



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 03:08 AM UTC

PDB ID : 3B63 / pdb_00003b63
EMDB ID : EMD-1088
Title : Actin filament model in the extended form of acromsomal bundle in the Limulus sperm
Authors : Cong, Y.; Topf, M.; Sali, A.; Matsudaira, P.; Dougherty, M.; Chiu, W.; Schmid, M.F.
Deposited on : 2007-10-26
Resolution : 9.50 Å(reported)
Based on initial models : 1YVN, 1ESV, 1T44, 1HIV, 1NWK, 1YAG, 1HLU, 1ATN, 1MDU

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

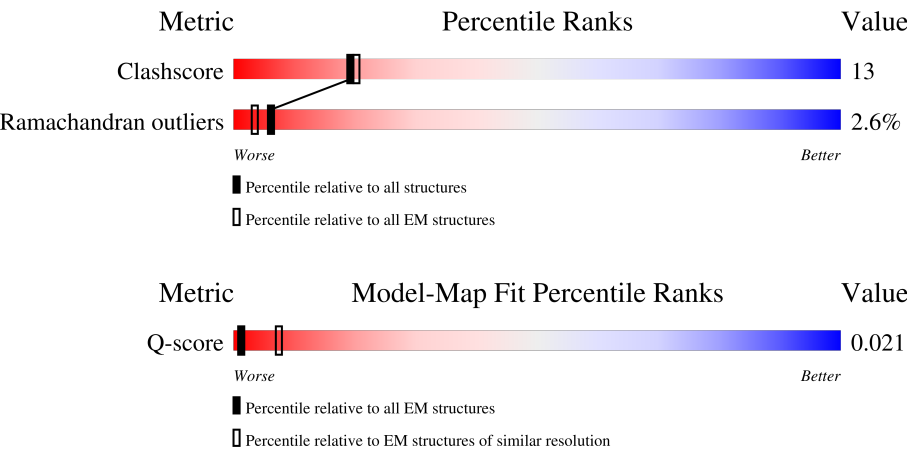
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 9.50 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	-
Q-score	-	25397	234 (9.00 - 10.00)

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	365	92% 67%31%
1	G	365	93% 68%30%
2	B	364	90% 59%34%6%
3	C	365	90% 67%31%
3	I	365	99% 62%34%

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Mol	Chain	Length	Quality of chain
4	D	357	92% 61% 32% 8%
5	E	365	92% 58% 37% 5%
5	H	365	97% 61% 34% . .
5	J	365	97% 62% 32% 6% .
5	K	365	96% 64% 32% .
5	N	365	93% 56% 38% 5%
6	F	357	90% 56% 38% 5% .
7	L	365	95% 60% 35% 5%
7	M	365	92% 63% 31% 5%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 39685 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 Actin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	365	Total	C	N	O	S	0	0
			2843	1800	480	545	18		
1	G	365	Total	C	N	O	S	0	0
			2843	1800	480	545	18		

- Molecule 2 is a protein called Actin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	364	Total	C	N	O	S	0	0
			2835	1796	474	545	20		

- Molecule 3 is a protein called Actin.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	365	Total	C	N	O	S	0	0
			2842	1801	479	544	18		
3	I	365	Total	C	N	O	S	0	0
			2842	1801	479	544	18		

- Molecule 4 is a protein called Actin.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	357	Total	C	N	O	S	0	0
			2791	1768	467	536	20		

- Molecule 5 is a protein called Actin.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	365	Total	C	N	O	S	0	0
			2845	1802	477	546	20		
5	H	365	Total	C	N	O	S	0	0
			2845	1802	477	546	20		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	365	Total	C	N	O	S	0	0
			2845	1802	477	546	20		
5	K	365	Total	C	N	O	S	0	0
			2845	1802	477	546	20		
5	N	365	Total	C	N	O	S	0	0
			2845	1802	477	546	20		

- Molecule 6 is a protein called Actin.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	357	Total	C	N	O	S	0	0
			2788	1767	467	534	20		

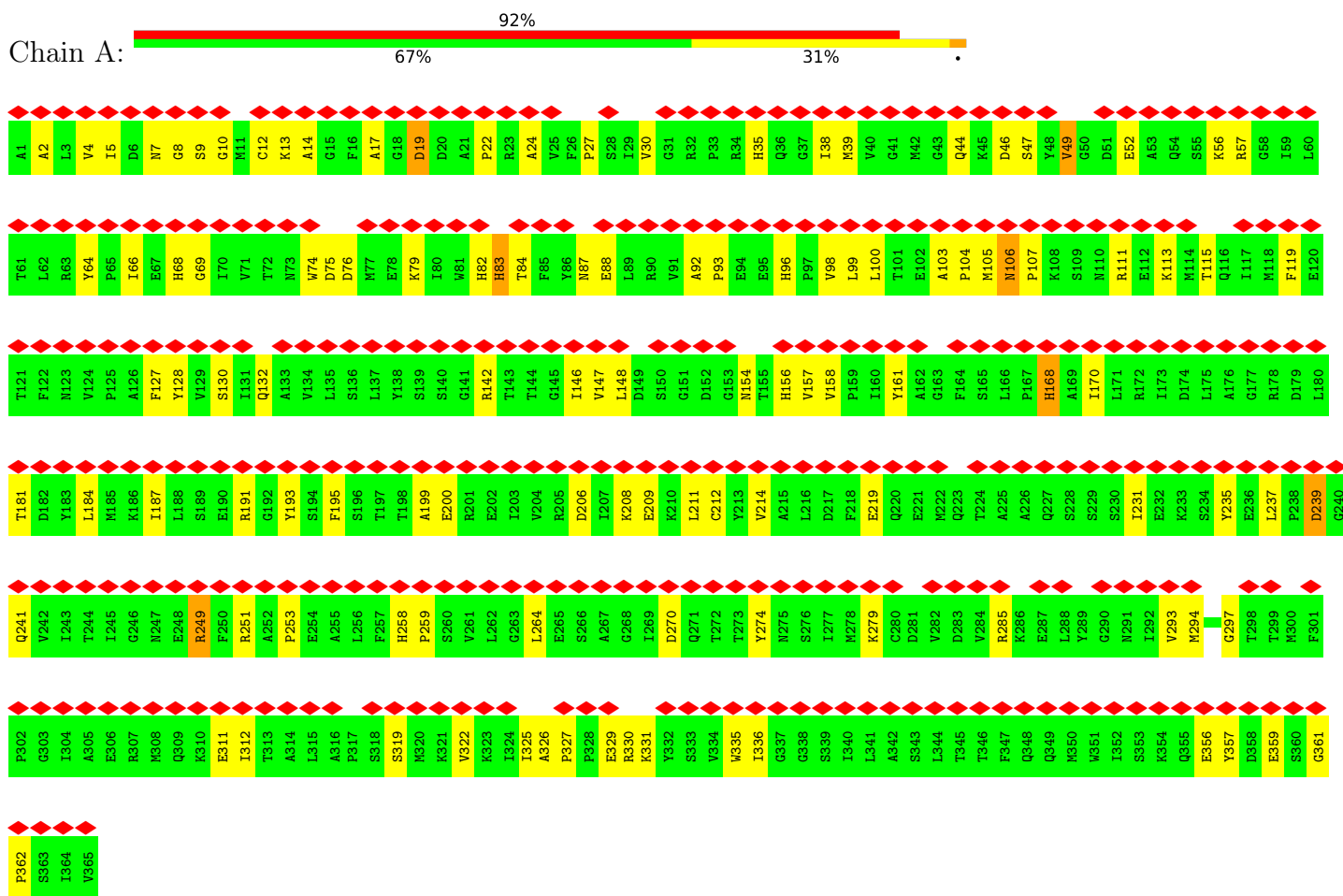
- Molecule 7 is a protein called Actin.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L	365	Total	C	N	O	S	0	0
			2838	1797	475	545	21		
7	M	365	Total	C	N	O	S	0	0
			2838	1797	475	545	21		

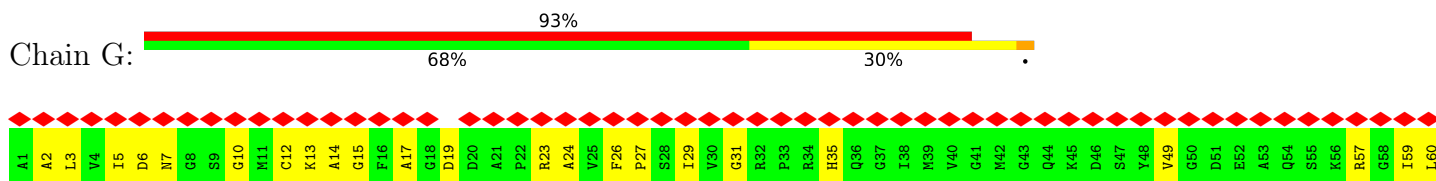
3 Residue-property plots

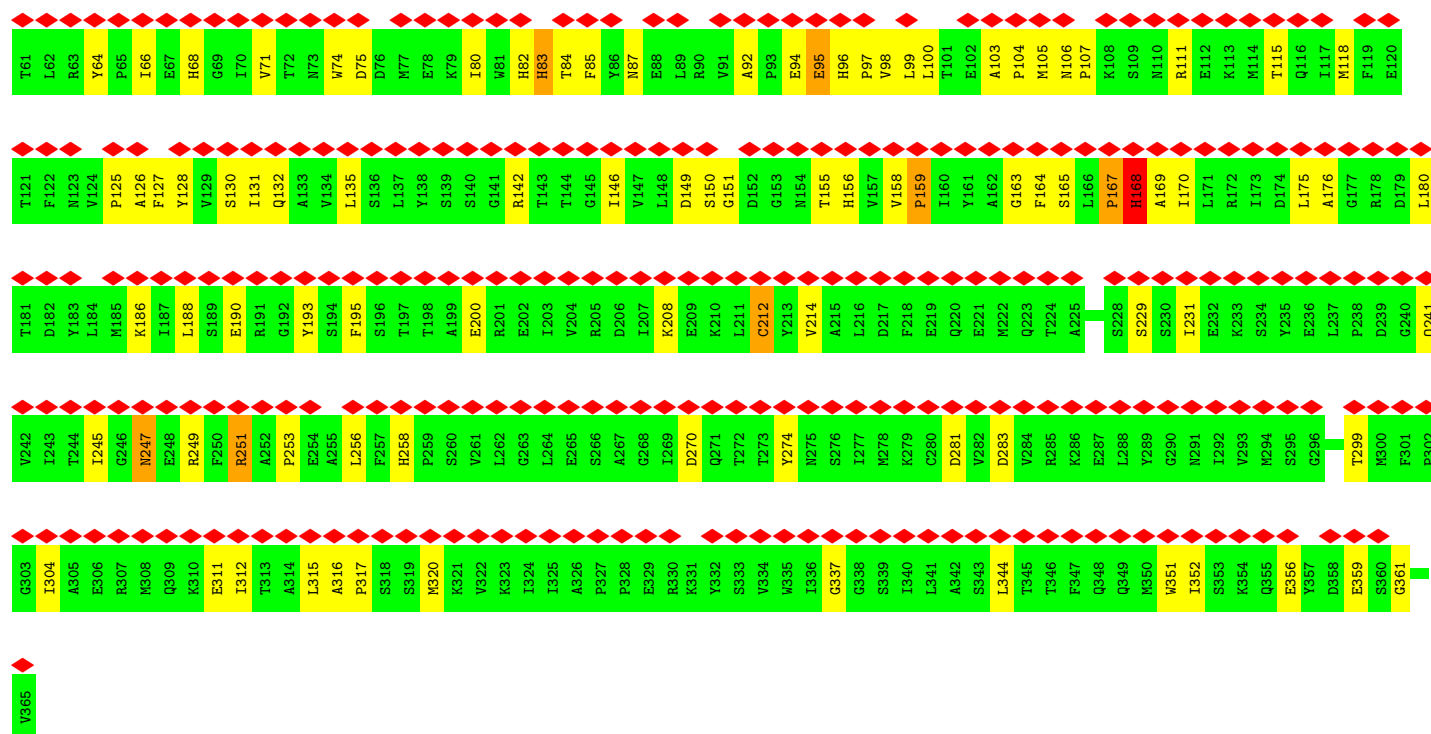
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

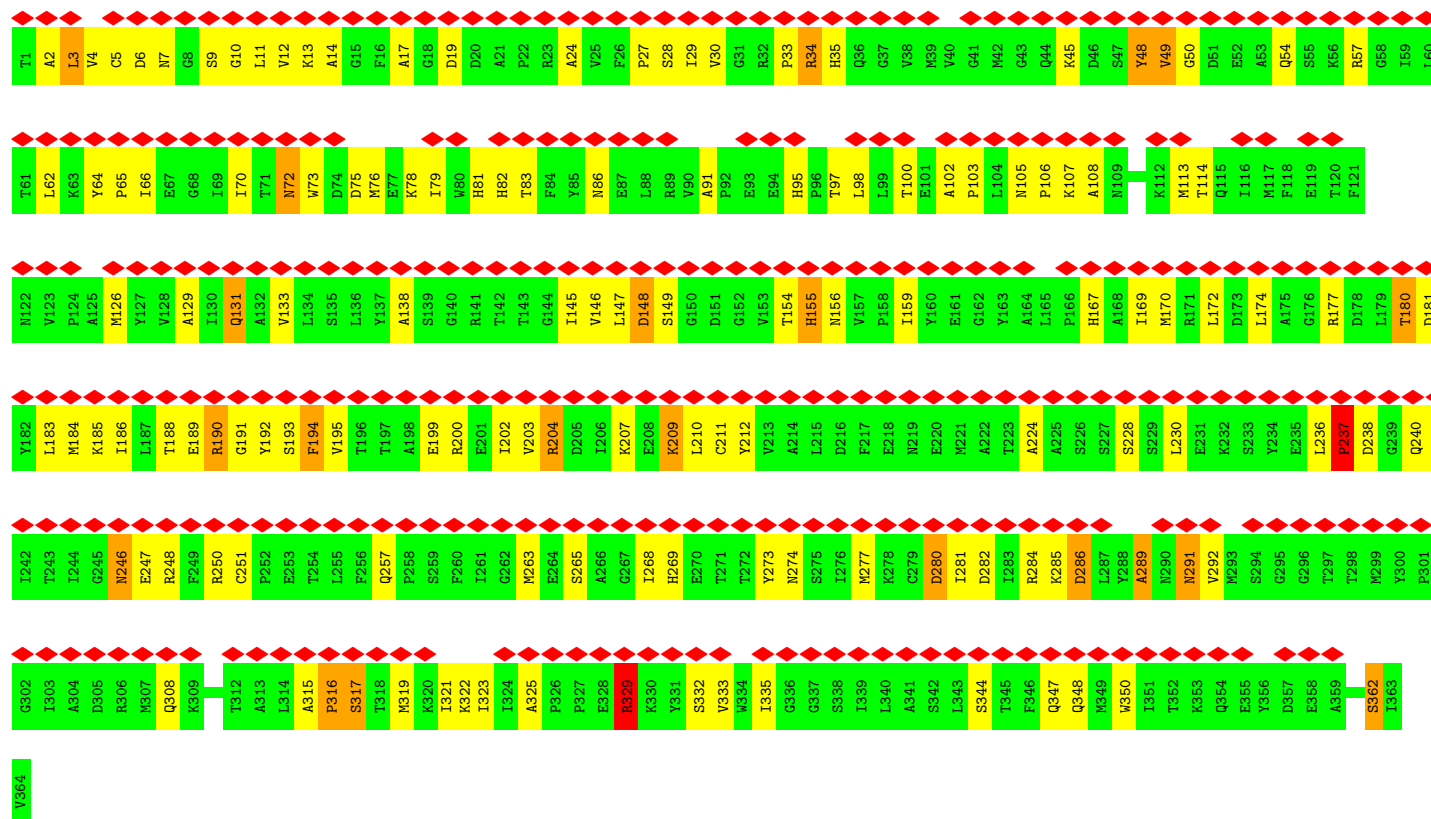
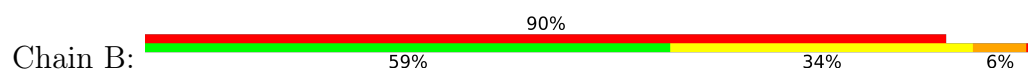


• Molecule 1: Actin

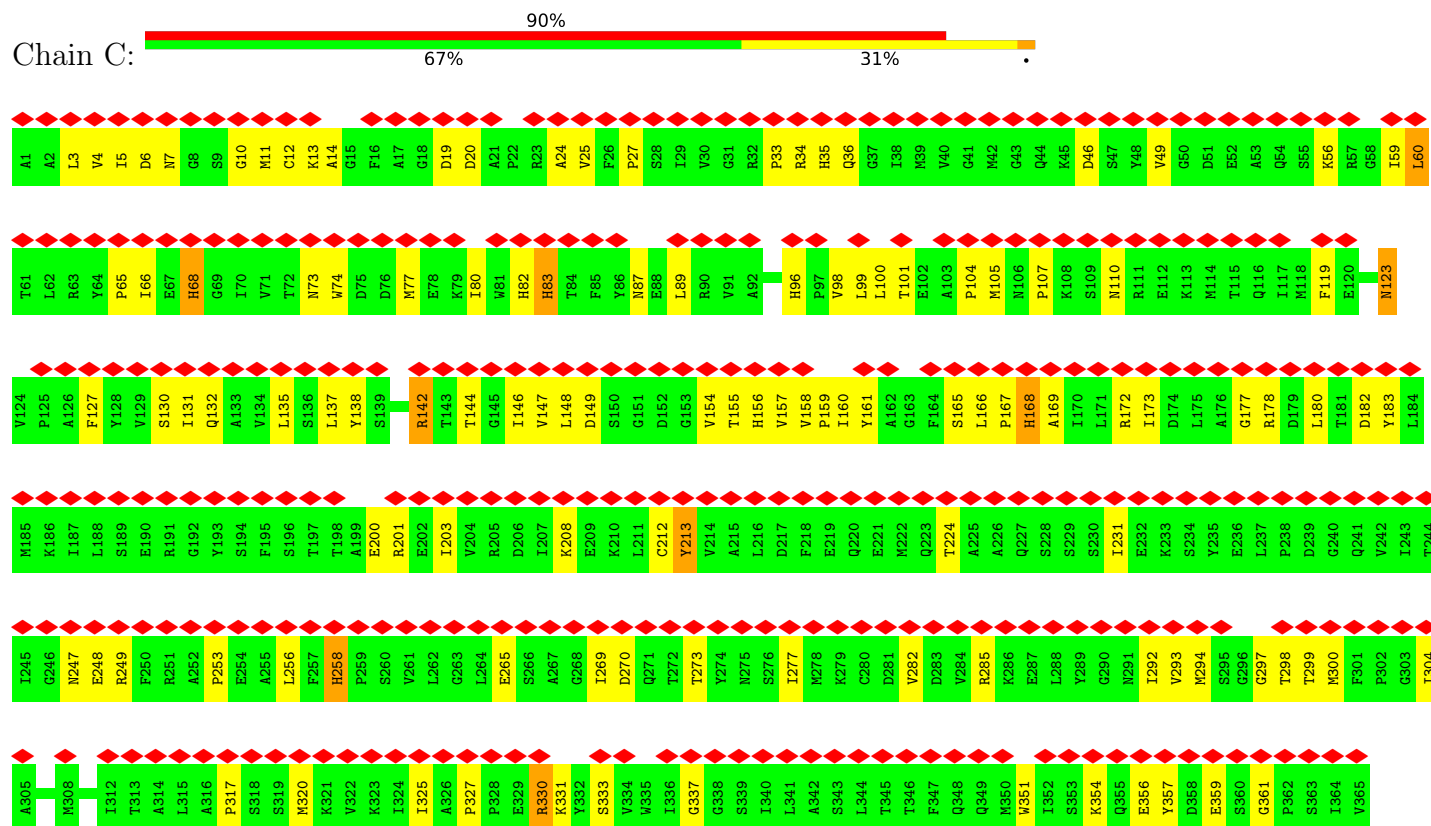




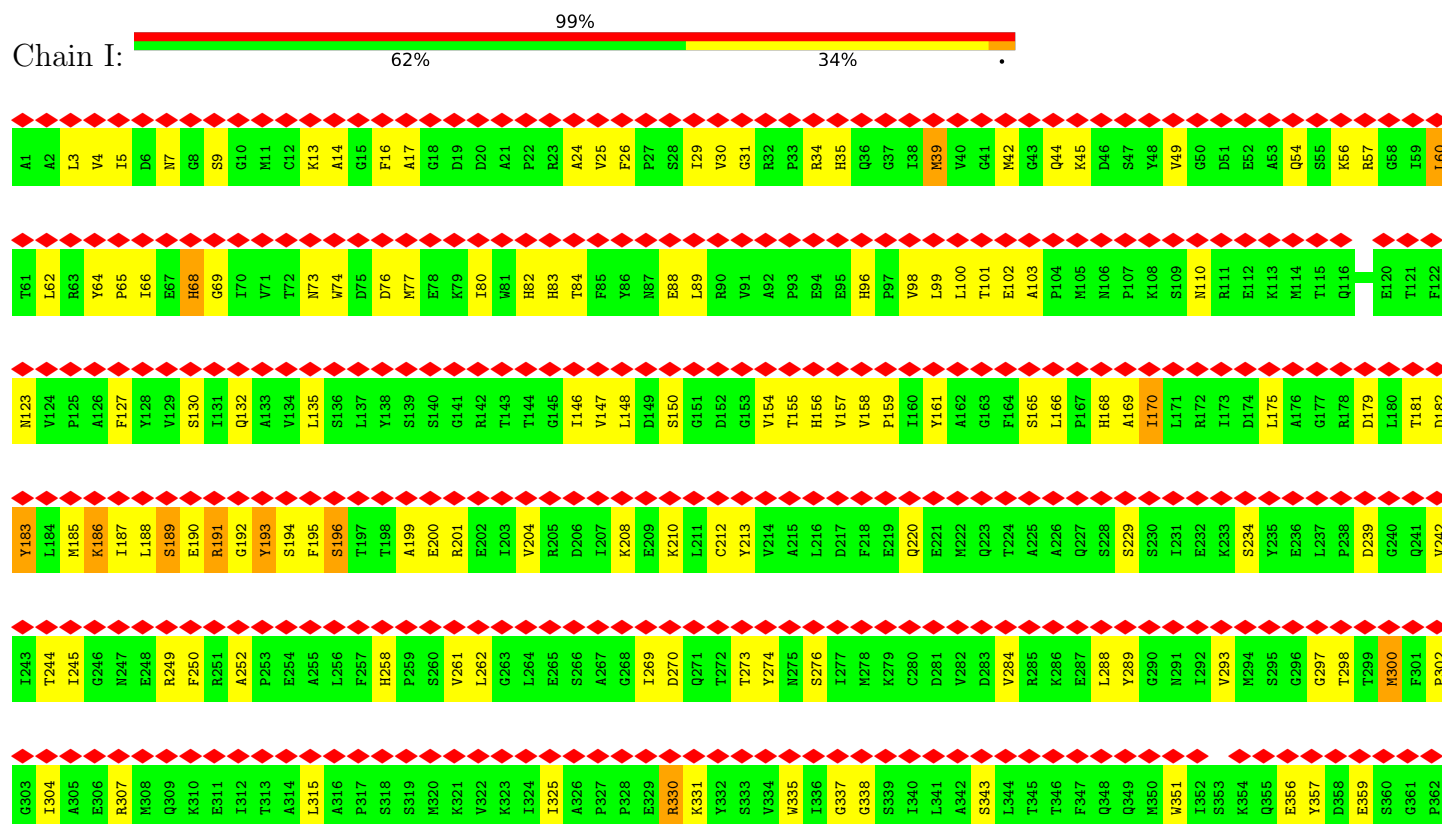
• Molecule 2: Actin



- Molecule 3: Actin

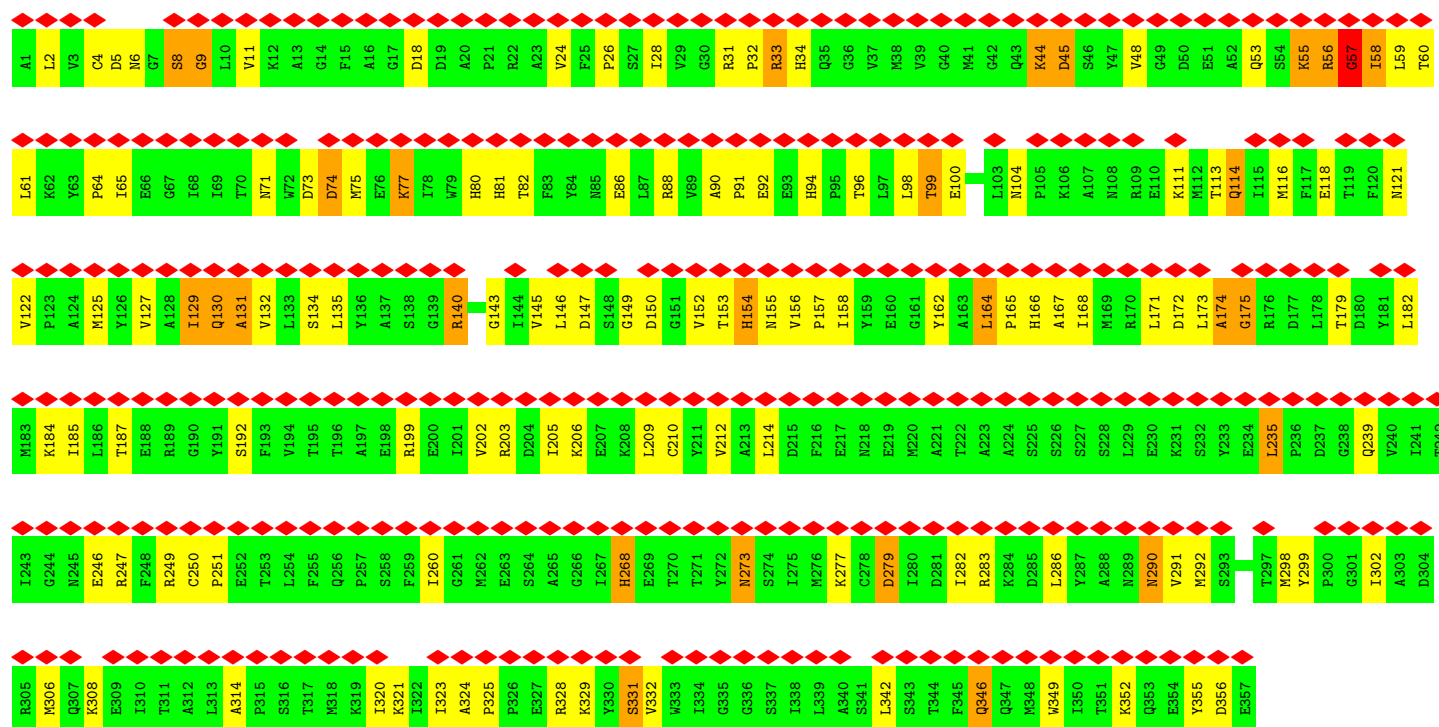
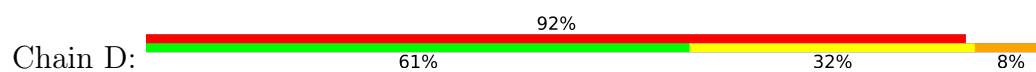


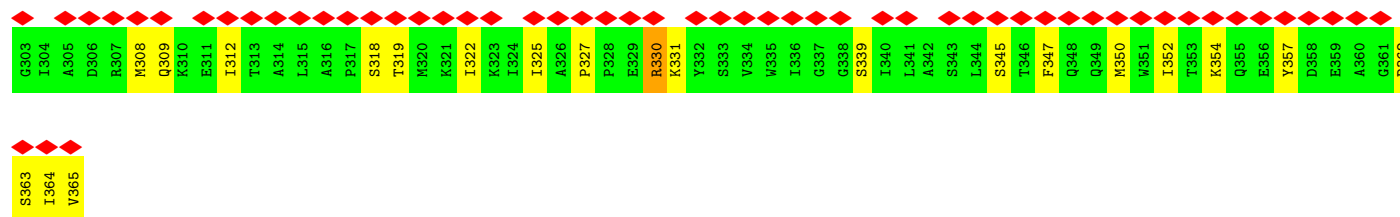
- Molecule 3: Actin



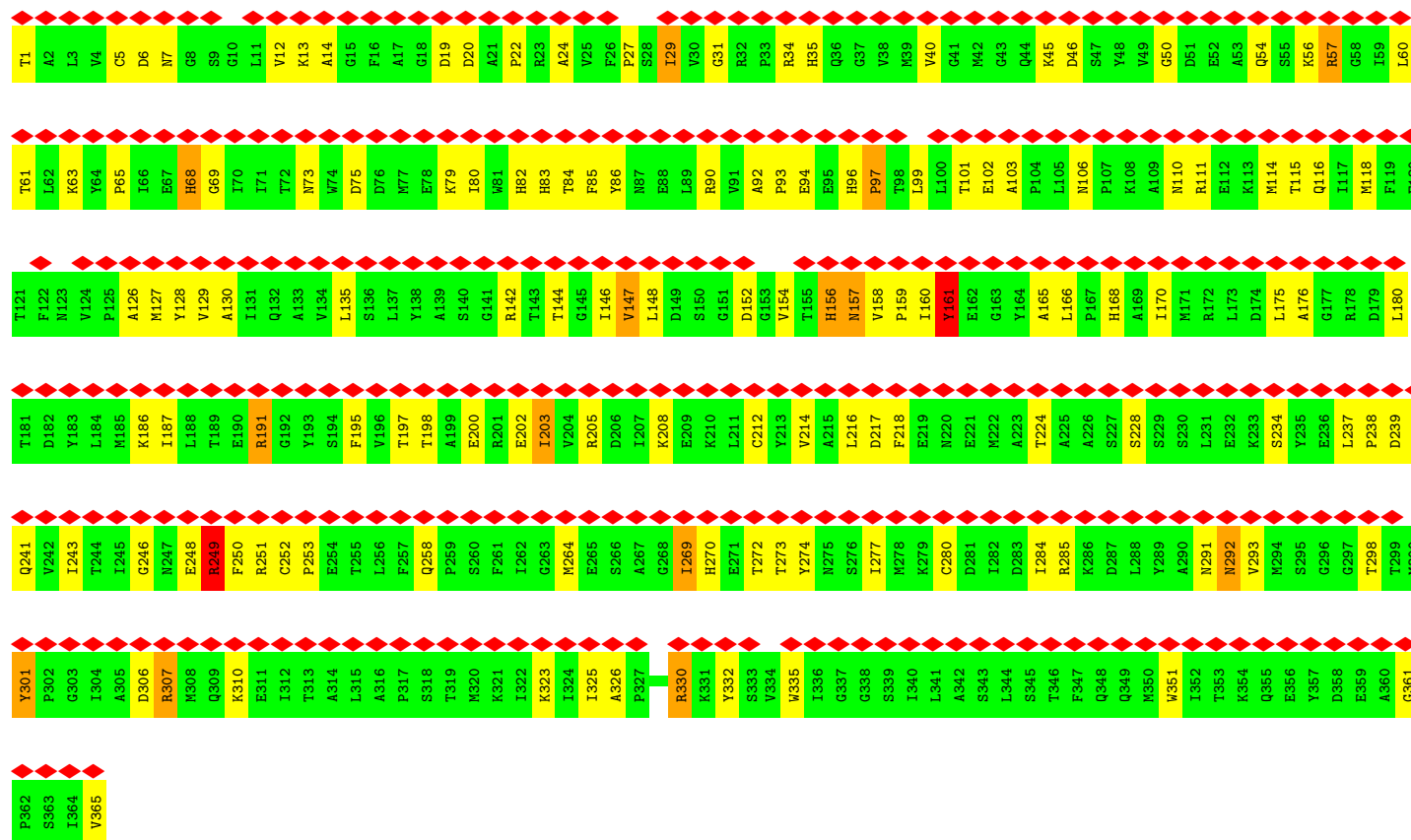


• Molecule 4: Actin





• Molecule 5: Actin

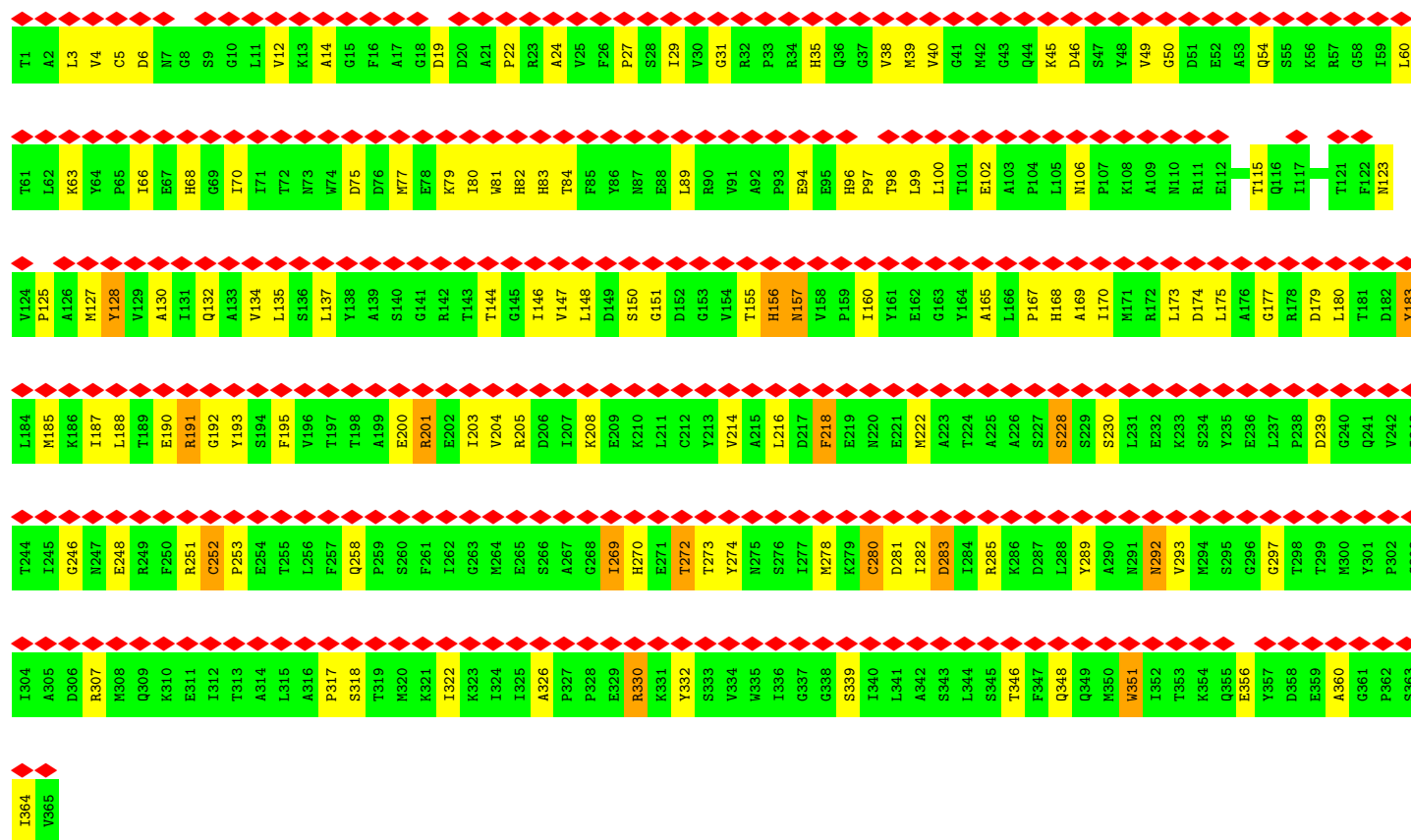


• Molecule 5: Actin



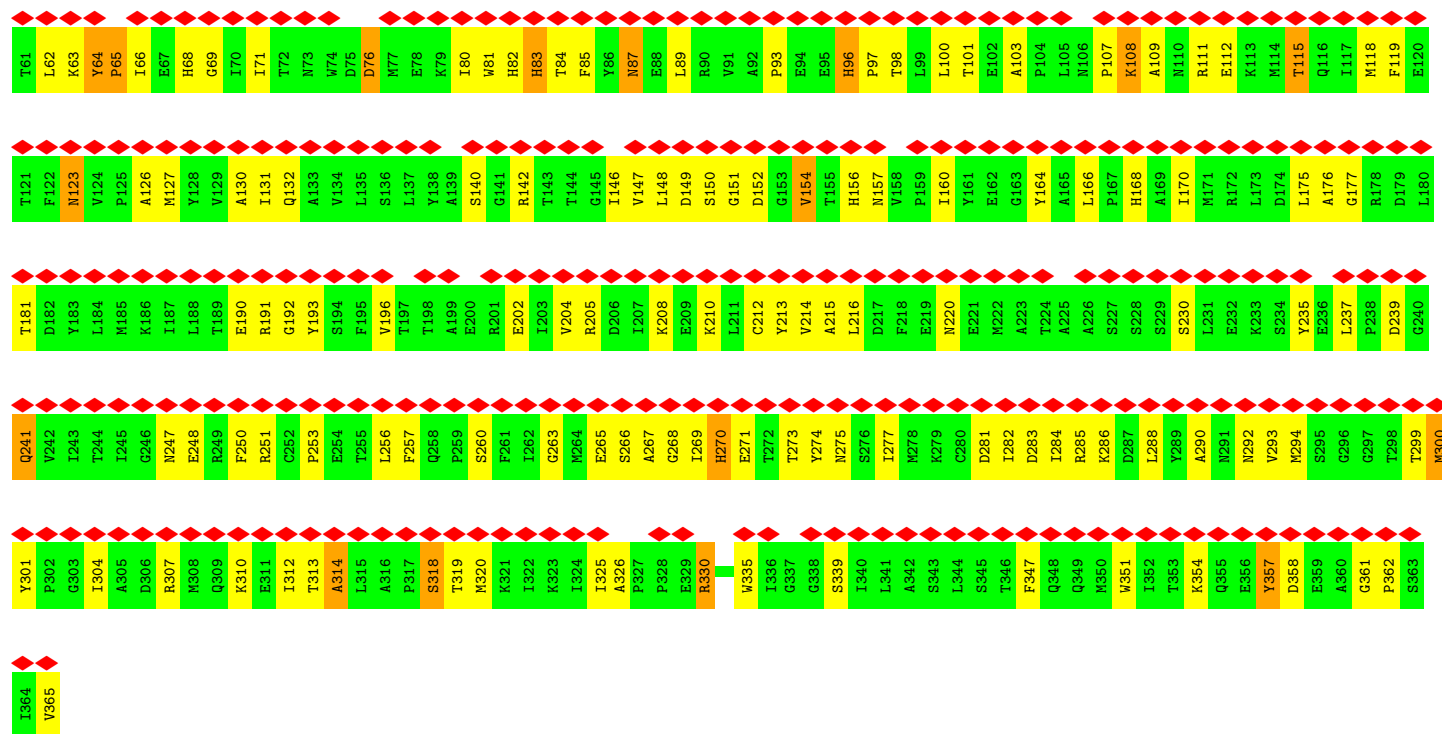


• Molecule 5: Actin

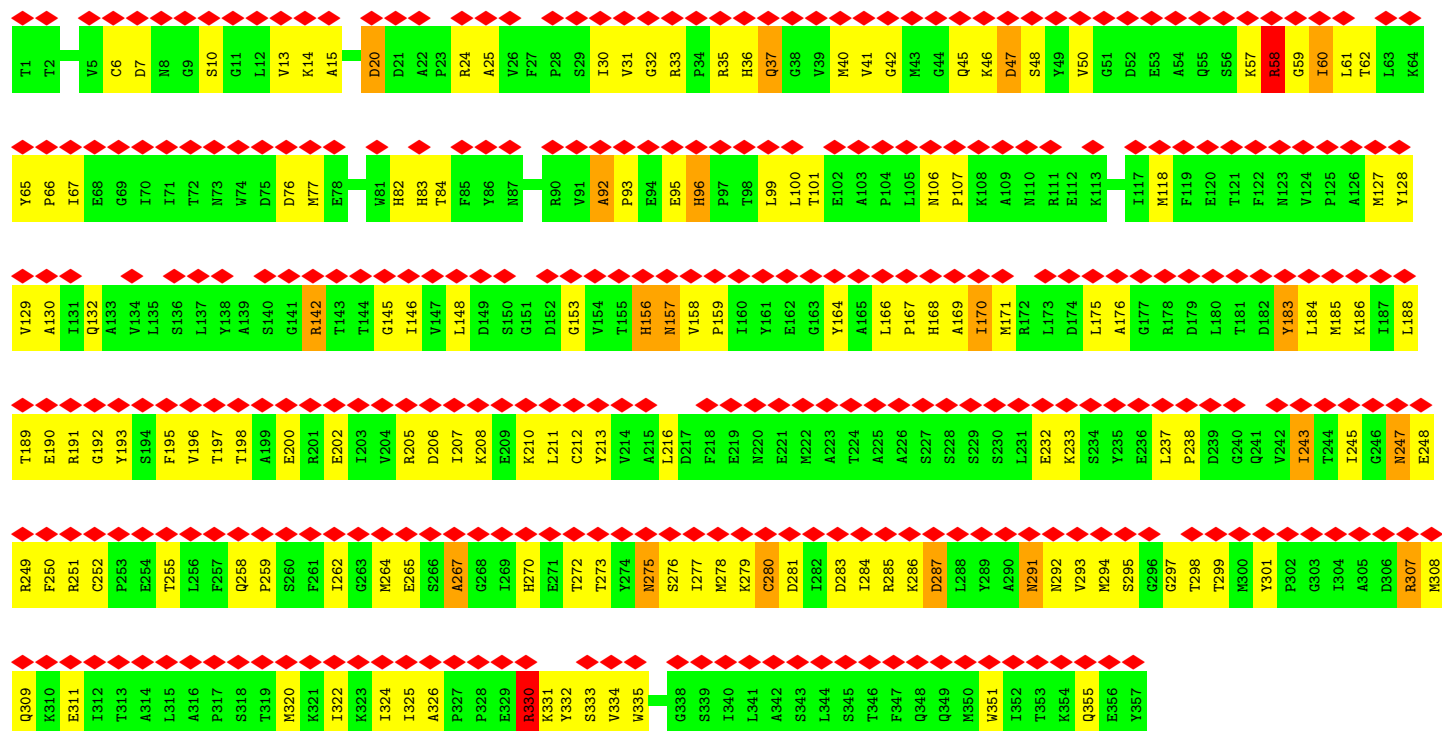


• Molecule 5: Actin



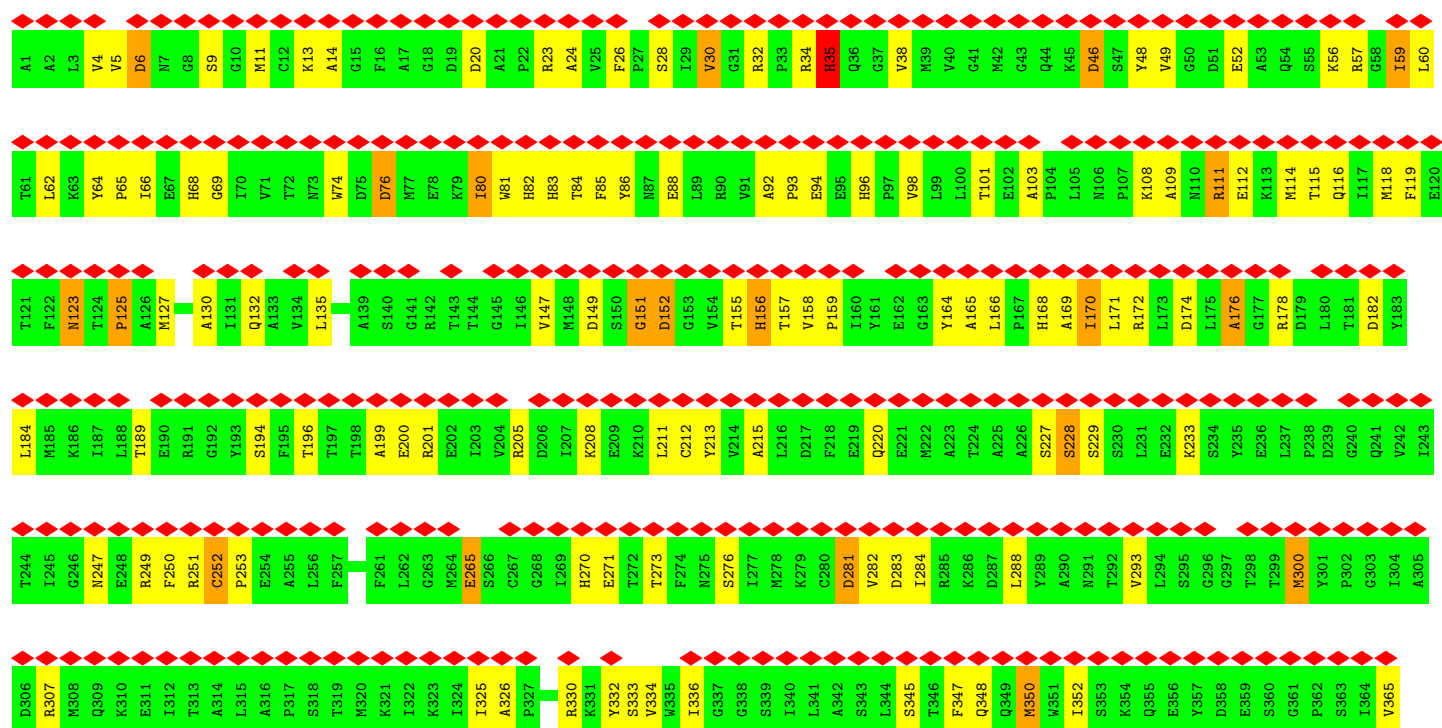


• Molecule 6: Actin



• Molecule 7: Actin





4 Experimental information

Property	Value	Source
EM reconstruction method	CRYSTALLOGRAPHY	Depositor
Imposed symmetry	3D CRYSTAL, a =Not provided Å, b =Not provided Å, c =Not provided Å, α =Not provided°, β =Not provided°, γ =Not provided°, space group=Not provided	Depositor
Number of images used	Not provided	
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	JEOL 4000EX	Depositor
Voltage (kV)	400	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	40000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	977.199	Depositor
Minimum map value	-974.403	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	215.097	Depositor
Recommended contour level	430	Depositor
Map size (Å)	255.99936, 148.00015, 765.7977	wwPDB
Map dimensions	576, 192, 112	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33333, 1.32143, 1.32951	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	0.76	8/2904 (0.3%)	1.56	36/3931 (0.9%)
1	G	0.76	8/2904 (0.3%)	1.53	39/3931 (1.0%)
2	B	0.75	8/2895 (0.3%)	1.65	59/3923 (1.5%)
3	C	0.75	8/2903 (0.3%)	1.56	31/3930 (0.8%)
3	I	0.74	8/2903 (0.3%)	1.59	41/3930 (1.0%)
4	D	0.75	7/2850 (0.2%)	1.63	45/3860 (1.2%)
5	E	0.77	9/2906 (0.3%)	1.63	45/3938 (1.1%)
5	H	0.75	8/2906 (0.3%)	1.61	44/3938 (1.1%)
5	J	0.77	9/2906 (0.3%)	1.65	59/3938 (1.5%)
5	K	0.77	10/2906 (0.3%)	1.62	35/3938 (0.9%)
5	N	0.76	9/2906 (0.3%)	1.60	44/3938 (1.1%)
6	F	0.75	7/2847 (0.2%)	1.62	36/3857 (0.9%)
7	L	0.77	8/2899 (0.3%)	1.69	47/3927 (1.2%)
7	M	0.77	9/2899 (0.3%)	1.63	44/3927 (1.1%)
All	All	0.76	116/40534 (0.3%)	1.61	605/54906 (1.1%)

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	12
1	G	0	7
2	B	0	9
3	C	0	6
3	I	0	9
4	D	0	5
5	E	0	8
5	H	0	7
5	J	0	6
5	K	0	9
5	N	0	8

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Mol	Chain	#Chirality outliers	#Planarity outliers
6	F	0	7
7	L	0	5
7	M	0	6
All	All	0	104

The worst 5 of 116 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	166	HIS	CD2-NE2	-7.16	1.29	1.37
1	G	168	HIS	CD2-NE2	-7.12	1.30	1.37
5	H	68	HIS	CD2-NE2	-7.04	1.30	1.37
5	E	168	HIS	CD2-NE2	-6.99	1.30	1.37
5	E	270	HIS	CD2-NE2	-6.99	1.30	1.37

The worst 5 of 605 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	L	285	ARG	N-CA-C	11.03	122.87	111.07
5	E	197	THR	N-CA-C	10.19	124.82	108.41
2	B	246	ASN	OD1-CG-ND2	-9.67	112.93	122.60
2	B	194	PHE	N-CA-C	9.37	124.27	111.90
1	G	75	ASP	CA-CB-CG	9.30	121.91	112.60

There are no chirality outliers.

5 of 104 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	111	ARG	Sidechain
1	A	142	ARG	Sidechain
1	A	161	TYR	Sidechain
1	A	57	ARG	Sidechain
1	A	64	TYR	Sidechain

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	2843	0	2818	54	0
1	G	2843	0	2818	60	0
2	B	2835	0	2813	83	0
3	C	2842	0	2821	72	0
3	I	2842	0	2821	80	0
4	D	2791	0	2766	81	0
5	E	2845	0	2820	78	0
5	H	2845	0	2820	68	0
5	J	2845	0	2820	84	0
5	K	2845	0	2820	72	0
5	N	2845	0	2820	88	0
6	F	2788	0	2770	110	0
7	L	2838	0	2812	80	0
7	M	2838	0	2812	70	0
All	All	39685	0	39351	1001	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 13.

The worst 5 of 1001 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)
5:E:198:THR:HA	6:F:265:GLU:HG3	1.51	0.91
5:E:248:GLU:HA	5:E:251:ARG:HB3	1.54	0.88
7:L:159:PRO:HG3	7:L:169:ALA:HB3	1.56	0.86
1:G:317:PRO:HG2	1:G:320:MET:HB2	1.58	0.85
7:L:259:PRO:HG2	7:L:266:SER:HB2	1.58	0.84

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	G	363/365 (100%)	333 (92%)	25 (7%)	5 (1%)	9	40
2	B	314/364 (86%)	275 (88%)	29 (9%)	10 (3%)	3	21
3	C	293/365 (80%)	269 (92%)	23 (8%)	1 (0%)	36	72
3	I	363/365 (100%)	328 (90%)	30 (8%)	5 (1%)	9	40
4	D	355/357 (99%)	307 (86%)	36 (10%)	12 (3%)	3	21
5	E	363/365 (100%)	314 (86%)	36 (10%)	13 (4%)	2	20
5	H	363/365 (100%)	319 (88%)	36 (10%)	8 (2%)	5	29
5	J	363/365 (100%)	309 (85%)	44 (12%)	10 (3%)	4	24
5	K	363/365 (100%)	315 (87%)	38 (10%)	10 (3%)	4	24
5	N	363/365 (100%)	322 (89%)	32 (9%)	9 (2%)	4	26
6	F	355/357 (99%)	295 (83%)	47 (13%)	13 (4%)	2	20
7	L	363/365 (100%)	305 (84%)	48 (13%)	10 (3%)	4	24
7	M	363/365 (100%)	307 (85%)	42 (12%)	14 (4%)	2	19
All	All	4584/4728 (97%)	3998 (87%)	466 (10%)	120 (3%)	6	25

5 of 120 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	280	ASP
2	B	329	ARG
2	B	362	SER
3	C	265	GLU
4	D	8	SER

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [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.

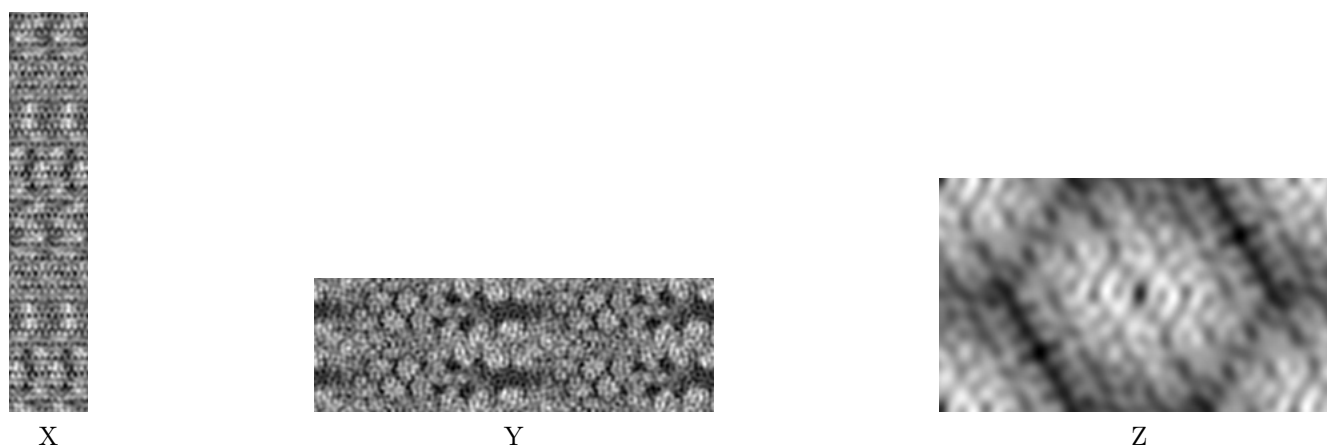
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1088. 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](#)

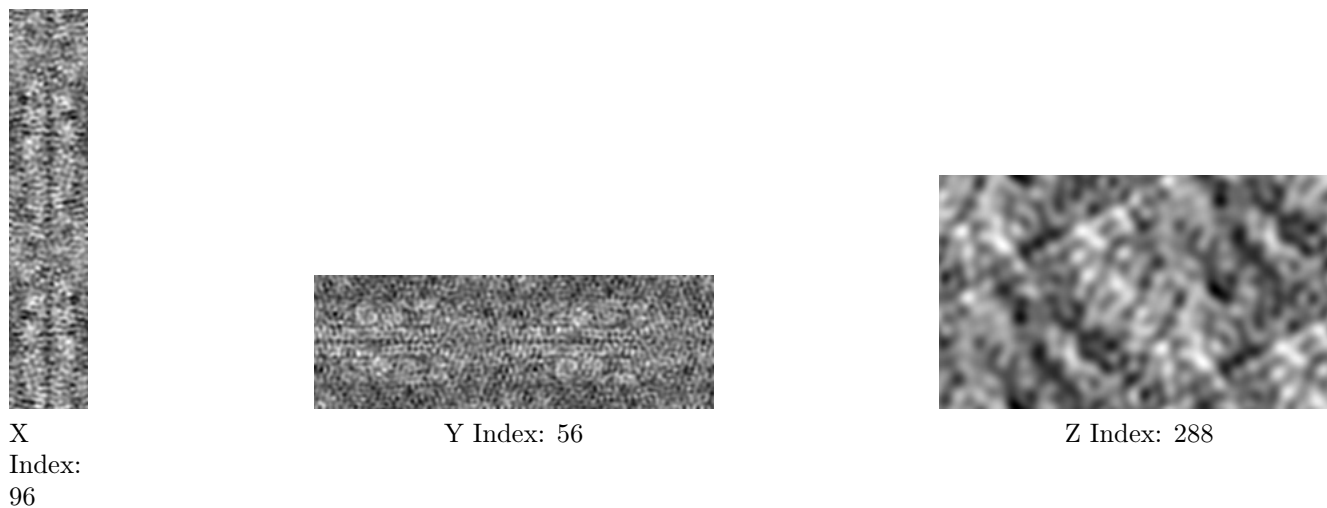
6.1.1 Primary map



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

6.2 Central slices [i](#)

6.2.1 Primary map



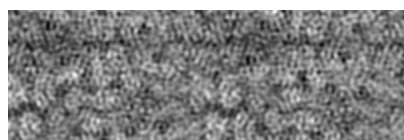
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X
Index:
123



Y Index: 84

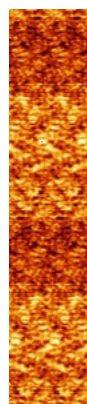


Z Index: 413

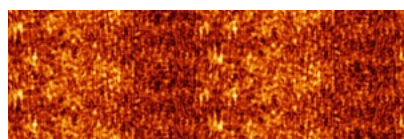
The images above show the largest variance slices of the map in three orthogonal directions.

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

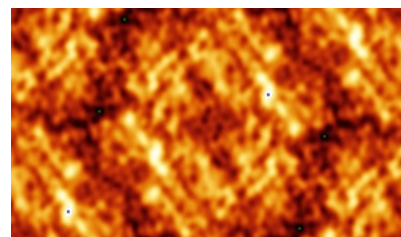
6.4.1 Primary map



X



Y

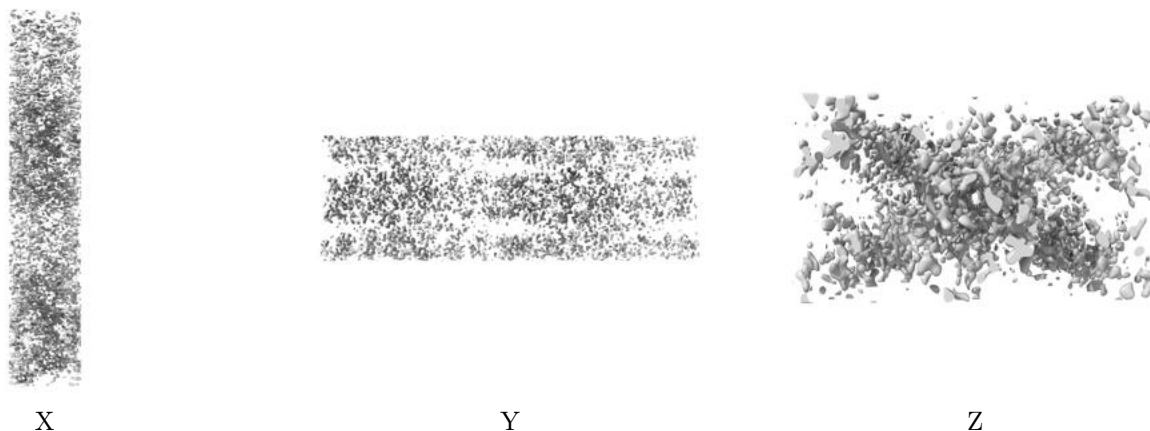


Z

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

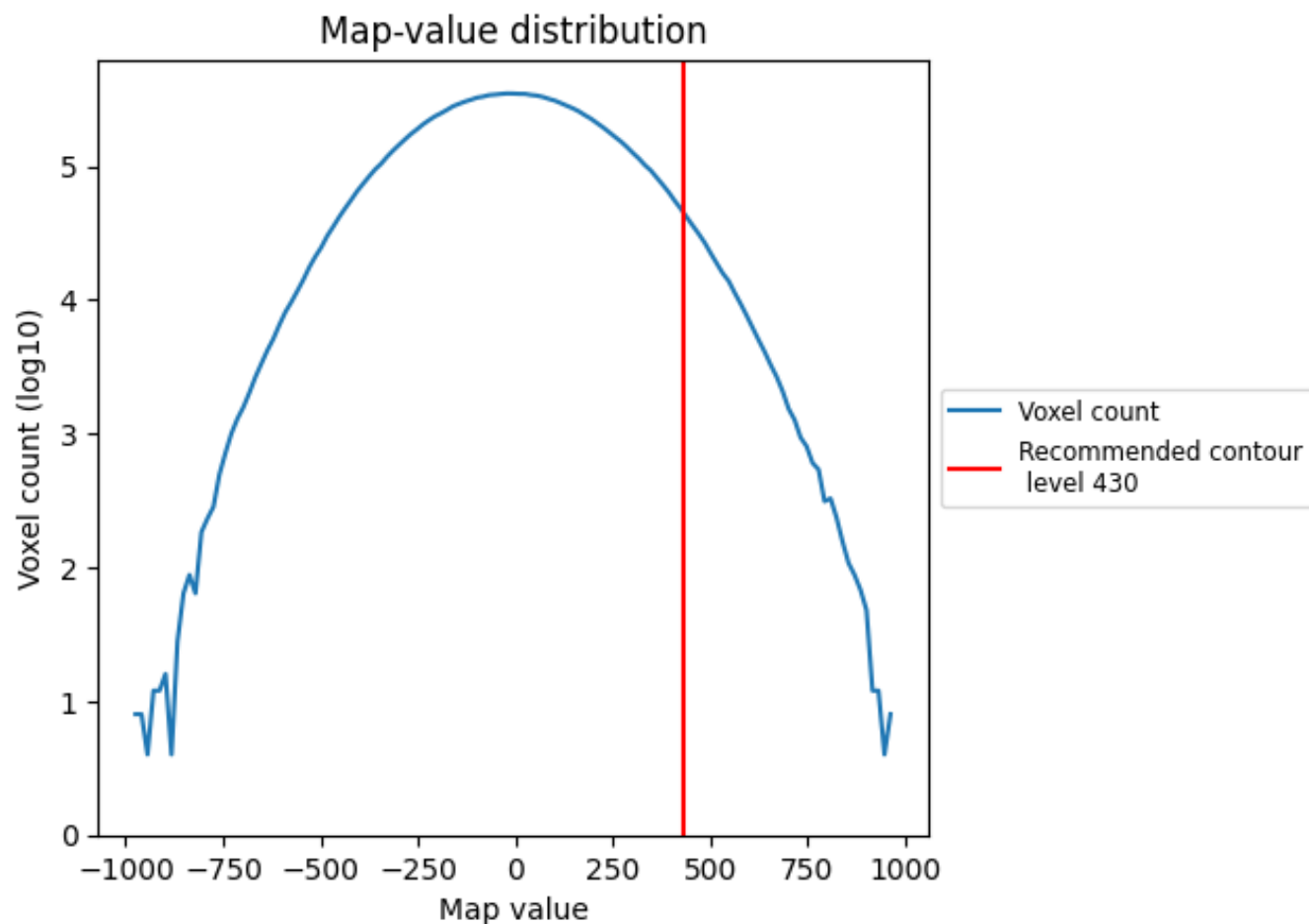
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

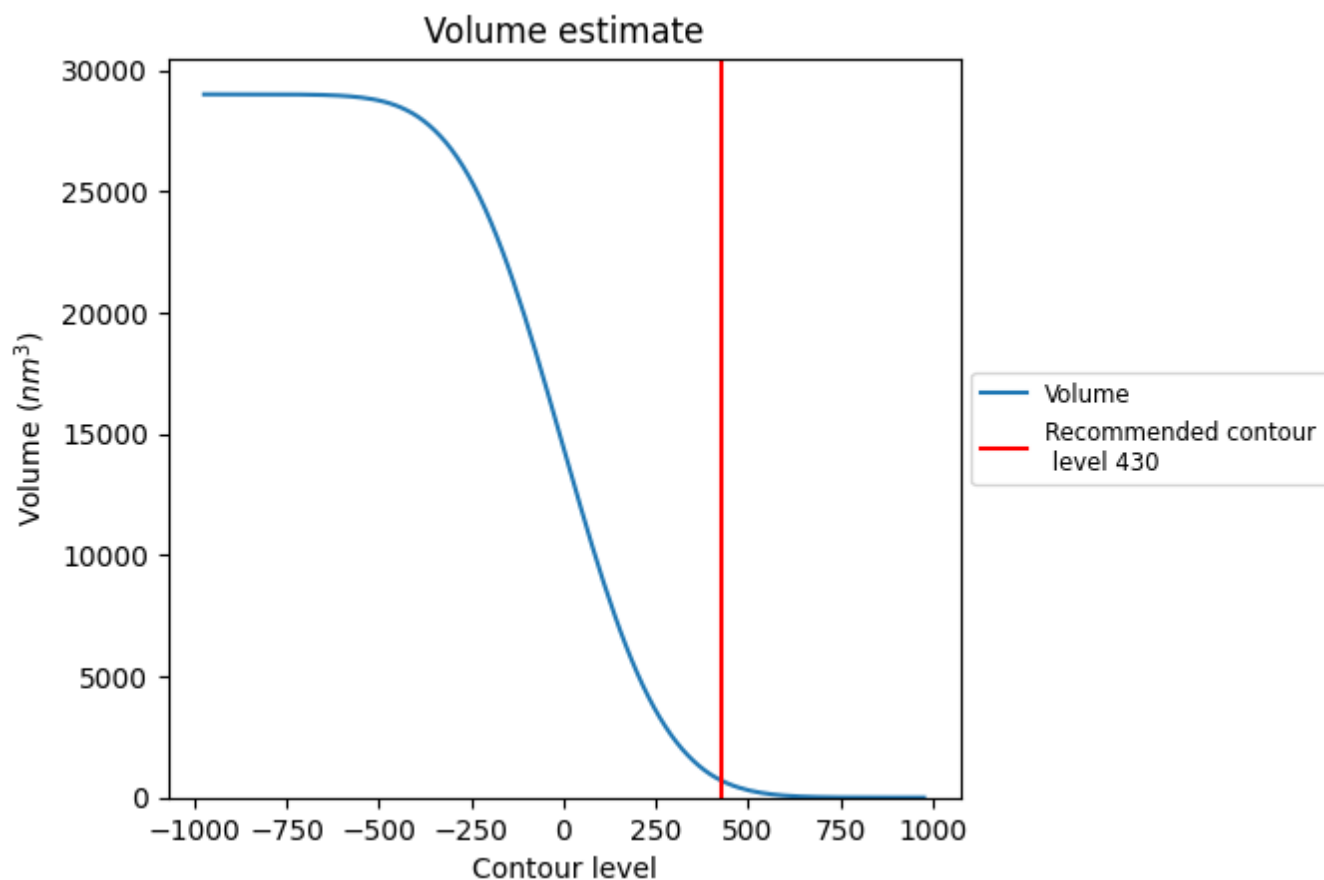
This section contains the results of statistical analysis of the map.

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 687 nm³; this corresponds to an approximate mass of 621 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](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

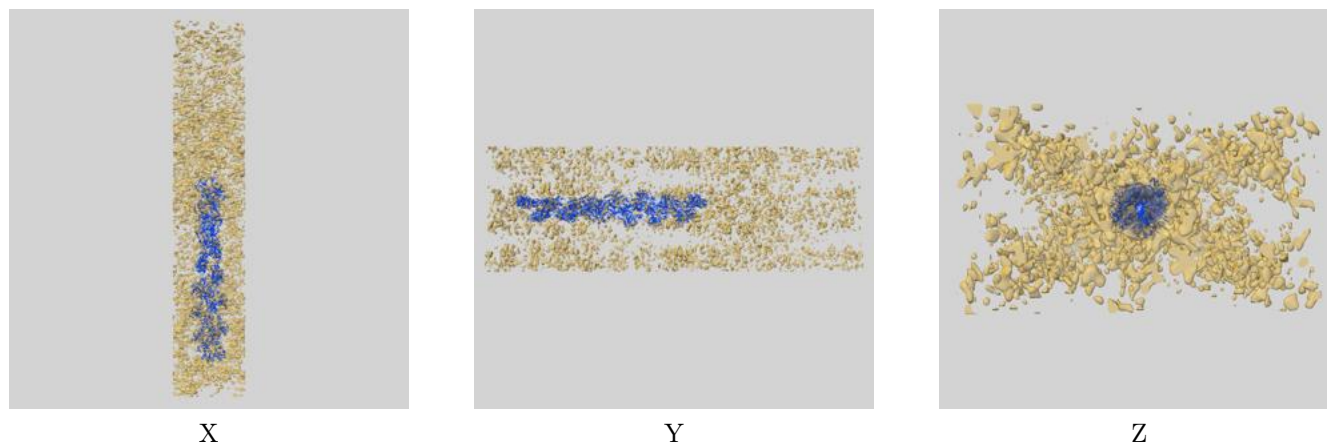
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

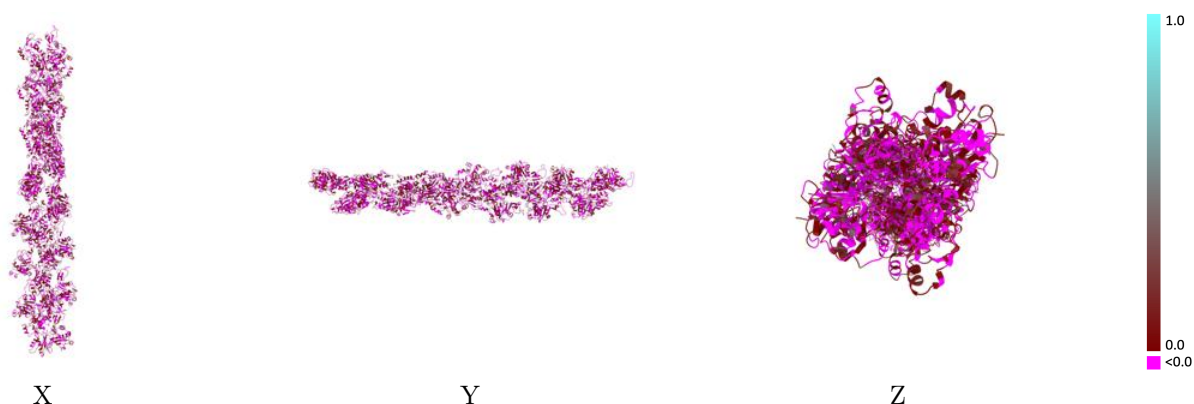
This section contains information regarding the fit between EMDB map EMD-1088 and PDB model 3B63. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



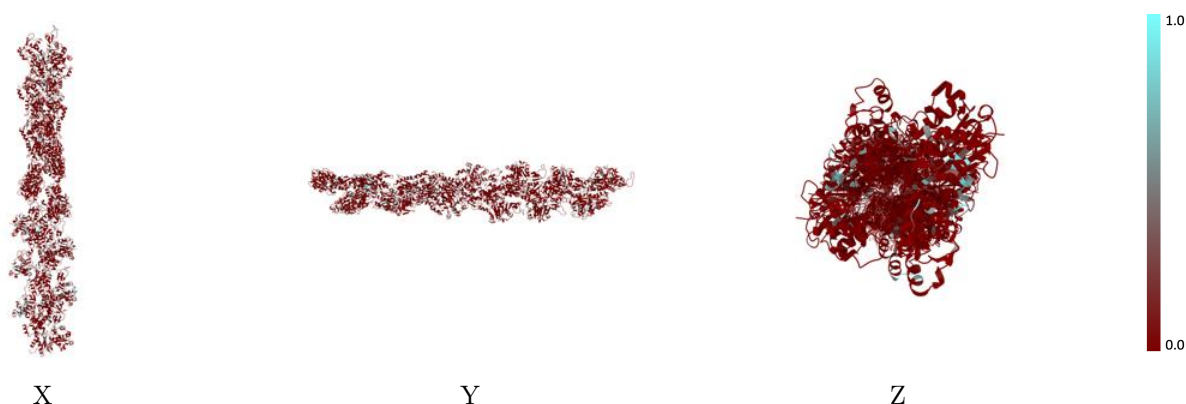
The images above show the 3D surface view of the map at the recommended contour level 430.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



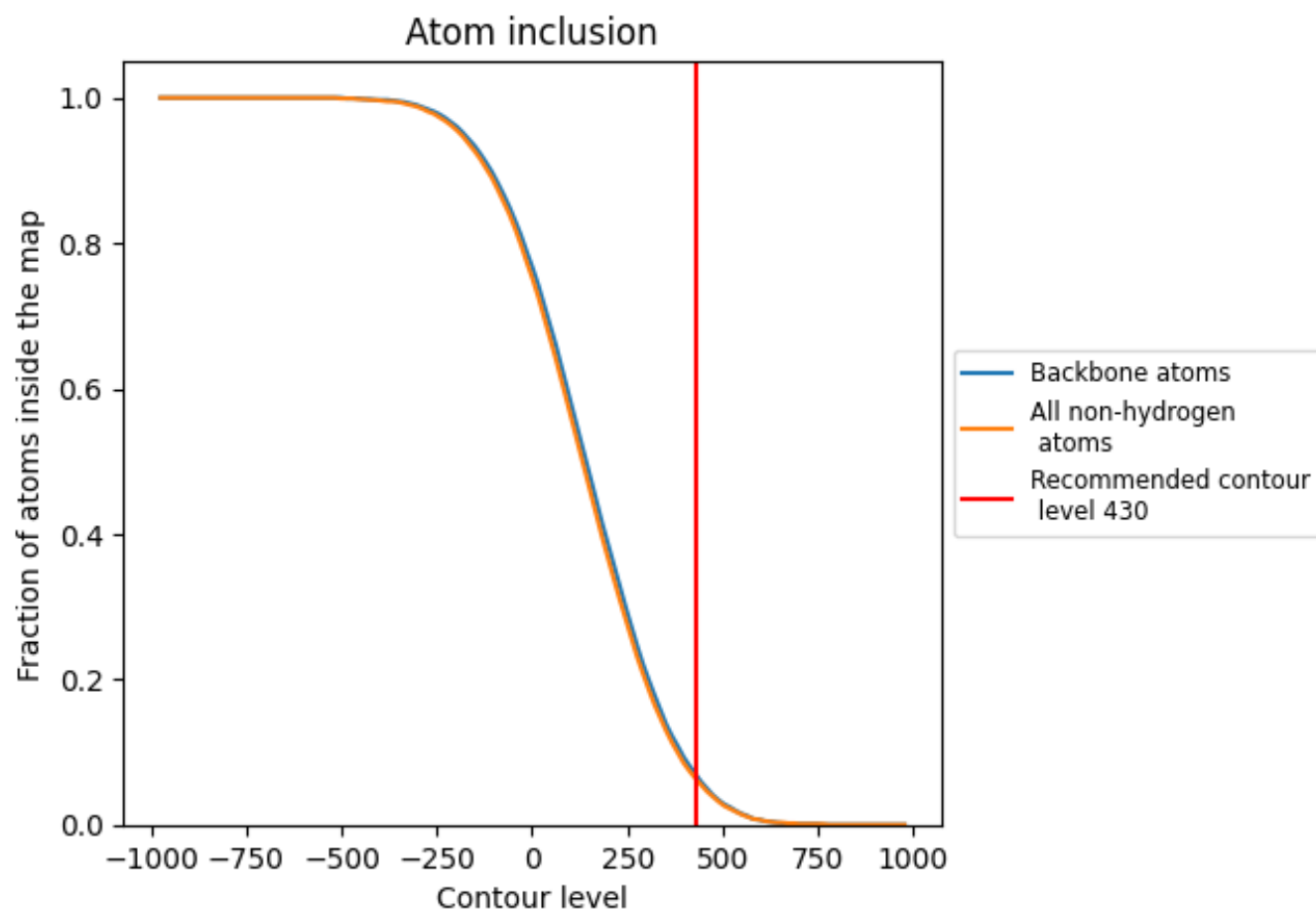
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (430).

9.4 Atom inclusion [i](#)



At the recommended contour level, 7% of all backbone atoms, 6% 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 (430) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.0630	 0.0210
A	 0.0670	 0.0210
B	 0.0970	 0.0030
C	 0.1090	 0.0310
D	 0.0810	 0.0140
E	 0.0780	 0.0340
F	 0.0810	 0.0260
G	 0.0640	 0.0240
H	 0.0340	 0.0130
I	 0.0130	 0.0240
J	 0.0300	 0.0110
K	 0.0330	 0.0240
L	 0.0560	 0.0330
M	 0.0740	 0.0240
N	 0.0700	 0.0110

