

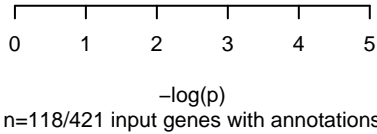
GO:BP
Elav_Nvec_vc1.1_XM_032381587.2

fraction genes in fg and expected value

| | |
|---------------------------------------------|------------|
| embryonic placenta development | GO:0001892 |
| lung epithelium development | GO:0060428 |
| cellular response to oxygen levels | GO:0071453 |
| regulation of odontoblast differentiatio... | GO:1901329 |
| swim bladder development | GO:0048794 |
| positive regulation of transcription fro... | GO:0061408 |
| magnesium ion transmembrane transport | GO:1903830 |
| positive regulation of transcription fro... | GO:0006990 |
| liver morphogenesis | GO:0072576 |
| positive regulation of DNA recombination | GO:0045911 |
| protein maturation | GO:0051604 |
| cellular response to lipid | GO:0071396 |
| somatic muscle development | GO:0007525 |
| antigen processing and presentation of p... | GO:0002474 |
| double-strand break repair via homologou... | GO:0000724 |
| regulation of osteoclast differentiation | GO:0045670 |
| apoptotic process | GO:0006915 |
| regulation of apoptotic process | GO:0042981 |
| determination of left/right symmetry | GO:0007368 |
| determination of heart left/right asymme... | GO:0061371 |
| adenylate cyclase-activating adrenergic ... | GO:0086023 |
| negative regulation of adenylate cyclase... | GO:0071878 |
| positive regulation of tyrosine phosphor... | GO:0042531 |
| cellular response to insulin-like growth... | GO:1990314 |
| regulation of adenylate cyclase-activati... | GO:0140192 |
| negative regulation of adenylate cyclase... | GO:0140199 |
| response to herbicide | GO:0009635 |
| G protein-coupled receptor signaling pat... | GO:0086103 |
| regulation of neurotrophin TRK receptor ... | GO:0051386 |
| positive regulation of neurotrophin TRK ... | GO:0051388 |

| | |
|-----------|------|
| p=1.9E-03 | n=5 |
| p=2.4E-03 | n=3 |
| p=3.9E-03 | n=8 |
| p=4.2E-03 | n=2 |
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| p=4.2E-03 | n=2 |
| p=4.2E-03 | n=2 |
| p=4.2E-03 | n=2 |
| p=4.6E-03 | n=3 |
| p=5.3E-03 | n=8 |
| p=7.7E-03 | n=11 |
| p=7.7E-03 | n=4 |
| p=7.7E-03 | n=3 |
| p=9.4E-03 | n=5 |
| p=1.0E-02 | n=4 |
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| p=1.1E-02 | n=23 |
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| p=1.2E-02 | n=2 |
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| p=1.2E-02 | n=2 |
| p=1.2E-02 | n=2 |
| p=1.2E-02 | n=2 |

| | |
|---------|---------|
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| fg=0.03 | bg=0.00 |
| fg=0.07 | bg=0.02 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
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| fg=0.07 | bg=0.02 |
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| fg=0.03 | bg=0.01 |
| fg=0.03 | bg=0.00 |
| fg=0.04 | bg=0.01 |
| fg=0.03 | bg=0.01 |
| fg=0.22 | bg=0.14 |
| fg=0.19 | bg=0.12 |
| fg=0.06 | bg=0.02 |
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| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
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| fg=0.02 | bg=0.00 |



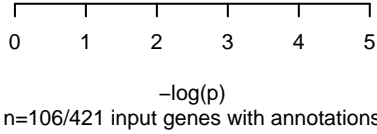
GO:MF
Elav_Nvec_vc1.1_XM_032381587.2

fraction genes in fg and expected value

| | |
|---------------------------------------------|------------|
| protein self-association | GO:0043621 |
| magnesium ion transmembrane transporter ... | GO:0015095 |
| N4-(beta-N-acetylglucosaminy)-L-asparag... | GO:0003948 |
| 3'-5' DNA helicase activity | GO:0043138 |
| pre-mRNA intronic binding | GO:0097157 |
| G-quadruplex DNA binding | GO:0051880 |
| ATP hydrolysis activity | GO:0016887 |
| cis-regulatory region sequence-specific ... | GO:0000987 |
| RNA polymerase II cis-regulatory region ... | GO:0000978 |
| DNA helicase activity | GO:0003678 |
| intronic transcription regulatory region... | GO:0001161 |
| misfolded protein binding | GO:0051787 |
| nucleoside-triphosphatase activity | GO:0017111 |
| ATP-dependent activity | GO:0140657 |
| DNA-binding transcription repressor acti... | GO:0001227 |
| DNA-binding transcription repressor acti... | GO:0001217 |
| hydrolase activity, acting on acid anhyd... | GO:0016817 |
| hydrolase activity, acting on acid anhyd... | GO:0016818 |
| pyrophosphatase activity | GO:0016462 |
| chromatin DNA binding | GO:0031490 |
| DNA-binding transcription factor binding | GO:0140297 |
| aryl hydrocarbon receptor binding | GO:0017162 |
| transcription regulatory region nucleic ... | GO:0001067 |
| DNA binding | GO:0003677 |
| hydrolase activity | GO:0016787 |
| transcription cis-regulatory region bind... | GO:0000976 |
| insulin-like growth factor II binding | GO:0031995 |
| four-way junction DNA binding | GO:0000400 |
| poly(A)-specific ribonuclease activity | GO:0004535 |
| lipopolysaccharide binding | GO:0001530 |

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|-----------|------|
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| p=4.4E-03 | n=2 |
| p=4.4E-03 | n=2 |
| p=1.3E-02 | n=2 |
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| p=3.2E-02 | n=3 |
| p=3.8E-02 | n=2 |
| p=3.8E-02 | n=2 |
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| p=4.6E-02 | n=4 |
| p=4.7E-02 | n=13 |
| p=4.7E-02 | n=13 |
| p=4.7E-02 | n=13 |
| p=5.0E-02 | n=3 |
| p=5.0E-02 | n=6 |
| p=5.5E-02 | n=2 |
| p=5.6E-02 | n=11 |
| p=5.7E-02 | n=18 |
| p=6.5E-02 | n=29 |
| p=6.6E-02 | n=10 |
| p=6.7E-02 | n=1 |
| p=6.7E-02 | n=1 |
| p=6.7E-02 | n=1 |
| p=6.7E-02 | n=1 |

| | |
|---------|---------|
| fg=0.04 | bg=0.01 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
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| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.09 | bg=0.05 |
| fg=0.08 | bg=0.04 |
| fg=0.08 | bg=0.04 |
| fg=0.03 | bg=0.01 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.12 | bg=0.07 |
| fg=0.09 | bg=0.05 |
| fg=0.04 | bg=0.01 |
| fg=0.04 | bg=0.01 |
| fg=0.12 | bg=0.07 |
| fg=0.12 | bg=0.07 |
| fg=0.12 | bg=0.07 |
| fg=0.03 | bg=0.01 |
| fg=0.06 | bg=0.03 |
| fg=0.02 | bg=0.00 |
| fg=0.10 | bg=0.06 |
| fg=0.17 | bg=0.12 |
| fg=0.27 | bg=0.20 |
| fg=0.09 | bg=0.06 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
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| fg=0.01 | bg=0.00 |



GO:CC
Elav_Nvec_vc1.1_XM_032381587.2

fraction genes in fg and expected value

| | |
|---------------------------------------------|------------|
| euchromatin | GO:0000791 |
| M band | GO:0031430 |
| COPII vesicle coat | GO:0030127 |
| I band | GO:0031674 |
| endoplasmic reticulum membrane | GO:0005789 |
| Golgi-associated vesicle | GO:0005798 |
| extracellular space | GO:0005615 |
| Golgi-associated vesicle membrane | GO:0030660 |
| Prp19 complex | GO:0000974 |
| Fanconi anaemia nuclear complex | GO:0043240 |
| condensed chromosome | GO:0000793 |
| membrane-enclosed lumen | GO:0031974 |
| intracellular organelle lumen | GO:0070013 |
| organelle lumen | GO:0043233 |
| nucleoplasm | GO:0005654 |
| Z disc | GO:0030018 |
| intracellular organelle | GO:0043229 |
| secretory granule lumen | GO:0034774 |
| transport vesicle | GO:0030133 |
| nuclear lumen | GO:0031981 |
| secretory vesicle | GO:0099503 |
| centrosome | GO:0005813 |
| vesicle lumen | GO:0031983 |
| cytoplasmic vesicle lumen | GO:0060205 |
| protein phosphatase type 2A complex | GO:0000159 |
| mitotic spindle pole | GO:0097431 |
| smooth endoplasmic reticulum | GO:0005790 |
| condensed chromosome, centromeric region | GO:0000779 |
| lysosome | GO:0005764 |
| integral component of endoplasmic reticu... | GO:0030176 |

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|-----------|-------|
| p=9.8E-04 | n=4 |
| p=2.7E-03 | n=4 |
| p=4.2E-03 | n=2 |
| p=5.3E-03 | n=6 |
| p=6.9E-03 | n=17 |
| p=7.2E-03 | n=7 |
| p=7.8E-03 | n=9 |
| p=1.0E-02 | n=4 |
| p=1.2E-02 | n=2 |
| p=1.2E-02 | n=2 |
| p=1.3E-02 | n=6 |
| p=1.4E-02 | n=58 |
| p=1.4E-02 | n=58 |
| p=1.4E-02 | n=58 |
| p=1.5E-02 | n=43 |
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| p=2.6E-02 | n=6 |
| p=2.7E-02 | n=12 |
| p=3.0E-02 | n=47 |
| p=3.0E-02 | n=15 |
| p=3.3E-02 | n=11 |
| p=3.4E-02 | n=6 |
| p=3.4E-02 | n=6 |
| p=3.7E-02 | n=2 |
| p=3.7E-02 | n=2 |
| p=3.9E-02 | n=3 |
| p=4.3E-02 | n=4 |
| p=4.4E-02 | n=11 |
| p=4.7E-02 | n=6 |

| | |
|---------|---------|
| fg=0.03 | bg=0.00 |
| fg=0.03 | bg=0.01 |
| fg=0.02 | bg=0.00 |
| fg=0.05 | bg=0.01 |
| fg=0.14 | bg=0.08 |
| fg=0.06 | bg=0.02 |
| fg=0.08 | bg=0.03 |
| fg=0.03 | bg=0.01 |
| fg=0.02 | bg=0.00 |
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| fg=0.05 | bg=0.02 |
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| fg=0.36 | bg=0.27 |
| fg=0.04 | bg=0.01 |
| fg=0.92 | bg=0.84 |
| fg=0.05 | bg=0.02 |
| fg=0.10 | bg=0.04 |
| fg=0.40 | bg=0.32 |
| fg=0.13 | bg=0.08 |
| fg=0.09 | bg=0.05 |
| fg=0.05 | bg=0.02 |
| fg=0.05 | bg=0.02 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.03 | bg=0.01 |
| fg=0.03 | bg=0.01 |
| fg=0.09 | bg=0.05 |
| fg=0.05 | bg=0.02 |

