

Ashwin	p=8.7E-02	n=1
ATP-synt_ab_Xtn	p=8.7E-02	n=1
Atthog	p=8.7E-02	n=2
BIRC6	p=8.7E-02	n=1
CASP_C	p=8.7E-02	n=1
CBFD_NFYB_HMF	p=8.7E-02	n=2
COQ7	p=8.7E-02	n=1
CTF_NFI	p=8.7E-02	n=1
Cu_amine_oxid	p=8.7E-02	n=1
Cu_amine_oxidN2	p=8.7E-02	n=1
DFP	p=8.7E-02	n=1
DNA_methylase	p=8.7E-02	n=1
DUF21	p=8.7E-02	n=1
DUF2370	p=8.7E-02	n=1
DUF3454	p=8.7E-02	n=1
DUF3715	p=8.7E-02	n=1
DUF4495	p=8.7E-02	n=1
DUF4611	p=8.7E-02	n=1
DUF4795	p=8.7E-02	n=1
DUF726	p=8.7E-02	n=1
DUF758	p=8.7E-02	n=1
E3_UbLigase_R4	p=8.7E-02	n=1
EF-hand_5	p=8.7E-02	n=3
ELM2	p=8.7E-02	n=2
FAM53	p=8.7E-02	n=1
FDF	p=8.7E-02	n=1
Fer4_24	p=8.7E-02	n=1
FHA_2	p=8.7E-02	n=1
Fra10Ac1	p=8.7E-02	n=1
HAND	p=8.7E-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=0.01	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
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fg=0.00	bg=0.00
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fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
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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



$-\log_{10}(p)$
n=263/233 input genes with annotations



fraction