



wwPDB EM Validation Summary Report ⓘ

Apr 20, 2025 – 12:17 AM JST

PDB ID : 9LW8 / pdb_00009lw8
EMDB ID : EMD-63434
Title : Bottom cap of bacteriophage Mycofy1 mature head (C5 symmetry)
Authors : Li, X.; Shao, Q.; Li, L.; Xie, L.; Ruan, Z.; Fang, Q.
Deposited on : 2025-02-13
Resolution : 3.53 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 : **FAILED**
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

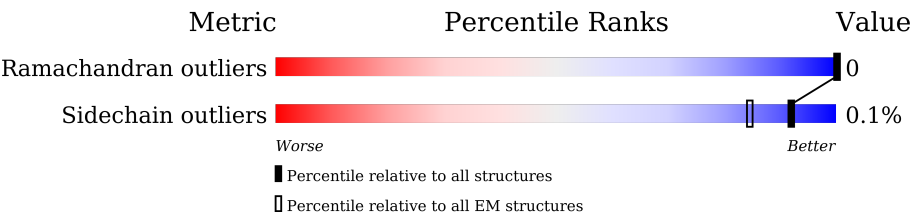
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY











The reported resolution of this entry is 3.53 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.














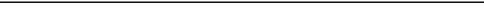





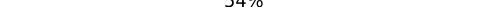
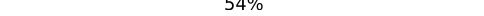
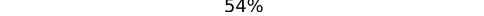
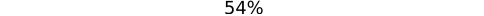
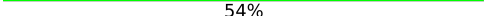



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain	
1	1	543	 53%	47%
1	2	543	 53%	47%
1	3	543	 53%	47%
1	4	543	 53%	47%
1	5	543	 53%	47%
1	A	543	 54%	46%
1	B	543	 46%	54%
1	C	543	 54%	46%
1	D	543	 54%	46%
1	E	543	 54%	46%



















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Mol	Chain	Length	Quality of chain	
1	F	543	 54%	46%
1	G	543	 54%	46%
1	H	543	 54%	46%
1	I	543	 54%	46%
1	J	543	 54%	46%
1	K	543	 54%	46%
1	L	543	 54%	46%
1	M	543	 54%	46%
1	N	543	 54%	46%
1	O	543	 54%	46%
1	P	543	 54%	46%
1	Q	543	 54%	46%
1	R	543	 54%	46%
1	S	543	 54%	46%
1	T	543	 54%	46%
1	U	543	 54%	46%
1	V	543	 54%	46%
1	W	543	 54%	46%
1	X	543	 54%	46%
1	Y	543	 54%	46%
1	Z	543	 54%	46%
1	a	543	 54%	46%
1	b	543	 54%	46%
1	c	543	 54%	46%
1	d	543	 54%	46%

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Mol	Chain	Length	Quality of chain	
1	e	543	 54%	46%
1	f	543	 54%	46%
1	g	543	 54%	46%
1	h	543	 54%	46%
1	i	543	 54%	46%
1	j	543	 54%	46%
1	k	543	 54%	46%
1	l	543	 54%	46%
1	m	543	 54%	46%
1	n	543	 54%	46%
1	o	543	 54%	46%
1	p	543	 54%	46%
1	q	543	 54%	46%
1	r	543	 54%	46%
1	s	543	 54%	46%
1	t	543	 54%	46%
1	u	543	 54%	46%
1	v	543	 54%	46%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 118260 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 Phage capsid-like C-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	288	Total	C	N	O	S	0	0
			2208	1397	379	428	4		
1	2	288	Total	C	N	O	S	0	0
			2208	1397	379	428	4		
1	3	288	Total	C	N	O	S	0	0
			2208	1397	379	428	4		
1	4	288	Total	C	N	O	S	0	0
			2208	1397	379	428	4		
1	5	288	Total	C	N	O	S	0	0
			2208	1397	379	428	4		
1	A	292	Total	C	N	O	S	0	0
			2235	1413	384	434	4		
1	B	249	Total	C	N	O	S	0	0
			1905	1207	324	371	3		
1	C	293	Total	C	N	O	S	0	0
			2241	1416	385	436	4		
1	D	293	Total	C	N	O	S	0	0
			2241	1416	385	436	4		
1	E	293	Total	C	N	O	S	0	0
			2241	1416	385	436	4		
1	F	292	Total	C	N	O	S	0	0
			2235	1413	384	434	4		
1	G	293	Total	C	N	O	S	0	0
			2241	1416	385	436	4		
1	H	293	Total	C	N	O	S	0	0
			2241	1416	385	436	4		
1	I	293	Total	C	N	O	S	0	0
			2241	1416	385	436	4		
1	J	293	Total	C	N	O	S	0	0
			2241	1416	385	436	4		
1	K	293	Total	C	N	O	S	0	0
			2241	1416	385	436	4		
1	L	293	Total	C	N	O	S	0	0
			2241	1416	385	436	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	M	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	N	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	O	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	P	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	Q	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	R	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	S	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	T	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	U	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	V	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	W	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	X	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	Y	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	Z	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	a	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	b	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	c	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	d	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	e	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	f	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	g	293	Total 2241	C 1416	N 385	O 436	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	h	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	i	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	j	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	k	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	l	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	m	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	n	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	o	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	p	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	q	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	r	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	s	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	t	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	u	293	Total 2241	C 1416	N 385	O 436	S 4	0	0
1	v	293	Total 2241	C 1416	N 385	O 436	S 4	0	0

There are 53 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	197	HIS	LYS	conflict	UNP Q854Z2
2	197	HIS	LYS	conflict	UNP Q854Z2
3	197	HIS	LYS	conflict	UNP Q854Z2
4	197	HIS	LYS	conflict	UNP Q854Z2
5	197	HIS	LYS	conflict	UNP Q854Z2
A	197	HIS	LYS	conflict	UNP Q854Z2
B	197	HIS	LYS	conflict	UNP Q854Z2
C	197	HIS	LYS	conflict	UNP Q854Z2
D	197	HIS	LYS	conflict	UNP Q854Z2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	197	HIS	LYS	conflict	UNP Q854Z2
F	197	HIS	LYS	conflict	UNP Q854Z2
G	197	HIS	LYS	conflict	UNP Q854Z2
H	197	HIS	LYS	conflict	UNP Q854Z2
I	197	HIS	LYS	conflict	UNP Q854Z2
J	197	HIS	LYS	conflict	UNP Q854Z2
K	197	HIS	LYS	conflict	UNP Q854Z2
L	197	HIS	LYS	conflict	UNP Q854Z2
M	197	HIS	LYS	conflict	UNP Q854Z2
N	197	HIS	LYS	conflict	UNP Q854Z2
O	197	HIS	LYS	conflict	UNP Q854Z2
P	197	HIS	LYS	conflict	UNP Q854Z2
Q	197	HIS	LYS	conflict	UNP Q854Z2
R	197	HIS	LYS	conflict	UNP Q854Z2
S	197	HIS	LYS	conflict	UNP Q854Z2
T	197	HIS	LYS	conflict	UNP Q854Z2
U	197	HIS	LYS	conflict	UNP Q854Z2
V	197	HIS	LYS	conflict	UNP Q854Z2
W	197	HIS	LYS	conflict	UNP Q854Z2
X	197	HIS	LYS	conflict	UNP Q854Z2
Y	197	HIS	LYS	conflict	UNP Q854Z2
Z	197	HIS	LYS	conflict	UNP Q854Z2
a	197	HIS	LYS	conflict	UNP Q854Z2
b	197	HIS	LYS	conflict	UNP Q854Z2
c	197	HIS	LYS	conflict	UNP Q854Z2
d	197	HIS	LYS	conflict	UNP Q854Z2
e	197	HIS	LYS	conflict	UNP Q854Z2
f	197	HIS	LYS	conflict	UNP Q854Z2
g	197	HIS	LYS	conflict	UNP Q854Z2
h	197	HIS	LYS	conflict	UNP Q854Z2
i	197	HIS	LYS	conflict	UNP Q854Z2
j	197	HIS	LYS	conflict	UNP Q854Z2
k	197	HIS	LYS	conflict	UNP Q854Z2
l	197	HIS	LYS	conflict	UNP Q854Z2
m	197	HIS	LYS	conflict	UNP Q854Z2
n	197	HIS	LYS	conflict	UNP Q854Z2
o	197	HIS	LYS	conflict	UNP Q854Z2
p	197	HIS	LYS	conflict	UNP Q854Z2
q	197	HIS	LYS	conflict	UNP Q854Z2
r	197	HIS	LYS	conflict	UNP Q854Z2
s	197	HIS	LYS	conflict	UNP Q854Z2
t	197	HIS	LYS	conflict	UNP Q854Z2

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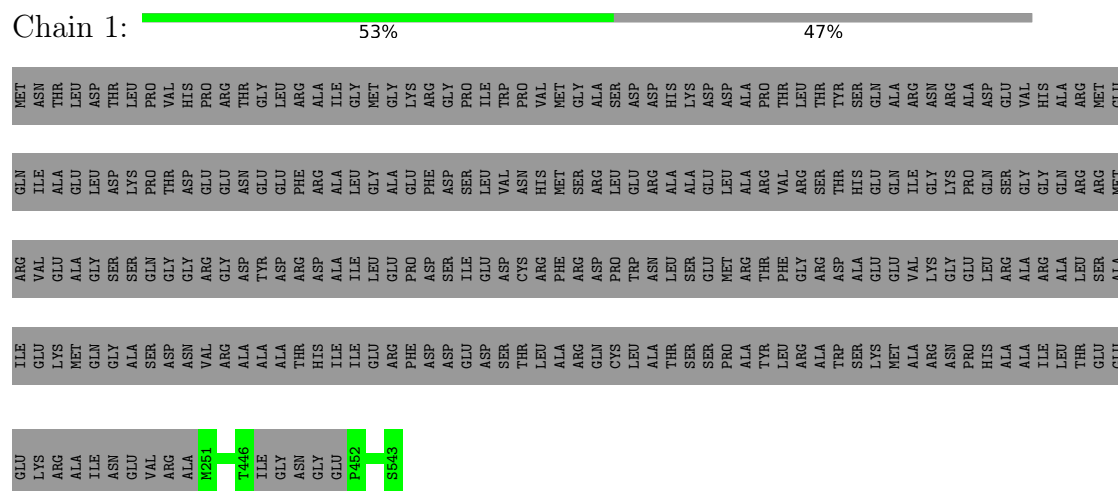
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Chain	Residue	Modelled	Actual	Comment	Reference
u	197	HIS	LYS	conflict	UNP Q854Z2
v	197	HIS	LYS	conflict	UNP Q854Z2

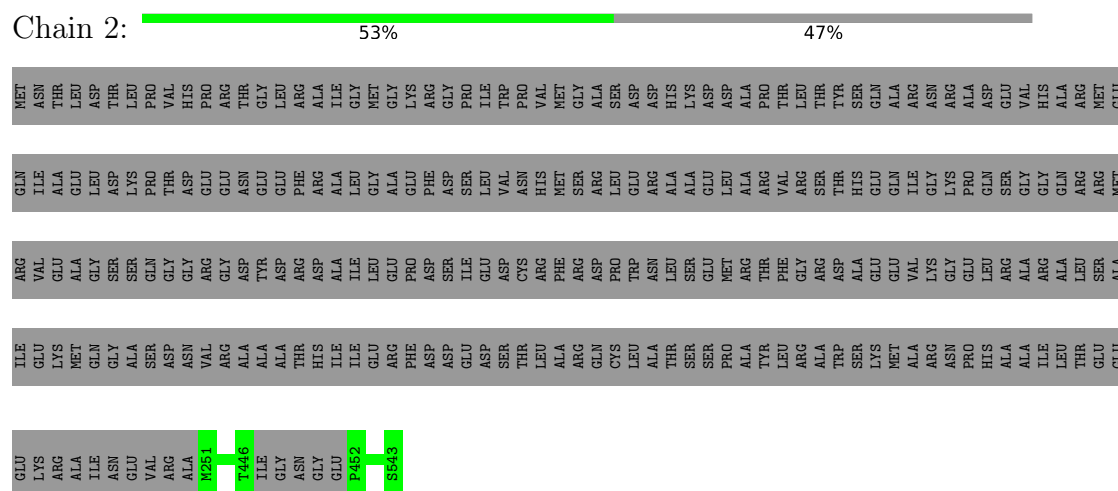
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

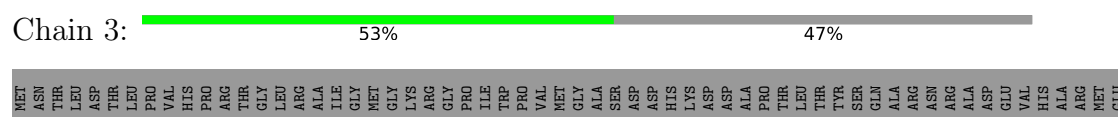
- Molecule 1: Phage capsid-like C-terminal domain-containing protein

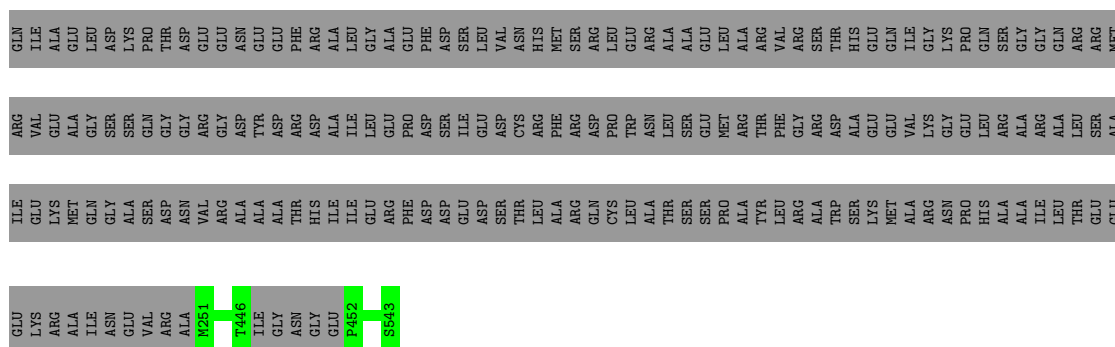


- Molecule 1: Phage capsid-like C-terminal domain-containing protein



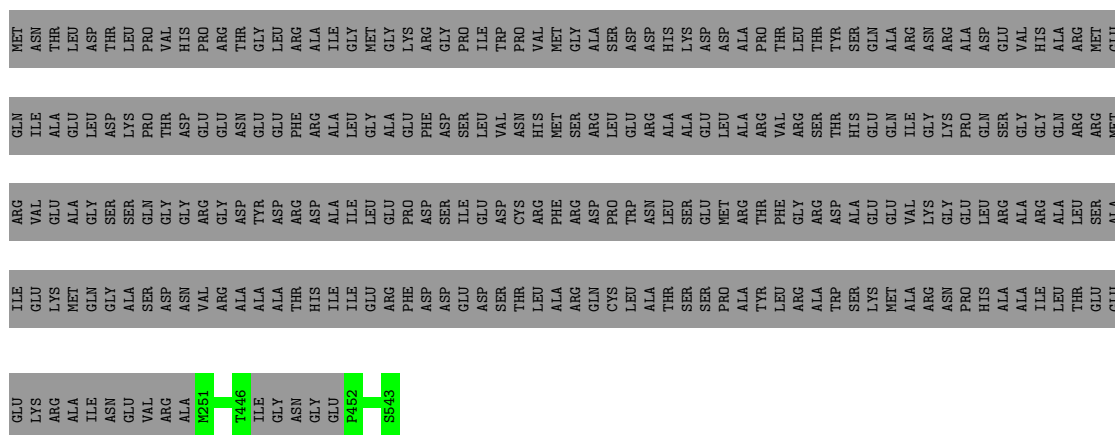
- Molecule 1: Phage capsid-like C-terminal domain-containing protein





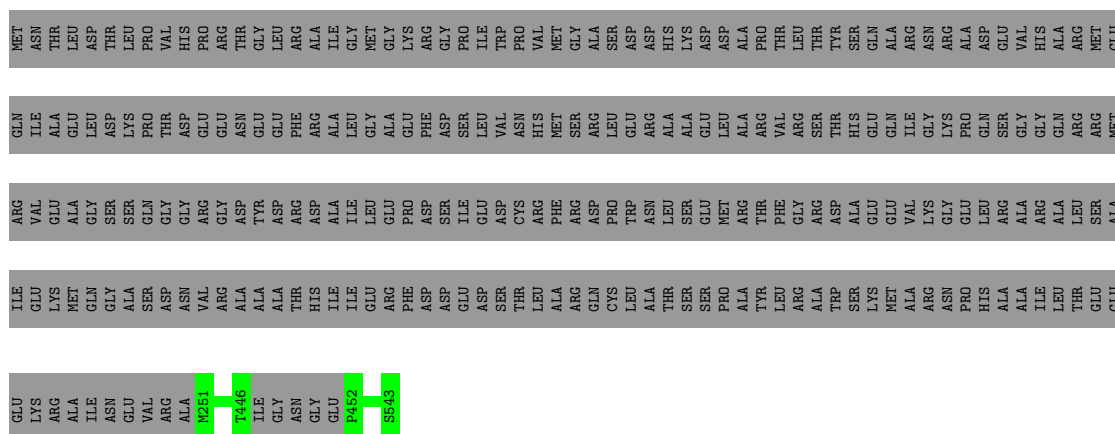
- Molecule 1: Phage capsid-like C-terminal domain-containing protein.

Chain 4: 53% 47%



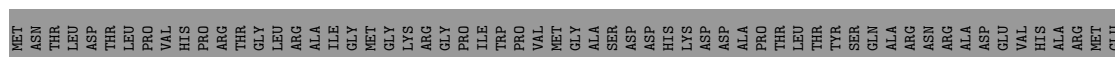
- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain 5: 53% 47%



- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain A:  54% 46%



[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain H:  54% 46%

GLU	LYS	TLE	ARG	GLN	MET
ARG	ARG	GLU	VAL	ILE	ASN
ALA	ALA	GLN	ALA	GLU	THR
ILE	ILE	GLN	GLY	LEU	LEU
ASN	ASN	GLY	SER	ASP	THR
GLU	ALA	ALA	SER	LYS	LEU
VAL	SER	SER	GLN	PRO	PRO
ARG	ASP	ASP	GLY	THR	GLY
ALA	ASN	ASN	GLY	ASP	HIS
M2E1	VAL	VAL	ARG	GLU	PRO
S543	ARG	ARG	GLY	GLU	ARG
	ALA	ALA	ASP	ASN	THR
	ALA	ALA	TYR	GLU	GLY
	ALA	ALA	ASP	LEU	LEU
	THR	THR	ARG	PHE	ARG
	HIS	HIS	ASP	ARG	ALA
	ILE	ILE	ALA	ALA	TLE
	ILE	ILE	ILE	LEU	GLY
	GLU	ARG	GLU	GLY	MET
	ARG	PHE	PRO	GLU	LYS
	ASP	ASP	SER	ASP	GLY
	GLU	ILE	ILE	SER	PRO
	ASP	GLU	GLU	LEU	ILE
	SER	SER	ASP	VAL	TRP
	THR	THR	CYS	ASN	ASN
	LEU	LEU	ARG	HIS	VAL
	ALA	ALA	PHE	MET	MET
	GLN	GLN	ARG	SER	GLY
	CYS	CYS	ASP	ARG	ALA
	LEU	LEU	PRO	LEU	SER
	ALA	ALA	TRP	GLU	ASP
	THR	THR	ASN	ARG	ASP
	SER	SER	LEU	ALA	HIS
	SER	SER	SER	ALA	LYS
	PRO	PRO	GLU	GLU	ASP
	THR	THR	THR	ARG	PRO
	LEU	LEU	PHE	VAL	THR
	ARG	ARG	GLY	ARG	THR
	ALA	ALA	ARG	SER	THR
	TRP	TRP	ASP	THR	TYR
	SER	SER	ALA	HIS	SER
	LYS	LYS	GLU	GLN	GLN
	MET	MET	GLU	TLE	ALA
	ALA	ALA	VAL	ILE	ARG
	ASN	ASN	GLY	LYS	ASN
	PRO	PRO	GLU	PRO	ALA
	HIS	HIS	LEU	GLN	ASP
	ALA	ALA	ARG	SER	GLU
	ILE	ILE	ALA	GLY	VAL
	LEU	LEU	ALA	GLN	HIS
	THR	THR	LEU	ARG	ARG
	GLU	GLU	SER	MET	ARG
	GLU	GLU	ALA	MET	GLN

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain I: 54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain J:  54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain K:  54% 46%

GLU	LYS	TLE	ARG	GLN	MET
ARG	ARG	GLU	VAL	ILE	ASN
ALA	ALA	GLN	ALA	GLU	THR
ILE	ILE	GLN	GLY	LEU	LEU
ASN	ASN	GLY	SER	ASP	THR
GLU	ALA	ALA	SER	LYS	LEU
VAL	SER	SER	GLN	PRO	PRO
ARG	ASP	ASP	GLY	THR	GLY
ALA	ASN	ASN	GLY	ASP	HIS
M2E1	VAL	VAL	ARG	GLU	PRO
S543	ARG	ARG	GLY	GLU	ARG
	ALA	ALA	ASP	ASN	THR
	ALA	ALA	TYR	GLU	GLY
	ALA	ALA	ASP	LEU	GLY
	THR	THR	ARG	PHE	ARG
	HIS	HIS	ASP	ARG	ALA
	ILE	ILE	ILE	ALA	TLE
	ILE	ILE	ILE	LEU	GLY
	GLU	ARG	GLU	GLY	MET
	ARG	PHE	PRO	GLU	LYS
	ASP	ASP	SER	ASP	GLY
	GLU	ILE	ILE	SER	PRO
	ASP	GLU	GLU	LEU	ILE
	SER	SER	GLU	VAL	TRP
	THR	THR	CYS	ASN	ASN
	LEU	LEU	ARG	HIS	VAL
	ALA	ALA	PHE	MET	MET
	GLN	GLN	ARG	SER	GLY
	CYS	CYS	ASP	ARG	ALA
	LEU	LEU	PRO	LEU	SER
	ALA	ALA	TRP	GLU	ASP
	THR	THR	ASN	ARG	ASP
	SER	SER	LEU	ALA	HIS
	SER	SER	SER	ALA	LYS
	PRO	PRO	GLU	GLU	ASP
	THR	THR	THR	ARG	PRO
	LEU	LEU	PHE	VAL	THR
	ARG	ARG	GLY	ARG	THR
	ALA	ALA	ARG	SER	THR
	TRP	TRP	ASP	THR	TYR
	SER	SER	ALA	HIS	SER
	LYS	LYS	GLU	GLN	GLN
	MET	MET	GLU	TLE	ALA
	ALA	ALA	VAL	GLY	ARG
	ARG	ARG	LYS	LYS	ASN
	ASN	ASN	GLY	PRO	ALA
	PRO	PRO	GLU	GLN	ASP
	HIS	HIS	ARG	SER	GLU
	ALA	ALA	ALA	GLY	VAL
	ILE	ILE	ARG	GLY	HIS
	LEU	LEU	ALA	GLN	ALA
	THR	THR	LEU	ARG	ARG
	GLU	GLU	SER	MET	GLN
	GLU	GLU	ALA	MET	GLN

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain L: 54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain M:  54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain N: 54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain O:  54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain P:  54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain Q: 54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain R:  54% 46%

M251 K360 S543	GLU	LYS	ARG	ALA	ILE	ASN	GLU	VAL	THR	LEU	ASP	GLY	THR	GLN	ILE	ASN	MET
	LYS	ARG	ALA	ILE	ASN	GLU	VAL	THR	LEU	ASP	GLY	THR	GLN	ILE	ASN	MET	
	ILE	ASN	GLU	VAL	THR	LEU	ASP	GLY	THR	GLN	ILE	ASN	MET	GLU	VAL	THR	
	ASN	GLU	VAL	THR	LEU	ASP	GLY	THR	GLN	ILE	ASN	MET	GLU	VAL	THR		
	GLU	VAL	THR	LEU	ASP	GLY	THR	GLN	ILE	ASN	MET	GLU	VAL	THR			
	VAL	THR	LEU	ASP	GLY	THR	GLN	ILE	ASN	MET	GLU	VAL	THR				
	ARG	ALA	ILE	ASN	GLU	VAL	THR	LEU	ASP	GLY	THR	GLN	ILE	ASN	MET		
	M251	K360	S543	GLU	VAL	THR	LEU	ASP	GLY	THR	GLN	ILE	ASN	MET	GLU	VAL	
	K360	S543	GLU	VAL	THR	LEU	ASP	GLY	THR	GLN	ILE	ASN	MET	GLU	VAL		
	S543	GLU	VAL	THR	LEU	ASP	GLY	THR	GLN	ILE	ASN	MET	GLU	VAL			
	GLU	VAL	THR	LEU	ASP	GLY	THR	GLN	ILE	ASN	MET	GLU	VAL				
	VAL	THR	LEU	ASP	GLY	THR	GLN	ILE	ASN	MET	GLU	VAL					
	THR	LEU	ASP	GLY	THR	GLN	ILE	ASN	MET	GLU	VAL						
	LEU	ASP	GLY	THR	GLN	ILE	ASN	MET	GLU	VAL							
	ASP	GLY	THR	GLN	ILE	ASN	MET	GLU	VAL								
	THR	GLN	ILE	ASN	MET	GLU	VAL										

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain S: 54% 46%

GLU	LYS	TLE	ARG	GLN	MET
ARG	ARG	GLU	VAL	ILE	ASN
ALA	ALA	MET	GLY	ALA	THR
ILE	ILE	GLN	GLY	LEU	ASP
ASN	ASN	GLY	SER	ASP	THR
GLU	GLU	ALA	SER	LYS	LEU
VAL	SER	SER	GLN	PRO	PRO
ARG	ASP	GLY	GLY	THR	VAL
ALA	ASN	ASN	GLY	ASP	HIS
M2E1	VAL	ARG	ARG	GLU	PRO
S543	ARG	GLY	GLY	GLU	ARG
	ALA	ALA	ASP	ASN	THR
	ALA	ALA	ASP	GLU	GLY
	ALA	THR	ARG	PHE	ARG
	HIS	ASP	ALA	ARG	ALA
	ILE	ILE	ALA	LEU	TLE
	ILE	GLU	LEU	GLY	MET
	PHE	PHE	GLU	ALA	GLY
	ASP	ASP	SER	SER	ARG
	GLU	GLU	ILE	SER	PRO
	ASP	ASP	GLU	SER	GLY
	THR	THR	CYS	ASN	THR
	LEU	LEU	ARG	HIS	VAL
ALA	ALA	PHE	MET	MET	
GLN	GLN	ARG	SER	GLY	
CYS	LYS	ASP	PRO	ALA	
LEU	THR	TRP	LEU	SER	
ALA	ALA	ASN	ARG	ASP	
THR	THR	LEU	ALA	HIS	
SER	SER	SER	SER	LYS	
PRO	SER	PRO	GLU	ASP	
ALA	ALA	ALA	ALA	ALA	
THR	THR	THR	ARG	PRO	
ARG	ARG	LEU	PHE	THR	
ALA	ALA	GLY	GLY	THR	
TRP	TRP	ASP	ARG	SER	
SER	SER	ALA	HIS	TYR	
GLN	GLN	GLU	THR	SER	
ALA	ALA	VAL	GLU	GLN	
TLE	TLE	GLU	ILE	ALA	
ARG	ARG	THR	ASP	ARG	
ASN	ASN	LEU	ASP	ARG	
GLY	GLY	ILE	ILE	THR	
THR	THR	ALA	ASP	GLY	
PRO	PRO	GLU	GLY	ARG	
ASN	ASN	ASN	TYR	GLY	
ARG	ARG	ASN	GLY	ASN	
GLU	GLU	GLY	GLY	GLY	
THR	THR	GLY	GLY	THR	
ASP	ASP	GLY	GLY	ASP	
PRO	PRO	GLY	GLY	GLU	
VAL	VAL	GLY	ALA	VAL	
GLU	GLU	GLY	ALA	GLY	
ARG	ARG	THR	ARG	ARG	
GLY	GLY	LEU	LEU	ARG	
THR	THR	ALA	ALA	THR	
ASP	ASP	SER	ARG	MET	
GLU	GLU	GLY	GLY	GLU	

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain T: 54% 46%

GLU	LYS	TLE	ARG	GLN	MET
ARG	ARG	GLU	VAL	ILE	ASN
ALA	ALA	GLN	ALA	GLU	THR
ILE	ILE	GLN	GLY	LEU	LEU
ASN	ASN	GLY	SER	ASP	THR
GLU	GLU	ALA	SER	LYS	LEU
VAL	VAL	SER	GLN	PRO	PRO
ARG	ASP	ASP	GLY	THR	GLY
ALA	ALA	ASN	GLY	ASP	HIS
M2E1	M2E1	VAL	ARG	GLU	PRO
S543	S543	ARG	GLY	GLU	ARG
		ALA	ASP	ASN	THR
		ALA	TYR	GLU	GLY
		ALA	ASP	LEU	GLY
		THR	ARG	PHE	ARG
		HIS	ASP	ARG	ALA
		ILE	ILE	ALA	TLE
		ILE	ILE	LEU	GLY
		GLU	GLU	GLY	MET
		ARG	PHE	GLU	LYS
		ASP	SER	ASP	ARG
		GLU	ILE	SER	PRO
		ASP	GLU	LEU	THR
		SER	GLY	VAL	TRP
		THR	CYS	ASN	PRO
		LEU	ARG	HIS	VAL
		ALA	PHE	MET	MET
		GLN	ARG	SER	GLY
		GLN	ASP	ARG	ALA
		CYS	PRO	LEU	SER
		LEU	TRP	GLU	ASP
		ALA	ASN	ARG	ASP
		THR	LEU	ALA	HIS
		SER	SER	ALA	LYS
		SER	GLU	GLU	ASP
		PRO	MET	LEU	ASP
		LYS	GLY	ARG	ALA
		MET	VAL	GLN	ALA
		ALA	VAL	TLE	ARG
		ARG	LYS	GLY	ASN
		ASN	GLY	LYS	ARG
		PRO	GLU	PRO	ALA
		HIS	LEU	GLN	ASP
		ALA	ARG	SER	GLU
		ALA	ALA	GLY	VAL
		ILE	ARG	GLY	HIS
		LEU	ALA	GLN	ALA
		THR	LEU	ARG	ARG
		THR	SER	MET	ARG
		GLU	ALA	MET	GLU

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain U: 54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain V:  54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain W:  54% 46%

GLU	LYS	TLE	ARG	GLN	MET
ARG	ARG	GLU	VAL	ILE	ASN
ALA	ALA	GLN	ALA	GLU	THR
ILE	ILE	GLN	GLY	LEU	LEU
ASN	ASN	GLY	SER	ASP	THR
GLU	GLU	ALA	SER	LYS	LEU
VAL	VAL	SER	GLN	PRO	PRO
ARG	ASP	ASP	GLY	THR	GLY
ALA	ALA	ASN	GLY	ASP	HIS
M2E1	M2E1	VAL	ARG	GLU	PRO
S543	S543	ARG	GLY	GLU	ARG
		ALA	ASP	ASN	THR
		ALA	TYR	GLU	GLY
		ALA	ASP	LEU	GLY
		THR	ARG	PHE	ARG
		HIS	ASP	ARG	ALA
		ILE	ILE	ALA	TLE
		ILE	ILE	LEU	GLY
		GLU	GLU	GLY	MET
		ARG	PHE	GLU	LYS
		ASP	SER	ASP	ARG
		GLU	ILE	SER	PRO
		ASP	GLU	LEU	THR
		SER	GLY	VAL	TRP
		THR	CYS	ASN	PRO
		LEU	ARG	HIS	VAL
		ALA	PHE	MET	MET
		GLN	ARG	SER	GLY
		CYS	ASP	ARG	ALA
		LEU	PRO	LEU	SER
		ALA	TRP	GLU	ASP
		THR	ASN	ARG	ASP
		SER	LEU	ALA	HIS
		SER	SER	ALA	LYS
		SER	GLU	LEU	ASP
		TRP	THR	LEU	ASP
		LYS	THR	ARG	PRO
		MET	PHE	VAL	THR
		ALA	ARG	LEU	THR
		ALA	ARG	SER	THR
		THR	ASP	THR	TYR
		SER	ALA	HIS	SER
		THR	GLY	GLN	GLN
		MET	GLU	TLE	ALA
		ALA	VAL	ILE	ARG
		ARG	GLY	GLY	ASN
		ASN	GLY	LYS	ARG
		PRO	GLU	PRO	ALA
		HIS	LEU	GLN	ASP
		ALA	ARG	SER	GLU
		ALA	ALA	GLY	VAL
		ILE	ARG	GLY	HIS
		LEU	ALA	GLN	ALA
		THR	LEU	ARG	ARG
		THR	SER	MET	ARG
		GLU	ALA	MET	GLN

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain X: 54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain Y:  54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain Z:  54% 46%

GLU	LYS	TLE	ARG	GLN	MET
ARG	ARG	GLU	VAL	ILE	ASN
ALA	ALA	GLN	ALA	GLU	THR
ILE	ILE	GLN	GLY	LEU	LEU
ASN	ASN	GLY	SER	ASP	THR
GLU	GLU	ALA	SER	LYS	LEU
VAL	VAL	SER	GLN	PRO	PRO
ARG	ARG	ASP	GLY	THR	GLY
ALA	ALA	ASN	GLY	ASP	HIS
M2E1	M2E1	VAL	ARG	GLU	PRO
S543	S543	ARG	GLY	GLU	ARG
		ALA	ASP	ASN	THR
		ALA	TYR	GLU	GLY
		ALA	ASP	LEU	GLY
		THR	ARG	PHE	ARG
		HIS	ASP	ARG	ALA
		ILE	ILE	ALA	TLE
		ILE	ILE	LEU	GLY
		GLU	GLU	GLY	MET
		ARG	PHE	GLU	LYS
		ASP	SER	ASP	ARG
		GLU	ILE	SER	PRO
		ASP	GLU	LEU	THR
		SER	CYS	ASN	VAL
		LEU	ARG	HIS	VAL
		ALA	PHE	MET	MET
		GLN	ARG	SER	GLY
		GLN	ASP	ARG	ALA
		CYS	PRO	LEU	SER
		LEU	TRP	GLU	ASP
		ALA	ASN	ARG	ASP
		THR	LEU	ALA	HIS
		SER	SER	ALA	LYS
		SER	GLU	GLU	ASP
		PRO	MET	LEU	ASP
		ALA	THR	ALA	ALA
		TYR	THR	ARG	PRO
		LEU	PHE	VAL	THR
		ARG	GLY	ARG	THR
		ALA	ARG	SER	THR
		TRP	ASP	THR	TYR
		SER	ALA	HIS	SER
		LYS	GLU	GLN	GLN
		MET	GLU	TLE	ALA
		ALA	VAL	ILE	ARG
		ARG	LYS	GLY	ASN
		ASN	GLY	LYS	ARG
		PRO	GLU	PRO	ALA
		HIS	LEU	GLN	ASP
		ALA	ARG	SER	GLU
		ALA	ALA	GLY	VAL
		ILE	ARG	GLY	HIS
		LEU	ALA	GLN	ALA
		THR	LEU	ARG	ARG
		THR	SER	MET	ARG
		GLU	ALA	MET	GLN

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain a: 54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain b: 54% 46%

GLU	LYS	TLE	ARG	GLN	MET
ARG	ARG	GLU	VAL	ILE	ASN
ALA	ALA	MET	GLU	ALA	THR
ILE	ILE	GLN	GLY	LEU	ASP
ASN	ASN	GLY	SER	ASP	THR
GLU	GLU	ALA	SER	LYS	LEU
VAL	SER	SER	GLN	PRO	PRO
ARG	ASP	GLY	GLY	THR	VAL
ALA	ASN	ASN	GLY	ASP	HIS
M2E1	VAL	ARG	ARG	GLU	PRO
S543	ARG	GLY	GLY	GLU	ARG
	ALA	ALA	ASP	ASN	THR
	ALA	ALA	ASP	GLU	GLY
	THR	THR	ARG	PHE	ARG
	HIS	ALA	ASP	ARG	ALA
	ILE	ILE	ALA	LEU	TLE
	ILE	ILE	ILE	LEU	GLY
	GLU	GLU	ILE	SER	MET
	PHE	PHE	PRO	SER	PRO
	ASP	ASP	SER	ASP	GLY
GLU	GLU	ILE	SER	PRO	
ASP	ASP	GLU	VAL	ILE	
SER	SER	THR	CYS	ASN	
THR	LEU	ARG	HIS	VAL	
ALA	ALA	PHE	MET	MET	
GLN	GLN	ARG	SER	GLY	
CYS	LYS	THR	PRO	ALA	
LEU	THR	TRP	LEU	SER	
ALA	ALA	ASN	ARG	ASP	
THR	THR	LEU	ALA	HIS	
SER	SER	SER	SER	LYS	
SER	SER	GLU	GLU	ASP	
PRO	PRO	ALA	ALA	ALA	
THR	THR	THR	ARG	PRO	
ARG	ARG	PHE	VAL	THR	
ALA	ALA	GLY	ARG	THR	
THR	THR	ASP	SER	THR	
TYR	THR	HIS	SER	TYR	
SER	SER	ALA	HIS	SER	
GLN	GLN	GLU	GLN	GLN	
ALA	ALA	MET	GLU	ALA	
TLE	ALA	VAL	TLE	ARG	
LYS	LYS	GLY	GLY	ASN	
PRO	PRO	GLU	GLU	ARG	
ALA	ALA	LEU	LEU	ASP	
HIS	HIS	THR	ARG	GLU	
ALA	ALA	ARG	ALA	VAL	
TLE	TLE	ILE	ALA	VAL	
THR	THR	LEU	ARG	THR	
ARG	ARG	LEU	LEU	ARG	
MET	MET	ALA	SER	MET	

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain c:  54% 46%

GLU	LYS	TLE	ARG	GLN	MET
ARG	ARG	GLU	VAL	ILE	ASN
ALA	ALA	GLN	ALA	GLU	THR
ILE	ILE	GLN	GLY	LEU	LEU
ASN	ASN	GLY	SER	ASP	THR
GLU	ALA	ALA	SER	LYS	LEU
VAL	SER	SER	GLN	PRO	PRO
ARG	ASP	ASP	GLY	THR	GLY
ALA	ASN	ASN	GLY	ASP	HIS
M2E1	VAL	VAL	ARG	GLU	PRO
S543	ARG	ARG	GLY	GLU	ARG
	ALA	ALA	ASP	ASN	THR
	ALA	ALA	TYR	GLU	GLY
	ALA	ALA	ASP	LEU	GLY
	THR	THR	ARG	PHE	ARG
	HIS	HIS	ASP	ARG	ALA
	ILE	ILE	ALA	ALA	TLE
	ILE	ILE	ILE	LEU	GLY
	GLU	ARG	GLU	GLY	MET
	ARG	PHE	PRO	GLU	LYS
	ASP	ASP	SER	ASP	GLY
	GLU	ILE	ILE	SER	PRO
	ASP	GLU	GLU	LEU	ILE
	SER	SER	GLU	VAL	TRP
	THR	THR	CYS	ASN	ASN
	LEU	LEU	ARG	HIS	VAL
	ALA	ALA	PHE	MET	MET
	GLN	GLN	ARG	SER	GLY
	CYS	CYS	ASP	ARG	ALA
	LEU	LEU	PRO	LEU	SER
	ALA	ALA	TRP	GLU	ASP
	THR	THR	ASN	ARG	ASP
	SER	SER	LEU	ALA	HIS
	SER	SER	SER	ALA	LYS
	PRO	PRO	GLU	GLU	ASP
	THR	THR	THR	ARG	PRO
	LEU	LEU	PHE	VAL	THR
	ARG	ARG	GLY	ARG	THR
	ALA	ALA	ARG	SER	THR
	TRP	TRP	ASP	THR	TYR
	SER	SER	ALA	HIS	SER
	LYS	LYS	GLU	GLN	GLN
	MET	MET	GLU	TLE	ALA
	ALA	ALA	VAL	ILE	ARG
	ASN	ASN	GLY	LYS	ASN
	PRO	PRO	GLU	PRO	ALA
	HIS	HIS	LEU	GLN	ASP
	ALA	ALA	ARG	SER	GLU
	ILE	ILE	ALA	GLY	VAL
	LEU	LEU	ALA	GLN	HIS
	THR	THR	LEU	ARG	ARG
	GLU	GLU	SER	MET	ARG
	GLU	GLU	ALA	MET	GLN

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain d: 54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain e:  54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain f: 54% 46%

GLU	LYS	TLE	ARG	GLN	MET
ARG	ARG	GLU	VAL	ILE	ASN
ALA	ALA	GLN	ALA	GLU	THR
ILE	ILE	GLN	GLY	LEU	LEU
ASN	ASN	GLY	SER	ASP	THR
GLU	GLU	ALA	SER	LYS	LEU
VAL	SER	SER	GLN	PRO	PRO
ARG	ASP	ASP	GLY	THR	GLY
ALA	ASN	ASN	GLY	ASP	HIS
M2E1	VAL	ARG	GLY	GLU	PRO
S543	ALA	ARG	GLY	GLU	ARG
	ALA	TYP	ASP	ASN	THR
	ALA	ASP	GLY	GLU	GLY
	ALA	ARG	ARG	PHE	ARG
	THR	THR	ASP	ARG	ALA
	HIS	ILE	ILE	ALA	TLE
	ILE	ILE	ILE	LEU	GLY
	GLU	ARG	GLU	GLY	MET
	ARG	PHE	PRO	GLU	LYS
	ASP	ASP	SER	ASP	GLY
	GLU	ILE	ILE	SER	PRO
	ASP	GLU	GLY	LEU	ILE
	ASP	THR	CYS	ASN	TRP
	LEU	LEU	ARG	HIS	VAL
	ALA	ALA	PHE	MET	MET
	GLN	GLN	ARG	SER	GLY
	CYS	CYS	ASP	ARG	ALA
	LEU	LEU	PRO	LEU	SER
	ALA	TRP	TRP	GLU	ASP
	THR	ALA	ASN	ARG	ASP
	SER	THR	LEU	ALA	HIS
	SER	SER	SER	ALA	LYS
	SER	SER	GLU	LEU	ASP
	TRP	TRP	THR	VAL	THR
	ALA	ARG	PHE	ARG	PRO
	ALA	LEU	THR	ARG	ALA
	ALA	GLU	GLY	LEU	ASP
	ALA	ALA	ARG	SER	THR
	ALA	ALA	ARG	THR	TYR
	LYS	GLY	ALA	HIS	SER
	MET	GLN	GLU	GLN	ALA
	ALA	TLE	VAL	ILE	ARG
	ALA	VAL	VAL	GLN	ASP
	ASN	GLY	GLY	LYS	ASN
	PRO	GLU	GLU	PRO	ALA
	HIS	ALA	ARG	GLN	ASP
	ALA	ALA	ALA	SER	GLU
	ILE	ILE	ALA	GLY	VAL
	LEU	LEU	ALA	GLN	HIS
	THR	THR	LEU	ARG	ARG
	GLU	GLU	SER	MET	ARG
	GLU	ALA	ALA	MET	GLU

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain g:  54% 46%

GLU	LYS	ILE	ARG	VAL	GLN	MET
ARG	GLY	GLU	VAL	VAL	ILE	ASN
ALA	MET	ALA	ALA	ALA	ALA	THR
ASN	GLN	GLY	GLY	GLY	LEU	LEU
GLU	ALA	SER	SER	SER	ASP	THR
VAL	SER	ALA	GLN	GLN	LYS	PRO
ARG	ASP	GLY	GLY	GLY	THR	PRO
ALA	ASN	VAL	ASP	ASP	ASP	HIS
M251	ARG	ARG	GLY	GLY	GLU	PRO
5643	ALA	ALA	TYR	ASP	ASN	THR
	ALA	ALA	ARG	ARG	GLU	GLY
	THR	THR	ARG	ARG	PHE	ARG
	HIS	ILE	ALA	ALA	ALA	ALA
	ILE	ILE	ILE	ILE	LEU	GLY
	GLU	GLU	GLU	GLU	GLY	MET
	PHE	PHE	PRO	PRO	ALA	GLY
	ASP	ASP	ASP	SER	PHE	LYS
	GLU	GLU	ILE	ILE	SER	GLY
	ASP	ASP	GLY	GLY	ASP	PRO
	THR	THR	THR	CYS	ASN	PRO
	LEU	LEU	ARG	ARG	HIS	VAL
	ALA	ALA	PHE	PHE	MET	VAL
	ARG	ARG	ARG	ARG	GLY	MET
	GLN	GLN	ASP	ASP	SER	GLY
	CYS	CYS	PRO	PRO	LEU	SER
	LEU	LEU	TRP	TRP	GLU	ASP
	ALA	ALA	ASN	ASN	ARG	ASP
	THR	THR	LEU	LEU	ALA	HIS
	SER	SER	SER	SER	ALA	LYS
	SER	SER	GLY	GLY	LEU	ASP
	LYS	LYS	GLU	GLU	GLN	GLN
	MET	MET	VAL	VAL	ILE	ALA
	ALA	ALA	VAL	VAL	GLY	ASN
	ARG	ARG	GLY	GLY	LYS	ARG
	PRO	PRO	GLU	GLU	PRO	ALA
	HIS	HIS	LEU	LEU	GLN	ASP
	ALA	ALA	ARG	ARG	SER	GLU
	ILE	ILE	ALA	ALA	GLY	VAL
	THR	THR	LEU	LEU	GLN	HIS
	THR	THR	LEU	LEU	ARG	ARG
	GLU	GLU	SER	SER	MET	ARG
	ALA	ALA	ALA	ALA	MET	GLY

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain h: 54% 46%

GLU	LYS	ARG	ILE	GLU	VAL	ARG	GLN	MET
LYS	ARG	GLU	LYS	GLU	VAL	GLU	ILE	ASN
ALA	ILE	MET	GLN	GLY	ALA	GLY	ALA	THR
ASN	GLY	GLY	ALA	SER	SER	SER	ASP	THR
GLU	ALA	ALA	SER	GLN	GLN	LYS	LYS	LEU
VAL	SER	SER	SER	GLY	GLY	THR	THR	PRO
ARG	ASP	ASP	ASN	GLY	GLY	ASP	ASP	HIS
ALA	VAL	VAL	VAL	ARG	GLY	GLU	PRO	PRO
M251	ARG	ARG	ARG	ASP	ASP	ASN	THR	THR
S543	ALA	ALA	ALA	TYR	GLY	GLU	ASN	GLY
	THR	THR	THR	ASP	GLY	LEU	PHE	ARG
	HIS	ILE	ILE	ALA	ALA	ALA	ILE	ILE
	ILE	GLU	ILE	ILE	ILE	LEU	GLY	MET
	GLY	GLY	GLY	GLY	GLU	ALA	ALA	GLY
	PHE	PHE	PHE	PRO	PRO	PHE	GLY	LYS
	ASP	ASP	ASP	ASP	SER	SER	ASP	ARG
	GLU	GLU	GLU	ILE	ILE	SER	SER	GLY
	ASP	ASP	ASP	GLU	VAL	LEU	LEU	ILE
	SER	SER	SER	ASP	CYS	ASN	ASN	PRO
	THR	THR	THR	ARG	HIS	HIS	VAL	VAL
	ALA	ALA	ALA	PHE	MET	MET	MET	GLY
	ARG	ARG	GLN	ASP	ARG	ALA	ALA	ALA
	LYS	LYS	LYS	PRO	PRO	LEU	SER	ASP
	THR	THR	THR	THR	TRP	GLY	ASP	ASP
	THR	THR	ALA	ASN	ASN	ARG	ALA	HIS
	SER	SER	SER	LEU	SER	ALA	LYS	LYS
	SER	SER	SER	GLU	GLU	GLU	ASP	ASP
	TRAP	TRAP	TRAP	ALA	ARG	SER	THR	THR
	ALA	ALA	ALA	ALA	PHE	VAL	THR	PRO
	LEU	LEU	LEU	GLY	GLY	ARG	ALA	ALA
	ARG	ARG	MET	GLU	VAL	ILE	ALA	ALA
	ALA	ARG	ALA	VAL	GLY	GLY	ASN	ASN
	ASN	ASN	ASN	GLY	GLY	LYS	LYS	ARG
	PRO	PRO	PRO	GLU	GLU	PRO	ALA	ALA
	HIS	HIS	HIS	LEU	ARG	GLN	GLN	ASP
	ALA	ALA	ALA	ARG	SER	SER	GLU	GLU
	THR	THR	THR	ALA	ALA	GLY	VAL	VAL
	ILE	ILE	ILE	ARG	ARG	GLY	ARG	ARG
	LEU	LEU	LEU	THR	LEU	GLN	ASP	GLY
	THR	THR	THR	THR	THR	THR	THR	THR
	GLU	GLU	GLU	ALA	ALA	MET	GLU	GLU

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain i:  54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain j: 54% 46%

GLU	LYS	ARG	ILE	GLU	VAL	ARG	ASN	MET
LYS	ARG	GLU	LYS	GLU	VAL	GLU	ASN	GLN
ALA	ILE	GLN	MET	ALA	GLY	ALA	LEU	ILE
ASN	GLU	GLY	ALA	SER	SER	SER	ASP	GLY
VAL	VAL	SER	ALA	GLN	GLN	GLN	LYS	PRO
ARG	ARG	ASP	ASP	GLY	GLY	ASP	THR	VAL
M251	M251	ASN	ASN	VAL	ARG	ARG	PRO	HIS
S543	S543	THR	ALA	ARG	GLY	ASP	THR	ARG
		ALA	ALA	ALA	TYR	ASP	GLY	GLY
		ALA	ALA	ASP	ASP	ASP	LEU	LEU
		THR	THR	THR	ASP	ASP	PHE	GLY
		ILE	ILE	ILE	ALA	ALA	ALA	ILE
		ILE	ILE	ILE	ILE	ILE	ILE	GLY
		GLU	GLU	GLU	GLU	GLU	GLY	MET
		ARG	PHE	PRO	PRO	ASP	LYS	GLY
		ASP	ASP	ASP	SER	SER	GLY	ARG
		GLU	GLU	ILE	ILE	ILE	PRO	PRO
		ASP	ASP	ASP	GLU	LEU	ILE	ILE
		SER	SER	GLU	VAL	TRP	TRP	TRP
		THR	THR	ASN	CYS	ASN	ASN	ASN
		ALA	LEU	ARG	ARG	HIS	VAL	VAL
		ALA	ALA	PHE	PHE	MET	MET	MET
		GLN	GLN	ARG	ARG	GLY	GLY	GLY
		CYS	CYS	ASP	ASP	LEU	SER	SER
		LEU	LEU	TRP	TRP	GLU	ASP	ASP
		ALA	ALA	ASN	ASN	ARG	ASP	ASP
		THR	THR	LEU	ALA	ALA	HIS	HIS
		SER	SER	SER	SER	ALA	LYS	LYS
		SER	SER	SER	GLU	GLU	ALA	ALA
		LYS	LYS	THR	THR	ARG	PRO	PRO
		MET	MET	LEU	PHE	VAL	THR	THR
		ALA	ALA	ARG	GLY	ARG	LEU	LEU
		ALA	ALA	ALA	GLY	ARG	THR	THR
		ASN	ASN	ASP	ASP	SER	TYR	TYR
		PRO	PRO	THR	THR	HIS	GLN	GLN
		GLY	GLY	GLY	GLY	GLY	ALA	ALA
		THR	THR	THR	THR	THR	ASP	ASP
		GLU	GLU	GLU	SER	SER	GLU	GLU
		VAL	VAL	VAL	ALA	ALA	VAL	VAL
		ARG	ARG	ARG	ALA	ALA	ARG	ARG
		GLU	GLU	GLU	GLU	GLU	ARG	ARG
		ILE	ILE	ILE	ILE	ILE	MET	MET
		GLU	GLU	GLU	GLU	GLU	GLU	GLU

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain k:  54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain 1:  54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain m:  54% 46%

GLU	LYS	ARG	ALA	ILE	ARG	ILE	GLU	VAL	ASN	GLN	MET
LYS	ARG	ALA	ILE	GLN	GLY	GLY	GLU	ALA	THR	ALA	ASN
ASN	GLU	ASN	GLY	ALA	SER	GLY	LEU	GLY	THR	LEU	ASP
GLU	VAL	ARG	ASN	SER	GLN	ASP	PRO	GLN	PRO	LEU	THR
ALA	ALA	ALA	VAL	ASP	GLY	VAL	ASP	GLY	HIS	ASP	GLY
M261			ARG	ARG	ARG	ILE	GLU	GLY	PRO	ARG	THR
S543			ALA	ALA	ASP	ILE	GLU	TYR	ASN	ASN	GLY
			ALA	THR	ARG	ALA	GLU	ASP	ARG	ARG	THR
			HIS	ILE	ASP	ILE	ALA	ASP	ALA	ILE	ILE
			ILE	ILE	ILE	GLY	LEU	LEU	GLY	GLY	MET
			ARG	ARG	PRO	GLU	ALA	GLU	GLY	ALA	GLY
			ASP	ASP	ASP	ASP	PHE	PRO	ARG	ARG	LYS
			ASP	ASP	SER	ILE	SER	SER	ASP	GLY	GLY
			GLU	GLU	ASP	GLU	LEU	LEU	VAL	SER	PRO
			SER	SER	ASP	SER	THR	CYS	ASN	ASN	ILE
			LEU	LEU	ARG	ARG	HIS	THR	VAL	VAL	MET
			ALA	ARG	PHE	THR	MET	THR	GLY	GLY	GLY
			GLN	GLN	ASP	ASP	ARG	ASP	ALA	ALA	ALA
			CYS	LEU	PRO	LEU	LEU	LEU	ASP	ASP	ASP
			TRP	LEU	TRP	GLU	ARG	ARG	ASP	ALA	THR
			ALA	ALA	ASN	ASN	ALA	LEU	HIS	LYS	ASP
			THR	SER	SER	SER	ALA	SER	ASP	THR	THR
			SER	SER	SER	GLY	HIS	GLY	GLN	ALA	ALA
			MET	MET	GLU	VAL	ILE	VAL	ARG	ALA	ARG
			ALA	ARG	LYS	GLY	LYS	GLY	ASN	ASN	ASN
			ASN	ASN	GLY	GLY	GLY	GLY	ARG	ASP	ASP
			PRO	PRO	GLU	GLU	GLN	GLN	ALA	ALA	ALA
			HIS	HIS	LEU	ARG	SER	GLY	GLY	GLU	GLU
			ALA	ALA	ALA	ALA	GLY	ALA	HIS	VAL	VAL
			ILE	ILE	ARG	ARG	ARG	ARG	THR	HIS	HIS
			LEU	LEU	ALA	ALA	GLN	ALA	SER	ARG	ARG
			THR	THR	LEU	THR	ARG	THR	THR	GLY	GLY
			GLU	GLU	SER	GLU	MET	ALA	THR	MET	GLY

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain n: 54% 46%

GLU	LYS	TLE	ARG	GLN	MET
ARG	ARG	GLU	VAL	ILE	ASN
ALA	ALA	MET	GLU	ALA	THR
ILE	ILE	GLN	GLY	LEU	ASP
ASN	ASN	GLY	SER	ASP	THR
GLU	GLU	ALA	SER	LYS	LEU
VAL	SER	SER	GLN	PRO	PRO
ARG	ASP	GLY	GLY	THR	VAL
ALA	ASN	ASN	GLY	ASP	HIS
M2E1	VAL	ARG	ARG	GLU	PRO
S543	ARG	GLY	GLY	GLU	ARG
	ALA	ALA	ASP	ASN	THR
	ALA	ALA	ASP	GLU	GLY
	ALA	THR	ARG	PHE	ARG
	HIS	ASP	ALA	ARG	ALA
	ILE	ILE	ALA	LEU	TLE
	ILE	GLU	LEU	GLY	MET
	PHE	GLU	GLU	ALA	GLY
	ASP	ASP	PRO	PHE	LYS
	ASP	ASP	SER	SER	ARG
	GLU	GLU	ILE	ILE	PRO
	ASP	ASP	GLU	SER	THR
	THR	THR	CYS	ASN	PRO
LEU	LEU	ARG	HIS	VAL	
ALA	ALA	PHE	MET	VAL	
GLN	GLN	ARG	SER	GLY	
CYS	THR	ASP	ARG	ALA	
LEU	LEU	PRO	LEU	SER	
THR	THR	TRP	GLU	ASP	
ALA	ALA	ASN	ARG	ASP	
THR	THR	LEU	ALA	HIS	
SER	SER	SER	SER	LYS	
SER	SER	GLU	GLU	ASP	
PRO	PRO	ALA	ALA	ALA	
PRO	PRO	THR	ARG	PRO	
THR	THR	PHE	VAL	THR	
ARG	ARG	GLY	ARG	THR	
ALA	ALA	ARG	SER	THR	
TRP	TRP	ALA	SER	TYR	
LYS	LYS	GLU	HIS	SER	
MET	MET	GLU	GLN	GLN	
ALA	ALA	VAL	TLE	ALA	
ARG	ARG	LYS	GLY	ASN	
ASN	ASN	GLY	LYS	ARG	
PRO	PRO	GLU	PRO	ALA	
HIS	HIS	LEU	ARG	ASP	
ALA	ALA	ARG	SER	GLU	
TLE	TLE	ALA	ALA	VAL	
THR	THR	ILE	ARG	GLY	
LEU	LEU	LEU	ALA	HIS	
ARG	ARG	THR	LEU	ARG	
ALA	ALA	GLU	LEU	ALA	
MET	MET	GLU	SER	ARG	
GLU	GLU	ALA	ALA	MET	

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain r:  54% 46%

[illegible]

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain s:  54% 46%

GLU	LYS	ARG	ALA	ILE	ARG	ILE	GLU	VAL	ASN	GLN	MET
LYS	ARG	ALA	ILE	GLN	GLY	GLY	GLU	ALA	THR	ALA	ASN
ASN	GLU	ASN	GLY	ALA	SER	SER	LYS	ASP	THR	LEU	LEU
GLU	VAL	ARG	ASN	SER	GLN	GLY	PRO	GLY	PRO	THR	GLY
ALA	ALA	ALA	VAL	VAL	ARG	ASP	GLU	GLU	PRO	ASP	HIS
M261			ARG	ARG	GLY	ASP	ASN	ASN	THR	THR	GLY
S543			ALA	ALA	TYR	GLU	GLU	GLU	ASN	GLN	GLY
			ALA	THR	ARG	ASP	PHE	ARG	ARG	ARG	ALA
			HIS	ILE	ASP	ALA	ILE	ILE	ALA	ILE	ILE
			ILE	ILE	ILE	LEU	GLY	GLY	MET	GLY	MET
			ARG	PHE	PRO	GLU	ALA	ALA	GLY	LYS	GLY
			ASP	ASP	ASP	SER	PHE	ASP	ARG	GLY	ARG
			GLU	ILE	ILE	SER	SER	SER	GLY	PRO	GLY
			ASP	ASP	ASP	GLU	LEU	LEU	THR	ILE	ILE
			THR	THR	CYS	ASN	HIS	ASN	VAL	VAL	VAL
			LEU	LEU	ARG	ARG	PHE	PHE	MET	MET	MET
			ALA	ARG	ARG	ARG	ARG	ARG	GLY	GLY	GLY
			GLN	GLN	ASP	ASP	GLN	ASP	ALA	ALA	ALA
			CYS	PRO	PRO	PRO	LEU	LEU	SER	SER	SER
			LEU	LEU	TRP	GLU	GLU	TRP	ASP	ASP	ASP
			ALA	ALA	ASN	ASN	ALA	ALA	HIS	ASP	ASP
			THR	THR	LEU	LEU	THR	ARG	ALA	ALA	ALA
			SER	SER	SER	SER	THR	PHE	PRO	THR	THR
			SER	ARG	GLY	ARG	LEU	GLY	THR	LEU	LEU
			TRP	TRP	ASP	THR	ALA	ARG	SER	THR	THR
			SER	SER	ASP	THR	ALA	ASP	TYR	TYR	TYR
			LYS	LYS	GLY	GLY	HIS	HIS	SER	SER	SER
			MET	MET	GLU	GLU	GLN	GLN	GLN	GLN	GLN
			ALA	ALA	VAL	VAL	ILE	ILE	ALA	ALA	ALA
			ARG	ARG	LYS	LYS	GLY	GLY	ASN	ASN	ASN
			PRO	PRO	GLU	GLU	GLY	GLY	ASP	ASP	ASP
			HIS	HIS	LEU	LEU	SER	ARG	ALA	ALA	ALA
			ALA	ALA	ARG	ARG	THR	THR	GLU	GLU	GLU
			ILE	ILE	ALA	ALA	GLY	GLY	VAL	VAL	VAL
			LEU	LEU	ALA	ALA	ARG	ARG	HIS	HIS	HIS
			THR	THR	LEU	LEU	ALA	ALA	ARG	ARG	ARG
			GLU	GLU	SER	SER	THR	THR	MET	MET	MET
			CTR	CTR	ALA	ALA	CTR	CTR	CTR	CTR	CTR

- Molecule 1: Phage capsid-like C-terminal domain-containing protein

Chain t: 54% 46%

GLU	LYS	ARG	ALA	ILE	ASN	GLN	MET
LYS	ARG	ALA	ILE	ASN	GLU	ILE	THR
ILE	ASN	GLU	VAL	GLY	LEU	GLU	ASP
GLU	VAL	ARG	ALA	THR	PRO	THR	THR
ALA	ARG	ALA	ASN	GLY	THR	ASP	LEU
M251	GLU	VAL	THR	GLY	ASP	GLU	PRO
M426	ALA	ARG	ILE	ASN	GLY	GLU	ARG
S543	ILE	THR	ILE	THR	GLY	ASP	THR
	GLU	PHE	GLU	ASP	LEU	GLY	GLY
	VAL	THR	ASP	GLU	VAL	THR	TRP
	THR	LEU	ALA	CYS	ASN	HIS	VAL
	ALA	ARG	PHE	MET	MET	GLY	THR
	GLN	GLN	ASP	ARG	SER	ARG	GLY
	CYS	THR	PRO	PRO	LEU	LEU	SER
	LEU	LEU	TRP	GLU	GLU	ASP	ASP
	ALA	THR	ASN	ARG	ALA	ALA	HIS
	THR	LEU	LEU	SER	ALA	GLU	LYS
	SER	SER	GLU	GLU	LEU	ASP	ASP
	PRO	PRO	MET	MET	LEU	ASP	ASP
	ALA	ALA	THR	THR	ARG	PRO	THR
	TYR	LEU	PHE	GLY	VAL	THR	THR
	ARG	ALA	GLY	SER	ARG	LEU	THR
	THR	TRP	ASP	THR	SER	TYR	SER
	SER	SER	ALA	HIS	HIS	GLN	GLN
	MET	LYS	GLY	GLN	ALA	ARG	ALA
	ALA	ARG	VAL	ILE	ILE	ASN	ALA
	LYS	THR	GLY	LYS	GLY	LYS	ASN
	HIS	HIS	LEU	GLN	PRO	ALA	ALA
	ALA	ALA	ARG	SER	SER	ASP	GLU
	ILE	ILE	ALA	GLY	GLY	THR	HIS
	THR	THR	ALA	ALA	GLN	ARG	ALA
	LEU	LEU	LEU	LEU	ARG	ARG	ARG
	GLU	GLU	SER	MET	ARG	THR	GLN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C5	Depositor
Number of particles used	19700	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 ($e^-/\text{\AA}^2$)	25.7	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	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	1	0.26	0/2258	0.48	0/3081
1	2	0.26	0/2258	0.48	0/3081
1	3	0.26	0/2258	0.48	0/3081
1	4	0.27	0/2258	0.48	0/3081
1	5	0.26	0/2258	0.49	0/3081
1	A	0.27	0/2286	0.49	0/3121
1	B	0.27	0/1947	0.48	0/2658
1	C	0.27	0/2292	0.48	0/3129
1	D	0.27	0/2292	0.49	0/3129
1	E	0.27	0/2292	0.49	0/3129
1	F	0.28	0/2286	0.48	0/3121
1	G	0.27	0/2292	0.49	0/3129
1	H	0.28	0/2292	0.49	0/3129
1	I	0.27	0/2292	0.48	0/3129
1	J	0.27	0/2292	0.49	0/3129
1	K	0.27	0/2292	0.49	0/3129
1	L	0.28	0/2292	0.49	0/3129
1	M	0.27	0/2292	0.48	0/3129
1	N	0.26	0/2292	0.47	0/3129
1	O	0.27	0/2292	0.49	0/3129
1	P	0.28	0/2292	0.48	0/3129
1	Q	0.27	0/2292	0.49	0/3129
1	R	0.26	0/2292	0.48	0/3129
1	S	0.26	0/2292	0.48	0/3129
1	T	0.26	0/2292	0.48	0/3129
1	U	0.26	0/2292	0.48	0/3129
1	V	0.27	0/2292	0.48	0/3129
1	W	0.27	0/2292	0.49	0/3129
1	X	0.27	0/2292	0.48	0/3129
1	Y	0.27	0/2292	0.49	0/3129
1	Z	0.26	0/2292	0.49	0/3129
1	a	0.27	0/2292	0.49	0/3129
1	b	0.26	0/2292	0.47	0/3129
1	c	0.27	0/2292	0.49	0/3129

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	d	0.28	0/2292	0.51	0/3129
1	e	0.27	0/2292	0.48	0/3129
1	f	0.27	0/2292	0.49	0/3129
1	g	0.27	0/2292	0.49	0/3129
1	h	0.27	0/2292	0.49	0/3129
1	i	0.26	0/2292	0.49	0/3129
1	j	0.27	0/2292	0.48	0/3129
1	k	0.27	0/2292	0.48	0/3129
1	l	0.26	0/2292	0.49	0/3129
1	m	0.27	0/2292	0.48	0/3129
1	n	0.26	0/2292	0.48	0/3129
1	o	0.26	0/2292	0.48	0/3129
1	p	0.27	0/2292	0.49	0/3129
1	q	0.27	0/2292	0.51	0/3129
1	r	0.26	0/2292	0.48	0/3129
1	s	0.26	0/2292	0.48	0/3129
1	t	0.27	0/2292	0.48	0/3129
1	u	0.26	0/2292	0.49	0/3129
1	v	0.27	0/2292	0.49	0/3129
All	All	0.27	0/120949	0.49	0/165110

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	1	284/543 (52%)	280 (99%)	4 (1%)	0	100	100
1	2	284/543 (52%)	281 (99%)	3 (1%)	0	100	100
1	3	284/543 (52%)	280 (99%)	4 (1%)	0	100	100
1	4	284/543 (52%)	279 (98%)	5 (2%)	0	100	100
1	5	284/543 (52%)	281 (99%)	3 (1%)	0	100	100
1	A	290/543 (53%)	284 (98%)	6 (2%)	0	100	100
1	B	243/543 (45%)	240 (99%)	3 (1%)	0	100	100
1	C	291/543 (54%)	285 (98%)	6 (2%)	0	100	100
1	D	291/543 (54%)	286 (98%)	5 (2%)	0	100	100
1	E	291/543 (54%)	288 (99%)	3 (1%)	0	100	100
1	F	290/543 (53%)	285 (98%)	5 (2%)	0	100	100
1	G	291/543 (54%)	287 (99%)	4 (1%)	0	100	100
1	H	291/543 (54%)	286 (98%)	5 (2%)	0	100	100
1	I	291/543 (54%)	288 (99%)	3 (1%)	0	100	100
1	J	291/543 (54%)	288 (99%)	3 (1%)	0	100	100
1	K	291/543 (54%)	286 (98%)	5 (2%)	0	100	100
1	L	291/543 (54%)	286 (98%)	5 (2%)	0	100	100
1	M	291/543 (54%)	289 (99%)	2 (1%)	0	100	100
1	N	291/543 (54%)	286 (98%)	5 (2%)	0	100	100
1	O	291/543 (54%)	289 (99%)	2 (1%)	0	100	100
1	P	291/543 (54%)	290 (100%)	1 (0%)	0	100	100
1	Q	291/543 (54%)	288 (99%)	3 (1%)	0	100	100
1	R	291/543 (54%)	283 (97%)	8 (3%)	0	100	100
1	S	291/543 (54%)	286 (98%)	5 (2%)	0	100	100
1	T	291/543 (54%)	286 (98%)	5 (2%)	0	100	100
1	U	291/543 (54%)	289 (99%)	2 (1%)	0	100	100
1	V	291/543 (54%)	286 (98%)	5 (2%)	0	100	100
1	W	291/543 (54%)	285 (98%)	6 (2%)	0	100	100
1	X	291/543 (54%)	289 (99%)	2 (1%)	0	100	100
1	Y	291/543 (54%)	288 (99%)	3 (1%)	0	100	100
1	Z	291/543 (54%)	283 (97%)	8 (3%)	0	100	100
1	a	291/543 (54%)	291 (100%)	0	0	100	100

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Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	291/543 (54%)	289 (99%)	2 (1%)	0	100	100
1	c	291/543 (54%)	287 (99%)	4 (1%)	0	100	100
1	d	291/543 (54%)	280 (96%)	11 (4%)	0	100	100
1	e	291/543 (54%)	287 (99%)	4 (1%)	0	100	100
1	f	291/543 (54%)	287 (99%)	4 (1%)	0	100	100
1	g	291/543 (54%)	288 (99%)	3 (1%)	0	100	100
1	h	291/543 (54%)	285 (98%)	6 (2%)	0	100	100
1	i	291/543 (54%)	280 (96%)	11 (4%)	0	100	100
1	j	291/543 (54%)	288 (99%)	3 (1%)	0	100	100
1	k	291/543 (54%)	287 (99%)	4 (1%)	0	100	100
1	l	291/543 (54%)	288 (99%)	3 (1%)	0	100	100
1	m	291/543 (54%)	289 (99%)	2 (1%)	0	100	100
1	n	291/543 (54%)	286 (98%)	5 (2%)	0	100	100
1	o	291/543 (54%)	287 (99%)	4 (1%)	0	100	100
1	p	291/543 (54%)	285 (98%)	6 (2%)	0	100	100
1	q	291/543 (54%)	284 (98%)	7 (2%)	0	100	100
1	r	291/543 (54%)	287 (99%)	4 (1%)	0	100	100
1	s	291/543 (54%)	286 (98%)	5 (2%)	0	100	100
1	t	291/543 (54%)	291 (100%)	0	0	100	100
1	u	291/543 (54%)	284 (98%)	7 (2%)	0	100	100
1	v	291/543 (54%)	287 (99%)	4 (1%)	0	100	100
All	All	15338/28779 (53%)	15110 (98%)	228 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	1	226/432 (52%)	226 (100%)	0	100	100
1	2	226/432 (52%)	226 (100%)	0	100	100
1	3	226/432 (52%)	226 (100%)	0	100	100
1	4	226/432 (52%)	226 (100%)	0	100	100
1	5	226/432 (52%)	226 (100%)	0	100	100
1	A	228/432 (53%)	228 (100%)	0	100	100
1	B	193/432 (45%)	192 (100%)	1 (0%)	86	93
1	C	229/432 (53%)	229 (100%)	0	100	100
1	D	229/432 (53%)	229 (100%)	0	100	100
1	E	229/432 (53%)	229 (100%)	0	100	100
1	F	228/432 (53%)	228 (100%)	0	100	100
1	G	229/432 (53%)	229 (100%)	0	100	100
1	H	229/432 (53%)	229 (100%)	0	100	100
1	I	229/432 (53%)	229 (100%)	0	100	100
1	J	229/432 (53%)	228 (100%)	1 (0%)	89	95
1	K	229/432 (53%)	229 (100%)	0	100	100
1	L	229/432 (53%)	229 (100%)	0	100	100
1	M	229/432 (53%)	228 (100%)	1 (0%)	89	95
1	N	229/432 (53%)	229 (100%)	0	100	100
1	O	229/432 (53%)	229 (100%)	0	100	100
1	P	229/432 (53%)	229 (100%)	0	100	100
1	Q	229/432 (53%)	229 (100%)	0	100	100
1	R	229/432 (53%)	228 (100%)	1 (0%)	89	95
1	S	229/432 (53%)	229 (100%)	0	100	100
1	T	229/432 (53%)	229 (100%)	0	100	100
1	U	229/432 (53%)	229 (100%)	0	100	100
1	V	229/432 (53%)	229 (100%)	0	100	100
1	W	229/432 (53%)	229 (100%)	0	100	100
1	X	229/432 (53%)	229 (100%)	0	100	100
1	Y	229/432 (53%)	229 (100%)	0	100	100
1	Z	229/432 (53%)	229 (100%)	0	100	100
1	a	229/432 (53%)	229 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	229/432 (53%)	229 (100%)	0	100	100
1	c	229/432 (53%)	229 (100%)	0	100	100
1	d	229/432 (53%)	229 (100%)	0	100	100
1	e	229/432 (53%)	229 (100%)	0	100	100
1	f	229/432 (53%)	229 (100%)	0	100	100
1	g	229/432 (53%)	229 (100%)	0	100	100
1	h	229/432 (53%)	229 (100%)	0	100	100
1	i	229/432 (53%)	229 (100%)	0	100	100
1	j	229/432 (53%)	229 (100%)	0	100	100
1	k	229/432 (53%)	229 (100%)	0	100	100
1	l	229/432 (53%)	228 (100%)	1 (0%)	89	95
1	m	229/432 (53%)	229 (100%)	0	100	100
1	n	229/432 (53%)	229 (100%)	0	100	100
1	o	229/432 (53%)	229 (100%)	0	100	100
1	p	229/432 (53%)	228 (100%)	1 (0%)	89	95
1	q	229/432 (53%)	229 (100%)	0	100	100
1	r	229/432 (53%)	229 (100%)	0	100	100
1	s	229/432 (53%)	229 (100%)	0	100	100
1	t	229/432 (53%)	229 (100%)	0	100	100
1	u	229/432 (53%)	229 (100%)	0	100	100
1	v	229/432 (53%)	228 (100%)	1 (0%)	89	95
All	All	12084/22896 (53%)	12077 (100%)	7 (0%)	92	97

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	R	360	LYS
1	l	374	GLN
1	v	426	ASN
1	p	510	ARG
1	M	532	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	n	419	GLN
1	q	275	ASN
1	X	430	ASN
1	a	279	ASN
1	a	430	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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.