



Full wwPDB EM Validation Report ⓘ

Nov 19, 2022 – 05:57 PM 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 Full wwPDB EM Validation 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.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

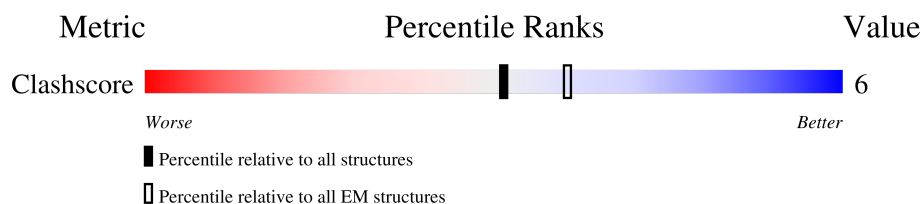
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

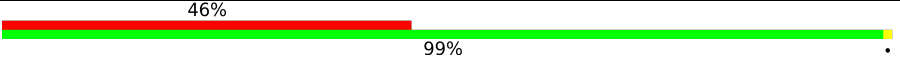
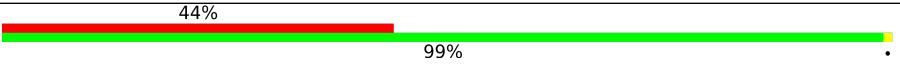
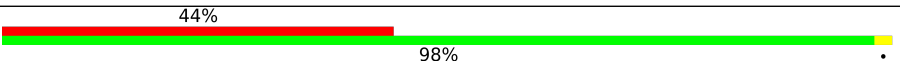
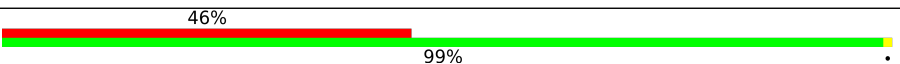
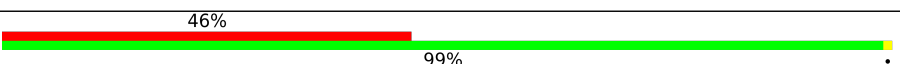
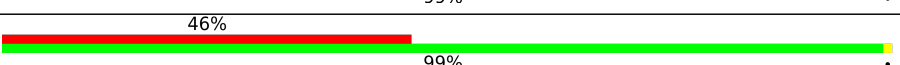
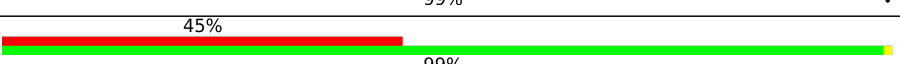
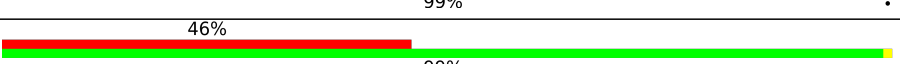
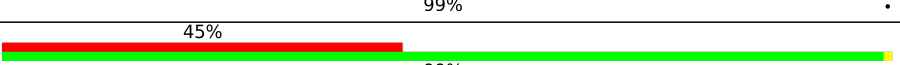
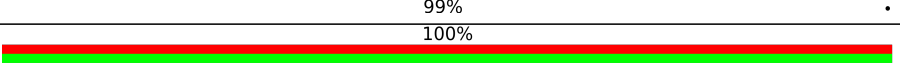
The reported resolution of this entry is 7.90 Å.

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	
1	B	1630	
1	C	1630	
1	D	1630	
1	E	1630	
1	F	1630	
1	G	1630	
1	H	1630	
1	I	1630	
2	J	70	

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Mol	Chain	Length	Quality of chain
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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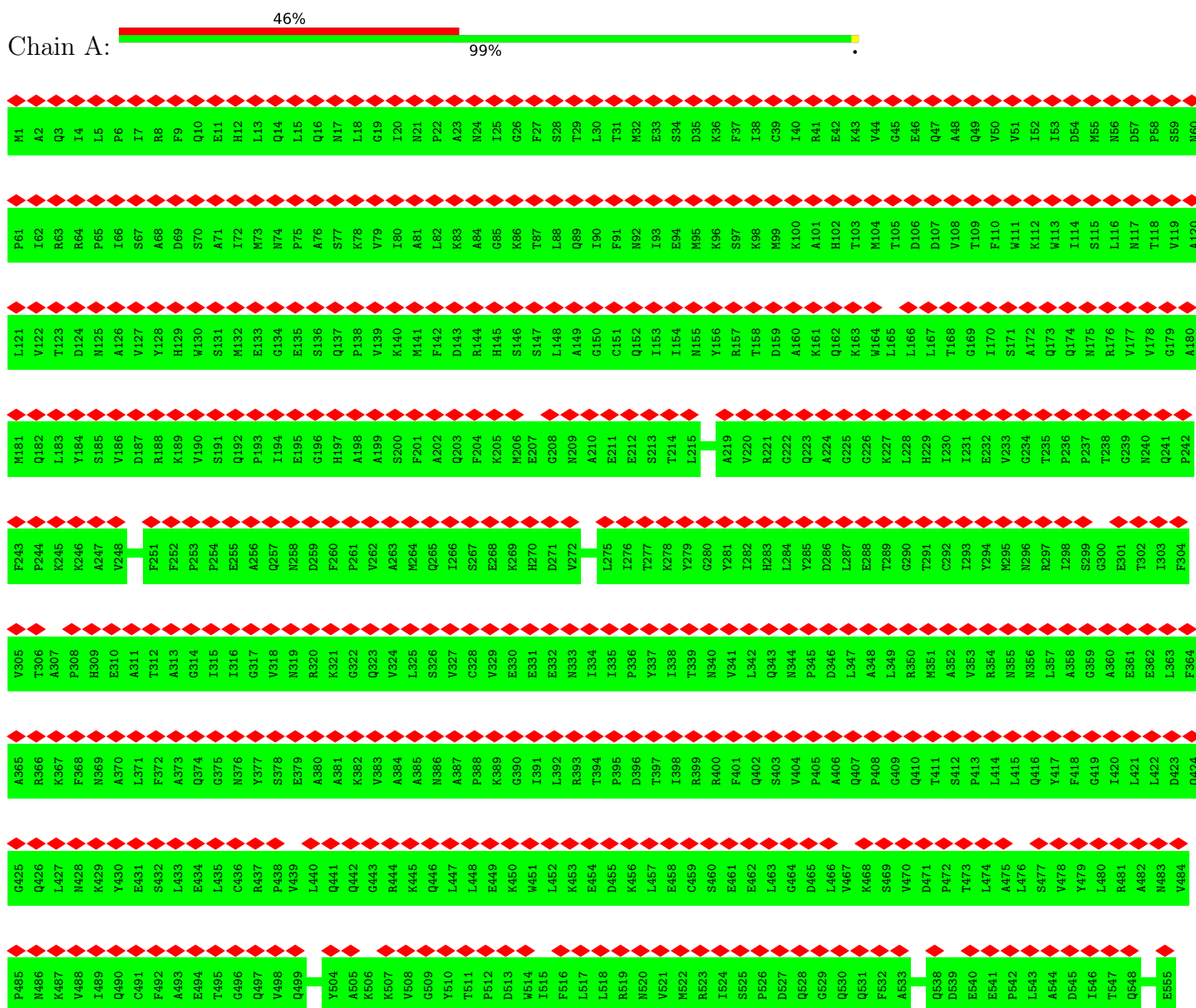
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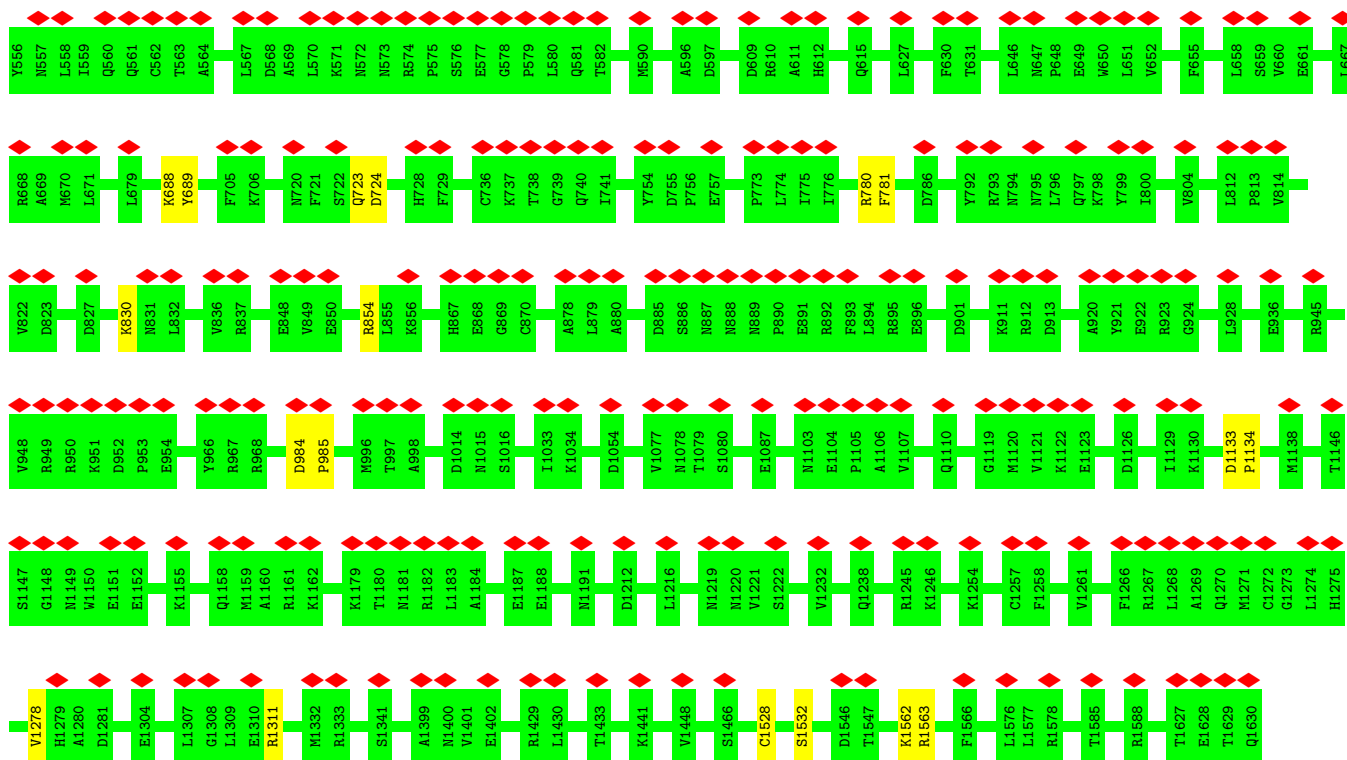
Mol	Chain	Residues	Atoms		AltConf	Trace
2	P	70	Total 70	C 70	0	70
2	Q	70	Total 70	C 70	0	70
2	R	70	Total 70	C 70	0	70

3 Residue-property plots

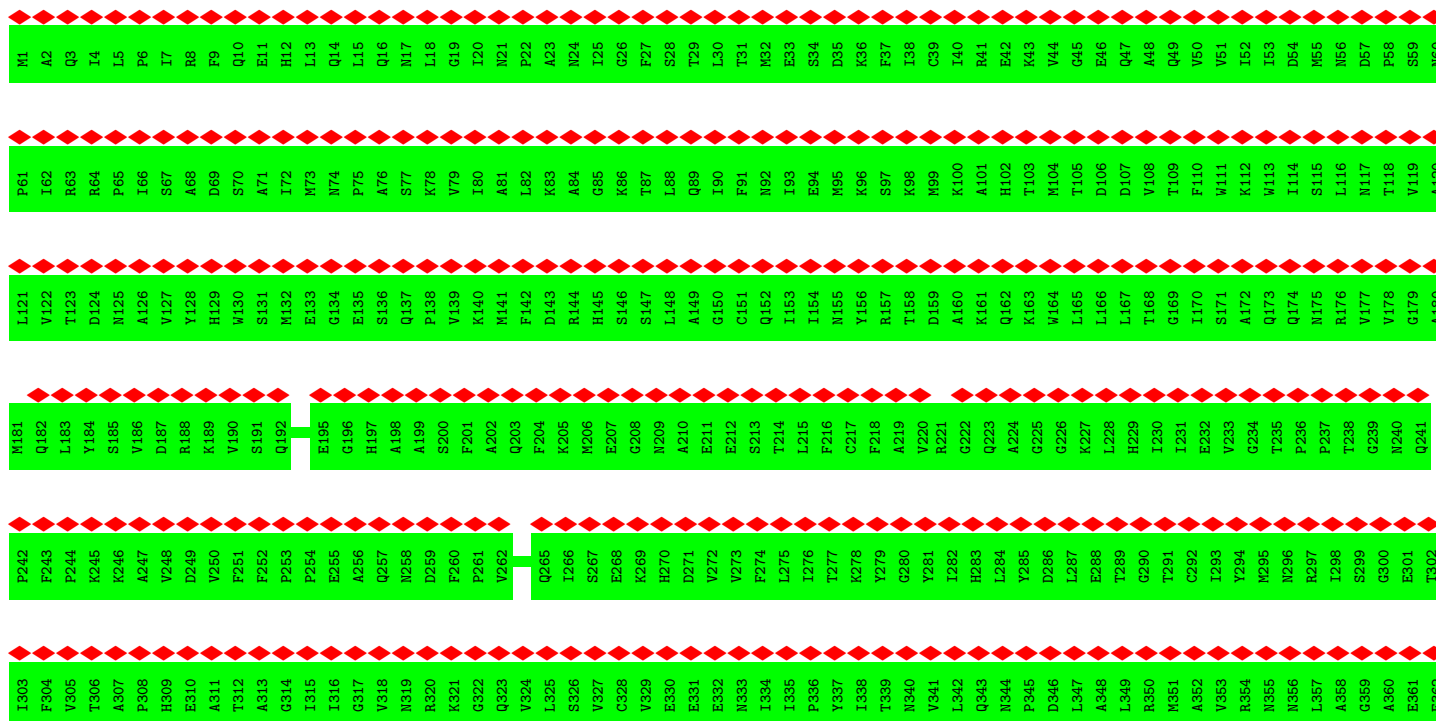
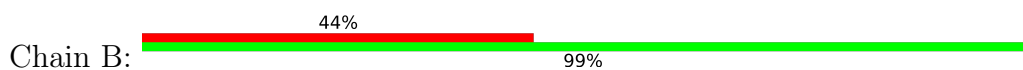
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

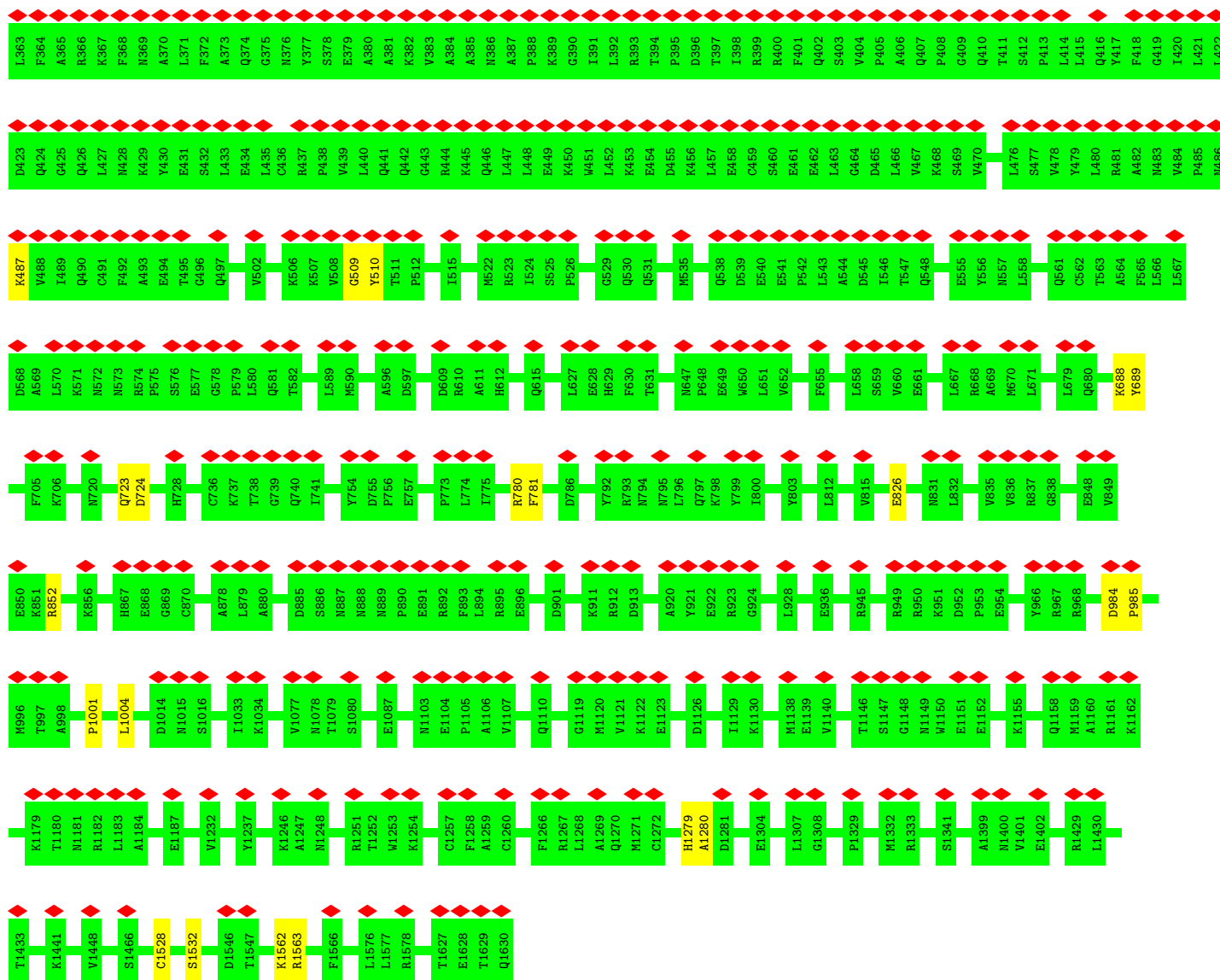
• Molecule 1: Clathrin heavy chain



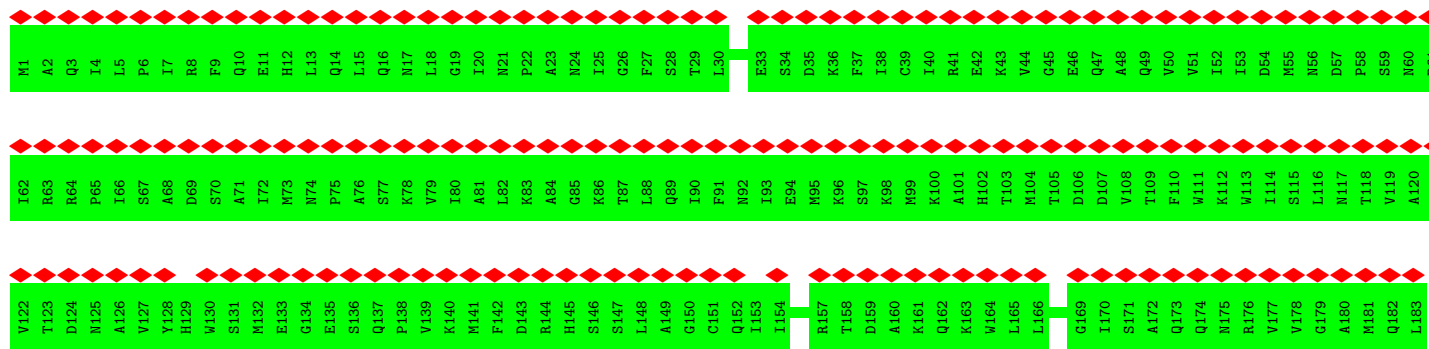
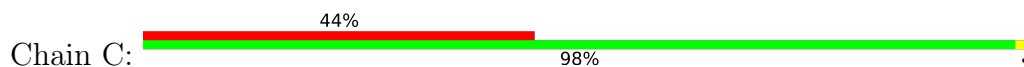


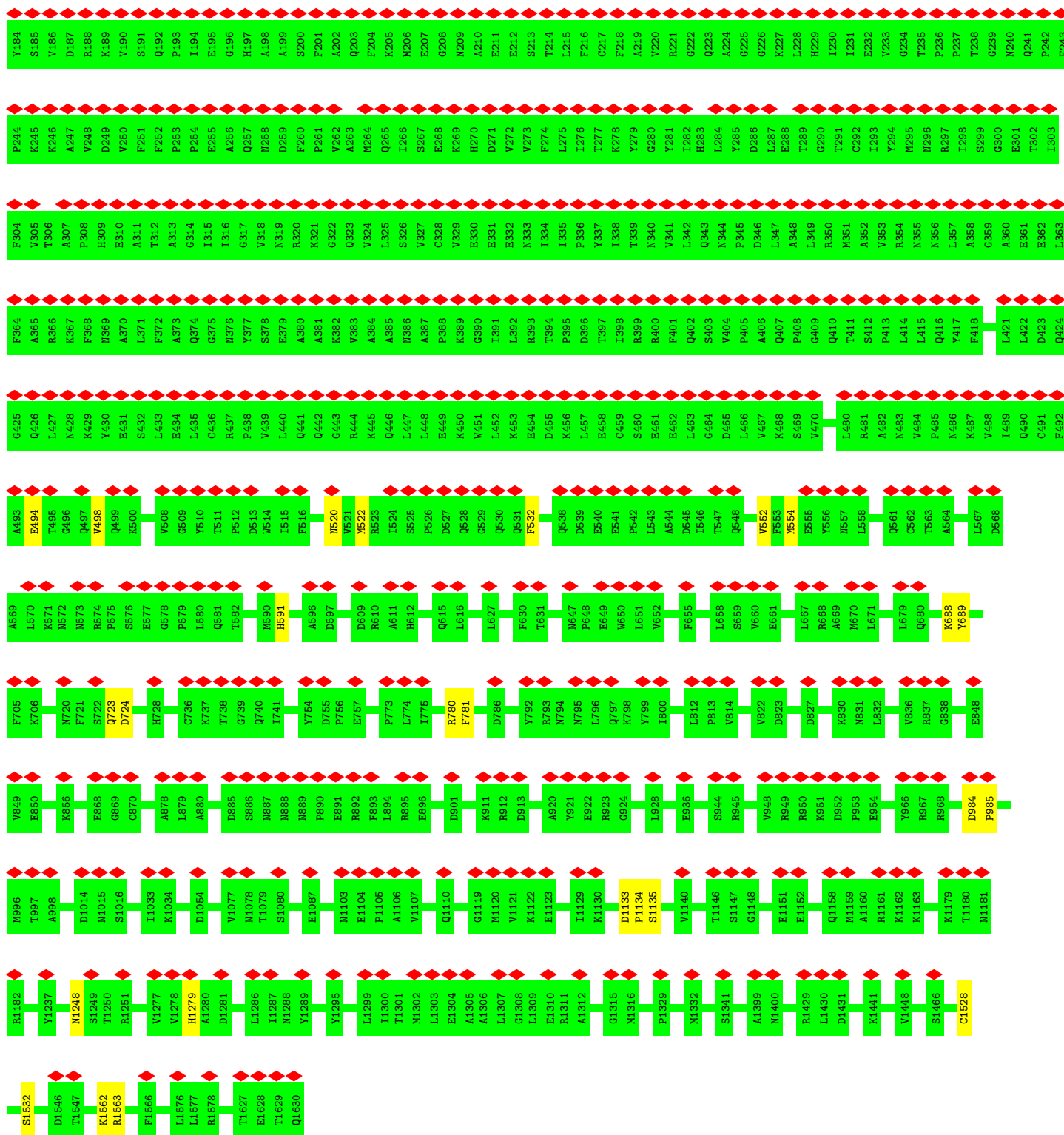
• Molecule 1: Clathrin heavy chain





• Molecule 1: Clathrin heavy chain

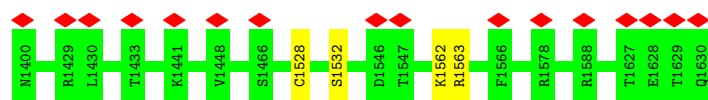




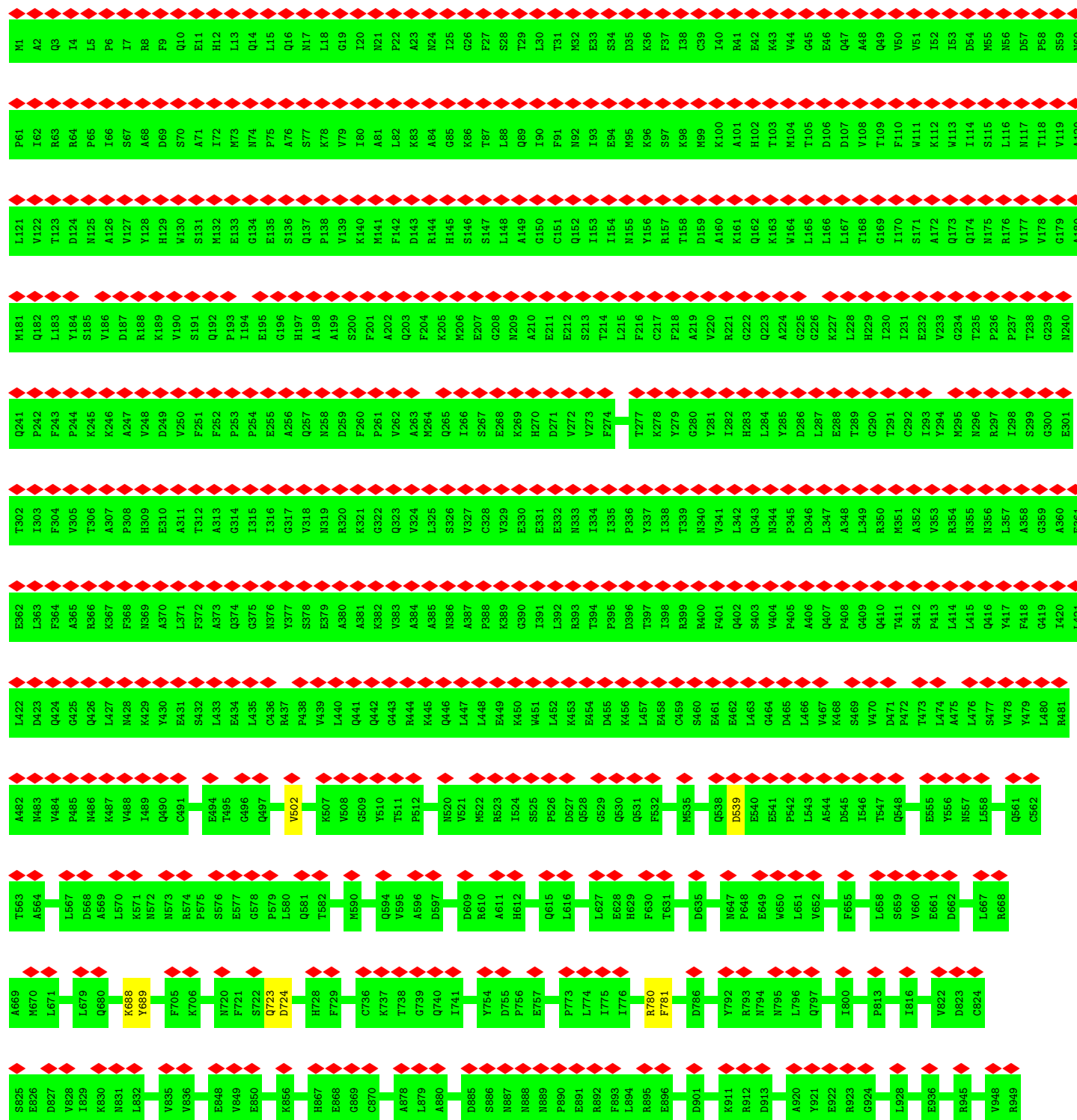
• Molecule 1: Clathrin heavy chain

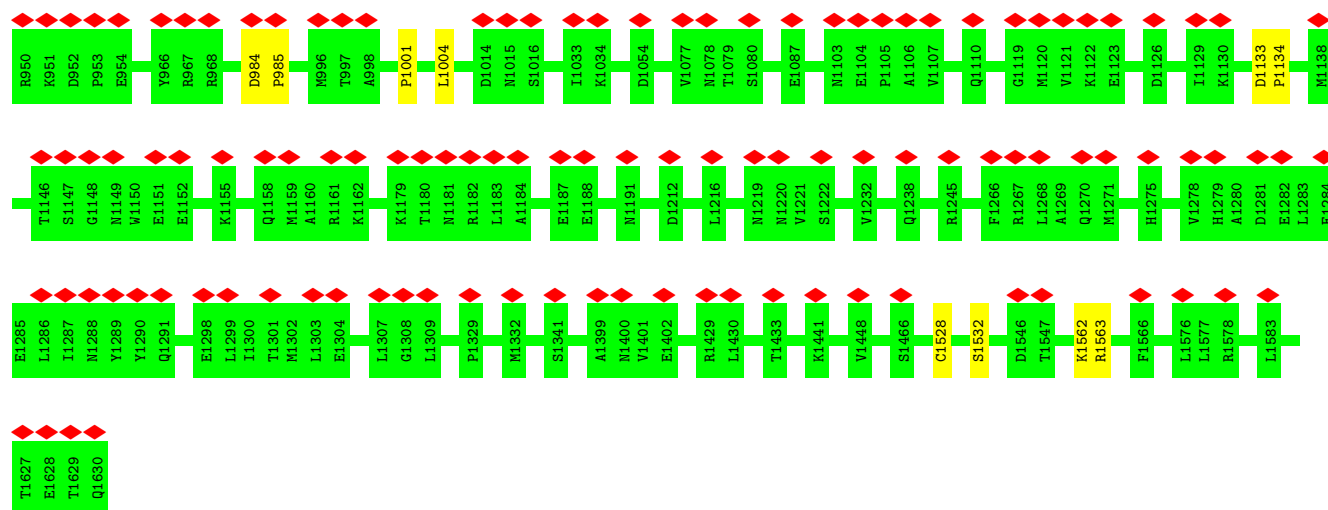


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I1129	E936	D843	A669	L558	N483	D423	L363	I303	T123	L183	T123	Q3
K1130	S944	E844	M670	Q560	V484	Q424	F364	F304	D124	Y184	D124	L4
D1133	R945	L845	L671	Q561	N486	G425	A365	T306	M125	S185	M125	L5
P1134	R945	L845	L671	Q561	N486	Q426	R366	T306	A126	V186	A126	P6
T1146	V948	E848	L679	C562	K487	L427	K367	A307	V127	D187	V127	I7
R949	R949	V849	Q680	T563	V488	N428	F368	P308	H128	R188	H128	R8
R950	R949	E850	K688	A564	I489	K429	N369	H309	D249	I189	D249	F9
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N952	K951	R852	F705	D668	C491	E431	L371	A311	S131	A71	S131	E11
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W1150	P953	R854	N720	L570	G496	L433	A373	A313	E133	P193	E133	L13
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E1152	Y965	K856	S722	N572	Q499	L435	G375	I315	E135	E195	E135	L15
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T1180	P985	E868	F729	E577	L503	L440	A380	R320	V139	A199	V139	G19
G969	T997	C870	C736	P579	K507	Q441	A381	K321	K140	S200	K140	I20
L1182	A998	E871	T738	L580	V508	Q442	K382	G322	F142	A202	F142	P22
A1184	P1001	E872	G739	T582	G509	R444	A384	Q323	D143	Q203	D143	A23
Y1237	L1004	A878	Q740	M590	Y510	K445	A385	L325	R144	F204	R144	N24
K1246	K1246	L879	I741	D590	D513	L447	A387	V327	H145	K205	H145	I25
E1265	F1266	R881	Y754	Q594	F516	L448	P388	C328	S146	M206	S146	G26
R1267	R1267	K881	D755	A596	L517	E449	K389	V329	I147	E207	I147	F27
I1033	K1034	R887	E757	D597	N520	L452	L391	E331	L148	Q208	L148	S28
E1265	F1266	S886	P773	D609	V521	E454	T394	N333	A149	M209	A149	T29
R1267	R1267	N887	L774	R610	M522	E454	P395	I334	G150	Q89	G150	L30
Q1270	D1054	N888	I775	A611	I524	D455	D396	P336	C151	F91	C151	T31
M1271	V1077	P890	R780	Q615	S525	L457	T397	Y337	Q152	N92	Q152	M32
C1272	T1079	R892	F781	L616	P526	E458	I398	I338	I153	I93	I153	E33
G1273	S1080	F893	D786	F630	D527	C459	R399	T339	E94	E94	E94	S34
H1275	E1087	R894	Y792	T631	Q528	S460	R400	N340	M95	M95	M95	D35
D1281	E1304	R896	L774	N647	R523	E461	F401	V341	K96	K96	K96	K36
E1304	E1104	N897	I775	P648	I524	D465	Q402	L342	R157	S97	R157	F37
E1104	P1105	D901	R780	E649	S525	L466	T397	L338	T158	K98	T158	I38
L1307	A1106	K911	F781	W650	P526	L466	Q407	T339	D159	M99	D159	C39
Q1308	V1107	R912	D786	L651	D527	V467	P408	V220	K100	K100	K100	I40
M1332	R1333	D913	I829	V652	Q538	K468	Q409	R221	A101	A101	A101	R41
S1341	A1399	A920	K830	F655	D539	S469	Q410	Q222	H102	H102	H102	E42
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		K1122	V836	S659	P542	P472	S412	V233	W164	W164	W164	V44
		V1121	R837	V660	L543	T473	P413	I293	T105	T105	T105	G45
		K1122		E661	A544	L474	L414	G294	D106	D106	D106	E46
				D662	D545	L476	L415	N296	D107	D107	D107	Q47
					I546	S477	Q416	R297	T108	T108	T108	A48
					T547	V478	Y417	L298	Q49	Q49	Q49	Q49
					Q548	Y479	F418	G239	F110	F110	F110	V50
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									K112	K112	K112	I53
									Q174	Q174	Q174	D54
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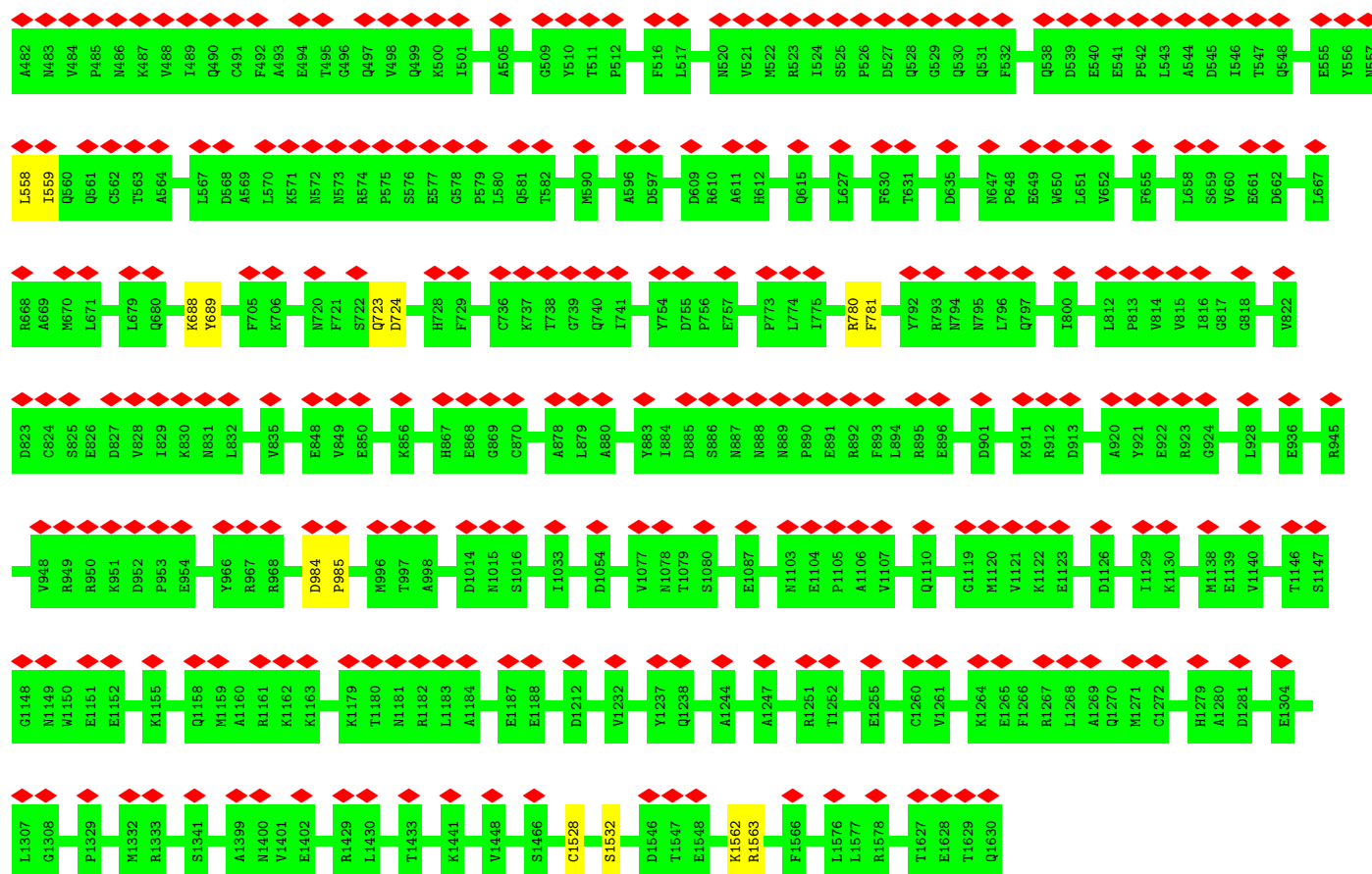
● Molecule 1: Clathrin heavy chain



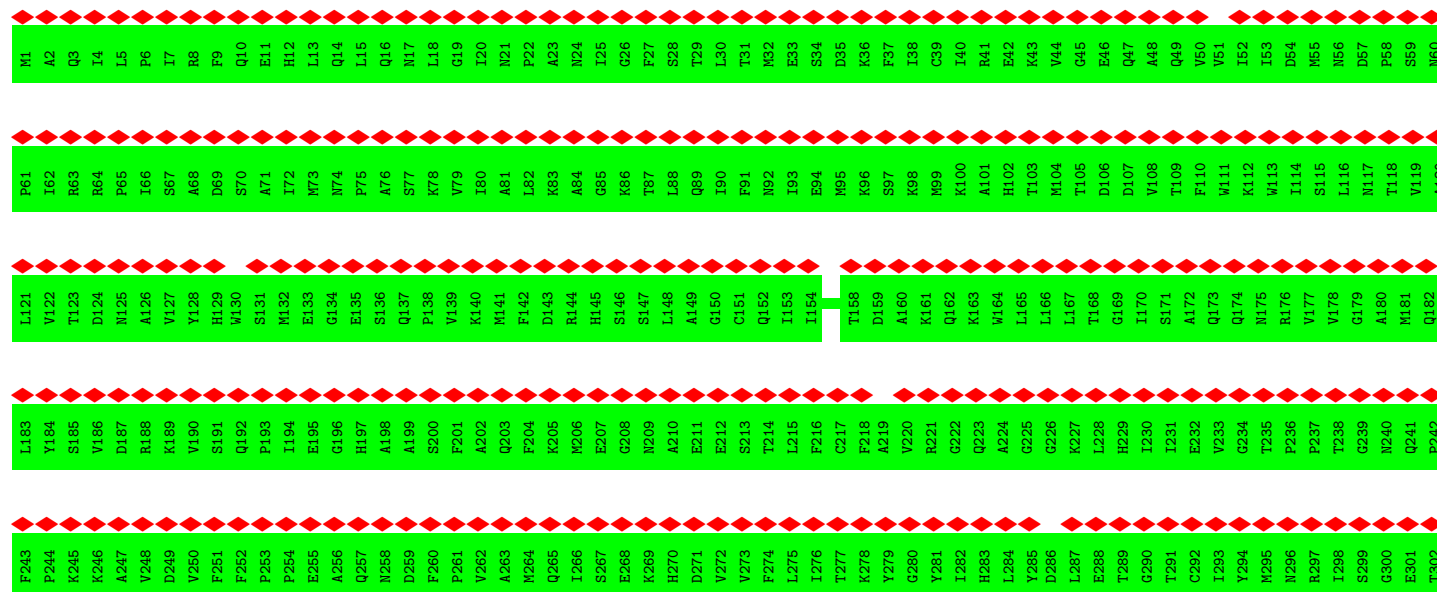


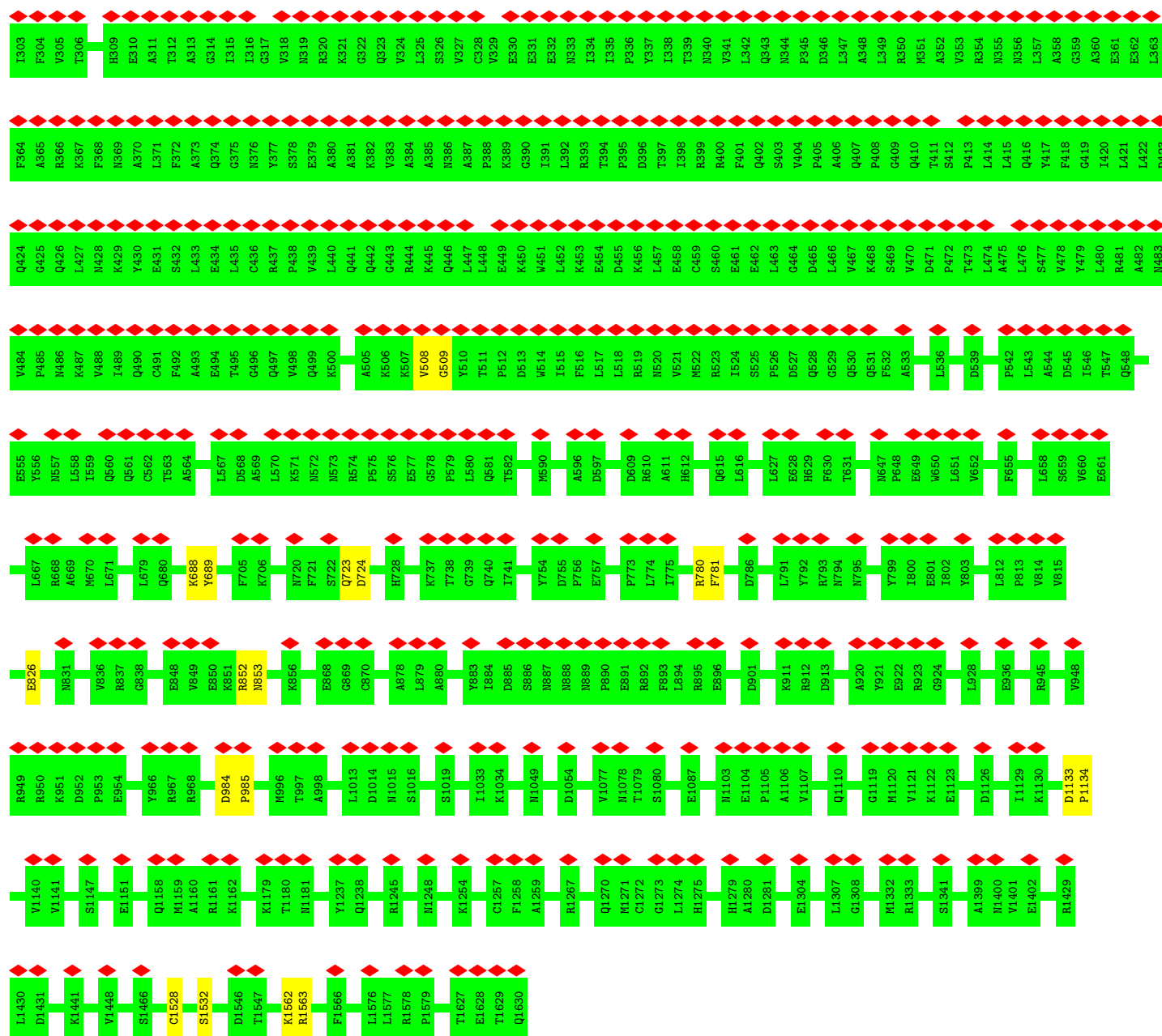
● Molecule 1: Clathrin heavy chain





• Molecule 1: Clathrin heavy chain

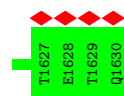




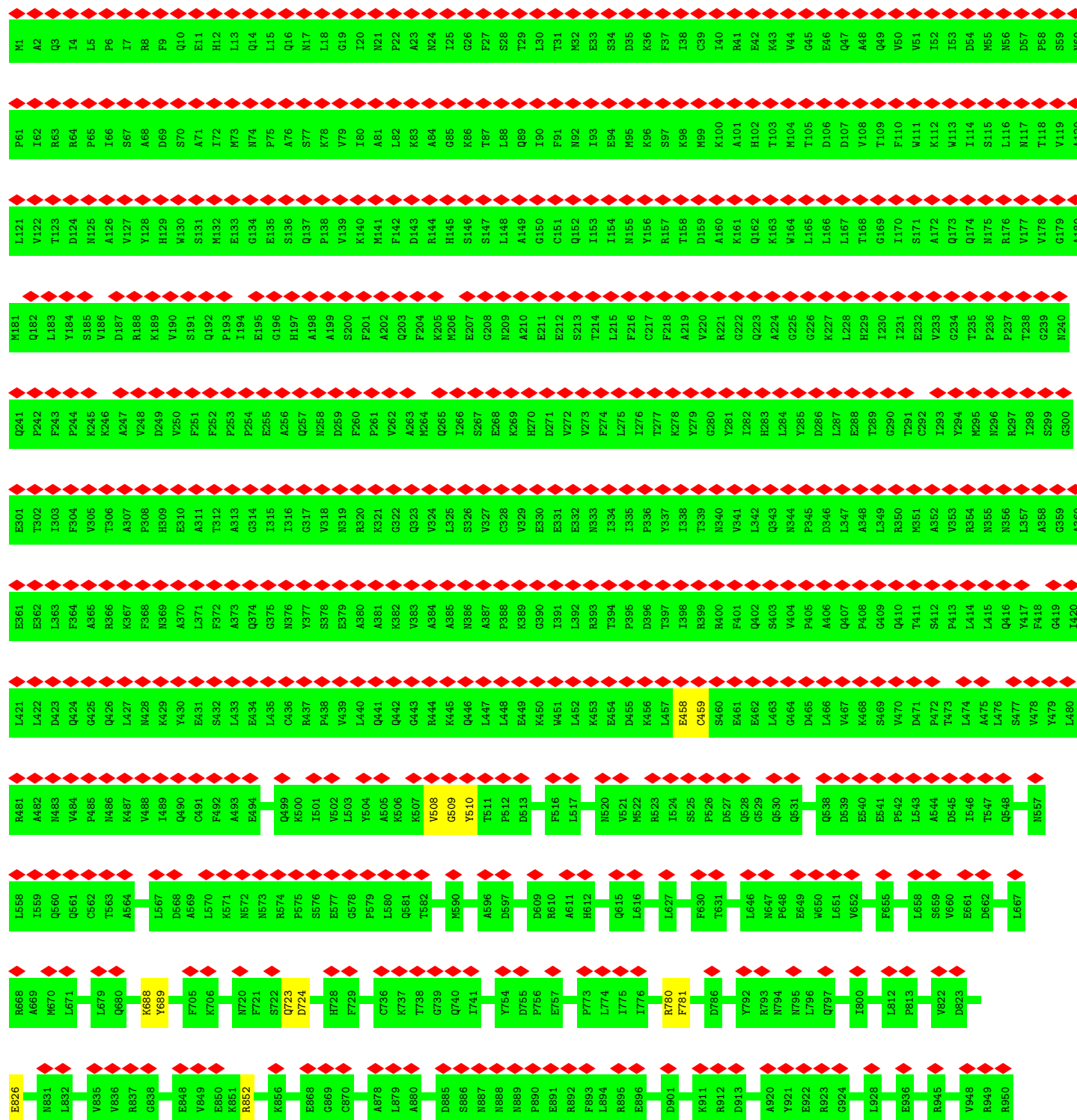
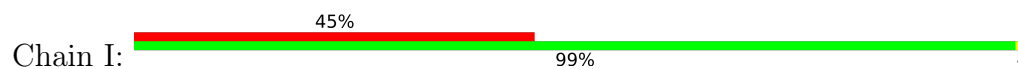
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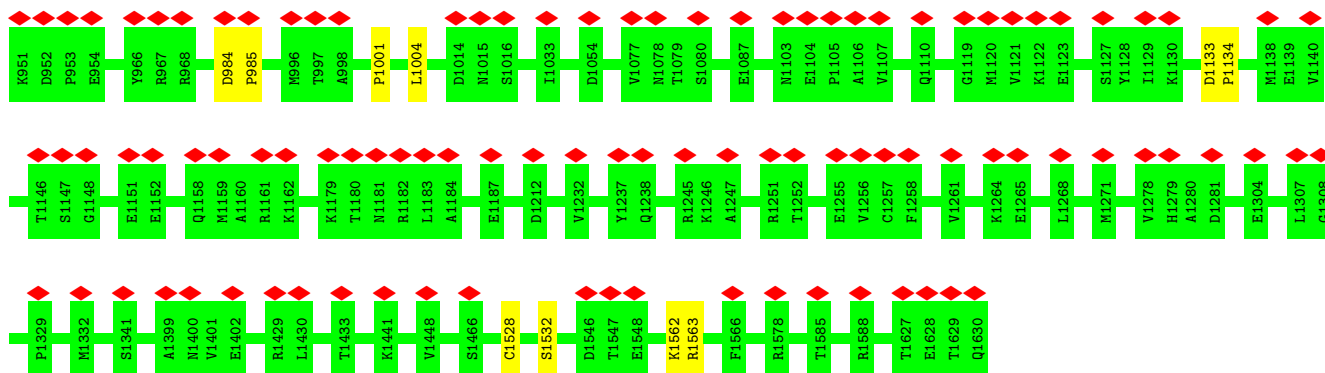


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L183	Y184	S185	V186	D187	R188	K189	V190	S191	Q192	P193	I194	E195	G196	H197	A198	A199	S200	F201	A202	Q203	F204	K205	M206	E207	G208	N209	A210	D211	E212	S213	T214	L215	T216	C217	F218	A219	V220	R221	Q222	K223	A224	G225	G226	K227	L228	H229	I230	I231	E232	I233	Y234	M235	N236	R237	I238	S239	G300	N240	Q241	P242										
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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	L397	I398	R399	R400	F401	Q402	S403	V404	P405	A406	Q407	P408	G409	Q410	T411	A412	P413	L414	L415	Q416	Y417	F418	G419	R420	L421	L422	N423											
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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	R895	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	N1081	L1082	H1021	R1022	I1033			K1034	M1049			Y1050	D1051	D1054			V1077	N1078	T1079	S1080	E1087			N1103			E1104	P1105	A1106	D1107	Q1110	G1119			M1120	V1121
K1122	E1123	I1129			K1130	D1133	P1134	M1138	T1146			S1147	G1148	M1149	W1150	E1151	E1152	K1155	Q1158	M1159	A1160	R1161	K1162	K1179	T1180	N1181	R1182	L1183	A1184	E1187	E1188	D1212	L1216	M1219	N1220	V1221	S1222	V1232	Y1237	Q1238	R1245	K1246	A1247	N1248	S1249	T1250	R1251	D1262																						
G1263	K1264	E1265	F1266	R1267	L1268	M1271	C1272	H1275	D1281	S1147	E1304	L1307	G1308	M1332	S1341	G1389	A1399	N1400	V1401	E1402	R1429	L1430	T1433	K1441	V1448	S1466	C1528	S1532	D1546	T1547	K1562	R1563	F1566	L1576	K1577	L1578	T1585	R1588																																

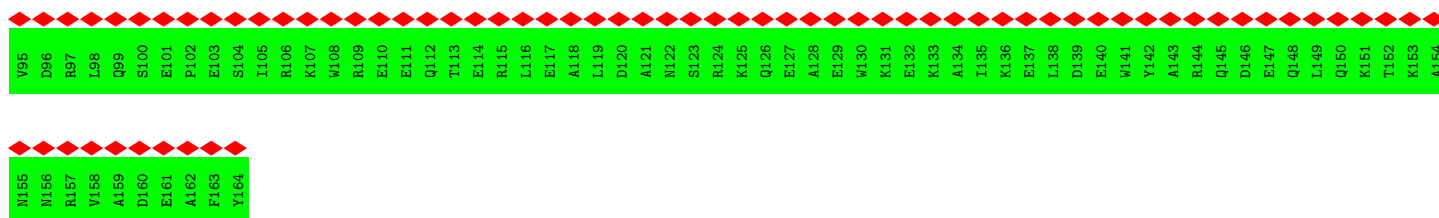


● Molecule 1: Clathrin heavy chain

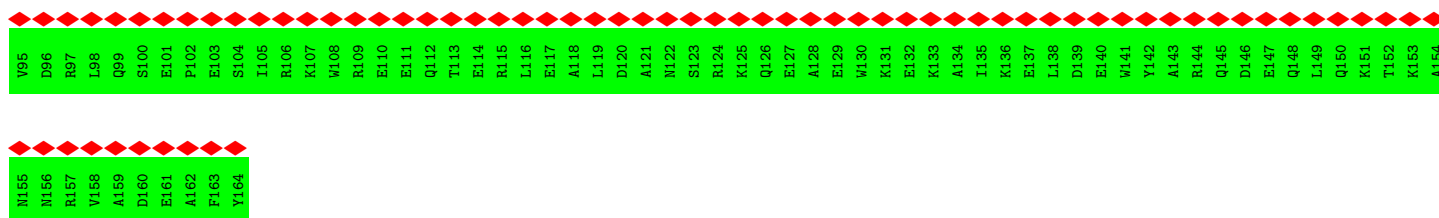




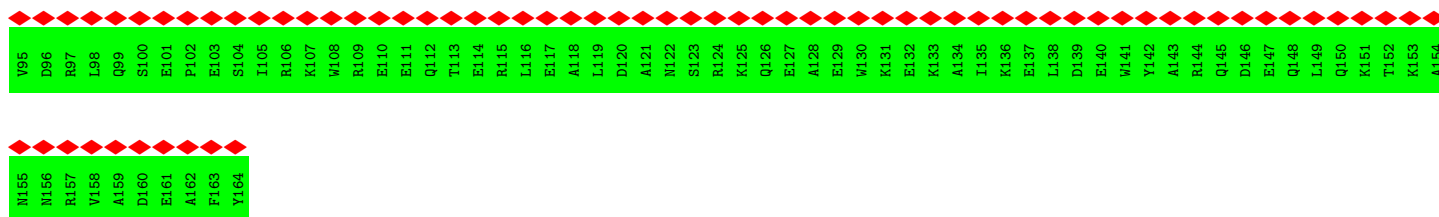
• Molecule 2: Clathrin light chain A



• 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



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
-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

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

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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.

All (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
1:B:723:GLN:CA	1:B:724:ASP:CA	2.24	1.15
1:E:723:GLN:CA	1:E:724:ASP:CA	2.24	1.15
1:F:723:GLN:CA	1:F:724:ASP:CA	2.24	1.15
1:H:723:GLN:CA	1:H:724:ASP:CA	2.24	1.15
1:D:723:GLN:CA	1:D:724:ASP:CA	2.24	1.15
1:I:723:GLN:CA	1:I:724:ASP:CA	2.24	1.13
1:G:1133:ASP:CA	1:G:1134:PRO:CA	2.27	1.13
1:H:1133:ASP:CA	1:H:1134:PRO:CA	2.27	1.13
1:A:1133:ASP:CA	1:A:1134:PRO:CA	2.27	1.12
1:C:1133:ASP:CA	1:C:1134:PRO:CA	2.27	1.12
1:E:1133:ASP:CA	1:E:1134:PRO:CA	2.27	1.12
1:D:508:VAL:CA	1:D:509:GLY:CA	2.27	1.10
1:B:984:ASP:CA	1:B:985:PRO:CA	2.30	1.10
1:H:984:ASP:CA	1:H:985:PRO:CA	2.30	1.10
1:A:984:ASP:CA	1:A:985:PRO:CA	2.30	1.09
1:C:984:ASP:CA	1:C:985:PRO:CA	2.30	1.09
1:F:984:ASP:CA	1:F:985:PRO:CA	2.30	1.08
1:D:984:ASP:CA	1:D:985:PRO:CA	2.30	1.08
1:I:984:ASP:CA	1:I:985:PRO:CA	2.30	1.08
1:E:984:ASP:CA	1:E:985:PRO:CA	2.30	1.07
1:G:984:ASP:CA	1:G:985:PRO:CA	2.30	1.07
1:A:1278:VAL:CA	1:A:1311:ARG:CA	2.38	1.01
1:H:780:ARG:CA	1:H:781:PHE:CA	2.50	0.90
1:F:780:ARG:CA	1:F:781:PHE:CA	2.50	0.90
1:A:780:ARG:CA	1:A:781:PHE:CA	2.50	0.90
1:G:780:ARG:CA	1:G:781:PHE:CA	2.50	0.90
1:C:780:ARG:CA	1:C:781:PHE:CA	2.50	0.90
1:B:780:ARG:CA	1:B:781:PHE:CA	2.50	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:780:ARG:CA	1:D:781:PHE:CA	2.50	0.89
1:E:780:ARG:CA	1:E:781:PHE:CA	2.50	0.89
1:I:780:ARG:CA	1:I:781:PHE:CA	2.50	0.89
1:C:494:GLU:CA	1:C:520:ASN:CA	2.53	0.86
1:G:1562:LYS:CA	1:G:1563:ARG:CA	2.56	0.84
1:H:1562:LYS:CA	1:H:1563:ARG:CA	2.56	0.84
1:A:1562:LYS:CA	1:A:1563:ARG:CA	2.56	0.83
1:B:1562:LYS:CA	1:B:1563:ARG:CA	2.56	0.83
1:D:1562:LYS:CA	1:D:1563:ARG:CA	2.56	0.83
1:I:1562:LYS:CA	1:I:1563:ARG:CA	2.56	0.82
1:C:1562:LYS:CA	1:C:1563:ARG:CA	2.56	0.82
1:E:1562:LYS:CA	1:E:1563:ARG:CA	2.56	0.82
1:F:1562:LYS:CA	1:F:1563:ARG:CA	2.56	0.82
1:B:826:GLU:CA	1:B:852:ARG:CA	2.57	0.82
1:I:1133:ASP:CA	1:I:1134:PRO:CA	2.59	0.81
1:I:509:GLY:CA	1:I:510:TYR:CA	2.60	0.80
1:D:1133:ASP:CA	1:D:1134:PRO:CA	2.64	0.76
1:G:826:GLU:CA	1:G:852:ARG:CA	2.63	0.76
1:E:502:VAL:CA	1:E:539:ASP:CA	2.67	0.72
1:C:554:MET:CA	1:C:591:HIS:CA	2.70	0.68
1:C:1248:ASN:CA	1:D:864:ALA:CA	2.75	0.64
1:B:509:GLY:CA	1:B:510:TYR:CA	2.76	0.64
1:C:498:VAL:CA	1:C:532:PHE:CA	2.77	0.63
1:G:508:VAL:CA	1:G:509:GLY:CA	2.78	0.61
1:H:688:LYS:CA	1:H:689:TYR:CA	2.80	0.60
1:A:688:LYS:CA	1:A:689:TYR:CA	2.80	0.60
1:B:688:LYS:CA	1:B:689:TYR:CA	2.80	0.60
1:G:688:LYS:CA	1:G:689:TYR:CA	2.80	0.60
1:E:688:LYS:CA	1:E:689:TYR:CA	2.80	0.60
1:F:688:LYS:CA	1:F:689:TYR:CA	2.80	0.60
1:C:688:LYS:CA	1:C:689:TYR:CA	2.80	0.59
1:D:688:LYS:CA	1:D:689:TYR:CA	2.80	0.59
1:I:826:GLU:CA	1:I:852:ARG:CA	2.81	0.59
1:I:688:LYS:CA	1:I:689:TYR:CA	2.80	0.59
1:F:558:LEU:CA	1:F:559:ILE:CA	2.81	0.58
1:A:830:LYS:CA	1:A:854:ARG:CA	2.81	0.58
1:C:1279:HIS:CA	1:D:895:ARG:CA	2.83	0.56
1:F:1528:CYS:CA	1:F:1532:SER:CA	2.84	0.56
1:H:1528:CYS:CA	1:H:1532:SER:CA	2.84	0.56
1:E:1528:CYS:CA	1:E:1532:SER:CA	2.84	0.56
1:I:1528:CYS:CA	1:I:1532:SER:CA	2.84	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1528:CYS:CA	1:B:1532:SER:CA	2.84	0.56
1:C:1528:CYS:CA	1:C:1532:SER:CA	2.84	0.56
1:A:1528:CYS:CA	1:A:1532:SER:CA	2.84	0.56
1:D:1528:CYS:CA	1:D:1532:SER:CA	2.84	0.55
1:G:1528:CYS:CA	1:G:1532:SER:CA	2.84	0.55
1:I:508:VAL:CA	1:I:510:TYR:CA	2.84	0.55
1:I:458:GLU:CA	1:I:459:CYS:CA	2.87	0.53
1:B:1279:HIS:CA	1:B:1280:ALA:CA	2.96	0.43
1:C:522:MET:CA	1:C:552:VAL:CA	2.96	0.43
1:B:487:LYS:CA	1:B:510:TYR:CA	2.98	0.41
1:I:1001:PRO:CA	1:I:1004:LEU:CA	3.00	0.40
1:B:1001:PRO:CA	1:B:1004:LEU:CA	3.00	0.40
1:D:1001:PRO:CA	1:D:1004:LEU:CA	3.00	0.40
1:E:1001:PRO:CA	1:E:1004:LEU:CA	3.00	0.40

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.

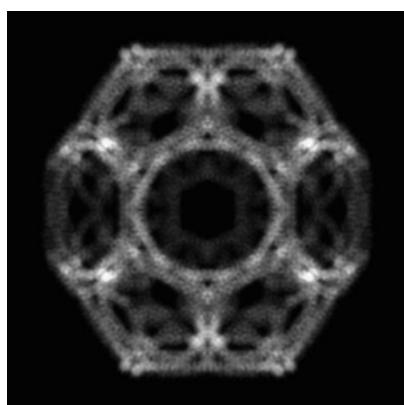
6 Map visualisation [i](#)

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.

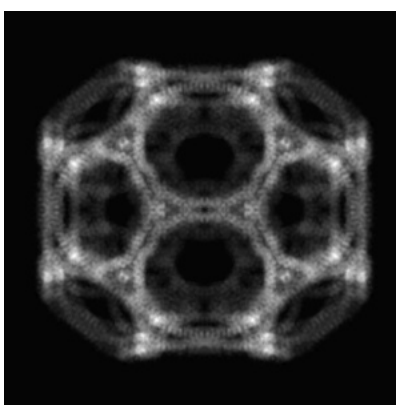
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

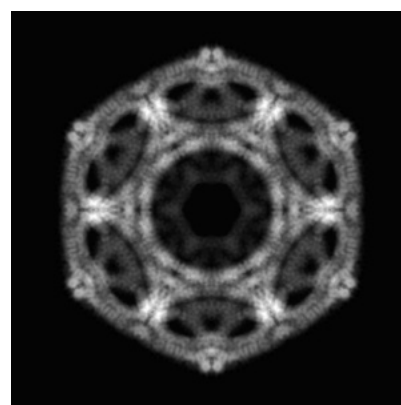
6.1.1 Primary map



X



Y

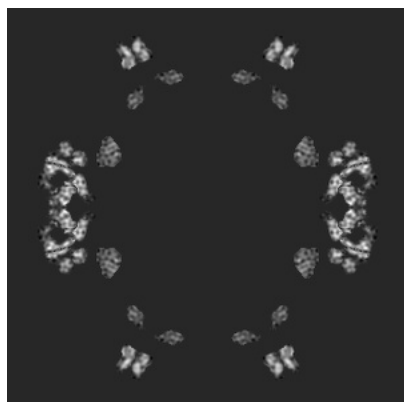


Z

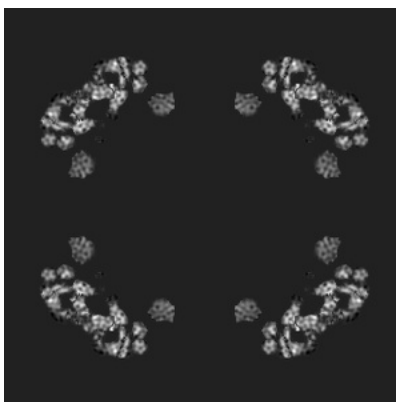
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

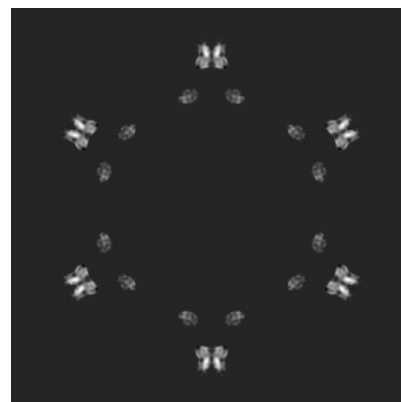
6.2.1 Primary map



X Index: 156



Y Index: 156

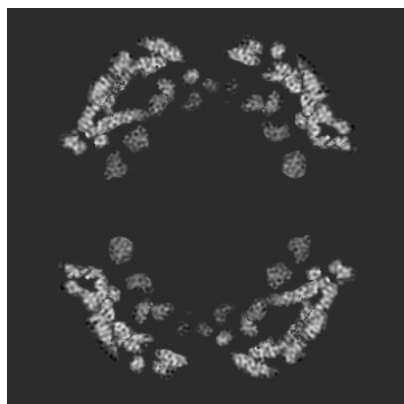


Z Index: 156

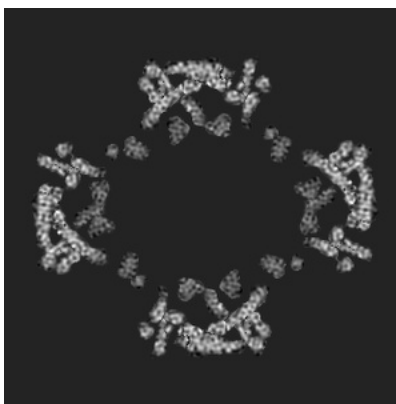
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

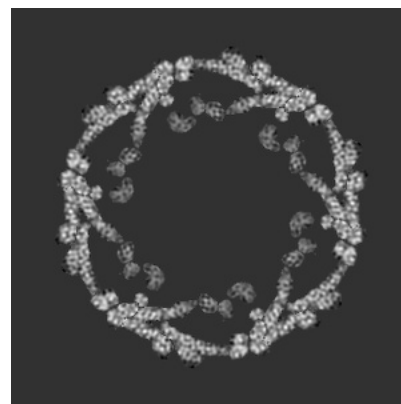
6.3.1 Primary map



X Index: 114



Y Index: 101

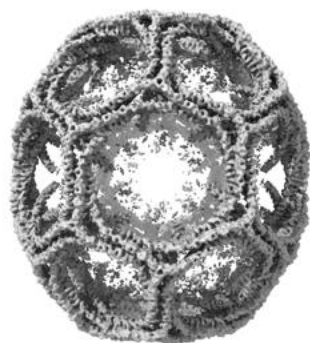


Z Index: 205

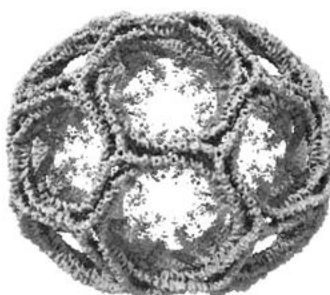
The images above show the largest variance slices of the map in three orthogonal directions.

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

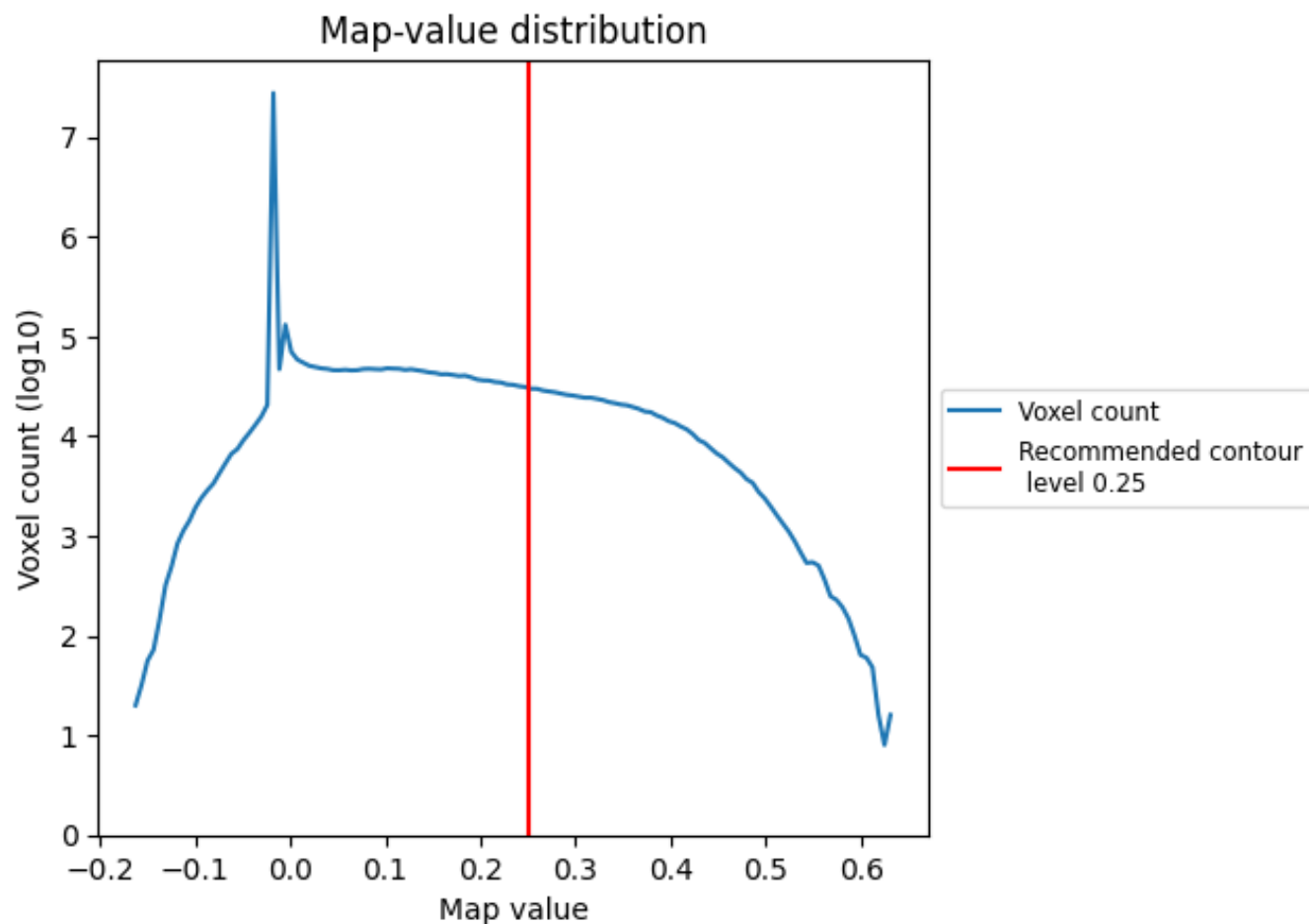
6.5 Mask visualisation

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

7 Map analysis [i](#)

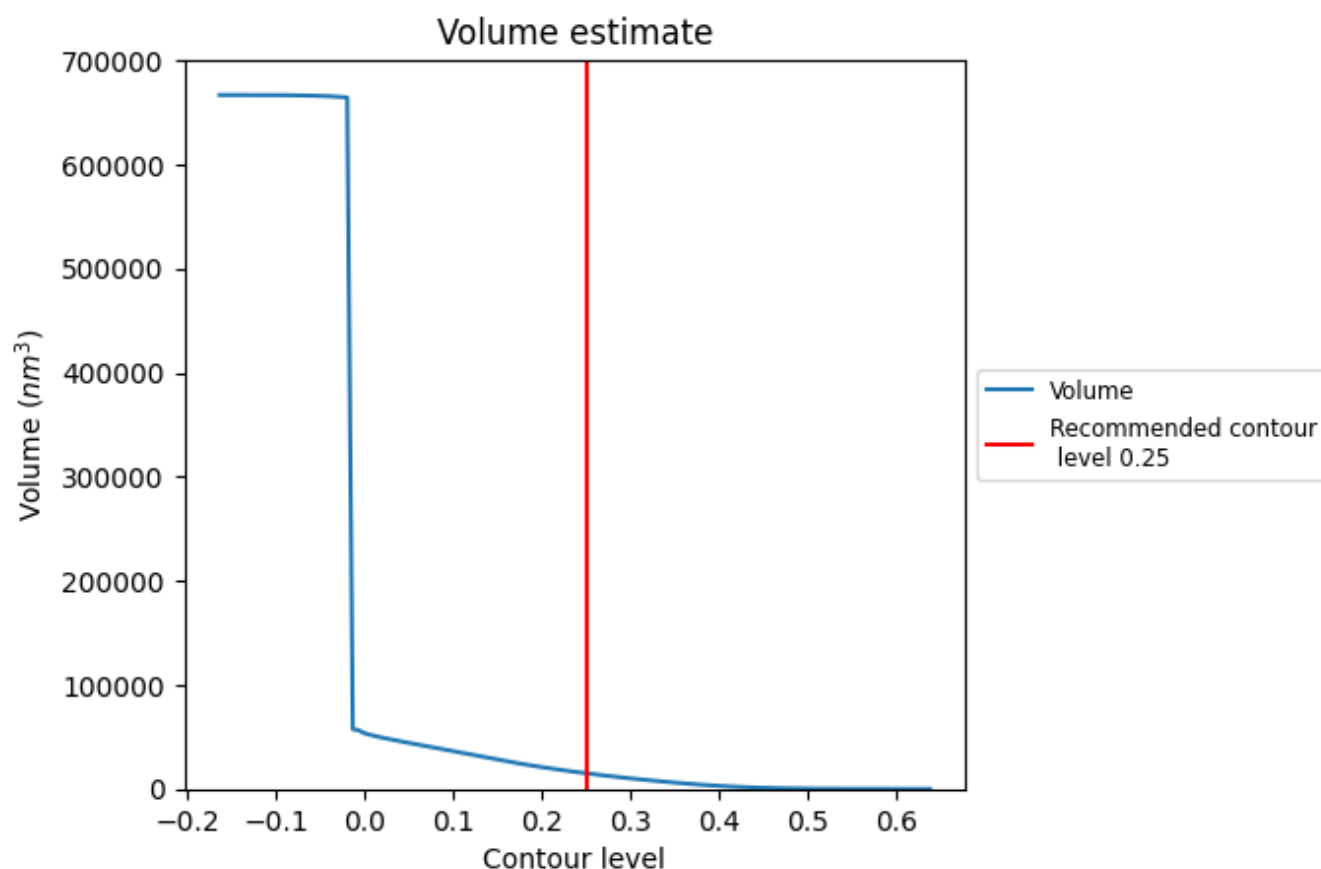
This section contains the results of statistical analysis of the map.

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.

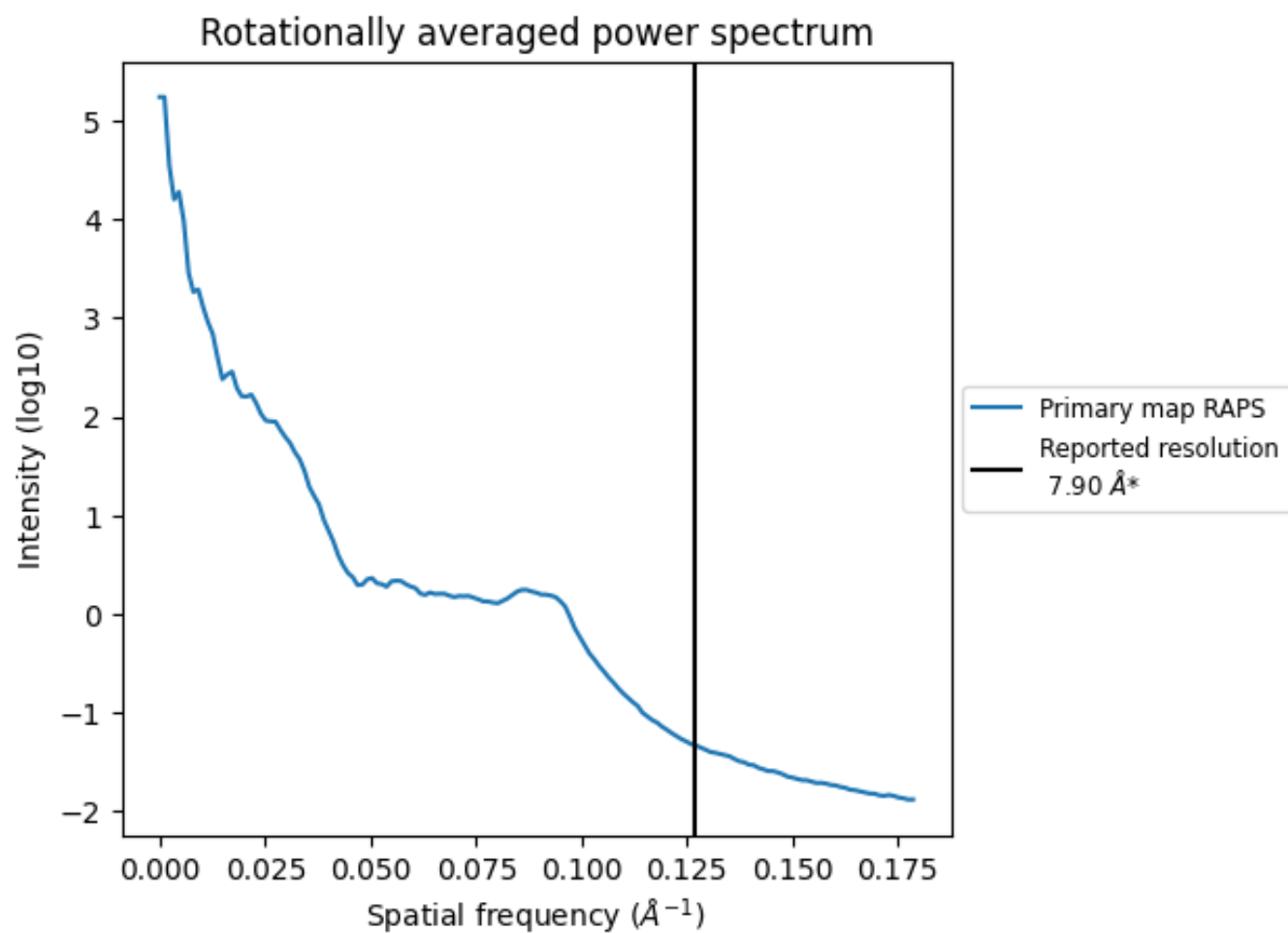
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 15047 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 ⓘ



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

8 Fourier-Shell correlation ⓘ

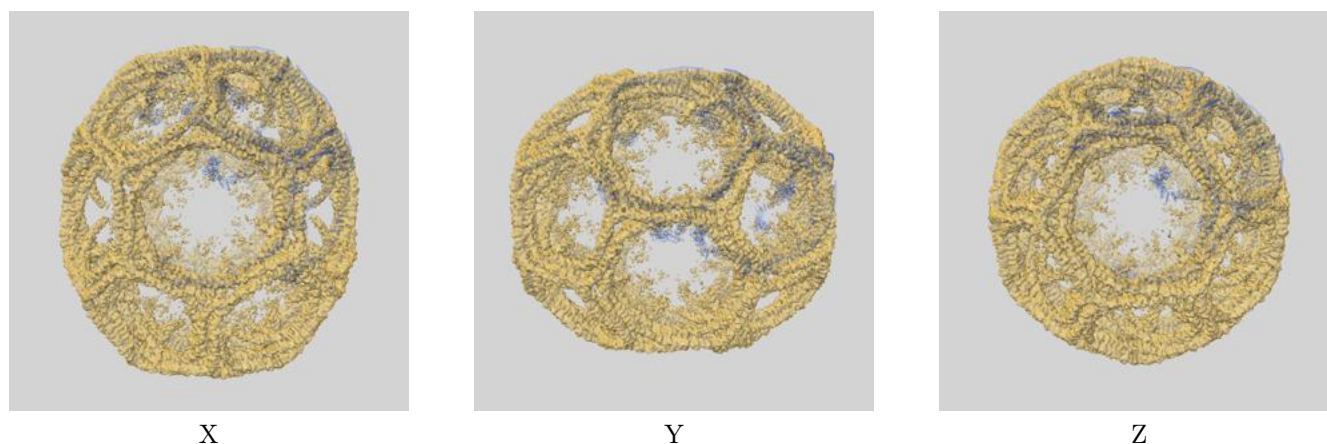
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

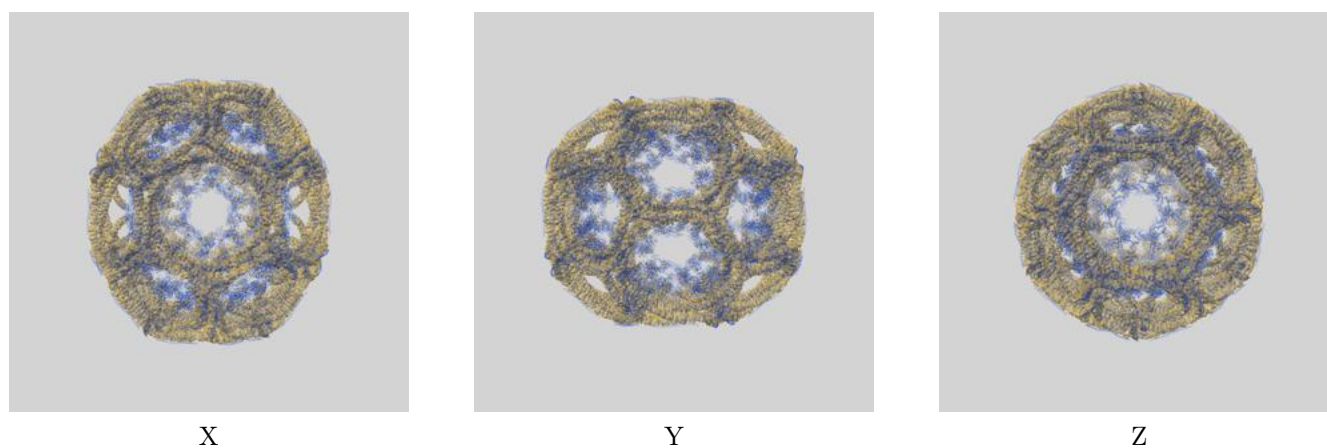
This section contains information regarding the fit between EMDB map EMD-5119 and PDB model 3IYV. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)



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



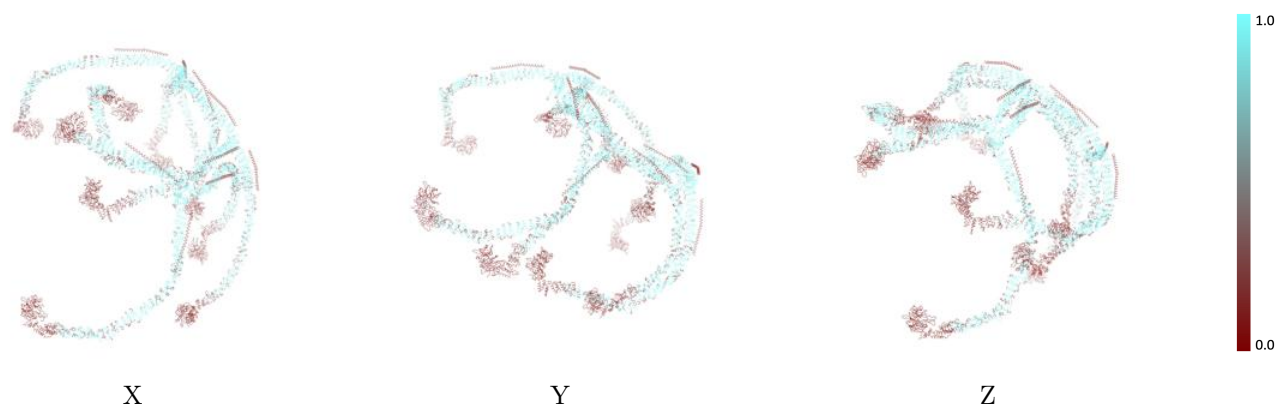
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



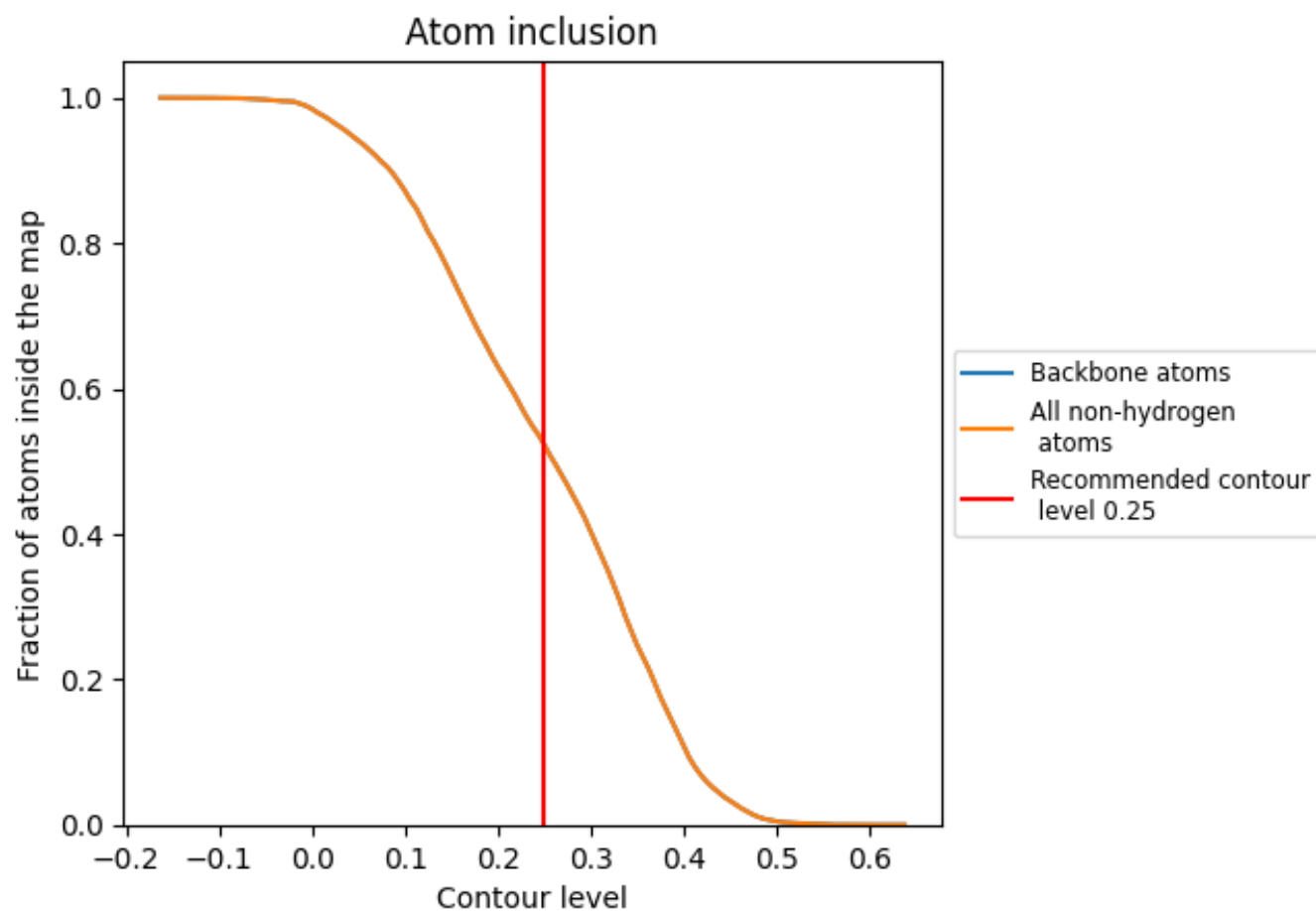
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.5228	 0.0550
A	 0.5380	 0.0530
B	 0.5552	 0.0610
C	 0.5601	 0.0620
D	 0.5442	 0.0580
E	 0.5387	 0.0570
F	 0.5387	 0.0580
G	 0.5491	 0.0630
H	 0.5374	 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

