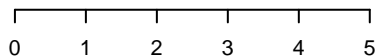


Carb_anhydrase	p=1.3E-01	n=1
CCDC154	p=1.3E-01	n=1
DSL	p=1.3E-01	n=1
DUF1387	p=1.3E-01	n=1
DUF3583	p=1.3E-01	n=1
Dynactin	p=1.3E-01	n=1
EF-hand_9	p=1.3E-01	n=1
KASH_CCD	p=1.3E-01	n=1
Lectin_C	p=1.3E-01	n=2
LRR_4	p=1.3E-01	n=1
MNNL	p=1.3E-01	n=1
MRVI1	p=1.3E-01	n=1
NPDC1	p=1.3E-01	n=1
PAE	p=1.3E-01	n=1
PDEase_I_N	p=1.3E-01	n=1
Pkinase_Tyr	p=1.3E-01	n=3
Plug_translocon	p=1.3E-01	n=1
SBF_like	p=1.3E-01	n=1
SBF2	p=1.3E-01	n=1
SecY	p=1.3E-01	n=1
Spec3	p=1.3E-01	n=1
Trefoil	p=1.3E-01	n=1
VWA	p=1.3E-01	n=2
7tm_1	p=1.7E-01	n=11
Amidase	p=1.7E-01	n=1
CAP_GLY	p=1.7E-01	n=1
FAM181	p=1.7E-01	n=1
Globin	p=1.7E-01	n=1
Inhibitor_I29	p=1.7E-01	n=1
LRR_9	p=1.7E-01	n=1

-log<sub>10</sub>(p)

n=79/81 input genes with annotations

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fg=0.02	bg=0.00
fg=0.11	bg=0.07
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fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
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fg=0.01	bg=0.00



fraction