



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 23, 2018 – 11:21 AM EST

PDB ID : 5WRC  
Title : Crystal structure of proteinase K from Engyodontium album  
Authors : Sugahara, M.; Nakane, T.; Suzuki, M.; Masuda, T.; Inoue, S.; Numata, K.  
Deposited on : 2016-12-01  
Resolution : 1.50 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030736  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030736

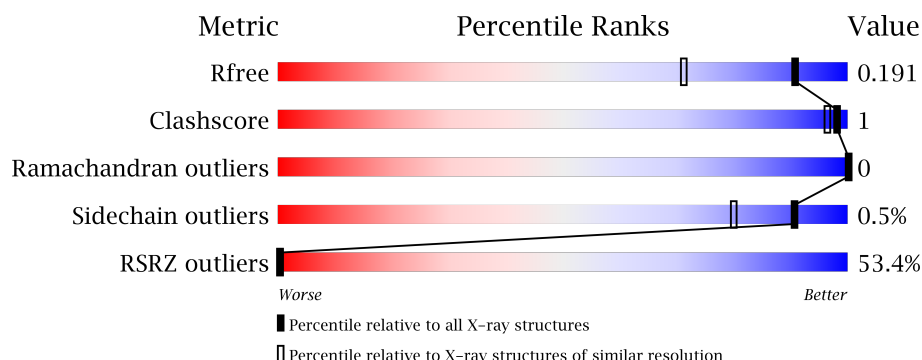
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.50 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	2279 (1.50-1.50)
Clashscore	112137	2503 (1.50-1.50)
Ramachandran outliers	110173	2445 (1.50-1.50)
Sidechain outliers	110143	2443 (1.50-1.50)
RSRZ outliers	101464	2305 (1.50-1.50)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	279	<div> <div>53%</div> <div>97%</div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2252 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.

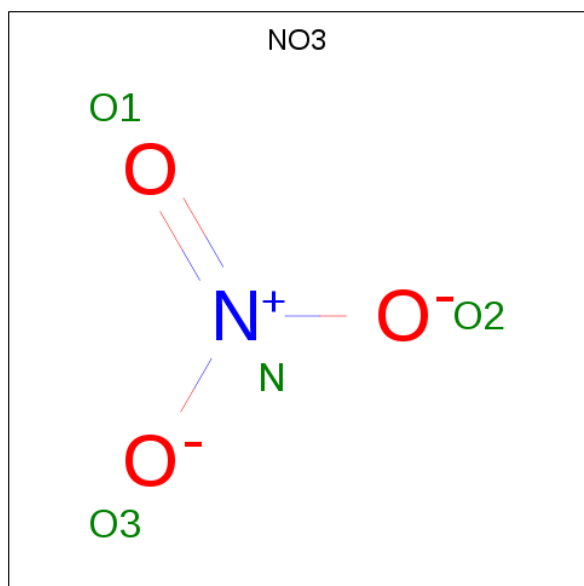
- Molecule 1 is a protein called Proteinase K.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	279	2031	1248	357	416	10	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	207	ASP	SER	conflict	UNP P06873

- Molecule 2 is NITRATE ION (three-letter code: NO3) (formula: NO<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	N	O		
2	A	1	4	1	3	0	0

- Molecule 3 is PRASEODYMIUM ION (three-letter code: PR) (formula: Pr).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total 2	Pr 2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	215	Total 215	O 215	0	0

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Proteinase K



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	68.60 Å 68.60 Å 108.80 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.70 – 1.50 32.71 – 1.31	Depositor EDS
% Data completeness (in resolution range)	100.0 (32.70-1.50) 85.0 (32.71-1.31)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.86 (at 1.31 Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, $R_{free}$	0.176 , 0.193 0.176 , 0.191	Depositor DCC
$R_{free}$ test set	1350 reflections (3.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	16.0	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 47.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2252	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PR, NO3

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	0.45	0/2070	0.51	1/2813 (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( $^{\circ}$ )
1	A	250	ARG	NE-CZ-NH2	-5.55	117.53	120.30

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	2031	0	1934	3	0
2	A	4	0	0	1	0
3	A	2	0	0	0	0
4	A	215	0	0	0	0
All	All	2252	0	1934	3	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 1.

All (3) 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:68:GLY:HA2	1:A:213:ILE:HG23	1.91	0.53
1:A:97:ASP:HB2	2:A:1001:NO3:O3	2.19	0.43
1:A:8:TRP:CH2	1:A:204:PRO:HB3	2.54	0.42

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	277/279 (99%)	269 (97%)	8 (3%)	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	213/213 (100%)	212 (100%)	1 (0%)	91	80

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	225	MET



Some 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	NO3	A	1001	-	1,3,3	4.24	1 (100%)	0,3,3	0.00	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NO3	A	1001	-	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	NO3	O1-N	4.24	1.39	1.23

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	NO3	1	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	279/279 (100%)	2.22	149 (53%)  	11, 15, 24, 37	0

All (149) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	278	GLN	6.5
1	A	279	ALA	4.6
1	A	186	TYR	4.5
1	A	177	VAL	4.4
1	A	77	VAL	4.4
1	A	35	VAL	4.4
1	A	84	VAL	4.3
1	A	104	TYR	4.2
1	A	213	ILE	4.2
1	A	264	ILE	4.1
1	A	73	CYS	4.0
1	A	37	VAL	3.9
1	A	230	VAL	3.8
1	A	74	ALA	3.8
1	A	252	ILE	3.8
1	A	277	TYR	3.8
1	A	233	LEU	3.7
1	A	208	ILE	3.7
1	A	107	ILE	3.6
1	A	103	GLN	3.6
1	A	266	PHE	3.5
1	A	42	ILE	3.5
1	A	24	TYR	3.5
1	A	231	ALA	3.4
1	A	64	ARG	3.4
1	A	101	SER	3.4
1	A	120	ASN	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	76	THR	3.4
1	A	148	LEU	3.3
1	A	144	ALA	3.3
1	A	273	ALA	3.3
1	A	128	VAL	3.3
1	A	5	ASN	3.3
1	A	153	VAL	3.2
1	A	201	ILE	3.2
1	A	10	LEU	3.2
1	A	226	ALA	3.2
1	A	95	VAL	3.2
1	A	227	THR	3.1
1	A	99	ASN	3.1
1	A	38	ILE	3.1
1	A	61	TYR	3.1
1	A	54	GLN	3.1
1	A	234	ALA	3.1
1	A	212	TRP	3.1
1	A	129	ALA	3.1
1	A	157	VAL	3.1
1	A	180	VAL	3.1
1	A	246	ALA	3.1
1	A	62	SER	3.1
1	A	88	THR	3.0
1	A	220	ILE	3.0
1	A	156	ALA	3.0
1	A	93	VAL	3.0
1	A	228	PRO	3.0
1	A	250	ARG	3.0
1	A	155	VAL	3.0
1	A	8	TRP	3.0
1	A	243	THR	3.0
1	A	159	ALA	3.0
1	A	237	LEU	3.0
1	A	127	VAL	2.9
1	A	249	CYS	2.9
1	A	182	ALA	2.9
1	A	265	PRO	2.9
1	A	49	PHE	2.9
1	A	96	LEU	2.9
1	A	158	ALA	2.8
1	A	47	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	114	VAL	2.8
1	A	23	TYR	2.8
1	A	25	TYR	2.8
1	A	179	THR	2.7
1	A	261	LEU	2.7
1	A	2	ALA	2.7
1	A	223	THR	2.7
1	A	269	VAL	2.7
1	A	22	THR	2.7
1	A	123	CYS	2.7
1	A	162	ASN	2.7
1	A	56	VAL	2.7
1	A	1	ALA	2.7
1	A	276	ASN	2.7
1	A	240	LEU	2.7
1	A	178	CYS	2.6
1	A	235	ALA	2.6
1	A	36	TYR	2.6
1	A	53	ALA	2.6
1	A	122	ASN	2.6
1	A	34	CYS	2.6
1	A	71	THR	2.6
1	A	31	GLN	2.5
1	A	108	ILE	2.5
1	A	232	GLY	2.5
1	A	236	TYR	2.5
1	A	90	LEU	2.5
1	A	209	LEU	2.5
1	A	172	ALA	2.5
1	A	18	PRO	2.5
1	A	175	PRO	2.4
1	A	202	PHE	2.4
1	A	27	GLU	2.4
1	A	141	VAL	2.4
1	A	131	LEU	2.4
1	A	40	THR	2.4
1	A	198	VAL	2.4
1	A	210	SER	2.4
1	A	82	TYR	2.4
1	A	169	TYR	2.4
1	A	251	TYR	2.4
1	A	256	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	167	ARG	2.3
1	A	267	GLY	2.3
1	A	85	ALA	2.3
1	A	253	ALA	2.3
1	A	16	THR	2.3
1	A	106	THR	2.3
1	A	19	GLY	2.3
1	A	145	ALA	2.3
1	A	58	THR	2.3
1	A	211	THR	2.3
1	A	21	SER	2.2
1	A	29	ALA	2.2
1	A	259	GLY	2.2
1	A	274	TYR	2.2
1	A	124	PRO	2.2
1	A	4	THR	2.2
1	A	248	ALA	2.2
1	A	78	GLY	2.2
1	A	7	PRO	2.2
1	A	225	MET	2.2
1	A	20	THR	2.2
1	A	13	ILE	2.1
1	A	75	GLY	2.1
1	A	204	PRO	2.1
1	A	214	GLY	2.1
1	A	217	THR	2.1
1	A	80	ARG	2.1
1	A	130	SER	2.1
1	A	224	SER	2.1
1	A	133	LEU	2.1
1	A	60	TYR	2.1
1	A	97	ASP	2.1
1	A	206	THR	2.1
1	A	45	SER	2.0
1	A	166	ALA	2.0
1	A	70	GLY	2.0
1	A	59	TYR	2.0
1	A	183	SER	2.0

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

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NO3	A	1001	4/4	0.81	0.16	-0.84	24,28,28,32	0
3	PR	A	1002	1/1	1.00	0.15	-1.05	11,11,11,11	1
3	PR	A	1003	1/1	0.96	0.13	-	21,21,21,21	1

### 6.5 Other polymers [i](#)

There are no such residues in this entry.