Electronic Supplementary Material (ESI) for Environmental Science: Nano.

Supporting information

Metabonomics-Assisted Label-Free Quantitative Proteomics and Transcriptome Analysis Reveals Novel Insights into Antifungal Effect of Graphene Oxide for controlling *Fusarium graminearum*

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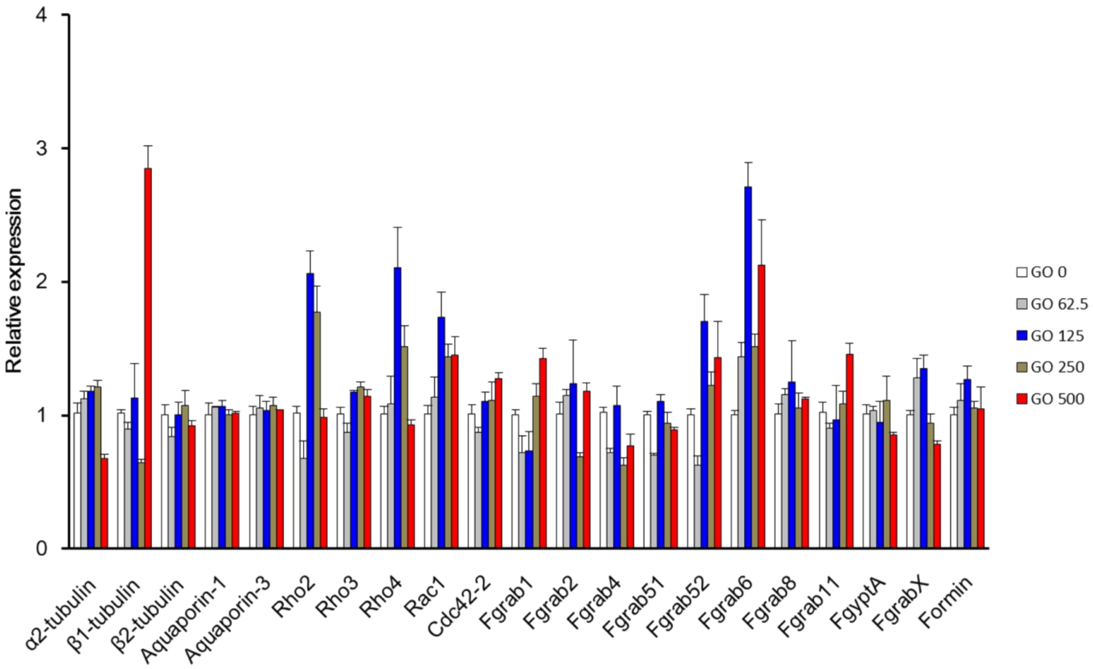


Figure S1. qRT-PCR validation of expression profiles of 22 genes associated with mycelial growth and cell wall development of FG strains PH-1 after treatment with different GO concentrations.

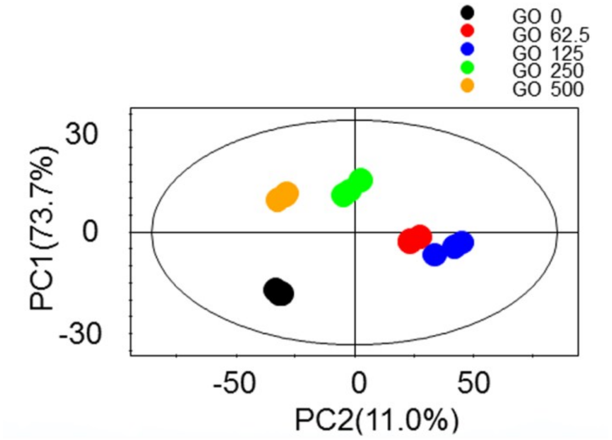
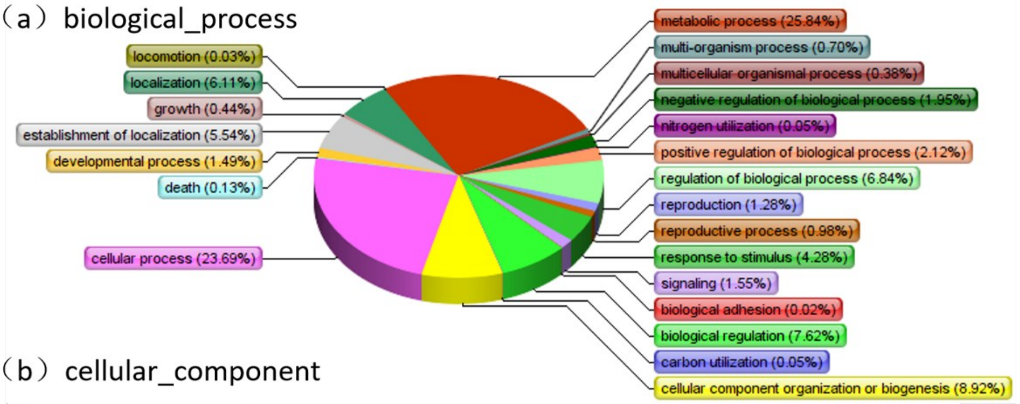
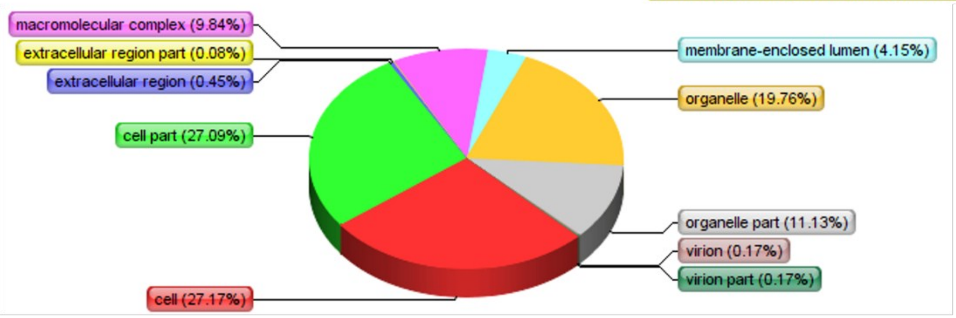


Figure S2. Scores plot from the PCA for the proteins of FG strains PH-1 treated with GO with 0 μg mL^{-1} (●), 62.5 μg mL^{-1} (●), 125 μg mL^{-1} (●), 250 μg mL^{-1} (●), 500 μg mL^{-1} (●). n=3.

（a）biological_process



（b）cellular_component



（c）molecular_function

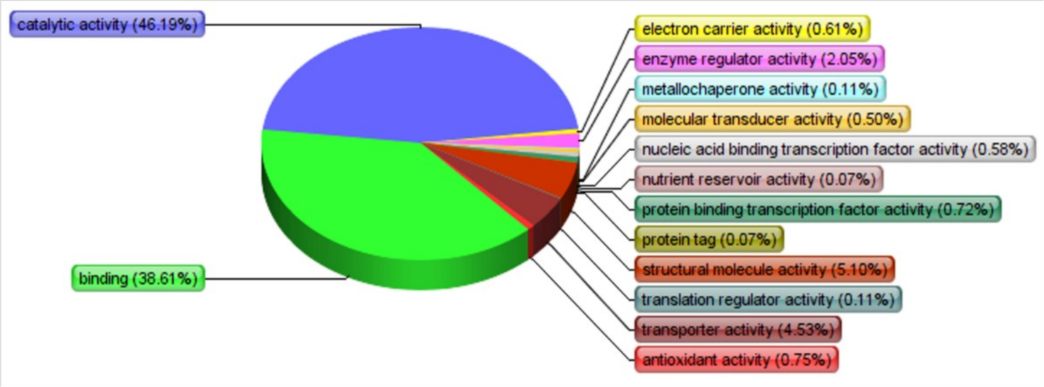


Figure S3. Gene ontology annotation class classification pie chart.

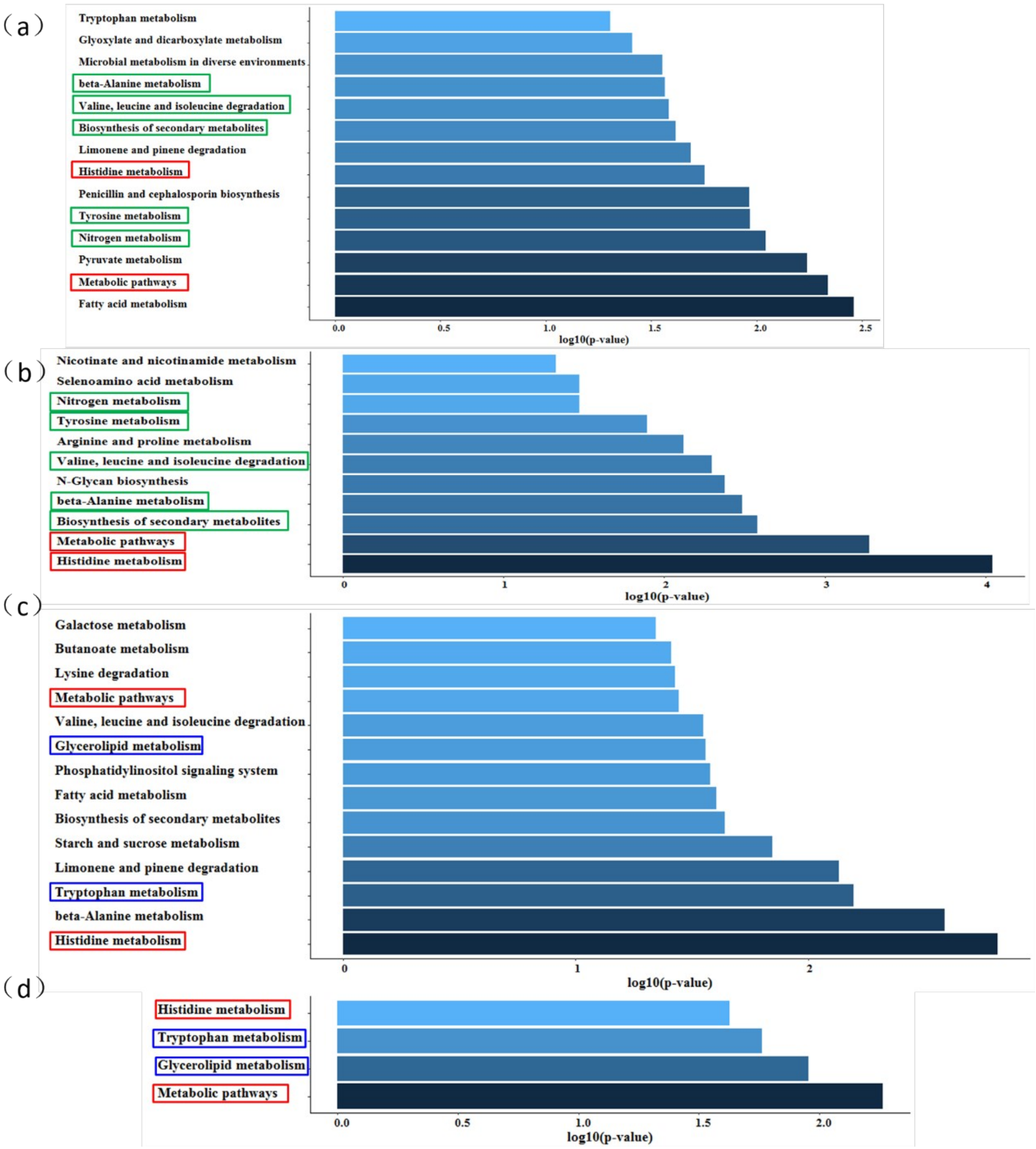


Figure S4. Pathway enrichment analysis of differential proteins. (a)-(d) represent in the 62.5/0, 125/0, 250/0 and 500/0 comparison groups, respectively. The red box indicates the pathways in all four control groups, the blue box indicates the pathways shared in 250/0 and 500/0 comparison groups, and the green box indicates the pathways shared by 125/0 and 62.5/0 comparison groups.

Table S1. T_1 Values for the protons of some selected metabolites (Unit: s).

Metabolites	δ(ppm)	T_1 Values	
		Mean	SD
TSP	0	3.36	0.02
isoleucine	1.01 (d)	1.05	0.01
valine	1.04 (d)	1.14	0.01
threonine	1.33 (d)	0.82	0.04
alanine	1.48 (d)	1.62	0.01
glutamate	2.34 (t)	1.31	0.05
pyruvate	2.37 (s)	1.45	0.06
glutamine	2.45 (m)	1.31	0.07
citrate	2.55 (d)	0.17	0.02
methionine	2.65 (t)	1.34	0.07
aspartate	2.80 (dd)	1.31	0.07
asparagine	2.87(dd)	1.41	0.02
γ-aminobutyrate	3.01 (t)	1.03	0.01
malonate	3.12 (s)	1.58	0.01
choline	3.20 (s)	2.35	0.01
betaine	3.26 (s)	1.51	0.02
syllo-inositol	3.30 (s)	3.31	0.02
glycine	3.57 (s)	2.38	0.01
β-glucose	4.65 (d)	1.36	0.04
trehalose	5.19 (d)	1.15	0.01
α-glucose	5.24(d)	1.95	0.02
sucrose	5.42 (d)	0.79	0.08
uridine	5.90 (d)	3.55	0.03
fumarate	6.52 (s)	8.62	0.07
tyrosine	6.90 (d)	2.57	0.02
histidine	7.09 (s)	1.70	0.02
phenylalanine	7.33 (m)	2.43	0.02
tryptophan	7.74 (d)	4.37	0.14
guanine	8.01 (s)	1.98	0.03
hypoxanthine	8.22 (s)	2.73	0.04
adenosine	8.35 (s)	3.61	0.06

Table S2. Gene expression levels of 35 predicted genes sequences by qRT-PCR.

Description	Sequence (F: Forward, 5'-3'; R: Reverse，5'-3')	Lotus tag
Actin	F:CGATTCCGTGCTCCTGAG R:ATGTTTCCGTAGAGATCCTTTC	FG07335.1
α1-tubulin	F:CCAACAAGAGCGAGCACGAGAGC R:TTGAGGGAGGCGATAGCGGCATT	FG00397.1
α2-tubulin	F:AGGACCCCGACCAGGGATTTAGC R:CGACGGTGTAGTGACCACGAGCA	FG00639.1
β1-tubulin	F:GACCGTATGATGGCAACTTT R:AACGGAGACAGGTAGTGACG	FG09530.1
β2-tubulin	F:TCCAAACTTCCGTCTGTTCCGTG R:TCGGCGTCTTGGTATTGCTGGTA	FG06611.1
Aquaporin-1	F:CTGGCCCTTTTCGTCGCACTTAT R:TGTCCAGGGTTTGCTTCCTCGTA	FG03680.1
Aquaporin-2	F:AGCACCCATCTTGCCCCCAT R:CCGAAAGCCAGGAGAGAACCC	FG00811.1
Aquaporin-3	F:CTCAACGGCTTCAACATCACCAC R:GCAAAGGCAAAGAAAAGGAACATAG	FG10816.1
RAS2	F:GGACACCGCTGGACAGGAAGAGT R:GGGTTTGCCGAGGAGATAGGAGA	FG10114.1
MAP1 (motigen-activated protein kinase)	F:ACATTCAGAAGCCCCGAAGTTAC R:GCGTTGAGGAGGAGGTTGGA	AF448230
Septin	F:CCAACCAATGGCACCGAAAG R:GACGAACACCAGCCTCCTCAAT	FG05315.1
Formins	F:AGAAAATGAACCAGCTTCGCCTG R:TTCCGTGCTGCTGTCCCTCG	FG07443.1
Pod1	F:ATGTGACTGGGAATGTCCTGGTT R:GCTGTGTCGTCGGTTTGGGTT	FG10787.1
Pod2	F:CGGTATCTACTGTGTCGCCCTCG R:CCATCCTTATCATCATCGTCATTGCT	FG06483.1
1,3-glucan synthase	F:CCCAATCTCTGTCCACACCTATC R:TGTTCTTCTCGTCCTTGTCGTTT	FG07946.1
VeA	F:TAACAATGCTGGAAACAACGGC R:GACCAGATGACTCGCCAAAAGC	JN635273.1
Myo2	F:CTGCCCTTTGCCCCACTCTC R:CCTTGTTGGCGTCGTAGCCG	FG09719.1
Rho1	F:CCTATTAGCCTTGGCCTCTGGGA R:CCGACGAGAATGATGGGGATGTT	FG08857.1
Rho2	F:ATGGCGGTTGTCGCTACTATCA R:CGCAGTCGGTCGTAATCTTCTTG	FG05447.1
Rho3	F:CTGCTTCGCCGTTGACTCTCC R:CGGGCTTCTGGCTGGTCTTT	FG04400.1
Rho4	F:CTGGTCATTATCGGTGATGGTGC R:GGTCGTAATCGCTCGTAGTCTTCC	FG04068.1
Rac1	F:GTAGCCCTCAAGTGCGACCTCC R:GCCTCGTTGACGCCCCTGTT	FG00170.1
Cdc42-1	F:TTCTACACTTCTGCCCATACACTCC R:CGCCTCGCATCTCCTTACTACTG	FG00304.1
Cdc42-2	F:ATGGCGGTTGTCGCTACTATCA R:CGCAGTCGGTCGTAATCTTCTTG	FG05447.1
Rho1-GTPase	F:AAAGAGGGCAAGGACAAGAAGTATG	FG08568.1

	R:GAACCAGTTGGGGTCAGGGAT	
FgRab1	F:CCGAACGATAGAACTCGATGGC R:CGAACTCCTTGGCTACGCTG	FG10873.1
FgRab2	F:GGCAAGTCCAGTCTCACCATTCG R:GGGGTTCAGGGAGCCCATCT	FG01534.1
FgRab4	F:TAGCATCCCCGAACCTTAGCC R:GCTCTTGTGACTTCTCTGCCCTCT	FG00808.1
FgRab51	F:GATTCCACCAACGCCCCCAA R:AGGAGCCAGCGAGGCAAAAC	FG05501.1
FgRab52	F:AGTCCACTATCGGTGCTGCTTTC R:GGCTGCTCGGTGACCAAATC	FG11808.1
FgRab6	F:TCTGATTCCATCCTATATCCGTGA R:TCTTAGCCTCTTCCTCGCCC	FG02479.1
FgRab7	F:AGAAGTTCAGTGCGAGCTACAAGG R:CAAATGGGAAGTTGGGAGGG	FG05141.1
FgRab8	F:GGCAACAAGTGCGACTGGGA R:GCAGGTTGGTCGTTCTTGGAGT	FG06209.1
FgRab11	F:CGGAAAGTCCAACCTTCTCAGTCG R:GCGTGATCTCGCAGCTCCTTG	FG04327.1
FgyptA	F:AATCTTCCCCACGATGTTGTTCTC R:GATGTGGTAGGGAGTTGCTGTCG	FG09550.1
FgrabX	F:CCGTGCCTCTGTGAACTACTACC R:TTCCTCAGTCCTAACAGCCCTC	FG07573.1
UspA1 (universal stress protein A1)	F:ATGGCGACGCTAACCGAGAC R:CGCGCACGCATACAACTTCG	FG02572.1
UspA2 (universal stress protein A2)	F:CGCGCAACCAACCCATGAGC R:CTTCGGACTCTGGGTGGAGG	FG08418.1
Sim (stress-induced morphogen)	F:TGCTCCTCTACGCACCCTCC R:CTGGACGAGCAGTTCGGTAG	FG06577.1

Table S3 Inhibitory activity of GO and fungicide on the mycelial biomass of F. graminearum strain PH-1.

Treatment	Linear regression equation	IC_{50} (μg mL^{-1})(95% CL)	Correlation coefficient
GO	y=3.88+1.65x	4.82 (3.53-6.58)	0.97
Carbendazol	y=3.69+1.64x	6.25 (4.94-7.90)	0.98
Mancozeb	y=3.46+1.46x	11.37 (8.64-14.96)	0.98

Table S4 Homology searches, domain predictions

22 common elements in "62.5/0", "125/0", "250/0" and "500/0":

Protein Index	Protein ID	Samesets	Descrption	ProtSeq	Pfam Domain prediction results	Number of domain predictions	The best match result obtained by NR database comparison
161	tr|I1RJK0|I1RJK0_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG04022.1 PE=4 SV=1	MKLLSLSLAAGLIVNQGASAKPSPQDEPLFSYNANLLPLEKNVGSSDLFPMADCNGFKLEEATFTQMQNAMKAGKLTSVQLVTCYLIRTYQTEEYTNSIMQINPDAFAIAAERDAERAKGKVRGPLHGIPFTVKDNIGTKDSLETTAGSWALLGNVVPRDAHVVKKLRDAGAVLFGKAALSEWADMRSNDYSEGYSARGGQVRSAYNFTINPGGSSTGSAVGVGANAIAFSLGTETDGSVINPANRNALVGIKPTVGLTSRAGVIPESEHQDSVGTFARTVRDATLVLDAIYGLDERDNYTSAQKDKTPKGGYAQYLSKKKALKGATFGLPWKSFWVHADEDMQSQLLELVDLIKSAGATIINGTEITNYETIVSPDGWNWDYGSTRGFPNESEYTYIKVDFYRNIETYLSEVENTSVRNLEDIVEFNKKYDGTEGGYPYKNGKGHPAFASGQDGFLASLETKGERDETYWQALDFCQSSTRKGINDALSYKGKKLSGLLVPPQVAQAPQIAAQAGYPVITIPGGYSKESGMPFGLGIMQTAWAESELIKWASAIEDLQHSTDAPSKRRLPKWLGYLERNVPVPF	81-375,PF01425.21,Amidase,;	1	ref|XP_011321633.1| hypothetical protein FGSG_04022 [Fusarium graminearum PH-1] >gb|ESU09134.1| hypothetical protein FGSG_04022 [Fusarium graminearum PH-1] >emb|CEF78941.1| unnamed protein product [Fusarium graminearum]
313	tr|I1RAM3|I1RAM3_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG00555.1 PE=4 SV=1	MLTIEETRALGDAHPEFEPVIRAHNPMLNGWDMNTDLDGFREMMAQLRQFQPKPDPETLSYQMQDFKIPLRDGFEVNARSYTPKDDVPSDGRPGLIIFHGGGFVTGDLETEAGLCAQFTKLGGVALNVDYRHAPEHVFPQAINDAFDATVWASQNGDRFGINPSKGFIIGGTSSGADISLAVSHLYRDNKNDPPLTGVYAPITSGVSDQTVPEKYRDHFISFEQCAKAPVFSTESIKFIHSKYKPDMKSPLAFPVAFPSHAGLPKTYFQACGMDPLRDCSIVLEQVYKDEGVPTKIDIYPGLPHAFWAMFPELEISQKRERDAAEGLKWLLAG	95-307,PF07859.13,Abhydrolase_3,CL0028;	1	ref|XP_011316236.1| hypothetical protein FGSG_00555 [Fusarium graminearum PH-1] >gb|ESU05751.1| hypothetical protein FGSG_00555 [Fusarium graminearum PH-1] >gb|EYB22384.1| hypothetical protein FG05_00555 [Fusarium graminearum] >gb|PCD18429.1| hypothetical protein FGRA07_07066 [Fusarium graminearum] >emb|CEF72508.1| unnamed protein product [Fusarium graminearum]
566	tr|A0A1C3YJ47|A0A1C3YJ47_GIBZE	tr|I1S0L7|I1S0L7_GIBZE	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FGRAMPH1_01T07647 PE=4 SV=1	MRTVLCRLALTARTFTSSSSSPTPLSLLQRTARNMSSATAPVLKQRVKLSLIQLASGSDKKANLDSAASHVARVASSGAKIVVLPECFNSPYGTDHFPQYAETLLPSPPSKDDAPSYHALSSMAVDNKVYLIGGSIPEYSPDTKKYYNTTLIFGPDGSLLGTHRKVHLFDIDIPGKITFRESDILSPGNKVTLVDLPEYGKIAVAICYDVRFPELATIAARKGAFALIYPGAFNTTTGPLHWQLLGRARAADNQLYVALCSPARAETGYPAYGHSLVADPMAQVQVEADEKETTVDWELDPEKITEARKAIPLNTQRRFDVYPDVSEGKVQFEES	49-309,PF00795.22,CN_hydrolase,;	1	gb|EYB28764.1| hypothetical protein FG05_10250 [Fusarium graminearum] >gb|PCD18786.1| nitrilase[Fusarium graminearum] >emb|SCB64584.1| unnamed protein product [Fusarium graminearum]
649	tr|I1S2I0|I1S2I0_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG10974.1 PE=4 SV=1	MSYTLYDAAILHTKEALQSLSAILKKASTHANASSFPEAKLAPDMLDLNFQVFFMTDLSQKLVARTTGVEPLTLSRDDCTNFEQYQARIAQVLEIVEKADKATVDKRADEIVTIGLGPGKSADMKSRDFVQGFAIPNIFFHLTTAYAILRKEGVEIGKQDFLGPFIGQYLQ	5-162,PF09351.10,DUF1993,CL0310;	1	ref|XP_011325398.1| hypothetical protein FGSG_10974 [Fusarium graminearum PH-1] >gb|ESU17776.1| hypothetical protein FGSG_10974 [Fusarium graminearum PH-1] >gb|EYB28963.1| hypothetical protein FG05_10974 [Fusarium graminearum] >gb|PCD36728.1| hypothetical protein FGRA07_07732 [Fusarium graminearum] >emb|CEF86777.1| unnamed protein product [Fusarium graminearum]
684	tr|I1REZ6|I	--	Uncharacterized protein	MKFSTITSLFLANAGLSLAAPTKTLAQATAIEVKTGDNGIETPLPIQPGMVD	□	0	ref|XP_011318155.1| hypothetical protein FGSG_02255 [Fusarium graminearum PH-1]

	1REZ6_GIBZE		OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG02255.1 PE=4 SV=1	NCDRFHFVAKNTGCLQIANMYGITFEQFKEWNPTVGDDCRTLWADANVCVRTIGYKYPVSVACYGSSDILPWGSNKAAALTAARDWCYNGGGGGIYEIYETKTGCVNAPSGAGKFVFEVKTTHGTRIGLTGGRCQTFLNLGINGCKEGAQTNTEGWTMETTFETGKCKA			>gb|ESU07670.1| hypothetical protein FGSG_02255 [Fusarium graminearum PH-1] >gb|EYB30925.1| hypothetical protein FG05_02255 [Fusarium graminearum] >emb|CEF74523.1| unnamed protein product [Fusarium graminearum]
722	tr|A0A098DHN6|A0A098DHN6_GIBZE	tr|A0A1C3YMU5|A0A1C3YMU5_GIBZE	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG03191.1 PE=3 SV=1	MFSLSLSLCPSCRPSHKTTHALHCNIRCSPRVLAFSSLVTMFSALTALAGSLVLYIICTSIYYITFHPLASIPGPKICGITRIPYWLVAFRGEDVRWMKTLHDKYGPVVRFGPTDVSYAATQAWNDIHGPKDSEKAQEFSVQPVNGVPSMLTTDVENHTRMRRLFSPAFSERALKKQEPLFKKYSELLMYKISEVGDNGAKPVEMCQLLNFTTFDVMAELCFGDHLDLLAKNEYSPWVRSIFESLKMLPIASMINYYPILNALFTRFEPKSVTQQRVTHCKHSEERVNRRLENGSDQPDVWNLVLEAKEGKGITVKEMHSNAELFMLAGSETTATLLSGCLYYLLSCPDKMDILLKEIRSKFDKVDDITFERLAELKYMNVCIKEALRIYPPVPIGSPRVVSPGGQQILGKYIPAETRVSVHHWSTYRSESNFKDADKFVPERWLKTEARYAGDALEAHQPFGFGPRNCLGQNMAMHEMRLILTTLVFSFDFELCEESKNWADQKSFALWIKNPLMIRATPVTTHARLNI	96-507,PF00067.22,p450,;	1	gb|EYB25587.1| hypothetical protein FG05_03191 [Fusarium graminearum] >emb|SCB65763.1| unnamed protein product [Fusarium graminearum]
956	tr|I1RFI9|I1RFI9_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG02467.1 PE=4 SV=1	MGSVGKDYPQELPLRGKTGTAAFGSSMKNDFMLDPEWRNMNHGSFGTYPKAVQTKFREYQDASEARPDPFIRYEYPKLLDESRAAVAKIINAPLDTVVFVPNATTGVNTVFRNLKWNEDGKDVIISFSTIYEACGKVADYLVDYYDEKVTHREVQLEYPLDDAEIIKKFEDAVKKIEDDGKRARICTFDVVSSRPGVVFPWEEMIKTCRKLNVLSMVDGAQGVGMVKLDMKSADPDFFVSNCHKWLHVPRGCAVFYVPLRNQELLPTTLATSHGYIPKRVQRITPLPPSKKSRFVTNFEFVGTLDNSPYLCVKDAIKWREEALGGEDAILEYLWDLNKKGSELVAKKLGTTYMENSTGTMRNCAMANIALPVWSAKEGKEGEFVVSAEETQTAFQWILNTLIGDYKTFVALFLHGGRFWIRTSAQVYLGIEDYEWLGGVLKELCERVAKKEYLK	68-270,PF00266.19,Aminotran_5,CL0061;	1	ref|XP_011318393.1| hypothetical protein FGSG_02467 [Fusarium graminearum PH-1] >gb|ESU07908.1| hypothetical protein FGSG_02467 [Fusarium graminearum PH-1] >gb|EYB31637.1| hypothetical protein FG05_02467 [Fusarium graminearum] >gb|PCD39483.1| hypothetical protein FGRA07_00754 [Fusarium graminearum] >emb|CEF74764.1| unnamed protein product [Fusarium graminearum]
1110	tr|I1RSP4|I1RSP4_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG07172.1 PE=3 SV=1	MSGSLVAQGGISDPALITLVNKLQDVFATVGVNNPIDLPQIAVVGSQSSGKSSVLENIVGRDFLPRGSGIVTRRPLVLQLINRPAESNSASAEEIDTSNDKQANADEWGEFLHAPGQKFYDFSKIRDEISRETEAKVGKNAGISPAPINLRIYSPNVLTLTLVDLPGLTKVPVGDQPRDIERQIREMVLKHIGKSNAIILAVTAANQDLANSDGLKLAREVDPEGQRTIGVLTKVDLMDEGTDVIDILSNRVIPLRLGYVPVVNRGQRDIDNRKAINQALEAEKNFFENHKAYRNKSSYCGTPYLARKLNLILMMHIKQTLPDIKARISSSLQKYTAELESLGPSMLGNSANIVLNIITEFTNEWRTVLDGNNTELSSTELSGGARISFVFHELYSNGVKAIDPFDVVKDVDIRTILYNSSGSSPALFVGTTAFELIVKQQIKRLEDPSLKCVSLVYDELVRILSQLLAKQLYRRYPSLKEKMHGVVIAFFKKAMEPTNKLVRDLVSMESCYVNTGHPDFLNGHRAMAMVNERYNPKPVQVDPKTGKPLAGTPRAASPTVPDGENAGNSGFFGSFFAAKNKKKAAAMEAPPPTLKASGTLSERENIEVEVIKLLISSYYNIVKRTMIDMVPKAVMLNLVQFTKDEMQRELLENMYRTDTLDDLLKESDFTIRRRKECQQMVESLGKASEIVSQVQ	244-528,PF01031.20,Dynamin_M,;41-235,PF00350.23,Dynamin_N,CL0023;603-694,PF02212.18,GED,;40-211,PF01926.23,MMR_HSR1,CL0023;	4	ref|XP_009254606.1| hypothetical protein FPSE_03212 [Fusarium pseudograminearum CS3096] >ref|XP_011326892.1| vacuolar protein sorting-associated protein 1 [Fusarium graminearum PH-1] >gb|EYB26571.1| hypothetical protein FG05_07172 [Fusarium graminearum] >gb|PTD10228.1| Vacuolar protein sorting-associated protein 1 [Fusarium culmorum] >gb|EKJ76662.1| hypothetical protein FPSE_03212 [Fusarium pseudograminearum CS3096] >gb|ESU13385.1| vacuolar protein sorting-associated protein 1 [Fusarium graminearum PH-1] >gb|PCD40583.1| vacuolar protein sorting-associated protein 1 [Fusarium graminearum]

1229	tr|I1RM69|I1RM69_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG05052.1 PE=4 SV=1	MRVATVASLLASASLTIAFDWQQVIGTSDNRAPSAVSTDSDAPWYRSELLSLHKSLIETSSVSGTEHDVGVWLESYLEKKGYTTARQALEPFENTPDGKPRFNVLAWRQDGKKTFDPKIAVSSHIDVVPPHIPYGIDDGEVTKETMITGRGSVDAKGSVAAQITAVEHLVEHDKIDPHKVLLLFVVGEEVKGDGMRRFSTALEKKELPYNLDAVIFGEPTELKLACGHKGMLGCDVTTKGFPGHSGYPWLGKSANELMIRAFAKIFETDLGSSDLFGNTTVNVGRFNGGVAANVIPEEAKVGLAVRVASGKQDDGHIAVHNKIQAIFDEVDKDAFIFDCTHGYGPVEANCDVDGFEKITVNYGTDIPNLKGDHTRYLYGPGNILVAHGARENLTVADLETAVEGYQKLILHALEQ	121-410,PF01546.28,Peptidase_M20,CL0035;227-330,PF07687.14,M20_dimer,;	2	ref|XP_011323536.1| hypothetical protein FGSG_05052 [Fusarium graminearum PH-1] >gb|ESU10960.1| hypothetical protein FGSG_05052 [Fusarium graminearum PH-1] >gb|EYB31803.1| hypothetical protein FG05_05052 [Fusarium graminearum] >gb|PCD39930.1| hypothetical protein FGRA07_01201 [Fusarium graminearum] >emb|CEF88852.1| unnamed protein product [Fusarium graminearum]
1254	tr|I1RRM5|I1RRM5_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG06757.1 PE=3 SV=1	MTKRTKKVGVTGKYGTRYGASLRKQVKKMEITQHAKYTCTFCGKVTVKRQATGIWDCKSCKRTVAGGAYTVATPAAAAMRSTLRRLREIAEV	4-88,PF01780.19,Ribosomal_L37ae,CL0167;	1	ref|XP_009260497.1| hypothetical protein FPSE_09105 [Fusarium pseudograminearum CS3096] >ref|XP_011326404.1| hypothetical protein FGSG_06757 [Fusarium graminearum PH-1] >gb|EYB28222.1| hypothetical protein FG05_06757 [Fusarium graminearum] >gb|KPA42324.1| ribosomal protein l37ae [Fusarium langsethiae] >gb|PTD09412.1| 60S ribosomal protein L43 [Fusarium culmorum] >gb|RGP69310.1| ribosomal l37ae [Fusarium sporotrichioides] >gb|EKJ70735.1| hypothetical protein FPSE_09105 [Fusarium pseudograminearum CS3096]
1490	tr|A0A098DV34|A0A098DV34_GIBZE	tr|I1RYP5|I1RYP5_GIBZE	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) PE=3 SV=1	MRIIPSPQLLYYITLSYIIAKMGVTDRIIQIGGQISGNPTAGGREKILQKNPDDIVVTAACRSAFTKGGRGGFKDTHAADLMAGVLKAILDRSKINPALVEDLCVGTVLAPGGGATEMRAASLVAGFPESIAVRTLNRQCSSGLQATVDVANQIKTGMIDIGIGAGVESMSINYGPGAVGEFSEEFEKVPEAANCKVPMGVLSEQMAKDLGITRQAQDTFAASSYQKALKAQKEGLFDEEIAPLKVKFEDKEGNTKEITVSKDDGVREGITVESLGKIRPAFAKDGSIHAGNASQISDGAAAVLLMKRSTAEKLGQKIIGKYVCASIVGVKPLLMGQGPWKAIPKALDLAGISKDDVDIWEINEAFASQCLWCANELGIPQEKINPKGGAIAFGHPLGCTGARQVSTLLYELKRTGQKVGATSMCVGTGMGMAAIWVAE	55-309,PF00108.23,Thiolase_N,CL0046;317-435,PF02803.18,Thiolase_C,CL0046;	2	ref|XP_025582932.1| uncharacterized protein FVRRES_13234 [Fusarium venenatum] >emb|CEI40698.1| unnamed protein product [Fusarium venenatum]
1577	tr|I1RY67|I1RY67_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG09304.1 PE=4 SV=1	MVAQAQAISVSLNDLKDGNIPFGTLKQAFGPDSLGILVVKDVPQEFPELRHQALSYASYLEKLENARAKYLTGWSLGKETLKNGQVDTFKGSYYANCAFYIDPSLECAKPTQEFSTDNFPEYLSPNVWPPEDVLPGFKPSVTSLCRLIIDVAVLVARACDRFAQEDIPGYPAGYLEHVVSTSSTTKARLLHYYPQESEPSAAGGDEDDWCATHLDHGCLTGLTSAMFIDEHKTSPSVPDVTNLNGASLPPLEELPSSPDPSAGLYIKSRTGETVQVKIPRDCIAFQTGEALERITAGRFKAVPHFVRGVRASVSDGKVARNTLAVFTQPNLGEEVDIEQHLTFGEFARGIVNKNTVS	□	0	ref|XP_011328457.1| hypothetical protein FGSG_09304 [Fusarium graminearum PH-1] >gb|ESU15859.1| hypothetical protein FGSG_09304 [Fusarium graminearum PH-1] >emb|CEF84585.1| unnamed protein product [Fusarium graminearum]
1767	tr|I1RQC0|I1RQC0_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG06261.1 PE=4 SV=1	MKISTSLITGIFAIFATTFASTIGRHDDSYPNFIREAEPTCITPGAIPNITGSQIRTVGVVLFQGFDMIDVFGPLDPLQLMSLGVQKLNLHLIAETLDPVTTKPVAMNKFDSSFFPTVPPTNTFDDELDLDLLIVPGGSGARNPNLQAVTSYIAKMFPKVKILMTICTGAGVAARSGVLDGHMATTNKNAWATMKEMGPKVNWVSPARYVIDGKIWSSSGVTSGLDLIFEFIATFWGKEQSERLAGIAEHVPREATDDPFSKHYNITPTEAQPCPQP	57-233,PF01965.24,DJ-1_PfpI,CL0014;	1	ref|XP_011324911.1| hypothetical protein FGSG_06261 [Fusarium graminearum PH-1] >gb|ESU12335.1| hypothetical protein FGSG_06261 [Fusarium graminearum PH-1] >gb|EYB33286.1| hypothetical protein FG05_06261 [Fusarium graminearum] >gb|PCD19146.1| hypothetical protein FGRA07_05951 [Fusarium graminearum] >emb|CEF87198.1| unnamed protein product [Fusarium graminearum]

1843	tr|A0A1C3YNA9|A0A1C3YNA9_GIBZE	tr|I1RKX5|I1RKX5_GIBZE	Carboxypeptidase OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FGRAMPH1_01T15555 PE=3 SV=1	MGLKTVVLAALSLVTLTNASAIDSRTNKPANTQYYNTKTSQFYVDPKGIPEVSFDVGESYAGQIPVDLKKNGSKDSKFFYWFFPTVNPAGKDDVVIWFNGGPGCSSLEGFIQENGPFKWQYGTYKPVPNAWSWHKLANVIWVEYPIGTGFSTGPVTAHNNTQTADEFVKWWKNLVDTFSLQGKKIYVTGESYAGVYIPYVGAAMLDKKDKKYYDVQGALYYDPVMPYADELHLDKAAFPAFFRHWESVFAIPNKNKKILENDNEKCGLDKYREAHLTYPPPPKPWKSVPTKGCDITSHFDEIIPVINPCFNVYHVQDTCPVLWDILGFPSVEYVAPGASIYFNLPDVRKAIHAPSTPKNWTSCSGPVFVKDDPHYDPAEHEKKFQTLVEKTNNVIIGSGMADYIITSNTTALAVQGLKWNGKQGFQKAPSQEFVVPIINNTALNTENWAGGSVQGEVHSERGFTLATVKTSGHMVPQYAPPAAFRQLEHLLGRVESLTEPEPFSINISTSFKWPY	58-489,PF00450.22,Peptidase_S10,CL0028;	1	emb|SCB65976.1| unnamed protein product [Fusarium graminearum]
1910	tr|V6RDP1|V6RDP1_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG03247.1 PE=3 SV=1	MPLLNGKANTAFIGAIDQGTTSSRFLIFDPSGDVVATHQIEFKQYYPHPGWHEHDPEELISSVEQCIDGAVETFESQGHSREQIKAVGITNQRETTVVWDKTTGKALHNAIVWTDTRSKDLVRRLKRRLGSSELIGRCGIPLSTYPSVSKLLWLLDNIPEVKDAYERGVLAFGTVDTWLTYKLNGATDRDVYVSDPSNASRTMFMNLETLKYDEDILDWFRIDDSKITLPRIVRSSDNKAYGSLAGTSLKGVKITGCLGDQSAALVGQKAFTPGLAKNTYGTGCFLLYNVGTKPVISSHGLLTTVAFDFGEGNTMYALEGSIAVAGSSVKFLVDNFGFIESSAKLSALAETVEDNGGCTFVTAFSGLFAPYWIDDARGTIFGITSYTQRGHIARATLEATCFQTKAILDSMEKDSGHALTELAVDGGMCNSDLIMQTQSDLIGIPVNRPGMRETTALGAAIAAGFAVGIWKSFDDLKEVNTQGRTIFKPQIAEEEATKRFGRWTKAVEMSKGWANE	276-466,PF02782.16,FGGY_C,CL0108;13-267,PF00370.21,FGGY_N,CL0108;	2	ref|XP_011322504.1| hypothetical protein FGSG_03247 [Fusarium graminearum PH-1] >gb|ESU10005.1| hypothetical protein FGSG_03247 [Fusarium graminearum PH-1] >gb|EYB32503.1| hypothetical protein FG05_03247 [Fusarium graminearum] >gb|PCD34188.1| hypothetical protein FGRA07_08506 [Fusarium graminearum] >emb|CEF78011.1| unnamed protein product [Fusarium graminearum]
2023	tr|I1S568|I1S568_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FGRAMPH1_01T04095 PE=4 SV=1	MAIPHRIVIVGSGVFGLSTAYYMSLDQKFSNSQIILLDAWNFEPDSRSTSVQNPGAANSDTSRIVRRAYPKGPYAALAYESVERWRTDWGADGRYVEQRLLFSGEGGPLEAPKKKGETVNYVKDAYATGCEMTPGGAGALEIWDSLDEIRSELQASERENSSSGKTEESSLRGFVSKDCGYANSGATIEWLRQKIIRMGRVDLRVGQVEKLVYSSGGARIDGVVLVDGTEIHADLTVIAAGCHSSRLLQLPNMCTVESAFVAYIQLTESEAQELRRREWPLIVNTHRGVFCVGPDQDNCLKLGQCSTGSRVEILKSAHLMDRDEAARLRSEADSSVQPDWANPGTGWGGKVTLTKTGEVVDDDPESAAVNKALAAFRGFLLELLGPQDDFASLDVSGRHDPLLNSIAVRPFARVRRCWYNDTPSYDFIVDYHPSFGISLFVASGGCDHAFKFMPVLGEKAVSIILRRLGDVPMASSREEASLLEELCRLWKFPDHLVSEQERRGAKL	6-461,PF01266.24,DAO,CL0063;	1	ref|XP_011317510.1| hypothetical protein FGSG_11986 [Fusarium graminearum PH-1] >gb|ESU07025.1| hypothetical protein FGSG_11986 [Fusarium graminearum PH-1] >gb|EYB22761.1| hypothetical protein FG05_11986 [Fusarium graminearum] >emb|CEF73855.1| unnamed protein product [Fusarium graminearum]

2109	tr|I1RZV5|I1RZV5_GIBZE	--	Aldehyde dehydrogenase OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG09960.1 PE=3 SV=1	MADNTTSYTTGPLEHTPLDEINAKVDLVRKTFRSGRTKDIEFRMRQIRKLYWAIVDNTELMQDALLKDLGKCKYEAVLAEIDWCKQECLDMTNNMEKWLRDEPVPNVPLQFRLMKHRTRFEPLGVILNIGAFNFPFQLTLPVVVGAIACGNCVVLKPSESSPNSAMVLKKIFDESLDPECFTYVNGALSETQRLLEQKFDKICFTGGKVVGKIIAKKAAETLTPVLLELGGQNPAFVTKNANLKLAARRLLWQKTLNAGQVCMSHNYILVERSVLSPFLGELNNQLRTFFPKGAKNSTDLAHIVSASHFNRLKKMLDGSKGKIVLGGSMDESTLFMEPTAVLVDDIEDSMMVDEAFGPIFAIMAIDSLDQAIDIANSVDPTPLSLSTFGSKDENKKVLDNVTSGGATCNDAFFHSQIPQSPLGGVGQSGMGNYHGIYSIRTFSHQRTIAEVPYWADALFRVRYMPYQWPNMNRLKSIAQPKPNFDRDGNKTKGFSYFVALVFGLGSKKAKGALLRWAFLVVAAAVLEAKKGTLSQLLTR	19-448,PF00171.22,Aldedh,CL0099;118-406,PF05893.14,LuxC,CL0099;	2	ref|XP_011318869.1| hypothetical protein FGSG_09960 [Fusarium graminearum PH-1] >gb|ESU16607.1| hypothetical protein FGSG_09960 [Fusarium graminearum PH-1] >gb|EYB26960.1| hypothetical protein FG05_09960 [Fusarium graminearum] >gb|PCD31578.1| hypothetical protein FGRA07_10121 [Fusarium graminearum] >emb|CEF75268.1| unnamed protein product [Fusarium graminearum]
2134	tr|I1RJV4|I1RJV4_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG04137.1 PE=4 SV=1	MVSAKKHVPIVKKRTKRFERHQHDRFMRVSPSWRKPKGIDSRVRRRFRGTIAMPSIGYGSNKKTRYMAPSGFKAFIVSNKSDLELLLMHNKTHAAEIAHNVSSRKRVDIIARAKQLGVKVTNPKAKVTTEV	15-122,PF01655.18,Ribosomal_L32e,;	1	ref|XP_009251552.1| hypothetical protein FPSE_00157 [Fusarium pseudograminearum CS3096] >ref|XP_011321494.1| 60S ribosomal protein L32 [Fusarium graminearum PH-1] >gb|EYB32386.1| hypothetical protein FG05_04137 [Fusarium graminearum] >gb|PTD07794.1| 60S ribosomal protein L32 [Fusarium culmorum] >gb|EKJ79703.1| hypothetical protein FPSE_00157 [Fusarium pseudograminearum CS3096] >gb|ESU08995.1| 60S ribosomal protein L32 [Fusarium graminearum PH-1] >gb|PCD28034.1| 60S ribosomal protein L32 [Fusarium graminearum]
2183	tr|A0A0E0SJJ3|A0A0E0SJJ3_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG11097.1 PE=4 SV=1	MLVLRFAALAAASLPLTSASAIFRRDLTAPESPRDGWSYLGCYIDSTSKRALDGPVHYDETGLTAETCVAHCVGLGYAFAGMEYSKECFCGSKRPTTKTDEADCNMPCTGDDEQPCGAGDRLTVFGKASAGGTSVPSGSPTETVSATASASGTASPVASDLPGTWSYAGCYTDPPGRALQAAGTSKSMTPQKCIATCIADGFKIAGVEYAEECFCGNALNNAASKVKESDCNMPCSGDSSQMCGAGSRLSLYSDGDFEVNPIPVAKKDGLPGDWEYKGCVFDNNNPYLLQWLYEDAGSYATSNMTIETCLNRCQKFGYSAGGVEYGRQCVCGDLKAVENRGDVWKDDSFCSMACPGDRNSTCGAGNHINYYEWTGASLNTFHYASGPKAGKYDHFSTSPIIPLISSVGINDKIVFVEKHGTSDDDTEGSFEFDYTTNIYRELALKTDVFCSASFTLPDKAGRIINIGGWSAESVYGIRFFTPDSPQGVDNGTNVWEEDYTQLRLFDPRWYPTALVLSNGSILAMGGESGSDAPIVPTAEVLPHPAGVTESTYVDYLERAENIGRTNSYPHMAILPSGNIFFTQFNESRLLSQVDFQSIKKLPDMPGQINNPLTGRNYPLQGTLMVLPHKAPYSDPVEILICGGTTHEPGNDALDNCVLMAPDVEGAEWAIERMPSKRVMPNMVALPDGRYLILGGAQVGRGGFGLADNANLNAVMYDPEEPLGQRMTVLANTTIARLYHSEAVLLSDGKVLVSGSDPQDQGKHPQEKRIEYFWPDYLLSGATQPNFTISDRDWTYGESYTFTLTSDLEEGASKLRVSLMASVGATHGVSMGQRTLFPEFSCSGKTCSVTAPPNAFVSPPSWYQMFVLDGPTPSHAIWVRIGGDPGKLGDWPKLPGFTPPGV	39-117,PF01822.19,WSC,;167-244,PF01822.19,WSC,;276-363,PF01822.19,WSC,;423-643,PF07250.11,Glyoxal_oxid_N,;784-880,PF09118.11,DUF1929,CL0159;	5	gb|EYB29075.1| hypothetical protein FG05_11097 [Fusarium graminearum] >gb|PCD36607.1| hypothetical protein FGRA07_07611 [Fusarium graminearum] >emb|CEF86606.1| unnamed protein product [Fusarium graminearum]

2238	tr|A0A098DK45|A0A098DK45_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG04337.1 PE=4 SV=1	MPLKVATIPSQSPLDNPSSVPGVTPTTIQTRLDHAHSTRGGSASASLLDDTDPVPRQQYQRDTTANTSEQFELVDYPPIQARRDAADREARRKEKRDEKRRWLQEQDEMKFSHSIQFNAVPDWSSHYIAYSNLKKLIYHLEKNAHQARGSTGDAESRPLINQEDAEEVFSRALGVELEKICSFYVSKEGELLEEAAQLLRDVGDEAEDAIADNRYLRRLSVSSANNRTGRNGFRSRSPRSRSSDNEESGSEEGDETTGLTTRRRSSGGRRRTIPSINKSRSEDLNASTDLGRDMRRLSTAADENEENLMFSSGIFSSAIMLKKRIIGLYVSLCELKSFIQLNRTGFTKVLKKFDKILDKELKGPYLRAHVETAYPFKDETKCMLEENIAKMEKAFAEIVTGGDEALARKDLRSHLREHVVWERNTVWRDLIGIERRAEAAGLGQALLGQERGNVTRRLQGDEAKGAQITQFRTPFGRVTLPPWLASSSLWTLIACFTVFALLLLLPIMEKPEQQNCLAMLVFVSLLWATETIPLFVTSLLIPFLSVVLNVVRDETPGKPQKRLGSKEATSAIFAAMWTPVIMLLLGGFTLAAALSKCTIDKRLATLVLSKAGTQPKTVLIANMFVAAFASMLISNVAAPVLCYSIIEPMLRTLPSDSNMSKAVIIGIALASNIGGMLSPIASPQNVVAMGIMQPAPTWLQWFFIVIPVGTVSIVLIWLILLVTFQPGKGTTIAPIRPVKEKFTALQWFVTIVTISTIALWCASHQLEAEFGDMGVIAIIPIVLFFGIGLLTKEDFNNFPWTIIILAAGGLSLGKAVRSSGLLHTLAEIVSEKVEGMSLYGVLVVFSTLILVIATFISHTVAALIFLPLVFDVGAAMDQPHPNLLVMGGVLMCSAAMGLPTSGFPNMTQLPAVIGSSSLSFVSVLYMLMDYNVMREIFRGDGVLYSFELAGAMLSAFTARPIIELKQQTKAKIETILAHGDRVLVGLNNGALRIYRLNGLVDPSLIGSADADAAAATSPNGENGASPITKSSSPTDLMREVERFSTRAIEQLAIIKDANTIVSLSNYHVSFHDLKTYELIETLPRTKNATCFASTSNIVKDPDTGIPEIVSRLAVAVKRKLLLWSWLESELSDDVDEIVLTESIRSVTWASATKLVCGLNGGYVMVNVVTREIEDVVSPGSGPAAGQNSRFGAMSSAGMGYMGLGGYMPKPLATKLAEGEILLAKDINTLFIDDNGKPLDRRQIPWQHAPESIGYSYPYILALQAPSKGSLEVRNPSTLSSLQNLSLPGAAQLHFPPPTYSLAHAGKGFHISSERCVWKMDATDYDSQIQELVDGGHFDEAISILEMLEDALLRNKTQTLREVKMLKAEGLFKKKKYRQAMDLFNEDTVHAPPERVLKMFPPSIAGELSSWAGREDEESQESDEAPATPKKANGTRTTTPEPSESPHDTPQSSKGGFARYLTGSYRRPQADTASIFSKKDTTDGDDTASVKEPDSADDQPLKDKNLTNAVLELNSYLAGTRARLQRVLDPVTGKLKPRSERNGSTEEIAENFLRIGLDESEELLQEELRNTFRLVDTTLFRAYMFSRPTLASSLFRIPNFCDPNVVNEKLLEHNRYNELVDFFYGKKLHKEALELLRRFGAAEKPDDAAPALHGPQRTIEYLKTLPPSEIDLILEHAEWTLKASPNAALEIFIGDTENAETLPREKIVSFIHDIDTQLECRYLEHIINELEDMTPDLHNRLVELYVENLKDKEEHGEEWNEMMNRFVEFLRHEFLREPVQVYSLSKAFQLIPRDDPAFYEAQAVVLSKMGQHKQALEIYVFKMKDYQKAEQYCNRVNATQDATPSAQQNTKNDAGDDPEKTTPSIYHTLLSLYLQPSSPNEPNLEPALDLLSKHGSRLPATSTLGLIPDDLPVRSLESYFRGRIRSANSLVNESRIVAGLRQAEGVSIAARLHLGDDVQGRQGGRNRHVAITDERHCVWCTMAV	109-165,PF03105.19,SPX,;153-366,PF03105.19,SPX,;1574-1680,PF10366.9,Vps39_1,CL0020;488-905,PF00939.19,Na_sulph_symp,CL0182;525-886,PF03600.16,CitMHS,CL0182;1887-1980,PF10367.9,Vps39_2,;1037-1286,PF00780.22,CNH,;	7	gb|PTD07037.1| putative transporter C3B8.04c [Fusarium culmorum]

2555	tr|I1S5U0|I1S5U0_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FGRAMPH1_01T15757 PE=4 SV=1	MSKILTVFGATGNQGGSVVRAILNDPALSKEFKIRGITRDVSKPAAKELASKGVEVVAADMNTAEQVAPAVKDAHTVFLVTNYWETNSGNGEIAQGKAVADACKTAGVKQLVFSSLLDTKKISNGRLAHIKHFEGKAEIEEYIRQINVPATFVLPGFFASNLFTSIRKNEDGSYAWALPGHGDKTQVPIFDVQGDMGKFVKAAIKNFPGTLNKRVFAATDYYSPNRIISEFSEVMGKPATFNQVPADVFKTFLPAAVADELTENMMLLEDPGYYGGADLKESLDMLDEKPITWKDFVEKNKSKWE	6-243,PF05368.13,NmrA,CL0063;9-160,PF13460.6,NAD_binding_10,CL0063;	2	ref|XP_011320939.1| hypothetical protein FGSG_12211 [Fusarium graminearum PH-1] >gb|ESU08440.1| hypothetical protein FGSG_12211 [Fusarium graminearum PH-1] >gb|PCD28520.1| hypothetical protein FGRA07_03659 [Fusarium graminearum] >emb|CEF79678.1| unnamed protein product [Fusarium graminearum]
2591	tr|A0A1C3YN33|A0A1C3YN33_GIBZE	tr|I1RIX7|I1RIX7_GIBZE	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FGRAMPH1_01T13677 PE=4 SV=1	MTTGVFHYIDPASSTDATGNLVKPWAKVDVDVSSFQRKLVKREVVDIRSAASLKAFDVDLSGFDVFKSPAKETEFTDESAVRNGYYAEVDALLKERIPAIKKIVIFDHTIRRREKTSPRQPVQQVHVDQTPGAAEARVRRHTDPSEAEELLKGRYQIINVWRPIGHPATDFPLAVIDYRSTKPEDMIKVDLLYPNRDDNDDDDRGKEVLPDEGTLKSTEGYTVKGETYSVAANPEHKLYYAKDMTPDEVMLIKCFDSKSEVHEGGKHGIAGYTPHTAFVDPDTPEDAPGRQSIEVRCLVFY	□	0	ref|XP_011321913.1| hypothetical protein FGSG_03774 [Fusarium graminearum PH-1] >gb|ESU09414.1| hypothetical protein FGSG_03774 [Fusarium graminearum PH-1]

18 common elements in "62.5/0", "125/0", "250/0" and "500/0":

Protein Index	Protein ID	Samesets	Description	ProtSeq	Pfam Domain prediction results	Number of domain predictions	The best match result obtained by NR database comparison
48	tr|V6QVH8|V6QVH8_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG00722.1 PE=3 SV=1	MSAQDPLSSTNPSSVTNNTQDASGRQPSSAAAGSSELSSAKISLRKSLRSFPDFPIPGINFVDIMPLFADPTAHATLVEALELQIAEAFPTKPDVIVGLDARGFLFGPGLALRLGVPFAAVRKQGKLPGPCVTAEYIKEYGKDLFQMQEDAVREGQKVLIVDDIIATGGSAKAAAELVQQLKGEVMGYLFILEIPGLNGRDKLGAPPTKILLEDA	76-189,PF00156.27,Pribosyltran,CL0533;	1	ref|XP_011316429.1| adenine phosphoribosyltransferase [Fusarium graminearum PH-1] >gb|ESU05944.1| adenine phosphoribosyltransferase [Fusarium graminearum PH-1] >emb|CEF72716.1| unnamed protein product [Fusarium graminearum]
123	tr|I1RM30|I1RM30_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG05007.1 PE=4 SV=1	MPPLRLAILEADTPQPQTRDRYGGYTGVFTALLEAAAKPKKLSELVSIKGYDVVNELHSYPVIEDIDAILITGSRHTAFDNDPWILKLVEYTKKAIASNRVRVVGVCFGHQIVGRAEGAKCGRSNNGWEVAVTEVDLTAKGKEVFGLDKMRIHQMHRDIVDAFPKNSIPLGSNNICEVQGFYSPGKYITVQGHPEFNEEIISEILFNRHTVGIFTDEVYNDAMKRAPLPHDGVAIAKAFLKFWREG	58-207,PF00117.28,GATase,CL0014;	1	ref|XP_011323488.1| hypothetical protein FGSG_05007 [Fusarium graminearum PH-1] >gb|ESU10912.1| hypothetical protein FGSG_05007 [Fusarium graminearum PH-1] >gb|EYB31760.1| hypothetical protein FG05_05007 [Fusarium graminearum] >gb|PCD39882.1| hypothetical protein FGRA07_01153 [Fusarium graminearum] >emb|CEF85837.1| unnamed protein product [Fusarium graminearum]
180	tr|I1RQE0|I1RQE0_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG06281.1 PE=3 SV=1	MKTSTFRIARGAAAGLQKRAYTKATTAPRHLMTIADLTPTEFANLVRDANTRKIAVKGGAPASYLNAGLAGKTVAMMFSKRSTRTRVSTEAAVTMLGGHPMFLGKDDIQLGVISSMTSCMVARVGPHSDVATLAKHSSVPVINALSDDFHPLQTIADFLTLAETFPASTSKGATLGLNGLKVAWVGDANNVLFDLAIGCVKMGVDISVAAPKGYEIPDAMRQLITSAGDGLSSPGKLIETNVPEEAVKDANVLVTDTWVSMGQEADTQKRLKDFAGFQITNDLAKRGGAKADWKFMHCLPRHPEEVADEVFYSPRSLVFPEAENRLWAALSALEGFVVNKGKF	179-329,PF00185.24,OTCace,CL0399;29-163,PF02729.21,OTCace_N,;	2	ref|XP_011324931.1| ornithine carbamoyltransferase [Fusarium graminearum PH-1] >gb|ESU12355.1| ornithine carbamoyltransferase [Fusarium graminearum PH-1] >gb|EYB33305.1| hypothetical protein FG05_06281 [Fusarium graminearum] >emb|CEF86191.1| unnamed protein product [Fusarium graminearum]

793	tr|I1RZM4|I1RZM4_GIBZE	--	Serine hydroxymethyltransferase OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG09873.1 PE=3 SV=1	MSLTGVRGTSRVLRTIAKPVAISATCTRPASSLAVEDQQQALSAHLNKADPAVFDIIEKEKNRQKHFINLIPSENFTSQAVLDALGSVMQNKYSEGYPGARYYGGNEFIDQSERLCQQRALESFGLDPKQWGVNVQALSGAPANLYVYSALLNTHDRLMGLDLPHGGHLSHGYQTLTKKISAISKYFETLPYRLNETTGYIDYEKLDEVASVYRPKIIVAGASAYSRLIDYQRMREICDKVNAYLLADIAHISGLVAAKVIPGPFAHADIVTTTSHKSLRGPRGAMIFYRKGIRRQHPKTKEDILYDLEGPINNSVFPGHQGGPHNHTITALAVALKQAQTPEFQAYQSQVLKNAKAFAKRLSEPKGKGGLGYKLVSGGTDNHLVLADLKPHGIDGGRVERVLELVGVAANKNTVPGDRSALVPGGLRMGTPAMTTRGFNEDDFVRVADVVDRAVTIASRIDKAARKAAEEKGDKSPGKIKVFLEHLGDGETQSEIVQLRSEVEDWVGTYPVPWNTSQ	46-450,PF00464.19,SHMT,CL0061;	1	ref|XP_011318775.1| serine hydroxymethyltransferase [Fusarium graminearum PH-1] >gb|ESU16513.1| serine hydroxymethyltransferase [Fusarium graminearum PH-1] >gb|EYB22206.1| hypothetical protein FG05_09873 [Fusarium graminearum] >gb|PCD31496.1| serine hydroxymethyltransferase [Fusarium graminearum] >emb|CEF75168.1| unnamed protein product [Fusarium graminearum]
918	tr|I1RAJ3|I1RAJ3_GIBZE	--	Uncharacterized protein OS=Gibberellazeae(strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG00523.1 PE=4 SV=1	MKYTIATIAAFATMALAKPAFLNTDFALTEGKPYTIRYSGCDSGCTIILQNGESTDLKDYKTLTSGAKGDSFTFTPSQLPSDTYNFKITDSAGDINYSAQFTYEGSYDAPSVTSATKSAVETTAAQTTEQATTLASVTKPVEEATTAKPIIPTHVPVPPKNATTPIATPTKTGGAGQTGVPEVPVSGATRMTSSLALIAGAAMAMVYLN	28-102,PF10342.9,GPI-anchored,CL0159;	1	ref|XP_011316199.1| hypothetical protein FGSG_00523 [Fusarium graminearum PH-1] >gb|ESU05714.1| hypothetical protein FGSG_00523 [Fusarium graminearum PH-1] >gb|EYB28074.1| hypothetical protein FG05_00523 [Fusarium graminearum] >gb|PCD18396.1| hypothetical protein FGRA07_07033 [Fusarium graminearum] >emb|CEF72467.1| unnamed protein product [Fusarium graminearum]
1017	tr|A0A098DRL8|A0A098DRL8_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG09809.1 PE=4 SV=1	MDEKQPSQRVMLPIQARRSRPTMTLIVMAIVTYTFWIWQPFRPLIDDESWVHITNDDIQPTDSLVPLEAHIMSKCPDAKEALELLVLPVMQRVHDKVNFTLSYIGRPTANDGVDCMHGPSECMGNIIELCARELYPDPKINLGFIMCLSRDYSDIPGRSLVEDCALESAIDFQQLNECAVKEDGGYGLSLLRHSIKRTADAGVTKSATIRLNGEIYCIRDGGEWSDCPHGSSVNDLLIAIEKLRRQS	67-165,PF03227.16,GILT,CL0172;	1	emb|CEF84004.1| unnamed protein product [Fusarium graminearum]
1170	tr|A0A1C3YMD1|A0A1C3YMD1_GIBZE	tr|I1S920|I1S920_GIBZE	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FGRAMPH1_01T10169 PE=4 SV=1	MIRSSAPINKYLNNELPRFFQLQKRSLTLSRALGFNVIHPSTSTSTTRLGSSSSTSITTPIRNRSFSSSSQLHSQEPIFSAMSSKLIPSDPDHVMVIRNVTPNIATFSVPFSRFGKVKIGGRGTLVKLTSGGLAVFSPVALTKATQAKVIEMGGDVRYIVALDYEHHIFISEWAKEYPTAKIIGPEGLPEKRAKQTDDPKIGNEQFAVVFNKETKRETRIDPEFDTDFDYEYVDGHANLEIVFCYKPERVLIQADLLFNLPPTEQYSKVPEAELPDDGAVGKLFACVQNPRGDTKWLQRFNWYLLAKNRDSFNDSMAVIAQWDFTTMIPCHGDVLEGDGKEVFMKVFDWHIQGGK	116-183,PF14234.6,DUF4336,;	1	emb|SCB65614.1| unnamed protein product [Fusarium graminearum]
1274	tr|A0A1C3YI49|A0A1C3YI49_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FGRAMPH1_01T03359 PE=3 SV=1	MDLVNSLEGRLLFAVPKKGRLNAATLNLLEGADVQFRRENRLDIALVKNLPIALIFLPAADIPTFVGEGRCDLGITGWDQVQEHDASVRAYNQLRRSSVDLTSTEDKVAGSDMVMELGFGSCKLQVQVPEKGQYKTPQDLVGKTIGTSFVHLAADYFLKLEQGENADGELSPRKMRTKIVELSGSVEAACALGVAEGIVDLVESGETMRAAGLKAIDTVVDSTAVLIKSRTPSNPELIDLITSRIRGVITAKSYVLCQYNIERNRLVEATKITPGKRSATVTTLDEEGWVAVSSMVEKKKIALVMDDLTRLGAEDILVLDIHNAR	58-247,PF01634.18,HisG,CL0177;251-323,PF08029.11,HisG_C,CL0089;	2	gb|EYB22533.1| hypothetical protein FG05_11938 [Fusarium graminearum] >gb|PCD22828.1| ATP phosphoribosyltransferase [Fusarium graminearum] >emb|SCB64227.1| unnamed protein product [Fusarium graminearum]
1334	tr|I1RQX9|I1RQX9_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG06480.1	MSKTLKVAAIQAEPVWQDLQGGVEKSIRLIQDAASNGANVIGFPEVFIPGYPWSIWANSPVENAAWINEYFKNSLERESPEMDQIRAAVREAGVFVVLGYSERYRGTLYIAQSFIDETGTIVLHRRKIKPTHVERAIYGDGQGESLNNVIQTTFGKVAGLNCWEHTQPLLRYYEYSQDVDIHVSSWPSIFPENSDQWPYHITPNCCKAFSHIVSMEGACFVILSSQILTAENFEKANVKGFDYTKNGGGG	6-287,PF00795.22,CN_hydrolase,;	1	ref|XP_011326083.1| hypothetical protein FGSG_06480 [Fusarium graminearum PH-1] >gb|ESU12576.1| hypothetical protein FGSG_06480 [Fusarium graminearum PH-1] >gb|EYB24576.1| hypothetical

			PE=4 SV=1	FTMIFSPFGKELVKALDPGVEGIVYADIDLEDKYKAKQNLDIVGHYARPDALSLRVNRHPAKPVFFANDL			protein FG05_06480 [Fusarium graminearum] >gb|PCD25589.1| hypothetical protein FGRA07_10994 [Fusarium graminearum] >emb|CEF83150.1| unnamed protein product [Fusarium graminearum]
1352	tr|A0A098DJ03|A0A098DJ03_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG03180.1 PE=4 SV=1	MSQAFVQRPAPEFTATTLFPGGEFKDIKLSDYQGQWVVLLFYPMDFTFVCPTEIIQYNNALDRFKEINTTVFGVSTDSHFTHLAWVEKPRKQGGLGPDLELPLIADKSTKISRNYGVLIEDEGIALRGLFIIDPKGVLRQITVNDLPVGRDVEETIRLVKAFQFTDEYGEVCPAGWQEGGKTMKADPKGSLEYFSAQGENGESESRKRPRTD	6-140,PF00578.21,AhpC-TSA,CL0172;9-151,PF08534.10,Redoxin,CL0172;161-195,PF10417.9,1-cysPrx_C,;	3	ref|XP_009257392.1| hypothetical protein FPSE_05999 [Fusarium pseudograminearum CS3096] >gb|EKJ73876.1| hypothetical protein FPSE_05999 [Fusarium pseudograminearum CS3096] >gb|PCD34251.1| peroxiredoxin 1 [Fusarium graminearum] >emb|CEF77926.1| unnamed protein product [Fusarium graminearum]
1509	tr|I1RPR4|I1RPR4_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG06043.1 PE=4 SV=1	MRFSSSTVLAALPALAAAQDSPVDQYKAQFQNVIGQFASYIPNPAYHDPVAAAEAKAGSMRLSVLTLDNWKETLYEPVSADATTPEEWWLLVSGGNKTCYGRCGTVEQAFNETAAKFALLDKTPHMAYLNCDNQPILCNSWSAGPPSLYVFEMLPEPAAVEVYSKRLNLTTTTSDTLVALQASGSKEEFHRHTSAWFHPVNGKLAEHGLAIPFGYLMWAMNLVPNWLFMLVVSFGSRAMMSRRMQGVNGAPQAGAQPAR	□	0	ref|XP_011324663.1| hypothetical protein FGSG_06043 [Fusarium graminearum PH-1] >gb|ESU12087.1| hypothetical protein FGSG_06043 [Fusarium graminearum PH-1] >gb|EYB33078.1| hypothetical protein FG05_06043 [Fusarium graminearum] >gb|PCD19366.1| hypothetical protein FGRA07_06171 [Fusarium graminearum] >emb|CEF85848.1| unnamed protein product [Fusarium graminearum]
1553	tr|A0A098E3C5|A0A098E3C5_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG11183.1 PE=4 SV=1	MSQIAEPTSQDEGMARLDTVQPATLLEPSHWVQKGEAADANNDALDTAIDSDGGSTSASITSSILQYRTIHGRTYHSEQGNAQGSNDEQQKDLMDLTHHILTLGLGDKLHLAPLIQYDVKQVIDIGTGTGIWAIDFADQYPNAEIIGTDLSPIQPSWIPPNLQFIIEDCTREWTFKSTSADYIHARWLMGSIGNWDSFFSEAFRVCKPGGWVESHEAASTISSDDNTVDPSSAMGHWGKFFIEGSKKIGTSFTVVEDGTQRKAMEKAGFVNIQEFDFRNPIGSWPDDPVEKQMGSYTKHGLDTDSEGFVLFMAHTLGWSREDILAYVAQFRREIRSGKHHGYFAQKVVWGQKPN	116-273,PF13489.6,Methyltransf_23,CL0063;122-210,PF13649.6,Methyltransf_25,CL0063;124-212,PF08241.12,Methyltransf_11,CL0063;	3	emb|CEF88606.1| unnamed protein product [Fusarium graminearum]
1630	tr|I1RME1|I1RME1_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG05130.1 PE=4 SV=1	MDPLNVLMIGTGEYTTGFVGGGASGSDKKVGVVGLSLFDLRRREKVNKLGMVGVNGKKFPAIREHLNKNIQQVYNDLDTSFDSFPANDKVDPDAYKSAIDALSPGDAITIFTPDPTHFPIAKYAIERGIHVMITKPAVKALEEHQQLVELAQKKGVYVYVEHHKRYDPAYADARAKAQKLGDFNYFYSYMSQPKSQLETFKAWAGKESDISYYLNSHHIDINDSMVQERGYVPVSVNASSSKGVAVELGCDPCTEDTISLLVTWNKNGEPTKRAVGVYTASWTAPQKAGVHSNQYFHYLAANGEIRVDQAKRGYDVADDSVGQMMWYNPFYMKYAPDEDGNFAGQTGYGYISIEKFVDGCRAVNSGKLKPEDLDAKPLPTLKNTIATTAILEAGRRSIDENREVKIVIENGKWRLE	49-162,PF01408.22,GFO_IDH_MocA,CL0063;	1	ref|XP_011323628.1| hypothetical protein FGSG_05130 [Fusarium graminearum PH-1] >gb|EYB31879.1| hypothetical protein FG05_05130 [Fusarium graminearum] >gb|PTD05422.1| hypothetical protein FCULG_00000470 [Fusarium culmorum] >gb|ESU11052.1| hypothetical protein FGSG_05130 [Fusarium graminearum PH-1] >gb|PCD40004.1| hypothetical protein FGRA07_01275 [Fusarium graminearum] >emb|CEF86401.1| unnamed protein product [Fusarium graminearum]
1676	tr|A0A098DU58|A0A098DU58_GIBZE	--	Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG07377.1	MRPEAFSSSFKMSAGDMQDEQLKEALITYEKLQGIEDDFEDVELEILRQQDKLTKDLYVRRAEVVSKIPQFWPLVFEQSPPEVDEYIQPSDSELLLNALTGLSVERFELPNGDPRSIAIKWEFKENEWFEDKVLEKKFYWRFHKDGWAGLVSEPVDIKWKEGKDLTNGMLSLAKKVHDEEKAGQKPGETENSKKLLKLMEETGMGGVSFFSWFGFRGRKVTPEESEEGRKIDEQKKADRKAGKIEEDD	66-290,PF00956.18,NAP,;	1	emb|CEF84358.1| unnamed protein product [Fusarium graminearum]

<table>
<tr><td></td><td></td><td></td><td>PE=3 SV=1</td><td>DDDMDEDDDDDEYEYEIFPTADDLAVFIAEDLWPGAIKYFTNAQDADDIPSDLEFEEMDEDDSDDEAPALAKA</td><td></td><td></td><td></td></tr>
<tr><td>1731</td><td>tr|I1RLA5|I1RLA5_GIBZE</td><td>--</td><td>Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG04692.1 PE=4 SV=1</td><td>MPKQHVYHLHPLGWENDPEEERFKVTTLDYLTVCSYNNYALFFKLEDSEKERAAEILKAGLERTLAQARHYCGTIEKDPGGGHSFTKKRNSTVRFFVQWLDAPEDADKYPSFEDLEKTNFSAVTLGDLEQWSVPPMTYGEKPEAHPDNSPVVSAFKANFIRGGLVFNIHHHHYTNDVMGWAGFVHQLAENCYAAVNGTKHPTWDPLNLDVSRLIKQEPPEDQKIDGPAPPERHPAHQVGMSLLFHLPKSKAAELKAKATPTDGTWISTYDAFSAFIWRNLTRIRAPVFNPDPKSTLYWCEAIDMRRRMHSPKVPPRIQHNVMFAVTSPTAPVTQPTVAQIMSEWSLSELASYIRRLTNSVTQENLDKTLEMVATIRDKTSLNTRVDAQPPLSILQTDHRDANITSADFGFAKPATYRHLLDRITEGVIIVYPPRDPLPESDEGCEFAIFYEKRLAQDLINDDEWSEYFEYRGVDAEDASEAKKANGTNGTNGVNGSS</td><td>20-443,PF02458.15,Transferase,CL0149;</td><td>1</td><td>ref|XP_011323124.1| hypothetical protein FGSG_04692 [Fusarium graminearum PH-1] >gb|ESU10548.1| hypothetical protein FGSG_04692 [Fusarium graminearum PH-1] >gb|EYB31472.1| hypothetical protein FG05_04692 [Fusarium graminearum] >emb|CEF87675.1| unnamed protein product [Fusarium graminearum]</td></tr>
<tr><td>1980</td><td>tr|A0A098DQF0|A0A098DQF0_GIBZE</td><td>tr|A0A1C3YLD0|A0A1C3YLD0_GIBZE</td><td>Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG07171.1 PE=4 SV=1</td><td>MALYSYHITALPRHMPYPHPPPPTSSNVSTANSNHSSAAPLTQSSTPSSTHQQNRNRARTGIANIGPSVANPARLPGQTPAQTLGRRQRSPASDGPSDPQPDSSQAPDNDLTEPPTKRRRENNTMGGSDILDPHNGAPLGFSNGSTEPSVGVTNGHKSAMNGSTNRDNNSTITKSHGMPSEYFGHNREEVTRLLIQALSDMGYQTAADNVSRESGYELESPTVAGFRSAVLSGSWSKAEELLTGASFETEGQGNGLVLAPSADRNAIRFWLRQQKFLELLEQKDTSRALVVLRSELTPLSHDTGKLHFLSSLLMCRSVDDLMAKADWDGANGQSRKLLLSELSKCISPSVMLPENRLAVLLEQVKQSQIDTCLYHTQALSPSLYSDHFCDRRWFPTEVALDLVDMNDEIWQVQFSHDGSKLAACGSGRQVIIWDTHTYSVAEILDDHDEGVGNMSFSPDDTMILCCARDGYARLWSTSDGRLIRQFNRFAEPVSGCVWAHDNRSLILGTLDPTFSLRTINLQTNEEYDWGKKHRVEDLCGSLDGRWLVALDNEKRIHVYNAITRELEFDMELNKRPTSVSISQDSRHLLINKSDGEAQLIDLVTRNSVQKFFGHTGGAYMIRSAFGGANESFVVSGSEDGNILIWHKNTGAAIERLPGHHPRCNAVAWNPTDPYVIASCGDDGRLKIWTNKSHSVEIRARYLQNRANDADTWDRDER</td><td>409-434,PF00400.32,WD40,CL0186;444-476,PF00400.32,WD40,CL0186;608-645,PF00400.32,WD40,CL0186;656-688,PF00400.32,WD40,CL0186;</td><td>4</td><td>gb|PCD40582.1| hypothetical protein FGRA07_01853 [Fusarium graminearum]</td></tr>
<tr><td>2295</td><td>tr|I1RFP5|I1RFP5_GIBZE</td><td>--</td><td>Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG02529.1 PE=4 SV=1</td><td>MKVSFSLAALLAASLSQAQYLISELSFGHAGRISPAESRGQIPNFAVQGNPNTPEILSNRIILTPLAPGNQRGAIWGQQPLLRTQWIADVDFRANGPDRGRGNLNIWLVRNGPATIGAGSIYTVGKFDGLALVIDTSGGSSGMVRGFLNDGNTDYSRQNNVDELSFGHCPYNYRNLGRPSQVKLRQTARAFRVELDGKLCFESDKISIPTGYQFGVTAATPDNPDSFEVFKMVVMADNSDTGAVRNDPPKQQNQNQNQNQNQNQNQNQNQARGQPAKANSNNNNNRNDGEYADEDPDIFSTSKTQFMDLHNRLQNTNHQLSSLQRTSSRHQQQDEKRHEDLTSLIGQLRADMRKLDDITALNSRISELEKDIQGLRKELTRKLQSTERTFKTTLSDHHSTLSEVVMNKTPGHKFLIFSIIGTQCILVAAYVVYKRRRASMPKKYL</td><td>37-235,PF03388.13,Lectin_leg-like,CL0004;</td><td>1</td><td>ref|XP_011318464.1| hypothetical protein FGSG_02529 [Fusarium graminearum PH-1] >gb|ESU07979.1| hypothetical protein FGSG_02529 [Fusarium graminearum PH-1] >gb|EYB31698.1| hypothetical protein FG05_02529 [Fusarium graminearum] >emb|CEF74839.1| unnamed protein product [Fusarium graminearum]</td></tr>
<tr><td>2485</td><td>tr|I1RC55|I1RC55_GIBZE</td><td>--</td><td>Uncharacterized protein OS=Gibberellazeae (strain PH-1 / ATCC MYA-4620 / FGSC 9075 / NRRL 31084) GN=FG01158.1 PE=3 SV=1</td><td>MAFFPRNFYNSDASFTPLFRLLDDFDSYSRQGTNGNGGARRSGLSHWQPKFDVRETGESYELHGELPGMNKSDVHIEFTEPQTMLIRGKTERTYTAGTPPAGLVEGTEARGAITDDSEEHSNSHHATVEDEEQAKAHEASTEVTHHEQPQEVEKKPVDQSKYWLTERSFGEFSRSFNFPTRVDQENVSAKFNDGILSIVVPKAKKHESRRINVE</td><td>151-213,PF00011.21,HSP20,CL0190;59-198,PF17886.1,ArsA_HSP20,CL0190;</td><td>2</td><td>ref|XP_011316926.1| 30 kDa heat shock protein [Fusarium graminearum PH-1] >gb|ESU06441.1| 30 kDa heat shock protein [Fusarium graminearum PH-1] >gb|EYB33841.1| hypothetical protein FG05_01158 [Fusarium graminearum] >gb|PCD22624.1| 30 kDa heat shock protein [Fusarium graminearum] >emb|CEF73238.1| unnamed protein product [Fusarium graminearum]</td></tr>
</table>

Table S5 GO Ontology enrichment analysis of differential proteins

GO62.5-GO0_Cellular Component

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value	Genes annotated to the term
microbody	12 out of 220 genes, 5.5%	33 out of 1646 genes, 2.0%	0.00065	tr|I1RCK2|I1RCK2_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|I1S9T6|I1S9T6_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1RWM4|I1RWM4_GIBZE, tr|I1S0X1|I1S0X1_GIBZE, tr|I1RJU4|I1RJU4_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|V6R476|V6R476_GIBZE
oligosaccharyltransferase complex	3 out of 220 genes, 1.4%	3 out of 1646 genes, 0.2%	0.00236	tr|I1RAH0|I1RAH0_GIBZE, tr|I1RZM0|I1RZM0_GIBZE, tr|I1R9N7|I1R9N7_GIBZE
peroxisome	10 out of 220 genes, 4.5%	31 out of 1646 genes, 1.9%	0.00508	tr|I1RCK2|I1RCK2_GIBZE, tr|I1S9T6|I1S9T6_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1S0X1|I1S0X1_GIBZE, tr|I1RJU4|I1RJU4_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|V6R476|V6R476_GIBZE
fatty acid synthase complex	2 out of 220 genes, 0.9%	2 out of 1646 genes, 0.1%	0.01779	tr|I1RMW9|I1RMW9_GIBZE, tr|I1RMW8|I1RMW8_GIBZE
glyoxysome	2 out of 220 genes, 0.9%	2 out of 1646 genes, 0.1%	0.01779	sp|Q4HYR2|ACEA_GIBZE, tr|I1RWM4|I1RWM4_GIBZE
AMP-activated protein kinase complex	2 out of 220 genes, 0.9%	2 out of 1646 genes, 0.1%	0.01779	tr|I1RZP6|I1RZP6_GIBZE, tr|A0A0E0SEM1|A0A0E0SEM1_GIBZE
peroxisomal matrix	3 out of 220 genes, 1.4%	5 out of 1646 genes, 0.3%	0.01917	tr|I1S0X1|I1S0X1_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE
microbody lumen	3 out of 220 genes, 1.4%	5 out of 1646 genes, 0.3%	0.01917	tr|I1S0X1|I1S0X1_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE
extracellular region	8 out of 220 genes, 3.6%	27 out of 1646 genes, 1.6%	0.02042	tr|I1RA13|I1RA13_GIBZE, tr|A0A098DGQ1|A0A098DGQ1_GIBZE, tr|I1S2I0|I1S2I0_GIBZE, tr|I1RHQ0|I1RHQ0_GIBZE, tr|A0A0E0SI42|A0A0E0SI42_GIBZE, tr|I1REI0|I1REI0_GIBZE, tr|I1S6S5|I1S6S5_GIBZE, tr|I1RR45|I1RR45_GIBZE
site of polarized growth	14 out of 220 genes, 6.4%	66 out of 1646 genes, 4.0%	0.04807	tr|I1S559|I1S559_GIBZE, tr|I1S8E0|I1S8E0_GIBZE, tr|I1RPQ7|I1RPQ7_GIBZE, tr|A0A0E0SJS1|A0A0E0SJS1_GIBZE, tr|I1RVZ7|I1RVZ7_GIBZE, tr|I1S0X0|I1S0X0_GIBZE, sp|Q4HY71|DBP5_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1S1Z9|I1S1Z9_GIBZE, tr|I1RAB7|I1RAB7_GIBZE, tr|I1RZS5|I1RZS5_GIBZE, tr|V6R476|V6R476_GIBZE, tr|A0A098DQJ8|A0A098DQJ8_GIBZE, tr|I1RZ91|I1RZ91_GIBZE
nuclear envelope lumen	2 out of 220 genes, 0.9%	3 out of 1646 genes, 0.2%	0.04866	tr|I1RZP6|I1RZP6_GIBZE, tr|A0A0E0SEM1|A0A0E0SEM1_GIBZE
cytoplasmic dynein complex	2 out of 220 genes, 0.9%	3 out of 1646 genes, 0.2%	0.04866	tr|A0A1C3YLL9|A0A1C3YLL9_GIBZE, tr|A0A1C3YLK5|A0A1C3YLK5_GIBZE

<table>
<tr><td>dynein complex</td><td>2 out of 220 genes, 0.9%</td><td>3 out of 1646 genes, 0.2%</td><td>0.04866</td><td>tr|A0A1C3YLL9|A0A1C3YLL9_GIBZE, tr|A0A1C3YLK5|A0A1C3YLK5_GIBZE</td></tr>
</table>

GO62.5-GO0_Molecular Function

<table>
<tr><th>Gene Ontology term</th><th>Cluster frequency</th><th>Protein frequency of use</th><th>P-value</th><th>Genes annotated to the term</th></tr>
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<tr><td>catalytic activity</td><td>203 out of 264 genes, 76.9%</td><td>1275 out of 1819 genes, 70.1%</td><td>0.00492</td><td>tr|I1RCK2|I1RCK2_GIBZE, tr|I1RAD8|I1RAD8_GIBZE, tr|G4XVC2|G4XVC2_GIBZA, tr|I1RPV8|I1RPV8_GIBZE, tr|I1RUB2|I1RUB2_GIBZE, tr|A0A098DLP1|A0A098DLP1_GIBZE, tr|I1RWE4|I1RWE4_GIBZE, tr|A0A0E0SER1|A0A0E0SER1_GIBZE, tr|I1S0B0|I1S0B0_GIBZE, tr|I1RAG2|I1RAG2_GIBZE, tr|A0A1C3YM63|A0A1C3YM63_GIBZE, tr|V6R2Z2|V6R2Z2_GIBZE, tr|A0A098D8R7|A0A098D8R7_GIBZE, tr|A0A098DCS9|A0A098DCS9_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|I1RJ37|I1RJ37_GIBZE, tr|V6QVH8|V6QVH8_GIBZE, tr|I1RAU6|I1RAU6_GIBZE, tr|I1RVI8|I1RVI8_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1S6S5|I1S6S5_GIBZE, tr|I1RJU4|I1RJU4_GIBZE, tr|I1S570|I1S570_GIBZE, tr|A0A098DET1|A0A098DET1_GIBZE, tr|I1RVY2|I1RVY2_GIBZE, tr|A0A098E1Q7|A0A098E1Q7_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1S4P4|I1S4P4_GIBZE, tr|I1S6R1|I1S6R1_GIBZE, tr|I1RUH3|I1RUH3_GIBZE, tr|I1RKK5|I1RKK5_GIBZE, tr|I1RZ21|I1RZ21_GIBZE, tr|I1RML4|I1RML4_GIBZE, tr|I1RAH0|I1RAH0_GIBZE, tr|I1RPQ7|I1RPQ7_GIBZE, tr|A0A0E0SDV0|A0A0E0SDV0_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|I1RW41|I1RW41_GIBZE, tr|I1RG54|I1RG54_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RWM4|I1RWM4_GIBZE, tr|I1RZV5|I1RZV5_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|A0A1C3YLC3|A0A1C3YLC3_GIBZE, sp|Q4HTS9|ISN1_GIBZE, tr|V6R476|V6R476_GIBZE, tr|A0A1C3YKH0|A0A1C3YKH0_GIBZE, tr|I1RF16|I1RF16_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1RZM0|I1RZM0_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|V6RG06|V6RG06_GIBZE, tr|A0A1C3YHU9|A0A1C3YHU9_GIBZE, tr|A0A1C3YHQ3|A0A1C3YHQ3_GIBZE, tr|A0A098D6R7|A0A098D6R7_GIBZE, tr|I1RDJ7|I1RDJ7_GIBZE, tr|A0A1C3YKM4|A0A1C3YKM4_GIBZE, tr|I1REI0|I1REI0_GIBZE, tr|I1RN16|I1RN16_GIBZE, tr|I1RI19|I1RI19_GIBZE, tr|A0A0E0SEM1|A0A0E0SEM1_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|A0A098D7M9|A0A098D7M9_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|A0A098DHN6|A0A098DHN6_GIBZE, tr|V6REA4|V6REA4_GIBZE, tr|I1S958|I1S958_GIBZE, tr|I1RMW8|I1RMW8_GIBZE, tr|A0A1C3YLL9|A0A1C3YLL9_GIBZE, tr|I1RSK0|I1RSK0_GIBZE, tr|I1RQU9|I1RQU9_GIBZE, tr|I1RSW5|I1RSW5_GIBZE, tr|I1RXH3|I1RXH3_GIBZE, tr|I1RLW6|I1RLW6_GIBZE, tr|I1RPE5|I1RPE5_GIBZE, tr|I1RH70|I1RH70_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A0E0SGN2|A0A0E0SGN2_GIBZE, tr|A0A098DGQ1|A0A098DGQ1_GIBZE, tr|I1S2I7|I1S2I7_GIBZE, tr|I1RN80|I1RN80_GIBZE, tr|I1RX83|I1RX83_GIBZE, tr|I1RAB7|I1RAB7_GIBZE, tr|A0A1C3YIT5|A0A1C3YIT5_GIBZE, tr|I1RC58|I1RC58_GIBZE, tr|I1S0F3|I1S0F3_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|I1RME1|I1RME1_GIBZE, sp|Q4I7L0|HAT2_GIBZE, tr|I1RCY4|I1RCY4_GIBZE, tr|I1RVR0|I1RVR0_GIBZE, tr|A0A1C3YJ47|A0A1C3YJ47_GIBZE, tr|I1RLA5|I1RLA5_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1SAJ9|I1SAJ9_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|I1RT88|I1RT88_GIBZE, tr|A0A0E0SI42|A0A0E0SI42_GIBZE, tr|I1RJG4|I1RJG4_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|A0A0E0SGT0|A0A0E0SGT0_GIBZE, tr|I1RY35|I1RY35_GIBZE, tr|A0A0E0RMB3|A0A0E0RMB3_GIBZE, tr|I1S9T6|I1S9T6_GIBZE, tr|I1RNW4|I1RNW4_GIBZE, tr|I1RJK0|I1RJK0_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|I1R9N7|I1R9N7_GIBZE, tr|I1RM69|I1RM69_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|A0A098D4K1|A0A098D4K1_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|I1S0I8|I1S0I8_GIBZE,</td></tr>
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transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	5 out of 264 genes, 1.9%	10 out of 1819 genes, 0.5%	0.00838	sp|Q4HYR2|ACEA_GIBZE, tr|I1RY35|I1RY35_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|I1RWM4|I1RWM4_GIBZE
transferase activity	52 out of 264 genes, 19.7%	269 out of 1819 genes, 14.8%	0.01141	tr|A0A0E0RWK1|A0A0E0RWK1_GIBZE, tr|I1RNW4|I1RNW4_GIBZE, tr|G4XVC2|G4XVC2_GIBZA, tr|A0A1C3YHU3|A0A1C3YHU3_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1RZM0|I1RZM0_GIBZE, tr|I1R9N7|I1R9N7_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A1C3YHU9|A0A1C3YHU9_GIBZE, tr|A0A0E0SER1|A0A0E0SER1_GIBZE, tr|A0A098D4K1|A0A098D4K1_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|I1RZP6|I1RZP6_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|V6RDP1|V6RDP1_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1RJ37|I1RJ37_GIBZE, tr|V6QVH8|V6QVH8_GIBZE, tr|I1RMW8|I1RMW8_GIBZE, tr|I1RVI8|I1RVI8_GIBZE, tr|I1RYU0|I1RYU0_GIBZE, tr|I1RC24|I1RC24_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1RSK0|I1RSK0_GIBZE, tr|I1RSW5|I1RSW5_GIBZE, tr|I1RPE5|I1RPE5_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|I1RVY2|I1RVY2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1S4P4|I1S4P4_GIBZE, tr|I1RX83|I1RX83_GIBZE, tr|I1RKK5|I1RKK5_GIBZE,

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<tr><td>transferase activity, transferring pentosyl groups</td><td>5 out of 264 genes, 1.9%</td><td>11 out of 1819 genes, 0.6%</td><td>0.01356</td><td>tr|V6QVH8|V6QVH8_GIBZE, tr|I1RPF5|I1RPF5_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RYU0|I1RYU0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
<tr><td>transferase activity, transferring glycosyl groups</td><td>10 out of 264 genes, 3.8%</td><td>33 out of 1819 genes, 1.8%</td><td>0.01483</td><td>tr|G4XVC2|G4XVC2_GIBZA, tr|I1RAH0|I1RAH0_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RZM0|I1RZM0_GIBZE, tr|I1R9N7|I1R9N7_GIBZE, tr|V6QVH8|V6QVH8_GIBZE, tr|I1RPF5|I1RPF5_GIBZE, tr|I1RX83|I1RX83_GIBZE, tr|I1RYU0|I1RYU0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
<tr><td>oxidoreductase activity</td><td>65 out of 264 genes, 24.6%</td><td>355 out of 1819 genes, 19.5%</td><td>0.01619</td><td>tr|I1S9T6|I1S9T6_GIBZE, tr|I1RAG2|I1RAG2_GIBZE, tr|I1S0I8|I1S0I8_GIBZE, tr|V6R2Z2|V6R2Z2_GIBZE, tr|I1RF05|I1RF05_GIBZE, tr|I1RYP2|I1RYP2_GIBZE, tr|I1RYN2|I1RYN2_GIBZE, tr|A0A0E0SGB3|A0A0E0SGB3_GIBZE, tr|I1RKP5|I1RKP5_GIBZE, tr|I1S0P0|I1S0P0_GIBZE, tr|I1RJU4|I1RJU4_GIBZE, tr|A0A098DET1|A0A098DET1_GIBZE, tr|I1RDV8|I1RDV8_GIBZE, tr|I1RHQ0|I1RHQ0_GIBZE, tr|V6R0W1|V6R0W1_GIBZE, tr|I1RY12|I1RY12_GIBZE, tr|I1S6R1|I1S6R1_GIBZE, tr|I1RZ21|I1RZ21_GIBZE, tr|I1REW2|I1REW2_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A1C3YKF3|A0A1C3YKF3_GIBZE, tr|I1RG54|I1RG54_GIBZE, tr|I1RZV5|I1RZV5_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RHL9|I1RHL9_GIBZE, tr|I1S223|I1S223_GIBZE, tr|I1RCR6|I1RCR6_GIBZE, tr|I1RW64|I1RW64_GIBZE, tr|A0A098DJ03|A0A098DJ03_GIBZE, tr|I1RF16|I1RF16_GIBZE, tr|I1RK26|I1RK26_GIBZE, tr|A0A1C3YHQ3|A0A1C3YHQ3_GIBZE, tr|A0A098D6R7|A0A098D6R7_GIBZE, tr|A0A1C3YKM4|A0A1C3YKM4_GIBZE, tr|I1REV6|I1REV6_GIBZE, tr|I1RI19|I1RI19_GIBZE, tr|I1RN16|I1RN16_GIBZE, tr|I1RR45|I1RR45_GIBZE, tr|I1REY8|I1REY8_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|A0A098DHN6|A0A098DHN6_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A1C3YIR5|A0A1C3YIR5_GIBZE, tr|V6REA4|V6REA4_GIBZE, tr|I1S958|I1S958_GIBZE, tr|I1RMW8|I1RMW8_GIBZE, tr|A0A098DPL1|A0A098DPL1_GIBZE, tr|A0A098DGQ1|A0A098DGQ1_GIBZE, tr|I1RV02|I1RV02_GIBZE, tr|A0A0E0SDM0|A0A0E0SDM0_GIBZE, tr|I1RFJ1|I1RFJ1_GIBZE, tr|I1S8F9|I1S8F9_GIBZE, tr|V6RPN0|V6RPN0_GIBZE, tr|I1RCY4|I1RCY4_GIBZE, tr|I1RME1|I1RME1_GIBZE, tr|V6RAM6|V6RAM6_GIBZE, tr|I1RVW1|I1RVW1_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|I1RT88|I1RT88_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RJG4|I1RJG4_GIBZE, tr|A0A0E0SI42|A0A0E0SI42_GIBZE, tr|I1RFV9|I1RFV9_GIBZE, tr|I1RY16|I1RY16_GIBZE, tr|I1RKZ4|I1RKZ4_GIBZE</td></tr>
<tr><td>oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor</td><td>4 out of 264 genes, 1.5%</td><td>8 out of 1819 genes, 0.4%</td><td>0.01879</td><td>tr|I1S9T6|I1S9T6_GIBZE, tr|I1RF16|I1RF16_GIBZE, tr|I1RHL9|I1RHL9_GIBZE, tr|I1RZ21|I1RZ21_GIBZE</td></tr>
<tr><td>adenylylsulfate kinase activity</td><td>2 out of 264 genes, 0.8%</td><td>2 out of 1819 genes, 0.1%</td><td>0.021</td><td>tr|I1RCL0|I1RCL0_GIBZE, sp|Q4I1N3|MET3_GIBZE</td></tr>
</table>

fatty-acid synthase activity	2 out of 264 genes, 0.8%	2 out of 1819 genes, 0.1%	0.021	tr|I1RMW9|I1RMW9_GIBZE, tr|I1RMW8|I1RMW8_GIBZE
oligosaccharyl transferase activity	2 out of 264 genes, 0.8%	2 out of 1819 genes, 0.1%	0.021	tr|I1RAH0|I1RAH0_GIBZE, tr|I1RZM0|I1RZM0_GIBZE
dolichyl-diphosphooligosaccharide-protein glycotransferase activity	2 out of 264 genes, 0.8%	2 out of 1819 genes, 0.1%	0.021	tr|I1RAH0|I1RAH0_GIBZE, tr|I1RZM0|I1RZM0_GIBZE
5'-nucleotidase activity	2 out of 264 genes, 0.8%	2 out of 1819 genes, 0.1%	0.021	tr|I1REI0|I1REI0_GIBZE, sp|Q4HTS9|ISN1_GIBZE
enoyl-[acyl-carrier-protein] reductase activity	2 out of 264 genes, 0.8%	2 out of 1819 genes, 0.1%	0.021	tr|I1RMW9|I1RMW9_GIBZE, tr|I1RW64|I1RW64_GIBZE
oxygen binding	2 out of 264 genes, 0.8%	2 out of 1819 genes, 0.1%	0.021	tr|I1RUM6|I1RUM6_GIBZE, tr|I1RKP5|I1RKP5_GIBZE
oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	9 out of 264 genes, 3.4%	30 out of 1819 genes, 1.6%	0.02187	tr|V6RAM6|V6RAM6_GIBZE, tr|I1RDV8|I1RDV8_GIBZE, tr|A0A1C3YIR5|A0A1C3YIR5_GIBZE, tr|V6R0W1|V6R0W1_GIBZE, tr|I1RK26|I1RK26_GIBZE, tr|A0A0E0SGB3|A0A0E0SGB3_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RZV5|I1RZV5_GIBZE, tr|V6R2Z2|V6R2Z2_GIBZE
transferase activity, transferring acyl groups	12 out of 264 genes, 4.5%	45 out of 1819 genes, 2.5%	0.02243	tr|I1RMW9|I1RMW9_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|I1RLA5|I1RLA5_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|A0A1C3YHU3|A0A1C3YHU3_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RWM4|I1RWM4_GIBZE, tr|I1RMW8|I1RMW8_GIBZE, tr|A0A098DS79|A0A098DS79_GIBZE, tr|I1RY35|I1RY35_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE
oxidoreductase activity, acting on the aldehyde or oxo group of donors	10 out of 264 genes, 3.8%	35 out of 1819 genes, 1.9%	0.02254	tr|V6RAM6|V6RAM6_GIBZE, tr|I1RDV8|I1RDV8_GIBZE, tr|A0A1C3YIR5|A0A1C3YIR5_GIBZE, tr|V6R0W1|V6R0W1_GIBZE, tr|I1RY12|I1RY12_GIBZE, tr|I1RK26|I1RK26_GIBZE, tr|A0A0E0SGB3|A0A0E0SGB3_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RZV5|I1RZV5_GIBZE, tr|V6R2Z2|V6R2Z2_GIBZE

aldehyde dehydrogenase (NAD) activity	4 out of 264 genes, 1.5%	9 out of 1819 genes, 0.5%	0.03003	tr|I1RDV8|I1RDV8_GIBZE, tr|A0A1C3YIR5|A0A1C3YIR5_GIBZE, tr|A0A0E0SGB3|A0A0E0SGB3_GIBZE, tr|V6R2Z2|V6R2Z2_GIBZE
ligase activity, forming carbon-sulfur bonds	4 out of 264 genes, 1.5%	9 out of 1819 genes, 0.5%	0.03003	tr|I1RA13|I1RA13_GIBZE, tr|I1S0X1|I1S0X1_GIBZE, tr|I1RPV8|I1RPV8_GIBZE, tr|I1RCT9|I1RCT9_GIBZE
motor activity	3 out of 264 genes, 1.1%	6 out of 1819 genes, 0.3%	0.04312	tr|I1RTG5|I1RTG5_GIBZE, tr|A0A1C3YLL9|A0A1C3YLL9_GIBZE, tr|A0A1C3YLK5|A0A1C3YLK5_GIBZE
calcium ion binding	5 out of 264 genes, 1.9%	15 out of 1819 genes, 0.8%	0.05393	tr|I1RSK9|I1RSK9_GIBZE, tr|A0A098DGS4|A0A098DGS4_GIBZE, tr|I1RE20|I1RE20_GIBZE, tr|I1RAB7|I1RAB7_GIBZE, tr|I1RZ91|I1RZ91_GIBZE

GO62.5-GO0_Biological Process

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value	Genes annotated to the term
organic acid metabolic process	52 out of 269 genes, 19.3%	241 out of 1882 genes, 12.8%	0.00065	tr|I1RW64|I1RW64_GIBZE, tr|I1S9T6|I1S9T6_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A098DLP1|A0A098DLP1_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|I1RA13|I1RA13_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RXJ0|I1RXJ0_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1S0X1|I1S0X1_GIBZE, tr|I1RVI8|I1RVI8_GIBZE, tr|I1RYU0|I1RYU0_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|I1RJU4|I1RJU4_GIBZE, tr|I1RQU9|I1RQU9_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A0E0SGN2|A0A0E0SGN2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RNG4|I1RNG4_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|A0A098DVI8|A0A098DVI8_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|I1S2V9|I1S2V9_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RWM4|I1RWM4_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RFV9|I1RFV9_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1S223|I1S223_GIBZE, tr|A0A1C3YKH0|A0A1C3YKH0_GIBZE, tr|I1RCR6|I1RCR6_GIBZE
carboxylic acid metabolic process	51 out of 269 genes, 19.0%	237 out of 1882 genes, 12.6%	0.00079	tr|I1RW64|I1RW64_GIBZE, tr|I1S9T6|I1S9T6_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A098DLP1|A0A098DLP1_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|I1RA13|I1RA13_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RXJ0|I1RXJ0_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1S0X1|I1S0X1_GIBZE, tr|I1RVI8|I1RVI8_GIBZE, tr|I1RYU0|I1RYU0_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1RQU9|I1RQU9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A0E0SGN2|A0A0E0SGN2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RNG4|I1RNG4_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, sp|Q4HYR2|ACEA_GIBZE,

				tr|A0A098DVI8|A0A098DVI8_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|I1S2V9|I1S2V9_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RWM4|I1RWM4_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RFV9|I1RFV9_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1S223|I1S223_GIBZE, tr|A0A1C3YKH0|A0A1C3YKH0_GIBZE, tr|I1RCR6|I1RCR6_GIBZE
oxoacid metabolic process	51 out of 269 genes, 19.0%	237 out of 1882 genes, 12.6%	0.00079	tr|I1RW64|I1RW64_GIBZE, tr|I1S9T6|I1S9T6_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A098DLP1|A0A098DLP1_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|I1RA13|I1RA13_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RXJ0|I1RXJ0_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1S0X1|I1S0X1_GIBZE, tr|I1RVI8|I1RVI8_GIBZE, tr|I1RYU0|I1RYU0_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1RQU9|I1RQU9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A0E0SGN2|A0A0E0SGN2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RNG4|I1RNG4_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|A0A098DVI8|A0A098DVI8_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|I1S2V9|I1S2V9_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RWM4|I1RWM4_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RFV9|I1RFV9_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1S223|I1S223_GIBZE, tr|A0A1C3YKH0|A0A1C3YKH0_GIBZE, tr|I1RCR6|I1RCR6_GIBZE
cellular ketone metabolic process	51 out of 269 genes, 19.0%	238 out of 1882 genes, 12.6%	0.00088	tr|I1RW64|I1RW64_GIBZE, tr|I1S9T6|I1S9T6_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A098DLP1|A0A098DLP1_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|I1RA13|I1RA13_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RXJ0|I1RXJ0_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1S0X1|I1S0X1_GIBZE, tr|I1RVI8|I1RVI8_GIBZE, tr|I1RYU0|I1RYU0_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1RQU9|I1RQU9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A0E0SGN2|A0A0E0SGN2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RNG4|I1RNG4_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|A0A098DVI8|A0A098DVI8_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|I1S2V9|I1S2V9_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RWM4|I1RWM4_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RFV9|I1RFV9_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1S223|I1S223_GIBZE, tr|A0A1C3YKH0|A0A1C3YKH0_GIBZE, tr|I1RCR6|I1RCR6_GIBZE
aspartate family amino acid metabolic process	11 out of 269 genes, 4.1%	30 out of 1882 genes, 1.6%	0.00181	sp|Q4HVQ9|LYS4_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RFV9|I1RFV9_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|I1RCR6|I1RCR6_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE

long-chain fatty acid metabolic process	3 out of 269 genes, 1.1%	3 out of 1882 genes, 0.2%	0.00289	tr|I1RMW9|I1RMW9_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|I1RF24|I1RF24_GIBZE
lysine biosynthetic process via aminoadipic acid	3 out of 269 genes, 1.1%	3 out of 1882 genes, 0.2%	0.00289	tr|I1S2D5|I1S2D5_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE
amine metabolic process	40 out of 269 genes, 14.9%	189 out of 1882 genes, 10.0%	0.00433	tr|I1S9T6|I1S9T6_GIBZE, tr|A0A0E0RWK1|A0A0E0RWK1_GIBZE, tr|G4XVC2|G4XVC2_GIBZA, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RF16|I1RF16_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A098DLP1|A0A098DLP1_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1RQU9|I1RQU9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RNG4|I1RNG4_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|A0A098DVI8|A0A098DVI8_GIBZE, tr|V6RXE7|V6RXE7_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RFV9|I1RFV9_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1RHL9|I1RHL9_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1RCR6|I1RCR6_GIBZE, tr|A0A1C3YKH0|A0A1C3YKH0_GIBZE
cellular amino acid metabolic process	34 out of 269 genes, 12.6%	158 out of 1882 genes, 8.4%	0.00651	tr|I1S9T6|I1S9T6_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A098DLP1|A0A098DLP1_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1RQU9|I1RQU9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RNG4|I1RNG4_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|A0A098DVI8|A0A098DVI8_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RFV9|I1RFV9_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1RCR6|I1RCR6_GIBZE, tr|A0A1C3YKH0|A0A1C3YKH0_GIBZE
cellular amine metabolic process	34 out of 269 genes, 12.6%	158 out of 1882 genes, 8.4%	0.00651	tr|I1S9T6|I1S9T6_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A098DLP1|A0A098DLP1_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1RQU9|I1RQU9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RNG4|I1RNG4_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|A0A098DVI8|A0A098DVI8_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RFV9|I1RFV9_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1RCR6|I1RCR6_GIBZE, tr|A0A1C3YKH0|A0A1C3YKH0_GIBZE

cellular amino acid and derivative metabolic process	39 out of 269 genes, 14.5%	190 out of 1882 genes, 10.1%	0.00841	tr|I1S9T6|I1S9T6_GIBZE, tr|A0A0E0RWK1|A0A0E0RWK1_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A098DLP1|A0A098DLP1_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1RQU9|I1RQU9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A0E0SGN2|A0A0E0SGN2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RNG4|I1RNG4_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|A0A098DVI8|A0A098DVI8_GIBZE, tr|V6RXE7|V6RXE7_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RFV9|I1RFV9_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|A0A098DS79|A0A098DS79_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1RCR6|I1RCR6_GIBZE, tr|A0A1C3YKH0|A0A1C3YKH0_GIBZE
oxidation reduction	59 out of 269 genes, 21.9%	313 out of 1882 genes, 16.6%	0.00879	tr|I1S9T6|I1S9T6_GIBZE, tr|I1RF16|I1RF16_GIBZE, tr|A0A098DJ03|A0A098DJ03_GIBZE, tr|I1RK26|I1RK26_GIBZE, tr|A0A098D6R7|A0A098D6R7_GIBZE, tr|A0A1C3YHQ3|A0A1C3YHQ3_GIBZE, tr|I1REV6|I1REV6_GIBZE, tr|A0A1C3YKM4|A0A1C3YKM4_GIBZE, tr|I1RAG2|I1RAG2_GIBZE, tr|I1RN16|I1RN16_GIBZE, tr|I1RI19|I1RI19_GIBZE, tr|I1RR45|I1RR45_GIBZE, tr|I1S0I8|I1S0I8_GIBZE, tr|V6R2Z2|V6R2Z2_GIBZE, tr|I1RF05|I1RF05_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|I1REY8|I1REY8_GIBZE, tr|I1RYP2|I1RYP2_GIBZE, tr|V6REA4|V6REA4_GIBZE, tr|A0A1C3YIR5|A0A1C3YIR5_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1RYN2|I1RYN2_GIBZE, tr|A0A0E0SGB3|A0A0E0SGB3_GIBZE, tr|I1S958|I1S958_GIBZE, tr|I1RKP5|I1RKP5_GIBZE, tr|I1S0P0|I1S0P0_GIBZE, tr|I1RMW8|I1RMW8_GIBZE, tr|I1RJU4|I1RJU4_GIBZE, tr|A0A098DPL1|A0A098DPL1_GIBZE, tr|A0A098DET1|A0A098DET1_GIBZE, tr|I1RDV8|I1RDV8_GIBZE, tr|A0A098DGQ1|A0A098DGQ1_GIBZE, tr|I1RHQ0|I1RHQ0_GIBZE, tr|I1RV02|I1RV02_GIBZE, tr|A0A0E0SDM0|A0A0E0SDM0_GIBZE, tr|V6R0W1|V6R0W1_GIBZE, tr|I1RY12|I1RY12_GIBZE, tr|I1S6R1|I1S6R1_GIBZE, tr|I1RFJ1|I1RFJ1_GIBZE, tr|I1S8F9|I1S8F9_GIBZE, tr|I1RZ21|I1RZ21_GIBZE, tr|V6RPN0|V6RPN0_GIBZE, tr|I1RME1|I1RME1_GIBZE, tr|I1RCY4|I1RCY4_GIBZE, tr|V6RAM6|V6RAM6_GIBZE, tr|I1RVW1|I1RVW1_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A1C3YKF3|A0A1C3YKF3_GIBZE, tr|I1RT88|I1RT88_GIBZE, tr|I1RG54|I1RG54_GIBZE, tr|A0A0E0SI42|A0A0E0SI42_GIBZE, tr|I1RJG4|I1RJG4_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RFV9|I1RFV9_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RHL9|I1RHL9_GIBZE, tr|I1RY16|I1RY16_GIBZE, tr|I1RKZ4|I1RKZ4_GIBZE, tr|I1RCR6|I1RCR6_GIBZE
lysine metabolic process	4 out of 269 genes, 1.5%	7 out of 1882 genes, 0.4%	0.01002	tr|I1S2D5|I1S2D5_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|I1RCR6|I1RCR6_GIBZE
lysine biosynthetic process	4 out of 269 genes, 1.5%	7 out of 1882 genes, 0.4%	0.01002	tr|I1S2D5|I1S2D5_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|I1RCR6|I1RCR6_GIBZE
cellular carbohydrate metabolic process	45 out of 269 genes, 16.7%	230 out of 1882 genes, 12.2%	0.01163	tr|I1S9T6|I1S9T6_GIBZE, tr|G4XVC2|G4XVC2_GIBZA, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1RZM0|I1RZM0_GIBZE, tr|I1R9N7|I1R9N7_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A098DLP1|A0A098DLP1_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|V6RDP1|V6RDP1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1RQU9|I1RQU9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|I1RHQ0|I1RHQ0_GIBZE, tr|I1RW06|I1RW06_GIBZE,

<table>
<tr><td></td><td></td><td></td><td></td><td>tr|I1S2H3|I1S2H3_GIBZE, tr|I1RX83|I1RX83_GIBZE, tr|I1RNG4|I1RNG4_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|A0A098DVI8|A0A098DVI8_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RAH0|I1RAH0_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|I1RWM4|I1RWM4_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|A0A0E0SI42|A0A0E0SI42_GIBZE, tr|I1RFV9|I1RFV9_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|A0A1C3YIZ4|A0A1C3YIZ4_GIBZE, tr|I1RCR6|I1RCR6_GIBZE, tr|A0A1C3YKH0|A0A1C3YKH0_GIBZE</td></tr>
<tr><td>aspartate family amino acid biosynthetic process</td><td>8 out of 269 genes, 3.0%</td><td>24 out of 1882 genes, 1.3%</td><td>0.0145</td><td>sp|Q4HVQ9|LYS4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|I1RCR6|I1RCR6_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE</td></tr>
<tr><td>cellular metabolic compound salvage</td><td>6 out of 269 genes, 2.2%</td><td>16 out of 1882 genes, 0.9%</td><td>0.01838</td><td>tr|I1REI0|I1REI0_GIBZE, tr|V6QVH8|V6QVH8_GIBZE, tr|I1RFV9|I1RFV9_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RZ21|I1RZ21_GIBZE, sp|Q4HTS9|ISN1_GIBZE</td></tr>
<tr><td>response to abiotic stimulus</td><td>8 out of 269 genes, 3.0%</td><td>25 out of 1882 genes, 1.3%</td><td>0.01875</td><td>tr|A0A098DRP2|A0A098DRP2_GIBZE, tr|A0A098D8N2|A0A098D8N2_GIBZE, tr|I1RBS5|I1RBS5_GIBZE, tr|I1S0X0|I1S0X0_GIBZE, tr|A0A0E0SI42|A0A0E0SI42_GIBZE, tr|A0A098DDH9|A0A098DDH9_GIBZE, tr|I1RC24|I1RC24_GIBZE, tr|I1RKZ4|I1RKZ4_GIBZE</td></tr>
<tr><td>positive regulation of cellular carbohydrate metabolic process</td><td>2 out of 269 genes, 0.7%</td><td>2 out of 1882 genes, 0.1%</td><td>0.02036</td><td>tr|I1RZP6|I1RZP6_GIBZE, tr|A0A0E0SEM1|A0A0E0SEM1_GIBZE</td></tr>
<tr><td>positive regulation of glucose metabolic process</td><td>2 out of 269 genes, 0.7%</td><td>2 out of 1882 genes, 0.1%</td><td>0.02036</td><td>tr|I1RZP6|I1RZP6_GIBZE, tr|A0A0E0SEM1|A0A0E0SEM1_GIBZE</td></tr>
<tr><td>peptidyl-asparagine modification</td><td>2 out of 269 genes, 0.7%</td><td>2 out of 1882 genes, 0.1%</td><td>0.02036</td><td>tr|I1RAH0|I1RAH0_GIBZE, tr|I1R9N7|I1R9N7_GIBZE</td></tr>
<tr><td>protein amino acid N-linked glycosylation via asparagine</td><td>2 out of 269 genes, 0.7%</td><td>2 out of 1882 genes, 0.1%</td><td>0.02036</td><td>tr|I1RAH0|I1RAH0_GIBZE, tr|I1R9N7|I1R9N7_GIBZE</td></tr>
<tr><td>sulfate assimilation, phosphoadenylyl sulfate reduction by</td><td>2 out of 269 genes, 0.7%</td><td>2 out of 1882 genes, 0.1%</td><td>0.02036</td><td>tr|I1RCL0|I1RCL0_GIBZE, sp|Q4I1N3|MET3_GIBZE</td></tr>
</table>

phosphoadenylyl-sulfate reductase (thioredoxin)				
alditol biosynthetic process	2 out of 269 genes, 0.7%	2 out of 1882 genes, 0.1%	0.02036	tr|A0A0E0SI42|A0A0E0SI42_GIBZE, tr|A0A1C3YIZ4|A0A1C3YIZ4_GIBZE
sulfate reduction	2 out of 269 genes, 0.7%	2 out of 1882 genes, 0.1%	0.02036	tr|I1RCL0|I1RCL0_GIBZE, sp|Q4I1N3|MET3_GIBZE
methionine salvage	2 out of 269 genes, 0.7%	2 out of 1882 genes, 0.1%	0.02036	tr|I1RFV9|I1RFV9_GIBZE, tr|I1RW06|I1RW06_GIBZE
propionate metabolic process, methylcitrate cycle	2 out of 269 genes, 0.7%	2 out of 1882 genes, 0.1%	0.02036	tr|I1RA13|I1RA13_GIBZE, tr|I1RVI8|I1RVI8_GIBZE
long-chain fatty acid catabolic process	2 out of 269 genes, 0.7%	2 out of 1882 genes, 0.1%	0.02036	tr|I1RCT9|I1RCT9_GIBZE, tr|I1RF24|I1RF24_GIBZE
amino acid salvage	2 out of 269 genes, 0.7%	2 out of 1882 genes, 0.1%	0.02036	tr|I1RFV9|I1RFV9_GIBZE, tr|I1RW06|I1RW06_GIBZE
positive regulation of gluconeogenesis	2 out of 269 genes, 0.7%	2 out of 1882 genes, 0.1%	0.02036	tr|I1RZP6|I1RZP6_GIBZE, tr|A0A0E0SEM1|A0A0E0SEM1_GIBZE
positive regulation of carbohydrate metabolic process	2 out of 269 genes, 0.7%	2 out of 1882 genes, 0.1%	0.02036	tr|I1RZP6|I1RZP6_GIBZE, tr|A0A0E0SEM1|A0A0E0SEM1_GIBZE
D-amino acid metabolic process	2 out of 269 genes, 0.7%	2 out of 1882 genes, 0.1%	0.02036	tr|I1S9T6|I1S9T6_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE

amine biosynthetic process	21 out of 269 genes, 7.8%	94 out of 1882 genes, 5.0%	0.02046	tr|A0A0E0RWK1|A0A0E0RWK1_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RW06|I1RW06_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RNG4|I1RNG4_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|I1RCR6|I1RCR6_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YKH0|A0A1C3YKH0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE
cellular amino acid biosynthetic process	20 out of 269 genes, 7.4%	89 out of 1882 genes, 4.7%	0.02205	tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RW06|I1RW06_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RNG4|I1RNG4_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|I1RCR6|I1RCR6_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YKH0|A0A1C3YKH0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE
organic acid catabolic process	13 out of 269 genes, 4.8%	51 out of 1882 genes, 2.7%	0.02293	tr|I1RA13|I1RA13_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|A0A098DVI8|A0A098DVI8_GIBZE, tr|I1RXJ0|I1RXJ0_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|A0A098DLP1|A0A098DLP1_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1S0X1|I1S0X1_GIBZE, tr|I1S223|I1S223_GIBZE
carboxylic acid catabolic process	13 out of 269 genes, 4.8%	51 out of 1882 genes, 2.7%	0.02293	tr|I1RA13|I1RA13_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|A0A098DVI8|A0A098DVI8_GIBZE, tr|I1RXJ0|I1RXJ0_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|A0A098DLP1|A0A098DLP1_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1S0X1|I1S0X1_GIBZE, tr|I1S223|I1S223_GIBZE
synapsis	3 out of 269 genes, 1.1%	5 out of 1882 genes, 0.3%	0.02313	tr|A0A098DVZ3|A0A098DVZ3_GIBZE, tr|A0A1C3YLK5|A0A1C3YLK5_GIBZE, tr|A0A098DSW9|A0A098DSW9_GIBZE
histone acetylation	3 out of 269 genes, 1.1%	5 out of 1882 genes, 0.3%	0.02313	tr|A0A0E0S6D3|A0A0E0S6D3_GIBZE, tr|I1S0R2|I1S0R2_GIBZE, sp|Q4I7L0|HAT2_GIBZE
hydrogen peroxide catabolic process	3 out of 269 genes, 1.1%	5 out of 1882 genes, 0.3%	0.02313	tr|A0A098DJ03|A0A098DJ03_GIBZE, tr|I1RR45|I1RR45_GIBZE, tr|A0A1C3YKF3|A0A1C3YKF3_GIBZE
chromosome organization involved in meiosis	3 out of 269 genes, 1.1%	5 out of 1882 genes, 0.3%	0.02313	tr|A0A098DVZ3|A0A098DVZ3_GIBZE, tr|A0A1C3YLK5|A0A1C3YLK5_GIBZE, tr|A0A098DSW9|A0A098DSW9_GIBZE
methionine metabolic process	6 out of 269 genes, 2.2%	17 out of 1882 genes, 0.9%	0.02509	tr|I1RFV9|I1RFV9_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RW06|I1RW06_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RE58|I1RE58_GIBZE

<table>
<tr><td>multicellular organismal development</td><td>7 out of 269 genes, 2.6%</td><td>22 out of 1882 genes, 1.2%</td><td>0.02829</td><td>sp|Q4I1H6|SNX3_GIBZE, tr|I1RX83|I1RX83_GIBZE, tr|I1RWK8|I1RWK8_GIBZE, tr|I1S2V9|I1S2V9_GIBZE, tr|A0A0E0SGT0|A0A0E0SGT0_GIBZE, tr|I1RH70|I1RH70_GIBZE, tr|V6RN44|V6RN44_GIBZE</td></tr>
<tr><td>response to osmotic stress</td><td>4 out of 269 genes, 1.5%</td><td>9 out of 1882 genes, 0.5%</td><td>0.02853</td><td>tr|A0A098DRP2|A0A098DRP2_GIBZE, tr|A0A098DDH9|A0A098DDH9_GIBZE, tr|I1S0X0|I1S0X0_GIBZE, tr|I1RKZ4|I1RKZ4_GIBZE</td></tr>
<tr><td>regulation of cellular carbohydrate metabolic process</td><td>4 out of 269 genes, 1.5%</td><td>9 out of 1882 genes, 0.5%</td><td>0.02853</td><td>tr|A0A098DQF0|A0A098DQF0_GIBZE, tr|I1RZP6|I1RZP6_GIBZE, tr|V6R476|V6R476_GIBZE, tr|A0A0E0SEM1|A0A0E0SEM1_GIBZE</td></tr>
<tr><td>second-messenger-mediated signaling</td><td>4 out of 269 genes, 1.5%</td><td>9 out of 1882 genes, 0.5%</td><td>0.02853</td><td>tr|I1RSV0|I1RSV0_GIBZE, tr|I1RC58|I1RC58_GIBZE, tr|I1RVZ7|I1RVZ7_GIBZE, tr|V6RN44|V6RN44_GIBZE</td></tr>
<tr><td>regulation of carbohydrate biosynthetic process</td><td>4 out of 269 genes, 1.5%</td><td>9 out of 1882 genes, 0.5%</td><td>0.02853</td><td>tr|A0A098DQF0|A0A098DQF0_GIBZE, tr|I1RZP6|I1RZP6_GIBZE, tr|V6R476|V6R476_GIBZE, tr|A0A0E0SEM1|A0A0E0SEM1_GIBZE</td></tr>
<tr><td>developmental process</td><td>20 out of 269 genes, 7.4%</td><td>94 out of 1882 genes, 5.0%</td><td>0.03821</td><td>*tr|I1RCK2|I1RCK2_GIBZE, tr|A0A098DVZ3|A0A098DVZ3_GIBZE, tr|I1RSV0|I1RSV0_GIBZE, tr|I1S1Z9|I1S1Z9_GIBZE, tr|I1RX83|I1RX83_GIBZE, tr|I1RAB7|I1RAB7_GIBZE, tr|I1RZP6|I1RZP6_GIBZE, tr|I1RR45|I1RR45_GIBZE, tr|A0A0E0SEM1|A0A0E0SEM1_GIBZE, sp|Q4I1H6|SNX3_GIBZE, tr|I1REC4|I1REC4_GIBZE, tr|I1RWK8|I1RWK8_GIBZE, tr|A0A0E0SDV0|A0A0E0SDV0_GIBZE, tr|I1S2V9|I1S2V9_GIBZE, tr|I1RPQ7|I1RPQ7_GIBZE, tr|V6RN44|V6RN44_GIBZE, tr|A0A0E0SGT0|A0A0E0SGT0_GIBZE, tr|I1RZS5|I1RZS5_GIBZE, tr|I1RH70|I1RH70_GIBZE, tr|I1RZ91|I1RZ91_GIBZE*</td></tr>
<tr><td>oxygen and reactive oxygen species metabolic process</td><td>5 out of 269 genes, 1.9%</td><td>14 out of 1882 genes, 0.7%</td><td>0.03832</td><td>tr|A0A098DGQ1|A0A098DGQ1_GIBZE, tr|A0A098DJ03|A0A098DJ03_GIBZE, tr|I1RR45|I1RR45_GIBZE, tr|A0A1C3YKF3|A0A1C3YKF3_GIBZE, tr|I1RKZ4|I1RKZ4_GIBZE</td></tr>
<tr><td>organic acid biosynthetic process</td><td>22 out of 269 genes, 8.2%</td><td>106 out of 1882 genes, 5.6%</td><td>0.03942</td><td>tr|I1RW64|I1RW64_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RW06|I1RW06_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RNG4|I1RNG4_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|I1RCR6|I1RCR6_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YKH0|A0A1C3YKH0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
<tr><td>carboxylic acid biosynthetic process</td><td>22 out of 269 genes, 8.2%</td><td>106 out of 1882 genes, 5.6%</td><td>0.03942</td><td>tr|I1RW64|I1RW64_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RW06|I1RW06_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RNG4|I1RNG4_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|I1RCR6|I1RCR6_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YKH0|A0A1C3YKH0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
</table>

regulation of gluconeogenesis	3 out of 269 genes, 1.1%	6 out of 1882 genes, 0.3%	0.04142	tr|A0A098DQF0|A0A098DQF0_GIBZE, tr|I1RZP6|I1RZP6_GIBZE, tr|A0A0E0SEM1|A0A0E0SEM1_GIBZE
protein amino acid acetylation	3 out of 269 genes, 1.1%	6 out of 1882 genes, 0.3%	0.04142	tr|A0A0E0S6D3|A0A0E0S6D3_GIBZE, tr|I1S0R2|I1S0R2_GIBZE, sp|Q4I7L0|HAT2_GIBZE
regulation of glucose metabolic process	3 out of 269 genes, 1.1%	6 out of 1882 genes, 0.3%	0.04142	tr|A0A098DQF0|A0A098DQF0_GIBZE, tr|I1RZP6|I1RZP6_GIBZE, tr|A0A0E0SEM1|A0A0E0SEM1_GIBZE
hydrogen peroxide metabolic process	3 out of 269 genes, 1.1%	6 out of 1882 genes, 0.3%	0.04142	tr|A0A098DJ03|A0A098DJ03_GIBZE, tr|I1RR45|I1RR45_GIBZE, tr|A0A1C3YKF3|A0A1C3YKF3_GIBZE
protein retention in Golgi apparatus	3 out of 269 genes, 1.1%	6 out of 1882 genes, 0.3%	0.04142	tr|I1REC4|I1REC4_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|I1RG99|I1RG99_GIBZE
regulation of carbohydrate metabolic process	4 out of 269 genes, 1.5%	10 out of 1882 genes, 0.5%	0.04231	tr|A0A098DQF0|A0A098DQF0_GIBZE, tr|I1RZP6|I1RZP6_GIBZE, tr|V6R476|V6R476_GIBZE, tr|A0A0E0SEM1|A0A0E0SEM1_GIBZE
fatty acid beta-oxidation	4 out of 269 genes, 1.5%	10 out of 1882 genes, 0.5%	0.04231	tr|I1RCT9|I1RCT9_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|I1S223|I1S223_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE
fatty acid oxidation	4 out of 269 genes, 1.5%	10 out of 1882 genes, 0.5%	0.04231	tr|I1RCT9|I1RCT9_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|I1S223|I1S223_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE
alditol metabolic process	4 out of 269 genes, 1.5%	10 out of 1882 genes, 0.5%	0.04231	tr|A0A0E0SI42|A0A0E0SI42_GIBZE, tr|I1RHQ0|I1RHQ0_GIBZE, tr|V6RDP1|V6RDP1_GIBZE, tr|A0A1C3YIZ4|A0A1C3YIZ4_GIBZE
lipid oxidation	4 out of 269 genes, 1.5%	10 out of 1882 genes, 0.5%	0.04231	tr|I1RCT9|I1RCT9_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|I1S223|I1S223_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE
multicellular organismal process	7 out of 269 genes, 2.6%	24 out of 1882 genes, 1.3%	0.04466	sp|Q4I1H6|SNX3_GIBZE, tr|I1RX83|I1RX83_GIBZE, tr|I1RWK8|I1RWK8_GIBZE, tr|I1S2V9|I1S2V9_GIBZE, tr|A0A0E0SGT0|A0A0E0SGT0_GIBZE, tr|I1RH70|I1RH70_GIBZE, tr|V6RN44|V6RN44_GIBZE
mycelium development	5 out of 269 genes, 1.9%	15 out of 1882 genes, 0.8%	0.05097	sp|Q4I1H6|SNX3_GIBZE, tr|I1RWK8|I1RWK8_GIBZE, tr|I1S2V9|I1S2V9_GIBZE, tr|I1RH70|I1RH70_GIBZE, tr|V6RN44|V6RN44_GIBZE

GO125-GO0_Cellular Component

<table>
<tr><th>Gene Ontology term</th><th>Cluster frequency</th><th>Protein frequency of use</th><th>P-value</th><th>Genes annotated to the term</th></tr>
<tr><td>commitment complex</td><td>4 out of 219 genes, 1.8%</td><td>6 out of 1646 genes, 0.4%</td><td>0.00368</td><td>tr|I1S7M3|I1S7M3_GIBZE, tr|I1RT35|I1RT35_GIBZE, tr|I1RCD6|I1RCD6_GIBZE, tr|A0A098D2V8|A0A098D2V8_GIBZE</td></tr>
<tr><td>cell surface</td><td>3 out of 219 genes, 1.4%</td><td>4 out of 1646 genes, 0.2%</td><td>0.00839</td><td>tr|I1RTU1|I1RTU1_GIBZE, tr|I1RF16|I1RF16_GIBZE, tr|I1RZX4|I1RZX4_GIBZE</td></tr>
<tr><td>plasma membrane part</td><td>8 out of 219 genes, 3.7%</td><td>26 out of 1646 genes, 1.6%</td><td>0.01576</td><td>tr|V6R3U5|V6R3U5_GIBZE, tr|I1RZX4|I1RZX4_GIBZE, tr|I1RJS2|I1RJS2_GIBZE, tr|I1S0N8|I1S0N8_GIBZE, tr|A0A098DD75|A0A098DD75_GIBZE, tr|A0A1C3YIN0|A0A1C3YIN0_GIBZE, tr|V6R7A6|V6R7A6_GIBZE, tr|I1RSV0|I1RSV0_GIBZE</td></tr>
<tr><td>presequence translocase-associated import motor</td><td>2 out of 219 genes, 0.9%</td><td>2 out of 1646 genes, 0.1%</td><td>0.01763</td><td>tr|A0A1C3YIX0|A0A1C3YIX0_GIBZE, tr|I1R9Y8|I1R9Y8_GIBZE</td></tr>
<tr><td>fatty acid synthase complex</td><td>2 out of 219 genes, 0.9%</td><td>2 out of 1646 genes, 0.1%</td><td>0.01763</td><td>tr|I1RMW9|I1RMW9_GIBZE, tr|I1RMW8|I1RMW8_GIBZE</td></tr>
<tr><td>chromosome, centromeric outer repeat region</td><td>2 out of 219 genes, 0.9%</td><td>2 out of 1646 genes, 0.1%</td><td>0.01763</td><td>sp|Q4IJU0|POB3_GIBZE, tr|I1S7M3|I1S7M3_GIBZE</td></tr>
<tr><td>pICln-Sm protein complex</td><td>2 out of 219 genes, 0.9%</td><td>2 out of 1646 genes, 0.1%</td><td>0.01763</td><td>tr|I1S7M3|I1S7M3_GIBZE, tr|A0A098D2V8|A0A098D2V8_GIBZE</td></tr>
<tr><td>extracellular region</td><td>8 out of 219 genes, 3.7%</td><td>27 out of 1646 genes, 1.6%</td><td>0.0199</td><td>tr|I1RA13|I1RA13_GIBZE, tr|I1S2I0|I1S2I0_GIBZE, tr|I1RTU1|I1RTU1_GIBZE, tr|I1REI0|I1REI0_GIBZE, tr|I1RHQ0|I1RHQ0_GIBZE, tr|I1S2W9|I1S2W9_GIBZE, tr|I1S6S5|I1S6S5_GIBZE, tr|I1S379|I1S379_GIBZE</td></tr>
<tr><td>extrinsic to plasma membrane</td><td>3 out of 219 genes, 1.4%</td><td>6 out of 1646 genes, 0.4%</td><td>0.03417</td><td>tr|I1RSV0|I1RSV0_GIBZE, tr|I1RJS2|I1RJS2_GIBZE, tr|I1S0N8|I1S0N8_GIBZE</td></tr>
<tr><td>cell wall</td><td>4 out of 219 genes, 1.8%</td><td>11 out of 1646 genes, 0.7%</td><td>0.04707</td><td>tr|I1RR60|I1RR60_GIBZE, tr|I1RF16|I1RF16_GIBZE, tr|I1RJD9|I1RJD9_GIBZE, tr|I1RZX4|I1RZX4_GIBZE</td></tr>
<tr><td>mitochondrial inner membrane presequence translocase complex</td><td>2 out of 219 genes, 0.9%</td><td>3 out of 1646 genes, 0.2%</td><td>0.04824</td><td>tr|A0A1C3YIX0|A0A1C3YIX0_GIBZE, tr|I1R9Y8|I1R9Y8_GIBZE</td></tr>
</table>

<table>
<tr><td>oligosaccharyltransferase complex</td><td>2 out of 219 genes, 0.9%</td><td>3 out of 1646 genes, 0.2%</td><td>0.04824</td><td>tr|I1RAH0|I1RAH0_GIBZE, tr|I1RZM0|I1RZM0_GIBZE</td></tr>
<tr><td>SMN-Sm protein complex</td><td>2 out of 219 genes, 0.9%</td><td>3 out of 1646 genes, 0.2%</td><td>0.04824</td><td>tr|I1S7M3|I1S7M3_GIBZE, tr|A0A098D2V8|A0A098D2V8_GIBZE</td></tr>
<tr><td>periplasmic space</td><td>2 out of 219 genes, 0.9%</td><td>3 out of 1646 genes, 0.2%</td><td>0.04824</td><td>tr|I1RTU1|I1RTU1_GIBZE, tr|V6RV57|V6RV57_GIBZE</td></tr>
<tr><td>fungal-type cell wall</td><td>3 out of 219 genes, 1.4%</td><td>7 out of 1646 genes, 0.4%</td><td>0.05402</td><td>tr|I1RF16|I1RF16_GIBZE, tr|I1RJD9|I1RJD9_GIBZE, tr|I1RZX4|I1RZX4_GIBZE</td></tr>
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GO125-GO0_Molecular Function

<table>
<tr><th>Gene Ontology term</th><th>Cluster frequency</th><th>Protein frequency of use</th><th>P-value</th><th>Genes annotated to the term</th></tr>
<tr><td>catalytic activity</td><td>208 out of 263 genes, 79.1%</td><td>1275 out of 1819 genes, 70.1%</td><td>0.00027</td><td>tr|I1RAD8|I1RAD8_GIBZE, tr|I1RCK2|I1RCK2_GIBZE, tr|G4XVC2|G4XVC2_GIBZA, tr|I1RPV8|I1RPV8_GIBZE, tr|A0A098DT41|A0A098DT41_GIBZE, tr|I1RUB2|I1RUB2_GIBZE, tr|I1RWE4|I1RWE4_GIBZE, tr|A0A0E0SER1|A0A0E0SER1_GIBZE, tr|I1S0B0|I1S0B0_GIBZE, tr|I1RAG2|I1RAG2_GIBZE, tr|A0A098DJH8|A0A098DJH8_GIBZE, tr|I1RIG1|I1RIG1_GIBZE, tr|A0A098DS29|A0A098DS29_GIBZE, tr|V6R2Z2|V6R2Z2_GIBZE, tr|I1RCA7|I1RCA7_GIBZE, tr|A0A098DCS9|A0A098DCS9_GIBZE, tr|I1RVU9|I1RVU9_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|I1S0N8|I1S0N8_GIBZE, tr|V6QVH8|V6QVH8_GIBZE, tr|I1RAU6|I1RAU6_GIBZE, tr|I1RVI8|I1RVI8_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1S6S5|I1S6S5_GIBZE, tr|I1RJU4|I1RJU4_GIBZE, tr|I1S570|I1S570_GIBZE, tr|I1RX90|I1RX90_GIBZE, tr|I1RLX7|I1RLX7_GIBZE, tr|A0A098E1Q7|A0A098E1Q7_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1S6R1|I1S6R1_GIBZE, tr|I1RZ21|I1RZ21_GIBZE, tr|I1RML4|I1RML4_GIBZE, tr|I1RAH0|I1RAH0_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RZV5|I1RZV5_GIBZE, tr|A0A1C3YLG3|A0A1C3YLG3_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1RKR9|I1RKR9_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE, tr|I1RF16|I1RF16_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1RZM0|I1RZM0_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A098D6R7|A0A098D6R7_GIBZE, tr|I1RDJ7|I1RDJ7_GIBZE, tr|I1RHP6|I1RHP6_GIBZE, tr|A0A1C3YHK0|A0A1C3YHK0_GIBZE, tr|I1REI0|I1REI0_GIBZE, tr|I1RTU1|I1RTU1_GIBZE, tr|A0A098DQK4|A0A098DQK4_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|A0A1C3YIS5|A0A1C3YIS5_GIBZE, tr|I1RN16|I1RN16_GIBZE, tr|I1RI19|I1RI19_GIBZE, tr|I1RKE1|I1RKE1_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|A0A098DHN6|A0A098DHN6_GIBZE, tr|I1S958|I1S958_GIBZE, tr|I1S210|I1S210_GIBZE, tr|I1RQE1|I1RQE1_GIBZE, tr|A0A1C3YJX2|A0A1C3YJX2_GIBZE, tr|I1RMW8|I1RMW8_GIBZE, tr|I1RGB2|I1RGB2_GIBZE, tr|I1S6V0|I1S6V0_GIBZE, tr|A0A098DJ29|A0A098DJ29_GIBZE, tr|I1RLW6|I1RLW6_GIBZE, tr|I1RPE5|I1RPE5_GIBZE, tr|I1RH70|I1RH70_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A0E0SGN2|A0A0E0SGN2_GIBZE, tr|A0A0E0RS58|A0A0E0RS58_GIBZE, tr|I1RSA3|I1RSA3_GIBZE, tr|I1RJQ5|I1RJQ5_GIBZE, tr|I1S2I7|I1S2I7_GIBZE, tr|V6RUB1|V6RUB1_GIBZE, tr|V6RK40|V6RK40_GIBZE, tr|I1RN80|I1RN80_GIBZE, tr|A0A098DBF9|A0A098DBF9_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RPN1|I1RPN1_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|I1RME1|I1RME1_GIBZE, tr|V6RSF3|V6RSF3_GIBZE, tr|I1RR72|I1RR72_GIBZE, tr|A0A0E0RVC1|A0A0E0RVC1_GIBZE, tr|A0A1C3YJ47|A0A1C3YJ47_GIBZE, tr|I1RLA5|I1RLA5_GIBZE, tr|I1RJC5|I1RJC5_GIBZE, tr|A0A1C3YI05|A0A1C3YI05_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|A0A0E0RTW2|A0A0E0RTW2_GIBZE,</td></tr>
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<tr><td>oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor</td><td>10 out of 263 genes, 3.8%</td><td>30 out of 1819 genes, 1.6%</td><td>0.00699</td><td>tr|V6RAM6|V6RAM6_GIBZE, tr|I1RDV8|I1RDV8_GIBZE, tr|I1RJC5|I1RJC5_GIBZE, tr|V6R0W1|V6R0W1_GIBZE, tr|A0A0E0SGB3|A0A0E0SGB3_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RZV5|I1RZV5_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|V6R2Z2|V6R2Z2_GIBZE</td></tr>
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<tr><td>oxidoreductase activity, acting on the aldehyde or oxo group of donors</td><td>11 out of 263 genes, 4.2%</td><td>35 out of 1819 genes, 1.9%</td><td>0.00777</td><td>tr|V6RAM6|V6RAM6_GIBZE, tr|I1RDV8|I1RDV8_GIBZE, tr|I1RJC5|I1RJC5_GIBZE, tr|V6R0W1|V6R0W1_GIBZE, tr|I1RY12|I1RY12_GIBZE, tr|A0A0E0SGB3|A0A0E0SGB3_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RZV5|I1RZV5_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|V6R2Z2|V6R2Z2_GIBZE</td></tr>
<tr><td>transferase activity, transferring acyl groups</td><td>13 out of 263 genes, 4.9%</td><td>45 out of 1819 genes, 2.5%</td><td>0.00859</td><td>tr|I1RMW9|I1RMW9_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|I1RX90|I1RX90_GIBZE, tr|I1RLA5|I1RLA5_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|A0A1C3YHU3|A0A1C3YHU3_GIBZE, tr|A0A0E0RSR0|A0A0E0RSR0_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RMW8|I1RMW8_GIBZE, tr|A0A098DS79|A0A098DS79_GIBZE, tr|I1RY35|I1RY35_GIBZE, tr|I1RVX9|I1RVX9_GIBZE</td></tr>
<tr><td>quinone binding</td><td>4 out of 263 genes, 1.5%</td><td>7 out of 1819 genes, 0.4%</td><td>0.01045</td><td>tr|I1S0P0|I1S0P0_GIBZE, tr|I1RF16|I1RF16_GIBZE, tr|I1RHL9|I1RHL9_GIBZE, tr|A0A0E0RTW2|A0A0E0RTW2_GIBZE</td></tr>
<tr><td>carbon-oxygen lyase activity, acting on phosphates</td><td>3 out of 263 genes, 1.1%</td><td>4 out of 1819 genes, 0.2%</td><td>0.01069</td><td>tr|I1RK93|I1RK93_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE</td></tr>
<tr><td>oxidoreductase activity</td><td>65 out of 263 genes, 24.7%</td><td>355 out of 1819 genes, 19.5%</td><td>0.01484</td><td>tr|I1RAG2|I1RAG2_GIBZE, tr|I1RIG1|I1RIG1_GIBZE, tr|I1S0I8|I1S0I8_GIBZE, tr|V6R2Z2|V6R2Z2_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RVU9|I1RVU9_GIBZE, tr|I1RYN2|I1RYN2_GIBZE, tr|A0A098D8J9|A0A098D8J9_GIBZE, tr|A0A0E0SGB3|A0A0E0SGB3_GIBZE, tr|I1RKP5|I1RKP5_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1S0P0|I1S0P0_GIBZE, tr|I1RJU4|I1RJU4_GIBZE, tr|I1RDV8|I1RDV8_GIBZE, tr|I1RHQ0|I1RHQ0_GIBZE, tr|V6R0W1|V6R0W1_GIBZE, tr|I1RYC8|I1RYC8_GIBZE, tr|I1RY12|I1RY12_GIBZE, tr|I1RZI8|I1RZI8_GIBZE, tr|I1S6R1|I1S6R1_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|I1RZ21|I1RZ21_GIBZE, tr|I1REW2|I1REW2_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A0E0SAR4|A0A0E0SAR4_GIBZE, tr|I1RZV5|I1RZV5_GIBZE, tr|A0A1C3YLG3|A0A1C3YLG3_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RHL9|I1RHL9_GIBZE, tr|I1RW64|I1RW64_GIBZE, tr|A0A098DJ03|A0A098DJ03_GIBZE, tr|I1RF16|I1RF16_GIBZE, tr|A0A098D6R7|A0A098D6R7_GIBZE, tr|I1RHP6|I1RHP6_GIBZE, tr|I1RI19|I1RI19_GIBZE, tr|I1RN16|I1RN16_GIBZE, tr|I1REY8|I1REY8_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|A0A098DHN6|A0A098DHN6_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S958|I1S958_GIBZE, tr|I1S210|I1S210_GIBZE, tr|I1RMW8|I1RMW8_GIBZE, tr|A0A1C3YJX2|A0A1C3YJX2_GIBZE, tr|A0A098DJ29|A0A098DJ29_GIBZE, tr|A0A1C3YKE3|A0A1C3YKE3_GIBZE, tr|A0A0E0SDM0|A0A0E0SDM0_GIBZE, tr|V6RK40|V6RK40_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RFJ1|I1RFJ1_GIBZE, tr|I1RPN1|I1RPN1_GIBZE, tr|I1RME1|I1RME1_GIBZE, tr|V6RAM6|V6RAM6_GIBZE, tr|I1RJC5|I1RJC5_GIBZE, tr|I1RVW1|I1RVW1_GIBZE, tr|A0A0E0RTW2|A0A0E0RTW2_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|I1RT88|I1RT88_GIBZE, tr|I1RBF3|I1RBF3_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|A0A1C3YIV0|A0A1C3YIV0_GIBZE, tr|V6R0H4|V6R0H4_GIBZE, tr|I1RY16|I1RY16_GIBZE, tr|I1RKZ4|I1RKZ4_GIBZE</td></tr>
</table>

oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor	4 out of 263 genes, 1.5%	8 out of 1819 genes, 0.4%	0.01854	tr|I1RF16|I1RF16_GIBZE, tr|I1RHL9|I1RHL9_GIBZE, tr|A0A0E0RTW2|A0A0E0RTW2_GIBZE, tr|I1RZ21|I1RZ21_GIBZE
serine-type peptidase activity	6 out of 263 genes, 2.3%	16 out of 1819 genes, 0.9%	0.01938	tr|I1RP45|I1RP45_GIBZE, tr|I1RR60|I1RR60_GIBZE, tr|I1S2I7|I1S2I7_GIBZE, tr|I1RBZ6|I1RBZ6_GIBZE, tr|I1RJH8|I1RJH8_GIBZE, tr|A0A1C3YNA9|A0A1C3YNA9_GIBZE
acetolactate synthase activity	2 out of 263 genes, 0.8%	2 out of 1819 genes, 0.1%	0.02084	tr|I1RQE1|I1RQE1_GIBZE, tr|I1RBY9|I1RBY9_GIBZE
fatty-acid synthase activity	2 out of 263 genes, 0.8%	2 out of 1819 genes, 0.1%	0.02084	tr|I1RMW9|I1RMW9_GIBZE, tr|I1RMW8|I1RMW8_GIBZE
oligosaccharyl transferase activity	2 out of 263 genes, 0.8%	2 out of 1819 genes, 0.1%	0.02084	tr|I1RAH0|I1RAH0_GIBZE, tr|I1RZM0|I1RZM0_GIBZE
dolichyl-diphosphooligosaccharide-protein glycotransferase activity	2 out of 263 genes, 0.8%	2 out of 1819 genes, 0.1%	0.02084	tr|I1RAH0|I1RAH0_GIBZE, tr|I1RZM0|I1RZM0_GIBZE
enoyl-[acyl-carrier-protein] reductase activity	2 out of 263 genes, 0.8%	2 out of 1819 genes, 0.1%	0.02084	tr|I1RMW9|I1RMW9_GIBZE, tr|I1RW64|I1RW64_GIBZE
oxygen binding	2 out of 263 genes, 0.8%	2 out of 1819 genes, 0.1%	0.02084	tr|I1RUM6|I1RUM6_GIBZE, tr|I1RKP5|I1RKP5_GIBZE
amine transmembrane transporter activity	3 out of 263 genes, 1.1%	5 out of 1819 genes, 0.3%	0.02387	tr|I1RSK9|I1RSK9_GIBZE, tr|I1RDH9|I1RDH9_GIBZE, tr|I1RL54|I1RL54_GIBZE
amino acid transmembrane transporter activity	3 out of 263 genes, 1.1%	5 out of 1819 genes, 0.3%	0.02387	tr|I1RSK9|I1RSK9_GIBZE, tr|I1RDH9|I1RDH9_GIBZE, tr|I1RL54|I1RL54_GIBZE

carbon-sulfur lyase activity	3 out of 263 genes, 1.1%	5 out of 1819 genes, 0.3%	0.02387	tr|A0A0E0SML0|A0A0E0SML0_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A0E0SGN2|A0A0E0SGN2_GIBZE
transferase activity, transferring acyl groups other than amino-acyl groups	8 out of 263 genes, 3.0%	26 out of 1819 genes, 1.4%	0.02537	tr|I1RMW9|I1RMW9_GIBZE, tr|I1RMW8|I1RMW8_GIBZE, tr|I1RX90|I1RX90_GIBZE, tr|I1RLA5|I1RLA5_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|A0A0E0RSR0|A0A0E0RSR0_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1RVX9|I1RVX9_GIBZE
serine hydrolase activity	6 out of 263 genes, 2.3%	17 out of 1819 genes, 0.9%	0.02642	tr|I1RP45|I1RP45_GIBZE, tr|I1RR60|I1RR60_GIBZE, tr|I1S2I7|I1S2I7_GIBZE, tr|I1RBZ6|I1RBZ6_GIBZE, tr|I1RJH8|I1RJH8_GIBZE, tr|A0A1C3YNA9|A0A1C3YNA9_GIBZE
aldehyde dehydrogenase (NAD) activity	4 out of 263 genes, 1.5%	9 out of 1819 genes, 0.5%	0.02965	tr|I1RDV8|I1RDV8_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|A0A0E0SGB3|A0A0E0SGB3_GIBZE, tr|V6R2Z2|V6R2Z2_GIBZE
acyltransferase activity	7 out of 263 genes, 2.7%	22 out of 1819 genes, 1.2%	0.02994	tr|I1RMW9|I1RMW9_GIBZE, tr|I1RMW8|I1RMW8_GIBZE, tr|I1RX90|I1RX90_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|A0A0E0RSR0|A0A0E0RSR0_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1RVX9|I1RVX9_GIBZE
transferase activity, transferring glycosyl groups	9 out of 263 genes, 3.4%	33 out of 1819 genes, 1.8%	0.03893	tr|G4XVC2|G4XVC2_GIBZA, tr|V6QVH8|V6QVH8_GIBZE, tr|I1RAH0|I1RAH0_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RYU0|I1RYU0_GIBZE, tr|I1RZM0|I1RZM0_GIBZE, tr|I1RZ78|I1RZ78_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|A0A0E0RS58|A0A0E0RS58_GIBZE
carbon-oxygen lyase activity	8 out of 263 genes, 3.0%	28 out of 1819 genes, 1.5%	0.03899	tr|I1RMW9|I1RMW9_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|A0A1C3YJI5|A0A1C3YJI5_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|I1S1W8|I1S1W8_GIBZE
amine oxidase activity	3 out of 263 genes, 1.1%	6 out of 1819 genes, 0.3%	0.04269	tr|I1RF16|I1RF16_GIBZE, tr|I1RHL9|I1RHL9_GIBZE, tr|A0A0E0RTW2|A0A0E0RTW2_GIBZE
hydrolase activity, hydrolyzing O-glycosyl compounds	11 out of 263 genes, 4.2%	45 out of 1819 genes, 2.5%	0.05003	tr|A0A0E0RVC1|A0A0E0RVC1_GIBZE, tr|I1RE20|I1RE20_GIBZE, tr|I1RPK1|I1RPK1_GIBZE, tr|A0A098DCS9|A0A098DCS9_GIBZE, tr|A0A098DT41|A0A098DT41_GIBZE, tr|I1SAK0|I1SAK0_GIBZE, tr|I1RWE4|I1RWE4_GIBZE, tr|I1RYC1|I1RYC1_GIBZE, tr|A0A1C3YIS5|A0A1C3YIS5_GIBZE, tr|I1RMM6|I1RMM6_GIBZE, tr|I1RZ78|I1RZ78_GIBZE

GO125-GO0_Biological Process

<table>
<tr><th>Gene Ontology term</th><th>Cluster frequency</th><th>Protein frequency of use</th><th>P-value</th><th>Genes annotated to the term</th></tr>
<tr><td>organic acid metabolic process</td><td>50 out of 264 genes, 18.9%</td><td>241 out of 1882 genes, 12.8%</td><td>0.00139</td><td>tr|I1RW64|I1RW64_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RWE8|I1RWE8_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RX22|I1RX22_GIBZE, tr|I1RA13|I1RA13_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RXJ0|I1RXJ0_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1S210|I1S210_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1RQE1|I1RQE1_GIBZE, tr|I1RGB2|I1RGB2_GIBZE, tr|I1RVI8|I1RVI8_GIBZE, tr|I1RYU0|I1RYU0_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1RJU4|I1RJU4_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A0E0SGN2|A0A0E0SGN2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RR68|I1RR68_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|V6RV57|V6RV57_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|I1S2V9|I1S2V9_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1S1W8|I1S1W8_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE</td></tr>
<tr><td>cellular carbohydrate metabolic process</td><td>48 out of 264 genes, 18.2%</td><td>230 out of 1882 genes, 12.2%</td><td>0.00154</td><td>tr|G4XVC2|G4XVC2_GIBZA, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RWE8|I1RWE8_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1RZM0|I1RZM0_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RE86|I1RE86_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|I1RKE1|I1RKE1_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RX22|I1RX22_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RKR5|I1RKR5_GIBZE, tr|V6RDP1|V6RDP1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|I1RQE1|I1RQE1_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1RZ78|I1RZ78_GIBZE, tr|I1RMM6|I1RMM6_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|I1RSA3|I1RSA3_GIBZE, tr|I1RJQ5|I1RJQ5_GIBZE, tr|I1RX90|I1RX90_GIBZE, tr|I1RHQ0|I1RHQ0_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|V6RV57|V6RV57_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RPK1|I1RPK1_GIBZE, tr|I1RAH0|I1RAH0_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S1W8|I1S1W8_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE</td></tr>
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<tr><th></th><th></th><th></th><th></th><th></th></tr>
<tr><td>carboxylic acid metabolic process</td><td>49 out of 264 genes, 18.6%</td><td>237 out of 1882 genes, 12.6%</td><td>0.0017</td><td>tr|I1RW64|I1RW64_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RWE8|I1RWE8_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RX22|I1RX22_GIBZE, tr|I1RA13|I1RA13_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RXJ0|I1RXJ0_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1S210|I1S210_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1RQE1|I1RQE1_GIBZE, tr|I1RGB2|I1RGB2_GIBZE, tr|I1RVI8|I1RVI8_GIBZE, tr|I1RYU0|I1RYU0_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A0E0SGN2|A0A0E0SGN2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RR68|I1RR68_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|V6RV57|V6RV57_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|I1S2V9|I1S2V9_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1S1W8|I1S1W8_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE</td></tr>
<tr><td>oxoacid metabolic process</td><td>49 out of 264 genes, 18.6%</td><td>237 out of 1882 genes, 12.6%</td><td>0.0017</td><td>tr|I1RW64|I1RW64_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RWE8|I1RWE8_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RX22|I1RX22_GIBZE, tr|I1RA13|I1RA13_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RXJ0|I1RXJ0_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1S210|I1S210_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1RQE1|I1RQE1_GIBZE, tr|I1RGB2|I1RGB2_GIBZE, tr|I1RVI8|I1RVI8_GIBZE, tr|I1RYU0|I1RYU0_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A0E0SGN2|A0A0E0SGN2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RR68|I1RR68_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|V6RV57|V6RV57_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|I1S2V9|I1S2V9_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1S1W8|I1S1W8_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE</td></tr>
<tr><td>cellular ketone metabolic process</td><td>49 out of 264 genes, 18.6%</td><td>238 out of 1882 genes, 12.6%</td><td>0.00187</td><td>tr|I1RW64|I1RW64_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RWE8|I1RWE8_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RX22|I1RX22_GIBZE, tr|I1RA13|I1RA13_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RXJ0|I1RXJ0_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1S210|I1S210_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1RQE1|I1RQE1_GIBZE, tr|I1RGB2|I1RGB2_GIBZE, tr|I1RVI8|I1RVI8_GIBZE, tr|I1RYU0|I1RYU0_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A0E0SGN2|A0A0E0SGN2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RR68|I1RR68_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|V6RV57|V6RV57_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|I1S2V9|I1S2V9_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1S1W8|I1S1W8_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE</td></tr>
</table>

<table>
<tr><td>amine biosynthetic process</td><td>23 out of 264 genes, 8.7%</td><td>94 out of 1882 genes, 5.0%</td><td>0.00387</td><td>tr|A0A0E0RWK1|A0A0E0RWK1_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RW06|I1RW06_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1RQE1|I1RQE1_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S1W8|I1S1W8_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
<tr><td>cellular amino acid biosynthetic process</td><td>22 out of 264 genes, 8.3%</td><td>89 out of 1882 genes, 4.7%</td><td>0.00412</td><td>tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RW06|I1RW06_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1RQE1|I1RQE1_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S1W8|I1S1W8_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
<tr><td>organic acid biosynthetic process</td><td>25 out of 264 genes, 9.5%</td><td>106 out of 1882 genes, 5.6%</td><td>0.00446</td><td>tr|I1RW64|I1RW64_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RR68|I1RR68_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1RQE1|I1RQE1_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S1W8|I1S1W8_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
<tr><td>carboxylic acid biosynthetic process</td><td>25 out of 264 genes, 9.5%</td><td>106 out of 1882 genes, 5.6%</td><td>0.00446</td><td>tr|I1RW64|I1RW64_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RR68|I1RR68_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1RQE1|I1RQE1_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S1W8|I1S1W8_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
<tr><td>protein import into mitochondrial matrix</td><td>4 out of 264 genes, 1.5%</td><td>6 out of 1882 genes, 0.3%</td><td>0.00451</td><td>tr|I1RBS5|I1RBS5_GIBZE, tr|A0A1C3YIX0|A0A1C3YIX0_GIBZE, tr|I1R9Y8|I1R9Y8_GIBZE, tr|I1RJT3|I1RJT3_GIBZE</td></tr>
<tr><td>carbohydrate metabolic process</td><td>57 out of 264 genes, 21.6%</td><td>300 out of 1882 genes, 15.9%</td><td>0.00553</td><td>tr|G4XVC2|G4XVC2_GIBZA, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RWE8|I1RWE8_GIBZE, tr|A0A098DT41|A0A098DT41_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1SAK0|I1SAK0_GIBZE, tr|I1RZM0|I1RZM0_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RE86|I1RE86_GIBZE, tr|I1RWE4|I1RWE4_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|A0A1C3YIS5|A0A1C3YIS5_GIBZE, tr|I1RKE1|I1RKE1_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RX22|I1RX22_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RKR5|I1RKR5_GIBZE, tr|V6RDP1|V6RDP1_GIBZE, tr|A0A098DCS9|A0A098DCS9_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1RQE1|I1RQE1_GIBZE, tr|I1RGB2|I1RGB2_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1S6S5|I1S6S5_GIBZE, tr|I1RZ78|I1RZ78_GIBZE, tr|I1RMM6|I1RMM6_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|I1RSA3|I1RSA3_GIBZE, tr|I1RJQ5|I1RJQ5_GIBZE, tr|I1RX90|I1RX90_GIBZE, tr|I1RHQ0|I1RHQ0_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RYC1|I1RYC1_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|I1RC39|I1RC39_GIBZE,</td></tr>
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<table>
<tr><td></td><td></td><td></td><td></td><td>tr|I1RE58|I1RE58_GIBZE, tr|V6RV57|V6RV57_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RPK1|I1RPK1_GIBZE, tr|I1RAH0|I1RAH0_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1S1W8|I1S1W8_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE</td></tr>
<tr><td>protein targeting to mitochondrion</td><td>7 out of 264 genes, 2.7%</td><td>18 out of 1882 genes, 1.0%</td><td>0.0079</td><td>tr|I1RZI8|I1RZI8_GIBZE, sp|Q4IB65|TIM9_GIBZE, tr|I1RFS5|I1RFS5_GIBZE, tr|I1RBS5|I1RBS5_GIBZE, tr|A0A1C3YIX0|A0A1C3YIX0_GIBZE, tr|I1R9Y8|I1R9Y8_GIBZE, tr|I1RJT3|I1RJT3_GIBZE</td></tr>
<tr><td>protein localization in mitochondrion</td><td>7 out of 264 genes, 2.7%</td><td>18 out of 1882 genes, 1.0%</td><td>0.0079</td><td>tr|I1RZI8|I1RZI8_GIBZE, sp|Q4IB65|TIM9_GIBZE, tr|I1RFS5|I1RFS5_GIBZE, tr|I1RBS5|I1RBS5_GIBZE, tr|A0A1C3YIX0|A0A1C3YIX0_GIBZE, tr|I1R9Y8|I1R9Y8_GIBZE, tr|I1RJT3|I1RJT3_GIBZE</td></tr>
<tr><td>metabolic process</td><td>228 out of 264 genes, 86.4%</td><td>1525 out of 1882 genes, 81.0%</td><td>0.00908</td><td>tr|I1RAD8|I1RAD8_GIBZE, tr|I1RCK2|I1RCK2_GIBZE, tr|G4XVC2|G4XVC2_GIBZA, tr|I1RPV8|I1RPV8_GIBZE, tr|A0A098DT41|A0A098DT41_GIBZE, tr|I1RWE4|I1RWE4_GIBZE, tr|I1S0B0|I1S0B0_GIBZE, tr|I1RAG2|I1RAG2_GIBZE, tr|I1RPA6|I1RPA6_GIBZE, tr|A0A098DJH8|A0A098DJH8_GIBZE, tr|I1S1D0|I1S1D0_GIBZE, tr|I1RIG1|I1RIG1_GIBZE, tr|A0A098DS29|A0A098DS29_GIBZE, tr|V6R2Z2|V6R2Z2_GIBZE, tr|I1RCA7|I1RCA7_GIBZE, tr|A0A098DCS9|A0A098DCS9_GIBZE, tr|I1RVU9|I1RVU9_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|I1S0N8|I1S0N8_GIBZE, tr|V6QVH8|V6QVH8_GIBZE, tr|I1RAU6|I1RAU6_GIBZE, tr|I1RVI8|I1RVI8_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1S6S5|I1S6S5_GIBZE, tr|I1RJU4|I1RJU4_GIBZE, tr|I1RSK9|I1RSK9_GIBZE, tr|I1RX90|I1RX90_GIBZE, tr|I1RLX7|I1RLX7_GIBZE, tr|A0A098E1Q7|A0A098E1Q7_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1S6R1|I1S6R1_GIBZE, tr|I1RZ21|I1RZ21_GIBZE, sp|Q4HTT1|H2A_GIBZE, tr|I1RML4|I1RML4_GIBZE, tr|I1RAH0|I1RAH0_GIBZE, tr|I1S2V9|I1S2V9_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|A0A098E0N0|A0A098E0N0_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|A0A1C3YLG3|A0A1C3YLG3_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1RKR9|I1RKR9_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE, tr|I1RVX0|I1RVX0_GIBZE, tr|I1RF16|I1RF16_GIBZE, tr|I1RDH6|I1RDH6_GIBZE, tr|I1RMV1|I1RMV1_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1RZM0|I1RZM0_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A098D6R7|A0A098D6R7_GIBZE, tr|I1RDJ7|I1RDJ7_GIBZE, tr|I1RHP6|I1RHP6_GIBZE, tr|I1S123|I1S123_GIBZE, tr|A0A1C3YHK0|A0A1C3YHK0_GIBZE, tr|I1REI0|I1REI0_GIBZE, tr|I1RTU1|I1RTU1_GIBZE, tr|A0A098DQK4|A0A098DQK4_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|A0A1C3YIS5|A0A1C3YIS5_GIBZE, tr|I1RN16|I1RN16_GIBZE, tr|I1RI19|I1RI19_GIBZE, tr|I1RKE1|I1RKE1_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1S958|I1S958_GIBZE, tr|I1S210|I1S210_GIBZE, tr|I1RQE1|I1RQE1_GIBZE, tr|A0A1C3YJX2|A0A1C3YJX2_GIBZE, tr|I1RMW8|I1RMW8_GIBZE, tr|I1RGB2|I1RGB2_GIBZE, tr|I1S6V0|I1S6V0_GIBZE, tr|A0A098DJ29|A0A098DJ29_GIBZE, tr|I1RCD6|I1RCD6_GIBZE, tr|I1RPE5|I1RPE5_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A0E0SGN2|A0A0E0SGN2_GIBZE, tr|A0A0E0RS58|A0A0E0RS58_GIBZE, tr|I1RSA3|I1RSA3_GIBZE, tr|I1RJQ5|I1RJQ5_GIBZE, tr|I1S2I7|I1S2I7_GIBZE, tr|V6RUB1|V6RUB1_GIBZE, tr|V6RK40|V6RK40_GIBZE, tr|I1RN80|I1RN80_GIBZE, tr|A0A098DBF9|A0A098DBF9_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RPN1|I1RPN1_GIBZE, tr|I1R9Y8|I1R9Y8_GIBZE, tr|I1RZD3|I1RZD3_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|I1S444|I1S444_GIBZE, tr|I1RME1|I1RME1_GIBZE, tr|V6RSF3|V6RSF3_GIBZE, tr|I1RR72|I1RR72_GIBZE, tr|A0A1C3YJ47|A0A1C3YJ47_GIBZE, tr|I1RLA5|I1RLA5_GIBZE, tr|I1RJC5|I1RJC5_GIBZE, tr|A0A1C3YI05|A0A1C3YI05_GIBZE, tr|I1RF24|I1RF24_GIBZE, tr|A0A0E0RTW2|A0A0E0RTW2_GIBZE, tr|I1S0R2|I1S0R2_GIBZE, tr|I1RT88|I1RT88_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|A0A1C3YIV0|A0A1C3YIV0_GIBZE, tr|I1S1W8|I1S1W8_GIBZE, tr|A0A0E0SGT0|A0A0E0SGT0_GIBZE, tr|I1RY35|I1RY35_GIBZE, tr|A0A0E0RMB3|A0A0E0RMB3_GIBZE, tr|I1RJK0|I1RJK0_GIBZE, tr|I1RWE8|I1RWE8_GIBZE, tr|I1RD15|I1RD15_GIBZE, tr|I1SAK0|I1SAK0_GIBZE, tr|I1RM69|I1RM69_GIBZE, tr|I1RE86|I1RE86_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|I1S0I8|I1S0I8_GIBZE, tr|I1RX22|I1RX22_GIBZE, sp|Q4I5I4|SPT5_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RP45|I1RP45_GIBZE, tr|V6QUE6|V6QUE6_GIBZE, tr|I1RD38|I1RD38_GIBZE,</td></tr>
</table>

				tr|I1RXJ0|I1RXJ0_GIBZE, tr|V6R3U5|V6R3U5_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|I1RYN2|I1RYN2_GIBZE, tr|A0A098D8J9|A0A098D8J9_GIBZE, tr|A0A0E0SGB3|A0A0E0SGB3_GIBZE, tr|I1RKP5|I1RKP5_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1S0P0|I1S0P0_GIBZE, tr|I1RT35|I1RT35_GIBZE, tr|I1RMM6|I1RMM6_GIBZE, tr|I1RDV8|I1RDV8_GIBZE, tr|I1RFI9|I1RFI9_GIBZE, tr|I1RHQ0|I1RHQ0_GIBZE, tr|V6R0W1|V6R0W1_GIBZE, tr|I1RYC8|I1RYC8_GIBZE, tr|I1RY12|I1RY12_GIBZE, tr|I1RQX9|I1RQX9_GIBZE, tr|I1RR68|I1RR68_GIBZE, tr|I1S379|I1S379_GIBZE, tr|A0A0E0SC40|A0A0E0SC40_GIBZE, tr|I1RZI8|I1RZI8_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|A0A1C3YIE7|A0A1C3YIE7_GIBZE, tr|I1RN63|I1RN63_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|A0A1C3YLK5|A0A1C3YLK5_GIBZE, tr|V6RV57|V6RV57_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|I1RBZ6|I1RBZ6_GIBZE, tr|A0A1C3YJI5|A0A1C3YJI5_GIBZE, tr|A0A0E0SAR4|A0A0E0SAR4_GIBZE, tr|I1RAM3|I1RAM3_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RHL9|I1RHL9_GIBZE, tr|I1RCR2|I1RCR2_GIBZE, tr|I1RSL6|I1RSL6_GIBZE, tr|I1RB05|I1RB05_GIBZE, tr|V6RR76|V6RR76_GIBZE, tr|I1RTG5|I1RTG5_GIBZE, tr|I1RW64|I1RW64_GIBZE, tr|A0A0E0RWK1|A0A0E0RWK1_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RAN2|I1RAN2_GIBZE, tr|A0A098DJ03|A0A098DJ03_GIBZE, tr|I1RJD9|I1RJD9_GIBZE, tr|I1S7M3|I1S7M3_GIBZE, tr|A0A1C3YHU3|A0A1C3YHU3_GIBZE, tr|I1RBS5|I1RBS5_GIBZE, tr|I1RPD9|I1RPD9_GIBZE, tr|I1RPI5|I1RPI5_GIBZE, sp|Q4IJU0|POB3_GIBZE, tr|I1RJH8|I1RJH8_GIBZE, tr|I1RWH4|I1RWH4_GIBZE, tr|I1RZP6|I1RZP6_GIBZE, tr|I1S362|I1S362_GIBZE, tr|I1RWW7|I1RWW7_GIBZE, tr|I1RA13|I1RA13_GIBZE, tr|I1REY8|I1REY8_GIBZE, tr|V6RDP1|V6RDP1_GIBZE, tr|I1S2W9|I1S2W9_GIBZE, tr|A0A098DQF0|A0A098DQF0_GIBZE, tr|I1RE20|I1RE20_GIBZE, tr|I1RKR5|I1RKR5_GIBZE, tr|A0A1C3YNA9|A0A1C3YNA9_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A098D2V8|A0A098D2V8_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1RAE5|I1RAE5_GIBZE, tr|I1RYU0|I1RYU0_GIBZE, tr|V6RCJ5|V6RCJ5_GIBZE, tr|I1RZ78|I1RZ78_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|A0A0E0SML0|A0A0E0SML0_GIBZE, tr|I1RDK8|I1RDK8_GIBZE, tr|A0A1C3YKE3|A0A1C3YKE3_GIBZE, tr|A0A0E0SDM0|A0A0E0SDM0_GIBZE, tr|I1RFS5|I1RFS5_GIBZE, tr|A0A098D9M4|A0A098D9M4_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|A0A0E0RSR0|A0A0E0RSR0_GIBZE, tr|I1RYC1|I1RYC1_GIBZE, tr|I1RR60|I1RR60_GIBZE, sp|Q4I948|RUVB2_GIBZE, tr|I1RFJ1|I1RFJ1_GIBZE, tr|A0A098E4P3|A0A098E4P3_GIBZE, tr|I1RUG3|I1RUG3_GIBZE, tr|A0A098DK45|A0A098DK45_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|V6RAM6|V6RAM6_GIBZE, tr|A0A0E0SFP4|A0A0E0SFP4_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RPK1|I1RPK1_GIBZE, tr|I1RVW1|I1RVW1_GIBZE, tr|I1RT23|I1RT23_GIBZE, tr|I1RKS0|I1RKS0_GIBZE, tr|I1RT94|I1RT94_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|I1RYZ9|I1RYZ9_GIBZE, tr|I1RBF3|I1RBF3_GIBZE, tr|A0A098DS79|A0A098DS79_GIBZE, tr|V6R0H4|V6R0H4_GIBZE, tr|I1RY16|I1RY16_GIBZE, tr|I1RKZ4|I1RKZ4_GIBZE
amine metabolic process	38 out of 264 genes, 14.4%	189 out of 1882 genes, 10.0%	0.00963	tr|A0A0E0RWK1|A0A0E0RWK1_GIBZE, tr|G4XVC2|G4XVC2_GIBZA, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RF16|I1RF16_GIBZE, tr|I1RWE8|I1RWE8_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RX22|I1RX22_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|I1RQE1|I1RQE1_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|A0A0E0RTW2|A0A0E0RTW2_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1RHL9|I1RHL9_GIBZE, tr|I1S1W8|I1S1W8_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE
cellular amino acid and derivative	38 out of 264 genes, 14.4%	190 out of 1882 genes, 10.1%	0.01052	tr|A0A0E0RWK1|A0A0E0RWK1_GIBZE, tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RWE8|I1RWE8_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RX22|I1RX22_GIBZE, tr|I1RTD3|I1RTD3_GIBZE,

<table>
<tr><td>metabolic process</td><td></td><td></td><td></td><td>tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1RQE1|I1RQE1_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|A0A0E0SGN2|A0A0E0SGN2_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|A0A098DBF9|A0A098DBF9_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RPN1|I1RPN1_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S1W8|I1S1W8_GIBZE, tr|A0A098DS79|A0A098DS79_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE</td></tr>
<tr><td>oxidation reduction</td><td>57 out of 264 genes, 21.6%</td><td>313 out of 1882 genes, 16.6%</td><td>0.01409</td><td>tr|I1RF16|I1RF16_GIBZE, tr|A0A098DJ03|A0A098DJ03_GIBZE, tr|A0A098D6R7|A0A098D6R7_GIBZE, tr|I1RHP6|I1RHP6_GIBZE, tr|I1S123|I1S123_GIBZE, tr|I1RAG2|I1RAG2_GIBZE, tr|I1RN16|I1RN16_GIBZE, tr|I1RI19|I1RI19_GIBZE, tr|I1RIG1|I1RIG1_GIBZE, tr|I1S0I8|I1S0I8_GIBZE, tr|V6R2Z2|V6R2Z2_GIBZE, tr|I1RMW9|I1RMW9_GIBZE, tr|I1REY8|I1REY8_GIBZE, tr|I1RVU9|I1RVU9_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1RYN2|I1RYN2_GIBZE, tr|A0A098D8J9|A0A098D8J9_GIBZE, tr|A0A0E0SGB3|A0A0E0SGB3_GIBZE, tr|I1RKP5|I1RKP5_GIBZE, tr|I1S958|I1S958_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1S0P0|I1S0P0_GIBZE, tr|A0A1C3YJX2|A0A1C3YJX2_GIBZE, tr|I1RMW8|I1RMW8_GIBZE, tr|A0A098DJ29|A0A098DJ29_GIBZE, tr|I1RJU4|I1RJU4_GIBZE, tr|I1RDV8|I1RDV8_GIBZE, tr|I1RHQ0|I1RHQ0_GIBZE, tr|A0A1C3YKE3|A0A1C3YKE3_GIBZE, tr|A0A0E0SDM0|A0A0E0SDM0_GIBZE, tr|V6RK40|V6RK40_GIBZE, tr|V6R0W1|V6R0W1_GIBZE, tr|I1RY12|I1RY12_GIBZE, tr|I1RZI8|I1RZI8_GIBZE, tr|I1S6R1|I1S6R1_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|I1RFJ1|I1RFJ1_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RPN1|I1RPN1_GIBZE, tr|I1RZ21|I1RZ21_GIBZE, tr|I1RME1|I1RME1_GIBZE, tr|V6RAM6|V6RAM6_GIBZE, tr|I1RVW1|I1RVW1_GIBZE, tr|A0A0E0RTW2|A0A0E0RTW2_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|I1RBF3|I1RBF3_GIBZE, tr|I1RT88|I1RT88_GIBZE, tr|A0A0E0SAR4|A0A0E0SAR4_GIBZE, tr|A0A1C3YIV0|A0A1C3YIV0_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|A0A1C3YLG3|A0A1C3YLG3_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RHL9|I1RHL9_GIBZE, tr|V6R0H4|V6R0H4_GIBZE, tr|I1RY16|I1RY16_GIBZE, tr|I1RKZ4|I1RKZ4_GIBZE</td></tr>
<tr><td>cellular amino acid metabolic process</td><td>32 out of 264 genes, 12.1%</td><td>158 out of 1882 genes, 8.4%</td><td>0.01555</td><td>tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RWE8|I1RWE8_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RX22|I1RX22_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RQE1|I1RQE1_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1S1W8|I1S1W8_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE</td></tr>
<tr><td>cellular amine metabolic process</td><td>32 out of 264 genes, 12.1%</td><td>158 out of 1882 genes, 8.4%</td><td>0.01555</td><td>tr|A0A098D9N3|A0A098D9N3_GIBZE, tr|I1RWE8|I1RWE8_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|I1RDE7|I1RDE7_GIBZE, tr|I1RFK3|I1RFK3_GIBZE, tr|A0A098E1W8|A0A098E1W8_GIBZE, tr|I1RC39|I1RC39_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RX22|I1RX22_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1S1P8|I1S1P8_GIBZE, tr|A0A098DQ44|A0A098DQ44_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A098DUS9|A0A098DUS9_GIBZE, tr|I1RQE1|I1RQE1_GIBZE, tr|I1RK93|I1RK93_GIBZE, tr|I1RKZ7|I1RKZ7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1S1W8|I1S1W8_GIBZE, tr|I1RBY9|I1RBY9_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE</td></tr>
</table>

<table>
<tr><td>sodium ion transport</td><td>2 out of 264 genes, 0.8%</td><td>2 out of 1882 genes, 0.1%</td><td>0.01961</td><td>tr|I1S1W8|I1S1W8_GIBZE, tr|A0A098DK45|A0A098DK45_GIBZE</td></tr>
<tr><td>propionate metabolic process, methylcitrate cycle</td><td>2 out of 264 genes, 0.8%</td><td>2 out of 1882 genes, 0.1%</td><td>0.01961</td><td>tr|I1RA13|I1RA13_GIBZE, tr|I1RVI8|I1RVI8_GIBZE</td></tr>
<tr><td>histidine biosynthetic process</td><td>3 out of 264 genes, 1.1%</td><td>5 out of 1882 genes, 0.3%</td><td>0.02195</td><td>tr|I1RPW1|I1RPW1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
<tr><td>histidine metabolic process</td><td>3 out of 264 genes, 1.1%</td><td>5 out of 1882 genes, 0.3%</td><td>0.02195</td><td>tr|I1RPW1|I1RPW1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
<tr><td>histidine family amino acid metabolic process</td><td>3 out of 264 genes, 1.1%</td><td>5 out of 1882 genes, 0.3%</td><td>0.02195</td><td>tr|I1RPW1|I1RPW1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
<tr><td>histidine family amino acid biosynthetic process</td><td>3 out of 264 genes, 1.1%</td><td>5 out of 1882 genes, 0.3%</td><td>0.02195</td><td>tr|I1RPW1|I1RPW1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
<tr><td>urea metabolic process</td><td>4 out of 264 genes, 1.5%</td><td>9 out of 1882 genes, 0.5%</td><td>0.02676</td><td>tr|I1RN80|I1RN80_GIBZE, tr|I1RJU4|I1RJU4_GIBZE, tr|A0A1C3YIV7|A0A1C3YIV7_GIBZE, tr|I1RQE0|I1RQE0_GIBZE</td></tr>
<tr><td>mitochondrial transport</td><td>7 out of 264 genes, 2.7%</td><td>23 out of 1882 genes, 1.2%</td><td>0.0327</td><td>tr|I1RZI8|I1RZI8_GIBZE, sp|Q4IB65|TIM9_GIBZE, tr|I1RFS5|I1RFS5_GIBZE, tr|I1RBS5|I1RBS5_GIBZE, tr|A0A1C3YIX0|A0A1C3YIX0_GIBZE, tr|I1R9Y8|I1R9Y8_GIBZE, tr|I1RJT3|I1RJT3_GIBZE</td></tr>
<tr><td>polyol metabolic process</td><td>5 out of 264 genes, 1.9%</td><td>14 out of 1882 genes, 0.7%</td><td>0.03563</td><td>tr|I1RSA3|I1RSA3_GIBZE, tr|I1RHQ0|I1RHQ0_GIBZE, tr|V6RDP1|V6RDP1_GIBZE, tr|V6RV57|V6RV57_GIBZE, tr|I1RE86|I1RE86_GIBZE</td></tr>
<tr><td>intracellular protein transmembrane transport</td><td>5 out of 264 genes, 1.9%</td><td>14 out of 1882 genes, 0.7%</td><td>0.03563</td><td>tr|I1RZI8|I1RZI8_GIBZE, tr|I1RBS5|I1RBS5_GIBZE, tr|A0A1C3YIX0|A0A1C3YIX0_GIBZE, tr|I1R9Y8|I1R9Y8_GIBZE, tr|I1RJT3|I1RJT3_GIBZE</td></tr>
<tr><td>alditol metabolic process</td><td>4 out of 264 genes, 1.5%</td><td>10 out of 1882 genes, 0.5%</td><td>0.03979</td><td>tr|I1RSA3|I1RSA3_GIBZE, tr|I1RHQ0|I1RHQ0_GIBZE, tr|V6RDP1|V6RDP1_GIBZE, tr|V6RV57|V6RV57_GIBZE</td></tr>
<tr><td>nucleosome organization</td><td>6 out of 264 genes, 2.3%</td><td>20 out of 1882 genes, 1.1%</td><td>0.05014</td><td>sp|Q4IJU0|POB3_GIBZE, tr|I1S219|I1S219_GIBZE, sp|Q4I948|RUVB2_GIBZE, tr|A0A098D8N2|A0A098D8N2_GIBZE, tr|A0A098DU58|A0A098DU58_GIBZE, tr|A0A098E4P3|A0A098E4P3_GIBZE</td></tr>
</table>

long-chain fatty acid metabolic process	2 out of 264 genes, 0.8%	3 out of 1882 genes, 0.2%	0.05337	tr|I1RMW9|I1RMW9_GIBZE, tr|I1RF24|I1RF24_GIBZE
acetate metabolic process	2 out of 264 genes, 0.8%	3 out of 1882 genes, 0.2%	0.05337	tr|I1RA13|I1RA13_GIBZE, tr|I1RVI8|I1RVI8_GIBZE
mitotic metaphase plate congression	2 out of 264 genes, 0.8%	3 out of 1882 genes, 0.2%	0.05337	tr|A0A1C3YLK5|A0A1C3YLK5_GIBZE, tr|A0A0E0SNM6|A0A0E0SNM6_GIBZE
farnesyl diphosphate biosynthetic process, mevalonate pathway	2 out of 264 genes, 0.8%	3 out of 1882 genes, 0.2%	0.05337	tr|I1RY35|I1RY35_GIBZE, tr|I1RPE5|I1RPE5_GIBZE
sister chromatid biorientation	2 out of 264 genes, 0.8%	3 out of 1882 genes, 0.2%	0.05337	tr|A0A1C3YLK5|A0A1C3YLK5_GIBZE, tr|A0A0E0SNM6|A0A0E0SNM6_GIBZE
heterotrimeric G-protein complex cycle	2 out of 264 genes, 0.8%	3 out of 1882 genes, 0.2%	0.05337	tr|I1RSV0|I1RSV0_GIBZE, tr|I1RJS2|I1RJS2_GIBZE
chromosome localization	2 out of 264 genes, 0.8%	3 out of 1882 genes, 0.2%	0.05337	tr|A0A1C3YLK5|A0A1C3YLK5_GIBZE, tr|A0A0E0SNM6|A0A0E0SNM6_GIBZE
establishment of chromosome localization	2 out of 264 genes, 0.8%	3 out of 1882 genes, 0.2%	0.05337	tr|A0A1C3YLK5|A0A1C3YLK5_GIBZE, tr|A0A0E0SNM6|A0A0E0SNM6_GIBZE
metaphase plate congression	2 out of 264 genes, 0.8%	3 out of 1882 genes, 0.2%	0.05337	tr|A0A1C3YLK5|A0A1C3YLK5_GIBZE, tr|A0A0E0SNM6|A0A0E0SNM6_GIBZE
establishment of mitochondrion localization	2 out of 264 genes, 0.8%	3 out of 1882 genes, 0.2%	0.05337	tr|I1RCK2|I1RCK2_GIBZE, tr|I1RKR9|I1RKR9_GIBZE

GO250-GO0_Cellular Component

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value	Genes annotated to the term

<table>
<tr><td>endosome</td><td>10 out of 145 genes, 6.9%</td><td>38 out of 1646 genes, 2.3%</td><td>0.00113</td><td>sp|Q4I1H6|SNX3_GIBZE, tr|I1REC4|I1REC4_GIBZE, tr|I1RW38|I1RW38_GIBZE, tr|I1RMA7|I1RMA7_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|A0A1C3YJJ7|A0A1C3YJJ7_GIBZE, tr|A0A098D760|A0A098D760_GIBZE, tr|I1RG99|I1RG99_GIBZE, tr|A0A098DVM4|A0A098DVM4_GIBZE, tr|I1S9S4|I1S9S4_GIBZE</td></tr>
<tr><td>late endosome</td><td>4 out of 145 genes, 2.8%</td><td>7 out of 1646 genes, 0.4%</td><td>0.00164</td><td>sp|Q4I1H6|SNX3_GIBZE, tr|A0A098DVM4|A0A098DVM4_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|I1RG99|I1RG99_GIBZE</td></tr>
<tr><td>vacuolar transporter chaperone complex</td><td>2 out of 145 genes, 1.4%</td><td>2 out of 1646 genes, 0.1%</td><td>0.00771</td><td>tr|I1RCV0|I1RCV0_GIBZE, tr|A0A1C3YHU9|A0A1C3YHU9_GIBZE</td></tr>
<tr><td>extracellular region</td><td>6 out of 145 genes, 4.1%</td><td>27 out of 1646 genes, 1.6%</td><td>0.02635</td><td>tr|I1S2I0|I1S2I0_GIBZE, tr|I1RHQ0|I1RHQ0_GIBZE, sp|I1S2N3|GAOA_GIBZE, tr|I1RLY2|I1RLY2_GIBZE, tr|A0A0E0SBV6|A0A0E0SBV6_GIBZE, tr|I1RKV6|I1RKV6_GIBZE</td></tr>
<tr><td>retromer complex</td><td>2 out of 145 genes, 1.4%</td><td>4 out of 1646 genes, 0.2%</td><td>0.04108</td><td>tr|I1REC4|I1REC4_GIBZE, tr|I1RG99|I1RG99_GIBZE</td></tr>
<tr><td>peroxisome</td><td>6 out of 145 genes, 4.1%</td><td>31 out of 1646 genes, 1.9%</td><td>0.04896</td><td>tr|I1RY32|I1RY32_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|I1RRW0|I1RRW0_GIBZE, tr|I1RJU4|I1RJU4_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1RE58|I1RE58_GIBZE</td></tr>
</table>

GO250-GO0_Molecular Function

<table>
<tr><th>Gene Ontology term</th><th>Cluster frequency</th><th>Protein frequency of use</th><th>P-value</th><th>Genes annotated to the term</th></tr>
<tr><td>hydrolase activity, acting on glycosyl bonds</td><td>13 out of 189 genes, 6.9%</td><td>49 out of 1819 genes, 2.7%</td><td>0.00098</td><td>tr|A0A0E0RVC1|A0A0E0RVC1_GIBZE, tr|A0A098DXB4|A0A098DXB4_GIBZE, tr|I1RPK1|I1RPK1_GIBZE, tr|A0A098DT41|A0A098DT41_GIBZE, tr|I1SAK0|I1SAK0_GIBZE, tr|I1RI39|I1RI39_GIBZE, tr|I1RYC1|I1RYC1_GIBZE, tr|A0A1C3YID4|A0A1C3YID4_GIBZE, tr|A0A098DE56|A0A098DE56_GIBZE, tr|I1RLY2|I1RLY2_GIBZE, tr|A0A1C3YIS5|A0A1C3YIS5_GIBZE, tr|V6QVM5|V6QVM5_GIBZE, tr|I1RJ55|I1RJ55_GIBZE</td></tr>
<tr><td>hydrolase activity, hydrolyzing O-glycosyl compounds</td><td>12 out of 189 genes, 6.3%</td><td>45 out of 1819 genes, 2.5%</td><td>0.00146</td><td>tr|A0A0E0RVC1|A0A0E0RVC1_GIBZE, tr|A0A098DXB4|A0A098DXB4_GIBZE, tr|I1RPK1|I1RPK1_GIBZE, tr|A0A098DT41|A0A098DT41_GIBZE, tr|I1SAK0|I1SAK0_GIBZE, tr|I1RI39|I1RI39_GIBZE, tr|I1RYC1|I1RYC1_GIBZE, tr|A0A1C3YID4|A0A1C3YID4_GIBZE, tr|A0A098DE56|A0A098DE56_GIBZE, tr|I1RLY2|I1RLY2_GIBZE, tr|A0A1C3YIS5|A0A1C3YIS5_GIBZE, tr|I1RJ55|I1RJ55_GIBZE</td></tr>
<tr><td>serine-type peptidase activity</td><td>6 out of 189 genes, 3.2%</td><td>16 out of 1819 genes, 0.9%</td><td>0.00382</td><td>tr|I1RR60|I1RR60_GIBZE, tr|A0A1C3YK08|A0A1C3YK08_GIBZE, tr|I1RJH8|I1RJH8_GIBZE, tr|I1RKV6|I1RKV6_GIBZE, tr|A0A1C3YNA9|A0A1C3YNA9_GIBZE, tr|I1RB96|I1RB96_GIBZE</td></tr>
<tr><td>serine hydrolase activity</td><td>6 out of 189 genes, 3.2%</td><td>17 out of 1819 genes, 0.9%</td><td>0.0054</td><td>tr|I1RR60|I1RR60_GIBZE, tr|A0A1C3YK08|A0A1C3YK08_GIBZE, tr|I1RJH8|I1RJH8_GIBZE, tr|I1RKV6|I1RKV6_GIBZE, tr|A0A1C3YNA9|A0A1C3YNA9_GIBZE, tr|I1RB96|I1RB96_GIBZE</td></tr>
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<table>
<tr><td>oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen</td><td>6 out of 189 genes, 3.2%</td><td>18 out of 1819 genes, 1.0%</td><td>0.00741</td><td>tr|I1RE90|I1RE90_GIBZE, tr|A0A1C3YK95|A0A1C3YK95_GIBZE, tr|A0A0E0SAE0|A0A0E0SAE0_GIBZE, tr|A0A1C3YJ69|A0A1C3YJ69_GIBZE, tr|I1RIU6|I1RIU6_GIBZE, tr|A0A098DPL1|A0A098DPL1_GIBZE</td></tr>
<tr><td>alpha,alpha-trehalase activity</td><td>2 out of 189 genes, 1.1%</td><td>2 out of 1819 genes, 0.1%</td><td>0.01074</td><td>tr|A0A0E0RVC1|A0A0E0RVC1_GIBZE, tr|A0A098DXB4|A0A098DXB4_GIBZE</td></tr>
<tr><td>trehalase activity</td><td>2 out of 189 genes, 1.1%</td><td>2 out of 1819 genes, 0.1%</td><td>0.01074</td><td>tr|A0A0E0RVC1|A0A0E0RVC1_GIBZE, tr|A0A098DXB4|A0A098DXB4_GIBZE</td></tr>
<tr><td>catalytic activity</td><td>145 out of 189 genes, 76.7%</td><td>1275 out of 1819 genes, 70.1%</td><td>0.0202</td><td>tr|G4XVC2|G4XVC2_GIBZA, tr|I1RPV8|I1RPV8_GIBZE, tr|I1RPF1|I1RPF1_GIBZE, tr|A0A098DT41|A0A098DT41_GIBZE, tr|A0A1C3YJJ7|A0A1C3YJJ7_GIBZE, tr|I1RTF0|I1RTF0_GIBZE, tr|A0A098DLP1|A0A098DLP1_GIBZE, tr|A0A0E0SER1|A0A0E0SER1_GIBZE, tr|I1RAG2|I1RAG2_GIBZE, tr|I1RLY2|I1RLY2_GIBZE, tr|I1RKV6|I1RKV6_GIBZE, tr|I1RHA8|I1RHA8_GIBZE, tr|I1RCA7|I1RCA7_GIBZE, tr|A0A1C3YK08|A0A1C3YK08_GIBZE, tr|A0A098DM02|A0A098DM02_GIBZE, tr|I1S0K9|I1S0K9_GIBZE, tr|A0A1C3YKH2|A0A1C3YKH2_GIBZE, tr|V6QVH8|V6QVH8_GIBZE, tr|I1RJU4|I1RJU4_GIBZE, tr|I1RK49|I1RK49_GIBZE, tr|I1RRS8|I1RRS8_GIBZE, tr|I1RNU7|I1RNU7_GIBZE, tr|I1RLX7|I1RLX7_GIBZE, tr|I1RKH9|I1RKH9_GIBZE, tr|A0A1C3YJ69|A0A1C3YJ69_GIBZE, tr|A0A098E1Q7|A0A098E1Q7_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RSA5|I1RSA5_GIBZE, tr|I1S267|I1S267_GIBZE, tr|I1RUH3|I1RUH3_GIBZE, tr|I1RVV3|I1RVV3_GIBZE, tr|I1RB96|I1RB96_GIBZE, tr|I1RZV5|I1RZV5_GIBZE, tr|A0A1C3YLC3|A0A1C3YLC3_GIBZE, tr|I1RF16|I1RF16_GIBZE, tr|I1RYB8|I1RYB8_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|A0A1C3YHU9|A0A1C3YHU9_GIBZE, tr|I1RPM6|I1RPM6_GIBZE, tr|A0A1C3YHQ3|A0A1C3YHQ3_GIBZE, tr|A0A098D6R7|A0A098D6R7_GIBZE, tr|A0A1C3YK95|A0A1C3YK95_GIBZE, tr|A0A1C3YIS5|A0A1C3YIS5_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|A0A098DHN6|A0A098DHN6_GIBZE, tr|A0A0E0SNZ9|A0A0E0SNZ9_GIBZE, tr|I1RZP1|I1RZP1_GIBZE, sp|I1S2N3|GAOA_GIBZE, tr|I1S6V0|I1S6V0_GIBZE, tr|I1RSW5|I1RSW5_GIBZE, tr|I1RLW6|I1RLW6_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|I1RXB6|I1RXB6_GIBZE, tr|V6QVH2|V6QVH2_GIBZE, tr|A0A098DTS1|A0A098DTS1_GIBZE, tr|I1RX83|I1RX83_GIBZE, tr|A0A1C3YML2|A0A1C3YML2_GIBZE, tr|I1RC58|I1RC58_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|I1RME1|I1RME1_GIBZE, tr|A0A0E0RVC1|A0A0E0RVC1_GIBZE, tr|A0A1C3YJ47|A0A1C3YJ47_GIBZE, tr|I1RLA5|I1RLA5_GIBZE, tr|I1RT88|I1RT88_GIBZE, tr|A0A1C3YIV0|A0A1C3YIV0_GIBZE, tr|I1RXF1|I1RXF1_GIBZE, sp|Q4I7K4|DED1_GIBZE, tr|I1RJK0|I1RJK0_GIBZE, tr|I1RNW4|I1RNW4_GIBZE, tr|A0A1C3YLH6|A0A1C3YLH6_GIBZE, tr|I1SAK0|I1SAK0_GIBZE, tr|I1RIU6|I1RIU6_GIBZE, tr|I1RM69|I1RM69_GIBZE, tr|I1RE86|I1RE86_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|I1RFJ5|I1RFJ5_GIBZE, tr|V6QVM5|V6QVM5_GIBZE, tr|I1RF05|I1RF05_GIBZE, tr|I1RG57|I1RG57_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|A0A098DXZ6|A0A098DXZ6_GIBZE, tr|I1RFI9|I1RFI9_GIBZE, tr|I1RQ38|I1RQ38_GIBZE, tr|I1RHQ0|I1RHQ0_GIBZE, tr|I1RWN7|I1RWN7_GIBZE, tr|I1RF55|I1RF55_GIBZE, tr|I1RQX9|I1RQX9_GIBZE, tr|I1RY12|I1RY12_GIBZE, tr|I1RE90|I1RE90_GIBZE, tr|A0A1C3YNC7|A0A1C3YNC7_GIBZE, tr|I1RM66|I1RM66_GIBZE, tr|I1RMJ4|I1RMJ4_GIBZE, tr|A0A098DUZ2|A0A098DUZ2_GIBZE, tr|I1RAM3|I1RAM3_GIBZE, tr|I1RHL9|I1RHL9_GIBZE, tr|A0A0E0SAE0|A0A0E0SAE0_GIBZE, tr|I1RTG5|I1RTG5_GIBZE, tr|I1RRS6|I1RRS6_GIBZE, tr|A0A098DJ03|A0A098DJ03_GIBZE, tr|I1RBS5|I1RBS5_GIBZE, tr|I1RMW4|I1RMW4_GIBZE, tr|A0A098DEB5|A0A098DEB5_GIBZE, tr|I1RPI5|I1RPI5_GIBZE, tr|I1RPD9|I1RPD9_GIBZE,</td></tr>
</table>

<table>
<tr><td></td><td></td><td></td><td></td><td>tr|A0A1C3YJZ1|A0A1C3YJZ1_GIBZE, tr|I1REV6|I1REV6_GIBZE, tr|A0A1C3YID4|A0A1C3YID4_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RJH8|I1RJH8_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RNZ1|I1RNZ1_GIBZE, tr|A0A098DXB4|A0A098DXB4_GIBZE, tr|V6RDP1|V6RDP1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1RA43|I1RA43_GIBZE, tr|A0A1C3YNA9|A0A1C3YNA9_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1RLV0|I1RLV0_GIBZE, tr|A0A098DE56|A0A098DE56_GIBZE, tr|I1RYU0|I1RYU0_GIBZE, tr|I1RJ55|I1RJ55_GIBZE, tr|A0A098DPL1|A0A098DPL1_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RF60|I1RF60_GIBZE, tr|I1RF85|I1RF85_GIBZE, tr|I1RMC0|I1RMC0_GIBZE, tr|A0A098DF44|A0A098DF44_GIBZE, tr|A0A098D760|A0A098D760_GIBZE, tr|I1RI39|I1RI39_GIBZE, tr|I1RYC1|I1RYC1_GIBZE, tr|I1S8P4|I1S8P4_GIBZE, tr|I1RR60|I1RR60_GIBZE, tr|I1RTI3|I1RTI3_GIBZE, tr|I1S4S5|I1S4S5_GIBZE, tr|I1S8F9|I1S8F9_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|V6RXE7|V6RXE7_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RPK1|I1RPK1_GIBZE, tr|I1RW54|I1RW54_GIBZE, tr|A0A1C3YM35|A0A1C3YM35_GIBZE, tr|I1RXX8|I1RXX8_GIBZE</td></tr>
<tr><td>transferase activity, transferring pentosyl groups</td><td>4 out of 189 genes, 2.1%</td><td>11 out of 1819 genes, 0.6%</td><td>0.02074</td><td>tr|V6QVH8|V6QVH8_GIBZE, tr|A0A098DF44|A0A098DF44_GIBZE, tr|I1RYU0|I1RYU0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
<tr><td>cytidylyltransferase activity</td><td>2 out of 189 genes, 1.1%</td><td>3 out of 1819 genes, 0.2%</td><td>0.03002</td><td>tr|V6RXE7|V6RXE7_GIBZE, tr|I1RK49|I1RK49_GIBZE</td></tr>
<tr><td>enzyme binding</td><td>7 out of 189 genes, 3.7%</td><td>31 out of 1819 genes, 1.7%</td><td>0.03535</td><td>tr|I1RZE1|I1RZE1_GIBZE, tr|I1RSP1|I1RSP1_GIBZE, tr|A0A098DES7|A0A098DES7_GIBZE, tr|A0A098DUT9|A0A098DUT9_GIBZE, tr|I1RRW0|I1RRW0_GIBZE, tr|A0A098DK45|A0A098DK45_GIBZE, sp|Q4I5I4|SPT5_GIBZE</td></tr>
<tr><td>monooxygenase activity</td><td>5 out of 189 genes, 2.6%</td><td>19 out of 1819 genes, 1.0%</td><td>0.03978</td><td>tr|I1RE90|I1RE90_GIBZE, tr|I1RAG2|I1RAG2_GIBZE, tr|A0A0E0SAE0|A0A0E0SAE0_GIBZE, tr|I1RIU6|I1RIU6_GIBZE, tr|A0A098DPL1|A0A098DPL1_GIBZE</td></tr>
<tr><td>ubiquitin-protein ligase activity</td><td>3 out of 189 genes, 1.6%</td><td>8 out of 1819 genes, 0.4%</td><td>0.04171</td><td>tr|I1RLX7|I1RLX7_GIBZE, tr|I1RG57|I1RG57_GIBZE, tr|A0A098D760|A0A098D760_GIBZE</td></tr>
<tr><td>tubulin binding</td><td>3 out of 189 genes, 1.6%</td><td>8 out of 1819 genes, 0.4%</td><td>0.04171</td><td>tr|I1RQF2|I1RQF2_GIBZE, tr|A0A0E0SNZ9|A0A0E0SNZ9_GIBZE, tr|I1RAI0|I1RAI0_GIBZE</td></tr>
<tr><td>transferase activity, transferring glycosyl groups</td><td>7 out of 189 genes, 3.7%</td><td>33 out of 1819 genes, 1.8%</td><td>0.0481</td><td>tr|G4XVC2|G4XVC2_GIBZA, tr|V6QVH8|V6QVH8_GIBZE, tr|I1RX83|I1RX83_GIBZE, tr|A0A098DF44|A0A098DF44_GIBZE, tr|I1RYU0|I1RYU0_GIBZE, tr|A0A098DM02|A0A098DM02_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
<tr><td>guanyl-nucleotide exchange factor activity</td><td>4 out of 189 genes, 2.1%</td><td>14 out of 1819 genes, 0.8%</td><td>0.0491</td><td>tr|I1RZP1|I1RZP1_GIBZE, tr|I1RRZ0|I1RRZ0_GIBZE, tr|A0A098DK45|A0A098DK45_GIBZE, tr|A0A1C3YKK9|A0A1C3YKK9_GIBZE</td></tr>
</table>

GO250-GO0_Biological Process

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value	Genes annotated to the term
histidine biosynthetic process	3 out of 195 genes, 1.5%	5 out of 1882 genes, 0.3%	0.00936	tr|I1RPW1|I1RPW1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE
histidine metabolic process	3 out of 195 genes, 1.5%	5 out of 1882 genes, 0.3%	0.00936	tr|I1RPW1|I1RPW1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE
histidine family amino acid metabolic process	3 out of 195 genes, 1.5%	5 out of 1882 genes, 0.3%	0.00936	tr|I1RPW1|I1RPW1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE
histidine family amino acid biosynthetic process	3 out of 195 genes, 1.5%	5 out of 1882 genes, 0.3%	0.00936	tr|I1RPW1|I1RPW1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE
mitochondrion morphogenesis	3 out of 195 genes, 1.5%	5 out of 1882 genes, 0.3%	0.00936	tr|I1S0R9|I1S0R9_GIBZE, tr|I1RTF0|I1RTF0_GIBZE, tr|I1RRS8|I1RRS8_GIBZE
adenine salvage	2 out of 195 genes, 1.0%	2 out of 1882 genes, 0.1%	0.01069	tr|V6QVH8|V6QVH8_GIBZE, tr|A0A098DF44|A0A098DF44_GIBZE
polyphosphate metabolic process	2 out of 195 genes, 1.0%	2 out of 1882 genes, 0.1%	0.01069	tr|I1RCV0|I1RCV0_GIBZE, tr|A0A1C3YHU9|A0A1C3YHU9_GIBZE
glycerophospholipid biosynthetic process	5 out of 195 genes, 2.6%	15 out of 1882 genes, 0.8%	0.01432	tr|V6RXE7|V6RXE7_GIBZE, tr|A0A098DM02|A0A098DM02_GIBZE, tr|A0A1C3YLC3|A0A1C3YLC3_GIBZE, tr|A0A1C3YJJ7|A0A1C3YJJ7_GIBZE, tr|I1RK49|I1RK49_GIBZE
glycerophospholipid metabolic process	7 out of 195 genes, 3.6%	27 out of 1882 genes, 1.4%	0.01683	tr|V6RXE7|V6RXE7_GIBZE, tr|A0A098DM02|A0A098DM02_GIBZE, tr|A0A1C3YLC3|A0A1C3YLC3_GIBZE, tr|I1RC58|I1RC58_GIBZE, tr|A0A1C3YJJ7|A0A1C3YJJ7_GIBZE, tr|I1RK49|I1RK49_GIBZE, tr|I1RE86|I1RE86_GIBZE
cysteine metabolic process	3 out of 195 genes, 1.5%	6 out of 1882 genes, 0.3%	0.0173	tr|A0A098DTS1|A0A098DTS1_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RE58|I1RE58_GIBZE
cell part morphogenesis	3 out of 195 genes, 1.5%	6 out of 1882 genes, 0.3%	0.0173	tr|I1S0R9|I1S0R9_GIBZE, tr|I1RTF0|I1RTF0_GIBZE, tr|I1RRS8|I1RRS8_GIBZE

<table>
<tr><td>protein retention in Golgi apparatus</td><td>3 out of 195 genes, 1.5%</td><td>6 out of 1882 genes, 0.3%</td><td>0.0173</td><td>tr|I1REC4|I1REC4_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|I1RG99|I1RG99_GIBZE</td></tr>
<tr><td>establishment of protein localization</td><td>25 out of 195 genes, 12.8%</td><td>159 out of 1882 genes, 8.4%</td><td>0.01822</td><td>tr|I1RZE1|I1RZE1_GIBZE, tr|I1RBS5|I1RBS5_GIBZE, tr|A0A098D760|A0A098D760_GIBZE, tr|I1RG99|I1RG99_GIBZE, tr|I1RBS3|I1RBS3_GIBZE, tr|I1RE68|I1RE68_GIBZE, tr|I1RSP1|I1RSP1_GIBZE, tr|I1S9S4|I1S9S4_GIBZE, tr|I1RY32|I1RY32_GIBZE, tr|A0A098DVM4|A0A098DVM4_GIBZE, tr|I1RJH8|I1RJH8_GIBZE, tr|A0A098DK45|A0A098DK45_GIBZE, tr|I1RZH5|I1RZH5_GIBZE, tr|I1RFP5|I1RFP5_GIBZE, sp|Q4I1H6|SNX3_GIBZE, tr|A0A0E0SNZ9|A0A0E0SNZ9_GIBZE, tr|I1REC4|I1REC4_GIBZE, tr|I1RW38|I1RW38_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|A0A1C3YIX0|A0A1C3YIX0_GIBZE, tr|A0A098DEH9|A0A098DEH9_GIBZE, tr|I1RZP1|I1RZP1_GIBZE, tr|I1RRW0|I1RRW0_GIBZE, tr|A0A0E0SNM6|A0A0E0SNM6_GIBZE, tr|I1RRS8|I1RRS8_GIBZE</td></tr>
<tr><td>maintenance of protein location in cell</td><td>4 out of 195 genes, 2.1%</td><td>11 out of 1882 genes, 0.6%</td><td>0.02055</td><td>tr|I1REC4|I1REC4_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|A0A0E0SNM6|A0A0E0SNM6_GIBZE, tr|I1RG99|I1RG99_GIBZE</td></tr>
<tr><td>protein transport</td><td>24 out of 195 genes, 12.3%</td><td>155 out of 1882 genes, 8.2%</td><td>0.02451</td><td>tr|I1RZE1|I1RZE1_GIBZE, tr|I1RBS5|I1RBS5_GIBZE, tr|A0A098D760|A0A098D760_GIBZE, tr|I1RG99|I1RG99_GIBZE, tr|I1RBS3|I1RBS3_GIBZE, tr|I1RE68|I1RE68_GIBZE, tr|I1RSP1|I1RSP1_GIBZE, tr|I1S9S4|I1S9S4_GIBZE, tr|I1RY32|I1RY32_GIBZE, tr|A0A098DVM4|A0A098DVM4_GIBZE, tr|I1RJH8|I1RJH8_GIBZE, tr|A0A098DK45|A0A098DK45_GIBZE, tr|I1RZH5|I1RZH5_GIBZE, tr|I1RFP5|I1RFP5_GIBZE, sp|Q4I1H6|SNX3_GIBZE, tr|A0A0E0SNZ9|A0A0E0SNZ9_GIBZE, tr|I1REC4|I1REC4_GIBZE, tr|I1RW38|I1RW38_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|A0A1C3YIX0|A0A1C3YIX0_GIBZE, tr|A0A098DEH9|A0A098DEH9_GIBZE, tr|I1RZP1|I1RZP1_GIBZE, tr|I1RRW0|I1RRW0_GIBZE, tr|I1RRS8|I1RRS8_GIBZE</td></tr>
<tr><td>glycerolipid metabolic process</td><td>7 out of 195 genes, 3.6%</td><td>29 out of 1882 genes, 1.5%</td><td>0.02476</td><td>tr|V6RXE7|V6RXE7_GIBZE, tr|A0A098DM02|A0A098DM02_GIBZE, tr|A0A1C3YLC3|A0A1C3YLC3_GIBZE, tr|I1RC58|I1RC58_GIBZE, tr|A0A1C3YJJ7|A0A1C3YJJ7_GIBZE, tr|I1RK49|I1RK49_GIBZE, tr|I1RE86|I1RE86_GIBZE</td></tr>
<tr><td>intracellular protein transport</td><td>23 out of 195 genes, 11.8%</td><td>148 out of 1882 genes, 7.9%</td><td>0.02643</td><td>tr|I1RZE1|I1RZE1_GIBZE, tr|I1RBS5|I1RBS5_GIBZE, tr|A0A098D760|A0A098D760_GIBZE, tr|I1RG99|I1RG99_GIBZE, tr|I1RBS3|I1RBS3_GIBZE, tr|I1RE68|I1RE68_GIBZE, tr|I1RSP1|I1RSP1_GIBZE, tr|I1S9S4|I1S9S4_GIBZE, tr|I1RY32|I1RY32_GIBZE, tr|I1RJH8|I1RJH8_GIBZE, tr|A0A098DK45|A0A098DK45_GIBZE, tr|I1RZH5|I1RZH5_GIBZE, tr|I1RFP5|I1RFP5_GIBZE, sp|Q4I1H6|SNX3_GIBZE, tr|A0A0E0SNZ9|A0A0E0SNZ9_GIBZE, tr|I1REC4|I1REC4_GIBZE, tr|I1RW38|I1RW38_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|A0A1C3YIX0|A0A1C3YIX0_GIBZE, tr|A0A098DEH9|A0A098DEH9_GIBZE, tr|I1RZP1|I1RZP1_GIBZE, tr|I1RRW0|I1RRW0_GIBZE, tr|I1RRS8|I1RRS8_GIBZE</td></tr>
<tr><td>inner mitochondrial membrane organization</td><td>3 out of 195 genes, 1.5%</td><td>7 out of 1882 genes, 0.4%</td><td>0.02798</td><td>tr|I1S0R9|I1S0R9_GIBZE, tr|I1RQJ1|I1RQJ1_GIBZE, tr|I1RRS8|I1RRS8_GIBZE</td></tr>
<tr><td>protein localization in Golgi apparatus</td><td>3 out of 195 genes, 1.5%</td><td>7 out of 1882 genes, 0.4%</td><td>0.02798</td><td>tr|I1REC4|I1REC4_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|I1RG99|I1RG99_GIBZE</td></tr>
<tr><td>mitochondrial membrane organization</td><td>4 out of 195 genes, 2.1%</td><td>12 out of 1882 genes, 0.6%</td><td>0.02838</td><td>tr|I1S0R9|I1S0R9_GIBZE, tr|I1RQJ1|I1RQJ1_GIBZE, tr|I1RTF0|I1RTF0_GIBZE, tr|I1RRS8|I1RRS8_GIBZE</td></tr>
<tr><td>maintenance of protein location</td><td>4 out of 195 genes, 2.1%</td><td>12 out of 1882 genes, 0.6%</td><td>0.02838</td><td>tr|I1REC4|I1REC4_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|A0A0E0SNM6|A0A0E0SNM6_GIBZE, tr|I1RG99|I1RG99_GIBZE</td></tr>
</table>

<table>
<tr><td>maintenance of location in cell</td><td>4 out of 195 genes, 2.1%</td><td>12 out of 1882 genes, 0.6%</td><td>0.02838</td><td>tr|I1REC4|I1REC4_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|A0A0E0SNM6|A0A0E0SNM6_GIBZE, tr|I1RG99|I1RG99_GIBZE</td></tr>
<tr><td>L-phenylalanine catabolic process</td><td>2 out of 195 genes, 1.0%</td><td>3 out of 1882 genes, 0.2%</td><td>0.02986</td><td>tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE</td></tr>
<tr><td>mitochondrial fusion</td><td>2 out of 195 genes, 1.0%</td><td>3 out of 1882 genes, 0.2%</td><td>0.02986</td><td>tr|I1RTF0|I1RTF0_GIBZE, tr|I1RRS8|I1RRS8_GIBZE</td></tr>
<tr><td>cytoplasmic transport</td><td>2 out of 195 genes, 1.0%</td><td>3 out of 1882 genes, 0.2%</td><td>0.02986</td><td>tr|I1RW38|I1RW38_GIBZE, tr|I1RZH5|I1RZH5_GIBZE</td></tr>
<tr><td>phosphoinositide-mediated signaling</td><td>2 out of 195 genes, 1.0%</td><td>3 out of 1882 genes, 0.2%</td><td>0.02986</td><td>tr|I1RC58|I1RC58_GIBZE, tr|I1RVZ7|I1RVZ7_GIBZE</td></tr>
<tr><td>carbohydrate metabolic process</td><td>40 out of 195 genes, 20.5%</td><td>300 out of 1882 genes, 15.9%</td><td>0.04397</td><td>tr|G4XVC2|G4XVC2_GIBZA, tr|A0A098DT41|A0A098DT41_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1SAK0|I1SAK0_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|A0A098DLP1|A0A098DLP1_GIBZE, tr|I1RE86|I1RE86_GIBZE, tr|I1RPM6|I1RPM6_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|A0A1C3YID4|A0A1C3YID4_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RLY2|I1RLY2_GIBZE, tr|A0A1C3YIS5|A0A1C3YIS5_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|V6RDP1|V6RDP1_GIBZE, tr|A0A098DXB4|A0A098DXB4_GIBZE, tr|A0A098DM02|A0A098DM02_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|A0A098DE56|A0A098DE56_GIBZE, tr|I1RJ55|I1RJ55_GIBZE, tr|A0A098DXZ6|A0A098DXZ6_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RNU7|I1RNU7_GIBZE, tr|I1RHQ0|I1RHQ0_GIBZE, tr|I1RI39|I1RI39_GIBZE, tr|I1RSA5|I1RSA5_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RYC1|I1RYC1_GIBZE, tr|A0A098DTS1|A0A098DTS1_GIBZE, tr|I1RVV3|I1RVV3_GIBZE, tr|I1RX83|I1RX83_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RPK1|I1RPK1_GIBZE, tr|A0A1C3YM35|A0A1C3YM35_GIBZE</td></tr>
<tr><td>amine metabolic process</td><td>27 out of 195 genes, 13.8%</td><td>189 out of 1882 genes, 10.0%</td><td>0.04499</td><td>tr|G4XVC2|G4XVC2_GIBZA, tr|I1RF16|I1RF16_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|A0A1C3YJJ7|A0A1C3YJJ7_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|A0A098DLP1|A0A098DLP1_GIBZE, tr|I1RPM6|I1RPM6_GIBZE, tr|I1S2H3|I1S2H3_GIBZE, tr|I1RSA5|I1RSA5_GIBZE, tr|A0A1C3YKS6|A0A1C3YKS6_GIBZE, tr|A0A098DTS1|A0A098DTS1_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1S4S5|I1S4S5_GIBZE, tr|I1RE58|I1RE58_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|V6RXE7|V6RXE7_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|I1RBE7|I1RBE7_GIBZE, tr|I1RHL9|I1RHL9_GIBZE, tr|A0A1C3YM35|A0A1C3YM35_GIBZE, tr|A0A098DXZ6|A0A098DXZ6_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
<tr><td>sulfur amino acid biosynthetic process</td><td>5 out of 195 genes, 2.6%</td><td>20 out of 1882 genes, 1.1%</td><td>0.04825</td><td>tr|A0A098DTS1|A0A098DTS1_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|A0A1C3YM35|A0A1C3YM35_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RE58|I1RE58_GIBZE</td></tr>
<tr><td>methionine biosynthetic process</td><td>4 out of 195 genes, 2.1%</td><td>14 out of 1882 genes, 0.7%</td><td>0.04869</td><td>tr|I1RFL2|I1RFL2_GIBZE, tr|A0A1C3YM35|A0A1C3YM35_GIBZE, sp|Q4I1N3|MET3_GIBZE, tr|I1RE58|I1RE58_GIBZE</td></tr>
</table>

maintenance of location	4 out of 195 genes, 2.1%	14 out of 1882 genes, 0.7%	0.04869	tr|I1REC4|I1REC4_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|A0A0E0SNM6|A0A0E0SNM6_GIBZE, tr|I1RG99|I1RG99_GIBZE
cellular protein localization	24 out of 195 genes, 12.3%	167 out of 1882 genes, 8.9%	0.05402	tr|I1RZE1|I1RZE1_GIBZE, tr|I1RBS5|I1RBS5_GIBZE, tr|A0A098D760|A0A098D760_GIBZE, tr|I1RG99|I1RG99_GIBZE, tr|I1RBS3|I1RBS3_GIBZE, tr|I1RE68|I1RE68_GIBZE, tr|I1RSP1|I1RSP1_GIBZE, tr|I1S9S4|I1S9S4_GIBZE, tr|I1RY32|I1RY32_GIBZE, tr|I1RJH8|I1RJH8_GIBZE, tr|A0A098DK45|A0A098DK45_GIBZE, tr|I1RZH5|I1RZH5_GIBZE, tr|I1RFP5|I1RFP5_GIBZE, sp|Q4I1H6|SNX3_GIBZE, tr|A0A0E0SNZ9|A0A0E0SNZ9_GIBZE, tr|I1REC4|I1REC4_GIBZE, tr|I1RW38|I1RW38_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|A0A1C3YIX0|A0A1C3YIX0_GIBZE, tr|A0A098DEH9|A0A098DEH9_GIBZE, tr|I1RZP1|I1RZP1_GIBZE, tr|I1RRW0|I1RRW0_GIBZE, tr|A0A0E0SNM6|A0A0E0SNM6_GIBZE, tr|I1RRS8|I1RRS8_GIBZE

GO500-GO0_Cellular Component

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value	Genes annotated to the term
extracellular region	11 out of 177 genes, 6.2%	27 out of 1646 genes, 1.6%	4.59E-05	tr|I1RA13|I1RA13_GIBZE, tr|I1S2I0|I1S2I0_GIBZE, tr|I1RR78|I1RR78_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|A0A0E0SI42|A0A0E0SI42_GIBZE, tr|I1RTU1|I1RTU1_GIBZE, tr|A0A0E0SBV6|A0A0E0SBV6_GIBZE, sp|I1S2N3|GAOA_GIBZE, tr|I1RKV6|I1RKV6_GIBZE, tr|I1RLD7|I1RLD7_GIBZE, tr|I1RR45|I1RR45_GIBZE
mitochondrial intermembrane space	7 out of 177 genes, 4.0%	24 out of 1646 genes, 1.5%	0.01043	tr|I1RZI8|I1RZI8_GIBZE, sp|Q4IB65|TIM9_GIBZE, tr|V6RH92|V6RH92_GIBZE, sp|Q4IJW4|TIM8_GIBZE, tr|I1RZ21|I1RZ21_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|A0A1C3YKH2|A0A1C3YKH2_GIBZE
microbody	8 out of 177 genes, 4.5%	33 out of 1646 genes, 2.0%	0.01996	sp|Q4HYR2|ACEA_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|A0A098D5A0|A0A098D5A0_GIBZE, tr|A0A0E0SEN1|A0A0E0SEN1_GIBZE, tr|I1RZ25|I1RZ25_GIBZE, tr|I1RRW0|I1RRW0_GIBZE
organelle envelope lumen	7 out of 177 genes, 4.0%	27 out of 1646 genes, 1.6%	0.02025	tr|I1RZI8|I1RZI8_GIBZE, sp|Q4IB65|TIM9_GIBZE, tr|V6RH92|V6RH92_GIBZE, sp|Q4IJW4|TIM8_GIBZE, tr|I1RZ21|I1RZ21_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|A0A1C3YKH2|A0A1C3YKH2_GIBZE
oligosaccharyltransferase complex	2 out of 177 genes, 1.1%	3 out of 1646 genes, 0.2%	0.03207	tr|I1RZM0|I1RZM0_GIBZE, tr|I1R9N7|I1R9N7_GIBZE
periplasmic space	2 out of 177 genes, 1.1%	3 out of 1646 genes, 0.2%	0.03207	tr|I1RTU1|I1RTU1_GIBZE, tr|I1RR96|I1RR96_GIBZE
mitochondrial intermembrane space protein transporter complex	2 out of 177 genes, 1.1%	3 out of 1646 genes, 0.2%	0.03207	sp|Q4IB65|TIM9_GIBZE, sp|Q4IJW4|TIM8_GIBZE
peroxisome	7 out of 177 genes, 4.0%	31 out of 1646 genes, 1.9%	0.04149	tr|A0A098D5A0|A0A098D5A0_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|A0A0E0SEN1|A0A0E0SEN1_GIBZE, tr|I1RRW0|I1RRW0_GIBZE, tr|I1RZ25|I1RZ25_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE

GO500-GO0_MolecularFunction

<table>
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<tr><th>Gene Ontology term</th><th>Cluster frequency</th><th>Protein frequency of use</th><th>P-value</th><th>Genes annotated to the term</th></tr>
</thead>
<tbody>
<tr><td>catalytic activity</td><td>172 out of 217 genes, 79.3%</td><td>1275 out of 1819 genes, 70.1%</td><td>0.00082</td><td>tr|I1RAD8|I1RAD8_GIBZE, tr|A0A098DT41|A0A098DT41_GIBZE, tr|I1RUB2|I1RUB2_GIBZE, tr|I1RCS1|I1RCS1_GIBZE, tr|A0A0E0SER1|A0A0E0SER1_GIBZE, tr|I1RKV6|I1RKV6_GIBZE, tr|A0A098DJH8|A0A098DJH8_GIBZE, tr|I1RWP8|I1RWP8_GIBZE, tr|I1RIG1|I1RIG1_GIBZE, tr|I1RR96|I1RR96_GIBZE, tr|I1RCA7|I1RCA7_GIBZE, tr|I1RDN6|I1RDN6_GIBZE, tr|A0A1C3YKH2|A0A1C3YKH2_GIBZE, tr|I1RZE4|I1RZE4_GIBZE, tr|V6QVH8|V6QVH8_GIBZE, tr|I1RAU6|I1RAU6_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1RRS8|I1RRS8_GIBZE, tr|I1RX90|I1RX90_GIBZE, tr|I1RLX7|I1RLX7_GIBZE, tr|I1RGI5|I1RGI5_GIBZE, tr|A0A1C3YJ69|A0A1C3YJ69_GIBZE, tr|I1S6R1|I1S6R1_GIBZE, tr|I1RUH3|I1RUH3_GIBZE, tr|I1RVV3|I1RVV3_GIBZE, tr|V6QWD8|V6QWD8_GIBZE, tr|I1RZ21|I1RZ21_GIBZE, tr|I1RZ25|I1RZ25_GIBZE, tr|I1RB96|I1RB96_GIBZE, tr|I1RJ45|I1RJ45_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|I1RUW4|I1RUW4_GIBZE, tr|I1RZV5|I1RZV5_GIBZE, tr|A0A0E0SQQ3|A0A0E0SQQ3_GIBZE, tr|I1RYB8|I1RYB8_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1RZM0|I1RZM0_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|V6RG06|V6RG06_GIBZE, tr|A0A1C3YHU9|A0A1C3YHU9_GIBZE, tr|I1RPM6|I1RPM6_GIBZE, tr|A0A1C3YHQ3|A0A1C3YHQ3_GIBZE, tr|A0A1C3YHK0|A0A1C3YHK0_GIBZE, tr|I1RTU1|I1RTU1_GIBZE, tr|I1S0A3|I1S0A3_GIBZE, tr|I1RYG3|I1RYG3_GIBZE, tr|I1RR22|I1RR22_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|A0A098DHN6|A0A098DHN6_GIBZE, tr|A0A0E0SNZ9|A0A0E0SNZ9_GIBZE, tr|A0A098DI12|A0A098DI12_GIBZE, tr|I1RHK2|I1RHK2_GIBZE, tr|I1RFQ1|I1RFQ1_GIBZE, tr|I1S3M2|I1S3M2_GIBZE, tr|I1S958|I1S958_GIBZE, sp|I1S2N3|GAOA_GIBZE, tr|A0A098DJ29|A0A098DJ29_GIBZE, tr|A0A0E0SEN1|A0A0E0SEN1_GIBZE, tr|I1RSW5|I1RSW5_GIBZE, tr|I1RXH3|I1RXH3_GIBZE, tr|I1RLW6|I1RLW6_GIBZE, tr|I1RSI2|I1RSI2_GIBZE, tr|I1RPE5|I1RPE5_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|V6RH92|V6RH92_GIBZE, tr|I1RCT7|I1RCT7_GIBZE, tr|A0A1C3YML2|A0A1C3YML2_GIBZE, tr|I1RME1|I1RME1_GIBZE, tr|I1RVR0|I1RVR0_GIBZE, tr|A0A1C3YJ47|A0A1C3YJ47_GIBZE, tr|I1RLA5|I1RLA5_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|A0A0E0RTW2|A0A0E0RTW2_GIBZE, tr|I1RTE4|I1RTE4_GIBZE, tr|A0A0E0SI42|A0A0E0SI42_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RFJ6|I1RFJ6_GIBZE, tr|I1REI6|I1REI6_GIBZE, tr|A0A0E0RMB3|A0A0E0RMB3_GIBZE, tr|I1RJK0|I1RJK0_GIBZE, tr|A0A0E0RSG8|A0A0E0RSG8_GIBZE, tr|I1RAZ1|I1RAZ1_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|I1R9N7|I1R9N7_GIBZE, tr|I1RM69|I1RM69_GIBZE, tr|I1RFJ5|I1RFJ5_GIBZE, tr|I1S0R8|I1S0R8_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|I1S0I8|I1S0I8_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|V6QWB1|V6QWB1_GIBZE, tr|I1RF05|I1RF05_GIBZE, tr|I1RSP4|I1RSP4_GIBZE, tr|A0A0E0SGB3|A0A0E0SGB3_GIBZE, tr|A0A0E0S3A4|A0A0E0S3A4_GIBZE, tr|A0A0E0RU55|A0A0E0RU55_GIBZE, tr|I1RKP5|I1RKP5_GIBZE, tr|I1RT76|I1RT76_GIBZE, sp|Q4IAA0|FAL1_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|I1RFI9|I1RFI9_GIBZE, tr|I1RF55|I1RF55_GIBZE, tr|I1RQX9|I1RQX9_GIBZE, tr|I1RYW6|I1RYW6_GIBZE, tr|I1RZI8|I1RZI8_GIBZE, tr|V6R4J1|V6R4J1_GIBZE, tr|A0A1C3YLK5|A0A1C3YLK5_GIBZE, tr|I1RDQ1|I1RDQ1_GIBZE, tr|I1S8X0|I1S8X0_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|I1RBZ6|I1RBZ6_GIBZE, tr|A0A1C3YJI5|A0A1C3YJI5_GIBZE, tr|I1RAM3|I1RAM3_GIBZE, tr|A0A098DUZ2|A0A098DUZ2_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RCR2|I1RCR2_GIBZE, tr|I1RLD7|I1RLD7_GIBZE, tr|I1S223|I1S223_GIBZE, tr|I1RCC2|I1RCC2_GIBZE, tr|A0A0E0RWK1|A0A0E0RWK1_GIBZE, tr|A0A098DJ03|A0A098DJ03_GIBZE, tr|I1RBS5|I1RBS5_GIBZE, tr|I1RPD9|I1RPD9_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RR45|I1RR45_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|I1RA13|I1RA13_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1SAH9|I1SAH9_GIBZE, tr|I1REY8|I1REY8_GIBZE, tr|I1S1K3|I1S1K3_GIBZE, tr|V6RDP1|V6RDP1_GIBZE, tr|A0A0E0SA95|A0A0E0SA95_GIBZE, tr|A0A098DXB4|A0A098DXB4_GIBZE,</td></tr>
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<tr><td>dioxygenase activity</td><td>5 out of 217 genes, 2.3%</td><td>12 out of 1819 genes, 0.7%</td><td>0.00902</td><td>tr|A0A0E0SQQ3|A0A0E0SQQ3_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE, tr|I1S958|I1S958_GIBZE</td></tr>
<tr><td>acetyltransferase activity</td><td>5 out of 217 genes, 2.3%</td><td>13 out of 1819 genes, 0.7%</td><td>0.01326</td><td>tr|I1RPW2|I1RPW2_GIBZE, tr|I1RX90|I1RX90_GIBZE, tr|A0A098D5A0|A0A098D5A0_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1RVX9|I1RVX9_GIBZE</td></tr>
<tr><td>amino-acid N-acetyltransferase activity</td><td>2 out of 217 genes, 0.9%</td><td>2 out of 1819 genes, 0.1%</td><td>0.01417</td><td>tr|I1RPW2|I1RPW2_GIBZE, tr|I1RVX9|I1RVX9_GIBZE</td></tr>
<tr><td>homogentisate 1,2-dioxygenase activity</td><td>2 out of 217 genes, 0.9%</td><td>2 out of 1819 genes, 0.1%</td><td>0.01417</td><td>tr|I1RF80|I1RF80_GIBZE, tr|I1RVR7|I1RVR7_GIBZE</td></tr>
<tr><td>triacylglycerol lipase activity</td><td>2 out of 217 genes, 0.9%</td><td>2 out of 1819 genes, 0.1%</td><td>0.01417</td><td>tr|I1RJ45|I1RJ45_GIBZE, tr|I1RPD9|I1RPD9_GIBZE</td></tr>
<tr><td>motor activity</td><td>3 out of 217 genes, 1.4%</td><td>6 out of 1819 genes, 0.3%</td><td>0.02546</td><td>tr|A0A0E0SNZ9|A0A0E0SNZ9_GIBZE, tr|A0A098D3M4|A0A098D3M4_GIBZE, tr|A0A1C3YLK5|A0A1C3YLK5_GIBZE</td></tr>
<tr><td>N-acetyltransferase activity</td><td>3 out of 217 genes, 1.4%</td><td>6 out of 1819 genes, 0.3%</td><td>0.02546</td><td>tr|I1RPW2|I1RPW2_GIBZE, tr|I1RX90|I1RX90_GIBZE, tr|I1RVX9|I1RVX9_GIBZE</td></tr>
<tr><td>intramolecular oxidoreductase activity, interconverting aldoses and ketoses</td><td>3 out of 217 genes, 1.4%</td><td>6 out of 1819 genes, 0.3%</td><td>0.02546</td><td>tr|I1RKR5|I1RKR5_GIBZE, tr|I1RVV3|I1RVV3_GIBZE, tr|A0A0E0RU55|A0A0E0RU55_GIBZE</td></tr>
<tr><td>transferase activity, transferring pentosyl groups</td><td>4 out of 217 genes, 1.8%</td><td>11 out of 1819 genes, 0.6%</td><td>0.033</td><td>tr|V6QVH8|V6QVH8_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|A0A098DF44|A0A098DF44_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
</table>

transferase activity, transferring acyl groups	10 out of 217 genes, 4.6%	45 out of 1819 genes, 2.5%	0.03473	sp|Q4HYR2|ACEA_GIBZE, tr|I1RPW2|I1RPW2_GIBZE, tr|I1RX90|I1RX90_GIBZE, tr|I1RLA5|I1RLA5_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|A0A098D5A0|A0A098D5A0_GIBZE, tr|A0A098DS79|A0A098DS79_GIBZE, tr|I1S8X0|I1S8X0_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE
microtubule motor activity	2 out of 217 genes, 0.9%	3 out of 1819 genes, 0.2%	0.03917	tr|A0A0E0SNZ9|A0A0E0SNZ9_GIBZE, tr|A0A1C3YLK5|A0A1C3YLK5_GIBZE
N-acyltransferase activity	3 out of 217 genes, 1.4%	7 out of 1819 genes, 0.4%	0.04069	tr|I1RPW2|I1RPW2_GIBZE, tr|I1RX90|I1RX90_GIBZE, tr|I1RVX9|I1RVX9_GIBZE
intramolecular oxidoreductase activity	4 out of 217 genes, 1.8%	12 out of 1819 genes, 0.7%	0.04499	tr|I1RKR5|I1RKR5_GIBZE, tr|I1RYB8|I1RYB8_GIBZE, tr|I1RVV3|I1RVV3_GIBZE, tr|A0A0E0RU55|A0A0E0RU55_GIBZE

GO500-GO0_Biological Process

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value	Genes annotated to the term
L-phenylalanine catabolic process	3 out of 211 genes, 1.4%	3 out of 1882 genes, 0.2%	0.00139	tr|I1RF80|I1RF80_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE
lysine biosynthetic process via aminoadipic acid	3 out of 211 genes, 1.4%	3 out of 1882 genes, 0.2%	0.00139	tr|I1S2D5|I1S2D5_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE
L-phenylalanine metabolic process	3 out of 211 genes, 1.4%	4 out of 1882 genes, 0.2%	0.0051	tr|I1RF80|I1RF80_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE
tyrosine metabolic process	3 out of 211 genes, 1.4%	4 out of 1882 genes, 0.2%	0.0051	tr|I1RF80|I1RF80_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE
thiamin biosynthetic process	3 out of 211 genes, 1.4%	4 out of 1882 genes, 0.2%	0.0051	tr|I1S0B7|I1S0B7_GIBZE, tr|I1RDH6|I1RDH6_GIBZE, tr|I1RFJ1|I1RFJ1_GIBZE
amine biosynthetic process	19 out of 211 genes, 9.0%	94 out of 1882 genes, 5.0%	0.00635	tr|I1RPW2|I1RPW2_GIBZE, tr|A0A0E0RWK1|A0A0E0RWK1_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RCT7|I1RCT7_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|A0A098DQF2|A0A098DQF2_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE,

				tr|I1RQE0|I1RQE0_GIBZE
cellular amino acid biosynthetic process	18 out of 211 genes, 8.5%	89 out of 1882 genes, 4.7%	0.0078	tr|I1RPW2|I1RPW2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RCT7|I1RCT7_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|A0A098DQF2|A0A098DQF2_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE
cellular amino acid and derivative metabolic process	32 out of 211 genes, 15.2%	190 out of 1882 genes, 10.1%	0.00892	tr|I1RPW2|I1RPW2_GIBZE, tr|A0A0E0RWK1|A0A0E0RWK1_GIBZE, tr|A0A0E0RSG8|A0A0E0RSG8_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE, tr|I1RCT7|I1RCT7_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|A0A098D5A0|A0A098D5A0_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|V6RXE7|V6RXE7_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|A0A098DQF2|A0A098DQF2_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RHK2|I1RHK2_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DS79|A0A098DS79_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE
thiamin metabolic process	3 out of 211 genes, 1.4%	5 out of 1882 genes, 0.3%	0.01171	tr|I1S0B7|I1S0B7_GIBZE, tr|I1RDH6|I1RDH6_GIBZE, tr|I1RFJ1|I1RFJ1_GIBZE
thiamin and derivative metabolic process	3 out of 211 genes, 1.4%	5 out of 1882 genes, 0.3%	0.01171	tr|I1S0B7|I1S0B7_GIBZE, tr|I1RDH6|I1RDH6_GIBZE, tr|I1RFJ1|I1RFJ1_GIBZE
thiamin and derivative biosynthetic process	3 out of 211 genes, 1.4%	5 out of 1882 genes, 0.3%	0.01171	tr|I1S0B7|I1S0B7_GIBZE, tr|I1RDH6|I1RDH6_GIBZE, tr|I1RFJ1|I1RFJ1_GIBZE
adenine salvage	2 out of 211 genes, 0.9%	2 out of 1882 genes, 0.1%	0.01252	tr|V6QVH8|V6QVH8_GIBZE, tr|A0A098DF44|A0A098DF44_GIBZE
amine metabolic process	31 out of 211 genes, 14.7%	189 out of 1882 genes, 10.0%	0.01471	tr|I1RPW2|I1RPW2_GIBZE, tr|A0A0E0RWK1|A0A0E0RWK1_GIBZE, tr|A0A0E0RSG8|A0A0E0RSG8_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE, tr|I1RCT7|I1RCT7_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|A0A098D5A0|A0A098D5A0_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|V6RXE7|V6RXE7_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|A0A098DQF2|A0A098DQF2_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|A0A0E0RTW2|A0A0E0RTW2_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE

<table>
<tr><td>vitamin metabolic process</td><td>9 out of 211 genes, 4.3%</td><td>37 out of 1882 genes, 2.0%</td><td>0.01768</td><td>tr|I1RSL2|I1RSL2_GIBZE, tr|I1RDH6|I1RDH6_GIBZE, tr|A0A0E0RU55|A0A0E0RU55_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1RFJ1|I1RFJ1_GIBZE, tr|A0A098D5A0|A0A098D5A0_GIBZE, tr|A0A098DJH8|A0A098DJH8_GIBZE, tr|I1RZ21|I1RZ21_GIBZE, tr|I1RAQ4|I1RAQ4_GIBZE</td></tr>
<tr><td>water-soluble vitamin metabolic process</td><td>9 out of 211 genes, 4.3%</td><td>37 out of 1882 genes, 2.0%</td><td>0.01768</td><td>tr|I1RSL2|I1RSL2_GIBZE, tr|I1RDH6|I1RDH6_GIBZE, tr|A0A0E0RU55|A0A0E0RU55_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1RFJ1|I1RFJ1_GIBZE, tr|A0A098D5A0|A0A098D5A0_GIBZE, tr|A0A098DJH8|A0A098DJH8_GIBZE, tr|I1RZ21|I1RZ21_GIBZE, tr|I1RAQ4|I1RAQ4_GIBZE</td></tr>
<tr><td>cellular carbohydrate metabolic process</td><td>36 out of 211 genes, 17.1%</td><td>230 out of 1882 genes, 12.2%</td><td>0.01791</td><td>tr|A0A0E0RSG8|A0A0E0RSG8_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1RZM0|I1RZM0_GIBZE, tr|I1R9N7|I1R9N7_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|V6RDP1|V6RDP1_GIBZE, tr|A0A098DXB4|A0A098DXB4_GIBZE, tr|I1RKR5|I1RKR5_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1RAQ4|I1RAQ4_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RPW2|I1RPW2_GIBZE, tr|I1RX90|I1RX90_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RI39|I1RI39_GIBZE, tr|I1RCT7|I1RCT7_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|A0A098DQF2|A0A098DQF2_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|A0A0E0SI42|A0A0E0SI42_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE</td></tr>
<tr><td>cellular amino acid metabolic process</td><td>26 out of 211 genes, 12.3%</td><td>158 out of 1882 genes, 8.4%</td><td>0.02403</td><td>tr|I1RPW2|I1RPW2_GIBZE, tr|A0A0E0RSG8|A0A0E0RSG8_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE, tr|I1RCT7|I1RCT7_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|A0A098DQF2|A0A098DQF2_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
<tr><td>cellular amine metabolic process</td><td>26 out of 211 genes, 12.3%</td><td>158 out of 1882 genes, 8.4%</td><td>0.02403</td><td>tr|I1RPW2|I1RPW2_GIBZE, tr|A0A0E0RSG8|A0A0E0RSG8_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE, tr|I1RCT7|I1RCT7_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|A0A098DQF2|A0A098DQF2_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE</td></tr>
<tr><td>sulfur compound biosynthetic process</td><td>8 out of 211 genes, 3.8%</td><td>33 out of 1882 genes, 1.8%</td><td>0.02533</td><td>tr|I1RCT7|I1RCT7_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RDH6|I1RDH6_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RFJ1|I1RFJ1_GIBZE, tr|I1RHK2|I1RHK2_GIBZE, tr|I1RUI6|I1RUI6_GIBZE</td></tr>
<tr><td>cellular metabolic compound salvage</td><td>5 out of 211 genes, 2.4%</td><td>16 out of 1882 genes, 0.9%</td><td>0.0262</td><td>tr|A0A1C3YHK0|A0A1C3YHK0_GIBZE, tr|V6QVH8|V6QVH8_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|A0A098DF44|A0A098DF44_GIBZE, tr|I1RZ21|I1RZ21_GIBZE</td></tr>
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<table>
<tr><td>aromatic amino acid family catabolic process</td><td>4 out of 211 genes, 1.9%</td><td>11 out of 1882 genes, 0.6%</td><td>0.02684</td><td>tr|I1RSL2|I1RSL2_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE</td></tr>
<tr><td>carboxylic acid metabolic process</td><td>36 out of 211 genes, 17.1%</td><td>237 out of 1882 genes, 12.6%</td><td>0.02779</td><td>tr|A0A0E0RSG8|A0A0E0RSG8_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|I1RR96|I1RR96_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RA13|I1RA13_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RPW2|I1RPW2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|V6RH92|V6RH92_GIBZE, tr|I1RCT7|I1RCT7_GIBZE, tr|A0A098D5A0|A0A098D5A0_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|A0A098DQF2|A0A098DQF2_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1S223|I1S223_GIBZE</td></tr>
<tr><td>oxoacid metabolic process</td><td>36 out of 211 genes, 17.1%</td><td>237 out of 1882 genes, 12.6%</td><td>0.02779</td><td>tr|A0A0E0RSG8|A0A0E0RSG8_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|I1RR96|I1RR96_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RA13|I1RA13_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RPW2|I1RPW2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|V6RH92|V6RH92_GIBZE, tr|I1RCT7|I1RCT7_GIBZE, tr|A0A098D5A0|A0A098D5A0_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|A0A098DQF2|A0A098DQF2_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1S223|I1S223_GIBZE</td></tr>
<tr><td>cellular ketone metabolic process</td><td>36 out of 211 genes, 17.1%</td><td>238 out of 1882 genes, 12.6%</td><td>0.0295</td><td>tr|A0A0E0RSG8|A0A0E0RSG8_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|I1RR96|I1RR96_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RA13|I1RA13_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RPW2|I1RPW2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|V6RH92|V6RH92_GIBZE, tr|I1RCT7|I1RCT7_GIBZE, tr|A0A098D5A0|A0A098D5A0_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|A0A098DQF2|A0A098DQF2_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1S223|I1S223_GIBZE</td></tr>
<tr><td>lysine metabolic process</td><td>3 out of 211 genes, 1.4%</td><td>7 out of 1882 genes, 0.4%</td><td>0.03454</td><td>tr|I1S2D5|I1S2D5_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE</td></tr>
<tr><td>inner mitochondrial membrane organization</td><td>3 out of 211 genes, 1.4%</td><td>7 out of 1882 genes, 0.4%</td><td>0.03454</td><td>sp|Q4IB65|TIM9_GIBZE, sp|Q4IJW4|TIM8_GIBZE, tr|I1RRS8|I1RRS8_GIBZE</td></tr>
</table>

lysine biosynthetic process	3 out of 211 genes, 1.4%	7 out of 1882 genes, 0.4%	0.03454	tr|I1S2D5|I1S2D5_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE
purine salvage	3 out of 211 genes, 1.4%	7 out of 1882 genes, 0.4%	0.03454	tr|V6QVH8|V6QVH8_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|A0A098DF44|A0A098DF44_GIBZE
pyridoxine biosynthetic process	2 out of 211 genes, 0.9%	3 out of 1882 genes, 0.2%	0.03477	tr|I1RZ21|I1RZ21_GIBZE, tr|A0A0E0RU55|A0A0E0RU55_GIBZE
vitamin B6 biosynthetic process	2 out of 211 genes, 0.9%	3 out of 1882 genes, 0.2%	0.03477	tr|I1RZ21|I1RZ21_GIBZE, tr|A0A0E0RU55|A0A0E0RU55_GIBZE
organic acid metabolic process	36 out of 211 genes, 17.1%	241 out of 1882 genes, 12.8%	0.03513	tr|A0A0E0RSG8|A0A0E0RSG8_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|I1RZM4|I1RZM4_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|A0A098DDD2|A0A098DDD2_GIBZE, tr|I1RR96|I1RR96_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|I1RA13|I1RA13_GIBZE, tr|I1RSL2|I1RSL2_GIBZE, tr|I1RTD3|I1RTD3_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|I1RQE0|I1RQE0_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RPW2|I1RPW2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|V6RH92|V6RH92_GIBZE, tr|I1RCT7|I1RCT7_GIBZE, tr|A0A098D5A0|A0A098D5A0_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, sp|Q4HYR2|ACEA_GIBZE, tr|A0A098DY09|A0A098DY09_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, tr|A0A098DQF2|A0A098DQF2_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1S223|I1S223_GIBZE
mitochondrial transport	6 out of 211 genes, 2.8%	23 out of 1882 genes, 1.2%	0.03632	tr|I1RZI8|I1RZI8_GIBZE, sp|Q4IB65|TIM9_GIBZE, sp|Q4IJW4|TIM8_GIBZE, tr|I1RBS5|I1RBS5_GIBZE, tr|I1RZH5|I1RZH5_GIBZE, tr|I1RRS8|I1RRS8_GIBZE
vitamin biosynthetic process	6 out of 211 genes, 2.8%	23 out of 1882 genes, 1.2%	0.03632	tr|I1RSL2|I1RSL2_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1RDH6|I1RDH6_GIBZE, tr|I1RFJ1|I1RFJ1_GIBZE, tr|I1RZ21|I1RZ21_GIBZE, tr|A0A0E0RU55|A0A0E0RU55_GIBZE
water-soluble vitamin biosynthetic process	6 out of 211 genes, 2.8%	23 out of 1882 genes, 1.2%	0.03632	tr|I1RSL2|I1RSL2_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1RDH6|I1RDH6_GIBZE, tr|I1RFJ1|I1RFJ1_GIBZE, tr|I1RZ21|I1RZ21_GIBZE, tr|A0A0E0RU55|A0A0E0RU55_GIBZE
sulfur metabolic process	11 out of 211 genes, 5.2%	55 out of 1882 genes, 2.9%	0.03739	tr|I1RDH6|I1RDH6_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RHK2|I1RHK2_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|I1RCT7|I1RCT7_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RFJ1|I1RFJ1_GIBZE, tr|A0A098DS79|A0A098DS79_GIBZE, tr|I1RSI2|I1RSI2_GIBZE
cellular aromatic compound metabolic process	14 out of 211 genes, 6.6%	77 out of 1882 genes, 4.1%	0.04268	tr|I1RSL2|I1RSL2_GIBZE, tr|I1RDH6|I1RDH6_GIBZE, tr|A0A098DQF2|A0A098DQF2_GIBZE, tr|A0A098DF44|A0A098DF44_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE, tr|I1RYW6|I1RYW6_GIBZE, tr|A0A1C3YHK0|A0A1C3YHK0_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|V6QVH8|V6QVH8_GIBZE, tr|I1S0B7|I1S0B7_GIBZE, tr|I1RFJ1|I1RFJ1_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE

protein targeting to mitochondrion	5 out of 211 genes, 2.4%	18 out of 1882 genes, 1.0%	0.04269	tr|I1RZI8|I1RZI8_GIBZE, sp|Q4IB65|TIM9_GIBZE, sp|Q4IJW4|TIM8_GIBZE, tr|I1RBS5|I1RBS5_GIBZE, tr|I1RRS8|I1RRS8_GIBZE
aromatic compound catabolic process	5 out of 211 genes, 2.4%	18 out of 1882 genes, 1.0%	0.04269	tr|I1RSL2|I1RSL2_GIBZE, tr|V6RF62|V6RF62_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE
lipid modification	5 out of 211 genes, 2.4%	18 out of 1882 genes, 1.0%	0.04269	tr|I1RAZ1|I1RAZ1_GIBZE, tr|I1RCT9|I1RCT9_GIBZE, tr|I1S223|I1S223_GIBZE, tr|I1RSI2|I1RSI2_GIBZE, tr|A0A098DV34|A0A098DV34_GIBZE
protein localization in mitochondrion	5 out of 211 genes, 2.4%	18 out of 1882 genes, 1.0%	0.04269	tr|I1RZI8|I1RZI8_GIBZE, sp|Q4IB65|TIM9_GIBZE, sp|Q4IJW4|TIM8_GIBZE, tr|I1RBS5|I1RBS5_GIBZE, tr|I1RRS8|I1RRS8_GIBZE
organic acid biosynthetic process	18 out of 211 genes, 8.5%	106 out of 1882 genes, 5.6%	0.043	tr|I1RPW2|I1RPW2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RCT7|I1RCT7_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|A0A098DQF2|A0A098DQF2_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE
carboxylic acid biosynthetic process	18 out of 211 genes, 8.5%	106 out of 1882 genes, 5.6%	0.043	tr|I1RPW2|I1RPW2_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RCT7|I1RCT7_GIBZE, tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1RYX6|I1RYX6_GIBZE, tr|I1RVX9|I1RVX9_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE, tr|I1RPW1|I1RPW1_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|A0A098DQF2|A0A098DQF2_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|A0A098DHF2|A0A098DHF2_GIBZE, tr|A0A1C3YI49|A0A1C3YI49_GIBZE, tr|I1RQE0|I1RQE0_GIBZE
aspartate family amino acid metabolic process	7 out of 211 genes, 3.3%	30 out of 1882 genes, 1.6%	0.04317	tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RW06|I1RW06_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE
aspartate family amino acid biosynthetic process	6 out of 211 genes, 2.8%	24 out of 1882 genes, 1.3%	0.04405	tr|I1RFL2|I1RFL2_GIBZE, tr|I1RCL0|I1RCL0_GIBZE, tr|I1S2D5|I1S2D5_GIBZE, sp|Q4HVQ9|LYS4_GIBZE, tr|I1RUI6|I1RUI6_GIBZE, tr|A0A098DLT9|A0A098DLT9_GIBZE
aromatic amino acid family metabolic process	6 out of 211 genes, 2.8%	24 out of 1882 genes, 1.3%	0.04405	tr|I1RSL2|I1RSL2_GIBZE, tr|A0A098DQF2|A0A098DQF2_GIBZE, tr|I1RCZ9|I1RCZ9_GIBZE, tr|I1RF80|I1RF80_GIBZE, tr|I1RVR7|I1RVR7_GIBZE, tr|I1RPM6|I1RPM6_GIBZE
response to abiotic stimulus	6 out of 211 genes, 2.8%	25 out of 1882 genes, 1.3%	0.05274	tr|A0A0E0SI42|A0A0E0SI42_GIBZE, tr|A0A098D8N2|A0A098D8N2_GIBZE, tr|I1RBS5|I1RBS5_GIBZE, tr|I1RT35|I1RT35_GIBZE, tr|A0A098DKQ4|A0A098DKQ4_GIBZE, tr|I1S0X0|I1S0X0_GIBZE

Table S6. Metabolite assignments from NMR spectroscopy for FG strains PH-1 under different GO concentration treatments.

no.	metabolites	group	δ ^{1}H（multiplicity）	Experiments
1	lipid	CH_3, $(CH_2)_n$, CH=CH	0.89 (m), 1.27 (m), 5.33 (m)	TOCSY, HSQC
2	leucine	δ-CH_3, δ′-CH_3, γ-CH, β-CH_2, α-CH	0.96 (t, 6.6 Hz), 0.94 (t, 7.4 Hz), 1.69 (m), 1.72 (m), 3.69 (t, 9.5 Hz)	TOCSY, HSQC, HMBC
3	isoleucine	γ′-CH_3, δ-CH_3, γ-CH_2, β-CH, α-CH	1.01 (d, 7.0 Hz), 0.94 (t, 7.4 Hz), 1.25 (m), 1.96 (m), 3.65 (m)	TOCSY, HSQC, HMBC
4	valine	γ-CH_3, γ′-CH_3, β-CH, α-CH, COOH	1.04 (d, 7.0 Hz), 0.99 (d, 7.0 Hz), 2.27 (m), 3.61 (d, 4.5 Hz）	TOCSY, HSQC, HMBC
5	threonine	CH_3, α-CH, β-CH, COOH	1.33 (d, 6.6 Hz), 3.59 (d, 4.8 Hz), 4.27 (m)	TOCSY, HSQC, HMBC
6	alanine	β-CH_3, α-CH, COOH	1.48 (d, 7.3 Hz), 3.78 (q, 7.3 Hz)	TOCSY, HMBC
7	lysine	γ-CH_2, δ-$CH_{2,}$ β-CH_2, ε-CH_2, α-CH	1.45 (m), 1.51 (m), 1.72 (m), 1.91 (m), 3.02 (t, 7.3 Hz), 3.77 (t, 5.1 Hz)	TOCSY, HSQC
8	acetate	CH_3, COOH	1.92 (s)	HSQC, HMBC
9	glutamate	β-CH_2, γ-CH_2, α-CH	2.02 (m), 2.09 (m), 2.34 (m), 3.75 (m)	TOCSY, HSQC
10	citrate	α, α′CH_2, γ, γ′CH_2	2.55 (d, 15.7 Hz), 2.68 (d, 15.7 Hz）	TOCSY, HMBC
11	aspartate	β-CH, β′-CH, α-CH, γ-COOH, COOH	2.68 (dd,7.6, 16.5 Hz), 2.80 (dd,3.8, 17.5 Hz), 3.89 (dd, 3.6, 7.6 Hz)	TOCSY, HSQC, HMBC
12	asparagine	β-CH, β′-CH, α-CH, γ-$CONH_2$, COOH	2.87 (dd,7.6, 16.5 Hz), 2.95 (dd,4.6, 16.5 Hz), 4.00 (dd, 4.6, 7.6 Hz)	TOCSY, HSQC, HMBC
13	γ-aminobutyrate	2 CH, 3 CH_2, 4 CH_2, COOH	2.30 (t, 7.6 Hz), 1.91 (m), 3.02 (t, 7.3 Hz)	TOCSY, HSQC, HMBC
14	choline	N-$(CH_3)_3$, O-CH_2, N-CH_2	3.20 (s), 4.07 (m), 3.52 (m)	TOCSY, HSQC, HMBC
15	phosphocholine	N-$(CH_3)_3$, O-CH_2, N-CH_2	3.23 (s), 4.23 (t, 5.3 Hz), 3.61 (t, 4.4 Hz)	TOCSY, HSQC
16	glycine betaine	CH_3, CH_2, COOH	3.26 (s), 3.91 (s)	TOCSY, HSQC, HMBC
17	β-glucose	1 CH, 2 CH, 3 CH, 4 CH, 5 CH, 6, 6′-CH	4.65 (d, 8.0 Hz), 3.25 (dd, 1.5, 8.0 Hz), 3.49 (m), 3.42 (m), 3.47 (m), 3.73, 3.90 (m)	TOCSY, HSQC
18	trehalose	1 CH, 2 CH, 3 CH, 4 CH, 5 CH, 6,6′ CH	5.19 (d, 3.8 Hz), 3.65 (dd, 3.8, 9.9 Hz), 3.86 (dd, 2.2, 4.9 Hz), 3.46 (t, 9.5 Hz), 3.83 (m), 3.89 (dd, 2.3, 12.4 Hz)	TOCSY, HSQC
19	α-glucose	1 CH, 2 CH, 3 CH, 4 CH, 5 CH, 6,6′ CH	5.24 (d, 3.7 Hz), 3.53 (dd, 3.8, 9.8 Hz), 3.73 (m), 3.42 (m), 3.86 (m), 3.74, 3.83 (m)	TOCSY, HSQC
20	sucrose	G-1 CH, G-2 CH, G-3 CH	5.42 (d, 3.9 Hz), 3.56 (m), 3.77 (m)	TOCSY, HSQC
21	GlcNAc-1-P	1 CH, 2 CH, 3 CH	5.46 (dd, 3.5, 7.4 Hz), 3.78 (m), 3.46 (m)	TOCSY, HMBC

22	UDP-GlcNac	1 CH, 10 CH, 11CH, 13 CH, 12 CH, NH	5.59 (t, 5.5Hz), 4.36 (m), 5.95 (d, 8.0 Hz), 5.97 (d, 8.0 Hz), 7.94 (d, 8.0 Hz), 8.34 (d, 8.4 Hz)	TOCSY, HMBC
23	uracil	5 CH, 6 CH	5.80 (d, 7.7 Hz), 7.54 (d, 7.6 Hz)	TOCSY, HSQC
24	uridine	11 CH, 12 CH, 7 CH, 6 CH	7.88 (d, 8.0 Hz), 5.90 (d, 8.1 Hz), 5.92 (d, 4.5 Hz), 4.36 (t, 4.9 Hz)	TOCSY, HSQC, HMBC
25	5′-UMP	12 CH, 7 CH, 11 CH, 6 CH	5.99 (d, 3.4 Hz), 6.00 (d, 3.7 Hz), 8.11 (d, 7.6 Hz), 4.42 (m)	TOCSY, HSQC
26	fumarate	2,3 CH, COOH	6.52 (s)	TOCSY, HMBC
27	tyrosine	3,5 CH, ring, 2,6 CH, ring, β-CH$_2$, α-CH, COOH	6.90 (d, 8.5), 7.20 (d, 8.5), 3.05 (dd,7.8, 14.8 Hz), 3.15 (dd, 8.6, 14.5 Hz), 3.93 (m)	TOCSY, HSQC
28	histidine	4 CH, ring, 2 CH, ring, β-CH$_2$, α-CH, COOH	7.09 (s), 7.92 (s), 3.20(dd, 5.1, 14.7 Hz), 3.25 (dd, 9.4, 14.6 Hz), 4.00 (m)	TOCSY, HSQC
29	phenylalanine	4 CH, ring, 3,5 CH, ring, 2,6 CH, ring, β-CH$_2$, α-CH	7.33 (m), 7.38 (m), 7.43 (m), 3.12 (dd,7.9, 14.9 Hz), 3.25 (dd, 5.2, 14.6 Hz), 4.00 (m)	TOCSY, HSQC
30	tryptophan	6 CH, ring, 7 CH, ring, 4 CH, ring, β-CH$_2$,⍰⍰-CH, COOH	7.29 (t, 7.3 Hz), 7.53 (d, 8.3 Hz), 7.74 (d, 8.1 Hz), 3.31 (dd,4.9, 14.3 Hz), 3.48 (dd, 9.1, 14.0 Hz), 4.05 (m)	TOCSY, HSQC, HMBC
31	guanosine	CH	8.01 (s)	TOCSY, HMBC
32	adenosine	14 CH, 8 CH, 1 CH	8.33 (s), 8.22 (s), 6.06 (d, 6.3 Hz)	TOCSY, HSQC
33	formate	CH	8.46 (s)	JRES, TOCSY
34	NMNA	2 CH, 6 CH, 1 CH$_3$,	9.13 (s), 8.84, 4.44 (s)	TOCSY, HSQC
35	inosine	2 CH, 7 CH, 12 CH	6.10 (d, 5.7 Hz), 8.24 (s), 8.35 (s)	JRES, TOCSY
36	hypoxanthine	2 CH, 7 CH	8.20 (s), 8.22 (s)	JRES, TOCSY
37	malonate	CH2	3.12 (s)	HSQC
38	dimethylamine	CH$_3$	2.72 (s)	HSQC
39	methionine	γ-CH$_2$, β-CH$_2$, α-CH, δ-CH$_3$, COOH	2.65 (t, 7.5 Hz), 2.17 (m), 3.78 (m), 2.14 (s)	TOCSY, HSQC
40	propionate	CH$_3$, CH$_2$	1.06 (t, 7.3 Hz), 2.19 (q, 4.0 Hz)	TOCSY, HSQC
41	quinone	CH	6.80 (s)	JRES, TOCSY
42	dTMP	CH	7.87 (s)	TOCSY, HSQC
43	α-ketoglutarate	β-CH$_2$, γ-CH$_2$	2.45 (t, 7.9 Hz), 3.02 (t, 8.5 Hz)	TOCSY, HSQC
44	succinate	CH$_3$, COOH	2.41 (s)	HSQC, HMBC
45	pyruvate	CH$_3$	2.37 (s)	HSQC
46	glycine	CH$_2$	3.57 (s)	JRES, TOCSY
47	1,3-dimethyluracil	5 CH, 6 CH	5.88 (d, 7.7 Hz), 7.54 (d, 7.6 Hz)	JRES

48	malate	α-CH, β-CH, β’-CH, COOH	4.31 (dd, 3.1, 10.2 Hz), 2.68 (dd, 3.1, 15.4 Hz), 2.37 (dd,10.2,15.4 Hz)	TOCSY, HSQC, HMBC
49	glutamine	β-CH$_2$, γ-CH$_2$, α-CH, C=O, COOH	2.14 (m), 2.45 (m), 3.79 (m)	TOCSY, HSQC, HMBC
50	proline	α-CH, β-CH$_2$, γ-CH$_2$, δ-CH$_2$, COOH	4.14 (m), 2.36 (m), 2.02 (m), 3.37 (m), 3.41 (m)	TOCSY, HSQC, HMBC
51	arginine	γ,γ’-CH, β-CH$_2$, δ-CH$_2$, α-CH	1.68 (m), 1.72 (m), 1.91 (m), 3.25 (m), 3.78 (t, 4.7 Hz)	TOCSY, HMBC, HSQC
52	xanthine		7.76 (s)	
53	U1	\	7.59, 6.99, 6.39	COSY, TOCSY
54	U2	\	7.56, 6.37	COSY, TOCSY
55	ascorbate	\	4.50 (d, 1.9Hz)	COSY, TOCSY, HSQC
		\	3.73 (m)	
56	syllo-inositol	CH	3.30 (s)	COSY, TOCSY
57	myo-inositol	2-CH, 1,3 CH, 4,6 CH, 5 CH	4.07 (t, 2.4 Hz), 3.52 (dd, 3.7, 9.8 Hz), 3.61 (t, 4.4 Hz), 3.29 (t, 4.5 Hz)	TOCSY，HSQC，HMBC
58	nicotinic acid	2 CH, 3 CH, 4 CH	8.64 (d, 2.0 Hz), 7.60 (dd, 5.1, 7.6 Hz), 8.06 (dt, 1.9, 8.2 Hz)	TOCSY，HSQC，HMBC
59	guanidoacetate	\	3.80 (s)	JRES, TOCSY
60	U3	\	3.70 (s)	JRES, TOCSY
61	U4	\	6.14, 6.68	COSY, TOCSY

Multiplicity: s, singlet; d, doublet; dd, doublet of doublets; t, triplet; q, quartet; spin-coupling system; U, unidentified signal; \, signals or multiplicities were not determined; GlcNAc-1-P, N-acetylglucosamine phosphotransferase 1; UDP-GlcNac, uridine diphosphate N-acetylglucosamine; NMNA, N-Methylnicotinamide.