Sequence Listing Free Text

SEQ ID NO:1

Tgcatc gaattc AGGAGAAATT AACTatg AACGAGTACGCCC CCCTGCGTTTGC

SEQ ID NO:2

Tgcatc aagctt TCAGATATGCAAGGCGTGGC CCAG

SEQ ID NO:3

tgtacggtat taatgtcgac AGGAGAAATT AACTATGCTT CAACTCCAAA AACAAGAAAC

SEQ ID NO:4

TGATCATGCGCCATAGTTAATTTCTCCTGGATCCTTAGACGC

TGGCAGGGGTGGCCTGTT

SEQ ID NO:5

GI:26991173, Protein name: acetyl-CoA synthetase ACS_[Pseudomonas putida KT2440]

```
        1 msaaplypvr pevaattltd eatykamyqq svinpdgfwr eqaqridwik
pftkvkqtsf
       61 ddhhvdikwf adgtlnvssn cldrhleerg dqlaiiwegd dpsehrnity
relheqvckf
      121 analrgqdvh rgdvvtiymp mipeavvaml acarigaihs vvfggfspea
lagriidcks
      181 kvvitadegv rggrrtplka nvdlaltnpe tssvqkiivc krtggdiawh
qhrdiwyedl
      241 mkvasshcap kemgaeealf ilytsgstgk pkgvlhttgg ylvyaalthe
rvfdyrpgev
      301 ywctadvgwv tghsyivygp langattllf egvpnypdit rvskivdkhk
vnilytapta
      361 irammaegqa avegadgssl rllgsvgepi npeawnwyyk tvgkercpiv
dtwwqtetgg
      421 ilisplpgat glkpgsatrp ffgvvpalvd nlgnlidgaa egnlvildsw
pgqsrslygd
      481 hdrfvdtyfk tfrgmyftgd garrdedgyy witgrvddvl nvsghrmgta
eiesamvahs
      541 kvaeaavvgv phdikgqgiy vyvtlnagie aseqlrlelk nwvrkeigpi
aspdviqwap
      601 glpktrsgki mrrilrkiat geydalgdis tladpgvvqh lidthkamnl asa
```

SEQ ID NO: 6

GI:260770658, Protein name: acetyl-CoA synthetase [Vibrio furnissii CIP 102972]

```
        1 mseahiypvk enikahthad detylamyqq svsdpegfws ehgkivdwmk
pftqvkhtsf
       61 dtghvdirwf edgtlnvsan cidrhlaerg ddvaiiwegd dpaddktltf
nelhrdvcrf
      121 snalkaqgvr kgdvvclymp mvpeaavaml actrigavht vvfggfspea
lagriidsds
      181 kvvitadegv rggravplkk nvdealtnpe vktiskvivf krtggevawh
ehrdvwwhda
      241 vaaasdvcpp eemnaedplf ilytsgstgk pkgvlhttgg ylvyatmtfk
yvfdyqpget
      301 fwctadvgwi tghtyliygp lsngaktilf egvpnypsta rmsevvdkhq
vnilytapta
      361 iralmakgde avkgtsrssl rimgsvgepi npeawewyyk tignekspiv
dtwwqtetgg
      421 ilitplpgat alkpgsatrp ffgvqpalvd nmgevidgaa egnlvildsw
pgqmrtvygd
      481 herfeqtyfs tfkgmyftgd garrdedgyy witgrvddvl nvsghrmgta
eiesalvafd
      541 kiaeaavvgv phdikgqaiy ayitlndgvy psaelhkevk dwvrkeigpi
atpdvlhwtd
      601 alpktrsgki mrrilrkiat gdtgnlgdts tladpsvvdk liaekaqlv
```

SEQ ID NO:7
GI:167623628, Protein name: acetyl-CoA synthetase [Shewanella halifaxensis HAW-EB4]

```
        1 mstqslykvp seiaanalvn deqykkmyqe sivnpegfwr ehgnridwik
pftkvkktsf
       61 ddhnlfikwf ydgtlnasan cldrhlenna dklaiiwegd dakdqrtlty
gqlhtqvckf
      121 analrsqgvr rgdvvtiymp mvpeaavaml acarigaihs vvfggfspds
iasrvidgns
      181 kvvitadegv ragriiplka nidealshpd vncvekvivm krtggdinwv
egrdiwwdsl
      241 mdtasehcia eemgaedplf llytsgstgn pkgvlhttgg ymvyaamthe
yvfdykenev
      301 ywctadvgwi tghsymvygp langatvlih egvpnypspa rlgemvdrhk
vnilytaptl
      361 iralmaegke qfagfdgssl rimgsvgepi npeawrwynd vighekcpiv
dtwwqtetgg
      421 ilisplpgat dtkpgsatrp ffgvqpalvd nmgnivdgas egnlvildsw
pgqmrtvfgd
      481 hdrfvltyfk tfrgmyftgd gakrdedgyy witgrvddvi nvsghrlgta
evesalvahe
      541 fvaeaavvgy phdikgqgiy ayvtltkgsv eteelrqelr qwvrkeigal
atpdliqwag
      601 glpktrsgki mrrflrkiaa nevsnlgdss tladpavidt lietrlnrse
```

SEQ ID NO:8
GI:330830937, Protein name: acetyl-CoA synthetase [Aeromonas veronii B565]

```
        1 mstqslykvp seiaanalvn deqykkmyqe sivnpegfwr ehgnridwik
pftkvkktsf
       61 ddhnlfikwf ydgtlnasan cldrhlenna dklaiiwegd dakdqrtlty
gqlhtqvckf
```

121 analrsqgvr rgdvvtiymp mvpeaavaml acarigaihs vvfggfspds iasrvidgns
181 kvvitadegv ragriiplka nidealshpd vncvekvivm krtggdinwv egrdiwwdsl
241 mdtasehcia eemgaedplf llytsgstgn pkgvlhttgg ymvyaamthe yvfdykenev
301 ywctadvgwi tghsymvygp langatvlih egvpnypspa rlgemvdrhk vnilytaptl
361 iralmaegke qfagfdgssl rimgsvgepi npeawrwynd vighekcpiv dtwwqtetgg
421 ilisplpgat dtkpgsatrp ffgvqpalvd nmgnivdgas egnlvildsw pgqmrtvfgd
481 hdrfvltyfk tfrgmyftgd gakrdedgyy witgrvddvi nvsghrlgta evesalvahe
541 fvaeaavvgy phdikgqgiy ayvtltkgsv eteelrqelr qwvrkeigal atpdliqwag
601 glpktrsgki mrrflrkiaa nevsnlgdss tladpavidt lietrlnrse

SEQ ID NO:9
GI:209696237, Protein name: acetyl-CoA synthetase [Aliivibrio salmonicida LFI1238]

1 msdihvypvn qdiaknahad edkyremyqq svinpegfwr ehgqivdwmt pytkvkntsf
61 dtghvdikwf edgelnvsan cidrhlaarg devaiiwegd dpqddasitf nelheqvckf
121 snalksqgvr kgdvvciymp mvaeaaiaml actrigavht vvfggfspea lagrivdsda
181 kvvitadegv rggrtvplkk nvddalnnpe vttiekvvvf qrtgndidwn eerdvwwhea
241 tavasahcep eamnaedplf ilytsgstgk pkgvlhttgg ylvyaamtfk yifdyqegev
301 fwctadvgwi tghtyliygp langaktilf egvpnypsts rmsevvdkhn vnilytapta
361 iralmahgnd avegtsrssl rvmgsvgepi npeawewyyn tigdarcpiv dtwwqtetgg
421 ilisplpgat alkpgsatrp ffgvqpalvd nmgnliegaa dgnlvitdsw pgqmrtiygd
481 hdrfeqtyfs tfkgmyftsd garrdedgyy witgrvddvl nvsghrmgta evesalvsfs
541 kiaeaaivgv phdikgqaiy ayitlnsgey psaelhkevk dwvrkeigpi atpdflhwtd
601 slpktrsgki mrrilrkiat gdtsnlgdts tladpsvvnk lieeqrkia

SEQ ID NO:10
GI:54310469, Protein name: acetyl-CoA synthetase [Photobacterium profundum SS9]

1 msevhvypvn qeiaatahvn deqyremyqq svinpegfwr ehgqivdwik pftkvkhtsf
61 dtghvsvkwf edgtlnvsan cidrhlatrg dqpaiiwegd dptddatfty nelheqvckf
121 snalksqgvr kgdvvclymp mvaeaaiaml actrigavht ivfggfspea lagrivdsna

```
      181 klvitadegv ragravplkk nvddalankn vtsiekvivl krtggnvewh
serdvwwhea
      241 tavasshcep eemnaedplf ilytsgstgk pkgvlhttgg ylvyatmtfk
yvfdyqegdv
      301 ywctadvgwi tghsylvygp langattvlf egvpnypsts rmsevvdkhn
vsilytapta
      361 iralmakgte aikgtsrssl rimgsvgepi npeawewyhh tigdsrcpiv
dtwwqtetgg
      421 ilitplpgat alkpgsatrp ffgvqpaivd nmgnilegva egnlvmvdsw
pgqmrtlwgd
      481 herfeqtyfs tfqgmyftgd garrdedgyy witgrvddvl nisghrmgta
eiesalvafd
      541 kiaeaaivgv phdikgqaiy ayitlndgei psaelhkevk dwvrkeigpi
atpdflhwtd
      601 alpktrsgki mrrilrkiat gdtgslgdts tladpsvvdk liaekqtil
```

SEQ ID NO:11
GI:6320852, Protein name: acetyl-CoA synthetase Faa2p[*S. cerevisiae*]

```
        1 maapdyaltd liesdprfes lktrlagytk gsdeyieely sqlpltsypr
yktflkkqav
       61 aisnpdneag fssiyrssls senlvscvdk nlrtaydhfm fsarrwpqrd
clgsrpidka
      121 tgtweetfrf esystvskrc hnigsgilsl vntkrkrple andfvvails
hnnpewiltd
      181 lacqaysltn talyetlgpn tseyilnlte apilifaksn myhvlkmvpd
mkfvntlvcm
      241 delthdelrm lnesllpvkc nslnekitff sleqveqvgc fnkipaippt
pdslytisft
      301 sgttglpkgv emshrniasg iafafstfri ppdkrnqqly dmcflplahi
fermviaydl
      361 aigfgigflh kpdptvlved lkilkpyava lvpriltrfe agiknaldks
tvqrnvanti
      421 ldsksarfta rggpdksimn flvyhrvlid kirdslglsn nsfiitgsap
iskdtllflr
      481 saldigirqg ygltetfagv clsepfekdv gscgaigisa ecrlksvpem
gyhadkdlkg
      541 elqirgpqvf eryfknpnet skavdqdgwf stgdvafidg kgrisvidrv
knffklahge
      601 yiapekieni ylsscpyitq ifvfgdplkt flvgivgvdv daaqpilaak
hpevktwtke
      661 vlvenlnrnk klrkeflnki nkctdglqgf eklhnikvgl epltleddvv
tptfkikrak
      721 askffkdtld qlyaegslvk tekl
```

SEQ ID NO:12
GI:255717016, Protein name: acetyl-CoA synthetase [Lachancea thermotolerans]

```
        1 mskqdgyisl selietdkrf qnlreelavy dknskeylsn lisklpltnh
vsyrqflkeq
       61 avslesskkh gyspvfrssl speclvsnvh prlstffelf nfsverfpdn
dclgqrsqdr
      121 vtghwgqhye fesyreiqer sqnlgsgimt vvnlkrkrrf gsndfivsfl
stnrkewvis
```

181 dlacqgyslg ntalyetlgl dtseyilnvt espvlilske niyrvmemvp klphlstivc
241 mdelsdlela qlngpllpqh tnskgerisi lnfrqverig asnkvplipp tpdslytisf
301 tsgttgtpkg vqmkqshvaa avafvlstlr mprlkhrsqa ydlcflplah iferqivafd
361 lssgtaigfl hkpdpsvlve dlkllkpdvf psvpriltkf eagiknslqn gdgsavtknv
421 astilnkrle rtthhggkdh silntvvfhr vlidkirssl glenldvvit gsapisndtl
481 lfmksaldcg vrqgygltet fagiclsear erdsgtcggm avttecrlrs ipemgydaeh
541 dlkgevqlrg sqvfrgyykn pqetsralge dgwystgdvg fidskgrlsi idrvknffkl
601 aqgeyiapek iesvylsscp yltqisvhgd slqtflvavi glelditapi ihkkipelrg
661 fsgkdlvdei nksrahrkal ivlinsfieg lqgfekihnl yvgieplkvt ddtitptlkv
721 kranaakhfr kilenlyeeg slikvekl

SEQ ID NO:13
GI:45187925, Protein name: acetyl-CoA synthetase [Ashbya gossypii ATCC 10895]

1 msnetevnry pgmgpislve virtdarfae lwkrlslfqq gsvefykely dnmplfagmd
61 gmalsapvpg sgkkgyspvf rnvlvpegkl lsaidegvdt gyhvfklsar mypdnhclgm
121 raydeatgkw ldeyrwetys qverraenlg agllsvvnvk rskpldtndf ivammsansk
181 ewvltdlacq tfslvntaly etlgpntsey imnltespvv vvskpnllri falasklral
241 ntivimddmd lqevdrlasl lpvtknakge tisvltlrqv ekigelnnia pippspdsfh
301 tisftsgtts lpkgvqlthr aycaalafac shvrcepnkq ryalcllplt hiyqrqmtgl
361 nlmhafgigf lhkpnpdlfi eamcvlrpam vslvprvltk leagiknsiq gadvstfkrk
421 laktvidakd krfsavsgpd dsymnrfiyr kifvdkirdk lgftnvplvt tgsapispet
481 lrfiqcamdi gilqgyglte tfggnflsvp yetdcgscgp pamttevrlr dvpgmsynae
541 kdhmgevvvr sqqqferyyk mpektaevld kdgwfstgdv gyidkkgrlf itdrvknifk
601 lsqgeyiape kvencylssc pfitqifvhg nslnnylvgv vgidvvpfka ildsrtskws
661 klpleevipt inkdpalkql tlkiinsfvt aelqgfekig nlyadvepls vdgetltptf
721 kvkrevctkv fkdilsslyd eghilkagkl

SEQ ID NO:14
GI:380351855, Protein name: acetyl-CoA synthetase [Candida orthopsilosis]

1 maslfnekpe hiwktitesf pldqsvtsra lplpnsevpg fspiyrnays qkelktvpyp

```
       61 gittlhdtfe lsvannghkr alghrvkkad gsfgeyvwqd yktvqqrrnn
lgsgiffvlq
      121 nnpyktdsea hkklkydpls ddsfvltifa hnrpewvlad vtstaysitn
talydtlgpd
      181 tskyilnlte cpiilcskdk vkslvelkeq npeelsnlic lvsmddltte
davlknychd
      241 hnislfdykq veklgeinpl apippkpetk fsitftsgtt ganpkgvllt
hetavagitf
      301 vysgitlpra davfysflpl ahiyerqgih faltygaaig fpqgpspltl
lediqvlepd
      361 ylalvprvlt kleagikaqt inndekpilk slftkaintk lalqsnpane
ntnpshllyd
      421 rvlgllrkkl gmknlkiims gsapispetl kflkaslntg vgqgygmset
fagvmasstf
      481 etdasscgpi svttecktrd lpamgytskd eggprgellv rgpqifleyy
knpeetaksf
      541 dedgwfytgd varidsktgr tyiidrvknf fklaqgeyvt perientyls
cfpyiaqlfv
      601 hgdslrthlv gvvgvdpasi tqyikqrhge titdaadlvr ffqdpkrkre
llvdmnaslg
      661 nklqgfeklh nievdvepls veknlitptm kikrpictky fkdtldklye
egslirndkl
```

SEQ ID NO:15
GI:126136683,Protein name: acetyl-CoA synthetase [Scheffersomyces stipitis CBS 6054]

```
       1 mslfqedpkn ihnfiraslp ldpkklcesv plpysekpgy savyrnkysv
dglitrphps
      61 latlfdlhev aarsqpdspc fgvrhkqadg tygpyqwiny qevydrkvhf
gsgvffilqn
     121 npyrtnspvh qkihydpqat espfvlsifs anraewvttd macsayslts
talydslgaq
     181 tskyilsste spivvsskdk lksliklkae dpetlsnlit lvsmdpldpk
tdealvkyan
     241 dnritlfdfd qvlklgeink lpqippkpet iytisftsgt tganpkgvll
thanavcavt
     301 fcysnitlpe sptvycflpl ahiyermsis falsmcaaig fpqspspltl
mddikhlrph
     361 flnlvprvyt kleaalkaqt fnsdkpiiks lfsaainkkm elqavedgaq
gkhivydqvv
     421 qllrkkigfd rliavttgsa pispetlkfi kaslntgmsq gygltesfag
vctslkyean
     481 pgscgaisit temrlrevpe mnyhahdkgg prgelmlrgp qifreyfknp
eetakaidse
     541 gwfatgdiar idatngnriy iidrvknffk laqgeyitpe kientylsqf
pfiqqlyvhg
     601 dplkthlvai vgldpatvds yikrkfndil snqddivdff rnpkhrlall
edmnssvggl
     661 lqgyerihni kvdfnpltie dnvitptlki krpiavkffk edfdalyeeg
slikpdahkl
```

SEQ ID NO:16
GI:294656605, Protein name: acetyl-CoA synthetase [Debaryomyces hansenii CBS767]

```
        1 mtssdvydhg dspyvfkpsk tpasqlirdh lplpekmfkd svslpgteke gysaiyrnkm
       61 fpgrlkealt peldtyyrlf knsvltfgdk sclayrkydy vnkksaddys
fltyrevdem
      121 kqrygsgfly llqnnpfkns ekfeshrkid nhvkdyknfd isdmsfvati
ysanrmewvl
      181 sdlmcssysi tntalydtlg adtseyilqt tqspvviatk ehvmdivnlk
ekypeklehv
      241 isivcldpld lknetslsae dqalvtacks hritlvdinq vmkvgeifpt
pelppspetl
      301 ytisftsgtt gahpkgvlls qkictagvtf vltqlpripd arsfsflpla
hiferqvcaf
      361 glscgncigf pqnggtpltl iedlklfkpn ymcnvprvft kyeaaiksat
vdhptstfkr
      421 gifdkvistk iqaqekydga dgshlvydrl flssirkafg fdnmefivtg
sapispstvk
      481 flkatlcvgm pqgygstesf agfaigipye aepgscgsvg vtvemklrel
pamgynlddp
      541 egprgelllr gpqifkqyfh neeetkksfd degwfhtgdv arfsknngrl
fiidrvknff
      601 klsqgeyvtp ekvenkylss ssilnqlyvh gdslrhflvg ivgidpegav
nflvekckvs
      661 ksqlssseqi lneinkkenr ellvayinsr isnqlsgfek lhniyvefep
lrldrdvvta
      721 tqklkrpvaf kffkpqidvm ydegslvkgp kl
```

SEQ ID NO:17
GI:6319264, Protein name: Acs1p [Saccharomyces cerevisiae S288c]

```
        1 mspsavqssk leeqsseidk lkakmsqsaa taqqkkehey ehltsvkivp
qrpisdrlqp
       61 aiathysphl dglqdyqrlh kesiedpakf fgskatqfln wskpfdkvfi
pdpktgrpsf
      121 qnnawflngq lnacyncvdr halktpnkka iifegdepgq gysitykell
eevcqvaqvl
      181 tysmgvrkgd tvavympmvp eaiitllais rigaihsvvf agfssnslrd
rindgdskvv
      241 ittdesnrgg kvietkrivd dalretpgvr hvlvyrktnn psvafhaprd
ldwatekkky
      301 ktyypctpvd sedplfllyt sgstgapkgv qhstagyllg alltmrytfd
thqedvffta
      361 gdigwitght yvvygpllyg catlvfegtp aypnysrywd iidehkvtqf
yvaptalrll
      421 kragdsyien hslkslrclg svgepiaaev wewysekigk neipivdtyw
qtesgshlvt
      481 plaggvtpmk pgsasfpffg idavvldpnt geelntshae gvlavkaawp
sfartiwknh
      541 dryldtylnp ypgyyftgdg aakdkdgyiw ilgrvddvvn vsghrlstae
ieaaiiedpi
      601 vaecavvgfn ddltgqavaa fvvlknkssw statddelqd ikkhlvftvr
kdigpfaapk
      661 liilvddlpk trsgkimrri lrkilagesd qlgdvstlsn pgivrhlids vkl
```

SEQ ID NO:18
GI:254579411, Protein name: ZYRO0C00682p [Zygosaccharomyces rouxii]

```
        1 mtvnyvyagm wrnlfpesic rlrdkrkehi pysmspstta tgtsptggti
gdlkarlvha
       61 aerentspat tnnvstekdh eaetntpttd ydhlisvhtv qqkpithrlq
selschycph
      121 isgfreyekl yresidqpse ffgnkarqfl nwfkdfdqvf ipdprtgkps
lnnnawflng
      181 qtnacyncvd rhaletpdkp aiiyetdepg qgytltysel leqvcqlaqv
lrysmgvrkg
      241 dtvavympmi pqavislmai arigaihsvv fagfscnslr drindadshv
vittdetkrg
      301 gkivetkriv ddalketpgv snvlvyrrtn nprvprqvsr dldwdgelrk
ykgycpcepv
      361 dsehplflly tsgstgtpkg vqhstagyll salltmrysf dthredvfft
agdvgwitgh
      421 tyvvygplly gcttlvfegt payptyaryw diidqykvtq fyvaptalrl
lkragdsfie
      481 ghslqslral gtvgepiaae vwewysekig knelpivdty wqtesgshml
tpmaggvtpm
      541 kpgsagfpfi gidscildpt tgqeltkplv egvlavrcgw psfartiwkd
hdrfldtylk
      601 pypgyyftgd gaardkdgyi wilgrvddvv nisghrlsta eiesavldda
ivaecavvgf
      661 nddltgqava afvvlknkss wstaseeell dikkhlilav rkdigpfaap
klivlvddlp
      721 ktrsgkimrr ilrkilagec dqlgdvstls npgvvrhlid svkl
```

SEQ ID NO:19

GI:45188280, Protein name: ADR408Wp [Ashbya gossypii ATCC 10895]

```
        1 mvtsagvgha eynngadvqh adyahltsvg qveqkplggr lgalaeyykp
nvasmeeyra
       61 mhaqsitdpa afygerarty vdwfrpfdav flpgpdgrps fdnnawfvng
qlnacynlvd
      121 rhaartpdkv aiiyeadepg egysltyrel laqvckvaqv lqysmgvrkg
dtvavympmi
      181 pqalvtllai srigaihsvv fagfssnslr drindarsev vvttdeskrg
gkiietkriv
      241 ddaiketpql rkvlvykrtc npsvsyvadr dldwdtevkk yksycpcepv
dsehplflly
      301 tsgstgapkg vqhstagyll qaylsmlysf dvhsddifft agdigwitgh
tyvvygplfs
      361 gcttvvfegt paypsysryw diidkysvtq fyvaptalrl lkragdsyvd
gyslrtlrsl
      421 gtvgepiaae vwewyytvig kreipvidty wqtesgahlv tplaggstpm
kpgsasfpff
      481 gidlaildpq tgeellgpnv egvlavkqpw psftrtiwnn hdryldtyln
pykgyyfagd
      541 gaardsqgfi wilgrvddvv nvsghrlsta eveaaiiqes mvaecavvgf
adeltgqaia
      601 afvvlkqkss wntaserelq eikkhlilsv rrdigpfaap klivlvddlp
ktrsgkimrr
      661 ilrkilagea dqlgdvstls npgivkhlie svkf
```

SEQ ID NO:20
GI:3139035, Protein name: acetyl-CoA synthetase [Kluyveromyces lactis]

```
        1 mksnasaaaa dqiktheyeh ltsvpivqpl pitdrlssea aqkykpnlpg
gfeeykslhk
       61 eslenpakfy heraqllnwf kpydqvfipd tegkptfenn awftngqlna
cynlvdrhaf
      121 tqpnkvaily eadepgqgys ltyaelleqv ckvaqilqys mnvkkgdtva
vympmipqal
      181 itllaitrig aihsvvfagf ssnslrdrin daysktvitt deskrggkti
etkrivdeal
      241 kdtpqvtnvl vfkrthneni kyipgrdldw deevkkyksy tpcepvdseh
plfllytsgs
      301 tgapkgvqhs tagyllqall smkytfdiqn ddifftagdi gwitghtycv
ygpllqgctt
      361 lvfegtpayp nfsryweivd kyqvtqfyva ptalrllkra gdsftegfsl
kslrslgsvg
      421 epiaaevwew ysekigknel pivdtywqte sgshlvtpla ggatpmkpga
aafpffgidl
      481 avldpttgie qtgehaegvl aikrpwpsfa rtiwknndrf ldtylkpypg
yyftgdgvar
      541 dkdgffwilg rvddvvnvsg hrlstaeiea aiieddmvae cavvgfndel
tgqavaafvv
      601 lknkssltaa seselqdikk hliitvrkdi gpfaapkliv lvddlpktrs
gkimrrilrk
      661 ilagesdqla tsphyptlvs lst
```

SEQ ID NO:21
GI:320580699, Protein name: Acetyl-coA synthetase isoform [Ogataea parapolymorpha DL-1]

```
        1 mpekhleneh lmreralepp agflerhpsk pylssldeyk kmyeesirdp
gsffggmaeq
       61 hlswfkpftv pkvpnapflk dnngepsawf vdgelnacyn cvdrwaiknp
dkpaiiyead
      121 epdqgeiity gellkqvckv sqvllnlgvk kgdtvavylp mipeaivtlm
aivrigaihs
      181 vvfagfssgs lrdrindans kvvittdesk rggkiietkk ivddallacp
qvtnvlvykr
      241 tgnshipwte grdlwwheev kkypsyypat pvsaedtlfl lytsgstgkp
kgiqhstagy
      301 llgallttky vfdvhpedil ftagdvgwit ghsyvvygpl lngattvvfe
gtpaypnysr
      361 yweivdkykv tqfyvaptal rllkragesy iepyslqslr vlgsvgepia
kdvwewynah
      421 igrgkahicd tywqtesgsh litplagvtp tkpgsaslpf fgidpaiidp
vsgkelegne
      481 vegvlairss wpsmartiwr dysrfldtyl rpyhgyyfsg dgaardkdgf
ywilgrvddv
      541 vnvsghrlst aeieaalieh smvaesavvg fpdeltgsav aafvslknrs
iedpsaikke
      601 liltvrkeig pfaapklill vndlpktrsg kimrrilrki lsgeedqlgd
tstlsnpqvv
      661 shlievvkak
```

SEQ ID NO:22
GI:190348910,Protein name: acetyl-coenzyme A synthetase 1 [Meyerozyma guilliermondii ATCC 6260]

```
        1 mpestdhldh ekmldppkgf ferstskpnl asldeykkly kqsiedpatf
fgnaaksfld
       61 wdrpfdytrf pvdpkddfkn gdipswfing qlnasynavd rwamknpekp
aiiyeadevn
      121 egrtitygel lkdvsklaat ltnlgvkkgd svavylpmip eaivtllaiv
rigalhsvvf
      181 agfsstslrd riidadsriv itadeskrgg ktietkkivd dalkecphvr
nvlvfkrtgn
      241 shvpfsagrd lwwhdelqky gpyfppvpvn sedplflyt sgstgkpkgv
qhntagyllg
      301 almtakytfd lheediifta gdvgwitght yvvygpllcg attvvfegtp
aypdysrywd
      361 vvdkykvnqf yvaptalrll kragtkyvek hdlsslrvlg svgepiaaev
whwyndnigr
      421 gkahivdtyw qtesgshllt plagvtptkp gsaslpffgi darildpvsg
kdlvdnnveg
      481 vlcvksawps itrgiyhdya ryietylkpy pnhyfsgdga ardkdgffwi
lgrvddvvnv
      541 sghrlstaei eaaliehelv gesavvgyad eltgqavaay vslksnvevd
dleaikkeli
      601 ltvrkeigpf aapklillvd dlpktrsgki mrrilrkvla geedqlgdis
tlsnpqvvsq
      661 vievvkasrk
```

SEQ ID NO:23
GI:29893231, Protein name: acyl-activating enzyme 11 –AAE11[Arabidopsis thaliana]

```
        1 mdnlvlcean nvpltpitfl krasecypnr tsiiygqtrf twpqtydrcc
rlaasllsln
       61 itrndvvsil apnvpamyem hfsvpmtgav lnpintrlda ktiaiilrha
epkilfvdye
      121 fapliqevlr liptdqsqah priilineid sttkpfskel dyeglirkge
ptpsssasmf
      181 rvhnehdpis lnytsgttad pkgvvishrg aylsalssii gwemgifpvy
lwtlpmfhcn
      241 gwthtwsvaa rggtnvcirh vtapeiykni elhgvthmsc vptvfrflle
gsrtdqspks
      301 spvqvltggs sppavlikkv eqlgfhvmhg yglteatgpv lfcewqdewn
klpehqqmel
      361 qqrqgvrnlt ladvdvkntk tlesvprdgk tmgeivikgs slmkgylknp
katseafkhg
      421 wlntgdigvi hpdgyveikd rskdiiisgg enissievek vlymyqqvle
aavvamphpl
      481 wgetpcafvv lkkgdeesvt segdlikycr enmphfmcpk kvvffqelpk
nsngkilksk
      541 lrdiakalvv reddagskkv hqrsiehvss rl
```

SEQ ID NO:24
GI:29893229, Protein name: acyl-activating enzyme 12 [Arabidopsis thaliana]

```
        1 mdnlalcean nvpltpitfl krasecypnr tsiiygktrf twpqtydrcc
rlaaslisln
       61 igkndvvsvv apntpamyem hfavpmagav lnpintrlda tsiaailrha
kpkilfidrs
      121 feplareilq llssedsnln lpvifiheid fpkrvssees dyecliqrge
ptpsllarmf
      181 ciqdehdpis lnytsgttad pkgvvishrg aylstlsaii gwemgtcpvy
lwtlpmfhcn
      241 gwtftwgtaa rggtsvcmrh vtapeiykni emhnvthmcc vptvfnillk
gnsldlshrs
      301 gpvhvltggs pppaalvkkv qrlgfqvmha yglteatgpv lfcewqdewn
rlpenqqmel
      361 karqglsilg ltevdvrnke tqesvprdgk tmgeivmkgs simkgylknp
katyeafkhg
      421 wlnsgdvgvi hpdghveikd rskdiiisgg enissveven iiykypkvle
tavvamphpt
      481 wgetpcafvv lekgetnned redklvtker dlieycrenl phfmcprkvv
fldelpkngn
      541 gkilkpklrd iakglvaede vnvrskvqrp vehftsrl
```

SEQ ID NO:25
GI:224065064, Protein name: acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa]

```
        1 mdqllkcdan yvpltpitfl kranavyanr tsviyegtrf twsqtyercc
rladslrsln
       61 vgkndvvsvl apnipavyem hfavpmagav lntinirlda kniatilshs
gakvffvdyq
      121 ykelaskals fldgavpsii aciddidtpt gvqfgqleye qlvqrgnpgy
tgelvqdewd
      181 pialnytsgt tsapkgvvys hrgaylssls lilgwemgna pvylwslpmf
hcngwtftwg
      241 vaarggtnvc irntsakdmy hniaehavth mccapivfnv llearpherr
eitspveilt
      301 ggapppasll qdierlgfhv thayglteat gpalvcewqk kwnklpqqdq
aklkarqgis
      361 iltladadvk dldtmvsvpr dgktmgeivl rgssimkgyf kdpeatskaf
rngwfatgdv
      421 gvihpdgyle ikdrskdvii sggenissve lesvlyrhpr vleaavvamp
hpkwgespca
      481 fisvkknsng dtndvkesdi iayckknlph ftvpkrvefm aelpktstgk
iqkfqlrala
      541 qnfvvneilp skkinghsqp sasgrvntev teyaqgheqv lalsrl
```

SEQ ID NO:26
GI:226508754, Protein name: acyl-activating enzyme 11 [Zea mays]

```
        1 mdqlpkrpan yvplspvgfl pranavygdr tsviyrgvrf twrqtyarcr
rlasallslg
```

```
       61 vvrrgdvvsv lapnvpamye mhfavpmaga vlntintrld aaavatilrh
sgaklffvdy
      121 dyvrlasdal rlldaadvpl vaviddihsp tgarlgeley eallahgdpd
adlpplqdew
      181 davtlsytsg ttsapkgvvy shrgaylstt slllqwgvpa epvylwtlpm
fhcngwtftw
      241 gmaarggvnv cirdarpadi yraiarhrvt hmccapvvfs illdgdgdsd
gaarqlqapv
      301 hvltggappp aallerveri gfnvthaygl teatgpalac ewrdqwdrlp
lperarlkar
      361 qgvsvlslad advknadtml svprdgrtvg eivlrgssvm kgylnnpean
esafragwfl
      421 tgdvgvvhpd gyieikdrsk dviisggeni cskeleevlf rhpavadaav
vamphprwge
      481 tpcafvvprd kaavlsegdv lafcskrmar fmvpkkvevv galprnalgk
vekvklreaa
      541 rklaptvaaa qkpkaktttv ggrrdgqpva hvmavsrl
```

SEQ ID NO:27
GI:357491641, Protein name: 2-succinylbenzoate-CoA ligase [Medicago truncatula]

```
        1 mnqltrnqan staltpltfl eraatvygns isiiynntsf twsqthkrcl
qlasslsslg
       61 iqkgdvvsvl spntpamyel hfsvpmsgai lnnlnfrldh ktlsvllihs
esklifvdil
      121 slsltlnals lfptniqqpk lvlimdetla phqipplpkn vniintyegl
vakgdpyfkw
      181 irpdsewdpi tlnytsgtts spkgvvhchr atfivsldsl idwsvpvqpv
flwtlpmfhs
      241 ngwsypwama avgginictr rtdaptiytl ieshgvthmc aapvvlnmls
nfnkteplkk
      301 pvhvltggss pptailtrae rlgfevshgf gmtevigviv scawkrewdr
fpatekarmk
      361 arqgvrkvgv aevdvvgptg esvkndgvtv geivvkgacv mlgyfkdeia
tsqcikkngw
      421 fytgdvavmh edgyleikdr skdliisgge nmssvevegv lymhsavkea
avvarpddfw
      481 getpcgfvsl kdelkkndip tdneikefck eklphfmmpk tivfmkelpk
tstgkvqkhv
      541 lrkvakkmgs lslpppprli sri
```

SEQ ID NO:28
GI:149375957, Protein name: acyl-CoA synthase [Marinobacter algicola DG893]

```
        1 mnsifdkgle ptdannatlt pldflartas vypeypavih gatrrnwqqt yercrrlasa
       61 ladrgvgkgd tvaamlpnip pmlechfgip mlgavlnaln trldakaiaf mlehgeakvl
      121 iadrefgdvi neavgmldnp pqvidvndpe fsgagtqvsd ldydafvasg dpafdwqmpa
      181 dewdaislcy tsgttgnpkg vvyhhrgaye namgnqavws mgmhpvylwt lpmfhcngwc
      241 fpwtitafag thvclrkvep ekilqliseh kvshmcgapi vlntllgase aakssfshtv
      301 qamtagaapp akvieaienm gfrvthvygl tevygpvtvc awksewddlp vedrarikar
      361 qgvryhtlag mmvgdpetme avpkdgntig eiflrgntvm kgylknpkat eeafrggwfh
      421 tgdlavwhad gyaeikdrlk diiisggeni stievedvly rhpdileaav varpdekwge
      481 tpcafvtlkp eagevseddi iafcrermak fkvpktivfs elpktstgki qkfvlrddak
      541 kl
```

SEQ ID NO:29
GI:26991093, Protein name: lpdV gene product [Pseudomonas putida KT2440]

```
        1 mqqiiqttll iigggpggyv aairagqlgi ptvlvegqal ggtclnigci
pskalihvae
       61 qfhqasrfte psplgisvas prldigqsvt wkdgivdrlt tgvaallkkh
gvkvvhgwak
      121 vldgkqvevd gqriqcehll latgsssvel pmlplggpvi sstealapkt
lpqhlvvvgg
      181 gyiglelgia yrklgaqvsv vearerilpt ydseltapva eslkklgial
hlghsvegye
      241 ngcllasdgk ggqlrleadq vlvavgrrpr tkgfnlecld lkmngaaiai
derchtsmhn
      301 vwaigdvage pmlahramaq gemvaeiiag karrfeptai aavcftdpev
vvvgktpeqa
      361 sqqgldciva qfpfaangra msleskgfv rvvarrdnhl ivgwqavgva
vselstafaq
      421 slemgacled vagtihahpt lgeavqeaal ralghalhi
```

SEQ ID NO:30,
GI:6325162, Protein name: Eeb1p [Saccharomyces cerevisiae S288c]

```
        1 mfrsgyyptv tpshwgyngt vkhvlgekgt kslafrdskr qiplhefvtk
hvptlkdgan
       61 frlnslftg ylqtlylsag dfskkfqvfy greiikfsdg gvctadwvmp
eweqtyslna
      121 ekasfnekqf sndekathpk gwprlhprtr ylsseelekc hskgysyplv
vvlhglaggs
      181 hepliralse dlskvgdgkf qvvvlnargc srskvttrri ftalhtgdvr
eflnhqkalf
      241 pqrkiyavgt sfgaamltny lgeegdncpl naavalsnpw dfvhtwdkla
hdwwsnhifs
      301 rtltqfltrt vkvnmnelqv penfevshkp tvekpvfyty trenlekaek
ftdilefdnl
      361 ftapsmglpd gltyyrkass inrlpnikip tliinatddp vtgenvipyk
qarenpcvll
      421 cetdlgghla yldnesnswl tkqaaeflgs fdelvl
```

SEQ ID NO:31
GI:207340567, Protein name: YPL095Cp-like protein [Saccharomyces cerevisiae AWRI1631]

```
        1 mfrsgyyptv tpshwgyngt vkhvlgekgt rslafrdskr qiplhefvtk
hvptlkdgan
       61 frlnslftg ylqtlylsag dfskkfqvfy greiikfsdg gvctadwvmp
eweqtyslna
      121 ekasfnekqf sndekathpk gwprlhprtr ylsseelekc hskgysyplv
vvlhglaggs
      181 hepliralse dlskvgdgkf qvvvlnargc srskvttrri ftalhtgdvr
eflnhqkalf
      241 pqrkiyavgt sfgaamltny lgeegdncpl naavalsnpw dfvhtwdkla
hdwwsnhifs
      301 rtltqfltrt vkvnmnelqv penfevshkp tvekpsfiri pekiwkrlkn lqty
```

SEQ ID NO:32
GI:255715549, Protein name: KLTH0E13310p [Lachancea thermotolerans]

```
        1 mplpifnpfh wgyhgtieqv snpngtvalt lkdekkpvqf sdfvsreipg
lkdkakfevn
       61 pllftgylqt lylggadfsk sfpvyygrei vkfsdggict adwvmkswks
kygadtssfk
      121 tdeqathpen wprlhprtrf leesekkdvh nsekplvvvl hglaggshep
iirsltqdls
      181 nagdskfdvv vlncrgcars kittrklfya vftsdirefi arekarhpsr
kiyavgfsfg
      241 atmlghylge egekapieaa sflcnpwdly qsalkmnqdw wsrnlfskni
aqflirlvkv
      301 nikelefkeg dvmpaepasl ehpsfcvfts knlrkarefg staefdnlft
apclgfdnam
      361 dyykacgsih qlpnikvpsl iinskddpvv gedsipykca kesdnlvlcv
sdlgghlafl
      421 dkkynswats kiaaffdkfe elvq
```

SEQ ID NO:33
GI:254584546, Protein name: ZYRO0F14740p [Zygosaccharomyces rouxii]

```
        1 msnlpiinpf hwgsrgtlkh tsapsgttkl tlnhdktkid fqhfvsqyvp
alkdgskfkl
       61 nnflftgilq tmylsgadyt kwfpvfygre ilelsdggvc tvdnvmvswe
ekyqlrqnsg
      121 sfnklefekd ekdthpqnwp rlqartrylt akelaevhgd qrplvvvlhg
laggshetii
      181 rsltsklski dggkfqvavl ncrgcarski tnkklfsafq tgdlkeylar
eksrnpnrki
      241 yavgfsfgas llanylgetg sesnltaavt lccpwdfllc aekmkkdyws
knlfskaitq
      301 flvrlvkvnm gelespegsk pefqpdienp clymctksnl eraksftqml
efdgtftaps
      361 mgfssaeeyy ragsainnlh kvqvptliin stddpiidas sipysqvkmn
pnllllatdl
      421 gghlayldet wdswmnthia sffstfdefl v
```

SEQ ID NO:34
GI:45185426, Protein name: ABR194Cp [Ashbya gossypii ATCC 10895]

```
        1 mglptfaprs wgyrgtithr pheeglvklp lkdkekepvt lsdllnehvp
elkdgarfyl
       61 hpylyngilq tmylygadfs qqykpfygre ivsysdggvs tadwamrewd
dlyaapegyn
      121 kekfdadaak thpenwprlq pntrfldeee lakipkdtrp livvahglag
gsheniiral
      181 vtellsvgng qfnvvvlnsr gcarskiank klfsafhtmd irefinreha
rqperkiygl
      241 gfsfgsvifg nylgeegdks plsgavccag pwdmfasskm lnddfwisrl
fgknlvkhls
```

```
      301 rllhvnrkel eydgskgddv edasptnpas hiftkenlar astmactrdf
dnfftapalg
      361 fknandyyka aspvnivgki rvptllinal ddpmvgaegf lpieklrsnk
hillcttdig
      421 ghlayldkny tpwmagrvae flskmdtlva
```

SEQ ID NO:35
GI:294659670, Protein name: DEHA2G12430p [Debaryomyces hansenii CBS767]

```
       1 mvfpwgfrsn vkihqsnsdk sidlplrnge ktikyadfik delpiideke klwlnpllfn
      61 gllqtlyyss anlshkfqvy ygreiftyed ggvcsidhvi pqpenteefk
alhdktlpeg
     121 wpklhprsry fsneeleqvn spsegsqstk picvvlhgla ggsheplirn
laeylstgkn
     181 enkwdtlvin srgccrtkit ngklftalst gdihevlvel kkrnpnrpiy
tvgfsfgaai
     241 lanylaeikd dtmitaaclv gcpwdlidsa yhiekswsgs ylfnpaltsf
lnklvknnft
     301 elnhhnpelf neenlkrgmk qtktwqfdsv ytchtigysn pfeyyrdasp
vnriskihtp
     361 tlilnstddp avgvrlpwme vennphlcmv etdlgghlgy vqssgkfwcv
qlveeffakf
     421 delias
```

SEQ ID NO:36
GI:75150384, Protein name: Benzoyl coenzyme A:benzyl alcohol benzoyl transferase[Clarkia breweri]

```
       1 mahdqslsfe vcrrkpelir pakqtphefk klsdvedqeg lrfqipviqf
ykhnnesmqe
      61 rdpvqvireg iaralvyyyp fagrlrevdg rklvvectge gvmfieadad
vtleqfgdal
     121 qppfpcfdql lfdvpgsggi ldsplliqv trlkcgsfif alrlnhtmad
aagivlfmka
     181 vgemargaat pstlpvwdrh ilnarvppqv tfnhreyeev kgtiftpfdd
lahrsfffgs
     241 teisamrkqi pphlrscstt ievltaclwr crtlaikpnp deevrmiciv
narskfnppl
     301 pdgyygnafa ipaavttagk lcnnplgfal elirkakrev teeymhsvad
lmvatgrphf
     361 tvvntylvsd vtragfgevd fgwgeavygg pakggvgvip gvtsfyiplr
nrqgekgivl
     421 piclpsaame ifaealnntl ngkeieiakh ftqssl
```

SEQ ID NO:37
GI:49798480, Protein name: benzoyl coenzyme A: benzyl alcohol benzoyl transferase [Petunia x hybrida]

```
       1 mdskqsselv ftvrrqepel iapakptpre tkflsdiddq eglrfqipvi
nfyrkdssmg
```

61 gkdpvevikk aiaetlvfyy pfagrlregn drklmvdctg egvmfveana dvtleefgde
121 lqppfpclee llydvpgsag vlhcpllliq vtrlrcggfi falrlnhtms dapglvqfmt
181 avgemargat apstlpvwcr ellnarnppq vtcthheyee vpdtkgtlip lddmvhrsff
241 fgptevsalr rfvpphlhnc stfevltaal wrcrtisikp dpeeevrvlc ivnarsrfnp
301 qlpsgyygna fafpvavtta eklcknplgy alelvkktks dvteeymksv adlmvikgrp
361 hftvvrtylv sdvtragfge vdfgwgkavy ggpakggvga ipgvasfyip frnkkgengi
421 vvpiclpgfa mekfvkelds mlkgdaqldn kkyafitpal

SEQ ID NO:38
GI:1171577, Protein name: hsr201 [Nicotiana tabacum]

1 mdskqsselv ftvrrqkpel iapakptpre tkflsdiddq eglrfqipvi qfyhkdssmg
61 rkdpvkvikk aiaetlvfyy pfagrlregn grklmvdctg egimfveada dvtleqfgde
121 lqppfpclee llydvpdsag vlncpllliq vtrlrcggfi falrlnhtms dapglvqfmt
181 avgemarggs apsilpvwcr ellnarnppq vtcthheyde vrdtkgtiip lddmvhksff
241 fgpsevsalr rfvphhlrkc stfelltavl wrcrtmslkp dpeeevralc ivnarsrfnp
301 plptgyygna fafpvavtta aklsknplgy alelvkktks dvteeymksv adlmvlkgrp
361 hftvvrtflv sdvtrggfge vdfgwgkavy ggpakggvga ipgvasfyip fknkkgengi
421 vvpiclpgfa metfvkeldg mlkvdaplvn snyaiirpal

SEQ ID NO:39
GI:84578877, Protein name: benzoyl CoA benzoic acid benzoyltransferase [Verbena x hybrida]

1 maqnntlltf tvrrnepeli apakptprel kplsdiddqe glrfqipviq fyrhdpkmrn
61 knparvirea lakvlvfyyp fagrlkegpa kklmvdcsge gvlfieaead vtlnqfgdal
121 qppfpcleel lydvpgsggv ldsplliqv trllcggfif alrlnhtmsd apglvqfmta
181 lgemaqgapr psilpvwqre llfarvqphv tcthheydev kdtkgtiipl ddmahrsfff
241 gptevaalrr fvpsslqkcs tfevltaclw rcrtialkpd peeemriici vnarakfnpp
301 lpkgyygngf afpvaisrag dlstkplgha lklvmqakna vndeymrslt dlmvikgrph
361 ftvvrsylvs dvtragfdav dfgwgnaayg gpakggvgai pgvasfyipf tnhkgetgiv
421 lpiclpnaam etfvkelnnm lakgnndqvl kehnynvlsr l

SEQ ID NO:40
GI:254771941, Protein name: alcohol acyltransferase [Vasconcellea cundinamarcensis]

```
        1 maekasslmf nvrrhepeli tpakptprei kllsdiddqd glrfqvpiiq
fyknnssmqg
       61 knpakiiksa laetlvhyyp lagrlregfg rklmvectge gilfieadad
vtlhefgddl
      121 pppfpclvel lydvpgssgi idtpllliqv trlkcggfif alrlnhtmsd
asglvqfmta
      181 vgemargqrs lsiqpvwerh llnardpprv thihheyddl edtkgtiipl
ddmvhrsfff
      241 gpsemaairr lvpahfhrst tsevltaylw rcytialqpd peeemrvicv
vnsrtklnpp
      301 lptgfygngi afpaaisqak kicenpfgyt lqlvkqtkvd vteeymrsaa
dlmamkgrph
      361 ftvvrrymvs dvtragfglv dfgwgrpepv yggpakggvg pipgvtsffv
pfknrkgekg
      421 ivvptclptp amerfaklmn eilqnqllvs aeenksvfiv sai
```

SEQ ID NO:41
GI:161089458,Protein name: acyltransferase [Vanda hybrid cultivar]

```
        1 masstlhfsv rrrppqlvap asptprelkr lsdiddqegl rfqipviqfy
rhepamagqn
       61 pasvirdala rtlvfyypfa grlregagkk lfvdctgegv lfieaeadvk
lkdfgdalhp
      121 pfpcleellf dvdgssavln tpllliqvtl lscggfilal rlnhtmsdap
glvqlmtavg
      181 elargsssps vipvwrrell earpspapff phpeyeqvpd tegtitpldn
tahrsfifgp
      241 reisilrsrl psqlrgasst fdiltacvwr srtralqpad pkenfriici
vnirgrinpp
      301 lpsgfygnaf glpvaiatag elcsrpldya velvkraksq vsgdylhsva
dymvmkgrph
      361 ftvvrtyvis dltragfgdv dfgwgkpvyg gpakggvgvs pgvfnffipf
vnasgekgiv
      421 vpiclpppam rrfvaeiqsl lsaqsal
```

SEQ ID NO:42
GI:57471999, Protein name: putative alcohol acyl-transferases CmAAT3 [Cucumis melo]

```
        1 masslvfqvq rsqpqlipps dptphefkql sdiddqeglr fqipviqfyr
hdprmagtdp
       61 arvikeaiak alvfyypfag rlregpgrkl fvectgegvm fieadadvsl
eqfgdalqpp
      121 fpcleeplfd vpnssgvldc pllliqvtrl kcggfifalr lnhtmsdasg
lvqfmmavge
      181 margatapsv rpvwqralln ardppkvtch hreydevvdt kgtiipllddm
ahrsfffgps
      241 eisairkalp shlrqcssfe vltaclwrfr tislqpdpee evrvlcivns
rskfnpplpt
```

```
      301 gyygnafafp valttagklc qnplgyalel vrkakadvte dymksvadlm
vikgrphftv
      361 vrtylvsdvt ragfedvdfg wgkamyggpa kggvgaipgv asfyipfknk
kgergilvpl
      421 clpapamerf vkeldallka gktidgvdnk kplfiasal
```

SEQ ID NO:43
GI:49798480, Protein name: benzoyl coenzyme A: benzyl alcohol benzoyl transferase [Petunia x hybrida]

```
        1 mdskqsselv ftvrrqepel iapakptpre tkflsdiddq eglrfqipvi
nfyrkdssmg
       61 gkdpvevikk aiaetlvfyy pfagrlregn drklmvdctg egvmfveana
dvtleefgde
      121 lqppfpclee llydvpgsag vlhcpllliq vtrlrcggfi falrlnhtms
dapglvqfmt
      181 avgemargat apstlpvwcr ellnarnppq vtcthheyee vpdtkgtlip
lddmvhrsff
      241 fgptevsalr rfvpphlhnc stfevltaal wrcrtisikp dpeeevrvlc
ivnarsrfnp
      301 qlpsgyygna fafpvavtta eklcknplgy alelvkktks dvteeymksv
adlmvikgrp
      361 hftvvrtylv sdvtragfge vdfgwgkavy ggpakggvga ipgvasfyip
frnkkgengi
      421 vvpiclpgfa mekfvkelds mlkgdaqldn kkyafitpal
```

SEQ ID NO:44
GI:75150383, Protein name: Benzoyl coenzyme A:benzyl alcohol benzoyl transferase [Nicotiana tabacum]

```
        1 mdskqsselv ftvrrqkpel iapakptpre ikflsdiddq eglrfqipvi
qfyhkdssmg
       61 rkdpvkvikk aiaetlvfyy pfagrlregn grklmvdctg egimfveada
dvtleqfgde
      121 lqppfpclee llydvpdsag vlncpllliq vtrlrcggfi falrlnhtms
dapglvqfmt
      181 avgemargas apsilpvwcr ellnarnppq vtcthheyde vrdtkgtiip
lddmvhksff
      241 fgpsevsalr rfvphhlrkc stfelltavl wrcrtmslkp dpeeevralc
ivnarsrfnp
      301 plptgyygna fafpvavtta aklsknplgy alelvkktks dvteeymksv
adlmvlkgrp
      361 hftvvrtflv sdvtrggfge vdfgwgkavy ggpakggvga ipgvasfyip
fknkkgengi
      421 vvpiclpgfa metfvkeldg mlkvdapldn snyaiirpal
```

SEQ ID NO:45
GI:224144897, Protein name: predicted protein [Populus trichocarpa]

```
        1 masspasllf kvhrrepeli kpakptphef kllsdiddqe glrfhipvmq
fyrnnpsmqg
```

```
       61 kdpvkiirea laktlvfyyp fagrlregpn rklmvectge gilfieadad
vtleqfgdal
      121 qppfpcleel lfdvpgssgv lncpllliqv trlkcggflf alrlnhtmsd
avglvqfmaa
      181 vgemargana psvpavwerq vlnasdpprv tcthreyeev adtkgtiipl
ddmahrsfff
      241 gpsemsalrk fvpphlshcs tfeiltaclw kcrtialqpd pteemrilci
vnarekfnpp
      301 lprgyygngf afpvavatae elsknpfgya lelvrkakad vteeymrsvs
slmvikgrph
      361 ftvvraylvs dlrragfeev dfgwgnaiyg gaakggvgai pgvasfyipf
tnkkgengvv
      421 vpfclpapam erfvkeldgm lkddqtvsaq tkskfivssl
```

SEQ ID NO:46
GI:356500043, Protein name: PREDICTED: benzyl alcohol O-benzoyltransferase-like [Glycine max]

```
        1 mdtslvftvr rseaeliapa kptprevkll sdiddqdglr fqipviqfyr
hdpsmagkdp
       61 vdvirkavak tlvfyypfag rlreglgrkl mvdctgegvl fieadadvtl
kqfgdalqpp
      121 fpcweellyd vpgsqgvlnt pllliqvtrl kcggfilavr lnhtmsdaag
lvqfmsalge
      181 iargrqepsi ppvwrrelln ardpprvtct hreyehvpdt kgtiipldhm
ahrsfffgps
      241 evaairslip qtdqrcsnfe vltaclwrcr tialqpdkde evrilcivna
rskfdpplps
      301 gyygnafafp vavttagklc dnplgyalel vrkakadvte eymhsvadlm
vtkgrphftv
      361 vrsylvsdvt ragfgniefg wgkavyggpa kggvgaipgv asfyipfkna
kgeeglvipv
      421 clpseamerf qkeldcvlnh hivqpsaiap nsrfivssl
```

SEQ ID NO:47
GI:133874202, Protein name: putative acyltransferase [Clitoria ternatea]

```
        1 matstssssl mfqvqkreae liapakptpr evkllsdidd qeglrfqipv
iqfyrynetm
       61 agkdpvevir kalaktlvfy ypfagrlreg pgrklmvdct gegvlfieah
advtlqqfgd
      121 slqppfpgld hllynlpnsd gvlnspllli qvtrlkcggf ilalrlnhtm
sdaaglvqfm
      181 savgeiargm eepsippvwr rellnarnpp kvtcthreye qvpdskgtii
plddmahrsf
      241 ffgpaeisai rrlipaqqqr qcsnfeilta clwrcrtial qpdsdeevri
lcivnargkf
      301 npplpagyyg nafafpvavt tagklcgnpl gyalelvrka kgdvseeymh
sladlmvtkg
      361 rphftvvrsy lvsdvtragf gdvdfgwgkp vyggpakggv gaipgvasfy
ipfrnskgee
      421 glvipvclps qamdrfvrel dtilnhhlqp ppksplvlss l
```

SEQ ID NO:48
GI:49798480, Protein name: benzyl alcohol benzoyl transferase(BPBT) [Petunia x hybrida]

```
        1 mdskqsselv ftvrrqepel iapakptpre tkflsdiddq eglrfqipvi
nfyrkdssmg
       61 gkdpvevikk aiaetlvfyy pfagrlregn drklmvdctg egvmfveana
dvtleefgde
      121 lqppfpclee llydvpgsag vlhcpllliq vtrlrcggfi falrlnhtms
dapglvqfmt
      181 avgemargat apstlpvwcr ellnarnppq vtcthheyee vpdtkgtlip
lddmvhrsff
      241 fgptevsalr rfvpphlhnc stfevltaal wrcrtisikp dpeeevrvlc
ivnarsrfnp
      301 qlpsgyygna fafpvavtta eklcknplgy alelvkktks dvteeymksv
adlmvikgrp
      361 hftvvrtylv sdvtragfge vdfgwgkavy ggpakggvga ipgvasfyip
frnkkgengi
      421 vvpiclpgfa mekfvkelds mlkgdaqldn kkyafitpal
```

SEQ ID NO:49
GI:1171577, Protein name: hsr201 [Nicotiana tabacum]

```
        1 mdskqsselv ftvrrqkpel iapakptpre tkflsdiddq eglrfqipvi
qfyhkdssmg
       61 rkdpvkvikk aiaetlvfyy pfagrlregn grklmvdctg egimfveada
dvtleqfgde
      121 lqppfpclee llydvpdsag vlncpllliq vtrlrcggfi falrlnhtms
dapglvqfmt
      181 avgemarggs apsilpvwcr ellnarnppq vtcthheyde vrdtkgtiip
lddmvhksff
      241 fgpsevsalr rfvphhlrkc stfelltavl wrcrtmslkp dpeeevralc
ivnarsrfnp
      301 plptgyygna fafpvavtta aklsknplgy alelvkktks dvteeymksv
adlmvlkgrp
      361 hftvvrtflv sdvtrggfge vdfgwgkavy ggpakggvga ipgvasfyip
fknkkgengi
      421 vvpiclpgfa metfvkeldg mlkvdaplvn snyaiirpal
```

SEQ ID NO:50
GI:57471999, Protein name: putative alcohol acyl-transferases [Cucumis melo]

```
        1 masslvfqvq rsqpqlipps dptphefkql sdiddqeglr fqipviqfyr
hdprmagtdp
       61 arvikeaiak alvfyypfag rlregpgrkl fvectgegvm fieadadvsl
eqfgdalqpp
      121 fpcleeplfd vpnssgvldc plliqvtrl kcggfifalr lnhtmsdasg
lvqfmmavge
      181 margatapsv rpvwqralln ardppkvtch hreydevvdt kgtiiplddm
ahrsfffgps
      241 eisairkalp shlrqcssfe vltaclwrfr tislqpdpee evrvlcivns
rskfnpplpt
```

301 gyygnafafp valttagklc qnplgyalel vrkakadvte dymksvadlm vikgrphftv
361 vrtylvsdvt ragfedvdfg wgkamyggpa kggvgaipgv asfyipfknk kgergilvpl
421 clpapamerf vkeldallka gktidgvdnk kplfiasal

SEQ ID NO:51
GI:133874202, Protein name: putative acyltransferase [Clitoria ternatea]

1 matstssssl mfqvqkreae liapakptpr evkllsdidd qeglrfqipv iqfyrynetm
61 agkdpvevir kalaktlvfy ypfagrlreg pgrklmvdct gegvlfieah advtlqqfgd
121 slqppfpgld hllynlpnsd gvlnspllli qvtrlkcggf ilalrlnhtm sdaaglvqfm
181 savgeiargm eepsippvwr rellnarnpp kvtcthreye qvpdskgtii plddmahrsf
241 ffgpaeisai rrlipaqqqr qcsnfeilta clwrcrtial qpdsdeevri lcivnargkf
301 npplpagyyg nafafpvavt tagklcgnpl gyalelvrka kgdvseeymh sladlmvtkg
361 rphftvvrsy lvsdvtragf gdvdfgwgkp vyggpakggv gaipgvasfy ipfrnskgee
421 glvipvclps qamdrfvrel dtilnhhlqp ppksplvlss l

SEQ ID NO:52
GI:224144897, Protein name: predicted protein [Populus trichocarpa]

1 masspasllf kvhrrepeli kpakptphef kllsdiddqe glrfhipvmq fyrnnpsmqg
61 kdpvkiirea laktlvfyyp fagrlregpn rklmvectge gilfieadad vtleqfgdal
121 qppfpcleel lfdvpgssgv lncpllliqv trlkcggflf alrlnhtmsd avglvqfmaa
181 vgemargana psvpavwerq vlnasdpprv tcthreyeev adtkgtiipl ddmahrsfff
241 gpsemsalrk fvpphlshcs tfeiltaclw kcrtialqpd pteemrilci vnarekfnpp
301 lprgyygngf afpvavatae elsknpfgya lelvrkakad vteeymrsvs slmvikgrph
361 ftvvraylvs dlrragfeev dfgwgnaiyg gaakggvgai pgvasfyipf tnkkgengvv
421 vpfclpapam erfvkeldgm lkddqtvsaq tkskfivssl

SEQ ID NO:53
GI:225454593, Protein name: benzyl alcohol O-benzoyltransferase [Vitis vinifera]

1 mapppslvfs vrrskpelva pakptphefk plsdiddqeg lrfqipviqf ykkvpsmhgr
61 dpakvikdav aralvfyypf agrlreeagr klvvectgeg ivfieadadv tleqfgdalq

```
      121 ppfpgleeli ydapgsggvl nsplliqvt rlqcggfifg lrlnhtmsda
aglvqfmsav
      181 gemargasap sippvwrrdl lnardpprvt rthheydeva dtkgtiipld
dmehrsfffg
      241 ptefaalrrl lsphlrtcst felltaclwr crtialrpdp eeevrvlciv
narsrlqppl
      301 pagyygnvfg fpvalssagk lcrnpleyal dlvkgaknsv dqeymksvad
lmvstgrrhf
      361 tvvrsylvsd ltragfgdvd fgwgkavygg aakggvgaip gvasfyipfr
nhkgedgivv
      421 pfclpaaame ifvkelnsll keehplpsnk sstfiisal
```

SEQ ID NO:54

GI:52139953, Protein name: alcohol acyl transferase (MpAAT1) [Malus x domestica]

```
        1 mmsfsvlqvk rlqpelitpa kstpqetkfl sdiddqeslr vqipiimcyk
dnpslnknrn
       61 pvkaireals ralvyyypla grlregpnrk lvvdcngegi lfveasadvt
leqlgdkilp
      121 pcplleefly nfpgsdgiid cpllliqvtc ltcggfilal rlnhtmcdaa
glllfltaia
      181 emargahaps ilpvwerell fardppritc ahheyedvig hsdgsyassn
qsnmvqrsfy
      241 fgakemrvlr kqipphlist cstfdlitac lwkcrtlaln inpkeavrvs
civnargkhn
      301 nvrlplgyyg nafafpaais kaeplcknpl gyalelvkka katmneeylr
svadllvlrg
      361 rpqysstgsy livsdntrvg fgdvnfgwgq pvfagpvkal dlisfyvqhk
nntedgilvp
      421 mclpssamer fqqeleritq epkedicnnl rstsq
```

SEQ ID NO:55

GI:44887628, Protein name: alcohol acyl transferase [Pyrus communis]

```
        1 mmslsvlqvk rlqpelitpa kptpqetkfl sdiddqeglr fqlpvimcyk
dnpslnknrn
       61 pikvikeals ralvyyypla grlregpnrk lmvncngegi lfveasadvt
leqlgdkilp
      121 pcplleeflf nfpgsdgiig cplllvqvtc ltcggfilal rlnhtmcdat
gllmfltait
      181 emgrgadaps ilpvwerell fardppritc ahyeyedvid hsdgsyafsn
qsnmvqrsfy
      241 fgakemrvlr kqipphlist cstfdlitac lwkcrtlvlk inpkqavrvs
civnargkhn
      301 nvhiplgyyg nafafpaavs kaeplcknpl gyalelvkka katmneeylr
svadllvlrg
      361 rpqysstgsy livsdntrag fgdvnfgwgq pvfagpakal dlisfyvqhk
nniedgilvp
      421 mclpssamer fqqeleritt gt
```

SEQ ID NO:56

GI:147801410, Protein name: hypothetical protein VITISV_042062 [Vitis vinifera]

```
        1 masswsplvf svkrcapefv rptnltprev kqlsdiddqe glrfqipvim
fypnnplmkg
       61 kdpvkvirea lgkalvyyyp fagrliegdn rklmvdctge gvlfieadad
ttlenlgdai
      121 qpmcpcfeel lydvpgsggi lgspliliqv trlrcggfif alrlnhtmsd
algliqflna
      181 isemaqglsv psllpiwere llnarnppri trihheyeev tnnkgtlmam
dennlvhrsf
      241 ffgpkeiral rnrlpaslga cstfevltay vwrcrtiafa vdpdevvris
clinmrgkrg
      301 fdlppgyygn afvypasitk agmlcknple yairllkkak aemsqeyiks
vadlmvikgr
      361 psftqpgnyf vsdvtragfg evnfgwgkpv ygglaralsi isfctrfrns
kgeegnvipi
      421 clpppvmerf eqelkrmtke aepvrliksm l
```

SEQ ID NO:57

GI:49798480, Protein name: benzyl alcohol benzoyl transferase [Petunia x hybrida]

```
        1 mdskqsselv ftvrrqepel iapakptpre tkflsdiddq eglrfqipvi
nfyrkdssmg
       61 gkdpvevikk aiaetlvfyy pfagrlregn drklmvdctg egvmfveana
dvtleefgde
      121 lqppfpclee llydvpgsag vlhcpllliq vtrlrcggfi falrlnhtms
dapglvqfmt
      181 avgemargat apstlpvwcr ellnarnppq vtcthheyee vpdtkgtlip
lddmvhrsff
      241 fgptevsalr rfvpphlhnc stfevltaal wrcrtisikp dpeeevrvlc
ivnarsrfnp
      301 qlpsgyygna fafpvavtta eklcknplgy alelvkktks dvteeymksv
adlmvikgrp
      361 hftvvrtylv sdvtragfge vdfgwgkavy ggpakggvga ipgvasfyip
frnkkgengi
      421 vvpiclpgfa mekfvkelds mlkgdaqldn kkyafitpal
```

SEQ ID NO:58

GI:158828372, Protein name: alcohol acyl transferase [Citrus sinensis]

```
        1 mvftfsqgll vtrkapeliv perptprevk qisdiddqes lrfqipllff
ykndpspsmq
       61 grdpvkvire aiskalvfyy plagrlkegy nrklmvecna egvlfieada
nftleqlrdd
      121 vqppcpylnq liydvpgseg ilgcpllliq vtrltcggfi fairfnhtmc
dafglvqflk
      181 aiedmarger sptlfpiwqr lilnarnppq vtcihheyde intnevpsdn
mahksfffsl
      241 kgikalrnql pfqlkdcstf elllaflwkc rtialklqpe eiakvccivn
vrgksyemdi
      301 ppgyygnaft fsavcskaeq lcknpigyav elvkkakaqm neeyirsaad
lmvikgrrik
      361 fstrgnfivs dlrnvglgdv dfgwgkpiya gtagavavis fftkyqnkng
epgilvpicl
      421 pqsamerlqe elkglmiqgs aedlcninqt qifskl
```

SEQ ID NO:59
GI:255552914, Protein name: Taxadien-5-alpha-ol O-acetyltransferase, putative [Ricinus communis]

```
       1 malppppftf avrrsppeli vparptprel kkvsdiddqe glrfqisfvm fyrslpsmkg
      61 rdpveiirka lsealvfyyp fagrliegpn rklivdcnge gilfieadad
itieqlgdsm
     121 qppcpcieel lydvpgssgi igcpllliqi trlacggfvf avrlnhvmsd
svglakffka
     181 tgeiakgacm pslfpvwqre ilsarnppqv thkleeyeei khtddksilt
ldspdmvqra
     241 fffgpkemrs lrrqlpshlr ncssfemlaa clwrcrtiaf dippnevvrl
scimnvrgkk
     301 glqlpdgycg nsfifpavls raehlcknpl gyavelvrks kskmseeyir
stidlmeikg
     361 rphyvtawnl llvdmshvgl advdfgwgnp vyfgptgsfp nismfsrfkn
skgengfvvp
     421 mwlprtvmek fqdeflkmte esaenlndar rqriistl
```

SEQ ID NO:60
GI:10121328, Protein name: alcohol acyltransferase (SAAT) [Fragaria x ananassa]

```
       1 mekievsins khtikpstss tplqpykltl ldqltppayv pivffypitd
hdfnlpqtla
      61 dlrqalsetl tlyyplsgrv knnlyiddfe egvpylearv ncdmtdflrl
rkieclnefv
     121 pikpfsmeai sderypllgv qvnvfdsgia igvsvshkli dggtadcflk
swgavfrgcr
     181 eniihpslse aallfpprdd lpekyvdqme alwfagkkva trrfvfgvka
issiqdeaks
     241 esvpkpsrvh avtgflwkhl iaasraltsg ttstrlsiaa qavnlrtrmn
metvldnatg
     301 nlfwwaqail elshttpeis dlklcdlvnl lngsvkqcng dyfetfkgke
gygrmceyld
     361 fqrtmssmep apdiylfssw tnffnpldfg wgrtswigva gkiesasckf
iilvptqcgs
     421 gieawvnlee ekmamleqdp hflalaspkt li
```

SEQ ID NO:61
GI:374498907, Protein name: alcohol acyl-transferase [Rosa rugosa]

```
       1 mekievsiis rdtikpsaas sslhpyklsi idqftpttyf pviffypitd
pvfnlpqtlt
      61 dlkitvsqtl tlyyplsgri knnlyiddfe agipylearv nchmidflrl
pkiewlnefv
     121 piapyrketi sellpllgiq vnifdsgiai gvsfshkind getancflks
wvaifrgyrn
     181 kiihpnlsqa allfpsrddl sekyvammer wwfgekkvvt rrfvfdtkai
salqhegkse
     241 yvpkpsrvqa ltgflwkhql aatralssgt strfslaiqa vnlrsrmnmk
ttldnaigni
```

301 flwapaflel nyttpessdh klcdlvnllk esvkeynsdy letlkgekgy ggmcdwldlm
361 degssiepal eiysfsswtr mfdqvdfgwg kpfwigvtgk vqttytnstv lvetqcengi
421 eawvtldqkr mamleqdpqf lafasptpgi smassvgid

SEQ ID NO:62
GI:255585363, Protein name: Anthranilate N-benzoyltransferase protein, putative [Ricinus communis]

1 mvtkmqvdii srevikpssp tihhykpfkf plfsqltptt yspviffypt tkpnlnitqt
61 lihlkktlae tltlyypfsg rvvdnlsidh fdegvpffia rvtglvlsdf lknpeielln
121 gflpykpftk etdkgvpqma fqvnvfscgg ivigwssshk lvdgptgaaf ihawatmsrt
181 gslsdvikpn cdeasiffpp rnpfpeehls lmeslwftkg nyiskrfvfd skaiaslrvk
241 argegnekkn mpsrvealsc fiwkccmaas raasgtpkps ilveavnlrt rtkppmskvs
301 igdifwwata vadpslhnke lhelatllde aialydsdym eslqgedgfe tmseycnqlr
361 glfsieepdi faftswsrlg iydmdfgfgn pfwigilgkv gpafrnltvf letrdgkgie
421 awitldeerm allerdpefl anaspnprfs sl

SEQ ID NO:63
GI:380863876, Protein name: BAHD acyltransferase [Erythroxylum coca]

1 mevhivsret vkpsspatlt kkpyklslfd qltpgtytpt iffypknrpn sdttqvlarl
61 krslsetlds yfflsgrtrd nrfidcfdeg vpffeasvsv glsdflkhhe hewlnrlvay
121 rpytkealds pllsiqvsvf acggivigts ashklidalt gsfilktwaa mfrgdvsdgi
181 spqideasmy fptrdsfpqn hlslmeslwf teanyvtrrf vfgaksisai kemakskpes
241 kqsriealsc fiwkhcmsas kavsgspqvs ilveavnlrt rttppmssss igdlfwwata
301 asnnddtkst elpelanllk eaielydtdf tkslqgnegd eaiyqyceql eglfslekpd
361 ifaftswcyv gftklnfgwg epiwvgtvgk agpafrnltv fietrdgkgi eawitldqkr
421 msvlehdpqf lafaslnpki ssl

SEQ ID NO:64
GI:255577416, Protein name: Anthranilate N-benzoyltransferase protein, putative [Ricinus communis]

1 mevhivsrem mkpsspaikh qkpyklclld qltpttyipi iffypmnnlf tkstlahlke

61 slvktlnfyy pfsgrakdnl yidrfeegvp ffeakvncsm syflkhyete slsnlfipsh
121 pfskeidmsi alvavqvsmf tcggiavglc lshklidaat assfvttwas fcrgdpknvi
181 qpdfeqpstf fpsstslpqn ylslmeriwf vkanyitkrf vfdakaiaal rvkakaklea
241 eptriatlsc fiwkcsmaas raisgapkps ilveavnlrq ktkppmkdss tgnlfwwava
301 lasptdtnst elnelvsmls eaiavyksdy thslqgengl kimseyceql egmfsleepd
361 ifgftswskm pvtrpnfgwg epfwvglmak agpefrnftv fidtkdgkgi eawitldear
421 mailqrdpef lafaspnpki ssl

SEQ ID NO:65
GI:359492333, Protein name: PREDICTED: vinorine synthase-like [Vitis vinifera]

1 mevtiisret ikpssptphh lrafklslld qlvpccytqv llfylidgfh gqsietshis
61 trlkdslset lthfyplags igddelqidc ndegvpyfea rvdcnlsefl qepelellnq
121 ffpcdplntp pmaklhlami qvnifnrggi aigvclshki adgvsisafl kawaaiargc
181 feeypsfeak slfpqneslp qdysmvlgkc lirtgkcvtk rvvfdasaia alkakasvdc
241 trvevvsafi wkramaaakq klgfqrssil thavnlrkkt ilslpessmg nlfwiaiteg
301 rvddeaeldl lvdktrkais kiscdfakkl qgeegfavaf ehvkevkaaf eedgvdfygf
361 sswckfevye gdfgwgrpiw vssfsgkgsv yknliffmdt rcgngieewv tldeeelgil
421 ecdpeflsfg smdpsplkla hfgqv

SEQ ID NO:66
GI:323331427, Protein name: Atf1p [Saccharomyces cerevisiae AWRI796]

1 mdlwkrlfea nptkirdkki knghfisitn tinlsalmne ideknqapvq qeclkemiqn
61 gharrmgsve dlyvalnrqn lyrnfctyge lsdyctrdql tlalreiclk nptllhivlp
121 trwpnhenyy rsseyysrph pvhdyisvlq elklsgvvln eqpeysavmk qileefknsk
181 gsytakifkl tttltipyfg ptgpswrlic lpeehtekwk kfifvsnhcm sdgrssihff
241 hdlrdelnni ktppkkldyi fkyeedyqll rklpepiekv idfrppylfi pksllsgfiy
301 nhlrfsskgv cmrmddvekt ddvvteiini sptefqaika niksniqgkc titpflhvcw
361 fvslhrwgkf fkplnfewlt difipadcrs qlpdddemrq myryganvgf idftpwisef
421 dmndnkenfw pliehyhevi sealrnkkhl hglgfniqgf vqkyvnidkv mcdraigkrr
481 ggtllsnvgl fnqleepdak ysicdlafgq fqgswhqafs lgvcstnvkg mnivvastkn
541 vvgsqeslee lcsiykalll gp

SEQ ID NO:67
GI:34485580, Protein name: lager alcohol acetyltransferase I [Saccharomyces pastorianus]

```
        1 meteesqfss itkiinpktl mntysektsl vqdeclvkmi qnghsrrmgs
vedlyaalnr
       61 qklyrnfsty selndyctkd qlalalrnic lknptllhiv lparwpdhkk
yylsseyysq
      121 prpkhdyisv lpelkldgvi lneqpehnal mkqileefan sngsytakif
klttaltipy
      181 tgptsptwrl iclpeeddtn kwkkfifvsn hcmcdgrssi hffqdlrdel
nniktlpkkl
      241 dyifeyekdy qllrklpepi enmidfrppy lfipksllsg fiyshlrfss
kgvctrmdei
      301 eksdeivtei inispsefqk irtkiklnip gkctitpfle vcwfvtlhkw
gkffkplkfe
      361 wltdvfipad crsllpedee vramyrygan vgfvdftpwi skfnmndske
nfwpliahyh
      421 evisgaikdk khlnglgfni qslvqkyvni dkvmrdralg ksrggtllsn
vgmfhqseet
      481 ehkyrirdla fgqfqgswhq afslgvsstn vkgmniliss tknvvgsqel
leelcamyka
      541 lllnp
```

SEQ ID NO:68
GI:365758173, Protein name: Atf1p [Saccharomyces cerevisiae x Saccharomyces kudriavzevii VIN7]

```
        1 miqngharrm gsvedlyval nrqnlyrnfs ayaelsdycs kdqltlalrn
iclknptllh
       61 ivlptrwpdh enyylsseyy shphpkhdyi svlpelkldg viineqpeng
kivrqileef
      121 rnsngtynak ifklttalti pyfgptspnw rliclpeeht dkwkkfifvs
nhcmsdgrss
      181 ihffhdlrae lndiktppkk ldylfkyend yqllrklpep iekvidfrpp
ylfipkslls
      241 gfiynhlrfa srgictrmdd meksddvvae iitispselq eirtkiksni
qgkctltpfl
      301 qvcwfvslhq wgkffkplnf ewltdifipa dcrpqlpdde evrqmyryga
nvgfvdftpw
      361 icesnmnenk enfwpliehy hqvisgalrd nkhlhglgln iqgfvqkyvn
idkamcdrai
      421 gkarggtlls nvgmfkqlds sncnysiktw llgnfkghgt khfhwvfvrl m
```

SEQ ID NO:69
GI:255712859, Protein name: KLTH0C11440p [Lachancea thermotolerans]

```
        1 mdslkergha rplghlenyf sitqrqklya nfsmycelsk pcspkqlaya
lrsiclqnpi
       61 lvhqvlpkhw pnhleyyasd eflaqptlqh edmrlldnvl lsdivmneqe
eygtvvseai
```

```
      121 eefsqnggqy skkifdiiad iripygdplk pnwrllcfpe gesnlwrkfi
yitnhcssdg
      181 rsaanlmrdl seqlnhvpet lpdsdiifny ssdyeglrkl pdpienridy
kppisyllql
      241 lsssyvrdyl gyyskgplvt ridevgenkt yysyflnfsa eqmktikqkl
ksrlpgctmt
      301 pflqacwlts myksgrvfsk smrewffdvv itmntaqmlp ddpelrsmyk
ygsnvggtry
      361 nylissfnvg edkdafwslv dyyqgvfnsa mekkhylfpl galmldslre
ksnmdkvimd
      421 dllgkprqgv ilsnvgyfqq kketdgyyvr dlvfaqslgs lrhtfvcnsc
ttdvggmniv
      481 acaaqgsvas ehdwadvcel fkeqtlal
```

SEQ ID NO:70
GI:156847986, Protein name: hypothetical protein Kpol_2002p89 [Vanderwaltozyma polyspora DSM 70294]

```
        1 meeyapfitq elvdrgharr mgqlenyfal lqrqnlyknf nvygeinepi
dkfqlgtafr
       61 qmllkypilm hvivprkyph heeyyasdey lnnpqpindy ikvmenidle
dillnsqpey
      121 eaivgklldq yksdgykytn rmieiigdis ipicdqtkpn wrllclptke
sdkkwhafvy
      181 isnhcaadgm tsmnffhdiv nglndksset vtevngrmnl vnyakdhkni
skfpkpiter
      241 veyrpslsql pkfmigniar tklnykspca ltttvdkvdm qtfdyilnft
neevgkirkh
      301 ikanthngvt ltpflqtclf vtlyqfgtif qktllewgld svlpvnarky
lpedaelrds
      361 ykygsnvggi hyfnlissfn ikndeaetfw slvdyyhany qkayhngdtf
vgfgllmsdf
      421 ivknknvdkl ikedyvnqkr ggvilsnlgf fpqdtrneyy lndlifaqtf
gsmkftfgls
      481 lcstnvngln igisvvrdaf ndretfekfc khyketiinf anl
```

SEQ ID NO:71
GI:255711342, Protein name: KLTH0B03806p [Lachancea thermotolerans]

```
        1 mttsqadtkl eelekrghar rlgnlenyfa lgqrqdlysn fgmfceldra
csenelaeal
       61 rgmcleypll lhtvlekkea qdvnfyqtse ylskpwpqhd yirvlqrvrf
advllndqee
      121 yaeivnaalk efasnggqys sevfelinkv ripychnsrp nwrimcfpee
gnaqsrewrk
      181 illlsnhcss dgmssanffh dlqdhlnnlp pslpqadvif dysqdhetlg
klpapietqi
      241 syvgpksyfa qlvgnqvlre yfgyksptpp iprvnepggn dfysyflkit
psevaavkkk
      301 lknkldpsct ltpffqacwf aalyksgivf sksfsqqlsn imvamntaql
lpedkqlkkq
      361 yryganvggs hynyqissfn vadkpeafwk lvryyqdvfv dakrkkhfly
plgalmidsi
```

421 yktknidlav tnsilgksrl gtmlsnvgyf pqkaratvgg fhiqdlifaq ttgsfrftfd
481 inlcatdigg lnitacvaeg alptredwkk lcelfktiil es

SEQ ID NO:72
GI:6321616, Protein name: Atf2p [Saccharomyces cerevisiae S288c]

1 mediegyeph itqelidrgh arrmghleny favlsrqkmy snftvyaeln kgvnkrqlml
61 vlkvllqkys tlahtiipkh yphheayyss eeylskpfpq hdfikvishl efddlimnnq
121 peyrevmeki seqfkkddfk vtnrlielis pviiplgnpk rpnwrliclp gkdtdgfetw
181 knfvyvtnhc gsdgvsgsnf fkdlallfck ieekgfdyde efiedqviid ydrdyteisk
241 lpkpitdrid ykpaltslpk ffltttfiyeh cnfktssest ltaryspssn anasynyllh
301 fstkqveqir aqikknvhdg ctltpfiqac flvalyrldk lftkslleyg fdvaipsnar
361 rflpndeelr dsykygsnvg gshyayliss fdipegdndk fwslveyyyd rflesydngd
421 hliglgvlql dfivenknid sllansylhq qrggaiisnt glvsqdttkp yyvrdlifsq
481 sagalrfafg lnvcstnvng mnmdmsvvqg tlrdrgewes fcklfyqtig efasl

SEQ ID NO:73
GI:156847986, Protein name: hypothetical protein Kpol_2002p89 [Vanderwaltozyma polyspora DSM 70294]

1 meeyapfitq elvdrgharr mgqlenyfal lqrqnlyknf nvygeinepi dkfqlgtafr
61 qmllkypilm hvivprkyph heeyyasdey lnnpqpindy ikvmenidle dillnsqpey
121 eaivgkslldq yksdgykytn rmieiigdis ipicdqtkpn wrllclptke sdkkwhafvy
181 isnhcaadgm tsmnffhdiv nglndksset vtevngrmnl vnyakdhkni skfpkpiter
241 veyrpslsql pkfmigniar tklnykspca ltttvdkvdm qtfdyilnft neevgkirkh
301 ikanthngvt ltpflqtclf vtlyqfgtif qktllewgld svlpvnarky lpedaelrds
361 ykygsnvggi hyfnlissfn ikndeaetfw slvdyyhany qkayhngdtf vgfgllmsdf
421 ivknknvdkl ikedyvnqkr ggvilsnlgf fpqdtrneyy lndlifaqtf gsmkftfgls
481 lcstnvngln igisvvrdaf ndretfekfc khyketiinf anl

SEQ ID NO:74
GI:50286475, Protein name: hypothetical protein [Candida glabrata CBS 138]

1 mapntksieq pliskakisg kgpdgfaiee sllerghsrr mghlenyfai mqrqklytnf

```
       61 nmygelnkev treqlavair qillrhpimm qaiipkkfpe heeyytsddy
yntpfpendf
      121 lrvitskikl sdiiineqse dygeiidmil seykkngykf daymqelign
ivipignpnk
      181 pnwrllclps aegggaqwkk fvyisnhccs daisavnlfq diaenvslie
qnswavpyad
      241 dvivdyeqdv adiaklpapi terveyrppl sklpkimlvs flktalnfks
daletrcnde
      301 ysgepetsav qmgdvcydsi lnytceevav irdrikhnvh gkctvtpfiq
aaffvamhqs
      361 rkllgqkqgf kewmsewgvd matpsstrry lpedpevrdm ykygsnvggi
hylymisgmk
      421 vereetekfw slveyyhdil lashsngdqt vglgtlmldv ivdkknvdkl
irdeylyqkr
      481 ggvimsnagy fhqdpaqayh vtdlvfgqrp galkfsfgvn vvstniggmn
lnvgmvrrtl
      541 rdraefrefi gildrvirdf tgln
```

SEQ ID NO:75
GI:367002213, Protein name: hypothetical protein TPHA_0E03170 [Tetrapisispora phaffii CBS 4417]

```
       1 mslealsfde ykpyiteeli ergharrmgh lqdyfaiiqr qklynnfniy celnekvnkv
       61 qlshafremf lqypalieyi vpkfypkhea yyrseeylsk pcpihdyirv
lnevnindii
      121 mneqdeyksi ttkisdifvk ndykfsneis emvstikiai cdpkkpnwri
iclpsktsst
      181 ewkdfilvsn hfdsdgtsav nffedltnil skqanvendt ivigndinii
nyskdyklis
      241 klpipiteri sytptlssip kfivgnickt klqytsdggd tpaefvsedp
ltydylinfs
      301 seevakmkkt iknclynsvt ltpfiqacff vamykynkil nlnnwwqwgv
dcalatnarr
      361 llpddpetrd lyrygsnvgg thyfnlisqf ninefeydkf fklvdyyhkn
yqnsyrngde
      421 lvgfgvlfsd liinntnmdk tikddytnhk rggllfsnvg yrnedltkkv
hvnniifsqs
      481 pgcmkftfgl nlistdkcgm nilmngvrgs vksrenfedf crffrktven fakl
```

SEQ ID NO:76
GI:366987729, Protein name: hypothetical protein NCAS_0A06920 [Naumovozyma castellii CBS 4309]

```
       1 mtqdqvtlde ykpyiadeli ergharrmgh lenyfallqr qklytnfsiy
gelnkevkdv
       61 dltralrsii fknpilahti vpkkypdqep fyqseeylna pypehdfikv
lpklslsdil
      121 ineqeefrei vddiltqfke angvitpdim kavayviipi cdpsrpnwrl
frlsptkffy
      181 isnhctsdai sgvnifqdic telsqndeep frddlqifny eedwesfhki
yipitdiiey
      241 rpaltslpki iasalvkgfl nyrnwptelt stndkgipfd fniitftnde
vnsiretvkk
```

```
      301 ynctftpflq acwfvamfnn gkifhmdswr ewgldvaips nsrrfladee
lkdiykygsn
      361 vgglhythli ssfniqldek ekfwdlvqyy qdgytksyen gdhfsglgll
mmdglvkrqn
      421 idkvissdyl hktragvlfs nagffpqdrt qayhvndllf tqsqgamkfs
fglniattni
      481 ggmniainva qgtfddeegi idlsqdfyrn iksfsnia
```

SEQ ID NO:77
GI:372463540, Protein name: hypothetical protein KAFR_0D01730 [Kazachstania africana CBS 2517]

```
        1 mglstkvees vrevqsqsda ssialledpv aeydipqeli drgharrmgh
lenyfamlqr
       61 qelysnfavy lkmnksvsrn dlkhalrevi lensvlahti vpkyypdhea
fyksekylnv
      121 pypkhdfmki lpslsledii indqseytev vnsiidqfvk dngkitnkls
eivsnicipi
      181 ydqsrpnwrl lclpdntdey snfvyisnhc csdgtsginl fqdlvkslng
kkspemtspd
      241 sliynyekdf dkisklpaai tdrvdyrpal wklpqfmlst lgkvffsyks
papvstkinm
      301 skpqpsfhni lnftpdelnk iriaikknac tmtsflqtcl fitlkehgif
anrkwnefgf
      361 ditvpsntrk dlpeelvtsq ykygsnvggl hysflissfi aenfwklcsy
ysavlkqadf
      421 lrplgtimld fvvnkqnids misdsylnkk rggiilsnvg yfeqnddece
ildlmlmqnv
      481 gglnfsyavn icstnlggmn iclsivegtl kdrddfnafc delkttvrqf cdin
```

SEQ ID NO:78
GI:26991090, Protein name: bkdA1 gene product [Pseudomonas putida KT2440]

```
        1 mneyaplrlh vpeptgrpgc qtdfsylrln dagqarkpai dvdaadtadl
syslvrvlde
       61 qgdaqgpwae didpqilrqg mramlktrif dsrmvvaqrq kkmsfymqsl
geeaigsgqa
      121 lalnrtdmcf ptyrqqsilm ardvslvemi cqllsnerdp lkgrqlpimy
svreagffti
      181 sgnlatqfvq avgwamasai kgdtkiasaw igdgataesd fhtaltfahv
yrapvilnvv
      241 nnqwaistfq aiaggesttf agrgvgcgia slrvdgndfv avyaasrwaa
erarrglgps
      301 liewvtyrag phstsddpsk yrpaddwshf plgdpiarlk qhlikighws
eeehqavtae
      361 leaaviaaqk eaeqygtlan ghipsaasmf edvykempdh lrrqrqelgv
```

SEQ ID NO:79
GI:26991091, Protein name: bkdA2 gene product [Pseudomonas putida KT2440]

```
        1 matttmtmiq alrsamdvml erddnvvvyg qdvgyfggvf rcteglqnky
gksrvfdapi
```

```
       61 sesgivgtav gmgayglrpv veiqfadyfy pasdqivsel arlryrsage
fiapltlrmp
      121 cgggiyggqt hsqspeamft qvcglrtvmp snpydakgll iasiecddpv
iflepkrlyn
      181 gpfdghhdrp vtpwskhphs avpdgyytvp ldkaaitrpg ndvtvltygt
tvyvaqvaae
      241 esgvdaevid lrslwpldld tivesvkktg rcvvvheatr tcgfgaelvs
lvqehcfhhl
      301 eapiervtgw dtpyphaqew ayfpgpsrvg aalkkvmev
```

SEQ ID NO:80
GI:26991092, Protein name: bkdB gene product [Pseudomonas putida KT2440]

```
        1 mgthvikmpd igegiaqvel vewfvkvgdi iaedqvvadv mtdkatveip
spvsgkvlal
       61 ggqpgevmav gselirieve gsgnhvdvpq pkpveapaap iaakpepqkd
vkpavyqapa
      121 nheaapivpr qpgdkplasp avrkraldag ielryvhgsg pagrilhedl
dafmskpqsn
      181 agqapdgyak rtdseqvpvi glrrkiaqrm qdakrrvahf syveeidvta
lealrqqlns
      241 khgdsrgklt llpflvralv valrdfpqin atyddeaqii trhgavhvgi
atqgdnglmv
      301 pvlrhaeags lwanageisr lanaarnnka sreelsgsti tltslgalgg
ivstpvvntp
      361 evaivgvnrm verpvvidgq ivvrkmmnls ssfdhrvvdg mdaalfiqav
rglleqpacl
      421 fve
```

SEQ ID NO:81

gaaaacgaaagctctctaaGCTGAGCAGGAGAAATTAACTATGGCGCATGATCAGAGCCT

SEQ ID NO:82

agcctttcgttttatttgatgcctctagaGCTCAGCTTACAGGCTGCTCTGGGTGAAATG

SEQ ID NO:83

cgaaagctctctaaGCTGAGCAGGAGAAATTAACTATGAATGAAATCGATGAGAAAAAT
C

SEQ ID NO:84

agcctttcgttttatttgatgcctctagaGCTCAGCTTAAGGGCCTAAAAGGAGAGCTTT

SEQ ID NO:85

cgaaagctctctaaGCTGAGCAGGAGAAATTAACTATGGAAGATATAGAAGGATACGA
AC

SEQ ID NO:86

cctttcgttttatttgatgcctctagaGCTCAGCTTAAAGCGACGCAAATTCGCCGATGG

SEQ ID NO:87

aaacgaaagctctctaaGCTGAGCAGGAGAAATTAACTATGGACAGCAAACAGAGCAGC
G

SEQ ID NO:88

cctttcgttttatttgatgcctctagaGCTCAGCTTAAAGCGCTGGGGTGATGAACGCAT

SEQ ID NO:89

aaacgaaagctctctaaGCTGAGCAGGAGAAATTAACTATGGAGAAAATAGAAGTGAGC
A

SEQ ID NO:90

cctttcgttttatttgatgcctctagaGCTCAGCTTAGATCAGCGTCTTTGGACTCGCCA

SEQ ID NO:91

GGGCCCgcatgcAGGAGAAATTAACTATGAACAACTTTAATCTGCACACCCC

SEQ ID NO:92

GGGCCCtctagaTTAGCGGGCGGCTTCGTATATACGGC