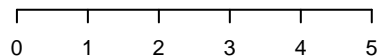


AA_permease_2	p=2.4E-01	n=3
AA_permease_C	p=2.4E-01	n=3
Ank_2	p=2.4E-01	n=4
ATP_Ca_trans_C	p=2.4E-01	n=1
Band_7	p=2.4E-01	n=2
Beta_helix	p=2.4E-01	n=1
BK_channel_a	p=2.4E-01	n=1
CaM_bdg_C0	p=2.4E-01	n=1
CDK5_activator	p=2.4E-01	n=1
CEBP_ZZ	p=2.4E-01	n=1
CG-1	p=2.4E-01	n=1
Cor1	p=2.4E-01	n=1
CSRNP_N	p=2.4E-01	n=1
Cu2_monoox_C	p=2.4E-01	n=1
Cu2_monooxygen	p=2.4E-01	n=1
Cytochrom_B561	p=2.4E-01	n=1
DBB	p=2.4E-01	n=1
DCX	p=2.4E-01	n=1
DHHC	p=2.4E-01	n=1
DUF3583	p=2.4E-01	n=1
Dynactin	p=2.4E-01	n=1
EF-hand_5	p=2.4E-01	n=2
ELM2	p=2.4E-01	n=2
ETS_PEA3_N	p=2.4E-01	n=1
Glyco_hydro_65m	p=2.4E-01	n=1
Hist_deacetyl	p=2.4E-01	n=1
HJURP_C	p=2.4E-01	n=1
HLH	p=2.4E-01	n=5
HSL_N	p=2.4E-01	n=1
HTH_Tnp_Tc5	p=2.4E-01	n=1

-log₁₀(p)

n=168/170 input genes with annotations

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fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.02	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00



fraction