



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 05:45 PM UTC

PDB ID : 3J2M / pdb_00003j2m
EMDB ID : EMD-1126
Title : The X-ray structure of the gp15 hexamer and the model of the gp18 protein fitted into the cryo-EM reconstruction of the extended T4 tail
Authors : Fokine, A.; Zhang, Z.; Kanamaru, S.; Bowman, V.D.; Aksyuk, A.; Arisaka, F.; Rao, V.B.; Rossmann, M.G.
Deposited on : 2012-11-09
Resolution : 15.00 Å(reported)

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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

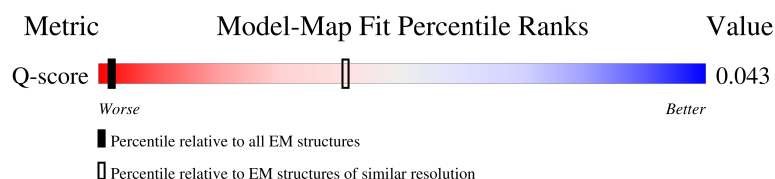
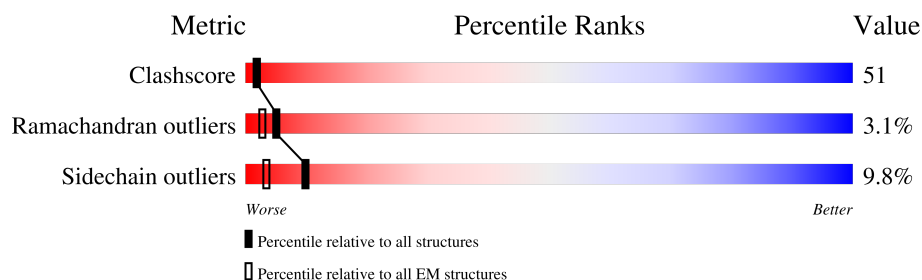
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 15.00 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.



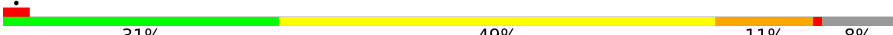
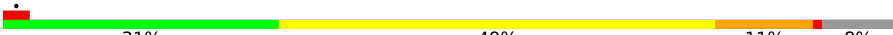
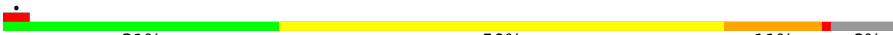
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	37 (14.50 - 15.50)

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	272	
1	B	272	
1	C	272	
1	D	272	

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Mol	Chain	Length	Quality of chain
1	E	272	
1	F	272	
2	U	659	
2	V	659	
2	W	659	
2	X	659	
2	Y	659	
2	Z	659	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 38334 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 Tail connector protein Gp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	211	Total	C	N	O	S	0	0
			1742	1123	283	328	8		
1	B	211	Total	C	N	O	S	0	0
			1742	1123	283	328	8		
1	C	211	Total	C	N	O	S	0	0
			1742	1123	283	328	8		
1	D	211	Total	C	N	O	S	0	0
			1742	1123	283	328	8		
1	E	211	Total	C	N	O	S	0	0
			1742	1123	283	328	8		
1	F	211	Total	C	N	O	S	0	0
			1742	1123	283	328	8		

- Molecule 2 is a protein called Tail sheath protein Gp18.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	U	609	Total	C	N	O	S	0	0
			4647	2929	785	923	10		
2	V	609	Total	C	N	O	S	0	0
			4647	2929	785	923	10		
2	W	609	Total	C	N	O	S	0	0
			4647	2929	785	923	10		
2	X	609	Total	C	N	O	S	0	0
			4647	2929	785	923	10		
2	Y	609	Total	C	N	O	S	0	0
			4647	2929	785	923	10		
2	Z	609	Total	C	N	O	S	0	0
			4647	2929	785	923	10		

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	100	GLU	ASP	SEE REMARK 999	UNP P13332
U	148	ALA	GLY	SEE REMARK 999	UNP P13332

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Chain	Residue	Modelled	Actual	Comment	Reference
U	150	ILE	ASN	SEE REMARK 999	UNP P13332
U	151	ILE	TYR	SEE REMARK 999	UNP P13332
U	301	GLY	GLU	SEE REMARK 999	UNP P13332
U	399	VAL	ALA	SEE REMARK 999	UNP P13332
U	454	TYR	HIS	SEE REMARK 999	UNP P13332
U	510	PRO	ARG	engineered mutation	UNP P13332
V	100	GLU	ASP	SEE REMARK 999	UNP P13332
V	148	ALA	GLY	SEE REMARK 999	UNP P13332
V	150	ILE	ASN	SEE REMARK 999	UNP P13332
V	151	ILE	TYR	SEE REMARK 999	UNP P13332
V	301	GLY	GLU	SEE REMARK 999	UNP P13332
V	399	VAL	ALA	SEE REMARK 999	UNP P13332
V	454	TYR	HIS	SEE REMARK 999	UNP P13332
V	510	PRO	ARG	engineered mutation	UNP P13332
W	100	GLU	ASP	SEE REMARK 999	UNP P13332
W	148	ALA	GLY	SEE REMARK 999	UNP P13332
W	150	ILE	ASN	SEE REMARK 999	UNP P13332
W	151	ILE	TYR	SEE REMARK 999	UNP P13332
W	301	GLY	GLU	SEE REMARK 999	UNP P13332
W	399	VAL	ALA	SEE REMARK 999	UNP P13332
W	454	TYR	HIS	SEE REMARK 999	UNP P13332
W	510	PRO	ARG	engineered mutation	UNP P13332
X	100	GLU	ASP	SEE REMARK 999	UNP P13332
X	148	ALA	GLY	SEE REMARK 999	UNP P13332
X	150	ILE	ASN	SEE REMARK 999	UNP P13332
X	151	ILE	TYR	SEE REMARK 999	UNP P13332
X	301	GLY	GLU	SEE REMARK 999	UNP P13332
X	399	VAL	ALA	SEE REMARK 999	UNP P13332
X	454	TYR	HIS	SEE REMARK 999	UNP P13332
X	510	PRO	ARG	engineered mutation	UNP P13332
Y	100	GLU	ASP	SEE REMARK 999	UNP P13332
Y	148	ALA	GLY	SEE REMARK 999	UNP P13332
Y	150	ILE	ASN	SEE REMARK 999	UNP P13332
Y	151	ILE	TYR	SEE REMARK 999	UNP P13332
Y	301	GLY	GLU	SEE REMARK 999	UNP P13332
Y	399	VAL	ALA	SEE REMARK 999	UNP P13332
Y	454	TYR	HIS	SEE REMARK 999	UNP P13332
Y	510	PRO	ARG	engineered mutation	UNP P13332
Z	100	GLU	ASP	SEE REMARK 999	UNP P13332
Z	148	ALA	GLY	SEE REMARK 999	UNP P13332
Z	150	ILE	ASN	SEE REMARK 999	UNP P13332
Z	151	ILE	TYR	SEE REMARK 999	UNP P13332

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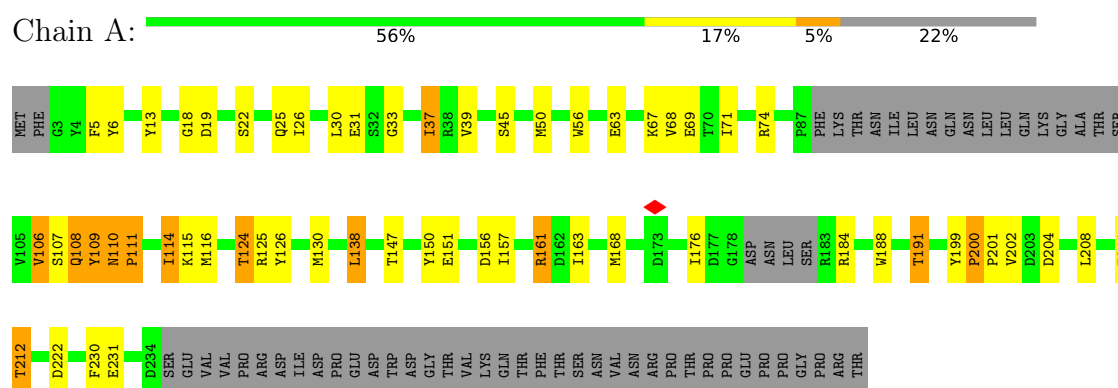
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Chain	Residue	Modelled	Actual	Comment	Reference
Z	301	GLY	GLU	SEE REMARK 999	UNP P13332
Z	399	VAL	ALA	SEE REMARK 999	UNP P13332
Z	454	TYR	HIS	SEE REMARK 999	UNP P13332
Z	510	PRO	ARG	engineered mutation	UNP P13332

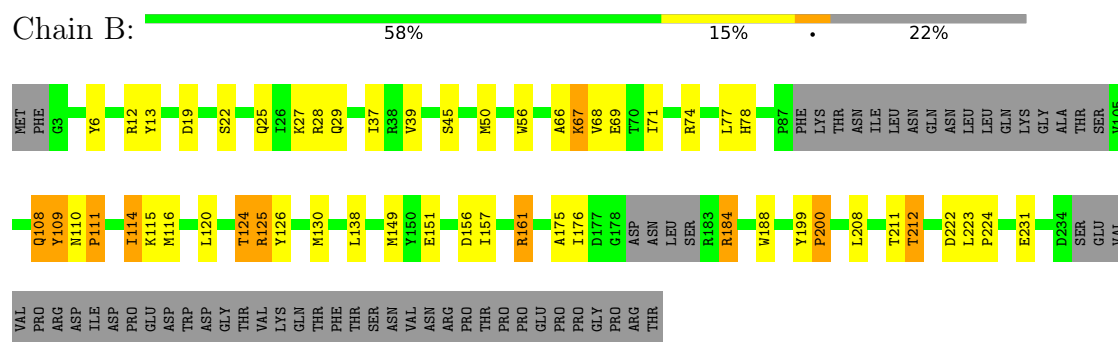
3 Residue-property plots

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.

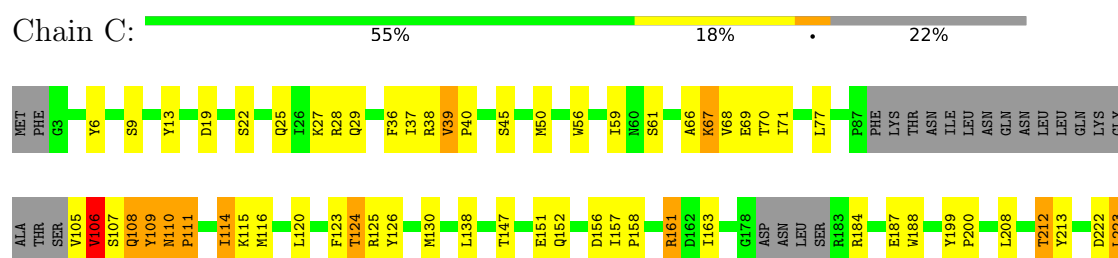
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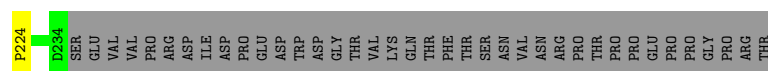


• Molecule 1: Tail connector protein Gp15

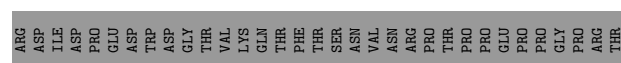


• Molecule 1: Tail connector protein Gp15

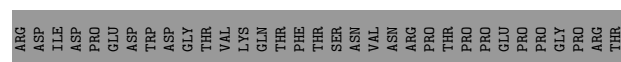
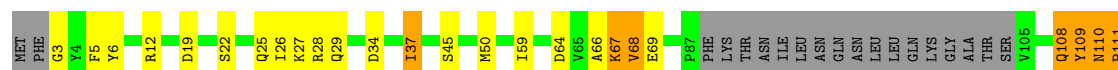




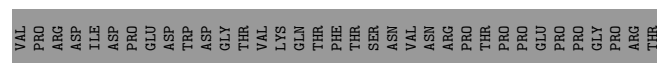
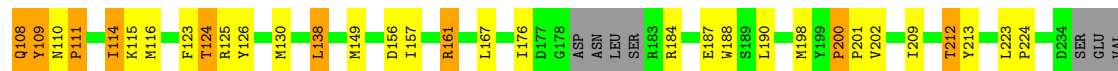
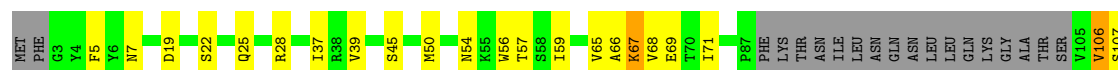
- Molecule 1: Tail connector protein Gp15



- Molecule 1: Tail connector protein Gp15

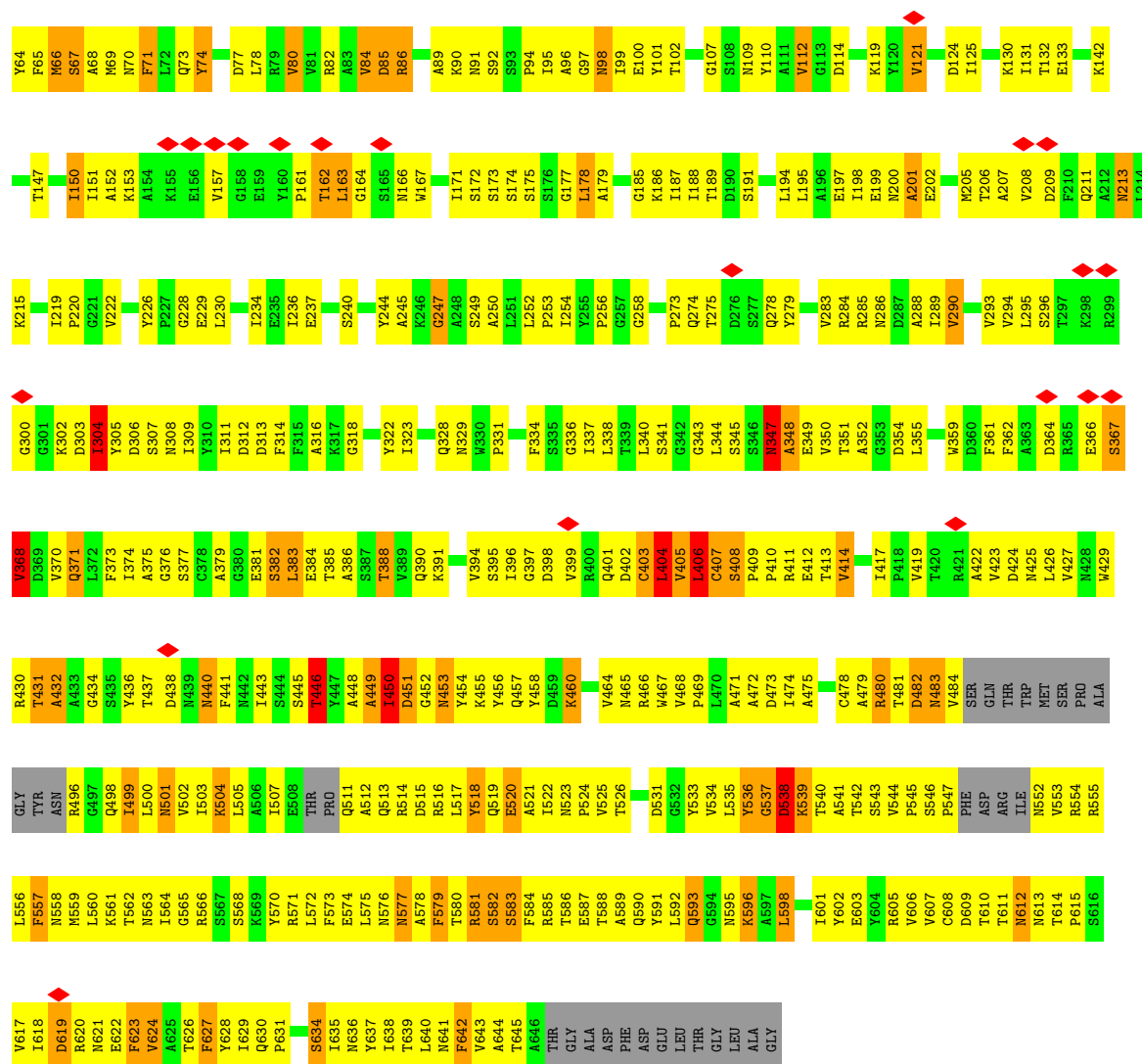


- Molecule 1: Tail connector protein Gp15

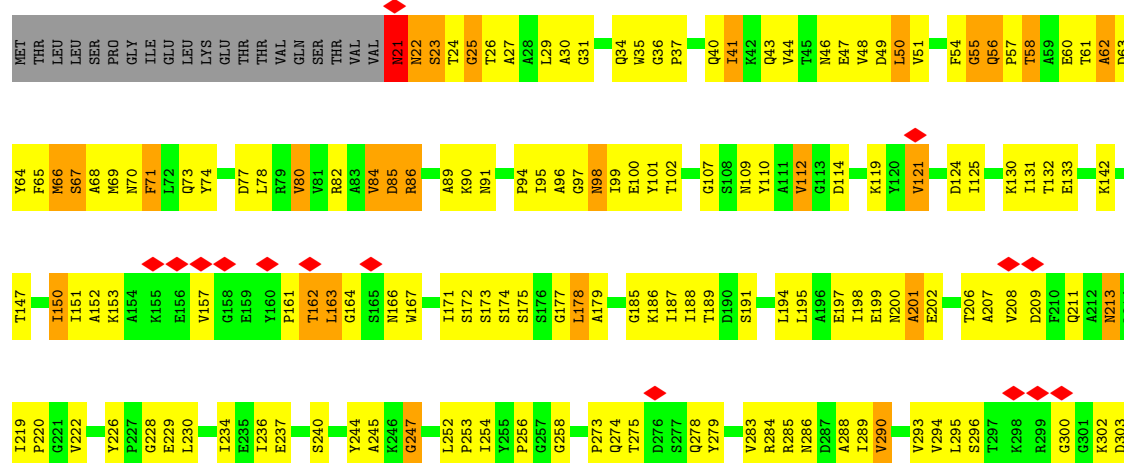


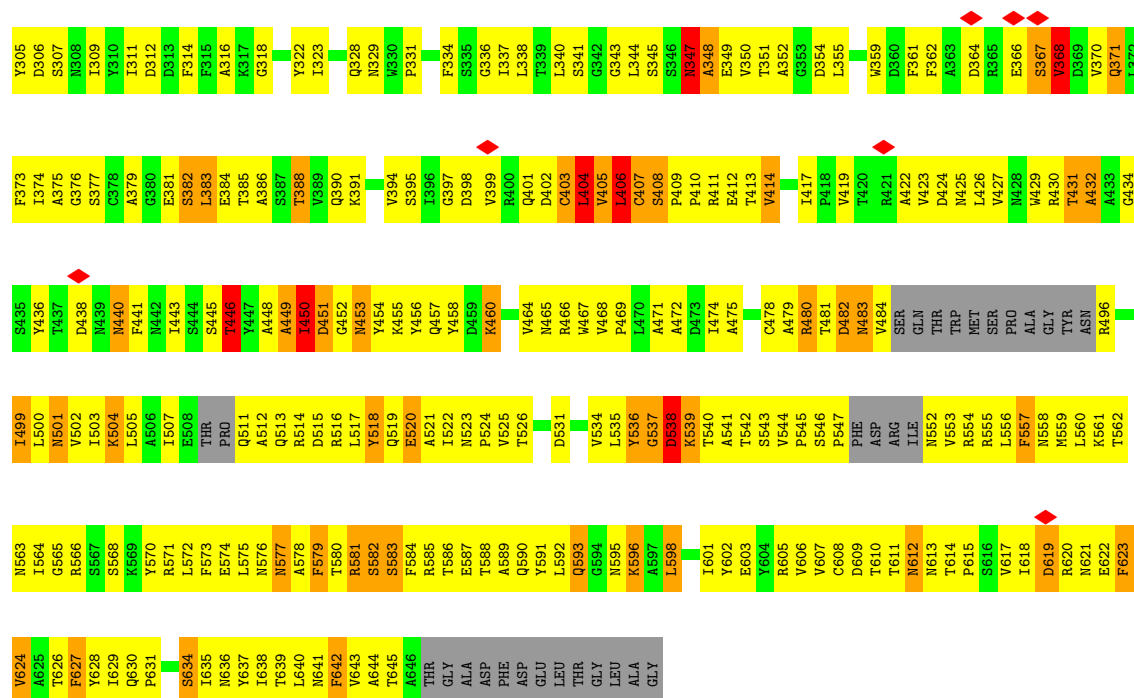
- Molecule 2: Tail sheath protein Gp18



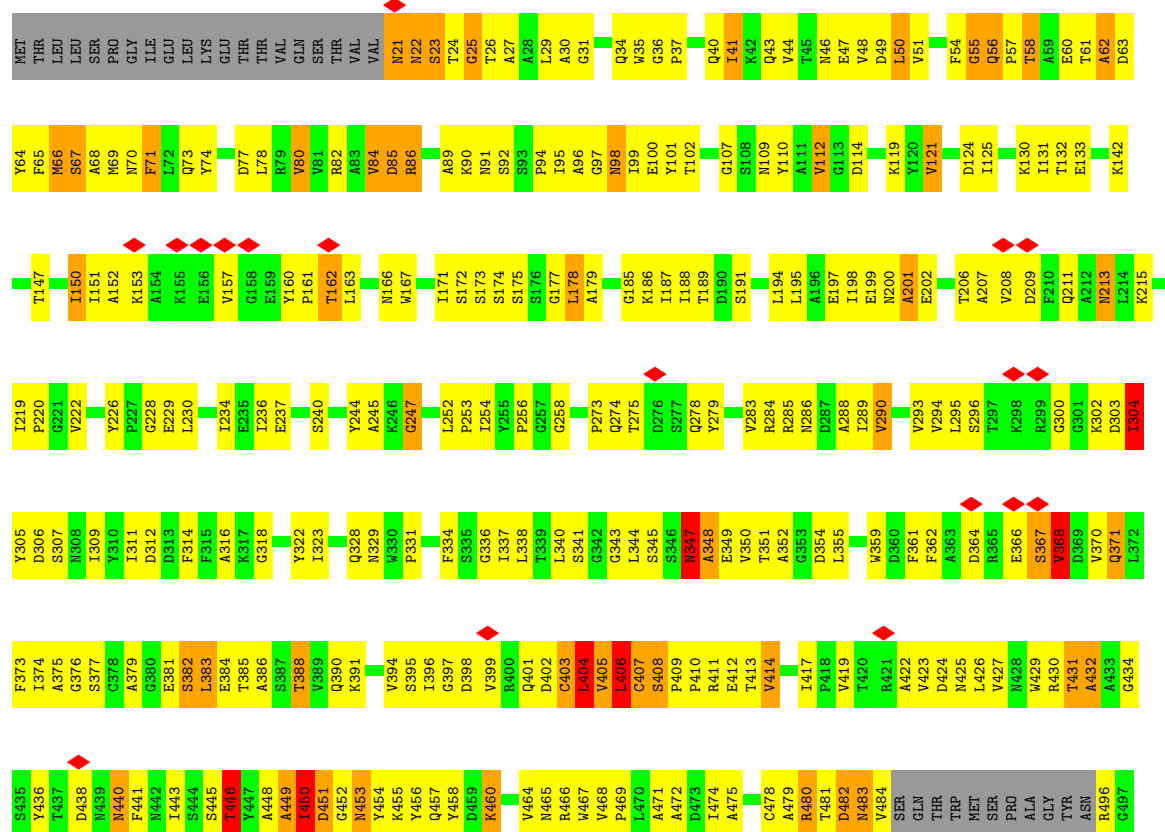


• Molecule 2: Tail sheath protein Gp18





• Molecule 2: Tail sheath protein Gp18



Q498 I499 N501 N502 I503 K504 L505 A506 I507 E508 THR Q511 A512 Q513 R514 D515 R516 L517 Q519 E520 A521 I522 N523 P524 V525 T526 D531 G532 Y533 G534 L535 Y536 G537 D538 K539 T540 A541 T542 S543 V544 P545 S546 P547 PHE ASP ARG ILE N552 V553 R554 R555 R556 F557 N558 M559 L560

K561 I562 N563 I564 G565 R566 S567 K568 I569 R571 L572 E573 E574 L575 N576 N577 L578 A578 R579 T580 R581 S582 S583 F584 I585 T586 E587 T588 A589 Q590 A591 L592 Q593 G594 N595 K596 A597 L598 I601 Y602 E603 Y604 R605 V606 V607 C608 D609 T610 T611 M612 N613 T614 P615 R616 S616 V617 I618 D619 N621

E622 F623 A624 A625 T626 F627 Y628 L629 Q630 P631 S634 I635 N636 Y637 I638 T639 L640 M641 F642 V643 T644 T645 THR GLY ALA ASP PHE ASP GLU LEU ALA GLY

• Molecule 2: Tail sheath protein Gp18

Chain X:  31% 49% 11% 8%

MET THR LEU SER PRO GLY ILE GLU LEU LYS GLU THR VAL THR VAL N21 N22 S23 T24 T25 T26 A27 L29 A30 G31 Q34 W35 Y101 G36 P37 Q40 I41 V44 T45 M46 V48 D49 L50 V51 F54 G55 Q56 P57 T58 A59 E60 T61 A62 D63 V64

R65 M66 S67 A68 N69 M70 F71 L72 G73 Y74 D77 L78 R79 V80 W81 R82 A83 R84 D85 R86 A89 K90 N91 S92 S93 P94 I95 I96 G97 N98 I99 E100 Y101 T102 I103 S104 G107 S108 N109 Y110 A111 V112 G113 D114 K119 Y120 V121 D124 I125 K130 T131 T132 E133

K142 T147 I150 I151 A152 K153 K154 K155 E156 G158 E159 Y160 P161 A162 L163 G164 N165 W167 I171 S172 S173 S174 S175 S176 G177 L178 A179 A180 V181 G185 K186 I187 T188 D189 S191 L194 L195 A196 E197 I198 E199 N200 D201 E202 T206 A207 I208 D209 Q211 A212

N213 L214 K215 I219 N220 G221 V222 Y226 G228 E229 L230 I234 E235 E236 E237 S240 Y244 A245 K246 G247 P253 I254 Y255 Y256 G257 G258 P273 Q274 T275 D276 S277 Q278 Y279 V283 R284 R285 N286 D287 L288 A288 I289 V290 V293 V294 L295 S296 T297 K298 R299 G301 A302

K302 D303 I304 Y305 D306 S307 N308 S309 Y310 I311 D312 D313 F314 F315 A316 K317 G318 Y322 I323 Q328 N329 W330 P331 F334 S335 G336 I337 L338 T339 L340 G343 L344 S345 S346 A347 A348 A349 V350 T351 A352 G353 D354 L355 W359 D360 F361 A362 A363 R364 R365 E366 S367 V368 V370

Q371 L372 F373 I374 A375 G376 S377 C378 A379 G380 E381 S382 L383 E384 T385 A386 S387 T388 T389 Q390 K391 V394 S395 I396 G397 D398 V399 Q400 Q401 D402 C403 L404 V405 L406 C407 S408 P409 R410 R411 E412 T413 T414 V415 I417 P418 V419 T420 R421 A422 V423 D424 M425 L426 V427 N428 W429 R430 T431 A432

A433 G434 S435 Y436 T437 D438 M439 N440 F441 M442 N443 S444 S445 T446 Y447 A448 A449 T450 T451 D452 M453 Y454 K455 Y456 Q457 Y458 D459 K460 Y464 M465 R466 V467 P468 P469 L470 A471 A472 D473 I474 A475 C478 A479 R480 T481 D482 M483 V484 SER GLN THR TRP MET SER PRO ALA GLY TYR ASN

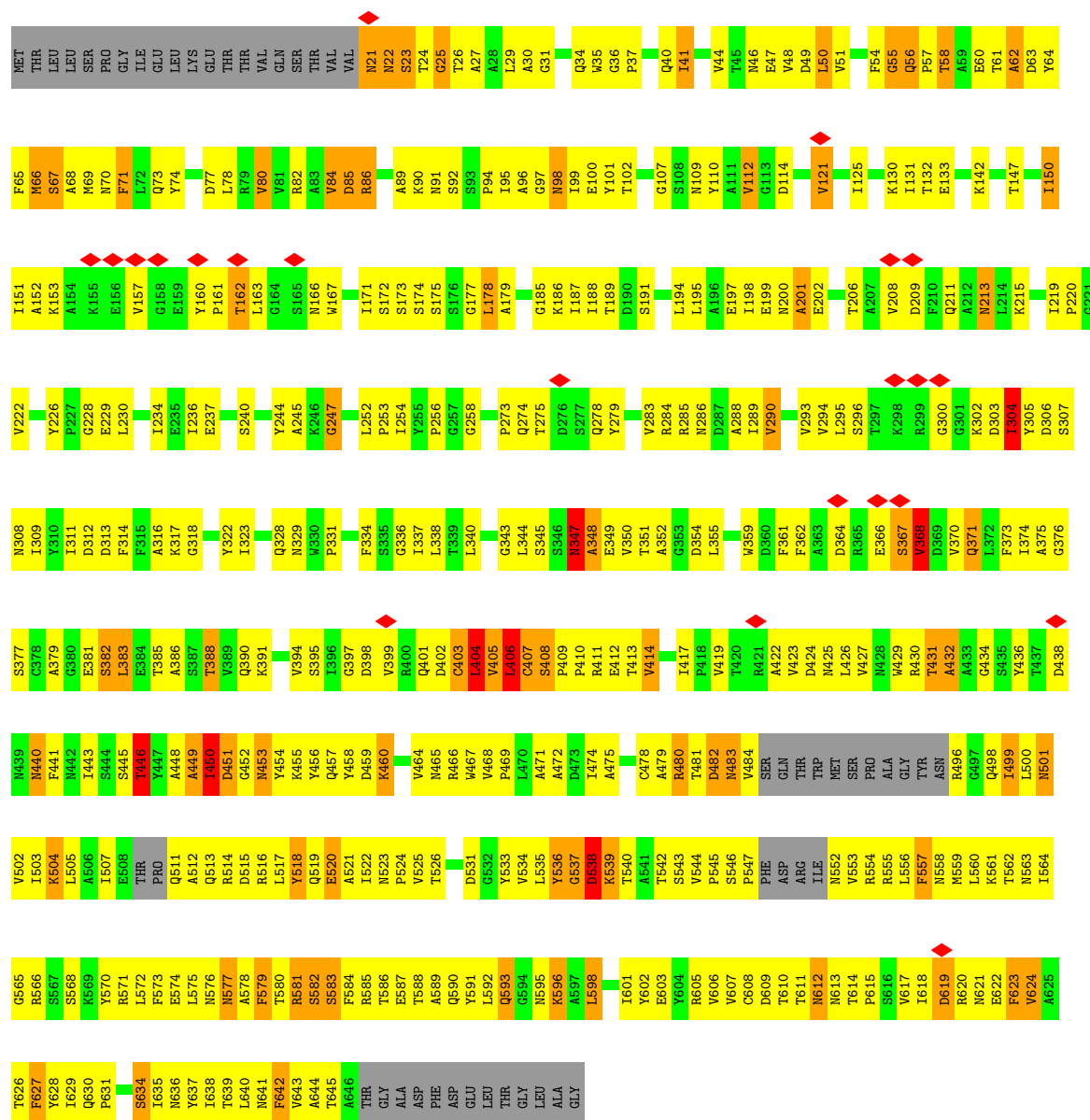
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M559 L560 K561 I562 N563 I564 G565 R566 S567 K568 I569 R571 L572 E573 E574 L575 N576 N577 L578 A578 R579 T580 R581 S582 S583 F584 I585 T586 E587 T588 A589 Q590 A591 L592 Q593 G594 N595 K596 A597 L598 I601 Y602 E603 Y604 R605 V606 V607 C608 D609 T610 T611 M612 N613 T614 P615 R616 S616 V617 I618 D619

R620 M621 E622 F623 A624 A625 T626 F627 Y628 L629 Q630 P631 S634 I635 N636 Y637 I638 T639 L640 M641 F642 V643 T644 T645 THR GLY ALA ASP PHE ASP GLU LEU ALA GLY

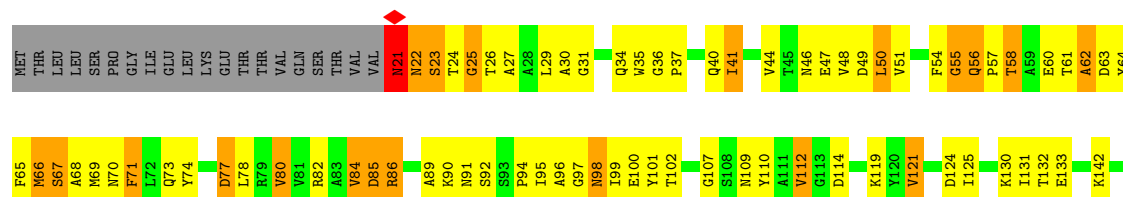
• Molecule 2: Tail sheath protein Gp18

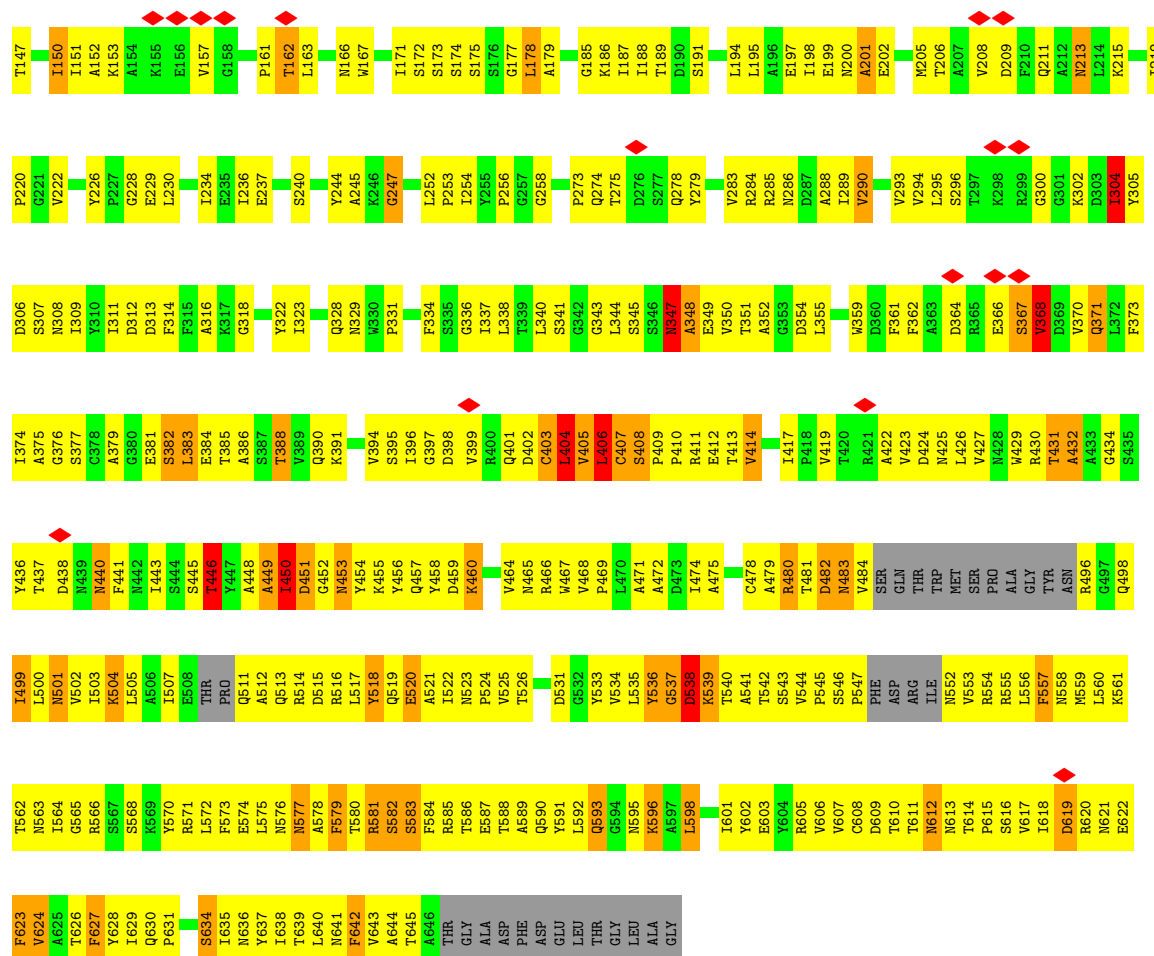
Chain Y:  31% 49% 11% 8%



• Molecule 2: Tail sheath protein Gp18

Chain Z:  31% 50% 11% 8%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of particles used	3029	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	each particle image	Depositor
Microscope	FEI/PHILIPS CM300FEG/ST	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	47000	Depositor
Image detector	Not provided	
Maximum map value	7.953	Depositor
Minimum map value	-2.953	Depositor
Average map value	0.059	Depositor
Map value standard deviation	0.533	Depositor
Recommended contour level	1.01	Depositor
Map size ($\text{\AA}$)	714.6, 714.6, 1508.6	wwPDB
Map dimensions	180, 180, 380	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing ($\text{\AA}$)	3.97, 3.97, 3.97	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	0.62	1/1787 (0.1%)	0.98	3/2421 (0.1%)
1	B	0.63	1/1787 (0.1%)	0.98	4/2421 (0.2%)
1	C	0.62	0/1787	0.99	6/2421 (0.2%)
1	D	0.63	0/1787	0.95	1/2421 (0.0%)
1	E	0.64	1/1787 (0.1%)	0.96	1/2421 (0.0%)
1	F	0.65	1/1787 (0.1%)	1.03	5/2421 (0.2%)
2	U	0.82	4/4729 (0.1%)	1.25	57/6427 (0.9%)
2	V	0.82	4/4729 (0.1%)	1.26	55/6427 (0.9%)
2	W	0.82	4/4729 (0.1%)	1.26	55/6427 (0.9%)
2	X	0.82	4/4729 (0.1%)	1.26	55/6427 (0.9%)
2	Y	0.82	4/4729 (0.1%)	1.25	55/6427 (0.9%)
2	Z	0.83	4/4729 (0.1%)	1.26	55/6427 (0.9%)
All	All	0.78	28/39096 (0.1%)	1.19	352/53088 (0.7%)

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
2	U	0	4
2	V	0	4
2	W	0	4
2	X	0	4
2	Y	0	4
2	Z	0	4
All	All	0	24

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Y	22	ASN	C-N	-7.35	1.23	1.33
2	X	22	ASN	C-N	-7.29	1.23	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Z	23	SER	C-O	7.29	1.33	1.24
2	U	22	ASN	C-N	-7.24	1.23	1.33
2	Z	22	ASN	C-N	-7.19	1.23	1.33

The worst 5 of 352 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	V	55	GLY	N-CA-C	19.05	158.33	113.18
2	U	55	GLY	N-CA-C	18.99	158.18	113.18
2	Y	55	GLY	N-CA-C	18.96	158.12	113.18
2	W	55	GLY	N-CA-C	18.95	158.08	113.18
2	X	55	GLY	N-CA-C	18.88	157.92	113.18

There are no chirality outliers.

5 of 24 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	U	21	ASN	Peptide
2	U	450	ILE	Peptide
2	U	451	ASP	Peptide
2	U	452	GLY	Peptide
2	V	21	ASN	Peptide

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	1742	0	1673	56	0
1	B	1742	0	1673	61	0
1	C	1742	0	1673	50	0
1	D	1742	0	1673	45	0
1	E	1742	0	1673	50	0
1	F	1742	0	1673	37	0
2	U	4647	0	4564	630	0
2	V	4647	0	4564	624	0
2	W	4647	0	4564	621	0
2	X	4647	0	4564	615	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Y	4647	0	4562	606	0
2	Z	4647	0	4564	605	0
All	All	38334	0	37420	3887	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 51.

The worst 5 of 3887 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:156:ASP:HB3	2:U:579:PHE:CE1	1.23	1.68
1:B:157:ILE:CD1	2:V:579:PHE:HB3	1.20	1.63
1:B:157:ILE:HG13	2:V:579:PHE:CB	1.21	1.57
1:B:156:ASP:HB3	2:V:579:PHE:CE1	1.39	1.54
1:A:157:ILE:HG13	2:U:579:PHE:CB	1.22	1.54

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	205/272 (75%)	184 (90%)	18 (9%)	3 (2%)	8	40
1	B	205/272 (75%)	184 (90%)	17 (8%)	4 (2%)	6	31
1	C	205/272 (75%)	184 (90%)	17 (8%)	4 (2%)	6	31
1	D	205/272 (75%)	184 (90%)	17 (8%)	4 (2%)	6	31
1	E	205/272 (75%)	183 (89%)	18 (9%)	4 (2%)	6	31
1	F	205/272 (75%)	184 (90%)	18 (9%)	3 (2%)	8	40
2	U	601/659 (91%)	479 (80%)	101 (17%)	21 (4%)	3	20
2	V	601/659 (91%)	480 (80%)	100 (17%)	21 (4%)	3	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	W	601/659 (91%)	479 (80%)	101 (17%)	21 (4%)	3	20
2	X	601/659 (91%)	479 (80%)	101 (17%)	21 (4%)	3	20
2	Y	601/659 (91%)	479 (80%)	101 (17%)	21 (4%)	3	20
2	Z	601/659 (91%)	480 (80%)	100 (17%)	21 (4%)	3	20
All	All	4836/5586 (87%)	3979 (82%)	709 (15%)	148 (3%)	5	22

5 of 148 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	108	GLN
1	B	67	LYS
1	B	108	GLN
1	C	67	LYS
1	C	108	GLN

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	192/250 (77%)	172 (90%)	20 (10%)	7	22
1	B	192/250 (77%)	177 (92%)	15 (8%)	11	32
1	C	192/250 (77%)	174 (91%)	18 (9%)	8	26
1	D	192/250 (77%)	176 (92%)	16 (8%)	10	30
1	E	192/250 (77%)	176 (92%)	16 (8%)	10	30
1	F	192/250 (77%)	176 (92%)	16 (8%)	10	30
2	U	494/536 (92%)	443 (90%)	51 (10%)	7	23
2	V	494/536 (92%)	444 (90%)	50 (10%)	7	23
2	W	494/536 (92%)	444 (90%)	50 (10%)	7	23
2	X	494/536 (92%)	444 (90%)	50 (10%)	7	23
2	Y	494/536 (92%)	444 (90%)	50 (10%)	7	23
2	Z	494/536 (92%)	442 (90%)	52 (10%)	6	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	4116/4716 (87%)	3712 (90%)	404 (10%)	10	24

5 of 404 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	W	404	LEU
2	X	430	ARG
2	Z	499	ILE
2	W	436	TYR
2	X	84	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 114 such sidechains are listed below:

Mol	Chain	Res	Type
2	W	523	ASN
2	Z	612	ASN
2	X	457	GLN
2	Z	590	GLN
2	Z	166	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

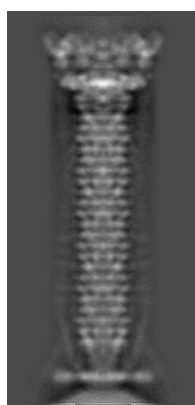
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1126. These allow visual inspection of the internal detail of the map and identification of artifacts.

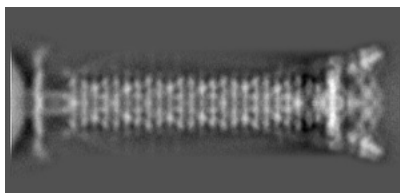
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

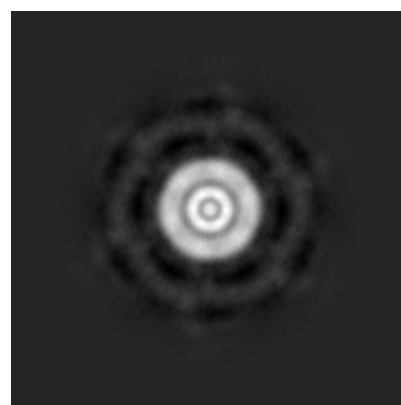
6.1.1 Primary map



X



Y

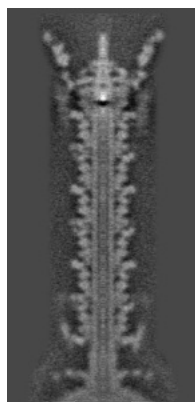


Z

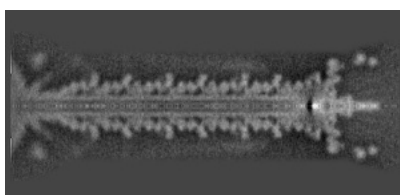
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

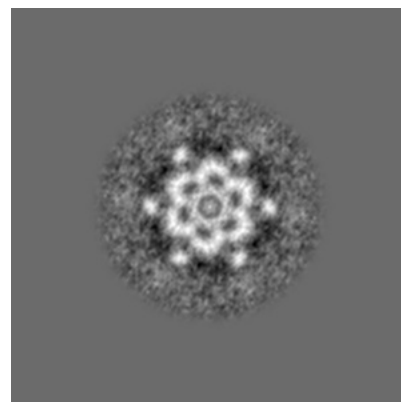
6.2.1 Primary map



X Index: 90



Y Index: 90

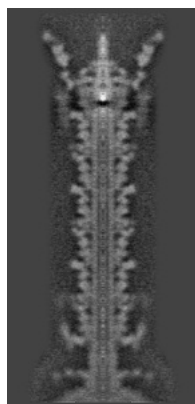


Z Index: 190

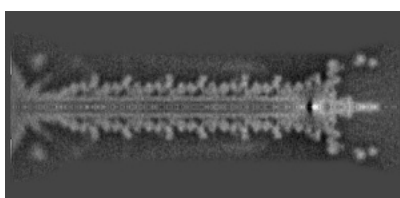
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

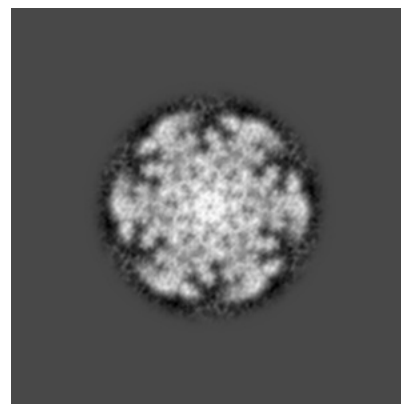
6.3.1 Primary map



X Index: 89



Y Index: 90

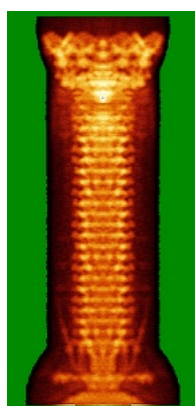


Z Index: 310

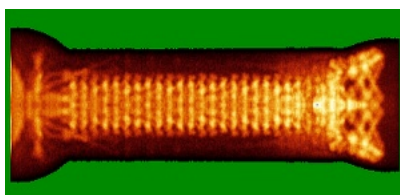
The images above show the largest variance slices of the map in three orthogonal directions.

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

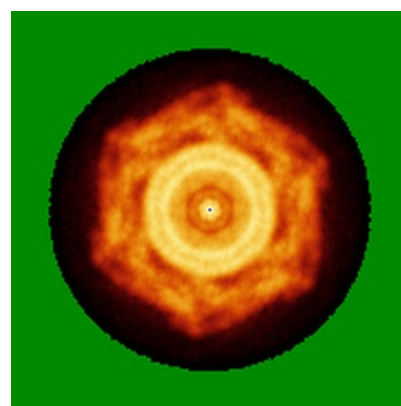
6.4.1 Primary map



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.

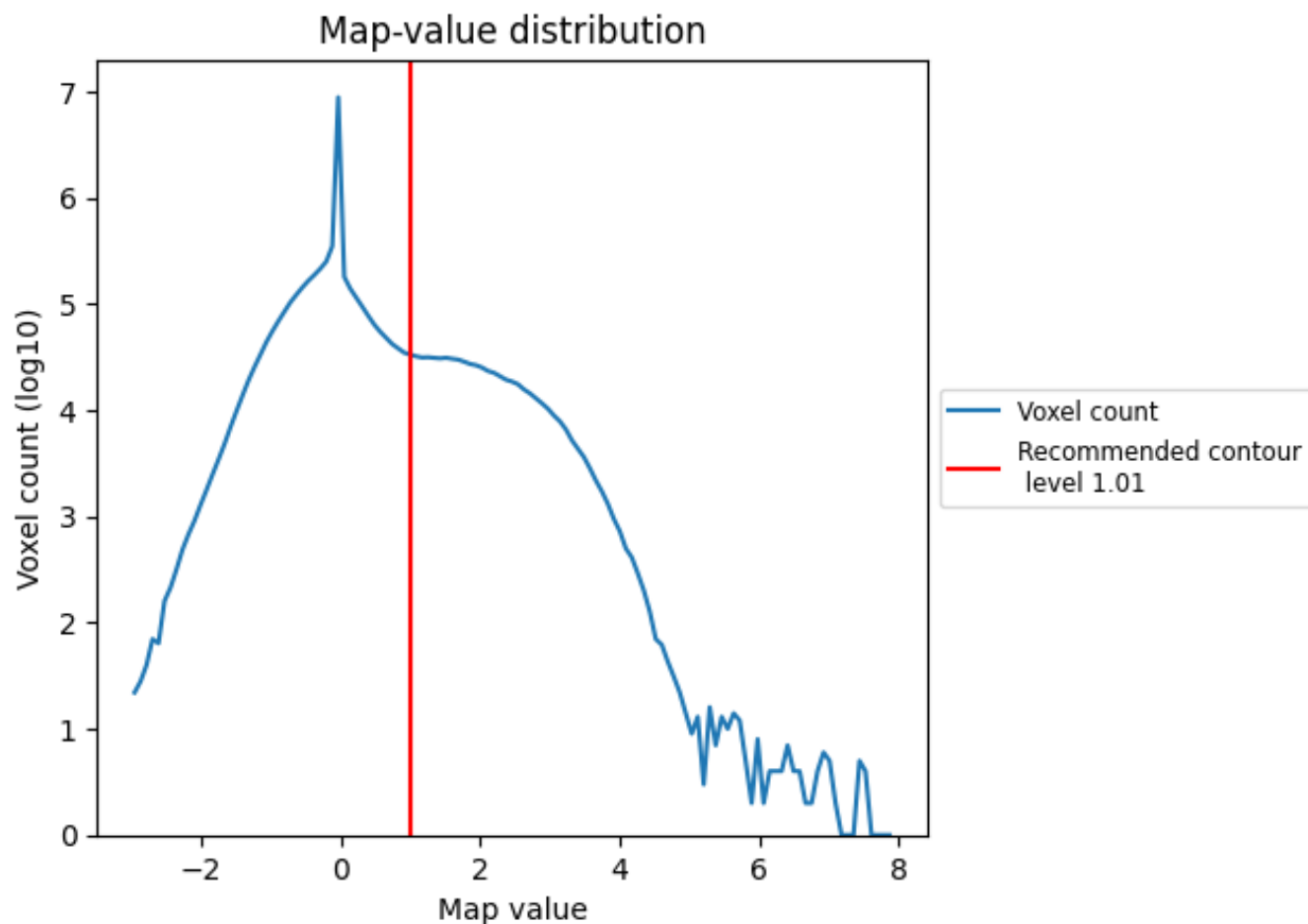
6.6 Mask visualisation

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

7 Map analysis [i](#)

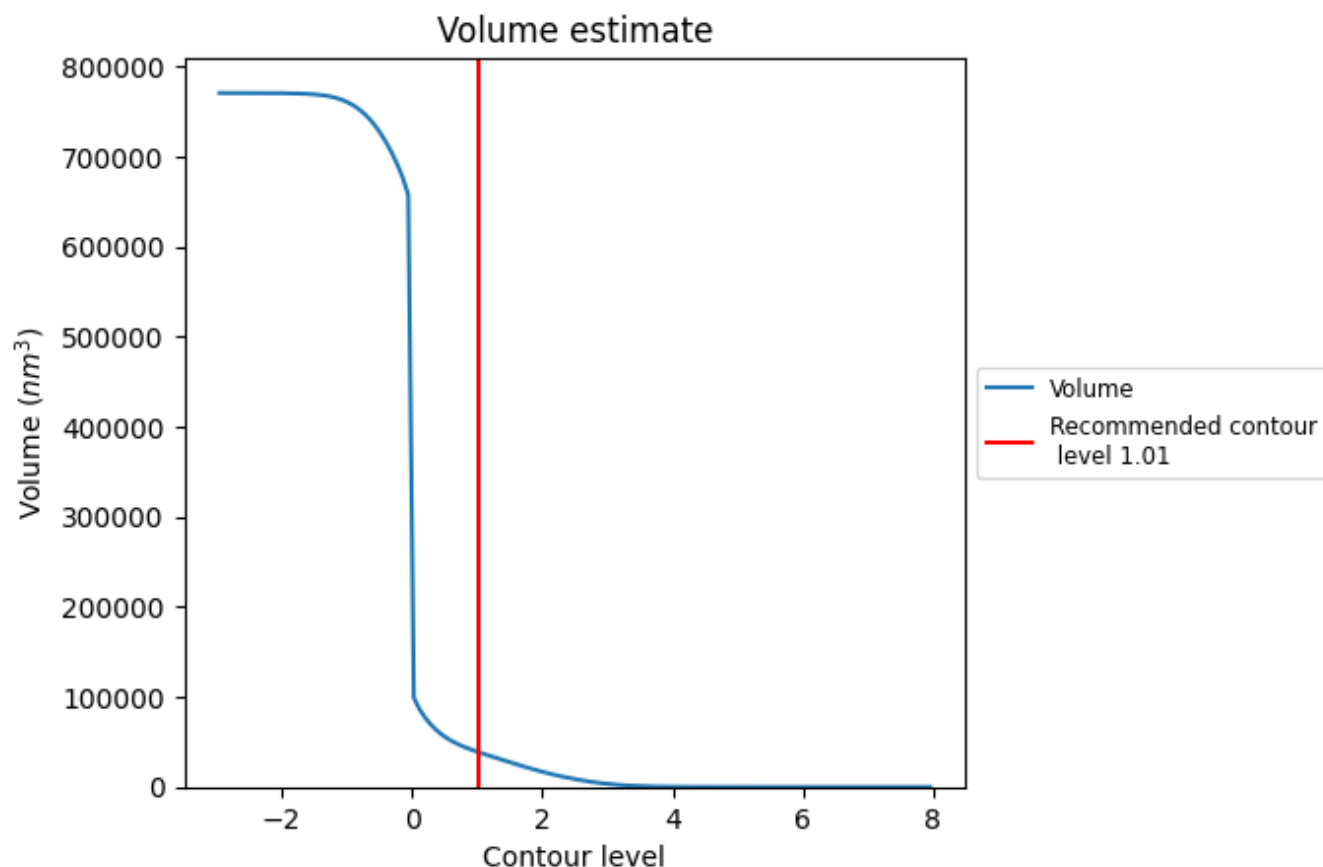
This section contains the results of statistical analysis of the map.

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 38892 nm³; this corresponds to an approximate mass of 35132 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

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

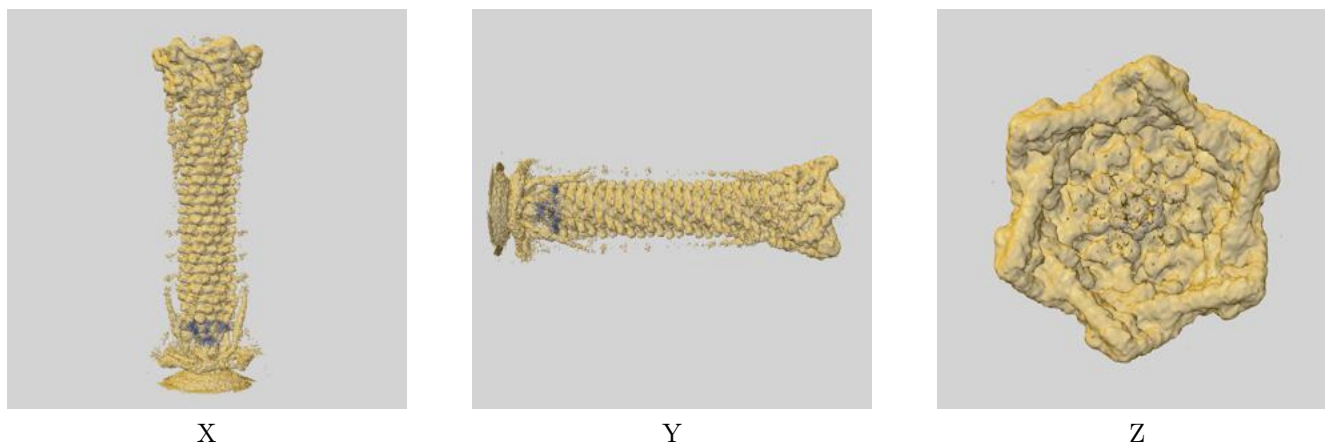
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

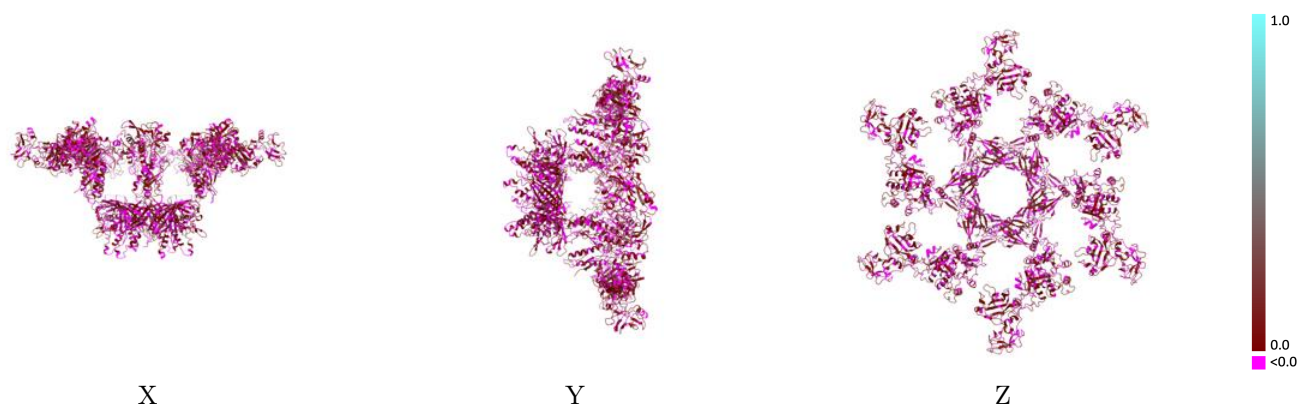
This section contains information regarding the fit between EMDB map EMD-1126 and PDB model 3J2M. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



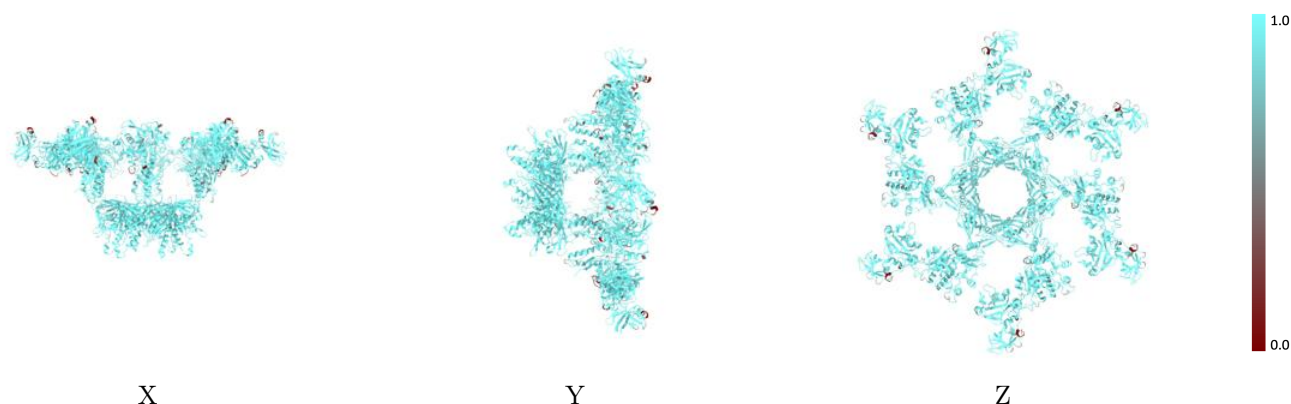
The images above show the 3D surface view of the map at the recommended contour level 1.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



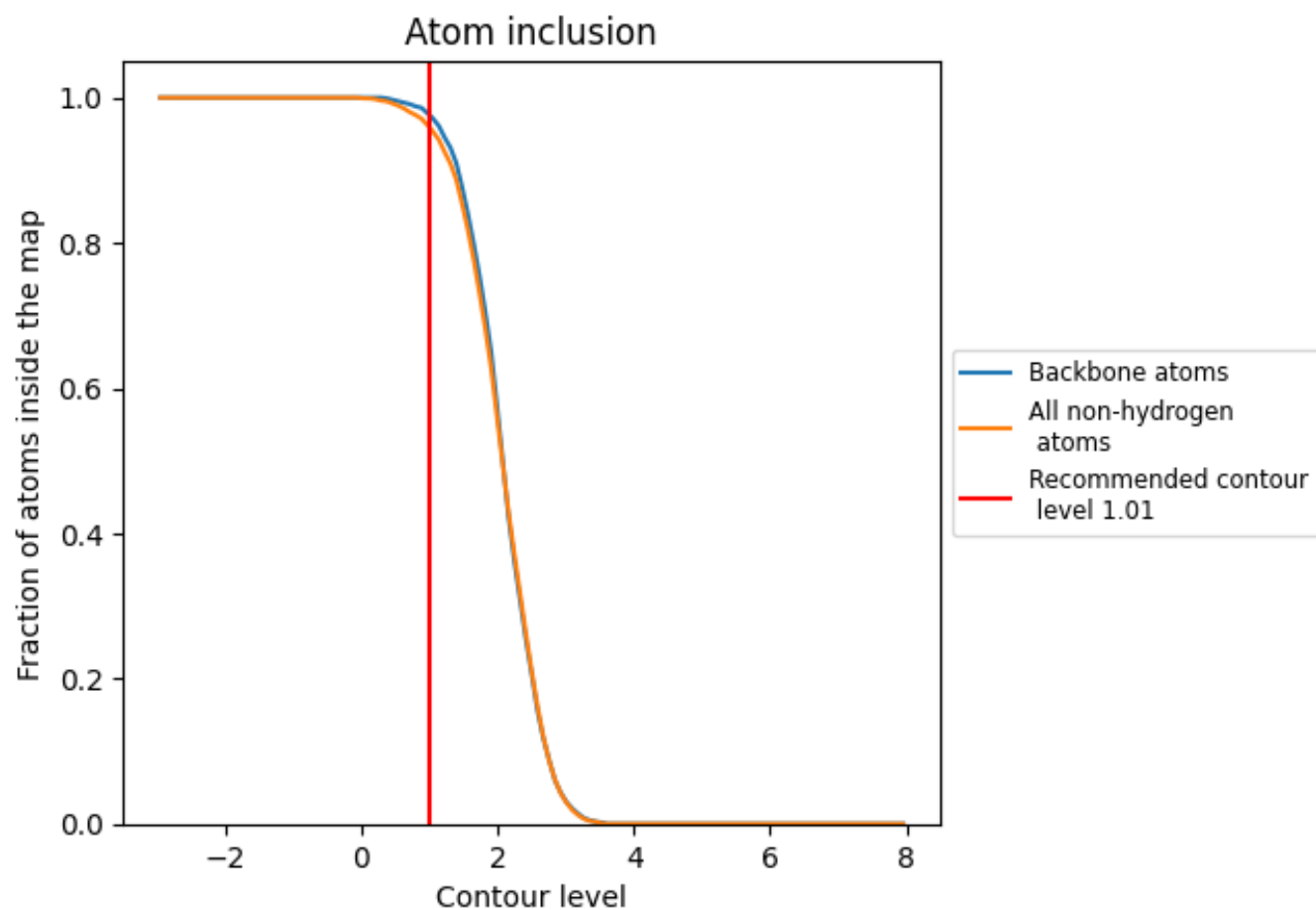
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.01).

9.4 Atom inclusion ⓘ



At the recommended contour level, 98% of all backbone atoms, 96% 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 (1.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9580	0.0430
A	0.9930	0.0230
B	0.9920	0.0260
C	0.9920	0.0260
D	0.9920	0.0220
E	0.9920	0.0260
F	0.9940	0.0250
U	0.9450	0.0540
V	0.9460	0.0500
W	0.9470	0.0480
X	0.9440	0.0510
Y	0.9460	0.0500
Z	0.9470	0.0490

1.0

0.0

<0.0