Supplementary Table 1. Protein Location Information

|  |  |  |  |
| --- | --- | --- | --- |
| cell cortex | cellular\_component | cellular bud | chromosome |
| cell wall | endomembrane system | cytoskeleton | cytoplasmic vesicle |
| cytoplasm | endoplasmic reticulum | Golgi apparatus | extracellular region |
| membrane | mitochondrial envelope | mitochondrion | nucleus |
| nucleolus | microtubule organizing center | peroxisome | plasma membrane |
| ribosome | site of polarized growth | vacuole | other |

Supplementary Algorithm 1. Spatiotemporal Hypergraph Construction

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| **Algorithm 1** Spatiotemporal Hypergraph Construction |
| **Input:** GO cellular components and time tags data (denoted as ), PPI data |
| **Output:** Constructed spatiotemporal hypergraph subnetworks |
| 1: // extract cellular components (cc) and time tags (tt) for each protein (p) in |
| 2: **for** each data in **do** |
| 3: **if** cc and tt p **then** |
| 4: PCT p, cc and tt // PCT is a dictionary containing p, cc and tt |
| 5: **end if** |
| 6: **end for** |
| 7: // initialize a map function reco(x), which returns the index of a GO term x |
| 8: **for** each cc in PCT **do** |
| 9: cmap reco(cc) // cmap is the index of GO term cc |
| 10: proteinmap cmap // proteinmap is the set of cmap and protein |
| 11: **end for** |
| 12: **for** each ppi in **do** |
| 13: **if** ppi in proteinmap **then** |
| 14: compute the flag list from intersected cc and tt sets |
| 15: **if** flag list is not empty **then** |
| 16: file ppi, flag // file is the spatiotemporal subnetwork |
| 17:  **end if** |
| 18: **end if** |
| 19: **end for** |
| 20: // Spatiotemporal hypergraph subnetwork construction |
| 21: **for** each data in file **do** |
| 22: **for** i in range () **do** |
| 23: **if** i in data(flag) **then** |
| 24: data(ppi) |
| 25: Hypergraph () |
| 26: **end if** |
| 27: **end for** |
| 28: **end for** |
| 29: **Return:** |

Supplementary Figure 1. Ko03008 Pathway

