**Supplementary Table 2:** Listing of proteins identified in global proteomics experiments with high confidence and differential expression, $\leq \frac{1}{10}$ %, $p \leq 0.1$, after exposure to BMP4 protein.

<table>
<thead>
<tr>
<th>RefSeq</th>
<th>IPI</th>
<th>Protein Name</th>
<th>Fold Change</th>
<th>p-value</th>
<th># of spectra utilized for quantification</th>
<th># of unique peptides</th>
<th>% Coverage*</th>
</tr>
</thead>
<tbody>
<tr>
<td>NP_002148</td>
<td>IPI00020362</td>
<td>10 kDa heat shock protein, mitochondrial</td>
<td>0.74</td>
<td>0.00</td>
<td>14</td>
<td>4</td>
<td>29.70%</td>
</tr>
<tr>
<td>NP_006102</td>
<td>IPI0001539</td>
<td>3-ketoacyl-CoA thiolase, mitochondrial</td>
<td>0.81</td>
<td>0.03</td>
<td>10</td>
<td>3</td>
<td>42.10%</td>
</tr>
<tr>
<td></td>
<td>IPI00472102</td>
<td>60 kDa heat shock protein, mitochondrial precursor</td>
<td>0.74</td>
<td>0.00</td>
<td>144</td>
<td>15</td>
<td>5.70%</td>
</tr>
<tr>
<td>NP_000007</td>
<td>IPI0005040, IPI00513827</td>
<td>Acyl-CoA dehydrogenase, medium-chain specific, mitochondrial precursor</td>
<td>1.13</td>
<td>0.04</td>
<td>6</td>
<td>2</td>
<td>10.20%</td>
</tr>
<tr>
<td>NP_005754</td>
<td>IPI00033217</td>
<td>Alpha-aminoadipic semialdehyde synthase, mitochondrial precursor</td>
<td>0.54</td>
<td>0.00</td>
<td>25</td>
<td>7</td>
<td>11.40%</td>
</tr>
<tr>
<td>NP_001001937</td>
<td>IPI00440493</td>
<td>ATP synthase alpha chain, mitochondrial precursor</td>
<td>0.85</td>
<td>0.03</td>
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<td>33.60%</td>
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<td>NP_001677</td>
<td>IPI00303476</td>
<td>ATP synthase beta chain, mitochondrial precursor</td>
<td>0.87</td>
<td>0.01</td>
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<td>23.30%</td>
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<td>IPI00027448</td>
<td>ATP synthase $g$ chain, mitochondrial</td>
<td>0.91</td>
<td>0.02</td>
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<tr>
<td>NP_005989</td>
<td>IPI00290770, IPI00553185</td>
<td>Chaperonin Containing TCP1, subunit 3 isoform b</td>
<td>0.82</td>
<td>0.06</td>
<td>16</td>
<td>6</td>
<td>19.90%</td>
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<td>NP_003312</td>
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<td>Elongation factor Tu, mitochondrial precursor</td>
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<td>8.67%</td>
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<td>Keratin, type I cytoskeletal 18</td>
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<td>80</td>
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<td>IPI00554648</td>
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<td>NADH-ubiquinone oxidoreductase 49 kDa subunit, mitochondrial precursor</td>
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<td>Ornithine aminotransferase, mitochondrial precursor</td>
<td>1.14</td>
<td>0.07</td>
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<tr>
<td>NP_036531</td>
<td>IPI00334907, IPI00395939</td>
<td>PhosPhatidylinositol transfer Protein, beta</td>
<td>1.23</td>
<td>0.09</td>
<td>3</td>
<td>2</td>
<td>8.67%</td>
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<tr>
<td>NP_005403</td>
<td>IPI00002520</td>
<td>Serine hydroxymethyltransferase, mitochondrial precursor</td>
<td>0.83</td>
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<td>3</td>
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<td>NP_003134</td>
<td>IPI00029744</td>
<td>Single-stranded DNA-binding protein, mitochondrial precursor</td>
<td>0.76</td>
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<td>11</td>
<td>2</td>
<td>16.20%</td>
</tr>
<tr>
<td>NP_006507</td>
<td>IPI000220194, IPI00641837</td>
<td>Solute carrier family 2, facilitated glucose transporter member 1</td>
<td>1.60</td>
<td>0.10</td>
<td>22</td>
<td>2</td>
<td>3.60%</td>
</tr>
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<td>NP_008862</td>
<td>IPI00003909, IPI00152505, IPI00607720</td>
<td>Solute carrier family 2, facilitated glucose transporter member 3</td>
<td>3.05</td>
<td>0.03</td>
<td>5</td>
<td>2</td>
<td>5.58%</td>
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<td>NP_001026854</td>
<td>IPI00003377, IPI00215907, IPI00332419</td>
<td>Splice Isoform 1 of Splicing factor, arginine/serine-rich 7</td>
<td>0.88</td>
<td>0.01</td>
<td>48</td>
<td>2</td>
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<td>IPI00012340</td>
<td>Splicing factor, arginine/serine-rich 9</td>
<td>0.83</td>
<td>0.04</td>
<td>12</td>
<td>2</td>
<td>9.96%</td>
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<td>NP_004125</td>
<td>IPI00007765</td>
<td>Stress-70 protein, mitochondrial precursor</td>
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<td>20.50%</td>
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<tr>
<td>NP_036205</td>
<td>IPI00010720</td>
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<td>0.88</td>
<td>0.03</td>
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<tr>
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<td>T-complex protein 1, theta subunit</td>
<td>0.85</td>
<td>0.01</td>
<td>17</td>
<td>6</td>
<td>10.90%</td>
</tr>
</tbody>
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* % Coverage = the # of amino acids in all unique peptides identified with 1 % FPR divided by the total # of amino acids in the protein listed. This is the largest % coverage identified for all three search algorithm identifications.
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<tr>
<th>RefSeq</th>
<th>IPI</th>
<th>Protein Name</th>
<th>Fold Change</th>
<th>p-value</th>
<th># of spectra utilized for quantification</th>
<th># of unique peptides</th>
<th>% Coverage*</th>
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<td>IPI00329633</td>
<td>Threonyl-tRNA synthetase, cytoplasmic</td>
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<td>5</td>
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<td></td>
<td>IPI00477182, IPI00556118</td>
<td>122 kDa protein</td>
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<td>0.09</td>
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<td>7</td>
<td>7.08%</td>
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<tr>
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<td>IPI00413331, IPI00418169, IPI00455315</td>
<td>36 kDa protein</td>
<td>1.77</td>
<td>0.00</td>
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<td>5</td>
<td>17.60%</td>
</tr>
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<td>NP_001002857</td>
<td>IPI00165360</td>
<td>3-mercaptopyruvate sulfurtransferase</td>
<td>1.19</td>
<td>0.04</td>
<td>3</td>
<td>2</td>
<td>7.10%</td>
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<tr>
<td>NP_001008</td>
<td>IPI00221089</td>
<td>40S ribosomal protein S13</td>
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<td>35</td>
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<td>40S ribosomal protein S18</td>
<td>0.82</td>
<td>0.10</td>
<td>18</td>
<td>3</td>
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<td>NP_000996</td>
<td>IPI00011253</td>
<td>40S ribosomal protein S3</td>
<td>0.79</td>
<td>0.03</td>
<td>8</td>
<td>3</td>
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<tr>
<td>NP_000970</td>
<td>IPI00419880, IPI00472119</td>
<td>40S ribosomal protein S3a</td>
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<tr>
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<td>IPI00027493, IPI00554481, IPI00021840</td>
<td>4F2 cell-surface antigen heavy chain</td>
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<td>60S ribosomal protein L10</td>
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<td>NP_002939</td>
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<td>60S ribosomal protein L15</td>
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<td>80</td>
<td>7</td>
<td>29.60%</td>
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<tr>
<td>NP_000976</td>
<td>IPI00413324, IPI00021840</td>
<td>60S ribosomal protein L17</td>
<td>0.85</td>
<td>0.05</td>
<td>21</td>
<td>3</td>
<td>17.50%</td>
</tr>
<tr>
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<td>60S ribosomal protein L17</td>
<td>0.85</td>
<td>0.05</td>
<td>21</td>
<td>3</td>
<td>17.50%</td>
</tr>
<tr>
<td>NP_000971</td>
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<td>60S ribosomal protein L18</td>
<td>0.67</td>
<td>0.01</td>
<td>8</td>
<td>2</td>
<td>13.40%</td>
</tr>
<tr>
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<td>60S ribosomal protein L18</td>
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<td>55</td>
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<td>15</td>
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</tr>
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<td>60S ribosomal protein L6</td>
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<td>9</td>
<td>3</td>
<td>13.20%</td>
</tr>
<tr>
<td>NP_000963</td>
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<td>60S ribosomal protein L7a</td>
<td>0.91</td>
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<td>10</td>
<td>2</td>
<td>9.81%</td>
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<td>Alpha-actinin 1</td>
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<td>14</td>
<td>16.30%</td>
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<td>NP_004915</td>
<td>IPI00013808</td>
<td>Alpha-actinin 4</td>
<td>1.38</td>
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<tr>
<td>NP_00691</td>
<td>IPI00218918, IPI00549413</td>
<td>Annexin A1</td>
<td>1.65</td>
<td>0.04</td>
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<td>2</td>
<td>11.60%</td>
</tr>
<tr>
<td>NP_001145</td>
<td>IPI00329801</td>
<td>Annexin A5</td>
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<tr>
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<td>IPI00220834</td>
<td>ATP-dependent DNA helicase II 80 kDa subunit</td>
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<tr>
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<td>1.50</td>
<td>0.01</td>
<td>4</td>
<td>4</td>
<td>1.30%</td>
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</tbody>
</table>

* % Coverage = the # of amino acids in all unique peptides identified with 1 % FPR divided by the total # of amino acids in the protein listed. This is the largest % coverage identified for all three search algorithm identifications.
<table>
<thead>
<tr>
<th>RefSeq</th>
<th>IPI</th>
<th>Protein Name</th>
<th>Fold Change</th>
<th>p-value</th>
<th># of spectra utilized for quantification</th>
<th># of unique peptides</th>
<th>% Coverage*</th>
</tr>
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<td>Calgizzarin</td>
<td>3.18</td>
<td>0.08</td>
<td>3</td>
<td>2</td>
<td>25.70%</td>
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<td>NP_004369 IPI00219930, IPI00010896, IPI00554767, IPI00640548, IPI00646484, IPI00647593</td>
<td>Cellular retinoic acid binding protein 1</td>
<td>0.61</td>
<td>0.01</td>
<td>9</td>
<td>3</td>
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<td>Chloride intracellular channel protein 1</td>
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<td>Creatine kinase B-type</td>
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<td>NP_001312 IPI00002824</td>
<td>Cysteine and glycine-rich protein 2</td>
<td>0.64</td>
<td>0.09</td>
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<td>2</td>
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<td>NP_061820 IPI00465315</td>
<td>Cytochrome c</td>
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<td>Dihydropyrimidinase-related protein 2</td>
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</tr>
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<td>Dipeptidyl-peptidase I precursor</td>
<td>0.80</td>
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<tr>
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<td>DNA replication licensing factor MCM2</td>
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<td>0.01</td>
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<td>NP_002379 IPI00013214</td>
<td>DNA replication licensing factor MCM3</td>
<td>0.79</td>
<td>0.07</td>
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<td>6</td>
<td>8.34%</td>
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<td>6</td>
<td>4</td>
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<td>167</td>
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* % Coverage = the # of amino acids in all unique peptides identified with 1 % FPR divided by the total # of amino acids in the protein listed. This is the largest % coverage identified for all three search algorithm identifications.
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* % Coverage = the # of amino acids in all unique peptides identified with 1 % FPR divided by the total # of amino acids in the protein listed. This is the largest % coverage identified for all three search algorithm identifications.
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<td>IPI00418471, IPI00646867</td>
<td>Vimentin</td>
<td>0.75</td>
<td>0.08</td>
<td>48</td>
<td>10</td>
<td>26.90%</td>
</tr>
</tbody>
</table>

* % Coverage = the # of amino acids in all unique peptides identified with 1 % FPR divided by the total # of amino acids in the protein listed. This is the largest % coverage identified for all three search algorithm identifications.
<table>
<thead>
<tr>
<th>RefSeq</th>
<th>IPI</th>
<th>Protein Name</th>
<th>Fold Change</th>
<th>P-value</th>
<th># of spectra utilized for quantification</th>
<th># of unique peptides</th>
<th>% Coverage*</th>
</tr>
</thead>
<tbody>
<tr>
<td>NP_057085</td>
<td>IPI00000733</td>
<td>WD-repeat protein 50</td>
<td>0.73</td>
<td>0.07</td>
<td>24</td>
<td>2</td>
<td>5.76%</td>
</tr>
<tr>
<td>NP_057396</td>
<td>IPI00170786</td>
<td>WW domain-binding protein 11</td>
<td>0.76</td>
<td>0.03</td>
<td>9</td>
<td>2</td>
<td>5.30%</td>
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<tr>
<td>NP_001203</td>
<td>IPI00014230</td>
<td>Complement component 1, Q subcomponent binding protein, mitochondrial precursor</td>
<td>0.61</td>
<td>0.04</td>
<td>10</td>
<td>3</td>
<td>19.20%</td>
</tr>
<tr>
<td>NP_006550</td>
<td>IPI00008575</td>
<td>Splice Isoform 1 of KH domain containing, RNA binding, signal transduction associated protein 1</td>
<td>0.86</td>
<td>0.05</td>
<td>7</td>
<td>4</td>
<td>10.40%</td>
</tr>
<tr>
<td>NP_00692</td>
<td>IPI00006482</td>
<td>Splice Isoform Long of Sodium/potassium-transporting ATPase alpha-1 chain precursor</td>
<td>1.10</td>
<td>0.01</td>
<td>18</td>
<td>3</td>
<td>2.93%</td>
</tr>
</tbody>
</table>

* % Coverage = the # of amino acids in all unique peptides identified with 1 % FPR divided by the total # of amino acids in the protein listed. This is the largest % coverage identified for all three search algorithm identifications.