



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:34 AM UTC

PDB ID : 3IYV / pdb_00003iyv
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 : 1B89, 1BPO

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

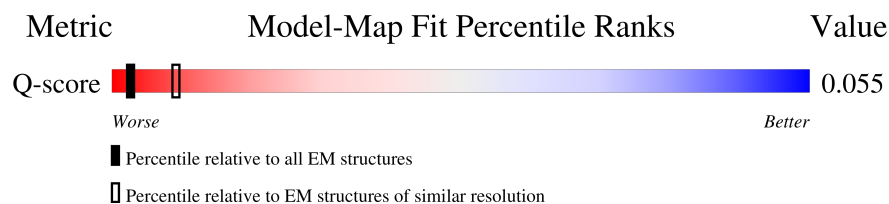
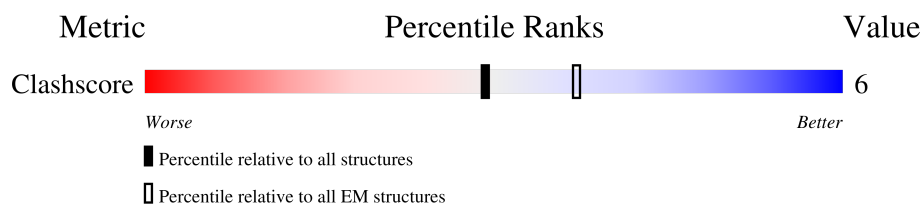
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

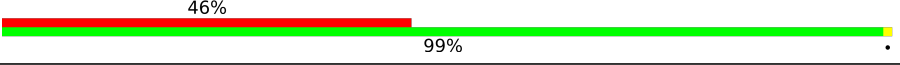
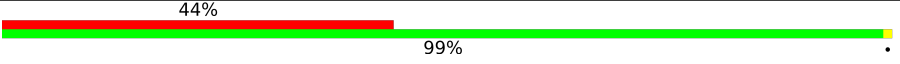
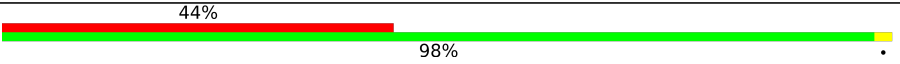
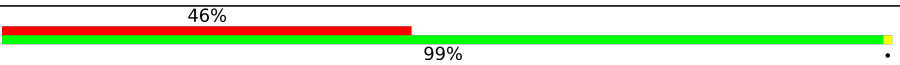
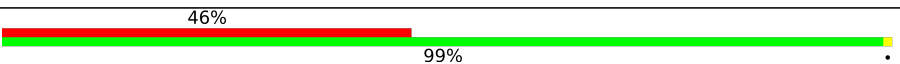
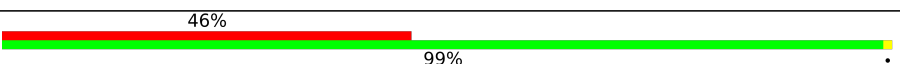
The reported resolution of this entry is 7.90 Å.

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Q-score	-	25397	366 (7.40 - 8.40)

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	
1	B	1630	
1	C	1630	
1	D	1630	
1	E	1630	
1	F	1630	

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Mol	Chain	Length	Quality of chain
1	G	1630	45% 99%
1	H	1630	46% 99%
1	I	1630	45% 99%
2	J	70	100%
2	K	70	100%
2	L	70	100%
2	M	70	100%
2	N	70	100%
2	O	70	100%
2	P	70	100%
2	Q	70	100%
2	R	70	100%

2 Entry composition

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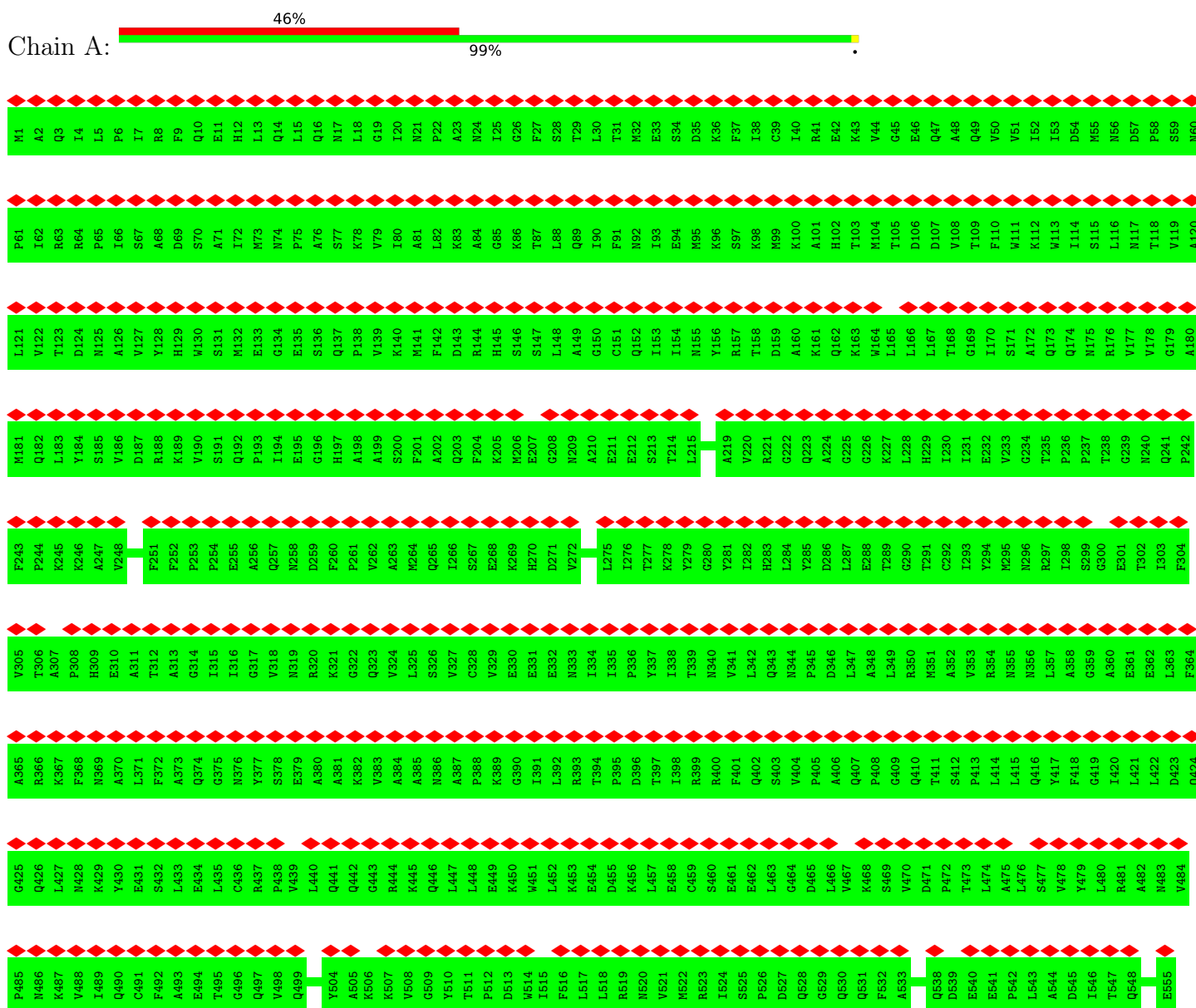
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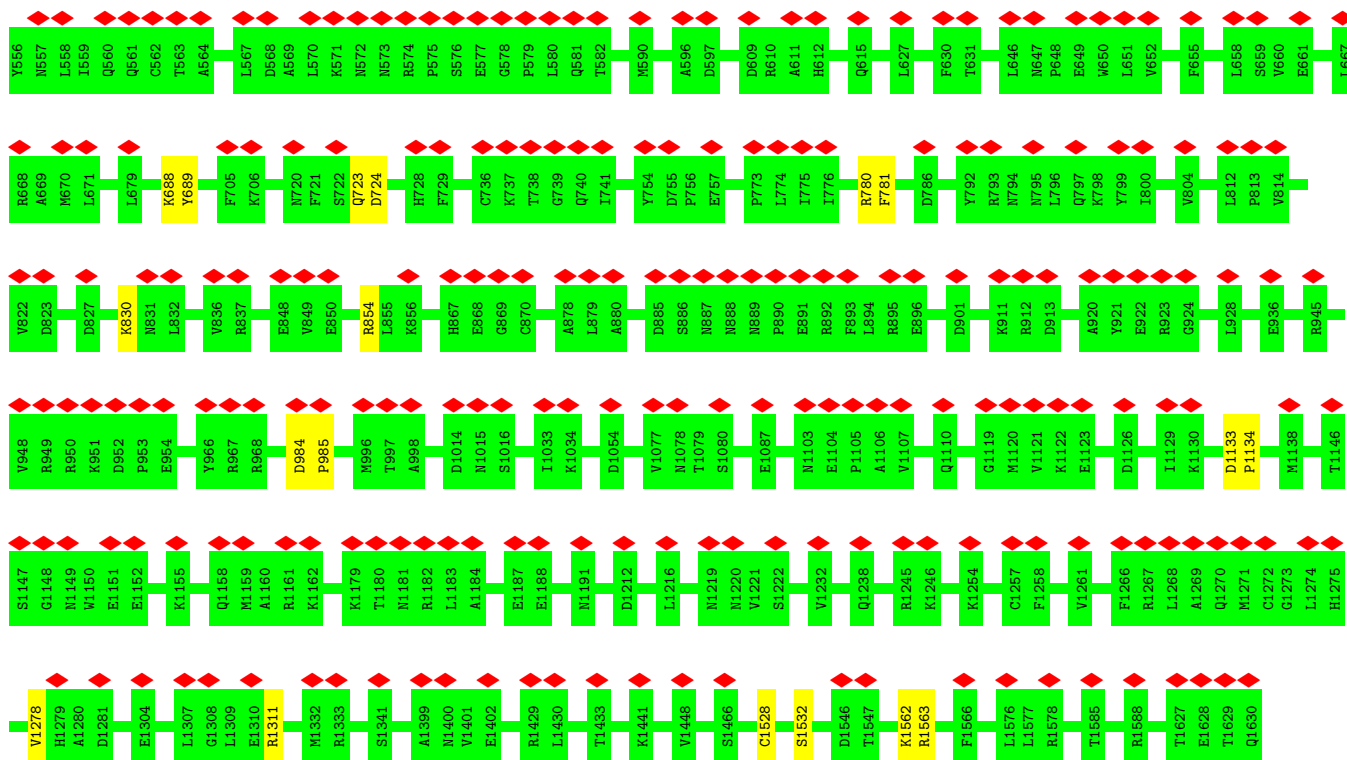
Mol	Chain	Residues	Atoms		AltConf	Trace
2	P	70	Total 70	C 70	0	70
2	Q	70	Total 70	C 70	0	70
2	R	70	Total 70	C 70	0	70

3 Residue-property plots

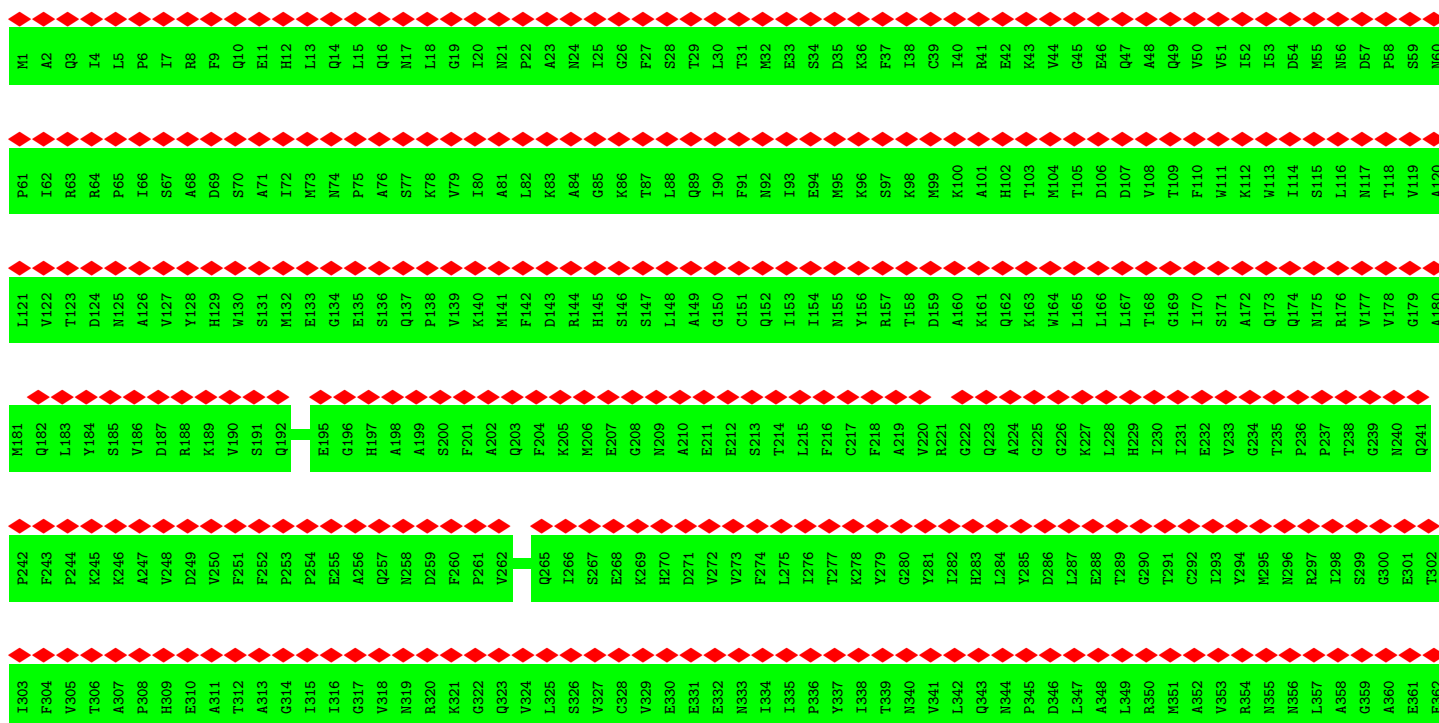
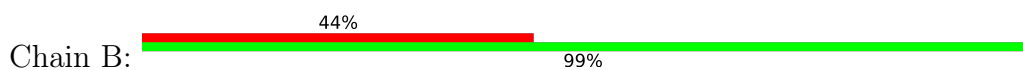
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

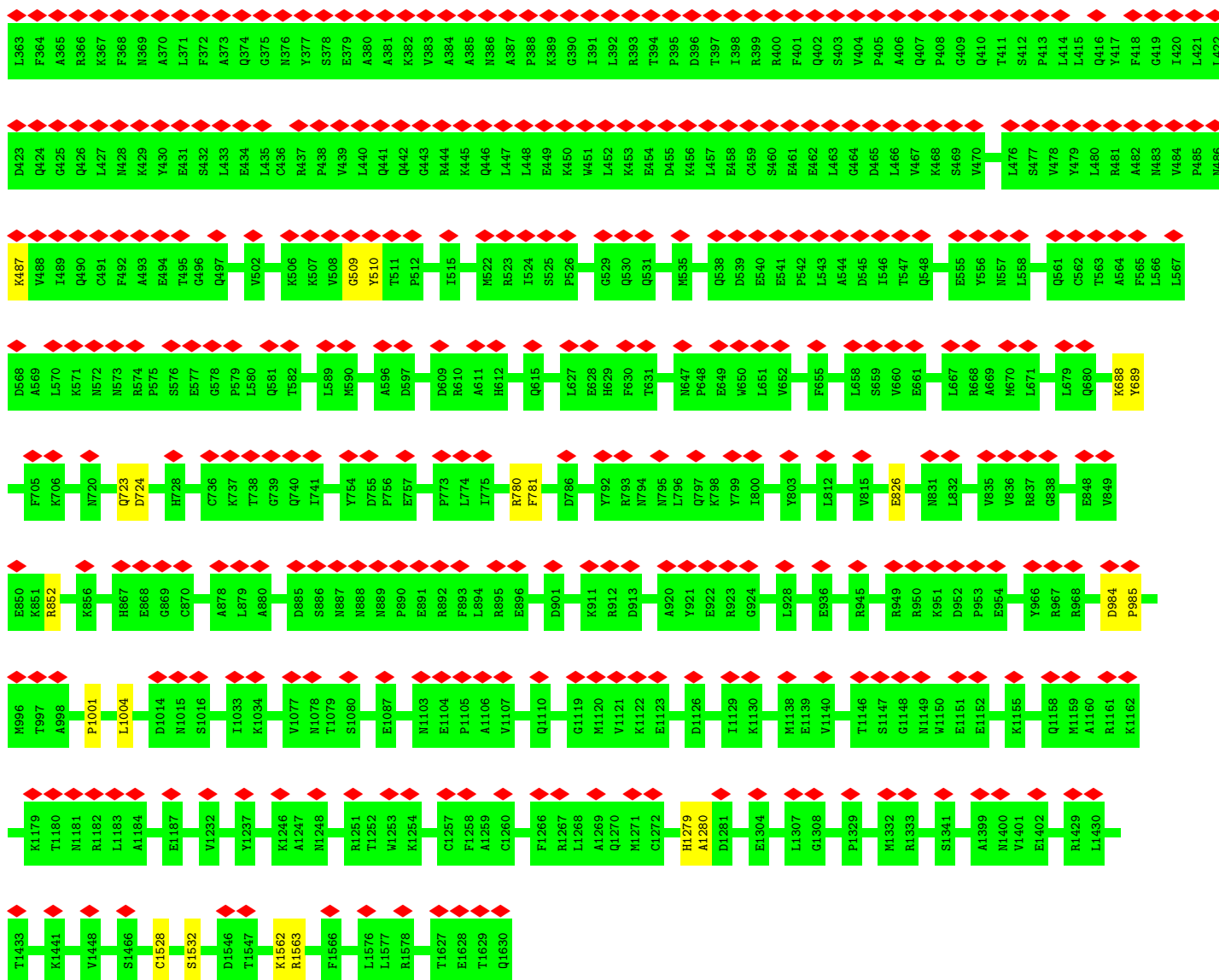
• Molecule 1: Clathrin heavy chain



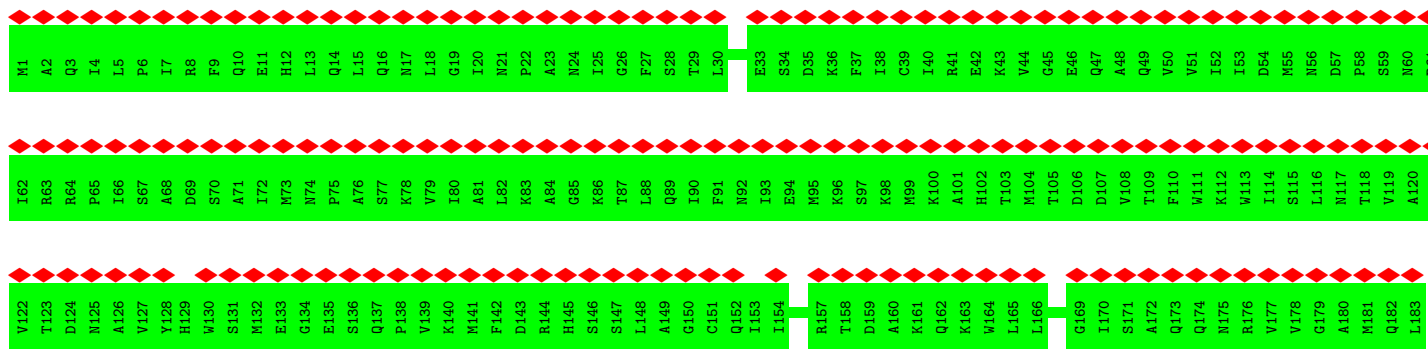
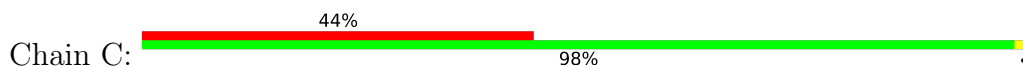


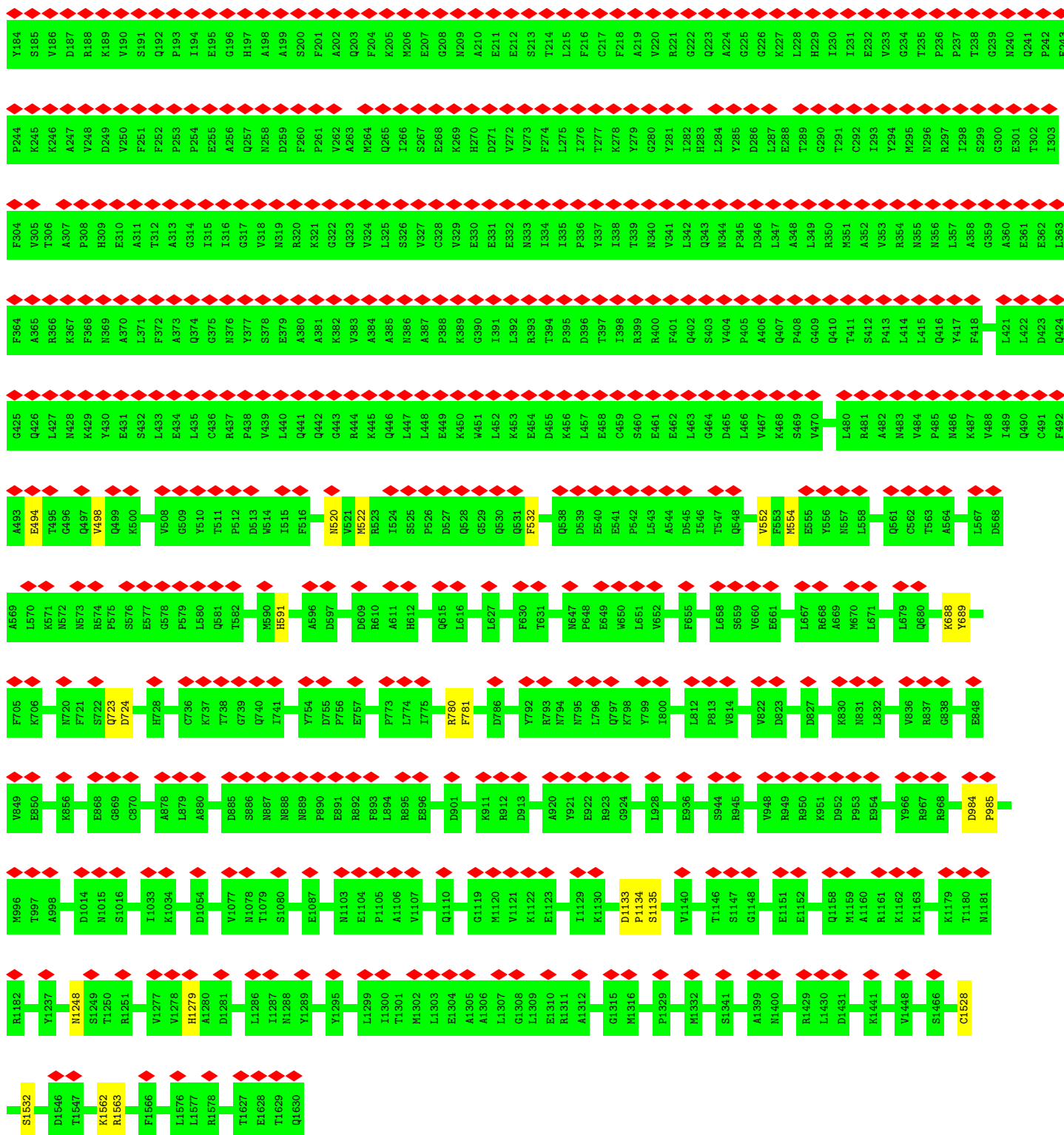
• Molecule 1: Clathrin heavy chain





• Molecule 1: Clathrin heavy chain

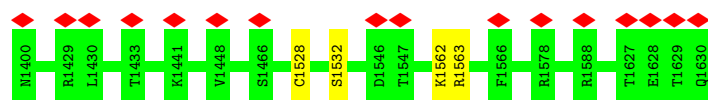




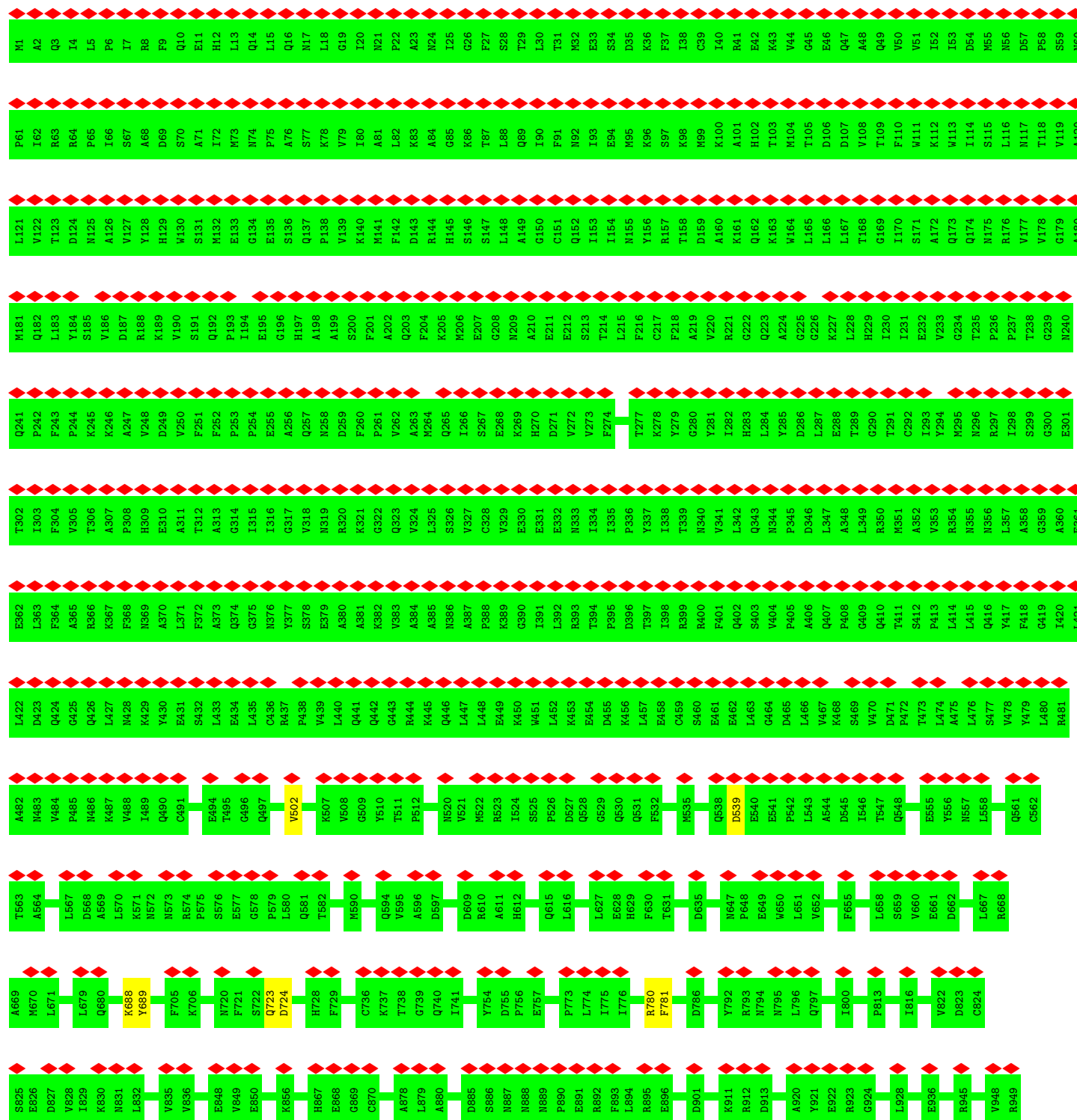
• Molecule 1: Clathrin heavy chain

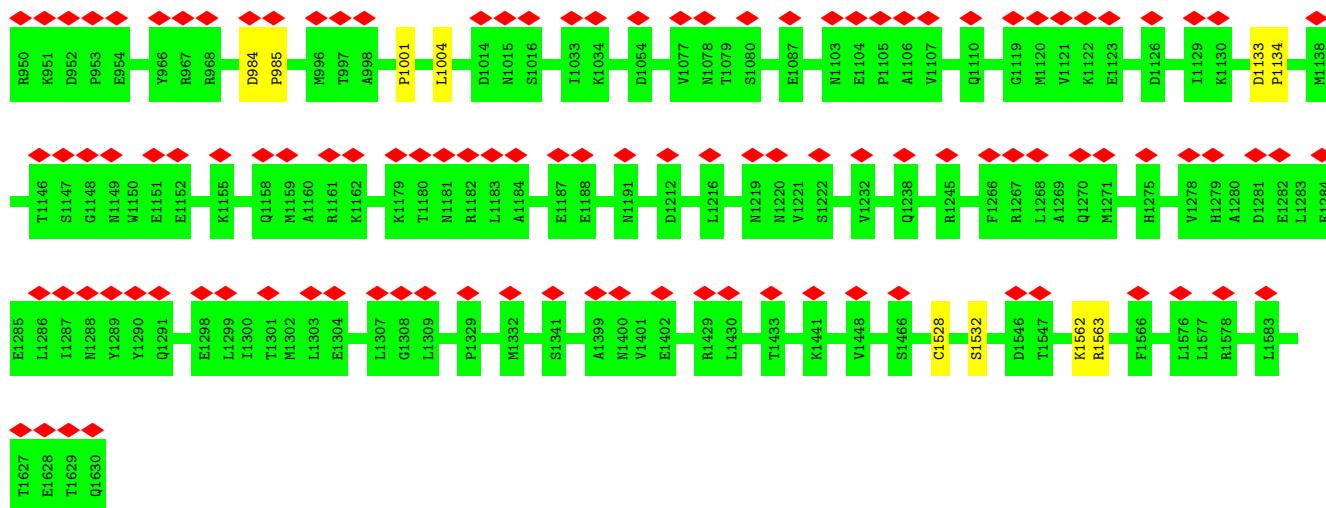


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Y1128	E936	T842	A669	L558	M483	D423	L363	I303	T123	Q183	163
I1129	E844	E844	M670	I559	V484	Q424	F364	F304	D124	Y184	164
K1130	S944	L845	L671	Q560	P485	G425	A365	V305	M125	S185	165
D1133	R945	L845	L679	Q561	N486	Q426	R366	T306	A126	V186	166
P1134	R945	L845	L679	C562	K487	L427	K367	A307	V127	D187	167
T1146	V948	E848	Q680	T563	V488	N428	F368	P308	I128	R188	168
R949	R949	V849	Q680	A564	I489	K429	N369	H309	H129	K189	169
R950	R950	E850	Y689	A564	Q490	Y430	A370	E310	M130	V190	170
K951	R951	K851	Y689	L567	C491	E431	L371	A311	S131	Q191	171
G1148	R952	R852	F705	D668	F492	S432	L371	T312	M132	Q192	172
D952	K148	N853	K706	A569	F492	S432	F372	T312	E131	Q192	172
N1149	R953	R853	K706	A569	F492	S432	F372	T312	E131	Q192	172
W1150	P953	R854	K706	A569	F492	S432	F372	T312	E131	Q192	172
E1151	E954	L855	L671	L570	G496	E434	Q374	G314	G134	I194	174
E1152	E954	K856	L671	L570	Q497	E434	Q374	G314	G134	I194	174
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R967	R968	L862	S722	N572	Q499	C436	N376	I316	E136	E196	176
K1162	R968	L862	Q723	N573	Q499	R437	N376	I316	E136	E196	176
A1178	R968	L862	D724	N574	K500	P438	N377	I317	Q137	H197	177
K1179	D984	H867	H728	P575	I501	V438	S378	V318	P138	A198	178
T1180	P985	E868	F729	S576	V502	L440	A380	N319	V139	I199	179
G869	P985	E868	F729	E577	L503	L440	A380	R320	K140	S200	180
N1181	M996	C870	C736	G578	L503	Q441	A381	K321	M141	F201	181
R1182	T997	E871	K737	P579	K507	Q442	K382	G322	F142	A202	182
L1183	A998	E872	T738	L580	Y508	G443	V383	Q323	D143	Q203	183
A1184	P1001	E872	T738	Q581	G509	R444	A384	V324	R144	F204	184
Y1237	P1001	E872	G739	T582	Y510	K445	A385	L325	H145	K205	185
K1246	L1004	A878	Q740	M590	D513	Q446	N386	S326	S146	M206	186
E1265	L1013	L879	I741	M590	D513	L447	A387	V327	S147	E207	187
F1266	D1014	L879	Y754	Q594	F516	L448	P388	C328	L148	Q208	188
R1267	R1251	K881	D755	V595	L517	E449	K389	V329	A149	N209	189
K1264	T1252	R882	F756	A596	L517	K450	G390	E330	G150	Q89	190
E1265	N1015	E883	E757	D597	N520	W451	I391	E331	C151	E211	191
F1266	S1016	T894	E757	D597	N520	L452	L392	E332	Q152	E212	192
R1267	I1033	D885	P773	D609	V521	K453	R393	N333	I153	S213	193
E1265	K1034	S886	L774	R610	M522	E454	T394	I334	I154	T214	194
R1267	D1054	N887	I775	A611	R523	D455	P395	I335	E94	E94	195
Q1270	M1077	N888	I775	H612	I524	K456	D396	P336	Y156	F216	196
M1271	N1078	N889	R780	Q615	S525	L457	T397	Y337	R157	C217	197
C1272	T1079	P890	F781	L616	P526	E458	I398	I338	T158	F218	198
L1274	S1080	R892	D786	L616	D527	C459	R399	T339	D159	Q98	199
H1275	E1087	F893	Y792	F630	Q528	S460	R400	N340	A160	V220	200
D1281	E1087	R894	Y792	T631	G529	E461	F401	V341	K161	R221	201
E1304	E1103	R895	R793	N647	Q530	E462	Q402	L342	Q162	Q222	202
E1304	E1104	E896	N794	P648	Q531	L463	S403	Q343	K163	H102	203
L1104	E1104	N897	N795	P648	F532	G464	V404	N344	W164	T103	204
P1105	P1105	N897	I800	E649	A533	G464	P405	P345	T105	M104	205
A1106	V1107	D901	I800	W650	Q534	L466	A406	D346	T106	Q226	206
M1332	Q1110	D901	I800	L651	M535	V467	Q407	L347	D107	K227	207
R1333	G1119	R912	F781	V652	Q538	K468	P408	A348	T108	D108	208
S1341	M1120	R912	V828	F655	D539	S469	Q409	L349	V108	Q109	209
A1399	V1121	D913	K830	F655	E540	V470	Q410	R350	F110	T230	210
	K1122	N831	N831	L658	E541	D471	T411	I231	W111	I170	211
				S659	P542	P472	S412	E232	S171	S171	212
				L543	F542	T473	P413	V233	A172	Q173	213
				A544	L543	L474	L414	G234	Q173	Q173	213
				D545	A544	A475	L414	T235	Q174	Q174	214
				I546	D545	L476	L415	M175	Q175	Q175	215
				T547	D545	S477	Q416	R176	L116	L116	216
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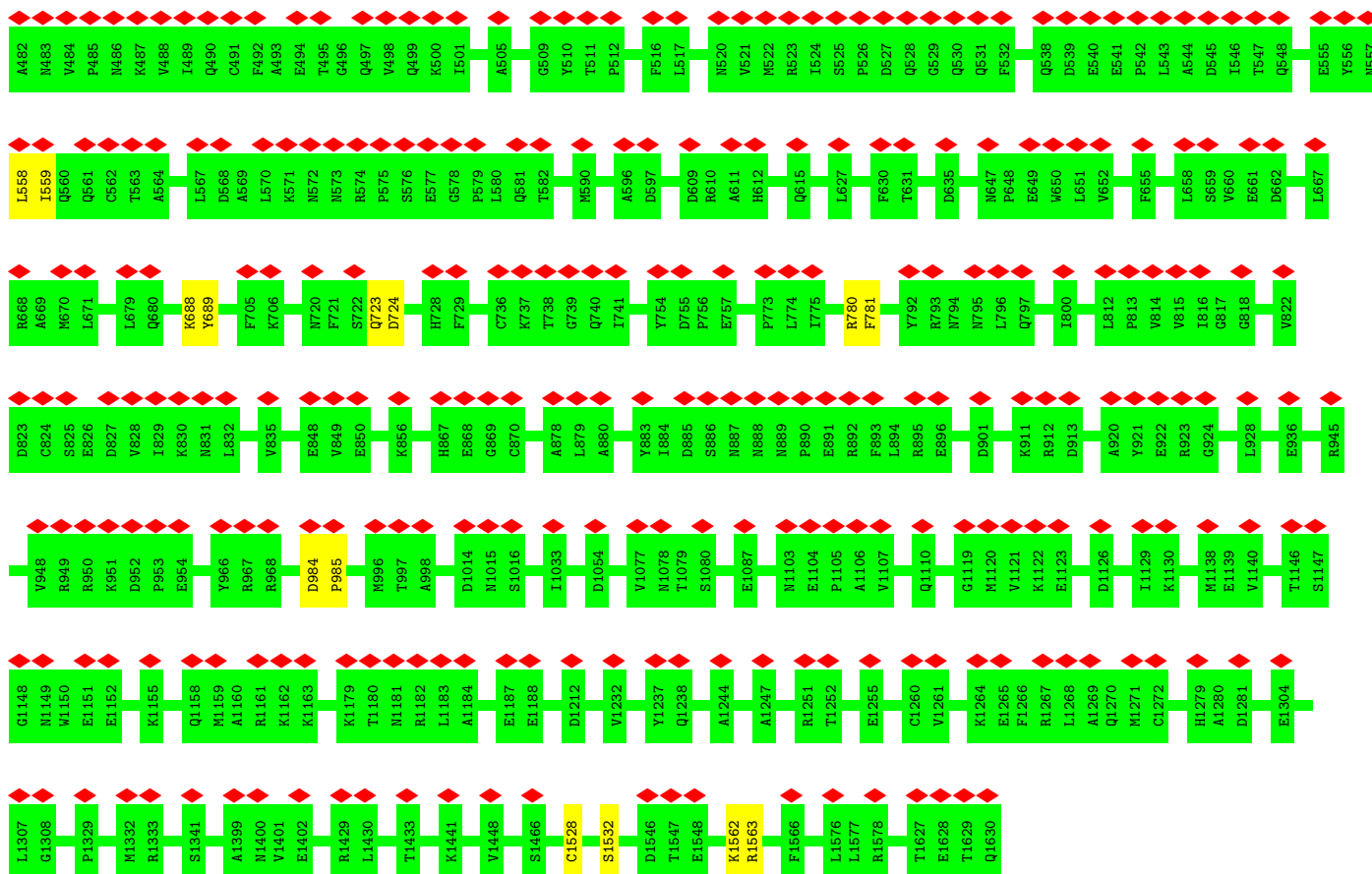
● Molecule 1: Clathrin heavy chain



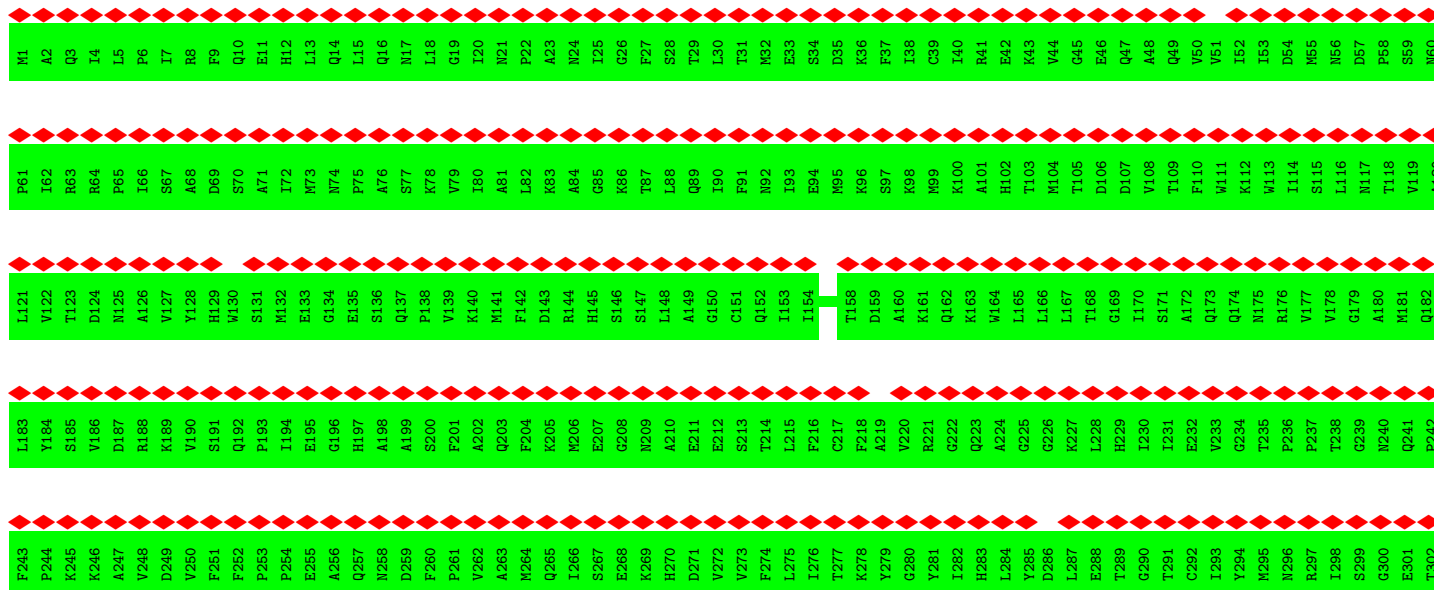


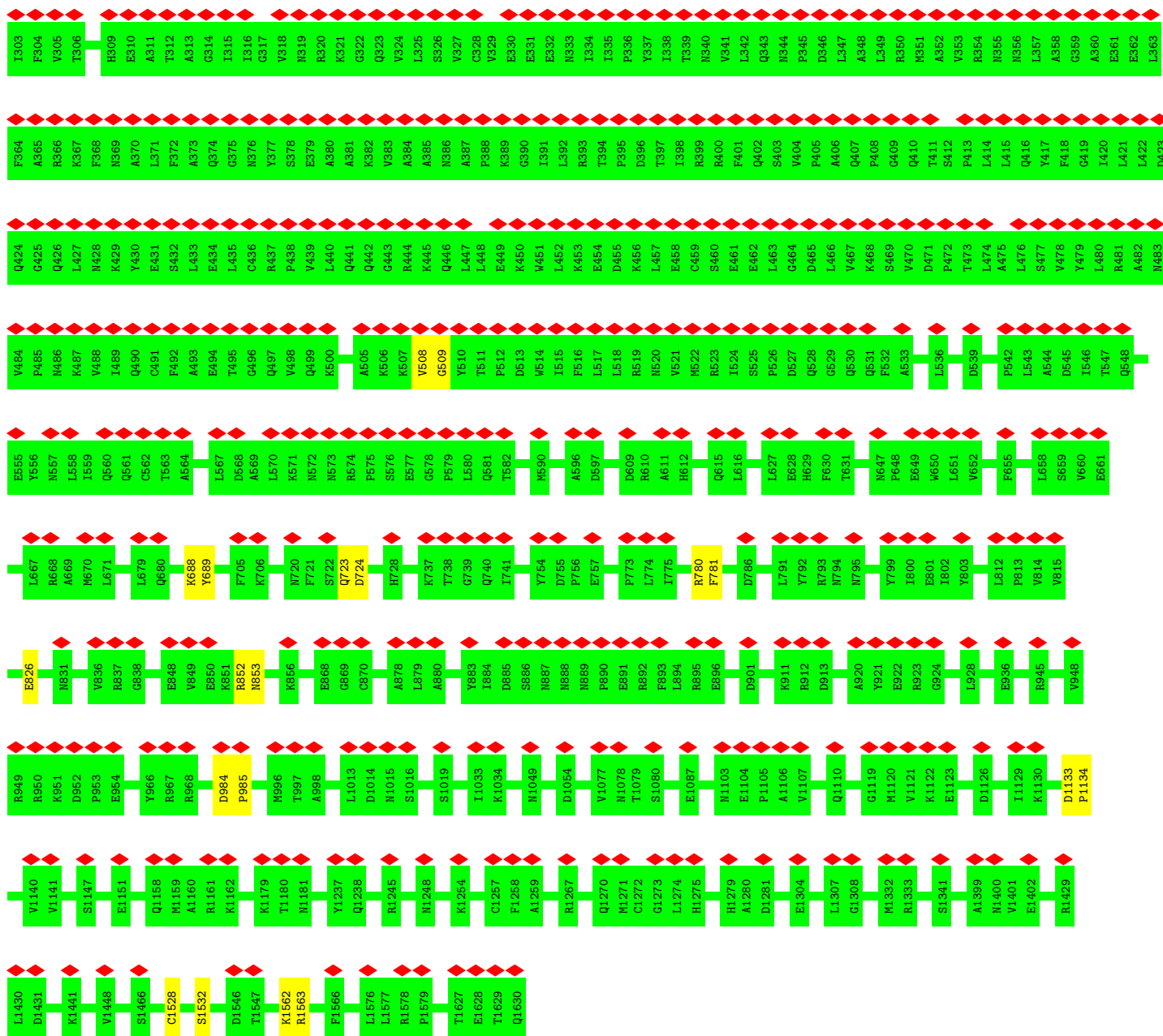
• Molecule 1: Clathrin heavy chain





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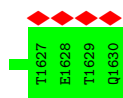




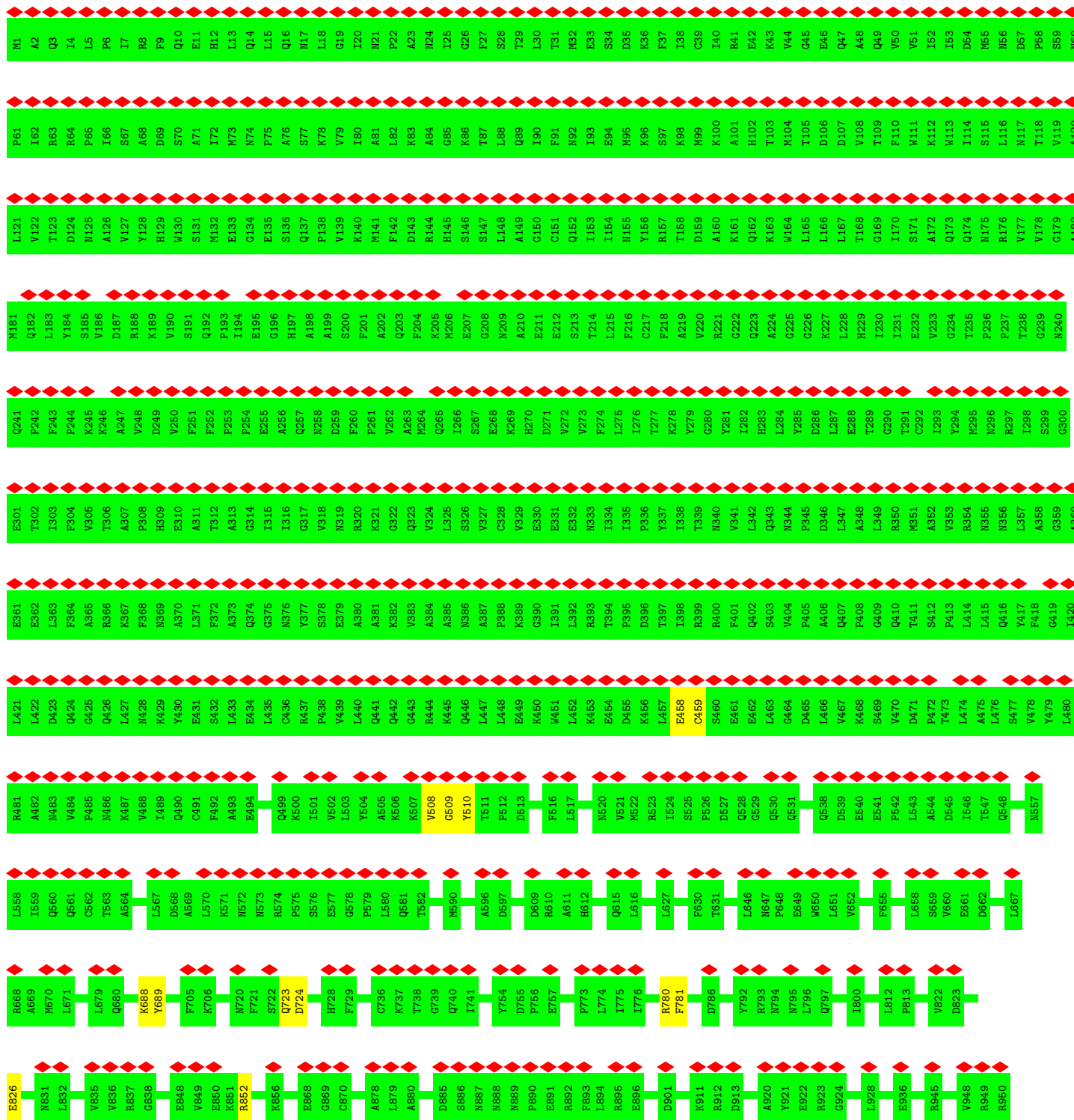
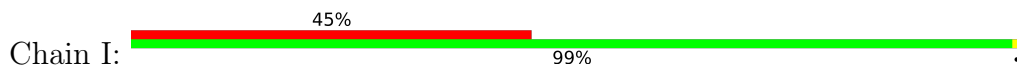
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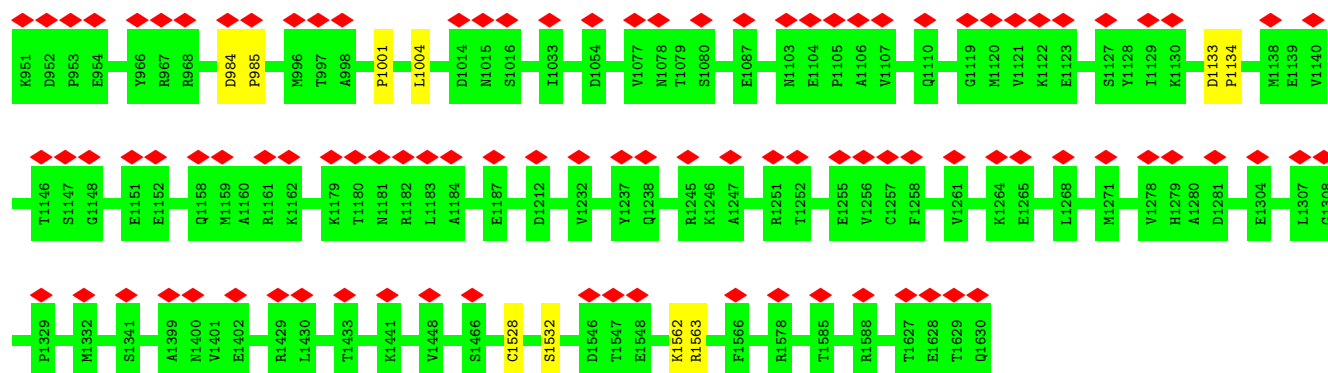


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F1266	K1130	R949	G838	R668	Q560	V488	L427	K367	P308	A247	V186	D124
R1267	D1133	R950	Q839	A669	Q561	L489	M428	F368	H309	V248	D187	N125
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C1272	M1138	P953	T842	A564	F492	F492	E431	L371	T312	F251	H129	Y128
H1275	T1146	E954	V846	L679	A493	E494	S432	F372	A313	F252	S191	H130
D1281	S1147	T966	A847	Q680	L567	T495	L433	A373	G314	P253	Q192	S131
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G1308	W1150	R984	E850	F705	L570	V498	C436	N376	G317	A256	G196	G134
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V1401	R1161	L1013	C870	F729	E577	K506	G443	V383	Q323	A263	Q203	K140
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R1578	S1222	N1078	F893	F781	P630	Q528	L463	S403	Q343	I282	Q222	Q162
T1585	V1232	T1079	R895	D786	T631	G529	G464	V404	N344	H283	Q223	K163
R1588	Y1237	S1080	E896	Y792	D635	Q530	D465	P405	D346	L284	A224	L164
	Q1238	E1087	D901	R793	L646	F532	L466	A406	L347	D286	G225	L165
	Q1238	N1103	K911	N794	N647	A533	V467	Q407	A348	L287	G226	L166
	R1245	E1104	R912	N795	P648	Q534	S469	G409	L349	E288	K227	L167
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	S1249	Q1110	E922	V828	V652	E541	L474	P413	V353	I293	E232	A172
	T1250	G1119	R923	I829	F655	P642	A475	L414	R354	Y294	V233	Q173
	R1251	M1120	Q924	K830	L658	L543	V478	Q416	N356	M295	G234	Q174
	D1262	V1121	L928	N831	S659	A544	Y479	Y417	L357	T235	R175	N175
			E936		V660	D545	F479	F418	A358	R297	P236	R176
						I546	L480	G359	G169	I298	T237	V177
						T547	R481	A419	S299	P237	V178	G179
						Q548	A482	I420	A360	G300	G239	A180
								L421	E362	E301	N240	M181
								L422	L363	T302	Q241	Q182



● Molecule 1: Clathrin heavy chain





• Molecule 2: Clathrin light chain A



• Molecule 2: Clathrin light chain A

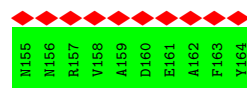
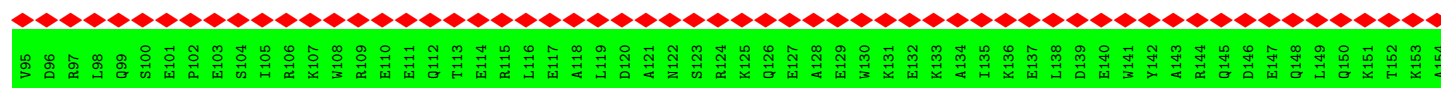


• Molecule 2: Clathrin light chain A

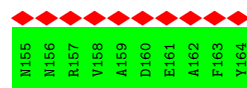


• Molecule 2: Clathrin light chain A

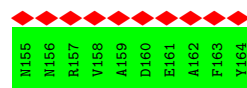
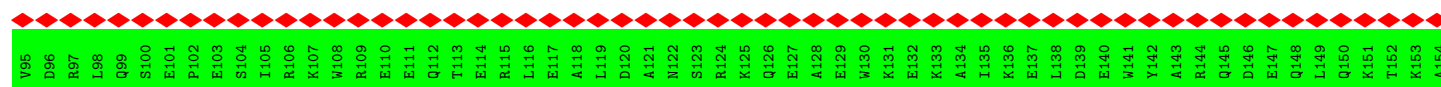




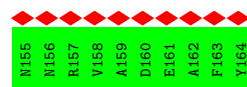
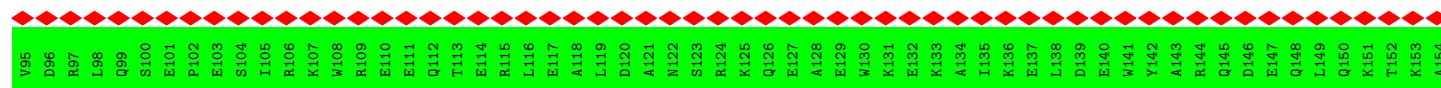
• Molecule 2: Clathrin light chain A



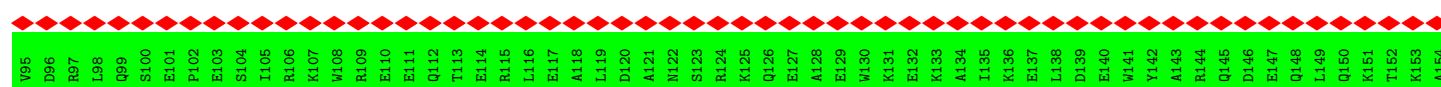
• Molecule 2: Clathrin light chain A



• Molecule 2: Clathrin light chain A



• Molecule 2: Clathrin light chain A



N155	N156	R157	V158	A159	D160	E161	A162	F163	Y164
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● Molecule 2: Clathrin light chain A



V95	D96	R97	L98	Q99	S100	E101	P102	E103	S104	I105	R106	K107	W108	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
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N155	N156	R157	V158	A159	D160	E161	A162	F163	Y164
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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 ($\text{\AA}$)	873.6, 873.6, 873.6	wwPDB
Map dimensions	312, 312, 312	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing ($\text{\AA}$)	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 oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

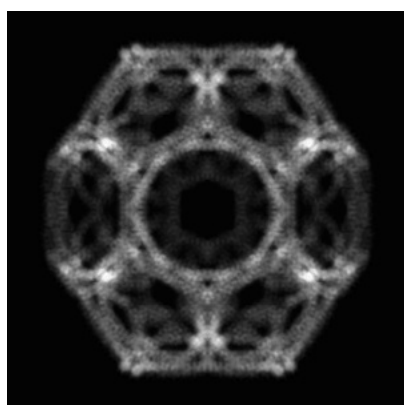
6 Map visualisation [i](#)

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.

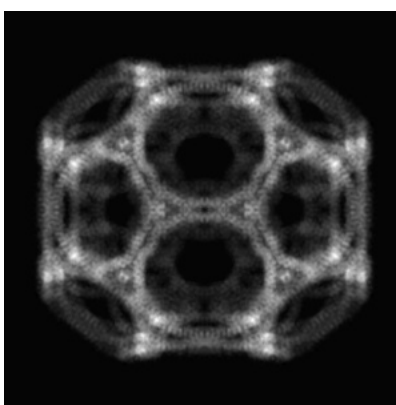
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

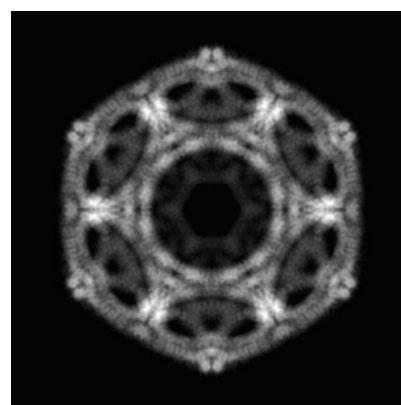
6.1.1 Primary map



X



Y

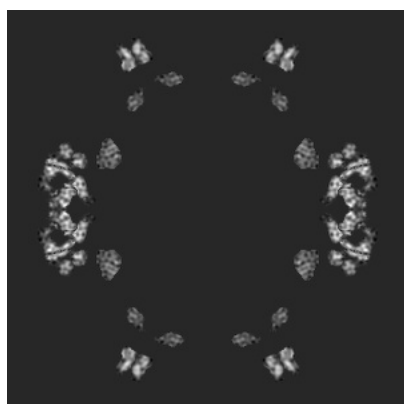


Z

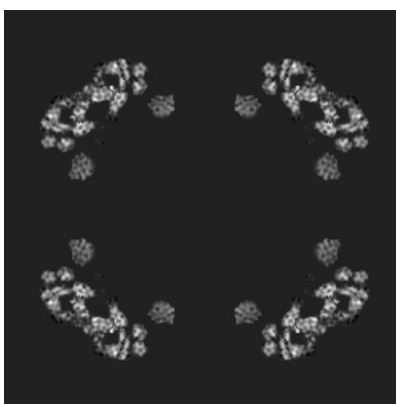
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

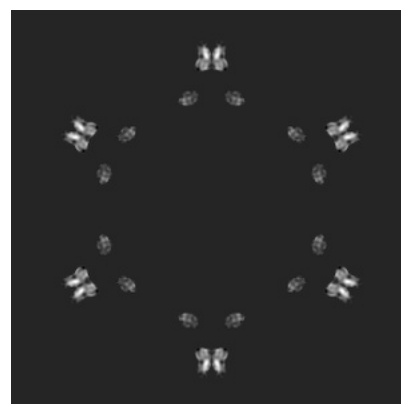
6.2.1 Primary map



X Index: 156



Y Index: 156

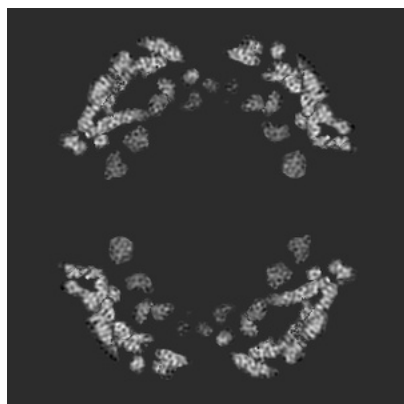


Z Index: 156

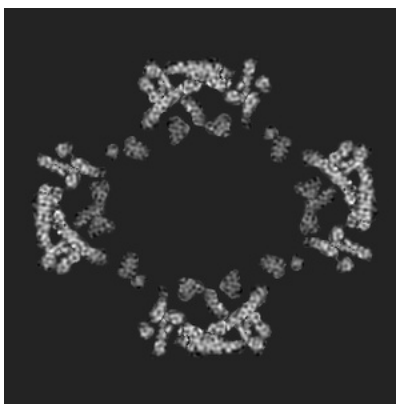
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

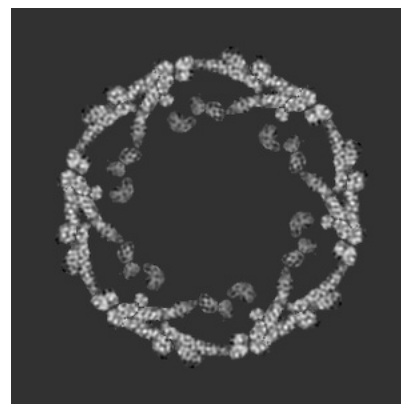
6.3.1 Primary map



X Index: 114



Y Index: 101

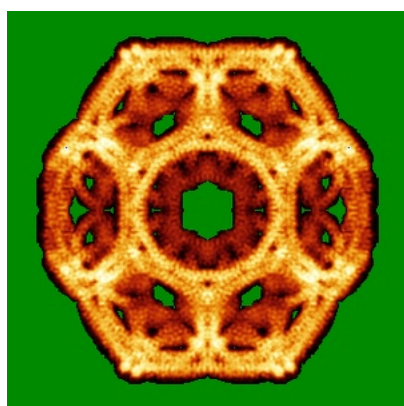


Z Index: 205

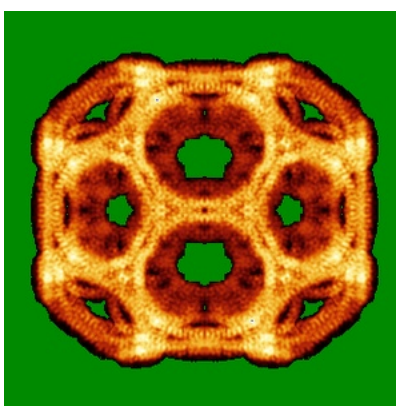
The images above show the largest variance slices of the map in three orthogonal directions.

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

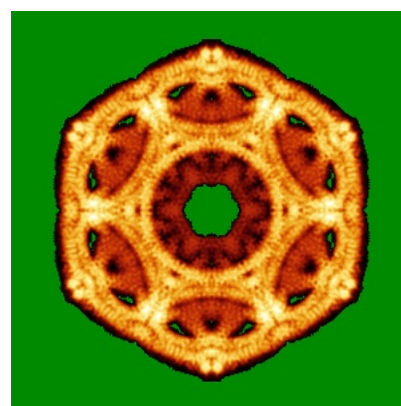
6.4.1 Primary map



X



Y

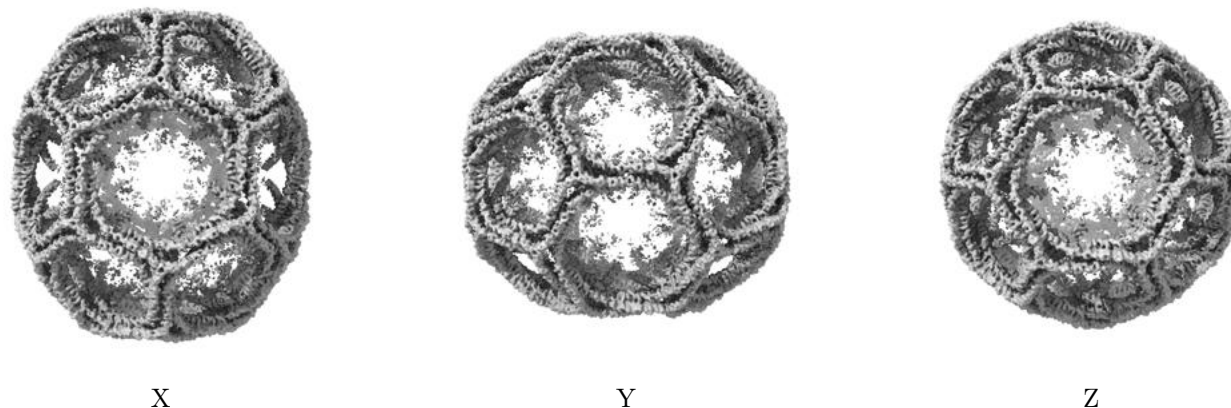


Z

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.

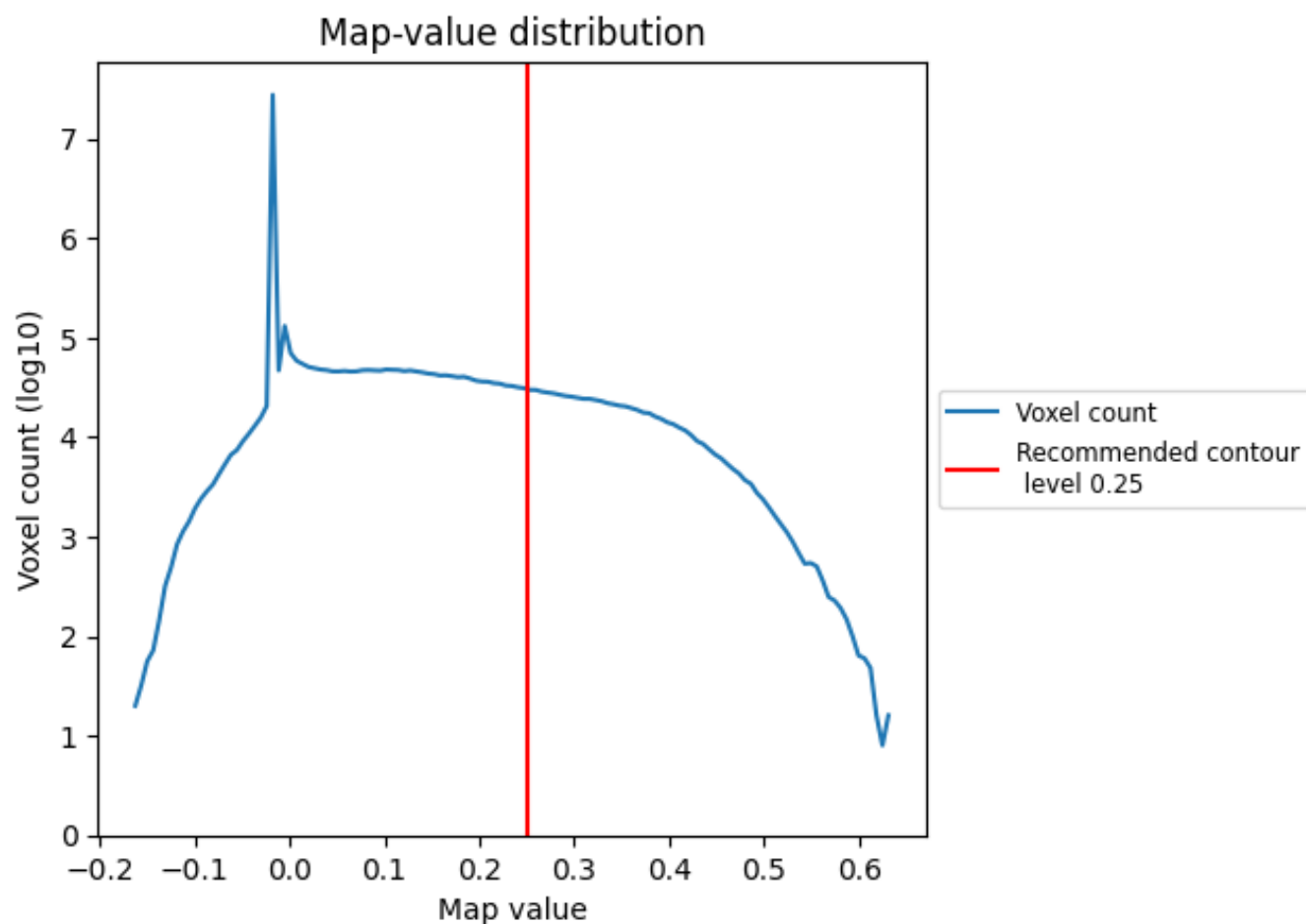
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

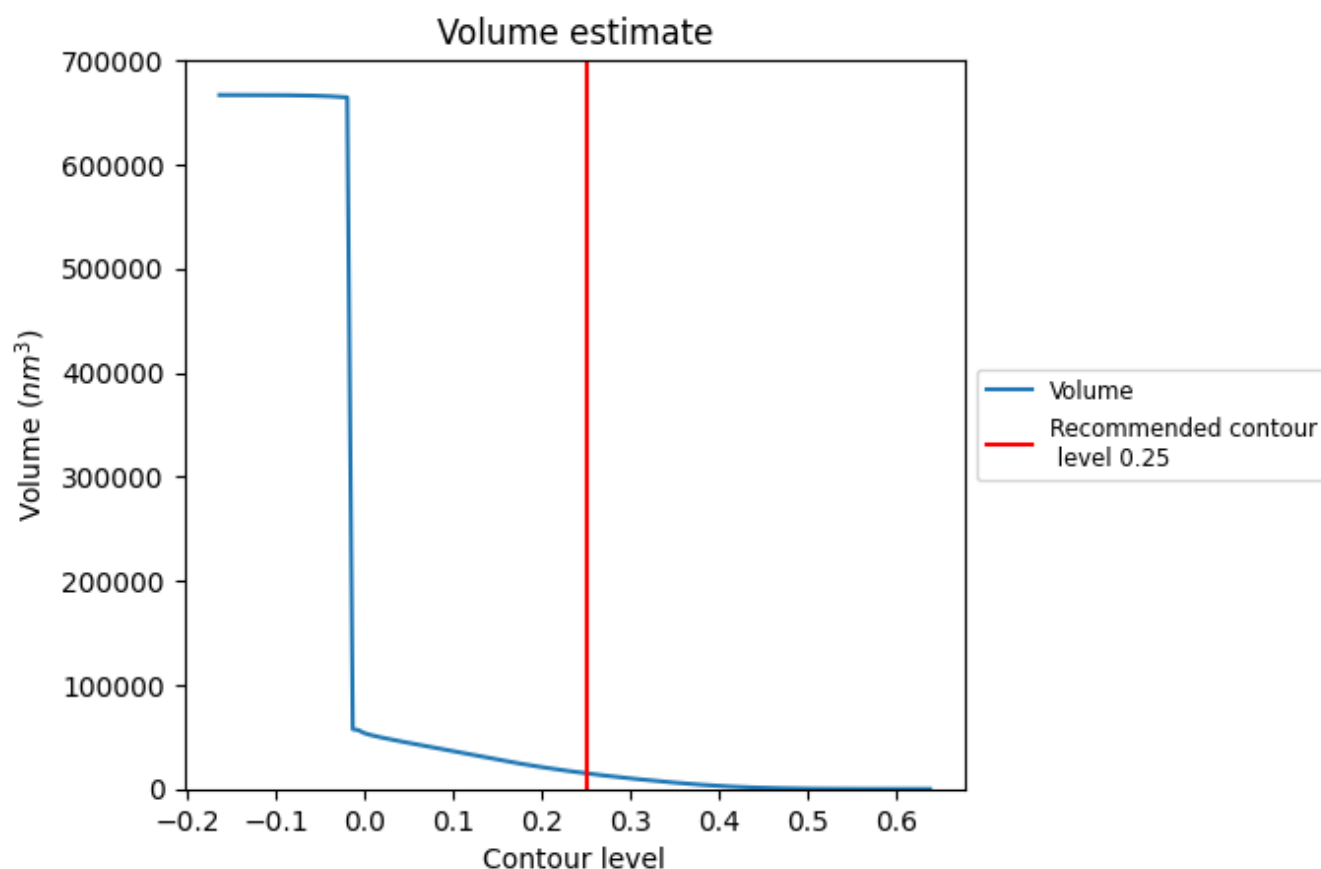
This section contains the results of statistical analysis of the map.

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.

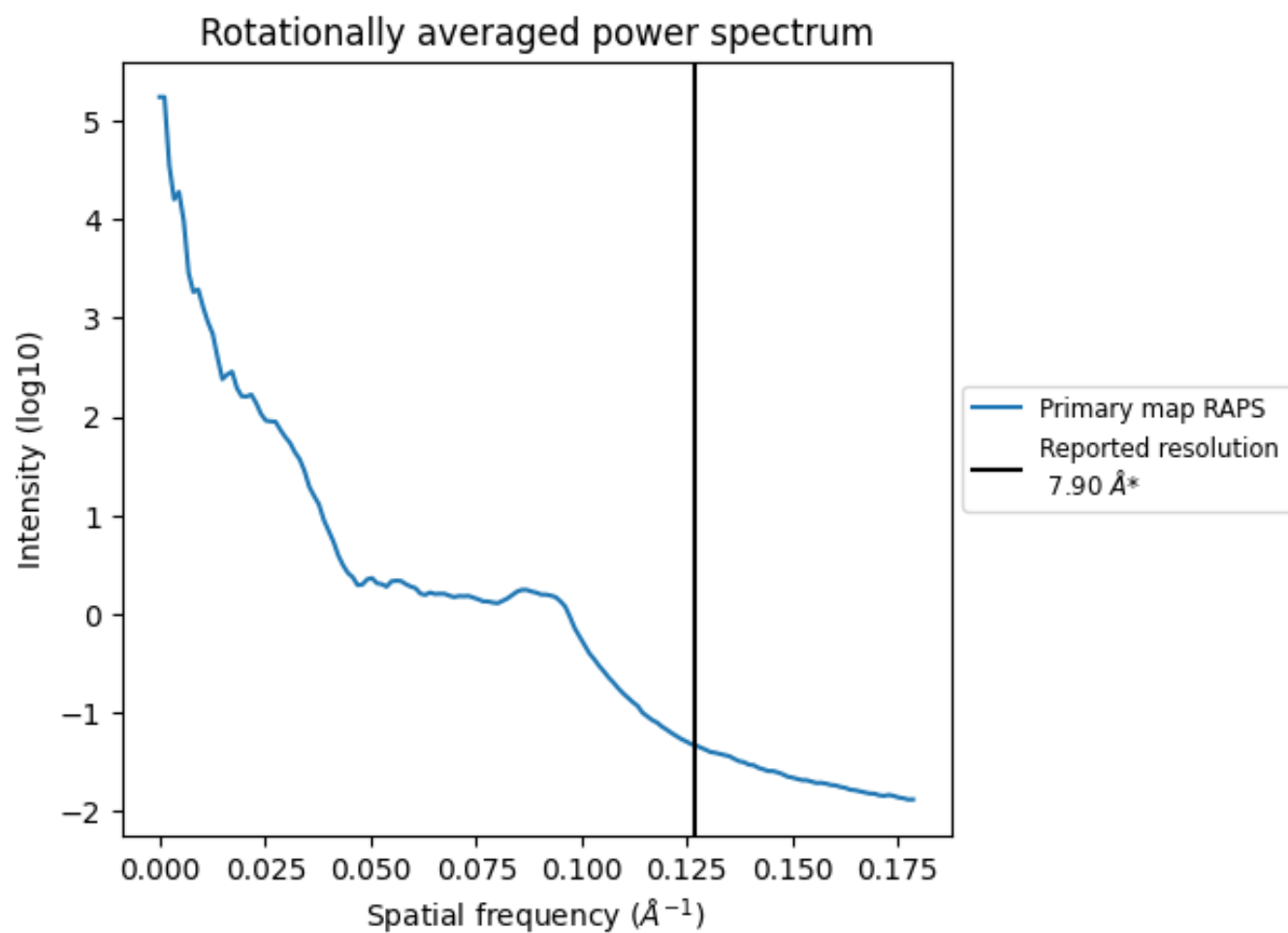
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 15047 nm^3 ; 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.127 Å⁻¹

8 Fourier-Shell correlation

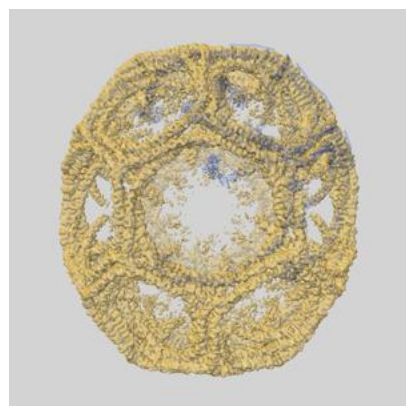
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

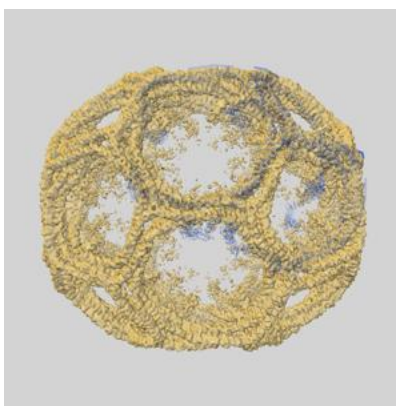
This section contains information regarding the fit between EMDB map EMD-5119 and PDB model 3IYV. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlays

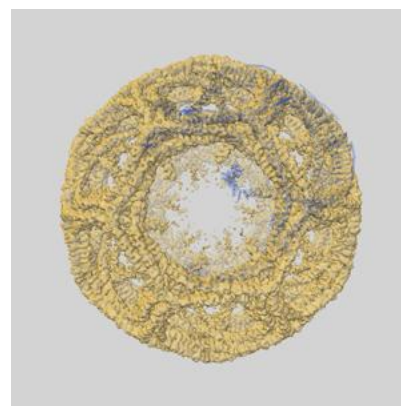
9.1.1 Map-model overlay [i](#)



X



Y



Z

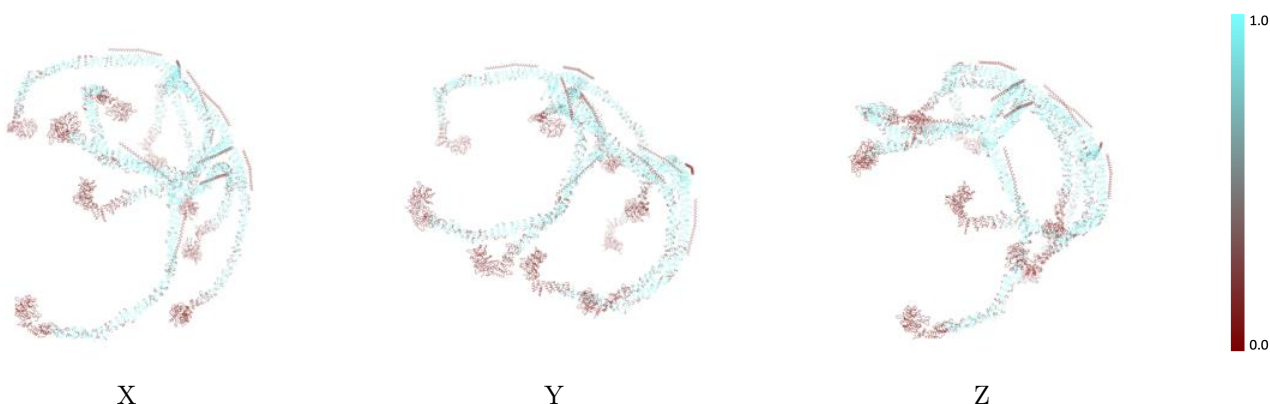
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



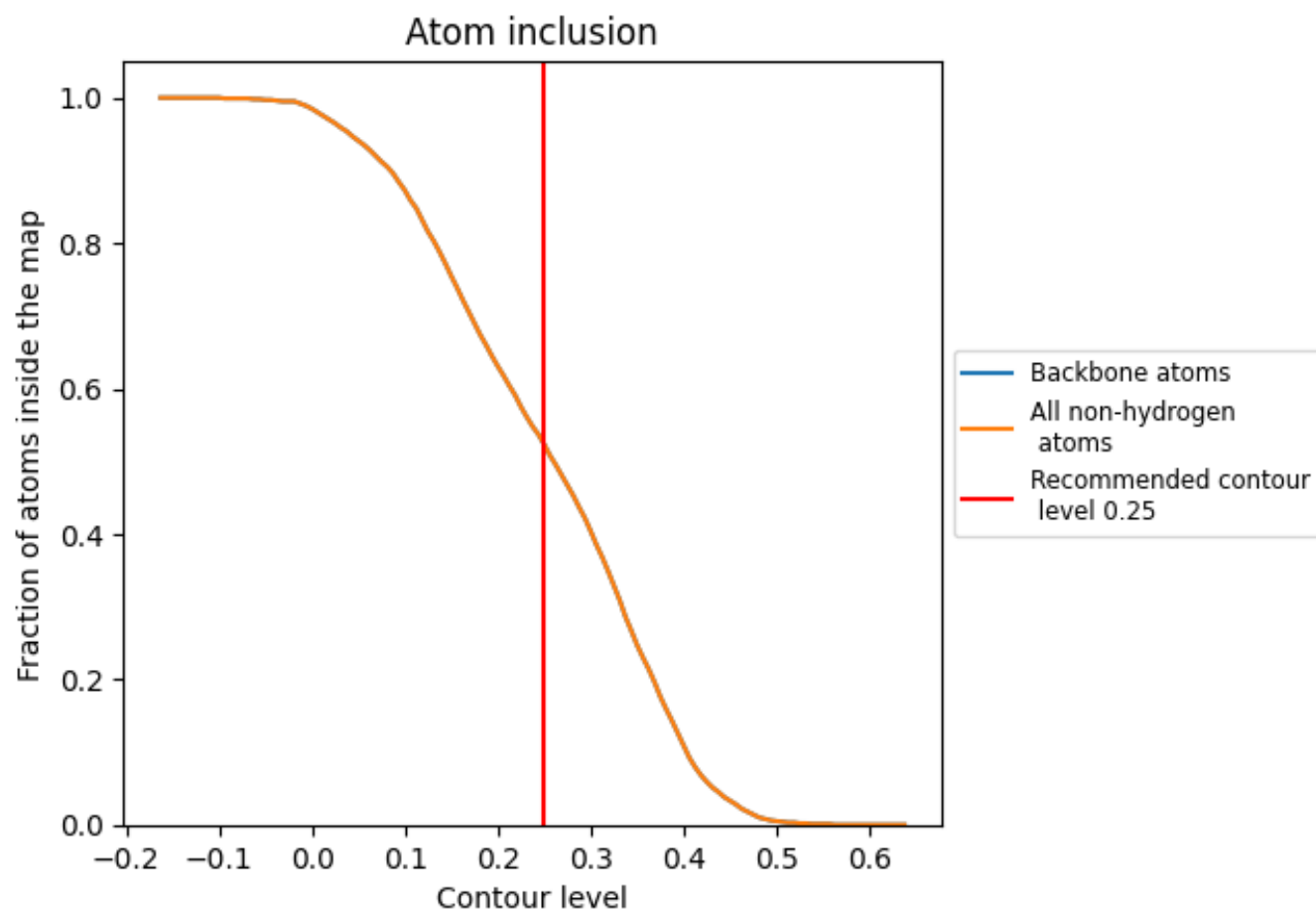
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

