Data Article

Dataset of proteins mapped on HepG2 cells and those differentially abundant after expression of the dengue non-structural 1 protein

Kíssila Rabeloa,1, Monique R.O. Trugilhob,1,2, Simone M. Costa a, André T.S. Ferreirab, Paulo C. Carvalhoc, Jonas Peralesb, Ada M.B. Alves a,*

a Laboratory of Biotechnology and Physiology of Viral Infections, Oswaldo Cruz Institute, Fiocruz, Rio de Janeiro, Brazil
b Laboratory of Toxinology, Oswaldo Cruz Institute, Fiocruz, Rio de Janeiro, Brazil
c Laboratory for Proteomics and Protein Engineering, Carlos Chagas Institute, Fiocruz, Paraná, Brazil

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ABSTRACT

The data supplied in this article are related to the research article entitled “The effect of the dengue non-structural 1 protein expression over the HepG2 cell proteins in a proteomic approach” (K. Rabelo, M.R. Trugillo, S.M. Costa, B.A. Pereira, O.C. Moreira, A.T. Ferreira et al., 2016) [1]. The present article provides the inventory of peptides and proteins mapped in a hepatocyte cell line (HepG2) by mass spectrometry in the presence of the non-structural protein 1 (NS1) of Dengue 2 virus (DENV2). Cells were transfected with pcENS1 plasmid, which encodes the DENV2 NS1 protein, or the controls pcDNA3 (negative control) or pMAXGFP, encoding the
green fluorescent protein (GFP), a protein unrelated to dengue. Differentially abundant protein lists were obtained by comparing cells transfected with pcENS1 and controls.

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**Specifications Table**

| Subject area                        | Biology                  |
|-------------------------------------|--------------------------|
| More specific subject area          | Proteomics, Virology     |
| Type of data                        | Table                    |
| How data was acquired               | Mass spectrometry        |
| Data format                         | Raw and analyzed         |
| Experimental factors                | HepG2 cells were transfected with plasmids expressing different proteins, lysed, trypsinized and submitted to Orbitrap |
| Experimental features               | All samples were analyzed LTQ-Orbitrap XL mass spectrometer |
| Data source location                | Oswaldo Cruz Foundation, Brazil |
| Data accessibility                  | Within this article      |

**Value of the data**

- These data describe the use of quantitative mass spectrometry-based proteomic experiments to assess the biological significance of cell alterations caused by DENV NS1 protein.
- 4756 proteins were mapped and we identify 41 or 81 differentially abundant proteins in the presence of NS1, comparing to controls.
- The data open new perspectives to identify the molecular mechanisms involving DENV NS1 protein in infected cells.

1. **Data**

HepG2 cells were transfected with the plasmids: pcENS1, pcDNA3 and pMAXGFP. To produce accurate data, we used three independent experimental biological replicates and samples were submitted to LTQ-Orbitrap XL (Thermo Scientific). Data analysis, using the PatternLab for Proteomics software, identified 14,138 peptides which mapped to 4756 proteins, from all conditions (HepG2 transfected with the three different plasmids and non-transfected cells) (Supplementary Table S1a-h). Applying the maximum parsimony principle we found 2314 proteins (Supplementary Table S1g). Using the Tfold module we generate the differential abundance distribution when comparing: non-transfected HepG2 x cell transfected with pcDNA3 (Table 1); HepG2 transfected with pcDNA3 x pcENS1 (Table 2) and cells transfected with pMAGFP x pcENS1 (Table 3)[1].

2. **Experimental design, materials and methods**

2.1. **Cell culture**

HepG2 cells (ATCC) were cultivated in Dulbecco’s modified Eagle's medium (DMEM) (SIGMA) supplemented with 10% fetal bovine serum (FBS) (Invitrogen). Cells were maintained at 37°C and
| Locus          | Fold Change | pValue   | Signal+ (pcDNA3) | Signal- (HepG2) | Description                                                                 |
|---------------|-------------|----------|-----------------|----------------|-----------------------------------------------------------------------------|
| sp1P20674     | 7.52        | 0.04600  | 1.29E-03        | 1.72E-04       | Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=2 |
| COX5A_HUMAN   |             |          |                 |                |                                                                             |
| sp1P39656     | 6.45        | 0.00016  | 9.18E-04        | 1.42E-04       | Dolichyl-diphosphooligosaccharide-protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4 |
| OST48_HUMAN   |             |          |                 |                |                                                                             |
| sp1P20674     | 4.20        | 0.02071  | 5.62E-03        | 1.34E-03       | Histone H2A.V OS=Homo sapiens GN=H2AFV PE=1 SV=3                             |
| H2AV_HUMAN    |             |          |                 |                |                                                                             |
| sp1P20674     | 4.18        | 0.02251  | 5.58E-03        | 1.34E-03       | Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2                             |
| H2AZ_HUMAN    |             |          |                 |                |                                                                             |
| sp1P20674     | 3.40        | 0.01591  | 6.34E-04        | 1.87E-04       | Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2                               |
| ALBU_HUMAN    |             |          |                 |                |                                                                             |
| tr1B4D1R8     | 3.32        | 0.01500  | 2.00E-03        | 6.04E-04       | NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NOQ1 PE=1 SV=1          |
| B4DLR8_HUMAN  |             |          |                 |                |                                                                             |
| sp1P15559     | 3.27        | 0.01639  | 1.45E-03        | 4.45E-04       | Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=1 SV=1 |
| NQ01_HUMAN    |             |          |                 |                |                                                                             |
| sp1P13073i    | 3.16        | 0.04534  | 5.81E-04        | 1.84E-04       | Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10 PE=1 SV=2    |
| COX41_HUMAN   |             |          |                 |                |                                                                             |
| sp1P9983D1C   | 3.14        | 0.02829  | 6.89E-04        | 2.19E-04       | Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=1 |
| DIC_HUMAN     |             |          |                 |                |                                                                             |
| tr1G3V576i    | 3.13        | 0.01342  | 1.92E-03        | 6.15E-04       | Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens GN=NOQ1 PE=1 SV=1 |
| G3V576i_HUMAN |             |          |                 |                |                                                                             |
| sp1P07910i    | 3.13        | 0.01342  | 1.45E-03        | 4.64E-04       | Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=1 |
| HNRNPC_HUMAN  |             |          |                 |                |                                                                             |
| tr1B4D2Y08    | 3.13        | 0.01342  | 1.54E-03        | 4.93E-04       | Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=NOQ1 PE=1 SV=1 |
| B4D2Y08_HUMAN |             |          |                 |                |                                                                             |
| tr1G3V2Q1i    | 3.13        | 0.01342  | 1.46E-03        | 4.66E-04       | Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=NOQ1 PE=1 SV=1 |
| G3V2Q1i_HUMAN |             |          |                 |                |                                                                             |
| tr1G3V4C1i    | 3.13        | 0.01342  | 1.52E-03        | 4.87E-04       | Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=NOQ1 PE=1 SV=1 |
| G3V4C1_HUMAN  |             |          |                 |                |                                                                             |
| sp1O15173i    | 3.11        | 0.00180  | 7.94E-04        | 2.55E-04       | Membrane-associated progesterone receptor component 2 OS=Homo sapiens GN=PGRMC2 PE=1 SV=1 |
| PGRC2_HUMAN   |             |          |                 |                |                                                                             |
| Gene ID     | Score | FDR   | p-value | Gene Description                                                                 |
|------------|-------|-------|---------|----------------------------------------------------------------------------------|
| spIP05787K2C8_HUMAN | 3.02  | 0.01302 | 8.22E-03 | Keratin, type II cytoskeletal 8 OS = Homo sapiens GN = KRT8 PE = 1 SV = 7; triF8VUG2/f8VUG2_HUMAN Keratin, type II cytoskeletal 8 (Fragment) OS = Homo sapiens GN = KRT8 PE = 1 SV = 7; triF8VP67/F8VP67_HUMAN Keratin, type II cytoskeletal 8 (Fragment) OS = Homo sapiens GN = KRT8 PE = 1 SV = 7; triF8VRG4/f8VRG4_HUMAN Keratin, type II cytoskeletal 8 (Fragment) OS = Homo sapiens GN = KRT8 PE = 1 SV = 7; triK7EQQ9/K7EQQ9_HUMAN 60S ribosomal protein L27 OS = Homo sapiens GN = RPL27 PE = 1 SV = 7 |
| spIP61353IRL27_HUMAN | 2.98  | 0.03444 | 9.43E-04 | 60S ribosomal protein L27 OS = Homo sapiens GN = RPL27 PE = 1 SV = 7; triK7EQQ9/K7EQQ9_HUMAN 60S ribosomal protein L27 (Fragment) OS = Homo sapiens GN = RPL27 PE = 1 SV = 7 |
| trtK7ELC7_K7ELC7_HUMAN | 2.98  | 0.03444 | 9.81E-04 | 60S ribosomal protein L27 (Fragment) OS = Homo sapiens GN = RPL27 PE = 1 SV = 7 |
| trtE9PCY7_E9PCY7_HUMAN | 2.81  | 0.02643 | 1.33E-03 | Heterogeneous nuclear ribonucleoprotein H OS = Homo sapiens GN = HNRNPH1 PE = 1 SV = 1; triH0YBG7/h0YBG7_HUMAN Heterogeneous nuclear ribonucleoprotein H (Fragment) OS = Homo sapiens GN = HNRNPH1 PE = 1 SV = 1; triE5RMG4/e5RMG4_HUMAN Heterogeneous nuclear ribonucleoprotein H (Fragment) OS = Homo sapiens GN = HNRNPH1 PE = 1 SV = 1; triE6RFM3/e6RFM3_HUMAN Heterogeneous nuclear ribonucleoprotein H (Fragment) OS = Homo sapiens GN = HNRNPH1 PE = 1 SV = 1 |
| trtE7EMC9_E7EMC9_HUMAN | 2.77  | 0.00863 | 5.78E-04 | Annexin OS = Homo sapiens GN = ANXA6 PE = 1 SV = 1 |
| spIP37108SRP14_HUMAN | 2.71  | 0.01021 | 8.50E-04 | Signal recognition particle 14 kDa protein OS = Homo sapiens GN = SRP14 PE = 1 SV = 2; triH0Y1W0/H0Y1W0_HUMAN Signal recognition particle 14 kDa protein OS = Homo sapiens GN = SRP14 PE = 1 SV = 1 |
| spIP53GQDv_DHB12_HUMAN | 2.42  | 0.01385 | 6.34E-04 | Estradiol 17-beta-dehydrogenase 12 OS = Homo sapiens GN = HSD17B12 PE = 1 SV = 2 |
| spIP54040CAT_A_HUMAN | 2.42  | 0.00728 | 7.06E-04 | Catalase OS = Homo sapiens GN = CAT PE = 1 SV = 3 |
| trtF8VM2V_F8VM2V_HUMAN | 2.41  | 0.00909 | 8.74E-04 | Phosphate carrier protein, mitochondrial OS = Homo sapiens GN = SLC25A3 PE = 1 SV = 1 |
| trtH0YLA2_H0YLA2_HUMAN | 2.30  | 0.00896 | 8.54E-04 | Signal recognition particle 14 kDa protein OS = Homo sapiens GN = SRP14 PE = 1 SV = 1 |
| spIP22087FBR_HUMAN | 2.21  | 0.01012 | 8.83E-04 | rRNA 2'-O-methyltransferase fibrillarin OS = Homo sapiens GN = FBL PE = 1 SV = 2; triM0R299/M0R299_HUMAN rRNA 2'-O-methyltransferase fibrillarin (Fragment) OS = Homo sapiens GN = FBL PE = 1 SV = 1 |
| trtH3BNX8_H3BNX8_HUMAN | 0.75  | 0.04600 | 1.27E-03 | Cytochrome c oxidase subunit 5A, mitochondrial OS = Homo sapiens GN = COX5A PE = 1 SV = 1 |
| trtH0Y449_H0Y449_HUMAN | –1.11 | 0.00212 | 2.27E-04 | Nucleoside-sensitive element-binding protein 1 (Fragment) OS = Homo sapiens GN = YBX1 PE = 1 SV = 1 |
| trtH3BRN4_H3BRN4_HUMAN | –1.70 | 0.00099 | 4.66E-04 | 4-aminobutyrate aminotransferase, mitochondrial OS = Homo sapiens GN = ABAT PE = 1 SV = 1; spIP80404l_gabt_HUMAN 4-aminobutyrate aminotransferase, mitochondrial OS = Homo sapiens GN = ABAT PE = 1 SV = 3 |
| spIP16401H15_HUMAN | –1.74 | 0.00435 | 2.18E-04 | Histone H1.5 OS = Homo sapiens GN = HIST1H1B PE = 1 SV = 3 |
| trtH3BNQ7_H3BNQ7_HUMAN | –2.14 | 0.00576 | 3.69E-04 | 4-aminobutyrate aminotransferase, mitochondrial OS = Homo sapiens GN = ABAT PE = 1 SV = 1 |
| trtA0A087WY63_A0A087WY63_HUMAN | –2.22 | 0.00267 | 4.43E-04 | Prostaglandin E synthase 3 OS = Homo sapiens GN = PTGES3 PE = 4 SV = 1 |
| spIP15185TEP_HUMAN | –2.37 | 0.00333 | 4.54E-04 | Prostaglandin E synthase 3 OS = Homo sapiens GN = PTGES3 PE = 1 SV = 1 |
| spIP14979_HNRDL_HUMAN | –2.55 | 0.01357 | 1.96E-04 | Heterogeneous nuclear ribonucleoprotein D-like OS = Homo sapiens GN = HNRPDL PE = 1 SV = 3 |
Table 1 (continued)

| Locus     | Fold Change | pValue  | Signal+ (pcDNA3) | Signal- (HepG2) | Description                                                                 |
|-----------|-------------|---------|------------------|-----------------|-----------------------------------------------------------------------------|
| triA0A087WUK2| -2.55       | 0.01357 | 2.27E-04         | 5.79E-04        | Heterogeneous nuclear ribonucleoprotein D-like OS = Homo sapiens GN = HNRNPDl PE = 4 SV = 1 |
| A0A087WUK2_HUMAN | -2.74       | 0.02442 | 2.45E-04         | 6.73E-04        | Alpha-1-antitrypsin OS = Homo sapiens GN = SERPINA1 PE = 1 SV = 3; triG3V2B9/G3V2B9_HUMAN Short peptide from AAT (Fragment) OS = Homo sapiens GN = SERPINA1 PE = 1 SV = 1; triG3V544/G3V544_HUMAN Short peptide from AAT (Fragment) OS = Homo sapiens GN = SERPINA1 PE = 1 SV = 1; triG3V387/G3V387_HUMAN Short peptide from AAT (Fragment) OS = Homo sapiens GN = SERPINA1 PE = 1 SV = 1; triG3V58R/G3V58R_HUMAN Short peptide from AAT (Fragment) OS = Homo sapiens GN = SERPINA1 PE = 1 SV = 1; |
| spIP0171294/AAT_HUMAN | -2.88       | 0.02516 | 2.26E-04         | 6.52E-04        | Lupus La protein OS = Homo sapiens GN = SSB PE = 1 SV = 1; triE7ER4/E7ER4_HUMAN Lupus La protein (Fragment) OS = Homo sapiens GN = SSB PE = 1 SV = 1; triE9PCX9/E9PCX9_HUMAN Lupus La protein (Fragment) OS = Homo sapiens GN = SSB PE = 1 SV = 1 |
| spIP054555/LA_HUMAN | -2.88       | 0.02516 | 2.26E-04         | 6.52E-04        | Lupus La protein OS = Homo sapiens GN = SSB PE = 1 SV = 1; |
| spIE7EMB3_HUMAN     | -0.31       | 0.04302 | 2.14E-04         | 6.44E-04        | Thioredoxin OS = Homo sapiens GN = TXN PE = 1 SV = 3 |
| spI0Y7A7_HUMAN      | -0.31       | 0.04674 | 6.16E-04         | 1.93E-03        | Calmodulin OS = Homo sapiens GN = CALM1 PE = 1 SV = 1 |
| spIE7ET20_HUMAN     | -0.31       | 0.04674 | 8.05E-04         | 2.52E-03        | Calmodulin OS = Homo sapiens GN = CALM1 PE = 1 SV = 1 |
| spIP62158/CALM_HUMAN| -3.16       | 0.04206 | 8.10E-04         | 2.56E-03        | Calmodulin OS = Homo sapiens GN = CALM1 PE = 1 SV = 2; triQ66HY3/Q66HY3_HUMAN CALM1 protein OS = Homo sapiens GN = CALM1 PE = 1 SV = 1; triG3V361/G3V361_HUMAN Calmodulin (Fragment) OS = Homo sapiens GN = CALM1 PE = 1 SV = 1 |
| triJ3QQX2/J3QQX2_HUMAN | -3.54       | 0.0702  | 2.84E-04         | 1.00E-03        | Rho GDP-dissociation inhibitor 1 OS = Homo sapiens GN = ARHGDA PE = 1 SV = 1; tri3J3KTF8/J3KTF8_HUMAN Rho GDP-dissociation inhibitor 1 (Fragment) OS = Homo sapiens GN = ARHGDA PE = 1 SV = 1; tri3J3K60/J3K60_HUMAN Rho GDP-dissociation inhibitor 1 OS = Homo sapiens GN = ARHGDA PE = 1 SV = 1 |
| spIE7ER40/HINT1_HUMAN | -3.59       | 0.00515 | 3.27E-04         | 1.17E-03        | Rho GDP-dissociation inhibitor 1 OS = Homo sapiens GN = ARHGDA PE = 1 SV = 1 |
| spIP52565/GDR1_HUMAN | -3.84       | 0.01529 | 1.68E-04         | 6.45E-04        | Acidic leucine-rich nuclear phosphoprotein 32 family member A OS = Homo sapiens GN = ANP32A PE = 1 SV = 1 |
| spIF39687/AN32A_HUMAN | -4.00       | 0.02378 | 3.39E-04         | 1.36E-03        | Proteasome subunit alpha type-2 OS = Homo sapiens GN = PSMA2 PE = 1 SV = 2 |
| spIP62158/OSPM_HUMAN | -4.00       | 0.01587 | 2.65E-04         | 1.09E-03        | Aspartate aminotransferase, cytoplasmic OS = Homo sapiens GN = GOT1 PE = 1 SV = 3 |
| spIE7EMB3_HUMAN     | -4.00       | 0.03401 | 1.33E-04         | 5.49E-04        | Eukaryotic translation initiation factor 3 subunit G (Fragment) OS = Homo sapiens GN = EIF3G PE = 1 SV = 1 |
| triJ3QQX2/J3QQX2_HUMAN | -4.20       | 0.02188 | 8.93E-04         | 3.75E-03        | Nucleophosmin OS = Homo sapiens GN = NPM1 PE = 1 SV = 2; triE5R198/E5R198_HUMAN Nucleophosmin (Fragment) OS = Homo sapiens GN = NPM1 PE = 1 SV = 1 |
| triJ3QLC8/J3QLC8_HUMAN | -4.24       | 0.01244 | 1.73E-04         | 7.34E-04        | 60S ribosomal protein L17 OS = Homo sapiens GN = RPL17 PE = 1 SV = 1 |
| triJ3QLC8/J3QLC8_HUMAN | -5.72       | 0.01114 | 6.04E-04         | 3.45E-03        | Histidine triad nucleotide-binding protein 1 OS = Homo sapiens GN = HINT1 PE = 1 SV = 2 |
| Gene Symbol       | Score | Value  | Log2FoldChange | FDR  | Description                                           | Species    |
|-------------------|-------|--------|----------------|------|------------------------------------------------------|------------|
| SP497731          | -6.14 | 0.04372| 2.79E-04       | 1.71E-03| Glutaredoxin-related protein 5, mitochondrial       | Homo sapiens |
| Q86SX6            |       |        |                |      |                                                      |            |
| GLRX5_HUMAN       | -6.55 | 0.03416| 8.78E-05       | 5.75E-04| Inorganic pyrophosphatase                             | Homo sapiens |
| Q15181            |       |        |                |      |                                                      |            |
| IPYR_HUMAN        | -7.66 | 0.00032| 7.86E-05       | 6.02E-04| FAD-AMP lyase (cyclizing) (Fragment)                 | Homo sapiens |

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| Locus                  | Fold Change | pValue   | Signal (+pcENS1) | Signal (-pcDNA3) | Description                                                                 |
|-----------------------|-------------|----------|------------------|------------------|-----------------------------------------------------------------------------|
| spiQ9UK22:FBX2_HUMAN  | 2.887204251 | 0.00294  | 0.000565646      | 0.000195915      | F-box only protein 2 OS=Homo sapiens GN=FBXO2 PE=1 SV=2                   |
| trfF2Z2V0             | 2.44891458  | 0.01885  | 0.000415618      | 0.000169717      | Copine-1 (Fragment) OS=Homo sapiens GN=CPNE1 PE=1 SV=1                    |
| spiP05386:RAL1_HUMAN  | 2.20861757  | 0.01819  | 0.002383141      | 0.001058645      | 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1         |
| spiP43243             | 2.106781667 | 0.00112  | 0.000262087      | 0.000297177      | Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2: trfB3KM87:B3KM87_HUMAN Matrin-3 |
| trfA8MXP9             | 2.106781667 | 0.00112  | 0.000592509      | 0.000281239      | Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=1                                |
| spiP51149:RAB7A_HUMAN | 1.93893554  | 0.00429  | 0.000768084      | 0.000344136      | Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1: trfC9J592:C9J592_HUMAN |
| spiQ9P035i            | 1.842287267 | 0.00587  | 0.00044159       | 0.000239697      | Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 OS=Homo sapiens GN=PTPLAD1 PE=1 SV=2 |
| spP52926              | -0.002597139 | 0.02916  | 0.000932861      | 0.000223981      | High mobility group protein HMGI-C OS=Homo sapiens GN=HMGA2 PE=1 SV=1       |
| trfF5H2A4i            | -0.002597139 | 0.02916  | 0.00086171       | 0.000223981      | High mobility group protein HMGI-C OS=Homo sapiens GN=HMGA2 PE=1 SV=1       |
| trF5H6H0i             | -0.002597139 | 0.02916  | 0.000691713      | 0.001796475      | High mobility group protein HMGI-C OS=Homo sapiens GN=HMGA2 PE=1 SV=1       |
| trfJ3QWR1i            | -0.018702242 | 0.00638  | 0.000248201      | 0.000464192      | 26S protease regulatory subunit 8 (Fragment) OS=Homo sapiens GN=PSMC5 PE=1 SV=1 |
| spiP00338:LDHA_HUMAN  | -0.267759662 | 0.03438  | 0.000725737      | 0.001934761      | > L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2: trfF5GXY2:F5GXY2_HUMAN -lactate dehydrogenase A chain (Fragment) OS=Homo sapiens GN=LDHA PE=1 SV=3 |
| spiP02765:FETUA_HUMAN | -0.475079452 | 0.0123   | 0.000111731      | 0.00053081       | Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1                 |
| spiP08233:HS90B_HUMAN | -1.523033786 | 0.0036   | 0.002236377      | 0.003406078      | Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4        |
| spiP02545:LMNA_HUMAN  | -1.560530275 | 0.00312  | 0.000879213      | 0.001372039      | Prelam-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1                               |
| spiP39023:RL3_HUMAN   | -2.033045505 | 0.00327  | 0.000226732      | 0.000460956      | 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2: trfG5E90G5E90_HUMAN 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=1: trfB5MCW2:B5MCW2_HUMAN 60S ribosomal protein L3 (Fragment) OS=Homo sapiens GN=RPL3 PE=1 SV=1 |
| spiP02768:ALBU_HUMAN  | -2.302973671 | 0.00479  | 0.000275409      | 0.000634261      | Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2                            |
| spiP26373:RL13_HUMAN  | -2.352456304 | 0.0203   | 0.000324859      | 0.000764216      | 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4: trfH3BUK8:H3BUK8_HUMAN 60S ribosomal protein L13 (Fragment) OS=Homo sapiens GN=RPL13 PE=1 SV=1: trfJ3QSB4:J3QSB4_HUMAN 60S ribosomal protein L13 (Fragment) OS=Homo sapiens GN=RPL13 PE=1 SV=1 |
| trfA0A87X1S2           | -2.401479196 | 0.00478  | 0.000370535      | 0.000889831      | Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=BX1 PE=4 SV=1 myocardylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=4 SV=1 |
| trfA0A87WZH7           | -2.408424932 | 0.00411  | 0.000303789      | 0.000731652      | Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=4 SV=1 |
| trtA0A087WWU8i A0A087WWU8_HUMAN | -2.440187743 | 0.00449 | 0.000253765 | 0.000619234 | Tropomyosin alpha-3 chain OS = Homo sapiens GN = TPM3 PE = 4 SV = 1 |
| spI29966i MARCS_HUMAN | -2.684863748 | 0.00191 | 0.00026381 | 0.000708295 | Myristoylated alanine-rich C-kinase substrate OS = Homo sapiens GN = MARCS PE = 1 SV = 4 |
| spI96273i SLIRP_HUMAN | -2.730197953 | 0.00514 | 0.000172275 | 0.000470346 | SRA stem-loop-interacting RNA-binding protein, mitochondrial OS = Homo sapiens GN = SLIRP PE = 1 SV = 1 |
| trtG3V259i G3V259_HUMAN | -2.730197953 | 0.00514 | 0.000151436 | 0.000413449 | SRA stem-loop-interacting RNA-binding protein, mitochondrial OS = Homo sapiens GN = SLIRP PE = 1 SV = 1 |
| trtH0YJ40H0YJ40_HUMAN | -2.730197953 | 0.00514 | 0.000195604 | 0.000534038 | SRA stem-loop-interacting RNA-binding protein, mitochondrial (Fragment) OS = Homo sapiens GN = SLIRP PE = 1 SV = 1 |
| trtA0A087WUN7i A0A087WUN7_HUMAN | -2.730197953 | 0.00514 | 0.000204109 | 0.000557257 | SRA stem-loop-interacting RNA-binding protein, mitochondrial OS = Homo sapiens GN = SLIRP PE = 4 SV = 1 |
| trtG3V4X6i G3V4X6_HUMAN | -2.899141374 | 0.03897 | 0.000143578 | 0.000416253 | Biliverdin reductase A OS = Homo sapiens GN = BLVRA PE = 1 SV = 2; trtJ9j1lC9j1e1_HUMAN Biliverdin reductase A (Fragment) OS = Homo sapiens GN = BLVRA PE = 1 SV = 1 |
| spI35004iBIEA_HUMAN | -3.082880329 | 0.02293 | 0.000536524 | 0.001654038 | Proteasome subunit alpha type-2 OS = Homo sapiens GN = PSMA2 PE = 4 SV = 1 |
| spI62269iRS18_HUMAN | -3.304625932 | 0.02144 | 0.000280286 | 0.000926242 | 40S ribosomal protein S18 OS = Homo sapiens GN = RPS18 PE = 1 SV = 3; trtJ3s69jJ3s69_HUMAN 40S ribosomal protein S18 OS = Homo sapiens GN = RPS18 PE = 1 SV = 1 |
| spI62269iRS18_HUMAN | -3.482472238 | 0.0473 | 0.000142247 | 0.00049537 | Serum albumin OS = Homo sapiens GN = ALB PE = 1 SV = 1 |
| spI62269iRS18_HUMAN | -3.482472238 | 0.0473 | 0.000191612 | 0.00052314 | Serum albumin OS = Homo sapiens GN = ALB PE = 1 SV = 1 |
| spI62269iRS18_HUMAN | -3.482472238 | 0.0473 | 0.000143578 | 0.000416253 | Serum albumin (Fragment) OS = Homo sapiens GN = ALB PE = 1 SV = 1 |
| spI62269iRS18_HUMAN | -3.818005689 | 0.03869 | 0.000206727 | 0.000789284 | Non-POU domain-containing octamer-binding protein (Fragment) OS = Homo sapiens GN = NONO PE = 1 SV = 3 |
| trtA0A087X0X3i A0A087X0X3_HUMAN | -3.895589738 | 0.04525 | 0.000131893 | 0.000513803 | Heterogeneous nuclear ribonucleoprotein M OS = Homo sapiens GN = HNRNPM PE = 4 SV = 1 |
| spI50515iEF1A3_HUMAN | -4.17671178 | 0.00362 | 0.001520654 | 0.006351333 | Putative elongation factor 1-alpha-like 3 OS = Homo sapiens GN = EEF1A1P5 PE = 5 SV = 1 |
| trtC9j0tC9j0t_HUMAN | -4.228640752 | 0.01546 | 0.000141501 | 0.000598356 | Proflnin-2 OS = Homo sapiens GN = PPN2 PE = 1 SV = 1 |
| trtC9j0tC9j0t_HUMAN | -4.228640752 | 0.01546 | 0.000117006 | 0.000495003 | Proflnin OS = Homo sapiens GN = PPN2 PE = 1 SV = 1 |
| trtQ5TAA0i Q5TAA0i_HUMAN | -4.374529519 | 0.01927 | 0.000236306 | 0.001032853 | Glutathione S-transferase omega-1 (Fragment) OS = Homo sapiens GN = GSTO1 PE = 1 SV = 1 |
| spI62269iRS18_HUMAN | -4.423436439 | 0.01596 | 0.000184689 | 0.000657539 | Sideroflexin-1 OS = Homo sapiens GN = SXFN1 PE = 1 SV = 4; trtD6RF00D6RF00_HUMAN Sideroflexin-1 (Fragment) OS = Homo sapiens GN = SXFN1 PE = 1 SV = 3 |
| spI62269iRS18_HUMAN | -9.640254654 | 0.00328 | 4.97959E-05 | 0.00480045 | Proteasome subunit alpha type-1 OS = Homo sapiens GN = PSMA1 PE = 1 SV = 1; trtF5G111i F5G111_HUMAN Proteasome subunit alpha type-1 OS = Homo sapiens GN = PSMA1 PE = 1 SV = 1 |
| Locus | Fold Change | pValue | Signal+ (pcENS1) | Signal- (pMAXGFP) | Description |
|-------|-------------|--------|-----------------|------------------|-------------|
| trE9PIZ4/E9PIZ4_HUMAN | 4.27 | 0.02884 | 5.1564100956E-04 | 1.206738747E-04 | Cysteine and histidine-rich domain-containing protein 1 OS=Homo sapiens GN=CHORDC1 PE=1 SV=1 |
| trH0YM16/H0YM16_HUMAN | 2.63 | 0.04622 | 3.6248916762E-04 | 1.3785223116E-04 | Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1 |
| spIP60900PSA6_HUMAN | 2.51 | 0.01497 | 6.5820719273E-04 | 2.6200153475E-04 | Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1 |
| trG3V295/G3V295_HUMAN | 2.51 | 0.01497 | 7.976309919E-04 | 3.174993680E-04 | Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=1 SV=1 |
| trG3V3I1/G3V3I1_HUMAN | 2.51 | 0.01497 | 1.0940470906E-03 | 4.3548903750E-03 | Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=1 SV=1 |
| spIP61626LYSC_HUMAN | 2.46 | 0.00250 | 8.0788085952E-04 | 3.2813609299E-04 | Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1 |
| spIP62081RS7_HUMAN | 2.07 | 0.00203 | 4.7837342096E-04 | 2.309690621E-04 | 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1 |
| spIO43175SERA_HUMAN | 2.05 | 0.02052 | 3.5415580623E-04 | 1.7288134062E-04 | > D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 |
| trM0R210/M0R210_HUMAN | 1.88 | 0.03982 | 1.8803502747E-03 | 1.0008461759E-03 | 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=1 |
| spIP62429RS16_HUMAN | 1.84 | 0.03469 | 1.6295554871E-03 | 8.8430929241E-04 | 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=1 |
| trA0A087WWZ27/A0A087WWZ27_HUMAN | 1.84 | 0.03469 | 1.6295554871E-03 | 8.8430929241E-04 | Zinc finger protein 90 OS=Homo sapiens GN=ZNF90 PE=4 SV=1 |
| spIP46782RS5_HUMAN | 1.82 | 0.04115 | 1.3188765458E-03 | 7.2344215749E-04 | 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4; trM0R0F0/M0R0F0_HUMAN |
| spIP50395GDIB_HUMAN | 1.82 | 0.04377 | 7.3807276416E-04 | 4.0635192954E-04 | 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1; trV9GYF8/V9GYF8_HUMAN Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2; trV9GYF8 |
| spIP62136PP1A_HUMAN | 1.81 | 0.04937 | 7.1055348515E-04 | 3.9154015749E-04 | Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens |
| trK7ERG4/K7ERG4_HUMAN | 1.79 | 0.03148 | 9.9775810350E-04 | 5.5628189049E-04 | Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1 |
| trM0R0R2/M0R0R2_HUMAN | 1.79 | 0.04224 | 1.1751143601E-03 | 6.5592088945E-04 | 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 |
sp|P47755|CAZA2_HUMAN 1.76 0.00907 3.8503391537E-04 2.1892360270E-04 0.00001 0.00002 F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3

tri|A8MXQ1|A8MXQ1_HUMAN 1.58 0.00171 1.8271019599E-03 1.1545048441E-03 Pituitary tumor-transforming gene 1 protein-interacting protein OS=Homo sapiens GN=PTTG1P PE=4 SV=1

sp|P43243|MATR3_HUMAN 1.56 0.00335 6.2608664580E-04 4.0083578369E-04 Matrix-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2: tri|B3KM87|B3KM87_HUMAN Matrix-3 OS=Homo sapiens GN=MATR3 PE=1 SV=1

tri|A8MXP9|A8MXP9_HUMAN 1.56 0.00335 5.9250881452E-04 3.793844557E-04 Matrix-3 OS=Homo sapiens GN=MATR3 PE=1 SV=1

tri|E9PSD5|E9PSD5_HUMAN 0.43 0.02884 4.9845297591E-04 1.1665384122E-03 Cysteine and histidine-rich domain-containing protein 1 OS=Homo sapiens GN=CHORDC1 PE=1 SV=1

sp|P18085|ARF4_HUMAN 0.18 0.01873 1.0283317157E-03 5.6312821438E-03 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3: tri|C9JPM4|C9JPM4_HUMAN ADP-ribosylation factor 4 (Fragment) OS=Homo sapiens GN=ARF4 PE=1 SV=1

tr|A0A087X1Z3|A0A087X1Z3_HUMAN 0.20 0.00919 2.9662475890E-04 5.9412009618E-04 Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=4 SV=1

tr|H0Y7M0|H0Y7M0_HUMAN 0.20 0.00919 3.3045038930E-04 6.6187063346E-03 Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=1: tri|H0YKU2|H0YKU2_HUMAN Proteasome activator complex subunit 2 (Fragment) OS=Homo sapiens GN=PSME2 PE=1 SV=1

tr|H3BT71|H3BT71_HUMAN 0.22 0.03725 3.6164761545E-04 7.882832196E-04 RNA-binding motif protein, X chromosome, N-terminally processed OS=Homo sapiens GN=RBMX PE=1 SV=1

tr|H0YMF4|H0YMF4_HUMAN 0.24 0.01281 4.5610249693E-04 1.0891334963E-03 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=1

sp|Q92928|RAB1C_HUMAN 0.33 0.00379 1.7941339393E-04 5.9502701116E-04 Putative Ras-related protein Rab-1C OS=Homo sapiens GN=RAB1C PE=5 SV=2

sp|Q9H0U4|RAB1B_HUMAN 0.33 0.00379 1.7941339393E-04 5.9502701116E-04 Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1

sp|P08238|HSB2_HUMAN 0.19 0.00037 2.2363769567E-03 6.508148171E-03 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HS90AB1 PE=1 SV=4

sp|P15531|NDK_HUMAN 0.13 0.00005 1.9216269100E-03 6.508648328E-03 Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1

sp|P22570|ADRO_HUMAN 0.14 0.00127 4.9680105400E-04 6.9510914103E-04 NADPH:adrenodoxin oxidoreductase, mitochondrial OS=Homo sapiens GN=FDXR PE=1 SV=3

sp|P02545|LMNA_HUMAN 0.14 0.00262 8.792129898E-04 1.235645125E-03 Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1

sp|Q8NBS9|LMNA_HUMAN 0.19 0.01047 4.3710044382E-04 6.7551841613E-04 Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 PE=1 SV=2

tr|K7ES89|K7ES89_HUMAN 0.55 0.00284 3.3391802783E-04 5.238721696E-04 Dual-specificity protein phosphatase 3 (Fragment) OS=Homo sapiens GN=DUSP3 PE=1 SV=1

sp|P60953|CDC42_HUMAN 0.15 0.01599 5.7952351298E-04 9.2218095833E-04 Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2: tri|Q5JYX0|Q5JYX0_HUMAN Cell division control protein 42 homolog (Fragment) OS=Homo sapiens GN=CDC42 PE=1 SV=1

tr|E3W990|E3W990_HUMAN 0.74 0.00295 2.067839368E-04 3.602949723E-04 Sequestosome-1 (Fragment) OS=Homo sapiens GN=SQSTM1 PE=1 SV=1

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| Locus                  | Fold Change | pValue | Signal (pENS1) | Signal (pMAXGFP) | Description                                                                                                                                 |
|-----------------------|-------------|--------|----------------|-----------------|----------------------------------------------------------------------------------------------------------------------------------------------|
| spiQ14847i            |             |        | 5.3129711808E-04 | 9.5247256550E-04 | LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2; trcQ9J9WZ2i C9J9W2_HUMAN LIM and SH3 domain protein 1 (Fragment) OS=Homo sapiens GN=LASP1 PE=1 SV=1 |
| LASP1_HUMAN           | 1.80        | 0.01301 | 4.6887694121E-04 | 8.4429729374E-04 | Myosin, light polypeptide 6, alkali, smooth muscle and non-muscle, isoform CRA_c OS=Homo sapiens GN=PDE6H PE=4 SV=1; trcQ8W175Homo sapiens GN=PDE6H PE=4 SV=1 |
| trcG3V1V0             | 1.80        | 0.01301 | 4.9992839427E-04 | 9.0021102564E-04 | Retinal cone rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma OS=Homo sapiens GN=PDE6H PE=1 SV=2 |
| G3V1V0_HUMAN          |             |        | 3.1718146023E-04 | 5.7114228937E-04 | Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2 |
| spiP606600MYL6_HUMAN  | 1.80        | 0.01301 | 5.0668605796E-04 | 1.0456297298E-03 | Retinal cone rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma OS=Homo sapiens GN=PDE6H PE=4 SV=1 |
| trcB726Z4i            | 1.80        | 0.01301 | 4.9663939168E-04 | 8.9428858468E-04 | Retinal cone rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma (Fragment) OS=Homo sapiens GN=PDE6H PE=4 SV=1 |
| B726Z4_HUMAN          |             |        | 2.1638459062E-04 | 4.2559598943E-04 | Retinal cone rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma OS=Homo sapiens GN=PDE6H PE=4 SV=1 |
| trcF8VPF3i            | 1.80        | 0.01301 | 1.389825096E-03 | 2.7257279358E-04 | Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=PRMT1 PE=1 SV=1 |
| F8VPF3_HUMAN          |             |        | 3.1524137556E-04 | 6.3140796832E-04 | Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=1 SV=3 |
| trcL7C211             | 1.99        | 0.01036 | 2.7412268027E-04 | 5.2623836772E-04 | Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1; spcQ99873i ANM1_HUMAN Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 |
| H7C211_HUMAN          |             |        | 2.1744009773E-04 | 4.4818711414E-04 | Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1; spcQ99873i ANM1_HUMAN Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 |
| spiQ9UL46i            | 2.00        | 0.00919 | 3.0738860599E-04 | 6.2309249752E-04 | Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4 |
| P5ME2_HUMAN           |             |        | 3.1524137556E-04 | 6.3140796832E-04 | Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4 |
| trcA0087WZH7i          | 2.05        | 0.01540 | 3.0378860599E-04 | 6.2309249752E-04 | Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=4 SV=1 |
| A0087WZH7_HUMAN       |             |        | 2.1744009773E-04 | 4.4818711414E-04 | MYCOS complex subunit MIC19 OS=Homo sapiens GN=CHCHD3 PE=1 SV=1 |
| spiQ9NX63i            | 2.06        | 0.04956 | 2.1744009773E-04 | 4.4818711414E-04 | MYCOS complex subunit MIC19 OS=Homo sapiens GN=CHCHD3 PE=1 SV=1 |
| MIC19_HUMAN           |             |        | 2.1275388873E-04 | 4.3852790643E-04 | MYCOS complex subunit MIC19 OS=Homo sapiens GN=CHCHD3 PE=1 SV=1 |
| trcC9JR26i            | 2.06        | 0.04956 | 2.1275388873E-04 | 4.3852790643E-04 | MYCOS complex subunit MIC19 OS=Homo sapiens GN=CHCHD3 PE=1 SV=1 |
| C9JR26_HUMAN          |             |        | 2.5741410440E-04 | 5.5640940806E-04 | Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1; trcQ5T68WQ5T68W8_HUMAN Acidic leucine-rich nuclear phosphoprotein 32 family member B (Fragment) OS=Homo sapiens GN=ANP32B PE=1 SV=1 |
| spiQ9SR88i            | 2.16        | 0.04445 | 2.5741410440E-04 | 5.5640940806E-04 | Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1; trcQ5T68WQ5T68W8_HUMAN Acidic leucine-rich nuclear phosphoprotein 32 family member B (Fragment) OS=Homo sapiens GN=ANP32B PE=1 SV=1 |
| AN32B_HUMAN           |             |        | 3.6660169237E-04 | 7.9908679213E-04 | RNA-binding motif protein, X chromosome, N-terminally processed (Fragment) OS=Homo sapiens GN=RBMX PE=1 SV=2 |
| trcH0Y6E7i            | 2.18        | 0.03725 | 3.6660169237E-04 | 7.9908679213E-04 | RNA-binding motif protein, X chromosome, N-terminally processed (Fragment) OS=Homo sapiens GN=RBMX PE=1 SV=2 |
| Protein | Description | Accession | Fold Change | p-value | Relative Expression |
|---------|-------------|-----------|--------------|---------|---------------------|
| Ras-related protein Rab-7a OS=Homo sapiens GN=RB7A PE=1 SV=1 | Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3; trC9JFG9l C9JFG9_HUMAN Actin-related protein 2/3 complex subunit 1B (Fragment) OS=Homo sapiens GN=ARPC1B PE=1 SV=3; trC9JGC8l C9JGC8_HUMAN Actin-related protein 2/3 complex subunit 1B (Fragment) OS=Homo sapiens GN=ARPC1B PE=1 SV=3; trC9JEY1l C9JEY1_HUMAN Actin-related protein 2/3 complex subunit 1B (Fragment) OS=Homo sapiens GN=ARPC1B PE=1 SV=3; trC9K057l C9K057_HUMAN Actin-related protein 2/3 complex subunit 1B (Fragment) OS=Homo sapiens GN=ARPC1B PE=1 SV=1 | 2.20 | 0.00773 | 3.7175544430E-04 |
| Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4 | Proteasome subunit alpha-type-2 OS=Homo sapiens GN=PSMA2 PE=4 SV=1 | 2.22 | 0.03550 | 8.4465213197E-04 |
| 60S ribosomal protein L27 (Fragment) OS=Homo sapiens GN=RPL27 PE=1 SV=1 | 2.21 | 0.00627 | 9.8605217655E-04 |
| 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3 | 2.59 | 0.06555 | 8.0938650796E-04 |
| 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=1 | 2.59 | 0.06555 | 7.1754677406E-04 |
| Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1 | 2.74 | 0.03035 | 1.0331761575E-03 |
| Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens GN=QPRT PE=1 SV=3; trC9JC5l C9JC5_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens GN=4 PE=4 SV=5 | 2.75 | 0.0691 | 5.6661625682E-04 |
| Protein RPL36A-HNRNPH2 OS=Homo sapiens GN=RPL36A-HNRNPH2 PE=3 SV=2 | 3.07 | 0.00710 | 6.9288128636E-04 |
| 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=3 SV=1; spIP83881l R36A_HUMAN 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2; trR4GN19l R4GN19_HUMAN 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=4 SV=1 | 3.07 | 0.00710 | 5.7577459007E-04 |
| 60S ribosomal protein L36a-like OS=Homo sapiens GN=RPL36AL PE=1 SV=3 | 3.07 | 0.00710 | 7.7132067726E-04 |
| Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=1 | 3.10 | 0.01904 | 4.7403637068E-04 |
| Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=1 | 3.10 | 0.01904 | 4.7403637068E-04 |
| Locus | Fold Change | pValue | Signal+ (pcENS1) | Signal- (pMAXGFP) | Description |
|-------|-------------|--------|-----------------|-------------------|-------------|
| triB7WNR0| B7WNR0_HUMAN | $-3.10$ | $0.01904$ | $1.4224658306E-04$ | Serum albumin (Fragment) OS=Homo sapiens GN=ALB PE=1 SV=1 |
| triH0YA55i | H0YA55_HUMAN | $-3.24$ | $0.02180$ | $1.2662540785E-04$ | GrpE protein homolog 1, mitochondrial OS=Homo sapiens GN=GRPEL1 PE=1 SV=2 |
| spiQ9HAV7i | GRP1_HUMAN | $-3.24$ | $0.01564$ | $2.8082634126E-04$ | 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3; triJ3S69iJ3S69_HUMAN |
| spiP62269iRS18_HUMAN | $-3.26$ | $0.01641$ | $1.1866193463E-04$ | $9.0884462029E-04$ | 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=1 |
| triC9Q83i | C9Q83_HUMAN | $-3.70$ | $0.04512$ | $1.5238542031E-04$ | Ras-related protein Rab-1B (Fragment) OS=Homo sapiens GN=RAB1B PE=3 SV=1 |
| triE9PLD0i | E9PLD0_HUMAN | $-3.81$ | $0.00228$ | $1.1344218542E-04$ | Ras GTPase-activating protein-binding protein 2 OS=Homo sapiens GN=G3BP2 PE=1 SV=2; triD6RB17D6RB17_HUMAN |
| spiQ9UN86i | G3BP2_HUMAN | $-3.82$ | $0.03844$ | $9.5943708277E-05$ | Ras GTPase-activating protein-binding protein 2 (Fragment) OS=Homo sapiens GN=G3BP2 PE=1 SV=1; triD6RC4J6RC4J_HUMAN |
| spiM0QXU7i | M0QXU7_HUMAN | $-4.04$ | $0.00033$ | $1.4864899148E-04$ | Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4; triD6RF0ID6RF0_HUMAN Side-roflexin-1 (Fragment) OS=Homo sapiens GN=SFXN1 PE=1 SV=3 |
| triJ3KRE2i | J3KRE2_HUMAN | $-4.63$ | $0.02210$ | $1.0372838583E-04$ | Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI1 PE=1 SV=1 |
| spiP04179i | SODM_HUMAN | $-5.14$ | $0.00047$ | $1.7132492605E-04$ | Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens GN=SOD2 PE=1 SV=2 |

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under humid atmosphere with 5% CO₂. In all experiments, cells were transfected between 86 and 89 cell passages with 70–80% confluence.

2.2. Plasmids

The recombinant plasmid pcENS1 was previously constructed in our laboratory [2], using the pcDNA3 mammalian expression vector (Invitrogen). It contains the sequence of 63 nucleotides that encodes 21 amino acids from the C-terminal portion of the DENV2 envelope (E) protein and the full length DENV2 ns1 gene. The vector pcDNA3 was used as a negative control, while the plasmid pMAXGFP (Amaxa), which encodes the green fluorescent protein (GFP) from Pontellina plumata copepod, was used as a control for expression of a DENV non-related protein.

2.3. Transfection

Transfection was performed by nucleofection with the Nucleofector V™ kit (Amaxa), according to manufacturer’s recommendation. Briefly, HepG2 cells were seeded on 75 cm² bottles, harvested after 4 or 5 days with the aid of cell scrapes in 3 ml of CMF solution (8 g/L of NaCl; 0.4 g/L of KCl; 0.1 g/L of Na₂SO₄; 0.39 g/L of Na₂HPO₄·12H₂O; 0.15 g/L of KH₂PO₄; 1.1 g/L of glucose; 0.0025 g/L of phenol red, pH 7.4), centrifuged at 500 g for 5 min and suspended in the nucleofection solution (Amaxa). Cell suspension with 5 μg of DNA plasmids (10⁶ cells/100 μl/cuvettes) was submitted to an electric shock in the Nucleofector 6 equipment (Amaxa), using the T-28 program. Nine cuvettes were used for each sample (pcDNA3, pcENS1 or pMAXGFP). After shock, cells received 500 μL of DMEM with 10% FBS and were immediately transferred to microcentrifuge tubes containing another 500 μL DMEM with 10% FBS. Cells were seeded on 25 cm² flasks, incubated in humid atmosphere with 5% CO₂ at 37 °C for 24 h.

2.4. Proteomic sample preparation

Cells were centrifuged at 500 g for 10 min and suspended in 50 mM ammonium bicarbonate buffer containing 0.2% of RapiGest™ SF (Waters). The protein concentration was determined using Qubit 2.0™ kit (Invitrogen) following the manufacturer’s instructions. A total of 50 μg protein was used for each sample. Samples were treated with 5 μL of 100 mM dithiothreitol for reduction, incubated for 3 h at 37 °C. After reaching room temperature, samples were alkylated with 5 μL of 400 mM iodoacetamide for 15 min, in the dark. Trypsin (Promega) was added in the ratio 1:50 enzyme/substrate and digestion was performed for 20 h, at 37 °C. The reaction was stopped after adding formic acid to final concentration of 1%. Aliquots from this digestion were desalted by using POROS R2 C8–18 resin (Invitrogen), packaged in micropipette tips (Millipore) and equilibrated in TFA 1%. After washing with 0.1% TFA, peptides were eluted in 0.1% TFA with 70% acetonitrile and completely dried in the vacuum centrifuge.

2.5. Isoelectric focalization of peptides (OFFGEL)

Twenty five micrograms of peptides were solubilized in 1.8 mL of 0.01% ampholytes (OFFGEL buffer pH 3–10) containing 4% (v/v) glycerol and was submitted to the 3100 OFFGEL Fractionator with the OFFGEL Low Res Kit pH 3–10 (Agilent Technologies) immobilized pH gradient (IPG) DryStrips, following the Agilent’s instructions. The peptides were also separated according to the manufacturer’s instruction and optimized as described in Hubner et al. [3]. Twelve well fractionations were focused for 20 kV with a maximum current of 50 mA and power of 200 mW for 24 h. Each fraction was separately desalted as previously described and suspended in 40 μL of 1% formic acid. All fractions were analyzed on 10 cm reversed phase (RP) column coupled to an LTQ-Orbitrap XL mass spectrometer.
2.6. Liquid chromatography-tandem mass spectrometry (LC-MS/MS) analysis

Desalted peptides fractions were loaded separately onto a 10 cm RP column coupled to the mass spectrometer by using a Proxeon easy-nLC-System (Thermo Scientific Easy-nLC II). Four microliters were initially applied to a 2 cm long (100 μm internal diameter) trap column packed with 5 μm, 200 Å Magic C18 AQ matrix (Michrom Bioresources) followed by separation on a 10 cm long (75 μm internal diameter) separation column packed with the same matrix directly on a self-pack 5–15 μm Tip empty column (New Objective). Samples were loaded onto the trap column at 2 μL/min while chromatographic separation occurred at 200 nL/min. Mobile phase A consisted of 0.1% formic acid in water while mobile phase B consisted of 0.1% formic acid in acetonitrile. Peptides were eluted with a gradient of 2–40% of B over 32 min followed by up to 80% B in 4 min, maintaining at this concentration for 2 min more, before column equilibration. The HPLC system was coupled to the LTQ-Orbitrap XL via a nanoscale LC interface (Thermo Scientific). Source voltage was set to 1.9 kV, the temperature of heated capillary was set to 200 °C and tube lens voltage to 48 and 100 V, respectively. The target precursor specters were acquired in ion trap full scan MS with 60,000 while FWHM full AGC target was set to 500,000. MS1 spectra were acquired on the Orbitrap analyzer (300–1700 m/z) at a 60,000 resolution (for m/z 445.1200). For each spectrum, the 10 most intense ions were submitted to CID fragmentation (minimum signal required of 10,000; isolation width of 2.5; normalized collision energy of 35.0; activation Q of 0.25 and activation time of 30 s, followed by MS2 acquisition on the linear trap quadrupole analyzer. Dynamic exclusion option was enabled and set with the following values for each parameter: repeat count = 1; repeat duration = 30 s; exclusion list size = 500; exclusion duration = 45 s and exclusion mass width = 10 ppm. Data were acquired in technical triplicates using the Xcalibur software (version 2.0.7).

2.7. Protein identification

The raw data files were processed and quantified using PatternLab for Proteomics software v 3.2 [4] (available at: http://max.ioc.fiocruz.br/mtrugilho/RabeloK2016/). Peptide sequence matching (PSM) was performed using the Comet algorithm [5] against the UniProt database (http://www.uniprot.org/) with human proteins entries downloaded January 2015, plus a FASTA file containing Dengue virus and GFP sequences, retrieved from the NCBI database. A target-reverse strategy was employed for increased confidence in protein identifications [6]. The search considered tryptic and semi-tryptic peptide candidates. The cysteine carbamidomethylation and oxidation of methionine were considered as fixed and variable modifications, respectively. The Comet search engine considered a precursor mass tolerance of 40 ppm and bins of 1.0005 for the MS/MS. The validity of the peptide spectrum matches were assessed using PatternLab’s Search Engine Processor (SEPro) module [7]. Briefly, identifications were grouped by charge state (+2 and > +3) and then by tryptic status (i.e., tryptic or semi-tryptic), resulting in four distinct subgroups. For each result, the XCorr, DeltaCN and Secondary Score values were used to generate a Bayesian discriminator. SEPro then automatically established a cutoff score to accept a false-discovery rate (FDR) of 1% based on the number of decoys, independently performed on each data subset, resulting in a false-positive rate that was independent of tryptic status or charge state [7]. Additionally, a minimum sequence length of 6 amino acid residues was required. Then, only PSMs with less than 5 ppm were considered to compose a final list of proteins supported by at least three independent evidences (e.g., identification of a peptide in different charge states, modified and non-modified version of the same peptide, or different peptides). All identification results are reported with less than 1% FDR, both peptide and protein level, by PatternLab’s SEPro module. Spectral counting for estimation of protein copy number was accomplished using the normalized spectral abundance factor (NSAF) [8]. These conditions generate 14,138 peptides which mapped to 4756 proteins, from all samples (HepG2 transfected with the three different plasmids and non-transfected cells) (Supplementary Table S1a–h). Applying the maximum parsimony principle we found 2314 proteins (Supplementary Table S1g). Differentially abundant proteins were pinpointed (Table 2a–c) using PatternLab’s TFold module with a Benjamini–Hochberg q-value of 0.05 [9].
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Transparency document. Supporting Material

Transparency data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2016.11.083.

Appendix A. Supporting Material

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2016.11.083.

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