**Tables S5.** Genome-wide prediction of CRE1 binding sites *in T. reesei*.

| Protein ID | Site 1* | Site 2 | Distance | Description | Functional category |
|---|---|---|---|---|---|
| **54283** | -709 | -700 | 9 | Predicted carbohydrate kinase, contains PfkB domain | General function prediction only |
| **102572** | -335 | -315 | 20 | Parvulin-like peptidyl-prolyl cis-trans isomerase | Posttranslational modification, protein turnover, chaperones |
| **43817** | -912 | -903 | 9 | PHD Zn-finger protein | General function prediction only |
| **53576** | -872 | -862 | 10 | CREB binding protein/P300 and related TAZ Zn-finger proteins | Transcription |
| **102743** | -500 | -489 | 11 | von Willebrand factor and related coagulation proteins | Defense mechanisms / Extracellular structures |
| **102743** | -191 | -183 | 8 | von Willebrand factor and related coagulation proteins | Defense mechanisms / Extracellular structures |
| **44330** | -1165 | -1155 | 10 | Dual-specificity tyrosine-phosphorylation regulated kinase | General function prediction only |
| **74258** | -1111 | -1084 | 27 | Phenylalanyl-tRNA synthetase beta subunit | Translation, ribosomal structure and biogenesis |
| **2087** | -1354 | -1345 | 9 | Exosomal 3'-5' exoribonuclease complex, subunit Rrp43 | Translation, ribosomal structure and biogenesis |
| **74486** | -247 | -238 | 9 | Uncharacterized conserved protein | Function unknown |
| **78176** | -1489 | -1477 | 12 | 1,3-beta-glucan synthase/callose synthase catalytic subunit | Cell wall/membrane/envelope biogenesis |
| **107779** | -835 | -829 | 6 | Predicted alpha/beta hydrolase BEM46 | General function prediction only |
| **122103** | -61 | -55 | 6 | Predicted nucleotidyltransferase | General function prediction only |
| **22538** | -1477 | -1466 | 11 | Vacuolar assembly/sorting protein PEP5/VPS11 | Intracellular trafficking, secretion, and vesicular transport |
| **78817** | -56 | -27 | 29 | 26S proteasome regulatory complex, ATPase RPT6 | Posttranslational modification, protein turnover, chaperones |
| **79124** | -807 | -798 | 9 | Kinesin-like protein | Cytoskeleton |
| **122476** | -536 | -530 | 6 | Protein involved in autophagy and nutrient starvation | Posttranslational modification, protein turnover, chaperones |
| **22647** | -85 | -58 | 27 | Microfibrillar-associated protein MFAP1 | Cytoskeleton |
| **108697** | -512 | -505 | 7 | Calcium-responsive transcription coactivator | Transcription |
| **108706** | -68 | -62 | 6 | Vacuolar sorting protein/ubiquitin receptor VPS23 | Intracellular trafficking, secretion, and vesicular transport / Posttranslational modification, protein turnover, chaperones |
| **64111** | -423 | -412 | 11 | Structural maintenance of chromosome protein SMC5/Spr18, SMC superfamily | Replication, recombination and repair / Chromatin structure and dynamics / Cell cycle control, cell division, chromosome partitioning |
| **108784** | -657 | -638 | 19 | Zinc-binding oxidoreductase | Energy production and conversion / General function prediction only |
| **64193** | -1329 | -1323 | 6 | Transferrin receptor and related proteins containing the protease-associated (PA) domain | Posttranslational modification, protein turnover, chaperones / Inorganic ion transport and metabolism / General function prediction only |

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|---|---|---|---|---|---|
| **64193** | -1323 | -1317 | 6 | Transferrin receptor and related proteins containing the protease-associated (PA) domain | Posttranslational modification, protein turnover, chaperones / Inorganic ion transport and metabolism / General function prediction only |
| **64193** | -1317 | -1311 | 6 | Transferrin receptor and related proteins containing the protease-associated (PA) domain | Posttranslational modification, protein turnover, chaperones / Inorganic ion transport and metabolism / General function prediction only |
| **22731** | -258 | -252 | 6 | Beclin-like protein | Signal transduction mechanisms |
| **4654** | -319 | -306 | 13 | Histidinol dehydrogenase | Amino acid transport and metabolism |
| **49832** | -839 | -810 | 29 | Translation initiation factor 2C (eIF-2C) and related proteins | Translation, ribosomal structure and biogenesis |
| **79673** | -677 | -670 | 7 | Serine/threonine protein kinase | Signal transduction mechanisms |
| **79741** | -266 | -242 | 24 | Sulfate/bicarbonate/oxalate exchanger SAT-1 and related transporters (SLC26 family) | Inorganic ion transport and metabolism |
| **122828** | -199 | -186 | 13 | Uncharacterized protein of the uridine kinase family | Nucleotide transport and metabolism |
| **79884** | -207 | -193 | 14 | Ubiquitin-like protein | Cell cycle control, cell division, chromosome partitioning / Posttranslational modification, protein turnover, chaperones |
| **80007** | -1059 | -1040 | 19 | WW domain binding protein WBP-2, contains GRAM domain | Signal transduction mechanisms |
| **4905** | -956 | -947 | 9 | VAMP-associated protein involved in inositol metabolism | Intracellular trafficking, secretion, and vesicular transport |
| **65969** | -224 | -201 | 23 | Cytoskeletal protein Adducin | Signal transduction mechanisms / Cytoskeleton |
| **4947** | -173 | -167 | 6 | TRAPP 20 K subunit | Intracellular trafficking, secretion, and vesicular transport |
| **27085** | -737 | -707 | 30 | KRR1-interacting protein involved in 40S ribosome biogenesis | Translation, ribosomal structure and biogenesis |
| **109779** | -134 | -127 | 7 | von Willebrand factor and related coagulation proteins | Defense mechanisms / Extracellular structures |
| **123030** | -796 | -785 | 11 | RhoGEF GTPase | Signal transduction mechanisms |
| **80231** | -133 | -127 | 6 | Hexokinase | Carbohydrate transport and metabolism |
| **66405** | -1363 | -1355 | 8 | Transcription initiation factor TFIID, subunit TAF5 (also component of histone acetyltransferase SAGA) | Transcription |
| **123114** | -1289 | -1262 | 27 | Molecular chaperone (HSP90 family) | Posttranslational modification, protein turnover, chaperones |
| **123226** | -754 | -742 | 12 | Neutral trehalase | Carbohydrate transport and metabolism |
| **120172** | -100 | -92 | 8 | Fe-S oxidoreductase | Energy production and conversion |
| **2384** | -543 | -535 | 8 | Signaling protein SWIFT and related BRCT domain proteins | Transcription / Replication, recombination and repair / Cell cycle control, cell division, chromosome partitioning / Signal transduction mechanisms |
| **55180** | -938 | -921 | 17 | COP9 signalosome, subunit CSN6 | Signal transduction mechanisms / Posttranslational modification, protein turnover, chaperones |
| **55172** | -782 | -767 | 15 | Isoamyl acetate-hydrolyzing esterase and related enzymes | General function prediction only |

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|---|---|---|---|---|---|
| **80833** | -1424 | -1398 | 26 | Chitinase | Carbohydrate transport and metabolism |
| **23050** | -1126 | -1118 | 8 | Small Nuclear ribonucleoprotein splicing factor | RNA processing and modification |
| **81102** | -1088 | -1070 | 18 | Flavin-containing monooxygenase | Secondary metabolites biosynthesis, transport and catabolism |
| **68107** | -979 | -973 | 6 | Ubiquitin-like/40S ribosomal S30 protein fusion | Translation, ribosomal structure and biogenesis / Posttranslational modification, protein turnover, chaperones |
| **81303** | -129 | -108 | 21 | Fumarate reductase, flavoprotein subunit | Energy production and conversion |
| **111102** | -308 | -302 | 6 | Glycosylphosphatidylinositol-specific phospholipase C | Signal transduction mechanisms |
| **111102** | -302 | -296 | 6 | Glycosylphosphatidylinositol-specific phospholipase C | Signal transduction mechanisms |
| **68622** | -1055 | -1046 | 9 | Uncharacterized conserved protein | Function unknown |
| **123705** | -1173 | -1145 | 28 | UDP-glucose/GDP-mannose dehydrogenase | Signal transduction mechanisms / Carbohydrate transport and metabolism |
| **111417** | -1083 | -1077 | 6 | Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) | Secondary metabolites biosynthesis, transport and catabolism |
| **5656** | -178 | -165 | 13 | Predicted transporter (major facilitator superfamily) | General function prediction only |
| **69122** | -859 | -848 | 11 | Fatty acid desaturase | Lipid transport and metabolism |
| **69068** | -760 | -751 | 9 | Predicted ubiquitin regulatory protein | Posttranslational modification, protein turnover, chaperones |
| **81843** | -287 | -275 | 12 | Alkaline phosphatase | Inorganic ion transport and metabolism |
| **81859** | -559 | -534 | 25 | Ubiquitin carboxyl-terminal hydrolase | Posttranslational modification, protein turnover, chaperones |
| **123946** | -580 | -562 | 18 | Predicted dehydrogenase | Secondary metabolites biosynthesis, transport and catabolism |
| **104180** | -197 | -173 | 24 | Ankyrin | Cell wall/membrane/envelope biogenesis |
| **56792** | -747 | -737 | 10 | Predicted mitochondrial cholesterol transporter | Signal transduction mechanisms / Lipid transport and metabolism |
| **56515** | -1465 | -1438 | 27 | Mismatch repair ATPase MSH4 (MutS family) | Replication, recombination and repair |
| **120391** | -76 | -61 | 15 | Serine/threonine protein kinase | Signal transduction mechanisms |
| **57010** | -692 | -686 | 6 | Protein geranylgeranyltransferase Type I, beta subunit | Posttranslational modification, protein turnover, chaperones |
| **75397** | -428 | -405 | 23 | Vacuolar assembly/sorting protein VPS9 | Intracellular trafficking, secretion, and vesicular transport |
| **2648** | -182 | -160 | 22 | Predicted component of NuA3 histone acetyltransferase complex | Chromatin structure and dynamics |
| **75444** | -89 | -74 | 15 | COP9 signalosome, subunit CSN4 | Signal transduction mechanisms / Posttranslational modification, protein turnover, chaperones |
| **75444** | -42 | -36 | 6 | COP9 signalosome, subunit CSN4 | Signal transduction mechanisms / Posttranslational modification, protein turnover, chaperones |
| **72661** | -106 | -99 | 7 | Serine/threonine protein kinase | Signal transduction mechanisms |

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|---|---|---|---|---|---|
| **104535** | -1485 | -1463 | 22 | Telomerase elongation inhibitor/RNA maturation protein PINX1 | RNA processing and modification / Cell cycle control, cell division, chromosome partitioning |
| **75568** | -1479 | -1463 | 16 | Thioredoxin-like protein | Posttranslational modification, protein turnover, chaperones |
| **2745** | -128 | -119 | 9 | Fumarase | Energy production and conversion |
| **124094** | -400 | -394 | 6 | Predicted methyltransferase | General function prediction only |
| **5927** | -259 | -232 | 27 | Serine carboxypeptidases (lysosomal cathepsin A) | Posttranslational modification, protein turnover, chaperones / Amino acid transport and metabolism |
| **70548** | -158 | -152 | 6 | Ras1 guanine nucleotide exchange factor | Signal transduction mechanisms |
| **124181** | -1059 | -1044 | 15 | Members of tubulin/FtsZ family | Cytoskeleton |
| **82499** | -201 | -177 | 24 | Predicted integral membrane protein | General function prediction only |
| **120623** | -901 | -894 | 7 | Nuclear receptor coregulator SMRT/SMRTER, contains Myb-like domains | Transcription |
| **120623** | -894 | -887 | 7 | Nuclear receptor coregulator SMRT/SMRTER, contains Myb-like domains | Transcription |
| **21752** | -1103 | -1092 | 11 | Amphiphysin | Intracellular trafficking, secretion, and vesicular transport |
| **46247** | -962 | -939 | 23 | WD40 repeat-containing protein | General function prediction only |
| **76117** | -159 | -146 | 13 | Defense-related protein containing SCP domain | Function unknown |
| **76117** | -146 | -140 | 6 | Defense-related protein containing SCP domain | Function unknown |
| **57609** | -1466 | -1450 | 16 | Heterochromatin-associated protein HP1 and related CHROMO domain proteins | Chromatin structure and dynamics |
| **105191** | -1220 | -1190 | 30 | RNA polymerase I and III, subunit RPA40/RPC40 | Transcription |
| **57335** | -195 | -172 | 23 | Uncharacterized conserved protein | Function unknown |
| **52847** | -604 | -589 | 15 | NADH:ubiquinone oxidoreductase, NDUFA5/B13 subunit | Energy production and conversion |
| **124285** | -674 | -665 | 9 | Small nuclear ribonucleoprotein SMD1 and related snRNPs | RNA processing and modification |
| **105342** | -766 | -749 | 17 | von Willebrand factor and related coagulation proteins | Defense mechanisms / Extracellular structures |
| **76336** | -1434 | -1428 | 6 | Mitofusin 1 GTPase, involved in mitochondrila biogenesis | Posttranslational modification, protein turnover, chaperones |
| **105432** | -947 | -938 | 9 | FOG: Immunoglobin and related proteins | Inorganic ion transport and metabolism / General function prediction only |
| **59014** | -1217 | -1211 | 6 | Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily | Secondary metabolites biosynthesis, transport and catabolism |
| **59014** | -1211 | -1199 | 12 | Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily | Secondary metabolites biosynthesis, transport and catabolism |
| **59014** | -1199 | -1193 | 6 | Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily | Secondary metabolites biosynthesis, transport and catabolism |

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| **59014** | -1193 | -1187 | 6 | Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily | Secondary metabolites biosynthesis, transport and catabolism |
| **58539** | -659 | -653 | 6 | Mitochondrial ribosome small subunit component, mediator of apoptosis DAP3 | Translation, ribosomal structure and biogenesis |
| **121158** | -1320 | -1297 | 23 | Serine/threonine protein kinase | Signal transduction mechanisms |
| **105931** | -761 | -755 | 6 | Beta-N-acetylhexosaminidase | Carbohydrate transport and metabolism |
| **105931** | -755 | -738 | 17 | Beta-N-acetylhexosaminidase | Carbohydrate transport and metabolism |
| **105931** | -738 | -721 | 17 | Beta-N-acetylhexosaminidase | Carbohydrate transport and metabolism |
| **105931** | -721 | -704 | 17 | Beta-N-acetylhexosaminidase | Carbohydrate transport and metabolism |
| **105931** | -704 | -680 | 24 | Beta-N-acetylhexosaminidase | Carbohydrate transport and metabolism |
| **106051** | -819 | -813 | 6 | Transcription factor TCF20 | Transcription |
| **106067** | -1137 | -1130 | 7 | Mitochondrial chaperonin | Posttranslational modification, protein turnover, chaperones |
| **47069** | -177 | -165 | 12 | 3'-5' exonuclease | Replication, recombination and repair |
| **60346** | -85 | -74 | 11 | Para-aminobenzoate (PABA) synthase ABZ1 | Translation, ribosomal structure and biogenesis |
| **60008** | -1339 | -1318 | 21 | Phosphatidylethanolamine binding protein | General function prediction only |
| **60873** | -84 | -55 | 29 | ATP-dependent DNA ligase I | Replication, recombination and repair |
| **61159** | -49 | -39 | 10 | Subunit of cis-Golgi transport vesicle tethering complex - Sec34p | Intracellular trafficking, secretion, and vesicular transport |
| **107187** | -1093 | -1077 | 16 | Reductases with broad range of substrate specificities | General function prediction only |
| **3889** | -1330 | -1324 | 6 | von Willebrand factor and related coagulation proteins | Defense mechanisms / Extracellular structures |
| **3889** | -1324 | -1306 | 18 | von Willebrand factor and related coagulation proteins | Defense mechanisms / Extracellular structures |
| **3889** | -1306 | -1300 | 6 | von Willebrand factor and related coagulation proteins | Defense mechanisms / Extracellular structures |
| **3889** | -1300 | -1282 | 18 | von Willebrand factor and related coagulation proteins | Defense mechanisms / Extracellular structures |
| **121777** | -1222 | -1216 | 6 | Halotolerance protein HAL3 (contains flavoprotein domain) | Cell cycle control, cell division, chromosome partitioning / Inorganic ion transport and metabolism |
| **107323** | -265 | -251 | 14 | Predicted 3-ketosphinganine reductase | Secondary metabolites biosynthesis, transport and catabolism |
| **121820** | -279 | -270 | 9 | Methionine synthase II (cobalamin-independent) | Amino acid transport and metabolism |
| **77991** | -578 | -561 | 17 | RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH, subunit SSL1 | Transcription / Replication, recombination and repair |
| **78072** | -617 | -596 | 21 | Amidases | Translation, ribosomal structure and biogenesis |
| **121915** | -894 | -884 | 10 | Microtubule-binding protein (translationally controlled tumor protein) | Cell cycle control, cell division, chromosome partitioning / Cytoskeleton |

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| **54991** | -893 | -884 | 9 | Hydroxysteroid 17-beta dehydrogenase 11 | Secondary metabolites biosynthesis, transport and catabolism |
| **53437** | -305 | -278 | 27 | Putative RNA polymerase II regulator | Transcription |
| **44041** | -403 | -394 | 9 | NADH-ubiquinone oxidoreductase, NDUFS1/75 kDa subunit | Energy production and conversion |
| **102947** | -165 | -135 | 30 | Speckle-type POZ protein SPOP and related proteins with TRAF, MATH and BTB/POZ domains | Cell cycle control, cell division, chromosome partitioning / General function prediction only |
| **21324** | -1145 | -1118 | 27 | Protein phosphatase 2A regulatory subunit A and related proteins | Signal transduction mechanisms |
| **54144** | -187 | -178 | 9 | Ferric reductase, NADH/NADPH oxidase and related proteins | Inorganic ion transport and metabolism / Secondary metabolites biosynthesis, transport and catabolism |
| **53685** | -1412 | -1405 | 7 | Type I phosphodiesterase/nucleotide pyrophosphatase | General function prediction only |
| **33273** | -1174 | -1165 | 9 | Mitochondrial/chloroplast ribosomal protein L17 | Translation, ribosomal structure and biogenesis |
| **103350** | -417 | -396 | 21 | Mitochondrial ribosomal protein S28 | Translation, ribosomal structure and biogenesis |
| **4064** | -1321 | -1311 | 10 | Threonine/serine dehydratases | Amino acid transport and metabolism |
| **34197** | -1201 | -1195 | 6 | Stress-induced protein UVI31+ | Signal transduction mechanisms |
| **62706** | -1095 | -1089 | 6 | Protein phosphatase 1, regulatory subunit, and related proteins | Signal transduction mechanisms |
| **62314** | -1329 | -1323 | 6 | Transcription initiation factor TFIID, subunit BDF1 and related bromodomain proteins | Transcription |
| **122124** | -899 | -879 | 20 | AAA+-type ATPase | Posttranslational modification, protein turnover, chaperones |
| **78582** | -723 | -708 | 15 | Protoheme ferro-lyase (ferrochelatase) | Coenzyme transport and metabolism |
| **4213** | -22 | -11 | 11 | Ribonuclease, T2 family | RNA processing and modification |
| **63206** | -1089 | -1074 | 15 | Putative zinc transporter | Inorganic ion transport and metabolism |
| **122240** | -337 | -328 | 9 | Carnitine O-acyltransferase CPT2/YAT1 | Lipid transport and metabolism |
| **36727** | -511 | -505 | 6 | SWI-SNF chromatin-remodeling complex protein | Chromatin structure and dynamics |
| **78909** | -1333 | -1324 | 9 | NDR and related serine/threonine kinases | General function prediction only |
| **4475** | -743 | -716 | 27 | C-3 sterol dehydrogenase/3-beta-hydroxysteroid dehydrogenase and related dehydrogenases | Amino acid transport and metabolism / Lipid transport and metabolism |
| **63882** | -622 | -613 | 9 | Enoyl-CoA hydratase | Lipid transport and metabolism |
| **79244** | -1310 | -1303 | 7 | Serine/threonine protein kinase | Signal transduction mechanisms |
| **108783** | -1188 | -1169 | 19 | Flavin-containing monooxygenase | Secondary metabolites biosynthesis, transport and catabolism |
| **79324** | -107 | -89 | 18 | Flavonol reductase/cinnamoyl-CoA reductase | Defense mechanisms |
| **79329** | -306 | -276 | 30 | Permease of the major facilitator superfamily | General function prediction only |

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| **79345** | -1160 | -1151 | 9 | Peroxisomal membrane protein MPV17 and related proteins | General function prediction only |
| **64545** | -391 | -385 | 6 | Monocarboxylate transporter | Carbohydrate transport and metabolism |
| **109007** | -953 | -947 | 6 | FOG: Low-complexity | Function unknown |
| **22785** | -604 | -581 | 23 | FOG: Zn-finger | General function prediction only |
| **22785** | -296 | -290 | 6 | FOG: Zn-finger | General function prediction only |
| **65142** | -84 | -78 | 6 | Aldehyde dehydrogenase | Energy production and conversion |
| **109397** | -1191 | -1178 | 13 | Uncharacterized conserved protein | Function unknown |
| **122886** | -1332 | -1305 | 27 | Beta tubulin | Cytoskeleton |
| **50335** | -1344 | -1335 | 9 | Ras-related small GTPase, Rho type | General function prediction only |
| **122988** | -488 | -463 | 25 | Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily | Secondary metabolites biosynthesis, transport and catabolism |
| **65925** | -937 | -914 | 23 | Cytosine deaminase FCY1 and related enzymes | Nucleotide transport and metabolism |
| **123015** | -1243 | -1213 | 30 | GTPase Rab5/YPT51 and related small G protein superfamily GTPases | Intracellular trafficking, secretion, and vesicular transport |
| **123029** | -1445 | -1437 | 8 | Cu2+/Zn2+ superoxide dismutase SOD1 | Inorganic ion transport and metabolism |
| **65965** | -350 | -326 | 24 | SAM-dependent methyltransferases | Lipid transport and metabolism / General function prediction only |
| **65821** | -1415 | -1397 | 18 | Uncharacterized conserved protein, contains WD40 repeats | Function unknown |
| **22911** | -64 | -39 | 25 | Glucose-repressible alcohol dehydrogenase transcriptional effector CCR4 and related proteins | Transcription |
| **66484** | -1140 | -1116 | 24 | Guanine nucleotide exchange factor | Intracellular trafficking, secretion, and vesicular transport |
| **5041** | -1238 | -1211 | 27 | Transcription initiation factor IIE, alpha subunit | Transcription |
| **123185** | -487 | -481 | 6 | Myosin class V heavy chain | Cytoskeleton |
| **66844** | -625 | -619 | 6 | Glycosylphosphatidylinositol anchor synthesis protein | Signal transduction mechanisms |
| **110158** | -1136 | -1130 | 6 | Predicted small molecule transporter involved in cellular pH homeostasis (Batten disease protein in human) | General function prediction only |
| **55912** | -1113 | -1088 | 25 | Septin CDC10 and related P-loop GTPases | Cell cycle control, cell division, chromosome partitioning / Signal transduction mechanisms / Cytoskeleton |
| **103470** | -1286 | -1276 | 10 | RNA-directed RNA polymerase QDE-1 required for posttranscriptional gene silencing and RNA interference | RNA processing and modification |
| **44878** | -1369 | -1351 | 18 | Arp2/3 complex-interacting protein VIP1/Asp1, involved in regulation of actin cytoskeleton | Cytoskeleton |

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| **2358** | -1085 | -1055 | 30 | Diadenosine polyphosphate hydrolase and related proteins of the histidine triad (HIT) family | Nucleotide transport and metabolism / General function prediction only |
| **2365** | -1183 | -1175 | 8 | Putative N2,N2-dimethylguanosine tRNA methyltransferase | RNA processing and modification |
| **21505** | -945 | -924 | 21 | G-protein alpha subunit (small G protein superfamily) | Cell cycle control, cell division, chromosome partitioning / Signal transduction mechanisms |
| **75069** | -806 | -782 | 24 | Predicted membrane protein, contains DoH and Cytochrome b-561/ferric reductase transmembrane domains | Signal transduction mechanisms |
| **110636** | -1088 | -1082 | 6 | RRM motif-containing protein | RNA processing and modification |
| **80961** | -1208 | -1197 | 11 | Transcription factor TCF20 | Transcription |
| **51212** | -808 | -802 | 6 | 60S ribosomal protein L5 | Translation, ribosomal structure and biogenesis |
| **67732** | -1034 | -1017 | 17 | Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily | Secondary metabolites biosynthesis, transport and catabolism |
| **51455** | -113 | -107 | 6 | ATP-dependent RNA helicase | RNA processing and modification |
| **110949** | -1127 | -1115 | 12 | C-type lectin | Defense mechanisms / Signal transduction mechanisms |
| **68122** | -772 | -755 | 17 | Permease of the major facilitator superfamily | Carbohydrate transport and metabolism |
| **111192** | -1420 | -1411 | 9 | Nucleolar GTPase/ATPase p130 | Nuclear structure |
| **111447** | -1281 | -1270 | 11 | Sulfatase | General function prediction only |
| **23276** | -978 | -969 | 9 | VAMP-associated protein involved in inositol metabolism | Intracellular trafficking, secretion, and vesicular transport |
| **81822** | -491 | -461 | 30 | Leucyl-tRNA synthetase | Translation, ribosomal structure and biogenesis |
| **69651** | -454 | -443 | 11 | Predicted transporter (major facilitator superfamily) | General function prediction only |
| **75195** | -438 | -432 | 6 | NADPH oxidase | Energy production and conversion |
| **75195** | -432 | -420 | 12 | NADPH oxidase | Energy production and conversion |
| **120384** | -1062 | -1035 | 27 | Notchless-like WD40 repeat-containing protein | Function unknown |
| **75383** | -1447 | -1441 | 6 | Reductases with broad range of substrate specificities | General function prediction only |
| **75403** | -642 | -620 | 22 | Cysteine desulfurase NFS1 | Amino acid transport and metabolism |
| **104418** | -84 | -78 | 6 | Kynurenine 3-monooxygenase and related flavoprotein monooxygenases | Energy production and conversion / General function prediction only |
| **75551** | -1201 | -1174 | 27 | Predicted sugar kinase | Carbohydrate transport and metabolism |
| **104593** | -166 | -157 | 9 | FOG: WD40 repeat | General function prediction only |
| **52521** | -1252 | -1246 | 6 | Uncharacterized conserved protein | Function unknown |

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|---|---|---|---|---|---|
| **6011** | -538 | -514 | 24 | Phosphatidic acid-preferring phospholipase A1, contains DDHD domain | Intracellular trafficking, secretion, and vesicular transport / Lipid transport and metabolism |
| **57870** | -690 | -684 | 6 | Histones H3 and H4 | Chromatin structure and dynamics |
| **104785** | -1099 | -1085 | 14 | Phosphoinositide phosphatase SAC1 | Lipid transport and metabolism |
| **75845** | -1442 | -1431 | 11 | Cysteine desulfurase NFS1 | Amino acid transport and metabolism |
| **45980** | -1431 | -1424 | 7 | Cell cycle control protein | Transcription / Cell cycle control, cell division, chromosome partitioning / Signal transduction mechanisms |
| **57472** | -201 | -187 | 14 | FOG: RRM domain | General function prediction only |
| **76057** | -761 | -753 | 8 | Vacuolar H+-ATPase V1 sector, subunit B | Energy production and conversion |
| **58011** | -620 | -611 | 9 | FOG: Zn-finger | General function prediction only |
| **57286** | -1396 | -1373 | 23 | Histone H3 (Lys4) methyltransferase complex, subunit CPS25/DPY-30 | Transcription |
| **82651** | -1170 | -1161 | 9 | Cullins | Cell cycle control, cell division, chromosome partitioning |
| **46463** | -968 | -962 | 6 | Serine palmitoyltransferase | Posttranslational modification, protein turnover, chaperones |
| **46613** | -161 | -155 | 6 | Predicted membrane protein | Function unknown |
| **76700** | -108 | -81 | 27 | FOG: Zn-finger | General function prediction only / Transcription |
| **105968** | -1071 | -1044 | 27 | Iron/ascorbate family oxidoreductases | Secondary metabolites biosynthesis, transport and catabolism / General function prediction only |
| **76905** | -1230 | -1203 | 27 | Flavin-containing monooxygenase | Secondary metabolites biosynthesis, transport and catabolism |
| **121298** | -1175 | -1145 | 30 | Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily) | Energy production and conversion |
| **121441** | -702 | -672 | 30 | Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily) | General function prediction only |
| **121529** | -1252 | -1227 | 25 | Mitochondrial carrier protein MRS3/4 | Energy production and conversion |
| **77495** | -1064 | -1035 | 29 | Uncharacterized conserved protein | Function unknown |
| **107014** | -248 | -239 | 9 | Nucleolar GTPase/ATPase p130 | Nuclear structure |
| **121786** | -1182 | -1168 | 14 | Uncharacterized conserved protein | Function unknown |
| **62493** | -384 | -372 | 12 | Chromatin remodeling complex RSC, subunit RSC1/Polybromo and related proteins | Transcription / Chromatin structure and dynamics |
| **27939** | -964 | -953 | 11 | Predicted transporter (major facilitator superfamily) | General function prediction only |
| **70750** | -1410 | -1395 | 15 | Vacuolar H+-ATPase V0 sector, subunit M9.7 (M9.2) | Energy production and conversion |
| **29619** | -113 | -83 | 30 | Annexin | Intracellular trafficking, secretion, and vesicular transport |

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|---|---|---|---|---|---|
| **34112** | -1179 | -1166 | 13 | 60S ribosomal protein L22 | Translation, ribosomal structure and biogenesis |
| **69217** | -1144 | -1121 | 23 | Cdk activating kinase (CAK)/RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH/TFIIK, kinase subunit CDK7 | Transcription / Replication, recombination and repair / Cell cycle control, cell division, chromosome partitioning |
| **30465** | -158 | -152 | 6 | U4/U6 small nuclear ribonucleoprotein Prp4 (contains WD40 repeats) | RNA processing and modification |
| **56872** | -273 | -264 | 9 | Serine/threonine specific protein phosphatase involved in glycogen accumulation, PP2A-related | Signal transduction mechanisms / Carbohydrate transport and metabolism |
| **55969** | -1040 | -1030 | 10 | Translation initiation factor 1A (eIF-1A) | Translation, ribosomal structure and biogenesis |
| **54471** | -320 | -295 | 25 | Serine/threonine protein kinase | Signal transduction mechanisms |
| **59546** | -1191 | -1184 | 7 | Transcription coactivator | Transcription |
| **41035** | -1398 | -1389 | 9 | Calcium-responsive transcription coactivator | Transcription |
| **69013** | -1375 | -1369 | 6 | Uncharacterized conserved protein | Function unknown |
| **69013** | -1369 | -1363 | 6 | Uncharacterized conserved protein | Function unknown |
| **33704** | -835 | -822 | 13 | Transcription initiation factor TFIID, subunit TAF9 (also component of histone acetyltransferase SAGA) | Transcription |
| **27649** | -767 | -742 | 25 | FOG: Zn-finger | General function prediction only |
| **63092** | -1377 | -1360 | 17 | Ribulose kinase and related carbohydrate kinases | Carbohydrate transport and metabolism |
| **25244** | -1165 | -1136 | 29 | FOG: Zn-finger | General function prediction only |
| **61032** | -364 | -354 | 10 | FOG: RCC1 domain | Function unknown |
| **39285** | -405 | -399 | 6 | Predicted DNA methylase | Function unknown |
| **55114** | -1056 | -1029 | 27 | Nucleoside phosphatase | Nucleotide transport and metabolism |
| **54736** | -776 | -770 | 6 | ATP-dependent RNA helicase | RNA processing and modification |
| **103131** | -597 | -591 | 6 | unknown protein | - |
| **53596** | -505 | -489 | 16 | unknown protein | - |
| **78189** | -218 | -212 | 6 | unknown protein | - |
| **62386** | -257 | -246 | 11 | unknown protein | - |
| **62537** | -1270 | -1258 | 12 | unknown protein | - |
| **62333** | -1237 | -1211 | 26 | unknown protein | - |
| **71532** | -715 | -686 | 29 | unknown protein | - |

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|---|---|---|---|---|---|
| **108025** | -1294 | -1270 | 24 | unknown protein | - |
| **4221** | -983 | -968 | 15 | unknown protein | - |
| **108202** | -245 | -236 | 9 | unknown protein | - |
| **108202** | -236 | -227 | 9 | unknown protein | - |
| **108573** | -574 | -565 | 9 | unknown protein | - |
| **108683** | -1011 | -981 | 30 | unknown protein | - |
| **79222** | -225 | -198 | 27 | unknown protein | - |
| **79222** | -198 | -171 | 27 | unknown protein | - |
| **79222** | -121 | -107 | 14 | unknown protein | - |
| **122576** | -1287 | -1281 | 6 | unknown protein | - |
| **79921** | -755 | -745 | 10 | unknown protein | - |
| **65572** | -201 | -182 | 19 | unknown protein | - |
| **80252** | -1433 | -1409 | 24 | unknown protein | - |
| **5011** | -622 | -616 | 6 | unknown protein | - |
| **123186** | -324 | -318 | 6 | unknown protein | - |
| **110159** | -978 | -972 | 6 | unknown protein | - |
| **110825** | -683 | -674 | 9 | unknown protein | - |
| **68026** | -841 | -835 | 6 | unknown protein | - |
| **81586** | -424 | -411 | 13 | unknown protein | - |
| **81586** | -411 | -405 | 6 | unknown protein | - |
| **81586** | -405 | -399 | 6 | unknown protein | - |
| **81586** | -399 | -393 | 6 | unknown protein | - |
| **81586** | -393 | -387 | 6 | unknown protein | - |
| **68876** | -1402 | -1389 | 13 | unknown protein | - |
| **68876** | -1389 | -1383 | 6 | unknown protein | - |
| **68876** | -1383 | -1377 | 6 | unknown protein | - |
| **68876** | -1377 | -1371 | 6 | unknown protein | - |
| **68876** | -1371 | -1365 | 6 | unknown protein | - |

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|---|---|---|---|---|---|
| **111439** | -1420 | -1402 | 18 | unknown protein | - |
| **68948** | -1395 | -1389 | 6 | unknown protein | - |
| **68948** | -1389 | -1383 | 6 | unknown protein | - |
| **123955** | -59 | -50 | 9 | unknown protein | - |
| **81979** | -1125 | -1116 | 9 | unknown protein | - |
| **104071** | -1404 | -1398 | 6 | unknown protein | - |
| **104419** | -17 | -11 | 6 | unknown protein | - |
| **56218** | -428 | -400 | 28 | unknown protein | - |
| **41699** | -920 | -896 | 24 | unknown protein | - |
| **57534** | -660 | -653 | 7 | unknown protein | - |
| **75935** | -879 | -869 | 10 | unknown protein | - |
| **105176** | -68 | -62 | 6 | unknown protein | - |
| **59073** | -774 | -767 | 7 | unknown protein | - |
| **58282** | -1373 | -1364 | 9 | unknown protein | - |
| **121091** | -1179 | -1154 | 25 | unknown protein | - |
| **106154** | -323 | -296 | 27 | unknown protein | - |
| **121337** | -741 | -735 | 6 | unknown protein | - |
| **106452** | -923 | -902 | 21 | unknown protein | - |
| **106452** | -726 | -720 | 6 | unknown protein | - |
| **60578** | -1093 | -1087 | 6 | unknown protein | - |
| **60422** | -21 | -12 | 9 | unknown protein | - |
| **107111** | -38 | -19 | 19 | unknown protein | - |
| **48178** | -71 | -41 | 30 | unknown protein | - |
| **54352** | -1375 | -1369 | 6 | unknown protein | - |
| **54426** | -343 | -334 | 9 | unknown protein | - |
| **103130** | -965 | -959 | 6 | unknown protein | - |
| **62198** | -1023 | -994 | 29 | unknown protein | - |
| **78706** | -1025 | -1016 | 9 | unknown protein | - |

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|---|---|---|---|---|---|
| **78706** | -1016 | -1007 | 9 | unknown protein | - |
| **78706** | -197 | -176 | 21 | unknown protein | - |
| **71676** | -231 | -222 | 9 | unknown protein | - |
| **63648** | -453 | -444 | 9 | unknown protein | - |
| **43418** | -1062 | -1043 | 19 | unknown protein | - |
| **65808** | -1246 | -1240 | 6 | unknown protein | - |
| **123256** | -1330 | -1321 | 9 | unknown protein | - |
| **103563** | -1396 | -1390 | 6 | unknown protein | - |
| **80685** | -1479 | -1472 | 7 | unknown protein | - |
| **80685** | -1472 | -1465 | 7 | unknown protein | - |
| **80685** | -1465 | -1458 | 7 | unknown protein | - |
| **67035** | -958 | -950 | 8 | unknown protein | - |
| **81149** | -1475 | -1461 | 14 | unknown protein | - |
| **51907** | -1468 | -1439 | 29 | unknown protein | - |
| **72488** | -369 | -356 | 13 | unknown protein | - |
| **56531** | -703 | -691 | 12 | unknown protein | - |
| **120407** | -1136 | -1127 | 9 | unknown protein | - |
| **75394** | -282 | -259 | 23 | unknown protein | - |
| **56259** | -530 | -508 | 22 | unknown protein | - |
| **111991** | -603 | -594 | 9 | unknown protein | - |
| **111991** | -594 | -588 | 6 | unknown protein | - |
| **111991** | -588 | -570 | 18 | unknown protein | - |
| **112212** | -223 | -196 | 27 | unknown protein | - |
| **105389** | -403 | -383 | 20 | unknown protein | - |
| **105520** | -761 | -755 | 6 | unknown protein | - |
| **105520** | -755 | -743 | 12 | unknown protein | - |
| **105520** | -743 | -737 | 6 | unknown protein | - |
| **105520** | -737 | -731 | 6 | unknown protein | - |

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|---|---|---|---|---|---|
| **105524** | -995 | -986 | 9 | unknown protein | - |
| **58634** | -744 | -738 | 6 | unknown protein | - |
| **121355** | -1442 | -1414 | 28 | unknown protein | - |
| **106444** | -1374 | -1358 | 16 | unknown protein | - |
| **60004** | -1409 | -1388 | 21 | unknown protein | - |
| **60004** | -1212 | -1206 | 6 | unknown protein | - |
| **60897** | -234 | -220 | 14 | unknown protein | - |
| **60665** | -1234 | -1224 | 10 | unknown protein | - |
| **3739** | -1305 | -1288 | 17 | unknown protein | - |
| **121638** | -177 | -171 | 6 | unknown protein | - |
| **32204** | -29 | -14 | 15 | unknown protein | - |
| **33058** | -769 | -757 | 12 | unknown protein | - |
| **59703** | -1203 | -1178 | 25 | unknown protein | - |
| **66865** | -83 | -65 | 18 | unknown protein | - |
| **55698** | -960 | -950 | 10 | unknown protein | - |
| **34353** | -1035 | -1029 | 6 | unknown protein | - |
| **65817** | -1389 | -1383 | 6 | unknown protein | - |
| **32293** | -815 | -792 | 23 | unknown protein | - |
| **32293** | -93 | -69 | 24 | unknown protein | - |
| **42953** | -794 | -776 | 18 | unknown protein | - |
| **26163** | -291 | -270 | 21 | unknown protein | - |

*Positions of Sites 1 and 2 are relative to the gene start codon.