W O R L D W I D E
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

May 13, 2020 – 11:28 pm BST

PDB ID	:	2BVA
Title	:	Crystal structure of the human P21-activated kinase 4
Authors	:	Debreczeni, J.E.; Bunkoczi, G.; Eswaran, J.; Filippakopoulos, P.; Das, S.; Fedorov, O.; Sundstrom, M.; Arrowsmith, C.; Edwards, A.; von Delft, F.; Knapp, S.
Deposited on	:	2005-06-23
Resolution	:	2.30 Å(reported)

The following versions of software and data (see references ⓘ) 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 ⓘ

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

The reported resolution of this entry is 2.30 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
Clashscore		25
Ramachandran outliers		1.7%
Sidechain outliers		26.4%
RSRZ outliers		0.7%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
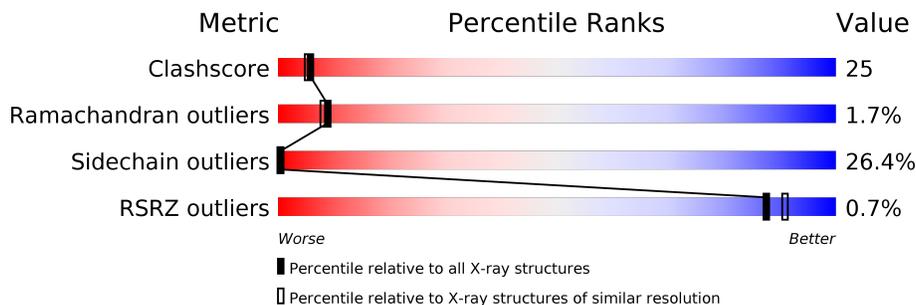
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	292	42% 38% 13% • 7%
1	B	292	% 35% 42% 14% • 6%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4287 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 P21-ACTIVATED KINASE 4.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	273	Total 2114	C 1359	N 362	O 379	P 1	S 13	0	0	0
1	B	275	Total 2137	C 1372	N 368	O 383	P 1	S 13	0	0	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	21	Total 21	O 21	0	0
2	B	15	Total 15	O 15	0	0

3 Residue-property plots ⓘ

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: P21-ACTIVATED KINASE 4

Chain A:
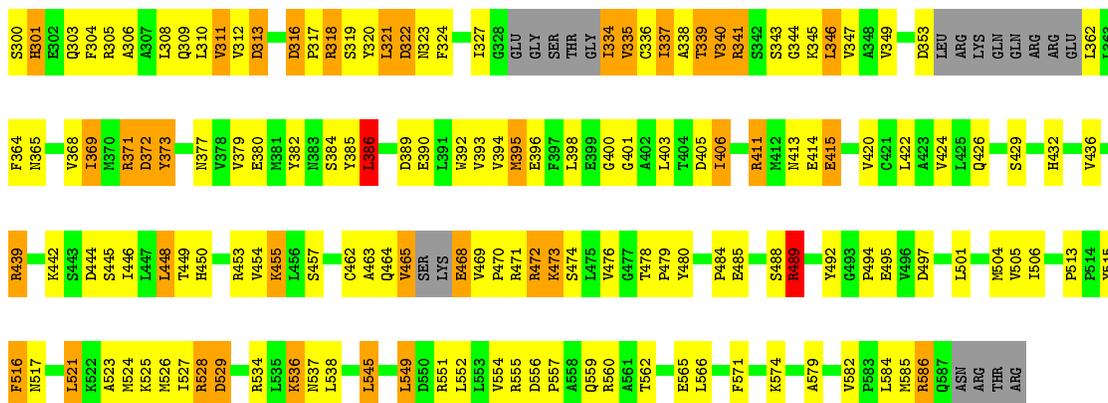
- Molecule 1: P21-ACTIVATED KINASE 4

Chain B:
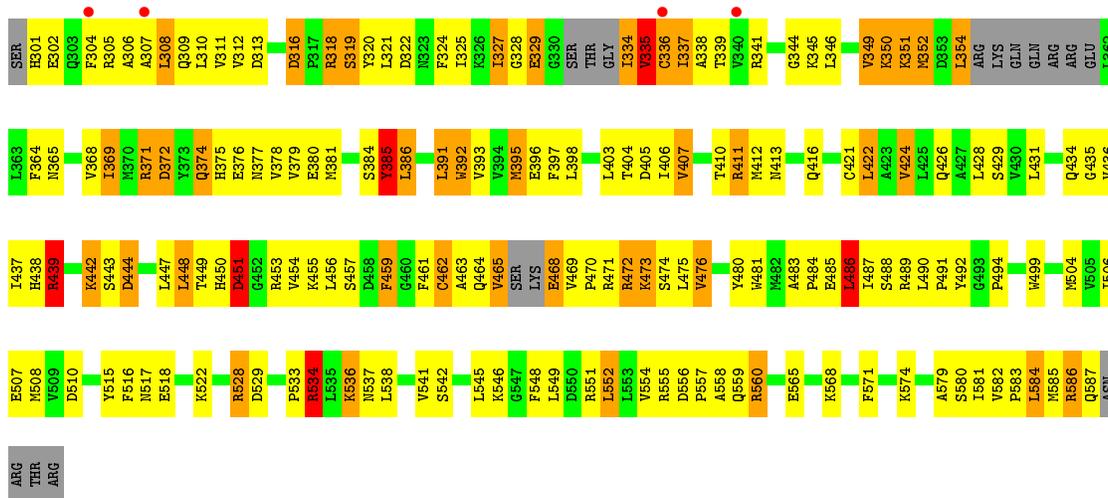
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α, β, γ	118.11Å　　118.11Å　　55.53Å 90.00°　　　90.00°　　　120.00°	Depositor
Resolution (Å)	20.00　　–　　2.30 19.84　　–　　2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (20.00-2.30) 95.0 (19.84-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	6.73 (at 2.30Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.192　　,　　　　0.269 0.199　　,　　(Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	16.1	Xtriage
Anisotropy	0.304	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 409.9	EDS
L-test for twinning[2]	$<|L|> = 0.44, <L^2> = 0.27$	Xtriage
Estimated twinning fraction	0.088 for -h,-k,l 0.068 for h,-h-k,-l 0.078 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	4287	wwPDB-VP
Average B, all atoms (Å^2)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.04% 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 (i)

5.1 Standard geometry (i)

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

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	0.41	0/2147	1.08	8/2917 (0.3%)
1	B	0.41	0/2170	1.07	12/2945 (0.4%)
All	All	0.41	0/4317	1.08	20/5862 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	551	ARG	CD-NE-CZ	11.04	139.05	123.60
1	B	551	ARG	NE-CZ-NH2	7.05	123.83	120.30
1	A	439	ARG	NE-CZ-NH2	-6.91	116.85	120.30
1	A	439	ARG	NE-CZ-NH1	6.87	123.73	120.30
1	B	371	ARG	NE-CZ-NH1	5.95	123.28	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	469	VAL	Peptide

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	2114	0	2122	100	0
1	B	2137	0	2160	116	0
2	A	21	0	0	1	0
2	B	15	0	0	0	0
All	All	4287	0	4282	216	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 25.

The worst 5 of 216 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:B:351:LYS:HG2	1:B:392:TRP:CH2	2.03	0.93
1:B:422:LEU:O	1:B:426:GLN:HG3	1.83	0.79
1:A:347:VAL:HG13	1:A:395:MET:O	1.83	0.79
1:A:579:ALA:O	1:A:582:VAL:HG22	1.83	0.79
1:B:472:ARG:HD2	1:B:474:SEP:O3P	1.84	0.77

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	264/292 (90%)	230 (87%)	30 (11%)	4 (2%)	10	10
1	B	266/292 (91%)	225 (85%)	36 (14%)	5 (2%)	8	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	530/584 (91%)	455 (86%)	66 (12%)	9 (2%)	9 8

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	335	VAL
1	B	335	VAL
1	A	301	HIS
1	A	311	VAL
1	B	352	MET

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	225/254 (89%)	168 (75%)	57 (25%)	0 0
1	B	229/254 (90%)	166 (72%)	63 (28%)	0 0
All	All	454/508 (89%)	334 (74%)	120 (26%)	0 0

5 of 120 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	549	LEU
1	B	334	ILE
1	B	536	LYS
1	A	585	MET
1	B	311	VAL

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	450	HIS
1	B	450	HIS
1	B	587	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are 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	$\#|Z| > 2$
1	SEP	B	474	1	8,9,10	0.88	0	8,12,14	2.15	2 (25%)
1	SEP	A	474	1	8,9,10	0.92	0	8,12,14	1.97	1 (12%)

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
1	SEP	B	474	1	-	1/5/8/10	-
1	SEP	A	474	1	-	3/5/8/10	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	474	SEP	P-OG-CB	-5.31	103.66	118.30
1	A	474	SEP	P-OG-CB	-4.93	104.71	118.30
1	B	474	SEP	OG-CB-CA	2.50	110.58	108.14

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	474	SEP	CB-OG-P-O1P

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Mol	Chain	Res	Type	Atoms
1	A	474	SEP	CB-OG-P-O2P
1	B	474	SEP	CA-CB-OG-P
1	A	474	SEP	CA-CB-OG-P

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	474	SEP	2	0
1	A	474	SEP	2	0

5.5 Carbohydrates (i)

There are no carbohydrates 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, 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	272/292 (93%)	-0.30	0	100 100	2, 16, 34, 46	0
1	B	274/292 (93%)	-0.25	4 (1%)	73 79	3, 17, 36, 49	0
All	All	546/584 (93%)	-0.28	4 (0%)	87 91	2, 17, 35, 49	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	336	CYS	2.5
1	B	304	PHE	2.3
1	B	340	VAL	2.1
1	B	307	ALA	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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
1	SEP	B	474	10/11	0.98	0.10	17,23,24,24	0
1	SEP	A	474	10/11	0.98	0.10	17,23,24,26	0

6.3 Carbohydrates (i)

There are no carbohydrates 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.