



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 11:55 AM UTC

PDB ID : 1FOQ / pdb_00001foq
Title : PENTAMERIC MODEL OF THE BACTERIOPHAGE PHI29 PROHEAD
RNA
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mann, M.G.
Deposited on : 2000-08-28
Resolution : 20.00 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB/EMDB 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:

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

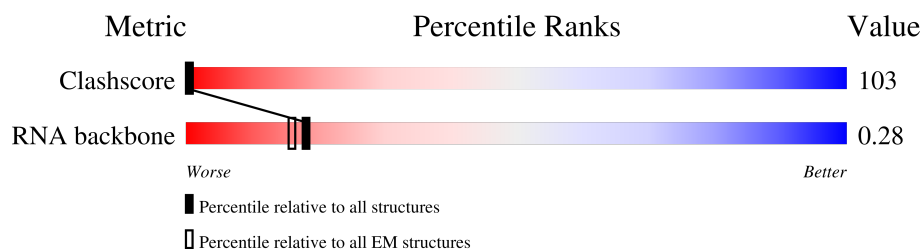
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 20.00 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)
Clashscore	229148	23984
RNA backbone	8273	3508

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	A	120	
1	B	120	
1	C	120	
1	D	120	
1	E	120	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 12095 atoms, of which 545 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.

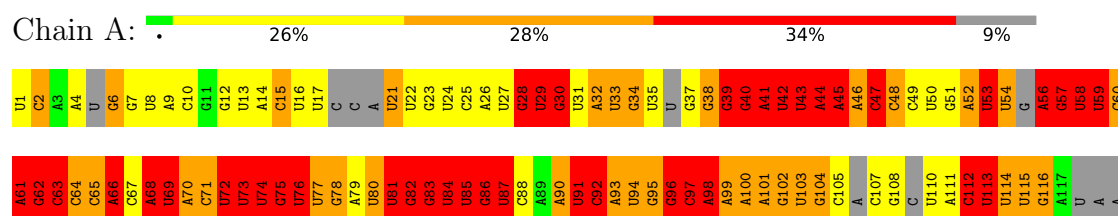
- Molecule 1 is a RNA chain called BACTERIOPHAGE PHI29 PROHEAD RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	109	Total	C	H	N	O	P	0	0
			2419	1033	109	393	775	109		
1	B	109	Total	C	H	N	O	P	0	0
			2419	1033	109	393	775	109		
1	C	109	Total	C	H	N	O	P	0	0
			2419	1033	109	393	775	109		
1	D	109	Total	C	H	N	O	P	0	0
			2419	1033	109	393	775	109		
1	E	109	Total	C	H	N	O	P	0	0
			2419	1033	109	393	775	109		

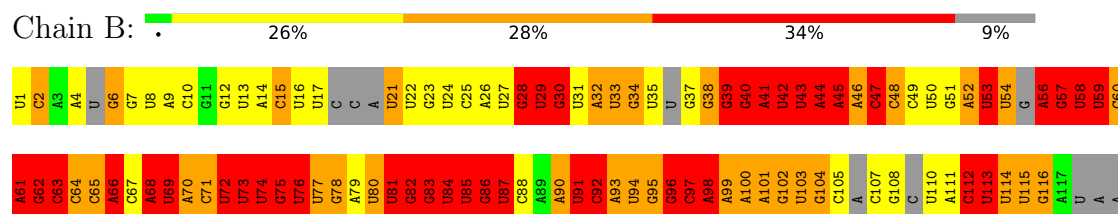
3 Residue-property plots [i](#)

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

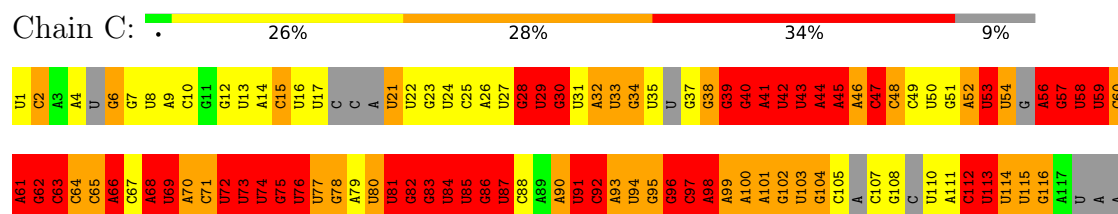
- Molecule 1: BACTERIOPHAGE PHI29 PROHEAD RNA



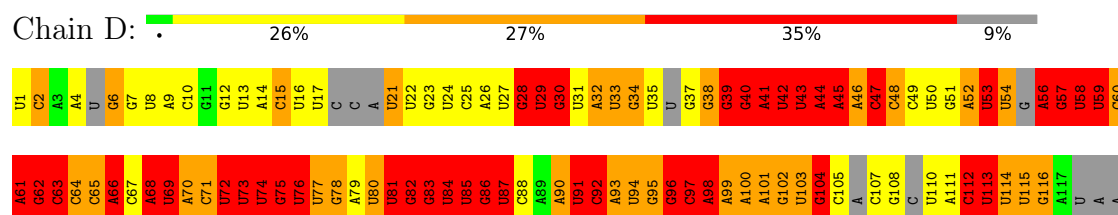
- Molecule 1: BACTERIOPHAGE PHI29 PROHEAD RNA



- Molecule 1: BACTERIOPHAGE PHI29 PROHEAD RNA



- Molecule 1: BACTERIOPHAGE PHI29 PROHEAD RNA



- Molecule 1: BACTERIOPHAGE PHI29 PROHEAD RNA



U1	C2	A3	A4	U	G6	G7	U8	A9	C10	G11	G12	U13	A14	C15	U16	U17	C	C	A	U21	U22	G23	U24	C25	A26	U27	G28	U29	G30	U31	A32	U33	G34	U35	U	G37	G38	G39	G40	A41	U42	U43	A44	A45	A46	C47	C48	C49	U50	G51	A52	U53	U54	G	A56	G57	U58	U59	C60
A61	G62	C63	C64	C65	A66	C67	A68	U69	A70	C71	U72	U73	U74	G75	U76	U77	G78	A79	U80	U81	G82	G83	U84	U85	G86	U87	C88	A89	A90	U91	C92	A93	U94	G95	G96	C97	G98	A99	A100	A101	G102	U103	G104	C105	A	C107	G108	C	U110	A111	C112	U113	U114	U115	G116	A117	U	A	A

4 Data and refinement statistics

Xtrriage (Phenix) and EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	1.00Å 1.00Å 1.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 20.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-20.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	unknown	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	12095	wwPDB-VP
Average B, all atoms (Å ²)	0.0	wwPDB-VP

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	3.48	71/2567 (2.8%)	3.30	215/3966 (5.4%)
1	B	3.48	71/2567 (2.8%)	3.30	216/3966 (5.4%)
1	C	3.48	71/2567 (2.8%)	3.30	216/3966 (5.4%)
1	D	3.48	71/2567 (2.8%)	3.30	215/3966 (5.4%)
1	E	3.48	71/2567 (2.8%)	3.30	215/3966 (5.4%)
All	All	3.48	355/12835 (2.8%)	3.30	1077/19830 (5.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	1
1	B	1	1
1	C	1	1
1	D	1	1
1	E	1	1
All	All	5	5

The worst 5 of 355 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	44	A	O3'-P	39.51	2.20	1.61
1	C	44	A	O3'-P	39.50	2.20	1.61
1	A	44	A	O3'-P	39.49	2.20	1.61
1	E	44	A	O3'-P	39.48	2.20	1.61
1	D	44	A	O3'-P	39.45	2.20	1.61

The worst 5 of 1077 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	41	A	O3'-P-O5'	41.75	166.62	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	41	A	O3'-P-O5'	41.73	166.60	104.00
1	A	41	A	O3'-P-O5'	41.73	166.59	104.00
1	C	41	A	O3'-P-O5'	41.71	166.56	104.00
1	E	41	A	O3'-P-O5'	41.70	166.55	104.00

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	40	G	C3'
1	B	40	G	C3'
1	C	40	G	C3'
1	D	40	G	C3'
1	E	40	G	C3'

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	87	U	Sidechain
1	B	87	U	Sidechain
1	C	87	U	Sidechain
1	D	87	U	Sidechain
1	E	87	U	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2310	109	1181	364	0
1	B	2310	109	1183	372	0
1	C	2310	109	1182	367	0
1	D	2310	109	1182	367	0
1	E	2310	109	1181	367	0
All	All	11550	545	5909	1784	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 103.

The worst 5 of 1784 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:A:29:U:C6	1:A:30:G:H4'	1.31	1.66
1:B:29:U:C6	1:B:30:G:H4'	1.31	1.66
1:D:29:U:C6	1:D:30:G:H4'	1.31	1.66
1:C:29:U:C6	1:C:30:G:H4'	1.31	1.65
1:C:28:G:H4'	1:C:29:U:C5'	1.22	1.62

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	108/120 (90%)	53 (49%)	12 (11%)
1	B	108/120 (90%)	53 (49%)	14 (12%)
1	C	108/120 (90%)	53 (49%)	14 (12%)
1	D	108/120 (90%)	53 (49%)	14 (12%)
1	E	108/120 (90%)	53 (49%)	14 (12%)
All	All	540/600 (90%)	265 (49%)	68 (12%)

5 of 265 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	C
1	A	6	G
1	A	21	U
1	A	29	U
1	A	30	G

5 of 68 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	E	41	A
1	E	58	U
1	E	91	U
1	B	103	U
1	B	91	U

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	53
1	B	53
1	C	53
1	D	53
1	E	53

The worst 5 of 265 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	51:G	O3'	52:A	P	3.32
1	B	51:G	O3'	52:A	P	3.32
1	C	51:G	O3'	52:A	P	3.32
1	D	51:G	O3'	52:A	P	3.32

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	51:G	O3'	52:A	P	3.32