



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 10:38 PM UTC

PDB ID : 3JBL / pdb_00003jbl
EMDB ID : EMD-6458
Title : Cryo-EM Structure of the Activated NAIP2/NLRC4 Inflammasome Reveals Nucleated Polymerization
Authors : Zhang, L.; Chen, S.; Ruan, J.; Wu, J.; Tong, A.B.; Yin, Q.; Li, Y.; David, L.; Lu, A.; Wang, W.L.; Marks, C.; Ouyang, Q.; Zhang, X.; Mao, Y.; Wu, H.
Deposited on : 2015-09-05
Resolution : 4.70 Å(reported)

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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:

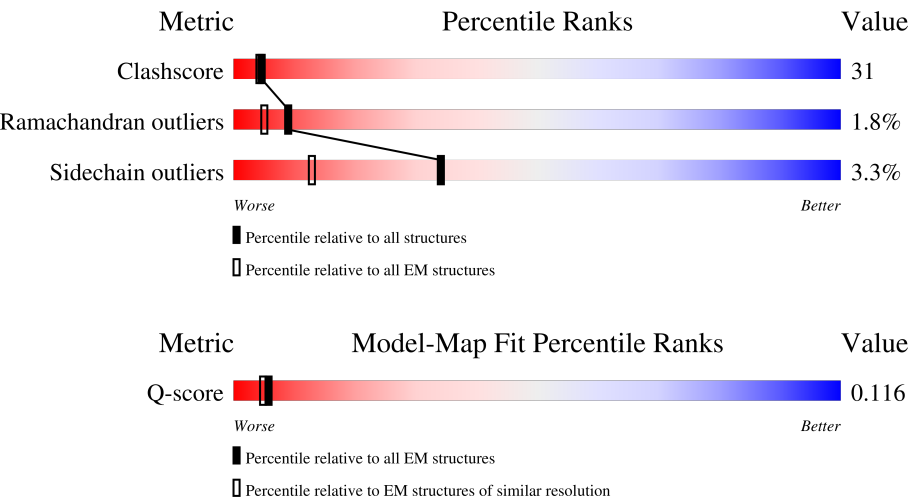
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.70 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.

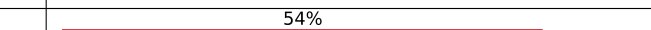
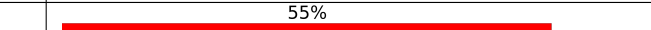


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	1989 (4.20 - 5.20)

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	932	55% 38%48%11%..
1	B	932	55% 38%48%11%..
1	C	932	55% 38%48%11%..
1	D	932	54% 38%48%11%..

Continued on next page...

Mol	Chain	Length	Quality of chain
1	E	932	
1	F	932	
1	G	932	
1	H	932	
1	I	932	
1	J	932	
1	K	932	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 80124 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.

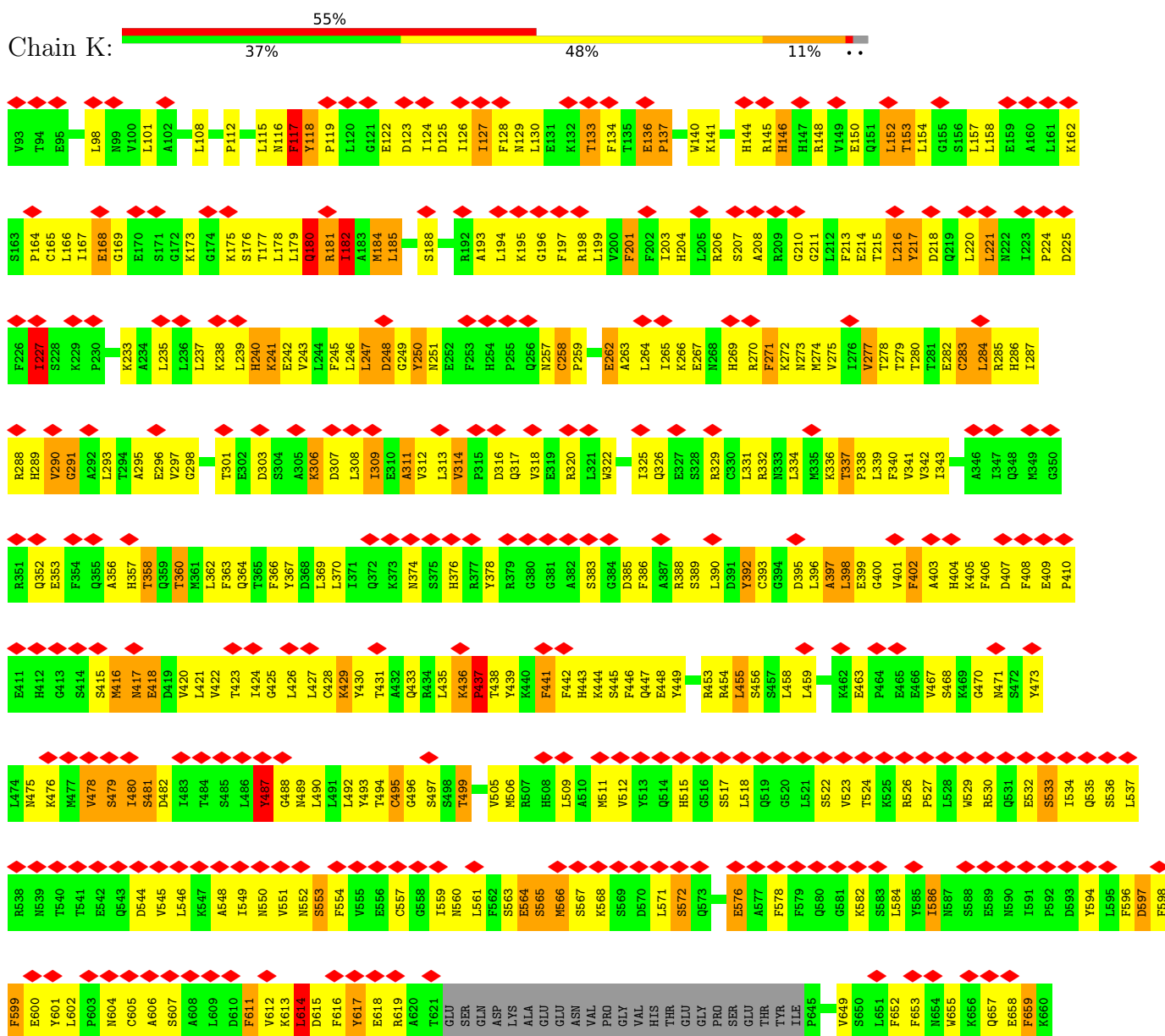
- Molecule 1 is a protein called NLR family CARD domain-containing protein 4.

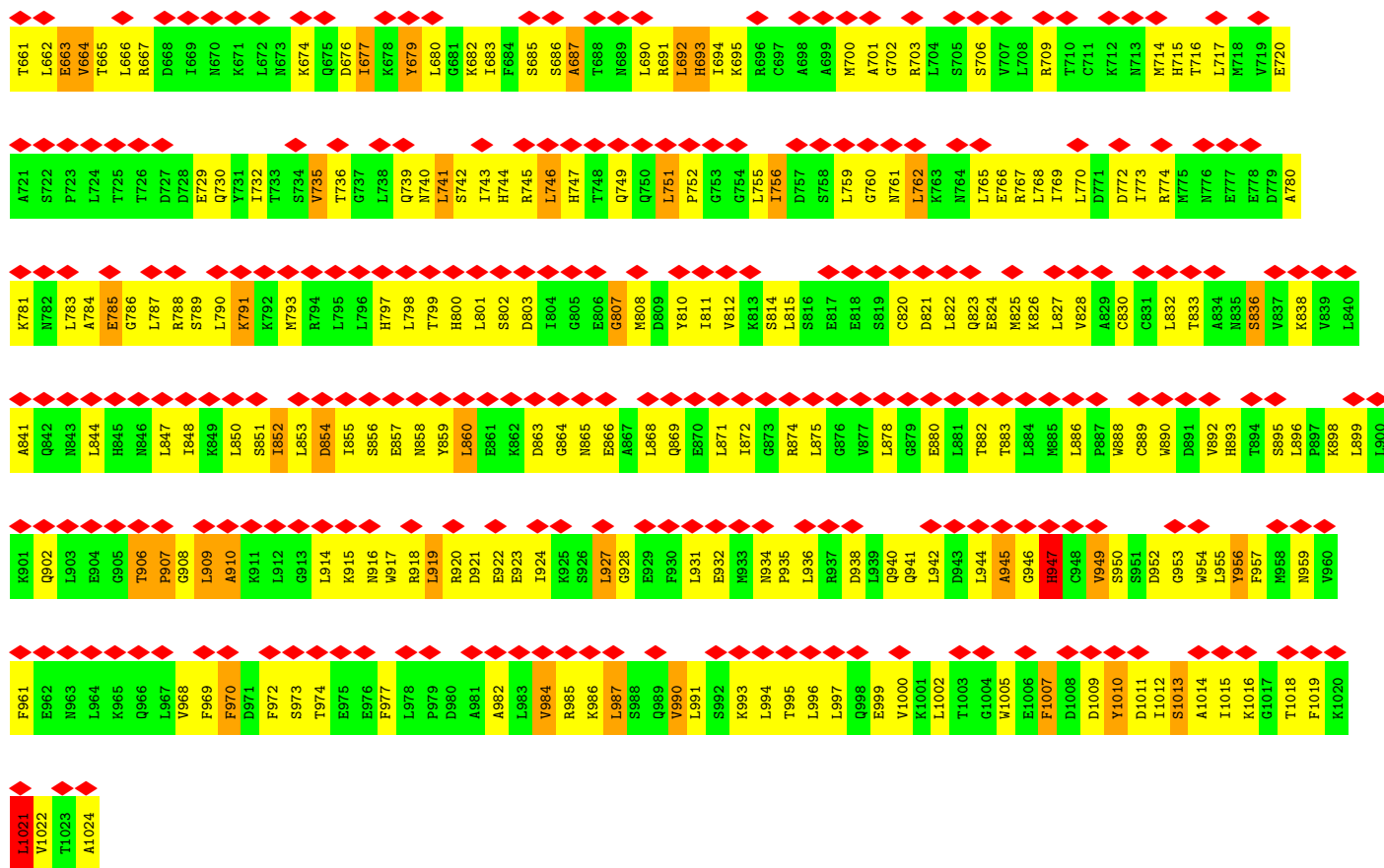
Mol	Chain	Residues	Atoms						AltConf	Trace
1	K	909	Total	C	N	O	P	S	0	0
			7284	4647	1233	1363	1	40		
1	A	909	Total	C	N	O	P	S	0	0
			7284	4647	1233	1363	1	40		
1	B	909	Total	C	N	O	P	S	0	0
			7284	4647	1233	1363	1	40		
1	C	909	Total	C	N	O	P	S	0	0
			7284	4647	1233	1363	1	40		
1	D	909	Total	C	N	O	P	S	0	0
			7284	4647	1233	1363	1	40		
1	E	909	Total	C	N	O	P	S	0	0
			7284	4647	1233	1363	1	40		
1	F	909	Total	C	N	O	P	S	0	0
			7284	4647	1233	1363	1	40		
1	G	909	Total	C	N	O	P	S	0	0
			7284	4647	1233	1363	1	40		
1	H	909	Total	C	N	O	P	S	0	0
			7284	4647	1233	1363	1	40		
1	I	909	Total	C	N	O	P	S	0	0
			7284	4647	1233	1363	1	40		
1	J	909	Total	C	N	O	P	S	0	0
			7284	4647	1233	1363	1	40		

3 Residue-property plots

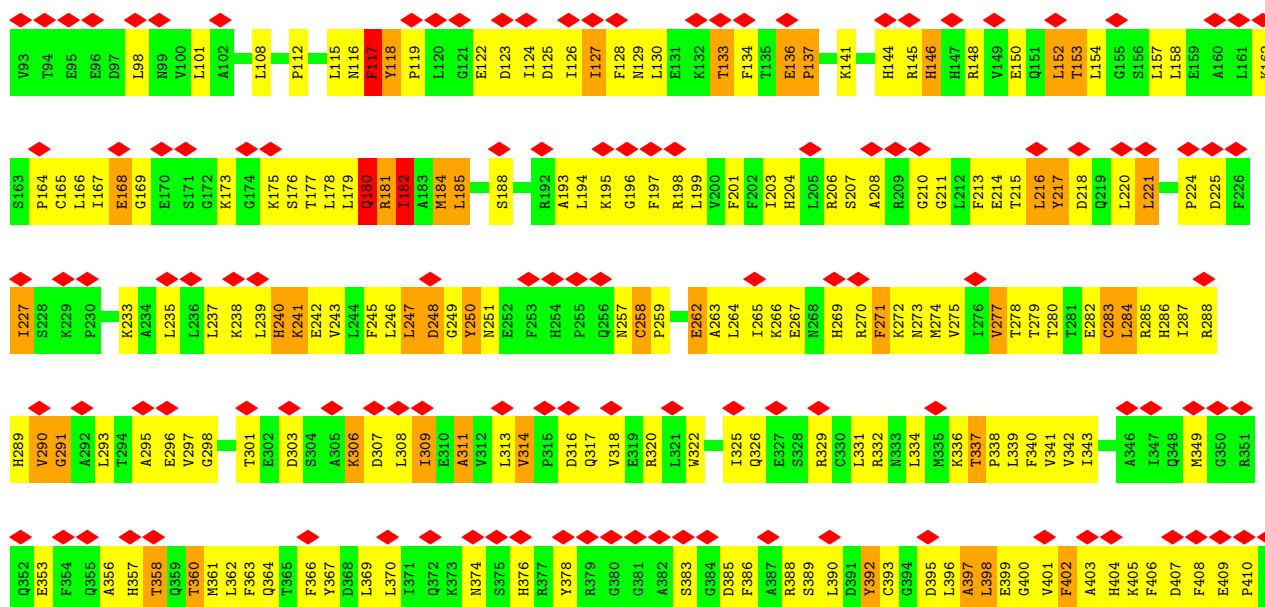
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: NLR family CARD domain-containing protein 4





• Molecule 1: NLR family CARD domain-containing protein 4

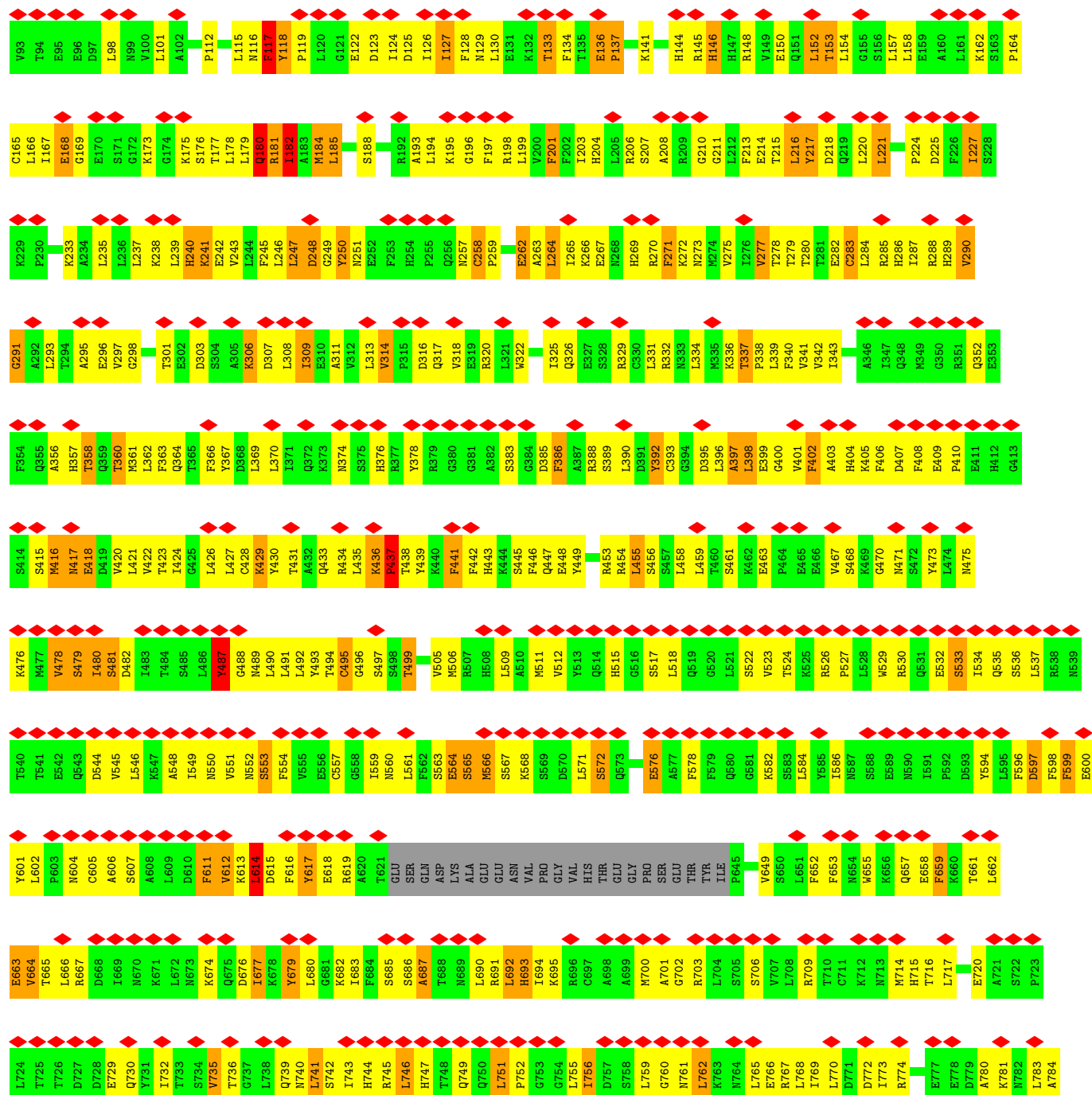


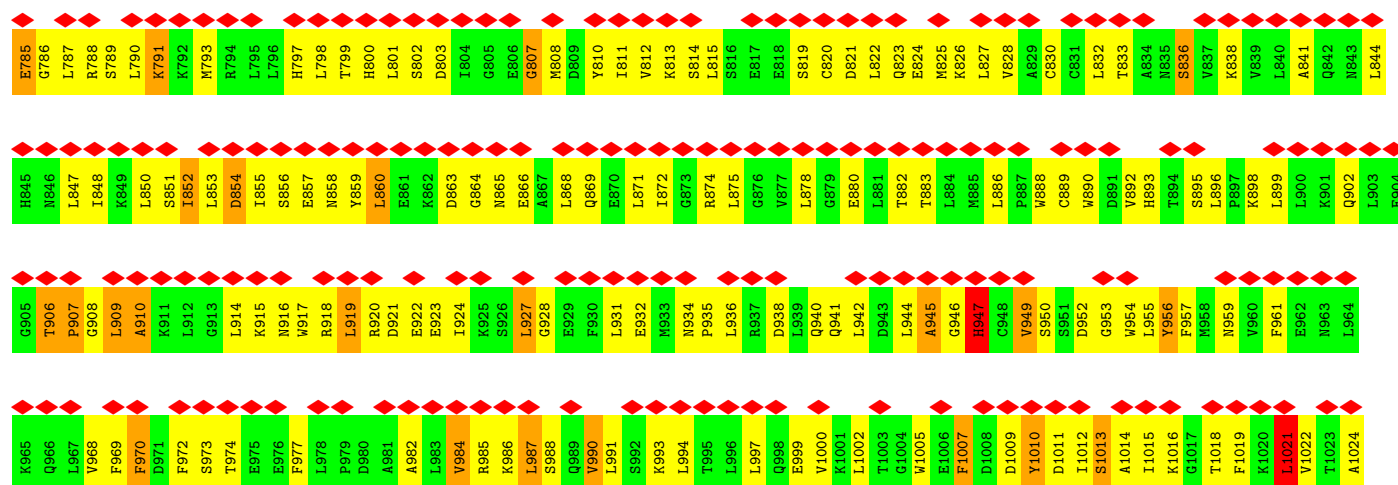




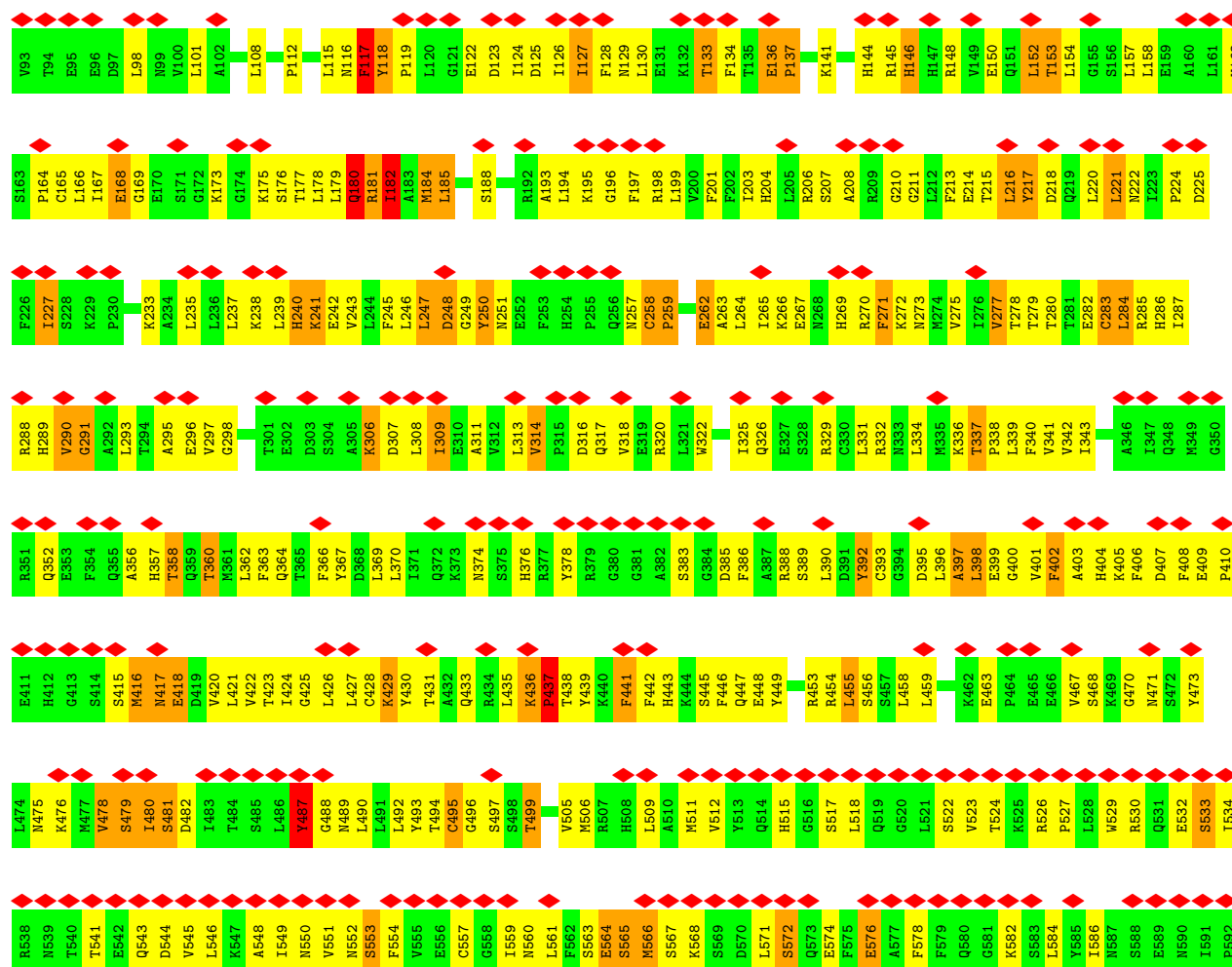
• Molecule 1: NLR family CARD domain-containing protein 4

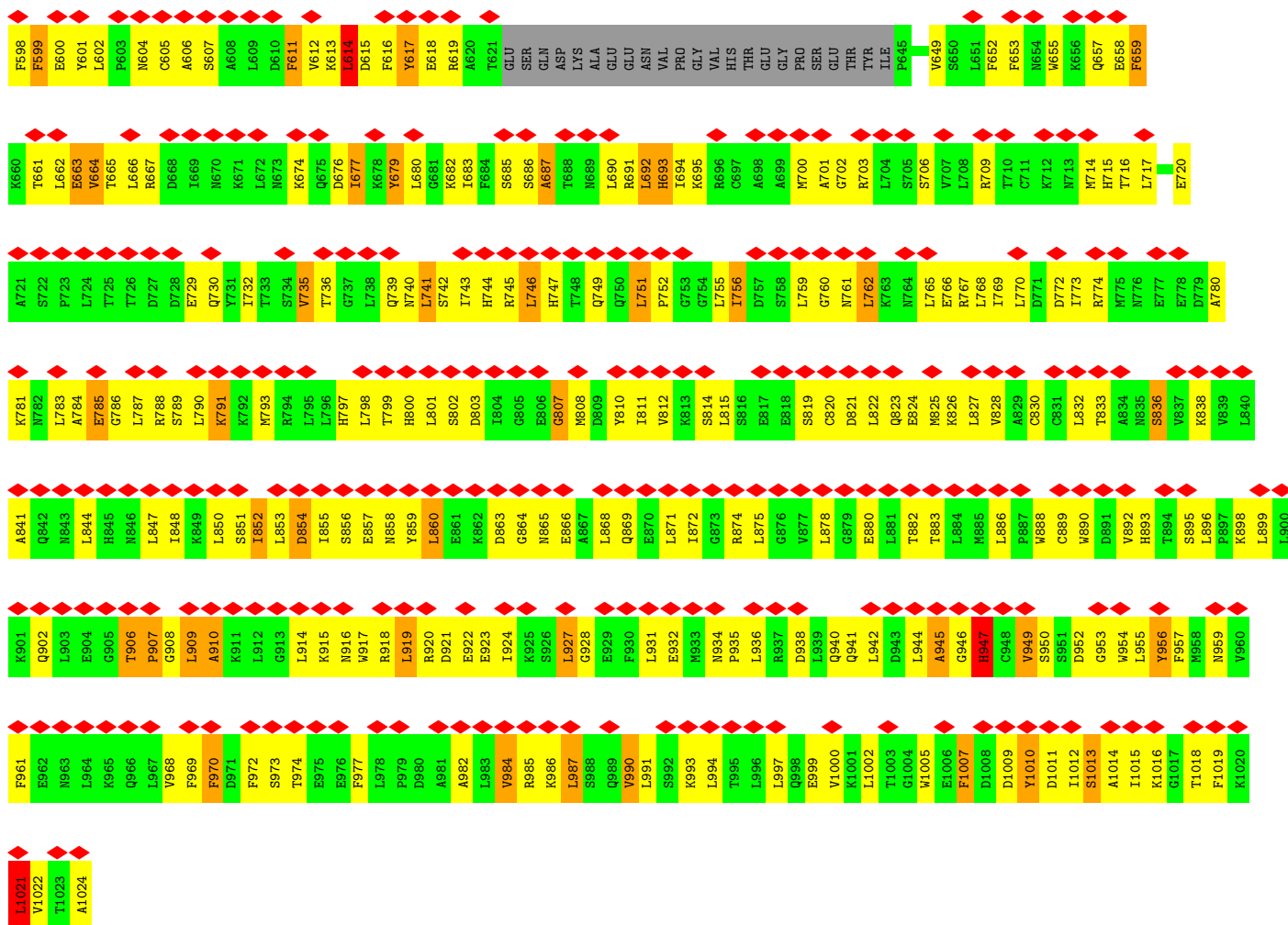
Chain C: 55% 38% 48% 11% ..



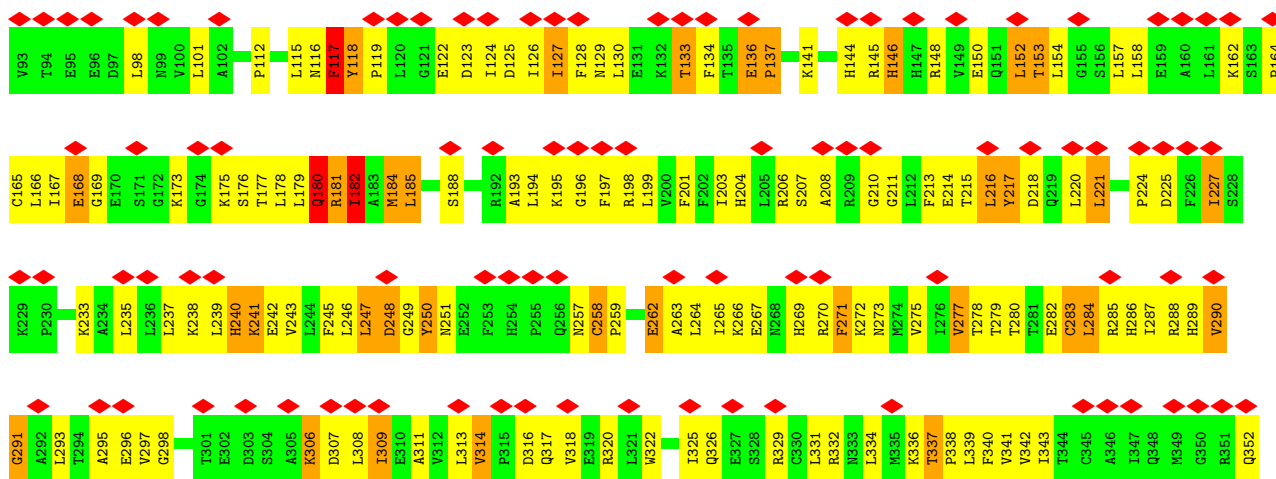


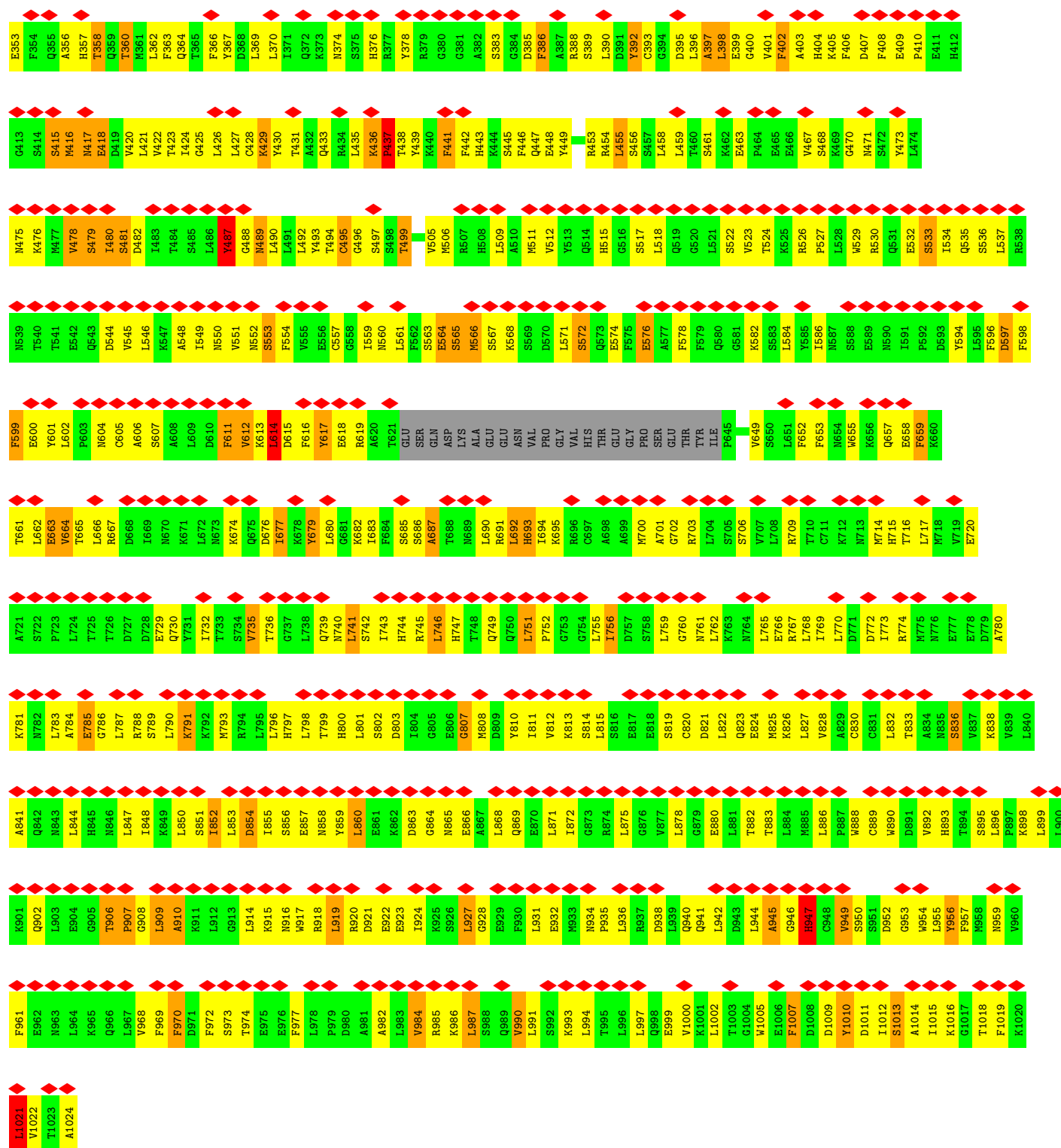
• Molecule 1: NLR family CARD domain-containing protein 4





• Molecule 1: NLR family CARD domain-containing protein 4





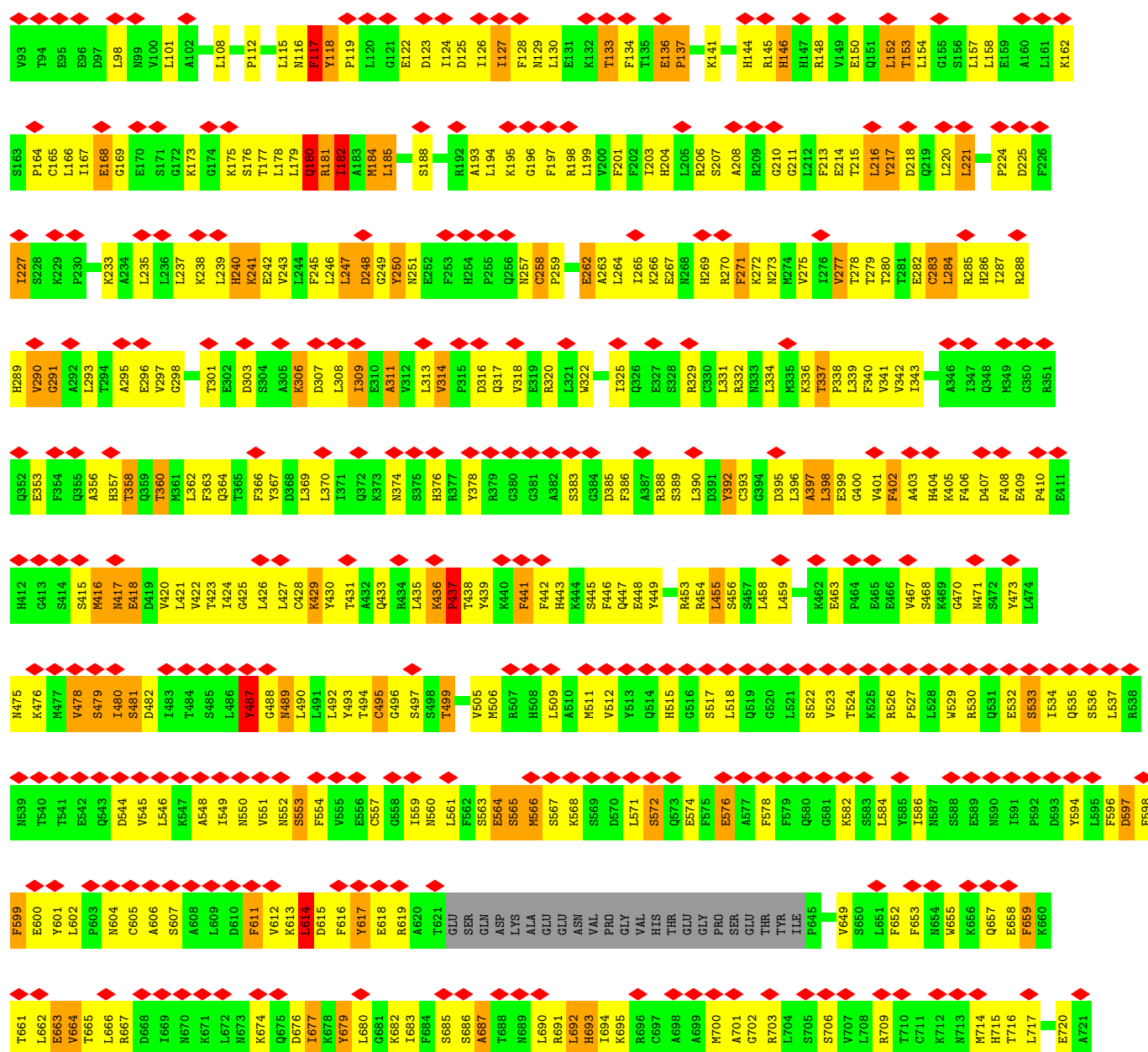
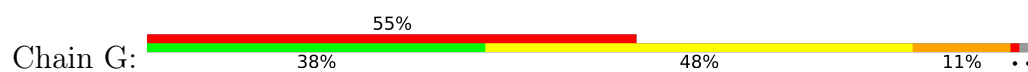
- Molecule 1: NLR family CARD domain-containing protein 4

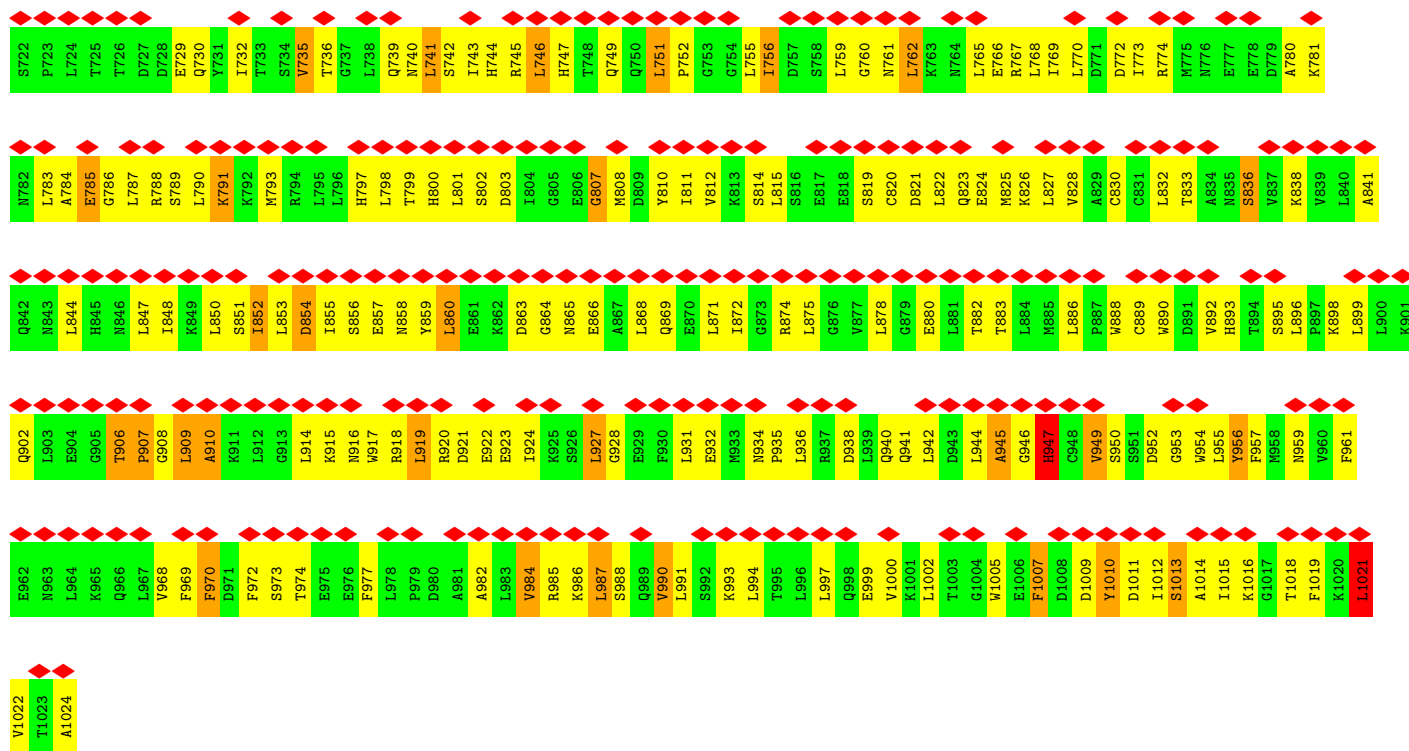




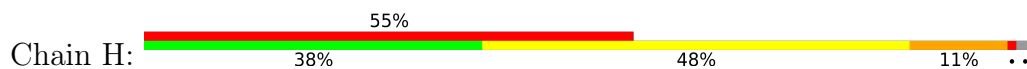


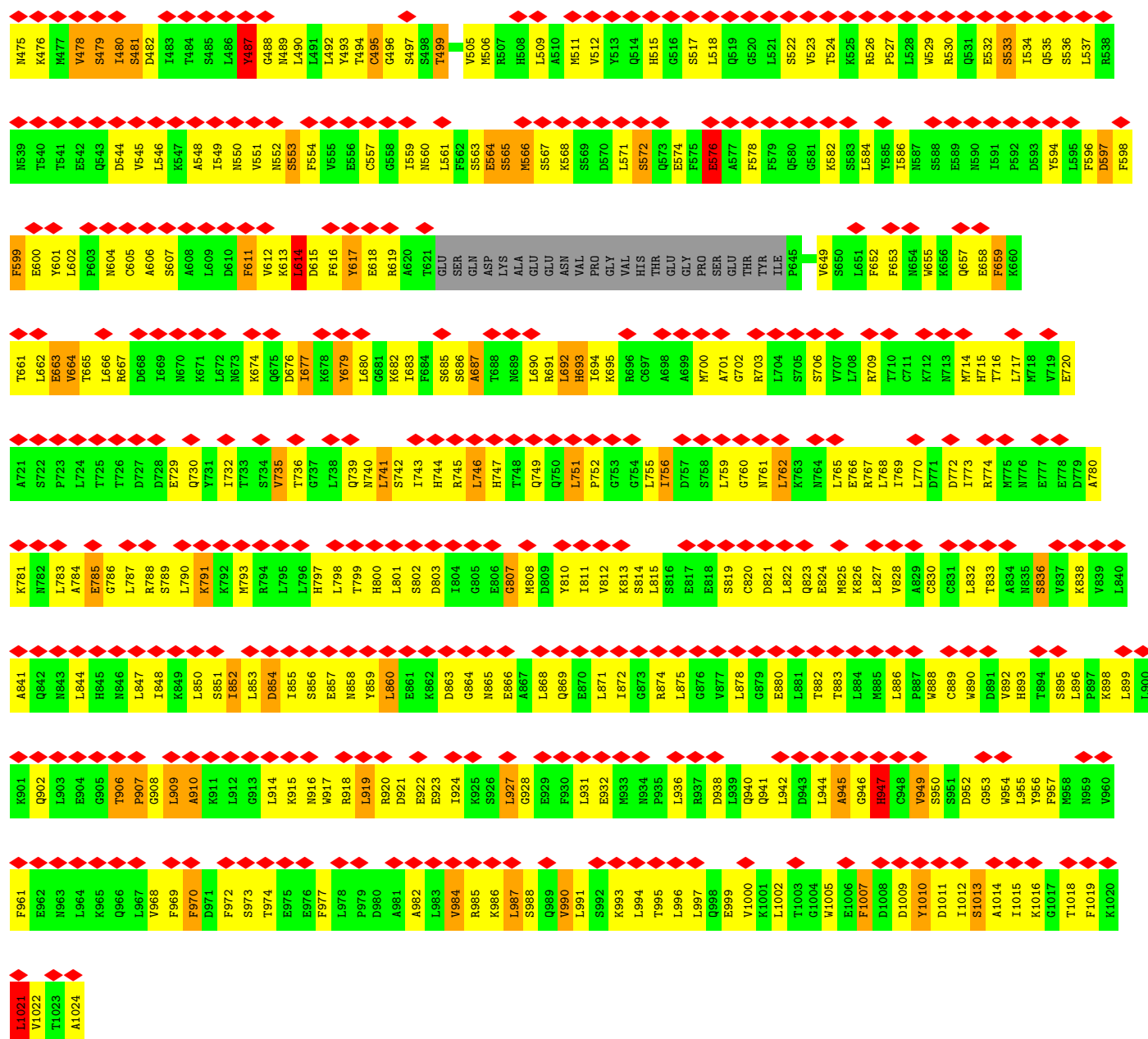
• Molecule 1: NLR family CARD domain-containing protein 4



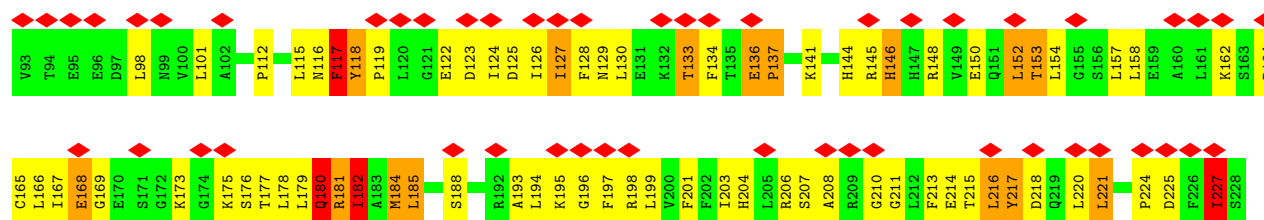


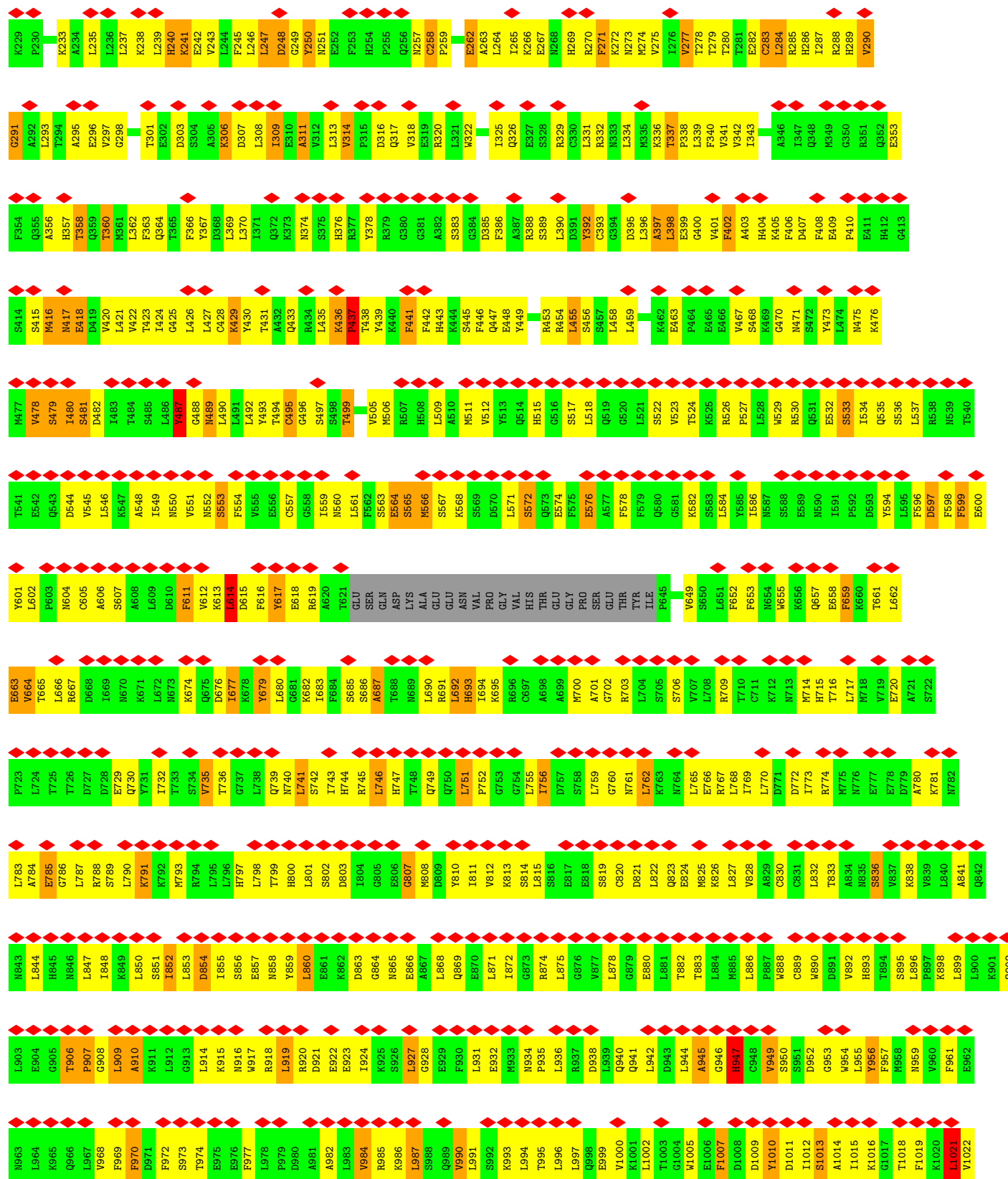
• Molecule 1: NLR family CARD domain-containing protein 4





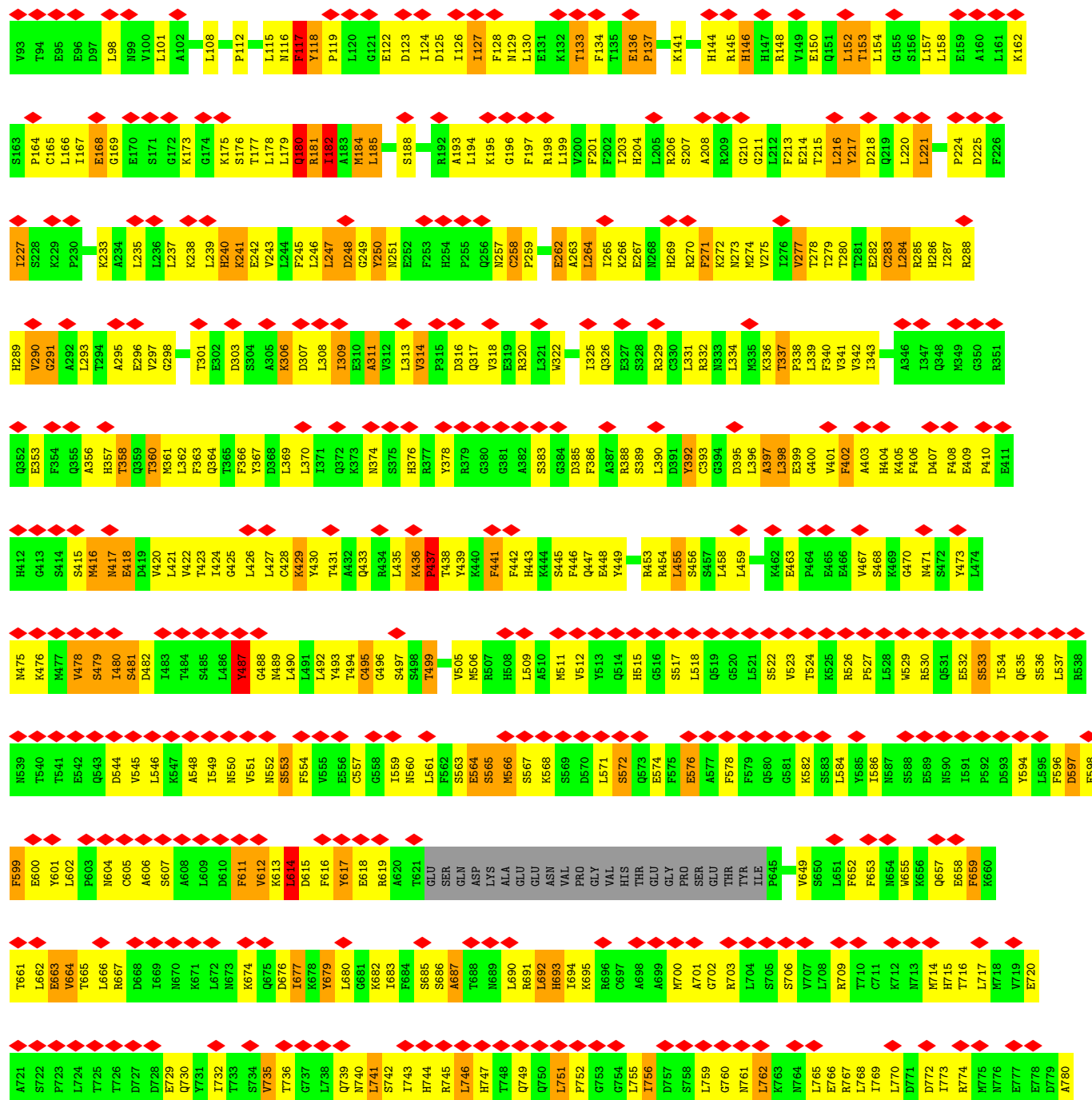
• Molecule 1: NLR family CARD domain-containing protein 4







• Molecule 1: NLR family CARD domain-containing protein 4



L1021	F961	K901	A941	K781
V1022	E962	Q902	Q842	W782
T1023	N963	L903	N963	L783
A1024	L964	E904	L844	A784
	K965	G905	H845	E785
	Q966	T906	N846	G786
	L967	P907	L847	L787
	V968	G908	I848	R788
	F969	L909	K849	S789
	F970	A910	L850	L790
	D971	K911	S851	K791
	F972	L912	I852	K792
	S973	G913	L853	W793
	T974	L914	D854	M794
	E975	K915	L855	L795
	E976	N916	S856	L796
	F977	W917	E857	H797
	L978	R918	E857	L798
	P979	L919	N858	T799
	D980	R920	Y859	H800
	A981	D921	L860	L801
	A982	E922	E861	S802
	L983	E923	K862	D803
	V984	I924	D863	I804
	K985	K925	G864	G905
	K986	S926	N865	E906
	L987	G927	E866	G807
	S988	G928	A867	M808
	Q989	E929	L868	D809
	V990	F930	Q869	Y810
	L991	L931	E870	I811
	S992	E932	L871	V812
	K993	M933	I872	K813
	L994	N934	G873	S814
	T995	P935	R874	L815
	L996	L936	L875	S816
	L997	R937	G876	E817
	Q998	D938	W877	E818
	E999	L939	L878	S819
	V1000	Q940	L878	C820
	K1001	Q941	G879	D821
	L1002	L942	E880	L822
	T1003	D943	L881	Q823
	G1004	L944	T882	E824
	W1005	A945	T883	M825
	F1007	G946	L884	K826
	D1008	H947	M885	L827
	D1009	C948	L886	V828
	Y1010	V949	P887	A829
	D1011	S950	W888	C830
	L1012	S951	C889	C831
	S1013	D952	W890	L832
	A1014	G953	D891	T833
	I1015	W954	V892	A834
	K1016	L955	H893	N835
	G1017	Y956	T894	S836
	T1018	P957	S895	V837
	F1019	N959	L896	K838
	K1020	V960	P897	V839
			K898	L840
			L899	
			L900	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C11	Depositor
Number of particles used	75114	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Wiener-type filter	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	28736	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor
Maximum map value	0.012	Depositor
Minimum map value	-0.008	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0045	Depositor
Map size ($\text{\AA}$)	385.28, 385.28, 385.28	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.86, 0.86, 0.86	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SEP

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	0.52	0/7412	1.55	171/10004 (1.7%)
1	B	0.52	0/7412	1.55	170/10004 (1.7%)
1	C	0.52	0/7412	1.55	166/10004 (1.7%)
1	D	0.52	0/7412	1.55	168/10004 (1.7%)
1	E	0.52	0/7412	1.55	169/10004 (1.7%)
1	F	0.52	0/7412	1.55	169/10004 (1.7%)
1	G	0.52	0/7412	1.55	169/10004 (1.7%)
1	H	0.52	0/7412	1.55	169/10004 (1.7%)
1	I	0.52	0/7412	1.55	169/10004 (1.7%)
1	J	0.52	0/7412	1.55	170/10004 (1.7%)
1	K	0.52	0/7412	1.55	167/10004 (1.7%)
All	All	0.52	0/81532	1.55	1857/110044 (1.7%)

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	2
1	B	0	2
1	C	0	2
1	D	0	2
1	E	0	2
1	F	0	2
1	G	0	2
1	H	0	2
1	I	0	2
1	J	0	2
1	K	0	2
All	All	0	22

There are no bond length outliers.

The worst 5 of 1857 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	280	THR	N-CA-C	-13.53	89.11	109.81
1	G	280	THR	N-CA-C	-13.53	89.11	109.81
1	K	280	THR	N-CA-C	-13.52	89.12	109.81
1	B	280	THR	N-CA-C	-13.52	89.12	109.81
1	C	280	THR	N-CA-C	-13.52	89.13	109.81

There are no chirality outliers.

5 of 22 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	117	PHE	Peptide
1	A	441	PHE	Peptide
1	B	117	PHE	Peptide
1	K	117	PHE	Peptide
1	K	441	PHE	Peptide

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	7284	0	7329	458	0
1	B	7284	0	7329	455	0
1	C	7284	0	7329	461	0
1	D	7284	0	7329	458	0
1	E	7284	0	7329	455	0
1	F	7284	0	7329	458	0
1	G	7284	0	7329	454	0
1	H	7284	0	7329	460	0
1	I	7284	0	7329	459	0
1	J	7284	0	7329	471	0
1	K	7284	0	7329	469	0
All	All	80124	0	80619	4922	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 31.

The worst 5 of 4922 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:K:125:ASP:H	1:J:433:GLN:HG2	1.28	0.95
1:A:433:GLN:HG2	1:B:125:ASP:H	1.33	0.94
1:F:433:GLN:HG2	1:G:125:ASP:H	1.33	0.93
1:G:433:GLN:HG2	1:H:125:ASP:H	1.33	0.93
1:D:433:GLN:HG2	1:E:125:ASP:H	1.34	0.93

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	904/932 (97%)	823 (91%)	65 (7%)	16 (2%)	6	33
1	B	904/932 (97%)	823 (91%)	65 (7%)	16 (2%)	6	33
1	C	904/932 (97%)	822 (91%)	66 (7%)	16 (2%)	6	33
1	D	904/932 (97%)	823 (91%)	65 (7%)	16 (2%)	6	33
1	E	904/932 (97%)	823 (91%)	65 (7%)	16 (2%)	6	33
1	F	904/932 (97%)	823 (91%)	65 (7%)	16 (2%)	6	33
1	G	904/932 (97%)	823 (91%)	65 (7%)	16 (2%)	6	33
1	H	904/932 (97%)	823 (91%)	65 (7%)	16 (2%)	6	33
1	I	904/932 (97%)	822 (91%)	66 (7%)	16 (2%)	6	33
1	J	904/932 (97%)	822 (91%)	66 (7%)	16 (2%)	6	33
1	K	904/932 (97%)	823 (91%)	65 (7%)	16 (2%)	6	33
All	All	9944/10252 (97%)	9050 (91%)	718 (7%)	176 (2%)	9	33

5 of 176 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	K	146	HIS
1	K	241	LYS
1	K	272	LYS
1	K	442	PHE
1	K	481	SER

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	810/830 (98%)	783 (97%)	27 (3%)	33	55
1	B	810/830 (98%)	783 (97%)	27 (3%)	33	55
1	C	810/830 (98%)	783 (97%)	27 (3%)	33	55
1	D	810/830 (98%)	783 (97%)	27 (3%)	33	55
1	E	810/830 (98%)	782 (96%)	28 (4%)	32	54
1	F	810/830 (98%)	783 (97%)	27 (3%)	33	55
1	G	810/830 (98%)	783 (97%)	27 (3%)	33	55
1	H	810/830 (98%)	783 (97%)	27 (3%)	33	55
1	I	810/830 (98%)	783 (97%)	27 (3%)	33	55
1	J	810/830 (98%)	783 (97%)	27 (3%)	33	55
1	K	810/830 (98%)	783 (97%)	27 (3%)	33	55
All	All	8910/9130 (98%)	8612 (97%)	298 (3%)	34	55

5 of 298 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	614	LEU
1	J	659	PHE
1	H	883	THR
1	I	663	GLU
1	C	663	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 132 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	715	HIS
1	J	273	ASN
1	J	869	GLN
1	D	273	ASN
1	C	998	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

11 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	SEP	J	533	1	8,9,10	1.60	1 (12%)	7,12,14	1.00	0
1	SEP	I	533	1	8,9,10	1.60	1 (12%)	7,12,14	1.00	0
1	SEP	C	533	1	8,9,10	1.60	1 (12%)	7,12,14	1.00	0
1	SEP	H	533	1	8,9,10	1.60	1 (12%)	7,12,14	0.99	0
1	SEP	B	533	1	8,9,10	1.61	1 (12%)	7,12,14	0.99	0
1	SEP	D	533	1	8,9,10	1.59	1 (12%)	7,12,14	0.99	0
1	SEP	E	533	1	8,9,10	1.60	1 (12%)	7,12,14	0.99	0
1	SEP	K	533	1	8,9,10	1.60	1 (12%)	7,12,14	0.99	0
1	SEP	F	533	1	8,9,10	1.60	1 (12%)	7,12,14	0.98	0
1	SEP	G	533	1	8,9,10	1.60	1 (12%)	7,12,14	0.98	0
1	SEP	A	533	1	8,9,10	1.60	1 (12%)	7,12,14	0.99	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SEP	J	533	1	-	0/6/8/10	-
1	SEP	I	533	1	-	0/6/8/10	-
1	SEP	C	533	1	-	0/6/8/10	-
1	SEP	H	533	1	-	0/6/8/10	-
1	SEP	B	533	1	-	0/6/8/10	-
1	SEP	D	533	1	-	0/6/8/10	-
1	SEP	E	533	1	-	0/6/8/10	-
1	SEP	K	533	1	-	0/6/8/10	-
1	SEP	F	533	1	-	0/6/8/10	-
1	SEP	G	533	1	-	0/6/8/10	-
1	SEP	A	533	1	-	0/6/8/10	-

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	533	SEP	P-O1P	3.54	1.61	1.50
1	F	533	SEP	P-O1P	3.54	1.61	1.50
1	C	533	SEP	P-O1P	3.54	1.61	1.50
1	B	533	SEP	P-O1P	3.53	1.61	1.50
1	K	533	SEP	P-O1P	3.53	1.61	1.50

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

11 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	J	533	SEP	2	0
1	I	533	SEP	2	0
1	C	533	SEP	2	0
1	H	533	SEP	2	0
1	B	533	SEP	2	0
1	D	533	SEP	2	0
1	E	533	SEP	2	0
1	K	533	SEP	2	0
1	F	533	SEP	2	0
1	G	533	SEP	2	0
1	A	533	SEP	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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.

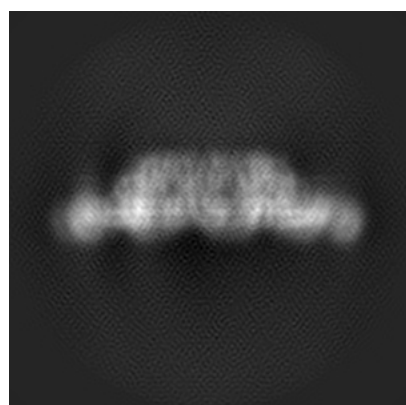
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6458. These allow visual inspection of the internal detail of the map and identification of artifacts.

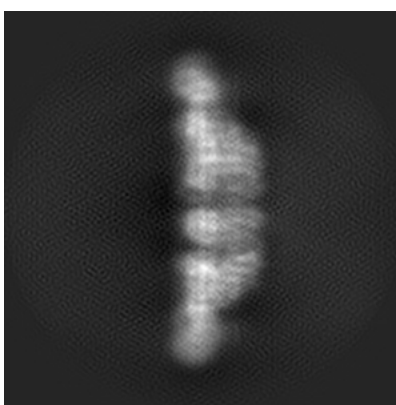
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

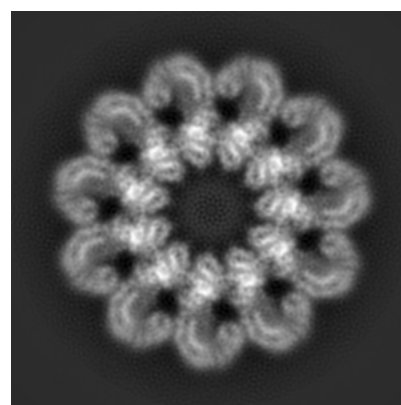
6.1.1 Primary map



X



Y

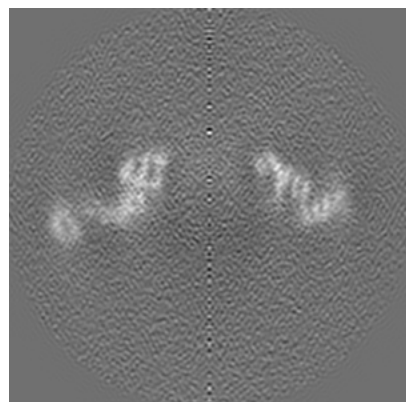


Z

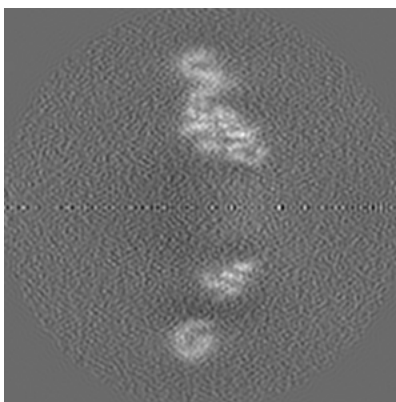
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

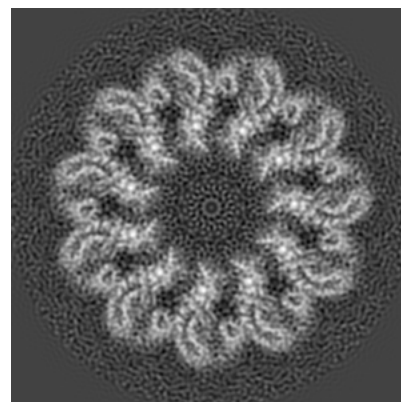
6.2.1 Primary map



X Index: 224



Y Index: 224

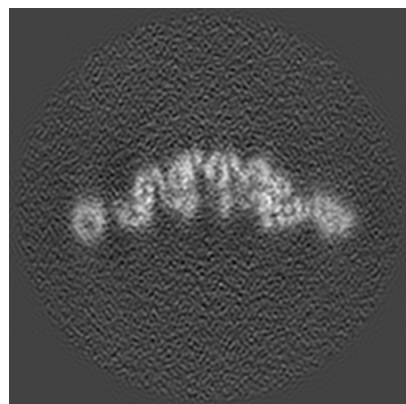


Z Index: 224

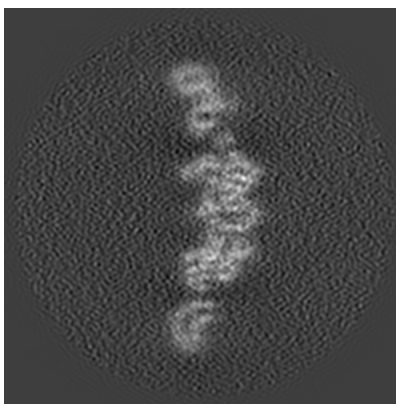
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

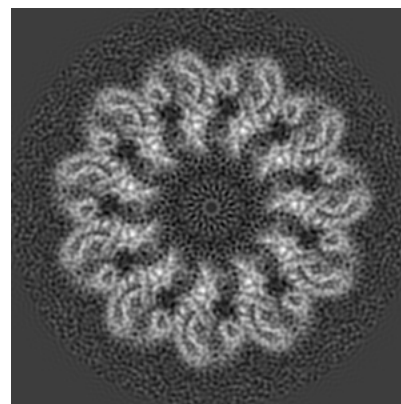
6.3.1 Primary map



X Index: 157



Y Index: 148

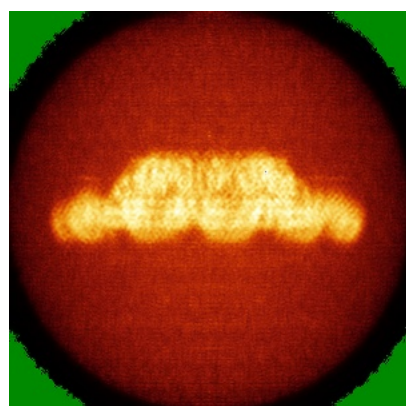


Z Index: 223

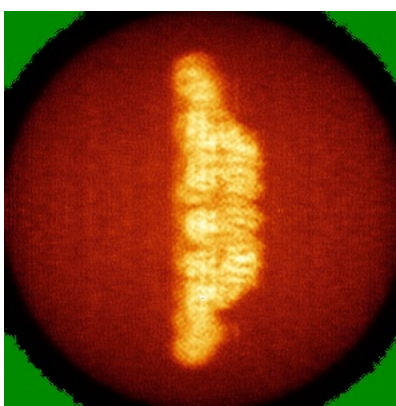
The images above show the largest variance slices of the map in three orthogonal directions.

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

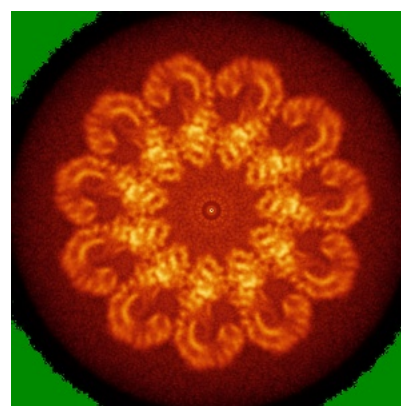
6.4.1 Primary map



X



Y

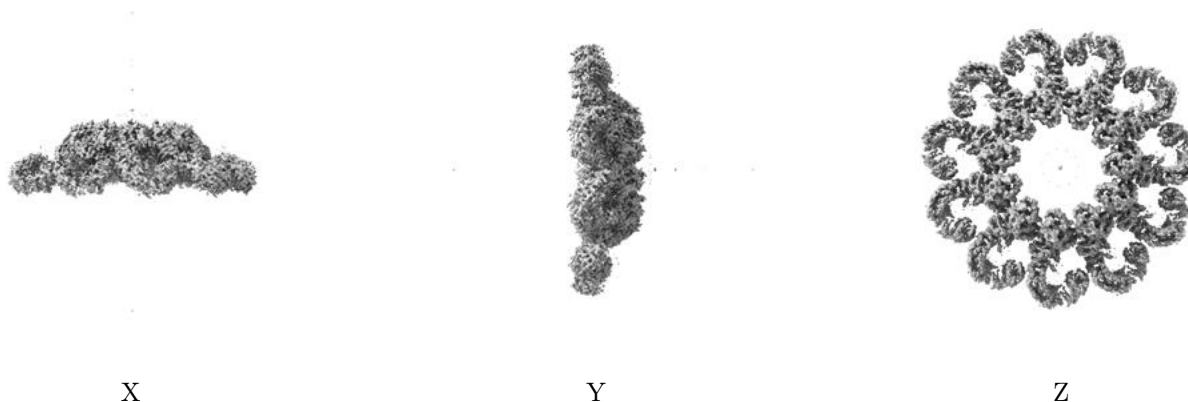


Z

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 0.0045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

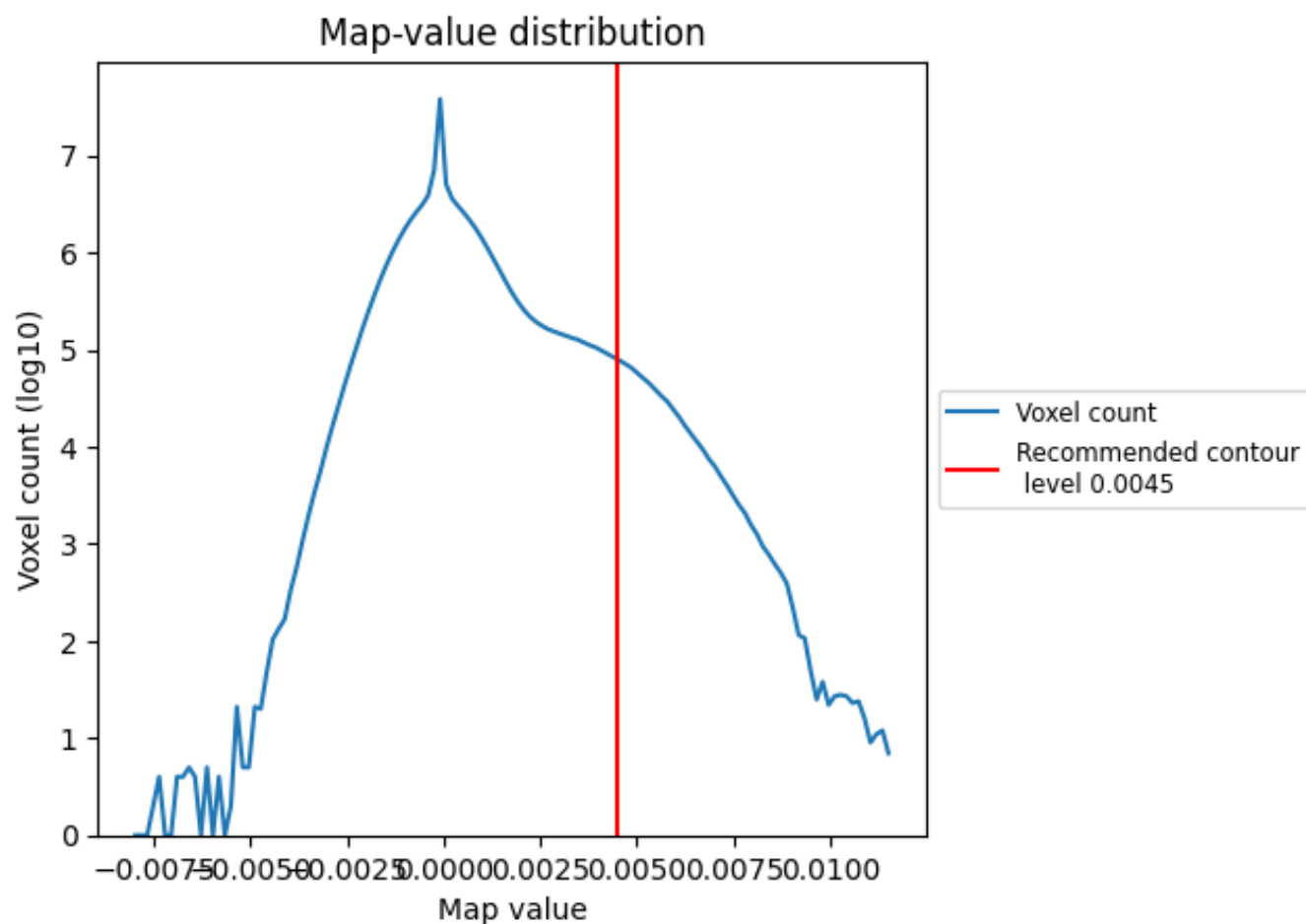
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

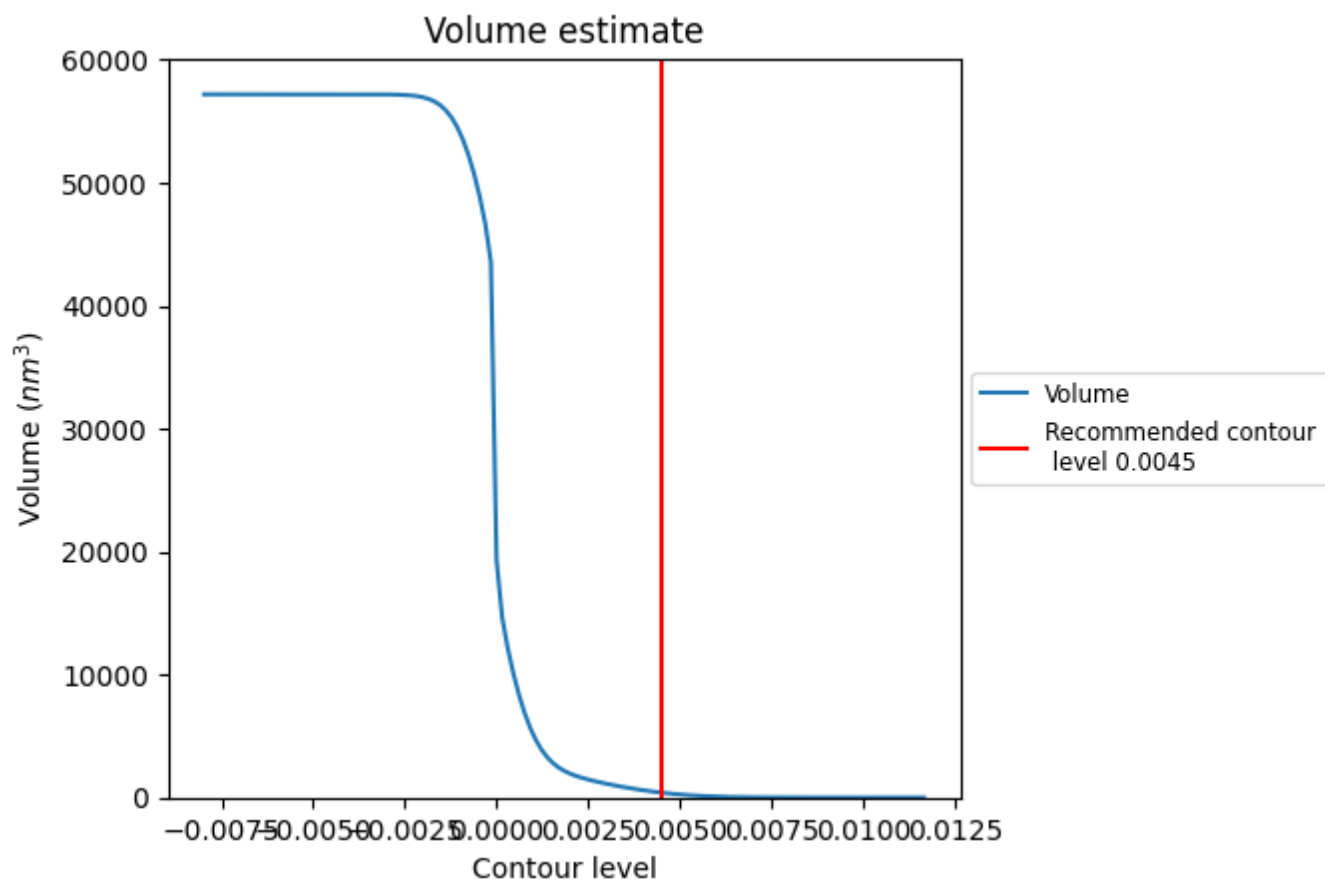
This section contains the results of statistical analysis of the map.

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.

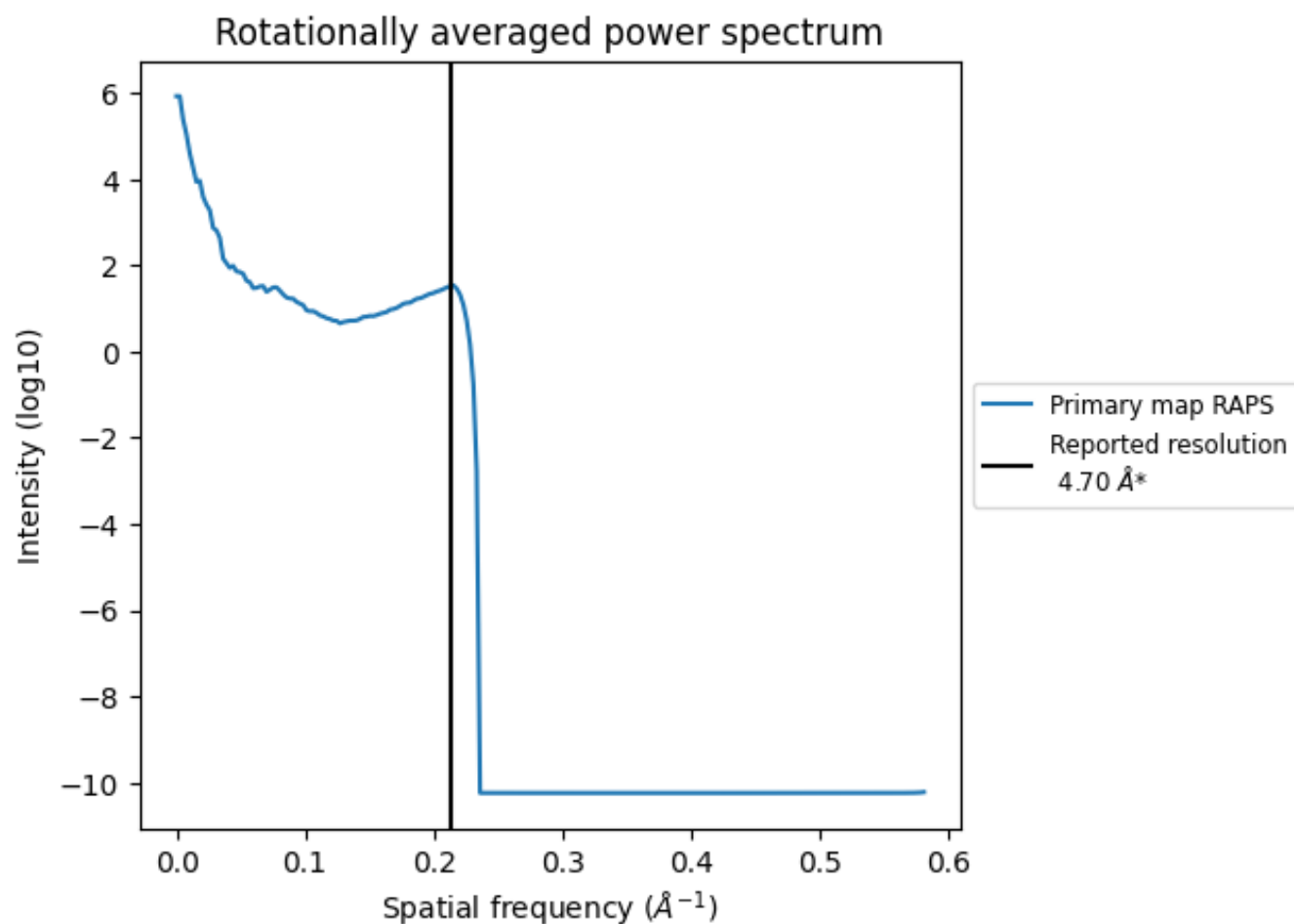
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 399 nm³; this corresponds to an approximate mass of 361 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 0.213 Å⁻¹

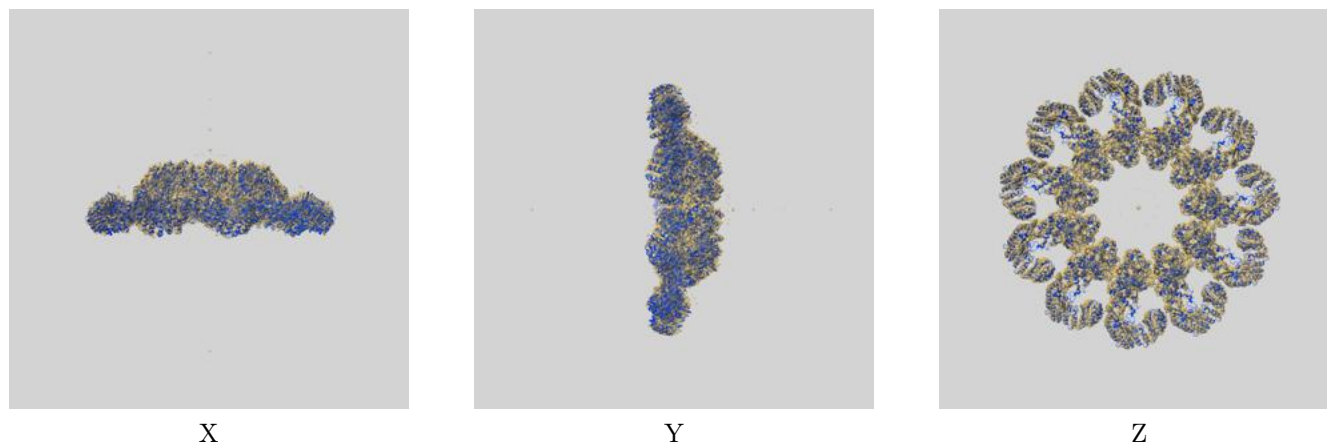
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

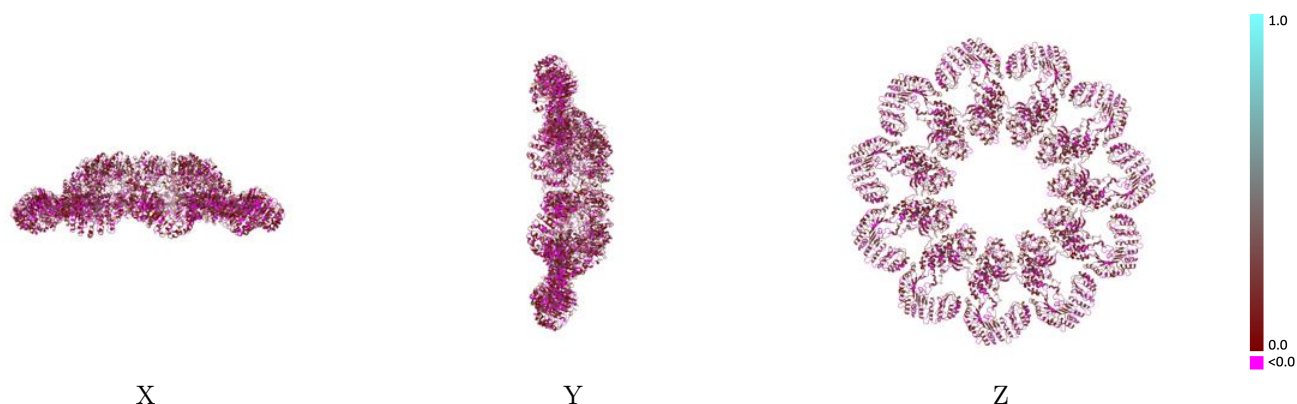
This section contains information regarding the fit between EMDB map EMD-6458 and PDB model 3JBL. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



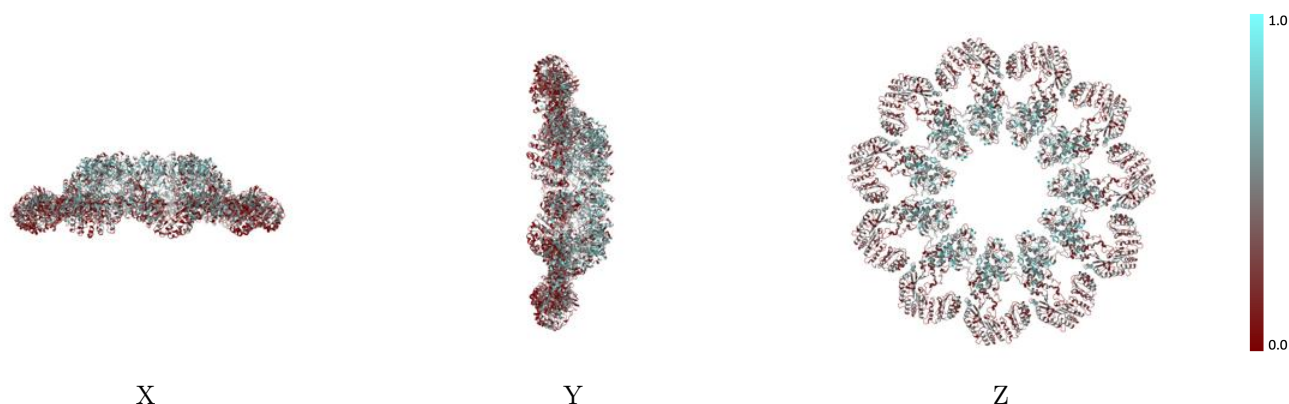
The images above show the 3D surface view of the map at the recommended contour level 0.0045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



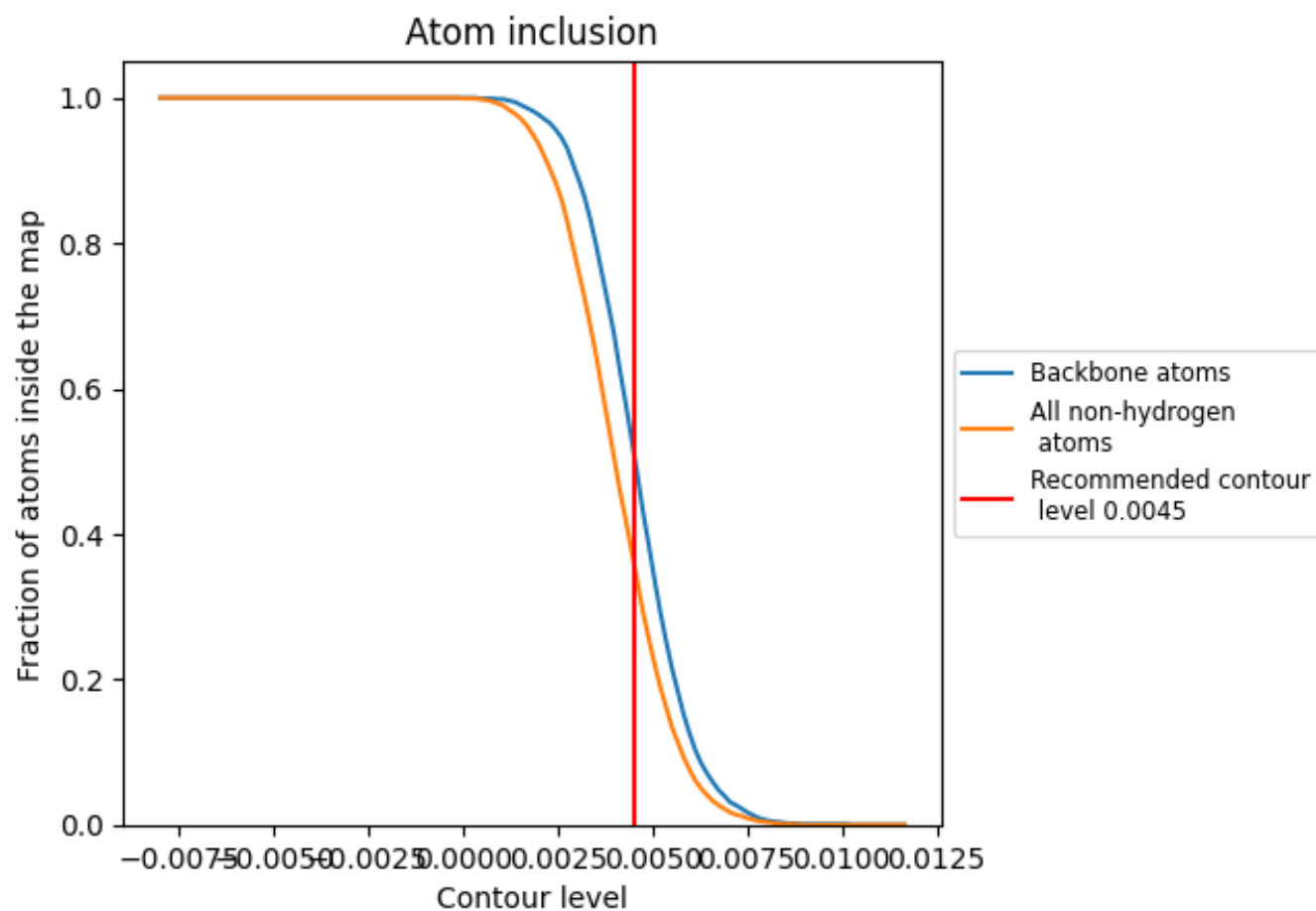
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0045).

9.4 Atom inclusion ⓘ



At the recommended contour level, 52% of all backbone atoms, 36% 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 (0.0045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3640	0.1160
A	0.3660	0.1160
B	0.3630	0.1170
C	0.3650	0.1160
D	0.3660	0.1170
E	0.3630	0.1160
F	0.3650	0.1170
G	0.3640	0.1170
H	0.3640	0.1170
I	0.3670	0.1160
J	0.3620	0.1160
K	0.3620	0.1160

1.0
0.0
<0.0