



## wwPDB EM Validation Summary Report ⓘ

Jun 1, 2025 – 12:56 AM JST

PDB ID : 9LR9 / pdb\_00009lr9  
EMDB ID : EMD-63322  
Title : Local reconstruction of bovine adenovirus type 3 capsid  
Authors : Xiao, H.; Liu, H.R.  
Deposited on : 2025-01-30  
Resolution : 3.30 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev118  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1



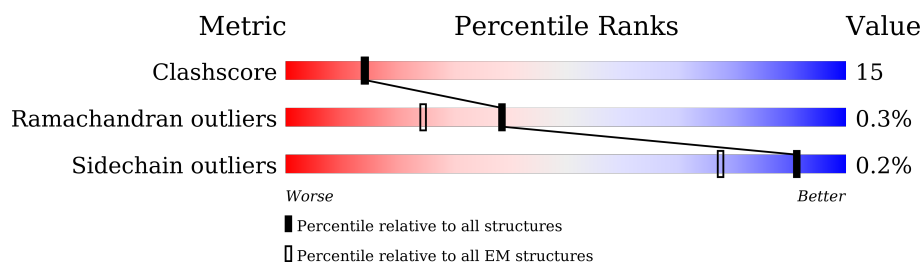
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.30 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415



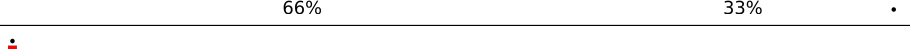
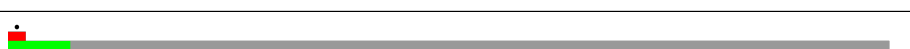


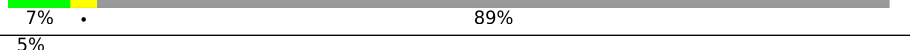
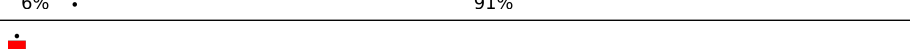


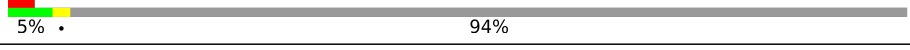
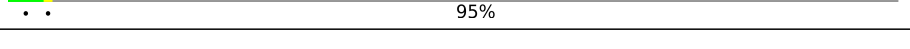
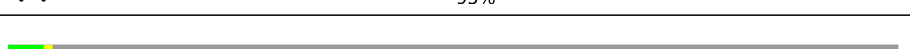
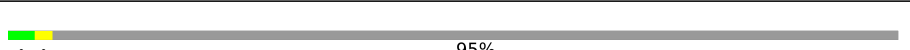


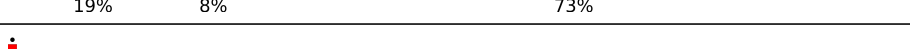







The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey 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	911	 62% 36% ..
1	D	911	 68% 31% .
1	F	911	 65% 34% .
1	G	911	 64% 35%
1	H	911	 63% 35% ..
1	I	911	 64% 34% ..
1	J	911	 65% 34%
1	X	911	 66% 33% .

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Mol	Chain	Length	Quality of chain
1	Y	911	
1	g	911	
1	h	911	
1	i	911	
2	B	263	
2	L	263	
2	S	263	
2	T	263	
2	Z	263	
2	a	263	
2	b	263	
2	c	263	
2	d	263	
3	C	171	
3	U	171	
3	e	171	
3	f	171	
4	E	80	
5	K	568	
6	M	410	
7	N	216	
7	R	216	
8	O	125	
8	P	125	
8	Q	125	

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Mol	Chain	Length	Quality of chain
8	V	125	
9	j	482	



## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 101800 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 Hexon protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	900	Total	C	N	O	S	0	0
			7183	4544	1257	1351	31		
1	D	903	Total	C	N	O	S	0	0
			7223	4574	1264	1354	31		
1	F	905	Total	C	N	O	S	0	0
			7238	4583	1267	1357	31		
1	G	907	Total	C	N	O	S	0	0
			7248	4589	1269	1359	31		
1	H	901	Total	C	N	O	S	0	0
			7209	4566	1262	1351	30		
1	I	899	Total	C	N	O	S	0	0
			7174	4539	1254	1351	30		
1	J	909	Total	C	N	O	S	0	0
			7260	4596	1271	1362	31		
1	X	904	Total	C	N	O	S	0	0
			7230	4579	1265	1355	31		
1	Y	904	Total	C	N	O	S	0	0
			7230	4579	1265	1355	31		
1	g	905	Total	C	N	O	S	0	0
			7238	4583	1267	1357	31		
1	h	905	Total	C	N	O	S	0	0
			7238	4583	1267	1357	31		
1	i	904	Total	C	N	O	S	0	0
			7230	4579	1265	1355	31		

- Molecule 2 is a protein called PVI.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	20	Total	C	N	O	S	0	0
			152	94	29	28	1		
2	L	50	Total	C	N	O	S	0	0
			374	239	65	68	2		
2	S	33	Total	C	N	O	S	0	0
			254	156	47	48	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	T	28	Total	C	N	O	S	0	0
			211	129	40	40	2		
2	Z	24	Total	C	N	O	S	0	0
			174	107	35	30	2		
2	a	27	Total	C	N	O	S	0	0
			200	123	39	36	2		
2	b	30	Total	C	N	O	S	0	0
			229	142	44	41	2		
2	c	26	Total	C	N	O	S	0	0
			196	121	38	35	2		
2	d	16	Total	C	N	O	S	0	0
			122	74	25	22	1		

- Molecule 3 is a protein called Pre-histone-like nucleoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	8	Total	C	N	O	S	0	0
			59	37	10	10	2		
3	U	8	Total	C	N	O	S	0	0
			59	37	10	10	2		
3	e	8	Total	C	N	O	S	0	0
			59	37	10	10	2		
3	f	8	Total	C	N	O	S	0	0
			59	37	10	10	2		

- Molecule 4 is a protein called PX.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	E	38	Total	C	N	O	0	0
			276	184	49	43		

- Molecule 5 is a protein called Pre-hexon-linking protein IIIa.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	262	Total	C	N	O	S	0	0
			2042	1284	361	395	2		

- Molecule 6 is a protein called PV.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	M	110	Total	C	N	O	S	0	0
			837	518	146	169	4		



- Molecule 7 is a protein called Pre-hexon-linking protein VIII.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	N	178	Total	C	N	O	S	0	0
			1407	887	254	261	5		
7	R	178	Total	C	N	O	S	0	0
			1407	887	254	261	5		

- Molecule 8 is a protein called PIX.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	111	Total	C	N	O	S	0	0
			863	531	160	169	3		
8	P	111	Total	C	N	O	S	0	0
			863	531	160	169	3		
8	Q	111	Total	C	N	O	S	0	0
			863	531	160	169	3		
8	V	111	Total	C	N	O	S	0	0
			863	531	160	169	3		

- Molecule 9 is a protein called Penton protein.

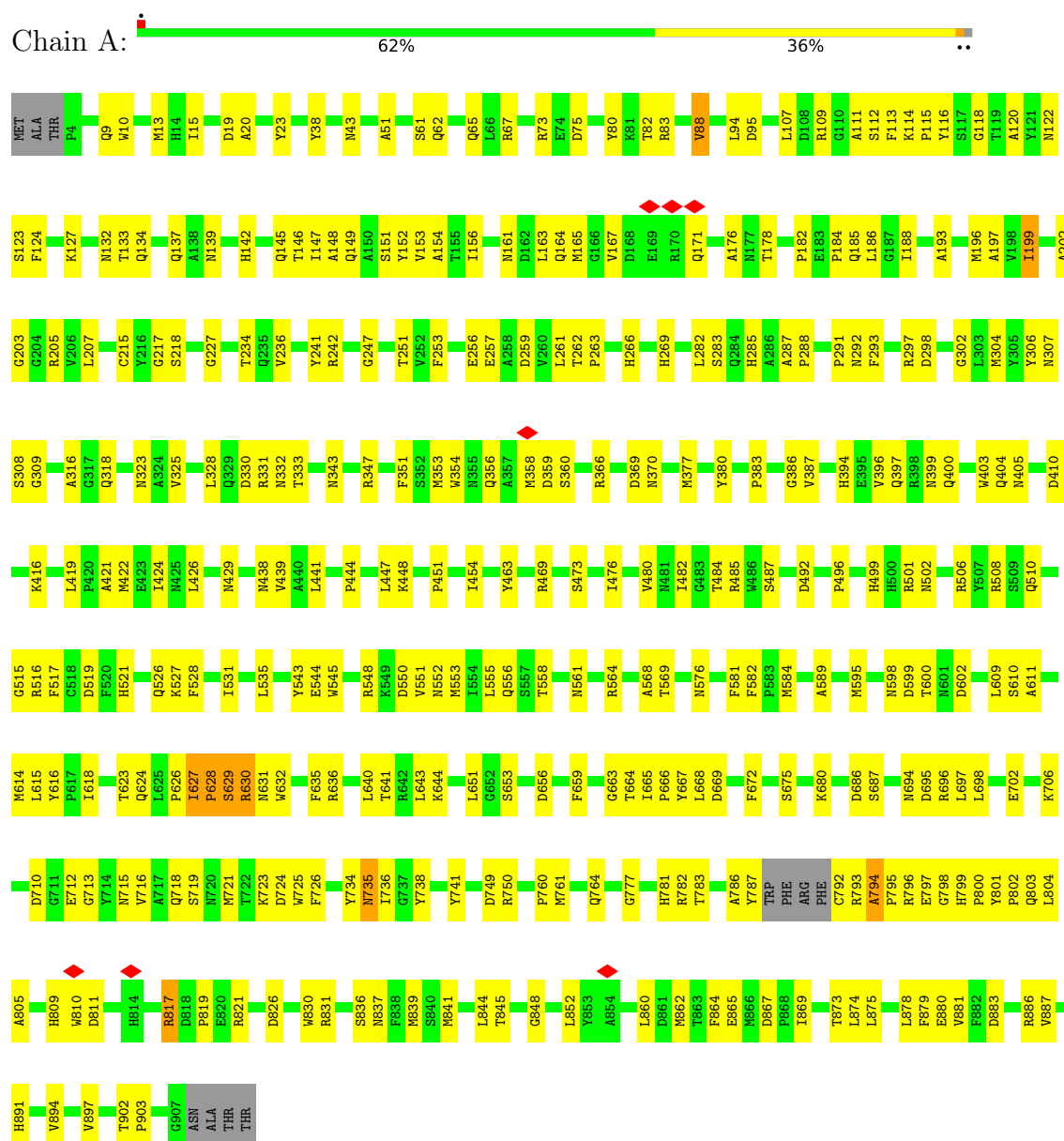
Mol	Chain	Residues	Atoms					AltConf	Trace
9	j	441	Total	C	N	O	S	0	0
			3530	2235	609	675	11		



### 3 Residue-property plots

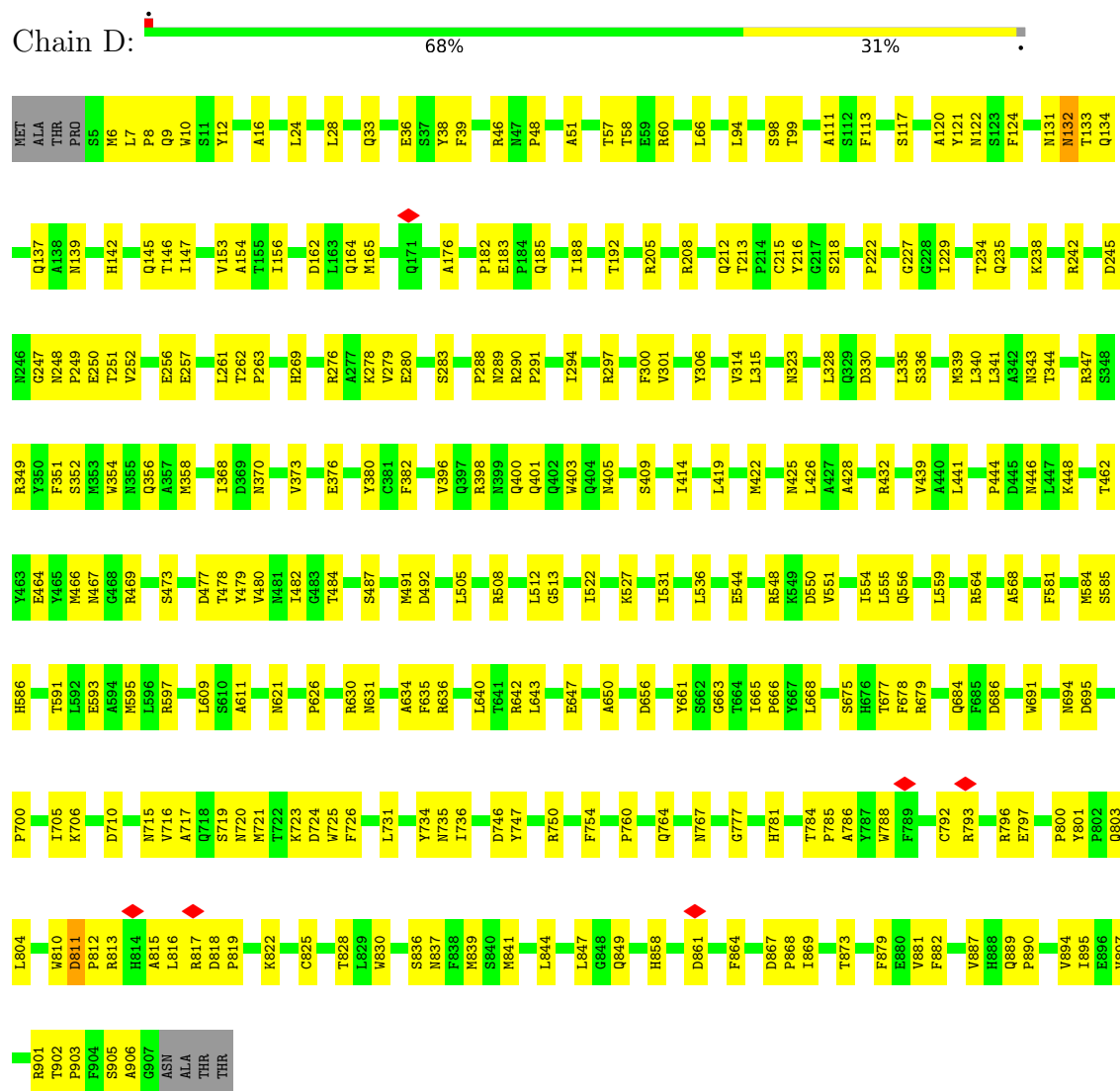
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

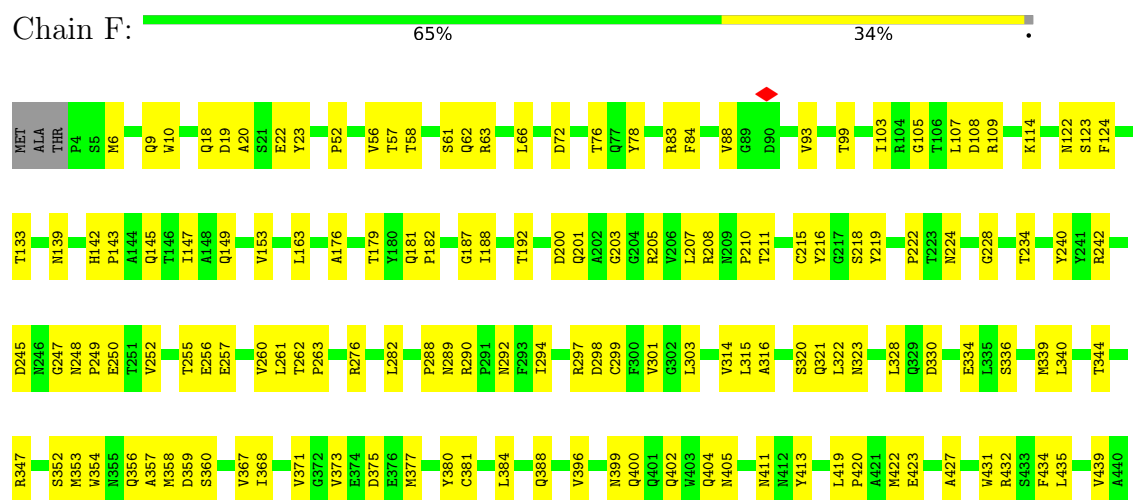


- Molecule 1: Hexon protein

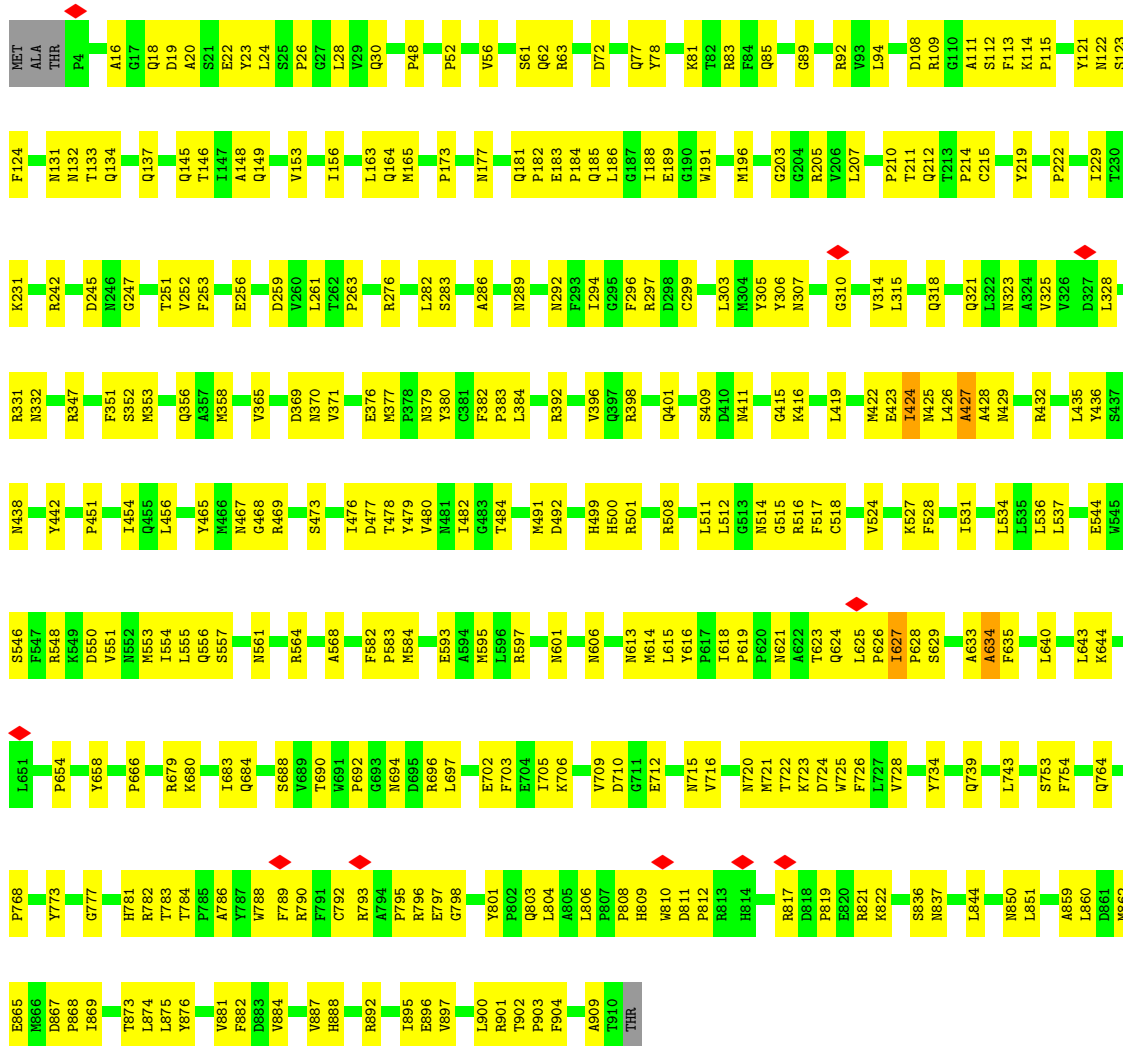




• Molecule 1: Hexon protein

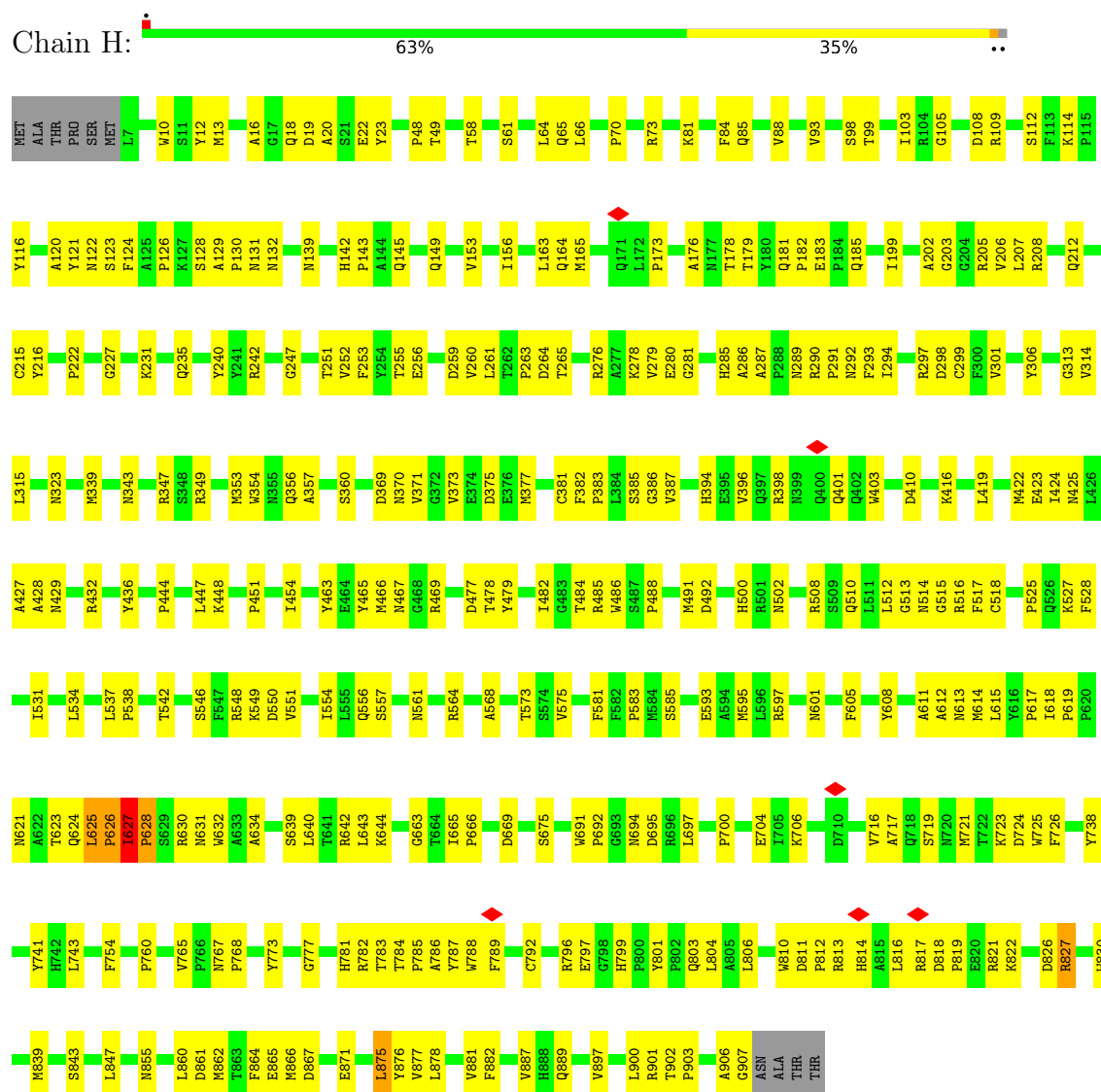




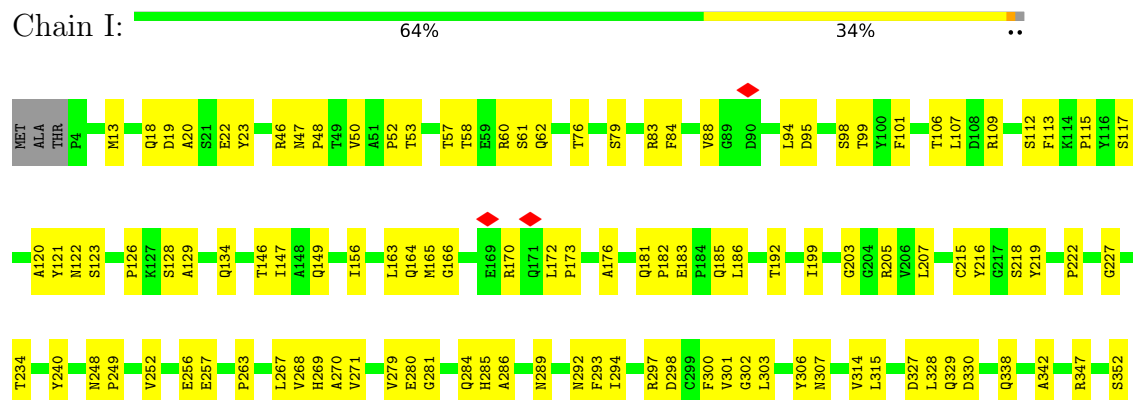




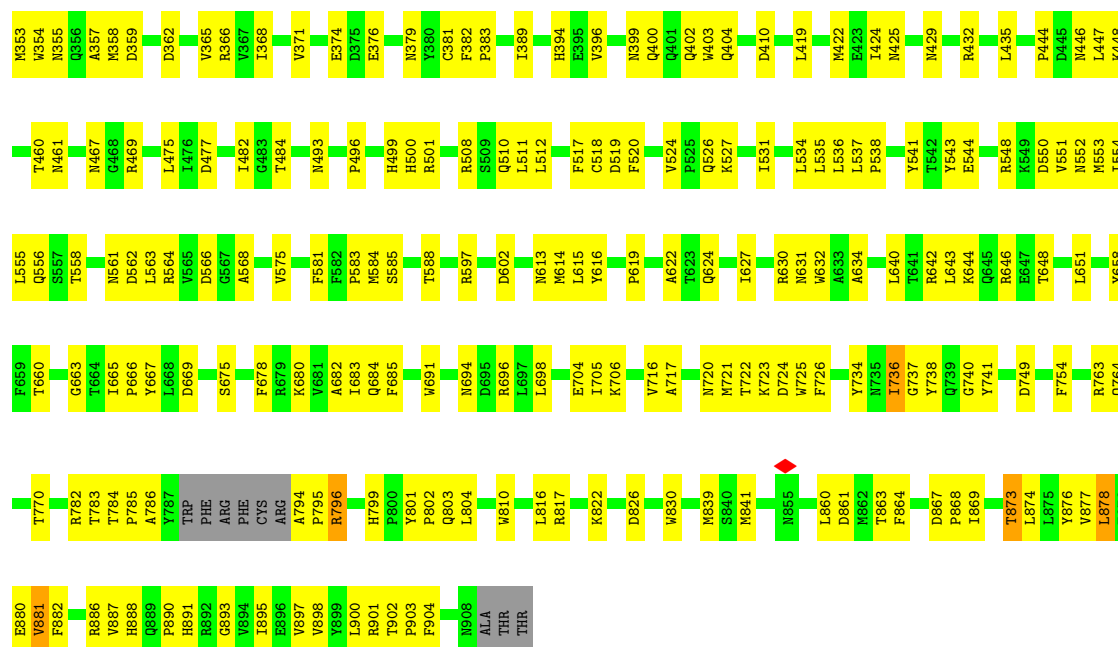
• Molecule 1: Hexon protein



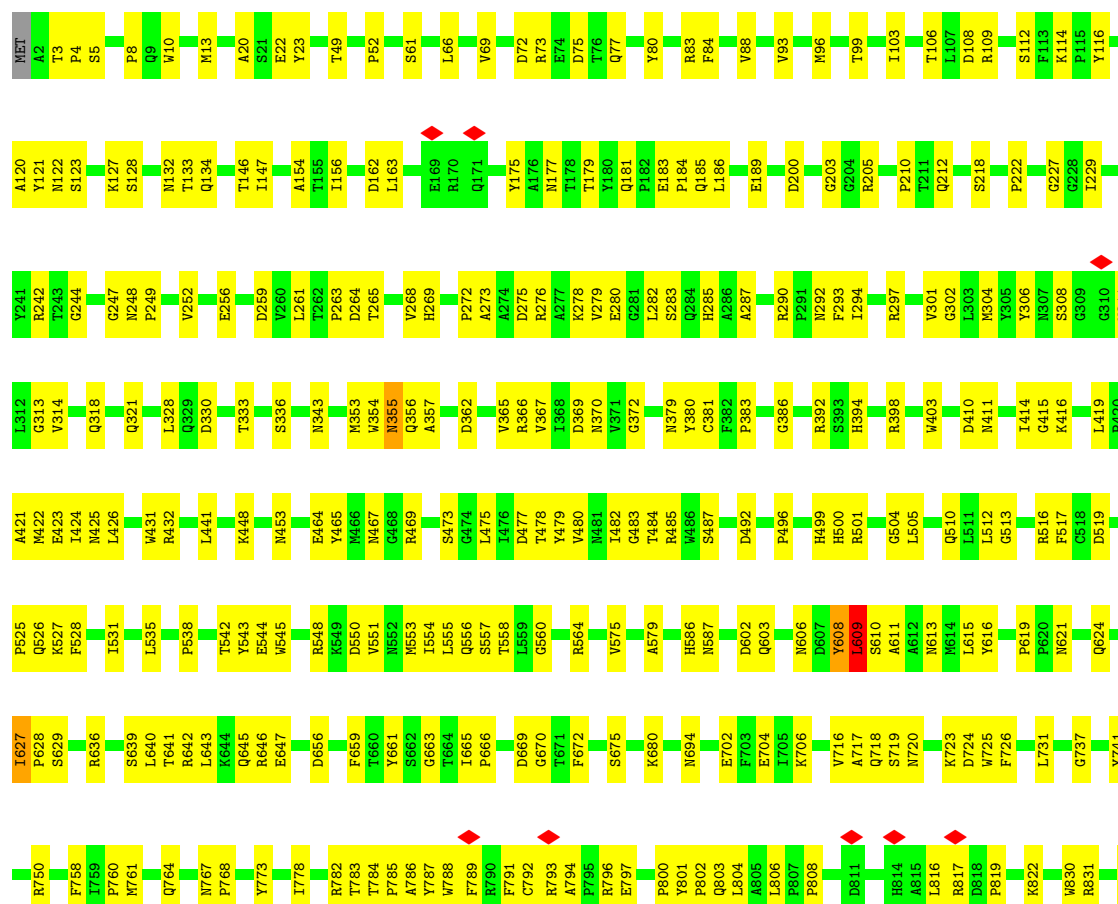
• Molecule 1: Hexon protein







• Molecule 1: Hexon protein

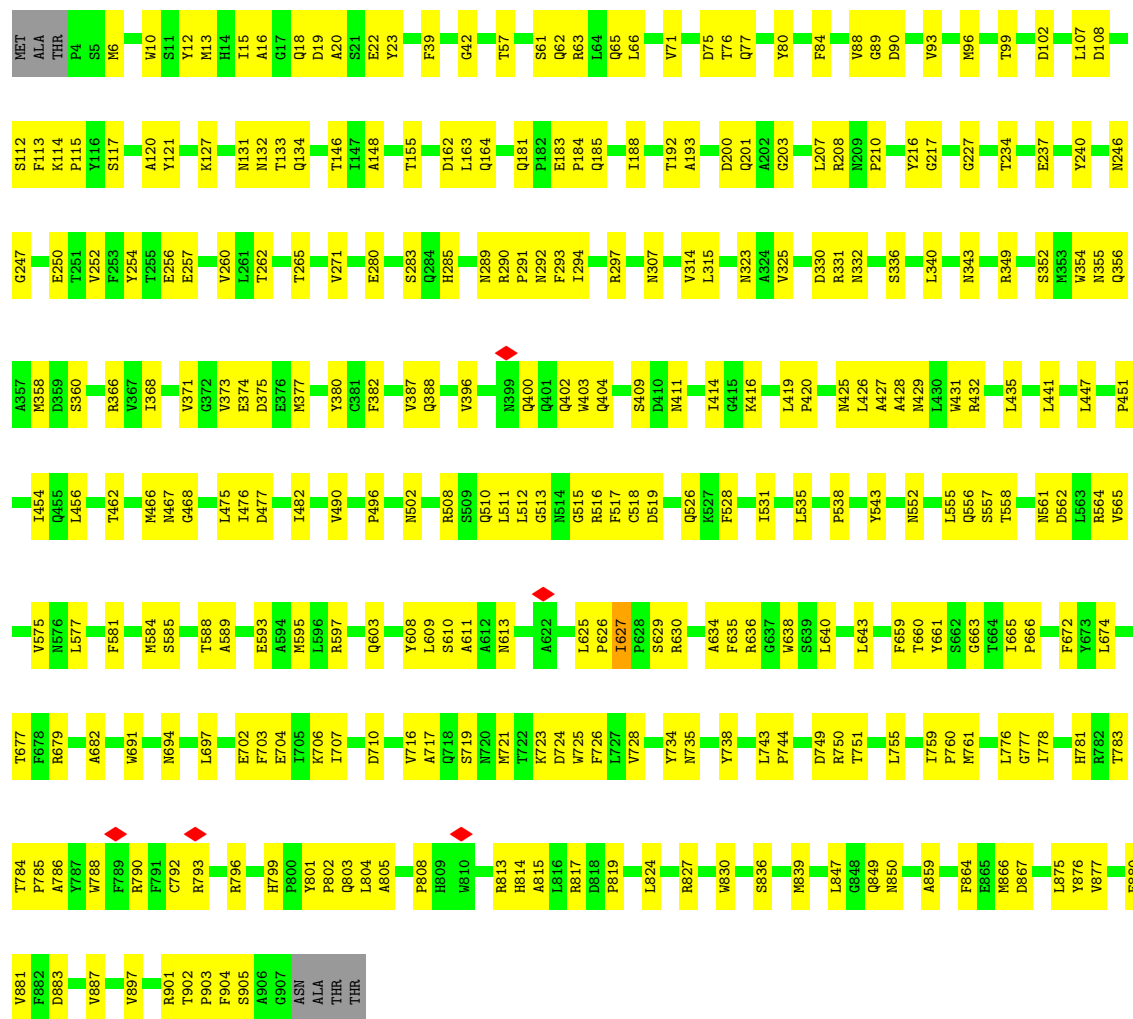






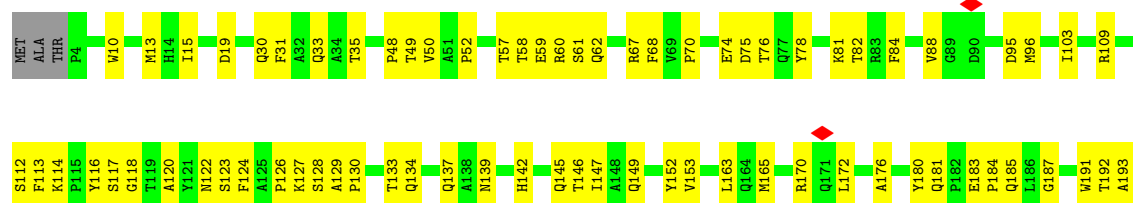
● Molecule 1: Hexon protein

Chain X: 66% 33%



● Molecule 1: Hexon protein

Chain Y: 60% 39%



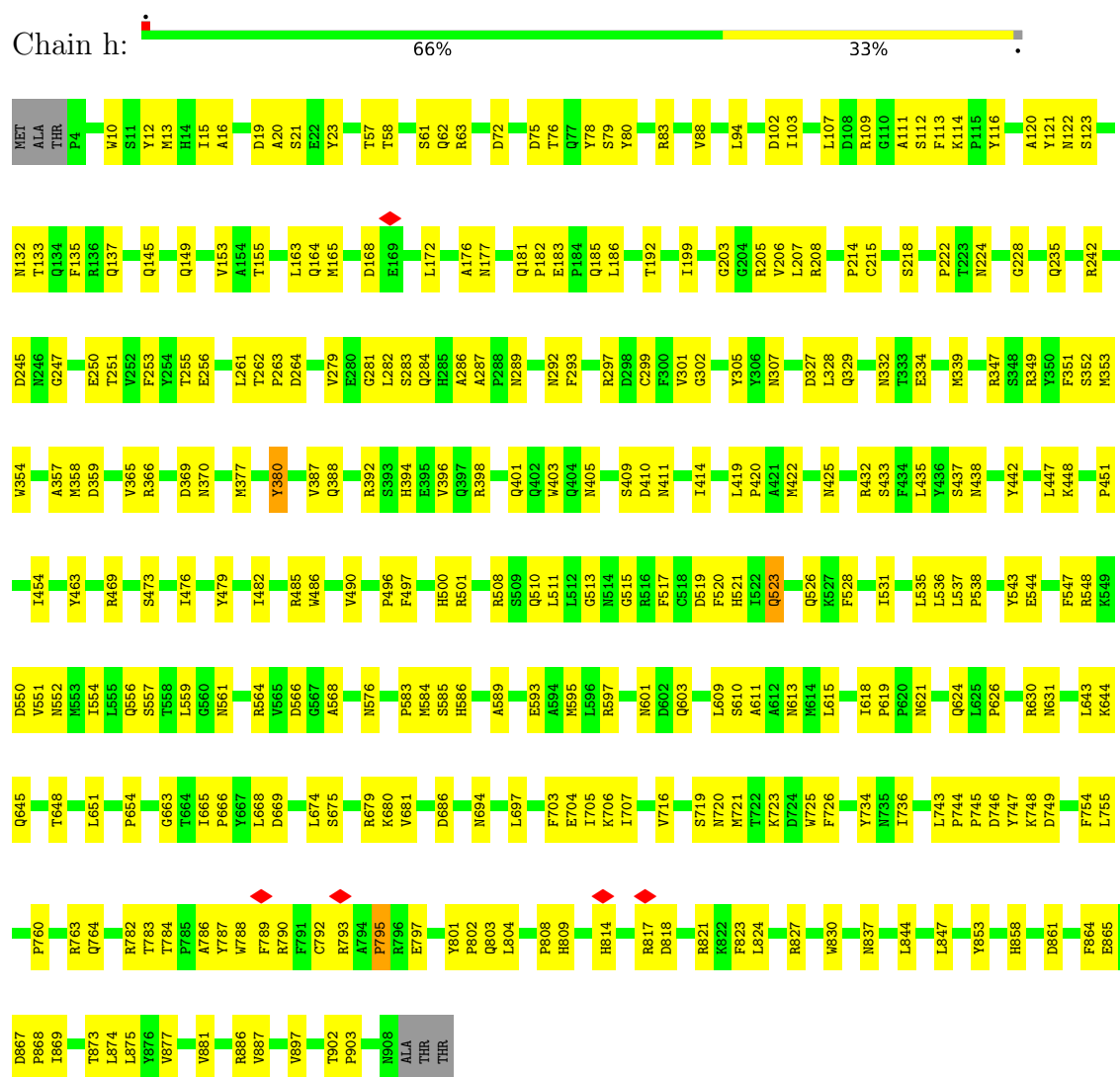




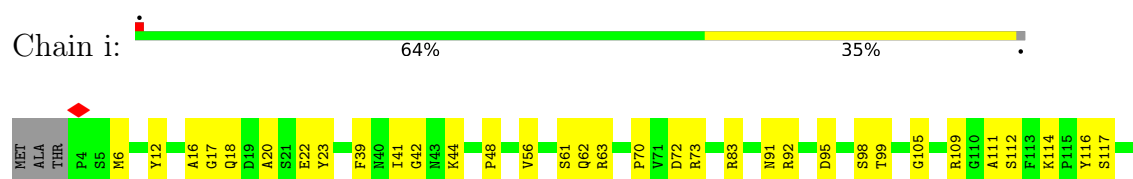




• Molecule 1: Hexon protein



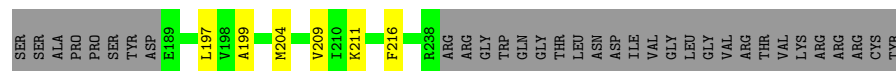
• Molecule 1: Hexon protein





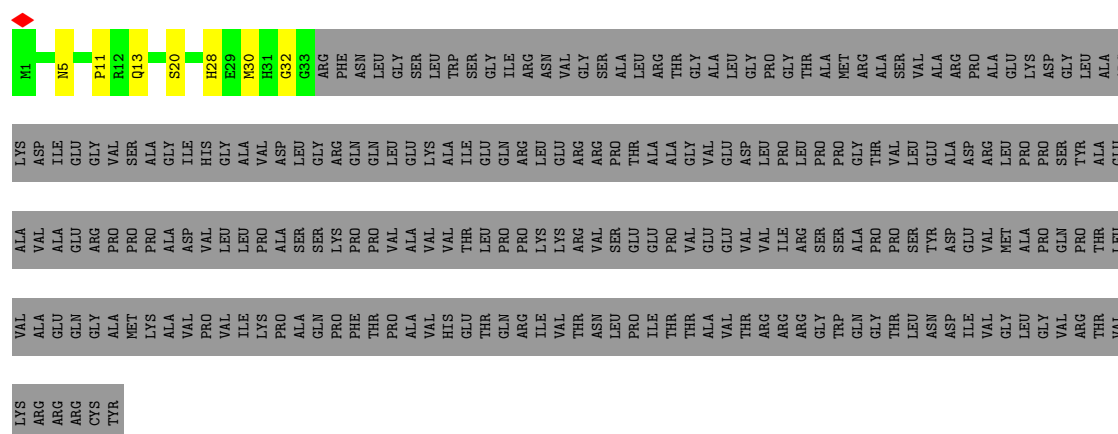






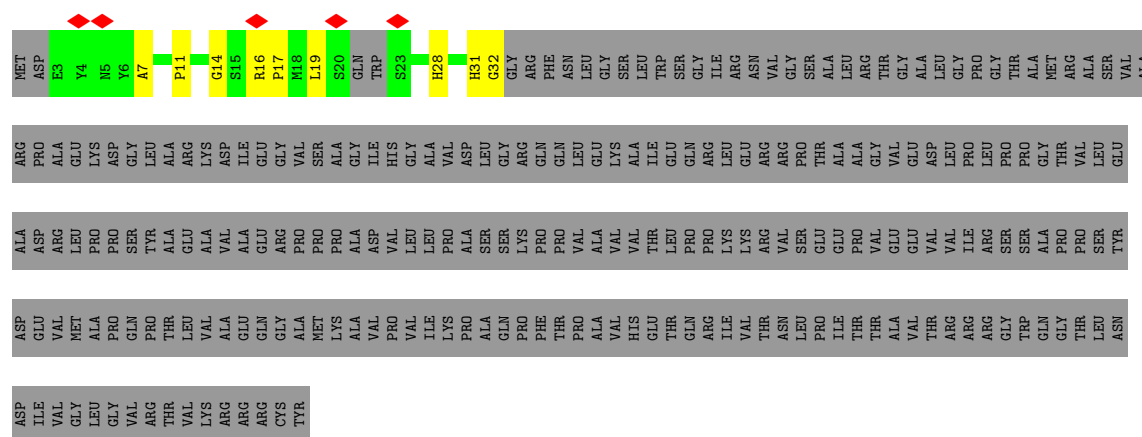
- Molecule 2: PVI

Chain S:  10% 87%



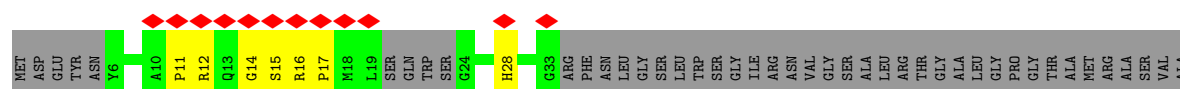
- Molecule 2: PVI

Chain T:  7% 89%



- Molecule 2: PVI

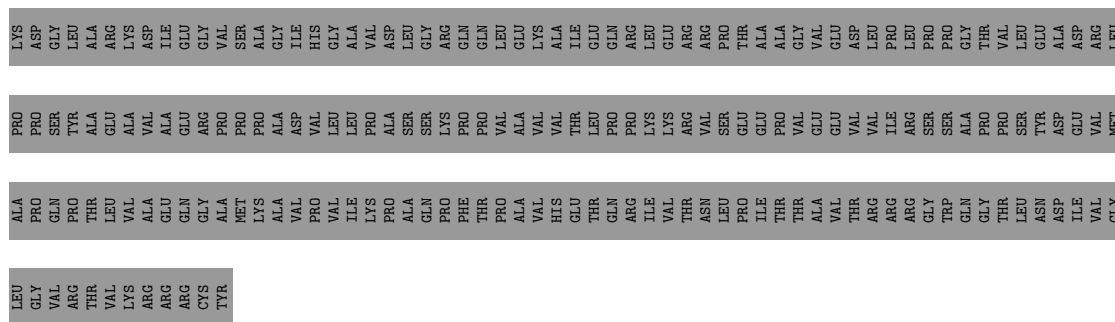
Chain Z:  5% 6% 91%





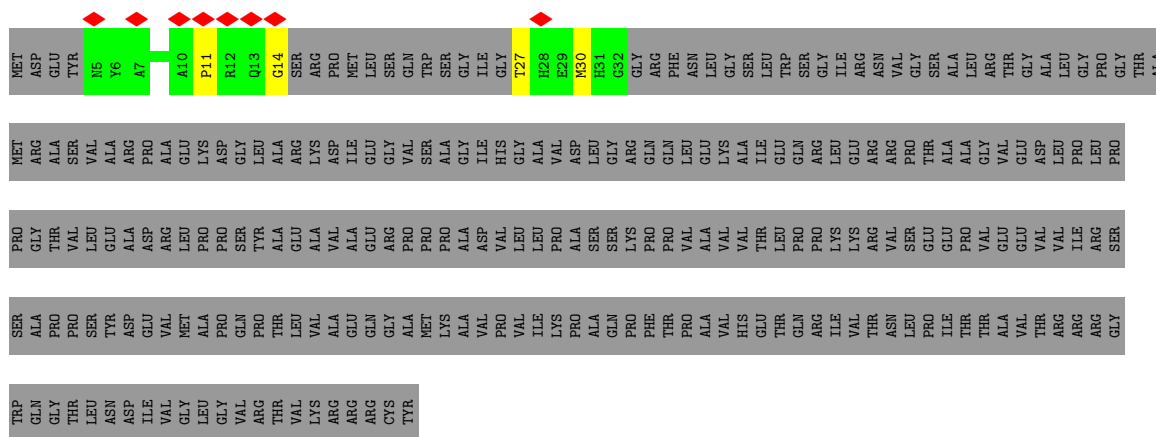






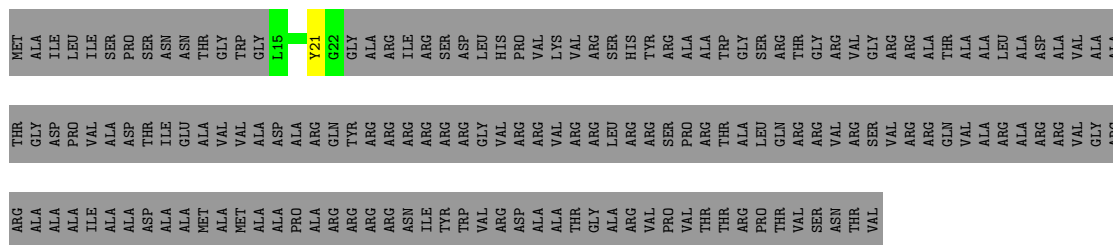
- Molecule 2: PVI

Chain d:  5% 94%



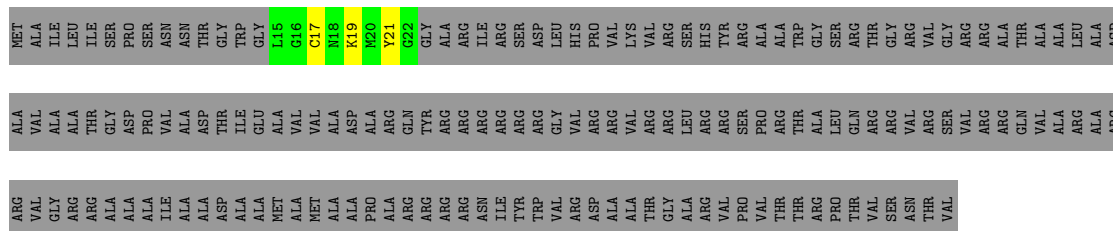
- Molecule 3: Pre-histone-like nucleoprotein

Chain C:  95%



- Molecule 3: Pre-histone-like nucleoprotein

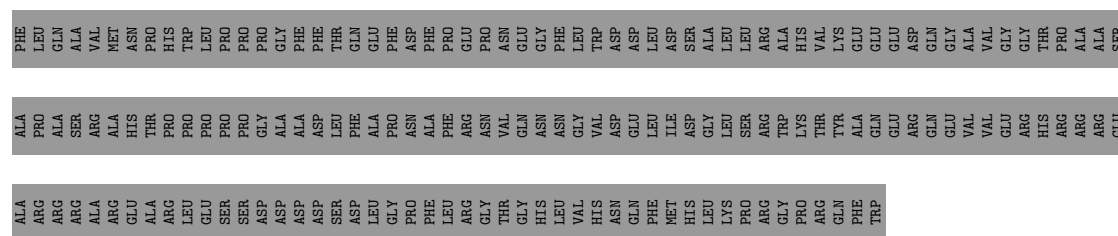
Chain U:  95%



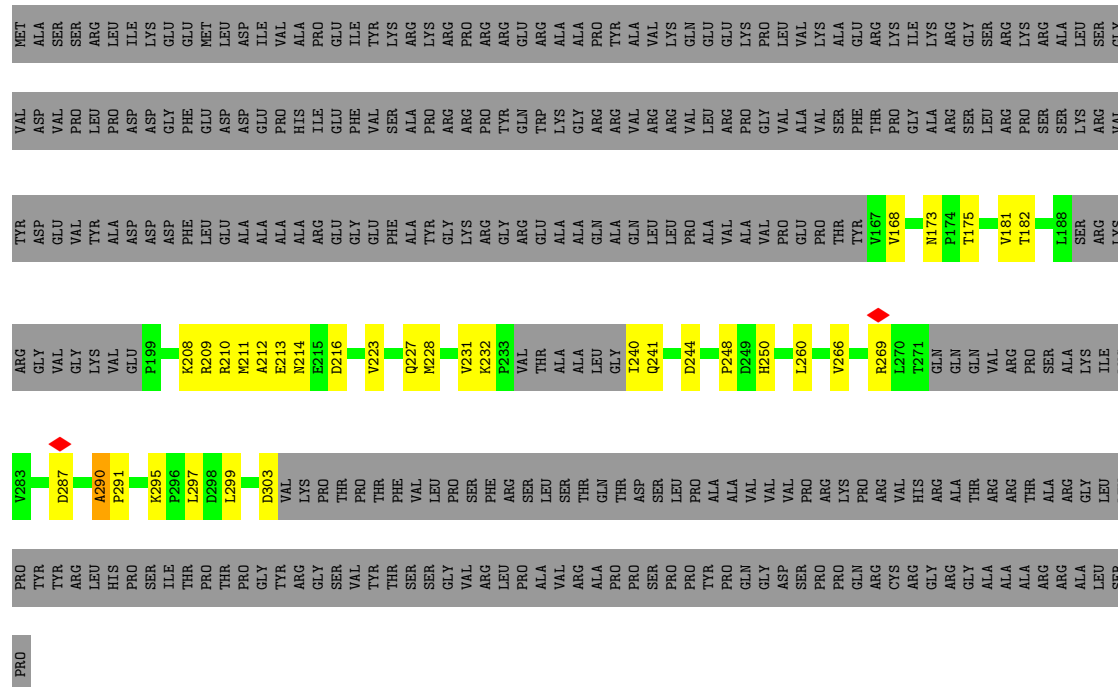




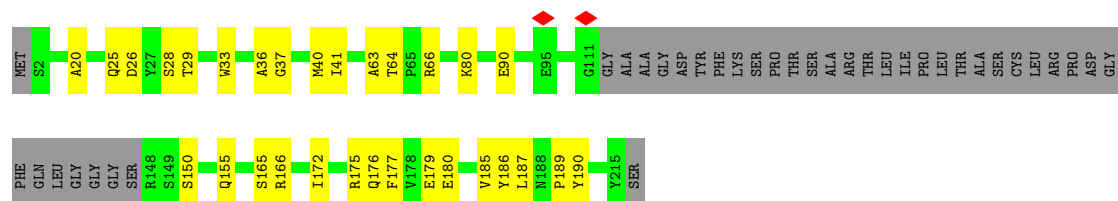




- Molecule 6: PV



- Molecule 7: Pre-hexon-linking protein VIII



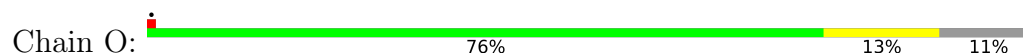
- Molecule 7: Pre-hexon-linking protein VIII



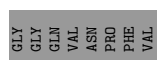
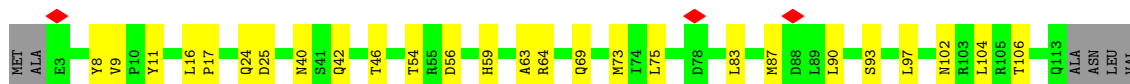




- Molecule 8: PIX



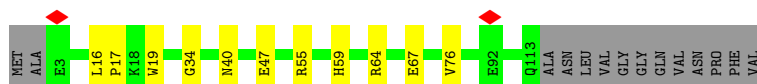
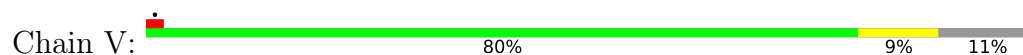
- Molecule 8: PIX



- Molecule 8: PIX



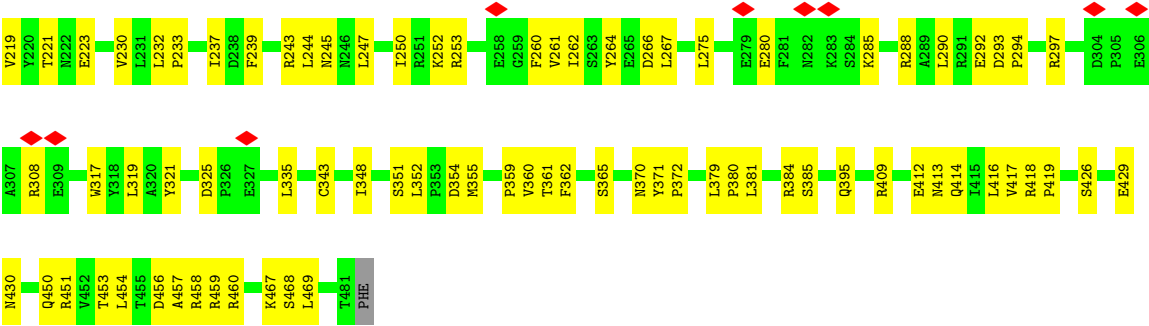
- Molecule 8: PIX



- Molecule 9: Penton protein









## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45262	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	35	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	51.946	Depositor
Minimum map value	-26.989	Depositor
Average map value	0.019	Depositor
Map value standard deviation	2.759	Depositor
Recommended contour level	5	Depositor
Map size ( $\text{\AA}$ )	467.36, 467.36, 467.36	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.27, 1.27, 1.27	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	0.22	0/7388	0.40	3/10078 (0.0%)
1	D	0.21	0/7432	0.37	0/10139
1	F	0.25	0/7448	0.40	2/10161 (0.0%)
1	G	0.24	0/7458	0.38	1/10175 (0.0%)
1	H	0.26	0/7418	0.40	3/10121 (0.0%)
1	I	0.22	0/7379	0.40	2/10067 (0.0%)
1	J	0.21	1/7470 (0.0%)	0.38	0/10193
1	X	0.14	0/7440	0.36	0/10150
1	Y	0.27	1/7440 (0.0%)	0.42	2/10150 (0.0%)
1	g	0.33	3/7448 (0.0%)	0.44	4/10161 (0.0%)
1	h	0.14	0/7448	0.33	0/10161
1	i	0.18	1/7440 (0.0%)	0.38	0/10150
2	B	0.11	0/155	0.35	0/207
2	L	0.11	0/382	0.32	0/526
2	S	0.13	0/261	0.38	0/351
2	T	0.11	0/215	0.36	0/287
2	Z	0.10	0/177	0.37	0/235
2	a	0.09	0/204	0.28	0/272
2	b	0.14	0/236	0.35	0/318
2	c	0.11	0/200	0.28	0/267
2	d	0.08	0/124	0.30	0/165
3	C	0.12	0/59	0.42	0/76
3	U	0.13	0/59	0.33	0/76
3	e	0.09	0/59	0.23	0/76
3	f	0.07	0/59	0.17	0/76
4	E	0.11	0/280	0.29	0/382
5	K	0.11	0/2077	0.28	0/2825
6	M	0.19	0/845	0.38	0/1145
7	N	0.14	0/1451	0.32	0/1980
7	R	0.14	0/1451	0.31	0/1980
8	O	0.10	0/876	0.27	0/1187
8	P	0.12	0/876	0.31	0/1187
8	Q	0.14	0/876	0.36	0/1187
8	V	0.11	0/876	0.28	0/1187



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
9	j	0.12	0/3614	0.33	0/4921
All	All	0.22	6/104621 (0.0%)	0.38	17/142619 (0.0%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	g	610	SER	CA-C	-7.49	1.43	1.52
1	g	627	ILE	N-CA	6.86	1.55	1.46
1	J	609	LEU	CA-C	-6.27	1.44	1.52
1	g	626	PRO	CA-C	5.57	1.60	1.52
1	i	463	TYR	CA-C	-5.33	1.46	1.52

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	817	ARG	N-CA-C	9.30	121.98	108.86
1	A	629	SER	N-CA-C	8.26	121.75	110.35
1	F	629	SER	N-CA-C	8.14	123.11	109.76
1	g	629	SER	N-CA-C	7.17	121.52	109.76
1	g	627	ILE	N-CA-C	6.94	123.86	108.88

There are no chirality outliers.

There are no planarity outliers.

## 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	7183	0	6847	309	0
1	D	7223	0	6881	235	0
1	F	7238	0	6895	286	0
1	G	7248	0	6902	303	0
1	H	7209	0	6867	291	0
1	I	7174	0	6835	281	0
1	J	7260	0	6913	285	0
1	X	7230	0	6889	257	0
1	Y	7230	0	6889	312	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	g	7238	0	6895	300	0
1	h	7238	0	6895	257	0
1	i	7230	0	6889	264	0
2	B	152	0	137	1	0
2	L	374	0	395	4	0
2	S	254	0	234	10	0
2	T	211	0	196	8	0
2	Z	174	0	168	7	0
2	a	200	0	188	5	0
2	b	229	0	212	3	0
2	c	196	0	185	3	0
2	d	122	0	109	6	0
3	C	59	0	58	1	0
3	U	59	0	58	2	0
3	e	59	0	58	1	0
3	f	59	0	58	3	0
4	E	276	0	308	10	0
5	K	2042	0	2015	28	0
6	M	837	0	857	31	0
7	N	1407	0	1331	21	0
7	R	1407	0	1331	37	0
8	O	863	0	860	10	0
8	P	863	0	860	21	0
8	Q	863	0	860	21	0
8	V	863	0	860	7	0
9	j	3530	0	3467	84	0
All	All	101800	0	97402	3057	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 15.

The worst 5 of 3057 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:F:627:ILE:HD12	1:F:628:PRO:HD2	1.28	1.10
1:A:627:ILE:HG23	1:A:860:LEU:O	1.49	1.09
1:A:623:THR:CG2	1:A:865:GLU:HG3	1.83	1.07
1:F:627:ILE:HG23	1:F:860:LEU:O	1.54	1.05
1:H:626:PRO:HB3	1:H:862:MET:H	1.19	1.04

There are no symmetry-related clashes.



## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	896/911 (98%)	800 (89%)	89 (10%)	7 (1%)	16	46
1	D	901/911 (99%)	810 (90%)	90 (10%)	1 (0%)	48	76
1	F	903/911 (99%)	811 (90%)	91 (10%)	1 (0%)	48	76
1	G	905/911 (99%)	811 (90%)	91 (10%)	3 (0%)	37	66
1	H	899/911 (99%)	803 (89%)	93 (10%)	3 (0%)	37	66
1	I	895/911 (98%)	813 (91%)	80 (9%)	2 (0%)	44	71
1	J	907/911 (100%)	818 (90%)	86 (10%)	3 (0%)	37	66
1	X	902/911 (99%)	828 (92%)	72 (8%)	2 (0%)	44	71
1	Y	902/911 (99%)	801 (89%)	97 (11%)	4 (0%)	30	61
1	g	903/911 (99%)	818 (91%)	79 (9%)	6 (1%)	19	50
1	h	903/911 (99%)	818 (91%)	83 (9%)	2 (0%)	44	71
1	i	902/911 (99%)	821 (91%)	79 (9%)	2 (0%)	44	71
2	B	16/263 (6%)	11 (69%)	5 (31%)	0	100	100
2	L	48/263 (18%)	45 (94%)	3 (6%)	0	100	100
2	S	31/263 (12%)	30 (97%)	1 (3%)	0	100	100
2	T	24/263 (9%)	22 (92%)	2 (8%)	0	100	100
2	Z	20/263 (8%)	18 (90%)	2 (10%)	0	100	100
2	a	23/263 (9%)	22 (96%)	1 (4%)	0	100	100
2	b	28/263 (11%)	27 (96%)	1 (4%)	0	100	100
2	c	22/263 (8%)	22 (100%)	0	0	100	100
2	d	12/263 (5%)	10 (83%)	2 (17%)	0	100	100
3	C	6/171 (4%)	5 (83%)	1 (17%)	0	100	100
3	U	6/171 (4%)	5 (83%)	1 (17%)	0	100	100
3	e	6/171 (4%)	6 (100%)	0	0	100	100
3	f	6/171 (4%)	6 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	E	34/80 (42%)	33 (97%)	1 (3%)	0	100	100
5	K	250/568 (44%)	239 (96%)	11 (4%)	0	100	100
6	M	102/410 (25%)	91 (89%)	9 (9%)	2 (2%)	6	28
7	N	174/216 (81%)	161 (92%)	12 (7%)	1 (1%)	22	53
7	R	174/216 (81%)	162 (93%)	12 (7%)	0	100	100
8	O	109/125 (87%)	105 (96%)	3 (3%)	1 (1%)	14	44
8	P	109/125 (87%)	105 (96%)	4 (4%)	0	100	100
8	Q	109/125 (87%)	106 (97%)	1 (1%)	2 (2%)	7	30
8	V	109/125 (87%)	107 (98%)	1 (1%)	1 (1%)	14	44
9	j	437/482 (91%)	401 (92%)	36 (8%)	0	100	100
All	All	12673/16455 (77%)	11491 (91%)	1139 (9%)	43 (0%)	38	66

5 of 43 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	634	ALA
1	H	626	PRO
1	H	827	ARG
1	I	796	ARG
1	J	355	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	777/786 (99%)	775 (100%)	2 (0%)	91	94
1	D	780/786 (99%)	779 (100%)	1 (0%)	92	96
1	F	782/786 (100%)	781 (100%)	1 (0%)	92	96
1	G	782/786 (100%)	782 (100%)	0	100	100
1	H	778/786 (99%)	774 (100%)	4 (0%)	86	91
1	I	776/786 (99%)	774 (100%)	2 (0%)	91	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	783/786 (100%)	782 (100%)	1 (0%)	92	96
1	X	781/786 (99%)	780 (100%)	1 (0%)	92	96
1	Y	781/786 (99%)	780 (100%)	1 (0%)	92	96
1	g	782/786 (100%)	780 (100%)	2 (0%)	91	94
1	h	782/786 (100%)	781 (100%)	1 (0%)	92	96
1	i	781/786 (99%)	781 (100%)	0	100	100
2	B	14/210 (7%)	14 (100%)	0	100	100
2	L	42/210 (20%)	42 (100%)	0	100	100
2	S	25/210 (12%)	25 (100%)	0	100	100
2	T	21/210 (10%)	21 (100%)	0	100	100
2	Z	16/210 (8%)	16 (100%)	0	100	100
2	a	19/210 (9%)	19 (100%)	0	100	100
2	b	22/210 (10%)	22 (100%)	0	100	100
2	c	19/210 (9%)	19 (100%)	0	100	100
2	d	11/210 (5%)	11 (100%)	0	100	100
3	C	6/127 (5%)	6 (100%)	0	100	100
3	U	6/127 (5%)	6 (100%)	0	100	100
3	e	6/127 (5%)	6 (100%)	0	100	100
3	f	6/127 (5%)	6 (100%)	0	100	100
4	E	27/55 (49%)	27 (100%)	0	100	100
5	K	222/474 (47%)	221 (100%)	1 (0%)	86	91
6	M	98/345 (28%)	98 (100%)	0	100	100
7	N	151/179 (84%)	151 (100%)	0	100	100
7	R	151/179 (84%)	151 (100%)	0	100	100
8	O	93/103 (90%)	93 (100%)	0	100	100
8	P	93/103 (90%)	93 (100%)	0	100	100
8	Q	93/103 (90%)	92 (99%)	1 (1%)	70	82
8	V	93/103 (90%)	93 (100%)	0	100	100
9	j	394/432 (91%)	394 (100%)	0	100	100
All	All	10993/13906 (79%)	10975 (100%)	18 (0%)	91	95

5 of 18 residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	Y	609	LEU
1	h	523	GLN
1	g	627	ILE
1	I	736	ILE
1	X	735	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 211 such sidechains are listed below:

Mol	Chain	Res	Type
5	K	130	ASN
1	Y	161	ASN
1	i	429	ASN
6	M	250	HIS
1	X	139	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 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.



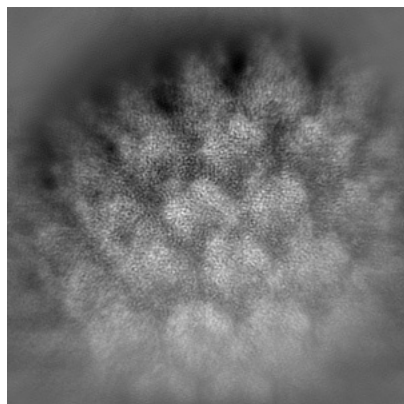
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63322. These allow visual inspection of the internal detail of the map and identification of artifacts.

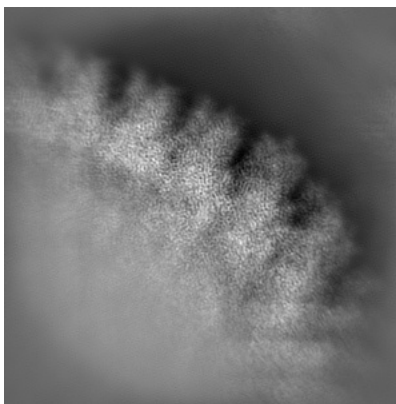
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

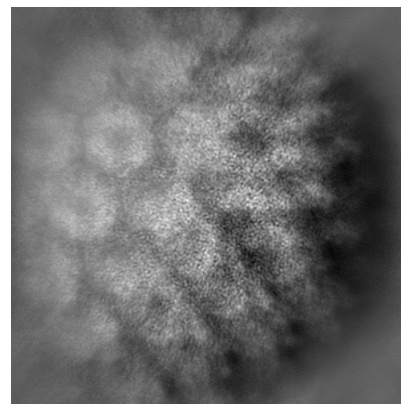
#### 6.1.1 Primary map



X

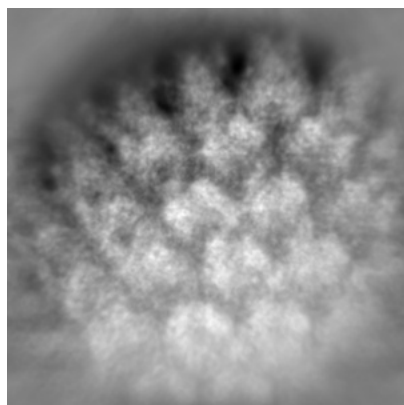


Y

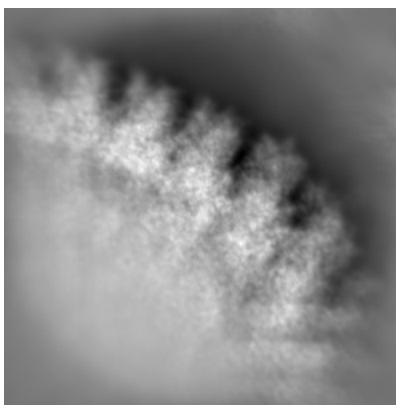


Z

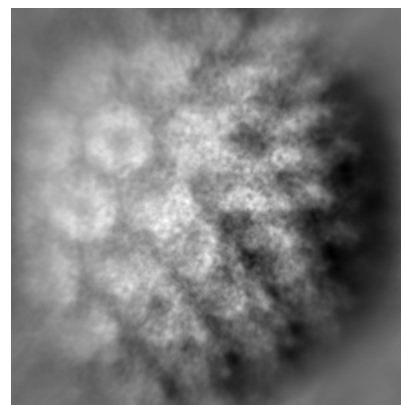
#### 6.1.2 Raw map



X



Y



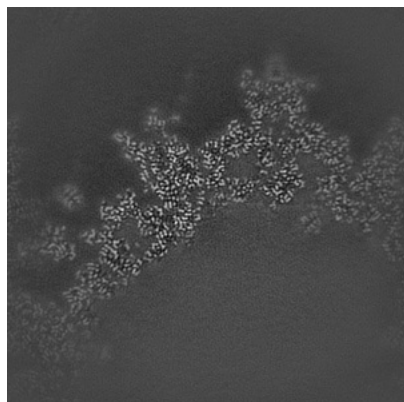
Z

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

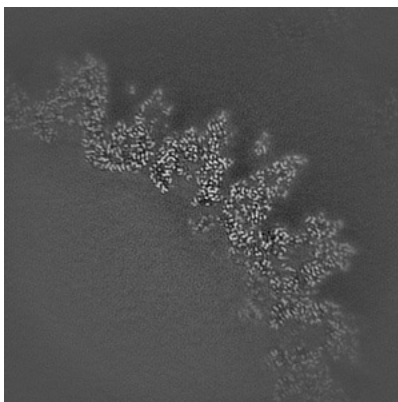


## 6.2 Central slices [i](#)

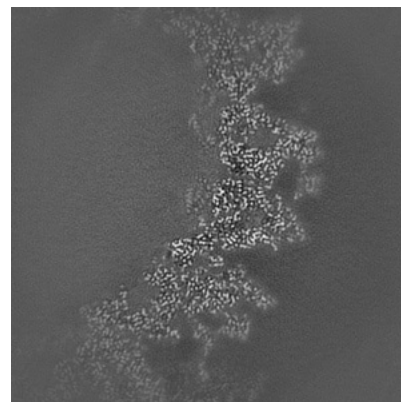
### 6.2.1 Primary map



X Index: 184

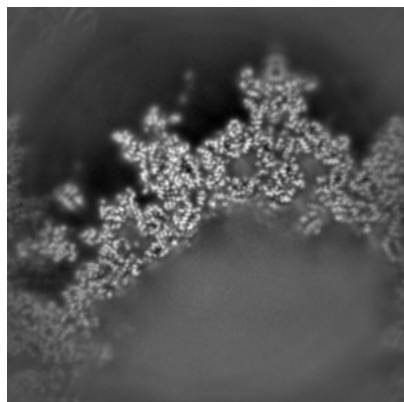


Y Index: 184

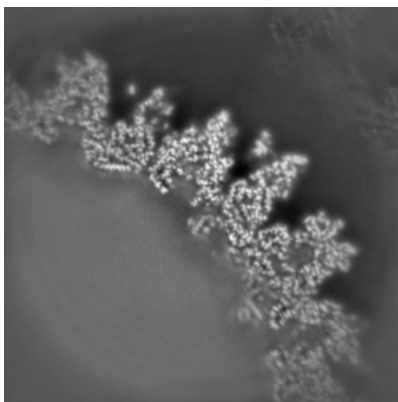


Z Index: 184

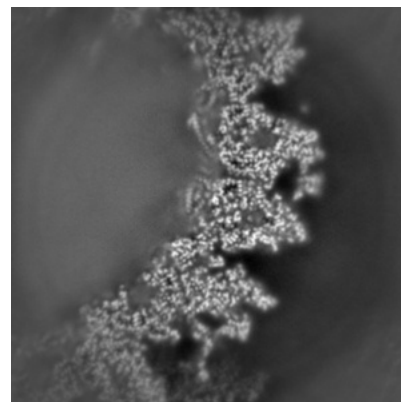
### 6.2.2 Raw map



X Index: 184



Y Index: 184



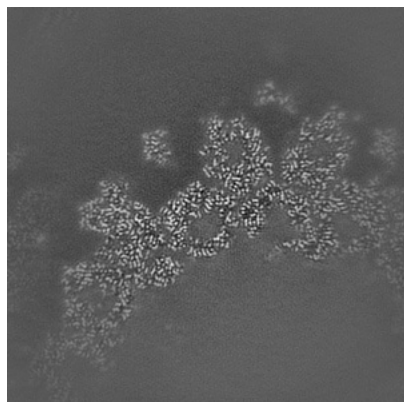
Z Index: 184

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

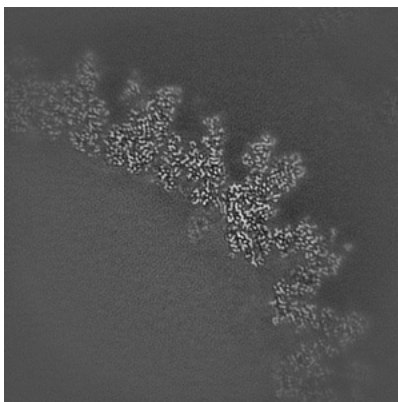


## 6.3 Largest variance slices [i](#)

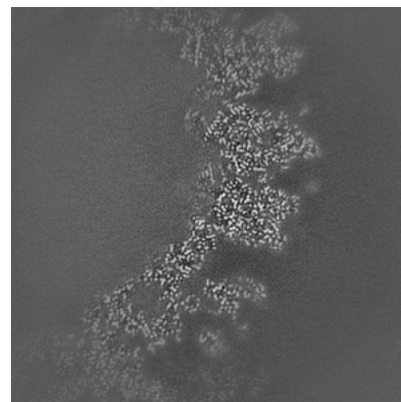
### 6.3.1 Primary map



X Index: 205

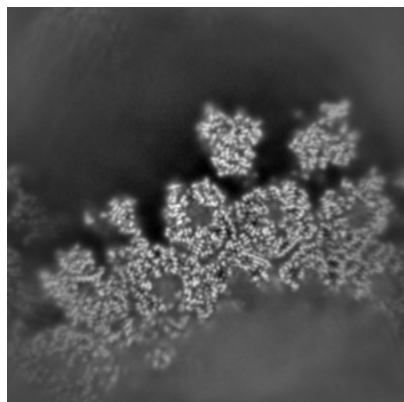


Y Index: 192

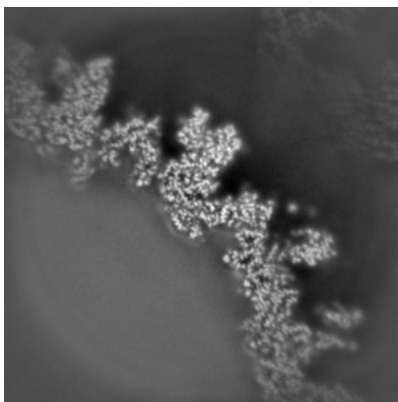


Z Index: 190

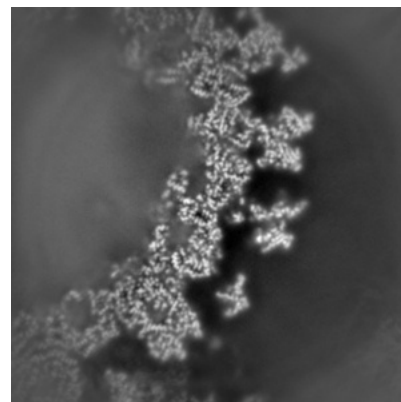
### 6.3.2 Raw map



X Index: 223



Y Index: 157



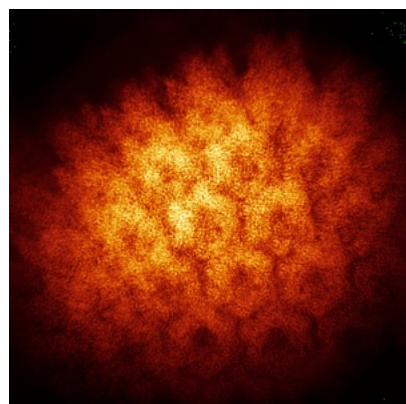
Z Index: 206

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

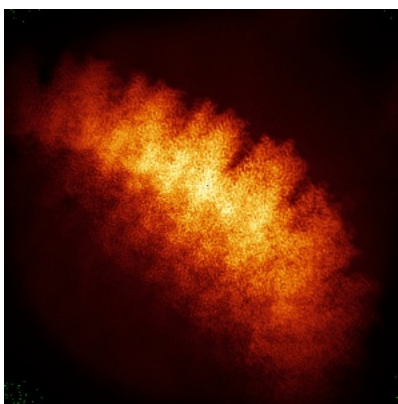


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

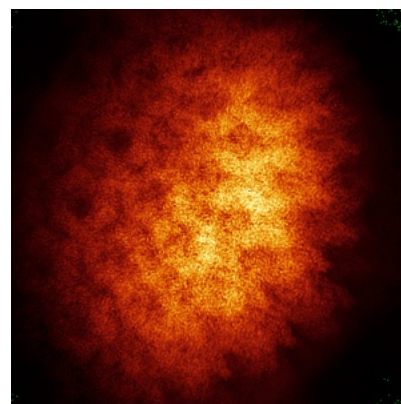
### 6.4.1 Primary map



X

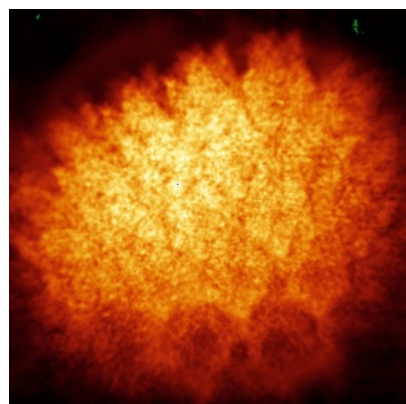


Y

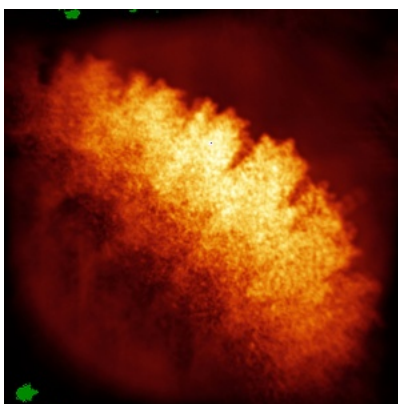


Z

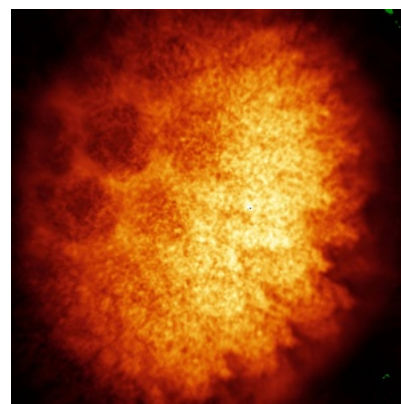
### 6.4.2 Raw map



X



Y



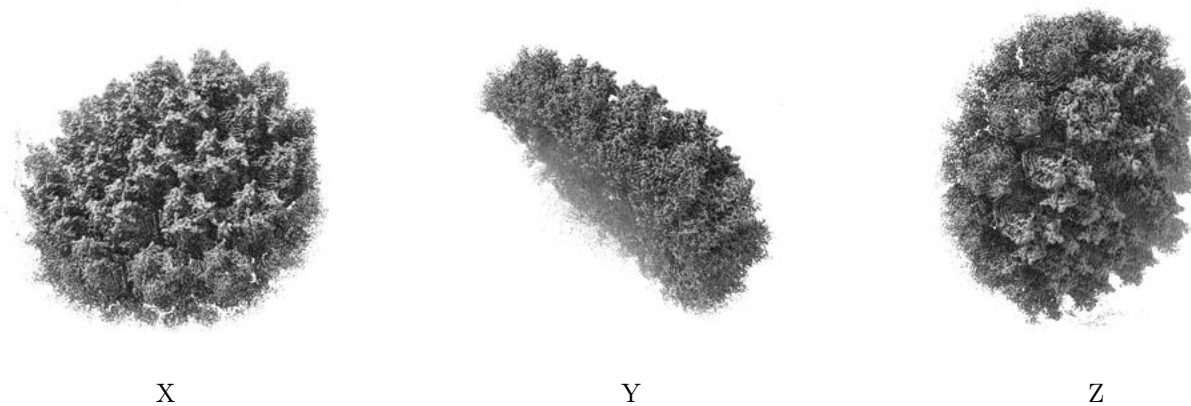
Z

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.



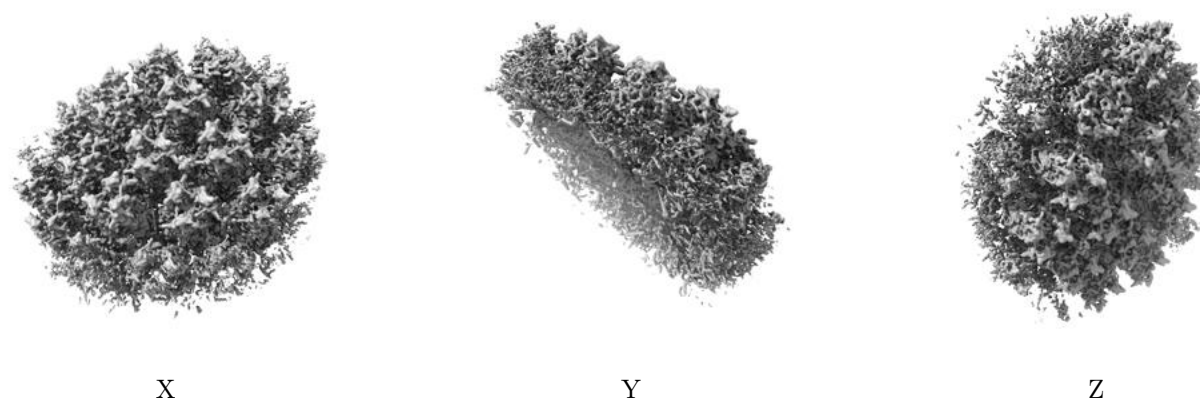
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

## 6.6 Mask visualisation [i](#)

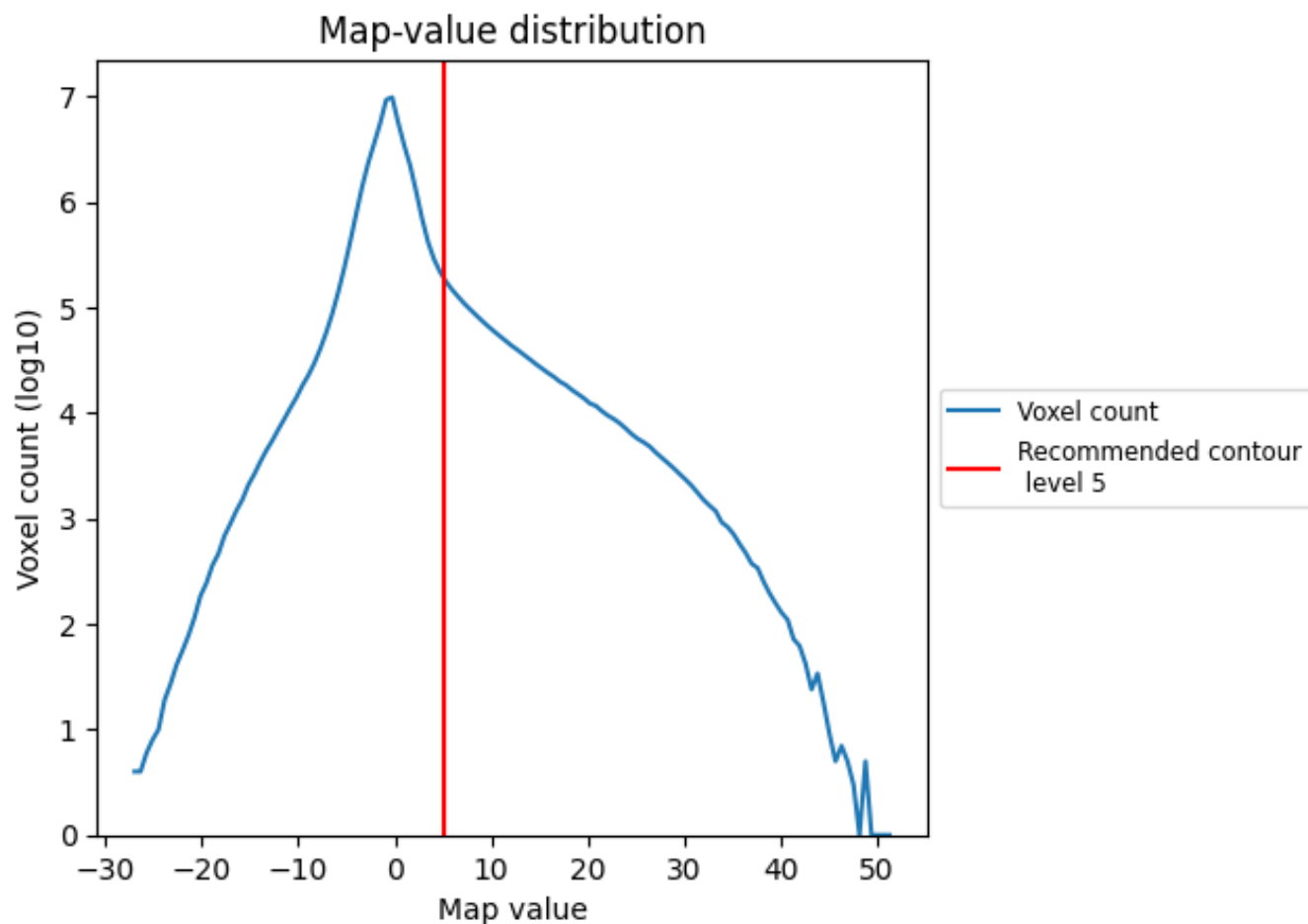
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

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

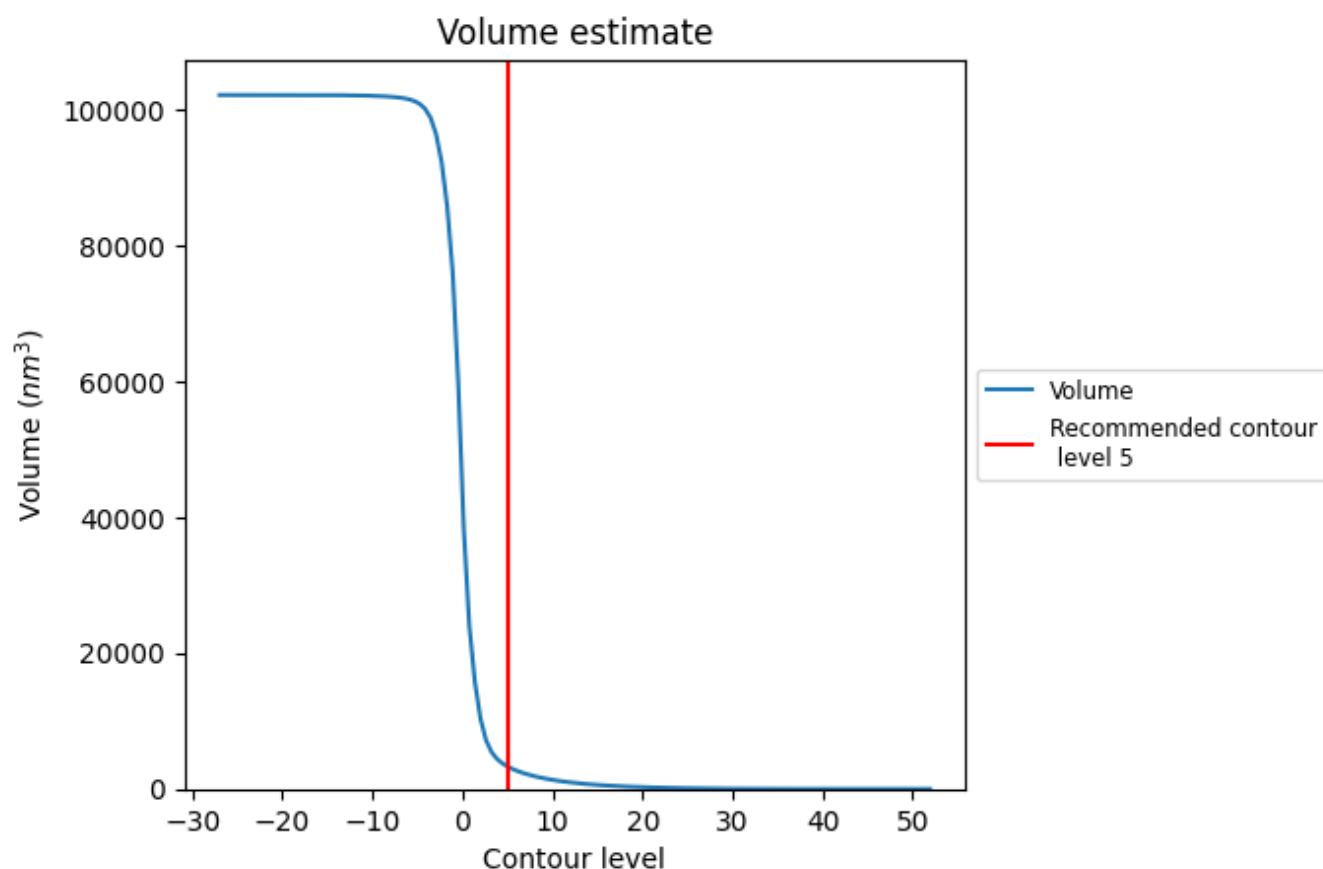
### 7.1 Map-value distribution [i](#)



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](#)

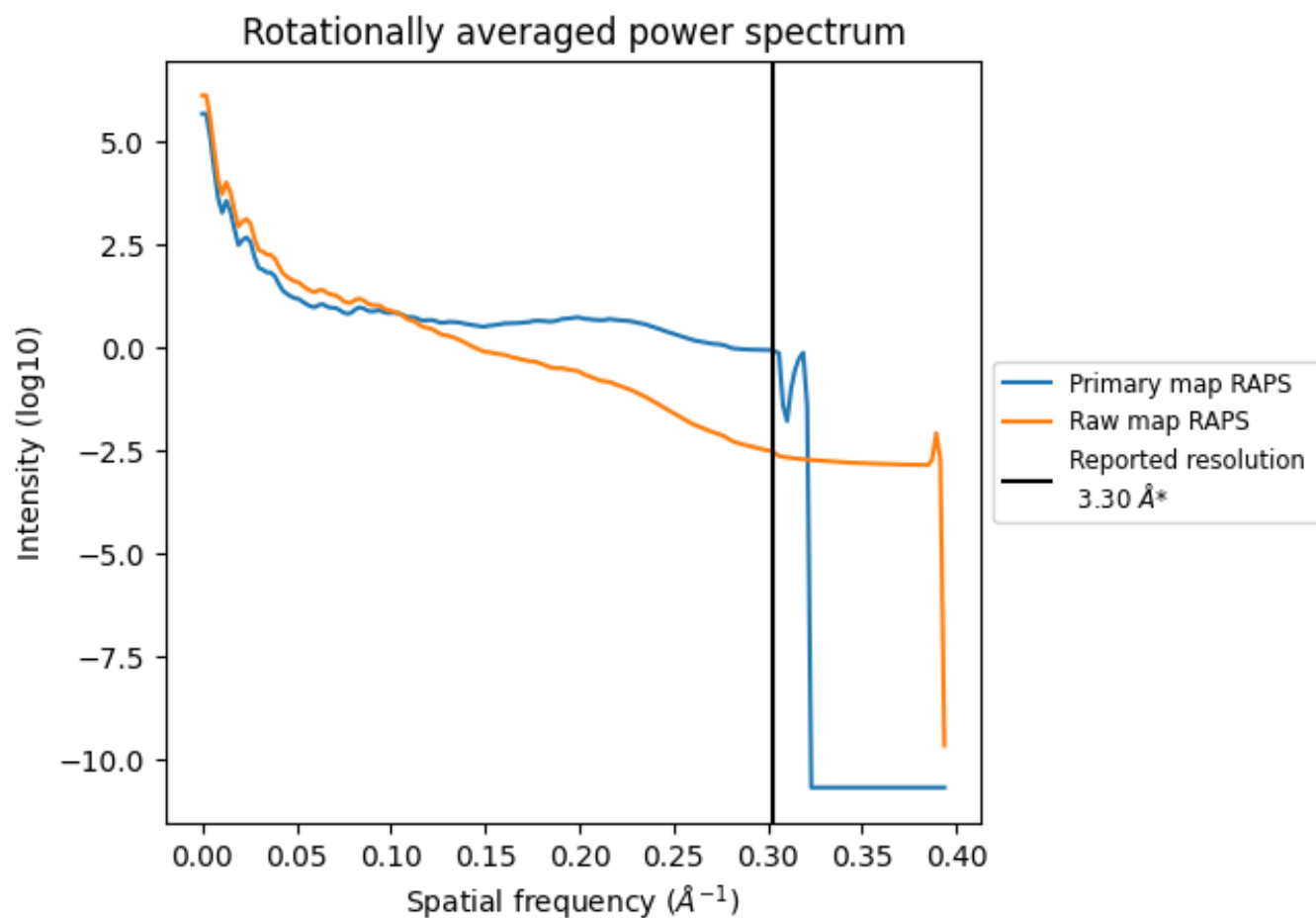


The volume at the recommended contour level is 3310 nm<sup>3</sup>; this corresponds to an approximate mass of 2990 kDa.

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 ⓘ



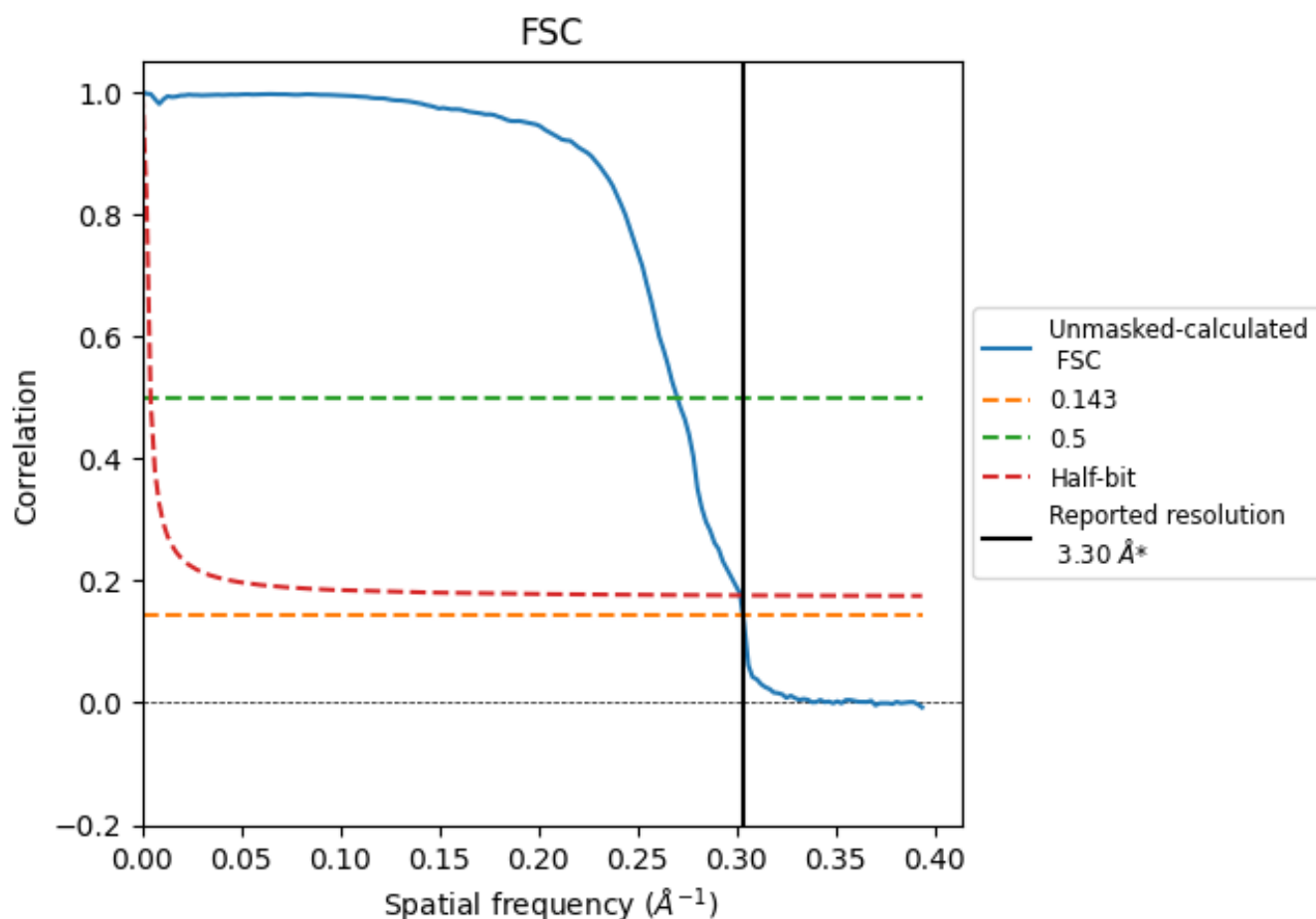
\*Reported resolution corresponds to spatial frequency of 0.303 Å<sup>-1</sup>



## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.303 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.30	3.70	3.31

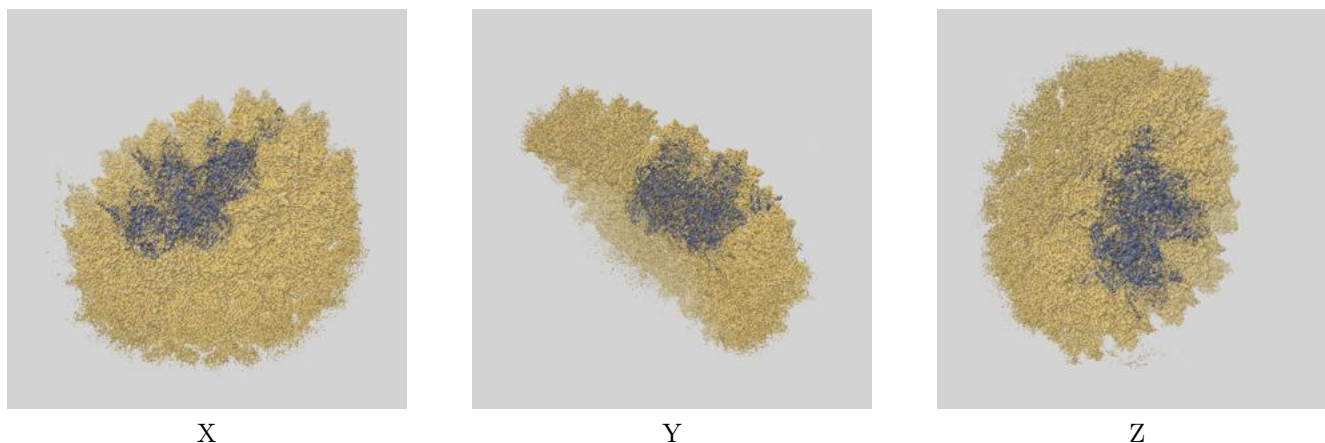
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-63322 and PDB model 9LR9. Per-residue inclusion information can be found in section [3](#) on page [8](#).

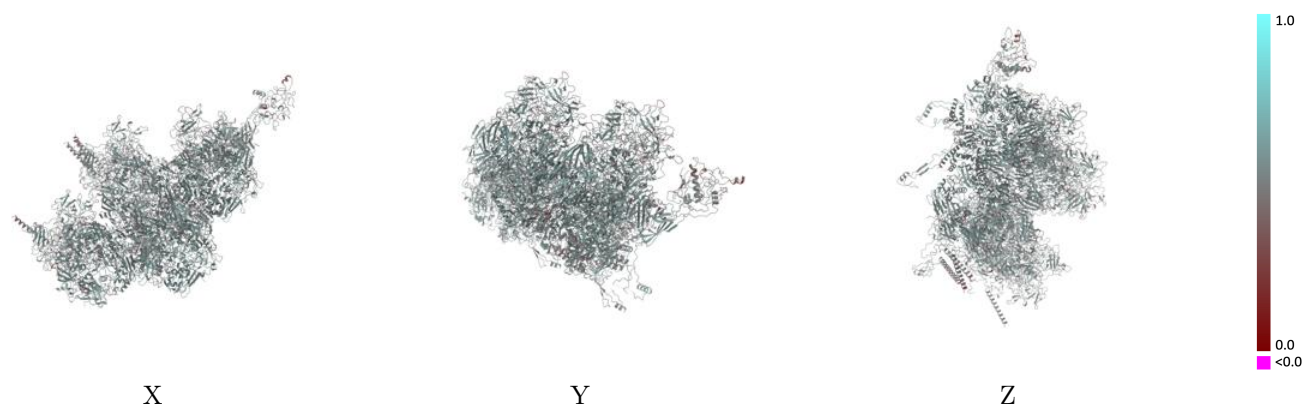
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 5.0 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.

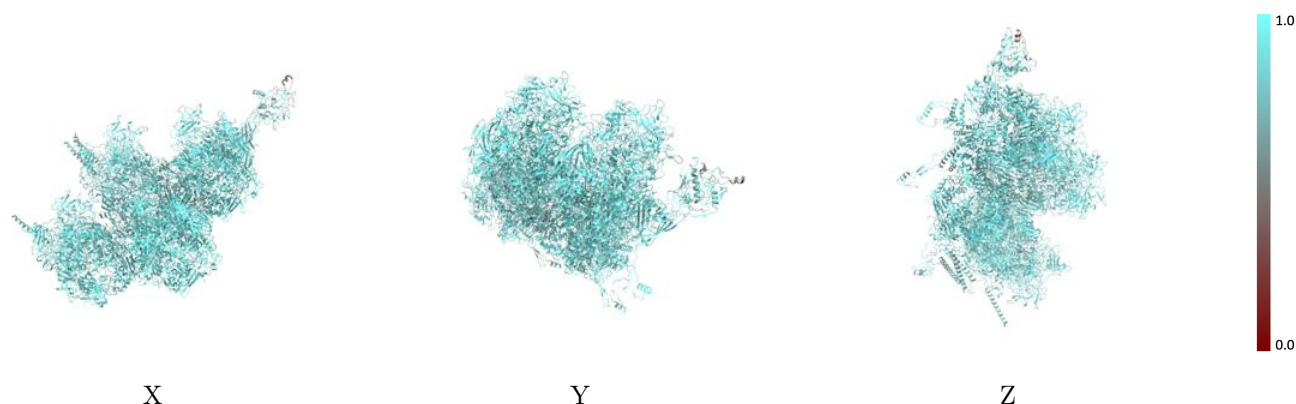


## 9.2 Q-score mapped to coordinate model [i](#)



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.

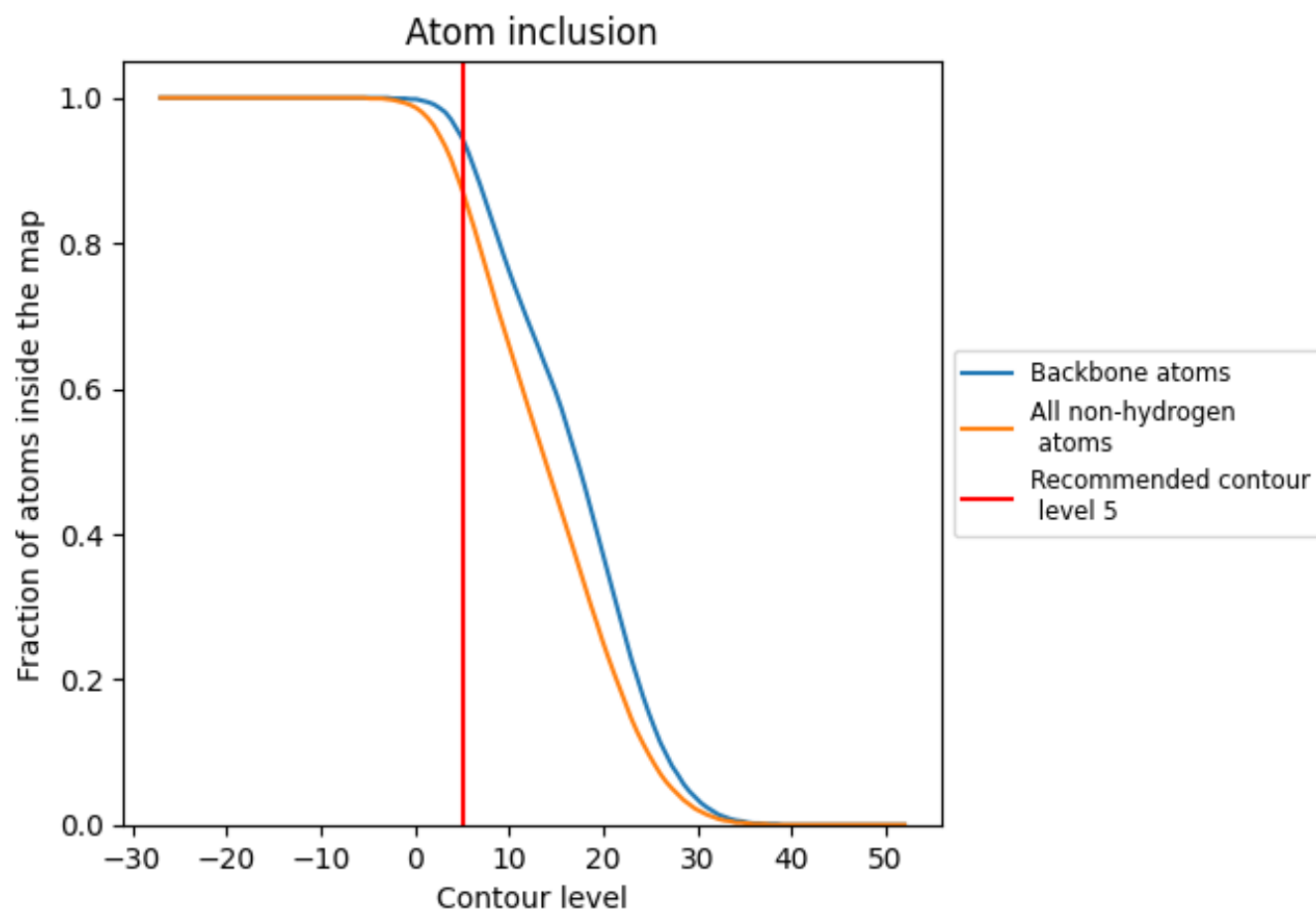
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (5).



## 9.4 Atom inclusion [i](#)











































































At the recommended contour level, 94% of all backbone atoms, 87% 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 (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8740	 0.5200
A	 0.8940	 0.5200
B	 0.5810	 0.4520
C	 0.7930	 0.5350
D	 0.9010	 0.5280
E	 0.6880	 0.4750
F	 0.9100	 0.5310
G	 0.8870	 0.5280
H	 0.8980	 0.5240
I	 0.8910	 0.5260
J	 0.9010	 0.5260
K	 0.7930	 0.4950
L	 0.6650	 0.5110
M	 0.7280	 0.4800
N	 0.8740	 0.5390
O	 0.7510	 0.4970
P	 0.7880	 0.4900
Q	 0.7890	 0.4990
R	 0.8840	 0.5370
S	 0.8220	 0.5240
T	 0.7070	 0.4970
U	 0.8100	 0.5160
V	 0.7480	 0.4810
X	 0.8960	 0.5220
Y	 0.8710	 0.5120
Z	 0.4260	 0.4150
a	 0.6030	 0.5000
b	 0.8380	 0.5280
c	 0.5950	 0.5050
d	 0.4030	 0.4390
e	 0.8280	 0.5670
f	 0.7240	 0.5150
g	 0.9050	 0.5280
h	 0.8800	 0.5260
i	 0.8630	 0.5170
j	 0.7650	 0.4910

