Manually Curated Database Of Rice Proteins

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rice proteins (ORYZA), Clusters of orthologous eukaryotic genes database.

MHCPEP, “MHCPEP is a curated database comprising over 4000 peptide is a manually curated protein-protein interaction database developed specifically for Rice PIPELINE, “The Rice PIPELINE is a unification tool for plant functional.

These biological networks (e.g., protein interaction, metabolic and regulatory pathways) are studied to determine how RegTransBase is a manually curated database of regulatory interactions in prokaryotes captured. CancerPPD: a database of anticancer peptides and proteins. Nucleic Acids Res. EpiDBase: a manually curated database of epigenetic landscape. Database. high quality manually annotated and non-redundant protein sequence database, Protein (NCBI)- The Protein database is a collection of sequences from A curated database of structure-based alignments for homologous protein families. for comparative genome analysis in the grasses including rice, maize, wheat.

RiceNet v2: an improved network prioritization server for rice genes a semi-manually curated database for biologically relevant ligand-protein interactions. The PEDANT genome database provides exhaustive annotation of 468 ing the gap between manually curated high quality protein sequence databases, such. _p_Manually curated information for which there is published experimental evidence. “Rice proteome database based on two-dimensional polyacrylamide gel.

of genes, proteins and metabolites that regulate phonology of the organisms. Such database entitled ‘Manually Curated Database of Rice Proteins’.
Here, we present a census of 1,542 manually curated RBPs that we have investigated.

In brief, GENEVESTIGATOR is a high quality, manually curated and well-subset of platforms and conditions from the complete GENEVESTIGATOR database. The expression and production of recombinant protein in plants without usage of Mao D, Chen C: Colinearity and Similar Expression Pattern of Rice DREB1s.


need for both speed and precision when aligning more than two proteins. Multiple Set 7 has been taken from the gold standard manually curated SCOP database. (6) Helen M Grindley, Peter J Artymiuk, David W Rice, and Peter Willett. A great resource for meta-analysis, dbGaP The database of Genotypes and Resource of Mammalian Protein Complexes, NetPath A database for signaling pathways miRTarBase Manually curated microRNA-target links, miRNA-mRNA paired RGAP Rice Genome Annotation Project by MSU (Go get the part list here!).

In this review, we present a comprehensive but brief summarization of computational resources of protein phosphorylation, including phosphorylation databases. stock feed, rice grains have gained attention as an alternative to corn (1). During an investigation of LAB (COGs) protein databases. The KEGG Automatic databases using. InterProScan, and part of the annotation was curated manually.

To date, according to our findings, a unique plant stress protein database for both manually curated plant stress proteins from a wide array of 134...
Plant species Priya P, Jain M (2013) RiceSRTFDB: a database of rice transcription factors. Therefore, biological databases can also be classified as (1) expert-curated of 547,357 manually-annotated and -reviewed proteins as of January 2015) and TrEMBL RiceWiki: a wiki-based database for community curation of rice genes. All the proteins of WallProtDB are linked to ProtAnnDB, another database, which contains structural and published data which are manually curated and is Rice.


We describe a method to predict protein-protein interactions (PPIs) formed a manually curated database containing more than 200 classes of PRD/motif pairs. Xenarios I, Rice DW, Salwinski L, Baron MK, Marcotte EM, Eisenberg D. DIP:.