Full wwPDB X-ray Structure Validation Report (i)

May 27, 2020 – 02:28 am BST

PDB ID	:	5AMX
Title	:	Crystal Structure of Proteinase K processed with the CrystalDirect automated mounting and cryo-cooling technology
Authors	:	Zander, U.; Hoffmann, G.; Cornaciu, I.; Cipriani, F.; Marquez, J.A.
Deposited on	:	2015-09-02
Resolution	:	1.01 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

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 1.01 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.
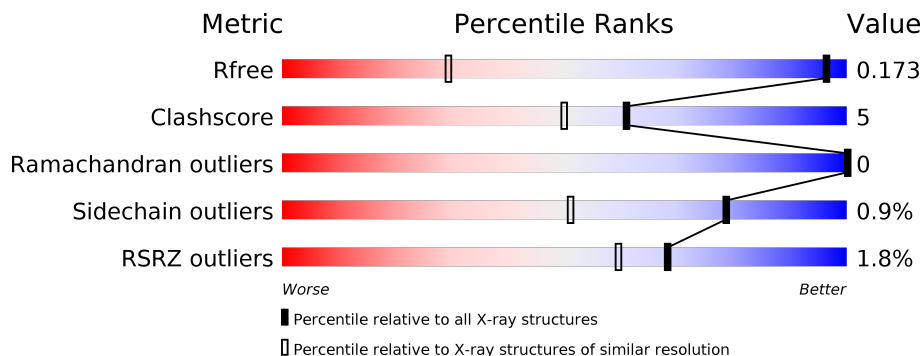
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1188 (1.08-0.96)
Clashscore	141614	1253 (1.08-0.96)
Ramachandran outliers	138981	1178 (1.08-0.96)
Sidechain outliers	138945	1180 (1.08-0.96)
RSRZ outliers	127900	1158 (1.08-0.96)

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 on 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	279	2% 85% 14%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2400 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
1	A	279	Total	C	N	O	S	0	1	0
			2036	1250	358	418	10			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	359	Total	O	0	0
			359	359		

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
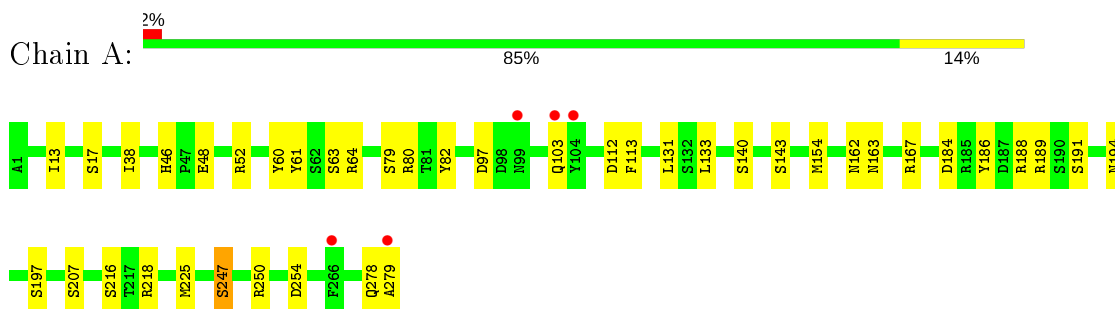
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	67.97Å 67.97Å 102.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.13 – 1.01 28.29 – 1.01	Depositor EDS
% Data completeness (in resolution range)	90.5 (29.13-1.01) 90.5 (28.29-1.01)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.52 (at 1.01Å)	Xtriage
Refinement program	REFMAC 5.8.0123	Depositor
R, R_{free}	0.157 , 0.166 0.167 , 0.173	Depositor DCC
R_{free} test set	5676 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	6.6	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.43 , 43.3	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	0.96	EDS
Total number of atoms	2400	wwPDB-VP
Average B, all atoms (Å^2)	9.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.90% 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: SO4

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	1.40	19/2075 (0.9%)	1.15	17/2818 (0.6%)

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	247	SER	CA-CB	15.66	1.76	1.52
1	A	143	SER	CB-OG	-10.25	1.28	1.42
1	A	63	SER	CB-OG	-10.08	1.29	1.42
1	A	112	ASP	CB-CG	9.96	1.72	1.51
1	A	60	TYR	CE2-CZ	-9.29	1.26	1.38
1	A	13	ILE	CB-CG1	-7.51	1.33	1.54
1	A	61	TYR	CD1-CE1	6.69	1.49	1.39
1	A	197	SER	CB-OG	-6.40	1.33	1.42
1	A	82	TYR	CE2-CZ	-6.27	1.30	1.38
1	A	61	TYR	CE1-CZ	-6.22	1.30	1.38
1	A	186	TYR	CB-CG	-5.98	1.42	1.51
1	A	113	PHE	CE2-CZ	-5.89	1.26	1.37
1	A	17	SER	CB-OG	-5.65	1.34	1.42
1	A	278	GLN	C-O	-5.52	1.12	1.23
1	A	207	SER	CB-OG	5.46	1.49	1.42
1	A	191	SER	CB-OG	-5.34	1.35	1.42
1	A	140	SER	CB-OG	-5.26	1.35	1.42
1	A	167	ARG	CG-CD	5.06	1.64	1.51
1	A	60	TYR	CD1-CE1	5.05	1.47	1.39

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	188	ARG	NE-CZ-NH1	15.76	128.18	120.30
1	A	64	ARG	NE-CZ-NH2	-8.29	116.16	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	97	ASP	CB-CG-OD1	7.35	124.92	118.30
1	A	61	TYR	CB-CG-CD1	7.03	125.22	121.00
1	A	80	ARG	NE-CZ-NH2	-6.84	116.88	120.30
1	A	184	ASP	CB-CG-OD1	6.79	124.41	118.30
1	A	250	ARG	NE-CZ-NH2	6.33	123.46	120.30
1	A	60	TYR	CG-CD1-CE1	-6.32	116.25	121.30
1	A	218	ARG	NE-CZ-NH2	-6.11	117.24	120.30
1	A	52	ARG	NE-CZ-NH1	5.91	123.26	120.30
1	A	184	ASP	CB-CG-OD2	-5.88	113.01	118.30
1	A	61	TYR	CD1-CE1-CZ	-5.84	114.54	119.80
1	A	254	ASP	CB-CG-OD2	-5.71	113.16	118.30
1	A	52	ARG	NE-CZ-NH2	-5.54	117.53	120.30
1	A	60	TYR	CB-CG-CD1	5.20	124.12	121.00
1	A	64	ARG	NE-CZ-NH1	5.05	122.83	120.30
1	A	188	ARG	NH1-CZ-NH2	-5.04	113.86	119.40

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	2036	0	1939	18	0
2	A	5	0	0	0	0
3	A	359	0	0	2	1
All	All	2400	0	1939	18	1

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 5.

All (18) 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:247:SER:CB	1:A:247:SER:CA	1.76	1.54
1:A:38:ILE:HB	1:A:131:LEU:HD23	1.48	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:ASN:HD22	1:A:194:ASN:HD21	1.31	0.79
1:A:46:HIS:HD2	1:A:48:GLU:H	1.32	0.76
1:A:38:ILE:HB	1:A:131:LEU:CD2	2.17	0.72
1:A:247:SER:CB	1:A:247:SER:N	2.55	0.68
1:A:38:ILE:HD12	1:A:131:LEU:HD21	1.81	0.62
1:A:279:ALA:HB2	3:A:2356:HOH:O	2.02	0.59
1:A:163:ASN:ND2	1:A:189:ARG:HH12	2.01	0.58
1:A:247:SER:CB	1:A:247:SER:C	2.67	0.57
1:A:46:HIS:HE1	1:A:216[A]:SER:O	1.87	0.57
1:A:46:HIS:CD2	1:A:48:GLU:H	2.21	0.53
1:A:46:HIS:HE1	1:A:216[B]:SER:O	1.95	0.49
1:A:38:ILE:CD1	1:A:131:LEU:HD21	2.43	0.48
1:A:163:ASN:HD22	1:A:189:ARG:HH12	1.61	0.46
1:A:103:GLN:HG2	3:A:2182:HOH:O	2.19	0.43
1:A:48:GLU:HB3	1:A:79:SER:HB2	2.01	0.42
1:A:133:LEU:C	1:A:133:LEU:HD12	2.40	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:2094:HOH:O	3:A:2341:HOH:O[7_545]	2.11	0.09

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	278/279 (100%)	270 (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	214/213 (100%)	212 (99%)	2 (1%)	78	51

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	154	MET
1	A	225	MET

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

Mol	Chain	Res	Type
1	A	46	HIS
1	A	162	ASN
1	A	163	ASN

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)

1 ligand is modelled in this entry.

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	SO4	A	1280	-	4,4,4	0.43	0	6,6,6	0.44	0

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 (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, 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	279/279 (100%)	0.26	5 (1%)	68	59	3, 6, 12, 30	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	266	PHE	3.6
1	A	279	ALA	3.5
1	A	103	GLN	2.5
1	A	104	TYR	2.5
1	A	99	ASN	2.4

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 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. The B-factors column lists the minimum, median, 95th 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	B-factors(Å^2)	Q<0.9
2	SO4	A	1280	5/5	0.99	0.06	6,7,10,11	0

6.5 Other polymers (i)

There are no such residues in this entry.