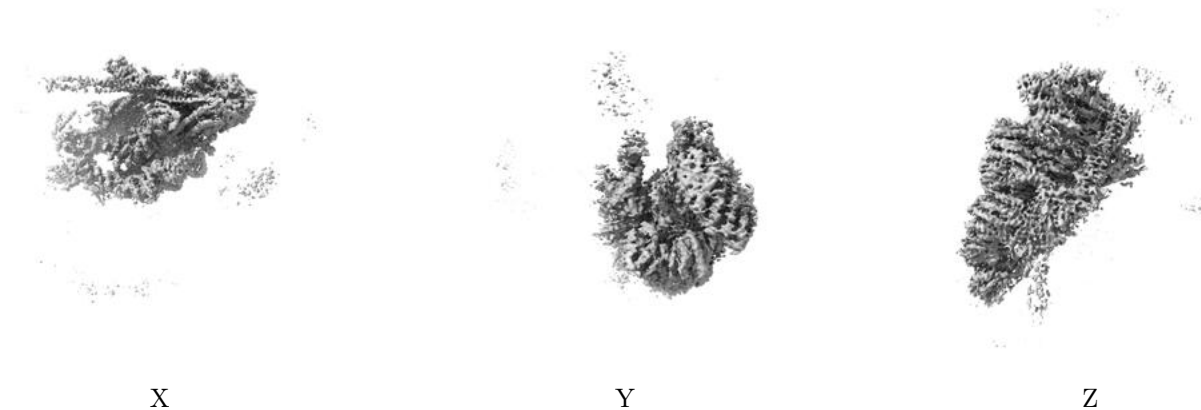


Z

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.

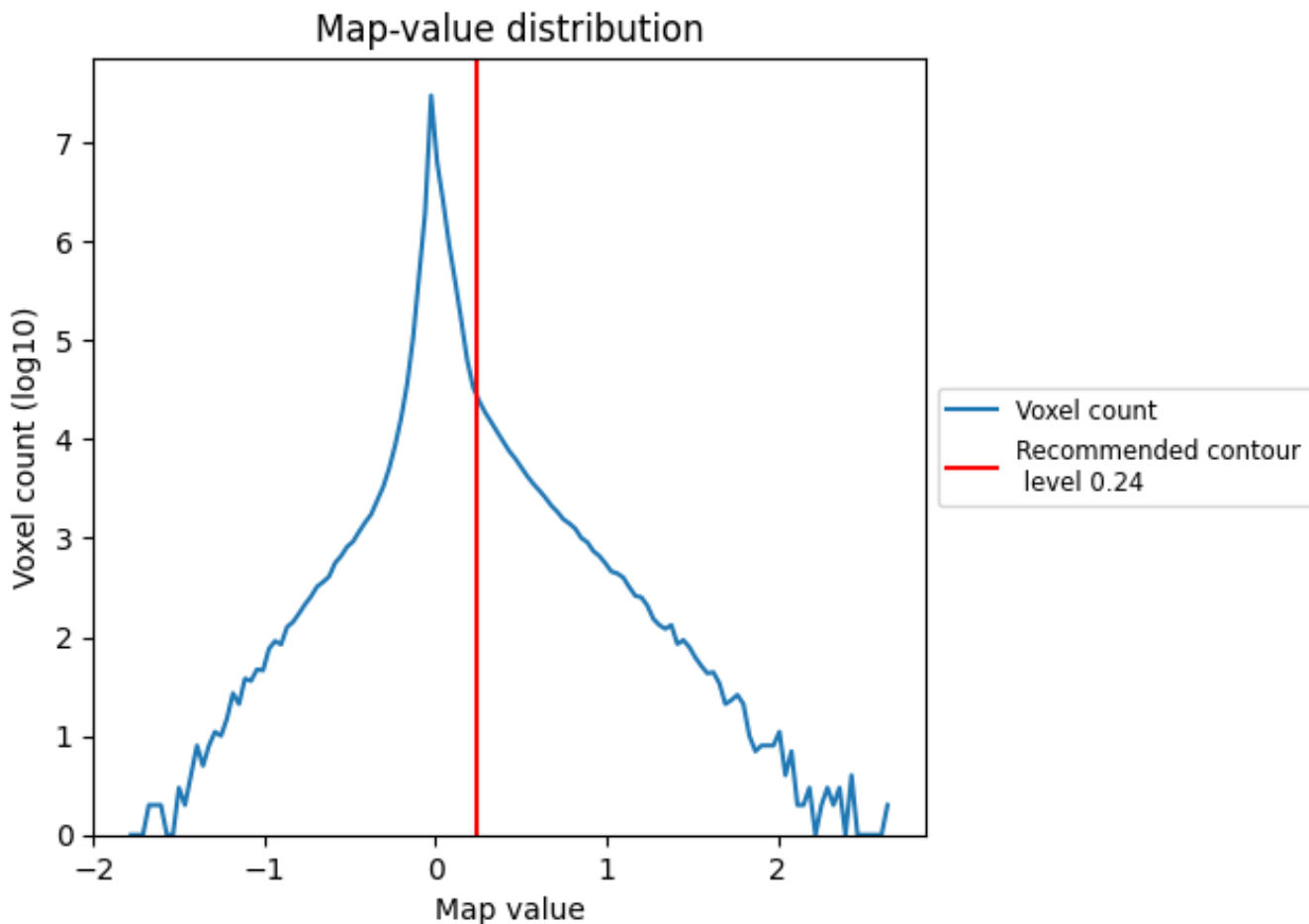
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

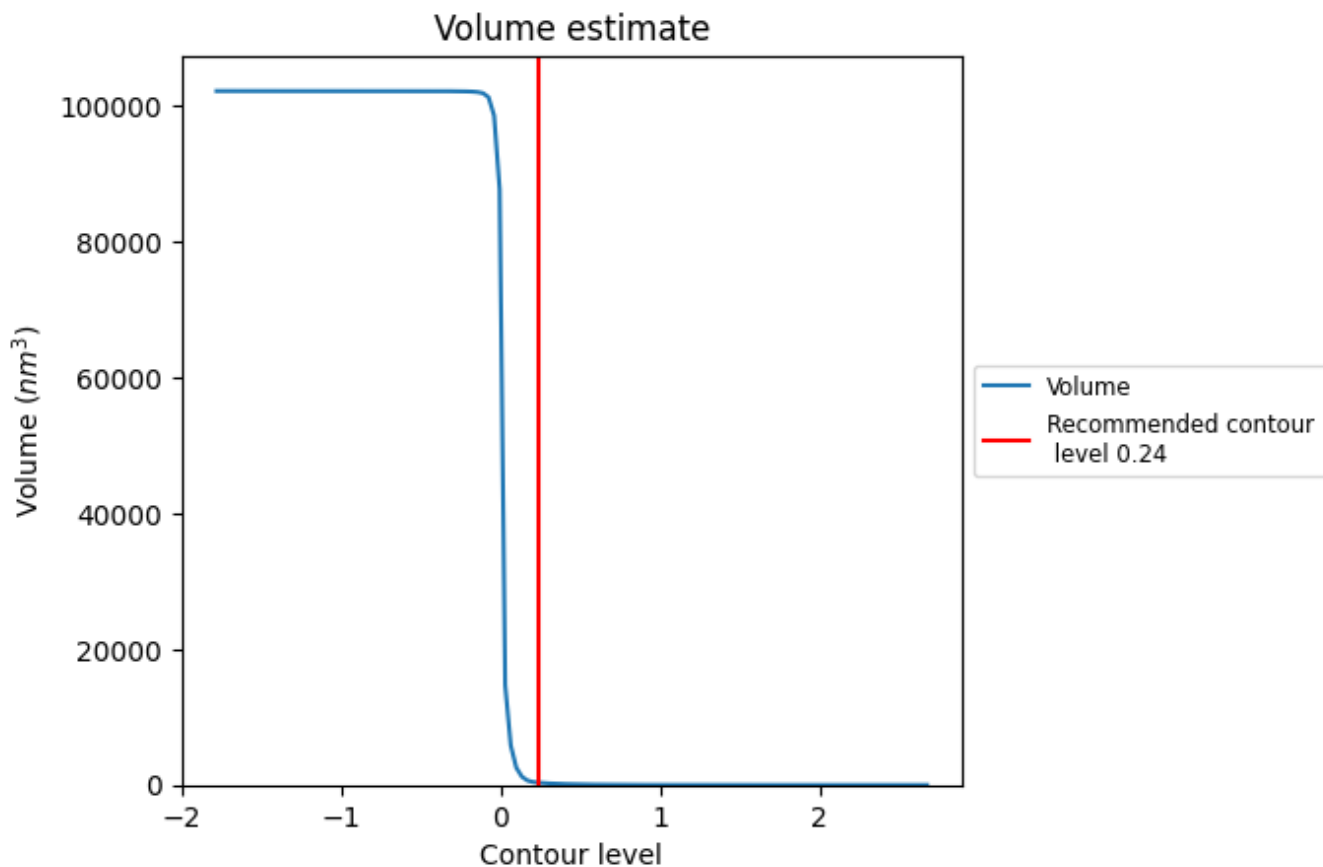
This section contains the results of statistical analysis of the map.

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.

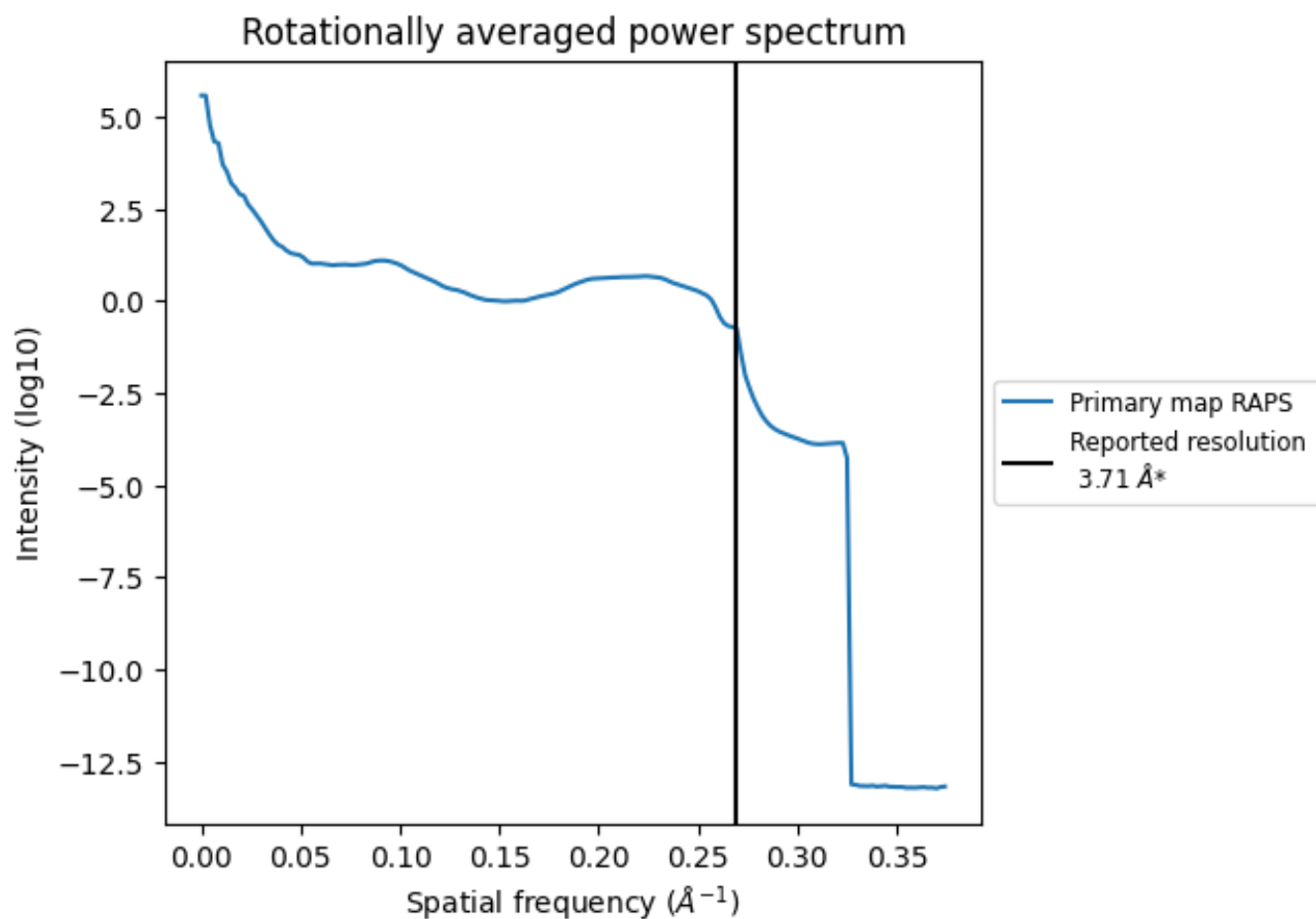
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 332 nm^3 ; 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.270\AA^{-1}

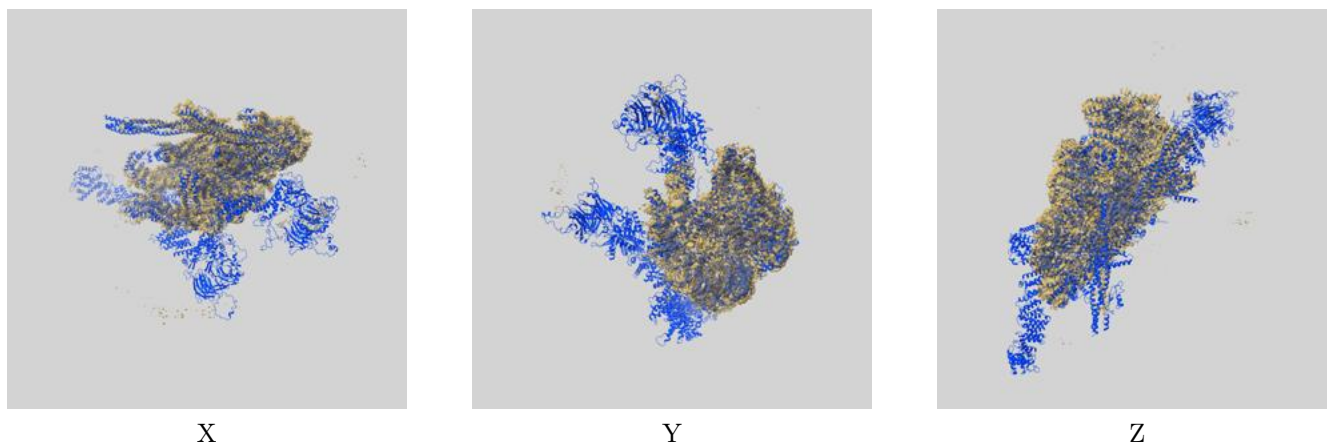
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

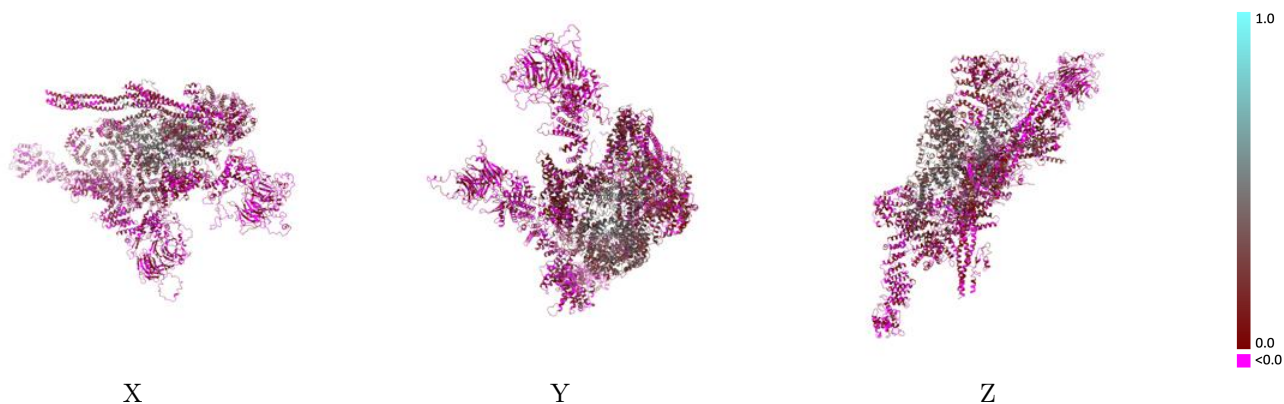
This section contains information regarding the fit between EMDB map EMD-32653 and PDB model 7WOO. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



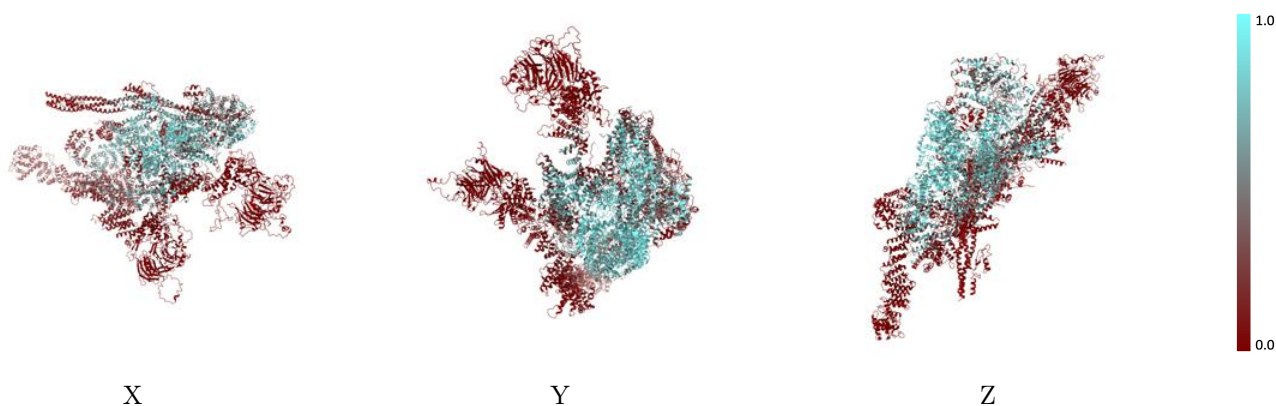
The images above show the 3D surface view of the map at the recommended contour level 0.24 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



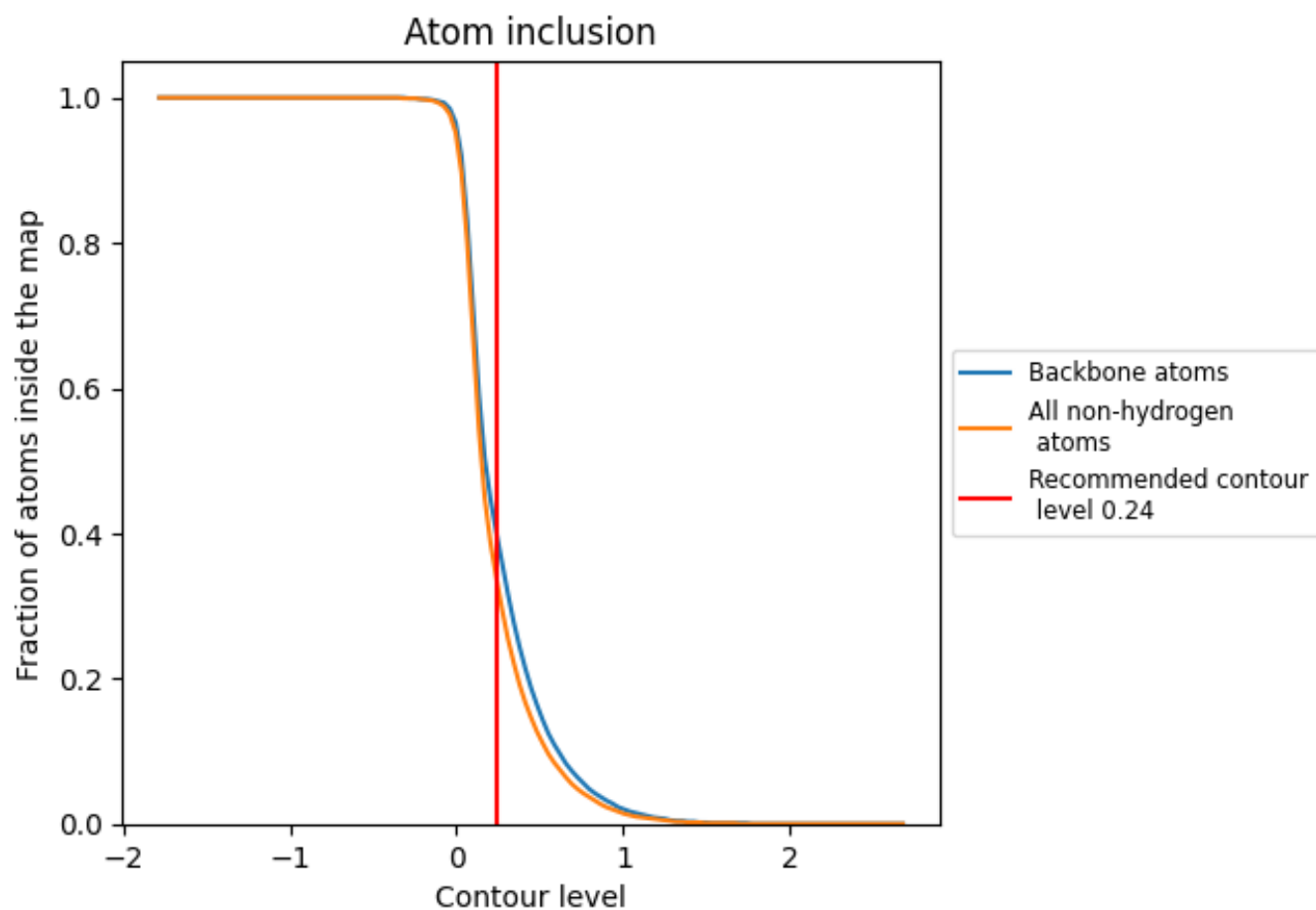
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

