

Table S2. Amino acid alignment of curated KS-domains of bacterial, fungal and animal PKS as well as animal FAS, including putative PKS/FAS from *A. longisetosus*. Sequences will be deposited in the NCBI database, and accession numbers provided upon acceptance of the manuscript.

>AAD43562.2_Fum1p_Fusarium_verticillioides_

-VAIVGMGMRLPGGIHTPDELWGMLVEKRST-RCEIPPTR-FSVDGFHSPSS--KPGSIAMR-HGHFLDDKD-
DLHRLDTSFFSMGMTEVSDIDPQQRMLLEVA YECMQS---SG-----QTNWRGSGNIGCYVGVWGEDW----LDLHSK--DLYDSGTYRVSGGHDF--AI-
SNRISYEDLKGPSFTIKAGCSSLIALHEAVRAIRAGDCDGAIVAGTNLVFSPMTMSVA--MTEQ-----GVL-SPDASCKTFDAN---A-NGYARGEA-INAIFLKP--
LNNALREGDP-IRALVRATSSNSDGKTP-----GMSMPSSSEHEALIRRAYGEVF--LD-PKD----TCFVEAHGTGTSVGDPLEATAIAR-VF----
GGSSDNKLYIGSVKPNLGHSEGASGVSSVMKA-VLALENRTIPPNNIFS--TP-NPKIP--FSEMNMVAVPVDAIPWP-----
RDRPLRVSVNSFGGANAHVILESGIP-----YLGSRSLPNESQ

>AAO62426.1_type_I_polyketide_synthase_Phoma_sp._C2932_

PIAIIIGMCRFPGNATSPEKLWELCAQGRSA-WSSIPKSR-FRQEGFYNPNAE-RVGTSHVV-GGHFLEE---
DPSLFDASFFNLSAEAAKTMDPQFRLQLESVYEAEMES---AGIT---LEHIAGSDTSVYAGACFRDY----HDSLVR--DPDLVPRFLLTGNG-A--
AMSSNRVSHFYDLRGASMTVDTGCSSTLTALHLACQGLRNRESKTSIVTGANVILNPDMPVT--MSSL-----GLL-GPEGKSHTFDAR---A-NGYGRGEG-
IATVVIKR--LDDALRAQDP-IRCIIRGTALNQDGRAT-----LTSPTSQAQSDLIRACYRAAA---LD-PND---TAFLLAAGTGTGTGDAVEIAAAAD-VFGEKRSP--
ERPLWIGSVKTNIGHSEATSGLASVIQAALALEKGLIPPNNIFK----EPNEKLGQVSAAVRVPNSLQKWPSVSG-----
VRRASVNNFGYGGANAHVILESGIP-----GHTPIANGS

>AAR85531.1_polyketide_synthase_Didymella_maydis_

PIAIVGLSFRGPGDATSAENLLRMVAESRES-RSPIPSQK-WNASGHYHPDPS-RQGS-HIVEYGHWFQ---
DVVEFDAPFFNLSA VESAALDPQQRMLLECTYEAFFEN---SGMP--LNKLVGTDTSVFTAVFCTDY----TDMLWR--DPEMVPMYQCTNSG-
ATRANMANRVSYFDFLKGPSITVDTACSGGLTALHLACQSLVTGESTQAVVSGSSLILGPETMVT--MSMM-----RFL-SPDGRCYAFDDR---A-NGYARGEG-
VTVLLKR--LDDALANGDT-IRAVIRGTGRNPDGKTT-----GIAMPSGLAQEALIRSVYAKTG--LD-LLD---TAYIECHGTGTQAGDTTEARAINN-VF---
GPGRQVPLAIGSVKTNIGHLEAASGLAGVLKCILMLENEIILPNRNFK----HANLNIPLEWKLVRPTTVEPWNSMT-----
TRRASVNSFGYGGTNVHAILESADNYMGQRADPQVFAVSAFDPTAGEACAKNLAYVVEERQDMTFLSSLAFTLSDRRT

>AAR90237.1_polyketide_synthase_partial_Botrytis_cinerea_

----TRGGNFKG-----DLAAFDPSPFFSITAEAKAMDPOHRLLETTYQALEN---AGIP---
LSKASGTKTGVYTGSMADY----RFTSLK--DPEDLPKYAVTGTA-M--
SLLANRLSWFFNLKGGPSINLDSACSSSLMALDIACQGLRNGDSSMAIVAGSCLISLETWIS--LCNM-----GFL-SPDRCYSFDNR---A-NGYARSEG-
VGVVVIKK--LSDALKDNDT-IRAVIRATGNSNDGHTP-----GITQPSREAQTRLIEETIYKGG--LD-PAK---TRYFEAHGTGTPLGDPGIEAGAIGS-VFREYRSA--
TEPLYVGALKSNIGHLEGGSGIAGLIKTVLVLEKGIIPNANFE-QA-NSNID--AEFFHLRFPTQAPWP--SQ---G-----
LRRASVNSFGFGGNSHCVNRATASFKFSVDPQLLVFSAVVDKDGIRRVAEAYRSYF-AGHALSFLRDLAYTLVSRRT

>AAR90238.1_polyketide_synthase_Botrytis_cinerea_

PIAIVGISCRFPAGANSPEELWLSISQKSA-WSDVPEDR-FNWKSFHLPSSD-VVGTINSR-GGHFIDQ---
DIRTFDAGFFGIPPAEANAMDPQHRLQLETA YEALEN---AGIS---LEKVRGSSTSVYVAIFNRDY----DRMMFK--DTNDIAKYHLLGSG-E--
AIASNRISYFFDLKGGPSMTVDTGCSGSLVALHQACQGLRSGDMDALVGGTSLILSPDTMVP--MSRM-----NVL-DPSGKSFVDDR---G-VGYGRGEG-
VATIVLKR--LKDALNAGDH-VRAVIRNTGINQDGKTS-----GIALPSQVAQALANHVFKQVG--LD-PCK---INVEAHGTGTIAGDLAETKSIAN-VF---
CTERKKTLYIGSIKSNIGHLESASGAAGLLKAILVLEKGLIPPVNLNLS---NHKKGLDLEQSNIVVPSKIEKLSVDEDEG-----
KSRIAINSFGYGGTNAHAILETAPLSQGSMAKLFSLSAKSKASLIENIKLRWASEFKATNQLENLSYTLNQRRS

>AAR90239.1_polyketide_synthase_Botrytis_cinerea_

PVAIIIGSSCRFTGA-SNTSKLWELLKEPRDV-LSKIPEER-FLAEGFYHQDQG-HHGTSNVL-HSYLLDE--
NPLAFDASFFHIHNREAEICDPQQRLLLENYETIES---ACYP--METIRGSDTGVFVGLMCADY----YDVQMR--DPETLPQYFSTGTA-R--
SIVSNRISYFFDWKGPSMTVDTACSSSLVAVHQAVSALRNGECSAV AAGVNLIFGPEMFNG--EANL-----KML-SPTGTCKMWDAS---A-DGYARREG-
CGSVMLKL--LEDAIRDGDR-IESVIRETGVNSDGRM-----GITMPSASSQEKLKETYRRAG--LD-PSKESDRQCFFEAHGTGTLAGDRQEAEAISR-
AFDLYQTSQDNLPLSVGSIKTVGHLEGCAGIAGLLKASLALQHSFIPNMHFQ-EL-NPEIE--PFYQNLKVVTSLQWPW--LI---PDNT----
PRRASINSFGFGGTNAHAILESYSAEQNTINTIVPLLLSASSEHSLVELTKKYLDHL-KTHPFQNLQDICWTALSCRS

>AAR90240.1_polyketide_synthase_Botrytis_cinerea_

PIAIIIRGRCRLAGGCQSPSELWNFLQTPYDV-SQEFFPDR-NSASRHSSTSTRGYFLSQ-----DVREFDASFFSLSPLEAQAMDPOHRLLETTYEALIEE--
AGIP---AETLRGSDTAVYTGVMFHDIY----LSLSSQ--DHMAIPKYHITGTA-P--
NKASNRISYFFDWKGPSMTVDTACSSSLVALDHAVVQQLRSGSSTLVAAGANLLLDGRPFIG--FNNM-----GML-SPTGSCCKMWDTE---A-DGYARREG-
ILAMLLKP--LRLALADGDN-IQCVIRETGVNHNHGRS-----GITLPSASAQTSLRIDVYHRAG--LD-PTNPSDRPQYIEAHGTGTQAGDPLEAEALAA-
AFSLTSSQDEAHMLVGSIKTVIGHTEGAAGLAGVLKASLAIHQHGIIPNLGFQ-QL-NKKVA--PYCTNMDVVTSVQWPW--AM---ASNT----
PRRVINSFGFGGANAHVILESVPLLSRSDSVLPYVFAAASEQSLISMLKRYENYL-QENPSINPNELTTTLASHRS

>AAR90241.1_polyketide_synthase_Botrytis_cinerea_

PIAIIIGMACRFPGGNSPSKLDLIKSPRNL-SKRVPDER-FNSEAFFHTNGS-YHGATDSR-EAYFLEE--
DVALFDNAFFNIQPGEAEEVDPQQRLLMETVYDSLCA---GGQT---IEGLRGSNTGIYVGMCCDDW-----AQAINR--DWESTMTYAATGQS-R--
AIVSNRISYFFDWKGPSMTVDTACSSSLVAVHQVTSRNGECPVVAAGVNLILGPMWIA--ESKL-----HML-SPTGTCKMWDDES---A-DGYARREG-
IASVVMKR--LSDALRDGDP-IECVIRGTGVNQDGK--TP--GLTMPNGKAQADLIRDYQYRAG--LD-
IHDPRDRPQFFHAHGTGTQAGDPQESQAIDSAFFSGPDKK--LETMAVGSIKTIIGHTEGTAGLASLIGSVMAIKHGVFPNLFHQ-NL-SPKVA--
PFYNHLHIPPTATPWP--EL---PSGV---PRRISCNSFGFGGLNAHAIIIESYESEATLASVFTPLTISAASALKATLSDIRSYL-EKSPDVNMHDLAHTLQSRRS

>AAR90242.1_polyketide_synthase__Botrytis_cinerea_

PIAVIGTGRCPGGASSPSKLWNLHHPYDL-TQKVPSSR-FNIKAFYHPNGE-HHGTTNAT-KSYFLNE---
DPTTFDAPFFNINPREAEALDPQQRLLLETVYEALAE---AGLS---IEEMQGTSTAVYVGLMCADY----FDVLMR--DIEDIPQYLATGTA-R--
SIMSNRISYFFDWKGPSTMTIDTACSSSLVAVHNAISTLRSGQSRATAAAGANLIFGPEMYIG--ESNL-----HML-SPTGRSQMWDSR---A-DGYARGEG-
TAAIVLKT--LKNALKEDDD-IEYIIRETGVNSDGKSK-----GITMPLAASQADLIRQTYARAG---LD-
CTKPSERCQYFEAHGTGTPAGDPVVEAEISSAFFPQRSIDLNSEPLHVSGIKTVIGHLEGAAGLAGIAGLALKEKTIIPPNLHFQ-SL-NSAIE--
PFYGNLNVPTAPLPWP--AV---EG-----PLRASVNSFGFGGTNAHAILESVEVPSLESTALIPFTISAISEDCLIQNTNFSYDI-EEHEGVNLDLGYSLGRSN

>AAR90244.1_polyketide_synthase__Botrytis_cinerea_

PIAIVGISCRPLGNVSTPDEFWELCSRARS-GWSEIPKER-FDTASFYHPNPG-KAGC-FNAAGGNFLKE---
DVGLFDAPFFSLTAQEATSMDPQQRILLECTFEALES---AGIP---KHEIVGKDVGVFVGGSFSEY----ESASFV--DTDSVPMYQATGKLF--
LSNRISHFFDLRGPSTMTIDTACSSSLVALHQACQSIRNGECKSAITGGCHLNMLPENWISIPFCEIPSNKYRLF-SDEGRSFSFDSR---G-TGYGRGEG-
CGLVILKP--LSQAQKQGF-IRAVVQNSVANQDGKTP-----GITMPLAASQADLIRQTYARAG---LD-
VFGEGRNA--RNPLFIGSVKSNIGHLEAASGIISVIKTAMMLERGFILPNHDFK---TPNENIPFSKWHLKVPISQRPWP-----
RAKKFASVNNFVGGGTNAHVVLERAPFSEKALQDRRMIALSANDKGALEALMKNIGIYLERPEFGLMSNVA YTLGQRR-

>AAR90247.1_polyketide_synthase__Botrytis_cinerea_

PIAVVGMSCRLSGDASDTQKLWELLKGRSA-WSKVPKDR-FNQEAFHDPSEAGKPGR-TSTDGGHFLKD---
DIKAFDAPFFNINPIEATAMDPQQRLLLEIAYEAFEN---AGLT---LEQLSGSNTGVYVGGWASDY----QEMLLR--DIDFPPIYQASVGV-A--
AISSNRISYCFNLHGPSLTLDTGCSASLVALHQAVHSLRAGETDKCFVAVGNLQLDPQRYGY--QNKL-----SMF-SKQGKSFTFDHRAKTA-SGYGRGEG-
CSGVVLMF--LSQAQKQGF-IRAVVQNSVANQDGKTP-----GITMPLAASQADLIRQTYARAG---LD-
ESDSPILIGSLKANIGHTESAAGLTGLIKA VLMLEHNMIPPQVNF-KA-NPEID--LDALNLRIPITLESRP-----
LKRISVNSFGYGGTNAHVVDAAAREEDASRAKERLFLVLSAASEKSCQDMSSKVAKYLESKADSTLLSRLAYTLRRSV

>AAR90260.1_polyketide_synthase__Bipolaris_maydis_

PLAIVGLATRFPPQEAYNTEQLWQFLLAKRCA-HTPIPEGR--MGPGHYHPDPE--HGGTHAVAGGHFLAE---
DPA YFDSFFGITKGEAMSLDPQQRV VLENVYLALEN---SGFT---LEQVAGSNTSVYVSGFNHHDH----LAILNS--DPETTLRHRVTGLT-N--
SMHSNRVSWFFDLKGPSTMTIDTACSSSMAALHLGQSLRTGESDMSIITGVITLNYPGDVNG--MSHQ-----GFL-SPDGRCSFDFHR---A-NGFARGEG-
AGTVILKP--LDALRDGDTP-IRAVVLRATATNEDGHTP-----GILTLPSSDAQERLIRRTYASAG---LN-FDD---TTLVEAHGTGTQGDIAEARGIAQ-AF-----
RKDKPL YLGSV KASVGHLEGAAGVAGIISVLALENGVIPPQANFE-KA-NPKIP--FQKWNLSIADKAVPWP-----
TQGLRRVNSVSGYGGTNAHVVDAAAREEDASRAKERLFLVLSAASEKSCQDMSSKVAKYLESKADSTLLSRLAYTLRRSV

>AAR90261.1_polyketide_synthase__partial__Bipolaris_maydis_

PIAIIAGFRGPGDARDPEAFYRMLIEGRSA-RTEIPKDR-YNVDAFYHPDPE-RLGSIQQR-YAHFLQ---
DFKAFDAPFFSITPKEAKAMDPTHRILLEAAYEGFEN---AGLT---LDQVSGTQTSCYIGTFTADF----PNLQAR--DNEGPSIYHATGMS-S--
SLASNRISYFFDLHGPSLTLDTACSSSLTAFHLACQSLRTGESEMSVVGANLMMFGPDMISL--LGAA-----KIL-SPEGKSKMWDAN---A-DGFARGEG-
FGTVILKP--LDALRDGDTP-IRAVVLRATATNEDGHTP-----GILTLPSSDAQERLIRRTYASAG---LN-FDD---TTLVEAHGTGTQGDIAEARGIAQ-AF-----
GRKSSLYVGSVKTNIHLEGAAGVAGVIKAAALVERGLIPQNLWFE-KL-NPEIN---LPENVEIPLKLTWPWSDG-----
PRRASINSFGYGGANAHVILEDTASLHDLQPTPKLFTISANDQEGVRRNVERLQRYLSAKTSAAFSLDLAFTLSAKRS

>AAR90262.1_polyketide_synthase__Bipolaris_maydis_

PIAIVGMSFRGPGSANNIENLFKMICERES-RTAIPKSR-WNNKAFYHPNFQ-RHGSHNVE-YGHFFHD---
DISKFDAPFFNMTKEEAALDPAQRLLLESTYEALEN---GGIP---LEKIVGTKTSVFGVGFATDY----TDLLTR--DPESVPMYQCTNSG-
QSRAMISNRISYFFDLHGPSLTLDTACSSSLVALHLACQSLRAGEAKSAIAAGVNVVNLNHEFMTT--MSMM-----KFL-SPDGRCYAFDER---G-NGYGRGEG-
FGTVILKP--LDALRDGDTP-IRAVVLRATATNEDGHTP-----GILTLPSSDAQERLIRRTYASAG---LN-FDD---TTLVEAHGTGTQGDIAEARGIAQ-AF-----
GAPEDRPLIIGSIKSNLGHLEGASGIAAVKAVLMLEQEVILPNQNF-KP-NPRIP--FVDWKLVRATNVQPWD--SS---G-----
PLRVNSVNSFGYGGANAHVILEDTASLHDLQPTPKLFTISANDQEGVRRNVERLQRYLSAKTSAAFSLDLAFTLSAKRS

>AAR90263.1_polyketide_synthase__Bipolaris_maydis_

PIAIIGMNMKFGDVAQSFVKLIVSARNV-SKEVPADR-FKI-AFYHPDPN-RLDSIRIR-NAHFMT---
DPRAFDAPFFNMSHAEASVLDPQQRGLLEGAYRTFEN---AGIP---MESLRTPTSVYCASFSRDG----ETITGR--DFASQSRYHATANG-S--
SMLSNRISHFFDLGAPSLTVDTACSSGLVALHLGVSILTGESTMSLVCGANTFITPESQAL-ALSNG-----GFL-SVDGKSYSDAK---A-NGYARGEG-
FGTVILKP--LDALRDGDTP-IRAVVLRATATNEDGHTP-----GILTLPSSDAQERLIRRTYASAG---LN-FDD---TTLVEAHGTGTQGDIAEARGIAQ-AF-----
RDGRSLDRPLYIGSVKASIGHLEGASGLAGVIKAVLSLEKAVIPPIAMFE-KV-NPAID--AADLQLAFPKEAIPWP--AS---E-----
VRRASVNSFGYGGANAHVILEDTASLHDLQPTPKLFTISANDQEGVRRNVERLQRYLSAKTSAAFSLDLAFTLSAKRS

>AAR90264.1_polyketide_synthase__Bipolaris_maydis_

PIAVVGFQFKFPQDVTNAETLWKLIERST-MTEIPKNR-WNIDGFYKENGH-RPGTVKNR-GGHFLSD---
DPRAFDAPFFSIQPAEAEACMDPQQRLLLESTYHALEN---AGIT---MQDAVGTRTSVHVGCLLQEY----SQISQR--DAQMPGDYRIVGSSGL--
AMLSNRISYFFDFGSPSMTVDTACSSGLVALHLGVSILTGESTMSLVCGANTFITPESQAL-ALSNG-----GFL-SVDGKSYSDAK---A-NGYARGEG-
FGTVILKP--LDALRDGDTP-IRAVVLRATATNEDGHTP-----GILTLPSSDAQERLIRRTYASAG---LN-FDD---TTLVEAHGTGTQGDIAEARGIAQ-AF-----
TPEDPIFVGALKSNMGHPGASGIAGVIKTLVLEKGIHPNVYPE-RI-NPAVT--AAGPNLRFPLEPVTWP-----
TSGVRRASVNSFGYGGTNAHVVIDDALS-----FLREQG-----

>AAR90265.1_polyketide_synthase__Bipolaris_maydis_

PIAIVIGLDAKPCDGDSSVQFFDFLIAGRSA-RKVPVSDR-YNADAFWHPDHH-RDGIHASK--QGHFMNS--
SVKAFDAPFFGITPAEAAALDPAQRLLLESTYHALEN---AGYT---LQELGNTGVYVGSFVYDY--RD-VMIK----DTDVALTYSGTGTV-P--
STLAGRVAWFFDFRGPFTVDTACSSSVALHQAIVIGLKSRECNLALACGTNVLSPFEGQQ--LNGL-----GVL-SPQGASKSFDKE---A-NGYGRGEG-
ISVVVLKR--MSDAIRDGDTP-IRAVIRNSGIGHDGK--GA--PLPAPVRESQVNLVRRCYAQAK--ID-PSE---TRLFEAHGTGTNAGDPTEAGAIISD-IF---
SRSEEEPIYIGALKSNIGHTEGNSVAFSIKAVLTLESIGIIPANAHFK-EV-NHAIP--KKWHFKFPTVATPYP--KT---PSG-----
VRRVNSVNSFGISGTNAHVVIDARHNGTAFAPQLFVLSAFDQDGVSRKCKAYAEYL--PKMITS-LYNLSYTLARKRS

>AAR90267.1_polyketide_synthase__Bipolaris_maydis_

PIAICGMALRLPGALKTPAQWFVTLTEKKDA-RAPIPFAR-FDAEAFYSASG--KSGYFNSK--
NGY YLDDSAEVLGALDTSLFRMSQESERMDPQAKILLELARECFES---AGET----DWRGKDIGTYVGSFGNDW--LE-MAAK---DRLDKNMYKVSQYS-D--
FLLSNRSLYEDYDLRGPSTIRTACSASLMGLHEACLAIIRNGDCSAAALVGGSNLFWSPDTMAD--MSEQ----GVT-SPNASCRSFDAD---A-DGYARAEA-
VNLVIYKP--LSAAIKHGNP-IRAIIRGSSLNADGK--TP---GPSMPSSSSQAALIRRAYQNAG--IP-ESE-IIRTAFFVECHATGTATGDPIEATAVGN-VF---G---
NGGVYIGSVKPNVGHSEGASGITSIIKAVLALENRVIPPNIKFE-TP-NPKIP--FLEKDLKVPDCLGWPF-----KDK---
LERVSVNFGIGGANAHFILDASAASFLESKWKGLFLITASTSESLEMQTRNLRDYA--LSN-TKAEHGSYTLACRRE

>AAR90269.1_polyketide_synthase__Bipolaris_maydis_

PIAIVGMGMRLPGNCHNSEAFWDLINQRDG-MIDIPSSR-WNSEGFYDPHG--RPGTTKVN-KGNFLGSI--
DPADFDSFFSMAAAQIAK VDPQHRVLETTYEALEN---AG----ESNFRGKKGVVYVGMFADDY----VEMQSK--DSEPHEFLSLTGHL-D--
LFGSNRVSHEFDWTPGSMITKTGCSASLVCLDQAVKALRAGDCDAIVGGANLIMSPALSCA--LVAQ----GVN-SADGICRSFADK---A-TGYGRGEA-
VSSLVVKR--LSDALADGNP-IRAIIRSTACNDDGKTP-----GITQPNVAHEALIRAAVYRTAGISEED-LNK-----TGFFECHGTGTAVGDPIEVAVAR-VF-----
GKDGMIIGSVKSNIGHSEGASGNTSVIKAILSMHQIIPNVNFE-TP-NPKIP--WKEANLRVPTCEMKWP--SD--R-----
LERASVNSFGIGGTNAHVILESAASTEQKPRLSLLFTARSEISLQESINKHADIYI-QKHGSSRLGDIA YTLGTRRE

>AAR90270.1_polyketide_synthase__partial__Bipolaris_maydis_

PIAIVGSACRFAGGANSPSKLWDLRNPDKI-RSNITDKR-FNANGFYHPDGS-HHGHMNVL-QSYLLEE--
DTRLFDAEFFGINPVEAKAMDPQQRLLLEVYYESIES--AGLS---IDRLRGSDTAVFAGLMCGDY----EARMLR--DLDQVPTHFATGTS-R--
AVMSNRVSYFFDWHGSPVITIDTACSSSLVAVHHAVQALRSGDASHAAVACGSNLIFGPEMYVI--ESKL-----KML-SPDLSLRMWDK---A-NGYARGEG-
VTAVVLKT--LSQALADGNH-IEVIRETGMSNDGA--TP---GITMPSASAQRDLIRSVYRKAG--LD-PESAEDRPQYIEAHGTGTAGDPIEAEALSTAFF----
GEKMTTPIYTGSIKTVLGHTEGSAGLAALLKVTQAMQNSTVPPNLWFQ-QI-NPKLK--PFYGNLQIPTHALIWP--KP--FGRR---
PKRASINNFVGGGTNAHAIVESYELASSAVTVSTPFVFAASTESELRSNLAAYATYL-DANPQTNTRDLAYTLRERRS

>AAS57290.1_polyketide_synthase__partial__Fusarium_graminearum_

----IGVGCRLPGGANLNDLWKLLESERNG-QTEIPKDR-WNADAWFDAYPD-AKQSMVTK--YGYFLQD--
DISQFQDAKFFGISSAEANMDPQQRLLMTTYEALED---AGIP--VETLRGSNTGVYASIFERSY--DR-MGHK----DLSTIGRTHLNGTG-E--
SDLSNRVSYCFDLRGPCMTIDTGCSGSLVGLHQACQSLRGESELAALVGGSQLVIQPDVLCI--MSGM-----GML-NPDGKSYAFDSR---G-AGYGRGEG-
VATIVLKR--LSDAALADGNH-IEVIRETGMSNDGK--TP---GLNTPSPDEAQAALSRVYQEAQ--LN-PAD----TSFVEAHGTGTAGDPIEAEALSTAFF----
CEGRTDDLYIGSVKTNIGHLEATSGIAGLLKSLILKHGQIPATLNF-KP-KPSLK--LYEKKIKIPSELTKLP--TP---QNG----PPRVSLNSFGYGG-----

>AAS57294.1_polyketide_synthase__partial__Fusarium_graminearum_

----IGTFCRFHGGANTPSKLWDLLEIKRDV-QSSIPPVR-FNVDAFIAVM-D-KNGCTDVK-KAYLWAE--
DTRLFDASFFKINPREAEAMDPQQRLLLEAVYEATE---SGLP---MEDLKGSDTAVYVGCMTGYY----HEMLMR--EPQDMPKYMATGTA-R--
SILSNRISYLFQDWKGPSMTIDTACSSSLVAVYDAVTAALRNGVSRIACAGGVNLIIGPEMMIS--ESKL-----HML-SPTGRSRMWDAS---A-NGYARGEG-
VAAIMMKT--LSQALADGNH-IEVIRETGMSNDGRTN-----GITLPSDEAQAALSRVYQEAQ--LN-PAD----RCQFFEAHGTGTAGDPIEAEALSTAFF----
DGSDIVNEPMYVGSVKTAIHLEGCAAGFAGMIKIVAEVKTGIIPNQLFE-TL-NPAVK--PYTSNLKLPVESQPWP--KL---TEGF---
PRRASVNSFGGGTNVHAIHQFDNSSVNEVICTPLVLSANCELS-----

>AAT28740.1_FUSS__Fusarium_verticillioides_

PIAIIGTSCRFPGGANTPSKLWDLLEIKRDV-QSRIPNDR-FNVDAFYSTNGD-KNGCTDVK-RAYLLSE--
DIRVFDASFFKINPREAEAMDPQQRLLLEAVYEATE---AGLP---MEDLKGSDTAVYVGCMTGDY----HEMLMR--DPQDMPKYMATGTA-R--
SILSNRISYLFQDWKGPSMTIDTACSSSLVAVYDAVTAALRNGVSKIACAGGANLILGPEMMIS--ESKL-----HML-SPTGRSRMWDAS---A-NGYARGEG-
VAAIMMKT--LSQALADGNH-IEVIRETGMSNDGRTN-----GITLPSDEAQAALSRVYQEAQ--LN-PAD----RCQFFEAHGTGTAGDPIEAEALSTAFF----
TDGDIVSEPMYVGSVKTAIHLEGCAAGLGLIKALEAVKRGVIPPNQLFE-NL-NPALK--PYVSNLRLPTESKPWP--KL---APGS---
PRRASVNSFGGGTNVHAIHQFDHSSADGIITPLVLSANSDLRLKQIAHFAEAI-EHNDKGEIDRIIFLAQRRS

>AFL91703.1_ArmB__Armillaria_mellea_

PIAICGMSVNMPGA-QSVAKLWEVLEKGINV-VSEVPEHR-FKVSNDYNDPKKKSRTMA---AHTGNFID---
EPDAFDNKFNFISPREARSMDPQQRLLLEAVYEATE---AGYV---PNSTPTNTFGCYVGVATNDYVQN-----LRNDIDVYYSTGTLR-R--
AFLSGRISYALQFSGPSIVVDTACSSSLVAVYQACRALMNRDCNAAVAGGVNIGSPDMFLG--LDRG-----HFL-SPTGQCKAFDAS---A-DGYSRSEG-
CGIFVLKR--LSDAVRNDQ-IRAVIRGVEVNSDGNAY-----SITRPHAPTQENLFTQTLERSG--LD-ASR---ISVVEAHGTGTAGDPIELESIRG-IFAKNRKT--
NNPLHITSVKANIGHLEAASGAALAKLLMLRHRITPRLISLK-NL-NPRIK-PLASDNVIIDTKQVAVAVPDE-----
SLPRVALLNFGAAGSNGALLLEEYIPEKIEVSSTFIVGLSAKNEQALVDLRASYIEYLRSPASAVSLADIAATATARRR

>AGI05041.1_fumagillin_dodecapentaenoate_synthase__Aspergillus_fumigatus_Af293_

PIAIVSACRLPGHVNGPHKLWELLQSGGTAVSNEVPQSR-FSSEG-HFDGSG-RPGTMKAL--SGMFIEDI-
DPAAFDAFFNLTRADAIAMDPQQRLLLEVYECFEN---GGIP---IEKVRGKQIGCYVGSNLGDY--HD-MQMR----DPEQRVSGHAVGTG-R--
AFLSNRISHFFDLRGSSTFIDTACSSSLVGVVDVACKNLRAAGTLTGAVVAGVNLWLSPEHTEE--RGTM-----RAAYSASGKCHTFDAK---A-DGYCRAEA-
VNAVYLRK--LSDAVRNDQ-IRAVIRGTASNDSGW--TP---GINSPSAAQAAMIREAYANAGIDSSE-YAE---TGYLECHGTGTAGDPIEAEALSTAFF----
AHPPASPLIIGSVKSNIGHSEPGAGLSGLIKAMLVVEEGEIPGNPTFL-NP-NPAID--FDNLRVYATRIRIPWP--KE---SSH---
YRRASVNSFGGGTNAHVILESAASTEQKPRLSLLFTARSEISLQESINKHADIYI-QKHGSSRLGDIA YTLGTRRE

>AIA58899.1_HRPKS__Penicillium_brefeldianum_

PIAVVGIACRLPGHSSTPKKLWDFLERGGIA-ANDTPSTR-FNLAA-HHDGSK-KPKMTRTP--GGMFIEDA-
DPRDFDAGFFGIGSADAAAMDPQQRLLLEVYECLEN---SGVP---FEKLYGAQVACHVGSYAVDY--DA-IQAR----DPEDRAPGAVVIG-R--
AMLSNRISHFFDLRGSSTFIDTACSSSLVGLDVAACRYLHTGEVDGAIIGGANMYFSPEHNLN--TGAM-----SVANSLSGRCHTFDVK---A-DGYCKAEA-
INCVYLRK--LSDAVRNDQ-IRAVIRGTASNDSGW--TP---GIASPSAAQAAMIREAYANAGIDSSE-YAE---TGYLECHGTGTAGDPIEAEALSTAFF----
SAKPEAPLYIGSVKSNIGHSEPAAGISGLIKALSIEKDLIPGNPTFI-TP-TPKID--FEGLKLPQSRANRRWP-----AAP---
FKRASVNSFGYGGNAHVIVVEPKV--VAGGRLQLLVLSANDEASLRANATTLKNYL--TNPNISLGDLSHTLSERRS

>AJG44381.1_MpaC_Penicillium_brevicompactum_

PIAITGMACRYPNA-DTLAQLWELLELGRCT-VKSPPESRFHMSDLQREPCKGP-----F-WGHFLE---
RPDVFDRHFFNISAREAESMDPQQRVALQVAYEAMES--AGYLKWQPNRLSQ-DIGCYVGVGSEDTENV-----ASRNANAFSITGTL-Q--
SFIAGRISHHFVGSWSPSISLDTACSSAAVAIHLACKALQTNDCCKIALAGGVNLTNPRVYQN--LSAA----SFL-SPSGACKPFDAS---A-DGYCRGEG-
AGLFLVLRP--LQDAIDNGDP-ILGVIAGS AVNQGSSNNS----PITVPDAEAQRSLYKAMSLAG---VS-PDE----VTYVEAHGTGTQVGDPIELDSLRRITFG---
GPHRRNMLHIGSIKGNIGHTETSSGAAGLLKTLMLQQQRIPRQANFN-QL-NPKVK-SLTPDRLVIASESTEWV--ST-----
KRVAMVSNYGASGSNAALIVKEHAPAPEYIQNKLAYNLMAMKQNRDLPLNL-----

>BAC20564.1_polyketide_synthase_Penicillium_citrinum_

PIVVVVGSGCRFPGGVNTPSKLLWELLKEPRDV-QTKIPKER-FDVDTFYSPDGT-HPGRTNAP-FAYLLQE---
DLRGFDASFFNIQAAGEAETIDPQQRLLLETVEAVSN--AGLR---IQGLQGSSTAVYVGMTHDY----ETIVTR--ELDSIPTYSATGVA-V--
SVASNRVSYFFDWHGSPMTIDTACSSSLAAVHLAVQQLRTGESTMAVAAGANLILGPMTFVM--ESKL----NML-SPNGRSRMWDAA---A-DGYARGEG-
VCSVLKLT--LSQALRDGDS-ILCVIRETGINQDGRIT-----GITMPNHSJAQELIRATYAKAG--LD-
ITNPQERCQFFEAGHTGTPAGDPQEAIAIATFFGHKDGTEKDELFGVGSIKTVLGHTEGTAGIAGLMKASFAVRNGVIPPNNLFE-KI-SPRVA--
PFYTHLKIATEATEWPIVAP-----GQPRRVSVNSFGFGGTNAHAIIEEYMATSDADACSLPLVLSKSKQRSMKATLENMLQFLETHDD-
VDMHDIAYTLLEKRS

>BAC20566.1_polyketide_synthase_Penicillium_citrinum_

PIAIVGMGCRFAGDATSPQKLWEMVERGSSA-WSKVPSSR-FNVRGVYHPNGE-RVGSTHVK-GGHFIDE---
DPALFDDAFAFFNMTEVASCMDPQYRLMLEVVYESLES---AGIT---IDGMAGSNTSVFVGGVMYHDY----QDLSNR--DPETVPRYFITGNS-G--
TMLSNRISHFYDLRGPSVTVDTACSSLTALHLACQSLRTGESDTAIVIGANLLNPDVFTV--MSNL----GFL-SPDGISYFDPR---A-NGYGRGEG-
IAALVIKA--LPNALRDQDP-IRAVIRETALNQDGKTP-----AITAPSDVAQKSLIQECYDKAG--LD-MSL----TSYVEAHGTGTPTGDPLEISAISA-AF-----
KGHPLHLGSKVANIGHTEASGLASIIKVALALEKGLIPPANRFL-----QKNSKMLMDQKNIKIPMSAQDWVPVKDG-----
TRRASVNVFVGGSNAHVLESYDRVEDGSKQRIYVVRKDEQACRRTIASLRDYIKSVADIPFLASLAYTLGSRRS

>BAD83684.1_PKS_N_polyketide_synthase_for_alternapyrone_biosynthesis_Alternaria_solani_

PVAIIGIARFGPDARDPEAFYRMLVEGRNA-RTEIPKDR-YNVDAFYHPDSE-RLGSIQQR-HAHFLQ---
DFKVFDAFFSITPKEAKAMPDTHRILLEATYEGFEN---AGLS---LEKVSQTQTSYIGTFTADF----PNLQAR--DNEGPSIYHATGMS-A--
SLASNRISWYFNLRGSPSLTVDTACSSSLTAFLHLACQSLRTGCEAEMSVVGGANLMMFGPDMISL--LGAA----KIL-SPEGKSKMWDAN---A-NGFARGEG-
FGVTILKP--LDAALRDGDN-IRAVVLATAANEDGHTP-----GISLPNSEAQOELIRRAYQIAG--VD-PAE---TAYVEAHGTGTQAGDPLEARAILK-
TIGSVEGR--KSDLVGVSKTNIGHLEGAAGVAGIKAALTVRGMIPPNLWFE-KL-NPEID---LPDNVKIASKLTPW-----
HSGPRRASINSFGFGGANAHAILEDAAASLRDVPKPLFVLSHSDQEGVKRSAERLQEYLASKTSTSFNLNLAAYTLAKRT

>BAJ09789.1_polyketide_synthase_Alternaria_solani_

PIAIVGMGCRVPGGVRDASSLWELLKNKRSR-YREFGDHR-FSRKGFHHPNSE-HPGT-VAT-EGGFLAE--
DPRLFDDHAFFGIGSLEVEDMPSQRKLLLEVVEAFEN---SGEP---WDSFSGSTTGTVFVGNFSSDH----LIQGR--DTDHPRPYASVGTG-T--
SILASNRVNYFNLRGSPSLTVDTACSSMYALHLAISAIRNGDCDAIIVAASNTIHPSTXLM--MTKL----GVL-SPTSTSHTFDSS---A-DGYARGEG-FSALYLKR-
-MSTAVDGDYP-IRALVRGSALNANGR--TG---GITHPGREGQEA VIRKAYENAGN--LP-MKD----TTFECHGTGTPVGDPIEISAIGN-VF---
GSTPEKPLLVGSIKTNIGHTEPASAIAGIMKVVLALENGFIPPSIGIK-KL-NPKLD--LKGGRINILTENTPWP--DG---R-----
VRRASVNSFGYGGANGHCHIDDVRTYKKRTANTSIGHINGHTNGHTNGHTNGHTNGH--TNGHTNGHTNGAH-----

>BAQ21221.1_polyketide_synthase_Oryzias_latipes_

GIAVVMGMCNFPGG-EGLENFWKVLLEGQNC-VVDIPSER-FDTSFWSADAT-KPGKTQTT-RAALID---
GFNEFDHKKFFGISEAEADVMDPQKLLQCSYRALED---AGTS---IESISGRTGVYVGLMNRDY--EM-LRNN----NPNTISHYNATGTA-T--
SVAANRISYTFDLQGPSFVDTACSSSLVALHVACQAMRLGDCCEMALCGGVNCHPEPRVFVA--LSKA----KMT-SPEGTSKPFSIR---A-DGYARGEG-
CGVLLKLP--LRSKRDRNK-IWGIHRTAINQDGRSVTP---ITKPSKVOQEELLRGIYS-----IAD---VQYIEAHGTGTPAGDTTEAGSISD-AI---
AEPGSKTLMVGSVKGNIGHTESAAGVAGVIVKLVLLMMKHETVPSVYFS-DD-SAGVD--MRALKLRVPIKAEKWE--AA---G---
PHGRVAGVNSFGFGGTNSHVVLREYTNATWL---KVCVLSAASEKSLILTINDTHRRLL---NQVDLRGLSYTSACGRS

>CAB04244.2_Fatty_Acid_Synthase_Caenorhabditis_elegans_

DIVISGVSGRFPRC-DNVKMFDMMLAGEDL---VTEDSLRWTPGFCDLPK--RHGKLL-----
VLNKFDAFFQVTPKQANFMDPQVRLLLEASWEAMVD---AGIN---PTDLRGSKTGVFVGCASSET----SGMLTQ--DPDVTGTGTLTGCV-R--
SMFSNRISYTFDLQGPSFVDTACSSSLVALHVACQAMRLGDCCEMALCGGVNCHPEPRVFVA--LSKA----KMT-SPEGTSKPFSIR---A-DGYARGEG-
VAAIFIQR--KKKAQR---LYATVVHAKSNTDGHKEHG---ITFPSGERQAQLLQEVYSEAG---ID-PNS---VYVEAHGTGTVKVPDQEA NAICE-VF---
CSKRTDSSLIGSVKSNMGAEPASGVCSLTKILLSIERQLIPPNLHYN-TP-NQYIP-GLTDGRGLKVVEPTALP-----
GGLIGINSFGFGGNSHVLKAADHPITPHPTKLVTYCGRTEQEA VENIFTEIESNK-DD---LYLQALLANQANMPA

>CAC44633.1_polyketide_synthase_partial_Fusarium_fujikuroi_

PIAIGSACRFPDSSPSKLLWLLKSPRDL-LTKVPPNR-YNADAFYHADSK-HHGTTNVR-HSYFLNE---
DPARFDDNFFNIQPEAEADPQQRLLMEVVYQGLCA---SGQT---IEGLRGSPTAVYVGMCDW----SGIITR--DLEVFPQYGATGMA-R--
SIMSNRISYTFDLQGPSFVDTACSSSLVALHVACQAMRLGDCCEMALCGGVNCHPEPRVFVA--LSKA----KMT-SPEGTSKPFSIR---A-DGYARGEG-
IAAVVLLKLP--LSAAIRDNDH-IDCIIRATGVNQDGR--TP---GLTMPSATAQADLIRSTYARAG--LD-INKPEDRPQFFHAHGTGTPAGDPREAEASTVRSI---
PDVKDDKLYVGSIKTVLGHTEGTAGLASLIGTALAIQNKTIIPNMHFD-VL-NPKIK--PFYDNLEVPKAIAPW--ET---HKGQ---
PRRASINSFGFGGTNAHAIIEAYEPDSAPGLFSPLTFSASSEPSLRSLSSYSDDL-KSNPDLKDLAYTLQTRRS

>CAG28797.1_polyketide_synthase/peptide_synthetase_Magnaporthe_grisea_

PIAIGSGCKFPGGSTTPSKLLWLLKDPKDI-VSEIRPDR-FDVVKYFHPDHK-HHGTSNVR-HSYFLNE---
NFKHFDKFFGIRPQEAAMADPQQRFLLETVEYESLEA---AGIT---ISDLKGSQAGVFGVMGVDY----SELLSQ--DIDAFPTYFAPGTA-R--
SILSNRISYTFDLHGSPVDTACSSSLVALHVACQSLRLGETPVAIVCGANLLTPGMAQYIA--ESKL----QML-SPNGRSRMWDAS---A-DGYARGEG-
FASIVLKP--LSVALANGDH-IECIHRETGCNQDGRIT-----GITMPSLAQCKLIQETYKRAAG--LD-
LSKSSDRPQYFEAHGTGTPAGDPVEAEAIATAFFGPESGFSHPDKLYVGSVKTVIGHTEGTAGLAGLIKASLAMKAKSIPPNNLHLE-RV-NPAVQ--

PFYGNLEIPTRLMDWP--EP---APGQ----PLRASVNSFGFGGANAHVILESYTPTAAAGPVFSPFVFSASSDKALASMLSAYS DYL-
SLNPTVDLRSVAYTLSQHR

>CAG29113.1_TPA__putative_polyketide_synthase__Magnaporthe_oryzae_7015_

PIAVVGTGCRFPGGANSKSLWEILEKPRGL-LKKVPAER-FDVSDFYHPDGS-FHGRNAA-NAYFLDQ---
NIRAFDANFFNIQHHEAEVTDPOHRLLETVYEALAT---AGLR---VEDLRGSSAVYCGQMMNDY----KDLVNF--DQDRLPTYTATGTA-A--
SILSNRVSYFFDWHGSPMTIDTACSSSLVAVHHA VQQLRSGSSKVAIAAGANLILGPVPLIV--ESKM-----NML-SPTGRSSMWDEK---A-NGYAR-EG-
VAAVVLKT--LSQALSDGDN-IECVIRETGVNQDGR--TP---GITMPHQAEALIRETYAAAG---LD-
LSRAEDRCQYFEAHGTGTPAGDPQEAEAISRFFGHGERPPREEPLYVGSIKTVIGHTEGTAGVAGLIKASLAMQNRITIPNMHFH-KL-SPKVA--
PFYQNLHVPTEAQPWP--EL---APGV---PMRASVNSFGFGGTNAHAILEAYPNQRSSAVPIWPIPIISANSELSLKATMQDLLQYL-
KSASGVRVQDLAWTLTNRSS

>CBX87032.1_BcBOA9_protein__Botrytis_cinerea_B05.10_

PV AIGMGCRFPDSDTPEDFWKMLAEERSG-LSRPPLSR-WNIDGFHANKA--RPGSLTPE-GGYFINE---
DIWKFDPAFFGIVQEEAKAMDPPQRKLLCEVYESFES---GGIT---LSQLSGSNTGCYIGNFTSDY----YLQGHR--DHNNPKPYSLLGSG-Y--
TIISNRVSYLFDLCGP-----RALQKEIDAAVVGTTNMLLAVETQMS--TDKV-----GVL-SATSTCHTFDES---A-DGYGRAEG-VGAIFLKR--
LSDAIRDNDP-IRGVIRGTATNANGKTS----GITQPSAKGHETVMRTAYEFAG---LD-PRD----TSYFETHGTGTQVGDPIEIKGVNFF--
NGTDRQKLLVGSVKTNVGHSEAAASALASIIK VCLAMEKRTIPATIGIK-KL-NPKID--FKGGRIEVVQKMTWPWP--KG---FS-----
VCRASINSFGYGGANATAIVEAADSRAVRSSEFLLLSAHADISTLKSNIERCRDVA-ED---YNILDLAYTLGCRRS

>EAA49993.1_hypothetical_protein_MG03752.4__Magnaporthe_grisea_7015_

PV AIVGMACRLPGSVSDPEAFYELCCLGRSG-WSEIPSHR-FSKEGYHHPND-RLGCFNPV-GGCFLESE---
DIGLFDAPFFKITEREAVAMDPOHRLILECTYEALEN---AGIP---MHSIAGRNVGCFAGGSFTDY----ELNLR--DLETQPMHQSTGNA-P--
TMMANRVSYFFDLRGPSTVETACSSSLTALHLAMQSLRCGDSSLVVLASSHLNVMDFHVA--MSSN-----GLL-SGDGRSYAFDSR---A-NGFGRGEG-
AGV VILKP--LADALRDGDN-IRALVVGSGVNDGRTN----GITMPNGESQLDMRKVYADNG--LD-PRD---CGYVEAHGTGTQVGDPLEMKALHD-
MFWEDR--SPRQLLVGSVKTNVGHLEGASGIVSLIKSAMMLERGYVLPNHDFR-EG-NKEIP--FDEWGVKVPKVMWPWP--RG-----
KKYISINSFGYGGANAHVAAPPR-----FRLPGEGLSLEE-----

>EAA58609.1_hypothetical_protein_AN6791.2__Aspergillus_nidulans_FGSC_A4_

PIAIVGLSCKFAGEASTPDRLEWMLAAGRSA-WSEIPSR-FNLKGA YHPSAD-RTNTVHVR--GGHFLEQ--
DLGLFDAQFFSFAETAASMDPQIRLQLESVYEALEN---AGIT---LPDVAGSNTAVYAAVSRDY--RD-GIIR----DEDRLPRFLTGTG-D--
AMFSNRVSHFFDLRGPSTLDTGCSGGLVALHEGVKSLRTGESDMALISGEGLTDEGRFF-----SPDGKSYAFDSR---A-NGYGRGEG-IATIVIKR--
LSDAIIAGDP-IRAVIRESGLNQDQK--TE--TITPSEEQAVALMRDCYRRAG--LD-YAD---TQYLEAHGTGTSTGDPICRAIAT-VF---
KDSSEQPLRIGSVKTNVGHTEAASGLASLIKVVMALEKGIKIPINSIFE-KP-NPKIA--LDEWNLRVVTTLEDWP--AG---PGG-----
VRRASINNSFGYGGTNAHLIVESQAASATNLDSDQIFVFSARDKQACVNMVNNLKKYL--RQNAL-LQRVAYTLGQR--

>EAA59818.1_hypothetical_protein_AN3610.2__Aspergillus_nidulans_FGSC_A4_

PIAIVGLGCRFPGGADTPEKLWQLAYEGRQC-WEEVPSNR-YNWHAFHHPDPE-ARGTHNAR-GGFFLQO---
DPAVFDANFFFAISAAEAIDPQRLLEVSYEALEN---AGMP---LEAIRGTQGTGVYVALVSRDY----DRMIYK--DPSQIPKYHLTGCG-D--
ATACGRISYTFDLKGPVSMGTGCSGSMVALHLACQALRLGETNAIVAGTNLLGPDMTIA--MSAL-----HMI-NENGRCPYFDSR--G-AGYGRAEG-
VAALVLRK--QADAVRDGDP-IRAVIRNTGINQDQKTN----GIMLPSEAAQQLTSTLYRQAG--LD-PNY---VCYIEAHGTGTQAGDAAEVTSIKQ-
VFASAART-RERPLFLGSIKANLGHSESTSLAGVIKTVIALENA TIPPLAAL-EL-KPDLHSLESTKIIPKVPVSWP--HE---G-----
TRLASVNSFGYGGTNAHVILESAPEPNEDGRPQLFIVSAKSRVLEAAIYNVRDWW-SRHGAIKRQELVKTLCRRS

>EAA61508.1_hypothetical_protein_AN9217.2__Aspergillus_nidulans_FGSC_A4_

PIAIVGMAARFSGEATNPSKLDMMVQGRGTG-HSAVPENR-FDAEAWHHPHSE-RRGTIQPR-SGFFLRE---
DPAVFDAPFFSMTAKEAA GMDPMQRKLEISYEFEN---AGIP---ITKLPGTATGVYSGVMNTDY----ELMTAG--DPMQLPQNAASGTS-R--
AMLANRISYFFDLRGPSTLDTACSSSLVALHLACQSLQAGETDQALVTVGNLILAPNFISQ--LSSM-----HML-SPDGKSHSFDNR--A-NGYARGEA-
LAAVVVKP--LYQALADGDT-IRAVIRGSGANQDQKTV----GITIPNQAQAEIRKTYATAG--LG-LEQ---TGYFEAHGTGTPVGDPIELSAIGT-SF---
GESQNCPLFVGSVKTNVGHTEGAAGLAGVKTVLALEAGIIPPLADFQ-EL-NEKLR--LEEWKALPLKATPWP--MP--G-----
LRRASVNSFGYGGANAHVILDDAYHDSGEGQSSKLLLSA YDGAGIKRTEASWNSHL-ADILAMGMNDLAYTSLDRRT

>EAA63960.1_hypothetical_protein_AN1784.2__Aspergillus_nidulans_FGSC_A4_

PIAIIGTGCRPLPGSSSRSLWTLKKNRNV-ASETPGDR-FDINAFYHEDPG-YPGTTNSK-EAYYISD---
DPRPFDAPFFNISATEAESIDPQRQLLETVYESLES---AGLR---LDALQGSSTGIFCGVMNNDW----GELQSA--DYKSLPQYLATGAA-R--
SIANRISYFFDWHGSPVVDTACSSSMVALHHA VTLAQNECTLALATGTNLIQAPNFIS--TTKI-----QML-SPTGRSRMWDAN---A-DGYARGEG-
VISIVLKR--LSDAIRDGD-IECVIRATGTNQDGRTM----GLTMPSSVSLQLIQSTYARAG--LD-
PRRVQDRQYFEAHGTGTLAGDPQEA AAIHHAFFGPPASPDNDILLVGSVKT VVGHTEGTAGLAGHIKASLNQHGLISPNLLEF-EL-NPALE--
PFASHLKVVTELTWPWP--SL--PTGA---PRRVSVNSFGYGGTNAHAILESYDAGQSLTAALLPFVFAASEGSLA AVLNSYAGYL-
KGGPALNLVDFAVTLRRTS

>EAA64652.1_hypothetical_protein_AN2547.2__Aspergillus_nidulans_FGSC_A4_

PIAVIGICRLSGSATDVSGLWDMKSGRSG-WTPGPGTR-FNMKAFQDPTGT-RSGTTNAT-GGHFIRE---
DISKFDATFFGINPVEAQAMDPOQRLLMLEVA YEAFEN---AGIT---MDALWGSNTGVYVQWASDY----HEIATR--DIERPPLYLVTGTG-P--
AITSNRVSYVFNLRGSPFTVDTGCSSSLVALHQA VLSLRNRETTQCFVGGVNLDDPQRFHY--QSRL-----KMF-SKDGRSFPFDAR---A-NGYGRGEG-
VTGVVLRK--LSVALRDGDP-VRAVIRNSVLNQDGR--TP---GISVPSAVAQKEAIIIRAYRQAK--LDLYAD-----YVEAHGTGTQVGDPIETSAIAAALT-----
SPSRPLPGSIKGNIGHTESAAGLAGLIKSVLLENGMIPPQVNYE-TT-NPDIH--LEEWNLRIPTKLERQT-----
LRRISLNSFGYGGTNAHVILDAHAHELHYHSEKPRVFMVSGASEKACQRVCARLARYL-VVNHRRALLARLAHTLAKQSI

>EAA67034.1_hypothetical_protein_AN8412.2__Aspergillus_nidulans_FGSC_A4_

LIAIVGSACRFPQSDSPSKLWTRLKEPIDL-RKTFPPQR-LNLARFYHPDGE-HHGSTDVDR-GTSYLLSE--
DPRQFDASFFNINPREAEGMDPQRLLETAFAEALAE---AGYS---LEAMNGSKTSVHVGVMSNSDF----SNIQLR--DPEVLPTYNATGTA-I--
SILSNRLSYFFNLKGPSVTIDTACSSSLVALHQA VQGLRAGDATAAIVAGANLIFDPAMYIA--ESSL----HML-SPDSCSRMWKDK---A-NGYARGEG-
VGVVLVLPK--LSRAIMDGDH-VEAVIRSTGVNSDGRK----GITMPNAESQTELIRQTYRDAG--LDPIRD--
RCQYFECHGTGTATGDPPEARVHDAFFPTETRTIPDGKLYVGSVKTIHGLEGCAGIAGVLAIKNRITIPPNMHFH-EP-NPRVI--PFCDRLEIPTVPIWPW-
-DT---GRS----PLRASINSFGGTTNAHAIIEGYDAITPDDLFIGLPLFSANSSSLVANVKNMAERI-RSDPSIDLESLLVWTLYARRS

>EAA67213.1_hypothetical_protein_FG02396.1_Gibberella_zeae_PH1_

-VAIVGLACRFPGDATSPSKFWDLLKSGKDA-YSET-TDR-YNAQAFYHPNSK-RQNVLPVT--GGHFLKQ--
DPHFVDAFAFFNITAAEAISLDPKQRIALEVA YEAFEN---AGKP---LKQVAGTTTACFVGSMSDY--RD-AVVR----DFAHNPKYHVLGTC-E--
EMLIANRISHFFDLHMGPSATVHTACSSSLVAIHLACQSLSGDAEMALAGVGMILTPDGMTQ--LNNL----GFL-NPEGHSRSDFKD---A-GGYGRGEG-
CGILVLKK--LDKAIQDGDN-IRAVIRASGVNSDGV--TQ--GVTMPSSEAAALIKHVYETRQ--LD-YGA---TQYVEAHGTGTAKADPVETGAIHR-TI---
GQSKNRKLW-----IGHLEAAAGVASVIKGVLA MENSLIPPNIHFA-SP-NPEIP--LDEWNMAVPTKLPWP-----AAR-----
TKRMSVNSFGMGGTNGHVLEAFNSYQPAHNGKRLFTFSSHDQAGLDRVSKSLVDHL--DSLQ-----

>EAA69154.1_hypothetical_protein_FG01790.1_Gibberella_zeae_PH1_

PIAICGMSVRLPGGLHSPQDLWEFLVSKGDA-RGPVPESR-YNASSYWSEKM--KPGTVKQ-YGYFLDESI-
DIASVDTSFMTMRKDEVGKADPQQRMLLEVARECLE---AG----EFDWKGRIPIGCFMGSFGEDW----VEMFAK--EAQQYGIYRVMGYG-D--
EMLIANRISHFFDLHMGPSATVHTACSSSLVAIHLACQSLSGDAEMALAGVGMILTPDGMTQ--LNNL----GFL-NPEGHSRSDFKD---A-GGYGRGEG-
ISAIKVPK--LSAAIRDGNP-IRAVIRSTASNSDGRGTAG---GIQVNDIAQETLIRRAYKMGAG---IDDYSQ---TAFVECHGTGTAGDPIETKAVGR-VF-----
GPSGGVLIGSVKPNLGHSEGASGLTSLIKAVMALENRTIPPNIKLS-QP-NPAIP--WTSCGLSVPTPEPTWP--SS---K-----
HERISVNSFGIGGTNAHVIIIDSACSVGRSATAPQLLVFSANGTDSLRLMITNYENYA-EKNPE-KIDDLAFTLGHKRE

>EAA69820.1_hypothetical_protein_FG10548.1_Gibberella_zeae_PH1_

PIAVVIGICRFPNGSSNPEALWKLSDARSC-YSKVPPDR-YNV DGRHPS-N-KLNTTIAE--GAHFLSE--
NIAAFDAFFNIAPIDAKSMDPQQRMLLEVYEGLES---AGIK---MEDTTGSDTSCYVGTFTRDW--SD-MLMR----DPETAPKYSAGIG-S--
GMQANRISYFFNLHGPSLTLDTCSSSLVALHLACQSLSGDAEMALAGVGMILTPDGMTQ--LNNL----GFL-NPEGHSRSDFKD---A-GGYGRGEG-
IAAVILKS--LDQAVRDRDP-IRAVIRGTGINHDGH--TP---GITLPSASAQADLISSVYKKSQ--LD-YDD---TMYFEAHGTGTAAAGDSVELRAIGA-SV----
TKDSSKTLVVGSIKSNIGHTEGAAGLAAFIKAVLVEKGLIPRNIHLN-NP-NPRIIP--FEELKIQVPTVEIPWP-----TPG-----
VRRASVNSFGYGGTNAHAILDDASSFKETTNRKLFVFSAAHEESAALNMKQRYATHL--EEEASYLDRLAY-----

>EAA71995.1_hypothetical_protein_FG08795.1_Gibberella_zeae_PH1_

DIAVVGIGLRFPGDASSPEELWVKVLGERGESQ-WSEFPKDR-LNIDGYHPGGD-RQGSISFR--GAHFIKS--
DFAAFDASFFVAVAEADAKAIDPQQRILLEASYEALEN---AGIR---KEDVDGTDAAVYVGSFVKDY--EQ-VCLR----DPDWQPQY AATGNG-I--
AIMANRISYFFNLHGPSLTLDTCSSSLVALHLACQSLSGDAEMALAGVGMILTPDGMTQ--LNNL----GFL-NPEGHSRSDFKD---A-GGYGRGEG-
IGVVMVKR--LSDALRNDT-IRAVIRATKVNQDGH--TTALKGITLPSKEAQV ANIHSVYESAG---LD-FSQ---TGYVECHGTGTAKAGDWRELKAISE-SL---
GSGIDNPVVGSLKPNIGHLEGAAGVAGLIKGVLTLEHAKIPPNIHLN-NP-NPDIID--FKNWVKVPTKLLDWP-----LPG-----
LRRVSVNCFGFGGTNAHVIMDEAPR-----QLFLFSAHERSGVQRVMESHLPYL--KSKTF-LRDYSYTLGCRRS

>EAA73063.1_hypothetical_protein_FG08208.1_Gibberella_zeae_PH1_

PIAVVGMSCRPLPGDATDTQKLWELITKGRSA-WSKVPTDR-WNQEAFHDPAAEGKPR-TSTDGGHFLKD--
DIAAFDASFFGNPIEATAMPDQQRLLVLEIAYEAFEN---AGLT---LQQLSGSNTGVYVGLWASDY----QEMLLR--DIDFPPIYQASGVG-A--
AIMANRISYFFNLHGPSLTLDTCSSSLVALHLACQSLSGDAEMALAGVGMILTPDGMTQ--LNNL----GFL-NPEGHSRSDFKD---A-GGYGRGEG-
CSGVVLMK--LSKAQKQGF-IRAVIRNSVANQDQKTN----GITVPSAAAQSAIEKAYAVQV--LT-PYA----DYVEAHGTGTAVGDPPIEKAKIAK-VL--
GAGRQSDSPLPIGSLKANIGHTESAAGLGLVKA VLMLENMIPPQVNYE-KP-NPEID--LDALNLRIPISLENK-----
LKRISVNSFGYGGTNAHVIVDAADAKDTRLVREQLFVLSAASEKSSQDLVLNVAKYLESKADAALLSRLAYTLRRTV

>NP_001012687.1_fatty_acid_synthase_Bos_taurus_

EVVITGMSGKLPES-ENLEEFWANLIGGVDM---VTDDRRWKAGLYGLPRR--GKLGK-----
DLSRFDASFFGVHPKQAHNMDPQLRLLLEVTYEAIVD---AGIN---PASIRGTNTGVVWVGVSGSEA----SEALSR--DPETLVGYSMVGCQ-R--
AMLANRISYFFFDKGPSITIDTACSSLLALQSA YQAIQGDCEMAMVGGVGNRLKPNQSVQ--FMKL----GML-SPEGTCKFFSDA---G-NGYCRAGA-
VMAILTK--KSLARR-----VYATILNAGTNTDGCKEKG---VTFPSGEAQEQLISSLYKPAG--LD-PET---LEYVEAHGTGTAVGDPQELNGIVQ-AL---
CGTRQSPRIGSTKSNMGHPEPASGLAALAKVLLSLEHGLWAPNLHFH-NP-NPKIP-ALQDGRQVVDRLPLV-----
GGNVGINSFGFGGNSVHVILQPNQAPHAALPRLLRASGRTLEGVQGLLELGLQHS-QN--LAFVSMNLNDIATPSP

>NP_001041530.1_uncharacterized_protein_LOC10000781_Danio_erio_

EIAIVGVGCHFPGG-EGLENFWRVLLLEGKNC-AVQIPNDR-FNLSQWYDPEES-KAGKTYTA-KAALID---
GLNAFDHKKFFGITEAESLMDPQHKLQLCTYRALED---AGIP---MEKASGTRTGVYVGLMNRDF--ELATVRN---NPKHISHTTGTGVA-M--
SIAANRISYFFNFTGPSVAIDCACSSSLVALHFACQAIQGDCEMAMVGGVGNRLKPNQSVQ--FMKL----GML-SPEGTCKFFSDA---G-NGYCRAGA-
CGVVLKPK--LKRALEDHHD-IWGVIGKTA VNVQDGHVSP---ITKPSMVQEQEELLRKIYST-E---AD-LCS---VQYIEAHGTGTAVGDPVEAGSMK-VI---
AKQKSGPLIGSVKSNIGHTESAAGVAGLIKVLLMMQHETIVPSLFYS-KE-NSSID--LKSLNMNIPTRVQKWI--SN---N-----
RAGRIAGINNFVGGTNAHIVKQYVQSPISKSCQYFVVSAASEKSMRNIIRDADQI--GAGKSDLQSLLYTSACRRS

>NP_001093400.1_fatty_acid_synthase_Sus_scrofa_

EVVIAGMSGKLPES-ENLEEFWANLIGGVDM---VTADRRWKAGLYGLPR--RMGKLGK-----
DLSRFDASFFGVHKSQANTMDPQLRMLLEVYEAIVD---GGIN---PASLRGTSTGVVWVGVSSSDA----SEALSR--DPETLVGYSMIGCQ-R--
AMMANRISYFFFDKGPSITIDTACSSLLALQSA YQAIQGDCEMAMVGGVGNRLKPNQSVQ--FMKL----GML-SQDGTCKRFFSDA---G-TGYCRAEA-
VVAVLLTK--KSLARR-----VYATILNAGTNTDGSKSEQ---VTFPSGDVQEQLIRSLYAPAG--PD-PES---LEYIEAHGTGTAVGDPQELNGIVN-AL---
CATRREPLIGSTKSNMGHPEPASVAAALIKVLLSLEHGLWAPNLHYH-TP-NPEIP-ALQDGRQVVDRLPIR-----
GGNVGINSFGFGGNSVHVILQPNRPAQHAALPRLLQASGRTLEAVQTLLEQLRHS-RD---LAFVGMNLNIAAVSP

>NP_001137778.2_fatty_acid_synthase_1_iform_C_Drosophila_melanogaster_

EIAITGFSGRLPES-STIEEFKQNLFDGVDM---VNDDPRRWERGLYGLPD---RIGKPKDS-----DLENFDQQFFGVHQQKAECDMDPLLRMLLELTHEAIID---
AGLN---PSDLRGSRTGVYIGVSNSET----EQHWCS--DADRNVNGYGLTGCA-R--
AMFANRISFTFDFKGPSYSDTACSSSLYALEQAFSDMREGKVDNALVAGAGLILKPTMSLQ--FKRL----NML-SPDGSKAFDES---G-NGYVRS-DG-
CVVLLQR--TSAARR----VYASILNVRTNTDGFKEQG---ITYPIGMQNRILIRETYEEIG---LN-PAD---VYVVEAHGTGTVGDPQEVSNTD-FF---
CKDRTPPLIGSVKSNMGHSEPASGVCSVAKILIAMEEGVIPGNLHYN-KP-NPDLV-GLVDGRLKVVDRLNPWN-----
GGIIGLSNFGFGGANAHVILKSNPKLTPKDGALKVVLASGRTEFAVEQLLESASTNA-DDDEYQLINEIHSKAIPNH

>NP_001239013.1_polyketide_synthase_2__Strongylocentrotus_purpuratus_

KVAIVGIGCRYANGINGVRFWEMLAKGMDC-TTPPSDR-FDSSFLLFPGSK-IQGMKYNK-CAGYLSQ--
NPEHFRDQFFRISPEEANHLDPQIRMLLEVVWESLQD---AGIP---AHSARGSKTVYMGVASEY--GV-LIGM---PNDNINQYNTSGTN-S--
CMTANRVSYEFDFRGPSTVDTACSSSMYSVHLACEALKNGQCEMAVAGVNVNLLPITSIG--FCQA-----GML-APDGCKKSFDS---A-DGYARREG-
VGA VILKP--LQRAIDDGDR-IYGVIRGGAIANR--TP---GIALPSYDQVSLIENAYKNAN---TL-PEE---VYVVEAHGTGTVGDRTEASAIGE-AM---
GLVEQPPLYLGSVKSNFGHSEGAAGIAGVKAALCLYHEIQPKVVFHR-SG-NESVD--FESLNIRVPGELTRWP-----KAA-----
KLVGCSSEFGFGGANAHVILEG---NERDSGKPSILFLSAASKDALKHLEEWGSYL--NEVIRAYNNALYTAAVRST

>NP_004095.4_fatty_acid_synthase__Homo_sapiens_

EVVIAGMSGKLPES-ENLQEFWDLNIGGVDM---VTDDRRWKAAGLYGLPRRSGKLIK-----
DLSRFDASFFGVHPKQAHTMDPQLRLLLEVTYEAIVD---GGIN---PDSLRTGTHGTGVWVGVSGSET-----SEALS--DPETLVGYSMVGCQ-R--
AMMANRISFFDFKGPSIALDTACSSSLMALQNA YQAIHSGECPAAIVGGINLLKPNTSVQ--FLRL-----GML-SPDGTCRSDFS---G-NGYCRSEG-
VAVLLTK--KSLARR----VYATILNAGTNTDGFKEQG---VTFPSGDIQEQLIRSLYQSAG---VA-PES---FEYIEAHGTGTVGDPQELNGITR-AL---
CATRQPELLIGSVKSNMGHSEPASGLAALAKVLLSLEHGLWAPNLHFN-SP-NPEIP-ALLDGRQLVVDQPLPVR-----
GGNVGINSFSGFGGSNVHILRPNTQPAPHATLPRLLRASGRTPAVQKLEEQLRHS-QD---LAFVSMNLNDIAAVPA

>NP_032014.3_fatty_acid_synthase__Mus_musculus_

EVVIAGMSGKLPES-ENLQEFWANLIGGVDM---VTDDRRWKAAGLYGLPKRS-GKLIK-----
DLSKFDASFFGVHPKQAHTMDPQLRLLLEVTYEAIVD---GGIN---PDSLRTGTHGTGVWVGVSGSEA-----SEALS--DPETLVGYSMVGCQ-R--
AMMANRISFFDFKGPSIALDTACSSSLMALQNA YQAIHSGECPAAIVGGINLLKPNTSVQ--FMKL-----GML-SPDGTCSRSDFS---G-NGYCRSEA-
VAVLLTK--KSLARR----VYATILNAGTNTDGSKEQG---VTFPSGEVQEQLICSLYQPPAG--LA-PES---LEYIEAHGTGTVGDPQELNGITR-SL---
CAFRQAPLLIGSVKSNMGHSEPASGLAALTKVLLSLEHGLWAPNLHFN-SP-NPEIP-ALLDGRQLVVDRLPVR-----
GGNVGINSFSGFGGSNVHILRPNTQRPTAHAALPHLLHAGSRTLEAVQDLLEQGRQHS-QD---LAFVSMNLNDIAATPT

>NP_059028.1_fatty_acid_synthase__Rattus_norvegicus_

EVVIAGMSGKLPES-ENLQEFWANLIGGVDM---VTDDRRWKAAGLYGLPK--RSGKLIK-----
DLSKFDASFFGVHPKQAHTMDPQLRLLLEVTYEAIVD---GGIN---PDSLRTGTHGTGVWVGVSGSEA-----SEALS--DPETLVGYSMVGCQ-R--
AMMANRISYTFDQGPSFSDTACSSSLALQNA YQAIHSGECPAAIVGGINLLKPNTSVQ--FMKL-----GML-SPDGTCSRSDFS---G-NGYCRSEA-
VAVLLTK--KSLARR----VYATILNAGTNTDGSKEQG---VTFPSGAEQEQILIRSLYQPPG--VA-PES---LEYIEAHGTGTVGDPQELNGITR-SL---
CAFRQSPLLIGSVKSNMGHSEPASGLAALTKVLLSLEHGLWAPNLHFN-SP-NPEIP-ALLDGRQLVVDRLPVR-----
GGVIGINSFSGFGGANVHILRPNTQAPHAALPHLLHAGSRTLEAVQDLLEQGRQHS-QD---LAFVSMNLNDIAATPT

>NP_492417.2_Fatty_Acid_Synthase__Caenorhabditis_elegans_

DIVISGVSGRFRPC-DNVKMFQMDLLAGEDL---VTEDSLRWTPGFCDLPKRH-GKLIK-----
VLNKFDAGFFQVTPKQANFMDPQVRLLEASWEAMVD---AGIN---PTDLRGSKTVGVFVGSASET-----SGMLTQ--DPDVTGYTLTGCV-R--
SMFSNRISYTFDQGPSFSDTACSSSLALQNA YQAIHSGECPAAIVGGINLLKPNTSVQ--FMKL-----GML-SPDGTCSRSDFS---G-DGYCRTEG-
VA AIFQR--KKKQR---LYATVVHAKSNTDGHKEHG---ITFPSGERQAQLLEQVYSEAG---ID-PNS---VYVVEAHGTGTVGDPQEANAICE-VF---
CSKRTDILLIGSVKSNMGHSEPASGVCSLTKILLSIERQLIPNHLHYN-TP-NQYIP-GLTDRGLKVVPTEPALP-----
GGLIGINSFSGFGGSNVHILKAADHPITPHPFTKLVTYCGRTEAVEIFTEIESNKDD---LYLQALLANQANMPA

>NP_608748.1_fatty_acid_synthase_1__isoform_A__Drosophila_melanogaster_

EIAITGFSGRLPES-STIEEFKQNLFDGVDM---VNDDPRRWERGLYGLPD---RIGKPKDS-----DLENFDQQFFGVHQQKAECDMDPLLRMLLELTHEAIID---
AGLN---PSDLRGSRTGVYIGVSNSET----EQHWCS--DADRNVNGYGLTGCA-R--
AMFANRISFTFDFKGPSYSDTACSSSLYALEQAFSDMREGKVDNALVAGAGLILKPTMSLQ--FKRL----NML-SPDGSKAFDES---G-NGYVRS-DG-
CVVLLQR--TSAARR----VYASILNVRTNTDGFKEQG---ITYPIGMQNRILIRETYEEIG---LN-PAD---VYVVEAHGTGTVGDPQEVSNTD-FF---
CKDRTPPLIGSVKSNMGHSEPASGVCSVAKILIAMEEGVIPGNLHYN-KP-NPDLV-GLVDGRLKVVDRLNPWN-----
GGIIGLSNFGFGGANAHVILKSNPKLTPKDGALKVVLASGRTEFAVEQLLESASTNA-DDDEYQLINEIHSKAIPNH

>NP_990486.2_fatty_acid_synthase__Gallus_gallus_

DVVIAGIAGKLPES-ENLQEFWENLLNGVDM---VTEDRRWKPQGIYGLPKRN-GKLIK-----DIKFDASFFGVHPKQAHTMDPQLRLLLEVSYEAILD--
-GGIN--PTALRGTDTGVWVVGASGSEA-----AEALSQ--DPELLGYSMTGCC-R--
AMLANRISYTFDFRGPSTVDTACSSSLMALENA YKAIHSGECPAAIVGGINLLKPNTSVQ--FMKL-----GML-SPDGACKAFDVS---G-NGYCRSEA-
VVVLLTK--KSMKR----VYATIVNAGSNTDGFKEQG---VTFPSGEMQQQVLGSLYREG--IK-PGD---VEYVEAHGTGTVGDPQEVNIGVN-VF---
CQCEREPLLIGSVKSNMGHSEPASGLAALAKVILLSLEHGLWAPNLHFN-DP-NPDIP-ALHDGSLKVCKPTPVK-----
GGLVINSFSGFGGSNAHVILRPNKQPETCNLPRVLCGRTEQAVEILIEESRKHGGC---SPFLSLLSDISAVPV

>pdb|3HHD|D_Chain_D__Fatty_acid_synthase

EVVIAGMSGKLPES-ENLQEFWDLNIGGVDM---VTDDRRWKAAGLYGLPR--RSGKLIK-----
DLSRFDASFFGVHPKQAHTMDPQLRLLLEVTYEAIVD---GGIN---PDSLRTGTHGTGVWVGVSGSET-----SEALS--DPETLVGYSMVGCQ-R--
AMMANRISFFDFRGPSTVDTACSSSLMALQNA YQAIHSGECPAAIVGGINLLKPNTSVQ--FLRL-----GML-SPEGTCKAFDVS---G-NGYCRSEG-
VAVLLTK--KSLARR----VYATILNAGTNTDGFKEQG---VTFPSGDIQEQLIRSLYQSAG---VA-PES---FEYIEAHGTGTVGDPQELNGITR-AL---
CATRQPELLIGSVKSNMGHSEPASGLAALAKVLLSLEHGLWAPNLHFN-SP-NPEIP-ALLDGRQLVVDQPLPVR-----
GGNVGINSFSGFGGSNVHILRPNTQPAPHATLPRLLRASGRTPAVQKLEEQLRHS-QD---LAFVSMNLNDIAAVPA

>pdb|5BP1|A_Chain_A__Mycoserocic_Acid_Synthase

PVAIIGMACRLPGAINSPQQLWEALLRGDDF-VTEIPTGR-WDAEEYYDPEPG-VPGR-SVSKWGAFLD----
DPAAFDPEFFGITEREAAAIDPQHRLLETAWEAVEH---SGLN---PAGLAGSATGVFMGLTHNDY----AHLAAD--AKALEGPYGFTGTS-F--
SLASGRVAYALGVHGPVITVDTACSSSLSAIHMACRSLHDGESDVALAGGVSVLLEPRKAAG--GSAA-----GML-SPTGRCHAFDTA---A-DGFVSAEG-
CVVLTLLKR--LDDAVADGDR-ILAVIRGTATNQDGRTV-----NIATPSADAQAKVYRMALKAAG---VE-PGT---VGLVEAHGTGTPVGDPLEFSSLAE-VY-----
GTDGPCALGSIKTNFGHTQSAAGALGVMKAVALAQHNVPQNLHFT----RLPDQMAEIETGLFVPEITPWPVREGQ-----
PRRAAVSAYGLSGTNVHAILEQAPEISPKAGNALVFPVSASSADALRSTAQHLADWLLRSGLD-----

>sp|A0A089QRB9.2|MSL3_MYCTU__Mycocerosic_acid_synthase-like_polyketide_synthase_

SVAVIGMACRLPGGIDSPQRLWEALLRGDDL-VGEIPADR-WDANVYDPEPG-VPGR-SVSRWGAFLD----
DVGGFDCDFGLTEREATAIDPQHRLLEVSWEAIEH---AGVD---PATLAESQTGVFVGLTHGDY----ELLSAD--CGAAEGPYGFTGTS-N--
SFASGRVAYTLGLHGPAITVDTACSSSLTAIHMACRSLHDGESDVALAGGVSVLLEPRKASV--GSLQ-----GML-SPTGRCHAFDTA---A-DGFVSAEG-
CVVLTLLKR--LPDAVRDGDGR-VLAVIRGTAAANQDGRTV-----NIAAPSAQAQIAVYQQALAAAG---VE-AST---VGMVEAHGTGTPVGDPEYASLAA-VY-----
-GTEGPCALTSVKTNFGHLQASAGPLGLMKTILALRHGVVPPQNLHFC----RLPDQLAEIDTELFVPEITPWPVREGQ-----
PRRAAVSAYGLSGTNVHAILEQAPEISPKAGNALVFPVSASSADALRSTAQHLADWVVDQNGNAVSMRDLGYTLSCRRRA

>sp|A0R1E8.1|PKS5_MYCS2_RecName__Full_Mycocerosic_acid_synthase-like_polyketide_synthase

PVAIIGMACRLPGAINSPQQLWEALLRGDDF-VTEIPTGR-WDAEEYYDPEPG-VPGR-SVSKWGAFLD----
DPAAFDPEFFGITEREAAAIDPQHRLLETAWEAVEH---SGLN---PAGLAGSATGVFMGLTHNDY----AHLAAD--AKALEGPYGFTGTS-F--
SLASGRVAYALGVHGPVITVDTACSSSLSAIHMACRSLHDGESDVALAGGVSVLLEPRKASV--GSLQ-----GML-SPTGRCHAFDTA---A-DGFVSAEG-
CVVLTLLKR--LDDAVADGDR-ILAVIRGTATNQDGRTV-----NIATPSADAQAKVYRMALKAAG---VE-PGT---VGLVEAHGTGTPVGDPLEFSSLAE-VY-----
GTDGPCALGSIKTNFGHTQSAAGALGVMKAVALAQHNVPQNLHFT----RLPDQMAEIETGLFVPEITPWPVREGQ-----
PRRAAVSAYGLSGTNVHAILEQAPEISPKAGNALVFPVSASSADALRSTAQHLADWLLRSGLD-----

>sp|B2HIL7.1|MSL7_MYCMM_RecName__Full_Phenolphthiocerol_synthase_polyketide_synthase_type_I_

PVAVVIGICRFPFGADGPEGLWDLVSQGRDA-VTEFPNDRGWDTGLFDPDPD-AEGKTYTR-WGAFVE----
NATNFDAGFFGIPPSEVLAMDPQQRLLMLEVSWEALEH---AGID---PMSLRGSSSTGVFTGIFAPSY-----GGK--DVGALQGYGLTGSP-V--
SVASGRVAYVYVLEGLGPAITVDTACSSSLVAIHMAASLRSGECMDALAGGVTVMLGPSIFV--FSRQ-----RGL-AADGRCKAFDFAA---A-DGTGWGEG-
AGVVLVLER--LSDAQRNGHN-VLAVVRGSAINQDGNASN-----GLTAPNGLAQQRVIAAALANCG--LT-SAD---VDVVEAHGTATTLGDPPIEAELLA-TY-----
GQPTDQPLWVGSIKSNMGTQAAAGVAGVIKVMQAMRHGLMPASLHVD-EP-SKRVD--WESGAVSVLAEARDWP--DA---GR-----
PRRAGVSSFGISGTNAHVILEEAPAKGEPSPVVPVVISARSAEALTAQAGRLLAHV-QADPQSNPVDIGFSLAGRSA

>sp|O31782.3|PKSN_BACSU_RecName__Full_Polyketide_synthase_PksN

PIAVIGISGIFPMA-KDVEAYWNILKEGKDC-MTEIPKDR-WDWREYEGDPAK-EVNKTNV-K-WGGFID----
GIADFDFPFPGIPSPREAEQMEPQQRLLTYAWKAIED---AGYS---AKRSLGKTGVFIGTGNTGY-----SLLSK--ANSAIEGSAANTS-P--
SVGPNRVSYFLNLHGPEPVDVDTACSSSLVAIHMAISIEEGTCMDALAGGVNTLILPEVYIS--FDKA-----GAL-SKEGKCKTFSNQ---A-DGFAHGE-
AGILFLK--LKAEEAGDH-IYGVIKGSAINHGGRAS-----LTPNPKAQADVIQSAAYQKAG--ID-PKT---VTYIEAHGTGTELDGPVEINGLKS-
AFKALGVNSANPYCGLGSVKTNIGHLSLAAAGAVIKILLQLKHKHTLVKSLHCE-----

>sp|O31784.2|PKSR_BACSU_RecName__Full_Polyketide_synthase_PksR

GIAIIGMSGQFPA-KNSVTEFWDNLVQGNK-VSEVPER-WDWRKY--AAAD-KEGQSSLQ-WGGFIE----
GIGFDPLFFGIPSPKEAANMDPQEFLLLIHAWKAMED---AGLT---GQVLSRPTGVFVAAGNTDT-----AVV-P--
SLIPNRISYALDVKGPSEYEAACSSALVALHRAIQSIRNGECEQAIVAVNLLSPPKGFIG--FDSM-----GYL-SEKQAKSFQAD---A-NGFVRSEG-
AGVLIIP--LQKAIEDSDH-IYSVIKGSVSHGGRGMS-----LHAPNPAKMDAMLKAYQGAQ--ID-PKT---VTYIEAHGASPLADAIEIEALKS-GC----SQ-
EEAPCYSSLPKPSIGHGELVSGMAALMKVSMAMKHQITPISGIFS-SL-NDQVS--LKGTRFRVTAENQQR--DL---
SDDAGKIPRRASINSYFSGGVNAHVILEEYIPVSMSENGAHIVVLSAKNQDRKAIQAQQQLDYV--NKQQLSLQDYAYTLQTGRE

>sp|O53901.2|PKS5_MYCTU_RecName__Full_Mycocerosic_acid_synthase-like_polyketide_synthase

PVAVIGMGCRPLPGGIDSPDRLWEALLRGDDL-VTEIPADR-WDIDEYYDPEPG-VPGRTDCK-WGAYLD----
NVGDFDPEFFGIGKEAIAIDPQHRLLETSWEAMEH---GGLT---PNQMAS-RTGVFVGLVHTDY----ILVHAD--NQTFEGPYGNTGTN-A--
CFASGRVAYAMGLQGPVITVDTACSSSLTAIHMACRSLHDGESDVALAGGVSVLLEPRRFAS--GSAL-----GML-SATGRCHAFDVS---A-DGFVSAEG-
CVMLALKR--LPDALADGDR-ILAVIRGTAAANQDGHV-----NIATPSRSQAQVAAVREALDVAG---VD-PAT---VGMVEAHGTPVGDPEYASLAE-VY-----
GNDGPCALASVKTNFGHTQSAAGALGLMKAVALAQHNVPQNLHFT----ALPDKLAAIETNLFVPEITPWPVREGQ-----
ETPRRAAVSAYGMTGTNVHAIVEQAPVATPGIDGALLFALSASSQDALRQTAARLADWVDAQGPELAPADLAYTLARRRG

>sp|P16540.1|KAS1_STRVN_RecName__Full_Granaticin_polyketide_putative_beta-ketoacyl_synthase_1_AltName__Full_ORF1

RVVITGVGVRAPGG-SGTFEFDWLLTAGRTA-----TRPISFFDASPFRRSIA-----GEIDFDAVAEGFSPREVRMRDRATQFAVACTRDALAD---
SGLD---TGALDPSRIGVALGSAVAYLVMSDSGREWL--DPAHLSMMFDYLS-P--
GVMPEAVAWAAGAEGPVTMVSVDGCTSGLDVGYAVQGTREGSADVAVAGADTPVSPVIVAC--FDAI-KATTPRNDPAHASRPFDDGT--R-NGFVLAEG-
AAMFVLEE--YEAQRRAH-IYAEVGGYATRQAYHMTG---LKKDGREMAESIRALDEAR--LD-RTA---VDYVNAHSGTGKQNDRHETAFAKRSGLG--
---EHAYAVPVSSIKSMGGHSLGAGSIEIASVLAIEHNVPPATANLH-----

>sp|P16541.2|KAS2_STRVN_RecName__Full_Granaticin_polyketide_putative_beta-ketoacyl_synthase_2_AltName__Full_ORF2

RAVVVTGLSVAAPGG-LGTERYWKSLTGTENG---IAELSRFDASRYPRLAG-----QIDDFEAS-EHLPSRLLPQTDVSTRYALAAADWALAD---
AGV--PESGLDDDLGVVSTAQGDFTHREFHKLWSQ--GPAVYVSYESFAWF-Y--
AVNTGQISIRNTMRGPSAALVGEQAGGLDAIGHARRTVRRGPGWCSAVASTRSTRGASSSQ--LSGG--LVSTVADPERAYLPFDVD--A-SGYVPGEG-
GAVLIVED--ADSARARGAERIV--RSPLRRDPAPGSG-----RPPALGRAEALALAEAG--LT-PAD---ISVVFADGAGVPELDRAEADTLAR-LF---GP--
RGVPVTAPKALTGRLCAGGGPADLAAALLALRDQVIPATGRH-----

>sp|P40806.3|PKSJ_BACSU_RecName__Full_Polyketide_synthase_PksJ_Short_PKS

PVAIVGISGRFPGA-MDIDEFWKNLEEGKDS-ITEVPKDR-WDWREHYGNPDT-DVNKTDIK-WGGFID---
GVAEFDPLFFGISPREADYVDPQRLMLTYVWKALED---AGCS---PQSLSGTGTGIFGTGNTGY----KDLFHR--ANLPIEGHAATGHMIP--
SVGPNRMSYFLNIHGSPSEPVETACSSSLVAIHRAVTA MQNGDCEMAIAAGVNTILTEEAHIS--YSKA----GML-STDGRCKTFSAD---A-NGYVRGEG-
VGMVMLKK--LEDAERDGNH-IYGVIRGTAENHGGGRANT-----LTSPNPKAQADLLVRA YRQAD---ID-PST---VTYIEAHGTGTSLGDPPIEINGLKA-
AFKELSNMVPDHRGIGSVKSNIGHLELAAGISGLIKVLLQMKHKTLVKS LHCE-TL-NPYLQ--LTDSPFYIVQEKQEWK--SV---
TDRDGNLPRRAGISFSGVGNNAHVIEEYMPHEATEQP NVIVLSAKNRSRLDRASQLLEVI-RNKKYQDLHRIAYTLQVGRE

>sp|P40872.4|PKSM_BACSU_RecName__Full_Polyketide_synthase_PksM

DIAIIGMAGRYPKA-KNIQEFWEQLKAGTDC-ITEIPNSR-WEWKESDGLDSP--AGKPLSK-WGGFIE---
EADCFDPQFFRISPREAEMMDPQERLFLETCEWAEIED---AGYT---PETIASPHVGVFAGVMHKDY----SLIGAE--ALSEHNPFPLSLNYAQ---
IANRVSYYCNFHGSPMAVDTVCSSSLTAVHLAIESIRNGECEAALAGVNL SLHPAKYIS--YGSV----GMH-SSDGYCHTFGKG--G-DGYVSGEG-
VGTVLLKP--LRKAEQDGR-IYAVIKGSAINHVGVKVS----GITVPSVAQADVIEACLEKGTG---ID-PRT---ISYVEAHGTGTSLGDPPIEVQGLVK-AFSRNTQD--
KQFCSIGSVKSNIGHAEAAAAGISGLTKTVLQLHHKTLVPSLHSE-EL-NPYLK--LDQTPFFVQHETKEWE--
QPSFTENGVDVYPRRAGLSFSGAGSNAHLILEEYIPQTPKDHPPALIVLSAKNMERLQEKAEQLLTAI-KQKRYTDLIRIAYTLQGTRE

>sp|P41175.1|KAS1_STRCM_RecName__Full_Putative_polyketide_beta-ketoacyl_synthase_1_AltName__Full_ORF1

RVAITGIEVLAPGG-LGRKEFWQLLSEGRTA-----TRGITFFDPAPFRSKVA-----AEADFCGLENGLSPEVRRMDRAAQFAVVTA-RAVED---
SGAE---LAHPPHRIGVVVGS AVGYR VVSDGGRLDLV--DHRYAVPHLYNYLV-P--
SSFAAEVAVAVGAEGPSTVVSTGCTSGIDAVGLAELVREGSVDVMVAGAVDAPISIPCVL-DAIKA---TTPRHADAPATASRPFDST---R-NGFVLGEG-
AAFFVLEE--LHSARRRGAH-IYAEIAGYATRSNAYHMTG-----LRDGAEMAEAIRLALDEAR---LN-PEQ---VDYINAHGSGTKQNDRHETA AFKALG-----
EHAYRTPVSSIKSMVGHSLGAIGSIEIAASALAMEYDVVPPTANLH-----

>sp|P41176.1|KAS2_STRCM_RecName__Full_Putative_polyketide_beta-ketoacyl_synthase_2_AltName__Full_ORF2

PVAVTGMGIAAPNGLGRPTTGRPPWAPRAAS-----AASRFDPSPGYAQLAG-----EIPGFRAA-EHLPGRLLVPQTDVTRLSLAAADWALAD---
AGVE---VAADFPLDMGVVTA SHAGEFGQDELQKLLGQ--GQPVLSAYQSAFW-Y--AVNSGQISIRHGMKGPSPGVVSDQAGGLDALAQARRLVRKG-
TPLIVCGAVEPRSPAGAGSP--SSPA--GGMSDSDEPNRAYLPFDRD---G-RGYVPGGGRGVVPPLER--AEAAPARGAE-VYGEAGPLARLPAPHSGRG-----
STRAHAIRALDDAG---TA-PGD---IRR VFADGGGRYPNDRAEAEASE-VF-----GPRGPVPTCPRTMTGRLHSGAAPLDVACALLAMRAGVIPPTVHID-----

>sp|P43678.2|KAS1_STRRM_RecName__Full_Oxytetracycline_polyketide_putative_beta-ketoacyl_synthase_1

RVVITGIGVAPGD-VGTPKPFWEMLTAGRTA---TRPISSFDASPFRSQVA-----AECDPFAAEGLSQRQVRAWDRTMQFAYVAAREALAD---
SGVT---GEADPRTGVMAGTACGYA VVSDEGRLWQV--DDAHGV PPLYDYFP-P--
SSMAAEIWLAEAEAGPAGVVSAGCTSGIDVLTHAADLVRDGAEMVAVAGASDAISIPITVAC--FDAI-KATTPRNDEPETASRPFDRT---R-NGFVLGEG-
AAFFVLEE--YAHARRR GAR-AYAEIAGYAGRCNAYSMTG-----LRSDGRELAEAVSRALDIAR---VD-PSE---VDYVNAHGSATKQNDLHETA AFKRSLG-----
-PHAYSVPISIKSMIGHSLGAICALEVAASALRIEHGVIPTANLR-----

>sp|P96202.2|PPSC_MYCTU_RecName__Full_Phthiocerol_synthase_polyketide_synthase_type_1

PIAVIGMGRFPGVGNNEQFWDLLCAGRSG-IVRVPAR-WDADAYYCDHT-VPGTICST-EGGFLTSW--
QPDEFDAEFFSISPREAAAMPQORLLIEVAWEALED---AGVP---QHTIRGTQTSVFGVTA YDYMLTLA GRLR----PVDLDA YIPTGNS-A--
NFAAGRLAYILGARGPAVVIDTACSSSLVA VHLACQSLRGRESMALVGGTNLLSPGPSIA--CSRW-----GML-SPEGRCKTFDAS---A-DGYVVRGEG-
AAVVVLKR--LDDAVRDGDR-ILAVIRGSAVNDGASS---GVTVPNGPAQALLAKALTSK---LT-AAD---IDYVEAHGTGTPLGDPPIEQLSLSK-
VFSRDRAGS---DQLVIGSVKTNLGHLEAAAGVAGLMAKVALAVHNGYIPRHLNFH-QL-TPHAS--EAASRLRIAADGIDWP--TT---GR-----
PRRAGVSSFGVSGTNAHVIEQAPDQRGPVAVSTLVVFGKTA PRVAATASVLADWL--DGPVPLADVAHTLNHRA

>sp|P9WQE0.1|PPSE_MYCTO_RecName__Full_Phthiocerol_synthase_polyketide_synthase_type_1

AIAVVGMAGRFPGA-KDVSAFWSNLRRGKES-IVTLSEQE-LRDAGVSDKTLA-DP--AYVR-RAPLLD---
GIDEFDAGFFGFPPLAAQVLDPOHRLFLQCAWHALED---AGAD---PARFDGS-IGVYGTSSPSGYLLHNLSHR----DPNAVLAEGLNFDQ-F--
SLLATRISHAFNLRGPIAVQVACSSSLVA VHLACL SLLSGECMALAGGSSLCIPHRVGYF--TSPG-----SMV-SAVGHCRPFVDV---A-DGTVFGSG-
VGLVVLKR--LAAAIDAADR-IHAVIRGSAINNDGSAKMG---YAAPNPAQAQDVIAEHAH VSG--ID-SST---VSYVECHGTGTPLGDPPIEQLLRA-AF---
EVSRSAPCVLGSVKSNIHLEVAAGIAGLIKTLCLKNKALPATLHYT-SP-NPELR--LDQSPFVQSKYGPWE--CD---G-----
VRRAGVSSFGVGGTNAHVVEEAPAAHAEPAGPVILLSAQTAAALGESRTALAAAL--ETQDPRLSDVAYTLARRRK

>sp|P9WQE1.1|PPSE_MYCTO_RecName__Full_Phthiocerol_synthase_polyketide_synthase_type_1

AIAVVGMAGRFPGA-KDVSAFWSNLRRGKES-IVTLSEQE-LRDAGVSDKTLA-DP--AYVR-RAPLLD---
GIDEFDAGFFGFPPLAAQVLDPOHRLFLQCAWHALED---AGAD---PARFDGS-IGVYGTSSPSGYLLHNLSHR----DPNAVLAEGLNFDQ-F--
SLLATRISHAFNLRGPIAVQVACSSSLVA VHLACL SLLSGECMALAGGSSLCIPHRVGYF--TSPG-----SMV-SAVGHCRPFVDV---A-DGTVFGSG-
VGLVVLKR--LAAAIDAADR-IHAVIRGSAINNDGSAKMG---YAAPNPAQAQDVIAEHAH VSG--ID-SST---VSYVECHGTGTPLGDPPIEQLLRA-AF---
EVSRSAPCVLGSVKSNIHLEVAAGIAGLIKTLCLKNKALPATLHYT-SP-NPELR--LDQSPFVQSKYGPWE--CD---G-----
VRRAGVSSFGVGGTNAHVVEEAPAAHAEPAGPVILLSAQTAAALGESRTALAAAL--ETQDPRLSDVAYTLARRRK

>sp|P9WQE2.1|PPSD_MYCTO_RecName__Full_Phthiocerol_synthase_polyketide_synthase_type_1

PVAVVIGCRFPGNVTGPESFWQLLADGVDT-IEQVPPDR-WDADAFYDPDPS-ASGRMTTK-WGGFVS---
DVDAFDADFFGITPREAVAMPDQHRMLLEVAVEALEH---AGIP---PDSLSGTRTGVMMLGSSWDY----TIVNIE--RRADIDAYLSTGTP-H--
CAAVGRIAYLLGLRGPVAVDTACSSSLVAIHLACQSLRLRETDVALAGGVQLTSPFTAIA--LSKW-----SAL-SPTGRCNSFDAN---A-DGFVRGEG-
CGVVIYLR--LADA VRDQDR-VLAVVRGSA TNDSGRSN---GMTAPNALAQORDVITSALKLAD---VT-PDS---VNYVETHGTGTPLGDPPIEFESLAA-
TYGLGKQG-GESPCALGSVKTNIHLEAAAGVAGFIKVALAVQRGHIPRNLFHT-RW-NPAID--ASATRLFVPTESAPWPAAG-----
PRRAAVSSFGVSGTNAHVVEEAPDAAGMPVYSALNVSGKTAARVASAAAVLADWMSGPGAAAPLADVAHTLNHRA

>sp|P9WQE3.1|PPSD_MYCTO_RecName__Full_Phthiocerol_synthase_polyketide_synthase_type_1

PVAVVIGICRFPNGVTGPESFWQLLADGVDT-IEQVPPDR-WDADAFYDPDPS-ASGRMTTK-WGGFVS----
DVDAFDADFFGITPREAVAMDQPHRMLEVAWEALEH---AGIP---PDSLSTRTGVMGLSSWDY----TIVNIE--RRADIDAYLSTGTP-H--
CAAVGRIAYLLGLRGPVAVDTACSSSLVAIHLACQSLRLRETDLALAGGVQLTSPPTAIA--LSKW-----SAL-SPTGRCSNFDAN---A-DGFVRGEG-
CGVVVLKR--LADAVRDQDR-VLAVVRGSAVNDGGRSN----GMTAPNALAQORDVITSALKLAD---VT-PDS---VNYVETHGTGTVLGDPIEFESLAA-
TYGLGKGQ-GESPCALGSKVKTNIGHLEAAAGVAGFIKAVLAVQRGHIPRNHFT-RW-NPAID--ASATRLFVPTESAPWPAAG-----
PRRAAVSSFLGSGTNAHVVEQAPDAAGMPYVSALNVSGKTAARVASAAAVLADWMSGPGAAAPLADVAHTLNRHRA

>sp|P9WQE4.1|PPSB_MYCTO_RecName__Full_Phthiocerol_synthesis_polyketide_synthase_type_I

PVAVVIGICRFPDGDVDPESFWDFLVAGRNA-ISTVPADR-WDAEAFYHPDPL-TPGRMTTK-WGGFVP---
DVAGFDAEFFGITPREAAAMDPQQRMLLEVAWEALEH---AGIP---PDSLGGTRTAVMMGVYFNEY----QSMMLAA--SPQNVDAVSGTGNA-H--
SITVGRISYLLGLRGPVAVDTACSSSLVAIHLACQSLRLRETDLALAGGVQITLSPETQIA--ISAW----GLL-SPQGRCAAFDAA---A-DGFVRGEG-
AGVVVLKR--LTDVAVRDGDQ-VLAVVRGSAVNDGGRSN----GVTAPNTAAQCDVIADALRSGD---VA-PDS---VNYVEAHGTGTVLGDPIEFALAA-TY---
GH-GGDACALGAVKTNIGHLEAAAGIAGFIKATLAVQRATIPPNLHFS-QW-NPAID--AASTRFFVPTQNSPWPTAEG-----
PRRAAVSSFLGSGTNAHVVEIQEGEGEDTGVSTLVVTGKTAQRMAATAQVLADWMEGPGAEVAVADVAHTVNHHR

>sp|P9WQE5.1|PPSB_MYCTU_RecName__Full_Phthiocerol_synthesis_polyketide_synthase_type_I

PVAVVIGICRFPDGDVDPESFWDFLVAGRNA-ISTVPADR-WDAEAFYHPDPL-TPGRMTTK-WGGFVP---
DVAGFDAEFFGITPREAAAMDPQQRMLLEVAWEALEH---AGIP---PDSLGGTRTAVMMGVYFNEY----QSMMLAA--SPQNVDAVSGTGNA-H--
SITVGRISYLLGLRGPVAVDTACSSSLVAIHLACQSLRLRETDLALAGGVQITLSPETQIA--ISAW----GLL-SPQGRCAAFDAA---A-DGFVRGEG-
AGVVVLKR--LTDVAVRDGDQ-VLAVVRGSAVNDGGRSN----GVTAPNTAAQCDVIADALRSGD---VA-PDS---VNYVEAHGTGTVLGDPIEFALAA-TY---
GH-GGDACALGAVKTNIGHLEAAAGIAGFIKATLAVQRATIPPNLHFS-QW-NPAID--AASTRFFVPTQNSPWPTAEG-----
PRRAAVSSFLGSGTNAHVVEIQEGEGEDTGVSTLVVTGKTAQRMAATAQVLADWMEGPGAEVAVADVAHTVNHHR

>sp|P9WQE6.1|PPSA_MYCTO_RecName__Full_Phthiocerol_synthesis_polyketide_synthase_type_I

PIAVVGMGCRFPFGISCEALWDFLCERRSS-ISQVPPQR-WQPFEGGPEVAALAR-TTR-WGSFLP---
DIDAFDAEFFEISPSEADKMDPQQRLLLEVAWEALEH---AGIP---PGTLRRSATGVFAGACLSEY----GAMASA--DLSQVDGWSNSGGA-M--
SIANRLSYFLDLRGPVAVDTACSSSLVAIHLACQSLRTQDCHLAIAAGVNLSSPAVFRG--FDQV----GAL-SPTGQCRAFDAT---A-DGFVRGEG-
AGVVVLKR--LTDVAVRDGDQ-VLAVICGSAVNDGGRSN----GLMAPNPAQMAVLRRAAYTNAG---MQ-PSE---VDYVEAHGTGTLLGDPIEARALGT-VL---
GRPESPLLIGSVKTNLGHTEAAAGIAGFIKTVLA VQHGIQIPPNQHFE-TA-NPHIP--FTDLRMKVVDQTTEWP--AT---GH-----
PRRAGVSSFGGTTNAHVVEIQEGEGQGLSPA VSTLVVAGKTMQRVSATAGMLADWM-EGPGAVALADVAHTLNRHRS

>sp|P9WQE7.1|PPSA_MYCTU_RecName__Full_Phthiocerol_synthesis_polyketide_synthase_type_I

PIAVVGMGCRFPFGISCEALWDFLCERRSS-ISQVPPQR-WQPFEGGPEVAALAR-TTR-WGSFLP---
DIDAFDAEFFEISPSEADKMDPQQRLLLEVAWEALEH---AGIP---PGTLRRSATGVFAGACLSEY----GAMASA--DLSQVDGWSNSGGA-M--
SIANRLSYFLDLRGPVAVDTACSSSLVAIHLACQSLRTQDCHLAIAAGVNLSSPAVFRG--FDQV----GAL-SPTGQCRAFDAT---A-DGFVRGEG-
AGVVVLKR--LTDVAVRDGDQ-VLAVICGSAVNDGGRSN----GLMAPNPAQMAVLRRAAYTNAG---MQ-PSE---VDYVEAHGTGTLLGDPIEARALGT-VL---
GRPESPLLIGSVKTNLGHTEAAAGIAGFIKTVLA VQHGIQIPPNQHFE-TA-NPHIP--FTDLRMKVVDQTTEWP--AT---GH-----
PRRAGVSSFGGTTNAHVVEIQEGEGQGLSPA VSTLVVAGKTMQRVSATAGMLADWM-EGPGAVALADVAHTLNRHRS

>sp|Q02059.2|KASA_STRCO_RecName__Full_Actinorhodin_polyketide_putative_beta-ketoacyl_synthase_1

RVVITGVGVRAPGG-NGTRQFWELTSGRTA-----TRRISFFDPSPYRSQVA-----AEADFDVPAEGFGPRELDRMDRASQFAVACAREAFAA--
SGLD---PDTLDPARVGVSLGSAVAYLLSDDSGRDWEV--DAAWLSRHMFDYLV-P--
SVMFAEVAWAVGAEQVPMVSTGCTSGLDVGNVRAIEGSAVDFMFAAGAADTPIVIVAC--FDAI-RATTARNDDPEHASRPFDDGT---R-DGFVLAEG-
AAMFVLED--YDSALARGAR-IHAEISGYATRCNAYHMTG----LKADGREMAETIRVALDESR---TD-ATD---IDYINAHGSGTRQNDRHETAAVKRALG-----
EHARRTPVSSIKSMVGHSLGAIGSLEIAACVLALEHGVVPTANLR-----

>sp|Q02062.1|KASB_STRCO_RecName__Full_Actinorhodin_polyketide_putative_beta-ketoacyl_synthase_2

SVLITGVGVVAPNG-LGLAPYWSAVLDGRHG--LGPVTR-FDVSRYPATLAG-----QIDDFHAP-DHIPGRLLPQTDPSRRLALTAADWALQD--
AKAD--PESLTDYDMGVVVTANACGDFTHREFRKLWSE--GPKSVSVYESFAWF-Y--AVNTGQISIRHGMRGPSALVAEQAGGLDALGHARRTIRRG-
TPLVSSGGVDSALDPGWVS-QIASG---RISTATDPDRAYLPFDER--A-AGYVPEGEG-GAILVLED--SAAAEARGRHDAYGELAGCASTFDPAPGSG-----
RPAGLERAIRLALNDAG---TG-PED---VDVVFADGAGVPELDAEAEARAIGR-VF-----
GREGVPVTPKTTTGRLYSGGGPLDVVTALMSLREGVIAPTAGVT-----

>sp|Q02251.2|MCAS_MYCBO_RecName__Full_Mycocerosic_acid_synthase

PVAVIGMGCRLPGGINSKDLWESLLRGDDL-VTEIPPDR-WDADDYDPEPG-VPGR-SVSRWGGFLD---
DVAGFDAEFFGISEREATSIDPQQRLLLETSWEAIEH---AGLD--PASLAGSSTAVFTGLTHEDY----LVLTIT--AGGLASPYVVTGLN-N--
SVASGRIAHTLGLHGPAMTFDTACSSGLMAVHLACRSLHDGEADLALAGGCAVLEPHACVA--ASAQ----GML-SSTGRCHSFADAD---A-DGFVRSEG-
CAMVLLKR--LPDALRDGNR-IFAVVRGTATNQDGRTE-----LTMPESDAQVAVYRAALAAAG---VQ-PET---GVVVEAHGTGTPIGDPIEYRSLAR-VY-----
GAGTPCALGSAKSNMGHSTASAGTVGLIKAILSLRHGVVPLLHFN---RLPDELSDVETGLFVQAVTPWPNGND-----
HTPKRVAVSSFGMSGTNVHAIVEEAPAPGDAEVPRLFMLSSTSSDALRQTARQLATWVEEHQDCVAASDLAYTLARGRA

>sp|Q03131.1|ERYA1_SACER_RecName__Full_6-deoxyerythronolide-B_synthase

-----AVLRGTAVNSDGA--SN---GLSAPNGRAQVRVVIQQALESQ---LG-PAD---
IDAVEAHGTGTGLDPIEARALFE-AY---GR--EQPLHLGSKVSNLGHQAAGVAGVIKMLAMRAGTLPRTLHAS-ER-SKEID--WSSGAILLDEPEPWP--
A-----GAR---PRRAGVSSFGISGTNAHAIIEEAPQ-----VAPVWLSASSAEGLRAQAARLAAHL--REHP-DPRDIAYSLATGRA

>sp|Q03132.3|ERYA2_SACER_RecName__Full_6-deoxyerythronolide-B_synthase

PIAIVGIGCRFPGGIGSPEQLWRVLAEGANL-TTGFPADRGWDIGRLYHPDPD-NPGTSYVD-KGGFLT---
DAADFDPGFFGITPREALAMPDQQRLLMLETAWEAVER---AGID---PDALRGTDGTGVFVGMNGQSY-----MQLLAG--EAERVDGYQGLGNS-A--
SVLSGRIA YTFGWEGPALTVDTACSSSLVGHILAMQALRRGECSLALAGGVTVMSPDYTFVD--FSTQ-----RGL-ASDGRCKAFSAR---A-DGFALSEG-
VAALVLEP--LSRARANGHQ-VLAVLRGSAVNQDQASN-----GLAAPNGPSQERVIRQALAAAG---VP-AAD---VDVVEAHGTGTGLDPIEAGALIA-TY---
GQDRDRPLRLGSKVKTNIHTQAAAGAAGVIVKVVLAAMRHGMPLRSLHAD-EL-SPHID--WESGAVEVLEEVVWPW--AG---ER-----
PRRAGVSSFGVSGTNAHVIEEAPAAARTERGLPFVLSGRSEAVVAQAARALAEHL-RDTPLEGLTDAAWTLATGRA

>sp|Q03133.4|ERYA3_SACER_RecName__Full_6-deoxyerythronolide-B_synthase

-----AVLAGSAVNQDGA--SN--GLTAPSGPAQQRVIRRALENAG---VR-AGD---
VDVVEAHGTGTRLDPIEVHALLS-TY---GADPDDPLWIGSVKSNIGHTQAAAGVAGVMKAVLALRHGEMPRTLHFD-EP-SPQIE--
WDLGAVSVVQARSWP--A-----GER---PRRAGVSSFGISGTNAHVIVIEEAP-----VPLVLSGRDEQAMRAQAGRLADHL--APEP-SLRDTGFTLATRAS

>sp|Q05470.3|PKSL_BACSU_RecName__Full_Polyketide_synthase_PksL_Short_PKS

EIAIIGISGRYPQA-DNIDELWEKLRDRGDC-ITEIPADR-WDHSLYYDEDKD-KPGKTYSK-WGGFMK---
DVKDFDPOFFHISPREAKLMDPQERLFLQCVYETMED---AGYT---REHLGRKSVGVYVGVMYEEY-----QLYGAQ--EQVRGRSLALTGNPSS---
IANRVSYFFDFHGPSIALDTCSSSLTAIHLACQSLQRGECEAAFGGVNVIHPNKYLM--LGQN----KFM-SSKGRCESFGQG--G-DGYVPGEG-
VGA VLLKP--LSKAVEDGDH-IYGIKGTAINHGGKTN-----GYSVNPNAQADVIKKAFVEAK---VD-PRT---VSYIEAHGTGTSLDPIEITGLSK-VFTQETDD-
KQFLAIGSAKSNIGHCESAAGVAVKLVLLQMKYRQLAPSLHSN-VL-NPNID--FLNSPFVKVQQUELEEWK--
RPIISVNGKDIELPRIAGVSSFGAGGVNAHILIEEYAPRLTKQHRSAFLVLSAKKEKQLKAYAEAMKDFV-TSNEDIDLEDMA YTLQTGRE

>sp|Q07017.1|OL56_STRAT_RecName__Full_Oleandomycin_polyketide_synthase_modules_5_and_6

-----AVVRGSAVNQDGA--SN--GLTAPNGPSQQRVIRAALADAG---LA-PAD---
VDVVEAHGTGTRLDPIEAQALLA-TY---GQAGGRPVLGWSVKSNIHTQAAAGVAGVMKMLVLRGGRVVPKTLHVD-EP-SPHVD--
WSAGAVELLTEERPW---EP---EAER---LRRAGISAFVSGTNAHVIVIEEAP-AAGD--LVVPWVVSGRDARALRAQAARLAAHV--S---
VSAVDVGSWSLVATRS

>AAR90242.1_polyketide_synthase__Botrytis_cinerea_1

RVAIVDYQ-PITGHPLDKTQFVQTLQEGEDA-LREHSAAH-VNAEAFVVRTTQQ-KLSTYIHR-TMSFPAHSPSDVALKKP---
MMPAKKQRLDVTQLYALNSCFERVAIIIASNLS---LSADRLQMRALWSGLPGSEG--AI-PLPELP--SINHWSWYGACGIG-----
TAQLAQYFGISADCYAVEAACASSLAAVHDAVRALQAGRYDAVIVGGIETATLERDLV---LCSA-----QMM-LSVSRIRPFSQG---A-DGFTPGDG-
GGFVMLTH-----HPVPR-AIATIEAISGSDSY-----SMTAPDPLGQALAIKKTLSLTA---ID-AQT---VQYLEAHGTGTGLDGRSEVMMLSKY-SY---
HRDKHSPLYIGSAKYNFHCFAGAGALSCKVLSAFEHERIPPTVSE--L-NVDLP--LGDIPAEVPPQAIPWR--LS---EDG-----
QRKAANAFGTGGINYL VIRQSS-----

>sp|Q7TXK8.1|MSL7_MYCBO_RecName__Full_Phenolphthiocerol_synthase_polyketide_synthase_type_1

PVAVVGIGCRFPFGVDGPDGLWVVSAGRVD-VSEFPTDRGWDVEGLYDPDPD-AEGKTYTR-WGAFLD---
DATGFDAGFFGIAPSEVLAMPDQQRLLMELVSWEALEH---AGID---PLSLRGSATGVYTGIFAASY-----GNR--DTGGLQGYGLTGTS-I--
SVASGRVSYVLGLGPAVSVDTACSSSLVAIHWAMSSLRSGECDLALAGGVTVMGLPSIFVG--FSRQ-----RGL-AADGRCKAFAAA---A-DGTGWGEG-
AGVVVLER--LDARRLGH-S-VLAVVRGSAVNQDQASN-----GLTAPNGLAQRVIAAALANAG---LS-AAD---VDVVEAHGTATTGLDPIEAQALLS-TY---
GQPAPQLVWVGSIKSNMGTQAAAGVAGVIMVQAMRHGVMPATLHVD-EP-SPRVD--WTSGAVSVLTEAREWS--VD---GR-----
PRRAVSSFGISGTNAHLILEEAPVTGGPRPSMVPVVISARSALTAQAQRLMAHV-QANPGLDPIVGC SLASRSV

>sp|Q7TXL6.1|PPSE_MYCBO_RecName__Full_Phthiocerol/phenolphthiocerol_synthase_polyketide_synthase_type_1

AIAVVMAGRFPGA-KDVSAFWSNLRGKES-IVTLSEQE-LRDAGVSDKTLA-DP--AYVR-RAPLLD---
GIDEFDAGFFGFPLAAQVLDPQHRLFLQCAWHALED---AGAD---PARFDGS-IGVYGTSSPSGYLLHNLSSH---DPNAVLAEGLNFDQ-F--
SLLATRISHAFNLGRGPAVAVDTACSSSLVAIHLACQSLRLETDVLAGGVQLTSPFTAIA--LSKW-----SAL-SPTGRCNSFDAN---A-DGTVRGE-
VGLVLLKP--LAA AIDAGR-IHAVIRGSAINNDGSAKMG---YAAPNPAQADVIAEAHAVSG--ID-SST---VSYVECHGTGTPLDPIEIQGLRA-AF---
EVSRSAPCVLGSVKSNIHLEVAAGIAGLIKITLCLKNKALPATLHYT-SP-NPELR--LDQSPFVQSKYGPWE--CD---G-----
VRRAGVSSFGVGGTNAHVVEEAPAAHAEPAGPVILLSAQTAALGESRTALAAAL--ETQDPRLSDVAYTLARRRK

>sp|Q7TXL7.1|PPSD_MYCBO_RecName__Full_Phthiocerol/phenolphthiocerol_synthase_polyketide_synthase_type_1

PVAVVGIGCRFPFNGVTPESFVQLLADGVDI-IEQVPPDR-WDADAFYDPDPS-ASGRMTTK-WGGFVS---
DVFADDFGFFGITPREAVAMPDQQRLLMELVSWEALEH---AGIP---PDSLGRTRTGVMMLGSSWDY-----TIVNIE--RRADIDAYLSTGTP-H--
CAAVGRIAYLLGLRGPAVAVDTACSSSLVAIHLACQSLRLETDVLAGGVQLTSPFTAIA--LSKW-----SAL-SPTGRCNSFDAN---A-DGTVRGE-
CGVVVLLK--LADAVRDQDR-VLAVVRGSAVNQDQASN-----GMTAPNALAQRDVITSALKLAD---VT-PDS---VNYVETHGTGTPLDPIEFESLAA-
TYGLGKQG--GESPCALGSVKTNIHLEAAAGVAGFIKAVLAVQRGHIPRNLFH-RW-NPAID--ASATRLFVPTESAPWAAAAG-----
PRRAVSSFGVSGTNAHVVEEAPDAAGGMPYVSALNVSGKTAARVASAAA VLADWMSGPAAAPLADVHTLNRHRA

>sp|Q7TXL8.1|PPSC_MYCBO_RecName__Full_Phthiocerol/phenolphthiocerol_synthase_polyketide_synthase_type_1

PIAVIGMGRFPFGVNNPEQFWDLLCAGRSG-IVRVPAQR-WDADAYYCDHT-VPGTICST-EGGFLTSW--
QPDEFDAEFFSISPREEAAMPDQQRLLMELVSWEALEH---AGVP---QHTIRGTQTSVFGVTA YDYMLTLAQRRL---PVDLDAYIPTGNS-A--
NFAAGRIAYILGARGPAVAVDTACSSSLVAIHLACQSLRLETDVLAGGVQLTSPFTAIA--LSKW-----SAL-SPTGRCNSFDAN---A-DGTVRGE-
AAVVVLLK--LDDAVRDGNR-ILAVVRGSAVNQDQASN-----GVTVPNGPAQALLAKALTSSK---LT-AAD---IDVVEAHGTGTPLDPIELDSLK-
VFSRDRAGS---DQLVIGSVKTNLGHLEAAAGVAGLMAKAVLAVHNGYIPRHLNFH-QL-TPHAS--EAASRLRIAADGIDWP--TT---GR-----
PRRAGVSSFGVSGTNAHVVEEAPDQGRPVAVSTLVVFGKTAAPRVAATASVLADWL--DGPVPLADVHTLNRHRA

>sp|Q7TXL9.1|PPSB_MYCBO_RecName__Full_Phthiocerol/phenolphthiocerol_synthase_polyketide_synthase_type_1

PVAVVGIGCRFPDGDGPEFVDFVLAGRNA-ISTVPADR-WDAEFYHPDPL-TPGRMTTK-WGGFVP---
DVAGFDAEFFGITPREAAAMPDQQRLLMELVSWEALEH---AGIP---PDSLGRTRTAVMMGVYFNEY-----QSMMLAA--SPQNVDAVSGTGNA-H--

SITVGRISYLLGLRGPVAVDTACSSSLVAVHLACQSLRLRETDLALAGGVSITLRPETQIA--ISAW----GLL-SPQGRCAAFDAA---A-DGFVRGEG-
AGVVVVKR--LTDVARDGDQ-VLAVVRGSAVNQDGRSN----GVTAPNTAAQCDDVIADALRSGD---VA-PDS----VNYVEAHGTGTVLGDPIEFALAA-TY---
GH-GGDACALGAVKTNIGHTLEAAAGIAGFIKATLAVQHRATIPPNLHFS-QW-NPAID--AASRFFVPTQNSPWPTAEG-----
PRRAAVSSFGGLGTTNAHVIIQEGSEEGEDTGVSTLVVTGKTAQRMAATAQVLADWMEGPGAEEVAVADV AHTVNHHR

>sp|Q7TXM0.1|PPSA_MYCBO_RecName__Full_Phthiocerol/phenolphthiocerol_synthesis_polyketide_synthase_type_I

PIAVVGMGCRFPGGISCEPALWDFLCERRSS-ISQVPPQR-WQPFEGGPPEVAALAR-TTR-WGSFLP---
DIDAFDAEFFEISPSEADKMDPQQRLLLEVAWEALEH---AGIP---PGTLRRSATGVFAGACLSEY----GAMASA--DLSQVDGWSNSGGA-M--
SIANRLSYFLDLRGPVAVDTACSSSLVAIHLACQSLRTQDCHLAIAGVNLNLSPAVFRG--FDQV----GAL-SPTGQCRAFADAT---A-DGFVRGEG-
AGVVVVKR--LTDVARDGDR-VLAVICGSAVTDQDGRSN----GLMAPNPAQAQMAVLRAAYTNAG---MQ-PSE----VDYVEAHGTGTLGDPIEARALGT-VL---
GRPEDSPLLIGSVKTNIGHTLEAAAGIAGFIKTVLAVQHRGQIPPNQHFV-TA-NHIP--FTDLRMKVVDVTQTEWP--AT---GH-----
PRRAGVSSFGGTTNAHVIEQEGQEGQLSPA VSTLVVAGKTMQRVSATAGMLADWM-EGPGAVALADV AHTLNHRS

>sp|Q9ZGI2.1|PIKA4_STRVZ_Full_Pikromycin_polyketide_synthaS

PMAIVGMSCRFAGGIRSPEDLWDAVAAGKDL-VSEVPEERGWDDISLYDPVPG-RKGTTYVR-NAAFDL---
DAAFGDAEFFEISPSEADKMDPQQRLLLEVAWEALEH---AGIP---PGTLRRSATGVFAGACLSEY----GAMASA--DLSQVDGWSNSGGA-M--
AVASGRIAYSLGLEPAVTVDTACSSSLVALHLALKGLRNGDCSTALVGGVAVLATPGAFIE--FSSQ----QAM-AADGRTKGFASA--A-DGLAWGEG-
VAVLLER--LSDARRKGHR-VLAVVRGSAVNQDGRSN----GLTAPHGSPQQLIRQALADAR---LT-SSD----VDVVEHGTGTRLGDPIEAQALLA-TY---
GQAPGSPLLRGLKSNIGHTLEAAAGIAGFIKTVLAVQHRGQIPPNQHFV-TA-NHIP--FTDLRMKVVDVTQTEWP--AT---GH-----
LRRAGVSAFVGTTNAHVLEEAPAEPPAGGGVVPVSAKTSAAALDAQIGQLAAYA-EDRTDVPDPAVAARALVDSRT

>sp|Q9ZGI3.1|PIKA3_STRVZ_Full_Pikromycin_polyketide_synthaS

PVAIVGMACRLPGGVASPEDLWQLVAGDGA-ISEFPQDRGWDVEGLYDPPDP-ASGRTYCR-SGGFLH---
DAGEFDAAFFGISPSEALAMDPQQRLLLEVAWEALEH---AGIP---PGTLRRSATGVFAGACLSEY----GAMASA--DLSQVDGWSNSGGA-M--
GFLSGRIAYSLGLEPAVTVDTACSSSLVALHLALVQALRKGECMDALAGGVTVMNADLFVQ--FSRQ----RGL-AADGRSKAFATS--A-DGFGPAEG-
AGVLLVER--LSDARRNGHR-VLAVVRGSAVNQDGRSN----GLTAPHGSPQQRVIRRALADAR---LA-PGD----VDVVEAHGTGTRLGDPIEAQALLA-TY---
GQSEIQPLRGLKSNIGHTLEAAAGIAGFIKTVLAVQHRGQIPPNQHFV-TA-NHIP--FTDLRMKVVDVTQTEWP--AT---GH-----
LRRAAVSSFGISGTNAHVLEEAPAEPPAGGGVVPVSAKTPAALDAQIGQLAAYA-DGRTDVPDPAVAARALVDSRT

>sp|Q9ZGI4.1|PIKA2_STRVZ_Pikromycin_polyketideS

PVAIVGMACRLPGGVASPEDLWRLVAGGEDA-ISGFPQDRGWDVEGLYDPPDP-ASGRTYCR-AGGFLD---
EAGEFDAAFFGISPSEALAMDPQQRLLLEVAWEALEH---AGIP---PGTLRRSATGVFAGACLSEY----GAMASA--DLSQVDGWSNSGGA-M--
SIMSGRVS YTLGLEPAVTVDTACSSSLVALHLALVQALRKGECGLALAGGVTVMSTPTTFVE--FSRQ----RGL-AEDGRSKAFAAS--A-DGFGPAEG-
VGMLLVER--LSDARRNGHR-VLAVVRGSAVNQDGRSN----GLTAPNGSPQQRVIRRALADAR---LT-TAD----VDVVEAHGTGTRLGDPIEAQALLA-TY---
GQDTEQPLRGLKSNIGHTLEAAAGIAGFIKTVLAVQHRGQIPPNQHFV-TA-NHIP--FTDLRMKVVDVTQTEWP--AT---GH-----
LRRAAVSSFGISGTNAHVLEEAPVDEPSVGGVVPWLVS AKTPAALDAQIGRLAFAA-SQGRADPGA VARVLADGRA

>sp|Q9ZGI5.1|PIKA1_STRVZFull_Pikromycin_polyketide_S

PVAIVGMACRLPGGVASPEDLWRLVAGGEDA-ISEFPQDRGWDVEGLYHPDPE-HPGTSYVR-QGGFIE---
NVAGFDAAFFGISPSEALAMDPQQRLLLEVAWEALEH---AGIP---PGTLRRSATGVFAGACLSEY----GAMASA--DLSQVDGWSNSGGA-M--
SVMSGRVS YTLGLEPAVTVDTACSSSLVALHLALVQALRKGECMDALAGGVTVMSTPTTFVE--FSRQ----RGL-AEDGRSKAFAAS--A-DGTSWSEG-
VGMLLVER--LSDARRNGHR-VLAVVRGSAVNQDGRSN----GLTAPNGSPQQRVIRRALADAR---LT-TSD----VDVVEAHGTGTRLGDPIEAQALLA-TY---
GQDDEQPLRGLKSNIGHTLEAAAGIAGFIKTVLAVQHRGQIPPNQHFV-TA-NHIP--FTDLRMKVVDVTQTEWP--AT---GH-----
LRRAAVSSFGISGTNAHVLEEAPVGSVGGVTPWVVS AKSAAALDAQIERLAFAA-SRDRTV DAVAHVLADGRA

>TRINITY_DN10243_c0_g1_i2_

-----HINTLEQSKTL-----RFLNKITMKIRFSFEIINCKILN---IGID---PNSLSGTNTGIFIGSCYDEF-----V--
NAYSNDHTKFGVGTK---QFFAEMVAHKFNLRGPKSLIDTACASSFSALHEAIVSLRSNQCDDRAIVMGLNICLRATTQLT--FTHM-----NMI-SPDGHCCKLDED--
-A-NGTAKGEA-LVVMILQK--KSEAKR----ITATVHTKTNCDGTTELQ---ITYPSTEFQRDLIRDTTSEIG---ID-PLN---
VKTCEAHCTGTQAGDPTEMRAICE-SM----CIERKDPLLIGALKSNIGHAEGASGFCSLTKVILSFENKCIPANMHMT-VP-NSRIE-GLVSGILKPVIKNTQFE----
-----GELACLNCFGFGGVNVHVIVKHNDKHQIVNQIPRLVQMCGRNEELNQTFTSLLRNP--EKLTRDYLSLINDISKTSP

>TRINITY_GG_3134_c21_g1__TRINITY_GG_3134_c21_g1_i2

DIVISGVGGRFPES-DSIDEFRDNLNNVDM---ITADDRRWPTPLYGMSPP---RMGKLK-----EIDKLDSTFFGIVPKVADEVDPQARILLETTYEAIFFD---
AGIN---PQTLRGSNTGVYGYTSVE-----VQEDLQ--SSKVESLLWFQGNS-K--
AFYANRVSFVDFHGPSMSIDVACAASMV ALDIAVTDIRLGLKCDQAIVAGVSINLQPFNTNHI--YQVN----NIG-SKEGMSRVWDQD---A-NGYVRGET-
VASLFLQR--KSDSKR----IYATILHSRTNIDGYKISG---MFFPSSSEQYDLMVTTYTEAG---IN-PHD----VNYFEHGTGTVGDPQEARAILE-AY---
CKDRKSVLPVGLLKSNIHGEGASGASLAKLLIVYENKKIPANLNLK---TLKTEIAEMV PPLVPVTENTDYE-----
PGIAGVNSFGIGGVNCHALLKPNKK-----LVNICGRTEEA VNYIFEFIEKNP--QKVRTDFLALIGEIVNPVS

>TRINITY_GG_3293_c9_g1__TRINITY_GG_3293_c9_g1_i10

-----NQRMGKLK-----EIDKFDGVFFGLMSEIADAVDPHSRILLETTYEAICD---AGVN---
PQTLRATKTGVYIGYSSIE-----IQLDSR--TSMKDSATWAPGSS-K--
AMYSNRISFFDFKGPSLVIDTACSSSMVAFDVA VTDLRLGKCDQAIVAGVGTNICLQPFNTNHI--YQTI----KFN-SPDGISRVWDEE---S-VGFVRGET-
VACLFLQR--KSDAKR----IYATVLHSRTNIDGYKMG---PFFPSSSEQYDLMVTTYTEAG---VD-PLD----VTYFEHGTGTVGDPQEARAIFN-AY---
CDGREGTLPGLLKSNIHGEGACGIASITKVIISYENECLPNLNLK---QLKTEISVMCPLFPVTENLTYI-----
PGIAGVNSFGVGGVNGHALLQPNYE-----LINICARNEDSLKSMFNIESHS--NKITQHFLALITDVMKTKP

>TRINITY_GG_3293_c9_g1__TRINITY_GG_3293_c9_g1_i4

EIVISGMSGRFPES-DSTDEFAQNLNKNVDM---ITEDRRRWPTDLYS---MNQRMGKLK-----EIDKFDGVFFGLMSEIADAVDPHSRILLETTYEAICD---
AGVN---PQTLRATKTGVYIGYSSIE-----IQLDSR--TSMKDSATWAPGSS-K--

AMYSNRISFFDFKGPSLVIDTACSSSMVAFDVAVTDLRLGKCDQAIVGGTNICLQPFTNHI--YQTI----KFN-SPDGISRVWDEE---S-VGFVRGET-
VACLFLQR--KSDAKR----IYATVLHSRTNIDGYKMG---PFFPSSECQRDLMTVTTYKEAN---VD-PLD---VTYFEAHGTGKAGDLQEARAIFN-AY----
CDGREGLPIGLLKSNIHGHEGACGIASITKVIISYENECIAPNLNLK-QL-KTEIS--VMCPPLFPVTENLTYI-----
PGIAGVNSFGVGGVNGHALLQPNYE-----LINICARNEDSLKSMFNFIESH--NKITQHFLALITDVMKTKP

>TRINITY_GG_3293_c9_g1__TRINITY_GG_3293_c9_g1_i8

-----NQRMGKLK-----EIDKFDGTVFFGLMSEIADAVDPHSRILLETYYEAICD---AGVN---
PQTLRATKTGVYIGYSSIE-----IQLDSR--TSMKDSATWAPGSS-K--
AMYSNRISFFDFKGPSLVIDTACSSSMVAFDVAVTDLRLGKCDQAIVGGTNICLQPFTNHI--YQTI----KFN-SPDGISRVWDEE---S-VGFVRGET-
VACLFLQR--KSDAKR----IYATVLHSRTNIDGYKMG---PFFPSSECQRDLMTVTTYKEAN---VD-PLD---VTYFEAHGTGKAGDLQEARAIFN-AY----
CDGREGLPIGLLKSNIHGHEGACGIASITKVIISYENECIAPNLNLK-QL-KTEIS--VMCPPLFPVTENLTYI-----
PGIAGVNSFGVGGVNGHALLQPNYE-----LINICARNEDSLKSMFNFIESH--NKITQHFLALITDVMKTKP

>TRINITY_GG_4863_c25_g1__TRINITY_GG_4863_c25_g1_i2

DIVISGVAGRFPES-DNIDELKENLYNNVDM---ITEDERRWPLGLYGLPTRS-GKIK-----DLSKFDAQFFGVHKGKANLMDPQARLLELTYYEAIAD--
AGIN---PQTLRGTGTGVYIGACVSEV-----EEGLAM--DISKVSQYALTGCS-R--
SMFANRVSYTFDFHGPSYSMDTACSSSFLALQQAVALGLRTGQCDMAVVGGVNICLRPVSALQ--FHLK----NML-AVDGKCKFLDAS---A-NGYVRSET-
CSVIFLQK--KSEAKR----IYATVIHAKTNTDGYKDGQ---ITYPSWQSQSALMNSTLREAG---IK-PTD---INFVEAHGTGTGAGDPTEQAIFD-VF---
CDGREGLPIGLLKSNIHGHEGACGIASITKVIISYENECIAPNLNLK-QL-KTEIS--VMCPPLFPVTENLTYI-----
DGVVAINSGFVGGVNVHVLKPKHQYRVIDNIPRLPICGRTEESVNYILDLEQNP--KKVTRDLLALLYDISQTN

>TRINITY_GG_6264_c208_g1__TRINITY_GG_6264_c208_g1_i1

-----NTLEQSKYL-----RFLNKITMKIRFSFEIINCKILN---IGID---PNSLSGTNTGIFIGSCYDEFV-----
NAYSNDHTKVFVGYK---QFFAEMVAHKFNLRGPKSLIDTACASSFSALHEAIVSLRSNCQDRAIVMGLNICLRATTQLY--FYHM----NMI-SPDGHCKCLDED-
--A-NGYAKGEA-LVVMILQK--KSEAKR----IYATVVHTKTNCDDGYTELG---ITYPSYEFQORDLIRDYSEIG---ID-PLN---
VKYCEAHCTGTQAGDPTEMAICESMC-----ERKDPDLLGALKSNIGHAEGASGFCSLTKVILSFENKIPANMHMT-VP-NSRIE-GLVSGILKPVIKNTQFE---
-----GELACLNCFGFGGVNVHVIVKHNDKHQIVNQIPRLVQMCGRNEELLNQFTTSLLRNPEKLT--RDYLSLINDISKTS

>TRINITY_GG_6449_c125_g1__TRINITY_GG_6449_c125_g1_i1

RVVVTGLGIVSPIG-VGVEKVVNNLISGRCG-ITEVIGSG-YES-----IPCK-IAAYVPK---NDLCLEQSF---AKNELRRLSKSTIYALIAAEEALTD---
AKWK---PTKERDKETGVAVGMGMVDEVVESGTVLRDV--GFNKISPHFVTKVL-M--
NMPAGHISMRYGLTGNHTVSTACTTGVSIGDAFNFIQRGAADVMICGGTEAVISPLSIAS--FARIRALCTQFNDNPSKASRPFDK---R-CGFVMGEG-
CGLVVLEE--LNHALNRKAK-IYAEIIGYGLSGDANHITA----PREDGKGAFECMKASIDDAH--IR-LDD---VTHINSHATSTPLGDKAELIAIKQ-LF---GE-
HSKNIAITSTKGTSTHLLGAAGSVEAIFILSCYNSLIPPTINLE-EPIDKELN-----IVANNPQEWN--TK---N-----RRIAITNSFGFGGTNASLVSINF-----

>TRINITY_GG_6449_c125_g1__TRINITY_GG_6449_c125_g1_i2

RVVVTGLGIVSPIG-VGVEKVVNNLISGRCG-ITEVIGSG-YES-----IPCK-IAAYVPK---NDLCLEQSF---AKNELRRLSKSTIYALIAAEEALTD---
AKWK---PTKERDKETGVAVGMGMVDEVVESGTVLRDV--GFNKISPHFVTKVL-M--
NMPAGHISMRYGLTGNHTVSTACTTGVSIGDAFNFIQRGAADVMICGGTEAVISPLSIAS--FARIRALCTQFNDNPSKASRPFDK---R-CGFVMGEG-
CGLVVLEE--LNHALNRKAK-IYAEIIGYGLSGDANHITA----PREDGKGAFECMKASIDDAH--IR-LDD---VTHINSHATSTPLGDKAELIAIKQ-LF---GE-
HSKNIAITSTKGTSTHLLGAAGSVEAIFILSCYNSLIPPTINLE-EPIDKELN-----IVANNPQEWN--TK---N-----RRIAITNSFGFGGTNASLVSINF-----

>TRINITY_GG_6602_c113_g1__TRINITY_GG_6602_c113_g1_i1

-----NLTQAPFSNGI--YQSI----GLL-ASDGKCKVWDKR--A-DGFVRSET-VGALFLQK--KSEAKR----IYATLLHAKTNTDGFKAIG---
LFSFVLRQRDLMIETYHEAG--VD-PND---IKFFESHGTGTNVGDPQEAKAIAAD-AY---
CHDRKEPLLLGAVKSNLGHSESSGLCSVAKVIVAFENKIPANLHFE-EP-KPEIE-CVVNKTLPVPMKNTPE-----
NGIVGNSFGVGGVNAHALLKSNKDYKIADPIPRLVNVSGRTEAAVKHIFDFIENNP-RKAHRALLNDSMKTLVIRGS

>XP_002589799.1_hypothetical_protein_BRAFLDRAFT_90481__Branchiostoma_floridae_

EVAIVGLWCRFPFA-EGPDEFWRVLENGEDC-MREIPPER-WNQEAWYNPDRN-TPGKSFVE-RAGFVD---
DFKDFDNRLFNISDLEASRMDPQQRWMLCSYKALEN---AGIP---LKNVYNTDTGVFVGMNYDY-----YWNSTLDMADVSSNTATGVS-I-
PVVANRVSYAFNLTGPSMTVDTACSSGMTALHLGCQAIRAGDCTMAICGGVNFILNPGMFVQ--LCRA-----GMV-CPDGRCKPFSAA---A-NGYARGEG-
CGVVIKS-----FRKEQLIRRLYEQHN--VD-PRH---IDYIEAHGTGTPVGDVPEARSLGKAIGQSRDSS--
EPPVLIGSVKSNFGHLESAAAMAGLIKVLLMMKHKKIAPTLHFN-EP-NPNID--FEGLIKVCTEPIWSSRNKD-----
KMMACVNSFGVGGNAHAILFSEPSLGRHEEPNIAVSANGKESLQASMKDLISFLEKNQC-TALSQAYTSSVKRT

>XP_002598380.1_hypothetical_protein_BRAFLDRAFT_96863__Branchiostoma_floridae_

KVAIVGIGCRYPGVHTPADFWTMAEGRDC-TIPPDVVR-FDTSFLWHPY-K-TPGKLYNR-CGGYLQ---
NVFEFDRQFFKIPPEANHLDPQIQLLEVTWEALEN---AGIP---PRSIRGNTGVYVGVTSSEY--LT-MTCS---PYSNISQYNTSGTN-S--
CMVSNRISYEFDLHGSPFSVDTACSSLSYIHLASEAIRKGDSCMAIAGGVNMLLPTISVG--FCQA-----GML-SPDGKCKSFDAS---A-DGYCRSEG-
AGVVLKPL--LSRALADGDR-VYAVIRGGTLTNDGR--TP--GIANPSYDAQLDLVEKACAAAK--VH-PHD---IQYVEAHGTGTVGDRTEANALGQ-IL---
GRKEDPPLYIGSVKSNFGHAEGAAGVAGIILKALMISKQIPRVVHFS-SP-NPDIH--FDALNIKVPSTLLQWE-----GKG-----
SRLAGCSSFGGGANAHILRPPTRGTERETKTIMLLSGNTKAALKEQVEHWISFL--SDTTDRFLQSLYTAANRG-

>XP_002599684.1_hypothetical_protein_BRAFLDRAFT_205831__partial__Branchiostoma_floridae_

SIAIVGLWCRFPHA-DSPDDFWRVVLVNGEDC-MEEIPDR-WSQDAWYSPDKN-APGKIFVQ-RAGFVQ---
GYKMFDPFLGLRDEEASRMDPQQRFMLECSYKAFEN---AGIT---MDELHGSDTGVFVGLMNTY-----LLDGDIL--DLQMTNHTITGTA-T--
SLVAARVAYTFNLTGPALTVDTACSSGLYAVHLGCQAIKTGDCSMAVCGGVSFILRPNMFVS--LCRA-----GMA-SPEGRCKPFSAA---A-DGYARGEG-

CGVVILKK--LSKALENNNDH-IWGVIIH-TAVNQDGRRTIP---ITAPSQSQEKLRLSILERYR---FD-PDH---IDYIEAHGTGTPVGDPEANSLGN-VI---
GKADDDPVLGKSVKGNHGLESAAGLAGLIKVLMMKQYKQIVPNVHFD-RP-NPNID--FDHLRLYVPTVLDWT-----LRG--
KDRRLACVNSFGFGGSNSHALVEQFPQVNEKQAYVVVVVSAKRESLKLSEVEDLIEHL-EQNPDISLERLAYTSTVRRRT

>XP_002605916.1_hypothetical_protein_BRAFLDRAFT_87410__Branchiostoma_floridae_

PIAVVGIGCRMPGGTTPSPKFWDVISEGRNV-ITEVPAER-WSLDQVYHSTDPH-QPGTHVTR-RAGFVD---
DIDMFDHTFFKISPREAAMMDPQQRHLLLEVITYEAFED---AGIT--PESVSES-CGVFVIGMMDY-----ALNMAD--DKHLFNSYANTGVA-H--
SVAANRISYAFNLKGPSLAVDTACAASMTALHLACSSLRNKECSVALVEGANVLLMPEVTVV--FSAM-----GVL-SPDGRSFPDAS---A-NGYVRSEG-
FGAAILKP--LSDAIRDRDH-VYSVIRGSAISDNQFSQS-----ITMPSSSQEKLRLMRTTYARFG--VP-LSS---VMYVEAHGTSTPVGDPAEAEAIK-TF---
GRRPASPLKIGSAKSNFGHMECAAGMVGVIKTALMLDRRALCPVSNYT-KP-SPKAD--FDELGISVQTEVETFP--DN---K-----
KVTLGVNSFGFGGSLAHVIMEANSAPDQEGDFILPLSGKSPDALRDLAKWLTYSK-DEKDA---INVSSWVATRRN

>XP_002608071.1_hypothetical_protein_BRAFLDRAFT_91451__Branchiostoma_floridae_

PVAIVGIGCRMPGGTTPSEKFWDVISEGRNV-ITEVPPER-WSLDQVYHSTDPH-QSGT-HVTRKAGFVD---
GIDMFDHTFFKISPREAAMMDPQQRHLLLEVITYEAFED---AGIV--PEKVSSES-CGVFVIGMMDY-----AMGLAP--NRHLFNSYASTGLE-H--
SLAANRISYAFNLKGPSLAVDTACAASMTALHLACSSLRNKECSVALVEGANVLLMPEVTVV--FSAM-----GVL-SPDGRSFPDAS---A-NGYVRSEG-
FGAAILVLP--LKDAAARDGDH-ICYVIRGTAADNNGFSQ-----SITMPSSSAQEILMKNTFARFG--VP-LSS---VSYIEAHGTSTPVGDPAEAEAIK-TF---
GPHRRSPLKIGSCKSNFGHMECASGIVGVIKTALMLDRRLTCLPSINFT-SP-NPEVD--FEALSVSQTKLEPFVTNE-----
KMIAGVNSFGFGGSLAHVIMEANSAPDQEGDFILPLSGKSSDALRDLSSKWLTFQ--DEKD--ALSWSWVATRRN

>XP_002610100.1_hypothetical_protein_BRAFLDRAFT_89867__Branchiostoma_floridae_

--AVVIGICRMPGGTTPSPKFWDVIREGRNV-ITEIPPER-WSLEAYHSTDPH-QSGTHVTR-KAGFVD---
DIDMFDHTFFKISPREAAMMDPQQRHLLLEVITYEAFED---AGIT--PESV-SESCGVFVIGMMDY--AL-FMAG---DKHLFNSYVNTGIA-H--
SVAANRISYAFNLKGPSLAVDTACAASMTALHLACSSLRNKECSVALVEGANVLLMPEVTVV--FSAM-----GVL-SPDGRSFPDAS---A-NGYVRSEG-
FGAVLIK--LSDAIRDRDH-VYSIIRGSAISDNQF--SH---SITMPSSSAQEQLMRTTYARFG--VP-LSD---VLYVEAHGTSTPVGDPAEAEAIK-AF---GP--
ASPMRIGSAKSNFGHMECAAGMVGVIKTALMLDKRTLCPVSNYT-SP-TPKTD--FEELGISVQTKVENFP--DN---Q-----
IVKLGVNSFGFGGSLAHVIMEANSAPDQEGDFILPLSGKSSDALRDLSSKWLTFQ--DEKD--ALSWSWVATRRN

>XP_003222100.1_PREDICTED__phthioceranic/hydroxyphthioceranic_acid_syntheselike__Anolis_carolinensis_

-IAITGICNFPGG-EGLDSEFWTVLENGRNC-TTEIPPER-FNISEWYEPDNN-KPNKICTT-RAALLD---
EFNAFDHQLFGINKEEAHIDPQKLLLECTYRALED---AGVT--RENISDTKTGVFVGLKNRDY--ES-IASR---AVGKTHYDGTGTA-S--
STAANRISYAFNLKGPSLAVDTGHSSFLSALHLGKAIKQGDCEAALCGGVNCHIEPRVVFV--LKA---KML-SPDGITKPFK---A-DGYGRGEG-
CGVLLKP--LMKAQEDLNK-IWGVLSITAVSQNGK---P---VTKLQVEQEKLRLSIYPA-Q--IN-PSV---VQYIETHSIGNPAQDTAEASLGN-II---
GTSNPLLLKIGSVMGNIHTESAAGAAGLIKVLMMHGHKIVPSLHFS-ES-NSSIN--TKKLNLIPTTVEKWD--ES---S---
EFGRVAGINCFGYEGNIIHAVVRQVQKRPV---ELFIISA VSGCSLRQTMEDTARYV--KRNDINLQNLAYTSACRRS

>XP_003222101.1_PREDICTED__phthioceranic/hydroxyphthioceranic_acid_syntheselike__Anolis_carolinensis_

EVAIVGICNFPGG-EGLDNFWQVLEVGKNC-VQEIPPER-FDTTEWYDTSN-KQKTTTK-HAAFID---
EFNTIDNKLFGINDVEVEYMDPQKLLLECTYRALED---AGVT--RENINGSSTGTGVFVGMNQDY--RI-TRSR---TSCTINHYDGTGTA-M--
SIAANRISYAFNLKGPSLAVDTACSSFLSALHLGKAIKQGDCEAALCGGVNCHIEPRVVFV--LKA---KMI-SPEGISKPFST---A-DGYGRGEG-CAVLLKLP--
LKAQEDFSK-IWGVISMASAVNQNGRSVTP---ITRPSQEQENLLRRIYPA-H---VD-PTT---VQYVEAHGTGTPAGDPVEAESVGN-VL---
GKSNFPPIKIGSVKGNIGHTESAAGAAGLIKVLMMHGHKIVPSLHFS-ES-TSSIN--TEKLNLIPTTVEKWD--EP---S---
EFGRIAGINSFGFGGTNAHVVRQVQKRPV---ELFLISSASVNSLKLTMEDMARYL--KTKDIALPNLAYTSACRRS

>XP_003222102.1_PREDICTED__probable_polyketide_synthase_1__Anolis_carolinensis_

EIAIVGICNFPGG-EGLDNFWQVLEVGKNC-VREIPPER-FDTTEWYDADSN-KQKTTTR-HAALIE---
EFNSFDNRLFGINEVEAEYMDPQKLLLECTYRALED---AGVT--RENINGSSTGTGVFVGMNQDY--RL-LRSR---TSSTFHYDGTGTS-M--
SIAANRISYAFNLKGPSLAVDTACSSFLSALHLGKAIKQGDCEAALCGGVNCHIEPRVVFV--LKA---KMI-SPEGISKPFST---A-DGYGRGEG-CAVLLKLP--
LRKAQEDFSK-IWGVISMASAVNQNGRSVTP---ITRPSQEQENLLCKIYPA-H---VD-PST---VQYVEAHGTGTPAGDPVEAESVGN-VL---
GKSNFPPIKIGSVKGNIGHTESAAGAAGLIKVLMMHGHKIVPSLHFS-ES-TSSIN--TEKLNLIPTTVEKWD--EP---S---
EFGRIAGINSFGFGGTNAHVVRQVQKRPV---ELFLISSASVNSFKLTMEDTARYL--KTKDIALPNLAYTSACRRS

>XP_004081384.1_equisetin_synthetase_eqxS__Oryzias_latipes_

GVA VVGICNFPGG-EGLENFWKVLVNGKNC-CVPIPRER-FDTRSWYDPPDT-KAGKSRTA-KAAFMD---
GFNEFDHRFFGISEVEEQMDPQKLLQCVYRALEN---AGIP--MEKASGTRTGVFVGMNQDY---ETNAAHM--HPSVINHWGTGLA-M--
SIAANRISYAFNLKGPSLAVDTACSSFLSALHLGKAIKQGDCEAALCGGVNCHIEPRVVFV--LKA---KMI-SPEGISKPFST---A-DGYGRGEG-
CGVLLKP--LKRALQDLHDH-IWGVITKTAIQDGRSVV---MTKPSVKQEQELLRRIYSEQD-----TAA---VQFIEAHGTGTPIGDPTEAESISN-VITKARPP-
GSQVLVWGSVKSNIHTESTAGMAGLIKVLMMHGHKIVPSLHFS-ES-EKSSVDVKALNIKIPQVVEKWE--CS---G-----
PRVAGVNNFGFGGTNAHVVRQVQKRPV---ELFLISSASVNSFKLTMEDTARYL--KTKDIALPNLAYTSACRRS

>XP_005144267.1_PREDICTED__fatty_acid_synthase__Melopsittacus_undulatus_

DVVIAGIAGKLPES-ENLQEFWENLLNGVDM---VTEDDRRWKPGMYGLPKRN-GKLGK-----
DISKFDASFFGVHPKQAHMTDPQLRLLLEVITYEAVLD---GGIN---PTTLRGDTGTGVVIGASGSEA-----AEAFSQ--DPEKLLGYSMTGCQ-R--
AMLANRISYAFNLKGPSLAVDTACSSFLSALHLGKAIKQGDCEAALCGGVNCHIEPRVVFV--LKA---GML-SPDGACKAFDAS--G-NGYCRSEA-
AVVLLTK--RSMKR-----IYATIVNAGSNTDGFKEQG---VTFPSGDMQQQLVRSLYKECN---IR-LED---VEYVEAHGTGTPVGDPEQINGVNI-IF--HQCK--
RKPLLGSTKSNMGHPPEPAGSLAALAKVILSLEHGLWAPNLHFN-TP-NPDIP-ALQDGTLEVVCCKPTPVK-----
GGLVCINSFGFGGANAHVILRPNENPLETFNIPRLVQICGRTQEA VETLIQESRKHGRC---SPFLSMLTDISTVPV

>XP_005153144.1_PREDICTED__polyketide_synthasenoribosomal_peptide_synthetase__Melopsittacus_undulatus_

EIAIVGICNFPGG-DGIDNFWKVLVEGRNC-TEEIPPER-FIVKEWYDPDEN-KPGKICTT-RAALLK---
EFNSFDNHLFGINNMEAMDPQKLLIECTFKALED---AGVP---VEAISGNTGTGVFVGMNQDY--EV-ITSR---IVIEMNHYDGTGSA-M--

SIANRVSTFNTLTPSLTIDTACSSFLFALHYALQTIKSGDCEAAICGAVNCIDPRTFVSS--LSKA----KMI-SPDGLSKPFSKQ--A-DGYGRGEG-CGVLFLLKP--
LKKAKEDHSK-IWGVINISAINQNGKATP----ITRPSQIQENLLRRIYET-H---VD-PSV----VQYIEAHGTGTAAAGDPTEAESLGN-VI---
SKSEVILKIGSVKGNIGHTESAAGAAALIKVLLMMHGGKFPVPSLHYS-KE-MSSID--TEKLNLEIPTTVEPWE--ES--G----
EYGRVAAINCFGFGGTNAHVVRQAKQKRPL---ELVLLSAASSKSLQMTMADTADQL--STRNITLPSLAYTSACRRS

>XP_005643614.1_hypothetical_protein_COCSUDRAFT_49000__Coccomyxa_subellipsoidea_C169_

--VDIMGFSCRFPES-ETPTQFWEVLVAGTDM---VTENDRRWPVGLHGTPGRF-GKLP-----EYHLFDAPFFSVHKGKQASKMDPQMRKLLLEVTHEAFVD-
--SGID---YKALRGRSRVGVYVGGCCGSEV----HAMWLS--DYNNTITGYEQGTCT-L--
SMFANRLSFFFDKGPSKAVDTACSSAFMALHDAVLDLQGRVVDYAVVGGSSAIFRPATSLA--FLRL----KML-SPDGACKSFDAS---G-NGYARAEG-
VASIILRRSDVFDTPVIVPREPYARVMGIGTNNNDGHTTEQG---ITFPSPGAQQLGTAVCRATG---ID-PSD---IQYVEAHGTGTVVGDSQELSAIDG-
LYGAGAGHTPEEPLIGSVKSNMGHCCEGCSGLAGLIKVLLSYENGLIPGNLHYK-EP-NPNE-SLKTGILKVVVTGATPWQ-----
GGLVAISSFGFGGSNVHAIAGCVREELFPPELPIVARTQEGSQSLEIAIKARA-FMADKLPKRLANHLSDVVG

>XP_005646747.1_ketoacilsyntdomaincontaining_protein__Coccomyxa_subellipsoidea_C169_

----IGLSRFPES-NGPAEFWTNLDIGTDM---LTTDDRRWPIAFQGLPPRS-GKAP-----GFDKFDAAFFSVHKGKQASKMDPQLRKLLEVAIEAWVD---
AGID---FRALRGRSRVGVYVGGCCGSEV----HAQWVA--DIDSITGYEQAGCA-R--
SMFANRLSFWFDHFGPSKCIDTACSSSLTAFNDASDFEAGRIDYAMVGGTSGIFKPQTSIA--FQRL----HML-SPDGTCKSFDAS---A-NGYARSDG-
IAAVLRRRPLSEAPVWAPRRPYARVLAACATNNDGHTKEG---ITFPSPGAQKALAQVCAKAG---LA-PSA---VGYIEAHGTGTVADGQELGAIEE-
WYGRAGARTPDNPLIGSVKSNMGHCCEGCSGLAGLIKVLLSYENGLIPGNLHYK-EP-NPNSA-GLRDGILKVVTEPTAF-----
EGIAALSNGFGGTTNVHLLQGGGWEQSRATGKVIPLACRTQEGMAEVVKILQGLP-GGEESVVDPMRCWANS CGGS

>XP_006815698.1_PREDICTED__uncharacterized_protein_LOC100373061__Saccoglossus_kowalevskii_

AIAVVGIAICRFPGA-NLDDEYWRVLSNGENH-LREIPKER-WNNDAFYSNDKK-EMGKNYVR-HAAFID---
RYDEWDRFRFQINDDEAMRMDPQQNILLECYKALEN---GGFP---VNELAGSNVGTYYIG-----
DCAMVCGGINLILSPTLFISS--LSRA----RMA-SATGKCPFSAD---A-DGYARGEG-CGVVVLKP--LQKAIKDGDI-IWGI-VGTGNCQDGHFATP---
ITAPSGKQEELENLVYAKY---VD-PSM---VTYIEAHGTGTVPDPIEANS LGH-FIGQARSQ-
GKPPCVYGVSKNIGHLEAGAGVAGLIKVLLMMKYRKNIPSLHFS-KA-NKKIN--FAELCLKVTEFVDWK-----VNEGDI--
SLTACVNSFGFGGTNAHAIVTSYSKPRCSQEKSHIALS AKTRESLILMIKHLKRSIQDQDQ-PTLSALAYTSTVRR

>XP_012938829.1_PREDICTED__lovastatin_nonaketide_syntheselike__Aplysia_californica_

-----ASVPGA-DNVEQFWRVLEQGENH-VVEIPKER-WNNDAFDFTDVH-AVGKSYVK-RAGLLK---
DPKAFDNKLFNINDFEADQMDPQKQFVLECCFMAMED---AGIT---REQLAGSNTGVYVGMANGDY----RGLFTA--KSPIVGNVYVTGIS-N--
SIIARSVSTFDLRGPMSTLDTACSSALVAIHVGAQALRTGDCDLALCGGTNFMSPDVFVH--LSKA----HNV-SPTGQCFASFDS---A-DGYTRGEG-
CGMVILKR--LKDALRDGDH-IWATI-ETGNSQDGHSTVP---ISAPSGDQQLRLETVYQDAA---MD-LEG---IDYIEAHGTGTSAGDPVEAKALGT-FF-----
GTRVYGVSKNIGHLEAGAGVAGLIKVLLMMKYRKNIPSLHFS-KA-NKKIN--FAELCLKVTEFVDWK-----VNEGDI--
RRNKIACVNSFGFGGTNCHAVVKAFFEQSEVLSIPICVCFSAKHEKSLKGSIEDFVQHPEVSS--LDVHDVSYTSTVRRD

>XP_013068913.1_PREDICTED__probable_polyketide_synthase_16__Biomphalaria_glabrata_

AIAIIGIAFKGPGA-ENLEQLWEVLEGGKNY-VLDLPKDR-WNVDAFYDPPDQ-ATGKYYTR-KAGLLS---
NPLDFNTFFDINDIESDQMDPQKQFVLECYRAMEH---AGIT---RRSIQSGKTGVYIGAMNCDY----RGLFTA--KSPIVGNVYVTGIS-N--
SIIARSVSTFDLRGPMSTLDTACSSALVAIHVGAQALRTGDCDLALCGGTNFMSPDVFVH--LSKA----QMV-SPTGQCFASFDS---A-DGYTRGEG-
CGVILK--LSD-----YE-----IEYIEAHGTGTQAGDYAEANALGK-FF-----
GSSKRLIGSIKTNIHLESAAGVAGLIKVLLMMQHNKFPVPSLFE-SL-NPKIN--FDDLNLVVPKVVREWS-----
TENKVGSVNSFGFGGSNCHAVVRSVVTQTNQVNNACVCFSGKTVTSLMGLSLRDLANYKRLK--LDVHDVSYTSTVRRD

>XP_013068917.1_PREDICTED__mycocerosic_acid_syntheselike__Biomphalaria_glabrata_

EIAVIGVGFKGPGA-DNLEQLWMVLENGENK-ISEIPKDR-WNSDAFYDSDTE-ATGKYYSR-KAGLLS---
NPHEFDCSFFNISEIESEQMDPQKQFVLECYRAMEH---AGIT---RDKIGSKTGVYIGAMNCDY----RGLFTA--KSPIVGNVYVTGIS-N--
SIIARSVSTFDLRGPMSTLDTACSSALVAIHVGAQALRTGDCDLALCGGTNFMSPDVFVH--LSKA----QML-SRSGQCFASFDS---A-DGYTRGEG-
CGVILK--LSDAERDNDP-ILAVI-TTGTNQDGHSTVP---ISAPSMSQIQLLEDMYRDLSS--LEQLDE---IEYIEAHGTGTQAGDYAEANALGK-FY-----
GSSKRLIGSIKTNIHLESAAGVAGLIKVLLMMQHNKFPVPSLFE-SL-NPKIN--FDDLNLVVPKVVREWS-----
TEKKVACVNSFGFGGSNCHAVVRSVVTQTNQVNNACVCFSGKTVTSLMGLSLRDLANYKRLK--LDVHDVSYTSTVRRD

>XP_013079084.1_PREDICTED__phthiocerol_synthesis_polyketide_synthase_type_I_PpsClike__Biomphalaria_glabrata_

QIAVIGISCKVPGA-DNVEQYWKLENGENH-VIDIPKER-WNNDAFYDPPDQ-AIGKSYVR-RAGLLK---
DPIAFDNKLFNINDFEADQMDPQKQFVLECYRAMEH---AGIT---REKLAGSNTGVYVGMANGDY----RGLFTA--KSPIVGNVYVTGIS-N--
SIIARSVSTFDLRGPMSTLDTACSSALVAIHVGAQALRTGDCDLALCGGTNFMSPDVFVH--LSKA----HNV-SPTGQCFASFDS---A-DGYTRGEG-
CGMVILKR--LKDALRDGDR-IWATI-ETGNSQDGHSTVP---ISAPSGDQQLRLETVYQDAA---MD-LEG---IDYIEAHGTGTSAGDPVEANALGK-FF-----
GAVRHRYIGSVKTNIGHLESAAGVAGLIKVLLMMQHNKFPVPSLFE-SL-NPKIN--FDDLNLVVPKVVREWS-----
SQNKVACVNSFGFGGTNCHAVVMEYEDMVEQKNIPCVCFSAKHEKSLKGSIEDFVNHPDVST--LDVHDVSYTSTVRRD

>XP_013396153.1_fusarin_C_synthetase__Lingula_anatina_

AIAVIGICRFPGA-NNIDEFWQVLVNGENH-LIEIPEDR-WNSAAFYDPPGRD-TPGKSYVK-QAAFVQ---
HHDAWDRFRFMINDAEARMDPQAMVLECYMALEN---AGIT---REDIFGTTGVYVGMANGDY----SALVNA--DLVEINHHAFTGSS-N--
SIIANRVSTFNTLQGPSLVDACSSAMVALHLLAAQALRTGECTTIAAGGCNLMITPENFVP--LCRA----KMM-SAKGQCQAFCAD---A-DGYARGEG-
CGMVIMKR--LKDALHDHDIWAVV-GTALNQDGHSTVP---ISAPASQETLLKHICYKYQ---VD-PAE---LQYAEAHGTGTPIGDPIEVALGK-
VLGKSRKE-DDLPLFVGVSKNIGHLESAAGVAGLIKVLLMMRAGKIAPSLHYTPERGNPKIN--FDEIRMKVPTVTDWPPSPKG-----
YRMCCVNSFGFGGTNGHAIVREHLNPEHGDDQTYIVAVSGTSEGSTQGLTHTLVERLRTGQ--YTLNEVAYTSTCRRT

>XP_013403200.1_phenolphthiocerol_synthesis_polyketide_synthase_type_I_PpsDlike__Lingula_anatina_

KVAIVGIGCRFPGEINNVKDFWEVLLKGIDC-TRPLPDDR-FDVNHFYHPTPK-TPGKLYVR-GGGYLEQ---
DLLSFDRLLFFKMPDPEANHMDDPQVRLLEVVWEAFED---GGIP---ARSIRGTNCGVYMGVTASEY--TT-LTSA----RSDAISQYSNSGTN-S--
CMVSNRISYEFDLHGPSLSIDTACSSSLYAVHLASEAIRNGDCDMAVAGGVNVMMPETIG--FCQA----GML-APDGRSKSFDSS---A-DGYRSEGE-
GGVILKS--LNKAVEDGDR-IVAVIRGGALSNDGR--TP---GIANPSYSAQVNLVYRACRHAM---IN-PQD---IQYVEAHGTGTQVGDTEANALGK-TI---
GQAKT-PLYIGSVKSNIGHCEGSSGIAGVIKVALMIHNELIPPVVHFH-KG-NPKIK--FKELNIKVPKELIWP--YV---EEM-----
PLIAGCSSFGGANAHVILEAPPS-----VVLISAATTTALSSRVDDFIELF--RKIQERFYDVAATTCLRSH

>XP_013405320.1_PREDICTED_phthiocerol_synthesis_polyketide_synthase_type_I_PpsClike_Lingula_anatina_

AIAIVGVGCRFPGA-DDIDEFWKVLNENGENH-VIDIPKER-WNNDAFFSSDPD-APGKTYVT-RAGFVK---
GHIEWDNRLFVNDLEAARMDDPQRFVLDCCYMALEN---AGIP---TPDIQGSRTGVYVGMNNDNF-----ADMFET--DVSSMNNYSLTGAS-N--
SITAARVSYVFNLLGPCMSVDTACSSAMVATHLGCQALKNCECNMALCGGVNAIMMPTMHVP--LSKA----RMV-SPTGQSQAFSSA---A-DGYARGE-
CGIVLKR--LKDALKDGR-IVAI-GTGVNQDGRTHP---ITAPSGSQAALLKEVFLRYH--VN-SDD---IQYVEAHGTGTQAGDPVECNAGS-
FLDRKARV--APECYIGSVKTNIGHLESAAGVAGLIKVLLMMKHEKIVPSLHFKGRPANPKIN--FHELRLRVPTVMNWTPEGK-----
PRLACVNSFSGGANAHVVMQFDRTEAFEKSPHIAISAQNVQWLEQITKNLMEKVSNE--YSLRDIARTSTCRRT

>XP_013759672.1_fatty_acid_synthase_Thecamonas_trahens_ATCC_50062_

KVVISGLSCRFPE-EDAETFFANLVAGTDM--VTADRRWDMTMDARSLPARSGK-----
SIAEFDARFFAVTGKAADKMDPQLRLLHATHEAVTD---AGWT---LDELAGSSTGVVWAGSFS-----DSHFDLLEDATAITGYEHTGCL-L--
NMFANRISYFNDLHGPSLSDTACSSAMVATHLGCQALKNCECNMALCGGVNAIMMPTMHVP--LSKA----RMV-SPTGQSQAFSSA---A-DGYARGE-
IAAIVLDA--ADTARN----AYLDDLVAACNNDGYTPQG---ITYPSSDAQVALIRSCLAAG---AT-PED---
VVYVEAHGTGTQAGDSVEANALDEVFVKHVLRSRSPENPLLGVSVKSNMHCENVSGLAGIHKVCLAARAGVLPNHYT-QP-NPKIP-
ALLSGTMRVVTQPTPWR-----GGLVAISSFGFGGTNAHALVRA---PQPARAADDSDQSTDLAALRAEVVQLLQSY-TGELAAALSRLASLFGSAP

>XP_015783256.1_fatty_acid_synthase_Tetranychus_urticae_

DIVISGISGRFAES-DNIDELAKNLFNDVDM--ITEDRRWPLGLYLPT--RSGKIK-----DLSKFDAQFFGVHKGQANLMDPQARMLELTYEALCD---
AGVN--PHSLRGRTRGVYVAGASVSEV---EELAQ--DVSKVSGYALTGCS-R--
SMFANRISYTFDFQGPSYADTACSSFLAFQALLGLRSGQDCQAIVGGVSI CLRPTVALQ--FHLK----NML-SNEGKCKHMDAS--A-DGYRSEA-
CSVVFLQR--KSAKR----IYATVIHKTNTDGYKKEG---ITPSPRDAQRDLMKEVLEESG--IS-PTD---VNFVEAHGTGTGLDPIEIDAIAE-VY---
CQGRTEPLLIGGVKSNLGHTEPASGLCSLAKVLI AFENKNIPANLHFN-TP-NPDIK-PLVRGQIKPIVENTPYN-----
GGIAINSFGFGGVNHALIKSNDK-----VVTMCRGTEGVNSFFDFIEKNP--TRVTKFLALVSEVSKVPA

>XP_015792919.1_fatty_acid_synthase_Tetranychus_urticae_

TIVISGLAGRFGA-DDVDQLWDLKLGKVL---YSEERDRHPSKLRNRPTALGQIN-----
DLSRFDQFFGYDAKAAEHMGTQNRVLFVYVEALWD---AGIL---VDSLGRSRTGFFLGISAG-----DGSDQYDLDETTDP--
VYIFNRLAYHFNWKGPSLSDTACSSFLADAIQAHWHIKHGLCDVAVVAGVNTIVDPFVNMT--AADM-----KML-SQSGFERCLDEN---A-DGFIRSET-
IAALILQR--KPAKR----IYGEILGTSVNDGYTEEG---ITFPNRYAQADAMRSALKIAN--IS-PSQ---IDYIEAHITGTQAGDAVETSAILD-AY---
RDNSDQPIKVGCIKSNIGHAEASAGINAVIRACKILQTSHLSPNAAYS-VP-NSRIS-GLLEGKHPVLEKQFN-----
ANILGVNTFGFGGSNGHILKGTQPLDSSLFPRLIVFCNRTRQIEGMAQHLLTKD-ALNED--LIAMLNLSLAKP

>XP_018429938.1_PREDICTED_probable_polyketide_synthase_16_Nanorana_parkeri_

QIAIVGIGCNFPGG-EGIDNFWKVIIEGQNC-TVEIPKER-FDTKHWYDSDYN-KPGKICTS-RAAIVE---
GIHMFDNKLFGIHNSESQMDPQHKLQLCTYRALED---AGYP---MESIGGTETGVYIGLMNKDA--EF-IYNN---YPEKINHFNGTGTS-M--
CIAANRISYQFNLTGPSLSLDTACSSSLVALHLACQAIKQGDCELAICGGVSCILDPRIVYA--LSKA----KMI-SPEGTSKPFSSK---A-DGYRSEGE-
CGIVLKP--LKQAKEDYSK-IWGVICASSINQDGRSVTP---ITKPSLEQERLLSRIYTA----ID-PCS---IQYLEAHGTGTPVGDPIEVTSIGN-TI---
GKSKMKSLKIGSVKGNIGHTES AAGMAGLIKVLLMMHHEVIPPSSLHYS-KE-LGIKQ--IEESKLVVPTAPEKWH--ED---V---
KFRGMAGINCFGFGGTNSHV VVKYKEKRPS---EILLSAASSKSLQLSIEDTKKEL-SKMPSISLENLVYTAACRRS

>XP_018430111.1_PREDICTED_LOW_QUALITY_PROTEIN_uncharacterized_protein_LOC108802755_Nanorana_parkeri_

AIAIVGMGNCNFPGG-EGIDNFWKVIIEGKNC-TVEIPEER-FNTKHWYDSDDN-KPGKIRTS-RAAIVE---
GIHMFDNKLFGIHNSESQMDPQHKLQLCTYRALED---AGYS---MESISGSNTGVYIGIMNKDS--EF-IYNN---SPENINHFNGTGTS-M--
SIAANRISYQFNLTGPSLSLDTACSSSLVALHLACQAIKQGDCELAICGGVSCILDPRIVYA--LSKA----KMI-SPEGTSKPFSSK---A-DGYRSEGE-
CGIVLKP--LKQAKEDYSK-IWGVICASSINQDGRSVTP---ITKPSQEQERLLSRIYTT----ID-PCS---IQYLEAHGTGTPVGDPIEATSIGN-TI---
GKSKMKPLKIGSVKGNIGHTES AAGMAGLIKVLFMMHHEVIPPSSLHYS-KE-LGIKQ--IEESKLVVPTAPEKWH--ED---V---
KFRGMAGINCFGFGGTNSHV VVKXKEKRPS---EILLSAASSKSLQLSIEDIKQL-SKMPSISLENLVYPAACRRS

>XP_026824077.1_fatty_acid_synthase_Ooceraea_biroi_

EIVISGIAGRYPDS-DNVELLKNNLFNKVDL---VTDDRRWRFDHAEIPQL-GKIN-----NVGKFDALFFGVHFKQAHTLDPMCRMLLEHAYEAVID--
-AGIN--PRQLRGSRTGVFIGTCSSES-----EKTWYF--EKLQVNGFGITGCS-R--
AMLANRISYWLGIHGPSYTLDSACSSSLYALENAYRSILDGQCDASIVGGSNLCLHPYVSLQ--YSRL----GVL-SSDGTCKCFDAS---A-NGYRSEA-
ICVFLQK--AKDAK----IYSTVHKTNCDFGKEQG---ITPSSVMQSAALLRDCYEEESG--MS-PSS---VSYVECHATGTQVGDPEELNTIEN-IF---
DRTPLLIGSVKSNIGHTEPVSGLCQITKVIAMETGTIPPNLHYK-TPLKGMKS--LEDGRKLVVTDTPWE-----
GGYVGINSGFGGANANCHVILKSHTKGAKTDDLPRV VVSGRTEESVKVFLNDRVERHAND---VEYVRLHDIHADDI

>XP_324222.1_hypothetical_protein_Neurospora_crassa_OR74A_

-IAIIGMSCRFAGDVSPLKLDLLAQGKSA-WSEIPKDR-FNIDGFHHPNFEKLNGT--NVIGGHFMKE---
DVGLFDAHFFNLSAETAAALDPQFRLQLESTYEALES---AGIT---LQDVAGSNTSVYAGSFFRDY----HESLIR--DPDTPRFLLMGTG-A--
AMASNRLSHFFDLRGPMSVDTGCSSTTLTALHQACQSLRSGESTMSIVGGANIMFNPDMFLA--MSSM----TLI-SKDGSRWAFDSR---A-NGYRSEGE-
SATVVLPK--LDAALRDGDP-IRAVIRDSGINQDGKTE---ITTPSGEAQALIRACYERAG--LD-PGQ---
TTYFEAHGTGTPDPIEVKAIARVFKDSRKGNGEDALLRIGSVKTNIGHTETASGVAIIVALALERQIPPSINF---
TPNALSLDEWKLKVPTELEEWWKDG-----
IRRASINNFYGGNSAHVIMEDYSSNNGDHHHSKVFLLSAKDEKATERMIANLKYTLHQKANIAENALLSNAHT--

>XP_324368.1_hypothetical_protein__Neurospora_crassa_OR74A_

-VAIVGMSCLPLGGVETPGDFYRMMCRGRSG-WSKVPKDR-FNQEAYNHPDPD-HKGTFFNSQ-GGYFIKQ---
DLSGFDAFFDVTREAEAMDPAQRLLMECTYEALLES---GGIP---REHIAAGTRTGVIFFGGNYGEH----RFSHIR--DLDTIPSFDFATGNQ-P--
AFLSGLRAYFFNLHGPTFTVDTACSSSLHALHLA VQSIRNGECDAAVVGASHLITQPDVWVS--MSML-----RLF-SDEGRTYAFDHR---ARSGYARREG-
CAVILKLP--VEKAFKDNDR-IFSVISHSGVSHNGRTV-----GIVAPSPDEQEQLLRDVFATAAK---ID-PRE----VGFVEAHGTGTRKGDPIEATAIYK-AVGRYL--
SADDPL YIGSSKPNVGHLECASGLVSVIKGVLSLYYGFILPNADFD-KE-NPGIP--FKEWNNMTVAKQKQKWPW--AH-----
KKYACVNNFSGFSNSSTCILAGPPIEHGAYTTPRLFVLSANDEQALRTSIKELGIWL--EQHAM-PRNLAYTLCQRRS

>XP_325868.1_hypothetical_protein__Neurospora_crassa_OR74A_

PIAIVGMACRMPGNVSTPAEFWELCTRARSG-WSETPKQR-FNSARFHPNQG-KGGTLNPNV-GGNFLNV---
DLA AFDAPFFGLTEKEAISMDPQQRLLLECTFEALEN---AGIP---KHTIAGKDVGVFVGGSFPEY----ESHFLR--DPDTIPMHQATGCA-Y--
AMQSNRISHFFDLRGPSTADTACSSSMVAIHLACQSLRTGESSAALVGGCHLNMLPEFWIS--FSTC-----RLL-SDAGRSFSDNR---G-TGFRGREG-
CGMIVLKP--LDQAIKDKDR-IRA VIAATGLNQGDKTP-----GITVPHGPAQ-----VYGRAG---LD-PNL----CGFVEAHGTGTRVGDPIEATAIHN-VL---
GQSPRNPPLWIGSVKSNIGHLEGASGIAGVKAALMLERGFILPNHDFK-QP-NPRIP--WKWNNLEVPVTPQRPWP-----
RGKKYISVNNFVGGTNGHVVLTAAPFSDKSGLRKLYVVT AHDKAALSQMKNIIVVYLEQRPEIDLTNSLAYTLGQRRS

>XP_329445.1_hypothetical_protein__Neurospora_crassa_OR74A_

PIAIVGSSCRFTGEATSPAKLWELLKDPKDL-TREVPKDR-FNVEGFYHPDGE-YHGTTNSA-KAYFLEQ---
DHLRFDAFFNITPKEAEIDPQQRMLLEV VYEALLES---AGYT---LDQVSDANIGCYVGNFVTFD-----ITMLQR--DDLSVSQYYATGNA-R--
SIISNRVSYFFNFHGPSMTIDTACSSSLVALHQA VLSLRSGEAMACVSGVNLITPEQFVV--ESSL-----HML-SPTGRCHMWDDR---A-DGYARREG-
VAAIFKP--LSKALADGDR-IEAIIRETGVNSDGRSK-----GITMPNWEAQSA LIQDTYRRSG---LN-
ARDPIDRCQFEAHGTGT AAGDPNEARAIEDAFFGRNVSTAEVSKLLVGSVKT VIGHTEGAAGLAGLKFV VHAMINGTVPPNLHFN-RL-QPAVA--
KYYSHLHVPTKALAWP--SV---AAGQ---PRRATVNSFVGGTNTAICEMVPLSADGQTRLPLVLSASSPRSMGAVAKCYRDYL-AQVS-
LPLEEAWAYAYKNRT

>XP_330106.1_hypothetical_protein__Neurospora_crassa_OR74A_

PIAII GMGCRLLPGGSHSSKLWELLKAGRTA-QSRFPSPR-FNIDGFYHPNSD-RPGSLNME-GGYFIED---
DIRGFENSFFGINNLEATYMDPQQRKLLLEVVFETFEN---AGFT---LDQVSDANIGCYVGNFVTFD-----ITMLQR--DSEYTHRYSATGLG-T--
TILANRISHVFNMGKPSFVIDTACSSSLYCLHAAVAALIA GECDSAIVAGANLIQSPEQQLA--TMKA-----GVL-SKTSTCHTFDSS---A-DGYARREG-
IGAILVKR--LSDAIRDGDP-IRSVIRGTAINSGKTN-----GITLPSADGQEA VIRKAYA QAG---LG-FNE---TDYIECHGTGTAVGDPIEVAEAVSR-VF---
KKPQGAPLLIGSVKSNLGHSEASGLSIIK VAMALEKGEIPPTYGVK-NI-NPKIK--TDEWNVQIVTETTPWP--KN---
LPHNAGRLFRRAAGVNSFGYGGANAHAI LEAPQMPASL TRSTLFLPFGSNTAALERRVTDIAAAI--DFENVNIADLAYTLGKVRT

>XP_330288.1_hypothetical_protein__Neurospora_crassa_OR74A_

PVAIVGMACRWPGGVHDPSQFWEFLRNKVNNG-WKEFD DPR-FSSAGFHHPNSD-RPGSMSMK--GAFLAEQ--
DARLFDHTFFGMTGLEVETMDPSQRKLLLEVAYEAIES---AGET---WESVSGTRTG VVGFVGNFCLDH--WM-IQSR----DWDNPRPYAFTGAG-T--
SILANRISYIFNL TGPSLFTVDTACSSSMYALHLAVNAIRAGDCESAI VASANWIADPGVQIA--LDKL-----GAL-SASARCHTFDAR---A-EGYARREG-
FGAIYVKR--PSLAIADMSP-IRAMIRGTAINSGR--TG---GITRPSANGQETVIREAYRNAGN--LP-FRD---TSYFECHGTGT VYVGDPIEVAALGR-VF---
APSSDDPLLIGSVKSNVGHGEGASALASIMKVVLAL EHGAIPIYDLQ-TR-NPNID--FEGAKVQPVTEVTPWP--KD---R-----
LQRASINSFGYGGANGHCHIIDHVNI PNANTRPLVLLPLSAHNENSLELNLKALSQVV-----LPLADVAYTLGARRS

>XP_682975.3_probable_polyketide_synthase_1_isoform_X2__Danio_erio_

DIAIIGICNFPGG-EGVDNFWKVLVEGRNC-VVQIPDER-FETSEWFHPDGE-EPGKTRTT-TAALIE---
GFNEFDQKFFGISEAEADYMDPQQRKLLQCA YRALED---AGIP---LEKVS GTRTG VYVIGLMNRDY--ET-LLNN----SPSTITHYNGTGTA-M--
SIAANRISYIFNL TGPSLFTVDTACSSSMYALHLAVNAIRAGDCESAI VASANWIADPGVQIA--LDKL-----GAL-SASARCHTFDAR---A-EGYARREG-
-LKKAIEDFDH-IWGI VNKTA V NQDGHVTVP---ITKPSMTQEQEALLRMIYSS-E---DF-LAN---VQYVEAHGTGTPAGDPVEAGSLSR-VI---
AKPSLGPLFVGSVKNIGHTESAAGVAGL IKILLMMKHETIVPSLFYS-AE-NSSID--AKALNLKIPTRA EKWL--YS---G-----
SRIK MAGLNSFGFGGTNAHAITEYVQLEPL----KLLPLSAATDQSLQLCIADTYQRI--SADEVDLQALAYTSACRRS

>XP_793564.2_PREDICTED__probable_polyketide_synthase_1__Strongylocentrotus_purpuratus_

PVAVVGIGTRHACAGANTTDDFWKVLKEGKEC-ILDIPPER-WAIDNFHDEDQ-T-RQGMVTK-RCGLID----
DLEGFDNLFFKISPREAASLDPQQRHLLLEVNYEAFED---AGIN---PDNLGES-CGVFV GIGMMDH-----AIQLV--DTSTTDAYTLTGIA-H--
SVSANRISYAFNLKGPSFVDTACASGLTALHLACTSLWNRECSVALMSACNGIQLPDITVG--FSAL----GVL-SPDGRCSFSS---A-NGYVREGE-
WGAIVLKP--LSQALADNDH-IYTVIRGSAIAANGLANS-----LTMPSPPAQEYV MKEAYEKFG---VS-MSD---VHYVEAHGTGTMVGDPLEAEAISR-AF---
NRTKDNPLKIGSVKSNFGHTEVAAGVTA AIKV ALMMENRTIPPTINFV-SS-NPHID--PEEMKLDIVTNVQPPF--TE---D-----
KHIIGLNSFGFAGALAHCFEEAPKSDSDEKQPIIPLSAKSPEALTAVAKQWQNLID-IDQDA--MSAVSWMSTRRRV