

AA_kinase	p=9.1E-02	n=1
Adaptin_binding	p=9.1E-02	n=1
ADP_ribosyl_GH	p=9.1E-02	n=2
AT_hook	p=9.1E-02	n=1
Auts2	p=9.1E-02	n=1
Caprin-1_dimer	p=9.1E-02	n=1
Chromo_shadow	p=9.1E-02	n=1
Creatinase_N	p=9.1E-02	n=1
Creatinase_N_2	p=9.1E-02	n=1
CREPT	p=9.1E-02	n=1
CUPID	p=9.1E-02	n=1
Dis3l2_C_term	p=9.1E-02	n=1
DMAP1	p=9.1E-02	n=1
DUF1075	p=9.1E-02	n=1
DUF3512	p=9.1E-02	n=1
DUF3827	p=9.1E-02	n=1
DUF547	p=9.1E-02	n=1
EGF_3	p=9.1E-02	n=2
Ependymin	p=9.1E-02	n=1
F-box	p=9.1E-02	n=2
FAM72	p=9.1E-02	n=1
GCV_H	p=9.1E-02	n=1
Gp_dh_C	p=9.1E-02	n=1
Gp_dh_N	p=9.1E-02	n=1
ILEI	p=9.1E-02	n=3
KLRAQ	p=9.1E-02	n=1
Mesd	p=9.1E-02	n=1
Mgm101p	p=9.1E-02	n=1
MRP-S31	p=9.1E-02	n=1
Muted	p=9.1E-02	n=1

fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.01	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.01	bg=0.00
fg=0.00	bg=0.00
fg=0.01	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.01	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00



-log10(p)

n=263/233 input genes with annotations



fraction