



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:38 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 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.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

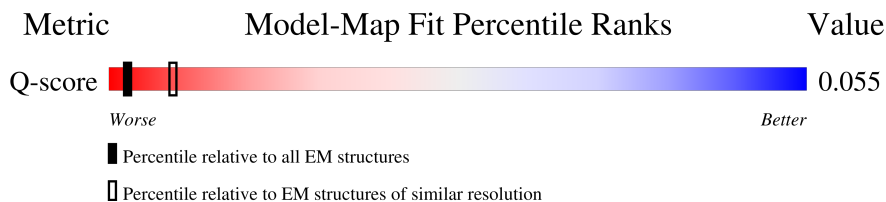
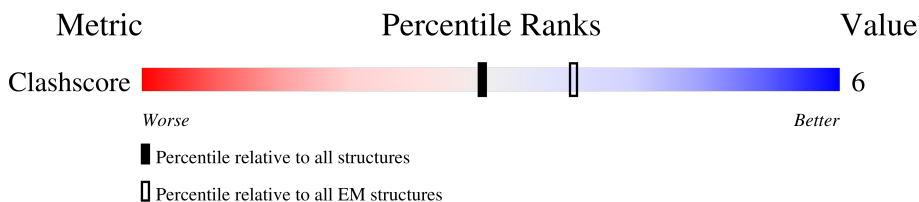
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

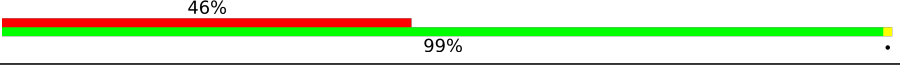
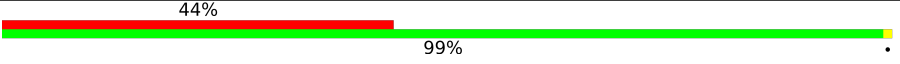
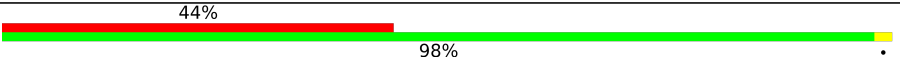
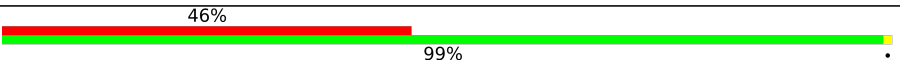
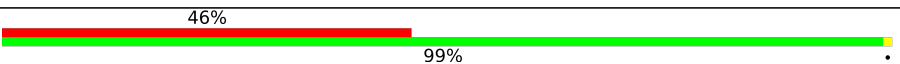
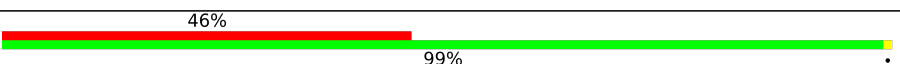
The reported resolution of this entry is 7.90 Å.

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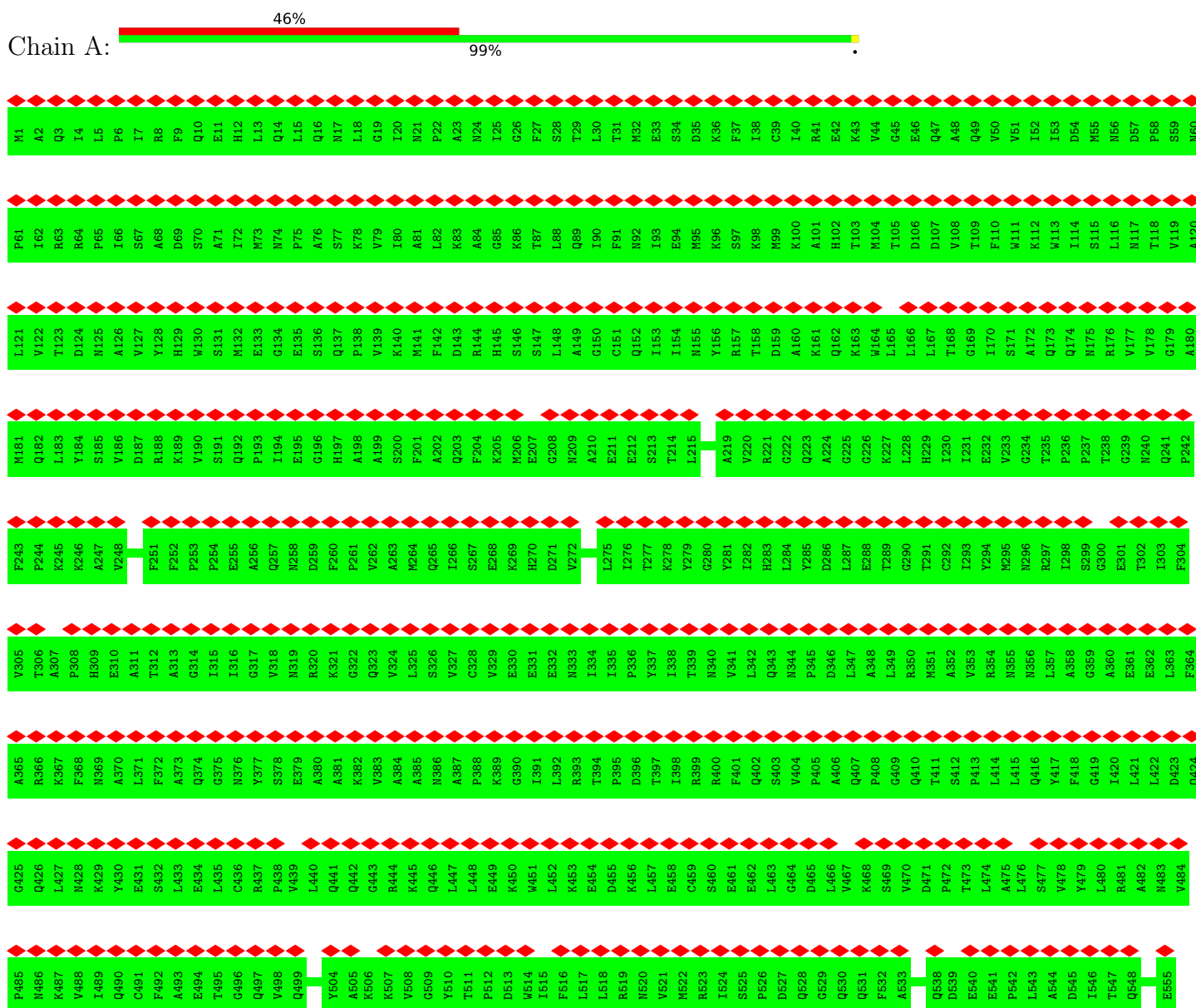
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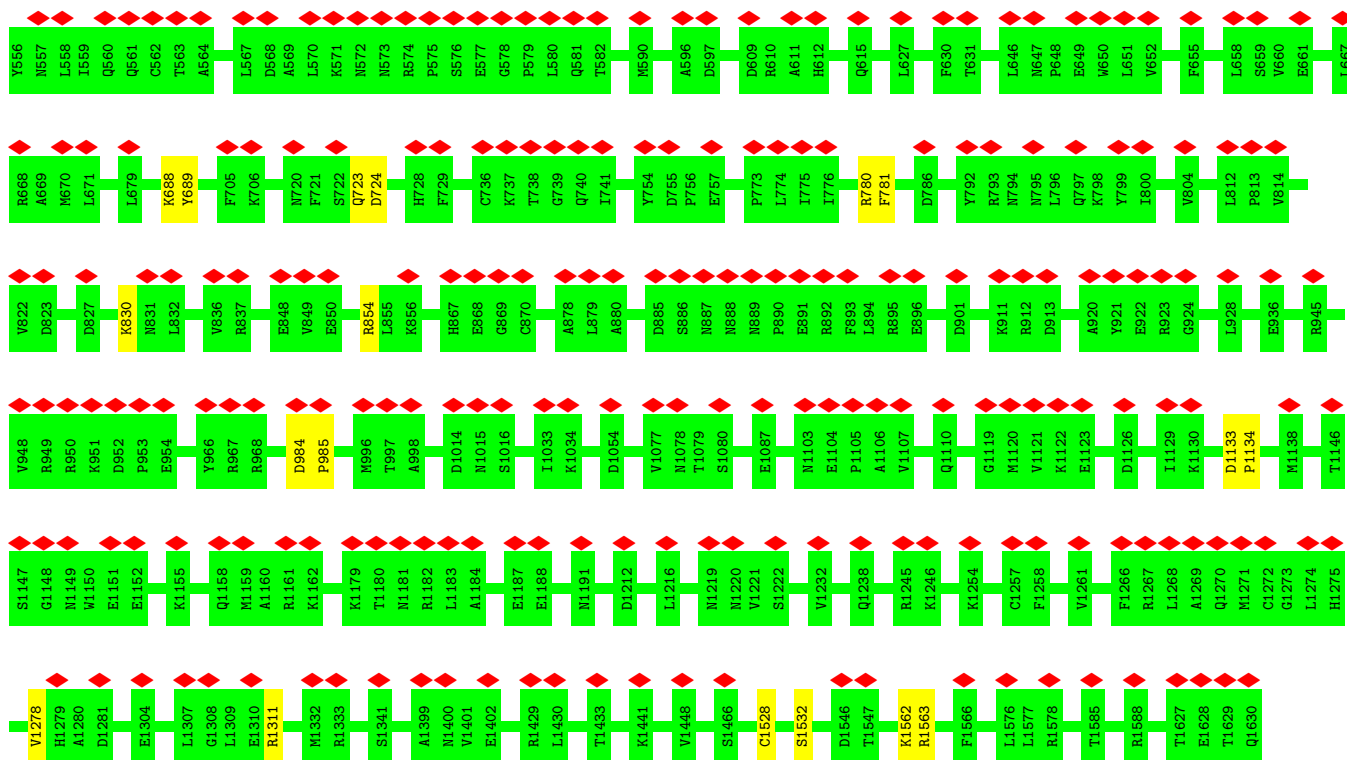
Mol	Chain	Residues	Atoms		AltConf	Trace
2	P	70	Total 70	C 70	0	70
2	Q	70	Total 70	C 70	0	70
2	R	70	Total 70	C 70	0	70

3 Residue-property plots

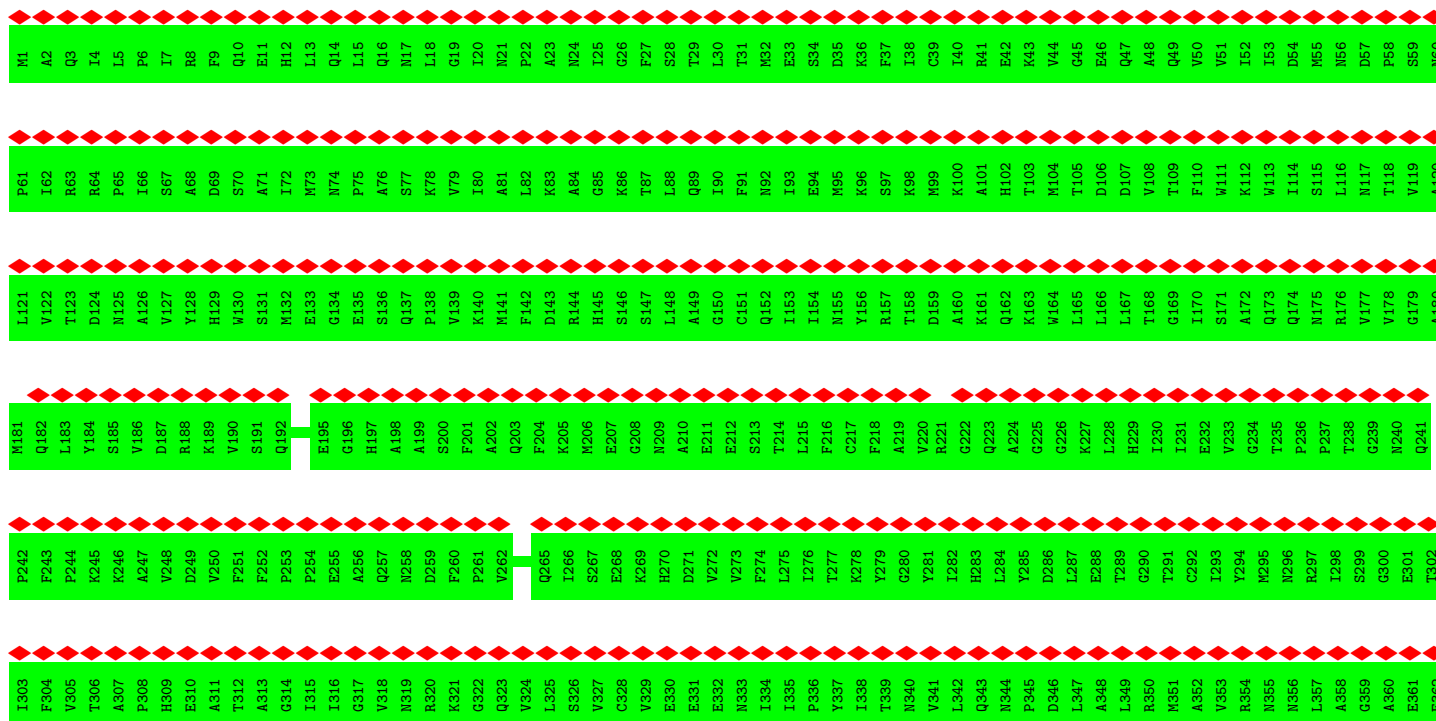
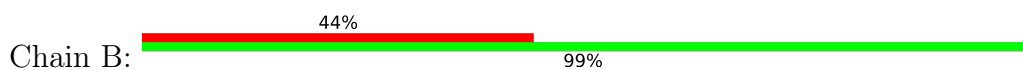
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

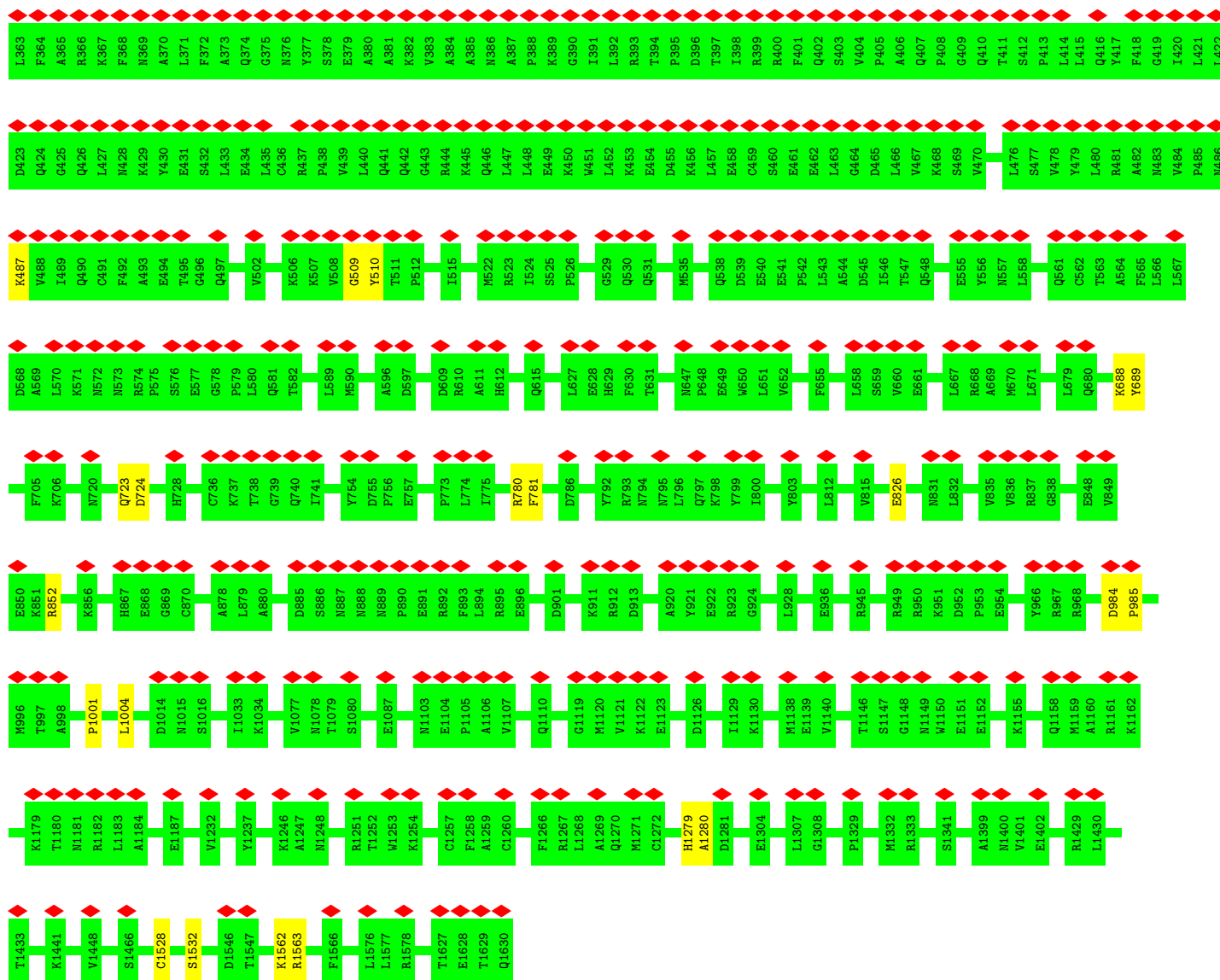
• Molecule 1: Clathrin heavy chain



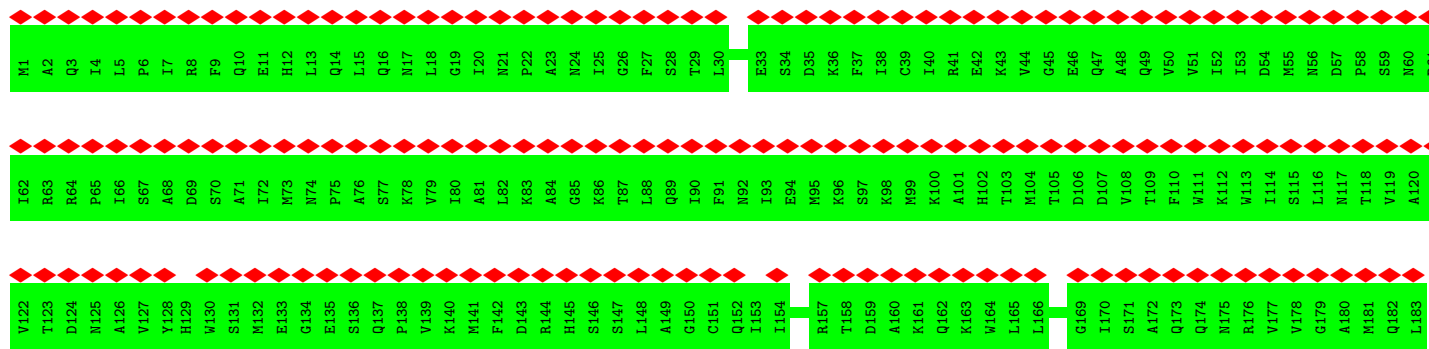
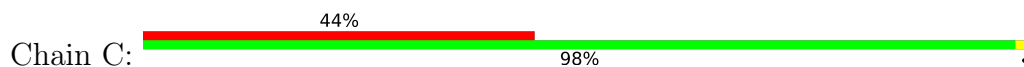


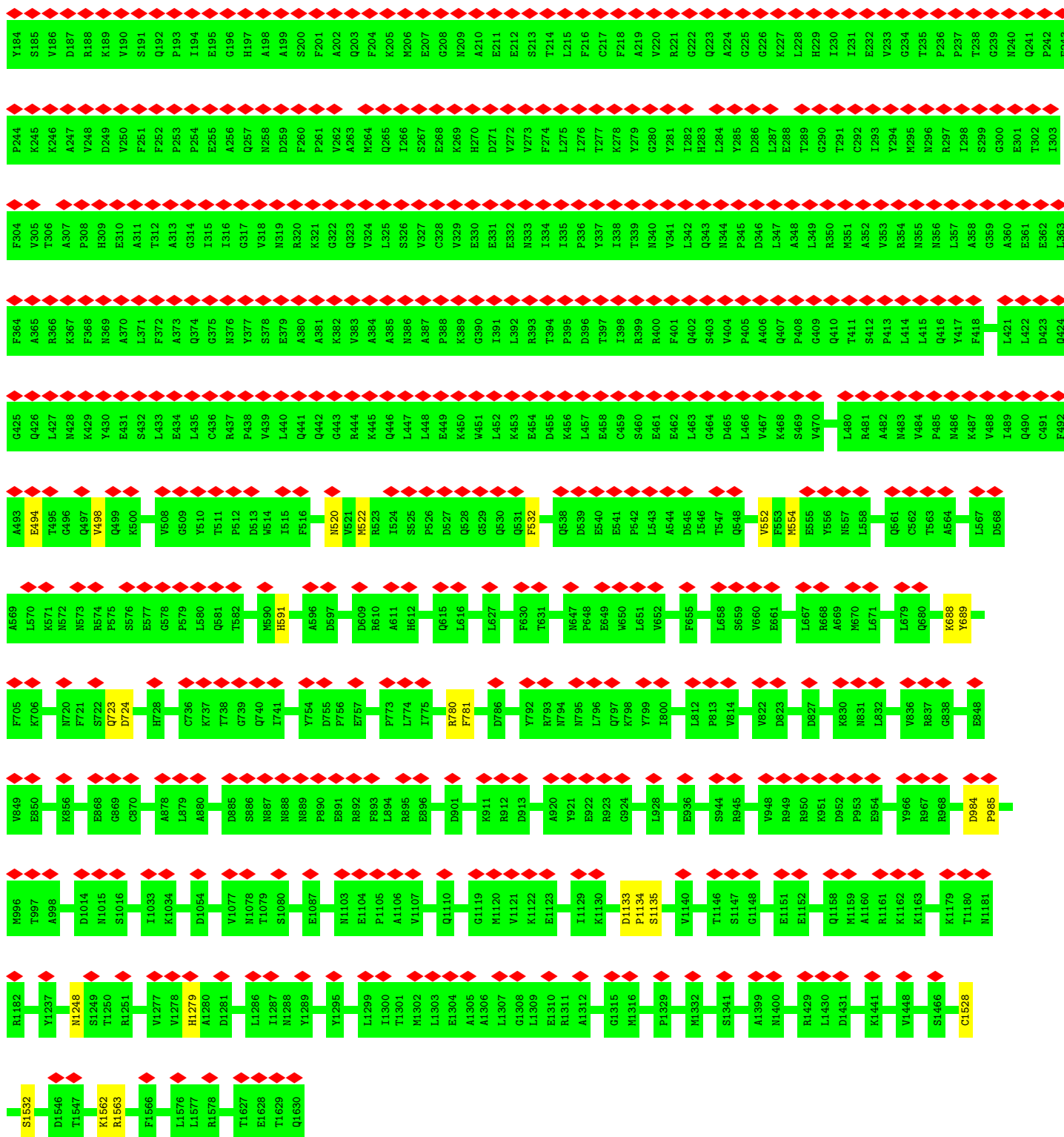
• Molecule 1: Clathrin heavy chain





• Molecule 1: Clathrin heavy chain

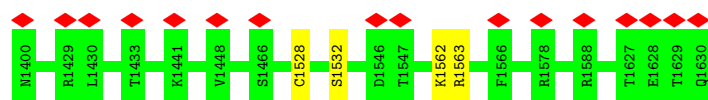




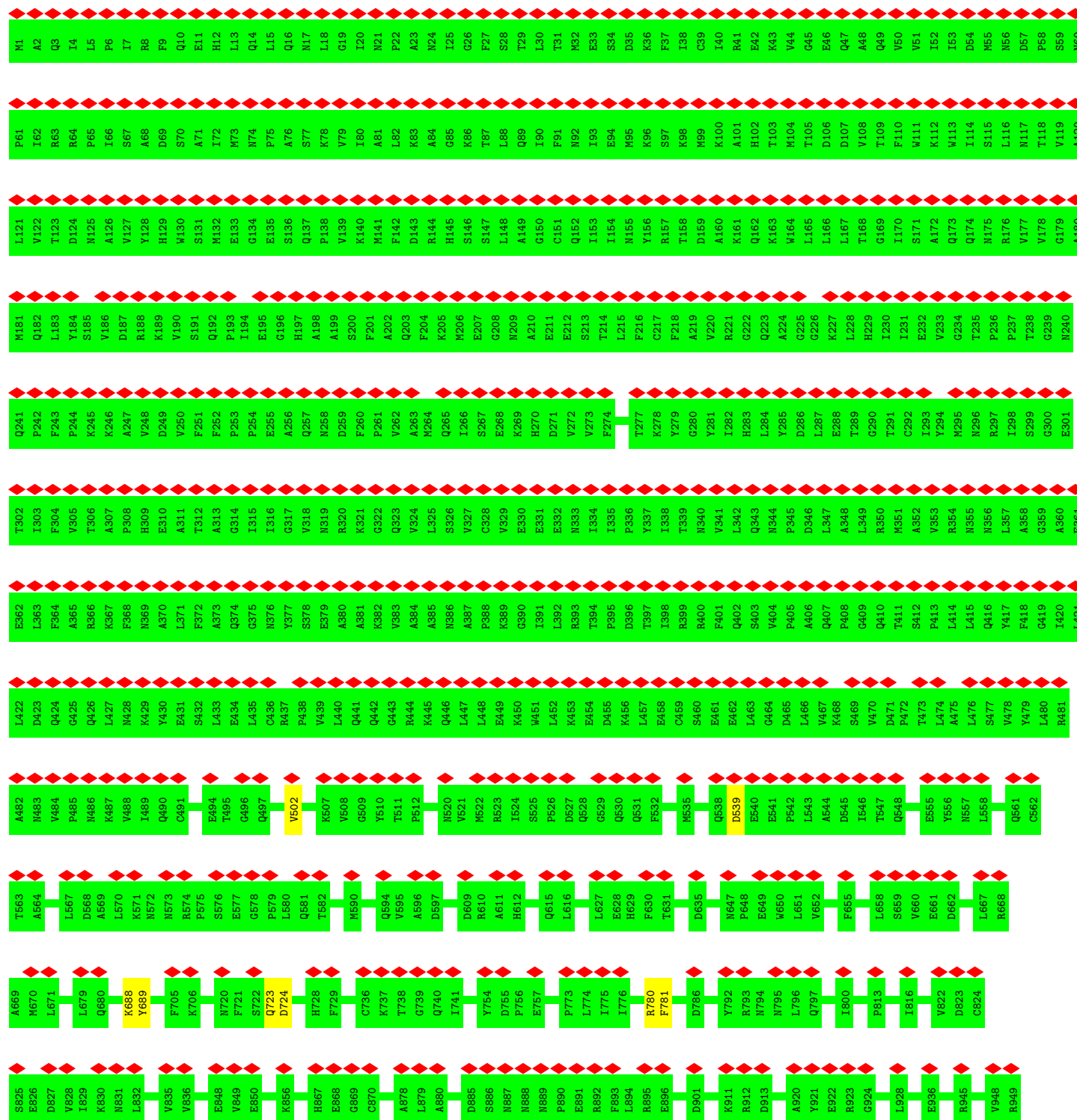
- Molecule 1: Clathrin heavy chain

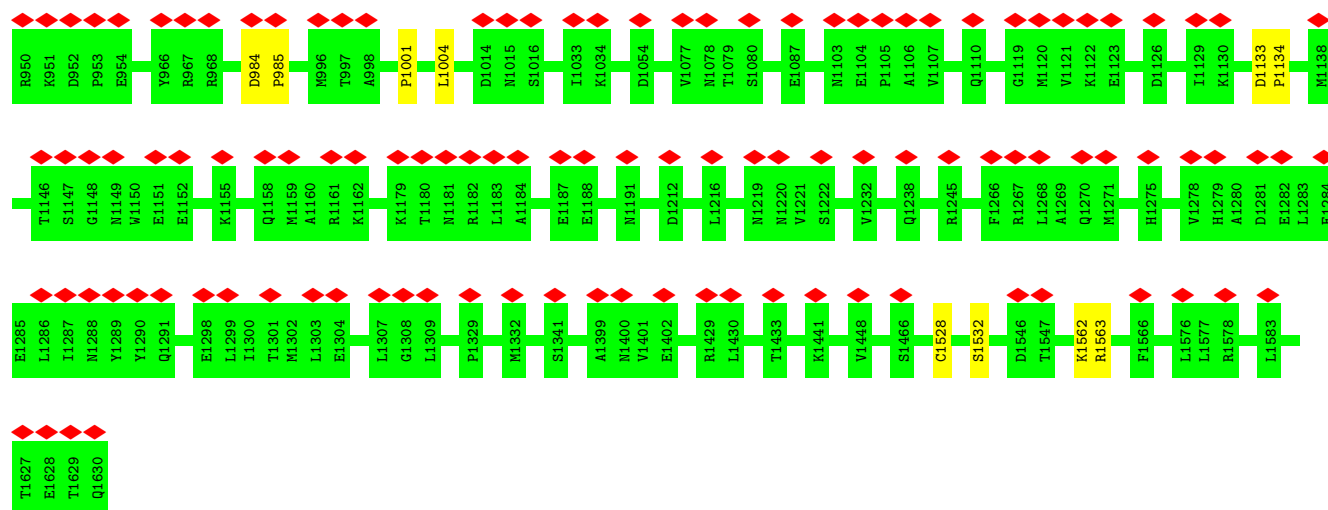


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S1127	E936	T842	R668	L558	A482	L422	E362	T302	V122	Q182	162
I1129	E936	D843	A669	L558	N483	D423	L363	I303	T123	L183	R63
K1130	S944	E844	M670	Q560	V484	Q424	F364	F304	D124	Y184	R64
D1133	R945	L845	L671	Q561	N486	G425	A365	V305	M125	S185	P65
P1134	R945	L845	L671	Q561	N486	Q426	R366	T306	A126	V186	166
T1146	V948	E848	L679	C562	K487	L427	K367	A307	V127	D187	S67
S1147	R949	V849	Q680	T563	V488	N428	F368	P308	H128	R188	A68
G1148	R950	E850	K688	A564	I489	K429	N369	H309	H129	D249	D69
N1149	R951	K851	Y689	L567	Q490	Y430	A370	E310	W130	V190	S70
P953	D952	R852	F705	D668	C491	E431	L371	A311	S131	S191	A71
W1150	R953	N853	K706	A569	F492	S432	F372	T312	M132	Q192	172
E1151	P954	R854	N720	L570	G496	L433	Q374	A313	E133	P193	M73
E1152	E954	L855	F721	K571	Q497	E434	G374	G314	G134	I194	M74
Y966	R967	K856	S722	N572	Q498	L435	G375	I315	E135	E195	P75
K1162	R968	L862	Q723	N573	Q499	C436	N376	I316	S136	G196	A76
A1178	D984	A864	D724	R574	K500	R437	Y377	G317	Q137	H197	S77
K1179	P985	E864	H728	P575	I501	P438	S378	V318	P138	A198	K78
T1180	E867	H878	F729	S576	V502	V439	E379	N319	V139	A199	V79
G869	E868	L879	F729	E577	L503	L440	A380	R320	K140	S200	180
N1181	E869	L879	F729	G578	E507	Q441	A381	K321	M141	F201	A81
R1182	C870	A880	C736	P579	K507	Q442	K382	G322	F142	A202	L82
L1183	T997	K881	K737	L580	V508	R443	V383	Q323	D143	Q203	K83
A998	A998	E871	T738	Q581	G509	R444	A384	V324	R144	F204	A84
A1184	E872	E872	G739	T582	Y510	K445	A385	L325	H145	K205	125
Y1237	P1001	E872	Q740	T592	D513	Q446	N386	S326	S146	M206	G26
K1246	L1004	L879	I741	M590	F516	L447	A387	V327	S147	E207	F27
R1251	L1013	L879	Y754	Q594	L517	L448	P388	C328	L148	G208	L88
T1252	D1014	K881	D755	V595	L517	E449	K389	V329	A149	M209	S28
K1264	M1015	E882	P756	A596	N520	K450	G390	E330	G150	A210	T29
E1265	S1016	Y883	E757	D597	V521	L452	L392	E331	C151	E211	F91
F1266	I1033	T884	P773	D609	M522	E454	R393	N333	Q152	E212	M92
R1267	K1034	S885	L774	R610	R523	E454	T394	I334	I153	T214	193
D1267	D1054	S886	I775	A611	I524	D455	P395	I335	I154	L215	E94
Q1270	V1077	N887	T775	H612	S525	K456	D396	P336	M155	F216	M95
M1271	N1078	N888	R780	Q615	P526	L457	T397	Y337	V156	C217	K96
C1272	T1079	P890	F781	L616	D527	E458	I398	I338	R157	C217	S97
G1273	S1080	R892	D786	F630	Q528	S460	R399	T339	T158	F218	K98
L1274	E1087	R893	Y792	T631	Q529	E461	R400	V220	D159	A219	M99
H1275	R895	L894	R793	N647	Q530	E462	F401	R221	K100	K100	140
D1281	E1087	E896	N794	P648	Q531	L463	Q402	Q223	A161	A101	R41
E1304	E1104	N897	N795	E649	F532	G464	V404	Q224	Q162	H102	E42
L1307	P1105	D901	I800	E649	A533	D465	P405	A224	M163	T103	K43
G1308	A1106	N897	L651	Q534	E533	D465	A406	G225	L165	T105	G45
M1332	V1107	D901	L651	W650	Q534	L466	A406	G226	L166	D106	E46
R1333	Q1110	K911	V652	L651	M535	V467	Q407	K227	L167	D107	Q47
S1341	G1119	R827	F655	L658	Q538	K468	P408	H229	T168	V108	A48
A1399	M1120	V828	L658	S659	D539	S469	Q409	I230	G169	T109	Q49
	V1121	I829	V660	E661	E541	V470	Q410	I170	F110	F110	V50
	K1122	N831	V660	E661	E541	P472	T411	S171	W111	W111	V51
		V836	E661	D662	P542	T473	S412	A172	K112	K112	I52
		R837	D662		L543	L474	P413	Q173	W113	W113	I53
					A544	A475	L414	Q174	K114	K114	D54
					D545	L476	L415	M175	S115	S115	M55
					I546	S477	Q416	R176	L116	L116	N56
					T547	V478	Y417	T237	M117	M117	D57
					Q548	V479	F418	T238	V177	V177	P58
						L480	G419	G239	G179	G179	N60



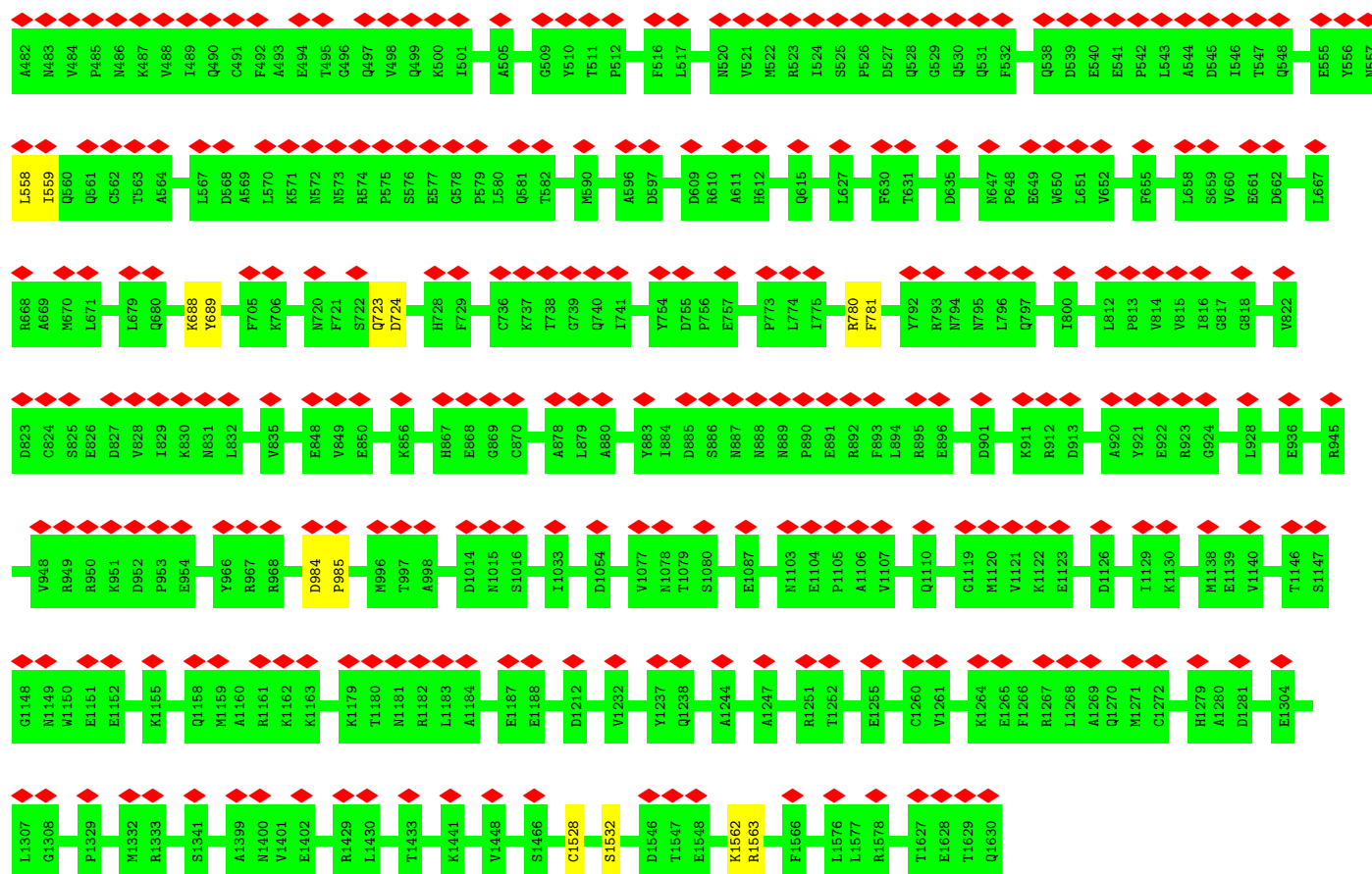
● Molecule 1: Clathrin heavy chain



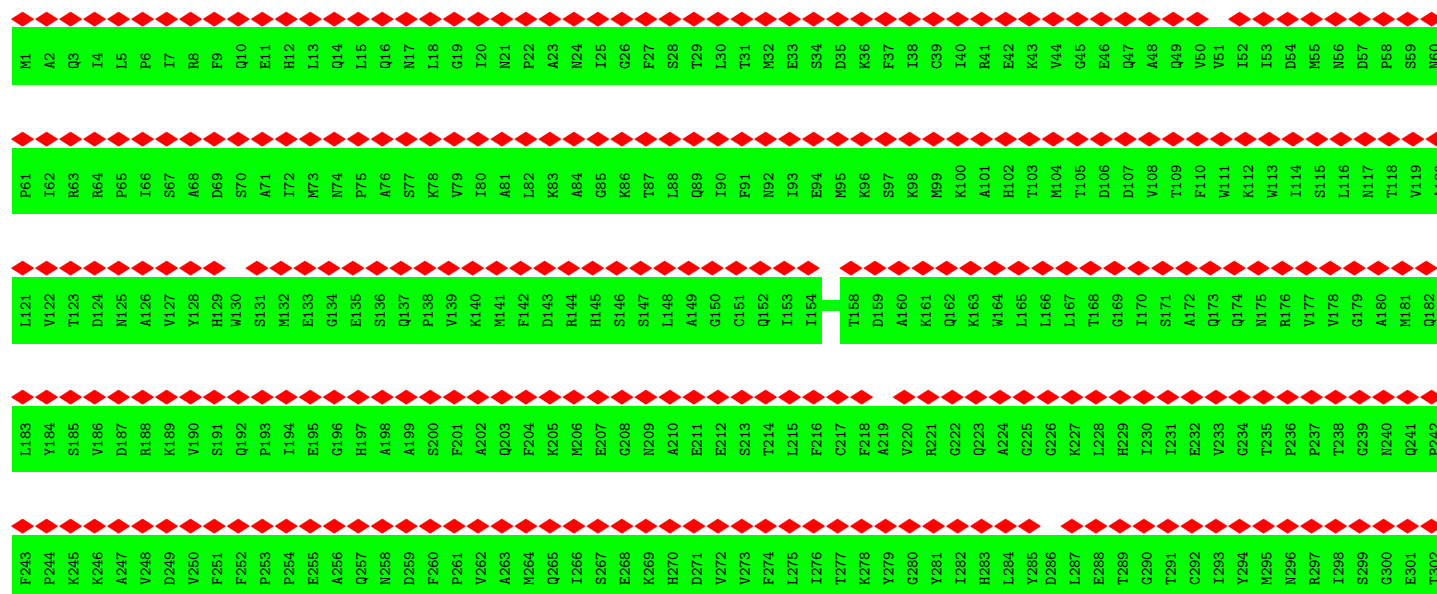


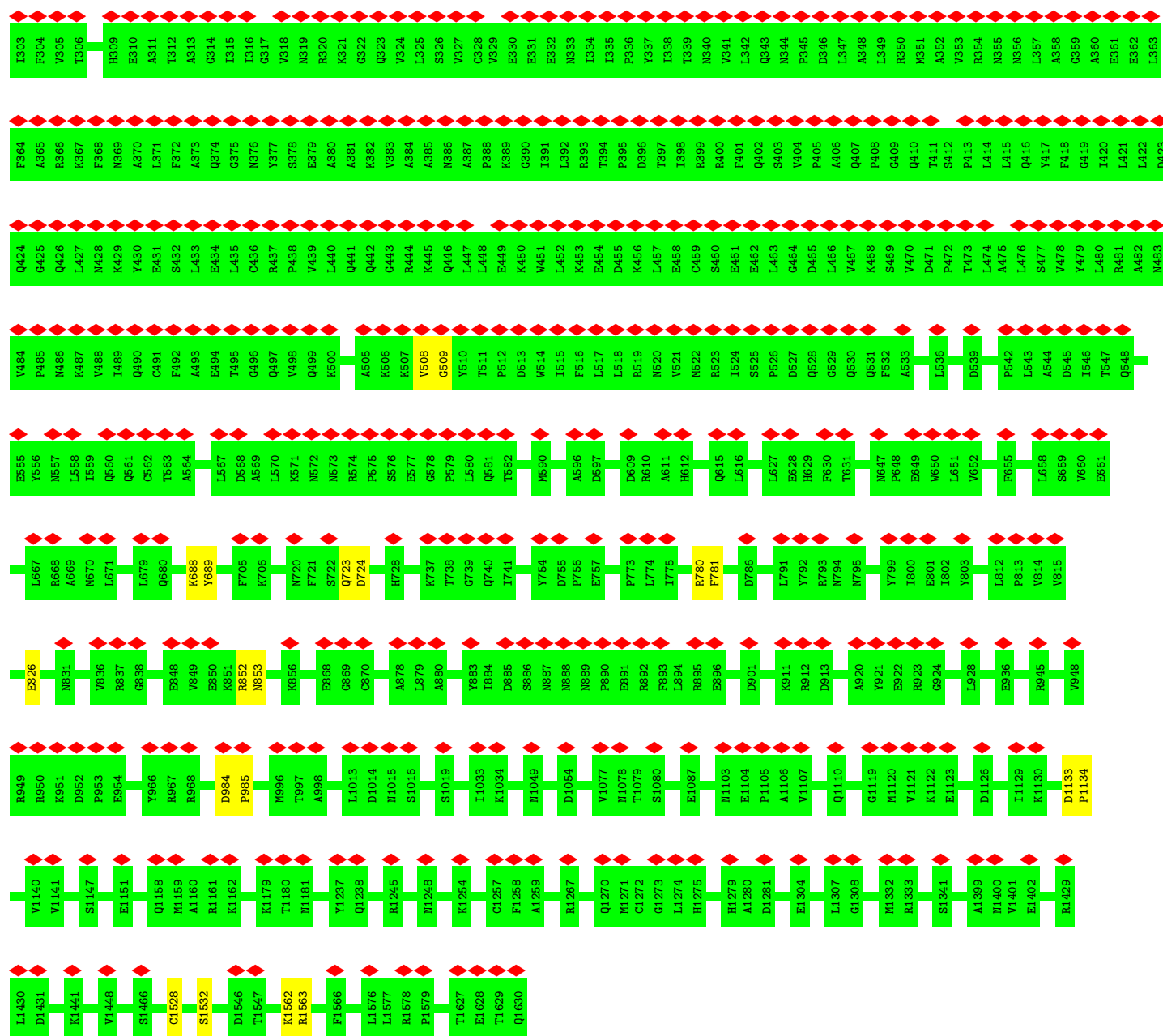
• Molecule 1: Clathrin heavy chain





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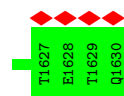




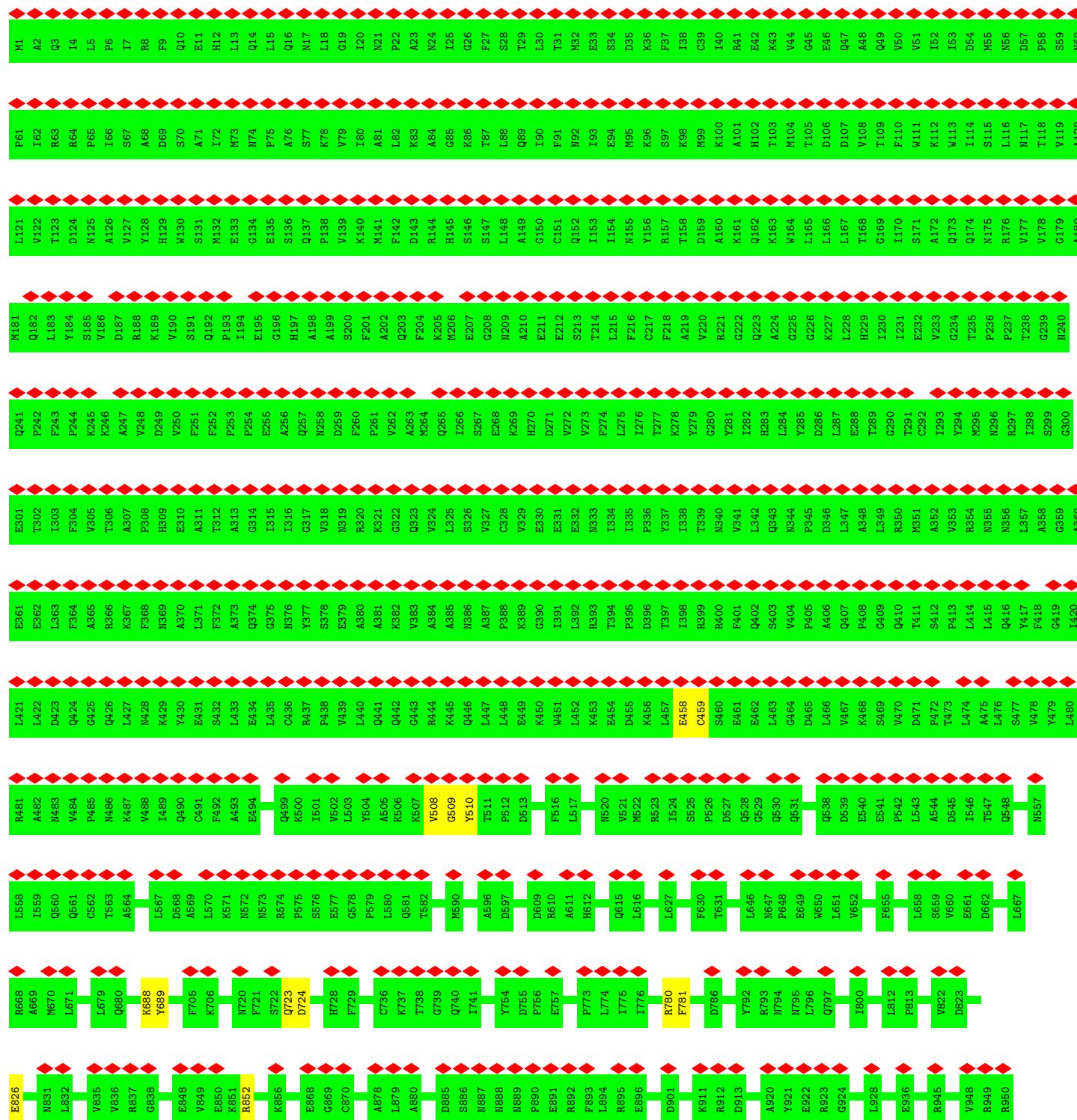
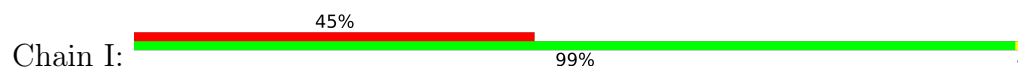
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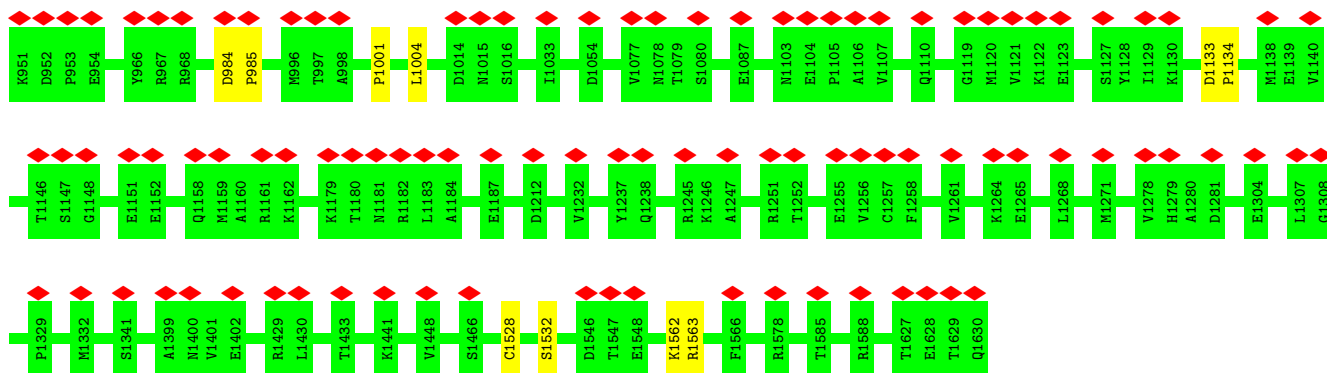


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K1122	E1123	I1129	K1130	D1133	P1134	M1138	T1146	S1147	G1148	M1149	W1150	E1151	E1152	K1155	Q1158	M1159	A1160	R1161	K1162	K1179	T1180	N1181	R1182	L1183	A1184	E1187	E1188	D1212	L1216	M1219	N1220	V1221	S1222	V1232	T1237	Q1238	R1245	K1246	A1247	N1248	S1249	T1250	R1251	D1262															
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	G924	L928	E936												
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	P773	L774	I775	R780	F781	D786	Y792	R793	M794	N795	I800	E826	D827	V828	I829	K830	R831															
P485	N486	K487	V488	L489	Q490	C491	F492	A493	E494	T495	G496	Q497	V498	Q499	V502	L503	Y504	A505	K506	K507	V508	G509	Y510	D513	W514	I515	F516	L517	N520	V521	N522	E523	S524	S525	P526	D527	E528	H529	F530	T531	D535	L546	N547	P548	E549	W550	L551	V552	F555	L558	S559	V560							
Q424	G425	Q426	L427	M428	K429	Y430	E431	S432	L433	E434	L435	A436	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	V478	Y479	L480	R481	A482	N483	V484	
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	E392	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	L420	L421	L422	D423
I303	F304	V305	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	V337	I338	T339	N340	V341	L342	Q343	N344	P345	D346	L347	A348	L349	R350	N351	A352	V353	R354	N355	N356	L357	A358	G359	A360	E361	E362	L363	
L121	V122	T123	D124	N125	A126	V127	Y128	H129	W130	S131	M132	E133	G134	E135	S136	Q137	P138	V139	K140	M141	F142	D143	K144	H145	S146	S147	L148	A149	G150	C151	Q152	I153	R157	T158	D159	A160	K161	Q162	K163	W164	L165	L166	T167	T168	G169	I170	S171	A172	Q173	Y174	N175	R176	V177	G178	G179	A180	M181	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



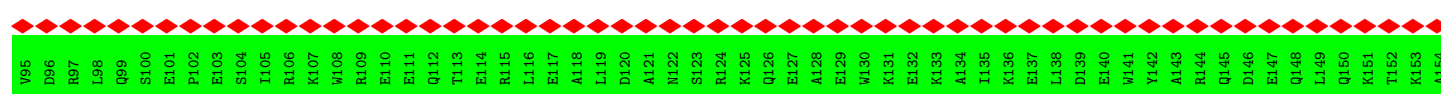
- Molecule 2: Clathrin light chain A



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

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

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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 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.

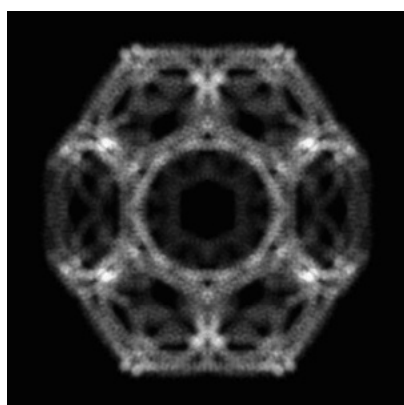
6 Map visualisation [i](#)

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.

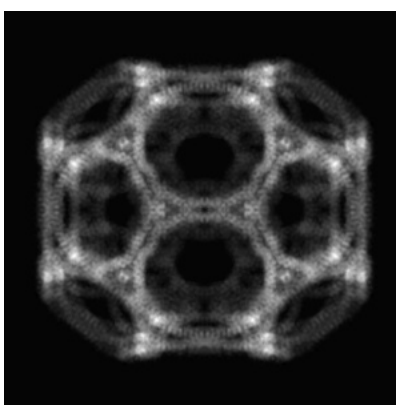
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

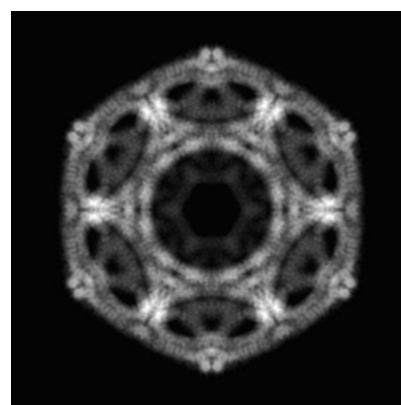
6.1.1 Primary map



X



Y

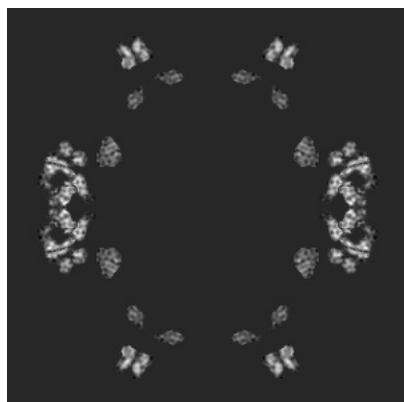


Z

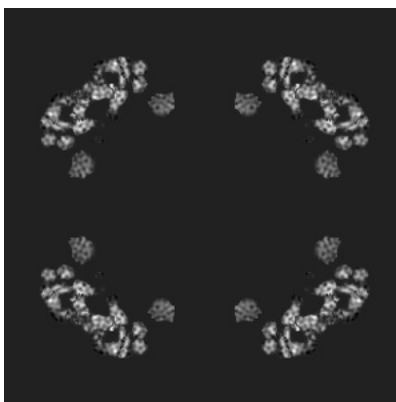
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

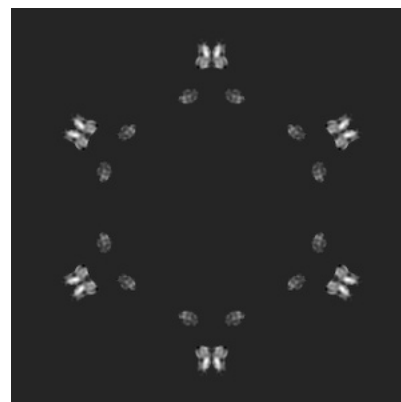
6.2.1 Primary map



X Index: 156



Y Index: 156

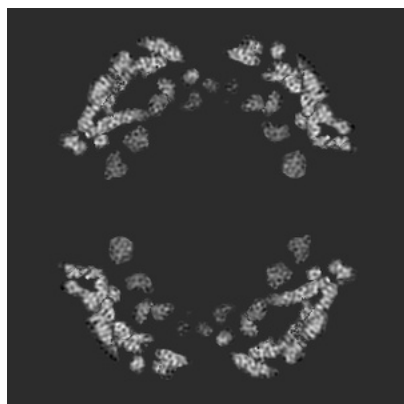


Z Index: 156

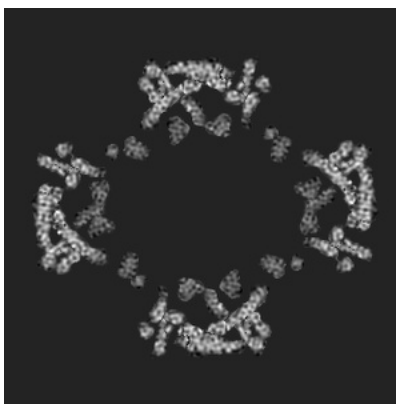
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

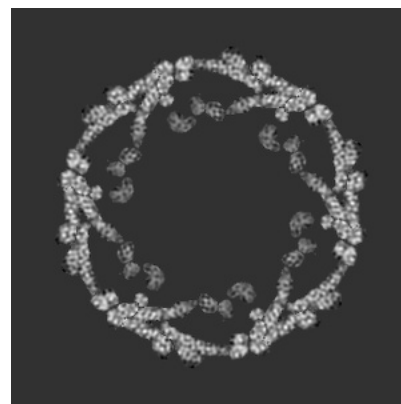
6.3.1 Primary map



X Index: 114



Y Index: 101

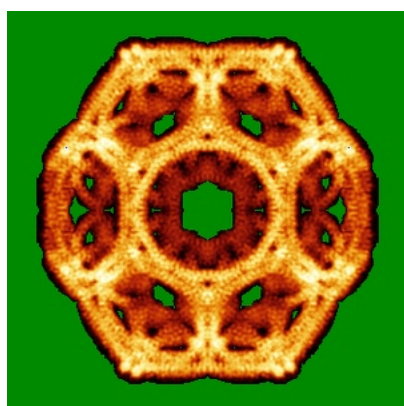


Z Index: 205

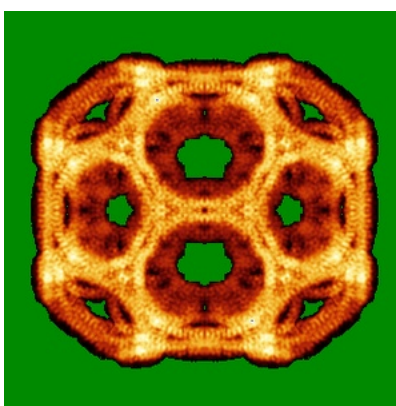
The images above show the largest variance slices of the map in three orthogonal directions.

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

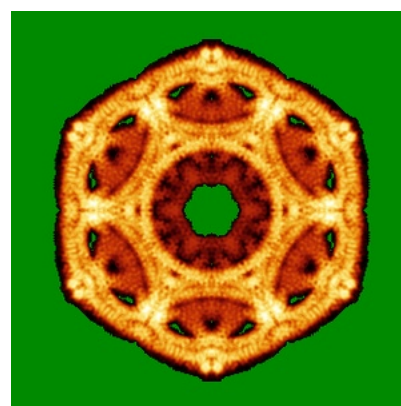
6.4.1 Primary map



X



Y

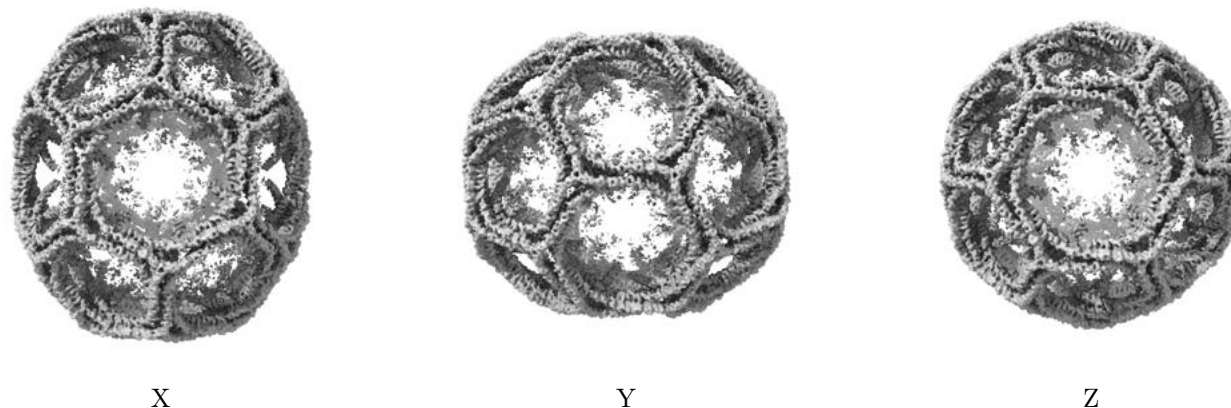


Z

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.

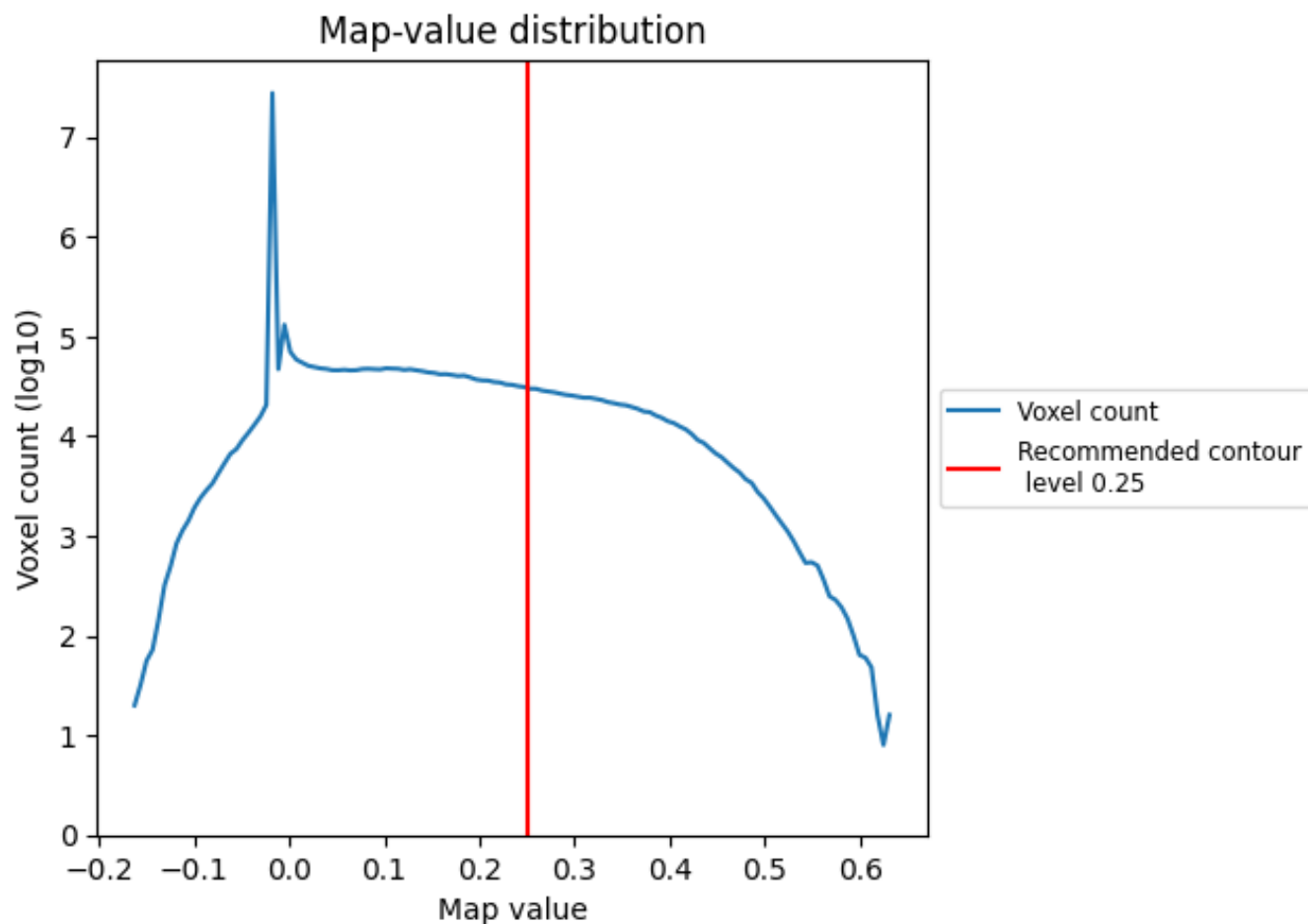
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

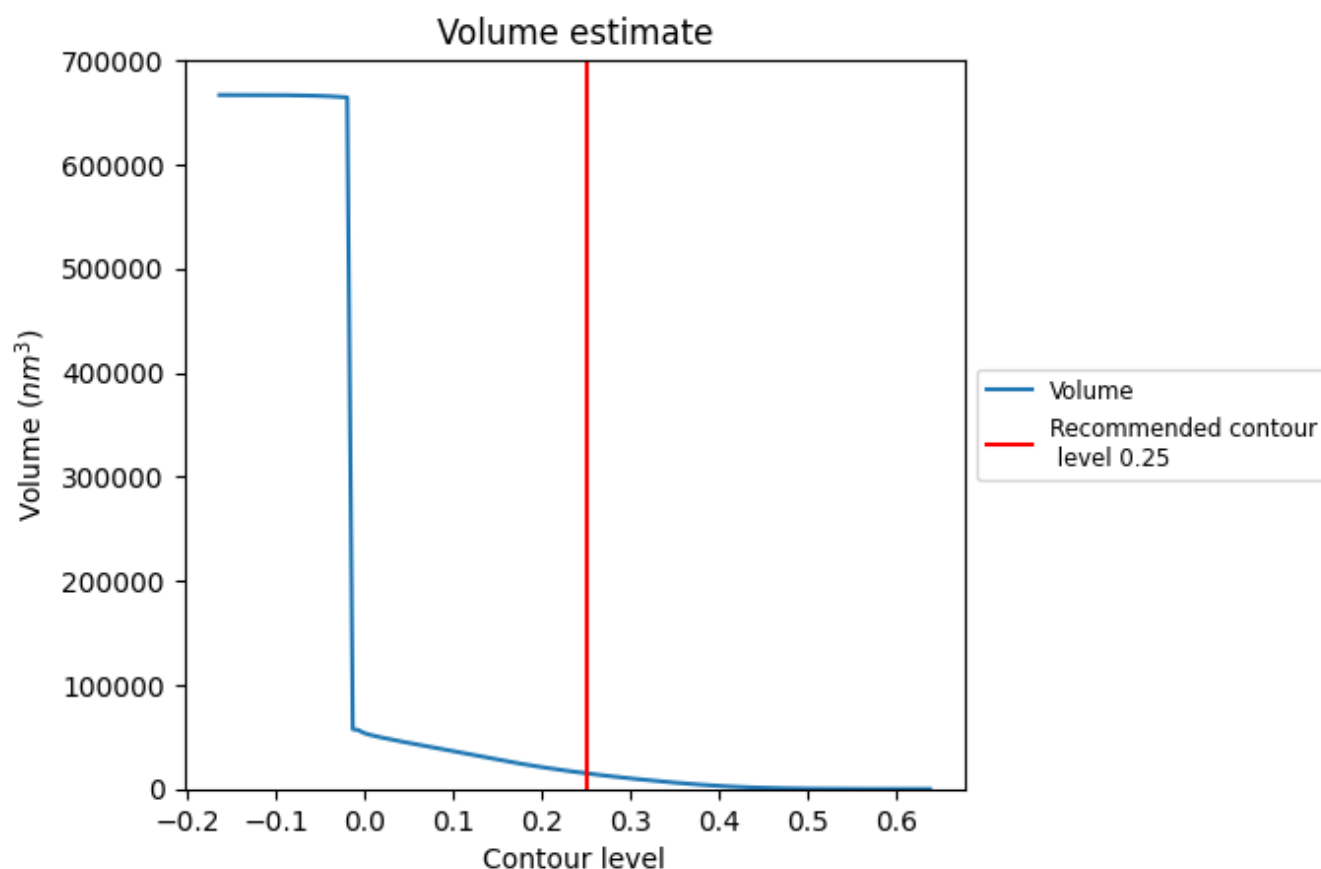
This section contains the results of statistical analysis of the map.

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.

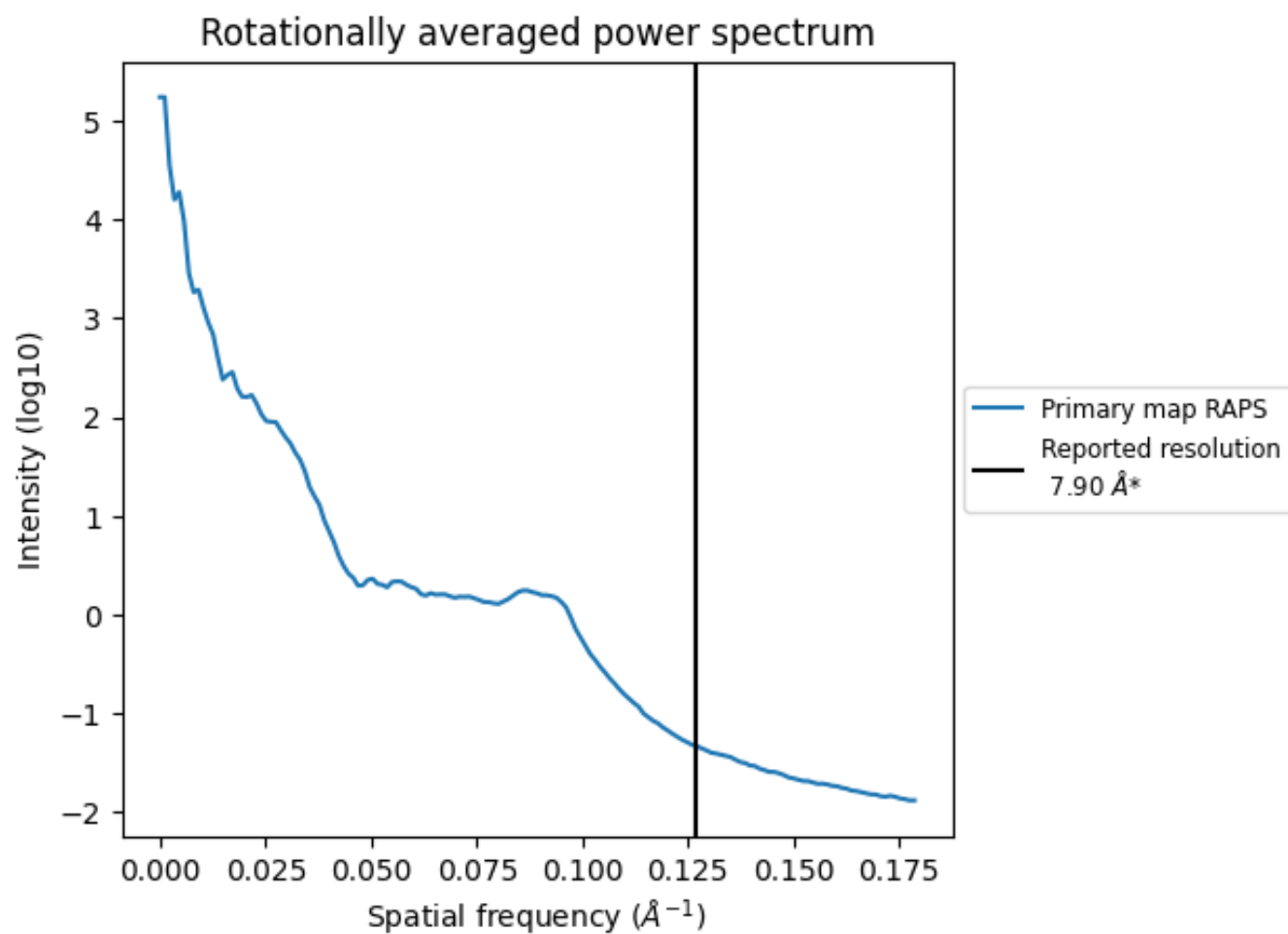
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 15047 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 ⓘ

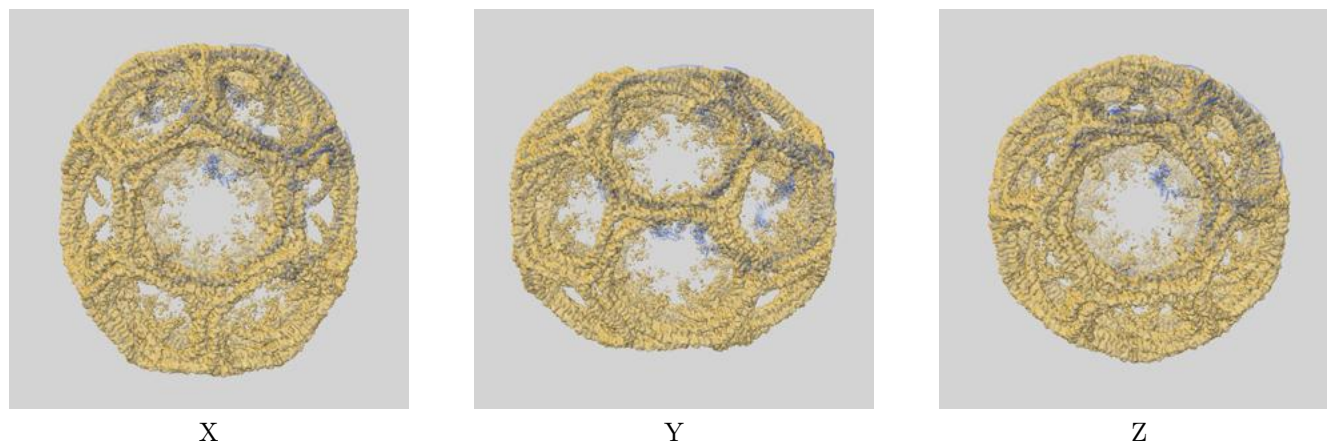
This section was not generated. No FSC curve or half-maps provided.

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](#)



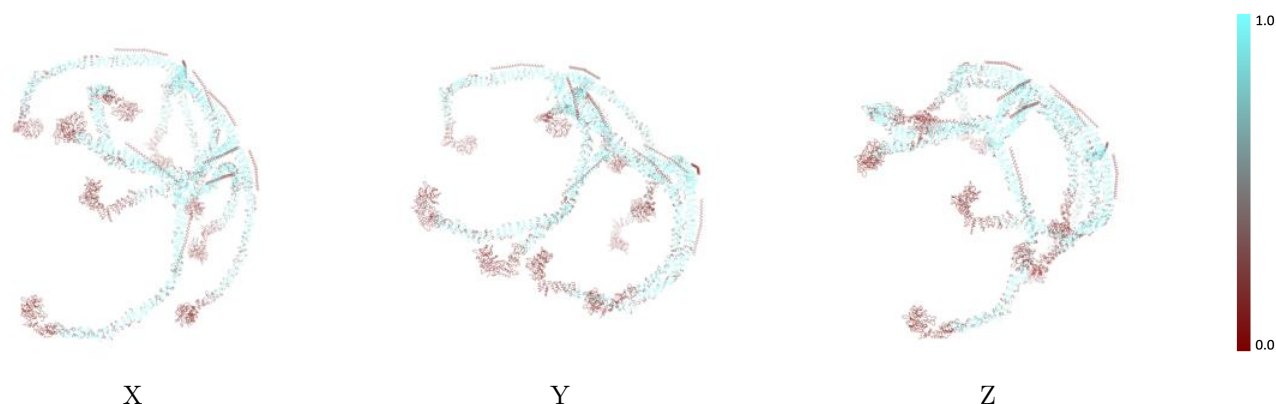
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



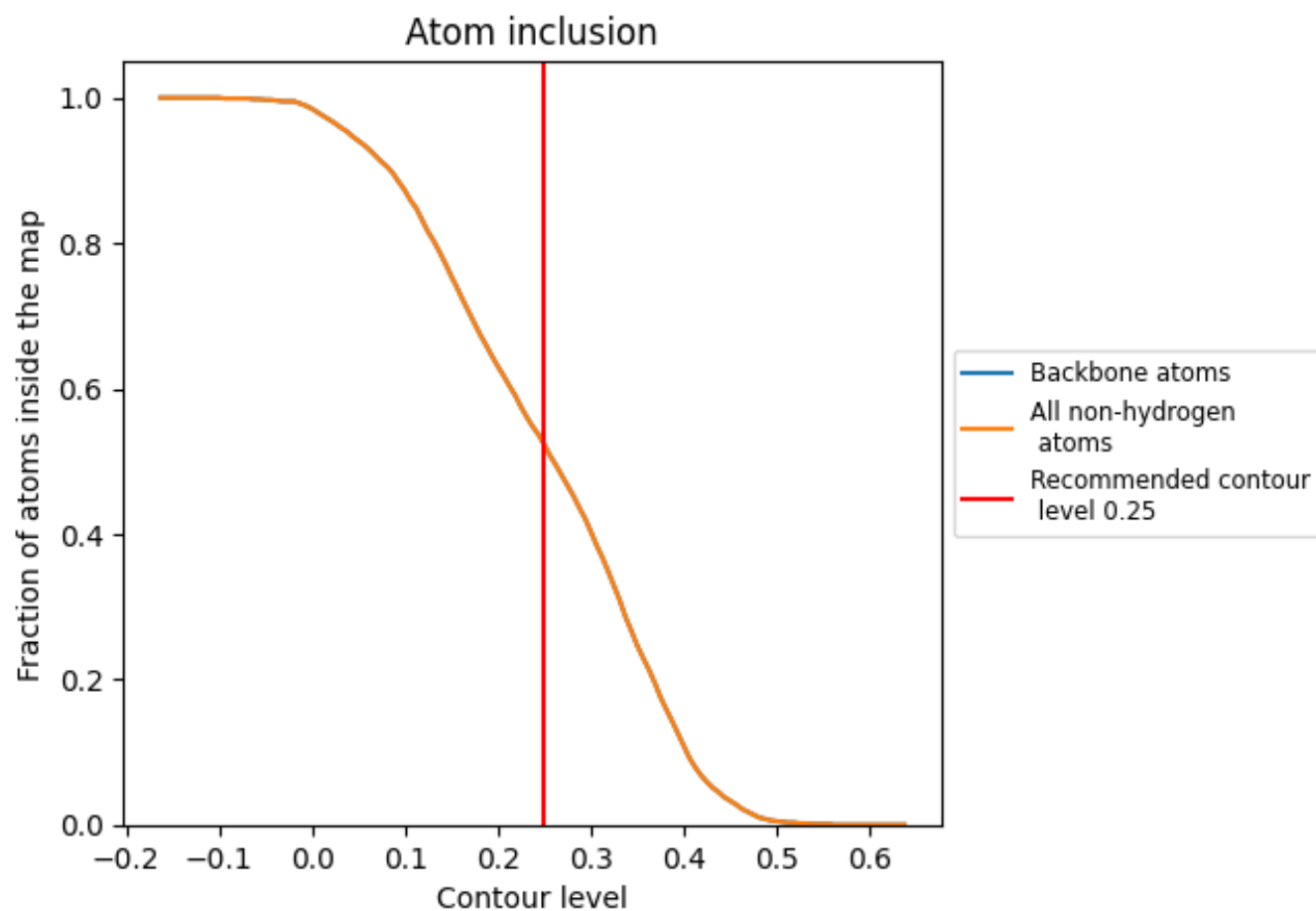
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

