wwPDB EM Validation Summary Report

Apr 29, 2024 – 11:00 pm BST

PDB ID	:	2WYY
EMDB ID	:	EMD-1663
Title	:	CRYOEM MODEL OF THE VESICULAR STOMATITIS VIRUS
Authors	:	Ge, P.; Tsao, J.; Green, T.J.; Luo, M.; Zhou, Z.H.
Deposited on	:	2009-11-20
Resolution	:	10.60 Å(reported)
Based on initial model	:	2WYY

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:

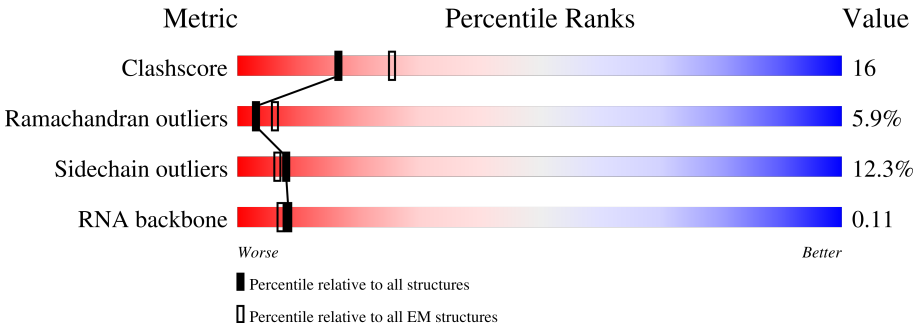
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 10.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 <=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	422	98% 67% 26% 6% •
1	C	422	98% 66% 26% 5% •
1	D	422	98% 68% 25% 5% •
1	F	422	98% 68% 25% 6% •
1	H	422	98% 67% 25% 6% •
1	I	422	98% 67% 26% 6% •
1	J	422	98% 68% 25% 6% •

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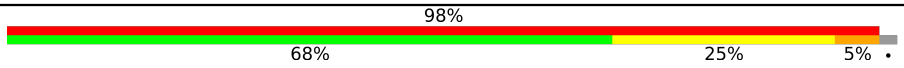
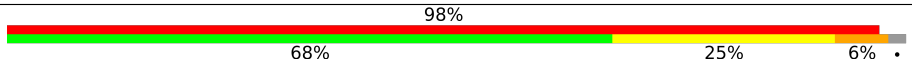
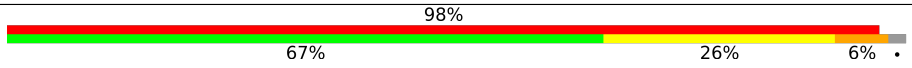
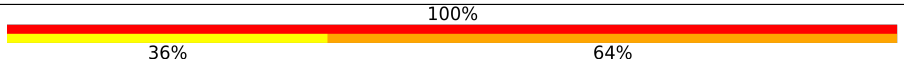
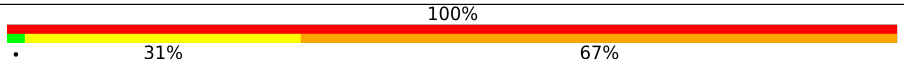
Mol	Chain	Length	Quality of chain
1	K	422	
1	L	422	
1	M	422	
2	R	45	
2	S	45	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 34620 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 NUCLEOPROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	C	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	D	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	F	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	H	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	I	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	J	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	K	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	L	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		
1	M	414	Total	C	N	O	S	0	0
			3282	2093	551	620	18		

- Molecule 2 is a RNA chain called POLY-URIDINE.

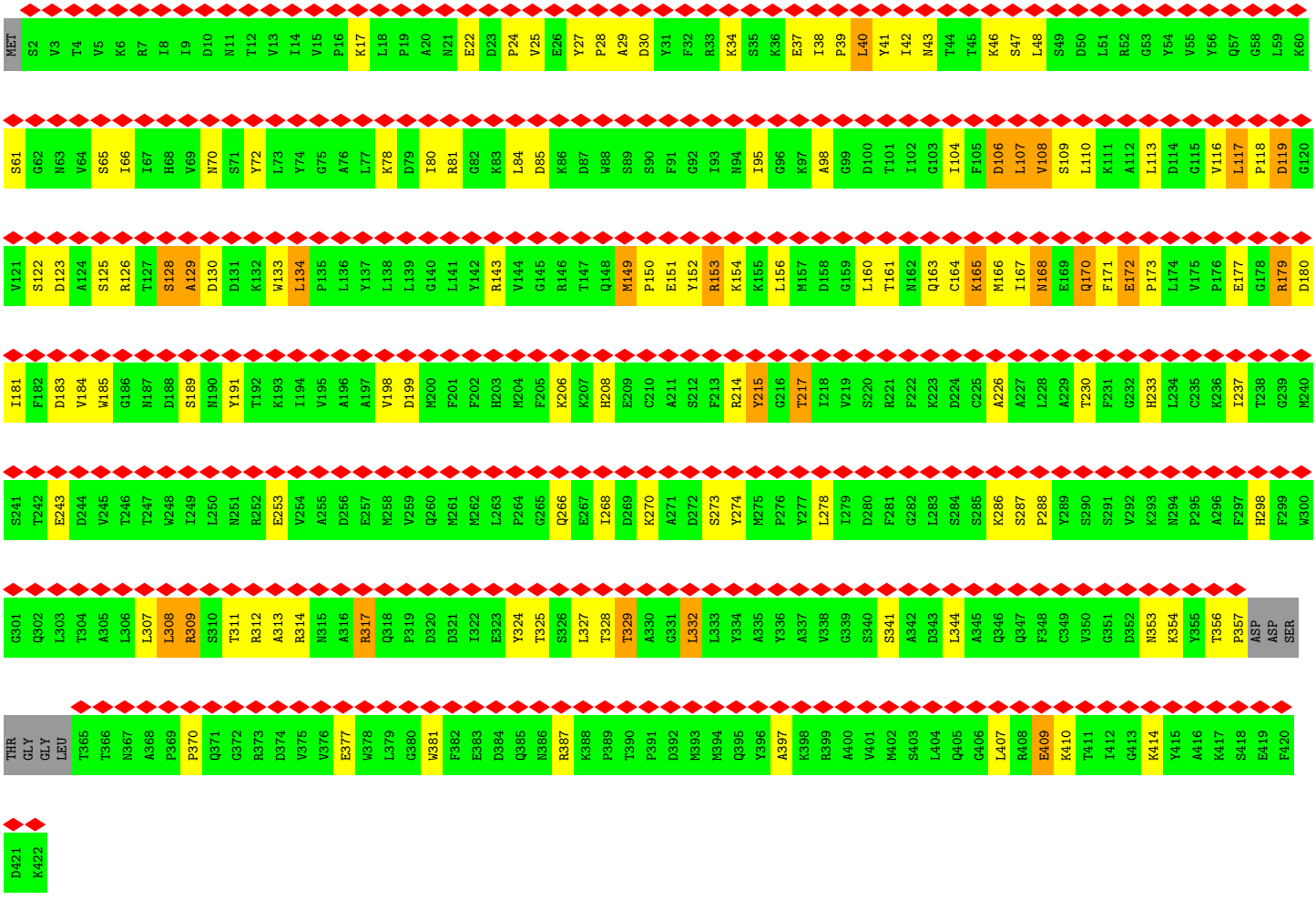
Mol	Chain	Residues	Atoms					AltConf	Trace
2	R	45	Total	C	N	O	P	0	0
			900	405	90	360	45		
2	S	45	Total	C	N	O	P	0	0
			900	405	90	360	45		

3 Residue-property plots (i)

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.

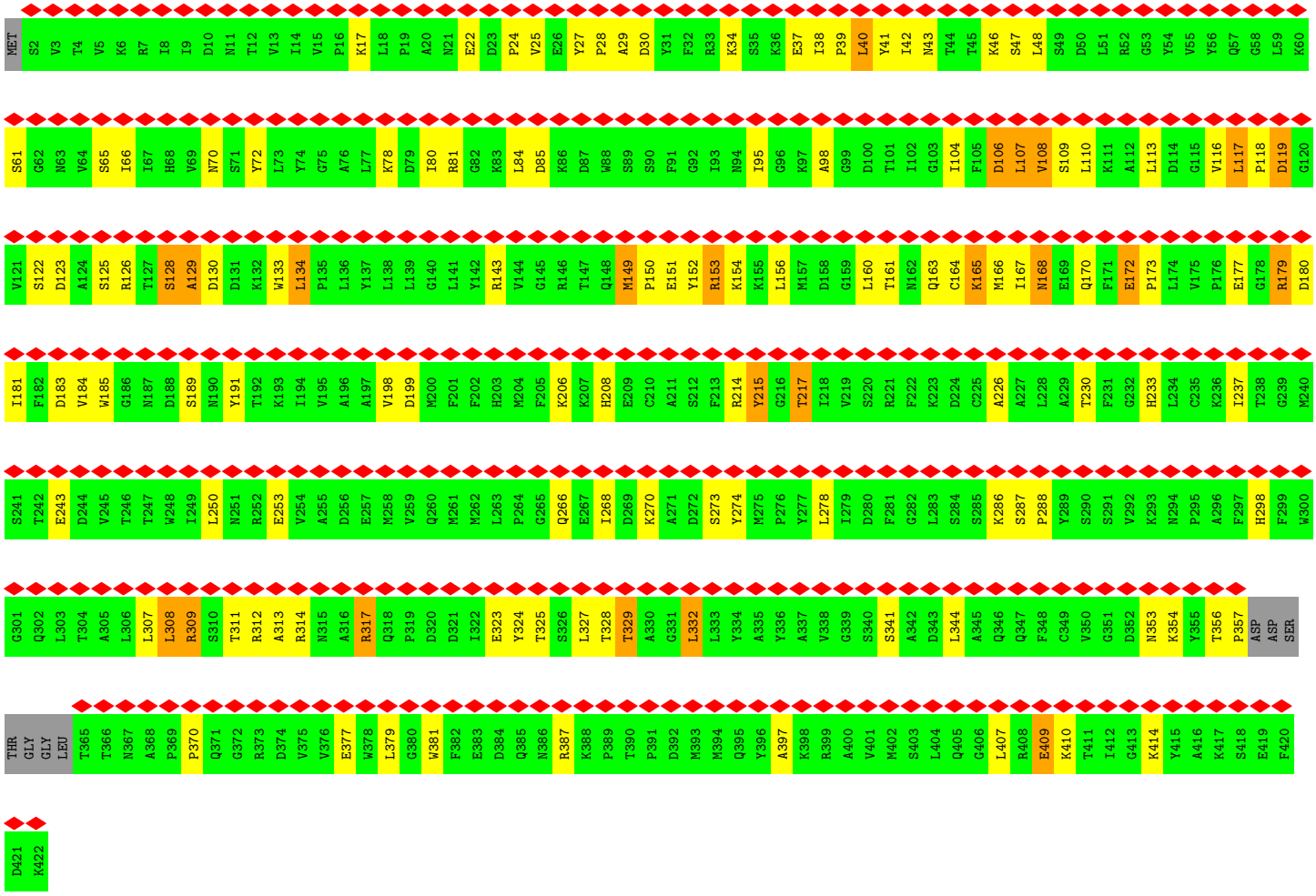
- Molecule 1: NUCLEOPROTEIN

Chain A:



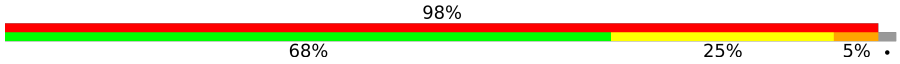
- Molecule 1: NUCLEOPROTEIN

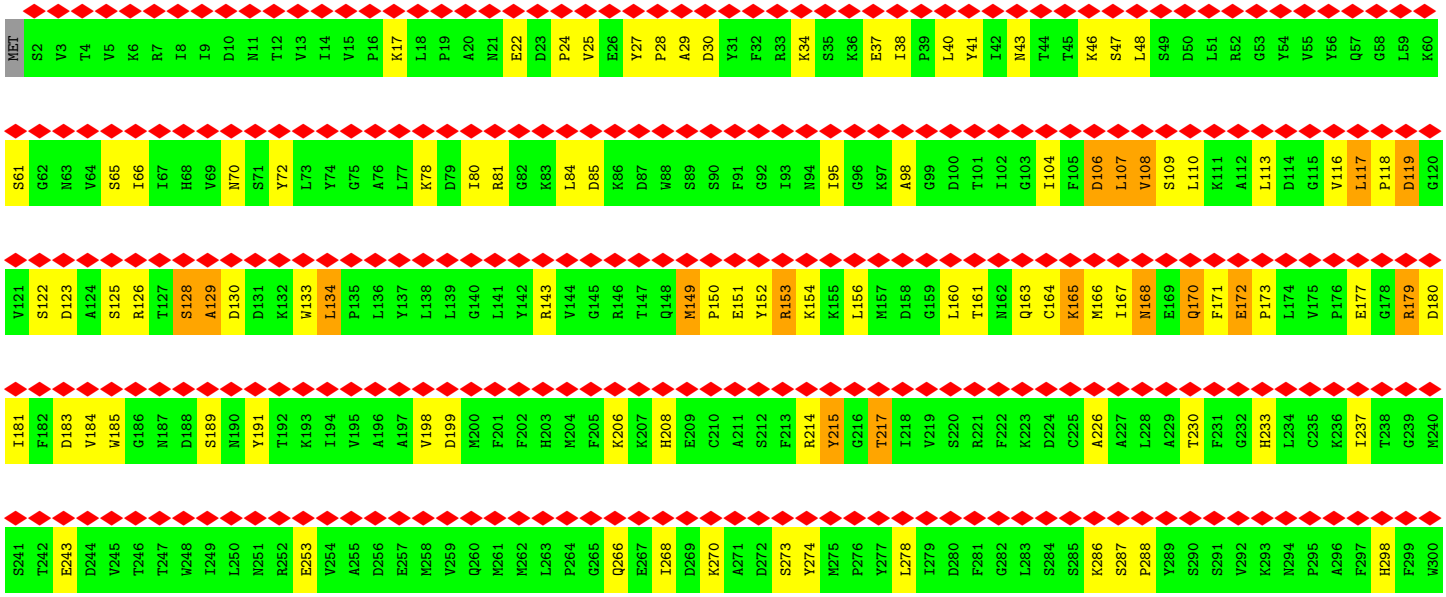
Chain C:

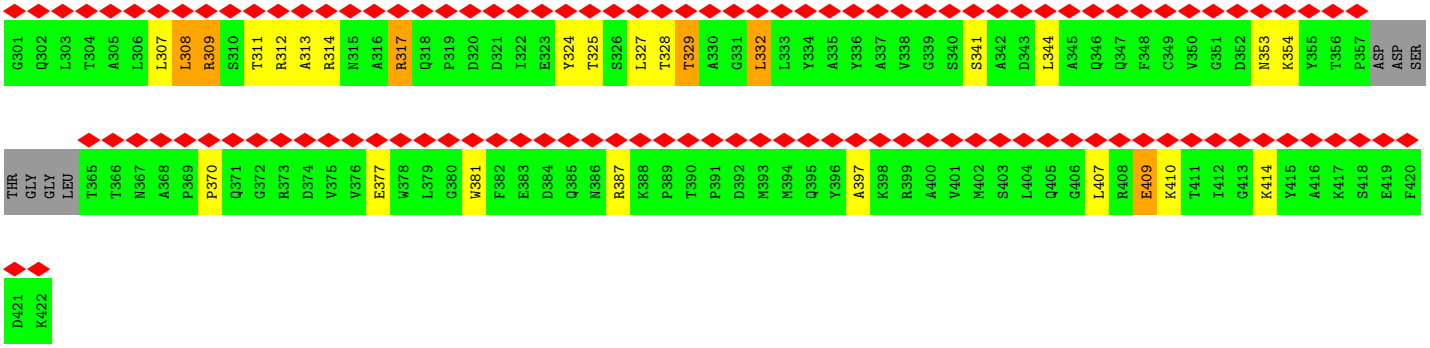


- Molecule 1: NUCLEOPROTEIN

Chain D:

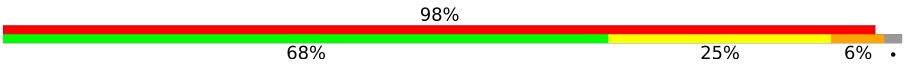


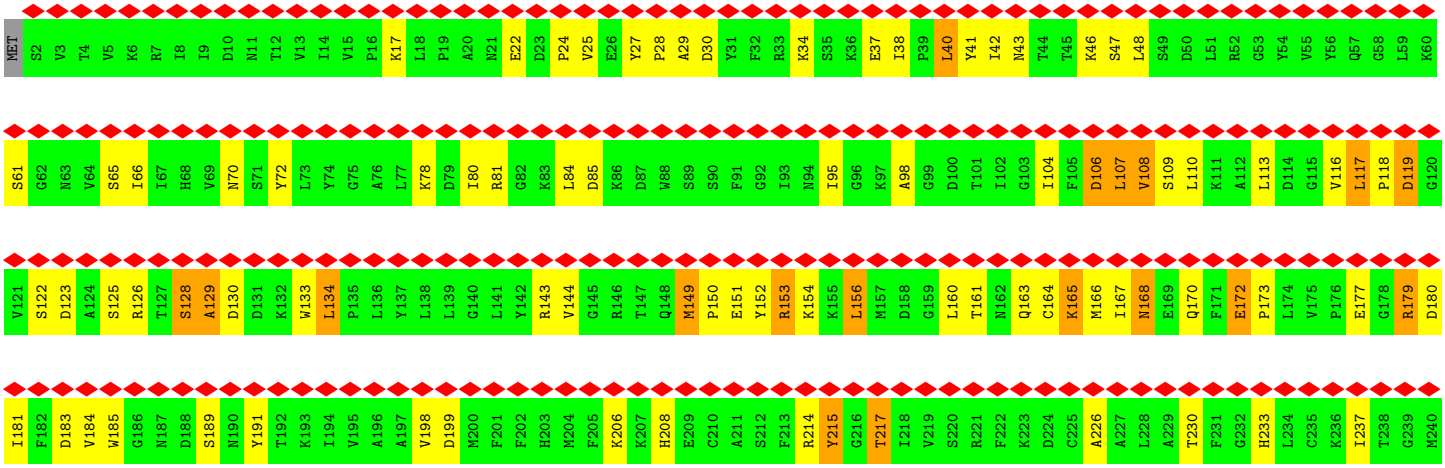




• Molecule 1: NUCLEOPROTEIN

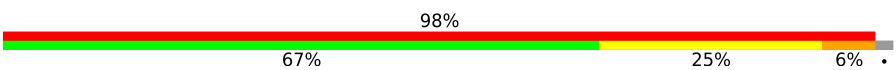
Chain F:

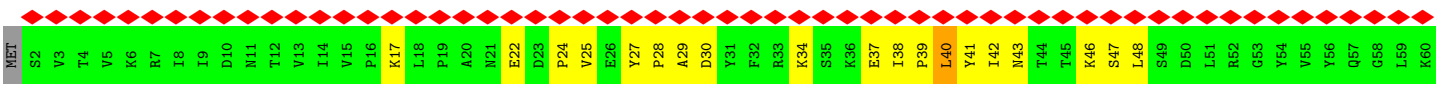


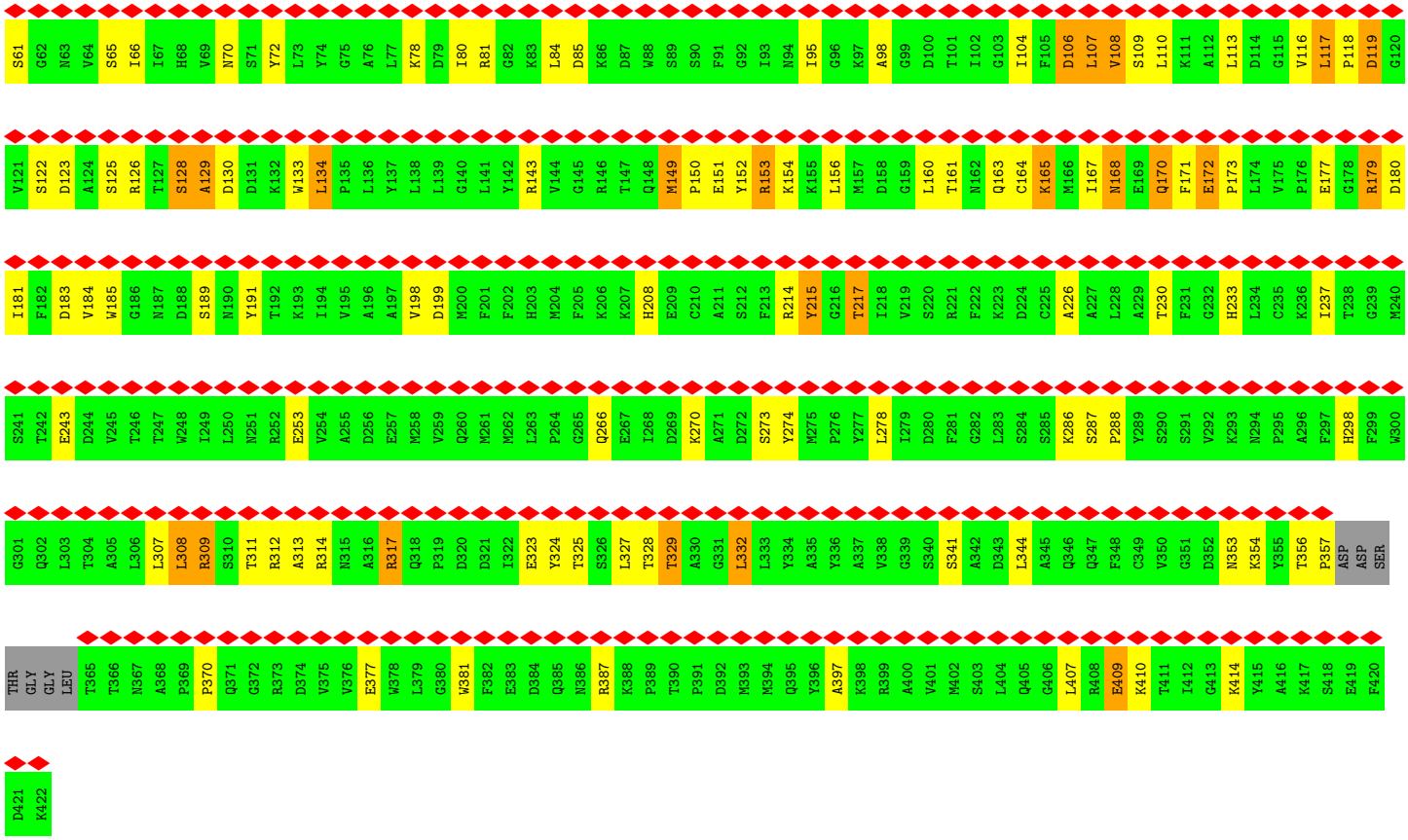


• Molecule 1: NUCLEOPROTEIN

Chain H:

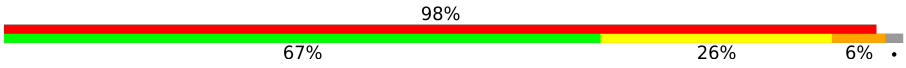


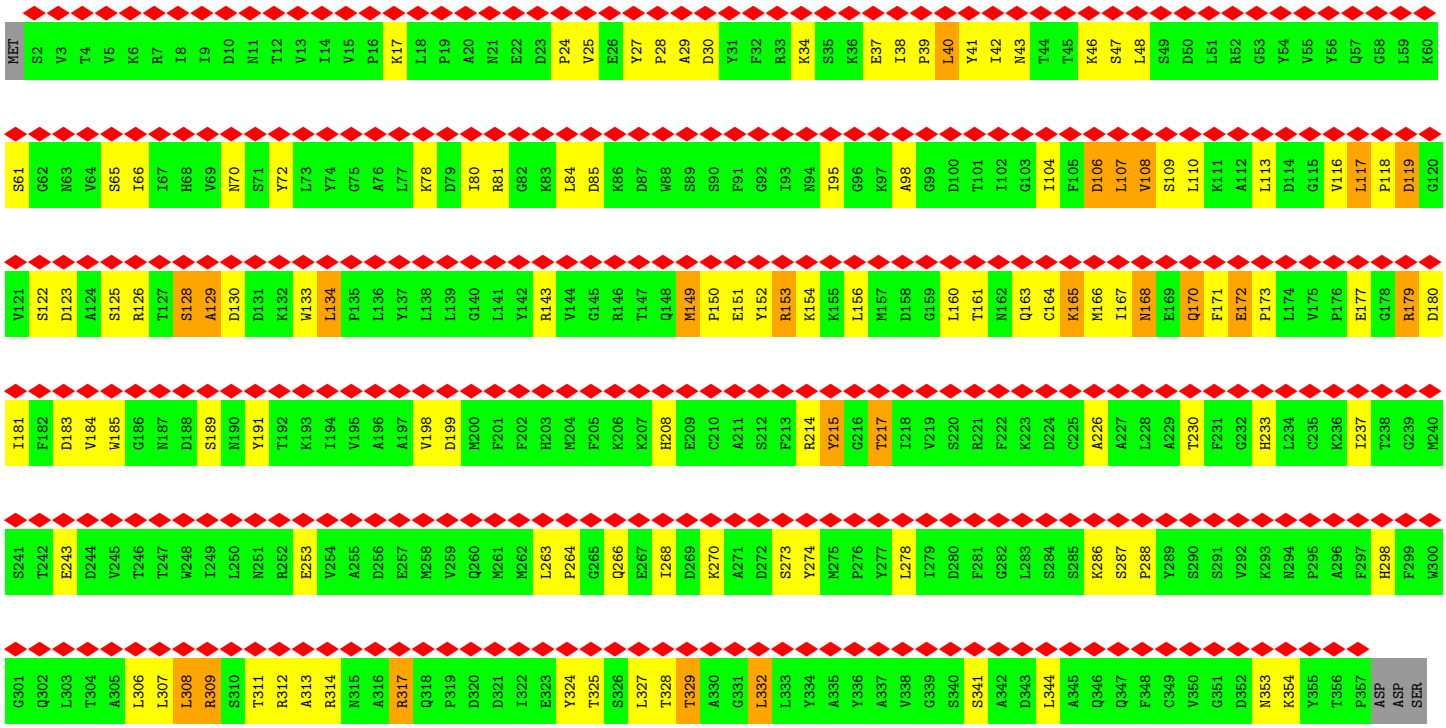


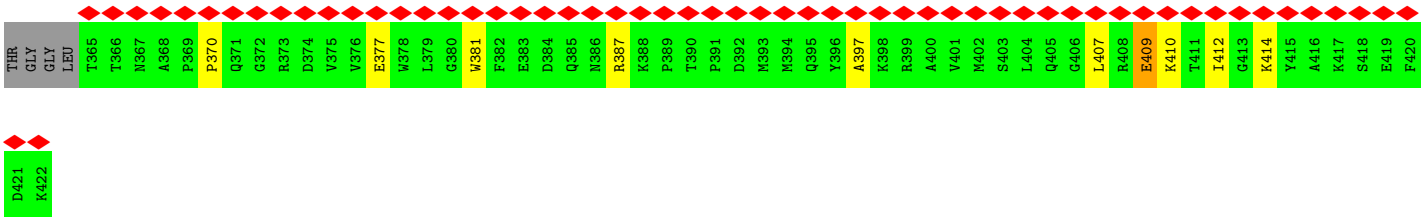


- Molecule 1: NUCLEOPROTEIN

Chain I:

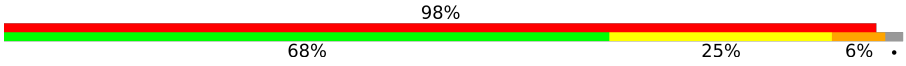


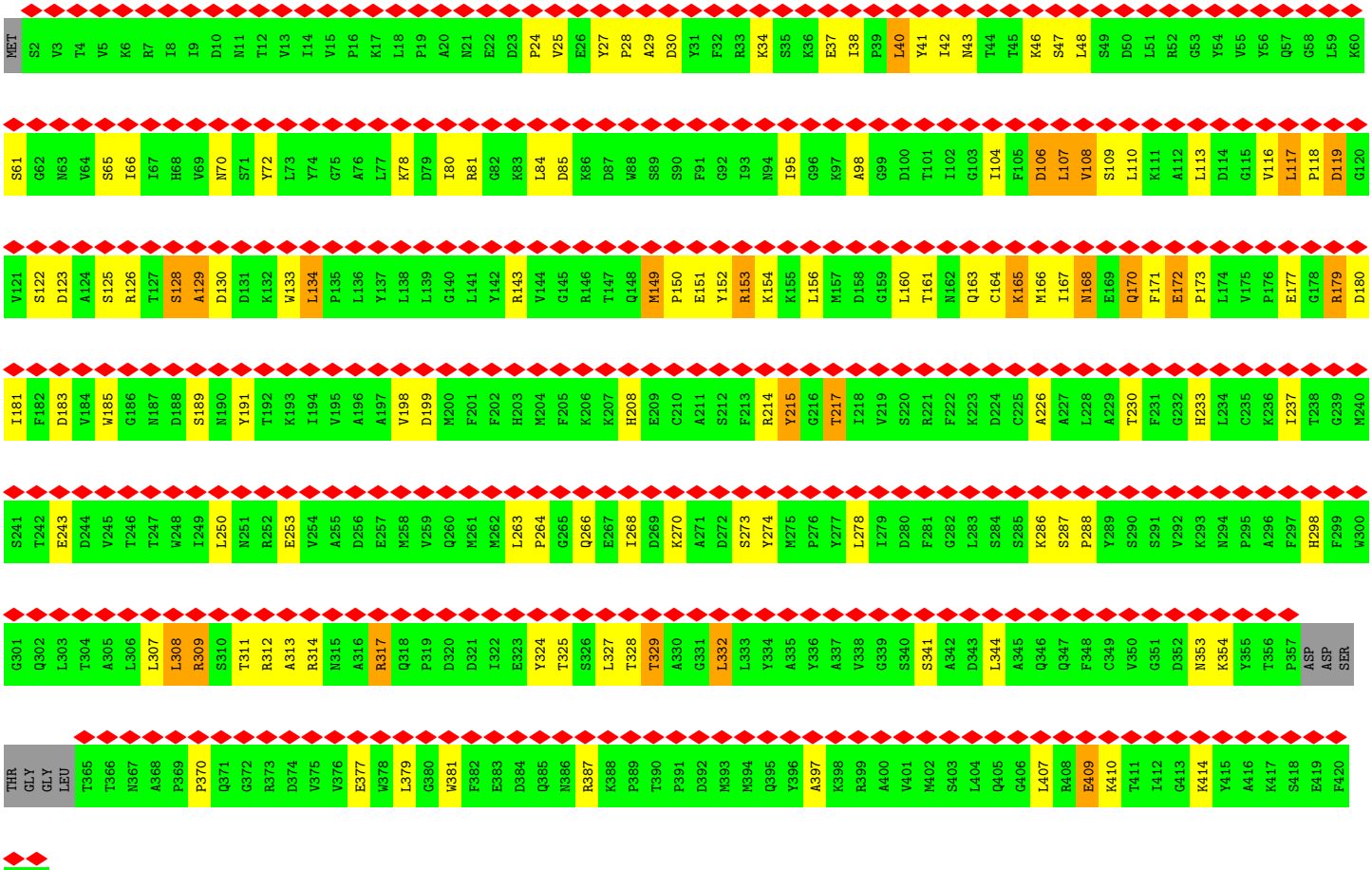




• Molecule 1: NUCLEOPROTEIN

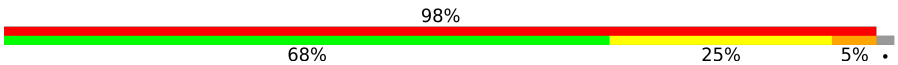
Chain J:





• Molecule 1: NUCLEOPROTEIN

Chain K:



V121 S122 D123 A124 S125 R126 T127 S128 A129 D130 D131 K132 W133 L134 P135 L136 Y137 L138 L139 G140 L141 Y142 R143 V144 G145 R146 T147 Q148 M149 P150 E151 Y152 R153 K154 K155 L156 M157 D158 G159 L160 T161 N162 Q163 C164 K165 M166 I167 N168 E169 Q170 F171 E172 P173 L174 V175 P176 E177 G178 R179 D180

I181 F182 D183 V184 W185 G186 N187 D188 S189 N190 Y191 T192 K193 I194 V195 A196 A197 V198 D199 M200 F201 F202 H203 M204 F205 K206 K207 H208 E209 C210 A211 S212 F213 R214 Y215 G216 T217 I218 V219 S220 R221 F222 K223 D224 C225 A226 A227 L228 A229 T230 F231 G232 H233 L234 C235 K236 I237 T238 G239 M240

S241 T242 E243 D244 V245 T246 T247 W248 I249 L250 N251 R252 E253 V254 A255 D256 E257 M258 V259 Q260 M261 M262 L263 P264 G265 Q266 E267 I268 D269 K270 A271 D272 S273 Y274 M275 P276 Y277 L278 I279 D280 F281 G282 L283 S284 S285 K286 S287 P288 Y289 S290 S291 V292 K293 N294 P295 A296 F297 H298 F299 W300

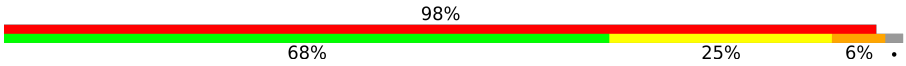
G301 Q302 L303 T304 A305 L306 L307 L308 R309 S310 T311 R312 A313 R314 N315 A316 R317 Q318 P319 D320 D321 I322 E323 Y324 T325 S326 L327 T328 T329 A330 G331 L332 L333 Y334 A335 Y336 A337 V338 G339 S340 S341 A342 D343 L344 A345 Q346 Q347 F348 C349 V350 G351 D352 N353 K354 Y355 T356 P357 ASP ASP SER

THR GLY GLY LEU T365 T366 N367 A368 P369 P370 Q371 G372 R373 D374 V375 V376 E377 W378 L379 G380 W381 F382 E383 D384 Q385 N386 R387 K388 P389 T390 P391 D392 M393 M394 Q395 Y396 A397 K398 R399 A400 V401 M402 S403 L404 Q405 G406 L407 R408 E409 K410 T411 I412 G413 K414 Y415 A416 K417 S418 E419 F420

D421 K422

- Molecule 1: NUCLEOPROTEIN

Chain L:



MET S2 V3 T4 V5 K6 R7 I8 I9 D10 N11 T12 V13 I14 V15 P16 K17 L18 P19 A20 N21 E22 D23 P24 V25 E26 Y27 P28 A29 D30 Y31 F32 R33 K34 S35 K36 E37 I38 P39 L40 Y41 I42 N43 T44 T45 K46 S47 L48 S49 D50 L51 R52 G53 Y54 V55 Y56 Q57 G58 L59 K60

S61 G62 N63 V64 S65 I66 I67 H68 V69 N70 S71 Y72 L73 Y74 G75 A76 L77 K78 D79 I80 R81 G82 K83 L84 D85 K86 D87 W88 S89 S90 F91 G92 I93 N94 I95 G96 K97 A98 G99 D100 T101 I102 G103 I104 F105 D106 L107 V108 S109 L110 K111 A112 L113 D114 G115 V116 L117 P118 D119 G120

V121 S122 D123 A124 S125 R126 T127 S128 A129 D130 D131 K132 W133 L134 P135 L136 Y137 L138 L139 G140 L141 Y142 R143 V144 G145 R146 T147 Q148 M149 P150 E151 Y152 R153 K154 K155 L156 M157 D158 G159 L160 T161 N162 Q163 C164 K165 M166 I167 N168 E169 Q170 F171 E172 P173 L174 V175 P176 E177 G178 R179 D180

I181 F182 D183 V184 W185 G186 N187 D188 S189 N190 Y191 T192 K193 I194 V195 A196 A197 V198 D199 M200 F201 F202 H203 M204 F205 K206 K207 H208 E209 C210 A211 S212 F213 R214 Y215 G216 T217 I218 V219 S220 R221 F222 K223 D224 C225 A226 A227 L228 A229 T230 F231 G232 H233 L234 C235 K236 I237 T238 G239 M240

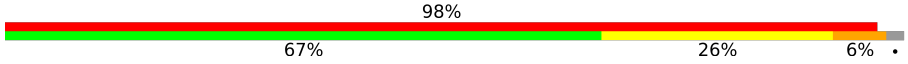
S241 T242 E243 D244 V245 T246 T247 W248 I249 L250 N251 R252 E253 V254 A255 D256 E257 M258 V259 Q260 M261 M262 L263 P264 G265 Q266 E267 I268 D269 K270 A271 D272 S273 Y274 M275 P276 Y277 L278 I279 D280 F281 G282 L283 S284 S285 K286 S287 P288 Y289 S290 S291 V292 K293 N294 P295 A296 F297 H298 F299 W300

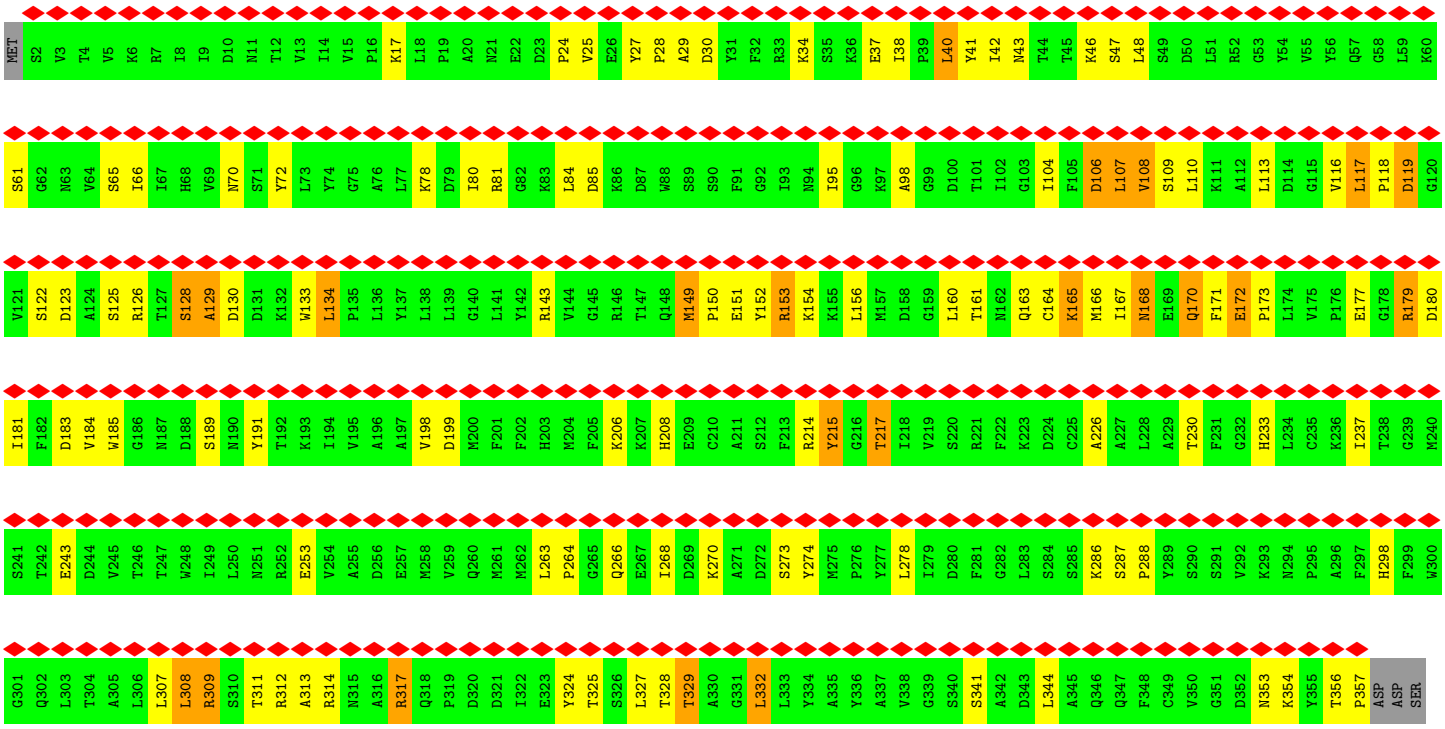
G301 Q302 L303 T304 A305 L306 L307 L308 R309 S310 T311 R312 A313 R314 N315 A316 R317 Q318 P319 D320 D321 I322 E323 Y324 T325 S326 L327 T328 T329 A330 G331 L332 L333 Y334 A335 Y336 A337 V338 G339 S340 S341 A342 D343 L344 A345 Q346 Q347 F348 C349 V350 G351 D352 N353 K354 Y355 T356 P357 ASP ASP SER

THR GLY GLY LEU T365 T366 N367 A368 P369 P370 Q371 G372 R373 D374 V375 V376 E377 W378 L379 G380 W381 F382 E383 D384 Q385 N386 R387 K388 P389 T390 P391 D392 M393 M394 Q395 Y396 A397 K398 R399 A400 V401 M402 S403 L404 Q405 G406 L407 R408 E409 K410 T411 I412 G413 K414 Y415 A416 K417 S418 E419 F420

• Molecule 1: NUCLEOPROTEIN

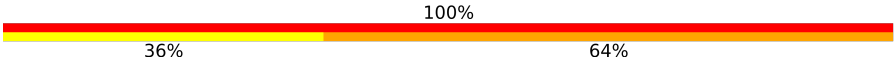
Chain M:

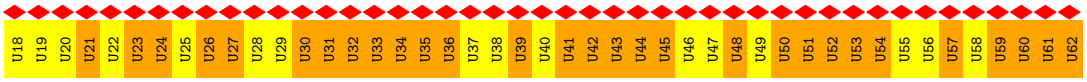




• Molecule 2: POLY-URIDINE

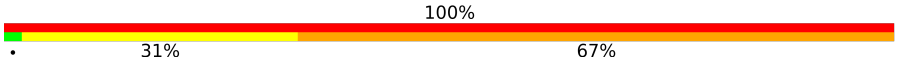
Chain R:

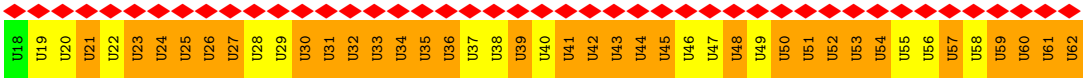




• Molecule 2: POLY-URIDINE

Chain S:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of segments used	Not provided	
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	98000	Depositor
Image detector	GENERIC TVIPS	Depositor
Maximum map value	5.997	Depositor
Minimum map value	-6.598	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.999	Depositor
Recommended contour level	1.0	Depositor
Map size (Å)	490.24, 490.24, 490.24	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90, 90, 90	wwPDB
Pixel spacing (Å)	1.532, 1.532, 1.532	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	0.54	0/3357	0.63	0/4543
1	C	0.54	0/3357	0.63	0/4543
1	D	0.50	0/3357	0.61	0/4543
1	F	0.54	0/3357	0.63	0/4543
1	H	0.54	0/3357	0.63	0/4543
1	I	0.54	0/3357	0.63	0/4543
1	J	0.54	0/3357	0.63	0/4543
1	K	0.50	0/3357	0.61	0/4543
1	L	0.54	0/3357	0.63	0/4543
1	M	0.54	0/3357	0.63	0/4543
2	R	0.90	0/989	1.18	1/1526 (0.1%)
2	S	0.90	0/989	1.18	1/1526 (0.1%)
All	All	0.56	0/35548	0.67	2/48482 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
1	D	0	1
1	F	0	1
1	H	0	1
1	I	0	1
1	J	0	1
1	K	0	1
1	L	0	1
1	M	0	1
All	All	0	10

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	R	31	U	C3'-C2'-C1'	5.04	105.53	101.50
2	S	31	U	C3'-C2'-C1'	5.03	105.52	101.50

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	106	ASP	Peptide
1	C	106	ASP	Peptide
1	D	106	ASP	Peptide
1	F	106	ASP	Peptide
1	H	106	ASP	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	3282	0	3249	109	0
1	C	3282	0	3249	112	0
1	D	3282	0	3249	109	0
1	F	3282	0	3249	109	0
1	H	3282	0	3249	103	0
1	I	3282	0	3249	113	0
1	J	3282	0	3249	101	0
1	K	3282	0	3249	110	0
1	L	3282	0	3249	109	0
1	M	3282	0	3249	111	0
2	R	900	0	451	70	0
2	S	900	0	450	70	0
All	All	34620	0	33391	1058	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 16.

The worst 5 of 1058 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:C:184:VAL:HG21	1:M:166:MET:CE	1.39	1.51
1:L:166:MET:CE	1:M:184:VAL:HG21	1.40	1.51
1:I:184:VAL:HG21	1:J:166:MET:CE	1.40	1.51
1:D:166:MET:CE	1:F:184:VAL:HG21	1.40	1.50
1:F:166:MET:CE	1:H:184:VAL:HG21	1.40	1.50

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	410/422 (97%)	341 (83%)	45 (11%)	24 (6%)	1	17
1	C	410/422 (97%)	341 (83%)	45 (11%)	24 (6%)	1	17
1	D	410/422 (97%)	341 (83%)	45 (11%)	24 (6%)	1	17
1	F	410/422 (97%)	341 (83%)	45 (11%)	24 (6%)	1	17
1	H	410/422 (97%)	340 (83%)	46 (11%)	24 (6%)	1	17
1	I	410/422 (97%)	341 (83%)	45 (11%)	24 (6%)	1	17
1	J	410/422 (97%)	341 (83%)	45 (11%)	24 (6%)	1	17
1	K	410/422 (97%)	341 (83%)	45 (11%)	24 (6%)	1	17
1	L	410/422 (97%)	341 (83%)	45 (11%)	24 (6%)	1	17
1	M	410/422 (97%)	340 (83%)	46 (11%)	24 (6%)	1	17
All	All	4100/4220 (97%)	3408 (83%)	452 (11%)	240 (6%)	3	17

5 of 240 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	24	PRO
1	A	98	ALA
1	A	128	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	150	PRO
1	A	168	ASN

5.3.2 Protein sidechains (i)

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	357/363 (98%)	313 (88%)	44 (12%)	4 19
1	C	357/363 (98%)	313 (88%)	44 (12%)	4 19
1	D	357/363 (98%)	313 (88%)	44 (12%)	4 19
1	F	357/363 (98%)	314 (88%)	43 (12%)	5 20
1	H	357/363 (98%)	313 (88%)	44 (12%)	4 19
1	I	357/363 (98%)	313 (88%)	44 (12%)	4 19
1	J	357/363 (98%)	313 (88%)	44 (12%)	4 19
1	K	357/363 (98%)	313 (88%)	44 (12%)	4 19
1	L	357/363 (98%)	314 (88%)	43 (12%)	5 20
1	M	357/363 (98%)	313 (88%)	44 (12%)	4 19
All	All	3570/3630 (98%)	3132 (88%)	438 (12%)	8 19

5 of 438 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	116	VAL
1	J	215	TYR
1	M	48	LEU
1	I	163	GLN
1	I	409	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	266	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	K	70	ASN
1	M	385	GLN
1	I	385	GLN
1	J	187	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	R	44/45 (97%)	34 (77%)	1 (2%)
2	S	44/45 (97%)	34 (77%)	1 (2%)
All	All	88/90 (97%)	68 (77%)	2 (2%)

5 of 68 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	R	19	U
2	R	21	U
2	R	23	U
2	R	24	U
2	R	25	U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	R	24	U
2	S	24	U

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

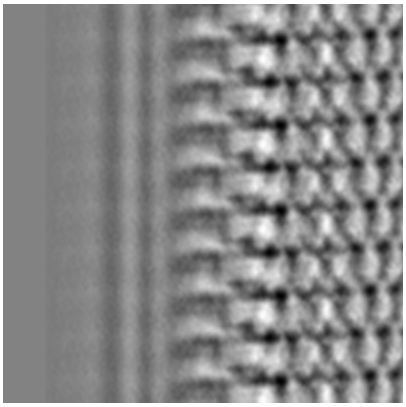
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-1663. These allow visual inspection of the internal detail of the map and identification of artifacts.

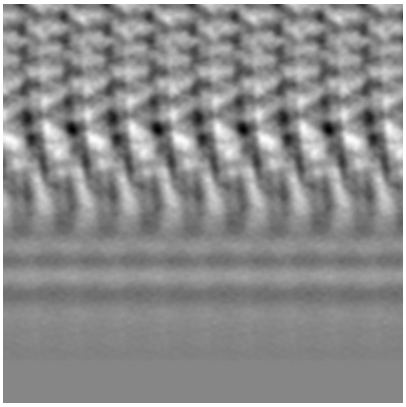
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

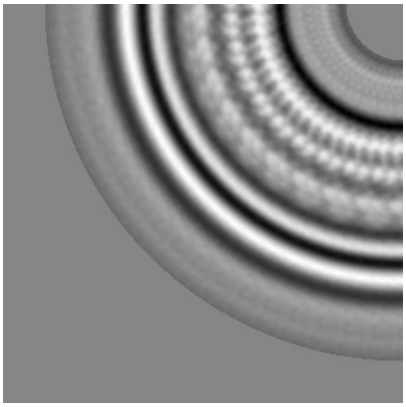
6.1.1 Primary map



X



Y

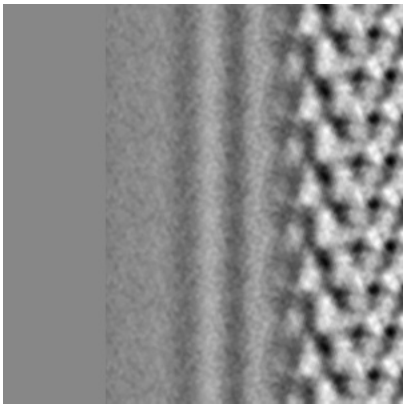


Z

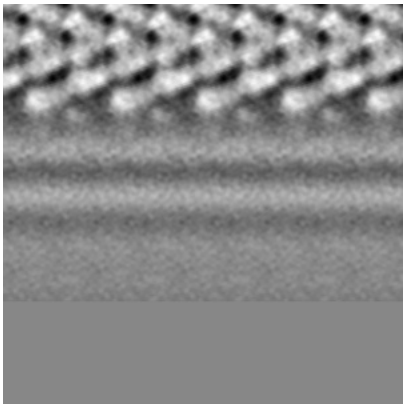
The images above show the map projected in three orthogonal directions.

6.2 Central slices

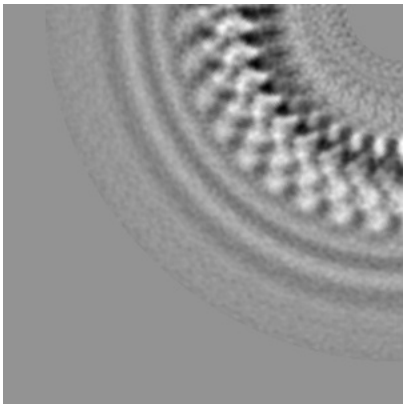
6.2.1 Primary map



X Index: 160



Y Index: 160

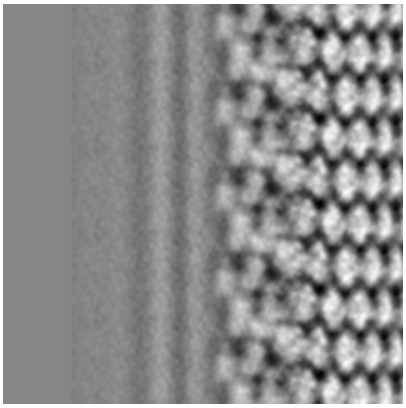


Z Index: 160

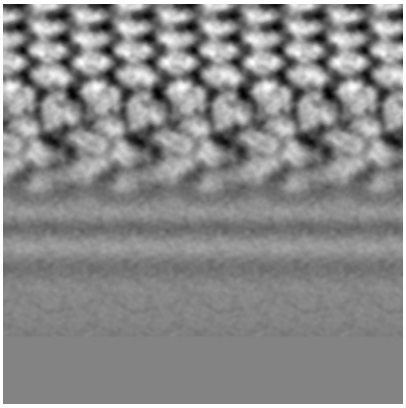
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

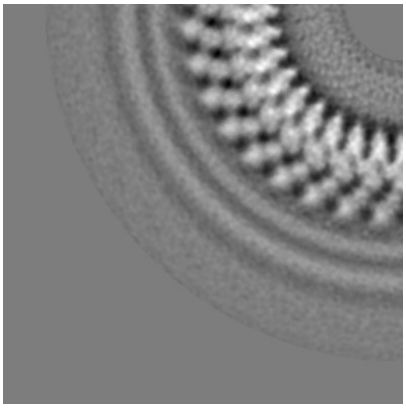
6.3.1 Primary map



X Index: 212



Y Index: 213

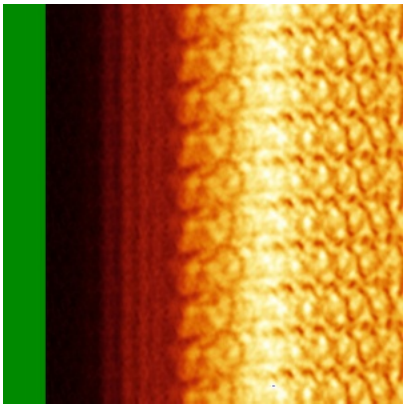


Z Index: 317

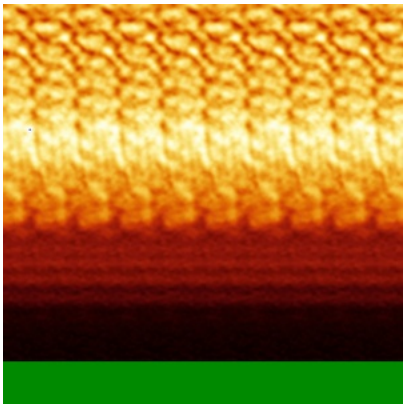
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

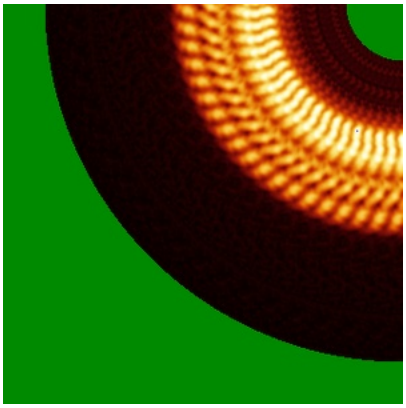
6.4.1 Primary map



X



Y

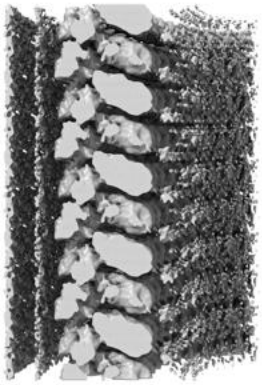


Z

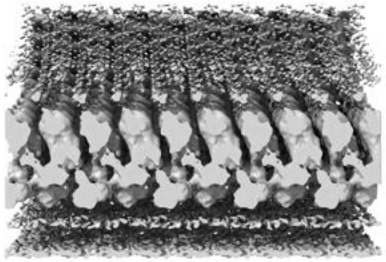
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

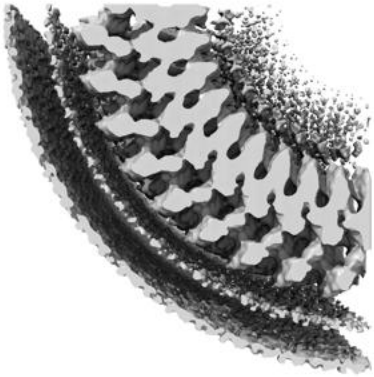
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

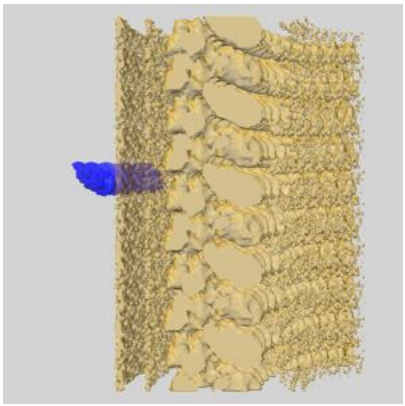
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

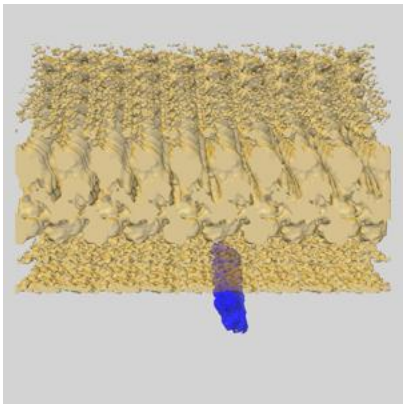
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

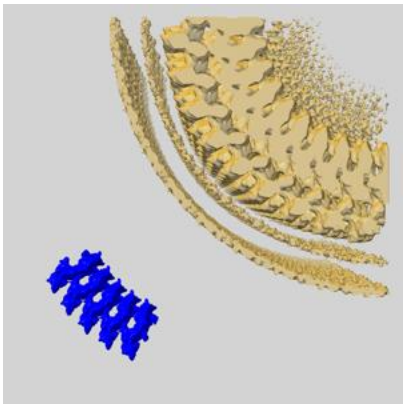
6.6.1 emd_1663_msk_1.map (i)



X

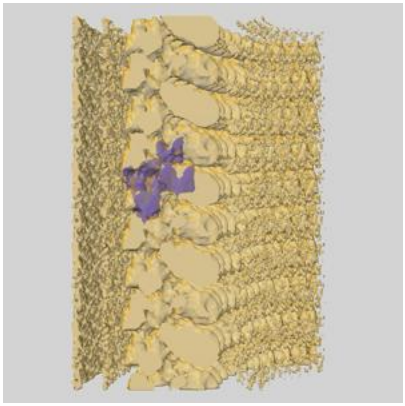


Y

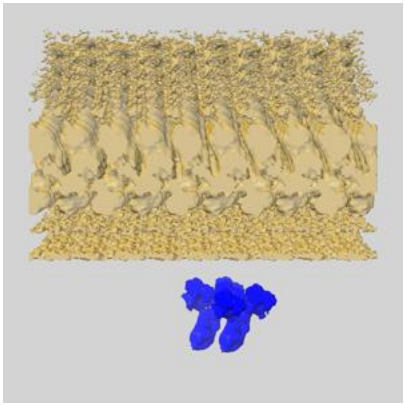


Z

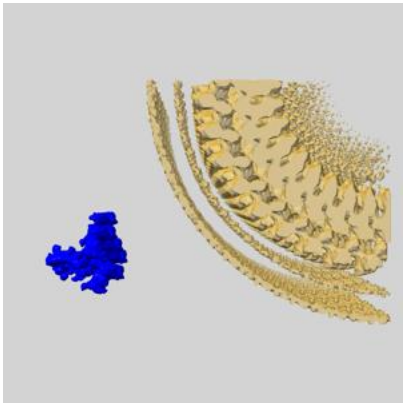
6.6.2 emd_1663_msk_2.map (i)



X



Y

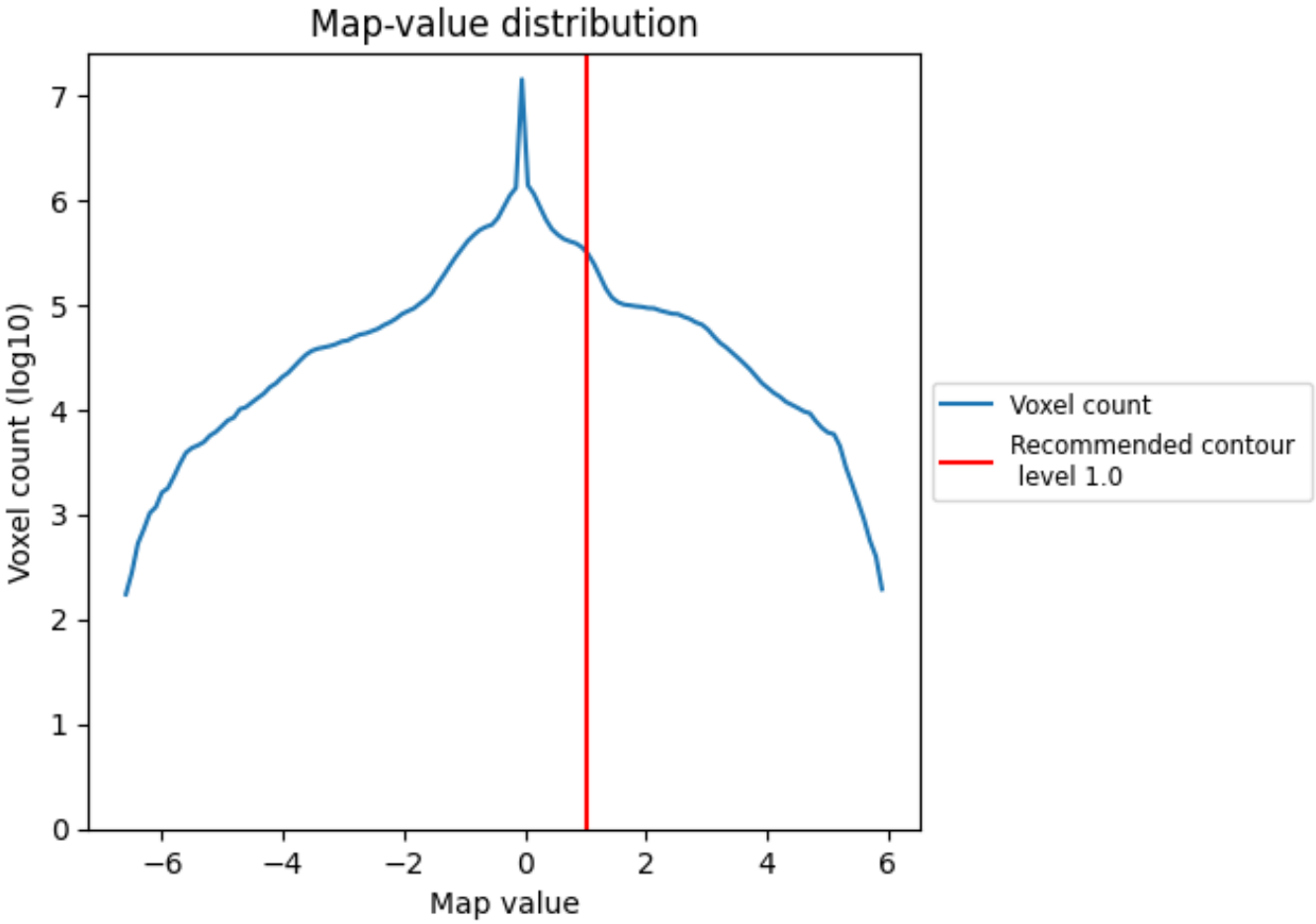


Z

7 Map analysis

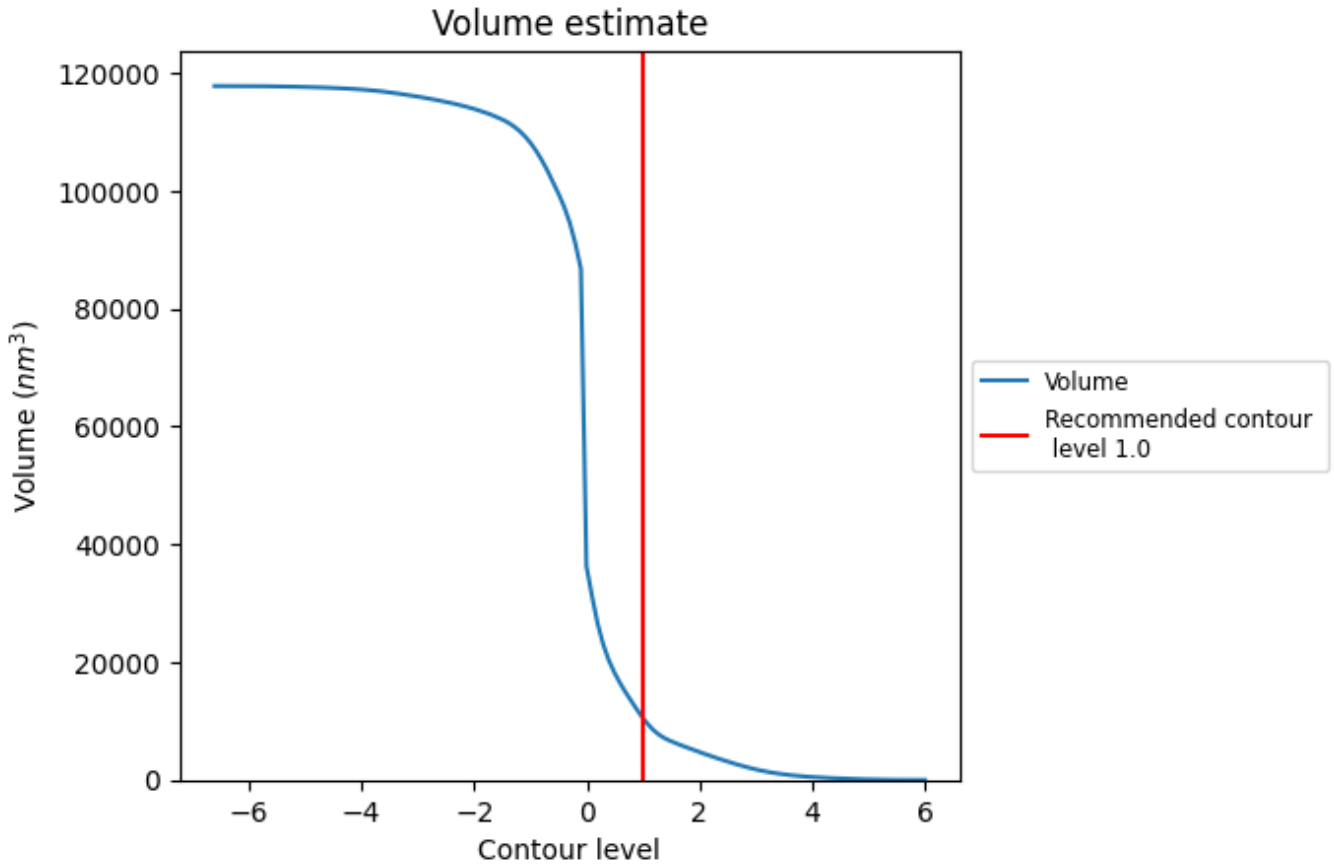
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

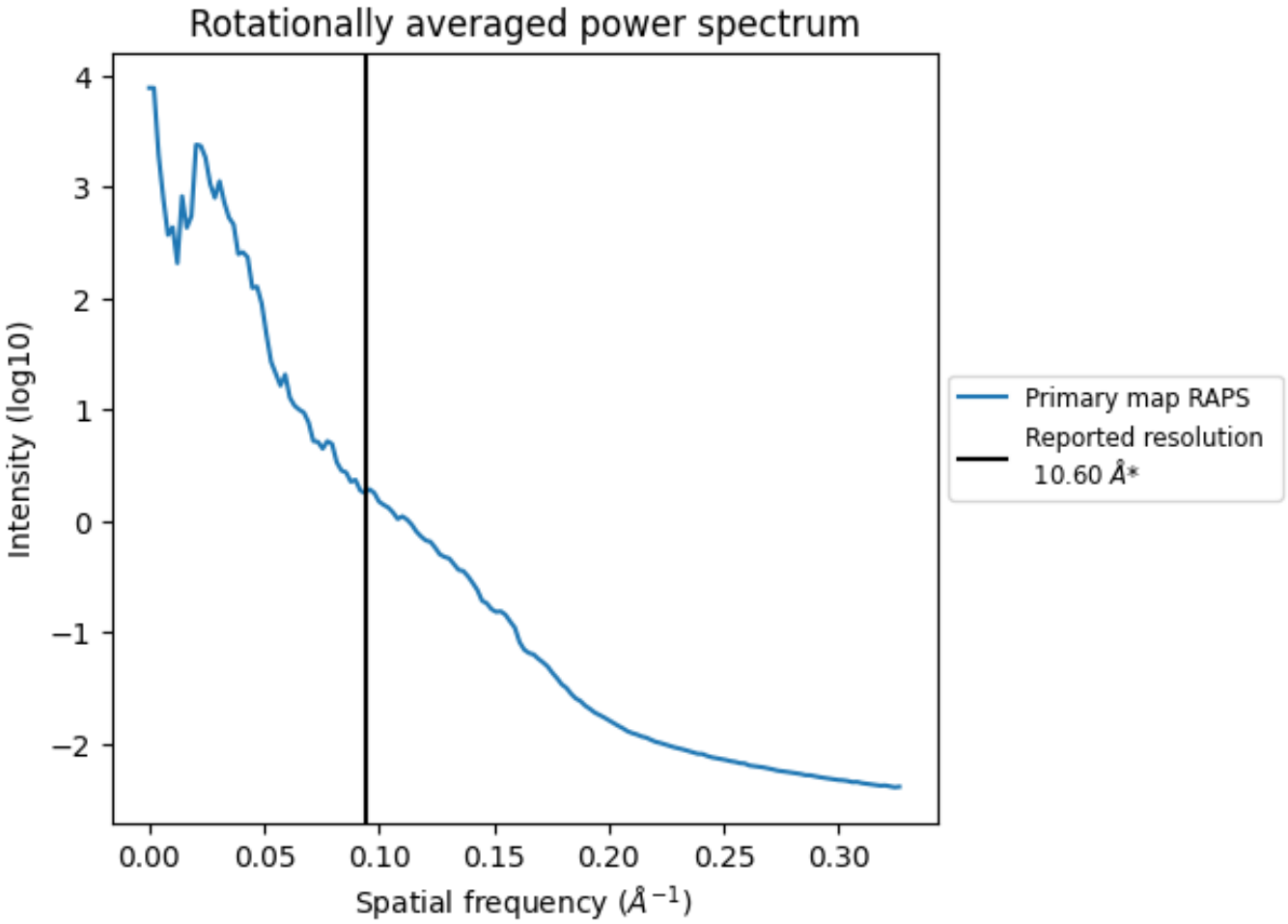
7.2 Volume estimate (i)



The volume at the recommended contour level is 10476 nm^3; this corresponds to an approximate mass of 9463 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)



*Reported resolution corresponds to spatial frequency of 0.094 Å^{-1}

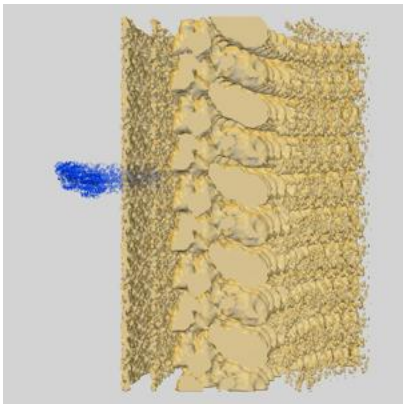
8 Fourier-Shell correlation (i)

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

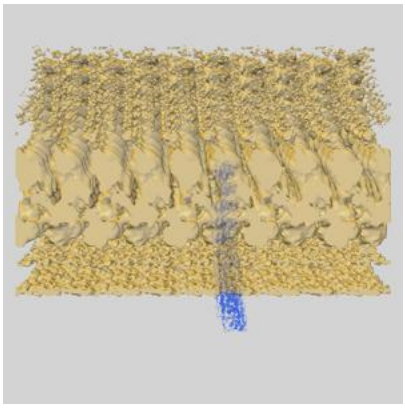
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-1663 and PDB model 2WYY. Per-residue inclusion information can be found in section 3 on page 5.

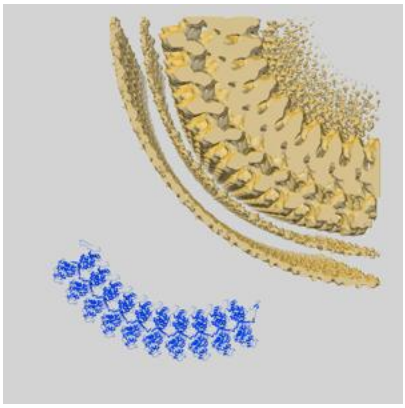
9.1 Map-model overlay



X



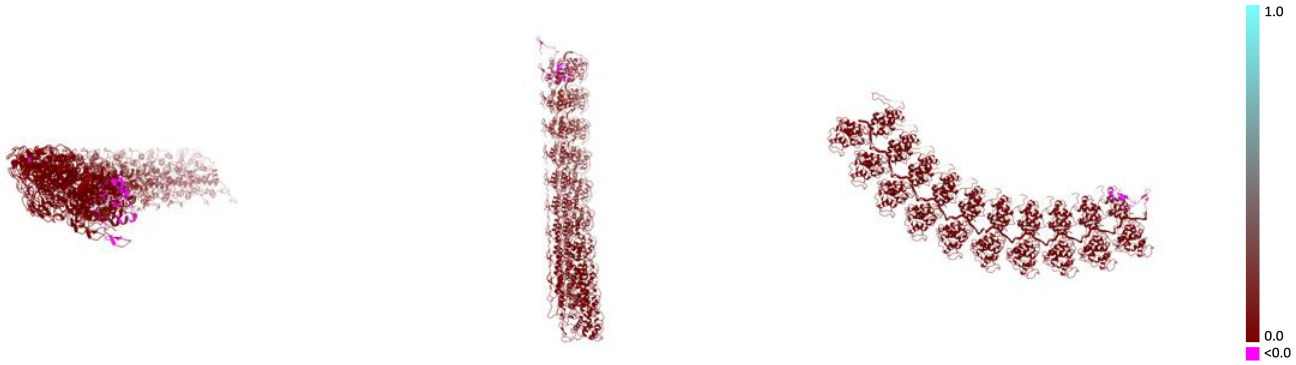
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.0 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.

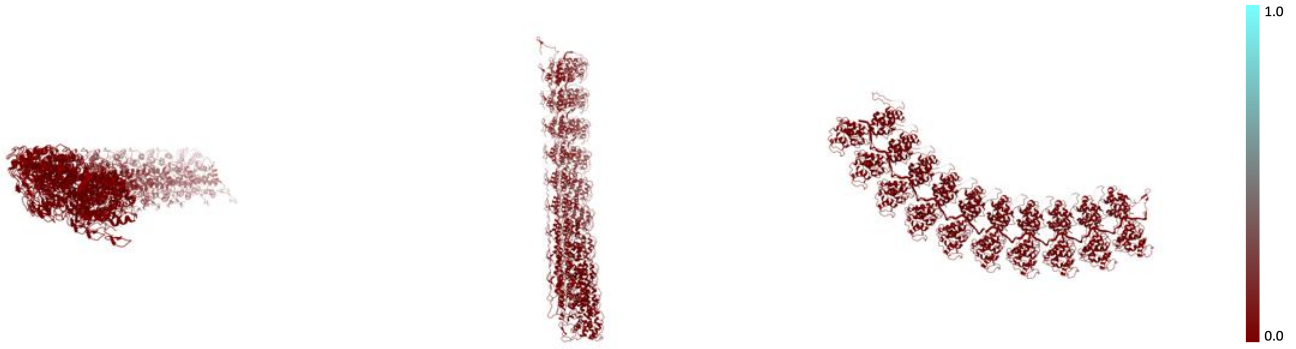
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according 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.

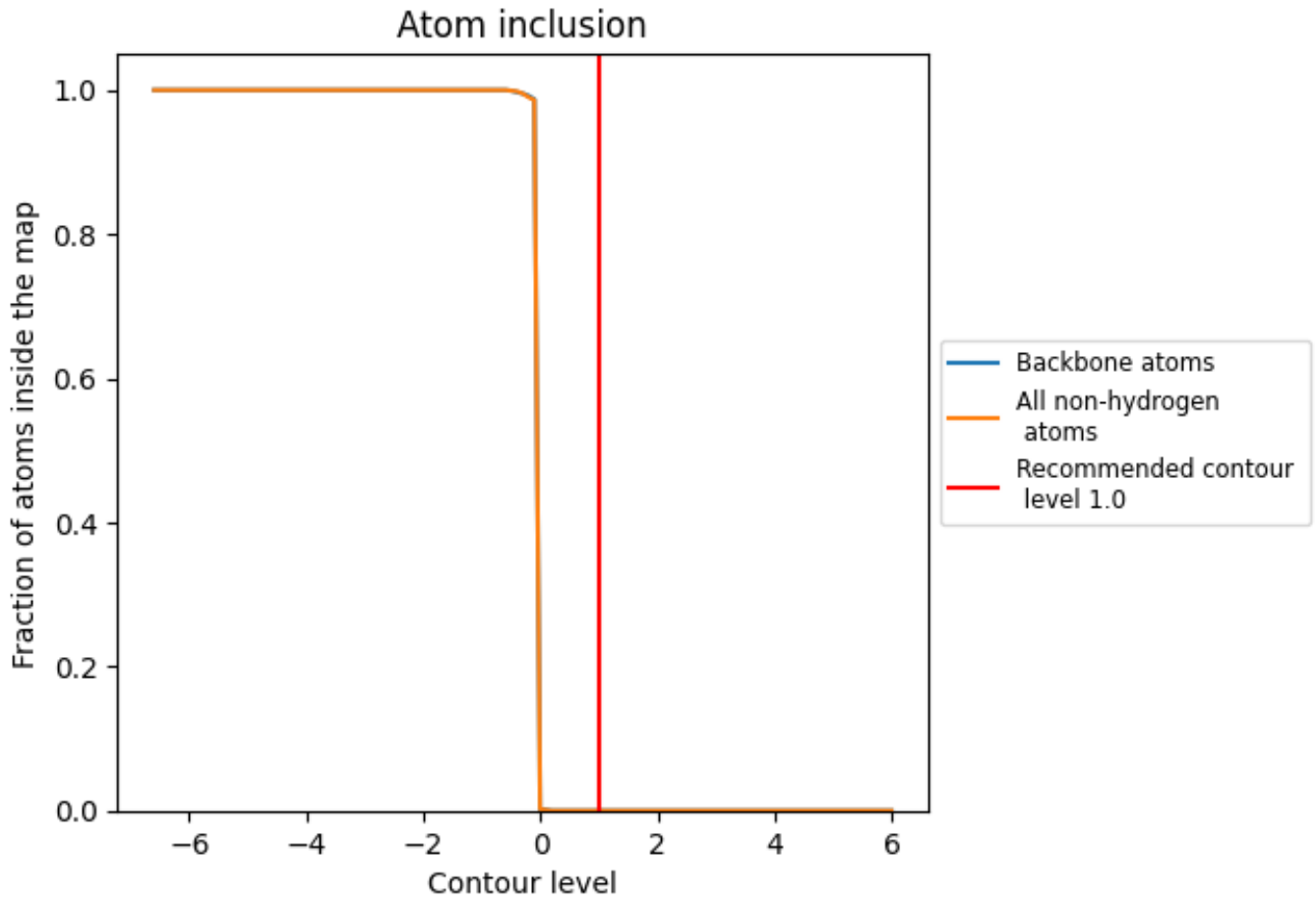
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (1.0).

9.4 Atom inclusion (i)



At the recommended contour level, 0% of all backbone atoms, 0% 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 (1.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.0000	0.0000
A	0.0000	0.0000
C	0.0000	0.0000
D	0.0000	0.0000
F	0.0000	0.0000
H	0.0000	0.0000
I	0.0000	0.0010
J	0.0000	0.0030
K	0.0000	0.0000
L	0.0000	-0.0000
M	0.0000	-0.0000
R	0.0000	0.0000
S	0.0000	0.0010