

Unique ID	NCU	Main FunCat	Desc
B14A6_060	NCU01083.1	METABOLISM	S-adenosylmethionine decar
17E5_070	NCU03737.1	PROTEIN SYNTHESIS_S	probable translation elongati
B2O8_210	NCU01596.1	PROTEIN FATE (folding, i	probable 26s proteasome p4
B12F1_050	NCU03439.1	UNCLASSIFIED PROTEIN	conserved hypothetical prote
B11N2_080	NCU03637.1	CELL FATE_CELL TYPE	probable zinc metallo-protea
90C4_230	NCU00768.1	TRANSCRIPTION	related to polyadenylate-bind
93G11_050	NCU03766.1	SUBCELLULAR LOCALIZ	probable U6 SNRNA-ASSOC
12F11_090	NCU01328.1	ENERGY	probable TRANSKETOLASE
7F4_360	NCU06713.1	UNCLASSIFIED PROTEIN	conserved hypothetical prote
B19C19_060	NCU03395.1	CELLULAR TRANSPORT	H+-transporting ATPase, vac
9G6_070	NCU04150.1	CELL CYCLE AND DNA F	probable MAK16 protein
65E11_080	NCU01305.1	BIOGENESIS OF CELLUL	related to membrane protein
B7A16_160	NCU04164.1	UNCLASSIFIED PROTEIN	conserved hypothetical prote
B1O14_280	NCU02472.1	CELLULAR TRANSPORT	NADH dehydrogenase (ubiqui
NCU06556.1	NCU06556.1	CELL RESCUE, DEFENS	probable thioredoxin
NCU05008.1	NCU05008.1	ENERGY_METABOLISM_	NADH2 dehydrogenase (ubiq
B2J23_070	NCU02027.1	METABOLISM	related to lysophospholipase

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123A4_170	NCU01163.1	UNCLASSIFIED PROTEIN	conserved hypothetical prote
B15B10_160	NCU04770.1	SUBCELLULAR LOCALIZ	probable TRANSCRIPTION
NCU06454.1	NCU06454.1	CELL CYCLE AND DNA F	probable GTP binding protei
NCU03292.1	NCU03292.1	CELLULAR TRANSPORT	putative calcium P-type ATP;
NCU06493.1	NCU06493.1	CELLULAR COMMUNICA	G protein alpha chain
B13D15_150	NCU01981.1	PROTEIN SYNTHESIS	probable translation initiation
B14D6_540	NCU06761.1	METABOLISM	probable sphingosine-1-phos
B24N4_120	NCU08744.1	TRANSCRIPTION	related to regulatory protein (
18F11_030	NCU01213.1	CELL RESCUE, DEFENS	manganese superoxide dism
NCU10028.1	NCU10028.1	UNCLASSIFIED PROTEIN	putative protein
NCU02549.1	NCU02549.1	PROTEIN FATE (folding, i	mitochondrial processing pe
NCU08344.1	NCU08344.1	PROTEIN SYNTHESIS_S	probable ribosomal protein L
NCU06432.1	NCU06432.1	PROTEIN SYNTHESIS	probable 40S ribosomal prot
B7N14_030	NCU03565.1	PROTEIN SYNTHESIS	probable ribosomal protein L
NCU02181.1	NCU02181.1	PROTEIN SYNTHESIS	probable ribosomal protein S
B17B1_040	NCU06843.1	PROTEIN SYNTHESIS	probable 60s ribosomal prote
B21D9_030	NCU01776.1	PROTEIN SYNTHESIS_S	probable ribosomal protein L
NCU07408.1	NCU07408.1	PROTEIN SYNTHESIS_P	60S acidic ribosomal protein
B8G12_400	NCU07182.1	PROTEIN SYNTHESIS	probable 40S RIBOSOMAL F
71B5_080	NCU09345.1	METABOLISM	probable thiamine repressed
B8B20_320	NCU05430.1	ENERGY_INTERACTION	H+-transporting ATP synthas
5C2_020	NCU03151.1	CLASSIFICATION NOT Y	probable peroxisomal memb
NCU08340.1	NCU08340.1	PROTEIN ACTIVITY REG	probable ADP-ribosylation fa
B14D6_160	NCU06804.1	METABOLISM	related to phenol 2-monooxy
NCU02160.1	NCU02160.1	CELLULAR COMMUNICA	probable GTP-binding protei

<b>Cluster</b>	<b>Dictyo orthologs</b>	<b>Dictyo cluster (Xu et al., 2004)</b>
Max0.5	SLE633	I
Max1~4	SLB469	I
Min0~0.5	SLF270	I
Min0~0.5	SLH404	I
Min0~0.5	SSC506	I
Max0.5	SSH321	II
Max1~4	SSM647	II
Min0~0.5	SLA731	II
Min0~0.5	SSA242	II
Min0~0.5	SSI279	II
Max1	CMP10_A04	III
Max1	SLI236	III
Max1	SSG642	III
Max8~16	SSH882	III
Min0~0.5	SLA657	III
Min0~0.5	SSF643	III
other	SSA104	III

<b>Cluster</b>	<b>Ustilago ortholog</b>	<b>Ustilago (Zahiri et al., 2005)</b>
Max0.5	UM06048.1	11h down
Max0.5	UM02394.1	11h down
Max1	UM00295.1	11h down
Max1	UM04461.1	11h down
Max1~4	UM05123.1	11h down
Min0~0.5	UM02665.1	11h down
Min0~0.5	UM05120.1	11h down
Min0~0.5	UM06385.1	11h down
other	UM03085.1	11h down
other	UM04553.1	11h down
Max1~4	UM05993.1	11h up
Max1~4	UM00198.1	11h up
Max1~4	UM01318.1	11h up
Max1~4	UM04855.1	11h up
Max1~4	UM02714.1	11h up
Max1~4	UM03846.1	11h up
Max1~4	UM04635.1	11h up
Max1~4	UM06055.1	11h up
Max1~4	UM02515.1	11h up
Max8~16	UM00816.1	11h up
Min0~0.5	UM03191.1	11h up
Min0~0.5	UM02947.1	11h up
Min0~0.5	UM00387.1	11h up
Max1~4	UM00640.1	4h down
Min0~0.5	UM00774.1	4h up