



Full wwPDB EM Validation Report ⓘ

Nov 20, 2022 – 02:56 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)

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

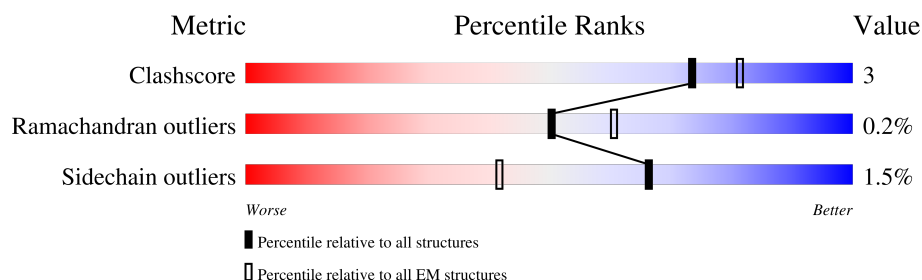
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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	<div> <div>66%</div> <div>90%</div> <div>10%</div> <div>.</div> </div>
1	B	491	<div> <div>65%</div> <div>90%</div> <div>10%</div> <div>.</div> </div>
1	C	491	<div> <div>66%</div> <div>90%</div> <div>9%</div> <div>.</div> </div>
1	D	491	<div> <div>65%</div> <div>90%</div> <div>9%</div> <div>.</div> </div>
1	E	491	<div> <div>66%</div> <div>91%</div> <div>8%</div> <div>.</div> </div>
1	F	491	<div> <div>65%</div> <div>90%</div> <div>10%</div> <div>.</div> </div>
1	G	491	<div> <div>66%</div> <div>90%</div> <div>9%</div> <div>.</div> </div>
1	H	491	<div> <div>65%</div> <div>90%</div> <div>9%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	I	491	<div> <div>65%</div> <div>90%</div> <div>10%</div> </div>
1	J	491	<div> <div>66%</div> <div>90%</div> <div>9%</div> </div>
1	K	491	<div> <div>65%</div> <div>90%</div> <div>10%</div> </div>
1	L	491	<div> <div>66%</div> <div>90%</div> <div>9%</div> </div>
1	M	491	<div> <div>65%</div> <div>90%</div> <div>9%</div> </div>
1	N	491	<div> <div>66%</div> <div>91%</div> <div>8%</div> </div>
1	O	491	<div> <div>65%</div> <div>90%</div> <div>9%</div> </div>
1	P	491	<div> <div>66%</div> <div>90%</div> <div>9%</div> </div>

2 Entry composition

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

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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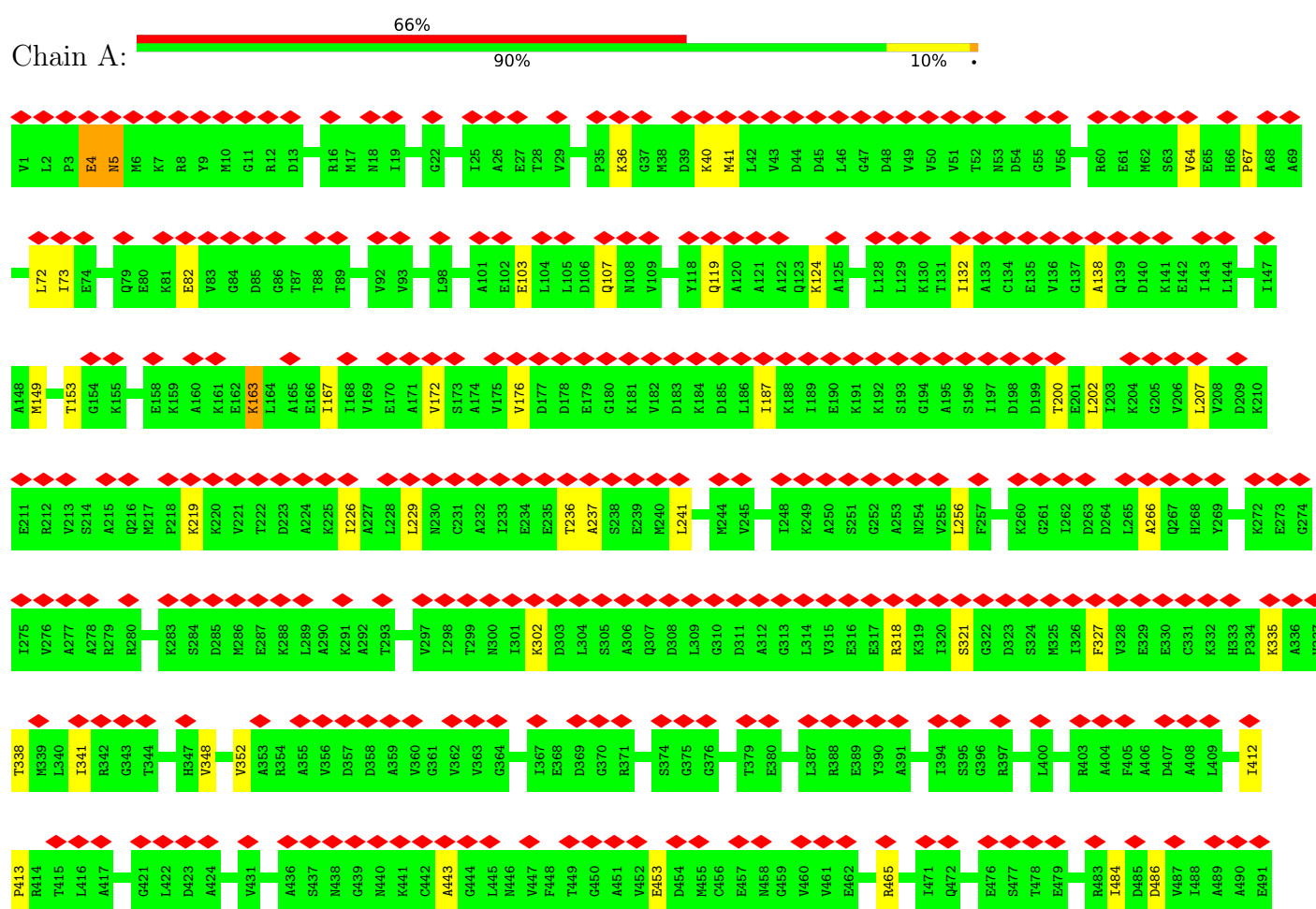
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Chain	Residue	Modelled	Actual	Comment	Reference
O	7110	THR	-	LINKER	UNP Q877G8
O	7111	ALA	-	LINKER	UNP Q877G8
O	7112	SER	-	LINKER	UNP Q877G8
O	7113	GLU	-	LINKER	UNP Q877G8
O	7114	MET	-	LINKER	UNP Q877G8
P	7600	GLU	-	LINKER	UNP Q877G8
P	7601	THR	-	LINKER	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

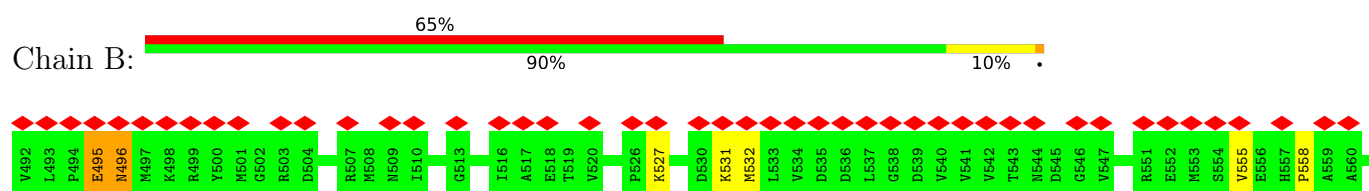
3 Residue-property plots

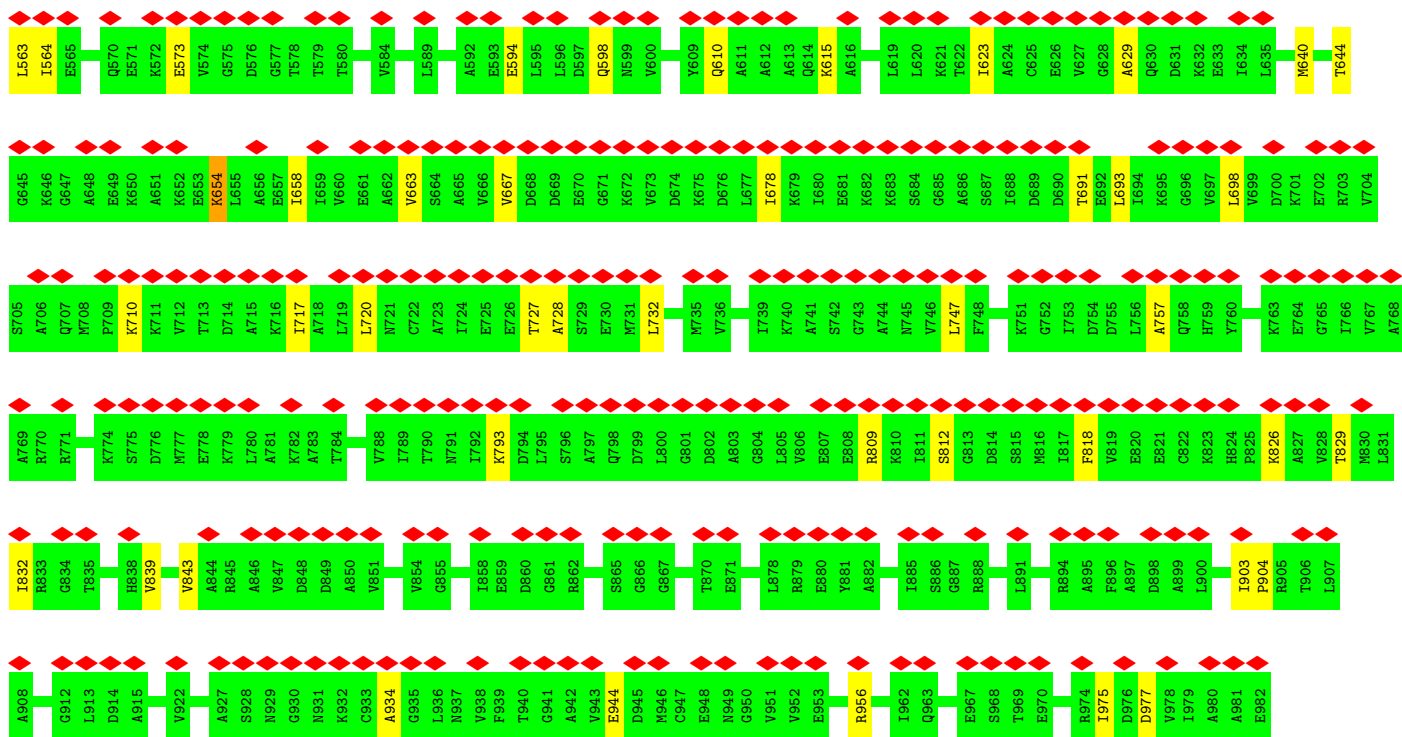
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

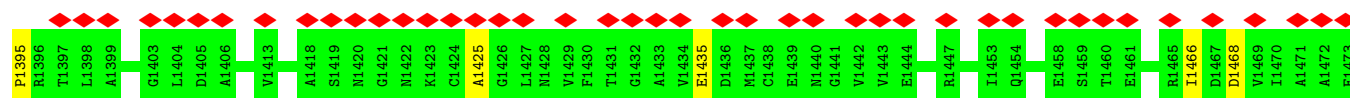
• Molecule 1: Lidless Mm-cpn



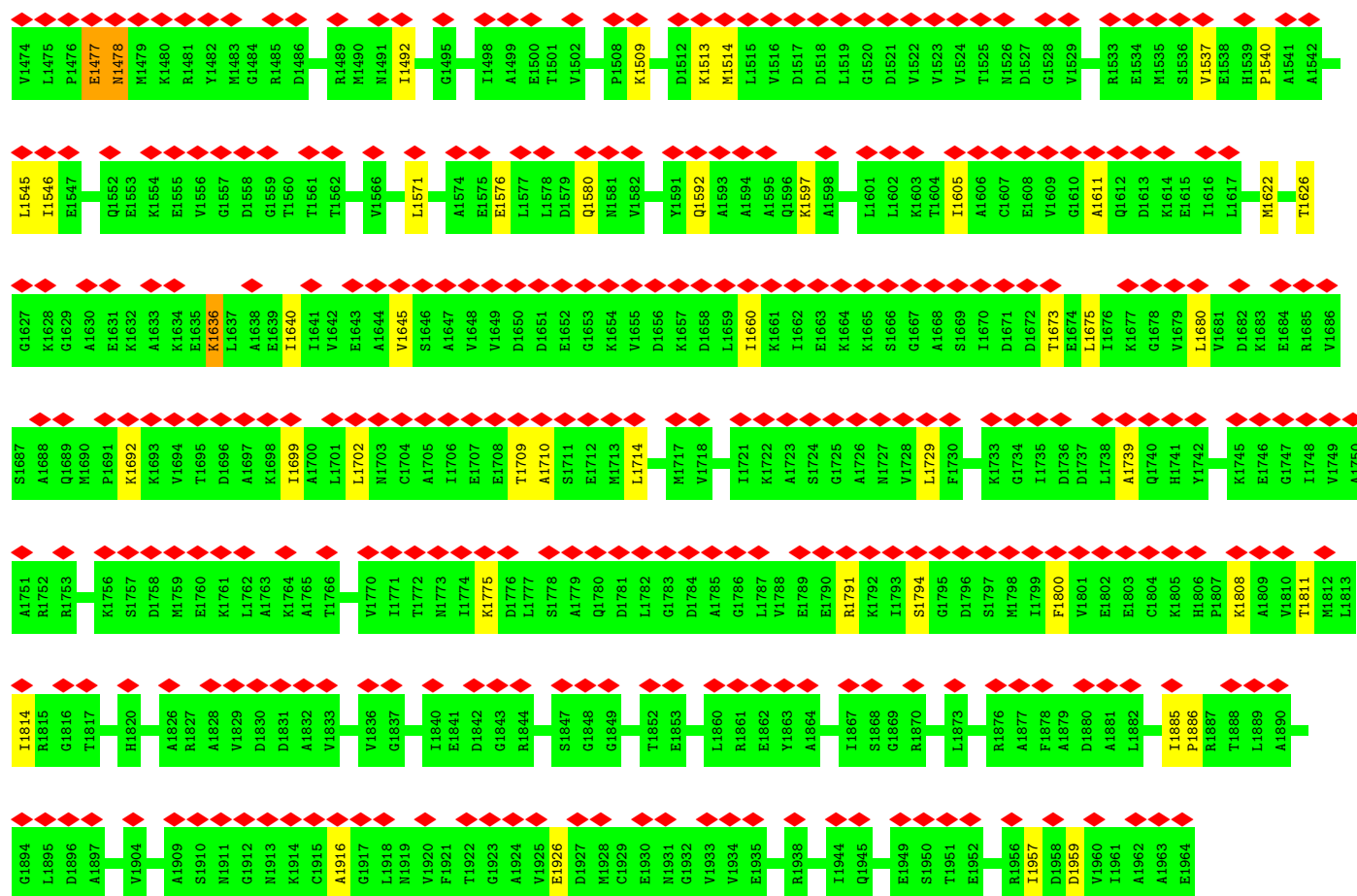
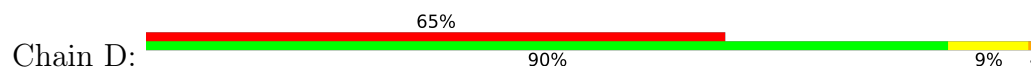
• Molecule 1: Lidless Mm-cpn



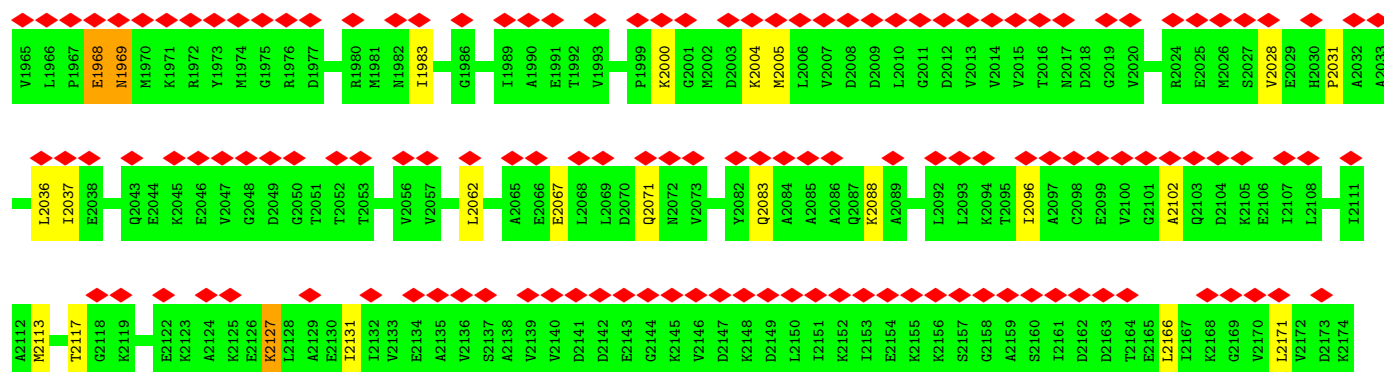
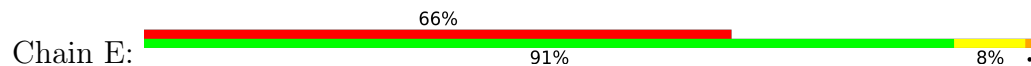


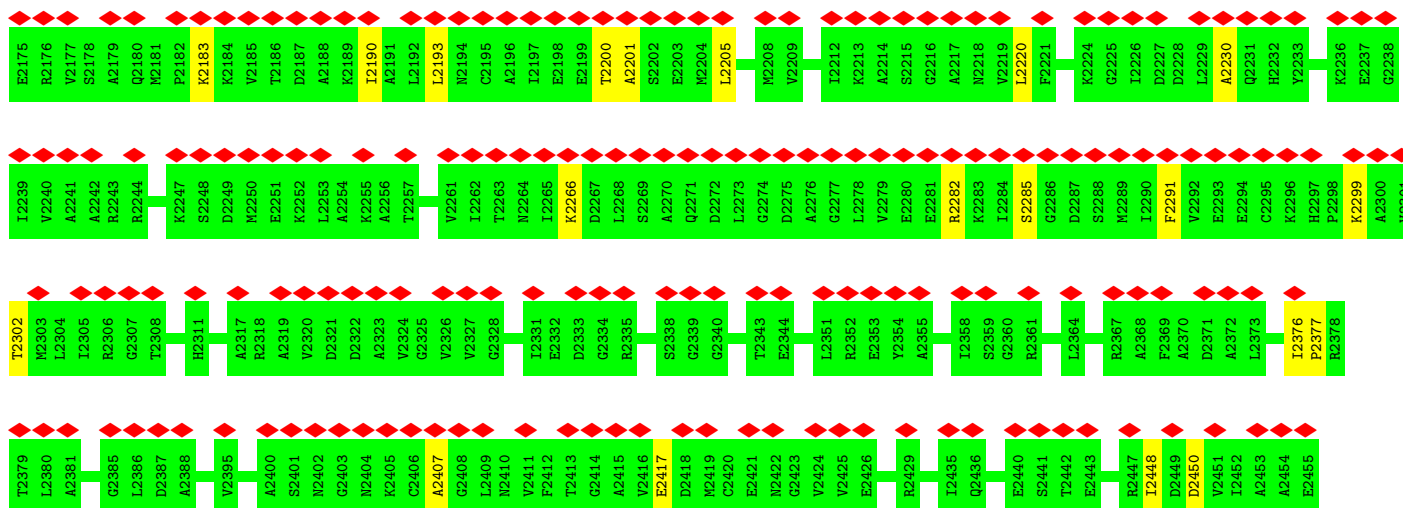


• Molecule 1: Lidless Mm-cpn

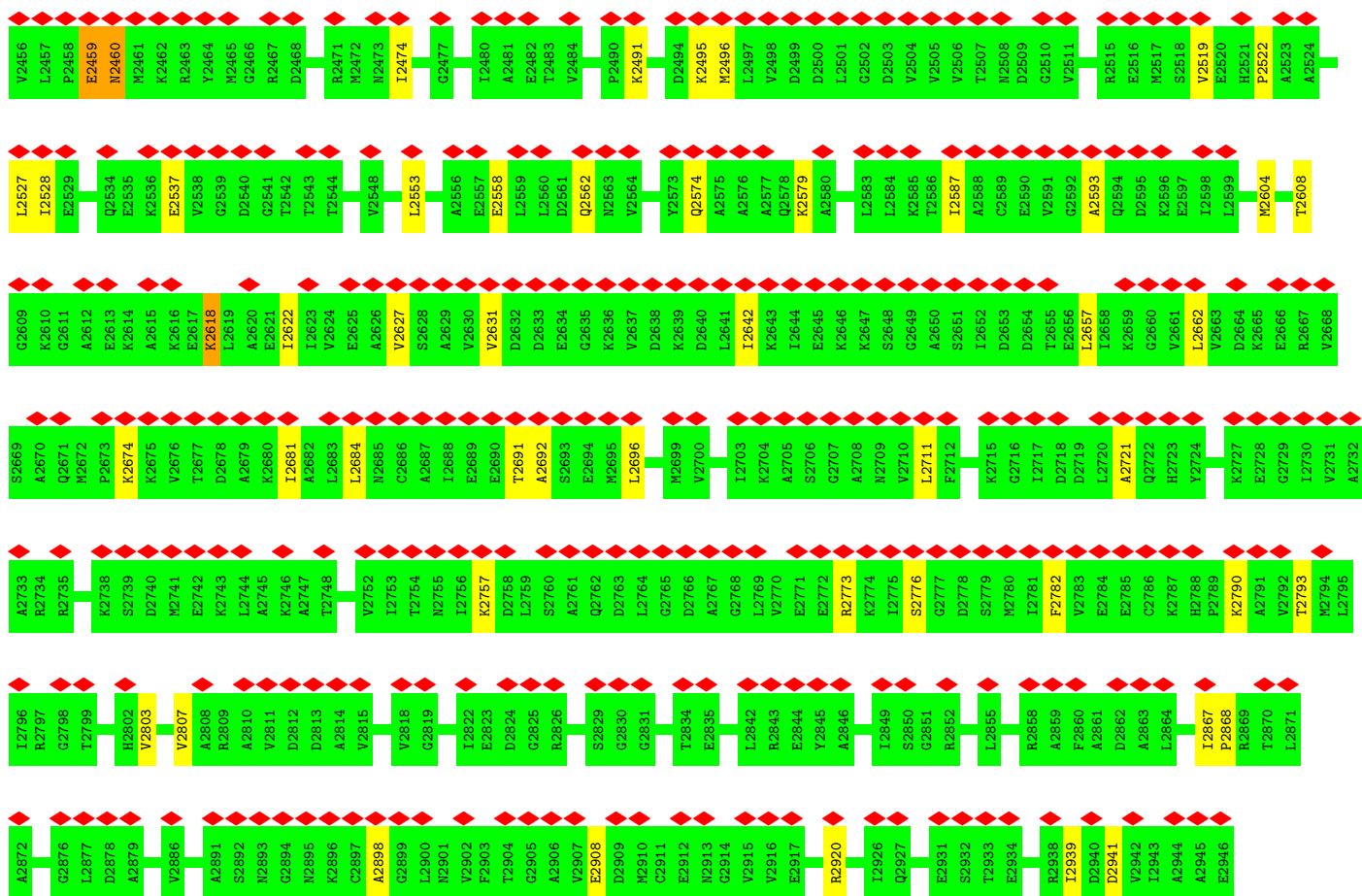
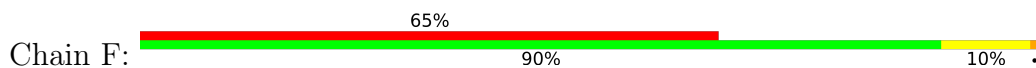


• Molecule 1: Lidless Mm-cpn

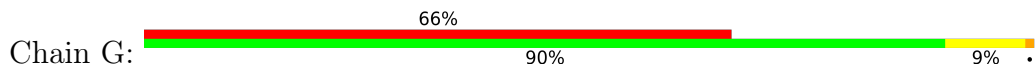


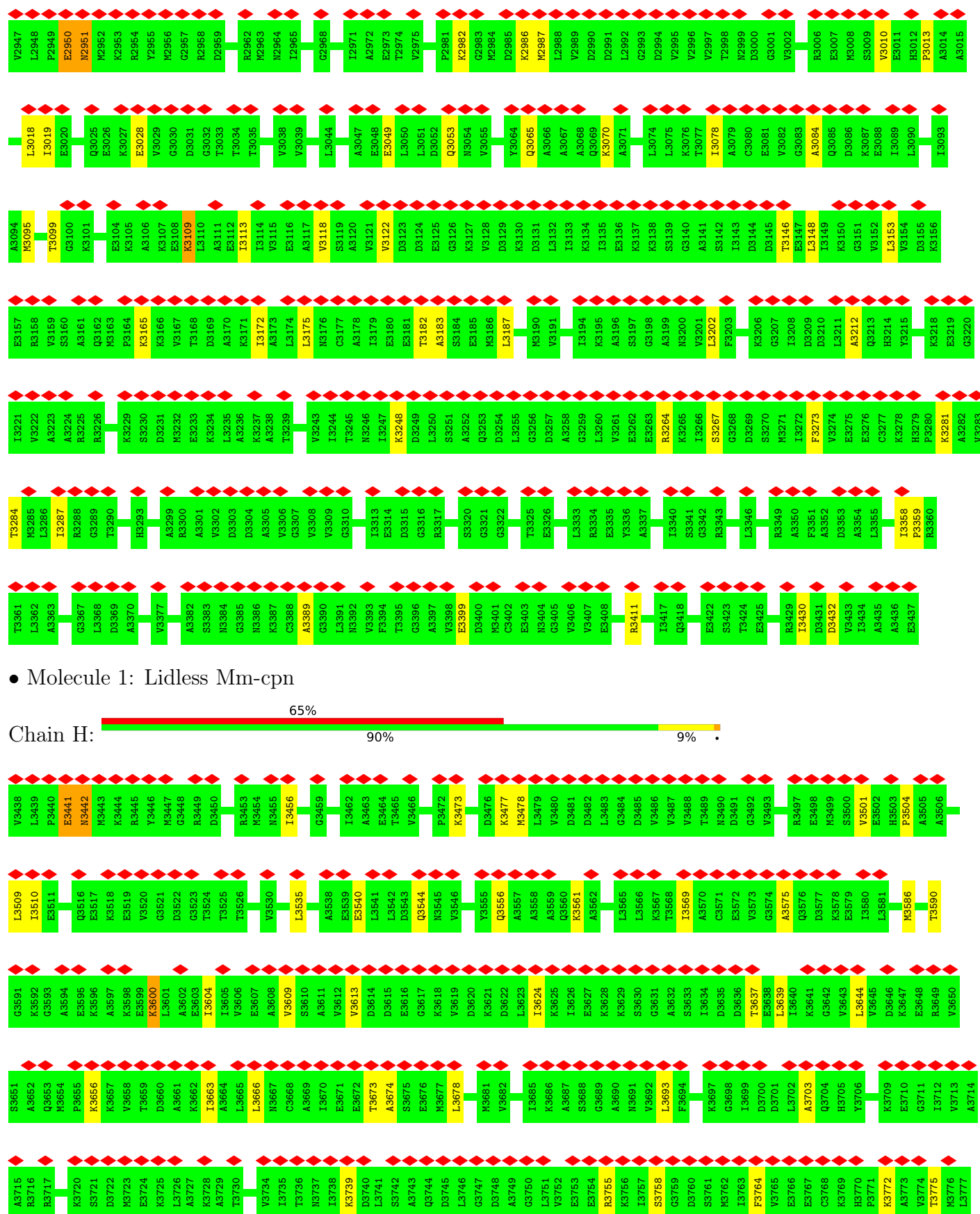


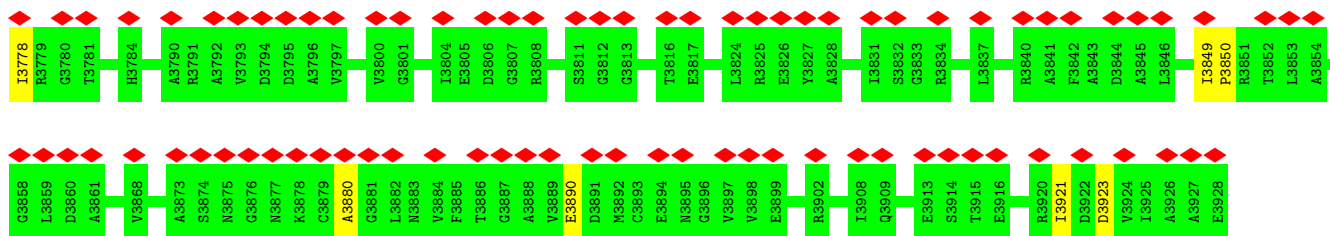
• Molecule 1: Lidless Mm-cpn



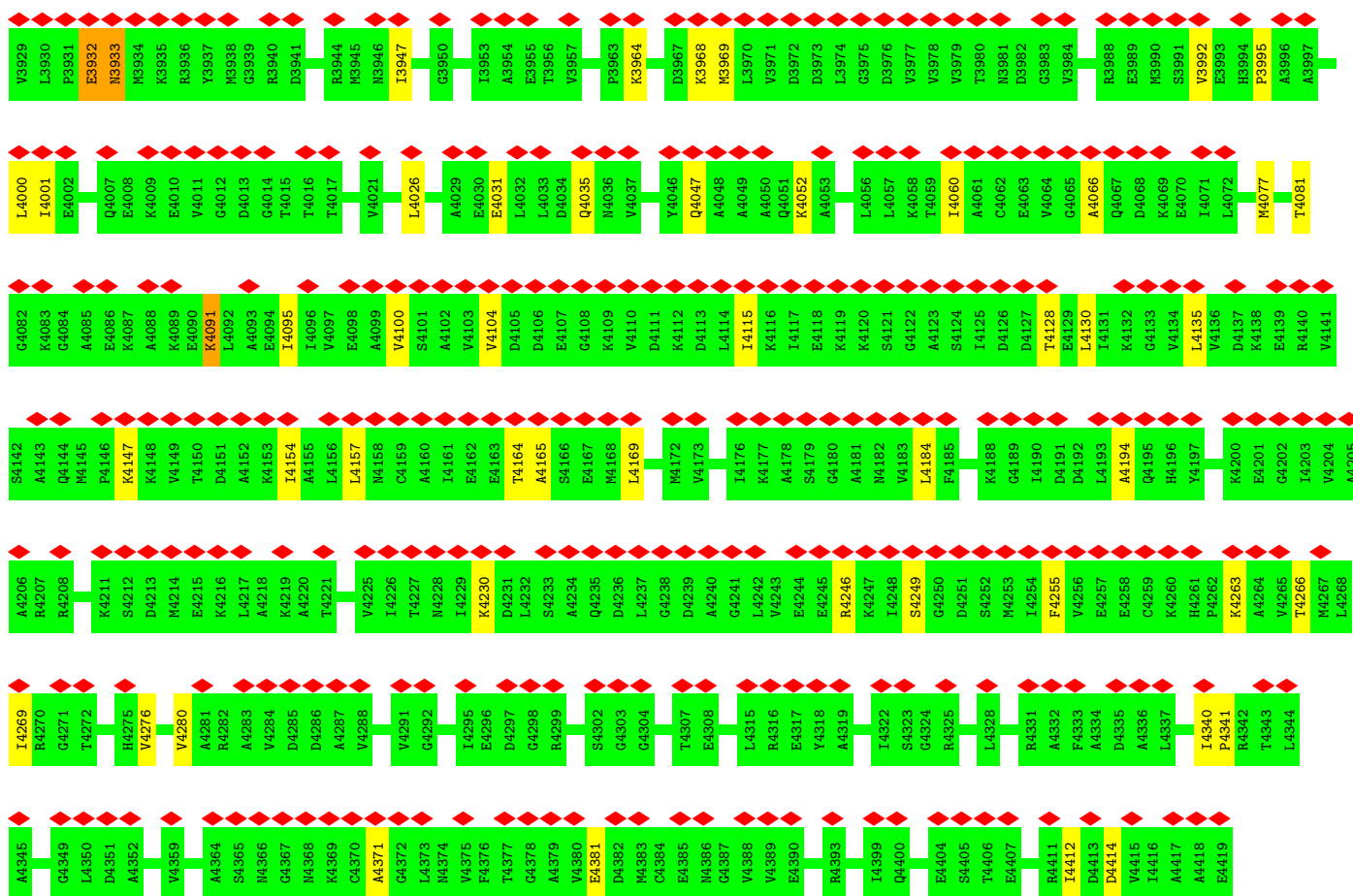
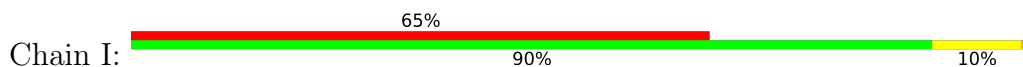
• Molecule 1: Lidless Mm-cpn



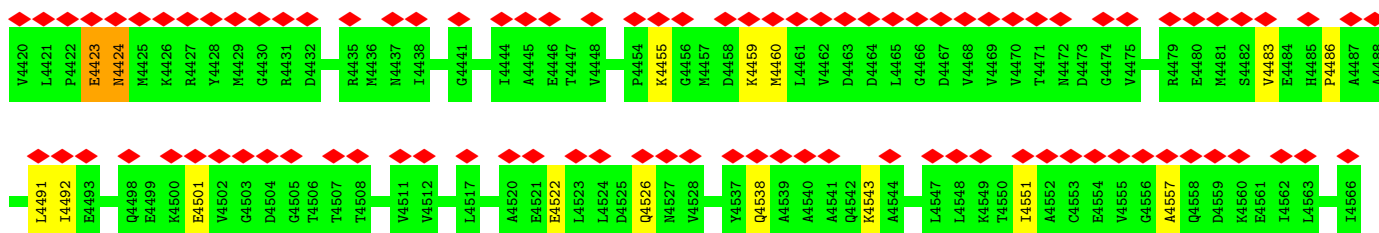
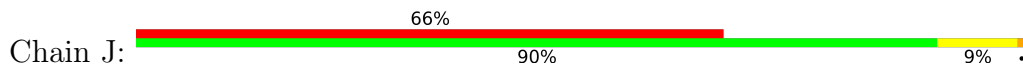


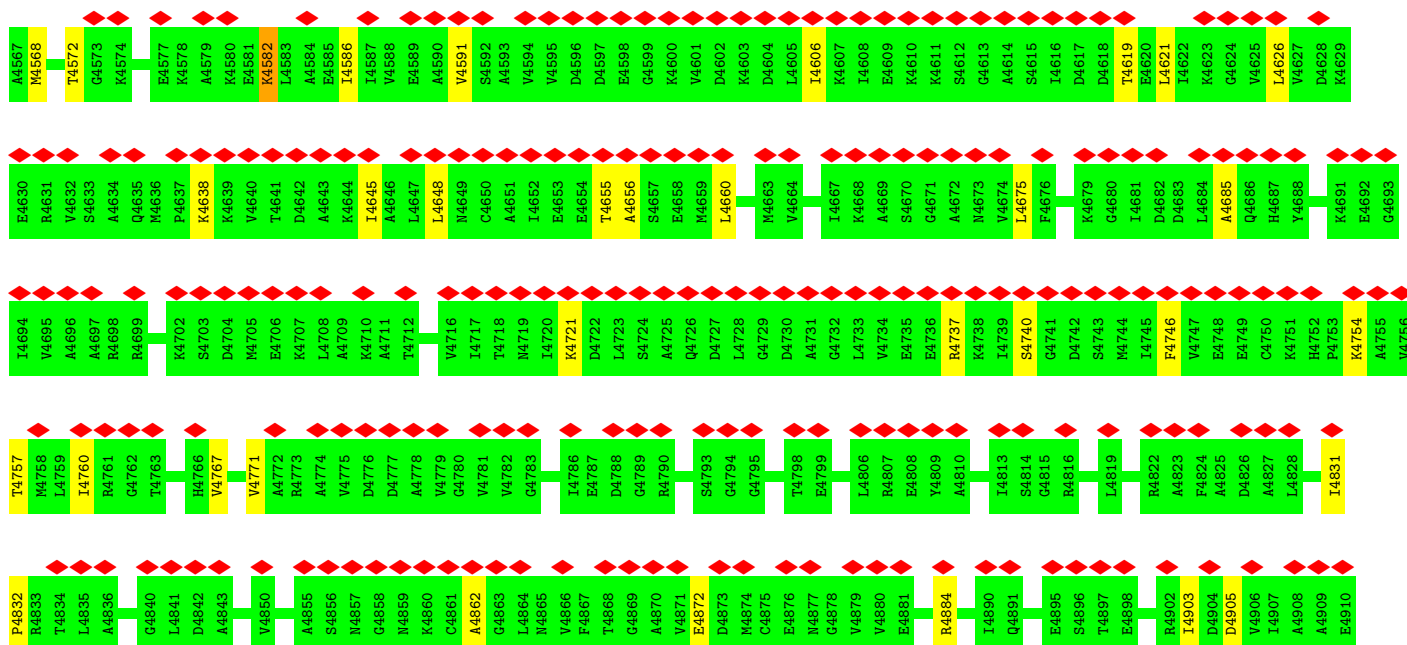


• Molecule 1: Lidless Mm-cpn

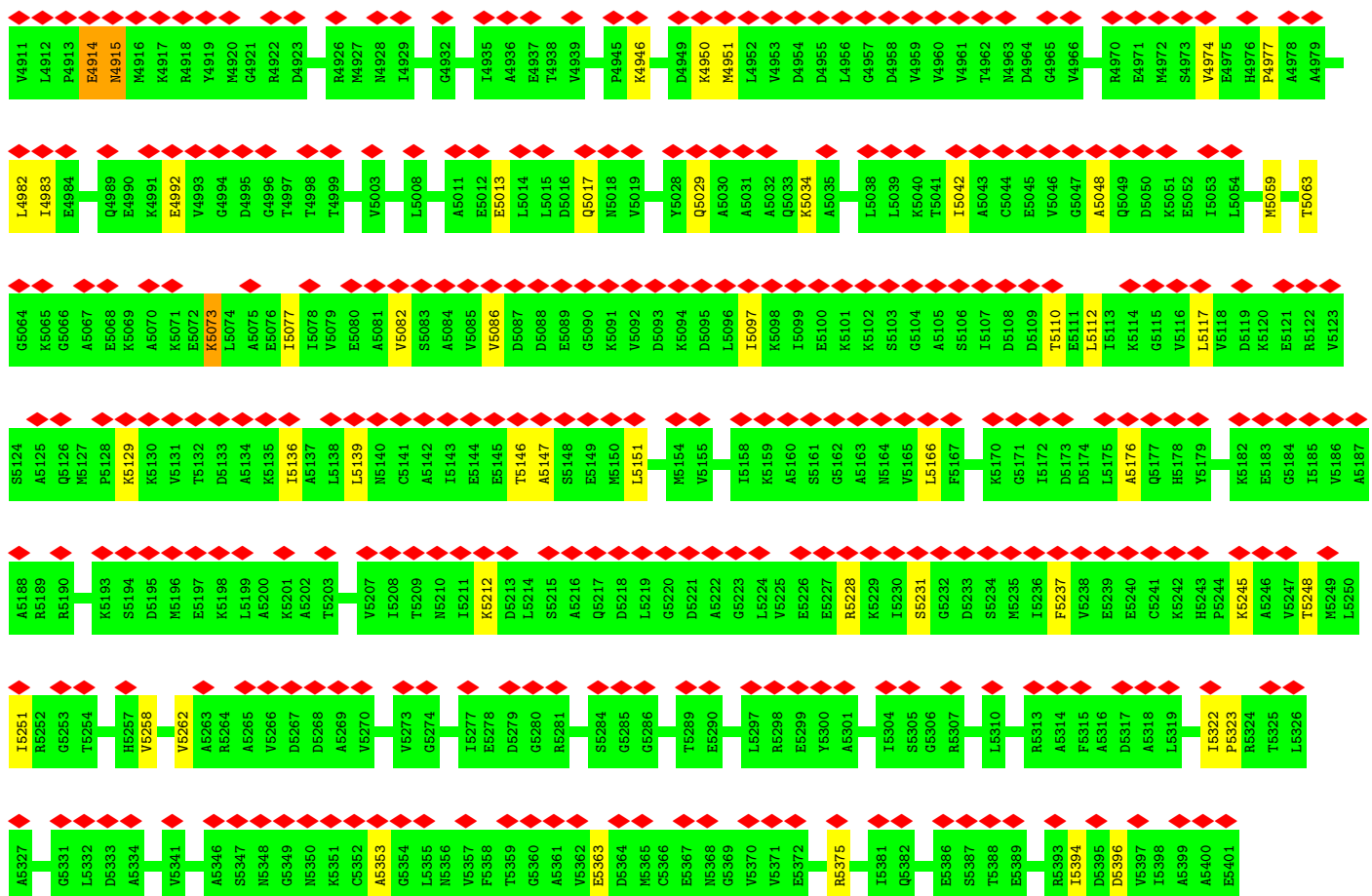
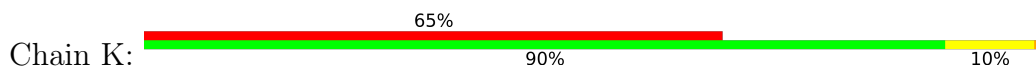


• Molecule 1: Lidless Mm-cpn

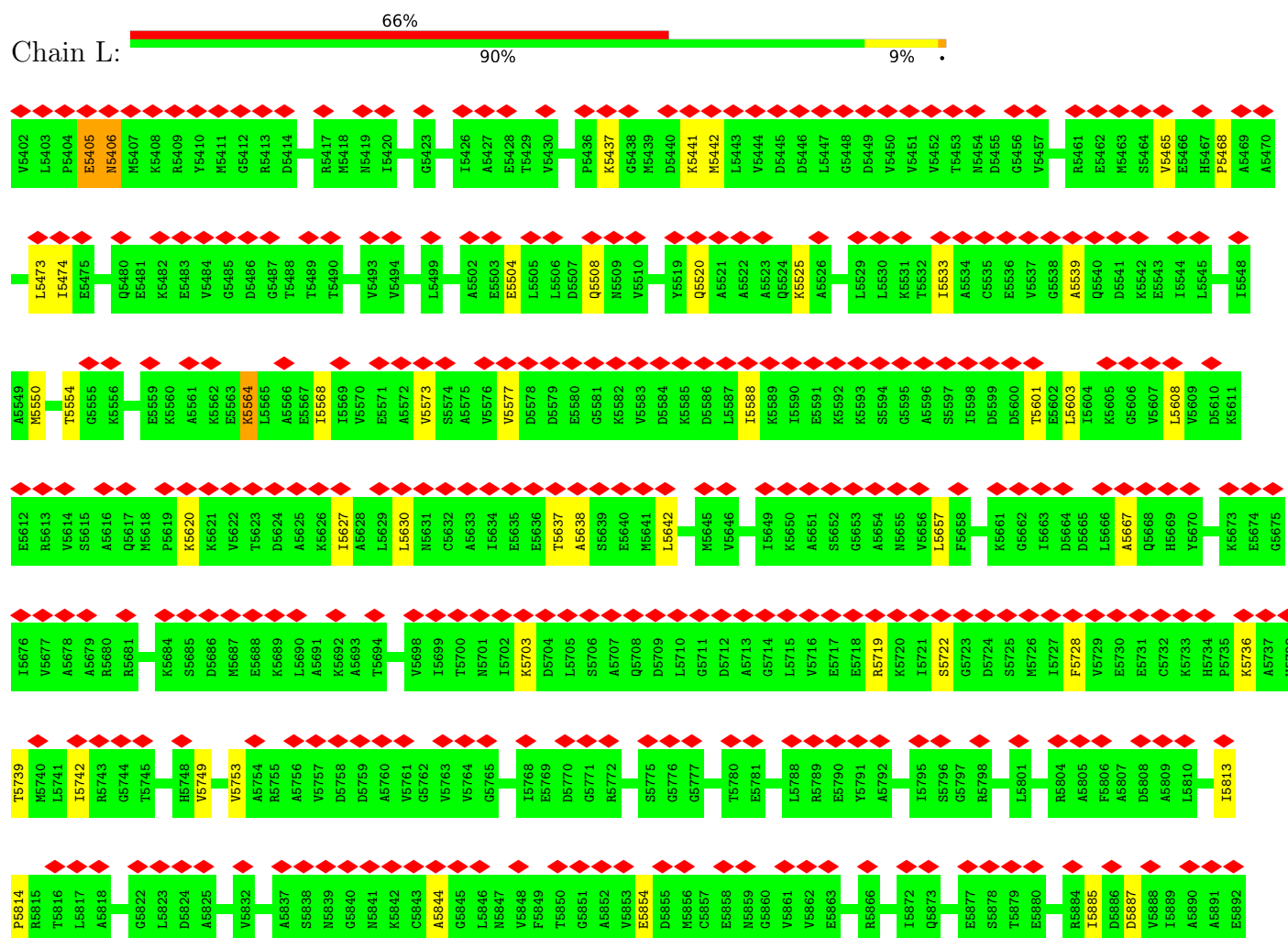




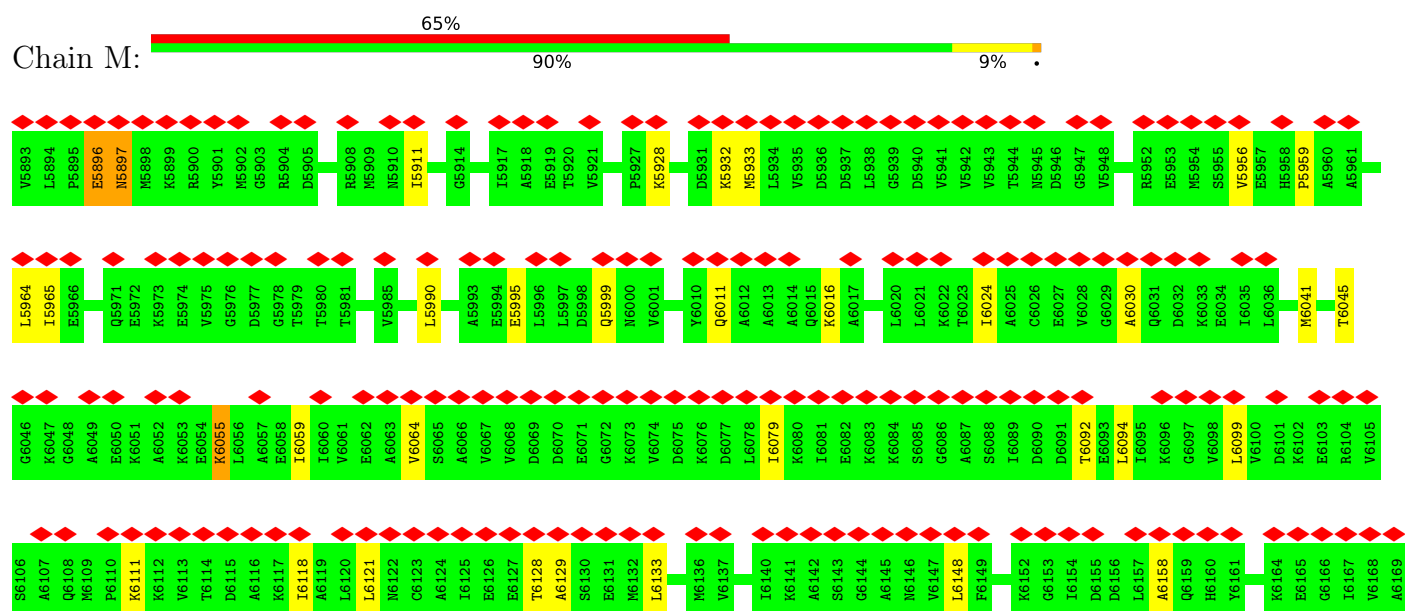
● Molecule 1: Lidless Mm-cpn

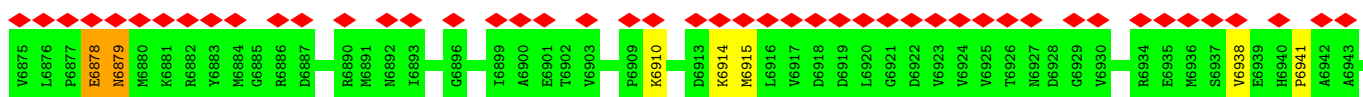


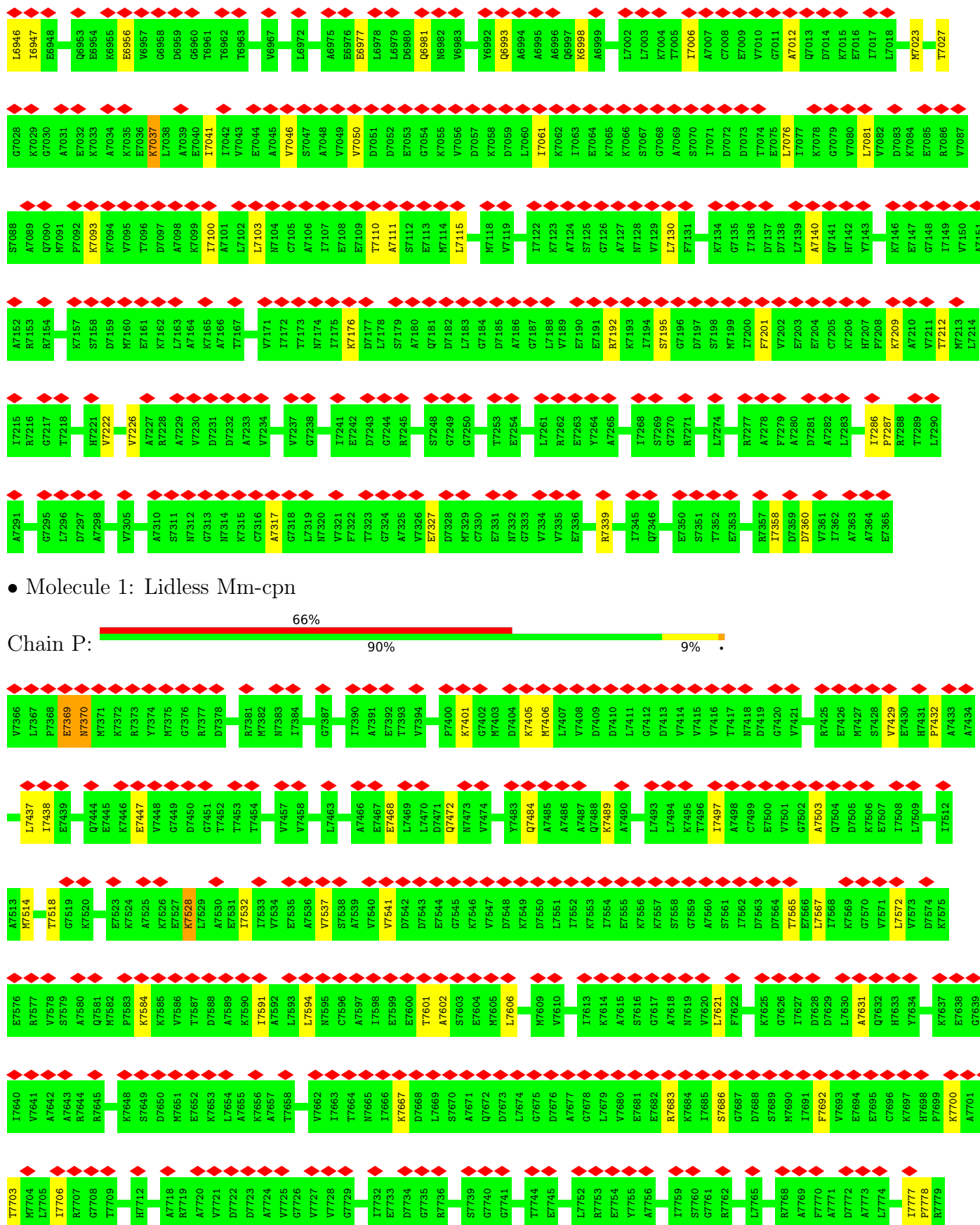
• Molecule 1: Lidless Mm-cpn



• Molecule 1: Lidless Mm-cpn







T7780	L7781	A7782	G7786	L7787	D7788	A7789	V7796	A7801	S7802	N7803	G7804	N7805	A7806	C7807	A7808	G7809	L7810	N7811	V7812	F7813	T7814	G7815	A7816	V7817	E7818	D7819	N7820	C7821	E7822	N7823	G7824	V7825	V7826	E7827	R7830	L7836	D7837	E7841	S7842	T7843	E7844	R7848	L7849	D7850	D7851	V7852	L7853	A7854	A7855	E7856
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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

5.1 Standard geometry

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

All (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
1	M	6335	ALA	C-O	5.07	1.32	1.23
1	O	7317	ALA	C-O	5.07	1.32	1.23
1	G	3389	ALA	C-O	5.05	1.32	1.23
1	J	4862	ALA	C-O	5.05	1.32	1.23
1	L	5844	ALA	C-O	5.05	1.32	1.23
1	P	7808	ALA	C-O	5.05	1.32	1.23
1	F	2898	ALA	C-O	5.05	1.32	1.23
1	C	1425	ALA	C-O	5.04	1.32	1.23
1	E	2407	ALA	C-O	5.04	1.32	1.23
1	N	6826	ALA	C-O	5.04	1.32	1.23
1	A	443	ALA	C-O	5.01	1.32	1.23

All (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
1	D	1477	GLU	CA-C-O	-6.61	106.22	120.10
1	P	7369	GLU	CA-C-O	-6.61	106.22	120.10
1	H	3441	GLU	CA-C-O	-6.61	106.23	120.10
1	L	5405	GLU	CA-C-O	-6.60	106.23	120.10
1	I	3932	GLU	CA-C-O	-6.60	106.23	120.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4	GLU	CA-C-O	-6.60	106.24	120.10
1	C	986	GLU	CA-C-O	-6.60	106.24	120.10
1	J	4423	GLU	CA-C-O	-6.60	106.24	120.10
1	K	4914	GLU	CA-C-O	-6.60	106.25	120.10
1	E	1968	GLU	CA-C-O	-6.59	106.26	120.10
1	O	6878	GLU	CA-C-O	-6.59	106.27	120.10
1	D	1702	LEU	CB-CG-CD2	-5.09	102.35	111.00
1	G	3175	LEU	CB-CG-CD2	-5.09	102.35	111.00
1	N	6612	LEU	CB-CG-CD2	-5.09	102.35	111.00
1	B	720	LEU	CB-CG-CD2	-5.08	102.36	111.00
1	P	7594	LEU	CB-CG-CD2	-5.08	102.37	111.00
1	H	3666	LEU	CB-CG-CD2	-5.07	102.38	111.00
1	A	229	LEU	CB-CG-CD2	-5.06	102.40	111.00
1	I	4157	LEU	CB-CG-CD2	-5.06	102.40	111.00
1	K	5139	LEU	CB-CG-CD2	-5.06	102.40	111.00
1	M	6121	LEU	CB-CG-CD2	-5.06	102.40	111.00
1	O	7103	LEU	CB-CG-CD2	-5.06	102.40	111.00
1	C	1211	LEU	CB-CG-CD2	-5.04	102.42	111.00
1	E	2193	LEU	CB-CG-CD2	-5.04	102.43	111.00
1	J	4648	LEU	CB-CG-CD2	-5.04	102.43	111.00
1	F	2684	LEU	CB-CG-CD2	-5.04	102.43	111.00
1	L	5630	LEU	CB-CG-CD2	-5.03	102.45	111.00

There are no chirality outliers.

All (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
1	B	944	GLU	Mainchain
1	C	1101	GLN	Mainchain
1	C	1120	ALA	Mainchain
1	C	1435	GLU	Mainchain
1	D	1592	GLN	Mainchain
1	D	1611	ALA	Mainchain
1	D	1926	GLU	Mainchain
1	E	2083	GLN	Mainchain
1	E	2102	ALA	Mainchain
1	E	2417	GLU	Mainchain

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Mol	Chain	Res	Type	Group
1	F	2574	GLN	Mainchain
1	F	2593	ALA	Mainchain
1	F	2908	GLU	Mainchain
1	G	3065	GLN	Mainchain
1	G	3084	ALA	Mainchain
1	G	3399	GLU	Mainchain
1	H	3556	GLN	Mainchain
1	H	3575	ALA	Mainchain
1	H	3890	GLU	Mainchain
1	I	4047	GLN	Mainchain
1	I	4066	ALA	Mainchain
1	I	4381	GLU	Mainchain
1	J	4538	GLN	Mainchain
1	J	4557	ALA	Mainchain
1	J	4872	GLU	Mainchain
1	K	5029	GLN	Mainchain
1	K	5048	ALA	Mainchain
1	K	5363	GLU	Mainchain
1	L	5520	GLN	Mainchain
1	L	5539	ALA	Mainchain
1	L	5854	GLU	Mainchain
1	M	6011	GLN	Mainchain
1	M	6030	ALA	Mainchain
1	M	6345	GLU	Mainchain
1	N	6502	GLN	Mainchain
1	N	6521	ALA	Mainchain
1	N	6836	GLU	Mainchain
1	O	6993	GLN	Mainchain
1	O	7012	ALA	Mainchain
1	O	7327	GLU	Mainchain
1	P	7484	GLN	Mainchain
1	P	7503	ALA	Mainchain
1	P	7818	GLU	Mainchain

5.2 Too-close contacts ⓘ

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.

All (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
1:H:3561:LYS:HA	1:H:3561:LYS:HE2	1.73	0.70
1:I:4052:LYS:HA	1:I:4052:LYS:HE2	1.73	0.70
1:J:4543:LYS:HE2	1:J:4543:LYS:HA	1.73	0.70
1:L:5525:LYS:HE2	1:L:5525:LYS:HA	1.73	0.70
1:C:1106:LYS:HE2	1:C:1106:LYS:HA	1.73	0.70
1:F:2579:LYS:HA	1:F:2579:LYS:HE2	1.73	0.70
1:O:6998:LYS:HE2	1:O:6998:LYS:HA	1.73	0.70
1:D:1597:LYS:HE2	1:D:1597:LYS:HA	1.73	0.70
1:M:6016:LYS:HE2	1:M:6016:LYS:HA	1.73	0.70
1:E:2088:LYS:HA	1:E:2088:LYS:HE2	1.73	0.69
1:N:6507:LYS:HE2	1:N:6507:LYS:HA	1.73	0.69
1:L:5813:ILE:HB	1:L:5814:PRO:HD3	1.83	0.61
1:A:412:ILE:HB	1:A:413:PRO:HD3	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1394:ILE:HB	1:C:1395:PRO:HD3	1.83	0.61
1:J:4831:ILE:HB	1:J:4832:PRO:HD3	1.83	0.61
1:E:2376:ILE:HB	1:E:2377:PRO:HD3	1.83	0.61
1:N:6795:ILE:HB	1:N:6796:PRO:HD3	1.83	0.61
1:G:3358:ILE:HB	1:G:3359:PRO:HD3	1.83	0.60
1:P:7777:ILE:HB	1:P:7778:PRO:HD3	1.83	0.60
1:B:747:LEU:C	1:B:747:LEU:HD13	2.23	0.60
1:B:903:ILE:HB	1:B:904:PRO:HD3	1.83	0.60
1:H:3849:ILE:HB	1:H:3850:PRO:HD3	1.83	0.60
1:K:5166:LEU:C	1:K:5166:LEU:HD13	2.23	0.60
1:K:5322:ILE:HB	1:K:5323:PRO:HD3	1.83	0.59
1:I:4340:ILE:HB	1:I:4341:PRO:HD3	1.83	0.59
1:J:4675:LEU:C	1:J:4675:LEU:HD13	2.23	0.59
1:A:256:LEU:HD13	1:A:256:LEU:C	2.23	0.59
1:C:1238:LEU:HD13	1:C:1238:LEU:C	2.23	0.59
1:L:5657:LEU:HD13	1:L:5657:LEU:C	2.23	0.59
1:D:1885:ILE:HB	1:D:1886:PRO:HD3	1.83	0.59
1:M:6148:LEU:HD13	1:M:6148:LEU:C	2.23	0.59
1:M:6304:ILE:HB	1:M:6305:PRO:HD3	1.83	0.59
1:D:1729:LEU:HD13	1:D:1729:LEU:C	2.23	0.59
1:P:7621:LEU:HD13	1:P:7621:LEU:C	2.23	0.59
1:G:3202:LEU:HD13	1:G:3202:LEU:C	2.23	0.59
1:F:2867:ILE:HB	1:F:2868:PRO:HD3	1.83	0.59
1:O:7286:ILE:HB	1:O:7287:PRO:HD3	1.83	0.58
1:I:4184:LEU:C	1:I:4184:LEU:HD13	2.23	0.58
1:H:3693:LEU:HD13	1:H:3693:LEU:C	2.23	0.58
1:E:2220:LEU:HD13	1:E:2220:LEU:C	2.23	0.58
1:N:6639:LEU:HD13	1:N:6639:LEU:C	2.23	0.58
1:F:2711:LEU:HD13	1:F:2711:LEU:C	2.23	0.58
1:O:7130:LEU:HD13	1:O:7130:LEU:C	2.23	0.58
1:C:1145:LYS:HE3	1:C:1145:LYS:HA	1.88	0.55
1:L:5564:LYS:HE3	1:L:5564:LYS:HA	1.88	0.55
1:E:2127:LYS:HE3	1:E:2127:LYS:HA	1.88	0.55
1:N:6546:LYS:HE3	1:N:6546:LYS:HA	1.88	0.55
1:F:2618:LYS:HA	1:F:2618:LYS:HE3	1.88	0.55
1:O:7037:LYS:HE3	1:O:7037:LYS:HA	1.88	0.55
1:D:1636:LYS:HE3	1:D:1636:LYS:HA	1.88	0.55
1:M:6055:LYS:HE3	1:M:6055:LYS:HA	1.88	0.55
1:J:4582:LYS:HE3	1:J:4582:LYS:HA	1.88	0.54
1:A:163:LYS:HA	1:A:163:LYS:HE3	1.88	0.54
1:P:7528:LYS:HA	1:P:7528:LYS:HE3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:3600:LYS:HA	1:H:3600:LYS:HE3	1.88	0.54
1:I:4091:LYS:HA	1:I:4091:LYS:HE3	1.88	0.54
1:G:3109:LYS:HE3	1:G:3109:LYS:HA	1.88	0.54
1:B:654:LYS:HE3	1:B:654:LYS:HA	1.88	0.53
1:K:5073:LYS:HE3	1:K:5073:LYS:HA	1.88	0.53
1:M:6378:ASP:HB3	1:N:6423:LYS:CD	2.43	0.48
1:J:4905:ASP:HB3	1:K:4950:LYS:CD	2.43	0.48
1:D:1959:ASP:HB3	1:E:2004:LYS:CD	2.44	0.48
1:A:486:ASP:HB3	1:B:531:LYS:CD	2.43	0.48
1:B:977:ASP:HB3	1:C:1022:LYS:CD	2.43	0.48
1:K:5396:ASP:HB3	1:L:5441:LYS:CD	2.44	0.48
1:E:2450:ASP:HB3	1:F:2495:LYS:CD	2.43	0.48
1:N:6869:ASP:HB3	1:O:6914:LYS:CD	2.43	0.48
1:C:1468:ASP:HB3	1:D:1513:LYS:CD	2.43	0.48
1:G:3432:ASP:HB3	1:H:3477:LYS:CD	2.43	0.48
1:L:5887:ASP:HB3	1:M:5932:LYS:CD	2.43	0.48
1:O:7360:ASP:HB3	1:P:7405:LYS:CD	2.43	0.48
1:F:2941:ASP:HB3	1:G:2986:LYS:CD	2.44	0.48
1:I:3968:LYS:CD	1:P:7851:ASP:HB3	2.44	0.48
1:A:40:LYS:CD	1:H:3923:ASP:HB3	2.43	0.47
1:E:2183:LYS:HD2	1:E:2183:LYS:N	2.30	0.47
1:I:4414:ASP:HB3	1:J:4459:LYS:CD	2.43	0.47
1:N:6602:LYS:HD2	1:N:6602:LYS:N	2.30	0.47
1:P:7584:LYS:HD2	1:P:7584:LYS:N	2.30	0.47
1:B:710:LYS:N	1:B:710:LYS:HD2	2.29	0.47
1:G:3165:LYS:N	1:G:3165:LYS:HD2	2.30	0.47
1:J:4638:LYS:HD2	1:J:4638:LYS:N	2.30	0.47
1:A:219:LYS:HD2	1:A:219:LYS:N	2.30	0.47
1:C:1201:LYS:HD2	1:C:1201:LYS:N	2.29	0.47
1:K:5129:LYS:HD2	1:K:5129:LYS:N	2.30	0.47
1:L:5620:LYS:HD2	1:L:5620:LYS:N	2.30	0.47
1:D:1692:LYS:HD2	1:D:1692:LYS:N	2.30	0.47
1:H:3656:LYS:HD2	1:H:3656:LYS:N	2.29	0.47
1:D:1680:LEU:HB3	1:D:1811:THR:HG21	1.97	0.47
1:I:4147:LYS:HD2	1:I:4147:LYS:N	2.30	0.47
1:M:6099:LEU:HB3	1:M:6230:THR:HG21	1.97	0.47
1:M:6111:LYS:HD2	1:M:6111:LYS:N	2.30	0.47
1:F:2674:LYS:N	1:F:2674:LYS:HD2	2.30	0.47
1:O:7093:LYS:HD2	1:O:7093:LYS:N	2.30	0.46
1:F:2662:LEU:HB3	1:F:2793:THR:HG21	1.97	0.46
1:N:6590:LEU:HB3	1:N:6721:THR:HG21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:7081:LEU:HB3	1:O:7212:THR:HG21	1.97	0.46
1:E:2171:LEU:HB3	1:E:2302:THR:HG21	1.97	0.46
1:L:5608:LEU:HB3	1:L:5739:THR:HG21	1.97	0.46
1:C:1189:LEU:HB3	1:C:1320:THR:HG21	1.97	0.46
1:J:4626:LEU:HB3	1:J:4757:THR:HG21	1.97	0.46
1:K:5077:ILE:HG23	1:K:5112:LEU:HB2	1.98	0.46
1:A:207:LEU:HB3	1:A:338:THR:HG21	1.97	0.46
1:B:658:ILE:HG23	1:B:693:LEU:HB2	1.98	0.46
1:G:3113:ILE:HG23	1:G:3148:LEU:HB2	1.98	0.46
1:P:7532:ILE:HG23	1:P:7567:LEU:HB2	1.98	0.46
1:P:7572:LEU:HB3	1:P:7703:THR:HG21	1.97	0.46
1:G:3049:GLU:O	1:G:3053:GLN:HG2	2.16	0.46
1:M:6059:ILE:HG23	1:M:6094:LEU:HB2	1.98	0.46
1:A:167:ILE:HG23	1:A:202:LEU:HB2	1.98	0.45
1:D:1640:ILE:HG23	1:D:1675:LEU:HB2	1.98	0.45
1:E:2067:GLU:O	1:E:2071:GLN:HG2	2.16	0.45
1:F:2558:GLU:O	1:F:2562:GLN:HG2	2.17	0.45
1:G:3153:LEU:HB3	1:G:3284:THR:HG21	1.97	0.45
1:N:6486:GLU:O	1:N:6490:GLN:HG2	2.17	0.45
1:O:6977:GLU:O	1:O:6981:GLN:HG2	2.17	0.45
1:A:103:GLU:O	1:A:107:GLN:HG2	2.16	0.45
1:D:1714:LEU:C	1:D:1714:LEU:HD23	2.37	0.45
1:J:4522:GLU:O	1:J:4526:GLN:HG2	2.17	0.45
1:P:7468:GLU:O	1:P:7472:GLN:HG2	2.16	0.45
1:F:2696:LEU:C	1:F:2696:LEU:HD23	2.37	0.45
1:J:4586:ILE:HG23	1:J:4621:LEU:HB2	1.98	0.45
1:M:6133:LEU:C	1:M:6133:LEU:HD23	2.37	0.45
1:O:7115:LEU:C	1:O:7115:LEU:HD23	2.37	0.45
1:L:5642:LEU:C	1:L:5642:LEU:HD23	2.37	0.45
1:C:1223:LEU:C	1:C:1223:LEU:HD23	2.37	0.45
1:H:3678:LEU:HD23	1:H:3678:LEU:C	2.37	0.45
1:I:4095:ILE:HG23	1:I:4130:LEU:HB2	1.98	0.45
1:B:594:GLU:O	1:B:598:GLN:HG2	2.17	0.45
1:B:698:LEU:HB3	1:B:829:THR:HG21	1.97	0.45
1:G:3187:LEU:HD23	1:G:3187:LEU:C	2.37	0.45
1:H:3604:ILE:HG23	1:H:3639:LEU:HB2	1.98	0.45
1:I:4169:LEU:HD23	1:I:4169:LEU:C	2.37	0.45
1:K:5013:GLU:O	1:K:5017:GLN:HG2	2.17	0.45
1:A:241:LEU:C	1:A:241:LEU:HD23	2.37	0.45
1:B:732:LEU:HD23	1:B:732:LEU:C	2.37	0.45
1:H:3644:LEU:HB3	1:H:3775:THR:HG21	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:5151:LEU:C	1:K:5151:LEU:HD23	2.37	0.45
1:M:5995:GLU:O	1:M:5999:GLN:HG2	2.16	0.45
1:D:1576:GLU:O	1:D:1580:GLN:HG2	2.16	0.45
1:I:4135:LEU:HB3	1:I:4266:THR:HG21	1.97	0.45
1:J:4660:LEU:HD23	1:J:4660:LEU:C	2.37	0.45
1:K:5117:LEU:HB3	1:K:5248:THR:HG21	1.97	0.45
1:O:7041:ILE:HG23	1:O:7076:LEU:HB2	1.98	0.45
1:P:7606:LEU:C	1:P:7606:LEU:HD23	2.37	0.45
1:E:2131:ILE:HG23	1:E:2166:LEU:HB2	1.98	0.45
1:F:2622:ILE:HG23	1:F:2657:LEU:HB2	1.98	0.45
1:H:3540:GLU:O	1:H:3544:GLN:HG2	2.16	0.45
1:C:1149:ILE:HG23	1:C:1184:LEU:HB2	1.98	0.44
1:N:6550:ILE:HG23	1:N:6585:LEU:HB2	1.98	0.44
1:C:1085:GLU:O	1:C:1089:GLN:HG2	2.17	0.44
1:I:4031:GLU:O	1:I:4035:GLN:HG2	2.17	0.44
1:L:5504:GLU:O	1:L:5508:GLN:HG2	2.16	0.44
1:L:5568:ILE:HG23	1:L:5603:LEU:HB2	1.98	0.44
1:E:1968:GLU:O	1:E:1969:ASN:HB2	2.18	0.44
1:J:4423:GLU:O	1:J:4424:ASN:HB2	2.18	0.44
1:A:4:GLU:O	1:A:5:ASN:HB2	2.18	0.44
1:E:2205:LEU:C	1:E:2205:LEU:HD23	2.37	0.44
1:N:6387:GLU:O	1:N:6388:ASN:HB2	2.18	0.44
1:O:6878:GLU:O	1:O:6879:ASN:HB2	2.18	0.44
1:F:2459:GLU:O	1:F:2460:ASN:HB2	2.18	0.44
1:K:4914:GLU:O	1:K:4915:ASN:HB2	2.18	0.44
1:N:6624:LEU:C	1:N:6624:LEU:HD23	2.37	0.44
1:G:2950:GLU:O	1:G:2951:ASN:HB2	2.18	0.44
1:H:3441:GLU:O	1:H:3442:ASN:HB2	2.18	0.44
1:P:7369:GLU:O	1:P:7370:ASN:HB2	2.18	0.44
1:B:495:GLU:O	1:B:496:ASN:HB2	2.18	0.44
1:I:3932:GLU:O	1:I:3933:ASN:HB2	2.18	0.44
1:A:318:ARG:HD2	1:A:327:PHE:CD1	2.53	0.43
1:D:1791:ARG:HD2	1:D:1800:PHE:CD1	2.53	0.43
1:L:5719:ARG:HD2	1:L:5728:PHE:CD1	2.53	0.43
1:O:7192:ARG:HD2	1:O:7201:PHE:CD1	2.53	0.43
1:D:1477:GLU:O	1:D:1478:ASN:HB2	2.18	0.43
1:I:4246:ARG:HD2	1:I:4255:PHE:CD1	2.53	0.43
1:M:6210:ARG:HD2	1:M:6219:PHE:CD1	2.53	0.43
1:F:2773:ARG:HD2	1:F:2782:PHE:CD1	2.54	0.43
1:G:3264:ARG:HD2	1:G:3273:PHE:CD1	2.53	0.43
1:M:5896:GLU:O	1:M:5897:ASN:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1300:ARG:HD2	1:C:1309:PHE:CD1	2.54	0.43
1:H:3755:ARG:HD2	1:H:3764:PHE:CD1	2.54	0.43
1:J:4737:ARG:HD2	1:J:4746:PHE:CD1	2.54	0.43
1:A:64:VAL:HG21	1:A:73:ILE:HD11	2.01	0.43
1:H:3501:VAL:HG21	1:H:3510:ILE:HD11	2.01	0.43
1:J:4483:VAL:HG21	1:J:4492:ILE:HD11	2.01	0.43
1:C:1046:VAL:HG21	1:C:1055:ILE:HD11	2.01	0.43
1:I:3992:VAL:HG21	1:I:4001:ILE:HD11	2.01	0.43
1:L:5405:GLU:O	1:L:5406:ASN:HB2	2.18	0.43
1:P:7683:ARG:HD2	1:P:7692:PHE:CD1	2.54	0.43
1:C:986:GLU:O	1:C:987:ASN:HB2	2.18	0.43
1:E:2028:VAL:HG21	1:E:2037:ILE:HD11	2.01	0.43
1:G:3010:VAL:HG21	1:G:3019:ILE:HD11	2.01	0.43
1:L:5465:VAL:HG21	1:L:5474:ILE:HD11	2.01	0.43
1:N:6447:VAL:HG21	1:N:6456:ILE:HD11	2.01	0.43
1:N:6701:ARG:HD2	1:N:6710:PHE:CD1	2.53	0.43
1:O:6938:VAL:HG21	1:O:6947:ILE:HD11	2.01	0.43
1:P:7429:VAL:HG21	1:P:7438:ILE:HD11	2.01	0.43
1:B:555:VAL:HG21	1:B:564:ILE:HD11	2.01	0.43
1:D:1537:VAL:HG21	1:D:1546:ILE:HD11	2.01	0.43
1:F:2519:VAL:HG21	1:F:2528:ILE:HD11	2.01	0.43
1:K:4974:VAL:HG21	1:K:4983:ILE:HD11	2.01	0.43
1:M:5956:VAL:HG21	1:M:5965:ILE:HD11	2.01	0.43
1:B:809:ARG:HD2	1:B:818:PHE:CD1	2.53	0.43
1:E:2282:ARG:HD2	1:E:2291:PHE:CD1	2.53	0.42
1:K:5228:ARG:HD2	1:K:5237:PHE:CD1	2.53	0.42
1:G:3078:ILE:C	1:G:3078:ILE:HD12	2.40	0.42
1:K:5042:ILE:HD12	1:K:5042:ILE:C	2.40	0.42
1:K:5394:ILE:HD12	1:K:5394:ILE:N	2.35	0.42
1:F:2587:ILE:C	1:F:2587:ILE:HD12	2.40	0.42
1:O:7006:ILE:C	1:O:7006:ILE:HD12	2.40	0.42
1:A:132:ILE:C	1:A:132:ILE:HD12	2.40	0.42
1:B:623:ILE:C	1:B:623:ILE:HD12	2.40	0.42
1:B:975:ILE:N	1:B:975:ILE:HD12	2.35	0.42
1:E:2113:MET:O	1:E:2117:THR:HG23	2.20	0.42
1:J:4551:ILE:HD12	1:J:4551:ILE:C	2.40	0.42
1:L:5533:ILE:HD12	1:L:5533:ILE:C	2.40	0.42
1:P:7497:ILE:C	1:P:7497:ILE:HD12	2.40	0.42
1:A:484:ILE:N	1:A:484:ILE:HD12	2.35	0.42
1:C:1114:ILE:C	1:C:1114:ILE:HD12	2.40	0.42
1:C:1131:MET:O	1:C:1135:THR:HG23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:2939:ILE:N	1:F:2939:ILE:HD12	2.35	0.42
1:H:3693:LEU:HD13	1:H:3693:LEU:O	2.20	0.42
1:J:4903:ILE:HD12	1:J:4903:ILE:N	2.35	0.42
1:L:5550:MET:O	1:L:5554:THR:HG23	2.20	0.42
1:N:6532:MET:O	1:N:6536:THR:HG23	2.20	0.42
1:O:7358:ILE:HD12	1:O:7358:ILE:N	2.35	0.42
1:P:7849:ILE:N	1:P:7849:ILE:HD12	2.35	0.42
1:B:640:MET:O	1:B:644:THR:HG23	2.20	0.42
1:C:1238:LEU:HD13	1:C:1238:LEU:O	2.20	0.42
1:G:3095:MET:O	1:G:3099:THR:HG23	2.20	0.42
1:G:3430:ILE:N	1:G:3430:ILE:HD12	2.35	0.42
1:H:3569:ILE:HD12	1:H:3569:ILE:C	2.40	0.42
1:J:4675:LEU:HD13	1:J:4675:LEU:O	2.20	0.42
1:L:5657:LEU:HD13	1:L:5657:LEU:O	2.20	0.42
1:P:7514:MET:O	1:P:7518:THR:HG23	2.20	0.42
1:A:256:LEU:HD13	1:A:256:LEU:O	2.20	0.42
1:I:4060:ILE:C	1:I:4060:ILE:HD12	2.40	0.42
1:I:4184:LEU:HD13	1:I:4184:LEU:O	2.20	0.42
1:K:5059:MET:O	1:K:5063:THR:HG23	2.20	0.42
1:D:1605:ILE:C	1:D:1605:ILE:HD12	2.40	0.42
1:E:2031:PRO:HB2	1:F:2496:MET:SD	2.60	0.42
1:J:4568:MET:O	1:J:4572:THR:HG23	2.20	0.42
1:L:5468:PRO:HB2	1:M:5933:MET:SD	2.60	0.42
1:M:6024:ILE:C	1:M:6024:ILE:HD12	2.40	0.42
1:A:149:MET:O	1:A:153:THR:HG23	2.20	0.41
1:C:1049:PRO:HB2	1:D:1514:MET:SD	2.60	0.41
1:D:1729:LEU:HD13	1:D:1729:LEU:O	2.20	0.41
1:F:2696:LEU:HD21	1:F:2721:ALA:CA	2.50	0.41
1:N:6450:PRO:HB2	1:O:6915:MET:SD	2.60	0.41
1:N:6867:ILE:HD12	1:N:6867:ILE:N	2.35	0.41
1:D:1714:LEU:HD21	1:D:1739:ALA:CA	2.50	0.41
1:L:5642:LEU:HD21	1:L:5667:ALA:CA	2.50	0.41
1:M:6133:LEU:HD21	1:M:6158:ALA:CA	2.50	0.41
1:M:6148:LEU:HD13	1:M:6148:LEU:O	2.20	0.41
1:O:7115:LEU:HD21	1:O:7140:ALA:CA	2.50	0.41
1:C:1223:LEU:HD21	1:C:1248:ALA:CA	2.50	0.41
1:C:1466:ILE:HD12	1:C:1466:ILE:N	2.35	0.41
1:E:2448:ILE:N	1:E:2448:ILE:HD12	2.35	0.41
1:H:3678:LEU:HD21	1:H:3703:ALA:CA	2.50	0.41
1:I:4169:LEU:HD21	1:I:4194:ALA:CA	2.50	0.41
1:O:6941:PRO:HB2	1:P:7406:MET:SD	2.61	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:747:LEU:HD13	1:B:747:LEU:O	2.20	0.41
1:C:1218:THR:O	1:C:1219:ALA:HB3	2.21	0.41
1:F:2522:PRO:HB2	1:G:2987:MET:SD	2.61	0.41
1:G:3182:THR:O	1:G:3183:ALA:HB3	2.21	0.41
1:G:3202:LEU:HD13	1:G:3202:LEU:O	2.20	0.41
1:H:3673:THR:O	1:H:3674:ALA:HB3	2.21	0.41
1:I:4164:THR:O	1:I:4165:ALA:HB3	2.21	0.41
1:K:5166:LEU:HD13	1:K:5166:LEU:O	2.20	0.41
1:L:5601:THR:HG23	1:L:5742:ILE:HA	2.02	0.41
1:L:5637:THR:O	1:L:5638:ALA:HB3	2.21	0.41
1:N:6515:ILE:C	1:N:6515:ILE:HD12	2.40	0.41
1:O:7023:MET:O	1:O:7027:THR:HG23	2.20	0.41
1:P:7601:THR:O	1:P:7602:ALA:HB3	2.21	0.41
1:P:7621:LEU:HD13	1:P:7621:LEU:O	2.20	0.41
1:B:663:VAL:HA	1:B:678:ILE:HD11	2.03	0.41
1:B:727:THR:O	1:B:728:ALA:HB3	2.21	0.41
1:F:2604:MET:O	1:F:2608:THR:HG23	2.20	0.41
1:F:2681:ILE:N	1:F:2681:ILE:HD12	2.36	0.41
1:H:3586:MET:O	1:H:3590:THR:HG23	2.20	0.41
1:J:4655:THR:O	1:J:4656:ALA:HB3	2.21	0.41
1:K:4977:PRO:HB2	1:L:5442:MET:SD	2.61	0.41
1:K:5146:THR:O	1:K:5147:ALA:HB3	2.21	0.41
1:L:5885:ILE:HD12	1:L:5885:ILE:N	2.35	0.41
1:A:236:THR:O	1:A:237:ALA:HB3	2.21	0.41
1:A:241:LEU:HD21	1:A:266:ALA:CA	2.50	0.41
1:C:1182:THR:HG23	1:C:1323:ILE:HA	2.03	0.41
1:C:1208:ILE:N	1:C:1208:ILE:HD12	2.36	0.41
1:E:2096:ILE:C	1:E:2096:ILE:HD12	2.40	0.41
1:I:4412:ILE:N	1:I:4412:ILE:HD12	2.35	0.41
1:J:4660:LEU:HD21	1:J:4685:ALA:CA	2.50	0.41
1:K:5082:VAL:HA	1:K:5097:ILE:HD11	2.03	0.41
1:O:7100:ILE:N	1:O:7100:ILE:HD12	2.36	0.41
1:B:558:PRO:HB2	1:C:1023:MET:SD	2.61	0.41
1:B:691:THR:HG23	1:B:832:ILE:HA	2.03	0.41
1:B:717:ILE:HD12	1:B:717:ILE:N	2.36	0.41
1:B:839:VAL:O	1:B:843:VAL:HG23	2.21	0.41
1:C:1154:VAL:HA	1:C:1169:ILE:HD11	2.03	0.41
1:D:1622:MET:O	1:D:1626:THR:HG23	2.20	0.41
1:D:1957:ILE:N	1:D:1957:ILE:HD12	2.35	0.41
1:G:3013:PRO:HB2	1:H:3478:MET:SD	2.60	0.41
1:H:3663:ILE:N	1:H:3663:ILE:HD12	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:4077:MET:O	1:I:4081:THR:HG23	2.20	0.41
1:K:5258:VAL:O	1:K:5262:VAL:HG23	2.21	0.41
1:L:5627:ILE:N	1:L:5627:ILE:HD12	2.36	0.41
1:L:5749:VAL:O	1:L:5753:VAL:HG23	2.21	0.41
1:N:6609:ILE:HD12	1:N:6609:ILE:N	2.36	0.41
1:N:6619:THR:O	1:N:6620:ALA:HB3	2.21	0.41
1:C:1330:VAL:O	1:C:1334:VAL:HG23	2.21	0.41
1:D:1709:THR:O	1:D:1710:ALA:HB3	2.21	0.41
1:E:2190:ILE:HD12	1:E:2190:ILE:N	2.36	0.41
1:E:2200:THR:O	1:E:2201:ALA:HB3	2.21	0.41
1:E:2220:LEU:HD13	1:E:2220:LEU:O	2.20	0.41
1:F:2691:THR:O	1:F:2692:ALA:HB3	2.21	0.41
1:H:3921:ILE:N	1:H:3921:ILE:HD12	2.35	0.41
1:I:4154:ILE:HD12	1:I:4154:ILE:N	2.36	0.41
1:J:4619:THR:HG23	1:J:4760:ILE:HA	2.03	0.41
1:K:5136:ILE:HD12	1:K:5136:ILE:N	2.36	0.41
1:M:6376:ILE:HD12	1:M:6376:ILE:N	2.35	0.41
1:A:41:MET:SD	1:H:3504:PRO:HB2	2.61	0.41
1:A:67:PRO:HB2	1:B:532:MET:SD	2.60	0.41
1:A:172:VAL:HA	1:A:187:ILE:HD11	2.03	0.41
1:A:200:THR:HG23	1:A:341:ILE:HA	2.03	0.41
1:A:348:VAL:O	1:A:352:VAL:HG23	2.21	0.41
1:D:1540:PRO:HB2	1:E:2005:MET:SD	2.61	0.41
1:G:3172:ILE:HD12	1:G:3172:ILE:N	2.36	0.41
1:H:3609:VAL:HA	1:H:3624:ILE:HD11	2.03	0.41
1:I:3969:MET:SD	1:P:7432:PRO:HB2	2.60	0.41
1:I:3995:PRO:HB2	1:J:4460:MET:SD	2.61	0.41
1:I:4100:VAL:HA	1:I:4115:ILE:HD11	2.03	0.41
1:J:4486:PRO:HB2	1:K:4951:MET:SD	2.60	0.41
1:J:4591:VAL:HA	1:J:4606:ILE:HD11	2.03	0.41
1:K:5110:THR:HG23	1:K:5251:ILE:HA	2.03	0.41
1:L:5573:VAL:HA	1:L:5588:ILE:HD11	2.03	0.41
1:M:5959:PRO:HB2	1:N:6424:MET:SD	2.61	0.41
1:M:6041:MET:O	1:M:6045:THR:HG23	2.20	0.41
1:M:6128:THR:O	1:M:6129:ALA:HB3	2.21	0.41
1:N:6639:LEU:HD13	1:N:6639:LEU:O	2.20	0.41
1:O:7110:THR:O	1:O:7111:ALA:HB3	2.21	0.41
1:P:7591:ILE:HD12	1:P:7591:ILE:N	2.36	0.41
1:C:1154:VAL:O	1:C:1158:VAL:HG23	2.21	0.41
1:E:1983:ILE:HG13	1:E:2062:LEU:HB3	2.04	0.41
1:J:4767:VAL:O	1:J:4771:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:6402:ILE:HG13	1:N:6481:LEU:HB3	2.03	0.41
1:B:663:VAL:O	1:B:667:VAL:HG23	2.22	0.40
1:B:732:LEU:HD21	1:B:757:ALA:CA	2.50	0.40
1:D:1699:ILE:N	1:D:1699:ILE:HD12	2.36	0.40
1:F:2803:VAL:O	1:F:2807:VAL:HG23	2.21	0.40
1:G:3187:LEU:HD21	1:G:3212:ALA:CA	2.50	0.40
1:K:5082:VAL:O	1:K:5086:VAL:HG23	2.22	0.40
1:L:5573:VAL:O	1:L:5577:VAL:HG23	2.22	0.40
1:M:6118:ILE:N	1:M:6118:ILE:HD12	2.36	0.40
1:O:7130:LEU:HD13	1:O:7130:LEU:O	2.20	0.40
1:O:7222:VAL:O	1:O:7226:VAL:HG23	2.21	0.40
1:P:7606:LEU:HD21	1:P:7631:ALA:CA	2.50	0.40
1:D:1492:ILE:HG13	1:D:1571:LEU:HB3	2.03	0.40
1:D:1673:THR:HG23	1:D:1814:ILE:HA	2.03	0.40
1:H:3609:VAL:O	1:H:3613:VAL:HG23	2.22	0.40
1:I:4100:VAL:O	1:I:4104:VAL:HG23	2.22	0.40
1:J:4645:ILE:N	1:J:4645:ILE:HD12	2.36	0.40
1:K:5151:LEU:HD21	1:K:5176:ALA:CA	2.50	0.40
1:M:6092:THR:HG23	1:M:6233:ILE:HA	2.03	0.40
1:A:82:GLU:OE2	1:A:465:ARG:NH2	2.55	0.40
1:F:2627:VAL:O	1:F:2631:VAL:HG23	2.21	0.40
1:H:3637:THR:HG23	1:H:3778:ILE:HA	2.03	0.40
1:I:4128:THR:HG23	1:I:4269:ILE:HA	2.03	0.40
1:J:4501:GLU:OE2	1:J:4884:ARG:NH2	2.55	0.40
1:M:5911:ILE:HG13	1:M:5990:LEU:HB3	2.04	0.40
1:N:6624:LEU:HD21	1:N:6649:ALA:CA	2.50	0.40
1:O:6956:GLU:OE2	1:O:7339:ARG:NH2	2.55	0.40
1:O:7046:VAL:O	1:O:7050:VAL:HG23	2.21	0.40
1:P:7537:VAL:O	1:P:7541:VAL:HG23	2.22	0.40
1:P:7565:THR:HG23	1:P:7706:ILE:HA	2.03	0.40
1:A:172:VAL:O	1:A:176:VAL:HG23	2.21	0.40
1:D:1645:VAL:HA	1:D:1660:ILE:HD11	2.03	0.40
1:E:2205:LEU:HD21	1:E:2230:ALA:CA	2.50	0.40
1:F:2537:GLU:OE2	1:F:2920:ARG:NH2	2.55	0.40
1:F:2711:LEU:HD13	1:F:2711:LEU:O	2.20	0.40
1:G:3028:GLU:OE2	1:G:3411:ARG:NH2	2.55	0.40
1:G:3118:VAL:O	1:G:3122:VAL:HG23	2.22	0.40
1:G:3146:THR:HG23	1:G:3287:ILE:HA	2.03	0.40
1:H:3456:ILE:HG13	1:H:3535:LEU:HB3	2.04	0.40
1:M:6064:VAL:HA	1:M:6079:ILE:HD11	2.03	0.40
1:P:7447:GLU:OE2	1:P:7830:ARG:NH2	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:ILE:N	1:A:226:ILE:HD12	2.36	0.40
1:B:573:GLU:OE2	1:B:956:ARG:NH2	2.55	0.40
1:F:2474:ILE:HG13	1:F:2553:LEU:HB3	2.03	0.40
1:F:2627:VAL:HA	1:F:2642:ILE:HD11	2.03	0.40
1:I:3947:ILE:HG13	1:I:4026:LEU:HB3	2.04	0.40
1:I:4276:VAL:O	1:I:4280:VAL:HG23	2.21	0.40
1:K:4992:GLU:OE2	1:K:5375:ARG:NH2	2.55	0.40
1:O:7046:VAL:HA	1:O:7061:ILE:HD11	2.03	0.40

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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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

All (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
1	F	2460	ASN
1	G	2951	ASN
1	H	3442	ASN
1	I	3933	ASN
1	J	4424	ASN
1	K	4915	ASN
1	L	5406	ASN
1	M	5897	ASN
1	N	6388	ASN
1	O	6879	ASN
1	P	7370	ASN

5.3.2 Protein sidechains ⓘ

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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

All (96) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	LYS
1	A	72	LEU
1	A	163	LYS
1	A	302	LYS
1	A	321	SER
1	A	335	LYS
1	B	527	LYS
1	B	563	LEU
1	B	654	LYS
1	B	793	LYS
1	B	812	SER
1	B	826	LYS
1	C	1018	LYS
1	C	1054	LEU
1	C	1145	LYS
1	C	1284	LYS
1	C	1303	SER
1	C	1317	LYS
1	D	1509	LYS
1	D	1545	LEU
1	D	1636	LYS

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Mol	Chain	Res	Type
1	D	1775	LYS
1	D	1794	SER
1	D	1808	LYS
1	E	2000	LYS
1	E	2036	LEU
1	E	2127	LYS
1	E	2266	LYS
1	E	2285	SER
1	E	2299	LYS
1	F	2491	LYS
1	F	2527	LEU
1	F	2618	LYS
1	F	2757	LYS
1	F	2776	SER
1	F	2790	LYS
1	G	2982	LYS
1	G	3018	LEU
1	G	3109	LYS
1	G	3248	LYS
1	G	3267	SER
1	G	3281	LYS
1	H	3473	LYS
1	H	3509	LEU
1	H	3600	LYS
1	H	3739	LYS
1	H	3758	SER
1	H	3772	LYS
1	I	3964	LYS
1	I	4000	LEU
1	I	4091	LYS
1	I	4230	LYS
1	I	4249	SER
1	I	4263	LYS
1	J	4455	LYS
1	J	4491	LEU
1	J	4582	LYS
1	J	4721	LYS
1	J	4740	SER
1	J	4754	LYS
1	K	4946	LYS
1	K	4982	LEU
1	K	5073	LYS

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Mol	Chain	Res	Type
1	K	5212	LYS
1	K	5231	SER
1	K	5245	LYS
1	L	5437	LYS
1	L	5473	LEU
1	L	5564	LYS
1	L	5703	LYS
1	L	5722	SER
1	L	5736	LYS
1	M	5928	LYS
1	M	5964	LEU
1	M	6055	LYS
1	M	6194	LYS
1	M	6213	SER
1	M	6227	LYS
1	N	6419	LYS
1	N	6455	LEU
1	N	6546	LYS
1	N	6685	LYS
1	N	6704	SER
1	N	6718	LYS
1	O	6910	LYS
1	O	6946	LEU
1	O	7037	LYS
1	O	7176	LYS
1	O	7195	SER
1	O	7209	LYS
1	P	7401	LYS
1	P	7437	LEU
1	P	7528	LYS
1	P	7667	LYS
1	P	7686	SER
1	P	7700	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	446	ASN
1	B	937	ASN
1	C	1428	ASN
1	D	1919	ASN
1	E	2410	ASN

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Mol	Chain	Res	Type
1	F	2901	ASN
1	G	3392	ASN
1	H	3883	ASN
1	I	4374	ASN
1	J	4865	ASN
1	K	5356	ASN
1	L	5847	ASN
1	M	6338	ASN
1	N	6829	ASN
1	O	7320	ASN
1	P	7811	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.

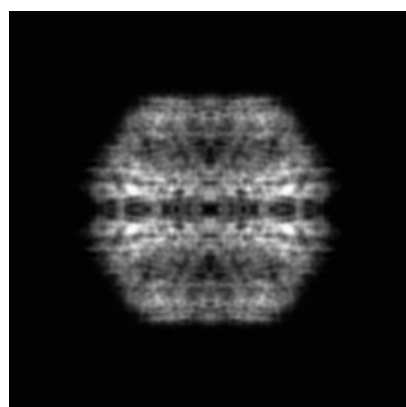
6 Map visualisation [i](#)

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.

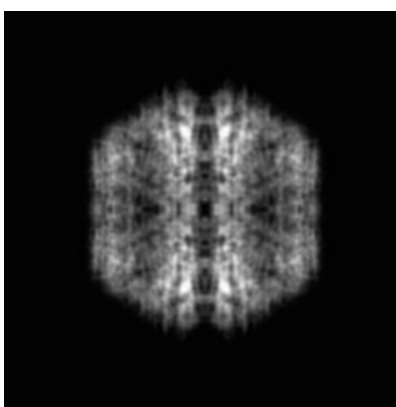
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

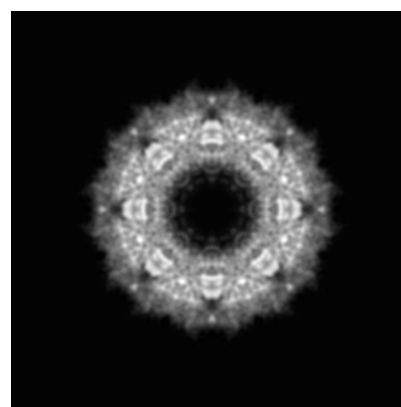
6.1.1 Primary map



X



Y

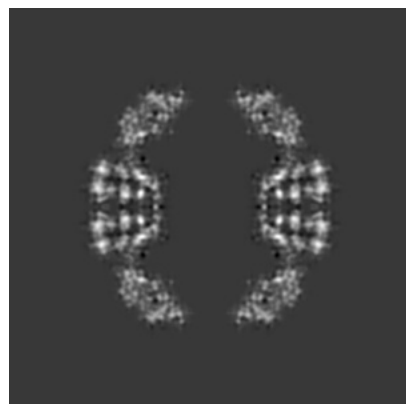


Z

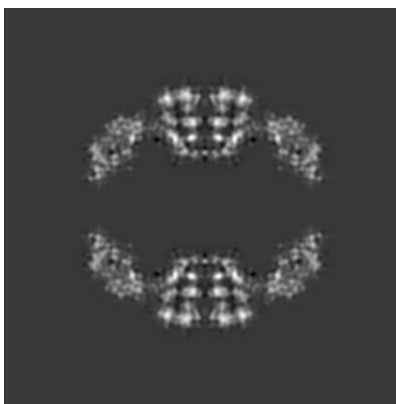
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

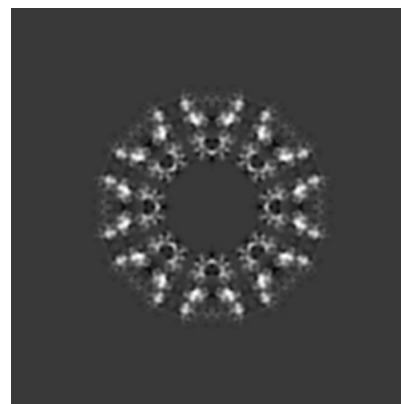
6.2.1 Primary map



X Index: 96



Y Index: 96

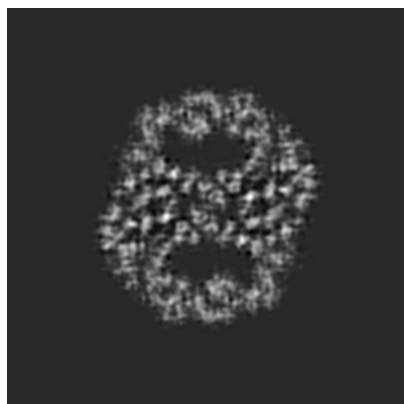


Z Index: 96

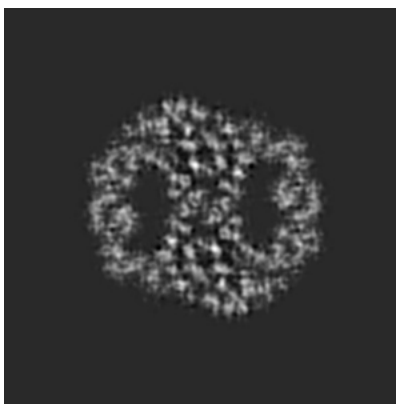
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 123



Y Index: 123

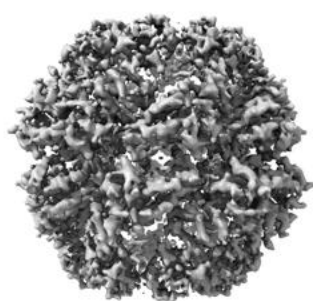


Z Index: 88

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

6.4 Orthogonal surface views [i](#)

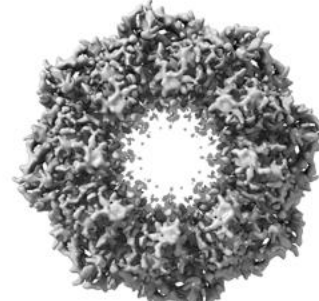
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

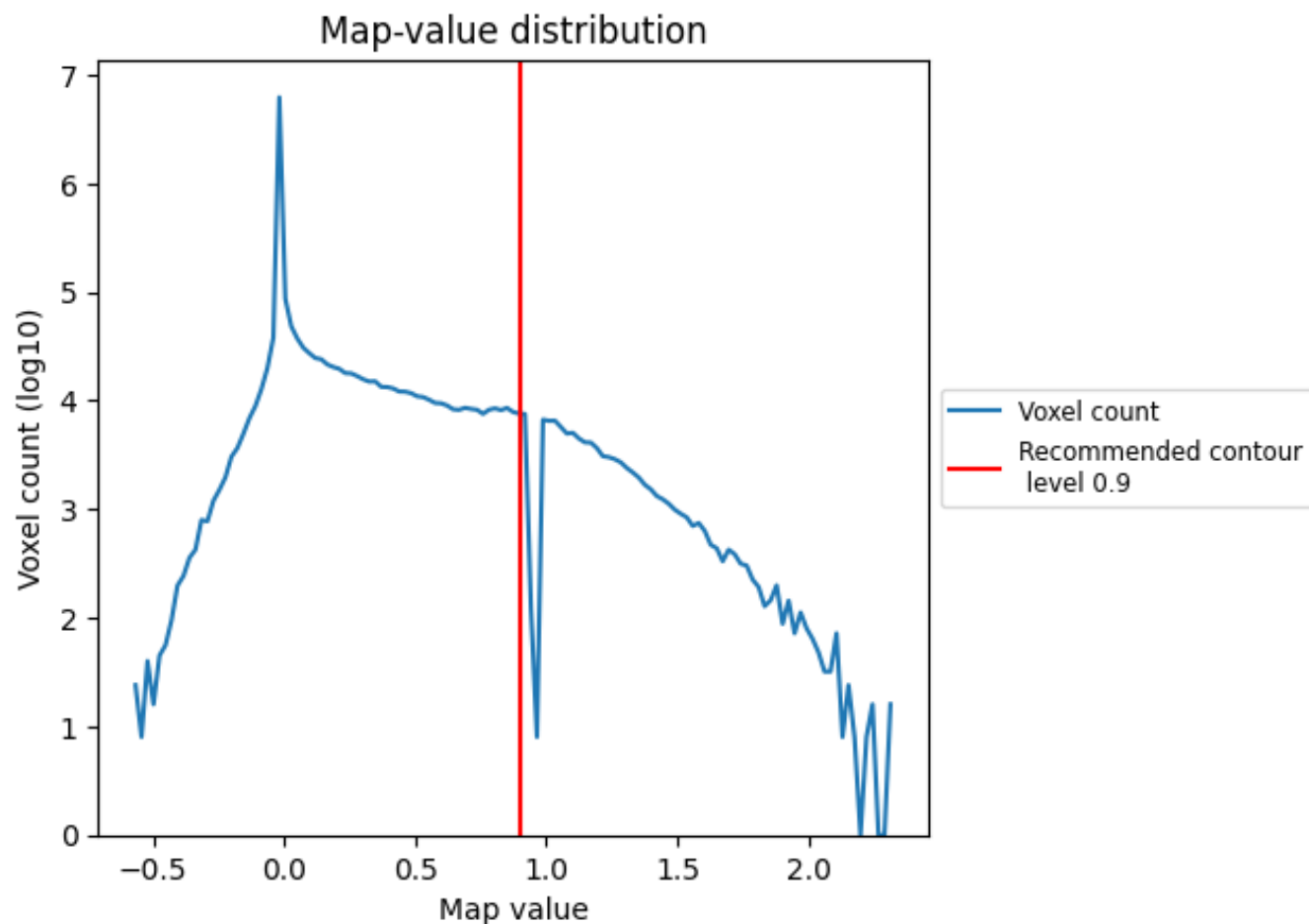
6.5 Mask visualisation

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

7 Map analysis [i](#)

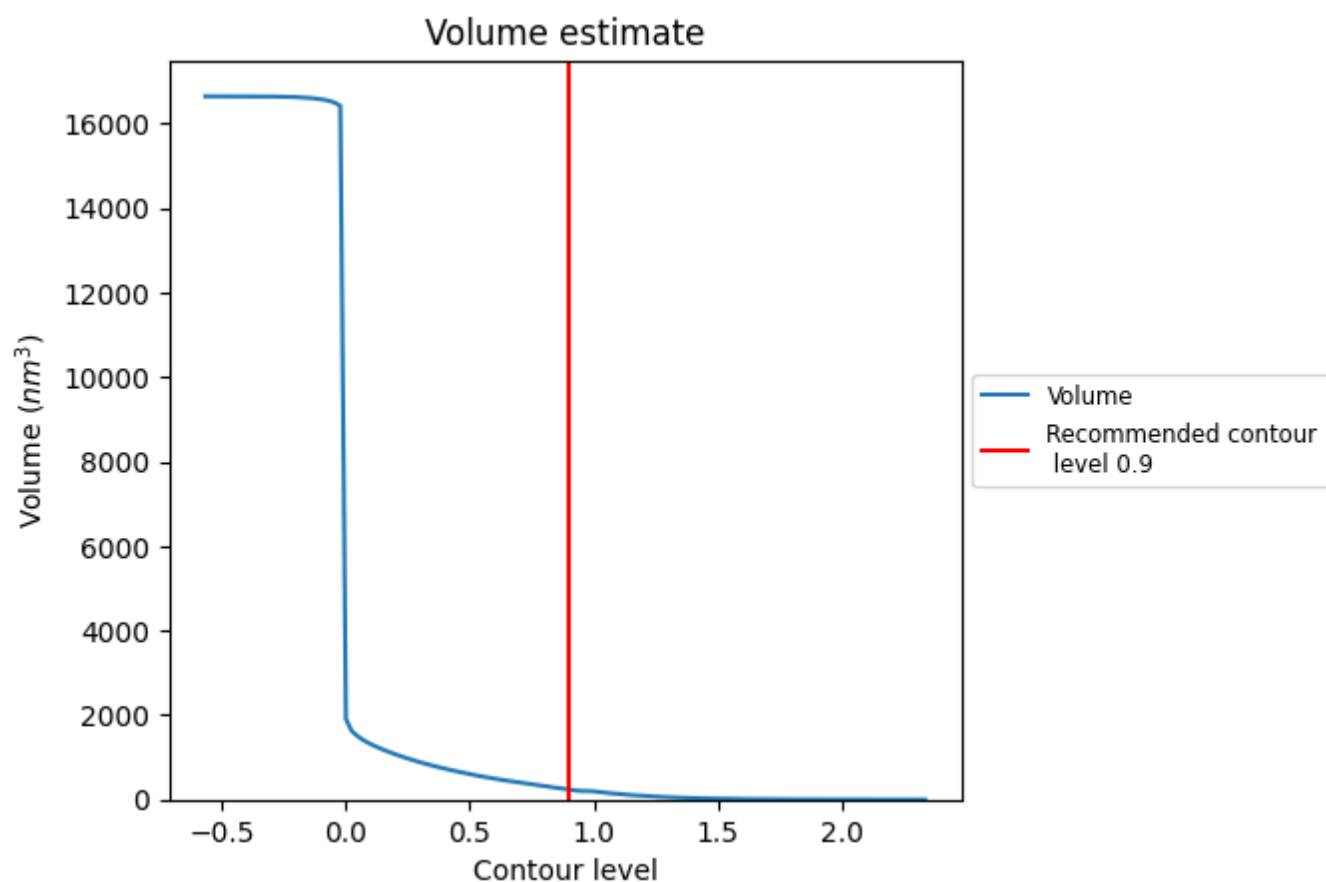
This section contains the results of statistical analysis of the map.

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.

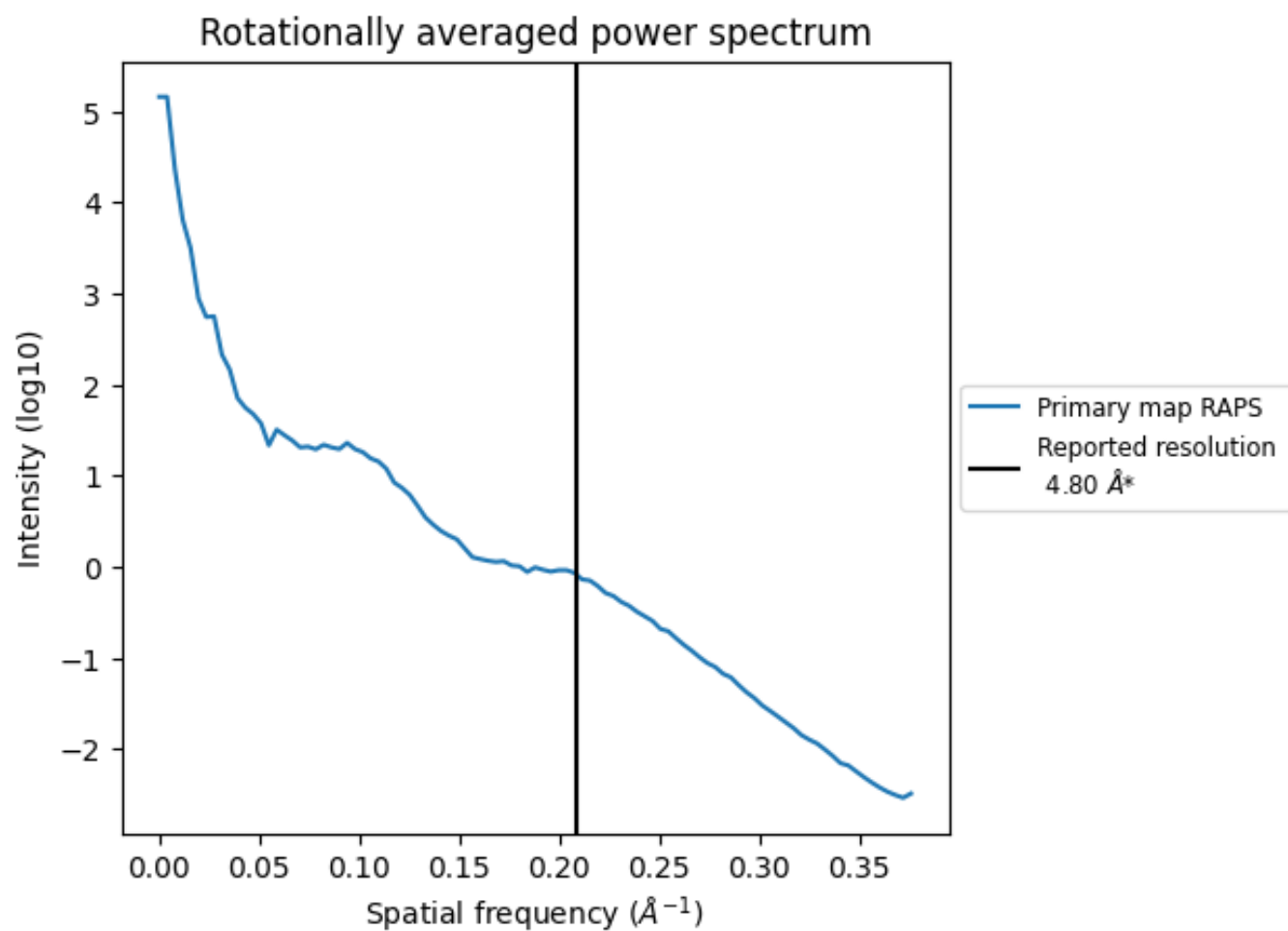
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 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 ⓘ



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

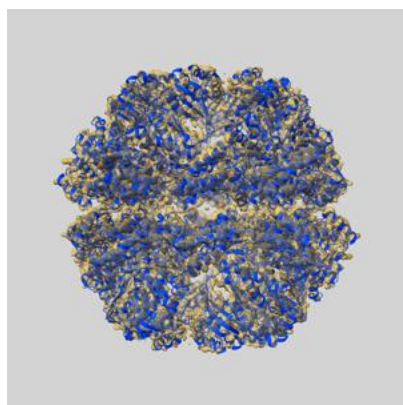
8 Fourier-Shell correlation

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

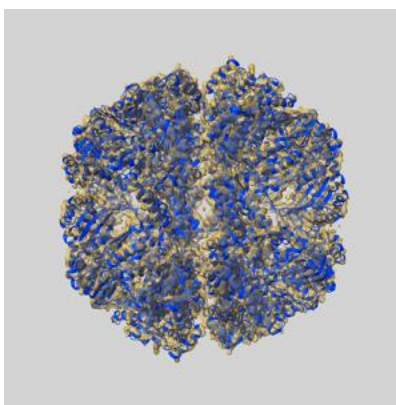
9 Map-model fit [i](#)

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](#).

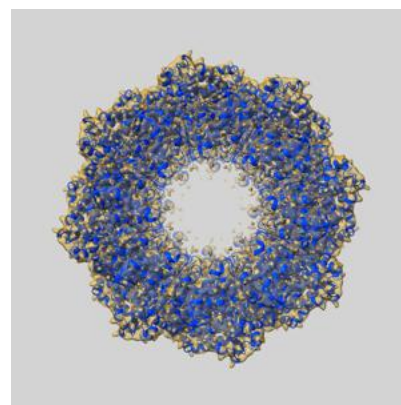
9.1 Map-model overlay [i](#)



X



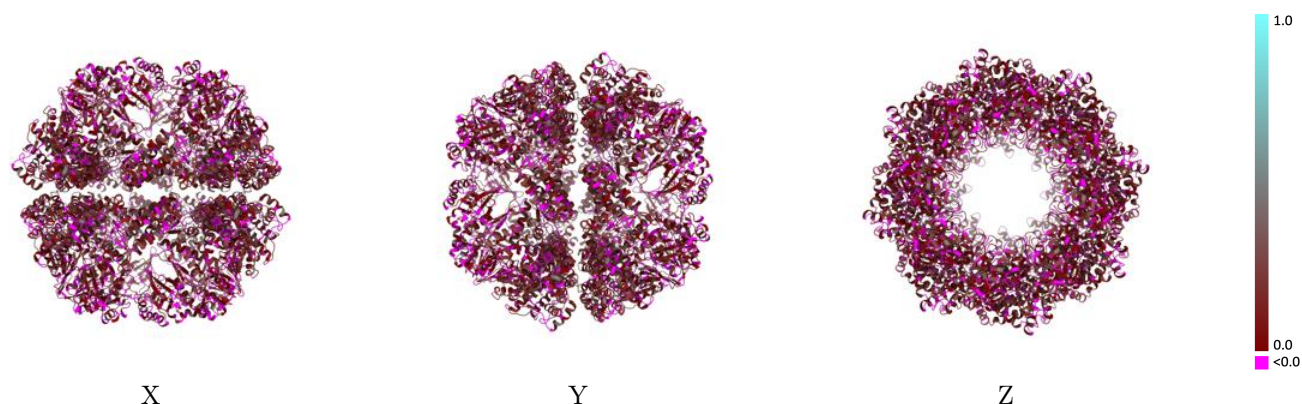
Y



Z

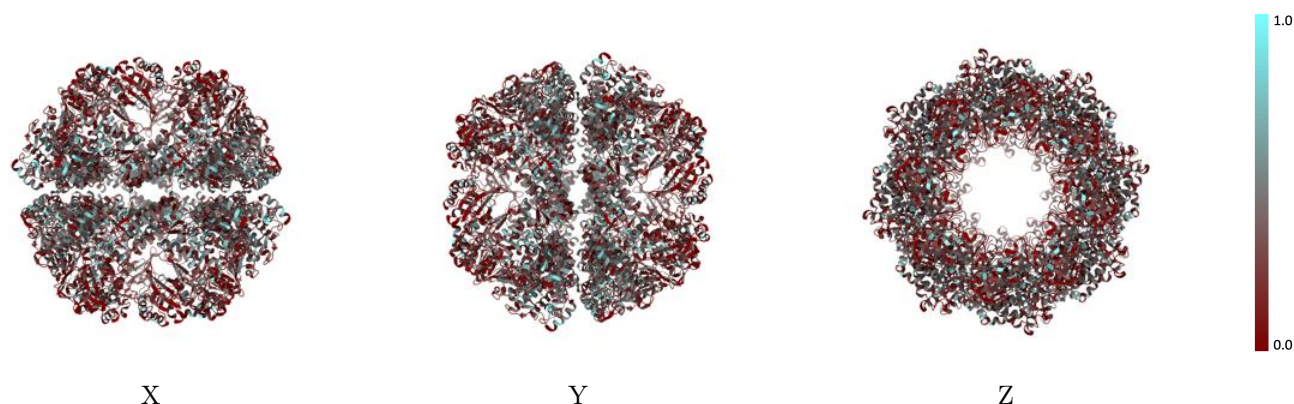
The images above show the 3D surface view of the map at the recommended contour level 0.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



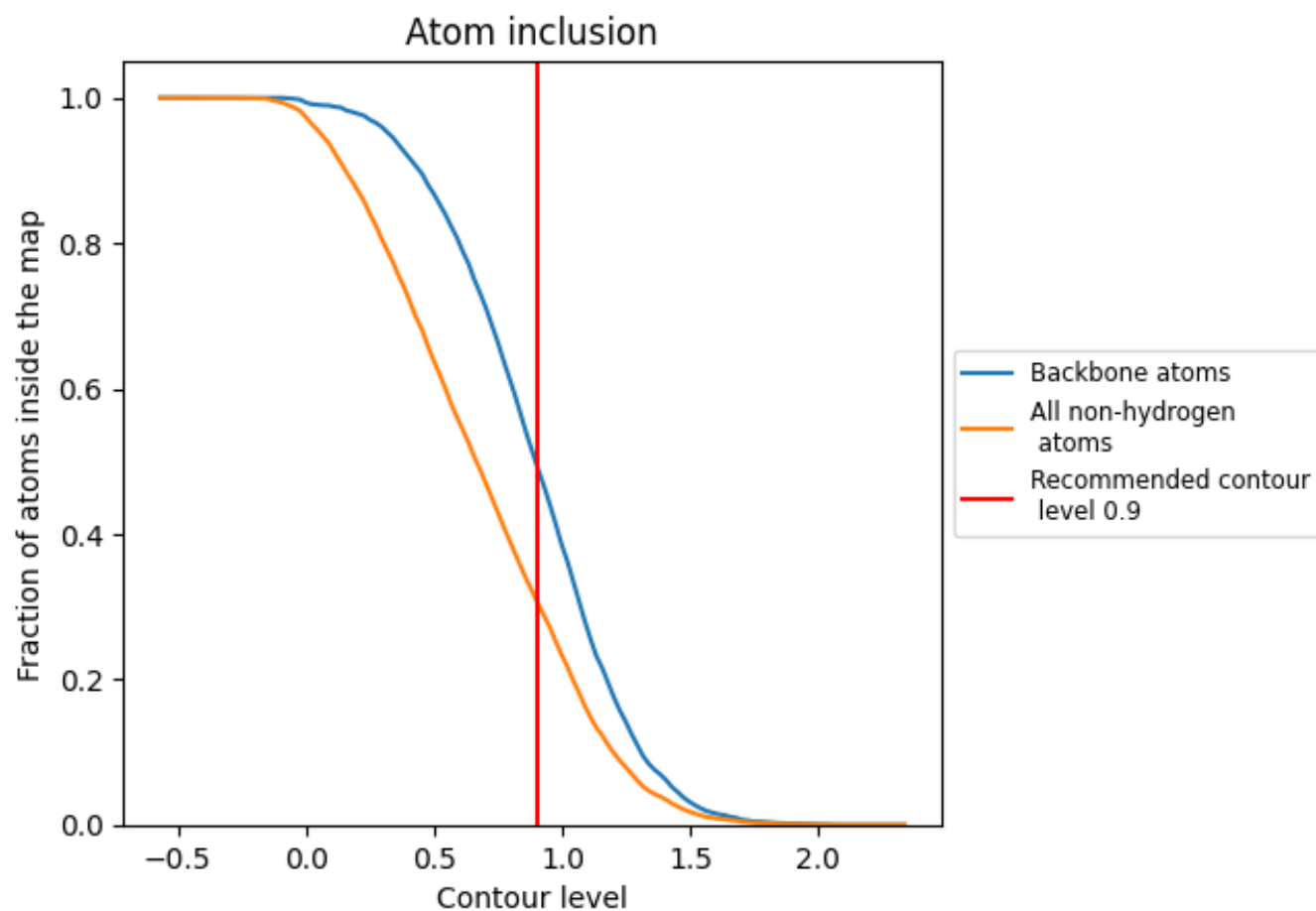
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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	<div><div></div></div> 0.3084	<div><div></div></div> 0.1090
A	<div><div></div></div> 0.3075	<div><div></div></div> 0.1090
B	<div><div></div></div> 0.3092	<div><div></div></div> 0.1100
C	<div><div></div></div> 0.3075	<div><div></div></div> 0.1090
D	<div><div></div></div> 0.3086	<div><div></div></div> 0.1090
E	<div><div></div></div> 0.3075	<div><div></div></div> 0.1090
F	<div><div></div></div> 0.3089	<div><div></div></div> 0.1100
G	<div><div></div></div> 0.3078	<div><div></div></div> 0.1100
H	<div><div></div></div> 0.3095	<div><div></div></div> 0.1100
I	<div><div></div></div> 0.3092	<div><div></div></div> 0.1100
J	<div><div></div></div> 0.3075	<div><div></div></div> 0.1090
K	<div><div></div></div> 0.3086	<div><div></div></div> 0.1100
L	<div><div></div></div> 0.3078	<div><div></div></div> 0.1100
M	<div><div></div></div> 0.3092	<div><div></div></div> 0.1100
N	<div><div></div></div> 0.3078	<div><div></div></div> 0.1090
O	<div><div></div></div> 0.3092	<div><div></div></div> 0.1090
P	<div><div></div></div> 0.3078	<div><div></div></div> 0.1080

1.0

0.0

<0.0