



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 10:30 AM UTC

PDB ID : 9JYZ / pdb_00009jyz
EMDB ID : EMD-61910
Title : portal-tail complex of mature T7
Authors : Liu, H.R.; Chen, W.Y.
Deposited on : 2024-10-13
Resolution : 2.70 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

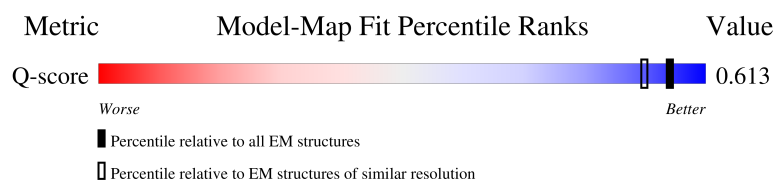
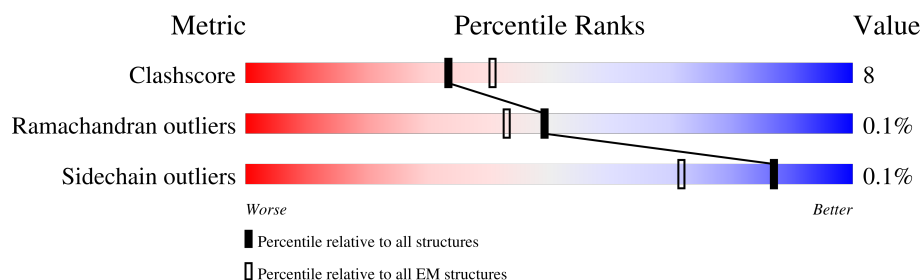
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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	10327 (2.20 - 3.20)

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	88	 5% 8% • 84%
1	3	88	 5% 8% • 5% 84%
1	4	88	 5% 10% • 84%
1	5	88	 7% 6% • 84%

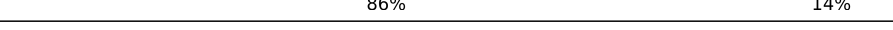
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Mol	Chain	Length	Quality of chain
1	6	88	5% 7% 5% 84%
1	7	88	6% 6% 9% 84%
1	8	88	5% 7% 7% 84%
1	9	88	7% 6% 9% 84%
1	AA	88	6% 5% 8% 84%
1	AB	88	7% 5% 5% 84%
1	AC	88	6% 11% 1% 84%
1	AD	88	6% 7% 7% 84%
2	1	99	12% 1% 85%
2	2	99	11% 1% 85%
2	v	99	12% 1% 85%
2	w	99	11% 1% 85%
2	y	99	11% 1% 85%
2	z	99	12% 1% 85%
3	A	553	20% 5% 75%
3	B	553	21% 5% 75%
3	C	553	21% 5% 75%
3	D	553	20% 5% 75%
3	E	553	20% 6% 75%
3	F	553	19% 5% 76%
3	G	553	19% 5% 76%
3	H	553	20% 5% 76%
3	I	553	19% 5% 76%
3	J	553	19% 5% 76%
3	K	553	18% 7% 75%

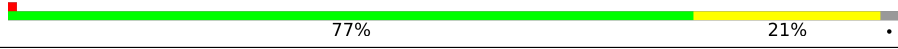
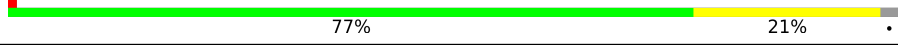
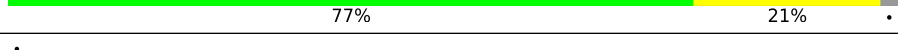
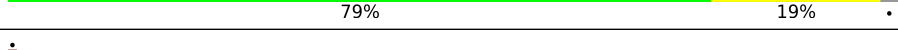
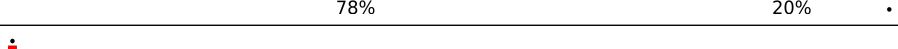
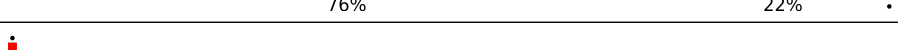
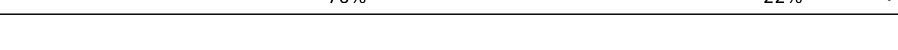
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Mol	Chain	Length	Quality of chain
3	L	553	
3	M	553	
3	N	553	
3	O	553	
3	a	553	
3	b	553	
3	c	553	
4	P	794	
4	Q	794	
4	R	794	
4	S	794	
4	T	794	
4	x	794	
5	U	196	
5	V	196	
5	W	196	
5	X	196	
5	Y	196	
5	Z	196	
5	d	196	
5	e	196	
5	f	196	
5	g	196	
5	h	196	
5	i	196	

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Mol	Chain	Length	Quality of chain	
6	j	536		.
6	k	536		.
6	l	536		.
6	m	536		.
6	n	536		.
6	o	536		.
6	p	536		.
6	q	536		.
6	r	536		.
6	s	536		.
6	t	536		.
6	u	536		.

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 126948 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 Protein 6.7.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	3	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	4	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	5	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	6	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	7	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	8	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	9	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	AA	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	AB	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	AC	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	AD	14	Total 110	C 70	N 18	O 20	S 2	0	0

- Molecule 2 is a protein called Protein 7.3.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	15	Total 101	C 60	N 21	O 20	0	0
2	2	15	Total 101	C 60	N 21	O 20	0	0
2	v	15	Total 101	C 60	N 21	O 20	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
2	w	15	Total 101	C 60	N 21	O 20	0	0
2	y	15	Total 101	C 60	N 21	O 20	0	0
2	z	15	Total 101	C 60	N 21	O 20	0	0

- Molecule 3 is a protein called Tail fiber protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	141	Total 1115	C 698	N 201	O 215	S 1	0	0
3	B	141	Total 1115	C 698	N 201	O 215	S 1	0	0
3	C	141	Total 1115	C 698	N 201	O 215	S 1	0	0
3	D	141	Total 1115	C 698	N 201	O 215	S 1	0	0
3	E	141	Total 1115	C 698	N 201	O 215	S 1	0	0
3	F	134	Total 1067	C 668	N 192	O 206	S 1	0	0
3	G	134	Total 1067	C 668	N 192	O 206	S 1	0	0
3	H	134	Total 1067	C 668	N 192	O 206	S 1	0	0
3	I	134	Total 1067	C 668	N 192	O 206	S 1	0	0
3	J	134	Total 1067	C 668	N 192	O 206	S 1	0	0
3	K	136	Total 1080	C 675	N 195	O 209	S 1	0	0
3	L	136	Total 1080	C 675	N 195	O 209	S 1	0	0
3	M	136	Total 1080	C 675	N 195	O 209	S 1	0	0
3	N	136	Total 1080	C 675	N 195	O 209	S 1	0	0
3	O	136	Total 1080	C 675	N 195	O 209	S 1	0	0
3	a	141	Total 1115	C 698	N 201	O 215	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	b	134	Total	C	N	O	S	0	0
			1067	668	192	206	1		
3	c	136	Total	C	N	O	S	0	0
			1080	675	195	209	1		

- Molecule 4 is a protein called Tail tubular protein gp12.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	P	793	Total	C	N	O	S	0	0
			6313	4003	1087	1208	15		
4	Q	793	Total	C	N	O	S	0	0
			6313	4003	1087	1208	15		
4	R	793	Total	C	N	O	S	0	0
			6313	4003	1087	1208	15		
4	S	793	Total	C	N	O	S	0	0
			6313	4003	1087	1208	15		
4	T	793	Total	C	N	O	S	0	0
			6313	4003	1087	1208	15		
4	x	793	Total	C	N	O	S	0	0
			6313	4003	1087	1208	15		

- Molecule 5 is a protein called Tail tubular protein gp11.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	U	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
5	V	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
5	W	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
5	X	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
5	Y	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
5	Z	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		
5	d	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		
5	e	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		
5	f	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	g	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		
5	h	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
5	i	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		

- Molecule 6 is a protein called Portal protein.

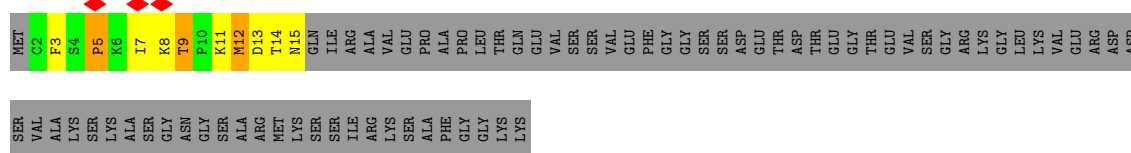
Mol	Chain	Residues	Atoms					AltConf	Trace
6	j	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	k	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	l	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	m	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	n	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	o	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	p	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	q	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	r	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	s	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	t	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	u	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		

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.

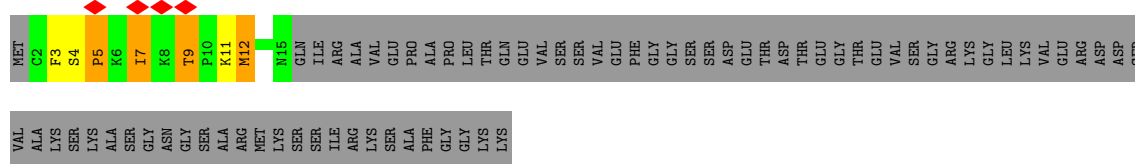
• Molecule 1: Protein 6.7

Chain 0: 84%



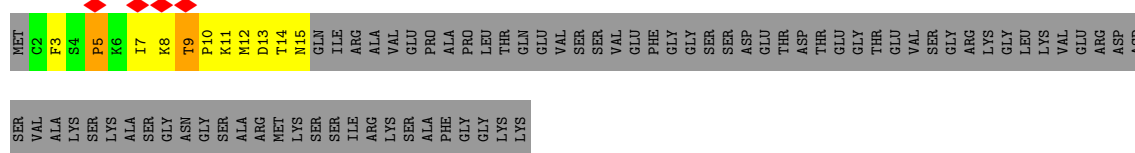
• Molecule 1: Protein 6.7

Chain 3: 84%



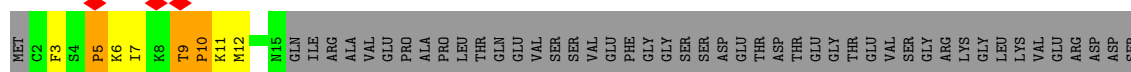
• Molecule 1: Protein 6.7

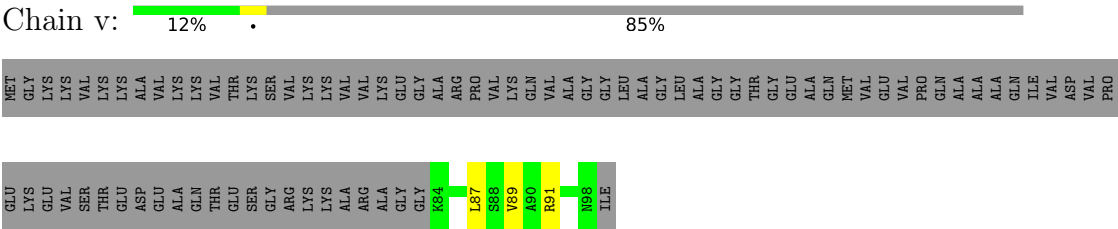
Chain 4: 84%



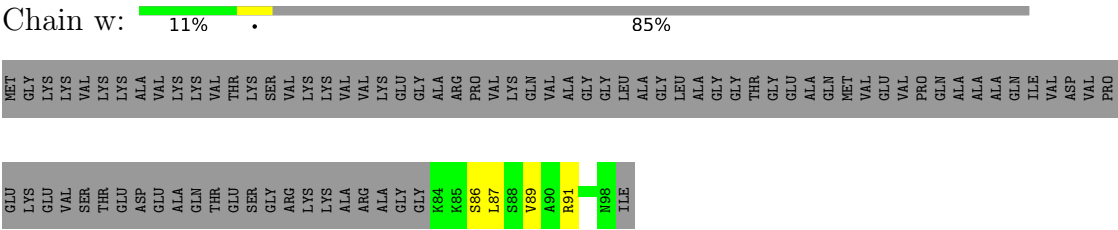
• Molecule 1: Protein 6.7

Chain 5: 84%

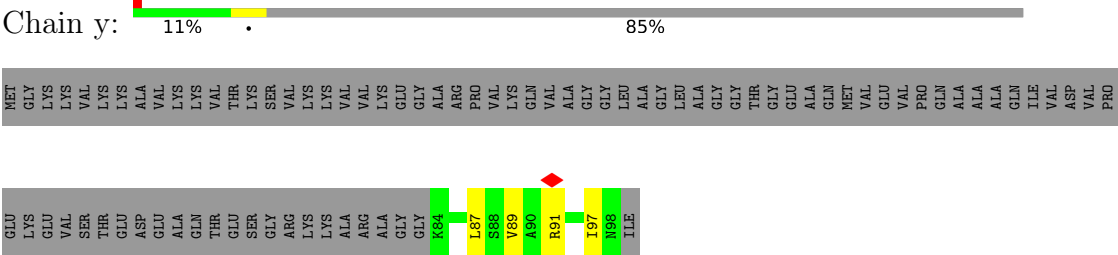




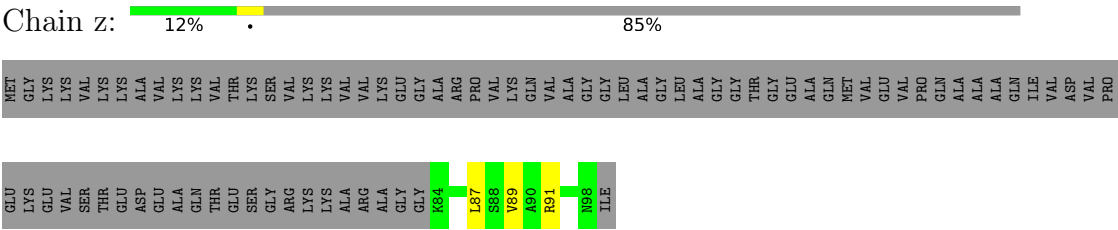
• Molecule 2: Protein 7.3



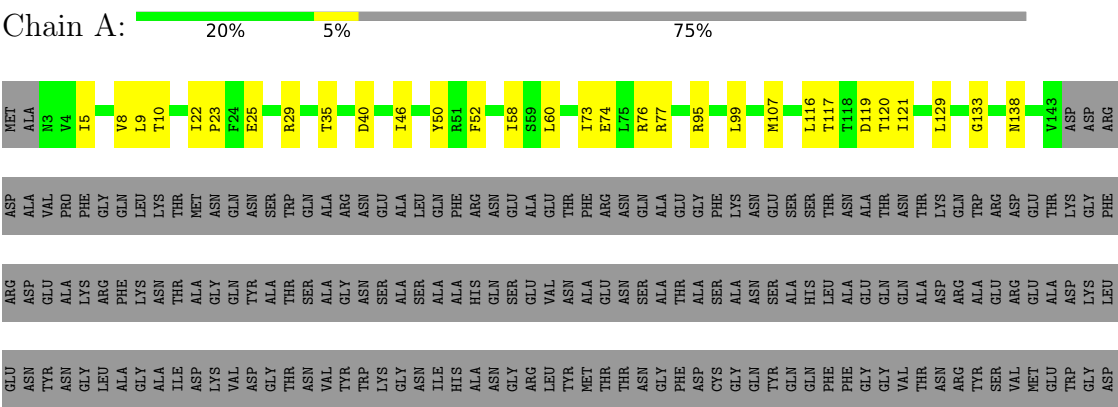
• Molecule 2: Protein 7.3



• Molecule 2: Protein 7.3



• Molecule 3: Tail fiber protein



[illegible]

- Molecule 3: Tail fiber protein

[illegible]

- Molecule 3: Tail fiber protein



LEU	GLY	LYS	PHE	MET
TYR	LEU	ARG	GLY	ALA
TRP	ALA	PHE	GLN	N3
GLN	GLY	LYS	LEU	V4
VAL	ALA	ASN	LYS	I5
ARG	ILE	THR	THR	
ARG	ASP	ALA	MET	V8
GLU	LYS	GLY	ASN	L9
TRP	VAL	GLN	GLN	T10
THR	ASP	TYR	ASN	
THR	GLY	ALA	SER	I22
ALA	GLY	THR	TRP	P23
ILE	ASN	SER	GLN	F24
GLY	VAL	ALA	ALA	E25
GLY	TYR	GLY	ARG	Y26
TRP	ASN	ASN	ASN	L27
ILE	LYS	SER	GLU	
GLN	GLY	ALA	ALA	I37
LEU	ASN	SER	LEU	
VAL	ILE	ALA	GLN	I68
VAL	HIS	ALA	PHE	S59
GLY	ALA	HIS	ARG	L60
GLN	ASN	GLN	ASN	
GLY	GLY	SER	GLU	I73
ILE	ARG	GLU	ALA	E74
ILE	LEU	VAL	THR	L75
THR	TYR	ASN	GLU	R76
GLN	MET	ALA	PHE	R77
GLY	THR	GLU	ARG	
GLY	THR	ASN	ASN	T81
ALA	ASN	SER	GLN	
MET	GLY	ALA	ALA	R95
THR	PHE	THR	GLU	
GLY	ASP	ALA	ALA	L99
GLN	CYS	SER	PHE	
LEU	GLY	ALA	LYS	I104
LYS	GLN	ASN	ASN	
LEU	TYR	SER	GLU	E111
LEU	GLN	ALA	SER	
ASN	GLN	HIS	SER	D115
GLY	PHE	LEU	THR	L116
HIS	PHE	ALA	ASN	T117
VAL	GLY	GLU	ALA	
LEU	GLY	GLN	THR	T120
LEU	THR	GLN	ASN	I121
LEU	THR	ALA	THR	
GLU	ASN	ASP	LYS	D130
SER	ARG	ARG	GLN	
ALA	TYR	ARG	TRP	R134
SER	SER	GLU	ARG	
ASP	VAL	ARG	ASP	A140
LYS	MET	GLU	GLU	
ALA	GLU	ALA	THR	V143
HIS	TRP	ASP	LYS	ASP
TYR	GLY	LYS	GLY	ASP
ILE	ASP	LEU	PHE	ARG
LEU	GLU	GLU	ASP	ASP
SER	ASN	ASN	ARG	ALA
LYS	GLY	TYR	GLU	VAL
TRP	TRP	ASN	ALA	

[illegible]

- Molecule 3: Tail fiber protein

[illegible]

- Molecule 3: Tail fiber protein



ILE	ASP	LEU	PHE	ARG	MET
LEU	GLU	GLU	ARG	ASP	ALA
SER	ASN	ASN	ASP	ALA	N3
ASP	GLY	TYR	GLU	VAL	V4
GLY	TRP	ASN	ALA	PRO	I5
ASN	MET	GLY	LYS	PHE	V8
ARG	TYR	ALA	PHE	GLN	L9
VAL	VAL	GLY	LYS	LEU	T10
ASN	GLN	ALA	ASN	LYS	
TRP	ARG	ILE	THR	THR	I22
TYR	ARG	ASP	ALA	MET	P23
ILE	GLU	LYS	GLY	ASN	F34
GLY	THR	VAL	GLN	GLN	E25
THR	THR	ASP	TYR	ASN	Y26
GLY	THR	GLY	ALA	SER	
SER	ALA	THR	THR	TRP	R29
ASP	ILE	ASN	SER	GLN	
ASN	GLY	VAL	ALA	ALA	T35
ASN	GLY	TYR	GLY	ARG	
ASN	ASN	TRP	ASN	ASN	D40
ASP	ILE	LYS	SER	GLU	
CYS	GLN	GLY	ALA	ALA	I46
THR	LEU	ASN	SER	LEU	
PHE	VAL	ILE	ALA	GLN	Y50
HIS	VAL	HIS	ALA	PHE	R51
SER	ASN	ALA	HIS	ARG	F52
TYR	GLY	ASN	GLN	ASN	
VAL	GLN	GLY	SER	GLU	R55
HIS	ILE	ARG	GLU	ALA	
GLY	ILE	LEU	VAL	GLU	I58
THR	THR	TYR	ASN	THR	S59
THR	GLN	MET	ALA	PHE	L60
LEU	GLY	GLY	GLU	ARG	
THR	GLY	THR	ASN	ASN	I73
LEU	ALA	ASN	SER	GLN	E74
LYS	MET	GLY	ALA	ALA	L75
GLN	THR	PHE	THR	GLU	R76
ASP	GLY	ASP	ALA	GLY	R77
TYR	GLY	CYS	SER	PHE	
ALA	LEU	GLY	ALA	LYS	R95
VAL	LYS	GLN	ASN	ASN	
VAL	LEU	TYR	SER	GLU	L99
ASN	GLN	GLN	ALA	GLU	
LYS	ASN	GLN	HIS	SER	M107
HIS	GLY	PHE	LEU	THR	
PHE	HIS	PHE	ALA	ASN	L116
HIS	VAL	GLY	GLU	ALA	T117
VAL	LEU	GLY	GLN	THR	T118
GLY	GLN	VAL	GLN	ASN	D119
GLN	THR	THR	ALA	THR	T120
ALA	GLU	ASN	ASP	LYS	I121
VAL	SER	ARG	ARG	GLN	
VAL	ALA	TYR	ALA	TRP	G133
ALA	SER	SER	GLU	ARG	
THR	ASP	VAL	ARG	ASP	N138
ASP	LYS	MET	GLU	GLU	
GLY	ALA	GLU	ALA	THR	V143
ASN	HIS	TRP	ALA	ASP	
ILE	TYR	GLY	TYG	GLY	ASP

[illegible]

- Molecule 3: Tail fiber protein

[illegible]

- Molecule 3: Tail fiber protein



VAL	ALA	TYR	ALA	TRP	ALA	LEU	MET
THR	SER	SER	SER	ARG	GLU	ASN	ALA
ASP	ASP	VAL	ASP	ASP	GLU	ASN	ALA
GLY	LYS	MET	GLU	THR	ALA	VAL	I5
ASN	HIS	TRP	ASP	LYS	ASP	LYS	V8
ILE	TYR	GLY	ASP	GLY	ASP	ASP	
GLN	ILE	ASP	LEU	PHE	LEU	ARG	Q12
THR	LEU	GLU	GLU	GLU	ASN	ASP	L13
THR	SER	ASN	ASN	ASP	ASP	ALA	L13
TRP	LYS	GLY	TYR	GLU	VAL	VAL	I22
TRP	ASP	TRP	ASN	ALA	PRO	ALA	
GLY	GLY	LEU	GLY	LYS	PHE	PHE	L36
GLY	ASN	MET	GLY	ARG	GLY	GLY	I37
LYS	ARG	TYR	ALA	PHE	GLN	GLN	
TRP	VAL	VAL	GLY	LYS	LEU	LEU	R41
LEU	ASN	GLN	ALA	ASN	LYS	LYS	
ASP	TRP	ARG	ILE	THR	THR	THR	L44
ALA	TYR	ARG	ASP	ALA	MET	MET	T45
TYR	ILE	GLU	LYS	GLY	GLY	ASN	I46
LEU	GLY	TRP	VAL	GLN	GLN	GLN	N47
ARG	ARG	THR	ASP	TYR	ASN	ASN	T48
ASP	GLY	THR	GLY	ALA	SER	SER	D49
SER	SER	ALA	THR	THR	THR	THR	Y50
PHE	ASP	ILE	ASN	SER	GLN	GLN	
VAL	ASN	GLY	VAL	ALA	ALA	ALA	A53
ALA	ASN	GLY	TYR	GLY	ARG	ARG	T54
LYS	ASN	ASN	TRP	ASN	GLU	GLU	T57
SER	ASP	ILE	LYS	SER	ASN	ASN	I58
LYS	CYS	GLN	GLY	ALA	ALA	ALA	S59
ALA	THR	LEU	ASN	SER	GLY	GLY	L60
THR	PHE	VAL	ILE	ALA	ILE	PHE	
GLY	HIS	VAL	ILE	ALA	ALA	ALA	M64
THR	HIS	ASN	GLY	HIS	ASN	ASN	
SER	VAL	TYR	GLY	GLN	GLN	GLU	T72
SER	HIS	ILE	ARG	GLU	ALA	ALA	
GLY	GLY	ILE	LEU	VAL	GLU	GLU	R76
SER	THR	THR	THR	ASN	ASN	PHE	
ALA	THR	GLN	MET	ALA	ALA	ARG	T81
GLY	LEU	GLY	THR	GLU	ASN	ASN	
THR	THR	GLY	THR	ASN	ASN	ASN	R84
GLY	LEU	ALA	ASN	SER	GLN	GLN	V101
VAL	LYS	MET	GLY	ALA	ALA	ALA	
VAL	ASP	THR	ASP	ALA	GLY	GLY	M107
THR	TYR	GLN	GLN	CYS	SER	PHE	
VAL	ALA	LEU	GLY	GLY	ALA	LYS	L116
SER	VAL	LYS	GLN	ASN	ASN	ASN	
ASP	VAL	LEU	LEU	SER	GLU	GLU	T120
GLN	ASN	GLN	GLN	ALA	SER	ALA	I121
LEU	LYS	ASN	GLN	HIS	THR	THR	
ARG	HIS	GLY	PHE	LEU	ALA	ASN	N124
PHE	PHE	HIS	PHE	ALA	GLU	ALA	
ARG	HIS	VAL	GLY	GLU	THR	THR	H128
ASN	VAL	LEU	LEU	GLN	ASN	ASN	L129
ILE	GLY	GLN	THR	ALA	THR	THR	D130
TRP	GLN	LEU	VAL	ALA	ASP	LYS	
ILE	ALA	GLU	ASN	ASP	ARG	GLN	N135
VAL	VAL	SER	ASP	ALA	ASP	GLN	

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• Molecule 3: Tail fiber protein

Chain H:  20% 5% 76%

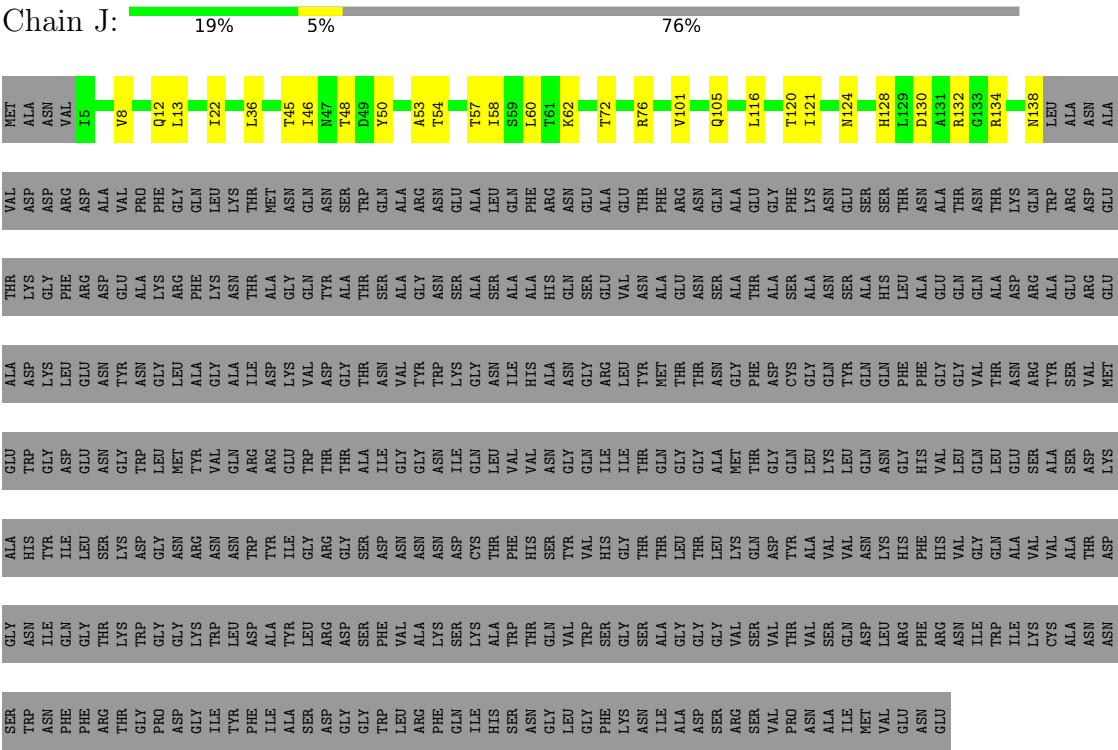
ARG	THR	GLY	GLY	PRO	ASP	GLY	GLY	LYS	TRP	LEU	ASP	ALA	TYR	LEU	SER	ASP	ASP	GLY	GLY	ASP	THR	THR	GLN	ASN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
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• Molecule 3: Tail fiber protein

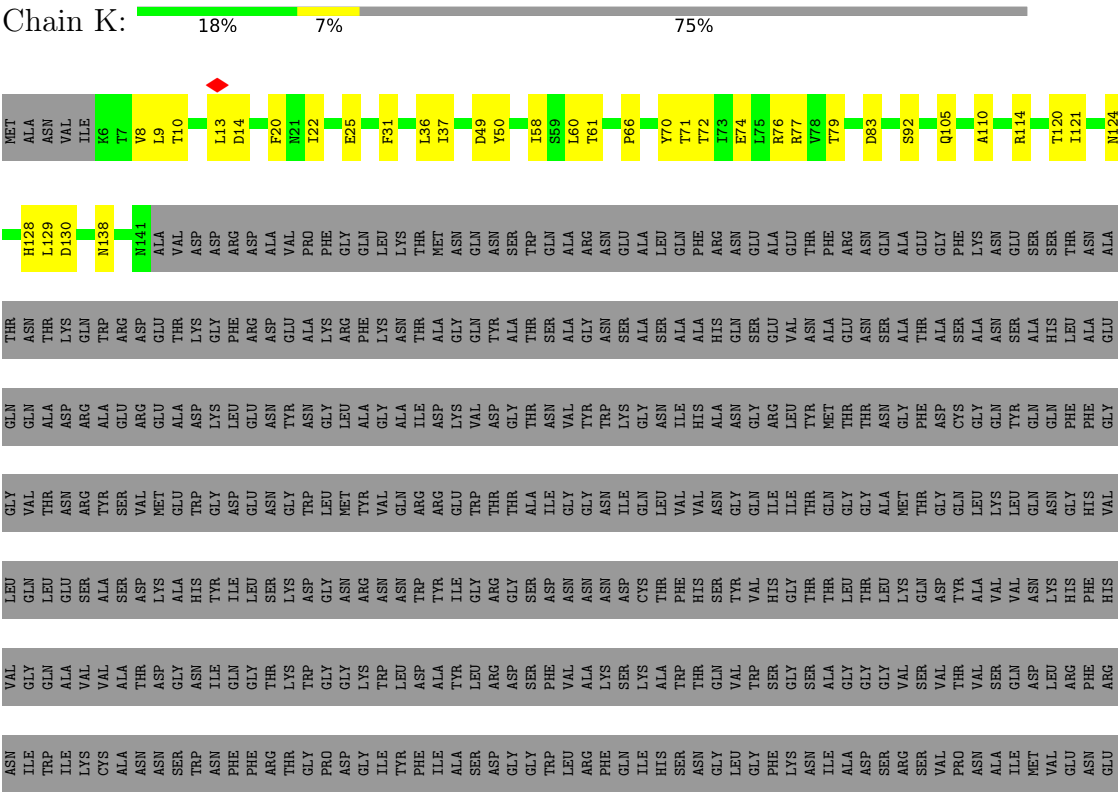
Chain I:  19% 5% 76%

TRP	ASN	HIS	TRP	ASP	LYS	ASP	LYS	ASP	MET
ASN	ILE	TYR	GLY	GLY	GLY	LEU	LEU	GLY	ALA
ASN	GLN	ILE	ASP	LEU	LEU	GLY	ASP	ASN	VAL
PHE	THR	LEU	GLU	ASN	ASN	GLY	ASP	ASP	I5
ARG	THR	SER	ASN	TYR	TYR	ASP	GLY	GLY	V8
THR	LYS	LYS	GLY	GLY	ALA	GLY	GLY	GLY	Q12
GLY	TRP	ASP	TRP	TRP	VAL	VAL	VAL	VAL	L13
PRO	GLY	GLY	TRP	TRP	GLN	GLN	GLY	LEU	I22
ASP	GLY	ASN	GLY	GLY	ASN	ASN	ASN	LYS	T45
ILE	TRP	ASN	VAL	VAL	ASN	ASP	THR	THR	T48
TYR	LEU	ASN	GLN	GLN	ASN	ASP	GLY	LYS	D49
PHE	ASP	THR	THR	THR	THR	GLY	ALA	ASN	Y50
ASN	ASP	ASP	ALA	THR	THR	THR	THR	THR	A53
ILE	ALA	TYR	ARG	ASP	ILE	ASN	SER	GLN	T54
ALA	TYR	ILE	GLU	GLY	GLU	VAL	ALA	ALA	T57
SER	LEU	GLY	TRP	VAL	VAL	TYR	GLY	ARG	I58
ASP	ARG	ASN	GLY	GLY	GLY	GLY	ASN	ASN	S59
PHE	ALA	ASN	ASN	THR	ASN	TRP	ASN	GLY	L60
GLN	LYS	ASN	ASN	THR	ILE	LYS	SER	ALA	T71
PHE	SER	ASP	ASN	GLY	GLY	GLY	ASN	ALA	T72
GLY	GLN	THR	VAL	GLY	THR	ASN	ASN	PHE	R76
LEU	VAL	TYR	GLY	ASN	GLN	ASN	GLY	ARG	T81
THR	TRP	VAL	GLN	GLY	SER	GLY	GLY	THR	B84
PHE	TRP	HIS	ILE	ILE	GLY	THR	GLY	GLY	V101
GLY	TRP	THR	ILE	ARG	ASN	THR	SER	ASN	Q105
ASN	GLY	GLY	ILE	GLY	GLY	THR	ALA	ALA	T120
SER	SER	GLN	THR	PHE	THR	ASP	THR	GLY	I121
VAL	VAL	ASP	GLY	GLY	ALA	GLY	ALA	PHE	
PRO	THR	TYR	GLN	CYS	SER	GLY	ALA	LYS	
ASN	VAL	VAL	LYS	GLN	ASN	ASN	ASN	ASN	N124
ALA	SER	VAL	VAL	GLY	THR	THR	SER	GLY	
ILE	GLN	VAL	LEU	GLN	GLN	GLN	ALA	THR	H128
VAL	LEU	LYS	ASN	ASN	GLY	GLY	HIS	SER	I129
GLY	ARG	HIS	GLY	PHE	THR	PHE	LEU	THR	D130
ASN	PHE	PHE	HIS	THR	THR	THR	ALA	ASN	A131
VAL	ARG	THR	VAL	VAL	GLY	GLY	GLY	ALA	R132
GLU	ASN	VAL	LEU	GLY	GLY	THR	GLN	THR	G133
THR	ILE	GLY	GLN	VAL	VAL	VAL	GLN	ASN	R134
ILE	THR	GLN	LEU	THR	THR	THR	ALA	THR	
LYS	VAL	ALA	GLU	ASN	ASP	ASP	ASP	LYS	V137
CYS	VAL	VAL	SER	GLY	ARG	ARG	GLN	GLN	N138
ALA	VAL	VAL	ALA	TYR	ALA	TRP	ALA	TRP	LEU
ASN	ALA	ALA	SER	VAL	ARG	ARG	GLY	ASP	ALA
GLY	ASN	THR	ASP	VAL	THR	THR	ASP	GLY	ASN
THR	ASN	GLY	LYS	THR	GLY	GLY	GLY	THR	ALA
SER	SER	THR	THR	THR	THR	THR	THR	THR	VAL
ASN	THR	GLY	ALA	THR	THR	THR	THR	THR	THR

● Molecule 3: Tail fiber protein



● Molecule 3: Tail fiber protein



● Molecule 3: Tail fiber protein

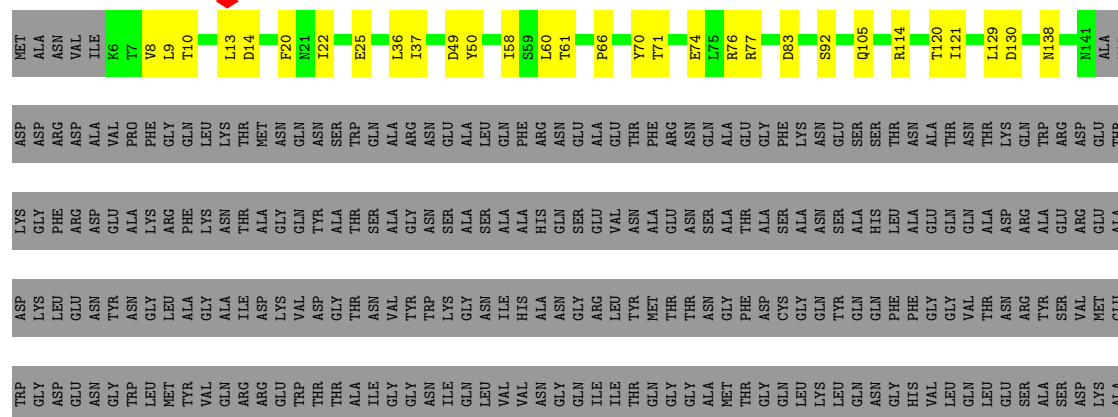
Chain L: 18% 7% 75%

VAL	GLU	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL	ASN	GLU	VAL
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● Molecule 3: Tail fiber protein

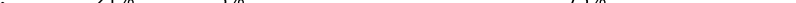
Chain M: 17% 7% 75%

MET	A110	LYS	ALA	ASN	GLN	GLY	LEU	VAL	ILE	K6	T7	V8	L9	L13	D14	F20	I21	T22	P23	F24	F31	V32	L36	I37	L44	D49	V50	T56	L60	T61	P66	Y70	T71	E74	L75	R76	T79	R84	D87	S92	R95	D98	Q105	T106	M107																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
ASN	R114	GLU	HIS	SER	ALA	THR	ASN	ASP	ARG	GLY	THR	THR	ASN	THR	GLN	ARG	ALA	VAL	ASP	ASP	ASP	ASP	VAL	PRO	PHE	GLY	LEU	ASN	THR	GLN	ASN	SER	TRP	GLN	ALA	ARG	ASN	GLU	ALA	GLY	THR	VAL	ASN	GLN	ALA	GLY	THR	ALA	GLY	PHE																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
VAL	M124	SER	ALA	ALA	LEU	THR	GLU	GLN	ALA	GLY	GLY	GLY	GLN	ALA	ASP	ARG	GLU	GLY	ASP	ASP	ASP	ASP	VAL	ASP	LYS	PHE	GLY	LYS	THR	LYS	GLN	ALA	THR	THR	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GL



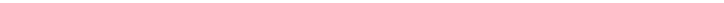
[illegible]

- Molecule 3: Tail fiber protein

Chain a:  21% 5% 75%

Tyr	Leu	Asn	Gln	Ala	Asn	Lys	Met
Phe	Asp	Trp	Arg	Ile	Thr	Thr	Ala
Ile	Ala	Tyr	Arg	Tyr	Ala	Met	Asn
Ala	Leu	Ile	Glu	Lys	Gln	Gln	V4
Ser	Leu	Gly	Trp	Val	Gln	Asn	V8
Asp	Arg	Arg	Thr	Asp	Tyr	Asn	L9
Gly	Asp	Gly	Thr	Gly	Ala	Ser	T10
Gly	Ser	Ser	Ala	Thr	Thr	Trp	T11
Trp	Phe	Asp	Ile	Gly	Ser	Gln	L13
Leu	Val	Asn	Gly	Val	Ala	Ala	I22
Arg	Ala	Asn	Asn	Tyr	Gly	Arg	P23
Phe	Lys	Asp	Gln	Trp	Asn	Asn	F24
Gln	Ser	Asp	Ile	Lys	Ser	Glu	E25
Ile	Lys	Cys	Gln	Gly	Ala	Ala	L36
His	Ala	Thr	Val	Ile	Ala	Gln	R85
Ser	Thr	Phe	Val	His	Ala	Phe	I58
Asn	Trp	His	Val	Ala	Ala	Arg	S59
Asn	Thr	Ser	Val	Ala	Asn	Thr	L60
Gly	Gln	Ser	Asn	Ala	His	Arg	I73
Leu	Val	Tyr	Gly	Ala	Gln	Asn	R76
Gly	Trp	Val	Gln	Gly	Ser	Glu	R77
Phe	Ser	His	Ile	Arg	Ser	Ala	L94
Leu	Val	His	Ile	Ala	Ala	Ala	L99
Ala	Val	Trp	Ala	Gly	Thr	Gly	T106
Ala	Val	Val	Met	Phe	Ala	Ala	M107
Ile	Gln	Val	Thr	Gly	Ser	Ser	E111
Ala	Val	Asn	Gln	Gln	Ala	Ala	T117
Glu	Arg	His	Gly	Phe	Leu	Thr	D119
Asn	Phe	Phe	His	Ala	Glu	Ala	T120
Glu	Arg	His	Val	Gly	Gln	Asn	L129
Asn	Trp	Val	Gln	Thr	Ala	Thr	D130
Trp	Lys	Val	Glu	Arg	Asp	Lys	A140
Ala	Val	Val	Ser	Val	Ala	Arg	V143
Ala	Ala	Ala	Ser	Met	Glu	Glu	ASP
Ala	Asn	Asp	Lys	Ala	Arg	Thr	ASP
Ala	Ser	Gly	His	Thr	Ala	Lys	ARG
Ala	Trp	Ala	Tyr	Trp	Lys	Gly	ASP
Ala	Gln	Gln	Ile	Asp	Leu	Phe	ARG
Ala	Gly	Thr	Leu	Glu	Glu	Arg	ASP
Ala	Phe	Thr	Ser	Asn	Asn	Ala	ASP
Ala	Arg	Lys	Ser	Gly	Thr	Val	VAL
Ala	Thr	Lys	Lys	Thr	Tyr	Glu	PRO
Ala	Trp	Asp	Asp	Gly	Ala	Lys	PHE
Ala	Gly	Gly	Gly	Met	Leu	Arg	GLY
Ala	Ala	Lys	Asn	Tyr	Gly	Phe	GLN
Ala	Trp	Trp	Arg	Val	Ala	Thr	GLN

- Molecule 3: Tail fiber protein

Chain b:  20% 5% 76%

[illegible]

THR	LVS	THR	GLY	PRO	ASP	GLY	ILE	THR	PHE	ILE	ALA	ALA	ASP	GLY	ARG	PHE	GLN	VAL	ASP	LEU	ARG	PHE	ASN	ILE	THR	THR	LVS	CYS	ALA	ASN	ASN	THR	PHE	PHE
ARG	THR	GLY	PRO	ASP	GLY	ILE	THR	PHE	ILE	ALA	ALA	ASP	GLY	ARG	PHE	GLN	VAL	ASP	LEU	ARG	PHE	ASN	ILE	THR	THR	LVS	CYS	ALA	ASN	ASN	THR	PHE	PHE	

- Molecule 3: Tail fiber protein

Chain c: 19% 6% 75%

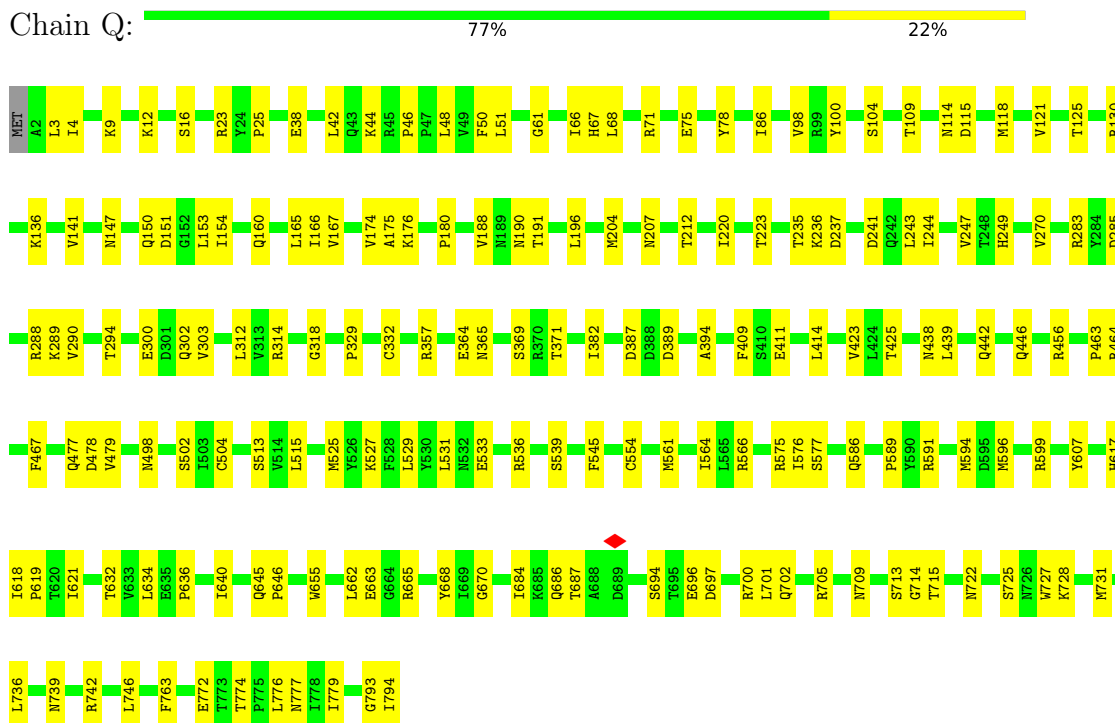
[illegible]

- Molecule 4: Tail tubular protein gp12

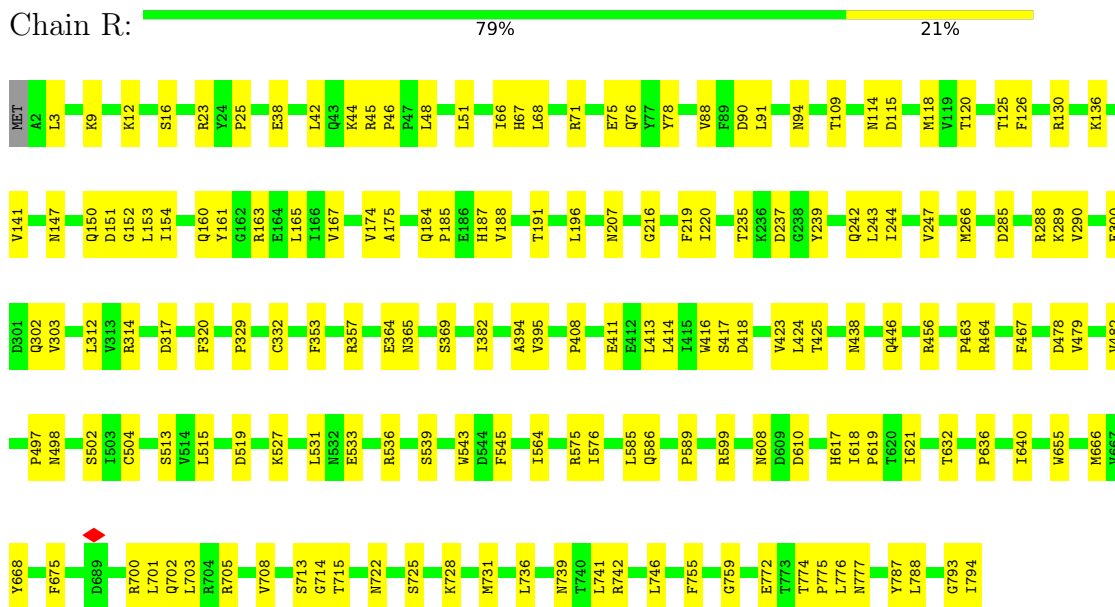
Chain P: 79% 21%

[illegible]

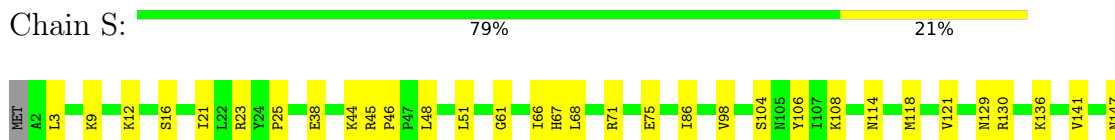
- Molecule 4: Tail tubular protein gp12

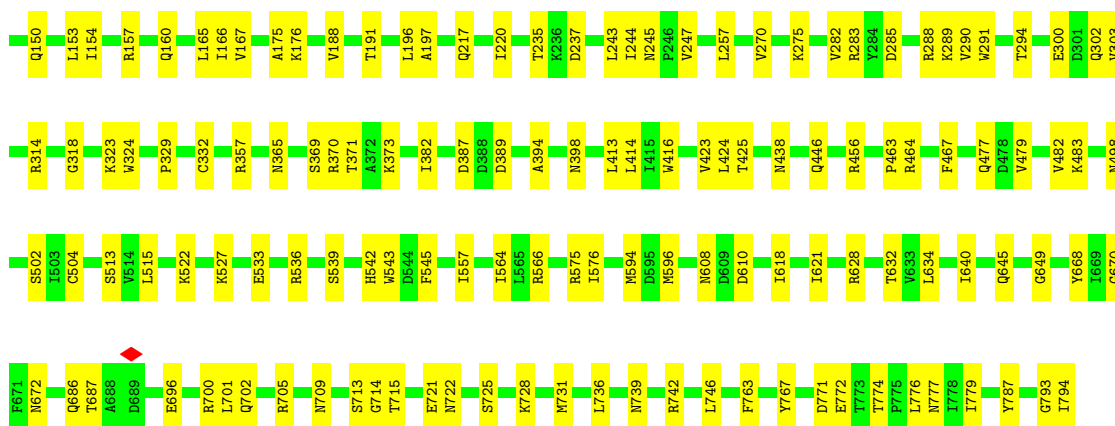


- Molecule 4: Tail tubular protein gp12



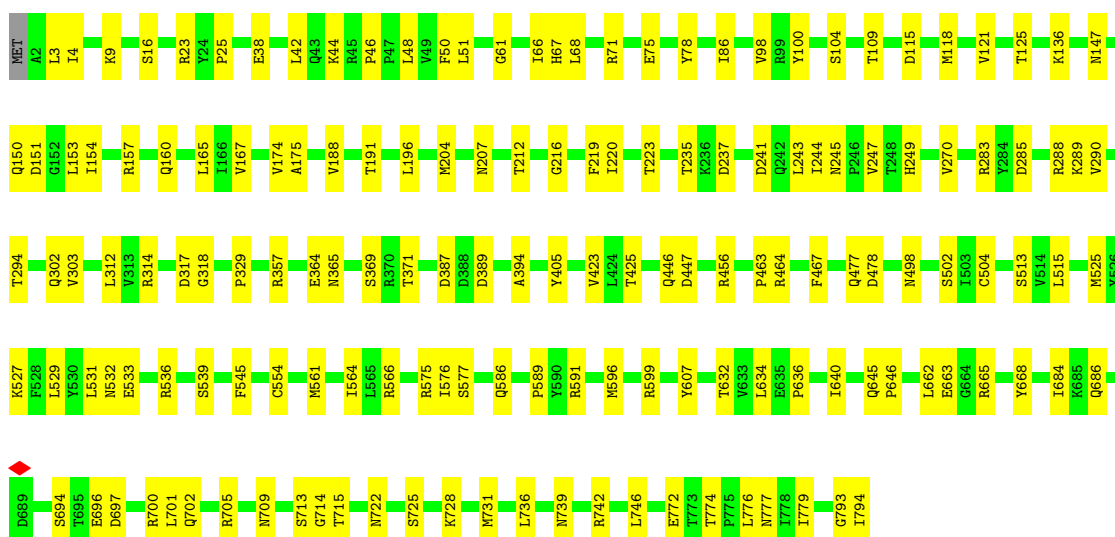
- Molecule 4: Tail tubular protein gp12





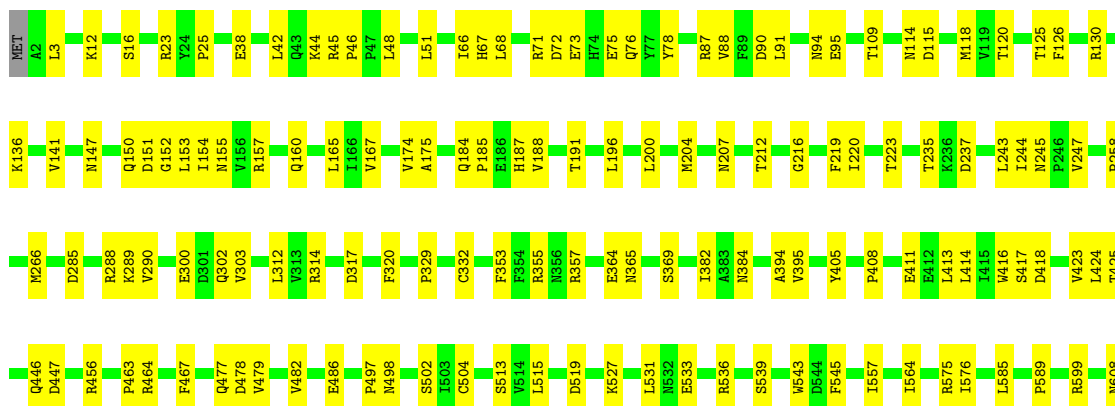
• Molecule 4: Tail tubular protein gp12

Chain T: 80% 20%



• Molecule 4: Tail tubular protein gp12

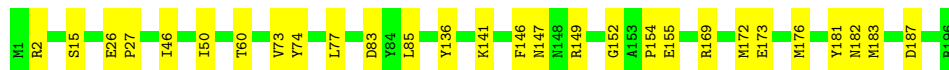
Chain x: 78% 22%





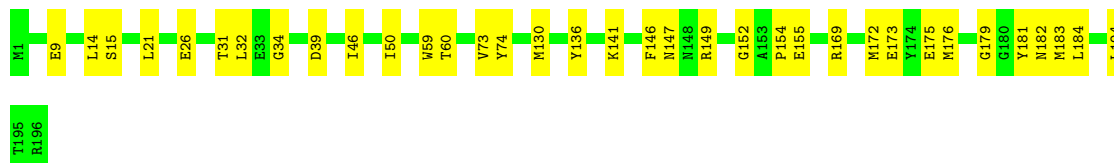
- Molecule 5: Tail tubular protein gp11

Chain U: 86% 14%



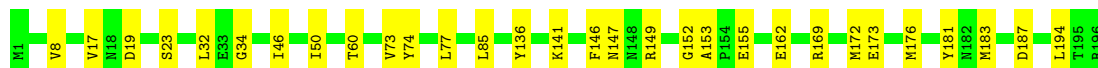
- Molecule 5: Tail tubular protein gp11

Chain V: 82% 18%



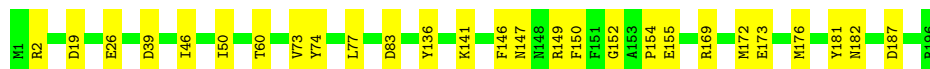
- Molecule 5: Tail tubular protein gp11

Chain W: 85% 15%



- Molecule 5: Tail tubular protein gp11

Chain X: 86% 14%



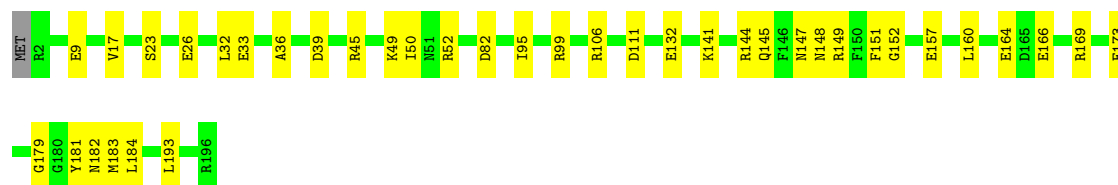
- Molecule 5: Tail tubular protein gp11

Chain Y: 88% 12%



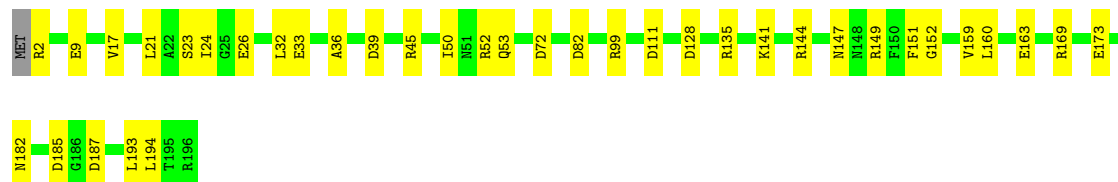
- Molecule 5: Tail tubular protein gp11

Chain Z: 80% 19%



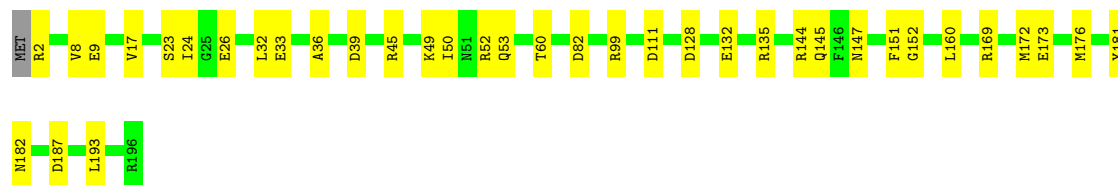
- Molecule 5: Tail tubular protein gp11

Chain d: 81% 19%



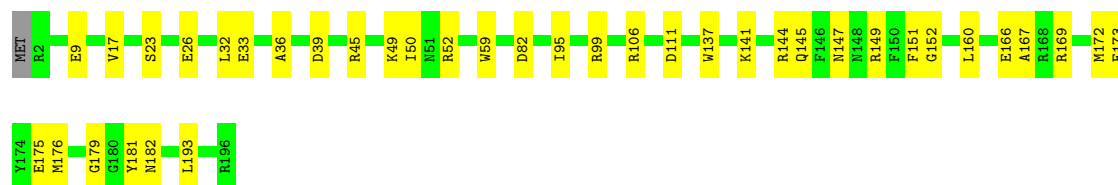
- Molecule 5: Tail tubular protein gp11

Chain e: 81% 19%



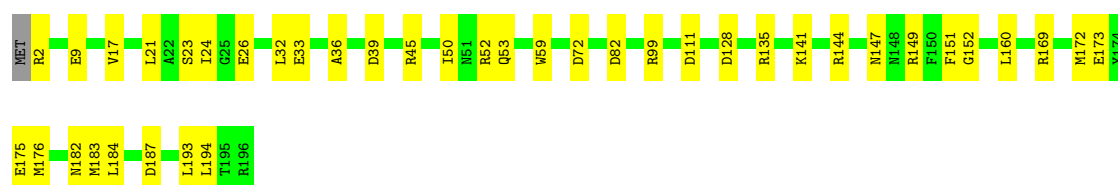
- Molecule 5: Tail tubular protein gp11

Chain f: 80% 19%



- Molecule 5: Tail tubular protein gp11

Chain g: 79% 20%



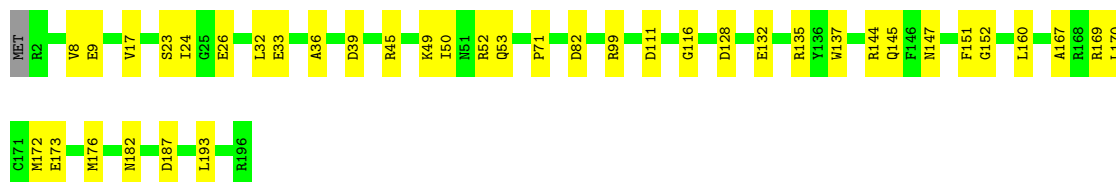
- Molecule 5: Tail tubular protein gp11

Chain h: 85% 15%



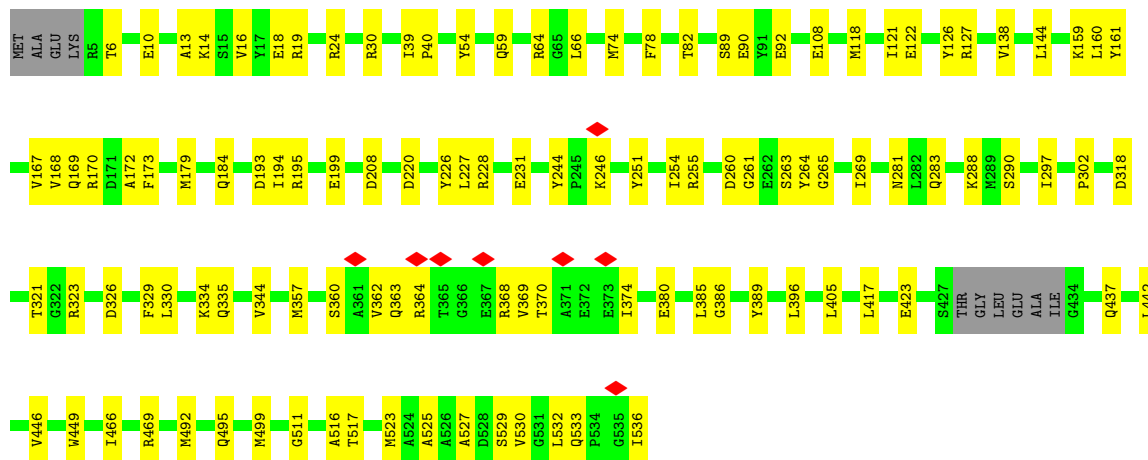
• Molecule 5: Tail tubular protein gp11

Chain i: 80% 20%



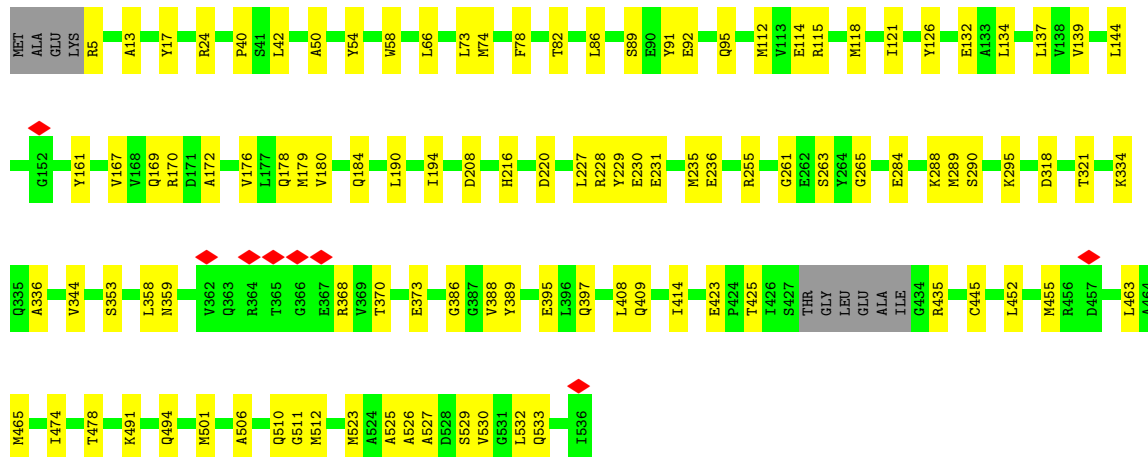
• Molecule 6: Portal protein

Chain j: 77% 21%

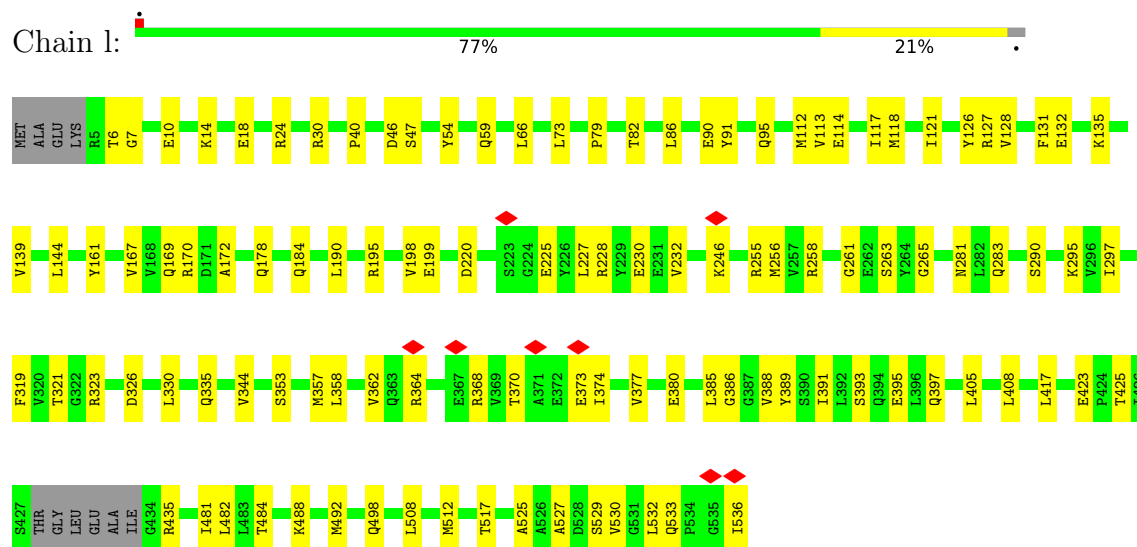


• Molecule 6: Portal protein

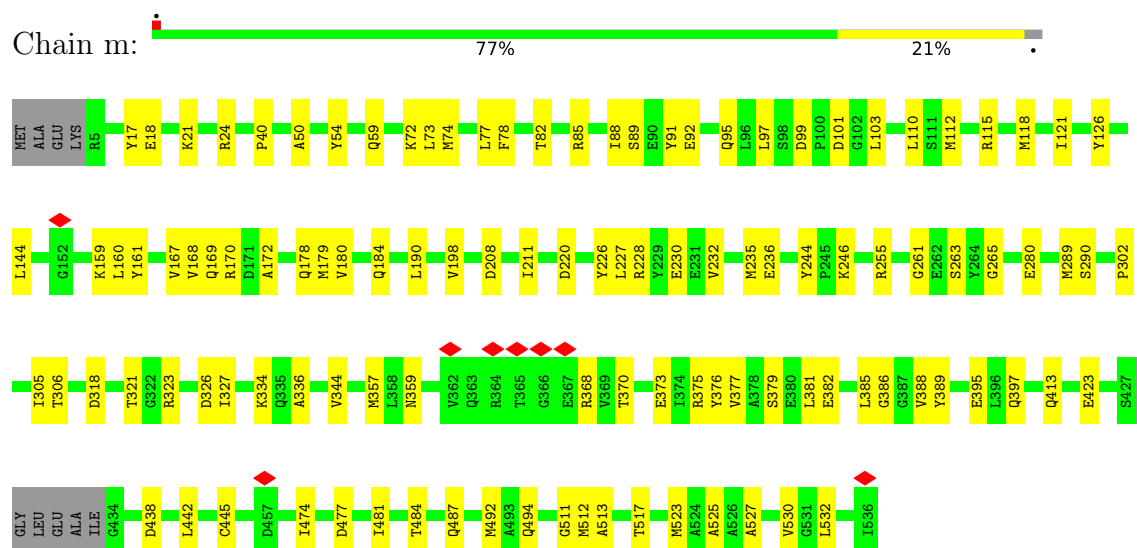
Chain k: 79% 20%



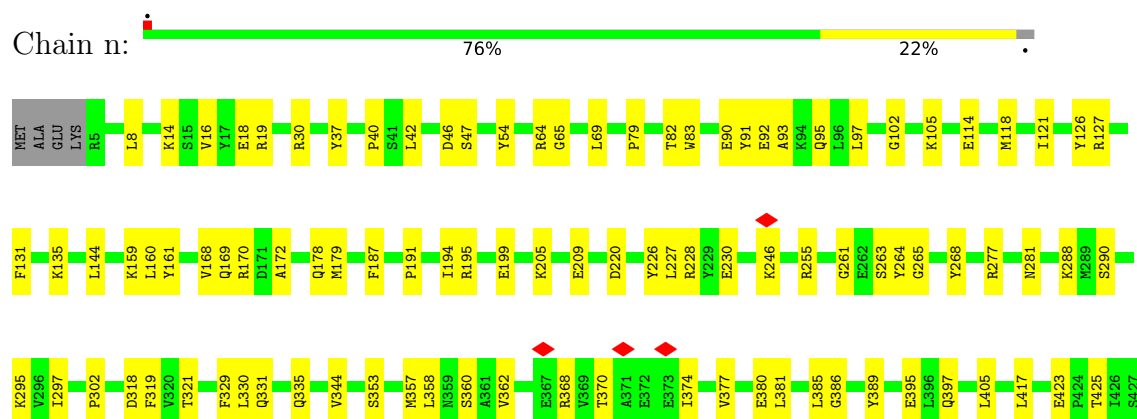
• Molecule 6: Portal protein



• Molecule 6: Portal protein



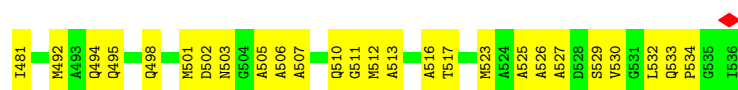
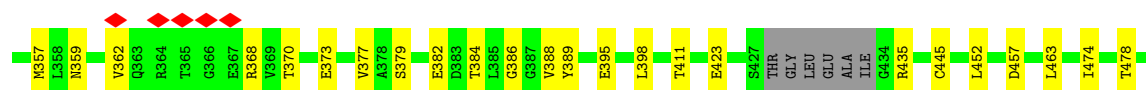
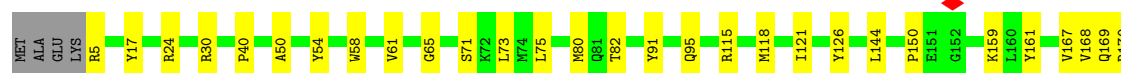
• Molecule 6: Portal protein





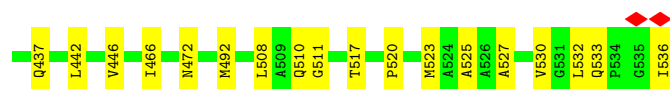
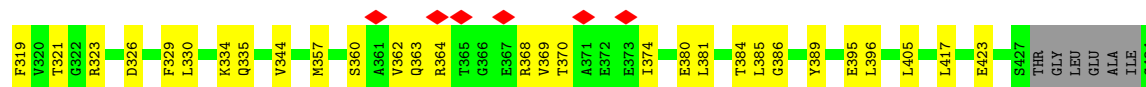
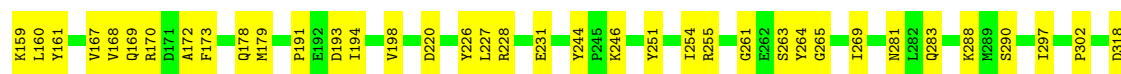
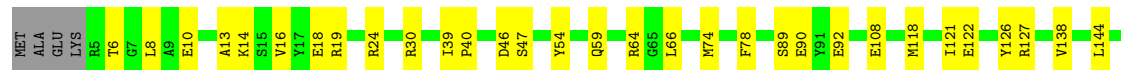
• Molecule 6: Portal protein

Chain o: 77% 21%



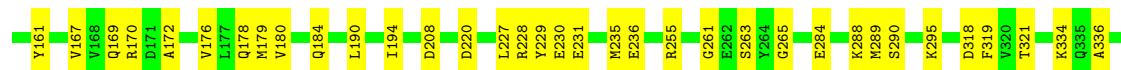
• Molecule 6: Portal protein

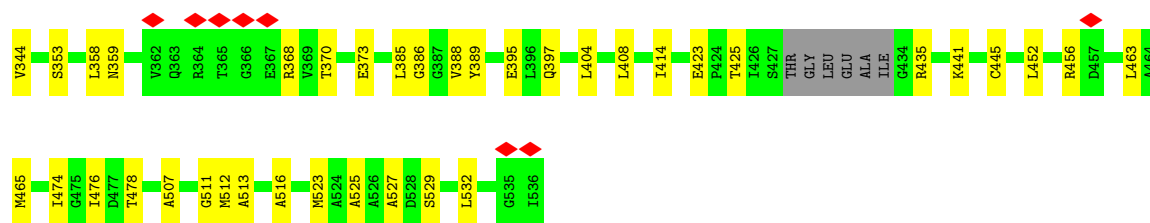
Chain p: 77% 21%



• Molecule 6: Portal protein

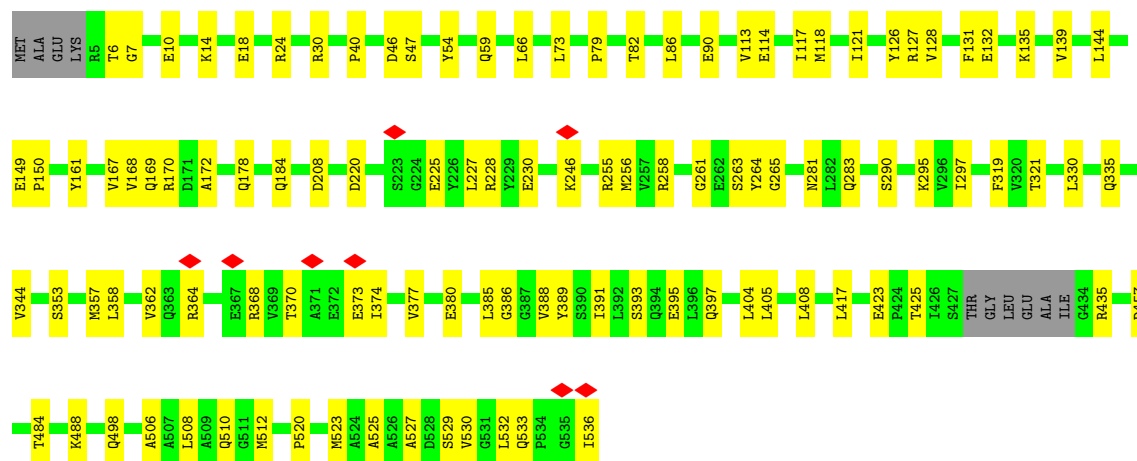
Chain q: 79% 19%





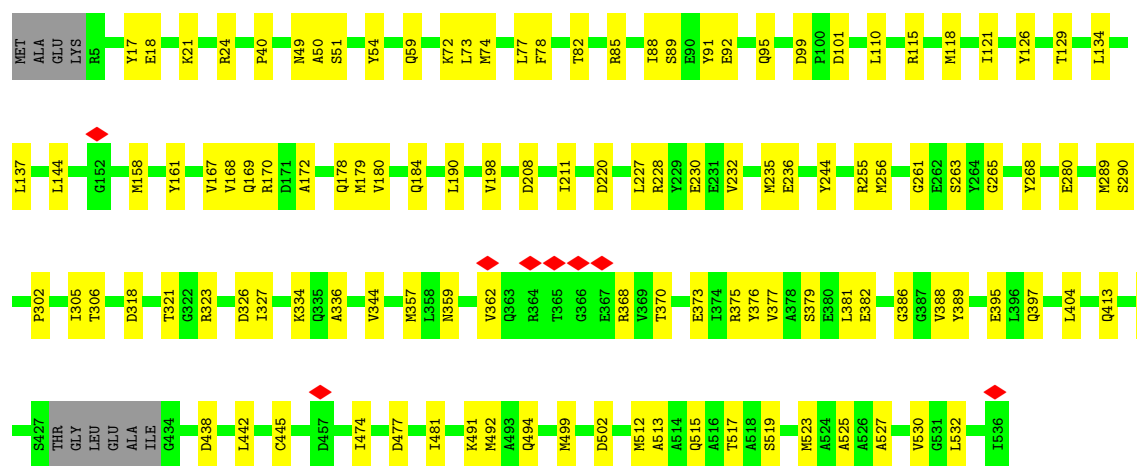
• Molecule 6: Portal protein

Chain r: 78% 20%



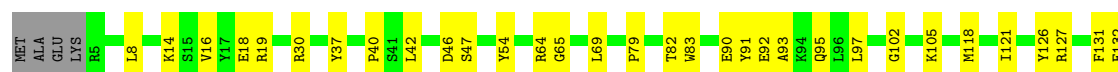
• Molecule 6: Portal protein

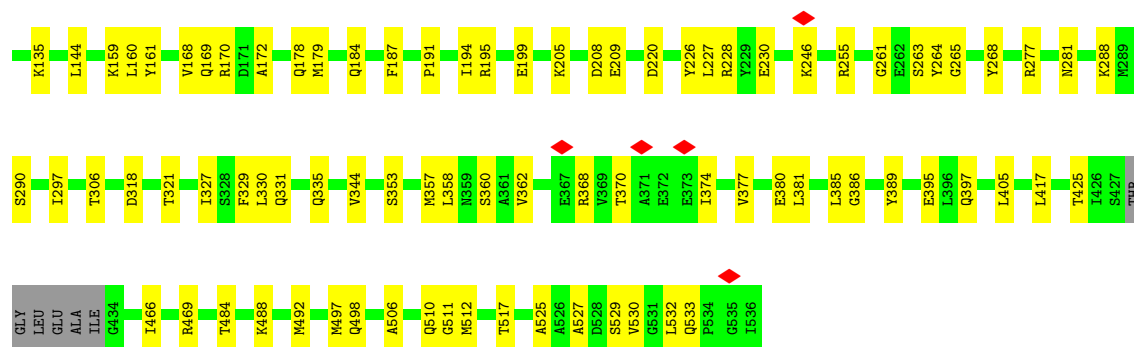
Chain s: 76% 22%



• Molecule 6: Portal protein

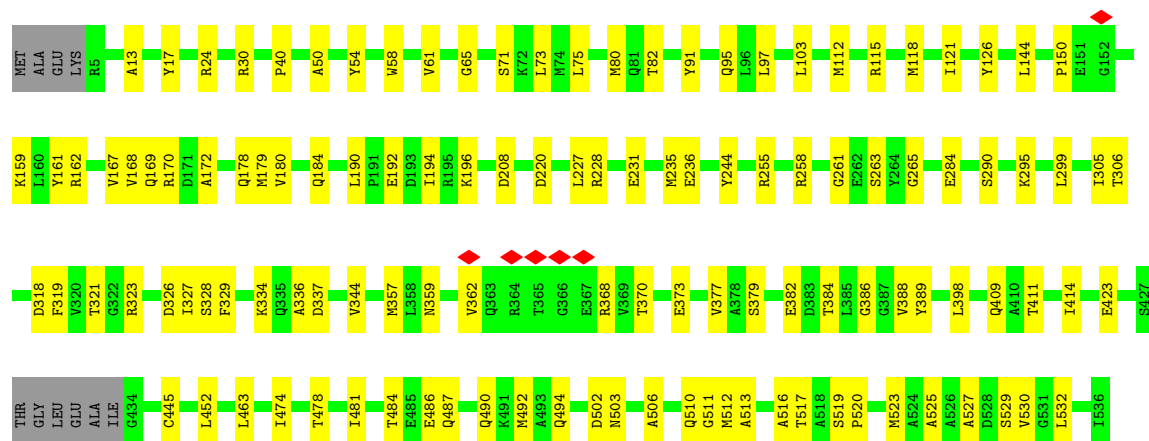
Chain t: 77% 21%





• Molecule 6: Portal protein

Chain u: 76% 22%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	65620	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	57.231	Depositor
Minimum map value	-33.541	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	2.152	Depositor
Recommended contour level	2	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 [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.61	0/112	1.38	2/149 (1.3%)
1	3	0.55	0/112	1.44	2/149 (1.3%)
1	4	0.60	0/112	1.40	3/149 (2.0%)
1	5	0.55	0/112	1.45	3/149 (2.0%)
1	6	0.63	0/112	1.40	4/149 (2.7%)
1	7	0.55	0/112	1.54	2/149 (1.3%)
1	8	0.58	0/112	1.41	5/149 (3.4%)
1	9	0.23	0/112	0.63	0/149
1	AA	0.53	0/112	1.47	4/149 (2.7%)
1	AB	0.63	0/112	1.39	4/149 (2.7%)
1	AC	0.52	0/112	1.50	4/149 (2.7%)
1	AD	0.58	0/112	1.32	3/149 (2.0%)
2	1	0.12	0/100	0.30	0/130
2	2	0.13	0/100	0.31	0/130
2	v	0.13	0/100	0.32	0/130
2	w	0.12	0/100	0.30	0/130
2	y	0.13	0/100	0.32	0/130
2	z	0.14	0/100	0.32	0/130
3	A	0.13	0/1130	0.30	0/1538
3	B	0.13	0/1130	0.28	0/1538
3	C	0.13	0/1130	0.28	0/1538
3	D	0.13	0/1130	0.30	0/1538
3	E	0.13	0/1130	0.30	0/1538
3	F	0.12	0/1082	0.30	0/1471
3	G	0.13	0/1082	0.31	0/1471
3	H	0.13	0/1082	0.30	0/1471
3	I	0.13	0/1082	0.32	0/1471
3	J	0.12	0/1082	0.29	0/1471
3	K	0.14	0/1095	0.38	0/1489
3	L	0.14	0/1095	0.38	0/1489
3	M	0.13	0/1095	0.37	0/1489
3	N	0.14	0/1095	0.37	0/1489
3	O	0.13	0/1095	0.38	0/1489
3	a	0.14	0/1130	0.30	0/1538

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	b	0.13	0/1082	0.32	0/1471
3	c	0.14	0/1095	0.37	0/1489
4	P	0.16	0/6473	0.31	0/8804
4	Q	0.15	0/6473	0.31	0/8804
4	R	0.15	0/6473	0.32	0/8804
4	S	0.16	0/6473	0.32	0/8804
4	T	0.15	0/6473	0.31	0/8804
4	x	0.15	0/6473	0.32	0/8804
5	U	0.16	0/1592	0.31	0/2153
5	V	0.17	0/1592	0.30	0/2153
5	W	0.15	0/1592	0.29	0/2153
5	X	0.15	0/1592	0.30	0/2153
5	Y	0.17	0/1592	0.32	0/2153
5	Z	0.17	0/1584	0.32	0/2143
5	d	0.16	0/1584	0.33	0/2143
5	e	0.16	0/1584	0.33	0/2143
5	f	0.16	0/1584	0.31	0/2143
5	g	0.16	0/1584	0.32	0/2143
5	h	0.15	0/1592	0.28	0/2153
5	i	0.16	0/1584	0.34	0/2143
6	j	0.14	0/4131	0.32	0/5590
6	k	0.14	0/4131	0.31	0/5590
6	l	0.14	0/4131	0.31	0/5590
6	m	0.15	0/4131	0.31	0/5590
6	n	0.15	0/4131	0.33	0/5590
6	o	0.14	0/4131	0.31	0/5590
6	p	0.14	0/4131	0.32	0/5590
6	q	0.14	0/4131	0.31	0/5590
6	r	0.14	0/4131	0.32	0/5590
6	s	0.15	0/4131	0.32	0/5590
6	t	0.15	0/4131	0.33	0/5590
6	u	0.16	0/4131	0.32	0/5590
All	All	0.16	0/129252	0.34	36/175236 (0.0%)

There are no bond length outliers.

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AC	14	THR	N-CA-C	8.22	120.25	111.28
1	7	14	THR	N-CA-C	7.26	119.19	111.28
1	AD	10	PRO	N-CA-C	7.16	123.71	113.47
1	4	5	PRO	N-CA-C	6.67	122.33	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	5	PRO	N-CA-C	6.64	122.75	113.53

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	110	0	115	13	0
1	3	110	0	115	11	0
1	4	110	0	115	17	0
1	5	110	0	115	10	0
1	6	110	0	115	11	0
1	7	110	0	115	12	0
1	8	110	0	115	11	0
1	9	110	0	115	13	0
1	AA	110	0	115	11	0
1	AB	110	0	115	12	0
1	AC	110	0	115	14	0
1	AD	110	0	115	11	0
2	1	101	0	109	5	0
2	2	101	0	109	5	0
2	v	101	0	109	4	0
2	w	101	0	109	5	0
2	y	101	0	109	6	0
2	z	101	0	109	5	0
3	A	1115	0	1122	26	0
3	B	1115	0	1122	21	0
3	C	1115	0	1122	21	0
3	D	1115	0	1122	25	0
3	E	1115	0	1122	25	0
3	F	1067	0	1071	20	0
3	G	1067	0	1071	21	0
3	H	1067	0	1071	18	0
3	I	1067	0	1071	23	0
3	J	1067	0	1071	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	K	1080	0	1082	24	0
3	L	1080	0	1082	24	0
3	M	1080	0	1082	26	0
3	N	1080	0	1082	23	0
3	O	1080	0	1082	19	0
3	a	1115	0	1122	22	0
3	b	1067	0	1071	22	0
3	c	1080	0	1082	19	0
4	P	6313	0	6075	114	0
4	Q	6313	0	6075	122	0
4	R	6313	0	6075	111	0
4	S	6313	0	6075	108	0
4	T	6313	0	6075	110	0
4	x	6313	0	6075	119	0
5	U	1565	0	1485	26	0
5	V	1565	0	1485	28	0
5	W	1565	0	1485	26	0
5	X	1565	0	1485	25	0
5	Y	1565	0	1485	22	0
5	Z	1557	0	1473	33	0
5	d	1557	0	1473	28	0
5	e	1557	0	1473	29	0
5	f	1557	0	1473	31	0
5	g	1557	0	1473	31	0
5	h	1565	0	1485	25	0
5	i	1557	0	1473	30	0
6	j	4070	0	4060	80	0
6	k	4070	0	4060	76	0
6	l	4070	0	4060	84	0
6	m	4070	0	4060	85	0
6	n	4070	0	4060	95	0
6	o	4070	0	4060	83	0
6	p	4070	0	4060	84	0
6	q	4070	0	4060	73	0
6	r	4070	0	4060	81	0
6	s	4070	0	4060	89	0
6	t	4070	0	4060	91	0
6	u	4070	0	4060	87	0
All	All	126948	0	124602	2088	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 8.

The worst 5 of 2088 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)
1:0:7:ILE:HA	6:n:530:VAL:HG21	1.39	1.01
1:4:7:ILE:HA	6:t:530:VAL:HG21	1.45	0.99
1:6:7:ILE:HA	6:r:530:VAL:HG21	1.46	0.97
1:AB:7:ILE:HA	6:l:530:VAL:HG21	1.49	0.93
1:AD:7:ILE:HA	6:j:530:VAL:HG21	1.51	0.90

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	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	3	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	4	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	5	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	6	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	7	12/88 (14%)	10 (83%)	1 (8%)	1 (8%)	0	1
1	8	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	9	12/88 (14%)	10 (83%)	1 (8%)	1 (8%)	0	1
1	AA	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	AB	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	AC	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	AD	12/88 (14%)	10 (83%)	1 (8%)	1 (8%)	0	1
2	1	13/99 (13%)	12 (92%)	1 (8%)	0	100	100
2	2	13/99 (13%)	12 (92%)	1 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	v	13/99 (13%)	12 (92%)	1 (8%)	0	100	100
2	w	13/99 (13%)	12 (92%)	1 (8%)	0	100	100
2	y	13/99 (13%)	12 (92%)	1 (8%)	0	100	100
2	z	13/99 (13%)	12 (92%)	1 (8%)	0	100	100
3	A	139/553 (25%)	135 (97%)	4 (3%)	0	100	100
3	B	139/553 (25%)	134 (96%)	5 (4%)	0	100	100
3	C	139/553 (25%)	134 (96%)	5 (4%)	0	100	100
3	D	139/553 (25%)	134 (96%)	5 (4%)	0	100	100
3	E	139/553 (25%)	135 (97%)	4 (3%)	0	100	100
3	F	132/553 (24%)	128 (97%)	4 (3%)	0	100	100
3	G	132/553 (24%)	129 (98%)	3 (2%)	0	100	100
3	H	132/553 (24%)	129 (98%)	3 (2%)	0	100	100
3	I	132/553 (24%)	128 (97%)	4 (3%)	0	100	100
3	J	132/553 (24%)	129 (98%)	3 (2%)	0	100	100
3	K	134/553 (24%)	127 (95%)	7 (5%)	0	100	100
3	L	134/553 (24%)	127 (95%)	7 (5%)	0	100	100
3	M	134/553 (24%)	127 (95%)	7 (5%)	0	100	100
3	N	134/553 (24%)	127 (95%)	7 (5%)	0	100	100
3	O	134/553 (24%)	127 (95%)	7 (5%)	0	100	100
3	a	139/553 (25%)	134 (96%)	5 (4%)	0	100	100
3	b	132/553 (24%)	128 (97%)	4 (3%)	0	100	100
3	c	134/553 (24%)	127 (95%)	7 (5%)	0	100	100
4	P	791/794 (100%)	773 (98%)	18 (2%)	0	100	100
4	Q	791/794 (100%)	775 (98%)	16 (2%)	0	100	100
4	R	791/794 (100%)	776 (98%)	15 (2%)	0	100	100
4	S	791/794 (100%)	774 (98%)	17 (2%)	0	100	100
4	T	791/794 (100%)	775 (98%)	16 (2%)	0	100	100
4	x	791/794 (100%)	774 (98%)	17 (2%)	0	100	100
5	U	194/196 (99%)	193 (100%)	1 (0%)	0	100	100
5	V	194/196 (99%)	192 (99%)	2 (1%)	0	100	100
5	W	194/196 (99%)	193 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	X	194/196 (99%)	193 (100%)	1 (0%)	0	100	100
5	Y	194/196 (99%)	193 (100%)	1 (0%)	0	100	100
5	Z	193/196 (98%)	191 (99%)	2 (1%)	0	100	100
5	d	193/196 (98%)	191 (99%)	2 (1%)	0	100	100
5	e	193/196 (98%)	191 (99%)	2 (1%)	0	100	100
5	f	193/196 (98%)	191 (99%)	2 (1%)	0	100	100
5	g	193/196 (98%)	191 (99%)	2 (1%)	0	100	100
5	h	194/196 (99%)	192 (99%)	2 (1%)	0	100	100
5	i	193/196 (98%)	191 (99%)	2 (1%)	0	100	100
6	j	522/536 (97%)	514 (98%)	8 (2%)	0	100	100
6	k	522/536 (97%)	513 (98%)	9 (2%)	0	100	100
6	l	522/536 (97%)	515 (99%)	7 (1%)	0	100	100
6	m	522/536 (97%)	515 (99%)	7 (1%)	0	100	100
6	n	522/536 (97%)	515 (99%)	7 (1%)	0	100	100
6	o	522/536 (97%)	513 (98%)	9 (2%)	0	100	100
6	p	522/536 (97%)	514 (98%)	8 (2%)	0	100	100
6	q	522/536 (97%)	515 (99%)	7 (1%)	0	100	100
6	r	522/536 (97%)	515 (99%)	7 (1%)	0	100	100
6	s	522/536 (97%)	514 (98%)	8 (2%)	0	100	100
6	t	522/536 (97%)	514 (98%)	8 (2%)	0	100	100
6	u	522/536 (97%)	514 (98%)	8 (2%)	0	100	100
All	All	15984/25152 (64%)	15660 (98%)	312 (2%)	12 (0%)	49	73

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	9	9	THR
1	0	9	THR
1	6	9	THR
1	AB	9	THR
1	AC	9	THR

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	14/73 (19%)	12 (86%)	2 (14%)	3	8
1	3	14/73 (19%)	12 (86%)	2 (14%)	3	8
1	4	14/73 (19%)	13 (93%)	1 (7%)	13	33
1	5	14/73 (19%)	14 (100%)	0	100	100
1	6	14/73 (19%)	14 (100%)	0	100	100
1	7	14/73 (19%)	13 (93%)	1 (7%)	13	33
1	8	14/73 (19%)	13 (93%)	1 (7%)	13	33
1	9	14/73 (19%)	14 (100%)	0	100	100
1	AA	14/73 (19%)	12 (86%)	2 (14%)	3	8
1	AB	14/73 (19%)	14 (100%)	0	100	100
1	AC	14/73 (19%)	12 (86%)	2 (14%)	3	8
1	AD	14/73 (19%)	13 (93%)	1 (7%)	13	33
2	1	11/72 (15%)	11 (100%)	0	100	100
2	2	11/72 (15%)	11 (100%)	0	100	100
2	v	11/72 (15%)	11 (100%)	0	100	100
2	w	11/72 (15%)	11 (100%)	0	100	100
2	y	11/72 (15%)	11 (100%)	0	100	100
2	z	11/72 (15%)	11 (100%)	0	100	100
3	A	122/451 (27%)	122 (100%)	0	100	100
3	B	122/451 (27%)	122 (100%)	0	100	100
3	C	122/451 (27%)	122 (100%)	0	100	100
3	D	122/451 (27%)	122 (100%)	0	100	100
3	E	122/451 (27%)	122 (100%)	0	100	100
3	F	117/451 (26%)	117 (100%)	0	100	100
3	G	117/451 (26%)	117 (100%)	0	100	100
3	H	117/451 (26%)	117 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	I	117/451 (26%)	117 (100%)	0	100	100
3	J	117/451 (26%)	117 (100%)	0	100	100
3	K	118/451 (26%)	118 (100%)	0	100	100
3	L	118/451 (26%)	118 (100%)	0	100	100
3	M	118/451 (26%)	118 (100%)	0	100	100
3	N	118/451 (26%)	118 (100%)	0	100	100
3	O	118/451 (26%)	118 (100%)	0	100	100
3	a	122/451 (27%)	122 (100%)	0	100	100
3	b	117/451 (26%)	117 (100%)	0	100	100
3	c	118/451 (26%)	118 (100%)	0	100	100
4	P	687/688 (100%)	687 (100%)	0	100	100
4	Q	687/688 (100%)	687 (100%)	0	100	100
4	R	687/688 (100%)	686 (100%)	1 (0%)	88	96
4	S	687/688 (100%)	687 (100%)	0	100	100
4	T	687/688 (100%)	687 (100%)	0	100	100
4	x	687/688 (100%)	686 (100%)	1 (0%)	88	96
5	U	169/169 (100%)	169 (100%)	0	100	100
5	V	169/169 (100%)	168 (99%)	1 (1%)	78	91
5	W	169/169 (100%)	169 (100%)	0	100	100
5	X	169/169 (100%)	169 (100%)	0	100	100
5	Y	169/169 (100%)	169 (100%)	0	100	100
5	Z	168/169 (99%)	168 (100%)	0	100	100
5	d	168/169 (99%)	168 (100%)	0	100	100
5	e	168/169 (99%)	168 (100%)	0	100	100
5	f	168/169 (99%)	168 (100%)	0	100	100
5	g	168/169 (99%)	168 (100%)	0	100	100
5	h	169/169 (100%)	169 (100%)	0	100	100
5	i	168/169 (99%)	168 (100%)	0	100	100
6	j	435/442 (98%)	435 (100%)	0	100	100
6	k	435/442 (98%)	435 (100%)	0	100	100
6	l	435/442 (98%)	435 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	m	435/442 (98%)	435 (100%)	0	100	100
6	n	435/442 (98%)	434 (100%)	1 (0%)	87	95
6	o	435/442 (98%)	434 (100%)	1 (0%)	87	95
6	p	435/442 (98%)	435 (100%)	0	100	100
6	q	435/442 (98%)	435 (100%)	0	100	100
6	r	435/442 (98%)	435 (100%)	0	100	100
6	s	435/442 (98%)	435 (100%)	0	100	100
6	t	435/442 (98%)	435 (100%)	0	100	100
6	u	435/442 (98%)	433 (100%)	2 (0%)	81	92
All	All	13740/20886 (66%)	13721 (100%)	19 (0%)	87	96

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	n	423	GLU
6	u	519	SER
4	x	71	ARG
6	u	30	ARG
1	AA	12	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 126 such sidechains are listed below:

Mol	Chain	Res	Type
5	h	93	GLN
6	t	359	ASN
6	k	487	GLN
6	t	335	GLN
6	u	498	GLN

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.

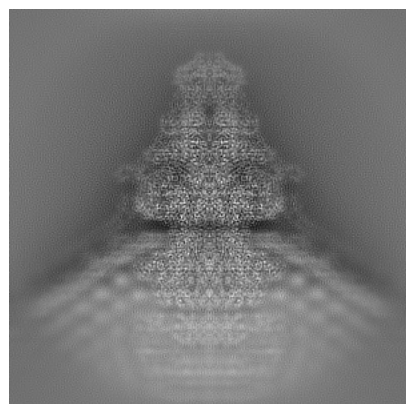
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61910. These allow visual inspection of the internal detail of the map and identification of artifacts.

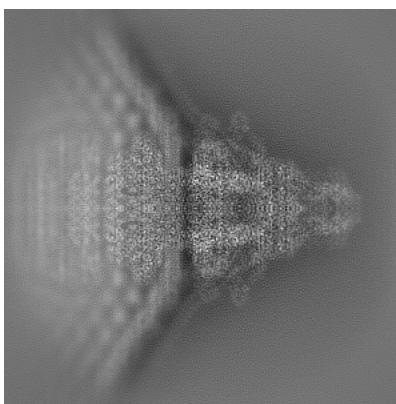
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

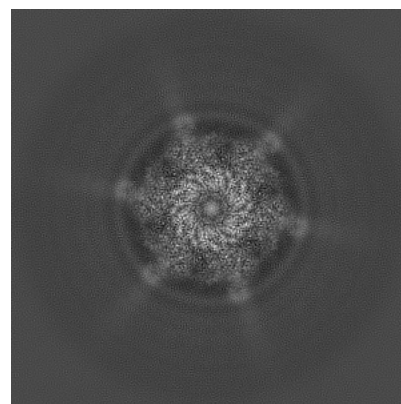
6.1.1 Primary map



X

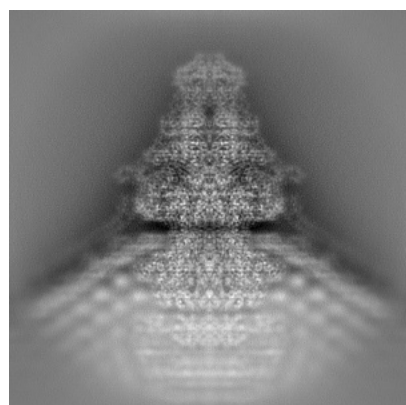


Y

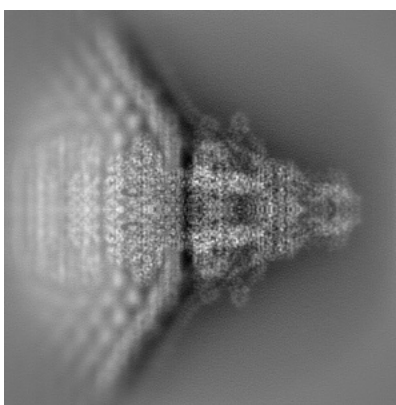


Z

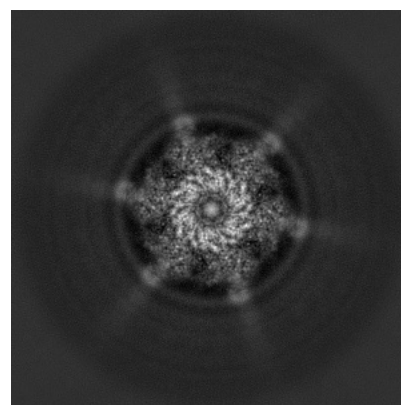
6.1.2 Raw map



X



Y

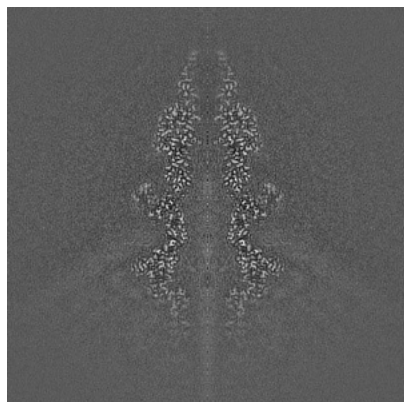


Z

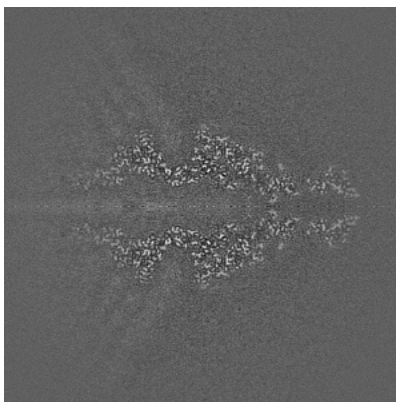
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

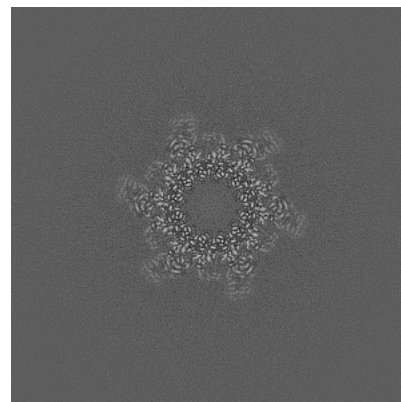
6.2.1 Primary map



X Index: 200

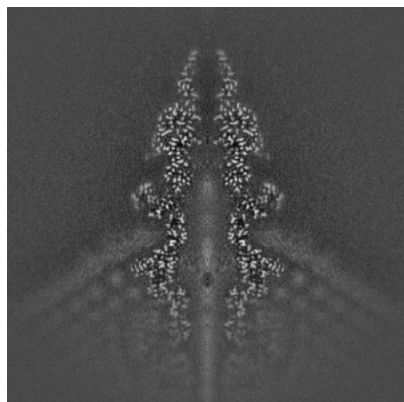


Y Index: 200

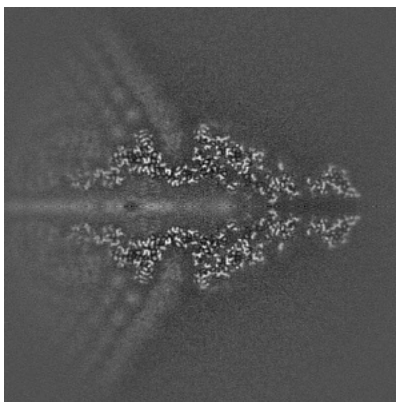


Z Index: 200

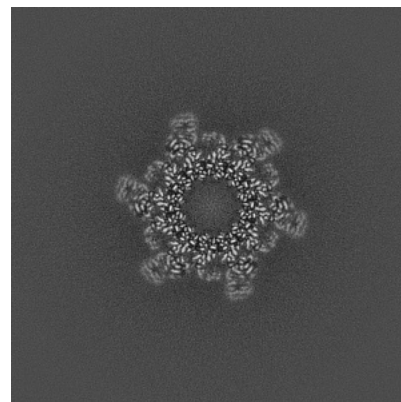
6.2.2 Raw map



X Index: 200



Y Index: 200

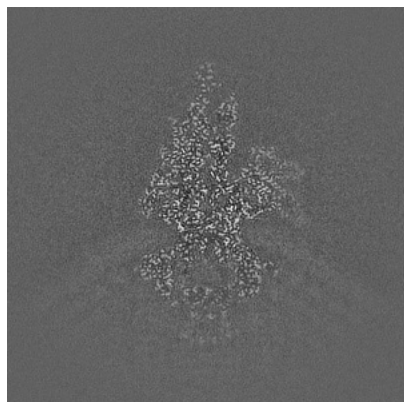


Z Index: 200

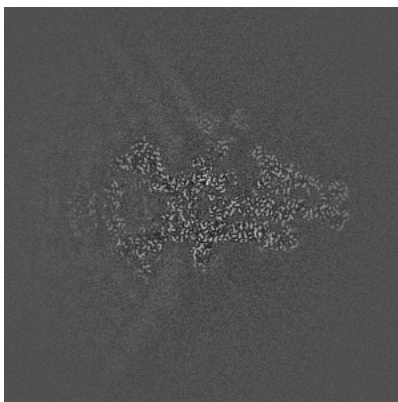
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

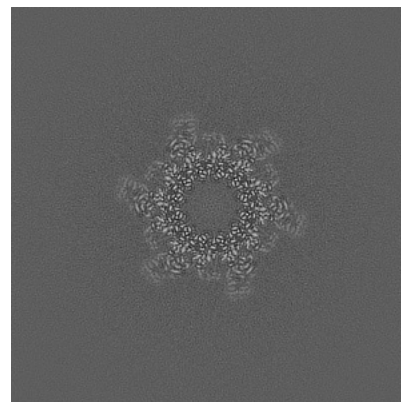
6.3.1 Primary map



X Index: 173

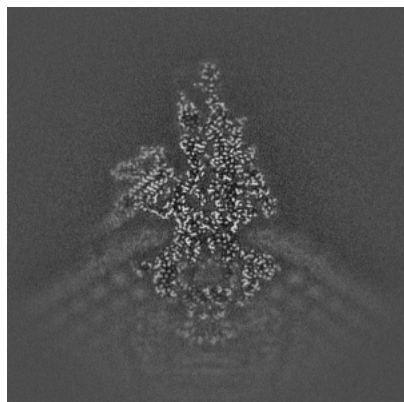


Y Index: 176

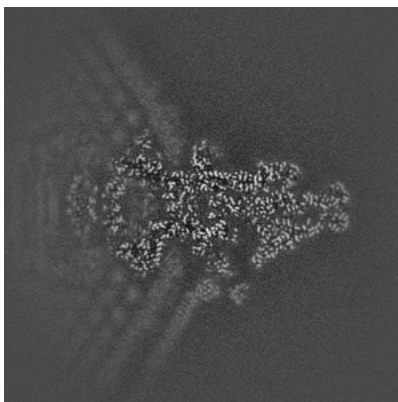


Z Index: 200

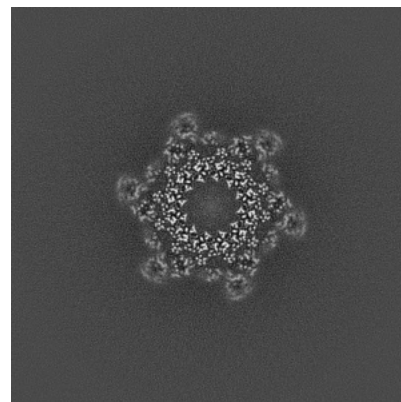
6.3.2 Raw map



X Index: 227



Y Index: 224

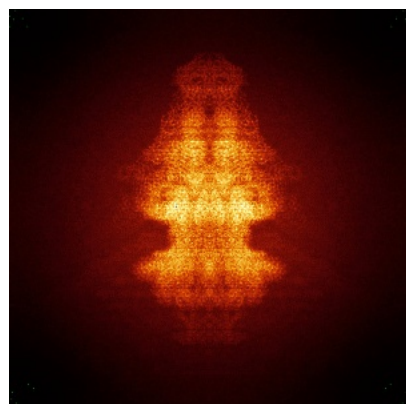


Z Index: 202

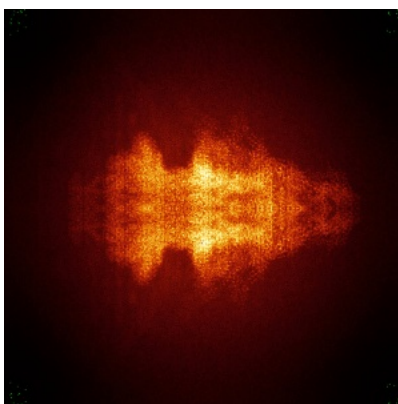
The images above show the largest variance slices of the map in three orthogonal directions.

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

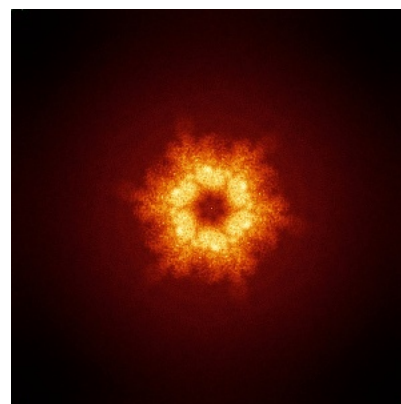
6.4.1 Primary map



X

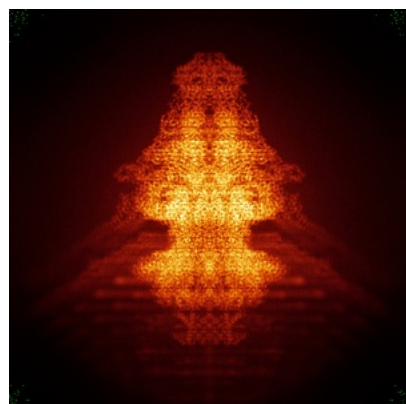


Y

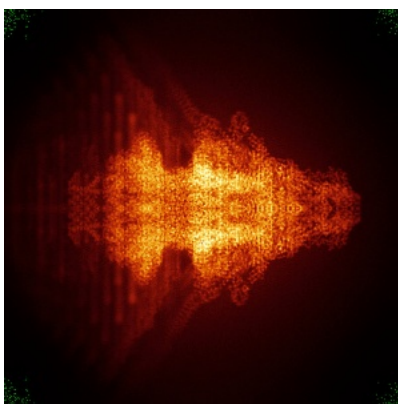


Z

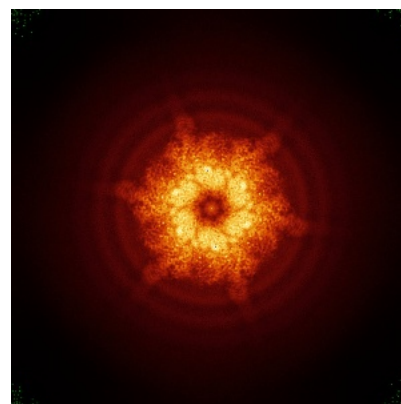
6.4.2 Raw map



X



Y

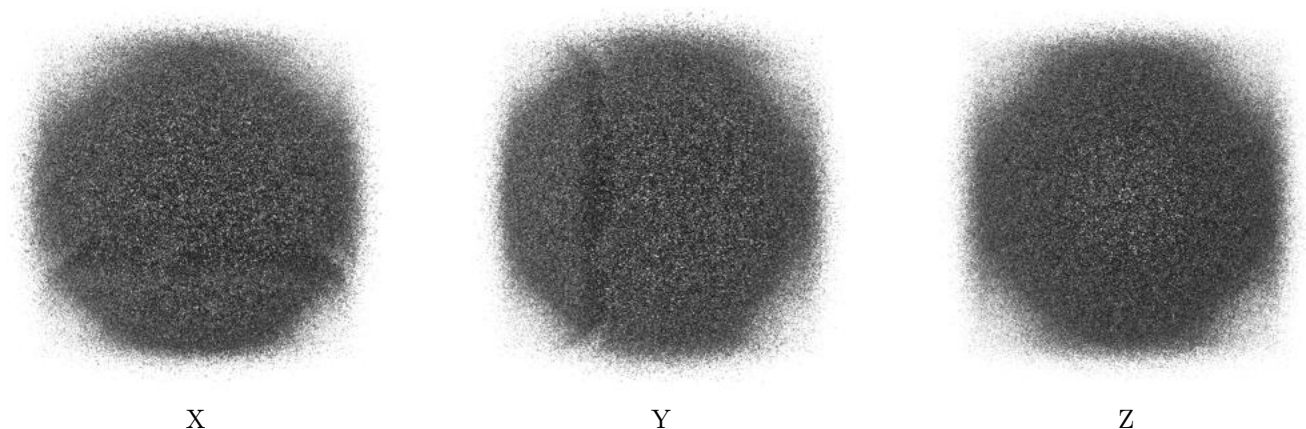


Z

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 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

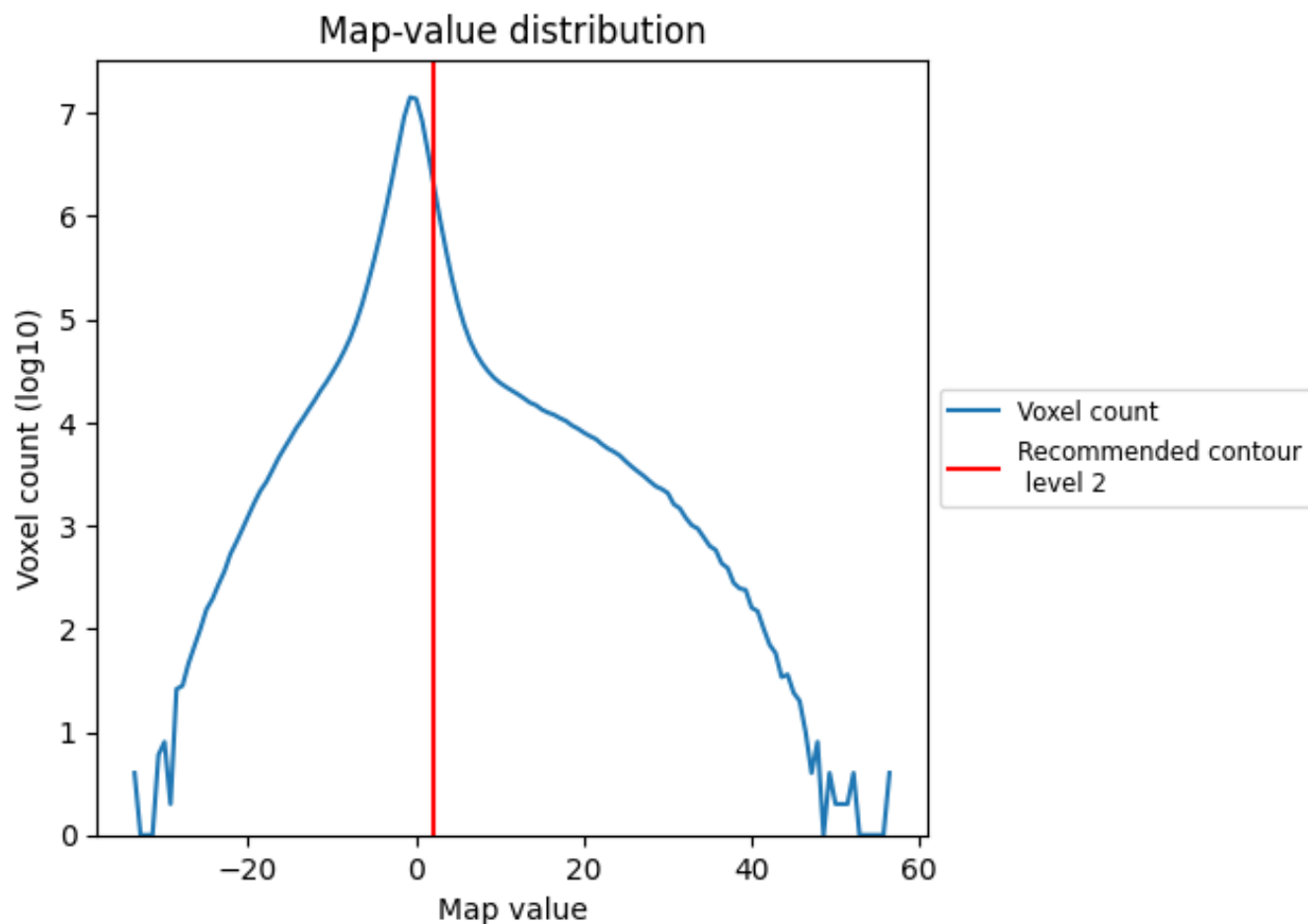
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

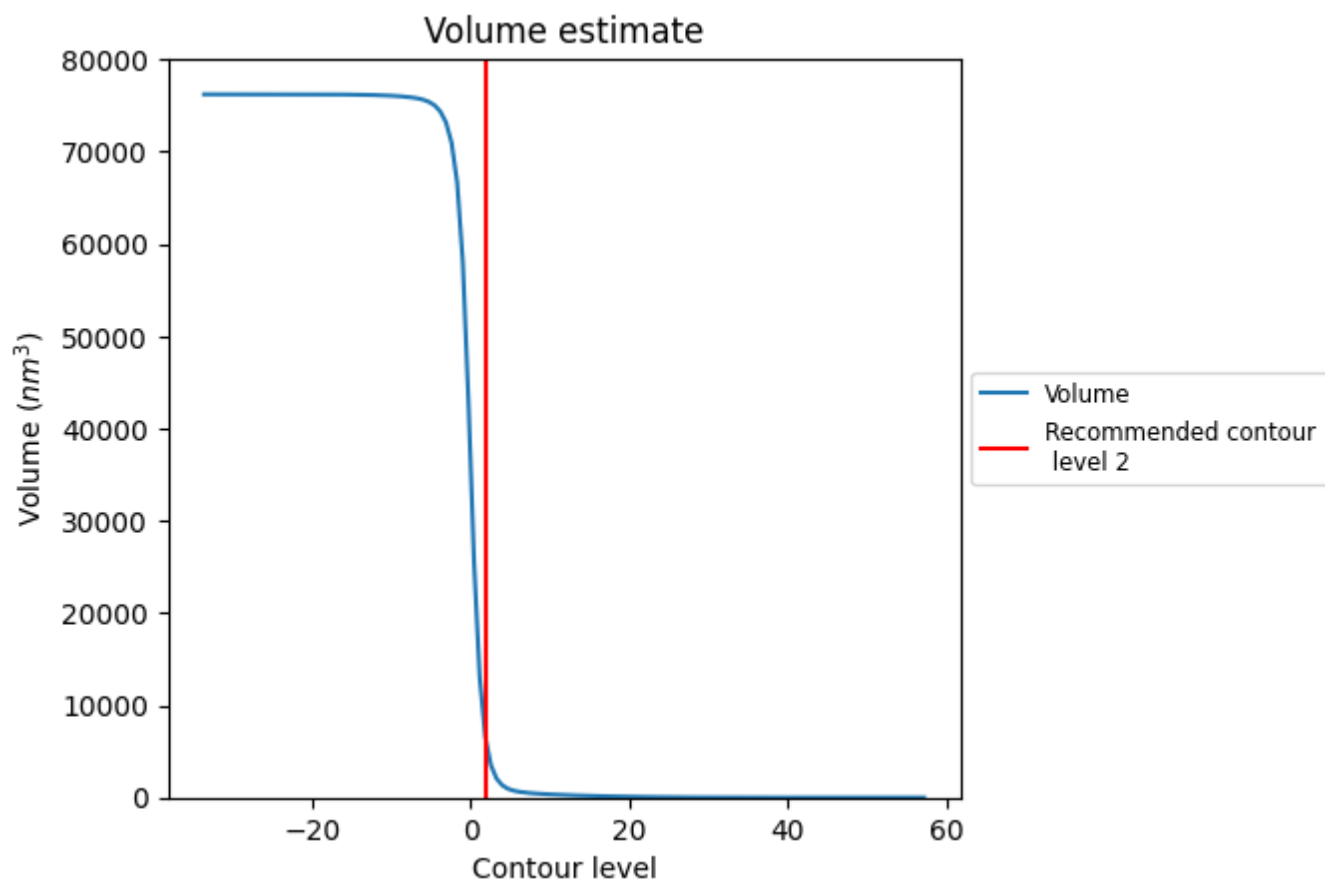
This section contains the results of statistical analysis of the map.

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.

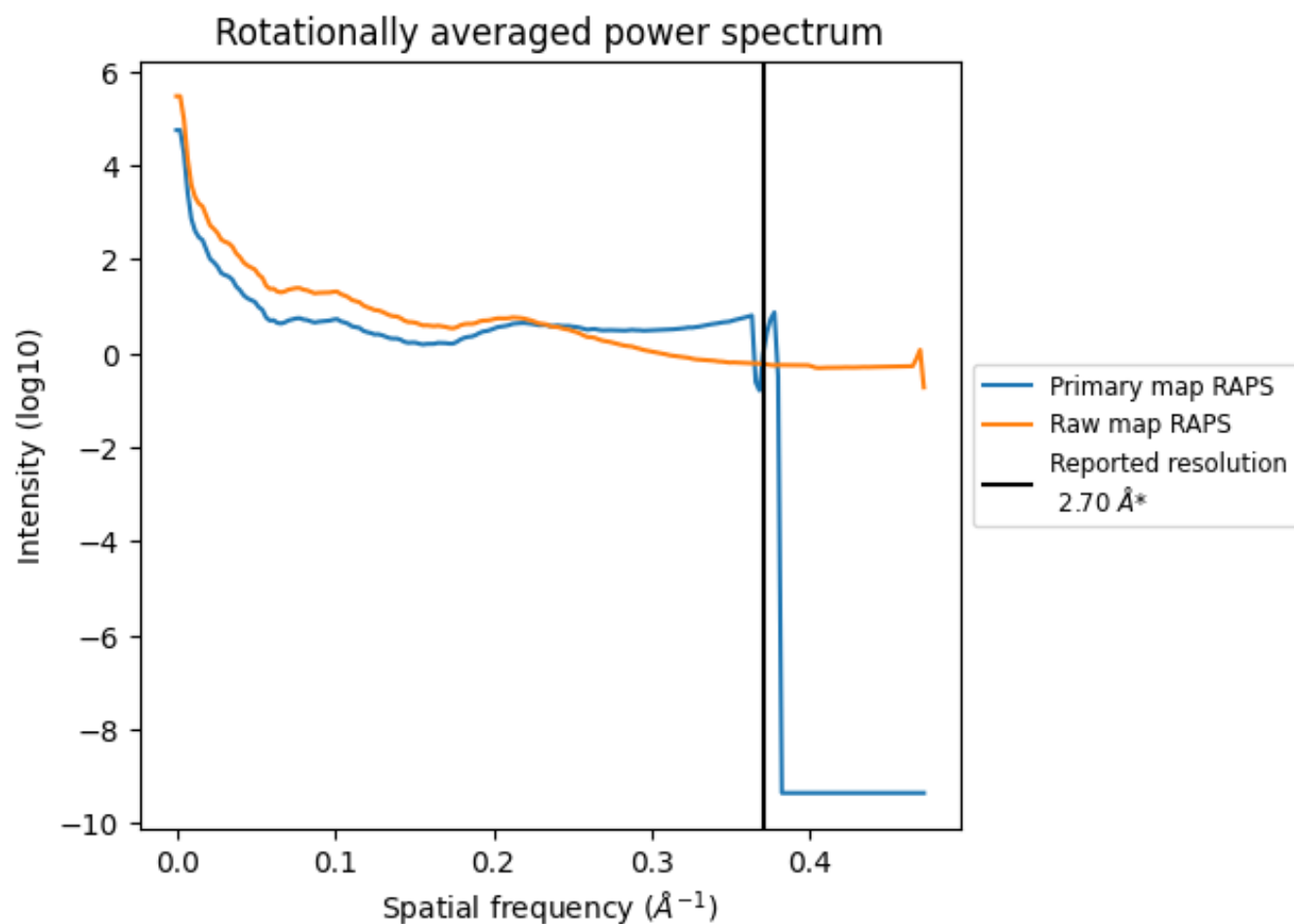
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6205 nm³; this corresponds to an approximate mass of 5605 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 ⓘ

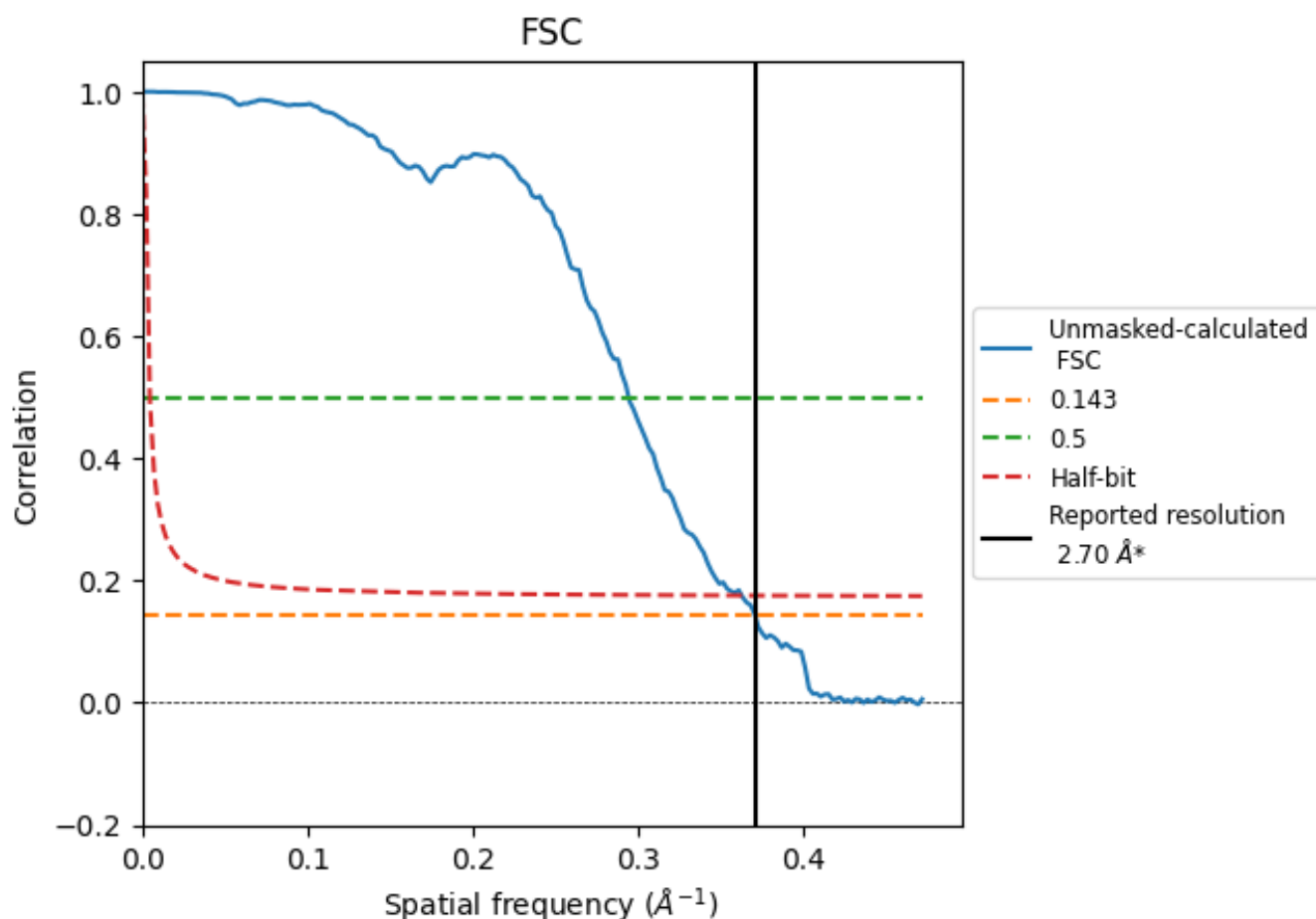


*Reported resolution corresponds to spatial frequency of 0.370 $\text{\AA}^{-1}$

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 0.370 Å⁻¹

8.2 Resolution estimates [i](#)

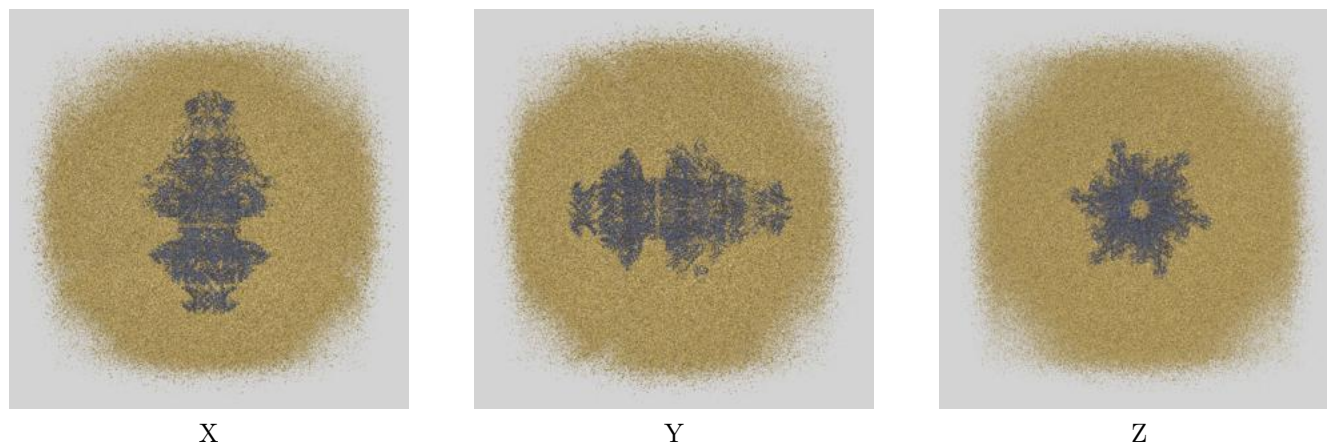
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.70	3.40	2.76

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

9 Map-model fit [i](#)

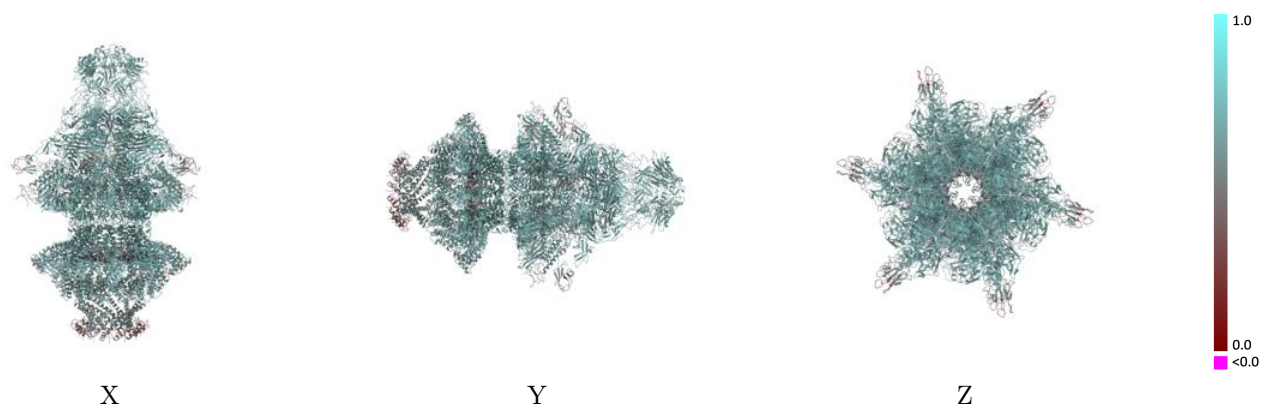
This section contains information regarding the fit between EMDB map EMD-61910 and PDB model 9JYZ. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



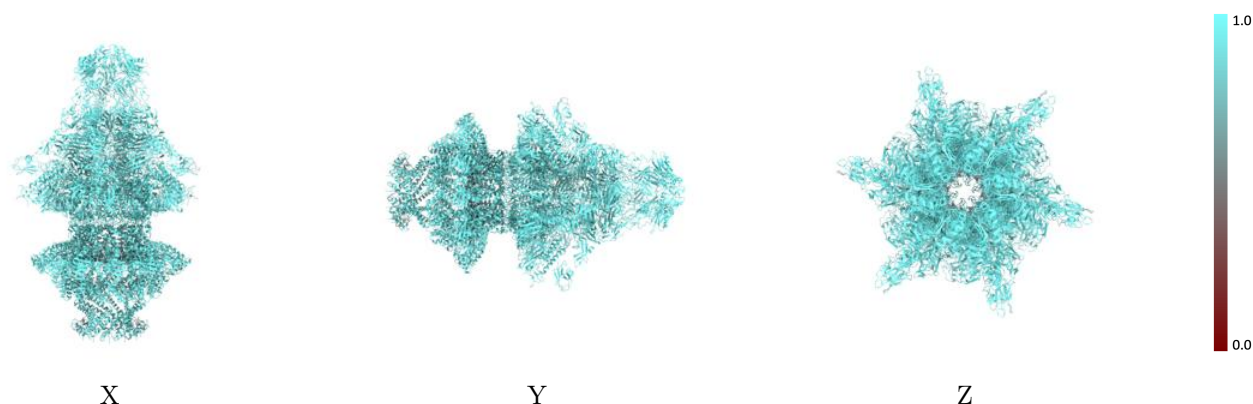
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



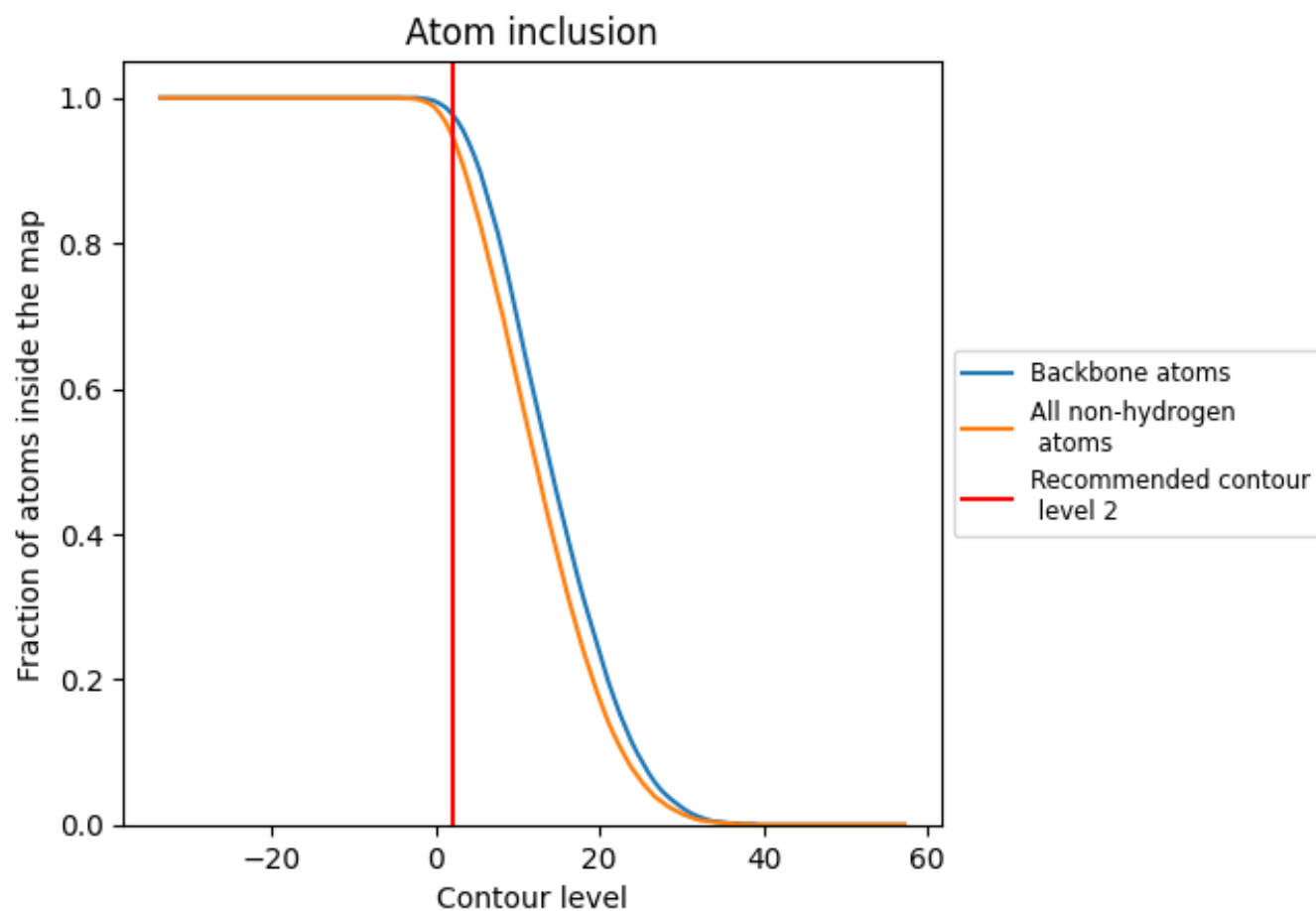
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 95% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9490	 0.6130
0	 0.6000	 0.3620
1	 0.7170	 0.4660
2	 0.7370	 0.4670
3	 0.4820	 0.2770
4	 0.6000	 0.3440
5	 0.5450	 0.3070
6	 0.5820	 0.3550
7	 0.5090	 0.2810
8	 0.5820	 0.3480
9	 0.4640	 0.2300
A	 0.9680	 0.6220
AA	 0.5180	 0.3240
AB	 0.5730	 0.3570
AC	 0.4820	 0.3260
AD	 0.6000	 0.3260
B	 0.9690	 0.6240
C	 0.9670	 0.6250
D	 0.9700	 0.6230
E	 0.9670	 0.6220
F	 0.9680	 0.6060
G	 0.9630	 0.6100
H	 0.9630	 0.6060
I	 0.9690	 0.6040
J	 0.9680	 0.6090
K	 0.9260	 0.5230
L	 0.9280	 0.5230
M	 0.9290	 0.5180
N	 0.9340	 0.5210
O	 0.9250	 0.5200
P	 0.9760	 0.6410
Q	 0.9770	 0.6420
R	 0.9770	 0.6410
S	 0.9760	 0.6410
T	 0.9780	 0.6430



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Chain	Atom inclusion	Q-score
U	 0.9780	 0.6600
V	 0.9760	 0.6640
W	 0.9730	 0.6610
X	 0.9780	 0.6610
Y	 0.9760	 0.6660
Z	 0.9770	 0.6600
a	 0.9700	 0.6230
b	 0.9700	 0.6030
c	 0.9350	 0.5220
d	 0.9740	 0.6560
e	 0.9780	 0.6600
f	 0.9780	 0.6580
g	 0.9730	 0.6550
h	 0.9760	 0.6630
i	 0.9780	 0.6610
j	 0.9270	 0.5900
k	 0.9310	 0.6000
l	 0.9290	 0.5910
m	 0.9290	 0.5970
n	 0.9280	 0.5910
o	 0.9320	 0.5960
p	 0.9270	 0.5900
q	 0.9290	 0.5980
r	 0.9290	 0.5910
s	 0.9300	 0.5960
t	 0.9290	 0.5910
u	 0.9330	 0.5970
v	 0.7580	 0.4670
w	 0.6970	 0.4620
x	 0.9760	 0.6410
y	 0.7480	 0.4770
z	 0.7480	 0.4670