

Figure S2

## Toxodb search

Step 1

STEP 1 : Exp Sim MIC2	
<b>Gene Id</b>	: TGME49_201780
<b>Distance Method</b>	: Pearson Correlation
<b># of Matches</b>	: 500
<b>% of missing data points</b>	: 10
<b>Experiment</b>	: M.White Cell Cycle Microarray spline smoothed - Interpolated
<b>Search Goal</b>	: Positive Correlation
<b>Time Shift</b>	: 0 hours

Results: 500 Genes

Give this search a weight

Step 2

STEP 2 : Exp Sim RON2	
<b>Gene Id</b>	: TGME49_300100
<b>Distance Method</b>	: Pearson Correlation
<b># of Matches</b>	: 500
<b>% of missing data points</b>	: 10
<b>Experiment</b>	: M.White Cell Cycle Microarray spline smoothed - Interpolated
<b>Search Goal</b>	: Positive Correlation
<b>Time Shift</b>	: 0 hours

Results: 500 Genes

Give this search a weight

Step 3

STEP 1 : Signal Pep	
<b>Organism</b>	: Toxoplasma gondii
<b>Minimum SignalP-NN Conclusion Score</b>	: 3
<b>Minimum SignalP-NN D-Score</b>	: 0.5
<b>Minimum SignalP-HMM Signal Probability</b>	: 0.5
<b>Matches any or all advanced parameters</b>	: any

Results: 5867 Genes

Give this search a weight

STEP 2 : Transmb Dom	
<b>Organism</b>	: Toxoplasma gondii
<b>Minimum Number of Transmembrane Domains</b>	: 1
<b>Maximum Number of Transmembrane Domains</b>	: 7

Results: 4540 Genes

Give this search a weight

Step 4

STEP 4 : Mass Spec	
<b>Experiment/Samples</b>	: Toxoplasma, Toxoplasma gondii, Oocyst Partially Sporulated Proteome (VEG) (Possenti et al.), Oocyst proteome, Oocyst proteome (M4 TypeII) (Wastling), Oocyst peptides, Oocyst proteome - Fractionated (M4 type II) (Fritz et al.), Oocyst Walls, Sporocysts/Sporozoites Cytosol, Sporocysts/Sporozoites Membrane, Proteome During Infection in H. sapiens (ME49 VEG GT1 RH) (Wastling), peptides from 16 hour infection time course in Homo sapien host cells (ME49), peptides from 16 hour infection time course in Homo sapien host cells (VEG), peptides from 44 hour infection time course in Homo sapien host cells (ME49), peptides from 44 hour infection time course in Homo sapien host cells (RH), peptides from 44 hour infection time course in Homo sapien host cells (VEG), peptides from infection in Homo sapien host cells (GT1), Tachyzoite Intra- and Extracellular Lysine-Acetylomes (RH) (Jeffers and Xue), extracellular acetylome, intracellular acetylome, Tachyzoite Rhopty proteome (RH) (Bradley et al.), purified rhodines, Tachyzoite conoid proteome (RH) (Hu et al.), conoid-depleted Fraction, conoid-enriched Fraction, Tachyzoite membrane and cytosolic proteomes (RH) (Dybas et al.), cytosolic fraction by LC-MS/MS, 05/2007, membrane biotin-purified fraction by LC-MS/MS, 5/22/2007, membrane fraction by 1DE, LC-MS/MS, 10/2006, membrane fraction by 1DE, LC-MS/MS, 12/2006, membrane fraction by 2DE, LC-MS/MS, membrane fraction by LC-MS/MS, 2/3/2006, membrane fraction by LC-MS/MS, 5/10/2006, membrane fraction by LC-MS/MS, 5/2/2006, membrane fraction by LC-MS/MS, 6/2006, Tachyzoite phosphoproteome - Calcium dependent (RH) (Nebi et al.), phosphopeptide-depleted (via Sequest), phosphopeptide-enriched (via Mascot), phosphopeptide-enriched (via Sequest), Tachyzoite phosphoproteome from purified parasite or infected host cell (RH) (Trecek et al.), Infected host cell, phosphopeptide-depleted (peptide discovery against TgME49), Infected host cell, phosphopeptide-depleted (peptide discovery against TgGT1), Infected host cell, phosphopeptide-enriched (peptide discovery against TgME49), Infected host cell, phosphopeptide-enriched (peptide discovery against TgGT1), Purified tachyzoites phosphopeptide-depleted (peptide discovery against TgGT1), Purified tachyzoites phosphopeptide-depleted (peptide discovery against TgME49), Purified tachyzoites phosphopeptide-enriched (peptide discovery against TgGT1), Purified tachyzoites phosphopeptide-enriched (peptide discovery against TgME49), Tachyzoite secretome (RH) (Zhou et al.), excreted/secreted antigen fraction by 2DE-MS, excreted/secreted antigen fraction by MudPIT, Tachyzoite subcellular fractions (Moreno), sample A, sample C, Tachyzoite total proteome (RH) (Wastling), Tris-insoluble fraction by 1DE, LC-MS/MS, Tris-insoluble fraction by MudPIT, Tris-soluble fraction by 1DE, LC-MS/MS, Tris-soluble fraction by MudPIT, total protein by 1DE, LC-MS/MS, total protein by 2DE-MS
<b>Minimum Number of Unique Peptide Sequences</b>	: 1
<b>Minimum Number of Spectra</b>	: 1

Results: 9985 Genes

Give this search a weight

Step 5

STEP 5 : Api Specific	
<b>Included Species</b>	: pfal
<b>Excluded Species</b>	: MAMM
<b>Organism</b>	: Toxoplasma gondii GT1, Toxoplasma gondii ME49, Toxoplasma gondii VEG

Results: 2626 Genes

Give this search a weight

## Plasmodb search

Step 1

STEP 1 : Exp Late Schiz	
<b>Experiment</b>	: Intraerythrocytic cycle transcriptome (3D7) sense strand
<b>Direction</b>	: up-regulated
<b>Reference Samples</b>	: 17-25
<b>Operation Applied to Reference Samples</b>	: minimum
<b>Comparison Samples</b>	: 40-5, 32-40
<b>Operation Applied to Comparison Samples</b>	: maximum
<b>fold difference &gt;=</b>	: 1.5
<b>Protein Coding Only</b>	: protein coding
<b>Global min / max in selected time points</b>	: Don't care

Results: 2696 Genes

Give this search a weight

Step 2

STEP 2 : Pf Gam/Spo fc	
<b>Experiment</b>	: Sexual Cycle Expression
<b>Direction</b>	: up-regulated
<b>Reference Samples</b>	: Gametocyte
<b>Operation Applied to Reference Samples</b>	: minimum
<b>Comparison Samples</b>	: Sporozoite
<b>Operation Applied to Comparison Samples</b>	: maximum
<b>fold difference &gt;=</b>	: 2
<b>Protein Coding Only</b>	: protein coding

Results: 547 Genes

Give this search a weight

Step 3

STEP 1 : Signal Pep	
<b>Organism</b>	: Plasmodium falciparum, Plasmodium falciparum 3D7, Plasmodium falciparum IT
<b>Minimum SignalP-NN Conclusion Score</b>	: 3
<b>Minimum SignalP-NN D-Score</b>	: 0.5
<b>Minimum SignalP-HMM Signal Probability</b>	: 0.5
<b>Matches any or all advanced parameters</b>	: any

Results: 2125 Genes

Give this search a weight

STEP 2 : Transmb Dom	
<b>Organism</b>	: Plasmodium falciparum
<b>Minimum Number of Transmembrane Domains</b>	: 1
<b>Maximum Number of Transmembrane Domains</b>	: 7

Results: 3106 Genes

Give this search a weight

Step 4

STEP 4 : Mass Spec	
<b>Experiment/Samples</b>	: Blood stage phospho- and total proteome (3D7) (Boothroyd), schizont phosphopeptide-depleted, schizont phosphopeptide-enriched, Schizont cytosolic extract, Infected erythrocytes from patient blood sample (Acharya et al.), P. falciparum infected erythrocytes from patient blood sample, Intraerythrocytic stages phosphoproteome (3D7) (Pease et al.), Intraerythrocytic stages, Merozoite Proteome (3D7) (Kahn), merozoite proteome (3D7), Merozoite phosphoproteome (3D7) (Lasonder et al.), Enriched merozoite phospho-proteins, Parasite rupture from erythrocyte (D10) (Bowyer et al.), schizont, 42 h post-infection, schizont, 48 h post-infection, Schizont Phosphoproteome (3D7)(2011) (Solyakov et al.), Enriched schizont phospho-proteins (2011), Schizont Phosphoproteome (3D7)(2012) (Lasonder et al.), Enriched schizont phospho-proteins (2012), merozoite (synchronized), sporozoite, 14 day purified, trophozoite (synchronized), Sporozoite Maturation Proteome (NF54) (Lasonder et al.), oocyst-derived sporozoite 13-14 days post-infection, oocysts 7-8 days post-infection, salivary gland sporozoites 18-22 days post-infection
<b>Minimum Number of Unique Peptide Sequences</b>	: 2
<b>Minimum Number of Spectra</b>	: 2

Results: 2572 Genes

Give this search a weight

Step 5

STEP 5 : Api Specific	
<b>Included Species</b>	: tgon
<b>Excluded Species</b>	: MAMM
<b>Organism</b>	: Plasmodium falciparum, Plasmodium falciparum 3D7, Plasmodium falciparum IT

Results: 1692 Genes

Give this search a weight