

NetREx

Gene ID	Name	TF	Description	MSU ID	ktotal	GO	Mapman	KEGG
Os01g0121500			Conserved hypothetical protein.	LOC_Os01g03130	21.6288395773726			[not assigned.unknown]
Os01g0159300			Zinc finger, RING/FYVE/PHD-type domain containing protein.	LOC_Os01g06590	47.3377961398288	Molecular Function: protein binding (GO:0005515), Molecular Function: zinc ion binding (GO:0008270)		[protein.degradation.ubiquitin.E3.RING]
Os01g0199400			Alpha/beta hydrolase family protein., Similar to predicted protein.	LOC_Os01g10250	18.3826950562483			[lipid metabolism.lipid degradation.lipases]
Os01g0246700	OsWRKY1v2	WRKY	Similar to WRKY transcription factor 1.	LOC_Os01g14440	21.2736183178468			[RNA.regulation of transcription.WRKY domain transcription factor family]
Os01g0261200	OsNTL3	NAC	No apical meristem (NAM) protein domain containing protein., Similar to NAC domain-containing protein 74.	LOC_Os01g15640	27.7648723945485	Biological Process: regulation of transcription, DNA-dependent (GO:0006355), Molecular Function: DNA binding (GO:0003677),		[development.unspecified]
Os01g0618000			Exonuclease domain containing protein.	LOC_Os01g43080	22.4643420419164	Cellular Component: intracellular (GO:0005622), Molecular Function: nucleic acid binding (GO:0003676), Molecular Function: exonuclease activity (GO:0004527)		[not assigned.unknown]
Os01g0623500			ATPase, AAA-type, core domain containing protein.	LOC_Os01g43480	23.8299483259502	Molecular Function: nucleotide binding (GO:0000166), Molecular Function: ATP binding (GO:0005524), Molecular Function: nucleoside-triphosphatase activity (GO:0017111)		[protein.degradation.AAA type]
Os01g0672400	OsDi19-3		Drought induced 19 family protein., Similar to Protein DEHYDRATION-INDUCED 19 homolog 3.	LOC_Os01g48190	25.8674371361883			[stress.abiotic.drought/salt]
Os01g0708900			Mitochondrial substrate carrier family protein.	LOC_Os01g51250	49.3267572959795	Biological Process: transport (GO:0006810), Biological Process: transmembrane transport (GO:0055085), Cellular Component: mitochondrial inner		[transport.metabolite transporters at the mitochondrial membrane]

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Os01g0709400			Survival protein SurE family protein.	LOC_Os01g51280	24.0210929097547	membrane (GO:0005743), Molecular Function: binding (GO:0005488) Molecular Function: hydrolase activity (GO:0016787)	[misc.acid and other phosphatases']	Purine metabolism, Pyrimidine metabolism, Nicotinate and nicotinamide metabolism, Metabolic pathways, Biosynthesis of secondary metabolites, Nucleotide metabolism
Os01g0747400			Protein kinase, core domain containing protein.	LOC_Os01g54350	37.472111695015	Biological Process: protein phosphorylation (GO:0006468), Molecular Function: protein kinase activity (GO:0004672), Molecular Function: protein serine/threonine kinase activity (GO:0004674), Molecular Function: ATP binding (GO:0005524), Molecular Function: transferase activity, transferring phosphorus-containing groups (GO:0016772)	[protein.postranslational modification']	
Os01g0748900			Membrane attack complex component/perforin/complement C9 family protein.	LOC_Os01g54510	21.4547277200377		[cell.cell death.plants']	
Os01g0793800			Conserved hypothetical protein.	LOC_Os01g58130	17.254642112296		[not assigned.unknown']	
Os01g0795600			Conserved hypothetical protein.	LOC_Os01g58310	17.8531671614703		[not assigned.unknown']	
Os01g0819000			Similar to transposon protein CACTA, En/Spm sub-class.	LOC_Os01g60309	20.4217028511527		[not assigned.unknown']	
Os01g0845000			Hypothetical conserved gene.	None	25.9920660656859			

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Os01g0846400			Conserved hypothetical protein.	LOC_Os01g62770	23.3908307132832			[not assigned.unknown]
Os01g0850100			Similar to Phosphatidic acid phosphatase-like protein.	LOC_Os01g63060	40.4312422157724			[misc.acid and other phosphatases]
Os01g0859100	ZOS1-17	C2H2	Similar to WIP1 protein (Fragment).	LOC_Os01g63980	22.2845712918944	Cellular Component: intracellular (GO:0005622), Molecular Function: nucleic acid binding (GO:0003676), Molecular Function: zinc ion binding (GO:0008270)	[RNA.regulation of transcription.C2H2 zinc finger family]	
Os01g0860800			Glycoside hydrolase, family 17 protein.	LOC_Os01g64170	31.906767961977	Biological Process: carbohydrate metabolic process (GO:0005975), Molecular Function: catalytic activity (GO:0003824), Molecular Function: hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004553), Molecular Function: cation binding (GO:0043169)	[misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase]	
Os01g0868000	ERF99, OsEREBP2, EREBP2, OsERF#099, OsERF099, OsERF99, AP2/EREBP#080, AP2/EREBP80	ERF	AP2/ERF transcription factor, Abiotic stress response, Salt stress response	LOC_Os01g64790	29.8351066628416	Biological Process: regulation of transcription, DNA-templated (GO:0006355), Molecular Function: DNA binding (GO:0003677), Molecular Function: transcription factor activity, sequence-specific DNA binding (GO:0003700)	[hormone metabolism.ethylene.signal transduction, 'RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family]	
Os01g0884300	OsNAC6	NAC	No apical meristem (NAM) protein domain containing protein.	LOC_Os01g66120	18.0405147235402	Biological Process: regulation of transcription, DNA-dependent (GO:0006355), Molecular Function: DNA binding (GO:0003677)	[development.unspecified]	
Os01g0908700			Similar to Hnrpa2b1-prov protein.	LOC_Os01g68060	52.1910824257723	Molecular Function: protein binding (GO:0005515), Molecular Function: zinc ion binding (GO:0008270)	[protein.degradation.ubiquitin.E3.RING]	
Os01g0919500			Zinc finger, RING/FYVE/PHD-type domain containing protein., Hypothetical	LOC_Os01g69040	35.8500277387632	Molecular Function: protein binding (GO:0005515), Molecular Function: zinc ion		[not assigned.unknown]

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Os01g0956075			conserved gene.	LOC_Os01g72600	19.2788642449716	binding (GO:0008270),	[not assigned.unknown]	
			Armadillo-like helical domain containing protein.			Molecular Function: binding (GO:0005488), Molecular Function: protein binding (GO:0005515)		
Os02g0146500	OsCDS1		Conserved hypothetical protein., Similar to cDNA clone:J013125B21, full insert sequence.	LOC_Os02g05320	15.8810293181607		[not assigned.unknown]	
Os02g0147800		HB-other	Hypothetical conserved gene., Similar to Homeo protein (Fragment).	LOC_Os02g05450	19.7022212730497	Molecular Function: protein binding (GO:0005515), Biological Process: regulation of transcription, DNA-dependent (GO:0006355), Molecular Function: DNA binding (GO:0003677), Molecular Function: sequence-specific DNA binding transcription factor activity (GO:0003700), Molecular Function: protein binding (GO:0005515), Molecular Function: sequence-specific DNA binding (GO:0043565)	[RNA.regulation of transcription.HB,Homeobox transcription factor family]	
Os02g0290300	OsWD40-40		WD40/YVTN repeat-like domain containing protein.	LOC_Os02g18820	13.985030546798	Molecular Function: protein binding (GO:0005515)	[development.unspecified]	
Os02g0300700	OseIF1A-1		Similar to Eukaryotic translation initiation factor 1A (EIF-1A) (EIF-4C).	LOC_Os02g19770	13.2410731555625	Biological Process: translational initiation (GO:0006413), Molecular Function: RNA binding (GO:0003723), Molecular Function: translation initiation factor activity (GO:0003743)	[protein.synthesis.initiation]	
Os02g0475300			Membrane attack complex component/perforin/complement C9 family protein., Similar to MAC/ Perforin domain containing protein.	LOC_Os02g27480	23.1841954348763		[cell.cell death.plants]	
Os02g0513000	OsPBL1		Similar to Receptor protein kinase-like protein.	LOC_Os02g30900	30.1732553382627	Biological Process: protein phosphorylation (GO:0006468), Molecular Function: protein	[protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII]	Plant-pathogen interaction

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						kinase activity (GO:0004672), Molecular Function: protein serine/threonine kinase activity (GO:0004674), Molecular Function: ATP binding (GO:0005524), Molecular Function: transferase activity, transferring phosphorus- containing groups (GO:0016772)		
Os02g0539200	OsPUB33		Zinc finger, RING/FYVE/PHD- type domain containing protein.	LOC_Os02g33590	26.0242856815913	Biological Process: protein ubiquitination (GO:0016567), Cellular Component: ubiquitin ligase complex (GO:0000151), Molecular Function: ubiquitin- protein ligase activity (GO:0004842), Molecular Function: binding (GO:0005488)	['RNA.regulation of transcription.PHOR1']	
Os02g0790500			Hypothetical protein., Similar to Trehalose-6-phosphate synthase., Similar to trehalose-6-phosphate synthase.	LOC_Os02g54820	16.0584044437305	, Biological Process: trehalose biosynthetic process (GO:0005992), Molecular Function: catalytic activity (GO:0003824)	['minor CHO metabolism.trehalose.potential TPS/TPP']	
Os02g0819400	LPA1, OsLpa1.3, Oslpa1, Lpa1, OsLpa1		Phytic acid metabolism	LOC_Os02g57400	18.2441893849221		['not assigned.unknown']	
Os03g0124300			Similar to ATP binding protein.	LOC_Os03g03290	26.9309499653932		['signalling.receptor kinases.Catharanthus roseus-like RLK1']	
Os03g0165050			Hypothetical genes.	None	20.5357802120153			
Os03g0186800			Modifier of rudimentary, Modr family protein.	LOC_Os03g08770	26.5111362518325		['not assigned.unknown']	Endocytosis
Os03g0187600	OsGRAM		GRAM domain containing protein.	LOC_Os03g08860	20.9918843053889		['hormone metabolism.abscisic acid.induced-regulated-responsive- activated']	
Os03g0187700			Target SNARE coiled-coil region domain containing protein.	LOC_Os03g08870	18.9247721286199	Molecular Function: protein binding (GO:0005515)	['not assigned.unknown']	SNARE interactions in vesicular transport
Os03g0194900			Uncharacterised conserved protein UCP037471 domain	LOC_Os03g09900	20.6487252432152	Cellular Component: integral to membrane (GO:0016021),	['hormone metabolism.auxin.induced- regulated-responsive-activated']	

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			containing protein., Similar to membrane protein.					
Os03g0224200	ORR1, ORR1, Orr1, OsRR21, Rrb1, OsRR19, OsRRB1	ARR-B	B-type response regulator, Cytokinin signaling, Similar to response regulator 8.	LOC_Os03g12350	41.6216743277943	Biological Process: two-component signal transduction system (phosphorelay) (GO:0000160), Biological Process: regulation of transcription, DNA-dependent (GO:0006355), Molecular Function: two-component response regulator activity (GO:0000156), Molecular Function: DNA binding (GO:0003677), Molecular Function: protein binding (GO:0005515), Biological Process: regulation of transcription, DNA-dependent (GO:0006355), Molecular Function: DNA binding (GO:0003677), Molecular Function: protein binding (GO:0005515)	['RNA.regulation of transcription.ARR']	Plant hormone signal transduction
Os03g0224700	HSFA9	HSF	Similar to HSP protein (Fragment).	LOC_Os03g12370	24.1458231620391	Biological Process: regulation of transcription, DNA-dependent (GO:0006355), Cellular Component: nucleus (GO:0005634), Molecular Function: sequence-specific DNA binding transcription factor activity (GO:0003700), Molecular Function: sequence-specific DNA binding (GO:0043565)	['RNA.regulation of transcription.HSF,Heat-shock transcription factor family']	
Os03g0264150			Hypothetical gene.	None	28.6180140154774			
Os03g0274000			Oxysterol-binding protein family protein., Similar to oxysterol-binding protein.	LOC_Os03g16690	39.8531681725476		['cell.vesicle transport']	
Os03g0331700	CML27		Similar to cDNA clone:002-120-A09, full insert sequence.	LOC_Os03g21380	21.0923586236831		['signalling.calcium']	Plant-pathogen interaction
Os03g0334200			Protein of unknown function	LOC_Os03g21640	17.0409954893373		['not assigned.unknown']	

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			DUF3133 domain containing protein.					
Os03g0655200			Similar to Membrin 11 (AtMEMB11) (Golgi SNAP receptor complex member 2-1) (27 kDa Golgi SNARE protein).	LOC_Os03g45260	20.4824005674662		['cell.vesicle transport']	SNARE interactions in vesicular transport
Os03g0693000			Similar to predicted protein.	LOC_Os03g48660	45.0175644450123		['not assigned.unknown']	
Os03g0740833			Conserved hypothetical protein.	None	20.9741739123653			
Os03g0761100	OsBIPP2C2, OsBIPP2C2b		Protein phosphatase 2C-like protein., Similar to protein phosphatase 2C family protein / PP2C family protein.	LOC_Os03g55320	17.5638349395865	Biological Process: protein dephosphorylation (GO:0006470), Cellular Component: protein serine/threonine phosphatase complex (GO:0008287), Molecular Function: catalytic activity (GO:0003824), Molecular Function: protein serine/threonine phosphatase activity (GO:0004722)	['protein.postranslational modification']	
Os03g0820300	ZFP182	C2H2	TFIIIA-type zinc finger protein, Transcription activator, Abiotic stress tolerance	LOC_Os03g60560	20.0219983485984	Molecular Function: metal ion binding (GO:0046872)	['not assigned.unknown']	
Os04g0402300			Similar to Cysteine-type peptidase.	LOC_Os04g32970	27.3633581153058		['protein.degradation.cysteine protease']	
Os04g0600000			Similar to Transfactor-like protein.	LOC_Os04g51130	22.406524472977	Biological Process: regulation of transcription, DNA-dependent (GO:0006355), Molecular Function: DNA binding (GO:0003677), Molecular Function: protein binding (GO:0005515)	['not assigned.unknown']	
Os04g0602300		Trihelix	Similar to B0403H10-OSIGBa0105A11.17 protein.	LOC_Os04g51320	37.0827082195673		['RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family']	
Os04g0609600	OsPP2C44		Similar to Protein phosphatase type 2C.	LOC_Os04g52000	56.4225662563757	Molecular Function: catalytic activity (GO:0003824)	['protein.postranslational modification']	
Os04g0660900	NPF2.6		TGF-beta receptor, type I/II extracellular region family	LOC_Os04g56560	29.0551965144995	Biological Process: oligopeptide transport (GO:0006857), Cellular	['transport.peptides and oligopeptides']	

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			protein.			Component: membrane (GO:0016020), Molecular Function: transporter activity (GO:0005215)		
Os04g0672900			Similar to H0322F07.6 protein.	LOC_Os04g57690	30.5067817445764			[not assigned.unknown']
Os05g0119200	OsGPRP3		Similar to EST C27893 corresponds to a region of the predicated gene.	LOC_Os05g02770	33.1263619900303			[not assigned.unknown']
Os05g0119300			Similar to ESTs AA754121.	LOC_Os05g02780	26.5813497233661			[not assigned.unknown']
Os05g0169000	TRXH8		Similar to Thioredoxin-like protein., Similar to Thioredoxin h-like protein.	LOC_Os05g07690	20.129746245603	Biological Process: glycerol ether metabolic process (GO:0006662), Biological Process: cell redox homeostasis (GO:0045454), Molecular Function: electron carrier activity (GO:0009055), Molecular Function: protein disulfide oxidoreductase activity (GO:0015035),		[redox.thioredoxin']
Os05g0305900	OsSTLK		Protein kinase, core domain containing protein.	LOC_Os05g24010	54.0334126599503	Biological Process: protein phosphorylation (GO:0006468), Molecular Function: protein kinase activity (GO:0004672), Molecular Function: protein serine/threonine kinase activity (GO:0004674), Molecular Function: protein tyrosine kinase activity (GO:0004713), Molecular Function: ATP binding (GO:0005524), Molecular Function: transferase activity, transferring phosphorus-containing groups (GO:0016772), Biological Process: protein phosphorylation (GO:0006468), Molecular Function: protein kinase activity (GO:0004672), Molecular Function: protein serine/threonine kinase activity		[signalling.receptor kinases.misc']

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						(GO:0004674), Molecular Function: ATP binding (GO:0005524), Molecular Function: transferase activity, transferring phosphorus-containing groups (GO:0016772)		
Os05g0312600	CML21		EF-Hand type domain containing protein.	LOC_Os05g24780	34.2440794097188	Molecular Function: calcium ion binding (GO:0005509)	[signalling.calcium']	Plant-pathogen interaction
Os05g0381700			Calmodulin-binding protein, plant domain containing protein., Similar to calmodulin-binding protein-related.	LOC_Os05g31690	49.2886801136929		[signalling.calcium']	
Os05g0474900			Protein of unknown function Cys-rich family protein.	LOC_Os05g39730	25.4198454554649		[stress']	
Os05g0529000	OsCOLE1		Tonoplast-localized DUF502-containing protein, COV-like protein, Regulation of intracellular auxin transport	LOC_Os05g45280	26.5905166897334		[hormone metabolism.auxin.induced-regulated-responsive-activated']	
Os05g0588900			Similar to mitochondrial chaperone BCS1.	LOC_Os05g51130	19.2378847020553	Molecular Function: nucleotide binding (GO:0000166), Molecular Function: ATP binding (GO:0005524), Molecular Function: nucleoside-triphosphatase activity (GO:0017111)	[protein.degradation.AAA type']	
Os06g0126000			LIM binding protein domain containing protein., Hypothetical conserved gene.	LOC_Os06g03600	26.8885264188022	Cellular Component: nucleus (GO:0005634), Molecular Function: transcription cofactor activity (GO:0003712)	[RNA.regulation of transcription.C2H2 zinc finger family', 'RNA.regulation of transcription.unclassified']	
Os06g0147300			Similar to cDNA clone:J023088C01, full insert sequence.	LOC_Os06g05470	26.6873008878271		[not assigned.unknown']	
Os06g0193400	OsPTF1	bHLH	Similar to Helix-loop-helix protein homolog., Similar to BHLH transcription factor.	LOC_Os06g09370	26.187359995159		[RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family']	
Os06g0200600			Non-protein coding transcript.	LOC_Os06g09990	14.4118851225382		[not assigned.unknown']	
Os06g0695600	OsMAR1		RING E3 ligase, Negative regulator for salt-stress	LOC_Os06g48040	38.7905146611839		[protein.degradation.ubiquitin.E3.RING']	

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			response					
Os07g0168800	ZFP177		Zinc finger, AN1-type domain containing protein.	LOC_Os07g07350	37.6117279721818	Molecular Function: DNA binding (GO:0003677), Molecular Function: zinc ion binding (GO:0008270)	['RNA.regulation of transcription.unclassified']	
Os07g0479600			Conserved hypothetical protein.	LOC_Os07g29640	29.2316297190471		['not assigned.unknown']	
Os07g0573300			FYVE finger-containing phosphoinositide kinase (EC 2.7.1.68) (1-phosphatidylinositol-4-phosphate 5-kinase) (PIP5K) (PtdIns(4)P-5- kinase) (PIKfyve) (p235). Splice isoform p235S., Similar to FYVE finger-containing phosphoinositide kinase (EC 2.7.1.68) (1-phosphatidylinositol-4-phosphate 5-kinase) (PIP5K) (PtdIns(4)P-5- kinase) (PIKfyve) (p235).	LOC_Os07g38580	56.7727262598883	Molecular Function: metal ion binding (GO:0046872)	['RNA.regulation of transcription.unclassified']	
Os07g0688200		MYB	Similar to Typical P-type R2R3 Myb protein (Fragment).	LOC_Os07g48870	48.8057285280857	Biological Process: regulation of transcription, DNA-dependent (GO:0006355), Molecular Function: DNA binding (GO:0003677), Molecular Function: protein binding (GO:0005515)	['RNA.regulation of transcription.MYB domain transcription factor family']	
Os08g0107400			Similar to GDP-mannose transporter., Similar to predicted protein.	LOC_Os08g01610	19.8608266189593		['transport.sugars', 'transport.NDP-sugars at the ER']	
Os08g0110300			Longin domain containing protein.	LOC_Os08g01880	17.154842883975	Biological Process: transport (GO:0006810), Biological Process: vesicle-mediated transport (GO:0016192), Cellular Component: integral to membrane (GO:0016021)	['cell.vesicle transport']	
Os08g0128300			Similar to Actin-like protein 3 (Actin-related protein 3).	LOC_Os08g03440	36.2264061068327	Biological Process: regulation of actin filament polymerization (GO:0030833), Cellular	['cell.organisation']	

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						Component: cytoskeleton (GO:0005856), Molecular Function: actin binding (GO:0003779), Molecular Function: ATP binding (GO:0005524)		
Os08g0157900	OsNTL2	NAC	Similar to NAM protein.	LOC_Os08g06140	18.280722778635	Biological Process: regulation of transcription, DNA-dependent (GO:0006355), Molecular Function: DNA binding (GO:0003677)	['development.unspecified']	
Os08g0408200	SRWD4, SRWD4, OsWD40-160		WD40 subfamily protein, Salt stress	LOC_Os08g31560	41.8299137042077	Molecular Function: protein binding (GO:0005515)	['development.unspecified']	
Os08g0480100			Signal recognition particle receptor, alpha subunit, N-terminal domain containing protein., Similar to predicted protein.	LOC_Os08g37444	35.1494272764869	Biological Process: GTP catabolic process (GO:0006184), Biological Process: SRP-dependent cotranslational protein targeting to membrane (GO:0006614), Biological Process: transport (GO:0006810), Biological Process: intracellular protein transport (GO:0006886), Cellular Component: signal recognition particle receptor complex (GO:0005785), Molecular Function: nucleotide binding (GO:0000166), Molecular Function: GTPase activity (GO:0003924), Molecular Function: signal recognition particle binding (GO:0005047), Molecular Function: GTP binding (GO:0005525), Molecular Function: nucleoside-triphosphatase activity (GO:0017111)	['protein.targeting.secretory pathway.unspecified']	Protein export
Os08g0512400			Protein of unknown function DUF296 domain containing protein., Similar to AT-hook protein 1.	LOC_Os08g40150	16.8940399577977	Molecular Function: DNA binding (GO:0003677)	['RNA.regulation of transcription.putative transcription regulator']	

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Os08g0540400	OsCPK21		Similar to Calcium-dependent protein kinase.	LOC_Os08g42750	20.0665201821505	Biological Process: protein phosphorylation (GO:0006468), Molecular Function: protein kinase activity (GO:0004672), Molecular Function: protein serine/threonine kinase activity (GO:0004674), Molecular Function: calcium ion binding (GO:0005509), Molecular Function: ATP binding (GO:0005524), Molecular Function: transferase activity, transferring phosphorus-containing groups (GO:0016772)	[signalling.calcium]	Plant-pathogen interaction
Os10g0492800			Similar to Ser/Thr protein phosphatase family.	LOC_Os10g35060	15.3280223131666		[not assigned.unknown]	
Os10g0500600			Zinc finger, C2H2-like domain containing protein., Similar to predicted protein.	LOC_Os10g35710	40.2624607488339	Cellular Component: intracellular (GO:0005622), Molecular Function: zinc ion binding (GO:0008270),	[not assigned.unknown]	
Os10g0516800	OsLCBK1		Long-chain base kinase, Regulation of disease resistance response and programmed cell death (PCD), Diacylglycerol kinase, catalytic region domain containing protein.	LOC_Os10g37280	38.1602214655354	Molecular Function: kinase activity (GO:0016301), Biological Process: activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway (GO:0007205), Molecular Function: diacylglycerol kinase activity (GO:0004143)	["lipid metabolism."exotics" (steroids, squalene etc).sphingolipids"]	
Os10g0518800			Serine/threonine protein kinase domain containing protein.	LOC_Os10g37480	17.1046862720932	Biological Process: protein phosphorylation (GO:0006468), Molecular Function: protein kinase activity (GO:0004672), Molecular Function: protein serine/threonine kinase activity (GO:0004674), Molecular Function: protein tyrosine kinase activity (GO:0004713), Molecular Function: ATP binding (GO:0005524), Molecular Function: transferase activity, transferring phosphorus-	[protein.postranslational modification]	

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						containing groups (GO:0016772)		
Os10g0520100			Cyclin-like F-box domain containing protein.	LOC_Os10g37570	21.4542544745964		[not assigned.unknown]	
Os10g0542800	OsBSK1-2		Brassinosteroid-signaling kinase, A member of the receptor-like cytoplasmic kinase (RLCK)-XII sub group, Major regulator in rice immunity	LOC_Os10g39670	24.2297319469875	Biological Process: protein phosphorylation (GO:0006468), Molecular Function: protein kinase activity (GO:0004672), Molecular Function: protein binding (GO:0005515), Molecular Function: ATP binding (GO:0005524)	[protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII']	
Os11g0114300			Conserved hypothetical protein.	LOC_Os11g02290	18.7727667901261		[not assigned.unknown]	
Os11g0133700			Similar to Glucosamine-fructose-6-phosphate aminotransferase, isomerizing family protein, expressed.	LOC_Os11g03900	30.7920614817706		[minor CHO metabolism.others']	
Os11g0141400			Similar to EF hand family protein, expressed.	LOC_Os11g04560	22.7578907946731	Molecular Function: calcium ion binding (GO:0005509)	[signalling.calcium']	
Os11g0168500	ERF118	ERF	Hypothetical conserved gene.	LOC_Os11g06770	24.9544795384736	Biological Process: regulation of transcription, DNA-dependent (GO:0006355), Molecular Function: DNA binding (GO:0003677), Molecular Function: sequence-specific DNA binding transcription factor activity (GO:0003700)	[RNA.regulation of transcription.AP2/ EREBP, APETALA2/Ethylene-responsive element binding protein family']	
Os11g0664500			Hypothetical conserved gene.	LOC_Os11g44310	16.2911746039573		[signalling.calcium']	
Os11g0703400			Similar to BRI1-KD interacting protein 109.	LOC_Os11g47710	23.2682414510744	Biological Process: protein transport (GO:0015031)	[RNA.regulation of transcription.SNF7']	
Os12g0114000			Conserved hypothetical protein.	LOC_Os12g02240	16.4279081138233		[not assigned.unknown]	
Os12g0131100			Similar to Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-	LOC_Os12g03720	39.0741143172027	Biological Process: carbohydrate metabolic process (GO:0005975), Molecular Function: sugar binding (GO:0005529)	Alanine, aspartate and glutamate metabolism, Amino sugar and nucleotide	

Gene ID	Name	TF	Description	MSU ID	ktotal	GO	Mapman	KEGG
			fructose-6- phosphate amidotransferase) (GFAT).					sugar metabolism, Metabolic pathways, Biosynthesis of nucleotide sugars
Os12g0131150			Similar to Glucosamine- fructose-6-phosphate aminotransferase, isomerizing family protein, expressed.	LOC_Os12g03720	30.2902018917927		[minor CHO metabolism.others']	
Os12g0147800	OsPSK5, PSK5		Similar to Phytosulfokines 5 precursor (Secretory protein SH27A).	LOC_Os12g05260	26.8548473955721	Biological Process: cell proliferation (GO:0008283), Cellular Component: extracellular region (GO:0005576), Molecular Function: growth factor activity (GO:0008083)	['development.unspecified']	
Os12g0639100			Major facilitator superfamily MFS_1 protein., Similar to nodulin-like protein.	LOC_Os12g44180	32.1825426603919	Biological Process: transmembrane transport (GO:0055085), Cellular Component: integral to membrane (GO:0016021)	['development.unspecified']	