



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:37 PM UTC

PDB ID : 8JOV / pdb_00008jov
EMDB ID : EMD-36463
Title : Portal-tail complex of phage GP4
Authors : Liu, H.; Chen, W.
Deposited on : 2023-06-08
Resolution : 3.80 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

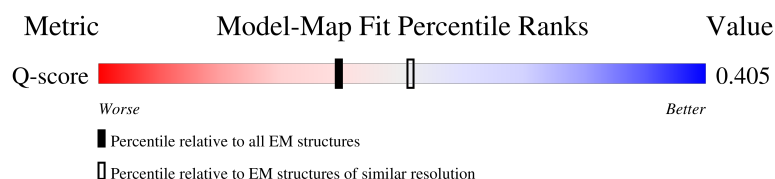
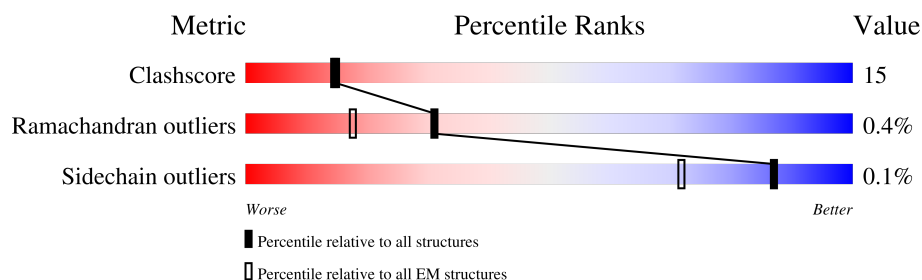
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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.



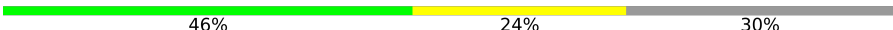
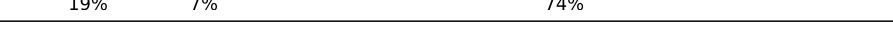
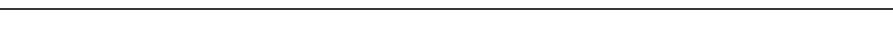
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	781	 46% 23% 30%
1	3	781	 48% 22% 30%
1	6	781	 48% 22% 30%
1	U	781	 48% 21% 30%

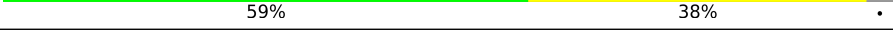
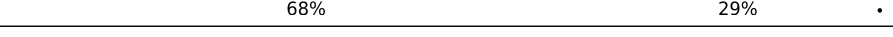
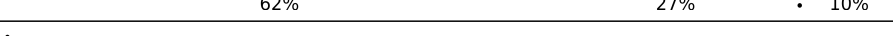
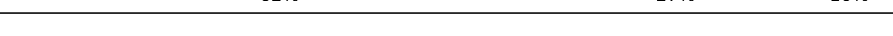
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Mol	Chain	Length	Quality of chain
1	Y	781	 46%24%30%
1	c	781	 49%21%30%
1	g	781	 47%22%30%
1	k	781	 50%20%30%
1	o	781	 49%21%30%
1	r	781	 49%21%30%
1	u	781	 48%22%30%
1	x	781	 50%20%30%
2	1	439	 17%10%74%
2	4	439	 18%8%74%
2	7	439	 18%8%74%
2	M	439	 16%10%74%
2	N	439	 19%7%74%
2	O	439	 19%7%74%
2	P	439	 18%9%74%
2	Q	439	 18%8%74%
2	R	439	 20%6%74%
2	V	439	 17%9%74%
2	Z	439	 17%9%74%
2	d	439	 18%8%74%
2	h	439	 18%8%74%
2	l	439	 19%7%74%
2	p	439	 19%7%74%
2	s	439	 18%8%74%
2	v	439	 17%9%74%

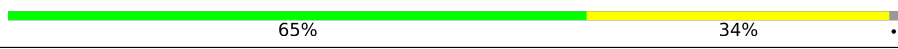
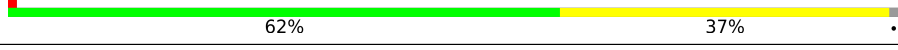
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Mol	Chain	Length	Quality of chain
2	y	439	
3	2	220	
3	5	220	
3	T	220	
3	X	220	
3	b	220	
3	f	220	
3	j	220	
3	n	220	
3	q	220	
3	t	220	
3	w	220	
3	z	220	
4	A	577	
4	B	577	
4	C	577	
4	D	577	
4	E	577	
4	F	577	
5	G	206	
5	H	206	
5	I	206	
5	J	206	
5	K	206	
5	L	206	

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Mol	Chain	Length	Quality of chain
5	S	206	
5	W	206	
5	a	206	
5	e	206	
5	i	206	
5	m	206	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 128070 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 Portal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	547	Total	C	N	O	S	0	0
			4297	2681	780	816	20		
1	3	547	Total	C	N	O	S	0	0
			4297	2681	780	816	20		
1	6	547	Total	C	N	O	S	0	0
			4297	2681	780	816	20		
1	U	547	Total	C	N	O	S	0	0
			4297	2681	780	816	20		
1	Y	547	Total	C	N	O	S	0	0
			4297	2681	780	816	20		
1	c	547	Total	C	N	O	S	0	0
			4297	2681	780	816	20		
1	g	547	Total	C	N	O	S	0	0
			4297	2681	780	816	20		
1	k	547	Total	C	N	O	S	0	0
			4297	2681	780	816	20		
1	o	547	Total	C	N	O	S	0	0
			4297	2681	780	816	20		
1	r	547	Total	C	N	O	S	0	0
			4297	2681	780	816	20		
1	u	547	Total	C	N	O	S	0	0
			4297	2681	780	816	20		
1	x	547	Total	C	N	O	S	0	0
			4297	2681	780	816	20		

- Molecule 2 is a protein called Putative tail fiber protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	116	Total	C	N	O	S	0	0
			829	507	150	170	2		
2	4	116	Total	C	N	O	S	0	0
			829	507	150	170	2		
2	7	116	Total	C	N	O	S	0	0
			829	507	150	170	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	M	116	Total	C	N	O	S	0	0
			829	507	150	170	2		
2	N	116	Total	C	N	O	S	0	0
			829	507	150	170	2		
2	O	116	Total	C	N	O	S	0	0
			829	507	150	170	2		
2	P	116	Total	C	N	O	S	0	0
			829	507	150	170	2		
2	Q	116	Total	C	N	O	S	0	0
			829	507	150	170	2		
2	R	116	Total	C	N	O	S	0	0
			829	507	150	170	2		
2	V	116	Total	C	N	O	S	0	0
			829	507	150	170	2		
2	Z	116	Total	C	N	O	S	0	0
			829	507	150	170	2		
2	d	116	Total	C	N	O	S	0	0
			829	507	150	170	2		
2	h	116	Total	C	N	O	S	0	0
			829	507	150	170	2		
2	l	116	Total	C	N	O	S	0	0
			829	507	150	170	2		
2	p	116	Total	C	N	O	S	0	0
			829	507	150	170	2		
2	s	116	Total	C	N	O	S	0	0
			829	507	150	170	2		
2	v	116	Total	C	N	O	S	0	0
			829	507	150	170	2		
2	y	116	Total	C	N	O	S	0	0
			829	507	150	170	2		

- Molecule 3 is a protein called Virion associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	213	Total	C	N	O	S	0	0
			1615	1013	281	316	5		
3	5	213	Total	C	N	O	S	0	0
			1615	1013	281	316	5		
3	T	213	Total	C	N	O	S	0	0
			1615	1013	281	316	5		
3	X	213	Total	C	N	O	S	0	0
			1615	1013	281	316	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	b	213	Total	C	N	O	S	0	0
			1615	1013	281	316	5		
3	f	213	Total	C	N	O	S	0	0
			1615	1013	281	316	5		
3	j	213	Total	C	N	O	S	0	0
			1615	1013	281	316	5		
3	n	213	Total	C	N	O	S	0	0
			1615	1013	281	316	5		
3	q	213	Total	C	N	O	S	0	0
			1615	1013	281	316	5		
3	t	213	Total	C	N	O	S	0	0
			1615	1013	281	316	5		
3	w	213	Total	C	N	O	S	0	0
			1615	1013	281	316	5		
3	z	213	Total	C	N	O	S	0	0
			1615	1013	281	316	5		

- Molecule 4 is a protein called Virion-associated phage protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	518	Total	C	N	O	S	0	0
			3812	2413	656	725	18		
4	B	518	Total	C	N	O	S	0	0
			3812	2413	656	725	18		
4	C	518	Total	C	N	O	S	0	0
			3812	2413	656	725	18		
4	D	518	Total	C	N	O	S	0	0
			3812	2413	656	725	18		
4	E	518	Total	C	N	O	S	0	0
			3812	2413	656	725	18		
4	F	518	Total	C	N	O	S	0	0
			3812	2413	656	725	18		

- Molecule 5 is a protein called gp81 of phage GP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	204	Total	C	N	O	S	0	0
			1611	1021	279	303	8		
5	H	204	Total	C	N	O	S	0	0
			1611	1021	279	303	8		
5	I	204	Total	C	N	O	S	0	0
			1611	1021	279	303	8		

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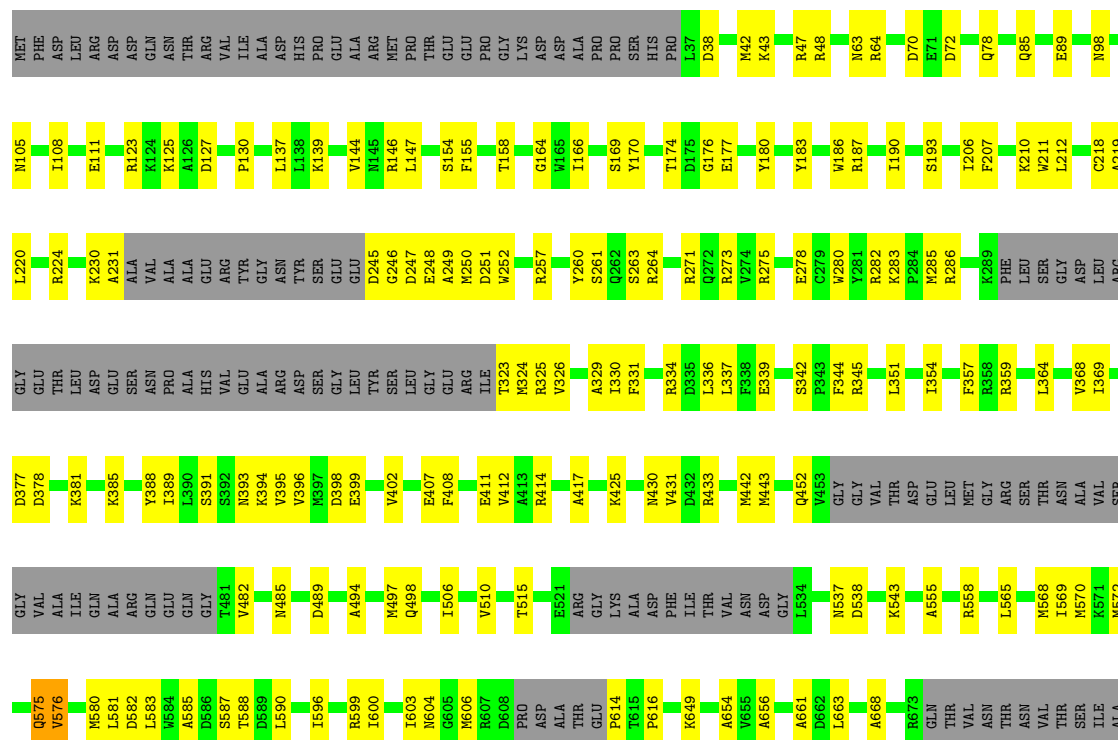
Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	204	Total 1611	C 1021	N 279	O 303	S 8	0	0
5	K	204	Total 1611	C 1021	N 279	O 303	S 8	0	0
5	L	204	Total 1611	C 1021	N 279	O 303	S 8	0	0
5	S	204	Total 1611	C 1021	N 279	O 303	S 8	0	0
5	W	204	Total 1611	C 1021	N 279	O 303	S 8	0	0
5	a	204	Total 1611	C 1021	N 279	O 303	S 8	0	0
5	e	204	Total 1611	C 1021	N 279	O 303	S 8	0	0
5	i	204	Total 1611	C 1021	N 279	O 303	S 8	0	0
5	m	204	Total 1611	C 1021	N 279	O 303	S 8	0	0

PRO	GLN	GLN	GLN	PRO	PRO	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	
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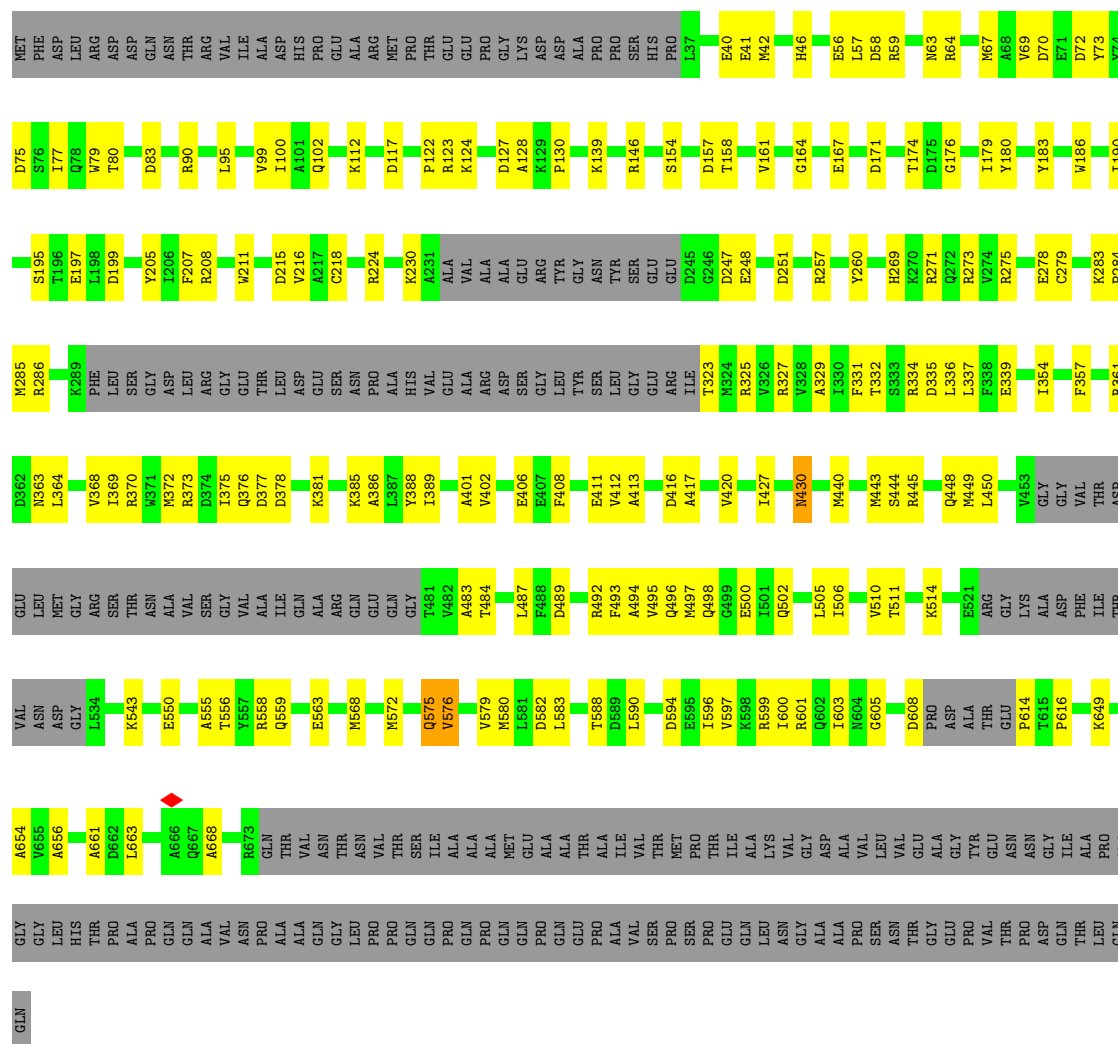
● Molecule 1: Portal protein

Chain 6:  48% 22% 30%

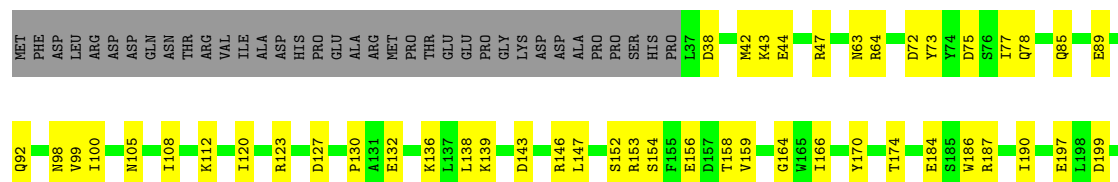
MET	PHE	ASP	LEU	ARG	ASP	ASP	GLN	ASN	THR	ARG	VAL	ILE	ALA	ASP	HIS	PRO	GLU	PRO	ALA	ARG	MET	THR	GLY	PRO	GLY	LYS	ASP	ASP	ALA	PRO	PRO	SER	HIS	PRO	L37	E40	E41	M42	K43	R47	E56	Q60	N63	R64	D70	E71	D72	Y73	Y74	D75	S76
I77	Q78	N98	Q102	N105	I108	G109	S110	E111	K112	R113	G114	R115	T116	D117	P122	R123	K124	K125	A126	D127	A128	K129	A130	E132	A133	K134	T135	K136	L137	L138	K139	V144	N145	R146	R153	S154	F155	T158	V161	G164	T174	D175	G176	I179	R182						
Y183	E184	S185	W186	R187	R208	W211	D215	V216	A217	C218	V221	R224	A231	ALA	VAL	ALA	ALA	ALA	GLU	ARG	TYR	GLY	ASN	TYR	SER	GLU	GLY	D245	G246	D247	E248	D251	W252	Y260	H269	K270	R271	Q272	R273	V274	R275	L276	E278	C279	W280	Y281	R282	M285			
K289	PHE	LEU	SER	GLY	ARG	GLY	THR	LEU	ASP	SER	ASN	PRO	ALA	HIS	VAL	GLU	ALA	VAL	ARG	ILE	T323	K324	R325	V326	R327	V328	A329	T330	F331	T332	D335	L336	L337	F338	E339	R345	I354	D357	R358	R359	G360	R361									
L364	V368	I369	R370	R373	D374	Q376	D377	D378	K381	R382	K385	A386	L387	Y388	I389	L390	S391	S392	N393	K394	D398	E399	G400	A401	V402	E406	E407	F408	E411	V412	A413	R414	P415	D416	V420	K425	Q426	I427	N430	V431	D432	R433	R445	M449	L450						
V453	GLY	VAL	THR	ASP	GLY	MET	GLY	ARG	SER	THR	ASN	ALA	VAL	VAL	ILE	GLN	ALA	ARG	GLN	GLY	GLY	T481	V482	A483	L484	M485	K486	L487	A494	Q502	I506	E507	V510	T511	K514	E521	ARG	GLY	LYS	ALA	ASP	PHE	ILE	THR	VAL	ASN					



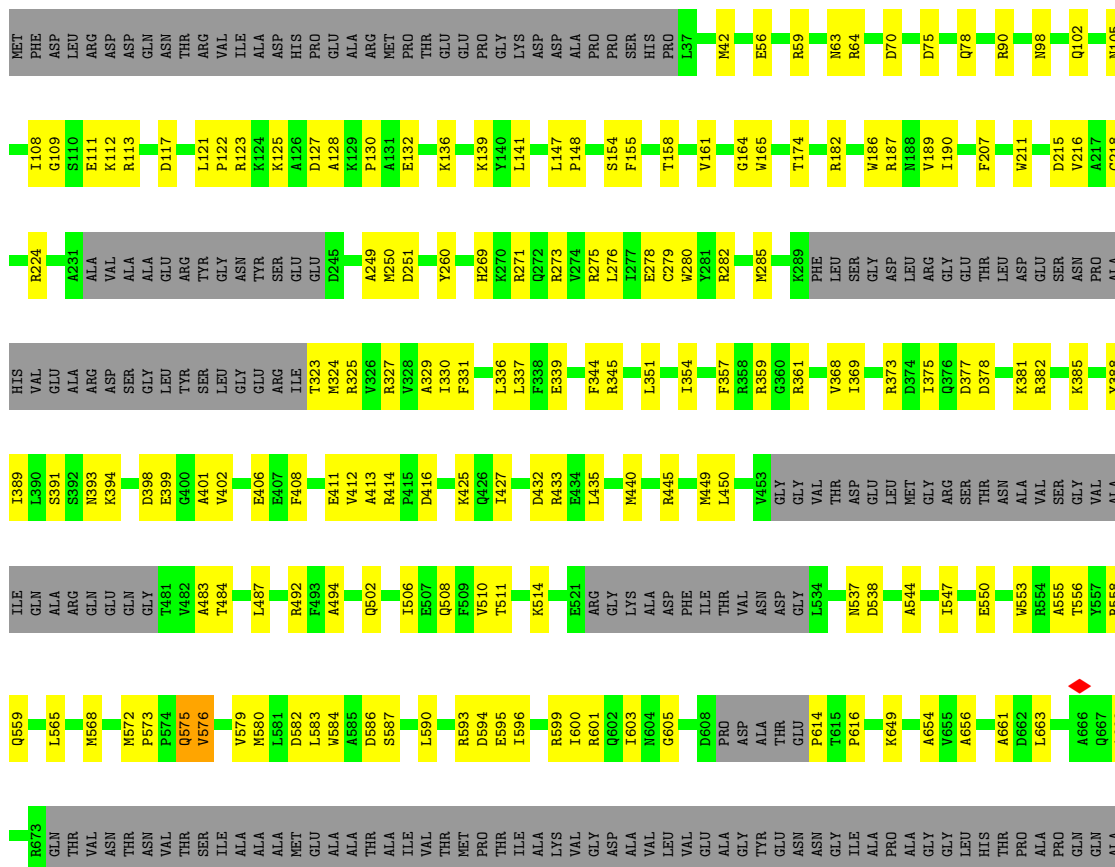
- Molecule 1: Portal protein

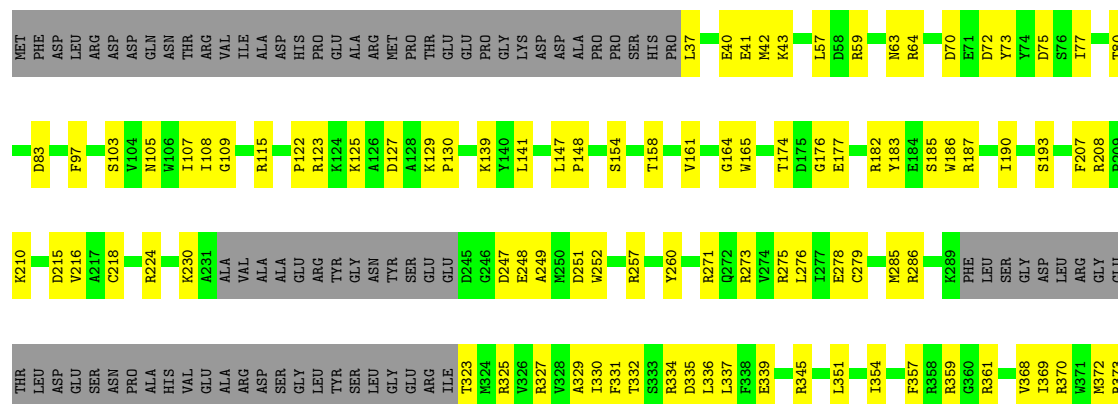


- Molecule 1: Portal protein



- Molecule 1: Portal protein









[illegible]

- Molecule 2: Putative tail fiber protein

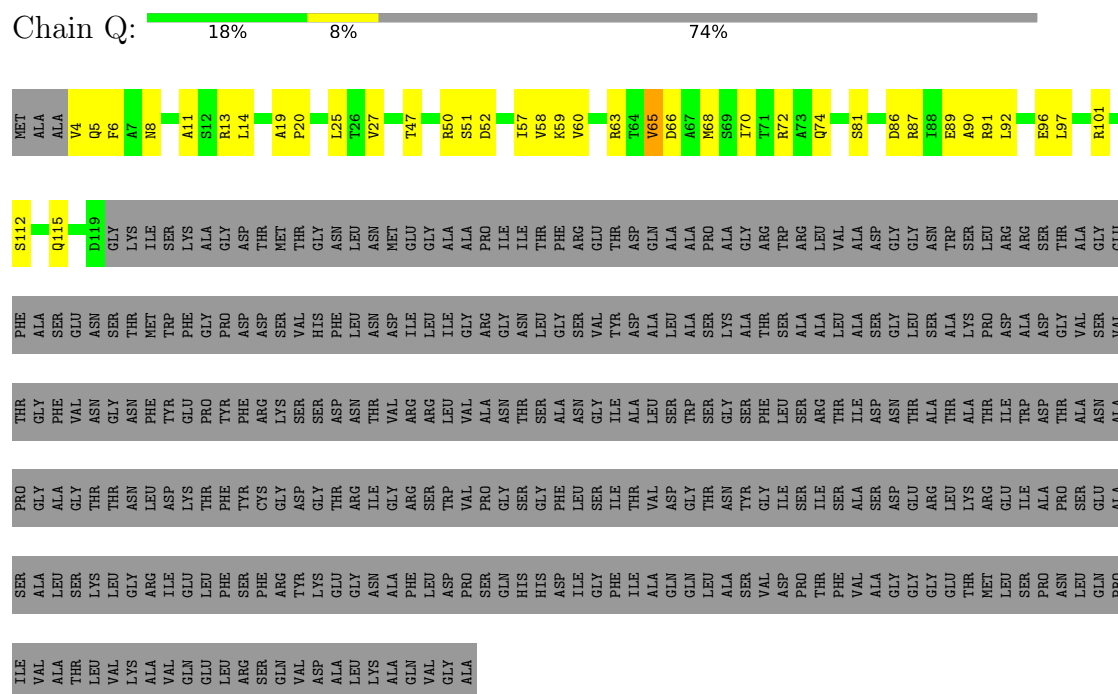
[illegible]

- Molecule 2: Putative tail fiber protein

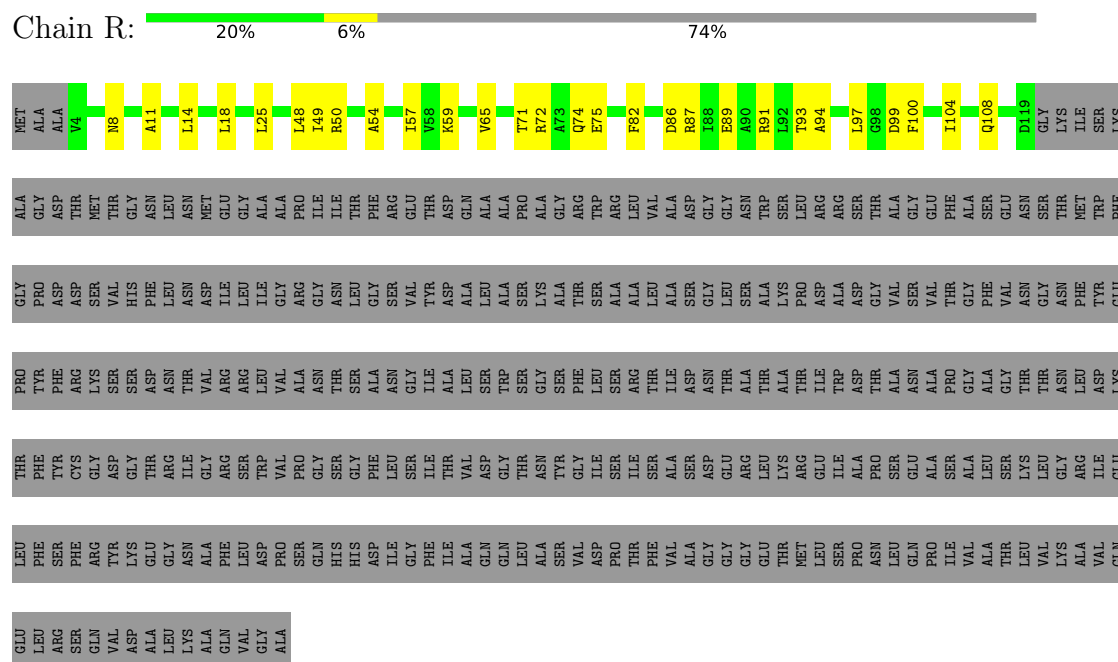


THR	THR	PRO	LEU	T93	MET
ILE	ASP	ASP	ARG	A94	ALA
TRP	ALA	TRP	ARG	G95	ALA
ASP	ASP	ASP	SER	V4	V4
THR	GLY	THR	THR	E96	Q5
ALA	VAL	ALA	ALA	I97	F6
ASN	SER	SER	GLY	G98	A7
ALA	VAL	ALA	GLU	D99	N8
PRO	GLY	THR	PHE	F100	
GLY	GLY	GLY	ALA	R101	
ALA	PHE	ALA	GLU	I104	L14
GLY	VAL	ASN	SER		L18
THR	GLY	GLY	ASN	D119	A19
THR	GLY	SER	SER	GLY	
ASN	ASN	THR	THR	LYS	G22
LEU	PHE	THR	MET	ILE	
ASP	THR	THR	THR	SER	L25
GLY	GLU	GLY	PHE	LYS	
THR	PRO	PRO	GLY	ALA	T28
PHE	TYR	TYR	PRO	GLY	P29
TYR	PHE	TYR	ASP	ASP	G30
CYS	ARG	ARG	ASP	THR	D31
GLY	LYS	LYS	SER	MET	
ASP	SER	SER	VAL	THR	L34
GLY	SER	SER	HIS	GLY	
THR	ASP	THR	PHE	ASN	L38
ARG	ASN	ASN	LEU	LEU	
ILE	THR	ILE	ASN	ASN	
GLY	VAL	VAL	ASP	MET	F44
ARG	ARG	ARG	ILE	GLU	M45
SER	ARG	ARG	LEU	GLY	A46
TRP	LEU	LEU	ILE	ALA	T47
VAL	VAL	VAL	GLY	ALA	L48
PRO	ALA	ALA	ARG	PRO	I49
GLY	ASN	ASN	GLY	ILE	R50
SER	THR	THR	ASN	ILE	S51
GLY	SER	SER	LEU	THR	D52
PHE	ALA	ALA	GLY	PHE	G53
LEU	ASN	ASN	SER	ARG	A54
SER	GLY	GLY	VAL	GLU	R55
ILE	ILE	ILE	TYR	THR	E56
THR	ALA	ALA	ASP	ASP	I57
VAL	LEU	LEU	ALA	GLN	V65
ASP	ASP	ASP	LEU	ALA	
GLY	TRP	TRP	ALA	ALA	T71
THR	THR	SER	SER	PRO	R72
ASN	GLY	LYS	LYS	ALA	A73
TYR	SER	SER	ALA	GLY	Q74
GLY	PHE	THR	THR	ARG	
ILE	LEU	SER	SER	TRP	S77
ILE	ARG	ALA	ALA	ARG	S78
SER	THR	THR	LEU	VAL	
ALA	ILE	ILE	ALA	ALA	F82
SER	ASP	ASN	SER	ASP	
ASP	ASN	ASP	GLY	GLY	D86
GLU	THR	THR	LEU	GLY	R87
ARG	ALA	ALA	SER	ASN	
LEU	THR	THR	ALA	THR	A90
LYS	ALA	ALA	LYS	SER	R91

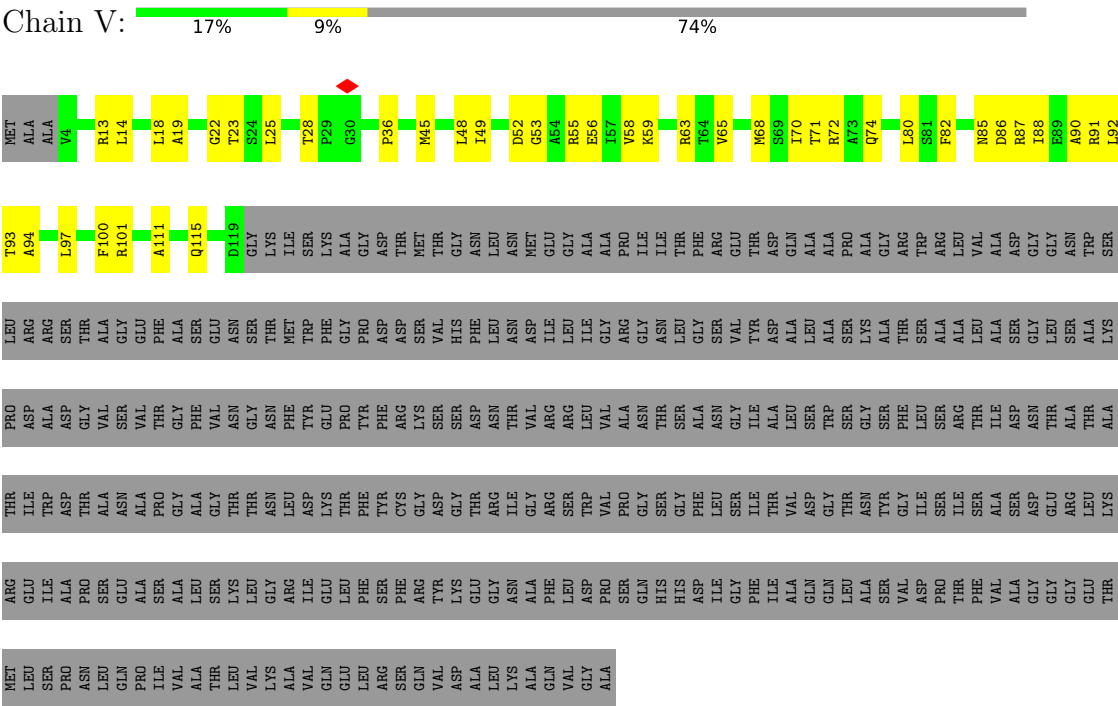
- Molecule 2: Putative tail fiber protein



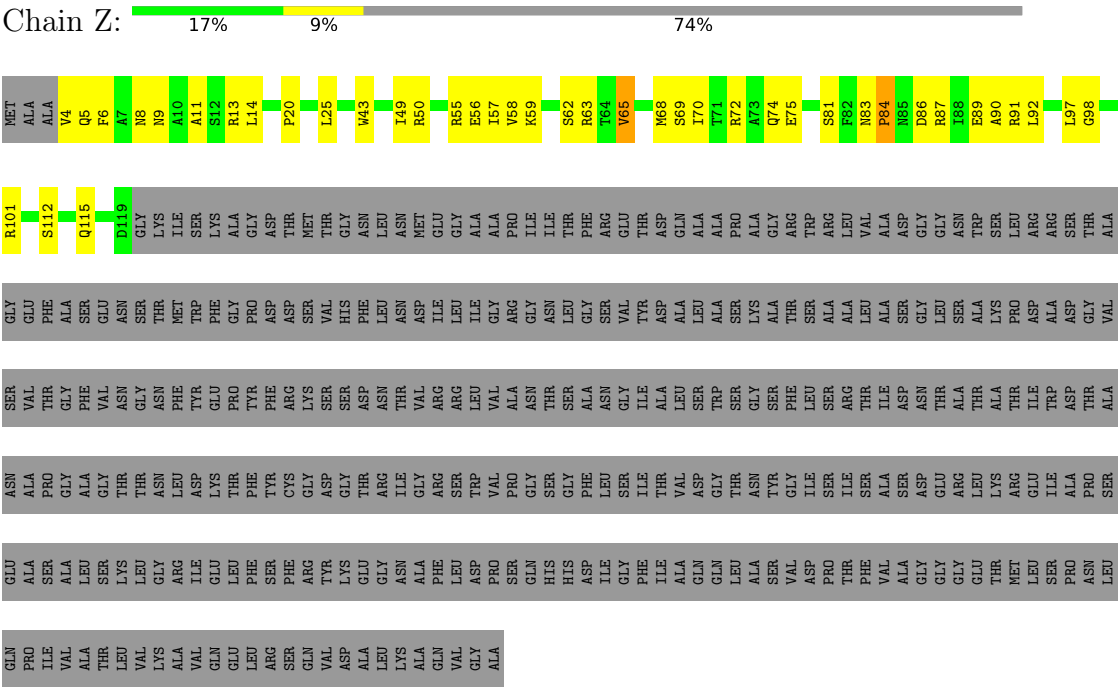
- Molecule 2: Putative tail fiber protein



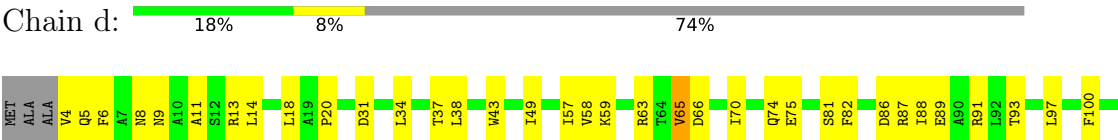
- Molecule 2: Putative tail fiber protein



● Molecule 2: Putative tail fiber protein

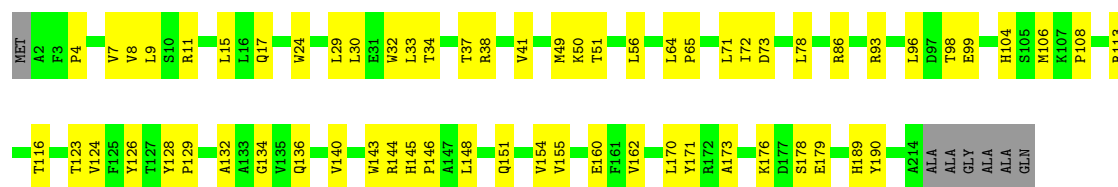


● Molecule 2: Putative tail fiber protein



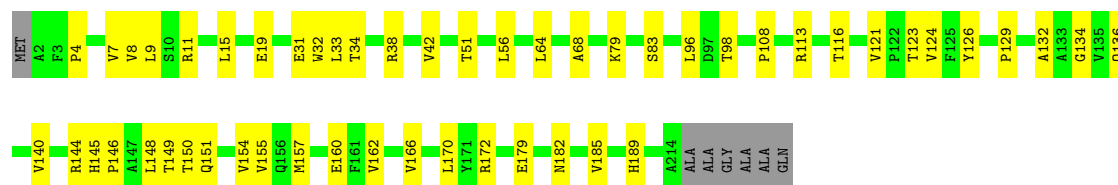


Chain 2:  68% 29% .



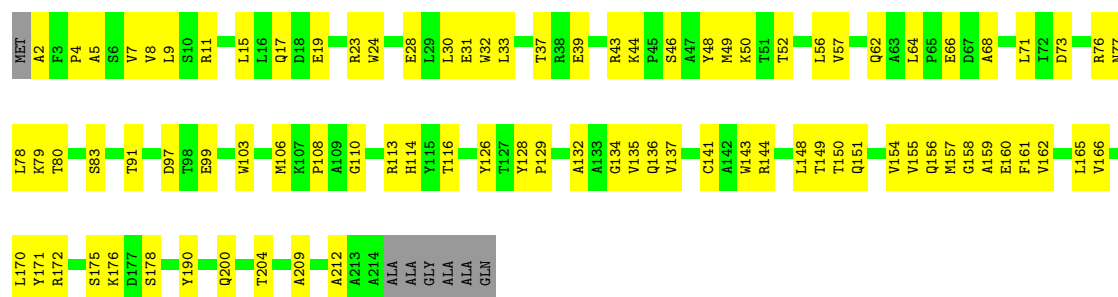
• Molecule 3: Virion associated protein

Chain 5:  73% 24% .



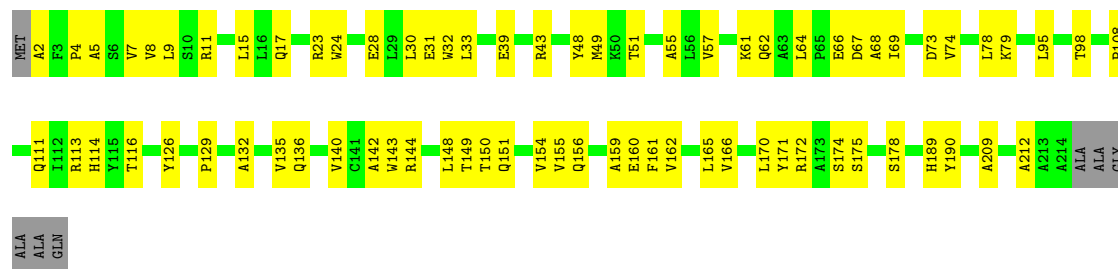
• Molecule 3: Virion associated protein

Chain T:  57% 40% .



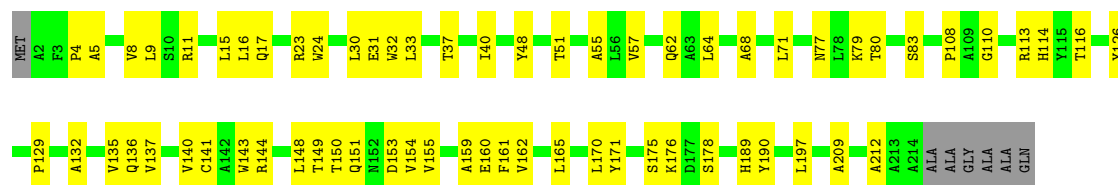
• Molecule 3: Virion associated protein

Chain X:  64% 33% .



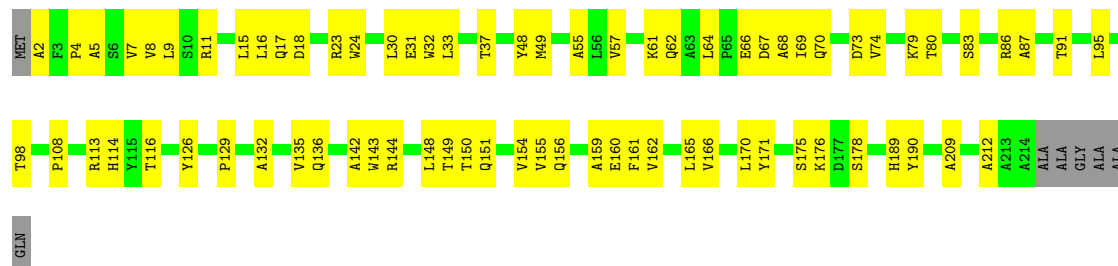
• Molecule 3: Virion associated protein

Chain b:  67% 30% .



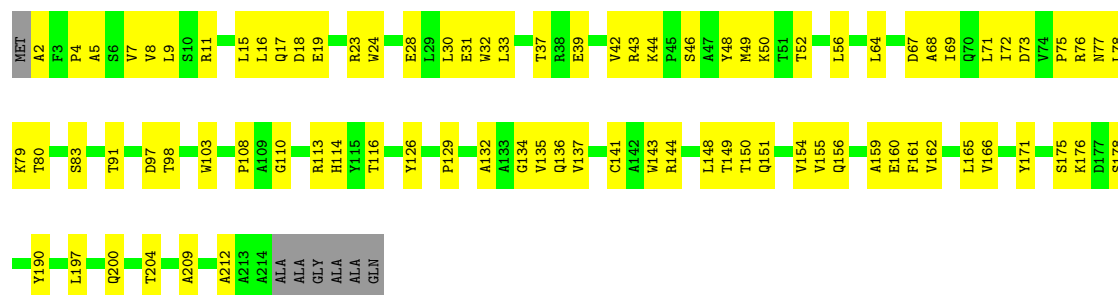
• Molecule 3: Virion associated protein

Chain f: 63% 34%



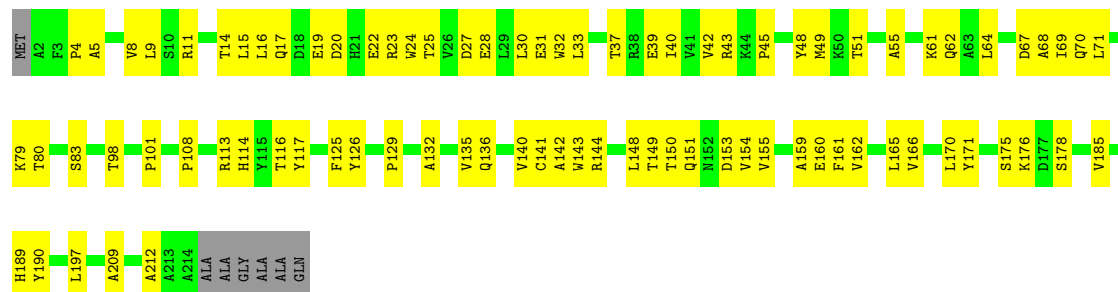
• Molecule 3: Virion associated protein

Chain j: 58% 39%



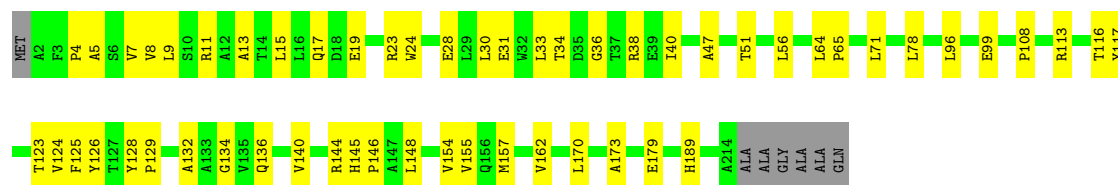
• Molecule 3: Virion associated protein

Chain n: 59% 38%



• Molecule 3: Virion associated protein

Chain q: 72% 25%



• Molecule 3: Virion associated protein



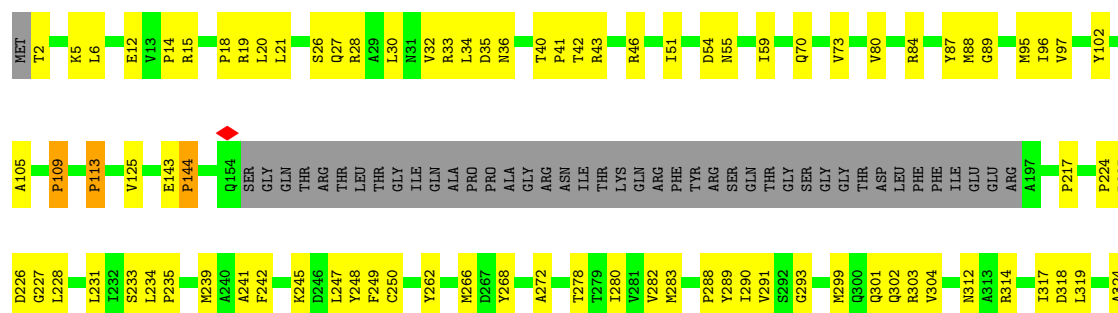
• Molecule 3: Virion associated protein

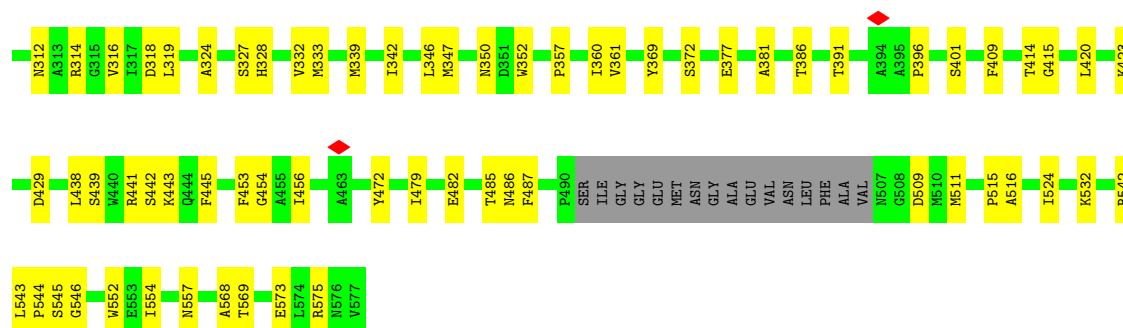


• Molecule 3: Virion associated protein

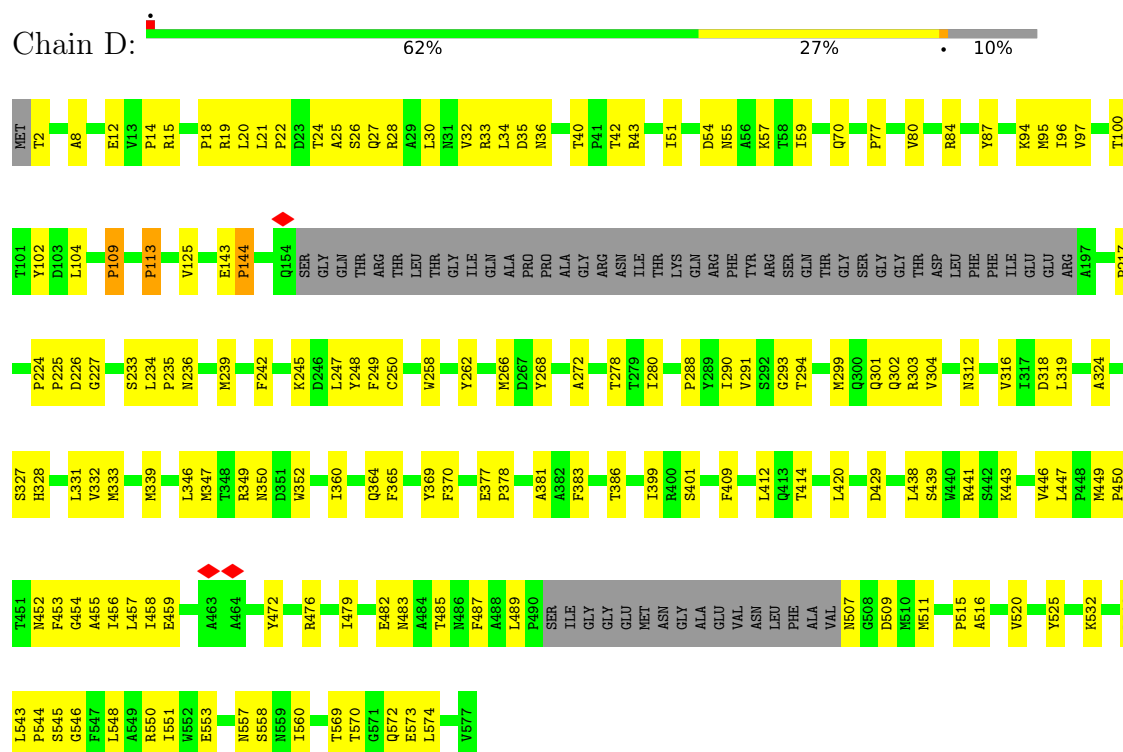


• Molecule 4: Virion-associated phage protein

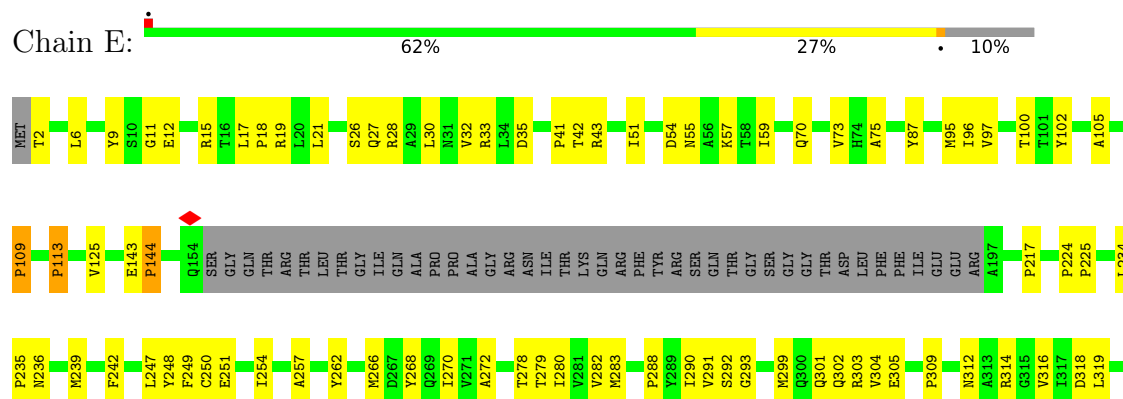


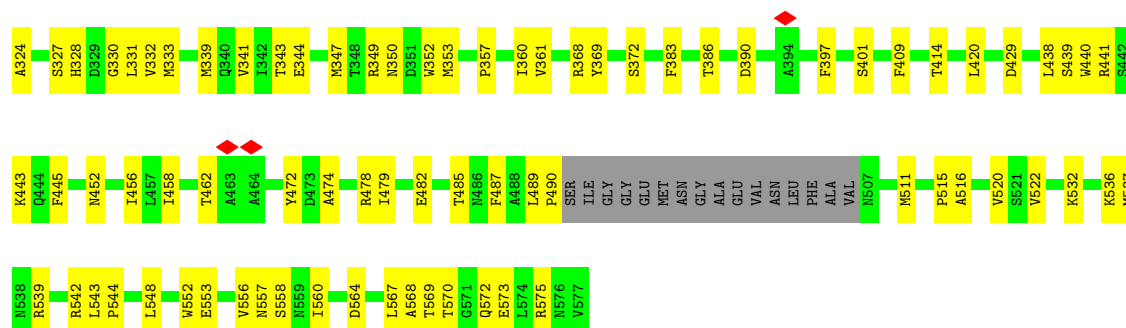


• Molecule 4: Virion-associated phage protein



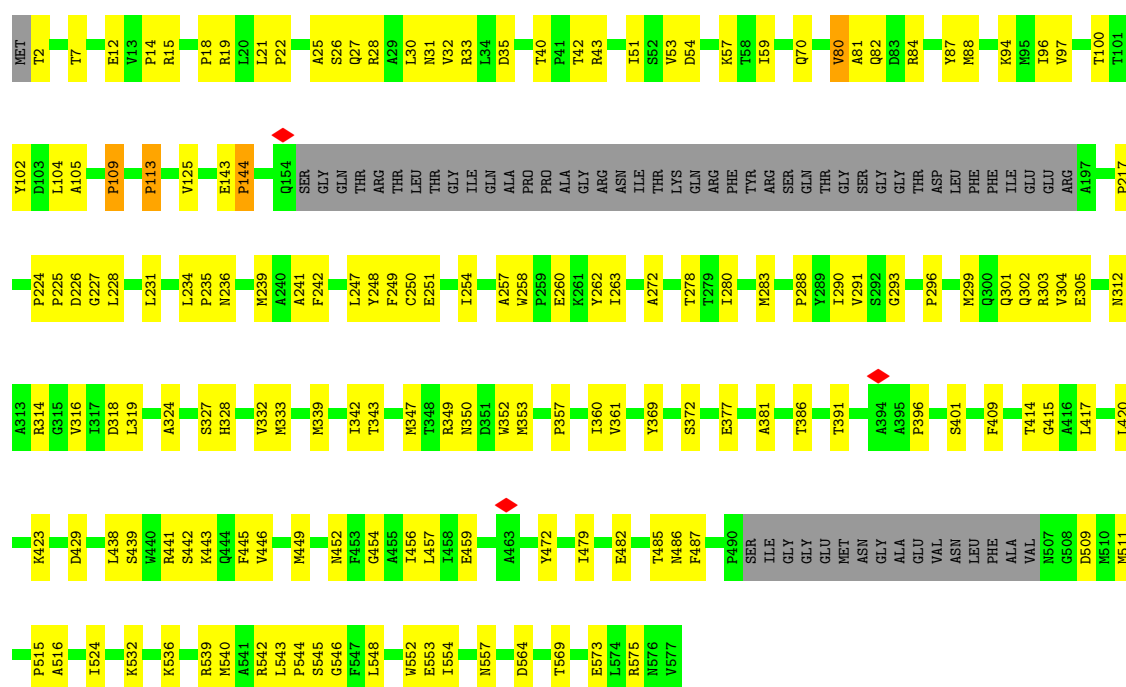
• Molecule 4: Virion-associated phage protein





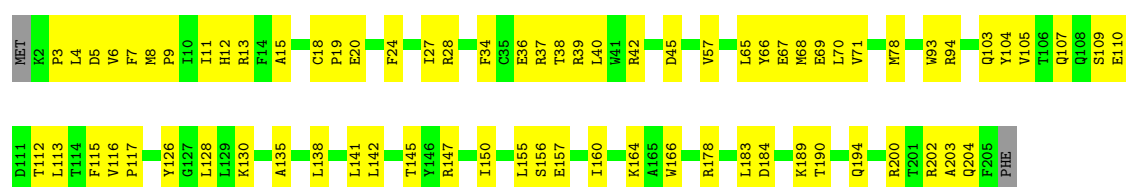
• Molecule 4: Virion-associated phage protein

Chain F: 62% 27% 10%



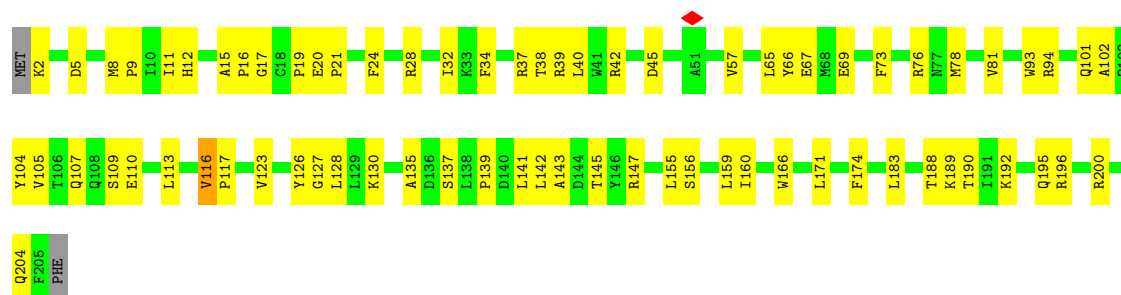
• Molecule 5: gp81 of phage GP4

Chain G: 64% 35%



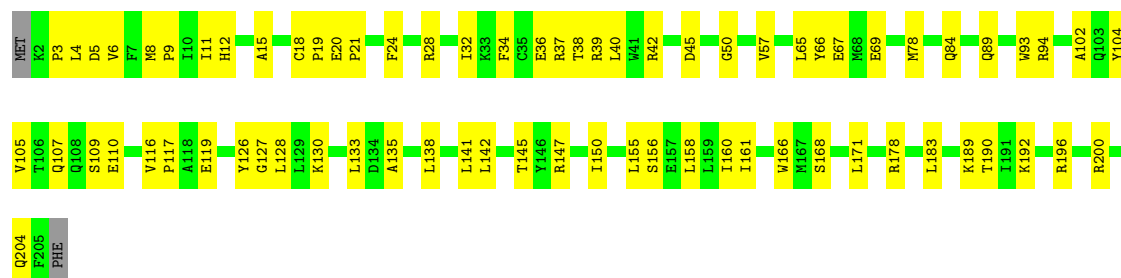
• Molecule 5: gp81 of phage GP4

Chain H: 64% 34%



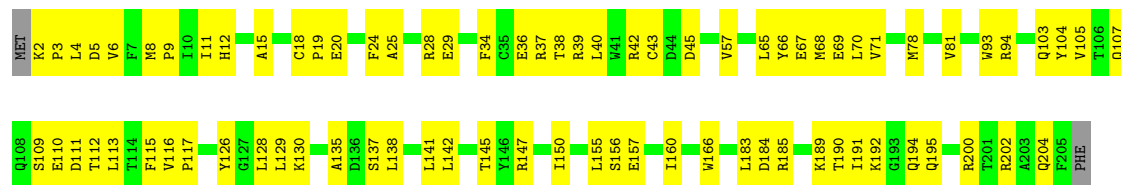
- Molecule 5: gp81 of phage GP4

Chain I: 64% 35% .



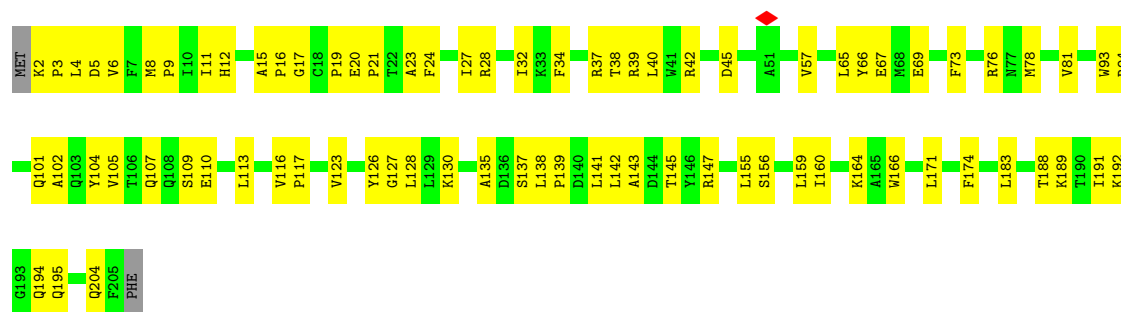
- Molecule 5: gp81 of phage GP4

Chain J: 61% 38% .



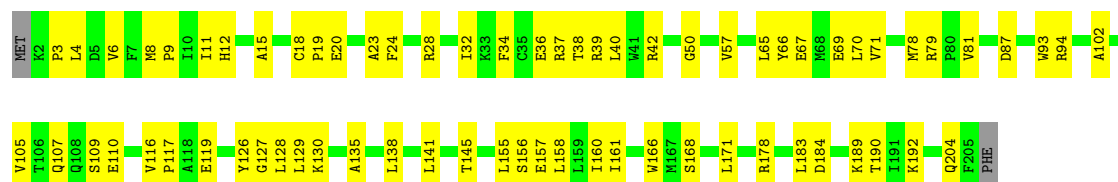
- Molecule 5: gp81 of phage GP4

Chain K: 61% 38% .

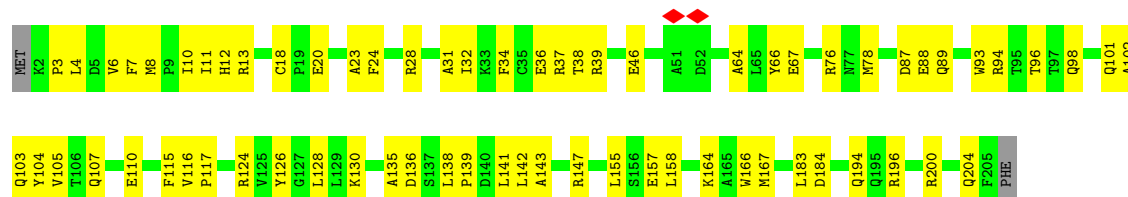


- Molecule 5: gp81 of phage GP4

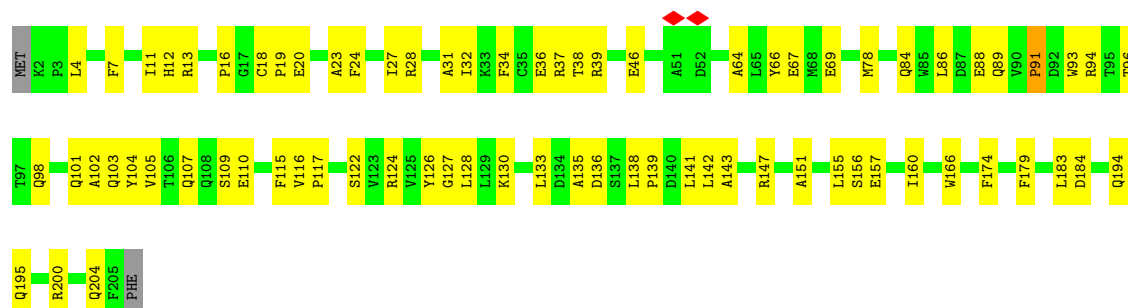
Chain L: 66% 33% .



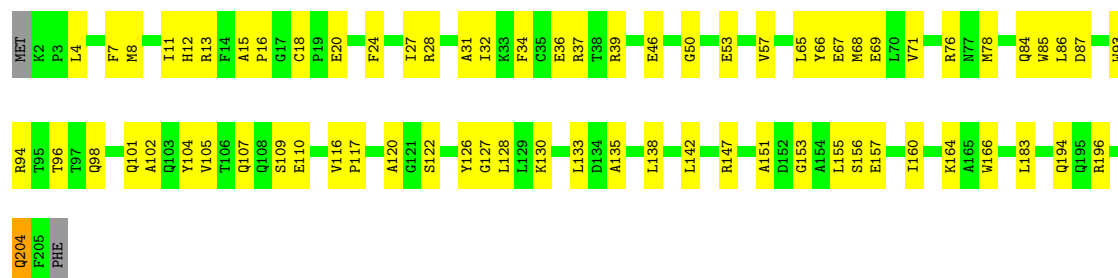
- Molecule 5: gp81 of phage GP4



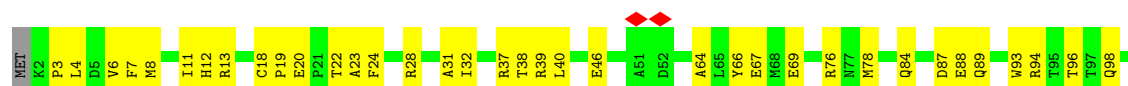
- Molecule 5: gp81 of phage GP4

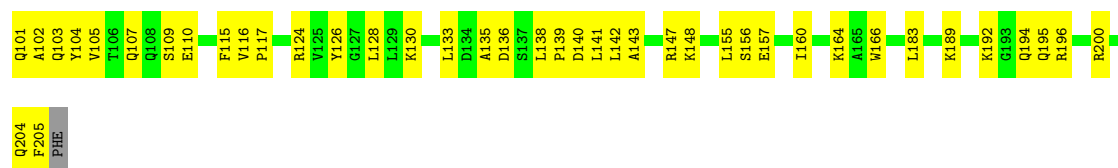


- Molecule 5: gp81 of phage GP4



- Molecule 5: gp81 of phage GP4





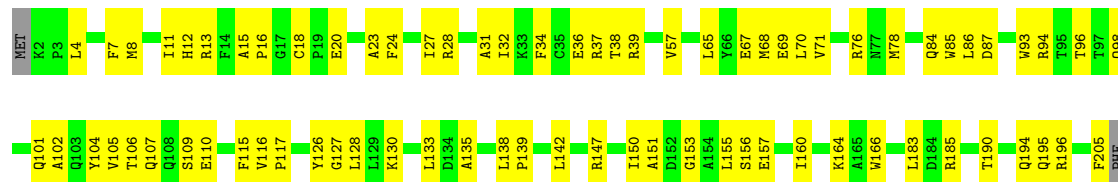
- Molecule 5: gp81 of phage GP4

Chain i: .



- Molecule 5: gp81 of phage GP4

Chain m: .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	39883	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	100	Depositor
Maximum defocus (nm)	3800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	31.901	Depositor
Minimum map value	-13.810	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.650	Depositor
Recommended contour level	3	Depositor
Map size (Å)	508.0, 508.0, 508.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.27, 1.27, 1.27	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	0.16	0/4368	0.41	4/5900 (0.1%)
1	3	0.14	0/4368	0.39	4/5900 (0.1%)
1	6	0.16	0/4368	0.40	4/5900 (0.1%)
1	U	0.14	0/4368	0.38	4/5900 (0.1%)
1	Y	0.17	0/4368	0.41	4/5900 (0.1%)
1	c	0.15	0/4368	0.39	4/5900 (0.1%)
1	g	0.15	0/4368	0.41	4/5900 (0.1%)
1	k	0.14	0/4368	0.37	2/5900 (0.0%)
1	o	0.16	0/4368	0.40	4/5900 (0.1%)
1	r	0.15	0/4368	0.40	4/5900 (0.1%)
1	u	0.17	0/4368	0.42	4/5900 (0.1%)
1	x	0.15	0/4368	0.39	4/5900 (0.1%)
2	1	0.16	0/840	0.41	0/1141
2	4	0.20	0/840	0.52	1/1141 (0.1%)
2	7	0.20	0/840	0.51	0/1141
2	M	0.19	0/840	0.46	0/1141
2	N	0.17	0/840	0.47	0/1141
2	O	0.17	0/840	0.49	0/1141
2	P	0.15	0/840	0.41	0/1141
2	Q	0.15	0/840	0.42	0/1141
2	R	0.17	0/840	0.48	0/1141
2	V	0.16	0/840	0.43	0/1141
2	Z	0.18	0/840	0.51	1/1141 (0.1%)
2	d	0.18	0/840	0.51	0/1141
2	h	0.19	0/840	0.45	0/1141
2	l	0.18	0/840	0.47	0/1141
2	p	0.16	0/840	0.43	0/1141
2	s	0.14	0/840	0.41	0/1141
2	v	0.19	0/840	0.54	1/1141 (0.1%)
2	y	0.16	0/840	0.44	0/1141
3	2	0.17	0/1653	0.38	0/2265
3	5	0.17	0/1653	0.38	0/2265
3	T	0.18	0/1653	0.44	0/2265
3	X	0.18	0/1653	0.41	0/2265

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	b	0.18	0/1653	0.43	0/2265
3	f	0.19	0/1653	0.43	0/2265
3	j	0.19	0/1653	0.43	0/2265
3	n	0.19	0/1653	0.44	0/2265
3	q	0.17	0/1653	0.37	0/2265
3	t	0.17	0/1653	0.39	0/2265
3	w	0.16	0/1653	0.37	0/2265
3	z	0.16	0/1653	0.37	0/2265
4	A	0.17	0/3893	0.46	4/5306 (0.1%)
4	B	0.16	0/3893	0.45	4/5306 (0.1%)
4	C	0.17	0/3893	0.46	4/5306 (0.1%)
4	D	0.17	0/3893	0.46	4/5306 (0.1%)
4	E	0.17	0/3893	0.46	4/5306 (0.1%)
4	F	0.17	0/3893	0.46	4/5306 (0.1%)
5	G	0.18	0/1648	0.40	0/2241
5	H	0.19	0/1648	0.41	0/2241
5	I	0.19	0/1648	0.42	0/2241
5	J	0.18	0/1648	0.40	0/2241
5	K	0.19	0/1648	0.42	0/2241
5	L	0.19	0/1648	0.41	0/2241
5	S	0.19	0/1648	0.39	0/2241
5	W	0.20	0/1648	0.43	1/2241 (0.0%)
5	a	0.18	0/1648	0.38	0/2241
5	e	0.18	0/1648	0.39	0/2241
5	i	0.20	0/1648	0.41	1/2241 (0.0%)
5	m	0.18	0/1648	0.38	0/2241
All	All	0.17	0/130506	0.42	75/177246 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	r	0	1
4	F	0	1
5	H	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 75 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	113	PRO	N-CA-CB	7.96	111.60	103.25
4	E	113	PRO	N-CA-CB	7.93	111.58	103.25
4	B	113	PRO	N-CA-CB	7.91	111.55	103.25
4	C	113	PRO	N-CA-CB	7.89	111.53	103.25
4	D	113	PRO	N-CA-CB	7.88	111.52	103.25

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	F	80	VAL	Peptide
5	H	116	VAL	Peptide
1	r	558	ARG	Sidechain

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	4297	0	4103	148	0
1	3	4297	0	4103	141	0
1	6	4297	0	4103	138	0
1	U	4297	0	4103	148	0
1	Y	4297	0	4103	160	0
1	c	4297	0	4103	142	0
1	g	4297	0	4103	140	0
1	k	4297	0	4103	123	0
1	o	4297	0	4103	138	0
1	r	4297	0	4103	131	0
1	u	4297	0	4103	137	0
1	x	4297	0	4103	134	0
2	1	829	0	810	35	0
2	4	829	0	810	29	0
2	7	829	0	810	27	0
2	M	829	0	810	33	0
2	N	829	0	810	26	0
2	O	829	0	810	26	0
2	P	829	0	810	35	0
2	Q	829	0	810	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	R	829	0	810	22	0
2	V	829	0	810	33	0
2	Z	829	0	810	34	0
2	d	829	0	810	26	0
2	h	829	0	810	28	0
2	l	829	0	810	23	0
2	p	829	0	810	24	0
2	s	829	0	810	34	0
2	v	829	0	810	35	0
2	y	829	0	810	22	0
3	2	1615	0	1565	56	0
3	5	1615	0	1565	47	0
3	T	1615	0	1565	69	0
3	X	1615	0	1565	61	0
3	b	1615	0	1565	55	0
3	f	1615	0	1565	66	0
3	j	1615	0	1565	66	0
3	n	1615	0	1565	73	0
3	q	1615	0	1565	48	0
3	t	1615	0	1565	57	0
3	w	1615	0	1565	56	0
3	z	1615	0	1565	52	0
4	A	3812	0	3582	122	0
4	B	3812	0	3582	120	0
4	C	3812	0	3582	117	0
4	D	3812	0	3582	120	0
4	E	3812	0	3582	122	0
4	F	3812	0	3582	137	0
5	G	1611	0	1583	64	0
5	H	1611	0	1583	61	0
5	I	1611	0	1583	65	0
5	J	1611	0	1583	71	0
5	K	1611	0	1583	71	0
5	L	1611	0	1583	61	0
5	S	1611	0	1583	59	0
5	W	1611	0	1583	68	0
5	a	1611	0	1583	65	0
5	e	1611	0	1583	71	0
5	i	1611	0	1583	67	0
5	m	1611	0	1583	71	0
All	All	128070	0	123084	3798	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 15.

The worst 5 of 3798 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:r:323:THR:N	1:u:174:THR:HG1	1.41	1.17
1:g:323:THR:N	1:k:174:THR:HG1	1.46	1.12
1:6:323:THR:N	1:U:174:THR:HG1	1.48	1.10
1:U:323:THR:N	1:Y:174:THR:HG1	1.51	1.07
1:c:323:THR:N	1:g:174:THR:HG1	1.52	1.07

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	535/781 (68%)	516 (96%)	17 (3%)	2 (0%)	30	62
1	3	535/781 (68%)	520 (97%)	13 (2%)	2 (0%)	30	62
1	6	535/781 (68%)	516 (96%)	17 (3%)	2 (0%)	30	62
1	U	535/781 (68%)	517 (97%)	16 (3%)	2 (0%)	30	62
1	Y	535/781 (68%)	523 (98%)	10 (2%)	2 (0%)	30	62
1	c	535/781 (68%)	519 (97%)	14 (3%)	2 (0%)	30	62
1	g	535/781 (68%)	518 (97%)	15 (3%)	2 (0%)	30	62
1	k	535/781 (68%)	518 (97%)	15 (3%)	2 (0%)	30	62
1	o	535/781 (68%)	519 (97%)	14 (3%)	2 (0%)	30	62
1	r	535/781 (68%)	517 (97%)	16 (3%)	2 (0%)	30	62
1	u	535/781 (68%)	520 (97%)	13 (2%)	2 (0%)	30	62
1	x	535/781 (68%)	520 (97%)	13 (2%)	2 (0%)	30	62
2	1	114/439 (26%)	106 (93%)	7 (6%)	1 (1%)	14	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	4	114/439 (26%)	107 (94%)	6 (5%)	1 (1%)	14	45
2	7	114/439 (26%)	106 (93%)	7 (6%)	1 (1%)	14	45
2	M	114/439 (26%)	108 (95%)	5 (4%)	1 (1%)	14	45
2	N	114/439 (26%)	105 (92%)	8 (7%)	1 (1%)	14	45
2	O	114/439 (26%)	106 (93%)	7 (6%)	1 (1%)	14	45
2	P	114/439 (26%)	107 (94%)	6 (5%)	1 (1%)	14	45
2	Q	114/439 (26%)	105 (92%)	8 (7%)	1 (1%)	14	45
2	R	114/439 (26%)	105 (92%)	8 (7%)	1 (1%)	14	45
2	V	114/439 (26%)	105 (92%)	8 (7%)	1 (1%)	14	45
2	Z	114/439 (26%)	107 (94%)	6 (5%)	1 (1%)	14	45
2	d	114/439 (26%)	105 (92%)	8 (7%)	1 (1%)	14	45
2	h	114/439 (26%)	107 (94%)	6 (5%)	1 (1%)	14	45
2	l	114/439 (26%)	106 (93%)	7 (6%)	1 (1%)	14	45
2	p	114/439 (26%)	107 (94%)	6 (5%)	1 (1%)	14	45
2	s	114/439 (26%)	108 (95%)	5 (4%)	1 (1%)	14	45
2	v	114/439 (26%)	107 (94%)	6 (5%)	1 (1%)	14	45
2	y	114/439 (26%)	106 (93%)	7 (6%)	1 (1%)	14	45
3	2	211/220 (96%)	200 (95%)	11 (5%)	0	100	100
3	5	211/220 (96%)	202 (96%)	9 (4%)	0	100	100
3	T	211/220 (96%)	196 (93%)	15 (7%)	0	100	100
3	X	211/220 (96%)	198 (94%)	13 (6%)	0	100	100
3	b	211/220 (96%)	196 (93%)	15 (7%)	0	100	100
3	f	211/220 (96%)	199 (94%)	12 (6%)	0	100	100
3	j	211/220 (96%)	197 (93%)	14 (7%)	0	100	100
3	n	211/220 (96%)	193 (92%)	18 (8%)	0	100	100
3	q	211/220 (96%)	203 (96%)	8 (4%)	0	100	100
3	t	211/220 (96%)	199 (94%)	12 (6%)	0	100	100
3	w	211/220 (96%)	201 (95%)	10 (5%)	0	100	100
3	z	211/220 (96%)	202 (96%)	9 (4%)	0	100	100
4	A	512/577 (89%)	483 (94%)	24 (5%)	5 (1%)	12	43
4	B	512/577 (89%)	480 (94%)	27 (5%)	5 (1%)	12	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	C	512/577 (89%)	477 (93%)	30 (6%)	5 (1%)	12	43
4	D	512/577 (89%)	480 (94%)	27 (5%)	5 (1%)	12	43
4	E	512/577 (89%)	481 (94%)	26 (5%)	5 (1%)	12	43
4	F	512/577 (89%)	479 (94%)	28 (6%)	5 (1%)	12	43
5	G	202/206 (98%)	198 (98%)	4 (2%)	0	100	100
5	H	202/206 (98%)	199 (98%)	3 (2%)	0	100	100
5	I	202/206 (98%)	194 (96%)	8 (4%)	0	100	100
5	J	202/206 (98%)	195 (96%)	7 (4%)	0	100	100
5	K	202/206 (98%)	197 (98%)	5 (2%)	0	100	100
5	L	202/206 (98%)	194 (96%)	8 (4%)	0	100	100
5	S	202/206 (98%)	199 (98%)	3 (2%)	0	100	100
5	W	202/206 (98%)	199 (98%)	3 (2%)	0	100	100
5	a	202/206 (98%)	196 (97%)	6 (3%)	0	100	100
5	e	202/206 (98%)	198 (98%)	4 (2%)	0	100	100
5	i	202/206 (98%)	198 (98%)	4 (2%)	0	100	100
5	m	202/206 (98%)	199 (98%)	3 (2%)	0	100	100
All	All	16500/25848 (64%)	15768 (96%)	660 (4%)	72 (0%)	31	62

5 of 72 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	576	VAL
1	3	576	VAL
1	6	576	VAL
4	A	109	PRO
4	A	113	PRO

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	432/657 (66%)	432 (100%)	0	100	100
1	3	432/657 (66%)	432 (100%)	0	100	100
1	6	432/657 (66%)	431 (100%)	1 (0%)	87	87
1	U	432/657 (66%)	431 (100%)	1 (0%)	87	87
1	Y	432/657 (66%)	432 (100%)	0	100	100
1	c	432/657 (66%)	432 (100%)	0	100	100
1	g	432/657 (66%)	431 (100%)	1 (0%)	87	87
1	k	432/657 (66%)	432 (100%)	0	100	100
1	o	432/657 (66%)	432 (100%)	0	100	100
1	r	432/657 (66%)	431 (100%)	1 (0%)	87	87
1	u	432/657 (66%)	432 (100%)	0	100	100
1	x	432/657 (66%)	432 (100%)	0	100	100
2	1	84/333 (25%)	84 (100%)	0	100	100
2	4	84/333 (25%)	83 (99%)	1 (1%)	63	72
2	7	84/333 (25%)	84 (100%)	0	100	100
2	M	84/333 (25%)	84 (100%)	0	100	100
2	N	84/333 (25%)	82 (98%)	2 (2%)	43	62
2	O	84/333 (25%)	84 (100%)	0	100	100
2	P	84/333 (25%)	84 (100%)	0	100	100
2	Q	84/333 (25%)	84 (100%)	0	100	100
2	R	84/333 (25%)	84 (100%)	0	100	100
2	V	84/333 (25%)	84 (100%)	0	100	100
2	Z	84/333 (25%)	83 (99%)	1 (1%)	63	72
2	d	84/333 (25%)	84 (100%)	0	100	100
2	h	84/333 (25%)	84 (100%)	0	100	100
2	l	84/333 (25%)	82 (98%)	2 (2%)	43	62
2	p	84/333 (25%)	84 (100%)	0	100	100
2	s	84/333 (25%)	84 (100%)	0	100	100
2	v	84/333 (25%)	84 (100%)	0	100	100
2	y	84/333 (25%)	84 (100%)	0	100	100
3	2	167/169 (99%)	167 (100%)	0	100	100
3	5	167/169 (99%)	167 (100%)	0	100	100

Continued on next page...

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	T	167/169 (99%)	167 (100%)	0	100	100
3	X	167/169 (99%)	167 (100%)	0	100	100
3	b	167/169 (99%)	167 (100%)	0	100	100
3	f	167/169 (99%)	167 (100%)	0	100	100
3	j	167/169 (99%)	167 (100%)	0	100	100
3	n	167/169 (99%)	167 (100%)	0	100	100
3	q	167/169 (99%)	167 (100%)	0	100	100
3	t	167/169 (99%)	167 (100%)	0	100	100
3	w	167/169 (99%)	167 (100%)	0	100	100
3	z	167/169 (99%)	167 (100%)	0	100	100
4	A	366/464 (79%)	366 (100%)	0	100	100
4	B	366/464 (79%)	366 (100%)	0	100	100
4	C	366/464 (79%)	366 (100%)	0	100	100
4	D	366/464 (79%)	366 (100%)	0	100	100
4	E	366/464 (79%)	366 (100%)	0	100	100
4	F	366/464 (79%)	366 (100%)	0	100	100
5	G	170/172 (99%)	170 (100%)	0	100	100
5	H	170/172 (99%)	170 (100%)	0	100	100
5	I	170/172 (99%)	170 (100%)	0	100	100
5	J	170/172 (99%)	170 (100%)	0	100	100
5	K	170/172 (99%)	170 (100%)	0	100	100
5	L	170/172 (99%)	170 (100%)	0	100	100
5	S	170/172 (99%)	170 (100%)	0	100	100
5	W	170/172 (99%)	170 (100%)	0	100	100
5	a	170/172 (99%)	169 (99%)	1 (1%)	78	79
5	e	170/172 (99%)	170 (100%)	0	100	100
5	i	170/172 (99%)	170 (100%)	0	100	100
5	m	170/172 (99%)	170 (100%)	0	100	100
All	All	12936/20754 (62%)	12925 (100%)	11 (0%)	87	89

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	g	430	ASN
2	l	9	ASN
1	r	391	SER
2	l	47	THR
1	U	485	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 124 such sidechains are listed below:

Mol	Chain	Res	Type
1	U	376	GLN
1	x	63	ASN
5	a	204	GLN
3	w	145	HIS
1	x	502	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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.

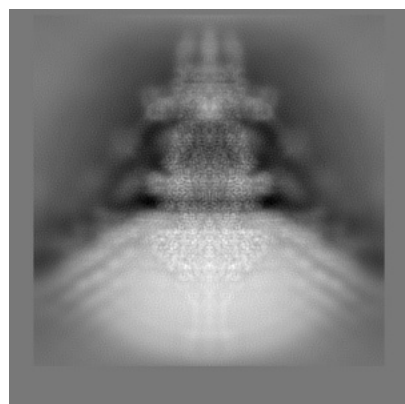
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36463. These allow visual inspection of the internal detail of the map and identification of artifacts.

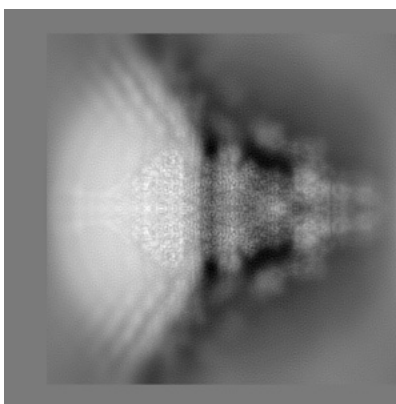
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

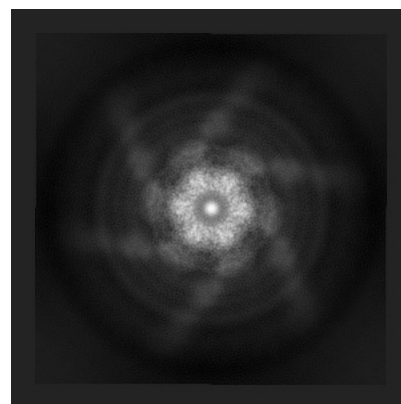
6.1.1 Primary map



X

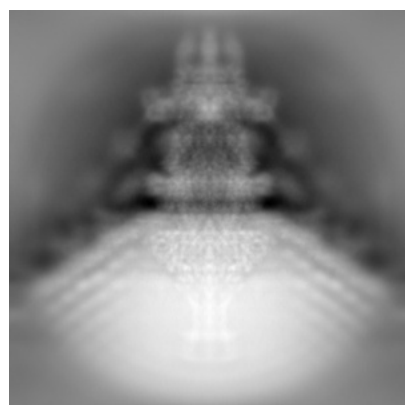


Y

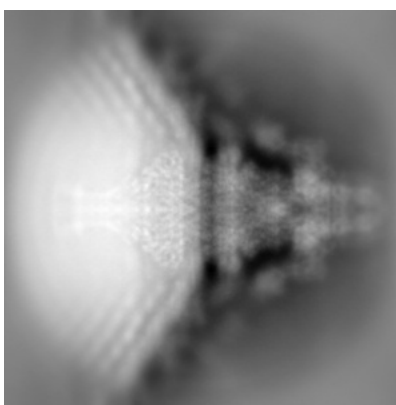


Z

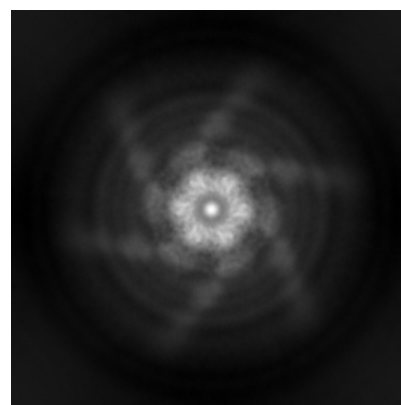
6.1.2 Raw map



X



Y

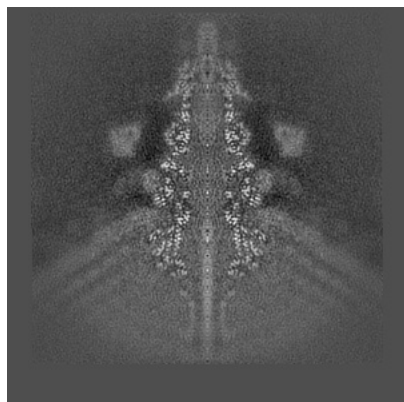


Z

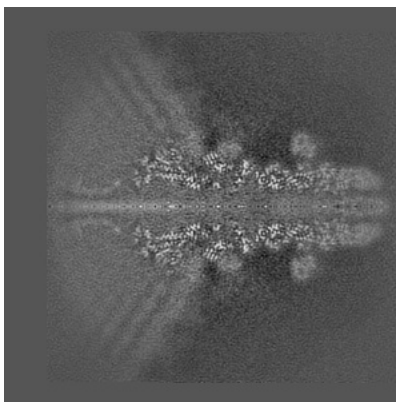
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

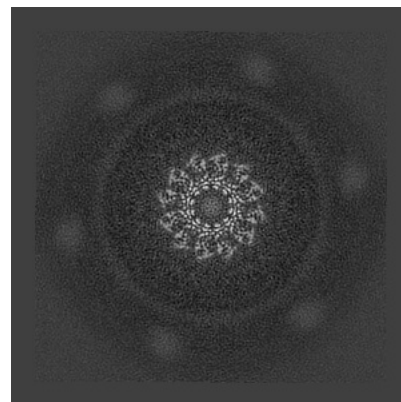
6.2.1 Primary map



X Index: 200

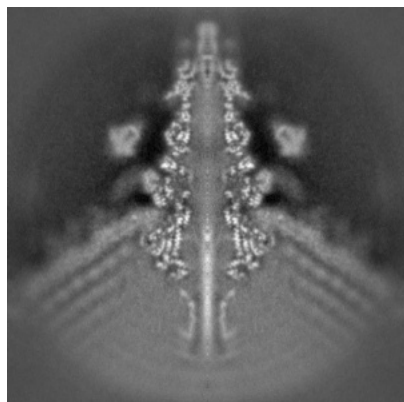


Y Index: 200

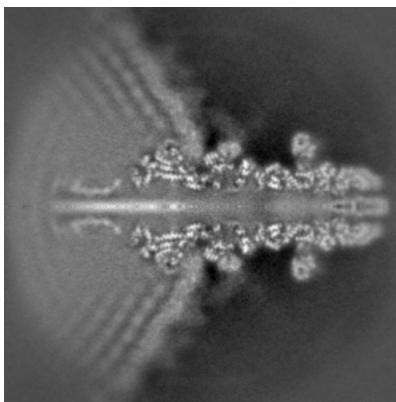


Z Index: 200

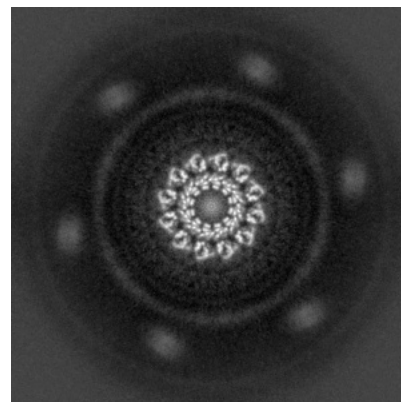
6.2.2 Raw map



X Index: 200



Y Index: 200

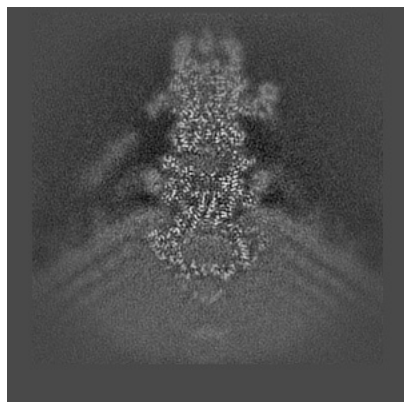


Z Index: 200

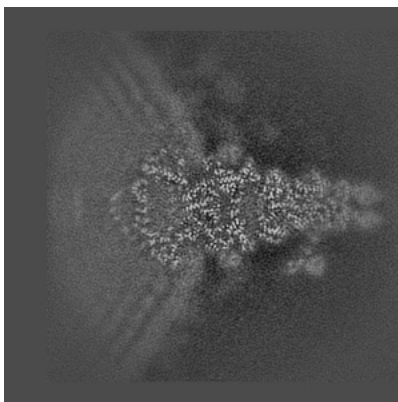
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

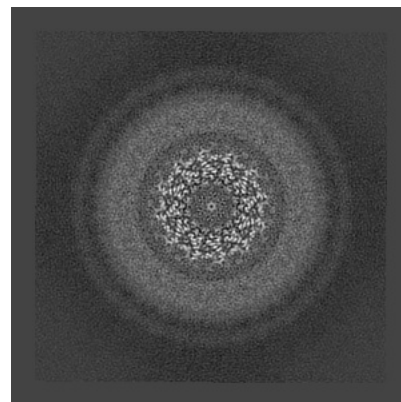
6.3.1 Primary map



X Index: 181

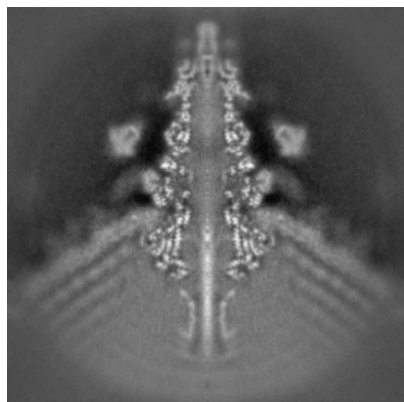


Y Index: 220

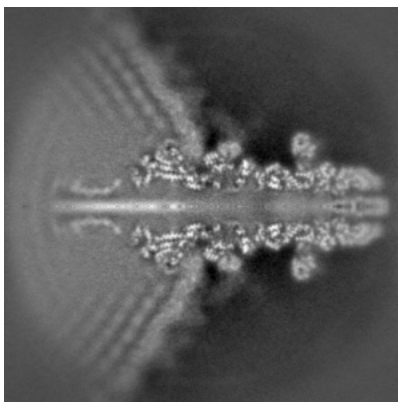


Z Index: 176

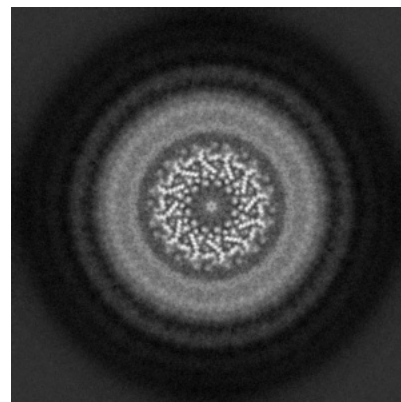
6.3.2 Raw map



X Index: 200



Y Index: 200

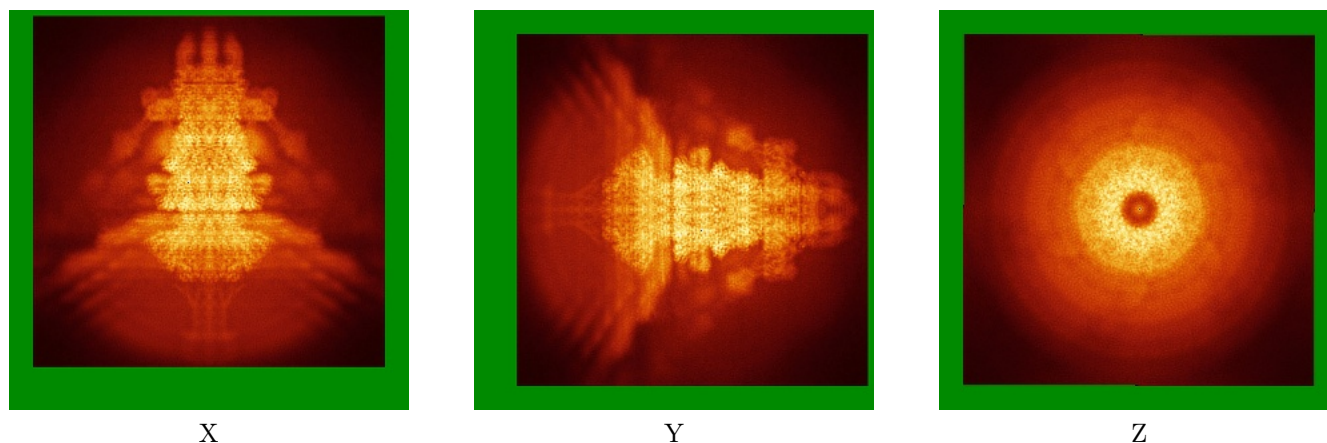


Z Index: 176

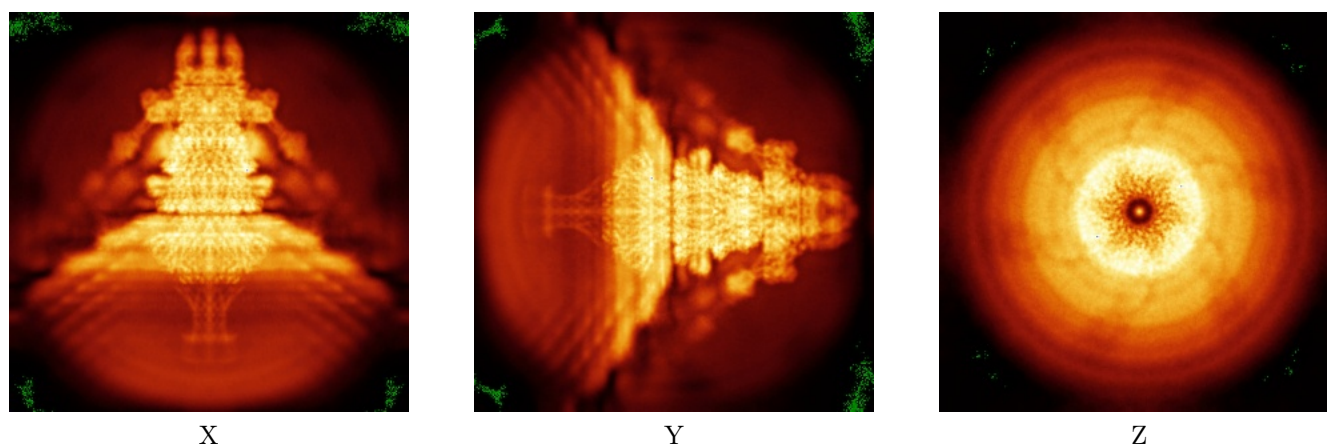
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

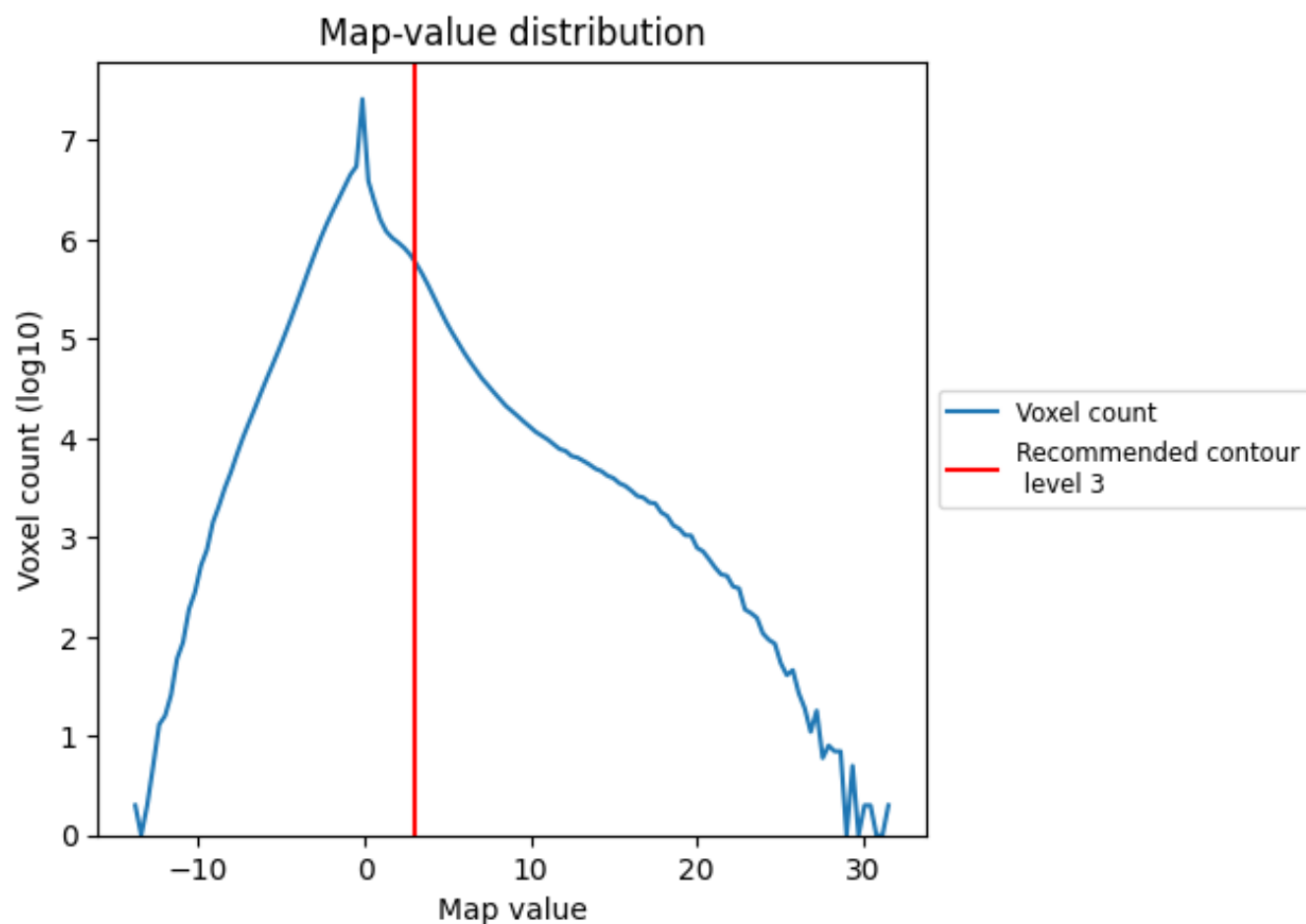
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

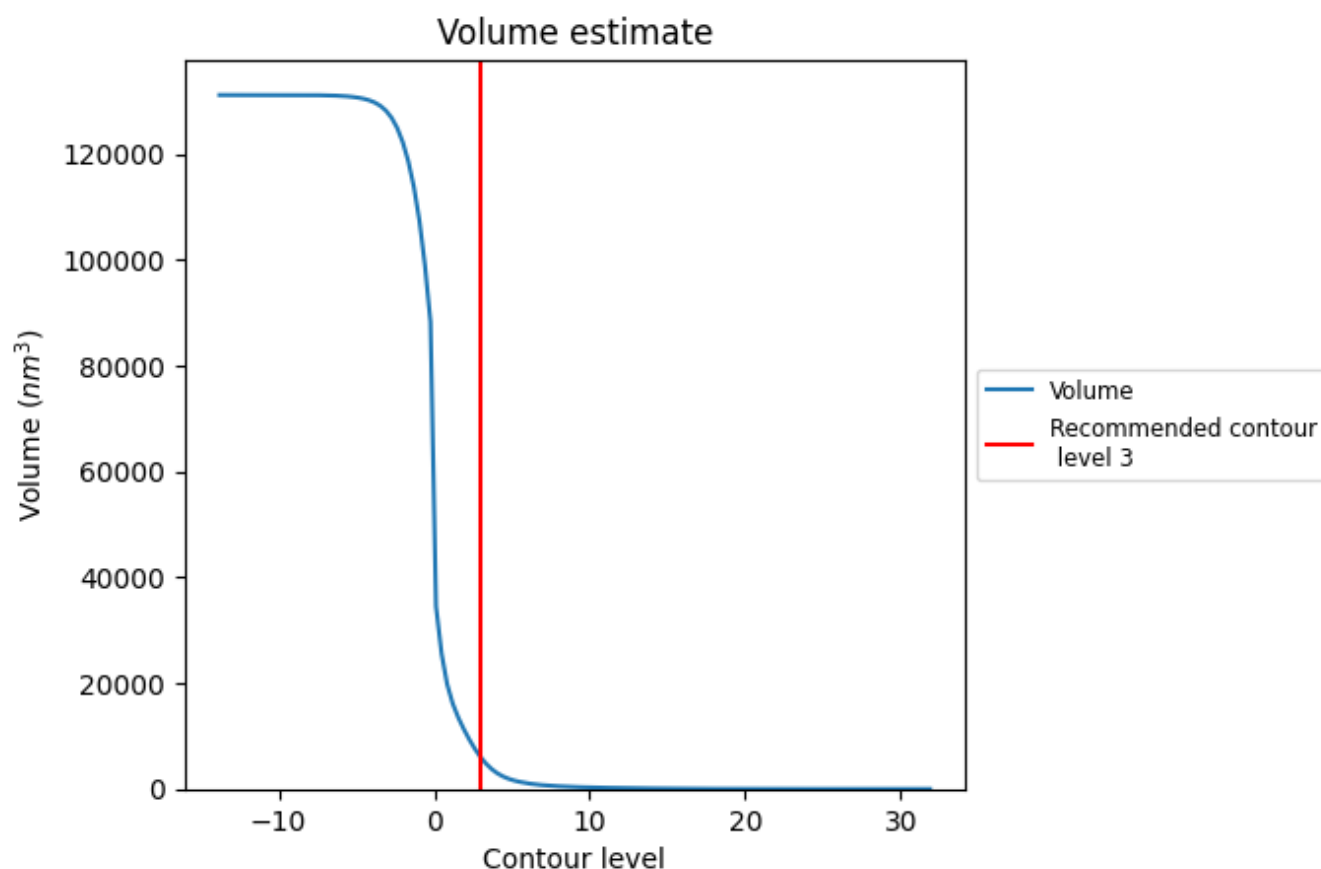
This section contains the results of statistical analysis of the map.

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.

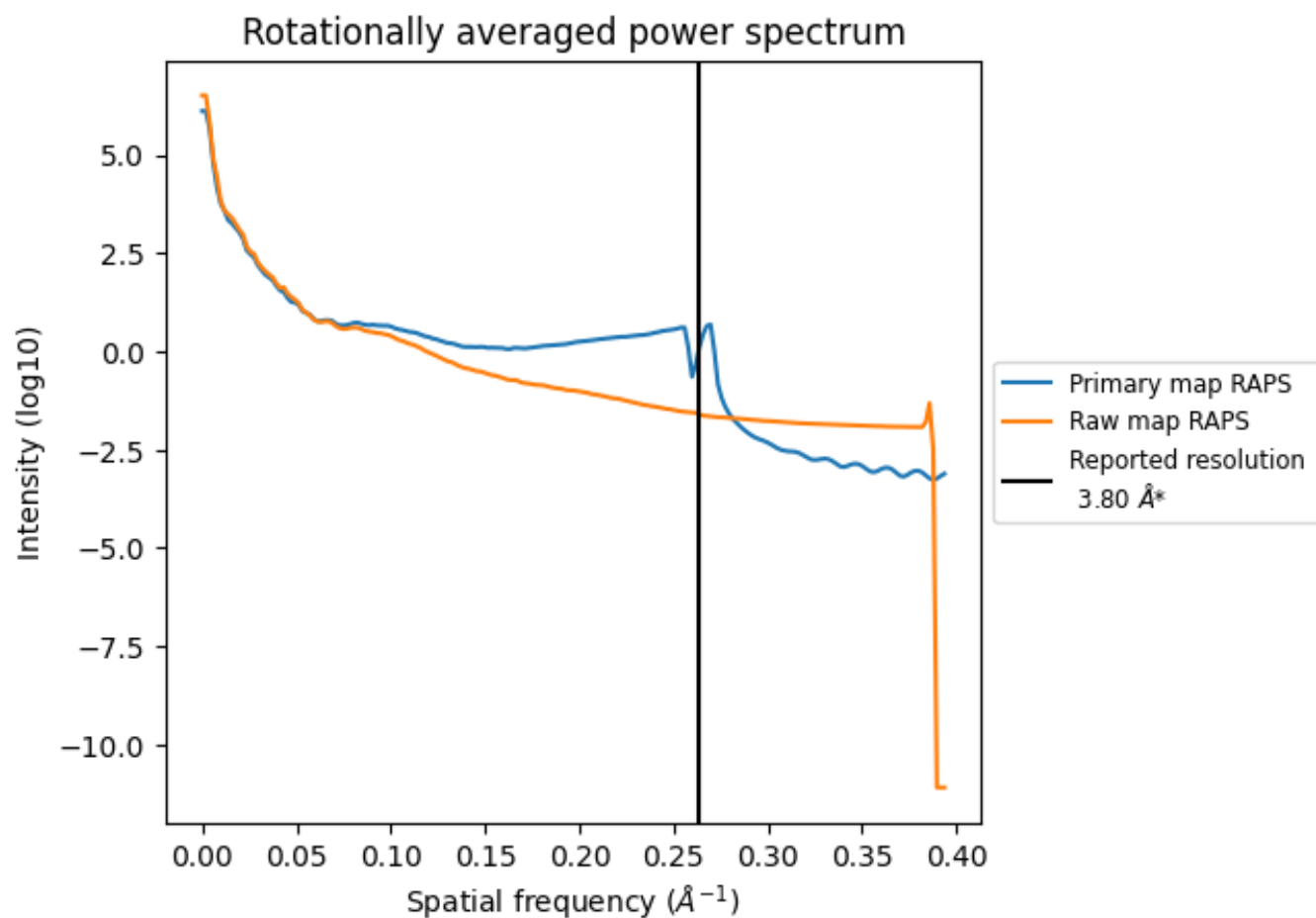
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5957 nm^3 ; this corresponds to an approximate mass of 5381 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 ⓘ

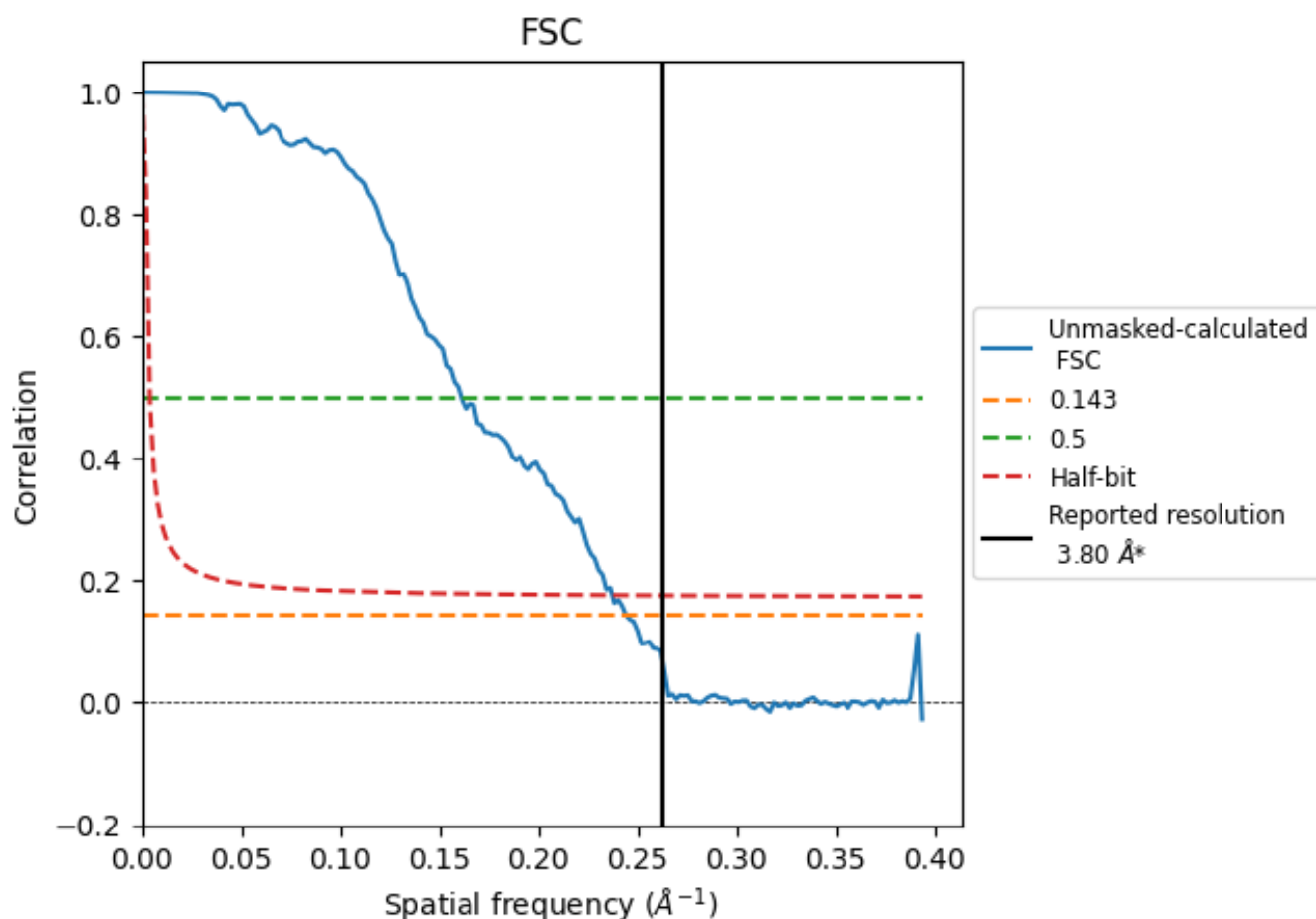


*Reported resolution corresponds to spatial frequency of 0.263 $\text{\AA}^{-1}$

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 0.263 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

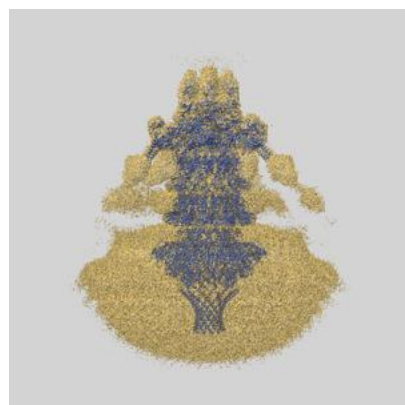
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.10	6.21	4.22

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

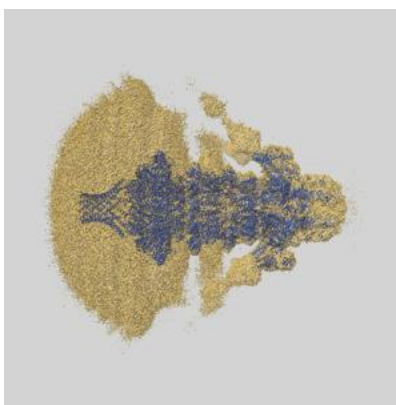
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-36463 and PDB model 8JOV. Per-residue inclusion information can be found in section [3](#) on page [10](#).

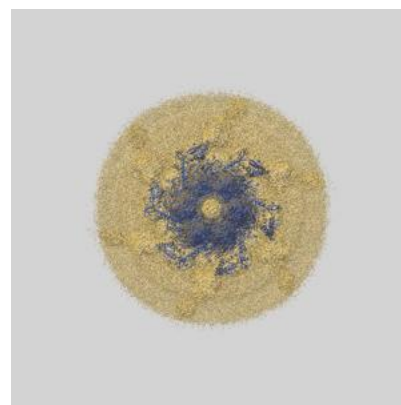
9.1 Map-model overlay [i](#)



X



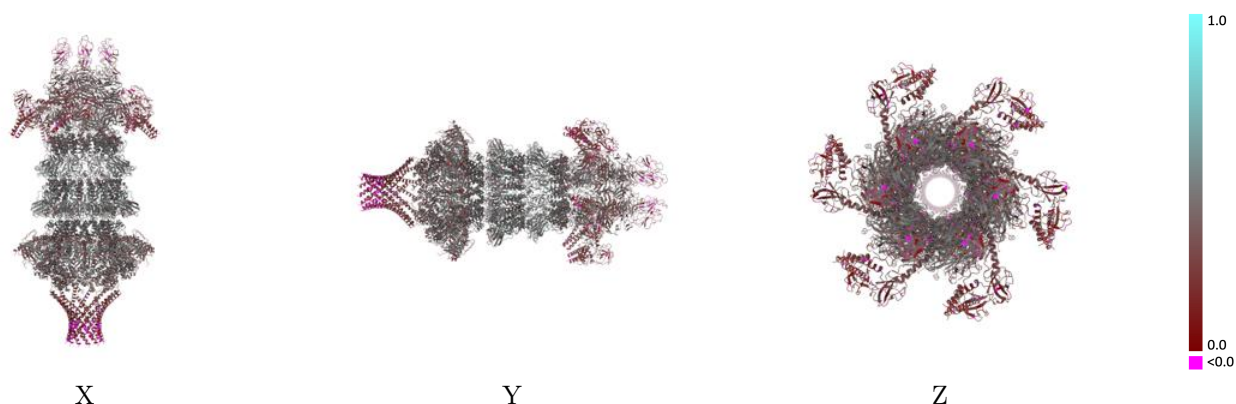
Y



Z

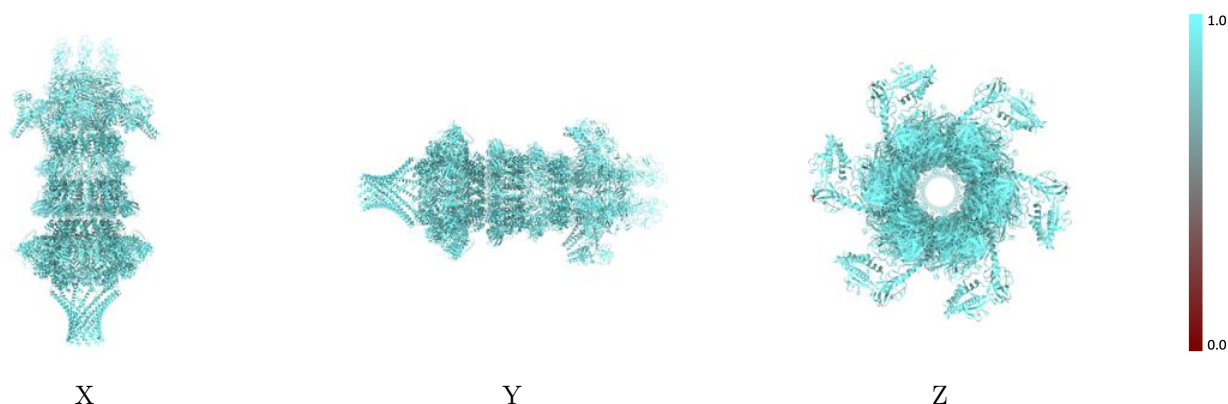
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



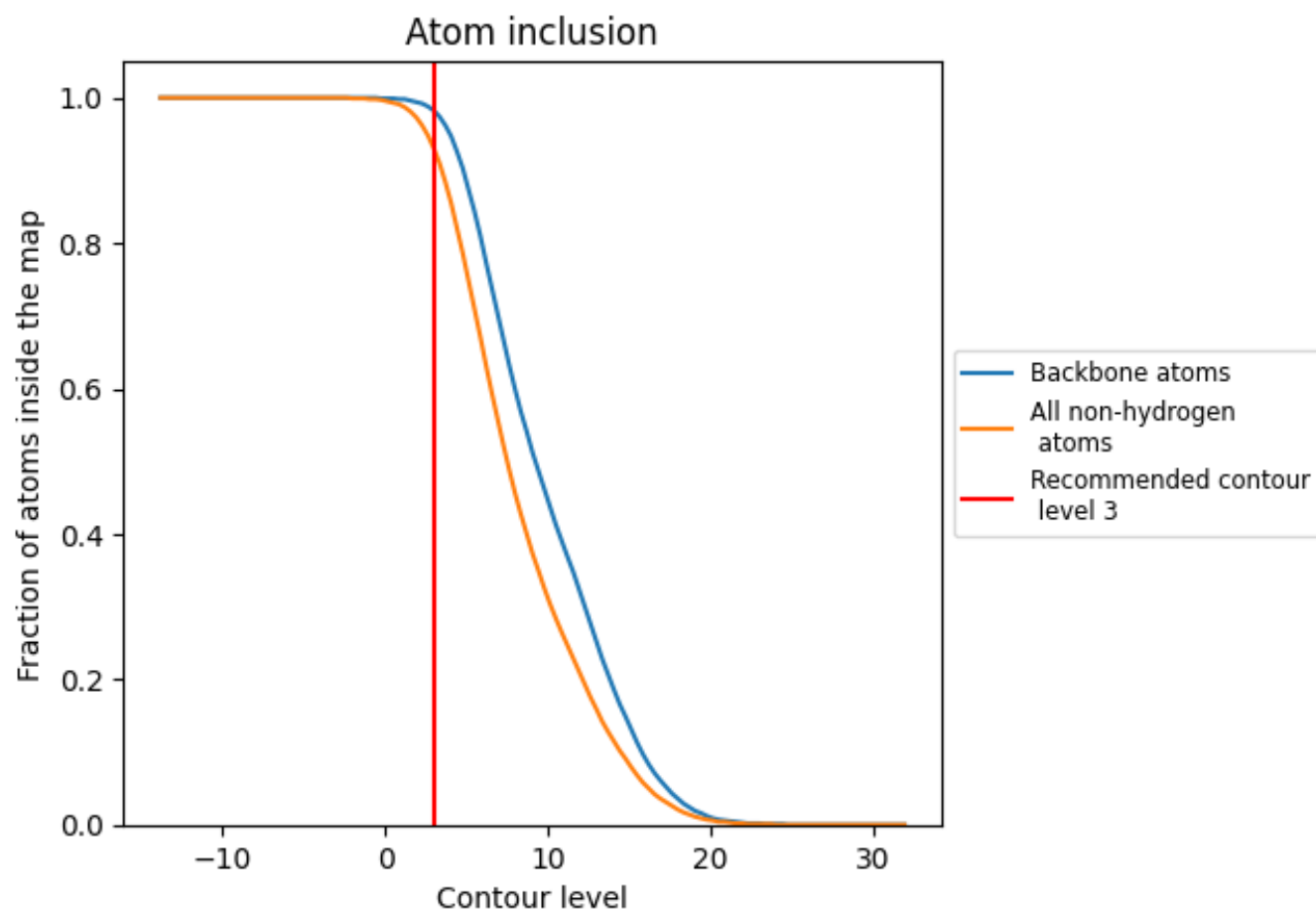
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 93% 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) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9290	 0.4050
0	 0.9310	 0.4100
1	 0.8900	 0.2720
2	 0.9530	 0.4690
3	 0.9280	 0.4080
4	 0.9040	 0.3510
5	 0.9550	 0.4700
6	 0.9260	 0.4120
7	 0.9040	 0.2300
A	 0.9350	 0.3860
B	 0.9390	 0.3850
C	 0.9330	 0.3850
D	 0.9360	 0.3880
E	 0.9400	 0.3870
F	 0.9340	 0.3860
G	 0.9180	 0.4580
H	 0.9190	 0.4520
I	 0.9170	 0.4500
J	 0.9150	 0.4550
K	 0.9190	 0.4530
L	 0.9170	 0.4520
M	 0.9040	 0.2770
N	 0.9100	 0.3410
O	 0.9030	 0.2240
P	 0.8900	 0.2780
Q	 0.9010	 0.3440
R	 0.9040	 0.2240
S	 0.9310	 0.4620
T	 0.9560	 0.4550
U	 0.9270	 0.4060
V	 0.8850	 0.2670
W	 0.9240	 0.4530
X	 0.9580	 0.4570
Y	 0.9280	 0.4100
Z	 0.9080	 0.3480



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Chain	Atom inclusion	Q-score
a	 0.9240	 0.4570
b	 0.9530	 0.4550
c	 0.9280	 0.4070
d	 0.9040	 0.2370
e	 0.9290	 0.4610
f	 0.9570	 0.4560
g	 0.9300	 0.4110
h	 0.8970	 0.2730
i	 0.9210	 0.4530
j	 0.9530	 0.4540
k	 0.9250	 0.4060
l	 0.9050	 0.3390
m	 0.9270	 0.4590
n	 0.9510	 0.4500
o	 0.9260	 0.4110
p	 0.9060	 0.2290
q	 0.9530	 0.4670
r	 0.9310	 0.4080
s	 0.8940	 0.2790
t	 0.9550	 0.4690
u	 0.9250	 0.4090
v	 0.9050	 0.3440
w	 0.9550	 0.4700
x	 0.9260	 0.4080
y	 0.9140	 0.2330
z	 0.9560	 0.4690