Table S3: Proteins not listed in Red Blood Cell protein databases: <http://141.61.102.16/rbc/>, <http://ebm.rsmjournals.com/cgi/content/full/232/11/1391#AFF3>, <http://proteomique.ipbs.fr/pairs/www/rbc_browser.htm>

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Gene | Protein | Expression level  | Coverage% | SC | Hits |
| RANBP1  | Ran-specific GTPase-activating protein  | N/A | 29.9 | 12 | 1 |
| TET1 | Tet oncogene 1  | N/A | 0.6 | 3 | 1 |
| *HARS* | Histidyl-tRNA synthetase, cytoplasmic  | N/A | 25.9 | 23 | 1 |
| *HERC1*  | Guanine nucleotide exchange factor p532  | N/A | 0.2 | 4 | 2 |
| TUBB | Tubulin beta chain  | HA21 🡹 | 52 | 104 | 1 |
| TUBB4 | Tubulin beta-4 chain  | HA21 🡹 | 49.5 | 51 | 1 |
| TUBA4A  | Tubulin alpha-4A chain  | HA21 🡹 | 46 | 41 | 1 |
| TUBB3 | Tubulin, beta- 3  | HA21 🡹 | 14.9 | 32 | 1 |
| TUBB6 | Tubulin, beta 6  | HA21 🡹 | 30.4 | 31 | 1 |
| RHOC | Ras homolog gene family, member C  | N/A | 25.5 | 7 | 1 |
| *FGD1*  | FYVE, RhoGEF and PH domain-containing protein 1  | N/A | 0.8 | 2 | 1 |
| *APOA1BP* | Isoform 1 of Apolipoprotein A-I-binding protein precursor  | HA19 🡻 | 24.3 | 53 | 5 |
| *GSTM3* | Glutathione S-transferase mu 3 (brain)  | N/A | 46.7 | 41 | 3 |
| PGAM1 | Phosphoglycerate mutase 1  | HA24 🡹 | 53.9 | 58  | 3 |
| *GMPR2*  | GMPR2 protein  | N/A | 24 | 20 | 3 |
| **POTEKP**  | POTE ankyrin domain family, member K | N/A | 6.9 | 17 | 1 |
| *HDHD2* | Haloacid dehalogenase-like hydrolase domain containing  | HA21 🡻 | 14.3 | 15 | 2 |
| PRPSAP1  | Phosphoribosyl pyrophosphate synthetase-associated protein 1 | N/A | 12.7 | 5 | 1 |
| *COL3A1*  | Isoform 1 of Collagen alpha-1(III) chain precursor  | HA21 🡹 | 1.2 | 2 | 1 |
| LETM1 | Leucine zipper-EF-hand-containing transmem.protein 1,mitochondrial precursor  | N/A | 3.5 | 2 | 1 |
| *SBNO1/2*  | Strawberry notch homolog 1 or 2  | N/A | 0.8 | 2 | 1 |

Gene: HGNC Symbol for coding human gene Protein: HGNC Symbol for protein identified

Expression level: Expression measured (normalized volume) in patient sample compared to average of controls

N/A: Protein not predominant protein running in that spot,

🡹 Patient expression higher than controls, 🡻: Patient expression lower than controls

Spectral count: Sum of spectral counts for peptides unique to identified protein from all spots where this protein was found

Coverage: Percentage of aminoacid sequence that is covered by unique peptides to identify protein

Hits: Number of spots where identified protein was found