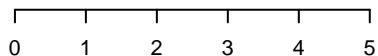


APOBEC_N	p=1.1E-01	n=1
APS_kinase	p=1.1E-01	n=1
ATP-sulfurylase	p=1.1E-01	n=1
Catalase	p=1.1E-01	n=1
Catalase-rel	p=1.1E-01	n=1
Cbl_N	p=1.1E-01	n=1
Cbl_N2	p=1.1E-01	n=1
Cbl_N3	p=1.1E-01	n=1
CCDC142	p=1.1E-01	n=1
Cluap1	p=1.1E-01	n=1
DER1	p=1.1E-01	n=1
DUF1151	p=1.1E-01	n=1
DUF1771	p=1.1E-01	n=1
DUF4419	p=1.1E-01	n=1
DUF4525	p=1.1E-01	n=1
DUF908	p=1.1E-01	n=1
DUF913	p=1.1E-01	n=1
EAF	p=1.1E-01	n=1
FA_FANCE	p=1.1E-01	n=1
FYVE	p=1.1E-01	n=3
Glyco_hydro_9	p=1.1E-01	n=1
Glyco_transf_18	p=1.1E-01	n=1
Glyco_transf_21	p=1.1E-01	n=1
Gryzun-like	p=1.1E-01	n=1
Hairy_orange	p=1.1E-01	n=1
Hrs_helical	p=1.1E-01	n=1
JAMP	p=1.1E-01	n=1
LID	p=1.1E-01	n=1
LIM_bind	p=1.1E-01	n=1
Limkain-b1	p=1.1E-01	n=1

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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



$-\log_{10}(p)$
n=234/188 input genes with annotations



fraction