

wwPDB X-ray Structure Validation Summary Report (i)

Oct 25, 2022 – 05:25 pm BST

PDB ID : 7R0K

Title: Crystal structure of Polymerase I from phage G20c

Authors: Welin, M.; Svensson, A.; Hakansson, M.; Al-Karadaghi, S.; Linares-Pasten,

J.A.; Jasilionis, A.; Nordberg Karlsson, E.; Ahlqvist, J.

Deposited on : 2022-02-02

Resolution : 2.97 Å(reported)

This is a wwPDB X-ray Structure 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/XrayValidationReportHelp with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

MolProbity: 4.02b-467 Xtriage (Phenix): 1.13

EDS : 2.31.2

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0267$

CCP4 : 7.1.010 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

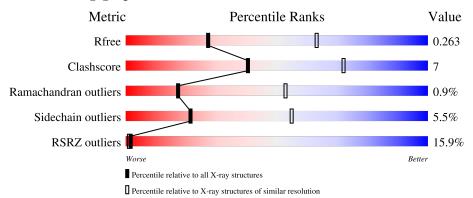
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\ DIFFRACTION$

The reported resolution of this entry is 2.97 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\AA)}) \end{array}$
R_{free}	130704	2754 (3.00-2.96)
Clashscore	141614	3103 (3.00-2.96)
Ramachandran outliers	138981	2993 (3.00-2.96)
Sidechain outliers	138945	2996 (3.00-2.96)
RSRZ outliers	127900	2644 (3.00-2.96)

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% 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	736	77%	18% • •
1	В	736	19% 73%	17% • 8%



2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 11067 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 DNA polymerase I.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	708	Total 5660	C 3626	N 962	O 1059	S 13	0	0	0
1	В	676	Total 5407	C 3459	N 922	O 1013	S 13	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

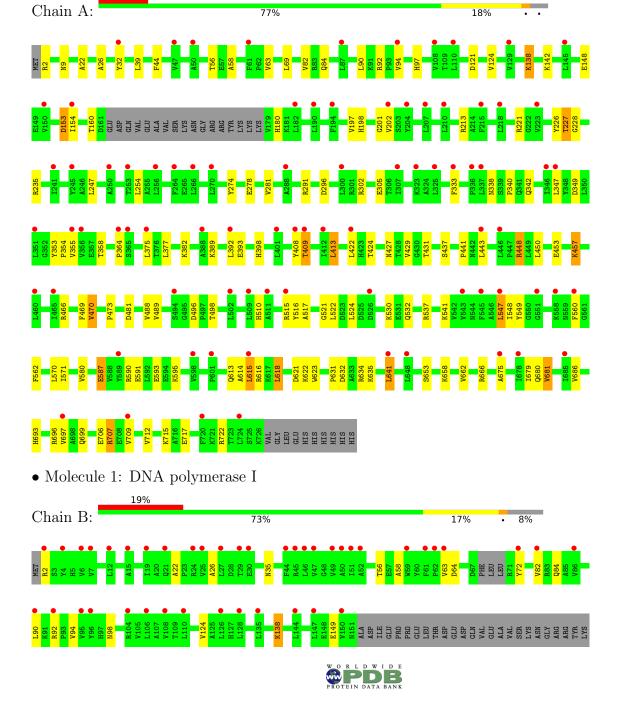
Chain	Residue	Modelled	Actual	Comment	Reference
A	729	LEU	-	expression tag	UNP A0A1L4BKI3
A	730	GLU	-	expression tag	UNP A0A1L4BKI3
A	731	HIS	-	expression tag	UNP A0A1L4BKI3
A	732	HIS	-	expression tag	UNP A0A1L4BKI3
A	733	HIS	-	expression tag	UNP A0A1L4BKI3
A	734	HIS	-	expression tag	UNP A0A1L4BKI3
A	735	HIS	-	expression tag	UNP A0A1L4BKI3
A	736	HIS	-	expression tag	UNP A0A1L4BKI3
В	729	LEU	-	expression tag	UNP A0A1L4BKI3
В	730	GLU	-	expression tag	UNP A0A1L4BKI3
В	731	HIS	-	expression tag	UNP A0A1L4BKI3
В	732	HIS	-	expression tag	UNP A0A1L4BKI3
В	733	HIS	-	expression tag	UNP A0A1L4BKI3
В	734	HIS	-	expression tag	UNP A0A1L4BKI3
В	735	HIS	-	expression tag	UNP A0A1L4BKI3
В	736	HIS	-	expression tag	UNP A0A1L4BKI3

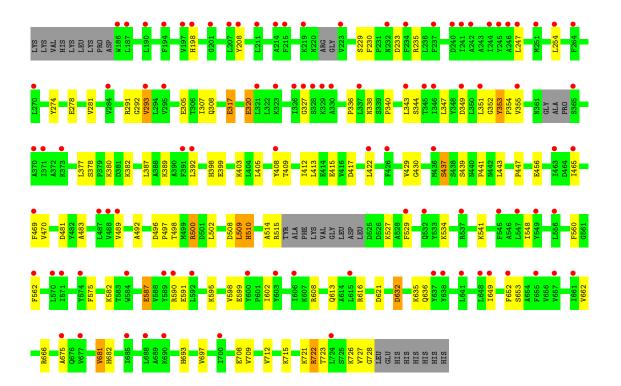


3 Residue-property plots (i)

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: DNA polymerase I







4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	309.77Å 98.01Å 77.61Å	Depositor
a, b, c, α , β , γ	90.00° 98.90° 90.00°	Depositor
Resolution (Å)	153.02 - 2.97	Depositor
resolution (A)	153.02 - 2.97	EDS
% Data completeness	68.9 (153.02-2.97)	Depositor
(in resolution range)	68.9 (153.02-2.97)	EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.59 (at 2.96Å)	Xtriage
Refinement program	BUSTER 2.11.8	Depositor
P.P.	0.216 , 0.260	Depositor
R, R_{free}	0.217 , 0.263	DCC
R_{free} test set	1564 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	107.0	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$ < L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11067	wwPDB-VP
Average B, all atoms (Å ²)	124.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.80% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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	0.47	0/5785	0.63	$2/7856 \ (0.0\%)$	
1	В	0.41	0/5520	0.59	0/7488	
All	All	0.44	0/11305	0.61	2/15344 (0.0%)	

There are no bond length outliers.

All (2) bond angle outliers are listed below:

	Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
	1	A	448	ARG	N-CA-C	-5.37	96.50	111.00
ĺ	1	A	470	VAL	N-CA-CB	-5.24	99.97	111.50

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	5660	0	5667	83	0
1	В	5407	0	5407	80	0
All	All	11067	0	11074	160	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 7.

The worst 5 of 160 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:B:447:PRO:HD2	1:B:465:ILE:HD13	1.58	0.83
1:A:489:VAL:HG21	1:A:653:SER:HB3	1.62	0.81
1:B:727:VAL:HG12	1:B:728:GLY:H	1.46	0.80
1:A:69:LEU:HD11	1:A:226:TYR:HB3	1.66	0.77
1:B:681:VAL:HG13	1:B:682:HIS:ND1	2.02	0.74

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 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	704/736 (96%)	656 (93%)	44 (6%)	4 (1%)	25 61
1	В	664/736 (90%)	616 (93%)	40 (6%)	8 (1%)	13 45
All	All	1368/1472 (93%)	1272 (93%)	84 (6%)	12 (1%)	17 53

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	615	LEU
1	В	327	GLY
1	В	514	ALA
1	A	228	GLY
1	В	509	LEU

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	Perce	ntiles
1	A	607/632 (96%)	574 (95%)	33 (5%)	22	55
1	В	580/632 (92%)	548 (94%)	32 (6%)	21	55
All	All	1187/1264 (94%)	1122 (94%)	65 (6%)	21	55

5 of 65 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	587	GLU
1	В	621	ASP
1	A	622	LYS
1	A	621	ASP
1	В	632	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	398	HIS
1	В	319	GLN
1	В	398	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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 monosaccharides 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 (i)

6.1 Protein, DNA and RNA chains (i)

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, 95^{th} 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 $>$	$\#\mathrm{RSRZ}{>}2$	1	$\mathrm{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	A	708/736 (96%)	0.90	82 (11%) 4	2	73, 106, 156, 165	0
1	В	676/736 (91%)	1.10	138 (20%) 1	0	92, 131, 190, 214	0
All	All	1384/1472 (94%)	1.00	220 (15%) 1	1	73, 118, 176, 214	0

The worst 5 of 220 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	194	PHE	7.4
1	В	7	VAL	6.8
1	В	245	TYR	6.7
1	В	27	LEU	6.3
1	В	190	LEU	6.1

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 monosaccharides 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.

