



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 09:44 AM UTC

PDB ID : 7Z4B / pdb_00007z4b
EMDB ID : EMD-14492
Title : Bacteriophage SU10 virion (C1)
Authors : Siborova, M.; Fuzik, T.; Prochazkova, M.; Novacek, J.; Plevka, P.
Deposited on : 2022-03-03
Resolution : 7.40 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 : **FAILED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
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 7.40 Å.

There are no overall percentile quality scores available for this entry.

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 284597 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 Major head protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AB	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AC	344	Total	C	N	O	S	0	0
			2663	1671	466	516	10		
1	AD	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AE	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	AF	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	AG	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AH	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AI	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AJ	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AK	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AL	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AM	344	Total	C	N	O	S	0	0
			2663	1671	466	516	10		
1	AN	344	Total	C	N	O	S	0	0
			2663	1671	466	516	10		
1	AO	344	Total	C	N	O	S	0	0
			2663	1671	466	516	10		
1	AP	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AQ	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	AR	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AS	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	AT	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	AU	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	AV	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	AW	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	AX	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	AY	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AZ	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BA	344	Total	C	N	O	S	0	0
			2663	1671	466	516	10		
1	BB	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BC	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	BD	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	BE	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BF	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BG	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BH	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BI	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BJ	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BK	344	Total	C	N	O	S	0	0
			2663	1671	466	516	10		
1	BL	344	Total	C	N	O	S	0	0
			2663	1671	466	516	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	BM	344	Total	C	N	O	S	0	0
			2663	1671	466	516	10		
1	BN	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BO	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BP	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BQ	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	BR	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	BS	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	BT	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	BU	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	BV	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	BW	345	Total	C	N	O	S	0	0
			2672	1676	467	519	10		
1	BX	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	BY	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BZ	345	Total	C	N	O	S	0	0
			2670	1675	467	518	10		
1	CA	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	CB	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	CC	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	CD	343	Total	C	N	O	S	0	0
			2657	1668	465	514	10		
1	CE	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	CF	342	Total	C	N	O	S	0	0
			2644	1656	464	514	10		
1	CG	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	CH	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	CI	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	CJ	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	CK	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	CL	343	Total	C	N	O	S	0	0
			2654	1665	464	515	10		
1	CM	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	CN	342	Total	C	N	O	S	0	0
			2644	1656	464	514	10		
1	CO	341	Total	C	N	O	S	0	0
			2637	1651	463	513	10		
1	CP	345	Total	C	N	O	S	0	0
			2668	1674	466	518	10		
1	CQ	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	CR	345	Total	C	N	O	S	0	0
			2670	1675	467	518	10		
1	CS	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	CT	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	CU	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	CV	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	CW	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	CX	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	CY	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	CZ	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	DA	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	DB	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	DC	345	Total	C	N	O	S	0	0
			2670	1675	467	518	10		
1	DD	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	DE	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	DF	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	DG	343	Total	C	N	O	S	0	0
			2657	1668	465	514	10		
1	DH	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	DI	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	DJ	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	DK	343	Total	C	N	O	S	0	0
			2654	1665	464	515	10		
1	DL	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	DM	345	Total	C	N	O	S	0	0
			2668	1674	466	518	10		
1	DN	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	DO	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	DP	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	DQ	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		

- Molecule 2 is a protein called Putative structural protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	DR	263	Total	C	N	O	S	0	0
			1420	809	289	317	5		
2	DS	263	Total	C	N	O	S	0	0
			1424	812	289	317	6		
2	DT	263	Total	C	N	O	S	0	0
			1424	812	289	317	6		

- Molecule 3 is a protein called Adaptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	DU	222	Total	C	N	O	S	0	0
			1813	1171	292	345	5		
3	DV	222	Total	C	N	O	S	0	0
			1813	1171	292	345	5		

- Molecule 4 is a protein called Surface protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	DW	910	Total	C	N	O	S	0	0
			7063	4465	1178	1404	16		

- Molecule 5 is a protein called Putative tail fiber.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	DX	87	Total	C	N	O	S	0	0
			683	430	112	139	2		
5	DY	80	Total	C	N	O	S	0	0
			628	397	102	127	2		
5	DZ	68	Total	C	N	O	S	0	0
			545	347	87	109	2		

- Molecule 6 is a protein called Putative tail tip fiber protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	EA	322	Total	C	N	O		0	0
			1289	644	322	323			
6	EB	322	Total	C	N	O		0	0
			1289	644	322	323			
6	EC	322	Total	C	N	O		0	0
			1289	644	322	323			

- Molecule 7 is a protein called Portal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	ED	604	Total	C	N	O	S	0	0
			4838	3038	835	942	23		
7	EE	604	Total	C	N	O	S	0	0
			4838	3038	835	942	23		

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	9418	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
5	DY	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	DY	81:LYS	C	82:ASP	N	3.02

5 Map visualisation

This section contains visualisations of the EMDB entry EMD-14492. 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.

5.1 Orthogonal projections

This section was not generated.

5.2 Central slices

This section was not generated.

5.3 Largest variance slices

This section was not generated.

5.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

5.5 Orthogonal surface views

This section was not generated.

5.6 Mask visualisation

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

6 Map analysis ⓘ

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

6.1 Map-value distribution ⓘ

This section was not generated.

6.2 Volume estimate versus contour level ⓘ

This section was not generated.

6.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

7 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

8 Map-model fit

This section was not generated.