



wwPDB EM Validation Summary Report ⓘ

Feb 13, 2024 – 11:04 AM EST

PDB ID : 3J03
EMDB ID : EMD-5138
Title : Lidless Mm-cpn in the closed state with ATP/AlFx
Authors : Zhang, J.; Ma, B.; DiMaio, F.; Douglas, N.R.; Joachimiak, L.; Baker, D.;
Frydman, J.; Levitt, M.; Chiu, W.
Deposited on : 2011-02-10
Resolution : 4.80 Å(reported)

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A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

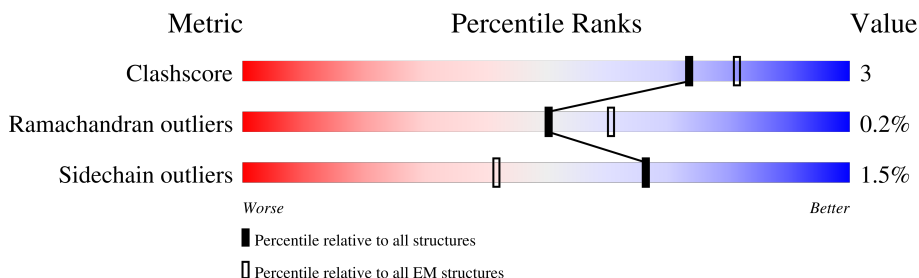
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	491	
1	B	491	
1	C	491	
1	D	491	
1	E	491	
1	F	491	
1	G	491	
1	H	491	

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Mol	Chain	Length	Quality of chain
1	I	491	
1	J	491	
1	K	491	
1	L	491	
1	M	491	
1	N	491	
1	O	491	
1	P	491	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 58640 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 Lidless Mm-cpn.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	491	3665	2272	635	734	24	0	0
1	B	491	3665	2272	635	734	24	0	0
1	C	491	3665	2272	635	734	24	0	0
1	D	491	3665	2272	635	734	24	0	0
1	E	491	3665	2272	635	734	24	0	0
1	F	491	3665	2272	635	734	24	0	0
1	G	491	3665	2272	635	734	24	0	0
1	H	491	3665	2272	635	734	24	0	0
1	I	491	3665	2272	635	734	24	0	0
1	J	491	3665	2272	635	734	24	0	0
1	K	491	3665	2272	635	734	24	0	0
1	L	491	3665	2272	635	734	24	0	0
1	M	491	3665	2272	635	734	24	0	0
1	N	491	3665	2272	635	734	24	0	0
1	O	491	3665	2272	635	734	24	0	0
1	P	491	3665	2272	635	734	24	0	0

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	235	GLU	-	linker	UNP Q877G8
A	236	THR	-	linker	UNP Q877G8
A	237	ALA	-	linker	UNP Q877G8
A	238	SER	-	linker	UNP Q877G8
A	239	GLU	-	linker	UNP Q877G8
A	240	MET	-	linker	UNP Q877G8
B	726	GLU	-	linker	UNP Q877G8
B	727	THR	-	linker	UNP Q877G8
B	728	ALA	-	linker	UNP Q877G8
B	729	SER	-	linker	UNP Q877G8
B	730	GLU	-	linker	UNP Q877G8
B	731	MET	-	linker	UNP Q877G8
C	1217	GLU	-	linker	UNP Q877G8
C	1218	THR	-	linker	UNP Q877G8
C	1219	ALA	-	linker	UNP Q877G8
C	1220	SER	-	linker	UNP Q877G8
C	1221	GLU	-	linker	UNP Q877G8
C	1222	MET	-	linker	UNP Q877G8
D	1708	GLU	-	linker	UNP Q877G8
D	1709	THR	-	linker	UNP Q877G8
D	1710	ALA	-	linker	UNP Q877G8
D	1711	SER	-	linker	UNP Q877G8
D	1712	GLU	-	linker	UNP Q877G8
D	1713	MET	-	linker	UNP Q877G8
E	2199	GLU	-	linker	UNP Q877G8
E	2200	THR	-	linker	UNP Q877G8
E	2201	ALA	-	linker	UNP Q877G8
E	2202	SER	-	linker	UNP Q877G8
E	2203	GLU	-	linker	UNP Q877G8
E	2204	MET	-	linker	UNP Q877G8
F	2690	GLU	-	linker	UNP Q877G8
F	2691	THR	-	linker	UNP Q877G8
F	2692	ALA	-	linker	UNP Q877G8
F	2693	SER	-	linker	UNP Q877G8
F	2694	GLU	-	linker	UNP Q877G8
F	2695	MET	-	linker	UNP Q877G8
G	3181	GLU	-	linker	UNP Q877G8
G	3182	THR	-	linker	UNP Q877G8
G	3183	ALA	-	linker	UNP Q877G8
G	3184	SER	-	linker	UNP Q877G8
G	3185	GLU	-	linker	UNP Q877G8
G	3186	MET	-	linker	UNP Q877G8
H	3672	GLU	-	linker	UNP Q877G8

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Chain	Residue	Modelled	Actual	Comment	Reference
H	3673	THR	-	linker	UNP Q877G8
H	3674	ALA	-	linker	UNP Q877G8
H	3675	SER	-	linker	UNP Q877G8
H	3676	GLU	-	linker	UNP Q877G8
H	3677	MET	-	linker	UNP Q877G8
I	4163	GLU	-	linker	UNP Q877G8
I	4164	THR	-	linker	UNP Q877G8
I	4165	ALA	-	linker	UNP Q877G8
I	4166	SER	-	linker	UNP Q877G8
I	4167	GLU	-	linker	UNP Q877G8
I	4168	MET	-	linker	UNP Q877G8
J	4654	GLU	-	linker	UNP Q877G8
J	4655	THR	-	linker	UNP Q877G8
J	4656	ALA	-	linker	UNP Q877G8
J	4657	SER	-	linker	UNP Q877G8
J	4658	GLU	-	linker	UNP Q877G8
J	4659	MET	-	linker	UNP Q877G8
K	5145	GLU	-	linker	UNP Q877G8
K	5146	THR	-	linker	UNP Q877G8
K	5147	ALA	-	linker	UNP Q877G8
K	5148	SER	-	linker	UNP Q877G8
K	5149	GLU	-	linker	UNP Q877G8
K	5150	MET	-	linker	UNP Q877G8
L	5636	GLU	-	linker	UNP Q877G8
L	5637	THR	-	linker	UNP Q877G8
L	5638	ALA	-	linker	UNP Q877G8
L	5639	SER	-	linker	UNP Q877G8
L	5640	GLU	-	linker	UNP Q877G8
L	5641	MET	-	linker	UNP Q877G8
M	6127	GLU	-	linker	UNP Q877G8
M	6128	THR	-	linker	UNP Q877G8
M	6129	ALA	-	linker	UNP Q877G8
M	6130	SER	-	linker	UNP Q877G8
M	6131	GLU	-	linker	UNP Q877G8
M	6132	MET	-	linker	UNP Q877G8
N	6618	GLU	-	linker	UNP Q877G8
N	6619	THR	-	linker	UNP Q877G8
N	6620	ALA	-	linker	UNP Q877G8
N	6621	SER	-	linker	UNP Q877G8
N	6622	GLU	-	linker	UNP Q877G8
N	6623	MET	-	linker	UNP Q877G8
O	7109	GLU	-	linker	UNP Q877G8

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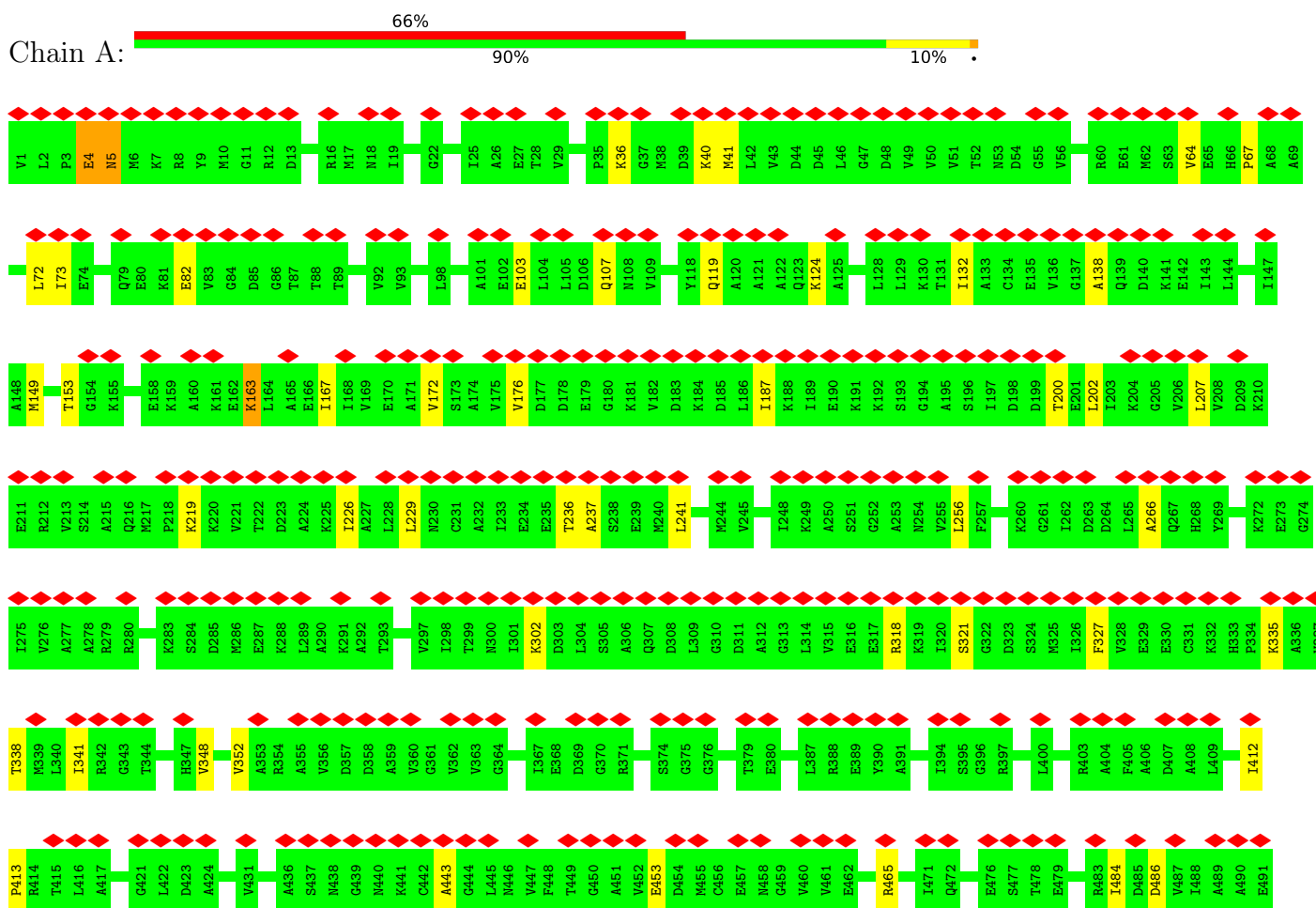
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Chain	Residue	Modelled	Actual	Comment	Reference
O	7110	THR	-	linker	UNP Q877G8
O	7111	ALA	-	linker	UNP Q877G8
O	7112	SER	-	linker	UNP Q877G8
O	7113	GLU	-	linker	UNP Q877G8
O	7114	MET	-	linker	UNP Q877G8
P	7600	GLU	-	linker	UNP Q877G8
P	7601	THR	-	linker	UNP Q877G8
P	7602	ALA	-	linker	UNP Q877G8
P	7603	SER	-	linker	UNP Q877G8
P	7604	GLU	-	linker	UNP Q877G8
P	7605	MET	-	linker	UNP Q877G8

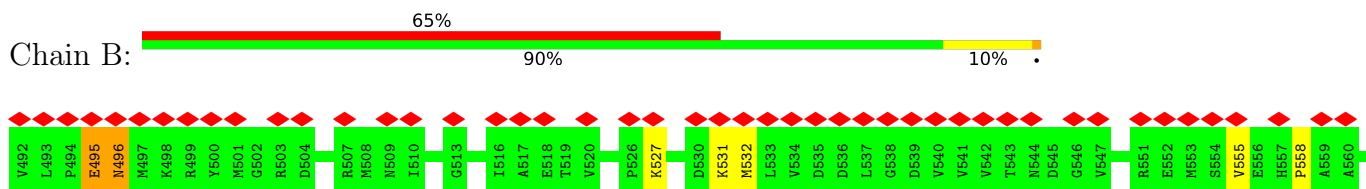
3 Residue-property plots [i](#)

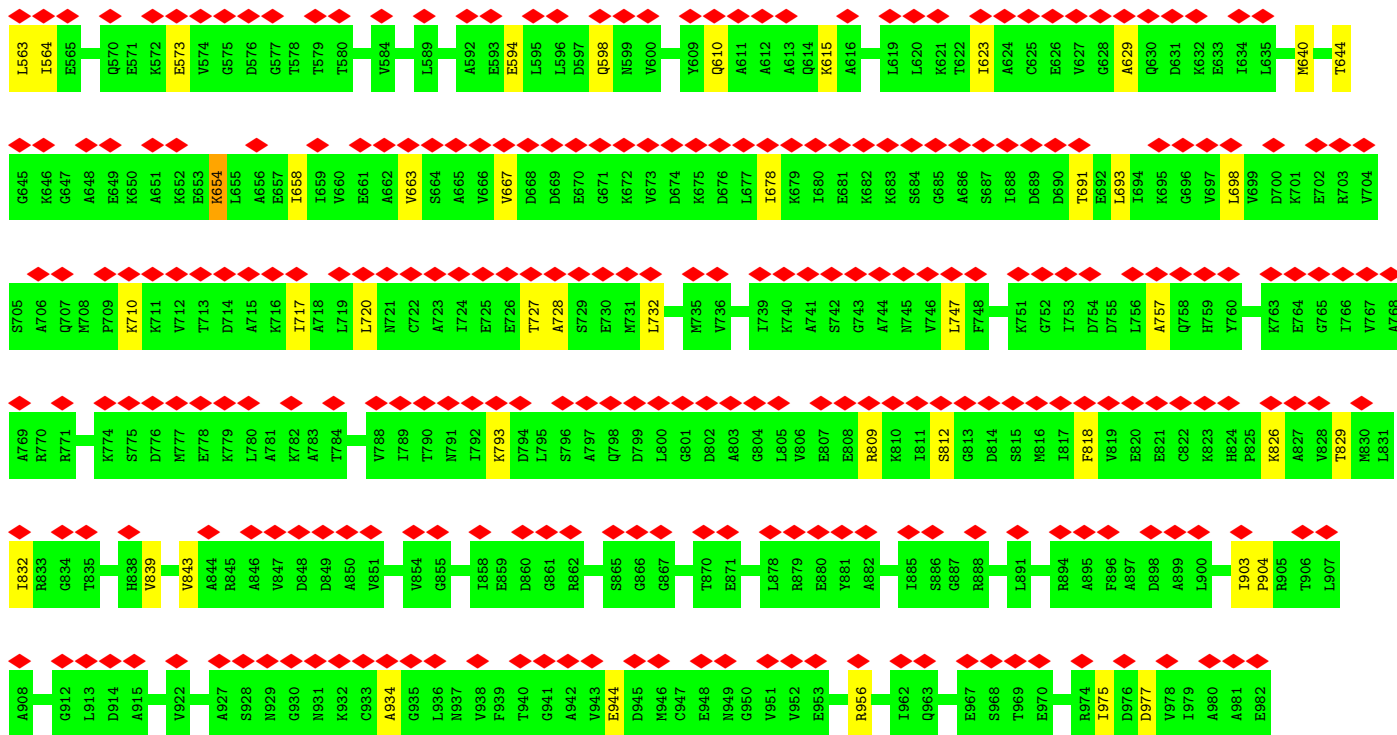
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

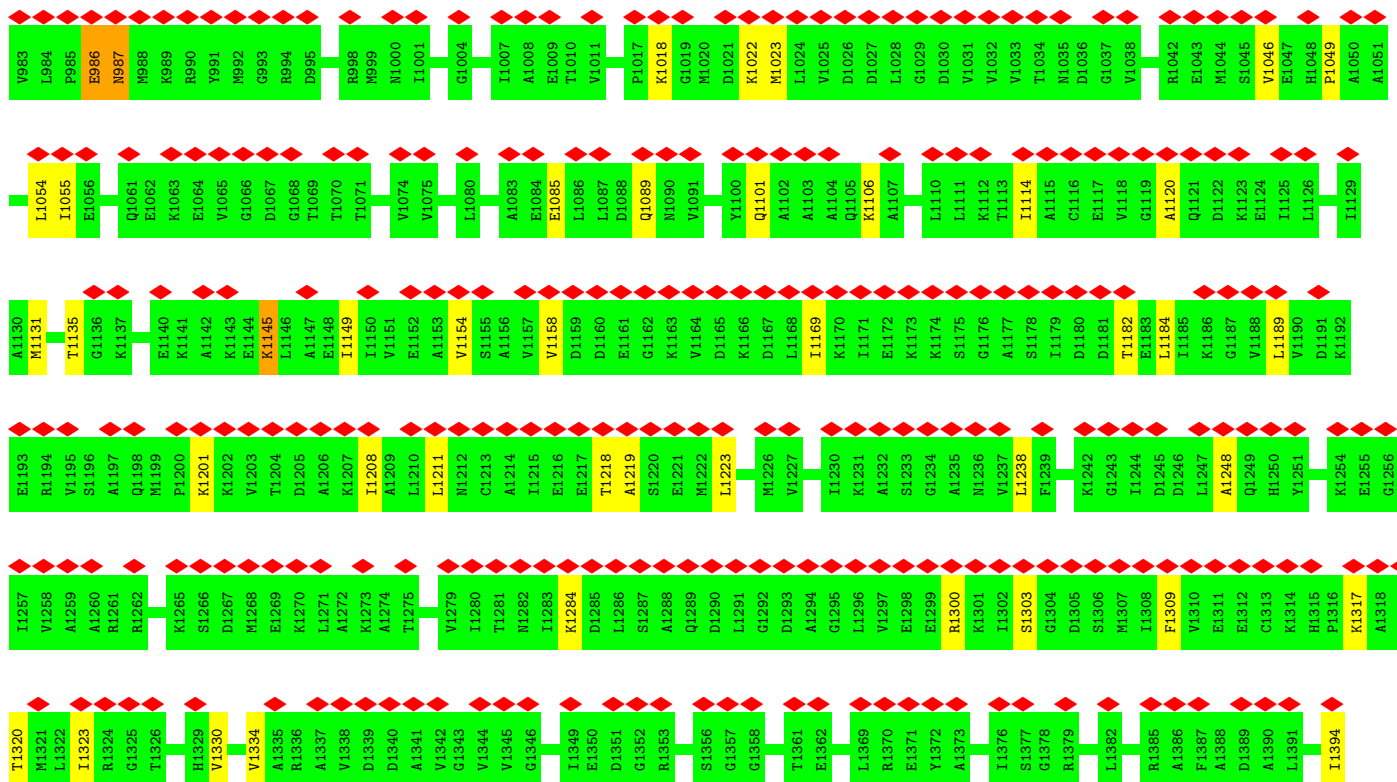


- Molecule 1: Lidless Mm-cpn



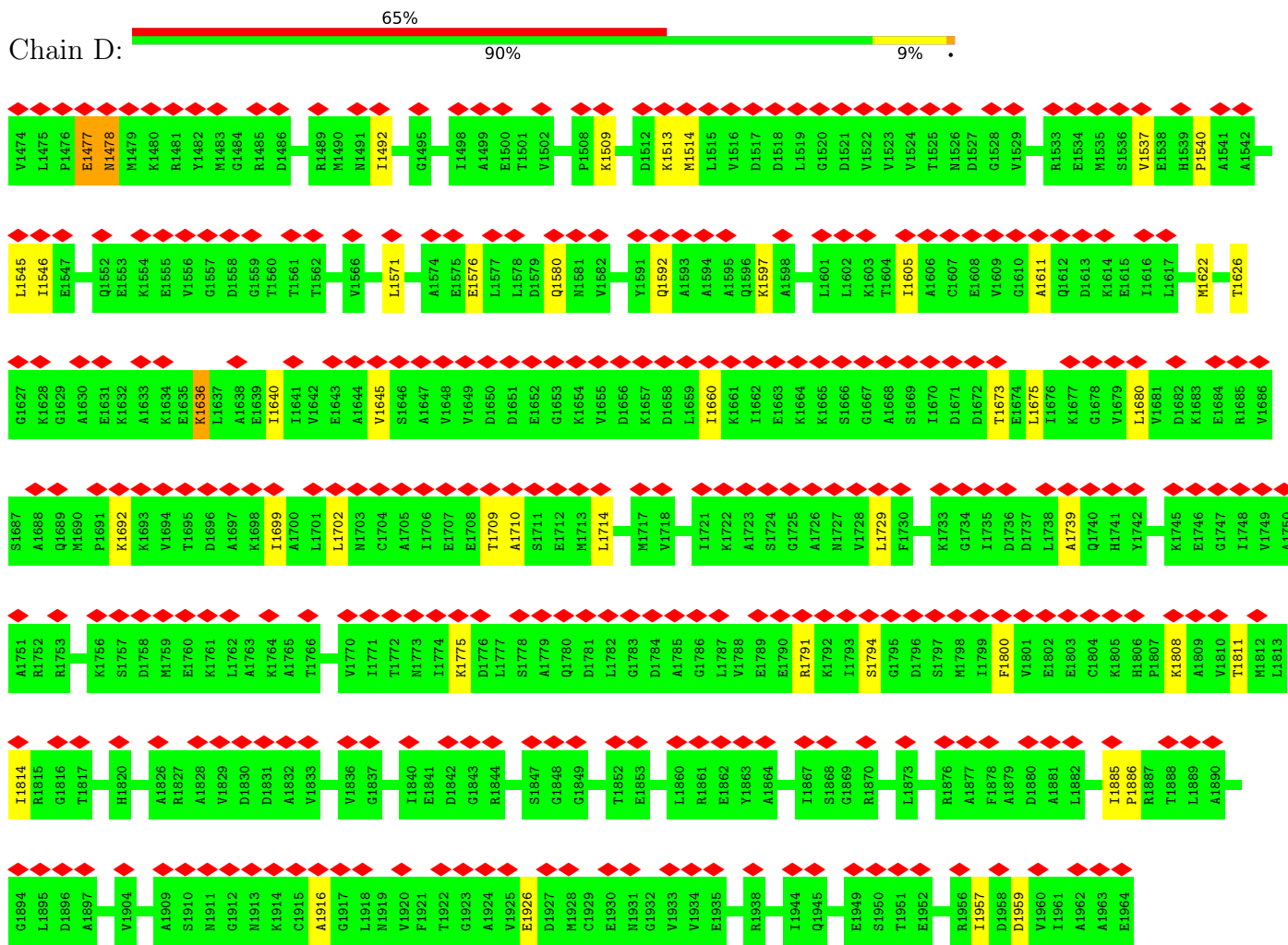


• Molecule 1: Lidless Mm-cpn

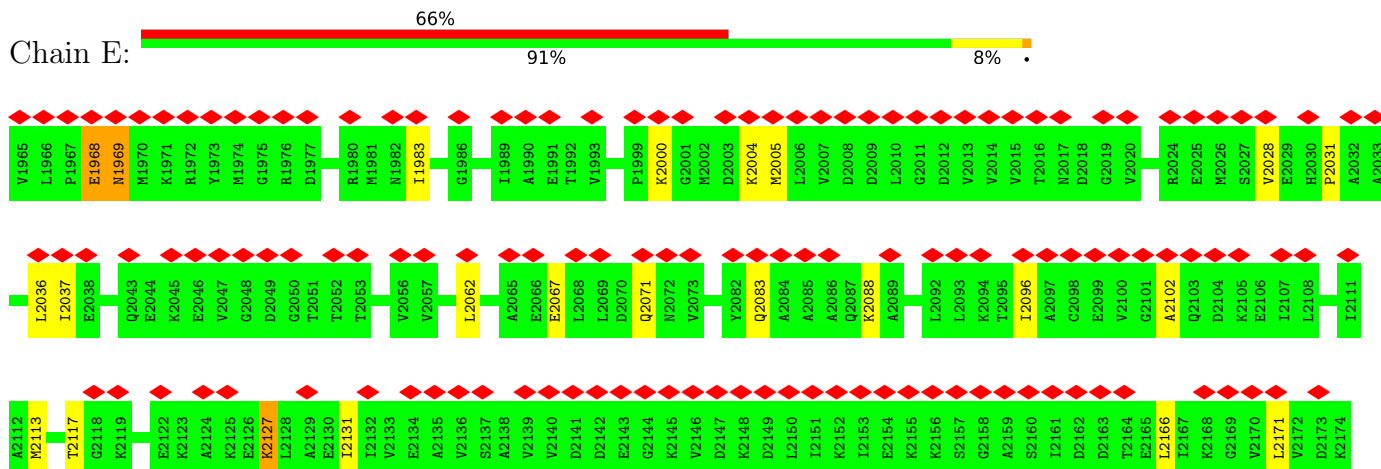


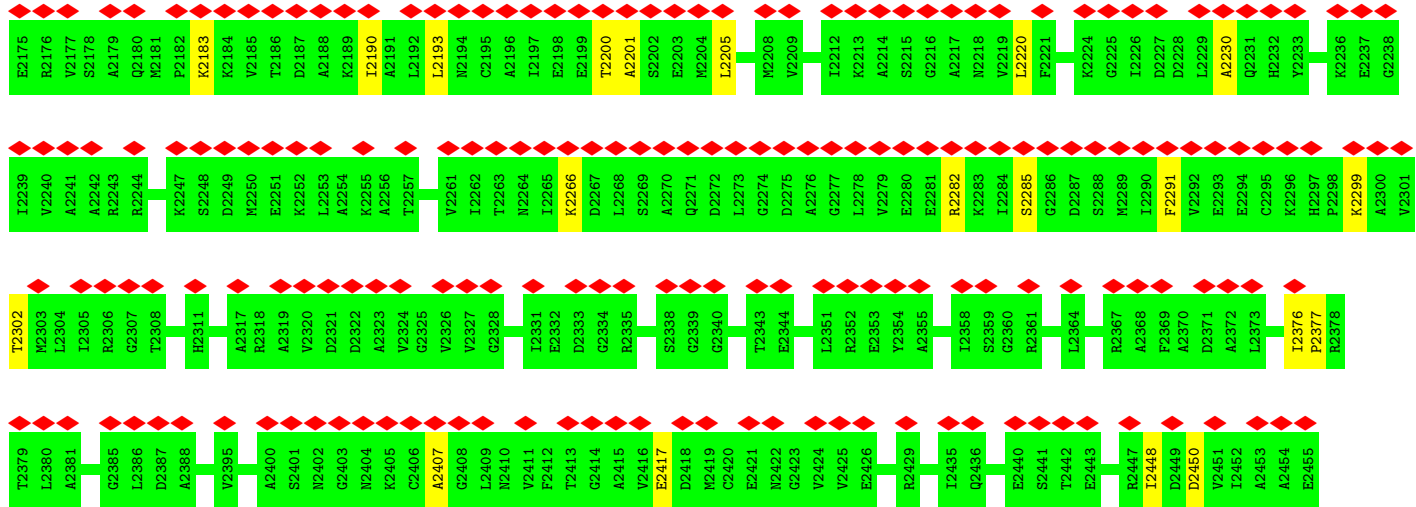


• Molecule 1: Lidless Mm-cpn

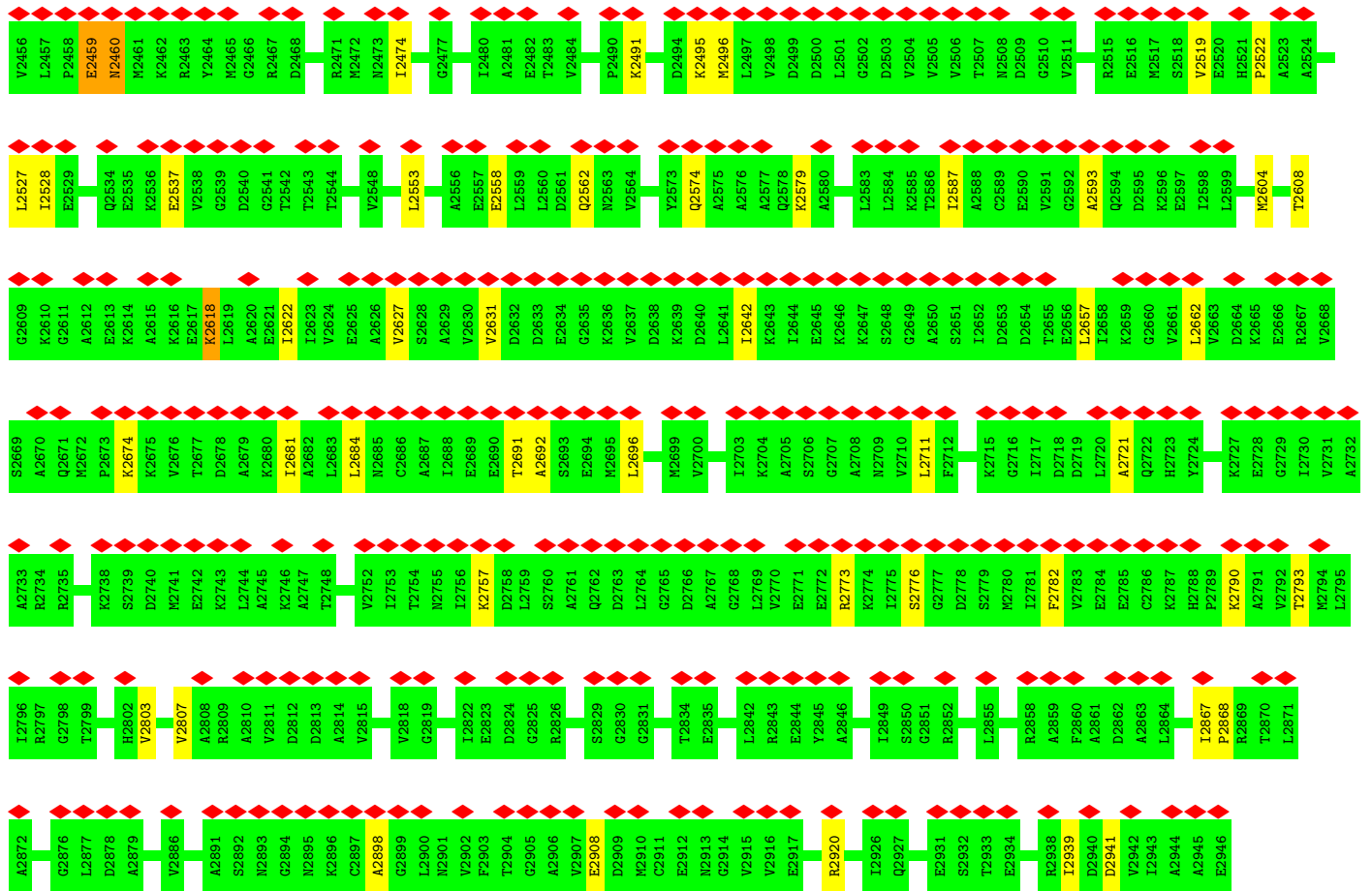
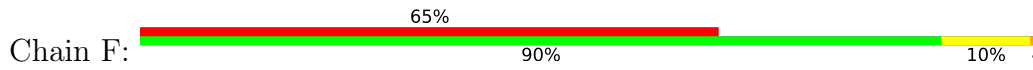


• Molecule 1: Lidless Mm-cpn

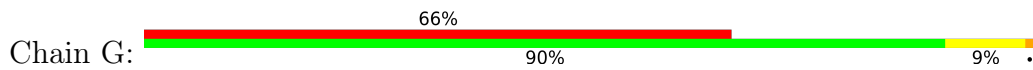


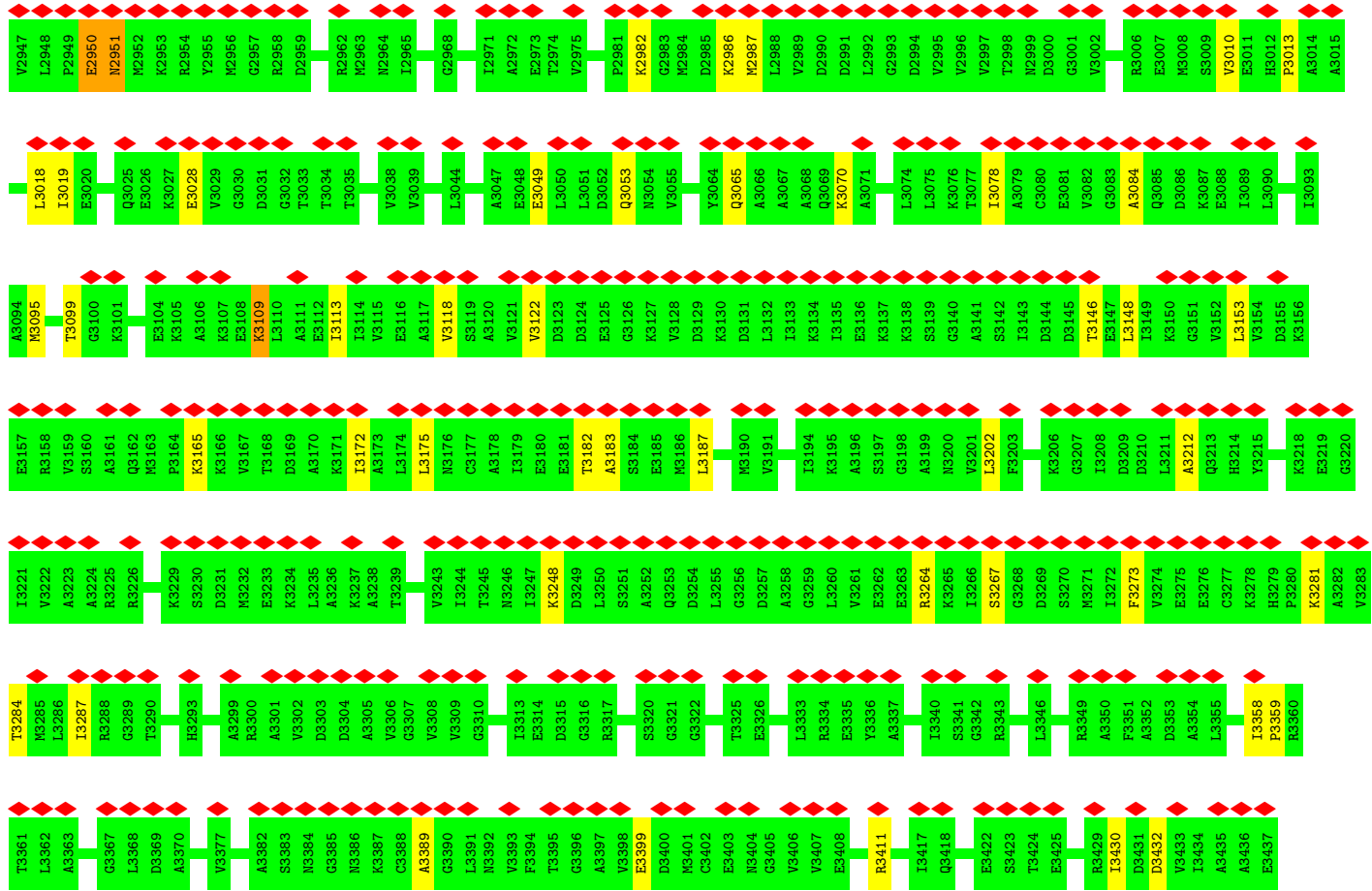


• Molecule 1: Lidless Mm-cpn

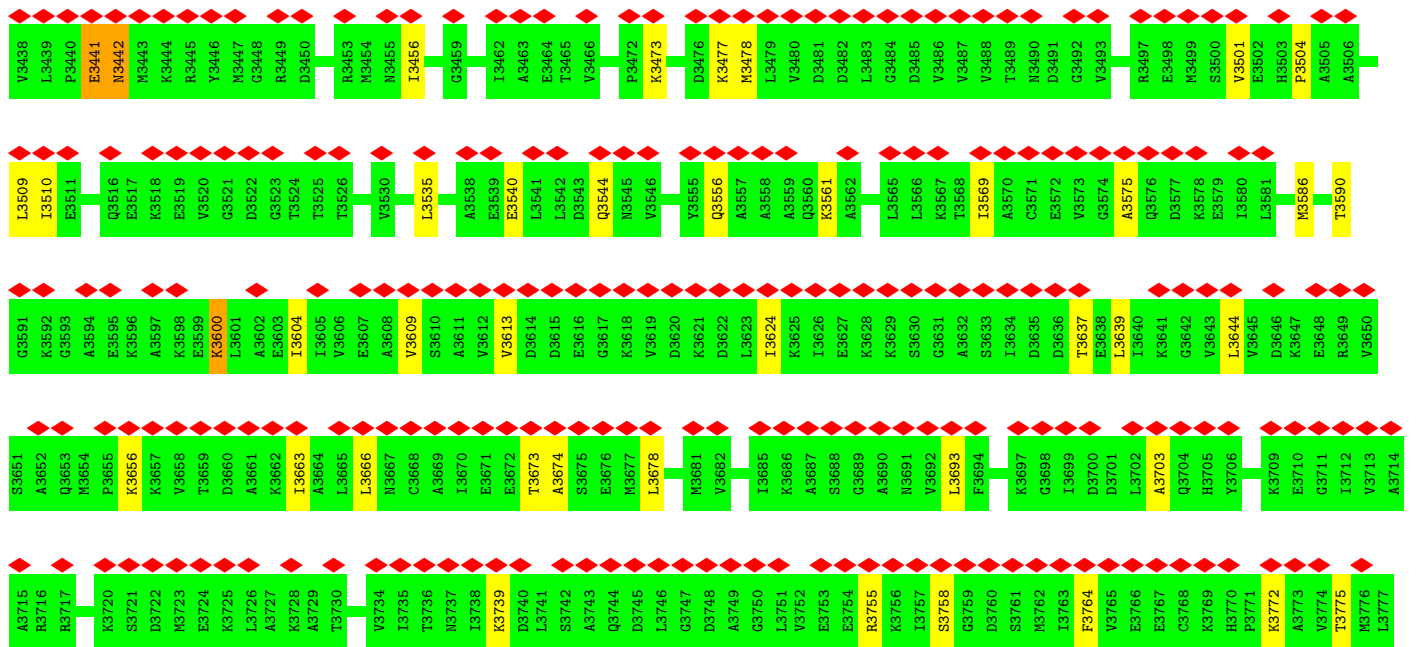


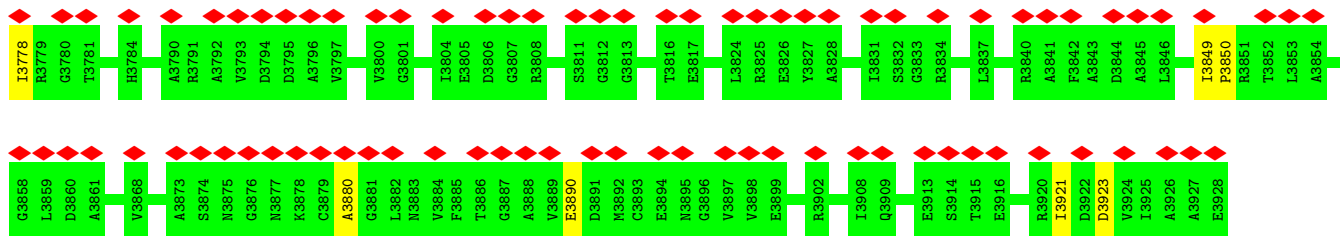
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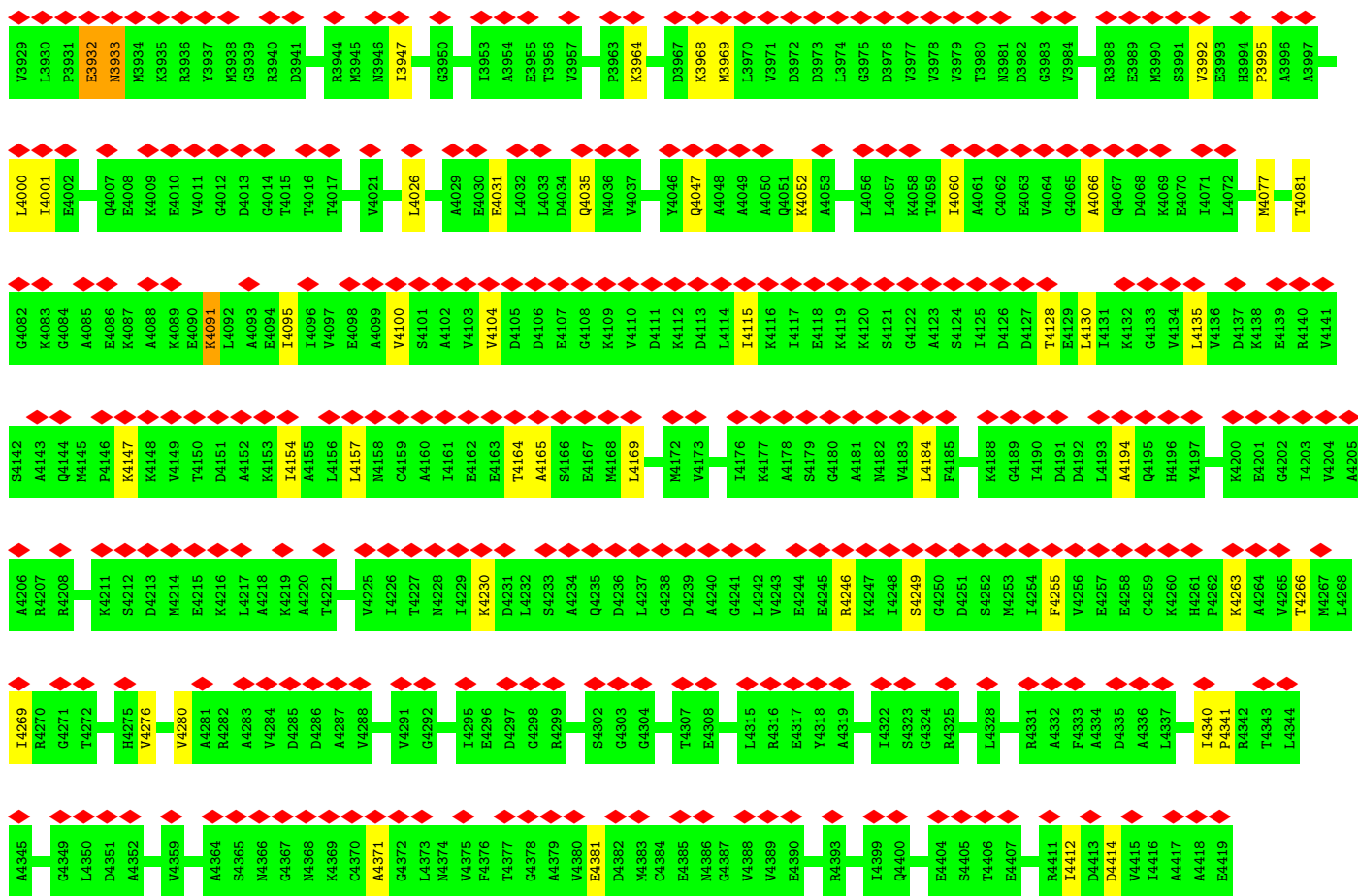
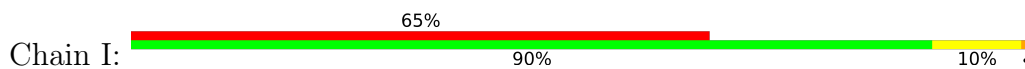


• Molecule 1: Lidless Mm-cpn

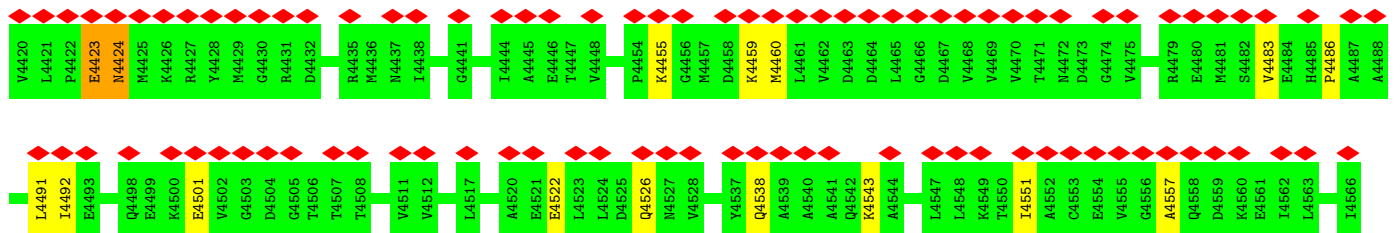
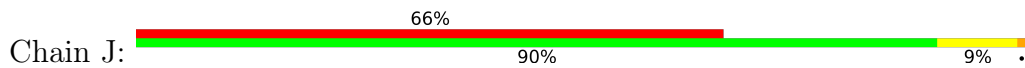


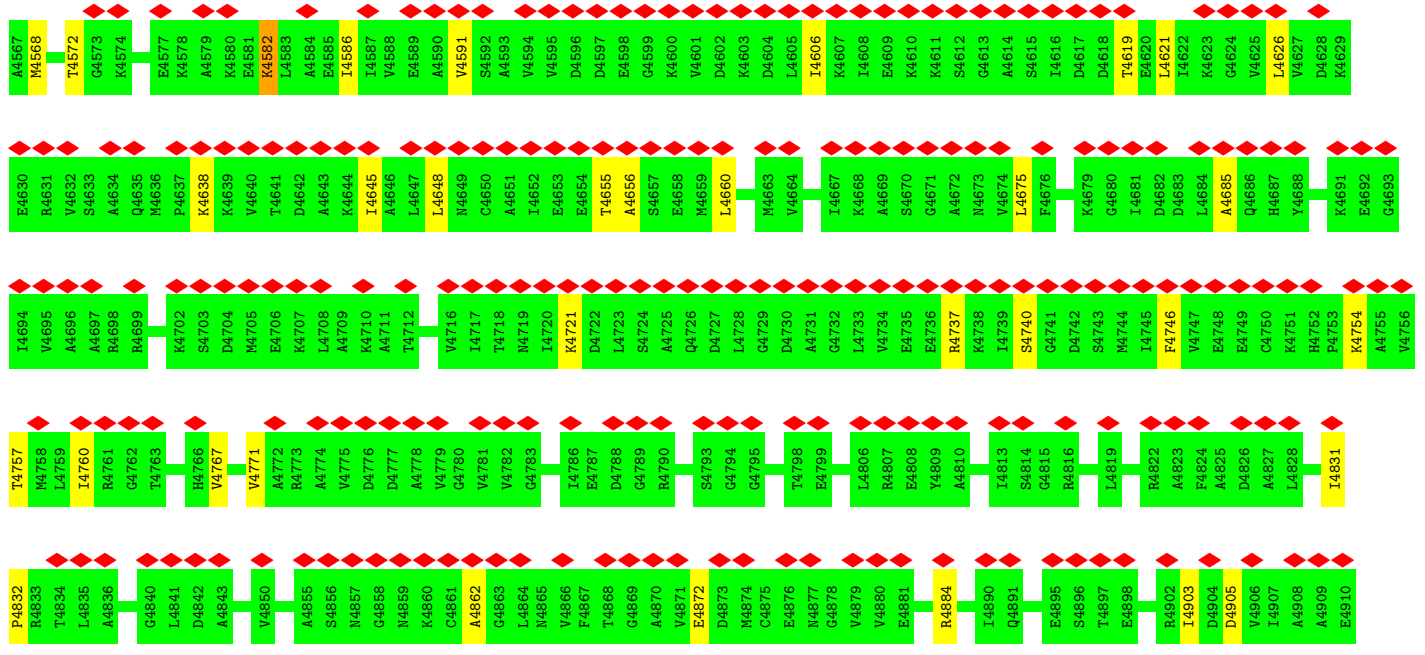


• Molecule 1: Lidless Mm-cpn

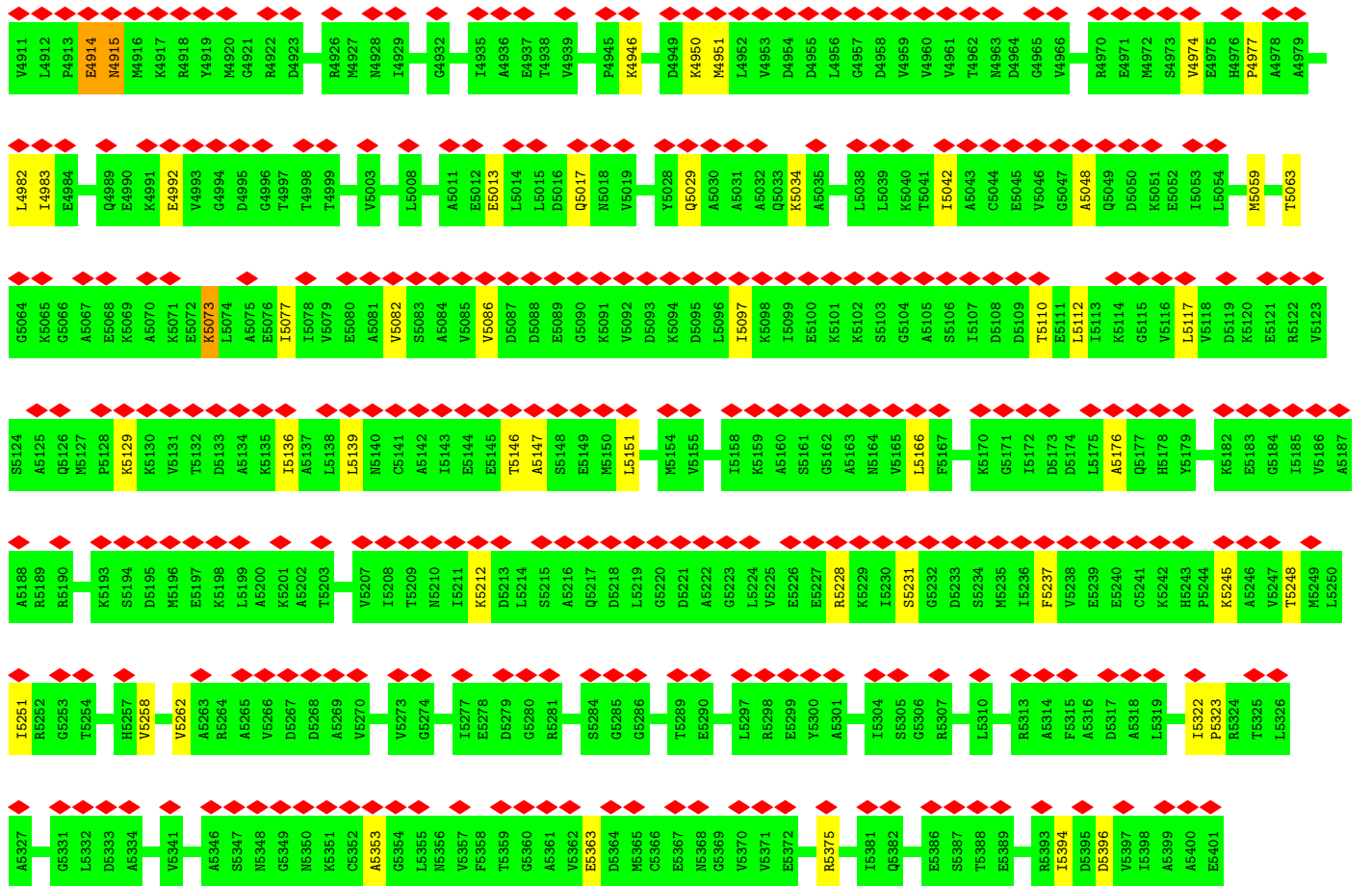
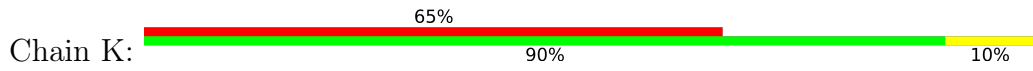


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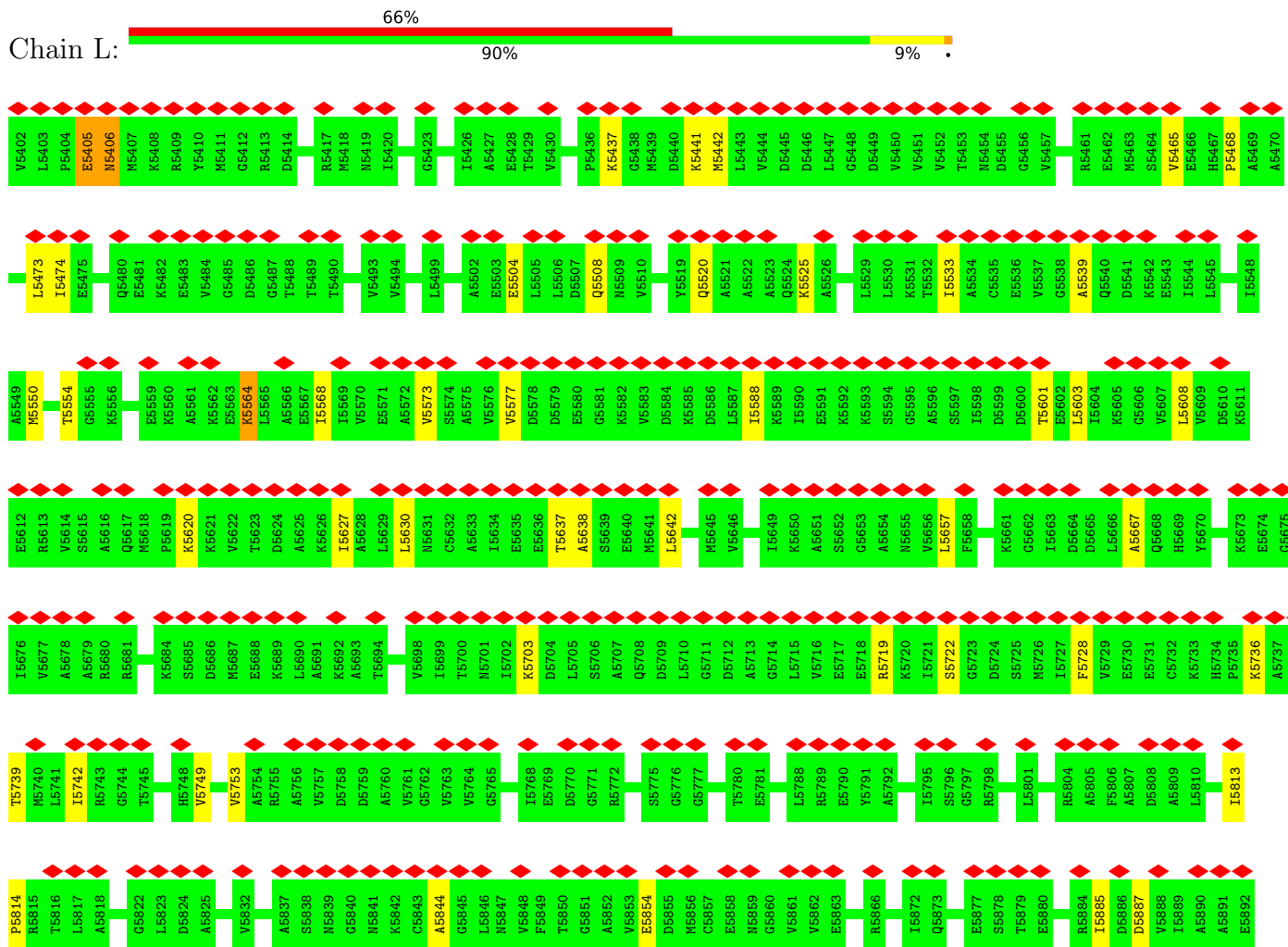




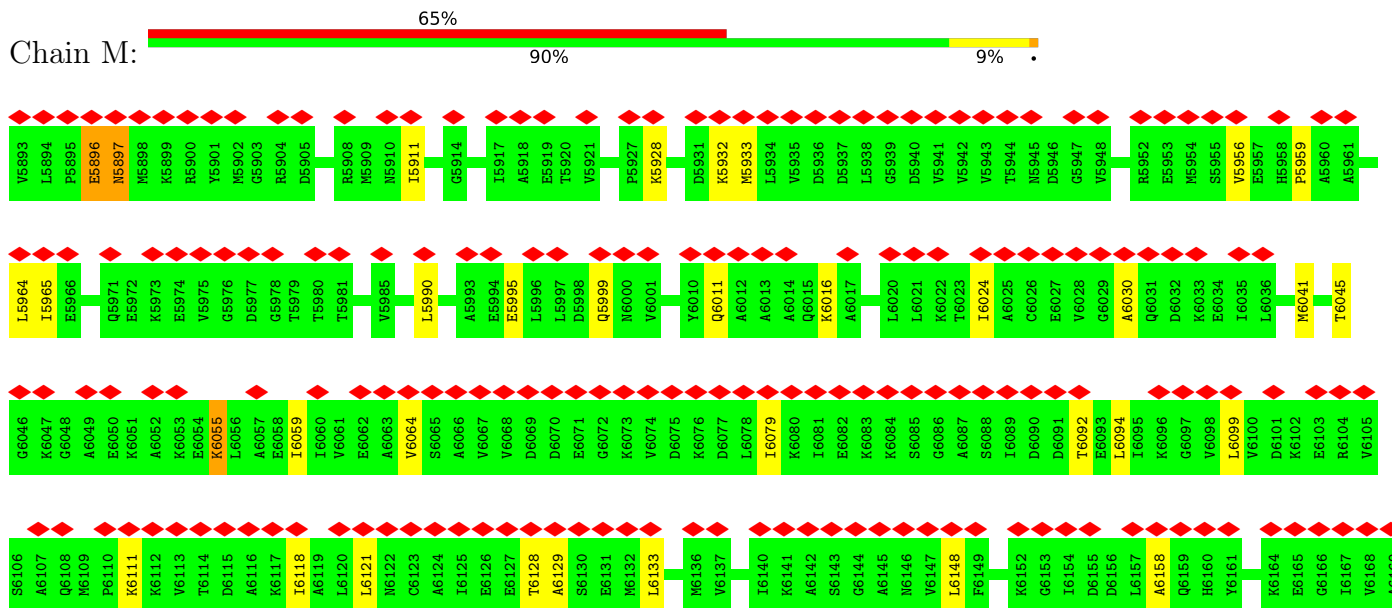
- Molecule 1: Lidless Mm-cpn

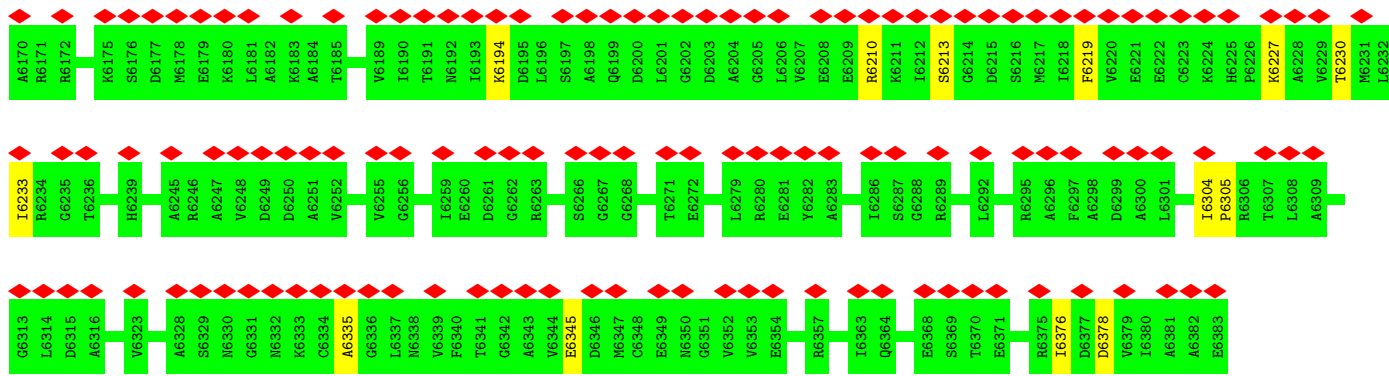


Molecule 1: Lidless Mm-cpn

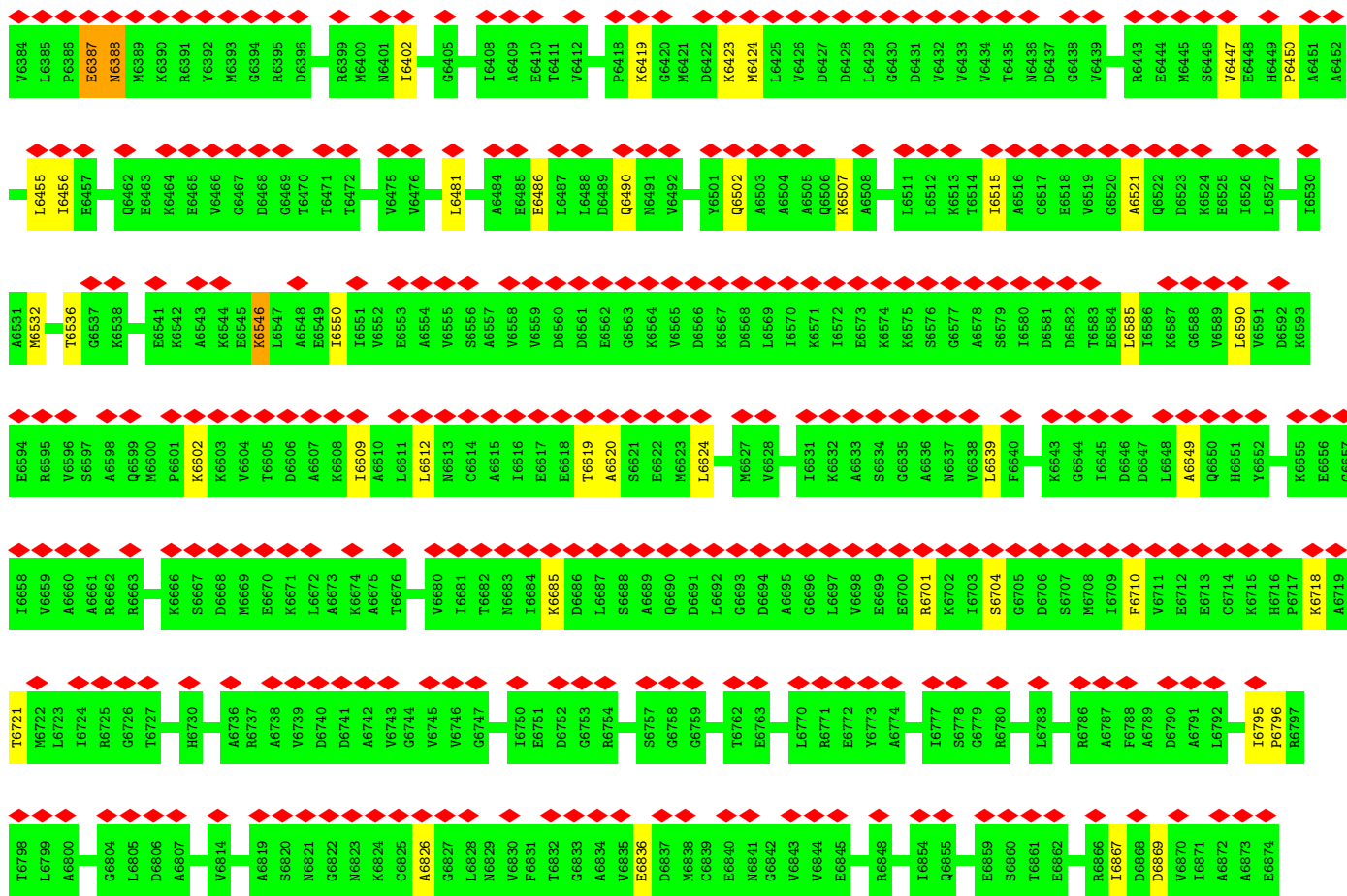


Molecule 1: Lidless Mm-cpn

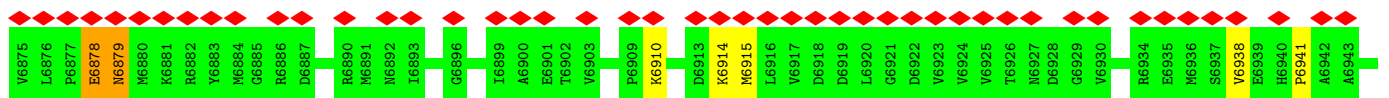
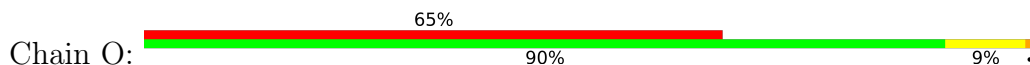


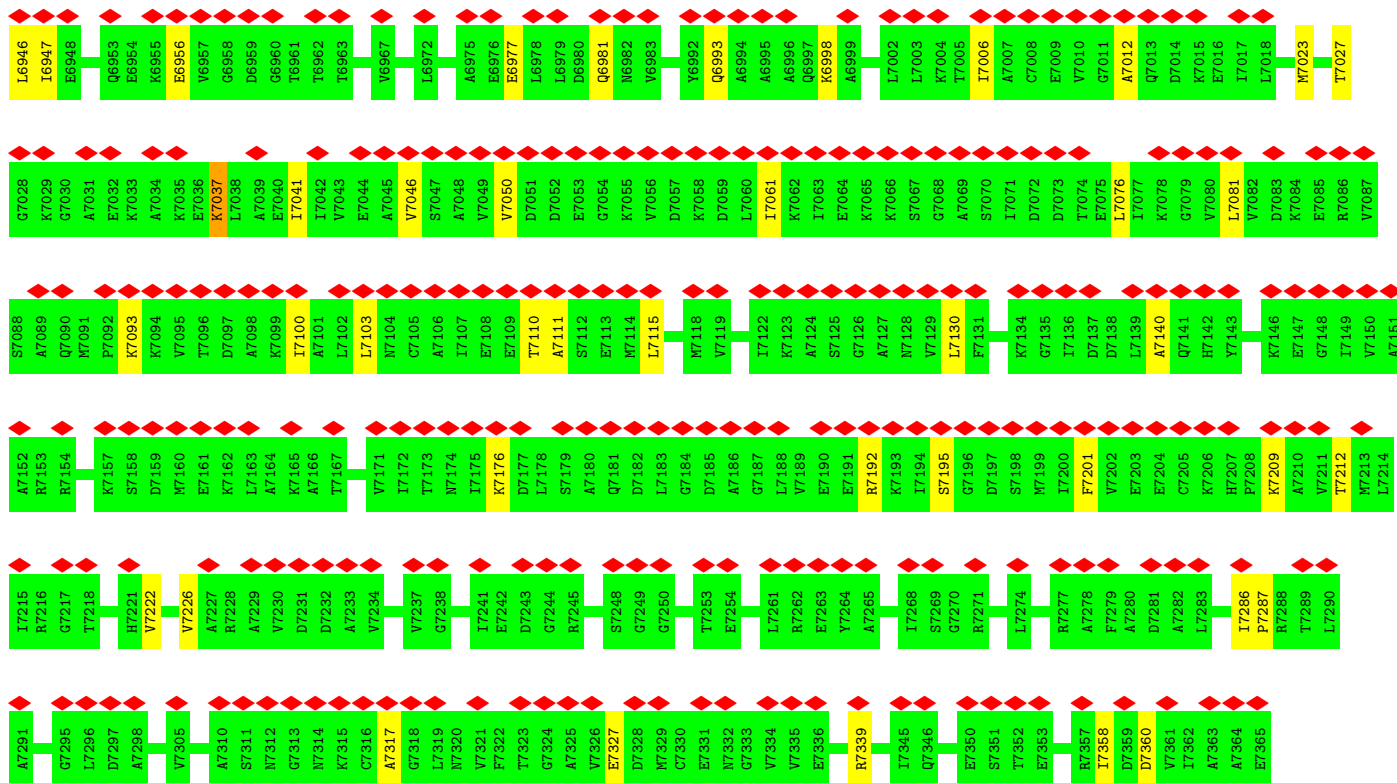


• Molecule 1: Lidless Mm-cpn

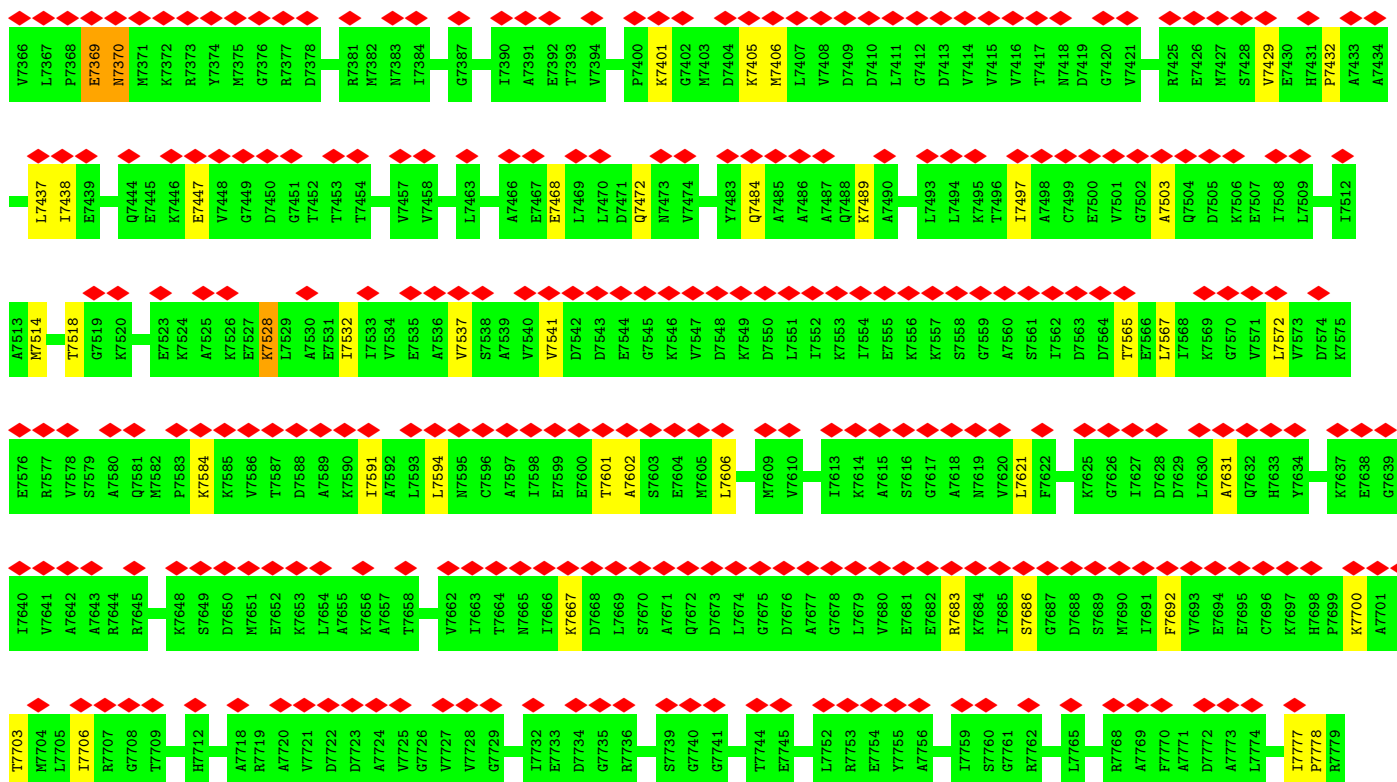
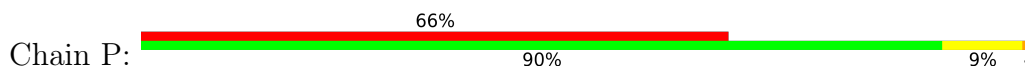


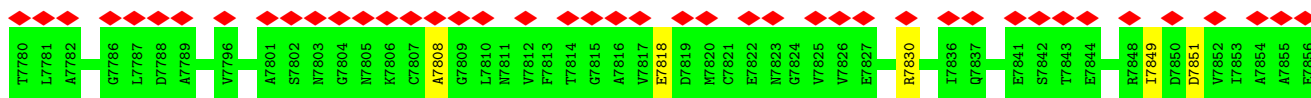
• Molecule 1: Lidless Mm-cpn





• Molecule 1: Lidless Mm-cpn





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D8	Depositor
Number of particles used	Not provided	
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Each micrograph	Depositor
Microscope	JEOL 3200FSC	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	112000	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	2.336	Depositor
Minimum map value	-0.567	Depositor
Average map value	0.043	Depositor
Map value standard deviation	0.182	Depositor
Recommended contour level	0.9	Depositor
Map size (\AA)	255.36, 255.36, 255.36	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing (\AA)	1.33, 1.33, 1.33	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.86	1/3686 (0.0%)	0.76	2/4961 (0.0%)
1	B	0.86	1/3686 (0.0%)	0.76	2/4961 (0.0%)
1	C	0.86	1/3686 (0.0%)	0.76	2/4961 (0.0%)
1	D	0.86	1/3686 (0.0%)	0.76	2/4961 (0.0%)
1	E	0.86	1/3686 (0.0%)	0.76	2/4961 (0.0%)
1	F	0.86	1/3686 (0.0%)	0.76	2/4961 (0.0%)
1	G	0.86	1/3686 (0.0%)	0.76	2/4961 (0.0%)
1	H	0.86	1/3686 (0.0%)	0.76	2/4961 (0.0%)
1	I	0.86	1/3686 (0.0%)	0.76	2/4961 (0.0%)
1	J	0.86	1/3686 (0.0%)	0.76	2/4961 (0.0%)
1	K	0.86	1/3686 (0.0%)	0.76	2/4961 (0.0%)
1	L	0.86	1/3686 (0.0%)	0.76	2/4961 (0.0%)
1	M	0.86	1/3686 (0.0%)	0.76	2/4961 (0.0%)
1	N	0.86	1/3686 (0.0%)	0.76	2/4961 (0.0%)
1	O	0.86	1/3686 (0.0%)	0.76	2/4961 (0.0%)
1	P	0.86	1/3686 (0.0%)	0.76	2/4961 (0.0%)
All	All	0.86	16/58976 (0.0%)	0.76	32/79376 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	3
1	C	0	3
1	D	0	3
1	E	0	3
1	F	0	3
1	G	0	3
1	H	0	3
1	I	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	J	0	3
1	K	0	3
1	L	0	3
1	M	0	3
1	N	0	3
1	O	0	3
1	P	0	3
All	All	0	48

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	1916	ALA	C-O	5.10	1.33	1.23
1	B	934	ALA	C-O	5.07	1.32	1.23
1	H	3880	ALA	C-O	5.07	1.32	1.23
1	I	4371	ALA	C-O	5.07	1.32	1.23
1	K	5353	ALA	C-O	5.07	1.32	1.23

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	6387	GLU	CA-C-O	-6.62	106.19	120.10
1	B	495	GLU	CA-C-O	-6.62	106.19	120.10
1	F	2459	GLU	CA-C-O	-6.62	106.19	120.10
1	M	5896	GLU	CA-C-O	-6.62	106.21	120.10
1	G	2950	GLU	CA-C-O	-6.61	106.21	120.10

There are no chirality outliers.

5 of 48 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	119	GLN	Mainchain
1	A	138	ALA	Mainchain
1	A	453	GLU	Mainchain
1	B	610	GLN	Mainchain
1	B	629	ALA	Mainchain

5.2 Too-close contacts [\(i\)](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3665	0	3804	28	0
1	B	3665	0	3801	28	0
1	C	3665	0	3801	27	0
1	D	3665	0	3801	26	0
1	E	3665	0	3801	24	0
1	F	3665	0	3801	28	0
1	G	3665	0	3801	26	0
1	H	3665	0	3801	27	0
1	I	3665	0	3801	28	0
1	J	3665	0	3801	27	0
1	K	3665	0	3801	28	0
1	L	3665	0	3801	27	0
1	M	3665	0	3801	26	0
1	N	3665	0	3801	24	0
1	O	3665	0	3801	27	0
1	P	3665	0	3801	26	0
All	All	58640	0	60819	395	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 3.

The worst 5 of 395 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:B:615:LYS:HA	1:B:615:LYS:HE2	1.73	0.71
1:P:7489:LYS:HA	1:P:7489:LYS:HE2	1.73	0.71
1:K:5034:LYS:HE2	1:K:5034:LYS:HA	1.73	0.71
1:G:3070:LYS:HE2	1:G:3070:LYS:HA	1.73	0.71
1:A:124:LYS:HA	1:A:124:LYS:HE2	1.73	0.70

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	489/491 (100%)	471 (96%)	17 (4%)	1 (0%)	47	81
1	B	489/491 (100%)	471 (96%)	17 (4%)	1 (0%)	47	81
1	C	489/491 (100%)	471 (96%)	17 (4%)	1 (0%)	47	81
1	D	489/491 (100%)	471 (96%)	17 (4%)	1 (0%)	47	81
1	E	489/491 (100%)	471 (96%)	17 (4%)	1 (0%)	47	81
1	F	489/491 (100%)	471 (96%)	17 (4%)	1 (0%)	47	81
1	G	489/491 (100%)	471 (96%)	17 (4%)	1 (0%)	47	81
1	H	489/491 (100%)	471 (96%)	17 (4%)	1 (0%)	47	81
1	I	489/491 (100%)	471 (96%)	17 (4%)	1 (0%)	47	81
1	J	489/491 (100%)	471 (96%)	17 (4%)	1 (0%)	47	81
1	K	489/491 (100%)	471 (96%)	17 (4%)	1 (0%)	47	81
1	L	489/491 (100%)	471 (96%)	17 (4%)	1 (0%)	47	81
1	M	489/491 (100%)	471 (96%)	17 (4%)	1 (0%)	47	81
1	N	489/491 (100%)	471 (96%)	17 (4%)	1 (0%)	47	81
1	O	489/491 (100%)	471 (96%)	17 (4%)	1 (0%)	47	81
1	P	489/491 (100%)	471 (96%)	17 (4%)	1 (0%)	47	81
All	All	7824/7856 (100%)	7536 (96%)	272 (4%)	16 (0%)	50	81

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	B	496	ASN
1	C	987	ASN
1	D	1478	ASN
1	E	1969	ASN

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	393/393 (100%)	387 (98%)	6 (2%)	65	80
1	B	393/393 (100%)	387 (98%)	6 (2%)	65	80
1	C	393/393 (100%)	387 (98%)	6 (2%)	65	80
1	D	393/393 (100%)	387 (98%)	6 (2%)	65	80
1	E	393/393 (100%)	387 (98%)	6 (2%)	65	80
1	F	393/393 (100%)	387 (98%)	6 (2%)	65	80
1	G	393/393 (100%)	387 (98%)	6 (2%)	65	80
1	H	393/393 (100%)	387 (98%)	6 (2%)	65	80
1	I	393/393 (100%)	387 (98%)	6 (2%)	65	80
1	J	393/393 (100%)	387 (98%)	6 (2%)	65	80
1	K	393/393 (100%)	387 (98%)	6 (2%)	65	80
1	L	393/393 (100%)	387 (98%)	6 (2%)	65	80
1	M	393/393 (100%)	387 (98%)	6 (2%)	65	80
1	N	393/393 (100%)	387 (98%)	6 (2%)	65	80
1	O	393/393 (100%)	387 (98%)	6 (2%)	65	80
1	P	393/393 (100%)	387 (98%)	6 (2%)	65	80
All	All	6288/6288 (100%)	6192 (98%)	96 (2%)	66	80

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	4721	LYS
1	L	5736	LYS
1	J	4754	LYS
1	K	5245	LYS
1	M	6194	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	O	7320	ASN
1	N	6829	ASN
1	I	4374	ASN
1	M	6338	ASN
1	H	3883	ASN

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.

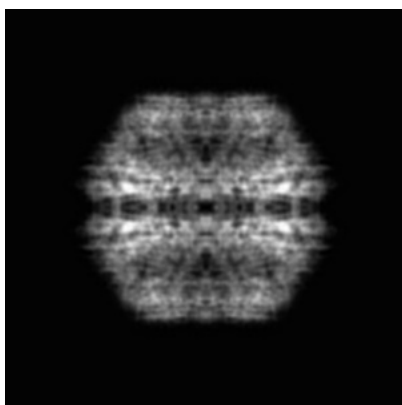
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5138. These allow visual inspection of the internal detail of the map and identification of artifacts.

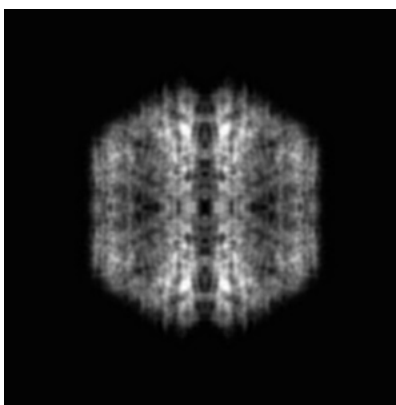
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

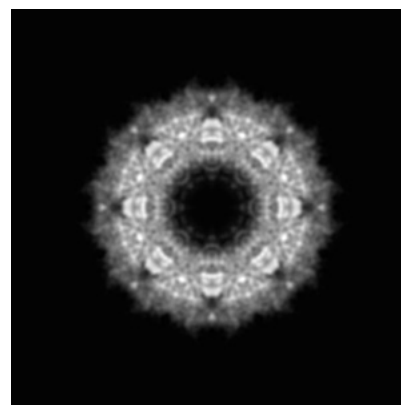
6.1.1 Primary map



X



Y

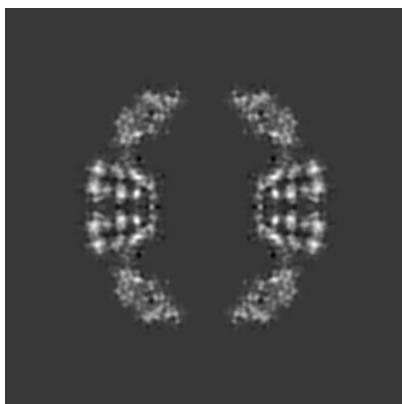


Z

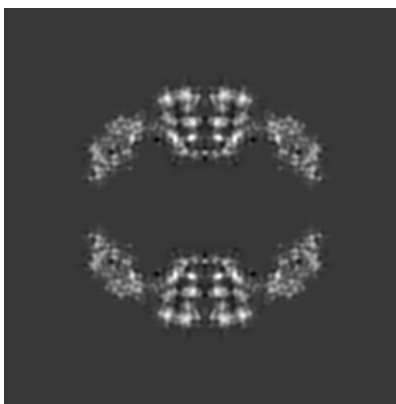
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

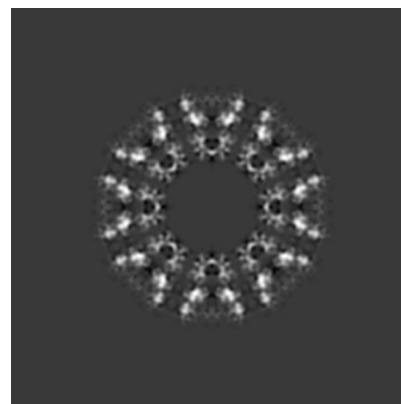
6.2.1 Primary map



X Index: 96



Y Index: 96

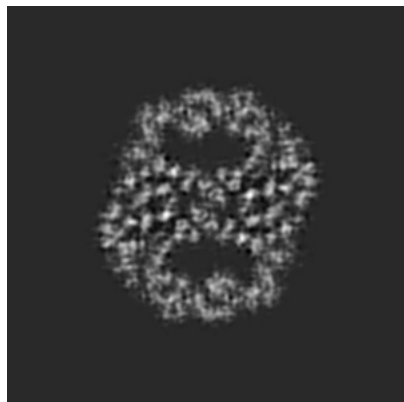


Z Index: 96

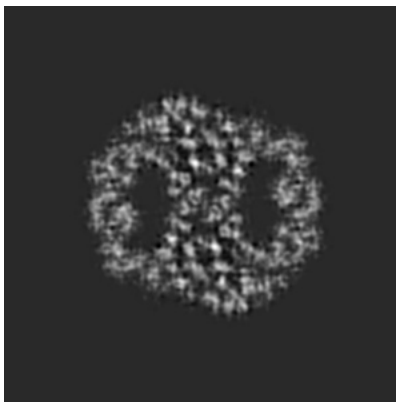
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

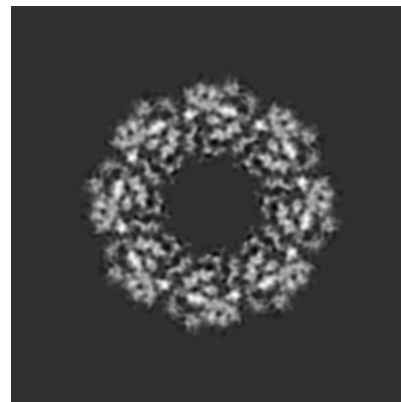
6.3.1 Primary map



X Index: 123



Y Index: 123

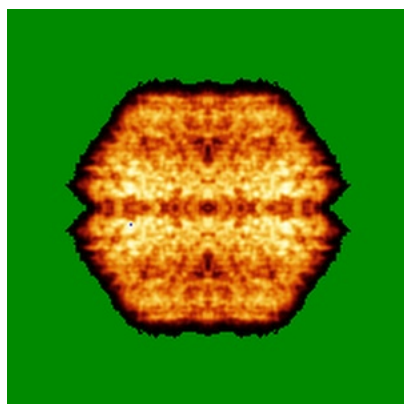


Z Index: 88

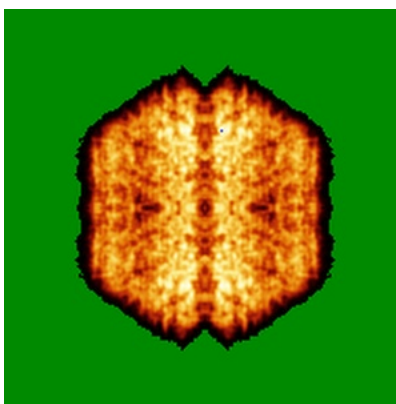
The images above show the largest variance slices of the map in three orthogonal directions.

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

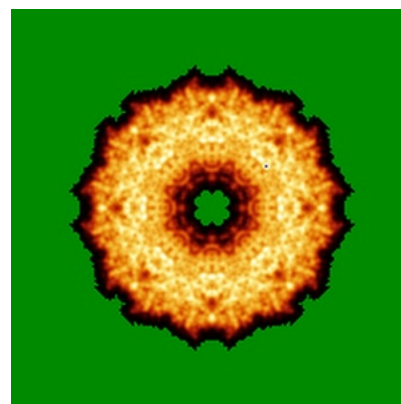
6.4.1 Primary map



X



Y

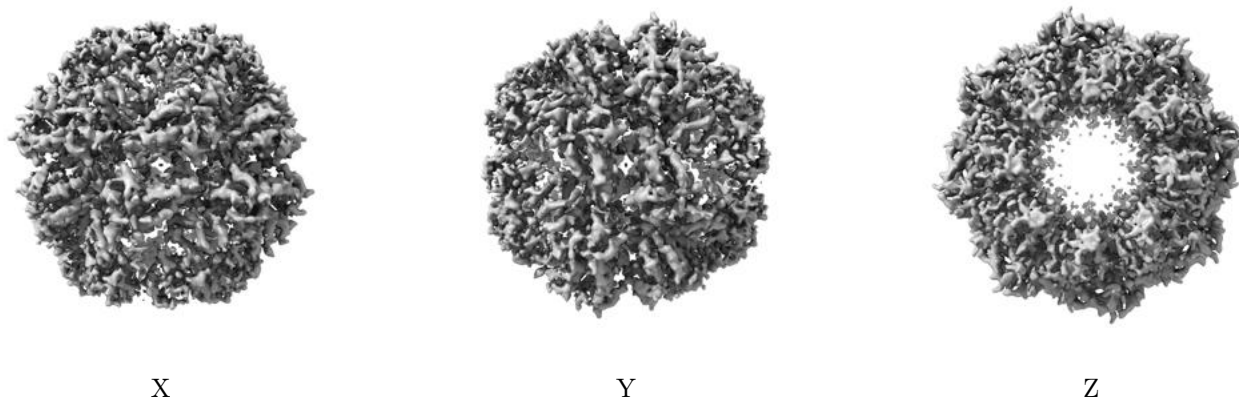


Z

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

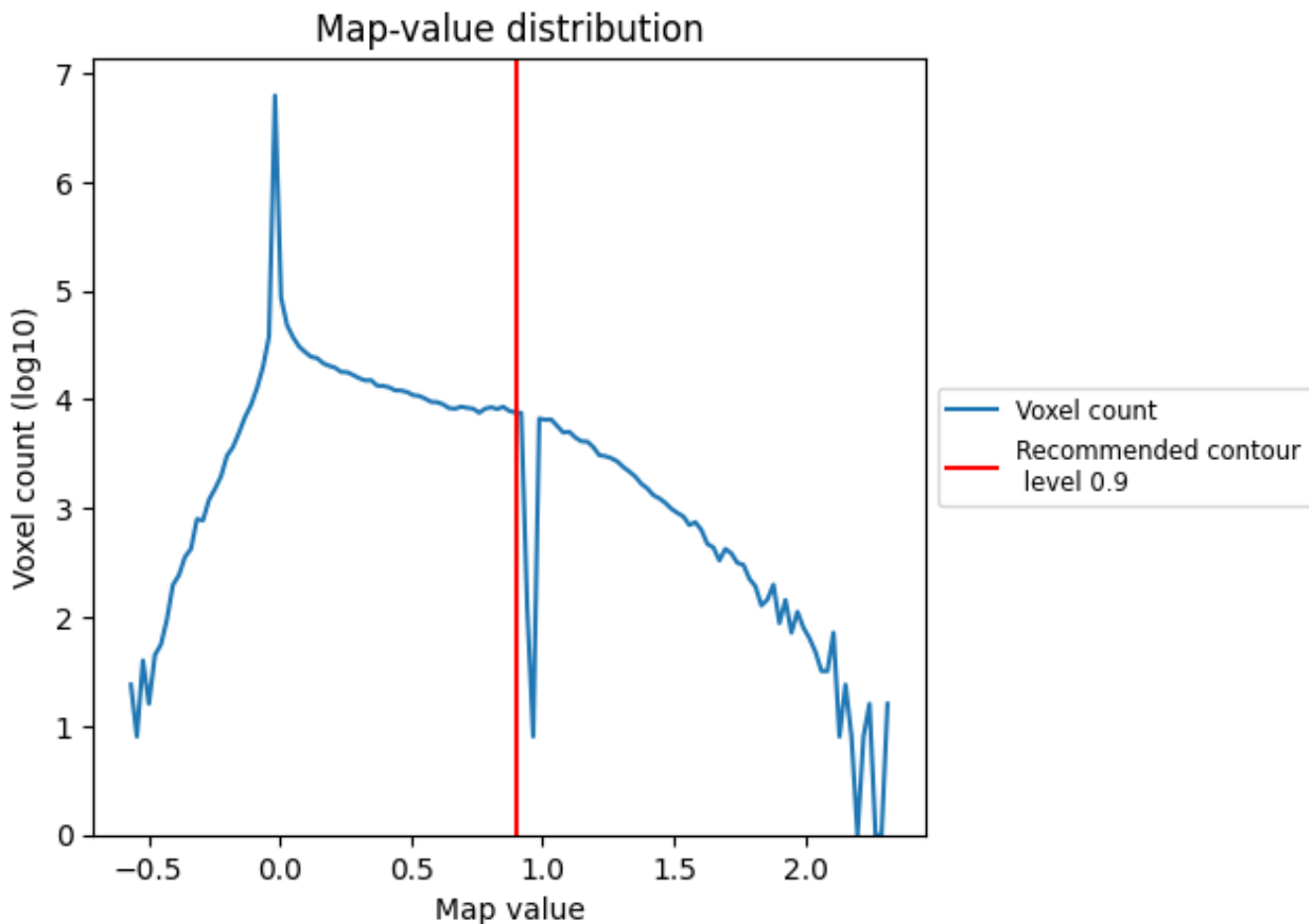
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

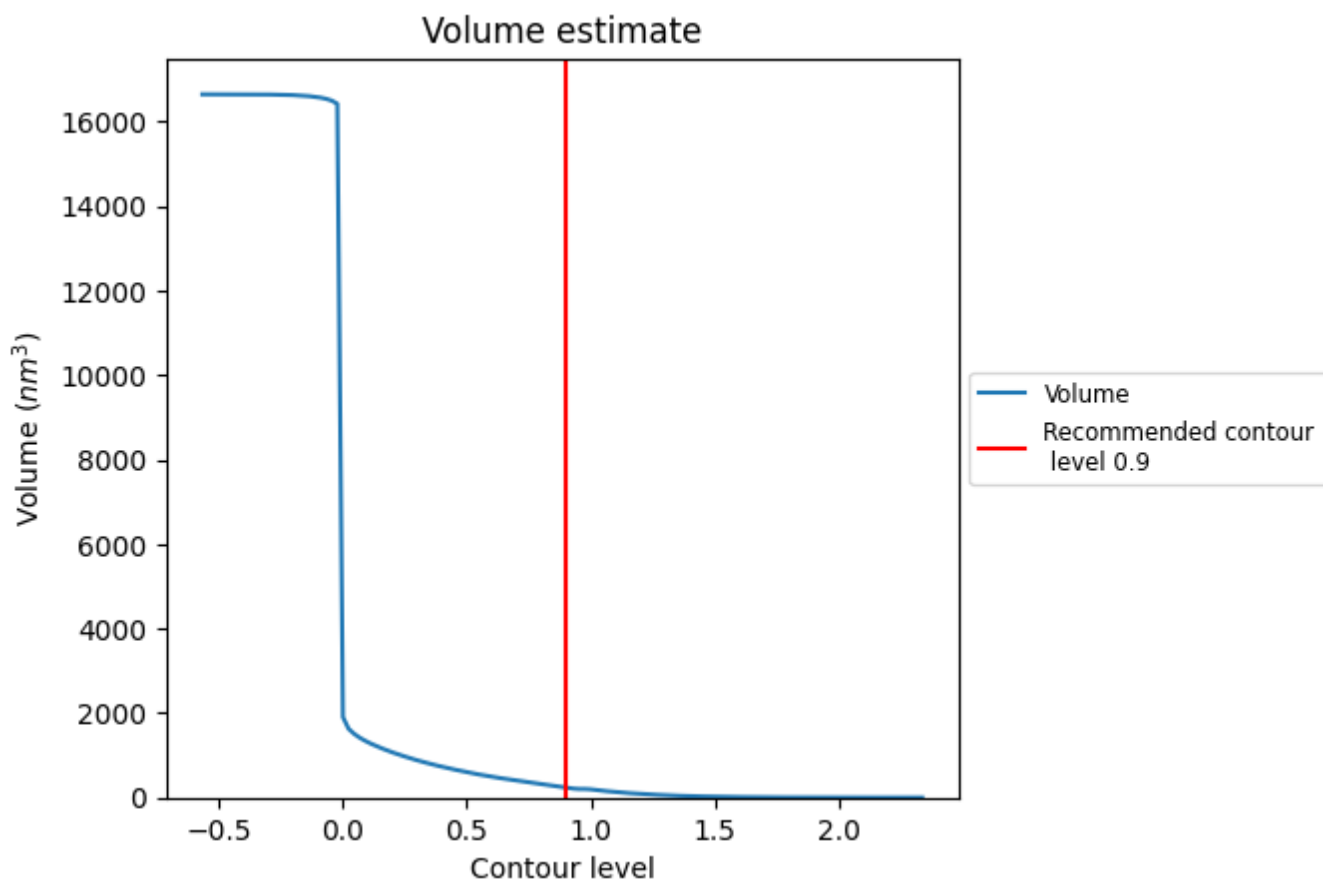
This section contains the results of statistical analysis of the map.

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.

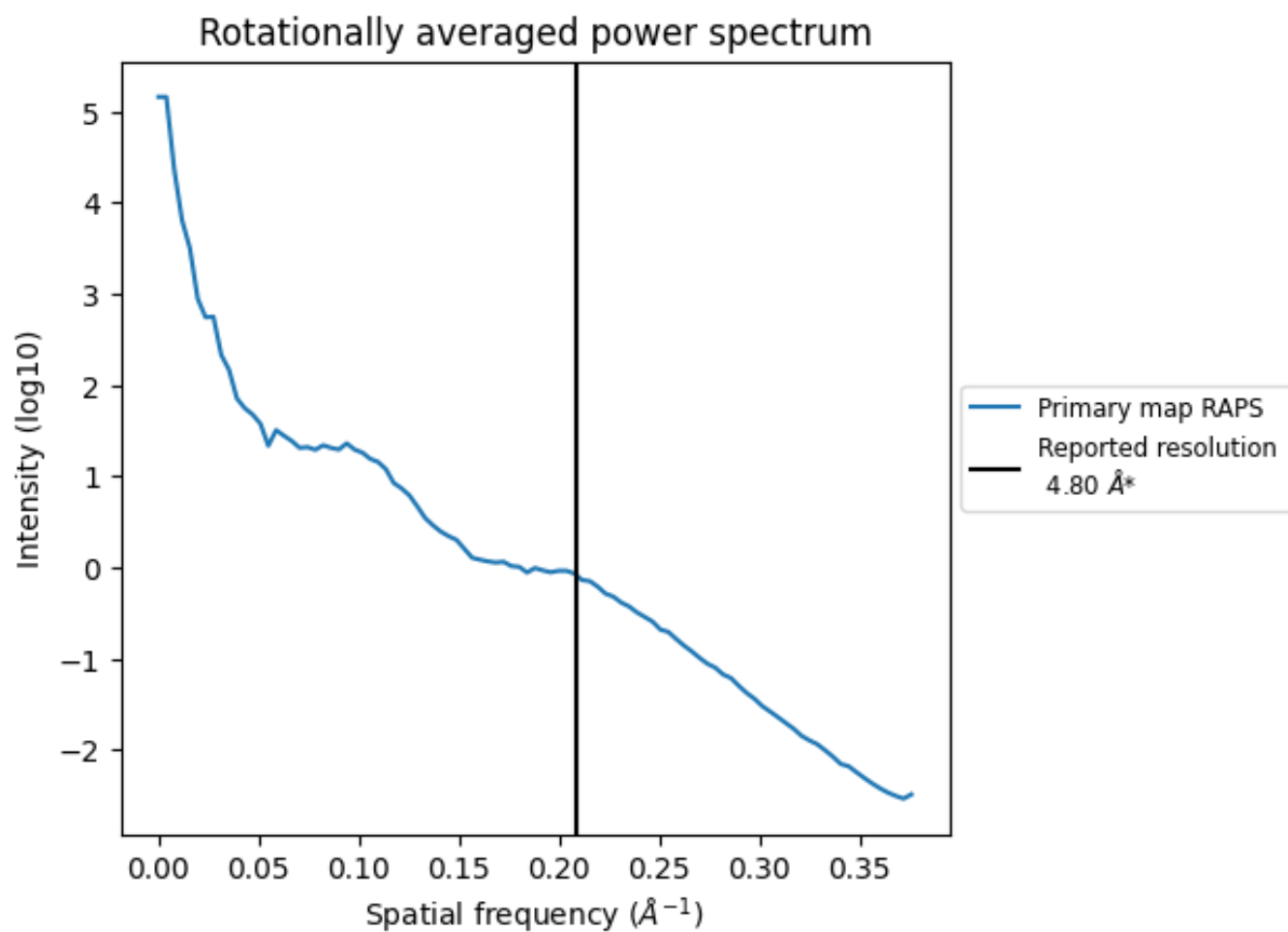
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 236 nm³; this corresponds to an approximate mass of 213 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.208 Å⁻¹

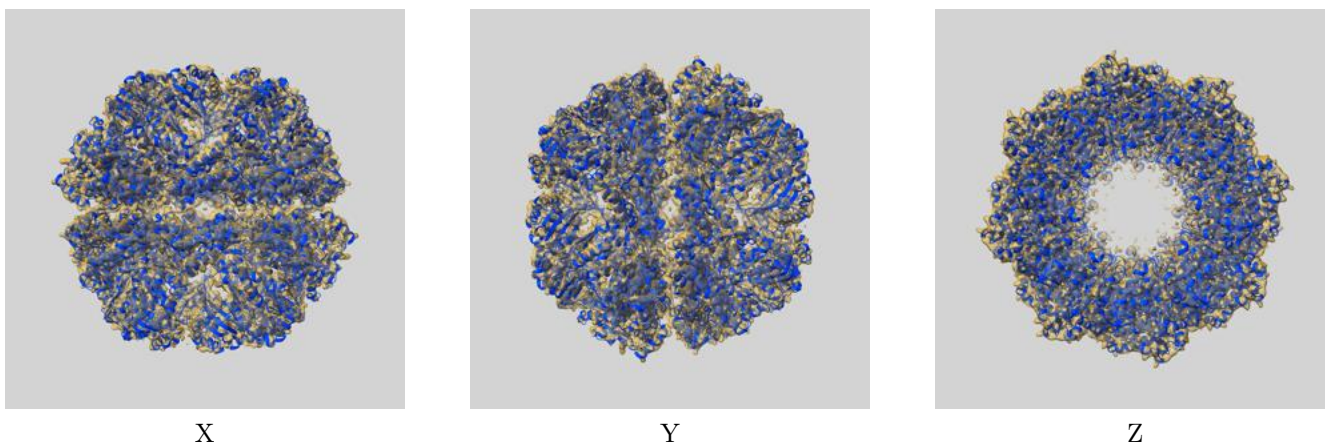
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

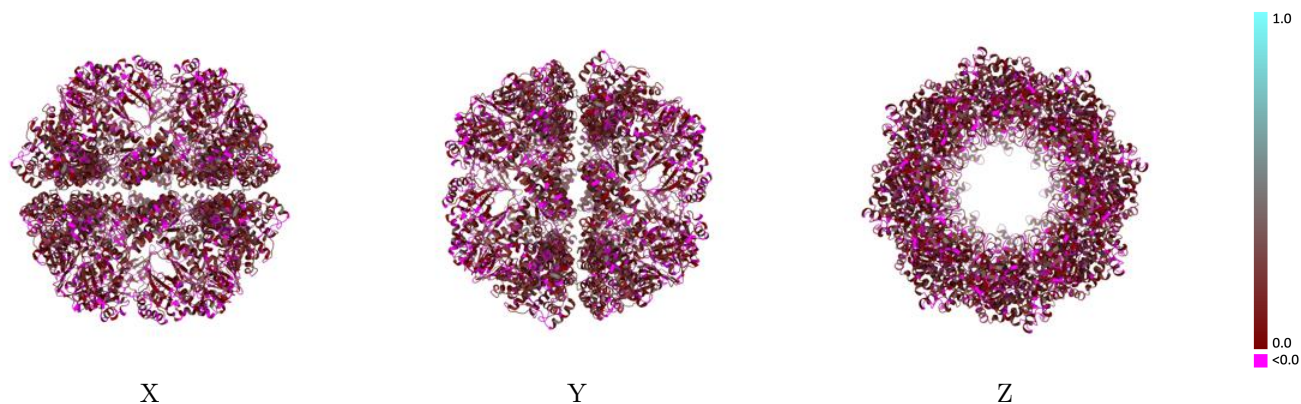
This section contains information regarding the fit between EMDB map EMD-5138 and PDB model 3J03. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



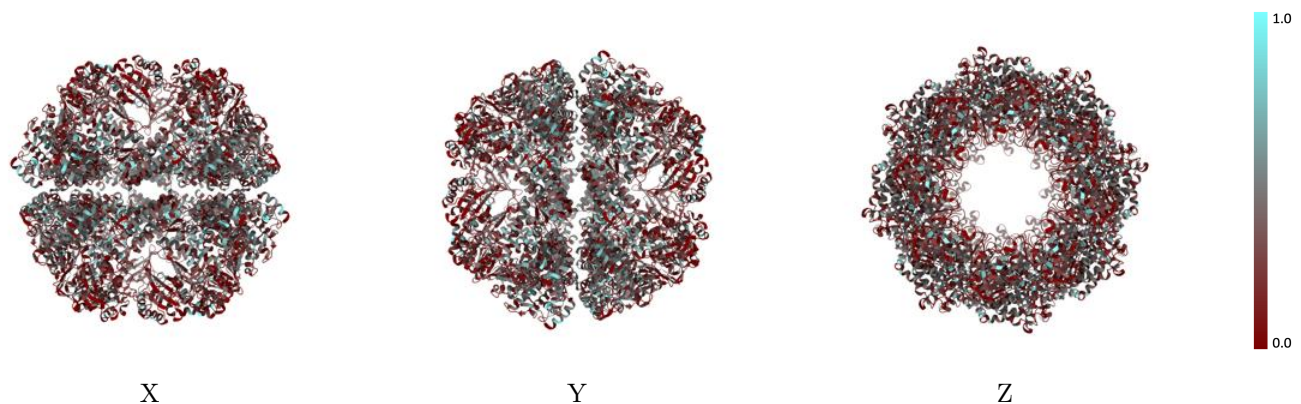
The images above show the 3D surface view of the map at the recommended contour level 0.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



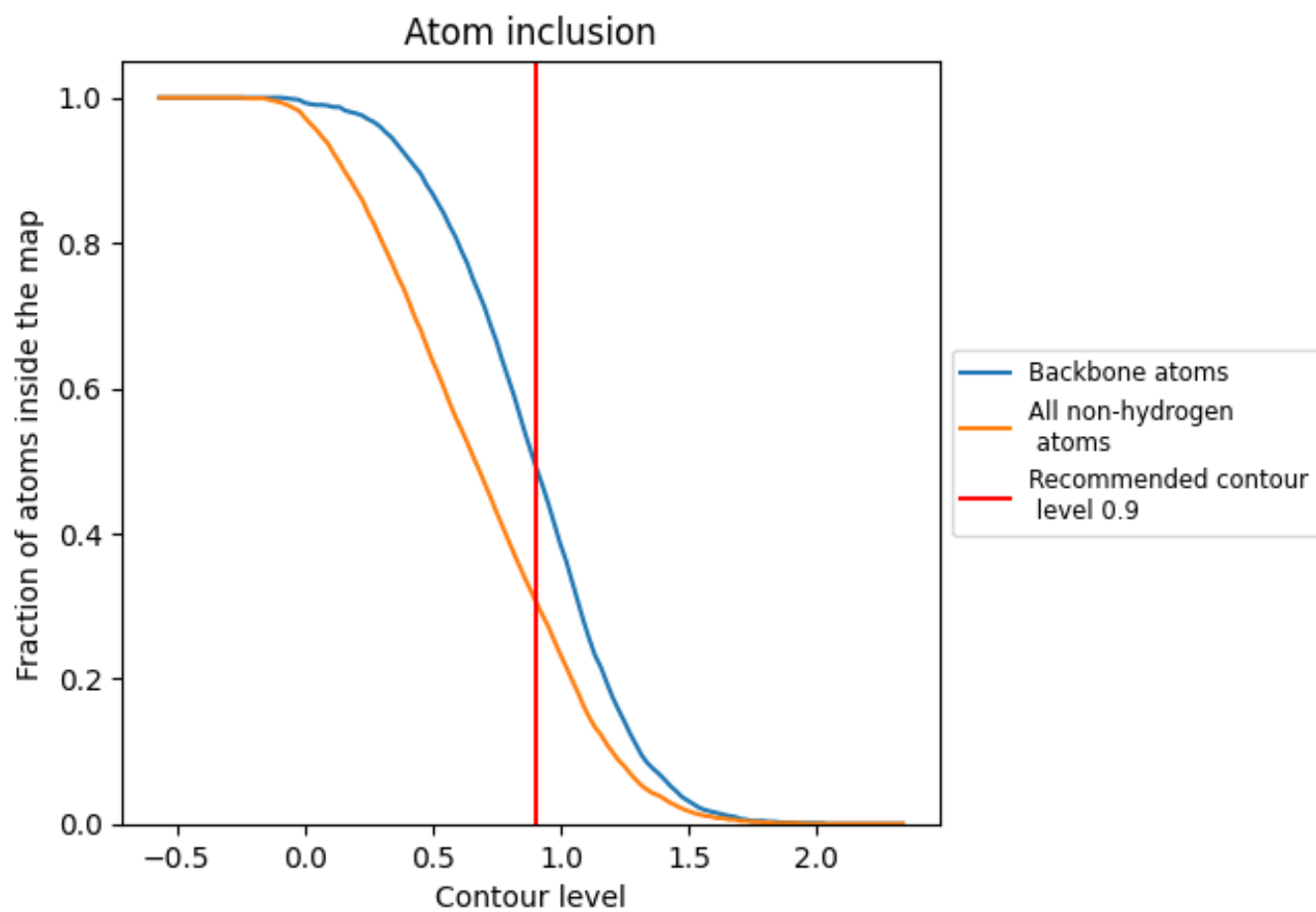
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.9).



































9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 31% 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 (0.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3080	 0.1090
A	 0.3070	 0.1090
B	 0.3090	 0.1100
C	 0.3070	 0.1090
D	 0.3090	 0.1090
E	 0.3070	 0.1090
F	 0.3090	 0.1100
G	 0.3080	 0.1100
H	 0.3090	 0.1100
I	 0.3090	 0.1100
J	 0.3070	 0.1090
K	 0.3090	 0.1100
L	 0.3080	 0.1100
M	 0.3090	 0.1100
N	 0.3080	 0.1090
O	 0.3090	 0.1090
P	 0.3080	 0.1080

