**Supplementary Information**

**PvP01-DB: Computational Structural and Functional Characterization of Soluble Proteome of PvP01 Strain of *Plasmodium vivax***

Ankita Singh1, 4, Rahul Kaushik1, 5, Dheeraj Kumar Chaurasia1, Manpreet Singh1, B. Jayaram1, 2, 3, \*

1Supercomputing Facility for Bioinformatics & Computational Biology, Indian Institute of Technology Delhi, Hauz Khas, New Delhi, India

2Kusuma School of Biological Sciences, Indian Institute of Technology Delhi, Hauz Khas, New Delhi, India

3Department of Chemistry, Indian Institute of Technology Delhi, Hauz Khas, New Delhi, India

4Present Address: Centre of Evolution and Medicine, Arizona State University, Tempe, USA

5Present Address: Laboratory for Structural Bioinformatics, Center for Biosystems Dynamics Research, RIKEN, Yokohama, Japan

E-mail: bjayaram@chemistry.iitd.ac.in; ankita@scfbio-iitd.res.in

Website: [www.scfbio-iitd.res.in](http://www.scfbio-iitd.res.in)

**Supplementary Information**

**Table S1.** A List Sequence Based Features Provided in the PvP01 Web Resource.

|  |  |
| --- | --- |
| Sequence Length | Amino Acid Compositions |
| Protein Sequence | Secondary Structural Content |
| Isoelectric Point | Deviation for Occurrence Frequencies |
| Molecular Weight | Predicted Secondary Structure |
| Instability Index | Structural Difficulty Index |
| Aliphatic Index | External Database Links |

**Table S2.** Details of Tools Used in Development of PvP01 Web Resource.

|  |  |
| --- | --- |
| **Tool Name** | **Tool Description** |
| *SD Index* | Structural Difficulty (SD) Index provides insights into the possibility of a reliable tertiary structure prediction of a protein based on its physico-chemical, secondary structural and homology based feature calculation. |
| PSIPRED | PSIPRED is PSI-BALST based protein secondary structure prediction tool which implements neural networks on sequence profiles adopted from PSI-BLAST to predict the secondary structure of a protein sequence. |
| PSSPred | PSSPred is another Protein Secondary Structure Prediction tool based on simple neural network training algorithm. The prediction is integration of seven differently trained neural network learning models and profile data. |
| SPIDER3 | SPIDER3 is an iterative deep learning neural network based prediction software which implements sequence based local and non-local protein information in each iteration of training and prediction. |
| BhageerathH+ | BhageerathH+ is an integrated software suite for protein tertiary structure prediction of globular proteins. It implements *ab initio*, homology and hybrid approaches for structure prediction through its various modules. |
| I-TASSER | I-TASSER is an iterative threading, assembly and refinement approach based protein tertiary structure prediction software suite. The potential templates are identified by using multiple threading approach. |
| RaptorX | RaptorX is a statistical model which performs protein tertiary structure prediction via remote homolog detection and protein threading methods without performing conventional profile-profile matching. |
| GalaxyRefine | GalaxyRefine is a protein structural quality refinement tool which first rebuilds side chains of input protein structure, followed by its side-chain repacking and finally performs overall structure relaxation by molecular dynamics simulation to improve local and global structural quality. |
| ProTSAV | ProTSAV is a protein tertiary structure analysis and validation method which integrates 10 different individual tools of protein structural property calculation to perform a comprehensive and reliable quality assessment. |
| ADDS | The AADS methodology implements physicochemical features of functional groups lining the cavities on the protein surface for ligand binding site prediction. |
| FPocket | F-pocket predicts the potential ligand binding sites based on Voronoi partition and alpha sphere theory and the pocket ranking is performed via Partial Least Square fitting. |
| LIGSITECSC | LigSite captures surface-solvent-surface events via protein’s Connolly surfaces and identified pockets are ranked on the basis of the extent of conservation of surface residues involved. |
| InterPro | InterPro performs an extensive protein sequence analysis and classification via various prediction models assembled from different databases. |
| SIFTER | SIFTER offers a statistical approach using phylogenetic analysis for representing protein relationships and functional characterization. |
| LocTree3 | LocTree is a machine learning based hierarchical system for experimental localizations and function prediction of proteins. |
| ProBis | ProBis is a protein structure surface conservation based similar protein binding sites detection which assigns protein function depending on the extent of similarity of binding sites of target protein to the known proteins. |
| KEGG | The KEGG pathway map is a molecular interaction/reaction network diagram represented in terms of the KEGG orthology (KO) groups, so that experimental evidence in specific organisms can be generalized. |

**Table S3.** A summary of structural property assessment tools used as a part of ProTSAV for performing the quality assessment of predicted model structures in PvP01 web resource.

|  |  |
| --- | --- |
| PROCHECK | Procheck evaluates stereo chemical quality of a given protein structure by calculating deviation in the geometry of residues from their standard values which are derived from well-refined, high-resolution native structures. |
| ProSA | ProSA calculates overall protein structure quality score in terms of Z-score and performs statistical comparison with experimental protein structures. It utilizes knowledge-based Cα potentials of mean force to estimate model accuracy. |
| ProQ | ProQ is a neural-network based method which utilizes various structural features, such as frequency of atom–atom contacts, solvent accessible surface area, residue–residue contacts etc. and generates LG Score and MaxSub Score. |
| Verify-3D | Verify-3D compares 3D-1D profiles of a protein structure. The match of an atomic model (3D) is assessed with its own amino acid sequence (1D) and a quality score is predicted with parameters derived from database of experimental structures. |
| Naccess | Naccess calculates solvent exposed surface area of all atoms and residues with defined probe size. It helps in better insights on structure by comparing residue-wise surface area with experimental structure. |
| ERRAT | ERRAT distinguishes correctly modeled regions from incorrectly modeled regions in the protein structures by evaluating certain characteristic atomic interactions. |
| D2N | D2N is a random forest approach based machine learning tool which predicts the quality of a protein structure derived from different physico-chemical features of native protein structures. |
| dFIRE | dFIRE is an energy function which reports for pair-wise atomic interactions and dipole-dipole interactions among the amino acid residues. For a given protein structure it provides a set of free energy scores. |
| MolProbity | MolProbity assesses all-atom contacts, side chain clashes, and Ramachandran distribution of backbone dihedral angles (ɸ and Ψ) as the major structural parameters. |

**Table S4.** A summary of search keywords which can be used for a systematic and specific browsing of PvP01 web resource.

|  |  |
| --- | --- |
| **Search Keyword** | **Brief Description** |
| Protein Sequence | User can provide amino acid sequence in single letter code of desired protein. The output will result in a PvP01 identifier corresponding to input sequence. |
| Chromosome Number | The genome of *P. vivax* consists of 14 chromosomes and user can browse the database for proteins corresponding to any of the chromosomes by selecting chromosome number(s). |
| UniProt Identifier | **It is a unique identifier (6 or 10 letter alphanumeric string) assigned to each protein deposited in UniProt.** |
| Protein Name | User can explore the database with the help of protein names. |
| Gene Ontology (GO)  | **The GO terms are unique accession numbers** of gene and gene product attributes across all species and can be used as search keywords in PvP01 web resource. |
| Protein Family or Pfam Identifier | Name of protein families or their Pfam identifiers can be used for exploring the databank. A Pfam identifier is a seven letter alphanumeric string. |
| InterPro Identifier | The InterPro database assigns each entry with a unique accession number in the form of an alphanumeric string starting with a prefix ‘IPR’ |
| RefSeq Identifier (RefSeq ID) | RefSeq Identifier is a unique identifier number for proteins in PvP01 we resource which refers to non-redundant and explicitly linked protein sequences. |
| PvP01 Identifier | PvP01 identifier is a 14 letter unique alphanumeric string assigned to all proteins of PvP01 strain of *P. vivax* by PlasmoDB.  |

**Table S5.** A list of PvP01 identifier(s) for which the metabolic pathways information in provided in PvP01 web resource along with corresponding metabolic pathway(s) name.

|  |  |
| --- | --- |
| **PVP01 ID** | **Pathways** |
| PVP01\_0116400 | Proteosome |
| PVP01\_0117900 | Ribosome Biogenesis |
| PVP01\_0118200 | Arginine Biosynthesis; Glutamate Metabolism; Terpenoid Backbone Biosynthesis; Metabolic Pathways |
| PVP01\_0203400 | RNA Transport |
| PVP01\_0208100 | Ribosome Biogenesis |
| PVP01\_0210300 | Terpenoid Backbone Biosynthesis; Biosynthesis of Antibiotics; Biosynthesis of Sec. Metabolites; Metabolic Pathways |
| PVP01\_0212000 | Mismatch Repair |
| PVP01\_0212500 | N-Glycan Biosynthesis; Metabolic Pathways; Protein Processing in Endoplasmic Reticulum |
| PVP01\_0303000 | Spliceosome |
| PVP01\_0308000 | Malaria |
| PVP01\_0308900 | DNA Replication; Homologous Recombination; Mismatch Repair; Nucleotide Excision Repair |
| PVP01\_0309700 | RNADegradation |
| PVP01\_0320000 | Ubiquinone Other Terpenoid-quinone Biosynthesis; Biosynthesis of Sec. Metabolites; Metabolic Pathways |
| PVP01\_0320700 | Mismatch Repair |
| PVP01\_0407900 | Metabolic Pathways; Oxidative Phosphorylation |
| PVP01\_0410800 | Protein Processing in Endoplasmic Reticulum |
| PVP01\_0413300 | N-Glycan Biosynthesis; Metabolic Pathways |
| PVP01\_0414200 | SNARE Interactions in Vesicular Transport |
| PVP01\_0415500 | Terpenoid Backbone Biosynthesis; Biosynthesis of Antibiotics; Biosynthesis of Sec. Metabolites; Metabolic Pathways |
| PVP01\_0418300 | Malaria |
| PVP01\_0418400 | Malaria |
| PVP01\_0419100 | Nucleotide Excision Repair |
| PVP01\_0421800 | Nucleotide Excision Repair |
| PVP01\_0506200 | Aminoacyl-tRNA Biosynthesis |
| PVP01\_0510700 | Lipoic Acid Metabolism; Metabolic Pathways |
| PVP01\_0512500 | Phagosome; Protein Processing in Endoplasmic Reticulum; Protein Export |
| PVP01\_0514100 | Glycerophospholipid Metabolism; Metabolic Pathways |
| PVP01\_0514400 | RNA Degradation; Spliceosome |
| PVP01\_0515500 | Ribosome Biogenesis |
| PVP01\_0519200 | Metabolic Pathways |
| PVP01\_0519400 | Glycine Serine and Threonine Metabolism; Glycolysis; Glyoxylate and Dicarboxylate Metabolism; Lysine Degradation; Propanoate Metabolism; Pyruvate Metabolism; TCA Cycle; Valine Leucine and Isoleucine Degradation; Biosynthesis of Antibiotics; Biosynthesis of Sec. Metabolites; Carbon Metabolism; Metabolic Pathways |
| PVP01\_0526600 | Folate Biosynthesis; Pyrimidine Metabolism; Metabolic Pathways |
| PVP01\_0529500 | Ribosome Biogenesis |
| PVP01\_0530500 | Fatty Acid Elongation; Biosynthesis of Sec. Metabolites; Biosynthesis of Unsaturated Fatty Acids; Fatty Acid Metabolism; Metabolic Pathways |
| PVP01\_0530800 | Phagosome |
| PVP01\_0530900 | Ribosome |
| PVP01\_0603100 | Proteosome |
| PVP01\_0608000 | Biosynthesis of Antibiotics; Biosynthesis of Sec. Metabolites; Metbolic Pathways |
| PVP01\_0612200 | Ribosome Biogenesis |
| PVP01\_0612900 | Ribosome |
| PVP01\_0617500 | Metabolic Pathways |
| PVP01\_0617600 | Protein Processing in Endoplasmic Reticulum |
| PVP01\_0619500 | TCA Cycle; Biosynthesis of Antibiotics; Biosynthesis of Sec. Metabolites; Carbon Metabolism; Metabolic Pathways; Oxidative Phosphorylation |
| PVP01\_0621200 | Metabolic Pathways |
| PVP01\_0622000 | Nucleotide Excision Repair |
| PVP01\_0702100 | Phagosome |
| PVP01\_0702800 | Protein Export |
| PVP01\_0704900 | Phagosome |
| PVP01\_0709100 | SNARE interactions in vesicular transport |
| PVP01\_0709500 | Metabolic Pathways |
| PVP01\_0710800 | Folate Biosynthesis; Metabolic Pathways |
| PVP01\_0716000 | Spliceosome |
| PVP01\_0717300 | Cysteine and Methionine Metabolism; Glutathione Metabolism; Metabolic Pathways |
| PVP01\_0718000 | N-Glycan Biosynthesis; Metabolic Pathways; Protein Processing in Endoplasmic Reticulum |
| PVP01\_0721400 | Biotin Metabolism; Fatty Acid Biosynthesis; Biosynthesis of Antibiotics; Fatty Acid Metabolism; Metabolic Pathways |
| PVP01\_0722100 | Lipoic Acid Metabolism; Metabolic Pathways |
| PVP01\_0722300 | Selenocompound Metabolism |
| PVP01\_0723800 | Aminoacyl-tRNA Biosynthesis |
| PVP01\_0724300 | RNA Transport; mRNA Surveillance |
| PVP01\_0725200 | Metabolic Pathways |
| PVP01\_0725800 | Pyruvate Metabolism; TCA Cycle; Biosynthesis of Antibiotics; Biosynthesis of Sec. Metabolites; Carbon Metabolism; Metabolic Pathways |
| PVP01\_0726400 | Glycerophospholipid Metabolism; Biosynthesis of Sec. Metabolites; Metabolic Pathways |
| PVP01\_0729100 | Glycerolipid Metabolism; Glycerophospholipid Metabolism; Biosynthesis of Sec. Metabolites; Metabolic Pathways |
| PVP01\_0734000 | Metabolic Pathways |
| PVP01\_0803300 | Ribosome |
| PVP01\_0808400 | Phagosome |
| PVP01\_0811300 | SNARE Interactions in Vesicular Transport |
| PVP01\_0811500 | Proteosome |
| PVP01\_0815100 | Biosynthesis of Sec. Metabolites; Metabolic Pathways |
| PVP01\_0815300 | Aminoacyl-tRNA Biosynthesis |
| PVP01\_0815900 | Glutathione Metabolism; Purine Metabolism; Pyrimidine Metabolism; Metabolic Pathways |
| PVP01\_0817900 | Glycerolipid Metabolism; Metabolic Pathways |
| PVP01\_0822500 | Ribosome Protein |
| PVP01\_0826100 | SNARE Interactions in Vesicular Transport |
| PVP01\_0829000 | Aminoacyl-tRNA Biosynthesis |
| PVP01\_0831600 | Spliceosome; Ubiquitin mediated proteolysis |
| PVP01\_0833100 | Ribosome Protein |
| PVP01\_0833200 | Ribosome |
| PVP01\_0833800 | Glycerophospholipid Metabolism; Biosynthesis of Sec. Metabolites |
| PVP01\_0836000 | Endocytosis |
| PVP01\_0837000 | Glycerolipid Metabolism; Glycerophospholipid Metabolism; Biosynthesis of Sec. Metabolites; Metabolic Pathways |
| PVP01\_0904500 | Ribosome Biogenesis; RNA Polymerase |
| PVP01\_0912500 | RNA Transport; Ribosome Biogenesis |
| PVP01\_0917200 | N-Glycan Biosynthesis; Metabolic Pathways; Protein Processing in Endoplasmic Reticulum |
| PVP01\_0918300 | RNA Transport; Ribosome Biogenesis |
| PVP01\_0919400 | Endocytosis |
| PVP01\_0920400 | Spliceosome |
| PVP01\_0922700 | Metabolic Pathways |
| PVP01\_0924000 | mRNA Surveillance |
| PVP01\_0924600 | Protein Processing in Endoplasmic Reticulum |
| PVP01\_0926700 | Aminoacyl-tRNA Biosynthesis |
| PVP01\_0926900 | Ribosome |
| PVP01\_0929400 | RNA Degradation |
| PVP01\_0930200 | Base Excision Repair |
| PVP01\_0930700 | Ribosome Protein |
| PVP01\_0936800 | Fatty Acid Elongation; Biosynthesis of Sec. Metabolites; Biosynthesis of Unsaturated Fatty Acids; Fatty Acid Metabolism; Metabolic Pathways |
| PVP01\_0938500 | Ribosome Protein |
| PVP01\_1005100 | Spliceosome |
| PVP01\_1005300 | Endocytosis |
| PVP01\_1005600 | RNA Transport |
| PVP01\_1013900 | Ribosome |
| PVP01\_1014600 | Porphyrin and Chlorophyll Metabolism; Biosynthesis of Sec. Metabolites; Metabolic Pathways; Oxidative Phosphorylation |
| PVP01\_1016500 | Amino Sugar and Nucleotide Sugar Metabolism; Galactose Metabolism; Biosynthesis of Antibiotics; Metabolic Pathways |
| PVP01\_1017000 | Ribosome Protein |
| PVP01\_1026300 | Protein Processing in Endoplasmic Reticulum |
| PVP01\_1026900 | Ribosome Protein |
| PVP01\_1031900 | Biosynthesis of Antibiotics; Biosynthesis of Sec. Metabolites; Metabolic Pathways |
| PVP01\_1032800 | Peroxisome |
| PVP01\_1104500 | Amino Sugar and Nucleotide Sugar Metabolism |
| PVP01\_1104900 | Spliceosome |
| PVP01\_1105200 | Glycerophospholipid Metabolism; Biosynthesis of Sec. Metabolites; Metabolic Pathways |
| PVP01\_1112700 | RNA Polymerase |
| PVP01\_1115600 | Ubiquitin Mediated Proteolysis |
| PVP01\_1118200 | Nucleotide Excision Repair |
| PVP01\_1121200 | Glycerophospholipid Metabolism; Biosynthesis of Sec. Metabolites; Metabolic Pathways |
| PVP01\_1121600 | RNA Transport; Ribosome Biogenesis |
| PVP01\_1121700 | Glycolysis; Glyoxylate and Dicarboxylate Metabolism; Propanoate Metabolism; Pyruvate Metabolism; Biosynthesis of Antibiotics; Biosynthesis of Sec. Metabolites; Carbon Metabolism; Metabolic Pathways |
| PVP01\_1125500 | Amino Sugar and Nucleotide Sugar Metabolism; Fructose Mannose Metabolism; Galactose Metabolism; Glycolysis; Biosynthesis of Antibiotics; Biosynthesis of Sec. Metabolites; Carbon Metabolism; Metabolic Pathways |
| PVP01\_1126500 | Biosynthesis of Amino Acids; Biosynthesis of Antibiotics; Biosynthesis of Sec. Metabolites; Metabolic Pathways |
| PVP01\_1130100 | Protein Processing in Endoplasmic Reticulum |
| PVP01\_1130600 | Metabolic Pathways |
| PVP01\_1132300 | Pyruvate Metabolism; TCA Cycle; Biosynthesis of Antibiotics; Biosynthesis of Sec. Metabolites; Carbon Metabolism; Metabolic Pathways |
| PVP01\_1133100 | Vitamin B6 Metabolism; Metabolic Pathways |
| PVP01\_1134000 | Biotin Metabolism; Fatty Acid Biosynthesis; Biosynthesis of Antibiotics; Fatty Acid Metabolism; Metabolic Pathways |
| PVP01\_1139500 | Glycerophospholipid Metabolism; Metabolic Pathways |
| PVP01\_1141500 | Ubiquinone Other Terpenoid-quinone Biosynthesis; Biosynthesis of Sec. Metabolites; Metabolic Pathways |
| PVP01\_1205600 | Aminoacyl-tRNA Biosynthesis; Porphyrin and Chlorophyll Metabolism; Biosynthesis of Sec. Metabolites; Metabolic Pathways |
| PVP01\_1207700 | Homologous Recombination |
| PVP01\_1209100 | Glutathione Metabolism; TCA Cycle; Biosynthesis of Amino Acids; Biosynthesis of Antibiotics; Biosynthesis of Sec. Metabolites; Carbon Metabolism; Metabolic Pathways; Peroxisome |
| PVP01\_1210200 | Lipoic Acid Metabolism; Metabolic Pathways |
| PVP01\_1210600 | Protein Processing in Endoplasmic Reticulum |
| PVP01\_1211200 | Amino Sugar and Nucleotide Sugar Metabolism; Biosynthesis of Antibiotics; Metabolic Pathways |
| PVP01\_1212000 | Glycolysis; Pyruvate Metabolism; TCA Cycle; Biosynthesis of Antibiotics; Biosynthesis of Sec. Metabolites; Carbon Metabolism; Metabolic Pathways |
| PVP01\_1212300 | Malaria |
| PVP01\_1213200 | Metabolic Pathways |
| PVP01\_1216500 | Ribosome Protein |
| PVP01\_1221800 | Aminoacyl-tRNA Biosynthesis |
| PVP01\_1221900 | Ribosome Biogenesis |
| PVP01\_1222100 | Base Excision Repair |
| PVP01\_1222700 | SNARE Interactions in Vesicular Transport |
| PVP01\_1223000 | Fatty Acid Elongation; Biosynthesis of Sec. Metabolites; Biosynthesis of Unsaturated Fatty Acids; Fatty Acid Metabolism; Metabolic Pathways |
| PVP01\_1223300 | Protein Export |
| PVP01\_1223800 | Metabolic Pathways |
| PVP01\_1229800 | Folate Biosynthesis; Metabolic Pathways |
| PVP01\_1229900 | SNARE Interactions in Vesicular Transport |
| PVP01\_1231600 | Biotin Metabolism; Fatty Acid Biosynthesis; Fatty Acid Metabolism; Metabolic Pathways |
| PVP01\_1238300 | Protein Processing in Endoplasmic Reticulum |
| PVP01\_1239500 | Biosynthesis of Antibiotics; Biosynthesis of Sec. Metabolites; Metabolic Pathways |
| PVP01\_1239700 | Base Excision Repair |
| PVP01\_1241500 | RNA Transport |
| PVP01\_1243100 | Nucleotide Excision Repair |
| PVP01\_1245200 | Spliceosome |
| PVP01\_1251000 | N-Glycan Biosynthesis |
| PVP01\_1253000 | Spliceosome |
| PVP01\_1254500 | SNARE Interactions in Vesicular Transport |
| PVP01\_1260000 | Ribosome Protein |
| PVP01\_1261900 | Aminoacyl-tRNA Biosynthesis |
| PVP01\_1262200 | Fructose Mannose Metabolism; Glycolysis; Pentose Phosphate Pathway; Biosynthesis of Amino Acids; Biosynthesis of Antibiotics; Biosynthesis of Sec. Metabolites; Carbon Metabolism; Metabolic Pathways |
| PVP01\_1263300 | Metabolic Pathways |
| PVP01\_1263500 | RNADegradation |
| PVP01\_1268500 | mRNA Surveillance |
| PVP01\_1268900 | Protein Export; Protein Processing in Endoplasmic Reticulum |
| PVP01\_1302500 | Protein Export |
| PVP01\_1302900 | Porphyrin and Chlorophyll Metabolism |
| PVP01\_1308100 | RNA Transport; mRNA Surveillance |
| PVP01\_1309300 | SNARE Interactions in Vesicular Transport |
| PVP01\_1310100 | Metabolic Pathways |
| PVP01\_1310900 | DNA Replication |
| PVP01\_1312600 | Purine Metabolism; Metabolic Pathways |
| PVP01\_1314500 | Porphyrin and Chlorophyll Metabolism; Biosynthesis of Sec. Metabolites; Metabolic Pathways; Oxidative phosphorylation |
| PVP01\_1315900 | Protein Export |
| PVP01\_1319700 | Ribosome Protein |
| PVP01\_1324700 | Ribosome Protein |
| PVP01\_1327700 | Ribosome Protein |
| PVP01\_1328500 | Aminoacyl-tRNA Biosynthesis |
| PVP01\_1329100 | Glutathione Metabolism; Metabolic Pathways |
| PVP01\_1334900 | Proteosome |
| PVP01\_1338300 | RNA Transport |
| PVP01\_1339000 | Glycerophospholipid Metabolism; Biosynthesis of Sec. Metabolites; Metabolic Pathways |
| PVP01\_1346200 | Ribosome Protein |
| PVP01\_1346800 | Purine Metabolism; Metabolic Pathways |
| PVP01\_1347000 | Glycerophospholipid Metabolism; Metabolic Pathways |
| PVP01\_1404100 | SNARE Interactions in Vesicular Transport |
| PVP01\_1405400 | Protein Processing in Endoplasmic Reticulum |
| PVP01\_1408500 | RNA Polymerase |
| PVP01\_1409900 | RNADegradation |
| PVP01\_1410300 | Spliceosome |
| PVP01\_1410500 | Ribosome Biogenesis |
| PVP01\_1411900 | Ribosome Protein |
| PVP01\_1416500 | Glycerophospholipid Metabolism; Metabolic Pathways |
| PVP01\_1416800 | RNA Transport |
| PVP01\_1417700 | SNARE Interactions in Vesicular Transport |
| PVP01\_1417900 | Spliceosome |
| PVP01\_1418700 | Ribosome |
| PVP01\_1421400 | Endocytosis |
| PVP01\_1426400 | Ribosome |
| PVP01\_1427500 | Spliceosome |
| PVP01\_1429500 | Folate Biosynthesis; Metabolic Pathways |
| PVP01\_1431400 | Glycerolipid Metabolism; Glycerophospholipid Metabolism; Biosynthesis of Sec. Metabolites; Metabolic Pathways |
| PVP01\_1431600 | RNA Transport |
| PVP01\_1432700 | RNA Transport |
| PVP01\_1435400 | Malaria |
| PVP01\_1442100 | Ribosome Protein |
| PVP01\_1442800 | Porphyrin and Chlorophyll Metabolism |
| PVP01\_1443100 | Spliceosome |
| PVP01\_1444000 | Ubiquitin Mediated Proteolysis |
| PVP01\_1449100 | Ribosome Biogenesis |
| PVP01\_1450200 | Aminoacyl-tRNA Biosynthesis |
| PVP01\_1450400 | Glycine Serine and Threonine Metabolism; Glycolysis; Glyoxylate and Dicarboxylate Metabolism; Lysine Degradation; Propanoate Metabolism; Pyruvate Metabolism; TCA Cycle; Valine Leucine and Isoleucine Degradation; Biosynthesis of Antibiotics; Biosynthesis of Sec. Metabolites; Carbon Metabolism; Metabolic Pathways |
| PVP01\_1452400 | Base Excision Repair; DNA Replication; Nucleotide Excision Repair |
| PVP01\_1455100 | Ubiquitin Mediated proteolysis |
| PVP01\_1457200 | Ribosome Protein |
| PVP01\_1458800 | DNA Replication; Mismatch Repair; Nucleotide Excision Repair |
| PVP01\_1459800 | Ribosome Protein |
| PVP01\_1460100 | SNARE Interactions in Vesicular Transport |
| PVP01\_1460700 | RNA Transport |
| PVP01\_1460900 | mRNA Survellance |
| PVP01\_1461300 | Nucleotide Excision Repair |
| PVP01\_1461700 | Endocytosis |
| PVP01\_1462500 | Ribosome Protein |
| PVP01\_1463900 | Protein Export |
| PVP01\_1464400 | Metabolic Pathways |
| PVP01\_1468800 | Aminoacyl-tRNA Biosynthesis |