

wwPDB X-ray Structure Validation Summary Report (i)

Oct 31, 2022 – 01:17 pm GMT

PDB ID : 706V

Title: Crystal structure of the VEL1 VEL polymerising domain (R643A K645D

I664D mutant)

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Deposited on : 2021-04-12

Resolution : 2.50 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)

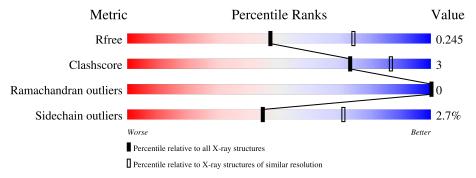
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.50 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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	77	82%	10%	8%
1	В	77	82%	9%	9%
1	С	77	77%	16%	8%
1	D	77	86%	5%	9%



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2308 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 VIN3-like protein 2.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	71	Total	С	N	Ο	S	0	0	0
1	A	71	577	366	96	112	3	0	0	
1	В	70	Total	С	N	О	S	0	1	0
1	Б	10	575	363	96	112	4	0	1	0
1	С	71	Total	С	N	О	S	0	0	0
1		7.1	578	365	96	114	3	0		
1	D	70	Total	С	N	О	S	0	0	0
1	ש	10	569	360	95	111	3	U	U	U

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	643	ALA	ARG	$\operatorname{conflict}$	UNP Q9SUM4
A	645	ASP	LYS	conflict	UNP Q9SUM4
A	664	ASP	ILE	$\operatorname{conflict}$	UNP Q9SUM4
В	643	ALA	ARG	$\operatorname{conflict}$	UNP Q9SUM4
В	645	ASP	LYS	$\operatorname{conflict}$	UNP Q9SUM4
В	664	ASP	ILE	$\operatorname{conflict}$	UNP Q9SUM4
С	643	ALA	ARG	$\operatorname{conflict}$	UNP Q9SUM4
С	645	ASP	LYS	$\operatorname{conflict}$	UNP Q9SUM4
С	664	ASP	ILE	$\operatorname{conflict}$	UNP Q9SUM4
D	643	ALA	ARG	$\operatorname{conflict}$	UNP Q9SUM4
D	645	ASP	LYS	$\operatorname{conflict}$	UNP Q9SUM4
D	664	ASP	ILE	conflict	UNP Q9SUM4

• Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	6	Total O 6 6	0	0
2	В	1	Total O 1 1	0	0

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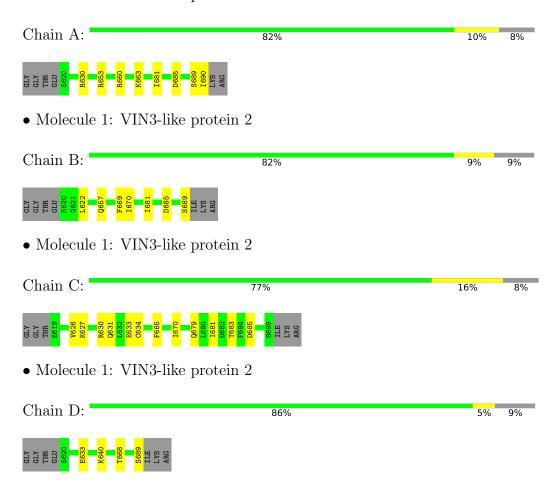
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	С	2	Total O 2 2	0	0



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: VIN3-like protein 2





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	52.07Å 58.05Å 119.99Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.04 - 2.50	Depositor
resolution (A)	29.03 - 2.50	EDS
% Data completeness	99.9 (29.04-2.50)	Depositor
(in resolution range)	100.0 (29.03-2.50)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.55 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
P. P.	0.214 , 0.241	Depositor
R, R_{free}	0.227 , 0.245	DCC
R_{free} test set	649 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	53.8	Xtriage
Anisotropy	0.378	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$ < L > = 0.49, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2308	wwPDB-VP
Average B, all atoms $(Å^2)$	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.89% 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	
IVIOI		RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	0.44	0/587	0.60	0/793
1	В	0.48	0/585	0.66	0/790
1	С	0.46	0/588	0.63	0/794
1	D	0.46	0/579	0.64	0/782
All	All	0.46	0/2339	0.63	0/3159

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 (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	577	0	561	7	0
1	В	575	0	554	3	0
1	С	578	0	556	6	0
1	D	569	0	550	3	0
2	A	6	0	0	1	0
2	В	1	0	0	0	0
2	С	2	0	0	0	0
All	All	2308	0	2221	15	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.

The worst 5 of 15 close contacts within the same asymmetric unit are listed below, sorted by their



clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:A:630:ARG:HD3	1:B:669:PHE:CE2	2.24	0.72
1:A:653:ARG:NH2	2:A:701:HOH:O	2.39	0.56
1:A:660:ARG:NH1	1:A:663:LYS:HD3	2.26	0.51
1:A:689:SER:C	1:A:690:ILE:HG13	2.31	0.51
1:C:627:LYS:O	1:C:631:GLN:HG3	2.12	0.48

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	Percen	$_{ m tiles}$
1	A	$69/77 \; (90\%)$	69 (100%)	0	0	100	100
1	В	$69/77 \; (90\%)$	69 (100%)	0	0	100	100
1	С	69/77 (90%)	69 (100%)	0	0	100	100
1	D	68/77 (88%)	68 (100%)	0	0	100	100
All	All	275/308~(89%)	275 (100%)	0	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	Perce	ntiles
1	A	$65/69 \ (94\%)$	65 (100%)	0	100	100
1	В	65/69~(94%)	62 (95%)	3 (5%)	27	50
1	С	65/69~(94%)	62 (95%)	3 (5%)	27	50
1	D	$64/69 \ (93\%)$	63 (98%)	1 (2%)	62	84
All	All	259/276~(94%)	252 (97%)	7 (3%)	44	71

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	С	633	GLU
1	С	634	CYS
1	D	689	SER
1	С	670	ILE
1	В	689	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

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

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

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

6.3 Carbohydrates (i)

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

6.4 Ligands (i)

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

6.5 Other polymers (i)

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

