Supplementary Table S1 contains data from six whole proteome datasets (available on request). Each dataset lists all proteins detected in one single-cell S7500 preparation from cytoplasmic homogenate. A multiconsensus report was generated from these six datasets. Redundancies in this report were resolved by manual inspection of the data. For any group of redundant hits, only the hit with highest Σ# PSMs was retained. Supplementary Table S1 includes the multiconsensus report for GAPDH, MDH1, TKTL2 and EEF2.1 (part A) and the information for each individual S7500 (part B, which includes the % of total Σ# peptide spectral matches and %rank calculations for the individual S7500s).

### A. Multiconsensus report - GAPDH, MDH1 TKTL2 and EEF2.1

| Accession | Xenbase gene symbol | Curated description | ΣCoverage | Σ# Proteins | Σ# Unique Peptides | Σ# Peptides | Σ# PSMs | MW [kDa] | calc. pI |
|-----------|---------------------|---------------------|-----------|-------------|------------------|-------------|---------|----------|----------|
| Q7ZY52    | gapdh               | Glyceraldehyde-3-phosphate dehydrogenase | 65.77     | 1           | 13               | 17          | 640     | 333      | 35.8     | 8.05     |
| A0A1L8G769| mdh1                | Malate dehydrogenase 1 | 53.89     | 1           | 7                | 14          | 430     | 334      | 36.4     | 6.58     |
| Q7ZXP8    | eef2.1              | Eukaryotic translation elongation factor 2, gene 1 | 51.05     | 3           | 16               | 40          | 506     | 858      | 95.4     | 6.93     |
| Q918J7    | tktl2               | Transketolase-like 2 | 51.20     | 1           | 23               | 23          | 319     | 625      | 67.4     | 6.73     |

**All Cytoplasmic S7500s**

|   | Score A3 | Coverage A3 | # Peptides A3 | # PSM A3 | % of total Σ# peptide spectral matches | %RANK.EXC |
|---|----------|-------------|---------------|----------|---------------------------------------|-----------|
| Cyto 1 | 2.201642478 | 0.9917 | 1.537655064 | 0.9696 | 1.24068063 | 0.964 |
| Cyto 2 | 1.867151319 | 0.9827 | 1.040978169 | 0.9481 | 0.82617315 | 0.9221 |
| Cyto 3 | 1.342356879 | 0.9583 | 1.040978169 | 0.9481 | 0.82617315 | 0.9221 |

**B. Individual cytoplasms - GAPDH, MDH1 TKTL2 and EEF2.1**

|   | Score A3 | Coverage A3 | # Peptides A3 | # PSM A3 | % of total Σ# peptide spectral matches | %RANK.EXC |
|---|----------|-------------|---------------|----------|---------------------------------------|-----------|
| Cyto 1 | 2.01642478 | 0.9917 | 1.537655064 | 0.9696 | 1.24068063 | 0.964 |
| Cyto 2 | 1.867151319 | 0.9827 | 1.040978169 | 0.9481 | 0.82617315 | 0.9221 |
| Cyto 3 | 1.342356879 | 0.9583 | 1.040978169 | 0.9481 | 0.82617315 | 0.9221 |

S7500 #1 - total Σ# peptide spectral matches for all detected proteins = 5723 (361 unique proteins)

S7500 #2 - total Σ# peptide spectral matches for all detected proteins = 6271 (365 unique proteins)

S7500 #3 - total Σ# peptide spectral matches for all detected proteins = 6052 (346 unique proteins)
| Peptide | Protein Name | Gene | Score A3 | Coverage A3 | # Peptides A3 | # PSM A3 | % of total Σ# peptide spectral matches | %RANK.EXC |
|---|---|---|---|---|---|---|---|---|
| Q7ZY52 | Glyceraldehyde-3-phosphate dehydrogenase gapdh | 257.96 | 53.45 | 13 | 89 | 1.602448649 | 0.9808 |
| A0A1L8G769 | Malate dehydrogenase 1 mdh1 | 212.41 | 43.71 | 10 | 69 | 1.242347829 | 0.9672 |
| Q7ZXQ8 | Eukaryotic translation elongation factor 2, gene 1 eef2.1 | 189.12 | 41.61 | 28 | 63 | 1.134317583 | 0.9617 |
| Q9I8J7 | Transketolase-like 2 tkt2 | 148.60 | 38.24 | 15 | 49 | 0.882247009 | 0.9262 |
| S7500 #4 - total Σ# peptide spectral matches for all detected proteins = 5554 (365 unique proteins) |  |
| Q7ZY52 | Glyceraldehyde-3-phosphate dehydrogenase gapdh | 412.93 | 64.86 | 16 | 142 | 2.027991886 | 0.9902 |
| A0A1L8G769 | Malate dehydrogenase 1 mdh1 | 256.42 | 49.10 | 12 | 82 | 1.399600034 | 0.9755 |
| Q7ZXQ8 | Eukaryotic translation elongation factor 2, gene 1 eef2.1 | 287.74 | 42.89 | 32 | 98 | 1.171093906 | 0.9608 |
| Q9I8J7 | Transketolase-like 2 tkt2 | 192.92 | 41.92 | 17 | 61 | 0.871179613 | 0.9413 |
| S7500 #5 - total Σ# peptide spectral matches for all detected proteins = 7002 (408 unique proteins) |  |
| Q7ZY52 | Glyceraldehyde-3-phosphate dehydrogenase gapdh | 380.62 | 62.46 | 16 | 126 | 2.058823494 | 0.9924 |
| A0A1L8G769 | Malate dehydrogenase 1 mdh1 | 279.73 | 49.10 | 13 | 88 | 1.437908472 | 0.9823 |
| Q7ZXQ8 | Eukaryotic translation elongation factor 2, gene 1 eef2.1 | 240.48 | 42.89 | 32 | 81 | 1.323529389 | 0.9671 |
| Q9I8J7 | Transketolase-like 2 tkt2 | 163.91 | 37.60 | 15 | 51 | 0.833333319 | 0.9292 |
| S7500 #6 - total Σ# peptide spectral matches for all detected proteins = 6120 (395 unique proteins) |  |