

translation factor activity, RNA binding GO:0008135 RNA binding GO:0003723 dynein light intermediate chain binding GO:0051959 poly(G) binding GO:0034046 tRNA (uracil) methyltransferase activity GO:0016300 hedgehog receptor activity GO:0008158 fibronectin binding GO:0001968 alpha–1,6–mannosylglycoprotein 2–beta–N-... GO:0008455 neuregulin binding GO:0031994 aspartic endopeptidase activity, intrame... GO:0042500 beta–2 adrenergic receptor binding GO:0031698 protein kinase A catalytic subunit bindi... GO:0034236 phosphatidylinositol–5–phosphate binding GO:0010314 p=2.6E-03 | n=3 p=1.1E-02 | n=7 fg=0.10 | bg=0.01 fg=0.24 | bg=0.09 p=1.8E-02 p=1.8E-02 n=1 fa=0.03 bg=0.00 fg=0.03 bg=0.00 n=1 fğ=0.03 p=1.8E-02 n=1bg=0.00 fg=0.03 bg=0.00 p=1.8E-02n=1fg=0.03 fg=0.03 p=1.8E-02 bg=0.00 p=1.8E-02ba=0.00n=1p=1.8E-02 p=1.8E-02 fg=0.03 fg=0.03 bg=0.00 bq=0.00 n=1p=3.6E-02 p=3.6E-02 fg=0.03 bg=0.00 bg=0.00 bg=0.00 fg=0.03 n=1p=3.6E-02 p=3.6E-02 fg=0.03 protein kinase A catalytic subunit bindi... GO:0034236 phosphatidylinositol–5–phosphate binding GO:0010314 cAMP–dependent protein kinase regulator ... GO:0008603 cAMP–dependent protein kinase inhibitor ... GO:0004862 insulin–like growth factor binding GO:0005520 lamin binding GO:0005521 heterocyclic compound binding GO:1901363 mRNA regulatory element binding translat... GO:0000900 catalytic activity, acting on a glycopro... GO:0140103 ribosomal small subunit binding GO:0043024 rDNA binding GO:000182 glutathione binding GO:00043295 fa=0.03 n=1bg = 0.00p=3.6E-02 fg=0.03 bg=0.00 p=3.6E-02 p=3.6E-02 p=3.6E-02 p=5.2E-02 p=5.4E-02 n=1fg=0.03 bg=0.00 bg=0.00 n=1fg=0.03 n=1bg=0.00 n=14 bg=0.27 fg=0.03 bg=0.00 bg=0.00 n=1p=5.4E-02 n=1p=5.4E-02 p=5.4E-02 n=1fg=0.03 bg=0.00 fg=0.03 bg=0.00 n=1 glutathione binding GO:000162 pre-mRNA 3'-splice site binding GO:0030628 laminin binding GO:0043236 oligopeptide binding GO:0050840 extracellular matrix binding GO:0050840 p=5.4E-02 **■**fg=0.03 bg=0.00 n=1p=5.4E-02 fg=0.03 bg=0.00 n=1 p=5.4E-02 p=5.4E-02 p=5.4E-02 p=5.4E-02 n=1fg=0.03 bg=0.00 bg=0.00 bg=0.00 fg=0.03 n=1fg=0.03 fg=0.03 n=1 tRNA methyltransferase activity GO:0008175 mRNA binding GO:0003729 n=1bq = 0.00p=5.7E-02 fg=0.10 bg=0.03 0 2 0.0 0.2 1 3 5 0.4 0.6 0.8 1.0 fraction –log(p) n=29/155 input genes with annotations

GO:CC Elav\_Nvec\_vc1.1\_XM\_048722339.1 fraction genes in fg and expected value

