Table /	A
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		UPREGULATED PATHWAYS	p-val	FDR q-va
	MPM:	PROTEASOME-MEDIATED DEGRADATION OF NON-NATIVE ER PROTEINS	0.00	0.05
	MPM:	GENES CODING FOR COMPONENTS OF THE PROTEASOME DEGRADATION	0.02	0.12
		MACHINERY AND THEIR TIMED TRANSCRIPTION		
Protein Turnover	MPM:	PEPTIDASES AND PROTEASES	0.02	0.12
	MPM:	PROTEASOME-MEDIATED PROTEOLYSIS OF UBIQUINATED PROTEINS	0.03	0.21
	GO:	RESPONSE TO HEAT	0.02	0.16
	GO:	UBIQUITIN-DEPENDENT PROTEIN CATABOLIC PROCESS	0.03	0.23
	GO:	ER-ASSOCIATED PROTEIN CATABOLIC PROCESS	0.01	0.13
	MPM:	S-GLUTATHIONYLATED PROTEINS	0.00	0.04
Oxidative Stress	MPM:	PROTEINS TARGETED BY THE THIOREDOXIN SUPERFAMILY ENZYMES	0.03	0.17
	GO:	OXIDOREDUCTASE ACTIVITY	0.00	0.04
	MPM:	GENES CODING FOR PROTEIN TRAFFIC RELATED PROTEINS	0.00	0.04
	MPM:	CLASSICAL COPII-MEDIATED VESICULAR TRANSPORT	0.01	0.13
	MPM:	SUBCELLULAR LOCATION OF ADAPTOR PROTEINS	0.01	0.13
Transport	MPM:	GENES CODING FOR TRANSPORT PROTEINS	0.02	0.16
I	MPM:	CLASSICAL CLATHRIN-MEDIATED VESICULAR TRANSPORT	0.04	0.21
	GO:	PROTEIN TRANSPORTER ACTIVITY	0.00	0.06
	GO:	INTRACELLULAR PROTEIN TRANSPORT	0.00	0.01
	GO:	VESICLE-MEDIATED TRANSPORT LOCALIZATION OF AMINOACYL-TRNA LIGASES IN THE THREE PROTEIN	0.01	0.13
Translational	MPM:	TRANSLATION OF AMINOACYL-TRNA LIGASES IN THE THREE PROTEIN	0.04	0.20
Elongation	GO:	TRANSLATIONAL COMPARTMENTS TRANSLATIONAL ELONGATION	0.04	0.24
•	MPM:	NUCLEAR GENES WITH MITOCHONDRIAL SIGNAL SEQUENCES	0.04	0.24
Mitochondrial	MPM:	MITOCHONDRIAL ELECTRON FLOW	0.00	0.03
Processes	MPM:	IMPORT OF PROTEINS INTO THE MITOCHONDRION	0.01	0.12
Cell cycle	GO:	REGULATION OF CELL CYCLE PROCESS	0.00	0.24
		DOWNREGULATED PATHWAYS	p-val	FDR q-va
	MPM:	FUNCTIONAL ANNOTATION OF MEROZOITE INVASION-RELATED PROTEINS	0.00	0.00
	MPM:	SUBCELLULAR LOCALIZATION OF PROTEINS INVOLVED IN INVASION	0.00	0.00
	MPM:	MEROZOITE LIGANDS THEIR ERYTHROCYTE RECEPTORS	0.01	0.08
	MPM:	PROTEIN-PROTEIN INTERACTIONS BETWEEN HUMAN ERYTHROCYTES AND	0.00	0.01
		PLASMODIUM FALCIPARUM		
Invacion			0.00	
Invasion	MPM:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL	0.00	0.00
Invasion, Pathogenesis and		INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL		
Pathogenesis and	MPM:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL <i>Pfemp1</i> DOMAIN ARCHITECTURES	0.00	0.00
	MPM: MPM:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL <i>Pfemp1</i> DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC	0.00 0.00	0.00 0.00
Pathogenesis and	MPM: MPM: GO:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL <i>Pfemp1</i> DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC CELL-CELL ADHESION	0.00 0.00 0.00	0.00 0.00 0.00
Pathogenesis and	MPM: MPM:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL <i>Pfemp1</i> DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC	0.00 0.00	0.00 0.00 0.00 0.00
Pathogenesis and	MPM: MPM: GO: GO: GO:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL <i>Pfemp1</i> DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC CELL-CELL ADHESION CYTOADHERENCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN MODULATION BY SYMBIONT OF HOST ERYTHROCYTE AGGREGATION	0.00 0.00 0.00 0.00 0.00	0.00 0.00 0.00 0.00 0.00
Pathogenesis and	MPM: GO: GO: GO: GO:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL Pfemp1 DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC CELL-CELL ADHESION CYTOADHERENCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN MODULATION BY SYMBIONT OF HOST ERYTHROCYTE AGGREGATION PATHOGENESIS	0.00 0.00 0.00 0.00 0.00 0.00	0.00 0.00 0.00 0.00 0.00 0.00
Pathogenesis and Cytoadherence	MPM: MPM: GO: GO: GO: GO: GO:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL Pfemp1 DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC CELL-CELL ADHESION CYTOADHERENCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN MODULATION BY SYMBIONT OF HOST ERYTHROCYTE AGGREGATION PATHOGENESIS ANTIGENIC VARIATION	0.00 0.00 0.00 0.00 0.00 0.00 0.00	0.00 0.00 0.00 0.00 0.00 0.00 0.00
Pathogenesis and Cytoadherence	MPM: MPM: GO: GO: GO: GO: MPM:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL Pfemp1 DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC CELL-CELL ADHESION CYTOADHERENCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN MODULATION BY SYMBIONT OF HOST ERYTHROCYTE AGGREGATION PATHOGENESIS ANTIGENIC VARIATION PEPTIDES WITH CONFIRMED METHYLATED LYSINE RESIDUES	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0
Pathogenesis and Cytoadherence	MPM:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL Pfemp1 DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC CELL-CELL ADHESION CYTOADHERENCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN MODULATION BY SYMBIONT OF HOST ERYTHROCYTE AGGREGATION PATHOGENESIS ANTIGENIC VARIATION PEPTIDES WITH CONFIRMED METHYLATED LYSINE RESIDUES CHAPERONE-MEDIATED MODULATION OF NUCLEOSOME-HISTONE INTERACTIONS	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0
Pathogenesis and Cytoadherence Chromatin Modification	MPM: MPM: GO: GO: GO: GO: MPM: MPM: GO:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL Pfemp1 DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC CELL-CELL ADHESION CYTOADHERENCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN MODULATION BY SYMBIONT OF HOST ERYTHROCYTE AGGREGATION PATHOGENESIS ANTIGENIC VARIATION PEPTIDES WITH CONFIRMED METHYLATED LYSINE RESIDUES CHAPERONE-MEDIATED MODULATION OF NUCLEOSOME-HISTONE INTERACTIONS RNA METABOLIC PROCESS	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0
Pathogenesis and Cytoadherence	MPM: GO: GO: GO: GO: GO: MPM: MPM: GO: GO:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL Pfemp1 DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC CELL-CELL ADHESION CYTOADHERENCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN MODULATION BY SYMBIONT OF HOST ERYTHROCYTE AGGREGATION PATHOGENESIS ANTIGENIC VARIATION PEPTIDES WITH CONFIRMED METHYLATED LYSINE RESIDUES CHAPERONE-MEDIATED MODULATION OF NUCLEOSOME-HISTONE INTERACTIONS RNA METABOLIC PROCESS REGULATION OF TRANSCRIPTION DNA-DEPENDENT	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0
Pathogenesis and Cytoadherence	MPM: MPM: GO: GO: GO: GO: MPM: MPM: GO: GO: MPM:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL Pfemp1 DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC CELL-CELL ADHESION CYTOADHERENCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN MODULATION BY SYMBIONT OF HOST ERYTHROCYTE AGGREGATION PATHOGENESIS ANTIGENIC VARIATION PEPTIDES WITH CONFIRMED METHYLATED LYSINE RESIDUES CHAPERONE-MEDIATED MODULATION OF NUCLEOSOME-HISTONE INTERACTIONS RNA METABOLIC PROCESS REGULATION OF TRANSCRIPTION DNA-DEPENDENT MATURATION AND EXPORT OF 60S AND 40S RIBOSOMAL SUBUNITS	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	0.00 0.00 0.00 0.00 0.00 0.00 0.01 0.12 0.14 0.16 0.10
Pathogenesis and Cytoadherence Chromatin Modification	MPM: MPM: GO: GO: GO: GO: MPM: MPM: GO: GO: MPM: MPM:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL Pfemp1 DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC CELL-CELL ADHESION CYTOADHERENCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN MODULATION BY SYMBIONT OF HOST ERYTHROCYTE AGGREGATION PATHOGENESIS ANTIGENIC VARIATION PEPTIDES WITH CONFIRMED METHYLATED LYSINE RESIDUES CHAPERONE-MEDIATED MODULATION OF NUCLEOSOME-HISTONE INTERACTIONS RNA METABOLIC PROCESS REGULATION OF TRANSCRIPTION DNA-DEPENDENT MATURATION AND EXPORT OF 60S AND 40S RIBOSOMAL SUBUNITS RIBOSOMAL PARTICLES ALONG THE 60S ASSEMBLY PATHWAY	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0
Pathogenesis and Cytoadherence Chromatin Modification Transcription	MPM: MPM: GO: GO: GO: GO: MPM: MPM: GO: MPM: MPM: MPM: MPM:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL Pfemp1 DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC CELL-CELL ADHESION CYTOADHERENCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN MODULATION BY SYMBIONT OF HOST ERYTHROCYTE AGGREGATION PATHOGENESIS ANTIGENIC VARIATION PEPTIDES WITH CONFIRMED METHYLATED LYSINE RESIDUES CHAPERONE-MEDIATED MODULATION OF NUCLEOSOME-HISTONE INTERACTIONS RNA METABOLIC PROCESS REGULATION OF TRANSCRIPTION DNA-DEPENDENT MATURATION AND EXPORT OF 60S AND 40S RIBOSOMAL SUBUNITS RIBOSOMAL PARTICLES ALONG THE 60S ASSEMBLY PATHWAY ACTIN BINDING	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0
Pathogenesis and Cytoadherence Chromatin Modification Transcription	MPM: MPM: GO: GO: GO: GO: MPM: MPM: GO: GO: MPM:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL Pfemp1 DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC CELL-CELL ADHESION CYTOADHERENCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN MODULATION BY SYMBIONT OF HOST ERYTHROCYTE AGGREGATION PATHOGENESIS ANTIGENIC VARIATION PEPTIDES WITH CONFIRMED METHYLATED LYSINE RESIDUES CHAPERONE-MEDIATED MODULATION OF NUCLEOSOME-HISTONE INTERACTIONS RNA METABOLIC PROCESS REGULATION OF TRANSCRIPTION DNA-DEPENDENT MATURATION AND EXPORT OF 60S AND 40S RIBOSOMAL SUBUNITS RIBOSOMAL PARTICLES ALONG THE 60S ASSEMBLY PATHWAY ACTIN BINDING MOTOR ACTIVITY	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0
Pathogenesis and Cytoadherence	MPM: MPM: GO: GO: GO: GO: MPM: MPM: GO: GO: MPM:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL Pfemp1 DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC CELL-CELL ADHESION CYTOADHERENCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN MODULATION BY SYMBIONT OF HOST ERYTHROCYTE AGGREGATION PATHOGENESIS ANTIGENIC VARIATION PEPTIDES WITH CONFIRMED METHYLATED LYSINE RESIDUES CHAPERONE-MEDIATED MODULATION OF NUCLEOSOME-HISTONE INTERACTIONS RNA METABOLIC PROCESS REGULATION OF TRANSCRIPTION DNA-DEPENDENT MATURATION AND EXPORT OF 60S AND 40S RIBOSOMAL SUBUNITS RIBOSOMAL PARTICLES ALONG THE 60S ASSEMBLY PATHWAY ACTIN BINDING MOTOR ACTIVITY PROTEIN PHOSPHORYLATION	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0
Pathogenesis and Cytoadherence Chromatin Modification Transcription	MPM: GO: GO: GO: GO: GO: MPM: MPM: GO: GO: GO: MPM: MPM:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL Pfemp1 DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC CELL-CELL ADHESION CYTOADHERENCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN MODULATION BY SYMBIONT OF HOST ERYTHROCYTE AGGREGATION PATHOGENESIS ANTIGENIC VARIATION PEPTIDES WITH CONFIRMED METHYLATED LYSINE RESIDUES CHAPERONE-MEDIATED MODULATION OF NUCLEOSOME-HISTONE INTERACTIONS RNA METABOLIC PROCESS REGULATION OF TRANSCRIPTION DNA-DEPENDENT MATURATION AND EXPORT OF 60S AND 40S RIBOSOMAL SUBUNITS RIBOSOMAL PARTICLES ALONG THE 60S ASSEMBLY PATHWAY ACTIN BINDING MOTOR ACTIVITY PROTEIN PHOSPHORYLATION THE PHOSPHOPROTEOME OF PLASMODIUM FALCIPARUM INFECTED RBCS	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0
Pathogenesis and Cytoadherence	MPM: MPM: GO: GO: GO: GO: MPM: MPM: GO: GO: MPM:	INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL Pfemp1 DOMAIN ARCHITECTURES ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC CELL-CELL ADHESION CYTOADHERENCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN MODULATION BY SYMBIONT OF HOST ERYTHROCYTE AGGREGATION PATHOGENESIS ANTIGENIC VARIATION PEPTIDES WITH CONFIRMED METHYLATED LYSINE RESIDUES CHAPERONE-MEDIATED MODULATION OF NUCLEOSOME-HISTONE INTERACTIONS RNA METABOLIC PROCESS REGULATION OF TRANSCRIPTION DNA-DEPENDENT MATURATION AND EXPORT OF 60S AND 40S RIBOSOMAL SUBUNITS RIBOSOMAL PARTICLES ALONG THE 60S ASSEMBLY PATHWAY ACTIN BINDING MOTOR ACTIVITY PROTEIN PHOSPHORYLATION	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0

Table B

Protein Turnover     MPM     CENTRAL POLSE OF DEURISULTINEXSES     0.03     0.15       Oxidative stress     MPM     CENTRAL ROLES OF DEURISULTINEXSES     0.00     0.05     0.20       Oxidative stress     MPM     CENTRS CODING FOR COMPORENTS OF THE PROTEASOME DEGRADATION     0.00     0.08       Oxidative stress     MPM     CULTRATINONULTED PROTEINS     0.00     0.00     0.00       CO     TRANSLATION     0.00     0.00     0.00     0.00     0.00       CO     TRANSLATION     0.01     0.01     0.01     0.01     0.04       Translation Initiation     MPM     REGOMAL STRUCTURE     0.00     0.00     0.03     0.03     0.05       Translation Initiation     MPM     REGOMAL STRUCTURE     0.00     0.06     0.00     0.00     0.06     0.00			UPREGULATED PATHWAYS	p-val	FDR q-val
Protein     Introducer     MMR:     CERNES CODING FOR COMPONENTS OF THE PROTEASOME DEGRADATION     0.05     0.20       Oxidative stress     MMR:     CUITATION OF TRANSLATION     0.00     0.00     0.00     0.00       Oxidative stress     MMR:     CUITATION OF TRANSLATION     0.00     0.00     0.00     0.00       Translation Initiation     MMR:     CUITATION OF TRANSLATION     0.01     0.01     0.01       Translation Initiation     MMR:     REDSOMAL STREET WOLVED IN RIBOSOME ASSEMBLY     0.00     0.00       MMR:     ORGANELLAR REDSOME ASSEMBLY PROTEINS AND THEIR PREDICTED TARGETING     0.00     0.00       MMR:     REDSOMAL STREET WOLVED IN RIBOSOME ASSEMBLY     0.00     0.00     0.00       MMR:     REDSOMAL STREET WOLVED IN REDSOME ASSEMBLY     0.00     0.00     0.00     0.00       MMR:     REDSOMAL STREET WOLVED IN REDSOME ASSEMBLY     0.01     0.04     0.03     0.05     0.20       MMR:     MARKERY     MMR:     REDSOMAL STREET WOLVED IN REDSOME ASSEMBLY     0.00     0.00     0.00       Transcription     MMR:     REDSOME ASSEMBLY <td></td> <td></td> <td></td> <td></td> <td></td>					
Instruction     Instruction     Instruction     Instruction     Instruction       Oxidative stress     MPM     CluritAHORY AND THER TIME OF TRANSCRIPTION     0.00     0.00       Oxidative stress     MPM     CluritAHORY AND THER TIME OF TRANSCRIPTION     0.00     0.00       GO     TRANSLATION INITIATION FRANCLATION     0.01     0.01     0.01       GO     TRANSLATION INITIATION FRANCLATION     0.01     0.01     0.04       GO     TRANSLATION INITIATION FRACTOR ACTIVITY     0.01     0.04       CO     TRANSLATION INITIATION FRACTOR ACTIVITY     0.01     0.04       Translation Initiation     MPM     ORGANELLAR RIBOSOME ASSEMBLY PROTEINS AND THEIR PREDICTED TARGETING     0.00     0.00       MPM     TRANSLATION INITIATION FRACTOR ACTIVITY     0.01     0.06     0.00     0.01     0.01     0.05     0.22     0.01     0.01 </td <td rowspan="2">Protein Turnover</td> <td></td> <td></td> <td></td> <td></td>	Protein Turnover				
MPM:     INITIATION OF TRANSLATION     0.00     0.00     0.00       GC:     TRANSLATIONAL INITIATION FACTOR ACTIVITY     0.01     0.01       Translation Initiation     0.07     TRANSLATIONAL INITIATION FACTOR ACTIVITY     0.01     0.04       Translation Initiation     MPM:     RIBOSOML STRUCTURE     0.00     0.00     0.00       MPM:     GENES CODING FOR COMPONENTS INVOLVED IN RIBOSOME ASSEMBLY     0.01     0.06     0.03       MPM:     GENES CODING FOR COMPONENTS INVOLVED IN RIBOSOME ASSEMBLY     0.01     0.06     0.06       MPM:     TRANSCRIPTION DE XPORT OF GAS AND 40S RIBOSOME ASSEMBLY     0.01     0.06     0.06       MPM:     TRANSCRIPTION ASSOCATED PROTEINS IMPLICATED IN THE TRANSCRIPTIONAL     0.04     0.16       MPM:     TRANSCRIPTION RELATED PROTEINS IMPLICATED IN THE TRANSCRIPTIONAL     0.04     0.07       MPM:     TRANSCRIPTION RELATED PROTEINS IN TROPHOZOITE AND SCHIZONTS     0.03     0.11       MPM:     TRANSCRIPTION RELATED PROTEINS IN TROPHOZOITE AND SCHIZONTS     0.00     0.01       MPM:     REVOCITE PROTEINS NETROPHIS INTROPHOZOITE AND SCHIZONTS     0.03     0.01       MPM		MPM:	MACHINERY AND THEIR TIMED TRANSCRIPTION	0.05	0.20
GC:     TRANSLATION     0.00     0.01       Translation Initiation     GC:     TRANSLATION NITIATION F ACTOR ACTIVITY     0.01     0.04       Translation Initiation     MPM:     RIBOSOML STRUCTURE     0.00     0.03       MPM:     GRO.     TRANSLATION NITIATION F ACTOR ACTIVITY     0.01     0.04       GC:     STRUCTURAL CONSTITUENT OF RIBOSOME ASSEMBLY PORTINS AND THEIR PREDICTED TARGETING     0.00     0.03       GC:     TRANSCRIPTION ASSOCIATED PROTEINS MULCATED IN THE TRANSCRIPTIONAL     0.04     0.04       MPM:     TRANSCRIPTION ASSOCIATED PROTEINS INFLICATED IN THE TRANSCRIPTIONAL     0.04     0.01       MPM:     TRANSCRIPTION RELATED PROTEINS INFLIP ADDAMIN-S-     0.04     0.01       Transcription     MPM:     TRANSCRIPTION RELATED PROTEINS INFLIP ADDAMIN-S-     0.04     0.01       MPM:     TRANSCRIPTION DE CONTAINING HARD DOMAIN-S-     0.00     0.04     0.01       MPM:     TRANSCRIPTION DE DE CONSTITUENT OF PLAUSIBLE STRESS HELICASES     0.01     0.04       MPM:     TRANSCRIPTION DE DE CONSTITUENT OF PLAUSIBLE STRESS HELICASES     0.01     0.02       MPM:     HEROLOPEN CONTAINING HISTOR PRODEDIN	Oxidative stress				
GC:     TRANSLATIONAL INITIATION FACTOR ACTIVITY     0.01     0.04       Translation Initiation     MPM.     RIBOSOMAL STRUCTURE.     0.00     0.00       MPM.     GRCANELLAR RIBOSOME ASSEMBLY PROTEINS AND THEIR PREDICTED TARGETING     0.00     0.00       MPM.     GRNE COUNDING FOR COMFONCTS INVOLVED IN RIBOSOME ASSEMBLY     0.01     0.06       GC:     STRUCTURAL CONSTITUENT OF RIBOSOME     0.00     0.05       MPM.     MATURATION AND EXPORT OF GRO SAND 40S RIBOSOMAL SUBUNITS     0.04     0.05       Transcription     MPM.     TRANSCRIPTION ASSOCIATED PROTEINS INFLICATED IN THE TRANSCRIPTIONAL     0.04     0.01       MPM.     TRANSCRIPTION RELATED REGISTIES ENCODING GENES     0.03     0.01       MPM.     TRANSCRIPTION RELATED REGISTIES ENCODING GENES     0.03     0.01       MPM.     PROTEINS CONTAINING HISTONE POST TRANSLATIONAL MODIFICATION BINDING     0.00     0.04       MPM.     PROTEINS CONTAINING HISTONE POST TRANSLATIONAL MODIFICATION BINDING     0.02     0.01       MPM.     PROTEINS CONTAINING HISTONE POST TRANSLATIONAL MODIFICATION BINDING     0.00     0.02       MPM.     REVOLED PROTEINS CONTAINING HISTONE POST TRANSLATIONAL MODIFIC					
GC     TRANSLATION NITIATION FACTOR ACTIVITY     0.01     0.00       MPM     RIBOSOMAL STRUCTURE     0.00     0.00       MPM     ORGANELLAR RIBOSOMAL STRUCTURE     0.00     0.00       GC     STRUCTURAL CONSTITUENT OF RIBOSOME ASSEMBLY     0.01     0.06       MPM     KEROSOMAL STRUCTURE     0.00     0.06       MPM     TRANSCRIPTION ASSCORTED PROTEINS INFOLVED IN RIBOSOME ASSEMBLY     0.01     0.04       Transcription     MPM     TRANSCRIPTION ASSCORTED PROTEINS INFOLVED IN THE TRANSCRIPTIONAL     0.04     0.16       MRM     TRANSCRIPTION RELATED PROTEINS INFOLVED IN THE TRANSCRIPTIONAL     0.04     0.01       MPM     TRANSCRIPTION DE CONSTRUCTIONS OF PLAUSIBLE STRESS HELICASES     0.03     0.01       MPM     READOLTED PROTEINS INFOLVED ONE TRANSCRIPTION SCHIPTONS OF PLAUSIBLE STRESS HELICASES     0.00     0.02       Chromatin     MPM     HISTORE CHARGENES     0.00     0.04       Modification     MPME     INTERACTORE OF THE STRUCTURES     0.00     0.04       Modification     MPME     HISTORE CHARGENES     0.00     0.04       MPME     HISTORE CHARG					
Translation Initiation     MPM.     RIBOSOMAL STRUCTURE     0.00     0.01     0.00     0.01     0.00     0.01     0.00     0.01     0.00     0.01     0.00     0.01     0.00     0.01     0.00     0.01     0.00     0.01     0.00     0.01     0.00     0.01     0.01     0.01     0.01					
MPM     ORGANELLAR RIBOSOME ASSEMBLY PROTEINS AND THEIR PREDICTED TAGETING     0.00     0.03       MPM     GENES CONDING FOR COMPONENTS INVOLVED IN RIBOSOME ASSEMBLY     0.01     0.06       GO     STRUCTURAL CONSTITUENT OF RIBOSOME     0.00     0.06       MPM     MATURATION AND EXPORT OF 60S AND 40S RIBOSOMAL SUBJINITS     0.05     0.20       Transcription     MPM     TRANSCRIPTION ASSOCIATED PROTEINS IMPLICATED IN THE TRANSCRIPTIONAL     0.04     0.16       MACHINERY     MPM     TRANSCRIPTION RELATED PROTEINS IMPLICATED INTERACTIONS SOCIATED PROTEINS THAN DO CONSTITUENTS OF PRODES     0.03     0.14       MPM     PRODED PROTEINS THAT COULD BE CONSTITUENTS OF PRODES     0.05     0.22       MPM     PROTEINS CONTAINING HISTONE POST TRANSLATIONAL MODIFICATION-BINDING     0.00     0.01       MPM     PROTEINS CONTAINING HISTONE POST TRANSLATIONAL MODIFICATION-BINDING     0.00     0.01       MPM     INTERACTOME OF THE SETH PROTEIN PHOSPHATASE TYPE 1     0.02     0.14       Phospholipid     MPM     INTERACTOME OF THE SETH PROTEIN PHOSPHATASE TYPE 1     0.02     0.14       Phospholipid     MPM     UTULATION OF PHOSPHATINE NULCLAR PORE     0.00     0.00 </td <td></td> <td></td> <td></td> <td></td> <td></td>					
MPMc     CENES CODING FOR COMPONENTS INVOLVED IN RIBOSOME ASSEMELY     0.01     0.06       MPMc     STRUCTURAL CONSTITUENT OF RIBOSOME     0.00     0.06       MPMc     TRANSCRIPTION ASD CLAYED PROTEINS IMPLICATED IN THE TRANSCRIPTIONAL     0.04     0.16       MPMc     TRANSCRIPTION ASD CLAYED PROTEINS INFLICATED IN THE TRANSCRIPTIONAL     0.04     0.17       MPMc     TRANSCRIPTION RELATED PROTEINS INTO PLOADINGS     0.04     0.17       MPMc     TRANSCRIPTION RELATED PROTEINS INTROPHOZOTE AND SCHIZONTS     0.00     0.01       MPMc     TRANSCRIPTION SCHITICUS IN TROPHOZOTE AND SCHIZONTS     0.00     0.01       MPMc     PREDICTED PROTEINS INTROPHOZOTE AND SCHIZONTS     0.00     0.01       MPMc     PROTEINS CONTAINING HISTONE POST TRANSLATIONAL MODIFICATION-BINDING     0.00     0.01       MODILES     MPMc     HISTONE CHAPERONES     0.00     0.04       MODILES     CHROMATINA AND EXPORT THROUGH THE ENDOPHATASE TYPE 1     0.02     0.14       metabolism     MPMc     FATTY ACIDS ELONGATION IN THE ENDOPHATASE TYPE 1     0.02     0.14       metabolism     MPMc     FATTY ACIDS ELONGATION IN THE ENDOPHATASE TYPE 1     0.02 <td>Translation Initiation</td> <td></td> <td></td> <td></td> <td></td>	Translation Initiation				
GO:     STRUCTURAL CONSTITUENT OF RIBOSOME     0.00     0.06       MPHE     MATURATION AND EXPORT OF 60S AND 40S RIBOSOMAL SUBUNTS     0.05     0.20       Transcription     MPME     TRANSCRIPTION ASSOCIATED PROTEINS IMPLICATED IN THE TRANSCRIPTIONAL     0.04       MPME     NARIABINING PROTEINS WIT AP2 DOMAIN-S-     0.04     0.03     0.16       MPME     RINA-BINDING PROTEINS INT ROPHOZOTES INCODING GENES     0.03     0.01       MPME     RINA-BINDING PROTEINS INT ROPHOZOTES HOLDSING SENESS     0.00     0.00       MPME     PROCODE PROTEINS THAT COULD BE CONSTITUENTS OF PRODESS     0.00     0.01       MPME     PROCOLE DROFTINS I STAT COULD BE CONSTITUENTS OF PRODESS     0.00     0.01       MODILES     MODILES     0.00     0.01     MODILES     0.00     0.02     0.14       Phospholipid     MPME     HISTONE CHAPERONES     0.00     0.00     0.01     0.02     0.14       Phospholipid     MPME     HISTONE CHAPERONES     0.00     0.02     0.14       Phospholipid     MPME     HISTONE CHAPERONES     0.00     0.02     0.14					
MPM.     MATURATION AND EXPORT OF 60S AND 40S RIBOSOMAL SUBUNITS     0.05     0.20       Transcription     MPM.     TRANSCRIPTION ASSOCIATED PROTEINS IMPLICATED IN THE TRANSCRIPTIONAL     0.04     0.16       MPM.     DNA BINDING PROTEINS WITH AP2 DOMAIN-S-     0.04     0.17       MPM.     DNA BINDING PROTEINS WITH AP2 DOMAIN-S-     0.04     0.17       MPM.     PREDICTED PROTEINS TRAT COULD BE CONSTITUENTS OF PLAUSIELS STRESS HELICASES     0.00     0.01       MPM.     PREDICTED PROTEINS THAT COULD BE CONSTITUENTS OF PLAUSIELS STRESS HELICASES     0.00     0.01       MPM.     PROTEINS CONTAINING HISTORE POST TRANSLATIONAL MODIFICATION-BINDING     0.00     0.01       MDDILES     MPM.     PROTEINS CONTAINING PROTEINS     0.02     0.14       Modification     MPM.     INTERACTONE OF THE SERTHAR PROTEIN PHOSPHATASE TYPE 1     0.02     0.14       Phospholipid     MPM.     FATTY ACIDS ELONGATION IN THE ENDOPLASING RETICULUM     0.03     0.19       Transport through the inclus     MPM.     FATTY ACIDS ELONGATION IN THE ENDOPLASING RETICULUM     0.03     0.03       Transport through the inclus     MPM.     FATTY ACIDS ELONGATION IN THE ENDOPLASING RETICULUM					
MPM:     Transcription     0.04     0.16       MCR.     MPM:     Transcription     0.04     0.16       MPM:     Transcription     MPM:     0.04     0.17       MPM:     Transcription     MPM:     0.04     0.17       MPM:     Transcription     MPM:     0.03     0.14       MPM:     MPM:     NEXDEX PROTEINS WITH AP2 DOMAIN-S:     0.00     0.01       MPM:     PROTEINS WIT RAPE ZOTE:     NEXDEX ZOTE:     0.00     0.01       MPM:     PROTEINS WITH AP2 DOMAIN-S:     0.00     0.01     0.04       MPM:     PROTEINS THAT COULD BE CONSTITUENTS SCHELICASES     0.00     0.01     0.02     0.14       MPM:     HISTORE COULD BE CONSTITUENTS SCHELICASES     0.00     0.00     0.02     0.14       Medification     MPM:     HISTORE CHAPERONES     0.00     0.00     0.02     0.14       Phospholipid     MPM:     INTERACTONE OF PROSENTER PROTEIN PHOSPHATASE TYPE 1     0.02     0.14       Prospholipid     MPM:     INTERACTONE OF PHOSPHOLIPIDS     0.00     0.00 <td></td> <td></td> <td>STRUCTURAL CONSTITUENT OF RIBOSOME</td> <td></td> <td></td>			STRUCTURAL CONSTITUENT OF RIBOSOME		
Machine Proteins     Machine Proteins     Utility       Transcription     MPM.     Transcription Proteins in Trophozoite And Schizonts     0.03     0.14       MPM.     MRNA-BINDING PROTEINS IN TROPHOZOITE AND SCHIZONTS     0.00     0.01       MPM.     PREDICTED PROTEINS IN TROPHOZOITE AND SCHIZONTS     0.00     0.01       MPM.     PREDICTED PROTEINS THAT COULD BE CONSTITUENTS OF P-BODIES     0.05     0.22       MPM.     ENCODED PROTEINS THAT COULD BE CONSTITUENTS OF P-BODIES     0.00     0.01       MPM.     ENCODED PROTEINS TONE POST TRANSLATIONAL MODIFICATION-BINDING     0.00     0.01       MOdification     MPM.     HISTONE CHAPERONES     0.00     0.01       Modification     MPM.     INTERACTOME OF THE SER THR PROTEINS     0.02     0.14       Phospholipid     MPM.     INTERACTOME OF THE SER THR PROTEINS     0.02     0.14       Phospholipid     MPM.     FATTY ACIDS ELONCATION IN THE ENDOPLASMIC RETICULUM     0.03     0.19       Inasport Through the     MPM.     FATTY ACIDS ELONCATION IN THE ENDOPLASMIC RETICULUM     0.03     0.01       Incleus     MPM.     FATTY ACIDS ELONCATION NIT THE		MPM:	MATURATION AND EXPORT OF 60S AND 40S RIBOSOMAL SUBUNITS	0.05	0.20
Transcription     MPM: HTANSCRIPTION RELATED PROTEINS SUTH AP2 DOMAIN-S:     0.04     0.17       MPM:     TRANSCRIPTION RELATED PROTEINS SUCODING GENES     0.03     0.14       MPM:     MRNA-BINDING PROTEINS IN TROPHOZOITE AND SCHIZONTS     0.00     0.01       MPM:     PREDICTED PROTEINS TATCOULD BE CODBING SCHIZONTS     0.05     0.22       MPM:     PROTEINS TATC COULD BE CONSTITUENTS OF PADDIES     0.05     0.22       Chromatin     MPM:     PROTEINS CONTAINING HISTONE POST TRANSLATIONAL MODIFICATION-BINDING     0.00     0.01       MODILES     MPM:     HISTONE CHAPE RONES     0.00     0.04       MPM:     HISTONE CHAPE RONES     0.02     0.14       Phospholipid     MPM:     HITCON OF PHOSPHOLIPIDS     0.02     0.14       Phospholipid     MPM:     KARYOPHERIN-EXPORT THEOUCH THE NUCLEAR EXPORT PATHWAYS     0.00     0.00       nucleus     MPM:     KARYOPHERIN-EXPORTI HENDUCLEAR EXPORT PATHWAYS     0.00     0.03       nucleus     MPM:     CHARONTIN OF PHOSPHORUS ASSOCIATED WITH HE MEMBRANE OF INFECTED     0.00     0.01       Reported proteins     MPM:     EXPORTED PORTEINS SO PLAS		MPM:		0.04	0.16
MPMI     TRANSCRIPTION     RELATED PROTEINS ENCODUNG SENSO     0.03     0.14       MPMI     PREDICTED PROTEINS INT ROPPOZOTE AND SCHIZONTS     0.00     0.01       MPMI     PREDICTED PROTEINS INT ROPPOZOTE AND SCHIZONTS     0.01     0.05     0.22       MPMI     PROTEINS TATA COULD BE CONSTITUENTS OF PBODIES     0.05     0.22       MPMI     PROTEINS STATA COULD BE CONSTITUENTS OF PBODIES     0.00     0.01       Modification     MPMI     INTERACTORE OF THE SENTH COULD BE CONSTITUENTS     0.00     0.01       Modification     MPMI     UTILIZATION OF PHOSPHOLIPIOS     0.02     0.14       Phospholipid     MPMI     UTILIZATION OF PHOSPHOLIPIOS     0.02     0.14       Instrapt through the     MPMI     UTILIZATION OF PHOSPHOLIPIOS     0.02     0.01       Instrapt through the     MPMI     INTERACTORE TROUCH THE ENDOLIAR PORT PATHWAYS     0.00     0.00       Incleus     MPMI     PARASITE ENCODED PROTEINS ASSOCIATED WITH THE MEMBRANE     0.00     0.01       Instructure     MPMI     CHARACTERISTICS OF PLASMODIUM FALCIPARUM WITH CONFIRMED LOCATION     0.01     0.02     0.11	Tasassiatisa	MPM:	DNA BINDING PROTEINS WITH AP2 DOMAIN-S-	0.04	0.17
MPM:     PREDICTE D PROTEIN. INTERACTIONS OF PLAUSIBLE STRESS HELICASES     0.01     0.04       MPM:     ENCODED PROTEINS THAT COULD BE CONSTITUENTS OF P-BODIES     0.05     0.22       Chromatin     MPM:     PROTEINS CONTAINING HISTONE POST TRANSLATIONAL MODIFICATION-BINDING     0.00     0.01       Modification     MPM:     PROTEINS CONTAINING HISTONE POST TRANSLATIONAL MODIFICATION-BINDING     0.02     0.14       Phospholipid     MPM:     HISTONE CHAPERONES     0.02     0.14       Phospholipid     MPM:     INTERACTORE OF THE SER-THIR PROTEIN PHOSPHATASE TYPE 1     0.02     0.14       Phospholipid     MPM:     INTERACTORE OF THE SER-THIR PROTEIN PHOSPHATASE TYPE 1     0.02     0.14       Irransport through the     MPM:     INTERACTORE OF THE SER-THIR PROTEIN PHOSPHATASE TYPE 1     0.02     0.14       realbolism     MPM:     KARYOPHERIN-EXPORTIN-MEDIATED NUCLEAR PORE     0.00     0.00     0.00       nucleus     MPM:     KARYOPHERIN-EXPORTIN-MEDIATED NUCLEAR PORE     0.00     0.01     0.05       Exported proteins     MPM:     KARAYOPHERIN-EXPORTIN-MEDIATED NUCLEAR PORTE NOTEIRED LOCATION     0.01     0.05	transcription				
MPM:     EXCODED PROTEINS THAT COULD BE CONSTITUENTS OF PADDIES     0.05     0.22       MPM:     PROTEINS CONTAINING HISTONE POST TRANSLATIONAL MODIFICATION-BINDING     0.00     0.01       Modification     MPM:     HISTONE CHAPERONES     0.00     0.01       Modification     MPM:     HISTONE CHAPERONES     0.02     0.14       Phospholipid     MPM:     INTERACTOME OF THE SER-THR PROTEINS     0.02     0.14       Phospholipid     MPM:     INTERACTOME OF THE SER-THR PROTEIN PHOSPHATASE TYPE 1     0.02     0.14       Phospholipid     MPM:     HITORE CATOR OF THE SER-THR PROTEIN PHOSPHATASE TYPE 1     0.02     0.14       Interaction     MPM:     FATTY ACIDS ELONGATION IN THE ENDOPLASMIC RETICULUM     0.03     0.09       Interaction     MPM:     KARYOPHERIN-EXPORT THROUGH THE NUCLEAR PORE     0.00     0.00       nucleus     MPM:     KARYOPHERIN-EXPORTINABED ADDIE DATAGE EXPORT PATHWAYS     0.00     0.01       Exported proteins     MPM:     PARASITE ENCODED PROTEINS ASSOCIATED WITH THE MEMBRANE OF INFECTED     0.00     0.01       MPM:     PROTEINS ASSOCIATED WITH THE MEMBRANE     0.02     0.11		MPM:	MRNA-BINDING PROTEINS IN TROPHOZOITE AND SCHIZONTS		
MPM:     PROTEINS CONTAINING HISTONE POST TRANSLATIONAL MODIFICATION-BINDING     0.00     0.01       Modification     MPM:     Chromatin     0.00     0.04       Modification     MPM:     CHROMATIN MODIFYING PROTEINS     0.02     0.14       MPM:     CHROMATIN MODIFYING PROTEINS     0.02     0.14       MPM:     INTERACTOME OF THE SER-THR PROTEIN PHOSPHATASE TYPE 1     0.02     0.14       metabolism     MPM:     INTERACTOME OF THE SER-THR PROTEIN PHOSPHATASE TYPE 1     0.02     0.14       metabolism     MPM:     INTELIZATION OF PHOSPHOLIPIDS     0.02     0.14       metabolism     MPM:     INTERACTOME OF THROUGH THE NUCLEAR PORE     0.00     0.00       nucleus     MPM:     KARYOPHERIN-EXPORTIN-MEDIATED NUCLEAR EXPORT PATHWAYS     0.00     0.03       exported proteins     MPM:     EXPORTED PROTEINS OF PLASMODIUM FALCIPARUM EXPORT PROTEINS THAT     0.02     0.11       MPM:     EXPORTED ROTEINS OF PLASMODIUM FALCIPARUM EXPORT PROTEINS THAT     0.02     0.11       Remotel     NPM:     EXPORTED PROTEINS OF PLASMODIUM FALCIPARUM EXPORT PROTEINS THAT     0.02     0.11       MPM:		MPM:	PREDICTED PROTEIN-PROTEIN INTERACTIONS OF PLAUSIBLE STRESS HELICASES	0.01	
Chromatin Modification     MPM: HISTORE CHAPERONES     0.00     0.004       MPM:     CHROMATIN MODIFYING PROTEINS     0.02     0.14       Phospholipid     MPM:     UTILIZATION OF PHOSPHOLIPIOS     0.02     0.14       Phospholipid     MPM:     UTILIZATION OF PHOSPHOLIPIOS     0.02     0.14       metabolism     MPM:     FATTY ACIDS ELONGATION IN THE ENDOPLASMIC RETICULUM     0.03     0.19       Transport through the     MPM:     IMPORT AND EXPORT THROUGH THE NUCLEAR EXPORT PATHWAYS     0.00     0.01       nucleus     MPM:     PARASITE ENCODED PROTEINS ASSOCIATED WITH THE MEMBRANE OF INFECTED     0.00     0.01       EXPORTED PROTEINS OF PLASMODIUM FALCIPARUM WITH CONFIRMED LOCATION     0.01     0.05       MPM:     EXPORTED PROTEINS OF PLASMODIUM FALCIPARUM EXPORT PROTEINS THAT     0.02     0.111       REMODEL INFECTED ERTITHROCYTE     0.00     0.00     0.03       MPM:     CHARACTERISTICS OF PLASMODIUM FALCIPARUM EXPORT PROTEINS THAT     0.02     0.011       REMODEL INFECTED ERTITHROCYTE     0.00     0.00     0.00     0.00     0.00       Others     MPM:     PROTEIN KINASE G-DEPE		MPM:		0.05	0.22
Modification     MPM: MPM: MPM:     INSTORE CHAPEROMES     0.00     0.04     0.02     0.14       MPM:     CHROMATIM MODE/VING PROTEINS     0.02     0.14     0.02     0.14       Phospholipid     MPM:     INTERACTOME OF THE SERTHR PROTEIN PHOSPHATASE TYPE 1     0.02     0.14       Phospholipid     MPM:     INTERACTOME OF PHOSPHOLIPIDS     0.02     0.14       metabolism     MPM:     KATY ACIDS ELONGATION IN THE ENDOPLASMIC RETICULUM     0.03     0.19       Transport through the metabolism     MPM:     KARYOPHERIN-EXPORTIN-MEDIATED NUCLEAR EXPORT PATHWAYS     0.00     0.00       MPM:     KARYOPHERIN-EXPORTIN-MEDIATED NUCLEAR EXPORT PATHWAYS     0.00     0.01       Exported proteins     MPM:     KARYOPHERIN-EXPORTIN-MEDIATED NUCLEAR EXPORT PROTEINS THAT     0.02     0.11       MPM:     CHARACTERISTICS OF PLASMODIUM FALCIPARUM WITH CONFIRMED LOCATION     0.01     0.05       MPM:     CHARACTERISTICS OF PLASMODIUM FALCIPARUM WITH CONFIRMED LOCATION     0.01     0.03       MPM:     AUTOPHAGY AND AUTOPHAGY RELATED PATHWAYS     0.00     0.00     0.00       Others     MPM:     PHOSPHOPOROTE	Chromotin	MPM:		0.00	0.01
MPM:     CHROMA TIM MODIF YING PROTEINS     0.02     0.14       MPM:     INTERACTOME OF THE SER-THR PROTEIN PHOSPHATASE TYPE 1     0.02     0.14       metabolism     MPM:     FATTY ACIDS ELONGATION IN THE ENDOPLASMIC RETICULUM     0.03     0.19       Transport through the nucleus     MPM:     FATTY ACIDS ELONGATION IN THE ENDOPLASMIC RETICULUM     0.03     0.00       MPM:     KARYOPHERIN-EXPORTIN-MEDIATED NUCLEAR EXPORT PATHWAYS     0.00     0.00       MPM:     KARYOPHERIN-EXPORTIN-MEDIATED NUCLEAR EXPORT PATHWAYS     0.00     0.01       ERYTHROCYTES     MPM:     EXPORTED PROTEINS ASSOCIATED WITH THE MEMBRANE OF INFECTED     0.00     0.01       Exported proteins     MPM:     EXPORTED PROTEINS OF PLASMODIUM FALCIPARUM WITH CONFIRMED LOCATION     0.01     0.05       MPM:     CHARACTERISTICS OF PLASMODIUM FALCIPARUM EXPORT PROTEINS THAT     0.02     0.11       REMODEL INFECTED ERYTHROCYTE     0.00     0.00     0.03       MPM:     HUTOPHAGY AND AUTOPHAGY RELATED PATHWAY     0.00     0.00       Others     MPM:     PHOTEIN KINASE G-DEPENDENT PHOSPHORYLATION IN SCHIZONTS     0.04     0.15       MPM:     DIF		MPM:	HISTONE CHAPERONES	0.00	0.04
Phospholipid metabolism     MPM: PATTY ACIDS ELONGATION IN THE ENDOPLASMIC RETICULUM     0.02     0.14       fransport through the nucleus     MPM:     FATTY ACIDS ELONGATION IN THE ENDOPLASMIC RETICULUM     0.03     0.19       reasport through the nucleus     MPM:     MPORT AND EXPORT THROUGH THE NUCLEAR PORE     0.00     0.00       MPM:     KARYOPHERIN-EXPORTIN-MEDIATED NUCLEAR EXPORT PATHWAYS     0.00     0.01       PARASITE ENCODE D PROTEINS ASSOCIATED WITH THE MEMBRANE OF INFECTED     0.00     0.01       Exported proteins     MPM:     EXPORTED PROTEINS OF PLASMODIUM FALCIPARUM WITH CONFIRMED LOCATION     0.01     0.05       MPM:     EXPORTED PROTEINS OF THE PARASITOPHOROUS VACUOLAR MEMBRANE     0.02     0.11       REMODEL INFECTED ERYTHROCYTE     0.00     0.03     0.04       Autophagy     MPM:     AUTOPHAGY AND AUTOPHAGY-RELATED PATHWAYS     0.00     0.00       Others     MPM:     PHOSPHOPROTEOME OF THE MEROZOITE     0.00     0.00     0.00       MPM:     DIFFERENTIAL PROTEOME OF THE MEROZOITE     0.00     0.00     0.00     0.00       MPM:     S-NITROSYLATED PROTEINS     0.01     0.13     0.00	woullication	MPM:	CHROMATIN MODIFYING PROTEINS	0.02	0.14
metabolismMPM:FATTY ACIDS ELONGATION IN THE ENDOPLASMIC RETICULUM0.030.19fransport through the nucleusMPM:IMPORT AND EXPORT THROUGH THE NUCLEAR EXPORT PATHWAYS0.000.03nucleusMPM:KARYOPHERIN-SKPORTIN-MEDATED NUCLEAR EXPORT PATHWAYS0.000.01Exported proteinsPARASITE ENCODED PROTEINS OF PLASMODIUM FALCIPARUM WITH CONFIRMED LOCATION0.010.05Exported proteinsMPM:PROTEINS OF PLASMODIUM FALCIPARUM WITH CONFIRMED LOCATION0.010.05MPM:CHARACTERISTICS OF PLASMODIUM FALCIPARUM WITH CONFIRMED LOCATION0.010.05MPM:CHARACTERISTICS OF PLASMODIUM FALCIPARUM EXPORT PROTEINS THAT0.020.11REMODEL INFECTED DERYTHROCYTE0.000.030.04AutophagyMPM:AUTOPHAGY AND AUTOPHAGY CATHWAY0.000.00MPM:PHOSPHOPROTEOME OF THE MEROZOITE0.000.000.00OthersMPM:PHOSPHOROTEOME OF THE MEROZOITE0.000.00MPM:PROTEIN KINASE G-DEPENDENPT PHOSPHORYLATION IN SCHIZONTS0.040.15MPM:DIFFERENTIAL PROTEOME ANALYSIS UNDER DRUG TREATMENT0.010.13MPM:INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL0.000.00Invasion,MPM:INTERACTIONS BETWEEN NORMAL AND INFECTED RBC0.000.00CytoadherenceGC:CYTOADHERENCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN0.000.00GO:CELL-CELL ADHESION0.010.090.000.00		MPM:	INTERACTOME OF THE SER-THR PROTEIN PHOSPHATASE TYPE 1	0.02	0.14
Transport through the nucleus     MPM:     IMPORT AND EXPORT THROUGH THE NUCLEAR PORE     0.00     0.00       nucleus     MPM:     KARYOPHERIN-EXPORTIN-MEDIATED NUCLEAR EXPORT PATHWAYS     0.00     0.03       Exported proteins     MPM:     PRASTIE ENCODED PROTEINS ASSOCIATED WITH THE MEMBRANE OF INFECTED     0.00     0.01       Exported proteins     MPM:     EXPORTED PROTEINS OF PLASMODIUM FALCIPARUM WITH CONFIRMED LOCATION     0.01     0.05       MPM:     PROFTINS OF THE PARASTOPHOROUS VACUOLAR MEMBRANE     0.02     0.11       MPM:     CHARACTERISTICS OF PLASMODIUM FALCIPARUM EXPORT PROTEINS THAT     0.02     0.11       MPM:     CHARACTERISTICS OF PLASMODIUM FALCIPARUM EXPORT PROTEINS THAT     0.02     0.11       MPM:     CHARACTERISTICS OF PLASMODIUM FALCIPARUM EXPORT PROTEINS THAT     0.02     0.11       MPM:     THE ATG AUTOPHAGY-RELATED PATHWAY     0.00     0.00     0.00       Others     MPM:     PHOSPHOROTEOME OF THE MEROZOITE     0.00     0.00     0.00       MPM:     INTERACTIONS BETWEEN MALANSI UNDER DRUGT REATMENT     0.01     0.13     MPM:     S-NITROSYLATED PROTEINS     0.00     0.00     0.00	Phospholipid	MPM:	UTILIZATION OF PHOSPHOLIPIDS	0.02	0.14
nucleusMPM:KARYOPHERIN-EXPORTIN-MEDIATED NUCLEAR EXPORT PATHWAYS0.000.03PARASITE ENCODED PROTEINS ASSOCIATED WITH THE MEMBRANE OF INFECTED0.000.01Exported proteinsMPM:EXPORTED PROTEINS OF PLASMODIUM FALCIPARUM WITH CONFIRMED LOCATION0.010.05MPM:EXPORTED PROTEINS OF PLASMODIUM FALCIPARUM WITH CONFIRMED LOCATION0.010.05MPM:PROTEINS OF THE PARASITOPHOROUS VACUOLAR MEMBRANE0.020.11MPM:CHARACTERISTICS OF PLASMODIUM FALCIPARUM EXPORT PROTEINS THAT0.020.11REMODEL INFECTED ERYTHROCYTE		MPM:	FATTY ACIDS ELONGATION IN THE ENDOPLASMIC RETICULUM	0.03	0.19
Exported proteins     MPM: EXPORTED PROTEINS ASSOCIATED WITH THE MEMBRANE OF INFECTED     0.00     0.01       Exported proteins     MPM: PROTEINS OF PLASMODIUM FALCIPARUM WITH CONFIRMED LOCATION     0.01     0.05       MPM: MPM: PROTEINS OF THE PARASITOPHOROUS VACUOLAR MEMBRANE     0.02     0.11       MPM: MPM: Autophagy     CHARACTERISTICS OF PLASMODIUM FALCIPARUM EXPORT PROTEINS THAT     0.02     0.11       MPM: MPM: MPM: MPM: MPM: MPM: MPM: MPM:	Transport through the	MPM:	IMPORT AND EXPORT THROUGH THE NUCLEAR PORE	0.00	0.00
Exported proteinsERYTHROCYTES EXPORTED PROTEINS OF PLASMODIUM FALCIPARUM WITH CONFIRMED LOCATION MPM: PROTEINS OF THE PARASITOPHOROUS VACUOLAR MEMBRANE CHARACTERISTICS OF PLASMODIUM FALCIPARUM EXPORT PROTEINS THAT REMODEL INFECTED ERYTHROCYTE0.020.11AutophagyMPM: MPM: MPM:AUTOPHAGY AND AUTOPHAGY-RELATED PATHWAYS MPM: PHOSPHOPROTEOME OF THE MEROZOITE MPM: DIFFERENTIAL PROTEINS COPE THE MEROZOITE MPM: DIFFERENTIAL PROTEINS COPE THE MEROZOITE MPM: DIFFERENTIAL PROTEINS0.000.000.00OthersMPM: MPM: MPM: DIFFERENTIAL PROTEINS MPM: DIFFERENTIAL PROTEINSDOWNREGULATED PATHWAYS MPM: S-NITROSYLATED PROTEINSp-valFDR q-vaOthersMPM: MPM: DIFFERENTIAL PROTEINSDOWNREGULATED PATHWAYS MPM: DIFFERENTIAL PROTEINS0.000.00OthersMPM: DIFFERENTIAL PROTEINSNITROSYLATED PROTEINS0.000.00MPM: Print DOWNREGULATED PATHWAYSp-valFDR q-vaPVDOWNREGULATED PATHWAYS MPM: NPM: NERSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC GO: CYTOADHERENCE TO MICROVASCULATURE MEDIATED RS MDM: CO: CO: CTIL-CELL ADHESION0.010.00OU CO: CO: CO: PATHOGENESISOU CO: PATHOGENESIS0.010.00Transcription reansportMPM: MPM: SUBCELLULAR LOCATION OF ADAPTOR PROTEINS MPM: SUBCELLULAR LOCATION OF ADAPTOR PROTEINS MPM: SUBCELLULAR LOCATION OF ADAPTOR PROTEINS MODI0.010.02Transcription reanslation elongation degestionMPM: MPM: MPM: MPM: SUBCELLULAR LOCATION FACTOR ACTIVITY0.030.11<	nucleus	MPM:		0.00	0.03
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Implicition     Implicition of the PARASITOPHOROUG VACUUAR MEMBRANE     0.02     0.11       MPM:     CHARACTERISTICS OF PLASMODIUM FALCIPARUM EXPORT PROTEINS THAT     0.02     0.11       Remodel INFECTED ERYTHROCYTE     0.00     0.03     0.00     0.03       Autophagy     MPM:     AUTOPHAGY AND AUTOPHAGY-RELATED PATHWAYS     0.00     0.00     0.04       MPM:     THE ATG AUTOPHAGIC PATHWAY     0.00     0.00     0.04       Others     MPM:     PHOSPHOPROTEOME OF THE MEROZOITE     0.00     0.00     0.00       MPM:     DIFFERENTIAL PROTEOME ANALYSIS UNDER DRUG TREATMENT     0.01     0.13     0.00     0.00       Others     MPM:     DIFFERENTIAL PROTEOME ANALYSIS UNDER DRUG TREATMENT     0.01     0.03       MPM:     INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL     0.00     0.00       Invasion,     MPM:     ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC     0.00     0.00       Pathogenesis,     GO:     ANTIGENIC VARIATION     0.00     0.00     0.00       Go:     CYLICADHERENCE TO MICROVASCULATURE MEDIATED RS YMBIONT PROTEIN     0.00     <	Europeted proteine	MPM:	EXPORTED PROTEINS OF PLASMODIUM FALCIPARUM WITH CONFIRMED LOCATION	0.01	0.05
REMODEL INFECTED ERYTHROCYTEAutophagyMPM:AUTOPHAGY AND AUTOPHAGY-RELATED PATHWAYS0.000.03MPM:THE ATG AUTOPHAGY AND AUTOPHAGY-RELATED PATHWAYS0.000.000.04OthersMPM:PHOSPHOPROTEOME OF THE MEROZOITE0.000.000.00OthersMPM:PROTEIN KINASE G-DEPENDENT PHOSPHORYLATION IN SCHIZONTS0.010.13MPM:DIFFERENTIAL PROTEOME ANALYSIS UNDER DRUG TREATMENT0.010.13MPM:S-NITROSYLATED PROTEINS <b>P-val</b> FDR q-vaDOWNREGULATED PATHWAYSp-valFDR q-vaMPM:INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL0.000.00Invasion,MPM:INTERACTIONS BETWEEN NORMAL AND INFECTED RBC0.000.00Invasion,MPM:Pfemp1 DOMAIN ARCHITECTURES0.000.00Pathogenesis, GO:GO:CYTOADHERNCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN0.000.00GO:PATHOGENESIS0.010.090.000.09TransportMPM:GLYCOSYLPHOSPHATIDYLINOSITOL -GPI- ANCHOR BIOSYNTHESIS0.010.09TranscriptionMPM:RNA POLYMERASE II TRANSCRIBES MRNA0.020.17Translation elongationGO:TRANSLATION ELONGATION FACTOR ACTIVITY0.030.19	Exported proteins	MPM:	PROTEINS OF THE PARASITOPHOROUS VACUOLAR MEMBRANE	0.02	0.11
AutopnagyMPM:THE ATG AUTOPHAGIC PATHWAY0.000.04OthersMPM:PHOSPHOPROTEOME OF THE MEROZOITE0.000.00MPM:PROTEIN KINASE G-DEPENDENT PHOSPHORYLATION IN SCHIZONTS0.040.15MPM:DIFFERENTIAL PROTEOME ANALYSIS UNDER DRUG TREATMENT0.010.13MPM:S-NITROSYLATED PROTEINS0.000.00DOWNREGULATED PATHWAYSp-valFDR q-vaPowalFDR q-vaMPM:INTERACTIONS BETWEEN MODIFIED HOST CELL MEMBRANE AND ENDOTHELIAL CELL0.000.00NPM:ROSETTE FORMATION BETWEEN NORMAL AND INFECTED RBC0.000.000.00Pathogenesis, GO:ANTIGENIC VARIATION0.000.000.00CytoadherenceGO:CYTOADHERENCE TO MICROVASCULATURE MEDIATED BY SYMBIONT PROTEIN0.000.00GO:PATHOGENESIS0.010.090.090.01GO:PATHOGENESIS0.010.090.010.09GO:PATHOGENESIS0.010.090.010.09GO:RNA POLYMERASE II TRANSCRIBES MRNA0.020.170.030.19Hemoglobin digestionMPM:RNA POLYMERASE II TRANSCRIBES MRNA0.020.17		MPM:		0.02	0.11
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ATP synthesis MPM: ATP SYNTHASE COMPLEX 0.04 0.24					
	ATP synthesis	MPM:	ATP SYNTHASE COMPLEX	0.04	0.24