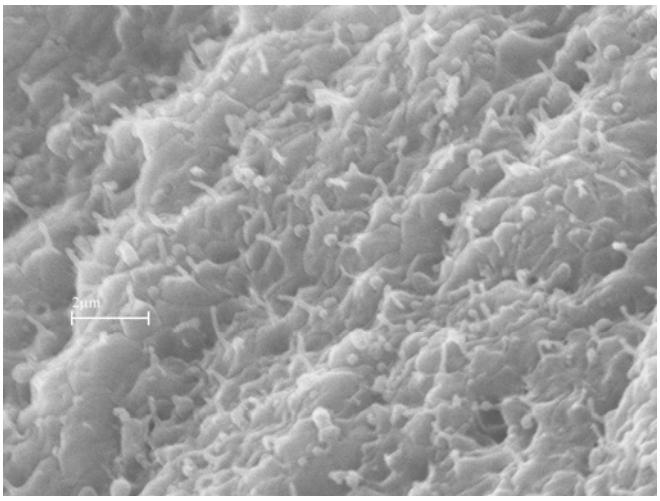
Analysis of the embryonic cerebrospinal fluid proteome

The progenitor cells of the developing cerebral cortex proliferate immediately adjacent to the cerebrospinal fluid (CSF)-filled ventricles of the brain. These progenitors also extend primary cilia directly into the CSF, raising the possibility that progenitor cells might obtain diffusible signals from the CSF that guide their development.

We carried out mass spectrometry on human fetal and embryonic rat CSF in order to investigate if the embryonic CSF contains important factors that might stimulate brain growth (Zappaterra et al., 2007). Rat and human CSF exhibited tremendous similarity and contained hundreds of proteins, including protease inhibitors, extracellular matrix proteins, transport proteins, and signaling proteins. This study provides a first step towards understanding when and how distinct factors in the CSF proteome might influence the development of the brain.



Scanning electron microscopy of the E12.5 mouse ventricular zone showing primary cilia extending into the ventricular space from cortical progenitor cells.

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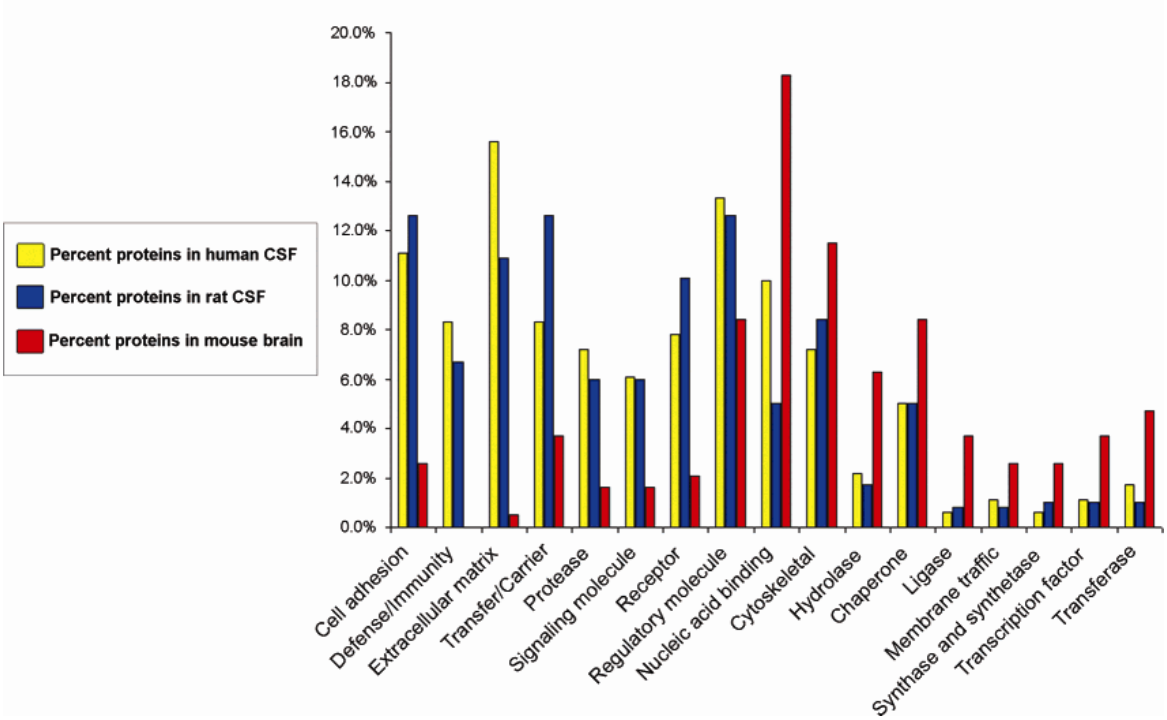

Comparison of proteins based on molecular function. Proteins present in embryonic human CSF, embryonic rat CSF, and embryonic mouse brain were analyzed using the Panther gene ontology database and classified according to molecular function. Chart includes protein category name, and percentage is calculated from number of proteins assigned to each category over total number of proteins analyzed. We show a comparison between human CSF, rat CSF, and mouse brain of the relative percentages from relevant categories based on molecular function.

Reference: A Comparative Proteomic Analysis of Human and Rat Embryonic Cerebrospinal Fluid. Zappaterra MD, Lisgo SN, Lindsay S, Gygi SP, Walsh CA, Ballif BA. J Proteome Res. 2007 Sep 7;6(9):3537-3548.