

**Supplemental Table 1.** Gene Ontology annotation of tea unigenes

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0001	436				
ug0002	1047				
ug0003	394				
ug0004	1175	GO:0005739,GO:0003824,GO:0005215		mitochondrion	catalytic activity,transporter activity
ug0005	643	GO:0005488,GO:0005			binding,protein binding
ug0006	751				
ug0007	863				
ug0008	699				
ug0009	688	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug0010	1096	GO:0016787,GO:0016043,GO:0009987	cellular component organization,cellular process		hydrolase activity
ug0011	604				
ug0012	180				
ug0013	739				
ug0014	730	GO:0005488			binding
ug0015	424				
ug0016	560				
ug0017	821				
ug0018	815				
ug0019	740				
ug0020	1008	GO:0016020,GO:0005794,GO:0005515,GO:0006810,GO:0009987,GO:0005198,GO:000573	transport,cellular process	membrane,Golgi apparatus,cytoplasm,plasma membrane	protein binding,structural molecule activity
ug0021	792				
ug0022	789	GO:0005618,GO:0016787,GO:0005576,GO:0005975,GO:0009987,GO:0009058,GO:000519,GO:0016301,GO:0008152,GO:0009987,GO:0000166,GO:000953	carbohydrate metabolic process,cellular process,catabolic process	cell wall,extracellular region	hydrolase activity
ug0023	489	GO:0009058,GO:000519,GO:0016301,GO:0008152,GO:0009987,GO:0000166,GO:000953	biosynthetic process,cellular amino acid and derivative metabolic process,metabolic process,cellular process	plastid	kinase activity,nucleotide binding
ug0024	772				
ug0025	176				
ug0026	800	GO:0003824,GO:0008152,GO:0016020,GO:0009536,GO:0005488	metabolic process	membrane,plastid	catalytic activity,binding
ug0027	120				
ug0028_1	571	GO:0005737,GO:0005737,GO:0005488,GO:0003	biosynthetic process,cellular amino acid and derivative metabolic process	cytoplasm,plasma membrane	binding,catalytic activity,transferase activity
ug0028_2	550	GO:0009058,GO:00066519,GO:0016740	acid and derivative metabolic process		
ug0029	760				
ug0030	831				
ug0031	300	GO:0005739,GO:0006091	generation of precursor metabolites and energy	mitochondrion	
ug0032	873	GO:0005739,GO:0009725,GO:0005783,GO:0003824		mitochondrion,plastid	
ug0033	515	GO:0019725,GO:0005783,GO:0003824	cellular homeostasis	endoplasmic reticulum	catalytic activity
ug0034_1	908	GO:0016020,GO:0008152,GO:0005488,GO:0005737,GO:0005488,GO:000515,GO:000719,GO:0007165,GO:0006091,GO:0009056,GO:000382	metabolic process	membrane	binding,catalytic activity
ug0034_2	571	GO:0005737,GO:0005488,GO:000515,GO:000719,GO:0007165,GO:0006091,GO:0009056,GO:000382	response to endogenous stimulus,signal transduction	cytoplasm,mitochondrion	
ug0035	760	GO:0005739,GO:0006091,GO:0005488,GO:0008152,GO:0016740,GO:0005618,GO:0006091,GO:0009056,GO:000382	generation of precursor metabolites and energy	mitochondrion	protein binding
ug0036	721				
ug0037	838	GO:0006091,GO:0003824,GO:0005488,GO:0008152,GO:0016740,GO:0005618,GO:0006091,GO:0009056,GO:000382	generation of precursor metabolites and energy	plastid	molecular_function,binding
ug0038	596	GO:0005488,GO:0008152,GO:0016740,GO:0005618,GO:0006091,GO:0009056,GO:000382	biological_process,generation of precursor metabolites and energy,catabolic process	cell wall,mitochondrion	binding,transferase activity,catalytic activity
ug0039	898				
ug0040_1	674	GO:0005739		mitochondrion	
ug0040_2	787				
ug0041_1	761	GO:0000003,GO:0009791,GO:0003700,GO:0006350,GO:0016020,GO:0005622,GO:0005215,GO:0005739,GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:001	reproduction,post-embryonic development,embryonic development,transcription transport,biosynthetic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		transcription factor activity
ug0041_2	973	GO:0005739,GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:001	metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane,intracellular,mitochondrion	transporter activity,hydrolase activity
ug0042	991				
ug0043	584	GO:0016740,GO:0005		mitochondrion	transferase activity
ug0044	766	GO:0005622		intracellular	
ug0045_1	455	GO:0019538,GO:0009056,GO:0016787	protein metabolic process,catabolic process		hydrolase activity

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0045_2	845	GO:0009536,GO:0009987,GO:0016020	cellular process	plastid,membrane	
ug0046	919	GO:0004872,GO:0005488,GO:0005737,GO:0009987,GO:0016020,GO:0005783,GO:000681	cellular process,transport	cytoplasm,membrane,endoplasmic reticulum	receptor activity,binding
ug0047_1	946	GO:0009653,GO:0007275,GO:0009058,GO:0006139,GO:0009536,GO:0016740	anatomical structure morphogenesis,multicellular organismal development,biosynthetic process,nucleobase, nucleoside, nucleotide and nucleic acid	plastid	transferase activity
ug0047_2	714	GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:0016020,GO:0005215	transport,biosynthetic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane	transporter activity
ug0048_1	246	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0009536,GO:00053	cellular component organization,cellular process	intracellular,plastid,nucleus	DNA binding
ug0048_2	397	GO:0005739		mitochondrion	
ug0049_1	504	GO:0005488			binding
ug0049_2	386	GO:0005737,GO:0006139,GO:0005515,GO:0009987,GO:0005634	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,flower development	cytoplasm,nucleus	protein binding
ug0050	381	GO:0005198,GO:0005886,GO:0005840,GO:0005829,GO:0009536,GO:000641	translation	plasma membrane,cell wall,ribosome,cytosol,plastid	structural molecule activity
ug0051	501	GO:0006950	response to stress		
ug0052	535	GO:0016020,GO:0009987,GO:0009536,GO:0006810,GO:000987,GO:0005886,GO:0016020,GO:0005773,GO:0016043,GO:000695	transport,cellular process,cellular component organization,response to stress,response to abiotic stimulus	plasma membrane,membrane,vacuole	
ug0053	313	GO:0005488,GO:0003824,GO:0008152,GO:0009058,GO:0009987,GO:0009536,GO:001597	metabolic process,biosynthetic process,cellular process,photosynthesis	plastid	binding,catalytic activity
ug0054	404	GO:0040007,GO:0005623,GO:0016043	growth,cellular component organization	cell	
ug0055_1	168	GO:0016020,GO:0009987,GO:0009536,GO:0006810,GO:000987,GO:0005886,GO:0016020,GO:0005773,GO:0016043,GO:000695	transport,cellular process,cellular component organization,response to stress,response to abiotic stimulus	plasma membrane,membrane,vacuole	
ug0055_2	660	GO:0005488,GO:0003824,GO:0008152,GO:0009058,GO:0009987,GO:0009536,GO:001597	metabolic process,biosynthetic process,cellular process,photosynthesis	plastid	binding,catalytic activity
ug0056	419	GO:0040007,GO:0005623,GO:0016043	growth,cellular component organization	cell	
ug0057	342	GO:0016020,GO:0009987,GO:0009536,GO:0006810,GO:000987,GO:0005886,GO:0016020,GO:0005773,GO:0016043,GO:000695	transport,cellular process,cellular component organization,response to stress,response to abiotic stimulus	plasma membrane,membrane,vacuole	
ug0058	960	GO:0005488,GO:0003824,GO:0008152,GO:0009058,GO:0009987,GO:0009536,GO:001597	metabolic process,biosynthetic process,cellular process,photosynthesis	plastid	binding,catalytic activity
ug0059	627	GO:0040007,GO:0005623,GO:0016043	growth,cellular component organization	cell	
ug0060	592	GO:0016020,GO:0009987,GO:0009536,GO:0006810,GO:000987,GO:0005886,GO:0016020,GO:0005773,GO:0016043,GO:000695	transport,cellular process,cellular component organization,response to stress,response to abiotic stimulus	plasma membrane,membrane,vacuole	
ug0061	849	GO:0005488,GO:0003824,GO:0008152,GO:0009058,GO:0009987,GO:0009536,GO:001597	metabolic process,biosynthetic process,cellular process,photosynthesis	plastid	binding,catalytic activity
ug0062	583	GO:0040007,GO:0005623,GO:0016043	growth,cellular component organization	cell	
ug0063	537	GO:0016020,GO:0009987,GO:0009536,GO:0006810,GO:000987,GO:0005886,GO:0016020,GO:0005773,GO:0016043,GO:000695	transport,cellular process,cellular component organization,response to stress,response to abiotic stimulus	plasma membrane,membrane,vacuole	
ug0064	994	GO:0005488,GO:0003824,GO:0008152,GO:0009058,GO:0009987,GO:0009536,GO:001597	metabolic process,biosynthetic process,cellular process,photosynthesis	plastid	binding,catalytic activity
ug0065	734	GO:0040007,GO:0005623,GO:0016043	growth,cellular component organization	cell	
ug0066_1	644	GO:0016020,GO:0009987,GO:0009536,GO:0006810,GO:000987,GO:0005886,GO:0016020,GO:0005773,GO:0016043,GO:000695	transport,cellular process,cellular component organization,response to stress,response to abiotic stimulus	plasma membrane,membrane,vacuole	
ug0066_2	848	GO:0005488,GO:0003824,GO:0008152,GO:0009058,GO:0009987,GO:0009536,GO:001597	metabolic process,biosynthetic process,cellular process,photosynthesis	plastid	binding,catalytic activity
ug0067	511	GO:0040007,GO:0005623,GO:0016043	growth,cellular component organization	cell	
ug0068_1	939	GO:0016020,GO:0009987,GO:0009536,GO:0006810,GO:000987,GO:0005886,GO:0016020,GO:0005773,GO:0016043,GO:000695	transport,cellular process,cellular component organization,response to stress,response to abiotic stimulus	plasma membrane,membrane,vacuole	
ug0068_2	842	GO:0005488,GO:0003824,GO:0008152,GO:0009058,GO:0009987,GO:0009536,GO:001597	metabolic process,biosynthetic process,cellular process,photosynthesis	plastid	binding,catalytic activity
ug0069	796	GO:0040007,GO:0005623,GO:0016043	growth,cellular component organization	cell	
ug0070_1	401	GO:0016020,GO:0009987,GO:0009536,GO:0006810,GO:000987,GO:0005886,GO:0016020,GO:0005773,GO:0016043,GO:000695	transport,cellular process,cellular component organization,response to stress,response to abiotic stimulus	plasma membrane,membrane,vacuole	
ug0070_2	909	GO:0005488,GO:0003824,GO:0008152,GO:0009058,GO:0009987,GO:0009536,GO:001597	metabolic process,biosynthetic process,cellular process,photosynthesis	plastid	binding,catalytic activity
ug0071	595	GO:0040007,GO:0005623,GO:0016043	growth,cellular component organization	cell	
ug0072	773	GO:0016020,GO:0009987,GO:0009536,GO:0006810,GO:000987,GO:0005886,GO:0016020,GO:0005773,GO:0016043,GO:000695	transport,cellular process,cellular component organization,response to stress,response to abiotic stimulus	plasma membrane,membrane,vacuole	
ug0073	924	GO:0005488,GO:0003824,GO:0008152,GO:0009058,GO:0009987,GO:0009536,GO:001597	metabolic process,biosynthetic process,cellular process,photosynthesis	plastid	binding,catalytic activity
ug0074	340	GO:0040007,GO:0005623,GO:0016043	growth,cellular component organization	cell	
ug0075	869	GO:0016020,GO:0009987,GO:0009536,GO:0006810,GO:000987,GO:0005886,GO:0016020,GO:0005773,GO:0016043,GO:000695	transport,cellular process,cellular component organization,response to stress,response to abiotic stimulus	plasma membrane,membrane,vacuole	
ug0076	560	GO:0005488,GO:0003824,GO:0008152,GO:0009058,GO:0009987,GO:0009536,GO:001597	metabolic process,biosynthetic process,cellular process,photosynthesis	plastid	binding,catalytic activity
ug0077	749	GO:0040007,GO:0005623,GO:0016043	growth,cellular component organization	cell	
ug0078	716	GO:0016020,GO:0009987,GO:0009536,GO:0006810,GO:000987,GO:0005886,GO:0016020,GO:0005773,GO:0016043,GO:000695	transport,cellular process,cellular component organization,response to stress,response to abiotic stimulus	plasma membrane,membrane,vacuole	
ug0079	621	GO:0005488,GO:0003824,GO:0008152,GO:0009058,GO:0009987,GO:0009536,GO:001597	metabolic process,biosynthetic process,cellular process,photosynthesis	plastid	binding,catalytic activity
ug0080	620	GO:0040007,GO:0005623,GO:0016043	growth,cellular component organization	cell	
ug0081	210	GO:0016020,GO:0009987,GO:0009536,GO:0006810,GO:000987,GO:0005886,GO:0016020,GO:0005773,GO:0016043,GO:000695	transport,cellular process,cellular component organization,response to stress,response to abiotic stimulus	plasma membrane,membrane,vacuole	
ug0082	865	GO:0005488,GO:0003824,GO:0008152,GO:0009058,GO:0009987,GO:0009536,GO:001597	metabolic process,biosynthetic process,cellular process,photosynthesis	plastid	binding,catalytic activity

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0083	612				
ug0084	1094	GO:0019538,GO:0009056	protein metabolic process,catabolic process		
ug0085	144				
ug0086	960	GO:0005829,GO:0005737		cytosol,cellular_component	
ug0087	718				
ug0088	616				
ug0089	412				
ug0090	290				
ug0091_1	587	GO:0003677,GO:000515,GO:0005634,GO:0005488,GO:0006350	transcription	nucleus	DNA binding,protein binding,binding
ug0091_2	813	GO:0009058,GO:0005975,GO:0016740	biosynthetic process,carbohydrate metabolic process		transferase activity
ug0092	207	GO:0006810,GO:000987,GO:0005737,GO:0005488,GO:0005794	transport,cellular process	cytoplasm,Golgi apparatus	binding
ug0093	766				
ug0094	807	GO:0005515,GO:0016807			protein binding,kinase translation factor activity, nucleic acid binding
ug0095	895	GO:0008135,GO:0005737,GO:0006412	translation	cytoplasm	
ug0096	1075	GO:0005623,GO:0005623		cell,cytoplasm	
ug0097	906	GO:0006810,GO:0005623,GO:0016020	transport	cell,membrane	
ug0098	754	GO:0005622,GO:0016327		intracellular,membrane	
ug0099_1	327				
ug0099_2	865	GO:0000166,GO:0006777	response to stress		nucleotide binding
ug0100_1	777	GO:0005623		cell	
ug0100_2	774				
ug0101	859	GO:0005886		plasma membrane	
ug0102_1	318				
ug0102_2	943	GO:0006950,GO:0006350,GO:0003700,GO:0005634,GO:0009719,GO:0007165	response to stress,transcription,response to endogenous stimulus,signal transduction	nucleus	transcription factor activity
ug0103	407				
ug0104	785				
ug0105	450				
ug0106	896	GO:0005215,GO:0016020,GO:0006810	transport	membrane	transporter activity
ug0107	612				
ug0108	795				
ug0109	1035	GO:0005783,GO:0000003,GO:0009791,GO:0000000	reproduction,post-embryonic development,embryonic	endoplasmic reticulum	
ug0110	838	GO:0003676,GO:0000166			nucleic acid binding,nucleotide binding
ug0111	403				
ug0112_1	340				
ug0112_2	866	GO:0006810,GO:0009058,GO:0003723,GO:000515,GO:0005654,GO:0006139,GO:0000166	transport,cellular process	nucleoplasm	RNA binding,protein binding,nucleotide binding
ug0113	667	GO:0006810,GO:0009058,GO:0003723,GO:000515,GO:0005654,GO:0006139,GO:0000166	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	nucleoplasm	RNA binding,protein binding,nucleotide binding
ug0114	481				
ug0115	549	GO:0003677,GO:0006350,GO:0005634	transcription	nucleus	DNA binding
ug0116	291				
ug0117	782	GO:0006464,GO:0016301,GO:0000166	protein modification process		kinase activity,nucleotide binding
ug0118	518	GO:0004871,GO:0007165,GO:0005488,GO:0006629,GO:0016787	signal transduction,lipid metabolic process		signal transducer activity,binding,hydrolase activity
ug0119	899	GO:0005783,GO:0000166,GO:0006950	response to stress	endoplasmic reticulum	nucleotide binding
ug0120	855				
ug0121	494	GO:0005515,GO:0006810,GO:0009987,GO:0005768,GO:0016020	transport,cellular process	endosome,membrane	protein binding
ug0122_1	974	GO:0005515			protein binding
ug0122_2	823				
ug0123	855	GO:0005886		plasma membrane	
ug0124	942	GO:0009719,GO:0006950,GO:0009628	response to endogenous stimulus,response to stress,response to abiotic stimulus		
ug0125	895	GO:0016020,GO:0005783,GO:0005623,GO:0005488,GO:0006810,G	transport,generation of precursor metabolites and energy	membrane,endoplasmic reticulum,cell	binding

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0126	471	GO:0016787,GO:0003824,GO:0016301,GO:008152,GO:0009987,GO:0009058,GO:0006629,GO:0000166,GO:0005840,GO:0005198,GO:0006412	metabolic process,cellular process,biosynthetic process,lipid metabolic process,carbohydrate metabolic process		hydrolase activity,catalytic activity,kinase activity,nucleotide binding
ug0127	629	GO:0016787,GO:0003824,GO:0016301,GO:008152,GO:0009987,GO:0009058,GO:0006629,GO:0000166,GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug0128	623	GO:0016787,GO:0003824,GO:0016301,GO:008152,GO:0009987,GO:0009058,GO:0006629,GO:0000166,GO:0005840,GO:0005198,GO:0006412	metabolic process,cellular process,biosynthetic process,lipid metabolic process,carbohydrate metabolic process		hydrolase activity,catalytic activity,kinase activity,nucleotide binding
ug0129_1	813	GO:0006810,GO:0000166,GO:0007165	transport,signal transduction		nucleotide binding
ug0129_2	525				
ug0130	897				
ug0131	560	GO:0006464,GO:0019538,GO:0009056,GO:009987,GO:0003677,GO:0006950,GO:000625	protein modification process,protein metabolic process,catabolic process,cellular process,response to stress,DNA	nucleus	DNA binding
ug0132	907				
ug0133	614	GO:0005777		peroxisome	
ug0134	425				
ug0135	745	GO:0016020,GO:0009058,GO:0016787,GO:0003677	response to biotic stimulus	membrane	hydrolase activity,transporter activity
ug0136	307				
ug0137_1	471	GO:0003723,GO:0016740,GO:0009058,GO:0003677	biosynthetic process,DNA metabolic process		RNA binding,transferase activity
ug0137_2	168				
ug0138	528				
ug0139	582				
ug0140	437				
ug0141	516	GO:0008152,GO:0003824,GO:0008150,GO:0005488,GO:000576,GO:0008152,GO:0006950,GO:0009056,GO:0009987,GO:000382	metabolic process,biological_process		catalytic activity
ug0142	866	GO:0008152,GO:0003824,GO:0009056,GO:0009987,GO:000382	metabolic process,response to stress,catabolic process,cellular process	extracellular region	binding,catalytic activity,molecular_function
ug0143_1	791	GO:0005737,GO:0016740,GO:0009058,GO:0003677		cytoplasm	hydrolase activity
ug0143_2	624				
ug0144	352				
ug0145	836				
ug0146	869	GO:0005488,GO:0008152,GO:0009987,GO:0003824,GO:0003674,GO:0005622,GO:0005840,GO:0016043,GO:0009987,GO:0003677,GO:0005198,GO:0003682,GO:0006412,GO:000	metabolic process,cellular process	plastid	binding,catalytic activity,molecular_function
ug0147	936	GO:0009987,GO:0003677,GO:0005198,GO:0003682,GO:0006412,GO:000	cellular component organization,cellular process,translation	intracellular,ribosome,mitochondrion	DNA binding,structural molecule activity,chromatin binding
ug0148	495				
ug0149	381	GO:0016787			hydrolase activity
ug0150	826				
ug0151	857	GO:0005737,GO:0009058,GO:0009653,GO:0016043,GO:0030154,GO:0016049,GO:0007275	pollination,anatomical structure morphogenesis,cellular component organization,cell differentiation,cell growth,multicellular organismal development	cytoplasm	
ug0152	915				
ug0153	428				
ug0154	504	GO:0016787,GO:0008152,GO:0003677,GO:0006350,GO:0009987	metabolic process		hydrolase activity
ug0155	805	GO:0003677,GO:0006350,GO:0009987	transcription,cellular process		DNA binding
ug0156	489	GO:0005794,GO:0006950,GO:0009628	response to stress,response to abiotic stimulus	Golgi apparatus	
ug0157	839	GO:0005634,GO:0003824,GO:0003674		nucleus	catalytic activity,molecular_function
ug0158	524	GO:0019538,GO:0009987,GO:0005515	protein metabolic process,cellular process		protein binding
ug0159_1	485				
ug0159_2	737	GO:0005737,GO:0006412,GO:0008135,GO:0016020,GO:0005634	translation	cytoplasm,membrane,nucleus	translation factor activity, nucleic acid binding
ug0160	561				
ug0161_1	481				
ug0161_2	412				
ug0162	719	GO:0005739,GO:0016020,GO:0005622		mitochondrion,membrane,intracellular	
ug0163_1	598				
ug0163_2	568				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0164	910	GO:0005829,GO:0005622,GO:0019538,GO:0	protein metabolic process,catabolic process	cytosol,intracellular	
ug0165	604				
ug0166	719	GO:0006810,GO:0005886,GO:0000166,GO:0	transport,signal transduction	plasma membrane	nucleotide binding
ug0167	341				
ug0168	190				
ug0169	501				
ug0170	948	GO:0005198,GO:0005840,GO:0016740,GO:0009536,GO:0006412,GO:0005886,GO:0009536,GO:0005773	translation	ribosome,plastid	structural molecule activity,transferase activity,RNA binding
ug0171	669			plasma membrane,plastid,vacuole	
ug0172	203				
ug0173	598				
ug0174_1	791				
ug0174_2	193				
ug0175	360				
ug0176_1	509				
ug0176_2	1084				
ug0177_1	781				
ug0177_2	376				
ug0178_1	1028				
ug0178_2	605	GO:0016301,GO:0004871,GO:0006464,GO:0	protein modification process		kinase activity,signal transducer activity,nucleotide
ug0179	950				
ug0180_1	325				
ug0180_2	662				
ug0181	555				
ug0182	885				
ug0183	625				
ug0184	609				
ug0185	548				
ug0186	877	GO:0016301,GO:0009628,GO:0009605,GO:0007165,GO:0005515,GO:0006139,GO:0009058,GO:0009579,GO:000166,GO:0005488,GO:0009536,GO:0009719,	response to abiotic stimulus,response to external stimulus,signal transduction,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process,response to endogenous	thylakoid,plastid,nucleus	kinase activity,protein binding,nucleotide binding,binding
ug0187	912				
ug0188	444	GO:0005576,GO:0006950,GO:0005618	response to stress	extracellular region,cell wall	
ug0189	813	GO:0003676,GO:0000166			nucleic acid binding,nucleotide binding
ug0190	730	GO:0009605,GO:0006950,GO:0006139,GO:0003676,GO:0005634,GO:0009607	response to external stimulus,response to stress,nucleobase, nucleoside, nucleotide and nucleic acid	nucleus	nucleic acid binding
ug0191	487				
ug0192	817	GO:0030528,GO:0003700,GO:0016043,GO:0006350,GO:0005634	cellular component organization,transcription	nucleus	transcription regulator activity,transcription factor activity
ug0193	791	GO:0005623		cell	
ug0194	883	GO:0003824,GO:0000166,GO:0008152,GO:0	metabolic process,transcription		catalytic activity,nucleotide binding
ug0195	890				
ug0196	705	GO:0003677			DNA binding
ug0197	103				
ug0198	182				
ug0199	1026	GO:0005515			protein binding
ug0200	908	GO:0006629,GO:0016740,GO:0000166,GO:0006139,GO:0009058,GO:0008150,GO:0040007,GO:0006950,GO:0009628	lipid metabolic process,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process,biological_process,growth, response to stress,response to abiotic stimulus		transferase activity,nucleotide binding
ug0201	522	GO:0005622		intracellular	
ug0202	613	GO:0005739		mitochondrion	
ug0203	316				
ug0204	848				
ug0205	393	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug0206	699				
ug0207	526				
ug0208	276	GO:0003824,GO:0008	metabolic process		catalytic activity
ug0209	1008				
ug0210	524	GO:0005739,GO:0009		mitochondrion,plastid	

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0211	909	GO:0005975,GO:0009056,GO:0016787,GO:000427	carbohydrate metabolic process,catabolic process		hydrolase activity,binding
ug0212	427				
ug0213	911	GO:0016787,GO:0005634,GO:0006464	protein modification process	nucleus	hydrolase activity
ug0214	787	GO:0005488,GO:0003824,GO:0008152,GO:0009058,GO:0006519	metabolic process,biosynthetic process,cellular amino acid and derivative metabolic process		binding,catalytic activity
ug0215	802	GO:0019538,GO:0003824,GO:0006464	protein metabolic process,protein modification process		catalytic activity
ug0216	535				
ug0217_1	898	GO:0003824,GO:0003674,GO:0008152,GO:0005488	metabolic process		catalytic activity,molecular_function,binding
ug0217_2	896	GO:0005515			protein binding
ug0218	780	GO:0009056,GO:0009987,GO:0006629,GO:0008152,GO:0003824,GO:0005777,GO:0009719,GO:0005634,GO:000421	catabolic process,cellular process,lipid metabolic process,metabolic process,response to endogenous stimulus	peroxisome,nucleus,cytosol	catalytic activity
ug0219	421				
ug0220	731	GO:0003677			DNA binding
ug0221	890	GO:0006950,GO:0009628,GO:0003824,GO:00008150,GO:0008152,GO:000000166,GO:0009530,GO:0005840,GO:0005427	response to stress,response to abiotic stimulus,biological_process,metabolic process	plastid,mitochondrion	catalytic activity,nucleotide binding
ug0222	427	GO:0009536,GO:0006412,GO:0003723	translation	ribosome,plastid	structural molecule activity,RNA binding
ug0223	486	GO:0016787			hydrolase activity
ug0224	1350				
ug0225	675				
ug0226	543	GO:0005488,GO:0003824,GO:0003674,GO:0006950,GO:0016740,GO:0016582	metabolic process,response to stress		binding,catalytic activity,molecular_function
ug0227	582	GO:0008152,GO:0009987,GO:0000166	metabolic process,cellular process		transferase activity,kinase activity,nucleotide binding
ug0228	546	GO:0005515			protein binding
ug0229	996	GO:0005730,GO:0016787,GO:0003676,GO:0008150,GO:0005618,GO:000139	biological_process	nucleolus,cell wall	hydrolase activity,nucleic acid binding,nucleotide binding
ug0230	139				
ug0231	387				
ug0232	721				
ug0233	851				
ug0234	691				
ug0235	780				
ug0236	458				
ug0237	836	GO:0008150	biological_process		
ug0238_1	484				
ug0238_2	684	GO:0016043,GO:0009987,GO:0019538,GO:0005515,GO:0005829,GO:0019538,GO:0009056	cellular component organization,cellular process,protein metabolic process,protein metabolic process,catabolic process	cytosol	protein binding
ug0239_1	517				
ug0239_2	568				
ug0240	328				
ug0241	424				
ug0242	120				
ug0243	432				
ug0244	623				
ug0245	682	GO:0005623		cell	
ug0246	488	GO:0005739		mitochondrion	
ug0247_1	612	GO:0005488,GO:0003824	metabolic process		binding,catalytic activity
ug0247_2	940				
ug0248	777				
ug0249	498	GO:0030528,GO:0006777	transcription		transcription regulator
ug0250	879	GO:0005623,GO:0005975,GO:0003824	carbohydrate metabolic process	cell	catalytic activity
ug0251	428				
ug0252_1	766	GO:0009536,GO:0005975		plastid	protein binding
ug0252_2	941	GO:0016740,GO:0003824	metabolic process		transferase activity

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0253	771	GO:0005737,GO:0009	biosynthetic process,carbohydrate	cytoplasm	catalytic activity
		058,GO:0005975,GO:0	metabolic process,cellular		
		009987,GO:0006629,G	process,lipid metabolic		
		O:0003824,GO:000613	process,nucleobase, nucleoside,		
ug0254	917	9,GO:0009056,GO:001	nucleotide and nucleic acid	intracellular,cytosol	RNA binding,translation
		9748,GO:0006091	metabolic process,catabolic		
		GO:0006950,GO:0009	process,secondary metabolic		
		607,GO:0005622,GO:0	process,generation of precursor		
ug0255	789	GO:000166,GO:0005	response to stress,response to biotic	nucleus	factor activity, nucleic acid
		515,GO:0006810,GO:0	stimulus,protein metabolic		
		009987,GO:0007165,G	process,catabolic process,cellular		
		O:0005634,GO:001678	process		
ug0256	888	GO:0009628,GO:0009	response to abiotic	nucleus	nucleotide binding,protein
		606,GO:0000166,GO:0	stimulus,tropism,post-embryonic		
		009791,GO:0000003,G	development,reproduction,anatomical		
		O:0009653,GO:000551	cal structure		
ug0257	357	5,GO:0009719,GO:000	morphogenesis,response to	nucleus	binding,transcription factor
		3700,GO:0006950,GO:	endogenous stimulus,response to		
		GO:0016301,GO:0005	generation of precursor metabolites		
		829,GO:0000166,GO:0	and energy,carbohydrate metabolic		
ug0258	949	006091,GO:0005975,G	process,catabolic process	cytosol	kinase activity,nucleotide
		569	carbohydrate metabolic process		
		459	GO:0005975,GO:0016		
		429	753		
ug0259	576	GO:0005515,GO:0007	multicellular organismal	mitochondrion,plastid,nucleus	protein binding,transcription
		275,GO:0005739,GO:0	development,cell		
		008219,GO:0009536,G	death,transcription		
		O:0003700,GO:000635			
ug0260	774	GO:0006139,GO:0003	nucleobase, nucleoside, nucleotide	plastid	RNA binding
		723,GO:0009536	and nucleic acid metabolic process		
		GO:0005622,GO:0006			
		350,GO:0016020,GO:0	transcription		
ug0261	569	003700,GO:0005488		intracellular,membrane	transcription factor
		GO:0009987,GO:0005			
		575,GO:0000166,GO:0	cellular process,cellular component		
		016043,GO:0005198,G	organization		
ug0262	429	O:0016787,GO:000585		cellular_component,cytoskeleton	nucleotide binding,structural
		GO:0005198,GO:0009			
		987,GO:0005575,GO:0	cellular process,response to		
		006950,GO:0009628,G	stress,response to abiotic		
ug0263_1	429	O:0000166,GO:001604	stimulus,cellular component	cellular_component,cytoskeleton	structural molecule
		3,GO:0016787,GO:000	organization		
		GO:0003676,GO:0000			
		166			
ug0263_2	753	GO:0005515		nucleus	nucleic acid
		GO:0030528,GO:0006	transcription		
		350,GO:0005634			
		203			
ug0264_1	860	GO:0006810,GO:0009	transport,cellular process	vacuole,membrane	hydrolase activity,nucleotide
		987,GO:0005773,GO:0			
		016020,GO:0016787,G			
		O:0000166,GO:000521			
ug0264_2	810	GO:0030528,GO:0006	transcription	nucleus	transcription regulator
		350,GO:0005634			
		GO:0005488,GO:0016	generation of precursor metabolites		
		020,GO:0006091,GO:0	and energy,photosynthesis		
ug0265	636	015979,GO:0009536,G		membrane,plastid,thylakoid	binding
		421			
		768			
		GO:0016740,GO:0005	biosynthetic process,cellular		
ug0266_1	900	737,GO:0009058,GO:0	process,lipid metabolic process	cytoplasm	transferase activity
		009987,GO:0006629			
		226			
		GO:0016020			
ug0266_2	903	GO:0005739,GO:0009		membrane	mitochondrion,plastid
		GO:0005622,GO:0019			
		538,GO:0009056,GO:0	protein metabolic process,catabolic		
		009987,GO:0005634,G	process,cellular process		
ug0267	574	O:0005829,GO:001678		intracellular,nucleus,cytosol	hydrolase activity
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
ug0268	668	GO:0005829,GO:001678		intracellular,nucleus,cytosol	hydrolase activity
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
ug0269	559	GO:0005829,GO:001678		intracellular,nucleus,cytosol	hydrolase activity
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
ug0270	435	GO:0005829,GO:001678		intracellular,nucleus,cytosol	hydrolase activity
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
ug0271	203	GO:0005829,GO:001678		intracellular,nucleus,cytosol	hydrolase activity
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
ug0272	644	GO:0005829,GO:001678		intracellular,nucleus,cytosol	hydrolase activity
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
ug0273	428	GO:0005829,GO:001678		intracellular,nucleus,cytosol	hydrolase activity
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
ug0274_1	615	GO:0005829,GO:001678		intracellular,nucleus,cytosol	hydrolase activity
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
ug0274_2	897	GO:0005829,GO:001678		intracellular,nucleus,cytosol	hydrolase activity
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
ug0275_1	421	GO:0005829,GO:001678		intracellular,nucleus,cytosol	hydrolase activity
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
ug0275_2	768	GO:0005829,GO:001678		intracellular,nucleus,cytosol	hydrolase activity
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
ug0276	1040	GO:0005829,GO:001678		intracellular,nucleus,cytosol	hydrolase activity
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
ug0277	226	GO:0005829,GO:001678		intracellular,nucleus,cytosol	hydrolase activity
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
ug0278	666	GO:0005829,GO:001678		intracellular,nucleus,cytosol	hydrolase activity
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
ug0279	871	GO:0005829,GO:001678		intracellular,nucleus,cytosol	hydrolase activity
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
ug0280	585	GO:0005829,GO:001678		intracellular,nucleus,cytosol	hydrolase activity
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			
		GO:0005829,GO:001678			

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0281	661				
ug0282	791				
ug0283_1	221				
ug0283_2	706				
ug0284_1	892				
ug0284_2	550	GO:0005739		mitochondrion	
ug0285	760				
ug0286	587	GO:0005886		plasma membrane	
ug0287	785	GO:0009058,GO:000987,GO:0006629,GO:0	biosynthetic process,cellular process,lipid metabolic process		transferase activity
ug0288	717	GO:0009536		plastid	
ug0289_1	566				
ug0289_2	454	GO:0005576,GO:0016043,GO:0009987,GO:0	cellular component organization,cellular process	extracellular region,membrane	
ug0290_1	294				
ug0290_2	503				
ug0291	797	GO:0008152,GO:0019538,GO:0003824	metabolic process,protein metabolic process		catalytic activity
ug0292	232				
ug0293	328	GO:0008152,GO:0003824,GO:0005739,GO:0	metabolic process	mitochondrion	catalytic activity,binding
ug0294	311				
ug0295	386				
ug0296_1	452	GO:0019538,GO:000987,GO:0000166	protein metabolic process,cellular process		nucleotide binding
ug0296_2	511	GO:0016020,GO:0005777,GO:0016043,GO:0	cellular component organization,cellular process	membrane,peroxisome	
ug0297	884	GO:0016301,GO:0005284			kinase activity,binding
ug0298	284				
ug0299_1	785	GO:0005829,GO:0003824,GO:0005739,GO:0008152,GO:0009058,GO:0009987,GO:0009056,GO:0006519,GO:0006629,GO:0019748,GO:0005515,GO:0009536,GO:0019725,GO:0030234,GO:0008150	metabolic process,biosynthetic process,cellular process,catabolic process,cellular amino acid and derivative metabolic process,lipid metabolic process,secondary metabolic process	cytosol,mitochondrion,plastid	catalytic activity,protein binding,binding
ug0299_2	913	GO:0006091,GO:0005975,GO:0009056,GO:0003824	homeostasis,biological_process generation of precursor metabolites and energy,carbohydrate metabolic process,catabolic process		enzyme regulator activity
ug0300	1308	GO:0005488,GO:0000166,GO:0005737,GO:0008152,GO:0009987,GO:0005730,GO:0005634,GO:0003723,GO:0006139,GO:0006950,GO:0009628,GO:000016	metabolic process,cellular process	cytoplasm	binding,nucleotide binding,transferase activity
ug0301_1	519	GO:0005198,GO:0005886,GO:0005783	metabolic process,cellular process	plasma membrane,endoplasmic reticulum	structural molecule activity
ug0301_2	768	GO:0005886,GO:000987,GO:0005730,GO:0005634,GO:0003723,GO:0006139,GO:0006950,GO:0009628,GO:000016	post-embryonic development,response to stress,response to biotic	plasma membrane	protein binding
ug0302	735				
ug0303	839				
ug0304	188				
ug0305	877	GO:0005488,GO:000987,GO:0000003,GO:000987,GO:0005515,GO:0	reproduction,post-embryonic development,multicellular		binding,protein binding
ug0306	332				
ug0307	807	GO:0005488,GO:0005739,GO:0005515,GO:0	organismal development,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	nucleoplasm	protein binding
ug0308	1017	GO:0006139,GO:0009908,GO:0005215,GO:0016020,GO:0005739,GO:0	development,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane,mitochondrion	transporter activity
ug0309	351	GO:0003677,GO:0005488,GO:0006259	DNA metabolic process		DNA binding,binding
ug0310	866	GO:0005886,GO:0005783		plasma membrane,endoplasmic reticulum	
ug0311	985				
ug0312	503				
ug0313	848				
ug0314_1	829	GO:0009536		plastid	
ug0314_2	682	GO:0006950,GO:000987,GO:0008152,GO:0009987,GO:0009536,GO:0005488,GO:0009579,GO:0005576,GO:000	response to stress,response to biotic stimulus,metabolic process,cellular process	plastid,thylakoid,extracellular region	binding,catalytic activity



Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0315	814	GO:0009719,GO:0007165,GO:0006950,GO:0	response to endogenous stimulus,signal		transferase activity
ug0316	413				
ug0317	673				
ug0318	364				
ug0319	764	GO:0016020,GO:0005783,GO:0005623,GO:0005488,GO:0006810,GO:0005975,GO:0009	transport,generation of precursor metabolites and energy	membrane,endoplasmic reticulum,cell	binding
ug0320_1	519	987,GO:0016787,GO:0005576,GO:0005618,G	carbohydrate metabolic process,cellular process	extracellular region,cell wall	hydrolase activity,transferase activity
ug0320_2	912				
ug0321	924	GO:0009719,GO:0007165,GO:0003824,GO:0	response to endogenous stimulus,signal transduction		catalytic activity,transferase activity
ug0322	621	GO:0003677,GO:0006435	transcription		DNA binding
ug0323	435				
ug0324_1	977	GO:0003824,GO:0009536,GO:0008150,GO:0005618,GO:0008152,GO:0005488,GO:0009058,GO:0006519,GO:000	biological_process,metabolic process,biosynthetic process,cellular amino acid and derivative metabolic process	plastid,cell wall,extracellular region,mitochondrion	catalytic activity,binding
ug0324_2	340	GO:0016043,GO:000987,GO:0005737,GO:0009653,GO:0016049,GO:0005576,GO:0016020,GO:0016787,GO:0006950,GO:0008219,GO:0005773,GO:0005975,G	cellular component organization,cellular process,anatomical structure morphogenesis,cell growth	cytoplasm,extracellular region,membrane	
ug0325_1	522	GO:0009056,GO:0009607,GO:0009987,GO:0005618,GO:0030246,GO:0008152,GO:000987,GO:0005488,GO:0	response to stress,cell death,carbohydrate metabolic process,catabolic process,response to biotic stimulus,cellular process	vacuole,cell wall,extracellular region	hydrolase activity,carbohydrate binding
ug0325_2	833	GO:0008152,GO:000987,GO:0005488,GO:0	metabolic process,cellular process		binding,catalytic activity
ug0326	534	GO:0009536		plastid	
ug0327	706				
ug0328	850	GO:0006464,GO:0016301,GO:0000166	protein modification process		kinase activity,nucleotide binding
ug0329_1	510	GO:0005975,GO:000987,GO:0016787,GO:0005576,GO:0005618,G	carbohydrate metabolic process,cellular process	extracellular region,cell wall	hydrolase activity,transferase activity
ug0329_2	689	GO:0005737,GO:0008152,GO:0005975,GO:0009987,GO:0009056,GO:0003824,GO:0016020,GO:0005	metabolic process,carbohydrate metabolic process,cellular process,catabolic process	cytoplasm	binding,catalytic activity
ug0330	858	737,GO:0005515,GO:0005215,GO:0006810,G	transport,cellular process	membrane,cytoplasm	protein binding,transporter activity
ug0331	611				
ug0332_1	505				
ug0332_2	752	GO:0006950,GO:0009607,GO:0009536,GO:0016020,GO:0009579,G	response to stress,response to biotic stimulus,transport	plastid,membrane,thylakoid	
ug0333	469				
ug0334	673	GO:0005623,GO:0005413,GO:0005215,GO:0006	transport	cell,cytoplasm	transporter activity
ug0335	413				
ug0336	765				
ug0337	1030				
ug0338	539				
ug0339	703	GO:0005515			protein binding
ug0340	841	GO:0005737		cytoplasm	
ug0341	695	GO:0003824,GO:0016020,GO:0005622		membrane,intracellular	catalytic activity
ug0342	583				
ug0343	134				
ug0344	330	GO:0005739,GO:0009739,GO:0005623,GO:0005739,GO:0016020		mitochondrion,plastid	
ug0345	793			cell,mitochondrion,membrane	
ug0346	834	GO:0005622		intracellular	
ug0347	357				
ug0348	545				
ug0349	875	GO:0005737,GO:0009739,GO:0005488,GO:0008152,GO:0003824,GO:0	metabolic process	cytoplasm,plastid	binding,catalytic activity,molecular_function
ug0350	665				
ug0351	569				
ug0352_1	178				
ug0352_2	863				
ug0353	716				
ug0354	699				
ug0355	919	GO:0016020		membrane	
ug0356	522				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0357	486	GO:0005773,GO:000515,GO:0005886		vacuole,plasma membrane	protein binding
ug0358_1	627				
ug0358_2	422	GO:0005886		plasma membrane	
ug0359_1	118				
ug0359_2	773				
ug0360	568				
ug0361_1	474	GO:0004872,GO:0005488,GO:0005737,GO:0009987,GO:0016020,GO:0005783,GO:000681	cellular process,transport	cytoplasm,membrane,endoplasmic reticulum	receptor activity,binding
ug0361_2	242				
ug0362	693	GO:0005730,GO:0003723,GO:0005515,GO:0003674,GO:0019725,GO:0005739,GO:0008152,GO:0000166,GO:0003824,GO:000573	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	nucleolus	RNA binding,protein binding
ug0363	433	GO:0006139,GO:0005975,GO:0009056,GO:019748,GO:0003824,GO:0009536	cellular homeostasis,metabolic process	mitochondrion,cytoplasm	molecular_function,nucleotide binding,catalytic activity
ug0364	822		nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,carbohydrate metabolic process,catabolic process,secondary metabolic	plastid	catalytic activity
ug0365	453				
ug0366	539	GO:0009579,GO:0016020,GO:0005515,GO:0009536,GO:0015979	photosynthesis	thylakoid,membrane,plastid	protein binding
ug0367_1	645				
ug0367_2	605	GO:0006464,GO:0006950,GO:0009628,GO:0005622,GO:0003723,GO:0005515,GO:0016301,GO:0000166,GO:000009719,GO:0008150,GO:0006350,GO:003700,GO:0005634,GO:0005488,GO:0006950,GO:0003824,GO:0008150,GO:0009719	protein modification process,response to stress,response to abiotic stimulus,response to endogenous stimulus	intracellular,nucleus	RNA binding,protein binding,kinase activity,nucleotide binding
ug0368	871		response to endogenous stimulus,biological_process,transcription,response to stress,response to abiotic stimulus	nucleus	transcription factor activity,binding
ug0369_1	475	GO:0003824,GO:0008150,GO:0009719	biological_process,response to endogenous stimulus		catalytic activity
ug0369_2	632	GO:0005488,GO:0008152,GO:0003824,GO:000536	metabolic process		binding,catalytic activity,molecular_function
ug0370	534				
ug0371	980				
ug0372	958	GO:0006810,GO:0009987,GO:0016020,GO:00019725,GO:0003674,GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634,GO:0005215,GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:0009536,GO:0016787,GO:0005773,GO:0006810,GO:0000166,GO:0007165	transport,cellular process	membrane,endosome	
ug0373	661		cellular homeostasis		molecular_function,catalytic activity
ug0374	733		cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug0375_1	851		transport,biosynthetic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	plastid,vacuole,membrane,plasma membrane	transporter activity,hydrolase activity
ug0375_2	975		transport,signal transduction		nucleotide binding
ug0376	756				
ug0377	780	GO:0006412,GO:0005622,GO:0006950,GO:0009607,GO:0005840,GO:0009536,GO:0005198,GO:0005515,GO:0016043,GO:0006810,GO:0009987,GO:0005794	translation,response to stress,response to biotic stimulus	intracellular,ribosome,plastid,membrane,thylakoid	structural molecule activity,protein binding
ug0378	675		transport,cellular process	Golgi apparatus	
ug0379	894	GO:0005488,GO:0008152,GO:0003824,GO:000536	metabolic process		binding,catalytic activity,molecular_function
ug0380	196				
ug0381	722	GO:0006950,GO:0009607,GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005515,GO:0009908,GO:0000030234,GO:0003677,GO:0006259,GO:0009058,GO:0005622,GO:0009987,GO:0005575,GO:0000166,GO:0016043,GO:0005198,GO:0016787,GO:000585	response to stress,response to biotic stimulus,cellular component organization,cellular process,flower development	intracellular,nucleus	DNA binding,protein binding
ug0382	822		DNA metabolic process,biosynthetic process	intracellular,nucleus	enzyme regulator activity,DNA binding
ug0383	894		cellular process,cellular component organization	cellular_component,cytoskeleton	nucleotide binding,structural molecule activity,hydrolase activity

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0384	689				
ug0385	201				
ug0386	571	GO:0006810,GO:0016020,GO:0005215	transport	membrane	transporter activity
ug0387	913	GO:0008152,GO:0005488,GO:0030528,GO:0000000	metabolic process		binding,transcription regulator activity,catalytic
ug0388	451				
ug0389	925	GO:0009536,GO:0005215,GO:0000003,GO:0009791,GO:0009790,GO:0016020,GO:0006810	reproduction,post-embryonic development,embryonic development,transport	plastid,membrane	transporter activity
ug0390	749				
ug0391	1023	GO:0006950	response to stress		
ug0392	804				
ug0393	438	GO:0005198,GO:0003723,GO:0005840,GO:0005783	translation	ribosome	structural molecule activity,RNA binding
ug0394	744				
ug0395	625	GO:0005783		endoplasmic reticulum	
ug0396	877				
ug0397	645	GO:0005739		mitochondrion	
ug0398	457	GO:0016740			transferase activity
ug0399	187				
ug0400	415	GO:0005198,GO:0005840,GO:0009536,GO:0006412,GO:0003723,GO:0005739,GO:0006091,GO:0015979,GO:0003674,GO:0005488,GO:0006810	translation	ribosome,plastid,mitochondrion	structural molecule activity,RNA binding
ug0401	374				
ug0402	901	GO:0000166,GO:0006091,GO:0016020,GO:0009579,GO:0006091,GO:0015979,GO:0003674,GO:0005488,GO:0006810	response to stress generation of precursor metabolites and energy,photosynthesis,transport	membrane,thylakoid,plastid	nucleotide binding molecular_function,binding
ug0403	458				
ug0404	449				
ug0405	557				
ug0406	524				
ug0407	610	GO:0003677,GO:000515,GO:0003700,GO:0005634,GO:0006350,GO:0005198,GO:0005840,GO:0006412	transcription	nucleus	DNA binding,protein binding,transcription factor activity
ug0408_1	518	GO:0005198,GO:0005840,GO:0006412	translation	ribosome	structural molecule activity
ug0408_2	303				
ug0409_1	906				
ug0409_2	371	GO:0005623		cell	
ug0410	1137	GO:0016020,GO:0005794,GO:0005515,GO:0006810,GO:0009987,GO:0005198,GO:0005739,GO:0016787,GO:0009536,GO:0000166,GO:0005488,GO:0006810	transport,cellular process	membrane,Golgi apparatus,cytoplasm,plasma membrane	protein binding,structural molecule activity
ug0411	872	GO:0016787,GO:0009536,GO:0000166,GO:0005488,GO:0006810	signal transduction	plastid	hydrolase activity,nucleotide binding
ug0412	126				
ug0413	653				
ug0414	831	GO:0003824,GO:0008152,GO:0000166	metabolic process		catalytic activity,nucleotide binding
ug0415	1047				
ug0416	716				
ug0417	718	GO:0005488,GO:0006091,GO:0003674,GO:0005739,GO:0006810	generation of precursor metabolites and energy,transport	mitochondrion	binding,molecular_function
ug0418	660	GO:0030234			enzyme regulator activity
ug0419_1	892				
ug0419_2	858				
ug0420	1056	GO:0005768,GO:0000166,GO:0006810,GO:0009987,GO:0016020,GO:0005515,GO:000716	transport,cellular process,signal transduction	endosome,membrane	nucleotide binding,protein binding,hydrolase activity
ug0421	452				
ug0422	359				
ug0423	492				
ug0424	588	GO:0005840,GO:0005198,GO:0006412,GO:0005773,GO:0005634,GO:0005886,GO:0005739,GO:0006412,GO:0006519,GO:0003824,GO:0000166	translation	ribosome,mitochondrion	structural molecule activity
ug0425	853			vacuole,nucleus,plasma membrane	nucleotide binding
ug0426	901				
ug0427	196				
ug0428	880	GO:0005737,GO:0006139,GO:0006412,GO:0006519,GO:0003824,GO:0000166	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,translation,cellular amino acid and derivative metabolic	cytoplasm	catalytic activity,nucleotide binding
ug0429	731	GO:0005623		cell	

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0430_1	744	GO:0016020,GO:0009579,GO:0009536,GO:0005794,GO:0005886		membrane,thylakoid,plastid,Golgi apparatus,plasma membrane	
ug0430_2	1094	GO:0003824			catalytic activity
ug0431	1039	GO:0019538,GO:0009056,GO:0016787	protein metabolic process,catabolic process		hydrolase activity
ug0432	667				
ug0433	495				
ug0434	837	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug0435	717	GO:0005739		mitochondrion	
ug0436	909	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug0437	695				
ug0438	742	GO:0006950,GO:0009056,GO:0009987,GO:0005777,GO:0005488,GO:0008152,GO:0003824	response to stress,catabolic process,cellular process,metabolic process	peroxisome	binding,catalytic activity
ug0439	778	GO:0016020,GO:0016713		membrane	hydrolase activity
ug0440	713				
ug0441	235				
ug0442	537				
ug0443	115				
ug0444	692				
ug0445_1	988	GO:0006139,GO:0005737,GO:0016787	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	cytoplasm	hydrolase activity
ug0445_2	732	GO:0007165,GO:0003700,GO:0005634,GO:0009791,GO:0006350	signal transduction,post-embryonic development,transcription	nucleus	transcription factor activity
ug0446	250				
ug0447_1	519	GO:0005886		plasma membrane	
ug0447_2	943				
ug0448	1124	GO:0016787,GO:0009536,GO:0009056,GO:0005515,GO:0005739,GO:0019538,GO:0009056	protein metabolic process,catabolic process	plastid,thylakoid	hydrolase activity
ug0449	522	GO:0019538,GO:0009987,GO:0006950,GO:0009628,GO:0009536,GO:0000166,GO:0016020,GO:0009579,GO:0006950,GO:0019725,GO:0005739,GO:0005515,GO:0005	protein metabolic process,cellular process,response to stress,response to abiotic stimulus,biological_process	mitochondrion,plastid,membrane,thylakoid,extracellular region	protein binding,nucleotide binding
ug0450_1	834	GO:0006950,GO:0019725,GO:0005739,GO:0005515,GO:0005	response to stress,cellular homeostasis	mitochondrion	catalytic activity
ug0450_2	738				
ug0451	483	GO:0005515,GO:0005215,GO:0006810,GO:0009987,GO:0016020,GO:0005737,GO:0016	transport,cellular process	membrane,cytoplasm	protein binding,transporter activity
ug0452	1003	GO:0005737,GO:0016020,GO:0009058,GO:0006519,GO:0003824,GO:000	biosynthetic process,cellular amino acid and derivative metabolic	cytoplasm	hydrolase activity
ug0453	1145			plastid	catalytic activity
ug0454	249				
ug0455	222				
ug0456	899	GO:0016020		membrane	
ug0457_1	876	GO:0003824,GO:0005000,GO:0003824,GO:0008	metabolic process,cellular		catalytic activity,binding
ug0457_2	820	GO:0009987,GO:0005975	process,carbohydrate metabolic process		catalytic activity
ug0458_1	1208	GO:0003723			RNA binding
ug0458_2	678	GO:0016020,GO:0006810,GO:0009987	transport,cellular process	membrane	
ug0459	312	GO:0016020,GO:0009536,GO:0016043,GO:000	cellular component organization,cellular process	membrane,plastid	
ug0460	862	GO:0006464	protein modification process		
ug0461	911	GO:0019725,GO:0003674,GO:0003824	cellular homeostasis		molecular_function,catalytic activity
ug0462	1222				
ug0463	391				
ug0464	703				
ug0465	497				
ug0466	715	GO:0016740,GO:000515,GO:0009058,GO:0005975,GO:0009987,GO:0016020,GO:000548	biosynthetic process,carbohydrate metabolic process,cellular process	membrane	transferase activity,protein binding,binding
ug0467	957	GO:0016787,GO:0019538,GO:0009987,GO:0016020,GO:0005783	protein metabolic process,cellular process	membrane,endoplasmic reticulum	hydrolase activity
ug0468	298				
ug0469	850	GO:0016043,GO:0009987,GO:0005737,GO:0005515,GO:0005856	cellular component organization,cellular process	cytoplasm,cytoskeleton	protein binding

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0470	213				
ug0471	192	GO:0019538,GO:0009	protein metabolic process,cellular process	endoplasmic reticulum	protein binding,binding
ug0472_1	191				
ug0472_2	1013				
ug0473	490	GO:0005975,GO:0009 987,GO:0005739,GO:0 016740,GO:0006091,G O:0009056,GO:000382	carbohydrate metabolic process,cellular process,generation of precursor metabolites and energy,catabolic process	mitochondrion	transferase activity,catalytic activity
ug0474	264				
ug0475	837				
ug0476	449				
ug0477_1	748	GO:0009058,GO:0009 987,GO:0006629,GO:0 005215,GO:0005488,G GO:0005488,GO:0005	biosynthetic process,cellular process,lipid metabolic process	plastid	transporter activity,binding
ug0477_2	469	515,GO:0005215,GO:0 016020,GO:0005739,G O:0006810,GO:001604	transport,cellular component organization,cellular process	membrane,mitochondrion	binding,protein binding,transporter activity
ug0478	820	GO:0005739		mitochondrion	
ug0479	615	GO:0005840,GO:0005 198,GO:0006412	translation	ribosome	structural molecule activity
ug0480	290				
ug0481	329				
ug0482	702	GO:0005576		extracellular region	
ug0483	497	GO:0006412,GO:0008 135	translation		translation factor activity, nucleic acid binding
ug0484	258				
ug0485	138				
ug0486	470				
ug0487	874				
ug0488	549	GO:0003677,GO:0003 700,GO:0005634,GO:0	transcription	nucleus	DNA binding,transcription factor activity
ug0489	767	GO:0005623,GO:0005 737,GO:0005739		cell,cytoplasm,mitochondrion	
ug0490	706	GO:0006091,GO:0016 020,GO:0005622,GO:0 003824,GO:0009058,G O:0009987,GO:000953	generation of precursor metabolites and energy,biosynthetic process,cellular process	membrane,intracellular,plastid,mitochondrion	catalytic activity
ug0491	692	GO:0008152,GO:0016	metabolic process		hydrolase activity
ug0492	1009	GO:0006464,GO:0005 623,GO:0016301,GO:0	protein modification process	cell	kinase activity,nucleotide binding
ug0493_1	556				
ug0493_2	444				
ug0494	530	GO:0005488,GO:0008 152,GO:0003824,GO:0	metabolic process		binding,catalytic activity,molecular_function
ug0495	553	GO:0016787,GO:0006 519	cellular amino acid and derivative metabolic process		hydrolase activity
ug0496	873				
ug0497	866	GO:0005622,GO:0016 787,GO:0019538,GO:0 009056,GO:0009987,G O:0000166,GO:000563 4,GO:0005829,GO:000	protein metabolic process,catabolic process,cellular process	intracellular,nucleus,cytosol	hydrolase activity,nucleotide binding,protein binding
ug0498_1	1080	GO:0009058,GO:0006 519,GO:0009536,GO:0	biosynthetic process,cellular amino acid and derivative metabolic process	plastid	catalytic activity
ug0498_2	469	GO:0005975,GO:0016	carbohydrate metabolic process		hydrolase activity
ug0499	430				
ug0500_1	701				
ug0500_2	796	GO:0016740,GO:0006 350,GO:0003677,GO:0	transcription	plastid	transferase activity,DNA binding
ug0501	440				
ug0502_1	996				
ug0502_2	245				
ug0503	434	GO:0016020,GO:0005 739,GO:0006091,GO:0	generation of precursor metabolites and energy,transport	membrane,mitochondrion	
ug0504	733	GO:0005488,GO:0009 GO:0006091,GO:0015	cellular process		binding
ug0505	913	979,GO:0016020,GO:0 009579,GO:0009536 GO:0009536,GO:0030 234,GO:0006950,GO:0	generation of precursor metabolites and energy,photosynthesis	membrane,thylakoid,plastid	
ug0506	684	003674,GO:0019725,G O:0008152,GO:000561 8,GO:0008150,GO:000 3824,GO:0016020,GO:	response to stress,cellular homeostasis,metabolic process,biological_process	plastid,cell wall,membrane,thylakoid	enzyme regulator activity,molecular_function,catalytic activity
ug0507	698				
ug0508	431				
ug0509	453				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0510	413				
ug0511	1121				
ug0512	1238				
ug0513	745				
ug0514	343				
ug0515	1016	GO:0008152,GO:0003824,GO:0009536	metabolic process	plastid	catalytic activity
ug0516	622	GO:0009058,GO:0006519,GO:0019748,GO:0008152,GO:0003824,GO:0005488	biosynthetic process,cellular amino acid and derivative metabolic process,secondary metabolic process,metabolic process		catalytic activity,binding
ug0517	431				
ug0518	768	GO:0005623		cell	
ug0519	817				
ug0520	673	GO:0009628,GO:0006950	response to abiotic stimulus,response to stress		
ug0521	861	GO:0009536		plastid	
ug0522	705				
ug0523	263				
ug0524_1	893	GO:0006350,GO:0003700,GO:0005634,GO:0009719,GO:0007165	transcription,response to endogenous stimulus,signal transduction	nucleus	transcription factor activity
ug0524_2	566	GO:0016787,GO:0008GO:0005737,GO:0008	metabolic process		hydrolase activity
ug0525	758	135,GO:0000166,GO:0006412,GO:0016787	translation	cytoplasm	translation factor activity, nucleic acid binding,nucleotide
ug0526	782	GO:0016043,GO:0009987,GO:0005737,GO:0005515,GO:0005856	cellular component organization,cellular process	cytoplasm,cytoskeleton	protein binding
ug0527	918				
ug0528_1	468	GO:0016787			hydrolase activity
ug0528_2	779				
ug0529	805				
ug0530	874				
ug0531	415				
ug0532	633				
ug0533_1	833	GO:0005840,GO:0005198,GO:0009536,GO:0016020,GO:0006412,G	translation	ribosome,plastid,membrane	structural molecule activity,RNA binding
ug0533_2	806				
ug0534	437				
ug0535	925	GO:0005488			binding
ug0536	857				
ug0537	601				
ug0538	1157	GO:0006091,GO:0000166,GO:0006950,GO:0003824,GO:0016020,GO:0005622,GO:000367	generation of precursor metabolites and energy,response to stress	membrane,intracellular,mitochondrion	nucleotide binding,catalytic activity,molecular_function
ug0539	462	GO:0005515			protein binding
ug0540	747	GO:0016740			transferase activity
ug0541	277				
ug0542_1	754				
ug0542_2	577				
ug0543	734				
ug0544_1	856	GO:0016020		membrane	
ug0544_2	447	GO:0005623		cell	
ug0545	736				
ug0546	491	GO:0005488,GO:0003824,GO:0008152,GO:0005623,GO:0009719,GO:0016020,GO:0006950,GO:0009628	metabolic process response to endogenous stimulus,response to stress,response to abiotic stimulus	cell,membrane	binding,catalytic activity,molecular_function
ug0547	627	GO:0006810,GO:0000166,GO:0007165,GO:0003677,GO:0003	transport,signal transduction		nucleotide binding
ug0548	798				
ug0549	676	824,GO:0000166,GO:0005622,GO:0006259	DNA metabolic process	intracellular	DNA binding,catalytic activity,nucleotide binding
ug0550	368				
ug0551	694	GO:0016740,GO:0008	metabolic process		transferase activity
ug0552	362				
ug0553	515				
ug0554	981	GO:0005739,GO:0016		mitochondrion,membrane	
ug0555	600				
ug0556_1	773				
ug0556_2	1129	GO:0016787,GO:0005622,GO:0019538,GO:0009056,GO:0009987	protein metabolic process,catabolic process,cellular process	intracellular	hydrolase activity
ug0557_1	793	GO:0005840,GO:0005198,GO:0009987,GO:0	cellular process,translation	ribosome	structural molecule activity
ug0557_2	1216				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0558	622	GO:0009536		plastid	
ug0559	289				
		GO:0005623,GO:0016			
ug0560	760	020,GO:0005215,GO:0006810,GO:0009987	transport,cellular process	cell,membrane	transporter activity
ug0561_1	275				
ug0561_2	871	GO:0000166,GO:0003677,GO:0006950,GO:0006810,GO:0016020,GO:0005215	response to stress,DNA metabolic process		nucleotide binding,DNA binding
ug0562	1161	GO:0006810,GO:0016020,GO:0005215	transport	membrane	transporter activity
		GO:0030234,GO:0008150,GO:0005737,GO:0005886,GO:0005576,GO:0008152,GO:000998	biological_process,metabolic process,cellular process	cytoplasm,plasma membrane,extracellular region	enzyme regulator activity
ug0563	1281				
ug0564	649	GO:0005615		extracellular space	
ug0565	631	GO:0006950	response to stress		
ug0566	1223				
ug0567	538				
ug0568	778	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug0569	597				
ug0570	699	GO:0005737		cytoplasm	
ug0571	363				
		GO:0009536,GO:0005198,GO:0005840,GO:0005829,GO:0016020,GO:0006412,GO:000372	translation	plastid,ribosome,cytosol,membrane	structural molecule activity,RNA binding
ug0572	906				
ug0573_1	849				
		GO:0006810,GO:0016043,GO:0009987,GO:0019538,GO:0009056,GO:0003824,GO:0006629,GO:0005515,GO:0005198,GO:000528,GO:0005515,GO:0005737,GO:0006350,GO:0009987,GO:0009987	transport,cellular component organization,cellular process,protein metabolic process,catabolic process,lipid metabolic process,protein		catalytic activity,protein binding
ug0573_2	825				
ug0574	898	GO:0030528,GO:0005515,GO:0006350,GO:0009987,GO:0009987	transcription	nucleus	transcription regulator activity,protein binding
ug0575	145	GO:0016020,GO:0009987,GO:0009536,GO:0003824,GO:0005829,GO:0008152,GO:0005215	photosynthesis	membrane,thylakoid,plastid	
ug0576	925		metabolic process,response to stress	cytosol	catalytic activity
ug0577	125				
ug0578_1	480	GO:0005829,GO:0005829,GO:0009579,GO:0009579		cytosol,plasma membrane	
		GO:0003674,GO:0005488,GO:0006810,GO:0016020,GO:0015979,GO:0005739,GO:0005488,GO:0008152,GO:0003824,GO:0005198,GO:0006810,GO:0005215,GO:0006810,GO:0005215	transport,photosynthesis,generation of precursor metabolites and energy	thylakoid,plastid,membrane,mitochondrion	molecular_function,binding
ug0578_2	475				
ug0579	875	GO:0005488,GO:0008152,GO:0003824,GO:0005198,GO:0006810,GO:0005215,GO:0006810,GO:0005215	metabolic process		binding,catalytic activity,molecular_function
ug0580	804	GO:0016020,GO:0005215,GO:0006810,GO:0005215	transport,cellular process	membrane	transporter activity
ug0581	189				
ug0582_1	599	GO:0005488,GO:0008150,GO:0009719	biological_process,response to endogenous stimulus		binding
ug0582_2	900				
ug0583	630	GO:0019538,GO:0009987,GO:0003824	protein metabolic process,cellular process		catalytic activity
ug0584	775	GO:0019538,GO:0009987,GO:0000166,GO:0006464,GO:000166,GO:0006464	protein metabolic process,catabolic process,cellular process,protein modification process		nucleotide binding,catalytic activity
ug0585	119				
ug0586	381				
ug0587	1042				
ug0588	695				
ug0589	818	GO:0003677,GO:0003700,GO:0005634,GO:0005488	transcription	nucleus	DNA binding,transcription factor activity
ug0590_1	779	GO:0005488			binding
ug0590_2	748	GO:0005623		cell	
ug0591_1	517				
ug0591_2	582	GO:0030528,GO:0006350,GO:0005634	transcription	nucleus	transcription regulator activity
ug0592	1113	GO:0005623,GO:0019538,GO:0009056,GO:0016020,GO:0009579,GO:0005488,GO:0009536,GO:0015979	protein metabolic process,catabolic process	cell	hydrolase activity
ug0593	829		photosynthesis	membrane,thylakoid,plastid	binding
ug0594	420				
ug0595	742				
ug0596	958	GO:0016043,GO:0006412,GO:0008135,GO:0006412,GO:0008135	cellular component organization,translation	mitochondrion	translation factor activity, nucleic acid binding

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0597	765	GO:0016020,GO:0005488,GO:0005737,GO:0		membrane,cytoplasm	binding,molecular_function
ug0598	484	GO:0005739,GO:0016001,GO:0016043,GO:000987,GO:0016020,GO:0	cellular component organization,cellular process	mitochondrion	hydrolase activity
ug0599	880	GO:0006810	transport	membrane,peroxisome	
ug0600	691	GO:0016787			hydrolase activity
ug0601	827				
ug0602	138				
ug0603	483	GO:0005737,GO:0016001,GO:0005840,GO:0005198,GO:0006412	translation	cytoplasm	hydrolase activity
ug0604	519			ribosome	structural molecule activity
ug0605_1	441				
ug0605_2	559				
ug0606	639	GO:0009536,GO:0006091,GO:0015979,GO:0005622,GO:0005488,GO:0016020,GO:000957	generation of precursor metabolites and energy,photosynthesis	plastid,intracellular,membrane,thylakoid	binding
ug0607	400				
ug0608	208				
ug0609	1095	GO:0003824,GO:0009058,GO:0006519	biosynthetic process,cellular amino acid and derivative metabolic		catalytic activity
ug0610	434				
ug0611	190	GO:0006259,GO:0003824,GO:0003677	DNA metabolic process		catalytic activity,DNA binding
ug0612	452	GO:0005618		cell wall	
ug0613	695	GO:0016787,GO:0005773,GO:0005975,GO:0009056,GO:0005488	carbohydrate metabolic process,catabolic process	vacuole	hydrolase activity,binding
ug0614_1	490				
ug0614_2	690				
ug0615	724	GO:0008289,GO:0006353	transport		lipid binding
ug0616	353				
ug0617	753	GO:0009058,GO:0005975,GO:0009987,GO:0016301,GO:0003824,GO:0019538,GO:0009	biosynthetic process,carbohydrate metabolic process,cellular process		kinase activity,catalytic activity,nucleotide binding
ug0618	1050	987,GO:0005515,GO:0001166,GO:0009536	protein metabolic process,cellular process	plastid	protein binding,nucleotide binding
ug0619	889				
ug0620	796	GO:0005737,GO:0005488,GO:0003824,GO:0008152,GO:0009058,GO:0006519,GO:000695	metabolic process,biosynthetic process,cellular amino acid and derivative metabolic process,response to stress,response	cytoplasm	binding,catalytic activity
ug0621	608	GO:0019538,GO:0009056,GO:0009987,GO:0	protein metabolic process,catabolic process,cellular process		protein binding
ug0622	454				
ug0623	637	GO:0003676,GO:0005135		intracellular	nucleic acid binding
ug0624	785	GO:0006412,GO:0008135	translation		translation factor activity, nucleic acid binding
ug0625	293				
ug0626	797				
ug0627	745	GO:0019725,GO:0009000,GO:0000166,GO:0016301,GO:0006139,GO:0	cellular homeostasis	plastid	nucleotide binding,kinase activity,transferase activity
ug0628	455	GO:0000166,GO:0016301,GO:0006139,GO:0	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		nucleotide binding,kinase activity,transferase activity
ug0629	444	GO:0000166,GO:0016301,GO:0006139,GO:0	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		activity,transferase activity
ug0630	800				
ug0631	943	GO:0016740			transferase activity
ug0632	715	GO:0006950,GO:0008219,GO:0009628,GO:0007049,GO:0030234,GO:0006350,GO:0000166,GO:0009607,GO:000	response to stress,cell death,response to abiotic stimulus,cell cycle,transcription,response to biotic stimulus	nucleus,plasma membrane	enzyme regulator activity,nucleotide binding
ug0633	824				
ug0634	531	GO:0005515			protein binding
ug0635	437	GO:0016020,GO:0005777,GO:0016043,GO:0009987,GO:0005739,GO:0006810,GO:0009058,GO:0006091,GO:0	cellular component organization,cellular process	membrane,peroxisome,mitochondrion	
ug0636	458	GO:006139,GO:0016787,GO:0005215,GO:0016020,GO:0006810,GO:0009058,GO:0006091,GO:0	metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane	hydrolase activity,transporter activity
ug0637	531	GO:006139,GO:0016787,GO:0005215,GO:0016020	transport,biosynthetic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane	hydrolase activity,transporter activity
ug0638	342				
ug0639	181				



Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0640_1	909	GO:0009536		plastid	
ug0640_2	1006	GO:0003677,GO:0006	transcription		DNA binding
ug0641	517				
ug0642	892	GO:0009536		plastid	
ug0643	955	GO:0005840,GO:0005 198,GO:0006412	translation	ribosome	structural molecule activity
ug0644	796				
ug0645	587				
ug0646	885	GO:0005488,GO:0008	biological_process		binding
ug0647	515				
ug0648	559	GO:0005840,GO:0005 198,GO:0006412	translation	ribosome	structural molecule activity
ug0649	453				
ug0650	1149	GO:0003723,GO:0005 737,GO:0006412,GO:0 GO:0009536,GO:0009	translation	cytoplasm	RNA binding,translation factor activity, nucleic acid
ug0651	818	058,GO:0009987,GO:0 015979,GO:0016020,G O:0009579,GO:001674	biosynthetic process,cellular process,photosynthesis	plastid,membrane,thylakoid	transferase activity
ug0652_1	438				
ug0652_2	686				
ug0653	413	GO:0016043,GO:0006 464,GO:0005634,GO:0	cellular component organization,protein modification	nucleus	hydrolase activity
ug0654	1027	GO:0005975,GO:0003 824,GO:0005488,GO:0 006139	process,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		catalytic activity,binding
ug0655	1207	GO:0019538,GO:0009 056,GO:0009987,GO:0 006464,GO:0009536,G O:0009628,GO:000979 1,GO:0005634,GO:001 6043,GO:0005515 GO:0009987,GO:0005	protein metabolic process,catabolic process,cellular process,protein modification process,response to abiotic stimulus,post-embryonic development,cellular component organization	plastid,nucleus	protein binding
ug0656	781	575,GO:0000166,GO:0 016043,GO:0005198,G O:0016787,GO:000585	cellular process,cellular component organization	cellular_component,cytoskeleton	nucleotide binding,structural molecule activity,hydrolase activity
ug0657	550				
ug0658	552	GO:0005886		plasma membrane	
ug0659	788	GO:0005576		extracellular region	
ug0660	727	GO:0030528,GO:0006 350,GO:0005634	transcription	nucleus	transcription regulator activity
ug0661	247				
ug0662	435				
ug0663	235				
ug0664_1	559	GO:0005840,GO:0009 536,GO:0005198,GO:0	translation	ribosome,plastid	structural molecule activity
ug0664_2	399				
ug0665	744	GO:0009536		plastid	
ug0666	558				
ug0667	841	GO:0009536		plastid	
ug0668	896	GO:0016020,GO:0009 579,GO:0009536		membrane,thylakoid,plastid	
ug0669	612	GO:0006091,GO:0005 975,GO:0009056,GO:0 016301	generation of precursor metabolites and energy,carbohydrate metabolic process,catabolic process		kinase activity
ug0670	505	GO:0006091,GO:0005 975,GO:0009056,GO:0 016301	generation of precursor metabolites and energy,carbohydrate metabolic process,catabolic process		kinase activity
ug0671	375				
ug0672	266				
ug0673	641	GO:0005737		cytoplasm	
ug0674	578	GO:0003824,GO:0005 488,GO:0006464	protein modification process		catalytic activity,binding
ug0675	754				
ug0676	856	GO:0003723			RNA binding
ug0677	202				
ug0678	549	GO:0019538,GO:0003 824,GO:0006464	protein metabolic process,protein modification process		catalytic activity
ug0679	261				
ug0680	617	GO:0030528,GO:0016 020,GO:0006350,GO:0 006810,GO:0005215,G	transcription,transport	membrane,nucleus	transcription regulator activity,transporter activity
ug0681	113				
ug0682	309				
ug0683	1177				
ug0684	659	GO:0006810,GO:0009 987,GO:0005773,GO:0 016020,GO:0005215,G	transport,cellular process	vacuole,membrane	transporter activity,hydrolase activity

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0685	927	GO:0005840,GO:0009536,GO:0006412,GO:0009058,GO:0005975,GO:0009987,GO:0006629,GO:0003723,GO:0005198,GO:0005829,GO:	translation,biosynthetic process,carbohydrate metabolic process,cellular process,lipid metabolic process	ribosome,plastid,cytosol,membrane	RNA binding,structural molecule activity,hydrolase activity
ug0686	203				
ug0687_1	786	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug0687_2	970	GO:0016301,GO:0005654,GO:0005739		nucleoplasm,mitochondrion	kinase activity
ug0688	437				
ug0689	834	GO:0006950,GO:0006350,GO:0007165,GO:0009719,GO:0030528,GO:0005515,GO:0003700,GO:0005488,GO:0003676,GO:0016043,GO:0009987,GO:0006350,GO:0005622,GO:0003680,GO:0019725,GO:0009579,GO:0005622,GO:	response to stress,transcription,signal transduction,response to endogenous stimulus	nucleus	transcription regulator activity,protein binding,transcription factor activity
ug0690	911	GO:0005488,GO:0003676,GO:0016043,GO:0009987,GO:0006350,GO:0005622,GO:0003680,GO:0019725,GO:0009579,GO:0005622,GO:	cellular component organization,cellular process,transcription	intracellular,nucleus	binding,nucleic acid binding,chromatin binding
ug0691_1	905	GO:0019725,GO:0009579,GO:0005622,GO:	cellular homeostasis	thylakoid,intracellular,plastid	
ug0691_2	270				
ug0692	756				
ug0693	453	GO:0000166			nucleotide binding
ug0694	427				
ug0695	331				
ug0696_1	856	GO:0016020,GO:0005739,GO:0003824,GO:0005215,GO:0003674,GO:0005488,GO:0006810,GO:0005488,GO:0008152,GO:0003824,GO:	transport,generation of precursor metabolites and energy	membrane,mitochondrion	catalytic activity,transporter activity,molecular_function,bi
ug0696_2	1076	GO:0005488,GO:0008152,GO:0003824,GO:	metabolic process,response to stress		binding,catalytic activity
ug0697	706				
ug0698	147				
ug0699	108				
ug0700	721				
ug0701	863	GO:0016740,GO:0009536,GO:0009058,GO:0005739,GO:0003824,GO:0008152,GO:0006091,GO:0005975,GO:0009056,GO:0005515	biosynthetic process,cellular amino acid and derivative metabolic process,generation of precursor metabolites and energy,carbohydrate metabolic process,catabolic process	plastid	transferase activity
ug0702	480	GO:0008152,GO:0006091,GO:0005975,GO:0009056,GO:0005515	precursor metabolites and energy,carbohydrate metabolic process,catabolic process	mitochondrion	catalytic activity
ug0703	1112	GO:0005515			protein binding
ug0704_1	604	GO:0003824,GO:0005622,GO:0008152,GO:0006091,GO:0005975,GO:0009056,GO:0016787,GO:0005515,GO:0006350,GO:000166,GO:0005634,GO:0005488	metabolic process,generation of precursor metabolites and energy,carbohydrate metabolic process,catabolic process	intracellular	catalytic activity
ug0704_2	517	GO:0006350,GO:000166,GO:0005634,GO:0005488	transcription	nucleus,plastid	hydrolase activity,protein binding,nucleotide binding
ug0705	1123	GO:0005488			binding
ug0706	936	GO:0019538,GO:0009056,GO:0009987	protein metabolic process,catabolic process,cellular process		
ug0707_1	470				
ug0707_2	839	GO:0009579,GO:0009536,GO:0005488,GO:		thylakoid,plastid	binding,catalytic activity
ug0708	519	GO:0005622		intracellular	
ug0709	899	GO:0003677,GO:0003700,GO:0005634,GO:	transcription	nucleus	DNA binding,transcription factor activity
ug0710	696				
ug0711	686				
ug0712_1	580	GO:0005488,GO:0016787,GO:0009538,GO:0009056,GO:0009987	protein metabolic process,catabolic process,cellular process		binding,transferase activity
ug0712_2	191				
ug0713_1	801				
ug0713_2	379				
ug0714_1	1050	GO:0005488			binding
ug0714_2	483				
ug0715	630				
ug0716	803	GO:0003824,GO:0005739,GO:0006091,GO:0015979,GO:0016020,GO:0009579,GO:0006464,GO:0005488,GO:0009538,GO:0016787,GO:0009987,GO:0009056,GO:00030246,GO:0005975	carbohydrate metabolic process		catalytic activity
ug0717	823	GO:0006091,GO:0015979,GO:0016020,GO:0009579,GO:0006464,GO:0005488,GO:0009538,GO:0016787,GO:0009987,GO:0009056,GO:00030246,GO:0005975	generation of precursor metabolites and energy,photosynthesis,protein modification process	membrane,thylakoid,plastid	binding
ug0718	870	GO:0016787,GO:0009987,GO:0009056,GO:00030246,GO:0005975	cellular process,catabolic process,carbohydrate metabolic process		hydrolase activity,carbohydrate binding
ug0719	493				
ug0720	590	GO:0005739,GO:0000003,GO:0009791,GO:	reproduction,post-embryonic development,embryonic	mitochondrion	

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0721	682				
ug0722	896	GO:0016020,GO:0009		membrane,plastid	
ug0723	460	GO:0005634		nucleus	
ug0724	660	GO:0005737		cytoplasm	
ug0725	543	GO:0005198,GO:0009 987,GO:0005840,GO:0 005829,GO:0005488,G O:0006412,GO:000372	cellular process,translation	ribosome,cytosol	structural molecule activity,binding,RNA binding
ug0726	642	GO:0003677,GO:0006			
ug0727	858	350,GO:0005634	transcription	nucleus	DNA binding
ug0728	841	GO:0005515,GO:0005		intracellular	protein binding
ug0729	810	GO:0000166,GO:0005			
ug0730	285	488,GO:0003674,GO:0 006810,GO:0008152,G O:0003824,GO:000953 6,GO:0009579,GO:001 6020,GO:0006091,GO:	transport,metabolic process,generation of precursor metabolites and energy,photosynthesis	plastid,thylakoid,membrane	nucleotide binding,binding,moleculer_fu nction,catalytic activity
ug0731	757	GO:0005840,GO:0009	cellular process	ribosome	
ug0732	316	GO:0005198,GO:0003			
ug0733	479	723,GO:0005840,GO:0 005829,GO:0016020,G	translation	ribosome,cytosol,membrane	structural molecule activity,RNA binding
ug0734	622	GO:0005773,GO:0005 739,GO:0009536,GO:0		vacuole,mitochondrion,plastid,plasm a membrane	
ug0735	517	GO:0009536		plastid	
ug0736	905	GO:0005488,GO:0005			binding,protein binding
ug0737_1	497	GO:0016787,GO:0030			hydrolase activity,enzyme regulator activity
ug0737_2	882	234			
ug0738	761	GO:0005198,GO:0005			
ug0739	335	840,GO:0009536,GO:0 006412,GO:0003723,G GO:0005488,GO:0009	translation	ribosome,plastid,mitochondrion	structural molecule activity,RNA binding
ug0740	899	058,GO:0009987,GO:0 003824,GO:0015979	biosynthetic process,cellular process,photosynthesis		binding,catalytic activity
ug0741	488	GO:0016301,GO:0005 829,GO:0000166,GO:0 006091,GO:0005975,G GO:0005488,GO:0005	generation of precursor metabolites and energy,carbohydrate metabolic process,catabolic process	cytosol	kinase activity,nucleotide binding
ug0742	659	515,GO:0005215,GO:0 016020,GO:0005739,G O:0006810,GO:001604	transport,cellular component organization,cellular process	membrane,mitochondrion	binding,protein binding,transporter activity
ug0743	560				
ug0744_1	627				
ug0744_2	671	GO:0005886		plasma membrane	
ug0745	169	GO:0019538,GO:0009			
ug0746	595	987,GO:0005515,GO:0 006950,GO:0005488,G	protein metabolic process,cellular process,response to stress	plasma membrane	protein binding,binding
ug0747	855	GO:0016020,GO:0005			
ug0748	827	737,GO:0005515,GO:0 006810,GO:0009987,G O:0005575,GO:000519	transport,cellular process	membrane,cytoplasm,cellular_comp onent	protein binding,structural molecule activity
ug0749_1	585	GO:0016043,GO:0009	cellular component		
ug0749_2	748	987,GO:0019538,GO:0 005515,GO:0005829	organization,cellular process,protein metabolic process	cytosol	protein binding
ug0750	726	GO:0000166,GO:0005			
ug0751	885	794,GO:0006810,GO:0 009987,GO:0005783	transport,cellular process	Golgi apparatus,endoplasmic reticulum	nucleotide binding
ug0752	705				
ug0753	233	GO:0003824,GO:0006			
ug0754	558	810,GO:0016020,GO:0 005739,GO:0006091	transport,generation of precursor metabolites and energy	membrane,mitochondrion	catalytic activity
ug0755	668				
ug0756	740				
ug0757_1	739				
ug0757_2	560				
ug0758	799	GO:0006091,GO:0005			
ug0759	787	737,GO:0003824,GO:0 006810,GO:0016020,G	generation of precursor metabolites and energy,transport	cytoplasm,membrane,mitochondrion	catalytic activity
ug0760	208				
ug0761	420				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0762	384	GO:0003824,GO:0006519,GO:0000003,GO:009791,GO:0009790	cellular amino acid and derivative metabolic process,reproduction,post-embryonic development,embryonic		catalytic activity
ug0763	144				
ug0764	954				
ug0765	499	GO:0016787			hydrolase activity
ug0766	661				
ug0767	1033	GO:0005886,GO:0009		plasma membrane,plastid	
ug0768	1169				
ug0769	879	GO:0009536		plastid	
ug0770	650	GO:0005576,GO:0030246,GO:0005975,GO:0005737,GO:0006	carbohydrate metabolic process	extracellular region	carbohydrate binding,hydrolase activity transferase
ug0771	843	350,GO:0016740,GO:003700,GO:0005634	transcription	cytoplasm,nucleus	activity,transcription factor activity
ug0772	487				
ug0773	405				
ug0774_1	544	GO:0006464,GO:0006519,GO:0005794,GO:005886,GO:0005488,GO:0003824,GO:000815	process,cellular amino acid and derivative metabolic process,metabolic process	Golgi apparatus,plasma membrane	binding,catalytic activity
ug0774_2	510	GO:0006464,GO:0006519,GO:0005794,GO:005886,GO:0005488,GO:0003824,GO:000815	process,cellular amino acid and derivative metabolic process,metabolic process	Golgi apparatus,plasma membrane	binding,catalytic activity
ug0775	545	GO:0005623,GO:0006950,GO:0006259,GO:0	response to stress,DNA metabolic process	cell	DNA binding
ug0776	771				
ug0777	902	GO:0030528,GO:0016043,GO:0006350,GO:0	cellular component organization,transcription	nucleoplasm	transcription regulator activity
ug0778	1135				
ug0779	600	GO:0005886		plasma membrane	
ug0780	811				
ug0781	460				
ug0782	1085				
ug0783_1	812				
ug0783_2	734				
ug0784	486	GO:0005515,GO:0005635,GO:0008219,GO:0016020,GO:0007165,GO:0006950,GO:000960	cell death,signal transduction,response to stress,response to biotic stimulus	nuclear envelope,membrane,endoplasmic reticulum	protein binding
ug0785	566	GO:0005515,GO:0005635,GO:0008219,GO:0016020,GO:0007165,GO:0006950,GO:000960	cell death,signal transduction,response to stress,response to biotic stimulus	nuclear envelope,membrane,endoplasmic reticulum	protein binding
ug0786_1	257				
ug0786_2	870				
ug0787	553				
ug0788	684	GO:0005634,GO:0000003,GO:0009791	reproduction,post-embryonic development	nucleus	
ug0789	848	GO:0006139,GO:0009058,GO:0016301	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process		kinase activity
ug0790	564	GO:0005623,GO:0016020,GO:0005737		cell,membrane,cytoplasm	
ug0791	827				
ug0792	738	GO:0005730,GO:0005622,GO:0009987	cellular process	nucleolus,intracellular	
ug0793	559	GO:0016020,GO:0005739,GO:0006091,GO:0	generation of precursor metabolites and energy,transport	membrane,mitochondrion	
ug0794_1	920				
ug0794_2	270				
ug0795	926				
ug0796	1025	GO:0005488,GO:0005			binding,protein binding
ug0797	564				
ug0798	570	GO:0000166,GO:0006	response to stress		nucleotide binding
ug0799	445				
ug0800	810	GO:0016020,GO:0007	signal transduction	membrane	
ug0801	555				
ug0802	906	GO:0019725,GO:0003824,GO:0008152,GO:0	cellular homeostasis,metabolic process	plastid	catalytic activity
ug0803	488				
ug0804	973	GO:0003677,GO:0003700,GO:0005634,GO:0	transcription	nucleus	DNA binding,transcription factor activity
ug0805	967	GO:0005886,GO:0016787,GO:0008152	metabolic process	plasma membrane	hydrolase activity
ug0806	503	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0807	1015	GO:0005488,GO:0008152,GO:0003824,GO:0003674,GO:0005739,G	metabolic process	mitochondrion	binding,catalytic activity,molecular_function,oxygen binding
ug0808_1	696				
ug0808_2	916	GO:0006810,GO:0009987,GO:0016020,GO:0	transport,cellular process	membrane,endosome	
ug0809	546				
ug0810	619				
ug0811	599	GO:0016020,GO:0009579,GO:0006810,GO:0006091,GO:0015979,GO:0006464,GO:0005488,GO:0009607,GO:0007165,GO:0006950,GO:0009628,GO:0030234	transport,generation of precursor metabolites and energy,photosynthesis,protein modification process response to biotic stimulus,signal transduction,response to stress,response to abiotic stimulus	membrane,thylakoid,plastid	binding
ug0812_1	879				enzyme regulator activity
ug0812_2	855				
ug0813	888	GO:0019538,GO:0009987,GO:0016020	protein metabolic process,cellular process	membrane	
ug0814	350				
ug0815	781	GO:0005856,GO:0003774,GO:0009987	cellular process	cytoskeleton	motor activity
ug0816_1	675	GO:0005739		mitochondrion	
ug0816_2	898				
ug0817	696	GO:0005886,GO:0005802,GO:0005737		plasma membrane,vacuole cytoplasm	
ug0818	802				
ug0819	269				
ug0820	379				
ug0821	920	GO:0005622,GO:0003920,GO:0008219,GO:0005515,GO:0006464	cell death,protein modification process	intracellular	DNA binding protein binding
ug0822_1	1111				
ug0822_2	843	GO:0005623		cell	
ug0823	750				
ug0824	594	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug0825	784	GO:0005737,GO:0006722,GO:0005737	response to stress	cytoplasm cytoplasm	
ug0826_1	1115	GO:0016020,GO:0005215,GO:0006810	transport	membrane	transporter activity
ug0826_2	1115				
ug0827	746	GO:0019725,GO:0003674,GO:0003824	cellular homeostasis		molecular_function,catalytic activity
ug0828	402				
ug0829	716	GO:0009056,GO:0006519,GO:0003824,GO:000166,GO:0005488,GO:0005737,GO:000573	catabolic process,cellular amino acid and derivative metabolic process	cytoplasm,mitochondrion	catalytic activity,nucleotide binding,protein binding
ug0830	959				
ug0831	550				
ug0832	717	GO:0006412,GO:0008135	translation		translation factor activity, nucleic acid binding
ug0833	628	GO:0005623,GO:00051166		cell,mitochondrion	
ug0834	1166				
ug0835	733	GO:0005198,GO:0005840,GO:0006412	translation	ribosome	structural molecule activity
ug0836	699	GO:0005198,GO:0005840,GO:0006412	translation	ribosome	structural molecule activity
ug0837	799	GO:0016020,GO:0009579,GO:0009536		membrane,thylakoid,plastid	
ug0838_1	875				
ug0838_2	613				
ug0839	848				
ug0840	546	GO:0005840,GO:0005198,GO:0005488,GO:0005886,GO:0005956,GO:0016787	translation protein metabolic process,catabolic process	ribosome plasma membrane	structural molecule activity,protein binding receptor binding
ug0841	593				
ug0842	526				hydrolase activity
ug0843	596	GO:0005739		mitochondrion	
ug0844	963	GO:0005618,GO:0005515,GO:0005886,GO:0009536,GO:0005634,GO:0007165,GO:000971	signal transduction,response to endogenous stimulus	cell wall,plasma membrane,plastid,nucleus	protein binding
ug0845	119				
ug0846	642				
ug0847	896	GO:0005634,GO:0003920,GO:0006091,GO:0005975,GO:0009056,GO:0003824	generation of precursor metabolites and energy,carbohydrate metabolic process,catabolic process	nucleus	DNA binding
ug0848_1	775				catalytic activity
ug0848_2	667				
ug0849_1	851	GO:0003824,GO:0009058,GO:0006519	biosynthetic process,cellular amino acid and derivative metabolic		catalytic activity

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0849_2	796	GO:0003824,GO:0009058,GO:0009987,GO:0006629,GO:0019748	biosynthetic process,cellular process,lipid metabolic process,secondary metabolic		catalytic activity
ug0850	982	GO:0006950	response to stress		
ug0851	567	GO:0005623,GO:0016787,GO:0006629	lipid metabolic process	cell	hydrolase activity
ug0852	812				
ug0853	568	GO:0005488			binding
ug0854	822	GO:0009536		plastid	
ug0855	620	GO:0019725,GO:0003	cellular homeostasis		catalytic activity
ug0856	707	GO:0005739,GO:0006950,GO:0016020	response to stress	mitochondrion,membrane	
ug0857	396				
ug0858	1043				
ug0859	697				
ug0860_1	909				
ug0860_2	667	GO:0016740,GO:0005829,GO:0003824,GO:0005488,GO:0006091,GO:0005975,GO:000905	generation of precursor metabolites and energy,carbohydrate metabolic process,catabolic process	cytosol	transferase activity,catalytic activity,binding
ug0861	870				
ug0862	1134	GO:0005488			binding
ug0863	902	GO:0005215,GO:0006	transport		transporter activity
ug0864	513				
ug0865	543	GO:0016740			transferase activity
ug0866	801				
ug0867	732	GO:0006950,GO:0009058,GO:0006519,GO:0019748	response to stress,biosynthetic process,cellular amino acid and derivative metabolic process,secondary metabolic		
ug0868	844				
ug0869	929	GO:0005576,GO:0016043,GO:0009987,GO:000	cellular component organization,cellular process	extracellular region,membrane	
ug0870	1336	GO:0000166,GO:0009GO:0005840,GO:0019		plastid	nucleotide binding
ug0871_1	884	538,GO:0009987,GO:0005783,GO:0005198,GO:0005737,GO:0005488,GO:0000166,GO:000	protein metabolic process,cellular process,translation	ribosome,endoplasmic reticulum,cytoplasm	structural molecule activity,binding,nucleotide binding,protein binding
ug0871_2	569				
ug0872	842	GO:0005198,GO:0005840,GO:0006412	translation	ribosome	structural molecule activity
ug0873	932	GO:0000166,GO:0005794,GO:0006810,GO:0009987,GO:0006464,GO:0009536,GO:000716GO:0005215,GO:0016020,GO:0005739,GO:0006950,GO:0009628,GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:0016787,GO:0019725,GO:0006	transport,cellular process,protein modification process,signal transduction	Golgi apparatus,plastid	nucleotide binding,transporter activity
ug0874	621	GO:0005215,GO:0016020,GO:0005739,GO:0006950,GO:0009628,GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:0016787,GO:0019725,GO:0006	response to stress,response to abiotic stimulus,transport,biosynthetic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic cellular homeostasis,generation of	membrane,mitochondrion	transporter activity,hydrolase activity
ug0875	631	GO:0005737,GO:0003674,GO:0003824,GO:0016020,GO:0006810,GO:0006	precursor metabolites and energy,transport	cytoplasm	molecular_function,catalytic activity
ug0876_1	452	GO:0016020,GO:0006810,GO:0005215	transport	membrane	transporter activity
ug0876_2	1130	GO:0019538,GO:0009987,GO:0005515,GO:000166,GO:0006950	protein metabolic process,cellular process,response to stress		protein binding,nucleotide binding
ug0877_1	871	GO:0006810,GO:0016020,GO:0005215	transport	membrane	transporter activity
ug0877_2	1061	GO:0005198,GO:0005840,GO:0006412,GO:0	translation	ribosome	structural molecule activity,RNA binding
ug0878	669	GO:0005623		cell	
ug0879	430				
ug0880	591	GO:0005488,GO:0009058,GO:0006519,GO:0	biosynthetic process,cellular amino acid and derivative metabolic		binding,catalytic activity
ug0881	622				
ug0882	689	GO:0005739,GO:0016020,GO:0005622		mitochondrion,membrane,intracellular	
ug0883	841				
ug0884	576				
ug0885_1	1116				
ug0885_2	888	GO:0006091,GO:0015979,GO:0016020,GO:0009579,GO:0005488,GO:0006464,GO:000953GO:0008152,GO:0003824,GO:0005488	generation of precursor metabolites and energy,photosynthesis,protein modification process	membrane,thylakoid,plastid	binding
ug0886	1173		metabolic process		catalytic activity,binding

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0887	635	GO:0016787,GO:0005575,GO:0019538,GO:0009056,GO:0000166,GO:0005634,GO:000582	protein metabolic process,catabolic process	cellular_component,nucleus,cytosol	hydrolase activity,nucleotide binding
ug0888	372	GO:0016787,GO:0019538,GO:0009056,GO:0009987,GO:0005634	protein metabolic process,catabolic process,cellular process	nucleus	hydrolase activity
ug0890	642	GO:0005515,GO:0005812		intracellular	protein binding
ug0891	812	GO:0019725,GO:0003824,GO:0005488,GO:0005886,GO:0006006,GO:0005730,GO:0005198,GO:0000003,GO:0009791,GO:0009790,GO:0005840,GO:0005829,GO:0006412,GO:000806	cellular homeostasis,transport		catalytic activity,binding
ug0892	456	GO:0019725,GO:0003824,GO:0005488,GO:0005886,GO:0006006,GO:0005730,GO:0005198,GO:0000003,GO:0009791,GO:0009790,GO:0005840,GO:0005829,GO:0006412,GO:000806	response to stress	plasma membrane	
ug0893	971	GO:0005886,GO:0006006,GO:0005730,GO:0005198,GO:0000003,GO:0009791,GO:0009790,GO:0005840,GO:0005829,GO:0006412,GO:000806	reproduction,post-embryonic development,embryonic development,translation	nucleolus,ribosome,cytosol,mitochondrion	structural molecule activity
ug0894_1	772	GO:0005840,GO:0005829,GO:0006412,GO:000806			
ug0894_2	806	GO:0005739,GO:0009807,GO:0006810	transport	mitochondrion,plastid	
ug0895	586	GO:0005739,GO:0009807,GO:0006810			
ug0896	807	GO:0006810	transport		
ug0897	647				
ug0898	694				
ug0899	126				
ug0900	812	GO:0003824,GO:0016740,GO:0009058,GO:0009987,GO:0005515,GO:0005488,GO:0009536,GO:0005634,GO:0005737,GO:0005739,GO:000999	biosynthetic process,cellular process,catabolic process,cellular amino acid and derivative metabolic process	plastid,nucleus,cytoplasm,mitochondrion	catalytic activity,transferase activity,protein binding,protein binding
ug0901	999				
ug0902	729				
ug0903	991	GO:0019725,GO:0005488,GO:0005886	cellular homeostasis	plasma membrane	binding
ug0904	526				
ug0905	604	GO:0016740,GO:0003824,GO:0006350,GO:0005634,GO:0005488	transcription	nucleus	transferase activity,DNA binding,protein binding
ug0906	697				
ug0907	580				
ug0908	1006	GO:0006810,GO:000999	transport,cellular process		
ug0909	1226	GO:0005576,GO:000999		extracellular region,plastid	
ug0910	1118	GO:0016787,GO:000999		plastid	hydrolase activity
ug0911	798				
ug0912	1236	GO:0005488,GO:0008152,GO:0003824,GO:0003674,GO:0006950	metabolic process,response to stress		binding,catalytic activity,molecular_function
ug0913	614				
ug0914	308	GO:0003824,GO:0006810,GO:0016020,GO:0006091,GO:0005739	transport,generation of precursor metabolites and energy	membrane,mitochondrion	catalytic activity
ug0915	1152	GO:0003824,GO:000818	metabolic process		catalytic activity
ug0916	818	GO:0005622		intracellular	
ug0917	682	GO:0016787,GO:0003824,GO:0000166,GO:0008135,GO:0006412	translation		hydrolase activity,RNA binding,nucleotide binding,translation factor activity, nucleic acid binding
ug0918	1007	GO:0005198,GO:0005840,GO:0006412,GO:0006091,GO:0016787,GO:0003824,GO:0000166,GO:0008135,GO:0006412	translation	ribosome	structural molecule activity
ug0919	993	GO:0005622,GO:0003824,GO:0005488,GO:0006810,GO:0005739,GO:0009058,GO:0005975,GO:0015979,GO:0016301,GO:0005739,GO:0009579,GO:0000166,GO:0006091,GO:0009056,GO:0009536,GO:0005488,GO:0005155,GO:0005215,GO:0016020,GO:0005739,GO:0006810,GO:001604	generation of precursor metabolites and energy,transport	membrane,intracellular,mitochondrion	catalytic activity,protein binding
ug0920	1035	GO:0005622,GO:0003824,GO:0005488,GO:0006810,GO:0005739,GO:0009058,GO:0005975,GO:0015979,GO:0016301,GO:0005739,GO:0009579,GO:0000166,GO:0006091,GO:0009056,GO:0009536,GO:0005488,GO:0005155,GO:0005215,GO:0016020,GO:0005739,GO:0006810,GO:001604	biosynthetic process,carbohydrate metabolic process,photosynthesis,generation of precursor metabolites and energy,catabolic process,biological process	mitochondrion,thylakoid,plastid,membrane	kinase activity,nucleotide binding
ug0921	637	GO:0005155,GO:0005215,GO:0016020,GO:0005739,GO:0006810,GO:001604	transport,cellular component organization,cellular process	membrane,mitochondrion	binding,protein binding,transporter activity
ug0922	1212	GO:0008135,GO:0016787,GO:0000166			translation factor activity, nucleic acid binding,hydrolase activity, nucleic acid binding
ug0923	782	GO:0006412,GO:0008135	translation		translation factor activity, nucleic acid binding
ug0924	728	GO:0019538,GO:000999,GO:0009987,GO:0005634,GO:000582	protein metabolic process,catabolic process,cellular process		protein binding

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0925	906	GO:0016787,GO:0005886,GO:0019538,GO:009987,GO:0009056,G	protein metabolic process,cellular process,catabolic process	plasma membrane,endoplasmic reticulum	hydrolase activity
ug0926	871	GO:0016020,GO:0009579,GO:0009536		membrane,thylakoid,plastid	
ug0927	1005	GO:0004872,GO:0005488,GO:0009987,GO:016020,GO:0005783,G	cellular process,transport	membrane,endoplasmic reticulum,mitochondrion	receptor activity,binding
ug0928	1541	O:0005739,GO:000681GO:0016020,GO:0005215,GO:0006810,GO:0	transport,cellular process	membrane	transporter activity
ug0929	847	GO:0016020,GO:0009579,GO:0009536,GO:0	photosynthesis	membrane,thylakoid,plastid	
ug0930	935				
ug0931	711				
ug0932	193				
ug0933	568	GO:0000003,GO:0009791,GO:0007275,GO:0005634	reproduction,post-embryonic development,multicellular organismal development	nucleus	
ug0934_1	838	GO:0006464,GO:0019538,GO:0009056,GO:009987,GO:0003824	protein modification process,protein metabolic process,catabolic process,cellular		catalytic activity
ug0934_2	878				
ug0935	1199	GO:0016787,GO:0016020,GO:0005215,GO:0005737,GO:0006	transport	membrane	hydrolase activity,transporter activity
ug0936	594	GO:0009058,GO:00016301,GO:0000166,G	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process	cytoplasm	kinase activity,nucleotide binding,binding
ug0937	690				
ug0938_1	627	GO:0005515			protein binding
ug0938_2	490				
ug0939	625	GO:0003824,GO:0008152,GO:0009058,GO:0009987,GO:0009536,G	metabolic process,biosynthetic process,cellular process,photosynthesis	plastid	catalytic activity
ug0940	910	GO:0005488,GO:0003824,GO:0008152,GO:0009058,GO:0009987,G	metabolic process,biosynthetic process,cellular process,photosynthesis	plastid	binding,catalytic activity
ug0941	850	O:0009536,GO:001597GO:0009058,GO:000987,GO:0005488,GO:0009536,GO:0003824	biosynthetic process,cellular process	plastid	binding,catalytic activity
ug0942_1	685				
ug0942_2	796	GO:0005215,GO:0006810,GO:0009058,GO:0006091,GO:0006139,G	transport,biosynthetic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane	transporter activity,hydrolase activity
ug0943	570				
ug0944	721	GO:0005515,GO:0005005198,GO:0005840,GO:0006412	translation	intracellular ribosome	protein binding structural molecule activity
ug0945_1	715	GO:0004872,GO:0005515,GO:0005215,GO:0006810,GO:0009987,G	transport,cellular process	membrane,mitochondrion	receptor activity,protein binding,transporter activity
ug0945_2	516	O:0016020,GO:000573			
ug0946	834				
ug0947	802				
ug0948	1057	GO:0005886,GO:0005791		plasma membrane	binding
ug0949_1	791				
ug0949_2	807	GO:0005488			binding
ug0950	971				
ug0951	657	GO:0005654,GO:0006350,GO:0016740,GO:0003677,GO:0005515	transcription	nucleoplasm	transferase activity,DNA binding,protein binding
ug0952	465	GO:0005737,GO:0005739,GO:0016020,GO:0		cytoplasm,mitochondrion,membrane, intracellular	
ug0953	711	GO:0019538,GO:0009987,GO:0003824	protein metabolic process,cellular process		catalytic activity
ug0954_1	313				
ug0954_2	680	GO:0005773		vacuole	
ug0955	709	GO:0005488,GO:0005897		intracellular	binding
ug0956	897				
ug0957_1	648	GO:0007165,GO:0009719,GO:0005634,GO:0	signal transduction,response to endogenous stimulus,transcription	nucleus	
ug0957_2	390				
ug0958	1145				
ug0959	449	GO:0016020,GO:0009844,GO:0005622,GO:0006810,GO:0005215	transport	membrane,plastid intracellular	transporter activity
ug0960	844				



Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug0961_1	941	GO:0016020,GO:0009579,GO:0009536,GO:004872,GO:0005739		membrane,thylakoid,plastid,mitochondrion	receptor activity
ug0961_2	1022	GO:0005737		cytoplasm	
ug0962	772	GO:0008152,GO:0005488,GO:0003824,GO:0005730,GO:0005198,GO:0005840,GO:0005829,GO:0006412,GO:0006950,GO:0008152,GO:0003824,GO:00008152,GO:0009536,GO:0005829,GO:0005730	metabolic process	plastid	binding,catalytic activity
ug0963	566				
ug0964	377	GO:0005730,GO:0005198,GO:0005840,GO:0005829,GO:0006412,GO:0006950,GO:0008152,GO:0003824,GO:00008152,GO:0009536,GO:0005829,GO:0005730	translation	nucleolus,ribosome,cytosol,mitochondrion	structural molecule activity
ug0965	959	GO:0008152,GO:0009536,GO:0005829,GO:0005730	stress,biological_process,metabolic process,response to abiotic stimulus	plastid,cytosol,mitochondrion	catalytic activity
ug0966	949	GO:0006810,GO:0000166,GO:0007165,GO:0019538,GO:000987,GO:0005515,GO:0005737,GO:0000166,GO:0005737,GO:0003824,GO:0006519,GO:0019748,GO:0009058,GO:0009056	transport,signal transduction		nucleotide binding
ug0967_1	1052	GO:0005515,GO:0005737,GO:0000166,GO:0005737,GO:0003824,GO:0006519,GO:0019748,GO:0009058,GO:0009056	protein metabolic process,cellular process,response to stress	cytoplasm	protein binding,nucleotide binding
ug0967_2	723				
ug0968_1	441	GO:0005737,GO:0003824,GO:0006519,GO:0019748,GO:0009058,GO:0009056	cellular amino acid and derivative metabolic process,secondary metabolic process,biosynthetic process,catabolic process	cytoplasm	catalytic activity
ug0968_2	1032				
ug0969	612				
ug0970	854				
ug0971	791				
ug0972	871				
ug0973	770	GO:0003676,GO:00050008152,GO:0005739,GO:0003824	metabolic process	intracellular mitochondrion	nucleic acid binding catalytic activity
ug0974	1017				
ug0975	453	GO:0009058,GO:000987,GO:0019748,GO:0019538,GO:000987,GO:0005737,GO:0003824,GO:0005634,GO:0008289,GO:0030234,GO:0007165,GO:0005840,GO:0005198,GO:0006412	biosynthetic process,cellular process,secondary metabolic process,cell cycle	cytoplasm,nucleus	catalytic activity
ug0976	784				
ug0977	911	GO:0008289,GO:0030234,GO:0007165,GO:0005840,GO:0005198,GO:0006412	signal transduction	membrane	lipid binding,enzyme regulator activity
ug0978	654	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug0979	322				
ug0980	994	GO:0006139,GO:0009058,GO:0016740	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process		transferase activity
ug0981	572				
ug0982	786				
ug0983	890	GO:0019725,GO:000674,GO:0003824,GO:0008152,GO:0009536	cellular homeostasis,metabolic process	plastid	molecular_function,catalytic activity
ug0984	1013				
ug0985	715	GO:0005737,GO:000791,GO:0016020,GO:0005635,GO:0005515,GO:0016043,GO:000704,GO:0005886,GO:000674,GO:0003824,GO:0005215,GO:0016020,GO:0005840,GO:0005198,GO:0006412	post-embryonic development,cellular component organization,cell cycle	cytoplasm,membrane,nuclear envelope	protein binding
ug0986	776				
ug0987	481	GO:0016020,GO:0005840,GO:0005198,GO:0006412		plasma membrane,membrane,mitochondrion	molecular_function,catalytic activity,transporter activity
ug0988	807	GO:0000166,GO:0003824,GO:0005737,GO:0005730		membrane,mitochondrion	nucleotide binding,RNA
ug0989_1	1007				
ug0989_2	771	GO:0019725,GO:000674,GO:0003824,GO:0009719,GO:000165,GO:0005576,GO:0005618,GO:0004872,GO:0003674,GO:000548,GO:0003723,GO:0016740,GO:0006139	cellular homeostasis,metabolic process		molecular_function,catalytic activity
ug0990	866				
ug0991	598	GO:0003723,GO:0016740,GO:0006139	response to endogenous stimulus,signal transduction	extracellular region,cell wall	receptor activity,molecular_function,binding
ug0992	1082	GO:0006810,GO:0000166,GO:0007165	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		RNA binding,transferase activity
ug0993	1098	GO:0016787	transport,signal transduction		nucleotide binding
ug0994	670	GO:0005488,GO:000674,GO:0005739,GO:0005730,GO:0005730,GO:0005730		mitochondrion,plastid	binding,molecular_function
ug0995	510	GO:0005840,GO:0005829,GO:0006412,GO:0005730	translation	nucleolus,ribosome,cytosol,mitochondrion	structural molecule activity
ug0996	809				



Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1029	787	GO:0005488,GO:0005886,GO:0003824		plasma membrane	binding,catalytic activity
ug1030	571	GO:0016787,GO:0000166			hydrolase activity,nucleotide binding
ug1031	588	GO:0016020		membrane	
ug1032_1	1119	GO:0006464,GO:0005737,GO:0000166,GO:0007165,GO:0016301,GO:0016787,GO:0005	protein modification process,signal transduction	cytoplasm,mitochondrion	nucleotide binding,kinase activity
ug1032_2	897	GO:0008152,GO:0009987,GO:0005488	metabolic process,cellular process	cytoplasm	hydrolase activity,binding
ug1033	675	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1034	506	GO:0008152,GO:0003824,GO:0005488	metabolic process		catalytic activity,binding
ug1035	941	GO:0005488			binding
ug1036	460	GO:0016020,GO:0005777,GO:0016043,GO:0	cellular component organization,cellular process	membrane,peroxisome	
ug1037	470	GO:0016020		membrane	
ug1038	787				
ug1039	507				
ug1040	799	GO:0016043,GO:0009987,GO:0005777,GO:0005739,GO:0005488,G	cellular component organization,cellular process	peroxisome,mitochondrion,plastid	binding
ug1041	774				
ug1042	865	GO:0005622,GO:0005886,GO:0019538,GO:0009056,GO:0009987,GO:0005634,GO:0005829,GO:0005576,GO:001	protein metabolic process,catabolic process,cellular process	intracellular,plasma membrane,nucleus,cytoplasm,extracellular region	hydrolase activity
ug1043_1	581	GO:0003824,GO:0006	translation		catalytic activity
ug1043_2	785	GO:0019538,GO:0009056,GO:0016787	protein metabolic process,catabolic process		hydrolase activity
ug1044	732	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1045	778	GO:0005623		cell	
ug1046	962	GO:0019725,GO:0003824,GO:0005488,GO:0006810,GO:0009536	cellular homeostasis,transport	plastid	catalytic activity,binding
ug1047	513	GO:0019725,GO:0005488,GO:0008152,GO:0003824,GO:0009536,G	cellular homeostasis,metabolic process,transport	plastid	binding,catalytic activity
ug1048	479				
ug1049_1	719	GO:0005886		plasma membrane	
ug1049_2	593	GO:0005856,GO:0005737,GO:0000166,GO:00016020,GO:0005622,GO:0005215,GO:0	transport,biosynthetic process,generation of precursor	cytoskeleton,cytoplasm	nucleotide binding,protein binding
ug1050	572	GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:001	metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane,intracellular,mitochondrion	transporter activity,hydrolase activity
ug1051_1	492	GO:0005975,GO:0009987,GO:0016787,GO:0005576,GO:0005618,G	carbohydrate metabolic process,cellular process	extracellular region,cell wall	hydrolase activity,transferase activity
ug1051_2	436	GO:0005975,GO:0009987,GO:0016787,GO:0005576,GO:0005618,G	carbohydrate metabolic process,cellular process	extracellular region,cell wall	hydrolase activity,transferase activity
ug1052	835				
ug1053	583	GO:0005975,GO:0009987,GO:0016787,GO:0005576,GO:0005618,G	carbohydrate metabolic process,cellular process	extracellular region,cell wall	hydrolase activity,transferase activity
ug1054	868	GO:0006412,GO:0008135	translation		translation factor activity, nucleic acid binding
ug1055	750	GO:0005488,GO:0005		intracellular	binding
ug1056	480				
ug1057	893	GO:0030246,GO:0007267,GO:0003677,GO:0006810,GO:0005886	cell-cell signaling,transport	plasma membrane	carbohydrate binding,DNA binding
ug1058	527	GO:0005773,GO:0005515,GO:0009536,GO:00009058,GO:0009		vacuole,plastid,plasma membrane	protein binding
ug1059	814	GO:0009058,GO:0009987,GO:0006629,GO:0005215,GO:0005488,G	biosynthetic process,cellular process,lipid metabolic process	plastid	transporter activity,binding
ug1060	592				
ug1061	899	GO:0005737,GO:0008135,GO:0000166,GO:0008152,GO:0006412,GO:0016787,GO:0030528	metabolic process,translation	cytoplasm	translation factor activity, nucleic acid binding,nucleotide binding,hydrolase activity,transcription
ug1062	671				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1063	337	GO:0016020,GO:0009536,GO:0006091,GO:0	generation of precursor metabolites and energy,photosynthesis	membrane,plastid	
ug1064_1	641				
ug1064_2	814	GO:0003824,GO:0008380	metabolic process		catalytic activity
ug1065	380				
ug1066	1221	GO:0005783,GO:0006810,GO:0009987,GO:0	transport,cellular process	endoplasmic reticulum,plasma membrane	
ug1067	926	GO:0005198			structural molecule activity
ug1068	425	GO:0005773		vacuole	
		GO:0000003,GO:0009791,GO:0009790,GO:0008152,GO:0009987,GO:0007275,GO:000372	reproduction,post-embryonic development,embryonic development,metabolic process,cellular		
ug1069	553	3,GO:0006950,GO:0009607,GO:0030154,GO:0009653,GO:0004518,GO:0009719,GO:0005515,GO:0009628,GO:0006810,GO:000987,GO:0000166,GO:0005515,GO:0007165,GO:0005634,GO:001678	process,multicellular organismal development,response to stress,response to biotic stimulus,cell differentiation,anatomical structure	cytoplasm,nucleus	RNA binding,nuclease activity,protein binding
ug1070	1002		transport,cellular process,signal transduction	nucleus	nucleotide binding,protein binding,hydrolase activity
ug1071	370				
ug1072	665	GO:0016740,GO:000958,GO:0005975,GO:0	biosynthetic process,carbohydrate metabolic process,cellular process		transferase activity
ug1073	187				
ug1074	453	GO:0005488,GO:0003908			binding,catalytic activity hydrolase activity
ug1075	908	GO:0016787			
ug1076	287				
ug1077	721	GO:0019725,GO:0006091,GO:0005737,GO:0003674,GO:0003824,GO:0005198,GO:0005	cellular homeostasis,generation of precursor metabolites and energy,transport	cytoplasm	molecular_function,catalytic activity
ug1078	454	840,GO:0009536,GO:0006412,GO:0003723	translation	ribosome,plastid	structural molecule activity,RNA binding
ug1079	494	215,GO:0016020,GO:0006810,GO:0009987	transport,cellular process	membrane	protein binding,transporter activity
ug1080	900	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1081	210				
ug1082	1194	GO:0005488			binding
ug1083	837	GO:0005515			protein binding
		GO:0005515,GO:0005215,GO:0009536,GO:0005773,GO:0016020,GO:0005739,GO:000588	transport	plastid,vacuole,membrane,mitochondrion,plasma membrane	protein binding,transporter activity
ug1084_1	1082				
ug1084_2	456	987,GO:0009056,GO:00030246,GO:0005975	cellular process,catabolic process,carbohydrate metabolic process		hydrolase activity,carbohydrate binding
ug1085	522	GO:0005488,GO:000958,GO:0006629,GO:0003824,GO:0009987,GO:0005737,GO:0006810,GO:0009987,GO:0005739,GO:000588	biosynthetic process,lipid metabolic process,cellular process	membrane	binding,catalytic activity
ug1086_1	274				
ug1086_2	688				
ug1087	664				
ug1088	593	GO:0016740,GO:000958,GO:0007165,GO:0006950,GO:0009628,GO:0009605,GO:0009719,GO:0000003,GO:0009791,GO:0005488,GO:0008150	biosynthetic process signal transduction,response to stress,response to abiotic stimulus,response to external stimulus,response to endogenous stimulus,reproduction,post-embryonic		transferase activity
ug1089	911				binding
ug1090	930				
ug1091	545				
ug1092	901	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1093	408				
ug1094	547				
ug1095_1	498				
ug1095_2	1195				
ug1096	1124	GO:0005737,GO:0006810,GO:0009058,GO:0	biosynthetic process,cellular amino acid and derivative metabolic	cytoplasm	transferase activity
ug1097	1081				
ug1098	874	GO:0006412,GO:0008135	translation		translation factor activity, nucleic acid binding
ug1099	625	GO:0005773,GO:0005515,GO:0005886		vacuole,plasma membrane	protein binding
ug1100_1	306	GO:0000166,GO:0003676			nucleotide binding,nucleic acid binding

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1100_2	1379	GO:0006810,GO:0005215,GO:0016020,GO:0	transport	membrane,mitochondrion	transporter activity
ug1101	806				
ug1102	838				
ug1103	651	GO:0016020,GO:0005622,GO:0005215,GO:0005739,GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:000	transport,biosynthetic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane,intracellular,mitochondrion	transporter activity,nucleotide binding,hydrolase activity
ug1104	568				
ug1105	776	GO:0009536,GO:0016		plastid,membrane	
ug1106	772				
ug1107	806				
ug1108	591				
ug1109	420				
ug1110	868	GO:0005623,GO:0005		cell,cytoplasm	
ug1111	286				
ug1112	1288	GO:0019725,GO:0005783,GO:0003824,GO:0009536,GO:0006950,GO:0008150,GO:0	cellular homeostasis response to stress,biological_process,generatio	endoplasmic reticulum	catalytic activity
ug1113	957	006091,GO:0005975,GO:0009056,GO:0003824,GO:0005739	n of precursor metabolites and energy,carbohydrate metabolic process,catabolic process	plastid,mitochondrion	catalytic activity
ug1114	364				
ug1115_1	570	GO:0005576,GO:0006950,GO:0005515,GO:0005618,GO:0016020	response to stress	extracellular region,cell wall,membrane	protein binding
ug1115_2	868				
ug1116	863	GO:0005488			binding
ug1117	975	GO:0005840,GO:0005198,GO:0009987,GO:0009536,GO:0006412,GO:0005623,GO:0003	cellular process,translation	ribosome,plastid	structural molecule activity,RNA binding
ug1118	578	824,GO:0008152,GO:0005618,GO:0000166	metabolic process	cell,cell wall	catalytic activity,nucleotide binding
ug1119	604				
ug1120	820	GO:0006350	transcription		
ug1121	525	GO:0005622		intracellular	
ug1122	581				
ug1123	911	GO:0016020,GO:0009536,GO:0006091,GO:0	generation of precursor metabolites and energy,photosynthesis	membrane,plastid	
ug1124	644	GO:0016301,GO:0005975,GO:0009987	carbohydrate metabolic process,cellular process		kinase activity
ug1125	440				
ug1126	685				
ug1127	650	GO:0005488,GO:0008152,GO:0003824	metabolic process		binding,catalytic activity
ug1128_1	456				
ug1128_2	825	GO:0016043,GO:0009987,GO:0005737,GO:0005515,GO:0005856	cellular component organization,cellular process	cytoplasm,cytoskeleton	protein binding
ug1129	688	GO:0019538,GO:0009536,GO:0016787,GO:0000166,GO:0005	protein metabolic process,catabolic process		hydrolase activity
ug1130_1	990	794,GO:0006810,GO:0009987,GO:0005783	transport,cellular process	Golgi apparatus,endoplasmic reticulum	nucleotide binding
ug1130_2	542				
ug1131	991				
ug1132	892	GO:0005975,GO:0016020,GO:0005515,GO:0006	carbohydrate metabolic process		hydrolase activity
ug1133	540	810,GO:0009987,GO:0005768,GO:0016020,GO:0006810,GO:0005	transport,cellular process	endosome,membrane	protein binding
ug1134	734	215,GO:0016020,GO:0005773,GO:0016787	transport	membrane,vacuole	transporter activity,hydrolase activity
ug1135	406				
ug1136_1	516				
ug1136_2	776				
ug1137_1	473				
ug1137_2	781	GO:0003676,GO:0000166,GO:0016787			nucleic acid binding,nucleotide
ug1138	477	GO:0005215,GO:0016020,GO:0006810,GO:0	transport,cellular process	membrane	transporter activity
ug1139	724	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1140	979				
ug1141	733				
ug1142_1	162				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1142_2	1022	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1143	747	GO:0005622,GO:0003677,GO:0016043,GO:009987,GO:0005634	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug1144	960	GO:0005840		ribosome	
ug1145	585	GO:0019538,GO:0009056,GO:0016787	protein metabolic process,catabolic process		hydrolase activity
ug1146_1	547	GO:0003824,GO:0005215,GO:0006091,GO:0005576	generation of precursor metabolites and energy	mitochondrion	catalytic activity,transporter activity
ug1146_2	867	GO:0005576		extracellular region	
ug1147	932	GO:0016020,GO:0005739,GO:0006091,GO:000678	generation of precursor metabolites and energy	membrane,mitochondrion	catalytic activity
ug1148	678				
ug1149_1	713	GO:0003676,GO:0005436		intracellular	nucleic acid binding
ug1149_2	436				
ug1150	400				
ug1151	881	GO:0005783		endoplasmic reticulum	
ug1152	489				
ug1153	735	GO:0005215,GO:0016020,GO:0006810,GO:009058,GO:0006091,GO:0006139,GO:0005773	transport,biosynthetic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane,vacuole	transporter activity
ug1154_1	666	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1154_2	880	GO:0007049,GO:0006259,GO:0009058,GO:0003677,GO:0005151,GO:0030234,GO:001630	cell cycle,DNA metabolic process,biosynthetic process		DNA binding,protein binding,enzyme regulator activity,kinase activity
ug1155	1060				
ug1156	413				
ug1157_1	942				
ug1157_2	869				
ug1158_1	791				
ug1158_2	635	GO:0016020,GO:0005570		membrane,intracellular	
ug1159	570				
ug1160	527				
ug1161_1	641	GO:0016787,GO:0006519	cellular amino acid and derivative metabolic process		hydrolase activity
ug1161_2	825	GO:0005737		cytoplasm	
ug1162_1	860	GO:0019538,GO:0009987,GO:0016020,GO:001164	protein metabolic process,cellular process	membrane	protein binding
ug1162_2	1164				
ug1163_1	909				
ug1163_2	823	GO:0000003,GO:0009791,GO:0009790	reproduction,post-embryonic development,embryonic		
ug1164	591	GO:0016787,GO:0005737,GO:0006629	lipid metabolic process	cytoplasm	hydrolase activity
ug1165_1	480	GO:0005198,GO:0009987,GO:0005840,GO:0005829,GO:0006412	cellular process,translation	ribosome,cytosol	structural molecule activity
ug1165_2	554	GO:0009536		plastid	
ug1166	908	GO:0005622,GO:0005886,GO:0019538,GO:0009056,GO:0009987,GO:0005634,GO:000582	protein metabolic process,catabolic process,cellular process	intracellular,plasma membrane,nucleus,cytosol	hydrolase activity
ug1167	725				
ug1168	916				
ug1169	903	GO:0003824			catalytic activity
ug1170	998				
ug1171	651				
ug1172	1000	GO:0016301,GO:0005634,GO:0005515,GO:0005622,GO:0005515,GO:0019538,GO:0009056,GO:0009987,GO:0003824,GO:0006464,GO:0006950,GO:000479	protein metabolic process,catabolic process,cellular process,protein modification process,response to stress,DNA metabolic process	nucleus,plastid	kinase activity,protein binding
ug1173	911	GO:0009056,GO:0009987,GO:0003824,GO:0006464,GO:0006950,GO:000479		intracellular	protein binding,catalytic activity
ug1174	479				
ug1175	414				
ug1176	1050	GO:0016740,GO:0005488,GO:0009058,GO:0006519,GO:0019748	biosynthetic process,cellular amino acid and derivative metabolic process,secondary metabolic		transferase activity,binding
ug1177_1	1242	GO:0005488,GO:0008152,GO:0003824,GO:000628	metabolic process		binding,catalytic activity,nucleotide binding
ug1177_2	628	GO:0009056	catabolic process		
ug1178	796				
ug1179_1	570				
ug1179_2	1085	GO:0008150,GO:0005488	biological_process	plasma membrane	

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1180_1	999	GO:0019725	cellular homeostasis		
ug1180_2	855	GO:0030528,GO:0005198,GO:0005840,GO:0006412	translation	ribosome	transcription regulator activity,structural molecule activity
ug1181	1136	GO:0005634,GO:0003676,GO:0005886		nucleus,plasma membrane	nucleic acid binding
ug1182	913				
ug1183	512				
ug1184	635	GO:0005618,GO:0005576,GO:0019538,GO:0009056,GO:0016787	protein metabolic process,catabolic process	cell wall,extracellular region	hydrolase activity
ug1185	1035				
ug1186	891	GO:0006810,GO:0005215,GO:0016020,GO:0005773,GO:0016787	transport	membrane,vacuole	transporter activity,hydrolase activity
ug1187	1047	GO:0005840,GO:0005739,GO:0005198,GO:0016740,GO:0009536,GO:0006412,GO:000372	translation	ribosome,mitochondrion,plastid	structural molecule activity,transferase activity,RNA binding
ug1188	767				
ug1189	926	GO:0000166,GO:0005794,GO:0006810,GO:0009987,GO:0006464,GO:0009536,GO:000716	transport,cellular process,protein modification process,signal transduction	Golgi apparatus,plastid	nucleotide binding,transporter activity
ug1190_1	763	GO:0016043,GO:000987,GO:0005737,GO:0005515,GO:0005856	cellular component organization,cellular process	cytoplasm,cytoskeleton	protein binding
ug1190_2	784				
ug1191	847	GO:0009719,GO:0007165,GO:0005576,GO:0005618,GO:0004872,GO:0003674,GO:000548	response to endogenous stimulus,signal transduction	extracellular region,cell wall	receptor activity,molecular_function,bi
ug1192_1	810	GO:0005198,GO:0006412	transport		structural molecule activity
ug1192_2	374				
ug1193_1	624				
ug1193_2	509	GO:0003676,GO:0005198		intracellular	nucleic acid binding
ug1194_1	532				
ug1194_2	715				
ug1195_1	1046	GO:0005737,GO:000987,GO:0006464,GO:0019538,GO:0009056,GO:0000166,GO:000382	cellular process,protein modification process,protein metabolic process,catabolic process	cytoplasm,nucleus	nucleotide binding,catalytic activity
ug1195_2	826	GO:0006950	response to stress		
ug1196	899	GO:0016020		membrane	
ug1197_1	857	GO:0005198			structural molecule activity
ug1197_2	953	GO:0005215,GO:0016020,GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:0016787,GO:0005773,GO:000	transport,biosynthetic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane,vacuole,plasma membrane	transporter activity,hydrolase activity
ug1198	611				
ug1199	893	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1200	795	GO:0006091,GO:0015979,GO:0016020,GO:0009579,GO:0005488,GO:0006464,GO:000953	generation of precursor metabolites and energy,photosynthesis,protein modification process	membrane,thylakoid,plastid	binding
ug1201	833	GO:0000166,GO:0003824			nucleotide binding,catalytic activity
ug1202	771	GO:0005730,GO:0005198,GO:0000003,GO:0009791,GO:0009790,GO:0005840,GO:0005829,GO:0006412,GO:000	reproduction,post-embryonic development,embryonic development,translation	nucleolus,ribosome,cytosol,mitochondrion	structural molecule activity
ug1203	627				
ug1204	435	GO:0005739,GO:0006091	generation of precursor metabolites and energy	mitochondrion	
ug1205	813	GO:0003723			RNA binding
ug1206	654				
ug1207	447	GO:0005198,GO:0005840,GO:0005829,GO:0006412,GO:0005739	translation	ribosome,cytosol,mitochondrion	structural molecule activity
ug1208	624				
ug1209	736	GO:0003824,GO:0005739,GO:0009058,GO:000	biosynthetic process,cellular process	mitochondrion	catalytic activity
ug1210	607	GO:0005886,GO:00050008150,GO:0005		plasma membrane	binding
ug1211	792	GO:0005488,GO:0005773,GO:0003824,GO:000	biological_process,carbohydrate metabolic process	vacuole,plasma membrane	binding,catalytic activity
ug1212	504	GO:0005829,GO:0005		cytosol,plasma membrane	

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1213	553	GO:0016787,GO:0008	metabolic process		hydrolase activity
		GO:0006810,GO:0006	transport,generation of precursor		
ug1214	541	091,GO:0006139,GO:0	metabolites and energy,nucleobase,	membrane,intracellular,thylakoid,pla	transporter activity
		009058,GO:0005215,G	nucleoside, nucleotide and nucleic	stid	
		O:0016020,GO:000562	acid metabolic process,biosynthetic		
		2,GO:0009579,GO:000	process		
ug1215	696				
ug1216	700				
ug1217	715				
ug1218	951				
ug1219	458				
ug1220	821	GO:0016043,GO:0009	cellular component		
		987,GO:0005737,GO:0	organization,cellular process	cytoplasm,cytoskeleton	protein binding
		005515,GO:0005856			
ug1221	829	GO:0030234			enzyme regulator activity
ug1222_1	911	GO:0003824,GO:0016	biosynthetic process,cellular	membrane,endoplasmic reticulum	catalytic activity
		020,GO:0005783,GO:0	process,lipid metabolic process		
		009058,GO:0009987,G			
ug1222_2	790				
		GO:0003674,GO:0005			
		488,GO:0003824,GO:0			
ug1223	942	006950,GO:0009628,G	response to stress,response to	cell wall,nucleus,extracellular region	molecular_function,binding,c
		O:0005618,GO:000016	abiotic stimulus,biosynthetic		atalytic activity,nucleotide
		6,GO:0009058,GO:000	process,cellular process		binding
		9987,GO:0005634,GO:			
		GO:0005622,GO:0003			
ug1224	1147	677,GO:0016043,GO:0	cellular component	intracellular,nucleus	DNA binding
		009987,GO:0005634	organization,cellular process		
ug1225	864	GO:0016020,GO:0009	photosynthesis	membrane,thylakoid,plastid	
		579,GO:0009536,GO:0			
ug1226	998				
ug1227	926	GO:0016740,GO:0003	transcription	nucleus	transferase activity,DNA
		677,GO:0006350,GO:0			binding
		GO:0016020,GO:0009			
ug1228_1	840	579,GO:0009536,GO:0	photosynthesis	membrane,thylakoid,plastid	
ug1228_2	785				
		GO:0009058,GO:0009	biosynthetic process,cellular		
ug1229	462	987,GO:0006629,GO:0	process,lipid metabolic	plastid	binding,catalytic activity
		005488,GO:0008152,G	process,metabolic process		
		O:0003824,GO:000953			
		GO:0006810,GO:0005			
ug1230	1036	886,GO:0000166,GO:0	transport,signal transduction	plasma membrane	nucleotide binding
ug1231	981	GO:0005488,GO:0009	metabolic process	plastid	binding,catalytic activity
		536,GO:0003824,GO:0			
ug1232	860				
		GO:0016787,GO:0005			
ug1233	932	737,GO:0008152,GO:0	metabolic process,cellular process	cytoplasm	hydrolase activity,binding
		009987,GO:0005488			
ug1234	677	GO:0005737,GO:0005	protein modification process	cytoplasm,nucleus	
		634,GO:0006464			
		GO:0009987,GO:0006	cellular process,lipid metabolic		
ug1235	471	629,GO:0005777,GO:0	process,reproduction,post-	peroxisome	molecular_function,catalytic
		003674,GO:0000003,G	embryonic development,embryonic		activity,nucleotide binding
		O:0009791,GO:000979	development,catabolic process		
		0,GO:0009056,GO:000			
ug1236	1098	GO:0009579,GO:0009		thylakoid,plastid	
ug1237_1	676	GO:0016020,GO:0005		membrane,mitochondrion	catalytic activity,transporter
		739,GO:0003824,GO:0			activity
ug1237_2	1524	GO:0005623,GO:0016		cell,membrane	
		GO:0019538,GO:0009	protein metabolic process,catabolic		
ug1238	945	056,GO:0009987,GO:0	process,cellular process,protein		catalytic activity
		006464,GO:0003824	modification process		
ug1239	920	GO:0005634,GO:0003		nucleus	DNA binding
ug1240	631	GO:0006950,GO:0009	response to stress,response to biotic		
		607,GO:0005576,GO:0	stimulus,metabolic process,cellular	extracellular region	hydrolase activity
		008152,GO:0009987,G	process		
ug1241	1163	GO:0006464,GO:0000	protein modification process		nucleotide binding,kinase
		166,GO:0016301			activity
		GO:0005515,GO:0005			
ug1242_1	602	215,GO:0006810,GO:0	transport,cellular component	membrane,mitochondrion,plastid	protein binding,transporter
		016043,GO:0009987,G	organization,cellular process		activity
		O:0016020,GO:000573			
		GO:0003824,GO:0003			
ug1242_2	863	674,GO:0005488,GO:0	transport,generation of precursor	membrane,thylakoid,plastid	catalytic
		006810,GO:0016020,G	metabolites and energy		activity,molecular_function,bi
		O:0009579,GO:000953			nding
		GO:0016301,GO:0005	generation of precursor metabolites		
ug1243	562	829,GO:0000166,GO:0	and energy,carbohydrate metabolic	cytosol	kinase activity,nucleotide
		006091,GO:0005975,G	process,catabolic process		binding



Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1244	611	GO:0005739,GO:0005886,GO:0016020,GO:0006091,GO:0000		mitochondrion,plasma membrane,membrane,intracellular	
ug1245	1043	166,GO:0016020,GO:005622,GO:0003674,GO:0008152,GO:000573	generation of precursor metabolites and energy,metabolic process	membrane,intracellular,mitochondrion	nucleotide binding,molecular_function,catalytic activity
ug1246	509	GO:0005840,GO:0005		ribosome,mitochondrion	
ug1247	1014	GO:0005886		plasma membrane	
ug1248_1	723	GO:0019538,GO:0009056,GO:0009987,GO:0	protein metabolic process,catabolic process,cellular process		protein binding
ug1248_2	839				
ug1249	647	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1250	609	GO:0009536		plastid	
ug1251	512				
ug1252	747	GO:0005622,GO:0003677,GO:0016043,GO:009987,GO:0005634,GO:0006950,GO:0009607,GO:0008152,GO:0	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug1253	943	009987,GO:0009536,GO:0005488,GO:0009579,GO:0005576,GO:0005488,GO:0005618,GO:0003824,GO:0005622,GO:0003677,GO:0016043,GO:009987,GO:0005634	response to stress,response to biotic stimulus,metabolic process,cellular process	plastid,thylakoid,extracellular region	binding,catalytic activity
ug1254	534	618,GO:0003824,GO:0005622,GO:0003677,GO:0016043,GO:009987,GO:0005634	response to stress	cell wall	binding,catalytic activity
ug1255	551	677,GO:0016043,GO:009987,GO:0005634	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug1256	712				
ug1257	595	GO:0006810,GO:0016020,GO:0005215	transport	membrane	transporter activity
ug1258	416				
ug1259	1353	GO:0009579,GO:0009536,GO:0006950,GO:0005488,GO:0008152,GO:0003824,GO:0016020,GO:0016043,GO:0007049,GO:0005488,GO:005856,GO:0005737,GO:0019538,GO:0009987,GO:0005737,GO:000166,GO:0005515,GO:0009579,GO:0003677	response to stress,metabolic process	thylakoid,plastid,membrane	binding,catalytic activity
ug1260	760	049,GO:0005488,GO:005856,GO:0005737,GO:0019538,GO:0009987,GO:0005737,GO:000166,GO:0005515,GO:0009579,GO:0003677	cellular component organization,cell cycle,cellular process	cytoskeleton,cytoplasm	binding
ug1261	770				
ug1262	751	GO:0019538,GO:0009987,GO:0005737,GO:000166,GO:0005515,GO:0009579,GO:0003677	protein metabolic process,cellular process	cytoplasm	nucleotide binding,protein binding
ug1263	662	824,GO:0016020,GO:009536,GO:0015979,GO:0005198,GO:0009	photosynthesis	thylakoid,membrane,plastid	catalytic activity
ug1264	542	987,GO:0005840,GO:005829,GO:0006412,GO:0005623,GO:0003	cellular process,translation	ribosome,cytosol	structural molecule activity
ug1265	565	824,GO:0005215,GO:0016020,GO:0005739		cell,membrane,mitochondrion	catalytic activity,transporter activity
ug1266	952	GO:0005737		cytoplasm	
ug1267	867	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1268	1311	GO:0016020,GO:0005739,GO:0005488,GO:0	transport	membrane,mitochondrion	binding
ug1269_1	1014				
ug1269_2	936	GO:0005215,GO:0016020,GO:0006810,GO:009058,GO:0006091,GO:0006139,GO:0016787,GO:0005773,GO:0005576,GO:0005488,GO:0003674	transport,biosynthetic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane,vacuole,plasma membrane	transporter activity,hydrolase activity
ug1270	479	GO:0005576,GO:0005488,GO:0003674		extracellular region	binding,molecular_function
ug1271	1054	GO:0005488,GO:0005737,GO:0003824,GO:0003723,GO:0006412,GO:0008135,GO:0009719,GO:0007165,GO:0005576,GO:005618,GO:0004872,GO:0003674,GO:000548	metabolic process	cytoplasm	binding,catalytic activity
ug1272	715	GO:0003723,GO:0006412,GO:0008135,GO:0009719,GO:0007165,GO:0005576,GO:005618,GO:0004872,GO:0003674,GO:000548	translation		RNA binding,translation factor activity, nucleic acid
ug1273	869	165,GO:0005576,GO:005618,GO:0004872,GO:0003674,GO:000548	response to endogenous stimulus,signal transduction	extracellular region,cell wall	receptor activity,molecular_function,bi nding
ug1274	635				
ug1275_1	812	GO:0006950,GO:0005	response to stress	vacuole	
ug1275_2	1275	GO:0005840,GO:0003723,GO:0005198,GO:0	translation	ribosome	RNA binding,structural molecule activity
ug1276	846				
ug1277_1	702				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1277_2	544	GO:0016740,GO:0003677,GO:0006350,GO:0	transcription	nucleus	transferase activity,DNA binding
ug1278	672				
ug1279	920				
ug1280	1087	GO:0016020,GO:0009579,GO:0006091,GO:015979,GO:0009536,GO:0005730,GO:0005	generation of precursor metabolites and energy,photosynthesis	membrane,thylakoid,plastid	
ug1281	841	198,GO:0005840,GO:0005829,GO:0006412	translation	nucleolus,ribosome,cytosol	structural molecule activity
ug1282	930				
ug1283	493	GO:0016020,GO:0005739,GO:0006091,GO:0	generation of precursor metabolites and energy,transport	membrane,mitochondrion	
ug1284	824	GO:0030528,GO:0009701		plastid	transcription regulator
ug1285_1	701				
ug1285_2	695	GO:0005739,GO:0005488,GO:0005515		mitochondrion	binding,protein binding
ug1286	754	GO:0005634		nucleus	
ug1287	546				
ug1288	1107	GO:0000166,GO:0005794,GO:0005737,GO:0006810,GO:0009987,GO:0005840,GO:0005198,GO:0006412	transport,cellular process	Golgi apparatus,cytoplasm,endoplasmic reticulum	nucleotide binding
ug1289	690	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1290	809				
ug1291	181				
ug1292	533	GO:0003824,GO:0005215,GO:0005739,GO:0	generation of precursor metabolites and energy	mitochondrion	catalytic activity,transporter activity
ug1293	620				
ug1294	960	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1295	573	GO:0005840,GO:0005198,GO:0006412,GO:0005488,GO:0005	translation	ribosome	structural molecule activity
ug1296	915	515,GO:0005215,GO:0016020,GO:0005739,GO:0006810,GO:001604,GO:0006412,GO:0008135	transport,cellular component organization,cellular process	membrane,mitochondrion	binding,protein binding,transporter activity
ug1297	1212	GO:0005515,GO:0005215,GO:0006810,GO:0016043,GO:0009987,GO:0016020,GO:0005739,GO:0005737,GO:0009058,GO:0006519,GO:0005488,GO:0016740	transport,cellular component organization,cellular process	membrane,mitochondrion,plastid	protein binding,transporter activity
ug1298	600	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1299	772	GO:0003824,GO:0008152,GO:0005488	metabolic process	cytoplasm	binding,transferase activity
ug1300	788	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1301	813				
ug1302_1	561	GO:0003824,GO:0008152,GO:0005488	metabolic process		catalytic activity,binding
ug1302_2	778	GO:0005488,GO:0003674,GO:0005739		mitochondrion	binding,molecular_function
ug1303_1	915	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1303_2	823				
ug1304	857	GO:0006810,GO:0009987,GO:0000166,GO:0005515,GO:0007165,GO:0005634,GO:001678	transport,cellular process,signal transduction	nucleus	nucleotide binding,protein binding,hydrolase activity
ug1305	753	GO:0019538,GO:0009987,GO:0003824,GO:0006464	protein metabolic process,catabolic process,cellular process,protein modification process		catalytic activity
ug1306	854	GO:0005488			binding
ug1307_1	1121				
ug1307_2	581	GO:0005840		ribosome	
ug1308	773	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug1309	1170	GO:0005488			binding
ug1310	784	GO:0006810,GO:0009987,GO:0005515,GO:0005635,GO:0005215	transport,cellular process	nuclear envelope	protein binding,transporter activity
ug1311	656				
ug1312	779				
ug1313	817				
ug1314	689	GO:0030528,GO:0005515,GO:0006350	transcription		transcription regulator activity,protein binding
ug1315	846				
ug1316	703				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1317	917	GO:0003677,GO:0003824,GO:0008152,GO:0005886,GO:0005	metabolic process,cellular process		DNA binding,catalytic activity
ug1318	1141	773,GO:0016020,GO:0005215,GO:0006810,GO:0005215,GO:0016020,GO:0005739,GO:0	transport	plasma membrane,vacuole,membrane	transporter activity
ug1319	846	006810,GO:0009058,GO:0006091,GO:0006139	metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane,mitochondrion	transporter activity
ug1320	245				
ug1321	827	GO:0006810	transport		
ug1322	1006				
ug1323	800				
ug1324	945				
ug1325_1	759	GO:0008150	biological_process		
ug1325_2	1441	GO:0006519,GO:0019748,GO:0003824	cellular amino acid and derivative metabolic process,secondary metabolic process		catalytic activity
ug1326	517				
ug1327	773	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1328	1042	GO:0016020,GO:0006810,GO:0009987,GO:0	transport,cellular process	membrane,Golgi apparatus	
ug1329	874	GO:0006350	transcription		
ug1330_1	576	GO:0006810	transport		
ug1330_2	815				
ug1331	759	GO:0016787,GO:0030234			hydrolase activity,enzyme regulator activity
ug1332_1	507	GO:0005488,GO:0016020,GO:0005618,GO:0003824,GO:0003674,G	response to stress	membrane,cell wall	binding,catalytic activity,molecular_function
ug1332_2	894				
ug1333	508				
ug1334_1	1008	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug1334_2	1137				
ug1335	918	GO:0006810,GO:000987,GO:0000166,GO:0005515,GO:0007165,GO:0005634,GO:001678	transport,cellular process,signal transduction	nucleus	nucleotide binding,protein binding,hydrolase activity
ug1336	669				
ug1337	937	GO:0006810,GO:000987,GO:0006950,GO:0009628,GO:0005773,GO:0009607,GO:0016787,GO:0005215,GO:0009605,GO:0005737,GO:0005515,GO:0005215,GO:0009536,GO:0	transport,cellular process,response to stress,response to abiotic stimulus,response to biotic stimulus,response to external stimulus	vacuole,cytoplasm,plasma membrane,membrane	hydrolase activity,transporter activity
ug1338	847	GO:0005840,GO:0005215,GO:0009536,GO:0	transport	plastid	protein binding,transporter activity
ug1339	792				
ug1340	730	GO:0005739,GO:0005		mitochondrion,plasma membrane	
ug1341	590	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1342	717				
ug1343	497	GO:0030246			carbohydrate binding
ug1344	979	GO:0005840,GO:0005198,GO:0003723,GO:0006412,GO:0006139	translation,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	ribosome	structural molecule activity,RNA binding
ug1345	979	GO:0030234,GO:0019725,GO:0009536,GO:0	cellular homeostasis,biological_process	plastid	enzyme regulator activity
ug1346	626	GO:0008289,GO:0006	transport		lipid binding
ug1347	544				
ug1348	1075	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1349	641				
ug1350	713	GO:0009536		plastid	
ug1351_1	769				
ug1351_2	1072	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug1352	654	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1353	1239	GO:0006810,GO:0016020,GO:0005215	transport	membrane	transporter activity
ug1354	633				
ug1355	769	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1356	750	GO:0005840,GO:0005198,GO:0009987,GO:0009536,GO:0006412,GO:0019725,GO:0003824,GO:0005488,GO:0003824,GO:0000166,GO:0008152,GO:0005198,GO:0005840,GO:0009536,GO:0006412,GO:0003723,GO:0016020,GO:0006810,GO:0009987	cellular process,translation	ribosome,plastid,mitochondrion	structural molecule activity
ug1357	463	GO:0019725,GO:0003824,GO:0005488,GO:0003824,GO:0000166,GO:0008152,GO:0005198,GO:0005840,GO:0009536,GO:0006412,GO:0003723,GO:0016020,GO:0006810,GO:0009987	cellular homeostasis,transport		catalytic activity,binding
ug1358	949	GO:0003824,GO:0000166,GO:0008152,GO:0005198,GO:0005840,GO:0009536,GO:0006412,GO:0003723,GO:0016020,GO:0006810,GO:0009987	metabolic process,transcription		catalytic activity,nucleotide binding
ug1359	640	GO:0005840,GO:0009536,GO:0006412,GO:0003723,GO:0016020,GO:0006810,GO:0009987	translation	ribosome,plastid,mitochondrion	structural molecule activity,RNA binding
ug1360	993	GO:0016020,GO:0006810,GO:0009987	transport,cellular process	membrane	
ug1361	1143	GO:0000166			nucleotide binding
ug1362	868	GO:0005488			binding
ug1363	963				
ug1364_1	971				
ug1364_2	960	GO:0005840,GO:0005198,GO:0003723,GO:0006412,GO:0006139,GO:0005576,GO:0006950,GO:0005618	translation,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	ribosome	structural molecule activity,RNA binding
ug1365	556	GO:0005576,GO:0006950,GO:0005618	response to stress	extracellular region,cell wall	
ug1366	971	GO:0019538,GO:0009987,GO:0005829,GO:0005634	protein metabolic process,cellular process	cytosol	protein binding
ug1367	621	GO:0005634		nucleus	
ug1368	212				
ug1369	704				
ug1370_1	876				
ug1370_2	631	GO:0006139,GO:0009987,GO:0000166,GO:0016020,GO:0016787,GO:0005634	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process	membrane	nucleotide binding,hydrolase activity,transporter activity
ug1371	548				
ug1372	926	GO:0005515			protein binding
ug1373	1354	GO:0019538,GO:0009987,GO:0008150,GO:0005634	protein metabolic process,catabolic process,biological_process		hydrolase activity
ug1374_1	255				
ug1374_2	1130				
ug1375	885	GO:0005737,GO:0005773,GO:0005886,GO:0019538,GO:0009987,GO:0005829,GO:0005634	protein metabolic process,catabolic process,cellular process,protein modification process	cytoplasm,vacuole,plasma membrane	
ug1376_1	797	GO:0005829,GO:0005634			catalytic activity
ug1376_2	368				
ug1377_1	878	GO:0005886		plasma membrane	
ug1377_2	752	GO:0005622,GO:000677,GO:0016043,GO:0009987,GO:0005634	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug1378	670	GO:0005840,GO:0005198,GO:0006412,GO:0008150,GO:0005840,GO:0009579,GO:0005739,GO:0009536	translation	ribosome	structural molecule activity
ug1379	916	GO:0005840,GO:0009579,GO:0005739,GO:0009536	biological_process	vacuole,thylakoid,mitochondrion,plastid	
ug1380	845	GO:0009536		plastid	
ug1381	874	GO:0005488,GO:0008152,GO:0003824	metabolic process		binding,catalytic activity
ug1382	611	GO:0006810	transport		
ug1383	678	GO:0005215,GO:0016020,GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:0005622,GO:0009536,GO:0019538,GO:0005840,GO:0005198,GO:0006412,GO:0005488,GO:0008152,GO:0003824,GO:0003674,GO:0006950	transport,biosynthetic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane,intracellular,plastid	transporter activity,hydrolase activity
ug1384	828	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1385	1262	GO:0005488,GO:0008152,GO:0003824,GO:0003674,GO:0006950	metabolic process,response to stress		binding,catalytic activity,molecular_function
ug1386	495	GO:0005739		mitochondrion	
ug1387	584	GO:0005856,GO:0009653,GO:0016043,GO:0009987,GO:0030154,GO:0007275,GO:0005515,GO:0005737	anatomical structure morphogenesis,cellular component organization,cellular process,cell differentiation,multicellular organismal development	cytoskeleton,cytoplasm	protein binding
ug1388	952				
ug1389	1625	GO:0005856,GO:0005737,GO:0000166,GO:0009058,GO:0009987,GO:0003824,GO:0008152,GO:0009536	biological_process		nucleotide binding,protein binding
ug1390	1480	GO:0003824,GO:0008152,GO:0009536	biosynthetic process,cellular process,metabolic process	plastid	catalytic activity
ug1391	1006	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1392	905				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1393	831	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1394	1014	GO:0005840,GO:0009536,GO:0003723,GO:0016020,GO:0009579,GO:0019725	cellular homeostasis	ribosome,plastid,membrane,thylakoid	RNA binding,nucleotide binding
ug1395	617	GO:0005840,GO:0005198,GO:0006412,GO:0005840,GO:0005198,GO:0006412,GO:0005840,GO:0005198,GO:0006412,GO:0005840,GO:0005198,GO:0006412,GO:0005840,GO:0005198,GO:0006412	translation	ribosome,mitochondrion	structural molecule activity
ug1396	697	GO:0005840,GO:0005198,GO:0006412,GO:0005840,GO:0005198,GO:0006412,GO:0005840,GO:0005198,GO:0006412,GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity,nucleotide binding
ug1397	727	GO:0005840,GO:0005198,GO:0006412,GO:0005840,GO:0005198,GO:0006412,GO:0005840,GO:0005198,GO:0006412,GO:0005840,GO:0005198,GO:0006412	transport,response to stress,response to abiotic stimulus		binding,protein binding
ug1398	633	488,GO:0005515,GO:0006950,GO:0009628			
ug1399	978				
ug1400	790				
ug1401	611				
ug1402	794				
ug1403	950	GO:0005829,GO:0003824,GO:0005488,GO:0006091,GO:0005975,GO:0005515,GO:0006412	generation of precursor metabolites and energy,carbohydrate metabolic process,catabolic process,protein modification	cytosol	catalytic activity,binding
ug1404	798	464,GO:0009719,GO:0005622,GO:0005488	process,response to endogenous stimulus	intracellular	protein binding,binding
ug1405	790				
ug1406_1	691	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1406_2	512	GO:0019538,GO:0009987,GO:0000166,GO:0006412,GO:0016043,GO:0009987,GO:0000003,GO:0009791,GO:0009790,GO:000813	protein metabolic process,cellular process,response to stress,translation,cellular component organization,cellular process,reproduction,post-embryonic development,embryonic		nucleotide binding
ug1407	1218				translation factor activity,nucleic acid binding,binding
ug1408	713				
ug1409	710	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634,GO:0016020,GO:0005737,GO:0005773,GO:005783,GO:0016740	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug1410	769	737,GO:0005773,GO:005783,GO:0016740		membrane,cytoplasm,vacuole,endoplasmic reticulum	transferase activity
ug1411	1197				
ug1412	760	GO:0019538,GO:0009987,GO:0005634,GO:0009987,GO:0005634	protein metabolic process,catabolic process,cellular process		protein binding
ug1413	1078	GO:0005840,GO:0005198,GO:0003723,GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity,RNA binding
ug1414	691	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1415	743	GO:0005576,GO:0007267,GO:0005618,GO:0005488	cell-cell signaling	extracellular region,cell wall	signal transducer activity
ug1416	1242	GO:0005488			binding
ug1417	988	GO:0005886		plasma membrane	
ug1418	720				
ug1419	887	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1420	814	GO:0005840,GO:0005198,GO:0009987,GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634	cellular process,translation	ribosome	structural molecule activity
ug1421	665	677,GO:0016043,GO:0009987,GO:0005634	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug1422	1136				
ug1423	808	GO:0008150,GO:0000003,GO:0009628,GO:0009791,GO:0009908,GO:0005634,GO:0007160,GO:0030246,GO:0019538,GO:0009987,GO:0005783,GO:0005488,GO:0005840,GO:0005198,GO:0006412	biological_process,reproduction,response to abiotic stimulus,post-embryonic development,flower development,signal transduction	nucleus	
ug1424	785	538,GO:0009987,GO:0005783,GO:0005488,GO:0005840,GO:0005198,GO:0006412	protein metabolic process,cellular process	endoplasmic reticulum	carbohydrate binding,binding,protein binding
ug1425	918	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1426	930				
ug1427	1278	GO:0008152,GO:0003824,GO:0005488	metabolic process		catalytic activity,binding
ug1428	642	GO:0006464	protein modification process		
ug1429	730	GO:0005975,GO:0009987,GO:0016301,GO:0005198,GO:0009987,GO:0005840,GO:0005198,GO:0006412,GO:0005739,GO:0016020,GO:0005622	carbohydrate metabolic process,cellular process		kinase activity
ug1430	867	987,GO:0005840,GO:0005829,GO:0006412	cellular process,translation	ribosome,cytosol	structural molecule activity
ug1431	665	GO:0005739,GO:0016020,GO:0005622		mitochondrion,membrane,intracellular	
ug1432	598			ar	

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1433	359				
ug1434	916	GO:0009719,GO:0007165,GO:0016740	response to endogenous stimulus,signal transduction		transferase activity
ug1435_1	916	GO:0006810,GO:0016020,GO:0005215	transport	membrane	transporter activity
ug1435_2	1054	GO:0016740			transferase activity
ug1436	768				
ug1437	1172	GO:0005975,GO:0009987,GO:0016787,GO:0005576,GO:0005618,GO:0005215,GO:0016020,GO:0005739,GO:0006810,GO:0009058,GO:0006091,GO:0006139	carbohydrate metabolic process,cellular process	extracellular region,cell wall	hydrolase activity,transferase activity
ug1438	964	GO:0006810,GO:0009058,GO:0006091,GO:0006139	metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane,mitochondrion	transporter activity
ug1439	795				
ug1440	478				
ug1441	537	GO:0006810,GO:0016020,GO:0005215	transport	membrane	transporter activity
ug1442	513				
ug1443	751	GO:0016043,GO:0007049,GO:0005737,GO:0003824,GO:0005634	cellular component organization,cell cycle	cytoplasm,nucleus	catalytic activity
ug1444	722	GO:0005198,GO:0005840,GO:0006412	translation	ribosome	structural molecule activity
ug1445	587	GO:0019538,GO:0009056,GO:0016787	protein metabolic process,catabolic process		hydrolase activity
ug1446	689	GO:0003677,GO:0006350,GO:0005634	transcription	nucleus	DNA binding
ug1447	853	GO:0005840,GO:0005198,GO:0006412,GO:0006950,GO:0009056,GO:0016787,GO:0005975,GO:0009056,GO:0009987,GO:003024	translation	ribosome	structural molecule activity,nucleotide binding
ug1448	695	GO:0003824,GO:0005488,GO:0006810,GO:0003674,GO:0016020,GO:0009536,GO:0009579,GO:0006091,GO:0016043,GO:0009987,GO:0006464,GO:00006	response to stress,response to biotic stimulus,carbohydrate metabolic process,catabolic process,cellular process		hydrolase activity,carbohydrate binding
ug1449	1324	GO:0003824,GO:0005488,GO:0006810,GO:0003674,GO:0016020,GO:0009536,GO:0009579,GO:0006091,GO:0016043,GO:0009987,GO:0006464,GO:00006	transport,generation of precursor metabolites and energy,photosynthesis	membrane,plastid,thylakoid	catalytic activity,binding,molecular function
ug1450	750	GO:0005737,GO:0005515,GO:0005856,GO:0009058,GO:0009987,GO:0005737,GO:0016740,GO:0000166,GO:0006464,GO:00006	cellular component organization,cellular process	cytoplasm,cytoskeleton	protein binding
ug1451	508	GO:0005737,GO:0016740,GO:0000166,GO:0006464,GO:00006	biosynthetic process,cellular process	cytoplasm	transferase activity,nucleotide binding,catalytic activity
ug1452	1558	GO:0005488,GO:0003824	protein modification process,cellular amino acid and derivative metabolic process		binding,catalytic activity
ug1453	507				
ug1454	1007	GO:0000166,GO:0005794,GO:0006810,GO:0009987,GO:0006464,GO:0009536,GO:000716	transport,cellular process,protein modification process,signal transduction	Golgi apparatus,plastid	nucleotide binding,transporter activity
ug1455	990				
ug1456	1226	GO:0005773		vacuole	
ug1457	561	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1458	593				
ug1459_1	1006	GO:0016043,GO:0009987,GO:0005737,GO:0005515,GO:0005856	cellular component organization,cellular process	cytoplasm,cytoskeleton	protein binding
ug1459_2	607				
ug1460	835	GO:0016020,GO:0005198,GO:0019538,GO:0009987,GO:0000166,GO:0003824,GO:0005488,GO:0008152,GO:0009536,GO:0005576,GO:0005737,GO:0005739,GO:0009056,GO:0009058,GO:0009987,GO:0006464,GO:0003824	protein metabolic process,cellular process	membrane,endoplasmic reticulum	nucleotide binding
ug1461	519	GO:0000166,GO:0003824,GO:0005488,GO:0008152,GO:0009536,GO:0005576,GO:0005737,GO:0005739,GO:0009056,GO:0009058,GO:0009987,GO:0006464,GO:0003824	metabolic process,catabolic process,cellular amino acid and derivative metabolic process	plastid,extracellular region,cytoplasm,mitochondrion	catalytic activity,binding
ug1462	1266	GO:0005737,GO:0005739,GO:0009056,GO:0009058,GO:0009987,GO:0006464,GO:0003824	biosynthetic process,cellular process	membrane,mitochondrion,intracellular	
ug1463	605	GO:0016020,GO:0005739,GO:0005622,GO:0019538,GO:0009056,GO:0009987,GO:0006464,GO:0003824	protein metabolic process,catabolic process,cellular process,protein modification process		catalytic activity
ug1464	905	GO:0005776,GO:0016043,GO:0009987,GO:00006	cellular component organization,cellular process	extracellular region,membrane	
ug1465	617	GO:0005776,GO:0016043,GO:0009987,GO:00006			

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1466	808	GO:0016740,GO:0003824,GO:0006091,GO:015979,GO:0009536,GO:0009058,GO:000998	generation of precursor metabolites and energy,photosynthesis,biosynthetic process,cellular process	plastid	transferase activity,catalytic activity
ug1467	406	GO:0005739,GO:0006091	generation of precursor metabolites and energy	mitochondrion	
ug1468	716				
ug1469	722				
ug1470	845	GO:0005515,GO:0005		intracellular	protein binding
ug1471	782	GO:0016740,GO:0006350,GO:0005622,GO:0	transcription	intracellular	transferase activity,DNA binding
ug1472	715				
ug1473	928	GO:0006950,GO:0008150,GO:0003824,GO:0008152,GO:0009536,GO:0005829,GO:000573	response to stress,biological_process,metabolic process,response to abiotic stimulus	plastid,cytosol,mitochondrion	catalytic activity
ug1474	685	GO:0005829,GO:0003824,GO:0005488,GO:0006091,GO:0005975,GO:0016020,GO:0005	generation of precursor metabolites and energy,carbohydrate metabolic process,catabolic process	cytosol	catalytic activity,binding
ug1475	997	GO:0009536,GO:0005979,GO:0005198,GO:0009	photosynthesis	membrane,plastid,thylakoid	binding
ug1476	708	GO:0005840,GO:0005829,GO:0005488,GO:0006412,GO:000372	cellular process,translation	ribosome,cytosol	structural molecule activity,binding,RNA binding
ug1477	762				
ug1478	636	GO:0006950,GO:0009607	response to stress,response to biotic stimulus		
ug1479	778	GO:0006810,GO:0005886,GO:0008289	transport	plasma membrane	lipid binding
ug1480	943	GO:0003676			nucleic acid binding
ug1481	812	GO:0009607,GO:0006950	response to biotic stimulus,response to stress		
ug1482	1426	GO:0016740			transferase activity
ug1483_1	717	GO:0005634,GO:0000166,GO:0003723		nucleus	nucleotide binding,RNA binding
ug1483_2	745				
ug1484	867	GO:0005737,GO:0005		cytoplasm	binding
ug1485	772	GO:0019725,GO:0003	cellular homeostasis		catalytic activity
ug1486_1	883	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1486_2	662	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1487	767	GO:0005488			binding
ug1488	990	GO:0016787			hydrolase activity
ug1489	951	GO:0005576,GO:0005488,GO:0003674		extracellular region	binding,molecular_function
ug1490	802	GO:0005840,GO:0006464,GO:0005198,GO:0006091,GO:0015	protein modification process,translation	ribosome	structural molecule activity
ug1491	897	GO:0009536,GO:0016020,GO:0009579,GO:0006464,GO:0005488,GO:000953	generation of precursor metabolites and energy,photosynthesis,protein modification process	membrane,thylakoid,plastid	binding
ug1492	1176				
ug1493	244				
ug1494	801	GO:0016020,GO:0005783,GO:0005623,GO:0005488,GO:0006810,GO:0005576,GO:0006	transport,generation of precursor metabolites and energy	membrane,endoplasmic reticulum,cell	binding
ug1495	1035	GO:0005576,GO:0006950,GO:0005618	response to stress	extracellular region,cell wall	
ug1496	1382	GO:0008152,GO:0009987,GO:0005488,GO:00019538,GO:0009	metabolic process,cellular process		binding,catalytic activity
ug1497	920	GO:0005515,GO:0001000166,GO:0006950	protein metabolic process,cellular process,response to stress		protein binding,nucleotide binding
ug1498	420				
ug1499	912	GO:0016301,GO:0009605,GO:0007165,GO:0009628,GO:0009058,GO:0006139,GO:0000166,GO:0005488	response to external stimulus,signal transduction,response to abiotic stimulus,biosynthetic process,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		kinase activity,nucleotide binding,binding
ug1500	726	GO:0006091,GO:0005488,GO:0003674	generation of precursor metabolites and energy		binding,molecular_function
ug1501	933	GO:0019538,GO:0009987,GO:0005515,GO:0006950,GO:0005488,G	protein metabolic process,cellular process,response to stress	plasma membrane	protein binding,binding
ug1502	1011				
ug1503	797				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1504	650	GO:0005488			binding
ug1505	914				
ug1506	607	GO:0005623		cell	
ug1507	879				
ug1508	573	GO:0016020,GO:0009		membrane,plastid	
ug1509	858	GO:0003824,GO:0005488,GO:0008152	metabolic process		catalytic activity,binding
ug1510	908	GO:0006464,GO:0019538,GO:0009056,GO:009987,GO:0003824,GO:0005737,GO:0006810,GO:0008152,GO:005215,GO:0006950,GO:0005488,GO:000563	protein modification process,protein metabolic process,catabolic process,cellular		catalytic activity
ug1511	1083	810,GO:0008152,GO:005215,GO:0006950,GO:0005488,GO:000563	transport,metabolic process,response to stress	cytoplasm,nucleus	transporter activity,binding,oxygen binding
ug1512	868				
ug1513	812	GO:0005488,GO:0003			binding,molecular_function
ug1514	921	GO:0008152,GO:0009987,GO:0005488,GO:0	metabolic process,cellular process		binding,catalytic activity
ug1515	1171	GO:0016740			transferase activity
ug1516	1216	GO:0016740,GO:0016020,GO:0009058,GO:009987,GO:0006629,GO:0009058,GO:0006519,GO:0019748,GO:0008152,GO:0003824,GO:0005488	biosynthetic process,cellular process,lipid metabolic process biosynthetic process,cellular amino acid and derivative metabolic process,secondary metabolic process,metabolic process	membrane	transferase activity
ug1517	876				catalytic activity,binding
ug1518	795				
ug1519	771	GO:0005622,GO:0003677,GO:0016043,GO:009987,GO:0005634,GO:0009719,GO:0007165,GO:0016740	cellular component organization,cellular process response to endogenous stimulus,signal transduction	intracellular,nucleus	DNA binding
ug1520	1140				transferase activity
ug1521	704				
ug1522	683	GO:0005739,GO:0006950,GO:0016020	response to stress	mitochondrion,membrane	
ug1523	944				
ug1524	609				
ug1525	893				
ug1526	946				
ug1527_1	635	GO:0019725,GO:0005829,GO:0008152,GO:009987,GO:0003674,GO:0003824,GO:0005	cellular homeostasis,metabolic process,cellular process	cytosol	molecular_function,catalytic activity
ug1527_2	1003	886,GO:0000166,GO:0008152,GO:0006350	metabolic process,transcription	plasma membrane	catalytic activity,nucleotide binding
ug1528	640				
ug1529	694	GO:0006091,GO:0015979,GO:0016020,GO:009579,GO:0005488,GO:0006464,GO:000953	generation of precursor metabolites and energy,photosynthesis,protein modification process	membrane,thylakoid,plastid	binding
ug1530	785	GO:0016787			hydrolase activity
ug1531_1	768	GO:0006950,GO:0005	response to stress	vacuole	
ug1531_2	711	GO:0006464	protein modification process		
ug1532	881	GO:0016787			hydrolase activity
ug1533	540	GO:0005623,GO:0016020,GO:0006950,GO:0000166,GO:0016787,GO:0006810,GO:009987,GO:0009536,GO:0007165,GO:000521	response to stress,response to abiotic stimulus transport,cellular process,signal transduction	cell,membrane	
ug1534	1214			plastid	nucleotide binding,hydrolase activity,transporter activity
ug1535	678				
ug1536	636	GO:0005737		cytoplasm	
ug1537_1	392	GO:0005623,GO:0016020,GO:0006950,GO:0	response to stress,response to abiotic stimulus	cell,membrane	
ug1537_2	752				
ug1538	510				
ug1539	655	GO:0015979,GO:0016020,GO:0009579	photosynthesis	membrane,thylakoid	
ug1540	898	GO:0005488			binding
ug1541	1008	GO:0003824,GO:0005829,GO:0009536,GO:0009058,GO:0006519,GO:0006950,GO:0009620,GO:0005840,GO:0006464,GO:0005198,GO:0006810,GO:0005886,GO:0008289	biosynthetic process,cellular amino acid and derivative metabolic process,response to stress,response to abiotic stimulus protein modification process,translation transport	cytosol,plastid	catalytic activity
ug1542	675			ribosome	structural molecule activity
ug1543	860			plasma membrane	lipid binding
ug1544	925				
ug1545	537	GO:0006950	response to stress		



Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1546	827	GO:0016020,GO:0005783,GO:0005623,GO:0005488,GO:0006810,G	transport,generation of precursor metabolites and energy	membrane,endoplasmic reticulum,cell	binding
ug1547	1108	GO:0005515			protein binding
ug1548	1226				
ug1549	670				
ug1550	780				
ug1551	1005				
ug1552	855				
ug1553	493	GO:0005488,GO:0008152,GO:0009987,GO:00016787,GO:0016	metabolic process,cellular process		binding,catalytic activity
ug1554	1158	043,GO:0009987,GO:0005618,GO:0030234	cellular component organization,cellular process	cell wall	hydrolase activity,enzyme regulator activity
ug1555	749	GO:0005515,GO:0006464,GO:0009719,GO:0005622,GO:0005488	protein modification process,response to endogenous stimulus	intracellular	protein binding,binding
ug1556	942	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1557_1	586	GO:0005840,GO:0005198,GO:0005488,GO:0006412,GO:0005739	translation	ribosome,mitochondrion	structural molecule activity,binding
ug1557_2	1101				
ug1558	941	GO:0009058,GO:0006519,GO:0019748,GO:0003824	biosynthetic process,cellular amino acid and derivative metabolic process,secondary metabolic		catalytic activity
ug1559	734	GO:0016020,GO:0009579,GO:0009536,GO:0005488,GO:0008	photosynthesis	membrane,thylakoid,plastid	
ug1560_1	802	GO:0005737,GO:0009987,GO:0003824,G	metabolic process,cellular process	cytoplasm	binding,catalytic activity,molecular_function
ug1560_2	835	GO:0019538,GO:0003824,GO:0006464	protein metabolic process,protein modification process		catalytic activity
ug1561	868	GO:0005737		cytoplasm	
ug1562	825				
ug1563	843	GO:0009058,GO:0006519,GO:0005488,GO:0	biosynthetic process,cellular amino acid and derivative metabolic		binding,transferase activity
ug1564	433				
ug1565	494	GO:0005623,GO:0005488,GO:0008152,GO:0005737,GO:0003824,G	metabolic process,response to stress	cell,cytoplasm	binding,catalytic activity,molecular_function
ug1566	1300				
ug1567_1	589	GO:0005737,GO:0000166,GO:0008152,GO:0005975,GO:0006091,G	metabolic process,carbohydrate metabolic process,generation of precursor metabolites and energy,catabolic process	cytoplasm	nucleotide binding,catalytic activity
ug1567_2	552	GO:0006810,GO:0016020,GO:0005215	transport	membrane	transporter activity
ug1568	1427	GO:0016740,GO:0009058,GO:0006519,GO:0019748	biosynthetic process,cellular amino acid and derivative metabolic process,secondary metabolic		transferase activity
ug1569	953				
ug1570	729	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1571	783	GO:0005515			protein binding
ug1572_1	722				
ug1572_2	947	GO:0008150	biological_process		
ug1573	578	GO:0003824,GO:0008152,GO:0005618,GO:0005488,GO:0016	metabolic process	cell wall	catalytic activity,nucleotide binding
ug1574	1259	GO:0006091,GO:00015979,GO:0009536,G	generation of precursor metabolites and energy,photosynthesis	membrane,plastid,thylakoid	binding
ug1575	943				
ug1576	1094	GO:0006464	protein modification process		
ug1577	1116	GO:0005488,GO:0003824,GO:0006350,GO:0009719,GO:0007165,GO:0030528,GO:0005515,G	transcription,response to endogenous stimulus,signal transduction	nucleus	binding,DNA binding transcription regulator activity,protein binding,transcription factor activity
ug1578	930	GO:0003700,GO:000563			
ug1579	837				
ug1580	1151				
ug1581	1020	GO:0009058,GO:0006519,GO:0019748,GO:0003824	biosynthetic process,cellular amino acid and derivative metabolic process,secondary metabolic		catalytic activity
ug1582	982	GO:0005975,GO:0016787,GO:0016740	carbohydrate metabolic process		hydrolase activity,transferase activity
ug1583_1	505				
ug1583_2	642	GO:0009607,GO:0009605,GO:0006950,GO:0	response to biotic stimulus,response to external	plastid	

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1584	762	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1585	504	GO:0005737,GO:0005198,GO:0009987,GO:000166,GO:0005856,GO:0016043,GO:0006950,GO:0009628,GO:0016020,GO:0009579,GO:0009536	cellular process,cellular component organization,response to stress,response to abiotic stimulus	cytoplasm,cytoskeleton	structural molecule activity,nucleotide binding,hydrolase activity
ug1586	814	GO:0003824,GO:0005215,GO:0006091,GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634	generation of precursor metabolites and energy,photosynthesis	membrane,thylakoid,plastid	
ug1587	953	GO:0003824,GO:0005215,GO:0006091,GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634	generation of precursor metabolites and energy	mitochondrion	catalytic activity,transporter activity
ug1588	855	GO:0003824,GO:0005215,GO:0006091,GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug1589	656	GO:0005737		cytoplasm	
ug1590	836	GO:0019538,GO:0009802,GO:0009987,GO:0006464,GO:0003824,GO:0005737,GO:0016043,GO:0009987,GO:0005634	protein metabolic process,catabolic process,cellular process,protein modification process		catalytic activity
ug1591	802	GO:0005737,GO:0016043,GO:0009987,GO:0005634	protein metabolic process,catabolic process	cytoplasm,plastid	hydrolase activity
ug1592	444	787,GO:0019538,GO:0009056,GO:0009536	protein metabolic process,catabolic process	cytoplasm,plastid	hydrolase activity
ug1593	468				
ug1594	828				
ug1595	1443	GO:0005622,GO:0005886,GO:0019538,GO:0009056,GO:0009987,GO:0005634,GO:000582	protein metabolic process,catabolic process,cellular process	intracellular,plasma membrane,nucleus,cytosol	hydrolase activity
ug1596	1043	GO:0016020,GO:0008464	cell death	membrane	
ug1597	464				
ug1598	1572	GO:0006350,GO:0003641	transcription		transcription factor activity
ug1599	641				
ug1600	949	GO:0005730,GO:0005737,GO:0000166,GO:0005886,GO:000515,GO:0007165,GO:001678,GO:0005840,GO:0005198,GO:0009987,GO:0006412,GO:0003723,GO:0016020,GO:000953	signal transduction	nucleolus,cytoplasm,plasma membrane	nucleotide binding,protein binding,hydrolase activity
ug1601_1	1100	GO:0005730,GO:0005737,GO:0000166,GO:0005886,GO:000515,GO:0007165,GO:001678,GO:0005840,GO:0005198,GO:0009987,GO:0006412,GO:0003723,GO:0016020,GO:000953	cellular process,translation	ribosome,membrane,plastid,thylakoid	structural molecule activity,RNA binding
ug1601_2	1018				
ug1602	697	GO:0006810	transport		
ug1603	828	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1604_1	657	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1604_2	460				
ug1605	731	GO:0000166			nucleotide binding
ug1606	1430	GO:0003677,GO:000005622,GO:0003677,GO:000005622,GO:0003677,GO:000005622,GO:0003677,GO:000005622	cellular component organization,cellular process	intracellular,nucleus,cytoskeleton	DNA binding,protein binding
ug1607	479	GO:0005634,GO:000585			binding
ug1608	522	GO:0005488			
ug1609	1061	GO:0016020,GO:0005783,GO:0005886,GO:0016787,GO:0006950,GO:0008219,GO:0005773,GO:0005975,GO:0009056,GO:0009607,GO:0009987,GO:0005618,GO:0030246,GO:0005840,GO:0005198,GO:0006412	response to stress,cell death,carbohydrate metabolic process,catabolic process,response to biotic stimulus,cellular process	membrane,endoplasmic reticulum,plasma membrane	hydrolase activity,carbohydrate binding
ug1610	1122	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1611	858	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1612	770				
ug1613	1107	GO:0006810,GO:0016020,GO:0005215,GO:0000166,GO:0016787,GO:0006810,GO:0009987,GO:0009536,GO:0007165,GO:000521	transport,cellular process,signal transduction	membrane	transporter activity
ug1614	1057	GO:0006810,GO:0016020,GO:0005215,GO:0000166,GO:0016787,GO:0006810,GO:0009987,GO:0009536,GO:0007165,GO:000521	transport,cellular process,signal transduction	plastid	nucleotide binding,hydrolase activity,transporter activity
ug1615	498				
ug1616	1038				
ug1617_1	647				
ug1617_2	894	GO:0005198,GO:0005840,GO:0006412,GO:0006810,GO:0016020,GO:0005215	translation	ribosome	structural molecule activity,RNA binding
ug1618	499	GO:0006810,GO:0016020,GO:0005215	transport	membrane	transporter activity

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1619	968	GO:0000166,GO:0005737,GO:0007165,GO:0	signal transduction,transport	cytoplasm	nucleotide binding
ug1620	983	GO:0006810,GO:0009	transport,cellular process		
ug1621	733	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1622	581	GO:0005730,GO:0005198,GO:0005840,GO:0005829,GO:0006412,GO:0005737,GO:0008	translation	nucleolus,ribosome,cytosol,mitochondrion	structural molecule activity
ug1623	665	GO:0000166,GO:0006412,GO:0016787,GO:0005515,GO:0005	translation	cytoplasm	translation factor activity, nucleic acid binding,nucleotide
ug1624	798	GO:0016020,GO:0009536,GO:0005622,GO:0005739,GO:000681	transport	membrane,plastid,intracellular,mitochondrion	protein binding,transporter activity
ug1625	593				
ug1626	573				
ug1627	977	GO:0005576,GO:0005488,GO:0003674		extracellular region	binding,molecular_function
ug1628	985				
ug1629	1075	GO:0003824,GO:0005618,GO:0016043,GO:0009987,GO:0005794,GO:0008152,GO:0005886,GO:0009058,GO:0005975,GO:0016740,GO:	cellular component organization,cellular process,metabolic process,biosynthetic process,carbohydrate metabolic process,photosynthesis	cell wall,Golgi apparatus,plasma membrane,plastid	catalytic activity,transferase activity
ug1630	522				
ug1631_1	864	GO:0009579,GO:0016020,GO:0009536,GO:0005829,GO:0003824,GO:0005488,GO:0005975,GO:0006091,GO:0009056	photosynthesis carbohydrate metabolic process,generation of precursor metabolites and energy,catabolic process	thylakoid,membrane,plastid cytosol	catalytic activity,binding
ug1631_2	772	GO:0008150	biological_process		
ug1632_1	1154				
ug1632_2	571				
ug1633	887	GO:0019538,GO:0009987,GO:0003824	protein metabolic process,cellular process		catalytic activity
ug1634	772				
ug1635	541				
ug1636	727	GO:0005739		mitochondrion	
ug1637	1172	GO:0005829,GO:0005		cytosol,cellular_component	
ug1638	1105	GO:0005488,GO:0005887,GO:0005730,GO:0005		nucleolus,intracellular	binding,protein binding
ug1639	887	GO:0005730,GO:0005			
ug1640	394	GO:0008289,GO:0006	transport		lipid binding
ug1641	691	GO:0008152,GO:0005488,GO:0009536,GO:0	metabolic process	plastid	binding,catalytic activity
ug1642	1242				
ug1643	1008	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1644	671	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1645	489	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1646	808	GO:0016740,GO:0009	biosynthetic process		transferase activity
ug1647	583				
ug1648	663	GO:0005198,GO:0009987,GO:0005840,GO:0005829,GO:0006412,GO:0006950,GO:0009056,GO:0006519,GO:0005739,GO:0009875,GO:0007275,GO:0000000	cellular process,translation response to stress,catabolic process,cellular amino acid and derivative metabolic process,pollen-pistil	ribosome,cytosol	structural molecule activity
ug1649	650	GO:0009856,GO:0009653,GO:0016043,GO:0030154,GO:0016049,GO:0016740,GO:0007610,GO:0009605,GO:0003723,GO:0006412,GO:0008135	interaction,multicellular organismal development,reproduction,pollination,anatomical structure morphogenesis,cellular component organization,cell di...	mitochondrion,plasma membrane	transferase activity,binding
ug1650	677	GO:0005840,GO:0005198,GO:0009987,GO:0009607,GO:0006950	cellular process,translation response to biotic stimulus,response to stress		RNA binding,translation factor activity, nucleic acid
ug1651	1102	GO:0005840,GO:0005198,GO:0009987,GO:0009607,GO:0006950	cellular process,translation	ribosome	structural molecule activity
ug1652	819				
ug1653	807				
ug1654	544				
ug1655	1443	GO:0016740,GO:0009058,GO:0006519,GO:0019748	biosynthetic process,cellular amino acid and derivative metabolic process,secondary metabolic		transferase activity
ug1656	543				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1657	817	GO:0009628,GO:0006950	response to abiotic stimulus,response to stress		
ug1658	839	GO:0005488			binding
ug1659_1	1180	GO:0005730,GO:0005198,GO:0009987,GO:0005840,GO:0005829,G	cellular process,translation	nucleolus,ribosome,cytosol	structural molecule activity
ug1659_2	516				
ug1660	1330	GO:0006810,GO:0016020,GO:0005215	transport	membrane	transporter activity
ug1661	920	GO:0003824,GO:0016740			catalytic activity,transferase activity
ug1662	683	GO:0005198,GO:0003723,GO:0005840,GO:0005730,GO:0005773,GO:0005198,GO:0005840,GO:0005829,G	translation	ribosome	structural molecule activity,RNA binding
ug1663	821	GO:0005198,GO:0005840,GO:0005829,G	translation	nucleolus,vacuole,ribosome,cytosol,membrane	structural molecule activity
ug1664	589	GO:0005215,GO:0016020,GO:0005739,GO:0006810,GO:0006091,G	transport,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic	membrane,mitochondrion	transporter activity,hydrolase activity
ug1665	1154	GO:0005840,GO:0005198,GO:0003723,GO:0005773,GO:0003824,GO:0009058,GO:0009058,GO:0009058	translation	ribosome	structural molecule activity,RNA binding
ug1666	557				
ug1667	558	GO:0005737,GO:0003824,GO:0009058,GO:0009058	biosynthetic process,cellular amino acid and derivative metabolic	cytoplasm	catalytic activity
ug1668	150				
ug1669	837				
ug1670	945	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1671	1084				
ug1672	1094	GO:0008152,GO:0009536,GO:0009579,GO:0006950,GO:0009628,G	metabolic process,response to stress,response to abiotic stimulus	plastid,thylakoid,mitochondrion	catalytic activity,transporter activity
ug1673	704	GO:0005198,GO:0003723,GO:0005840,GO:0009579,GO:0003824,GO:0009579,GO:0003824	translation	ribosome	structural molecule activity,RNA binding
ug1674	670	GO:0016020,GO:0009536,GO:0015979	photosynthesis	thylakoid,membrane,plastid	catalytic activity
ug1675	163				
ug1676	701	GO:0005623,GO:0006950,GO:0009058,GO:0006519,GO:0019748	response to stress,biosynthetic process,cellular amino acid and derivative metabolic process,secondary metabolic	cell	
ug1677	658	GO:0006412,GO:0000003,GO:0009791,GO:0009790,GO:0005730,G	translation,reproduction,post-embryonic development,embryonic development,protein modification process	nucleolus,ribosome,cytosol	structural molecule activity,protein binding
ug1678	846				
ug1679	590	GO:0016020,GO:0005739,GO:0003824,GO:0005886		membrane,mitochondrion	catalytic activity,transporter activity
ug1680	889	GO:0005886		plasma membrane	
ug1681	499	GO:0006950	response to stress		
ug1682	1878	GO:0005488,GO:0000003,GO:0009791,GO:0009790,GO:0016787,G	reproduction,post-embryonic development,embryonic development,regulation of gene expression, epigenetic,cellular process,metabolic process,cellular component	plasma membrane	binding,hydrolase activity
ug1683	666				
ug1684	843	GO:0009607,GO:0006950	response to biotic stimulus,response to stress		
ug1685	1761	GO:0016787,GO:000618,GO:0005773,GO:0005886,GO:0005576		cell wall,vacuole,plasma membrane,extracellular region	hydrolase activity
ug1686	903	GO:0005198,GO:0005840,GO:0006412	translation	ribosome	structural molecule activity
ug1687_1	981	GO:0000166,GO:0003824,GO:0000008			nucleotide binding,RNA catalytic activity
ug1687_2	1399		metabolic process		
ug1688	920				
ug1689	644				
ug1690	841				
ug1691	967	GO:0016020,GO:0006810,GO:0009987	transport,cellular process	membrane	
ug1692	601				
ug1693	1096	GO:0005886,GO:0016020,GO:0008150	biological_process	plasma membrane,membrane	
ug1694	543				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1695	773	GO:0005730,GO:0005198,GO:0000003,GO:0009791,GO:0009790,GO:0005840,GO:0005829,GO:0006412,GO:000	reproduction,post-embryonic development,embryonic development,translation	nucleolus,ribosome,cytosol,mitochondrion	structural molecule activity
ug1696	842	GO:0016020,GO:0005737,GO:0005739		membrane,cytoplasm,mitochondrion	
ug1697	536				
ug1698	480				
ug1699	895	GO:0005840,GO:0006464,GO:0005198,GO:0005840,GO:0000166,GO:0003723	protein modification process,translation	ribosome	structural molecule activity
ug1700	884	GO:0005840,GO:0000166,GO:0003723		ribosome	nucleotide binding,RNA binding
ug1701_1	561	GO:0006810	transport		
ug1701_2	1065				
ug1702	800	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1703	805	GO:0006412,GO:0008135	translation		translation factor activity, nucleic acid binding
ug1704	735	GO:0005198,GO:0005840,GO:0006412	translation	ribosome	structural molecule activity
ug1705	764				
ug1706	871	GO:0016301,GO:0009605,GO:0007165,GO:0009628,GO:0009058,GO:0006139,GO:0000166,GO:0005488	response to external stimulus,signal transduction,response to abiotic stimulus,biosynthetic process,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		kinase activity,nucleotide binding,binding
ug1707	1216	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634,GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005515,GO:0005634,GO:000585	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug1708	789	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005515,GO:0005634,GO:000585	cellular component organization,cellular process	intracellular,nucleus,cytoskeleton	DNA binding,protein binding
ug1709	963				
ug1710	1165	GO:0008135,GO:0005737,GO:0008150,GO:0005886,GO:0006412,GO:0003674,GO:0016020,GO:0009579,GO:0005488,GO:0006810,GO:0009536,GO:0015979,GO:0005739,GO:000	biological_process,translation	cytoplasm,plasma membrane	translation factor activity, nucleic acid binding
ug1711	1439	GO:0005488,GO:0006810,GO:0009536,GO:0015979,GO:0005739,GO:000	transport,photosynthesis,generation of precursor metabolites and energy	membrane,thylakoid,plastid,mitochondrion	molecular_function,binding
ug1712	609				
ug1713	532				
ug1714_1	1308				
ug1714_2	1200	GO:0016787,GO:0008150,GO:0008152	biological_process,metabolic process		hydrolase activity
ug1715_1	479				
ug1715_2	879	GO:0009536,GO:0003677,GO:0006091,GO:0015979,GO:0016020,GO:0019538,GO:0009	generation of precursor metabolites and energy,photosynthesis	plastid,membrane,thylakoid	DNA binding
ug1716	521				
ug1717	1240	GO:0019538,GO:0009987,GO:0003824,GO:0006810,GO:0008289	protein metabolic process,cellular process,transport		catalytic activity,lipid binding
ug1718	644				
ug1719	684				
ug1720	1206	GO:0005622,GO:0019538,GO:0009056,GO:0009987,GO:0005634,GO:0005829,GO:0016787,GO:0019538,GO:0003824,GO:0006464	protein metabolic process,catabolic process,cellular process	intracellular,nucleus,cytosol	hydrolase activity
ug1721	947	GO:0019538,GO:0003824,GO:0006464	protein metabolic process,protein modification process		catalytic activity
ug1722	1505	GO:0005488,GO:0008152,GO:0003824,GO:0003674,GO:0006950,GO:0005886,GO:0006810,GO:0009987,GO:0005515,GO:0016020,GO:0005794,GO:000519	metabolic process,response to stress	plasma membrane,membrane,Golgi apparatus	protein binding,structural molecule activity
ug1723	1165	GO:0005488,GO:0008152,GO:0003824,GO:0003674,GO:0006950,GO:0005886,GO:0006810,GO:0009987,GO:0005515,GO:0016020,GO:0005794,GO:000519	transport,cellular process		
ug1724	642	GO:0006464	protein modification process		
ug1725	876	GO:0005634,GO:0000166,GO:0003723		nucleus	nucleotide binding,RNA binding
ug1726	1254	GO:0005618		cell wall	
ug1727	601	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005515,GO:0005634,GO:000585	cellular component organization,cellular process	intracellular,nucleus,cytoskeleton	DNA binding,protein binding

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1728	568				
ug1729	1210				
ug1730	856				
ug1731	883	GO:0005737,GO:0006464,GO:0005515,GO:019538,GO:0009056,GO:0009987,GO:0005630,GO:0016020,GO:0009536,GO:0009579	protein modification process,protein metabolic process,catabolic process,cellular process	cytoplasm,nucleus	protein binding
ug1732	652	GO:0016020,GO:0009536,GO:0009579		membrane,plastid,thylakoid	
ug1733	845	GO:0016020,GO:0009536,GO:0005840,GO:0005198,GO:0006412	photosynthesis translation	membrane,thylakoid,plastid	
ug1734	768	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1735	732	GO:0006950	response to stress		
ug1736	629	GO:0005840,GO:0005198,GO:0005488,GO:0006412,GO:0005739	translation	ribosome,mitochondrion	structural molecule activity,protein binding
ug1737	1105	GO:0006464	protein modification process		
ug1738	1241	GO:0016787,GO:0009536,GO:0009987,GO:0006629,GO:0003824	biosynthetic process,cellular process,lipid metabolic process		hydrolase activity,catalytic activity
ug1739	854	GO:0005840,GO:0005198,GO:0006412,GO:0006464	translation	ribosome	structural molecule activity,RNA binding
ug1740	878				
ug1741_1	908	GO:0005623,GO:0005005		cell,cytoplasm	
ug1741_2	805	GO:0005634,GO:0000166,GO:0003723		nucleus	nucleotide binding,RNA binding
ug1742	960				
ug1743	1171	GO:0005622,GO:0019538,GO:0009056,GO:0009987,GO:0005634,GO:0005829,GO:0016787,GO:0005856,GO:0005737,GO:0000166,GO:0006464	protein metabolic process,catabolic process,cellular process	intracellular,nucleus,cytosol	hydrolase activity
ug1744	1671	GO:0005622,GO:0019538,GO:0009056,GO:0009987,GO:0005634,GO:0005829,GO:0016787,GO:0005856,GO:0005737,GO:0000166,GO:0006464		cytoskeleton,cytoplasm	nucleotide binding,protein binding
ug1745	842				
ug1746	731				
ug1747	612	GO:0008150,GO:0016787,GO:0003824,GO:0006950,GO:0005829,GO:0016787,GO:0005856,GO:0005739,GO:0009600,GO:0005730,GO:0009600	biological_process response to stress,response to biotic stimulus,metabolic process,carbohydrate metabolic process,generation of precursor metabolites and energy,catabolic process,biosynthetic process,cellular process,biological_process	membrane	
ug1748	839	GO:0008152,GO:0000166,GO:0005975,GO:0006091,GO:0009056,GO:0009058,GO:0009987,GO:0009536,GO:0006464,GO:0009987,GO:0006464	biosynthetic process,cellular amino acid and derivative metabolic process,secondary metabolic process,cellular process,catabolic process,carbohydrate metabolic process	cytosol,cell wall,mitochondrion,nucleolus,plastid,plasma membrane	catalytic activity,nucleotide binding
ug1749	1440	GO:0006519,GO:0019748,GO:0016787,GO:0009987,GO:0009056,GO:0005975,GO:0016740,GO:0009987,GO:0006519,GO:0019748	biosynthetic process,cellular amino acid and derivative metabolic process,secondary metabolic process,cellular process,catabolic process,carbohydrate metabolic process		transferase activity
ug1750_1	1414	GO:0009056,GO:0005975,GO:0016740,GO:0006464	process,carbohydrate metabolic process		hydrolase activity
ug1750_2	1186	GO:0003677,GO:0005515,GO:0009536,GO:0006950,GO:0009987	transcription	plastid	transferase activity,DNA binding,protein binding
ug1751_1	941	GO:0008152,GO:0009987,GO:0016020,GO:0005739,GO:0003824,GO:0005215,GO:0005886,GO:0006810,GO:0006090	response to stress,response to biotic stimulus,metabolic process,cellular process	membrane,mitochondrion,plasma membrane,plastid	catalytic activity,transporter activity
ug1751_2	1166	GO:0005215,GO:0005886,GO:0006810,GO:0006090	transport,generation of precursor metabolites and energy	membrane,mitochondrion,plasma membrane,plastid	catalytic activity,transporter activity
ug1752	740	GO:0005515,GO:0005005,GO:0005198,GO:0005005		extracellular region	protein binding
ug1753	927	GO:0005829,GO:0016020,GO:0006412	translation	ribosome,cytosol,membrane	structural molecule activity
ug1754	779	GO:0005737,GO:0006412,GO:0005198,GO:0003723,GO:0005840,GO:0005215,GO:0016020,GO:0006810,GO:0006090	response to stress	cytoplasm	
ug1755	1017	GO:0005198,GO:0003723,GO:0005840,GO:0005215,GO:0016020,GO:0006810,GO:0006090	translation	ribosome	structural molecule activity,RNA binding
ug1756	952	GO:00091,GO:0006139,GO:0009058,GO:0008289,GO:0005622,GO:0007165,GO:0005151,GO:0005488,GO:000628,GO:0009791,GO:0003677,GO:0006464	transport,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process	membrane,intracellular,plastid,thylakoid	transporter activity,lipid binding
ug1757	873	GO:0005488,GO:000628,GO:0009791,GO:0003677,GO:0006464	signal transduction,response to abiotic stimulus,post-embryonic development,biological_process		protein binding,protein binding
ug1758	1602	GO:0003677,GO:0006464	transcription		DNA binding

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1759	837	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug1760	1059	GO:0019538,GO:0009987,GO:0003824	protein metabolic process,cellular process		catalytic activity
ug1761	698				
ug1762	1043				
ug1763	767	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug1764	1203	GO:0005515			protein binding
ug1765	785	GO:0000003,GO:0009791,GO:0009790	reproduction,post-embryonic development,embryonic		
ug1766	836	GO:0019538,GO:0009987,GO:0003824	protein metabolic process,cellular process		catalytic activity
ug1767	968	GO:0005840,GO:0005198,GO:0009987,GO:0006464	cellular process,translation protein modification process	ribosome	structural molecule activity
ug1768	1210	GO:0016020,GO:0009987,GO:0005840,GO:0006091,GO:0005840,GO:0009987	generation of precursor metabolites and energy,photosynthesis	membrane,plastid	
ug1770_1	748	GO:0005198,GO:0005829,GO:0006412,GO:0019538,GO:0009987,GO:0009579,GO:0009536,GO:0005488,GO:0005737,GO:0003824,GO:0005773,GO:0005198	translation protein metabolic process,cellular process	ribosome,plastid,cytosol	structural molecule activity,RNA binding
ug1770_2	782	GO:0005198,GO:0005840,GO:0005829,GO:0006412,GO:0005198,GO:0005840,GO:0005488,GO:0005737,GO:0003824,GO:0005773,GO:0005198	translation protein metabolic process,cellular process	thylakoid,plastid,cytoplasm	binding,catalytic activity
ug1771	780	GO:0005198,GO:0005840,GO:0005829,GO:0006412,GO:0005198,GO:0005840,GO:0005488,GO:0005737,GO:0003824,GO:0005773,GO:0005198	translation	vacuole,ribosome,cytosol	structural molecule activity
ug1772	1200	GO:0005198,GO:0005840,GO:0005829,GO:0006412,GO:0005198,GO:0005840,GO:0005488,GO:0005737,GO:0003824,GO:0005773,GO:0005198	translation	ribosome	structural molecule activity
ug1773	948	GO:0005198,GO:0005840,GO:0005829,GO:0006412,GO:0005198,GO:0005840,GO:0005488,GO:0005737,GO:0003824,GO:0005773,GO:0005198	metabolic process,cellular process	cytoplasm	binding,catalytic activity,molecular_function
ug1774_1	625	GO:0008150,GO:000515,GO:0016787,GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634,GO:0005840,GO:0005198,GO:0006412,GO:0005198,GO:0006412	biological_process	plasma membrane	protein binding,hydrolase activity
ug1774_2	751	GO:0005198,GO:0005840,GO:0005829,GO:0006412,GO:0005198,GO:0005840,GO:0005488,GO:0005737,GO:0003824,GO:0005773,GO:0005198	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug1775	591	GO:0005198,GO:0005840,GO:0005829,GO:0006412,GO:0005198,GO:0005840,GO:0005488,GO:0005737,GO:0003824,GO:0005773,GO:0005198	translation	ribosome	structural molecule activity
ug1776	564	GO:0005198,GO:0005840,GO:0005829,GO:0006412,GO:0005198,GO:0005840,GO:0005488,GO:0005737,GO:0003824,GO:0005773,GO:0005198	cellular process,translation	ribosome,cytosol	structural molecule activity
ug1777	904	GO:0005198,GO:0005840,GO:0005829,GO:0006412,GO:0005198,GO:0005840,GO:0005488,GO:0005737,GO:0003824,GO:0005773,GO:0005198	protein modification process,protein metabolic process,catabolic process,cellular		catalytic activity
ug1778	212				
ug1779	786	GO:0003676,GO:0000166			nucleic acid binding,nucleotide binding
ug1780	682	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1781	1117	GO:0005737,GO:0009058,GO:0005975,GO:0009987,GO:0006629,GO:0003824,GO:0006139,GO:0009056,GO:0019748,GO:0006091	biosynthetic process,carbohydrate metabolic process,cellular process,lipid metabolic process,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,catabolic process,secondary metabolic process,generation of precursor	cytoplasm	catalytic activity
ug1782	563	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005515,GO:0005634,GO:000585	cellular component organization,cellular process	intracellular,nucleus,cytoskeleton	DNA binding,protein binding
ug1783	587				
ug1784_1	1063	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1784_2	985				
ug1785_1	624				
ug1785_2	1365	GO:0016740,GO:0009058,GO:0006519,GO:0019748,GO:0005515	biosynthetic process,cellular amino acid and derivative metabolic process,secondary metabolic		transferase activity,protein binding
ug1786	1545	GO:0016740			transferase activity
ug1787	929	GO:0006810,GO:0016020,GO:0005215,GO:0005198,GO:0005840	transport	membrane	transporter activity
ug1788	1497	GO:0005198,GO:0005840,GO:0005829,GO:0006412,GO:0003723,GO:0005198,GO:0005840,GO:0005488,GO:0005737,GO:0003824,GO:0005773,GO:0005198	translation	ribosome,plastid,mitochondrion	structural molecule activity,RNA binding

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1789	673	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0009536,G	cellular component organization,cellular process	intracellular,plastid,nucleus	DNA binding
ug1790	1462				
ug1791	858	GO:0007165,GO:000515,GO:0005488,GO:0016740,GO:0009628,GO:0009791,GO:000815	signal transduction,response to abiotic stimulus,post-embryonic development,biological_process		protein binding,transferase activity
ug1792	805	GO:0006412,GO:0008135,GO:0005739	translation	mitochondrion	translation factor activity, nucleic acid binding
ug1793	624	GO:0009719,GO:0008150	response to endogenous stimulus,biological_process		
ug1794	577				
ug1795	160				
ug1796	742				
ug1797	666	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		
ug1798_1	911	GO:0005488,GO:0008152,GO:0003824,GO:0	metabolic process,response to stress		binding,catalytic activity
ug1798_2	401				
ug1799	699	GO:0003677			DNA binding
ug1800	435				
ug1801_1	906	GO:0003824,GO:0009005,GO:0009058,GO:0009		plastid	catalytic activity
ug1801_2	854	987,GO:0006629,GO:0005215,GO:0005488,G	biosynthetic process,cellular process,lipid metabolic process	plastid	transporter activity,binding
ug1802	858				
ug1803	695				
ug1804	969	GO:0016043,GO:000987,GO:0005622,GO:0005634,GO:0003700,GO:0005198,GO:000368	cellular component organization,cellular process	intracellular,nucleus	transcription factor activity,structural molecule activity,chromatin binding
ug1805	613	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1806	700				
ug1807	444	GO:0005840,GO:0005198,GO:0006412,GO:0005622,GO:0003	translation	ribosome,mitochondrion	structural molecule activity
ug1808	733	677,GO:0016043,GO:0009987,GO:0009536,G	cellular component organization,cellular process	intracellular,plastid,nucleus	DNA binding
ug1809	625				
ug1810	1153	GO:0008152,GO:0005488,GO:0030528,GO:0005840,GO:0005198,GO:0006412	metabolic process		binding,transcription regulator activity,catalytic
ug1811	594	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1812	992	GO:0006950	response to stress		
ug1813_1	741				
ug1813_2	822	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug1814	590	GO:0005488,GO:0003677,GO:0005840,GO:0005198,GO:0006412	translation	ribosome	binding,molecular_function
ug1815	1078	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1816	631	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1817	1284	GO:0006091,GO:0015979,GO:0005737,GO:0016020,GO:0009579,G	generation of precursor metabolites and energy,photosynthesis	cytoplasm,membrane,thylakoid,plastid	
ug1818	1126	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0006950,G	cellular component organization,cellular process,response to stress	intracellular,nucleus	DNA binding
ug1819	686				
ug1820	921	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1821	719	GO:0005739		mitochondrion	
ug1822_1	832	GO:0005615		extracellular space	
ug1822_2	1767	GO:0005737,GO:0008135,GO:0000166,GO:0006412,GO:0016787	translation	cytoplasm	translation factor activity, nucleic acid binding,nucleotide
ug1823	1162	GO:0005618,GO:0005198,GO:0016301,GO:0005975,GO:0009987	carbohydrate metabolic process,cellular process	cell wall,plasma membrane	
ug1824	1310	GO:0009536,GO:0005622,GO:0006091,GO:0015979,GO:0016020,G	generation of precursor metabolites and energy,photosynthesis,protein modification process	plastid,intracellular,membrane,thylakoid	binding
ug1825	963	O:0009579,GO:000548			



Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1826	826	GO:0006091,GO:0015979,GO:0006950,GO:0003674,GO:0005488,GO:0016020,GO:0009579,GO:0006810,GO:000005737,GO:0005634,GO:0006464	generation of precursor metabolites and energy,photosynthesis,response to stress,transport	membrane,thylakoid,cytoplasm,plastid	molecular_function,binding
ug1827	1647	GO:0005737,GO:0005634,GO:0006464	protein modification process	cytoplasm,nucleus	
ug1828	178				
ug1829	798	GO:0016787,GO:0030234			hydrolase activity,enzyme regulator activity
ug1830	644				
ug1831	823	GO:0005737,GO:0005772		cytoplasm	binding
ug1832	772				
ug1833	675	GO:0005840		ribosome	
ug1834	762	GO:0006091,GO:0015979,GO:0016020,GO:0005622,GO:0008150,GO:0019538,GO:0009056,GO:0009987,GO:0005634,GO:0005829,GO:0016787,GO:0000019538,GO:0009056,GO:0009987,GO:0006464,GO:0003824,GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005515,GO:0005634,GO:0005850,GO:0006412,GO:0008135	generation of precursor metabolites and energy,photosynthesis	membrane,thylakoid	
ug1835	1059	GO:0019538,GO:0009056,GO:0009987,GO:0005634,GO:0005829,GO:0016787,GO:0000019538,GO:0009056,GO:0009987,GO:0006464,GO:0003824,GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005515,GO:0005634,GO:0005850	biological_process,protein metabolic process,catabolic process,cellular process,response to stress,response to abiotic stimulus	intracellular,nucleus,cytosol	hydrolase activity
ug1836	1027	GO:0019538,GO:0009056,GO:0009987,GO:0006464,GO:0003824,GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005515,GO:0005634,GO:0005850	protein metabolic process,catabolic process,cellular process,protein modification process		catalytic activity
ug1837	608	GO:0016043,GO:0009987,GO:0005515,GO:0005634,GO:0005850	cellular component organization,cellular process	intracellular,nucleus,cytoskeleton	DNA binding,protein binding
ug1838	1007	GO:0006412,GO:0008135	translation		translation factor activity,nucleic acid binding
ug1839	674	GO:0016020,GO:0005966		membrane,mitochondrion	
ug1840	966				
ug1841	1108	GO:0009719,GO:0007165,GO:0016740	response to endogenous stimulus,signal transduction		transferase activity
ug1842	770	GO:0005488,GO:0009794		plastid	binding
ug1843	794				
ug1844	1233	GO:0006950,GO:0009056,GO:0009987,GO:0005737,GO:0003674,GO:0005488,GO:0008152,GO:0003824,GO:0000019538,GO:0009056,GO:0009987,GO:0003824,GO:0006464	response to stress,catabolic process,cellular process,metabolic process	cytoplasm,extracellular region	molecular_function,binding,catalytic activity
ug1845	843	GO:0019538,GO:0009056,GO:0009987,GO:0003824,GO:0006464	protein metabolic process,catabolic process,cellular process,protein modification process		catalytic activity
ug1846	878				
ug1847	956				
ug1848_1	891				
ug1848_2	890	GO:0007165,GO:000515,GO:0005488,GO:0016740,GO:0009628,GO:0009791,GO:000815	signal transduction,response to abiotic stimulus,post-embryonic development,biological_process		protein binding,transferase activity
ug1849	1010				
ug1850	529				
ug1851	592	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1852	465				
ug1853	739	GO:0016020,GO:0009579,GO:0009536,GO:000009536	photosynthesis	membrane,thylakoid,plastid	
ug1854_1	632			plastid	
ug1854_2	1131	GO:0009058,GO:0006519,GO:0005488,GO:0003824,GO:0008152	biosynthetic process,cellular amino acid and derivative metabolic process,metabolic process		binding,catalytic activity
ug1855	665	GO:0016020,GO:0009579,GO:0015979,GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005618,GO:0005198,GO:0005840,GO:0006412	photosynthesis	membrane,thylakoid,plastid	
ug1856	802	GO:0016043,GO:0009987,GO:0005618,GO:0005198,GO:0005840,GO:0006412	cellular component organization,cellular process	intracellular,cell wall,nucleus	DNA binding
ug1857	794		translation	ribosome	structural molecule activity
ug1858	966				
ug1859	1049	GO:0003824,GO:0005737,GO:0008152,GO:0000016740,GO:0005488,GO:000003824,GO:0008152,GO:0009987,GO:0006091,GO:0009056,GO:0000009536,GO:0000009791,GO:000000003	metabolic process	cytoplasm	catalytic activity,binding
ug1860	1587	GO:0003824,GO:0008152,GO:0009987,GO:0006091,GO:0009056,GO:0000009536,GO:0000009791,GO:000000003	metabolic process,cellular process,generation of precursor metabolites and energy,catabolic process,carbohydrate metabolic process	plasma membrane	transferase activity,transferase activity,binding,catalytic activity
ug1861	798	GO:0009056,GO:0000009536,GO:0000009791,GO:000000003	reproduction,post-embryonic development,embryonic	plastid	



Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug1902	1116				
ug1903	475				
ug1904	721				
ug1905	750	GO:0016020,GO:0009579,GO:0015979	photosynthesis	membrane,thylakoid	
ug1906	1059	GO:0005198,GO:0006	transport		structural molecule activity
ug1907	920	GO:0008150	biological_process		
ug1908	846	GO:0006810	transport		
ug1909	551	GO:0005840,GO:0005198,GO:0006412,GO:0005730,GO:0005	translation	ribosome	structural molecule activity
ug1910	809	198,GO:0000003,GO:0009791,GO:0009790,GO:0005840,GO:0005829,GO:0006412,GO:0009	reproduction,post-embryonic development,embryonic development,translation	nucleolus,ribosome,cytosol,mitochondrion	structural molecule activity
ug1911	716	579,GO:0006091,GO:0015979,GO:0009536	generation of precursor metabolites and energy,photosynthesis	membrane,thylakoid,plastid	
ug1912	1084	GO:0009579,GO:0009536,GO:0006091,GO:0015979,GO:0005488,GO:0009628,GO:001602	generation of precursor metabolites and energy,photosynthesis,response to abiotic stimulus	thylakoid,plastid,membrane	binding
ug1913	733	GO:0016787,GO:0005840,GO:0005198,GO:0009058,GO:0005975,GO:0009987,GO:000662	biosynthetic process,carbohydrate metabolic process,cellular process,lipid metabolic process,translation	ribosome	hydrolase activity,structural molecule activity
ug1914	749	GO:0019725,GO:0005829,GO:0003824	cellular homeostasis	cytosol	catalytic activity
ug1915	1419	GO:0005737,GO:0005634,GO:0006464	protein modification process	cytoplasm,nucleus	
ug1916	916	GO:0016020,GO:0009579,GO:0005488,GO:0005198,GO:0009	photosynthesis	membrane,thylakoid	binding
ug1917	577	987,GO:0005840,GO:0005829,GO:0005488,GO:0006412,GO:000372	cellular process,translation	ribosome,cytosol	structural molecule activity,binding,RNA binding
ug1918	549	GO:0005737,GO:0008152,GO:0003824,GO:0	metabolic process	cytoplasm	catalytic activity,binding
ug1919	819				
ug1920	643	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1921	1433	GO:0005840,GO:0005198,GO:0009987,GO:0006412,GO:0009	cellular process,translation	ribosome	structural molecule activity
ug1922	702	GO:0016020,GO:0009579,GO:0005515,GO:0	photosynthesis	membrane,thylakoid	protein binding
ug1923	1035	GO:0006950	response to stress		
ug1924	770				
ug1925	1137	GO:0006950,GO:0009579,GO:0005773,GO:0006810,GO:0005886,GO:0016020,GO:000521	response to stress,response to abiotic stimulus,transport	vacuole,plasma membrane,membrane,plastid	transporter activity
ug1926	803	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug1927	855				
ug1928	753	GO:0016020,GO:0009579,GO:0009536,GO:0	photosynthesis	membrane,thylakoid,plastid	
ug1929	725				
ug1930	1036	GO:0005488,GO:0008152,GO:0006950,GO:0009987,GO:0005739,GO:0005840,GO:0006	metabolic process,response to stress,cellular process	mitochondrion	binding,catalytic activity
ug1931	431	464,GO:0005198,GO:0005634,GO:0006412	protein modification process,translation	ribosome,nucleus	structural molecule activity
ug1932	725	GO:0006810	transport		
ug1933	692	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1934	755	GO:0006412,GO:0008135	translation		translation factor activity, nucleic acid binding
ug1935	696	GO:0005215,GO:0016020,GO:0005739,GO:0006810,GO:0006091,GO:0006139,GO:0009058,GO:0008289,GO:000	transport,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process	membrane,mitochondrion,intracellular ar	transporter activity,lipid binding
ug1936	741	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug1937	1050	GO:0005488			binding
ug1938	661				





Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug2019_1	449	GO:000166,GO:0009058,GO:0009987,GO:006629,GO:0008152,GO:0016020,GO:0006139,GO:0003824,GO:00016020,GO:0008152,GO:0009058,GO:0009987,GO:0006629,GO:0006139,GO:0003824	biosynthetic process,cellular process,lipid metabolic process,metabolic process,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process,cellular process,lipid metabolic process,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane,endoplasmic reticulum	nucleotide binding,catalytic activity
ug2019_2	436	GO:0009987,GO:0006629,GO:0006139,GO:0003824	metabolic process,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane	nucleotide binding,catalytic activity
ug2020	453	GO:0000166			nucleotide binding
ug2021	443				
ug2022	427				
ug2023	448				
ug2024	437				
ug2025	485				
ug2026	444	GO:0016020,GO:0005773,GO:0006810,GO:006091,GO:0006139,GO:0009058,GO:0016787,GO:0005215,GO:0006519,GO:0019748,GO:0009653,GO:0016043,GO:0016049,GO:0009	transport,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process,cellular amino acid and derivative metabolic process,secondary metabolic process,anatomical structure mo...	membrane,vacuole,plastid,plasma membrane	hydrolase activity,transporter activity
ug2027	460				
ug2028	455				
ug2029	434				
ug2030	452				
ug2031	468				
ug2032	455	GO:0003676,GO:0000166			nucleic acid binding,nucleotide binding
ug2033	464	GO:0005488			binding
ug2034	413				
ug2035	382				
ug2036	448				
ug2037	455				
ug2038	452				
ug2039	480	GO:0009719,GO:0009628	response to endogenous stimulus,response to abiotic		
ug2040	399	GO:0005737,GO:0019538,GO:0009056,GO:0009987,GO:0006810	protein metabolic process,catabolic process,cellular process,transport	cytoplasm	
ug2041	413	GO:0005737,GO:0019538,GO:0009056,GO:0009987,GO:0006810	protein metabolic process,catabolic process,cellular process,transport	cytoplasm	
ug2042	431				
ug2043	354				
ug2044	309				
ug2045	405				
ug2046	422	GO:0005488,GO:0008152,GO:0003824,GO:0003674,GO:0006950	metabolic process,response to stress		binding,catalytic activity,molecular_function
ug2047	459	GO:0005623,GO:0003824,GO:0005488		cell	catalytic activity,binding
ug2048	500				
ug2049	441	GO:0005739,GO:0016506		mitochondrion,membrane	
ug2050	506	GO:0016787			hydrolase activity
ug2051	433				
ug2052	529				
ug2053	456				
ug2054	359				
ug2055	448				
ug2056	515	GO:0005730,GO:0003450		nucleolus	catalytic activity
ug2057	488				
ug2058	455				
ug2059_1	268				
ug2059_2	444	GO:0009536		plastid	
ug2060	309				
ug2061	296				
ug2062	456				
ug2063	396	GO:0016787,GO:0000166,GO:0009536,GO:0005886		plastid	hydrolase activity,nucleotide binding,transporter activity
ug2064	451	GO:0005886		plasma membrane	
ug2065	385				
ug2066		GO:0005515,GO:0007275,GO:0006464,GO:0019538,GO:0009056,GO:0009987,GO:0003824,GO:0005634,GO:000	multicellular organismal development,protein modification process,protein metabolic process,catabolic process,cellular process	nucleus	protein binding,catalytic activity,binding



Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug2104_1	253				
ug2104_2	497	GO:0005488,GO:0006139,GO:0016740,GO:0030528,GO:0006350,GO:0005634	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	mitochondrion	binding,transferase activity
ug2105_1	510		transcription	nucleus	transcription regulator activity
ug2105_2	433				
ug2106_1	530				
ug2106_2	556				
ug2107_1	420				
ug2107_2	476				
ug2108_1	420				
ug2108_2	562				
ug2109_1	423				
ug2109_2	538				
ug2110_1	425				
ug2110_2	525				
ug2111_1	431	GO:0008152,GO:0003824,GO:0016020,GO:000166,GO:0006139	metabolic process,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane	catalytic activity,nucleotide binding
ug2111_2	494				
ug2112_1	420	GO:0009058,GO:000987,GO:0009536,GO:0009058,GO:000987,GO:0005488,GO:016043,GO:0009536,GO:0000166,GO:0008152,GO:0003824,GO:0005840,GO:0003824,GO:0005777,GO:0003674,GO:0000166,GO:0008152,GO:0009536,GO:0016020,GO:000	biosynthetic process,cellular process	plastid	structural molecule activity
ug2112_2	527		biosynthetic process,cellular process,cellular component organization	plastid	binding,structural molecule activity
ug2113_1	309		metabolic process		nucleotide binding,catalytic activity,molecular_function
ug2113_2	514		metabolic process	ribosome,peroxisome,plastid,membrane,nucleus,extracellular region	catalytic activity,molecular_function,nucleotide binding
ug2114_1	261				
ug2114_2	292				
ug2115_1	272				
ug2115_2	503				
ug2116_1	215				
ug2116_2	516	GO:0005794		Golgi apparatus	
ug2117_1	428	GO:0006950,GO:0009835,GO:0006350,GO:0003700,GO:0005634,GO:0007165,GO:0009710,GO:0006950,GO:0009835,GO:0006350,GO:0003700,GO:0005634,GO:0007165,GO:0009710	response to stress,ripening,transcription,signal transduction,response to endogenous stimulus	nucleus	transcription factor activity
ug2117_2	506		stress,ripening,transcription,signal transduction,response to endogenous stimulus	nucleus	transcription factor activity
ug2118_1	415				
ug2118_2	344				
ug2119_1	421				
ug2119_2	572				
ug2120_1	413				
ug2120_2	443				
ug2121_1	164				
ug2121_2	512	GO:0006091,GO:0016020,GO:0005739,GO:0003824,GO:0005215	generation of precursor metabolites and energy	membrane,mitochondrion	catalytic activity,transporter activity
ug2122_1	381				
ug2122_2	551	GO:0004872,GO:0008152,GO:0016787	metabolic process		receptor activity,hydrolase activity
ug2123_1	427	GO:0008152,GO:0016787,GO:0009536	metabolic process	plastid	hydrolase activity
ug2123_2	563		metabolic process	plastid	hydrolase activity
ug2124_1	397				
ug2124_2	598				
ug2125_1	433				
ug2125_2	492				
ug2126_1	401	GO:0006464,GO:0016301,GO:0000166	protein modification process		kinase activity,nucleotide binding
ug2126_2	518		protein modification process		kinase activity,nucleotide binding
ug2127_1	402				
ug2127_2	543	GO:0009058,GO:0006519,GO:0016301	biosynthetic process,cellular amino acid and derivative metabolic response to abiotic stimulus,response to stress		kinase activity
ug2128_1	427				
ug2128_2	507				
ug2129_1	413				
ug2129_2	627	GO:0005488,GO:0003824			binding,nucleic acid binding



Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug2130_1	430	GO:0003723,GO:0016740,GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		RNA binding,transferase activity
ug2130_2	460	GO:0003723,GO:0016740,GO:0006139,GO:0	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	plastid	RNA binding,transferase activity
ug2131_1	416				
ug2131_2	188				
ug2132_1	435				
ug2132_2	580				
ug2133_1	426	GO:0006139,GO:0009056,GO:0016787,GO:0005829	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,catabolic process	cytosol	hydrolase activity
ug2133_2	520	GO:0006139,GO:0009056,GO:0016787,GO:0005829	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,catabolic process	cytosol	hydrolase activity
ug2134_1	404	GO:0005737,GO:0016043,GO:0009987,GO:0005515,GO:0016049,GO:0005737,GO:0016	cellular component organization,cellular process,cell growth	cytoplasm,nucleus	protein binding
ug2134_2	421	GO:0005737,GO:0016043,GO:0009987,GO:0005515,GO:0016049,GO	cellular component organization,cellular process,cell growth	cytoplasm,nucleus	protein binding
ug2135_1	446				
ug2135_2	529	GO:0005488			binding
ug2136_1	426				
ug2136_2	580				
ug2137_1	433	GO:0003824			catalytic activity
ug2137_2	600	GO:0003824			catalytic activity
ug2138_1	421	GO:0005576,GO:0000043,GO:0005618,GO:0016043,GO:0009987,GO:0009653,GO:0016049,GO:0005576,GO:0000000,GO:0004871,GO:0009	reproduction cellular component organization,cellular process,anatomical structure morphogenesis,cell response to abiotic stimulus,tropism	extracellular region cell wall,extracellular region	
ug2138_2	547	GO:0005576,GO:0000000,GO:0004871,GO:0009	reproduction cellular component organization,cellular process,anatomical structure morphogenesis,cell response to abiotic stimulus,tropism	extracellular region cell wall,extracellular region	
ug2139_1	414	GO:0005634,GO:0005515,GO:0004871,GO:0009	response to abiotic stimulus,tropism	nucleus	signal transducer activity,protein binding
ug2139_2	602	GO:0005634,GO:0005515,GO:0004871,GO:0009	response to abiotic stimulus,tropism	nucleus	signal transducer activity,protein binding
ug2140_1	430				
ug2140_2	495				
ug2141_1	413	GO:0003674,GO:0009058,GO:0009987,GO:0006629,GO:0003824,GO:0005488,GO:0009628,GO:0008152,GO:0006519,GO:0019748,GO:0016020,GO:0005576,GO:0009058,GO:0009987,GO:0006629,GO:0003824,GO:0009628,GO:0005488,GO:0008152,GO:0006519,GO:0019748,GO:0016020,GO:	biosynthetic process,cellular process,lipid metabolic process,response to abiotic stimulus,metabolic process,cellular amino acid and derivative metabolic process,secondary metabolic process biosynthetic process,cellular process,lipid metabolic process,response to abiotic stimulus,metabolic process,cellular amino acid and derivative metabolic process,secondary	membrane,extracellular region,endoplasmic reticulum	molecular_function,catalytic activity,protein binding
ug2141_2	523	GO:0003674,GO:0009058,GO:0009987,GO:0006629,GO:0003824,GO:0009628,GO:0005488,GO:0008152,GO:0006519,GO:0019748,GO:0016020,GO:	biosynthetic process,cellular process,lipid metabolic process,response to abiotic stimulus,metabolic process,cellular amino acid and derivative metabolic process,secondary	membrane,endoplasmic reticulum	catalytic activity,protein binding
ug2142_1	423				
ug2142_2	507				
ug2143_1	407	GO:0003824,GO:0005488,GO:0009058,GO:0009987,GO:0009628,GO:0009791,GO:0008152,GO:0009056,GO:0006519,GO:0016787,GO:0005739,GO:0016740,GO:0003824,GO:0005488,GO:0009058,GO:0009987,GO:0009628,GO:0009791,GO:0008152,GO:0009056,GO:0006519,GO:0016787,GO:0005739,GO:0016740,GO:0003824,GO:0005488,GO:0009058,GO:0009987,GO:0009628,GO:	biosynthetic process,cellular process,response to abiotic stimulus,post-embryonic development,metabolic process,catabolic process,cellular amino acid and derivative metabolic process biosynthetic process,cellular process,response to abiotic stimulus,post-embryonic development,metabolic process,catabolic process,cellular amino acid and derivative metabolic process	mitochondrion,membrane,nucleus	catalytic activity,protein binding,hydrolase activity,transferase activity
ug2143_2	597	GO:0009791,GO:0008152,GO:0009056,GO:0006519,GO:0016787,GO:0005739,GO:0016740,GO:0003824,GO:0005488,GO:0009058,GO:0009987,GO:0009628,GO:	development,metabolic process,catabolic process,cellular amino acid and derivative metabolic process biosynthetic process,cellular process,response to abiotic stimulus,post-embryonic development,metabolic process,catabolic process,cellular amino acid and derivative metabolic process	mitochondrion,nucleus	catalytic activity,protein binding,hydrolase activity,transferase activity
ug2144_1	391				
ug2144_2	575	GO:0005739		mitochondrion	
ug2145_1	419	GO:0006810,GO:0009987,GO:0016020,GO:0016043,GO:0005515,GO:0006810,GO:0009	transport,cellular process,cellular component organization	membrane	protein binding
ug2145_2	539	GO:0006810,GO:0009987,GO:0016020,GO:0016043,GO:0005515,GO:0007165,GO:0006629,GO:0016787	transport,cellular process,cellular component organization signal transduction,lipid metabolic process	membrane	protein binding
ug2146_1	378	GO:0007165,GO:0006629,GO:0016787	signal transduction,lipid metabolic process		hydrolase activity
ug2146_2	444				
ug2147_1	408				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug2147_2	593	GO:0016043,GO:0009987,GO:0005856,GO:0005515,GO:0000166,GO:0005737,GO:000563	cellular component organization,cellular process	cytoskeleton,cytoplasm,nucleus	protein binding,nucleotide binding
ug2148_1	126				
ug2148_2	583	GO:0016020		membrane	
ug2149_1	439				
ug2149_2	557				
ug2150_1	356				
ug2150_2	386	GO:0003700,GO:0005634,GO:0006350	transcription	nucleus	transcription factor activity
ug2151_1	456	GO:0003824,GO:0008152,GO:0006519,GO:0003824,GO:0008152,GO:0006519,GO:000	metabolic process,cellular amino acid and derivative metabolic		catalytic activity,binding
ug2151_2	558	GO:0003824,GO:0008152,GO:0006519,GO:000	metabolic process,cellular amino acid and derivative metabolic		catalytic activity,binding
ug2152_1	277				
ug2152_2	498	GO:0009536		plastid	
ug2153_1	322				
ug2153_2	617				
ug2154_1	428				
ug2154_2	498				
ug2155_1	299	GO:0005515			protein binding
ug2155_2	450				
ug2156_1	493	GO:0005773,GO:0006810,GO:0005215,GO:0005773,GO:0006810,GO:0005215,GO:0016020	transport	vacuole,membrane	transporter activity
ug2156_2	372	810,GO:0005886,GO:0005215,GO:0016020	transport	vacuole,plasma membrane,membrane	transporter activity
ug2157_1	527	GO:0016787,GO:0019538,GO:0009056	protein metabolic process,catabolic process		hydrolase activity
ug2157_2	382	GO:0016787,GO:0005737,GO:0019538,GO:000	protein metabolic process,catabolic process	cytoplasm	hydrolase activity
ug2158_1	523				
ug2158_2	117				
ug2159_1	498	GO:0005737,GO:0006464,GO:0005515	protein modification process	cytoplasm	protein binding
ug2159_2	391				
ug2160_1	498	GO:0005515			protein binding
ug2160_2	395	GO:0005515			protein binding
ug2161_1	515				
ug2161_2	376	GO:0003677,GO:0003700,GO:0005634,GO:000	transcription	nucleus	DNA binding,transcription factor activity
ug2162_1	473				
ug2162_2	392	GO:0016020,GO:0016740,GO:0009058,GO:0009987,GO:0006629,GO:0005737,GO:0006	biosynthetic process,cellular process,lipid metabolic process	membrane	transferase activity
ug2163_1	500	412,GO:0008135,GO:0005634,GO:0005488,GO:0005737,GO:0006	translation	cytoplasm,nucleus	translation factor activity, nucleic acid binding,binding
ug2163_2	355	412,GO:0008135,GO:0005634,GO:0005488	translation	cytoplasm,nucleus	translation factor activity, nucleic acid binding,binding
ug2164_1	484				
ug2164_2	504				
ug2165_1	259				
ug2165_2	423				
ug2166_1	423	GO:0008289			lipid binding
ug2166_2	529	GO:0008289			lipid binding
ug2167_1	279				
ug2167_2	468	GO:0016020,GO:0006519,GO:0006629,GO:0005488,GO:0016787	cellular amino acid and derivative metabolic process,lipid metabolic process	membrane	binding,hydrolase activity
ug2168_1	427				
ug2168_2	542	GO:0005737		cytoplasm	
ug2169_1	372	GO:0005488,GO:0008152,GO:0003824,GO:000	metabolic process		binding,catalytic activity,molecular_function
ug2169_2	148				
ug2170_1	470	GO:0003677,GO:0003700,GO:0005634,GO:000	transcription	nucleus	DNA binding,transcription factor activity
ug2170_2	587	GO:0003677,GO:0006	transcription		DNA binding
ug2171_1	437				
ug2171_2	546				
ug2172_1	123				
ug2172_2	487				
ug2173_1	409	GO:0005488,GO:0006519,GO:0003824	cellular amino acid and derivative metabolic process		binding,catalytic activity
ug2173_2	460				
ug2174_1	433				
ug2174_2	396				
ug2175_1	239				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug2175_2	578				
ug2176_1	443				
ug2176_2	597	GO:0003677,GO:000515,GO:0003700,GO:0005634,GO:0006350	transcription	nucleus	DNA binding,protein binding,transcription factor activity
ug2177_1	514	GO:0016301,GO:0004871,GO:0006464,GO:000166,GO:0007165,GO:0016301,GO:0004	protein modification process,signal transduction	mitochondrion	kinase activity,signal transducer activity,nucleotide binding
ug2177_2	546	GO:0016301,GO:0004871,GO:0006464,GO:000166,GO:0007165	protein modification process,signal transduction		kinase activity,signal transducer activity,nucleotide binding
ug2178_1	464				
ug2178_2	605				
ug2179_1	255				
ug2179_2	247				
ug2180_1	401				
ug2180_2	549	GO:0005488,GO:0019538,GO:0009056,GO:0009987,GO:0006464,GO:0003824,GO:000562	protein metabolic process,catabolic process,cellular process,protein modification process	intracellular	binding,catalytic activity
ug2181_1	350				
ug2181_2	488	GO:0003677,GO:000515,GO:0003700,GO:0005634,GO:0006350	transcription	nucleus	DNA binding,protein binding,transcription factor activity
ug2182_1	106				
ug2182_2	494	GO:0005488,GO:0008150,GO:0006950,GO:0	biological_process,response to stress		binding,protein binding
ug2183_1	243				
ug2183_2	544	GO:0005773		vacuole	
ug2184_1	417	GO:0005488,GO:0016787,GO:0006412,GO:0009536,GO:0005739	translation	plastid,mitochondrion	binding,hydrolase activity
ug2184_2	575	GO:0006464,GO:0005618,GO:0005488,GO:0016787,GO:0009536,GO:0006412,GO:000573	protein modification process,translation	cell wall,plastid,mitochondrion	binding,hydrolase activity
ug2185_1	598				
ug2185_2	549				
ug2186_1	608	GO:0005739,GO:0005		mitochondrion,endoplasmic	
ug2186_2	574	GO:0005739,GO:0005		mitochondrion,endoplasmic	
ug2187_1	637	GO:0008152,GO:0003	metabolic process		catalytic activity
ug2187_2	566				
ug2188_1	609	GO:0016740,GO:0008	metabolic process		transferase activity
ug2188_2	191				
ug2189_1	597	GO:0003824,GO:0005			catalytic activity,protein binding
ug2189_2	552	GO:0003824,GO:0005			catalytic activity,protein binding
ug2190_1	535	GO:0008152,GO:0003824,GO:0005488	metabolic process		catalytic activity,protein binding
ug2190_2	376	GO:0008152,GO:0003824,GO:0005488	metabolic process		catalytic activity,protein binding
ug2191_1	497	GO:0005622,GO:0000166,GO:0007165	signal transduction	intracellular	nucleotide binding
ug2191_2	407				
ug2192_1	474				
ug2192_2	421	GO:0016020		membrane	
ug2193_1	467				
ug2193_2	375				
ug2194_1	442				
ug2194_2	345	GO:0005515			protein binding
ug2195_1	519	GO:0005654,GO:0030528,GO:0016043,GO:0006350,GO:0000166,G	cellular component organization,transcription	nucleoplasm	transcription regulator activity,nucleotide binding,catalytic activity
ug2195_2	399				
ug2196_1	476				
ug2196_2	396				
ug2197_1	447	GO:0003723,GO:0008152,GO:0003824,GO:0016740,GO:0000166,GO:0006259,GO:000905	metabolic process,DNA metabolic process,biosynthetic process		RNA binding,catalytic activity,transferase activity,nucleotide binding
ug2197_2	412	GO:0008152,GO:0003676,GO:0003824,GO:0003824,GO:0019	metabolic process		nucleic acid binding,catalytic activity,nucleotide binding
ug2198_1	599	GO:0005488,GO:0009056,GO:0009987,GO:0005515	protein metabolic process,catabolic process,cellular process		catalytic activity,protein binding
ug2198_2	394	GO:0003824,GO:0005739,GO:0003723,GO:0005		mitochondrion	catalytic activity
ug2199_1	488	GO:0006412,GO:0005739,GO:0005634,GO:0000166	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	cytoplasm,nucleus	RNA binding,nucleotide binding
ug2199_2	262				
ug2200_1	488				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug2200_2	434				
ug2201_1	415	GO:0005515			protein binding
ug2201_2	427				
ug2202_1	427	GO:0005783,GO:0006810,GO:0009987	transport,cellular process	endoplasmic reticulum	
ug2202_2	445	GO:0005783,GO:0006810,GO:0009987	transport,cellular process	endoplasmic reticulum	
ug2203_1	561	GO:0009536		plastid	
ug2203_2	463				
ug2204_1	568	GO:0005488,GO:0008152,GO:0003824,GO:0005488	metabolic process		binding,catalytic activity,molecular_function
ug2204_2	468	GO:0003824,GO:0005488			catalytic activity,binding
ug2205_1	550	GO:0005488,GO:0008152,GO:0003824	metabolic process		binding,catalytic activity
ug2205_2	459				
ug2206_1	524	GO:0006412,GO:0008135,GO:0016020	translation	membrane	translation factor activity,nucleic acid binding
ug2206_2	461	GO:0005488			binding
ug2207_1	495				
ug2207_2	454	GO:0003824,GO:0009536,GO:0009058,GO:0005488	biosynthetic process,cellular process	plastid	catalytic activity
ug2208_1	449	GO:0005634,GO:0005488		nucleus,mitochondrion	
ug2208_2	483	GO:0005634,GO:0005488		nucleus,mitochondrion	
ug2209_1	447				
ug2209_2	441	GO:0005488			binding
ug2210_1	440	GO:0007165,GO:0005794,GO:0005515	signal transduction	Golgi apparatus	protein binding
ug2210_2	482	GO:0007165,GO:0005794,GO:0005515	signal transduction	Golgi apparatus	protein binding
ug2211_1	427				
ug2211_2	468	GO:0003677			DNA binding
ug2212_1	461				
ug2212_2	190				
ug2213_1	473	GO:0003824,GO:0008152	metabolic process		catalytic activity
ug2213_2	460	GO:0003824,GO:0008152	metabolic process		catalytic activity
ug2214_1	458	GO:0005488,GO:0016740,GO:0005515			binding,transferase activity,protein binding
ug2214_2	493	GO:0005488,GO:0005488			binding,protein binding
ug2215_1	454				
ug2215_2	470				
ug2216_1	474				
ug2216_2	440				
ug2217_1	430				
ug2217_2	397				
ug2218_1	450				
ug2218_2	454				
ug2219_1	598	GO:0009056,GO:0006519,GO:0016740,GO:0005488	catabolic process,cellular amino acid and derivative metabolic	plastid	transferase activity
ug2219_2	469				
ug2220_1	530	GO:0009790,GO:0009908,GO:0006350	embryonic development,flower development,transcription		
ug2220_2	431				
ug2221_1	433				
ug2221_2	404				
ug2222_1	322				
ug2222_2	443	GO:0006810,GO:0016020,GO:0005215	transport	membrane	transporter activity
ug2223_1	412	GO:0003824,GO:0005886,GO:0006519,GO:0008152,GO:000166,GO:0006950,GO:000962	cellular amino acid and derivative metabolic process,metabolic process,response to stress,response to abiotic stimulus	plasma membrane,mitochondrion	catalytic activity,nucleotide binding
ug2223_2	483	GO:0003824,GO:0005886,GO:0006519,GO:0008152,GO:000166,GO:0006950,GO:000962	cellular amino acid and derivative metabolic process,metabolic process,response to stress,response to abiotic stimulus	plasma membrane,mitochondrion	catalytic activity,nucleotide binding
ug2224_1	407	GO:0006950,GO:0003824,GO:0008152,GO:0005488	response to stress,metabolic process	plastid	catalytic activity
ug2224_2	373				
ug2225_1	428				
ug2225_2	537				
ug2226_1	506	GO:0006950,GO:0009628,GO:0009987,GO:0006810,GO:0005623,GO:0005488,GO:0005515	response to stress,response to abiotic stimulus,cellular process,transport	cell,plasma membrane	binding,protein binding
ug2226_2	200				
ug2227_1	475				
ug2227_2	432				
ug2228_1	479				
ug2228_2	411				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug2229_1	464	GO:0006810,GO:0009987,GO:0005215	transport,cellular process		transporter activity
ug2229_2	267				
ug2230_1	426				
ug2230_2	457				
ug2231_1	494	GO:0005975,GO:0006950,GO:0005576,GO:0016787,GO:0005488	carbohydrate metabolic process,response to stress	extracellular region	hydrolase activity,binding
ug2231_2	432	GO:0005975,GO:0016787,GO:0005488	carbohydrate metabolic process		hydrolase activity,binding
ug2232_1	502	GO:0006810,GO:0005259	transport		binding
ug2232_2	259				
ug2233_1	412				
ug2233_2	413				
ug2234_1	447	GO:0005488,GO:0003824,GO:0009058,GO:000444	biosynthetic process		binding,catalytic activity,transferase activity
ug2234_2	444				
ug2235_1	435				
ug2235_2	447				
ug2236_1	481	GO:0005783		endoplasmic reticulum	
ug2236_2	444	GO:0016020,GO:0005056,GO:0019538,GO:0009056,GO:0009987,GO:0006464,GO:0003824	protein metabolic process,catabolic process,cellular process,protein modification process	membrane,endoplasmic reticulum	catalytic activity
ug2237_1	483	GO:0019538,GO:0009056,GO:0009987,GO:0006464,GO:0003824	protein metabolic process,catabolic process,cellular process,protein modification process		catalytic activity
ug2237_2	354	GO:0019538,GO:0009056,GO:0009987,GO:0003824,GO:0006464	protein metabolic process,catabolic process,cellular process,protein modification process		catalytic activity
ug2238_1	430				
ug2238_2	461				
ug2239_1	387				
ug2239_2	378				
ug2240_1	870				
ug2240_2	395	GO:0005488,GO:0008152,GO:0003824,GO:000563	metabolic process		binding,catalytic activity,molecular_function
ug2241_1	563				
ug2241_2	492	GO:0005634,GO:0003676,GO:0005622,GO:0005215,GO:0009056		nucleus,intracellular	nucleic acid binding
ug2242_1	864	GO:0006810,GO:0009536,GO:0016020,GO:0005737	response to biotic stimulus,transport	plastid,membrane,mitochondrion	transporter activity
ug2242_2	855	GO:0005737		cytoplasm	
ug2243_1	591				
ug2243_2	466	GO:0005488,GO:0008152,GO:0003824,GO:0003674,GO:0005757	metabolic process	endoplasmic reticulum	binding,catalytic activity,molecular_function,oxygen binding
ug2244_1	757				
ug2244_2	944				
ug2245_1	100				
ug2245_2	851	GO:0009536		plastid	
ug2246_1	150				
ug2246_2	342				
ug2247_1	668				
ug2247_2	482				
ug2248_1	285				
ug2248_2	828	GO:0005623,GO:0006950,GO:0009058,GO:0006519,GO:0019748	response to stress,biosynthetic process,cellular amino acid and derivative metabolic process,secondary metabolic process	cell	
ug2249_1	295				
ug2249_2	716	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug2250_1	192				
ug2250_2	282				
ug2251_1	138				
ug2251_2	308	GO:0008150,GO:0000166,GO:0005829,GO:0006139,GO:0006412,GO:0006519,GO:0003824	biological_process,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,translation,cellular amino acid and derivative metabolic process	cytosol	nucleotide binding,catalytic activity
ug2252_1	113	GO:0005622,GO:0003723,GO:0005515		intracellular	RNA binding,protein binding
ug2252_2	167	GO:0016787,GO:0005975,GO:0016043,GO:0009987	carbohydrate metabolic process,cellular component organization,cellular process		hydrolase activity
ug2253_1	712	GO:0005623,GO:000488,GO:0003676,GO:0008152,GO:0003824,GO:0003674,GO:000016	metabolic process,response to stress	cell	binding,nucleic acid binding,catalytic activity,molecular_function,nucleotide binding
ug2253_2	265				
ug2254_1	727	GO:0016740			transferase activity

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug2254_2	206	GO:0016787,GO:0030234			hydrolase activity,enzyme regulator activity
ug2255_1	141				
ug2255_2	297	GO:0000003,GO:0009791,GO:0009790	reproduction,post-embryonic development,embryonic		
ug2256_1	240				
ug2256_2	432	GO:0009987,GO:000019538,GO:0009056,GO:0005622,GO:0005488,GO:0009987,G	cellular process protein metabolic process,catabolic process,cellular process	intracellular	nucleotide binding binding,enzyme regulator activity
ug2257_2	127				
ug2258_1	710	GO:0009536		plastid	
ug2258_2	411				
ug2259_1	377	GO:0003676			nucleic acid binding
ug2259_2	248				
ug2260_1	655	GO:0005515			protein binding
ug2260_2	360				
ug2261_1	323				
ug2261_2	674				
ug2262_1	480				
ug2262_2	525				
ug2263_1	744	GO:0006412,GO:0005622,GO:0005198,GO:0009987,GO:0005737,GO:0000166,GO:0016020	translation,cellular process	intracellular,cytoplasm,membrane	structural molecule activity,nucleotide binding
ug2263_2	351	GO:0016301,GO:0000125			kinase activity,nucleotide
ug2264_1	125				
ug2264_2	516				
ug2265_1	250	GO:0016020,GO:0019538,GO:0009056,GO:000538	protein metabolic process,catabolic process	membrane	hydrolase activity
ug2265_2	443				
ug2266_1	778				
ug2266_2	285				
ug2267_1	196				
ug2267_2	144				
ug2268_1	163				
ug2268_2	131				
ug2269_1	184				
ug2269_2	100				
ug2270_1	192				
ug2270_2	187	GO:0009719,GO:0005155,GO:0005739,GO:0009628,GO:0005886	response to endogenous stimulus,response to abiotic stimulus	mitochondrion,plasma membrane	protein binding
ug2271_1	188				
ug2271_2	155	GO:0005488,GO:0008152,GO:0003824	metabolic process		binding,catalytic activity
ug2272_1	180				
ug2272_2	151				
ug2273_1	215				
ug2273_2	180				
ug2274_1	191				
ug2274_2	220				
ug2275_1	198				
ug2275_2	133				
ug2276_1	173				
ug2276_2	127				
ug2277_1	143				
ug2277_2	151				
ug2278_1	192				
ug2278_2	331				
ug2279_1	121				
ug2279_2	314				
ug2280_1	682				
ug2280_2	161				
ug2281_1	713				
ug2281_2	714	GO:0009058,GO:0005975,GO:0009987,GO:0006629,GO:0016740,GO:0009536,GO:000573	biosynthetic process,carbohydrate metabolic process,cellular process,lipid metabolic process	plastid,mitochondrion	transferase activity
ug2282_1	336				
ug2282_2	694	GO:0019538,GO:0009056,GO:0009987,GO:0003824,GO:0006464	protein metabolic process,catabolic process,cellular process,protein modification process		catalytic activity
ug2283_1	199				
ug2283_2	749	GO:0008152,GO:0016740,GO:0009536	metabolic process	plastid	transferase activity
ug2284_1	193				
ug2284_2	377				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug2285_1	658	GO:0016787,GO:0003723,GO:0000166,GO:008135,GO:0006412	translation		hydrolase activity,RNA binding,nucleotide binding,translation factor activity, nucleic acid binding
ug2285_2	467				
ug2286_1	393				
ug2286_2	247				
ug2287_1	295				
ug2287_2	177				
ug2288_1	307	GO:0005783		endoplasmic reticulum	
ug2288_2	227				
ug2289_1	296				
ug2289_2	188	GO:0005488,GO:0016		membrane	binding
ug2290_1	159				
ug2290_2	427				
ug2291_1	620	GO:0005515,GO:0003			protein binding,DNA binding
ug2291_2	793	GO:0005737,GO:0005488,GO:0006950,GO:003824,GO:0005975,GO:0006091,GO:000905	response to stress,carbohydrate metabolic process,generation of precursor metabolites and energy,catabolic process	cytoplasm	binding,catalytic activity
ug2292_1	213				
ug2292_2	287				
ug2293_1	300				
ug2293_2	131	GO:0005488,GO:0016			binding,transferase activity
ug2294	204				
ug2295	230	GO:0005488,GO:000515,GO:0003824			binding,protein binding,catalytic activity
ug2296	142				
ug2297	128				
ug2298	198	GO:0006464,GO:0005886,GO:0016301,GO:0	protein modification process	plasma membrane	kinase activity,nucleotide binding
ug2299	330				
ug2300	124				
ug2301	305	GO:0008152,GO:000987,GO:0003824,GO:00016787,GO:0005975,GO:0009056,GO:008150,GO:0009987,GO:0030246	metabolic process,cellular process		catalytic activity,binding
ug2302	275		carbohydrate metabolic process,catabolic process,biological_process,cellular process		hydrolase activity,carbohydrate binding
ug2303	181				
ug2304	225				
ug2305	194				
ug2306	166				
ug2307	298	GO:0006464,GO:0000166,GO:0016301	protein modification process		nucleotide binding,kinase activity
ug2308	559	GO:0006091,GO:0009056,GO:0003824,GO:0008152,GO:0003	generation of precursor metabolites and energy,catabolic process,metabolic process		catalytic activity
ug2309	254	GO:0008152,GO:0003824,GO:0005488,GO:0030528	metabolic process		catalytic activity,binding,transcription regulator activity
ug2310	201				
ug2311	230				
ug2312	158	GO:0004872,GO:0006464,GO:0006950,GO:0005886,GO:0005515,GO:0000166,GO:0016020,GO:0008289,GO:001	protein modification process,response to stress	plasma membrane,membrane	receptor activity,protein binding,nucleotide binding,lipid binding,kinase activity
ug2313	202				
ug2314	157				
ug2315	400				
ug2316	245				
ug2317	300				
ug2318	240				
ug2319	313				
ug2320	645				
ug2321	274				
ug2322	597				
ug2323	302	GO:0003676			nucleic acid binding
ug2324	413				
ug2325	516				
ug2326	524	GO:0006810,GO:0005829,GO:0008289	transport	cytosol	lipid binding
ug2327	336				
ug2328	632	GO:0005488			binding
ug2329	825				
ug2330	769	GO:0005623,GO:0004518,GO:0003723		cell	nuclease activity,RNA binding

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug2331	428	GO:0005737,GO:0003824,GO:0006519,GO:019748,GO:0009058,GO:0009056	cellular amino acid and derivative metabolic process,secondary metabolic process,biosynthetic process,catabolic process	cytoplasm	catalytic activity
ug2332	554	GO:0005488,GO:0019538,GO:0009056,GO:009987,GO:0005886,GO:0006464,GO:000382	protein metabolic process,catabolic process,cellular process,protein modification process	plasma membrane,intracellular	binding,catalytic activity
ug2333	326	GO:0003677,GO:0005488,GO:0006259	DNA metabolic process		DNA binding,binding
ug2334	111				
ug2335	159				
ug2336	662				
ug2337	105				
ug2338	270				
ug2339	615				
ug2340	442	GO:0016740			transferase activity
ug2341	619	GO:0016020,GO:0005215,GO:0006810,GO:009607,GO:0005886	transport,response to biotic stimulus	membrane,plasma membrane	transporter activity
ug2342	380	GO:0005488			binding
ug2343	490				
ug2344	102				
ug2345	638				
ug2346	412	GO:0009987,GO:0009425	cellular process,catabolic process		
ug2347	425				
ug2348	760				
ug2349	816	GO:0005618,GO:0016043,GO:0009987,GO:0005794,GO:0005886,GO:0009058,GO:0005975,GO:0005576,GO:001	cellular component organization,cellular process,biosynthetic process,carbohydrate metabolic process	cell wall,Golgi apparatus,plasma membrane,extracellular region	transferase activity
ug2350	243				
ug2351	564	GO:0005515,GO:0000003,GO:0009791,GO:0	reproduction,post-embryonic development,embryonic		protein binding
ug2352	671				
ug2353	418				
ug2354	726	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug2355	342				
ug2356	302				
ug2357	341				
ug2358	321	GO:0005622,GO:0016787,GO:0019538,GO:009056,GO:0009987,GO:0000166,GO:000563	protein metabolic process,catabolic process,cellular process	intracellular,nucleus,cytosol	hydrolase activity,nucleotide binding
ug2359	211				
ug2360	851				
ug2361	482	GO:0006950,GO:0006259,GO:0003824,GO:0	response to stress,DNA metabolic process	plastid	catalytic activity
ug2362	327				
ug2363	104				
ug2364	705	GO:0005622,GO:0000916		intracellular	nucleotide binding
ug2365	916				
ug2366	485	GO:0030246,GO:0006464,GO:0000166,GO:0	protein modification process		carbohydrate binding,nucleotide
ug2367	440				
ug2368	427	GO:0005737		cytoplasm	
ug2369	822				
ug2370	428	GO:0003824,GO:0016740,GO:000515		membrane	catalytic activity transferase activity,protein binding
ug2371	216				
ug2372	418	GO:0008152,GO:0009987,GO:0003824,GO:0003824,GO:0008	metabolic process,cellular process		catalytic activity,binding
ug2373	810	GO:0005739,GO:0005488,GO:0016020,GO	biological_process,generation of precursor metabolites and energy	mitochondrion,membrane	catalytic activity,binding
ug2374	114				
ug2375	188				
ug2376	151				
ug2377	395				
ug2378	343	GO:0016787,GO:0005975,GO:0005618,GO:0005840,GO:0005488	carbohydrate metabolic process	cell wall,ribosome	hydrolase activity,binding
ug2379	243				
ug2380	264	GO:0005488			binding
ug2381	475	GO:0005623		cell	
ug2382	715	GO:0030528,GO:0003700,GO:0016043,GO:0006350,GO:0005634	cellular component organization,transcription	nucleus	transcription regulator activity,transcription factor activity



Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug2383	554	GO:0005488,GO:0008152,GO:0003824,GO:0003674,GO:0006950	metabolic process,response to stress		binding,catalytic activity,molecular_function
ug2384	468				
ug2385	876				
ug2386	252				
ug2387	192				
ug2388	405	GO:0009058,GO:0006519,GO:0016301,GO:0	biosynthetic process,cellular amino acid and derivative metabolic	plastid	kinase activity
ug2389	255				
ug2390	101				
ug2391	469				
ug2392	772	GO:0009719,GO:0006350,GO:0003700,GO:0	response to endogenous stimulus,transcription	nucleus	transcription factor activity
ug2393	945				
ug2394	261				
ug2395	214				
ug2396	773	GO:0019538,GO:0009987,GO:0005515	protein metabolic process,cellular process		protein binding
ug2397	562				
ug2398	185				
ug2399	716				
ug2400	637	GO:0006091,GO:0000166,GO:0016020,GO:0005622,GO:0003824,GO:0005488,GO:0005730,GO:0005488,GO:0016787,GO:0019538,GO:0009056,GO:0009536	generation of precursor metabolites and energy	membrane,intracellular,mitochondrion	nucleotide binding,catalytic activity,binding
ug2401	567	GO:0019538,GO:0009056,GO:0009536	protein metabolic process,catabolic process	plastid	binding,hydrolase activity
ug2402	226				
ug2403	752				
ug2404	833	GO:0030246,GO:0005757		cell	carbohydrate binding
ug2405	757				
ug2406	615	GO:0008152,GO:0003401,GO:0005634	metabolic process	nucleus	catalytic activity
ug2407	401				
ug2408	265				
ug2409	266				
ug2410	105				
ug2411	555				
ug2412	727	GO:0016740,GO:0009058,GO:0006519,GO:0	biosynthetic process,cellular amino acid and derivative metabolic		transferase activity,binding
ug2413	131				
ug2414	612				
ug2415	929				
ug2416	665	GO:0009536,GO:0016740,GO:0009058,GO:0005975,GO:0009987	biosynthetic process,carbohydrate metabolic process,cellular process	plastid	transferase activity
ug2417	185				
ug2418	409				
ug2419	575				
ug2420	150				
ug2421	679				
ug2422	321				
ug2423	609	GO:0005975,GO:0016787,GO:0005488	carbohydrate metabolic process		hydrolase activity,binding
ug2424	540				
ug2425	708	GO:0006464,GO:0016020,GO:0016787	protein modification process	membrane	hydrolase activity
ug2426	468				
ug2427	708	GO:0016740,GO:0009058,GO:0009987,GO:0005488,GO:0009058,GO:0009987,GO:0	biosynthetic process,cellular process,lipid metabolic process		transferase activity
ug2428	608	GO:0006629,GO:0005886,GO:0003824,GO:0000003,GO:0030154,GO:000	process,reproduction,cell differentiation,multicellular organismal development	plasma membrane	binding,catalytic activity
ug2429	852				
ug2430	342				
ug2431	205				
ug2432	250				
ug2433	671				
ug2434	831	GO:0009791,GO:0003723,GO:0003677,GO:0006950,GO:0009628,GO:0005739,GO:0000160,GO:0009605,GO:0006950,GO:0008150,GO:0005215,GO:0006810,GO:0019538,GO:0009056,GO:0016787,GO:0	post-embryonic development,response to stress,response to abiotic stimulus	mitochondrion	RNA binding,DNA binding,nucleotide binding
ug2435	909	GO:0009605,GO:0006950,GO:0008150,GO:0005215,GO:0006810,GO:0019538,GO:0009056,GO:0016787,GO:0	response to external stimulus,response to stress,biological_process,transport protein metabolic process,catabolic process		transporter activity
ug2436	754	GO:0019538,GO:0009056,GO:0016787,GO:0	protein metabolic process,catabolic process		hydrolase activity,protein binding











Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug2714	628	GO:0006464,GO:0000166,GO:0003824,GO:0016301,GO:0005622	protein modification process	intracellular	nucleotide binding,catalytic activity,kinase activity
ug2715	796				
ug2716	532				
ug2717	293				
ug2718	748	GO:0005737,GO:0006810,GO:0005215,GO:0008289,GO:0008150,GO:0008219,GO:0006950	transport,biological_process,cell death,response to stress,response to biotic stimulus	cytoplasm	transporter activity,lipid binding
ug2719	312	GO:0016740			transferase activity
ug2720	111				
ug2721	864	GO:0016020,GO:0005622,GO:0016787,GO:0005215,GO:0006810,GO:0006091,GO:0006139,GO:0009058,GO:0005305,GO:0005634,GO:0000000	transport,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process	membrane,intracellular	hydrolase activity,transporter activity,nucleotide binding
ug2722	332	GO:0030528,GO:0006350,GO:0005634,GO:0000000	transcription	nucleus,mitochondrion	transcription regulator activity
ug2723	302				
ug2724	863	GO:0016740			transferase activity
ug2725	772	GO:0006412,GO:0008135	translation		translation factor activity, nucleic acid binding
ug2726	442				
ug2727	221				
ug2728	281				
ug2729	846	GO:0016787,GO:0019538,GO:0009056,GO:0001166,GO:0016020,GO:0005488,GO:0009539	protein metabolic process,catabolic process	membrane,plastid,mitochondrion	hydrolase activity,nucleotide binding,binding
ug2730	212				
ug2731	862	GO:0009058,GO:0005975,GO:0005737,GO:0003666	biosynthetic process,carbohydrate metabolic process	cytoplasm	transferase activity
ug2732	366				
ug2733	793	GO:0016787,GO:0000003,GO:0009791,GO:0009790,GO:0009058,GO:0006519	reproduction,post-embryonic development,embryonic development,biosynthetic process,cellular amino acid and derivative metabolic process		hydrolase activity
ug2734	680	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		
ug2735	730	GO:0005840,GO:0009536,GO:0005198,GO:0003723,GO:0006412	translation	ribosome,plastid	structural molecule activity,RNA binding
ug2736	820	GO:0003676,GO:0004518			nucleic acid binding,nuclease activity
ug2737	891	GO:0016740			transferase activity
ug2738	874				
ug2739	519				
ug2740	933				
ug2741	907	GO:0005576,GO:0009812		extracellular region,plastid	
ug2742	812				
ug2743	105				
ug2744	126				
ug2745	109				
ug2746	461	GO:0005515,GO:0009719,GO:0007165,GO:0005634,GO:0006350	response to endogenous stimulus,signal transduction,transcription	nucleus	protein binding
ug2747	748				
ug2748	822	GO:0003676			nucleic acid binding
ug2749	897	GO:0016020,GO:0005739,GO:0005622,GO:0003674,GO:0003824,GO:0005488,GO:0006810	transport,generation of precursor metabolites and energy	membrane,mitochondrion,intracellular	molecular_function,catalytic activity,binding
ug2750	784				
ug2751	229				
ug2752	450				
ug2753	629	GO:0016020		membrane	
ug2754	727				
ug2755	621				
ug2756	565	GO:0016020,GO:0005739,GO:0005488,GO:0003674,GO:0006810,GO:0006091,GO:0003824	transport,generation of precursor metabolites and energy	membrane,mitochondrion	binding,molecular_function,catalytic activity,transporter activity
ug2757	853	GO:0009536		plastid	
ug2758	701	GO:0005488,GO:0008152,GO:0003824	metabolic process		binding,catalytic activity
ug2759	590	GO:0005488,GO:0003676,GO:0005622		intracellular	binding,nucleic acid binding





Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug2810	369	GO:0019538,GO:0009	protein metabolic process,catabolic		
ug2811	454	056,GO:0009987,GO:0003824,GO:0006464	process,cellular process,protein modification process		catalytic activity
ug2812	867	GO:0005975,GO:0016787,GO:0009536	carbohydrate metabolic process	plastid	hydrolase activity
ug2813	282				
ug2814	916	GO:0003824,GO:0009536,GO:0006950	response to stress	plastid	catalytic activity
ug2815	873	GO:0009536,GO:0003824,GO:0005515		plastid	catalytic activity,protein binding
ug2816	157				
ug2817	709	GO:0005886		plasma membrane	
ug2818	596				
ug2819	459	GO:0005488			binding
ug2820	839	GO:0005488,GO:0005			binding,protein binding
ug2821	114				
ug2822	335				
ug2823	771	GO:0005739		mitochondrion	
ug2824	757	GO:0008152,GO:0003824,GO:0009536	metabolic process	plastid	catalytic activity
ug2825	716	GO:0016787,GO:0008152,GO:0016020,GO:000166,GO:0005215	metabolic process	membrane	hydrolase activity,nucleotide binding,transporter activity
ug2826	792	GO:0005488			binding
ug2827	754	GO:0006139,GO:0030234	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		enzyme regulator activity
ug2828	719				
ug2829	196				
ug2830	646	GO:0016020,GO:0016043,GO:0009987,GO:0009056,GO:0009	cellular component organization,cellular process	membrane,plastid	
ug2831	810	987,GO:0005488,GO:0016787,GO:0005739	catabolic process,cellular process	mitochondrion	binding,hydrolase activity
ug2832	606				
ug2833	513				
ug2834	119				
ug2835	577	GO:0005623		cell	
ug2836	803	GO:0005488			binding
ug2837	243	GO:0005886,GO:0016740,GO:0009058,GO:0005975,GO:0009987	biosynthetic process,carbohydrate metabolic process,cellular process	plasma membrane	transferase activity
ug2838	457	GO:0004872,GO:0016020,GO:0003824		membrane	receptor activity,catalytic activity
ug2839	776				
ug2840	764	GO:0009536		plastid	
ug2841	566				
ug2842	578				
ug2843	166				
ug2844	642				
ug2845	713	GO:0008152,GO:0005488,GO:0030528,GO:0005623	metabolic process	cell	binding,transcription regulator activity,catalytic activity
ug2846	385	GO:0005623			
ug2847	153				
ug2848	467				
ug2849	460	GO:0003677,GO:0006	transcription		DNA binding
ug2850	718	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug2851	346	GO:0003676,GO:0005622,GO:0009536		intracellular,plastid	nucleic acid binding
ug2852	931	GO:0016787			hydrolase activity
ug2853	101				
ug2854	841				
ug2855	699	GO:0005737,GO:0016740,GO:0006464,GO:0016787,GO:0005623	protein modification process	cytoplasm,membrane	hydrolase activity
ug2856	281	GO:0016740,GO:0016787,GO:0005623		cell	
ug2857	718	GO:0009058,GO:000166,GO:0009536	biosynthetic process	plastid	transferase activity,kinase activity,nucleotide binding
ug2858	816	GO:0005773,GO:0005515,GO:0016787,GO:0006519,GO:0019538,GO:0005737,GO:0005515,GO:0006810,GO:0008135	cellular amino acid and derivative metabolic process,protein metabolic process,catabolic process	vacuole	protein binding,hydrolase activity
ug2859	596	GO:0005737,GO:0005515,GO:0006810,GO:0008135	transport,cellular process	cytoplasm	protein binding
ug2860	636	GO:0008135			translation factor activity, nucleic acid binding
ug2861	687	GO:0003723,GO:0004518,GO:0008150,GO:0005623	biological_process	intracellular	RNA binding,nuclease activity
ug2862	701				
ug2863	682				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug2864	280	GO:0000166,GO:0008141	cell death		nucleotide binding
ug2865	141				
ug2866	865	GO:0005623		cell	
ug2867	500				
ug2868	771	GO:0005488,GO:0005737,GO:0008152,GO:0009987,GO:0000166,GO:0006810,GO:0009	metabolic process,cellular process	cytoplasm	binding,nucleotide binding,catalytic activity
ug2869	884				
ug2870	618	GO:0006810,GO:000987,GO:0016020,GO:0005739,GO:0005488	transport,cellular process	membrane,mitochondrion	binding
ug2871	804				
ug2872	881				
ug2873	571	GO:0005488,GO:001020,GO:0005739,GO:0006810,GO:0009987,GO:0009536,GO:000521	transport,cellular process	membrane,mitochondrion,plastid	binding,transporter activity
ug2874	863	GO:0005737		cytoplasm	
ug2875	479	GO:0019538,GO:000987,GO:0005488,GO:0003674,GO:0005515,GO:0005737,GO:0003	protein metabolic process,cellular process	plastid	binding,molecular_function,protein binding
ug2876	474				
ug2877	725				
ug2878	732	GO:0005623,GO:0005		cell,cytoplasm	
ug2879	497	GO:0003676,GO:0000166			nucleic acid binding,nucleotide binding
ug2880	343	GO:0005488,GO:001740,GO:0009058,GO:0006519,GO:0003824,GO:0016020,GO:0009	biosynthetic process,cellular amino acid and derivative metabolic process	plastid	binding,transferase activity,catalytic activity
ug2881	880	GO:0006091,GO:0015979,GO:0005488,GO:0005622,GO:000953	generation of precursor metabolites and energy,photosynthesis	membrane,thylakoid,intracellular,plastid	binding
ug2882	905	GO:0005515,GO:0009		plastid	protein binding
ug2883	425				
ug2884	463	GO:0005737,GO:0003824,GO:0006139,GO:006412,GO:0006519,GO:0000166	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,translation,cellular amino acid and derivative metabolic	cytoplasm	catalytic activity,nucleotide binding
ug2885	728				
ug2886	488	GO:0016020,GO:0005215,GO:0009607,GO:0006810,GO:0005886	response to biotic stimulus,transport	membrane,plasma membrane	transporter activity
ug2887	644				
ug2888	818	GO:0005623		cell	
ug2889	416				
ug2890	207				
ug2891	798				
ug2892	772	GO:0005622,GO:000987,GO:0009056,GO:0005975,GO:0005	cellular process,catabolic process	intracellular	hydrolase activity
ug2893	131				
ug2894	349	GO:0005737,GO:0005576,GO:0016787,GO:0030246,GO:0009536,GO:0016	carbohydrate metabolic process	cellular_component,extracellular region	hydrolase activity,carbohydrate binding,binding
ug2895	536	GO:0019538,GO:000987,GO:0009987,GO:0005488,GO:0003824	protein metabolic process,catabolic process,cellular process,protein modification process	plastid,membrane	
ug2896	453	GO:0009536			catalytic activity
ug2897	441	GO:0009536		plastid	
ug2898	366				
ug2899	757	GO:0005618,GO:0006950,GO:0006259,GO:0005739,GO:0016787,GO:0003677,GO:0016043,GO:0009987,GO:0019538,GO:0000166,GO:0016020,GO:0009536,GO:0005515,GO:0009579,GO:0009058,GO:0	response to stress,DNA metabolic process,cellular component organization,cellular process,protein metabolic process,biosynthetic process,transport	cell wall,mitochondrion,membrane,plastid,thylakoid	hydrolase activity,DNA binding,nucleotide binding,protein binding,nuclease activity
ug2900	710				
ug2901	496				
ug2902	628				
ug2903	549	GO:0016787,GO:0016301,GO:0007275,GO:0040007,GO:0004872,GO:0005975,GO:0009987,GO:0009056,GO:0009653,GO:0007165,GO:0000166,GO:0005515,GO:0030154,GO:0009	multicellular organismal development,growth,carbohydrate metabolic process,cellular process,catabolic process,anatomical structure morphogenesis,signal transduction,cell differentiation,flower		hydrolase activity,kinase activity,receptor activity,nucleotide binding,protein binding

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug2904	155				
ug2905	334	GO:0003723,GO:0006139,GO:0005515,GO:0	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		RNA binding,protein binding,catalytic activity
ug2906	354				
ug2907	722	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug2908	360				
ug2909	373				
ug2910	380				
ug2911	586	GO:0016020,GO:0009		membrane,plastid	
ug2912	858				
ug2913	459	GO:0016787			hydrolase activity
ug2914	774	GO:0009536,GO:0016020,GO:0009579		plastid,membrane,thylakoid	
ug2915	820				
ug2916	703	GO:0005515			protein binding
ug2917	628				
ug2918	731				
ug2919	570	GO:0006350,GO:0040007,GO:0005634	transcription,growth	nucleus	
ug2920	369				
ug2921	799	GO:0030234,GO:0008152,GO:0009987,GO:0006139,GO:0009058,GO:0019748,GO:0008150,GO:0005488,GO:0006091,GO:0003824,GO:0005515,GO:0009536	metabolic process,cellular process,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process,secondary metabolic process,biological_process,generation of precursor metabolites and	plastid	enzyme regulator activity,protein binding,catalytic activity,protein binding
ug2922	164				
ug2923	540				
ug2924	339				
ug2925	542	GO:0008152,GO:0003824,GO:0005488	metabolic process		catalytic activity,protein binding
ug2926	727				
ug2927	712				
ug2928	412				
ug2929	696	GO:0016020,GO:0009579,GO:0009536,GO:0005886,GO:0006810,GO:0016787	photosynthesis	membrane,thylakoid,plastid	
ug2930	450	GO:0005886,GO:0006810,GO:0016787	transport	plasma membrane	hydrolase activity
ug2931	141				
ug2932	348	GO:0009058,GO:000987,GO:0009536,GO:0006464	biosynthetic process,cellular process	plastid	catalytic activity
ug2933	767	GO:0006464	protein modification process		
ug2934	180				
ug2935	772	GO:0005515,GO:0005		intracellular	protein binding
ug2936	455				
ug2937	719	GO:0009536,GO:0003824,GO:0016740,GO:0003677,GO:0006350,GO:0	transcription	mitochondrion	catalytic activity,transferase activity,DNA binding
ug2938	156				
ug2939	435				
ug2940	719	GO:0016020,GO:0009536,GO:0009579		membrane,plastid,thylakoid	
ug2941	841	GO:0005773,GO:0005		vacuole,plasma membrane	
ug2942	676				
ug2943	379				
ug2944	820	GO:0009536,GO:0006950,GO:0009628,GO:0005488,GO:0008152,GO:0016020,GO:000957	response to stress,response to abiotic stimulus,metabolic process	plastid,membrane,thylakoid	binding
ug2945	711	GO:0016787,GO:0003824,GO:0006139,GO:0005840,GO:0005198,GO:0006412	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		hydrolase activity,catalytic activity,kinase activity
ug2946	846	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug2947	659	GO:0003824,GO:0008152,GO:0005488	metabolic process		catalytic activity,protein binding
ug2948	854				
ug2949	860	GO:0016020,GO:0009536,GO:0006091,GO:0	generation of precursor metabolites and energy,photosynthesis	membrane,plastid	
ug2950	525				
ug2951	638	GO:0008152,GO:0016740,GO:0009536	metabolic process	plastid	transferase activity
ug2952	681	GO:0003676			nucleic acid binding
ug2953	346				
ug2954	573	GO:0005488,GO:0005886,GO:0016301,GO:0	cellular process	plasma membrane	binding,kinase activity
ug2955	125				
ug2956	830				
ug2957	827	GO:0016020,GO:0009536,GO:0009579		membrane,plastid,thylakoid	

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug2958	872				
ug2959	421	GO:0016787,GO:0003676,GO:0005622,GO:0005488,GO:0000166		intracellular	hydrolase activity,nucleic acid binding,binding,nucleotide
ug2960	446	GO:0016787,GO:0005215,GO:0016020,GO:0006139,GO:0009058,GO:0000166,GO:0005488,GO:0006810,GO:000	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process,transport	membrane,plasma membrane	hydrolase activity,transporter activity,nucleotide binding,binding
ug2961	517				
ug2962	351				
ug2963	855	GO:0003824,GO:0003677,GO:0006259	DNA metabolic process		catalytic activity,DNA binding
ug2964	716	GO:0003677,GO:0005488,GO:0005515,GO:0		plastid	DNA binding,binding,protein binding
ug2965	491				
ug2966	705	GO:0009719,GO:0005618,GO:0005488,GO:0000003,GO:0009791,GO:0005886,GO:000727	response to endogenous stimulus,reproduction,post-embryonic development,multicellular	cell wall,plasma membrane	binding
ug2967	111				
ug2968	728	GO:0019725,GO:0003824,GO:0008152,GO:0	cellular homeostasis,metabolic process	mitochondrion	catalytic activity
ug2969	736	GO:0003677,GO:0008	cell death		DNA binding
ug2970	251				
ug2971	793				
ug2972	627				
ug2973	485				
ug2974	488	GO:0005488,GO:0003824,GO:0009058,GO:00005737,GO:0006	biosynthetic process protein modification		binding,catalytic activity,transferase activity
ug2975	685	GO:0005515,GO:0009719,GO:0005634	process,response to endogenous stimulus	cytoplasm,nucleus	protein binding
ug2976	354				
ug2977	109				
ug2978	449				
ug2979	802				
ug2980	600	GO:0005198,GO:0005840,GO:0006412,GO:0	translation	ribosome,mitochondrion	structural molecule activity
ug2981	611				
ug2982	522	GO:0016020,GO:0005		membrane,plasma membrane	
ug2983	150	GO:0005215,GO:0019725,GO:0006810	cellular homeostasis,transport		transporter activity
ug2984	565	GO:0005739		mitochondrion	
ug2985	640				
ug2986	160				
ug2987	755	GO:0006464,GO:0019538,GO:0009056,GO:0009987,GO:0003824,GO:0016020,GO:0009	protein modification process,protein metabolic process,catabolic process,cellular		catalytic activity
ug2988	660	GO:0005739,GO:0008152,GO:0003824	metabolic process	membrane,plastid,thylakoid	catalytic activity
ug2989	392				
ug2990	757				
ug2991	125				
ug2992	792				
ug2993	534	GO:0005515,GO:0005975,GO:0006091,GO:0009056,GO:0003824,GO:0009536	carbohydrate metabolic process,generation of precursor metabolites and energy,catabolic process	plastid	protein binding,catalytic activity
ug2994	786	GO:0005739,GO:0016020,GO:0009536		mitochondrion,membrane,plastid	
ug2995	484				
ug2996	822	GO:0006810,GO:0009	transport,cellular process		
ug2997	415				
ug2998	804	GO:0005739		mitochondrion	
ug2999	512				
ug3000	574	GO:0005623		cell	
ug3001	460				
ug3002	573	GO:0009058,GO:0009987,GO:0009536,GO:0	biosynthetic process,cellular process	plastid	catalytic activity
ug3003	253				
ug3004	890	GO:0009536		plastid	
ug3005	691	GO:0009579,GO:0005488,GO:0009536		thylakoid,plastid	binding
ug3006	680				
ug3007	412				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug3008	870	GO:0006464,GO:0005618,GO:0005886,GO:0005515,GO:0016301,GO:0000166,GO:000716	protein modification process,signal transduction	cell wall,plasma membrane	protein binding,kinase activity,nucleotide binding
ug3009	191				
ug3010	393	GO:0005739,GO:0006091	generation of precursor metabolites and energy	mitochondrion	
ug3011	709	GO:0005488			binding
ug3012	671	GO:0009719	response to endogenous stimulus		
ug3013	763	GO:0005622		intracellular	
ug3014	879	GO:0005488,GO:0008152,GO:0003824,GO:0	metabolic process		binding,catalytic activity,molecular_function
ug3015	741	GO:0006810	transport		
ug3016	160				
ug3017	676				
ug3018	522				
ug3019	636	GO:0016020,GO:0009536,GO:0009579,GO:00019538,GO:0009		membrane,plastid,thylakoid,mitochondrion	
ug3020	812	987,GO:0005515,GO:0007275,GO:0016020,GO:0009536,GO:000957	protein metabolic process,cellular process,multicellular organismal development	membrane,plastid,thylakoid	protein binding
ug3021	796	GO:0016043,GO:0009987,GO:0005515,GO:0	cellular component organization,cellular process	cytoskeleton	protein binding
ug3022	812	GO:0005488,GO:0005		intracellular	binding
ug3023	445	GO:0005737,GO:0016		cytoplasm,membrane	
ug3024	771	GO:0005886		plasma membrane	
ug3025	170				
ug3026	397				
ug3027	877				
ug3028	284				
ug3029	394				
ug3030	519	GO:0005488,GO:0008152,GO:0009987,GO:0006519,GO:0016740,GO:0008	metabolic process,cellular process,cellular amino acid and derivative metabolic process	mitochondrion	binding,transferase activity
ug3031	182	GO:0016740,GO:0008	metabolic process		transferase activity
ug3032	240				
ug3033	807	GO:0005737		cytoplasm	
ug3034	476				
ug3035	872				
ug3036	722				
ug3037	801	GO:0005623,GO:0005		cell,cytoplasm	
ug3038	548				
ug3039	482				
ug3040	724				
ug3041	616				
ug3042	414				
ug3043	506				
ug3044	779	GO:0005623,GO:0005		cell,cytoplasm	
ug3045	521				
ug3046	751				
ug3047	799	GO:0016787			hydrolase activity
ug3048	772				
ug3049	671	GO:0016043,GO:0005515,GO:0005215,GO:0006810,GO:0009987,GO:00016020,GO:000573	cellular component organization,transport,cellular process	membrane,mitochondrion	protein binding,transporter activity
ug3050	805	GO:0005515			protein binding
ug3051	339				
ug3052	460	GO:0006950,GO:0009628,GO:0005730,GO:0003677,GO:0009719,GO:0003700,GO:0030528,GO:0005515,GO:00019538,GO:0009	response to stress,response to abiotic stimulus,response to endogenous stimulus,transcription,signal transduction	nucleolus	DNA binding,transcription factor activity,transcription regulator activity,protein binding
ug3053	667	987,GO:0005515	protein metabolic process,cellular process		protein binding
ug3054	252				
ug3055	552				
ug3056	845				
ug3057	930				
ug3058	902				
ug3059	761				
ug3060	759	GO:0009536,GO:0003824,GO:0003674,GO:0008152,GO:0005488,GO:00016020,GO:000957	metabolic process	plastid,membrane,thylakoid	catalytic activity,molecular_function,binding
ug3061	723	GO:0005773,GO:0016		vacuole	transferase activity
ug3062	625				
ug3063	561	GO:0005488,GO:0005515,GO:0005886		plasma membrane	binding,protein binding

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug3064	545				
ug3065	703				
ug3066	383	GO:0005739		mitochondrion	
ug3067	571				
ug3068	479				
ug3069	859	GO:0009579,GO:0009536,GO:0005515,GO:0		thylakoid,plastid,membrane	protein binding
ug3070	373				
ug3071	164				
ug3072	171				
		GO:0006950,GO:0009628,GO:0005488,GO:0	response to stress,response to abiotic stimulus,protein		
ug3073	453	006464,GO:0019538,GO:0009056,GO:0009987,GO:0008152,GO:0008150,GO:0003824,GO:	modification process,protein metabolic process,catabolic process,cellular process,metabolic process,biological process	cytosol,intracellular	binding,catalytic activity
ug3074	468				
ug3075	450	GO:0006810,GO:000987,GO:0016020,GO:0	transport,cellular process	membrane,endosome	
ug3076	131				
		GO:0006810,GO:000987,GO:0005623,GO:016020,GO:0005515	transport,cellular process	cell,membrane	protein binding
ug3078	304				
ug3079	400				
ug3080	388				
ug3081	314	GO:0003824,GO:0000166			catalytic activity,nucleotide binding
ug3082	265	GO:0003677,GO:0006350,GO:0005634	transcription	nucleus	DNA binding
ug3083	195				
ug3084	313				
ug3085	399	GO:0008150	biological_process		
ug3086	457	GO:0005488			binding
ug3087	238				
ug3088	372	GO:0005488			binding
ug3089	295				
ug3090	458	GO:0016787			hydrolase activity
ug3091	443				
		GO:0007165,GO:0009719,GO:0030528,GO:004871,GO:0005515,GO:0005634,GO:000635	signal transduction,response to endogenous stimulus,transcription	nucleus	transcription regulator activity,signal transducer activity,protein binding
ug3092	412				
ug3093	465	GO:0005576		extracellular region	
ug3094	404	GO:0005623,GO:0019538,GO:0009056,GO:0009653,GO:0030154,GO:0007275,GO:0	protein metabolic process,catabolic process,cellular process anatomical structure morphogenesis,cell	cell	
ug3095	479	005794,GO:0016043,GO:0016049,GO:0016020,GO:0005783	differentiation,multicellular organismal development,cellular component organization,cell	Golgi apparatus,membrane,endoplasmic reticulum	
ug3096	444				
ug3097	145				
ug3098	478				
ug3099	430	GO:0009536		plastid	
ug3100	462				
ug3101	432				
ug3102	390				
ug3103	379				
ug3104	428				
ug3105	427				
ug3106	461	GO:0005975,GO:0005618,GO:0016787,GO:00016020,GO:0005635,GO:0005768,GO:0	carbohydrate metabolic process	cell wall,membrane	hydrolase activity
ug3107	457	000166,GO:0006810,GO:0009987,GO:0005886,GO:0009719,GO:0005623,GO:0005829,GO:0006810,GO:0006091,GO:0006139,GO:0009058,GO:0016020,GO:0005215	transport,cellular process,response to endogenous stimulus	membrane,nuclear envelope,endosome,plasma membrane,cell,cytosol,endoplasmic reticulum	nucleotide binding
ug3108	445	GO:0005618,GO:0005576,GO:0005618,GO:0005576	transport,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic	membrane	transporter activity
ug3109	483	576,GO:0019538,GO:0009056,GO:0016787	protein metabolic process,catabolic process	cell wall,extracellular region	hydrolase activity
ug3110	468				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug3111	438	GO:0005515,GO:0005215,GO:0016020,GO:0006810,GO:0009987,GO:0016043,GO:000953	transport,cellular process,cellular component organization	membrane,plastid,thylakoid	protein binding,transporter activity
ug3112	330				
ug3113	234				
ug3114	361	GO:0006810,GO:0016020,GO:0005215	transport	membrane	transporter activity
ug3115	475				
ug3116	203				
ug3117	149				
ug3118	344				
ug3119	476				
ug3120	285				
ug3121	515	GO:0005975,GO:000987,GO:0016787,GO:0005576,GO:0005618,G	carbohydrate metabolic process,cellular process	extracellular region,cell wall	hydrolase activity,transferase activity
ug3122	169				
ug3123	397	GO:0016301,GO:0005829,GO:0000166,GO:0005975,GO:0006091,GO:0009056	carbohydrate metabolic process,generation of precursor metabolites and energy,catabolic process	cytosol	kinase activity,nucleotide binding
ug3124	113				
ug3125	473				
ug3126	443	GO:0003824,GO:0009446,GO:0005773		plastid vacuole	catalytic activity
ug3127	454	GO:0003824,GO:0005829,GO:0016787,GO:0016740,GO:0005975,GO:0	carbohydrate metabolic process		catalytic activity,binding hydrolase activity,transferase activity,binding
ug3128	343				
ug3129	407				
ug3130	407				
ug3131	407				
ug3132	385	GO:0005975,GO:000987,GO:0008150,GO:0016740,GO:0005739,GO:0000166,GO:0006091,GO:0009056,GO:0005975,GO:0003824	carbohydrate metabolic process,cellular process,biological_process,generation of precursor metabolites and energy,catabolic process	mitochondrion,plastid	transferase activity,nucleotide binding,catalytic activity
ug3133	414	GO:0003824			catalytic activity
ug3134	567				
ug3135	456				
ug3136	557				
ug3137	313				
ug3138	400	GO:0005488,GO:0008515,GO:0005488,GO:0005376	biological_process		binding
ug3139	515				binding,protein binding
ug3140	376				
ug3141	372	GO:0009987,GO:000987,GO:0003674,GO:0006519,GO:0005739	cellular process,catabolic process,cellular amino acid and derivative metabolic process	mitochondrion	molecular_function
ug3142	458				
ug3143	497	GO:0016020,GO:0005125		membrane	binding
ug3144	125				
ug3145	410				
ug3146	386				
ug3147	525				
ug3148	529				
ug3149	136				
ug3150	558	GO:0006464,GO:0005488,GO:0000166,GO:0005886	protein modification process	plasma membrane	binding,nucleotide binding,kinase activity
ug3151	367				
ug3152	600	GO:0009058,GO:000987,GO:0006629,GO:0005488,GO:0008152,GO:0003824,GO:000578	biosynthetic process,cellular process,lipid metabolic process,metabolic process	endoplasmic reticulum	binding,catalytic activity
ug3153	113				
ug3154	519				
ug3155	455	GO:0008289,GO:0006508	transport		lipid binding
ug3156	508				
ug3157	433				
ug3158	374				
ug3159	218				
ug3160	100				
ug3161	118				
ug3162	424	GO:0008135,GO:0006412,GO:0030528,GO:0005488,GO:0016043,GO:0006350,GO:000565	translation,cellular component organization,transcription	nucleoplasm	translation factor activity, nucleic acid binding,transcription regulator
ug3163	228				
ug3164	279				
ug3165	217				
ug3166	430				
ug3167	365				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug3168	476	GO:0005737,GO:0005198,GO:0009987,GO:000166,GO:0005856,GO:0016043,GO:0006950,GO:0009628,GO:001	cellular process,cellular component organization,response to stress,response to abiotic stimulus	cytoplasm,cytoskeleton	structural molecule activity,nucleotide binding,hydrolase activity
ug3170	519				
ug3171	511				
ug3172	142				
ug3173	123				
ug3174	577	GO:0005515,GO:0009000003,GO:0009653,GO:0009791,GO:0009790	reproduction,anatomical structure morphogenesis,post-embryonic development,embryonic	plastid	protein binding
ug3175	570				
ug3176	152				
ug3177	577				
ug3178	407	GO:0016301			kinase activity
ug3179	408				
ug3180	192				
ug3181	574	GO:0006950,GO:000886,GO:0019725,GO:003824,GO:0005783,G	response to stress,cellular homeostasis	plasma membrane,endoplasmic reticulum,mitochondrion	catalytic activity
ug3182	543				
ug3183	303				
ug3184	507				
ug3185	456	GO:0016020,GO:0005618,GO:0019538,GO:0009056,GO:0016787	protein metabolic process,catabolic process	membrane,cell wall	hydrolase activity
ug3186	585				
ug3187	194				
ug3188	455				
ug3189	535	GO:0005829,GO:0005488,GO:0006950,GO:00019725	response to stress,response to abiotic stimulus cellular homeostasis	cytosol	binding
ug3190	400				
ug3191	516				
ug3192	129				
ug3193	579	GO:0008152,GO:0005739,GO:0000166,GO:000	metabolic process	mitochondrion	nucleotide binding,catalytic activity
ug3194	452				
ug3195	501	GO:0005737,GO:0009058,GO:0009987,GO:0006629,GO:0003824,GO:0008150,GO:0016020,GO:0006950,GO:0009628,GO:0008150,GO:0003824,GO:0008152,GO:0000166,GO:0009530,GO:0016301,GO:0016740	biosynthetic process,cellular process,lipid metabolic process,biological_process,response to abiotic stimulus response to stress,response to abiotic stimulus,biological_process,metabolic process	cytoplasm,membrane	catalytic activity
ug3196	504				
ug3197	459				
ug3198	387	GO:0030246			kinase activity,transferase activity carbohydrate binding
ug3199	540	GO:0003700,GO:0005634,GO:0006350	transcription	nucleus	transcription factor activity
ug3200	568				
ug3201	108				
ug3202	392				
ug3203	275				
ug3204	346				
ug3205	414	GO:0005618,GO:0005151,GO:0005886,GO:0009536,GO:0005634,GO:0009719,GO:000716	response to endogenous stimulus,signal transduction	cell wall,plasma membrane,plastid,nucleus	protein binding
ug3206	490				
ug3207	393				
ug3208	380				
ug3209	410	GO:0004872,GO:001020,GO:0005783,GO:0005488,GO:0009987,G	cellular process,transport	membrane,endoplasmic reticulum	receptor activity,binding
ug3210	547				
ug3211	429	GO:0008152,GO:0003824,GO:0008150	metabolic process,biological_process		catalytic activity
ug3212	423				
ug3213	357				
ug3214	203				
ug3215	262				
ug3216	429				
ug3217	413	GO:0003677,GO:0006350,GO:0005634	transcription	nucleus	DNA binding
ug3218	430	GO:0005737,GO:0005111		cytoplasm,cell wall	
ug3219	111				
ug3220	369				



Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug3221	578				
ug3222	107				
ug3223	187				
ug3224	114				
ug3225	423				
ug3226	491	GO:0019725,GO:0003824,GO:0005488,GO:0005622,GO:0005886,GO:0019538,GO:0009056,GO:0009987,GO:0005634,GO:0005829,GO:0016787,GO:000	cellular homeostasis,transport protein metabolic process,catabolic process,cellular process,response to stress,response to abiotic stimulus	intracellular,plasma membrane,nucleus,cytosol	catalytic activity,binding hydrolase activity
ug3227	281				
ug3228	109				
ug3229	162				
ug3230	421	GO:0019725,GO:0005783,GO:0003824,GO:0006091,GO:0009	cellular homeostasis generation of precursor metabolites and energy,catabolic process	endoplasmic reticulum	catalytic activity catalytic activity,binding,transferase activity
ug3231	441	056,GO:0003824,GO:0005488,GO:0016740			
ug3232	501	GO:0009058,GO:0006139,GO:0016301	biosynthetic process,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		kinase activity
ug3233	389				
ug3234	404				
ug3235	457				
ug3236	498	GO:0005488,GO:0008488,GO:0008152,GO:0003824,GO:0009058,GO:0006091,GO:0009056,GO:000166,GO:0009536	metabolic process,biosynthetic process,cellular amino acid and derivative metabolic process,generation of precursor metabolites and energy,catabolic process	mitochondrion,plastid	binding,lipid binding binding,catalytic activity,nucleotide binding
ug3237	411				
ug3238	414				
ug3239	415	GO:0009605,GO:0006950,GO:0006350,GO:0016301,GO:0005515,GO:0007165,GO:000960	response to external stimulus,response to stress,transcription,signal transduction,response to biotic stimulus,protein modification	mitochondrion	kinase activity,protein binding,enzyme regulator activity,nucleotide binding
ug3240	378	7,GO:0030234,GO:0006464,GO:0009058,GO:0006519,GO:0009987,GO:0019748,GO:0009628,GO:0006810,GO:000	process,cellular amino acid and derivative metabolic process,cellular process,secondary cellular amino acid and derivative metabolic process,metabolic process		
ug3241	539	GO:0005488,GO:0006519,GO:0016740,GO:0008152,GO:0009987,GO:0009987,GO:0005			
ug3242	498				
ug3243	412	575,GO:0000166,GO:0016043,GO:0005198,GO:0016787,GO:000585	cellular process,cellular component organization	cellular_component,cytoskeleton	nucleotide binding,structural molecule activity,hydrolase activity
ug3244	183	GO:0005886		plasma membrane	
ug3245	591	GO:0016740			transferase activity
ug3246	246				
ug3247	389	GO:0016787,GO:0005634,GO:0006464	protein modification process	nucleus	hydrolase activity
ug3248	412	GO:0005737,GO:0005488,GO:0005515		cytoplasm	binding,protein binding
ug3249	386	GO:0005623		cell	
ug3250	504	GO:0005840,GO:0005198,GO:0006412,GO:000	translation	ribosome	structural molecule activity,nucleotide binding
ug3251	254				
ug3252	270				
ug3253	394				
ug3254	391	GO:0005737,GO:0005488,GO:0008152,GO:0003824	metabolic process	cytoplasm,plasma membrane	binding,catalytic activity
ug3255	442				
ug3256	299				
ug3257	155				
ug3258	511	GO:0016301,GO:0005829,GO:0000166,GO:0005975,GO:0006091,GO:0009056	carbohydrate metabolic process,generation of precursor metabolites and energy,catabolic process	cytosol	kinase activity,nucleotide binding
ug3259	323	GO:0016787			hydrolase activity
ug3260	183				
ug3261	353	GO:0016301,GO:0005515,GO:0007275,GO:000	multicellular organismal development,cell cycle		kinase activity,protein binding
ug3262	232				
ug3263	491				



Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug3318	477				
ug3319	401				
ug3320	488				
ug3321	283				
ug3322	479				
ug3323	488	GO:0016020,GO:0006810,GO:0005215	transport	membrane	transporter activity
ug3324	468	GO:0000166,GO:0016020,GO:0008152,GO:0005488,GO:0003824,GO:0003674,GO:000588	metabolic process	membrane,plasma membrane	nucleotide binding,binding,catalytic activity,molecular_function
ug3325	474				
ug3326	455				
ug3327	498	GO:0005488			binding
ug3328	384				
ug3329	507	GO:0006350,GO:0003700,GO:0005488	transcription		transcription factor activity,binding
ug3330	424				
ug3331	450	GO:0016301,GO:0006350,GO:0009058,GO:0005975,GO:0009987,GO:0005488	transcription,biosynthetic process,carbohydrate metabolic process,cellular process	nucleus	kinase activity
ug3332	455				
ug3333	355				
ug3334	482	GO:0030246,GO:0005975,GO:0009987,GO:0005488	carbohydrate metabolic process,cellular process		carbohydrate binding,catalytic activity
ug3335	448				
ug3336	425	GO:0008150,GO:0005488,GO:0005777,GO:0016740,GO:0006519,GO:0009058,GO:001602	biological_process,cellular amino acid and derivative metabolic process,biosynthetic process	peroxisome,membrane,plastid	binding,transferase activity
ug3337	432				
ug3338	359	GO:0003824,GO:0000166			catalytic activity,nucleotide binding
ug3339	455				
ug3340	134				
ug3341	348				
ug3342	469	GO:0016020,GO:0006810,GO:0005215	transport	membrane	transporter activity
ug3343	487	GO:0016020,GO:0003824,GO:0005488		membrane	catalytic activity,binding
ug3344	139				
ug3345	502				
ug3346	514				
ug3347	464				
ug3348	466				
ug3349	172				
ug3350	486				
ug3351	485				
ug3352	441	GO:0003676,GO:0000166,GO:0016787			nucleic acid binding,nucleotide
ug3353	482				
ug3354	474	GO:0016740			transferase activity
ug3355	473				
ug3356	432	GO:0003824,GO:0005488,GO:0009536		plastid	catalytic activity,binding
ug3357	416				
ug3358	469				
ug3359	441	GO:0006950,GO:0009056,GO:0009987,GO:0005777,GO:0005488,GO:0008152,GO:000382	response to stress,catabolic process,cellular process,metabolic process	peroxisome	binding,catalytic activity
ug3360	294				
ug3361	472	GO:0003824,GO:0005488,GO:0005783,GO:00006810,GO:0005215,GO:0016020		endoplasmic reticulum,membrane	catalytic activity,binding
ug3362	453	GO:0006810,GO:0005215,GO:0016020	transport	membrane	transporter activity
ug3363	476				
ug3364	507				
ug3365	164				
ug3366	479				
ug3367	583	GO:0005975,GO:0016000,GO:0005975,GO:0009987,GO:0005777,GO:0005488,GO:0008152,GO:000382	carbohydrate metabolic process		hydrolase activity
ug3368	455	GO:0005975,GO:0016787,GO:0005576,GO:0005618,GO:0003824,GO:0005	carbohydrate metabolic process,cellular process	extracellular region,cell wall	hydrolase activity,transferase activity
ug3369	659	GO:0003824,GO:0005			catalytic activity,binding
ug3370	642				













Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug3610	153				
ug3611	693				
ug3612	539				
		GO:0005618,GO:0006950,GO:0006259,GO:0005739,GO:0016787,GO:0003677,GO:001604	response to stress,DNA metabolic process,cellular component organization,cellular	cell wall,mitochondrion,membrane,plastid,thylakoid	hydrolase activity,DNA binding,nucleotide binding,protein binding,nuclease activity
ug3613	774	3,GO:0009987,GO:0019538,GO:0000166,GO:0016020,GO:0009536,GO:0005515,GO:0009579,GO:0009058,GO:0	process,protein metabolic process,biosynthetic process,transport		
ug3614	410	GO:0006091,GO:0015	generation of precursor metabolites and	membrane,plastid,thylakoid	catalytic activity,molecular_function
ug3615	413	979,GO:0003824,GO:0003674,GO:0006810,GO:0016020,GO:000953	energy,photosynthesis,transport		
ug3616	747	GO:0016043,GO:0007049,GO:0005515,GO:0	cellular component organization,cell cycle	nucleus	protein binding
ug3617	192				
ug3618	527	GO:0006810	transport		
ug3619	741	GO:0005622		intracellular	
ug3620	663	GO:0005623,GO:0005737,GO:0016787,GO:0		cell,cytoplasm	hydrolase activity,binding
ug3621	812	GO:0003676,GO:0000166,GO:0009536		plastid	nucleic acid binding,nucleotide binding
ug3622	315				
ug3623	203				
ug3624	197				
ug3625	740	GO:0009058,GO:000987,GO:0019748,GO:0006629,GO:0005515,GO:0016043	biosynthetic process,cellular process,secondary metabolic process,lipid metabolic process,cellular component		protein binding
ug3626	793				
ug3627	498	GO:0008150,GO:0005773,GO:0005576,GO:0005634,GO:0009536,GO:0005886,GO:000551	biological_process	vacuole,extracellular region,nucleus,plastid,plasma membrane	protein binding
ug3628	617	GO:0019538,GO:000987,GO:0009628,GO:0003676,GO:0004871,GO:0000166,GO:000548	protein metabolic process,cellular process,response to abiotic stimulus		nucleic acid binding,signal transducer activity,nucleotide binding,binding,protein binding
ug3629	311				
ug3630	648	GO:0009536		plastid	
ug3631	435	GO:0016787,GO:0005737,GO:0019538,GO:0009987,GO:0016020,GO	protein metabolic process,cellular process	cytoplasm,membrane,endoplasmic reticulum	hydrolase activity
ug3632	468				
ug3633	679				
ug3634	410				
ug3635	697	GO:0016020,GO:0003824,GO:0009536,GO:000003,GO:0009791,GO:0016740,GO:0006350,GO:0009536	reproduction,post-embryonic development,embryonic development	membrane,plastid	catalytic activity
ug3636	768	GO:0016740,GO:0006350,GO:0009536	transcription	plastid	transferase activity
ug3637	428	GO:0008152,GO:0016787,GO:0009536	metabolic process	plastid	hydrolase activity
ug3638	731	GO:0009058,GO:000987,GO:0003824,GO:0006950,GO:0009628,GO:0005783,GO:0009536,GO:0005886	biosynthetic process,cellular process,response to stress,response to abiotic stimulus		catalytic activity
ug3639	823			endoplasmic reticulum,plastid,plasma membrane	
ug3640	811				
ug3641	313				
ug3642	625	GO:0006810,GO:0009628,GO:0009606,GO:0016020,GO:0016787,GO:0005215,GO:0009791,GO:0009719,GO:0008150,GO:0000166,GO:0009605,GO:0005515,	transport,response to abiotic stimulus,tropism,post-embryonic development,response to endogenous stimulus,biological_process,response to external stimulus,flower development	membrane,plasma membrane	hydrolase activity,transporter activity,nucleotide binding,protein binding
ug3643	505				
ug3644	902	GO:0008150,GO:0009	biological_process	plastid	
ug3645	440				
ug3646	247				
ug3647	286	GO:0016020		membrane	
ug3648	411				
ug3649	554				
ug3650	385				
ug3651	173				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug3652	295				
ug3653	350				
ug3654	290				
ug3655	830	GO:0030246,GO:0005618,GO:0005975,GO:0005773,GO:0005488,GO:0005886,GO:001678	carbohydrate metabolic process	cell wall,vacuole,plasma membrane,cellular_component	carbohydrate binding,kinase,hydrolase activity
ug3656	745				
ug3657	176				
ug3658	483				
ug3659	184				
ug3660	632				
ug3661	777	GO:0003677,GO:0006	transcription		DNA binding
ug3662	871	GO:0005488,GO:0008152,GO:0003824,GO:0	metabolic process		binding,catalytic activity,molecular_function
ug3663	226				
ug3664	473				
ug3665	155				
ug3666	354				
ug3667	275				
ug3668	418				
ug3669	306	GO:0016301,GO:0006139,GO:0007275,GO:000166,GO:0009536,GO:0009058,GO:0006519,GO:0005634	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,multicellular organismal development,biosynthetic process,cellular amino acid and derivative metabolic process	plastid,nucleus	kinase activity,nucleotide binding
ug3670	324	GO:0008152,GO:0003824,GO:0006950	metabolic process,response to stress		catalytic activity
ug3671	253				
ug3672	144				
ug3673	124				
ug3674	626				
ug3675	215				
ug3676	485				
ug3677	164				
ug3678	453				
ug3679	794	GO:0006464,GO:0005886,GO:0005515,GO:0016301,GO:0000166,GO	protein modification process,signal transduction	plasma membrane	protein binding,kinase activity,nucleotide binding
ug3680	473				
ug3681	348				
ug3682	459				
ug3683	534	GO:0007049,GO:0005634,GO:0030234,GO:0005515,GO:0009987	cell cycle,cellular process	nucleus	enzyme regulator activity,protein binding
ug3684	571				
ug3685	451	GO:0003723,GO:0006139,GO:0009058,GO:0005739,GO:0000003,GO:0009791,GO:0009790,GO:0003824,GO:0008152,GO:0006259,GO:0016043,GO:0009987,GO:0000166,GO:0005515,GO:0005737,GO:0	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process,reproduction,post-embryonic development,embryonic development,metabolic process,DNA metabolic process,cellular component organization,cellular process	mitochondrion,cytoplasm,plastid	RNA binding,catalytic activity,nucleotide binding,protein binding,nuclease activity
ug3686	104				
ug3687	673	GO:0005794,GO:0009653,GO:0016043,GO:0016049,GO:0009987,GO:0016787	anatomical structure morphogenesis,cellular component organization,cell growth,cellular process	Golgi apparatus	hydrolase activity
ug3688	481				
ug3689	680				
ug3690	284	GO:0016787,GO:0005975,GO:0005737,GO:0	carbohydrate metabolic process	cytoplasm	hydrolase activity,kinase activity
ug3691	573	GO:0003676,GO:0000166			nucleic acid binding,nucleotide binding
ug3692	627				
ug3693	489				
ug3694	294	GO:0003676			nucleic acid binding
ug3695	444				
ug3696	352				
ug3697	327	GO:0006464,GO:0005886,GO:0005515,GO:0000166,GO:0016301	protein modification process	plasma membrane	protein binding,nucleotide binding,kinase activity
ug3698	411	GO:0009058,GO:0009	biosynthetic process,cellular		
ug3699	879	GO:0005737,GO:0005		cytoplasm,intracellular	
ug3700	383				
ug3701	774				
ug3702	807	GO:0016740,GO:0008	metabolic process		transferase activity

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug3703	136				
ug3704	596				
ug3705	115				
ug3706	272				
ug3707	401				
ug3708	791	GO:0007165,GO:0004	signal transduction		signal transducer activity
ug3709	341	GO:0005623		cell	
ug3710	175				
ug3711	543				
ug3712	460	GO:0009536		plastid	
			biosynthetic process,carbohydrate		
			metabolic process,cellular		
ug3713	685	GO:0005737,GO:0009 058,GO:0005975,GO:0 009987,GO:0006629,G O:0003824,GO:000613 9,GO:0009056,GO:001 9748,GO:0006091	process,lipid metabolic process,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,catabolic process,secondary metabolic process,generation of precursor	cytoplasm	catalytic activity
ug3714	920	GO:0005618,GO:0016 787,GO:0009536,GO:0 019538,GO:0009056,G	protein metabolic process,catabolic process	cell wall,plastid,extracellular region	hydrolase activity
ug3715	211	GO:0005576		extracellular region	
ug3716	879	GO:0009058,GO:0009 987,GO:0006629,GO:0	biosynthetic process,cellular process,lipid metabolic process		transporter activity
ug3717	412				
ug3718	356				
ug3719	939				
ug3720	596	GO:0005634,GO:0007 049,GO:0009987	cell cycle,cellular process	nucleus	
ug3721	135				
ug3722	727	GO:0005794		Golgi apparatus	
ug3723	242				
ug3724	887	GO:0005856,GO:0005 737,GO:0000166,GO:0		cytoskeleton,cytoplasm	nucleotide binding,protein binding
ug3725	343				
ug3726	766	GO:0006950,GO:0009 628,GO:0016740,GO:0 016787,GO:0006139,G O:0009058,GO:000953	response to stress,response to abiotic stimulus,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic	plastid	transferase activity,hydrolase activity
ug3727	147				
ug3728	861				
ug3729	741				
ug3730	898	GO:0005622,GO:0006 810,GO:0005215	transport	intracellular	transporter activity
ug3731	794	GO:0016787			hydrolase activity
ug3732	429				
ug3733	260				
ug3734	893				
ug3735	297				
ug3736	525	GO:0006259,GO:0009 058,GO:0005515,GO:0 016043,GO:0009987,G O:0009536,GO:000563	DNA metabolic process,biosynthetic process,cellular component organization,cellular process	plastid,nucleus	protein binding,kinase activity
ug3737	456				
ug3738	108				
ug3739	340				
ug3740	236				
ug3741	547				
ug3742	163				
ug3743	883	GO:0005737,GO:0016 787,GO:0009536		cytoplasm,plastid	hydrolase activity
ug3744	391				
ug3745	753	GO:0005737,GO:0005 634,GO:0005488,GO:0	protein modification process	cytoplasm,nucleus	binding
ug3746	585				
ug3747	951	GO:0006810,GO:0016 043,GO:0009987,GO:0 005737,GO:0016020,G O:0005777,GO:000551 5,GO:0009056,GO:000	transport,cellular component organization,cellular process,catabolic process,lipid metabolic process	cytoplasm,membrane,peroxisome	protein binding
ug3748	576	GO:0003723,GO:0006 139,GO:0005634,GO:0 GO:0003676,GO:0005 515,GO:0000003,GO:0 009628,GO:0009791,G O:0009605,GO:000716 5,GO:0003824,GO:000	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process reproduction,response to abiotic stimulus,post-embryonic development,response to external stimulus,signal	nucleus	RNA binding,nucleotide binding
ug3749	575	GO:0003824,GO:000 7275,GO:0005634,GO:	transduction,multicellular organismal development	nucleus	nucleic acid binding,protein binding,catalytic activity,nucleotide binding
ug3750	884				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug3751	536	GO:0007049,GO:0016301,GO:0005515	cell cycle		kinase activity,protein binding
ug3752	236	GO:0016787,GO:0000166,GO:0009536		plastid	hydrolase activity,nucleotide binding
ug3753	372				
ug3754	367	GO:0016020,GO:0005280		membrane,endosome	
ug3755	280				
ug3756	824	GO:0016787			hydrolase activity
ug3757	454	GO:0005739,GO:0009536,GO:0016020		mitochondrion,plastid,membrane	
ug3758	783	GO:0005488			binding
ug3759	892				
ug3760	243				
ug3761	715				
ug3762	930	GO:0005623,GO:000810,GO:0009987,GO:0016020,GO:0005768	transport,cellular process	cell,membrane,endosome	
ug3763	301				
ug3764	102				
ug3765	800	GO:0003677			DNA binding
ug3766	551	GO:0007275	multicellular organismal		
ug3767	280				
ug3768	838				
ug3769	869	GO:0019725	cellular homeostasis		
ug3770	429				
ug3771	269				
ug3772	410				
ug3773	803				
ug3774	341				
ug3775	761	GO:0005515,GO:0009628,GO:0004871	response to abiotic stimulus		protein binding,signal transducer activity
ug3776	709				
ug3777	724				
ug3778	292				
ug3779	837				
ug3780	174				
ug3781	482				
ug3782	467				
ug3783	572				
ug3784	396				
ug3785	118				
ug3786	600				
ug3787	634	GO:0005840		ribosome	
ug3788	869	GO:0005488,GO:000515,GO:0003677			binding,protein binding,DNA binding
ug3789	765	GO:0005488			binding
ug3790	538	GO:0005488			binding
ug3791	674				
ug3792	699				
ug3793	164				
ug3794	419	GO:0005886,GO:0005275,GO:0009653,GO:0007008,GO:0006350,GO:0008289,GO:0003677,GO:00030154,GO:0003700	anatomical structure morphogenesis,multicellular organismal development,transcription,cell	plasma membrane,vacuole nucleus	lipid binding,DNA binding,transcription factor activity
ug3796	716				
ug3797	374				
ug3798	194				
ug3799	621	GO:0004518,GO:001740,GO:0003677,GO:0016787,GO:0009987,GO:0005488,GO:0006250	cellular process,DNA metabolic process		nuclease activity,transferase activity,DNA binding,hydrolase activity,binding
ug3800	138				
ug3801	695	GO:0005215,GO:000886,GO:0006810	transport	plasma membrane	transporter activity
ug3802	317	GO:0009058,GO:0006139,GO:0000166,GO:0006810,GO:0016020,GO:0016787,GO:0005210	biosynthetic process,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,transport	membrane	nucleotide binding,hydrolase activity,transporter activity
ug3803	506	GO:0005488			binding
ug3804	575	GO:0005840,GO:0009099,GO:0005198,GO:0009987,GO:0006412	cellular process,translation	ribosome,plastid	structural molecule activity
ug3805	272				
ug3806	346				
ug3807	748	GO:0016020,GO:0009536,GO:0009579		membrane,plastid,thylakoid	
ug3808	833	GO:0016020,GO:000886,GO:0030246		membrane,plasma membrane	carbohydrate binding
ug3809	573				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug3810	284	GO:0003677,GO:0006	DNA metabolic process		DNA binding
ug3811	720	GO:0019538,GO:0009056,GO:0009987,GO:0	protein metabolic process,catabolic process,cellular process		protein binding
ug3812	158				
ug3813	175				
ug3814	175				
ug3815	608	GO:0003677,GO:0005151,GO:0007165,GO:0009719,GO:0005634,G	signal transduction,response to endogenous stimulus,transcription	nucleus	DNA binding,protein binding
ug3816	611				
ug3817	726				
ug3818	777	GO:0006139,GO:0003824	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		catalytic activity
ug3819	538	GO:0005488			binding
ug3820	328	GO:0016787,GO:0005737,GO:0007165,GO:0	signal transduction	cytoplasm,nucleus	hydrolase activity
ug3821	333	GO:0019725	cellular homeostasis		
ug3822	538				
ug3823	905	GO:0008152,GO:0009987,GO:0005488,GO:0	metabolic process,cellular process		binding,catalytic activity
ug3824	301				
ug3825	281				
ug3826	669				
ug3827	844	GO:0005488,GO:0005		Golgi apparatus	binding
ug3828	240				
ug3829	115				
ug3830	352				
ug3831	532	GO:0005618,GO:0009987,GO:0008152,GO:0003824,GO:0005739	response to endogenous stimulus metabolic process	cell wall mitochondrion	catalytic activity
ug3832	657	GO:0005730,GO:0005			
ug3833	678	GO:0005622,GO:0005634,GO:0006139,G	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	nucleolus,nucleoplasm,intracellular,nucleus,mitochondrion	
ug3834	268	GO:0000166,GO:0006139,GO:0016301	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		nucleotide binding,kinase activity
ug3835	181				
ug3836	380				
ug3837	711				
ug3838	373	GO:0016787,GO:0016043,GO:0009987	cellular component organization,cellular process		hydrolase activity
ug3839	347				
ug3840	626				
ug3841	174				
ug3842	371	GO:0005575,GO:0019538,GO:0009056,GO:000166,GO:0016787,G	protein metabolic process,catabolic process	cellular_component,nucleus,cytosol	nucleotide binding,hydrolase activity
ug3843	239	O:0005634,GO:000582			
ug3844	779				
ug3845	167				
ug3846	224				
ug3847	141				
ug3848	157				
ug3849	429				
ug3850	257				
ug3851	801				
ug3852	541				
ug3853	435				
ug3854	671	GO:0009536		plastid	
ug3855	638				
ug3856	176				
ug3857	310				
ug3858	268				
ug3859	441				
ug3860	192				
ug3861	652	GO:0016787,GO:0009987,GO:0003824,GO:0009536	biosynthetic process,cellular process	plastid	hydrolase activity,catalytic activity
ug3862	504				
ug3863	574	GO:0005488,GO:0008152,GO:0003824,GO:0	metabolic process		binding,catalytic activity,molecular_function
ug3864	270				
ug3865	792	GO:0006464,GO:0005773,GO:0005886,GO:0005515,GO:0016301,G	protein modification process,response to endogenous stimulus,signal transduction	vacuole,plasma membrane	protein binding,kinase activity,nucleotide binding
ug3866	704	O:0000166,GO:000971			
ug3867	801	GO:0005488,GO:0008152,GO:0003824,GO:0003674,GO:0006950	metabolic process,response to stress		binding,catalytic activity,molecular_function

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug3868	570	GO:0009058,GO:0009	biosynthetic process,cellular		
ug3869	782	987,GO:0006950,GO:0009607,GO:0016020,G	process,response to stress,response to biotic stimulus	membrane,plastid	
ug3870	255				
ug3871	340				
ug3872	531	GO:0005488			binding
		GO:0005488,GO:0016787,GO:0016301,GO:0007275,GO:0040007,G	multicellular organismal development,growth,carbohydrate metabolic process,cellular process,catabolic		
ug3873	487	O:0005975,GO:0009987,GO:0009056,GO:0009653,GO:0007165,GO:0000166,GO:0030154,GO:0009908,GO:0006	process,anatomical structure morphogenesis,signal transduction,cell differentiation,flower		binding,hydrolase activity,kinase activity,nucleotide binding
ug3874	313				
ug3875	805				
ug3876	810	GO:0006810,GO:0009987,GO:0005622,GO:0	transport,cellular process	intracellular	transporter activity
ug3877	170				
ug3878	882				
ug3879	429	GO:0005840,GO:0005198,GO:0009536,GO:0	translation	ribosome,plastid	structural molecule activity
ug3880	464	GO:0006464,GO:0000166,GO:0007165,GO:0	protein modification process,signal transduction		nucleotide binding,kinase activity
ug3881	360				
ug3882	860	GO:0006464,GO:0005488,GO:0000166,GO:0	protein modification process		binding,nucleotide binding,kinase activity
ug3883	194				
ug3884	525				
ug3885	381				
ug3886	771				
ug3887	882	GO:0006950,GO:0006259,GO:0003824	response to stress,DNA metabolic process		catalytic activity
		GO:0006139,GO:0005975,GO:0005622,GO:0009058,GO:0009653,G	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,carbohydrate metabolic process,biosynthetic		
ug3888	378	O:0016043,GO:0016049,GO:0003824,GO:0005488	process,anatomical structure morphogenesis,cellular component organization,cell growth	intracellular	catalytic activity,binding
ug3889	278				
ug3890	335				
ug3891	261				
		GO:0005730,GO:0005773,GO:0005198,GO:0005840,GO:0005829,G	translation	nucleolus,vacuole,ribosome,cytosol,membrane	structural molecule activity
ug3892	913	O:0016020,GO:000641			
ug3893	557				
ug3894	107				
		GO:0030246,GO:0019538,GO:0009987,GO:0	protein metabolic process,cellular process,response to stress,response to abiotic stimulus	vacuole,endoplasmic reticulum,mitochondrion	carbohydrate binding,protein binding
ug3895	571	005773,GO:0005783,GO:0006950,GO:0005488,GO:0005515,GO:000	carbohydrate metabolic process,cellular process,catabolic		
ug3896	852	787,GO:0005576,GO:0005975,GO:0009987,G	process,cellular process,catabolic process	cell wall,extracellular region	hydrolase activity
		GO:0004871,GO:0007165,GO:0005488,GO:0006629,GO:0016787	signal transduction,lipid metabolic process		signal transducer activity,protein binding,hydrolase activity
ug3897	706				
ug3898	364	GO:0016020,GO:0005		membrane,cell	
ug3899	294				
ug3900	654				
ug3901	121				
ug3902	874	GO:0006950,GO:0006259,GO:0030528,GO:0	response to stress,DNA metabolic process		transcription regulator activity,protein binding
ug3903	512				
ug3904	565	GO:0016020		membrane	
ug3905	792	GO:0006259,GO:0003676,GO:0005622,GO:0	DNA metabolic process	intracellular	nucleic acid binding,catalytic activity
ug3906	900	GO:0019538,GO:0009056,GO:0016787	protein metabolic process,catabolic process		hydrolase activity
ug3907	789	GO:0008152,GO:0009987,GO:0003824,GO:0	metabolic process,cellular process		catalytic activity,protein binding
		GO:0016020,GO:0005			
ug3908	735	515,GO:0005215,GO:0006810,GO:0009987,G	transport,cellular process	membrane,plasma membrane	protein binding,transporter activity

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug3909	622	GO:0009628,GO:0016787,GO:0005515,GO:000166,GO:0006950,GO:0019538,GO:000998	response to abiotic stimulus,response to stress,protein metabolic process,cellular process		hydrolase activity,protein binding,nucleotide binding
ug3910	664				
ug3911	781	GO:0005623,GO:000987,GO:0009056	cellular process,catabolic process	cell	
ug3912	306				
ug3913	175				
ug3914	119				
ug3915	768				
ug3916	182				
ug3917	630				
ug3918	169				
ug3919	432				
ug3920	422	GO:0009536		plastid	
ug3921	353	GO:0009058,GO:000987,GO:0006629	biosynthetic process,cellular process,lipid metabolic process		
ug3922	216	GO:0016020,GO:0009		membrane,plastid	
ug3923	591				
ug3924	757	GO:0019538,GO:000987,GO:0005829,GO:0	protein metabolic process,cellular process	cytosol	protein binding
ug3925	763				
ug3926	804	GO:0003676,GO:0000166			nucleic acid binding,nucleotide binding
ug3927	629	GO:0003723,GO:000908,GO:0005634	flower development	nucleus	RNA binding
ug3928	809	GO:0006350	transcription		
ug3929	532	GO:0016020,GO:0005777,GO:0016043,GO:00008135,GO:0005622,GO:0005730,GO:0	cellular component organization,cellular process	membrane,peroxisome	
ug3930	435	006412,GO:0016020,GO:0009536,GO:0009579,GO:0016787,GO:0005773,GO:0005	translation	intracellular,nucleolus,membrane,plastid,thylakoid,extracellular region	translation factor activity, nucleic acid binding,hydrolase activity,nucleotide binding
ug3931	148	886,GO:0005215,GO:0006810,GO:0016020	transport	vacuole,plasma membrane,membrane	transporter activity
ug3932	226				
ug3933	241				
ug3934	813	GO:0008152,GO:0003824,GO:0005488,GO:0009536,GO:0030528,GO:0005622,GO:0003	metabolic process	plastid	catalytic activity,binding,transcription regulator activity
ug3935	635	677,GO:0016043,GO:0009987,GO:0009536,G	cellular component organization,cellular process	intracellular,plastid,nucleus	DNA binding
ug3936	719				
ug3937	892	GO:0016740,GO:0009515,GO:0006810,GO:0		plastid	transferase activity
ug3938	831	009987,GO:0005635,GO:0030234,GO:0005783,GO:0006950,GO:000	transport,cellular process,response to stress,response to abiotic stimulus	plasma membrane,nuclear envelope,endoplasmic reticulum	protein binding,enzyme regulator activity
ug3939	188				
ug3940	539	GO:0016020,GO:0006950,GO:0005576,GO:0007165,GO:0005618,GO:0005515,GO:000953,GO:0005515,GO:0016020,GO:0005737,GO:0005215,GO:0006810,GO:0009987,GO:000573	response to stress,signal transduction	membrane,extracellular region,cell wall,plastid	protein binding
ug3941	805		transport,cellular process	membrane,cytoplasm,mitochondrion	protein binding,transporter activity
ug3942	204				
ug3943	555				
ug3944	754	GO:0016301,GO:0004871,GO:0006464,GO:000166,GO:0007165	protein modification process,signal transduction		kinase activity,signal transducer activity,nucleotide binding
ug3945	825	GO:0016787			hydrolase activity
ug3946	210				
ug3947	671				
ug3948	775				
ug3949	869	GO:0016020,GO:0005737,GO:0006810,GO:0	transport,cellular process	membrane,cytoplasm	
ug3950	274				
ug3951	752	GO:0019538,GO:000987,GO:0005515,GO:000166,GO:0009536	protein metabolic process,cellular process	plastid	protein binding,nucleotide binding
ug3952	547				
ug3953	100				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug3954	335	GO:0009987,GO:000575,GO:0000166,GO:016043,GO:0005198,GO:0016787,GO:000585	cellular process,cellular component organization	cellular_component,cytoskeleton	nucleotide binding,structural molecule activity,hydrolase activity
ug3955	209	GO:0016740,GO:0007267,GO:0040029,GO:0006139,GO:0003677,GO:0016043,GO:0006350,GO:0009987,GO:0005634	cell-cell signaling,regulation of gene expression, epigenetic,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,cellular component	nucleus	transferase activity,DNA binding
ug3956	287				
ug3957	715				
ug3958	776				
ug3959	319				
ug3960	881	GO:0019538,GO:0009056,GO:0009987,GO:0003824,GO:0006464	protein metabolic process,catabolic process,cellular process,protein modification process		catalytic activity
ug3961	664				
ug3962	107				
ug3963	322				
ug3964	803				
ug3965	534				
ug3966	183				
ug3967	137				
ug3968	147				
ug3969	709	GO:0005622,GO:0003677,GO:0016043,GO:0009987,GO:0005634	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug3970	202				
ug3971	460	GO:0006464,GO:0000166,GO:0016301	protein modification process		nucleotide binding,kinase activity
ug3972	464				
ug3973	645	GO:0008152,GO:0005737,GO:0003824,GO:0005618,GO:0003824,GO:0005488,GO:000824,GO:0005488,GO:0005886,GO:0009653,GO:0016043,GO:0016049,GO:0016020,GO:000604,GO:0016020,GO:0009	metabolic process	cytoplasm	catalytic activity
ug3974	909	GO:0005886,GO:0009653,GO:0016043,GO:0016049,GO:0016020,GO:000604,GO:0016020,GO:0009	anatomical structure morphogenesis,cellular component organization,cell growth	cell wall,plasma membrane,membrane,extracellular region	catalytic activity,binding
ug3975	604	GO:0016020,GO:0009	response to biotic stimulus	membrane	
ug3976	257				
ug3977	356				
ug3978	911	GO:0005886		plasma membrane	
ug3979	248				
ug3980	494				
ug3981	422				
ug3982	771				
ug3983	238				
ug3984	374				
ug3985	481				
ug3986	854	GO:0005737,GO:0016		cytoplasm	hydrolase activity
ug3987	414				
ug3988	606				
ug3989	202				
ug3990	683				
ug3991	791	GO:0003677,GO:0005634,GO:0006350	transcription	nucleus	DNA binding
ug3992	886				
ug3993	304				
ug3994	362				
ug3995	133				
ug3996	508				
ug3997	578				
ug3998	532	GO:0005739		mitochondrion	
ug3999	543				
ug4000	791	GO:0005840,GO:0005198,GO:0009536,GO:0006412,GO:0003723	translation	ribosome,plastid	structural molecule activity,RNA binding
ug4001	843	GO:0009058,GO:0009987,GO:0006629,GO:000	biosynthetic process,cellular process,lipid metabolic process		transferase activity
ug4002	274				
ug4003	428	GO:0009719	response to endogenous stimulus		
ug4004	313				
ug4005	208				
ug4006	206				
ug4007	854	GO:0016020,GO:0005886,GO:0005886,GO:0005		membrane,cell	
ug4008	757	GO:0016020,GO:0005215,GO:0006810	transport	plasma membrane,vacuole,membrane	transporter activity
ug4009	829				



Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4010	848	GO:0006464,GO:0005886,GO:0005515,GO:000166,GO:0016301	protein modification process	plasma membrane	protein binding,nucleotide binding,kinase activity
ug4011	566				
ug4012	503				
ug4013	512				
ug4014	279				
ug4015	881	GO:0009536		plastid	
ug4016	740				
ug4017	672				
ug4018	595	GO:0005515			protein binding
ug4019	699				
ug4020	736	GO:0016787,GO:0005670		cell wall	hydrolase activity
ug4021	670				
ug4022	650				
ug4023	339	GO:0008152,GO:0016737,GO:0003824	metabolic process		hydrolase activity
ug4024	376	GO:0019725,GO:0005515,GO:0003824	cellular homeostasis	cytoplasm	catalytic activity
ug4025	706	GO:0005215,GO:0006810,GO:0008152,GO:000336	transport,metabolic process	plasma membrane	transporter activity
ug4026	336				
ug4027	236	GO:0005488,GO:0009058,GO:0009987,GO:0003824,GO:0015979	biosynthetic process,cellular process,photosynthesis		binding,catalytic activity
ug4028	754				
ug4029	707	GO:0003824,GO:0009058,GO:0009987,GO:000659	biosynthetic process,cellular process	plastid	catalytic activity
ug4030	659				
ug4031	763	GO:0006350,GO:0003700,GO:0005634	transcription	nucleus	transcription factor activity
ug4032	789	GO:0000003,GO:0009791,GO:0009790,GO:0009536,GO:0006410,GO:0016740,GO:0009606	reproduction,post-embryonic development,embryonic development,translation	ribosome,plastid	structural molecule activity
ug4033	606	GO:0005975,GO:0009987,GO:0016020	biosynthetic process,carbohydrate metabolic process,cellular process	membrane	transferase activity
ug4034	507	GO:0016740,GO:0009058,GO:0005975,GO:000689	biosynthetic process,carbohydrate metabolic process,cellular process		transferase activity
ug4035	689				
ug4036	842				
ug4037	507	GO:0005488,GO:0005515,GO:0005215,GO:00016020,GO:0005739,GO:0006810,GO:001604	transport,cellular component organization,cellular process	membrane,mitochondrion	binding,protein binding,transporter activity
ug4038	738				
ug4039	840	GO:0008152,GO:0016737,GO:0016020,GO:0005739,GO:0003824,GO:0005215,GO:0016787,GO:0006810,GO:0019538,GO:0009056,GO:000691	metabolic process		hydrolase activity
ug4040	483	GO:0008152,GO:0016737,GO:0005215,GO:0016787,GO:0006810,GO:0019538,GO:0009056,GO:000691	transport,protein metabolic process,catabolic process,generation of precursor metabolites and energy	membrane,mitochondrion	catalytic activity,transporter activity,hydrolase activity,binding
ug4041	691	GO:0005739		mitochondrion	
ug4042	535	GO:0009058,GO:0009987,GO:0006629,GO:000604	biosynthetic process,cellular process,lipid metabolic process		transferase activity
ug4043	604				
ug4044	631				
ug4045	730				
ug4046	304				
ug4047	261				
ug4048	751	GO:0005739		mitochondrion	
ug4049	645	GO:0005215,GO:0005739,GO:000739,GO:0016020,GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:0008289,GO:0005488,GO:0005215,GO:0005739,GO:0003674,GO:0006091,GO:0009056,GO:000016	transport,biosynthetic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	mitochondrion,membrane,intracellular	transporter activity,lipid binding
ug4050	733	GO:0005488,GO:0005215,GO:0005739,GO:0006091		intracellular	binding
ug4051	901				
ug4052	526				
ug4053	894				
ug4054	605	GO:0016020,GO:0008152	cell death	membrane	
ug4055	379				
ug4056	213				
ug4057	106				
ug4058	513	GO:0005618,GO:0016020,GO:0005739,GO:0003674,GO:0006091,GO:0009056,GO:000016	generation of precursor metabolites and energy,catabolic process	cell wall,membrane,mitochondrion	molecular_function,nucleotide binding,catalytic activity
ug4059	526	GO:0016787,GO:0009281		plastid	hydrolase activity
ug4060	281				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4061	858				
ug4062	546	GO:0008152,GO:0008152	metabolic process,biological_process		catalytic activity,binding
ug4063	225	GO:0005515			protein binding
ug4064	853	GO:0005739		mitochondrion	
ug4065	898	GO:0005737,GO:0005152,GO:006810,GO:0009987,G	transport,cellular process	cytoplasm,membrane	protein binding,transporter activity
ug4066	816				
ug4067	662	GO:0005488,GO:0008152,GO:0009536,GO:016740,GO:0009058,G	biological_process,biosynthetic process,cellular amino acid and derivative metabolic process	plastid	binding,transferase activity
ug4068	357				
ug4069	771				
ug4070	667	GO:0005488,GO:000824,GO:0008152,GO:0009058,GO:0009987,GO:0009536,GO:001597	metabolic process,biosynthetic process,cellular process,photosynthesis	plastid	binding,catalytic activity
ug4071	341				
ug4072	325				
ug4073	195				
ug4074	863	GO:0005739,GO:0009		mitochondrion,plastid	
ug4075	379				
ug4076	197				
ug4077	698	GO:0016740,GO:0005794,GO:0009058,GO:006464,GO:0005975,GO:0016020,GO:000573	biosynthetic process,protein modification process,carbohydrate metabolic process	Golgi apparatus,membrane,mitochondrion	transferase activity
ug4078	575				
ug4079	797	GO:0016740			transferase activity
ug4080	167				
ug4081	196				
ug4082	663	GO:0009536		plastid	
ug4083	140				
ug4084	799	GO:0005739,GO:0005975,GO:0009987,GO:0009536,GO:0016301,GO:0005622,GO:0003	carbohydrate metabolic process,cellular process	mitochondrion,plastid	kinase activity
ug4085	604	GO:0016043,GO:0009987,GO:0005634,GO:0016020,GO:0005	cellular component organization,cellular process	intracellular,nucleus	DNA binding
ug4086	720	GO:0016020,GO:0005215,GO:0006810,GO:0	transport,cellular process	membrane	transporter activity
ug4087	878	GO:0000166,GO:0005777,GO:0008152,GO:0006139,GO:0005975,GO:0009056,GO:0019748,GO:0003824,GO:0006950,GO:0009628	metabolic process,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,carbohydrate metabolic process,catabolic process,secondary metabolic process,response to stress,response	peroxisome	nucleotide binding,catalytic activity
ug4088	144				
ug4089	816				
ug4090	267				
ug4091	510	GO:0006950,GO:0009607	response to stress,response to biotic stimulus		
ug4092	405				
ug4093	819	GO:0016020		membrane	
ug4094	745				
ug4095	274				
ug4096	406	GO:0005739		mitochondrion	
ug4097	699	GO:0003824,GO:0005737,GO:0005618,GO:0006091,GO:0005783,G	generation of precursor metabolites and energy	cytoplasm,cell wall,endoplasmic reticulum	catalytic activity,molecular_function
ug4098	339				
ug4099	431	GO:0003824,GO:0008152,GO:0005975,GO:0006091,GO:0009056,GO:0009536,GO:0009058,GO:0009	metabolic process,carbohydrate metabolic process,generation of precursor metabolites and energy,catabolic process	plastid	catalytic activity
ug4100	533	GO:0016020,GO:0005739,GO:0005622,GO:0016787,GO:0005215,GO:0005515,GO:0	biosynthetic process,cellular process	membrane,mitochondrion,intracellular	
ug4101	898	GO:0003824,GO:0005737,GO:0016020,GO:0009536,GO:0005783,GO:000		cytoplasm,membrane,plastid,endoplasmic reticulum,plasma membrane	hydrolase activity,transporter activity,protein binding,catalytic activity
ug4102	546				
ug4103	689	GO:0016787,GO:0005			hydrolase activity,binding
ug4104	663				
ug4105	277				
ug4106	173				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4107	520	GO:0005576,GO:0016043,GO:0009987,GO:0	cellular component organization,cellular process	extracellular region,membrane	
ug4108	372				
ug4109	321				
ug4110	621				
ug4111	342				
ug4112	488				
ug4113	806				
ug4114	841	GO:0005737,GO:0016		cytoplasm,membrane	
ug4115	473	GO:0005488,GO:0006950,GO:0009628	response to stress,response to abiotic stimulus		binding
ug4116	677				
ug4117	916				
ug4118	864	GO:0003824,GO:0019538,GO:0009056,GO:0009987,GO:0005515	protein metabolic process,catabolic process,cellular process		catalytic activity,protein binding
ug4119	460	GO:0016787			hydrolase activity
ug4120	176				
ug4121	506				
ug4122	829	GO:0009536		plastid	
ug4123	460	GO:0005488,GO:0008150,GO:0009536,GO:0016740,GO:0009058,G	biological_process,biosynthetic process,cellular amino acid and derivative metabolic process	plastid	binding,transferase activity
ug4124	787				
ug4125	191				
ug4126	151				
ug4127	531				
ug4128	527				
ug4129	880	GO:0006259,GO:0009058,GO:0005515,GO:0005634,GO:0008152,G	DNA metabolic process,biosynthetic process,metabolic process,cellular process,response to stress	nucleus	protein binding
ug4130	181				
ug4131	396	GO:0009536		plastid	
ug4132	274				
ug4133	549	GO:0016020,GO:0009		membrane,plastid	
ug4134	109				
ug4135	534				
ug4136	456	GO:0005488,GO:0003674,GO:0009536		plastid	binding,molecular_function
ug4137	856	GO:0005622,GO:0019538,GO:0009056,GO:0009987,GO:0005634,G	protein metabolic process,catabolic process,cellular process	intracellular,nucleus,cytosol	hydrolase activity
ug4138	189				
ug4139	176				
ug4140	703				
ug4141	805	GO:0003700,GO:0005634,GO:0005488,GO:0	transcription	nucleus	transcription factor activity,binding
ug4142	799	GO:0005840,GO:0005198,GO:0006412,GO:0	translation	ribosome,plastid	structural molecule activity
ug4143	660	GO:0005488			binding
ug4144	758	GO:0016787			hydrolase activity
ug4145	855	GO:0016301,GO:0005634,GO:0005488,GO:0		nucleus,plasma membrane	kinase activity,binding
ug4146	609	GO:0005886,GO:0005622,GO:0006810,GO:0009987,GO:0016020,G	transport,cellular process	plasma membrane,intracellular,membrane,G	
ug4147	837	GO:0005515,GO:0005737,GO:0003723		cytoplasm	protein binding,RNA binding
ug4148	302				
ug4149	103				
ug4150	563	GO:0005515			protein binding
ug4151	837	GO:0006091,GO:0015979,GO:0016020,GO:0009579,GO:0005488,G	generation of precursor metabolites and energy,photosynthesis,protein modification process	membrane,thylakoid,plastid	binding
ug4152	824	GO:0005515,GO:00050009058,GO:0005975,GO:0015979,GO:0		mitochondrion	protein binding
ug4153	676	GO:0003824,GO:0005515,G	biosynthetic process,carbohydrate metabolic process,photosynthesis	plastid,thylakoid,extracellular region,mitochondrion	catalytic activity,protein binding
ug4154	353				
ug4155	589	GO:0003677,GO:0006350,GO:0005634	transcription	nucleus	DNA binding
ug4156	857	GO:0000166			nucleotide binding
ug4157	629	GO:0006412,GO:0009	translation	plastid	
ug4158	333				
ug4159	297				

<b>Unigene ID</b>	<b>sequence length (bp)</b>	<b>GO-ID</b>	<b>Biological process</b>	<b>Cellular component</b>	<b>Molecular function</b>
ug4160	704	GO:0003676			nucleic acid binding
ug4161	523	GO:0005886		plasma membrane	
ug4162	861				
ug4163	868	GO:0005737,GO:0005773,GO:0005886		cytoplasm,vacuole,plasma membrane	
ug4164	353				
ug4165	787				
ug4166	434				
ug4167	473	GO:0016787,GO:000987,GO:0009056	cellular process,catabolic process		hydrolase activity
ug4168	638	GO:0000166,GO:0005737,GO:0003824,GO:0008152,GO:000166,GO:0005739		intracellular	nucleotide binding
ug4169	474	GO:0003824,GO:0008152,GO:0005488	metabolic process		catalytic activity,binding
ug4170	744				
ug4171	231	GO:0003824,GO:0008152,GO:000166,GO:0005739	biological_process,metabolic process	mitochondrion	catalytic activity,nucleotide binding
ug4172	210	GO:0009536		plastid	
ug4173	800	GO:0016020,GO:000635,GO:0005488,GO:0006810,GO:0016043,GO:0009987,GO:0005739	transport,cellular component organization,cellular process	membrane,nuclear envelope,cytoplasm	binding,transporter activity
ug4174	611				
ug4175	671	GO:0005840,GO:000198,GO:0006412	translation	ribosome	structural molecule activity
ug4176	301				
ug4177	438	GO:0005737		cytoplasm	
ug4178	399				
ug4179	477	GO:0005515,GO:000165,GO:0009719,GO:0003723	signal transduction,response to endogenous stimulus	mitochondrion	protein binding
ug4180	773				
ug4181	255				
ug4182	696	GO:0005622,GO:000677,GO:0016043,GO:0009987,GO:0009536,GO:0003676,GO:0005737,GO:0005622	cellular component organization,cellular process	intracellular,plastid,nucleus	DNA binding
ug4183	428			cytoplasm,intracellular	nucleic acid binding
ug4184	915				
ug4185	310				
ug4186	111				
ug4187	525				
ug4188	882	GO:0003723			RNA binding
ug4189	876	GO:0006464,GO:0000166,GO:0016301	protein modification process		nucleotide binding,kinase activity
ug4190	612	GO:0040029,GO:000259,GO:0003677,GO:0003677,GO:0030	regulation of gene expression, epigenetic,DNA metabolic process		DNA binding
ug4191	715	528,GO:0005654,GO:0003700,GO:0006350,GO:0009058,GO:000987,GO:0006629,GO:000003,GO:0008289,GO:0005737,GO:0006464,GO:0005515,GO:0019538,GO:0009056,GO:0009987,GO:000563	transcription	nucleoplasm	DNA binding,transcription regulator activity,transcription factor
ug4192	324		biosynthetic process,cellular process,lipid metabolic process,reproduction		lipid binding
ug4193	805		protein modification process,protein metabolic process,catabolic process,cellular process	cytoplasm,nucleus	protein binding
ug4194	744				
ug4195	828				
ug4196	862	GO:0005634,GO:0003676,GO:0005737,GO:0005739		nucleus	DNA binding
ug4197	631				
ug4198	564				
ug4199	605				
ug4200	654	GO:0005840,GO:000198,GO:0006412,GO:0005515,GO:0006810,GO:0016787,GO:0009987,GO:0016020,GO:0009536,GO:000578,GO:0019538,GO:000987,GO:0005634,GO:000622	translation	ribosome	structural molecule activity
ug4201	792		transport,cellular process	membrane,plastid,endoplasmic reticulum	protein binding,hydrolase activity,nucleotide binding
ug4202	879	056,GO:0030234,GO:0005622,GO:0005634,GO:0005515,GO:0006412,GO:0005515,GO:0006810,GO:0016787,GO:0009987,GO:0016020,GO:0009536,GO:000578,GO:0019538,GO:000987,GO:0005634,GO:000622	protein metabolic process,catabolic process	intracellular,nucleus,cytosol	enzyme regulator activity
ug4203	309				
ug4204	104				
ug4205	402				
ug4206	386				
ug4207	814				
ug4208	739				
ug4209	883	GO:0006629,GO:000576,GO:0016787	lipid metabolic process	extracellular region	hydrolase activity
ug4210	218				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4211	476	GO:0005623		cell	
ug4212	487				
ug4213	129				
ug4214	171				
ug4215	313				
ug4216	450	GO:0016020,GO:0009			
ug4217	351	579,GO:0009536,GO:005488,GO:0015979	photosynthesis	membrane,thylakoid,plastid	binding
ug4218	526	GO:0003723,GO:0016740,GO:0006259,GO:0692	DNA metabolic process, biosynthetic process		RNA binding,transferase activity
ug4219	692				
ug4220	413				
ug4221	818				
ug4222	353				
ug4223	550	GO:0016020		membrane	
ug4224	927	GO:0016043,GO:0009987,GO:0016020,GO:0005623,GO:0006950,GO:0009058,GO:0006519,GO:0019748	cellular component organization,cellular process response to stress,biosynthetic process,cellular amino acid and derivative metabolic process,secondary metabolic process	membrane	protein binding
ug4225	426	950,GO:0009058,GO:0006519,GO:0019748		cell	
ug4226	348				
ug4227	562				
ug4228	814	GO:0009536		plastid	
ug4229	349	GO:0003723			RNA binding
ug4230	739				
ug4231	799				
ug4232	774	GO:0016020,GO:0005737,GO:0009987,GO:0009987,GO:0009987	cellular process	membrane,cytoplasm	transferase activity
ug4233	677	GO:0016020,GO:0009536,GO:0016043,GO:0005488,GO:0016740,GO:0009058,GO:0006519,GO:0000166	cellular component organization,cellular process biosynthetic process,cellular amino acid and derivative metabolic process	membrane,plastid	
ug4234	753				binding,transferase activity,nucleotide binding
ug4235	496				
ug4236	363				
ug4237	572				
ug4238	294				
ug4239	565	GO:0003824,GO:0009058,GO:0006629,GO:0003674,GO:0016740	biosynthetic process,lipid metabolic process		catalytic activity,molecular_function,transferase activity
ug4240	200				
ug4241	906	GO:0016787,GO:0009536,GO:0005739,GO:0019538,GO:0009056,GO:0016020,GO:0009570,GO:0005515,GO:0006464,GO:0000166,GO:0009536	protein metabolic process,catabolic process	plastid,mitochondrion,membrane,thylakoid	hydrolase activity
ug4242	871	GO:0005515,GO:0006464,GO:0000166,GO:0009536	protein modification process		protein binding,nucleotide binding,kinase activity
ug4243	902				
ug4244	477	GO:0009536		plastid	
ug4245	215				
ug4246	855	GO:0009536		plastid	
ug4247	834	GO:0019538,GO:0009987,GO:0005737,GO:0005515,GO:0000166	protein metabolic process,cellular process	cytoplasm	protein binding,nucleotide binding
ug4248	177				
ug4249	882	GO:0005576,GO:0005757		extracellular region,cytoplasm	
ug4250	757				
ug4251	834				
ug4252	238	GO:0016740,GO:0006350,GO:0003677,GO:0009536	transcription	plastid	transferase activity,DNA binding
ug4253	104				
ug4254	124				
ug4255	123				
ug4256	878	GO:0016020,GO:0006810,GO:0005215,GO:0009536	transport	membrane,plasma membrane	transporter activity
ug4257	875				
ug4258	194				
ug4259	831	GO:0016787,GO:0016740,GO:0009579,GO:0009536,GO:0016020		membrane	hydrolase activity
ug4260	301			thylakoid,plastid,membrane	
ug4261	842	GO:0003676,GO:0000166,GO:0005622		intracellular	nucleic acid binding,nucleotide binding
ug4262	271				
ug4263	790	GO:0005623,GO:0005786,GO:0007275,GO:0005698,GO:0005488,GO:0005433	multicellular organismal	cell,cytoplasm	binding
ug4264	786				binding,protein binding
ug4265	698				
ug4266	433				
ug4267	138				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4268	113				
ug4269	156				
ug4270	199				
ug4271	226				
ug4272	540				
ug4273	548	GO:0016020,GO:0009536,GO:0009579,GO:00009		membrane,plastid,thylakoid	protein binding
ug4274	283				
ug4275	610	GO:0016740			transferase activity
ug4276	104				
ug4277	375				
ug4278	239				
ug4279	198	GO:0005886		plasma membrane	
ug4280	546				
ug4281	937	GO:0005488,GO:0003824,GO:0009058,GO:00009	biosynthetic process		binding,catalytic activity,transferase activity
ug4282	248				
ug4283	325				
ug4284	848				
ug4285	882				
ug4286	460				
ug4287	605	GO:0003677,GO:0005737,GO:0006810,GO:0009987,GO:0006259,GO:00009	transport,cellular process,DNA metabolic process	cytoplasm	DNA binding,RNA binding
ug4288	159				
ug4289	883	GO:0003674,GO:0005488,GO:0006810,GO:0006464,GO:0016020,GO:0009536,GO:0009579,GO:0009058,GO:0006810,GO:0016020,GO:0005215	transport,protein modification process,photosynthesis,generation of precursor metabolites and energy	membrane,plastid,thylakoid	molecular_function,binding
ug4290	379	GO:0006810,GO:0016020,GO:0005215	transport	membrane	transporter activity
ug4291	766	GO:0008152,GO:0016020,GO:0005634	metabolic process		transferase activity
ug4292	885	GO:0005634		nucleus	
ug4293	700	GO:0005488,GO:0003824			binding,nucleic acid binding
ug4294	734				
ug4295	225				
ug4296	391	GO:0009058,GO:0009987,GO:0003824,GO:0005488,GO:0009536	biosynthetic process,cellular process	plastid	catalytic activity,binding
ug4297	240	GO:0016740			transferase activity
ug4298	936	GO:0005737		cytoplasm	
ug4299	322				
ug4300	454				
ug4301	808	GO:0000166,GO:0005515,GO:0006810,GO:0009987,GO:0007165,GO:0005634,GO:001678	transport,cellular process,signal transduction	nucleus	nucleotide binding,protein binding,hydrolase activity
ug4302	575				
ug4303	344				
ug4304	390				
ug4305	368				
ug4306	838	GO:0016020,GO:0009536,GO:0009579,GO:00019538,GO:0009987,GO:0005515,GO:0000003,GO:0009791,GO:0009790,GO:0030234,GO:0000166,GO:00009	protein metabolic process,cellular process,reproduction,post-embryonic development,embryonic development	membrane,plastid,thylakoid	protein binding
ug4307	687	000003,GO:0009791,GO:0009790,GO:0030234,GO:0000166,GO:00009	protein metabolic process,cellular process,reproduction,post-embryonic development,embryonic development	plastid,thylakoid	protein binding,enzyme regulator activity,nucleotide binding
ug4308	742				
ug4309	577				
ug4310	425				
ug4311	891				
ug4312	527				
ug4313	404				
ug4314	351	GO:0005515			protein binding
ug4315	152				
ug4316	161				
ug4317	170				
ug4318	853				
ug4319	367				
ug4320	107				
ug4321	101				
ug4322	795	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug4323	751				
ug4324	745	GO:0016020,GO:0006139,GO:0019748,GO:0016787	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,secondary metabolic	membrane	hydrolase activity
ug4325	157				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4326	914	GO:0003824			catalytic activity
ug4327	177	GO:0016740,GO:0006259,GO:0009058,GO:0003723,GO:0009628,GO:0009058,GO:000987,GO:0016020,GO:0005739,GO:0005886,GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:0016020,GO:0005215	DNA metabolic process,biosynthetic process,response to abiotic process		transferase activity,RNA binding,binding
ug4328	102				
ug4329	710	GO:0009058,GO:000987,GO:0016020,GO:0005739,GO:0005886,GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:0016020,GO:0005215	biosynthetic process,cellular process	membrane,mitochondrion,plasma membrane,intracellular	
ug4330	208				
ug4331	254				
ug4332	582				
ug4333	248				
ug4334	419				
ug4335	312	GO:0016787			hydrolase activity
ug4336	409	GO:0005623		cell	
ug4337	703	GO:0003824			catalytic activity
ug4338	500				
ug4339	345				
ug4340	540				
ug4341	626	GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:0016020,GO:0005215	transport,biosynthetic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane	transporter activity
ug4342	743				
ug4343	282				
ug4344	874	GO:0003723,GO:0004518,GO:0009536,GO:0005975,GO:000987,GO:0016787,GO:0005576,GO:0005618,GO:0005777,GO:0005739,GO:0005515,GO:0016043,GO:0009987	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	plastid	RNA binding,nuclease activity
ug4345	230				
ug4346	212				
ug4347	819	GO:0005975,GO:000987,GO:0016787,GO:0005576,GO:0005618,GO:0005777,GO:0005739,GO:0005515,GO:0016043,GO:0009987	carbohydrate metabolic process,cellular process	extracellular region,cell wall	hydrolase activity,transferase activity
ug4348	173				
ug4349	297				
ug4350	116				
ug4351	222				
ug4352	778	GO:0005488,GO:0005318,GO:0005716,GO:0005759,GO:0005181,GO:0005333,GO:0005115,GO:0005334,GO:0005321			binding,protein binding
ug4353	318				
ug4354	716				
ug4355	759				
ug4356	181				
ug4357	333				
ug4358	115				
ug4359	334				
ug4360	321				
ug4361	412	GO:0005777,GO:0005739,GO:0005515,GO:0016043,GO:0009987	cellular component organization,cellular process	peroxisome,mitochondrion	protein binding
ug4362	252				
ug4363	122				
ug4364	336				
ug4365	595	GO:0016787,GO:0006950,GO:0006259	response to stress,DNA metabolic process		hydrolase activity
ug4366	424				
ug4367	552				
ug4368	441	GO:0005886		plasma membrane	
ug4369	730	GO:0016740,GO:0006950,GO:0009628,GO:0005794,GO:0009058,GO:0005975,GO:0009987,GO:0016020,GO:0006139,GO:0009058,GO:0006519,GO:000166,GO:0003824	response to stress,response to abiotic stimulus,biosynthetic process,carbohydrate metabolic process,cellular process	Golgi apparatus,membrane,endoplasmic reticulum	transferase activity
ug4370	498	GO:0006139,GO:0009058,GO:0006519,GO:000166,GO:0003824	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process,cellular amino acid and derivative metabolic process		nucleotide binding,catalytic activity
ug4371	698	GO:0006139,GO:0009058,GO:00019748,GO:0009536,GO:0016787	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,carbohydrate metabolic process,catabolic process,secondary metabolic process	plastid	hydrolase activity
ug4372	722	GO:0008289,GO:0005423		plasma membrane	lipid binding
ug4373	423				
ug4374	160				
ug4375	244				
ug4376	800	GO:0000166			nucleotide binding
ug4377	705	GO:0005975,GO:000987,GO:0006629,GO:0030246,GO:0016740	carbohydrate metabolic process,cellular process,lipid metabolic process		carbohydrate binding,transferase activity

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4378	358				
ug4379	795				
ug4380	676				
ug4381	594				
ug4382	559	GO:0007165,GO:0009719,GO:0016043,GO:0006412,GO:0005737,GO:0004872,GO:0007165,GO:0009719,GO:0009653,GO:0009908,GO:0009058,GO:0005975,GO:0016787	signal transduction,response to endogenous stimulus,cellular component organization,translation signal transduction,response to endogenous stimulus,anatomical structure morphogenesis,flower development,biosynthetic process,carbohydrate metabolic process	cytoplasm	protein binding
ug4383	610	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	receptor activity,hydrolase activity
ug4384	415				structural molecule activity
ug4385	234				
ug4386	759	GO:0005737,GO:000856,GO:0016043,GO:0009987,GO:0005623,GO:0005515,GO:000562GO:0005515,GO:000562	cellular component organization,cellular process	cytoplasm,cytoskeleton,cell,intracellular	protein binding
ug4387	776	GO:0006464,GO:0016009056,GO:0009987	protein metabolic process,catabolic process,cellular process	intracellular	protein binding
ug4388	803	GO:0006464,GO:001301,GO:0000166,GO:00005488,GO:0000166,GO:0008152,GO:0003824,GO:0003674	protein modification process	mitochondrion	kinase activity,nucleotide binding
ug4389	172				binding,nucleotide binding,catalytic activity,molecular_function
ug4390	390	GO:0005488,GO:0000166,GO:0008152,GO:0003824,GO:0003674	metabolic process		
ug4391	169				
ug4392	369				
ug4393	423				
ug4394	769	GO:0006464,GO:001538,GO:0009056,GO:0009987,GO:0003824,GO:0000166,GO:0016005488,GO:0000166,GO:0008152,GO:0003824,GO:0003674	protein modification process,protein metabolic process,catabolic process,cellular		catalytic activity
ug4395	316	GO:0006464,GO:001787,GO:0003677,GO:0005488,GO:0005515	protein modification process,protein metabolic process,catabolic process,cellular		nucleotide binding,hydrolase activity,DNA binding,protein
ug4396	356				
ug4397	440	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug4398	192				
ug4399	233				
ug4400	201				
ug4401	342				
ug4402	802				
ug4403	486				
ug4404	223				
ug4405	261				
ug4406	741	GO:0005515,GO:000810,GO:0009987,GO:0005488,GO:0005739	transport,cellular process	mitochondrion	protein binding,protein binding
ug4407	141				
ug4408	843	GO:0005622,GO:0000166,GO:0007165	signal transduction	intracellular	nucleotide binding
ug4409	557				
ug4410	314				
ug4411	387				
ug4412	142	GO:0005215,GO:0016020,GO:0005739,GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:0016787	transport,biosynthetic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane,mitochondrion	transporter activity,hydrolase activity
ug4413	497				
ug4414	607	GO:0016787			hydrolase activity
ug4415	648				
ug4416	166				
ug4417	452				
ug4418	413	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug4419	296	GO:0000003,GO:0009791,GO:0006464,GO:0016787,GO:0019538,GO:0009056,GO:0005634,GO:0006950,GO:000019725,GO:0003824,GO:0008152	reproduction,post-embryonic development,protein metabolic process,protein metabolic process,catabolic process,response to stress,response to abiotic cellular homeostasis,metabolic process	nucleus	hydrolase activity
ug4420	375				
ug4421	707	GO:0019725,GO:0003824,GO:0008152	cellular homeostasis,metabolic process		catalytic activity
ug4422	851	GO:0003676,GO:0000166			nucleic acid binding,nucleotide binding



Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4423	246				
ug4424	715	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug4425	271	GO:0016787,GO:0005215,GO:0005886,GO:0006810,GO:0000166,G	transport	plasma membrane,membrane	hydrolase activity,transporter activity,nucleotide binding
ug4426	570				
ug4427	104				
ug4428	147				
ug4429	520	GO:0005840,GO:0005198,GO:0006412,GO:0006350,GO:0008135,GO:0003677,GO:0030528,GO:0005515,G	translation	ribosome,mitochondrion	structural molecule activity
ug4430	727	GO:0005634,GO:0005480	transcription	nucleus	translation factor activity,nucleic acid binding,DNA binding,transcription regulator activity,protein
ug4431	545				
ug4432	860	GO:0005622,GO:0019538,GO:0009056,GO:0009987,GO:0005634,G	protein metabolic process,catabolic process,cellular process	intracellular,nucleus,cytosol	hydrolase activity
ug4433	424				
ug4434	445				
ug4435	606				
ug4436	484	GO:0009536		plastid	
ug4437	714				
ug4438	443	GO:0009536		plastid	
ug4439	331				
ug4440	146				
ug4441	332				
ug4442	697				
ug4443	843	GO:0009058,GO:000987,GO:0006629,GO:0003824,GO:0016740,G	biosynthetic process,cellular process,lipid metabolic process	membrane,endoplasmic reticulum,plasma membrane	catalytic activity,transferase activity
ug4444	840	GO:0005488			binding
ug4445	446	GO:0005730,GO:0006139,GO:0005634,GO:0005622,GO:0003723	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	nucleolus,nucleus,intracellular	RNA binding
ug4446	117				
ug4447	738				
ug4448	379				
ug4449	388				
ug4450	157				
ug4451	269				
ug4452	438				
ug4453	748	GO:0005739		mitochondrion	
ug4454	421				
ug4455	594	GO:0005773,GO:0005886,GO:0016787,GO:0005215,GO:0006810,G	transport	vacuole,plasma membrane,membrane	hydrolase activity,transporter activity,nucleotide binding
ug4456	673				
ug4457	483	GO:0005737,GO:0009628,GO:0009606,GO:0005515,GO:0005856,G	response to abiotic stimulus,tropism	cytoplasm,cytoskeleton,nucleus	protein binding
ug4458	164				
ug4459	831	GO:0016787,GO:0000166,GO:0005215			hydrolase activity,nucleotide binding,transporter activity
ug4460	698				
ug4461	337				
ug4462	638	GO:0005856,GO:0005515,GO:0016043,GO:0000159	cellular component organization,cellular process	cytoskeleton	protein binding
ug4463	159				
ug4464	420				
ug4465	360				
ug4466	652	GO:0003824,GO:0005488,GO:0005515,GO:0006950,GO:0008219,G	response to stress,cell death	plasma membrane	catalytic activity,activity,protein binding
ug4467	118				
ug4468	119				
ug4469	690				
ug4470	347	GO:0003824,GO:0008135,GO:0006810,GO:000987,GO:0005215,GO:0019725,GO:0016020	metabolic process		catalytic activity
ug4471	822	GO:0019538,GO:000987,GO:0003824,GO:0000159	transport,cellular process,cellular homeostasis	membrane	transporter activity
ug4472	507				
ug4473	171				
ug4474	726	GO:0005198,GO:0009058,GO:0009987,GO:0000159	biosynthetic process,cellular process		structural molecule activity,protein binding

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4475	698	GO:0008152,GO:0009987,GO:0016787	metabolic process,cellular process		hydrolase activity
ug4476	299				
ug4477	764				
ug4478	751				
ug4479	551	GO:0016301,GO:0006464,GO:0005488,GO:0	protein modification process		kinase activity, binding, nucleotide
ug4480	186				
ug4481	633				
ug4482	173				
ug4483	277				
ug4484	293	GO:0019538,GO:0009987,GO:0005515	protein metabolic process,cellular process		protein binding
ug4485	389				
ug4486	437	GO:0016740,GO:0008831	metabolic process		transferase activity
ug4487	831				
ug4488	615	GO:0009987,GO:0005829,GO:0003824	cellular process	cytosol	catalytic activity
ug4489	111				
ug4490	316				
ug4491	174				
ug4492	291				
ug4493	538				
ug4494	216	GO:0006259,GO:0003676,GO:0016787	DNA metabolic process		nucleic acid binding, hydrolase activity, transferase activity
ug4495	592	GO:0016740			
ug4496	608	GO:0005634,GO:0005305,GO:0005488,GO:0005708,GO:0005622		nucleus, cytosol, intracellular, intracellular	binding
ug4497	305				
ug4498	708				
ug4499	506	GO:0003824,GO:0008831	metabolic process		catalytic activity
ug4500	273	GO:0009987,GO:0006629,GO:0003824	cellular process, lipid metabolic process		catalytic activity
ug4501	210				
ug4502	396	GO:0016740,GO:0008831	metabolic process		transferase activity
ug4503	187				
ug4504	602				
ug4505	192				
ug4506	677				
ug4507	636	GO:0005794,GO:0009987,GO:0009058,GO:0005975,GO:0016740,GO:0	cellular process, biosynthetic process, carbohydrate metabolic process	Golgi apparatus, membrane	transferase activity
ug4508	108				
ug4509	318				
ug4510	250				
ug4511	274				
ug4512	257				
ug4513	680	GO:0019538,GO:0009056	protein metabolic process, catabolic process		
ug4514	357				
ug4515	665				
ug4516	267	GO:0030528,GO:0005198,GO:0005840,GO:0006412	translation	ribosome	transcription regulator activity, structural molecule activity
ug4517	148				
ug4518	242				
ug4519	305				
ug4520	159				
ug4521	555	GO:0006412,GO:0005515,GO:0000003,GO:0009653,GO:0016043,GO:0030154,GO:0009790,GO:0030528,GO:0045182,GO:0003700,GO:0004871,GO:0006350,	translation, reproduction, anatomical structure morphogenesis, cellular component organization, cell differentiation, embryonic development, transcription	cytoplasm, nucleus	protein binding, transcription regulator activity, translation regulator activity, transcription factor activity, signal transducer activity
ug4522	380				
ug4523	566				
ug4524	299				
ug4525	278				
ug4526	169				
ug4527	109				
ug4528	732	GO:0016740			transferase activity
ug4529	297				
ug4530	618				
ug4531	142				
ug4532	325				
ug4533	145				
ug4534	148				
ug4535	859	GO:0008152,GO:0003824,GO:0005488	metabolic process		catalytic activity, binding

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4536	482	GO:0016740,GO:0005654,GO:0006350,GO:0	transcription	nucleoplasm	transferase activity,nucleotide binding
ug4537	252				
ug4538	128				
ug4539	113				
ug4540	372				
ug4541	403				
ug4542	219				
ug4543	234				
ug4544	474	GO:0006350,GO:000908,GO:0005515,GO:0003700,GO:0007165,GO:0009719,GO:000563	transcription,flower development,signal transduction,response to endogenous stimulus	nucleus	protein binding,transcription factor activity
ug4545	275				
ug4546	247				
ug4547	347	GO:0005737,GO:0016		cytoplasm,membrane	
ug4548	716				
ug4549	112				
ug4550	293				
ug4551	444	GO:0016020,GO:0005215,GO:0006810,GO:0	transport,cellular process	membrane	transporter activity
ug4552	810				
ug4553	534	GO:0005488,GO:0003824,GO:0003674,GO:0016740			binding,catalytic activity,molecular_function,transferase activity
ug4554	789	GO:0005488,GO:0003824,GO:0005618,GO:0005737			binding,molecular_function
ug4555	755	GO:0016787,GO:0019538,GO:0009056,G	protein metabolic process,catabolic process	cell wall,cytoplasm,membrane	hydrolase activity
ug4556	631				
ug4557	113				
ug4558	334	GO:0016787,GO:0005975,GO:0005737	carbohydrate metabolic process	cytoplasm	hydrolase activity
ug4559	106				
ug4560	260				
ug4561	740	GO:0009536		plastid	
ug4562	831	GO:0005886		plasma membrane	
ug4563	913	GO:0016020		membrane	
ug4564	568	GO:0005840,GO:0005198,GO:0006412,GO:0	translation	ribosome	structural molecule activity,nucleotide binding
ug4565	106				
ug4566	301				
ug4567	461				
ug4568	554	GO:0005737,GO:0019538,GO:0009987,GO:0005886,GO:0005618,GO:0000166,GO:0005515,GO:0005215,GO:0009	protein metabolic process,cellular process	cytoplasm,plasma membrane,cell wall	nucleotide binding,protein binding
ug4569	907	GO:0006810,GO:0009536,GO:0016020	response to biotic stimulus,transport	plastid,membrane	transporter activity
ug4570	217				
ug4571	829	GO:0003700,GO:0005634,GO:0005739,GO:0	transcription	nucleus,mitochondrion	transcription factor activity
ug4572	212				
ug4573	411	GO:0016740,GO:0009058,GO:0005488	biosynthetic process		transferase activity,binding
ug4574	856				
ug4575	129				
ug4576	105				
ug4577	377	GO:0019538,GO:0009987,GO:0005829,GO:0	protein metabolic process,cellular process	cytosol	protein binding
ug4578	874	GO:0005623,GO:0006	response to stress	cell	
ug4579	161				
ug4580	514				
ug4581	552				
ug4582	175	GO:0003824,GO:0003674,GO:0006091,GO:0009056,GO:0016020,GO:0006464,GO:0016301,GO:0000166	generation of precursor metabolites and energy,catabolic process	membrane,mitochondrion	catalytic activity,molecular_function
ug4583	867		protein modification process		kinase activity,nucleotide binding
ug4584	658				
ug4585	161				
ug4586	756	GO:0003677,GO:0003700,GO:0006350	transcription		DNA binding,transcription factor activity
ug4587	122				
ug4588	105				
ug4589	807	GO:0005488,GO:0005618,GO:0016787		cell wall	binding,hydrolase activity
ug4590	259				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4591	444	GO:0005488,GO:0019538,GO:0009056,GO:009987,GO:0006464,GO:0007049,GO:0003824,GO:0005634,GO:000	protein metabolic process,catabolic process,cellular process,protein modification process,cell cycle	nucleus,intracellular	binding,catalytic activity
ug4592	812				
ug4593	285	GO:0003824			catalytic activity
ug4594	762	GO:0005488,GO:0005			binding,protein binding
ug4595	306				
ug4596	543				
ug4597	195				
ug4598	390				
ug4599	175				
ug4600	316				
ug4601	385				
ug4602	794	GO:0008152,GO:000987,GO:0016787	metabolic process,cellular process		hydrolase activity
ug4603	152				
ug4604	395				
ug4605	796				
ug4606	349	GO:0005840,GO:0007275,GO:0005198,GO:000	multicellular organismal development,translation	ribosome	structural molecule activity
ug4607	895	GO:0006950,GO:0003824,GO:0006139,GO:0005975,GO:0009056,GO:0019748,GO:0005488,GO:0006519,GO:0005829	response to stress,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,carbohydrate metabolic process,catabolic process,secondary metabolic process,cellular amino acid and	cytosol	catalytic activity,binding
ug4608	482				
ug4609	145				
ug4610	146				
ug4611	277				
ug4612	668				
ug4613	494	GO:0016740,GO:0009058,GO:0005975	biosynthetic process,carbohydrate metabolic process		transferase activity
ug4614	193	GO:0003677,GO:0006	transcription		DNA binding
ug4615	728	GO:0016740,GO:0009058,GO:0006519	biosynthetic process,cellular amino acid and derivative metabolic		transferase activity
ug4616	162				
ug4617	829	GO:0004872,GO:0006464,GO:0016301,GO:000	protein modification process		receptor activity,kinase activity,nucleotide binding
ug4618	825	GO:0005730,GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	nucleolus	
ug4619	496				
ug4620	550	GO:0005737		cytoplasm	
ug4621	120				
ug4622	912				
ug4623	919				
ug4624	136				
ug4625	467				
ug4626	231	GO:0005488,GO:0008152,GO:0003824,GO:000	metabolic process		binding,catalytic activity,molecular_function signal transducer activity
ug4627	841	GO:0007165,GO:0004	signal transduction		
ug4628	477				
ug4629	135				
ug4630	769	GO:0005773,GO:0005		vacuole	binding
ug4631	121				
ug4632	866	GO:0006950,GO:0009628	response to stress,response to abiotic stimulus		
ug4633	536				
ug4634	344	GO:0008150,GO:0006810,GO:0009991,GO:0007154,GO:0006950	biological_process,transport,response to extracellular stimulus,cell communication,response to stress		
ug4635	873	GO:0016787			hydrolase activity
ug4636	608				
ug4637	781	GO:0005515,GO:0005215,GO:0006810,GO:0009987,GO:0016020,GO:0003677,GO:0005	transport,cellular process	membrane,cytoplasm	protein binding,transporter activity
ug4638	614	515,GO:0003700,GO:0005634,GO:0006350	transcription	nucleus	DNA binding,protein binding,transcription factor activity
ug4639	195				
ug4640	607	GO:0005622,GO:0003		intracellular	DNA binding
ug4641	642				
ug4642	521	GO:0005198,GO:0005840,GO:0006412,GO:000	translation	ribosome,mitochondrion	structural molecule activity
ug4643	254				
ug4644	214				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4645	908	GO:0009987,GO:0005829,GO:0005515,GO:0006950,GO:0005488,GO:0003824,GO:000597	cellular process,response to stress,carbohydrate metabolic process	cytosol	protein binding,protein binding,catalytic activity
ug4646	836	GO:0009536		plastid	
ug4647	778	GO:0005198,GO:0005840,GO:0006412	translation	ribosome	structural molecule activity
ug4648	405	GO:0016020		membrane	
ug4649	785	GO:0009536		plastid	
ug4650	520	GO:0005488,GO:0008152,GO:0009987,GO:0	metabolic process,cellular process		binding,catalytic activity
ug4651	263	GO:0005737		cytoplasm	
ug4652	763				
ug4653	572	GO:0016020		membrane	
ug4654	669				
ug4655	331				
ug4656	465	GO:0016020		membrane	
ug4657	367				
ug4658	664	GO:0006950,GO:0009628	response to stress,response to abiotic stimulus		
ug4659	609				
ug4660	572				
ug4661	147				
ug4662	480				
ug4663	209				
ug4664	102				
ug4665	594				
ug4666	866				
ug4667	806	GO:0005737,GO:0009056,GO:0009987,GO:0016787,GO:0005488	catabolic process,cellular process	cytoplasm	hydrolase activity,protein binding
ug4668	318				
ug4669	311				
ug4670	516				
ug4671	434	GO:0016020,GO:0006810,GO:0005215,GO:0005198,GO:0005618,GO:0000003,GO:0	transport	membrane,plasma membrane	transporter activity
ug4672	603	GO:009791,GO:0009790,GO:0005840,GO:0005829,GO:0009536,GO:0016020,GO:0006412,GO:0	reproduction,post-embryonic development,embryonic development,translation	cell wall,ribosome,cytosol,plastid,membrane	structural molecule activity,RNA binding
ug4673	830	GO:0005634,GO:0006259,GO:0009058,GO:0005773,GO:0006950,GO:0009628,GO:0005622,GO:0008150,GO:0	DNA metabolic process,biosynthetic process	nucleus	
ug4674	889	GO:0005886,GO:0019538,GO:0009056,GO:0009987,GO:0005634,GO:0005829,GO:0005576,	response to stress,response to abiotic stimulus,biological_process,protein metabolic process,catabolic process,cellular process	vacuole,intracellular,plasma membrane,nucleus,cytosol,extracellular region	hydrolase activity
ug4675	567				
ug4676	301	GO:0005515			protein binding
ug4677	566				
ug4678	731	GO:0005488,GO:0016740,GO:0006519,GO:0009058,GO:0005739	cellular amino acid and derivative metabolic process,biosynthetic process	mitochondrion	binding,transferase activity
ug4679	271	GO:0016301			kinase activity
ug4680	550	GO:0016043,GO:0009987,GO:0005856	cellular component organization,cellular process	cytoskeleton	
ug4681	378	GO:0005488,GO:0005886,GO:0005773,GO:0		plasma membrane,vacuole	binding,molecular_function
ug4682	580				
ug4683	420	GO:0005739		mitochondrion	
ug4684	659				
ug4685	787	GO:0006464,GO:0016301,GO:0000166	protein modification process		kinase activity,nucleotide binding
ug4686	464	GO:0005623,GO:0019538,GO:0009056,GO:00030528,GO:0005198,GO:0005840,GO:0006412	protein metabolic process,catabolic process	cell	hydrolase activity
ug4687	768	GO:0005739	translation	ribosome	transcription regulator activity,structural molecule activity
ug4688	554				
ug4689	238				
ug4690	187				
ug4691	173				
ug4692	368				
ug4693	746	GO:0005618		cell wall	
ug4694	381				
ug4695	100				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4696	699	GO:0009987,GO:0005515,GO:0006810	cellular process,transport		protein binding
ug4697	374	GO:0003677			DNA binding
ug4698	208				
ug4699	308				
ug4700	238	GO:0005886		plasma membrane	
ug4701	201				
ug4702	559				
ug4703	208				
ug4704	721				
ug4705	579	GO:0016787,GO:0016043,GO:0009987,GO:0005618,GO:0005739	cellular component organization,cellular process	cell wall,mitochondrion	hydrolase activity
ug4706	345	GO:0004518,GO:0005622,GO:0005488		intracellular	nuclease activity,binding
ug4707	775	GO:0005488,GO:0016787,GO:0009058,GO:0009987,GO:0009536	biosynthetic process,cellular process	plastid	binding,hydrolase activity
ug4708	133				
ug4709	136				
ug4710	812	GO:0003723,GO:0016787,GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		RNA binding,hydrolase activity
ug4711	412				
ug4712	789	GO:0005488,GO:0005			binding,protein binding
ug4713	274				
ug4714	209				
ug4715	855	GO:0016301,GO:0005730,GO:0005737,GO:0		nucleolus,cytoplasm	kinase activity,protein binding
ug4716	457				
ug4717	624				
ug4718	751	GO:0009536		plastid	
ug4719	118				
ug4720	710				
ug4721	226				
ug4722	115				
ug4723	301	GO:0005515,GO:0003700,GO:0007165,GO:0009719,GO:0005634,GO:0016787,GO:0005737,GO:0003723,GO:0	signal transduction,response to endogenous stimulus,transcription	nucleus	protein binding,transcription factor activity
ug4724	921	GO:0005488,GO:0006810,GO:0009987,GO:0016043,GO:0005515,GO:000	transport,cellular process,cellular component organization	cytoplasm,plastid	hydrolase activity,RNA binding,binding,protein binding,nucleotide binding
ug4725	310				
ug4726	369				
ug4727	781	GO:0005488			binding
ug4728	560	GO:0008289			lipid binding
ug4729	207				
ug4730	651	GO:0005488,GO:0006350,GO:0009908,GO:0006464,GO:0030528,GO:0005515,GO:000563	transcription,flower development,protein modification process	nucleus	binding,transcription regulator activity,protein binding
ug4731	719				
ug4732	605				
ug4733	867				
ug4734	102				
ug4735	643	GO:0003824			catalytic activity
ug4736	605				
ug4737	289				
ug4738	191				
ug4739	621				
ug4740	115				
ug4741	825	GO:0006350,GO:0005575,GO:0016043,GO:0007275,GO:0005886,GO:0005515,GO:0030154,GO:0009987,GO:0005622,GO:0005737,GO:	transcription,cellular component organization,multicellular organismal development,cell differentiation,cellular process,anatomical structure morphogenesis,embryonic	cellular_component,plasma membrane,intracellular,cytoplasm	protein binding
ug4742	157				
ug4743	611	GO:0005975	carbohydrate metabolic process		
ug4744	372				
ug4745	443	GO:0005737,GO:0005488,GO:0016740		cytoplasm	binding,transferase activity
ug4746	817				
ug4747	575	GO:0005737,GO:0016301,GO:0005488,GO:0005975,GO:0006091,GO:0009056	carbohydrate metabolic process,generation of precursor metabolites and energy,catabolic process	cytoplasm	kinase activity,binding

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4748	708	GO:0005739,GO:0005975,GO:0009987,GO:0009536,GO:0016301	carbohydrate metabolic process,cellular process	mitochondrion,plastid	kinase activity
ug4749	195	GO:0005737,GO:0003824,GO:0000166,GO:0006139,GO:0006412,GO:0006519	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,translation,cellular amino acid and derivative metabolic	cytoplasm	catalytic activity,nucleotide binding
ug4750	291				
ug4751	153				
ug4752	366				
ug4753	118				
ug4754	591	GO:0008150,GO:0003677,GO:0000166,GO:0016787,GO:0040029,GO:0016043,GO:000635	biological_process,regulation of gene expression, epigenetic,cellular component organization,transcription		DNA binding,nucleotide binding,hydrolase activity
ug4755	121				
ug4756	130				
ug4757	665				
ug4758	714	GO:0005623,GO:0016020,GO:0005737		cell,membrane,cytoplasm	
ug4759	729	GO:0005783		endoplasmic reticulum	
ug4760	346	GO:0005515,GO:0007275,GO:0006464,GO:0019538,GO:0009056,GO:0009987,GO:0003824,GO:0005634,GO:000	multicellular organismal development,protein modification process,protein metabolic process,catabolic process,cellular process	nucleus	protein binding,catalytic activity,binding
ug4761	684				
ug4762	302				
ug4763	327				
ug4764	293				
ug4765	645				
ug4766	751	GO:0008135,GO:0000166,GO:0009536,GO:0016787		plastid	translation factor activity, nucleic acid binding,nucleotide transcription regulator
ug4767	787	GO:0030528			
ug4768	274				
ug4769	704				
ug4770	389	GO:0009536		plastid	
ug4771	307				
ug4772	535	GO:0009536		plastid	
ug4773	110				
ug4774	464	GO:0003824,GO:0019538,GO:0009056,GO:0009987,GO:0006464,GO:0009536,GO:0016	protein metabolic process,catabolic process,cellular process,protein modification process	plastid,membrane	catalytic activity,nucleotide binding
ug4775	579	GO:0009536,GO:0016			
ug4776	556				
ug4777	799	GO:0005198,GO:0006	transport		structural molecule activity
ug4778	684				
ug4779	456	GO:0016301,GO:0000166,GO:0016740,GO:0003824,GO:0006139,GO:0006464,GO:0000166,GO:0016301,GO:000	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process protein modification process		kinase activity,nucleotide binding,transferase activity,catalytic activity nucleotide binding,kinase activity,protein binding
ug4780	258	GO:0009058,GO:0009987,GO:0006629,GO:0009605,GO:0006950,GO:0006519,GO:0019748,GO:0009628,GO:0016020,GO:0016740	biosynthetic process,cellular process,lipid metabolic process,response to external stimulus,response to stress,cellular amino acid and derivative metabolic process,secondary metabolic process,response to	membrane	transferase activity
ug4781	389	GO:0016020,GO:0005215,GO:0006810	transport	membrane	transporter activity
ug4782	692				
ug4783	506				
ug4784	464	GO:0016740,GO:0003677,GO:0005488,GO:0	DNA metabolic process		transferase activity,DNA binding,binding
ug4785	322				
ug4786	648	GO:0019538,GO:0009987,GO:0005829,GO:0005198,GO:0009	protein metabolic process,cellular process	cytosol	protein binding
ug4787	386	987,GO:0005840,GO:0005829,GO:0006412	cellular process,translation	ribosome,cytosol	structural molecule activity
ug4788	401				
ug4789	249				
ug4790	261	GO:0005488			binding
ug4791	197				
ug4792	262				
ug4793	764	GO:0005215,GO:0019725,GO:0016020,GO:0009536,GO:0005515,GO:0006810,GO:000998	cellular homeostasis,transport,cellular process	membrane,plastid	transporter activity,protein binding

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4794	771	GO:0016020,GO:0009536,GO:0009579		membrane,plastid,thylakoid	
ug4795	414				
ug4796	168				
ug4797	591	GO:0016020,GO:0005737,GO:0003824,GO:00016787	lipid metabolic process	membrane,cytoplasm	catalytic activity
ug4798	538	GO:0016787			hydrolase activity
ug4799	118				
ug4800	570				
ug4801	132				
ug4802	483				
ug4803	466				
ug4804	202				
ug4805	565	GO:0005622,GO:0009605,GO:0007165,GO:0009628,GO:0009791,GO:0003677,GO:0005515,GO:0006350,GO:000392	response to external stimulus,signal transduction,response to abiotic stimulus,post-embryonic development,transcription	intracellular,nucleus	DNA binding,protein binding
ug4806	392				
ug4807	719	GO:0005488,GO:0009536,GO:0003824,GO:000154	metabolic process	plastid	binding,catalytic activity
ug4808	154				
ug4809	824	GO:0006464,GO:0005488,GO:0000166,GO:000405	protein modification process		binding,nucleotide binding,kinase activity
ug4810	405	GO:0005488			binding
ug4811	494				
ug4812	245	GO:0003677,GO:000515,GO:0005634,GO:0005488,GO:0006350	transcription	nucleus	DNA binding,protein binding,kinase activity
ug4813	103				
ug4814	433				
ug4815	902	GO:0003677,GO:0006350,GO:0005634	transcription	nucleus	DNA binding
ug4816	690	GO:0005623,GO:000629,GO:0016787	lipid metabolic process	cell	hydrolase activity
ug4817	858	GO:0016020,GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:0005773,GO:0016787,GO:0005215,GO:0006464,GO:0000166,GO:0016301	transport,biosynthetic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane,vacuole,plasma membrane	hydrolase activity,transporter activity
ug4818	937	GO:0006464,GO:0000166,GO:0016301	protein modification process		nucleotide binding,kinase activity
ug4819	894	GO:0016740			transferase activity
ug4820	343				
ug4821	933				
ug4822	894	GO:0005634,GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	nucleus	
ug4823	921				
ug4824	304				
ug4825	105				
ug4826	387				
ug4827	427	GO:0006259,GO:0009536,GO:0003677,GO:00016787,GO:0005622,GO:000392	DNA metabolic process,biosynthetic process	intracellular	DNA binding,hydrolase activity,nucleotide binding
ug4828	392				
ug4829	422				
ug4830	818	GO:0008150,GO:0003839	biological_process		transcription factor activity
ug4831	839	GO:0003723			RNA binding
ug4832	169				
ug4833	242				
ug4834	698	GO:0016020,GO:0009579,GO:0009536		membrane,thylakoid,plastid	
ug4835	491				
ug4836	730	GO:0003824,GO:0006139,GO:0006412,GO:0006519,GO:0000166	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,translation,cellular amino acid and derivative metabolic		catalytic activity,nucleotide binding
ug4837	242				
ug4838	680				
ug4839	146				
ug4840	333				
ug4841	247				
ug4842	690				
ug4843	119				
ug4844	132				
ug4845	203				
ug4846	436				
ug4847	112				
ug4848	765				



Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4849	794	GO:0005488,GO:0008152,GO:0003824,GO:0	metabolic process		binding,catalytic activity,molecular_function
ug4850	666				
ug4851	563				
ug4852	824	GO:0005739,GO:0016043,GO:0009987,GO:0	cellular component organization,cellular process	mitochondrion,plastid	
ug4853	333				
ug4854	408				
ug4855	431				
ug4856	555	GO:0003824,GO:0009536,GO:0008150,GO:005618,GO:0009058,GO:0006519,GO:0005488,GO:0005576,GO:00016740,GO:0009058,GO:0009987,GO:0006629,GO:0019748,GO:0	biological_process,biosynthetic process,cellular amino acid and derivative metabolic process	plastid,cell wall,extracellular region,mitochondrion	catalytic activity,binding
ug4857	892	GO:0016740,GO:0009058,GO:0009987,GO:0006629,GO:0019748,GO:0	biosynthetic process,cellular process,lipid metabolic process,secondary metabolic	plastid	transferase activity
ug4858	752				
ug4859	224				
ug4860	194				
ug4861	851	GO:0005515			protein binding
ug4862	617	GO:0016740,GO:0008150,GO:0016020,GO:0005622,GO:0009058,GO:0009987,GO:0000003,GO:0009791,GO:0009790,GO:0009536,GO:000	metabolic process biosynthetic process,cellular process,reproduction,post-embryonic development,embryonic development	membrane,intracellular,plastid,mitochondrion	transferase activity
ug4864	281				
ug4865	622				
ug4866	634				
ug4867	887	GO:0005618,GO:0008152,GO:0003824,GO:0	metabolic process	cell wall,plastid	catalytic activity
ug4868	334				
ug4869	610				
ug4870	165				
ug4871	555				
ug4872	494				
ug4873	208	GO:0009536		plastid	
ug4874	155				
ug4875	151				
ug4876	743	GO:0003677,GO:0006	transcription		DNA binding
ug4877	902				
ug4878	654				
ug4879	181				
ug4880	482				
ug4881	122				
ug4882	106				
ug4883	333				
ug4884	723	GO:0016020,GO:0005739,GO:0009536		membrane,mitochondrion,plastid	
ug4885	411				
ug4886	888	GO:0003824,GO:0005975,GO:0006091,GO:0009056,GO:0009536	carbohydrate metabolic process,generation of precursor metabolites and energy,catabolic process	plastid	catalytic activity
ug4887	725	GO:0000166,GO:0016787			nucleotide binding,hydrolase activity
ug4888	435	GO:0016787,GO:0005		peroxisome	hydrolase activity
ug4889	360				
ug4890	116				
ug4891	434				
ug4892	822				
ug4893	135				
ug4894	835	GO:0016740,GO:0006519,GO:0009536	cellular amino acid and derivative metabolic process	plastid	transferase activity
ug4895	134				
ug4896	779				
ug4897	272				
ug4898	288				
ug4899	155				
ug4900	814				
ug4901	143				
ug4902	448	GO:0005739,GO:0006	transport	mitochondrion	
ug4903	677	GO:0016020,GO:0005215,GO:0009536,GO:0	transport	membrane,plastid	transporter activity
ug4904	578				
ug4905	234				
ug4906	270				
ug4907	726	GO:0009987	cellular process		
ug4908	779				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4909	684				
ug4910	346				
ug4911	305				
ug4912	282				
ug4913	499	GO:0006259,GO:0003676,GO:0003824	DNA metabolic process		nucleic acid binding,catalytic activity
ug4914	825	GO:0003824,GO:0000166			catalytic activity,nucleotide binding
ug4915	498	GO:0006139,GO:0016740	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		transferase activity
ug4916	394	GO:0019538,GO:000987,GO:0005515,GO:000166,GO:0009536	protein metabolic process,cellular process	plastid	protein binding,nucleotide binding
ug4917	731	GO:0005737,GO:0016125		cytoplasm	hydrolase activity
ug4918	125				
ug4919	315				
ug4920	424	GO:0016020,GO:0007GO:0006259,GO:0009058,GO:0000166,GO:0009536,GO:0003824,GO:0009056,GO:0006519,GO:0016740,GO:0005737,GO:0005739	signal transduction DNA metabolic process,biosynthetic process,response to stress catabolic process,cellular amino acid and derivative metabolic process	membrane	
ug4921	682	GO:0009056,GO:0006519,GO:0016740,GO:0005737,GO:0005739		plastid	nucleotide binding,catalytic activity
ug4922	700	GO:0016787,GO:0005975,GO:0005773,GO:0003723,GO:0005488,GO:0006259,GO:0009058,GO:0005739,GO:0016043,GO:0009987,GO:0016740,GO:0003677,GO:0019538,GO:0009056,GO:0005622,GO:0016787,GO:0003473	carbohydrate metabolic process	cytoplasm,mitochondrion	transferase activity
ug4923	559			vacuole	hydrolase activity
ug4924	473			mitochondrion,intracellular,nucleus	RNA binding,binding,transferase activity,DNA binding,hydrolase activity,chromatin binding
ug4925	485				
ug4926	170				
ug4927	845	GO:0005515			protein binding
ug4928	207				
ug4929	809	GO:0016043,GO:0009987,GO:0005515,GO:0009653,GO:0016049	cellular component organization,cellular process,anatomical structure		protein binding
ug4930	185				
ug4931	129				
ug4932	775				
ug4933	405				
ug4934	443				
ug4935	261				
ug4936	179				
ug4937	632				
ug4938	857	GO:0003674,GO:0019725,GO:0008152,GO:0009536,GO:0003824	cellular homeostasis,metabolic process	plastid	molecular_function,catalytic activity
ug4939	188				
ug4940	421	GO:0005488,GO:0008135,GO:0000166			binding,translation factor activity, nucleic acid binding,nucleotide binding
ug4941	571	GO:0005515,GO:0005215,GO:0005886,GO:0006810,GO:0009987,GO:0009536	transport,cellular process	plasma membrane,mitochondrion	protein binding,transporter activity
ug4942	335	GO:0009536		plastid	
ug4943	434	GO:0005737,GO:0005488,GO:0005975,GO:0009987,GO:0009056,GO:0006259	carbohydrate metabolic process,cellular process,catabolic process	cytoplasm	binding,catalytic activity
ug4944	211				
ug4945	714	GO:0016020,GO:0005739,GO:0005488,GO:0006810,GO:0005215	transport	membrane,mitochondrion	binding,transporter activity
ug4946	673	GO:0016020		membrane	
ug4947	734	GO:0004872,GO:0006464,GO:0005737,GO:0005886,GO:0005515,GO:0000166,GO:0016301,GO:0007165,GO:000438	protein modification process,signal transduction	cytoplasm,plasma membrane,mitochondrion	receptor activity,protein binding,nucleotide binding,kinase activity
ug4948	438				
ug4949	655	GO:0016020,GO:0009579,GO:0009536,GO:0005515,GO:0006810,GO:0009987,GO:0005737,GO:0016020,GO:0009653,GO:000979	photosynthesis transport,cellular process,anatomical structure morphogenesis,post-embryonic development	membrane,thylakoid,plastid	
ug4950	541			cytoplasm,membrane	protein binding
ug4951	443				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug4952	916	GO:0006139,GO:0006412,GO:0006519,GO:0005739,GO:0000003,GO:0009791,GO:0009790,GO:0001666,GO:0003824,GO:0009536	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,translation,cellular amino acid and derivative metabolic process,reproduction,post-embryonic development,embryonic	mitochondrion,plastid	nucleotide binding,catalytic activity
ug4953	108				
ug4954	652	GO:0005623,GO:0016787,GO:0006464,GO:0006350,GO:000908,GO:0003700,GO:0005634,GO:0005515	protein modification process	cell	hydrolase activity,binding
ug4955	218				
ug4956	384				
ug4957	945				
ug4958	759				
ug4959	457				
ug4960	461	GO:0016740,GO:0009058,GO:0006519,GO:0003824,GO:0009536	biosynthetic process,cellular amino acid and derivative metabolic process	plastid	transferase activity,catalytic activity
ug4961	215				
ug4962	106				
ug4963	931	GO:0005975,GO:0009987,GO:0008152,GO:0003824,GO:0000166	carbohydrate metabolic process,cellular process,metabolic process		catalytic activity,nucleotide binding
ug4964	126				
ug4965	370	GO:0006091,GO:001979,GO:0016020,GO:0009579,GO:0005488,GO:0006464,GO:000953	generation of precursor metabolites and energy,photosynthesis,protein modification process	membrane,thylakoid,plastid	binding
ug4966	132				
ug4967	205				
ug4968	773	GO:0005488,GO:0005515,GO:0016020		membrane	binding,protein binding
ug4969	325				
ug4970	110				
ug4971	897				
ug4972	255				
ug4973	186				
ug4974	252				
ug4975	389	GO:0016740,GO:0009058,GO:0009987,GO:0006629,GO:0009991,GO:0007154,GO:0006950,GO:0016787,GO:0003550,GO:0005634	biosynthetic process,cellular process,lipid metabolic process,response to extracellular stimulus,cell communication,response to stress	plastid	transferase activity,hydrolase activity
ug4976	789	GO:0003677,GO:0006350,GO:0005634	transcription	nucleus	DNA binding
ug4977	754	GO:0005488,GO:001979	cellular homeostasis		binding
ug4978	177				
ug4979	225				
ug4980	177				
ug4981	142				
ug4982	252				
ug4983	299				
ug4984	442				
ug4985	292				
ug4986	423				
ug4987	163	GO:0019538,GO:0009987,GO:0005737,GO:0005515,GO:0000166	protein metabolic process,cellular process	cytoplasm	protein binding,nucleotide binding
ug4988	422				
ug4989	160				
ug4990	126				
ug4991	279				
ug4992	211				
ug4993	604				
ug4994	154				
ug4995	427	GO:0005886,GO:0006320	response to stress	plasma membrane	
ug4996	320				
ug4997	694	GO:0005515,GO:0007049,GO:0016043,GO:0009987,GO:0005856,GO:0005737,GO:000563	cell cycle,cellular component organization,cellular process	cytoskeleton,cytoplasm,nucleus	protein binding
ug4998	423	GO:0000166,GO:0005737,GO:0003824,GO:000555	metabolic process	cytoplasm	nucleotide binding,catalytic activity
ug4999	555				
ug5000	816				
ug5001	141				
ug5002	827	GO:0019538,GO:0009987,GO:0003824,GO:0006464	protein metabolic process,catabolic process,cellular process,protein modification process		catalytic activity

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug5003	146				
ug5004	127				
		GO:0003774,GO:0005856,GO:0016043,GO:007049,GO:0009653,G	cellular component organization,cell cycle,anatomical structure morphogenesis,flower		motor activity,nucleotide binding,protein
ug5005	437	O:0009908,GO:0000166,GO:0007165,GO:0009719,GO:0009987,GO:0005515,GO:0003700,	development,signal transduction,response to endogenous stimulus,cellular process	cytoskeleton,cytoplasm,nucleus	binding,transcription factor activity
ug5006	631				
ug5007	849				
ug5008	832	GO:0005488,GO:0005		plasma membrane	binding
ug5009	183				
ug5010	275				
ug5011	140				
ug5012	192				
ug5013	306				
ug5014	573				
ug5015	286				
ug5016	212				
ug5017	187				
ug5018	256				
ug5019	249				
ug5020	731	GO:0016020,GO:0005737,GO:0009987,GO:0	cellular process,transport	membrane,cytoplasm	
ug5021	359				
ug5022	357	GO:0000166			nucleotide binding
ug5023	217				
ug5024	615				
ug5025	106				
ug5026	569	GO:0005886,GO:0005		plasma membrane	binding
ug5027	438				
ug5028	104				
		GO:0005773,GO:0016787,GO:0009056,GO:0006629,GO:0009987,G	catabolic process,lipid metabolic process,cellular process	vacuole	hydrolase activity,binding
ug5029	737				
ug5030	334				
ug5031	374				
ug5032	223				
		GO:0016740,GO:0009058,GO:0009987,GO:0006629,GO:0005886	biosynthetic process,cellular process,lipid metabolic process	plasma membrane	transferase activity
ug5033	804				
ug5034	566				
ug5035	510				
ug5036	869				
ug5037	146				
ug5038	158				
		GO:0003824,GO:0005488,GO:0005618		cell wall	catalytic activity,binding
ug5039	779				
ug5040	693				
ug5041	813				
ug5042	916				
ug5043	909	GO:0000166,GO:0003			nucleotide binding,RNA
ug5044	775				
ug5045	671	GO:0005623,GO:0009	response to biotic stimulus	cell	
ug5046	347				
ug5047	278				
ug5048	876				
ug5049	366				
ug5050	206				
ug5051	365				
ug5052	612				
ug5053	654				
		GO:0005737,GO:0007165,GO:0009719,GO:0	signal transduction,response to endogenous stimulus	cytoplasm,nucleus	
ug5054	889				
ug5055	681	GO:0005739		mitochondrion	
		GO:0005623,GO:0005488,GO:0008152,GO:0003824,GO:0003674,G	metabolic process	cell	binding,catalytic activity,molecular_function,oxygen binding
ug5056	249				
ug5057	716				
ug5058	623				
		GO:0006810,GO:0000166,GO:0007165	transport,signal transduction		nucleotide binding
ug5059	378				
		GO:0006139,GO:0009058,GO:0016301,GO:0000166,GO:0005739	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,biosynthetic process	mitochondrion	kinase activity,nucleotide binding
ug5060	770				
		GO:0005488,GO:0003824,GO:0006810,GO:0008152,GO:0016020,G	transport,metabolic process	membrane,plastid,thylakoid	binding,catalytic activity
ug5061	891				
		O:0009536,GO:000957			

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug5062	576				
ug5063	412				
ug5064	223				
ug5065	472				
ug5066	197	GO:0005215,GO:0006	transport		transporter activity
ug5067	141				
ug5068	206				
ug5069	166				
ug5070	465	GO:0005856,GO:0003774,GO:0009987	cellular process	cytoskeleton	motor activity
ug5071	811	GO:0016020,GO:0005739,GO:0005488,GO:0006810,GO:0005215	transport	membrane,mitochondrion	binding,transporter activity
ug5072	458				
ug5073	831	GO:0005618,GO:0006950,GO:0009628,GO:0005886,GO:0016020,GO:0005783,GO:0009058,GO:0006464,GO:000	response to stress,response to abiotic stimulus,biosynthetic process,protein modification process,carbohydrate metabolic process	cell wall,plasma membrane,membrane,endoplasmic reticulum	transferase activity
ug5074	433				
ug5075	894	GO:0016020,GO:0005622,GO:0005215,GO:0005739,GO:0006810,GO:0009058,GO:0006091,GO:0006139,GO:001	transport,biosynthetic process,generation of precursor metabolites and energy,nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	membrane,intracellular,mitochondrion	transporter activity,hydrolase activity
ug5076	864				
ug5077	697	GO:0003676,GO:0016		membrane	nucleic acid binding
ug5078	726				
ug5079	857				
ug5080	259				
ug5081	816	GO:0019538,GO:0009987,GO:0005515	protein metabolic process,cellular process		protein binding
ug5082	672	GO:0003723,GO:0006139,GO:0016740	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		RNA binding,transferase activity
ug5083	133				
ug5084	833				
ug5085	114				
ug5086	625	GO:0005488,GO:0005		intracellular	binding
ug5087	527				
ug5088	581				
ug5089	401	GO:0005840,GO:0005198,GO:0009987,GO:0009536,GO:0006412,GO	cellular process,translation	ribosome,plastid	structural molecule activity,RNA binding
ug5090	104				
ug5091	225				
ug5092	658				
ug5093	615	GO:0016020,GO:0009058,GO:0006629,GO:0	biosynthetic process,lipid metabolic process	membrane	transferase activity
ug5094	582				
ug5095	716	GO:0016020,GO:0005215,GO:0006810,GO:0009987,GO:0009835	transport,cellular process,ripening	membrane	transporter activity
ug5096	107				
ug5097	916				
ug5098	399				
ug5099	133				
ug5100	454				
ug5101	466	GO:0016740,GO:0005515,GO:0009058,GO:0005975,GO:0009987,GO:0016020,GO:000548	biosynthetic process,carbohydrate metabolic process,cellular process	membrane	transferase activity,protein binding,binding
ug5102	254				
ug5103	513				
ug5104	596				
ug5105	738	GO:0016020		membrane	
ug5106	524				
ug5107	380				
ug5108	105				
ug5109	218				
ug5110	150				
ug5111	110				
ug5112	819	GO:0005739		mitochondrion	
ug5113	928	GO:0008152,GO:0019538,GO:0003824	metabolic process,protein metabolic process		catalytic activity
ug5114	830				
ug5115	451				
ug5116	134				
ug5117	351				
ug5118	898				
ug5119	456				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug5120	774	GO:0009536		plastid	
ug5121	697	GO:0019538,GO:000987,GO:0005829,GO:0	protein metabolic process,cellular process	cytosol	protein binding
ug5122	578	GO:0005488			binding
ug5123	226				
ug5124	194	GO:0016301,GO:0030246			kinase activity,carbohydrate binding
ug5125	784				
ug5126	268				
ug5127	689	GO:0005615		extracellular space	
ug5128	690				
ug5129	312				
ug5130	417				
ug5131	405	GO:0006464,GO:0000166,GO:0016301,GO:0016787,GO:0005	protein modification process		nucleotide binding,kinase activity
ug5132	682	618,GO:0005840,GO:0005975,GO:0005488,G	carbohydrate metabolic process	cell wall,ribosome,cytoplasm	hydrolase activity,binding
ug5133	597				
ug5134	223				
ug5135	894	GO:0005488,GO:0008152,GO:0003824,GO:0006950,GO:0009987,GO:0003674,GO:0019	metabolic process,response to stress,cellular process	plastid	binding,catalytic activity
ug5136	912	725,GO:0003824,GO:0016020,GO:0009536,GO:0009579,GO:000573	cellular homeostasis	membrane,plastid,thylakoid,mitochondrion	molecular_function,catalytic activity
ug5137	329				
ug5138	846	GO:0005515			protein binding
ug5139	877				
ug5140	611	GO:0005622,GO:0019538,GO:0009056,GO:0009987,GO:0000003,GO:0009791,GO:0009790,GO:0005488,GO:000	protein metabolic process,catabolic process,cellular process,reproduction,post-embryonic development,embryonic development	intracellular,cytosol	binding
ug5141	393				
ug5142	258				
ug5143	277				
ug5144	248				
ug5145	793	GO:0016020		membrane	
ug5146	210				
ug5147	271				
ug5148	147				
ug5149	142				
ug5150	589				
ug5151	171				
ug5152	166				
ug5153	477				
ug5154	154				
ug5155	409	GO:0005623		cell	
ug5156	713				
ug5157	143				
ug5158	419				
ug5159	371				
ug5160	209				
ug5161	371				
ug5162	531				
ug5163	420				
ug5164	305	GO:0005576,GO:0007267,GO:0004871	cell-cell signaling	extracellular region	signal transducer activity
ug5165	134				
ug5166	375				
ug5167	900	GO:0008152,GO:0016	metabolic process		hydrolase activity
ug5168	413				
ug5169	101				
ug5170	362				
ug5171	391				
ug5172	267				
ug5173	207				
ug5174	628	GO:0009536,GO:0003		plastid	catalytic activity
ug5175	396				
ug5176	101				
ug5177	411				
ug5178	144				
ug5179	820				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug5180	913	GO:0006950,GO:0009607,GO:0008150,GO:0005488,GO:0009536,GO:0016787,GO:0009579,GO:0016020,GO:0008152,GO:0009987,GO:0008150,GO:0005488,GO:0005886,GO:0016043,GO:0007049,GO:0016049,GO:0008152,GO:000585	response to stress,response to biotic stimulus,biological_process,metabolic process,cellular process,response to abiotic stimulus	plastid,thylakoid,membrane	binding,hydrolase activity
ug5181	874	GO:0008150,GO:0005488,GO:0005886,GO:0016043,GO:0007049,GO:0016049,GO:0008152,GO:000585	biological_process		binding
ug5182	496	GO:0008150,GO:0005488,GO:0005886,GO:0016043,GO:0007049,GO:0016049,GO:0008152,GO:000585	cellular component organization,cell cycle,cell growth,metabolic process	plasma membrane,cytoskeleton	binding
ug5183	412				
ug5184	701	GO:0005198,GO:0003723,GO:0005840,GO:0009536,GO:0006412	translation	ribosome,plastid	structural molecule activity,RNA binding
ug5185	121				
ug5186	867	GO:0009058,GO:0006519,GO:0003824	biosynthetic process,cellular amino acid and derivative metabolic		catalytic activity
ug5187	794				
ug5188	893	GO:0008152,GO:0006091,GO:0009056,GO:0003824,GO:0005739	metabolic process,generation of precursor metabolites and energy,catabolic process	mitochondrion	catalytic activity
ug5189	594				
ug5190	179				
ug5191	602	GO:0005515,GO:0005215,GO:0000166,GO:0016020,GO:0009536,GO:0006810,GO:0009987,GO:0009536,GO:0016787,GO:0016043,GO:0009987,GO:0019538,GO:0009056,GO:001602	transport,cellular process	membrane,plastid,mitochondrion	protein binding,transporter activity,nucleotide binding
ug5192	844	GO:0009536,GO:0016787,GO:0016043,GO:0009987,GO:0019538,GO:0009056,GO:001602	cellular component organization,cellular process,protein metabolic process,catabolic process	plastid,membrane,thylakoid	hydrolase activity
ug5193	135				
ug5194	223				
ug5195	599				
ug5196	212				
ug5197	900	GO:0005840,GO:0005198,GO:0006412	translation	ribosome	structural molecule activity
ug5198	325				
ug5199	365				
ug5200	595	GO:0005488			binding
ug5201	123				
ug5202	414				
ug5203	381	GO:0016787,GO:0006810,GO:0005215,GO:000166,GO:0016020	transport	membrane	hydrolase activity,transporter activity,nucleotide binding
ug5204	189				
ug5205	110				
ug5206	361	GO:0005515,GO:0005215,GO:0000166,GO:0016020,GO:0009536,GO:0006810,GO:0009987,GO:0003824,GO:0005488,GO:0006139,GO:0006412,GO:0006519,GO:0009536	transport,cellular process	membrane,plastid	protein binding,transporter activity,nucleotide binding
ug5207	391	GO:0003824,GO:0005488,GO:0006139,GO:0006412,GO:0006519,GO:0009536	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,translation,cellular amino acid and derivative metabolic	plastid	catalytic activity,binding
ug5208	336	GO:0003723,GO:0006139,GO:0004518,GO:0005488	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	intracellular	RNA binding,nuclease activity
ug5209	138				
ug5210	126				
ug5211	177				
ug5212	312				
ug5213	249				
ug5214	408				
ug5215	486				
ug5216	807				
ug5217	101				
ug5218	263	GO:0009058,GO:0005975,GO:0015979,GO:0003824,GO:0008152,GO:0009536	biosynthetic process,carbohydrate metabolic process,photosynthesis,metabolic process	plastid	catalytic activity
ug5219	619	GO:0016787,GO:0005488		peroxisome	hydrolase activity
ug5220	381	GO:0009536		plastid	
ug5221	537	GO:0009607,GO:0009605,GO:0006950,GO:0005488	response to biotic stimulus,response to external	plastid	
ug5222	341				
ug5223	359				
ug5224	385				
ug5225	595				
ug5226	148				

Unigene ID	sequence length (bp)	GO-ID	Biological process	Cellular component	Molecular function
ug5227	132				
ug5228	548	GO:0005515			protein binding
ug5229	589				
ug5230	669				
ug5231	772	GO:0005739,GO:0005		mitochondrion	binding
ug5232	755	GO:0016020,GO:0005	transport	membrane,mitochondrion	transporter activity
ug5233	258				
ug5234	470	GO:0003824,GO:0005 488,GO:0008152,GO:0 005576,GO:0009056,G O:0006519,GO:001974	metabolic process,catabolic process,cellular amino acid and derivative metabolic process,secondary metabolic	extracellular region	catalytic activity,binding
ug5235	192				
ug5236	485				
ug5237	166				
ug5238	475				
ug5239	623				
ug5240	518	GO:0005739		mitochondrion	
ug5241	119				
ug5242	114				
ug5243	105				
ug5244	150				
ug5245	142				
ug5246	908				
ug5247	369	GO:0003824			catalytic activity
ug5248	171				
ug5249	306				
ug5250	170				
ug5251	120				
ug5252	651	GO:0019538,GO:0009 987,GO:0009579,GO:0 009536,GO:0005488,G O:0005515,GO:000382	protein metabolic process,cellular process	thylakoid,plastid	binding,protein binding,catalytic activity
ug5253	417				
ug5254	691	GO:0005515			protein binding
ug5255	624				
ug5256	823				
ug5257	739				
ug5258	177				
ug5259	100				
ug5260	105				
ug5261	432	GO:0003824,GO:0008 152,GO:0000166	metabolic process		catalytic activity,nucleotide binding
ug5262	678				