



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 04:22 PM UTC

PDB ID : 6YSZ / pdb_00006ysz
EMDB ID : EMD-10911
Title : Cryo-EM structure of T7 bacteriophage DNA translocation gp15 core protein intermediate assembly
Authors : Perez-Ruiz, M.; Pulido-Cid, M.; Luque-Ortega, J.R.; Cuervo, A.; Carrascosa, J.L.
Deposited on : 2020-04-23
Resolution : 3.60 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

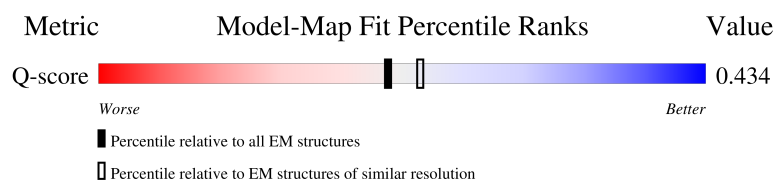
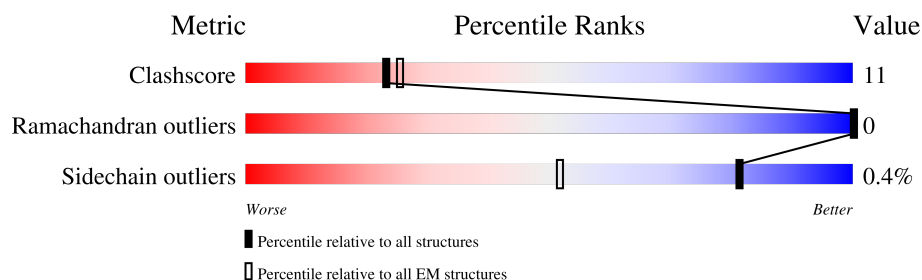
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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	12797 (3.10 - 4.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	782	
1	B	782	
1	C	782	
1	D	782	

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Mol	Chain	Length	Quality of chain
1	E	782	 31%10%60%
1	F	782	 30%10%60%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 15192 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Internal virion protein gp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	316	Total	C	N	O	S	0	0
			2532	1558	457	507	10		
1	B	316	Total	C	N	O	S	0	0
			2532	1558	457	507	10		
1	C	316	Total	C	N	O	S	0	0
			2532	1558	457	507	10		
1	D	316	Total	C	N	O	S	0	0
			2532	1558	457	507	10		
1	E	316	Total	C	N	O	S	0	0
			2532	1558	457	507	10		
1	F	316	Total	C	N	O	S	0	0
			2532	1558	457	507	10		

There are 210 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-34	MET	-	initiating methionine	UNP P03725
A	-33	ARG	-	expression tag	UNP P03725
A	-32	GLY	-	expression tag	UNP P03725
A	-31	SER	-	expression tag	UNP P03725
A	-30	HIS	-	expression tag	UNP P03725
A	-29	HIS	-	expression tag	UNP P03725
A	-28	HIS	-	expression tag	UNP P03725
A	-27	HIS	-	expression tag	UNP P03725
A	-26	HIS	-	expression tag	UNP P03725
A	-25	HIS	-	expression tag	UNP P03725
A	-24	GLY	-	expression tag	UNP P03725
A	-23	MET	-	expression tag	UNP P03725
A	-22	ALA	-	expression tag	UNP P03725
A	-21	SER	-	expression tag	UNP P03725
A	-20	MET	-	expression tag	UNP P03725
A	-19	THR	-	expression tag	UNP P03725
A	-18	GLY	-	expression tag	UNP P03725
A	-17	GLY	-	expression tag	UNP P03725

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	GLN	-	expression tag	UNP P03725
A	-15	GLN	-	expression tag	UNP P03725
A	-14	MET	-	expression tag	UNP P03725
A	-13	GLY	-	expression tag	UNP P03725
A	-12	ARG	-	expression tag	UNP P03725
A	-11	ASP	-	expression tag	UNP P03725
A	-10	LEU	-	expression tag	UNP P03725
A	-9	TYR	-	expression tag	UNP P03725
A	-8	ASP	-	expression tag	UNP P03725
A	-7	ASP	-	expression tag	UNP P03725
A	-6	ASP	-	expression tag	UNP P03725
A	-5	ASP	-	expression tag	UNP P03725
A	-4	LYS	-	expression tag	UNP P03725
A	-3	ASP	-	expression tag	UNP P03725
A	-2	PRO	-	expression tag	UNP P03725
A	-1	SER	-	expression tag	UNP P03725
A	0	SER	-	expression tag	UNP P03725
B	-34	MET	-	initiating methionine	UNP P03725
B	-33	ARG	-	expression tag	UNP P03725
B	-32	GLY	-	expression tag	UNP P03725
B	-31	SER	-	expression tag	UNP P03725
B	-30	HIS	-	expression tag	UNP P03725
B	-29	HIS	-	expression tag	UNP P03725
B	-28	HIS	-	expression tag	UNP P03725
B	-27	HIS	-	expression tag	UNP P03725
B	-26	HIS	-	expression tag	UNP P03725
B	-25	HIS	-	expression tag	UNP P03725
B	-24	GLY	-	expression tag	UNP P03725
B	-23	MET	-	expression tag	UNP P03725
B	-22	ALA	-	expression tag	UNP P03725
B	-21	SER	-	expression tag	UNP P03725
B	-20	MET	-	expression tag	UNP P03725
B	-19	THR	-	expression tag	UNP P03725
B	-18	GLY	-	expression tag	UNP P03725
B	-17	GLY	-	expression tag	UNP P03725
B	-16	GLN	-	expression tag	UNP P03725
B	-15	GLN	-	expression tag	UNP P03725
B	-14	MET	-	expression tag	UNP P03725
B	-13	GLY	-	expression tag	UNP P03725
B	-12	ARG	-	expression tag	UNP P03725
B	-11	ASP	-	expression tag	UNP P03725
B	-10	LEU	-	expression tag	UNP P03725

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-9	TYR	-	expression tag	UNP P03725
B	-8	ASP	-	expression tag	UNP P03725
B	-7	ASP	-	expression tag	UNP P03725
B	-6	ASP	-	expression tag	UNP P03725
B	-5	ASP	-	expression tag	UNP P03725
B	-4	LYS	-	expression tag	UNP P03725
B	-3	ASP	-	expression tag	UNP P03725
B	-2	PRO	-	expression tag	UNP P03725
B	-1	SER	-	expression tag	UNP P03725
B	0	SER	-	expression tag	UNP P03725
C	-34	MET	-	initiating methionine	UNP P03725
C	-33	ARG	-	expression tag	UNP P03725
C	-32	GLY	-	expression tag	UNP P03725
C	-31	SER	-	expression tag	UNP P03725
C	-30	HIS	-	expression tag	UNP P03725
C	-29	HIS	-	expression tag	UNP P03725
C	-28	HIS	-	expression tag	UNP P03725
C	-27	HIS	-	expression tag	UNP P03725
C	-26	HIS	-	expression tag	UNP P03725
C	-25	HIS	-	expression tag	UNP P03725
C	-24	GLY	-	expression tag	UNP P03725
C	-23	MET	-	expression tag	UNP P03725
C	-22	ALA	-	expression tag	UNP P03725
C	-21	SER	-	expression tag	UNP P03725
C	-20	MET	-	expression tag	UNP P03725
C	-19	THR	-	expression tag	UNP P03725
C	-18	GLY	-	expression tag	UNP P03725
C	-17	GLY	-	expression tag	UNP P03725
C	-16	GLN	-	expression tag	UNP P03725
C	-15	GLN	-	expression tag	UNP P03725
C	-14	MET	-	expression tag	UNP P03725
C	-13	GLY	-	expression tag	UNP P03725
C	-12	ARG	-	expression tag	UNP P03725
C	-11	ASP	-	expression tag	UNP P03725
C	-10	LEU	-	expression tag	UNP P03725
C	-9	TYR	-	expression tag	UNP P03725
C	-8	ASP	-	expression tag	UNP P03725
C	-7	ASP	-	expression tag	UNP P03725
C	-6	ASP	-	expression tag	UNP P03725
C	-5	ASP	-	expression tag	UNP P03725
C	-4	LYS	-	expression tag	UNP P03725
C	-3	ASP	-	expression tag	UNP P03725

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	PRO	-	expression tag	UNP P03725
C	-1	SER	-	expression tag	UNP P03725
C	0	SER	-	expression tag	UNP P03725
D	-34	MET	-	initiating methionine	UNP P03725
D	-33	ARG	-	expression tag	UNP P03725
D	-32	GLY	-	expression tag	UNP P03725
D	-31	SER	-	expression tag	UNP P03725
D	-30	HIS	-	expression tag	UNP P03725
D	-29	HIS	-	expression tag	UNP P03725
D	-28	HIS	-	expression tag	UNP P03725
D	-27	HIS	-	expression tag	UNP P03725
D	-26	HIS	-	expression tag	UNP P03725
D	-25	HIS	-	expression tag	UNP P03725
D	-24	GLY	-	expression tag	UNP P03725
D	-23	MET	-	expression tag	UNP P03725
D	-22	ALA	-	expression tag	UNP P03725
D	-21	SER	-	expression tag	UNP P03725
D	-20	MET	-	expression tag	UNP P03725
D	-19	THR	-	expression tag	UNP P03725
D	-18	GLY	-	expression tag	UNP P03725
D	-17	GLY	-	expression tag	UNP P03725
D	-16	GLN	-	expression tag	UNP P03725
D	-15	GLN	-	expression tag	UNP P03725
D	-14	MET	-	expression tag	UNP P03725
D	-13	GLY	-	expression tag	UNP P03725
D	-12	ARG	-	expression tag	UNP P03725
D	-11	ASP	-	expression tag	UNP P03725
D	-10	LEU	-	expression tag	UNP P03725
D	-9	TYR	-	expression tag	UNP P03725
D	-8	ASP	-	expression tag	UNP P03725
D	-7	ASP	-	expression tag	UNP P03725
D	-6	ASP	-	expression tag	UNP P03725
D	-5	ASP	-	expression tag	UNP P03725
D	-4	LYS	-	expression tag	UNP P03725
D	-3	ASP	-	expression tag	UNP P03725
D	-2	PRO	-	expression tag	UNP P03725
D	-1	SER	-	expression tag	UNP P03725
D	0	SER	-	expression tag	UNP P03725
E	-34	MET	-	initiating methionine	UNP P03725
E	-33	ARG	-	expression tag	UNP P03725
E	-32	GLY	-	expression tag	UNP P03725
E	-31	SER	-	expression tag	UNP P03725

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-30	HIS	-	expression tag	UNP P03725
E	-29	HIS	-	expression tag	UNP P03725
E	-28	HIS	-	expression tag	UNP P03725
E	-27	HIS	-	expression tag	UNP P03725
E	-26	HIS	-	expression tag	UNP P03725
E	-25	HIS	-	expression tag	UNP P03725
E	-24	GLY	-	expression tag	UNP P03725
E	-23	MET	-	expression tag	UNP P03725
E	-22	ALA	-	expression tag	UNP P03725
E	-21	SER	-	expression tag	UNP P03725
E	-20	MET	-	expression tag	UNP P03725
E	-19	THR	-	expression tag	UNP P03725
E	-18	GLY	-	expression tag	UNP P03725
E	-17	GLY	-	expression tag	UNP P03725
E	-16	GLN	-	expression tag	UNP P03725
E	-15	GLN	-	expression tag	UNP P03725
E	-14	MET	-	expression tag	UNP P03725
E	-13	GLY	-	expression tag	UNP P03725
E	-12	ARG	-	expression tag	UNP P03725
E	-11	ASP	-	expression tag	UNP P03725
E	-10	LEU	-	expression tag	UNP P03725
E	-9	TYR	-	expression tag	UNP P03725
E	-8	ASP	-	expression tag	UNP P03725
E	-7	ASP	-	expression tag	UNP P03725
E	-6	ASP	-	expression tag	UNP P03725
E	-5	ASP	-	expression tag	UNP P03725
E	-4	LYS	-	expression tag	UNP P03725
E	-3	ASP	-	expression tag	UNP P03725
E	-2	PRO	-	expression tag	UNP P03725
E	-1	SER	-	expression tag	UNP P03725
E	0	SER	-	expression tag	UNP P03725
F	-34	MET	-	initiating methionine	UNP P03725
F	-33	ARG	-	expression tag	UNP P03725
F	-32	GLY	-	expression tag	UNP P03725
F	-31	SER	-	expression tag	UNP P03725
F	-30	HIS	-	expression tag	UNP P03725
F	-29	HIS	-	expression tag	UNP P03725
F	-28	HIS	-	expression tag	UNP P03725
F	-27	HIS	-	expression tag	UNP P03725
F	-26	HIS	-	expression tag	UNP P03725
F	-25	HIS	-	expression tag	UNP P03725
F	-24	GLY	-	expression tag	UNP P03725

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-23	MET	-	expression tag	UNP P03725
F	-22	ALA	-	expression tag	UNP P03725
F	-21	SER	-	expression tag	UNP P03725
F	-20	MET	-	expression tag	UNP P03725
F	-19	THR	-	expression tag	UNP P03725
F	-18	GLY	-	expression tag	UNP P03725
F	-17	GLY	-	expression tag	UNP P03725
F	-16	GLN	-	expression tag	UNP P03725
F	-15	GLN	-	expression tag	UNP P03725
F	-14	MET	-	expression tag	UNP P03725
F	-13	GLY	-	expression tag	UNP P03725
F	-12	ARG	-	expression tag	UNP P03725
F	-11	ASP	-	expression tag	UNP P03725
F	-10	LEU	-	expression tag	UNP P03725
F	-9	TYR	-	expression tag	UNP P03725
F	-8	ASP	-	expression tag	UNP P03725
F	-7	ASP	-	expression tag	UNP P03725
F	-6	ASP	-	expression tag	UNP P03725
F	-5	ASP	-	expression tag	UNP P03725
F	-4	LYS	-	expression tag	UNP P03725
F	-3	ASP	-	expression tag	UNP P03725
F	-2	PRO	-	expression tag	UNP P03725
F	-1	SER	-	expression tag	UNP P03725
F	0	SER	-	expression tag	UNP P03725

3 Residue-property plots

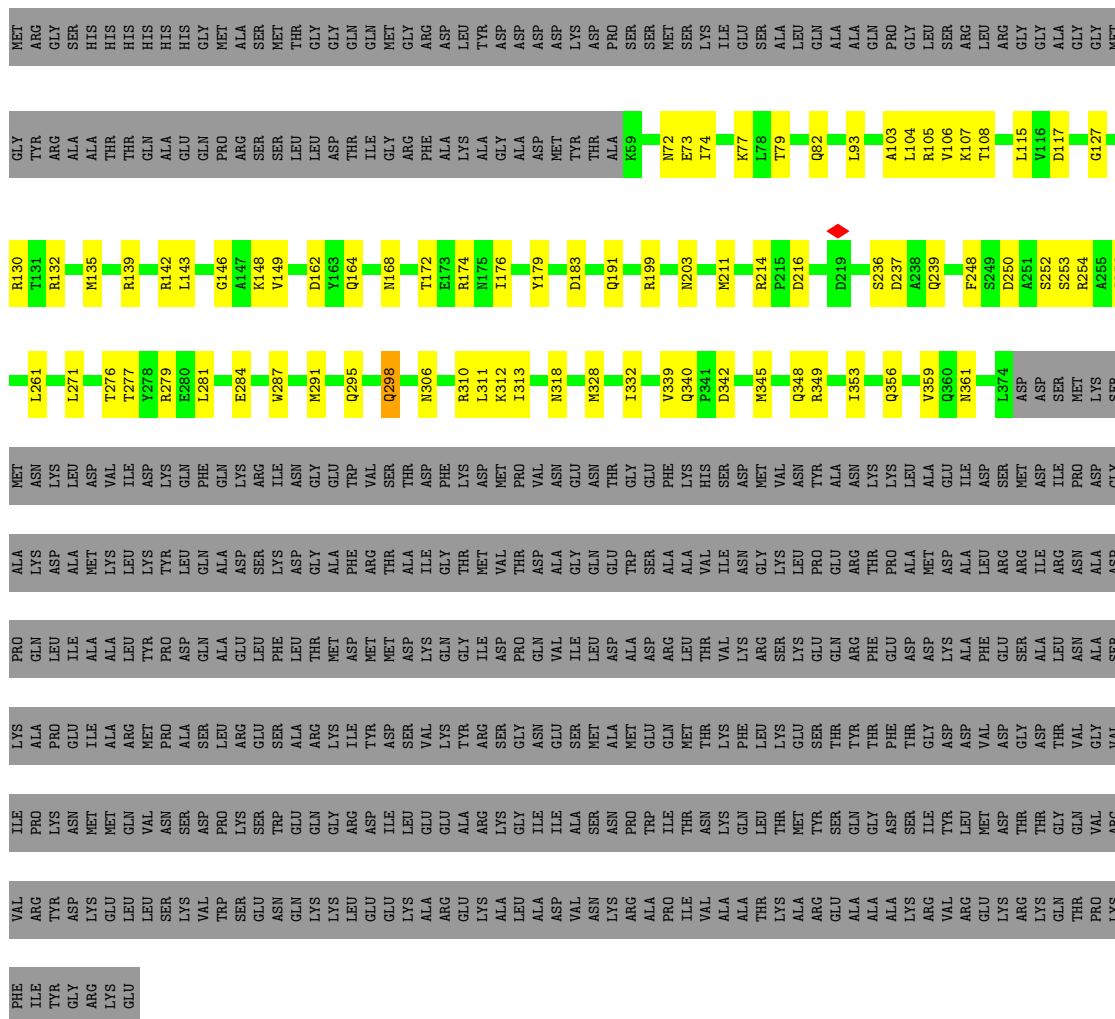
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Internal virion protein gp15

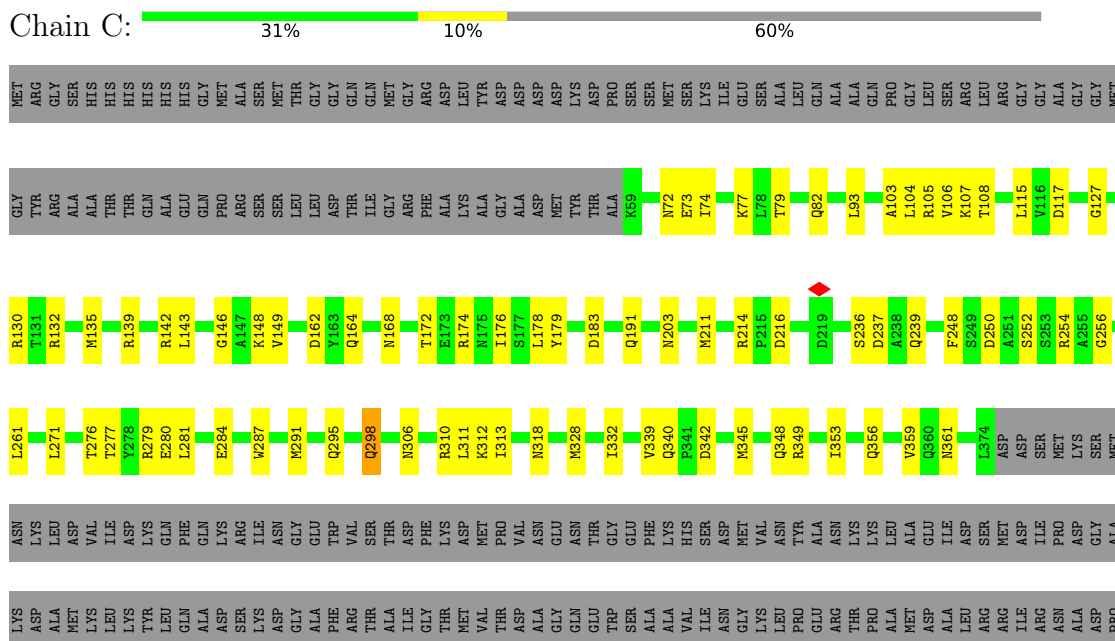


- Molecule 1: Internal virion protein gp15





- Molecule 1: Internal virion protein gp15



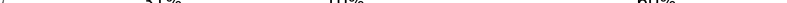
ILE	TYR	ARG	PRO	ALA	GLN	
	GLY	TYR	LYS			LEU
	ARG	ASN	ASN			PRO
	LYS	ASP	ASN			ASP
GLU	ARG	LEU	GLN	LEU	TYR	
	LYS	LEU	VAL	MET	ARG	
	GLY	LEU	GLN	MET	LEU	
	ILE	LEU	VAL	ASP	LEU	
GLY	GLY	GLN	ASP	GLU	PHE	
	ARG	ASN	TRP	SER	LEU	
	LYS	GLN	GLY	ARG	THR	
	ILE	LEU	ARG	LYS	MET	
TYR	ASP	GLU	ASP	TYR	ASP	
	ASN	GLU	ILE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

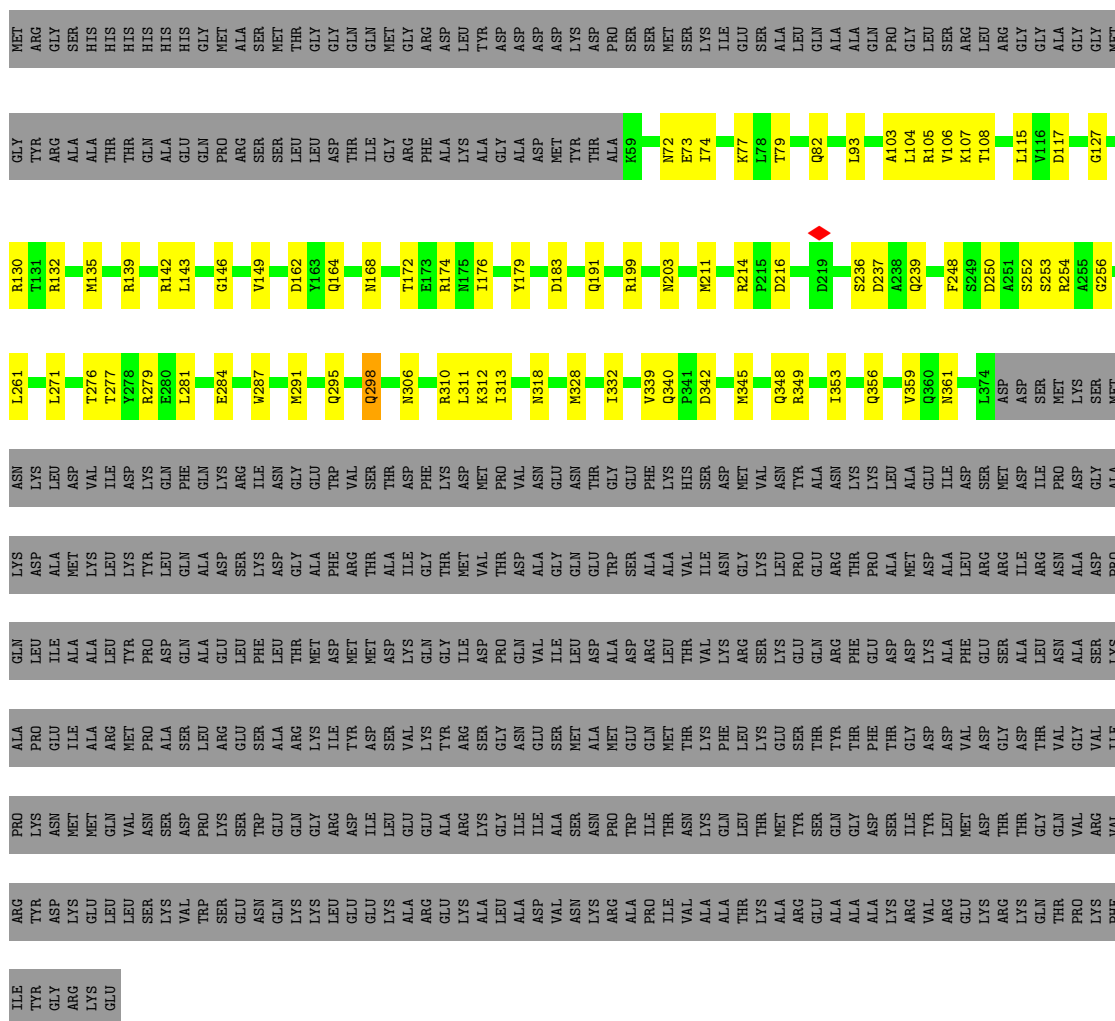
- Molecule 1: Internal virion protein gp15

Chain D:  31% 9% 60%

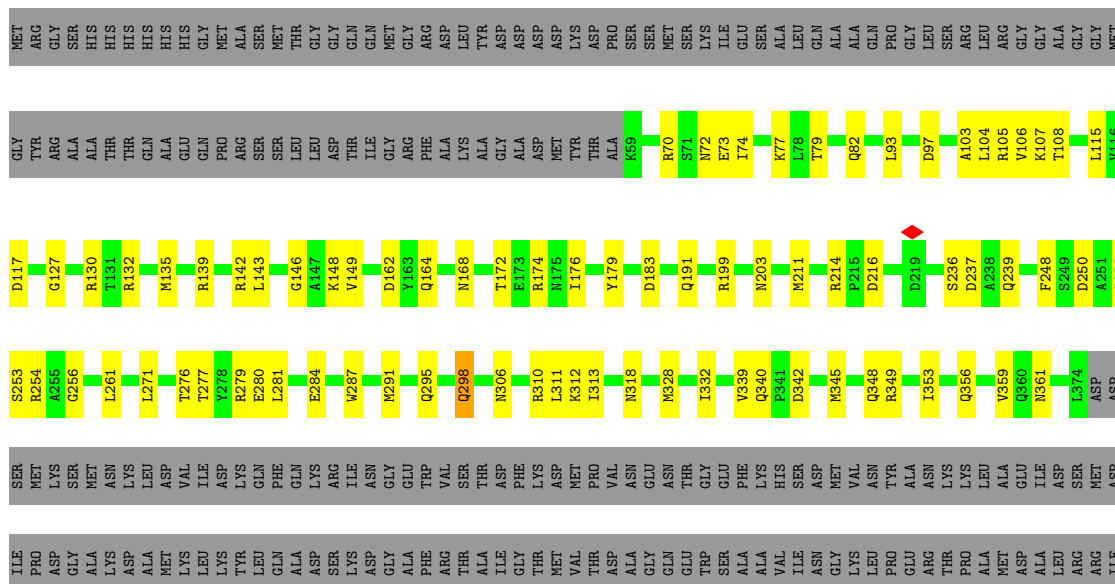
GLU	LEU	GLN	ARG	LEU	LEU	ILE	L271	R130	MET
LEU	LEU	VAL	MET	TYR	TYR	ASP	L271	R130	GLY
LEU	ASN	ASN	PRO	PRO	TYR	ASP	L271	R132	TYR
LYS	LYS	SER	ALA	ASP	LEU	GLN	T276	R132	GLY
VAL	VAL	ASP	SER	GLN	GLN	PHE	T277	M135	ALA
TRP	TRP	PRO	LEU	ALA	ALA	GLN	L281	R139	ALA
SER	SER	LYS	ARG	GLU	ASP	LYS	L281	R139	THR
GLU	GLU	SER	GLU	LEU	LEU	ARG	E284	R142	GLN
ASN	ASN	TRP	SER	PHE	LYS	ILE	E284	R143	ALA
GLN	GLN	GLU	ALA	LEU	ASP	ASN	M291	L143	ALA
LYS	LYS	GLN	ARG	THR	GLY	GLY	M291	G146	GLN
LYS	LYS	GLY	LYS	MET	ALA	GLU	Q295	G146	PRO
LEU	LEU	ARG	ILE	ASP	PHE	TRP	Q295	A147	ARG
GLU	GLU	ASP	TYR	MET	ARG	VAL	K148	A147	ALA
GLU	GLU	ILE	ASP	MET	THR	SER	Q298	V149	SER
LYS	LYS	LYS	SER	ASP	ALA	THR	Q298	V149	SER
ALA	ALA	GLU	VAL	LYS	ILE	ASP	N306	D162	LEU
ARG	ARG	GLU	LYS	GLN	GLY	PHE	N306	D162	GLY
GLU	GLU	ALA	TYR	GLY	THR	LYS	R310	Y163	ASP
LYS	LYS	ARG	ARG	ILE	MET	ASP	L311	Q164	THR
ALA	ALA	LYS	SER	ASP	THR	MET	K312	Q164	GLN
LEU	LEU	GLY	GLY	PRO	THR	PRO	I313	M168	GLY
ALA	ALA	ILE	ASN	GLN	ASP	VAL	N318	T172	ARG
ASP	ASP	ILE	GLU	VAL	ALA	ASN	N318	E173	ALA
VAL	VAL	ALA	SER	ILE	GLY	GLU	M328	R174	LYS
ASN	ASN	SER	MET	LEU	GLN	ASN	M328	M175	ALA
LYS	LYS	ASN	ALA	ASP	GLU	THR	I332	M176	GLY
ARG	ARG	PRO	MET	ALA	TRP	GLY	I332	Y179	ALA
ALA	ALA	TRP	GLU	ASP	SER	GLU	V339	Y179	ASP
PRO	PRO	ILE	GLN	ARG	ALA	PHE	V339	D183	ASP
ILE	ILE	THR	MET	LEU	ALA	LYS	Q340	D183	LYS
ASN	VAL	ASN	THR	THR	VAL	HIS	P341	Q191	THR
ALA	ALA	LYS	VAL	ILE	ILE	SER	D342	Q191	ASP
ALA	ALA	GLN	PHE	LYS	ASN	ASP	M345	N203	ALA
LEU	THR	LEU	LEU	ARG	GLY	MET	M345	N203	SER
LYS	LYS	THR	LYS	SER	LYS	VAL	Q348	M211	MET
ALA	ALA	MET	GLU	LYS	LEU	ASN	Q348	E73	THR
ARG	ARG	GLU	SER	GLU	PRO	TYR	R349	R74	LYS
GLU	GLU	SER	THR	GLN	GLU	ALA	R214	R214	ILE
ALA	ALA	GLN	TYR	ARG	THR	ASN	I353	P215	GLU
ALA	ALA	GLY	THR	PHE	THR	LYS	D215	D215	SER
ASP	ALA	ASP	PHE	GLU	PRO	LYS	Q356	T79	ALA
LYS	LYS	SER	THR	ASP	ALA	LEU	Q356	D219	ALA
ARG	ARG	ILE	GLY	ASP	MET	ALA	V359	Q82	LEU
VAL	VAL	TYR	ASP	LEU	ASP	GLU	Q380	S236	GLN
ARG	ARG	LEU	ASP	ALA	ALA	ILE	N361	D237	ALA
GLU	GLU	MET	VAL	PHE	LEU	ASP	L374	A238	ALA
LYS	LYS	ASP	ASP	GLU	ARG	SER	L374	Q239	GLN
THR	THR	THR	GLY	SER	ARG	MET	ASP	Q239	PRO
LYS	LYS	THR	ASP	ALA	ILE	ASP	ASP	L104	GLY
GLN	GLN	GLY	THR	LEU	ARG	ILE	SER	R105	LEU
THR	THR	GLN	VAL	ASN	ASN	ASN	F248	S249	SER
PRO	PRO	VAL	GLY	ALA	ALA	ASP	D250	K107	ARG
LYS	LYS	ARG	VAL	SER	ASP	GLY	A251	T108	LEU
PHE	PHE	VAL	ILE	LYS	PRO	ALA	SER	L115	ARG
ILE	ILE	ARG	PRO	ALA	ALA	ASN	MET	V116	GLY
TYR	TYR	TYR	ASN	LEU	LEU	ASP	LYS	D117	GLY
GLY	GLY	ASP	ASN	GLU	ILE	ALA	A255	D256	ALA
ARG	ARG	THR	MET	ILE	ALA	LYS	G256	G256	GLY
LYS	LYS	CTR	MET	ALA	ALA	THR	VAL	G127	GLY
THR	THR	THR	THR	THR	THR	THR	THR	THR	MET

- Molecule 1: Internal virion protein gp15

Chain E:  31% 10% 60%



- Molecule 1: Internal virion protein gp15



GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU	ASP	ALA	LYS	GLY	ASP	LEU	VAL	GLN	ASP	GLY	PRO	GLY	ASP	LEU	GLY	ASP	GLY	ASP	ALA
GLN	THR	PRO	LYS	PHE	ILE	TYR	GLY	ARG	LYS	GLU	LEU	SER	ASN	LEU	TYR	PRO	ASP	GLN	LEU	GLY	PHE	GLU																			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of particles used	50980	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	120000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.225	Depositor
Minimum map value	-0.004	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0114	Depositor
Map size (Å)	204.0, 204.0, 204.0	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.19	0/2569	0.35	0/3463
1	B	0.19	0/2569	0.35	0/3463
1	C	0.19	0/2569	0.35	0/3463
1	D	0.19	0/2569	0.35	0/3463
1	E	0.19	0/2569	0.35	0/3463
1	F	0.19	0/2569	0.35	0/3463
All	All	0.19	0/15414	0.35	0/20778

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

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2532	0	2453	68	0
1	B	2532	0	2453	71	0
1	C	2532	0	2453	69	0
1	D	2532	0	2453	68	0
1	E	2532	0	2453	70	0
1	F	2532	0	2453	73	0
All	All	15192	0	14718	332	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 11.

The worst 5 of 332 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:C:311:LEU:HD11	1:D:356:GLN:OE1	1.89	0.73
1:A:356:GLN:OE1	1:F:311:LEU:HD11	1.88	0.72
1:E:311:LEU:HD11	1:F:356:GLN:OE1	1.88	0.72
1:B:311:LEU:HD11	1:C:356:GLN:OE1	1.89	0.71
1:D:311:LEU:HD11	1:E:356:GLN:OE1	1.90	0.71

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	314/782 (40%)	305 (97%)	9 (3%)	0	100	100
1	B	314/782 (40%)	305 (97%)	9 (3%)	0	100	100
1	C	314/782 (40%)	305 (97%)	9 (3%)	0	100	100
1	D	314/782 (40%)	305 (97%)	9 (3%)	0	100	100
1	E	314/782 (40%)	305 (97%)	9 (3%)	0	100	100
1	F	314/782 (40%)	305 (97%)	9 (3%)	0	100	100
All	All	1884/4692 (40%)	1830 (97%)	54 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	266/653 (41%)	265 (100%)	1 (0%)	84	81
1	B	266/653 (41%)	265 (100%)	1 (0%)	84	81
1	C	266/653 (41%)	265 (100%)	1 (0%)	84	81
1	D	266/653 (41%)	265 (100%)	1 (0%)	84	81
1	E	266/653 (41%)	265 (100%)	1 (0%)	84	81
1	F	266/653 (41%)	265 (100%)	1 (0%)	84	81
All	All	1596/3918 (41%)	1590 (100%)	6 (0%)	81	81

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	298	GLN
1	E	298	GLN
1	F	298	GLN
1	B	298	GLN
1	A	298	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	246	GLN
1	E	203	ASN
1	F	340	GLN
1	D	286	GLN
1	D	344	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

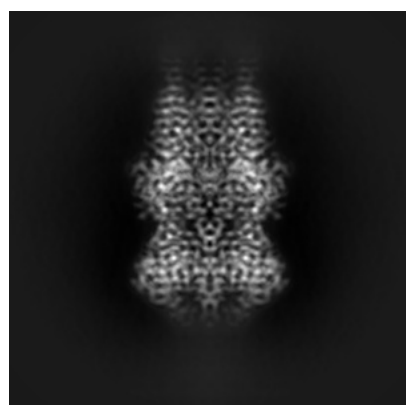
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10911. These allow visual inspection of the internal detail of the map and identification of artifacts.

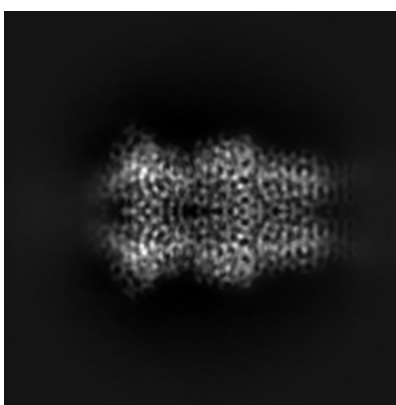
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

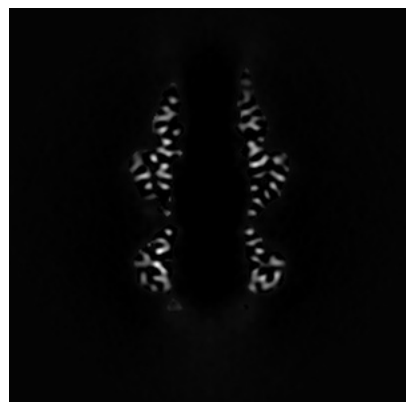


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 120



Y Index: 120



Z Index: 120

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: 140



Y Index: 94

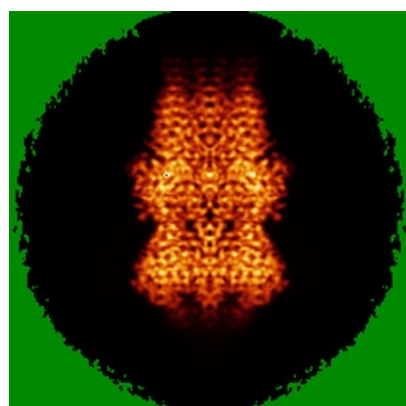


Z Index: 82

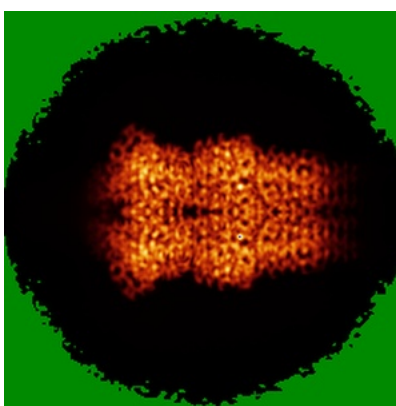
The images above show the largest variance slices of the map in three orthogonal directions.

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

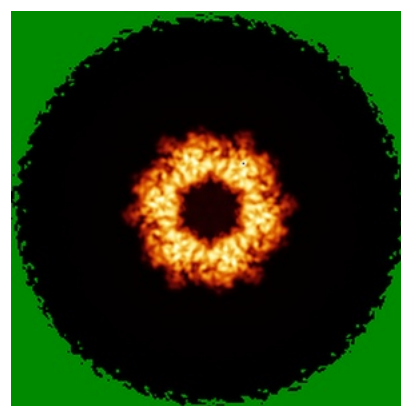
6.4.1 Primary map



X



Y

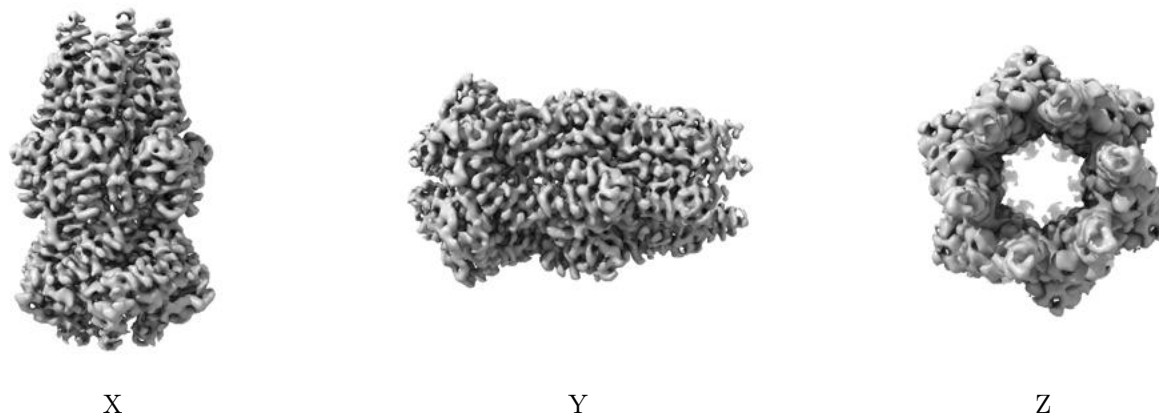


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0114. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

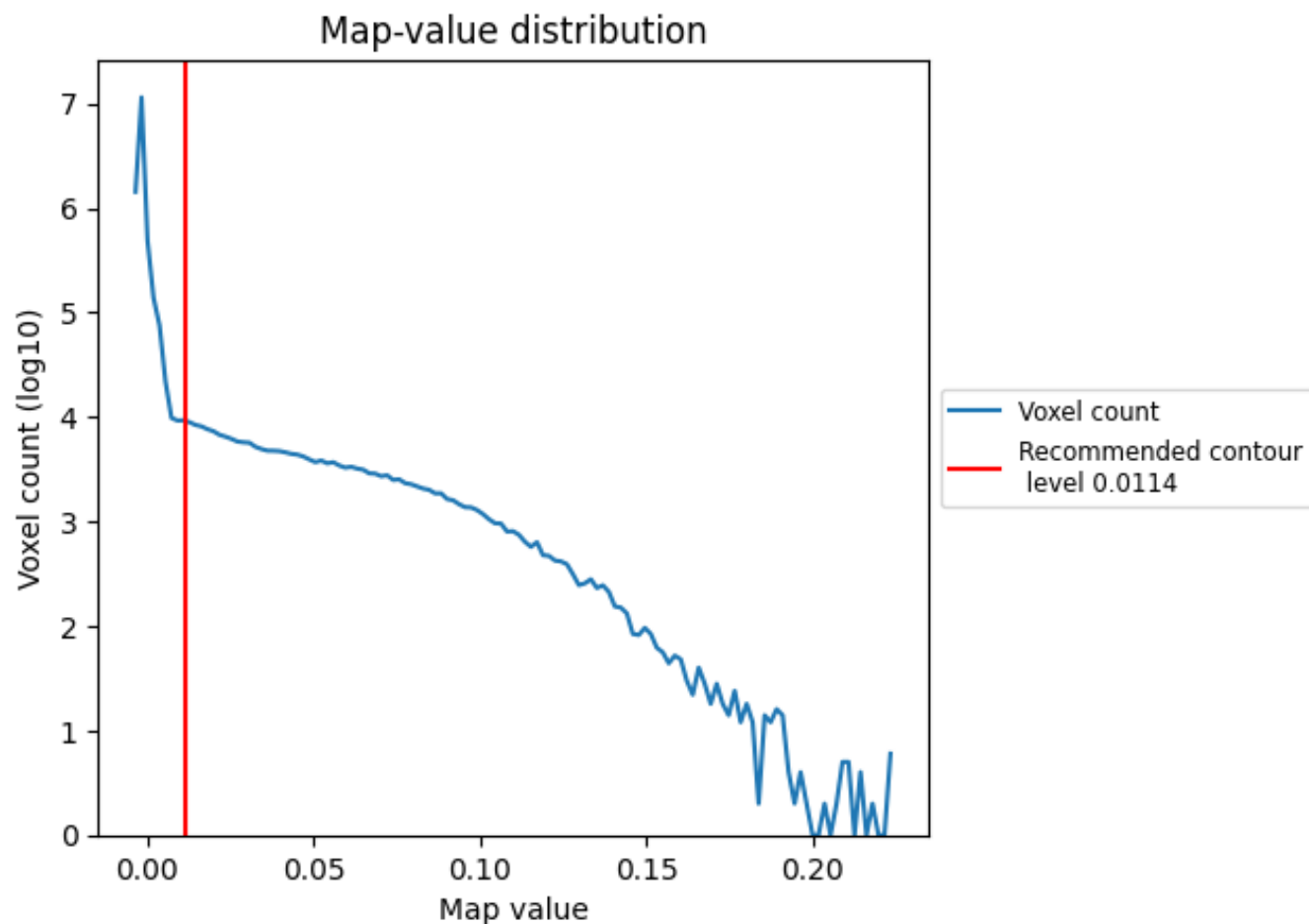
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

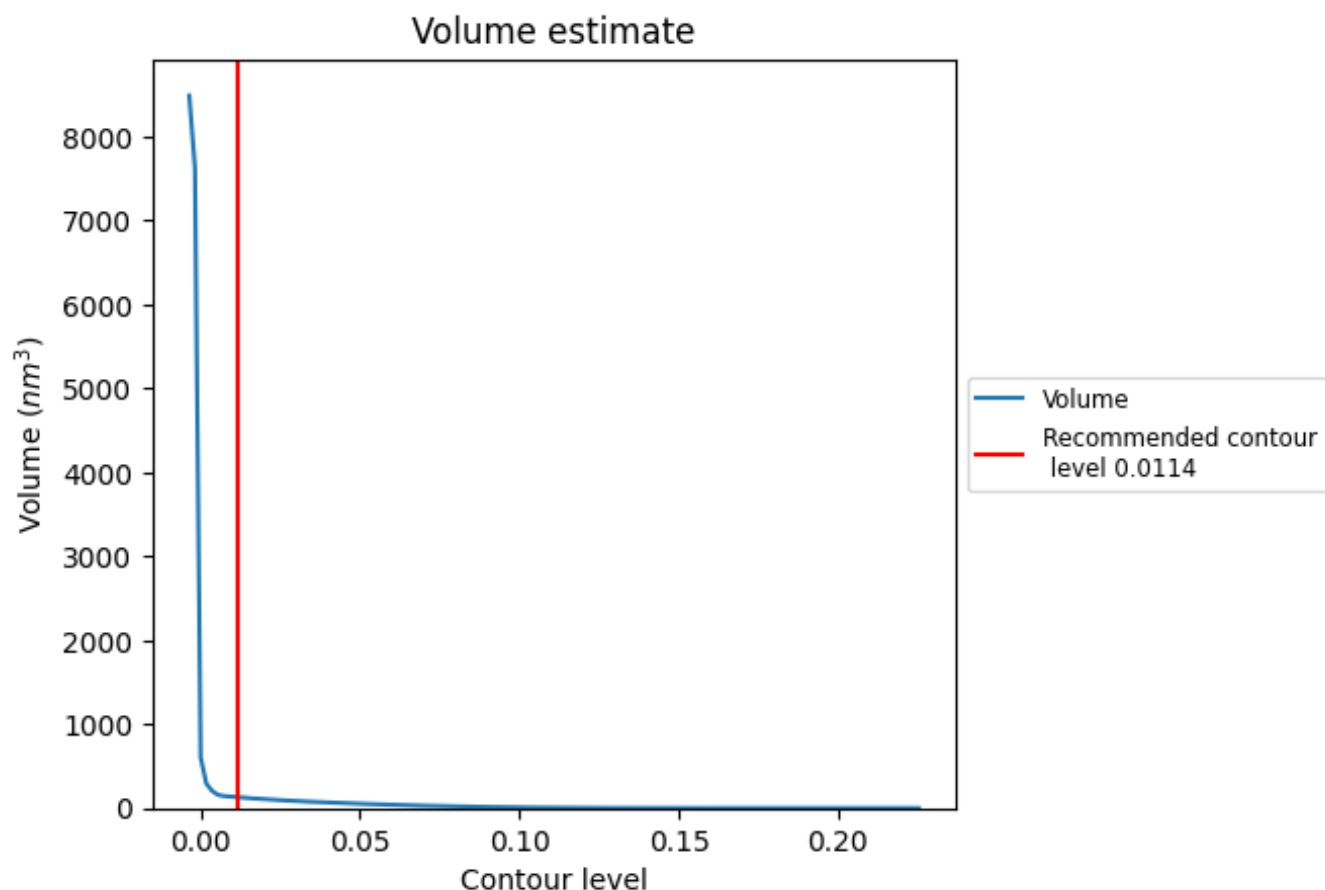
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

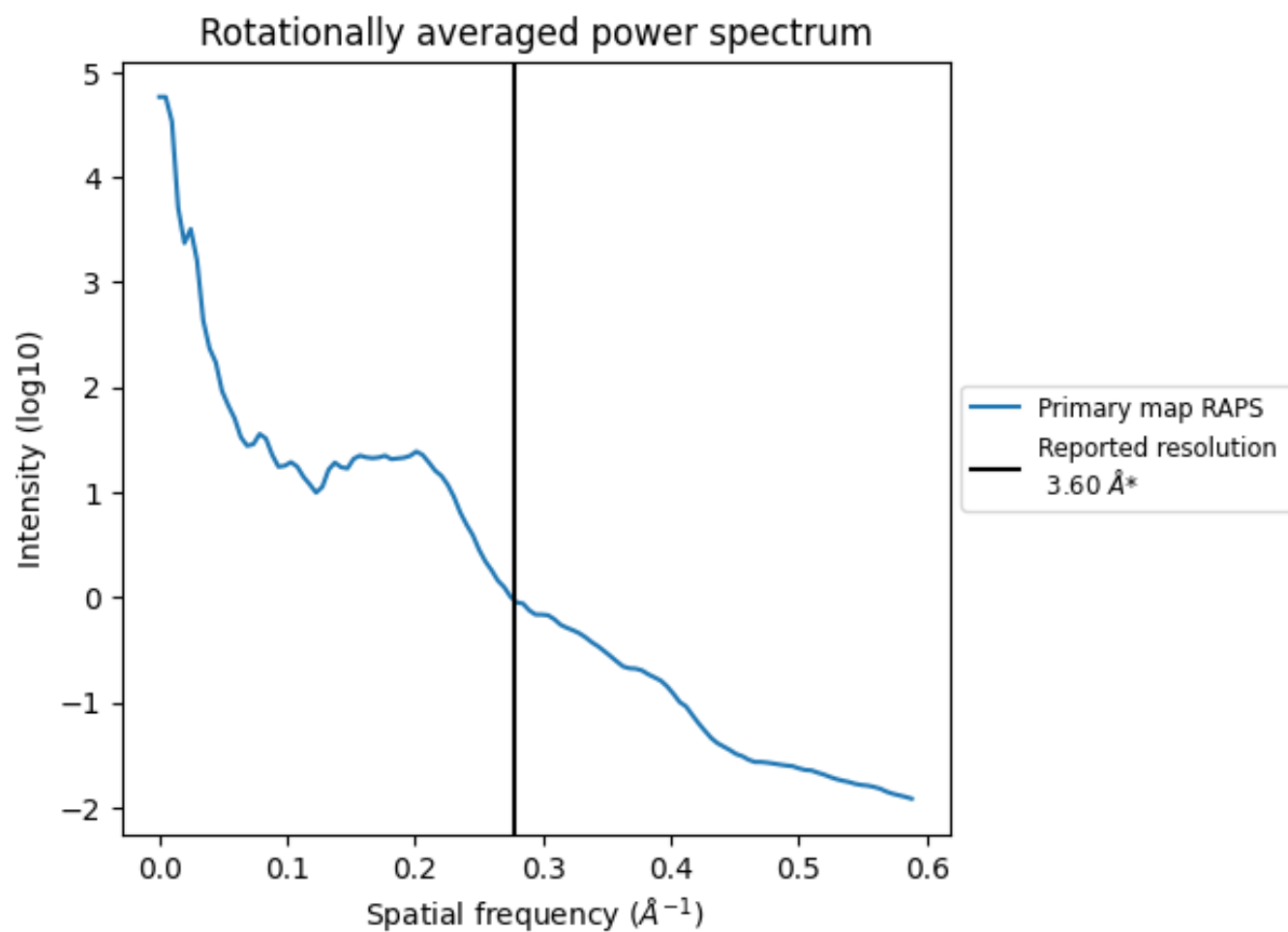
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 131 nm^3 ; this corresponds to an approximate mass of 119 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 ⓘ

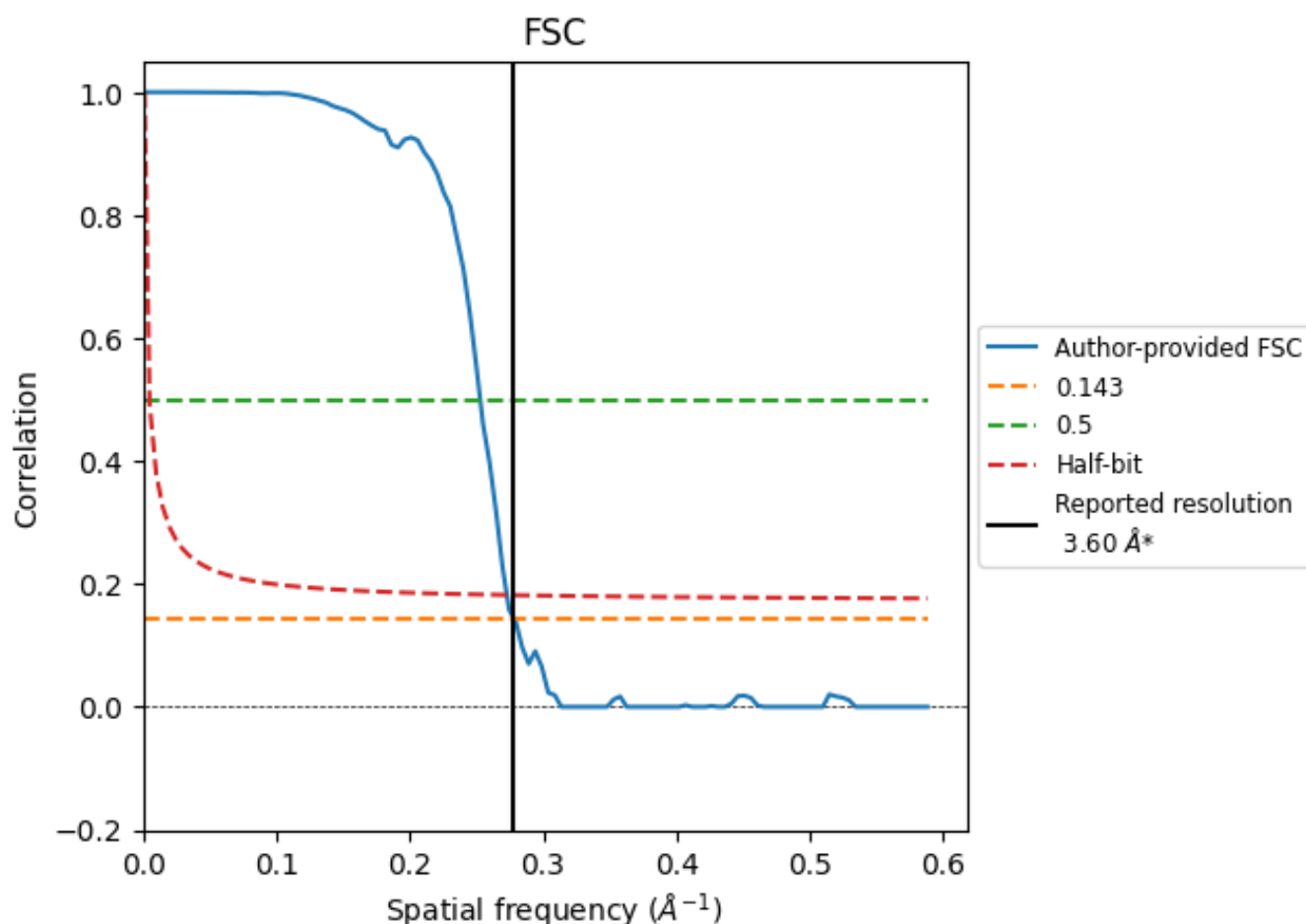


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

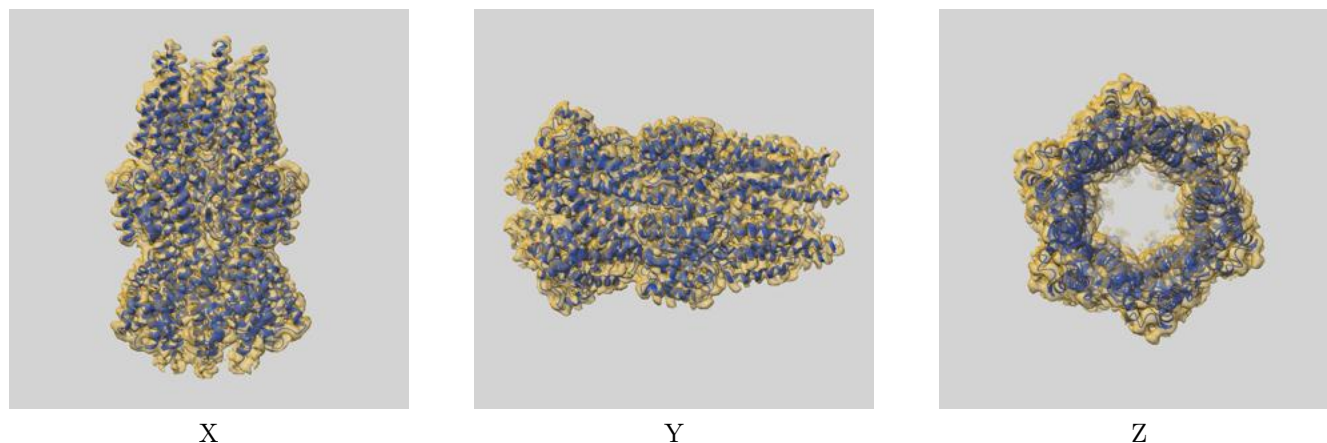
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.59	3.96	3.67
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

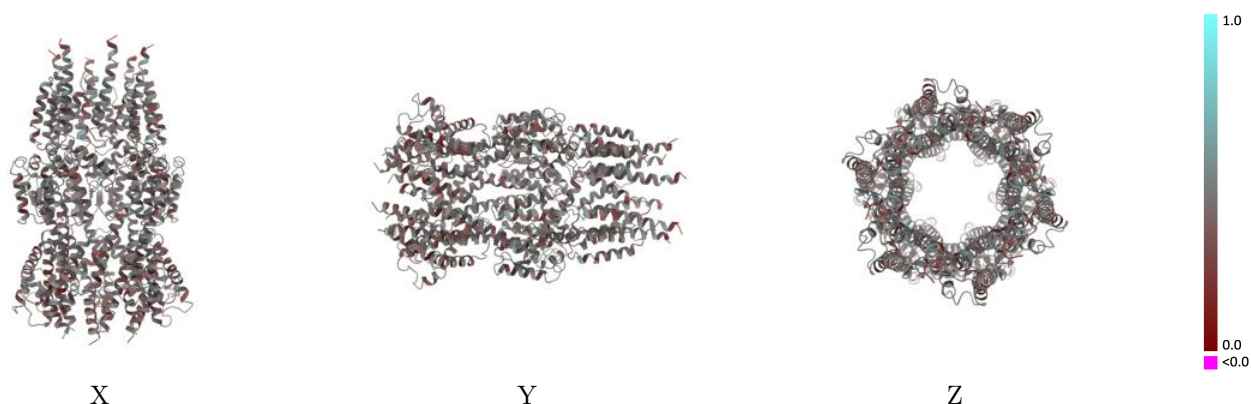
This section contains information regarding the fit between EMDB map EMD-10911 and PDB model 6YSZ. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



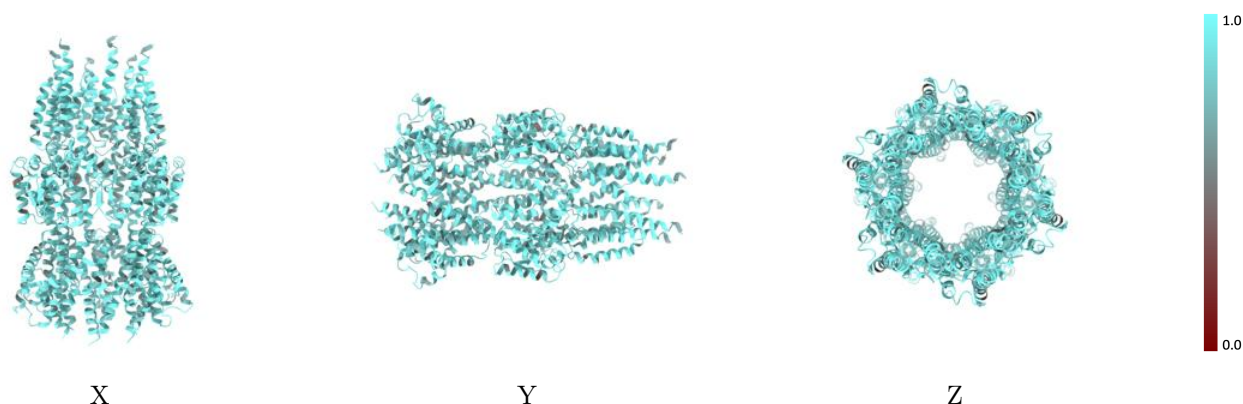
The images above show the 3D surface view of the map at the recommended contour level 0.0114 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



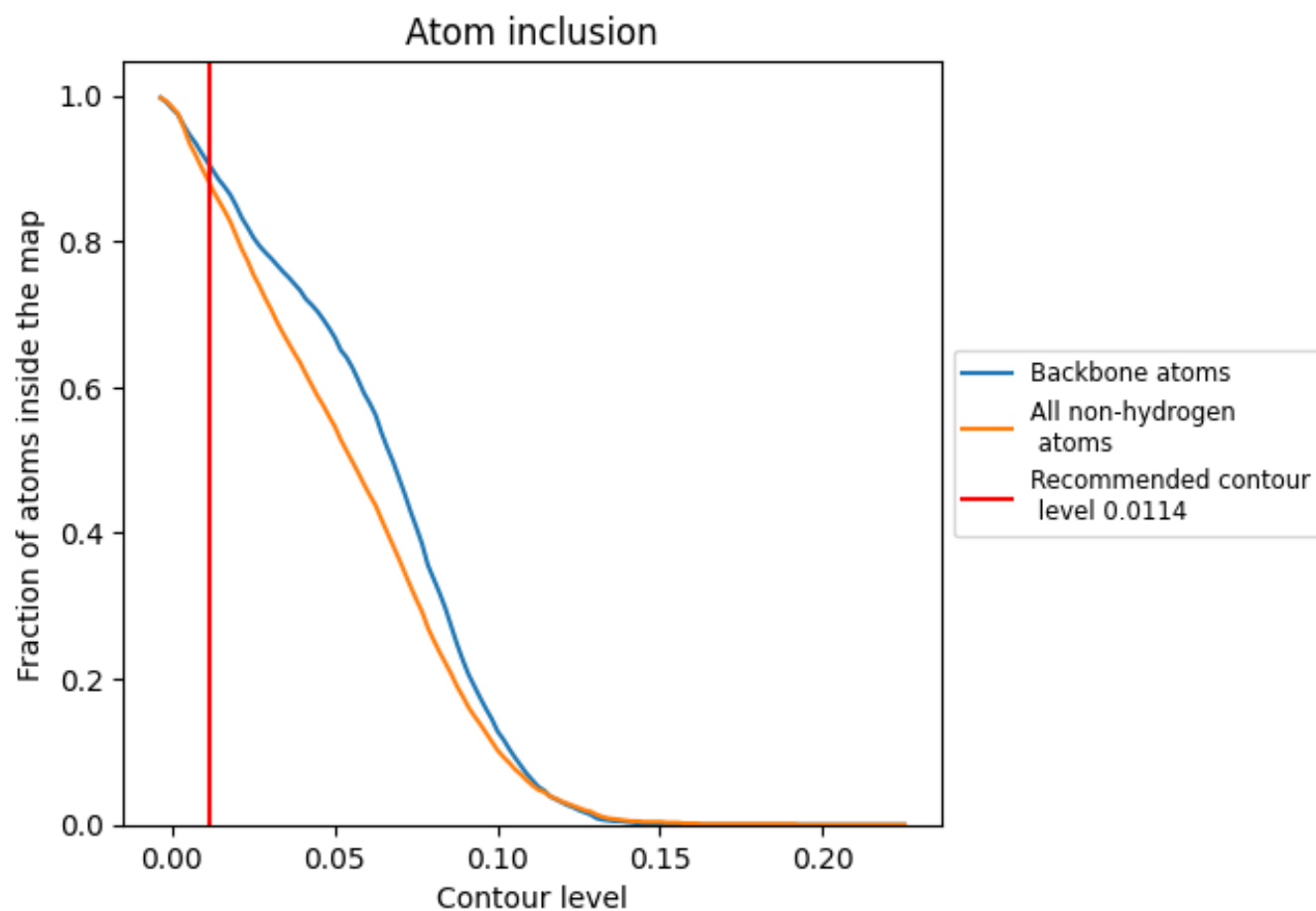
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0114).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 88% 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 (0.0114) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8810	0.4340
A	0.8830	0.4390
B	0.8810	0.4340
C	0.8810	0.4320
D	0.8830	0.4360
E	0.8790	0.4310
F	0.8800	0.4320

1.0

0.0

<0.0