Identifying transcription factors of pxdn and pxdnl in the cardiovascular system usingbioinformatics tools

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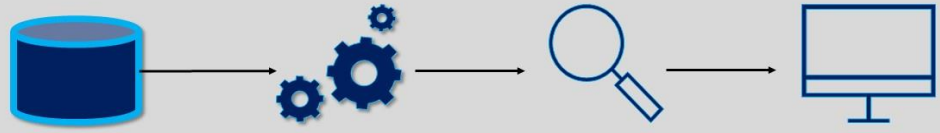
Identifying Transcription Factors (TFs) of *PXDN* and *PXDNL* in Cardiovascular Cells using Bioinformatics Tools

ChIP Atlas Database → Bioinformatics Tools → Data Analysis → Data Visualisation



Results

Number of TFs identified for PXDN and PXDNL using different bioinformatics tools

Bioinformatics Tool	No. of TFs identified for PXDN	No. of TFs identified for PXDNL
Peak Browser Tool	16	6
Peak Enrichment Tool	17	5
R Studios (ChIPseeker)	13	3

Conclusion

TFs identified in this study, including RELA (vital for immune system development and immune response), BRD4 (transcriptional activator of proteins involved in ECM formation), and TAL1 (vital for healthy heart formation), coupled with the known functions of PXDN and PXDNL, suggests that their dysregulation can promote the development of cardiovascular diseases through mechanisms involving extracellular matrix organization, immune system response, and cardiovascular cell development

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Introduction: Peroxidasin (*PXDN*) and Peroxidasin-like (*PXDNL*) proteins have been implicated in a variety of cardiovascular diseases. Peroxidasin is a haem-peroxidase involved in vital cell functions, such as cell development, extracellular matrix deposition, and immune response. Peroxidasin-like protein is a homolog of PXDN lacking enzymatic activity but thought to regulate PXDN function. Both genes are expressed in cardiovascular cells, but their roles in cardiovascular diseases remains unknown. This study aimed to identify transcription factors which regulate *PXDN* and *PXDNL* in cardiovascular cells using bioinformatics tools.

Methodology: ChIPseq data retrieved from the ChIP Atlas database was analysed using three tools: Peak Browser and Enrichment Analysis Tools were used to identify statistically significant transcription factors near the Transcription Start Sites (TSS) of both genes, and ChIPseeker package for R Studios was used to filter results and identify statistically significant transcription factors in the promoter and distal intergenic regions of both genes.

Results: 13 major transcription factors were identified for *PXDN* and 3 for *PXDNL*. Transcription factors EP300, RELA and TCF 21, were common to both genes, and are known to play important roles in cardiovascular cell development and immune system signalling.

Discussion and Conclusion: The transcription factors identified in this study, coupled with the known functions of PXDN and PXDNL, suggests that their dysregulation can promote the development of cardiovascular diseases through mechanisms involving the extracellular matrix organisation, immune system response and cell development. Future research can elucidate these mechanisms using a multi-omics approach.

Key References:

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Keywords: Peroxidasin, transcription factors, cardiovascular cells, gene regulation, bioinformatics, ChIPseq