

by ubiquitin-dependent pathway. Regulation of α -SMA by JNK signaling pathway may lead to new approaches in the treatment of progressive renal fibrosis

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A Functional Genomic Screen for Cardiogenic Genes Using RNA Interference in Developing *Drosophila* Embryos

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Identifying genetic components is an essential step toward understanding complex developmental processes. The primitive heart of the fruit fly, the dorsal vessel, which is a hemolymph-pumping organ, has provided a unique model system to identify cardiogenic genes and to further our understanding of the molecular mechanisms of cardiogenesis. Using RNA interference in developing *Drosophila* embryos, we performed a genomewide search

for cardiogenic genes. Through analyses of the >5,800 genes that cover 40% of all predicted *Drosophila* genes, we identified a variety of genes encoding transcription factors and cell signaling proteins required for different steps during heart development. Analysis of mutant heart phenotypes and identified genes suggests that the *Drosophila* heart tube is segmentally patterned, like axial patterning, but assembled with regional modules. One of the identified genes, *smjang*, was further characterized. In the *smjang* mutant embryo, we found that within each segment a subset of cardiac cells is missing. Interestingly, the *smjang* gene encodes a protein that is a component of the chromatin remodeling complex recruited by methyl-CpG-DNA binding proteins, suggesting that epigenetic information is crucial for specifying cardiac precursors. Together, these studies not only identify key regulators but also reveal mechanisms underlying heart development and disease.

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Overexpression of SMP30 Inhibits Radiation-Induced Apoptosis in Smad3-Knockout Mice Liver

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