wwPDB EM Validation Summary Report

Nov 19, 2022 – 10:30 AM EST

PDB ID	:	7LIV
EMDB ID	:	EMD-23386
Title	:	Structure of human transfer RNA visualized in the cytomegalovirus, a DNA virus
Authors	:	Liu, Y.T.; Strugatsky, D.; Liu, W.; Zhou, Z.H.
Deposited on	:	2021-01-28
Resolution	:	3.60 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:

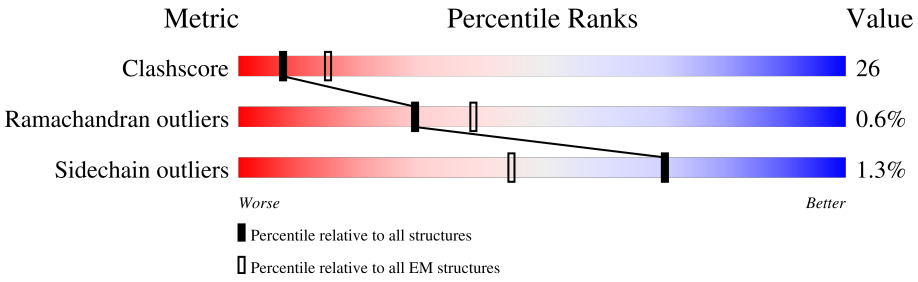
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 3.60 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

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	1370	65% 63% 33%
1	C	1370	64% 61% 37%
1	J	1370	67% 61% 36%
2	4	285	94% 67% 32%
2	5	285	86% 71% 29%
2	6	285	80% 68% 32%
3	D	75	63% 47% 37% 16%
3	E	75	65% 59% 25% 16%

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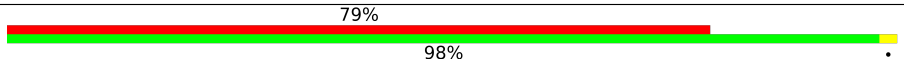
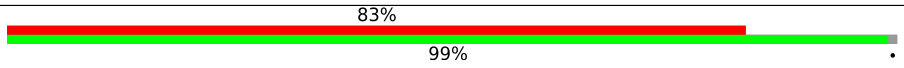
Mol	Chain	Length	Quality of chain
3	Z	75	
4	p	290	
5	q	306	
5	r	306	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 47058 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 Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	J	1348	Total	C	N	O	S	0	0
			10681	6802	1851	1967	61		
1	A	1328	Total	C	N	O	S	0	0
			10526	6706	1827	1934	59		
1	C	1348	Total	C	N	O	S	0	0
			10681	6802	1851	1967	61		

- Molecule 2 is a protein called Tegument protein pp150.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5	285	Total	C	N	O	S	0	0
			2328	1468	426	421	13		
2	6	285	Total	C	N	O	S	0	0
			2328	1468	426	421	13		
2	4	285	Total	C	N	O	S	0	0
			2328	1468	426	421	13		

- Molecule 3 is a protein called Small capsomere-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Z	63	Total	C	N	O	S	0	0
			513	321	97	91	4		
3	D	63	Total	C	N	O	S	0	0
			513	321	97	91	4		
3	E	63	Total	C	N	O	S	0	0
			513	321	97	91	4		

- Molecule 4 is a protein called Triplex capsid protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	p	290	Total	C	N	O	S	0	0
			2325	1485	411	417	12		

- Molecule 5 is a protein called Triplex capsid protein 2.

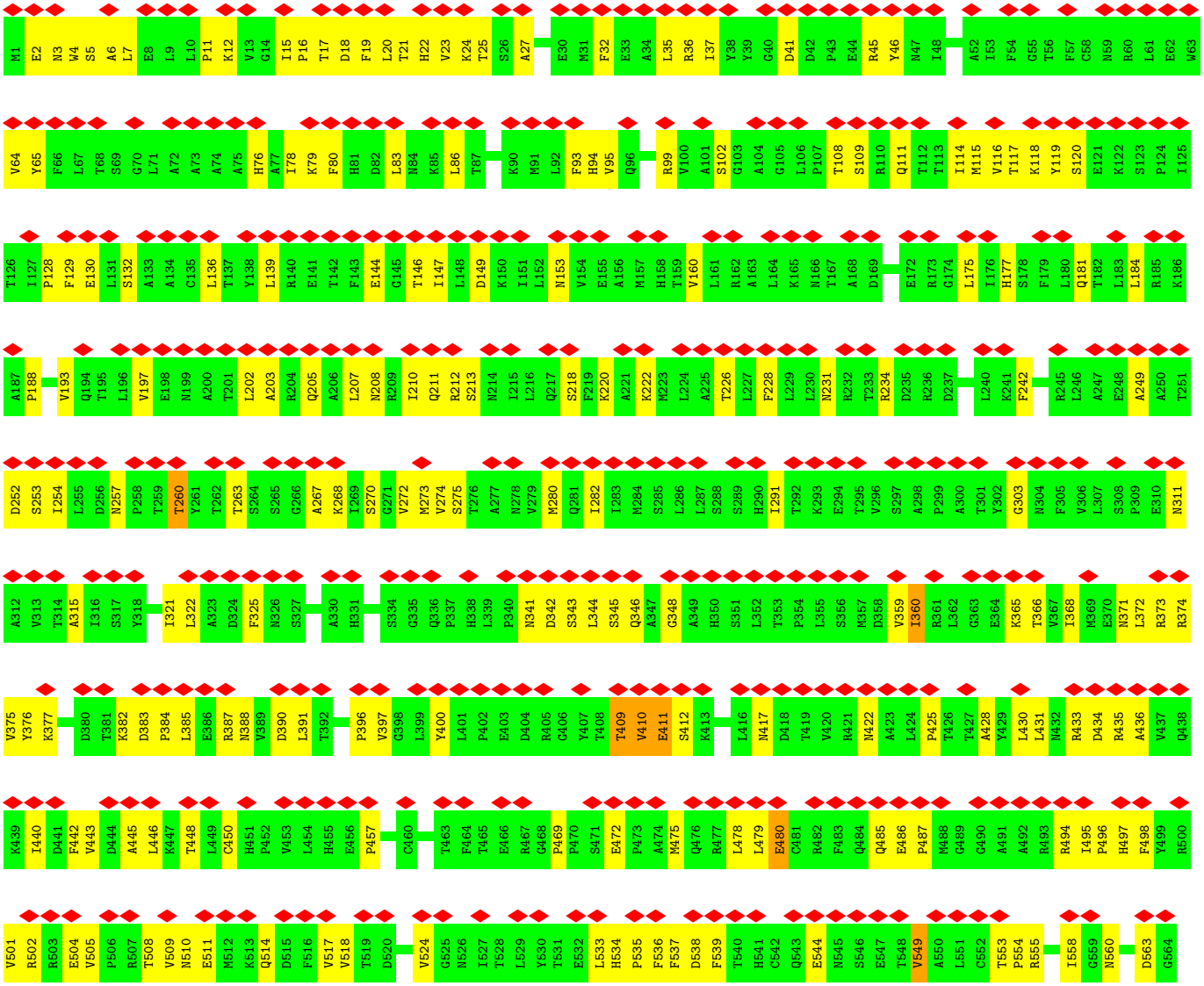
Mol	Chain	Residues	Atoms					AltConf	Trace
5	q	241	Total	C	N	O	S	0	0
			1911	1236	328	331	16		
5	r	304	Total	C	N	O	S	0	0
			2411	1544	420	429	18		

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.

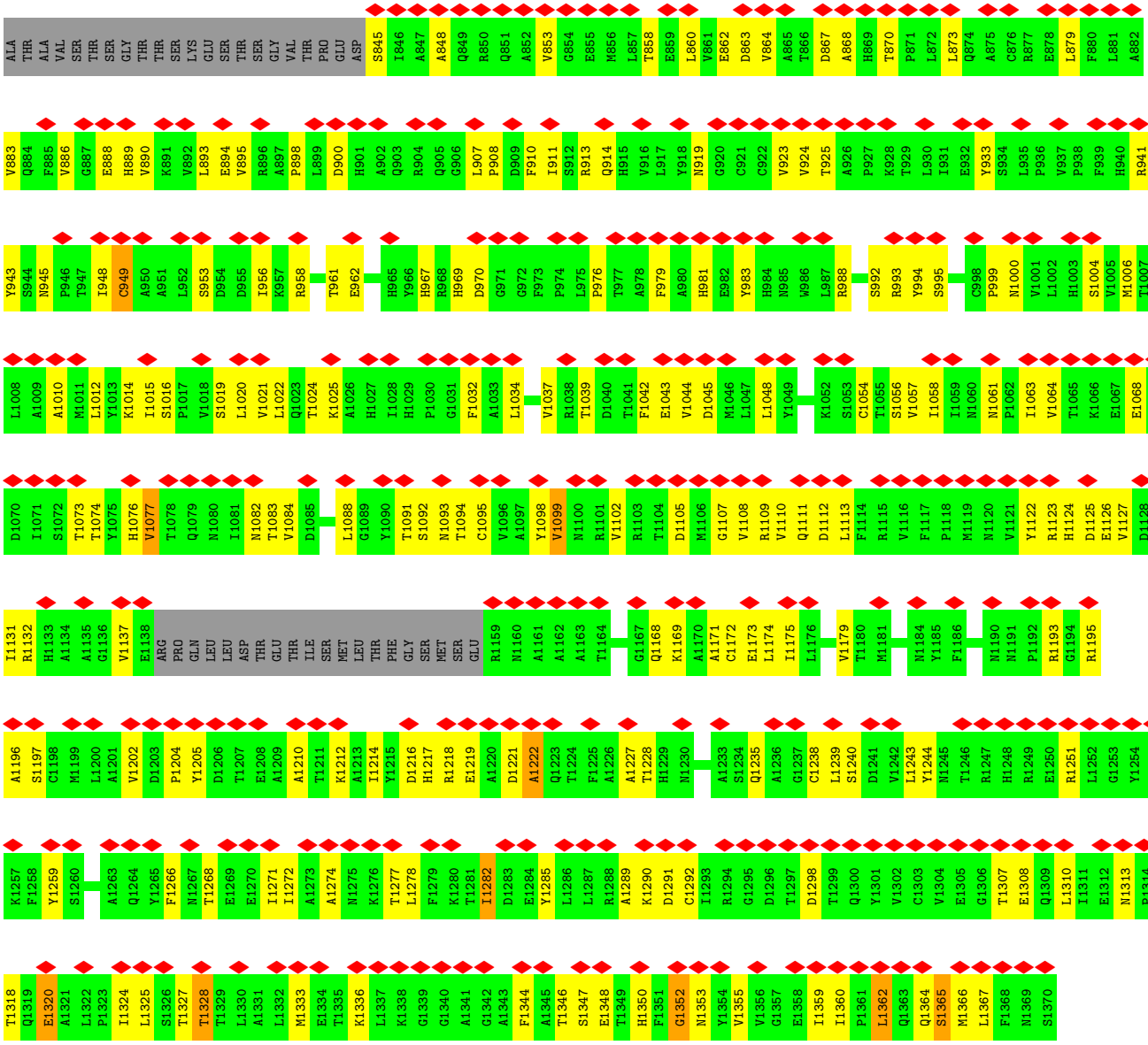
- Molecule 1: Major capsid protein

Chain J:



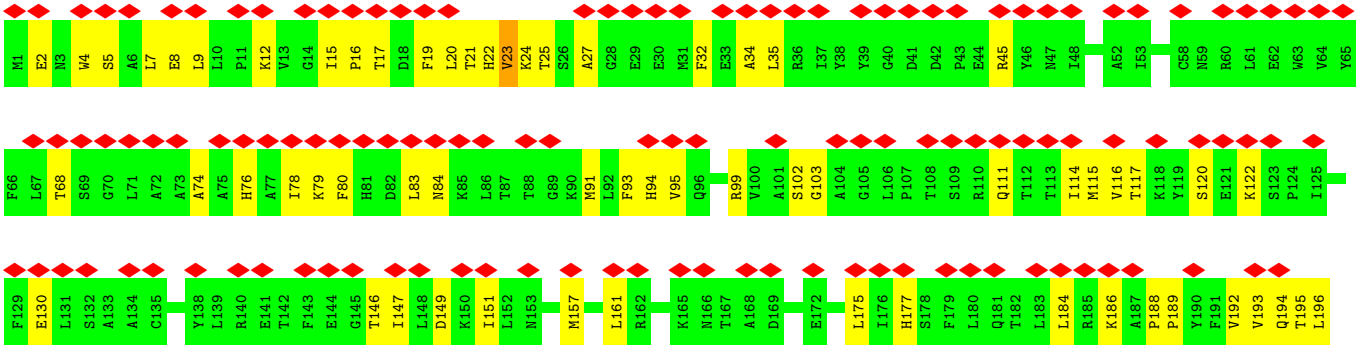
• Molecule 1: Major capsid protein

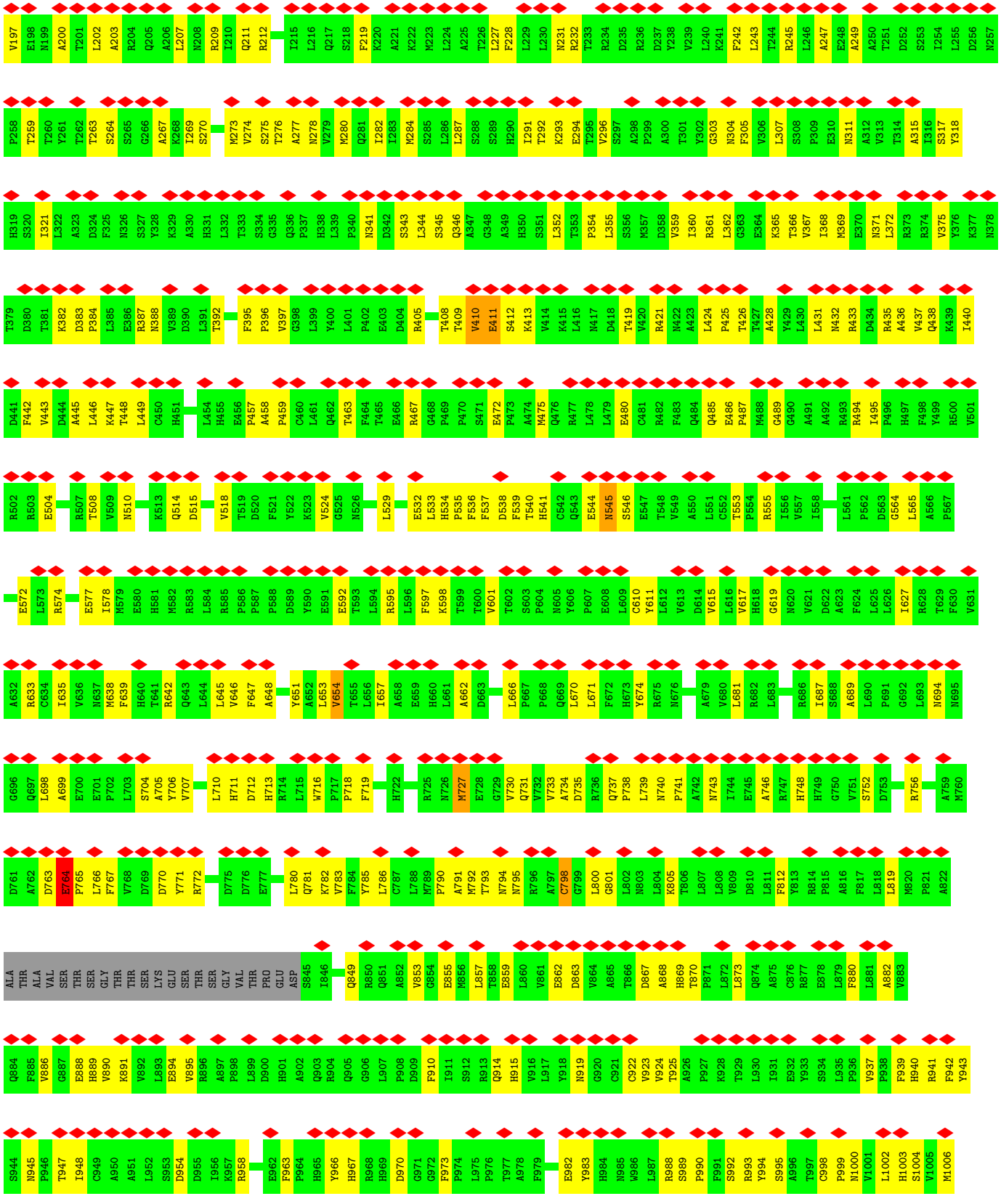
Chain A:

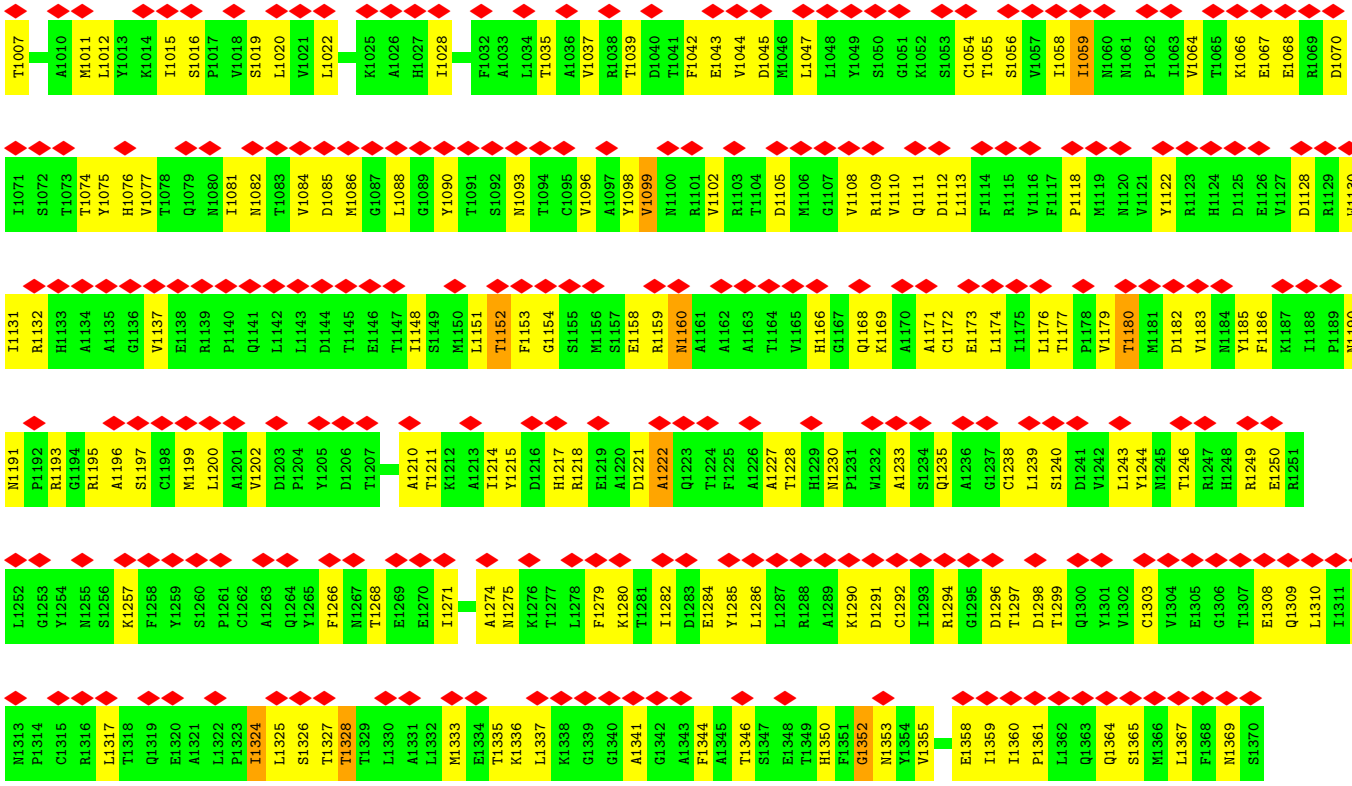


• Molecule 1: Major capsid protein

Chain C:

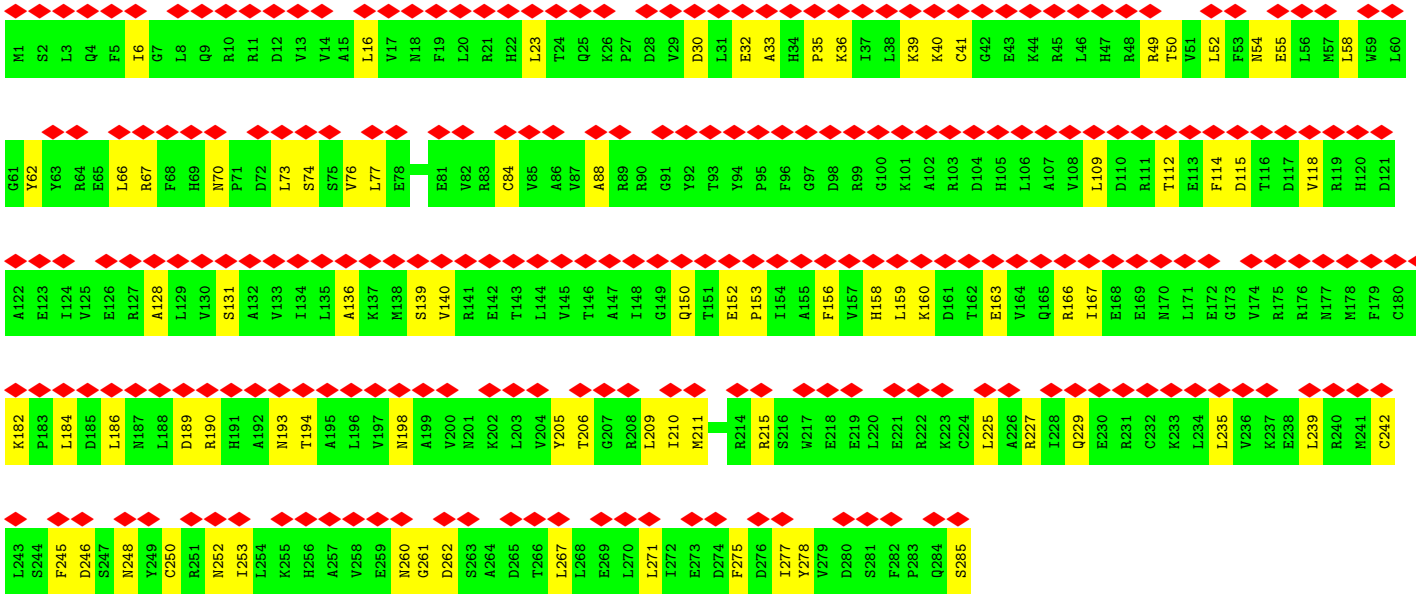



V197 E198 N199 A200 T201 L202 A203 R204 Q205 A206 L207 N208 R209 I210 Q211 R212 I215 L216 Q217 S218 F219 K220 A221 K222 M223 L224 A225 T226 L227 F228 L229 L230 N231 R232 T233 R234 D235 R236 D237 Y238 V239 L240 K241 F242 L243 T244 R245 L246 A247 E248 A249 A250 T251 D252 S253 I254 L255 D256 N257
P258 T259 T260 Y261 T262 T263 S264 S265 G266 A267 K268 I269 S270 M273 V274 S275 T276 A277 N278 V279 M280 Q281 I282 I283 M284 S285 L286 L287 S288 S289 H290 I291 T292 K293 E294 T295 V296 S297 A298 P299 A300 T301 Y302 G303 N304 F305 V306 L307 S308 P309 E310 N311 A312 V313 T314 A315 I316 S317 Y318
H319 S320 I321 L322 A323 D324 F325 N326 S327 Y328 K329 A330 H331 L332 T333 S334 G335 Q336 P337 H338 L339 P340 N341 D342 S343 L344 S345 Q346 A347 G348 A349 H350 S351 L352 T353 P354 L355 S356 M357 D358 V359 I360 R361 L362 G363 E364 K365 T366 V367 I368 M369 E370 N371 L372 R373 R374 V375 Y376 K377 N378
T379 D380 T381 K382 D383 P384 L385 E386 R387 N388 V389 D390 L391 T392 F395 P396 V397 G398 L399 Y400 L401 P402 E403 D404 R405 T408 T409 V410 E411 S412 K413 V414 K415 L416 N417 D418 T419 V420 R421 N422 A423 L424 P425 T426 T427 A428 Y429 L430 L431 N432 R433 D434 R435 A436 V437 Q438 K439 I440
D441 F442 V443 D444 A445 L446 K447 T448 L449 C450 H451 L454 H455 E456 P457 A458 P459 C460 L461 Q462 T463 F464 T465 E466 R467 G468 P469 P470 S471 E472 P473 A474 M475 Q476 R477 L478 L479 E480 C481 R482 F483 Q484 Q485 E486 P487 M488 G489 G490 A491 A492 R493 R494 I495 P496 H497 F498 Y499 R500 V501
R502 R503 E504 R507 T508 V509 N510 K513 Q514 D515 V518 T519 D520 F521 Y522 K523 V524 G525 N526 L529 E532 L533 H534 P535 F536 F537 D538 F539 T540 H541 C542 Q543 E544 N545 S546 E547 T548 V549 A550 L551 C552 T553 P554 R555 I556 V557 I558 L561 P562 D563 G564 L565 A566 P567
E572 L573 R574 E577 I578 M579 E580 H581 M582 R583 L584 R585 P586 P587 P588 D589 Y590 S591 E592 T593 L594 R595 L596 F597 K598 T599 T600 V601 T602 S603 P604 N605 Y606 P607 E608 L609 C610 Y611 L612 V613 D614 V615 L616 V617 H618 G619 N620 V621 D622 A623 F624 L625 L626 I627 R628 T629 F630 V631
A632 R633 C634 I635 V636 N637 M638 F639 H640 T641 R642 Q643 L644 L645 V646 F647 A648 Y651 A652 L653 V654 T655 L656 I657 A658 E659 H660 L661 A662 D663 L666 P667 P668 Q669 L670 L671 F672 H673 Y674 R675 N676 A679 V680 L681 R682 L683 R686 I687 S688 A689 L690 P691 G692 L693 N694 N695
G696 Q697 L698 A699 E700 E701 P702 L703 S704 A705 Y706 V707 L710 H711 D712 H713 R714 L715 W716 P717 P718 F719 H722 R725 N726 M727 E728 G729 V730 Q731 V732 V733 A734 D735 R736 Q737 P738 L739 N740 P741 A742 N743 I744 E745 A746 R747 H748 H749 G750 V751 S752 D753 R756 A759 M760
D761 A762 D763 E764 P765 L766 F767 V768 D769 D770 Y771 R772 D775 D776 E777 L780 Q781 K782 V783 F784 Y785 L786 C787 L788 M789 P790 A791 M792 T793 N794 N795 R796 A797 C798 G799 L800 G801 L802 N803 L804 K805 T806 L807 L808 V809 D810 L811 F812 Y813 R814 P815 A816 F817 L818 L819 M820 P821 A822
ALA THR ALA VAL SER THR SER GLY THR THR SER LYS GLU SER THR SER GLY VAL THR PRO GLU ASP S845 I846 Q849 R850 Q851 A852 V853 G854 E855 M856 L857 T858 E859 L860 V861 E862 D863 V864 A865 T866 D867 A868 H869 T870 P871 L872 L873 Q874 A875 C876 R877 E878 L879 F880 L881 A882 V883
Q884 P885 V886 G887 E888 H889 V890 K891 V892 L893 E894 V895 R896 A897 P898 L899 D900 H901 A902 Q903 R904 Q905 G906 L907 P908 D909 F910 I911 S912 R913 Q914 H915 V916 L917 Y918 N919 G920 C921 C922 V923 V924 T925 A926 P927 K928 T929 L930 I931 E932 Y933 S934 L935 P936 V937 P938 F939 H940 R941 F942 Y943
S944 N945 P946 T947 I948 C949 A950 A951 L952 S953 D954 D955 I956 K957 R958 E962 F963 P964 H965 Y966 H967 R968 H969 D970 G971 G972 F973 P974 L975 P976 T977 A978 F979 E982 Y983 H984 N985 W986 L987 R988 S989 P990 F991 S992 R993 Y994 S995 A996 T997 C998 P999 N1000 V1001 L1002 H1003 S1004 V1005 M1006



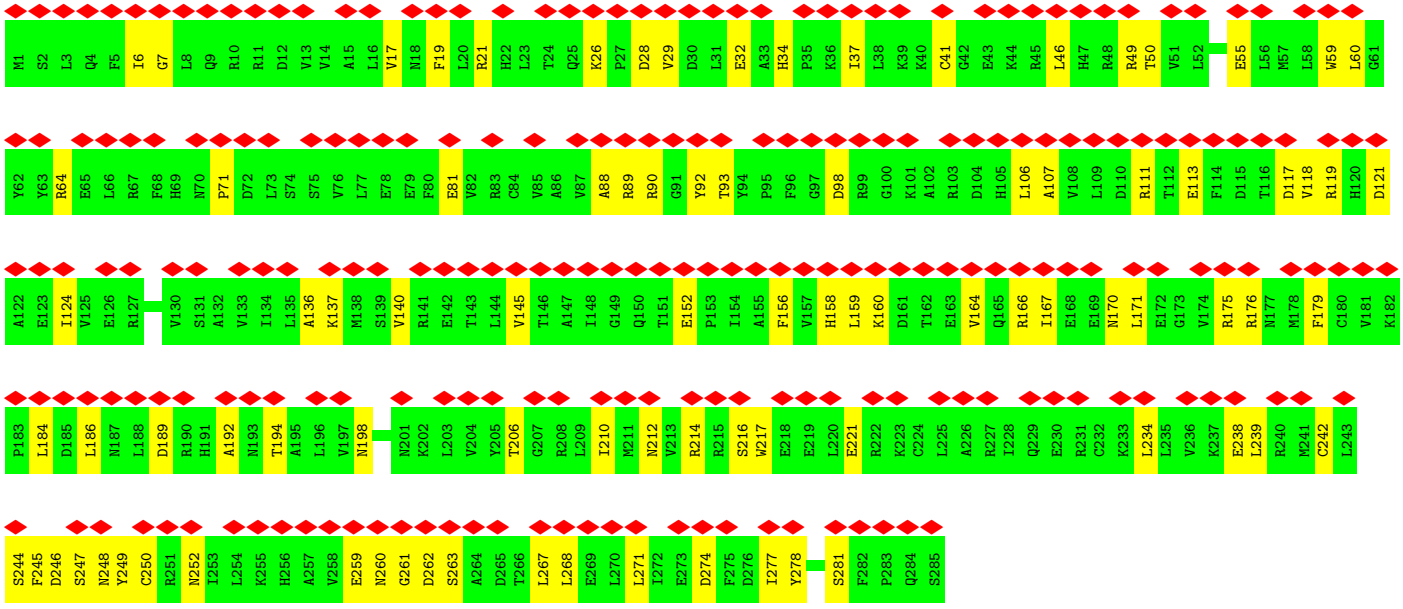
• Molecule 2: Tegument protein pp150

Chain 5:



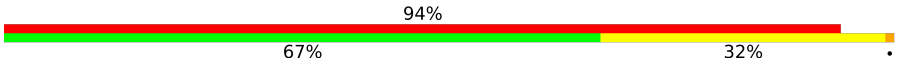
• Molecule 2: Tegument protein pp150

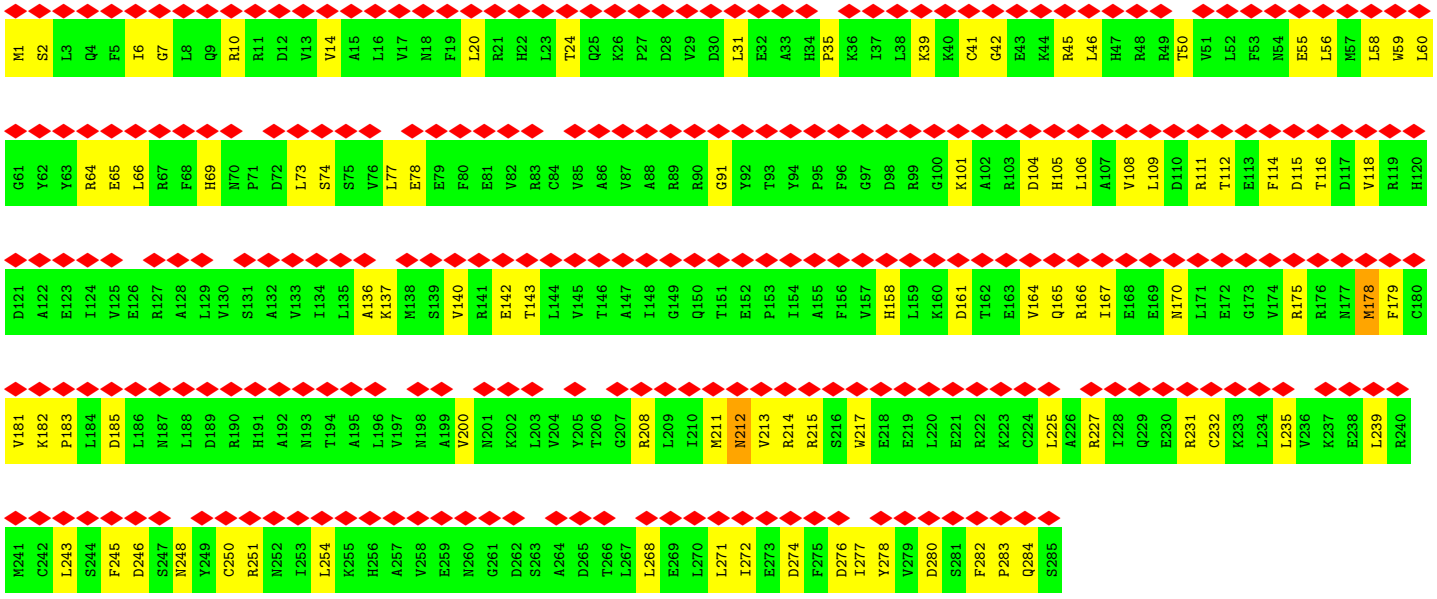
Chain 6:



• Molecule 2: Tegument protein pp150

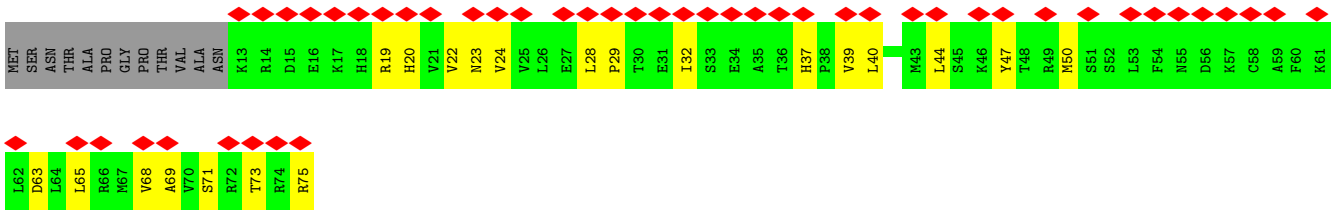
Chain 4:





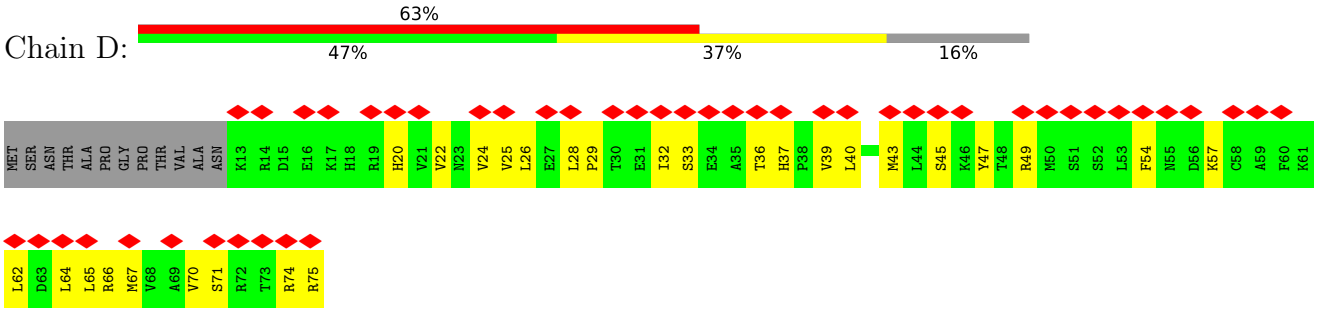
• Molecule 3: Small capsomere-interacting protein

Chain Z:



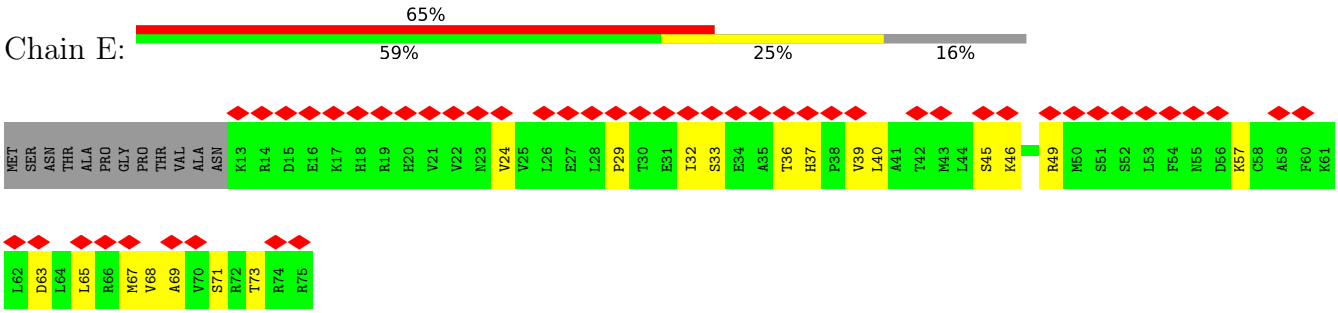
• Molecule 3: Small capsomere-interacting protein

Chain D:



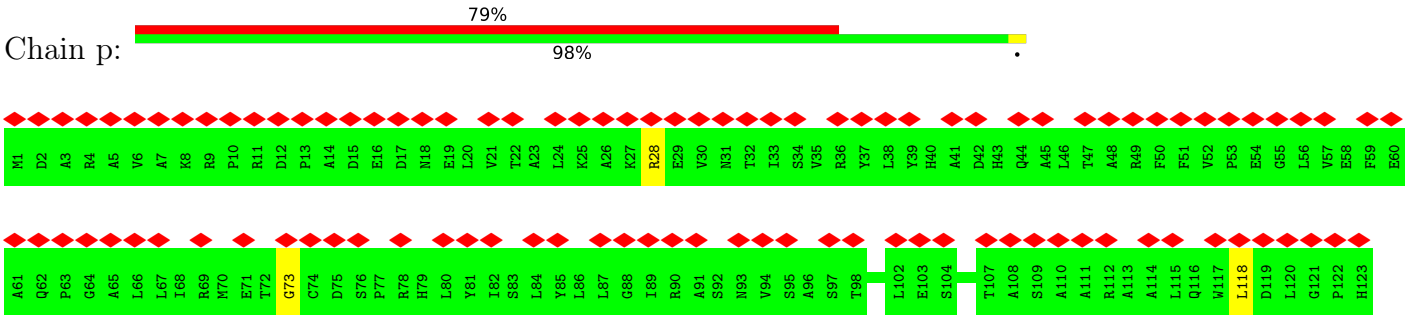
• Molecule 3: Small capsomere-interacting protein

Chain E:



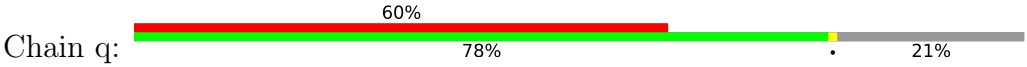
• Molecule 4: Triplex capsid protein 1

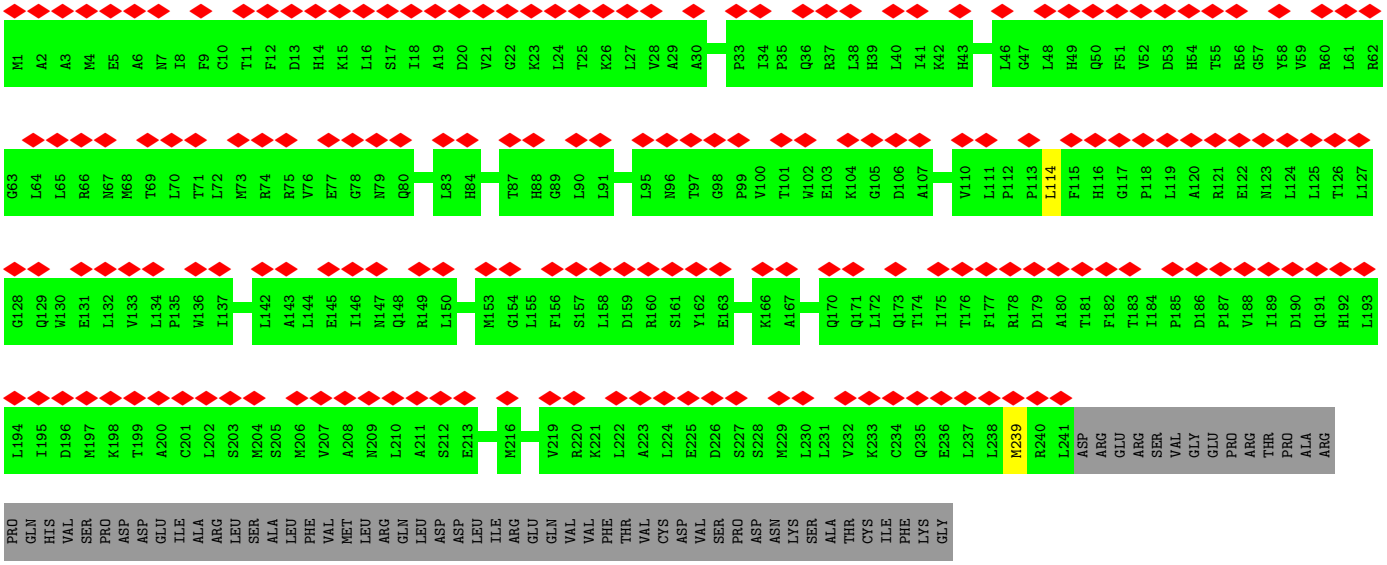
Chain p:



• Molecule 5: Triplex capsid protein 2

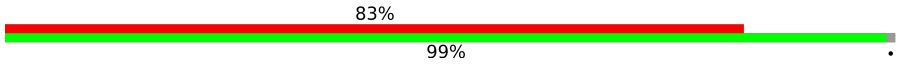
Chain q:

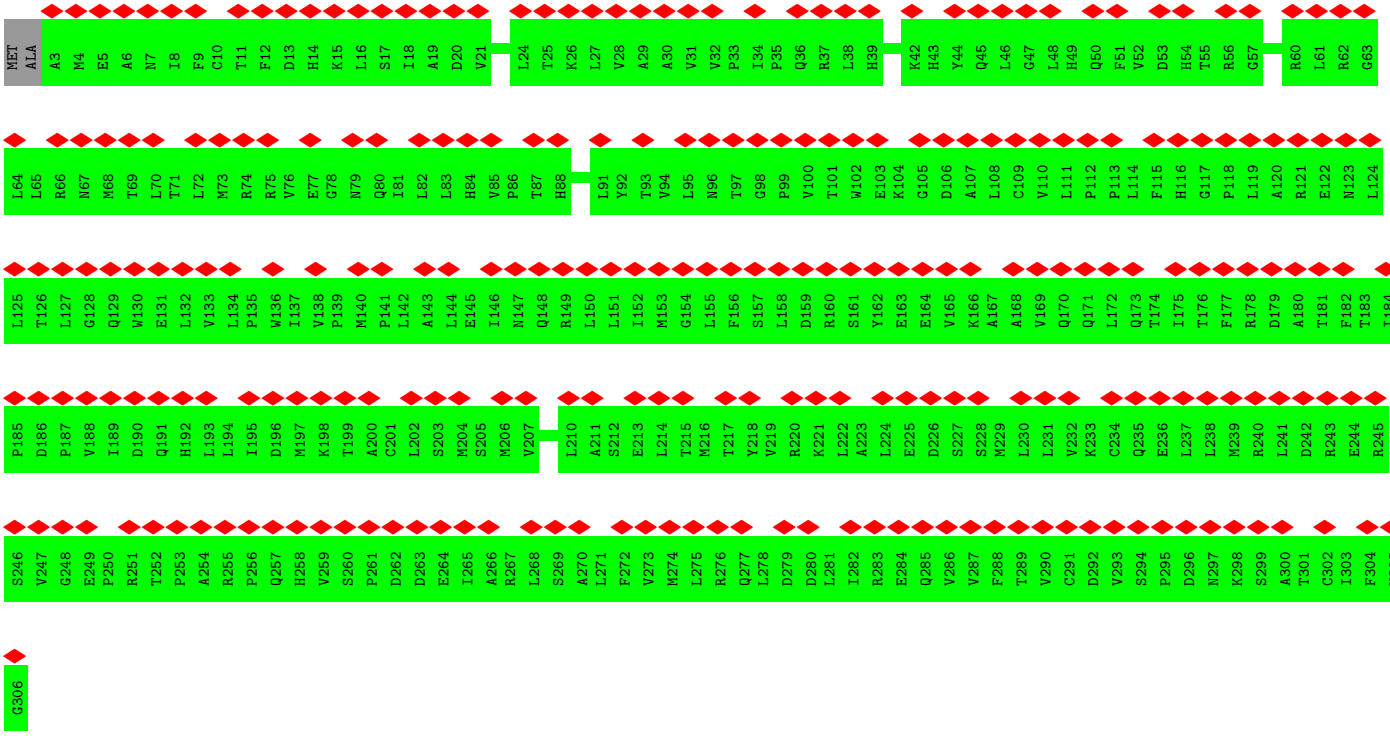




• Molecule 5: Triplex capsid protein 2

Chain r:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	97166	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	18.9	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.083	Depositor
Minimum map value	-0.047	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	412.16, 412.16, 412.16	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.61, 1.61, 1.61	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	0.48	0/10779	0.56	0/14684
1	C	0.49	0/10937	0.56	0/14899
1	J	0.48	0/10937	0.56	0/14899
2	4	0.38	0/2366	0.51	0/3192
2	5	0.36	0/2366	0.49	0/3192
2	6	0.40	0/2366	0.51	0/3192
3	D	0.42	0/520	0.50	0/697
3	E	0.41	0/520	0.57	0/697
3	Z	0.41	0/520	0.53	0/697
4	p	0.42	0/2374	0.57	0/3221
5	q	0.39	0/1949	0.55	0/2649
5	r	0.40	0/2458	0.59	0/3339
All	All	0.46	0/48092	0.55	0/65358

There are no bond length outliers.

There are no bond angle outliers.

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	10526	0	10468	605	0
1	C	10681	0	10620	681	0
1	J	10681	0	10618	630	0
2	4	2328	0	2363	81	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	5	2328	0	2363	70	0
2	6	2328	0	2363	81	0
3	D	513	0	539	56	0
3	E	513	0	539	26	0
3	Z	513	0	539	33	0
4	p	2325	0	2362	0	0
5	q	1911	0	2007	0	0
5	r	2411	0	2500	0	0
All	All	47058	0	47281	2125	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 26.

The worst 5 of 2125 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:203:ALA:CB	1:C:207:LEU:HD21	1.30	1.60
1:A:207:LEU:CD1	1:A:212:ARG:HG3	1.38	1.53
1:C:19:PHE:CE1	1:C:23:VAL:N	1.78	1.51
1:J:440:ILE:CD1	1:J:1108:VAL:HG11	1.38	1.50
1:A:207:LEU:HD11	1:A:212:ARG:CG	1.39	1.49

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	1322/1370 (96%)	1242 (94%)	73 (6%)	7 (0%)	29	68
1	C	1344/1370 (98%)	1255 (93%)	78 (6%)	11 (1%)	19	59
1	J	1344/1370 (98%)	1262 (94%)	71 (5%)	11 (1%)	19	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	4	283/285 (99%)	273 (96%)	10 (4%)	0	100	100
2	5	283/285 (99%)	271 (96%)	11 (4%)	1 (0%)	34	71
2	6	283/285 (99%)	274 (97%)	8 (3%)	1 (0%)	34	71
3	D	61/75 (81%)	60 (98%)	1 (2%)	0	100	100
3	E	61/75 (81%)	60 (98%)	1 (2%)	0	100	100
3	Z	61/75 (81%)	59 (97%)	2 (3%)	0	100	100
4	p	288/290 (99%)	273 (95%)	13 (4%)	2 (1%)	22	61
5	q	239/306 (78%)	231 (97%)	7 (3%)	1 (0%)	34	71
5	r	302/306 (99%)	288 (95%)	14 (5%)	0	100	100
All	All	5871/6092 (96%)	5548 (94%)	289 (5%)	34 (1%)	29	64

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	409	THR
1	J	410	VAL
1	J	764	GLU
1	J	1070	ASP
1	J	1238	CYS

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	1155/1192 (97%)	1137 (98%)	18 (2%)	62	83
1	C	1174/1192 (98%)	1156 (98%)	18 (2%)	65	84
1	J	1174/1192 (98%)	1149 (98%)	25 (2%)	53	78
2	4	256/257 (100%)	254 (99%)	2 (1%)	81	91
2	5	256/257 (100%)	255 (100%)	1 (0%)	91	97
2	6	256/257 (100%)	256 (100%)	0	100	100
3	D	59/68 (87%)	59 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	E	59/68 (87%)	59 (100%)	0	100 100
3	Z	59/68 (87%)	59 (100%)	0	100 100
4	p	252/252 (100%)	249 (99%)	3 (1%)	71 87
5	q	214/273 (78%)	213 (100%)	1 (0%)	88 95
5	r	272/273 (100%)	272 (100%)	0	100 100
All	All	5186/5349 (97%)	5118 (99%)	68 (1%)	70 86

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1292	CYS
1	C	1324	ILE
4	p	118	LEU
1	J	1365	SER
1	J	1353	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 93 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	901	HIS
2	5	34	HIS
1	C	914	GLN
1	C	1160	ASN
2	6	170	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 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.

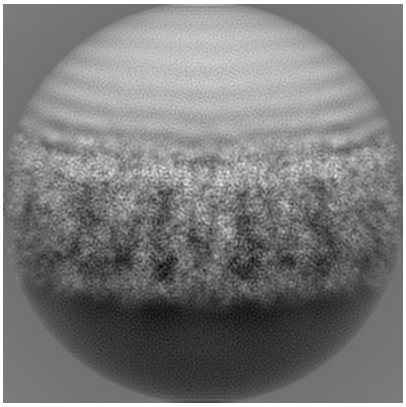
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-23386. These allow visual inspection of the internal detail of the map and identification of artifacts.

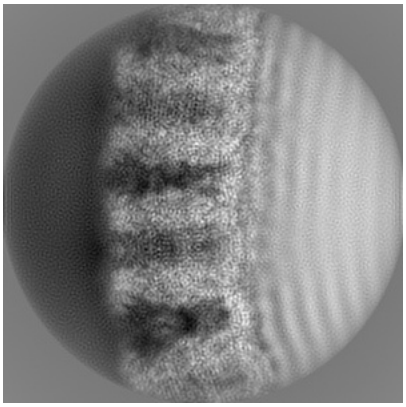
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

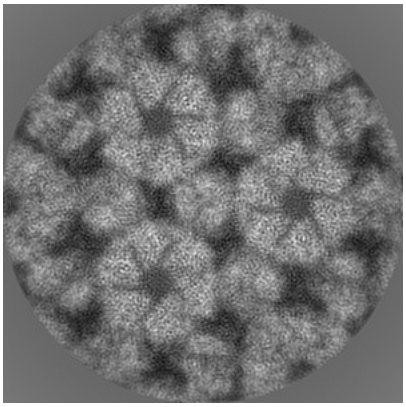
6.1.1 Primary map



X



Y

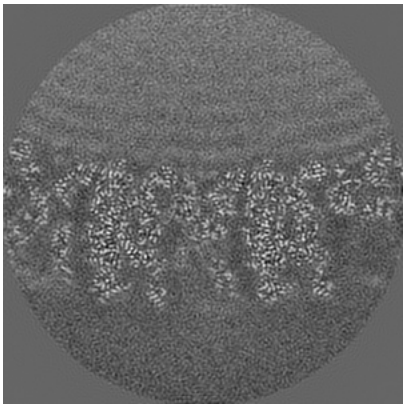


Z

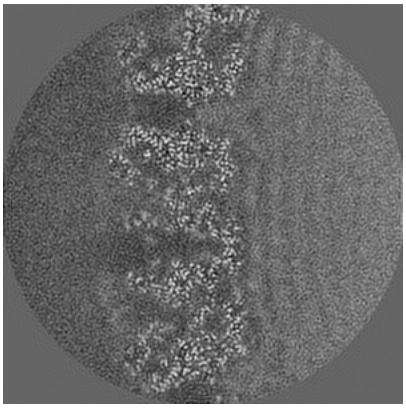
The images above show the map projected in three orthogonal directions.

6.2 Central slices

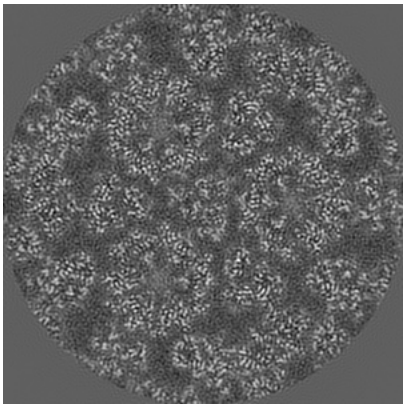
6.2.1 Primary map



X Index: 128



Y Index: 128

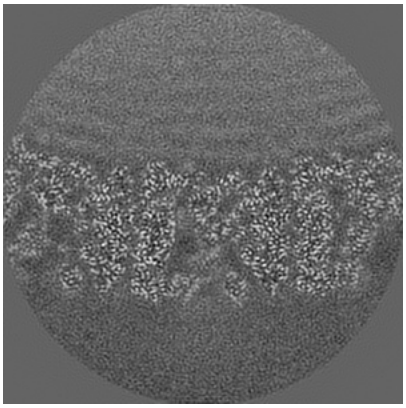


Z Index: 128

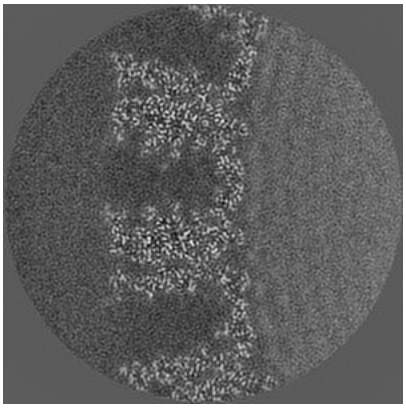
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

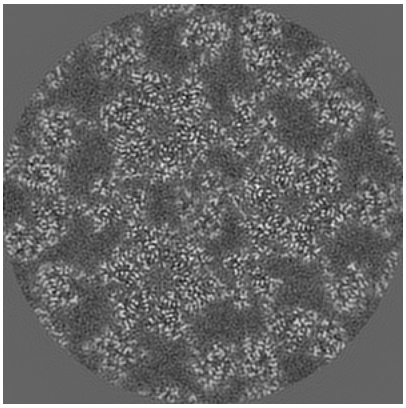
6.3.1 Primary map



X Index: 119



Y Index: 153

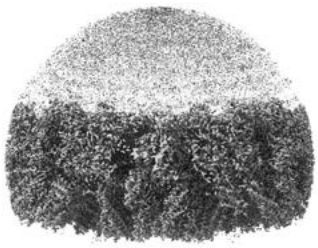


Z Index: 121

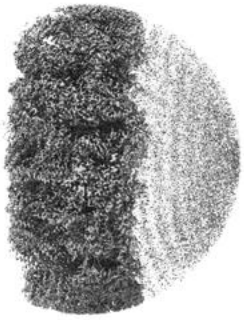
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

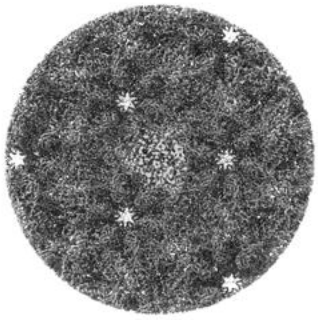
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

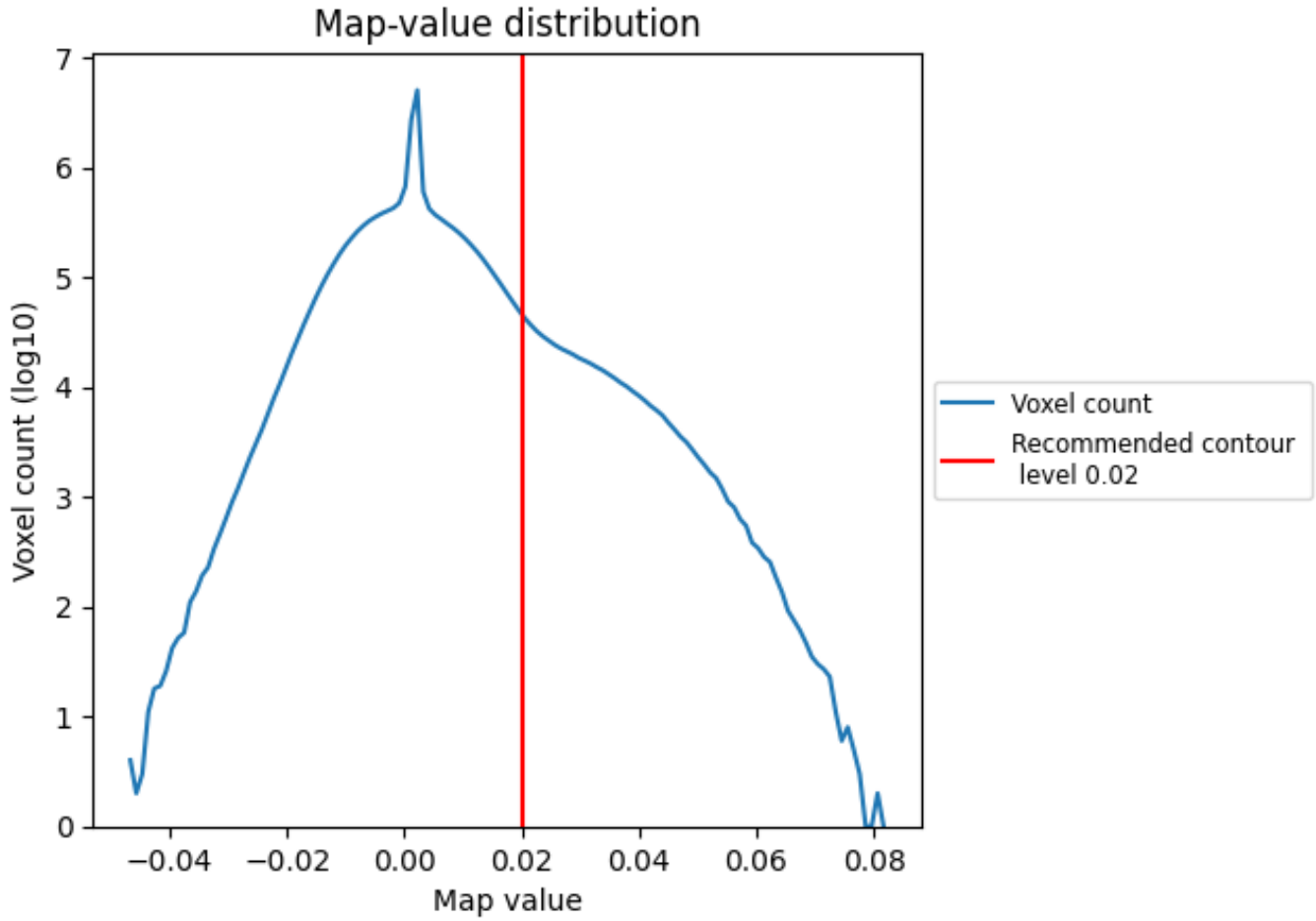
6.5 Mask visualisation (i)

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

7 Map analysis

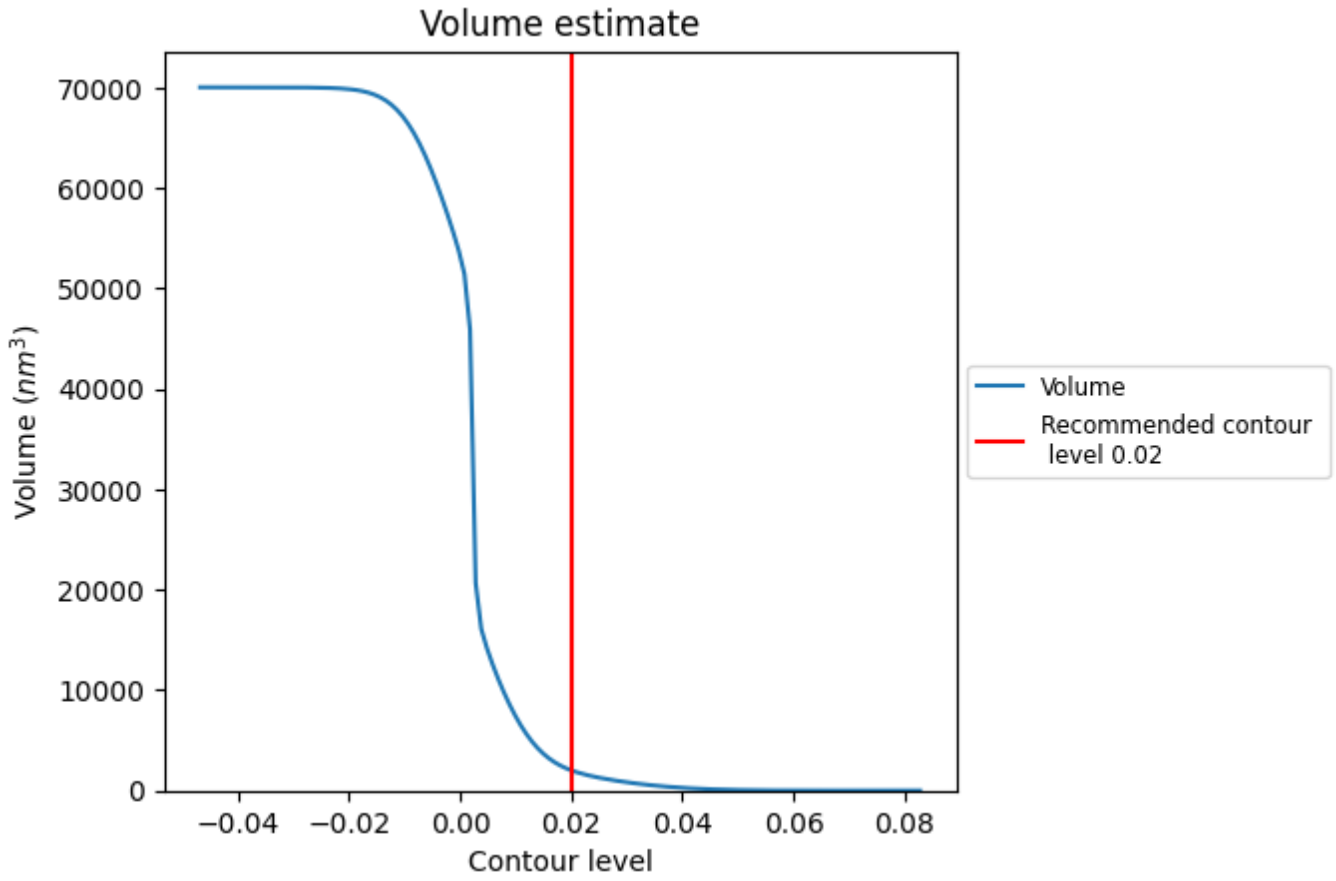
This section contains the results of statistical analysis of the map.

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.

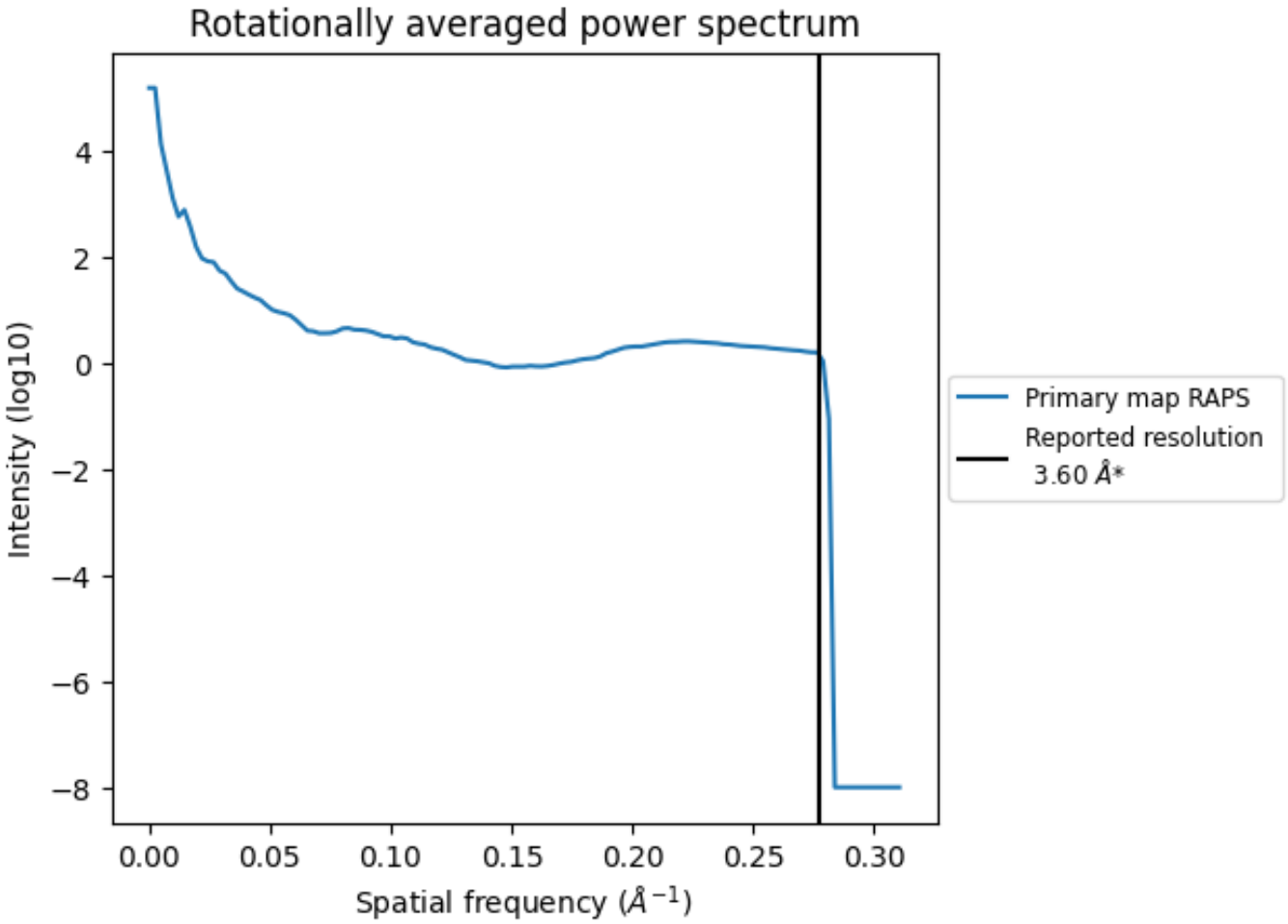
7.2 Volume estimate (i)



The volume at the recommended contour level is 2015 nm^3; this corresponds to an approximate mass of 1820 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 0.278 Å^{-1}

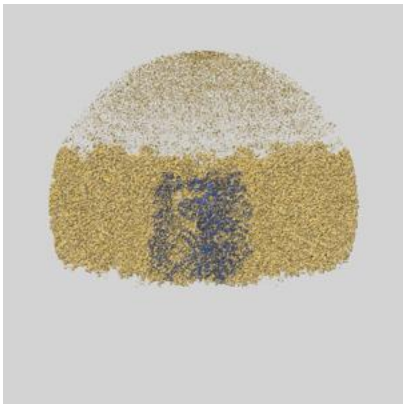
8 Fourier-Shell correlation

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

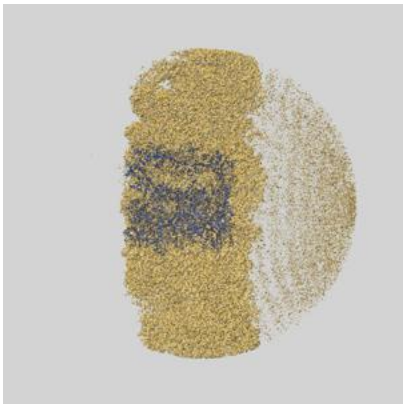
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-23386 and PDB model 7LIV. Per-residue inclusion information can be found in section 3 on page 6.

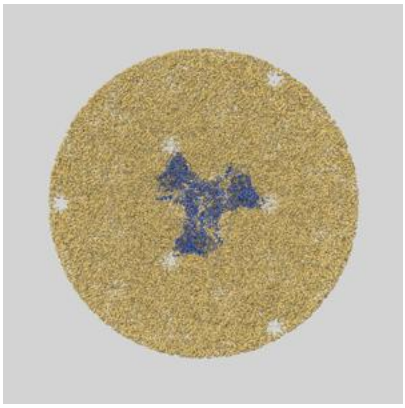
9.1 Map-model overlay



X



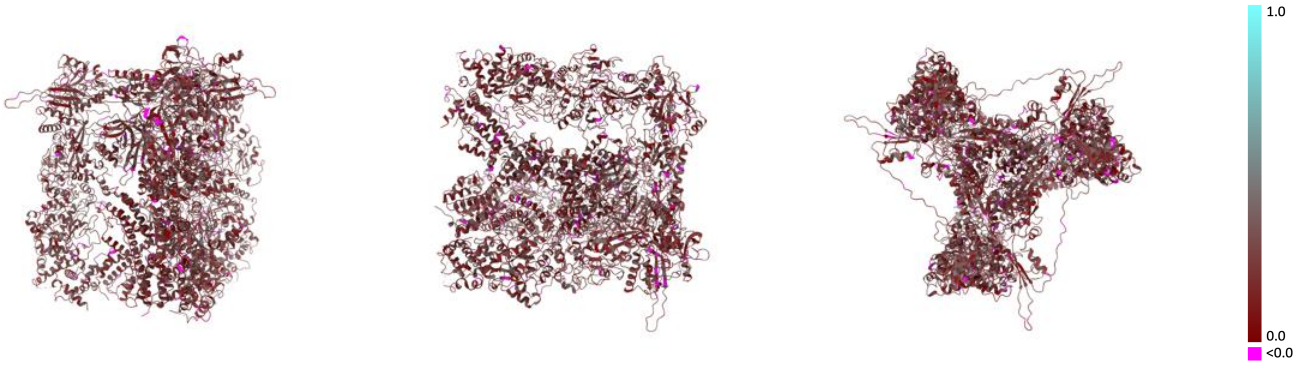
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02 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.

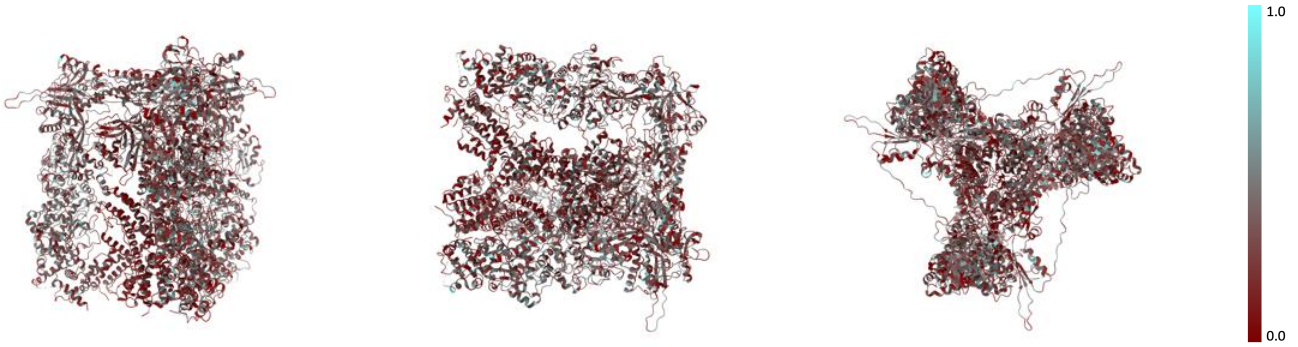
9.2 Q-score mapped to coordinate model (i)



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.

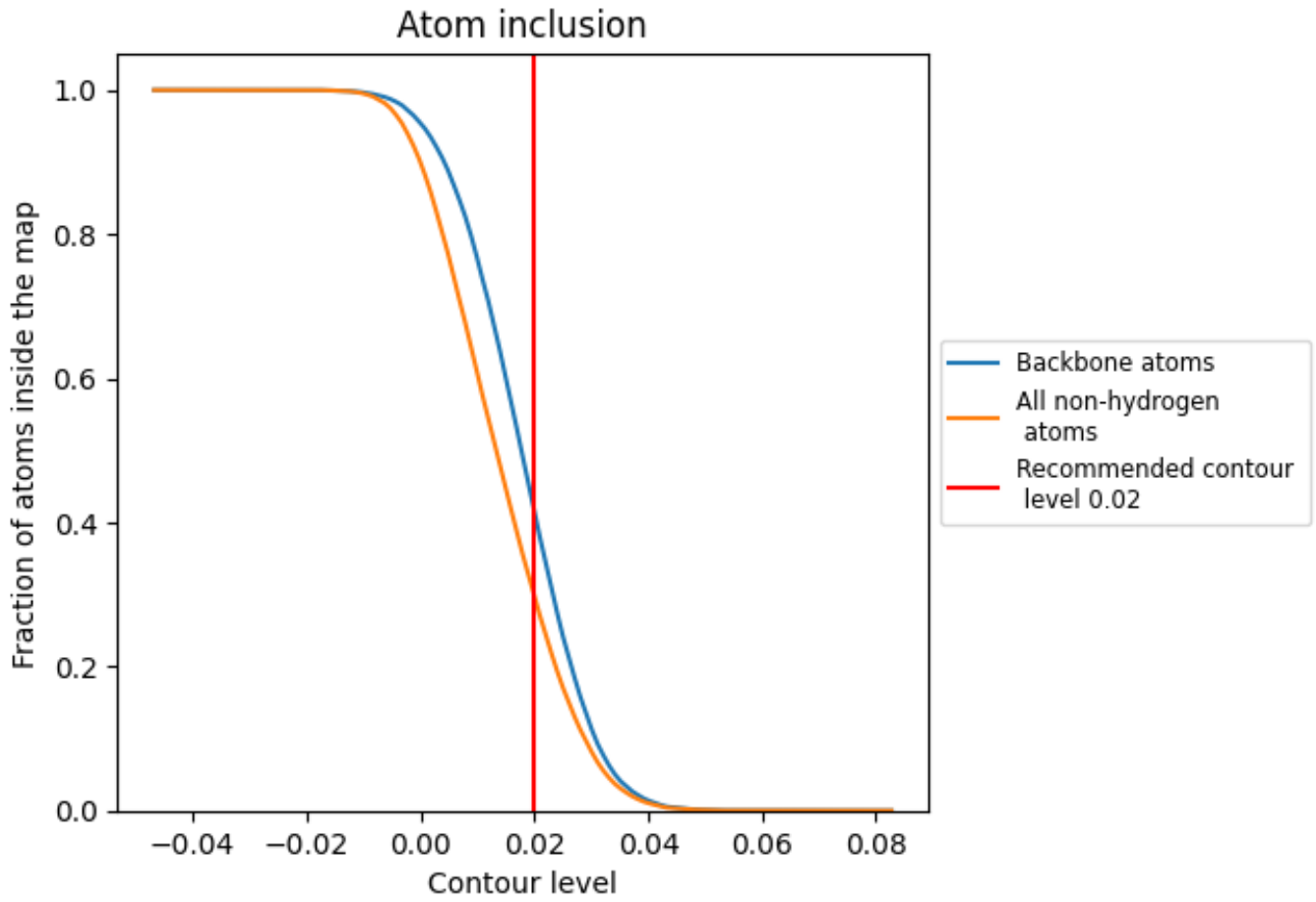
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.02).

9.4 Atom inclusion (i)



At the recommended contour level, 42% of all backbone atoms, 30% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.2976	0.2310
4	0.1420	0.2040
5	0.1787	0.2130
6	0.2366	0.2360
A	0.3338	0.2400
C	0.3416	0.2380
D	0.2550	0.2280
E	0.2711	0.2290
J	0.3306	0.2290
Z	0.2570	0.2250
p	0.2283	0.2260
q	0.2696	0.2350
r	0.2319	0.2150