



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:23 PM UTC

PDB ID : 3KMQ / pdb_00003kmq
Title : G62S mutant of foot-and-mouth disease virus RNA-polymerase in complex with a template- primer RNA, tetragonal structure
Authors : Ferrer-Orta, C.; Verdaguer, N.; Perez-Luque, R.
Deposited on : 2009-11-11
Resolution : 2.11 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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/XrayValidationReportHelp>

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
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

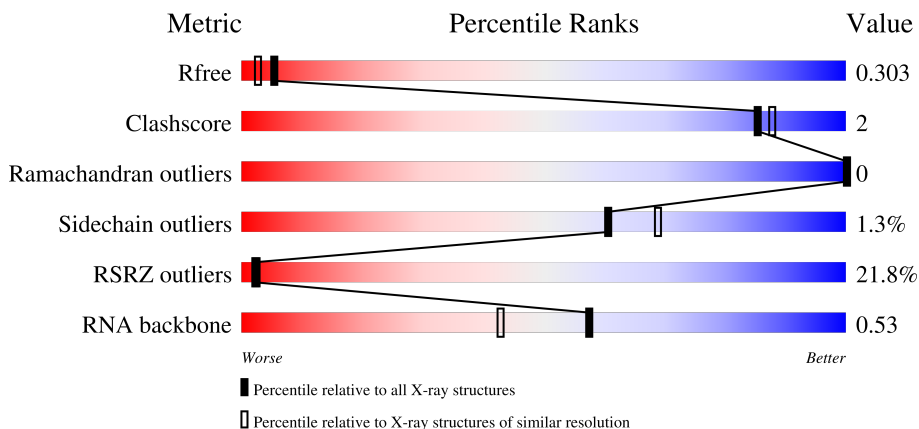
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.11 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	8290 (2.14-2.10)
Clashscore	190562	8817 (2.14-2.10)
Ramachandran outliers	187476	8738 (2.14-2.10)
Sidechain outliers	187428	8739 (2.14-2.10)
RSRZ outliers	180081	8294 (2.14-2.10)
RNA backbone	3983	1037 (2.46-1.78)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	476	21% 94% 6%
2	B	5	100% 40% 20% 20% 20%
3	C	5	40% 80% 20%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4065 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 3D polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	476	Total	C	N	O	S	0	0	0
			3758	2388	650	699	21			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	62	SER	GLY	engineered mutation	UNP Q9QCE3
A	471	ALA	-	expression tag	UNP Q9QCE3
A	472	ALA	-	expression tag	UNP Q9QCE3
A	473	LEU	-	expression tag	UNP Q9QCE3
A	474	GLU	-	expression tag	UNP Q9QCE3
A	475	HIS	-	expression tag	UNP Q9QCE3
A	476	HIS	-	expression tag	UNP Q9QCE3

- Molecule 2 is a RNA chain called RNA (5'-R(P*GP*GP*GP*CP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	5	Total	C	N	O	P	0	0	0
			109	48	21	35	5			

- Molecule 3 is a RNA chain called RNA (5'-R(*GP*GP*CP*CP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	5	Total	C	N	O	P	0	0	0
			103	47	19	33	4			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	93	Total	O	0	0
			93	93		

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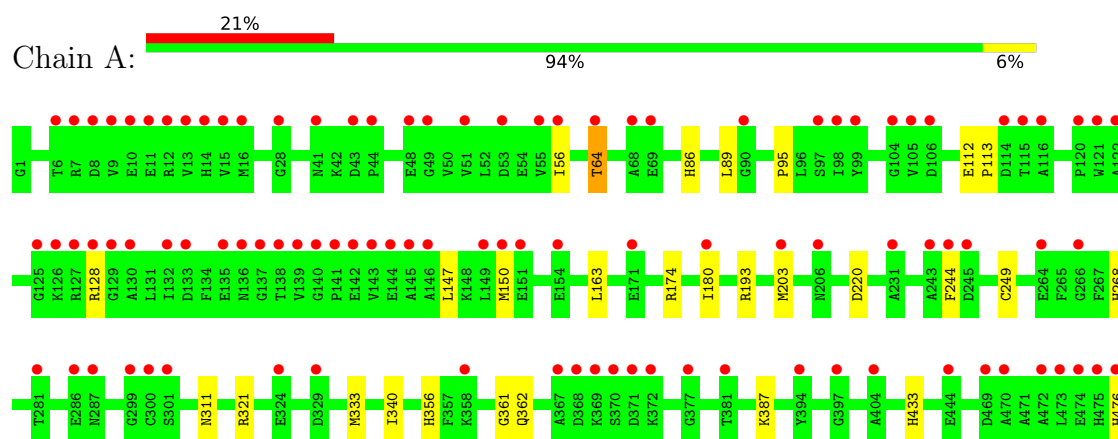
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	O	0	0
			1	1		
4	C	1	Total	O	0	0
			1	1		

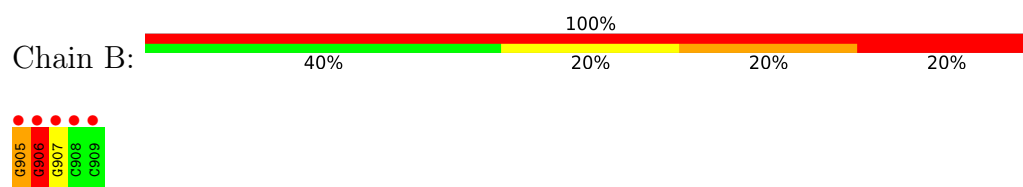
3 Residue-property plots [i](#)

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 and electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

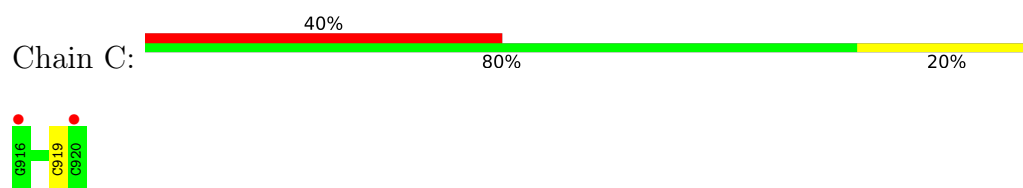
- Molecule 1: 3D polymerase



- Molecule 2: RNA (5'-R(P*GP*GP*GP*CP*C)-3')



- Molecule 3: RNA (5'-R(*GP*GP*CP*CP*C)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	93.66Å 93.66Å 121.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.11 20.00 – 2.11	Depositor EDS
% Data completeness (in resolution range)	98.8 (20.00-2.11) 98.8 (20.00-2.11)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.240 , 0.267 0.272 , 0.303	Depositor DCC
R_{free} test set	1584 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	43.3	Xtriage
Anisotropy	0.007	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 35.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4065	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.70% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	A	0.43	0/3849	0.74	0/5212
2	B	0.44	0/121	1.09	1/187 (0.5%)
3	C	0.51	0/114	0.69	0/176
All	All	0.43	0/4084	0.75	1/5575 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	906	G	C4'-C3'-C2'	-5.62	96.98	102.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	3758	0	3674	16	0
2	B	109	0	56	3	0
3	C	103	0	57	1	0
4	A	93	0	0	1	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
All	All	4065	0	3787	17	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 2.

All (17) 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:333:MET:HE3	1:A:340:ILE:HD13	1.72	0.71
1:A:193:ARG:NH1	2:B:906:G:OP2	2.33	0.60
1:A:95:PRO:HG3	1:A:268:HIS:HB2	1.85	0.59
1:A:333:MET:HE3	1:A:340:ILE:CD1	2.33	0.58
1:A:147:LEU:HA	1:A:150:MET:HE3	1.89	0.54
1:A:387:LYS:HD3	3:C:919:C:H5''	1.89	0.53
1:A:220:ASP:OD1	1:A:433:HIS:HE1	1.93	0.51
1:A:244:PHE:HA	1:A:362:GLN:HE22	1.73	0.51
1:A:86:HIS:HD2	4:A:491:HOH:O	1.94	0.51
1:A:89:LEU:HD11	1:A:203:MET:HG3	1.94	0.49
1:A:321:ARG:HH11	1:A:356:HIS:HD2	1.62	0.46
1:A:112:GLU:HA	1:A:113:PRO:HD3	1.83	0.45
1:A:128:ARG:HH12	2:B:905:G:P	2.40	0.45
1:A:64:THR:HG21	1:A:361:GLY:HA3	2.02	0.41
1:A:64:THR:HG23	1:A:249:CYS:HB3	2.02	0.41
1:A:56:ILE:HD11	1:A:163:LEU:HD21	2.03	0.41
2:B:906:G:H2'	2:B:907:G:C8	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	474/476 (100%)	466 (98%)	8 (2%)	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 X-ray entries followed by that with respect to entries of similar resolution.

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	399/400 (100%)	394 (99%)	5 (1%)	61	69

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	64	THR
1	A	174	ARG
1	A	180	ILE
1	A	311	ASN
1	A	476	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	HIS
1	A	86	HIS
1	A	124	GLN
1	A	160	GLN
1	A	280	ASN
1	A	287	ASN
1	A	311	ASN
1	A	356	HIS
1	A	362	GLN
1	A	378	HIS
1	A	433	HIS
1	A	464	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	5/5 (100%)	1 (20%)	2 (40%)
3	C	4/5 (80%)	0	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	9/10 (90%)	1 (11%)	2 (22%)

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	906	G

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	905	G
2	B	906	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	476/476 (100%)	1.27	99 (20%) 2 3	36, 46, 59, 62	0
2	B	5/5 (100%)	3.90	5 (100%) 0 0	55, 56, 56, 56	5 (100%)
3	C	5/5 (100%)	1.78	2 (40%) 1 1	43, 43, 44, 44	5 (100%)
All	All	486/486 (100%)	1.31	106 (21%) 2 2	36, 46, 59, 62	10 (2%)

All (106) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	15	VAL	5.8
1	A	136	ASN	5.7
1	A	14	HIS	5.6
2	B	905	G	5.3
1	A	301	SER	5.3
1	A	473	LEU	5.0
1	A	16	MET	5.0
1	A	476	HIS	4.5
1	A	53	ASP	4.4
1	A	287	ASN	4.4
1	A	144	GLU	4.2
1	A	370	SER	4.1
1	A	145	ALA	4.1
1	A	104	GLY	4.1
1	A	48	GLU	4.0
1	A	116	ALA	4.0
2	B	909	C	3.9
1	A	41	ASN	3.8
1	A	49	GLY	3.8
1	A	299	GLY	3.8
1	A	474	GLU	3.7
2	B	907	G	3.7
1	A	106	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	138	THR	3.7
1	A	149	LEU	3.6
1	A	146	ALA	3.6
2	B	906	G	3.6
1	A	329	ASP	3.5
1	A	130	ALA	3.5
1	A	120	PRO	3.5
1	A	140	GLY	3.5
1	A	150	MET	3.5
1	A	99	TYR	3.3
1	A	394	TYR	3.2
1	A	97	SER	3.2
1	A	367	ALA	3.2
1	A	8	ASP	3.2
1	A	300	CYS	3.2
1	A	142	GLU	3.1
1	A	56	ILE	3.1
1	A	139	VAL	3.1
2	B	908	C	3.0
1	A	397	GLY	3.0
1	A	372	LYS	2.9
1	A	11	GLU	2.9
1	A	469	ASP	2.9
1	A	472	ALA	2.9
1	A	129	GLY	2.8
1	A	132	ILE	2.8
1	A	180	ILE	2.8
1	A	369	LYS	2.8
1	A	231	ALA	2.8
1	A	143	VAL	2.8
1	A	122	ALA	2.8
1	A	9	VAL	2.8
1	A	151	GLU	2.7
1	A	98	ILE	2.7
1	A	137	GLY	2.7
1	A	133	ASP	2.6
1	A	245	ASP	2.6
1	A	12	ARG	2.6
1	A	121	TRP	2.6
1	A	154	GLU	2.6
1	A	135	GLU	2.6
1	A	6	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	404	ALA	2.5
1	A	28	GLY	2.5
1	A	127	ARG	2.5
1	A	371	ASP	2.5
1	A	266	GLY	2.5
1	A	368	ASP	2.4
1	A	470	ALA	2.4
1	A	64	THR	2.4
1	A	7	ARG	2.4
1	A	286	GLU	2.4
1	A	105	VAL	2.4
1	A	44	PRO	2.4
1	A	171	GLU	2.3
1	A	203	MET	2.3
1	A	324	GLU	2.3
3	C	916	G	2.3
1	A	55	VAL	2.2
1	A	43	ASP	2.2
1	A	114	ASP	2.2
1	A	475	HIS	2.2
1	A	206	ASN	2.2
1	A	243	ALA	2.2
1	A	126	LYS	2.2
1	A	358	LYS	2.2
1	A	115	THR	2.2
1	A	381	THR	2.1
1	A	10	GLU	2.1
1	A	264	GLU	2.1
1	A	444	GLU	2.1
1	A	141	PRO	2.1
1	A	244	PHE	2.1
1	A	51	VAL	2.1
1	A	128	ARG	2.1
1	A	377	GLY	2.1
1	A	13	VAL	2.1
1	A	68	ALA	2.1
1	A	281	THR	2.0
1	A	125	GLY	2.0
1	A	69	GLU	2.0
3	C	920	C	2.0
1	A	90	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.