



## wwPDB EM Validation Summary Report ⓘ

Nov 29, 2022 – 04:58 PM 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)

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

A user guide is available at

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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

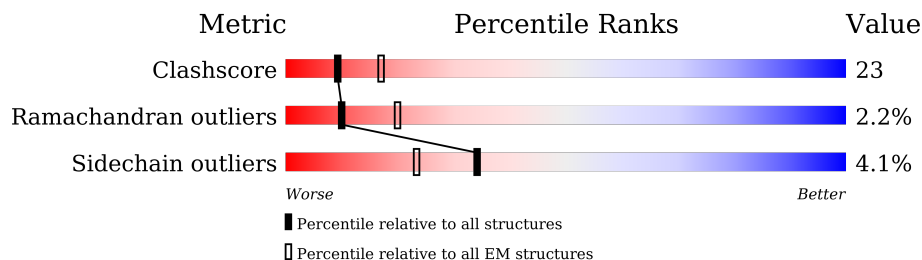
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.71 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  $\geq 3$ , 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	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">83%</div> </div>
1	Z	839	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">53%</div> </div>
2	C	1391	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">95%</div> </div>
3	D	1502	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">80%</div> </div>
4	E	1655	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">14%</div> </div>
5	F	1683	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">33%</div> </div>
6	G	472	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">24%</div> </div>
6	J	472	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">30%</div> </div>

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Mol	Chain	Length	Quality of chain
7	H	541	<p>28% 29% 14% 55%</p>
7	K	541	<p>34% 19% 23% 53%</p>
8	I	823	<p>10% 13% 7% 77%</p>
8	L	823	<p>14% 12% 10% 77%</p>

## 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.

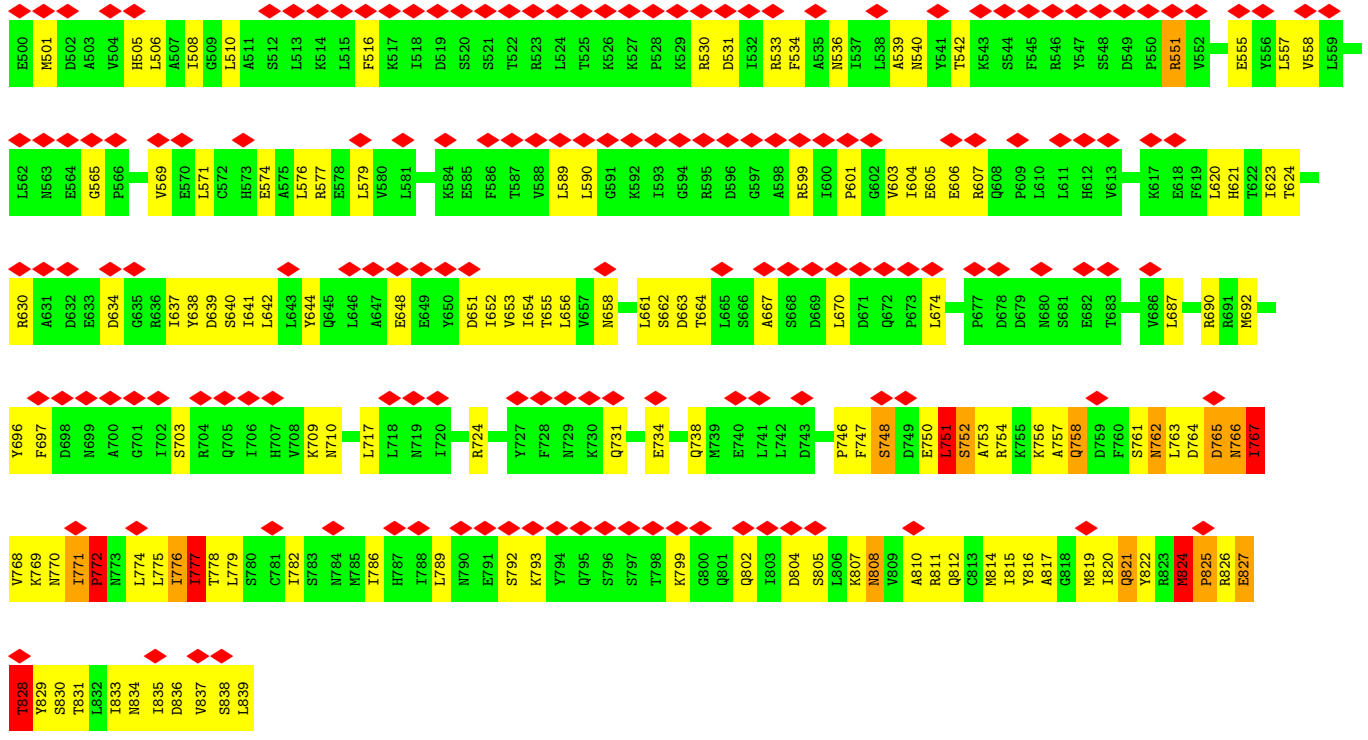
Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	246	Total	C	N	O	S	0	0
			1811	1128	332	348	3		
7	K	254	Total	C	N	O	S	0	0
			1808	1126	334	345	3		

- Molecule 8 is a protein called Nucleoporin NSP1.

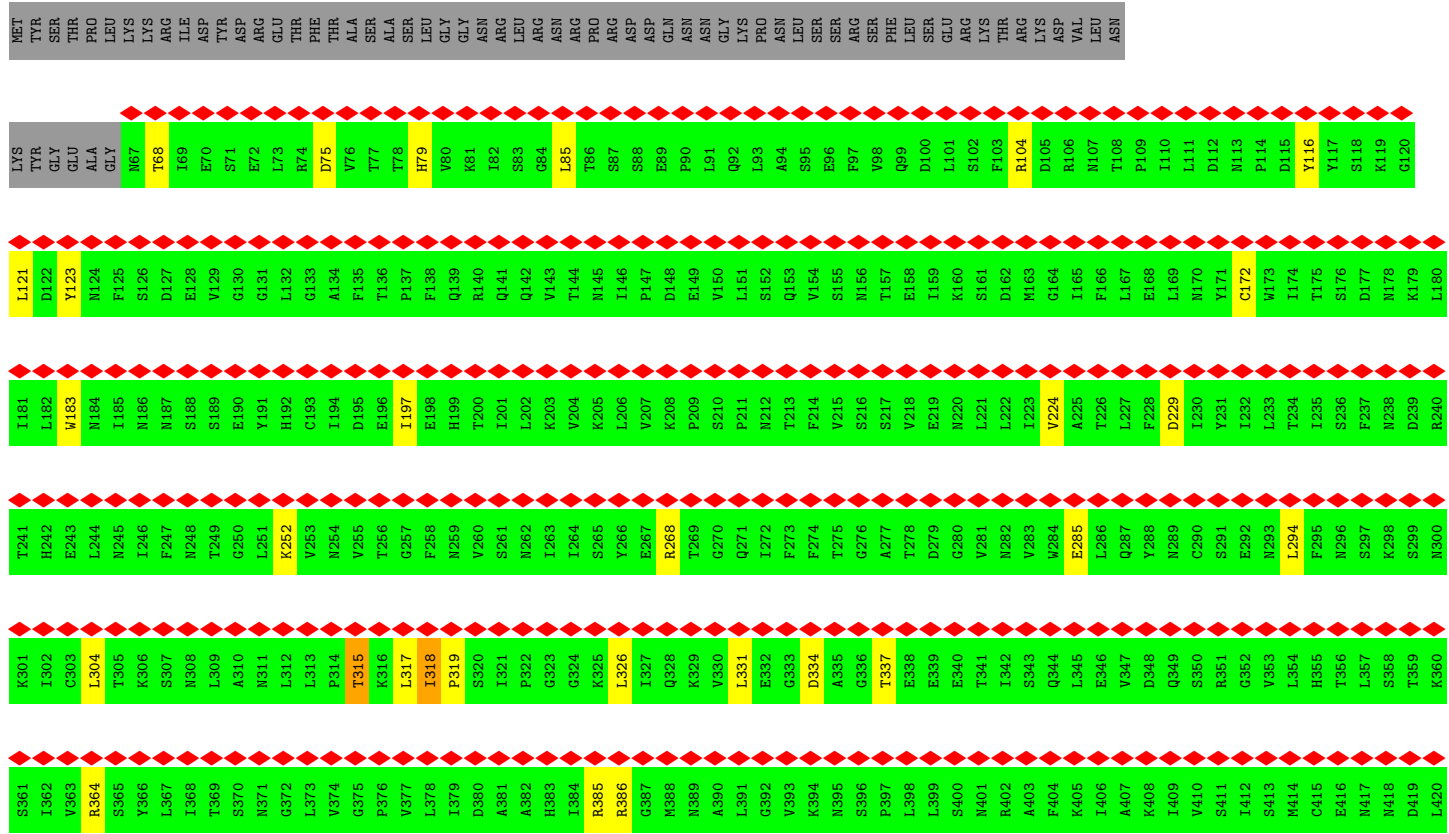
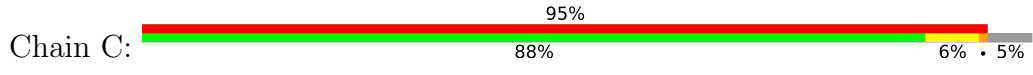
Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	187	Total	C	N	O	S	0	0
			1418	862	244	311	1		
8	L	187	Total	C	N	O	S	0	0
			1366	830	240	295	1		







• Molecule 2: Nucleoporin NUP157

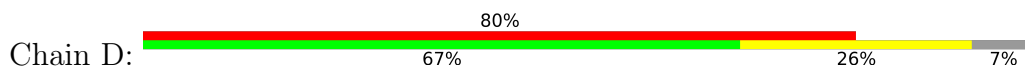




C1141	L1081	I1021	P961	I901	R841	G781	S721	A661	V601	S541	G481	F421
D1142	P1082	E1022	K962	L902	E842	S782	Q722	L662	A602	A542	P482	L422
S1143	Y1083	Q1023	T963	C903	Y843	M783	I723	A663	V603	P443	L483	A423
S1144	L1084	S1024	V964	Y904	F844	A784	M724	F664	L604	D544	S484	V424
T1145	K1085	P1025	G965	R905	F845	I785	E725	F665	T605	G545	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	R969	L910	H850	A790	F730	P670	E610	N550	S490	V430
P1151	S1091	A971	D851	E911	D851	E791	F731	G671	I611	Y551	T491	R431
A1152	L1092	D972	L852	A912	L852	S792	K732	V672	B612	G552	Y492	L432
L1153	E1093	K973	F853	A913	F853	I793	R733	E673	C613	K553	I493	Y433
V1154	I1094	I974	T854	Q914	T854	A794	A734	B674	B614	K554	I494	F434
Q1155	S1095	D975	P855	K915	P855	M795	S735	I675	R615	V555	T495	K435
N1096	N1096	K976	R856	F916	R856	M796	K736	K676	T616	E556	T496	G436
S1157	L1097	G977	A857	E917	A857	A797	T737	P677	P617	N557	C497	S437
E1158	N1098	N878	K858	M918	K858	L798	E738	K678	D618	T558	A498	I438
M1159	W1099	Q979	T859	I919	T859	I799	K739	S679	E619	A559	S499	S439
I1160	F1100	A980	K860	D920	K860	L800	M740	S680	V620	L560	T500	R440
H1161	Y1101	Q981	L861	S921	L861	L801	D741	R681	F621	L561	I501	R441
E1162	L1102	E982	L862	K922	L862	I802	A742	E682	E622	D562	I502	S442
L1163	F1103	Y983	I863	I923	I863	M803	F743	S883	S623	T563	S503	I443
F1164	K1104	V984	K864	S924	K864	S804	G744	G684	L624	T564	P504	G444
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I1166	N1106	R986	L866	N926	L866	K806	S746	V686	E626	E566	I506	L446
A1167	H1107	G987	L867	H927	L867	D807	I747	P687	M627	I567	Y507	K447
S1168	F1108	C988	L868	L928	L868	A808	T748	P688	P628	F508	F508	L448
L1169	L1109	N989	E869	D929	E869	L809	R749	I689	L629	E569	T509	D449
Q1170	E1110	S1050	V670	T930	V670	S810	P750	S690	P630	I570	C510	S450
D1171	A1111	M1051	V671	A931	V671	L811	Q751	Q891	F631	V571	V511	V451
D1172	A1112	N1052	N872	I932	N872	I812	V752	N692	I632	P572	R512	K452
L1173	D1113	R1053	A873	D933	A873	M813	E753	L693	H633	L573	K513	F453
L1174	V1114	F1054	N874	L934	N874	B614	V754	F694	S634	T574	R514	P454
M1175	L1115	K995	L875	Y835	L875	F615	Y755	D895	Y635	R575	A515	P455
L1176	Y1116	V996	A876	E936	A876	B616	L756	K696	G636	S576	N516	T456
F1177	A1117	Y1057	S877	R937	S877	E617	S757	S697	L637	F577	S457	S457
R1178	L1118	C1058	G878	C938	G878	D818	S758	E698	S638	N578	G518	I458
M1179	A1119	F1059	T879	A939	T879	I619	I759	E699	E639	Y579	E519	S459
E1180	S1120	Y1060	S880	E940	S880	D820	S760	C700	A640	T580	L520	S460
T1181	S1121	D1061	A881	N941	A881	A621	V761	D701	C641	S521	S461	S461
R1182	I1122	W1062	D882	I942	D882	F822	L762	G702	S642	K522	L462	L462
I1183	F1123	L1063	Y883	E943	Y883	K623	A763	I703	T643	P683	G523	E463
D1184	D1124	V1064	L884	L944	L884	S824	D764	V704	A644	Q584	I524	Q464
E1185	L1125	A1065	V885	C945	V885	L825	F765	L705	L645	G585	T525	N465
L1186	K1126	T1006	N886	E946	N886	L826	F766	S706	L646	N526	N526	K466
Y1187	L1127	K1067	V887	L947	V887	M827	M767	F707	L647	A67	K527	S467
R1188	S1128	R1068	L888	R948	L888	T828	I768	R708	A648	N588	A528	F468
K1189	F1009	Q1069	K889	R949	K889	L829	H769	F709	C649	N589	L529	I469
Q1190	E1010	D1070	E990	V950	E990	M830	R770	Y709	K649	F590	L530	L469
L1191	I1011	Y1071	R891	N951	R891	G631	F771	G711	F651	A591	E531	G471
T1192	V1012	L1072	F892	D952	F892	A832	S772	S712	N652	S192	N532	H472
L1193	L1073	L1073	G893	I953	G893	G633	F773	A713	K653	Q593	K533	H473
K1194	S1014	R1074	S894	M954	S894	G634	V774	L714	S654	Y594	E534	P474
L1195	A1135	L1075	F895	N955	F895	B635	S775	L715	E555	S595	E535	L475
M1196	D1016	D1076	C956	K956	C956	B636	F776	I716	H656	A596	H536	L475
G1197	L1017	S1077	H897	L957	H897	D637	V777	T717	I657	E597	K537	M476
R1198	A1138	Q1078	S898	N958	S898	S638	P778	R718	I658	E598	T477	H477
V1199	G1139	F1079	A899	Y959	A899	K639	P779	L719	S659	L599	Y539	D479
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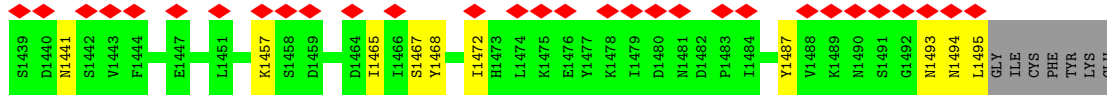
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L1205	I1265	S1325	R1385
F1206	S1266	S1326	D1386
N1207	N1267	N1327	H1387
D1208	T1268	I1328	H1388
C1209	L1269	I1329	G1389
A1210	I1270	E1330	L1390
D1211	R1271	M1331	K1391
P1212	I1272	S1332	
L1213	G1273	E1333	
D1214	K1274	G1334	
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Y1216	T1276	V1336	
E1217	T1277	E1337	
I1218	D1278	L1338	
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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	
V1254	A1314	P1374	
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V1256	V1316	T1376	
G1257	S1317	D1377	
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● Molecule 3: Nucleoporin NUP170

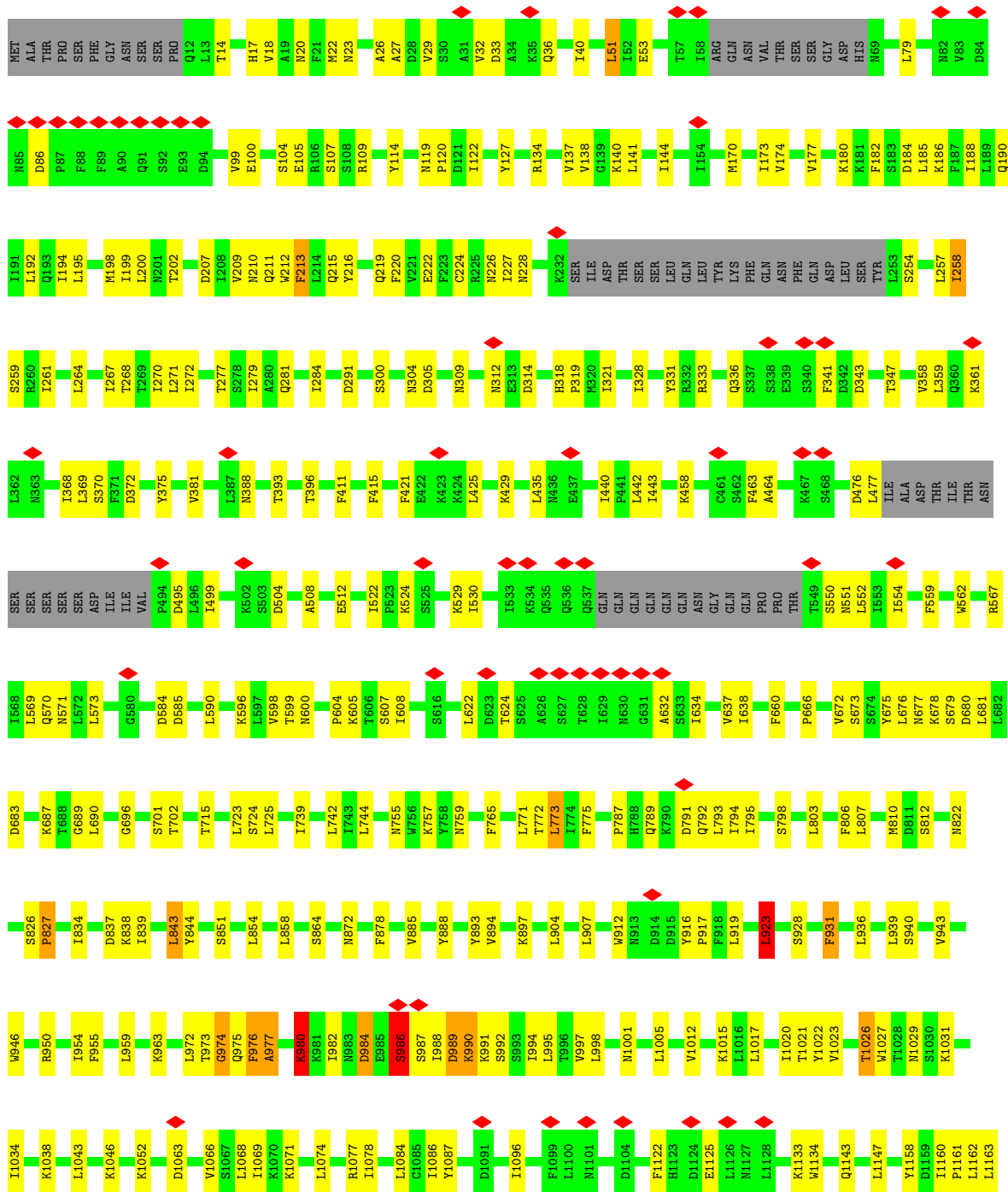


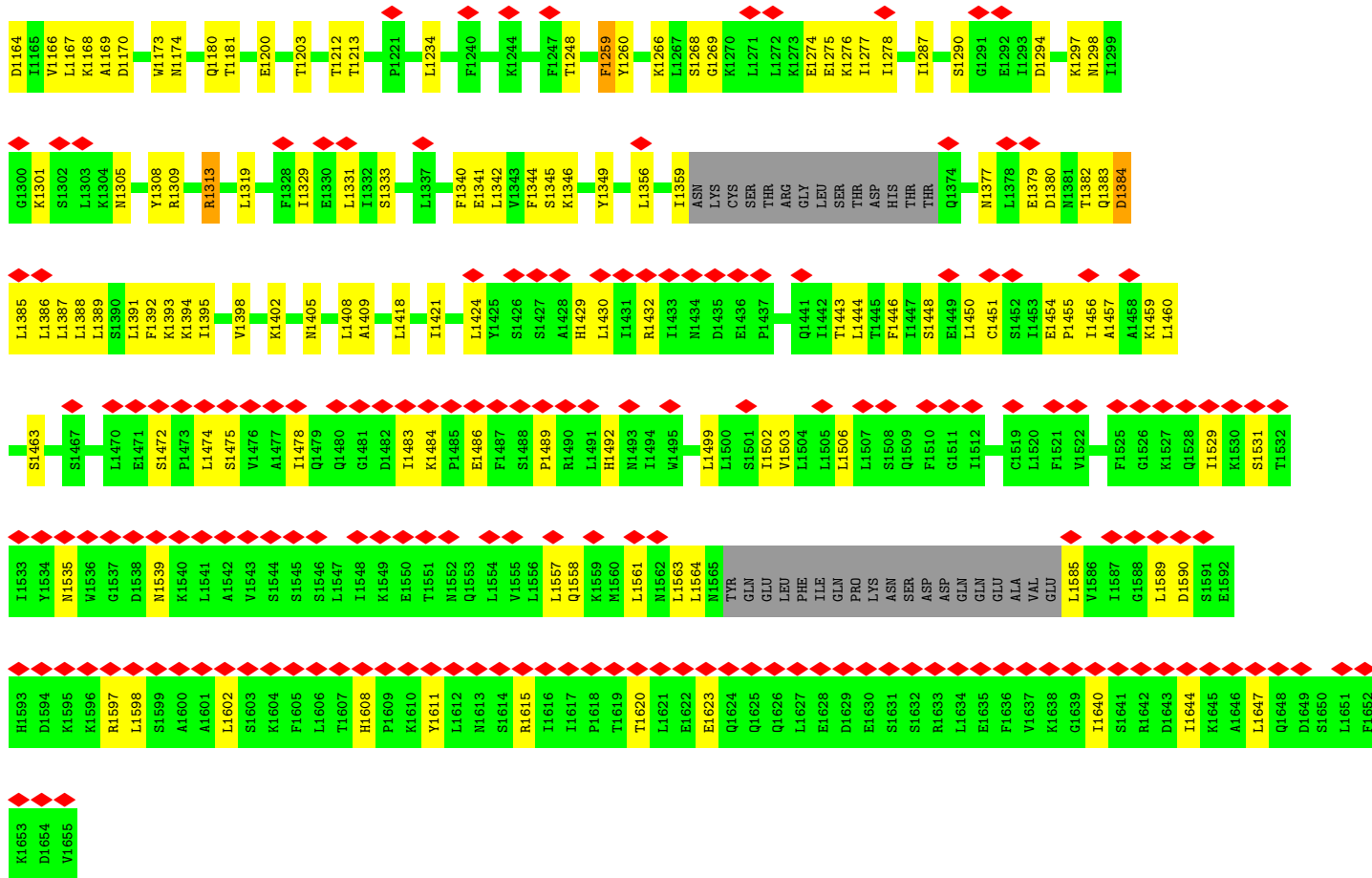
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GLN	SER	E123	W183	F243	D303	Q363	I423	H483
SER	ASN	R124	I184	A244	W304	Q364	S424	Q484
PRO	LEU	S125	T185	I245	F305	R365	S425	Q485
PHE	MET	Y126	I186	S246	N306	G366	V426	Q486
HIS	ARG	Y127	D187	L247	S307	I367	A427	E487
ASN	ALA	N128	N188	D248	K308	I368	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
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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	I338	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	I402	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	K1144	S1237	R1238	S1145	Y1146	E1147	F1242	C1243	A1149	L1150	K1151	V1246	Q1378	Q1379	D1380	S1381	E1382	F1388	E1389	L1390	F1391	F1392	I1393	V1394	C1395	M1396	F1397	F1398	I1399	E1400	T1401	L1402	P1403	K1404	E1405	H1406	I1407	S1409	G1410	S1411	T1418	A1419	G1420	V1421	S1422	F1423	M1426	I1429	L1430	K1431	E1432	L1433	I1434	E1435	T1436	S1437	D1438	Y1083	V1084	A1085	M1086	G1087	F1088	L1089	E1090	M1091	D1092	D1093	R1094	L1249	S1250	Q1251	K1252	R1254	I1255	M1161	Y1162	V1166	M1169	R1170	E1171	E1172	K1173	L1174	L1175	D1176	K1114	V1115	D1116	E1117	L1118	A1119	E1120	K1121	K1122	Q1123	S1124	S1125	K1126	T1127	Q1128	M1129	Q1130	I1131	S1132	I1133	S1134	M1135	D1136	D1137	E1138	V1139	K1140	L1141	R1142	Y1021	D1022	S1023	L1024	M1025	Y1026	H1027	L1028	K1029	M1030	A1031	T1032	A1033	L1034	L1035	E1036	Q1037	I1038	V1039	D1040	D1041	L1042	S1043	I1044	E1045	K1046	A987	L988	Q989	E990	R991	C992	G993	S994	F995	C996	S997	A998	S999	D1000	I1001	L1002	G1003	F1004	R1005	A1006	I1007	E1008	H1009	L1010	R1011	R1012	A1013	K1014	E1015	I1016	G1017	L1018	R1019	M1020	Q901	S902	I903	K904	E905	G906	L907	S908	F909	L910	M911	V912	L913	Y914	E915	E916	S917	E918	V919	E920	G921	F922	D923	N924	Q925	Y926	L927	G928	F929	K930	D931	I932	S933	S934	S935	V936	S937	L938	D939	V940	Q941	K942	D943	L944	V945	K946	L947	D948	F949	K950	D951	L952	F953	A954	P955	N956	D957	K958	T959	K960	Y841	Y842	L843	S844	E845	N846	N847	L848	L849	N850	E851	F852	F853	L854	T855	Y856	G857	D858	S859	I860	S861	Q862	I863	S864	A865	P866	Y867	V868	L869	A870	N871	N872	S873	N874	G875	R876	V877	I878	D879	K880	T881	E882	E883	V884	A885	N886	Q887	A888	S889	E890	I891	A892	I893	N894	A895	N896	I897	K898	M899	V900	Y781	Y782	S783	T784	W785	G786	R787	H788	F789	W790	M791	T792	F793	T794	D795	N796	R797	V798	T799	S800	H801	A802	F803	I804	S805	I745	S806	S807	D808	P809	I810	T811	S812	F813	A754	N815	N816	L817	E757	D758	F759	D820	E821	L761	I822	S823	Q824	N825	G826	N827	I828	I829	S830	K831	V832	S833	I834	S835	K836	T837	C838	I839	E840	D661	L662	I663	D664	N665	P666	P668	P669	V670	L671	S672	Y673	G674	A675	A676	E677	A678	C679	S680	T681	S681	P682	A682	L683	F684	A685	T686	C687	K688	S689	N690	K691	S692	E693	K694	L695	R696	S697	N698	A699	L700	T701	F702	L703	T704	M705	G706	I707	P708	G709	V710	V711	D712	I713	K714	P715	L716	Y717	N718	R719	Y720	L781	R782	D783	I784	W785	G786	R787	H788	F789	W790	M791	T792	F793	T794	D795	N796	R797	V798	T799	S800	H801	A802	F803	I804	S805	I745	S806	S807	D808	P809	I810	T811	S812	F813	A754	N815	N816	L817	E757	D758	F759	D820	E821	L761	I822	S823	Q824	N825	G826	N827	I828	I829	S830	K831	V832	S833	I834	S835	K836	T837	C838	I839	E840	Y641	Y642	L643	S644	E645	N646	N647	L648	L649	N650	E651	F652	F653	L654	T655	Y656	G657	D658	S659	I660	S661	Q662	I663	S664	A665	P666	Y667	V668	L669	A670	N671	N672	Y673	G674	A675	A676	E677	A678	C679	S680	T681	S681	P682	A682	L683	F684	A685	T686	C687	K688	S689	N690	K691	S692	E693	K694	L695	R696	S697	N698	A699	L700	T701	F702	L703	T704	M705	G706	I707	P708	G709	V710	V711	D712	I713	K714	P715	L716	Y717	N718	R719	Y720	L781	R782	D783	I784	W785	G786	R787	H788	F789	W790	M791	T792	F793	T794	D795	N796	R797	V798	T799	S800	H801	A802	F803	I804	S805	I745	S806	S807	D808	P809	I810	T811	S812	F813	A754	N815	N816	L817	E757	D758	F759	D820	E821	L761	I822	S823	Q824	N825	G826	N827	I828	I829	S830	K831	V832	S833	I834	S835	K836	T837	C838	I839	E840	Y841	Y842	L843	S844	E845	N846	N847	L848	L849	N850	E851	F852	F853	L854	T855	Y856	G857	D858	S859	I860	S861	Q862	I863	S864	A865	P866	Y867	V868	L869	A870	N871	N872	S873	N874	G875	R876	V877	I878	D879	K880	T881	E882	E883	V884	A885	N886	Q887	A888	S889	E890	I891	A892	I893	N894	A895	N896	I897	K898	M899	V900	Y541	Y542	L543	S544	E545	N546	N547	L548	L549	N550	E551	F552	F553	L554	T555	Y556	G557	D558	S559	I560	S561	Q562	I563	S564	A565	P566	Y567	V568	L569	A570	N571	N572	Y573	G574	A575	A576	E577	A578	C579	S580	T581	S581	P582	A582	L583	F584	A585	T586	C587	K588	S589	N590	K591	S592	E593	K594	L595	R596	S597	N598	A599	L600	T601	F602	L603	T604	M605	G606	I607	P608	G609	V610	V611	D612	I613	K614	P615	L616	Y617	N618	R619	Y620	L641	R642	D643	W644	N645	G646	R647	H648	F649	W650	M651	T652	F653	T654	D655	N656	R657	V658	T659	C660	D661	L662	I663	D664	N665	P666	P668	P669	V670	L671	S672	Y673	G674	A675	A676	E677	A678	C679	S680	T681	S681	P682	A682	L683	F684	A685	T686	C687	K688	S689	N690	K691	S692	E693	K694	L695	R696	S697	N698	A699	L700	T701	F702	L703	T704	M705	G706	I707	P708	G709	V710	V711	D712	I713	K714	P715	L716	Y717	N718	R719	Y720	L781	R782	D783	I784	W785	G786	R787	H788	F789	W790	M791	T792	F793	T794	D795	N796	R797	V798	T799	S800	H801	A802	F803	I804	S805	I745	S806	S807	D808	P809	I810	T811	S812	F813	A754	N815	N816	L817	E757	D758	F759	D820	E821	L761	I822	S823	Q824	N825	G826	N827	I828	I829	S830	K831	V832	S833	I834	S835	K836	T837	C838	I839	E840	Y841	Y842	L843	S844	E845	N846	N847	L848	L849	N850	E851	F852	F853	L854	T855	Y856	G857	D858	S859	I860	S861	Q862	I863	S864	A865	P866	Y867	V868	L869	A870	N871	N872	S873	N874	G875	R876	V877	I878	D879	K880	T881	E882	E883	V884	A885	N886	Q887	A888	S889	E890	I891	A892	I893	N894	A895	N896	I897	K898	M899	V900	Y641	Y642	L643	S644	E645	N646	N647	L648	L649	N650	E651	F652	F653	L654	T655	Y656	G657	D658	S659	I660	S661	Q662	I663	S664	A665	P666	Y667	V668	L669	A670	N671	N672	Y673	G674	A675	A676	E677	A678	C679	S680	T681	S681	P682	A682	L683	F684	A685	T686	C687	K688	S689	N690	K691	S692	E693	K694	L695	R696	S697	N698	A699	L700	T701	F702	L703	T704	M705	G706	I707	P708	G709	V710	V711	D712	I713	K714	P715	L716	Y717	N718	R719	Y720	L781	R782	D783	I784	W785	G786	R787	H788	F789	W790	M791	T792	F793	T794	D795	N796	R797	V798	T799	S800	H801	A802	F803	I804	S805	I745	S806	S807	D808	P809	I810	T811	S812	F813	A754	N815	N816	L817	E757	D758	F759	D820	E821	L761	I822	S823	Q824	N825	G826	N827	I828	I829	S830	K831	V832	S833	I834	S835	K836	T837	C838	I839	E840	Y841	Y842	L843	S844	E845	N846	N847	L848	L849	N850	E851	F852	F853	L854	T855	Y856	G857	D858	S859	I860	S861	Q862	I863	S864	A865	P866	Y867	V868	L869	A870	N871	N872	S873	N874	G875	R876	V877	I878	D879	K880	T881	E882	E883	V884	A885	N886	Q887	A888	S889	E890	I891	A892	I893	N894	A895	N896	I897	K898	M899	V900
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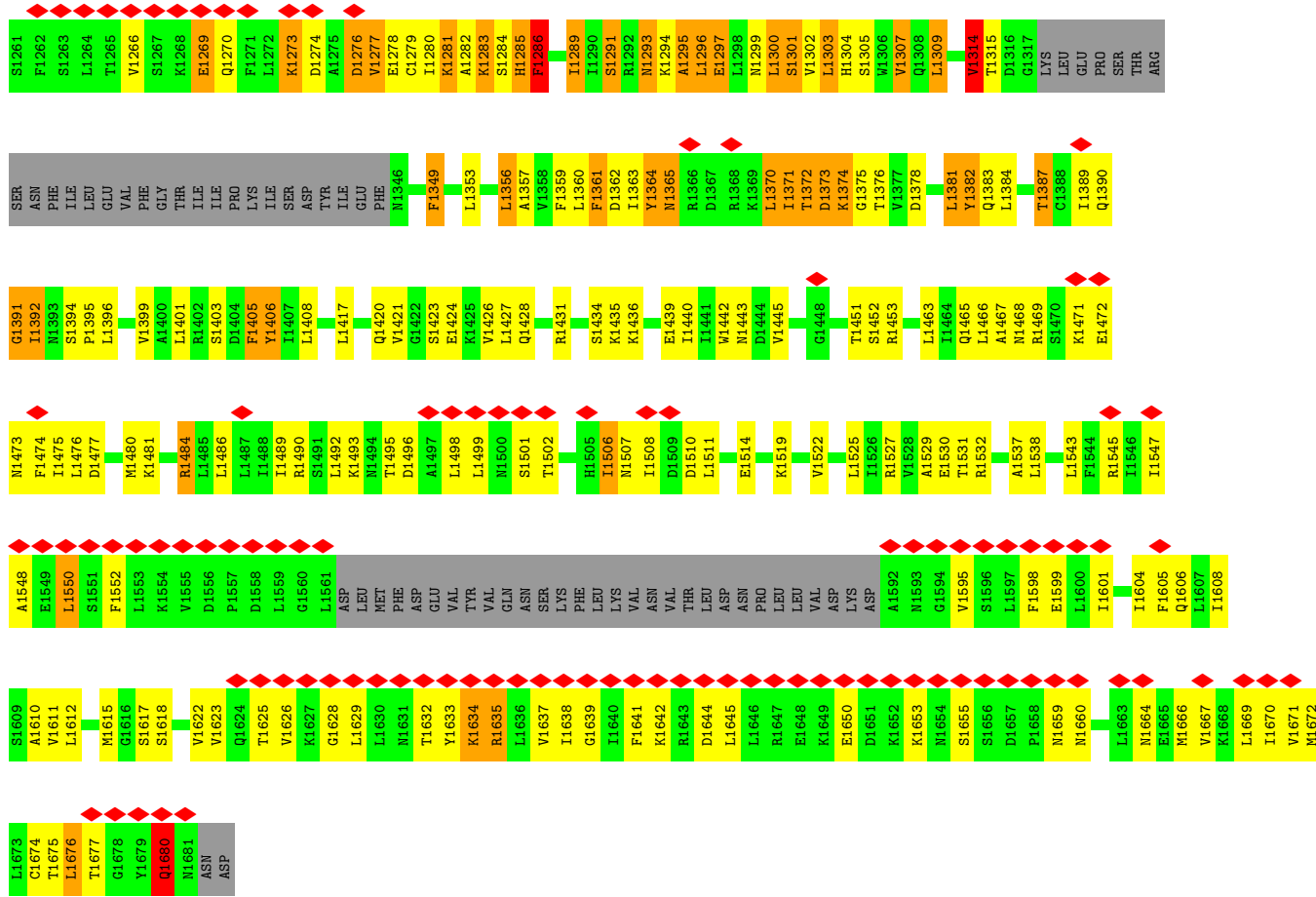


• Molecule 4: Nucleoporin NUP188

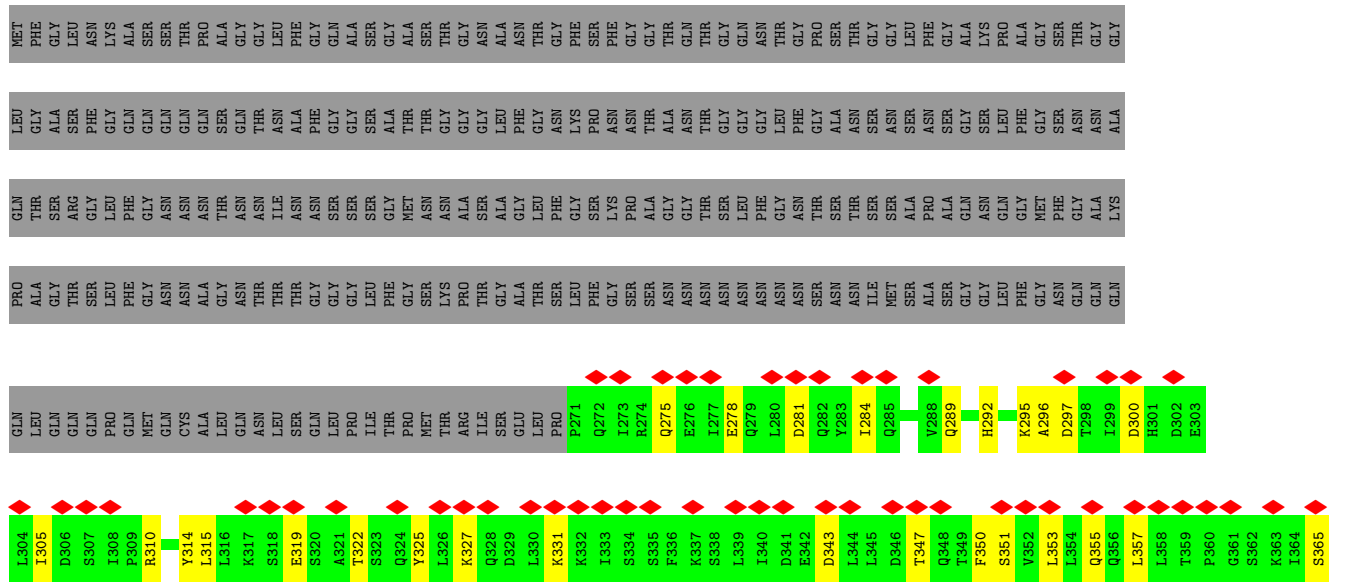
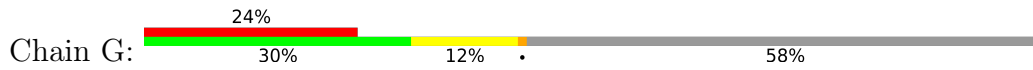








• Molecule 6: Nucleoporin NUP49/NSP49











E789	L721	K661	GLU	GLU	LYS	ASP	ALA	LYS	ALA	GLY	THR	ASN
M790	L722	I662	GLU	GLU	LYS	GLY	THR	LYS	PHE	GLY	THR	THR
I791	S723	M663	THR	THR	ASP	GLY	THR	ASN	ALA	THR	GLY	GLY
Q792	D724	S664	GLY	THR	GLY	GLY	GLY	ASP	PHE	GLY	THR	THR
L793	V725	W665	LYS	LYS	SER	ASP	GLY	ASP	ALA	ASP	ASP	ASN
I794	V726	D666	LYS	LYS	SER	ASP	GLY	ASP	ALA	ASP	ASP	ASN
K795	S727	Q667	THR	THR	ALA	ASP	GLY	GLY	PRO	LYS	PHE	LEU
I796	T728	W668	ALA	ALA	PHE	ASP	ALA	GLY	GLY	LYS	LYS	ASN
L797	S729	L669	ASP	ASP	THR	PRO	THR	ASP	GLY	GLY	THR	ASN
M798	S730	V670	VAL	VAL	PHE	ALA	ALA	LYS	GLY	LYS	GLY	THR
S799	S731	K671	LYS	LYS	THR	THR	THR	GLY	ASP	GLN	PRO	THR
H800	G731	K671	SER	SER	SER	SER	SER	ALA	ASP	PRO	ASP	ASN
F801	A732	G672	SER	SER	LYS	PHE	ALA	ALA	ASP	ASP	GLY	ASN
D802	A733	G673	ASP	ASP	LYS	THR	THR	PHE	LYS	ASP	GLY	ASN
A803	A734	E674	LEU	LEU	GLY	THR	THR	THR	ASN	PRO	PRO	ASN
L804	A734	Q675	LEU	LEU	LYS	LYS	LYS	PHE	ALA	THR	THR	THR
R805	N735	Q675	LYS	LYS	GLY	LYS	LYS	GLY	ALA	THR	THR	LYS
S806	N736	I676	LEU	LEU	GLU	ASN	ASN	ALA	PRO	GLY	PRO	PRO
L807	N737	S677	ASN	ASN	GLY	GLY	GLY	ALA	ALA	GLY	LEU	ASN
D808	D738	Q678	LYS	LYS	ASP	LYS	LYS	ALA	SER	VAL	GLY	ASN
D809	D738	L679	VAL	VAL	GLY	GLY	GLY	ALA	SER	PRO	GLY	ASN
T812	R741	Y680	GLY	GLY	LYS	LYS	LYS	ALA	ASP	ALA	LEU	ASN
K816	A744	S681	LEU	LEU	ALA	ALA	ALA	ALA	ASP	GLY	LEU	ASN
Q817	A744	D682	LYS	LYS	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
I818	T747	A683	PRO	PRO	ILE	ILE	ILE	ALA	ASP	GLY	LEU	ASN
N819	A748	V684	VAL	VAL	SER	PRO	PRO	ALA	ASP	GLY	LEU	ASN
S820	Q749	M685	SER	SER	PHE	ALA	ALA	ALA	ASP	GLY	LEU	ASN
I821	L750	A686	LEU	LEU	GLY	PHE	PHE	ALA	ASP	GLY	LEU	ASN
L822	L751	E687	ASP	ASP	ALA	ALA	ALA	ALA	ASP	GLY	LEU	ASN
K823	D752	H688	LYS	LYS	LYS	PHE	PHE	ALA	ASP	GLY	LEU	ASN
	L765	S689	THR	THR	GLY	GLY	GLY	ALA	ASP	GLY	LEU	ASN
	N756	Q690	THR	THR	GLN	GLY	GLY	ALA	ASP	GLY	LEU	ASN
	S759	M691	LYS	LYS	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	L762	K692	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	L765	I693	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	I766	D694	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	I767	Q695	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	E768	L697	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	I769	Q698	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	V772	Y699	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	S773	I700	THR	THR	PHE	ALA	ALA	ALA	ASP	GLY	LEU	ASN
	M774	E701	THR	THR	GLY	GLY	GLY	ALA	ASP	GLY	LEU	ASN
	T775	R702	THR	THR	ALA	ALA	ALA	ALA	ASP	GLY	LEU	ASN
	F776	Q703	THR	THR	GLN	GLN	GLN	ALA	ASP	GLY	LEU	ASN
	N777	Q704	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	K778	D705	THR	THR	ASP	ASP	ASP	ALA	ASP	GLY	LEU	ASN
	L779	E706	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	T780	L707	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	N781	E708	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	I782	N709	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	D783	F710	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	I784	L711	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	N785	D712	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	M786	L713	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	E787	F714	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
	D788	T715	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
		T716	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
		T717	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
		T718	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
		E719	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN
		A720	THR	THR	LYS	LYS	LYS	ALA	ASP	GLY	LEU	ASN

## 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 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

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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

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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	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

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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

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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.

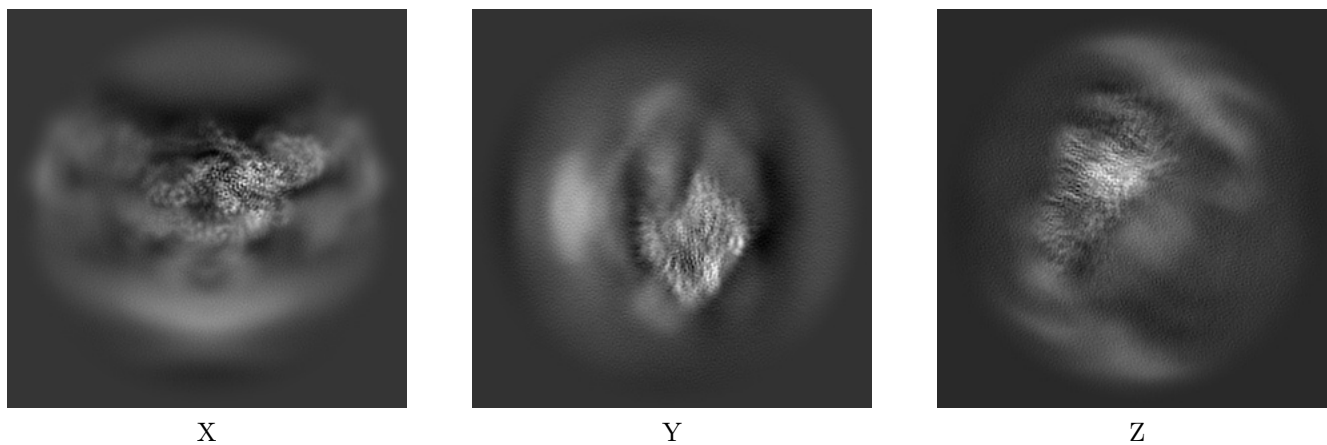
## 6 Map visualisation [i](#)

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](#)

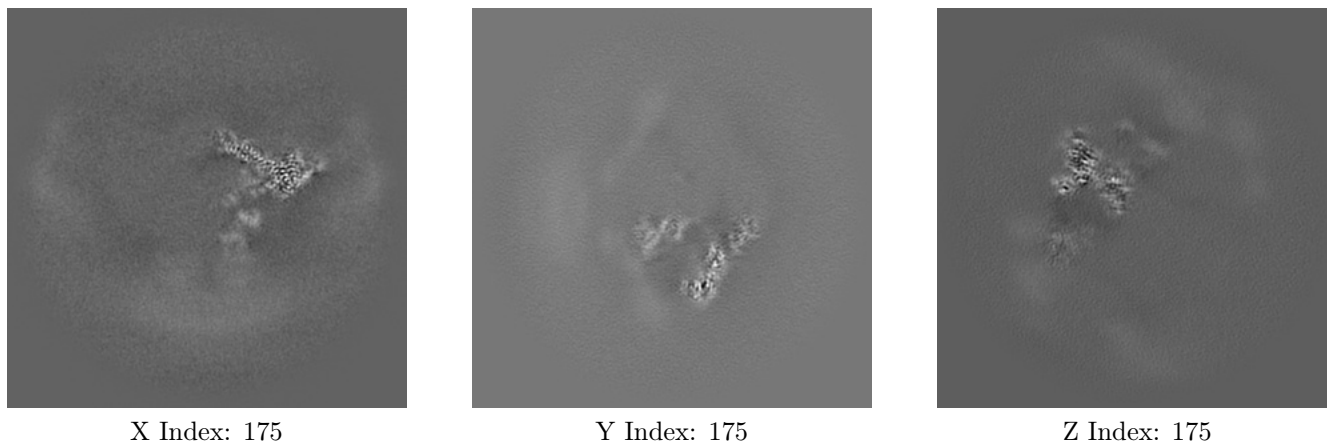
#### 6.1.1 Primary map



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

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

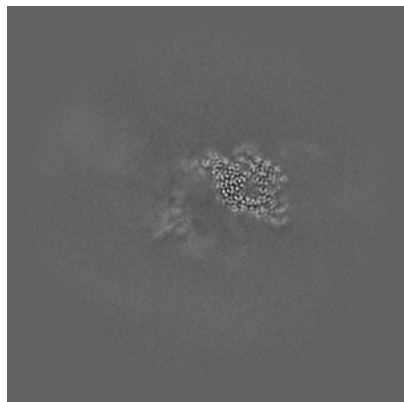
#### 6.2.1 Primary map



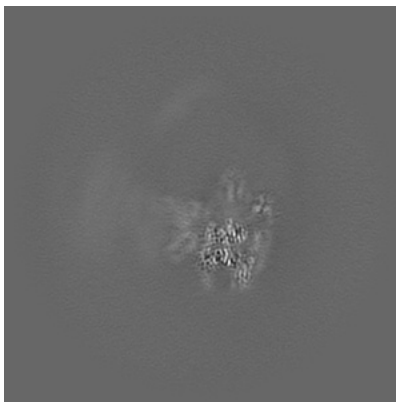
The images above show central slices of the map in three orthogonal directions.

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

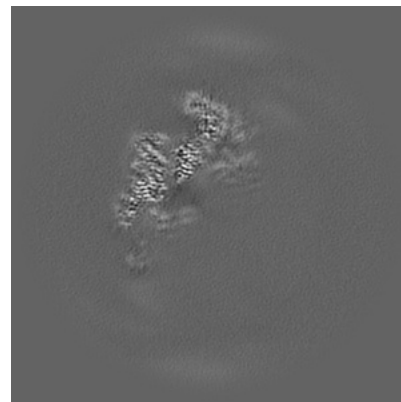
### 6.3.1 Primary map



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 surface views [i](#)

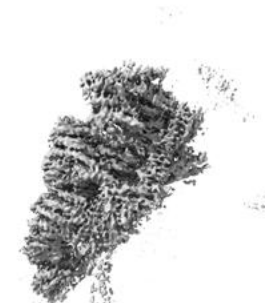
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.24. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

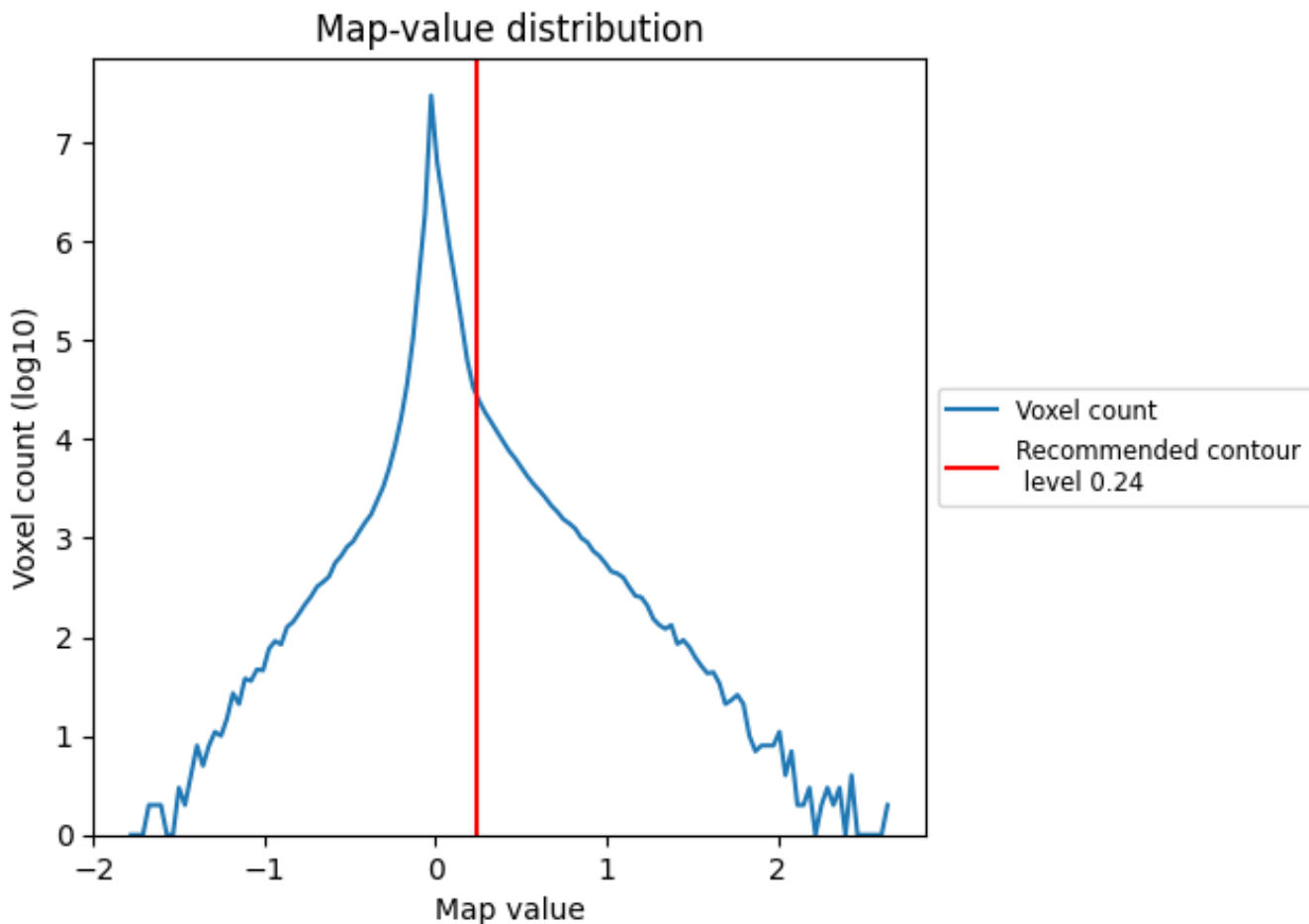
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

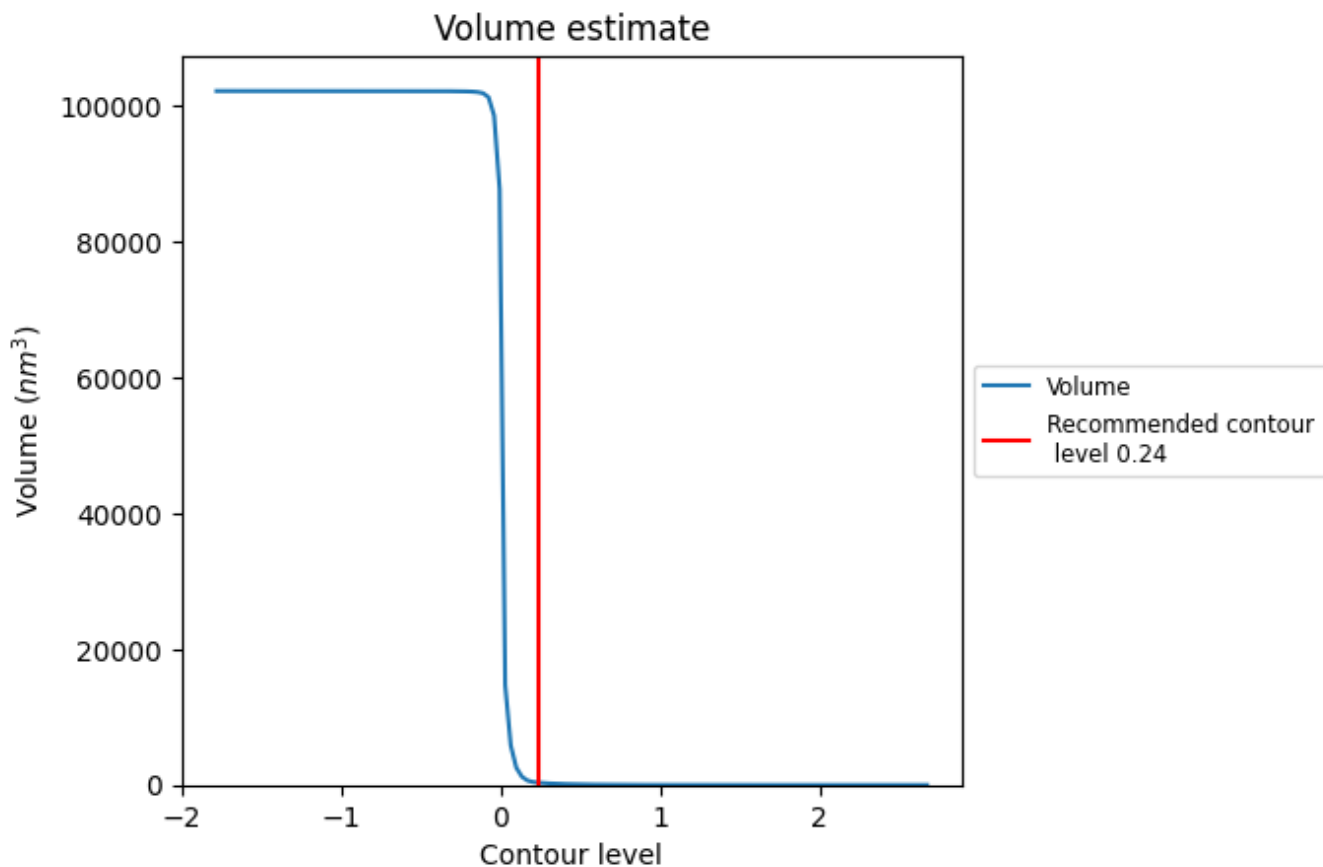
This section contains the results of statistical analysis of the map.

### 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.

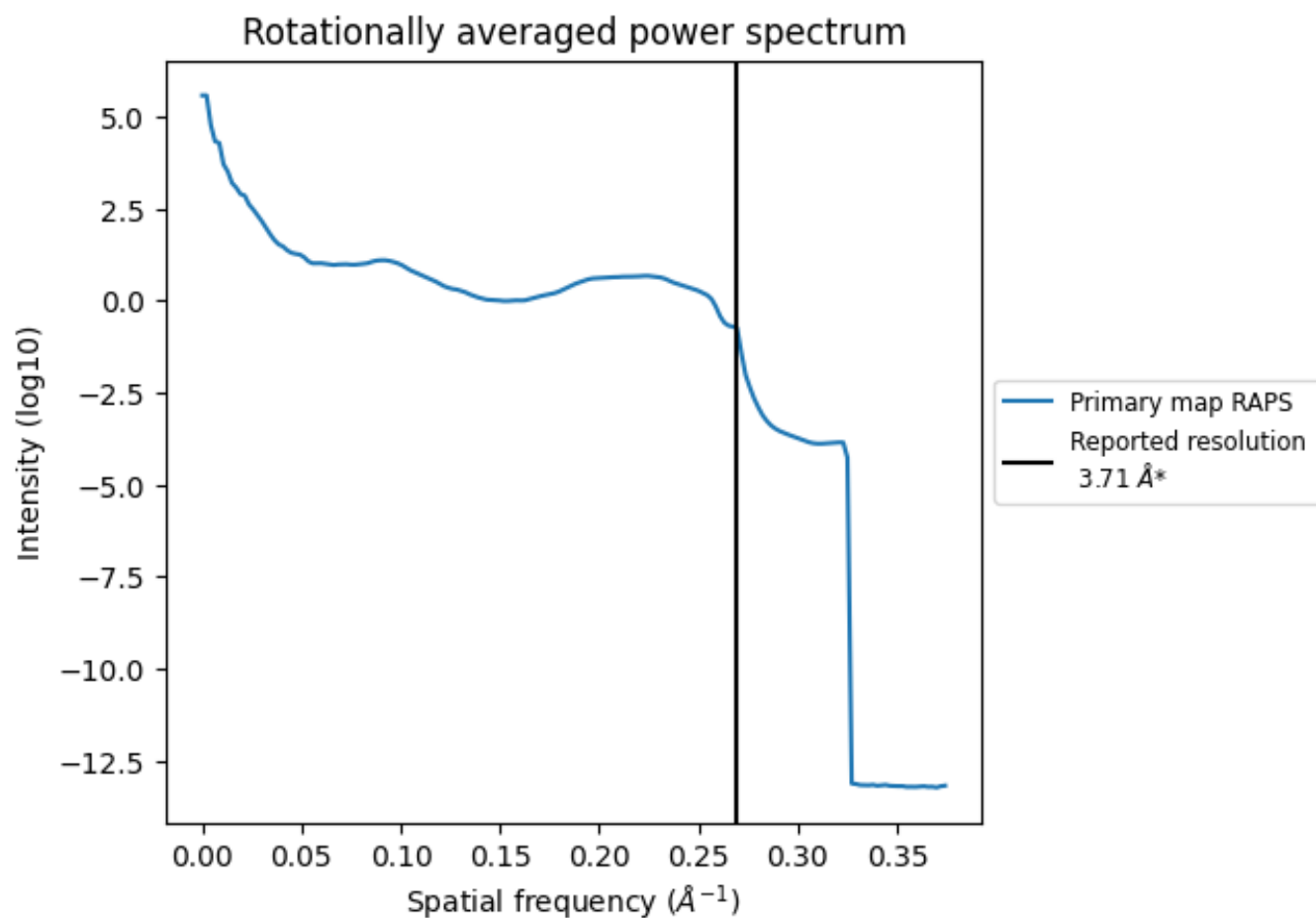
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 332  $\text{nm}^3$ ; 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 Å<sup>-1</sup>



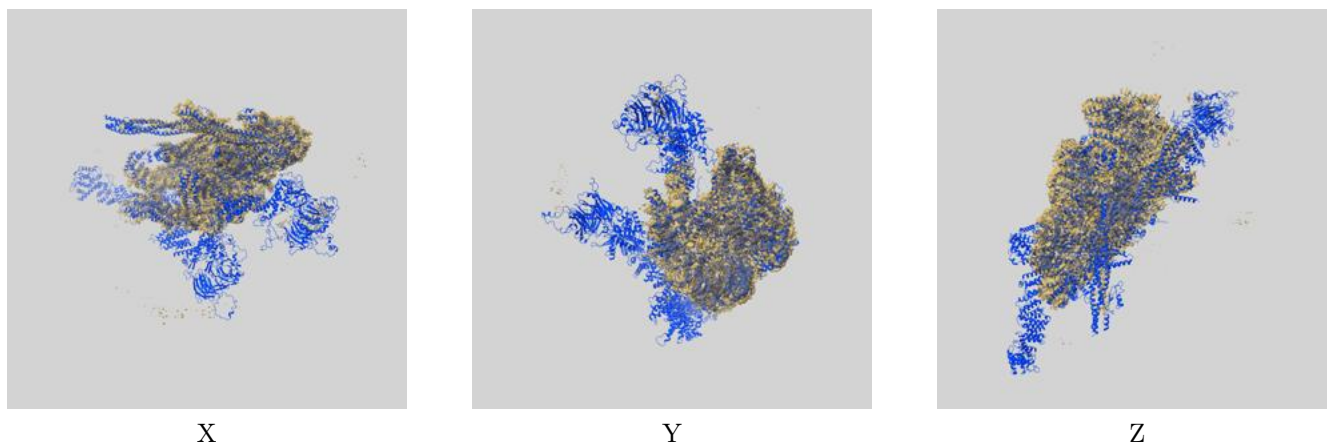
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

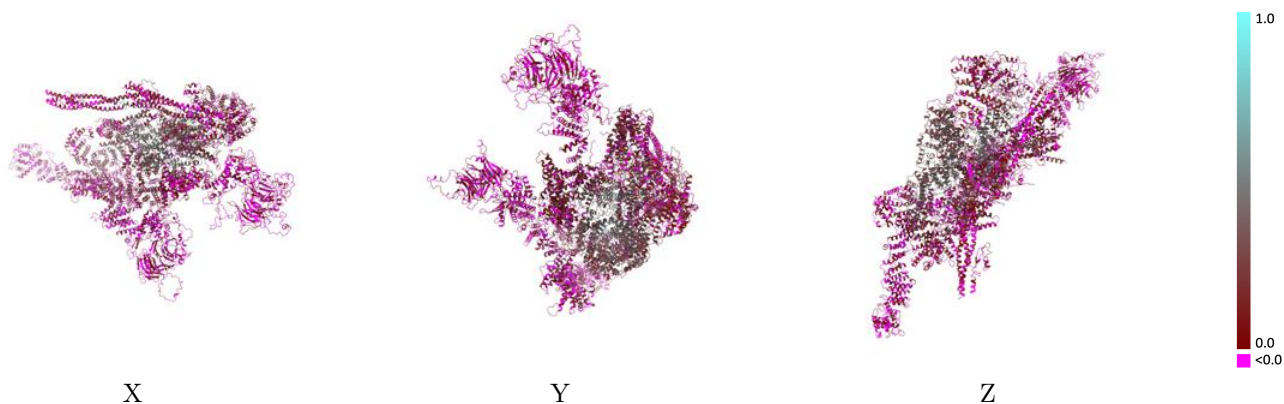
This section contains information regarding the fit between EMDB map EMD-32653 and PDB model 7WOO. Per-residue inclusion information can be found in section 3 on page 6.

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



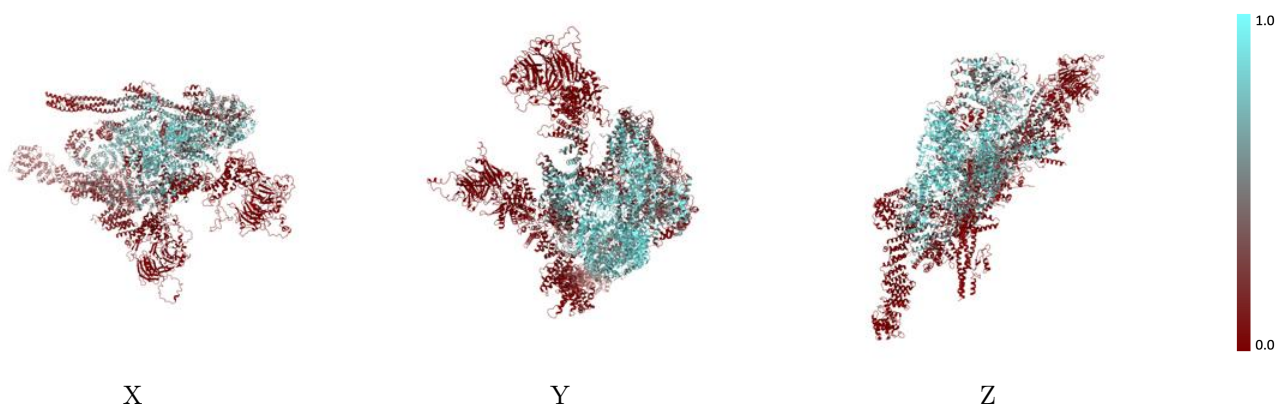
The images above show the 3D surface view of the map at the recommended contour level 0.24 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



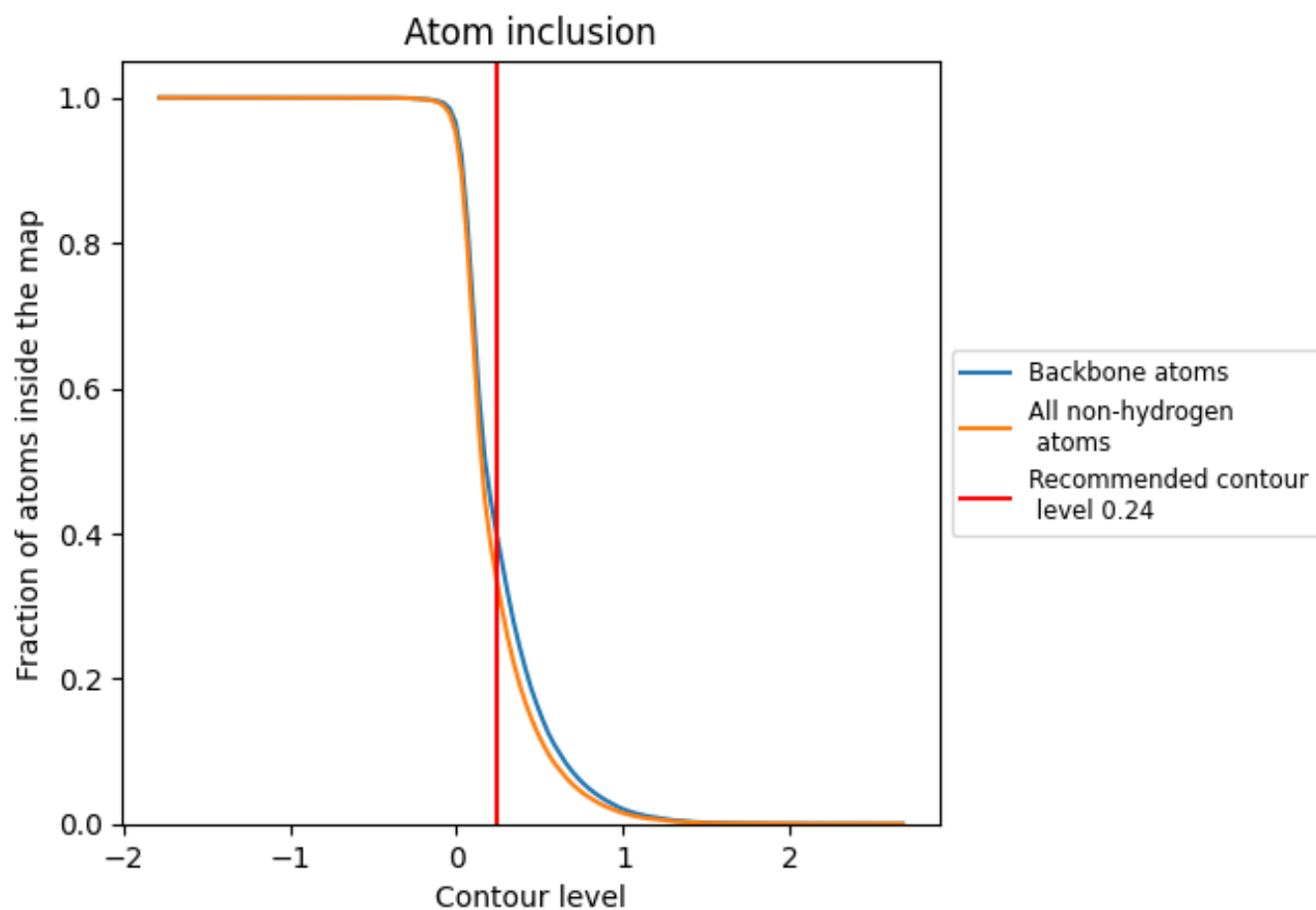
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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	 0.3366	 0.1340
A	 0.0352	 0.0150
C	 0.0006	 0.0220
D	 0.1244	 0.0320
E	 0.7097	 0.3120
F	 0.5687	 0.2180
G	 0.3909	 0.0730
H	 0.3423	 0.0980
I	 0.4901	 0.1220
J	 0.2858	 0.1480
K	 0.2424	 0.1210
L	 0.3038	 0.0820
Z	 0.3468	 0.1290

