

Gene	Description	Variant Type	Position	GO IDs	GO Descriptions
gene4306	hypothetical protein	missense_variant	p.Ala40Thr	GO:0016779, GO:0008152, GO:0016021	nucleotidyltransferase activity, metabolic process, integral component of membrane
gene4025	membrane protein	missense_variant	p.Arg284Cys	GO:0016021	integral component of membrane
gene3092	5'-nucleotidase	missense_variant	p.Arg371Cys	GO:0046872, GO:0004519, GO:0000166, GO:0008253, GO:0009166, GO:0090305, GO:0015949	metal ion binding, endonuclease activity, nucleotide binding, 5'-nucleotidase activity, nucleotide catabolic process, nucleic acid phosphodiester bond hydrolysis, nucleobase-containing small molecule interconversion
gene4104	cyclodextrin-binding protein	missense_variant	p.Asp313Asn	GO:0005363, GO:0015768	maltose transmembrane transporter activity, maltose transport
gene1593	penicillin-binding protein	frameshift_variant	p.Asp399fs	GO:0009252, GO:0016021, GO:0008658, GO:0016757	peptidoglycan biosynthetic process, integral component of membrane, penicillin binding, transferase activity, transferring glycosyl groups
gene5434	chemotaxis protein CheY	frameshift_variant	p.Asp45fs	GO:0008152, GO:0016740, GO:0000160, GO:0005622	metabolic process, transferase activity, phosphorelay signal transduction system, intracellular
gene3930	cell division protein FtsA	missense_variant	p.Gln83Arg	GO:0008360, GO:0051301, GO:0007049	regulation of cell shape, cell division, cell cycle
gene425	ABC transporter ATP-binding protein	missense_variant	p.Glu192Gly	GO:0042626, GO:0055085, GO:0008152, GO:0005524	ATPase activity, coupled to transmembrane movement of substances, transmembrane transport, metabolic process, ATP binding
gene936	alpha-acetolactate decarboxylase	frameshift_variant	p.Glu67fs	GO:0045151, GO:0006113, GO:0047605	acetoin biosynthetic process, fermentation, acetolactate decarboxylase activity
gene4168	transporter	missense_variant	p.Gly298Glu	GO:0006836, GO:0005328, GO:0016021, GO:0055085	neurotransmitter transport, neurotransmitter:sodium symporter activity, integral component of membrane, transmembrane transport

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gene383	5-methylribose kinase	missense_variant	p.His156Arg	GO:0016310, GO:0019509, GO:0005524, GO:0019284, GO:0046522	phosphorylation, L-methionine biosynthetic process from methylthioadenosine, ATP binding, L-methionine biosynthetic process from S-adenosylmethionine, S-methyl-5-thioribose kinase activity
gene3850	GTP-sensing transcriptional pleiotropic repressor CodY	missense_variant	p.Ile116Asn	GO:0003677, GO:0005737, GO:0005525, GO:0045892, GO:0003700	DNA binding, cytoplasm, GTP binding, negative regulation of transcription, DNA-templated, transcription factor activity, sequence-specific DNA binding
gene1823	transporter	frameshift_variant	p.Ile324fs	GO:0042891, GO:0005215, GO:0016021, GO:0055085	antibiotic transport, transporter activity, integral component of membrane, transmembrane transport
gene3226	diaminobutyrate--2-oxoglutarate transaminase	missense_variant	p.Ile380Val	GO:0047307, GO:0030170, GO:0045303, GO:0019491	diaminobutyrate-pyruvate transaminase activity, pyridoxal phosphate binding, diaminobutyrate-2-oxoglutarate transaminase activity, ectoine biosynthetic process
gene1791	hypothetical protein	missense_variant	p.Leu258His	GO:0016021	integral component of membrane
gene5251	membrane protein	missense_variant	p.Leu36Trp	GO:0016021	integral component of membrane
gene652	cadmium transporter	frameshift_variant	p.Leu773fs	GO:0070574, GO:0046872, GO:0016021, GO:0008551, GO:0008152, GO:0000166, GO:0005886	cadmium ion transmembrane transport, metal ion binding, integral component of membrane, cadmium-exporting ATPase activity, metabolic process, nucleotide binding, plasma membrane
gene679	cardiolipin synthase	frameshift_variant	p.Lys130fs	GO:0005886, GO:0008808, GO:0032049, GO:0016021	plasma membrane, cardiolipin synthase activity, cardiolipin biosynthetic process, integral component of membrane
gene4394	phosphotransferase	missense_variant	p.Lys168Asn	GO:0005524, GO:0006470, GO:0016776, GO:0004674, GO:0043531, GO:0006468	ATP binding, protein dephosphorylation, phosphotransferase activity, phosphate group as acceptor, protein serine/threonine kinase activity, ADP binding, protein phosphorylation
gene3246	N-acetylmuramoyl-L-alanine amidase	missense_variant	p.Lys219Glu	GO:0009253, GO:0008745	peptidoglycan catabolic process, N-acetylmuramoyl-L-alanine amidase activity

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gene1141	wall-associated protein	missense_variant	p.Lys991Glu	GO:0097264, GO:0016021	self proteolysis, integral component of membrane
gene3802	damage-inducible protein	missense_variant	p.Met133Thr	GO:0003677, GO:0016787, GO:0006259	DNA binding, hydrolase activity, DNA metabolic process
gene4381	hypothetical protein	missense_variant	p.Met164Lys	GO:0016021	integral component of membrane
gene4039	hypothetical protein	missense_variant	p.Met199Val	GO:0005524	ATP binding
gene692	sodium:alanine symporter	frameshift_variant	p.Met223fs	GO:0032328, GO:0016021, GO:0015655, GO:0006814	alanine transport, integral component of membrane, alanine:sodium symporter activity, sodium ion transport
gene2131	transporter	frameshift_variant	p.Phe217fs	GO:0055085, GO:0016021	transmembrane transport, integral component of membrane
gene56	ribose-phosphate pyrophosphokinase	missense_variant	p.Pro155Ser	GO:0004749, GO:0016301, GO:0005524, GO:0000287, GO:0016310, GO:0009165, GO:0005737, GO:0009156, GO:0006015	ribose phosphate diphosphokinase activity, kinase activity, ATP binding, magnesium ion binding, phosphorylation, nucleotide biosynthetic process, cytoplasm, ribonucleoside monophosphate biosynthetic process, 5-phosphoribose 1-diphosphate biosynthetic process
gene1428	sodium:dicarboxylate symporter	frameshift_variant	p.Pro26fs	GO:0017153, GO:0006835, GO:0016021	sodium:dicarboxylate symporter activity, dicarboxylic acid transport, integral component of membrane
gene4752	acetyl-CoA synthetase	missense_variant	p.Pro453Leu	GO:0008152, GO:0016874	metabolic process, ligase activity
gene1836	acetyltransferase	frameshift_variant	p.Pro6fs	GO:0008080, GO:0008152	N-acetyltransferase activity, metabolic process

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gene4105	alpha-amylase	frameshift_variant	p.Ser104fs	GO:0009313, GO:0004556, GO:0043169, GO:0031216	oligosaccharide catabolic process, alpha-amylase activity, cation binding, neopullulanase activity
gene2939	glutamate 5-kinase	missense_variant	p.Ser12Gly	GO:0005524, GO:0004349, GO:0003723, GO:0055129, GO:0005737, GO:0016310	ATP binding, glutamate 5-kinase activity, RNA binding, L-proline biosynthetic process, cytoplasm, phosphorylation
gene2724	DeoR family transcriptional regulator	frameshift_variant	p.Ser191fs	GO:0005622, GO:0006355, GO:0003700, GO:0003677	intracellular, regulation of transcription, DNA-templated, transcription factor activity, sequence-specific DNA binding, DNA binding
gene113	DNA-directed RNA polymerase subunit beta	missense_variant	p.Ser35Pro	GO:0003899, GO:0006351, GO:0000345, GO:0032549, GO:0003677	DNA-directed RNA polymerase activity, transcription, DNA-templated, cytosolic DNA-directed RNA polymerase complex, ribonucleoside binding, DNA binding
gene414	PTS trehalose transporter subunit IIBC	frameshift_variant	p.Ser75fs	GO:0008982, GO:0016021, GO:0016310, GO:0009401, GO:0016301, GO:0005886, GO:0034219	protein-N(P)-phosphohistidine-sugar phosphotransferase activity, integral component of membrane, phosphorylation, phosphoenolpyruvate-dependent sugar phosphotransferase system, kinase activity, plasma membrane, carbohydrate transmembrane transport
gene1797	two-component system sensor histidine kinase	missense_variant	p.Thr235Ala	GO:0000160, GO:0016021, GO:0000155, GO:0046983, GO:0023014, GO:0005622	phosphorelay signal transduction system, integral component of membrane, phosphorelay sensor kinase activity, protein dimerization activity, signal transduction by protein phosphorylation, intracellular
gene3189	MFS transporter	frameshift_variant	p.Thr306fs	GO:0055085, GO:0005215, GO:0016021	transmembrane transport, transporter activity, integral component of membrane
gene2984	tetracycline resistance protein	missense_variant	p.Thr41Met	GO:0003924, GO:0003746, GO:0006414, GO:0005525	GTPase activity, translation elongation factor activity, translational elongation, GTP binding
gene5299	BigG family transcription antiterminator	frameshift_variant	p.Thr424fs	GO:0005524, GO:0003677, GO:0006355, GO:0008134, GO:0009401, GO:0016021	ATP binding, DNA binding, regulation of transcription, DNA-templated, transcription factor binding, phosphoenolpyruvate-dependent sugar phosphotransferase system, integral component of membrane
gene4827	molybdopterin (MPT) converting factor%2C subunit 2	missense_variant	p.Thr86Ile	GO:0030366, GO:0006777	molybdopterin synthase activity, Mo-molybdopterin cofactor biosynthetic process

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gene3557	serine protease	frameshift_variant	p.Trp239fs	GO:0016021, GO:0004252, GO:0006508	integral component of membrane, serine-type endopeptidase activity, proteolysis
gene654	transcriptional regulator	missense_variant	p.Tyr193Ser	GO:0003700, GO:0043565, GO:0006355	transcription factor activity, sequence-specific DNA binding, sequence-specific DNA binding, regulation of transcription, DNA-templated
gene1783	cell surface protein	frameshift_variant	p.Tyr83fs	GO:0006508, GO:0016021, GO:0008233	proteolysis, integral component of membrane, peptidase activity
gene915	catalase	frameshift_variant	p.Val215fs	GO:0020037, GO:0046872, GO:0006979, GO:0055114, GO:0004096	heme binding, metal ion binding, response to oxidative stress, oxidation-reduction process, catalase activity
gene1445	ATP phosphoribosyltransferase regulatory subunit	frameshift_variant	p.Val364fs	GO:0000105, GO:0016757, GO:0004812, GO:0006418, GO:0005737	histidine biosynthetic process, transferase activity, transferring glycosyl groups, aminoacyl-tRNA ligase activity, tRNA aminoacylation for protein translation, cytoplasm
gene5405	ATP synthase subunit alpha	missense_variant	p.Val451Ile	GO:0046961, GO:0045262, GO:0015991, GO:0042777, GO:0005524, GO:0046933	proton-transporting ATPase activity, rotational mechanism, plasma membrane proton-transporting ATP synthase complex, catalytic core F(1), ATP hydrolysis coupled proton transport, plasma membrane ATP synthesis coupled proton transport, ATP binding, proton-transporting ATP synthase activity, rotational mechanism