

Browse the database per chromosome

All Chr01 Chr02 Chr03 Chr04 Chr05 Chr06 Chr07 Chr08 Chr09 Chr10 Chr11 Chr12

--- DATABASE SEARCH

WELCOME

Proteogenomics (PG) is a recent research trend aiming genomic features in both eukaryotic and prokaryotic organism transition evidence of the genes. While, the MS/MS proteomics data. Thus, the MS/MS based peptides-based proteogenomics projects.

The Rice Proteogenomics Project (RPP), in the Institute for the genome annotation of the rice following a Proteogenomics establishment of the analytical pipelines (experimental and an online database system for the storage of the resultant data.

OryzaPG-DB is the rice proteogenomics database developed proteomics of the rice undifferentiated cultured cells, the current novel proteogenomics features and the updated gene models.

The information is provides in three flavors browsing, see each novel peptide and the visualization of the new annotations.

For more information about how to use OryzaPG-DB, please

The Database Currently Contains:

Genes/us-mRNAs: 3182
Proteins/cDNA: 5034
Total Peptides: 15124
Novel Peptides: 166
Genes to Be Revised: 40

KEIO UNIVERSITY

Institute for Advanced Biosciences
Keio University

Advanced Search Result

Search parameters Chromosome # 1 Next Records 1 to 25 of 51

Chrf	Gene	Description	Details
1	LOC_Os01g33060	protein HEAT repeat family protein, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
1	LOC_Os01g24958	protein heat shock stable phosphoprotein, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
1	LOC_Os01g60040	protein HEAT repeat family protein, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
1	LOC_Os01g24958	protein HEAT repeat family protein, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
1	LOC_Os01g70250	protein HEAT repeat family protein, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
2	LOC_Os02g07310	protein HEAT repeat family protein, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
2	LOC_Os02g18020	protein heat shock protein DnaJ, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
2	LOC_Os02g40430	protein HEAT repeat family protein, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
2	LOC_Os02g40820	protein heat shock protein ST1, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
2	LOC_Os02g52150	protein heat shock 22 kDa protein, mitochondrial precursor, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
3	LOC_Os03g10540	protein HEAT repeat family protein, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
3	LOC_Os03g27460	protein heat shock protein DnaJ, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
3	LOC_Os03g19420	protein HEAT repeat family protein, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
3	LOC_Os03g51140	protein HEAT repeat family protein, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
3	LOC_Os03g21180	protein heat shock protein DnaJ, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
4	LOC_Os04g01740	protein heat shock protein, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
4	LOC_Os04g21100	protein heat shock protein binding protein, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
4	LOC_Os04g42840	protein HEAT repeat family protein, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
4	LOC_Os04g11180	protein heat shock protein ST1, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
4	LOC_Os04g21180	protein heat shock protein, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
4	LOC_Os04g21100	protein heat shock protein binding protein, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
4	LOC_Os04g42840	protein HEAT repeat family protein, putative, expressed	Protein Product(s) cDNA(s) Translat... Visualization Updated Annotation
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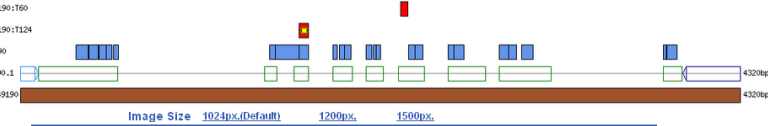
Gene Model Detailed View

Gene
MSUTJGR (V6.1) Locus: LOC_Os01g49190 Chromosome # 1 Gene Model Annotation: Updated Annotation (sG)P
Description: protein ATP synthase, putative, expressed
Total peptides: 193 Alternative Splice Products: 1

Peptides Assessment and Gene Model Visualization

Total peptides: 193 Novel Peptides and Genomic Features (2)
Peptides' sources: 1- Intrinsic Peptides: 0
1- From Protein DB: 191 2- Acceptor Spanning Peptides: 0
2- From cDNA DB: 0 3- Donor Spanning Peptides: 1
3- From Transcript DB: 2 ExonDef.details
4- From Genome DB: 0

Annotation and proteomic features of LOC_Os01g49190 gene
Annotation visualization and feature assessment by PGV v0.01



Protein(s)
MSUTJGR (V6.1) Locus: LOC_Os01g49190 Model Locus: LOC_Os01g49190.1
Model: 1310.1m05114 Leihgt: 558AA Sequence (FASTA)
Description: protein ATP synthase, putative, expressed

cDNA(s)
MSUTJGR (V6.1) Locus: LOC_Os01g49190 Model Locus: LOC_Os01g49190.1
Model: 1310.1m05114 Leihgt: 2130Bp Sequence (FASTA)
Description: cDNA ATP synthase, putative, expressed

Transcript (unspliced-mRNA)
MSUTJGR (V6.1) Locus: LOC_Os01g49190
Transcription Unit: 1310.1m05114 Leihgt: 4321Bp Sequence (FASTA)
Description: unspliced-genomic ATP synthase, putative, expressed

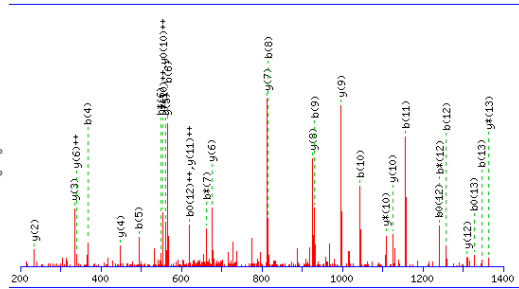
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lascot Peptide View

Peptide View

MS/MS Fragmentation of QAAALQALHDLITSK found in **chromosome01 IRGSP pseudomolecules Build05-1**, chromosome01 translated in frame 5 (nucleic acid sequence)

MS/MS Match to Query 6444: 1490.808212 from (746.411382,2+) Title: Elution from: 66.225 to 66.225 scan no 9804 polarity+ data file Rice01nm.mgf



monoisotopic mass of neutral peptide Mr (calc): 1490.8093
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
-term : Gln-pyrrro-Glu (N-term Q)
ions Score: 65 Expect: 0.0007
atches (Bold Red) : 31/138 fragment ions using 54 most intense peaks

#	b	b ⁺⁺	b ⁺	b ⁰	y	y ⁺⁺
1	112.0393	56.5233	95.0128	48.0100	Q	
2	183.0764	92.0419	166.0499	83.5286	A	1380.7845 690.8959
3	254.1135	127.5604	237.0870	119.0471	A	1309.7474 655.3774