



Human Muscle-Specific A-Kinase Anchoring Protein (mAKAP) Polymorphisms: Mechanistic Role in Cardiovascular Diseases

Santosh Suryavanshi¹, Kody Anderson², Shweta Jadhav¹, Olivier Lichtarge³ and Bradley K McConnell¹

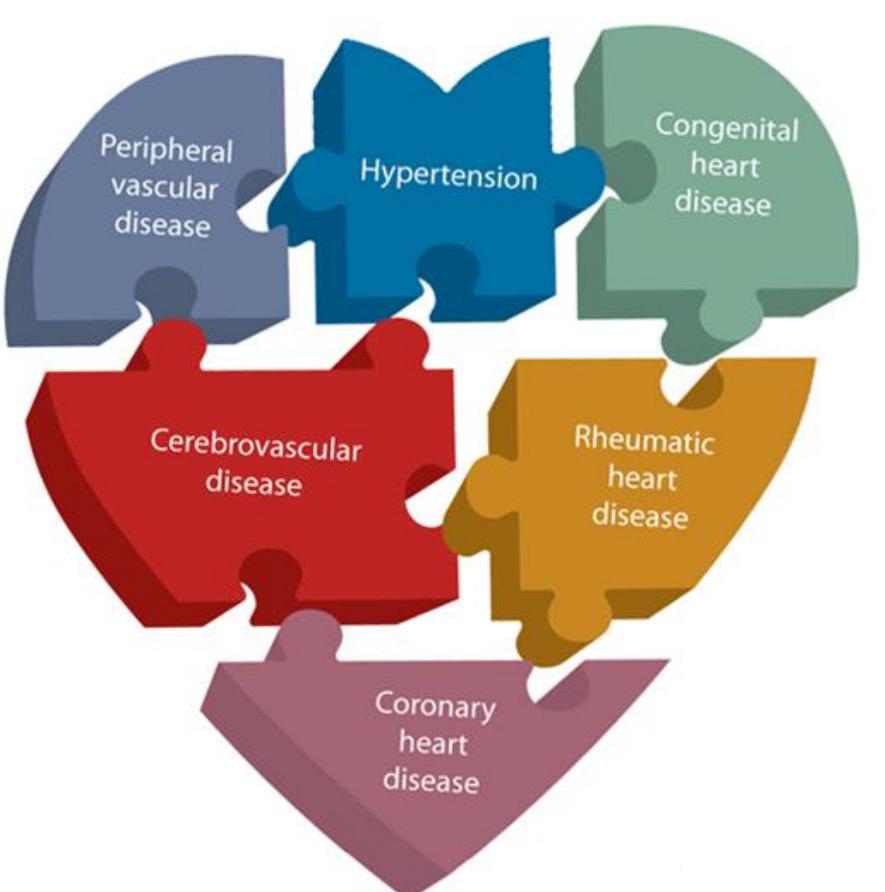
¹University of Houston College of Pharmacy, Houston, TX; ²University of Houston Cullen College of Engineering, Houston, TX

³Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX.

BACKGROUND

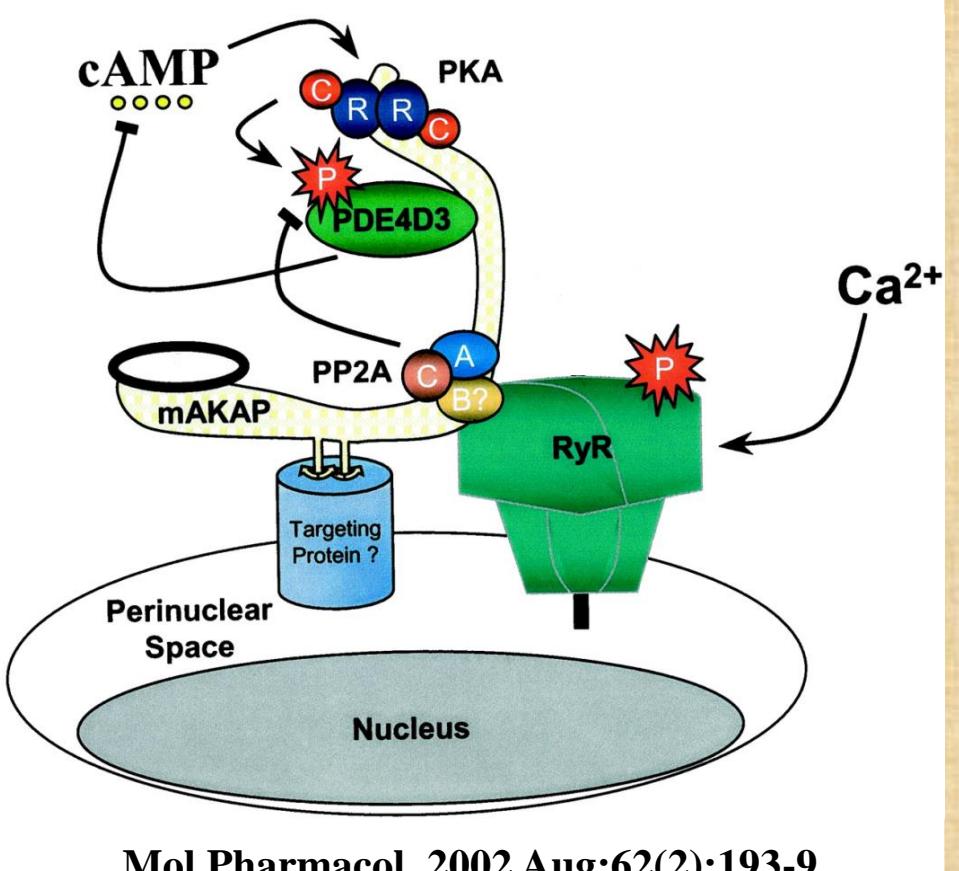
CARDIOVASCULAR DISEASES AND SINGLE NUCLEOTIDE POLYMORPHISMS

- Cardiovascular diseases (CVDs) are the leading cause of deaths globally with **17.7 million deaths every year**, more than all forms of cancer combined.
- The National Human Genome Research Institute reported **5585 SNPs with association to CVDs** at $P < 10^{-5}$ (Kathiresan and Srivastava 2012).
- Genetics** plays an incomparable role in the susceptibility of humans to CVDs.

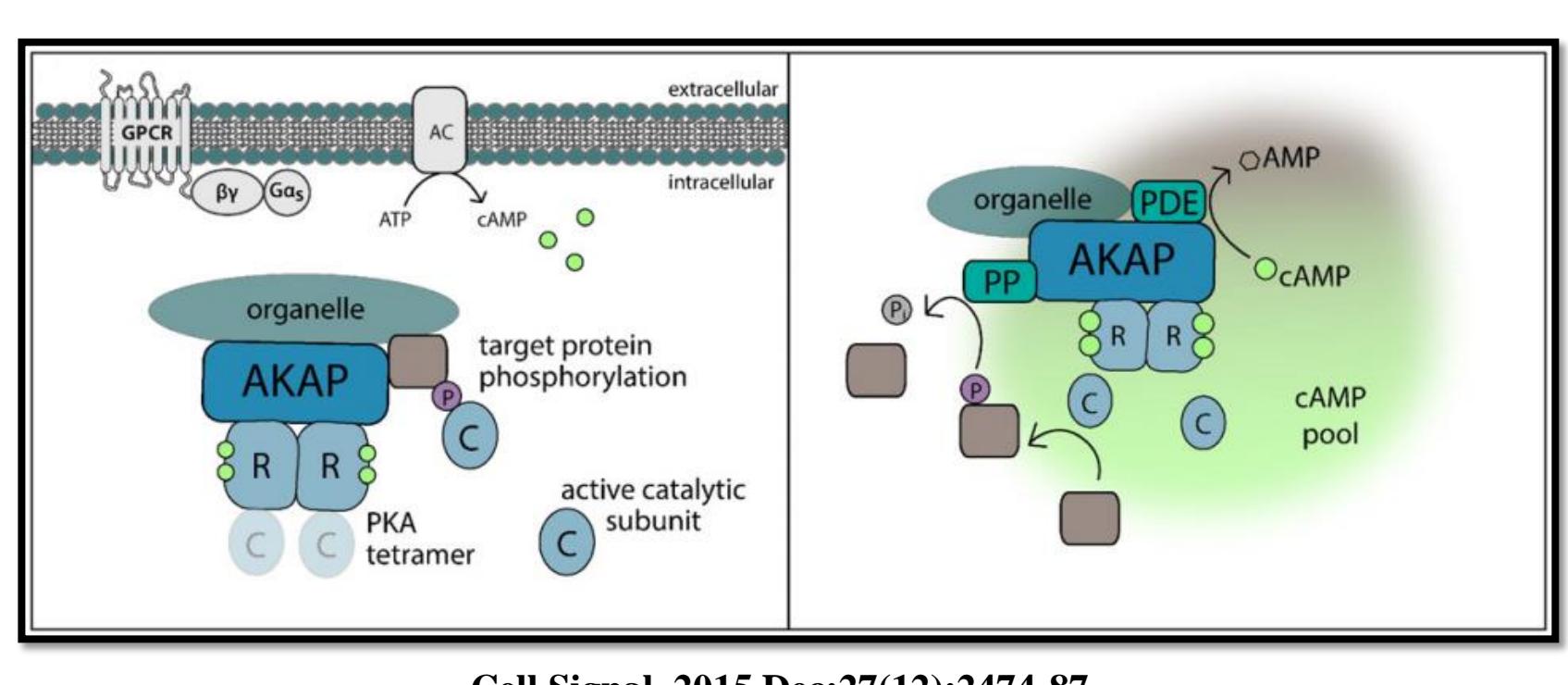


mAKAP: A Kinase Anchoring Protein (AKAP)

- AKAPs, by definition, bind protein kinase A (PKA) along with other crucial proteins in the body (Wong and Scott, 2004).
- mAKAP**, muscle-specific AKAP that is expressed in the heart, is a master scaffold for tight regulation of cAMP.
- By maintaining local cAMP pools, mAKAP organizes cardiac cAMP/PKA signaling.



cAMP/PKA/AKAP TRIAD



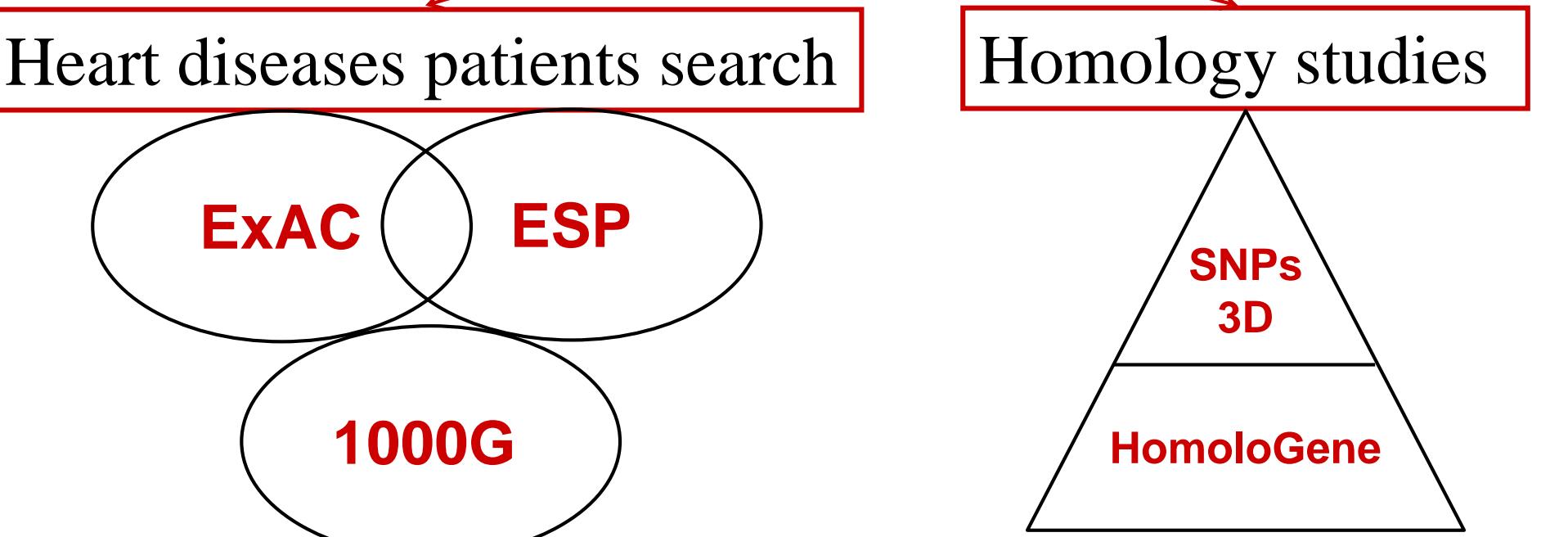
- Cyclic adenine monophosphate (cAMP) is a **universal intracellular second messenger** (Dema, Perets et al. 2015).
- cAMP **activates PKA** and modulates phosphorylation of PKA substrates; thus **controls basic heart functioning**.
- By binding to PKA, AKAPs regulate cAMP/PKA signaling where alterations in this signaling are implicated in CVDs.

OBJECTIVE

To study the mechanistic role of mAKAP polymorphisms in increasing risk of cardiovascular diseases

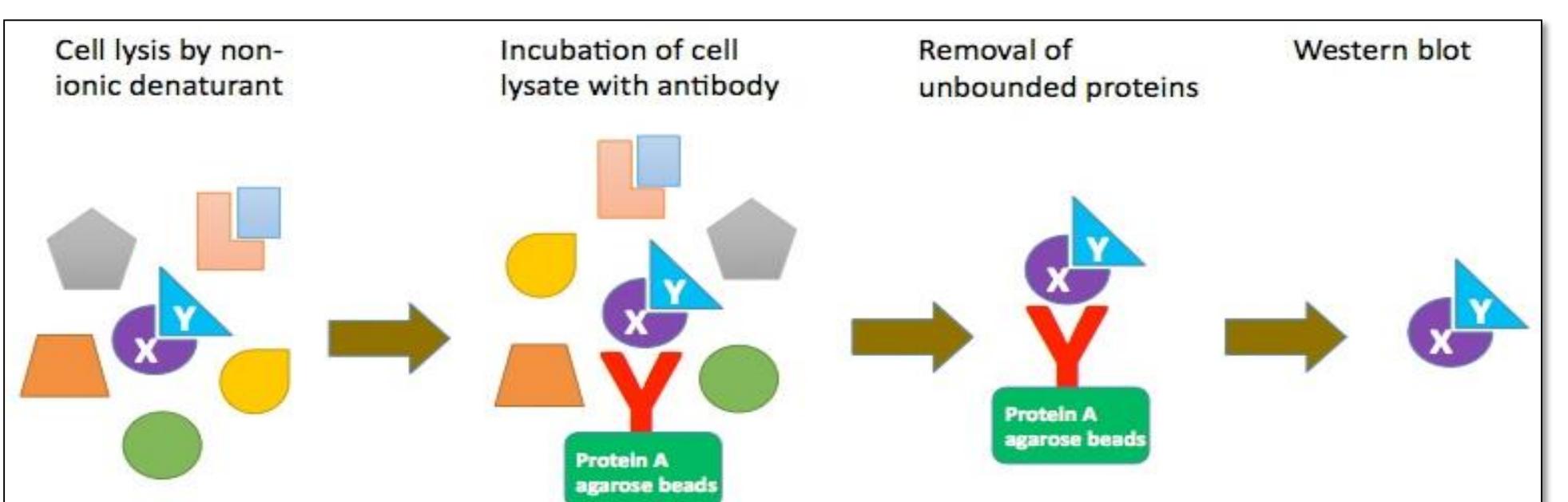
METHODS

COMPUTATIONAL STUDIES

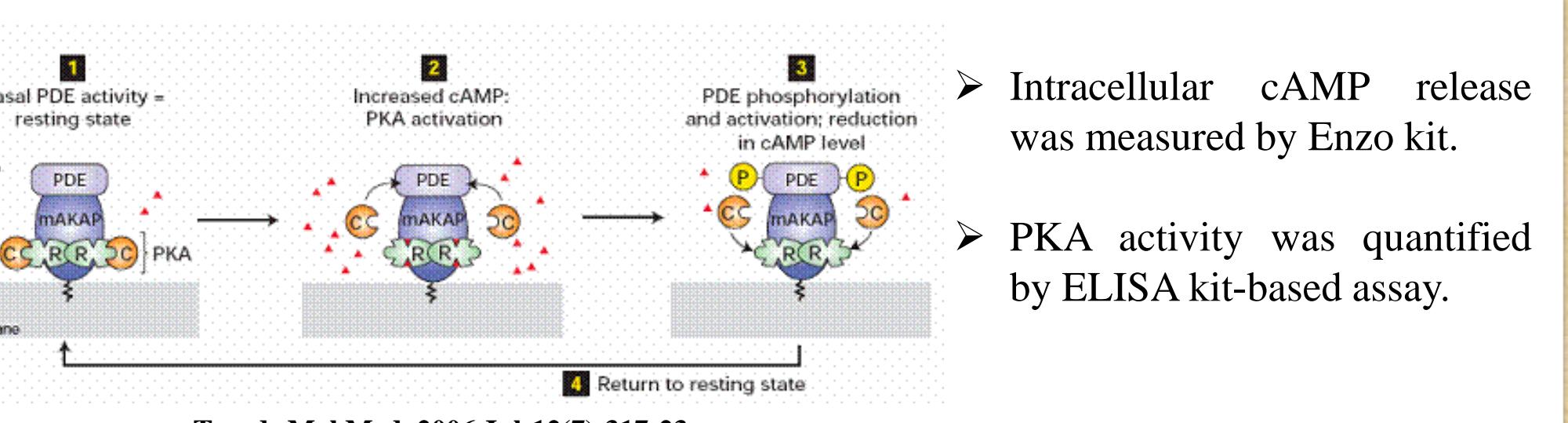


- ExAC:** Exome Aggregation Consortium
ESP: Exome Sequencing Project
1000G: 1000 Genome Project – Healthy people
SNPs3D and HomoloGene: Softwares that assign molecular functional effects of SNPs based on the structure and sequence analysis

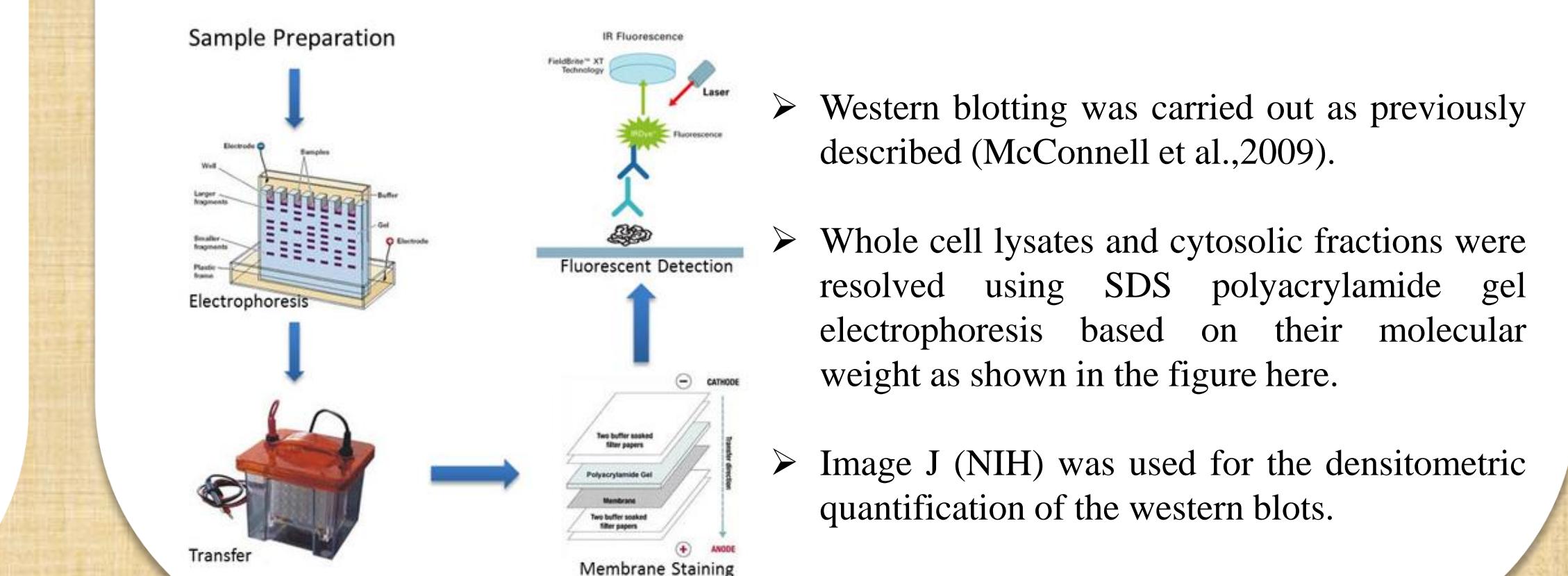
IMMUNOPRECIPITATION



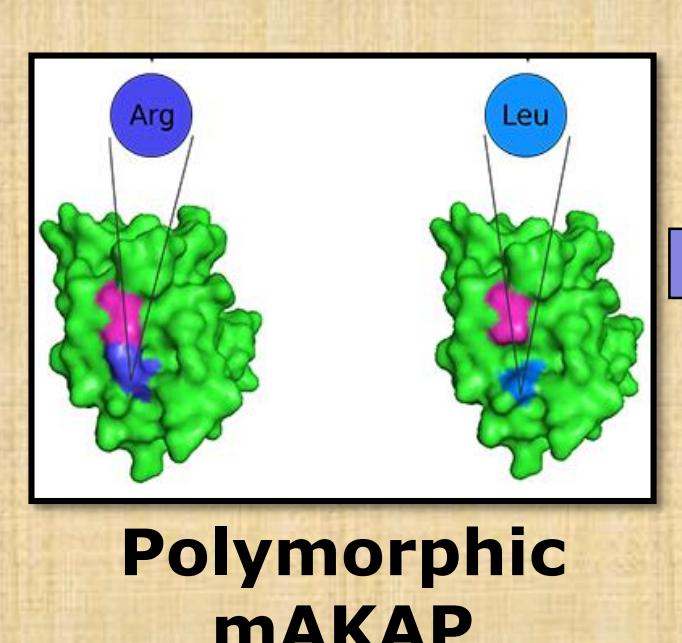
cAMP LEVELS AND PKA ACTIVITY ASSAY



WESTERN BLOTTING



SUMMARY OF RESULTS



Abrupt binding of PKA and PDE4D3

Changes in intracellular cAMP release

Change in PKA activity

Higher PKA phosphorylation of CREB

RESULTS

COMPUTATIONAL STUDIES DATA

SNPs #	Amino acid positions	Nucleotide change	Amino acid change	Binding domain	Occurrence
1	1653	A/C	Serine (S) to Arginine (R)	PDE4D3	Frequent in American, European, Canadian and Italian population
2	2124	A/G	Glutamic acid (E) to Glycine (G)	3'-PKA RII	Exclusively frequent in African American population

Figure 1: Summary of computational studies.
This table shows two mAKAP SNPs to be studied highlighting their position in the mAKAP protein and occurrence.

QUERY	1633 LDLLNRLENIQSPSEQKIKRSVSDI 2104 LRKGDFYSYLSLSSHSDCDEVNYIEE
dogs	1633 LDLLNRLENIQSPSEQKIKRSVSDI 2104 LRKGDFYSYLSLSSHSDCDEVNYIEE
mouse	1633 LDLLNRLENIQSPSEQKIKRSVSDI 2104 LRKGDFYSYLSLSSHSDCDEVNYIEE
domestic cow	1633 LDLLNRLENIQSPSEQKIKRSVSDI 2104 LRKGDFYSYLSLSSHSDCDEVNYIEE
rats	1633 LDLLNRLENIQSPSEQKIKRSVSDI 2104 LRKGDFYSYLSLSSHSDCDEVNYIEE
gray short duckbill platy	1633 LDLLNRLENIQSPSEQKIKRSVSDI 2104 LRKGDFYSYLSLSSHSDCDEVNYIEE

Figure 2: The homology studies for human mAKAP Serine1653 and Glutamic acid2124. The amino acid residues (serine 1653 and glutamic acid 2124; highlighted) are evolutionarily conserved among different species. This shows that Serine and Glutamic acid residues are extremely crucial for mAKAP function.

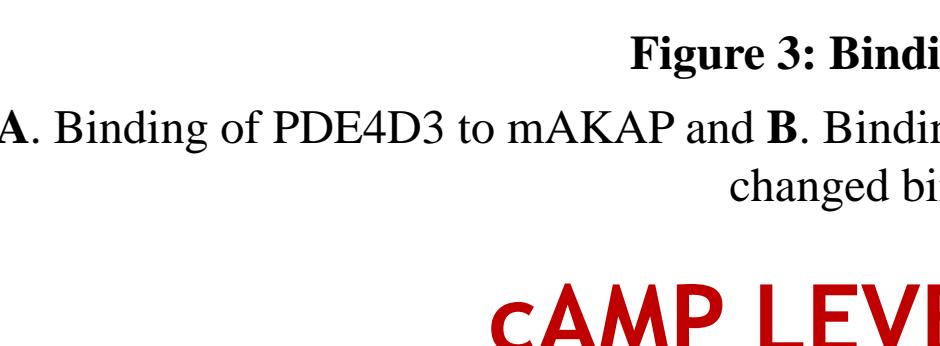
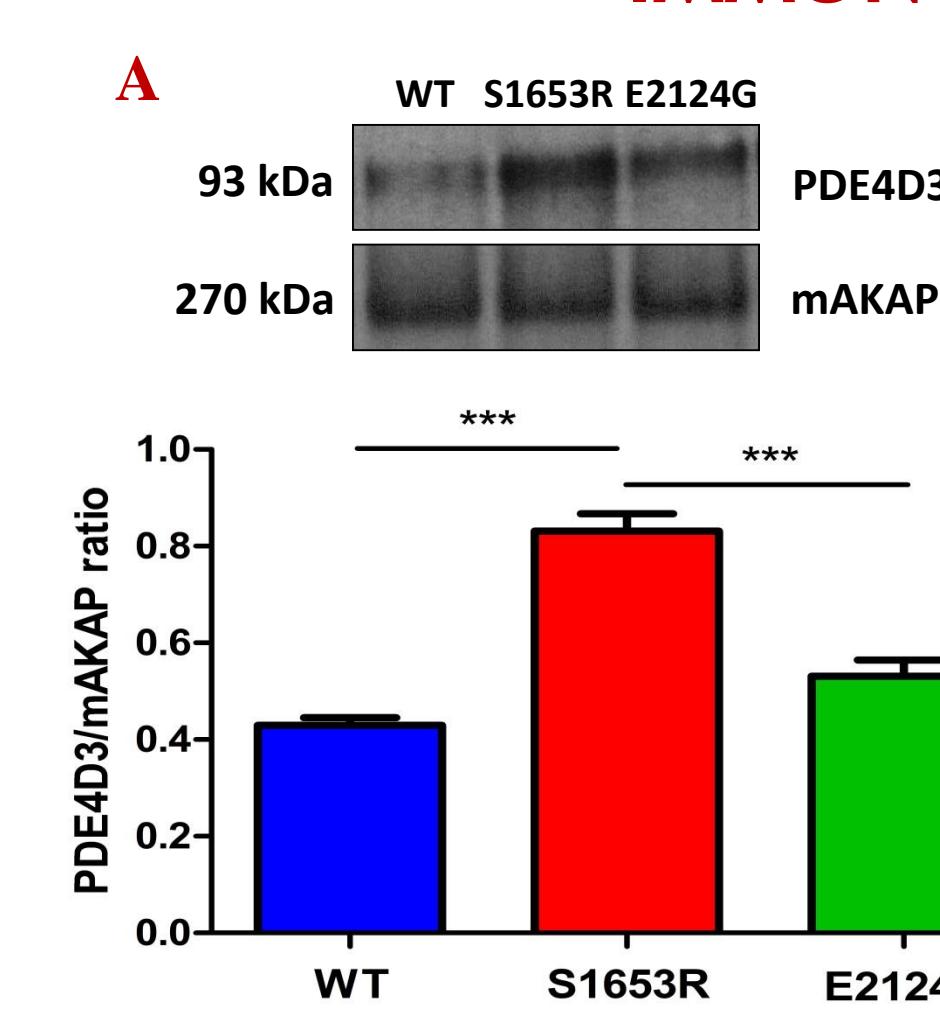
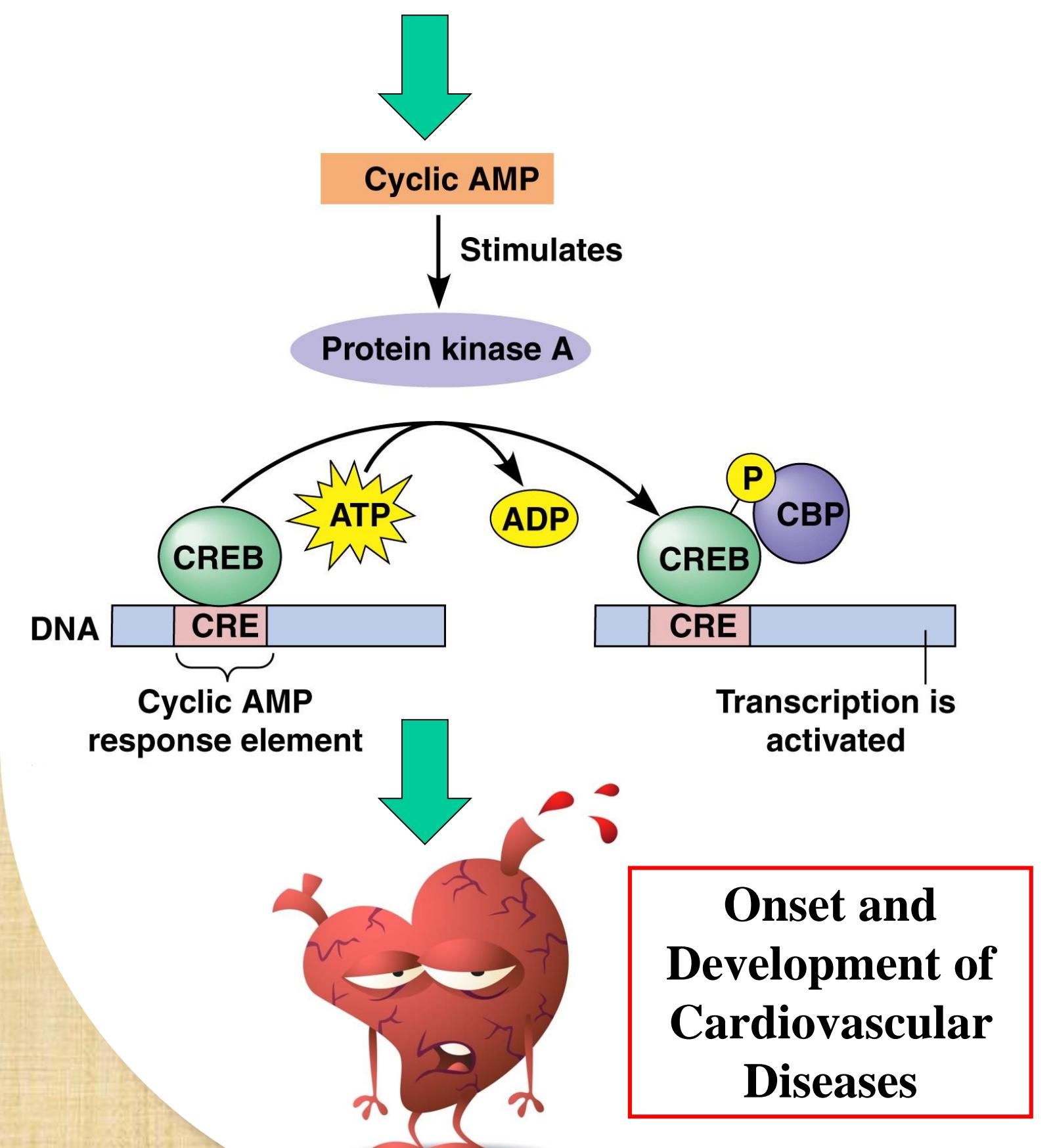
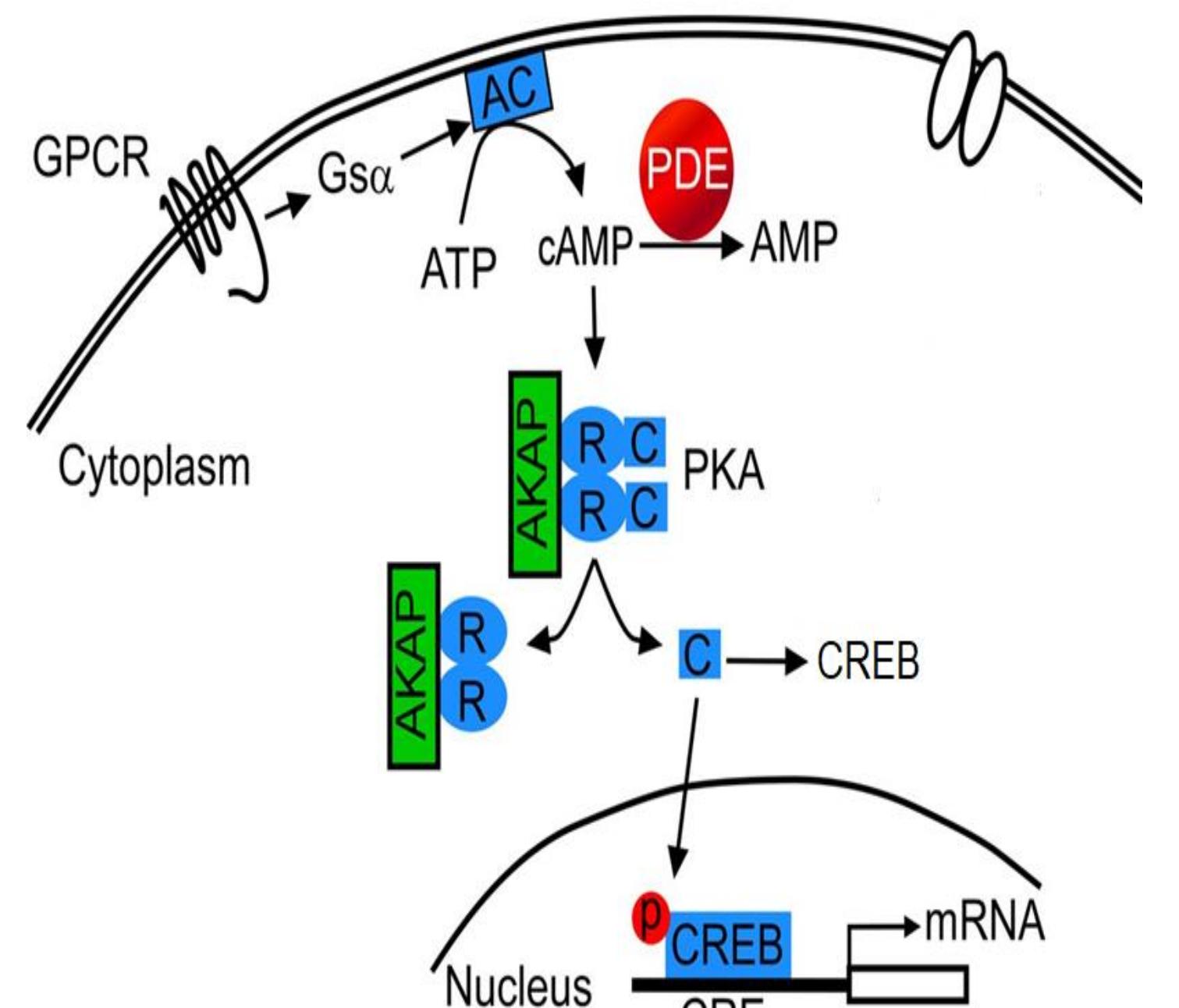


Figure 3: Binding of PDE4D3 and PKA to WT and mutant mAKAP. Immunoprecipitation results showed that mAKAP polymorphisms changed binding of PDE4D3 and PKA to mAKAP differently.

CAMP LEVELS and PKA ACTIVITY DATA

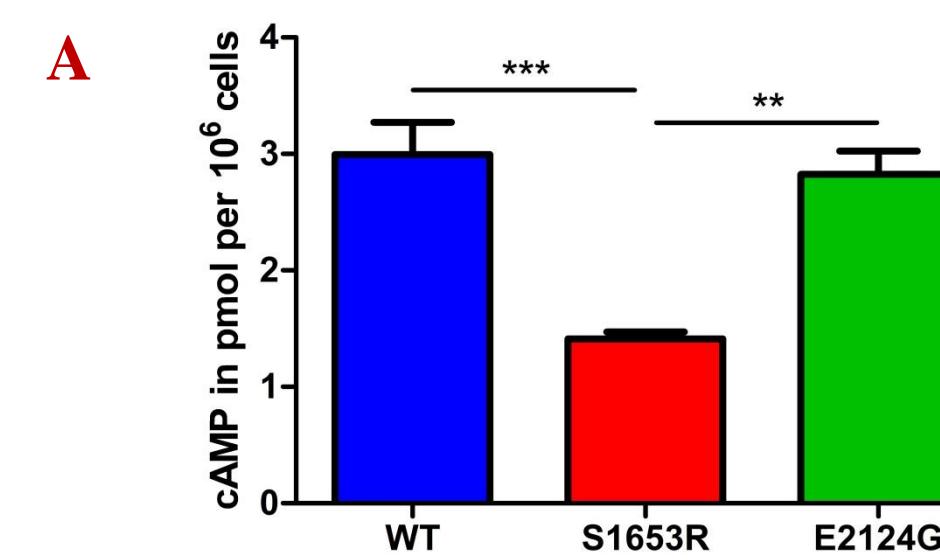


Figure 4: Direct cAMP levels and PKA activity assay. Intracellular cAMP measured as pmol/10⁶ cells. B. PKA activity normalized to per µg of protein. Each sample is performed in triplicate and four independent experiment were done for analyses.

CREB PHOSPHORYLATION

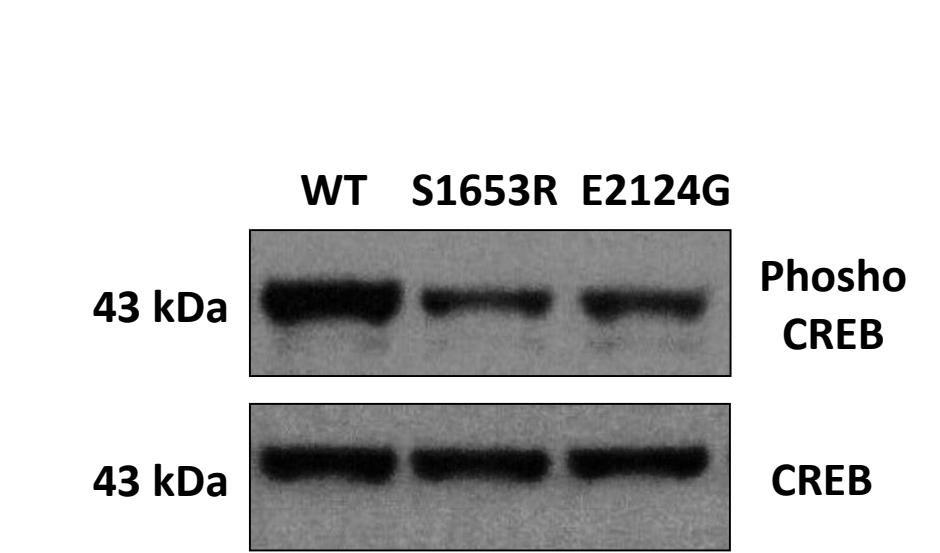


Figure 5: Western blotting. Western blot analysis of PKA phosphorylation of CREB. Left panel shows the bands with phospho-CREB and total CREB antibodies and right panel shows the corresponding quantifications graphs.

INNOVATION

- This is the **FIRST study** to find out the relationship between the genetics of AKAPs and heart disease.
- Abstract based on this poster is **accepted** for the world's no. 1 heart conference (AHA) in Anaheim, California.

CONCLUSIONS

- mAKAP polymorphisms may pre-dispose humans to CVDs by altering cAMP/PKA signaling in the heart.**
- PKA-mAKAP interaction modulators can be developed as therapeutic target to augment current treatment of CVDs.**