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PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2024 – 02:53 PM EST

PDB ID	:	3KMS
Title	:	G62S mutant of foot-and-mouth disease virus RNA-polymerase in complex with a template- primer RNA trigonal structure
Authors	:	Ferrer-Orta, C.; Verdaguer, N.; Perez-Luque, R.
Deposited on	:	2009-11-11
Resolution	:	2.20 Å(reported)

The following versions of software and data (see references ⓘ) were used in the production of this report:

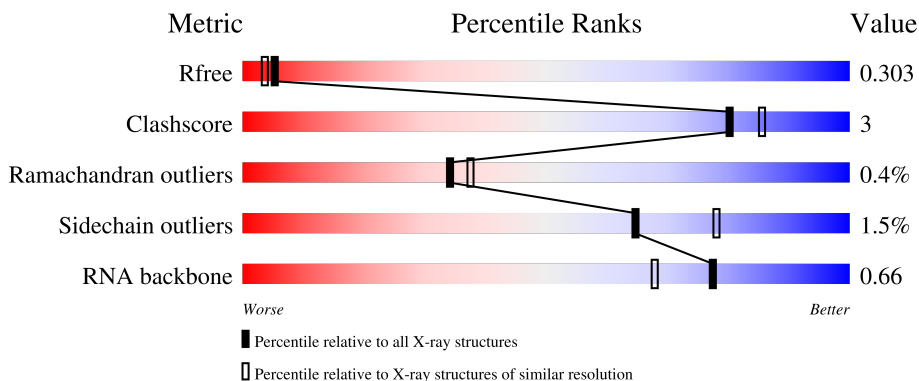|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.20 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	Percentile Ranks	Value
Rfree		0.303
Clashscore		3
Ramachandran outliers		0.4%
Sidechain outliers		1.5%
RNA backbone		0.66

Worse   *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RNA backbone	3102	1032 (2.60-1.80)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	476	93% 7%
2	B	7	71% 29%
3	C	5	80% 20%

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2 Entry composition ⓘ

There are 5 unique types of molecules in this entry. The entry contains 4051 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
			3731	2374	643	693	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(*AP*UP*GP*GP*GP*CP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	7	Total	C	N	O	P	62	0	0
			148	67	28	47	6			

- 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 MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		

- Molecule 5 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	59	Total 59	O 59	0	0
5	B	5	Total 5	O 5	0	0
5	C	4	Total 4	O 4	0	0

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.
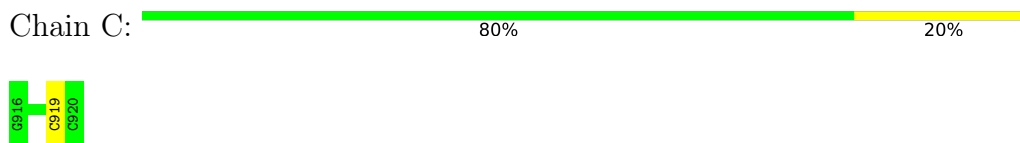
• Molecule 1: 3D polymerase

Chain A:
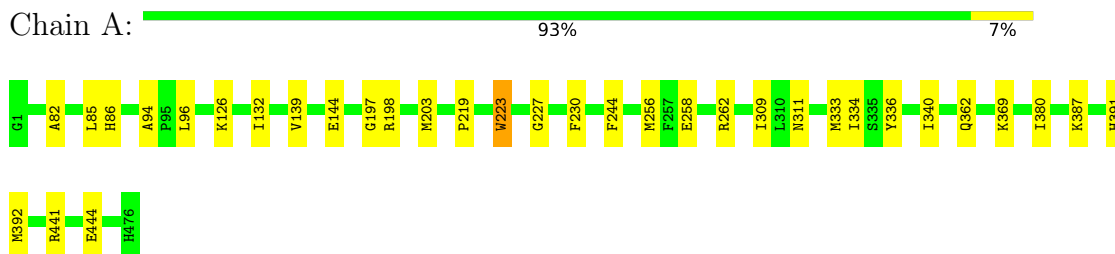
• Molecule 2: RNA (5'-R(*AP*UP*GP*GP*GP*CP*C)-3')

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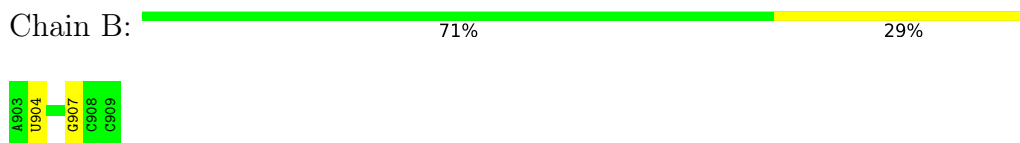
• Molecule 3: RNA (5'-R(*GP*GP*CP*CP*C)-3')

Chain C:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	93.95Å 93.95Å 100.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.40 – 2.20 29.39 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.0 (29.40-2.20) 99.0 (29.39-2.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	2.51 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.236 , 0.266 0.285 , 0.303	Depositor DCC
R_{free} test set	1320 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	45.3	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 41.5	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.033 for -h,-k,l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	4051	wwPDB-VP
Average B, all atoms (Å^2)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5   Model quality ⓘ

5.1   Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	0.33	0/3822	0.46	0/5180
2	B	0.59	0/165	1.00	0/256
3	C	0.60	0/114	0.97	0/176
All	All	0.35	0/4101	0.52	0/5612

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	3731	0	3631	21	0
2	B	148	0	78	0	0
3	C	103	0	57	1	0
4	A	1	0	0	0	0
5	A	59	0	0	3	0
5	B	5	0	0	0	0
5	C	4	0	0	0	0
All	All	4051	0	3766	21	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 3.

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All (21) 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:82:ALA:O	5:A:599:HOH:O	1.59	1.16
1:A:256:MET:HE2	1:A:309:ILE:HG21	1.49	0.94
1:A:230:PHE:HB2	1:A:380:ILE:HD12	1.49	0.92
1:A:387:LYS:HD3	3:C:919:C:H5"	1.77	0.67
1:A:94:ALA:O	1:A:198:ARG:HD2	2.03	0.58
1:A:227:GLY:HA2	1:A:380:ILE:HD13	1.86	0.57
1:A:256:MET:CE	1:A:309:ILE:HG21	2.30	0.56
1:A:441:ARG:O	1:A:444:GLU:HG2	2.08	0.53
1:A:256:MET:HE2	1:A:309:ILE:CG2	2.31	0.53
1:A:244:PHE:HA	1:A:362:GLN:HE22	1.73	0.53
1:A:85:LEU:HD11	1:A:203:MET:SD	2.52	0.49
1:A:132:ILE:HG12	1:A:139:VAL:HG12	1.96	0.47
1:A:86:HIS:HD2	5:A:525:HOH:O	1.98	0.47
1:A:230:PHE:CB	1:A:380:ILE:HD12	2.35	0.47
1:A:82:ALA:C	5:A:599:HOH:O	2.33	0.44
1:A:333:MET:CE	1:A:340:ILE:HD13	2.48	0.44
1:A:333:MET:HE1	1:A:340:ILE:HD13	1.99	0.43
1:A:96:LEU:HD22	1:A:197:GLY:HA3	2.00	0.42
1:A:258:GLU:O	1:A:262:ARG:HG2	2.19	0.42
1:A:219:PRO:O	1:A:223:TRP:HB2	2.19	0.42
1:A:139:VAL:HG23	1:A:144:GLU:HG3	2.03	0.41

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%)	461 (97%)	11 (2%)	2 (0%)	34	37

All (2) Ramachandran outliers are listed below:

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Mol	Chain	Res	Type
1	A	126	LYS
1	A	369	LYS

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 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	393/400 (98%)	387 (98%)	6 (2%)	65	78

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	223	TRP
1	A	311	ASN
1	A	334	ILE
1	A	336	TYR
1	A	391	HIS
1	A	392	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	86	HIS
1	A	160	GLN
1	A	280	ASN
1	A	311	ASN
1	A	322	HIS
1	A	356	HIS
1	A	362	GLN
1	A	447	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	6/7 (85%)	2 (33%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	C	4/5 (80%)	0	0
All	All	10/12 (83%)	2 (20%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	904	U
2	B	907	G

There are no RNA pucker outliers to report.

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 ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.