

ANNOTATING THE HUMAN PROTEOME

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The completion of the human genome has shifted the attention from deciphering the sequence to the identification and characterization of the encoded components. The identification and functional annotation of the proteome is here of special interest and reaches from the identification of genes and transcripts functional information on many human proteins. Public domain databases are required to manage and collate this information and present it to the user community in both a human and machine readable manner. My talk will concentrate on the current status of annotating the human proteome, achievements and shortcomings, and future prospects towards a more complete characterization of human gene products, especially in the light of large-scale sequencing projects aimed on studying human variation.