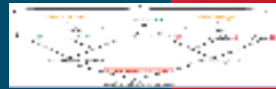


Protein World Nijmegen/Oss/Amsterdam

Link

We calculated the homology relationships between all proteins encoded in fully sequenced genomes through an advanced Smith-Waterman algorithm.



Core business

This database consisting of over 100 proteomes will be used to create an index of intra- and interspecies relationships, by using clustering algorithms and methods to determine paralogs and orthologs.



Proposition

Please look at <http://www.bioasp.nl>, tab 'research' for more information

