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Function
glycine-rich protein similar to H41 gene for histone protein GB:X15142 GI:3204 [Physarum polycephalum]
proline-rich family protein contains proline-rich extensin domains, INTERPRO:IPR002965
expressed protein
expressed protein
glycine/proline-rich protein contains similarity to flagelliform silk protein [Nephila clavipes] gi|7106224|gb|AAF360
oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to SP|Q9ZWQ9 Flavonol synthase (EC 1.14.11.-) {
expressed protein ; expression supported by MPSS
early-responsive to dehydration protein-related / ERD protein-related similar to ERD4 protein (early-responsive t
glycosyl transferase family 2 protein similar to cellulose synthase from Agrobacterium tumeficiens [gi:710492] an
peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein weak similarity to CARS-Cyp [Homo sapiens]
PAZ domain-containing protein / piwi domain-containing protein similar to SP|Q9XGW1 PINHEAD protein (ZWIL
MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:122312
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
delta 7-sterol-C5-desaturase, putative similar to delta7 sterol C-5 desaturase GI:5031219 from [Arabidopsis thali
potassium transporter family protein similar to HAK2 [Hordeum vulgare] GI:7108599, potassium transporter [Ara
peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein similar to cyclophylin [Digitalis lanata] GI:15637
proline-rich extensin-like family protein contains proline-rich extensin domains, INTERPRO:IPR002965
auxin efflux carrier protein, putative (PIN1) identical to putative auxin efflux carrier protein; AtPIN1 [Arabidopsis t
glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein similar to polygalacturonase
sec61beta family protein similar to SP|P52870 Protein transport protein SEC61 beta 1 subunit {Saccharomyces
sec61beta family protein similar to SP|P52870 Protein transport protein SEC61 beta 1 subunit {Saccharomyces
RNA-binding protein, putative similar to RNA-binding protein from [Solanum tuberosum] GI:15822705, [Nicotiana
thioredoxin family protein contains Pfam profile: PF00085 thioredoxin
universal stress protein (USP) family protein similar to ER6 protein [Lycopersicon esculentum] GI:5669654; cont
glycine-rich protein
senescence-associated family protein similar to senescence-associated protein 5 [Hemerocallis hybrid cultivar] g
expressed protein
oligouridylate-binding protein, putative similar to oligouridylate binding protein [Nicotiana plumbaginifolia] GI:699
sporozoite surface protein-related contains weak similarity to Sporozoite surface protein 2 precursor (Swiss-Prot
cytochrome P450, putative
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to 14 kDa polypeptide [Catharan
auxin-responsive AUX/IAA family protein identical to IAA14 (GI:972931) [Arabidopsis thaliana]; similar to SP|Q38
expressed protein
heavy-metal-associated domain-containing protein similar to farnesylated protein 1 (GI:23304411) {Hordeum vul
zinc finger (C3HC4-type RING finger) family protein similar to RING-H2 finger protein RHX1a [Arabidopsis thalia
MADS-box protein (AGL12) identical to GB:AAC49085 GI:862650 from (Arabidopsis thaliana) (Plant Cell 7 (8), 1
cryptochrome 1 apoprotein (CRY1) / flavin-type blue-light photoreceptor (HY4) contains Pfam PF03441: FAD bin
expressed protein
expressed protein
arginine/serine-rich splicing factor RSP41 (RSP41) nearly identical to SP|P92966 Arginine/serine-rich splicing fa
expressed protein similar to PrMC3 [Pinus radiata] GI:5487873
myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain
auxin-responsive protein / indoleacetic acid-induced protein 7 (IAA7) identical to SP|Q38825|AXI7_ARATH Auxin
hypothetical protein
calcium-dependent protein kinase, putative / CDPK, putative similar to calcium-dependent protein kinase, isoform
SC35-like splicing factor, 30a kD (SCL30a) almost identical to SC35-like splicing factor SCL30a GI:9843661 from
expressed protein

arginine/serine-rich splicing factor SC35 contains similarity to splicing factor; contains Pfam profile PF00076: RN
arginine/serine-rich splicing factor SC35 contains similarity to splicing factor; contains Pfam profile PF00076: RN
syntaxin, putative (SYP124) similar to syntaxin-related protein Nt-syr1 GI:4206787 from [Nicotiana tabacum]
glycine-rich protein
expressed protein contains Pfam domain, PF04578: Protein of unknown function, DUF594; expression supporte
tetratricopeptide repeat (TPR)-containing protein contains Pfam profile PF00515: TPR Domain
expressed protein
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam profile: PF00234 proteas
arginine/serine-rich splicing factor RSP41 (RSP41) nearly identical to SP|P92966 Arginine/serine-rich splicing fa
hypothetical protein
receptor-like protein kinase-related contains Pfam profile: PF01657 Domain of unknown function that is usually a
late embryogenesis abundant domain-containing protein / LEA domain-containing protein low similarity to LEA pr
expressed protein
expressed protein
expressed protein ; expression supported by MPSS
expressed protein
glycine-rich protein / late embryogenesis abundant protein (M17) identical to late-embryogenesis abundant M17
expressed protein
serine/threonine protein phosphatase, putative nearly identical to serine/threonine protein phosphatase [Arabido
two-component responsive regulator family protein / response regulator family protein contains Pfam profile: PF0
disease resistance-responsive family protein / fibroin-related contains similarity to silk fibroin heavy chain [Bomby
cell divsion control protein, putative similar to SWISS-PROT:P25859 cell division control protein 2 homolog B [Ar
cysteine protease inhibitor, putative / cystatin, putative similar to SP|P09229 Cysteine proteinase inhibitor-I (Oryz
glucose-1-phosphate adenylyltransferase large subunit 1 (APL1) / ADP-glucose pyrophosphorylase (ADG2) iden
floral homeotic protein APETALA1 (AP1) / agamous-like MADS box protein (AGL7) identical to SP|P35631 Flora
expressed protein
protein kinase family protein contains protein kinase domain, Pfam:PF00069
hypothetical protein
hypothetical protein
cation/hydrogen exchanger, putative (CHX27) monovalent cation:proton antiporter family 2 (CPA2) member, PM
F-box family protein contains F-box domain Pfam:PF00646 ; similar to SKP1 interacting partner 2 (SKIP2) TIGR
hypothetical protein
strictosidine synthase family protein similar to strictosidine synthase [Rauvolfia serpentina][SP|P15324]; contains
CHP-rich zinc finger protein, putative contains similarity to CHP-rich zinc finger protein
auxin-responsive GH3 protein, putative (DFL-1) identical to auxin-responsive GH3 homologue [Arabidopsis thalia
heavy-metal-associated domain-containing protein similar to farnesylated protein ATFP3 [GI:4097547]; contains
zinc finger (Ran-binding) family protein weak similarity to SP|Q01844 RNA-binding protein EWS (EWS oncogene
zinc finger (Ran-binding) family protein weak similarity to SP|Q01844 RNA-binding protein EWS (EWS oncogene
auxin-responsive protein / indoleacetic acid-induced protein 7 (IAA7) identical to SP|Q38825|AXI7_ARATH Auxin
proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family
expressed protein contains Pfam profile PF04749: Protein of unknown function, DUF614; expression supported
cyclic nucleotide-binding transporter 1 / CNBT1 (CNGC20) identical to cyclic nucleotide-binding transporter 1 (CI
ARF GTPase-activating domain-containing protein similar to GCN4-complementing protein (GCP1) GI:6465806
expressed protein contains Pfam profile PF04146: YT521-B-like family
broad-spectrum mildew resistance RPW8 family protein contains Pfam PF05659: Arabidopsis broad-spectrum m
translocon-associated protein alpha (TRAP alpha) family protein contains Pfam profile: PF03896 translocon-asso
thioredoxin family protein similar to thioredoxin [Nicotiana tabacum] GI:20047; contains Pfam profile: PF00085 T
sulfate transporter (ST1) identical to sulfate transporter [Arabidopsis thaliana] GI:2285885

aminotransferase, putative similar to nicotianamine aminotransferase from Hordeum vulgare [GI:6498122, GI:64
cytochrome P450 family protein contains Pfam PF00067: Cytochrome P450; similar to Cytochrome P450 86A2
F-box family protein contains F-box domain Pfam:PF00646
cytochrome P450 83B1 (CYP83B1) Identical to Cytochrome P450 (SP:O65782)[Arabidopsis thaliana]
myb family transcription factor (MYB4) contains Pfam profile: PF00249 myb-like DNA-binding domain
hypothetical protein
mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein
acyl CoA reductase, putative similar to acyl CoA reductase [Simmondsia chinensis] GI:5020215; contains Pfam
zinc knuckle (CCHC-type) family protein contains Pfam domain, PF00098: Zinc knuckle
calcium-dependent protein kinase, putative / CDPK, putative similar to calcium-dependent protein kinase GB:AA
arginine/serine-rich splicing factor RSP40 (RSP40) identical to SP|P92965 Arginine/serine-rich splicing factor RS
phospholipase/carboxylesterase family protein similar to lysophospholipase I [Mus musculus] GI:1864159; conta
basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
jacalin lectin family protein similar to myrosinase binding protein [Brassica napus] GI:1711296, myrosinase-bindi
protein kinase family protein / peptidoglycan-binding LysM domain-containing protein contains protein kinases A
invertase/pectin methylesterase inhibitor family protein low similarity to pectinesterase from Lycopersicon escule
lipocalin, putative similar to temperature stress-induced lipocalin [Triticum aestivum] GI:18650668
pentatricopeptide (PPR) repeat-containing protein contains INTERPRO:IPR002885 PPR repeats
remorin family protein contains Pfam domain, PF03763: Remorin, C-terminal region
lectin protein kinase family protein contains Pfam domains, PF01453: Lectin (probable mannose binding) and PF
nodulin MtN21 family protein similar to MtN21 GI:2598575 (root nodule development) from [Medicago truncatula
DNA-binding protein-related contains similarity to DNA-binding protein GI:170271 from [Nicotiana tabacum]
zinc finger (Ran-binding) family protein contains Pfam domain, PF00641: Zn-finger in Ran binding protein and ot
chitinase, putative similar to basic endochitinase CHB4 precursor SP:Q06209 from [Brassica napus]
hypothetical protein
expressed protein contains Pfam profile PF04525: Protein of unknown function (DUF567)
leucine-rich repeat transmembrane protein kinase, putative
calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase
serine carboxypeptidase S10 family protein similar to glucose acyltransferase GB:AAD01263 [Solanum berthaul
hypothetical protein contains Pfam PF04510 : Family of unknown function (DUF577)); common family comprised
MD-2-related lipid recognition domain-containing protein / ML domain-containing protein contains Pfam profile P
F-box family protein ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250
expressed protein
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein identical to pEARLI 1 (Accession No. L4
PHD finger family protein contains Pfam domain, PF00628: PHD-finger
glycosyl hydrolase family 17 protein similar to beta-1,3-glucanase precursor GI:4097946 from [Oryza sativa]
DC1 domain-containing protein contains Pfam protein PF03107 DC1 domain
zinc transporter (ZIP1) identical to putative zinc transporter GB:AAC24197 from [Arabidopsis thaliana], (Proc. N
expressed protein
oxidoreductase, 2OG-Fe(II) oxygenase family protein low similarity to alkB protein - Escherichia coli, PIR:BVECK
dehydration-responsive protein-related similar to early-responsive to dehydration stress ERD3 protein [Arabidop
leucine-rich repeat transmembrane protein kinase, putative contains leucine rich repeat (LRR) domains, Pfam:P
proline-rich family protein
expressed protein
cytochrome P450, putative similar to Cytochrome P450 72A1 (SP:Q05047) [Catharanthus roseus];
self-incompatibility protein-related similar to S3 self-incompatibility protein [Papaver rhoeas] GI:1107841
hypothetical protein contains Pfam profile: PF04842 plant protein of unknown function (DUF639)
cytochrome P450, putative similar to cytochrome p450 GI:438242 from [Solanum melongena]

protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains protease inhibitor/seed storage
expressed protein
gibberellin-responsive protein, putative similar to SP|P46689 Gibberellin-regulated protein 1 precursor {Arabidop
glycine-rich protein / late embryogenesis abundant protein (M17) identical to late-embryogenesis abundant M17
trehalose-6-phosphate synthase, putative similar to Alpha,alpha-trehalose-phosphate synthase [UDP-forming] (E
phosphatidylinositol 3- and 4-kinase family protein low similarity to 55 kDa type II phosphatidylinositol 4-kinase [F
S-adenosyl-L-methionine:carboxyl methyltransferase family protein similar to SAM:jasmonic acid carboxyl methy
amino acid permease family protein weak similarity to GABA permease [Emericella nidulans] GI:4972245; conta
hypothetical protein
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed s
expressed protein
senescence-associated protein, putative similar to senescence-associated protein 5 [Hemerocallis hybrid cultiva
U5 small nuclear ribonucleoprotein helicase, putative
F-box family protein contains F-box domain Pfam:PF00646
WD-40 repeat family protein / auxin-dependent protein (ARCA) / guanine nucleotide-binding protein beta subunit
thioredoxin family protein contains Pfam profile: PF00085 Thioredoxin; similar to ESTs gb|T46281, gb|R83933, g
expressed protein
hypothetical protein
pentatricopeptide (PPR) repeat-containing protein low similarity to post-transcriptional control of chloroplast gene
WRKY family transcription factor
nodulin MtN21 family protein similar to MtN21 GI:2598575 (root nodule development) from [Medicago truncatula
expressed protein
seven in absentia (SINA) family protein low similarity to siah-1A protein [Mus musculus] GI:297035; contains Pfa
hypothetical protein
disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of
branched-chain amino acid aminotransferase 1 / branched-chain amino acid transaminase 1 (BCAT1) nearly ide
cytochrome B561-related related to cytochrome b-561 (GI:20345443) [Mus musculus]; multidrug resistance prot
cytochrome P450, putative similar to cytochrome P450 GI:4688670 from [Catharanthus roseus]
myb family transcription factor (MYB123) contains PFAM profile: myb DNA-binding domain PF00249
expressed protein
CER1 protein, putative similar to CER1 GI:1199467 and maize gl1 homolog (glossy1 locus) GI:1209703 from [Ar
expressed protein
expressed protein contains Pfam profile PF04749: Protein of unknown function, DUF614
hypothetical protein
xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan trans
expressed protein similar to hypothetical protein GI:6524175 from [Arabidopsis thaliana]
beta-ketoacyl-CoA synthase family (FIDDLEHEAD) (FDH) identical to GB:AJ010713 (fiddlehead protein)
lipase class 3 family protein contains Pfam profile PF01764: Lipase
methyltransferase MT-A70 family protein low similarity to SP|P25583 Karyogamy protein KAR4 {Saccharomyces
light-responsive receptor protein kinase / senescence-responsive receptor-like serine/threonine kinase, putative
Ras-related GTP-binding protein, putative similar to GTP-binding protein RAB7A from [Lotus japonicus]
MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:122312
zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RI
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to pEARLI 1 (Accession No. L43
auxin efflux carrier family protein contains auxin efflux carrier domain, Pfam:PF03547
cinnamyl-alcohol dehydrogenase (CAD) identical to SP|P48523 Cinnamyl-alcohol dehydrogenase (EC 1.1.1.195
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to pEARLI 1 (Accession No. L43
tRNA synthetase class II (G, H, P and S) family protein similar to SP|O23627 Glycyl-tRNA synthetase (EC 6.1.1.

myb family transcription factor contains Pfam profile: PF00249 Myb DNA binding domain
semialdehyde dehydrogenase family protein similar to SP:O31219 Aspartate-semialdehyde dehydrogenase (EC
PQ-loop repeat family protein / transmembrane family protein similar to SP|Q10482 Seven transmembrane prote
CER1 protein, putative similar to CER1 GI:1199467 and maize gl1 homolog (glossy1 locus) GI:1209703 from [Ar
AP2 domain-containing protein RAP2.1 (RAP2.1) identical to AP2 domain containing protein RAP2.1 GI:228162
cold-shock DNA-binding family protein contains Pfam domains, PF00313: 'Cold-shock' DNA-binding domain and
cation/hydrogen exchanger, putative (CHX13) monovalent cation:proton antiporter family 2 (CPA2) member, PM
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to pEARLI 1 (Accession No. L43
transporter-related low similarity to D-xylose proton-symporter [Lactobacillus brevis] GI:2895856; contains Pfam
C2 domain-containing protein contains INTERPRO:IPR000008 C2 domain
expressed protein contains similarity to carboxyl-terminal proteinase contains Pfam profile PF03080: Arabidopsis
trihelix DNA-binding protein, putative similar to DNA-binding protein DF1 [Pisum sativum] GI:13646986
MADS-box protein (AGL13)
paired amphipathic helix repeat-containing protein similar to Sin3 protein [Yarrowia lipolytica] GI:18076824; conta
F-box family protein contains F-box domain Pfam:PF00646
expressed protein
glycosyl transferase family 20 protein / trehalose-phosphatase family protein contains Pfam profile: PF02358 trel
chloroplast outer membrane protein, putative similar to chloroplast protein import component Toc159 [Pisum sati
secY family protein low similarity to SP|P31159 Preprotein translocase secY subunit {Synechococcus sp}; contai
potassium transporter family protein similar to HAK2 [Hordeum vulgare] GI:7108599, potassium transporter HAK
galactinol synthase, putative similar to galactinol synthase, isoform GolS-1 GI:5608497 from [Ajuga reptans]
mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein
phosphatidylinositol 3- and 4-kinase family protein low similarity to phosphatidylinositol 4-kinase type-II beta [Hor
hypothetical protein
nodulin family protein similar to nodulin-like protein [Arabidopsis thaliana] GI:3329368, nodule-specific protein Nl
amino acid permease family protein weak similarity to GABA permease [Emericella nidulans] GI:4972245; conta
fip1 motif-containing protein contains Pfam profile PF05182: Fip1 motif
protein kinase family protein contains eukaryotic protein kinase domain, INTERPRO:IPR000719
hypothetical protein
phytochrome kinase substrate 1 (PKS1) identical to Swiss-Prot:Q9SWI1 phytochrome kinase substrate 1 [Arabid
hypothetical protein
cell elongation protein / DWARF1 / DIMINUTO (DIM) identical to GB:S71189 [SP|Q39085] from [Arabidopsis tha
cell elongation protein / DWARF1 / DIMINUTO (DIM) identical to GB:S71189 [SP|Q39085] from [Arabidopsis tha
glutamate receptor family protein (GLR1.2) plant glutamate receptor family, PMID:11379626
glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein weak similarity to polygalact
expressed protein contains Pfam profile: PF01363 FYVE zinc finger
pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
expressed protein
DC1 domain-containing protein contains Pfam protein PF03107 DC1 domain
protein kinase family protein contains Pfam domains, PF00069: Protein kinase domain
transport inhibitor response protein, putative E3 ubiquitin ligase SCF complex F-box subunit; similar to transport
leucine-rich repeat transmembrane protein kinase, putative Cf-2.2, Lycopersicon pimpinellifolium, PIR:T10515
U2 snRNP auxiliary factor small subunit, putative Strong similarity to gb|Y18349 U2 snRNP auxiliary factor, smal
protein kinase, putative contains protein kinase domain, Pfam:PF00069
glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIG
annexin 4 (ANN4) nearly identical to annexin (AnnAt4) [Arabidopsis thaliana] GI:6503084; contains Pfam profile
eukaryotic translation initiation factor SUI1, putative similar to P|P32911 Protein translation factor SUI1 {Sacchar

phytochrome kinase, putative contains similarity to Swiss-Prot:Q9SWI1 phytochrome kinase substrate 1 [Arabid
expansin, putative (EXP20) similar to alpha-expansin 3 GI:6942322 from [Triphysaria versicolor]; alpha-expansi
helicase-related similar to CHL1 potential helicase protein (GI:2632247) [Homo sapiens]; similar to helicase GB:
hypothetical protein and grail contains Pfam profile PF03080: Arabidopsis proteins of unknown function
expressed protein contains Pfam profile PF03087: Arabidopsis protein of unknown function
disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of
signal recognition particle receptor alpha subunit family protein similar to Signal recognition particle receptor alp
acyl CoA reductase, putative similar to acyl CoA reductase [Simmondsia chinensis] GI:5020215; contains Pfam
S-adenosyl-L-methionine:carboxyl methyltransferase family protein similar to defense-related protein cjs1 [Brass
hypothetical protein
expressed protein
hypothetical protein
26S proteasome AAA-ATPase subunit, putative similar to 26S proteasome AAA-ATPase subunit RPT1 SP:Q41
expressed protein contains Pfam profile: PF05097 protein of unknown function (DUF688)
membrane protein, putative similar to membrane protein SDR2 (GI:1747306) [Mus musculus]
expressed protein ; expression supported by MPSS
disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a
SPX (SYG1/Pho81/XPR1) domain-containing protein similar to PHO1 protein [Arabidopsis thaliana] GI:2006903
glycosyl transferase family 20 protein / trehalose-phosphatase family protein similar to trehalose-6-phosphate sy
chloride channel protein (CLC-a) identical to GI:1742952 (gb|AAC05742.1)
cyclophilin-RNA interacting protein, putative
sterile alpha motif (SAM) domain-containing protein contains Pfam profile PF00536: SAM domain (Sterile alpha
tetratricopeptide repeat (TPR)-containing protein contains Pfam profile PF00515 TPR Domain; similar to infertilit
proline transporter 2 (ProT2) identical to proline transporter 2 GI:1769903 from [Arabidopsis thaliana]
dehydrin family protein contains Pfam domain, PF00257: Dehydrin
leucine-rich repeat transmembrane protein kinase, putative
glutamate receptor family protein (GLR1.2) plant glutamate receptor family, PMID:11379626
zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein contains InterPro entry
myb family transcription factor similar to myb-related transcription factor (cpm10) GB:U33915 GI:1002795 from [
IWS1 C-terminus family protein contains Pfam profile PF05909: IWS1 C-terminus
sporulation protein-related isoform contains non-consensus AT-donor acceptor site at intron 6; similar to Stage II
glycine-rich protein contains non-consensus GG donor splice site at exon2; modeled to est match.
serine carboxypeptidase S10 family protein contains Pfam profile: PF00450 serine carboxypeptidase; similar to s
UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl a
nitrate transporter (NTP3) nearly identical to nitrate transporter [Arabidopsis thaliana] GI:4490323; contains Pfam
expressed protein contains Pfam profile: PF01925 domain of unknown function DUF81
RNA polymerase sigma subunit SigE (sigE) / sigma-like factor (SIG5) identical to RNA polymerase sigma subuni
sugar transporter family protein similar to D-xylose proton-symporter [Lactobacillus brevis] GI:2895856; contains
apoptosis inhibitory protein 5 (API5)-related contains weak hit to Pfam profile PF05918: Apoptosis inhibitory prot
expressed protein
CAX-interacting protein 4 (CAXIP4) contains Pfam domain PF00098: Zinc knuckle; identical to cDNA CAX-intera
expressed protein
thiamin pyrophosphokinase, putative similar to thiamin pyrophosphokinase [Mus musculus] gi|6468206|dbj|BAA8
polyadenylate-binding protein 5 (PABP5) identical to GB:Q05196 from [Arabidopsis thaliana]
calcineurin B-like protein 3 (CBL3) identical to calcineurin B-like protein 3 (GI:22136404) [Arabidopsis thaliana]
expressed protein
expressed protein similar to unknown protein (gb|AAB72163.1)
heavy-metal-associated domain-containing protein similar to farnesylated protein 1 (GI:23304411) {Hordeum vul

dynamin-like protein 6 (ADL6) identical to dynamin-like protein 6 (ADL6) [Arabidopsis thaliana] GI:6651399; cont
esterase, putative similar to ethylene-induced esterase [Citrus sinensis] GI:14279437, polyneuridine aldehyde es
early-responsive to dehydration protein-related / ERD protein-related similar to ERD4 protein (early-responsive t
ubiquitin activating enzyme, putative (ECR1) identical to putative ubiquitin activating enzyme E1 [Arabidopsis tha
serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza s
expressed protein contains Pfam profile PF01027: Uncharacterized protein family UPF0005
senescence-associated family protein similar to senescence-associated protein 5 [Hemerocallis hybrid cultivar] g
disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of
cation/hydrogen exchanger, putative (CHX17) similar to Na+/H+-exchanging protein slr1595 - Synechocystis sp.
beta-ketoacyl-CoA synthase family protein similar to GB:AAC99312 from [Arabidopsis thaliana] (Plant J. (1999) I
arginine/serine-rich splicing factor RSP40 (RSP40) identical to SP|P92965 Arginine/serine-rich splicing factor RS
rRNA processing protein-related contains weak similarity to rRNA processing protein EBP2 (EBNA1-binding prot
expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538
F-box family protein predicted protein, Caenorhabditis elegans, PIR2:S44609 ; similar to SKP1 interacting partne
major intrinsic family protein / MIP family protein contains Pfam profile: MIP PF00230
S1 RNA-binding domain-containing protein similar to SP|Q05022 rRNA biogenesis protein RRP5 {Saccharomyce
cyclic nucleotide-regulated ion channel / cyclic nucleotide-gated channel (CNGC1) almost identical to cyclic nucl
glycine-rich protein (GRP17) olesin; glycine-rich protein 17 (GRP17) PMID:11431566; function: pollen recognitio
myb family transcription factor (MYB38) contains Pfam profile: PF00249 myb-like DNA-binding domain
NAD-dependent epimerase/dehydratase family protein similar to nucleotide sugar epimerase from Vibrio vulnific
forkhead-associated domain-containing protein / FHA domain-containing protein weak similarity to SP|Q28147 N
expressed protein hypothetical protein - Synechocystis sp. (strain PCC 6803), PIR:S75899
hypothetical protein
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
sterile alpha motif (SAM) domain-containing protein contains Pfam profile PF00536: SAM domain (Sterile alpha
serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II chains A and B (SP:P08819) (E
glycosyl hydrolase family 35 protein similar to beta-galactosidase BG1 GI:15081596 from [Vitis vinifera]
40S ribosomal protein S3 (RPS3C)
phosphatidylinositol 3- and 4-kinase family protein low similarity to phosphatidylinositol 4-kinase type-II beta [Ho
leucine-rich repeat transmembrane protein kinase, putative may contain C-terminal ser/thr protein kinase domai
protein kinase, putative (MRK1) identical to ATMRK1 [Arabidopsis thaliana] gi|2351097|dbj|BAA22079
expressed protein
expressed protein
expressed protein
ADP-ribosylation factor identical to GP:166586 ADP-ribosylation factor {Arabidopsis thaliana}; ADP-ribosylation f
hydrolase, alpha/beta fold family protein low similarity to SP|Q40708 PIR7A protein {Oryza sativa}, polyneuridine
hypothetical protein
disease resistance protein RPP1-Ws[A,C]-like (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR e
disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of
cyclic nucleotide-binding transporter 2 / CNBT2 (CNGC19) identical to cyclic nucleotide-binding transporter 2 (CI
myb family transcription factor (MYB66) / werewolf (WER) contains PFAM profile: Myb DNA binding domain PF0
F-box family protein contains Pfam:PF00646 F-box domain ; similar to SKP1 interacting partner 2 (SKIP2) TIGR
expressed protein predicted proteins, Arabidopsis thaliana Pfam profile PF03080: Arabidopsis proteins of unknow
sec61beta family protein similar to SP|P52870 Protein transport protein SEC61 beta 1 subunit {Saccharomyces
calcium-dependent protein kinase 9 (CDPK9) identical to calcium-dependent protein kinase [Arabidopsis thaliana
cinnamyl-alcohol dehydrogenase, putative similar to cinnamyl alcohol dehydrogenase, Nicotiana tabacum [SP|P
loricrin-related contains weak similarity to Loricrin (Swiss-Prot:P23490) [Homo sapiens]
nodulin-related low similarity to MtN21 [Medicago truncatula] GI:2598575; contains Pfam profile PF00892: Integr

ribosomal protein L10A family protein contains similarity to Swiss-Prot:P53029 ribosomal protein L10A [Arabidop
potassium channel tetramerisation domain-containing protein contains Pfam profile PF02214: K+ channel tetram
expressed protein contains Pfam domain PF05003: protein of unknown function (DUF668)
protein kinase family protein contains protein kinase domain, Pfam:PF00069; similar to receptor-like serine/threo
expressed protein similar to H1-1flk [Arabidopsis thaliana] GI:388260
Ras-related GTP-binding protein, putative similar to GTP-binding protein RAB7A from [Lotus japonicus]
thiamin pyrophosphokinase, putative similar to thiamin pyrophosphokinase [Mus musculus] gi|6468206|dbj|BAA8
expressed protein ; expression supported by MPSS
calmodulin-binding family protein contains IQ calmodulin-binding motif, Pfam:PF00612
myb family transcription factor (MYB79) contains PFASM profile: myb DNA binding domain PF00249; identical to
serine carboxypeptidase S10 family protein similar to GI:8777303 from [Arabidopsis thaliana] (DNA Res. 7 (1), 3
RNA recognition motif (RRM)-containing protein
cysteine proteinase, putative similar to cysteine endopeptidase precursor [Ricinus communis] GI:2944446; conta
pathogenesis-related protein, putative similar to pathogenesis-related protein 1b precursor (pr-1b) GB:X03465 G
expressed protein nearly identical to At1g24996, At1g25170, At1g25097; similar to ESTs dbj AV530941.1, dbj|AV
expressed protein nearly identical to At1g24996, At1g25170, At1g24822; similar to ESTs dbj AV530941.1, dbj|AV
expressed protein nearly identical to At1g24996, At1g25097, At1g24822
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase, putative / vitamin-B12-independent met
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase, putative / vitamin-B12-independent met
glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein weak similarity to SP|P2764
mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein
actin 7 (ACT7) / actin 2 identical to SP|P53492 Actin 7 (Actin-2) {Arabidopsis thaliana}
cyclin-related contains weak similarity to Swiss-Prot:P35662 cylicin I (Multiple-band polypeptide I) [Bos taurus]
expressed protein
invertase/pectin methylesterase inhibitor family protein low similarity to pectinesterase from Arabidopsis thaliana
bZIP transcription factor family protein similar to bZIP transcription factor GI:1769891 from [Arabidopsis thaliana]
omega-3 fatty acid desaturase, endoplasmic reticulum (FAD3) identical to SP:48623
glucose-methanol-choline (GMC) oxidoreductase family protein similar to mandelonitrile lyase from Prunus serot
expressed protein contains Pfam domain PF05003: protein of unknown function (DUF668); expression supporte
expressed protein
expressed protein
proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family
haloacid dehalogenase-like hydrolase family protein low similarity to genetic modifier [Zea mays] GI:10444400; c
haloacid dehalogenase-like hydrolase family protein low similarity to genetic modifier [Zea mays] GI:10444400; c
MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:122312
expressed protein contains Pfam domain, PF03650: Uncharacterized protein family (UPF0041)
chloride channel protein (CLC-c) identical to gi:1742956
branched-chain amino acid aminotransferase 1 / branched-chain amino acid transaminase 1 (BCAT1) nearly ide
remorin family protein contains Pfam domain, PF03763: Remorin, C-terminal region
multi-copper oxidase type I family protein similar to pollen-specific BP10 protein [SP|Q00624][Brassica napus]; c
zinc finger (C2H2 type) family protein contains Pfam domain PF00096: Zinc finger, C2H2 type
ABC transporter family protein similar to PDR5-like ABC transporter GI:1514643 from [Spirodela polyrhiza]
cytochrome P450, putative
calcineurin B-like protein 3 (CBL3) identical to calcineurin B-like protein 3 (GI:22136404) [Arabidopsis thaliana]
ADP-ribosylation factor, putative similar to ADP-ribosylation factor GI:166586 from [Arabidopsis thaliana]
glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIG
cytochrome P450 family protein similar to Cytochrome P450 86A2 (SP:O23066) [Arabidopsis thaliana]contains P
thiamin pyrophosphokinase, putative similar to thiamin pyrophosphokinase [Mus musculus] gi|6468206|dbj|BAA8

hypothetical protein
expressed protein similar to enterophilin-2L (GI:12718845) [Cavia porcellus]; similar to Hyaluronan mediated mo
protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain
gibberellin-regulated protein 1 (GASA1) / gibberellin-responsive protein 1 identical to SP|P46689 Gibberellin-reg
serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza s
alcohol oxidase-related similar to long chain fatty alcohol oxidase from Candida cloacae [GI:6983581], Candida
ABC transporter family protein similar to ATP-binding cassette, sub-family G, member 2 (Placenta-specific ATP-
glycine-rich protein
60S ribosomal protein L10A (RPL10aC)
expressed protein unusual splice site at second intron; GA instead of conserved GT at donor site; similar to At14
epoxide hydrolase, putative strong similarity to ATsEH [Arabidopsis thaliana] GI:1109600
60S ribosomal protein L10A (RPL10aB)
60S ribosomal protein L10A (RPL10aB)
expressed protein
protein kinase, putative similar to protein kinase [Arabidopsis thaliana] gi|1054633|emb|CAA63387; contains pro
plant defensin-fusion protein, putative contains a plant defensin motif, personal communication, Bart Thomma (E
dyskerin, putative / nucleolar protein NAP57, putative similar to SP|P40615 Dyskerin (Nucleolar protein NAP57)
DNAJ heat shock N-terminal domain-containing protein contains Pfam profile PF00226 DnaJ domain
hypothetical protein
GHMP kinase-related contains similarity to D-glycero-D-manno-heptose 7-phosphate kinase [Aneurinibacillus th
expressed protein
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase / vitamin-B12-independent methionine s
invertase/pectin methylesterase inhibitor family protein low similarity to pistil-specific gene sts15 [Solanum tuber
serine carboxypeptidase S10 family protein contains Pfam profile: PF00450 serine carboxypeptidase ;similar to s
cytochrome P450 71B20, putative (CYP71B2) identical to cytochrome P450 71B20 (SP:Q9LTM3) [Arabidopsis t
glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)
auxin-responsive AUX/IAA family protein contains Pfam profile: PF02309 AUX/IAA family
kelch repeat-containing F-box family protein similar to SKP1 interacting partner 4 [Arabidopsis thaliana] GI:1071
leucine-rich repeat transmembrane protein kinase, putative
bacterial hemolysin-related similar to hemolysine GB:AAD36643 from [Thermotoga maritima], contains Pfam pro
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
DNAJ chaperone C-terminal domain-containing protein contains Pfam profile PF01556: DnaJ C terminal region
ubiquitin-specific protease 27, putative (UBP27) similar to GI:11993494; ubiquitin specific protease 66 - Gallus g
myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain
no apical meristem (NAM) family protein contains Pfam PF02365 : No apical meristem (NAM) protein; similar to
senescence-associated family protein similar to senescence-associated protein 5 [Hemerocallis hybrid cultivar] g
hypothetical protein
zinc finger protein-related similar to SP|Q09472 E1A-associated protein p300 {Homo sapiens}, SP|Q92793 CRE
phosphate translocator-related low similarity to SP|P52178 Triose phosphate/phosphate translocator, non-green
hypothetical protein
protein kinase, putative (MRK1) identical to ATMRK1 [Arabidopsis thaliana] gi|2351097|dbj|BAA22079
myb family transcription factor (MYB20) similar to myb-related transcription factor GI:1430846 from [Lycopersico
dormancy/auxin associated family protein contains Pfam profile: PF05564 dormancy/auxin associated protein
expressed protein
protein kinase, putative contains protein kinase domain, Pfam:PF00069
eukaryotic translation initiation factor 1A, putative / eIF-1A, putative / eIF-4C, putative strong similarity to translat
F-box family protein-related contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain; simila
zinc finger (GATA type) family protein contains Pfam profile:PF00320 GATA:GATA zinc finger

expressed protein similar to NLPE1 (GI:13022100) [Rhizobium etli];
expressed protein
cytochrome P450 family protein
expressed protein similar to H1-1flk [Arabidopsis thaliana] GI:388260
anion exchange protein family contains similarity to SWISS-PROT:P02730 anion transport protein (Anion exchar
calmodulin-binding protein-related contains similarity to potato calmodulin-binding protein PCBP GI:17933110 fro
basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 Helix-loop-helix DNA-binding domain
zinc finger homeobox family protein / ZF-HD homeobox family protein hypothetical protein T8K22.16, Arabidopsi
superoxide dismutase [Fe], chloroplast (SODB) / iron superoxide dismutase (FSD1) identical to Fe-superoxide d
superoxide dismutase [Fe], chloroplast (SODB) / iron superoxide dismutase (FSD1) identical to Fe-superoxide d
superoxide dismutase [Fe], chloroplast (SODB) / iron superoxide dismutase (FSD1) identical to Fe-superoxide d
thiamin pyrophosphokinase, putative similar to thiamin pyrophosphokinase [Mus musculus] gi|6468206|dbj|BAA8
hypothetical protein IB1C3-1 protein, Arabidopsis thaliana, AJ011845 contains Pfam profile PF03080: Arabidopsi
xyloglucan fucosyltransferase family protein contains Pfam profile: PF03254 xyloglucan fucosyltransferase
heat shock protein, putative strong similarity to SP|P55737 Heat shock protein 81-2 (HSP81-2) {Arabidopsis thal
purine permease-related low similarity to purine permease [Arabidopsis thaliana] GI:7620007; contains Pfam pro
expressed protein
OTU-like cysteine protease family protein contains Pfam profile PF02338: OTU-like cysteine protease
dormancy/auxin associated family protein contains Pfam profile: PF05564 dormancy/auxin associated protein
hypothetical protein
expressed protein
phospholipase/carboxylesterase family protein low similarity to lysophospholipase I [Mus musculus] GI:1864159;
eukaryotic translation initiation factor 4A-2 / eIF-4A-2 similar to eukaryotic translation initiation factor 4A GI:1969
OTU-like cysteine protease family protein contains Pfam profile PF02338: OTU-like cysteine protease
auxin-responsive protein / indoleacetic acid-induced protein 9 (IAA9) identical to SP|Q38827 Auxin-responsive p
auxin-responsive protein / indoleacetic acid-induced protein 9 (IAA9) identical to SP|Q38827 Auxin-responsive p
heat shock protein 81-2 (HSP81-2) nearly identical to SP|P55737 Heat shock protein 81-2 (HSP81-2) {Arabidops
DNA-binding family protein contains Pfam domain, PF02178: AT hook motif
prenylated rab acceptor (PRA1) family protein contains Pfam profile PF03208: Prenylated rab acceptor (PRA1)
fructokinase-related similar to fructokinase GI:2102691 from [Lycopersicon esculentum]
purple acid phosphatase, putative contains Pfam profile: PF00149 calcineurin-like phosphoesterase; identical to
CTP synthase, putative / UTP--ammonia ligase, putative similar to SP|P17812 CTP synthase (EC 6.3.4.2) (UTP-
expressed protein
glutathione S-transferase, putative similar to putative glutathione S-transferase GB:CAA10060 [Arabidopsis thali
ATPase, plasma membrane-type, putative / proton pump, putative strong similarity to P-type H(+)-transporting A
60S ribosomal protein L27 (RPL27C)
expressed protein contains weak similarity to reticulocyte-binding protein 2 homolog A [Plasmodium falciparum] g
hypothetical protein
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
expressed protein ; expression supported by MPSS
nuclear transport factor 2 (NTF2), putative similar to Swiss-Prot:P33331 nuclear transport factor 2 (NTF-2) (Nucl
myb family transcription factor similar to myb-related protein GI:2505876 from [Arabidopsis thaliana]
VHS domain-containing protein / GAT domain-containing protein weak similarity to HGF-regulated tyrosine kinas
senescence-associated family protein similar to senescence-associated protein 5 [Hemerocallis hybrid cultivar] g
expressed protein
expressed protein similar to Hypothetical protein RP404. (Swiss-Prot:Q9ZDC7) [Rickettsia prowazekii]; similar to
transcription factor CRC (CRABS CLAW) identical to transcription factor CRC (CRABS CLAW) GI:4836698 [Aral
leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00560: Leucine Rich

phospholipase A2 gamma, secretory low molecular weight identical to secretory low molecular weight phospholip
laccase, putative / diphenol oxidase, putative similar to laccase [Populus balsamifera subsp. trichocarpa][GI:380
DNA (cytosine-5-)-methyltransferase, putative strong similarity to cytosine-5 methyltransferase (METII) [Arabidop
heat shock protein, putative strong similarity to heat shock protein [Arabidopsis thaliana] GI:1906830; contains P
heat shock protein, putative strong similarity to heat shock protein [Arabidopsis thaliana] GI:1906830; contains P
acyl CoA reductase, putative similar to acyl CoA reductase [Simmondsia chinensis] GI:5020215; contains Pfam p
expressed protein
hypothetical protein
expressed protein
exocyst subunit EXO70 family protein strong similarity to unknown protein (emb|CAB83315.1); contains Pfam do
expressed protein similar to unknown protein (gb|AAF04428.1)
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to 14 kDa polypeptide [Catharan
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to 14 kDa polypeptide [Catharan
ubiquitin family protein weak similarity to PLIC-2 (ubiquitin-like type II) [Homo sapiens] GI:9937505; contains Pfa
glutathione S-transferase (103-1A) identical to Swiss-Prot:P46421 glutathione S-transferase 103-1A [Arabidopsis
protein kinase, putative contains protein kinase domain, Pfam:PF00069
glycine-rich RNA-binding protein similar to RNA-binding protein (RZ-1) GB:BAA12064 [Nicotiana sylvestris]; cont
glycosyl hydrolase family 17 protein similar to 3-glucanase GI:18483232 from [Sorghum bicolor]
myb family transcription factor (MYB105) contains Pfam profile: PF00249: Myb-like DNA-binding domain
expressed protein
expressed protein
hypothetical protein similar to unknown protein (pir |T17429)
60S ribosomal protein L30 (RPL30A) similar to GI:6984132 from [Euphorbia esula]
eukaryotic translation initiation factor 4A-1 / eIF-4A-1 eIF-4A-1 gi:15293046, gi:15450485; contains Pfam profile
MADS-box protein-related contains INTERPRO:IPR02100 MADS-box domain ;similar to MADS box transcription
patatin, putative similar to patatin-like latex allergen [Hevea brasiliensis][PMID:10589016]; contains patatin doma
glycine-rich protein
bifunctional dihydrofolate reductase-thymidylate synthase, putative / DHFR-TS, putative similar to THY-1 [SP| Q
expressed protein ; expression supported by MPSS
cyclin family protein similar to CycD3;2 [Lycopersicon esculentum] GI:6434199 ; contains Pfam profiles PF00134
no apical meristem (NAM) family protein similar to NAC2 (GI:6456751) [Arabidopsis thaliana]; contains Pfam PF
expressed protein contains Pfam profile PF04819: Family of unknown function (DUF716) (Plant viral-response fa
hypothetical protein
expressed protein
glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)
mitogen-activated protein kinase kinase (MAPKK), putative (MKK6) similar to NQK1 MAPKK [Nicotiana tabacum
F-box family protein / tubby family protein similar to Chain A, C-Terminal Domain Of Mouse Brain Tubby Protein
disease resistance-responsive family protein low similarity to disease resistance response protein 206-d [Pisum
MADS-box protein, putative
expressed protein
methyl-CpG-binding domain-containing protein contains Pfam profile PF01429: Methyl-CpG binding domain
peroxidase, putative identical to class III peroxidase ATP38 [Arabidopsis thaliana] gi|17530568|gb|AAL40851; sim
AAA-type ATPase family protein contains Pfam profile: PF00004 ATPase family
ATPase, plasma membrane-type, putative / proton pump, putative strong similarity to P-type H(+)-transporting AT
LOB domain protein 6 / lateral organ boundaries domain protein 6 (LBD6) / asymmetric leaves2 (AS2) identical t
protein kinase, putative similar to protein kinase p46XlEg22 [Xenopus laevis] gi|609280|emb|CAA78914; contain
leucine-rich repeat transmembrane protein kinase, putative identical to putative kinase-like protein TMKL1 precu
basix helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain

DC1 domain-containing protein contains Pfam protein PF03107 DC1 domain
two-component responsive regulator family protein / response regulator family protein contains Pfam profile: PF0
hypothetical protein
ATPase, plasma membrane-type, putative / proton pump, putative strong similarity to P-type H(+)-transporting A
expressed protein
ATPase 9, plasma membrane-type, putative / proton pump 9, putative / proton-exporting ATPase, putative strong
nodulin MtN21 family protein similar to MtN21 GI:2598575 (root nodule development) from [Medicago truncatula
pentatricopeptide (PPR) repeat-containing protein contains INTERPRO:IPR002885 PPR repeats
hevein-like protein (HEL) identical to SP|P43082 Hevein-like protein precursor {Arabidopsis thaliana}; similar to S
jacalin lectin family protein similar to myrosinase-binding protein homolog [Arabidopsis thaliana] GI:2997767; cor
thiamin pyrophosphokinase, putative similar to thiamin pyrophosphokinase [Mus musculus] gi|6468206|dbj|BAA8
pentatricopeptide (PPR) repeat-containing protein low similarity to leaf protein [Ipomoea nil] GI:3107905; contain
expressed protein
leucine-rich repeat family protein
protein kinase family protein contains protein kinase domain, Pfam:PF00069
serine/threonine protein phosphatase PP1 isozyme 4 (TOPP4) / phosphoprotein phosphatase 1 identical to SP|P
flowering locus T protein (FT) identical to SP|Q9SXZ2 FLOWERING LOCUS T protein {Arabidopsis thaliana}; co
ABC transporter family protein contains Pfam profile: PF00005 ABC transporter
zinc finger protein-related contains similarity to zinc finger proteins (CCCH type)
proline transporter 2 (ProT2) identical to proline transporter 2 GI:1769903 from [Arabidopsis thaliana]
protein kinase family protein contains protein kinase domain, Pfam:PF00069
expressed protein similar to SP|Q41706 A3 protein (unknown function) {Vigna unguiculata}
expressed protein
expressed protein similar to unknown protein (gb|AAF00631.1)
F-box family protein contains F-box domain Pfam:PF00646
nodulin-related weak similarity to nodule-specific protein Nlj70 [Lotus japonicus] GI:3329366
senescence/dehydration-associated protein-related (ERD7) similar to senescence-associated protein 12 [Hemer
leucine-rich repeat protein kinase, putative similar to protein kinase TMK1 gi|166888|gb|AAA32876; contains Pfa
UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl ar
expressed protein predicted proteins, Arabidopsis thaliana
vegetative storage protein 2 (VSP2) identical to SP|O82122 Vegetative storage protein 2 precursor {Arabidopsis
ubiquitin carboxyl-terminal hydrolase, putative / ubiquitin thiolesterase, putative similar to SP|Q9JKB1 Ubiquitin c
leucine-rich repeat protein kinase, putative smilar to light repressible receptor protein kinase [Arabidopsis thalian
MATE efflux protein-related contains Pfam profile PF01554: Uncharacterized membrane protein family
glucose-6-phosphate 1-dehydrogenase, putative / G6PD, putative strong similarity to SP|Q43839 Glucose-6-pho
alcohol dehydrogenase, putative similar to alcohol dehydrogenase GB:CAA37333 GI:297178 from [Solanum tub
Ras-related protein (RAB7) / AtRab75 / small GTP-binding protein, putative identical to SP:O04157 Ras-related
aminoacylase, putative / N-acyl-L-amino-acid amidohydrolase, putative similar to aminoacylase-1 (N-acyl-L-amin
lipid transfer protein, putative identical to anther-specific gene ATA7 [gi:2746339]; contains Pfam protease inhibit
calcineurin B-like protein 9 (CBL9) identical to calcineurin B-like protein 9 (GI:5866279) and calcium-binding prot
AAA-type ATPase family protein contains Pfam domain, PF00004: ATPase, AAA family
las1-like family protein similar to Las1p [Saccharomyces cerevisiae] GI:495504; contains Pfam profile PF04031:
heat shock protein 81-1 (HSP81-1) / heat shock protein 83 (HSP83) nearly identical to SP|P27323 Heat shock p
glycosyl hydrolase family 9 protein similar to cellulase GI:575404 from [Sambucus nigra].
plant defensin-fusion protein, putative (PDF1.4) plant defensin protein family member, personal communication,
lactoylglutathione lyase, putative / glyoxalase I, putative similar to putative lactoylglutathione lyase SP:Q39366, C
60S ribosomal protein L11 (RPL11D)
40S ribosomal protein S3 (RPS3B) ribosomal protein S3a - Xenopus laevis, PIR:R3XL3A

expressed protein
hypothetical protein
glutamate receptor family protein (GLR2.3) plant glutamate receptor family, PMID:11379626
expressed protein
transcriptional factor B3 family protein contains Pfam profile PF02362: B3 DNA binding domain
expressed protein contains Pfam profile PF05811: Eukaryotic protein of unknown function (DUF842)
expressed protein
protein kinase, putative similar to cyclin dependent kinase C [Lycopersicon esculentum] gi|15215944|emb|CAC5
terpene synthase/cyclase family protein
expressed protein similar to geranylgeranylated protein ATGP4 [GI:4097567]
aldehyde oxidase, putative similar to aldehyde oxidases from Arabidopsis thaliana: GI:3172023, GI:3172025, GI
universal stress protein (USP) family protein / responsive to dessication protein (RD2) strong similarity to RD2 pr
expressed protein contains Pfam profile PF05212: Protein of unknown function (DUF707)
basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
leucine-rich repeat family protein contains leucine rich repeat (LRR) domains, Pfam:PF00560
transducin family protein / WD-40 repeat family protein similar to PAK/PLC-interacting protein 1 (GI:4211689) {H
galactinol synthase, putative contains Pfam profile: PF01501 glycosyl transferase family 8
hypothetical protein
phosphoglycerate/bisphosphoglycerate mutase-related weak hit to Pfam profile PF00300: phosphoglycerate mut
multi-copper oxidase type I family protein contains Pfam profile: PF00394 Multicopper oxidase; similar to pollen-
hypothetical protein
zinc finger (C2H2 type) family protein contains Pfam domain, PF00096: Zinc finger, C2H2 type
Rac-like GTP-binding protein (ARAC7) identical to rac GTP binding protein Arac7 GI:3702962 from [Arabidopsis
histone-like transcription factor (CBF/NF-Y) family protein contains Pfam PF00808 : Histone-like transcription fac
cytochrome P450, putative similar to cytochrome P450 89A2 (CYPLXXXIX) (SP:Q42602) [Arabidopsis thaliana];
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
60S ribosomal protein L11 (RPL11D)
ubiquitin family protein contains INTERPRO:IPR000626 ubiquitin domain
hypothetical protein
expressed protein
zinc finger (C2H2 type) family protein ; contains Pfam profile: PF00096 Zinc finger, C2H2 type
dynein light chain, putative similar to SP|O02414 Dynein light chain LC6, flagellar outer arm {Anthocidaris crassi
universal stress protein (USP) family protein / responsive to dessication protein (RD2) strong similarity to RD2 pr
alcohol dehydrogenase, putative similar to alcohol dehydrogenase from Solanum tuberosum [SP|p14673]; conta
hypothetical protein
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
phototropic-responsive NPH3 family protein contains NPH3 family domain, Pfam:PF03000
phototropic-responsive NPH3 family protein contains NPH3 family domain, Pfam:PF03000
gibberellin 20-oxidase, putative similar to gibberellin 20-oxidase GB:CAA58295 from [Arabidopsis thaliana]
ovate family protein 57% similar to ovate protein (GI:23429649) [Lycopersicon esculentum]; contains TIGRFAM
expressed protein
expressed protein Since this genomic sequence region is unfinished, the annotated gene may be missing a stop
glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein similar to polygalacturonase
ammonium transporter 2 (AMT2) identical to SP|Q9M6N7 Ammonium transporter 2 (AtAMT2) {Arabidopsis thalia
zinc finger homeobox family protein / ZF-HD homeobox family protein predicted proteins, Arabidopsis thaliana
60S ribosomal protein L37 (RPL37C) similar to ribosomal protein L37 GB:BAA04888 from [Homo sapiens]
ubiquitin-specific protease 12 (UBP12) almost identical to ubiquitin-specific protease 12 GI:11993471 [Arabidops

ubiquitin-specific protease 12 (UBP12) almost identical to ubiquitin-specific protease 12 GI:11993471 [Arabidops
senescence-associated family protein similar to senescence-associated protein 5 [Hemerocallis hybrid cultivar] g
expressed protein
expressed protein similar to E6 (GI:1000090) [Gossypium barbadense]
amino acid carrier, putative / amino acid permease, putative strong similarity to amino acid carrier GI:3293031 fr
mitochondrial transcription termination factor-related / mTERF-related contains Pfam profile PF02536: mTERF
fasciclin-like arabinogalactan family protein similar to fasciclin-like arabinogalactan-protein 1 [Arabidopsis thalian
nodulin MtN21 family protein similar to MtN21 GI:2598575 (root nodule development) from [Medicago truncatula
expressed protein contains Pfam profile PF01027: Uncharacterized protein family UPF0005
ubiquitin family protein contains INTERPRO:IPR000626 ubiquitin domain
cysteine endopeptidase-related similar to cysteine endopeptidase precursor GI:2944446 from [Ricinus communis
hypothetical protein
OTU-like cysteine protease family protein contains Pfam profile PF02338: OTU-like cysteine protease
expressed protein
haloacid dehalogenase-like hydrolase family protein similar to SP|Q08623 GS1 protein {Homo sapiens}; contains
serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II chains A and B (SP:P08819) (E
metal transporter, putative (ZIP9) identical to putative metal transporter ZIP9 [Arabidopsis thaliana] gi|17385790|
F-box family protein contains F-box domain Pfam:PF00646
universal stress protein (USP) family protein contains Pfam PF00582: universal stress protein family
no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; NAC-dom
homeodomain-containing protein contains 'Homeobox' domain signature, Prosite:PS00027
homeodomain-containing protein contains 'Homeobox' domain signature, Prosite:PS00027
glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)
calmodulin-binding protein similar to anther ethylene-upregulated calmodulin-binding protein ER1 GI:11612392 f
myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain
myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain
subtilase family protein contains similarity to cucumisin-like serine protease GI:3176874 from [Arabidopsis thalia
60S ribosomal protein L28 (RPL28C) unknown protein chromosome II BAC F6F22 - Arabidopsis thaliana,PID:g3
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to pEARLI 1 (Accession No. L43
glycosyl hydrolase family 17 protein
expressed protein
proline-rich extensin-like family protein contains extensin-like region, Pfam:PF04554
ATPase, plasma membrane-type, putative / proton pump, putative similar to P-type H(+)-transporting ATPase fro
phototropic-responsive NPH3 family protein contains NPH3 family domain, Pfam:PF03000
homeobox-leucine zipper transcription factor (HB-14) identical to homeodomain transcription factor (ATHB-14)G
hypothetical protein
aldehyde oxidase 1 (AAO1) identical to aldehyde oxidase AAO1 from Arabidopsis thaliana [gi:3172023] isoform
aldehyde oxidase 1 (AAO1) identical to aldehyde oxidase AAO1 from Arabidopsis thaliana [gi:3172023] isoform
MIR domain-containing protein similar to SP|Q99470 Stromal cell-derived factor 2 precursor (SDF-2) {Homo sap
disease resistance-responsive protein-related / dirigent protein-related contains similarity to disease resistance r
serine carboxypeptidase S10 family protein SERINE CARBOXYPEPTIDASE I PRECURSOR - Hordeum vulgare
cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative identic
expressed protein
pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
cold-shock DNA-binding family protein / glycine-rich protein (GRP2) identical to Glycine-rich protein 2b (AtGRP2
leucine-rich repeat transmembrane protein kinase, putative similar to GI:3641252 from [Malus x domestica] (Pla
paired amphipathic helix repeat-containing protein low similarity to transcriptional repressor SIN3B [Mus musculu
glycosyl hydrolase family protein 17 similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from [Nicotiana

expressed protein
terminal flower 1 protein (TFL1) identical go SP|P93003 TERMINAL FLOWER 1 protein {Arabidopsis thaliana}; c
seryl-tRNA synthetase, putative / serine--tRNA ligase, putative similar to PIR|T03949 serine--tRNA ligase (EC 6.
dual specificity protein phosphatase family protein contains Pfam profile: PF00782 dual specificity phosphatase,
nodulin-related low similarity to MtN21 [Medicago truncatula] GI:2598575
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
paired amphipathic helix repeat-containing protein weak similarity to SP|P22579 Paired amphipathic helix protein
expressed protein
malate dehydrogenase [NAD], mitochondrial identical to mitochondrial NAD-dependent malate dehydrogenase C
MADS-box protein (AGL40) contains Pfam profile PF00319: SRF-type transcription factor (DNA-binding and dim
proline-rich family protein contains proline-rich extensin domains, INTERPRO:IPR002965; contains 1 predicted t
proline-rich family protein contains proline-rich extensin domains, INTERPRO:IPR002965; contains 1 predicted t
F-box family protein contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein inte
stigma-specific Stig1 family protein contains Pfam profile PF04885: Stigma-specific protein, Stig1
gibberellin 20-oxidase-related similar to gibberellin 20-oxidase from Pisum sativum [GI:1848146], Phaseolus vulg
MADS-box protein, putative
polygalacturonase inhibiting protein 2 (PGIP2) identical to polygalacturonase inhibiting protein 2 (PGIP2) [Arabid
expressed protein
paired amphipathic helix repeat-containing protein low similarity to transcriptional repressor SIN3B [Mus musculu
germin-like protein, putative similar to SP|Q9LEA7; contains PS00725 germin family signature
60S ribosomal protein L37 (RPL37B) similar to SP:Q43292 from [Arabidopsis thaliana]
photosystem I reaction center subunit VI, chloroplast, putative / PSI-H, putative (PSAH2) identical to SP|Q9SUI6
cyclin-related contains weak similarity to Swiss-Prot:P35662 cylicin I (Multiple-band polypeptide I) [Bos taurus]
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
sugar isomerase (SIS) domain-containing protein / CBS domain-containing protein similar to SP|Q47334 Polysia
thioredoxin family protein low similarity to thioredoxin [Gallus gallus] GI:212766; contains Pfam profile: PF00085
auxin-responsive AUX/IAA family protein contains Pfam profile: PF02309 AUX/IAA family
glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)
protein kinase, putative contains protein kinase domain, Pfam:PF00069
replication factor C 37 kDa, putative Similar to SWISS-PROT:P35249 activator 1 37 kDa subunit (Replication fac
expressed protein
expressed protein
expressed protein ; expression supported by MPSS
60S ribosomal protein L18 (RPL18B) similar to GB:P42791
late embryogenesis abundant protein (M10) / LEA protein M10 identical to GB:AF076979
expansin family protein (EXPL3) contains Pfam profile: PF01357 pollen allergen; expansin-like gene, PMID:1164
RuBisCO subunit binding-protein beta subunit, chloroplast / 60 kDa chaperonin beta subunit / CPN-60 beta ident
RuBisCO subunit binding-protein beta subunit, chloroplast / 60 kDa chaperonin beta subunit / CPN-60 beta ident
expressed protein
phosphatidic acid phosphatase-related / PAP2-related
DNA repair protein Rad4 family low similarity to SP|Q01831 DNA-repair protein complementing XP-C cells (Xero
xanthine/uracil permease family protein contains Pfam profile: PF00860 permease family
receptor-like protein kinase-related contains Pfam profile: PF01657 Domain of unknown function that is usually a
expressed protein
expressed protein
major latex protein-related / MLP-related low similarity to major latex protein {Papaver somniferum}[GI:294060] ;
cyclic nucleotide-regulated ion channel, putative (CNGC18) similar to cyclic nucleotide and calmodulin-regulated
expressed protein contains Pfam PF02594: Uncharacterized ACR, YggU family COG1872

zinc finger (B-box type) family protein / salt tolerance-like protein (STH) contains Pfam profile PF00643: B-box zi
hypothetical protein
CER1 protein identical to maize gl1 homolog (glossy1 locus) GI:1209703 and CER1 GI:1199467 from [Arabidops
hypothetical protein
paired amphipathic helix repeat-containing protein weak similarity to transcriptional repressor SIN3B [Mus muscu
ADP-ribosylation factor, putative similar to GTP-binding ADP-ribosylation factor homolog 1 protein (SP:P25160)
transcriptional regulator (FUSCA3) identical to FUSCA3 GB:AAC35247 [Arabidopsis thaliana] (Plant J. 6, 379-38
XH/XS domain-containing protein / XS zinc finger domain-containing protein contains Pfam domains PF03469: X
phototropic-responsive NPH3 family protein contains NPH3 family domain, Pfam:PF03000
oligouridylate-binding protein, putative similar to oligouridylate binding protein GI:6996560 from [Nicotiana plumb
glycosyl transferase family 2 protein similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from [
hypothetical protein
ADP-ribosylation factor, putative identical to GP:15450888 ADP-ribosylation factor-like protein {Arabidopsis thalia
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
isocitrate lyase, putative similar to isocitrate lyase GI:167144 from [Brassica napus]
CBL-interacting protein kinase 9 (CIPK9) identical to CBL-interacting protein kinase 9 [Arabidopsis thaliana] gi|13
Ca(2+)-dependent nuclease identical to Ca(2+)-dependent nuclease [Arabidopsis thaliana] GI:7684292; support
fructose-bisphosphate aldolase, putative similar to PIR|S65073 fructose-bisphosphate aldolase (EC 4.1.2.13) isc
ethylene-responsive family protein similar to Ethylene-regulated ER33 protein (GI:5669656) [Lycopersicon escul
DPB-1 transcription factor, putative (DPB) similar to Swiss-Prot:Q14186 transcription factor DP-1 [Homo sapiens
nucleosidase-related contains weak similarity to MTA/SAH nucleosidase (P46). (Swiss-Prot:P24247) [Shigella fle
glycosyl hydrolase family protein 17 similar to beta-1,3-glucanase GI:15150341 from [Camellia sinensis]; C-term
hypothetical protein ; expression supported by MPSS
ubiquitin family protein contains INTERPRO:IPR000626 ubiquitin domain
group II intron splicing factor CRS1-related contains weak similarity to CRS1 [Zea mays] gi|9837550|gb|AAG005
40S ribosomal protein S15A (RPS15aF) cytoplasmic ribosomal protein S15a, Arabidopsis thaliana, EMBL:ATAF1
dehydrin, putative similar to dehydrin ERD10 (Low-temperature-induced protein LTI45) [Arabidopsis thaliana] SW
cytochrome P450 family protein similar to Cytochrome P450 97B2 (SP:048921) [Glycine max]
F-box family protein similar to hypothetical protein GB:AAD18122 from [Arabidopsis thaliana];contains Pfam PF0
CBL-interacting protein kinase 9 (CIPK9) identical to CBL-interacting protein kinase 9 [Arabidopsis thaliana] gi|13
glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein similar to polygalacturonase
DNA-binding protein-related contains Pfam domain PF03479: Domain of unknown function (DUF296), found in A
ADP-ribosylation factor, putative similar to ADP-ribosylation factor GI:166586 from [Arabidopsis thaliana]
ribonucleoside-diphosphate reductase small chain, putative / ribonucleotide reductase, putative similar to ribonu
zinc knuckle (CCHC-type) family protein contains Pfam domain, PF00098: Zinc knuckle
expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is un
leucine-rich repeat transmembrane protein kinase, putative brassinosteroid-insensitive protein BRI1 - Arabidopsi
respiratory burst oxidase protein D (RbohD) / NADPH oxidase identical to respiratory burst oxidase protein D fro
mitochondrial import inner membrane translocase (TIM8) identical to mitochondrial import inner membrane trans
alcohol dehydrogenase, putative similar to alcohol dehydrogenase from Solanum tuberosum [SP|p14673]; conta
zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RI
expressed protein
synaptobrevin family protein similar to vesicle-associated membrane protein 7 [Rattus norvegicus] GI:9502258,
aminoacylase, putative / N-acyl-L-amino-acid amidohydrolase, putative similar to aminoacylase-1 (N-acyl-L-amin
zinc finger (DHHC type) family protein contains Pfam profile PF01529: DHHC zinc finger domain
sterile alpha motif (SAM) domain-containing protein contains Pfam profile PF00536: SAM domain (Sterile alpha
Ras-related GTP-binding protein (RAN3) identical to atran3 [Arabidopsis thaliana] GI:2058280
potassium channel protein 2 (AKT2) (AKT3) identical to potassium channel [Arabidopsis thaliana] gi|1100898|gb

histone H3 identical to histone H3 from Zea mays SP|P05203, Medicago sativa GI:166384, Encephalartos altens
expressed protein predicted protein, Arabidopsis thaliana
calmodulin-binding protein-related
ACT domain containing protein (ACR4) low similarity to uridylyltransferase [Gluconacetobacter diazotrophicus] G
xanthine/uracil permease family protein contains Pfam profile: PF00860 permease family
pumilio/Puf RNA-binding domain-containing protein contains Pfam profile: PF00806 Pumilio-family RNA binding
sucrose synthase, putative / sucrose-UDP glucosyltransferase, putative strong similarity to sucrose synthase GI:
guanylate kinase 1 (GK-1) identical to guanylate kinase (GK-1) [Arabidopsis thaliana] gi|7861795|gb|AAF70408
heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative contains Pfam profile: PF00076 RNA recog
ribosomal protein L19 family protein similar to plastid ribosomal protein L19 precursor [Spinacia oleracea] gi|758
glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIG
expressed protein
protein kinase family protein contains Pfam domains, PF00069: Protein kinase domain
ethanolamine-phosphate cytidylyltransferase, putative / phosphorylethanolamine transferase, putative / CTP:pho
expressed protein
clathrin adaptor complex small chain family protein contains Pfam profile: PF01217 clathrin adaptor complex sma
expressed protein similar to unknown protein (gb|AAF00631.1)
oxidoreductase family protein similar to AX110P [Daucus carota] GI:285739; contains Pfam profiles PF01408: Ox
kip-related protein 5 (KRP5) / cyclin-dependent kinase inhibitor 5 (ICK5) identical to cyclin-dependent kinase inh
ABC transporter family protein
hypothetical protein
cytochrome P450 71A12, putative (CYP71A12) Identical to Cytochrome P450 (SP:O49340) [Arabidopsis thalian
phosphatidylinositol 4-kinase, putative similar to phosphatidylinositol 4-kinase alpha [Daucus carota] GI:345227
elongation factor Tu family protein translation Elongation Factor 2, Schizosaccharomyces pombe, PIR:T39902
60S ribosomal protein L37 (RPL37A) almost identical to GB:Q43292
60S ribosomal protein L8 (RPL8A)
glycine-rich protein
Rho GDP-dissociation inhibitor family protein similar to SP|P52565 Rho GDP-dissociation inhibitor 1 (Rho GDI 1
phototropic-responsive NPH3 family protein contains NPH3 family domain, Pfam:PF03000
no apical meristem (NAM) family protein identical to no apical meristem protein CUC2 (GI:1944132) [Arabidopsis
receptor protein kinase-related contains Pfam profile: PF01657 Domain of unknown function
TATA-binding protein-associated phosphoprotein Dr1 protein, putative (DR1) identical to Dr1 protein homolog (S
hypothetical protein
OTU-like cysteine protease family protein contains Pfam profile PF02338: OTU-like cysteine protease
disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of
expressed protein
glutathione S-transferase, putative
amino acid permease, putative strong similarity to AUX1 GI:1531758 from [Arabidopsis thaliana]; contains Pfam
expressed protein contains Pfam profile PF01027: Uncharacterized protein family UPF0005
basic helix-loop-helix protein / bHLH protein contains Pfam profile PF00010: Helix-loop-helix DNA-binding domai
scarecrow-like transcription factor 3 (SCL3) identical to GB:AAD24404 GI:4580515 from [Arabidopsis thaliana] (
expressed protein EST gb|T21171 comes from this gene
ovule development protein, putative similar to ovule development protein AINTEGUMENTA (GI:1209099) [Arabid
hypothetical protein
hypothetical protein
hypothetical protein
jacalin lectin family protein similar to myrosinase-binding protein homolog [Arabidopsis thaliana] GI:2997767; cor
AAA-type ATPase family protein BCS1 nuclear gene encoding mitochondrial protein - Homo sapiens, EMBL:AF0

hypothetical protein
hypothetical protein
hypothetical protein
glycine-rich RNA-binding protein, putative similar to Glycine-rich RNA-binding protein 2, mitochondrial precursor
glycine-rich RNA-binding protein, putative similar to Glycine-rich RNA-binding protein 2, mitochondrial precursor
leucine-rich repeat family protein
pseudouridine synthase family protein contains Pfam profiles: PF00849 RNA pseudouridylate synthase, PF0147
oligouridylate-binding protein, putative similar to oligouridylate binding protein GI:6996560 from [Nicotiana plumb
hypothetical protein contains Pfam PF04510 : Family of unknown function (DUF577); common family comprised
hypothetical protein
expressed protein
zinc finger (C2H2 type) family protein contains Pfam profile: PF00096 zinc finger, C2H2 type
CBL-interacting protein kinase 9 (CIPK9) identical to CBL-interacting protein kinase 9 [Arabidopsis thaliana] gi|13
glycosyl hydrolase family protein 17 similar to glucan endo-1,3-beta-glucosidase precursor SP:P52409 from [Trit
phosphatidylinositol 3- and 4-kinase family protein low similarity to phosphatidylinositol 4-kinase type-II beta [Hor
expressed protein
PQ-loop repeat family protein / transmembrane family protein similar to SP|Q60441 Mannose-P-dolichol utilizatio
40S ribosomal protein S6 (RPS6B)
ceramidase family protein contains Pfam domain, PF04734: Neutral/alkaline nonlysosomal ceramidase
expressed protein
disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of
disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of
calcium-binding EF hand family protein contains Pfam profile: PF00036 EF hand
glycosyl hydrolase family 9 protein similar to endo-beta-1,4-D-glucanase GI:4165132 from [Lycopersicon esculen
expressed protein
exonuclease family protein contains exonuclease domain, Pfam:PF00929
ABI3-interacting protein 1 (AIP1) identical to pseudo-response regulator 1 GI:7576354 from [Arabidopsis thaliana
expressed protein contains Pfam profile PF04776: Protein of unknown function (DUF626)
glycosyl hydrolase family 9 protein
CCAAT-box binding transcription factor Hap5a, putative
expressed protein contains Prosite PS00012: Phosphopantetheine attachment site; similar to GLE1 (GI:328881
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
expressed protein
NAD-dependent glycerol-3-phosphate dehydrogenase family protein weak similarity to SP|P46919 Glycerol-3-ph
NAD-dependent glycerol-3-phosphate dehydrogenase family protein weak similarity to SP|P46919 Glycerol-3-ph
alcohol dehydrogenase, putative similar to alcohol dehydrogenase GI:551257 from [Nicotiana tabacum]
DNA-binding protein, putative strong similarity to DNA-binding proteins from [Arabidopsis thaliana] RAV1 GI:386
hypothetical protein
hypothetical protein
expressed protein
peroxidase, putative similar to peroxidase ATP6a [Arabidopsis thaliana] gi|1429215|emb|CAA67310
plastocyanin-like domain-containing protein
early-responsive to dehydration protein-related / ERD protein-related low similarity to ERD4 protein (early-respon
hypothetical protein
copine-related low similarity to SP|Q99829 Copine I {Homo sapiens}
tubulin gamma-2 chain / gamma-2 tubulin (TUBG2) identical to SP|P38558 Tubulin gamma-2 chain (Gamma-2 t
stress-inducible protein, putative similar to sti (stress inducible protein) [Glycine max] GI:872116; contains Pfam
3-phosphoshikimate 1-carboxyvinyltransferase, putative / 5-enolpyruvylshikimate-3-phosphate, putative / EPSP

dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family similar to dihydroflavonol 4-reductase
Ras-related GTP-binding protein, putative similar to GTP-binding protein GI:871510 from [Pisum sativum]; conta
UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl ar
auxin efflux carrier family protein contains auxin efflux carrier domain, Pfam:PF03547
auxin efflux carrier family protein contains auxin efflux carrier domain, Pfam:PF03547
auxin efflux carrier family protein contains auxin efflux carrier domain, Pfam:PF03547
zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RI
cytochrome P450 family protein similar to cytochrome P450 GI:984542 from [Sorghum bicolor]
RNA recognition motif (RRM)-containing protein contains InterPro entry IPR000504: RNA-binding region RNP-1
oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to flavonol synthase SP|Q96330 {Arabidopsis thalia
60S ribosomal protein L21 similar to 60S ribosomal protein L21 GI:3885884 from [Oryza sativa]
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
expressed protein
expressed protein
emsy N terminus domain-containing protein / ENT domain-containing protein contains Pfam profile PF03735: EN
emsy N terminus domain-containing protein / ENT domain-containing protein contains Pfam profile PF03735: EN
hypothetical protein contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287
esterase/lipase/thioesterase family protein similar to monoglyceride lipase from [Homo sapiens] GI:14594904, [M
hypothetical protein
expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is un
potassium transporter (KUP1) identical to potassium transporter [Arabidopsis thaliana] gi|2654088|gb|AAB87687
expressed protein contains Pfam domain, PF04367: Protein of unknown function (DUF502)
2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative stron
2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative stron
thioredoxin family protein low similarity to thioredoxin [Gallus gallus] GI:212766; contains Pfam profile: PF00085
expressed protein
zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RI
hypothetical protein
expressed protein
protein kinase family protein contains Pfam PF00069: Protein kinase domain
CP12 domain-containing protein contains Pfam domain PF02672: CP12 domain
ovule development protein, putative similar to ovule development protein AINTEGUMENTA (GI:1209099) [Arabid
glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIG
cytochrome P450 family protein similar to cytochrome P450 72A1 (SP:Q05047) [Catharanthus roseus]
protein kinase family protein contains protein kinase domain, Pfam:PF00069
expressed protein contains Pfam profile PF03140: Plant protein of unknown function
zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RI
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
glyoxal oxidase-related contains similarity to glyoxal oxidase precursor [Phanerochaete chrysosporium] gi|10503
photosystem I reaction center subunit VI, chloroplast, putative / PSI-H, putative (PSAH1) identical to SP|Q9SUI7
leucine-rich repeat transmembrane protein kinase, putative hypothetical proteins - Arabidopsis thaliana
mitogen-activated protein kinase kinase (MAPKK), putative (MKK3) similar to NPK2 [Nicotiana tabacum] gi|8623
phosphoglycerate/bisphosphoglycerate mutase family protein contains Pfam profile PF00300: phosphoglycerate
nodulin MtN3 family protein similar to MtN3 GI:1619602 (root nodule development) from [Medicago truncatula]
protein kinase, putative similar to protein kinase G11A [Oryza sativa] SWISS-PROT:P47997
expressed protein contains Pfam domain, PF04515: Protein of unknown function, DUF580
major latex protein-related / MLP-related low similarity to major latex protein {Papaver somniferum}[GI:294060] ;
DNAJ heat shock protein, putative (J3) identical to AtJ3 [Arabidopsis thaliana] GI:2641638, strong similarity to se

leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00560: Leucine Rich
heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative contains Pfam profile: PF00076 RNA recog
hypothetical protein
ChaC-like family protein contains Pfam profile: PF04752 ChaC-like protein
glycoside hydrolase family 19 protein similar to chitinase GI:17799 from [Brassica napus]; contains Pfam profiles
leucine-rich repeat transmembrane protein kinase, putative CLAVATA1 receptor kinase, Arabidopsis thaliana, EM
fasciclin-like arabinogalactan family protein similar to fasciclin-like arabinogalactan-protein 1 [Arabidopsis thalian
hypothetical protein various predicted proteins, Arabidopsis thaliana contains Pfam profile PF03080: Arabidopsis
expressed protein
expressed protein
integral membrane family protein contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569;
homeobox-leucine zipper transcription factor family protein similar to wuschel protein (GI:22087128) [Arabidopsi
expressed protein
bile acid:sodium symporter family protein low similarity to SP|Q12908 Ileal sodium/bile acid cotransporter {Homo
glutamate carboxypeptidase, putative (AMP1) identical to GI:15624092 glutamate carboxypeptidase {Arabidops
zinc finger (C2H2 type) protein (WIP2) identical to WIP2 protein [Arabidopsis thaliana] gi|18027012|gb|AAL5572
disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of
expressed protein
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to cysteine-rich 5B protein - Lyco
mitochondrial transcription termination factor family protein / mTERF family protein weak similarity to mtDBP pro
NADP-dependent oxidoreductase, putative similar to probable NADP-dependent oxidoreductase (zeta-crystallin
aspartyl protease family protein low similarity to CND41, chloroplast nucleoid DNA binding protein [Nicotiana tab
expressed protein
vacuolar sorting receptor, putative identical to GB:U79960 GI:1737220; contains a calcium-binding EGF-like dom
vacuolar sorting receptor, putative identical to GB:U79960 GI:1737220; contains a calcium-binding EGF-like dom
basix helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
serine/threonine protein kinase, putative similar to serine-threonine protein kinase [Triticum aestivum] gi|205537
29 kDa ribonucleoprotein, chloroplast / RNA-binding protein cp 29 nearly identical to SP|Q43349 29 kDa ribonuc
glycosyl transferase family 2 protein similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from [
homeobox-leucine zipper transcription factor family protein similar to wuschel protein (GI:22087128) [Arabidopsi
vacuolar processing enzyme alpha / alpha-VPE identical to SP|P49047 Vacuolar processing enzyme, alpha-isoz
ACT domain containing protein (ACR4) low similarity to uridylyltransferase [Gluconacetobacter diazotrophicus] G
flavin-containing monooxygenase family protein / FMO family protein similar to flavin-containing monooxygenase
Ras-related GTP-binding nuclear protein (RAN-2) identical to GTP-binding nuclear protein RAN-2 SP:P41917 fro
PQ-loop repeat family protein / transmembrane family protein similar to SP|Q60441 Mannose-P-dolichol utilizatio
thiol methyltransferase, putative similar to thiol methyltransferase 1 GI:14583119 from [Brassica oleracea]
TATA-binding protein-associated phosphoprotein Dr1 protein, putative (DR1) identical to Dr1 protein homolog (S
TATA-binding protein-associated phosphoprotein Dr1 protein, putative (DR1) identical to Dr1 protein homolog (S
3-phosphoshikimate 1-carboxyvinyltransferase, putative / 5-enolpyruvylshikimate-3-phosphate, putative / EPSP
hairpin-responsive protein, putative (HIN1) similar to harpin-induced protein hin1 (GI:1619321) [Nicotiana tabacu
60S ribosomal protein L21 (RPL21E) similar to 60S ribosomal protein L21 GB:Q43291 GI:2851508 from [Arabido
thioredoxin family protein similar to protein disulfide isomerase [Dictyostelium discoideum] GI:2627440; contains
transcriptional factor B3 family protein contains Pfam profile PF02362: B3 DNA binding domain
COP1 regulatory protein photomorphogenesis repressor; identical to COP1 regulatory protein/FUSCA protein FU
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
nodulin MtN21 family protein contains similarity to MtN21 [Medicago truncatula] GI:2598575; contains Pfam prof
cytochrome P450-related weak similarity to cytochrome P450 [Catharanthus roseus] GI:4688670
flavin-containing monooxygenase family protein / FMO family protein similar to flavin-containing monooxygenase

patatin-related contains Patatin domain PF01734
patatin-related contains Patatin domain PF01734
C2 domain-containing protein contains Pfam profile PF00168: C2 domain
purple acid phosphatase, putative contains Pfam profile: PF00149 calcineurin-like phosphoesterase; identical to
hypothetical protein contains Pfam profile PF03478: Protein of unknown function (DUF295)
receptor-like protein kinase-related contains Pfam profile: PF01657 Domain of unknown function that is usually a
protein kinase family protein contains protein kinase domain, Pfam:PF00069
MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:122312
BRCT domain-containing protein contains Pfam domain, PF00533: BRCA1 C Terminus (BRCT) domain
CBL-interacting protein kinase 3 (CIPK3) identical to CBL-interacting protein kinase 3 [Arabidopsis thaliana] gi|92
disease resistance protein RPP1-WsB-like (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exist
expressed protein no suitable start codon was identified.
universal stress protein (USP) family protein contains Pfam PF00582: universal stress protein family; similar to h
SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative similar to phosphatidylinositol trans
nodulin MtN21 family protein similar to MtN21 [Medicago truncatula] GI:2598575; contains Pfam profile PF00892
disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of
myb family transcription factor (MYB110) contains Pfam profile: PF00249 myb-like DNA-binding domain
exocyst subunit EXO70 family protein (EXO70-G1) tomato leucine zipper-containing protein - Lycopersicon escu
alkaline phytoceramidase family / aPHC family contains Pfam profile: PF05875: alkaline phytoceramidase (aPHC
nodulin family protein similar to nodulin-like protein [Arabidopsis thaliana] GI:3329368, nodule-specific protein Nl
hypothetical protein
transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related contains Pfam profiles: PF0230
squamosa promoter-binding protein-like 3 (SPL3) identical to squamosa-promoter binding protein like 3 [Arabido
glutathione S-transferase 6 (GST6) identical to GB:X95295. Based on identical cDNA hits, the translation is now
F-box family protein ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250
myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain
pre-mRNA splicing factor PRP38 family protein (SRL1) contains Pfam profile PF03371: PRP38 family
60S ribosomal protein L28 (RPL28A)
disease resistance protein RPP1-WsB-like (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exist
disease resistance protein RPP1-WsB-like (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exist
sec7 domain-containing protein similar to SP|Q42510 Pattern formation protein EMB30 (GNOM) {Arabidopsis th
delta 7-sterol-C5-desaturase (STE1) identical to sterol-C5-desaturase GB:AAD12944 GI:4234768 from [Arabido
TAZ zinc finger family protein / BTB/POZ domain-containing protein contains Pfam PF00651 : BTB/POZ domain
allene oxide cyclase, putative / early-responsive to dehydration protein, putative / ERD protein, putative similar to
29 kDa ribonucleoprotein, chloroplast / RNA-binding protein cp 29 nearly identical to SP|Q43349 29 kDa ribonuc
60S ribosomal protein L36 (RPL36A)
expressed protein contains Pfam domain, PF04515: Protein of unknown function, DUF580
speckle-type POZ protein-related contains Pfam PF00651 : BTB/POZ domain
cysteine proteinase, putative contains similarity to cysteine proteinase GI:479060 from [Glycine max]
hypothetical protein similar to mitochondrial protein-like protein (GI:11559424) [Cucumis sativus]
syntaxin 23 (SYP23) / PEP12-like protein identical to SP|O04378 Syntaxin 23 (AtSYP23) (AtPLP) (AtPEP12-like
subtilase family protein contains similarity to subtilase; SP1 GI:9957714 from [Oryza sativa]
tubulin family protein similar to spindle pole body protein [Homo sapiens][GI:2801701][PMID:9566967], gamma-t
DNA-binding protein-related similar to GT-2 factor [Arabidopsis thaliana GI:416490
expressed protein similar to unknown protein (emb|CAB88044.1)
RNA recognition motif (RRM)-containing protein contains InterPro entry IPR000504: RNA-binding region RNP-1
hypothetical protein
mitochondrial transcription termination factor-related / mTERF-related contains Pfam profile PF02536: mTERF

disease resistance family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR00
disease resistance family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR00
crooked neck protein, putative / cell cycle protein, putative similar to Swiss-Prot:P17886 crooked neck protein [D
protein kinase family protein / U-box domain-containing protein contains Pfam profiles PF00069 Eukaryotic prote
expressed protein
MADS-box family protein similar to MADS-box protein NMH 7 GI:2827300 from [Medicago sativa]
GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, E
cytochrome c biogenesis protein family low similarity to cytochrome c biogenesis protein CcdA [Paracoccus pant
hypersensitive response protein 1 (HR1) identical to HR1 [Arabidopsis thaliana] GI:12958166; contains Pfam pro
protein phosphatase 2C, putative / PP2C, putative protein phosphatase 2C, Schizosaccharomyces pombe, PIR2
leucine-rich repeat transmembrane protein kinase, putative
ankyrin repeat family protein contains ankyrin repeat domains, Pfam:PF00023
ubiquitin-conjugating enzyme, putative identical or nearly so to Ubiquitin-conjugating enzymes SP|P35132, SP|P
alpha-xylosidase, putative strong similarity to alpha-xylosidase precursor GI:4163997 from [Arabidopsis thaliana]
anion exchange family protein anion exchange protein 2, Homo sapiens, PIR2:S21086
expressed protein
expressed protein contains 1 transmembrane domain; similar to Protein E6 (Swiss-Prot:Q01197) [Gossypium hir
hypothetical protein
terpene synthase/cyclase family protein similar to sesquiterpene synthases [GI:11934937][Lycopersicon hirsutum
crooked neck protein, putative / cell cycle protein, putative similar to Swiss-Prot:P17886 crooked neck protein [D
MIF4G domain-containing protein / MA3 domain-containing protein similar to SP|Q9P6R9 Cell cycle control prote
DNA-binding protein-related contains Pfam domain PF03479: Domain of unknown function (DUF296), found in A
pathogenesis-related homeodomain protein (PRHA) identical to Pathogenesis-related homeodomain protein (PR
cytidine deaminase, putative / cytidine aminohydrolase, putative identical to cytidine deaminase 6 (CDA6) [Arabi
late embryogenesis abundant group 1 domain-containing protein / LEA group 1 domain-containing protein conta
hypothetical protein
calcium-dependent protein kinase, putative / CDPK, putative similar to calcium-dependent protein kinase GB:AA
expressed protein
BTB/POZ domain-containing protein Interpro IPR000210/ PS50097: BTBB/POZ domain; similar to POZ 56 prote
polygalacturonase, putative / pectinase, putative similar to polygalacturonase PG1 GI:5669846, PG2 GI:566984
two-component phosphorelay mediator 1 (HP1) identical to ATHP1 [Arabidopsis thaliana] GI:4156241
C2 domain-containing protein similar to zinc finger and C2 domain protein GI:9957238 from [Arabidopsis thaliana
hypothetical protein
SET domain-containing protein (SUVH5) identical to SUVH5 [Arabidopsis thaliana] GI:13517751; contains Pfam
expressed protein
lanthionine synthetase C-like family protein contains Pfam domain, PF05147: Lanthionine synthetase C-like prot
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
jacalin lectin family protein similar to myrosinase binding protein homolog GI:2997767 from [Arabidopsis thaliana
expressed protein contains Pfam domain PF04134: Protein of unknown function, DUF393
expressed protein
trans-cinnamate 4-monooxygenase / cinnamic acid 4-hydroxylase (C4H) (CA4H) / cytochrome P450 73 (CYP73)
myb family transcription factor (MYB117) contains Pfam profile: PF00249 myb-like DNA-binding domain
leucine-rich repeat transmembrane protein kinase, putative leucine-rich receptor-like protein (LRPKm1) - Malus
transcription initiation factor IIB-2 / general transcription factor TFIIB-2 (TFIIB2) identical to SP|Q9SS44 Transcri
endonuclease/exonuclease/phosphatase family protein similar to inositol polyphosphate 5-phosphatase I (GI:104
glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein similar to polygalacturonase
glycine-rich protein

expressed protein
ADP-ribosylation factor, putative similar to ADP-ribosylation factor GB:AAA32729 GI:166586 from (Arabidopsis t
hypothetical protein
aminopeptidase P, cytosolic, putative similar to cytosolic aminopeptidase P from [Homo sapiens] GI:8489879, [R
disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a
expressed protein
pentatricopeptide (PPR) repeat-containing protein low similarity to DNA-binding protein [Triticum aestivum] GI:69
hypothetical protein
protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain
ubiquitin-specific protease 1, putative (UBP1) similar to GI:11993461
ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023
dihydropterin pyrophosphokinase, putative / dihydropteroate synthase, putative / DHPS, putative similar to dihyd
expressed protein
protein kinase family protein contains protein kinase domain Pfam:PF00069
RNA-binding protein (XF41) identical to RNA binding protein GI:18181938 from (Arabidopsis thaliana); contains
expressed protein contains Pfam domain, PF04578: Protein of unknown function, DUF594
phosphate translocator-related low similarity to SP|P52178 Triose phosphate/phosphate translocator, non-green
ABC transporter family protein Bactrocera tryoni membrane transporter (white) gene, PID:g3676298
eukaryotic translation initiation factor 1A, putative / eIF-1A, putative / eIF-4C, putative strong similarity to translat
eukaryotic translation initiation factor 1A, putative / eIF-1A, putative / eIF-4C, putative strong similarity to translat
chalcone synthase / naringenin-chalcone synthase identical to SP|P13114
glycerophosphoryl diester phosphodiesterase family protein contains Pfam profile PF03009: Glycerophosphoryl
hypothetical protein
disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of
expressed protein contains Pfam profile PF04525: Protein of unknown function (DUF567)
protein kinase, putative similar to protein kinase APK1A [Arabidopsis thaliana] Swiss-Prot:Q06548
dual specificity protein phosphatase family protein contains Pfam profile: PF00782 dual specificity phosphatase,
pantoate-beta-alanine ligase, putative similar to pantoate--beta-alanine ligase [Lotus japonicus] GI:2292921; con
kinase interacting family protein similar to kinase interacting protein 1 (GI:13936326) [Petunia integrifolia]
ubiquitin-conjugating enzyme, putative strong similarity to SP|P35133 Ubiquitin-conjugating enzyme E2-17 kDa 1
calcium-dependent protein kinase 19 (CDPK19) identical to calcium-dependent protein kinase [Arabidopsis thali
calcium-dependent protein kinase 19 (CDPK19) identical to calcium-dependent protein kinase [Arabidopsis thali
purine permease, putative (PUP2) similar to purine permease [Arabidopsis thaliana] GI:7620007; contains Pfam
phosphatidic acid phosphatase family protein / PAP2 family protein similar to phosphatidic acid phosphatase 2a2
mitogen-activated protein kinase, putative / MAPK, putative (MPK2) identical to mitogen-activated protein kinase
mitogen-activated protein kinase, putative / MAPK, putative (MPK2) identical to mitogen-activated protein kinase
glutamate:glyoxylate aminotransferase 2 (GGT2) identical to glutamate:glyoxylate aminotransferase 2 [Arabidop
glutamate:glyoxylate aminotransferase 2 (GGT2) identical to glutamate:glyoxylate aminotransferase 2 [Arabidop
myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain
myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain
myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain
glycosyl hydrolase family protein 17 similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from [Nicotiana
expressed protein
CTP synthase, putative / UTP--ammonia ligase, putative similar to SP|P17812 CTP synthase (EC 6.3.4.2) (UTP-
basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed s
seed maturation family protein similar to embryonic cell protein [Daucus carota] GI:18337; contains Pfam profile
mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein

auxin-responsive protein-related similar to indole-3-acetic acid induced protein arg7 (SP:P32295) [Vigna radiata]
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
ubiquitin-conjugating enzyme 13 (UBC13) E2; identical to gi:992706
histone H3 identical to several histone H3 proteins, including Zea mays SP|P05203, Medicago sativa GI:166384
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to pEARLI 1 (Accession No. L43
germin-like protein (GLP9) identical to germin-like protein subfamily 1 member 8 [SP|Q9LEA7]
protein kinase, putative similar to ATMRK1 [Arabidopsis thaliana] gi|2351097|dbj|BAA22079
basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
polyubiquitin, putative similar to polyubiquitin GI:248337 from [Zea mays]
plant EC metallothionein-like family 15 protein identical to EC protein homolog 2 (SP:Q42377) {Arabidopsis thalia
replication factor C 37 kDa, putative Similar to SWISS-PROT:P35249 activator 1 37 kDa subunit (Replication fac
leucine-rich repeat transmembrane protein kinase, putative
transporter-related low similarity to SP|P39843 Multidrug resistance protein 2 (Multidrug-efflux transporter 2) {Ba
expressed protein contains Pfam profile PF04525: Protein of unknown function (DUF567)
glycine-rich protein cylicin II - bovine, PIR2:I46014
UDP-glucoronosyl/UDP-glucosyl transferase family protein glycosyltransferase family
clathrin adaptor complex small chain family protein contains Pfam profile: PF01217 clathrin adaptor complex sm
calcium-binding EF hand family protein contains Pfam profile: PF00036 EF hand
expressed protein
cytochrome P450 family protein flavonoid 3',5'-hydroxylase Hf1, Petunia x hybrida, PIR2:S38985
major intrinsic family protein / MIP family protein contains Pfam profile: MIP PF00230
expressed protein
expressed protein
hypothetical protein
Expressed protein
eukaryotic translation initiation factor 4A, putative / eIF-4A, putative similar to Eukaryotic initiation factor 4A-10 G
hypothetical protein
heat shock protein-related contains weak similarity to Pfam profile PF00011: Hsp20/alpha crystallin family
flavin-containing monooxygenase family protein / FMO family protein similar to flavin-containing monooxygenase
phosphatidylinositol-4-phosphate 5-kinase family protein similar to phosphatidylinositol-4-phosphate 5-kinase At
cyclopropane-fatty-acyl-phospholipid synthase family protein similar to cyclopropane synthase [Sterculia foetida]
homocysteine S-methyltransferase 1 (HMT-1) identical to GB:AAF23821 from [Arabidopsis thaliana]
expressed protein contains similarity to SKP1 interacting partner 3 [Arabidopsis thaliana] GI:10716951
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed s
leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR00
MADS-box family protein contains Pfam profile: PF00319 SRF-type transcription factor (DNA-binding and dimeri
trichome differentiation protein / GLABROUS1 protein (GL1) identical to trichome differentiation protein GL1 SP:
microtubule associated protein (MAP65/ASE1) family protein low similarity to SP|P50275 Anaphase spindle elon
cytochrome P450, putative similar to cytochrome P450 79B2 (SP:O81346) [Arabidopsis thaliana]
serine carboxypeptidase S10 family protein similar to retinoid-inducible serine carboxypeptidase precursor (GI:15
hypothetical protein contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287
hypothetical protein
DNA-binding protein-related similar to GTL1 [Arabidopsis thaliana] GI:2664198
expressed protein
syntaxin-related family protein similar to proteins At3g54160, At1g47920 (syntaxin SYP81), At5g41830, At3g441
LOB domain family protein / lateral organ boundaries domain family protein (LBD10) identical to SP|O64836 Put
protein kinase family protein Three false introns were added with non-consensus splice sites to circumenvent fra

transcription factor-related low similarity to tumor-related protein [Nicotiana glauca x Nicotiana langsdorffii] GI:68
calcineurin B-like protein 2 (CBL2) identical to calcineurin B-like protein 2 GI:3309084 from [Arabidopsis thaliana
tubulin family protein similar to spindle pole body protein [Homo sapiens][GI:2801701][PMID:9566967], gamma-t
(S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid o
expressed protein
CCAAT-box binding transcription factor, putative similar to CAAT-box DNA binding protein subunit B (NF-YB) (SP
CCAAT-box binding transcription factor, putative similar to CAAT-box DNA binding protein subunit B (NF-YB) (SP
2-oxoacid dehydrogenase family protein similar to SP|P36957 Dihydrolipoamide succinyltransferase component
pyruvate kinase, putative identical to probable pyruvate kinase, cytosolic isozyme (EC 2.7.1.40) [Arabidopsis tha
WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA -binding domain
60S ribosomal protein L18 (RPL18C) 60S ribosomal protein L18, Arabidopsis thaliana, SWISSPROT:RL18_ARA
heavy-metal-associated domain-containing protein low similarity to wound-responsive gene KED [Nicotiana taba
dehydration-responsive protein-related similar to early-responsive to dehydration stress ERD3 protein [Arabidops
glutathione S-transferase, putative Second of three repeated putative glutathione transferases. 72% identical to
expressed protein
expressed protein
heat shock protein 81-4 (HSP81-4) nearly identical to heat shock protein hsp81.4 [Arabidopsis thaliana] GI:1906
phosphatidylinositolglycan synthase family protein similar to SP|Q92535 Phosphatidylinositol-glycan biosynthesis
PHD finger family protein contains Pfam domain, PF00628: PHD-finger
sucrose synthase / sucrose-UDP glucosyltransferase (SUS1) identical to SP|P49040 Sucrose synthase (EC 2.4.
exonuclease family protein contains exonuclease domain, Pfam:PF00929
exonuclease family protein contains exonuclease domain, Pfam:PF00929
exonuclease family protein contains exonuclease domain, Pfam:PF00929
exonuclease family protein contains exonuclease domain, Pfam:PF00929
E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At6), putative E3 ubiquitin ligase; similar to Skp1 GI:4959
two-component phosphorelay mediator 1 (HP1) identical to ATHP1 [Arabidopsis thaliana] GI:4156241
chloride channel protein (CLC-b) identical to CLC-b chloride channel protein GB:CAA96058 from [Arabidopsis th
expressed protein
zinc finger (DHHC type) family protein contains Pfam profile PF01529: DHHC zinc finger domain
DJ-1 family protein low similarity to SP|Q51732 protease I from Pyrococcus furiosus; contains Pfam profile: PF0
splicing factor RSZp21 (RSZP21) / 9G8-like SR protein (SRZ21) nearly identical to 9G8-like splicing factor SRZ2
splicing factor RSZp21 (RSZP21) / 9G8-like SR protein (SRZ21) nearly identical to 9G8-like splicing factor SRZ2
terpene synthase/cyclase family protein similar to terpene synthase GB:CAA72074 from [Arabidopsis thaliana]
serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza s
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to tapetum-specific protein a9 pr
protein kinase (APK1a) identical to Protein kinase APK1A from [Arabidopsis thaliana] SWISS-PROT:Q06548
protein kinase (APK1a) identical to Protein kinase APK1A from [Arabidopsis thaliana] SWISS-PROT:Q06548
cytochrome P450 family protein similar to Cytochrome P450 90A1 (SP:Q42569) [Arabidopsis thaliana]; contains
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed s
glycine-rich protein / oleosin
wall-associated kinase, putative
serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II-3 precursor (SP:P52711) (CP-M
UDP-galactose/UDP-glucose transporter-related contains weak similarity to UDP-galactose/UDP-glucose transp
expressed protein
fatty acid hydroxylase (FAH1) identical to fatty acid hydroxylase Fah1p GB:AF021804 GI:2736147 from [Arabido
membrane protein, putative contains 7 transmembrane domains; similar to inhibitor of apoptosis-2 IAP-2 (GI:200
40S ribosomal protein S9 (RPS9B) 40S ribosomal protein S9, Chlamydomonas sp., EMBL:AU066528
ubiquinol-cytochrome C reductase complex 14 kDa protein, putative similar to SP|P48502 Ubiquinol-cytochrome

serine-rich protein-related contains some similarity to serine-rich proteins
DNAJ heat shock protein, putative (J3) identical to AtJ3 [Arabidopsis thaliana] GI:2641638, strong similarity to se
self-incompatibility protein-related similar to S3 self-incompatibility protein [Papaver rhoeas] GI:1107841
transducin family protein / WD-40 repeat family protein contains 5 (4 significant) WD-40 repeats; similar to perio
terpene synthase/cyclase family protein predicted protein, Arabidopsis thaliana
patatin, putative similar to patatin-like latex allergen [Hevea brasiliensis][PMID:10589016]; contains patatin doma
pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
40S ribosomal protein S6 (RPS6A) ribosomal protein S6, Arabidopsis thaliana, PID:g2662469
transporter-related low similarity to SP|P39843 Multidrug resistance protein 2 (Multidrug-efflux transporter 2) {Ba
transporter-related low similarity to SP|P39843 Multidrug resistance protein 2 (Multidrug-efflux transporter 2) {Ba
MATE efflux family protein Strong similarity to gi|4734005 F3L12.7 hypothetical protein from Arabidopsis thaliana
myosin heavy chain-related
purine permease, putative (PUP2) similar to purine permease [Arabidopsis thaliana] GI:7620007; contains Pfam
acid phosphatase class B family protein similar to SP|P15490 STEM 28 kDa glycoprotein precursor (Vegetative
hypothetical protein
curculin-like (mannose-binding) lectin family protein low similarity to Ser/Thr protein kinase [Zea mays] GI:25980
cyclin family protein similar to cyclin 2 [Trypanosoma brucei] GI:7339572, cyclin 6 [Trypanosoma cruzi] GI:12005
small nuclear ribonucleoprotein G, putative / snRNP-G, putative / Sm protein G, putative similar to SWISS-PROT
terpene synthase/cyclase family protein similar to terpene synthase GB:CAA72074 from [Arabidopsis thaliana]
plastocyanin-like domain-containing protein
hypothetical protein
serine/threonine protein phosphatase PP1 isozyme 6 (PP1BG) (TOPP6) identical to SP|P48486 Serine/threonin
ubiquitin-specific protease 24, putative (UBP24) identical to ubiquitin-specific protease 24 [Arabidopsis thaliana]
ubiquitin-specific protease 24, putative (UBP24) identical to ubiquitin-specific protease 24 [Arabidopsis thaliana]
rhomboid protein-related contains 6 transmembrane domains; similar to phosphatidyl inositol glycan class T (GI:
hypothetical protein
Cwf15 / Cwc15 cell cycle control family protein contains Pfam profile PF04889: Cwf15/Cwc15 cell cycle control p
oleosin / glycine-rich protein
expressed protein
expressed protein
expressed protein
expressed protein
paired amphipathic helix repeat-containing protein low similarity to transcription co-repressor Sin3 [Xenopus laev
senescence-associated family protein contains similarity to senescence-associated gene Ntdin from GI:7594903
expressed protein
expressed protein
glutathione S-transferase, putative
subtilase family protein contains Pfam domain, PF00082: Subtilase family; contains Pfam domain, PF02225: pro
basic helix-loop-helix (bHLH) family protein contains Pfam domain, PF00010: Helix-loop-helix DNA-binding doma
Rac-like GTP-binding protein (ARAC2) identical to RAC-like GTP binding protein ARAC2 SP:Q38903
expressed protein similar to cDNA bHLH transcription factor (bHLH zeta gene) GI:32563005
expressed protein
myb family transcription factor (MYB47) contains Pfam profile: PF00249 myb-like DNA-binding domain
clathrin adaptor complexes medium subunit family protein contains Pfam profile: PF00928 adaptor complexes m
pectinesterase family protein contains Pfam profile: PF01095 pectinesterase
PHD finger family protein contains Pfam domain, PF00628: PHD-finger
no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; similar to
aminotransferase, putative tsimilar to nicotianamine aminotransferase from Hordeum vulgare [GI:6498122, GI:64

EXS family protein / ERD1/XPR1/SYG1 family protein similar to PHO1 protein [Arabidopsis thaliana] GI:200690
hypothetical protein No suitable start codon could be identified.
ADP-ribosylation factor 1 (ARF1) identical to ADP-ribosylation factor ARF1({Arabidopsis thaliana} (SP:P36397) (
peroxiredoxin type 2, putative strong similarity to type 2 peroxiredoxin [Brassica rapa subsp. pekinensis] GI:4928
fip1 motif-containing protein contains Pfam profile PF05182: Fip1 motif
expressed protein
expressed protein
UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl ar
F-box family protein contains F-box domain Pfam:PF00646
expressed protein
expressed protein
beta-ketoacyl-CoA synthase, putative Strong similarity to beta-keto-Coa synthase gb|U37088 from Simmondsia
esterase/lipase/thioesterase family protein similar to ethylene-induced esterase [Citrus sinensis] GI:14279437, p
nascent polypeptide-associated complex (NAC) domain-containing protein similar to alpha-NAC, non-muscle for
F-box family protein similar to F-box protein family, AtFBX7 (GI:20197899) [Arabidopsis thaliana]
zinc finger (GATA type) family protein
WRKY family transcription factor
cytochrome P450, putative similar to cytochrome p450 GI:438240 from [Solanum melongena]
3-phosphoshikimate 1-carboxyvinyltransferase / 5-enolpyruvylshikimate-3-phosphate / EPSP synthase nearly ide
fasciclin-like arabinogalactan-protein, putative similar to gi_13377784_gb_AAK20861
tolA protein-related contains weak similarity to Swiss-Prot:P19934 TolA protein [Escherichia coli]
emsy N terminus domain-containing protein / ENT domain-containing protein contains Pfam profile PF03735: EN
12S seed storage protein, putative / cruciferin, putative strong similarity to SP|P33525 Cruciferin CRU1 precurso
1-aminocyclopropane-1-carboxylate synthase, putative / ACC synthase, putative similar to ACC synthases from A
protein kinase family protein contains Prosite:PS00108: Serine/Threonine protein kinases active-site signature a
mandelate racemase/muconate lactonizing enzyme C-terminal domain-containing protein / hydrolase, alpha/beta
expressed protein ; expression supported by MPSS
myb family transcription factor (MYB32) similar to myb DNA-binding protein GI:19052 from [Hordeum vulgare]
MATE efflux family protein contains Pfam profile PF01554: Uncharacterized membrane protein family
hypothetical protein
purine permease, putative similar to purine permease GI:7620007 from [Arabidopsis thaliana]
CBS domain-containing protein / transporter associated domain-containing protein contains Pfam profiles PF005
serine/threonine protein kinase, putative similar to Pto kinase interactor 1 (Pti1)[Lycopersicon esculentum] gi|366
kelch repeat-containing protein contains Pfam profile PF01344: Kelch motif
integral membrane family protein / nodulin MtN21-related low similarity to MtN21 [Medicago truncatula] GI:25985
cupin family protein contains Pfam profile PF00190: Cupin
lectin protein kinase family protein contains Pfam domains, PF00138: Legume lectins alpha domain, PF00139: L
carbohydrate kinase family contains Pfam profile PF01256: Carbohydrate kinase
carbohydrate kinase family contains Pfam profile PF01256: Carbohydrate kinase
hypothetical protein contains Pfam profile PF04525: Protein of unknown function (DUF567)
expressed protein
hypothetical protein
zinc finger (GATA type) family protein GATA transcription factor 3, Arabidopsis thaliana, Y13650
zinc finger (GATA type) family protein GATA transcription factor 3, Arabidopsis thaliana, Y13650
expressed protein
60S ribosomal protein L7 (RPL7A) similar to ribosomal protein L7 GB:AAA03081 GI:307388 from [Homo sapiens
peroxidase, putative similar to peroxidase isozyme [Armoracia rusticana] gi|217932|dbj|BAA14143
cytochrome P450 71B15, putative (CYP71B15) Identical to Cytochrome P450 (SP:Q9LW27) [Arabidopsis thalian

expressed protein putative zinc-finger protein - Arabidopsis thaliana,PID:g4406777
annexin 1 (ANN1) identical to annexin (AnnAt1) [Arabidopsis thaliana] GI:4959106
hydrolase, alpha/beta fold family protein contains Pfam profile: PF00561 alpha/beta hydrolase fold
expressed protein
protein kinase, putative similar to protein kinase KIPK (KCBP-interacting protein kinase) [Arabidopsis thaliana] gi
nodulin MtN21 family protein similar to MtN21 [Medicago truncatula] GI:2598575
zinc finger (C2H2 type) family protein contains Pfam profile: PF00096 zinc finger, C2H2 type
hypothetical protein hypothetical protein - Arabidopsis thaliana, EMBL:AC006438.2
reticulon family protein (RTNLB12) contains Pfam profile PF02453: Reticulon
cyclic nucleotide-regulated ion channel (CNGC10) (ACBK1) almost identical to CaM-regulated potassium ion cha
dehydration-responsive family protein similar to early-responsive to dehydration stress ERD3 protein [Arabidopsi
disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of
pfkB-type carbohydrate kinase family protein contains Pfam profile: PF00294 pfkB family carbohydrate kinase
expressed protein contains similarity to carboxyl-terminal proteinase contains Pfam profile PF03080: Arabidopsis
expressed protein contains Pfam profile PF03641: decarboxylase family protein
hypothetical protein
histone deacetylase (RPD3A) identical to SP|O22446 Histone deacetylase (HD) {Arabidopsis thaliana}
transcriptional adaptor (ADA2a) identical to transcriptional adaptor ADA2a [Arabidopsis thaliana] gi|13591698|gb
expressed protein
sporulation protein-related isoform contains non-consensus AT-donor acceptor site at intron 6; similar to Stage II
quercetin 3-O-methyltransferase 1 / flavonol 3-O-methyltransferase 1 / caffeic acid/5-hydroxyferulic acid O-meth
polyubiquitin (UBQ9) identical to polyubiquitin (ubq9) gene sequence GI:304120 from [Arabidopsis thaliana]
expressed protein
metallo-beta-lactamase family protein similar to Metal Dependent Hydrolase GB:AAD18619 from [Chlamydophil
adenylate kinase, putative similar to adenylate kinase (ATP-AMP transphosphorylase) [Arabidopsis thaliana] SW
hypothetical protein similar to unknown protein (gb|AAD26867.1)
glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIG
omega-3 fatty acid desaturase, chloroplast, temperature-sensitive (FAD8) identical to SP:48622 Temperature-se
bZIP transcription factor family protein similar to bZIP protein(G/HBF-1) GI:1905785 from [Glycine max]; contain
xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan trans
expressed protein similar to GI:2827651,GP:10764853, GI:10764852, GI:7527728, GI:4406788, GI:6063544 [Ar
subtilase family protein contains similarity to subtilase; SP1 GI:9957714 from [Oryza sativa]
hypothetical protein low similarity to SP|P07271 DNA repair and recombination protein PIF1, mitochondrial precu
expressed protein
auxilin-related low similarity to SP|Q27974 Auxilin {Bos taurus}
peroxidase, putative identical to peroxidase [Arabidopsis thaliana] gi|6822093|emb|CAB71009; identical to cDNA
F-box family protein contains F-box domain Pfam:PF00646
hypothetical protein
Rac-like GTP-binding protein (ARAC5) / Rho-like GTP-binding protein (ROP4) identical to RAC-like GTP-binding
expressed protein
proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family
expressed protein
patatin-related contains Patatin domain PF01734
phospholipid/glycerol acyltransferase family protein
expressed protein
MADS-box protein (AGL6)
expressed protein
protein phosphatase 2C-related / PP2C-related similar to protein phosphatase 2C GI:3242077 from (Arabidopsis

protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
hypothetical protein
expressed protein
expressed protein
cell division control protein 2 homolog B (CDC2B) identical to cell division control protein 2 homolog B [Arabidop
basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
expressed protein
F-box family protein contains F-box domain Pfam:PF00646
AAA-type ATPase family protein similar to SP|P18708 Vesicular-fusion protein NSF (N-ethylmaleimide-sensitive
1-aminocyclopropane-1-carboxylate synthase, putative / ACC synthase, putative similar to ACC synthases from
protein kinase (KIPK) identical to protein kinase KIPK (KCBP-interacting protein kinase) [Arabidopsis thaliana] gi
protein kinase (KIPK) identical to protein kinase KIPK (KCBP-interacting protein kinase) [Arabidopsis thaliana] gi
MADS-box protein (AGL28) similar to MADS-box transcription factor GI:6580943 from [Picea abies]; contains Pf
60S ribosomal protein L15 (RPL15A)
protein kinase family protein contains Pfam PF01657: Domain of unknown function; similar to receptor-like prote
hypothetical protein
xylose isomerase family protein contains similarity to Xylose isomerase (EC 5.3.1.5) (Swiss-Prot:P22842) [Therm
vacuolar proton ATPase, putative similar to vacuolar proton ATPase 100-kDa subunit from Dictyostelium discoide
lectin protein kinase family protein contains Pfam domains PF00069: Protein kinase domain and PF01453: Lecti
annexin 7 (ANN7) nearly identical to calcium-binding protein annexin 7 [Arabidopsis thaliana] GI:12667522
hypothetical protein
hypothetical protein
sinapoylglucose:malate sinapoyltransferase (SNG1) similar to serine carboxypeptidase I precursor (SP:P37890)
4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein similar to gi:112801 from Petr
tryptophan synthase, beta subunit, putative similar to SP|P14671 Tryptophan synthase beta chain 1, chloroplast
endonuclease/exonuclease/phosphatase family protein simlar to inositol polyphosphate 5-phosphatase I (GI:104
armadillo/beta-catenin repeat family protein / U-box domain-containing family protein contains Pfam domain, PF
transducin family protein / WD-40 repeat family protein contains 5 WD-40 repeats (PF00400); similar to beta tran
EXS family protein / ERD1/XPR1/SYG1 family protein similar to PHO1 protein [Arabidopsis thaliana] GI:200690
leucine-rich repeat family protein contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611;
ubiquitin family protein contains Pfam profiles PF00240: Ubiquitin family, PF00627: UBA/TS-N domain;
serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza s
ovule development protein, putative similar to ovule development protein AINTEGUMENTA (GI:1209099) [Arabid
S-adenosyl-L-methionine:carboxyl methyltransferase family protein similar to SAM:jasmonic acid carboxyl methy
2S seed storage protein 3 / 2S albumin storage protein / NWMU2-2S albumin 3 identical to SP|P15459
hypothetical protein
DNAJ heat shock N-terminal domain-containing protein contains Pfam profile PF00226 DnaJ domain; DNAJ dom
small nuclear ribonucleoprotein D2, putative / snRNP core protein D2, putative / Sm protein D2, putative similar t
small nuclear ribonucleoprotein D2, putative / snRNP core protein D2, putative / Sm protein D2, putative similar t
small nuclear ribonucleoprotein D2, putative / snRNP core protein D2, putative / Sm protein D2, putative similar t
hypothetical protein
3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein similar to steroid
expressed protein
protein kinase family protein contains Pfam profile: PF00069 Eukaryotic protein kinase domain
mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein contains P
mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein contains P
seven transmembrane MLO family protein / MLO-like protein 2 (MLO2) idenctical to membrane protein Mlo2 [Ara
polygalacturonase, putative / pectinase, putative similar to polygalacturonase 5 [Lycopersicon esculentum] GI:24

UDP-sulfoquinovose:DAG sulfoquinovosyltransferase / sulfolipid synthase (SQD2) identical to GI:20302857
expressed protein
pfkB-type carbohydrate kinase family protein similar to fructokinase GI:2102693 from [Lycopersicon esculentum]
hypothetical protein
ankyrin repeat family protein contains ankyrin repeat domains, Pfam:PF00023
auxin-responsive factor (ARF6) identical to ARF6 [Arabidopsis thaliana] GI:4102600 (Science 276 (5320), 1865-
CHP-rich zinc finger protein, putative
basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
DNAJ heat shock protein, putative simlar to SP|P25685 DnaJ homolog subfamily B member 1 (Heat shock 40 kD
hypothetical protein DYNAMIN-LIKE PROTEIN- Arabidopsis thaliana, EMBL:L36939
phosphatidic acid phosphatase family protein / PAP2 family protein similar to phosphatidic acid phosphatase 2a2
cytochrome P450 71A19, putative (CYP71A19) Identical to Cytochrome P450 (SP:Q9T0K0) [Arabidopsis thalian
expressed protein
H+-transporting two-sector ATPase, putative similar to SP|P54641 Vacuolar ATP synthase subunit d (EC 3.6.3.14
auxin transport protein, putative similar to auxin transport protein PIN7[Arabidopsis thaliana] gi|5817305|gb|AAD
hypothetical protein
zinc finger (C2H2 type) family protein contains Pfam PF00096: Zinc finger, C2H2 type
auxin transport protein (EIR1) identical to auxin transport protein EIR1 [Arabidopsis thaliana] gi|3377507|gb|AAC
serine decarboxylase identical to serine decarboxylase [Arabidopsis thaliana] GI:15011302; contains Pfam profil
pentatricopeptide (PPR) repeat-containing protein contains INTERPRO:IPR002885 PPR repeats
no apical meristem (NAM) family protein similar to NAC2 (GI:6456751) [Arabidopsis thaliana]; contains Pfam PF
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
cytochrome P450 71B20, putative (CYP71B2) identical to cytochrome P450 71B20 (SP:Q9LTM3) [Arabidopsis th
hypothetical protein
expressed protein
terpene synthase/cyclase family protein
integral membrane family protein contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569;
serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza s
nuclear movement family protein contains Pfam profile: PF03593 nuclear movement protein
zinc finger (C3HC4-type RING finger) family protein similar to Pfam domain, PF00097: Zinc finger, C3HC4 type (
zinc finger (C3HC4-type RING finger) family protein similar to Pfam domain, PF00097: Zinc finger, C3HC4 type (
auxin-responsive protein / indoleacetic acid-induced protein 19 (IAA19) identical to SP|O24409 Auxin-responsive
phosphoinositide phosphatase family protein contains similarity to phosphoinositide phosphatase SAC1 [Rattus
RNase Z 97% identical to RNase Z (GI:20975607) [Arabidopsis thaliana]; similar to RNase Z (GI:20975609) [Ara
hypothetical protein contains Pfam profile PF05056: Protein of unknown function (DUF674)
glycine-rich protein (GRP16) oleosin; glycine-rich protein 16 (GRP16) PMID:11431566
amino acid permease, putative strong similarity to AUX1 GI:1531758 from [Arabidopsis thaliana]; contains Pfam
senescence-associated family protein similar to senescence-associated protein 5 [Hemerocallis hybrid cultivar] g
ARP2/3 complex 21 kDa subunit family contains Pfam PF04062: P21-ARC (ARP2/3 complex 21 kDa subunit); si
heat shock factor protein 1 (HSF1) / heat shock transcription factor 1 (HSTF1) identical to heat shock transcriptio
cyclin-dependent kinase / CDK (CKS1) identical to Cks1 protein [Arabidopsis thaliana] gi|2274859|emb|CAA038
serine/threonine protein kinase, putative similar to Pto kinase interactor 1 (serine/threonine protein kinase) [Lyco
calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase
NADH-ubiquinone oxidoreductase-related contains weak similarity to NADH-ubiquinone oxidoreductase 15 kDa
protein phosphatase 2C, putative / PP2C, putative protein phosphatase 2C, Schizosaccharomyces pombe, PIR2
nucleoporin-related contains weak similarity to Nucleoporin NUP1 (Nuclear pore protein NUP1) (Swiss-Prot:P20
expressed protein ; expression supported by MPSS
expressed protein contains Pfam profile PF05212: Protein of unknown function (DUF707)

transcription initiation factor IID-2 (TFIID-2) / TATA-box factor 2 / TATA sequence-binding protein 2 (TBP2) identic
transcription initiation factor IID-2 (TFIID-2) / TATA-box factor 2 / TATA sequence-binding protein 2 (TBP2) identic
UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl ar
embryo-specific protein-related contains weak similarity to embryo-specific protein 3 (GI:3335171) [Arabidopsis t
glycerol kinase, putative similar to glycerol kinase (ATP:glycerol 3-phosphotransferase, Glycerokinase, GK)[Myc
late embryogenesis abundant protein (ECP31) / LEA protein identical to LEA protein in group 5 (AtECP31) [Arab
self-incompatibility protein-related low similarity to self-incompatibility [Papaver nudicaule] GI:3097262
phototropic-responsive NPH3 family protein contains NPH3 family domain, Pfam:PF03000
expressed protein
expressed protein
oxygenase-related similar to myo-inositol oxygenase [Sus scrofa] gi|17432544|gb|AAL39076
aldose 1-epimerase family protein similar to apospory-associated protein C; APOC [Chlamydomonas reinhardtii]
self-incompatibility protein-related simlar to self-incompatibility [Papaver rhoeas] GI:3097260
hypothetical protein
aspartyl protease family protein contains Pfam PF00026: Eukaryotic aspartyl protease
MATE efflux protein-related strong similarity to unknown protein (pir||T02324); contains Pfam profile PF01554 Ur
short-chain dehydrogenase/reductase (SDR) family protein similar to 3-beta-hydroxysteroiddehydrogenase GI:15
glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIG
transducin family protein / WD-40 repeat family protein contains 5 (4 significant) WD-40 repeats; similar to period
amino acid permease family protein similar to SP|P18581 Low-affinity cationic amino acid transporter-2 (CAT-2)
expansin, putative (EXP10) similar to expansin At-EXP1 GI:1041702 from [Arabidopsis thaliana]; alpha-expansin
transducin family protein / WD-40 repeat family protein contains Pfam profile: PF00400 WD domain, G-beta repe
subtilase family protein contains similarity to meiotic serine proteinase TMP GI:6468325 from [Lycopersicon escu
strictosidine synthase family protein similar to hemomucin [Drosophila melanogaster][GI:1280434], strictosidine s
protein kinase family protein contains protein kinase domain, Pfam:PF00069
auxin-responsive GH3 family protein similar to auxin-responsive GH3 product [Glycine max] GI:18591; contains
inorganic carbon transport protein-related contains weak similarity to Swiss-Prot:P27372 inorganic carbon transp
two-component responsive regulator family protein / response regulator family protein contains Pfam profile: PF0
hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains, INTERPRO:IPR002965
disease resistance protein-related contains Pfam domain, PF00931: NB-ARC domain, a novel signalling motif fo
leucine-rich repeat family protein / protein kinase family protein contains leucine rich repeat (LRR) domains, Pfar
nodulin MtN3 family protein similar to MtN3 GI:1619602 (root nodule development) from [Medicago truncatula]
transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related contains Pfam profiles: PF0230
inorganic pyrophosphatase, putative [soluble] / pyrophosphate phospho-hydrolase, putative / PPase, putative sir
UDP-glucoronosyl/UDP-glucosyl transferase family protein contains similarity to UDPG glucosyltransferase GB:A
expressed protein various predicted proteins, Arabidopsis thaliana
expressed protein
mitochondrial transcription termination factor-related / mTERF-related contains Pfam profile PF02536: mTERF
cytochrome P450 71B19, putative (CYP71B19) Identical to cytochrome P450 71B19 (SP:Q9LTM4)[Arabidopsis t
NLI interacting factor (NIF) family protein contains Pfam profile PF03031: NLI interacting factor
expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538
AP2 domain-containing transcription factor, putative similar to TINY GB:CAA64359; contains Pfam profile PF008
dehydration-responsive family protein similar to early-responsive to dehydration stress ERD3 protein [Arabidopsi
vacuolar sorting receptor, putative nearly identical to vacuolar sorting receptor homolog (GP:1737218) [Arabidop
hypothetical protein
cytochrome P450, putative cytochrome p450, Arabidopsis thaliana, PID:G2252844
expressed protein
expressed protein ; expression supported by MPSS

expressed protein contains Pfam PF05421: Protein of unknown function (DUF751)
SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein similar to polyphosphoinositide b
heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related low similarity to copper ho
protein kinase family protein contains Prosite:PS00108: Serine/Threonine protein kinases active-site signature a
glycine-rich protein
isoprenylcysteine carboxyl methyltransferase family protein / ICMT family protein similar to SP|O60725 Protein-S
translation elongation factor Ts (EF-Ts), putative similar to ethylene-responsive elongation factor EF-Ts precurso
disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of
expressed protein
NOL1/NOP2/sun family protein contains Pfam profile PF01189: NOL1/NOP2/sun family
vacuolar sorting receptor, putative nearly identical to vacuolar sorting receptor homolog [Arabidopsis thaliana] GI
vacuolar sorting receptor, putative nearly identical to vacuolar sorting receptor homolog [Arabidopsis thaliana] GI
leucine-rich repeat protein kinase, putative similar to light repressible receptor protein kinase, gi|2129635; contai
GDSL-motif lipase, putative similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:150543
suppressor of lin-12-like protein-related / sel-1 protein-related similar to Sel-1 homolog precursor (Suppressor of
farnesyl pyrophosphate synthetase 1, mitochondrial (FPS1) / FPP synthetase 1 / farnesyl diphosphate synthase
expressed protein
auxin transport protein, putative similar to auxin transport protein PIN7[Arabidopsis thaliana] gi|5817305|gb|AAD
NADP-dependent oxidoreductase, putative (P1) identical to probable NADP-dependent oxidoreductase P1, zeta
F-box family protein contains Pfam profile: PF00646 F-box domain; similar to SKP1 interacting partner 2 (SKIP2)
cytochrome P450 family protein similar to Cytochrome P450 72A1 (SP:Q05047) [Catharanthus roseus]; similar t
tRNA synthetase class II (G, H, P and S) family protein similar to SP|O23627 Glycyl-tRNA synthetase (EC 6.1.1.
cytochrome P450 71B28, putative (CYP71B28) Identical to Cytochrome P450 (SP:Q9SAE3) [Arabidopsis thalian
expressed protein
expansin, putative (EXP14) similar to alpha-expansin 3 GI:6942322 from [Triphysaria versicolor]; alpha-expansin
pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
T-complex protein 11 contains Pfam PF05794: T-complex protein 11
polyubiquitin (UBQ4) identical to GI:17677
hypothetical protein
agamous-like MADS box protein AGL5 / floral homeodomain transcription factor (AGL5) identical to SP|P29385 A
agamous-like MADS box protein AGL5 / floral homeodomain transcription factor (AGL5) identical to SP|P29385 A
hypothetical protein
F-box family protein
diacylglycerol kinase, putative contains INTERPRO domain, IPR001206, DAG-kinase catalytic domain
disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of
expressed protein
hypothetical protein
mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein
DNA (cytosine-5-)-methyltransferase, putative similar to cytosine-5 methyltransferase (METII) [Arabidopsis thalia
amino acid transporter family protein similar to amino acid carrier [Ricinus communis] GI:3293031; contains Pfam
endomembrane protein 70, putative TM4 family;
tRNA synthetase class I (W and Y) family protein contains Pfam profile: PF00579 tRNA synthetases class I (W a
expressed protein
glycine-rich RNA-binding protein similar to RNA-binding protein GB:S46286 from [Nicotiana sylvestris]
choline monooxygenase, putative (CMO-like) similar to Choline monooxygenase, chloroplast precursor (EC 1.14
expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is un
isoflavone reductase family protein similar to phenylcoumaran benzylic ether reductase homolog Fi1 [Forsythia x
peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein similar to cyclophylin [Digitalis lanata] GI:15637

basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
tRNA-splicing endonuclease positive effector-related contains similarity to SEN1, a positive effector of tRNA-spli
expressed protein
polyubiquitin (UBQ3) identical to GI:928809
polyubiquitin (UBQ3) identical to GI:928809
expressed protein contains similarity to hypothetical proteins of [Arabidopsis thaliana]
MADS-box protein (AGL62) contains Pfal profile PF00319: SRF-type transcription factor (DNA-binding and dime
expressed protein
oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to naringenin,2-oxoglutarate 3-dioxygenase (flavon
invertase/pectin methylesterase inhibitor family protein contains Pfam profile PF04043: Plant invertase/pectin me
protein kinase family protein contains protein kinase domain, Pfam:PF00069
expressed protein
hypothetical protein predicted proteins, Arabidopsis thaliana contains Pfam profile PF03080: Arabidopsis protein
expressed protein
WD-40 repeat protein (MSI4) contains 6 (4 significant) WD-40 repeats (PF0400); identical to WD-40 repeat prote
expressed protein
F-box family protein contains Pfam profile: PF00646 F-box domain
ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023
F-box family protein contains Pfam:PF00646 F-box domain ; similar to SKP1 interacting partner 2 (SKIP2) TIGR
WD-40 repeat family protein contains 5 WD-40 repeats (PF00400); similar to fizzy1 (GI:3298595) {Xenopus laev
glycosyl hydrolase family protein 17 similar to beta-1,3-glucanase GI:15150341 from [Camellia sinensis]; C-term
SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein contains Pfam PF00650 : CRAL/
myb family transcription factor (MYB39) contains Pfam profile: PF00249 myb-like DNA-binding domain
protein kinase family protein contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein k
ADP-ribosylation factor, putative similar to ADP-ribosylation factor-like protein 1 (SP:P40616) [Homo sapiens]; Al
glutamyl-tRNA(Gln) amidotransferase B family protein contains Pfam profiles: PF02934 PET112 family, N termin
expressed protein
expressed protein
expressed protein
seed maturation family protein similar to SP|P09444 Late embryogenesis abundant protein D-34 (LEA D-34) {Go
expressed protein
RIO1 family protein similar to extragenic suppressor of the bimD6 mutation (SUDD) [Emericella nidulans] GI:233
kelch repeat-containing protein contains Pfam profile PF01344: Kelch motif
hypothetical protein
expressed protein identical to senescence-associated protein SAG102 (GI::22331931) [Arabidopsis thaliana] (un
peroxidase, putative peroxidase [Arabidopsis thaliana] gi|6822093|emb|CAB71009; identical to cDNA class III pe
expressed protein
copper-binding family protein similar to copper homeostasis factor gi:3168840 from Arabidopsis thaliana; contain
peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein similar to SP|P87051 Peptidyl-prolyl cis-trans is
photosystem II 5 kD protein 100% identical to GI:4836947 (F5D21.10)
far-red impaired responsive protein, putative similar to far-red impaired response protein FAR1 [Arabidopsis thali
terpene synthase/cyclase family protein contains Pfam profile: PF01397 terpene synthase family
splicing factor, putative similar to Splicing factor 3B subunit 10 (SF3b10) (Pre-mRNA splicing factor SF3b 10 kDa
hypothetical protein
F-box family protein contains F-box domain Pfam:PF00646
U-box domain-containing protein low similarity to immediate-early fungal elicitor protein CMPG1 [Petroselinum cr
proline-rich family protein contains proline-rich region, INTERPRO:IPR000694
cell division control protein, putative cdc2MsF [Medicago sativa] gi|1806146|emb|CAA65982

expressed protein
expressed protein
protein kinase, putative similar to receptor serine/threonine kinase PR5K gi|1235680|gb|AAC49208
auxin-responsive protein, putative similar to small auxin-up regulated protein SAUR (GI:3043536) [Raphanus sa
galactosyltransferase family protein contains Pfam profile: PF01762 galactosyltransferase
peroxiredoxin type 2, putative strong similarity to type 2 peroxiredoxin [Brassica rapa subsp. pekinensis] GI:4928
no apical meristem (NAM) family protein similar to NAC2 (GI:6456751) [Arabidopsis thaliana]; contains Pfam PF
zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RI
NADP-dependent oxidoreductase, putative similar to probable NADP-dependent oxidoreductase (zeta-crystallin
expressed protein
DNA-directed RNA polymerase, putative identical to RNA polymerase subunit [Arabidopsis thaliana] GI:514322;
DNA-directed RNA polymerase, putative identical to RNA polymerase subunit [Arabidopsis thaliana] GI:514322;
60S ribosomal protein L35a (RPL35aC) similar to ribosomal protein L33B GB:NP_014877 from [Saccharomyces
leucine-rich repeat transmembrane protein kinase, putative contains similarity to many predicted protein kinases
expressed protein ; expression supported by MPSS
60S ribosomal protein L32 (RPL32A) ribosomal protein L32, human, PIR1:R5HU32
cell division cycle protein 48, putative / CDC48, putative very strong similarity to SP|P54609 Cell division cycle p
expressed protein contains Pfam profile PF03087: Arabidopsis protein of unknown function
hypothetical protein
no apical meristem (NAM) family protein similar to OsNAC7 protein GB:BAA89801 GI:6730944 from [Oryza sativ
heat shock protein-related contains weak similarity to 17.6 kDa class I heat shock protein (HSP 17.6) (Swiss-Pro
hypothetical protein contains Pfam profile PF03080: Arabidopsis proteins of unknown function
chitinase, putative similar to basic endochitinase CHB4 precursor SP:Q06209 from [Brassica napus]
transducin family protein / WD-40 repeat family protein contains 4 (3 significant) WD-40 repeats; similar to perio
homeobox-leucine zipper family protein / lipid-binding START domain-containing protein similar to Anthocyaninle
expressed protein
40S ribosomal protein S21 (RPS21B) ribosomal protein S21, cytosolic - Oryza sativa, PIR:S38357
formin-binding protein-related similar to formin binding protein 21 (GI:3550080) [Homo sapiens]; similar to formin
expressed protein
kinase interacting family protein similar to kinase interacting protein 1 (GI:13936326) [Petunia integrifolia]
14-3-3 protein GF14 phi (GRF4) identical to GF14 protein phi chain GI:1493805, SP:P46077 from [Arabidopsis t
myb family transcription factor contains Pfam domain, PF00249: Myb-like DNA-binding domain
myb family transcription factor similar to myb-related protein mixta GI:485867 from [Antirrhinum majus]
transcriptional factor B3 family protein contains Pfam profile PF02362: B3 DNA binding domain
expressed protein
glycosyl hydrolase family 9 protein
transcriptional factor B3 family protein low similarity to reproductive meristem protein 1 [Arabidopsis thaliana] GI:
tonoplast intrinsic protein, putative similar to tonoplast intrinsic protein GI:5081419 from [Brassica napus]
40S ribosomal protein S9 (RPS9C) 40S ribosomal protein S9 - Chlamydomonas sp.,EMBL:AU066528
paired amphipathic helix repeat-containing protein contains Pfam profile PF02671: Paired amphipathic helix repe
inositol-3-phosphate synthase isozyme 2 / myo-inositol-1-phosphate synthase 2 / MI-1-P synthase 2 / IPS 2 iden
MutT/nudix family protein similar to mRNA-decapping enzyme [Homo sapiens] GI:23268269; contains Pfam prof
vesicle-associated membrane protein, putative / VAMP, putative similar to VAP27 GI:6688926 [Nicotiana plumba
arginine/serine-rich splicing factor, putative similar to SP|P92964 Arginine/serine-rich splicing factor RSP31 {Aral
transmembrane protein-related low similarity to transmembrane protein OTMP [Ovis aries] GI:9965379
omega-3 fatty acid desaturase, endoplasmic reticulum (FAD3) identical to SP:48623
receptor-like protein kinase-related contains Pfam profile: PF01657 Domain of unknown function that is usually a
expressed protein

WD-40 repeat protein (MSI2) contains 5 WD-40 repeats (PF0400); identical to WD-40 repeat protein MSI2 (SP:C
expressed protein
IWS1 C-terminus family protein contains Pfam PF05909: IWS1 C-terminus;
circadian clock coupling factor-related similar to circadian clock coupling factor ZGT [Nicotiana tabacum] GI:142
proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family
receptor-like protein kinase-related contains Pfam profile: PF01657 Domain of unknown function that is usually a
protein phosphatase 2C, putative / PP2C, putative
expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538
F-box family protein / tubby family protein similar to Tubby protein (SP:P50586) {Mus musculus}; similar to Chain
F-box family protein / tubby family protein similar to Tubby protein (SP:P50586) {Mus musculus}; similar to Chain
IAA-amino acid hydrolase, putative (ILL3) identical to IAA-amino acid hydrolase homolog ILL3 [Arabidopsis thalia
invertase/pectin methylesterase inhibitor family protein low similarity to SP|P83326 Pectinesterase inhibitor (Pect
hypothetical protein
cytochrome P450 family protein
GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, E
expressed protein
permease-related low similarity to purine permease [Arabidopsis thaliana] GI:7620007
CCAAT-box binding transcription factor Hap5a, putative
lipoxygenase (LOX1) identical to SP|Q06327
aldose 1-epimerase family protein similar to ALDOSE 1-EPIMERASE PRECURSOR GB:P05149 [SP|P05149] fr
ABC transporter family protein ABC family transporter, Entamoeba histolytica, EMBL:EH058
splicing factor RSZp22 (RSZP22) / 9G8-like SR protein (SRZ22) identical to RSZp22 protein [Arabidopsis thalian
unusual floral organ (UFO) / F-box family protein (FBX1) E3 ubiquitin ligase SCF complex F-box subunit; almost
disease resistance-responsive family protein / dirigent family protein similar to dirigent protein GB:AAF25365 GI:
family II extracellular lipase 1 (EXL1) EXL1 (PMID:11431566); similar to anter-specific proline-rich protein (APG)
family II extracellular lipase 1 (EXL1) EXL1 (PMID:11431566); similar to anter-specific proline-rich protein (APG)
protein phosphatase 2C, putative / PP2C, putative protein phosphatase-2C, Mesembryanthemum crystallinum, A
expressed protein
EXS family protein / ERD1/XPR1/SYG1 family protein similar to PHO1 protein [Arabidopsis thaliana] GI:200690
oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to leucoanthocyanidin dioxygenase [Malus domesti
cyclic nucleotide-regulated ion channel / cyclic nucleotide-gated channel (CNGC4) identical to cyclic nucleotide a
cyclic nucleotide-regulated ion channel / cyclic nucleotide-gated channel (CNGC4) identical to cyclic nucleotide a
RNA and export factor-binding protein, putative similar to GI:7159943 from [Mus musculus] (RNA 6 (4), 638-650
tryptophan synthase, beta subunit, putative similar to SP|P14671 Tryptophan synthase beta chain 1, chloroplast
F-box family protein contains F-box domain Pfam:PF00646
F-box family protein contains F-box domain Pfam:PF00646
prolylcarboxypeptidase-related weak similarity to SP|P42785| Lysosomal Pro-X carboxypeptidase precursor (EC
expressed protein
expressed protein
bZIP transcription factor family protein / ABA-responsive element-binding protein, putative similar to ABA-respon
expressed protein nearly identical to At1g25170, At1g25097, At1g24822; similar to ESTs dbj AV530941.1, dbj|AV
plant basic secretory protein (BSP) family protein similar to NtPRp27 [Nicotiana tabacum] GI:5360263; contains
armadillo/beta-catenin repeat family protein / U-box domain-containing family protein contains Pfam domain, PF
MADS-box protein (AGL47)
CBL-interacting protein kinase 24 (CIPK24) / serine/threonine protein kinase (SOS2) identical to CBL-interacting
transferase family protein similar to deacetylvindoline 4-O-acetyltransferase from Catharanthus roseus GI:40918
glutathione S-transferase, putative similar to glutathione S-transferase GI:860955 from [Hyoscyamus muticus]
calmodulin-binding protein-related (PICBP) contains similarity to potato calmodulin-binding protein PCBP GI:179

expressed protein
DNA polymerase family B protein similar to SP|Q61493 DNA polymerase zeta catalytic subunit (EC 2.7.7.7) {Mus
F-box family protein contains F-box domain Pfam:PF00646
cytochrome P450 family protein similar to Cytochrome P450 85 (SP:Q43147) {Lycopersicon esculentum};
ABA-responsive protein (HVA22c) identical to AtHVA22c [Arabidopsis thaliana] GI:4884936
formin homology 2 domain-containing protein / FH2 domain-containing protein contains formin homology 2 doma
self-incompatibility protein-related similar to S1 self-incompatibility protein GB:CAA52380 [Papaver rhoeas] (Proc
pentatricopeptide (PPR) repeat-containing protein contains Pfam profile: PF01535 PPR repeat
F-box family protein contains Pfam:PF00646 F-box domain ; similar to SKP1 interacting partner 2 (SKIP2) TIGR
DNA helicase (RECQl4A) nearly identical to DNA Helicase [Arabidopsis thaliana] GI:11121449
inositol-3-phosphate synthase, putative / myo-inositol-1-phosphate synthase, putative / MI-1-P synthase, putative
hypothetical protein
glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein contains Pfam profile: PF02485
33 kDa secretory protein-related contains Pfam PF01657: Domain of unknown function, duplicated in 33 KDa se
pre-mRNA splicing factor PRP38 family protein (SRL1) contains Pfam profile PF03371: PRP38 family
brassinosteroid signalling positive regulator (BZR1) identical to to BZR1 protein [Arabidopsis thaliana] gi|202709
brassinosteroid signalling positive regulator (BZR1) identical to to BZR1 protein [Arabidopsis thaliana] gi|202709
CBL-interacting protein kinase 21, putative (CIPK21) identical to CBL-interacting protein kinase 21 [Arabidopsis
expressed protein
cytochrome P450, putative similar to cytochrome P450 CYP89 (SP:Q42602)[Arabidopsis thaliana]; similar to cyt
thioredoxin family protein low similarity to SP|P29451 Thioredoxin [Rhesus macaque] {Macaca mulatta}; contains
embryonic flower 1 (EMF1) identical to embryonic flower 1 [Arabidopsis thaliana] GI:15430697
pentatricopeptide (PPR) repeat-containing protein contains INTERPRO:IPR002885 PPR repeats
glutamate receptor family protein (GLR1.3) plant glutamate receptor family, PMID:11379626
zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RI
exostosin family protein contains Pfam domain, PF03016: Exostosin family
copper-binding family protein similar to copper homeostasis factor gi:3168840 from Arabidopsis thaliana; contain
hypothetical protein
protein kinase family protein contains Pfam PF00069: Protein kinase domain
expressed protein
expressed protein
serine carboxypeptidase S10 family protein contains Pfam profile: PF00450 serine carboxypeptidase; similar to s
Expressed protein
glycine-rich protein
expressed protein weakly similar to drought-induced protein SDi-6 (PIR:S71562) common sunflower (fragment)
preprotein translocase secY subunit, chloroplast (CpSecY) Identical to SP|Q38885 Preprotein translocase secY
beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative similar
nodulin MtN21 family protein similar to MtN21 [Medicago truncatula] GI:2598575; contains Pfam profile PF00892
multi-copper oxidase type I family protein similar to pollen-specific BP10 protein [SP|Q00624][Brassica napus]; c
transporter-related low similarity to SP|Q9NTN3 UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter (U
autophagy protein Apg5 family contains Pfam profile: PF04106 autophagy protein Apg5
tRNA synthetase class I (W and Y) family protein contains Pfam profile: PF00579 tRNA synthetases class I (W a
expressed protein similar to unknown protein (pir||T05226)
expressed protein similar to unknown protein (pir||T05226)
expressed protein
hypothetical protein
mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein contains Pfam PF0
exonuclease family protein contains Pfam domain PF00929: exonuclease

exonuclease family protein contains Pfam domain PF00929: exonuclease
zinc finger (C2H2 type) protein 3 (AZF3) identical to Cys2/His2-type zinc finger protein 3 [Arabidopsis thaliana] g
DNA-directed RNA polymerase, putative identical to RNA polymerase subunit [Arabidopsis thaliana] GI:514322;
expansin family protein (EXPL2) contains Pfam profile: PF01357 pollen allergen; expansin-like gene, PMID:1164
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to auxin down regulated GB:X69
COP1-interacting protein-related similar to COP1-interacting protein 4 (CIP4) [Arabidopsis thaliana] GI:1316064
pectate lyase family protein similar to pectate lyase GP:14289169 from [Salix gilgiana];contains Pfam profile: PF
homeobox protein knotted-1 like 5 (KNAT5) / homeodomain containing protein 1 (H1) identical to homeobox prot
methyladenine glycosylase family protein similar to SP|P05100 DNA-3-methyladenine glycosylase I (EC 3.2.2.20
PHD finger family protein contains Pfam profile: PF00628: PHD-finger
MADS-box protein (AGL3)
zinc finger protein-related contains low similarity to zinc finger proteins and Pfam PF01485: IBR domain
senescence-associated family protein similar to senescence-associated protein 5 [Hemerocallis hybrid cultivar] g
syntaxin 73 (SYP73) identical to syntaxin 73 (AtSYP73) (Swiss-Prot:Q94KK5) [Arabidopsis thaliana]
histone H3 identical to histone H3 from Zea mays SP|P05203, Medicago sativa GI:166384, Encephalartos altens
expressed protein similarity to predicted protein, Arabidopsis thaliana
hypothetical protein hypothetical protein T3B23.10 - Arabidopsis thaliana,PID:g4803958
40S ribosomal protein S19 (RPS19C) 40S ribsomal protein S19, Oryza sativa, SWISSPROT:RS19_ORYSA
hypothetical protein
leucine-rich repeat protein kinase, putative similar to light repressible receptor protein kinase [Arabidopsis thalian
protein kinase family protein contains protein kinase domain, Pfam:PF00069
protein phosphatase 2C-related / PP2C-related contains protein phosphatase 2C domain
multi-copper oxidase type I family protein similar to pollen-specific BP10 protein [SP|Q00624][Brassica napus]; c
expressed protein contains Pfam domain, PF03650: Uncharacterized protein family (UPF0041)
serine/threonine protein kinase, putative similar to Pto kinase interactor 1 (Pti1)[Lycopersicon esculentum] gi|366
expressed protein predicted proteins, Arabidopsis thaliana
transducin family protein / WD-40 repeat family protein contains Pfam PF00400: WD domain, G-beta repeat (4 c
transducin family protein / WD-40 repeat family protein contains Pfam PF00400: WD domain, G-beta repeat (4 c
expressed protein contains Pfam profile PF05078: Protein of unknown function (DUF679)
hypothetical protein
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
gibberellin 20-oxidase identical to GI:1109699
nodulin MtN3 family protein similar to MtN3 GI:1619602 (root nodule development) from [Medicago truncatula]
mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein contains Pfam PF0
expressed protein
expressed protein
chlorophyll A-B binding protein / LHCII type III (LHCB3) identical to Lhcb3 protein [Arabidopsis thaliana] GI:4741
60S ribosomal protein L7A (RPL7aB) 60S RIBOSOMAL PROTEIN L7A - Oryza sativa, SWISSPROT:RL7A_ORY
protein kinase, putative similar to nuclear serine/threonine protein kinase GI:3582644 from [Rattus norvegicus]
expressed protein
glutamate receptor family protein (GLR2.9) plant glutamate receptor family, PMID:11379626
transducin family protein / WD-40 repeat family protein contains 5 WD-40 repeats (PF00400); AND-1 protein - H
hypothetical protein
tetrachloro-p-hydroquinone reductive dehalogenase-related contains similarity to tetrachloro-p-hydroquinone red
KOW domain-containing transcription factor family protein
F-box family protein contains F-box domain Pfam:PF00646
expressed protein
glycosyl hydrolase family 18 protein similar to chitinase/lysozyme GI:467689 from [Nicotiana tabacum]

expressed protein
expressed protein similar to En/Spm-like transposon protein GB:AAB95292 GI:2088658 from [Arabidopsis thalia
hypothetical protein
peroxidase, putative identical to peroxidase ATP24a [Arabidopsis thaliana] gi|1890313|emb|CAA72484
DEAD/DEAH box helicase carpel factory / CAF identical to RNA helicase/RNAseIII CAF protein GB:AAF03534 G
expressed protein
cytidine/deoxycytidylate deaminase family protein similar to SP|Q9URQ3 tRNA-specific adenosine deaminase 3
agamous-like MADS box protein AGL1 / shatterproof 1 (AGL1) (SHP1) identical to SP|P29381 Agamous-like MA
expressed protein PA26, p53 regulated PA26-T3 nuclear protein, Homo sapiens, EMBL:AF033121
hypothetical protein contains similarity to hypothetical proteins of [Arabidopsis thaliana]
cytidine deaminase 4 (CDA4) (desH) / cytidine aminohydrolase identical to cytidine deaminase homolog DesH [
protein kinase-related similar to serine/threonine protein kinase [Chlamydomonas reinhardtii] GI:18139937
copine-related low similarity to SP|Q99829 Copine I {Homo sapiens}
copine-related low similarity to SP|Q99829 Copine I {Homo sapiens}
copine-related low similarity to SP|Q99829 Copine I {Homo sapiens}
copine-related low similarity to SP|Q99829 Copine I {Homo sapiens}
phospholipid/glycerol acyltransferase family protein contains Pfam profile PF01553: Acyltransferase
tRNA synthetase class I (W and Y) family protein contains Pfam profile: PF00579 tRNA synthetases class I (W a
hypothetical protein
alpha, alpha-trehalose-phosphate synthase, UDP-forming, putative / trehalose-6-phosphate synthase, putative /
F-box family protein contains F-box domain Pfam:PF00646
FAD-binding domain-containing protein similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-form
DegP protease, putative contains similarity to DegP2 protease GI:13172275 from [Arabidopsis thaliana]
pollen coat receptor kinase, putative contains Pfam profile: PF01657 Domain of unknown function that is usually
pollen coat receptor kinase, putative contains Pfam profile: PF01657 Domain of unknown function that is usually
cytochrome P450 family protein contains Pfam profile: PF00067 cytochrome P450
sinapoylglucose:malate sinapoyltransferase (SNG1) similar to serine carboxypeptidase I precursor (SP:P37890)
zinc finger (C3HC4-type RING finger) family protein similar to RING-H2 finger protein RHX1a [Arabidopsis thalia
transaldolase, putative similar to transaldolase [Solanum tuberosum] gi|2078350|gb|AAB54016
UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl ar
homeobox-leucine zipper transcription factor (HB-9) identical to HD-Zip protein GB:CAA71854 GI:2145358 from
guanine nucleotide-binding family protein / activated protein kinase C receptor, putative / RACK, putative contain
hypothetical protein
DNA-binding protein, putative strong similarity to DNA-binding proteins from [Arabidopsis thaliana] RAV1 GI:386
hypothetical protein
oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to gibberellin 20-oxidase from A. thaliana [gi:11096
diphthine synthase, putative (DPH5) similar to Diphthine synthase (Diphtamide biosynthesis methyltransferase)
diphthine synthase, putative (DPH5) similar to Diphthine synthase (Diphtamide biosynthesis methyltransferase)
protein kinase, putative similar to protein kinase ATMRK1 [Arabidopsis thaliana] gi|2351097|dbj|BAA22079
transcriptional factor B3 family protein contains Pfam profile PF02362: B3 DNA binding domain
expressed protein non-consensus GC donor splice site at exon boundary 21576
ubiquitin-conjugating enzyme, putative nearly identical to ubiquitin-conjugating enzyme E2 [Catharanthus roseus
acireductone dioxygenase (ARD/ARD') family protein similar to iron-deficiency induced gene [Hordeum vulgare]
small nuclear ribonucleoprotein F, putative / U6 snRNA-associated Sm-like protein, putative / Sm protein F, putat
transcription initiation factor IID-1 (TFIID-1) / TATA-box factor 1 / TATA sequence-binding protein 1 (TBP1) identic
ADP-ribosylation factor, putative similar to ADP-ribosylation factor DcARF1 (GI:965483) [Daucus carota].
60S ribosomal protein L27A (RPL27aA) similar to GB:BAA96068 from [Panax ginseng]
hypothetical protein

sinapoylglucose:malate sinapoyltransferase (SNG1) similar to serine carboxypeptidase I precursor (SP:P37890)
hypothetical protein
cysteine endopeptidase, papain-type (XCP2) identical to papain-type cysteine endopeptidase XCP2 GI:670818
ankyrin repeat family protein contains ankyrin repeat domains, Pfam:PF00023
pumilio/Puf RNA-binding domain-containing protein contains Pfam profile: PF00806: Pumilio-family RNA binding
fructose-bisphosphate aldolase, putative similar to PIR|S65073 fructose-bisphosphate aldolase (EC 4.1.2.13) iso
glutamyl-tRNA(Gln) amidotransferase B family protein contains Pfam profiles: PF02934 PET112 family, N termin
lectin protein kinase family protein contains Pfam domains, PF00138: Legume lectins alpha domain, PF00139: L
actin-related protein 2 (ARP2) nearly identical to actin-related protein 2 (ARP2) [Arabidopsis thaliana] GI:381862
tropinone reductase, putative / tropine dehydrogenase, putative similar to tropinone reductase SP:P50165 from
zinc finger (B-box type) family protein contains Pfam profile: PF01760 CONSTANS family zinc finger
40S ribosomal protein S8 (RPS8A) ribosomal protein S8 - Zea mays, PIR:T04088
Ras-related GTP-binding protein, putative similar to GTP-binding protein GI:1208537 from [Glycine max]
expressed protein
expressed protein
expressed protein
expressed protein
ribosomal protein L1 family protein ribosomal protein L1, S.oleracea, EMBL:SORPL1
expressed protein
9-cis-epoxycarotenoid dioxygenase / neoxanthin cleavage enzyme / NCED1 / carotenoid cleavage dioxygenase
40S ribosomal protein S3 (RPS3A)
expressed protein
expressed protein
hypothetical protein ; expression supported by MPSS
hypothetical protein predicted protein - Arabidopsis thaliana, EMBL:AL163852
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
transducin family protein / WD-40 repeat family protein contains contains Pfam PF00400: WD domain, G-beta re
universal stress protein (USP) family protein similar to ER6 protein GB:AAD46412 GI:5669654 from [Lycopersico
universal stress protein (USP) family protein similar to ER6 protein GB:AAD46412 GI:5669654 from [Lycopersico
glycosyl hydrolase family 3 protein exhydrolase II - Zea mays, EMBL:AF064707
DNAJ heat shock N-terminal domain-containing protein contains Pfam profile PF00226 DnaJ domain
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed s
expressed protein
protein phosphatase 2C, putative / PP2C, putative protein phosphatase 2C, Medicago sativa, PID:g2582800
40S ribosomal protein S27 (RPS27D)
glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolas
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
inorganic phosphate transporter, putative similar to brain specific Na+-dependent inorganic phosphate cotranspo
no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; nap gene,
hypothetical protein
60S ribosomal protein L26 (RPL26A) 60S RIBOSOMAL PROTEIN L26, Brassica rapa, EMBL:BRD495
zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RI
hypothetical protein predicted proteins, Arabidopsis thaliana
expressed protein
expressed protein
expressed protein predicted protein, Drosophila melanogaster
hypothetical protein contains Pfam profile PF03478: Protein of unknown function (DUF295)
cytochrome P450 family protein CYTOCHROME P450 71B7 - Arabidopsis thaliana, EMBL:X97864

expressed protein
zinc knuckle (CCHC-type) family protein contains Pfam domain, PF00098: Zinc knuckle
myb family transcription factor (MYB60)
expressed protein ; expression supported by MPSS
early-responsive to dehydration protein-related / ERD protein-related low similarity to ERD4 protein (early-respor
universal stress protein (USP) family protein similar to ER6 protein GB:AAD46412 GI:5669654 from [Lycopersico
WRKY family transcription factor identical to WRKY transcription factor 24 (WRKY24) GI:15384230 from [Arabid
WRKY family transcription factor
vacuolar processing enzyme beta / beta-VPE identical to SP|Q39044 Vacuolar processing enzyme, beta-isozym
glycine-rich protein / oleosin contains similarity to Pfam profile: PF01277 Oleosin
expressed protein similar to hypothetical protein GB:CAB10284 contains Pfam profile PF03080: Arabidopsis pro
proline-rich family protein
expressed protein
hypothetical protein
expressed protein contains 3 transmembrane domains; contains Pfam profile PF05832: Eukaryotic protein of un
expressed protein contains Pfam profile: PF04782 protein of unknown function (DUF632)
expressed protein contains Pfam profile: PF04782 protein of unknown function (DUF632)
galactosyltransferase family protein contains Pfam profile: PF01762 galactosyltransferase
serine/threonine protein kinase (RFK3) identical to receptor-like serine/threonine kinase [Arabidopsis thaliana] gi
early-responsive to dehydration protein-related / ERD protein-related low similarity to ERD4 protein (early-respor
inositol-3-phosphate synthase isozyme 2 / myo-inositol-1-phosphate synthase 2 / MI-1-P synthase 2 / IPS 2 iden
caleosin-related family protein similar to caleosin GB:AAF13743 GI:6478218 from [Sesamum indicum]; similar to
copper transporter, putative similar to SP|Q39065 Copper transporter 1 (COPT1) {Arabidopsis thaliana}; contain
seven in absentia (SINA) family protein similar to siah-1A protein [Mus musculus] GI:297035; contains Pfam prof
hypothetical protein
serine carboxypeptidase S10 family protein similar to retinoid-inducible serine carboxypeptidase precursor (GI:15
pectinesterase family protein contains Pfam profile: PF01095 pectinesterase
palmitoyl protein thioesterase family protein
expressed protein
CDP-diacylglycerol--inositol 3-phosphatidyltransferase / phosphatidylinositol synthase (PIS1) identical to phosph
serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II chains A and B (SP:P08819) (E
serine carboxypeptidase S10 family protein similar to serine carboxypeptidase II (CP-MII) GB:CAA70815 (SP:P0
myb family transcription factor (MYB89) identical to transcription factor (MYB89) GI:5823322 from [Arabidopsis t
squamosa promoter-binding protein-like 12 (SPL12) identical to squamosa promoter binding protein-like 12 [Aral
hypothetical protein
MADS-box family protein contains Pfam profile: PF00319 SRF-type transcription factor (DNA-binding and dimeri
expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is un
basix helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
tetratricopeptide repeat (TPR)-containing protein low similarity to SP|P46825 Kinesin light chain (KLC) {Loligo pe
calcium-binding EF hand family protein contains INTERPRO:IPR002048 calcium-binding EF-hand domain
expressed protein ; expression supported by MPSS
glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein similar to glucosaminyl (N-acety
cytochrome P450 71A13, putative (CYP71A13) Identical to Cytochrome P450 71A13 (SP:O49342) [Arabidopsis
inorganic phosphate transporter identical to inorganic phosphate transporter [Arabidopsis thaliana] GI:3869190
Rho GDP-dissociation inhibitor family protein similar to SP|P52565 Rho GDP-dissociation inhibitor 1 (Rho GDI 1
beta-1,3-glucanase-related similar to beta-1,3-glucanase-like protein (GI:14279169) [Olea europaea] similar to G
C2 domain-containing protein contains INTERPRO:IPR000008 C2 domain
expressed protein

expressed protein
hypothetical protein
hypothetical protein
histone H2A identical to histone H2A Arabidopsis thaliana GI:7595337
expressed protein low similarity to N-methyl-D-aspartate receptor-associated protein [Drosophila melanogaster]
self-incompatibility protein-related contains similarity to S3 self-incompatibility protein [Papaver rhoeas] GI:11078
basic helix-loop-helix (bHLH) family protein contains Pfam domain, PF00010: Helix-loop-helix DNA-binding doma
multi-copper oxidase type I family protein similar to pollen-specific BP10 protein [SP|Q00624][Brassica napus]; c
RNA recognition motif (RRM)-containing protein
expressed protein
cell division protein kinase, putative similar to cell division protein kinase 7 [Homo sapiens] SWISS-PROT:P5061
fatty acid hydroxylase, putative similar to fatty acid hydroxylase Fah1p GB:AF021804 GI:2736147 from [Arabido
phosphate translocator-related low similarity to SP|P52178 Triose phosphate/phosphate translocator, non-green
phosphate translocator-related low similarity to SP|P52178 Triose phosphate/phosphate translocator, non-green
amino acid permease 2 (AAP2) identical to amine acid permease AAP2 [Arabidopsis thaliana] GI:510236
C2 domain-containing protein contains INTERPRO:IPR000008 C2 domain
pyruvate kinase, putative similar to pyruvate kinase isozyme G, chloroplast precursor [Nicotiana tabacum] SWIS
vacuolar sorting receptor, putative similar to vacuolar sorting receptor homolog [Arabidopsis thaliana] GI:173721
hypothetical protein
60S ribosomal protein L35 (RPL35A) similar to 60S ribosomal protein L35 GB:AAC27830
MADS-box protein, putative strong similarity to DNA-binding protein [Brassica rapa subsp. pekinensis] GI:64693
2-oxoglutarate dehydrogenase E1 component, putative / oxoglutarate decarboxylase, putative / alpha-ketoglutar
expressed protein
cytochrome P450 71B22, putative (CYP71B22) Identical to cytochrome P450 71B22 (SP:Q9LTM1)[Arabidopsis
expressed protein
PHD finger family protein / SWIB complex BAF60b domain-containing protein / GYF domain-containing protein c
BURP domain-containing protein similarity to SP|Q08298 Dehydration-responsive protein RD22 precursor {Arab
calmodulin, putative identical to SP|P30188 Calmodulin-like protein {Arabidopsis thaliana}
copper amine oxidase, putative similar to copper amine oxidase [Cicer arietinum] gi|3819099|emb|CAA08855
DNAJ heat shock family protein SP|Q9UDY4 DnaJ homolog subfamily B member 4 (Heat shock 40 kDa protein
starch phosphorylase, putative similar to alpha-glucan phosphorylase, H isozyme SP:P32811 from [Solanum tub
subtilase family protein subtilisin-like protease AIR3, Arabidopsis thaliana, EMBL:AF098632
hypothetical protein
expressed protein contains Pfam profile PF03140: Plant protein of unknown function
F-box family protein contains Pfam profile: PF00646 F-box domain
DNAJ heat shock N-terminal domain-containing protein similar to SP|P39101 CAJ1 protein [Saccharomyces cer
beta-galactosidase, putative / lactase, putative similar to beta-galactosidase precursor [Brassica oleracea] SWIS
expressed protein
calcium-dependent protein kinase, putative / CDPK, putative similar to calmodulin-domain protein kinase CDPK
zinc transporter (ZIP2) identical to zinc transporter ZIP2 [Arabidopsis thaliana] gi|3252868|gb|AAC24198; memb
band 7 family protein similar to hypersensitive-induced response protein [Zea mays] GI:7716468; contains Pfam
myb family transcription factor (MYB68) identical to putative transcription factor (MYB68) GI:3941493 from [Arab
basic helix-loop-helix (bHLH) family protein
ribosome-binding factor A family protein contains PFam PF02033: Ribosome-binding factor A
adenosine/AMP deaminase family protein low similarity to SP|P03958 Adenosine deaminase (EC 3.5.4.4) (Aden
DNAJ heat shock family protein similar to SP|Q9S5A3 Chaperone protein dnaJ {Listeria monocytogenes}; conta
peroxiredoxin type 2, putative strong similarity to type 2 peroxiredoxin [Brassica rapa subsp. pekinensis] GI:4928
expressed protein hypothetical protein F1N19.27 - Arabidopsis thaliana, EMBL:AC009519

FAD-dependent oxidoreductase family protein
peroxidase, putative identical to peroxidase [Arabidopsis thaliana] gi|1483222|emb|CAA67551
cation/hydrogen exchanger, putative (CHX14) monovalent cation:proton antiporter family 2 (CPA2) member, PM
leucine-rich repeat transmembrane protein kinase, putative
serine/threonine protein kinase, putative similar to serine-threonine protein kinase [Triticum aestivum] gi|205537
serine/threonine protein kinase, putative similar to serine-threonine protein kinase [Triticum aestivum] gi|205537
transport inhibitor response protein, putative E3 ubiquitin ligase SCF complex F-box subunit; similar to transport
expressed protein
expressed protein contains Pfam profile PF02713: Domain of unknown function DUF220
U-box domain-containing protein several hypothetical proteins - Arabidopsis thaliana
signal peptidase, putative similar to chloroplast thylakoidal processing peptidase GB:CAA71502 GI:2769566 fro
ubiquitin-conjugating enzyme family protein low similarity to ubiquitin-conjugating BIR-domain enzyme APOLLO
glycosyl hydrolase family 5 protein / cellulase family protein contains Pfam profile: PF00150 cellulase (glycosyl h
expressed protein contains Pfam profile PF04819: Family of unknown function (DUF716) (Plant viral-response fa
ubiquitin-conjugating enzyme, putative nearly identical to ubiquitin-conjugating enzyme E2 [Catharanthus roseus
glutathione S-transferase, putative similar to glutathione S-transferase, GST 10b GB:CAA10662 [Arabidopsis tha
glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)
poly [ADP-ribose] polymerase, putative / NAD(+) ADP-ribosyltransferase, putative / poly[ADP-ribose] synthetase
sterile alpha motif (SAM) domain-containing protein contains Pfam profile PF00536: SAM domain (Sterile alpha
pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
allene oxide cyclase family protein similar to ERD12 [GI:15320414], allene oxide cyclase GI:8977961 from [Lyco
wall-associated kinase, putative contains similarity to wall-associated kinase 4 GI:3355308 from [Arabidopsis tha
expressed protein
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
protein kinase family protein contains protein kinase domain, Pfam:PF00069 (likely that this cDNA contains a sin
guanine nucleotide-binding family protein / activated protein kinase C receptor (RACK1) identical to guanine nuc
acyl carrier protein 3, chloroplast (ACP-3) nearly identical to SP|P25702 Acyl carrier protein 3, chloroplast precur
histone H2A, putative strong similarity to histone H2A Arabidopsis thaliana GI:7595337, Triticum aestivum GI:53
RWP-RK domain-containing protein similar to nodule inception protein GI:6448579 from (Lotus japonicus); conta
leucine-rich repeat family protein / extensin family protein contains Pfam PF00560: Leucine Rich Repeat domain
expressed protein
glutathione S-transferase, putative
expressed protein contains similarity to glutamic acid/alanine-rich protein GI:6707830 from [Trypanosoma congo
glycoside hydrolase family 47 protein Similar to gb|U04299 mannosyl-oligosaccharide alpha-1,2-mannosidase fr
disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of
hypothetical protein and genefinder; expression supported by MPSS
phototropic-responsive NPH3 family protein contains NPH3 family domain, Pfam:PF03000
oxidoreductase, 2OG-Fe(II) oxygenase-related contains weak hit to Pfam PF03171: oxidoreductase, 2OG-Fe(II)
terpene synthase/cyclase family protein
rhodanese-like domain-containing protein contains rhodanese-like domain PF:00581
hypothetical protein
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
expressed protein
hypothetical protein
glutamate decarboxylase, putative similar to glutamate decarboxylase GB:Q07346 [Petunia x hybrida] (J. Biol. C
F-box family protein (FBX13) contains similarity to fimbriata GI:547307 from [Antirrhinum majus]
alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXD motif-containing protein low
rhodanese-like domain-containing protein contains Rhodanese-like domain PF:00581

zinc finger homeobox family protein / ZF-HD homeobox family protein contains Pfam domain, PF04770: ZF-HD
hypothetical protein
expressed protein
short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002198 Short-chain
FtsH protease, putative contains similarity to FtsH protease GI:13183728 from [Medicago sativa]
cytochrome P450, putative Similar to Cytochrome P450 89A2 (SP:Q42602)[Arabidopsis thaliana]; contains Pfa
senescence-associated family protein similar to senescence-associated protein 5 [Hemerocallis hybrid cultivar]
C2 domain-containing protein similar to zinc finger and C2 domain protein GI:9957238 from [Arabidopsis thalian
expressed protein
ethylene receptor, putative (EIN4) similar to ethylene receptor GB:AAC31123 [Malus domestica], identical to put
ethylene receptor, putative (EIN4) similar to ethylene receptor GB:AAC31123 [Malus domestica], identical to put
F-box family protein contains F-box domain Pfam:PF00646
F-box family protein contains F-box domain Pfam:PF00646
glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIG
60S ribosomal protein L31 (RPL31C)
senescence-associated family protein contains similarity to ketoconazole resistant protein GI:928938 and senes
expressed protein
expressed protein
protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed s
SF2/ASF-like splicing modulator (SRP30) nearly identical to SF2/ASF-like splicing modulator Srp30 [Arabidopsis
proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family
NADP-dependent oxidoreductase, putative strong similarity to probable NADP-dependent oxidoreductase (zeta-
SNF2 domain-containing protein / helicase domain-containing protein similar to SP|P46100 Transcriptional regul
14-3-3 protein GF14 psi (GRF3) (RCI1) identical to 14-3-3 protein GF14 psi GI:1168200, SP:P42644
chloroplast outer membrane protein-related low similarity to chloroplastic outer envelope membrane protein (OE
zinc knuckle (CCHC-type) family protein contains Pfam domain PF00098: Zinc knuckle
receptor-like protein kinase 5 (RLK5) identical to receptor-like protein kinase 5 [Arabidopsis thaliana] GI:135067
zinc-binding family protein similar to zinc-binding protein [Pisum sativum] GI:16117799; contains Pfam profile PF
expressed protein contains Pfam domain, PF03650: Uncharacterized protein family (UPF0041)
60S ribosomal protein-related contains weak similarity to 60S ribosomal protein L10A (CSA-19) (NEDD-6) (Swis
expressed protein
hypothetical protein contains Pfam profile PF04852: Protein of unknown function (DUF640)
speckle-type POZ protein-related contains Pfam PF00651 : BTB/POZ domain; similar to Speckle-type POZ prote
glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIG
basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
AAA-type ATPase family protein contains Pfam profile: ATPase family PF00004
defense protein-related weak similarity to SP|Q8GYN5 RPM1-interacting protein 4 {Arabidopsis thaliana}
lateral root primordium (LRP) protein-related similar to lateral root primordium 1 (LRP1) [Arabidopsis thaliana] G
fasciclin-like arabinogalactan-protein (FLA12)
malate oxidoreductase, putative similar to NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (SP:P1262
phytochelatin synthetase family protein / COBRA cell expansion protein COBL2 similar to phytochelatin synthetase
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
BSD domain-containing protein contains Pfam profile PF03909: BSD domain
expressed protein
expressed protein contains Pfam profile PF03759: Domain of unknown function (DUF315)
cytochrome P450 71B21, putative (CYP71B21) identical to Cytochrome P450 71B21 (SP:Q9LTM2) [Arabidopsis
12S seed storage protein (CRB) identical to 12S seed storage protein, gi|808937 [SP|P15456] [Plant Mol Biol 11
transducin family protein / WD-40 repeat family protein contains 3 WD-40 repeats (PF00400); mRNA-associated

expressed protein
expressed protein
expressed protein ; expression supported by MPSS
DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain
wound-responsive family protein similar to wound inducive gene (GI:8096273)[Nicotiana tabacum]
leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR00
expressed protein
reversibly glycosylated polypeptide, putative similar to reversibly glycosylatable polypeptide (RGP1) [Pisum sativ
reversibly glycosylated polypeptide, putative similar to reversibly glycosylatable polypeptide (RGP1) [Pisum sativ
hypothetical protein
hypothetical protein
glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein weak similarity to polygalact
early-responsive to dehydration stress protein (ERD12) nearly identical to early-responsive to dehydration (ERD
E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At3), putative E3 ubiquitin ligase; similar to fimbriata-asso
phragmoplast-associated kinesin-related protein 2 (PAKRP2) identical to cDNA phragmoplast-associated kinesin
pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
senescence-associated protein, putative similar to senescence-associated protein 5 [Hemerocallis hybrid cultiva
myb family transcription factor contains PFAM profile: myb DNA binding domain PF00249
cytochrome P450, putative similar to SP:Q42569 from [Arabidopsis thaliana]
gibberellin 20-oxidase identical to GI:1109695
expressed protein
protein kinase family protein contains protein kinase domain, Pfam:PF00069
sodium/dicarboxylate cotransporter, putative similar to SWISS-PROT:Q13183 renal sodium/dicarboxylate cotran
heavy-metal-associated domain-containing protein contains Pfam profile PF00403: Heavy-metal-associated dom
glycosyltransferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transfera
ORMDL family protein contains Pfam domain PF04061: ORMDL family
expressed protein ; expression supported by MPSS
expressed protein probable membrane protein YBL102w, yeast, PIR2:S45393
cytochrome P450 family protein similar to Cytochrome P450 78A4 (SP:O65012) Cytochrome P450 78A4 [Pinus
protein kinase family protein contains protein kinase domain, Pfam:PF00069
12S seed storage protein, putative / cruciferin, putative strong similarity to SP|P33525 Cruciferin CRU1 precurso
reticulon family protein (RTNLB15) contains PFam profile PF02453: Reticulon
cytochrome P450 90A1 (CYP90A1) (CYP90) (CPD) identical to Cytochrome P450 90A1 (SP:Q42569) [Arabidop
Ras-related protein (ARA-5) / small GTP-binding protein, putative identical to Ras-related protein ARA-5 SP:P28
peptidase M50 family protein / sterol-regulatory element binding protein (SREBP) site 2 protease family protein c
kelch repeat-containing F-box family protein contains Pfam PF00646: F-box domain; contains Pfam PF01344 : K
expressed protein
octicosapeptide/Phox/Bem1p (PB1) domain-containing protein contains Pfam profile PF00564: PB1 domain
pfkB-type carbohydrate kinase family protein contains Pfam profile: PF00294 pfkB family carbohydrate kinase
leucine-rich repeat transmembrane protein kinase, putative
glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)
expressed protein
DNAJ heat shock N-terminal domain-containing protein low similarity to AHM1 [Triticum aestivum] GI:6691467; c
sucrose-phosphate synthase, putative similar to sucrose-phosphate synthase (EC 2.4.1.14) isoform 1 - Citrus un
integral membrane protein, putative contains 3 transmembrane domains; contains Pfam PF04535 : Domain of u
calmodulin-domain protein kinase isoform 7 (CPK7) identical to calmodulin-domain protein kinase CDPK isoform
cyclic nucleotide-regulated ion channel / cyclic nucleotide-gated channel (CNGC6) identical to cyclic nucleotide a
cinnamoyl-CoA reductase family similar to cinnamoyl-CoA reductase from Pinus taeda [GI:17978649], Eucalyptu

expressed protein
invertase/pectin methylesterase inhibitor family protein low similarity to pistil-specific gene sts15 [Solanum tuber
expressed protein
expressed protein
ubiquinol-cytochrome C reductase complex 14 kDa protein, putative similar to SP|P48502 Ubiquinol-cytochrome
myb family transcription factor (MYB17) contains PFAM profile: Myb-like DNA-binding domain PF00249
auxin-responsive protein, putative similar to auxin-inducible SAUR (Small Auxin Up RNAs) (GI:3043536) [Rapha
expressed protein contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266
disease resistance family protein / LRR family protein contains leucine rich-repeat domains Pfam:PF00560, INTE
PHD finger family protein contains Pfam domain, PF00628: PHD-finger
basic helix-loop-helix (bHLH) family protein contains Pfam domain, PF00010: Helix-loop-helix DNA-binding doma
phospholipase A2, putative similar to secretory low molecular weight phospholipase A2 gamma [Arabidopsis thal
leucine-rich repeat transmembrane protein kinase, putative
expressed protein
meprin and TRAF homology domain-containing protein / MATH domain-containing protein contains Pfam profile
delta 1-pyrroline-5-carboxylate synthetase B / P5CS B (P5CS2) identical to SP|P54888
fringe-related protein similarity to predicted proteins + similar to hypothetical protein GB:AAC23643 [Arabidopsis
expressed protein
expressed protein and genefinder
ribosomal protein L10 family protein ribosomal protein L10- Nicotiana tabacum, EMBL:AB010879
universal stress protein (USP) family protein similar to ER6 protein [Lycopersicon esculentum] GI:5669654; cont
2S seed storage protein 2 / 2S albumin storage protein / NWMU2-2S albumin 2 identical to SP|P15458
expressed protein low similarity to SP|P51572 B-cell receptor-associated protein 31 (6C6-AG tumor-associated a
galactosyltransferase family protein contains Pfam profile: PF01762 galactosyltransferase
protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
serine carboxypeptidase S10 family protein contains Pfam profile: PF00450 serine carboxypeptidase; similar to s
nucleotidyltransferase family protein contains Pfam profiles: PF01909 nucleotidyltransferase domain, PF04926
transcriptional coactivator p15 (PC4) family protein (KELP) similar to SP|P53999 Activated RNA polymerase II tra
hypothetical protein
ubiquitin-conjugating enzyme 7 (UBC7) E2; identical to gi:992703, SP:P42747
beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative similar to beta-amylase GI:13560977 from
expressed protein ; expression supported by MPSS
expressed protein
peroxisomal protein PEX19 family protein contains Pfam profile: PF04614 Pex19 protein family
expressed protein predicted proteins, Arabidopsis thaliana, D.melanogaster, C.elegans and S.pombe
calcineurin B-like protein 1 (CBL1) identical to calcineurin B-like protein 1 (GI:3309082) [Arabidopsis thaliana]
protein kinase family protein contains protein kinase domain, Pfam:PF00069
hypothetical protein various predicted proteins, Arabidopsis thaliana
MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:122312
thylakoid lumenal 17.4 kDa protein, chloroplast identical to SP:P81760 Thylakoid lumenal 17.4 kDa protein, chlo
thylakoid lumenal 17.4 kDa protein, chloroplast identical to SP:P81760 Thylakoid lumenal 17.4 kDa protein, chlo
phototropic-responsive NPH3 family protein contains NPH3 family domain, Pfam:PF03000
GTP-binding protein-related low similarity to SP|Q99ME9 Nucleolar GTP-binding protein 1 (Chronic renal failure
synbindin, putative similar to Swiss-Prot:Q9ES56 synbindin (TRS23 homolog) [Mus musculus]
expressed protein ; expression supported by MPSS
MADS-box protein (AGL3)
trehalose-6-phosphate phosphatase, putative similar to trehalose-6-phosphate phosphatase (AtTPPA) GI:29441
expressed protein identical to ORF1 [Arabidopsis thaliana] gi|457716|emb|CAA50905

human Rev interacting-like family protein / hRIP family protein similar to ARF GAP-like zinc finger-containing pro
auxin efflux carrier protein, putative similar to efflux carrier of polar auxin transport [Brassica juncea] gi|1233173
peroxisomal biogenesis factor 11 family protein / PEX11 family protein contains Pfam PF05648: Peroxisomal bio
methylcrotonyl-CoA carboxylase alpha chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 1 (MCCA) nearly
actin 2 (ACT2) identical to SP|Q96292 Actin 2 {Arabidopsis thaliana}; nearly identical to SP|Q96293 Actin 8 [Aral
expressed protein
AAA-type ATPase family protein contains Pfam profile: ATPase family PF00004
expressed protein contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292
RNA-binding protein-related contains weak similarity to Swiss-Prot:Q01844 RNA-binding protein EWS (EWS onc
expressed protein
ferric-chelate reductase, putative similar to ferric-chelate reductase (FRO1) [Pisum sativum] GI:15341529; conta
ethylene-responsive element-binding protein, putative contains Pfam profile: PF00847 AP2 domain; similar to eth
expressed protein
expressed protein
expressed protein contains Pfam domains, PF04782: Protein of unknown function (DUF632) and PF04783: Prot
complex 1 family protein / LVR family protein contains Pfam PF05347: Complex 1 protein (LYR family)
complex 1 family protein / LVR family protein contains Pfam PF05347: Complex 1 protein (LYR family)
hypothetical protein
phototropic-responsive NPH3 family protein contains some similarity to root phototropism RPT2 [Arabidopsis tha
hypothetical protein
clathrin assembly protein AP19 identical to clathrin assembly protein AP19 GI:2231698 from [Arabidopsis thalian
ankyrin repeat family protein contains Pfam PF00023: Ankyrin repeat

Length	Observed Volatility	Expected Volatility	Observed-Expected	Variance
615	0.703632043	0.695243080	0.008388963	0.001022420
762	0.700863618	0.694266430	0.006597191	0.000693290
228	0.702812213	0.691221540	0.011590669	0.000946030
179	0.727390983	0.714587610	0.012803378	0.001184650
1505	0.698710097	0.694075690	0.004634405	0.001490360
365	0.727213208	0.717715590	0.009497613	0.001562830
242	0.730003648	0.718802480	0.011201166	0.001476920
757	0.718605417	0.711658670	0.006946748	0.001837370
693	0.717929313	0.710614640	0.007314677	0.001877790
838	0.705912448	0.698782860	0.007129589	0.002196230
991	0.718409590	0.712771030	0.005638556	0.001707570
507	0.711167865	0.702694080	0.008473786	0.002002536
719	0.719730171	0.714734825	0.004995346	0.001008900
280	0.740882002	0.730464408	0.010417594	0.001755616
797	0.716432143	0.710254435	0.006177707	0.001764542
571	0.714063218	0.707166342	0.006896876	0.001618899
438	0.702244092	0.696871606	0.005372487	0.000772970
623	0.717548579	0.710926173	0.006622405	0.001671198
459	0.729913785	0.722778971	0.007134814	0.001449367
82	0.726266884	0.710039584	0.016227300	0.001354567
82	0.726266884	0.710039584	0.016227300	0.001354567
310	0.709271551	0.702211562	0.007059989	0.000969931
155	0.734368617	0.722597628	0.011770989	0.001373176
161	0.721392976	0.709211999	0.012180978	0.001558853
172	0.703976326	0.696200097	0.007776229	0.000690572
273	0.729646587	0.720078517	0.009568070	0.001675007
362	0.719056828	0.710705218	0.008351610	0.001727924
420	0.720509136	0.713898508	0.006610627	0.001258284
153	0.731642862	0.721555532	0.010087330	0.001071625
512	0.726600582	0.719707817	0.006892764	0.001678596
138	0.702388039	0.687603626	0.014784413	0.002092408
229	0.732610409	0.723836158	0.008774251	0.001223140
210	0.716803413	0.706003068	0.010800345	0.001713463
479	0.739949272	0.736846740	0.003102532	0.000349053
473	0.718068772	0.710754633	0.007314139	0.001934622
212	0.731457321	0.721363354	0.010093967	0.001695973
682	0.717465849	0.711818613	0.005647236	0.001713515
151	0.719111953	0.707383318	0.011728635	0.001653726
580	0.672567063	0.668910133	0.003656930	0.000619728
358	0.715278901	0.707758597	0.007520304	0.001621050
359	0.714445396	0.706924093	0.007521303	0.001630229
433	0.716720571	0.710324296	0.006396275	0.001427378
211	0.729318602	0.720758629	0.008559973	0.001253505
396	0.727010511	0.719822519	0.007187992	0.001676954
584	0.723760225	0.718319577	0.005440648	0.001416967
263	0.707798038	0.698666643	0.009131395	0.001799091
735	0.730307341	0.726434970	0.003872371	0.000916896

304	0.708227370	0.699449408	0.008777962	0.001953865
304	0.708227370	0.699449408	0.008777962	0.001953865
304	0.726531275	0.718522083	0.008009193	0.001627685
291	0.686508964	0.681745636	0.004763328	0.000551435
804	0.721603575	0.716293351	0.005310224	0.001908178
589	0.725449440	0.719363588	0.006085852	0.001836817
329	0.720995682	0.713430378	0.007565304	0.001592168
134	0.701047960	0.687393132	0.013654829	0.002119654
357	0.715108936	0.707815194	0.007293742	0.001616136
80	0.733518965	0.725020190	0.008498775	0.000495987
249	0.724709391	0.715706167	0.009003224	0.001733424
636	0.716172605	0.712688618	0.003483987	0.000666154
443	0.714212307	0.707881529	0.006330778	0.001546706
175	0.731804553	0.722058125	0.009746428	0.001451762
195	0.732239965	0.723165538	0.009074427	0.001403883
234	0.724247888	0.714987456	0.009260432	0.001763657
281	0.719067268	0.713254024	0.005813244	0.000834680
334	0.718415183	0.710440420	0.007974763	0.001871747
304	0.725867578	0.718325989	0.007541589	0.001534083
293	0.730558388	0.722531969	0.008026419	0.001676715
448	0.692632497	0.686813142	0.005819355	0.001350560
258	0.716054397	0.706861299	0.009193098	0.001943683
123	0.718190775	0.706266943	0.011923833	0.001560088
523	0.718994177	0.712725714	0.006268463	0.001837993
257	0.728928449	0.720291683	0.008636766	0.001730090
161	0.728450428	0.719051577	0.009398851	0.001294945
495	0.717662310	0.711533630	0.006128680	0.001693159
268	0.713545135	0.705292960	0.008252175	0.001673825
328	0.703246220	0.696552983	0.006693237	0.001351860
733	0.715238761	0.709804124	0.005434636	0.002006265
417	0.709949671	0.702386003	0.007563669	0.002212201
217	0.731337608	0.723811158	0.007526450	0.001141558
395	0.723679768	0.717249550	0.006430218	0.001519322
306	0.726406612	0.719123848	0.007282764	0.001527976
613	0.716361977	0.711035358	0.005326619	0.001646471
359	0.734440179	0.729604420	0.004835760	0.000798043
423	0.708208295	0.703327395	0.004880901	0.000961579
423	0.708208295	0.703327395	0.004880901	0.000961579
244	0.729533530	0.722079310	0.007454220	0.001295168
571	0.722022942	0.716828649	0.005194294	0.001490351
527	0.724138850	0.718229885	0.005908965	0.001781153
765	0.712351988	0.707230942	0.005121046	0.001957924
769	0.713337876	0.708522684	0.004815192	0.001750232
540	0.725934047	0.720661081	0.005272966	0.001478787
201	0.742493652	0.733481689	0.009011963	0.001609226
259	0.706044855	0.697522691	0.008522164	0.001871337
101	0.729736040	0.718825921	0.010910120	0.001199957
659	0.715182852	0.709991553	0.005191299	0.001777694

446	0.723158446	0.717402281	0.005756165	0.001483521
506	0.725309311	0.719676852	0.005632459	0.001611771
533	0.714056303	0.707877498	0.006178805	0.002052689
500	0.721451036	0.715626765	0.005824271	0.001715860
283	0.725249243	0.717367386	0.007881857	0.001783791
308	0.732518874	0.726544459	0.005974415	0.001115881
297	0.706542685	0.698904050	0.007638635	0.001769638
410	0.725667413	0.719336440	0.006330973	0.001679144
269	0.728166069	0.721909643	0.006256426	0.001080001
324	0.732204558	0.725140045	0.007064513	0.001665942
310	0.717888893	0.710883377	0.007005516	0.001594642
256	0.716934426	0.709046474	0.007887952	0.001674951
353	0.723839604	0.717687008	0.006152595	0.001405743
731	0.711901921	0.708399680	0.003502241	0.000943365
652	0.715110230	0.710180228	0.004930002	0.001674026
201	0.719911438	0.710272394	0.009639044	0.001975966
187	0.731597203	0.723763833	0.007833371	0.001222275
698	0.729002086	0.724439737	0.004562349	0.001549444
348	0.730346716	0.724864444	0.005482273	0.001115927
830	0.713838492	0.709462320	0.004376172	0.001696064
298	0.721584525	0.714627865	0.006956661	0.001547592
290	0.737832918	0.731015285	0.006817633	0.001448772
171	0.725663421	0.717404392	0.008259029	0.001259209
215	0.718971121	0.710944227	0.008026893	0.001495654
148	0.739629974	0.732363659	0.007266315	0.000844876
197	0.730433923	0.721769619	0.008664303	0.001608913
896	0.711625723	0.707054030	0.004571693	0.002039111
390	0.715346689	0.708862943	0.006483746	0.001793746
438	0.723991587	0.718192134	0.005799453	0.001613019
608	0.721553926	0.716195032	0.005358894	0.001912625
161	0.717004514	0.706943338	0.010061176	0.001788049
115	0.728492246	0.716223273	0.012268973	0.001899229
423	0.716955048	0.711288305	0.005666743	0.001494413
169	0.701933688	0.692129894	0.009803794	0.001788418
253	0.732170438	0.725880465	0.006289973	0.001115860
364	0.720262417	0.714372626	0.005889792	0.001408290
668	0.724289557	0.719879021	0.004410536	0.001450599
356	0.716288568	0.709399727	0.006888841	0.001887611
109	0.683153940	0.670573484	0.012580456	0.001937193
450	0.715268196	0.709362701	0.005905495	0.001766989
612	0.721328840	0.716397794	0.004931046	0.001677071
967	0.710070330	0.705663141	0.004407188	0.002118610
603	0.714676413	0.710020206	0.004656207	0.001475675
169	0.722285411	0.713017245	0.009268166	0.001639738
513	0.721774742	0.715970099	0.005804643	0.001954888
123	0.734508665	0.723180311	0.011328354	0.001787754
704	0.726376237	0.721824663	0.004551574	0.001653387
512	0.717978976	0.712230217	0.005748759	0.001920583

109	0.703247149	0.690004577	0.013242572	0.002171186
127	0.700759551	0.693670213	0.007089338	0.000726032
89	0.717476858	0.704391620	0.013085239	0.001737442
226	0.719660919	0.713898675	0.005762244	0.000855987
857	0.719368807	0.715256770	0.004112037	0.001657981
534	0.712244847	0.706870840	0.005374008	0.001768399
372	0.723586514	0.717473424	0.006113090	0.001594327
438	0.714551667	0.708429846	0.006121821	0.001883919
180	0.724163995	0.714775287	0.009388708	0.001821504
150	0.703282391	0.692763417	0.010518974	0.001906031
327	0.716110368	0.710263670	0.005846697	0.001284822
264	0.727932737	0.720530218	0.007402519	0.001666729
2173	0.713246473	0.710565141	0.002681333	0.001800971
474	0.715859710	0.709906329	0.005953381	0.001937851
328	0.717372131	0.710703662	0.006668468	0.001685684
276	0.716739468	0.710021738	0.006717730	0.001443867
570	0.723217795	0.719093353	0.004124442	0.001124098
85	0.734486202	0.726463095	0.008023107	0.000638854
856	0.718002499	0.714130972	0.003871527	0.001502827
381	0.711650589	0.705541737	0.006108853	0.001677992
340	0.713122378	0.705986840	0.007135537	0.002043681
149	0.727973432	0.718262054	0.009711379	0.001660412
234	0.728964501	0.721897699	0.007066803	0.001381383
118	0.730400961	0.721594500	0.008806461	0.001082002
1104	0.718941943	0.715034139	0.003907804	0.001996289
310	0.713486644	0.706937900	0.006548744	0.001577761
546	0.720477834	0.715437568	0.005040266	0.001646477
521	0.729576107	0.724382497	0.005193610	0.001673717
259	0.722759280	0.714808489	0.007950791	0.001955644
580	0.708911358	0.704040467	0.004870891	0.001649700
624	0.722160872	0.717255411	0.004905460	0.001803909
138	0.713861021	0.703601537	0.010259485	0.001746797
243	0.718475758	0.711313891	0.007161868	0.001500928
362	0.725000213	0.719331091	0.005669122	0.001407246
283	0.729777159	0.723821905	0.005955254	0.001215422
149	0.733438689	0.726062212	0.007376477	0.000983304
551	0.718972219	0.714012578	0.004959641	0.001644290
365	0.724362009	0.718114226	0.006247783	0.001732015
776	0.718317410	0.714497535	0.003819874	0.001377640
877	0.712364835	0.708294986	0.004069849	0.001777812
207	0.723120545	0.716139243	0.006981302	0.001239239
484	0.706240613	0.700511930	0.005728683	0.001957173
256	0.721014761	0.714168527	0.006846234	0.001479659
183	0.694532939	0.685510650	0.009022289	0.001838558
458	0.707022163	0.701041300	0.005980863	0.002030286
366	0.716213156	0.710663699	0.005549457	0.001401435
118	0.704830645	0.691789664	0.013040981	0.002497262
464	0.717705964	0.712712247	0.004993717	0.001442111

589	0.738629370	0.734797166	0.003832204	0.001078633
376	0.716613362	0.711174793	0.005438569	0.001389104
377	0.714912228	0.708531989	0.006380239	0.001921104
628	0.722096959	0.717321130	0.004775829	0.001797794
154	0.718618244	0.709464109	0.009154135	0.001628446
302	0.713240257	0.708180900	0.005059357	0.000980444
832	0.715174435	0.710961494	0.004212941	0.001874846
112	0.703459616	0.691491923	0.011967693	0.002036771
735	0.712900818	0.708381552	0.004519266	0.001910921
777	0.717107531	0.712971830	0.004135701	0.001692592
421	0.727695350	0.722819015	0.004876335	0.001276604
592	0.726543605	0.722233141	0.004310464	0.001405067
245	0.716068736	0.708509609	0.007559127	0.001790162
161	0.722992496	0.714395835	0.008596661	0.001523421
379	0.730608272	0.724697162	0.005911110	0.001696110
126	0.738264422	0.729867766	0.008396657	0.001141647
863	0.715561753	0.711627009	0.003934744	0.001718170
899	0.715590330	0.711818396	0.003771934	0.001646056
557	0.716046879	0.710723195	0.005323684	0.002034543
793	0.715185115	0.711025319	0.004159796	0.001769125
336	0.727495747	0.722357923	0.005137825	0.001144457
313	0.711077614	0.704784653	0.006292961	0.001603860
531	0.717431473	0.712664627	0.004766845	0.001561637
144	0.739581057	0.730819641	0.008761416	0.001431189
547	0.707942828	0.702776019	0.005166809	0.001901056
517	0.712579565	0.707313003	0.005266562	0.001867555
981	0.725324770	0.722077432	0.003247339	0.001348044
496	0.707865838	0.702325438	0.005540400	0.001984413
125	0.727959125	0.718201066	0.009758059	0.001556006
440	0.720719085	0.715621363	0.005097721	0.001495896
88	0.714486764	0.706130248	0.008356516	0.000804871
562	0.727801711	0.723492382	0.004309329	0.001370092
562	0.727801711	0.723492382	0.004309329	0.001370092
868	0.716066634	0.711976822	0.004089812	0.001913593
472	0.716976528	0.711656284	0.005320244	0.001762065
311	0.724232639	0.718585083	0.005647555	0.001308975
666	0.718098836	0.713609930	0.004488906	0.001773175
487	0.729742594	0.724908647	0.004833946	0.001511313
89	0.724873454	0.713752844	0.011120610	0.001462141
662	0.723798592	0.719700617	0.004097975	0.001477774
692	0.719828845	0.715882907	0.003945938	0.001435199
576	0.712357954	0.707310743	0.005047210	0.001958517
1250	0.704041345	0.700360811	0.003680534	0.002263371
297	0.721037061	0.714527180	0.006509881	0.001683006
499	0.712762713	0.707807639	0.004955074	0.001640725
542	0.721300861	0.717083276	0.004217585	0.001291208
320	0.718243724	0.711761832	0.006481892	0.001807144
114	0.720656103	0.711494577	0.009161526	0.001288444

443	0.722949162	0.717755632	0.005193530	0.001613845
257	0.715919396	0.709077260	0.006842136	0.001625045
883	0.717647150	0.713804378	0.003842772	0.001761840
402	0.719764629	0.714255350	0.005509279	0.001650015
326	0.719170960	0.712707956	0.006463004	0.001847093
981	0.717802757	0.713943462	0.003859295	0.001987668
635	0.713920025	0.709711487	0.004208538	0.001535621
450	0.725569350	0.720622243	0.004947107	0.001503744
349	0.722038255	0.716319324	0.005718931	0.001561625
153	0.731500777	0.722843078	0.008657699	0.001574906
783	0.723503287	0.719821480	0.003681808	0.001458761
458	0.723711021	0.718441618	0.005269403	0.001750094
465	0.721734892	0.716858426	0.004876466	0.001525800
524	0.719754434	0.715102894	0.004651539	0.001566302
258	0.721989994	0.714400712	0.007589282	0.002056317
798	0.728785298	0.725111805	0.003673493	0.001495751
875	0.715745574	0.711662930	0.004082644	0.002026146
319	0.716306853	0.710186521	0.006120332	0.001667296
863	0.722370430	0.718731252	0.003639179	0.001595924
776	0.708834201	0.704636965	0.004197236	0.001914279
507	0.724135360	0.719708925	0.004426435	0.001391851
461	0.709031677	0.703555520	0.005476157	0.001941647
273	0.715415386	0.709297310	0.006118076	0.001435657
440	0.715503806	0.710088739	0.005415067	0.001813423
99	0.748567197	0.740905910	0.007661287	0.000817610
891	0.705628106	0.701558086	0.004070020	0.002076746
751	0.715696980	0.711461833	0.004235147	0.001897374
541	0.712846765	0.708013604	0.004833161	0.001783009
244	0.731250404	0.724161828	0.007088576	0.001732900
407	0.730108765	0.724842878	0.005265887	0.001600446
304	0.715278105	0.708602947	0.006675158	0.001921840
280	0.741271955	0.736977520	0.004294435	0.000734611
436	0.721690045	0.716436753	0.005253291	0.001712665
482	0.724556968	0.720047681	0.004509287	0.001396538
591	0.714759267	0.710253103	0.004506164	0.001713078
460	0.714475880	0.708861843	0.005614037	0.002069852
518	0.714696045	0.709767222	0.004928823	0.001797183
730	0.712374884	0.708101910	0.004272974	0.001908447
661	0.722624730	0.718417457	0.004207273	0.001675338
260	0.727006082	0.720430830	0.006575252	0.001612971
333	0.720989951	0.715288964	0.005700987	0.001557339
106	0.740918373	0.732411918	0.008506456	0.001103827
268	0.717353215	0.710122631	0.007230585	0.002016413
669	0.714828103	0.710971767	0.003856337	0.001432893
227	0.726945372	0.719839721	0.007105652	0.001651624
181	0.695575598	0.686467819	0.009107780	0.002174725
362	0.731939089	0.726365825	0.005573264	0.001633244
578	0.734093839	0.731706895	0.002386944	0.000478433

915	0.706489067	0.702817652	0.003671415	0.001793811
154	0.722071720	0.713621703	0.008450017	0.001600164
757	0.717074069	0.713034541	0.004039528	0.001797919
455	0.714142472	0.709259372	0.004883099	0.001583086
438	0.728069830	0.723000840	0.005068990	0.001646093
539	0.716433689	0.711786008	0.004647681	0.001705385
196	0.727279869	0.720803617	0.006476252	0.001204363
1086	0.716502403	0.712976164	0.003526239	0.001982402
821	0.706784432	0.702736460	0.004047973	0.001974961
479	0.722153556	0.717029393	0.005124163	0.001848306
351	0.718336609	0.712923490	0.005413119	0.001511543
294	0.729588666	0.724298280	0.005290386	0.001209657
158	0.731948130	0.722497478	0.009450652	0.002075392
334	0.726414770	0.720105299	0.006309471	0.001956315
251	0.702697946	0.696335383	0.006362563	0.001495671
1839	0.712197995	0.709704166	0.002493829	0.001685401
717	0.719577981	0.715334331	0.004243650	0.001903604
544	0.717825862	0.713699378	0.004126485	0.001367587
299	0.735806705	0.729874737	0.005931968	0.001556840
431	0.710589704	0.705645295	0.004944409	0.001560598
315	0.719958709	0.713887864	0.006070845	0.001726105
273	0.703883853	0.697083157	0.006800697	0.001877554
128	0.722329903	0.713899203	0.008430700	0.001353058
598	0.724319382	0.719868568	0.004450814	0.001765848
204	0.720017659	0.712693275	0.007324383	0.001633940
493	0.721967214	0.717552590	0.004414624	0.001435777
846	0.721081025	0.717846511	0.003234514	0.001323663
249	0.712211793	0.705912450	0.006299344	0.001479021
651	0.716049275	0.712064749	0.003984526	0.001550119
803	0.702318846	0.698015853	0.004302994	0.002230751
345	0.715453296	0.710369391	0.005083905	0.001338508
248	0.727559607	0.720931134	0.006628473	0.001636245
248	0.727559607	0.720931134	0.006628473	0.001636245
248	0.727559607	0.720931134	0.006628473	0.001636245
182	0.724276119	0.716235889	0.008040230	0.001769244
264	0.722691220	0.716640494	0.006050726	0.001454792
399	0.702925173	0.697056411	0.005868762	0.002069242
873	0.714509771	0.710490042	0.004019729	0.002126008
1026	0.711795041	0.708097955	0.003697086	0.002114088
744	0.713640135	0.709380799	0.004259336	0.002038378
204	0.736782077	0.729662271	0.007119806	0.001563694
572	0.719503139	0.714840819	0.004662320	0.001882819
431	0.723659138	0.718878369	0.004780770	0.001492310
83	0.718591005	0.708271127	0.010319878	0.001339286
491	0.723064730	0.718428764	0.004635967	0.001599314
358	0.717966187	0.712793616	0.005172571	0.001453688
635	0.711333922	0.707579647	0.003754275	0.001358691
375	0.714248490	0.708462978	0.005785512	0.001910899

82	0.729898808	0.717579680	0.012319128	0.001895146
442	0.722646490	0.717547820	0.005098670	0.001750709
600	0.716865462	0.712489245	0.004376216	0.001751752
391	0.713960587	0.708469617	0.005490970	0.001799621
553	0.718746265	0.714193118	0.004553147	0.001750206
173	0.724589519	0.718104459	0.006485060	0.001112829
265	0.713479442	0.706281482	0.007197960	0.002106548
129	0.743068977	0.734559345	0.008509632	0.001434308
146	0.731593606	0.722650523	0.008943083	0.001793505
262	0.728578112	0.722408787	0.006169325	0.001532388
447	0.718935213	0.713912529	0.005022684	0.001733187
749	0.719561188	0.716115665	0.003445524	0.001366822
365	0.724827364	0.720062654	0.004764710	0.001275133
227	0.713404047	0.707598806	0.005805242	0.001177919
217	0.729076213	0.722378366	0.006697847	0.001500479
217	0.729076213	0.722378366	0.006697847	0.001500479
217	0.729076213	0.722378366	0.006697847	0.001500479
766	0.714445482	0.710777819	0.003667664	0.001588483
766	0.714445482	0.710777819	0.003667664	0.001588483
476	0.717301684	0.712386728	0.004914955	0.001776876
310	0.713876829	0.708019616	0.005857213	0.001643944
378	0.723153891	0.718085000	0.005068891	0.001501642
885	0.714266350	0.711409685	0.002856665	0.001116990
202	0.728845407	0.721736565	0.007108843	0.001578998
195	0.706517070	0.697733583	0.008783487	0.002327115
166	0.735216235	0.727215207	0.008001027	0.001648065
289	0.724427293	0.718472760	0.005954533	0.001592066
502	0.712167085	0.707818001	0.004349085	0.001478185
523	0.718613219	0.713963288	0.004649931	0.001761593
420	0.725205188	0.720385438	0.004819750	0.001520034
420	0.725205188	0.720385438	0.004819750	0.001520034
489	0.720106125	0.715179572	0.004926553	0.001849060
366	0.720654527	0.715159029	0.005495498	0.001723105
366	0.721565274	0.716069776	0.005495498	0.001723105
486	0.710911330	0.705845837	0.005065493	0.001950030
109	0.733094689	0.724099017	0.008995672	0.001379342
780	0.707090761	0.703078412	0.004012349	0.001965998
385	0.712079520	0.706985059	0.005094461	0.001565111
443	0.724812946	0.720069282	0.004743664	0.001561699
542	0.712160707	0.707780088	0.004380619	0.001630599
272	0.717014880	0.711817915	0.005196965	0.001152197
1470	0.717482918	0.714831843	0.002651074	0.001621807
513	0.715868909	0.710903555	0.004965354	0.001987578
231	0.726464796	0.719749660	0.006715136	0.001637637
158	0.734117863	0.726665698	0.007452165	0.001379869
457	0.721033388	0.716820341	0.004213047	0.001276763
479	0.725436459	0.720943684	0.004492775	0.001525354
266	0.717566645	0.710669133	0.006897511	0.001999465

43	0.735692265	0.720626963	0.015065302	0.001543119
360	0.717687878	0.713122790	0.004565087	0.001186745
647	0.719458390	0.715388636	0.004069754	0.001699187
99	0.713782653	0.703224840	0.010557814	0.001751196
438	0.727776320	0.722920870	0.004855450	0.001638781
747	0.714416837	0.710746772	0.003670065	0.001597012
1093	0.714352416	0.711152024	0.003200392	0.001777476
138	0.701095287	0.692844035	0.008251252	0.001492212
218	0.723610069	0.716844702	0.006765368	0.001588878
394	0.724062814	0.719061018	0.005001796	0.001570990
321	0.721283116	0.715877638	0.005405478	0.001497480
217	0.723420279	0.716691242	0.006729037	0.001570957
217	0.723420279	0.716691242	0.006729037	0.001570957
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334	0.715948420	0.710025878	0.005922542	0.001875082
123	0.720206817	0.711378485	0.008828332	0.001534918
566	0.722017565	0.718237272	0.003780294	0.001295213
674	0.723534217	0.720177818	0.003356399	0.001215917
126	0.750448415	0.742366722	0.008081694	0.001319050
273	0.719193855	0.712779242	0.006414613	0.001803265
160	0.710614693	0.701668756	0.008945937	0.002055966
766	0.713599724	0.710069936	0.003529788	0.001533882
200	0.718116540	0.710712080	0.007404460	0.001766038
185	0.735238114	0.727332465	0.007905649	0.001862545
369	0.718135585	0.712460621	0.005674964	0.001916084
141	0.722685024	0.714000955	0.008684069	0.001716487
144	0.717142430	0.709189989	0.007952441	0.001470136
435	0.720136676	0.715129467	0.005007209	0.001762238
1253	0.704567734	0.701242773	0.003324961	0.002240048
302	0.712814753	0.707153971	0.005660782	0.001569076
1611	0.719355836	0.716762781	0.002593055	0.001756700
358	0.717853337	0.712679245	0.005174092	0.001557563
495	0.711621505	0.706601218	0.005020287	0.002032598
236	0.727165523	0.720347748	0.006817776	0.001789815
339	0.723949106	0.719192259	0.004756847	0.001252083
265	0.711194274	0.704244361	0.006949914	0.002092445
414	0.735049478	0.731241549	0.003807929	0.000981382
1358	0.721567153	0.719103728	0.002463425	0.001347697
317	0.724199139	0.718282087	0.005917052	0.001816305
191	0.735009742	0.728383495	0.006626246	0.001373959
392	0.718477008	0.714006036	0.004470972	0.001284650
283	0.729748162	0.723316388	0.006431774	0.001919490
109	0.721133665	0.712969597	0.008164068	0.001191186
135	0.722557912	0.714282482	0.008275431	0.001516382
430	0.719073847	0.713732190	0.005341658	0.002013239
146	0.736850680	0.729158317	0.007692363	0.001417929
392	0.723899618	0.718907684	0.004991934	0.001604108
191	0.724276371	0.717114501	0.007161869	0.001609471

320	0.714486255	0.708702475	0.005783780	0.001758710
540	0.717902919	0.714021461	0.003881458	0.001336721
503	0.723681094	0.719513566	0.004167528	0.001435707
532	0.719625660	0.715186091	0.004439569	0.001723474
642	0.715807033	0.711512300	0.004294734	0.001947066
418	0.718692942	0.713845177	0.004847766	0.001615765
415	0.720960145	0.716172214	0.004787931	0.001565332
221	0.722216196	0.716802368	0.005413828	0.001065856
213	0.721664688	0.715513820	0.006150868	0.001328280
213	0.721664688	0.715513820	0.006150868	0.001328280
213	0.721664688	0.715513820	0.006150868	0.001328280
268	0.714046589	0.707159750	0.006886839	0.002095562
376	0.732791141	0.728146769	0.004644371	0.001339100
908	0.714822702	0.711328247	0.003494455	0.001832616
700	0.727075140	0.723443039	0.003632101	0.001529035
316	0.710246582	0.703961163	0.006285419	0.002067863
94	0.686604795	0.675388562	0.011216233	0.001962727
246	0.719283072	0.712834438	0.006448634	0.001700298
107	0.722151740	0.713901146	0.008250594	0.001212645
355	0.731423744	0.727280326	0.004143417	0.001017099
407	0.711675304	0.706317434	0.005357870	0.001950787
256	0.712236748	0.705800769	0.006435979	0.001771225
413	0.714426443	0.709526075	0.004900368	0.001657107
317	0.721463084	0.716282852	0.005180232	0.001421908
337	0.717305577	0.712141666	0.005163911	0.001504549
339	0.717006822	0.711873377	0.005133446	0.001495673
700	0.726156430	0.722525696	0.003630734	0.001545650
303	0.696398144	0.691281271	0.005116873	0.001329367
210	0.719564304	0.712184729	0.007379575	0.001917081
147	0.715716721	0.707632348	0.008084373	0.001611243
336	0.724624564	0.719222353	0.005402211	0.001644546
592	0.709821727	0.705889289	0.003932439	0.001536581
69	0.726401947	0.714105488	0.012296459	0.001751138
233	0.722615689	0.716281348	0.006334341	0.001569378
961	0.715752304	0.712513735	0.003238569	0.001694767
136	0.721889256	0.713750054	0.008139201	0.001515145
275	0.722030698	0.715883753	0.006146945	0.001747978
210	0.719248167	0.712553335	0.006694832	0.001584497
579	0.728381438	0.724635346	0.003746093	0.001372193
75	0.714381484	0.703781570	0.010599913	0.001424923
127	0.725275642	0.717476767	0.007798875	0.001307751
288	0.721976675	0.716603534	0.005373141	0.001410454
608	0.719824277	0.716296672	0.003527605	0.001285632
285	0.716772941	0.710369707	0.006403235	0.001987024
79	0.727194213	0.717472581	0.009721631	0.001273670
434	0.721603337	0.716853888	0.004749450	0.001670384
182	0.720281773	0.713328658	0.006953115	0.001504218
929	0.707785488	0.704513982	0.003271507	0.001699961

188	0.719001887	0.712254141	0.006747746	0.001465694
581	0.714071084	0.710334626	0.003736457	0.001388989
1513	0.718133545	0.715691887	0.002441658	0.001544658
778	0.718543998	0.715051301	0.003492696	0.001626373
781	0.718712751	0.715233471	0.003479280	0.001620126
403	0.716192272	0.711162534	0.005029738	0.001747156
309	0.720352898	0.714903938	0.005448960	0.001573708
195	0.739588403	0.733684762	0.005903641	0.001165799
272	0.728981988	0.723948769	0.005033220	0.001182336
696	0.715897687	0.712011520	0.003886167	0.001805455
102	0.744183808	0.734777430	0.009406377	0.001551312
130	0.699261964	0.689940574	0.009321390	0.001943980
130	0.699261964	0.689940574	0.009321390	0.001943980
552	0.712961574	0.708916787	0.004044786	0.001557634
225	0.726564798	0.720060547	0.006504252	0.001642076
443	0.715095751	0.710626982	0.004468769	0.001527513
246	0.719213537	0.713775024	0.005438513	0.001259688
476	0.713686177	0.709313843	0.004372333	0.001576361
331	0.731834090	0.726735266	0.005098824	0.001491384
289	0.708795541	0.702961237	0.005834304	0.001707806
289	0.708795541	0.702961237	0.005834304	0.001707806
245	0.728235215	0.721417238	0.006817977	0.001977848
113	0.719900235	0.710028881	0.009871354	0.001913772
413	0.715399294	0.710610580	0.004788714	0.001646218
465	0.718887097	0.715426985	0.003460113	0.000968540
415	0.712245089	0.707404526	0.004840562	0.001694024
171	0.714703384	0.709363526	0.005339858	0.000849979
493	0.723125447	0.718738541	0.004386906	0.001654247
825	0.713691243	0.710016433	0.003674810	0.001942585
303	0.721321523	0.715231094	0.006090429	0.001962298
395	0.728564497	0.724073934	0.004490563	0.001391173
303	0.711768828	0.705361153	0.006407675	0.002174844
74	0.717852778	0.705167088	0.012685690	0.002083138
176	0.719467688	0.712247732	0.007219957	0.001608024
103	0.728454461	0.718055092	0.010399369	0.001952409
357	0.715610830	0.710357938	0.005252892	0.001727018
407	0.712881950	0.708062991	0.004818958	0.001657911
307	0.703541628	0.698101468	0.005440160	0.001595251
248	0.717679051	0.711110671	0.006568380	0.001880320
82	0.734183830	0.723848986	0.010334844	0.001539283
187	0.730699755	0.725052358	0.005647397	0.001048639
347	0.712273528	0.706843892	0.005429635	0.001798766
507	0.718886296	0.714314738	0.004571558	0.001863148
932	0.714576109	0.711332304	0.003243805	0.001724612
200	0.709792609	0.703264528	0.006528082	0.001500212
295	0.716560807	0.710686408	0.005874399	0.001792125
675	0.705436651	0.701309015	0.004127636	0.002025473
175	0.722381259	0.713879353	0.008501906	0.002229386

727	0.722587176	0.718880183	0.003706992	0.001762824
522	0.717777908	0.713455090	0.004322818	0.001721463
269	0.724690719	0.719439555	0.005251164	0.001309065
957	0.715212003	0.712039761	0.003172242	0.001699626
558	0.722828726	0.718710501	0.004118225	0.001671483
955	0.717029476	0.713855018	0.003174458	0.001700221
381	0.718061127	0.713212561	0.004848566	0.001582938
512	0.720198690	0.715557122	0.004641568	0.001949787
213	0.720727839	0.715129122	0.005598717	0.001180712
602	0.722433281	0.718935018	0.003498263	0.001304734
198	0.717567544	0.709907051	0.007660493	0.002058445
843	0.726971895	0.723787615	0.003184280	0.001515856
253	0.714677777	0.708939739	0.005738038	0.001477510
1052	0.710854910	0.707593796	0.003261114	0.001989154
343	0.713793762	0.708233002	0.005560759	0.001885970
322	0.719284171	0.713867790	0.005416381	0.001681907
176	0.712385239	0.705195483	0.007189756	0.001619976
738	0.710602996	0.706744659	0.003858337	0.001956378
677	0.721048543	0.717897853	0.003150690	0.001196787
384	0.715399336	0.710123618	0.005275718	0.001905337
630	0.715171641	0.711357479	0.003814162	0.001634180
391	0.711928165	0.706756412	0.005171753	0.001866088
157	0.728729446	0.721673683	0.007055763	0.001394979
281	0.727276513	0.721852733	0.005423780	0.001478531
361	0.725137317	0.720059665	0.005077652	0.001664862
526	0.715740019	0.711171490	0.004568530	0.001963741
453	0.713345138	0.708952815	0.004392324	0.001563508
944	0.706829069	0.703564797	0.003264272	0.001800188
488	0.725121121	0.720800290	0.004320831	0.001630648
328	0.719901235	0.714749742	0.005151494	0.001559526
266	0.714743241	0.708561855	0.006181386	0.001820985
235	0.723125323	0.716979212	0.006146112	0.001590676
882	0.710368424	0.707044067	0.003324357	0.001746721
506	0.708726124	0.703991273	0.004734851	0.002036353
600	0.711053810	0.706974673	0.004079137	0.001793500
395	0.716239043	0.711837581	0.004401462	0.001375821
204	0.722104872	0.715770601	0.006334271	0.001472007
431	0.713361016	0.708752531	0.004608485	0.001651335
181	0.724369219	0.716918492	0.007450727	0.001812953
214	0.729159003	0.722803883	0.006355120	0.001560646
727	0.715087977	0.711337384	0.003750592	0.001846779
612	0.713544525	0.709266786	0.004277738	0.002023317
706	0.726480717	0.723040642	0.003440075	0.001511185
487	0.716985752	0.712887239	0.004098513	0.001481428
79	0.742675441	0.732775207	0.009900234	0.001406625
351	0.715807613	0.710897126	0.004910487	0.001537766
173	0.719276736	0.711987399	0.007289336	0.001674653
250	0.710705971	0.704860233	0.005845737	0.001556529

405	0.716657744	0.711948124	0.004709620	0.001638191
95	0.723096983	0.715273450	0.007823532	0.001060967
896	0.715024676	0.711842886	0.003181790	0.001656201
212	0.718617026	0.711575958	0.007041068	0.001919696
301	0.728083556	0.722812812	0.005270744	0.001528265
150	0.735930765	0.729240071	0.006690694	0.001228430
404	0.722875233	0.717872463	0.005002770	0.001851661
446	0.711357431	0.706538673	0.004818758	0.001896625
599	0.728212338	0.724351883	0.003860455	0.001635360
121	0.729824070	0.720985881	0.008838189	0.001732949
1338	0.713056515	0.710448655	0.002607859	0.001669052
194	0.715214945	0.709042699	0.006172246	0.001356641
439	0.727997963	0.723518859	0.004479104	0.001616855
287	0.715080576	0.709682712	0.005397864	0.001535704
287	0.715080576	0.709682712	0.005397864	0.001535704
963	0.709409144	0.706049263	0.003359881	0.001997018
1116	0.717083771	0.714030896	0.003052875	0.001911138
335	0.725241654	0.720849688	0.004391966	0.001188084
91	0.728624477	0.718106117	0.010518361	0.001851451
261	0.720456446	0.714238563	0.006217883	0.001857605
593	0.722607518	0.718953275	0.003654243	0.001459009
166	0.722356945	0.715463362	0.006893583	0.001453518
261	0.715030583	0.709025174	0.006005410	0.001735816
210	0.715730600	0.709503844	0.006226755	0.001502122
140	0.727348340	0.719975119	0.007373221	0.001404727
511	0.716333626	0.711776926	0.004556700	0.001960355
711	0.723548301	0.720271735	0.003276566	0.001412397
183	0.720189325	0.713174000	0.007015326	0.001666704
155	0.713464276	0.705365474	0.008098802	0.001882371
259	0.690001128	0.683381706	0.006619422	0.002102316
291	0.715643726	0.710014750	0.005628975	0.001709931
173	0.727760388	0.720990879	0.006769509	0.001470270
210	0.732399787	0.726481569	0.005918218	0.001364274
188	0.715535838	0.709390102	0.006145736	0.001318598
353	0.717044259	0.712313044	0.004731214	0.001468325
126	0.707959266	0.699059471	0.008899795	0.001855793
441	0.728276976	0.724057810	0.004219166	0.001462853
632	0.713010331	0.708952138	0.004058193	0.001943515
632	0.713010331	0.708952138	0.004058193	0.001943515
377	0.722501347	0.717936198	0.004565149	0.001468679
321	0.725686161	0.720578635	0.005107525	0.001566906
345	0.710886412	0.705215450	0.005670962	0.002076233
449	0.712186570	0.707452693	0.004733876	0.001883943
395	0.722920749	0.718363058	0.004557691	0.001538524
476	0.712270437	0.708105422	0.004165015	0.001548962
192	0.722676639	0.716133680	0.006542959	0.001543095
96	0.720353533	0.711289751	0.009063782	0.001481059
1116	0.719953230	0.717363961	0.002589270	0.001405362

1117	0.719945455	0.717358503	0.002586952	0.001404104
286	0.723194716	0.717217467	0.005977249	0.001920894
162	0.718217683	0.710737044	0.007480639	0.001704598
336	0.736167980	0.732704037	0.003463943	0.000759604
477	0.716985468	0.712632278	0.004353190	0.001703865
334	0.720719454	0.715304962	0.005414491	0.001845798
279	0.711565891	0.705980023	0.005585868	0.001641692
385	0.716149123	0.711167732	0.004981391	0.001801750
561	0.712713831	0.708627638	0.004086193	0.001766847
539	0.715394266	0.711537304	0.003856963	0.001512471
106	0.739428127	0.732538258	0.006889869	0.000949245
91	0.747476179	0.737799635	0.009676544	0.001608388
333	0.721808943	0.717108446	0.004700497	0.001390230
148	0.739285949	0.731926426	0.007359523	0.001515278
241	0.723235414	0.717425728	0.005809686	0.001538320
408	0.724204434	0.719852334	0.004352100	0.001462480
345	0.712634839	0.707429749	0.005205089	0.001772913
449	0.720102407	0.715402055	0.004700352	0.001882872
161	0.728955641	0.721384725	0.007570916	0.001752954
148	0.736812136	0.729769275	0.007042861	0.001395973
681	0.719937309	0.716760043	0.003177266	0.001308132
681	0.719937309	0.716760043	0.003177266	0.001308132
103	0.723519946	0.713522286	0.009997660	0.001963933
907	0.717668030	0.714660515	0.003007515	0.001565659
397	0.717302211	0.712454262	0.004847949	0.001782741
397	0.717302211	0.712454262	0.004847949	0.001782741
755	0.708014052	0.704709190	0.003304862	0.001576163
144	0.717390625	0.710097412	0.007293212	0.001465345
178	0.693517864	0.686009577	0.007508287	0.001919857
550	0.726352741	0.722985254	0.003367488	0.001193544
559	0.707760878	0.704051273	0.003709605	0.001472734
257	0.697032384	0.691707151	0.005325232	0.001395656
962	0.717424987	0.714480290	0.002944697	0.001598054
615	0.712929185	0.708733150	0.004196036	0.002075979
853	0.712080898	0.708950302	0.003130596	0.001603880
317	0.728883108	0.723989695	0.004893413	0.001456991
1369	0.712034770	0.709619828	0.002414942	0.001532741
1369	0.712034770	0.709619828	0.002414942	0.001532741
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323	0.703298024	0.698330176	0.004967847	0.001531417
485	0.721266162	0.717273084	0.003993078	0.001488027
369	0.718841671	0.714192017	0.004649654	0.001535786
354	0.717381985	0.712787179	0.004594806	0.001438945
623	0.728458612	0.724833168	0.003625444	0.001578264
202	0.706611683	0.701678438	0.004933244	0.000947945
1096	0.706893929	0.703768019	0.003125910	0.002066298
242	0.718824258	0.713199771	0.005624487	0.001477317
184	0.704574951	0.698018534	0.006556417	0.001527398

229	0.727216886	0.721761739	0.005455148	0.001317786
178	0.721569698	0.715166145	0.006403553	0.001412511
403	0.712489242	0.707682058	0.004807184	0.001803169
189	0.722414214	0.715936496	0.006477719	0.001536864
271	0.706459251	0.699987074	0.006472177	0.002201219
669	0.725826543	0.722521810	0.003304733	0.001416768
156	0.735001196	0.728394778	0.006606418	0.001320717
270	0.710521682	0.705021597	0.005500085	0.001584966
342	0.706309239	0.701427325	0.004881914	0.001582178
249	0.728638880	0.723118331	0.005520550	0.001473527
233	0.725084565	0.719824148	0.005260417	0.001252700
233	0.725084565	0.719824148	0.005260417	0.001252700
431	0.730489271	0.725959396	0.004529875	0.001719553
122	0.725926119	0.717886110	0.008040008	0.001534017
337	0.723024518	0.718105380	0.004919138	0.001586262
253	0.718306589	0.712131557	0.006175031	0.001876918
331	0.710867923	0.705063541	0.005804382	0.002173687
259	0.721615884	0.716150469	0.005465415	0.001509362
223	0.715733214	0.709156650	0.006576564	0.001884577
223	0.707729298	0.702133651	0.005595647	0.001369852
96	0.720644672	0.711993043	0.008651629	0.001410736
146	0.701836384	0.694419829	0.007416555	0.001577529
898	0.714714036	0.712208544	0.002505492	0.001108441
542	0.724077566	0.720397531	0.003680036	0.001444190
351	0.706262341	0.701019550	0.005242791	0.001898889
172	0.720553182	0.713423809	0.007129372	0.001721203
192	0.718095893	0.711607681	0.006488212	0.001595858
137	0.714197387	0.705688564	0.008508822	0.001959340
360	0.723229786	0.718335689	0.004894097	0.001704425
340	0.714172403	0.709168535	0.005003868	0.001683371
421	0.721870453	0.717337367	0.004533086	0.001711048
331	0.705238516	0.700053385	0.005185131	0.001763793
312	0.724227799	0.719486316	0.004741482	0.001393237
188	0.709302128	0.702507595	0.006794533	0.001723999
108	0.719895773	0.712600494	0.007295280	0.001142451
216	0.720901399	0.715625269	0.005276130	0.001195389
601	0.706954205	0.703444829	0.003509376	0.001472157
601	0.706954205	0.703444829	0.003509376	0.001472157
416	0.726076527	0.721800886	0.004275640	0.001513148
306	0.709232663	0.703592359	0.005640305	0.001938940
866	0.715765704	0.712828782	0.002936922	0.001488321
527	0.708966998	0.704700202	0.004266796	0.001912403
265	0.721818791	0.716305812	0.005512979	0.001605855
524	0.733915278	0.730266875	0.003648403	0.001391690
232	0.733560314	0.728076703	0.005483611	0.001391986
153	0.743678639	0.737765254	0.005913385	0.001067950
707	0.713494363	0.709843571	0.003650792	0.001883145
233	0.711005453	0.705161730	0.005843723	0.001591586

239	0.718156281	0.712671534	0.005484747	0.001438516
104	0.710756446	0.701521155	0.009235291	0.001774763
626	0.716679731	0.712816929	0.003862802	0.001869583
74	0.711251068	0.701246796	0.010004272	0.001482934
253	0.711736143	0.706202513	0.005533630	0.001553917
166	0.722206510	0.714663209	0.007543300	0.001897102
314	0.722059207	0.717190782	0.004868426	0.001495746
636	0.717713992	0.714029817	0.003684175	0.001736445
453	0.710901773	0.706390676	0.004511097	0.001855140
431	0.719471129	0.715643078	0.003828051	0.001272909
553	0.726387519	0.722465488	0.003922032	0.001715889
253	0.725667024	0.720613083	0.005053941	0.001304149
185	0.723324272	0.716159455	0.007164817	0.001917683
663	0.723809579	0.720479740	0.003329840	0.001485160
577	0.719731784	0.716321599	0.003410185	0.001358191
448	0.720758050	0.716736157	0.004021893	0.001467181
324	0.714808502	0.709969068	0.004839435	0.001538651
359	0.705856996	0.701301247	0.004555749	0.001511510
363	0.723996321	0.719287016	0.004709305	0.001634597
386	0.719051776	0.714878867	0.004172908	0.001364943
96	0.718645340	0.709078394	0.009566946	0.001784690
195	0.706722942	0.700802915	0.005920027	0.001388850
93	0.736380079	0.727413431	0.008966648	0.001519673
198	0.733025617	0.727056802	0.005968815	0.001434178
492	0.727510520	0.723726571	0.003783949	0.001433118
131	0.728676584	0.720817267	0.007859317	0.001646309
164	0.738461112	0.733914303	0.004546809	0.000689811
540	0.711444211	0.707369211	0.004075000	0.001826152
397	0.725347345	0.720766972	0.004580373	0.001696516
450	0.720517644	0.716513981	0.004003663	0.001471097
382	0.725153488	0.720757154	0.004396334	0.001506177
340	0.711527546	0.707252674	0.004274872	0.001269337
182	0.722243349	0.715260545	0.006982804	0.001813121
817	0.718544071	0.715555040	0.002989030	0.001491430
261	0.728691942	0.723530562	0.005161380	0.001421042
590	0.714417825	0.710493165	0.003924660	0.001859340
837	0.702456227	0.699041088	0.003415139	0.001998531
922	0.719558080	0.716595081	0.002962999	0.001660410
78	0.760451693	0.751282634	0.009169059	0.001345378
382	0.716695138	0.712394180	0.004300957	0.001449959
160	0.707827665	0.699853517	0.007974148	0.002087904
331	0.710733497	0.705738347	0.004995150	0.001694923
286	0.723909345	0.718752422	0.005156923	0.001561327
434	0.712624782	0.708310630	0.004314152	0.001659799
719	0.710828617	0.707609369	0.003219248	0.001534092
457	0.709118509	0.704586027	0.004532482	0.001933547
222	0.719597809	0.714545477	0.005052332	0.001167551
803	0.715697601	0.712300697	0.003396904	0.001909519

137	0.706981443	0.699148098	0.007833346	0.001732591
155	0.726934787	0.719837495	0.007097291	0.001609464
552	0.716990966	0.713487301	0.003503665	0.001397039
456	0.715525872	0.711400470	0.004125402	0.001602245
399	0.709818030	0.704969163	0.004848867	0.001937571
962	0.715745778	0.712964382	0.002781397	0.001537317
810	0.716813857	0.713648287	0.003165571	0.001678698
388	0.720680170	0.716195386	0.004484783	0.001615385
495	0.711926833	0.708688504	0.003238330	0.001074977
230	0.715322079	0.709119367	0.006202712	0.001834376
518	0.723748018	0.720022966	0.003725052	0.001491021
766	0.715996983	0.712679747	0.003317235	0.001749766
702	0.717077838	0.713830494	0.003247344	0.001537002
422	0.717834165	0.713544411	0.004289754	0.001613369
103	0.725785682	0.716718205	0.009067477	0.001760346
144	0.738602668	0.731041034	0.007561634	0.001712430
252	0.728365152	0.723040372	0.005324780	0.001486622
353	0.719036514	0.714405501	0.004631013	0.001575614
190	0.720163292	0.713882958	0.006280333	0.001560216
590	0.699913321	0.695434007	0.004479314	0.002465137
249	0.699003559	0.692163934	0.006839625	0.002426271
504	0.717032851	0.712694462	0.004338388	0.001977170
526	0.714448575	0.710426451	0.004022124	0.001778089
974	0.716454337	0.713726374	0.002727963	0.001514637
96	0.720224625	0.711745319	0.008479306	0.001445000
259	0.710214411	0.705362852	0.004851559	0.001277247
1648	0.720269257	0.718186888	0.002082369	0.001499410
224	0.729085037	0.723535633	0.005549403	0.001447651
560	0.712504565	0.708476227	0.004028338	0.001908677
376	0.714429964	0.710277093	0.004152871	0.001363118
276	0.721681187	0.716217439	0.005463748	0.001734337
147	0.730212136	0.724373216	0.005838920	0.001054957
149	0.720570938	0.712807207	0.007763731	0.001891145
241	0.720374698	0.714647535	0.005727163	0.001664695
1040	0.710773969	0.707682033	0.003091936	0.002094140
330	0.716709798	0.712005071	0.004704727	0.001538957
215	0.719034332	0.712765775	0.006268557	0.001781403
409	0.718368706	0.713955133	0.004413573	0.001680137
549	0.720118345	0.716283619	0.003834726	0.001703293
329	0.720803895	0.716272778	0.004531117	0.001425784
483	0.713468384	0.709152927	0.004315457	0.001898798
207	0.721826761	0.715448551	0.006378210	0.001777906
429	0.714214490	0.710070279	0.004144211	0.001556278
259	0.690144752	0.684003269	0.006141483	0.002064240
259	0.690144752	0.684003269	0.006141483	0.002064240
259	0.690144752	0.684003269	0.006141483	0.002064240
452	0.717585083	0.713869669	0.003715414	0.001318837
471	0.726251959	0.722158428	0.004093531	0.001671039

487	0.720118162	0.715951208	0.004166954	0.001791274
487	0.720118162	0.715951208	0.004166954	0.001791274
487	0.720118162	0.715951208	0.004166954	0.001791274
137	0.714457879	0.707186257	0.007271621	0.001534753
137	0.714457879	0.707186257	0.007271621	0.001534753
1064	0.710517553	0.707544302	0.002973251	0.001993127
431	0.708074614	0.703591036	0.004483578	0.001836134
427	0.719409551	0.715669448	0.003740102	0.001265929
178	0.724901358	0.717862565	0.007038793	0.001870128
121	0.694674583	0.684120833	0.010553749	0.002859474
130	0.725583939	0.718378213	0.007205726	0.001432238
216	0.713412375	0.707752504	0.005659871	0.001469326
452	0.720691668	0.716794205	0.003897463	0.001461665
115	0.730667750	0.722244628	0.008423121	0.001741420
623	0.714508929	0.711053571	0.003455359	0.001588560
283	0.718062813	0.712947143	0.005115670	0.001581745
236	0.708718340	0.702464507	0.006253834	0.001973959
250	0.708819624	0.703137258	0.005682365	0.001730094
734	0.714087037	0.710982956	0.003104081	0.001516914
329	0.724479518	0.720246949	0.004232569	0.001265005
1069	0.716218258	0.713296041	0.002922217	0.001960355
1069	0.716218258	0.713296041	0.002922217	0.001960355
390	0.729790392	0.725333365	0.004457027	0.001665335
516	0.719416664	0.715711809	0.003704855	0.001522652
110	0.733717339	0.727411152	0.006306188	0.000940514
223	0.722937584	0.717183597	0.005753988	0.001588334
619	0.718601134	0.715266902	0.003334233	0.001480631
287	0.724759171	0.719881645	0.004877526	0.001471655
491	0.715707735	0.712162674	0.003545060	0.001330106
251	0.721578297	0.716839138	0.004739160	0.001215701
612	0.721788740	0.718428137	0.003360603	0.001493017
330	0.735346751	0.731492590	0.003854161	0.001059338
229	0.721713133	0.716427188	0.005285945	0.001383315
463	0.712660230	0.708349838	0.004310392	0.001859757
463	0.712660230	0.708349838	0.004310392	0.001859757
397	0.715092123	0.710856099	0.004236024	0.001540251
174	0.724232614	0.717901683	0.006330931	0.001507966
387	0.715314163	0.710994342	0.004319821	0.001561658
298	0.720697079	0.715386617	0.005310462	0.001817758
123	0.714666392	0.706561007	0.008105386	0.001749507
338	0.712070309	0.706995757	0.005074552	0.001884933
175	0.704705391	0.698829974	0.005875417	0.001308588
647	0.715725536	0.712171941	0.003553595	0.001771543
105	0.715355322	0.705930678	0.009424644	0.002023857
368	0.720979824	0.716703488	0.004276336	0.001460501
475	0.716949660	0.712870302	0.004079359	0.001716371
573	0.721878650	0.718749229	0.003129421	0.001218616
490	0.710869689	0.707046208	0.003823481	0.001555770

365	0.716884219	0.712573563	0.004310656	0.001473253
219	0.722929277	0.717176149	0.005753128	0.001574817
481	0.705557862	0.701522383	0.004035478	0.001703768
397	0.716252030	0.711480602	0.004771429	0.001966621
397	0.716252030	0.711480602	0.004771429	0.001966621
397	0.716252030	0.711480602	0.004771429	0.001966621
494	0.712886227	0.708718657	0.004167570	0.001869585
531	0.724476439	0.720542559	0.003933880	0.001791922
305	0.715600625	0.710733446	0.004867178	0.001576423
358	0.720306726	0.715660182	0.004646544	0.001686817
165	0.721265803	0.715472618	0.005793184	0.001208575
539	0.727840126	0.724566292	0.003273834	0.001261379
476	0.714913915	0.711205238	0.003708677	0.001429515
476	0.714913915	0.711205238	0.003708677	0.001429515
328	0.720147864	0.715510064	0.004637800	0.001540488
328	0.720147864	0.715510064	0.004637800	0.001540488
735	0.732836055	0.730430471	0.002405585	0.000929171
349	0.722369100	0.717866387	0.004502712	0.001548670
282	0.720356651	0.715423466	0.004933185	0.001506012
569	0.713863579	0.710118308	0.003745271	0.001753484
713	0.715698808	0.712444049	0.003254760	0.001662168
262	0.719878800	0.714631721	0.005247079	0.001587887
561	0.712902438	0.709532194	0.003370244	0.001403591
561	0.712902438	0.709532194	0.003370244	0.001403591
205	0.718733971	0.712585295	0.006148677	0.001707393
348	0.717794744	0.712613301	0.005181443	0.002058453
284	0.715002749	0.709198311	0.005804437	0.002108553
130	0.721921670	0.715804879	0.006116791	0.001072303
392	0.728839167	0.724877722	0.003961444	0.001357840
526	0.719792328	0.716080832	0.003711496	0.001600006
132	0.724967529	0.718810785	0.006156743	0.001104987
424	0.714233628	0.710147730	0.004085897	0.001563350
548	0.718278329	0.714744451	0.003533877	0.001512201
519	0.714955522	0.710825144	0.004130378	0.001956897
753	0.716371569	0.713252335	0.003119234	0.001619548
681	0.712613978	0.709049372	0.003564606	0.001914289
107	0.732828358	0.725040998	0.007787360	0.001435718
683	0.722883336	0.719766568	0.003116768	0.001468159
548	0.711076841	0.707312909	0.003763933	0.001718544
146	0.699645034	0.692277265	0.007367769	0.001754393
720	0.703269117	0.699659579	0.003609537	0.002077732
521	0.710972445	0.707029292	0.003943153	0.001794565
272	0.717094902	0.711861899	0.005233003	0.001650617
290	0.712057413	0.706773477	0.005283936	0.001797940
507	0.712012023	0.708387720	0.003624303	0.001482154
483	0.712127868	0.707878219	0.004249649	0.001942075
140	0.744291271	0.737596903	0.006694368	0.001397443
421	0.719936157	0.716334323	0.003601834	0.001218303

639	0.711797903	0.708163895	0.003634007	0.001882856
496	0.711765860	0.708645267	0.003120593	0.001078268
248	0.731857382	0.726459167	0.005398215	0.001613577
200	0.720045021	0.714732344	0.005312678	0.001260534
282	0.717419491	0.713171569	0.004247921	0.001137626
1003	0.701208933	0.698117093	0.003091840	0.002144349
281	0.703300472	0.698382508	0.004917963	0.001520598
353	0.724877143	0.720709944	0.004167199	0.001372612
198	0.719960760	0.713579801	0.006380959	0.001805398
198	0.719960760	0.713579801	0.006380959	0.001805398
207	0.706100250	0.700028951	0.006071299	0.001708804
232	0.718723521	0.713319170	0.005404351	0.001518634
530	0.719637480	0.715932061	0.003705420	0.001631076
410	0.700931441	0.696171235	0.004760206	0.002083075
706	0.708015507	0.704701789	0.003313718	0.001740452
384	0.727802117	0.724038827	0.003763290	0.001221582
1148	0.715042819	0.712186100	0.002856719	0.002105811
320	0.714322982	0.709510949	0.004812032	0.001666481
126	0.714027794	0.706117667	0.007910127	0.001773356
542	0.713547723	0.709566320	0.003981404	0.001933399
347	0.719893875	0.715439661	0.004454215	0.001549753
408	0.705791253	0.701203543	0.004587710	0.001933234
351	0.730743472	0.726667964	0.004075508	0.001312858
629	0.724306740	0.721358381	0.002948360	0.001231410
629	0.724306740	0.721358381	0.002948360	0.001231410
222	0.712788512	0.707091183	0.005697328	0.001624107
351	0.721708191	0.717296947	0.004411244	0.001540081
335	0.705980504	0.701527752	0.004452752	0.001497809
536	0.722725881	0.719038158	0.003687723	0.001644622
252	0.723877595	0.718650328	0.005227267	0.001556510
479	0.717358696	0.713698798	0.003659897	0.001451749
452	0.714737208	0.710770880	0.003966328	0.001608956
463	0.722164069	0.718498519	0.003665550	0.001409150
222	0.719788702	0.715002024	0.004786678	0.001152346
240	0.711813792	0.705412528	0.006401264	0.002229079
228	0.722605092	0.717595936	0.005009156	0.001296959
160	0.731703057	0.726223578	0.005479478	0.001089682
160	0.731703057	0.726223578	0.005479478	0.001089682
522	0.709324908	0.705579939	0.003744969	0.001663198
208	0.718686126	0.712501585	0.006184541	0.001808461
165	0.721149028	0.715472618	0.005676410	0.001208575
362	0.710630444	0.706579093	0.004051351	0.001350783
331	0.720942207	0.716340936	0.004601271	0.001595001
676	0.719758837	0.716574717	0.003184121	0.001560118
557	0.724415240	0.720766310	0.003648929	0.001688557
376	0.715902895	0.711371432	0.004531463	0.001758112
168	0.725810711	0.718536044	0.007274667	0.002024962
458	0.723147981	0.719495707	0.003652273	0.001391597

802	0.715911045	0.712816605	0.003094440	0.001749676
802	0.715911045	0.712816605	0.003094440	0.001749676
375	0.730323157	0.726367092	0.003956066	0.001337267
308	0.725535868	0.720792561	0.004743307	0.001580350
400	0.718962122	0.714593635	0.004368486	0.001742199
251	0.730748398	0.725901657	0.004846742	0.001346143
643	0.719081840	0.715793785	0.003288055	0.001587237
503	0.716165418	0.711984593	0.004180825	0.002007601
766	0.714340155	0.711261191	0.003078964	0.001658178
442	0.722778303	0.718935099	0.003843204	0.001490816
1241	0.715771104	0.713081517	0.002689587	0.002052974
206	0.715979737	0.709802787	0.006176950	0.001798102
220	0.714063187	0.708193106	0.005870081	0.001734423
561	0.726635322	0.723206975	0.003428348	0.001508837
371	0.718096037	0.713617587	0.004478450	0.001704546
1302	0.712135279	0.709469994	0.002665284	0.002121850
234	0.735080641	0.729680919	0.005399723	0.001568495
688	0.711477766	0.708002307	0.003475459	0.001911801
256	0.731700623	0.726446804	0.005253819	0.001626848
585	0.707858697	0.704100044	0.003758653	0.001904291
134	0.733276439	0.725745044	0.007531395	0.001753009
602	0.714995616	0.711630034	0.003365582	0.001572921
132	0.728456654	0.721863877	0.006592777	0.001323825
264	0.716565117	0.711218276	0.005346841	0.001744737
164	0.725119393	0.718029855	0.007089538	0.001906912
220	0.724683728	0.719098698	0.005585030	0.001592500
386	0.717981046	0.713636871	0.004344175	0.001690632
144	0.718169360	0.711920709	0.006248651	0.001305010
1215	0.715442516	0.712768456	0.002674059	0.002019900
1215	0.715442516	0.712768456	0.002674059	0.002019900
1376	0.718817818	0.716426133	0.002391685	0.001830500
282	0.735926743	0.730947738	0.004979005	0.001626430
365	0.719744924	0.715052542	0.004692382	0.001869957
259	0.708785870	0.703477558	0.005308311	0.001699087
343	0.705526743	0.701212932	0.004313811	0.001487413
114	0.716365318	0.708346397	0.008018920	0.001710250
483	0.711324601	0.707162248	0.004162352	0.001953182
210	0.720697752	0.714581962	0.006115790	0.001835325
212	0.719098363	0.714004709	0.005093654	0.001287308
258	0.729328938	0.723990026	0.005338913	0.001721197
256	0.712102691	0.706849930	0.005252761	0.001653584
763	0.714532382	0.711665683	0.002866699	0.001468859
680	0.714097907	0.710540858	0.003557048	0.002018083
497	0.730801449	0.727307382	0.003494068	0.001423416
616	0.712494898	0.709250725	0.003244174	0.001522745
400	0.713374487	0.709011518	0.004362969	0.001789088
126	0.714308248	0.706495957	0.007812292	0.001806958
275	0.711567110	0.705932062	0.005635048	0.002052430

984	0.709589728	0.706478582	0.003111145	0.002239159
984	0.709589728	0.706478582	0.003111145	0.002239159
706	0.726265373	0.723162134	0.003103239	0.001599698
835	0.713634029	0.710627628	0.003006401	0.001776170
295	0.716552745	0.711353197	0.005199548	0.001877158
340	0.716067035	0.712147672	0.003919363	0.001229434
362	0.719984903	0.715991817	0.003993086	0.001358888
355	0.691407576	0.686338674	0.005068902	0.002147577
190	0.724478856	0.717358363	0.007120493	0.002269384
276	0.724177231	0.719529443	0.004647789	0.001405236
1007	0.709738041	0.706949909	0.002788133	0.001845337
574	0.717028054	0.713375870	0.003652184	0.001805863
149	0.726219957	0.719858177	0.006361780	0.001422613
869	0.718918419	0.716179167	0.002739252	0.001538275
711	0.715600350	0.712226603	0.003373746	0.001910081
249	0.724811462	0.719501592	0.005309870	0.001658405
268	0.731750028	0.727958923	0.003791105	0.000909981
222	0.730793843	0.725761688	0.005032156	0.001328419
607	0.720421871	0.716895557	0.003526314	0.001785078
658	0.726135904	0.722993747	0.003142158	0.001536616
901	0.715924443	0.713008042	0.002916400	0.001813723
420	0.709743045	0.706033937	0.003709107	0.001368486
797	0.725331653	0.722608588	0.002723065	0.001399695
294	0.715109730	0.710534903	0.004574827	0.001457740
135	0.737668369	0.733915706	0.003752663	0.000450487
237	0.726330100	0.721274947	0.005055153	0.001435904
535	0.723707315	0.720176381	0.003530934	0.001581403
437	0.714015963	0.709433988	0.004581975	0.002176280
244	0.717952438	0.712620018	0.005332420	0.001646859
381	0.722857217	0.719103369	0.003753847	0.001274488
115	0.717086721	0.709549321	0.007537399	0.001552008
169	0.720429138	0.713628560	0.006800578	0.001856742
212	0.718215349	0.712530697	0.005684652	0.001628174
795	0.720501706	0.717707733	0.002793973	0.001475465
313	0.716714755	0.712096499	0.004618255	0.001587171
406	0.711080559	0.706851790	0.004228769	0.001726525
610	0.726456473	0.723272752	0.003183721	0.001471583
823	0.725323174	0.722476422	0.002846752	0.001587535
446	0.717975528	0.714555172	0.003420356	0.001242442
215	0.728399017	0.723252353	0.005146664	0.001356961
154	0.718408498	0.711324469	0.007084029	0.001841648
506	0.717424955	0.713563684	0.003861271	0.001798376
281	0.731128350	0.726409877	0.004718473	0.001491894
968	0.700855376	0.697799163	0.003056213	0.002157374
313	0.716044802	0.711422209	0.004622592	0.001595934
548	0.717547347	0.713926815	0.003620533	0.001714715
333	0.723890499	0.719634247	0.004256252	0.001441794
820	0.713931241	0.711195826	0.002735415	0.001467212

794	0.712053837	0.709072138	0.002981699	0.001688877
191	0.730098506	0.724637820	0.005460686	0.001362787
238	0.729668782	0.725015915	0.004652867	0.001232924
570	0.716021683	0.712629180	0.003392503	0.001570369
812	0.708487624	0.705241242	0.003246383	0.002048662
166	0.722344562	0.715499503	0.006845059	0.001862324
493	0.721005087	0.717290289	0.003714798	0.001629281
64	0.750173651	0.740987931	0.009185719	0.001294064
660	0.717468777	0.714233238	0.003235538	0.001655887
1084	0.715523512	0.713107075	0.002416437	0.001517084
176	0.717173016	0.711113162	0.006059854	0.001549343
460	0.724757682	0.720740548	0.004017135	0.001780041
136	0.712916426	0.705546989	0.007369437	0.001772186
1170	0.718379099	0.715995351	0.002383747	0.001595260
361	0.720222004	0.716750113	0.003471891	0.001044458
878	0.720686053	0.717756515	0.002929539	0.001808663
310	0.710315607	0.705140101	0.005175506	0.001993463
578	0.698053857	0.693727099	0.004326758	0.002598488
146	0.734798201	0.728279068	0.006519133	0.001492009
146	0.734798201	0.728279068	0.006519133	0.001492009
396	0.714767977	0.710694243	0.004073734	0.001581194
362	0.719351052	0.714983418	0.004367634	0.001662232
210	0.718913923	0.713387067	0.005526855	0.001545313
1195	0.715507483	0.712848647	0.002658835	0.002037517
192	0.722547965	0.717191610	0.005356355	0.001328750
491	0.711706915	0.708004346	0.003702569	0.001626595
181	0.720566483	0.714863738	0.005702746	0.001423816
311	0.716697765	0.712076336	0.004621430	0.001607564
270	0.741665283	0.737034720	0.004630563	0.001401758
149	0.726298809	0.719869632	0.006429177	0.001492847
534	0.723123677	0.719791459	0.003332219	0.001441177
534	0.723123677	0.719791459	0.003332219	0.001441177
348	0.707912242	0.703208968	0.004703275	0.001872109
328	0.718548383	0.714012752	0.004535631	0.001641309
377	0.720307391	0.715862880	0.004444512	0.001811897
377	0.720307391	0.715862880	0.004444512	0.001811897
482	0.715935690	0.712244175	0.003691515	0.001598716
482	0.715935690	0.712244175	0.003691515	0.001598716
401	0.716414497	0.712124688	0.004289809	0.001797969
403	0.716278281	0.712009762	0.004268519	0.001789046
403	0.716278281	0.712009762	0.004268519	0.001789046
135	0.725325277	0.719135676	0.006189601	0.001260644
164	0.713197079	0.706571384	0.006625695	0.001756411
564	0.713165762	0.709740560	0.003425202	0.001614547
248	0.721634032	0.716087733	0.005546298	0.001862018
116	0.710935641	0.702759185	0.008176456	0.001893360
183	0.707900912	0.702867954	0.005032958	0.001132672
413	0.705834603	0.701754140	0.004080463	0.001680377

140	0.724750337	0.717166372	0.007583965	0.001968543
605	0.720357561	0.717104850	0.003252711	0.001565660
208	0.732444275	0.726822938	0.005621338	0.001609080
167	0.730893103	0.725023979	0.005869124	0.001408724
137	0.706333829	0.699148098	0.007185731	0.001732591
162	0.697869452	0.691019121	0.006850331	0.001862703
223	0.704823573	0.699487195	0.005336378	0.001556948
412	0.721926910	0.718057845	0.003869065	0.001515262
259	0.718564777	0.713249302	0.005315475	0.001798064
295	0.710172900	0.705213203	0.004959696	0.001784563
86	0.729784052	0.725249624	0.004534428	0.000435252
328	0.715108039	0.710549024	0.004559015	0.001678560
961	0.707987049	0.704972093	0.003014956	0.002150989
479	0.705818784	0.701461167	0.004357617	0.002239710
211	0.710809695	0.705147504	0.005662191	0.001666072
453	0.713596058	0.710393554	0.003202504	0.001144868
480	0.724026742	0.720423335	0.003603407	0.001537215
163	0.722668850	0.715754804	0.006914047	0.001924263
530	0.719862187	0.716113817	0.003748370	0.001839902
196	0.719535587	0.714057946	0.005477641	0.001454852
558	0.717061049	0.713510571	0.003550478	0.001742248
306	0.705274084	0.700856761	0.004417323	0.001479525
304	0.715840810	0.711150712	0.004690098	0.001657201
304	0.715840810	0.711150712	0.004690098	0.001657201
56	0.743032640	0.733204389	0.009828252	0.001340774
142	0.738254283	0.731718585	0.006535698	0.001504350
415	0.715832773	0.711845347	0.003987426	0.001637155
250	0.718867185	0.713630935	0.005236250	0.001702314
491	0.714270994	0.711132773	0.003138221	0.001201088
460	0.717627209	0.714129335	0.003497874	0.001400038
716	0.722707872	0.719900074	0.002807798	0.001404342
407	0.725501445	0.721412145	0.004089300	0.001696556
269	0.712672936	0.707626941	0.005045994	0.001708834
164	0.731185201	0.724909067	0.006276134	0.001611930
105	0.716173380	0.708929698	0.007243682	0.001376029
865	0.704427129	0.701189774	0.003237354	0.002265428
179	0.731612732	0.725993469	0.005619263	0.001414955
229	0.729336172	0.724257507	0.005078665	0.001478863
708	0.717579147	0.714422775	0.003156372	0.001766373
544	0.721683855	0.718095730	0.003588125	0.001755737
390	0.719815061	0.715742594	0.004072468	0.001623454
703	0.730549551	0.728034302	0.002515249	0.001116304
233	0.732099210	0.727195780	0.004903430	0.001407889
399	0.726113474	0.722159962	0.003953512	0.001568364
402	0.722588509	0.718276041	0.004312468	0.001881576
536	0.714022752	0.710197908	0.003824844	0.001973574
312	0.724642042	0.720661521	0.003980521	0.001244454
1090	0.703039086	0.700167146	0.002871940	0.002263266

226	0.718793070	0.712966364	0.005826705	0.001933621
227	0.721490546	0.716103318	0.005387229	0.001660488
679	0.714006805	0.710574713	0.003432092	0.002016084
364	0.716760896	0.712585567	0.004175330	0.001600189
387	0.718882706	0.714950964	0.003931742	0.001510315
174	0.729814102	0.724547140	0.005266962	0.001219826
174	0.729814102	0.724547140	0.005266962	0.001219826
366	0.713759251	0.709813746	0.003945506	0.001439943
498	0.718057529	0.714482506	0.003575023	0.001609305
347	0.726442294	0.722913013	0.003529281	0.001093331
188	0.708814972	0.702716115	0.006098857	0.001768971
196	0.745785094	0.741336537	0.004448557	0.000981302
685	0.719919985	0.716662956	0.003257029	0.001838568
222	0.732320161	0.727005635	0.005314526	0.001586635
68	0.731929981	0.721472870	0.010457110	0.001882107
219	0.717960718	0.712325703	0.005635015	0.001762102
700	0.726308971	0.723381852	0.002927119	0.001520345
304	0.706762844	0.701126559	0.005636285	0.002449276
372	0.717176551	0.713171390	0.004005161	0.001513937
809	0.712653430	0.709731806	0.002921624	0.001754189
317	0.710666281	0.705630698	0.005035583	0.002043407
317	0.710666281	0.705630698	0.005035583	0.002043407
317	0.710666281	0.705630698	0.005035583	0.002043407
317	0.710666281	0.705630698	0.005035583	0.002043407
86	0.750533471	0.741929432	0.008604040	0.001620283
157	0.718120582	0.711880194	0.006240388	0.001556289
781	0.706933584	0.703869141	0.003064443	0.001867117
370	0.715587224	0.711381699	0.004205525	0.001669300
707	0.706916037	0.703931651	0.002984386	0.001606501
400	0.712078057	0.708229711	0.003848347	0.001511817
188	0.705331497	0.699112431	0.006219065	0.001856971
188	0.705331497	0.699112431	0.006219065	0.001856971
606	0.720537287	0.717229421	0.003307866	0.001693685
409	0.722705227	0.718564262	0.004140965	0.001791984
96	0.713415943	0.705395610	0.008020332	0.001577946
411	0.707750890	0.703597617	0.004153273	0.001812551
411	0.707750890	0.703597617	0.004153273	0.001812551
513	0.716998570	0.713256361	0.003742208	0.001837244
123	0.712268542	0.704985662	0.007282880	0.001670015
142	0.709395197	0.702909379	0.006485818	0.001529607
787	0.717725832	0.714917601	0.002808231	0.001589347
464	0.723092447	0.719686107	0.003406339	0.001378963
348	0.716077261	0.711722801	0.004354460	0.001690102
788	0.703013004	0.700027417	0.002985587	0.001800275
238	0.728599475	0.723975632	0.004623844	0.001305347
469	0.719621963	0.715698718	0.003923244	0.001851977
199	0.712605183	0.706318809	0.006286374	0.002017903
102	0.730492013	0.721813251	0.008678762	0.001971460

111	0.709855403	0.701335904	0.008519499	0.002067627
344	0.719249439	0.715473098	0.003776340	0.001259245
129	0.737641938	0.731657776	0.005984162	0.001186061
495	0.725601371	0.722374156	0.003227215	0.001324661
536	0.718434312	0.714644739	0.003789573	0.001980481
340	0.719840930	0.715520229	0.004320702	0.001633826
634	0.718580492	0.715356530	0.003223962	0.001697247
251	0.709464005	0.704348933	0.005115073	0.001691493
485	0.705963035	0.701746263	0.004216772	0.002223063
485	0.705963035	0.701746263	0.004216772	0.002223063
488	0.707128066	0.703038544	0.004089522	0.002104151
958	0.705041414	0.702529419	0.002511995	0.001558541
359	0.708315501	0.703826742	0.004488759	0.001866563
273	0.721781800	0.717025136	0.004756664	0.001593914
541	0.717511972	0.714226008	0.003285964	0.001508102
444	0.715707161	0.712261957	0.003445204	0.001361308
211	0.713470444	0.707835282	0.005635162	0.001732745
80	0.731401580	0.723238382	0.008163198	0.001378656
603	0.719631610	0.716212282	0.003419327	0.001823307
211	0.722078306	0.716896773	0.005181533	0.001465289
203	0.710586426	0.704480631	0.006105794	0.001958783
323	0.714596534	0.710046622	0.004549912	0.001731986
552	0.710670597	0.707291984	0.003378613	0.001632819
552	0.710670597	0.707291984	0.003378613	0.001632819
305	0.706074513	0.700935789	0.005138724	0.002088303
266	0.708733138	0.703875034	0.004858104	0.001628460
231	0.726880701	0.721830284	0.005050417	0.001528523
231	0.698336892	0.693996531	0.004340361	0.001129645
444	0.726403271	0.722860987	0.003542284	0.001447208
92	0.724447631	0.716030736	0.008416894	0.001693427
184	0.714766275	0.708550311	0.006215964	0.001847362
128	0.740813756	0.733933332	0.006880425	0.001575041
187	0.732685459	0.727069322	0.005616137	0.001535290
141	0.724917273	0.719731026	0.005186247	0.000987610
343	0.714434482	0.709721399	0.004713083	0.001984299
343	0.714434482	0.709721399	0.004713083	0.001984299
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767	0.706110174	0.703272385	0.002837789	0.001609341
302	0.718313344	0.713885940	0.004427404	0.001543269
202	0.713625800	0.708161369	0.005464431	0.001573600
157	0.722933932	0.716507823	0.006426109	0.001691439
132	0.731708238	0.725153753	0.006554485	0.001480756
268	0.735794764	0.730993325	0.004801439	0.001614531
429	0.720368871	0.716559771	0.003809100	0.001626826
384	0.715591399	0.711921480	0.003669919	0.001352556
256	0.728249369	0.724177231	0.004072138	0.001111067
251	0.726883104	0.721983213	0.004899890	0.001577851
390	0.716520938	0.712526168	0.003994771	0.001633497

757	0.722626855	0.719750228	0.002876627	0.001645214
225	0.717474251	0.712369287	0.005104964	0.001540858
182	0.721379377	0.715221700	0.006157678	0.001813595
163	0.715094753	0.709397771	0.005696982	0.001390931
1193	0.717859561	0.715810685	0.002048876	0.001316788
452	0.719404149	0.716072980	0.003331168	0.001319331
452	0.719404149	0.716072980	0.003331168	0.001319331
492	0.719370237	0.715725837	0.003644400	0.001719310
353	0.719936905	0.715500712	0.004436193	0.001827833
142	0.726818410	0.720504002	0.006314408	0.001489775
74	0.756825497	0.748407357	0.008418140	0.001380272
529	0.712872868	0.709141001	0.003731868	0.001941744
263	0.712799623	0.707882689	0.004916934	0.001676579
218	0.721113664	0.716644549	0.004469115	0.001148465
368	0.727060106	0.722977906	0.004082201	0.001617859
511	0.717848260	0.714354884	0.003493376	0.001647484
394	0.719692243	0.716125837	0.003566406	0.001325021
507	0.713174066	0.709299098	0.003874967	0.002013969
521	0.709872533	0.706412796	0.003459737	0.001651445
248	0.699552540	0.694201959	0.005350581	0.001880739
119	0.723228735	0.716878687	0.006350047	0.001271116
224	0.729344719	0.724515665	0.004829054	0.001385780
395	0.709848518	0.706264937	0.003583581	0.001345753
471	0.717433051	0.713710024	0.003723026	0.001732992
637	0.711351696	0.708043182	0.003308514	0.001855054
657	0.714259878	0.711044861	0.003215017	0.001807015
591	0.707994015	0.704337356	0.003656659	0.002103765
275	0.720235643	0.715136108	0.005099534	0.001904370
483	0.704152973	0.700048477	0.004104496	0.002167718
394	0.712843933	0.708400303	0.004443630	0.002073550
352	0.711871821	0.707259636	0.004612185	0.001996456
654	0.715136402	0.712079782	0.003056619	0.001629584
389	0.712561239	0.708590265	0.003970974	0.001636843
229	0.736237988	0.731757588	0.004480401	0.001227602
360	0.710691766	0.705991294	0.004700472	0.002125994
708	0.722886012	0.720016164	0.002869847	0.001559250
650	0.714538116	0.711399892	0.003138224	0.001712311
366	0.704219786	0.699695530	0.004524256	0.002004577
366	0.704219786	0.699695530	0.004524256	0.002004577
207	0.730112051	0.724604467	0.005507584	0.001680748
190	0.707342309	0.701241114	0.006101195	0.001893214
189	0.724654103	0.719955700	0.004698404	0.001117039
323	0.721789810	0.717742555	0.004047255	0.001416744
323	0.721789810	0.717742555	0.004047255	0.001416744
330	0.717439093	0.713094945	0.004344148	0.001667619
248	0.723617525	0.718722002	0.004895523	0.001594056
347	0.711719951	0.707285656	0.004434295	0.001830184
491	0.718779583	0.715121930	0.003657653	0.001763245

159	0.724865475	0.718429354	0.006436121	0.001768672
318	0.712353812	0.707744480	0.004609332	0.001814823
648	0.702521590	0.699164256	0.003357334	0.001963532
448	0.715185388	0.711359599	0.003825790	0.001762974
950	0.709515209	0.706886761	0.002628448	0.001764881
354	0.703522180	0.698475315	0.005046865	0.002426414
215	0.723976561	0.718574395	0.005402166	0.001688549
123	0.721422236	0.714258657	0.007163579	0.001699666
204	0.720234576	0.713855440	0.006379136	0.002235949
707	0.712610456	0.709413882	0.003196574	0.001945909
507	0.723872941	0.720816685	0.003056255	0.001275661
1235	0.719208255	0.716792622	0.002415633	0.001942422
489	0.713056808	0.709547415	0.003509394	0.001624166
364	0.721133644	0.717322691	0.003810953	0.001428641
229	0.716998910	0.712111998	0.004886913	0.001478148
318	0.725589572	0.720909265	0.004680306	0.001883459
502	0.719944444	0.716912339	0.003032105	0.001250968
478	0.717455149	0.713837146	0.003618003	0.001696240
557	0.721444410	0.718244840	0.003199570	0.001546267
380	0.714453949	0.710176425	0.004277524	0.001885718
364	0.720272703	0.716280980	0.003991724	0.001573461
323	0.710922624	0.706175643	0.004746981	0.001976237
361	0.711088663	0.706838647	0.004250016	0.001770957
362	0.710976374	0.706470962	0.004505412	0.001996581
249	0.718982657	0.714407346	0.004575310	0.001417156
237	0.720545185	0.715382092	0.005163094	0.001717969
528	0.721963745	0.718911049	0.003052696	0.001338556
436	0.722041742	0.718455202	0.003586540	0.001525784
174	0.729920780	0.723672385	0.006248396	0.001849203
293	0.729532508	0.725804102	0.003728406	0.001108851
339	0.719871195	0.715381171	0.004490024	0.001861144
766	0.707220291	0.704546423	0.002673867	0.001491490
1100	0.722660684	0.720365322	0.002295362	0.001578796
287	0.723910851	0.719030055	0.004880796	0.001863424
910	0.711976216	0.709615462	0.002360753	0.001382892
332	0.708795215	0.704221512	0.004573703	0.001894589
423	0.711469708	0.707272392	0.004197316	0.002035662
105	0.712031359	0.703581219	0.008450140	0.002048713
197	0.717672474	0.712605729	0.005066745	0.001382090
125	0.716946670	0.710100941	0.006845730	0.001602069
602	0.713766144	0.710475492	0.003290652	0.001782773
827	0.715718171	0.713107532	0.002610639	0.001541541
288	0.709213375	0.704246209	0.004967167	0.001944460
501	0.708170852	0.704470369	0.003700483	0.001880427
390	0.719212698	0.715308264	0.003904434	0.001629928
253	0.720017786	0.715331082	0.004686704	0.001523588
499	0.711424998	0.708184493	0.003240504	0.001437384
180	0.717161113	0.711256580	0.005904533	0.001722047

655	0.718692073	0.715671053	0.003021020	0.001641652
171	0.717320018	0.711522905	0.005797113	0.001578344
99	0.716498631	0.708174673	0.008323958	0.001884472
324	0.730607085	0.726623481	0.003983604	0.001412631
310	0.711194058	0.706574668	0.004619390	0.001817450
227	0.720176962	0.714459708	0.005717253	0.002038745
225	0.724781018	0.719487370	0.005293648	0.001734182
416	0.716515175	0.712291885	0.004223290	0.002041421
743	0.711443782	0.708521606	0.002922177	0.001748787
471	0.718398333	0.714732341	0.003665993	0.001747475
935	0.711063163	0.708485123	0.002578040	0.001718271
935	0.711063163	0.708485123	0.002578040	0.001718271
248	0.722264401	0.717696459	0.004567941	0.001430923
205	0.715602768	0.710154002	0.005448766	0.001684166
266	0.710215892	0.705241869	0.004974023	0.001821280
1900	0.716773626	0.714936606	0.001837020	0.001774550
288	0.728967857	0.725059210	0.003908647	0.001218213
822	0.718891979	0.716197800	0.002694179	0.001652040
588	0.716690587	0.713257760	0.003432826	0.001918756
317	0.718995706	0.714589386	0.004406320	0.001704899
279	0.730008102	0.725888406	0.004119696	0.001311948
395	0.726077389	0.722411881	0.003665508	0.001472359
417	0.727627608	0.724002019	0.003625589	0.001520991
543	0.711606722	0.708352536	0.003254186	0.001595596
466	0.707449208	0.703910235	0.003538973	0.001619583
586	0.719079696	0.715857289	0.003222408	0.001688618
633	0.707496022	0.704154797	0.003341225	0.001961262
316	0.721472616	0.717422357	0.004050258	0.001438872
808	0.718863431	0.716096325	0.002767106	0.001719050
809	0.705048495	0.701916716	0.003131778	0.002205311
300	0.703876866	0.700325086	0.003551780	0.001052117
442	0.718398334	0.714798456	0.003599877	0.001592582
426	0.716951015	0.713533993	0.003417022	0.001383047
387	0.709645569	0.705907662	0.003737907	0.001503643
165	0.716212812	0.710808636	0.005404176	0.001340773
120	0.735952622	0.729343687	0.006608936	0.001458631
113	0.725183942	0.718830183	0.006353759	0.001271599
109	0.736730633	0.729723274	0.007007359	0.001492538
109	0.736730633	0.729723274	0.007007359	0.001492538
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633	0.720424695	0.717695992	0.002728703	0.001314536
269	0.717175612	0.712048622	0.005126989	0.001972622
151	0.701173965	0.695765565	0.005408399	0.001232452
766	0.722403868	0.719625636	0.002778232	0.001649796
735	0.714807499	0.711939310	0.002868189	0.001688165
735	0.714807499	0.711939310	0.002868189	0.001688165
574	0.716002711	0.712825373	0.003177337	0.001618342
395	0.712039108	0.708638184	0.003400924	0.001276053

511	0.712398273	0.708867808	0.003530465	0.001779169
159	0.726223396	0.719968189	0.006255208	0.001738984
346	0.714010530	0.709906843	0.004103687	0.001629219
311	0.726959703	0.722709940	0.004249762	0.001570896
678	0.712183563	0.709141133	0.003042430	0.001755512
934	0.711387828	0.708920678	0.002467150	0.001590513
269	0.717648900	0.713418369	0.004230532	0.001347140
429	0.722321785	0.718670615	0.003651170	0.001601141
348	0.717256087	0.713720425	0.003535662	0.001218582
107	0.727690007	0.720606710	0.007083297	0.001503854
303	0.717642654	0.713286080	0.004356574	0.001611020
491	0.715842620	0.712033654	0.003808965	0.001996693
124	0.718820404	0.711160630	0.007659774	0.002039957
352	0.724161242	0.720067694	0.004093548	0.001654274
617	0.715058320	0.711916894	0.003141427	0.001709251
87	0.746631357	0.739721435	0.006909922	0.001166584
388	0.726403513	0.723420144	0.002983369	0.000969958
648	0.716956105	0.713982195	0.002973910	0.001609762
483	0.719200968	0.715844456	0.003356512	0.001528639
613	0.713924665	0.710718782	0.003205884	0.001769913
293	0.726309387	0.722020014	0.004289373	0.001514557
687	0.720930585	0.718191583	0.002739002	0.001448542
503	0.716981802	0.713380196	0.003601606	0.001835389
813	0.720566709	0.717908395	0.002658314	0.001616380
307	0.697426764	0.692324165	0.005102599	0.002249166
558	0.726644132	0.723318357	0.003325775	0.001737284
213	0.713590039	0.708120879	0.005469160	0.001794517
436	0.723106720	0.719370916	0.003735804	0.001714071
305	0.728794347	0.725038335	0.003756011	0.001212201
521	0.711604086	0.708084957	0.003519129	0.001818269
521	0.711604086	0.708084957	0.003519129	0.001818269
198	0.725564489	0.720672399	0.004892090	0.001336018
832	0.717771058	0.715048215	0.002722842	0.001739239
355	0.713271236	0.709125883	0.004145353	0.001720713
486	0.719331053	0.715748448	0.003582605	0.001759884
191	0.699448385	0.694445900	0.005002485	0.001349173
489	0.718499990	0.715096578	0.003403412	0.001601840
328	0.725844074	0.721522218	0.004321856	0.001733245
175	0.713324645	0.707646756	0.005677889	0.001596915
496	0.721305487	0.718150227	0.003155260	0.001398126
88	0.730585256	0.722954350	0.007630906	0.001450932
339	0.708336342	0.704210310	0.004126032	0.001634168
616	0.721328788	0.718581922	0.002746867	0.001316388
84	0.742580826	0.735056203	0.007524623	0.001347419
358	0.722543264	0.718839478	0.003703786	0.001392398
763	0.709073072	0.706442409	0.002630663	0.001498177
863	0.714625704	0.711988038	0.002637666	0.001703633
336	0.730156845	0.726047208	0.004109638	0.001610433

201	0.715926938	0.710540487	0.005386451	0.001655165
201	0.715926938	0.710540487	0.005386451	0.001655165
481	0.714704208	0.711128135	0.003576073	0.001746101
191	0.713386463	0.707901714	0.005484749	0.001631364
523	0.719211010	0.716018533	0.003192477	0.001516847
257	0.706873450	0.703163098	0.003710352	0.001007542
131	0.740689031	0.734445503	0.006243528	0.001455536
518	0.713399367	0.709702571	0.003696796	0.002017906
358	0.729052331	0.725351882	0.003700448	0.001398731
358	0.729052331	0.725351882	0.003700448	0.001398731
312	0.729612771	0.725647068	0.003965703	0.001400202
318	0.719050633	0.714720509	0.004330124	0.001702253
151	0.731897865	0.725596221	0.006301644	0.001712098
692	0.722002884	0.719173754	0.002829130	0.001581998
486	0.711992727	0.708452440	0.003540286	0.001740484
487	0.706774837	0.702906544	0.003868293	0.002082621
380	0.706624867	0.702729330	0.003895537	0.001649215
561	0.725721235	0.722813844	0.002907391	0.001357035
462	0.725729405	0.722572912	0.003156493	0.001317455
636	0.703385339	0.700168804	0.003216535	0.001883370
250	0.717522211	0.713371387	0.004150824	0.001233747
765	0.715379997	0.712625550	0.002754446	0.001662518
816	0.708779867	0.706377541	0.002402326	0.001349080
371	0.714994395	0.710891122	0.004103273	0.001790218
381	0.706281927	0.702227021	0.004054906	0.001796592
596	0.717708786	0.714561075	0.003147711	0.001695306
192	0.725678452	0.720051427	0.005627026	0.001747166
597	0.717700998	0.714763343	0.002937655	0.001483666
256	0.726884133	0.723235423	0.003648711	0.000981825
386	0.718454010	0.714521519	0.003932491	0.001720191
967	0.702304525	0.699439628	0.002864897	0.002290604
286	0.711234910	0.706515477	0.004719434	0.001838731
515	0.716478655	0.713148710	0.003329945	0.001648955
217	0.726753707	0.721896281	0.004857426	0.001478855
436	0.711626914	0.707877157	0.003749757	0.001771007
199	0.718060597	0.713150426	0.004910171	0.001387089
326	0.725091449	0.721278220	0.003813229	0.001371490
445	0.705855486	0.701838904	0.004016582	0.002078238
503	0.716851898	0.713306941	0.003544957	0.001832268
466	0.719312580	0.716113029	0.003199551	0.001383633
162	0.706507366	0.699908745	0.006598621	0.002046229
184	0.728877087	0.723891245	0.004985842	0.001329629
590	0.717879209	0.714826933	0.003052276	0.001597898
624	0.722980434	0.720343357	0.002637078	0.001261707
694	0.715872329	0.712949051	0.002923277	0.001724839
507	0.719536101	0.716020031	0.003516070	0.001822984
436	0.717734845	0.714382583	0.003352262	0.001426641
261	0.715488635	0.710579725	0.004908910	0.001831395

186	0.712286255	0.706058279	0.006227976	0.002102268
410	0.721219610	0.717732603	0.003487007	0.001452887
159	0.722058212	0.717254229	0.004803982	0.001070051
636	0.710943041	0.707774107	0.003168934	0.001864016
305	0.719986528	0.716687850	0.003298678	0.000968809
198	0.725113419	0.719412327	0.005701092	0.001880283
396	0.710758345	0.707068043	0.003690303	0.001575905
1191	0.711548130	0.709084281	0.002463848	0.002113039
303	0.724114694	0.720184870	0.003929825	0.001367972
784	0.718785473	0.716141521	0.002643951	0.001602884
629	0.722315480	0.719691500	0.002623980	0.001266779
629	0.722315480	0.719691500	0.002623980	0.001266779
844	0.711667234	0.708950844	0.002716390	0.001821840
321	0.715653908	0.711506969	0.004146939	0.001614915
679	0.714951604	0.712190385	0.002761219	0.001515259
385	0.718788747	0.714782705	0.004006042	0.001808482
199	0.735718338	0.732541703	0.003176635	0.000587971
613	0.715132939	0.712045151	0.003087788	0.001712602
346	0.719244459	0.715733223	0.003511235	0.001250216
448	0.720325113	0.716501997	0.003823116	0.001919215
533	0.722720143	0.719483342	0.003236801	0.001637255
277	0.719645370	0.715264079	0.004381291	0.001559470
491	0.718432366	0.714688994	0.003743373	0.002018030
165	0.715416480	0.708743581	0.006672898	0.002155660
256	0.725696125	0.721765995	0.003930130	0.001160173
518	0.723985507	0.720702597	0.003282911	0.001638751
1132	0.710275951	0.707885585	0.002390366	0.001899010
383	0.708683076	0.704587141	0.004095935	0.001886768
165	0.704234852	0.697872482	0.006362370	0.001963174
247	0.715163123	0.710192331	0.004970792	0.001794063
249	0.715160497	0.710229631	0.004930866	0.001779653
151	0.722053629	0.716096204	0.005957425	0.001575392
180	0.726770027	0.720821075	0.005948952	0.001873198
489	0.720058666	0.716847346	0.003211320	0.001485328
1008	0.716103384	0.713540993	0.002562391	0.001949417
143	0.720975541	0.714192009	0.006783532	0.001938703
151	0.717650109	0.712596524	0.005053585	0.001137605
338	0.702950457	0.698839894	0.004110564	0.001685052
1405	0.719703938	0.717772157	0.001931781	0.001547144
468	0.713916133	0.710370551	0.003545583	0.001736195
645	0.720418334	0.717396737	0.003021597	0.001740183
409	0.713671866	0.709805238	0.003866628	0.001807776
656	0.709821076	0.707052012	0.002769064	0.001487757
290	0.707817075	0.704513753	0.003303322	0.000936010
423	0.717038645	0.713516796	0.003521849	0.001552908
424	0.717433579	0.713915316	0.003518264	0.001553722
307	0.715611550	0.711347635	0.004263915	0.001653417
388	0.713551554	0.709917324	0.003634230	0.001518852

261	0.720386678	0.715747436	0.004639242	0.001666008
639	0.713369149	0.710136407	0.003232742	0.001981006
143	0.733054363	0.727324429	0.005729935	0.001392941
307	0.709364079	0.704814990	0.004549089	0.001885280
307	0.709364079	0.704814990	0.004549089	0.001885280
303	0.725236712	0.721399603	0.003837109	0.001323974
300	0.728091091	0.724292957	0.003798134	0.001284582
86	0.730720447	0.722422947	0.008297500	0.001757737
349	0.720759735	0.716959367	0.003800368	0.001498219
168	0.713160437	0.707339433	0.005821003	0.001693088
296	0.723455332	0.718850583	0.004604750	0.001868719
424	0.720862401	0.717497518	0.003364884	0.001430245
1022	0.718690814	0.716432925	0.002257889	0.001552360
401	0.716355877	0.712746327	0.003609550	0.001556783
508	0.717406134	0.714512265	0.002893869	0.001268645
105	0.726648023	0.720584623	0.006063400	0.001151220
389	0.725442233	0.721665462	0.003776770	0.001655002
653	0.709871312	0.706773553	0.003097759	0.001869031
567	0.719863812	0.716688074	0.003175738	0.001706357
445	0.714081356	0.710558348	0.003523008	0.001648439
202	0.703022863	0.698248355	0.004774508	0.001375129
541	0.720383238	0.717746792	0.002636446	0.001123064
361	0.720155541	0.716300365	0.003855176	0.001602643
468	0.714764156	0.711355070	0.003409086	0.001624817
185	0.720934513	0.715130454	0.005804059	0.001862946
551	0.712205799	0.708950374	0.003255424	0.001746201
542	0.708602031	0.705239642	0.003362389	0.001833022
140	0.728039015	0.723880543	0.004158473	0.000724720
151	0.703108391	0.697707988	0.005400402	0.001318434
160	0.711326085	0.706149188	0.005176897	0.001283886
64	0.732258246	0.723602225	0.008656021	0.001436120
538	0.718743066	0.715664441	0.003078625	0.001528012
573	0.715663251	0.712785478	0.002877773	0.001422061
188	0.715139589	0.709669534	0.005470056	0.001686658
264	0.720596510	0.716431962	0.004164549	0.001373182
339	0.713663949	0.709460425	0.004203525	0.001797155
222	0.721044497	0.716020986	0.005023511	0.001683217
263	0.745115003	0.741452177	0.003662827	0.001060150
632	0.721882449	0.719235984	0.002646465	0.001329994
107	0.725318274	0.719073853	0.006244421	0.001254277
733	0.724479156	0.721915677	0.002563478	0.001448921
605	0.721330715	0.718124022	0.003206692	0.001872454
88	0.735710047	0.727991835	0.007718212	0.001577825
78	0.734747142	0.727166057	0.007581085	0.001349374
492	0.711188880	0.707618163	0.003570717	0.001888924
578	0.715498788	0.712253534	0.003245253	0.001833543
562	0.711220055	0.707972240	0.003247815	0.001786317
316	0.718415367	0.714210117	0.004205251	0.001683952

100	0.736306041	0.730517764	0.005788277	0.001009957
79	0.718053952	0.710052715	0.008001237	0.001524680
667	0.714755033	0.711757455	0.002997578	0.001807426
94	0.712463887	0.704816112	0.007647774	0.001658209
682	0.718186398	0.715355947	0.002830452	0.001647964
163	0.716081227	0.710635033	0.005446193	0.001458507
366	0.736705707	0.733284078	0.003421629	0.001292702
546	0.708636612	0.705289512	0.003347100	0.001845578
354	0.715287287	0.711675016	0.003612271	0.001394184
610	0.714027573	0.711068468	0.002959105	0.001613139
376	0.718563502	0.715026179	0.003537323	0.001421884
376	0.718563502	0.715026179	0.003537323	0.001421884
113	0.728518567	0.722411362	0.006107205	0.001274126
656	0.704392227	0.701324401	0.003067826	0.001867013
278	0.720419505	0.715878430	0.004541076	0.001733676
134	0.720590947	0.714252366	0.006338580	0.001628259
816	0.715006505	0.712511987	0.002494518	0.001535713
256	0.707132811	0.701524991	0.005607820	0.002436769
87	0.724814406	0.718034154	0.006780252	0.001210774
359	0.728044478	0.724444827	0.003599651	0.001409277
193	0.724235804	0.719078605	0.005157199	0.001555382
397	0.733314332	0.730172072	0.003142260	0.001188819
265	0.714479251	0.710519750	0.003959501	0.001260030
415	0.727786861	0.724478573	0.003308288	0.001377671
683	0.716091347	0.713112594	0.002978753	0.001838202
144	0.704717071	0.699256135	0.005460936	0.001303125
83	0.724373412	0.717449603	0.006923809	0.001207606
243	0.719362027	0.715250910	0.004111117	0.001246972
352	0.723185954	0.719124545	0.004061409	0.001763606
518	0.723989251	0.720676966	0.003312285	0.001727178
268	0.718634615	0.714156254	0.004478361	0.001633606
358	0.723644386	0.719990367	0.003654019	0.001453241
366	0.721633180	0.717699277	0.003933903	0.001722710
462	0.722626441	0.719390272	0.003236169	0.001471717
661	0.711402752	0.708577954	0.002824799	0.001606738
492	0.716745112	0.713798036	0.002947077	0.001301736
683	0.720569703	0.717710748	0.002858955	0.001701216
254	0.705114937	0.700707613	0.004407324	0.001503964
198	0.711611283	0.705963852	0.005647431	0.001926298
242	0.714449115	0.709615864	0.004833251	0.001725033
381	0.720249250	0.716567938	0.003681313	0.001576642
374	0.715684674	0.711849160	0.003835514	0.001680269
150	0.726571259	0.721205605	0.005365654	0.001319170
225	0.713975606	0.709276664	0.004698942	0.001518218
236	0.708773061	0.702911309	0.005861752	0.002478285
387	0.720529330	0.716860197	0.003669133	0.001592660
257	0.719473794	0.714751536	0.004722257	0.001753169
115	0.723320122	0.717837966	0.005482155	0.001057443

416	0.724628416	0.721441008	0.003187408	0.001294271
241	0.722929233	0.718360613	0.004568620	0.001540570
405	0.720403358	0.716794436	0.003608921	0.001616381
250	0.722262563	0.717451394	0.004811169	0.001773448
584	0.714169327	0.711088062	0.003081265	0.001699344
301	0.721351010	0.717132284	0.004218726	0.001642009
280	0.721891494	0.717819772	0.004071721	0.001424242
157	0.708050806	0.701285923	0.006764883	0.002204773
456	0.711975201	0.708416207	0.003558994	0.001775215
456	0.711975201	0.708416207	0.003558994	0.001775215
429	0.711495244	0.707902021	0.003593223	0.001702393
180	0.708733386	0.702838869	0.005894517	0.001922243
113	0.741895220	0.735230665	0.006664555	0.001542882
504	0.711368846	0.707830124	0.003538722	0.001940287
354	0.705585920	0.701770521	0.003815399	0.001584404
53	0.714427493	0.703081928	0.011345566	0.002098800
369	0.708693200	0.704539828	0.004153372	0.001960920
235	0.718417108	0.714240284	0.004176824	0.001262997
860	0.715549873	0.713101660	0.002448213	0.001588573
359	0.715543147	0.711991876	0.003551272	0.001395480
889	0.711972042	0.709419816	0.002552226	0.001785296
201	0.702204407	0.697056920	0.005147487	0.001642094
443	0.707787045	0.704074493	0.003712552	0.001883647
183	0.732433310	0.728051109	0.004382201	0.001084168
375	0.710261275	0.706468951	0.003792324	0.001665590
376	0.710145332	0.706363094	0.003782238	0.001661160
338	0.717754767	0.713970504	0.003784263	0.001494936
178	0.710471313	0.705203677	0.005267637	0.001525476
795	0.715633636	0.712977143	0.002656493	0.001733626
350	0.720554446	0.716824906	0.003729540	0.001504677
695	0.715710185	0.712779543	0.002930642	0.001845098
695	0.715710185	0.712779543	0.002930642	0.001845098
296	0.704609797	0.700462976	0.004146821	0.001573637
373	0.707439684	0.703725552	0.003714133	0.001590808
460	0.713585273	0.709964423	0.003620850	0.001864727
460	0.713585273	0.709964423	0.003620850	0.001864727
200	0.727047660	0.721871552	0.005176108	0.001656840
263	0.720104969	0.716016370	0.004088599	0.001359683
292	0.713324011	0.708710348	0.004613663	0.001922248
443	0.710023826	0.707052177	0.002971650	0.001210132
150	0.727066009	0.721731025	0.005334985	0.001321174
226	0.721707419	0.717296715	0.004410703	0.001360639
661	0.709212509	0.706271083	0.002941426	0.001769920
278	0.731189450	0.727559492	0.003629957	0.001133967
447	0.717450917	0.713932431	0.003518487	0.001715385
332	0.726788590	0.722834574	0.003954017	0.001609370
257	0.727138211	0.722882770	0.004255441	0.001444000
1496	0.717048679	0.715157600	0.001891079	0.001659971

160	0.718912990	0.712850768	0.006062222	0.001825967
1891	0.711935268	0.710232893	0.001702374	0.001702249
400	0.734987888	0.731265759	0.003722130	0.001721501
469	0.719450824	0.716007060	0.003443763	0.001728081
185	0.732068964	0.726793965	0.005274999	0.001599866
761	0.709135458	0.706578742	0.002556716	0.001546319
141	0.735568667	0.729965075	0.005603592	0.001376598
483	0.717876469	0.714498049	0.003378421	0.001715575
569	0.718560069	0.715478132	0.003081937	0.001683226
1189	0.714130399	0.712025307	0.002105093	0.001642424
511	0.721264564	0.718317353	0.002947211	0.001384033
200	0.719342288	0.713536690	0.005805598	0.002102182
379	0.713292619	0.708962073	0.004330546	0.002216729
264	0.711800815	0.707377653	0.004423163	0.001613022
394	0.715673341	0.711896725	0.003776616	0.001755153
337	0.715181313	0.711675117	0.003506196	0.001294035
337	0.715181313	0.711675117	0.003506196	0.001294035
417	0.715888339	0.712190994	0.003697345	0.001780621
295	0.716529327	0.712491037	0.004038290	0.001502916
512	0.715170982	0.711739493	0.003431489	0.001883765
127	0.729245602	0.723076904	0.006168698	0.001510093
1097	0.717294924	0.715259070	0.002035854	0.001421571
720	0.716499168	0.713713576	0.002785592	0.001747065
861	0.712576240	0.709931977	0.002644263	0.001883128
222	0.727942566	0.723714543	0.004228023	0.001242227
454	0.718843577	0.715300485	0.003543092	0.001784279
142	0.739862722	0.735067295	0.004795427	0.001022575
318	0.723504767	0.719451733	0.004053034	0.001636876
353	0.714775199	0.710856605	0.003918595	0.001698699
164	0.732590636	0.726966181	0.005624455	0.001626278
72	0.719367579	0.712944472	0.006423108	0.000931249
438	0.719826377	0.716318512	0.003507865	0.001689925
72	0.740218569	0.734232340	0.005986228	0.000809104
200	0.713410421	0.709170650	0.004239771	0.001127457
156	0.715025863	0.710739242	0.004286621	0.000899293
552	0.697650820	0.694193765	0.003457055	0.002069709
462	0.724561580	0.721132680	0.003428901	0.001704438
369	0.703601910	0.699347515	0.004254395	0.002096202
552	0.714011660	0.711115361	0.002896299	0.001453890
241	0.699420260	0.694167360	0.005252900	0.002088127
338	0.722618795	0.718675825	0.003942969	0.001650785
413	0.714044874	0.710317788	0.003727087	0.001803257
246	0.726033676	0.721759818	0.004273858	0.001412601
247	0.725793323	0.721536769	0.004256554	0.001406882
174	0.723243709	0.717825891	0.005417817	0.001606127
105	0.738693554	0.733003874	0.005689680	0.001069511
179	0.711158811	0.706031835	0.005126976	0.001480750
345	0.716330727	0.712338715	0.003992012	0.001730349

345	0.716330727	0.712338715	0.003992012	0.001730349
194	0.713753434	0.708850146	0.004903288	0.001469439
303	0.720262305	0.716303680	0.003958624	0.001496489
266	0.716026536	0.711949225	0.004077311	0.001395308
298	0.686285536	0.682349924	0.003935612	0.001457808
318	0.719686075	0.715990519	0.003695556	0.001372481
369	0.720402555	0.716848915	0.003553640	0.001472833
384	0.718465357	0.714897453	0.003567904	0.001545918
313	0.719347993	0.715400866	0.003947127	0.001542366
698	0.716141965	0.713264074	0.002877891	0.001828816
259	0.718786543	0.714223497	0.004563046	0.001706414
553	0.726862606	0.724201934	0.002660672	0.001238908
259	0.718913800	0.714111616	0.004802185	0.001890352
264	0.717675820	0.712917561	0.004758258	0.001892230
137	0.705468399	0.699148098	0.006320302	0.001732591
541	0.710529495	0.707170526	0.003358969	0.001933886
220	0.729203651	0.724678021	0.004525629	0.001428014
144	0.713676385	0.707827031	0.005849354	0.001562394
81	0.729447567	0.721623312	0.007824254	0.001573208
878	0.713306163	0.710807278	0.002498885	0.001740065
569	0.724605976	0.721692843	0.002913134	0.001533230
494	0.706361524	0.702959640	0.003401884	0.001818106
539	0.715637328	0.712508380	0.003128948	0.001679447
109	0.737136608	0.731477550	0.005659058	0.001112511
362	0.708425543	0.704817191	0.003608353	0.001502815
241	0.715673568	0.710954200	0.004719368	0.001711897
329	0.716443801	0.712408836	0.004034964	0.001708670
332	0.716613371	0.712614867	0.003998504	0.001693230
208	0.706247425	0.701170981	0.005076444	0.001709988
212	0.731639999	0.727344087	0.004295912	0.001248161
628	0.721463445	0.718751192	0.002712253	0.001475524
381	0.722475268	0.719094016	0.003381251	0.001391276
259	0.714125413	0.709181082	0.004944332	0.002022357
177	0.711661547	0.706516582	0.005144965	0.001496994
422	0.715411598	0.711674126	0.003737472	0.001884454
242	0.725522108	0.721058887	0.004463220	0.001541214
266	0.712545349	0.708494192	0.004051157	0.001397071
257	0.716158040	0.711885884	0.004272156	0.001501146
1153	0.716703667	0.714611668	0.002091999	0.001615395
407	0.719518914	0.715983142	0.003535772	0.001630268
941	0.718688271	0.716416254	0.002272017	0.001557379
952	0.711822943	0.709482722	0.002340220	0.001672315
304	0.730192371	0.726342211	0.003850160	0.001445580
267	0.720642960	0.715789389	0.004853571	0.002018516
1494	0.722340044	0.720839678	0.001500366	0.001079529
340	0.714777421	0.710745292	0.004032129	0.001774424
827	0.714741991	0.712321268	0.002420723	0.001556276
380	0.711487106	0.708062313	0.003424793	0.001431858

286	0.723286158	0.718804554	0.004481604	0.001845604
1149	0.712523399	0.710459481	0.002063919	0.001572662
125	0.742139498	0.736064978	0.006074520	0.001482405
320	0.707327364	0.703407609	0.003919756	0.001580827
1910	0.714016823	0.712460036	0.001556787	0.001489084
170	0.729201293	0.723828032	0.005373261	0.001579029
433	0.717208788	0.713853426	0.003355361	0.001568480
249	0.714591928	0.709964704	0.004627225	0.001715363
94	0.733155593	0.725534182	0.007621410	0.001758348
225	0.730675950	0.726862721	0.003813230	0.001053620
252	0.710015720	0.705430004	0.004585717	0.001711141
288	0.731158686	0.727036448	0.004122238	0.001580521
469	0.715033383	0.711935078	0.003098306	0.001454157
469	0.715033383	0.711935078	0.003098306	0.001454157
469	0.715033383	0.711935078	0.003098306	0.001454157
469	0.715033383	0.711935078	0.003098306	0.001454157
586	0.707125343	0.703892891	0.003232452	0.001978511
397	0.714304866	0.710565572	0.003739294	0.001793831
209	0.730442774	0.726305920	0.004136854	0.001156235
822	0.719010453	0.716613196	0.002397257	0.001527086
465	0.716533406	0.712981120	0.003552286	0.001897362
542	0.715405255	0.712488219	0.002917036	0.001491541
560	0.715327306	0.712383795	0.002943512	0.001569206
267	0.719651509	0.715237044	0.004414464	0.001683570
279	0.720293122	0.716037106	0.004256016	0.001635508
560	0.719739512	0.716683661	0.003055851	0.001695200
459	0.725435038	0.722224047	0.003210991	0.001534166
424	0.713560386	0.709725429	0.003834957	0.002021642
439	0.705926995	0.702439548	0.003487446	0.001731073
456	0.717404320	0.713974745	0.003429576	0.001739441
842	0.709658109	0.707191984	0.002466125	0.001661815
327	0.717234126	0.713295606	0.003938519	0.001646319
78	0.733023126	0.725849763	0.007173363	0.001305612
245	0.724770475	0.720716567	0.004053908	0.001309821
247	0.735459808	0.731782798	0.003677010	0.001087260
294	0.729632873	0.725866575	0.003766299	0.001358225
278	0.715703355	0.711612939	0.004090416	0.001515200
278	0.715703355	0.711612939	0.004090416	0.001515200
365	0.720286879	0.716854354	0.003432526	0.001401040
287	0.723095936	0.719128694	0.003967241	0.001471785
413	0.720424513	0.716963858	0.003460655	0.001611887
154	0.718831741	0.712692313	0.006139428	0.001891844
200	0.733892513	0.729288185	0.004604328	0.001382011
92	0.723547947	0.717256305	0.006291642	0.001187285
201	0.720142965	0.715218372	0.004924593	0.001590299
189	0.721475570	0.716097939	0.005377630	0.001783824
105	0.718746490	0.712008594	0.006737896	0.001555873
134	0.731619552	0.725430925	0.006188627	0.001676103

434	0.727670139	0.724405900	0.003264239	0.001510747
240	0.726546068	0.722502446	0.004043622	0.001282433
357	0.722317019	0.718880079	0.003436939	0.001378232
663	0.715087461	0.712392799	0.002694662	0.001573680
518	0.713606309	0.710501946	0.003104363	0.001632147
360	0.706978562	0.703469435	0.003509127	0.001449764
489	0.711357351	0.708030449	0.003326902	0.001770260
670	0.711709042	0.708833895	0.002875148	0.001811963
390	0.723388997	0.719952218	0.003436779	0.001507146
272	0.710865458	0.706648834	0.004216624	0.001583658
122	0.715171101	0.709057444	0.006113657	0.001493679
223	0.716446574	0.711841343	0.004605231	0.001549675
206	0.720631081	0.716100806	0.004530275	0.001385466
332	0.724131165	0.720378260	0.003752905	0.001532533
332	0.724131165	0.720378260	0.003752905	0.001532533
332	0.724131165	0.720378260	0.003752905	0.001532533
397	0.714875786	0.711388457	0.003487329	0.001582691
347	0.711855480	0.708175933	0.003679546	0.001540998
483	0.715809336	0.712425376	0.003383961	0.001814468
539	0.720902799	0.718055311	0.002847488	0.001433758
251	0.708758222	0.704468449	0.004289773	0.001515506
123	0.702240690	0.697381300	0.004859390	0.000953203
123	0.702240690	0.697381300	0.004859390	0.000953203
193	0.728260495	0.723457015	0.004803480	0.001462536
93	0.731465294	0.723905724	0.007559570	0.001745998
518	0.722377750	0.719406807	0.002970944	0.001502575
472	0.721876384	0.718956111	0.002920273	0.001322955
200	0.717915537	0.713373057	0.004542480	0.001356380
201	0.717660567	0.713140687	0.004519880	0.001349632
651	0.717489609	0.715022641	0.002466968	0.001303669
113	0.721155066	0.715914486	0.005240580	0.001021654
103	0.732373556	0.726420510	0.005953046	0.001201684
285	0.720459578	0.716550062	0.003909516	0.001435100
312	0.715240550	0.711434113	0.003806437	0.001489548
85	0.721010529	0.714057091	0.006953438	0.001354723
471	0.719218494	0.716281739	0.002936754	0.001339047
705	0.726229028	0.723595268	0.002633760	0.001614195
513	0.715261865	0.711920629	0.003341236	0.001890704
342	0.727456419	0.724090902	0.003365516	0.001278881
378	0.711720132	0.707883499	0.003836633	0.001836990
147	0.722497558	0.716887992	0.005609567	0.001527247
255	0.720019134	0.716011633	0.004007501	0.001353327
401	0.720013301	0.716645410	0.003367891	0.001503477
125	0.714647767	0.707821797	0.006825970	0.001927491
41	0.760376450	0.752744497	0.007631954	0.000790501
307	0.728843968	0.725422588	0.003421380	0.001190345
166	0.726063281	0.720587797	0.005475484	0.001648552
500	0.716649946	0.713297925	0.003352021	0.001861141

203	0.715844384	0.711031259	0.004813125	0.001558045
536	0.730298267	0.727688936	0.002609331	0.001210739
198	0.736641972	0.731932156	0.004709816	0.001457690
456	0.709578056	0.706249945	0.003328111	0.001676430
704	0.708324809	0.705404704	0.002920105	0.001992541
227	0.718700051	0.714393172	0.004306879	0.001397827
180	0.725766512	0.720913750	0.004852762	0.001407227
250	0.727056338	0.722929851	0.004126488	0.001413518
487	0.717307740	0.714387044	0.002920696	0.001381132
167	0.710495951	0.705003909	0.005492043	0.001674741
397	0.730147416	0.727070586	0.003076830	0.001249610
226	0.709611082	0.706070342	0.003540740	0.000942448
326	0.713157784	0.709013978	0.004143806	0.001862608
105	0.716830381	0.710001626	0.006828755	0.001629886
187	0.720827110	0.715518203	0.005308908	0.001754640
399	0.727419612	0.723968190	0.003451422	0.001583009
399	0.727419612	0.723968190	0.003451422	0.001583009
339	0.723730601	0.720085878	0.003644723	0.001500636
618	0.705455598	0.702590286	0.002865312	0.001690966
618	0.716345687	0.713286182	0.003059505	0.001928182
511	0.720085707	0.717184952	0.002900756	0.001434300
185	0.724054564	0.719042498	0.005012066	0.001550909
146	0.729562010	0.723899054	0.005662956	0.001563157
328	0.719545017	0.715943876	0.003601141	0.001420559
229	0.696117200	0.692684316	0.003432884	0.000901771
462	0.720608618	0.717400803	0.003207815	0.001588904
340	0.725068381	0.721482974	0.003585407	0.001460860
317	0.710798535	0.707074505	0.003724030	0.001470341
117	0.730478674	0.724508913	0.005969761	0.001395036
228	0.715435960	0.710331557	0.005104403	0.001988365
481	0.718804954	0.715760607	0.003044347	0.001492165
474	0.716977090	0.713830511	0.003146579	0.001572615
191	0.732325724	0.727253177	0.005072547	0.001647121
928	0.714644171	0.712267241	0.002376930	0.001757566
214	0.704836075	0.699429798	0.005406276	0.002099482
372	0.728102061	0.724860700	0.003241361	0.001313148
471	0.717080672	0.713768234	0.003312438	0.001736342
495	0.712242907	0.709068695	0.003174212	0.001677130
1798	0.709638432	0.708050600	0.001587832	0.001525784
184	0.733820421	0.728332617	0.005487803	0.001865495
172	0.723248361	0.717466598	0.005781763	0.001937094
396	0.716675663	0.713013812	0.003661851	0.001789388
504	0.715527239	0.712104097	0.003423143	0.001991325
517	0.715342739	0.712198864	0.003143876	0.001723536
241	0.726876760	0.722612936	0.004263824	0.001477920
198	0.703050315	0.698507905	0.004542410	0.001378230
774	0.715946868	0.713377888	0.002568981	0.001724336
184	0.709097578	0.703035009	0.006062570	0.002283418

184	0.709097578	0.703035009	0.006062570	0.002283418
359	0.718378922	0.714438859	0.003940063	0.001883277
241	0.717637286	0.712745132	0.004892155	0.001949248
131	0.701037239	0.694900029	0.006137210	0.001669865
257	0.703140087	0.698043232	0.005096855	0.002260426
151	0.734787835	0.729040041	0.005747794	0.001689605
479	0.720111187	0.717322374	0.002788813	0.001262002
547	0.713255876	0.710348069	0.002907807	0.001567261
117	0.711973358	0.705599761	0.006373597	0.001610734
210	0.703273724	0.697792588	0.005481135	0.002139276
392	0.712251637	0.708680084	0.003571553	0.001695885
238	0.715470945	0.710897968	0.004572978	0.001688248
415	0.718695755	0.715332784	0.003362971	0.001592075
415	0.718695755	0.715332784	0.003362971	0.001592075
494	0.719750654	0.716776303	0.002974351	0.001483339
1013	0.710175863	0.707976616	0.002199246	0.001663448
572	0.715561637	0.712556316	0.003005321	0.001754575
626	0.721509894	0.719002671	0.002507223	0.001336701
141	0.724527806	0.718680492	0.005847314	0.001637594
124	0.710365245	0.703416303	0.006948941	0.002035300
256	0.720608331	0.715961178	0.004647153	0.001879485
1026	0.713886066	0.711764746	0.002121320	0.001570871
433	0.714203454	0.710824935	0.003378518	0.001684403
501	0.719242992	0.716049105	0.003193887	0.001742088
168	0.723523615	0.718061235	0.005462381	0.001710988
825	0.715642783	0.713246550	0.002396232	0.001616910
281	0.719557620	0.715441908	0.004115712	0.001624846
217	0.715856861	0.711103240	0.004753621	0.001673980
567	0.723018831	0.720451112	0.002567719	0.001276557
338	0.718984041	0.715783503	0.003200538	0.001182480
842	0.716558227	0.714230706	0.002327522	0.001557939
779	0.710206785	0.707935180	0.002271606	0.001372962
351	0.724311658	0.720628656	0.003683002	0.001627266
477	0.716276774	0.712921250	0.003355524	0.001836710
388	0.728758291	0.725299216	0.003459075	0.001588224
392	0.718288469	0.715107866	0.003180604	0.001356724
787	0.723427813	0.721261652	0.002166161	0.001263950
165	0.722362739	0.717095239	0.005267500	0.001568027
426	0.723297257	0.720026993	0.003270264	0.001560487
354	0.711603342	0.707780296	0.003823047	0.001773296
293	0.720097710	0.716350872	0.003746838	0.001410884
375	0.725191528	0.721846451	0.003345077	0.001439971
572	0.727976678	0.725356905	0.002619773	0.001348016
216	0.718952037	0.714315921	0.004636116	0.001595053
356	0.714118812	0.710223820	0.003894992	0.001856971
443	0.711548795	0.708460169	0.003088626	0.001453168
163	0.716513754	0.711451007	0.005062747	0.001437799
188	0.709986663	0.704901250	0.005085412	0.001673467

421	0.705909701	0.702285381	0.003624320	0.001903761
329	0.702227158	0.698444289	0.003782869	0.001621556
830	0.711462557	0.708827896	0.002634661	0.001985736
947	0.707475407	0.705130727	0.002344680	0.001794519
344	0.718336638	0.714579904	0.003756735	0.001673557
344	0.718336638	0.714579904	0.003756735	0.001673557
578	0.710981718	0.707860383	0.003121335	0.001941299
76	0.724947437	0.718369668	0.006577769	0.001134214
218	0.736911542	0.733024065	0.003887477	0.001136693
436	0.725015264	0.721655896	0.003359368	0.001697847
368	0.718502959	0.715039790	0.003463169	0.001523142
908	0.718511391	0.716375223	0.002136168	0.001431842
509	0.718672138	0.715622820	0.003049318	0.001635870
277	0.717620271	0.712859680	0.004760590	0.002170173
121	0.721133028	0.714563004	0.006570025	0.001806396
592	0.717377690	0.714445223	0.002932467	0.001761078
103	0.723120414	0.715818717	0.007301697	0.001900325
984	0.721506968	0.719375438	0.002131530	0.001547270
207	0.713534527	0.708759435	0.004775092	0.001633620
584	0.724491425	0.721782216	0.002709209	0.001483891
255	0.707316091	0.703092716	0.004223375	0.001575178
691	0.715861697	0.713182711	0.002678986	0.001717717
222	0.721343700	0.716099845	0.005243854	0.002114582
343	0.723817892	0.720179017	0.003638875	0.001573525
762	0.718509075	0.716042649	0.002466426	0.001606093
327	0.715386459	0.711491056	0.003895402	0.001720139
137	0.707380652	0.701373838	0.006006813	0.001713745
132	0.701892969	0.695786008	0.006106962	0.001707705
975	0.712890246	0.710718460	0.002171786	0.001595267
416	0.705990320	0.702454418	0.003535902	0.001804280
142	0.735649234	0.730435078	0.005214156	0.001339300
241	0.718940108	0.714282451	0.004657657	0.001814134
434	0.709603938	0.705973398	0.003630541	0.001985183
575	0.714039185	0.711014644	0.003024541	0.001825655
1305	0.712261140	0.710113007	0.002148132	0.002090554
311	0.731921742	0.728505892	0.003415850	0.001259961
662	0.715471321	0.712611049	0.002860272	0.001882213
287	0.730645624	0.726924778	0.003720846	0.001381205
612	0.719709227	0.716957209	0.002752018	0.001611304
235	0.707938136	0.703389847	0.004548290	0.001690919
281	0.724062634	0.720145805	0.003916829	0.001499970
652	0.722173801	0.719584338	0.002589462	0.001521577
256	0.720016908	0.716062062	0.003954845	0.001393886
75	0.758978743	0.753957930	0.005020813	0.000658245
495	0.724267281	0.721387233	0.002880048	0.001430565
418	0.719215932	0.715850579	0.003365353	0.001651049
436	0.708221946	0.704330037	0.003891909	0.002305173
147	0.726763921	0.721193331	0.005570590	0.001592348

311	0.730027762	0.726654763	0.003372999	0.001235280
100	0.740031503	0.734452396	0.005579107	0.001086907
383	0.713441065	0.710347056	0.003094008	0.001280660
322	0.715440043	0.711588277	0.003851765	0.001669915
803	0.703341170	0.700880790	0.002460380	0.001699415
498	0.717892373	0.714637518	0.003254855	0.001849813
283	0.720069087	0.715859002	0.004210085	0.001760522
178	0.715080288	0.709575213	0.005505075	0.001893737
402	0.727940418	0.724991762	0.002948656	0.001227095
767	0.717012996	0.714319061	0.002693934	0.001954664
767	0.717012996	0.714319061	0.002693934	0.001954664
592	0.725255357	0.722503260	0.002752097	0.001575640
328	0.708892294	0.704499024	0.004393270	0.002224972
472	0.717968024	0.714958202	0.003009822	0.001503009
120	0.727268369	0.721394400	0.005873969	0.001455730
137	0.713336783	0.707873722	0.005463061	0.001437852
223	0.696796113	0.691100733	0.005695379	0.002544365
211	0.714964132	0.710229039	0.004735093	0.001664334
178	0.722739694	0.717717075	0.005022620	0.001579793
269	0.713598247	0.709153231	0.004445016	0.001870188
603	0.714854229	0.711902308	0.002951922	0.001848992
344	0.720557178	0.717348794	0.003208384	0.001246169
1458	0.719574321	0.717794829	0.001779492	0.001624932
256	0.720929060	0.716650843	0.004278217	0.001649606
363	0.708985109	0.705361926	0.003623183	0.001680264
285	0.710545732	0.706482343	0.004063389	0.001659682
681	0.707658287	0.704958646	0.002699641	0.001750669
228	0.723781943	0.719274028	0.004507915	0.001634825
110	0.738352408	0.732685286	0.005667123	0.001246897
447	0.720523120	0.717531935	0.002991185	0.001412791
285	0.714734919	0.710981960	0.003752959	0.001418264
202	0.713697219	0.709136773	0.004560445	0.001484780
225	0.717717922	0.712670708	0.005047214	0.002025950
512	0.714084752	0.711302439	0.002782313	0.001401135
220	0.723288899	0.718382921	0.004905978	0.001872514
393	0.720648181	0.717098765	0.003549416	0.001751444
220	0.725320679	0.721674654	0.003646025	0.001034649
347	0.719418499	0.716385895	0.003032604	0.001129446
250	0.703049109	0.698811289	0.004237820	0.001589022
589	0.708770625	0.705979985	0.002790639	0.001623438
442	0.722848236	0.719857881	0.002990355	0.001399054
686	0.728214846	0.725879445	0.002335401	0.001324435
430	0.722791319	0.719633588	0.003157730	0.001518801
247	0.726776025	0.722650089	0.004125936	0.001489841
549	0.714529496	0.711508896	0.003020600	0.001775496
500	0.716779416	0.713614934	0.003164482	0.001775229
456	0.713148884	0.710011945	0.003136939	0.001591041
141	0.731121800	0.726020929	0.005100870	0.001301230

372	0.718117316	0.714570107	0.003547209	0.001660313
150	0.729638874	0.724603514	0.005035360	0.001349966
435	0.720390000	0.717453426	0.002936574	0.001331560
657	0.725472677	0.722900412	0.002572265	0.001543840
330	0.716799824	0.713179419	0.003620405	0.001536393
730	0.701230180	0.698186751	0.003043428	0.002401836
160	0.713403419	0.707247005	0.006156415	0.002154545
349	0.718394507	0.715008574	0.003385933	0.001422618
349	0.718394507	0.715008574	0.003385933	0.001422618
197	0.727485807	0.723739305	0.003746501	0.000983769
148	0.726570962	0.721088100	0.005482862	0.001583526
485	0.718964219	0.715923644	0.003040576	0.001596078
255	0.704641149	0.700371661	0.004269488	0.001655216
164	0.732194567	0.727779941	0.004414626	0.001138159
870	0.717344889	0.715112542	0.002232347	0.001544626
612	0.722325381	0.719644817	0.002680564	0.001567851
270	0.717443436	0.712745322	0.004698114	0.002125020
311	0.734027492	0.730360415	0.003667077	0.001492589
640	0.725871160	0.723112280	0.002758880	0.001738569
378	0.718801117	0.715190445	0.003610672	0.001759145
387	0.723364874	0.720209452	0.003155422	0.001375498
677	0.719355064	0.717001684	0.002353380	0.001339352
541	0.711411623	0.708378479	0.003033144	0.001778808
127	0.721654936	0.717090688	0.004564248	0.000945789
454	0.718626040	0.715382622	0.003243418	0.001707782
155	0.727534637	0.722511329	0.005023308	0.001398569
302	0.720965919	0.717027153	0.003938766	0.001676954
226	0.714985261	0.710193351	0.004791910	0.001857974
538	0.717850939	0.714776939	0.003073999	0.001820502
490	0.716730045	0.713672719	0.003057326	0.001640164
525	0.709643433	0.706918339	0.002725094	0.001397390
161	0.715993168	0.710032759	0.005960408	0.002050690
473	0.712271870	0.708964210	0.003307660	0.001856314
204	0.724017329	0.719581438	0.004435891	0.001440177
557	0.702723712	0.699659139	0.003064573	0.001877858
396	0.721888606	0.718332042	0.003556564	0.001798330
93	0.732011914	0.725811257	0.006200657	0.001283812
289	0.714098460	0.710160177	0.003938282	0.001609496
330	0.713129258	0.709373143	0.003756115	0.001672101
854	0.710229447	0.707742505	0.002486941	0.001897663
103	0.720003579	0.712626217	0.007377362	0.002014083
253	0.726092077	0.721912099	0.004179978	0.001588777
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