

GO_ID	LEVEL(S)	TERM	NB_IN_REF	NB_IN_SET	P_VALUE	GENES_IN_SET
GO:0005622	4,3	intracellular	519	45	4.36E-11	Tb11.50.0007, Tb09.160.4240, Tb09.211.1750, Tb11.01.1740, Tb927.8.2540, NDHK, Tb11.02.2950, CYPA, PPK, TK, Tb927.2.4210, CAP17, eIF-5A, Tb11.02.1480, NDPK, NHP2, Tb11.02.4700, TCP-1-eta, TCP-1-gamma, Tb11.02.0290, TRYP2, TbPPK, Tb927.8.5120, Tb11.02.4440, Tb927.8.3530, Tb11.47.0004, TCP-1-beta, Tb927.3.3780, GDH, Tb11.01.1920, Tb927.8.730, RISP, TIM, Tb927.8.5260, TCP-1-alpha, Nopp44/46, Tb927.7.4170, NOP86, Tb11.01.0355, Tb09.160.3270, TCP-1-zeta, Tb927.3.5050, Tb11.02.0250, Tb927.3.1380, gim5B
GO:0044424	5,4,3	intracellular part	510	44	1.18E-10	Tb11.50.0007, Tb09.160.4240, Tb09.211.1750, Tb11.01.1740, Tb927.8.2540, NDHK, Tb11.02.2950, CYPA, PPK, TK, Tb927.2.4210, CAP17, eIF-5A, Tb11.02.1480, NDPK, NHP2, Tb11.02.4700, TCP-1-eta, TCP-1-gamma, Tb11.02.0290, TRYP2, TbPPK, Tb927.8.5120, Tb927.8.3530, Tb11.47.0004, TCP-1-beta, Tb927.3.3780, GDH, Tb11.01.1920, Tb927.8.730, RISP, TIM, Tb927.8.5260, TCP-1-alpha, Nopp44/46, Tb927.7.4170, NOP86, Tb11.01.0355, Tb09.160.3270, TCP-1-zeta, Tb927.3.5050, Tb11.02.0250, Tb927.3.1380, gim5B
GO:0005737	6,5,4	cytoplasm	301	31	7.94E-09	Tb09.211.1750, Tb11.01.1740, Tb927.8.2540, NDHK, Tb11.02.2950, CYPA, TK, eIF-5A, Tb11.02.1480, NHP2, TCP-1-eta, TCP-1-gamma, Tb11.02.0290, TRYP2, Tb927.8.5120, Tb927.8.3530, Tb11.47.0004, TCP-1-beta, Tb927.3.3780, GDH, Tb11.01.1920, RISP, Tb927.8.5260, TCP-1-alpha, Tb927.7.4170, Tb11.01.0355, Tb09.160.3270, TCP-1-zeta, Tb927.3.5050, Tb11.02.0250, Tb927.3.1380
GO:0044444	7,6,5,4	cytoplasmic part	264	28	3.26E-08	Tb09.211.1750, Tb11.01.1740, Tb927.8.2540, NDHK, Tb11.02.2950, CYPA, Tb11.02.1480, NHP2, TCP-1-eta, TCP-1-gamma, Tb11.02.0290, TRYP2, Tb927.8.5120, Tb927.8.3530, Tb11.47.0004, TCP-1-beta, GDH, Tb11.01.1920, RISP, Tb927.8.5260, TCP-1-alpha, Tb927.7.4170, Tb11.01.0355, Tb09.160.3270, TCP-1-zeta, Tb927.3.5050, Tb11.02.0250, Tb927.3.1380
GO:0005623	2	cell	763	49	2.18E-07	Tb927.6.480, Tb11.50.0007, Tb09.160.4240, Tb09.211.1750, Tb11.01.1740, Tb927.8.2540, TbNT10, NDHK, Tb11.02.2950, CYPA, Tb927.8.8300, PPK, TK, Tb927.2.4210, CAP17, eIF-5A, Tb11.02.1480, NDPK, NHP2, Tb11.02.4700, TCP-1-eta, TCP-1-gamma, Tb11.02.0290, TRYP2, TbPPK, Tb927.8.5120, Tb11.02.4440, Tb927.8.3530, Tb927.6.520, Tb11.47.0004, TCP-1-beta, Tb927.3.3780, GDH, Tb11.01.1920, Tb927.8.730, RISP, TIM, Tb927.8.5260, TCP-1-alpha, Nopp44/46, Tb927.7.4170, NOP86, Tb11.01.0355, Tb09.160.3270, TCP-1-zeta, Tb927.3.5050, Tb11.02.0250, Tb927.3.1380, gim5B

GO:0044464	3,2	cell part	763	49	2.18E-07	Tb927.6.480, Tb11.50.0007, Tb09.160.4240, Tb09.211.1750, Tb11.01.1740, Tb927.8.2540, TbNT10, NDHK, Tb11.02.2950, CYPA, Tb927.8.8300, PPDk, TK, Tb927.2.4210, CAP17, eIF-5A, Tb11.02.1480, NDPK, NHP2, Tb11.02.4700, TCP-1-eta, TCP-1-gamma, Tb11.02.0290, TRYP2, TbPfk, Tb927.8.5120, Tb11.02.4440, Tb927.8.3530, Tb927.6.520, Tb11.47.0004, TCP-1-beta, Tb927.3.3780, GDH, Tb11.01.1920, Tb927.8.730, RISP, TIM, Tb927.8.5260, TCP-1-alpha, Nopp44/46, Tb927.7.4170, NOP86, Tb11.01.0355, Tb09.160.3270, TCP-1-zeta, Tb927.3.5050, Tb11.02.0250, Tb927.3.1380, gim5B
GO:0043231	7,6,5,4	intracellular membrane-bounded organelle	270	27	2.30E-07	Tb09.160.4240, Tb09.211.1750, Tb11.01.1740, Tb927.8.2540, NDHK, Tb11.02.2950, PPDk, Tb927.2.4210, Tb11.02.1480, NDPK, Tb11.02.4700, Tb11.02.0290, TRYP2, TbPfk, Tb927.8.5120, Tb927.8.3530, Tb11.47.0004, GDH, Tb927.8.730, RISP, TIM, Nopp44/46, Tb927.7.4170, NOP86, Tb11.02.0250, Tb927.3.1380, gim5B
GO:0043227	3	membrane-bounded organelle	270	27	2.30E-07	Tb09.160.4240, Tb09.211.1750, Tb11.01.1740, Tb927.8.2540, NDHK, Tb11.02.2950, PPDk, Tb927.2.4210, Tb11.02.1480, NDPK, Tb11.02.4700, Tb11.02.0290, TRYP2, TbPfk, Tb927.8.5120, Tb927.8.3530, Tb11.47.0004, GDH, Tb927.8.730, RISP, TIM, Nopp44/46, Tb927.7.4170, NOP86, Tb11.02.0250, Tb927.3.1380, gim5B
GO:0005832	10,9,8,7,6,4	chaperonin-containing T-complex	6	5	3.75E-07	TCP-1-eta, TCP-1-gamma, TCP-1-beta, TCP-1-alpha, TCP-1-zeta
GO:0043226	2	organelle	418	34	4.81E-07	Tb11.50.0007, Tb09.160.4240, Tb09.211.1750, Tb11.01.1740, Tb927.8.2540, NDHK, Tb11.02.2950, PPDk, Tb927.2.4210, CAP17, Tb11.02.1480, NDPK, NHP2, Tb11.02.4700, Tb11.02.0290, TRYP2, TbPfk, Tb927.8.5120, Tb927.8.3530, Tb11.47.0004, GDH, Tb11.01.1920, Tb927.8.730, RISP, TIM, Tb927.8.5260, Nopp44/46, Tb927.7.4170, NOP86, Tb11.01.0355, Tb927.3.5050, Tb11.02.0250, Tb927.3.1380, gim5B
GO:0043229	6,5,4,3	intracellular organelle	418	34	4.81E-07	Tb11.50.0007, Tb09.160.4240, Tb09.211.1750, Tb11.01.1740, Tb927.8.2540, NDHK, Tb11.02.2950, PPDk, Tb927.2.4210, CAP17, Tb11.02.1480, NDPK, NHP2, Tb11.02.4700, Tb11.02.0290, TRYP2, TbPfk, Tb927.8.5120, Tb927.8.3530, Tb11.47.0004, GDH, Tb11.01.1920, Tb927.8.730, RISP, TIM, Tb927.8.5260, Nopp44/46, Tb927.7.4170, NOP86, Tb11.01.0355, Tb927.3.5050, Tb11.02.0250, Tb927.3.1380, gim5B
GO:0006082	4	organic acid metabolic process	57	12	1.12E-06	Tb11.01.1740, Tb927.2.4210, Tb927.7.4970, Tb927.8.6060, Tb11.47.0004, GDH, Tb09.211.3330, Tb927.7.3620, Tb927.5.1090, Tb927.7.4170, Tb927.7.4390, Tb11.02.3120
GO:0019752	5	carboxylic acid metabolic process	57	12	1.12E-06	Tb11.01.1740, Tb927.2.4210, Tb927.7.4970, Tb927.8.6060, Tb11.47.0004, GDH, Tb09.211.3330, Tb927.7.3620, Tb927.5.1090, Tb927.7.4170, Tb927.7.4390, Tb11.02.3120
GO:0051726	5,4	regulation of cell cycle	11	6	1.37E-06	Tb11.02.4700, TCP-1-eta, TCP-1-gamma, TCP-1-beta, TCP-1-alpha, TCP-1-zeta
GO:0006520	5,6	cellular amino acid metabolic process	35	9	4.82E-06	Tb11.01.1740, Tb927.7.4970, Tb927.8.6060, Tb11.47.0004, GDH, Tb09.211.3330, Tb927.7.3620, Tb927.5.1090, Tb927.7.4390
GO:0020015	8,7,6,5	glycosome	15	6	8.24E-06	PPDK, Tb927.2.4210, TbPfk, Tb927.8.3530, TIM, gim5B

GO:0009987	2	cellular process	975	57	8.52E-06	Tb11.01.3110, Tb11.50.0007, Tb09.211.0930, Tb09.160.4240, Tb11.01.1740, DRBD3, NDHK, CYPA, PPDK, TK, Tb927.2.4210, Tb11.01.1290, Tb927.7.4970, Tb927.8.5600, CAP17, Tb927.8.6440, Tb11.03.0090, eIF-5A, NDPK, NHP2, Tb927.8.6060, Tb11.02.4700, TCP-1-eta, TCP-1-gamma, Tb927.8.5120, Tb09.211.0050, ZFP2, Tb09.211.2150, Tb927.8.3530, Tb11.47.0004, Tb09.211.3510, TCP-1-beta, Tb927.3.3780, GDH, Tb11.01.1920, Tb09.211.3330, Tb927.8.730, Tb927.7.3620, RISP, Tb927.5.1090, TIM, Tb927.8.5260, TCP-1-alpha, Nopp44/46, Tb927.7.4170, rtb2, NOP86, UBP1, Tb927.7.4390, Tb11.02.1120, Tb11.02.3120, Tb11.01.0355, Tb927.8.6650, TCP-1-zeta, Tb927.3.5050, Tb927.5.1000, Tb11.02.0250
GO:0015980	5	energy derivation by oxidation of organic com	10	5	1.97E-05	Tb11.01.1740, NDHK, Tb927.8.5120, Tb11.47.0004, RISP
GO:0045333	6	cellular respiration	10	5	1.97E-05	Tb11.01.1740, NDHK, Tb927.8.5120, Tb11.47.0004, RISP
GO:0006519	4	cellular amino acid and derivative metabolic p	42	9	2.35E-05	Tb11.01.1740, Tb927.7.4970, Tb927.8.6060, Tb11.47.0004, GDH, Tb09.211.3330, Tb927.7.3620, Tb927.5.1090, Tb927.7.4390
GO:0009308	5	cellular amine metabolic process	42	9	2.35E-05	Tb11.01.1740, Tb927.7.4970, Tb927.8.6060, Tb11.47.0004, GDH, Tb09.211.3330, Tb927.7.3620, Tb927.5.1090, Tb927.7.4390
GO:0044237	3	cellular metabolic process	792	49	2.43E-05	Tb11.01.3110, Tb09.211.0930, Tb11.01.1740, DRBD3, NDHK, CYPA, PPDK, TK, Tb927.2.4210, Tb927.7.4970, Tb927.8.5600, Tb927.8.6440, Tb11.03.0090, eIF-5A, NDPK, NHP2, Tb927.8.6060, TCP-1-eta, TCP-1-gamma, Tb927.8.5120, Tb09.211.0050, Tb09.211.2150, Tb927.8.3530, Tb11.47.0004, Tb09.211.3510, TCP-1-beta, Tb927.3.3780, GDH, Tb11.01.1920, Tb09.211.3330, Tb927.8.730, Tb927.7.3620, RISP, Tb927.5.1090, TIM, Tb927.8.5260, TCP-1-alpha, Nopp44/46, Tb927.7.4170, UBP1, Tb927.7.4390, Tb11.02.1120, Tb11.02.3120, Tb11.01.0355, Tb927.8.6650, TCP-1-zeta, Tb927.3.5050, Tb927.5.1000, Tb11.02.0250
GO:0034641	4	cellular nitrogen compound metabolic process	43	9	2.87E-05	Tb11.01.1740, Tb927.7.4970, Tb927.8.6060, Tb11.47.0004, GDH, Tb09.211.3330, Tb927.7.3620, Tb927.5.1090, Tb927.7.4390
GO:0006807	3	nitrogen compound metabolic process	43	9	2.87E-05	Tb11.01.1740, Tb927.7.4970, Tb927.8.6060, Tb11.47.0004, GDH, Tb09.211.3330, Tb927.7.3620, Tb927.5.1090, Tb927.7.4390
GO:0009066	6,7	aspartate family amino acid metabolic process	6	4	3.43E-05	Tb11.01.1740, Tb927.8.6060, Tb11.47.0004, Tb927.7.4390
GO:0005739	8,7,6,5	mitochondrion	114	14	3.73E-05	Tb09.211.1750, Tb11.01.1740, Tb927.8.2540, NDHK, Tb11.02.2950, Tb11.02.1480, Tb11.02.0290, TRYP2, Tb927.8.5120, Tb11.47.0004, GDH, RISP, Tb11.02.0250, Tb927.3.1380
GO:0016491	3	oxidoreductase activity	81	12	5.09E-05	Tb11.02.2310, Tb11.01.1740, COXIV, NDHK, TRYP2, Tb927.8.3530, Tb11.47.0004, Tb927.3.3780, GDH, Tb927.7.210, RISP, Tb11.02.3120

GO:0008152	2	metabolic process	890	52	5.64E-05	Tb11.01.3110, Tb09.211.0930, Tb11.01.1740, DRBD3, NDHK, CYPA, PPDK, TK, Tb927.2.4210, Tb927.7.4970, Tb927.8.5600, Tb927.8.6440, Tb11.03.0090, eIF-5A, Tb11.02.1480, NDPK, NHP2, Tb927.8.6060, TCP-1-eta, TCP-1-gamma, Tb11.02.0290, Tb927.8.5120, Tb09.211.0050, Tb11.02.4440, Tb09.211.2150, Tb927.8.3530, Tb11.47.0004, Tb09.211.3510, TCP-1-beta, Tb927.3.3780, GDH, Tb11.01.1920, Tb09.211.3330, Tb927.8.730, Tb927.7.3620, RISP, Tb927.5.1090, TIM, Tb927.8.5260, TCP-1-alpha, Nopp44/46, Tb927.7.4170, UBP1, Tb927.7.4390, Tb11.02.1120, Tb11.02.3120, Tb11.01.0355, Tb927.8.6650, TCP-1-zeta, Tb927.3.5050, Tb927.5.1000, Tb11.02.0250
GO:0009068	7,8	aspartate family amino acid catabolic process	3	3	6.36E-05	Tb11.01.1740, Tb927.8.6060, Tb11.47.0004
GO:0005829	8,7,6,5	cytosol	30	7	7.11E-05	CYPA, TCP-1-eta, TCP-1-gamma, TCP-1-beta, TCP-1-alpha, Tb09.160.3270, TCP-1-zeta
GO:0007049	3	cell cycle	29	7	9.08E-05	Tb11.02.4700, TCP-1-eta, TCP-1-gamma, TCP-1-beta, TCP-1-alpha, NOP86, TCP-1-zeta
GO:0015078	9	hydrogen ion transmembrane transporter activity	8	4	1.51E-04	COXIV, Tb11.02.2950, RISP, Tb927.3.1380
GO:0015077	8	monovalent inorganic cation transmembrane transporter activity	8	4	1.51E-04	COXIV, Tb11.02.2950, RISP, Tb927.3.1380
GO:0006091	4	generation of precursor metabolites and energy	24	6	2.42E-04	Tb11.01.1740, NDHK, Tb927.8.5120, Tb11.47.0004, RISP, TIM
GO:0009060	7	aerobic respiration	9	4	2.56E-04	Tb11.01.1740, Tb927.8.5120, Tb11.47.0004, RISP
GO:0050794	4,3	regulation of cellular process	59	9	3.53E-04	Tb09.211.0930, Tb11.01.1290, Tb11.02.4700, TCP-1-eta, TCP-1-gamma, TCP-1-beta, TCP-1-alpha, rtb2, TCP-1-zeta
GO:0050789	3,2	regulation of biological process	61	9	4.52E-04	Tb09.211.0930, Tb11.01.1290, Tb11.02.4700, TCP-1-eta, TCP-1-gamma, TCP-1-beta, TCP-1-alpha, rtb2, TCP-1-zeta
GO:0022890	7	inorganic cation transmembrane transporter activity	11	4	6.34E-04	COXIV, Tb11.02.2950, RISP, Tb927.3.1380
GO:0006066	4	cellular alcohol metabolic process	31	6	1.01E-03	TK, Tb927.2.4210, Tb927.8.5600, Tb11.03.0090, Tb927.8.3530, TIM
GO:0005753	12,11,10,13,9,8,7,6,5	mitochondrial proton-transporting ATP synthase complex	2	2	1.39E-03	Tb11.02.2950, Tb927.3.1380
GO:0045252	6,5,4	oxoglutarate dehydrogenase complex	2	2	1.39E-03	Tb11.01.1740, Tb11.47.0004
GO:0045259	6,5,7,4	proton-transporting ATP synthase complex	2	2	1.39E-03	Tb11.02.2950, Tb927.3.1380
GO:0005996	5,6	monosaccharide metabolic process	23	5	1.59E-03	TK, Tb927.2.4210, Tb927.8.5600, Tb11.03.0090, TIM
GO:0006554	8,9	lysine catabolic process	2	2	1.61E-03	Tb11.01.1740, Tb11.47.0004
GO:0009072	6,5,7	aromatic amino acid family metabolic process	2	2	1.61E-03	Tb11.01.1740, Tb11.47.0004
GO:0006568	8,7,6	tryptophan metabolic process	2	2	1.61E-03	Tb11.01.1740, Tb11.47.0004
GO:0006566	7,8	threonine metabolic process	2	2	1.61E-03	Tb927.8.6060, Tb927.7.4390
GO:0006553	7,8	lysine metabolic process	2	2	1.61E-03	Tb11.01.1740, Tb11.47.0004
GO:0006586	7	indolalkylamine metabolic process	2	2	1.61E-03	Tb11.01.1740, Tb11.47.0004
GO:0042434	6	indole derivative metabolic process	2	2	1.61E-03	Tb11.01.1740, Tb11.47.0004
GO:0042430	5	indole and derivative metabolic process	2	2	1.61E-03	Tb11.01.1740, Tb11.47.0004
GO:0019200	6	carbohydrate kinase activity	2	2	1.63E-03	Tb11.03.0090, TbPfk
GO:0004591	6	oxoglutarate dehydrogenase (succinyl-transferase) activity	2	2	1.63E-03	Tb11.01.1740, Tb11.47.0004
GO:0016624	5	oxidoreductase activity, acting on the aldehyde or ketone group, NAD(P)+ as acceptor	2	2	1.63E-03	Tb11.01.1740, Tb11.47.0004
GO:0016744	4	transferase activity, transferring aldehyde or ketone group	2	2	1.63E-03	TK, Tb927.8.5600
GO:0003727	5	single-stranded RNA binding	2	2	1.63E-03	Tb09.211.0930, Tb09.211.2150
GO:0008143	6,7	poly(A) RNA binding	2	2	1.63E-03	Tb09.211.0930, Tb09.211.2150
GO:0070717	6	poly-purine tract binding	2	2	1.63E-03	Tb09.211.0930, Tb09.211.2150
GO:0044445	9,8,7,6,5	cytosolic part	25	5	1.68E-03	TCP-1-eta, TCP-1-gamma, TCP-1-beta, TCP-1-alpha, TCP-1-zeta

GO:0044238	3	primary metabolic process	797	44	1.82E-03	Tb11.01.3110, Tb09.211.0930, Tb11.01.1740, DRBD3, CYPA, TK, Tb927.2.4210, Tb927.7.4970, Tb927.8.5600, Tb927.8.6440, Tb11.03.0090, eIF-5A, Tb11.02.1480, NDPK, NHP2, Tb927.8.6060, TCP-1-eta, TCP-1-gamma, Tb09.211.0050, Tb11.02.4440, Tb09.211.2150, Tb11.47.0004, Tb09.211.3510, TCP-1-beta, GDH, Tb11.01.1920, Tb09.211.3330, Tb927.8.730, Tb927.7.3620, Tb927.5.1090, TIM, Tb927.8.5260, TCP-1-alpha, Nopp44/46, Tb927.7.4170, UBP1, Tb927.7.4390, Tb11.02.1120, Tb11.01.0355, Tb927.8.6650, TCP-1-zeta, Tb927.3.5050, Tb927.5.1000, Tb11.02.0250
GO:0009063	6,7	cellular amino acid catabolic process	7	3	1.90E-03	Tb11.01.1740, Tb927.8.6060, Tb11.47.0004
GO:0031090	5,4,3	organelle membrane	40	6	2.61E-03	Tb09.211.1750, Tb11.02.2950, Tb927.2.4210, Tb927.7.4170, Tb927.3.1380, gim5B
GO:0065007	2	biological regulation	79	9	2.73E-03	Tb09.211.0930, Tb11.01.1290, Tb11.02.4700, TCP-1-eta, TCP-1-gamma, TCP-1-beta, TCP-1-alpha, rtb2, TCP-1-zeta
GO:0006732	5	coenzyme metabolic process	16	4	2.81E-03	Tb11.01.1740, TK, Tb927.8.5600, Tb11.47.0004
GO:0009310	6	amine catabolic process	8	3	2.92E-03	Tb11.01.1740, Tb927.8.6060, Tb11.47.0004
GO:0044270	5	nitrogen compound catabolic process	8	3	2.92E-03	Tb11.01.1740, Tb927.8.6060, Tb11.47.0004
GO:0006006	7,8	glucose metabolic process	17	4	3.53E-03	TK, Tb927.2.4210, Tb927.8.5600, TIM
GO:0044262	4,5	cellular carbohydrate metabolic process	28	5	3.81E-03	TK, Tb927.2.4210, Tb927.8.5600, Tb11.03.0090, TIM
GO:0044455	11,10,9,12,8,7,6,5,4	mitochondrial membrane part	3	2	4.02E-03	Tb11.02.2950, Tb927.3.1380
GO:0051186	4	cofactor metabolic process	18	4	4.36E-03	Tb11.01.1740, TK, Tb927.8.5600, Tb11.47.0004
GO:0008324	6	cation transmembrane transporter activity	18	4	4.46E-03	COXIV, Tb11.02.2950, RISP, Tb927.3.1380
GO:0016903	4	oxidoreductase activity, acting on the aldehyd	3	2	4.70E-03	Tb11.01.1740, Tb11.47.0004
GO:0005730	11,10,8,9,7,6,5	nucleolus	10	3	4.72E-03	Tb927.8.730, Nopp44/46, NOP86
GO:0006753	6	nucleoside phosphate metabolic process	20	4	6.39E-03	TK, Tb927.8.5600, NDPK, Tb11.02.1120
GO:0009117	7	nucleotide metabolic process	20	4	6.39E-03	TK, Tb927.8.5600, NDPK, Tb11.02.1120
GO:0032991	2	macromolecular complex	257	17	6.39E-03	Tb11.50.0007, Tb11.01.1740, Tb11.02.2950, NHP2, TCP-1-eta, TCP-1-gamma, Tb927.8.3530, Tb11.47.0004, TCP-1-beta, Tb11.01.1920, RISP, Tb927.8.5260, TCP-1-alpha, Tb11.01.0355, TCP-1-zeta, Tb927.3.5050, Tb927.3.1380
GO:0006457	7,6	protein folding	75	8	6.66E-03	Tb11.01.3110, CYPA, TCP-1-eta, TCP-1-gamma, TCP-1-beta, TCP-1-alpha, TCP-1-zeta, Tb11.02.0250
GO:0005975	4	carbohydrate metabolic process	32	5	6.68E-03	TK, Tb927.2.4210, Tb927.8.5600, Tb11.03.0090, TIM
GO:0016874	3	ligase activity	45	6	6.70E-03	Tb927.7.4970, Tb09.211.0050, Tb927.7.3620, Tb927.5.1090, Tb11.02.1120, Tb927.5.1000
GO:0003824	2	catalytic activity	778	41	8.21E-03	Tb11.50.0007, Tb11.02.2310, Tb11.01.1740, Tb927.8.2540, COXIV, NDHK, Tb11.02.2950, CYPA, PPDk, TK, Tb927.2.4210, Tb927.7.4970, Tb927.8.5600, Tb11.03.0090, NDPK, Tb927.8.6060, Tb11.02.0290, TRYP2, TbPfk, Tb09.211.0050, Tb11.02.4440, AK_Tb09.160.4560, Tb927.8.3530, Tb11.47.0004, Tb09.211.3510, Tb927.3.3780, GDH, Tb09.211.3330, Tb927.7.210, Tb927.7.3620, RISP, Tb927.5.1090, TIM, Tb927.7.4170, rtb2, Tb927.7.4390, Tb11.02.1120, Tb11.02.3120, Tb09.160.3270, Tb927.5.1000, Tb11.02.0250
GO:0003723	4	RNA binding	95	9	8.80E-03	Tb09.211.0930, DRBD3, Tb927.8.6440, Tb09.211.2150, Tb927.8.730, Nopp44/46, UBP1, Tb927.8.6650, Tb09.160.3270
GO:0019318	6,7	hexose metabolic process	22	4	8.91E-03	TK, Tb927.2.4210, Tb927.8.5600, TIM
GO:0003729	5	mRNA binding	4	2	9.03E-03	Tb09.211.0930, Tb09.211.2150