



wwPDB EM Validation Summary Report ⓘ

Feb 14, 2024 – 12:28 AM EST

PDB ID : 3IYV
EMDB ID : EMD-5119
Title : Clathrin D6 coat as full-length Triskelions
Authors : Johnson, G.T.; Fotin, A.; Cheng, Y.; Sliz, P.; Grigorieff, N.; Harrison, S.C.;
Kirchhausen, T.; Walz, T.
Deposited on : 2010-06-17
Resolution : 7.90 Å (reported)
Based on initial models : 1BPO, 1B89

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.dev70
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) : 2.36

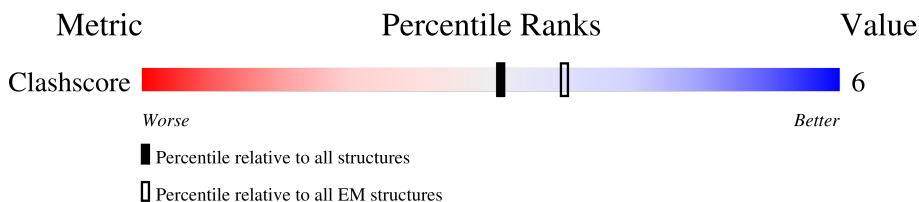
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

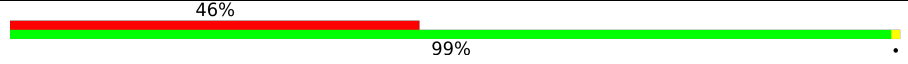
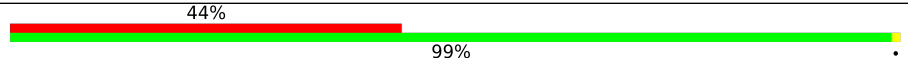
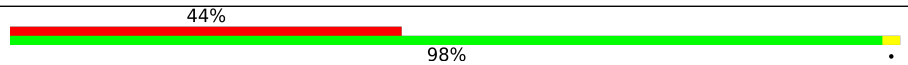
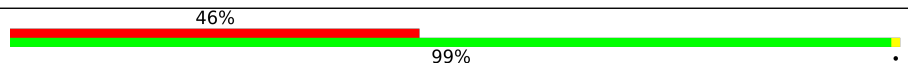
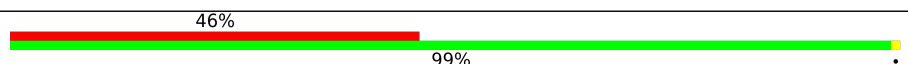
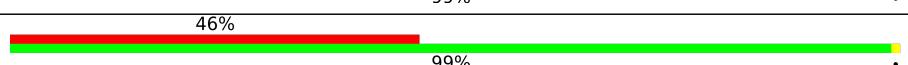
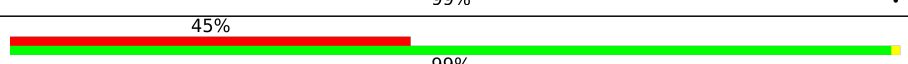
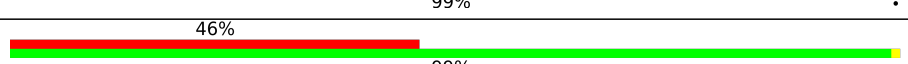
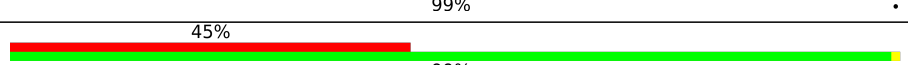
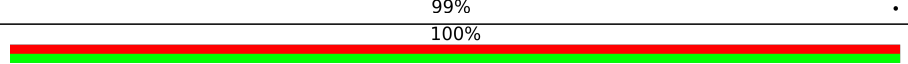
The reported resolution of this entry is 7.90 Å.

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

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	1630	 46% 99%
1	B	1630	 44% 99%
1	C	1630	 44% 98%
1	D	1630	 46% 99%
1	E	1630	 46% 99%
1	F	1630	 46% 99%
1	G	1630	 45% 99%
1	H	1630	 46% 99%
1	I	1630	 45% 99%
2	J	70	 100% 100%

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Mol	Chain	Length	Quality of chain
2	K	70	100% 100%
2	L	70	100% 100%
2	M	70	100% 100%
2	N	70	100% 100%
2	O	70	100% 100%
2	P	70	100% 100%
2	Q	70	100% 100%
2	R	70	100% 100%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 15300 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 Clathrin heavy chain.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	A	1630	Total C 1630 1630	0	1630
1	B	1630	Total C 1630 1630	0	1630
1	C	1630	Total C 1630 1630	0	1630
1	D	1630	Total C 1630 1630	0	1630
1	E	1630	Total C 1630 1630	0	1630
1	F	1630	Total C 1630 1630	0	1630
1	G	1630	Total C 1630 1630	0	1630
1	H	1630	Total C 1630 1630	0	1630
1	I	1630	Total C 1630 1630	0	1630

- Molecule 2 is a protein called Clathrin light chain A.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	J	70	Total C 70 70	0	70
2	K	70	Total C 70 70	0	70
2	L	70	Total C 70 70	0	70
2	M	70	Total C 70 70	0	70
2	N	70	Total C 70 70	0	70
2	O	70	Total C 70 70	0	70

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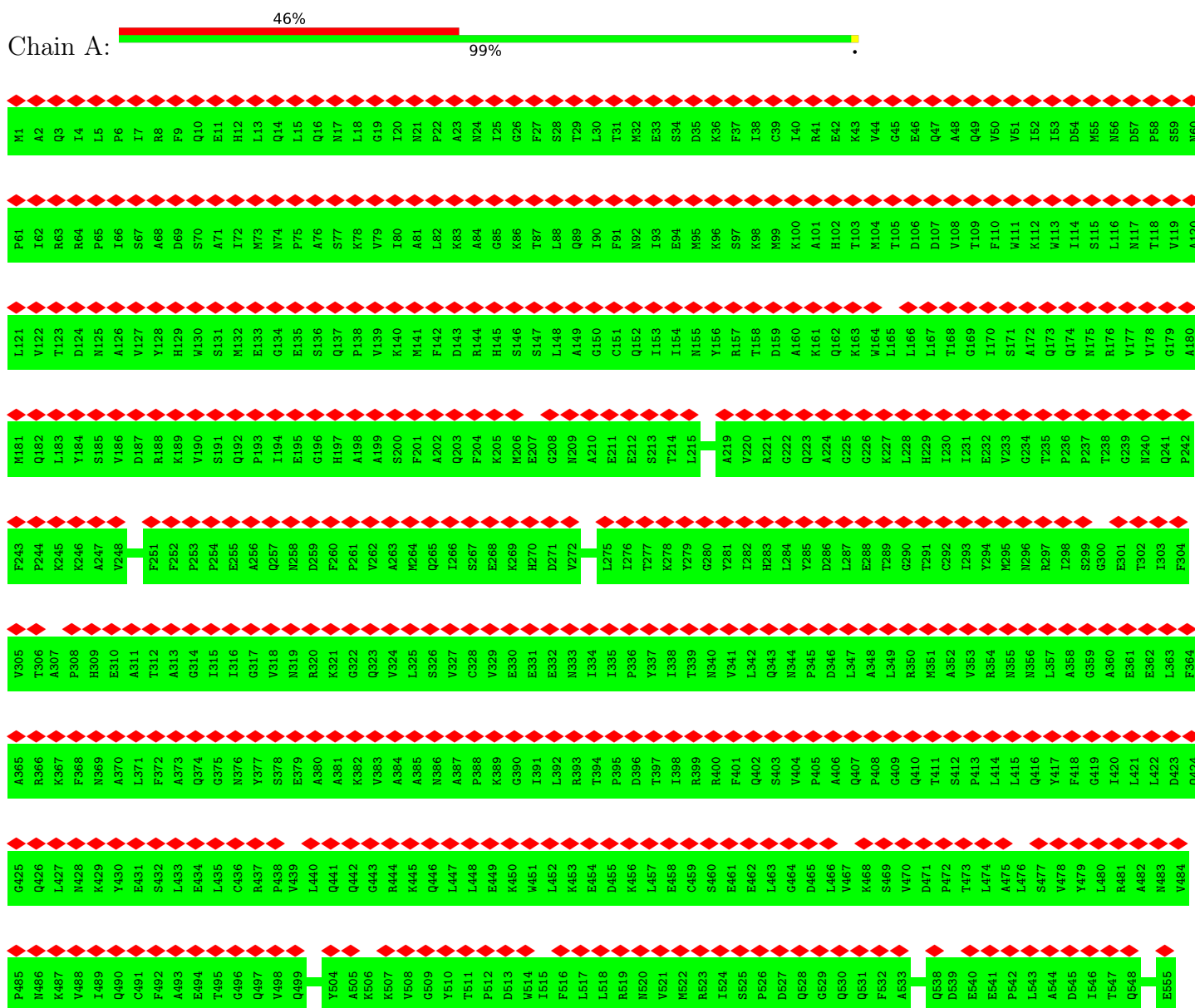
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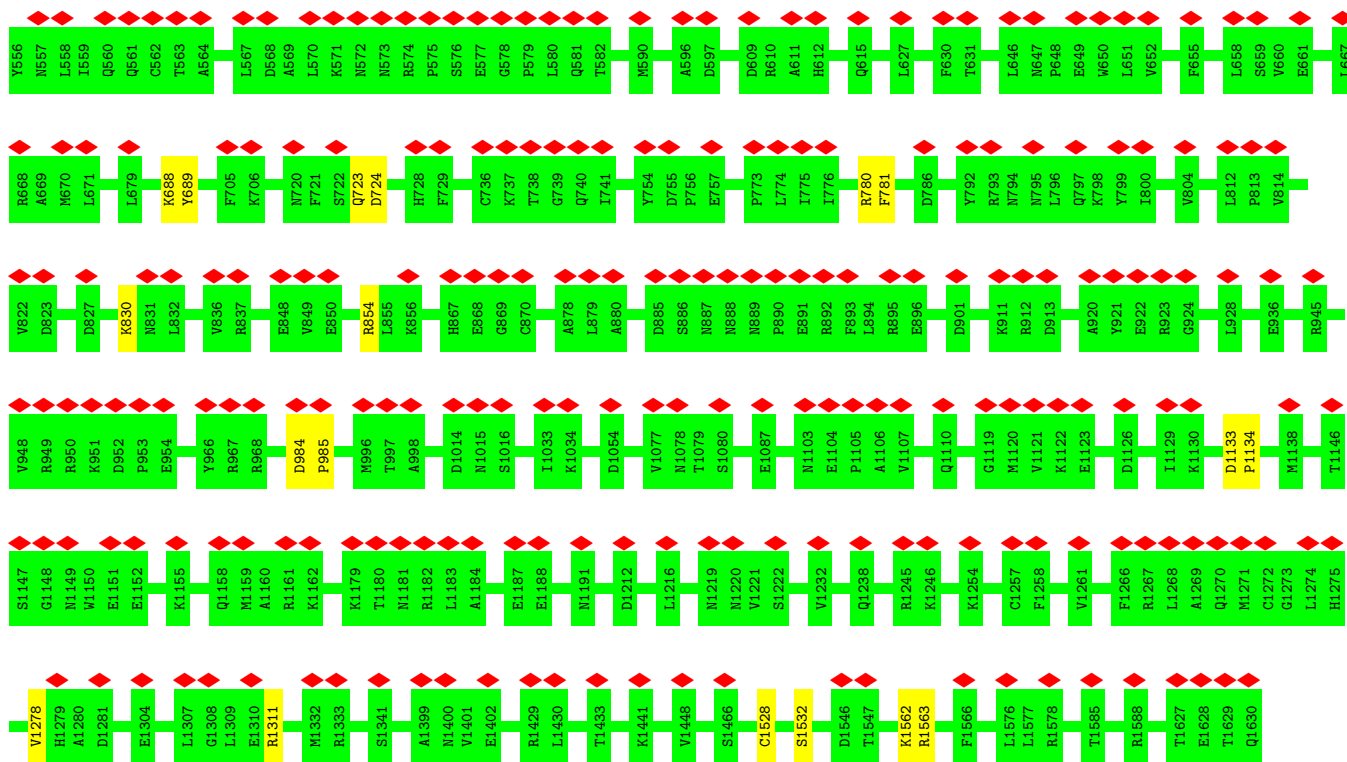
Mol	Chain	Residues	Atoms	AltConf	Trace
2	P	70	Total C 70 70	0	70
2	Q	70	Total C 70 70	0	70
2	R	70	Total C 70 70	0	70

3 Residue-property plots

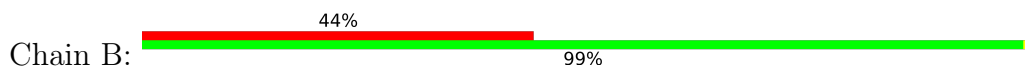
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

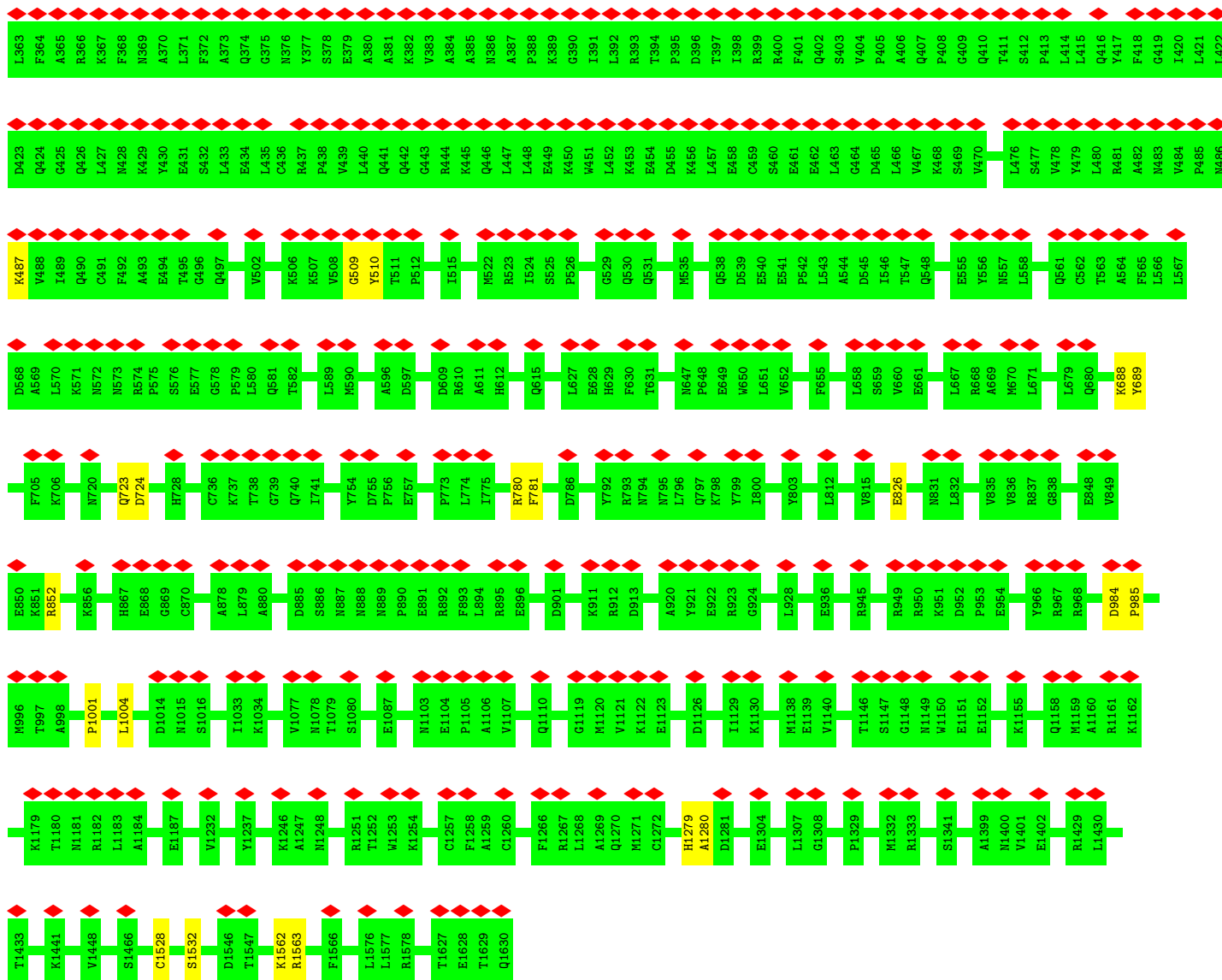
- Molecule 1: Clathrin heavy chain



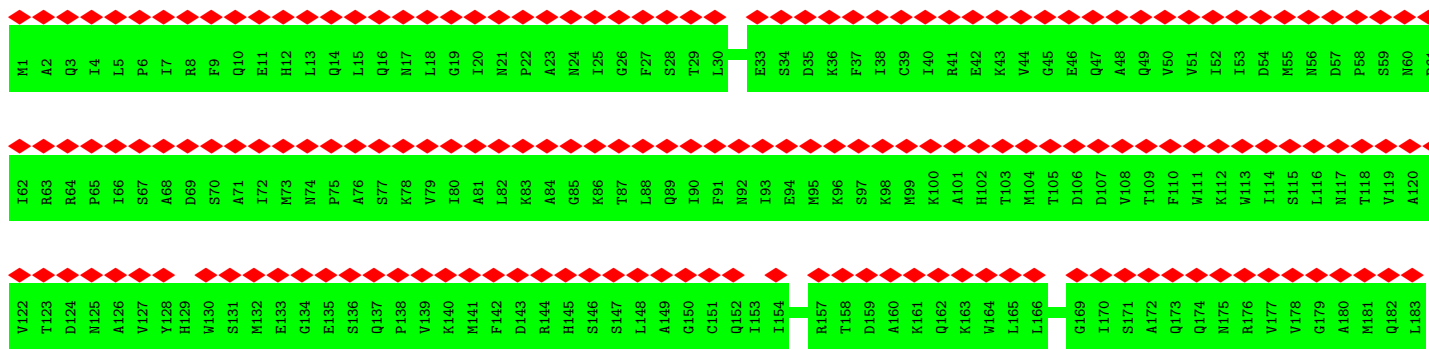
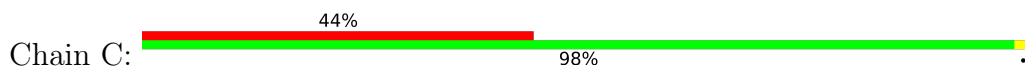


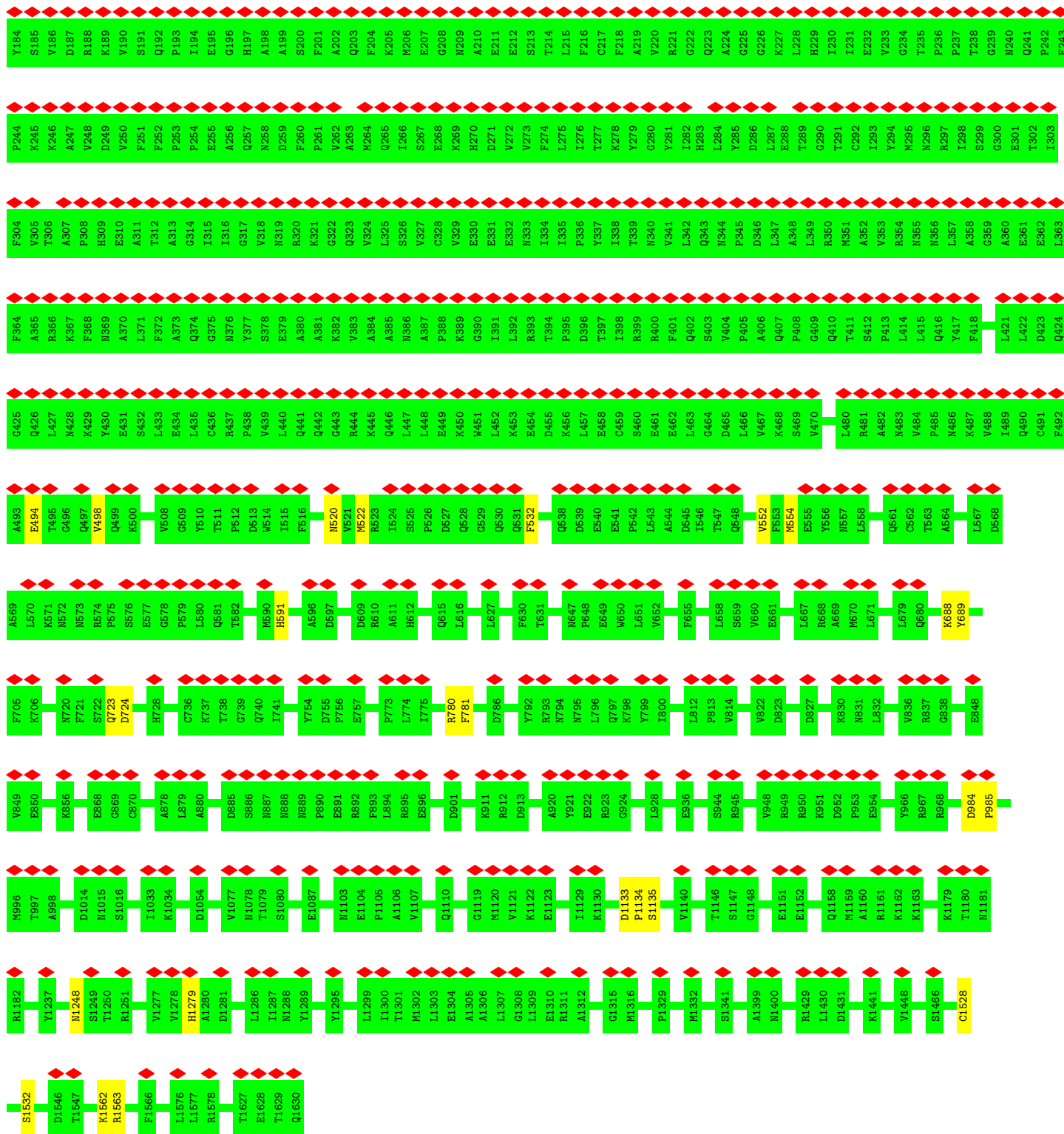
• Molecule 1: Clathrin heavy chain





• Molecule 1: Clathrin heavy chain

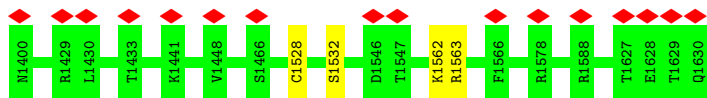




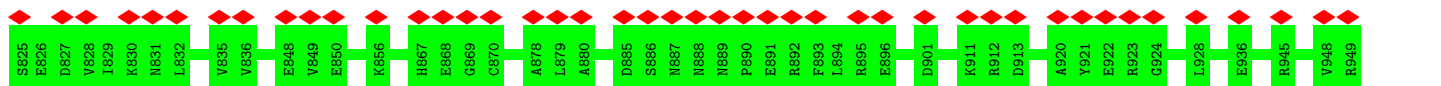
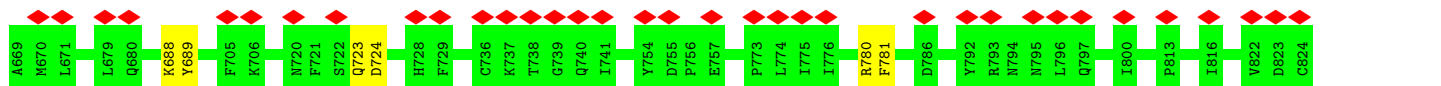
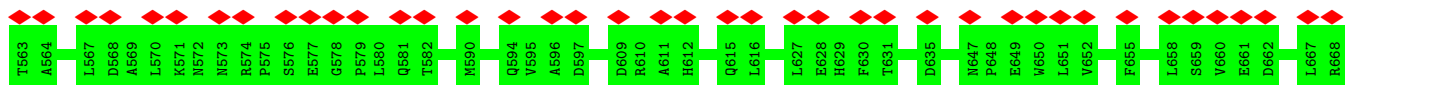
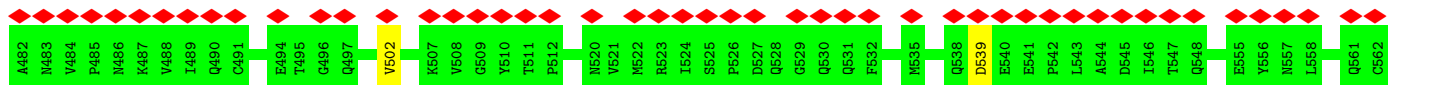
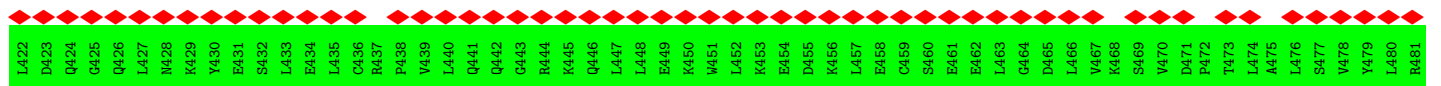
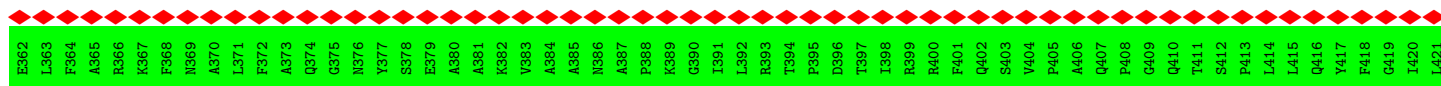
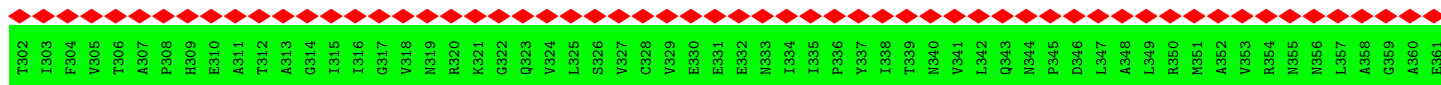
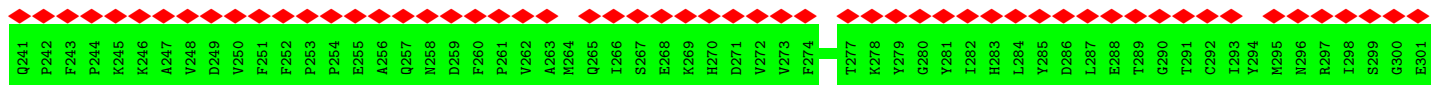
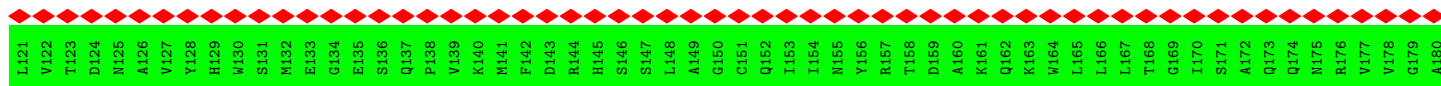
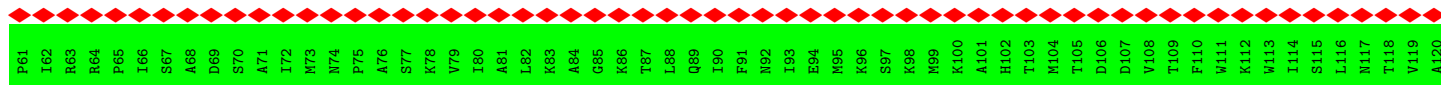
• Molecule 1: Clathrin heavy chain

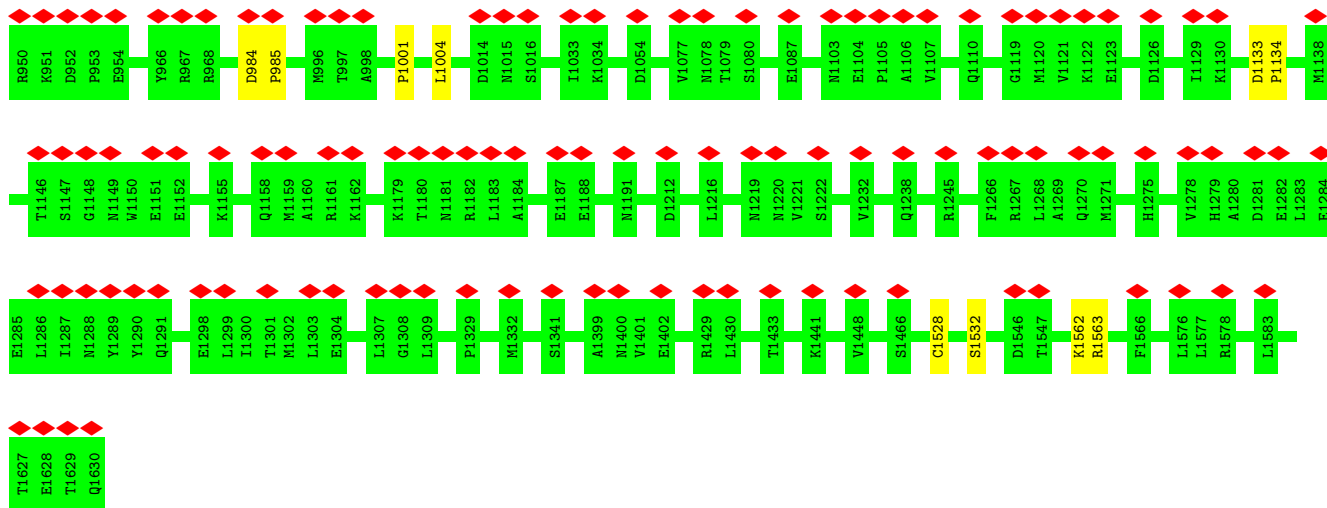


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Q3	R63	T123	L183	F243	I303	L363	D423	N483	L559	A669	D943	E937	I1128
T4	R64	D124	Y194	P244	F304	F364	Q424	V484	Q560	M670	E944	S944	I1129
L5	P65	M125	S185	K245	V305	A365	G425	P485	Q561	L671	L945	R945	K1130
P6	L66	A126	V186	K246	T306	R366	Q426	N486	C562	L679	E948	V948	D1133
I7	S67	I127	D187	A247	A307	F367	L427	K487	T563	Q680	V949	R949	P1134
H8	A68	Y128	R188	V248	P308	F368	N428	V488	A564	K688	E950	R950	T1146
F9	D69	K129	K189	D249	H309	N369	K429	I489	L567	Y689	R951	R951	S1147
Q10	S70	W130	V190	V250	E310	A370	Y430	Q490	D568	K689	R952	R952	G1148
E11	A71	S131	S191	F251	A311	L371	E431	C491	A569	F705	R953	D952	N1149
H12	I72	M132	Q192	F252	T312	F372	S432	F492	L570	K706	N954	R954	W1150
L13	M73	E133	P193	P253	A313	A373	L433	G496	N571	N720	L955	E954	E1151
Q14	M74	G134	I194	P254	G314	Q374	E434	Q497	N572	F721	L956	Y966	E1152
L15	P75	E135	I195	E255	I315	G375	L435	V498	N573	S722	L962	R967	K1182
Q16	A76	S136	G196	A256	I316	N376	C436	Q499	R574	Q723	L963	R968	A1178
M17	S77	I137	H197	Q257	G317	Y377	R437	K500	P575	D724	A964	D984	K1179
L18	K78	P138	A198	N258	V318	S378	V439	I501	S576	H728	H677	P985	T1180
G19	V79	V139	A199	D259	N319	E379	L440	V502	E577	F729	E687	M996	R1182
T20	I80	K140	S200	F260	R320	A380	L441	L503	G578	C736	E688	C970	L1183
M21	A81	M141	F201	P261	K321	A381	Q441	L504	P579	K737	G689	E971	A1184
P22	L82	F142	A202	V262	G322	K382	Q442	K507	L580	T738	C971	E972	Y1237
A23	R83	D143	Q203	A263	Q323	V383	G443	V508	L581	C738	C972	E973	K1246
N24	A84	R144	F204	M264	V324	A384	R444	G509	Q596	T739	E973	E974	R1251
I25	G85	H145	K205	Q265	L325	A385	K445	Y510	D597	I775	E974	E975	T1252
G26	K86	I146	M206	I266	S326	N386	Q446	D513	M599	Q740	A878	P1001	K1264
F27	T87	S147	E207	S267	V327	A387	L447	L513	Q594	I741	L879	L1004	E1265
S28	L88	L148	G208	E268	C328	P388	L448	F516	V595	Y754	L880	L1013	F1266
T29	R89	A149	M209	K269	V329	K389	E449	L517	A596	M755	A881	D1014	R1267
L30	I90	G150	A210	H270	E330	G390	K450	L518	D597	P756	I882	M1015	Q1270
T31	F91	C151	E211	D271	E331	I391	W451	N520	M609	E757	Y883	S1016	C1272
E32	N92	Q152	E212	V272	E332	L392	L452	M521	R610	P773	I884	I1033	G1273
K33	I93	I153	S213	V273	N333	R393	K453	V522	A611	L774	D885	I1034	L1274
S34	E94	I154	T214	F274	I334	T394	E454	M523	B612	I775	P886	K1034	H1275
D35	M95	M155	L215	L275	I335	P395	D455	R523	Q615	R780	N887	D1054	D1281
K36	K96	Y156	F216	I276	P336	D396	K456	S525	L616	F781	N888	V1077	M1271
F37	S97	I157	C217	T277	V337	T397	L457	P526	L617	D786	N889	M1078	C1272
I38	K98	T158	F218	K278	I338	I398	E458	D527	F630	E786	P890	T1079	G1273
C39	M99	D159	A219	Y279	T339	R399	C459	Q528	T631	Y792	E891	S1080	L1274
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K43	T103	K163	Q223	H283	Q343	S403	L463	F532	E649	N794	R895	N997	L1307
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A48	V108	T168	L228	E288	L347	P408	K468	D538	F655	I829	G901	R913	A1399
Q49	T109	I170	H229	T289	L349	G409	S469	E540	L658	I830	D902	D913	G1119
V50	F110	I171	I230	T291	L349	Q410	V470	E541	S659	K830	E903	K911	M1120
W51	M111	S171	I231	T291	N351	T411	D471	E542	V660	H831	E904	R912	V1121
L52	K112	Q172	E232	C292	A352	S412	P472	E543	D662	H831	F655	D913	K1122
I53	W113	A173	V233	I293	V353	P413	T473	P542	L659	V836	L658	A920	G1119
D54	Q174	Q174	G234	Y294	R354	L414	L474	L543	S660	R837	S659	Y921	M1120
M55	S115	M175	T235	M295	N355	L415	A475	A544	E661		E661	E922	V1121
N56	L116	R176	P236	R296	N356	Q416	L476	D545	D662		D662	R923	A1399
D57	T117	P237	R237	R297	N357	L417	L477	L546				R924	
P58	V178	V177	T238	I298	L357	Y417	L478	T547				G924	
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N60	A120	A180	M240	G300	G359	G419	L480						

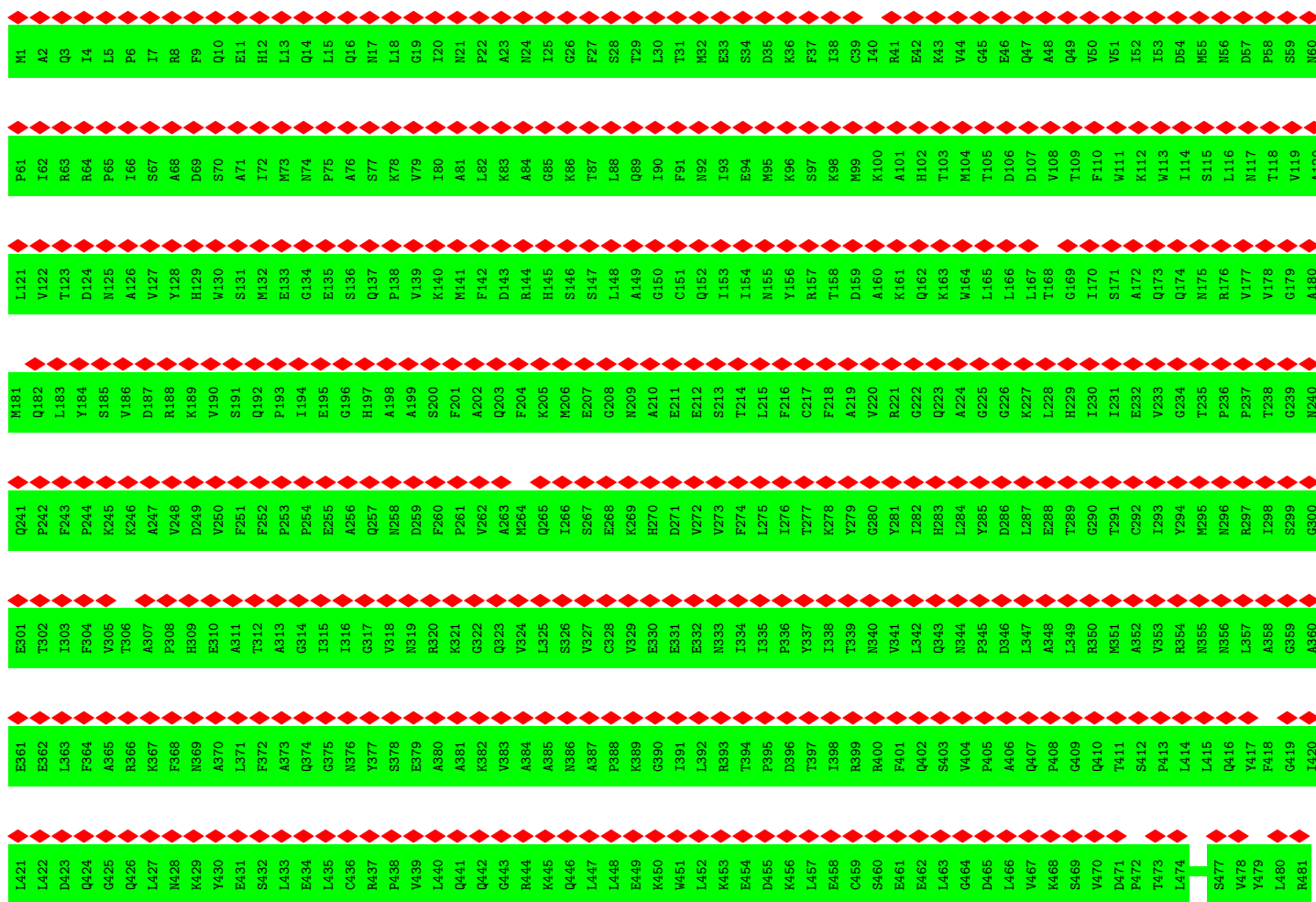


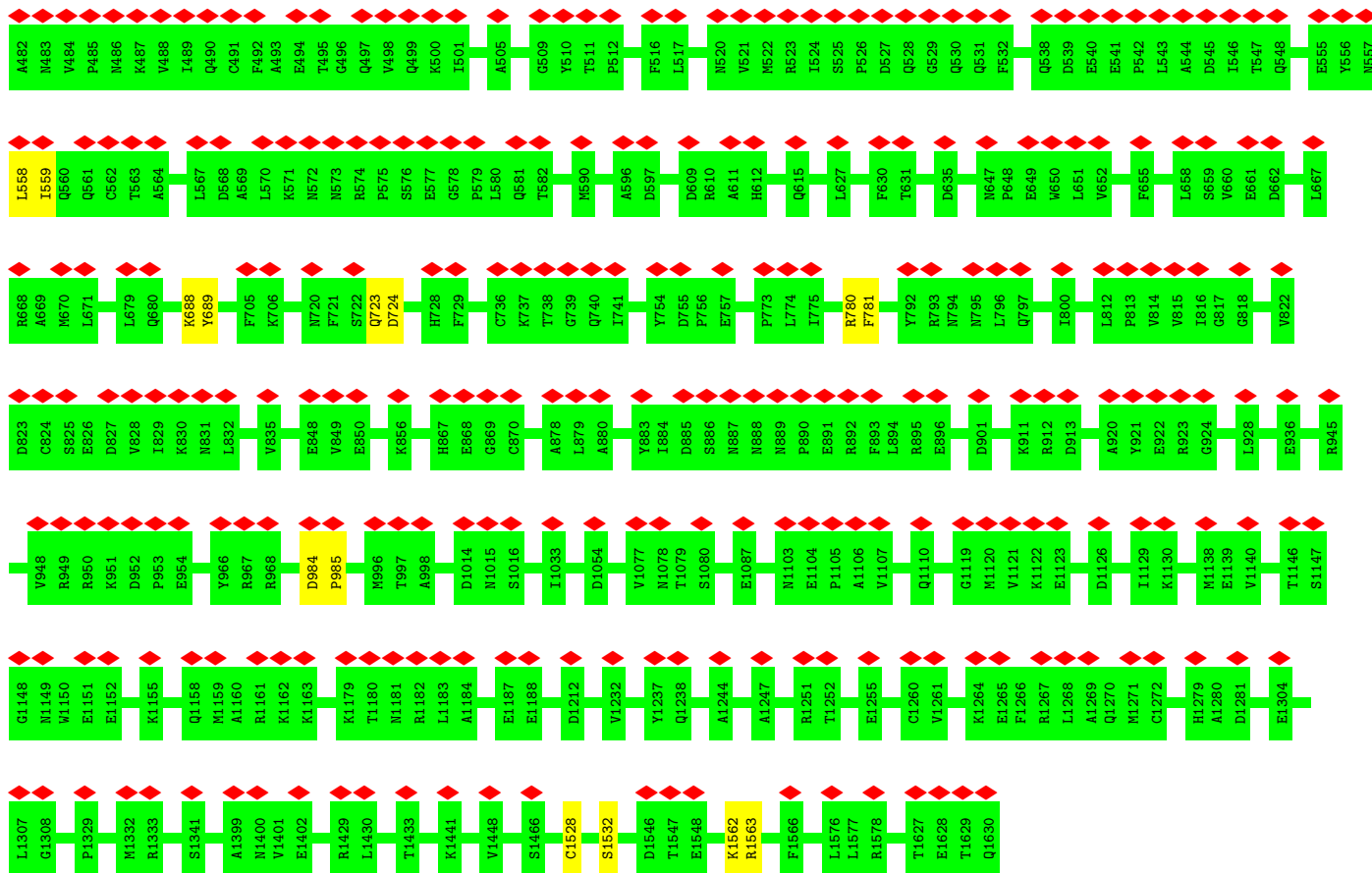
● Molecule 1: Clathrin heavy chain



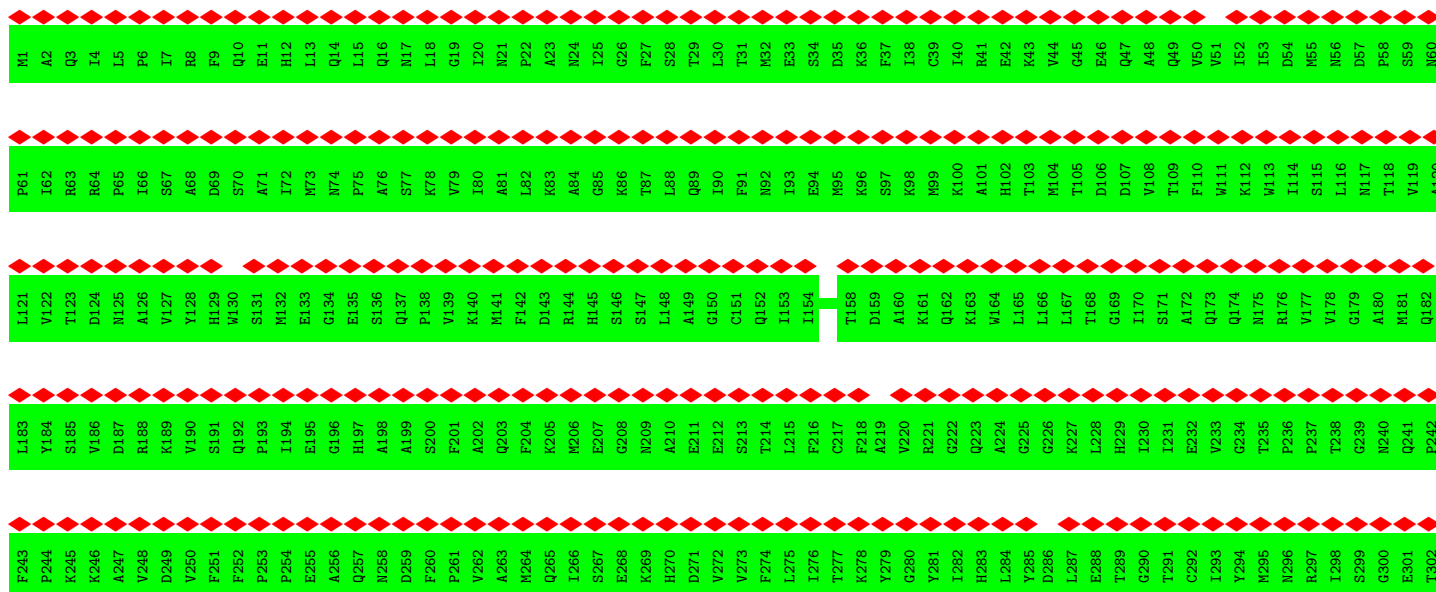


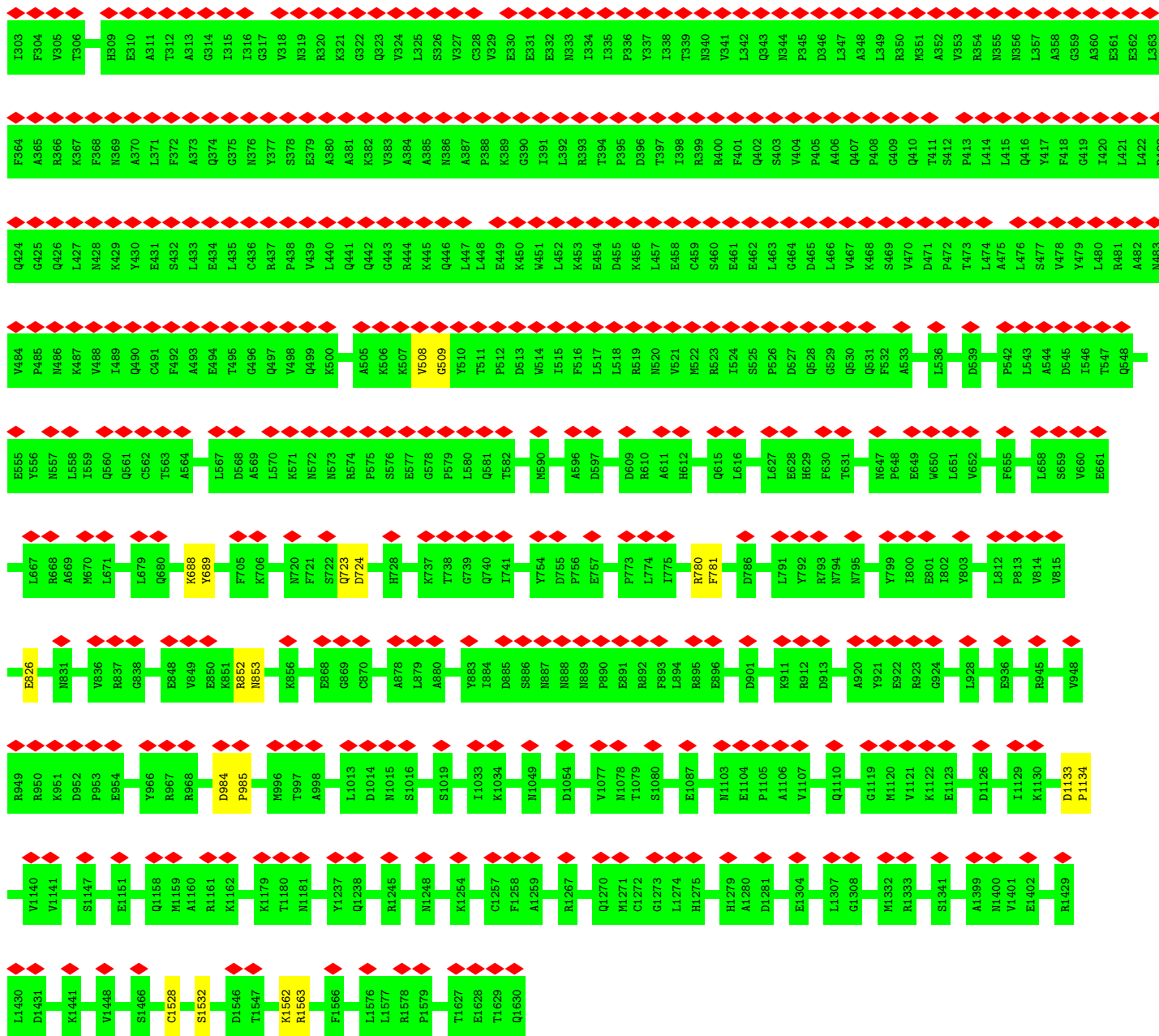
• Molecule 1: Clathrin heavy chain



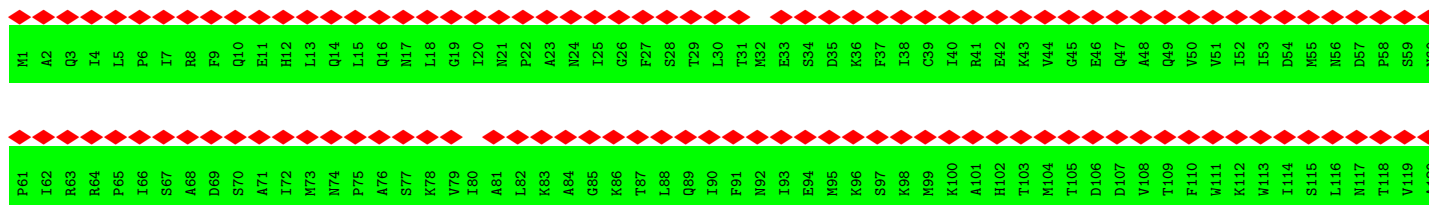


• Molecule 1: Clathrin heavy chain

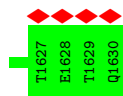




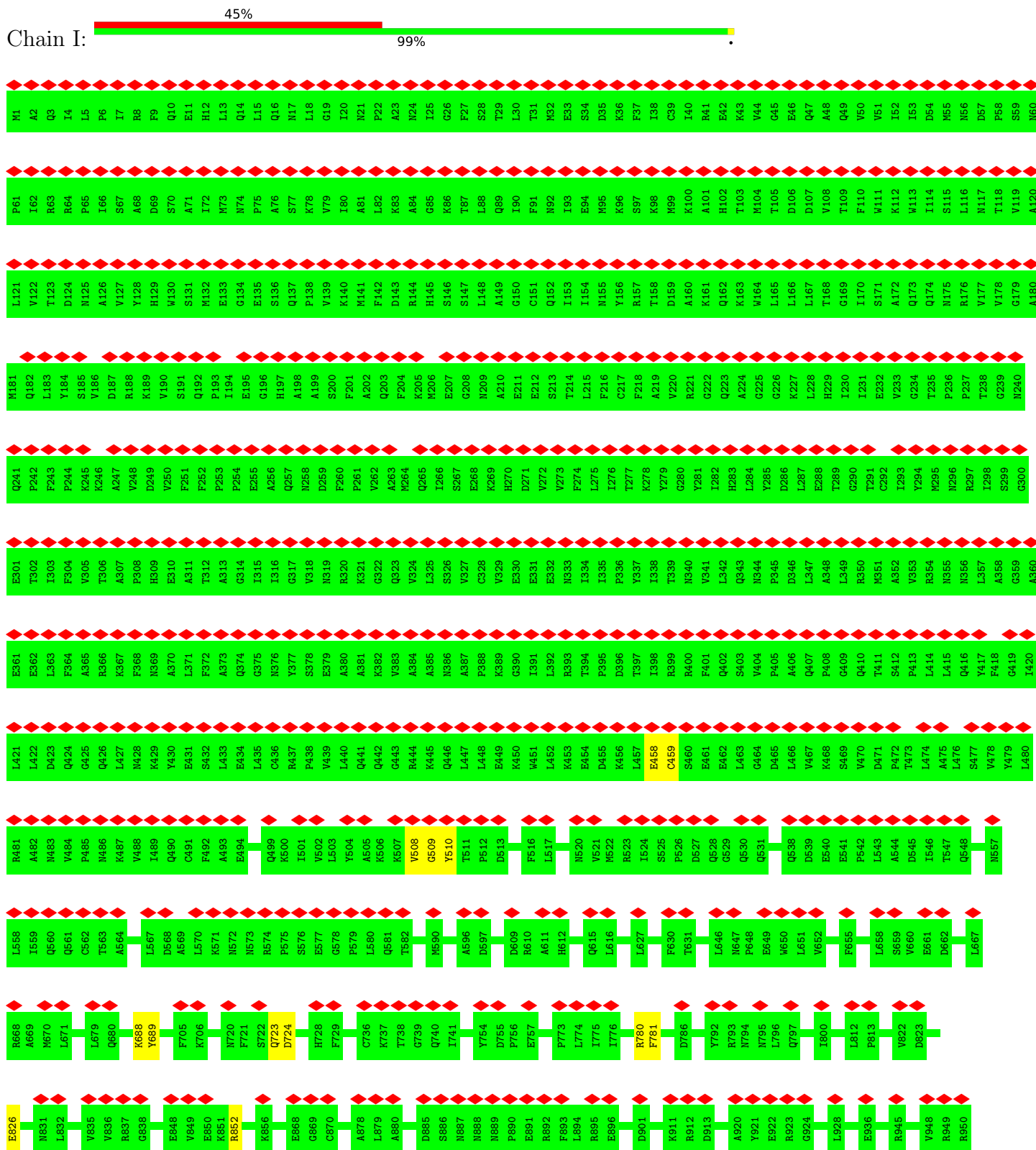
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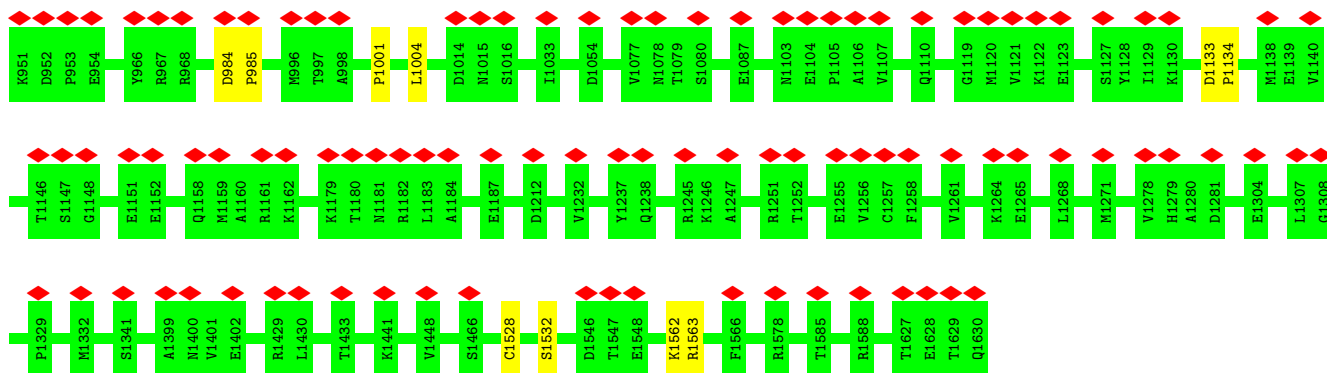


L121	V122	T123	D124	M125	A126	V127	Y128	H129	W130	S131	M132	E133	G134	E135	S136	Q137	P138	K140	V139	M141	F142	D143	R144	H145	S146	S147	L148	A149	G150	C151	Q152	I153	R157	T158	D159	A160	K161	Q162	K163	W164	L165	L166	T168	G169	I170	S171	A172	Q173	Q174	M175	R176	V177	V178	G179	A180	M181	Q182			
L183	Y184	S185	V186	D187	R188	K189	V190	S191	Q192	P193	I194	E195	G196	H197	A198	A199	S200	F201	A202	Q203	F204	K205	M206	E207	G208	N209	A210	D211	E212	S213	T214	L215	L216	F216	C217	F218	A219	V220	R221	G222	Q223	A224	G225	G226	K227	L228	H229	I230	I231	E232	V233	G234	T235	P236	F237	T238	G239	N240	Q241	P242
F244	P244	K246	A247	V248	D249	V250	F251	F252	P253	P254	E255	A256	Q257	N258	D259	F260	P261	A262	A263	M264	Q265	I266	S267	E268	K269	H270	D271	E272	V273	F274	L275	I276	T277	K278	Y279	G280	Y281	I282	H283	L284	Y285	D286	E288	T289	G290	I291	C292	I293	Y294	M295	N296	R297	I298	S299	G300	E301	T302			
I303	F304	Y305	P308	H309	E310	A311	T312	A313	G314	I315	I316	G317	V318	N319	R320	K321	G322	Q323	V324	L325	S326	V327	C328	V329	E330	E331	E332	N333	I334	I335	P336	Y337	I338	T339	N340	V341	L342	Q343	N344	P345	D346	L347	A348	L349	R350	K351	A352	V353	R354	Y354	N355	N356	L357	A358	G359	A360	E361	E362	L363	
F364	A365	R366	K367	F368	N369	A370	L371	F372	A373	Q374	G375	N376	Y377	S378	E379	A380	A381	K382	V383	A384	A385	N386	A387	P388	K389	G390	I391	L392	R393	T394	P395	D396	T397	I398	R399	R400	F401	Q402	S403	V404	P405	A406	Q407	P408	G409	Q410	T411	S412	P413	L414	L415	Q416	Y417	F418	G419	L420	L421	L422	D423	
Q424	G425	Q426	L427	M428	K429	Y430	E431	S432	L433	E434	L435	C436	R437	P438	V439	L440	Q441	Q442	G443	R444	K445	Q446	L447	L448	E449	K450	W451	L452	K453	E454	D455	K456	L457	E458	C459	S460	E461	E462	L463	G464	D465	L466	V467	K468	S469	V470	D471	P472	T473	L474	A475	V476	Y477	L480	R481	A482	N483	V484		
P485	N486	K487	V488	I489	Q490	C491	F492	A493	E494	T495	G496	Q497	V498	Q499	W500	L503	Y504	A505	K506	K507	V508	G509	Y510	D511	W514	I515	F516	L517	N520	V521	M522	A523	E524	S525	P526	D527	E528	H529	F530	G531	F532	A533	Q534	M535	Q538	D539	E540	E541	P542	L543	A544	D545	I546	T547	Q548					
M557	L558	I559	Q560	Q561	C562	T563	A564	L567	D568	A569	L570	K571	N572	N573	R574	F575	S576	E577	G578	P579	L580	Q581	T582	M590	A596	D597	D609	R610	A611	H612	D615	L627	E628	H629	F630	T631	D635	L646	N647	P648	E649	H650	L651	V652	F655	L658	S659	V660												
E661	D662	L667	R668	A669	H670	L671	L679	Q680	K688	Y689	F705	K706	N720	Q723	D724	H728	F729	C736	K737	T738	G739	Q740	I741	Y754	D755	P756	E757	F773	L774	I775	R780	F781	D786	Y792	R793	M794	N795	I800	E826	D827	W828	I829	K830	H831																
L832	V836	R837	G838	Q839	F840	S841	T842	V846	A847	E848	V849	E850	K856	L857	P860	W861	L862	G869	C870	E871	E872	A878	L879	A880	D885	S886	N887	N888	N889	P890	E891	R892	F893	L894	E896	D901	K911	R912	D913	A920	Y921	E922	R923	Q924	L928	E936														
R945	V948	R949	R950	K951	D952	P953	E954	Y966	R967	R968	D984	P985	M996	T997	A998	L1013	D1014	N1015	S1016	V1017	F1018	S1019	E1020	H1021	R1022	I1033	K1034	N1049	Y1050	D1051	D1054	V1077	N1078	I1079	S1080	E1087	N1103	E1104	P1105	A1106	V1107	Q1110	G1119	M1120	V1121															
K1122	E1123	I1129	K1130	D1133	P1134	M1138	T1146	S1147	I1148	M1149	M1150	E1151	E1152	K1155	Q1158	M1159	A1160	R1161	K1162	K1179	T1180	M1181	N1182	L1183	A1184	E1187	E1188	D1212	L1216	M1219	M1220	V1221	S1222	V1232	Y1237	Q1238	R1245	K1246	A1247	M1248	S1249	T1250	R1251	D1262																
G1263	K1264	E1265	F1266	R1267	L1268	M1271	C1272	H1275	D1281	E1304	L1307	G1308	M1332	S1341	G1389	A1399	N1400	V1401	E1402	R1429	L1430	T1433	K1441	V1448	S1466	C1528	S1532	D1546	T1547	K1562	R1563	F1566	L1576	L1577	R1578	M1585	R1588																							

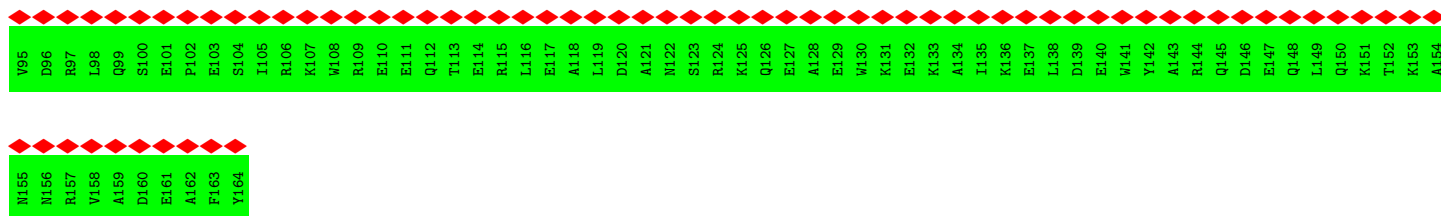


● Molecule 1: Clathrin heavy chain

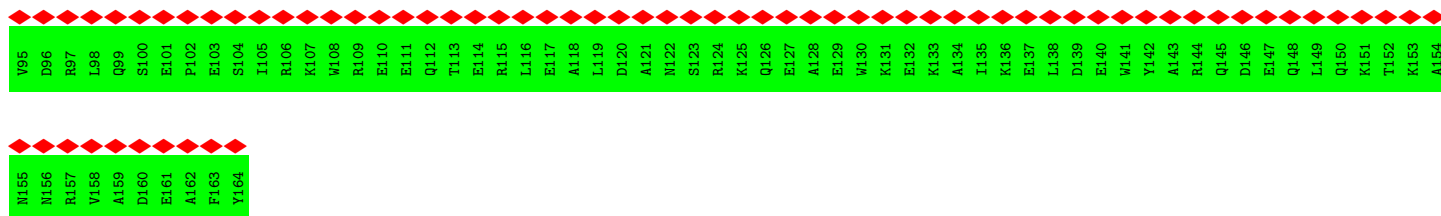




• Molecule 2: Clathrin light chain A



• Molecule 2: Clathrin light chain A

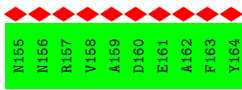
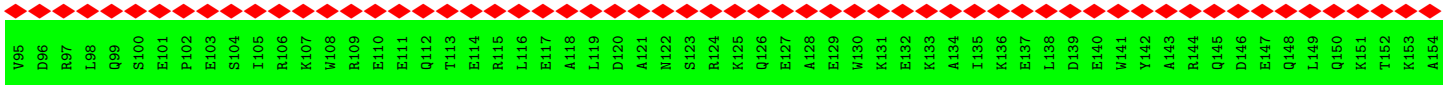


• Molecule 2: Clathrin light chain A

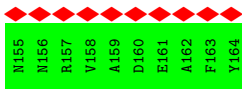
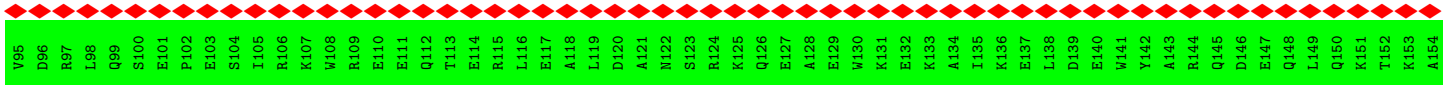


• Molecule 2: Clathrin light chain A

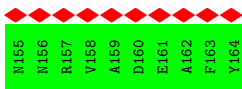
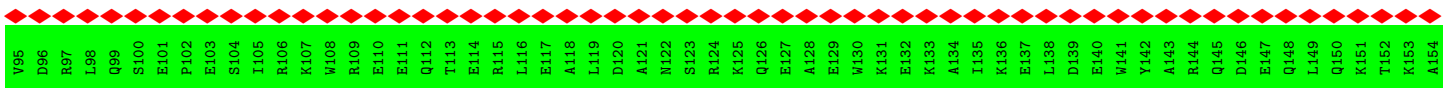




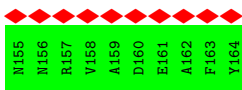
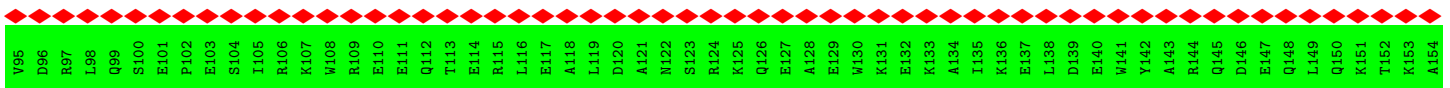
• Molecule 2: Clathrin light chain A



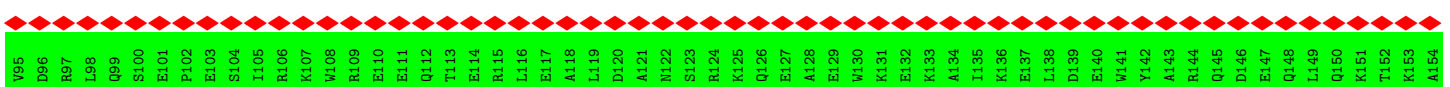
• Molecule 2: Clathrin light chain A



• Molecule 2: Clathrin light chain A



• Molecule 2: Clathrin light chain A



N155
N156
R157
V158
A159
D160
E161
A162
F163
Y164

• Molecule 2: Clathrin light chain A

Chain R: 

V95
D96
R97
L98
Q99
S100
E101
P102
E103
S104
I105
R106
K107
V108
R109
E110
E111
Q112
T113
E114
R115
L116
E117
A118
L119
D120
A121
M122
S123
R124
K125
Q126
E127
A128
E129
W130
K131
E132
K133
A134
I135
K136
E137
L138
D139
E140
W141
Y142
A143
R144
Q145
D146
E147
Q148
L149
Q150
K151
T152
K153
A154

N155
N156
R157
V158
A159
D160
E161
A162
F163
Y164

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D6	Depositor
Number of particles used	1450	Depositor
Resolution determination method	Not provided	
CTF correction method	CTFTILT, FREALIGN V.6.07	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2000.00	Depositor
Maximum defocus (nm)	5000.00	Depositor
Magnification	51160	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	0.638	Depositor
Minimum map value	-0.163	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.063	Depositor
Recommended contour level	0.25	Depositor
Map size (\AA)	873.6, 873.6, 873.6	wwPDB
Map dimensions	312, 312, 312	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing (\AA)	2.8, 2.8, 2.8	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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1630	0	0	9	0
1	B	1630	0	0	11	0
1	C	1630	0	0	14	0
1	D	1630	0	0	11	0
1	E	1630	0	0	9	0
1	F	1630	0	0	7	0
1	G	1630	0	0	10	0
1	H	1630	0	0	7	0
1	I	1630	0	0	12	0
2	J	70	0	0	0	0
2	K	70	0	0	0	0
2	L	70	0	0	0	0
2	M	70	0	0	0	0
2	N	70	0	0	0	0
2	O	70	0	0	0	0
2	P	70	0	0	0	0
2	Q	70	0	0	0	0
2	R	70	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	15300	0	0	88	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 6.

The worst 5 of 88 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:C:1134:PRO:CA	1:C:1135:SER:CA	1.84	1.53
1:G:826:GLU:CA	1:G:853:ASN:CA	1.92	1.47
1:G:723:GLN:CA	1:G:724:ASP:CA	2.24	1.16
1:C:723:GLN:CA	1:C:724:ASP:CA	2.24	1.15
1:A:723:GLN:CA	1:A:724:ASP:CA	2.24	1.15

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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.

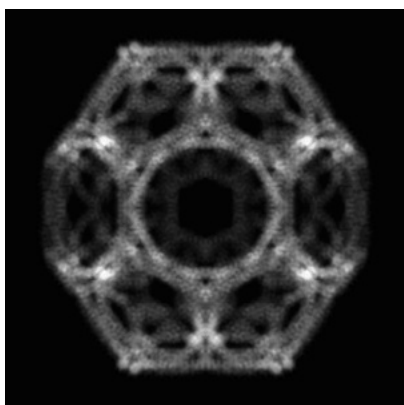
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5119. These allow visual inspection of the internal detail of the map and identification of artifacts.

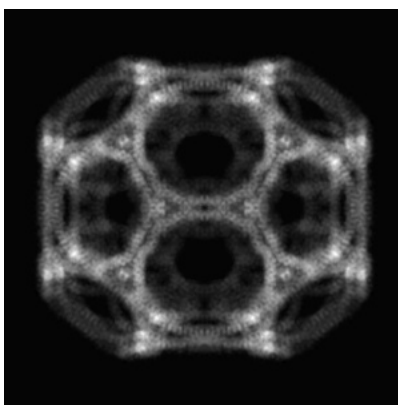
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

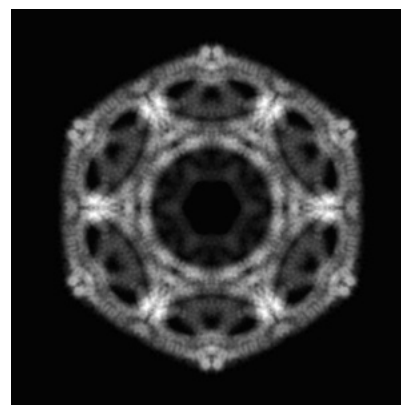
6.1.1 Primary map



X



Y

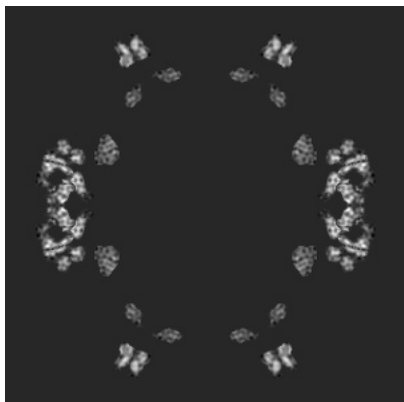


Z

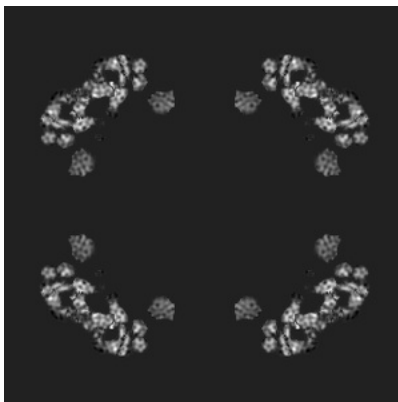
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

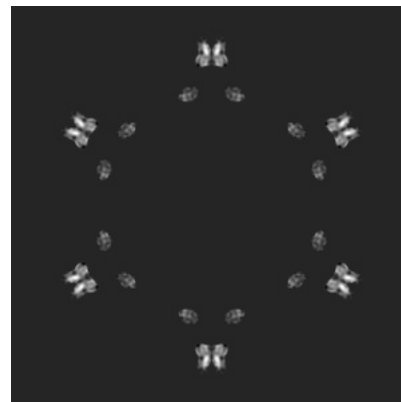
6.2.1 Primary map



X Index: 156



Y Index: 156

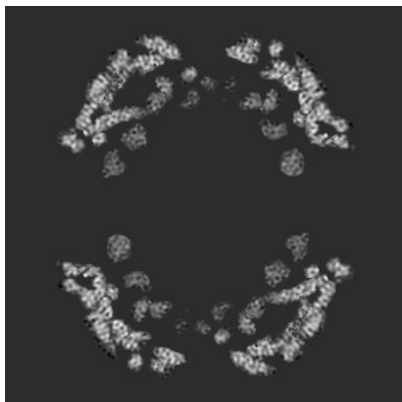


Z Index: 156

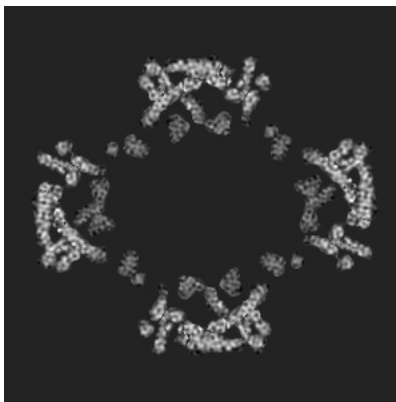
The images above show central slices of the map in three orthogonal directions.

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

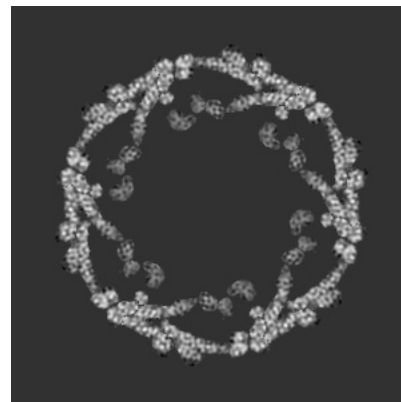
6.3.1 Primary map



X Index: 114



Y Index: 101

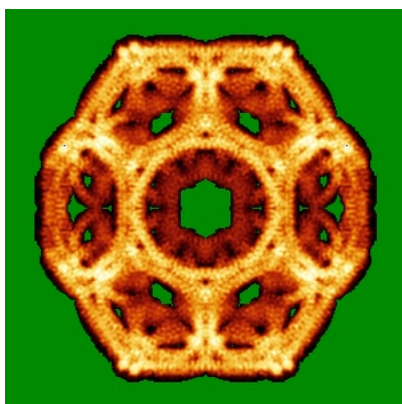


Z Index: 205

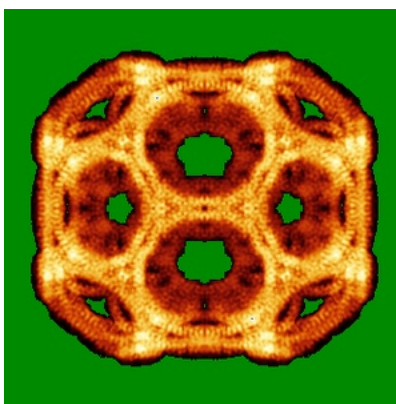
The images above show the largest variance slices of the map in three orthogonal directions.

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

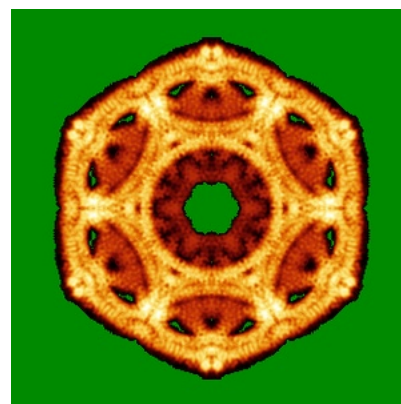
6.4.1 Primary map



X



Y

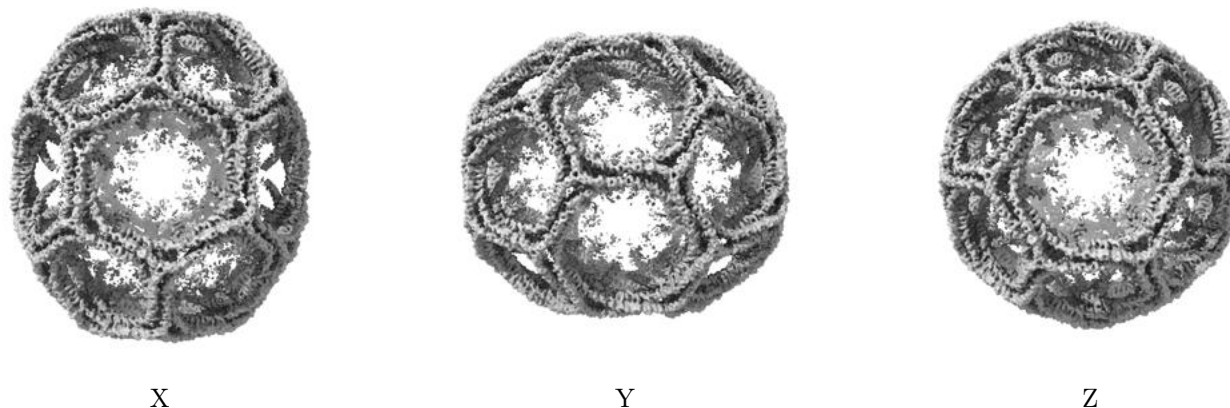


Z

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

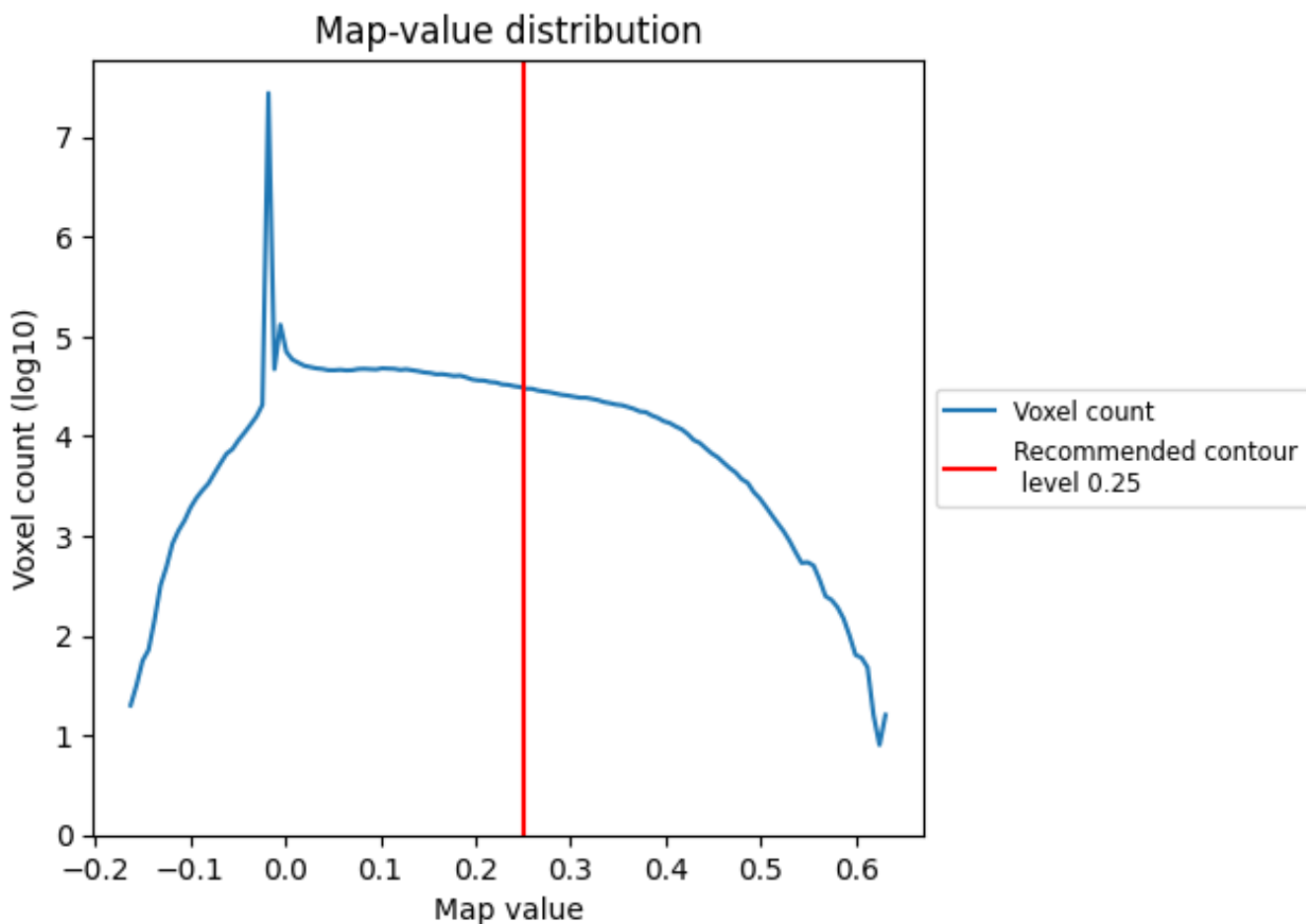
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

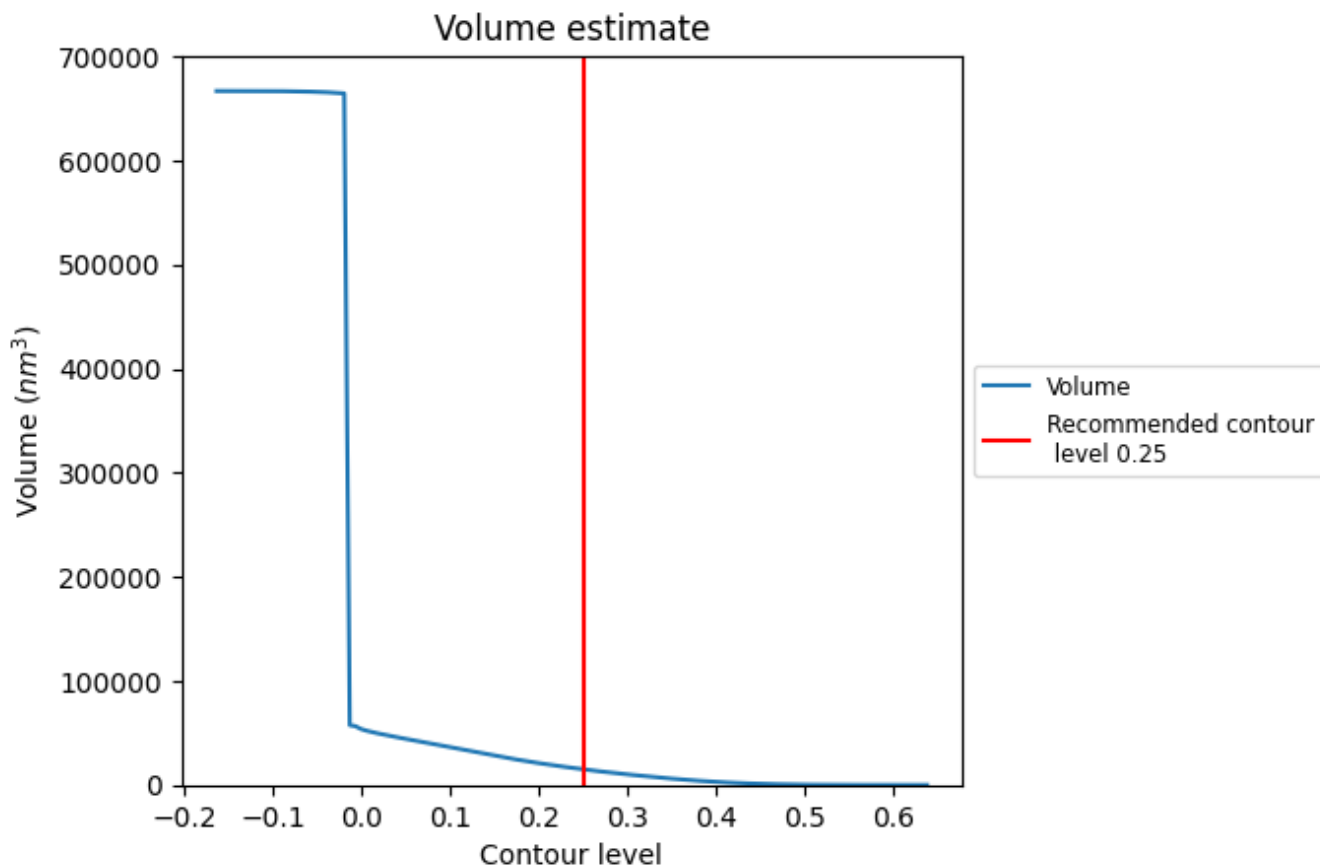
This section contains the results of statistical analysis of the map.

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.

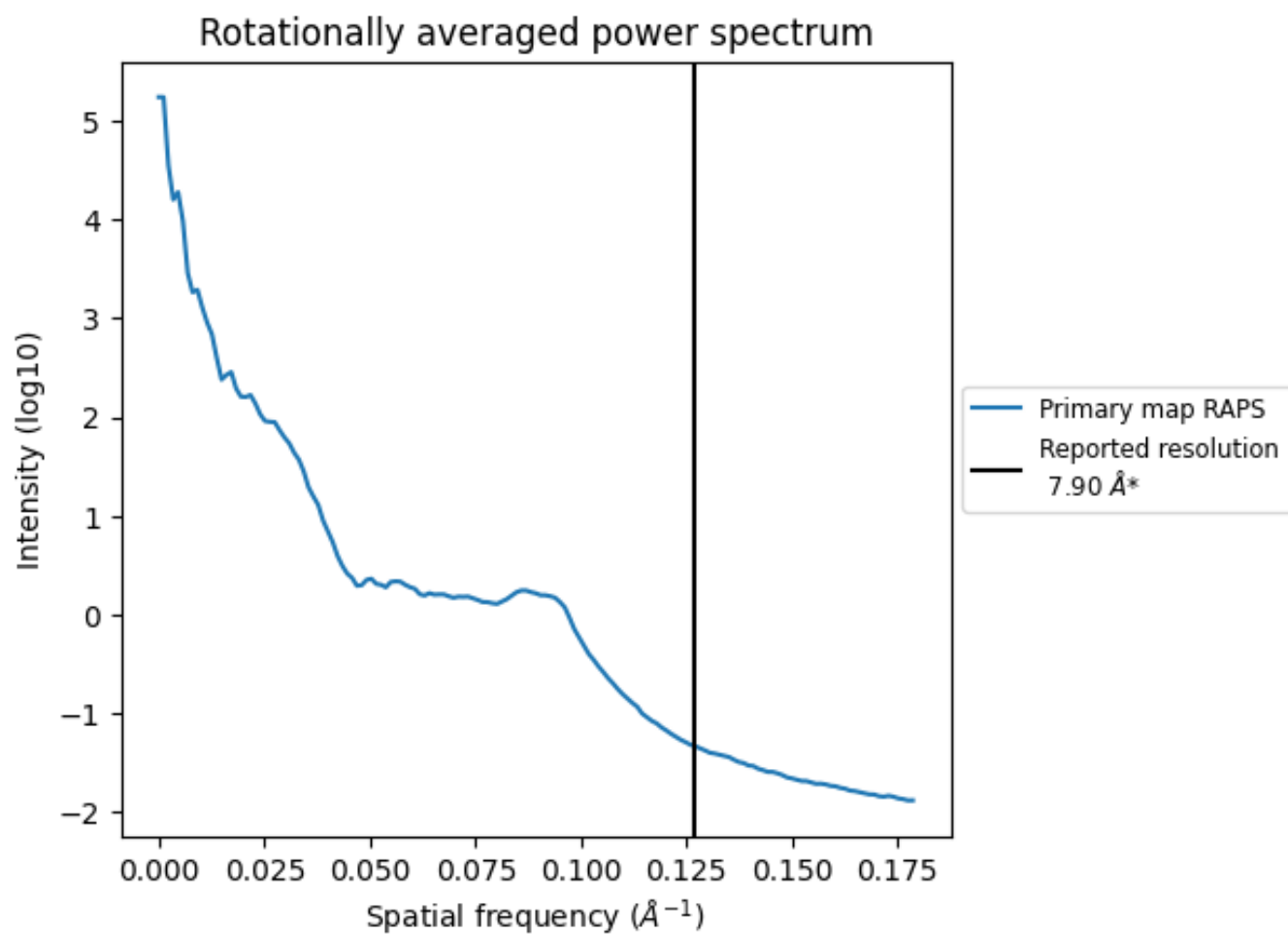
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 150470 nm³; this corresponds to an approximate mass of 13592 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 0.127 Å⁻¹

8 Fourier-Shell correlation

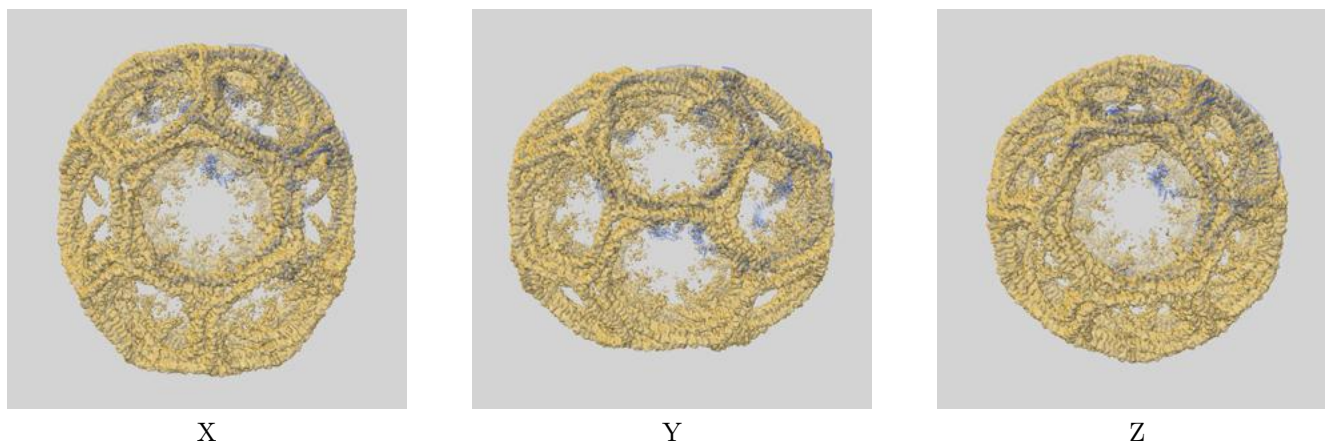
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

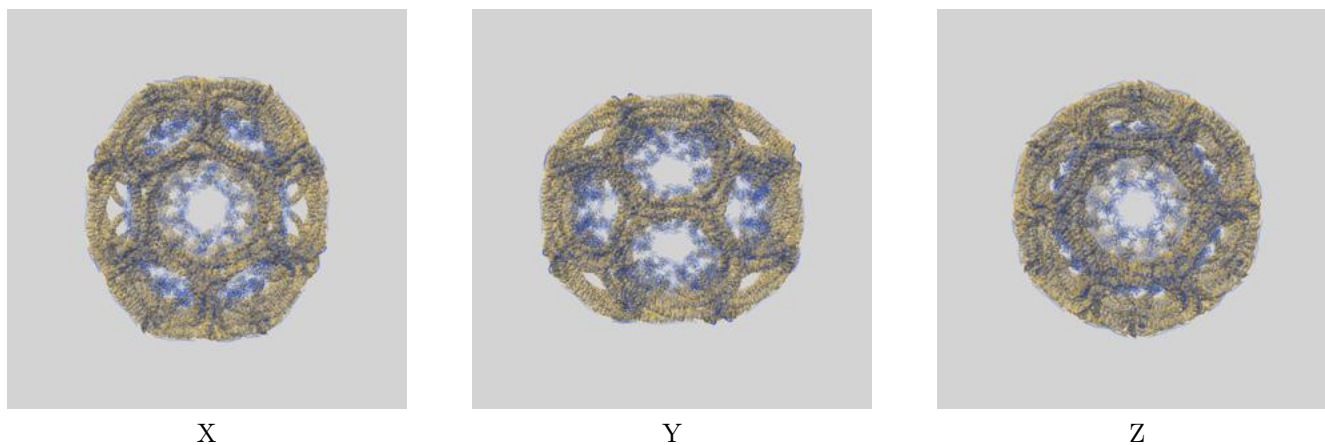
This section contains information regarding the fit between EMDB map EMD-5119 and PDB model 3IYV. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

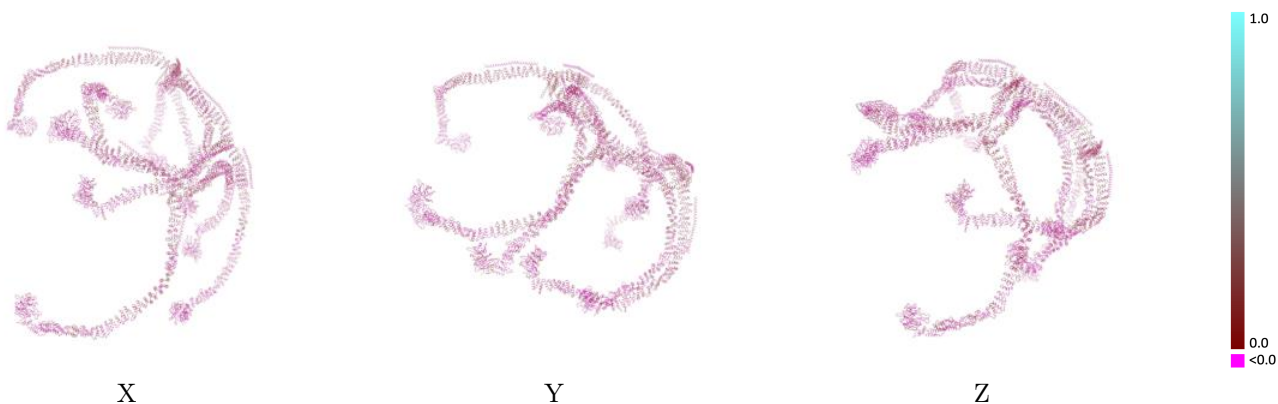


9.1.2 Map-model assembly overlay [i](#)



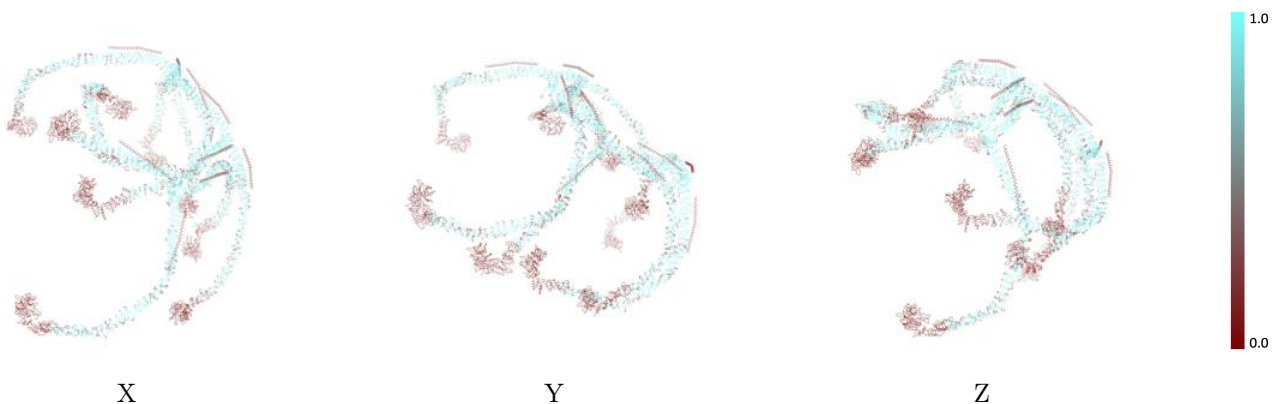
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



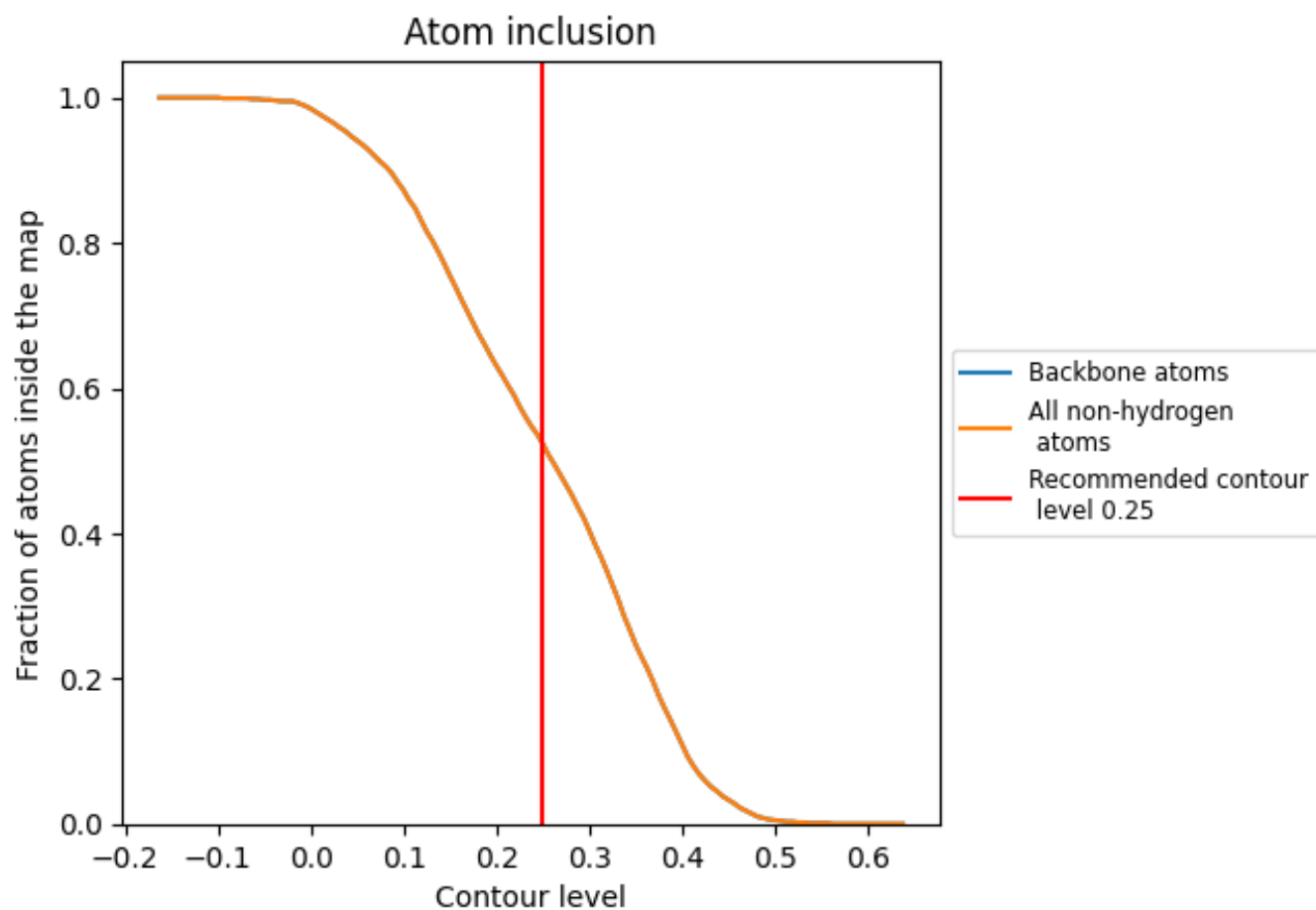
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).







































9.4 Atom inclusion [i](#)



At the recommended contour level, 52% of all backbone atoms, 52% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5230	 0.0550
A	 0.5380	 0.0530
B	 0.5550	 0.0610
C	 0.5600	 0.0620
D	 0.5440	 0.0580
E	 0.5390	 0.0570
F	 0.5390	 0.0580
G	 0.5490	 0.0630
H	 0.5370	 0.0530
I	 0.5460	 0.0590
J	 0.0000	 -0.0250
K	 0.0000	 -0.0310
L	 0.0000	 0.0050
M	 0.0000	 0.0110
N	 0.0000	 -0.0150
O	 0.0000	 -0.0380
P	 0.0000	 -0.0440
Q	 0.0000	 -0.0190
R	 0.0000	 -0.0300

