

CentHub : Designing a database of centrosomal proteins identified by mass spectrometry

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The centriole is a macromolecular structure that plays a key role in the formation of flagella, cilia and centrosomes. Knowledge about the structure and composition of this cellular organelle has been mainly gathered by immunofluorescence. Over the last twenty years, mass spectrometry has been used to generate a list of proteins that may be part of the centriole. Recently, the combination of cryo-ET and structure prediction algorithms has allowed the mapping of individual proteins within the centriole. In this context, we designed *CentHub*, an online resource, to centralize and organize information from centriole proteomics. *CentHub* is initialized with the proteins identified in published papers and includes the orthologous proteins of each entry.

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