**S7 Table. Homology detection of novel motifs identified in MEME analysis**

(Three best hits for each motif is shown)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Motif** | **Hit (PDB id)** | **Prob.**  | **E-value** | **P-value** | **Score** |
| **Motif 1** | T-cell receptor gamma chain (1ypz\_F) | 75 | 4.5 | 0.00014 | 24.1 |
| Immunoglobulin A1 heavy chain (3m8o\_H) | 68.3 | 4.1 | 0.00013 | 25.9 |
| IG MU chain C region secreted form (4ba8\_A) | 59.0 | 13 | 0.00039 | 20.0 |
| **Motif 2** | DNA-directed RNA polymerase II subunit RPB1 (4jxt\_B) | 23.4 | 26 | 0.00081 | 16.2 |
| Phosphorylated peptide from C-terminal of RNA polymerase II (1p16\_C) | 21.5 | 30 | 0.00093 | 16.0 |
| EIAV capsid protein P26 (1eia\_A) | 17.1 | 49 | 0.0015 | 21.3 |
| **Motif 3** | Cyclin-dependent kinase inhibitor 1 (2zvv\_Y) | 81.7 | 0.27 | 8.4E-06 | 21.1 |
| Pfadf1, cofilin/actin-depolymerizing factor homolog 1 (3q2b\_A) | 28.0 | 17 | 0.00052 | 17.9 |
| V1AR, vasopressin V1A receptor (1ytv\_M) | 27.4 | 12 | 0.00036 | 19.4 |
| **Motif 4** | AP endonuclease (3ngf\_A) | 47.9 | 3.7 | 0.00011 | 21.0 |
| Tetrahydrodipicolinate acetyltransferase (3bv8\_A) | 24.0 | 23 | 0.00071 | 19.3 |
| HTRA, putative serine protease (2l97\_A) | 22.0 | 29 | 0.00089 | 17.3 |
| **Motif 5** | Maltose-binding protein (3iot\_A) | 53.6 | 3.1 | 9.4E-05 | 27.4 |
| Maltose-binding periplasmic protein (4feb\_A) | 44.1 | 5.3 | 0.00016 | 25.9 |
| Maltose-binding periplasmic protein (4feb\_A) | 35.9 | 7.2 | 0.00022 | 25.2 |
| **Motif 6** | Wiskott-aldrich syndrome protein family member 2 (2a40\_C) | 82.3 | 0.32 | 9.9E-06 | 23.6 |
| YFLH protein (3d0w\_A) | 40.2 | 4.3 | 0.00013 | 23.2 |
| P7TM2, P7 polypeptide (2k8j\_X) | 38.0 | 11 | 0.00035 | 17.7 |
| **Motif 7** | CG4944-PC, isoform C; protein-protein complex (2ff6\_H) | 12.6 | 32 | 0.00097 | 15.7 |
| Golgi to ER traffic protein 2 (3sjd\_D) | 8.4 | 82 | 0.0025 | 16.0 |
| Golgi to ER traffic protein 2 (3zs9\_C) | 6.9 | 1.4E+02 | 0.0042 | 14.6 |
| **Motif 8** | Mannosyl-oligosaccharide 1,2-alpha-mannosidase (4ayo\_A) | 39.2 | 3.6 | 0.00011 | 25.9 |
| Methionine synthase (B12-independent) (3rpd\_A) | 35.1 | 17 | 0.00054 | 20.5 |
| Anti-sigma F factor (1th8\_A) | 28.4 | 4.1 | 0.00013 | 21.3 |
| **Motif 9** | Probable insulin-like peptide 5 A chain (2wfu\_A) | 27.2 | 5.2 | 0.00016 | 20.1 |
| NADH dehydrogenase I subunit E (2lxr\_A) | 25.9 | 22 | 0.00068 | 21.6 |
| SWI5, zinc finger DNA binding domain (1zfd\_A) | 24.7 | 21 | 0.00063 | 17.8 |
| **Motif 10** | Protein (immunoglobulin), virus-antibody complex (1qgc\_4) | 77.5 | 1.4 | 4.4E-05 | 27.6 |
| IG gamma-2A chain C region, A allele (3zo0\_A)  | 72.9 | 2.6 | 7.9E-05 | 23.3 |
| IGY FCU3-4, immunoglobulin (2w59\_A) | 72.4 | 4.1 | 0.00013 | 22.6 |
| **Motif 11** | DNA replication protein DNAC (3ec2\_A) | 44.2 | 5.5 | 0.00017 | 22.7 |
| Hypothetical UPF0131 protein PH0828 (v30\_A) | 23.7 | 6.4 | 0.0002 | 21.6 |
| Cytosine/guanine deaminase related protein (2i9u\_A) | 23.0 | 19 | 0.0006 | 19.3 |
| **Motif 12** | Putative nucleotidyltransferase (1ylq\_A) | 33.9 | 9.9 | 0.0003 | 22.8 |
| Hypothetical protein HI0073 (1no5\_A) | 27.8 | 21 | 0.00065 | 21.3 |
| RE55538P, BEN domain (4ix7\_A)  | 21.3 | 33 | 0.001 | 21.3 |
| **Motif 13** | Photosystem 1 reaction centre subunit II (1jb0\_D) | 24.8 | 17 | 0.00053 | 21.9 |
| Photosystem I subunit II (4kt0\_D) | 23.6 | 19 | 0.00058 | 21.8 |
| Photosystem I reaction center subunit II (2wsc\_D) | 18.2 | 32 | 0.001 | 21.9 |
| **Motif 14** | Glucan endo-1,3-beta-D-glucosidase (3ur8\_A) | 59.5 | 3 | 9.2E-05 | 27.4 |
| CAG38821; archeal virus, viral protein (3ur8\_A) | 50.8 | 2.5 | 7.6E-05 | 24.2 |
| Brassinosteroid insensitive 1-associated receptor (4mn8\_B) | 43.8 | 5.4 | 0.00017 | 25.0 |
| **Motif 15** | Protein FDRA, predicted actyl-COA synthetase (3dmy\_A) | 48.6 | 4.4 | 0.00014 | 27.7 |
| VP12.5, KP6 killer toxin subunit beta (4gvb\_B) | 40.0 | 6.5 | 0.0002 | 21.6 |
| Serine/threonine-protein kinase PAK 4 (4l67\_B) | 29.3 | 13 | 0.0004 | 16.8 |