



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 04:37 PM UTC

PDB ID : 9JZ0 / pdb_00009jz0
EMDB ID : EMD-61911
Title : portal-tail complex of DNA-ejected T7
Authors : Liu, H.R.; Chen, W.Y.
Deposited on : 2024-10-13
Resolution : 3.50 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

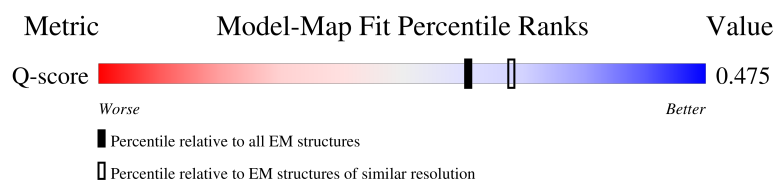
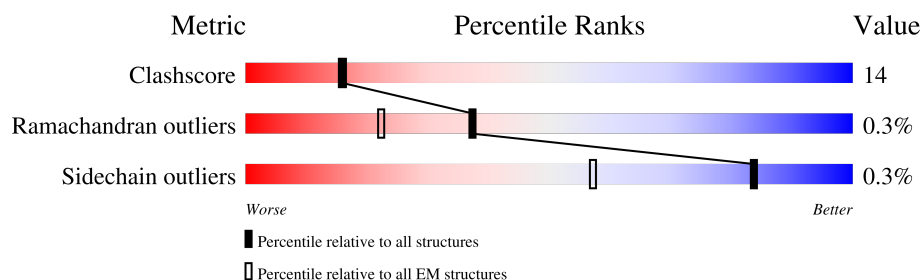
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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.



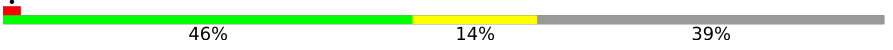
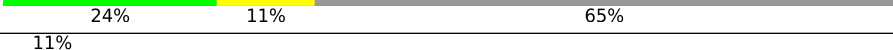
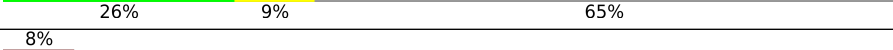
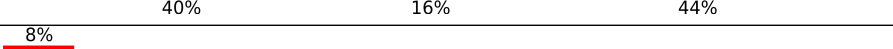
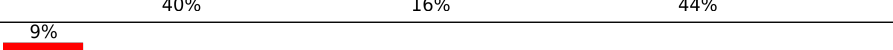
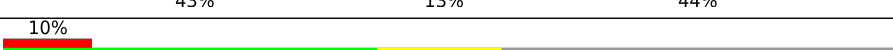
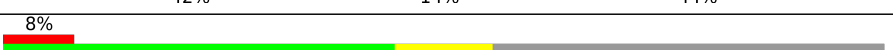
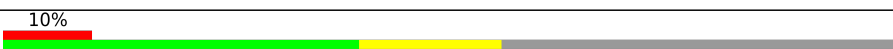
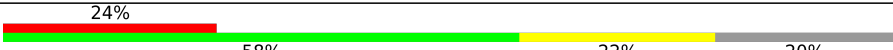
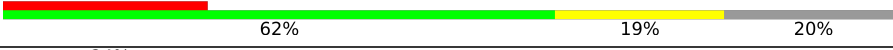
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	0	196	
1	1	196	
1	Y	196	
1	Z	196	

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Mol	Chain	Length	Quality of chain
1	y	196	
1	z	196	
2	2	88	
2	3	88	
2	4	88	
2	5	88	
2	6	88	
2	7	88	
2	8	88	
2	9	88	
2	AA	88	
2	AB	88	
2	AC	88	
2	AD	88	
3	A	536	
3	B	536	
3	C	536	
3	D	536	
3	E	536	
3	F	536	
3	G	536	
3	H	536	
3	I	536	
3	J	536	
3	K	536	

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Mol	Chain	Length	Quality of chain
3	L	536	
4	M	196	
4	N	196	
4	O	196	
4	P	196	
4	Q	196	
4	R	196	
4	S	196	
4	T	196	
4	U	196	
4	V	196	
4	W	196	
4	X	196	
5	a	553	
5	b	553	
5	c	553	
5	d	553	
5	e	553	
5	f	553	
5	g	553	
5	h	553	
5	i	553	
5	j	553	
5	k	553	
5	l	553	

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Mol	Chain	Length	Quality of chain
5	m	553	15%6%79%
5	n	553	11%9%80%
5	o	553	13%8%80%
5	p	553	15%6%79%
5	q	553	11%9%80%
5	r	553	12%8%80%
6	s	794	57%42%. .
6	t	794	56%43%..
6	u	794	57%42%..
6	v	794	56%43%... .
6	w	794	57%41%..
6	x	794	56%42%... .

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 122376 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 Internal virion protein gp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	119	Total	C	N	O	S	0	0
			920	556	172	185	7		
1	1	119	Total	C	N	O	S	0	0
			920	556	172	185	7		
1	Y	119	Total	C	N	O	S	0	0
			920	556	172	185	7		
1	Z	119	Total	C	N	O	S	0	0
			920	556	172	185	7		
1	y	119	Total	C	N	O	S	0	0
			920	556	172	185	7		
1	z	119	Total	C	N	O	S	0	0
			920	556	172	185	7		

- Molecule 2 is a protein called Protein 6.7.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	31	Total	C	N	O	S	0	0
			231	139	38	53	1		
2	3	31	Total	C	N	O	S	0	0
			231	139	38	53	1		
2	4	31	Total	C	N	O	S	0	0
			231	139	38	53	1		
2	5	31	Total	C	N	O	S	0	0
			231	139	38	53	1		
2	6	31	Total	C	N	O	S	0	0
			231	139	38	53	1		
2	7	31	Total	C	N	O	S	0	0
			231	139	38	53	1		
2	8	49	Total	C	N	O	S	0	0
			368	219	64	84	1		
2	9	49	Total	C	N	O	S	0	0
			368	219	64	84	1		
2	AA	49	Total	C	N	O	S	0	0
			368	219	64	84	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	49	Total	C	N	O	S	0	0
			368	219	64	84	1		
2	AC	49	Total	C	N	O	S	0	0
			368	219	64	84	1		
2	AD	49	Total	C	N	O	S	0	0
			368	219	64	84	1		

- Molecule 3 is a protein called Portal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	429	Total	C	N	O	S	0	0
			3363	2120	562	667	14		
3	B	431	Total	C	N	O	S	0	0
			3378	2128	567	669	14		
3	C	429	Total	C	N	O	S	0	0
			3363	2120	562	667	14		
3	D	431	Total	C	N	O	S	0	0
			3378	2128	567	669	14		
3	E	429	Total	C	N	O	S	0	0
			3363	2120	562	667	14		
3	F	431	Total	C	N	O	S	0	0
			3378	2128	567	669	14		
3	G	429	Total	C	N	O	S	0	0
			3363	2120	562	667	14		
3	H	431	Total	C	N	O	S	0	0
			3378	2128	567	669	14		
3	I	429	Total	C	N	O	S	0	0
			3363	2120	562	667	14		
3	J	431	Total	C	N	O	S	0	0
			3378	2128	567	669	14		
3	K	429	Total	C	N	O	S	0	0
			3363	2120	562	667	14		
3	L	431	Total	C	N	O	S	0	0
			3378	2128	567	669	14		

- Molecule 4 is a protein called Tail tubular protein gp11.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	M	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
4	N	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	O	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
4	P	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		
4	Q	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
4	R	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		
4	S	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
4	T	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		
4	U	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
4	V	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		
4	W	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
4	X	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		

- Molecule 5 is a protein called Tail fiber protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	a	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
5	b	113	Total	C	N	O	S	0	0
			907	575	157	174	1		
5	c	113	Total	C	N	O	S	0	0
			907	575	157	174	1		
5	d	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
5	e	113	Total	C	N	O	S	0	0
			907	575	157	174	1		
5	f	113	Total	C	N	O	S	0	0
			907	575	157	174	1		
5	g	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
5	h	113	Total	C	N	O	S	0	0
			907	575	157	174	1		
5	i	113	Total	C	N	O	S	0	0
			907	575	157	174	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	j	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
5	k	113	Total	C	N	O	S	0	0
			907	575	157	174	1		
5	l	113	Total	C	N	O	S	0	0
			907	575	157	174	1		
5	m	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
5	n	113	Total	C	N	O	S	0	0
			907	575	157	174	1		
5	o	113	Total	C	N	O	S	0	0
			907	575	157	174	1		
5	p	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
5	q	113	Total	C	N	O	S	0	0
			907	575	157	174	1		
5	r	113	Total	C	N	O	S	0	0
			907	575	157	174	1		

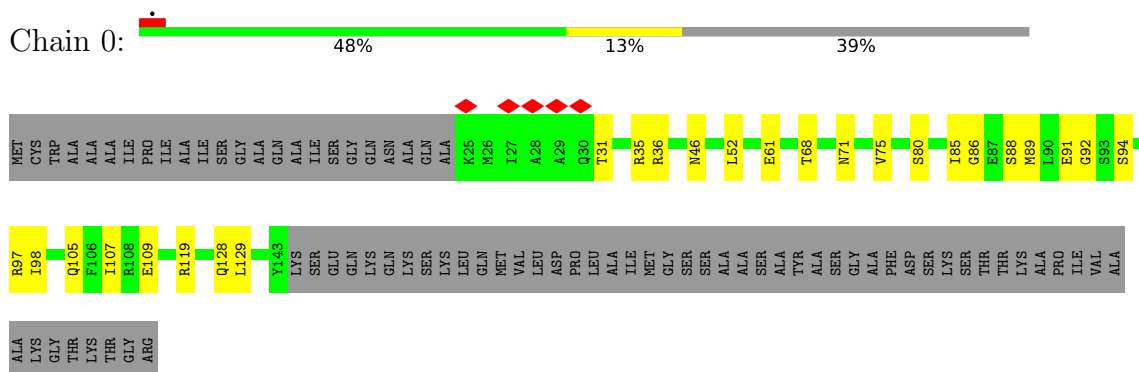
- Molecule 6 is a protein called Tail tubular protein gp12.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	s	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		
6	t	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		
6	u	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		
6	v	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		
6	w	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		
6	x	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		

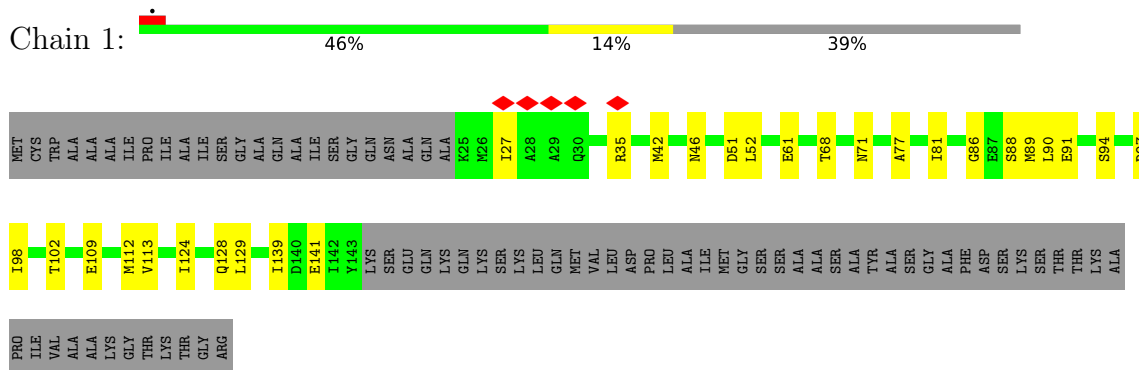
3 Residue-property plots [i](#)

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.

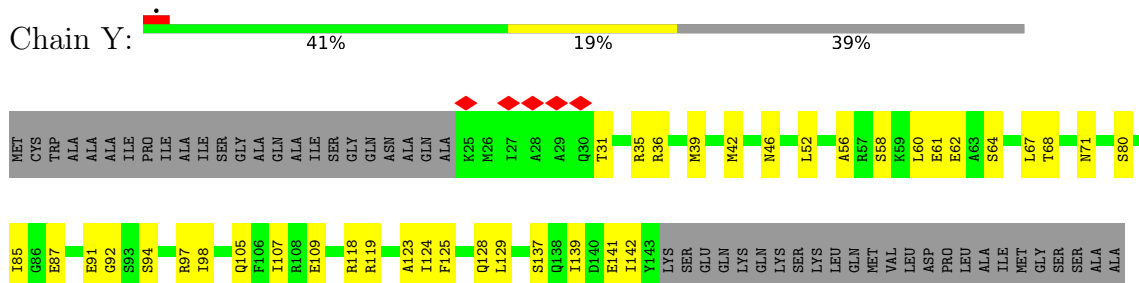
- Molecule 1: Internal virion protein gp14



- Molecule 1: Internal virion protein gp14



- Molecule 1: Internal virion protein gp14



GLY ASN GLY SER ALA ARG MET LYS SER PRO SER ILE ARG LYS SER ALA PHE GLY LYS LYS

• Molecule 2: Protein 6.7

Chain 3: 13% 26% 9% 65%

MET CYS PHE SER PRO LYS ILE LYS THR PRO K11 T14 V20 E21 P22 A23 P24 L25 T26 Q27 E28 V29 S30 S31 V32 E33 S37 S38 D39 E40 T41 ASP THR GLU GLY THR GLU GLY THR VAL SER GLY ARG LYS LYS LEU VAL VAL GLU ARG ASP ASP VAL SER VAL LYS SER LYS ALA

SER GLY ASN GLY SER ALA ARG MET LYS SER PRO SER ILE ARG LYS SER ALA PHE GLY LYS LYS

• Molecule 2: Protein 6.7

Chain 4: 9% 25% 10% 65%

MET CYS PHE SER PRO LYS ILE LYS THR PRO K11 K12 D13 T14 Q16 R15 V20 E21 P22 V29 S30 S31 V32 E33 S37 S38 D39 E40 T41 ASP THR GLU GLY THR GLU GLY THR VAL SER GLY ARG LYS LYS LEU VAL VAL GLU ARG ASP ASP VAL LYS SER LYS ALA SER GLY

ASN GLY SER ALA ARG MET LYS SER PRO SER ILE ARG LYS SER ALA PHE GLY LYS LYS

• Molecule 2: Protein 6.7

Chain 5: 14% 25% 10% 65%

MET CYS PHE SER PRO LYS ILE LYS THR PRO K11 T14 V20 E21 P22 A23 P24 L25 V29 S30 S31 V32 E33 S37 S38 D39 E40 T41 ASP THR GLU GLY THR GLU GLY THR VAL SER GLY ARG LYS LYS LEU VAL VAL GLU ARG ASP ASP VAL LYS SER LYS ALA SER GLY

ASN GLY SER ALA ARG MET LYS SER PRO SER ILE ARG LYS SER ALA PHE GLY LYS LYS

• Molecule 2: Protein 6.7

Chain 6: 11% 24% 11% 65%

MET CYS PHE SER PRO LYS ILE LYS THR PRO K11 K12 T14 Q16 R15 V20 E21 P22 V29 S30 S31 V32 E33 S37 S38 D39 E40 T41 ASP THR GLU GLY THR GLU GLY THR VAL SER GLY ARG LYS LYS LEU VAL VAL GLU ARG ASP ASP VAL LYS SER LYS ALA SER GLY

ASN GLY SER ALA ARG MET LYS SER PRO SER ILE ARG LYS SER ALA PHE GLY LYS LYS

• Molecule 2: Protein 6.7

Chain 7: 11% 26% 9% 65%

MET CYS PHE SER PRO LYS ILE LYS THR PRO K11 T14 I17 V20 E21 P22 A23 P24 L25 V29 S30 S31 V32 E33 S37 S38 D39 E40 T41 ASP THR GLU GLY THR GLU GLY THR VAL SER GLY ARG LYS LYS LEU VAL VAL GLU ARG ASP ASP VAL LYS SER LYS ALA SER GLY

SER
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ALA
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PRO
SER
SER
SER
ILE
ARG
LYS
ALA
ALA
PHE
GLY
GLY
LYS
LYS

• Molecule 2: Protein 6.7



MET CYS PHE SER PRO LYS ILE THR PRO K11 I17 V20 E21 P22 L25 V29 V32 E33 D39 E40 T41 D42 T43 E44 G45 T46 E47 L54 K56 V56 E57 R58 D59 ASP SER VAL ALA LYS SER LYS ALA SER LYS ALA SER ASN GLY GLY ALA ARG MET LYS SER SER

ILE
ARG
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SER
ALA
PHE
GLY
GLY
LYS
LYS

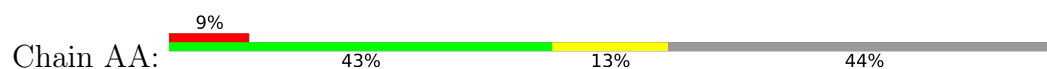
• Molecule 2: Protein 6.7



MET CYS PHE SER PRO LYS ILE THR PRO K11 M12 D13 Q16 I17 V20 E21 P22 Q27 V32 E33 G36 D39 E40 T41 D42 T43 E44 G45 L54 K55 D59 ASP SER VAL ALA LYS SER LYS ALA SER LYS ALA SER ASN GLY GLY ALA ARG MET LYS SER SER ILE

ARG
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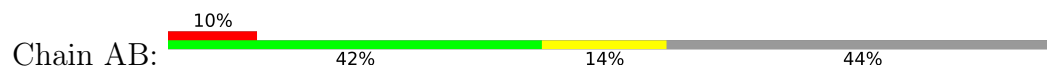
• Molecule 2: Protein 6.7



MET CYS PHE SER PRO LYS ILE THR PRO K11 M12 D13 I17 E21 S30 S31 V32 E33 D39 E40 T41 D42 T43 E44 G45 T46 E47 K52 K55 D59 ASP SER VAL ALA LYS SER LYS ALA SER LYS ALA SER ASN GLY GLY ALA ARG MET LYS SER SER ILE LYS

SER
ALA
PHE
GLY
GLY
LYS
LYS

• Molecule 2: Protein 6.7



MET CYS PHE SER PRO LYS ILE THR PRO K11 M12 D13 Q16 E21 P22 L25 V29 V32 E33 G36 D39 E40 T41 D42 T43 E44 G45 L54 R58 D59 ASP SER VAL ALA LYS SER LYS ALA SER LYS ALA SER ASN GLY GLY ALA ARG MET LYS SER SER ILE

ARG
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LYS
LYS

• Molecule 2: Protein 6.7



MET CYS PHE SER PRO LYS ILE THR PRO K11 T14 I17 V20 V32 E33 D39 E40 T41 D42 T43 E44 G45 T46 E47 L54 K55 D59 ASP SER VAL ALA LYS SER LYS ALA SER LYS ALA SER ASN GLY GLY ALA ARG MET LYS SER SER ILE ARG MET LYS SER SER ALA PHE

GLY
GLY
LYS
LYS

• Molecule 2: Protein 6.7



MET CYS PHE SER PRO LYS ILE THR LYS PRO K11 K12 D13 Q16 I17 V20 E21 P22 V32 E33 D39 E40 T41 T42 T43 T44 E45 T46 K52 K55 R53 D59 ASP SER VAL ALA LYS SER LYS LYS ALA SER SER ASN GLY SER ALA ARG MET LYS SER SER SER ILE ARG

LYS SER ALA PHE GLY GLY LYS LYS

• Molecule 3: Portal protein



MET ALA GLU LYS ARG T6 G7 E10 D11 K14 S15 V16 Y17 E18 R19 K21 K22 D23 R24 T38 L42 S47 D48 T52 Q55 W58 Q59 A60 L66 N67 N68 L75 A76 L77 F78 P79 M80 Q81 L86 T87 I88 S89 E90 Y91 E92 A93 K94 Q95

L96 L97 S98 D99 P100 D101 G102 L103 K105 V106 D107 E108 L110 L111 S112 M113 E114 R115 I116 I117 M118 N119 Y120 I121 E122 V128 T129 L130 L134 V138 V139 L144 L145 Y146 L147 E151 G152 S153 N154 Y155 M158 Y159 L160 Y161 R162 L163 S164 V168 Q169 R170

F173 G174 N175 M179 Q184 I185 A186 F187 G188 A189 L190 P191 E192 D193 I194 R195 K196 E199 G200 Q201 G202 G203 E204 K205 D208 E209 T210 I211 D212 V213 Y214 Y215 H216 L219 D220 E221 D222 S223 G224 E225 Y226 L227 R228 Y229 E230 E231 V232 E233 G234 M235 E236 V237 Q238 G239

S240 T243 Y244 P245 K246 E247 A248 Y251 M256 V257 L259 D260 S263 Y264 G265 R266 T269 Y272 L273 G274 D275 L279 L282 Q283 E284 K288 M289 S290 Y296 L299 V300 N301 P302 I305 P308 L311 A314 Q315 T316 G317 D318 F319 V320

R323 I327 S328 I348 R351 F354 A355 F356 M357 L358 A361 V362 Q363 R364 T365 G366 E367 R368 V369 T370 A371 E372 E373 I374 R375 A378 S379 E380 D383 V388 Y389 S390 I391 L392 S393 Q394 E395 L396 Q397 L398 P399 L400 V401 R402 Y403 L404 L405 K406 Q407 L408 Q409 A410

T411 Q412 Q413 I414 P415 E416 L417 P418 K419 E420 A421 V422 E423 P424 T425 I426 S427 T428 G429 L430 E431 A432 I433 G434 ARG GLY ASP ASN GLN ALA LEU ASP LYS LEU ALA GLN GLY MET CYS VAL THR ALA GLN TRP ALA ALA THR ALA LEU ALA SER PRO GLU MET ARG ASP MET ALA ASP ASN ILE LEU ALA MET ILE LYS LEU ARG ILE

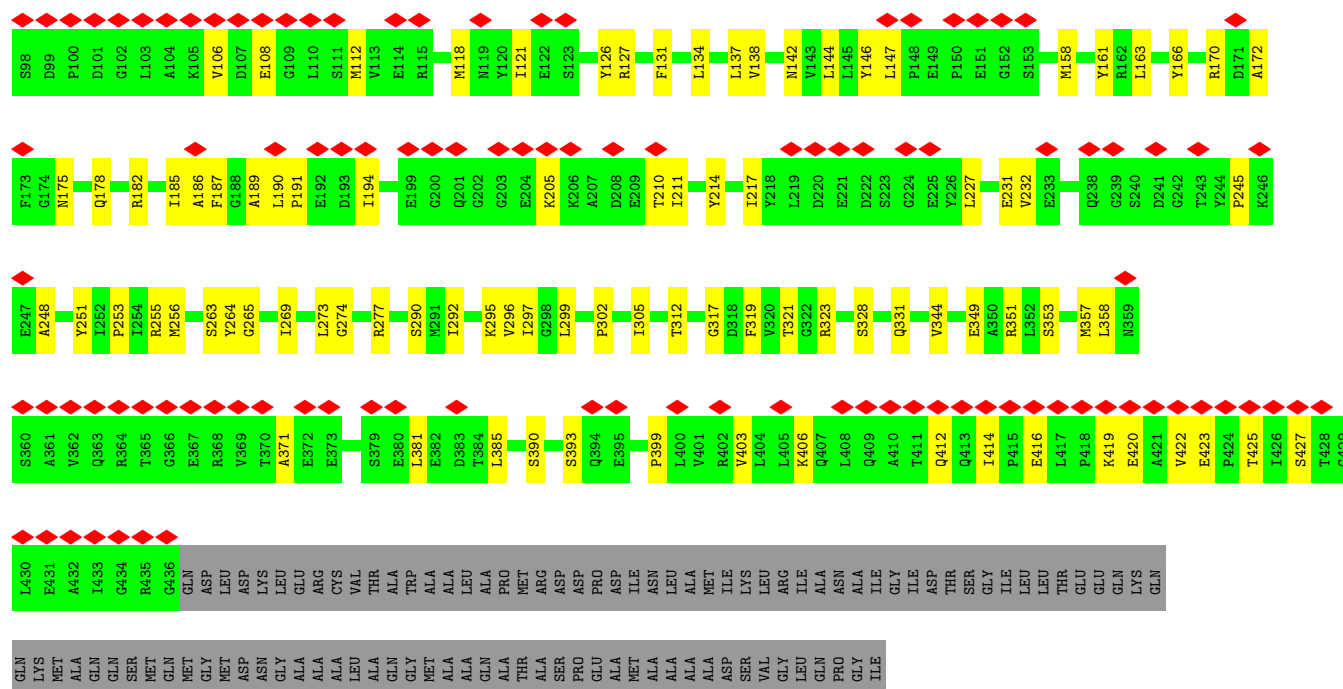
ALA ASN ALA ILE GLY ASP THR SER ILE LEU LEU THR GLU GLN LYS GLN GLN LYS MET MET GLY MET ASP ASN GLY ALA ALA LEU LEU ALA GLN GLY MET VAL ALA GLN TRP ALA ALA THR ALA SER PRO GLU MET ARG ASP MET ALA ASP ASN ILE LEU ALA MET ILE LYS LEU ARG ILE

GLY LEU GLN PRO GLY ILE

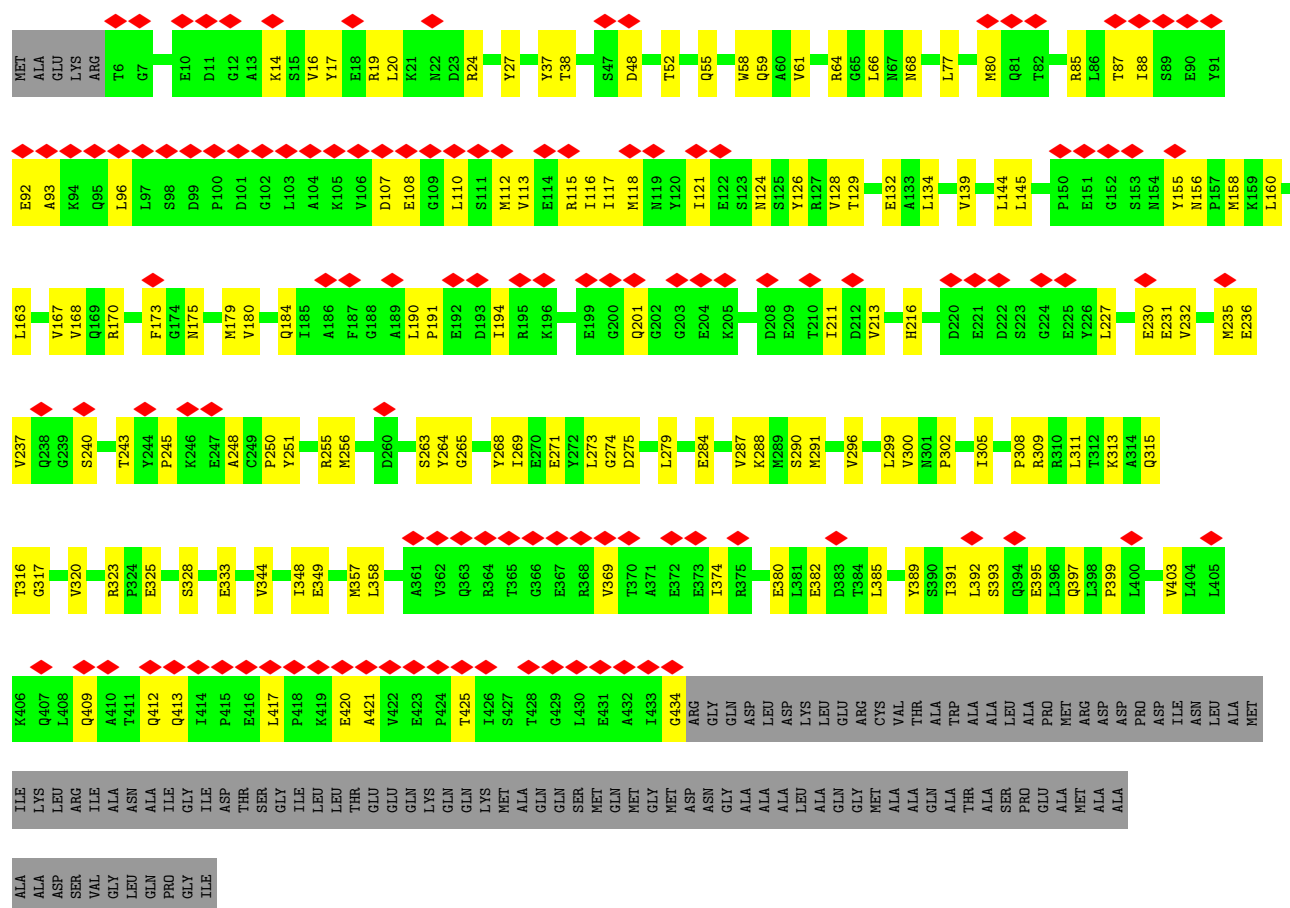
• Molecule 3: Portal protein



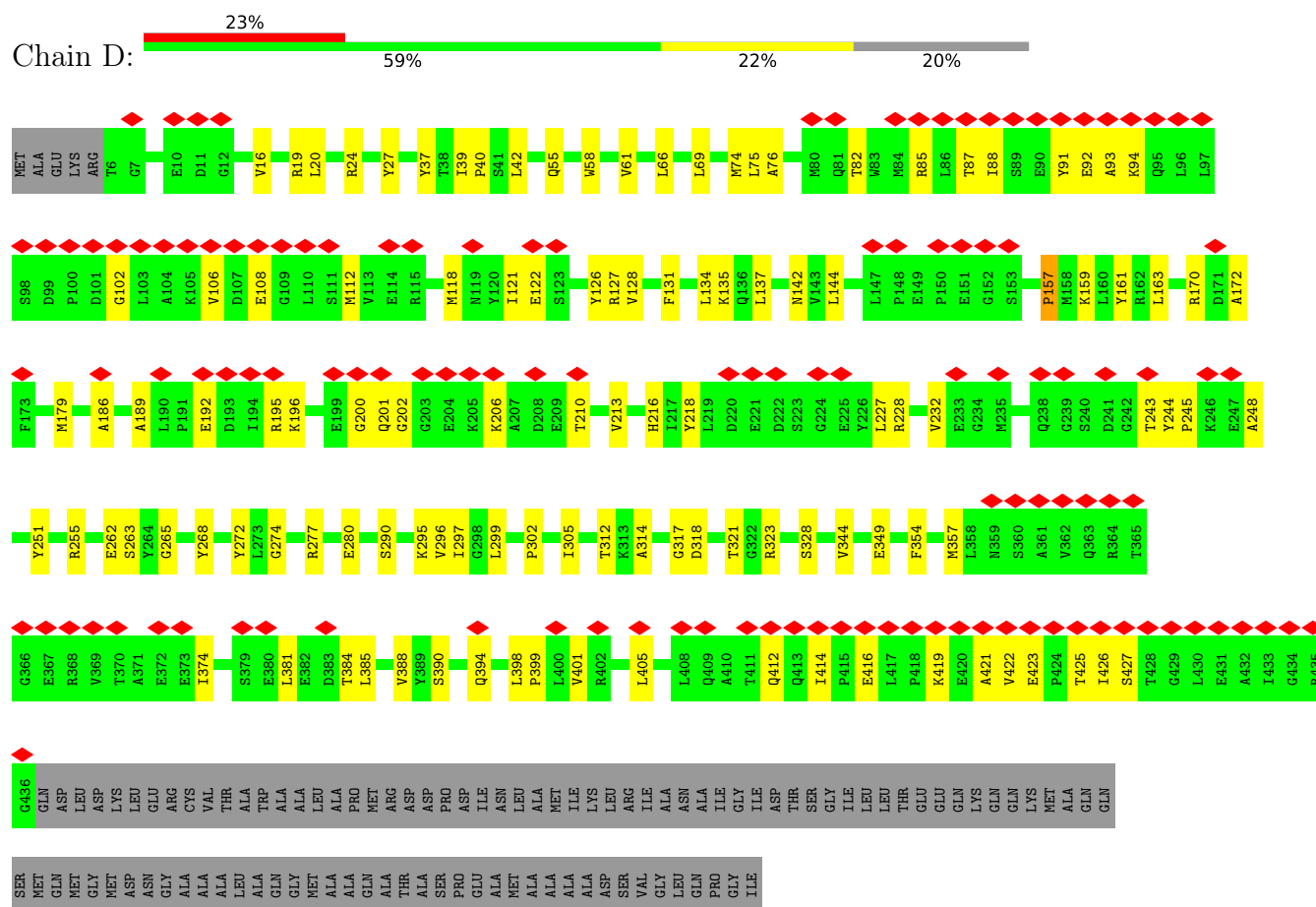
MET ALA GLU LYS ARG T6 G7 L8 A9 E10 D11 G12 G13 K14 S15 V16 R19 R24 Y27 C34 T38 I39 D48 T52 W58 V61 N68 L69 L73 M74 M80 Q81 T82 T83 M84 M85 L86 T87 I88 S89 E90 Y91 E92 A93 Q95 L96 L97



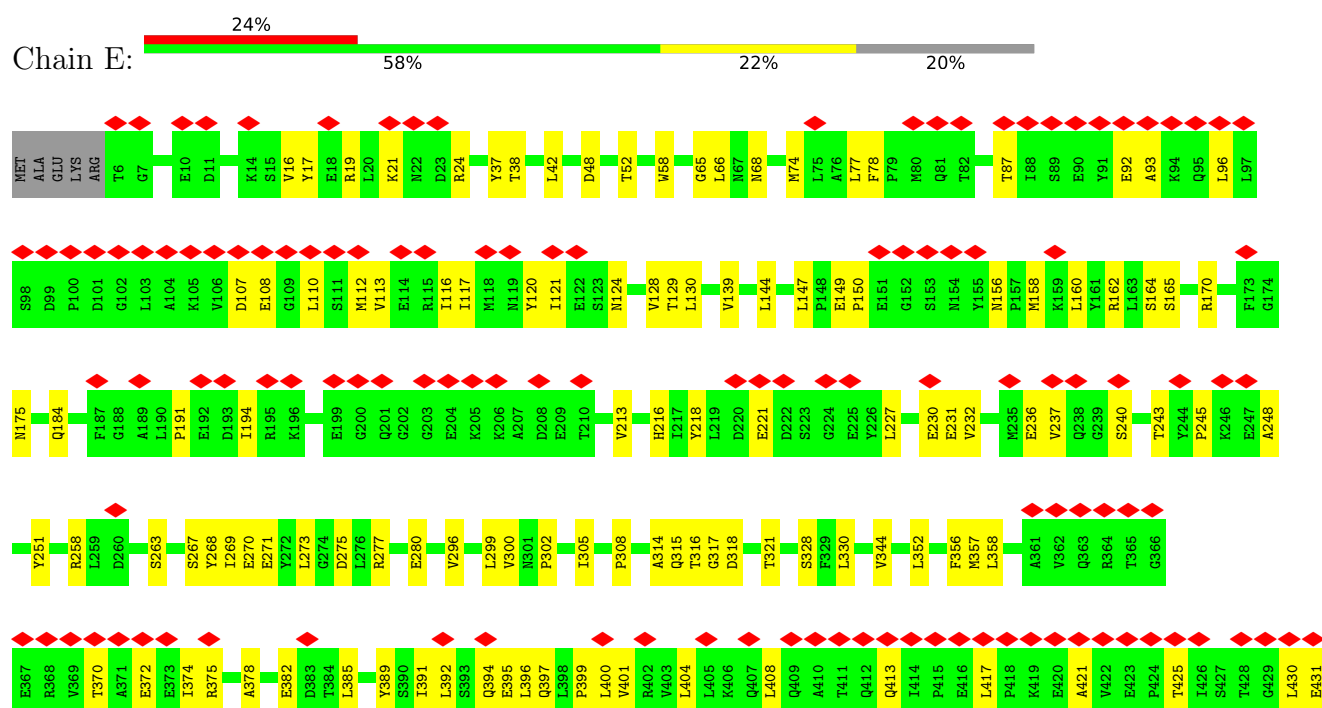
• Molecule 3: Portal protein

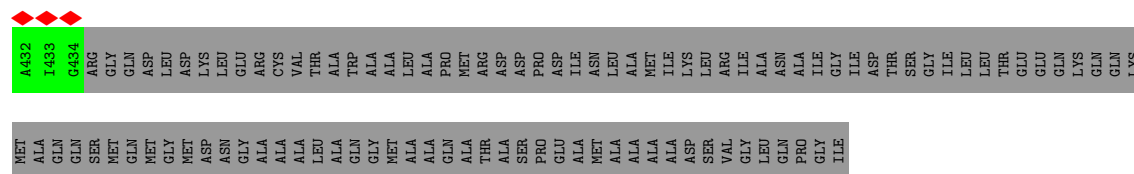


- Molecule 3: Portal protein

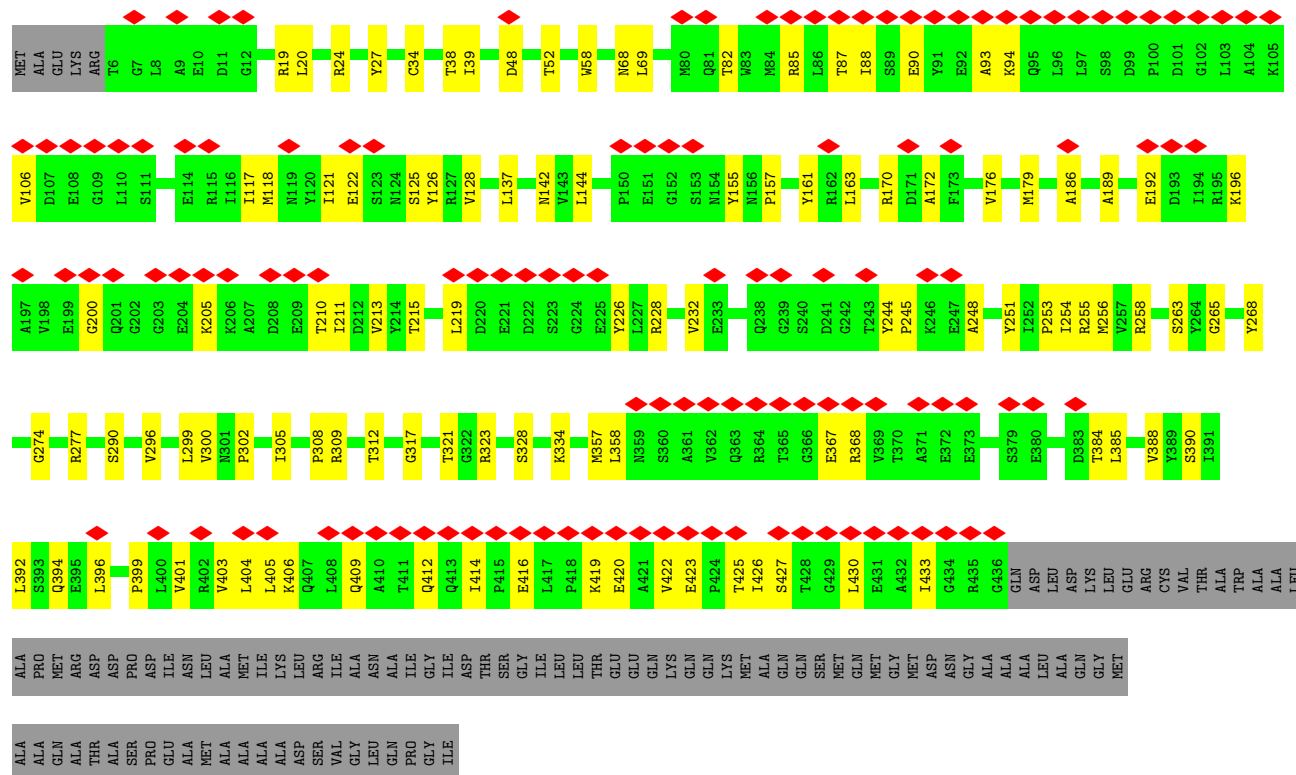


- Molecule 3: Portal protein

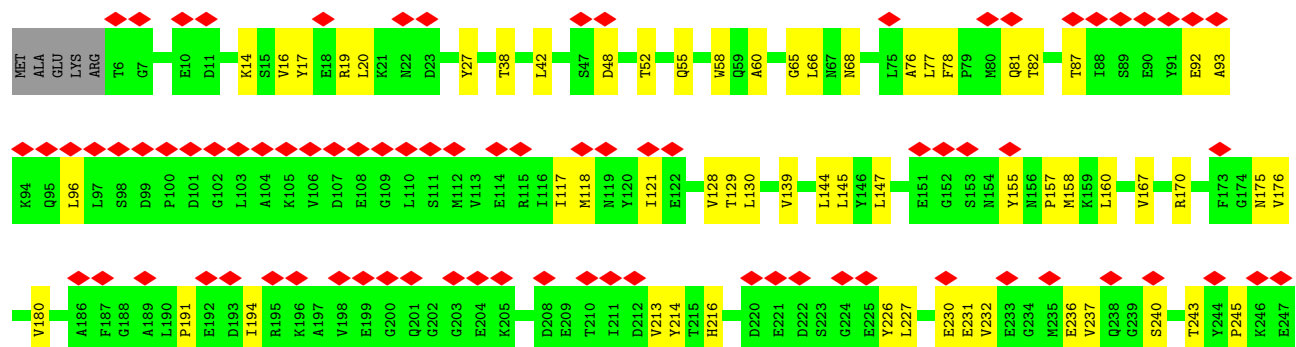


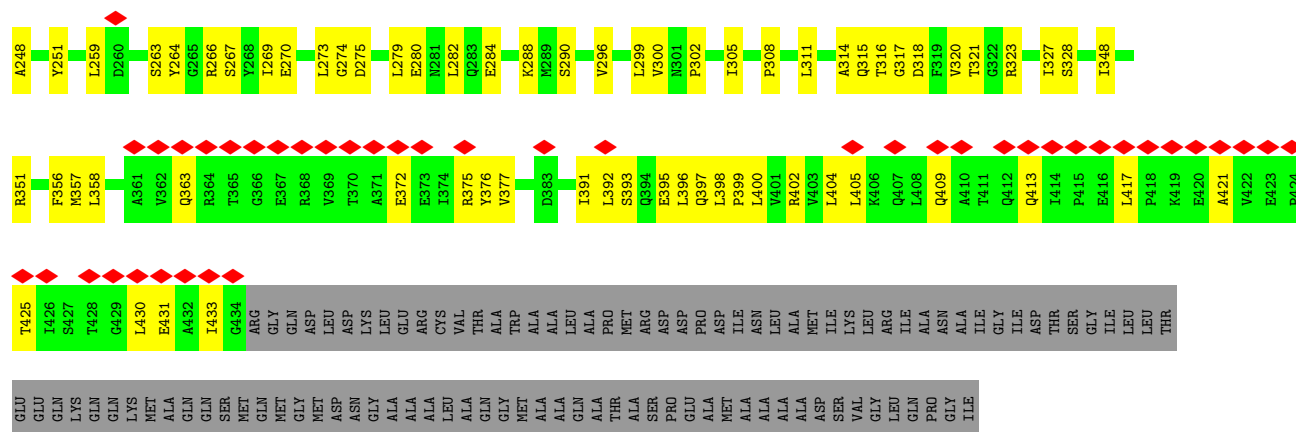


• Molecule 3: Portal protein

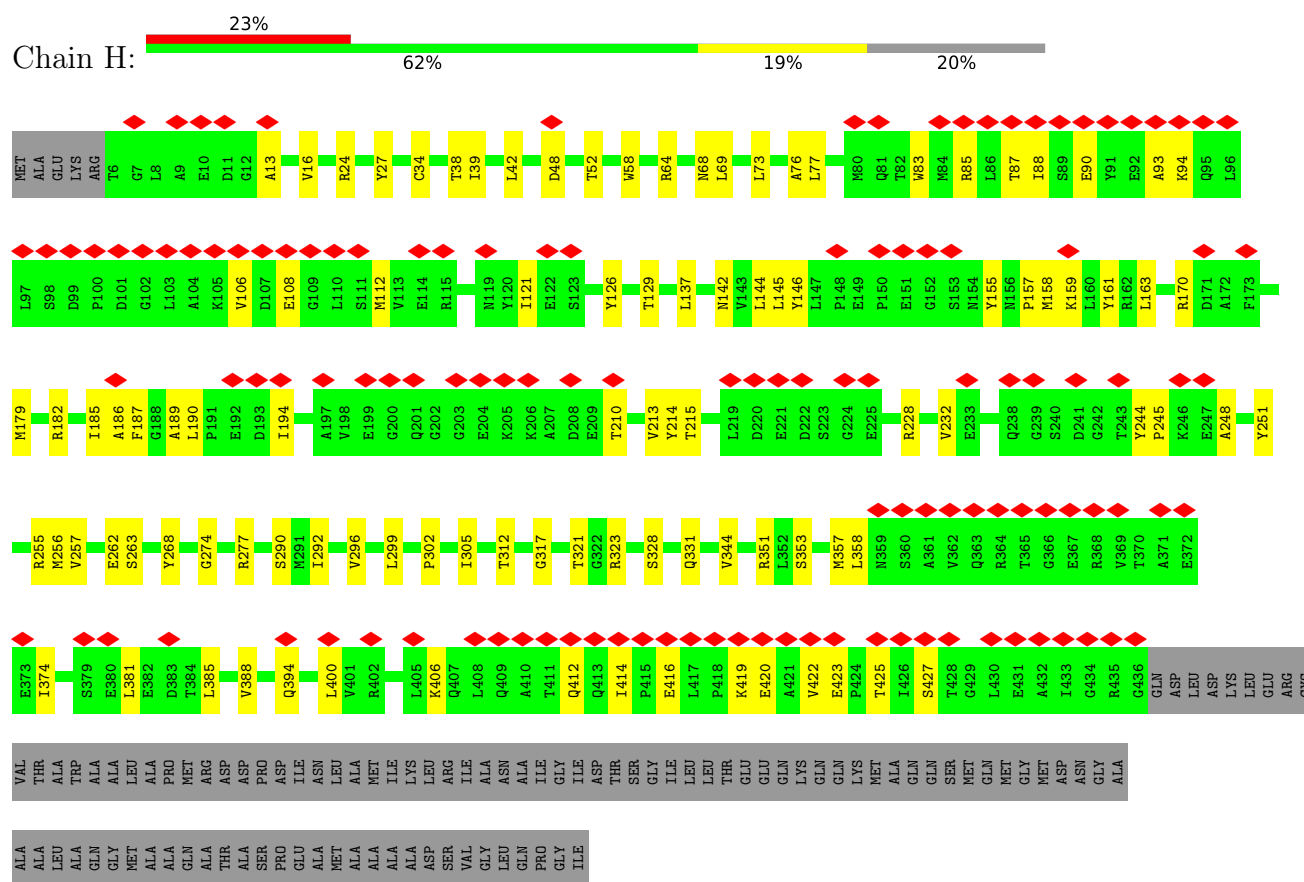


• Molecule 3: Portal protein

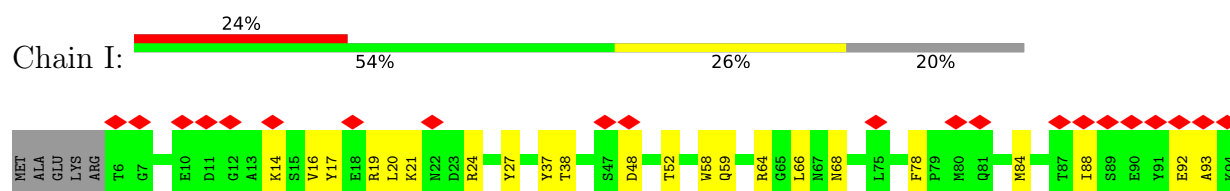


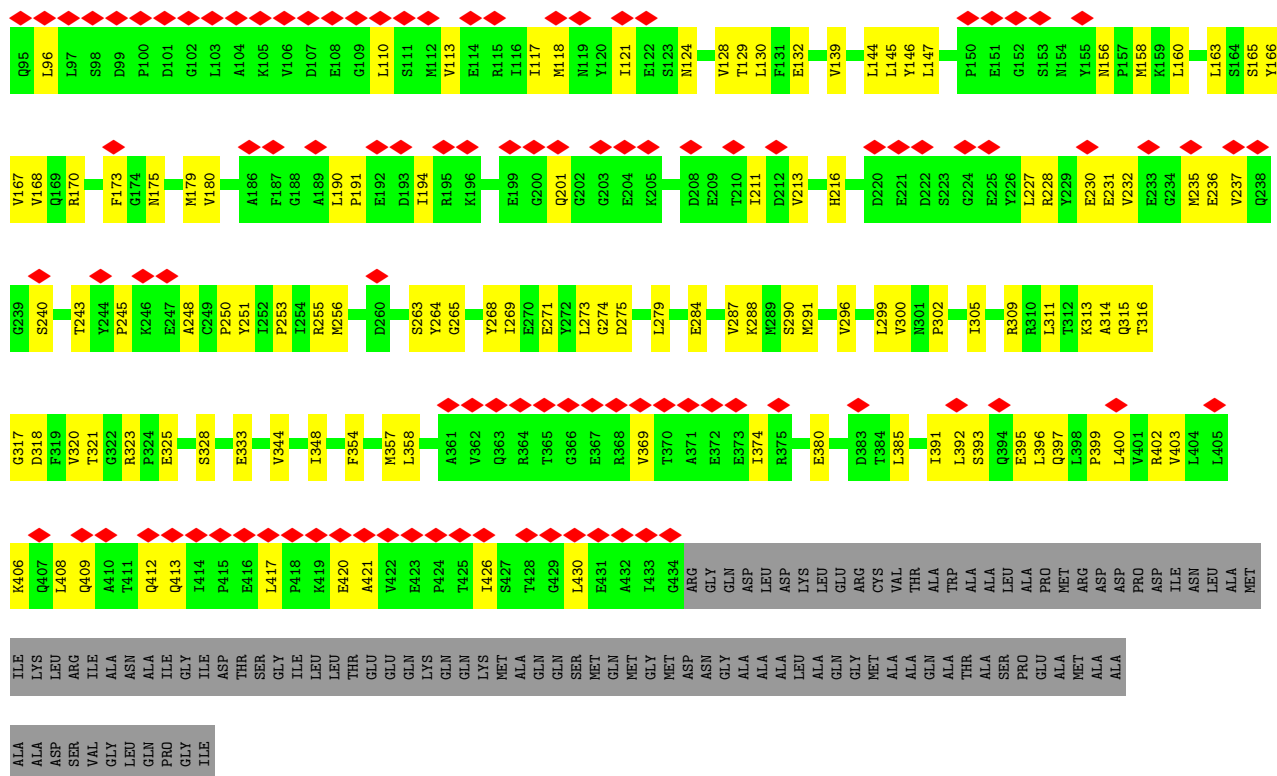


• Molecule 3: Portal protein

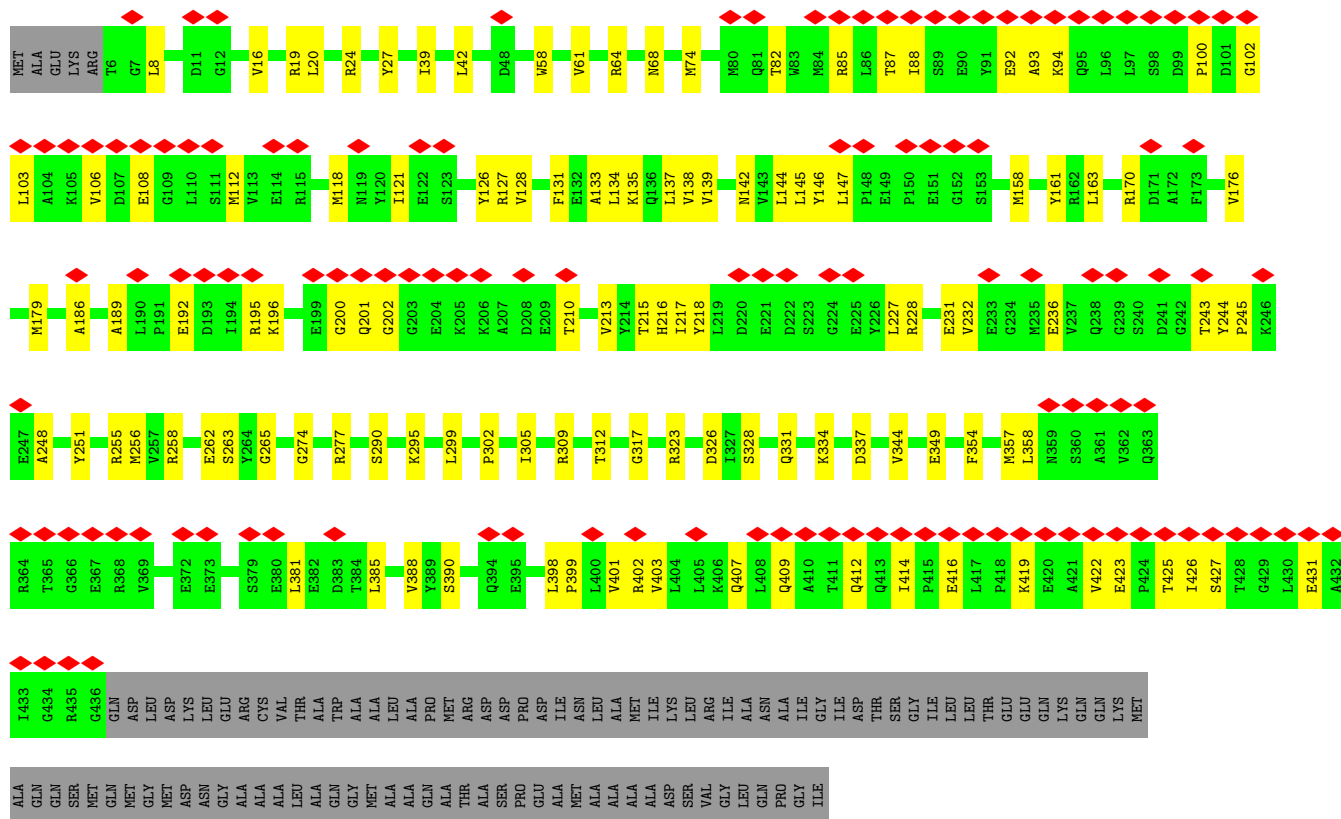


• Molecule 3: Portal protein

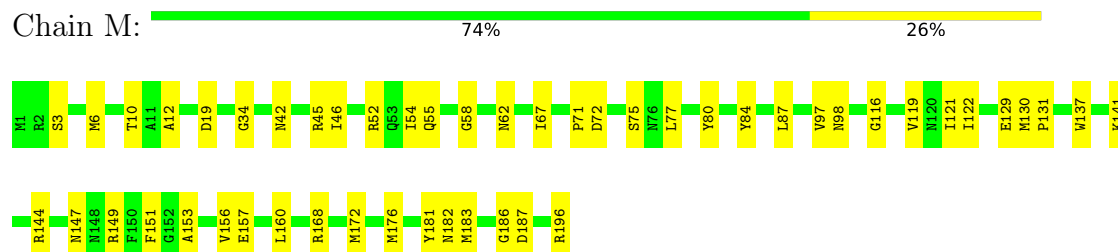




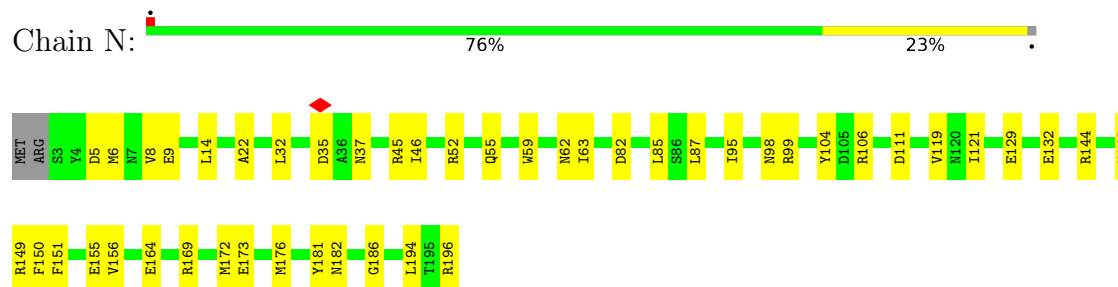
• Molecule 3: Portal protein



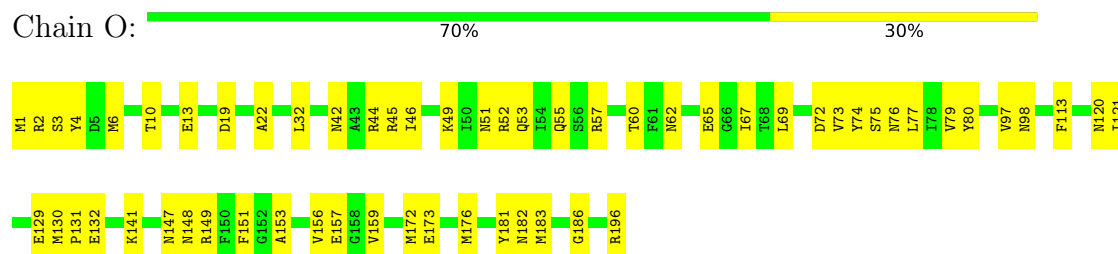
- Molecule 4: Tail tubular protein gp11



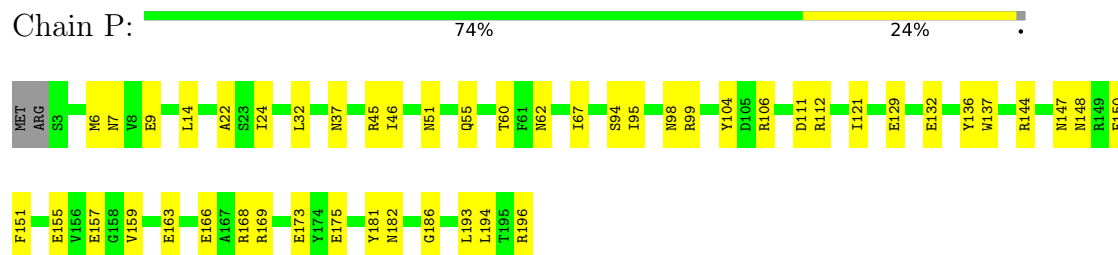
- Molecule 4: Tail tubular protein gp11



- Molecule 4: Tail tubular protein gp11

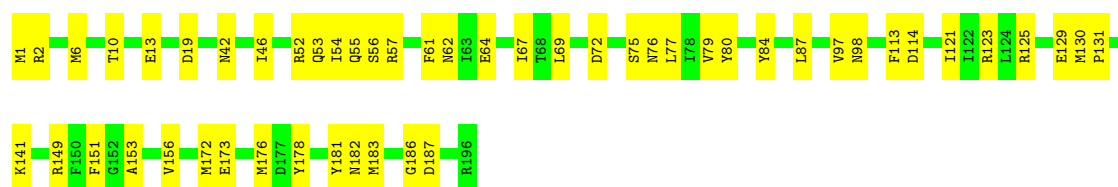


- Molecule 4: Tail tubular protein gp11



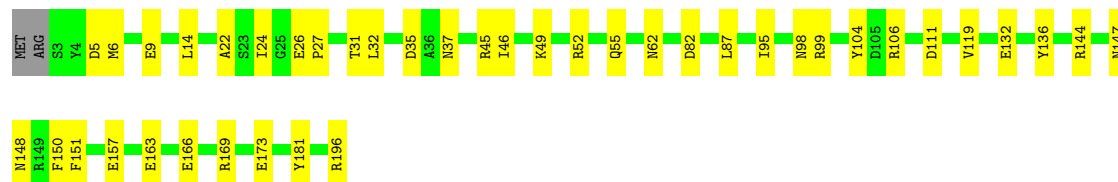
- Molecule 4: Tail tubular protein gp11





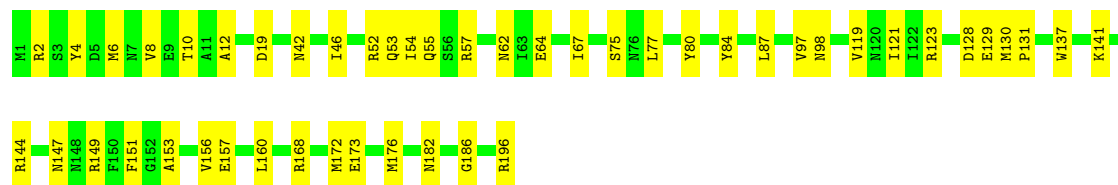
- Molecule 4: Tail tubular protein gp11

Chain R: 78% 21%



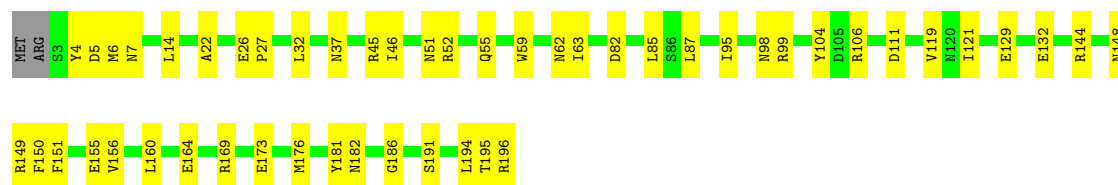
- Molecule 4: Tail tubular protein gp11

Chain S: 76% 24%



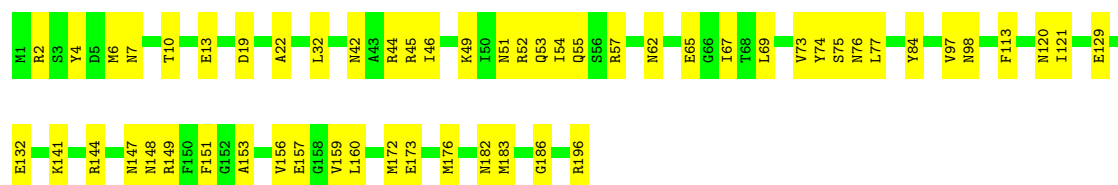
- Molecule 4: Tail tubular protein gp11

Chain T: 73% 26%



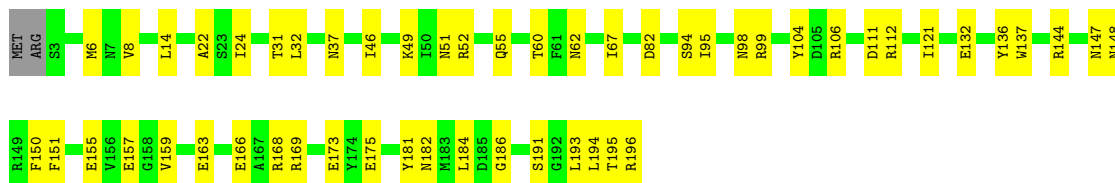
- Molecule 4: Tail tubular protein gp11

Chain U: 72% 28%

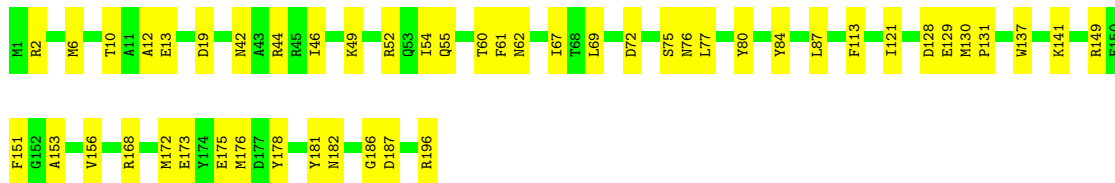
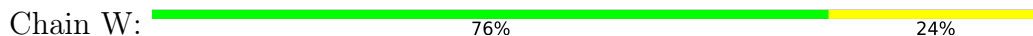


- Molecule 4: Tail tubular protein gp11

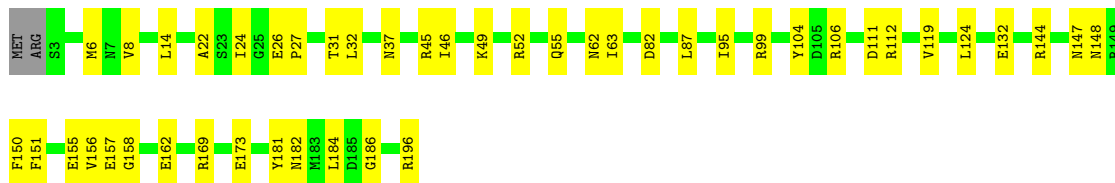
Chain V: 72% 27%



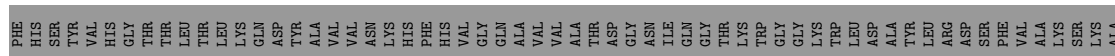
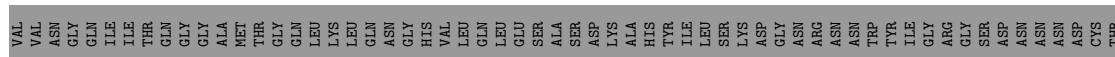
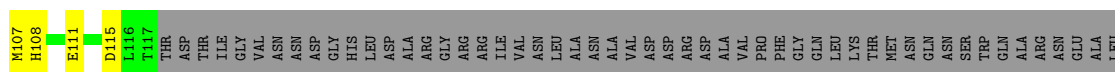
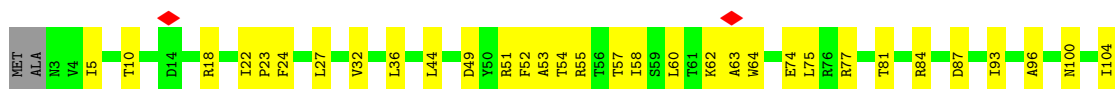
- Molecule 4: Tail tubular protein gp11



- Molecule 4: Tail tubular protein gp11



- Molecule 5: Tail fiber protein



- Molecule 5: Tail fiber protein

- Molecule 5: Tail fiber protein



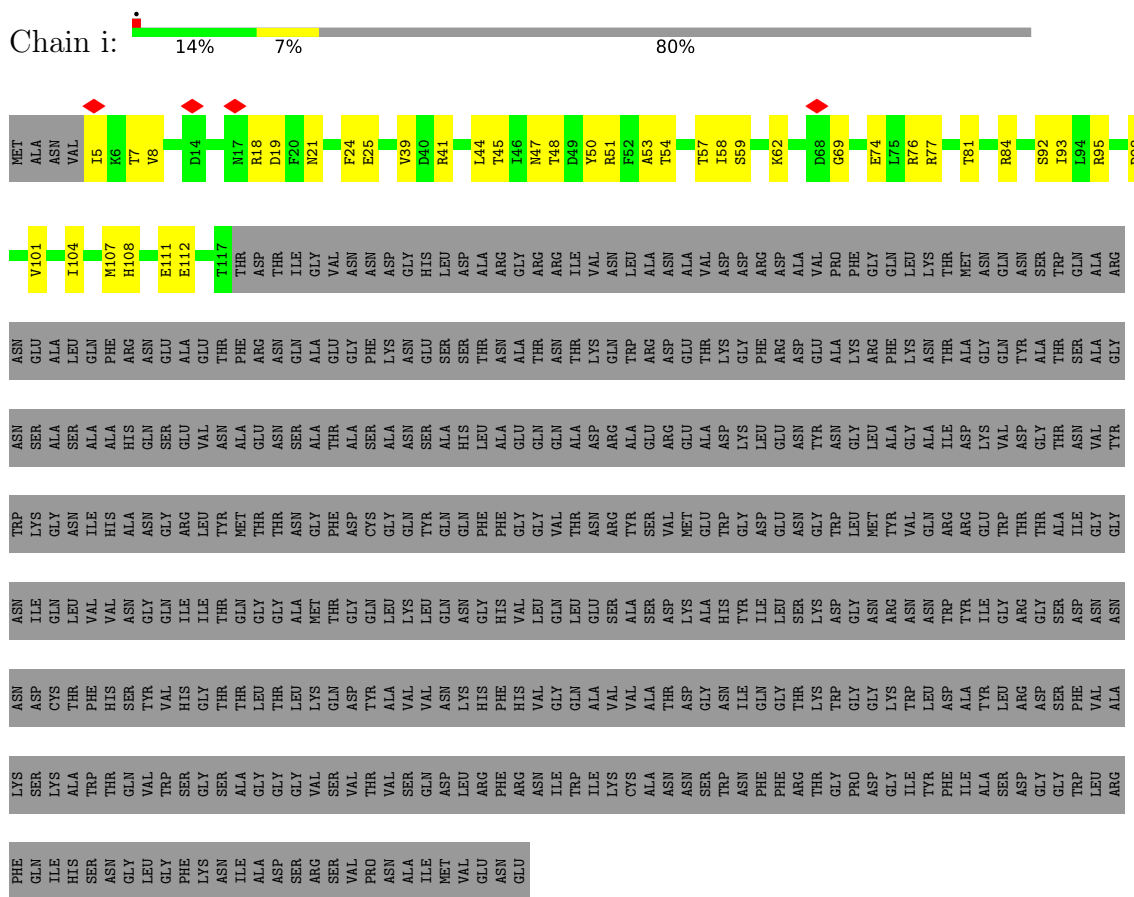




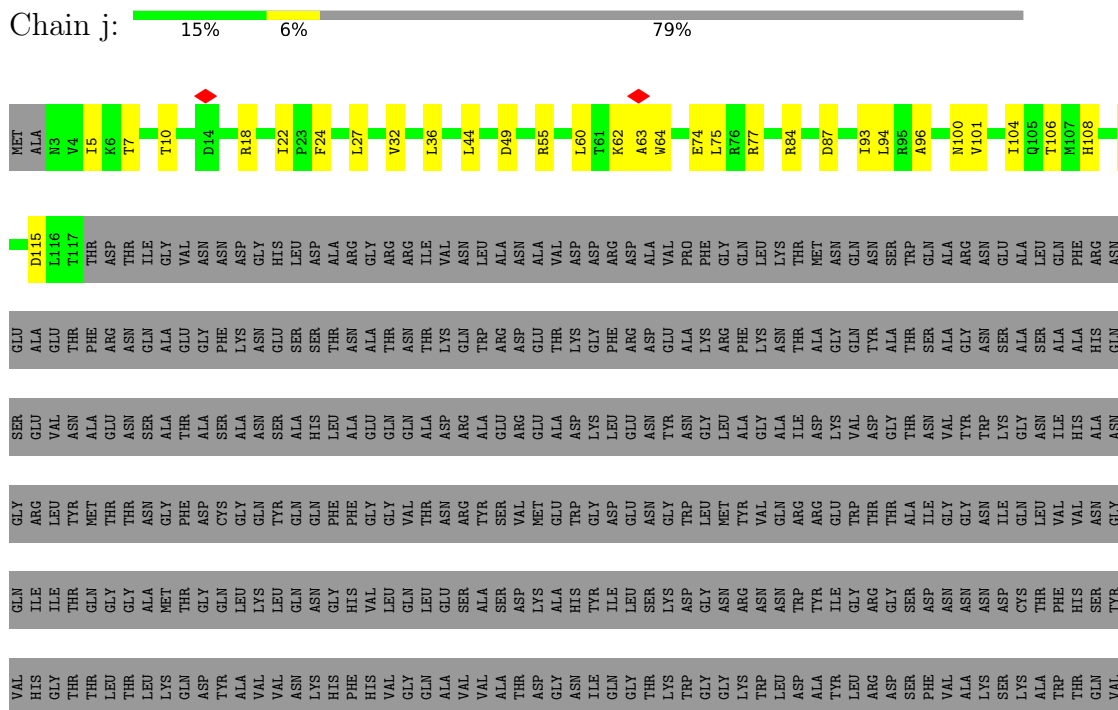
- Molecule 5: Tail fiber protein

[illegible]

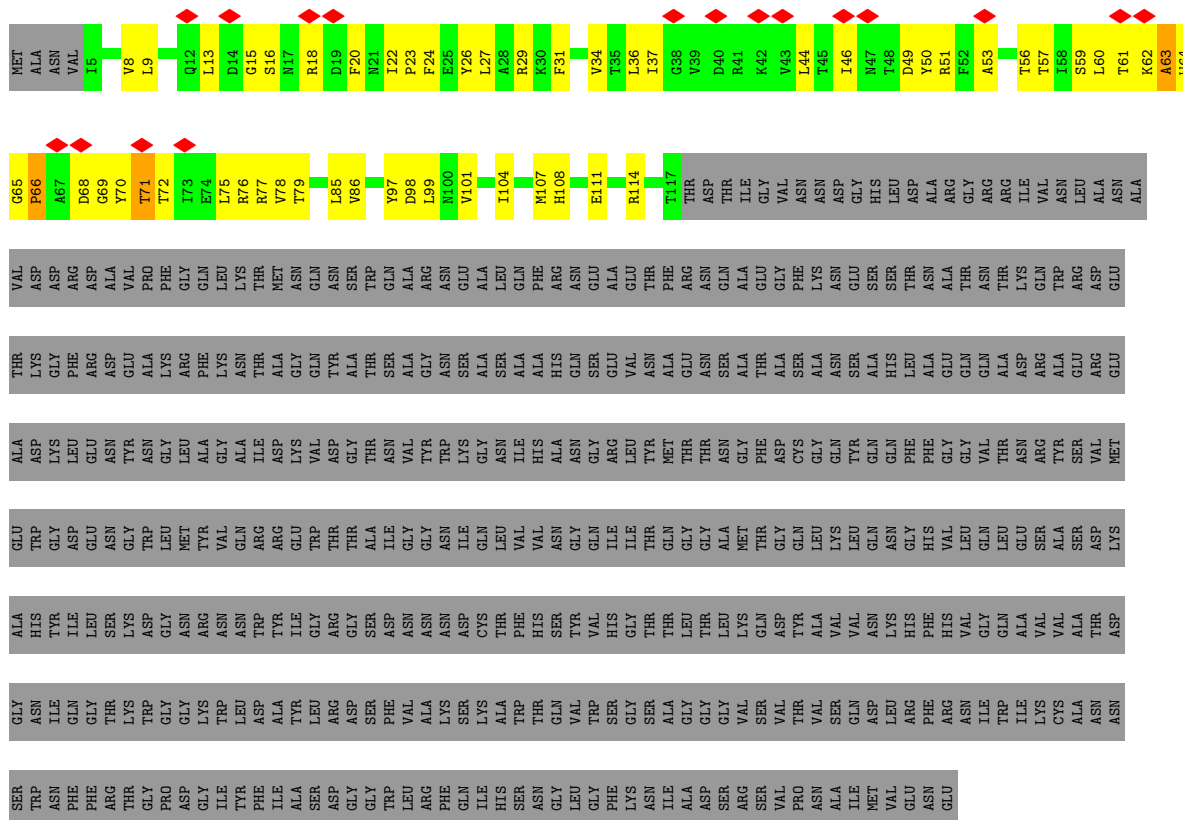
- Molecule 5: Tail fiber protein



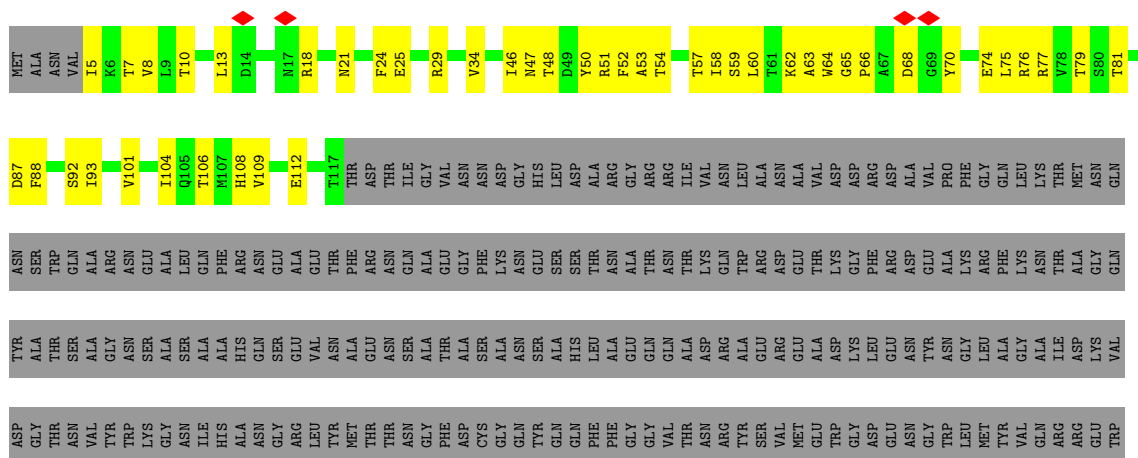
- Molecule 5: Tail fiber protein

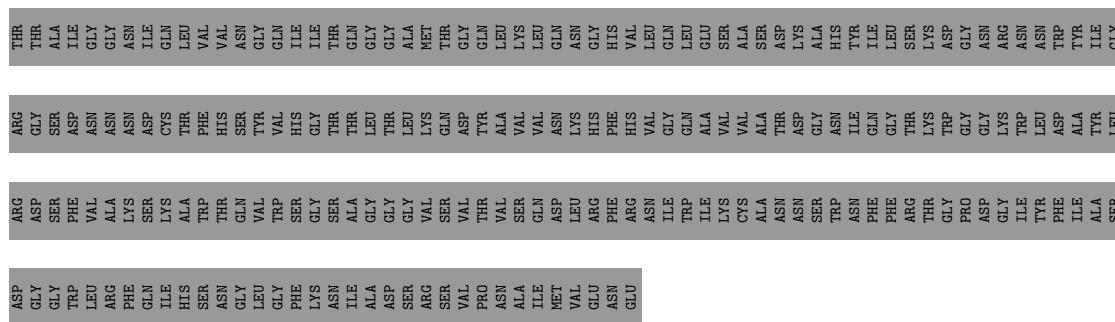


- Molecule 5: Tail fiber protein

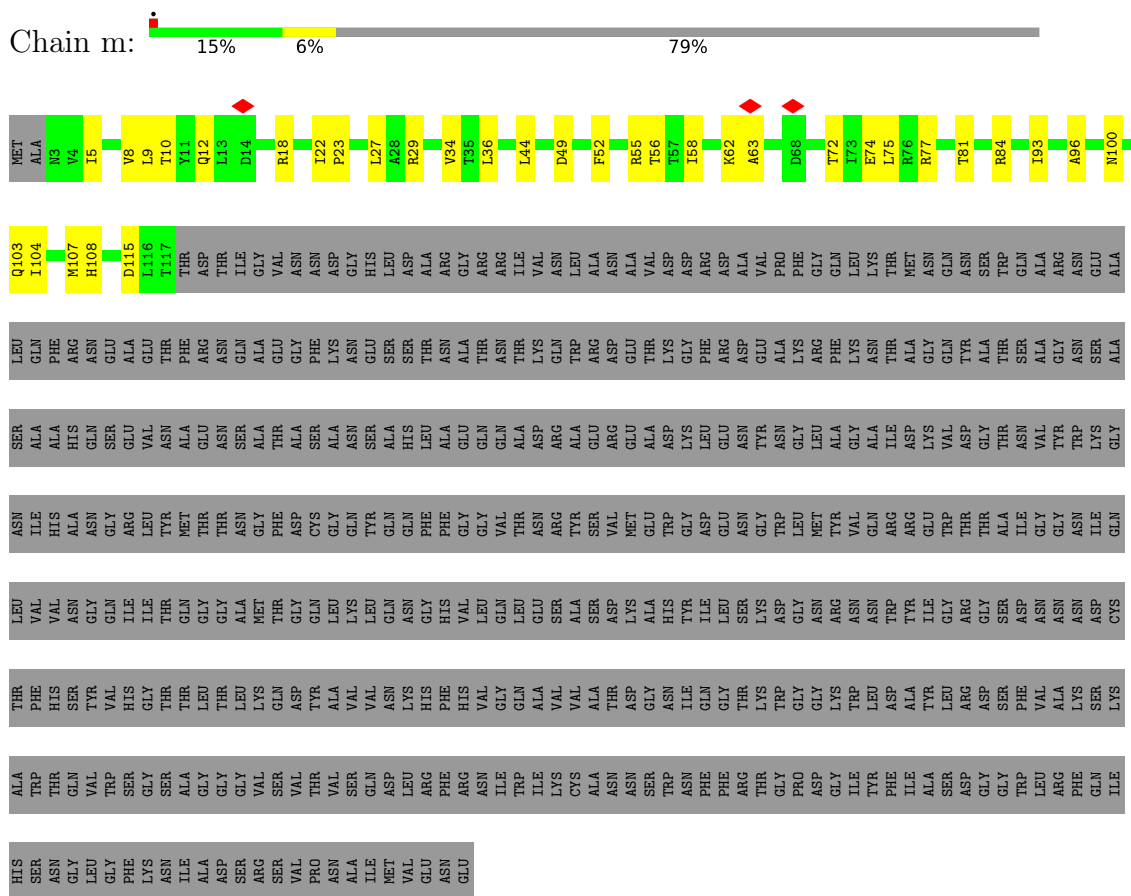


- Molecule 5: Tail fiber protein

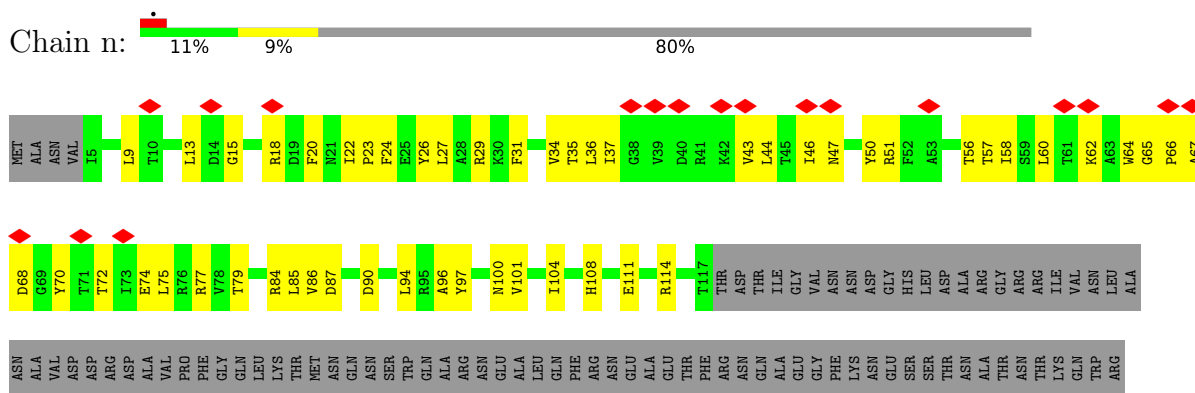




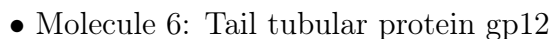
- Molecule 5: Tail fiber protein

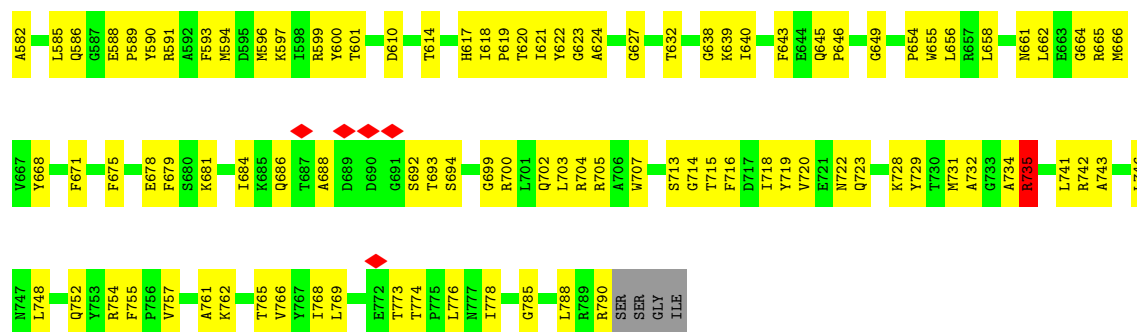


- Molecule 5: Tail fiber protein

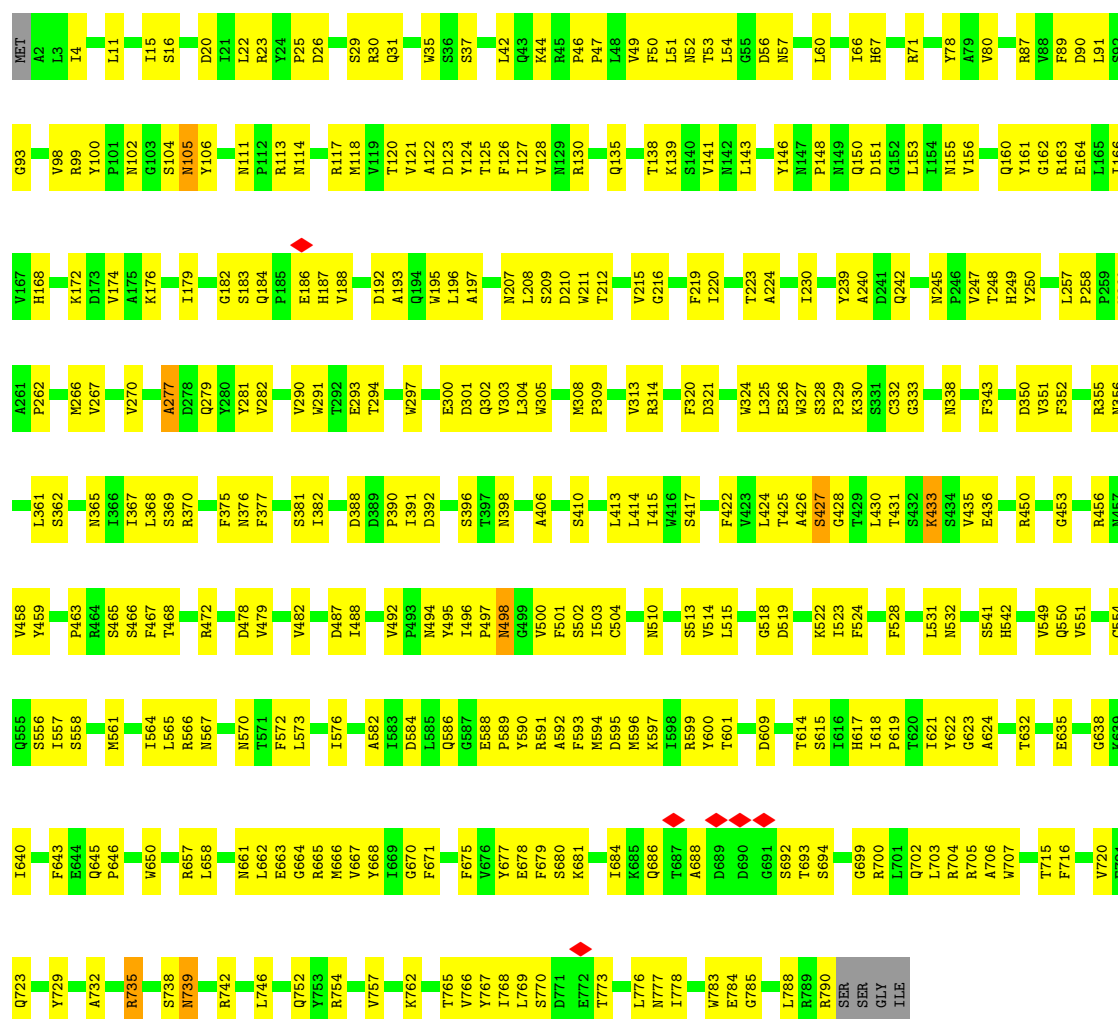


MET	ALA	N3	V4	I5	T10	L13	D14	N17	R18	N21	I22	P23	F24	L27	A28	R29	V32	L36	L44	D49	W64	G65	Y70	E74	L75	R76	R77	T81	I93	L94	R95	A96	N100	I104	G105	T106	M107	H108	V109	A110	E111
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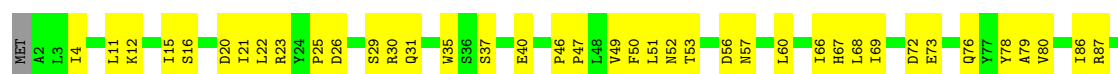


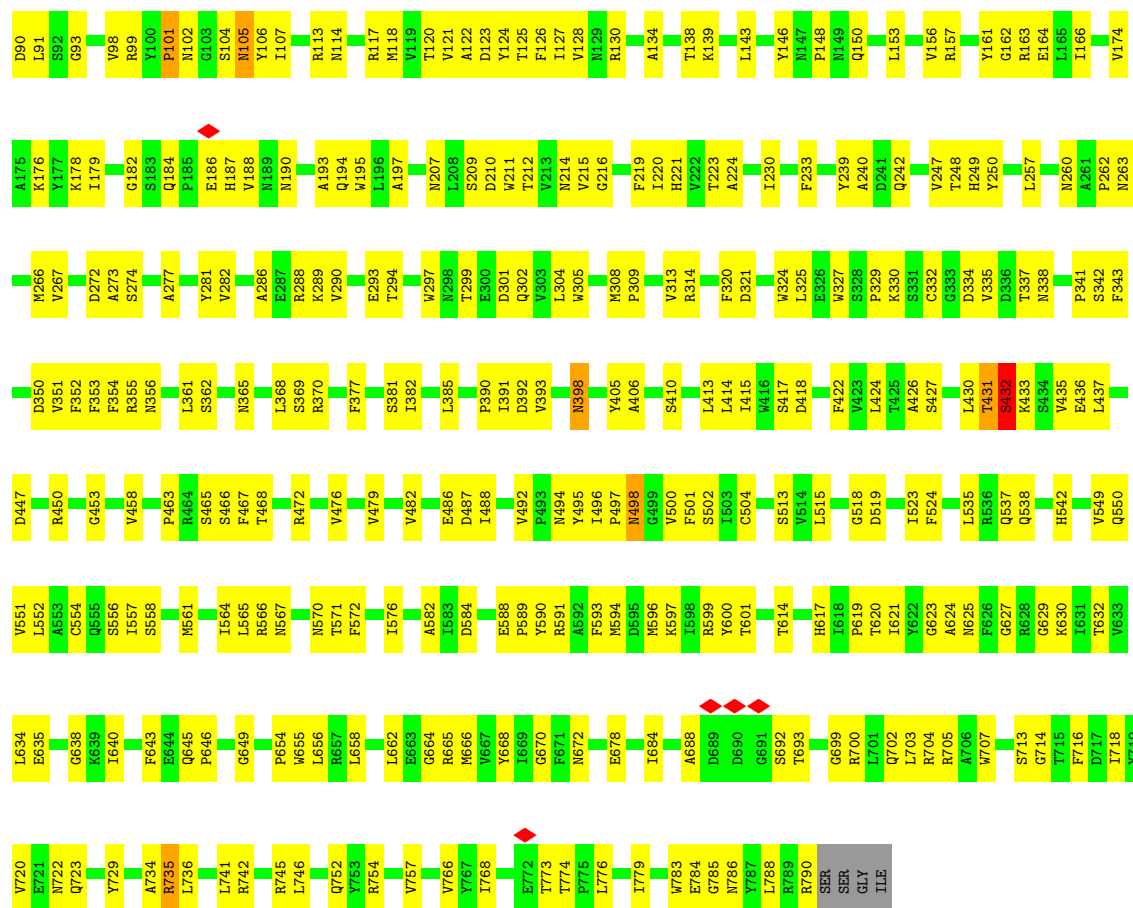


• Molecule 6: Tail tubular protein gp12

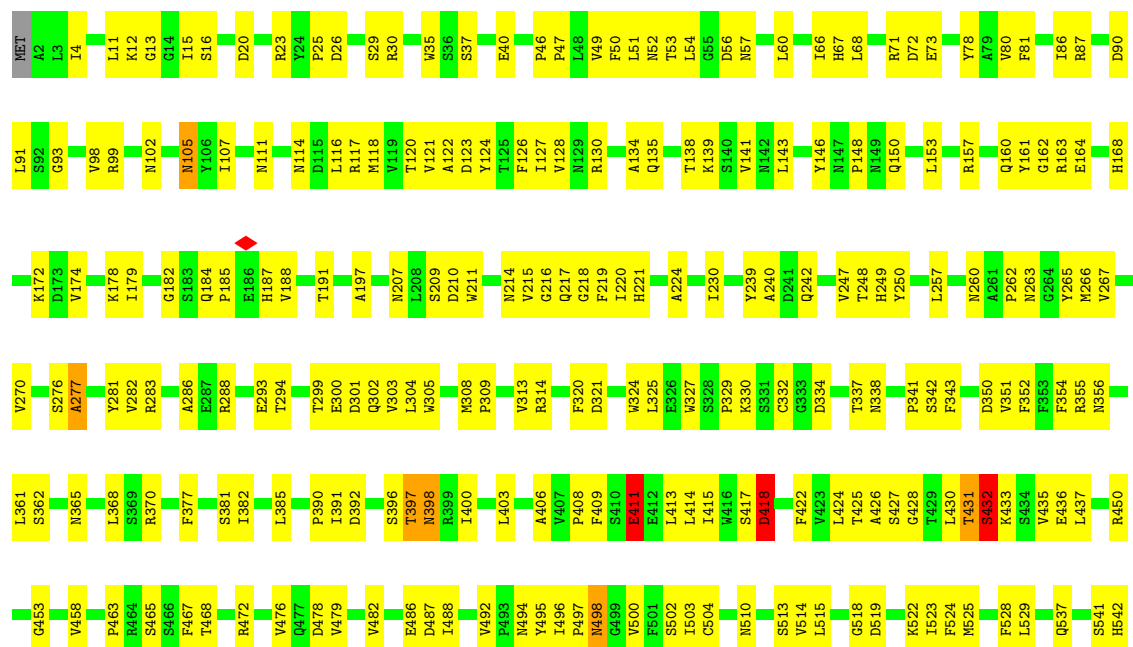


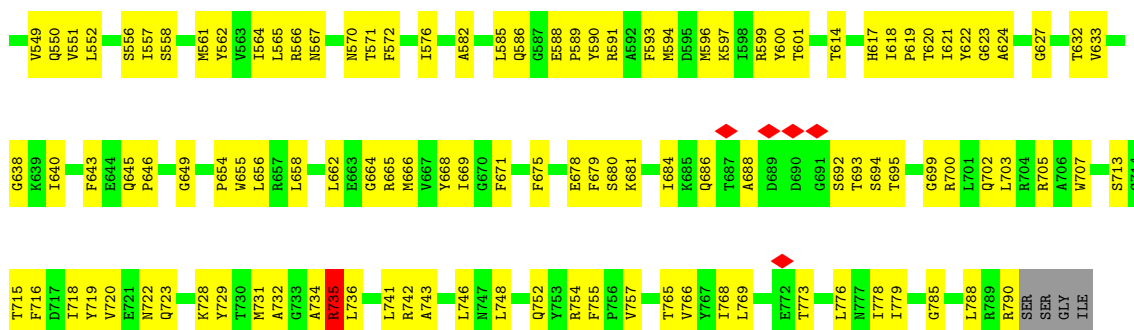
• Molecule 6: Tail tubular protein gp12



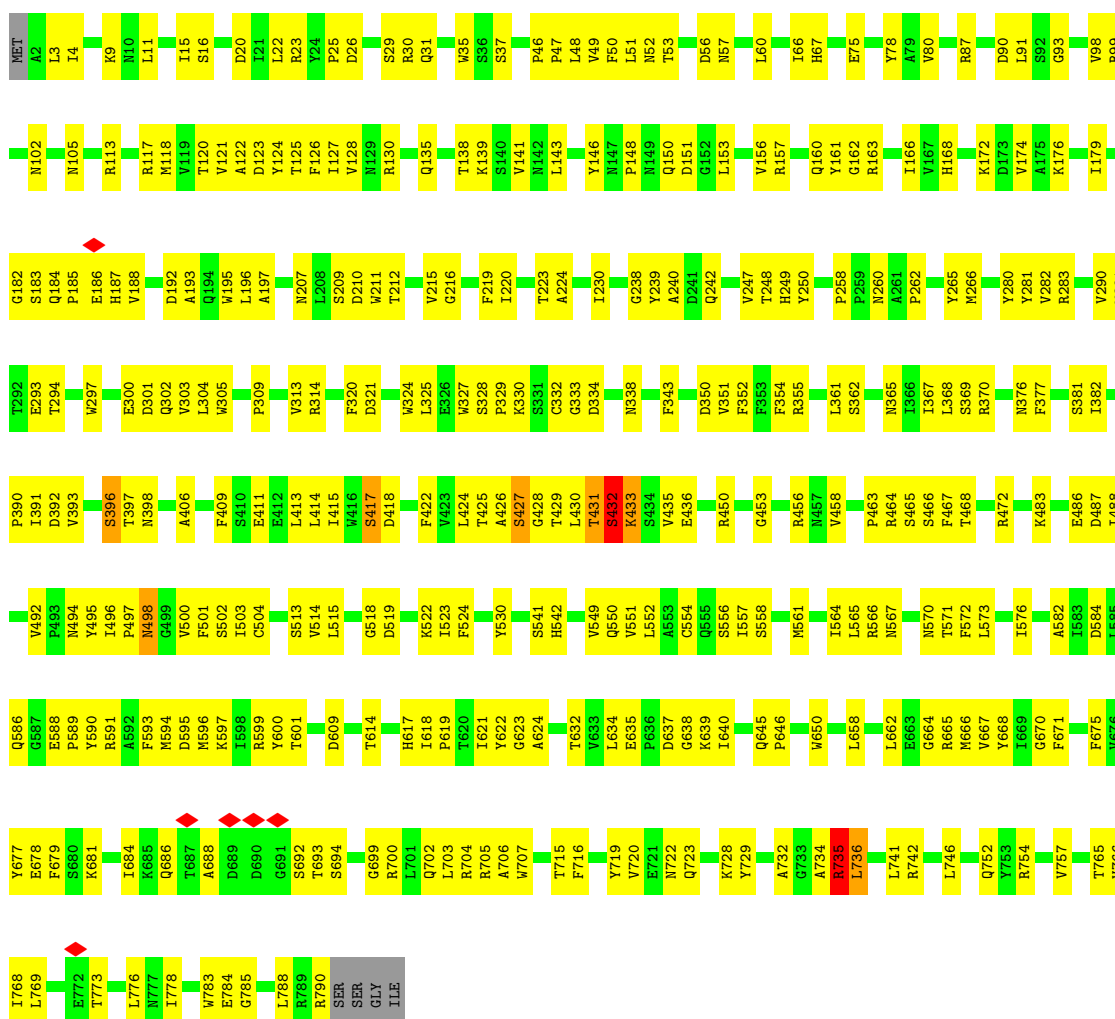


• Molecule 6: Tail tubular protein gp12





• Molecule 6: Tail tubular protein gp12



• Molecule 6: Tail tubular protein gp12



Y719	W720	E721	N722	Q723	Y729	A734	R735	L736	G737	W738	N739	T740	L741	R742	R745	L746	Q752	Y753	R754	V757	T765	V766	Y767	I768	L769	S770	D771	E772	T773	T774	P775	L776	N777	I778	I779	W783	E784	G785	L788	R789	SER	SER	GLY	ILE							
G638	K639	V551	L552	A653	G554	Q645	P646	G649	P654	W655	L656	R657	L658	L662	E663	G664	R665	Y668	F671	F675	V676	Y677	E678	K681	I684	T687	A688	D689	D690	S692	T693	S694	T695	G699	R700	L701	Q702	L703	R704	R705	A706	W707	G714	T715	F716	D717	I718				
Q550	V435	E436	L437	T441	D447	R450	G453	V458	P463	R464	S465	S466	F467	T468	R472	V476	E486	D487	I488	V492	P493	N494	Y495	I496	P497	N498	G499	V500	F501	S502	I503	C504	S513	V514	L515	G518	D519	I523	F524	Q537	Q538	S541	V549								
S434	D350	V351	F352	F353	F354	R355	N356	L361	S362	N365	I366	I367	L368	S369	R370	F377	S381	I382	P390	I391	D392	V393	A394	V395	S396	T397	Y405	A406	F409	S410	E411	E412	L413	L414	I415	D418	E419	A420	Q421	F422	W423	L424	T425	A426	S427	G428	T429	L430	T431	S432	K433
P262	N263	M266	V267	K268	I269	V270	A277	D278	Q279	Y280	Y281	V282	A286	V290	W291	T292	E293	T294	W297	N298	S209	D210	W211	T212	V213	N214	V215	G216	Q217	G218	F219	I220	H221	T222	A224	I230	F233	Y239	A240	D241	Q242	V247	T248	H249	Y250	L257	P258	N260	A261		
K178	I179	G182	S183	Q184	P185	I269	V270	A277	D278	Q279	Y280	Y281	V282	A286	V290	W291	T292	E293	T294	W297	N298	S209	D210	W211	T212	V213	N214	V215	G216	Q217	G218	F219	I220	H221	T222	A224	I230	F233	Y239	A240	D241	Q242	V247	T248	H249	Y250	L257	P258	N260	A261	
L91	S92	G93	N94	E95	V98	R99	Y100	H187	V188	P101	N105	Y106	I107	R113	R117	M118	V119	T120	V121	A122	D123	Y124	T125	F126	I127	V128	N129	R130	A134	T138	K139	L143	Y146	N147	P148	N149	Q150	L153	R157	Y161	G162	R163	E164	L165	I166	V174	A175	K176	Y177		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23461	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	30.188	Depositor
Minimum map value	-18.529	Depositor
Average map value	0.012	Depositor
Map value standard deviation	1.377	Depositor
Recommended contour level	3.9	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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	0	0.14	0/924	0.30	0/1235
1	1	0.15	0/924	0.34	0/1235
1	Y	0.16	0/924	0.32	0/1235
1	Z	0.15	0/924	0.32	0/1235
1	y	0.15	0/924	0.32	0/1235
1	z	0.17	0/924	0.31	0/1235
2	2	0.17	0/233	0.36	0/315
2	3	0.17	0/233	0.34	0/315
2	4	0.16	0/233	0.35	0/315
2	5	0.18	0/233	0.35	0/315
2	6	0.16	0/233	0.36	0/315
2	7	0.17	0/233	0.36	0/315
2	8	0.20	0/370	0.38	0/497
2	9	0.17	0/370	0.36	0/497
2	AA	0.16	0/370	0.33	0/497
2	AB	0.16	0/370	0.40	0/497
2	AC	0.14	0/370	0.33	0/497
2	AD	0.14	0/370	0.33	0/497
3	A	0.15	0/3419	0.35	0/4632
3	B	0.15	0/3434	0.32	0/4651
3	C	0.15	0/3419	0.34	0/4632
3	D	0.16	0/3434	0.34	1/4651 (0.0%)
3	E	0.15	0/3419	0.35	0/4632
3	F	0.14	0/3434	0.31	0/4651
3	G	0.15	0/3419	0.35	0/4632
3	H	0.14	0/3434	0.31	0/4651
3	I	0.15	0/3419	0.34	0/4632
3	J	0.14	0/3434	0.31	0/4651
3	K	0.14	0/3419	0.34	0/4632
3	L	0.14	0/3434	0.31	0/4651
4	M	0.20	0/1592	0.35	0/2153
4	N	0.20	0/1573	0.35	0/2129
4	O	0.19	0/1592	0.33	0/2153
4	P	0.19	0/1573	0.35	0/2129

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	Q	0.19	0/1592	0.35	0/2153
4	R	0.19	0/1573	0.35	0/2129
4	S	0.20	0/1592	0.35	0/2153
4	T	0.22	0/1573	0.37	0/2129
4	U	0.19	0/1592	0.35	0/2153
4	V	0.20	0/1573	0.35	0/2129
4	W	0.19	0/1592	0.34	0/2153
4	X	0.19	0/1573	0.35	0/2129
5	a	0.18	0/936	0.36	0/1274
5	b	0.19	0/921	0.46	0/1253
5	c	0.19	0/921	0.45	0/1253
5	d	0.18	0/936	0.35	0/1274
5	e	0.20	0/921	0.41	0/1253
5	f	0.18	0/921	0.42	0/1253
5	g	0.18	0/936	0.35	0/1274
5	h	0.17	0/921	0.41	1/1253 (0.1%)
5	i	0.18	0/921	0.39	0/1253
5	j	0.18	0/936	0.32	0/1274
5	k	0.20	0/921	0.54	2/1253 (0.2%)
5	l	0.17	0/921	0.40	0/1253
5	m	0.19	0/936	0.35	0/1274
5	n	0.22	0/921	0.55	1/1253 (0.1%)
5	o	0.20	0/921	0.46	1/1253 (0.1%)
5	p	0.21	0/936	0.39	0/1274
5	q	0.18	0/921	0.40	0/1253
5	r	0.23	0/921	0.54	4/1253 (0.3%)
6	s	0.32	0/6449	0.58	8/8772 (0.1%)
6	t	0.29	0/6449	0.55	5/8772 (0.1%)
6	u	0.30	0/6449	0.55	4/8772 (0.0%)
6	v	0.30	0/6449	0.59	12/8772 (0.1%)
6	w	0.31	0/6449	0.57	7/8772 (0.1%)
6	x	0.32	0/6449	0.59	10/8772 (0.1%)
All	All	0.22	0/124632	0.43	56/168984 (0.0%)

There are no bond length outliers.

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	v	736	LEU	N-CA-C	9.92	122.10	111.28
6	x	736	LEU	N-CA-C	8.98	121.07	111.28
6	x	105	ASN	N-CA-C	-8.61	102.53	113.72
6	s	12	LYS	N-CA-C	-8.22	102.28	111.07

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Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	w	105	ASN	N-CA-C	-7.91	103.44	113.72

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	0	920	0	919	25	0
1	1	920	0	919	23	0
1	Y	920	0	919	37	0
1	Z	920	0	919	30	0
1	y	920	0	919	20	0
1	z	920	0	919	33	0
2	2	231	0	217	9	0
2	3	231	0	217	9	0
2	4	231	0	217	10	0
2	5	231	0	217	9	0
2	6	231	0	217	8	0
2	7	231	0	217	8	0
2	8	368	0	352	19	0
2	9	368	0	352	12	0
2	AA	368	0	352	10	0
2	AB	368	0	352	15	0
2	AC	368	0	352	11	0
2	AD	368	0	352	17	0
3	A	3363	0	3347	95	0
3	B	3378	0	3363	96	0
3	C	3363	0	3347	97	0
3	D	3378	0	3363	87	0
3	E	3363	0	3347	84	0
3	F	3378	0	3363	82	0
3	G	3363	0	3347	91	0
3	H	3378	0	3363	77	0
3	I	3363	0	3347	100	0
3	J	3378	0	3363	90	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	K	3363	0	3347	83	0
3	L	3378	0	3363	74	0
4	M	1565	0	1485	41	0
4	N	1546	0	1460	44	0
4	O	1565	0	1485	55	0
4	P	1546	0	1460	45	0
4	Q	1565	0	1485	42	0
4	R	1546	0	1460	34	0
4	S	1565	0	1485	46	0
4	T	1546	0	1460	45	0
4	U	1565	0	1485	47	0
4	V	1546	0	1460	49	0
4	W	1565	0	1485	42	0
4	X	1546	0	1460	38	0
5	a	922	0	931	30	0
5	b	907	0	916	36	0
5	c	907	0	916	35	0
5	d	922	0	931	35	0
5	e	907	0	916	36	0
5	f	907	0	916	40	0
5	g	922	0	931	31	0
5	h	907	0	916	28	0
5	i	907	0	916	31	0
5	j	922	0	931	27	0
5	k	907	0	916	41	0
5	l	907	0	916	33	0
5	m	922	0	931	33	0
5	n	907	0	916	41	0
5	o	907	0	916	30	0
5	p	922	0	931	29	0
5	q	907	0	916	39	0
5	r	907	0	916	35	0
6	s	6289	0	6051	261	0
6	t	6289	0	6051	262	0
6	u	6289	0	6051	250	0
6	v	6289	0	6051	266	0
6	w	6289	0	6051	263	0
6	x	6289	0	6051	257	0
All	All	122376	0	119742	3482	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 14.

The worst 5 of 3482 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)
5:o:18:ARG:HH22	5:o:63:ALA:HB2	1.35	0.91
6:s:570:ASN:HD21	6:s:624:ALA:HB3	1.39	0.88
6:u:570:ASN:HD21	6:u:624:ALA:HB3	1.38	0.85
6:w:570:ASN:HD21	6:w:624:ALA:HB3	1.40	0.85
6:v:570:ASN:HD21	6:v:624:ALA:HB3	1.39	0.85

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	0	117/196 (60%)	115 (98%)	2 (2%)	0	100	100
1	1	117/196 (60%)	116 (99%)	1 (1%)	0	100	100
1	Y	117/196 (60%)	115 (98%)	2 (2%)	0	100	100
1	Z	117/196 (60%)	115 (98%)	2 (2%)	0	100	100
1	y	117/196 (60%)	115 (98%)	2 (2%)	0	100	100
1	z	117/196 (60%)	116 (99%)	1 (1%)	0	100	100
2	2	29/88 (33%)	25 (86%)	4 (14%)	0	100	100
2	3	29/88 (33%)	26 (90%)	3 (10%)	0	100	100
2	4	29/88 (33%)	23 (79%)	6 (21%)	0	100	100
2	5	29/88 (33%)	25 (86%)	4 (14%)	0	100	100
2	6	29/88 (33%)	23 (79%)	6 (21%)	0	100	100
2	7	29/88 (33%)	24 (83%)	5 (17%)	0	100	100
2	8	47/88 (53%)	45 (96%)	2 (4%)	0	100	100
2	9	47/88 (53%)	45 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AA	47/88 (53%)	45 (96%)	2 (4%)	0	100	100
2	AB	47/88 (53%)	45 (96%)	2 (4%)	0	100	100
2	AC	47/88 (53%)	44 (94%)	3 (6%)	0	100	100
2	AD	47/88 (53%)	44 (94%)	3 (6%)	0	100	100
3	A	427/536 (80%)	419 (98%)	8 (2%)	0	100	100
3	B	429/536 (80%)	422 (98%)	7 (2%)	0	100	100
3	C	427/536 (80%)	416 (97%)	11 (3%)	0	100	100
3	D	429/536 (80%)	422 (98%)	7 (2%)	0	100	100
3	E	427/536 (80%)	417 (98%)	10 (2%)	0	100	100
3	F	429/536 (80%)	422 (98%)	7 (2%)	0	100	100
3	G	427/536 (80%)	418 (98%)	9 (2%)	0	100	100
3	H	429/536 (80%)	423 (99%)	6 (1%)	0	100	100
3	I	427/536 (80%)	414 (97%)	13 (3%)	0	100	100
3	J	429/536 (80%)	425 (99%)	4 (1%)	0	100	100
3	K	427/536 (80%)	417 (98%)	10 (2%)	0	100	100
3	L	429/536 (80%)	423 (99%)	6 (1%)	0	100	100
4	M	194/196 (99%)	190 (98%)	4 (2%)	0	100	100
4	N	192/196 (98%)	185 (96%)	7 (4%)	0	100	100
4	O	194/196 (99%)	190 (98%)	4 (2%)	0	100	100
4	P	192/196 (98%)	185 (96%)	7 (4%)	0	100	100
4	Q	194/196 (99%)	190 (98%)	4 (2%)	0	100	100
4	R	192/196 (98%)	187 (97%)	5 (3%)	0	100	100
4	S	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
4	T	192/196 (98%)	185 (96%)	7 (4%)	0	100	100
4	U	194/196 (99%)	191 (98%)	3 (2%)	0	100	100
4	V	192/196 (98%)	184 (96%)	8 (4%)	0	100	100
4	W	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
4	X	192/196 (98%)	186 (97%)	6 (3%)	0	100	100
5	a	113/553 (20%)	107 (95%)	6 (5%)	0	100	100
5	b	111/553 (20%)	106 (96%)	5 (4%)	0	100	100
5	c	111/553 (20%)	105 (95%)	5 (4%)	1 (1%)	14	47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	d	113/553 (20%)	108 (96%)	5 (4%)	0	100	100
5	e	111/553 (20%)	103 (93%)	7 (6%)	1 (1%)	14	47
5	f	111/553 (20%)	106 (96%)	5 (4%)	0	100	100
5	g	113/553 (20%)	110 (97%)	3 (3%)	0	100	100
5	h	111/553 (20%)	105 (95%)	4 (4%)	2 (2%)	6	34
5	i	111/553 (20%)	107 (96%)	4 (4%)	0	100	100
5	j	113/553 (20%)	109 (96%)	4 (4%)	0	100	100
5	k	111/553 (20%)	104 (94%)	5 (4%)	2 (2%)	6	34
5	l	111/553 (20%)	107 (96%)	4 (4%)	0	100	100
5	m	113/553 (20%)	109 (96%)	4 (4%)	0	100	100
5	n	111/553 (20%)	103 (93%)	8 (7%)	0	100	100
5	o	111/553 (20%)	108 (97%)	3 (3%)	0	100	100
5	p	113/553 (20%)	107 (95%)	5 (4%)	1 (1%)	14	47
5	q	111/553 (20%)	106 (96%)	5 (4%)	0	100	100
5	r	111/553 (20%)	106 (96%)	5 (4%)	0	100	100
6	s	787/794 (99%)	701 (89%)	80 (10%)	6 (1%)	16	49
6	t	787/794 (99%)	702 (89%)	78 (10%)	7 (1%)	14	47
6	u	787/794 (99%)	699 (89%)	80 (10%)	8 (1%)	12	44
6	v	787/794 (99%)	699 (89%)	79 (10%)	9 (1%)	11	43
6	w	787/794 (99%)	699 (89%)	83 (10%)	5 (1%)	21	54
6	x	787/794 (99%)	702 (89%)	80 (10%)	5 (1%)	21	54
All	All	15342/25734 (60%)	14513 (95%)	782 (5%)	47 (0%)	37	67

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	c	68	ASP
6	s	432	SER
6	s	498	ASN
6	s	735	ARG
6	t	498	ASN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	95/149 (64%)	95 (100%)	0	100	100
1	1	95/149 (64%)	95 (100%)	0	100	100
1	Y	95/149 (64%)	95 (100%)	0	100	100
1	Z	95/149 (64%)	95 (100%)	0	100	100
1	y	95/149 (64%)	95 (100%)	0	100	100
1	z	95/149 (64%)	95 (100%)	0	100	100
2	2	27/73 (37%)	27 (100%)	0	100	100
2	3	27/73 (37%)	27 (100%)	0	100	100
2	4	27/73 (37%)	27 (100%)	0	100	100
2	5	27/73 (37%)	27 (100%)	0	100	100
2	6	27/73 (37%)	27 (100%)	0	100	100
2	7	27/73 (37%)	27 (100%)	0	100	100
2	8	42/73 (58%)	42 (100%)	0	100	100
2	9	42/73 (58%)	42 (100%)	0	100	100
2	AA	42/73 (58%)	42 (100%)	0	100	100
2	AB	42/73 (58%)	42 (100%)	0	100	100
2	AC	42/73 (58%)	42 (100%)	0	100	100
2	AD	42/73 (58%)	42 (100%)	0	100	100
3	A	365/442 (83%)	365 (100%)	0	100	100
3	B	366/442 (83%)	366 (100%)	0	100	100
3	C	365/442 (83%)	365 (100%)	0	100	100
3	D	366/442 (83%)	366 (100%)	0	100	100
3	E	365/442 (83%)	365 (100%)	0	100	100
3	F	366/442 (83%)	366 (100%)	0	100	100
3	G	365/442 (83%)	365 (100%)	0	100	100
3	H	366/442 (83%)	366 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	I	365/442 (83%)	365 (100%)	0	100	100
3	J	366/442 (83%)	366 (100%)	0	100	100
3	K	365/442 (83%)	365 (100%)	0	100	100
3	L	366/442 (83%)	366 (100%)	0	100	100
4	M	169/169 (100%)	169 (100%)	0	100	100
4	N	167/169 (99%)	167 (100%)	0	100	100
4	O	169/169 (100%)	169 (100%)	0	100	100
4	P	167/169 (99%)	167 (100%)	0	100	100
4	Q	169/169 (100%)	169 (100%)	0	100	100
4	R	167/169 (99%)	167 (100%)	0	100	100
4	S	169/169 (100%)	169 (100%)	0	100	100
4	T	167/169 (99%)	167 (100%)	0	100	100
4	U	169/169 (100%)	169 (100%)	0	100	100
4	V	167/169 (99%)	167 (100%)	0	100	100
4	W	169/169 (100%)	169 (100%)	0	100	100
4	X	167/169 (99%)	167 (100%)	0	100	100
5	a	102/451 (23%)	102 (100%)	0	100	100
5	b	100/451 (22%)	99 (99%)	1 (1%)	68	75
5	c	100/451 (22%)	100 (100%)	0	100	100
5	d	102/451 (23%)	102 (100%)	0	100	100
5	e	100/451 (22%)	100 (100%)	0	100	100
5	f	100/451 (22%)	99 (99%)	1 (1%)	68	75
5	g	102/451 (23%)	102 (100%)	0	100	100
5	h	100/451 (22%)	99 (99%)	1 (1%)	68	75
5	i	100/451 (22%)	100 (100%)	0	100	100
5	j	102/451 (23%)	102 (100%)	0	100	100
5	k	100/451 (22%)	99 (99%)	1 (1%)	68	75
5	l	100/451 (22%)	99 (99%)	1 (1%)	68	75
5	m	102/451 (23%)	102 (100%)	0	100	100
5	n	100/451 (22%)	99 (99%)	1 (1%)	68	75
5	o	100/451 (22%)	99 (99%)	1 (1%)	68	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	p	102/451 (23%)	102 (100%)	0	100	100
5	q	100/451 (22%)	100 (100%)	0	100	100
5	r	100/451 (22%)	99 (99%)	1 (1%)	68	75
6	s	684/688 (99%)	677 (99%)	7 (1%)	68	75
6	t	684/688 (99%)	678 (99%)	6 (1%)	70	76
6	u	684/688 (99%)	683 (100%)	1 (0%)	88	87
6	v	684/688 (99%)	681 (100%)	3 (0%)	84	81
6	w	684/688 (99%)	678 (99%)	6 (1%)	70	76
6	x	684/688 (99%)	675 (99%)	9 (1%)	61	72
All	All	13302/21348 (62%)	13262 (100%)	40 (0%)	84	83

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	w	433	LYS
6	x	419	GLU
6	w	735	ARG
6	x	397	THR
6	x	538	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 153 such sidechains are listed below:

Mol	Chain	Res	Type
6	u	538	GLN
6	x	338	ASN
6	u	645	GLN
6	v	645	GLN
1	y	49	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

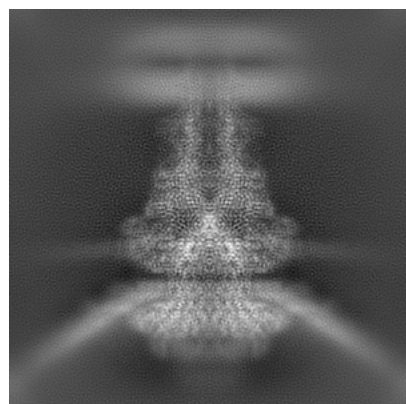
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61911. These allow visual inspection of the internal detail of the map and identification of artifacts.

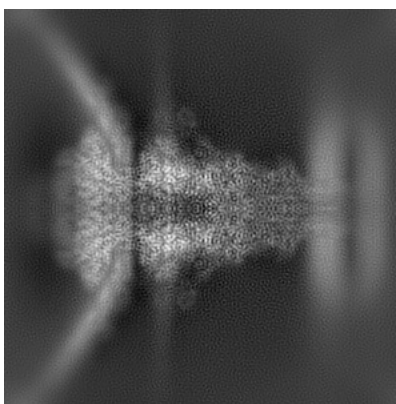
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

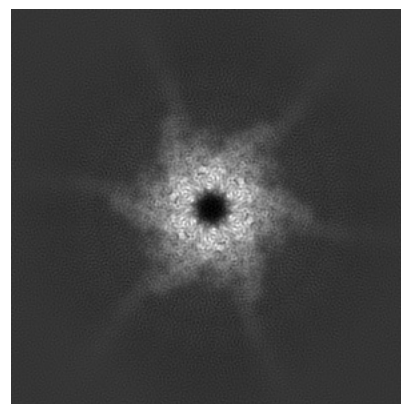
6.1.1 Primary map



X

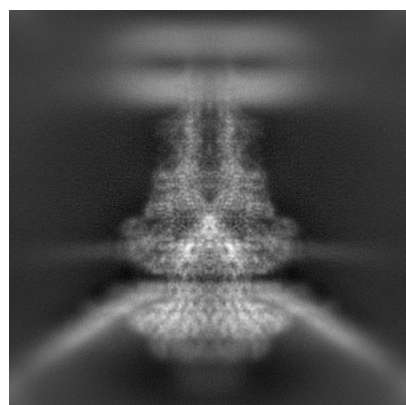


Y

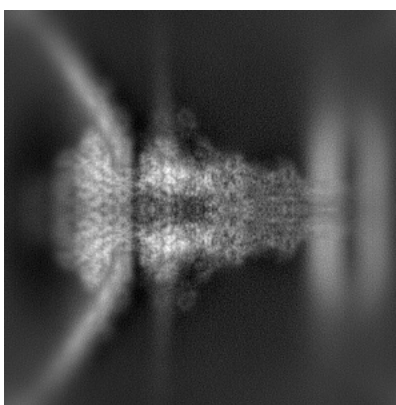


Z

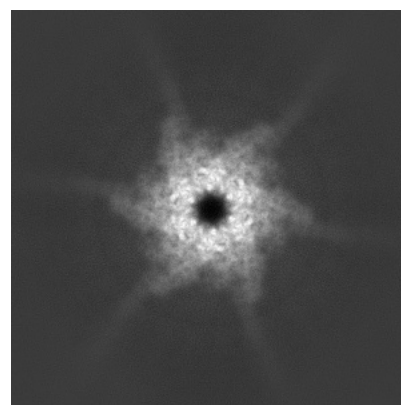
6.1.2 Raw map



X



Y

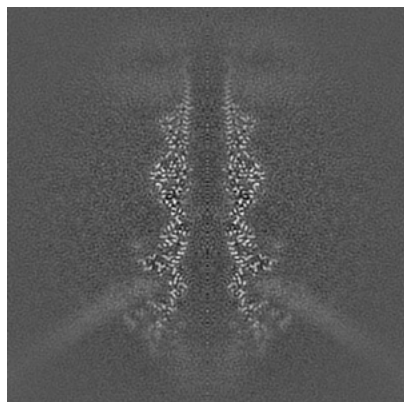


Z

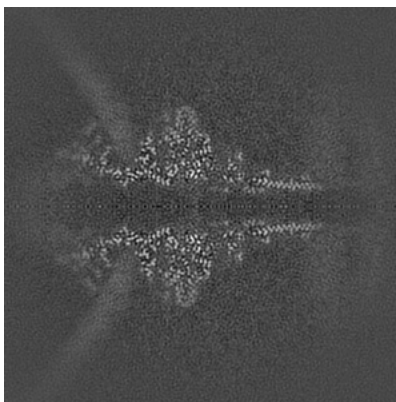
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

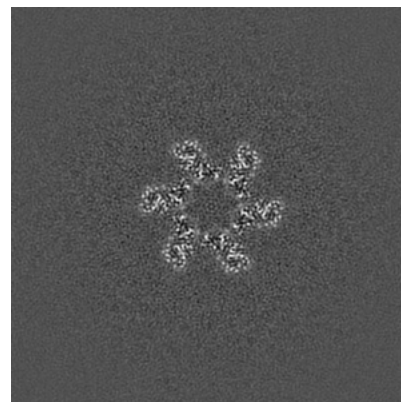
6.2.1 Primary map



X Index: 200

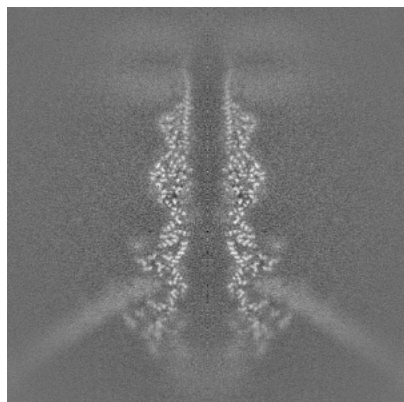


Y Index: 200

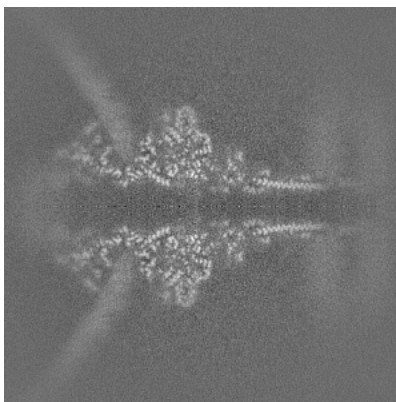


Z Index: 200

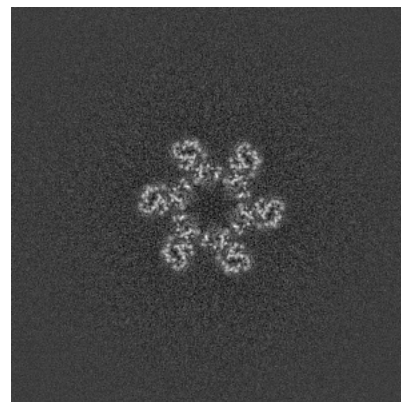
6.2.2 Raw map



X Index: 200



Y Index: 200

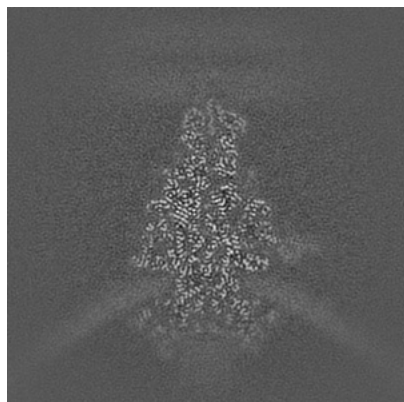


Z Index: 200

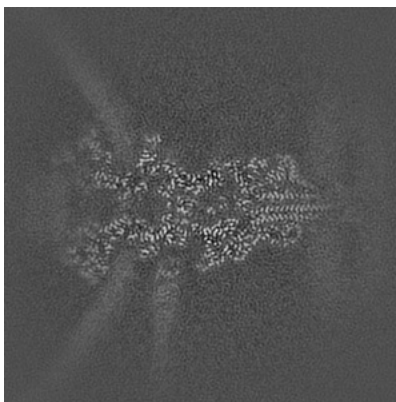
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

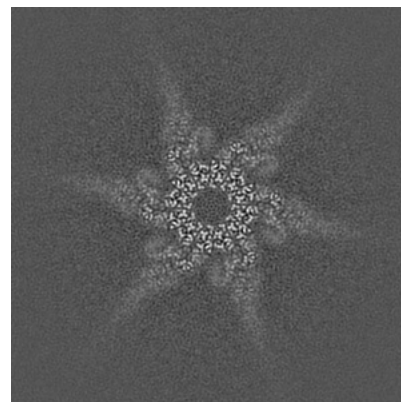
6.3.1 Primary map



X Index: 171

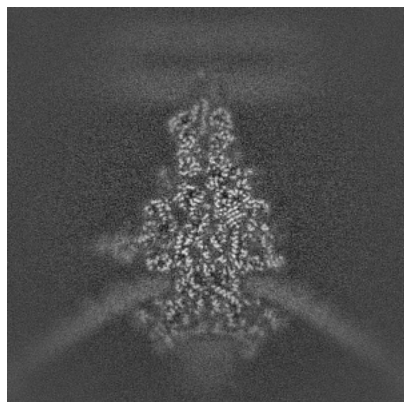


Y Index: 220

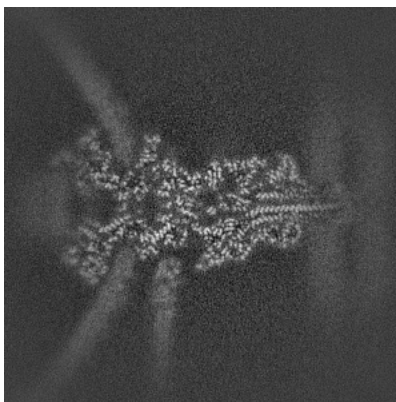


Z Index: 164

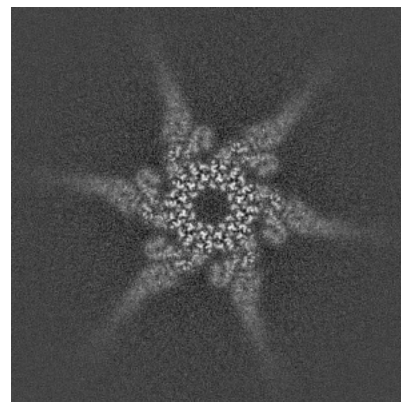
6.3.2 Raw map



X Index: 229



Y Index: 221

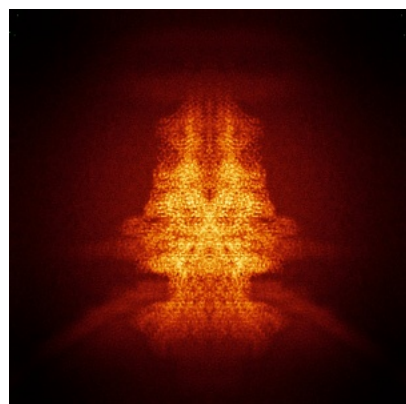


Z Index: 164

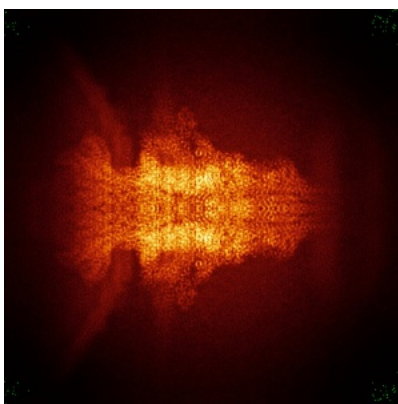
The images above show the largest variance slices of the map in three orthogonal directions.

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

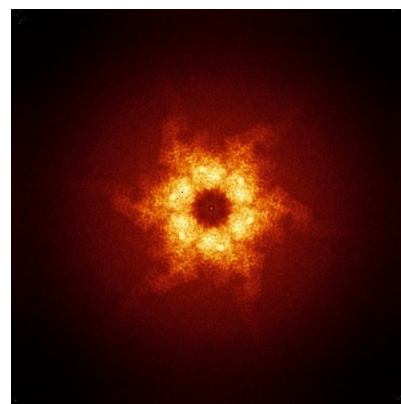
6.4.1 Primary map



X

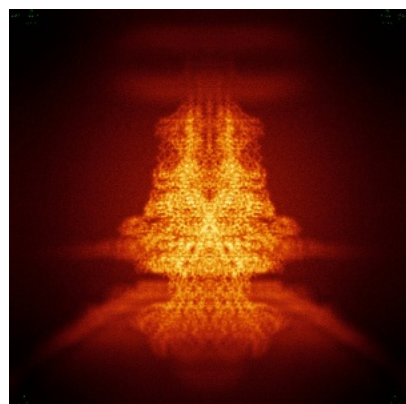


Y

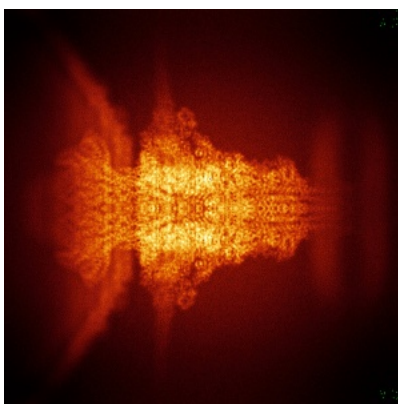


Z

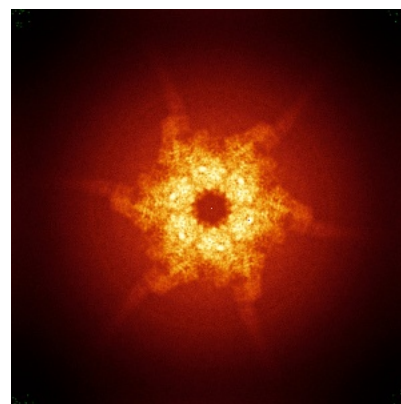
6.4.2 Raw map



X



Y

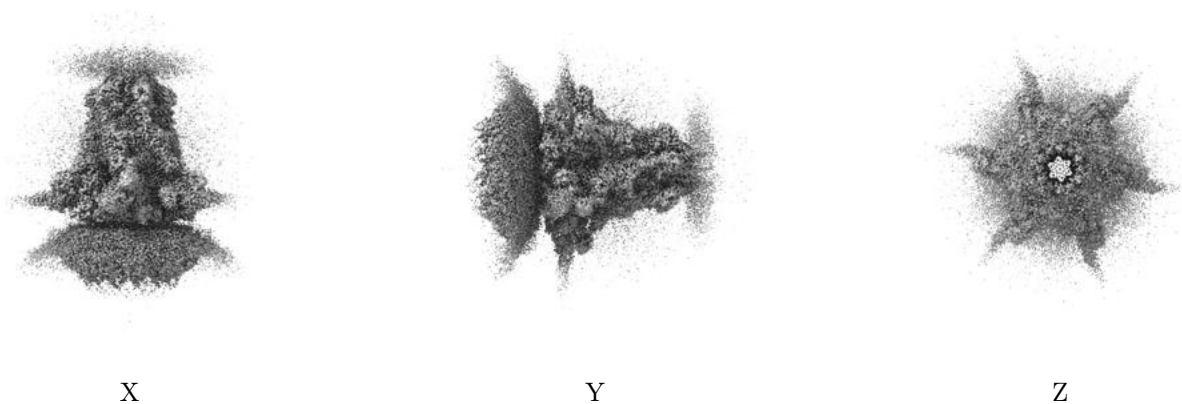


Z

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

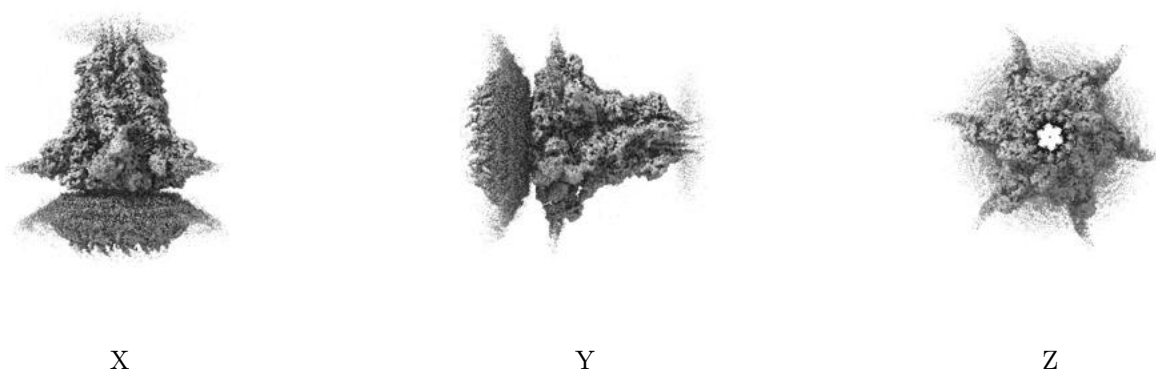
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

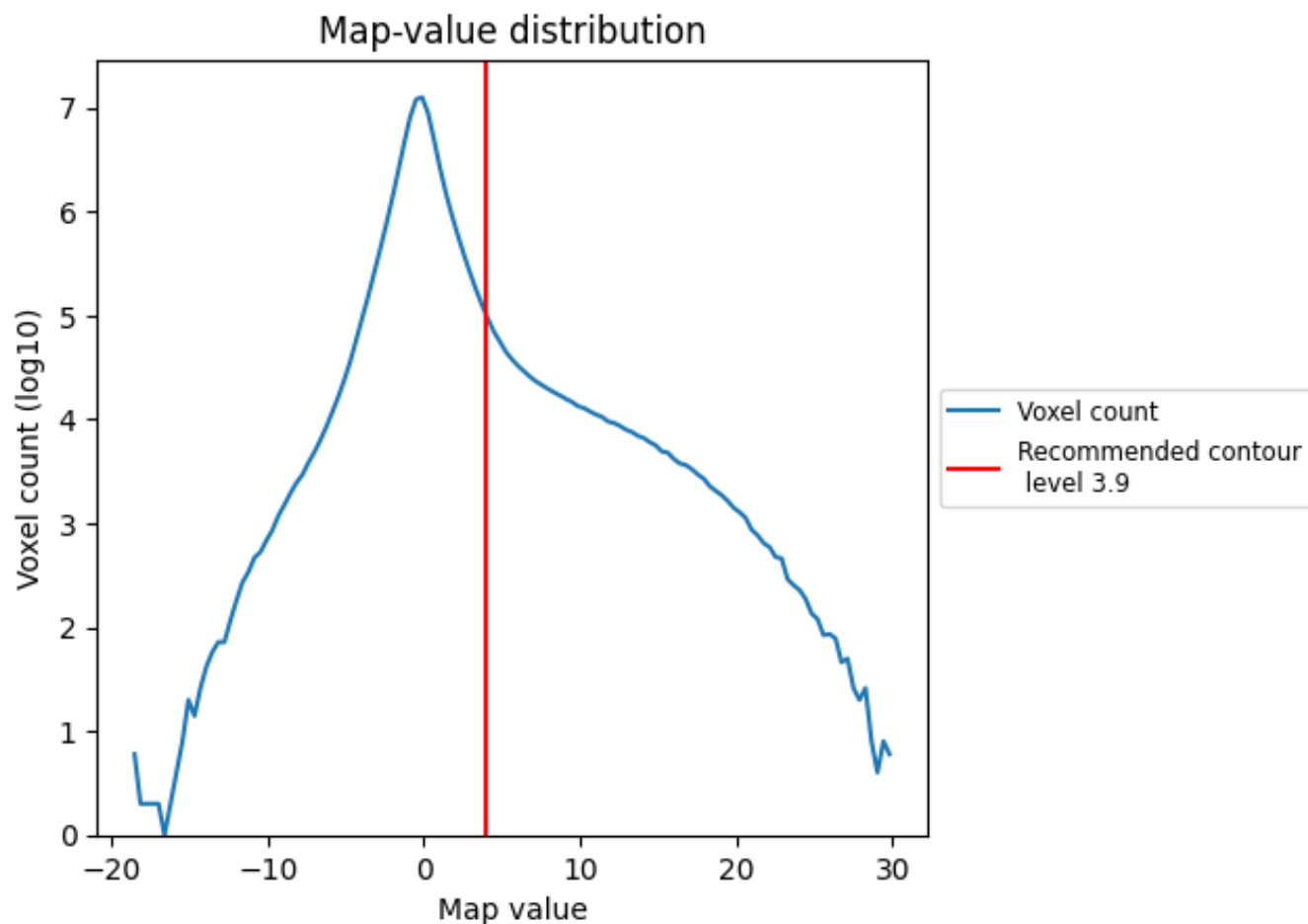
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

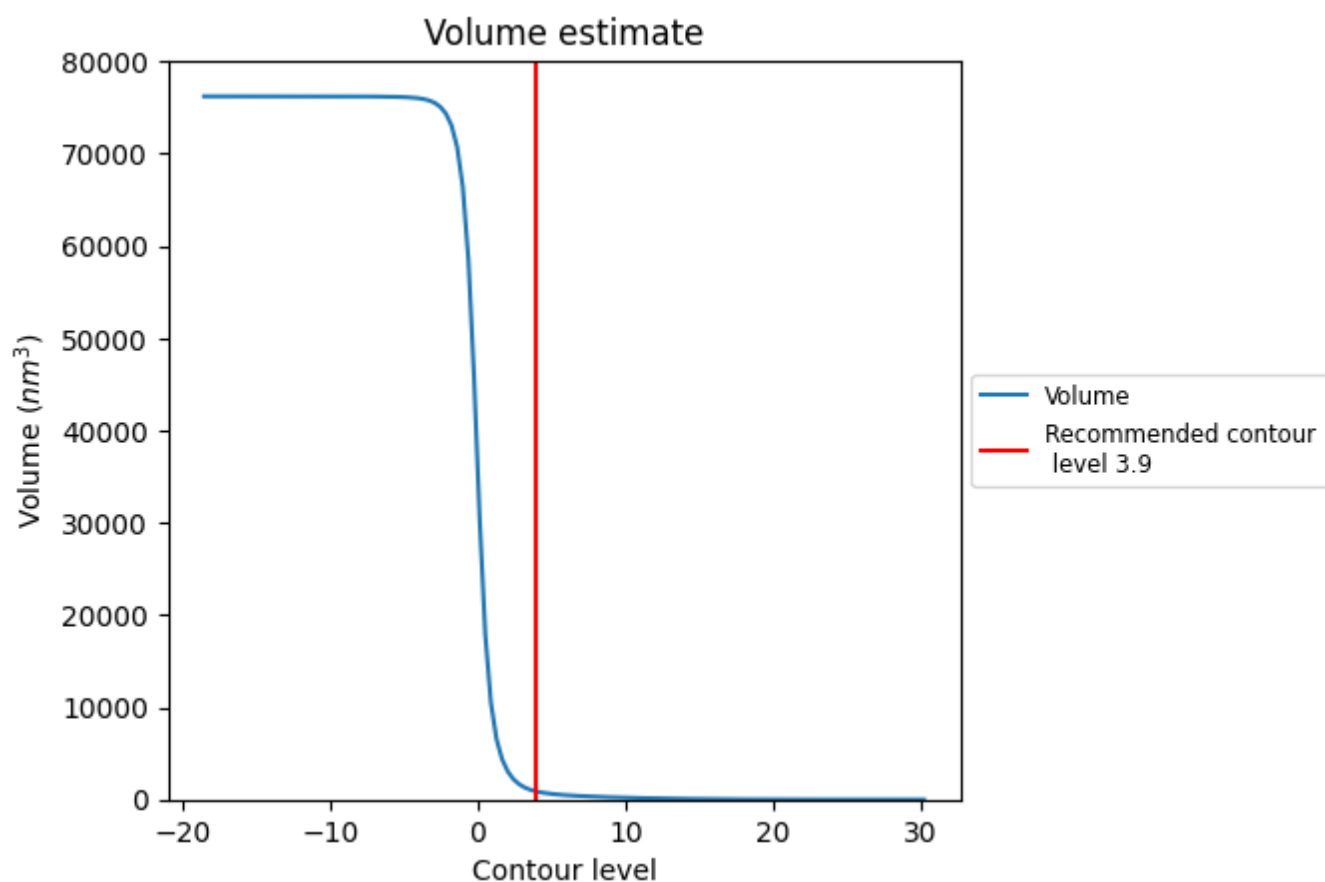
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

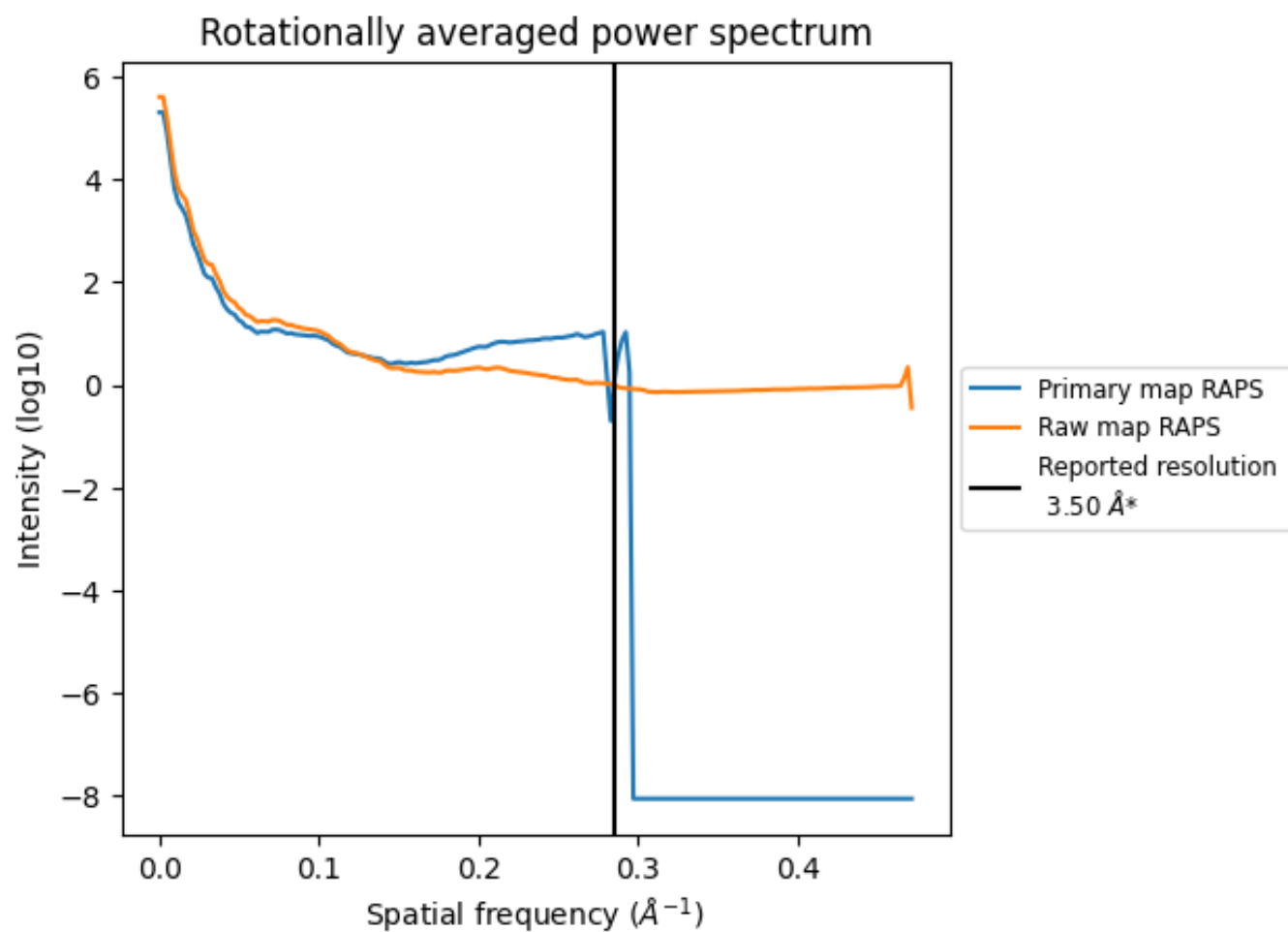
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 902 nm³; this corresponds to an approximate mass of 815 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

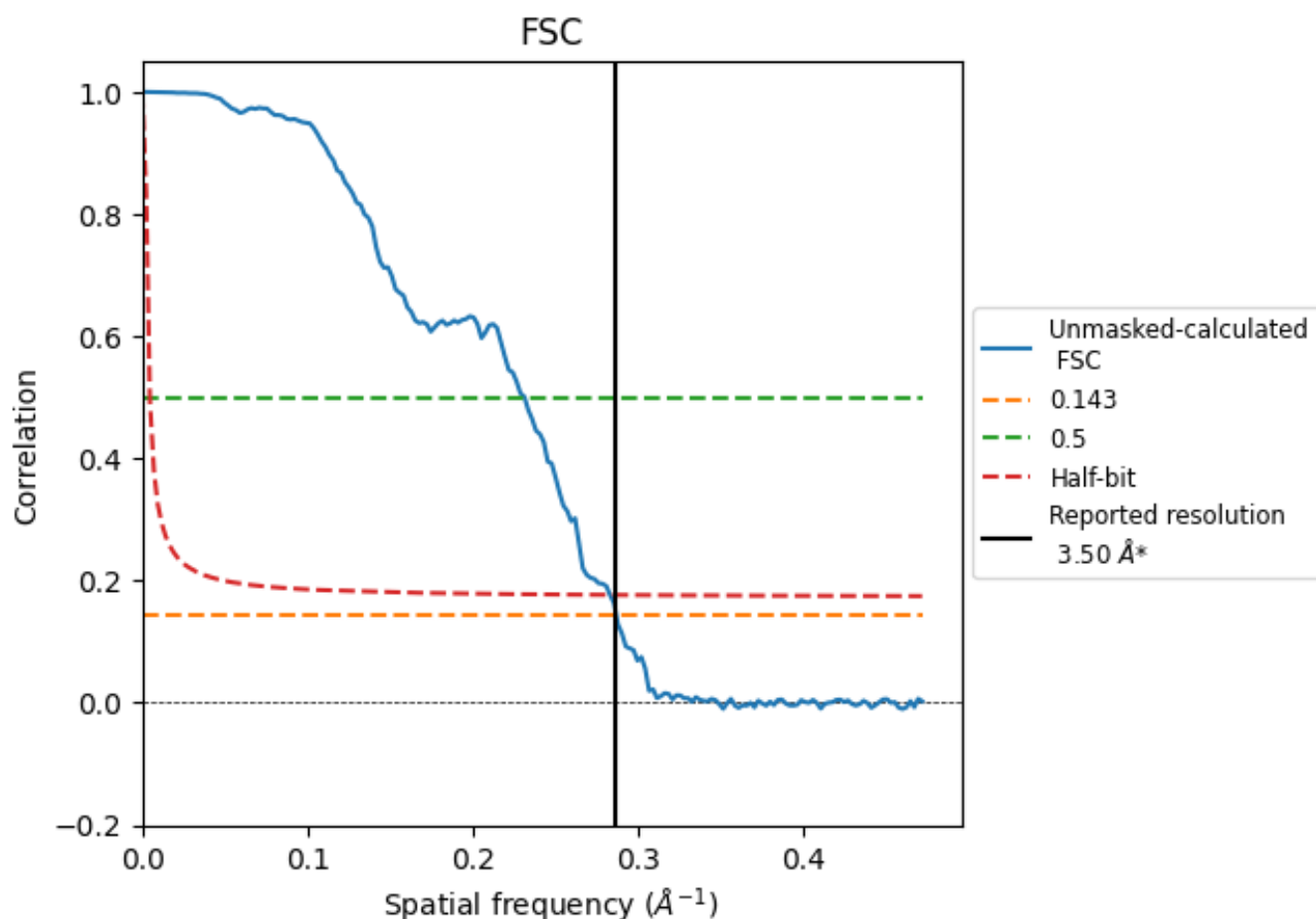


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.286 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

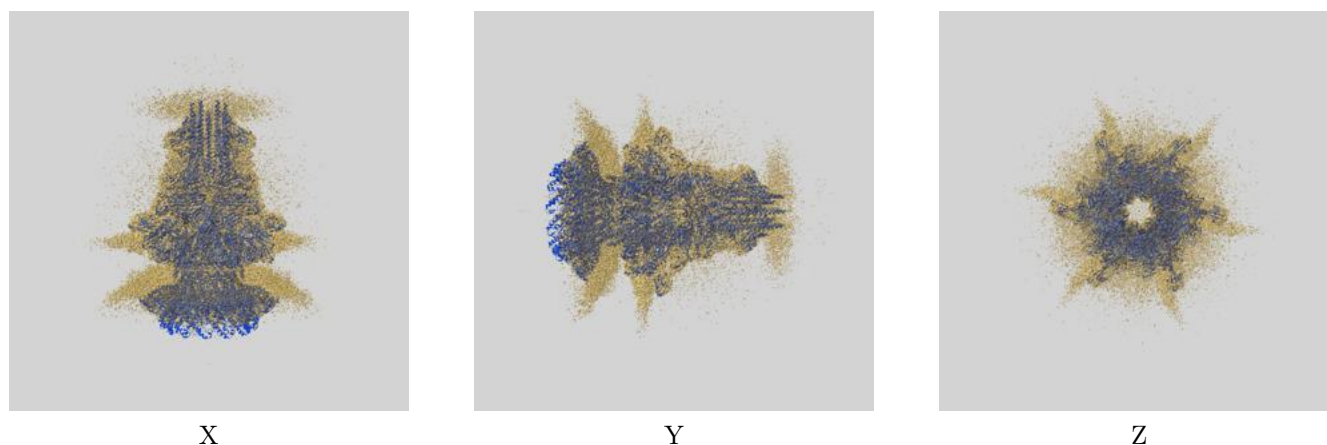
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.49	4.33	3.53

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

9 Map-model fit [i](#)

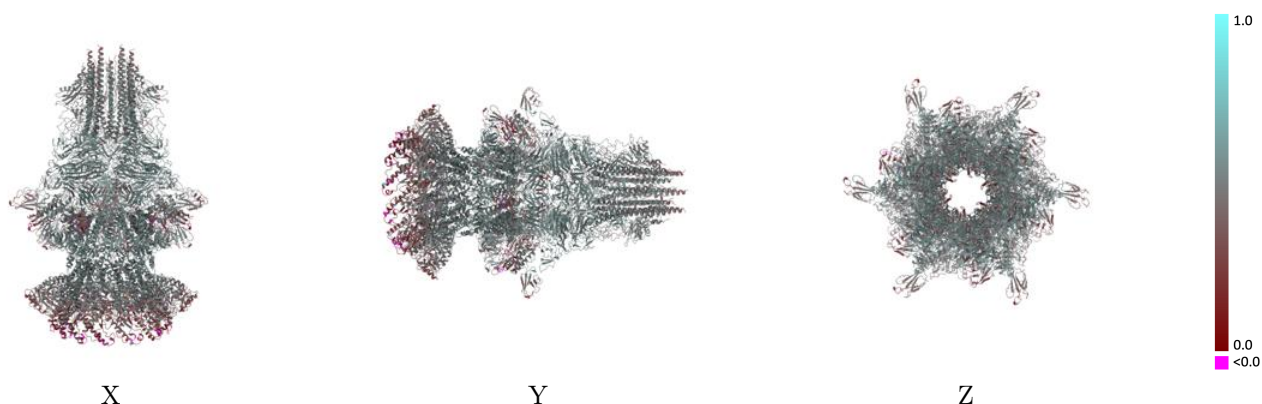
This section contains information regarding the fit between EMDB map EMD-61911 and PDB model 9JZ0. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



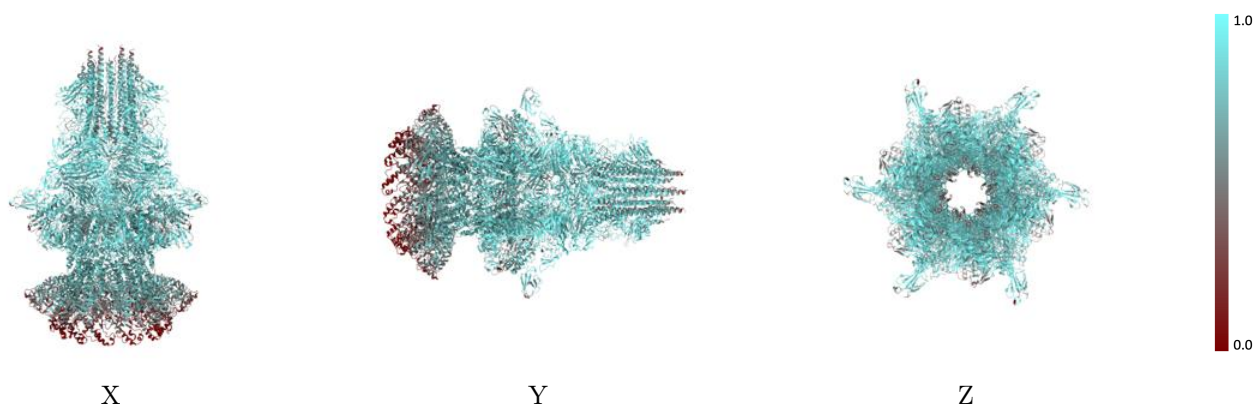
The images above show the 3D surface view of the map at the recommended contour level 3.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



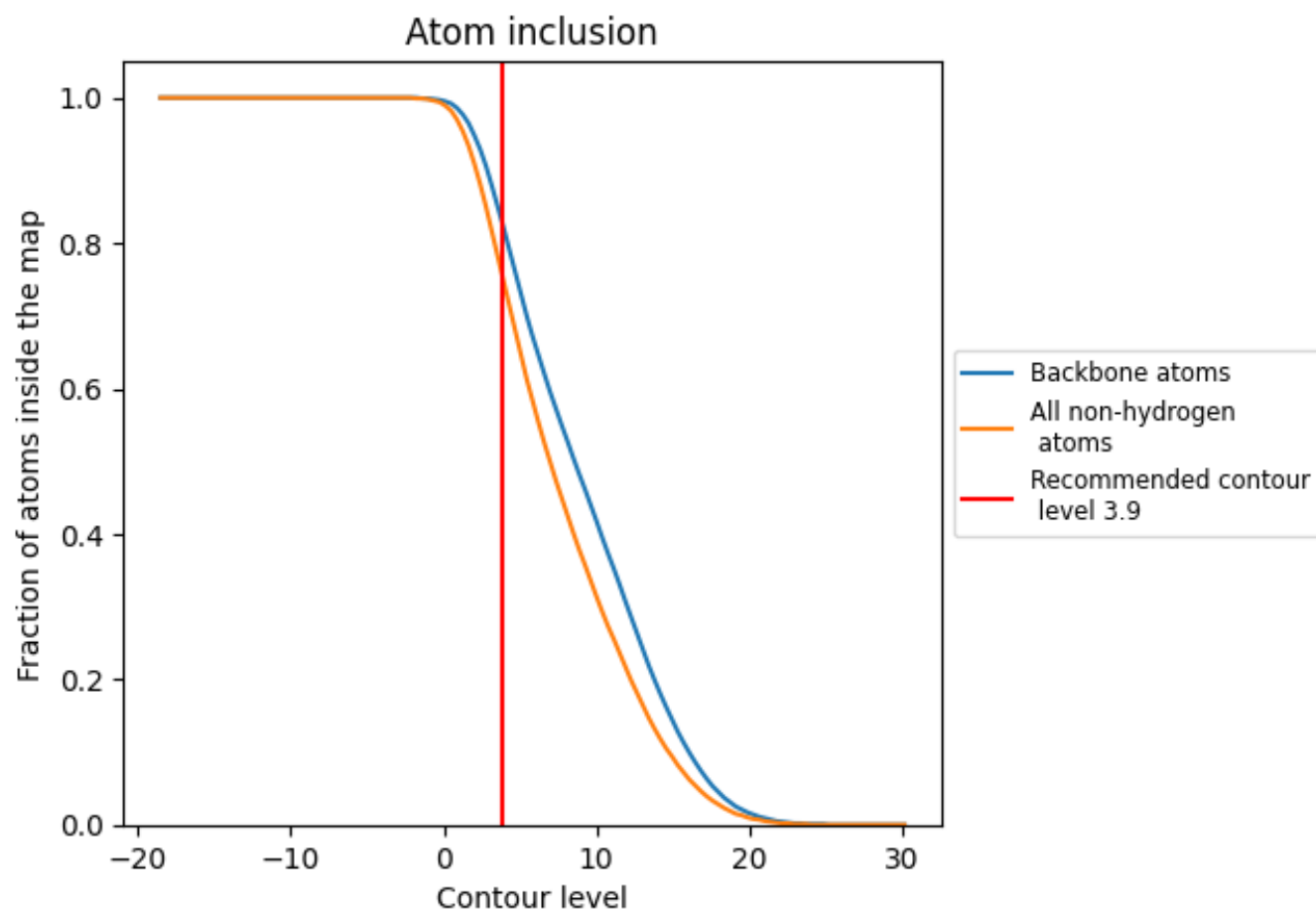
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.9).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 75% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (3.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7500	 0.4750
0	 0.7900	 0.4990
1	 0.7810	 0.4970
2	 0.4850	 0.3780
3	 0.4500	 0.3820
4	 0.4800	 0.3770
5	 0.4540	 0.3820
6	 0.4670	 0.3770
7	 0.4630	 0.3880
8	 0.6770	 0.4550
9	 0.6770	 0.4620
A	 0.5730	 0.4250
AA	 0.6490	 0.4660
AB	 0.6680	 0.4580
AC	 0.6740	 0.4610
AD	 0.6570	 0.4600
B	 0.5680	 0.4180
C	 0.5720	 0.4250
D	 0.5680	 0.4160
E	 0.5760	 0.4260
F	 0.5670	 0.4170
G	 0.5700	 0.4240
H	 0.5710	 0.4180
I	 0.5720	 0.4240
J	 0.5650	 0.4190
K	 0.5780	 0.4270
L	 0.5670	 0.4170
M	 0.8780	 0.5370
N	 0.8640	 0.5310
O	 0.8870	 0.5370
P	 0.8650	 0.5280
Q	 0.8780	 0.5370
R	 0.8580	 0.5310
S	 0.8740	 0.5350
T	 0.8650	 0.5310



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Chain	Atom inclusion	Q-score
U	 0.8820	 0.5360
V	 0.8660	 0.5310
W	 0.8760	 0.5350
X	 0.8580	 0.5310
Y	 0.7900	 0.4970
Z	 0.7860	 0.5030
a	 0.8100	 0.4750
b	 0.6720	 0.3580
c	 0.8090	 0.4520
d	 0.8110	 0.4780
e	 0.6690	 0.3690
f	 0.7950	 0.4460
g	 0.8270	 0.4800
h	 0.6670	 0.3680
i	 0.7980	 0.4510
j	 0.8160	 0.4790
k	 0.6760	 0.3670
l	 0.8060	 0.4540
m	 0.8140	 0.4780
n	 0.6740	 0.3610
o	 0.8000	 0.4490
p	 0.8350	 0.4820
q	 0.6700	 0.3670
r	 0.7890	 0.4440
s	 0.8880	 0.5250
t	 0.8910	 0.5240
u	 0.8850	 0.5250
v	 0.8860	 0.5230
w	 0.8890	 0.5220
x	 0.8870	 0.5240
y	 0.7870	 0.4990
z	 0.7770	 0.4970