

## CHARACTERIZATION OF ADRBK1 KINASE IN THE HUMAN PROTEOME USING ONLINE BIOINFORMATICS TOOLS

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### Abstract

*Non-receptor tyrosine-protein kinase that plays a role in many key processes linked to cell growth and survival such as cytoskeleton remodeling in response to extracellular stimuli, cell motility and adhesion, receptor endocytosis, autophagy, DNA damage response and apoptosis. Coordinates actin remodeling through tyrosine phosphorylation of proteins controlling cytoskeleton dynamics like WASF3 (involved in branch formation); ANXA1 (involved in membrane anchoring); DBN1, DBNL, CTTN, RAPH1 and ENAH (involved in signaling); or MAPT and PXN (microtubule-binding proteins). Phosphorylation of WASF3 is critical for the stimulation of lamellipodia formation and cell migration. Involved in the regulation of cell adhesion and motility through phosphorylation of key regulators of these processes such as BCAR1, CRK, CRKL, DOK1, EFS or NEDD9. Phosphorylates multiple receptor tyrosine kinases and more particularly promotes endocytosis of EGFR, facilitates the formation of neuromuscular synapses through MUSK,*

**Keywords:** Kinase, beta androgenic receptor, Homosaiens



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### Introduction

ADRBK1 (ADRBK1 Beta-adrenergic receptor kinase 1)

The ADRBK1 kinase is a G protein-Coupled receptor kinase1

The product of this gene phosphorelates the beta2 adrenergic receptor and appears to mediate agonist specific desensitization observed at high agonist concentration. this protein is an ubiquitous cytosolic enzyme that specifically phosphorelates the activated form of the beta androgenic and related G Protein Coupled receptors (Benovic et al 1991)

Following are the pathways where it involves

- Cardiac Beta-adrenergic signalling
- cAMP- mediated signalling
- Gαq signalling
- Sonic Hedgehog signalling
- Opioid signalling

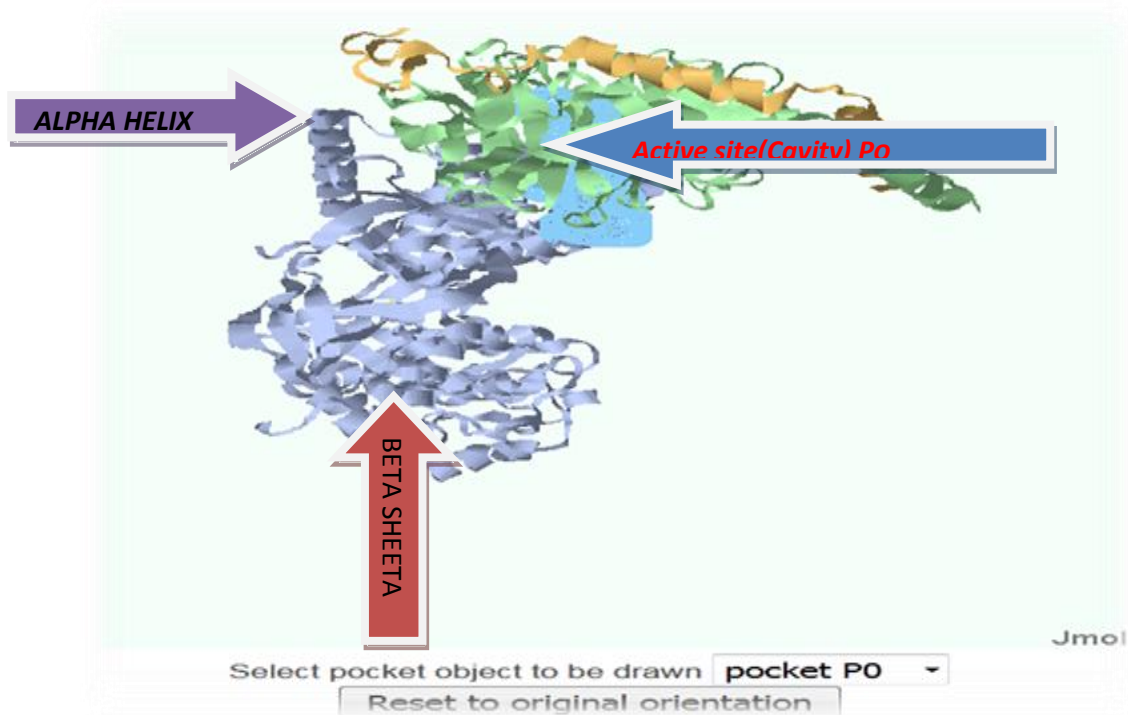
- GPCR Signaling
- Colorectal cancer Metastasis Signaling

As its a specific type of regulator involved in cell function

The ADBRK1 is kinase protein belonging to AGC Ser /Thr protein kinase family kinase,the kinase makes impact by means of phosphorylation of ADP protein on Colorectal cancer Metastasis signaling pathway,it catalyzes the transfer of phosphate usually from ATP to substrate,three dimensional sturcture for ADBRK1 was identified with the use of PDB dababse the server witht the use of DOGSITE scorer server detailed in methods part which has been explained in chapter no II

**Fig.No 1 shows the three dimensional structure**

The below fig is the 3 D Structure of the ADRBK1 Beta-adrenergic receptor kinase 1,the active site is shown by the arrow indicating the largest cavity of the protein shown in **Blue colour** it has volume  $900.91 \text{ \AA}^3$ ,the surface area is about  $903.74 \text{ \AA}^2$ ,Depth  $27.73 \text{ \AA}$



The presence of functional groups in the ADBRK1 was carried out with the use of DOGSITE scorer an online server .the functional group descriptors are shown in table no1 .

**Functional group descriptors**

Descriptor	Number
Hydrogen bond donors	23
Hydrogen bond acceptors	65
Metals	0
Hydrophobicity interactions	33
Hydrophobicity ratio	0.27

### Tab 1 A

The Tab.No1A Shows the information about the functional descriptors which is the molecular characterizations of the cavity showing 23 Hydrogen bond donors,65 Hydrogen bond acceptors,hydrophobic interactions are 33 ,andHydrophobicity ratio 0.27

The (value) is the total number, it is calculated by the DOGSITE scorer server

The functional group means the side chain of the amino acid which actually takes part in to the chemical reaction the functional group descriptor word can be raplaced by the description word

### Element descriptors

Descriptor	Value
Pocket atoms	191
Carbons (C)	123
Nitrogens (N)	30
Oxygens	34
Sulphurs (S)	4

### Tab 1B

Tab No 1B is the actual element descriptors showing the annotation of total number of Pocket atoms 191 involved in the active site ,Carbon atoms 123,Nitrogen atoms 30,Oxygen atoms 34 ,sulfor atoms 4

### Materials and Methods

The databases used for the annotation of the ADRBK1 is swissprot and Uiprot The three dimensional structure of the protein is viewed by by the online JMOL software, it can be viewd by other software tools also like CHIMERA, RASWIN, Swisspdb Viewer ,CN3D etc.

### Conclusion

The gene represented in this entry is involved in disease pathogenesis.

Disease descriptionA clonal myeloproliferative disorder of a pluripotent stem cell with a specific cytogenetic abnormality, the Philadelphia chromosome (Ph), involving myeloid, erythroid, megakaryocytic, B-lymphoid, and sometimes T-lymphoid cells, but not marrow fibroblasts.

A chromosomal aberration involving ABL1 has been found in patients with chronic myeloid leukemia. Translocation t(9;22)(q34;q11) with BCR. The translocation produces a BCR-ABL found also in acute myeloid leukemia (AML) and acute lymphoblastic leukemia. A chromosomal aberration involving ABL1 is found in a form of acute lymphoblastic leukemia (PubMed:15361874). Translocation t(9;9)(q34;q34) with NUP214 (PubMed:15361874)

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