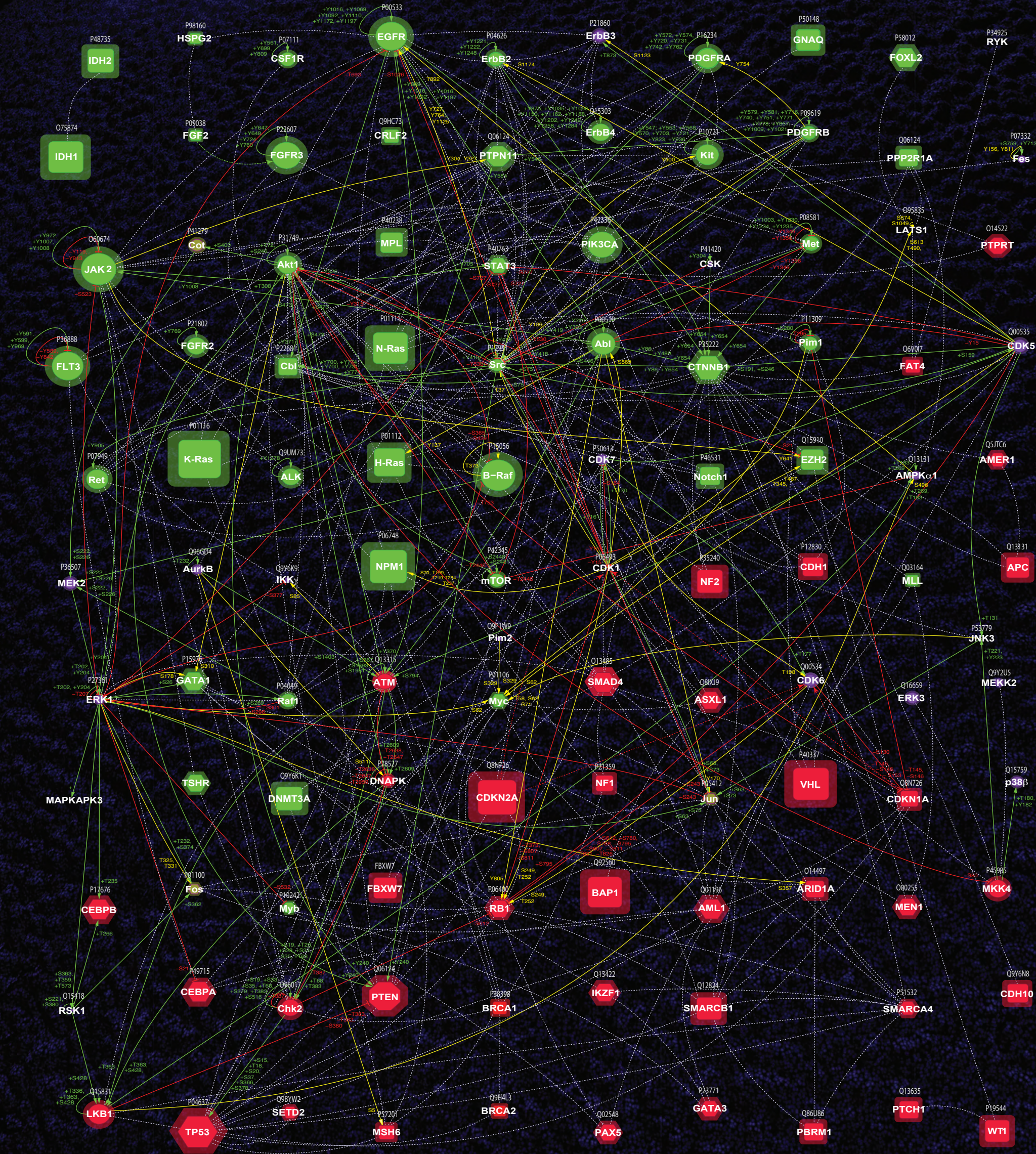




## www.OncoNET.ca Human Cancer Protein Interaction Network



This protein interaction map displays those oncoproteins (red icons) and tumour suppressor proteins (green icons) that have demonstrated the highest rates of mutation (per 100 amino acids residues) in over 24,000 human tumours as well as a few proteins with some of the lowest rates, which appear to be tumour requiring proteins (purple icons). The size of each protein icon is related to the log<sub>10</sub> of the mutation rate for the protein as determined on the [www.onconet.ca](http://www.onconet.ca) website, which is based primarily on data collected from the Wellcome Trust Sanger Institute's Catalogue of Somatic Mutations in Cancer (COSMIC) database. Protein icon shape: Kinases - round; Phosphatases - octagon; Transcription factors - hexagon; Other proteins - square.

Kinase-substrate interactions were retrieved from [www.kinasenet.ca](http://www.kinasenet.ca) and other protein-protein interactions were obtained from [www.kinatlas.ca](http://www.kinatlas.ca) and the STRING database ([www.string-db.org](http://www.string-db.org)). Cytoscape v3.4 was used to initially render the map. Activating phosphorylation is shown with green solid arrows and green text for the phosphosites. Inhibitory phosphorylation are depicted with red solid lines and red text for the phosphosites. Undefined phosphorylation is indicated with yellow solid arrows and yellow text for the phosphosites. All other protein-protein interactions are shown with light grey dashed lines. More information about these proteins and their phosphorylation is available at [www.onconet.ca](http://www.onconet.ca), [www.kinasenet.ca](http://www.kinasenet.ca) and [www.phosphonet.ca](http://www.phosphonet.ca).