The phylogenetic tree depicts the relationships between members of the complete superfamily of human protein kinases. Protein kinases constitute one of the largest superfamilies of protein-coding genes. They are defined by the presence of protein kinase catalytic domains, which control protein activity by catalyzing the addition of a negatively charged phosphate group to other proteins. Protein-kinase domains have a wide variety of biological functions, especially those that carry signals from the cell membrane to intracellular targets and coordinate complex biological functions. The phylogenetic tree belonging to a single superfamily of enzymes where catalytic domains are related to sequence and structure. The phylogenetic tree depicts the relationships between proteins based on sequence similarity between proteins in the protein sequence alignment of these catalytic domains. Most kinases fall into small families of highly related sequences, and most families are part of larger groups. The seven major groups are labeled and colored distinctly. Other kinases are shown in the center of the tree, colored gray. The relationships shown on the phylogenetic tree illustrate the nature and biological function for many of the over 100 uncharacterized kinases presented here.

The main dendrogram shows the sequence similarity between protein kinase domains, derived from public sequences and gene-prediction methods detailed in Manning et al. (Science 2002). Dendrograms derived from Motif Matrix model profile analysis and multiple sequence alignment. To infer evolutionary relationships between protein kinases, a Markov model profile analysis and multiple sequence alignment. The initial branching pattern was built from a neighbor-joining tree derived from a ClustalW Markov model profile analysis and multiple sequence alignment. The initial branch lengths are semiquantitative, but the branching pattern was modified by extensive pairwise sequence alignment of kinase domains. The new tree was extensively modified by extensive pairwise sequence alignment of kinase domains. The new tree was extensively modified by extensive pairwise sequence alignment of kinase domains. The new tree was extensively modified by extensive pairwise sequence alignment of kinase domains. The new tree was extensively modified by extensive pairwise sequence alignment of kinase domains. The new tree was extensively modified by extensive pairwise sequence alignment of kinase domains. The new tree was extensively modified by extensive pairwise sequence alignment of kinase domains.

Mapping Proteomes
The new developed shows the sequence similarity between protein kinases. The tree was derived from public sequences and gene-prediction methods. The protein sequence alignment of the domains. The tree was extensively modified by extensive pairwise sequence alignment of kinase domains. The new tree was extensively modified by extensive pairwise sequence alignment of kinase domains. The new tree was extensively modified by extensive pairwise sequence alignment of kinase domains. The new tree was extensively modified by extensive pairwise sequence alignment of kinase domains.

The inset diagram shows trees for seven atypical protein kinase families. These proteins have verified or strongly predicted kinase activity, but have little or no sequence similarity to members of the protein kinase superfamily. A further eight atypical protein kinases in small families of one or two genes are not shown.

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Authors

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