Supplementary information

Each column lists the most granular correct terms with P-score > 50%. More than one term indicates hits to more than one branch. Each term is listed as GO ID, I-score ± s.d., P-score, (description)

Manual assessment of false positives – IEA annotation included

Gene name and annotated product description	**Original human GO annotation**	**With IEA annotations**	
		Lowest scoring true positive	Highest scoring false positive with P-score > 50%
PFL2465 Thymidylate kinase	GO:0006235 (dTTP biosynthesis)	GO:0006235, 0.59±0.48, 98% (dTTP biosynthesis) GO:0006233, 0.59±0.48, 100% (dTDP biosynthesis)	n/a
	GO:0008372 (cellular_component unknown)	n/a	n/a
	GO:0004798 (thymidylate kinase activity) GO:0005524 (ATP binding)	GO:0004798, 0.9893±0.0142, 100% (thymidylate kinase activity) GO:0005524, 0.40±0.49, 68% (ATP binding)	n/a
PFL1875w hypothetical protein	GO:0000004 (biological process unknown)	GO:0008152, 0.53±0.38, 67% (metabolism) GO:0006813, 0.65±0.46, 100% (potassium ion transport)	n/a
	GO:00016020 (membrane)	GO:0008076, 0.66+/-0.47, 69% (voltage-gated potassium channel complex)	n/a
	GO:00005554 (Molecular function unknown	GO:0005249, 0.65+/-0.46, 58% (voltage-gated potassium channel)	n/a
PFL1835w hypothetical protein	GO:0000004 (biological process unknown)	n/a	GO:0009190, 0.0009±0.0019, 88% (cyclic nucleotide biosynthesis) GO:0006304, 0.0015±0.0030, 56% (DNA modification)
	GO:00016020 (membrane) GO:0020011 (apicoplast)	GO:0016021, 0.0069±0.0124, 74% (integral to membrane)	GO:0005891, 0.01±.0.01, 74% (voltage-gated calcium channel complex) GO:0005884, 3e-05±7e-05, 56% (actin filament)
	GO:00005554 (Molecular function unknown	n/a	GO:0015078, 0.001±0.003, 96% (hydrogen ion transporter)

			GO:0004601, 0.0003±0.0007, 68% (peroxidase) GO:0003890, 3e-05±7e-05, 96% (beta DNA polymerase) GO:0003889, 0.0001±0.0002, 100% (alpha DNA polymerase) GO:0003902, 0.0002±0.0005, 56% (DNA-directed RNA polymerase III) GO:0015399, 0.0758±0.1380, 58% (primary active transporter) GO:0004842, 0.0196±0.0167, 79% (ubiquitin-protein ligase) GO:0004222, 0.0033±0.0064, 80% (metalloendopeptidase) GO:0005525, 0.0014±0.0021, 64% (GTP binding) GO:0008270, 0.0014±0.0029, 56% (zinc ion binding)
PFL1825w hypothetical protein	GO:0000004 (biological process unknown)	n/a	GO:0015980, 0.8536±0, 65% (energy derivation by oxidation of organic compounds)
	GO:00016020 (membrane)	GO:0005623, 1±0, 68% (cell)	
	GO:00005554 (Molecular function unknown)	n/a	GO:0004026, 0.8536, ±0, 60% (alcohol O-acetyltransferase)
PFL1780w hypothetical protein	GO:0000004 (biological process unknown)	n/a	n/a
	GO:00016020 (membrane) GO:0020011 (apicoplast)	GO:0016020, 0.6512±0.4609, 91% (membrane)	n/a
	GO:00005554 (Molecular function unknown)	GO:0004671, 0.6512±0.4609, 70% (protein-S-isoprenylcysteine O-methyltransferase)	n/a
PFL1710c tetQ family GTPase, putative	GO:0000004 (biological process unknown)	GO:0006414, 0.7538±0.1860, 99% (translational elongation)	n/a
	GO:0005739 (mitochondrion)		GO:0005737, 0.5442±0.4546, 52%

	GO:0020011 (apicoplast)		(cytoplasm)
	GO:0005525 (GTP binding)	GO:0005525, 0.3693±0.3237, 98% (GTP binding) GO:0003746, 0.71±0.17, 99% (translation elongation factor)	
PFC0495w aspartyl protease, putative	GO:0006508 (proteolysis and peptidolysis)	GO:0006508, 0.5244±0.4754, 76% (proteolysis and peptidolysis)	n/a
	GO:0008372 (cellular_component unknown)	n/a	n/a
	GO:0004190 (aspartic-type endopeptidase activity)	GO:0004194, 0.4976±0.4976, 100% (pepsin A)	n/a
PFB0795w ATP synthase F1, alpha subunit, putative	GO:0000004 (biological process unknown)	GO:0015986, 0.3333±0.4082, 100% (ATP synthesis coupled proton transport)	n/a
	GO:0005739 (mitochondrion)	GO:0016469, 0.3437±0.4302, 90% (hydrogen-transporting two-sector ATPase complex)	n/a
	GO:00005554 (Molecular function unknown)	GO:0003936, 0.9638±0.0648, 100% (hydrogen-transporting two-sector ATPase)	GO:0005224, 0.1695±0.3199, 100% (ATP-binding and phosphorylation-dependent chloride channel)

Manual assessment of false positives – IEA annotation excluded.

Gene name and annotated product description	**Original human GO annotation**	Without IEA annotations	
		Lowest scoring true positive	Highest scoring false positive with P-score > 50%
PFL2465 Thymidylate kinase	GO:0006235 (dTTP biosynthesis)	GO:0006233, 0.32±0.45, 26% (dTDP biosynthesis) GO:0006235, 0.32±0.45, 26% (dTTP biosynthesis)	GO:0019222, 0.002±00.003, 64% (regulation of metabolism)
	GO:0008372 (cellular_component unknown)	n/a	GO:0005737, 0.66±0.46, 76% (cytoplasm)
	GO:0004798 (thymidylate kinase activity) GO:0005524 (ATP binding)	GO:0004798, 0.98±0.02, 86% (thymidylate kinase activity)	n/a
PFL1875w	GO:0000004 (biological process	GO:0008152,0.85±0.15, 73% (metabolism)	n/a

hypothetical protein	unknown)		
	GO:00016020 (membrane)	GO:0005623, 0.85±0.15, (cell)	GO:0005622, 0.85±0.15, 71% (intracellular)
	GO:00005554 (Molecular function unknown	n/a	GO:0005554, 0.15±0.15, 70% (molecular_function unknown)
PFL1835w hypothetical protein	GO:0000004 (biological process unknown)	GO:0007582, 0.6145±0.2521, 75% (physiological processes) GO:0009987, 0.6223±0.2971, 82% (cellular process)	GO:0008151, 0.5920±0.2932, 70% (cell growth and/or maintenance)
	GO:00016020 (membrane) GO:0020011 (apicoplast)	GO:0016021, 0.0069±0.0124, 58% (integral to membrane)	GO:0005625, 0.0017±0.0035, 65% (soluble fraction) GO:0005624, 0.0001±0.0003, 52% (membrane fraction)
	GO:00005554 (Molecular function unknown)	n/a	GO:0005525, 0.0011±0.0022, 52% (GTP binding) GO:0004930, 0.0011±0.0023, 71% (G-protein coupled receptor)
PFL1825w hypothetical protein	GO:0000004 (biological process unknown)	n/a	GO:0006113, 0.8536±0, 54% (fermentation) GO:0008151,1±0,100% (cell growth and/or maintenance) GO:0006091, 0.8536±0, 82% (energy pathways) GO:0015980, 0.8536±0, 81% (energy derivation by oxidation of organic compounds)
	GO:00016020 (membrane)	GO:0000267, 0.8536±0, 63% (cell fraction)	
	GO:00005554 (Molecular function unknown	n/a	GO:0008374, 0.8536±0, 70% (O-acyltransferase) GO:0016407, 0.8536±0, 70% (acetyltransferase)
PFL1780w hypothetical protein	GO:0000004 (biological process unknown)	GO:0006464, 0.4769±0.4769, 83% (protein modification)	GO:0007323, 0.4769±0.4769, 83% (peptide pheromone maturation)
	GO:00016020 (membrane) GO:0020011 (apicoplast)	GO:0005783, 0.4769±0.4769, 52% (endoplasmic reticulum) GO:0012505, 0.4769±0.4769, 51% (endomembrane system)	n/a
	GO:00005554 (Molecular function unknown	GO:0008171, 0.9769±0.0230, 92% (O-methyltransferase) GO:0008757, 0.9769±0.0230, 92% (S-adenosylmethionine-dependent methyltransferase) GO:0008276, 0.9769±0.0230, 92% (protein	n/a

		methyltransferase)	
PFL1710c tetQ family GTPase, putative	GO:0000004 (biological process unknown)	GO:0006412, 0.4782±0.4060, 56% (protein biosynthesis)	n/a
	GO:0005739 (mitochondrion) GO:0020011 (apicoplast)	n/a	GO:0005737, 0.3462±0.4325, 52% (cytoplasm)
	GO:0005525 (GTP binding)	GO:0005525, 0.1341±0.0840, 54% (GTP binding) GO:0003746, 0.4905±0.2708, 63% (translation elongation factor)	GO:0004930, 0.0017±0.0035, 71% (G-protein coupled receptor)
PFC0495w aspartyl protease, putative	GO:0006508 (proteolysis and peptidolysis)	GO:0008152, 0.6529±0.4620, 72% (metabolism)	GO:0006351, 0.3333±0.4714, 53% (transcription, DNA-dependent)
	GO:0008372 (cellular_component unknown)	n/a	GO:0005622, 0.2276±0.3219, 56% (intracellular)
	GO:0004190 (aspartic-type endopeptidase activity)	GO:0004190, 0.6558±0.4639, 80% (aspartic-type endopeptidase)	n/a
PFB0795w ATP synthase F1, alpha subunit, putative	GO:0000004 (biological process unknown)	GO:0016887, 0.7943±0.3972, 82% (ATPase) GO:0015405, 0.7642±0.3872, 72% (P-P-bond-hydrolysis-driven transporter)	
	GO:0005739 (mitochondrion)	GO:0005754, 0.3108±0.3825, 60% (hydrogen-transporting ATP synthase, catalytic core (sensu Eukarya))	
	GO:00005554 (Molecular function unknown)	GO:0015075, 0.2349±0.3884, 50% (ion transporter)	GO:0016820, 0.7642±0.3872, 62% (hydrolase, acting on acid anhydrides, catalyzing transmembrane movement of substances) GO:0015442, 0.7642±0.3872, 72% (hydrogen-/sodium-translocating ATPase)