



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 07:19 AM UTC

PDB ID : 6B1T / pdb_00006b1t
EMDB ID : EMD-7034
Title : Improved cryoEM structure of human adenovirus type 5 with atomic details of minor proteins VI and VII
Authors : Dai, X.H.; Wu, L.; Sun, R.; Zhou, Z.H.
Deposited on : 2017-09-18
Resolution : 3.20 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

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:

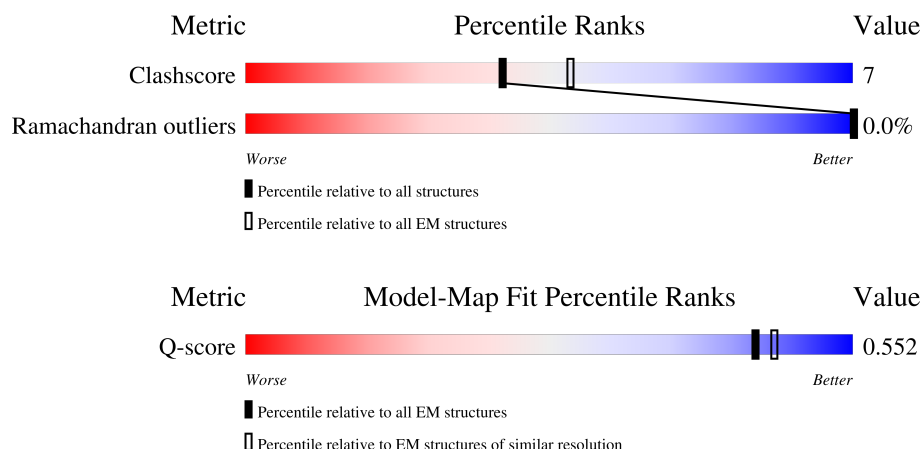
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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	952	
1	B	952	
1	C	952	
1	D	952	
1	E	952	

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Mol	Chain	Length	Quality of chain
1	F	952	
1	G	952	
1	H	952	
1	I	952	
1	J	952	
1	K	952	
1	L	952	
2	M	571	
3	N	585	
4	O	227	
4	P	227	
5	Q	140	
5	R	140	
5	S	140	
5	T	140	
6	U	33	
6	V	33	
6	Y	33	
7	W	11	
8	X	217	

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 100134 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	908	Total	C	N	O	S	0	0
			7286	4639	1231	1380	36		
1	B	910	Total	C	N	O	S	0	0
			7299	4647	1233	1383	36		
1	C	910	Total	C	N	O	S	0	0
			7302	4650	1232	1383	37		
1	D	906	Total	C	N	O	S	0	0
			7273	4631	1229	1378	35		
1	E	914	Total	C	N	O	S	0	0
			7325	4662	1237	1390	36		
1	F	910	Total	C	N	O	S	0	0
			7300	4647	1233	1384	36		
1	G	909	Total	C	N	O	S	0	0
			7293	4643	1232	1382	36		
1	H	913	Total	C	N	O	S	0	0
			7319	4659	1236	1387	37		
1	I	910	Total	C	N	O	S	0	0
			7300	4647	1233	1384	36		
1	J	913	Total	C	N	O	S	0	0
			7318	4658	1236	1388	36		
1	K	910	Total	C	N	O	S	0	0
			7299	4646	1233	1384	36		
1	L	912	Total	C	N	O	S	0	0
			7311	4654	1235	1386	36		

- Molecule 2 is a protein called Penton protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	M	455	Total	C	N	O	S	0	0
			3642	2309	630	691	12		

- Molecule 3 is a protein called Pre-hexon-linking protein IIIa.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	N	288	Total	C	N	O	S	0	0
			2236	1385	410	437	4		

- Molecule 4 is a protein called Pre-hexon-linking protein VIII.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	O	180	Total	C	N	O	S	0	0
			1383	870	244	264	5		
4	P	180	Total	C	N	O	S	0	0
			1383	870	244	264	5		

- Molecule 5 is a protein called Hexon-interlacing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Q	119	Total	C	N	O	S	0	0
			874	541	155	176	2		
5	R	93	Total	C	N	O	S	0	0
			698	432	123	141	2		
5	S	86	Total	C	N	O	S	0	0
			647	397	115	133	2		
5	T	88	Total	C	N	O	S	0	0
			663	409	118	134	2		

- Molecule 6 is a protein called Pre-protein VI.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	U	29	Total	C	N	O	S	0	0
			216	132	42	40	2		
6	V	29	Total	C	N	O	S	0	0
			216	132	42	40	2		
6	Y	28	Total	C	N	O	S	0	0
			208	128	40	38	2		

- Molecule 7 is a protein called Pre-histone-like nucleoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	W	11	Total	C	N	O	S	0	0
			83	55	15	12	1		

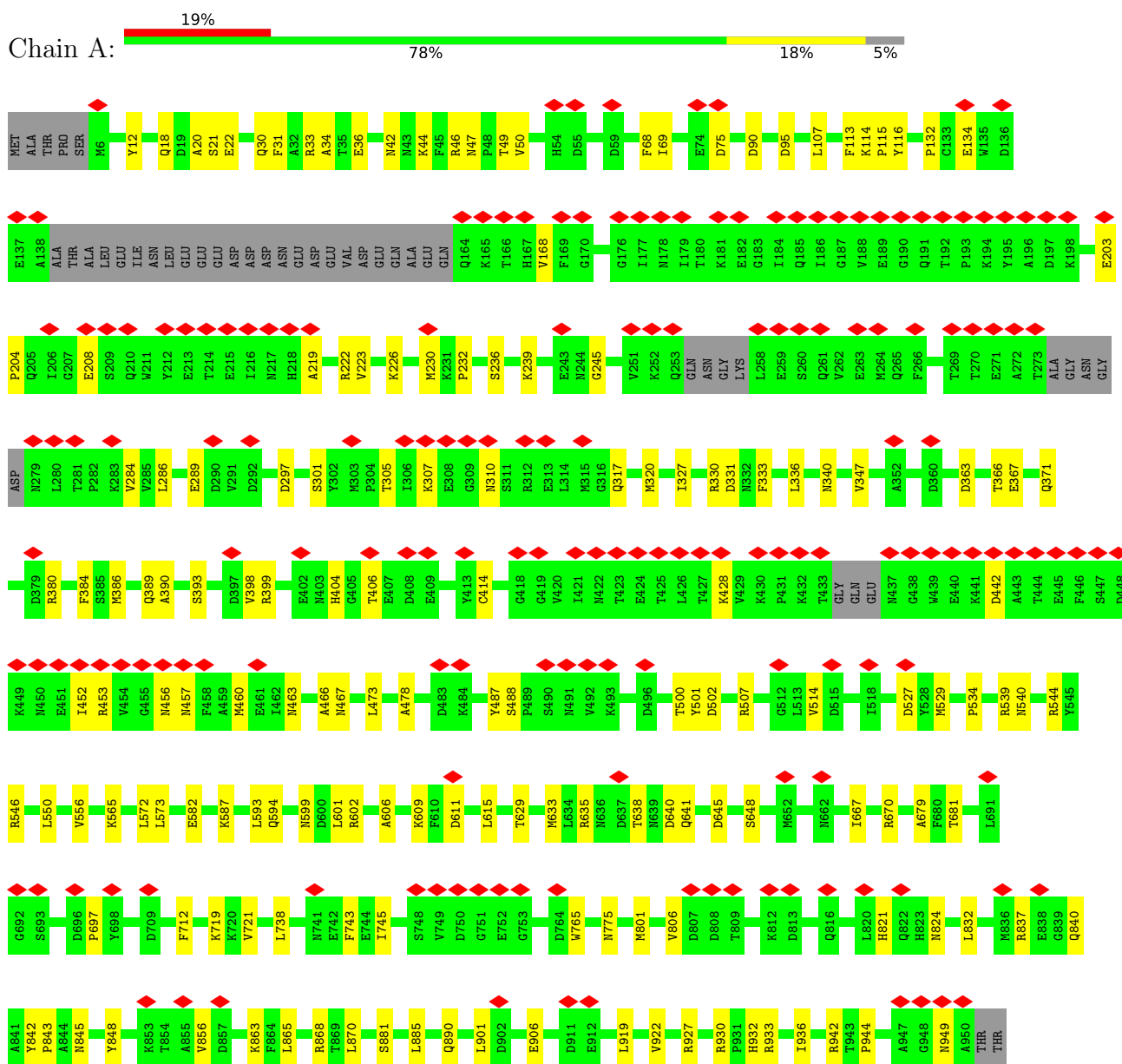
- Molecule 8 is a protein called Pre-protein VI.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	X	33	Total 260	C 158	N 49	O 53	0	0

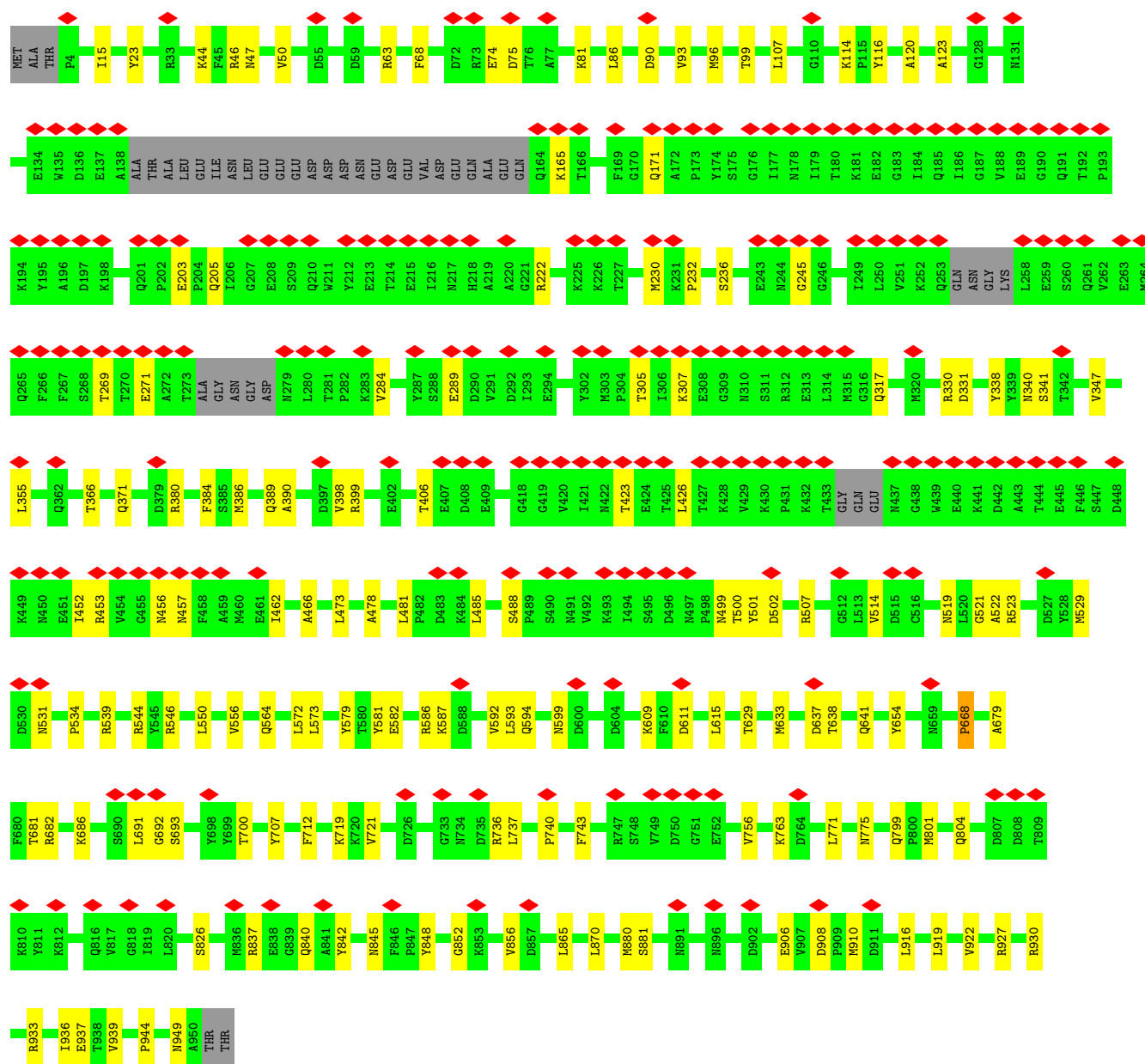
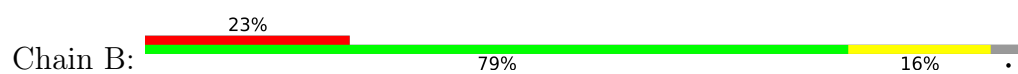
3 Residue-property plots

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.

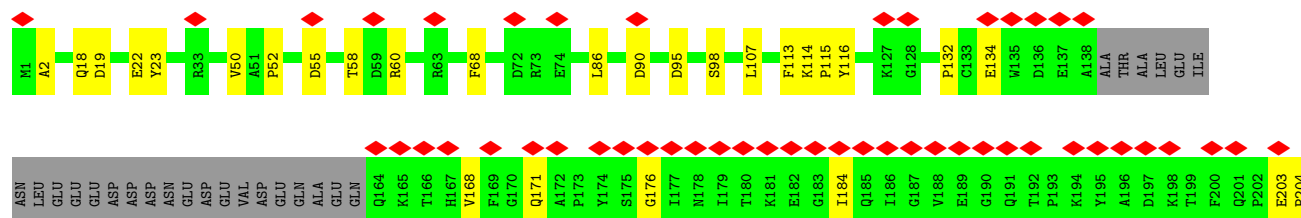
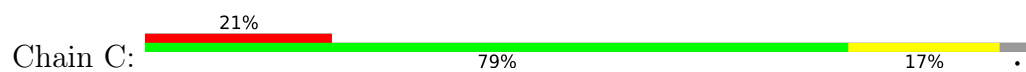
- Molecule 1: Hexon protein

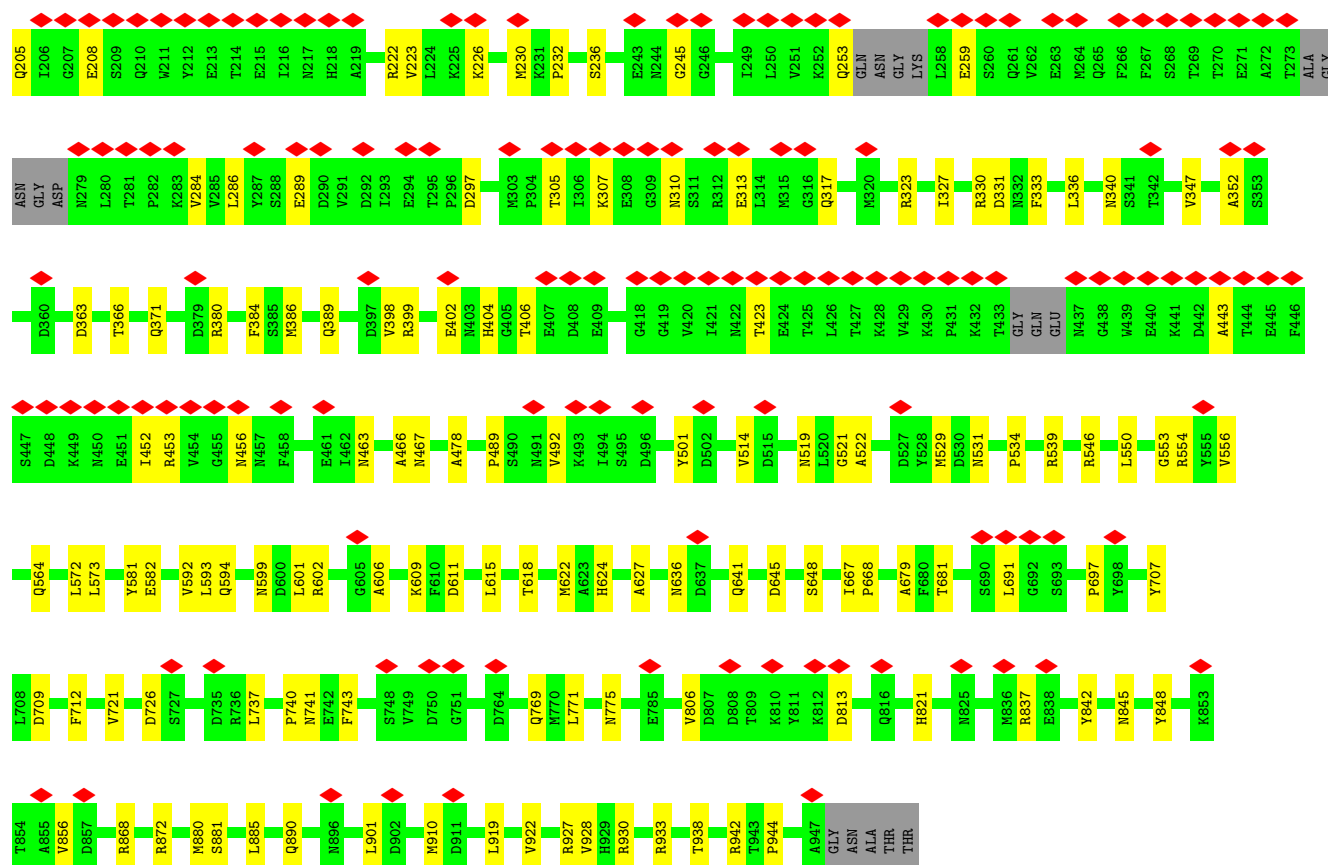


- Molecule 1: Hexon protein

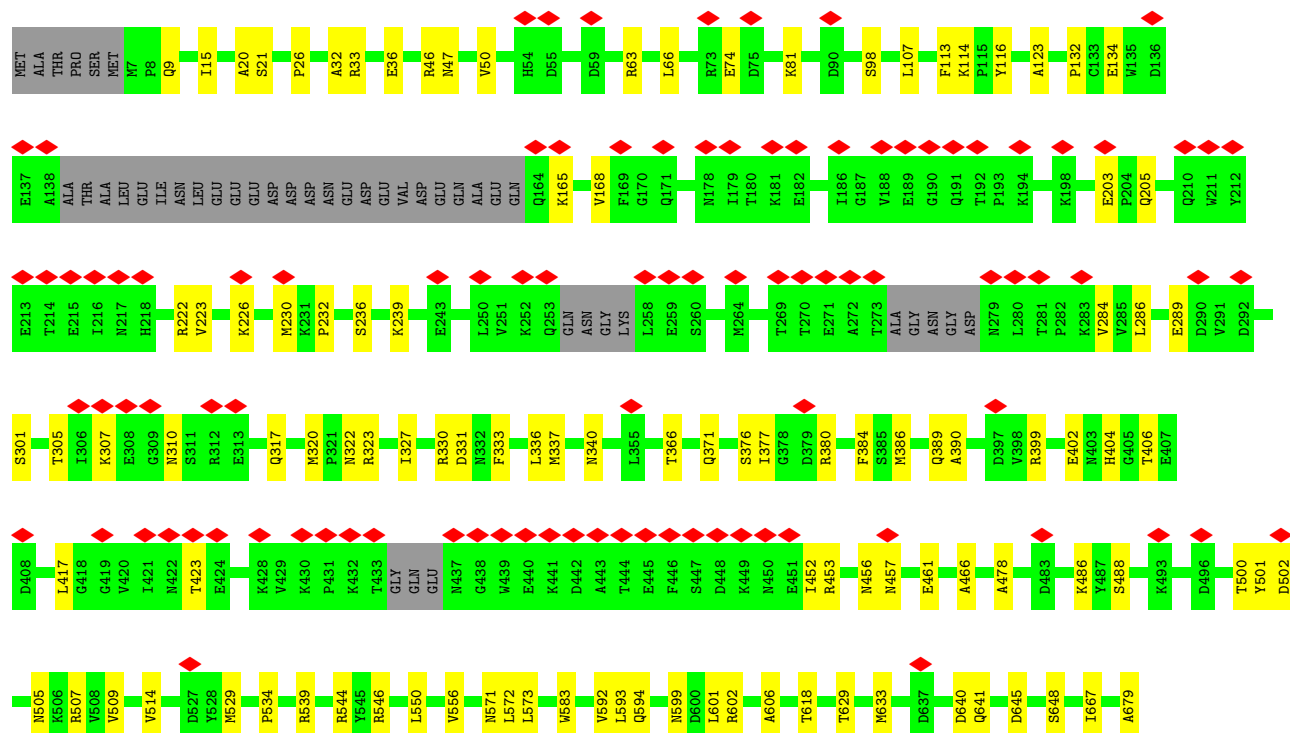
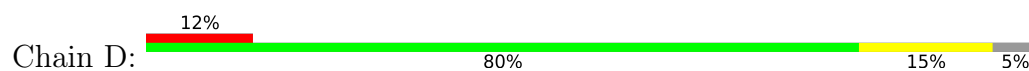


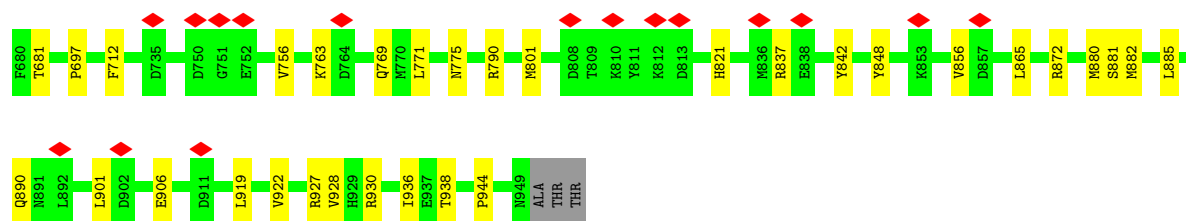
• Molecule 1: Hexon protein



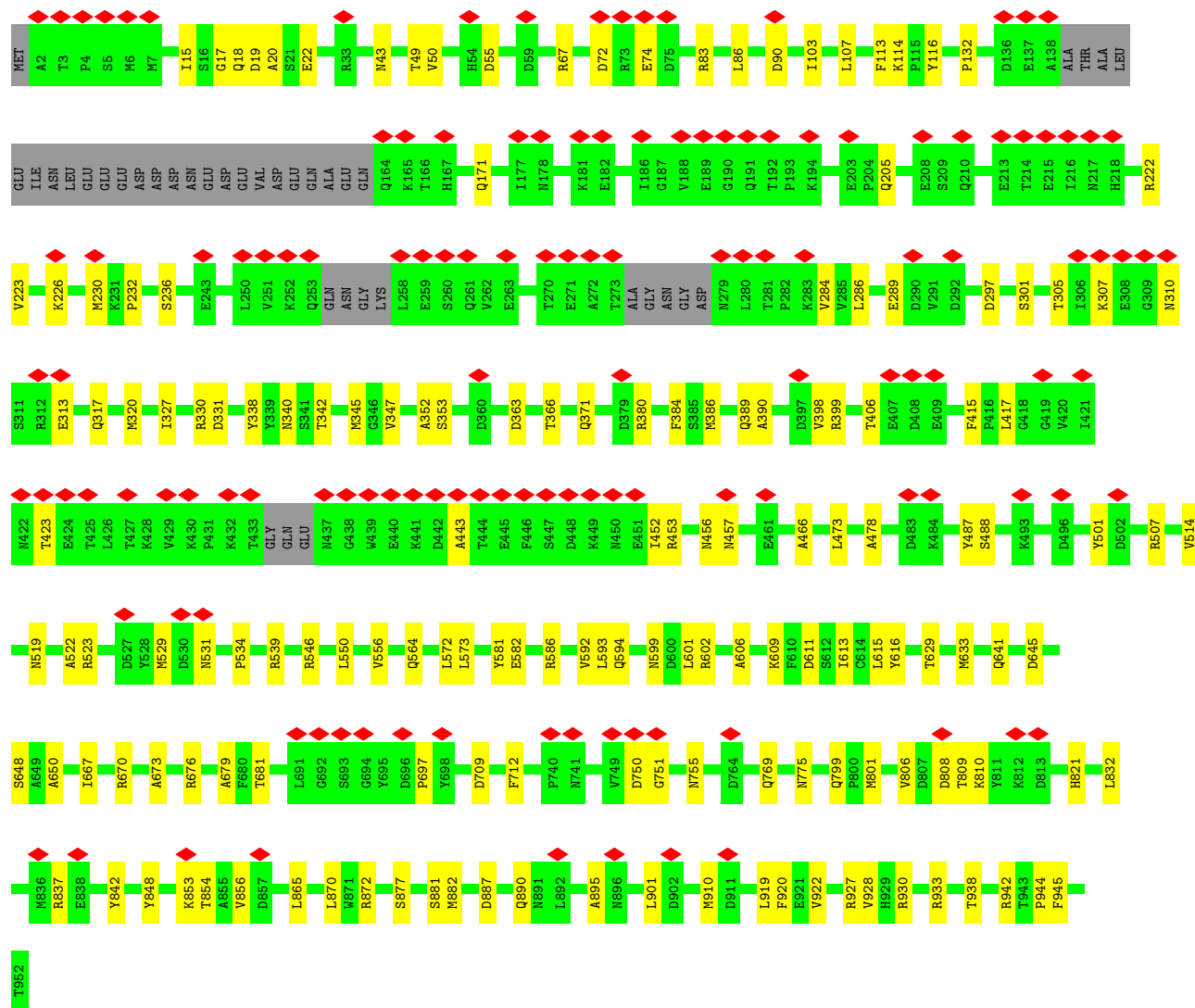
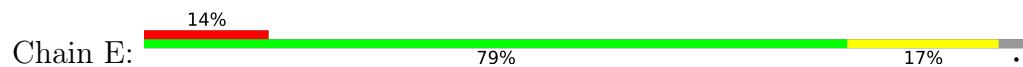


• Molecule 1: Hexon protein

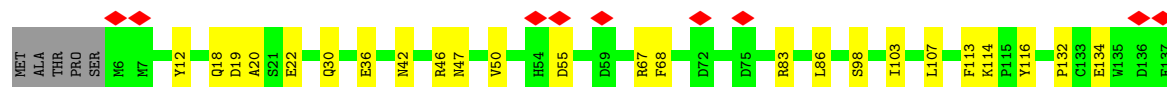
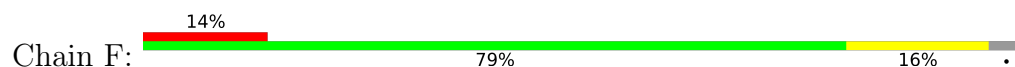


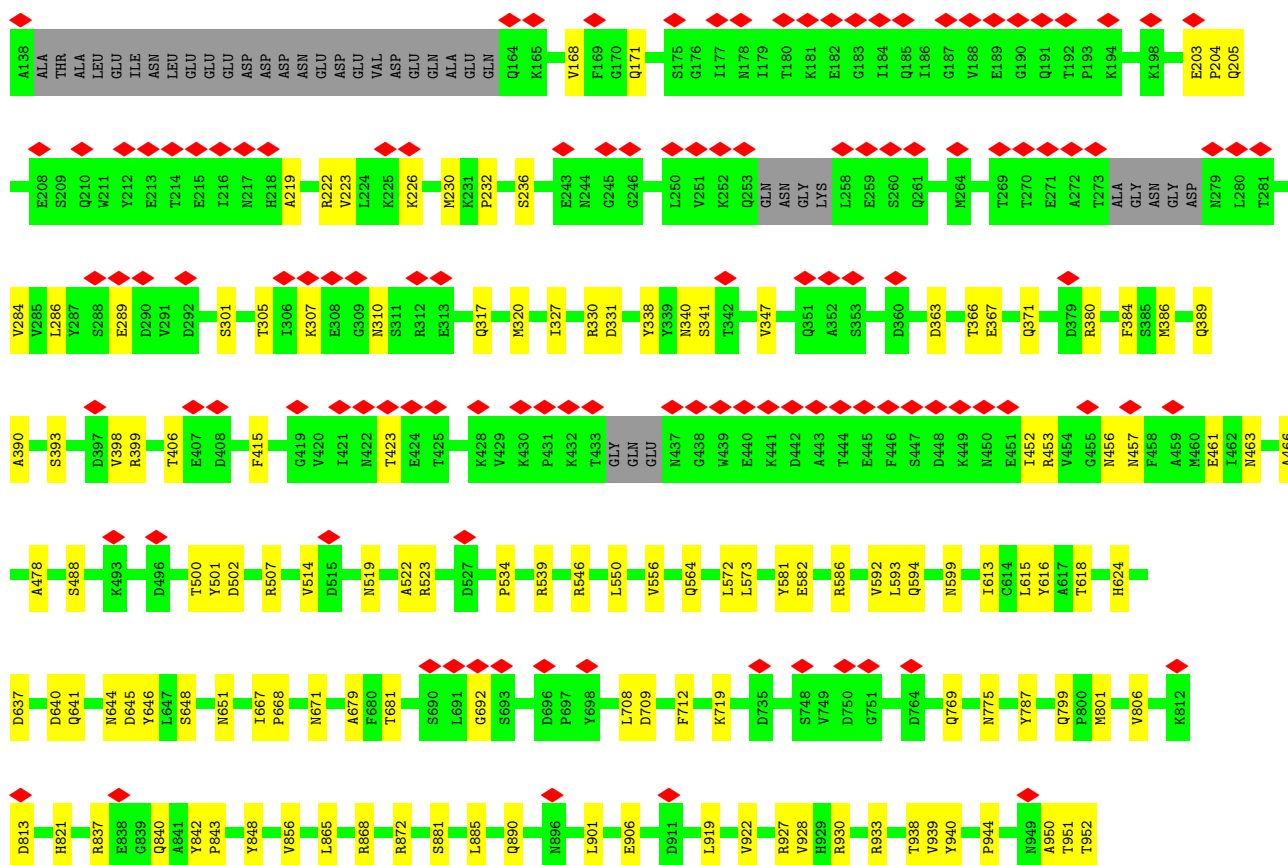


• Molecule 1: Hexon protein

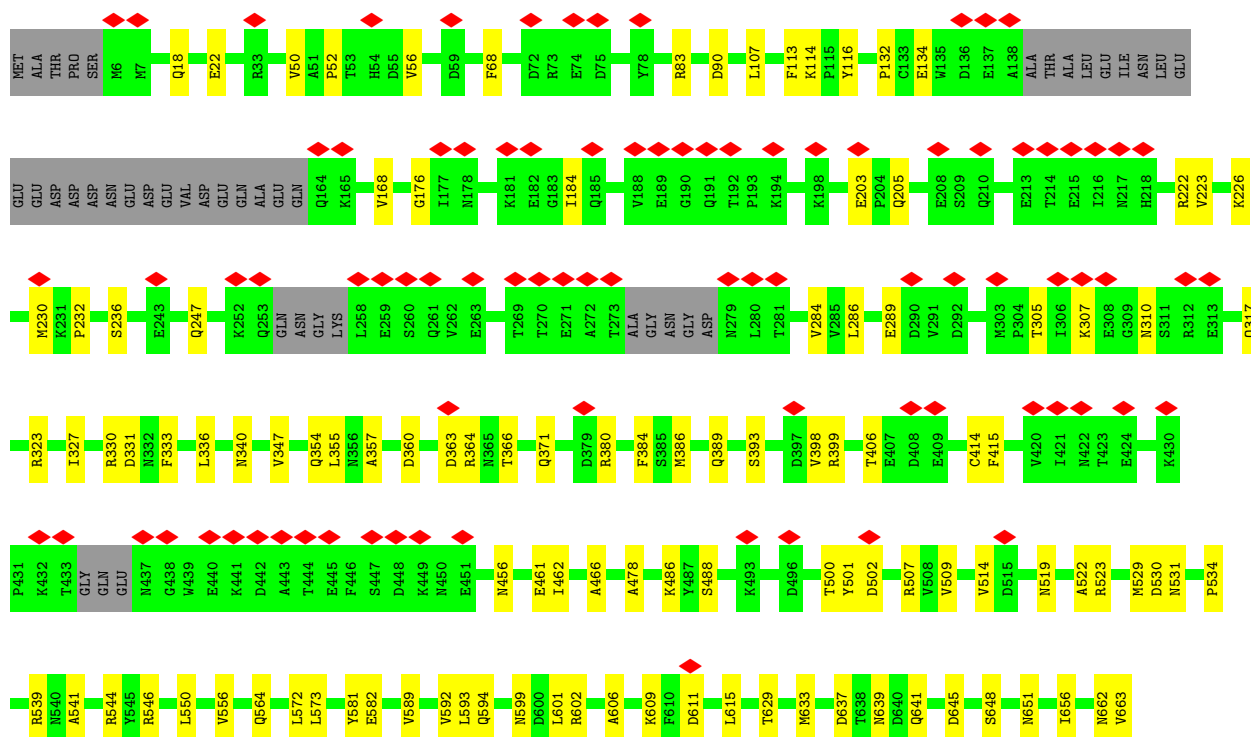
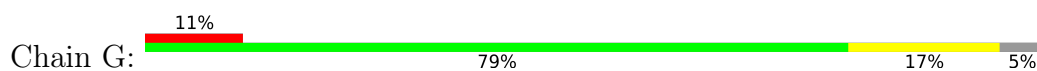


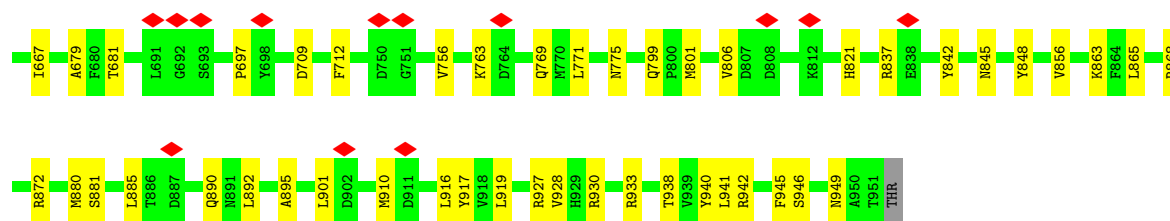
• Molecule 1: Hexon protein



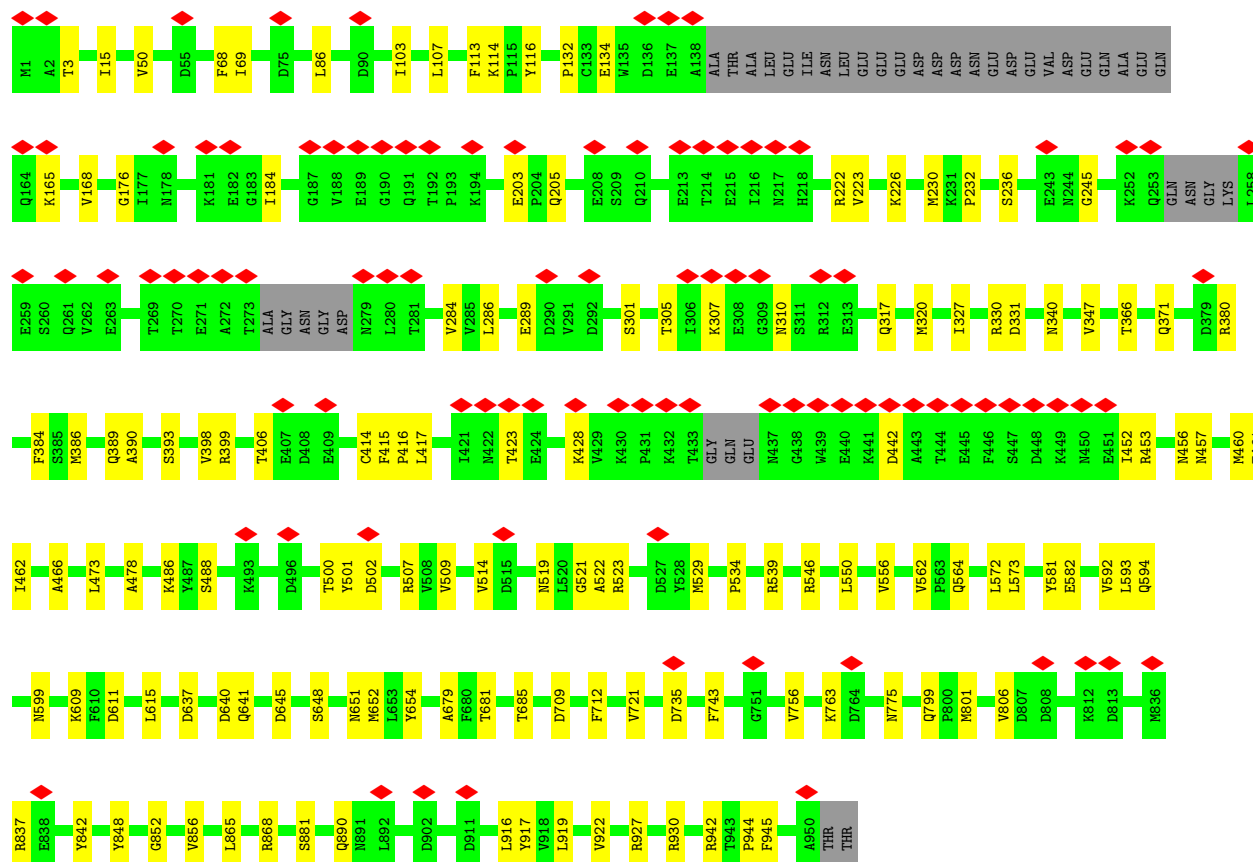
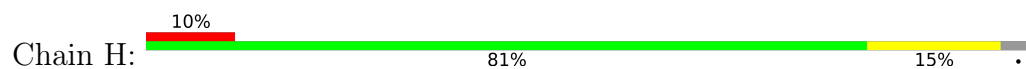


• Molecule 1: Hexon protein

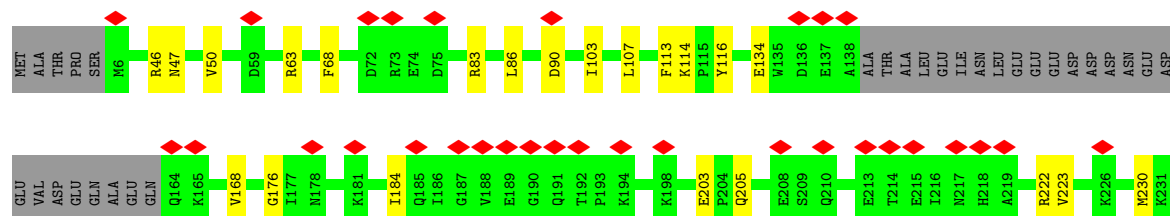
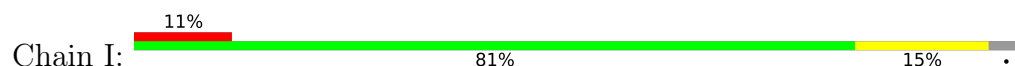


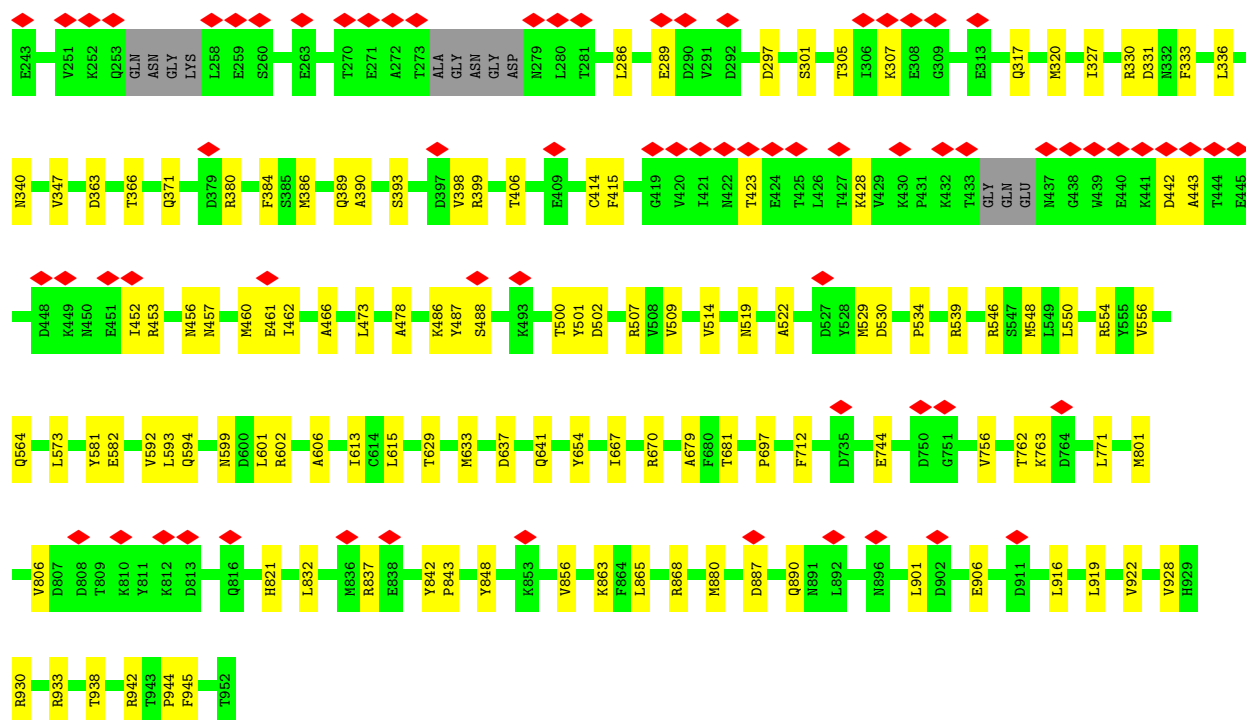


• Molecule 1: Hexon protein

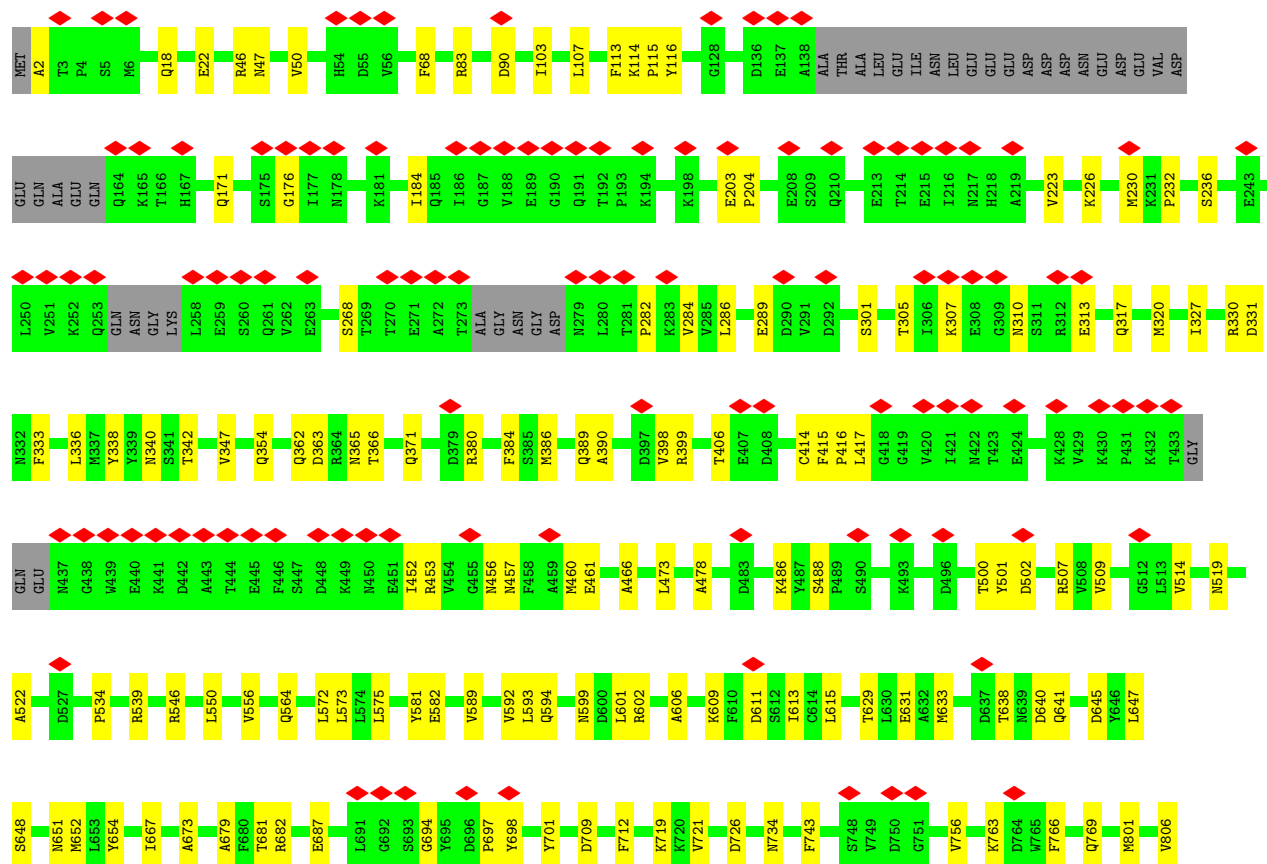
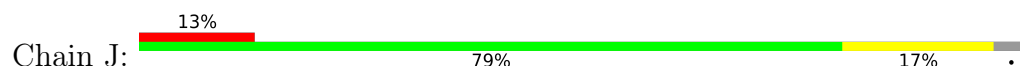


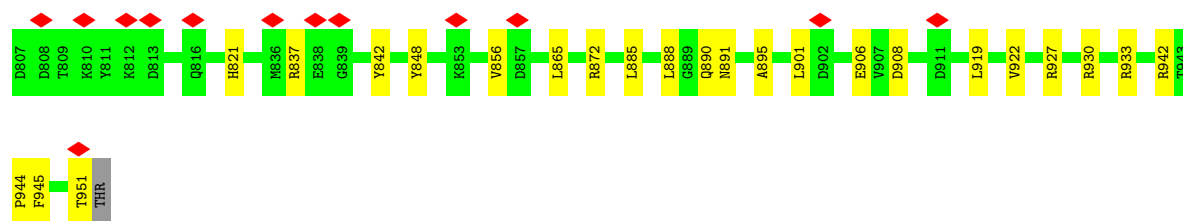
• Molecule 1: Hexon protein



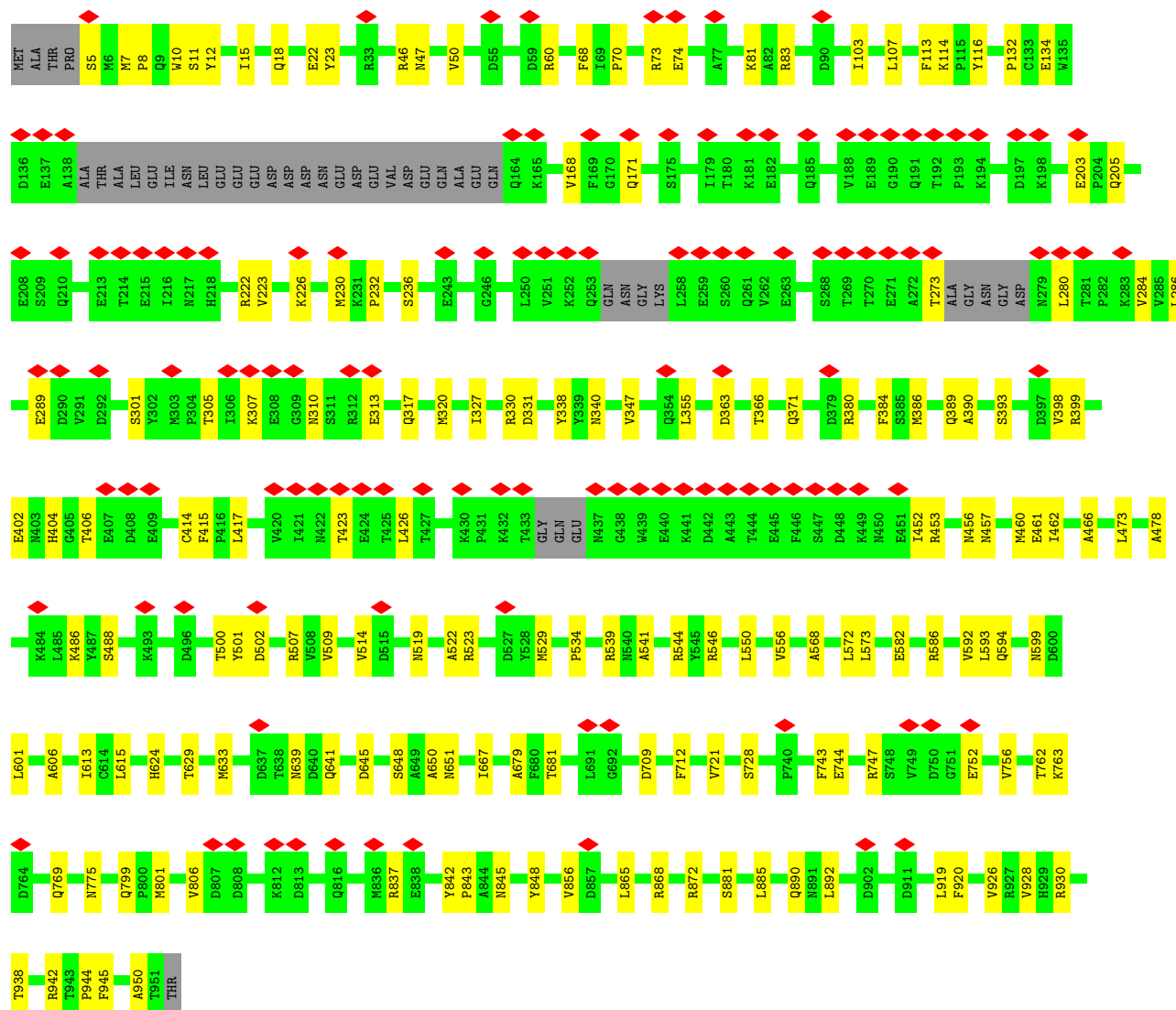
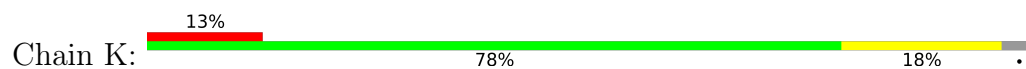


• Molecule 1: Hexon protein

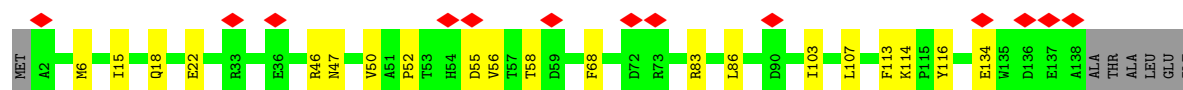
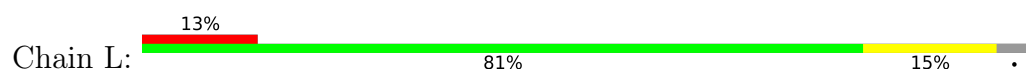


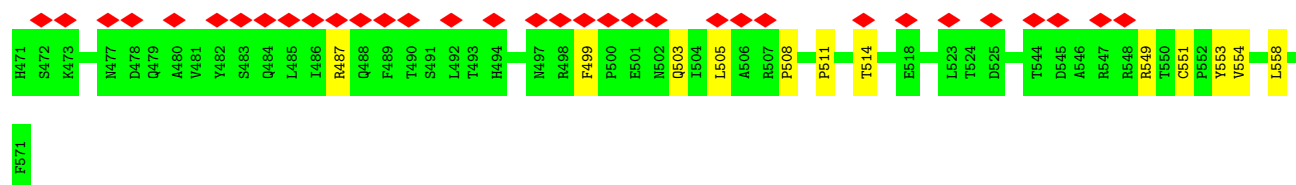


• Molecule 1: Hexon protein

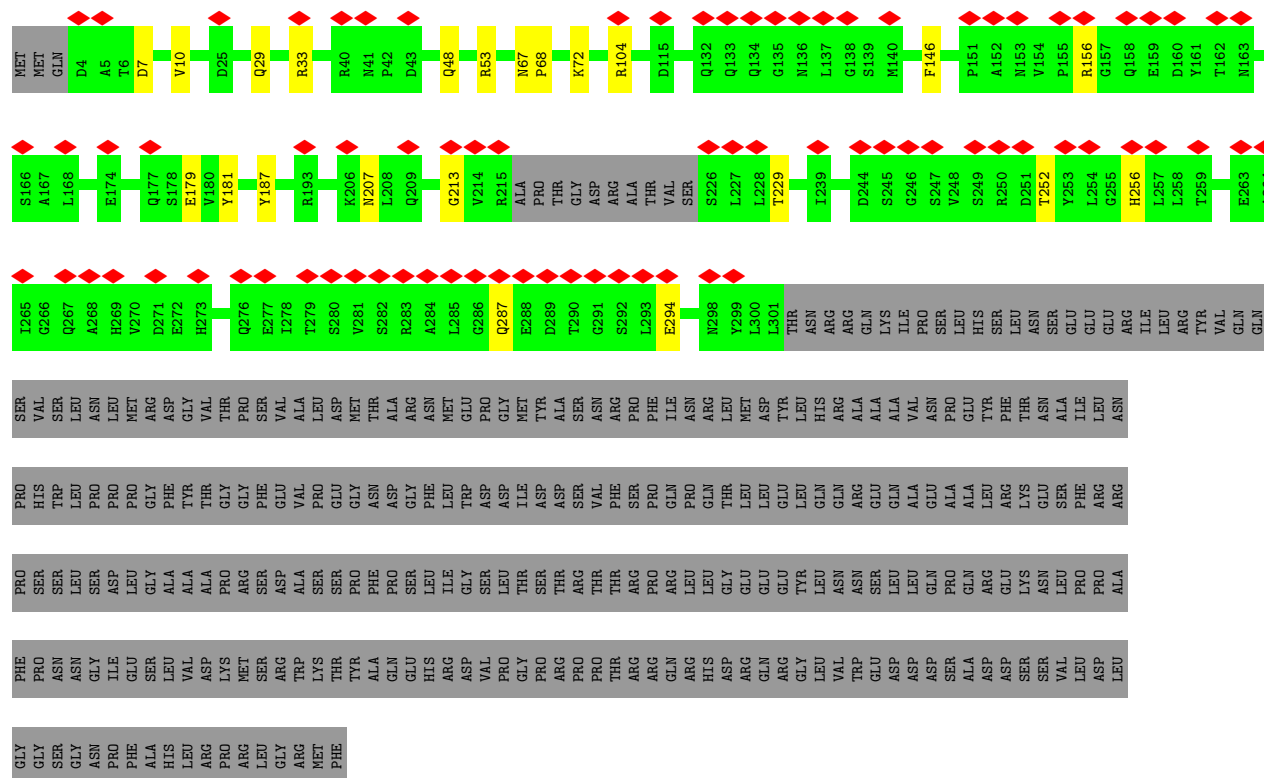


• Molecule 1: Hexon protein

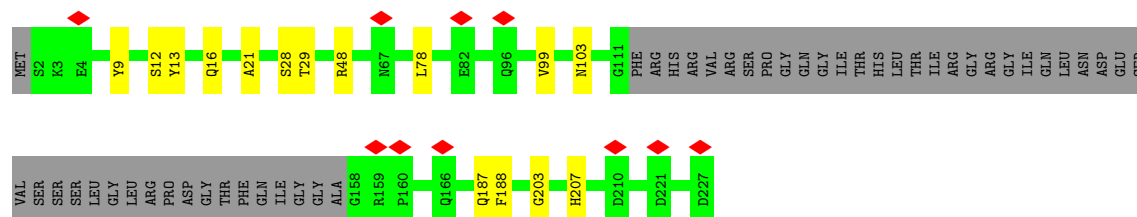




• Molecule 3: Pre-hexon-linking protein IIIa



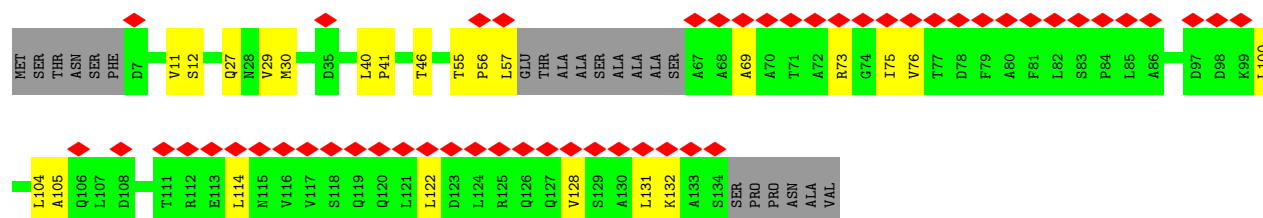
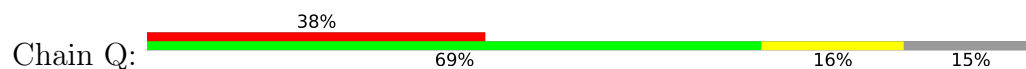
• Molecule 4: Pre-hexon-linking protein VIII



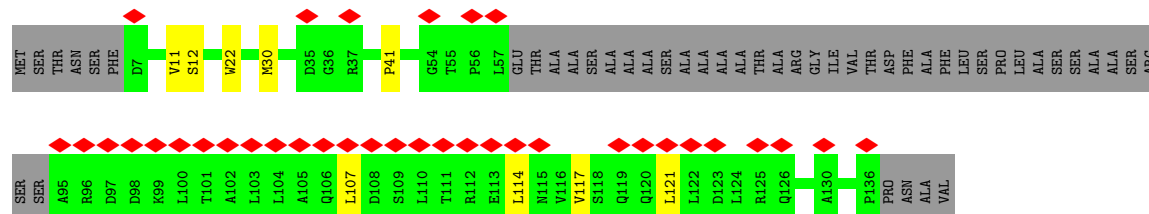
• Molecule 4: Pre-hexon-linking protein VIII



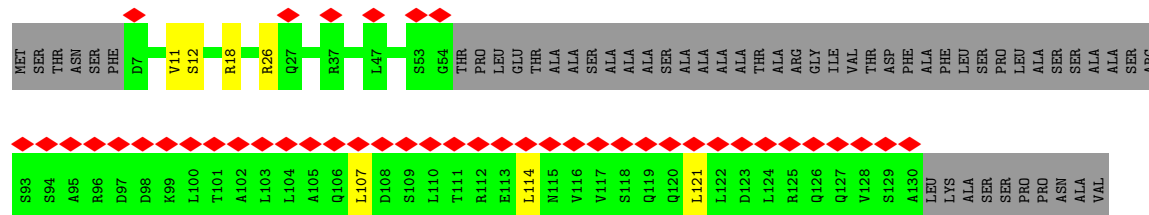
- Molecule 5: Hexon-interlacing protein



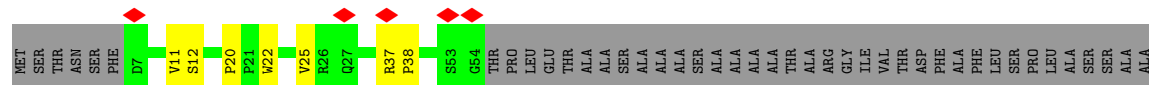
- Molecule 5: Hexon-interlacing protein



- Molecule 5: Hexon-interlacing protein



- Molecule 5: Hexon-interlacing protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	53000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	16.748	Depositor
Minimum map value	-11.582	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.876	Depositor
Recommended contour level	3	Depositor
Map size (Å)	1088.0, 1088.0, 1088.0	wwPDB
Map dimensions	1280, 1280, 1280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	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	0.25	0/7481	0.46	0/10170
1	B	0.24	0/7495	0.46	0/10189
1	C	0.25	0/7498	0.49	2/10194 (0.0%)
1	D	0.27	0/7468	0.47	0/10153
1	E	0.26	0/7521	0.48	0/10227
1	F	0.27	0/7495	0.47	0/10190
1	G	0.28	0/7488	0.50	0/10180
1	H	0.28	0/7515	0.50	0/10217
1	I	0.27	0/7495	0.48	0/10190
1	J	0.27	0/7514	0.49	0/10217
1	K	0.27	0/7494	0.48	0/10188
1	L	0.27	0/7507	0.48	0/10207
2	M	0.25	1/3734 (0.0%)	0.49	1/5091 (0.0%)
3	N	0.22	0/2271	0.48	0/3090
4	O	0.31	0/1422	0.50	0/1942
4	P	0.32	0/1422	0.52	0/1942
5	Q	0.21	0/884	0.57	0/1204
5	R	0.18	0/706	0.46	0/962
5	S	0.18	0/653	0.48	0/888
5	T	0.18	0/669	0.47	0/909
6	U	0.28	0/222	0.50	0/298
6	V	0.31	0/222	0.47	0/298
6	Y	0.26	0/214	0.48	0/287
7	W	0.27	0/85	0.49	0/110
8	X	0.27	0/265	0.57	0/359
All	All	0.26	1/102740 (0.0%)	0.48	3/139702 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	M	508	PRO	CA-C	-7.54	1.47	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	2	ALA	CA-C-N	9.55	134.04	120.49
1	C	2	ALA	C-N-CA	9.55	134.04	120.49
2	M	508	PRO	O-C-N	-7.61	117.57	121.15

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	7286	0	6998	134	0
1	B	7299	0	7011	110	0
1	C	7302	0	7020	115	0
1	D	7273	0	6984	134	0
1	E	7325	0	7036	124	0
1	F	7300	0	7012	134	0
1	G	7293	0	7004	103	0
1	H	7319	0	7033	93	0
1	I	7300	0	7011	94	0
1	J	7318	0	7029	112	0
1	K	7299	0	7010	120	0
1	L	7311	0	7022	99	0
2	M	3642	0	3562	39	0
3	N	2236	0	2207	15	0
4	O	1383	0	1326	11	0
4	P	1383	0	1326	20	0
5	Q	874	0	890	17	0
5	R	698	0	713	7	0
5	S	647	0	652	6	0
5	T	663	0	676	13	0
6	U	216	0	196	40	0
6	V	216	0	196	44	0
6	Y	208	0	190	38	0
7	W	83	0	84	18	0
8	X	260	0	256	36	0
All	All	100134	0	96444	1311	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 7.

The worst 5 of 1311 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:A:30:GLN:NE2	6:Y:22:TRP:CZ3	1.83	1.43
1:D:790:ARG:HH21	8:X:137:ARG:NE	1.25	1.34
1:A:30:GLN:NE2	6:Y:22:TRP:HZ3	1.16	1.31
4:P:203:GLY:O	4:P:208:TYR:CE1	1.82	1.31
1:D:872:ARG:NH2	7:W:23:GLY:CA	1.94	1.30

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	898/952 (94%)	860 (96%)	38 (4%)	0	100	100
1	B	900/952 (94%)	856 (95%)	43 (5%)	1 (0%)	48	79
1	C	900/952 (94%)	859 (95%)	40 (4%)	1 (0%)	48	79
1	D	896/952 (94%)	856 (96%)	40 (4%)	0	100	100
1	E	904/952 (95%)	866 (96%)	38 (4%)	0	100	100
1	F	900/952 (94%)	865 (96%)	34 (4%)	1 (0%)	48	79
1	G	899/952 (94%)	859 (96%)	40 (4%)	0	100	100
1	H	903/952 (95%)	867 (96%)	36 (4%)	0	100	100
1	I	900/952 (94%)	865 (96%)	35 (4%)	0	100	100
1	J	903/952 (95%)	869 (96%)	34 (4%)	0	100	100
1	K	900/952 (94%)	864 (96%)	36 (4%)	0	100	100
1	L	902/952 (95%)	867 (96%)	35 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	M	451/571 (79%)	426 (94%)	25 (6%)	0	100	100
3	N	284/585 (48%)	276 (97%)	8 (3%)	0	100	100
4	O	176/227 (78%)	171 (97%)	5 (3%)	0	100	100
4	P	176/227 (78%)	171 (97%)	4 (2%)	1 (1%)	21	56
5	Q	115/140 (82%)	109 (95%)	6 (5%)	0	100	100
5	R	89/140 (64%)	86 (97%)	3 (3%)	0	100	100
5	S	82/140 (59%)	79 (96%)	3 (4%)	0	100	100
5	T	84/140 (60%)	81 (96%)	3 (4%)	0	100	100
6	U	27/33 (82%)	27 (100%)	0	0	100	100
6	V	27/33 (82%)	27 (100%)	0	0	100	100
6	Y	26/33 (79%)	24 (92%)	2 (8%)	0	100	100
7	W	9/11 (82%)	9 (100%)	0	0	100	100
8	X	29/217 (13%)	28 (97%)	1 (3%)	0	100	100
All	All	12380/13921 (89%)	11867 (96%)	509 (4%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	P	204	PRO
1	C	668	PRO
1	F	668	PRO
1	B	668	PRO

5.3.2 Protein sidechains [i](#)

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

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.

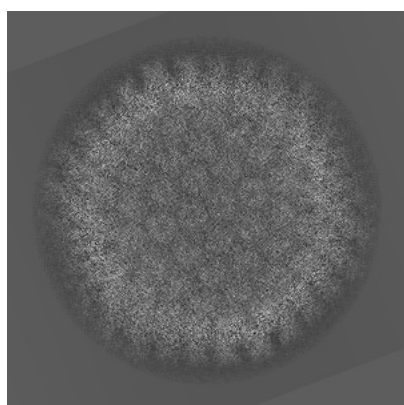
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7034. These allow visual inspection of the internal detail of the map and identification of artifacts.

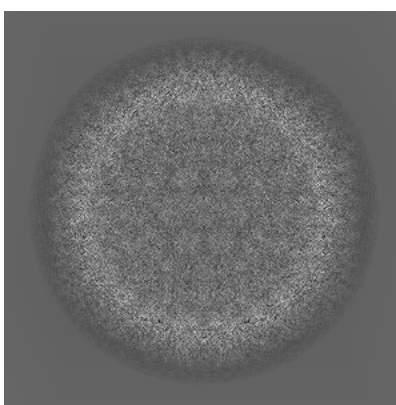
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

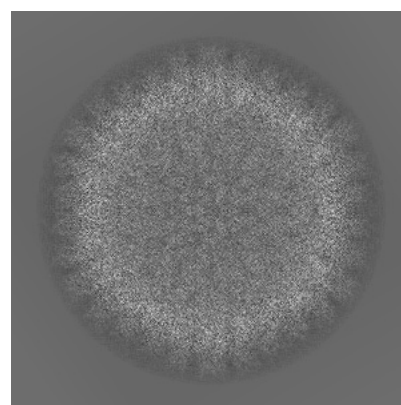
6.1.1 Primary map



X



Y

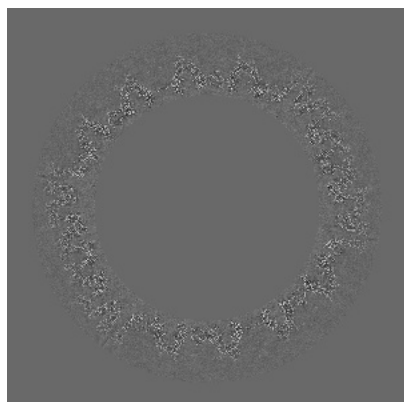


Z

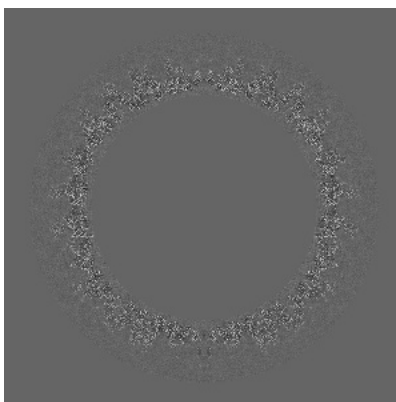
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

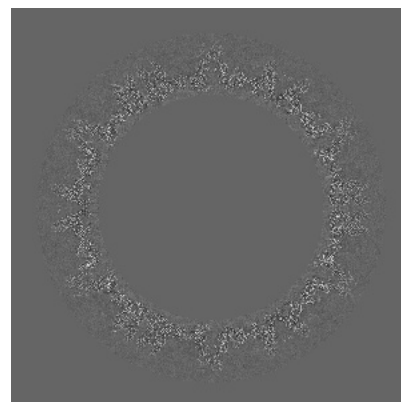
6.2.1 Primary map



X Index: 640



Y Index: 640

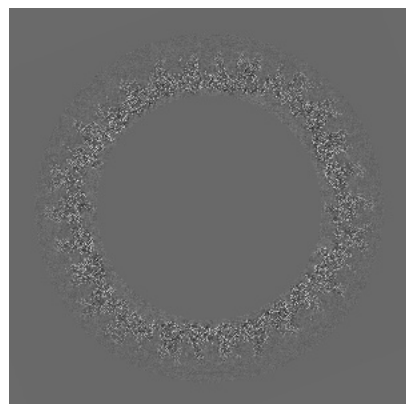


Z Index: 640

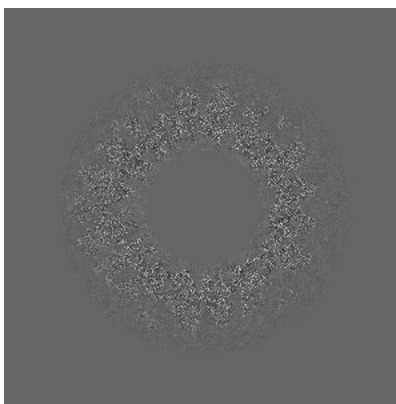
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

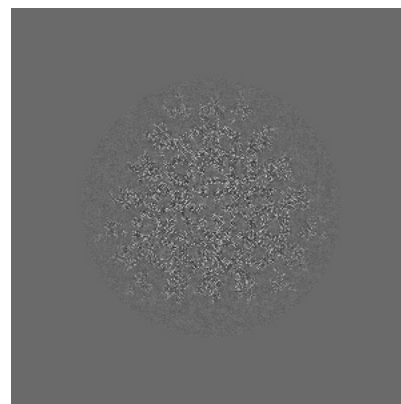
6.3.1 Primary map



X Index: 617



Y Index: 329

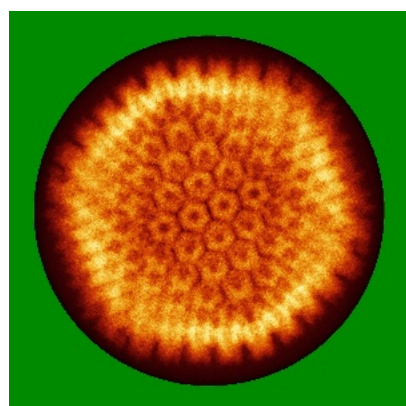


Z Index: 1017

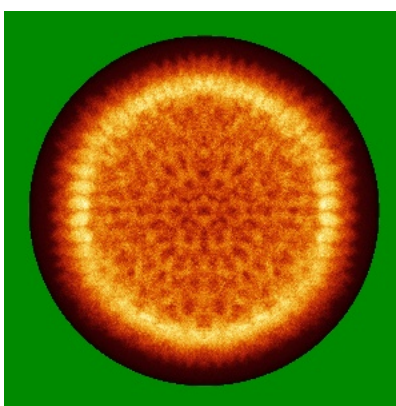
The images above show the largest variance slices of the map in three orthogonal directions.

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

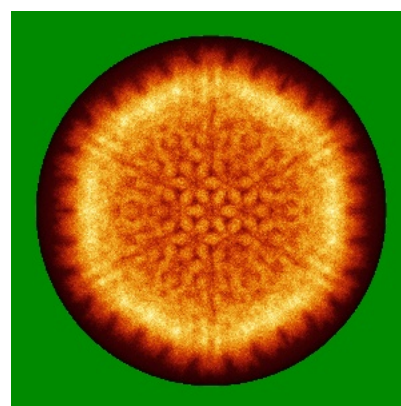
6.4.1 Primary map



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

This section was not generated.

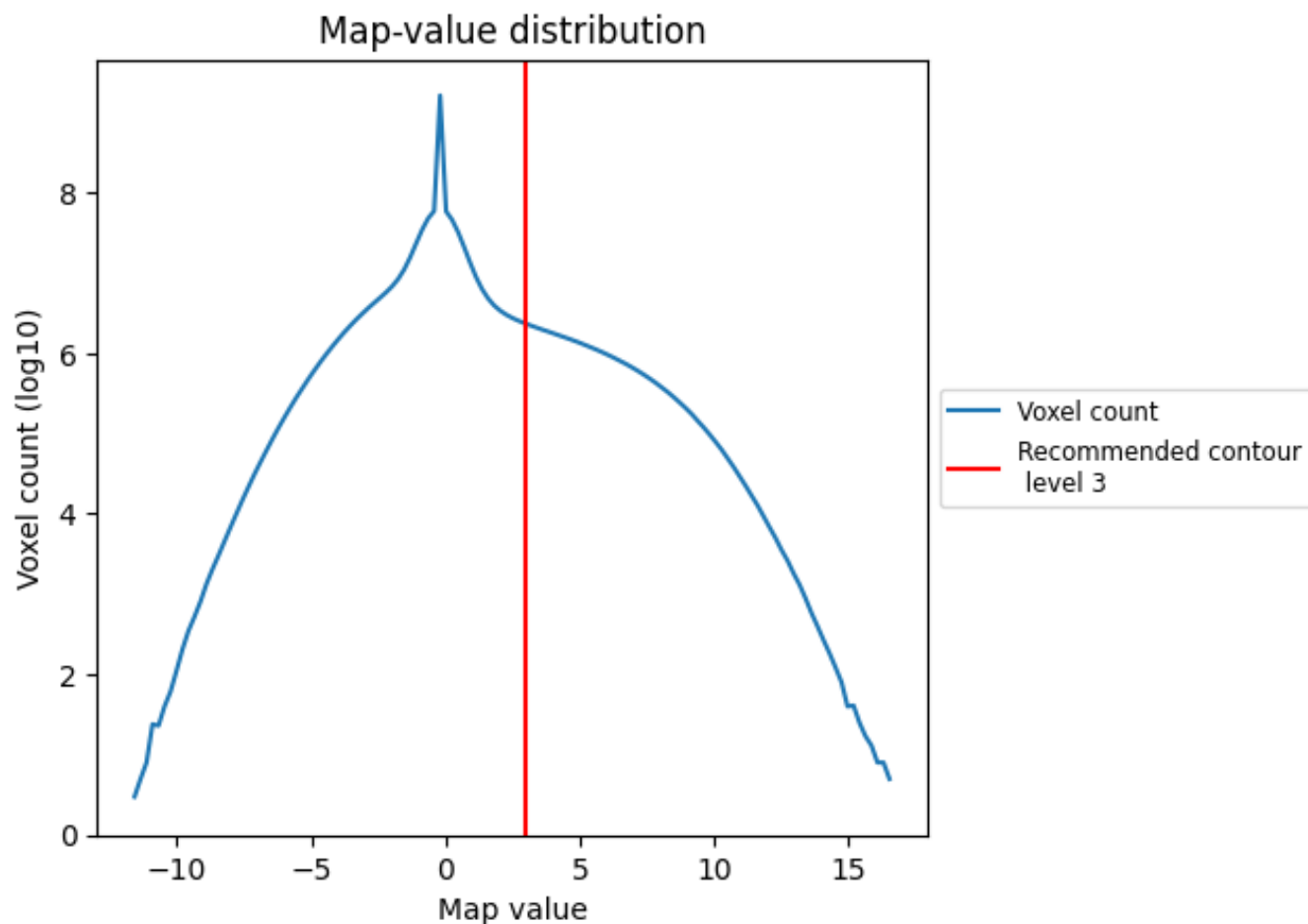
6.6 Mask visualisation

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

7 Map analysis [i](#)

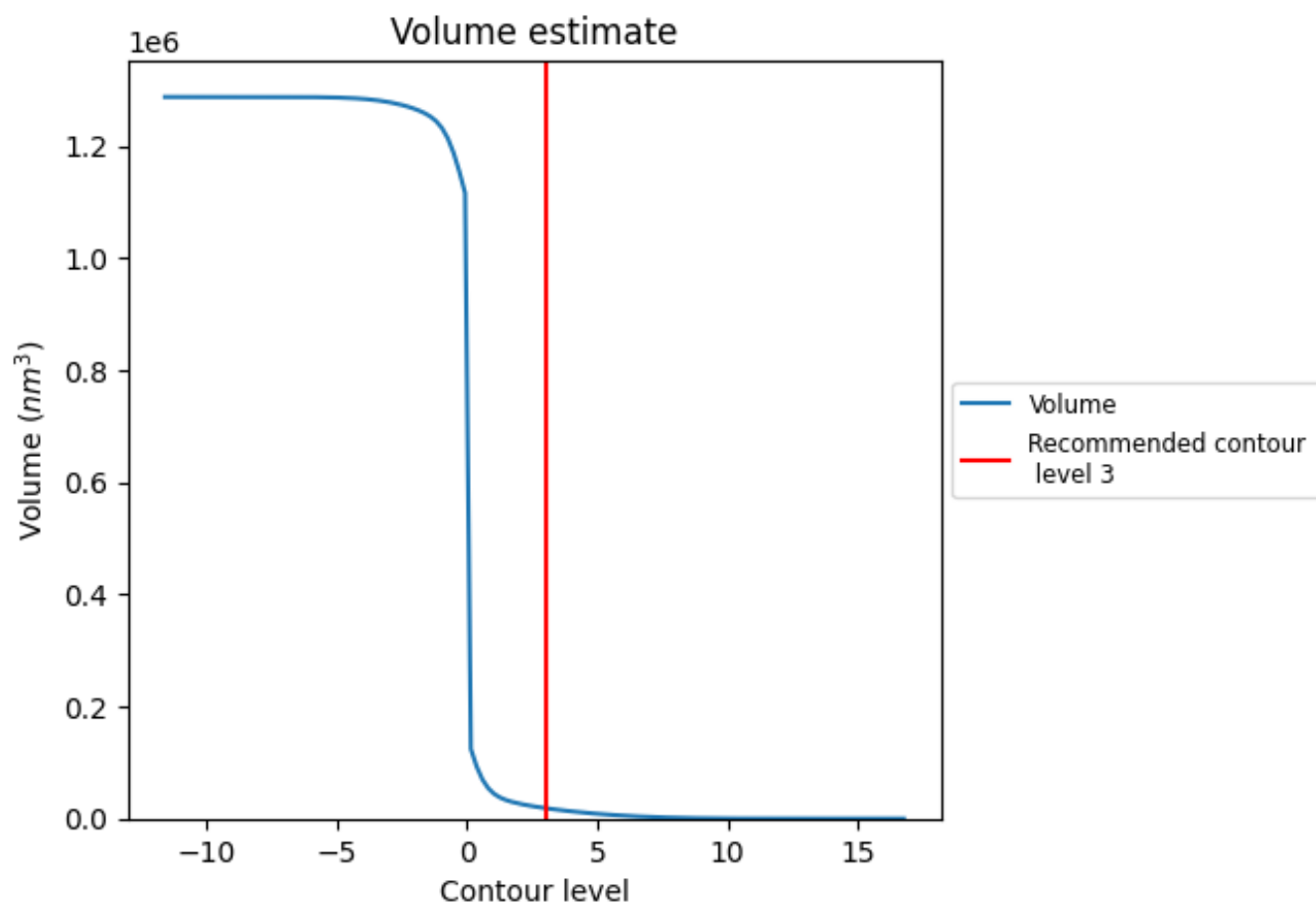
This section contains the results of statistical analysis of the map.

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.

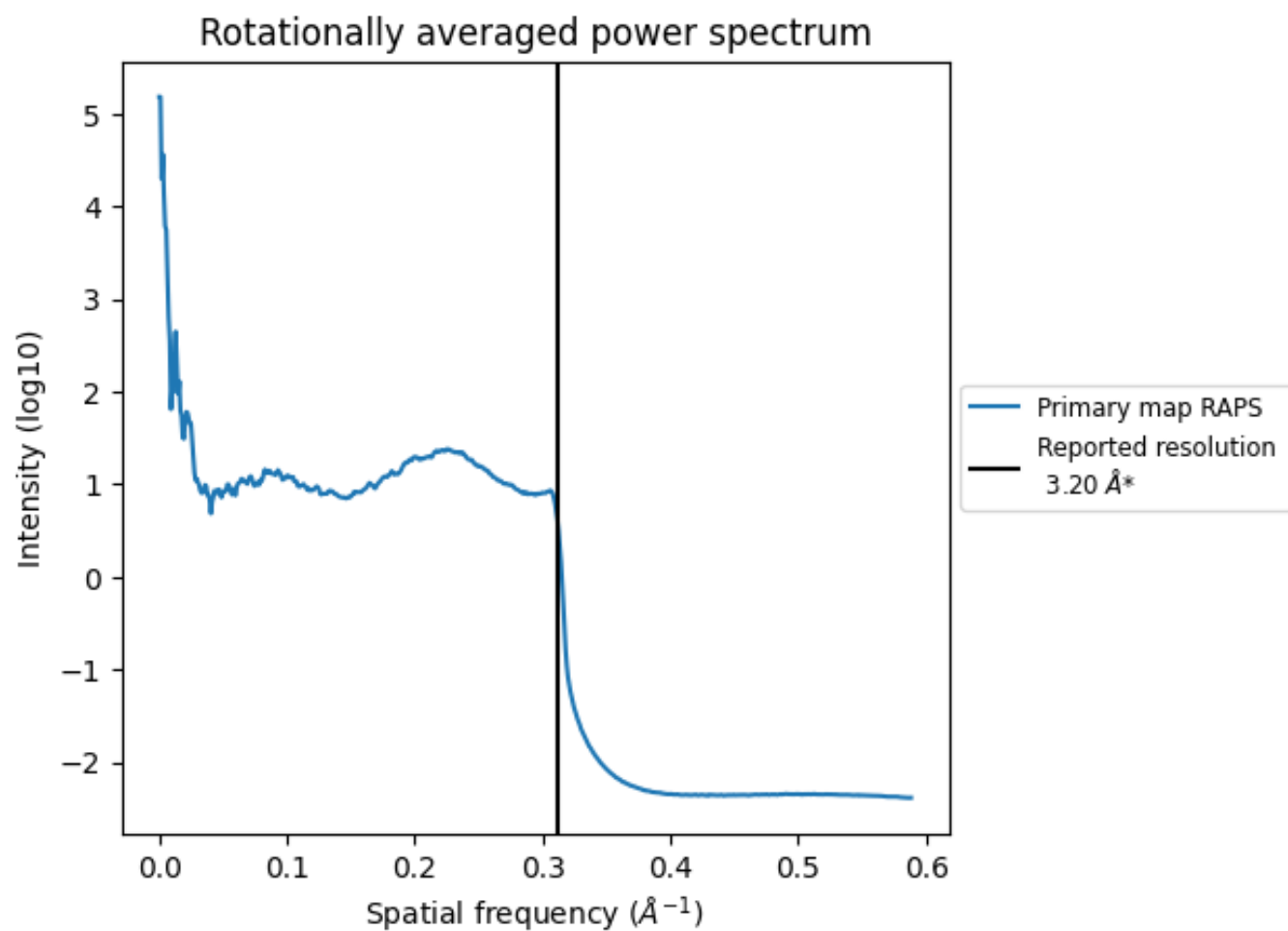
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 18707 nm³; this corresponds to an approximate mass of 16898 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 0.312 Å⁻¹

8 Fourier-Shell correlation

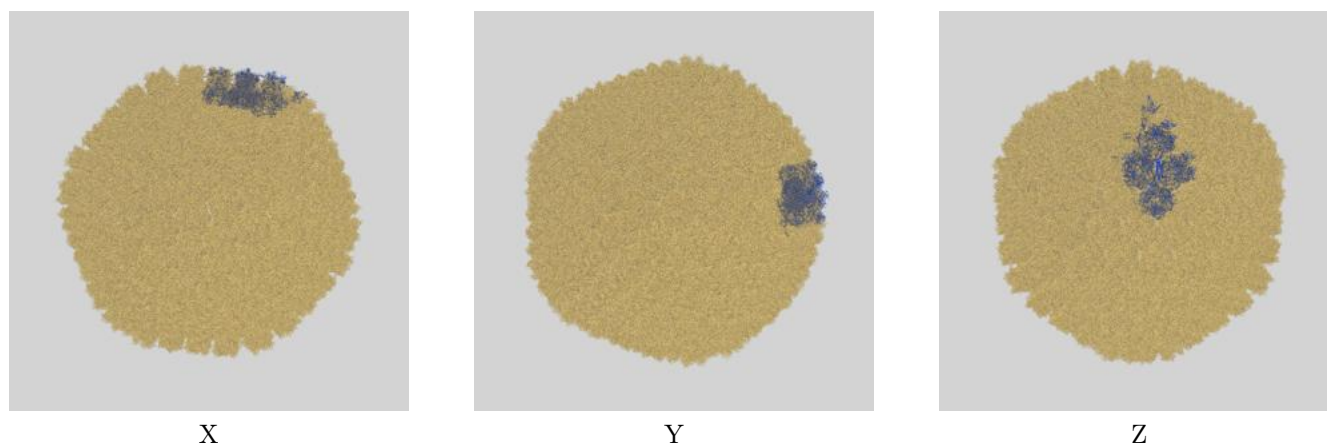
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

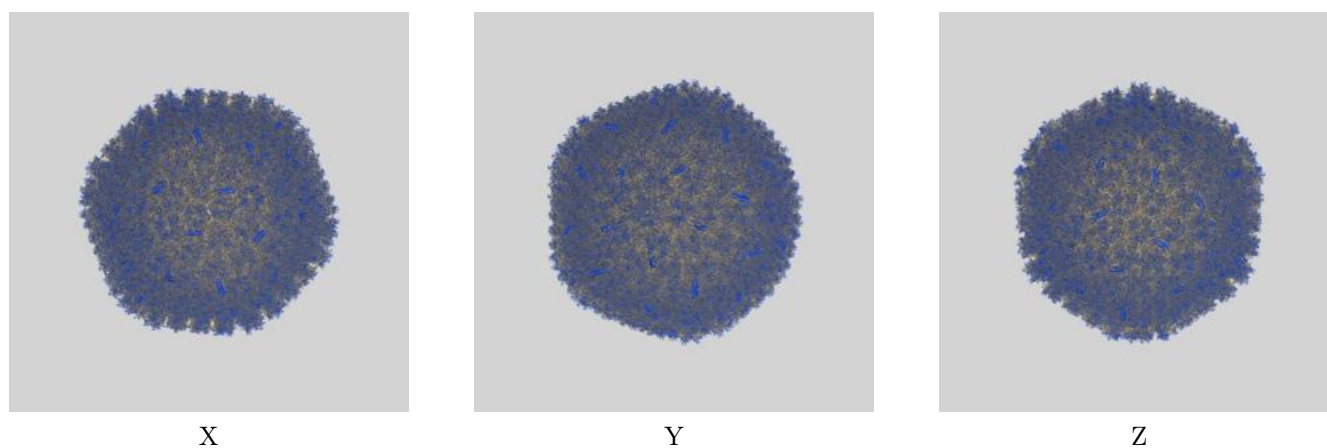
This section contains information regarding the fit between EMDB map EMD-7034 and PDB model 6B1T. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

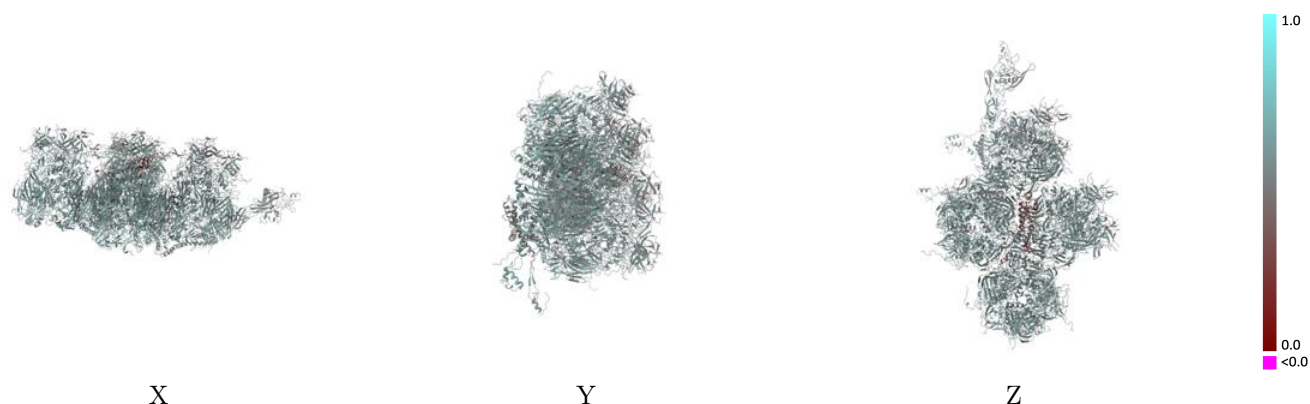


9.1.2 Map-model assembly overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 3.0 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](#)

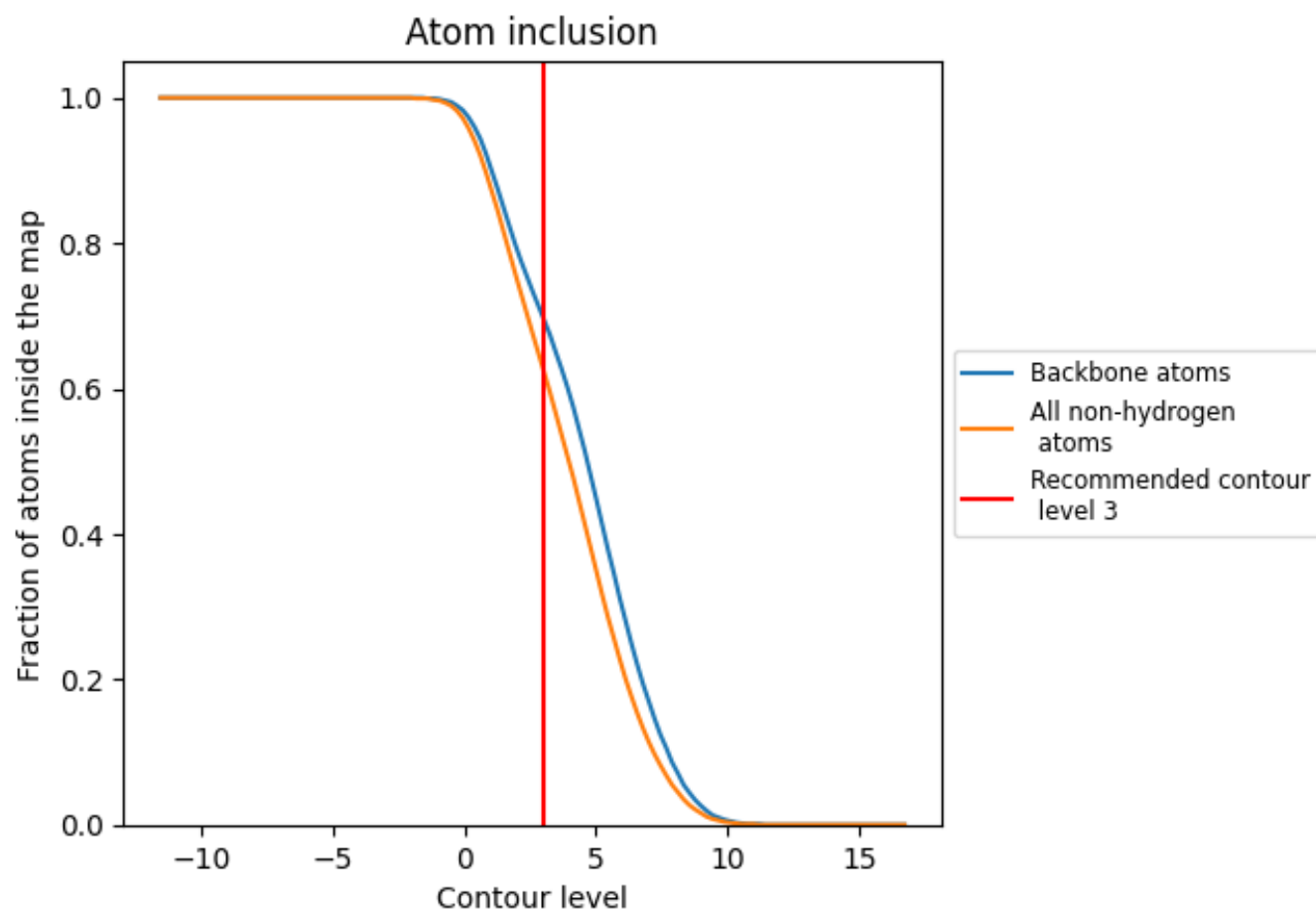


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 62% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6250	 0.5520
A	 0.5990	 0.5510
B	 0.5760	 0.5450
C	 0.5900	 0.5470
D	 0.6650	 0.5620
E	 0.6390	 0.5570
F	 0.6470	 0.5590
G	 0.6730	 0.5640
H	 0.6750	 0.5640
I	 0.6770	 0.5620
J	 0.6470	 0.5590
K	 0.6450	 0.5580
L	 0.6510	 0.5610
M	 0.4690	 0.5150
N	 0.5260	 0.5100
O	 0.6830	 0.5510
P	 0.7140	 0.5560
Q	 0.3970	 0.4600
R	 0.4220	 0.4780
S	 0.3370	 0.4600
T	 0.3430	 0.4700
U	 0.6020	 0.5750
V	 0.6440	 0.5760
W	 0.6670	 0.5800
X	 0.3160	 0.5320
Y	 0.6800	 0.5610

