**Supplementary Table 1. Regulated proteins of *P. brasiliensis*, *Pb*18 after 6 h infection, in INF-γ activated alveolar macrophages**

|  |  |  |  |
| --- | --- | --- | --- |
| **Accession number1** | **Protein description** | **Score2** | ***Pb*18\_P x CTRL****Ratio3** |
| **Functional categories4** |  |  |
| **AMINO ACID METABOLISM**  |  |  |
| **Amino acid degradation** |  |  |
| PADG\_00822 | glutaminase A | 651.49 | *\** |
| PADG\_04686 | glutamine synthetase  | 496.27 | *\** |
| PADG\_05922 | glutamate carboxypeptidase  | 3500.33 | 1.75 |
| PADG\_04516 | NADP-specific glutamate dehydrogenase  | 651.57 | 1.59 |
| PADG\_05085 | 1-pyrroline-5-carboxylate dehydrogenase  | 3215.32 | 1.44 |
| PADG\_06546 | puromycin-sensitive aminopeptidase  | 499.08 | 1.59 |
| PADG\_04689 | N-acetyl-gamma-glutamyl-phosphate reductase | 686.12 | *\** |
| PADG\_02214 | 4-aminobutyrate aminotransferase  | 4656.87 | 0.44 |
| PADG\_03627 | 2-oxoisovalerate dehydrogenase subunit beta  | 674.79 | 0.64 |
| PADG\_03466 | 3-hydroxyisobutyrate dehydrogenase  | 504.5 | + |
| PADG\_07369 | isovaleryl-CoA dehydrogenase  | 3828.73 | 0.52 |
| PADG\_07370 | methylcrotonoyl-CoA carboxylase beta chain  | 1047.22 | 0.6 |
| PADG\_00637 | arginase  | 1161.3 | 0.37 |
| PADG\_01418 | cysteine dioxygenase  | 767.22 | *+* |
| PADG\_03686 | aspartate aminotransferase  | 395.76 | + |
| PADG\_00832 | adenylosuccinate synthetase  | 969.84 | + |
| PADG\_01718 | saccharopine dehydrogenase [NADP+, L-glutamate-forming] | 584.09 | + |
| PADG\_08468 | 4-hydroxyphenylpyruvate dioxygenase  | 5519.57 | 0.71 |
| PADG\_08464 | maleylacetoacetate isomerase  | 1624.24 | 0.71 |
| PADG\_00215 | aromatic-L-amino-acid decarboxylase  | 579.63 | + |
| PADG\_08466 | homogentisate 1,2-dioxygenase  | 1254.23 | 0.53 |
| **Amino acid biosynthesis** |  |  |
| PADG\_07029 | acetylornithine aminotransferase  | 522.48 | *\** |
| PADG\_00888 | argininosuccinate synthase | 652.7 | 1.97 |
| PADG\_01615 | homocitrate synthase, mitochondrial | 559.95 | 3.18 |
| PADG\_08376 | aspartate-semialdehyde dehydrogenase | 696.7 | 1.68 |
| PADG\_05111 | serine hydroxymethyltransferase, cytosolic | 1716.94 | 2.01 |
| PADG\_02914 | glycine cleavage system T protein | 1568.09 | 1.4 |
| PADG\_05896 | phosphoglycerate dehydrogenase  | 313.7 | *\** |
| PADG\_02726 | cysteine synthase | 898.45 | 1.43 |
| PADG\_03522 | methylthioadenosine phosphorylase | 479.79 | 1.44 |
| PADG\_08662 | cystathionine beta-lyase | 398.91 | *\** |
| PADG\_08328 | 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase | 4196.01 | 1.89 |
| PADG\_07907 | acetolactate synthase  | 1231.54 | 1.46 |
| PADG\_07609 | dihydroxy-acid dehydratase | 505.55 | 2.18 |
| PADG\_03114 | 3-deoxy-7-phosphoheptulonate synthase | 523.88 | *\** |
| **NITROGEN METABOLISM** |  |  |
| PADG\_06490 | formamidase  | 1170.68 | 1.47 |
| PADG\_07010 | urease accessory protein UreG | 643.89 | *\** |
| **NUCLEOTIDE/NUCLEOSIDE/NUCLEOBASE METABOLISM** |  |  |
| PADG\_08066 | purine nucleoside phosphorylase I, inosine and guanosine-specific | 1433.7 | 1.46 |
| PADG\_01424 | inosine-uridine preferring nucleoside hydrolase | 435.72 | *\** |
| PADG\_02246 | adenosine kinase | 1864.44 | 1.43 |
| PADG\_04828 | adenylosuccinate lyase | 614.73 | 1.91 |
| PADG\_06297 | phosphoribosylamine-glycine ligase | 410.55 | *\** |
| PADG\_07585 | inosine-5'-monophosphate dehydrogenase | 914.88 | 1.8 |
| PADG\_07970 | dihydroorotase, homodimeric type | 580.91 | *\** |
| PADG\_04288 | endoribonuclease L-PSP  | 22381.84 | 0.67 |
| **C-COMPOUND AND CARBOHYDRATE METABOLISM** |  |  |
| PADG\_04374 | UTP-glucose-1-phosphate uridylyltransferase  | 722.26 | *\** |
| PADG\_11132 | Phosphoglucomutase | 367.02 | *\** |
| PADG\_03943 | Phosphomannomutase | 388.32 | *\** |
| PADG\_04761 | mannosyl-oligosaccharide glucosidase  | 667.61 | 1.84 |
| PADG\_07523 | neutral alpha-glucosidase AB  | 600.23 | 1.91 |
| PADG\_06221 | formate dehydrogenase  | 632.87 | + |
| **PENTOSE-PHOSPHATE PATHWAY** |  |  |
| PADG\_03651 | 6-phosphogluconate dehydrogenase, decarboxylating 1 | 567.53 | 2.27 |
| PADG\_07420 | transaldolase  | 3551.69 | 0.71 |
| **GLYCOLYSIS/GLUCONEOGENESIS** |  |  |
| PADG\_03813 | Hexokinase | 587.08 | 2.45 |
| PADG\_07950 | glucokinase  | 433.94 | 1.78 |
| PADG\_00451 | glucose-6-phosphate isomerase | 919.44 | 1.87 |
| PADG\_05109 | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase | 1255.36 | 1.71 |
| PADG\_08503 | phosphoenolpyruvate carboxykinase | 3649.92 | 1.55 |
| PADG\_02411 | glyceraldehyde-3-phosphate dehydrogenase  | 29527.63 | 0.42 |
| PADG\_01896 | phosphoglycerate kinase | 6553.54 | 0.58 |
| **PYRUVATE METABOLISM** |  |  |
| PADG\_01797 | pyruvate dehydrogenase protein X component | 576.86 | 2.05 |
| PADG\_04165 | pyruvate dehydrogenase complex component Pdx1 | 691.24 | 1.43 |
| PADG\_06494 | dihydrolipoyl dehydrogenase | 3577,44 | 1.4 |
| PADG\_00714 | pyruvate decarboxylase  | 2477.21 | 0.61 |
| PADG\_03276 | S-(hydroxymethyl)glutathione dehydrogenase  | 1082.77 | + |
| **FERMENTATION** |  |  |  |
| PADG\_00171 | L-lactate dehydrogenase  | 3625.04 | 0.71 |
| **TRICARBOXYLIC ACID CYCLE** |  |  |
| PADG\_08387 | citrate synthase, mitochondrial | 665.29 | 1.84 |
| PADG\_04994 | citrate synthase subunit 1  | 2691.59 | 0.63 |
| PADG\_11845 | aconitate hydratase, mitochondrial | 2588.05 | 1.76 |
| PADG\_00317 | succinyl-CoA ligase subunit beta  | 356.85 | 4.09 |
| PADG\_01762 | oxoglutarate dehydrogenase (succinyl-transferring), E1 component | 566.44 | 1.40 |
| PADG\_00052 | succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial | 1339.48 | 1.61 |
| PADG\_08013 | succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial | 768.68 | 2.48 |
| PADG\_08119 | fumarate hydratase, mitochondrial | 596.3 | 2.31 |
| **METHYLCITRATE CYCLE** |  |  |
| PADG\_04718 | 2-methylcitrate dehydratase | 11210.66 | 1.55 |
| PADG\_04709 | methyl-isocitrate lyase | 900.43 | 1.55 |
| PADG\_04710 | 2-methylcitrate synthase, mitochondrial  | 1868.25 | 0.65 |
| **GLYOXALATE CYCLE** |  |  |
| PADG\_01483 | isocitrate lyase | 1754.4 | 1.4 |
| **ELECTRON TRANSPORT AND RESPIRATION** |  |  |
| PADG\_01366 | NADH-ubiquinone oxidoreductase | 3175.48 | 1.82 |
| PADG\_07749 | NAD(P)H:quinone oxidoreductase, type IV | 41840.44 | 1.59 |
| PADG\_05750 | putative cytochrome c oxidase subunit Via | 4381.04 | 2.5 |
| PADG\_04397 | cytochrome c oxidase subunit 4, mitochondrial | 1429.9 | 2.88 |
| PADG\_11468 | electron transfer flavoprotein beta-subunit  | 471.59 | *\** |
| PADG\_11981 | V-type proton ATPase catalytic subunit A | 430.31 | 2.36 |
| PADG\_03175 | V-type proton ATPase subunit F | 877.44 | 1.87 |
| PADG\_04319 | V-type ATPase, G subunit | 448.84 | 1.75 |
| PADG\_00688 | F-type H+-transporting ATPase subunit H | 2589.81 | 2.11 |
| PADG\_08391 | plasma membrane ATPase | 442.15 | 1.76 |
| PADG\_08394 | cytochrome b-c1 complex subunit 2  | 904.65 | 0.61 |
| **ATP SYNTHESIS** |  |  |
| PADG\_07042 | ATP synthase F1, delta subunit | 514.91 | *\** |
| PADG\_04729 | ATP synthase subunit D, mitochondrial | 2219.02 | 2.09 |
| PADG\_07813 | ATP synthase F1, gamma subunit | 1367.33 | 2.38 |
| PADG\_08349 | ATP synthase subunit beta, mitochondrial | 17882.4 | 3.38 |
| PADG\_07789 | ATP synthase subunit delta, mitochondrial | 2026.9 | 1.84 |
| **FATTY ACID BIOSYNTHESIS** |  |  |
| PADG\_00255 | fatty acid synthase subunit beta dehydratase  | 889.54 | 1.75 |
| PADG\_05783 | farnesyl pyrophosphate synthetase  | 3596.45 | *\** |
| **DEGRADATION OF KETONE BODIES** |  |  |
| PADG\_04939 | succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B  | 1703.1 | 1.68 |
| **OXIDATION OF FATTY ACIDS** |  |  |
| PADG\_01209 | enoyl-CoA hydratase  | 5708.9 | 0.36 |
| PADG\_03194 | 3-ketoacyl-CoA thiolase B  | 2030.96 | 0.57 |
| PADG\_01687 | 3-ketoacyl-CoA thiolase  | 3955.45 | 0.67 |
| PADG\_03449 | isopentenyl-diphosphate delta-isomerase  | 795.96 | + |
| PADG\_04343 | short chain dehydrogenase/reductase  | 620.43 | + |
| PADG\_02751 | acetyl-CoA acetyltransferase  | 2879.73 | 0.41 |
| **METABOLISM OF VITAMINS. COFACTORS. AND PROSTHETIC GROUPS** |  |  |
| PADG\_00443 | dihydropteroate synthase  | 1863.88 | 1.52 |
| PADG\_01886 | adenosylhomocysteinase  | 3209.32 | 1.69 |
| PADG\_00513 | 2-succinylbenzoate-CoA ligase  | 567.59 | *\** |
| **SECONDARY METABOLISM** |  |  |
| PADG\_04899 | metallo-beta-lactamase domain-containing protein  | 1103.5 | *\** |
| PADG\_08108 | coproporphyrinogen III oxidase  | 526.04 | *\** |
| PADG\_04636 | dienelactone hydrolase family protein  | 1042.89 | 1.43 |
| PADG\_04175 | inorganic pyrophosphatase | 2372.74 | 1.41 |
| PADG\_02981 | ThiJ/PfpI family protein  | 2110.74 | 0.65 |
| **SIGNAL TRANSDUCTION** |  |  |
| PADG\_02017 | calmodulin  | 917.7 | 2.58 |
| PADG\_01565 | calnexin  | 1309.53 | 1.89 |
| PADG\_01243 | rab GDP-dissociation inhibitor  | 838.81 | 2.15 |
| PADG\_05517 | rho GDP-dissociation inhibitor  | 620.8 | 2.69 |
| PADG\_04440 | 14-3-3-like protein 2  | 22781.86 | 1.41 |
| PADG\_05608 | GTP-binding protein ypt7  | 512.66 | *\** |
| PADG\_03544 | ser/Thr protein phosphatase family protein  | 456.22 | 1.99 |
| PADG\_11275 | CMGC/MAPK protein kinase  | 439.81 | + |
| PADG\_00172 | ras-like GTP-binding protein  | 506.63 | + |
| **CYTOSKELETON** |  |  |
| PADG\_00945 | actin like protein 2/3 complex, subunit 5  | 1210.25 | 1.52 |
| PADG\_00422 | actin cytoskeleton protein (VIP1)  | 3501.22 | 1.69 |
| PADG\_05538 | actin  | 517.74 | 1.99 |
| PADG\_05239 | tubulin-specific chaperone Rbl2 | 949.14 | 1.64 |
| **CELL CYCLE** |  |  |
| PADG\_05683 | cell division control protein 48 | 3099.11 | 1.95 |
| PADG\_05875 | centromere/microtubule-binding protein cbf5 | 473.9 | *\** |
| PADG\_04056 | 14-3-3 family protein épsilon | 11315.76 | 1.43 |
| PADG\_07930 | ARP2/3 complex 20 kDa subunit  | 1565.37 | *\** |
| PADG\_07733 | ARP2/3 complex 34 kDa subunit  | 693.88 | + |
| PADG\_02763 | cyclin-dependent kinase regulatory subunit | 763.95 | + |
| **DNA PROCESSING** |  |  |
| PADG\_02683 | UV excision repair protein Rad23 | 1951.91 | 1.58 |
| PADG\_00656 | non-histone chromosomal protein 6 | 6855.17 | 1.64 |
| PADG\_00718 | histone chaperone asf1 | 625.3 | 1.89 |
| PADG\_00872 | Histone | 3651.58 | 3.45 |
| PADG\_00873 | histone H3 | 2817.56 | 3.93 |
| PADG\_07134 | histone H4 | 3673.03 | 4.13 |
| PADG\_08423 | RuvB-like helicase 2 | 443.26 | *\** |
| **TRANSCRIPTION**  |  |  |
| PADG\_11711 | ATP-dependent RNA helicase eIF4A  | 523.13 | 3.59 |
| PADG\_00067 | polymerase II polypeptide D  | 1667.1 | *\** |
| PADG\_01151 | DNA-directed RNA polymerase II subunit RPB11  | 475.45 | *\** |
| PADG\_04657 | nascent polypeptide-associated complex subunit beta  | 2060.21 | 3.32 |
| PADG\_04730 | nascent polypeptide-associated complex subunit alpha  | 2511.44 | 1.89 |
| PADG\_07888 | eukaryotic translation initiation factor 5A  | 938.57 | *\** |
| PADG\_02825 | small nuclear ribonucleoprotein Lsm8  | 936.12 | 1.52 |
| PADG\_03696 | nuclear polyadenylated RNA-binding protein Nab2  | 580.16 | *\** |
| PADG\_04981 | nucleoporin p58/p45  | 881.57 | *\** |
| PADG\_05393 | mRNA decapping hydrolase  | 487.75 | 2.8 |
| PADG\_04672 | ATP-dependent RNA helicase SUB2  | 1324.65 | *\** |
| PADG\_04796 | pre-mRNA-splicing factor rse1  | 687.99 | *\** |
| PADG\_06734 | U6 snRNA-associated Sm-like protein LSm7  | 2200.35 | *\** |
| PADG\_00676 | RNApii degradation factor def1  | 568.85 | 1.89 |
| PADG\_11958 | small nuclear ribonucleoprotein  | 860.29 | *\** |
| PADG\_11062 | bZIP transcription factor  | 817.23 | 2.22 |
| **PROTEIN SYNTHESIS** |  |  |
| PADG\_02759 | ribosome recycling factor  | 787.37 | 3.42 |
| PADG\_00784 | 40S ribosomal protein S0  | 4550.38 | 1.43 |
| PADG\_00995 | ubiquitin-40S ribosomal protein S27a  | 2933.72 | 2.33 |
| PADG\_02056 | ribosomal protein L7/L12  | 6872.26 | 1.93 |
| PADG\_02446 | 60S acidic ribosomal protein P2  | 14965.78 | 5.00 |
| PADG\_04030 | 60S acidic ribosomal protein P0  | 1428.5 | 1.89 |
| PADG\_05939 | 60S ribosomal protein L27a  | 1823.21 | 1.8 |
| PADG\_07891 | ubiquitin-60S ribosomal protein L40  | 2561.7 | 2.58 |
| PADG\_08244 | 60S acidic ribosomal protein P1 | 14587.27 | 1.58 |
| PADG\_08605 | 40S ribosomal protein S28  | 5195.73 | 1.71 |
| PADG\_02206 | DnaJ domain protein Psi  | 707.66 | 1.5 |
| PADG\_01949 | translation elongation factor Tu  | 3152.3 | 1.64 |
| PADG\_02296 | eukaryotic translation initiation factor 3 subunit F  | 1272.06 | *\** |
| PADG\_04083 | eukaryotic translation initiation factor 2 subunit gamma  | 904.31 | *\** |
| PADG\_07977 | eukaryotic translation initiation factor 1A, Y-chromosomal  | 703.74 | *\** |
| PADG\_08033 | eukaryotic translation initiation factor 3 subunit B  | 557.3 | 1.63 |
| PADG\_01558 | histidyl-tRNA synthetase  | 469.31 | 2.03 |
| PADG\_07582 | phenylalanine-tRNA ligase, alpha subunit  | 691.71 | 1.75 |
| PADG\_00066 | tRNA (guanine(37)-N1)-methyltransferase  | 384.07 | *\** |
| PADG\_00333 | 40S ribosomal protein S16  | 1144.09 | 0.71 |
| PADG\_00335 | 40S ribosomal protein S14  | 4602.27 | 0.66 |
| PADG\_00354 | 40S ribosomal protein S17  | 1524.81 | 0.51 |
| PADG\_00942 | 40S ribosomal protein S7  | 4390.69 | 0.63 |
| PADG\_01083 | 60S ribosomal protein L32 | 1109.4 | 0.44 |
| PADG\_01267 | 40S ribosomal protein S11 | 5706.97 | 0.41 |
| PADG\_01281 | mitochondrial 37S ribosomal protein MRPS8 | 463.22 | + |
| PADG\_01407 | 40S ribosomal protein | 7497.56 | 0.62 |
| PADG\_01654 | 40S ribosomal protein S6-A  | 2963.94 | 0.58 |
| PADG\_01914 | 60S ribosomal protein L35  | 1408.15 | 0.67 |
| PADG\_02445 | 40S ribosomal protein S15  | 6405.8 | 0.58 |
| PADG\_02797 | mitochondrial 54S ribosomal protein YmL3  | 428.68 | + |
| PADG\_03315 | 40S ribosomal protein S4  | 3899.5 | 0.58 |
| PADG\_03326 | 40S ribosomal protein S9  | 4494.77 | 0.39 |
| PADG\_03778 | 60S ribosomal protein L10-A | 3782.16 | 0.55 |
| PADG\_03781 | 60S ribosomal protein L30 | 2485.54 | 0.71 |
| PADG\_12253 | 60S ribosomal protein L3 | 1750.4 | 0.63 |
| PADG\_12365 | 40S ribosomal protein S8-A | 2524.96 | 0.53 |
| PADG\_03856 | 60S ribosomal protein L15  | 2106.51 | 0.48 |
| PADG\_04106 | 60S ribosomal protein L11  | 4743.63 | 0.50 |
| PADG\_07469 | RNase III domain-containing protein  | 465.89 | + |
| PADG\_04848 | 60S ribosomal protein L8-B | 6589.56 | 0.68 |
| PADG\_05025 | ribosomal protein L24 | 1716.08 | + |
| PADG\_05338 | 60S ribosomal protein L18-B | 4386.56 | 0.2 |
| PADG\_06313 | 40S ribosomal protein S18 | 2306.16 | 0.57 |
| PADG\_06525 | 40S ribosomal protein S1 | 4906.3 | 0.64 |
| PADG\_06680 | 40S ribosomal protein S2 | 3503.9 | 0.61 |
| PADG\_06838 | 40S ribosomal protein S5 | 5075.18 | 0.53 |
| PADG\_07583 | 40S ribosomal protein S21 | 3306.23 | 0.65 |
| PADG\_07803 | 60S ribosomal protein L12 | 4692.42 | 0.65 |
| PADG\_07870 |  30S ribosomal protein S7 | 638.76 | + |
| PADG\_08213 | ribosomal protein S2 | 593.74 | + |
| PADG\_08602 | 40S ribosomal protein S2 | 3621.3 | 0.46 |
| PADG\_11832 | 60S ribosomal protein L31 | 3256.39 | 0.39 |
| PADG\_00355 | 40S ribosomal protein S17  | 802.28 | + |
| PADG\_00692 | elongation factor 1-alpha | 7568.61 | 0.29 |
| PADG\_06265 | elongation factor 1 gamma domain-containing protein  | 5531 | 0.57 |
| PADG\_08125 | elongation factor 2 | 3952.23 | 0.48 |
| PADG\_07105 | arginine-tRNA ligase | 554.11 | + |
| PADG\_08472 | lysine-tRNA ligase | 503.01 | + |
| **PROTEIN FOLDING, MODIFICATION, DESTINATION** |  |  |
| PADG\_07515 | UBX domain-containing protein  | 573.32 | 1.49 |
| PADG\_01852 | small glutamine-rich tetratricopeptide repeat-containing protein  | 991 | 2.2 |
| PADG\_04034 | chaperone DnaJ  | 924.8 | 1.5 |
| PADG\_02637 | ubiquitin-conjugating enzyme  | 795.87 | *\** |
| PADG\_01605 | polyubiquitin  | 2988.76 | 2.24 |
| PADG\_03424 | ubiquitin-activating enzyme E1  | 1565.4 | 1.52 |
| PADG\_07558 | ubiquitin carboxyl-terminal hydrolase  | 735.58 | 1.49 |
| PADG\_07715 | hsp90-like protein  | 21307.69 | 0.35 |
| PADG\_08369 | hsp60-like protein | 31486.72 | 0.69 |
| **PROTEIN DEGRADATION** |  |  |
| PADG\_00599 | 26S protease regulatory subunit 6A  | 436.54 | *\** |
| PADG\_01935 | 26S proteasome non-ATPase regulatory subunit 10  | 726.98 | 1.5 |
| PADG\_03192 | proteasome component PUP2  | 484.74 | 1.59 |
| PADG\_03221 | thimet oligopeptidase  | 769.99 | 2.03 |
| PADG\_03735 | proline iminopeptidase | 574.84 | *\** |
| PADG\_03967 | proteasome component C5  | 3676.41 | 1.44 |
| PADG\_04952 | AAA ATPase  | 491.31 | *\** |
| PADG\_05160 | dipeptidyl-peptidase  | 435.87 | 1.87 |
| PADG\_04167 | aspartyl aminopeptidase | 456.35 | 1.43 |
| PADG\_05193 | xaa-Pro aminopeptidase  | 465.6 | *\** |
| PADG\_05560 | 26S proteasome regulatory subunit rpn-1 | 757.72 | *\** |
| PADG\_05820 | xaa-Pro aminopeptidase  | 606.66 | 1.59 |
| PADG\_06766 | mitochondrial-processing peptidase subunit beta  | 944.78 | 3.18 |
| PADG\_05837 | E3 ubiquitin ligase complex SCF subunit sconC | 3142.06 | 1.55 |
| PADG\_03727 | proteasome component PUP1  | 2198.59 | 0.67 |
| **PROTEIN BINDING** |  |  |
| PADG\_07884 | polyadenylate-binding protein, cytoplasmic and nuclear  | 459.2 | 2.63 |
| PADG\_07249 | actin binding protein  | 460.77 | 1.99 |
| PADG\_01529 | TPR repeat protein  | 640.89 | *\** |
| **CELLULAR TRANSPORT** |  |  |
| PADG\_03203 | BAR domain-containing protein  | 1831.27 | 1.71 |
| PADG\_08188 | vacuolar-sorting protein snf7 | 895.93 | *\** |
| PADG\_02833 | ADP-ribosylation fator | 2358.28 | + |
| **CELL RESCUE, DEFENSE AND VIRULENCE** |  |  |
| PADG\_01551 | thioredoxin reductase  | 976.26 | 1.56 |
| PADG\_01954 | superoxide dismutase 2 Fe-Mn | 1379.02 | 1.99 |
| PADG\_07418 | superoxide dismutase 1 Cu-Zn | 2464.72 | 1.99 |
| PADG\_02030 | Hsp90 co-chaperone Cdc37  | 2932.07 | 2.22 |
| PADG\_02785 | heat shock protein Hsp88  | 9518.65 | 1.5 |
| PADG\_03963 | 30 kDa heat shock protein | 6432.9 | 1.84 |
| PADG\_04379 | heat shock protein STI1  | 4552.74 | 1.99 |
| PADG\_01479 | gamma-glutamyltransferase | 545.4 | 1.76 |
| PADG\_07422 | serine proteinase | 380.41 | 1.8 |
| PADG\_07460 | vacuolar aminopeptidase  | 487.7 | 1.53 |
| PADG\_00324 | catalase P  | 1207.99 | 0.60 |
| PADG\_03095 | mitochondrial peroxiredoxin PRX1  | 2391.55 | 0.67 |
| PADG\_03163 | cytochrome c peroxidase mitochondrial | 7277.58 | 0.47 |
| PADG\_08651 | peroxisomal hydratase-dehydrogenase-epimerase | 724.34 | + |
| PADG\_07946 | peroxisomal matrix protein | 4560.11 | 0.6 |
| PADG\_02048 | nitroreductase family protein | 636.86 | + |
| **CELL DEATH** |  |  |
| PADG\_06087 | programmed cell death protein 5 | 578.79 | 2.22 |
| **UNCLASSIFIED** |  |  |
| PADG\_06289 | hypothetical protein | 749.22 | 1.4 |
| PADG\_03869 | hypothetical protein  | 785.98 | *\** |
| PADG\_03827 | hypothetical protein  | 2531.19 | *\** |
| PADG\_01010 | hypothetical protein  | 690.72 | 2.20 |
| PADG\_01871 | hypothetical protein  | 725.03 | *\** |
| PADG\_03210 | hypothetical protein  | 1477.99 | 1.85 |
| PADG\_00496 | hypothetical protein  | 515.07 | *\** |
| PADG\_08480 | hypothetical protein  | 646.53 | 3.85 |
| PADG\_11936 | hypothetical protein  | 1140.44 | *\** |
| PADG\_02307 | hypothetical protein  | 740.98 | *\** |
| PADG\_04442 | hypothetical protein  | 452.53 | *\** |
| PADG\_04229 | hypothetical protein  | 583.82 | 1.56 |
| PADG\_07627 | 4-carboxymuconolactone decarboxylase family protein  | 628.84 | 1.93 |
| PADG\_12437 | EF hand domain-containing protein  | 391.93 | *\** |
| PADG\_05837 | E3 ubiquitin ligase complex SCF subunit sconC | 3142.06 | 1.55 |
| PADG\_03526 | M protein repeat protein  | 467.91 | *\** |
| PADG\_00344 | hypothetical protein | 1008.02 | + |
| PADG\_00211 | hypothetical protein | 2047.72 | + |
| PADG\_00921 | hypothetical protein | 2142.99 | 0.63 |
| PADG\_01488 | hypothetical protein | 1980.81 | + |
| PADG\_03660 | hypothetical protein | 860.43 | + |
| PADG\_02764 | hypothetical protein | 2170.39 | 0.71 |
| PADG\_08212 | hypothetical protein | 2557.19 | 0.26 |
| PADG\_08368 | hypothetical protein | 716.93 | 0.34 |
| PADG\_01849 | GTP-binding protein YchF | 416.64 | + |
| PADG\_07287 | WD repeat-containing protein  | 579.21 | + |
| PADG\_08483 | chromobox protein 1  | 411.76 | 0.58 |
| PADG\_07412 | DUF1479 domain-containing protein  | 861.11 | + |
| PADG\_05356 | isochorismatase domain-containing protein  | 871.15 | 0.55 |
| PADG\_04559 | progesterone binding protein | 1333.07 | + |
| PADG\_06196 | 12-oxophytodienoate reductase  | 2364.81 | 0.63 |

1Accession number obtained in the *Paracoccidioides* database available at <http://www.broadinstitute.org/annotation/genome/paracoccidioides_brasiliensis/MultiHome.html>.

2PLGS score is the result of different mathematical models for peptide and fragment assign prediction. Acceptable score values consider protein identification with a minimum confidence level of 95% and a false discovery rate of 6%.

3Ratio values were obtained by dividing the values of protein abundance (in fmol) from *Pb*18 during infection of activated macrophages by the abundance in control**.** Proteins with a minimum fold change of 40% were considered regulated.

4Biological process of differentially expressed proteins from MIPS (http://mips.helmholtz-muenchen.de/funcatDB/) and Uniprot databases (http://www.uniprot.org/).

*\** Proteins detected in *P. brasiliensis* *Pb*18 only during activated macrophage infection.

+ Proteins detected in *P. brasiliensis* *Pb*18 only in the control condition.