Supplemental Figure 1. Alignment of protein sequences from the β-ketoacyl synthase (KS) and acyltransferase (AT) domains of fungal PKS and PKS/NRPS. Protein sequences were aligned using AlignX. A similar alignment was obtained with ClustalW. The active sites of the KS and AT domains are indicated by green lines above the alignment. The following sequences were included in this analysis (see Methods for accession numbers): *M. grisea* (Ace1, Syn2, Syn6,7,8, mg03810, mg03818, mg09589); *A. fumigatus* (af04917); *A. nidulans* (AN8412, AnpksST, AnWA); *F. graminearum* (FG10464); *N. crassa* (ncu08399, ncu09638, ncu02918); *A. terreus* (LNKS, LDKS, AtMSAS, Atat1); *P. griseofulvum* (PgPKS2), *C. heterostrophus* (ChPKS1,2,16,17); *G. moniliformis* (FUM1, GmPKS1,9,10), *C. lagenarium* (ClPKS1) and, *B. fuckeliana* (BfPKS3,4,5,6,8). Bacterial PKS sequences (epoD, MxaC, MxaD) were included as references.

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                 1                                                50
     ACE1    (1) EPIAIIGSGCKFPGGSTTPSKLWELLKDPK-----DIVSEIRPD-RFDVD
     Syn7    (1) EPIAIIGSACRFPGDLSTPSDLWDFLQSPR-----DLQTEVPKD-RFNAD
     Syn6    (1) EPIAVVGTGCRFPGGANSPSKLWEILEKPR-----GLLKKVPAE-RFDVD
     LNKS    (1) EPIVVVGSGCRFPGDANTPSKLWELLQHPR-----DVQSRIPKE-RFDVD
   GmPKS9    (1) EPIAVVGTACRFPGGCNTPSKLWDLVFSSR-----DVLQKVPPA-RFNVD
   GmPKS1    (1) EPIAIIGSACRFPGDSSSPSKLWDLLKSPR-----DLLTKVPPN-RYNAD
   BfPKS5    (1) EPIAIIGMACRFPGGSNSPSKLWDLIKSPR-----NLSKRVPDE-RFNSE
  ChPKS16    (1) EPIAIVGSACRFAGGANSPSKLWDLLRNPK-----DIRSNITDK-RFNAN
  FG10464    (1) EPIAIIGTGCRFPGGSNTASKLWDLLKDPK-----DVSKEVPED-RFNLD
  mg03818    (1) EPIAVIGIGCRFPG-ASSLHKLQEALSAPS-----DLSQTIPDD-RFHVD
     Syn2    (1) EPIAIIGTGCRFPGSCDSPSKLWELLEKPR-----DLLKKIPND-RFSAD
  mg03810    (1) EPIAIVGTGFRFPGGASTPSKLWDLLHSPR-----DVLAPIPQS-RFNAE
  ChPKS17    (1) EPIAVVGVGCRFPGGCNTPSKLWDLICEQR-----DIQSKIPAE-RYNSD
  GmPKS10    (1) EPIAIIGTSCRFPGGANTPSKLWDLLIEKR-----DVQSSIPPE-RFNVD
  af04917    (1) EPIAIIGTGCRFPGGSTSPSKLWDLLYSPR-----DLTREVPAESRFNPK
 ncu08399    (1) EPIAIVGSSCRFTGEATSPAKLWELLKDPK-----DLTREVPKD-RFNVE
   BfPKS6    (1) EPIAVIGTGCRFPGGASSPSKLWNLLHHPY-----DLTQKVPSS-RFNIK
   BfPKS3    (1) KPVAIIGSSCRFTG-ASNTSKLWELLKEPR-----DVLSKIPEE-RFLAE
   BfPKS4    (1) EPIAIIGRGCRLAGGCQSPSELWNFLQTPY-----DVSQEFPPD-RNSAS
   AN8412    (1) DLIAIVGSACRFPGQSDSPSKLWTRLKEPI-----DLRKTFPPQ-RLNLA
  mg09589    (1) EPIAVIGLANRFPGGADTPARLWTILKDAASAEAADLSREPPPG-RMNLR
     Syn8    (1) EPVAIIGYSLRFPGGADTPSKFWELLTSGR-----DISREPDPR-RLNLS
   ChPKS2    (1) MPLAIIGMSCRFPGKVASLEDFWDMLSNSK-----HGYRQFPRE-RFNWE
   ChPKS1    (1) -PIAVVGMSFRGPGDATNVEKLLNMISEGR-----ESRAEVQAK-KWDPE
   BfPKS8    (1) IPIAIVGISCRLPGNVSTPDEFWELCSRAR-----SGWSEIPKE-RFDTA
     LDKS    (1) APIAMVGMGCRFGGGATDPQKLWKLLEEGG-----SAWSKIPPS-RFNVG
 ncu04865    (1) MPIAIIGMSCRFAGDVDSPSKLWDLLAQGK-----SAWSEIPKD-RFNID
     FUM1    (1) LPVAIVGMGMRLPGGIHTPDELWGMLVEKR-----STRCEIPPT-RFSVD
 ncu09638    (1) STDVGVWPACRWPGGVHDPSQFWEFLRNKV-----NGWKEFDDP-RFSSA
 ncu02918    (1) EPIAIIGMGCRLPGGSHSSSKLWELLKAGR-----TAQSRFPPS-RFNID
   AtMSAS    (1) NEVAVVGMACRLAGGNNSPEELWQSILNRK-----DASGEIPSM-RWEPY
   PgPKS2    (1) DDIAIIGMACRVPGDVKSPSALWQFLLQKG-----DASGDMPSW-RWDPY
     EpoD    (1) EPIAIVGIGCRFPGGADAPEAFWELLDAER-----DAVQPLDR--RWALV
     MxaC    (1) EPIAIVGMACRFP-QADNVEAFWRLLQGGV-----DAVREIPLE-RWPKD
     MxaD    (1) EPIAIVGTSCRVPGGARTPEAFWRLLHGGV-----DAITEVPRD-RWDAE
   pks ST    (1) GKLAIVSMSGRFP-EAPSTDSFWDLLYKGL-----DVCKEVPLR-RWDVK
     AnWA    (1) SKIAIIGMSGRFP-EADSPQDFWNLLYKGL-----DVHRKVPED-RWDAD
   ClPKS1    (1) CKLAIVGMAGRFP-DAASHEKLWELLAKGL-----DVHRVVPAD-RFPVA
    Atat1    (1) QKIAIVGMAGRFP-NSDDLESFWSTLRQGL-----DLHRRVPPD-RFDID
Consensus    (1) EPIAIVG GCRFPGGA SPSKLWDLL    R     DL   IP D RF VD
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             51                                                100
     ACE1   (45) KYFHPDHKHHG-TSNVRHSYFLE---ENFKHFDAKFFGIRPQEAMAMDPQ
     Syn7   (45) AFHHADGSHHG-RTNARHGYFLN----NVKTFDAQFFGVQAGEAESMDPQ
     Syn6   (45) SFYHPDGSFHG-RTNAANAYFLD---QNIRAFDANFFNIQHHEAEVTDPQ
     LNKS   (45) TFYHPDGKHHG-RTNAPYAYVLQ---DDLGAFDAAFFNIQAGEAESMDPQ
   GmPKS9   (45) SFYHSDPTHHG-TTNVTQSYFLD---EDVTKFDNGFFGIQPMEAEAMDPQ
   GmPKS1   (45) AFYHADSKHHG-TTNVRHSYFLN---EDPARFDNNFFNIQPGEAEAIDPQ
   BfPKS5   (45) AFFHTNGSYHG-ATDSREAYFLE---EDVALFDNAFFNIQPGEAEAVDPQ
  ChPKS16   (45) GFYHPDGSHHG-HMNVLQSYLLE---EDTRLFDAEFFGINPVEAKAMDPQ
  FG10464   (45) RFYHKDSSHHG-TANVRRSYLLD---EDVRLFDTQFFGISPGEAQAMDPQ
  mg03818   (44) GFYHPNAQHHA-STNVRKSYFLD---VNVRKFDHNFFNITAVEAAAMDPQ
     Syn2   (45) GFYHPKNSHHG-TSNVRHSYLLD---EDLRTYDAQFFGVKAIEASSMDPQ
  mg03810   (45) GFYHQDGEYGG-HSNVRDSYTIA---EDVAAWDAGFFNVAAAEASAIDPQ
  ChPKS17   (45) AFYNEDGSKPG-CTNVNHGYFLD---EDIRAFDAAFFRMNPAEVEAVDPQ
  GmPKS10   (45) AFYSSNGDKNG-CTDVKKAYLLA---EDIRLFDASFFKINPREAEAMDPQ
  af04917   (46) GFYNVDGEHHG-ASNATNAYFIE---EDPRYFDAGFFSIAPREAESIDPQ
 ncu08399   (45) GFYHPDGEYHG-TTNSAKAYFLE---QDHRLFDASFFNITPKEAEAIDPQ
   BfPKS6   (45) AFYHPNGEHHG-TTNATKSYFLN---EDPTTFDAPFFNINPREAEALDPQ
   BfPKS3   (44) GFYHQDGQHHG-TSNVLHSYLLD---ENPLAFDSAFFHIHNREAECIDPQ
   BfPKS4   (45) -------R----HSTSTRGYFLS---QDVREFDASFFSLSPLEAQAMDPQ
   AN8412   (45) RFYHPDGEHHGSTDVRGTSYLLS---EDPRQFDASFFNINPREAEGMDPQ
  mg09589   (50) KFYHPDGDRHG-RTPVGKAYFLSEDL-DPALFDASFFGISPLEAEAMDPQ
     Syn8   (45) KFHHAKGEHHG-SSNVLKSYFL--DQ-DPCLFDGSFFGISPLEAEAMDPQ
   ChPKS2   (45) AFYHPNQSRKD-CIDVNCGYFLD---GDIAEFDAQFFKMNG---TDADPQ
   ChPKS1   (44) GFYHPDSSRHG-THNVEYGHWFQ---QDVYNFDAPFFNVSPAEAAALDPQ
   BfPKS8   (45) SFYHPNPGKAG-CFNAAGGNFLK---EDVGLFDAPFFSLTAQEATSMDPQ
     LDKS   (45) GVYHPNGQRVG-SMHVRGGHFLD---EDPALFDASFFNMSTEVASCMDPQ
 ncu04865   (45) GFHHPNFEKLN-GTNVIGGHFMK---EDVGLFDAHFFNLSAETAAALDPQ
     FUM1   (45) GFHSPSSK-PG-SIAMRHGHFLDDK-DDLHRLDTSFFSMGMTEVSDIDPQ
 ncu09638   (45) GFHHPNSDRPG-SMSMKGAFLAEQ---DARLFDHTFFGMTGLEVETMDPS
 ncu02918   (45) GFYHPNSDRPG-SLNMEGGYFIED---DIRGFENSFFGINNLEATYMDPQ
   AtMSAS   (45) YRRDIRNP-KILDQTTKRGYFLD----HVENFDAAFFGVSPKEAEQMDPQ
   PgPKS2   (45) RQRHPRNA-AALAKTTAKGYFVN----DIDHFDAAFFAISPREAEQMDPQ
    EpoD    (44) GVAPVEAVP-------HWAGLLTEP---IDCFDAAFFGISPREARSLDPQ
    MxaC    (44) EVADIGDG------AMRWGGFLDS----VDSFDPGFFGISPREAVRMDPQ
     MxaD   (45) ALFDPDPNKQG-RTYARWGGFIDG----VDRFDAAFFGVSPREASRMDPQ
   pks ST   (44) THVDPSGKARN-KGATRWGCWLD----FAGEFDPRFFSISPKEAPQMDPA
     AnWA   (44) AHVDLTGTATN-TSKVPYGCWIR----EPGLFDPRFFNMSPREALQADPA
   ClPKS1   (44) THYDITGKAVN-TSHSQYGCWIE----NPGYFDPRFFNMSPREAFQTDPM
    Atat1   (44) AHYDPTGKKLN-STHTPYGCFIE----KPGLFDPRFFNMSQREAYQTDPM
Consensus   (51) GFYHP G   G  TNV   GYFLD     DV   FDA FF ISP EA AMDPQ
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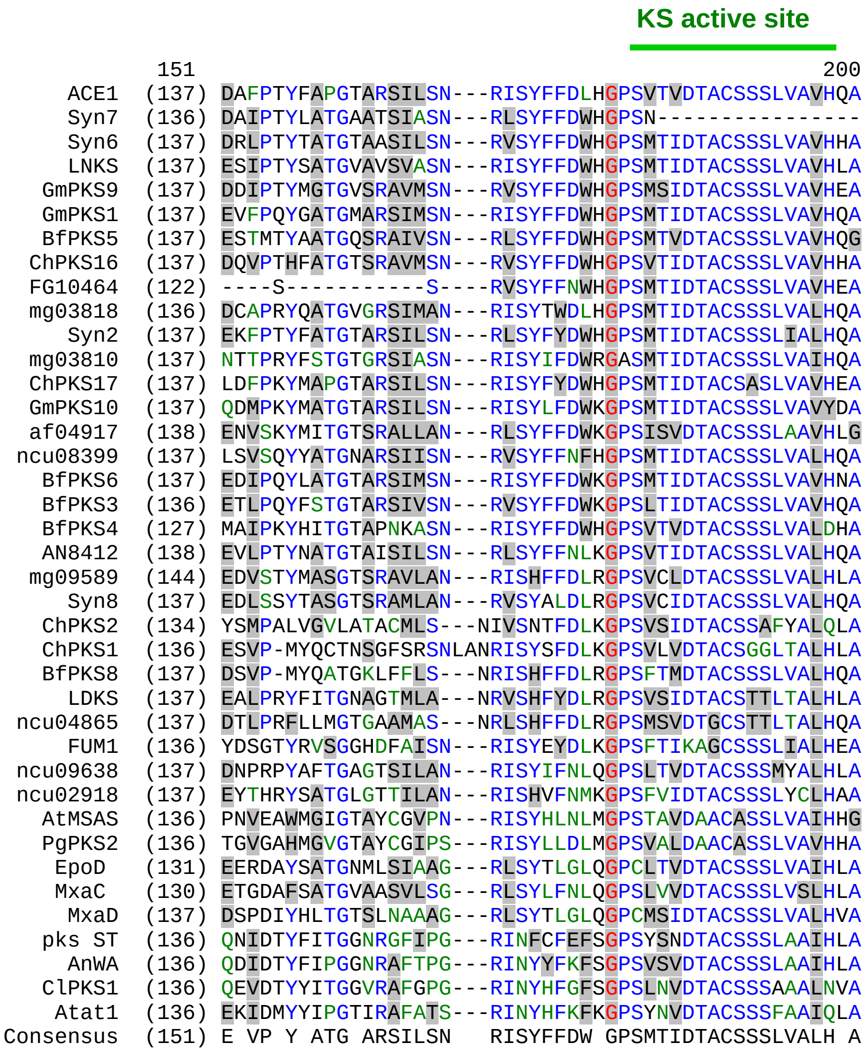
            101                                                 150
     ACE1  (91) QRFLLETVYESLEAAGITISDLKGS---QAGVFVGNMGVDYSELLSQDI-
     Syn7  (90) QRQLLEATYDALCAAGQTLGALKGS---DTAVYVGIMTHDFELTKVGDL-
     Syn6  (91) HRLLLETVYEALATAGLRVEDLRGS---STAVYCGQMMNDYKDLVNFDQ-
     LNKS  (91) HRLLLETVYEAVTNAGMRIQDLQGT---STAVYVGVMTHDYETVSTRDL-
   GmPKS9  (91) QRLLLETVYDSVVDAGLAMEDLKGS---DTSVFVGQMCDDWAQMLAKDW-
   GmPKS1  (91) QRLLMEVVYQGLCASGQTIEGLRGS---PTAVYVGVMCDDWSGIITRDL-
   BfPKS5  (91) QRLLMETVYDSLCAGGQTIEGLRGS---NTGIYVGMMCDDWAQAINRDW-
  ChPKS16  (91) QRLLLEVVYESIESAGLSIDRLRGS---DTAVFAGLMCGDYEARMLRDL-
  FG10464  (91) HRVLLEVVYEAIESAGKTIHGLHNS---DTAVNA----------------
  mg03818  (90) QRLLLETVYEALENASVSDKQLKGS---DTGVYVGLMCGDYENILMRDI-
     Syn2  (91) QRLLMETVYEALESAGLSIKQLQGS---DTAVYVGVMSADFMDMLARDV-
  mg03810  (91) QRLLTECVYEALESGGHSVQALRGS---DTAVYVGLVNEEYSDIHYREL-
  ChPKS17  (91) QRMLLETVFEALESAGTTIDQLQGT---DTAVYVGCMTSDYVEMLLRDP-
  GmPKS10  (91) QRLLLEAVYEATETAGLPMEDLKGS---DTAVYVGCMTGDYHEMLMREP-
  af04917  (92) QRLLLETVYEAMENAGLTLNGMRGS---ATSAYMGAMSADYTDTQLRDI-
 ncu08399  (91) QRMLLEVVYEALESAGYTLQDYSGK---KVAVFAGVMTADYDTLSQRDD-
   BfPKS6  (91) QRLLLETVYEALEAAGLSIEEMQGT---STAVYVGLMCADYFDVLMRDI-
   BfPKS3  (90) QRLLLENVYETIESACYPMETIRGS---DTGVFVGLMCADYYDVQMRDP-
   BfPKS4  (81) HRLLLETVYEALEEAGIPAETLRGS---DTAVYTGVMFHDYLSLSSQDH-
   AN8412  (92) QRLLLETAFEALEAAGYSLEAMNGS---KTSVHVGVMNSDFSNIQLRDP-
  mg09589  (98) QRMLLETVYEASESAGMPLDKLKAA---NCAVYVGAMTADYAELPTRDV-
     Syn8  (91) QRLLLETVYEAAESAGATLEGLRGS---RTSVHVGVMTGDYADVQARDA-
   ChPKS2  (88) GRMILECVYEALENAGGSQESIVGS---KVGVFSTSNTSDYTLSLKDDI-
   ChPKS1  (90) QRMLLECSYEAFENSGTPMSKIVGT---DTSVFVSSFATDYTDMLWRDP-
   BfPKS8  (91) QRILLECTFEALESAGIPKHEIVGK---DVGVFVGGSFSEYESASFVDT-
     LDKS  (91) YRLILEVVYEALEAAGIPLEQVSGS---KTGVFAGTMYHDYQGSFQRQP-
 ncu04865  (91) FRLQLESTYEALESAGITLQDVAGS---NTSVYAGSFFRDYHESLIRDP-
     FUM1  (92) QRMLLEVAYECMQSSGQTNWRGS-----NIGCYVGVWGEDWLDLHSKDL-
 ncu09638  (91) QRKLLEVAYEAIESAGETWESVSGT---RTGVFVGNFCLDHWMIQSRDW-
 ncu02918  (91) QRKLLEVVFETFENAGFTLDQVSDA---NIGCYVGNFVTDFITMQLKDS-
   AtMSAS  (90) QRLSLEVTWEALEDAGIPPQSLSGS---ETAVFMGVNSDDYSKLLLEDI-
   PgPKS2  (90) QRIALEVAWEALENAGISPSRLAGS---DTSVYMGVNSDDYGKLVLEDL-
     EpoD  (84) HRLLLEVAWEGLEDAGIPPRSIDGS---RTGVFVGAFTADYARTVARLPR
     MxaC  (84) QRLLLEVAWEALEDAGLDVDKLSGS---RSGVFIGACNDDYHCMQVERP-
     MxaD  (90) QRMLLEVAWEALERAGQPPDQLAGS---RTGVFLGIIGSDYAQLQARLLG
   pks ST  (89) QRMALMSTYEAMERGGIVPDTTPSTQRNRIGVFHGVTSNDWMETNTA---
     AnWA  (89) QRLALLTAYEALEGAGFVPDSTPSTQRDRVGIFYGMTSDDYREVNSG---
   ClPKS1  (89) QRMALTTAYEALEMCGYVPNRTPSTRLDRIGTFYGQTSDDWREINAA---
    Atat1  (89) GRLALVTAYEALEMSGFVPNRTPSSMLDRIGTFYGQTSDDWRTLNAA---
Consensus (101) QRLLLE VYEALESAGITIE L GS    TGVFVGVM  DY  L  RD
```



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            151                                                 200
     ACE1  (137) DAFPTYFAPGTARSILSN---RISYFFDLHGPSVTVDTACSSSLVAVHQA
     Syn7  (136) DAIPTYLATGAATSIASN---RLSYFFDWHGPSN----------------
     Syn6  (137) DRLPTYTATGTAASILSN---RVSYFFDWHGPSMTIDTACSSSLVAVHHA
     LNKS  (137) ESIPTYSATGVAVSVASN---RISYFFDWHGPSMTIDTACSSSLVAVHLA
   GmPKS9  (137) DDIPTYMGTGVSRAVMSN---RVSYFFDWHGPSMSIDTACSSSLVAVHEA
   GmPKS1  (137) EVFPQYGATGMARSIMSN---RISYFFDWHGPSMTIDTACSSSLVAVHQA
   BfPKS5  (137) ESTMTYAATGQSRAIVSN---RLSYFFDWHGPSMTVDTACSSSLVAVHQG
  ChPKS16  (137) DQVPTHFATGTSRAVMSN---RVSYFFDWHGPSVTIDTACSSSLVAVHHA
  FG10464  (122) ----S-----------S----RVSYFFNWHGPSMTIDTACSSSLVAVHEA
  mg03818  (136) DCAPRYQATGVGRSIMAN---RISYTWDLHGPSMTIDTACSSSLVALHQA
     Syn2  (137) EKFPTYFATGTARSILSN---RLSYFYDWHGPSMTIDTACSSSLIALHQA
  mg03810  (137) NTTPRYFSTGTGRSIASN---RISYIFDWRGASMTIDTACSSSLVAIHQA
  ChPKS17  (137) LDFPKYMAPGTARSILSN---RISYFYDWHGPSMTIDTACSASLVAVHEA
  GmPKS10  (137) QDMPKYMATGTARSILSN---RISYLFDWKGPSMTIDTACSSSLVAVYDA
  af04917  (138) ENVSKYMITGTSRALLAN---RLSYFFDWKGPSISVDTACSSSLAAVHLG
 ncu08399  (137) LSVSQYYATGNARSIISN---RVSYFFNFHGPSMTIDTACSSSLVALHQA
   BfPKS6  (137) EDIPQYLATGTARSIMSN---RISYFFDWKGPSMTIDTACSSSLVAVHNA
   BfPKS3  (136) ETLPQYFSTGTARSIVSN---RVSYFFDWKGPSLTIDTACSSSLVAVHQA
   BfPKS4  (127) MAIPKYHITGTAPNKASN---RISYFFDWHGPSVTVDTACSSSLVALDHA
   AN8412  (138) EVLPTYNATGTAISILSN---RLSYFFNLKGPSVTIDTACSSSLVALHQA
  mg09589  (144) EDVSTYMASGTSRAVLAN---RISHFFDLRGPSVCLDTACSSSLVALHLA
     Syn8  (137) EDLSSYTASGTSRAMLAN---RVSYALDLRGPSVCIDTACSSSLVALHQA
   ChPKS2  (134) YSMPALVGVLATACMLS---NIVSNTFDLKGPSVSIDTACSSAFYALQLA
   ChPKS1  (136) ESVP-MYQCTNSGFSRSNLANRISYSFDLKGPSVLVDTACSGGLTALHLA
   BfPKS8  (137) DSVP-MYQATGKLFFLS---NRISHFFDLRGPSFTMDTACSSSLVALHQA
     LDKS  (137) EALPRYFITGNAGTMLA---NRVSHFYDLRGPSVSIDTACSTTLTALHLA
 ncu04865  (137) DTLPRFLLMGTGAAMAS---NRLSHFFDLRGPSMSVDTGCSTTLTALHQA
     FUM1  (136) YDSGTYRVSGGHDFAISN---RISYEYDLKGPSFTIKAGCSSSLIALHEA
 ncu09638  (137) DNPRPYAFTGAGTSILAN---RISYIFNLQGPSLTVDTACSSSMYALHLA
 ncu02918  (137) EYTHRYSATGLGTTILAN---RISHVFNMKGPSFVIDTACSSSLYCLHAA
    AtMSAS (136) PNVEAWMGIGTAYCGVPN---RISYHLNLMGPSTAVDAACASSLVAIHHG
   PgPKS2  (136) TGVGAHMGVGTAYCGIPS---RISYLLDLMGPSVALDAACASSLVAVHHA
    EpoD   (131) EERDAYSATGNMLSIAAG---RLSYTLGLQGPCLTVDTACSSSLVAIHLA
    MxaC   (130) ETGDAFSATGVAASVLSG---RLSYLFNLQGPSLVVDTACSSSLVSLHLA
     MxaD  (137) DSPDIYHLTGTSLNAAAG---RLSYTLGLQGPCMSIDTACSSSLVALHVA
   pks ST  (136) QNIDTYFITGGNRGFIPG---RINFCFEFSGPSYSNDTACSSSLAAIHLA
     AnWA  (136) QDIDTYFIPGGNRAFTPG---RINYYFKFSGPSVSVDTACSSSLAAIHLA
    ClPKS1 (136) QEVDTYYITGGVRAFGPG---RINYHFGFSGPSLNVDTACSSSAAALNVA
   Atat1   (136) EKIDMYYIPGTIRAFATS---RINYHFKFKGPSYNVDTACSSSFAAIQLA
Consensus  (151) E VP Y ATG ARSILSN   RISYFFDW GPSMTIDTACSSSLVALH A
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            201                                              250
     ACE1  (184) VQSLRLG----ETPVAIVCGANLLLGPAQYIAESKLQMLS-------PNG
     Syn7  (167) -----------------------------FITESKLSMLS-------PTG
     Syn6  (184) VQQLRSG----SSKVAIAAGANLILGPVPLIVESKMNMLS-------PTG
     LNKS  (184) VQQLRTG----QSSMAIAAGANLILGPMTFVLESKLSMLS-------PSG
   GmPKS9  (184) VRTLRSG----ESNVAVAAGANLILLPGMYICESKLRMIS-------PTG
   GmPKS1  (184) IQTLRSG----ESEVAIAAGANLILTPGMYIAESKLSMLS-------PSG
   BfPKS5  (184) VTSLRNG----ECPVVIAAGVNLILGPGMWIAESKLHMLS-------PTG
  ChPKS16  (184) VQALRSG----DSHAAVACGSNLIFGPEMYVIESKLKMLS-------PDS
  FG10464  (153) VQALRNG----TSRMAVACGTNLILSPLPFISESNLSMLS-------PTG
  mg03818  (183) VQALRLG----ESRLAIVGGSNLLLG---------------------PEW
     Syn2  (184) VQVLRSK----QSKVAVAAGSNIILGPEQYIAESKLQMLS-------PDG
  mg03810  (184) VQTLRSG----AFKVAVAAGVNMLLGPEPYIVESSFHMLS-------PTG
  ChPKS17  (184) VQALRSG----ISRVACAAGSNAILGPENFVIESKLQLLS-------PTG
  GmPKS10  (184) VTALRNG----VSRIACAGGVNLILGPEMMISESKLHMLS-------PTG
  af04917  (185) FQALRAG----ECTISCVGGSNIILNPDCYLAATSLHLLS-------PTG
 ncu08399  (184) VLSLRSG----EAEMACVSGVNLILTPEQFVVESSLHMLS-------PTG
   BfPKS6  (184) ISTLRSG----QSRTAIAAGANLIFGPEMYIGESNLHMLS-------PTG
   BfPKS3  (183) VSALRNG----ECRSAVAAGVNLIFGPEMFNGEANLKMLS-------PTG
   BfPKS4  (174) VQQLRSG----SSTLAVAAGANLLLDGRPFIGFNNMGMLS-------PTG
   AN8412  (185) VQGLRAG----DATAAIVAGANLIFDPAMYIAESSLHMLS-------PDS
  mg09589  (191) CQDLRTG----CADMAVVAGSCLILSPDMFISESKLHMLS-------PTG
     Syn8  (184) VRDLAAEGGAAGSDMAIVAGCGLLLDPLMYIAESKLRMLS-------PTG
   ChPKS2  (181) SQSLRSG----ETEMCIVSGCALNISPWRWTMLSNLTMLN-------PDG
   ChPKS1  (185) CQSLLVG----DVRQALAAGSSLILGPEMMVTMSMMKFLS-------PDG
   BfPKS8  (183) CQSIRNG----ECKSAITGGCHLNMLPENWISIPFCEIPSNKYRLFSDEG
     LDKS  (184) IQSLRAG----ESDMAIVAGANLLLNPDVFTTMSNLGFLS-------SDG
 ncu04865  (184) CQSLRSG----ESTMSIVGGANIMFNPDMFLAMSSMTLIS-------KDG
     FUM1  (183) VRAIRAG----DCDGAIVAGTNLVFSPTMSVAMTEQGVLS-------PDA
 ncu09638  (184) VNAIRAG----DCDSAIVASANWIADPGVQIALDKLGALS-------ASA
 ncu02918  (184) VAALIAG----ECDSAIVAGANLIQSPEQQLATMKAGVLS-------KTS
   AtMSAS  (183) RQAILQG----ESEVAIVGGVNALCGPGLTRVLDKAGATS-------TEG
   PgPKS2  (183) RQAIRAG----ETDLAIAGGVNALLGPGLTRVLDEAGAIS-------ADG
    EpoD   (178) CRSLRAG----ESDLALAGGVSTLLSPDMMEAAARTQALS-------PDG
    MxaC   (177) CQSLRNR----ECNMALAGGVNLILSPQSVLLVSKLQALS-------PDG
     MxaD  (184) CQSLRNR----ECDLALSAGVNLMLMPDATIALSSSRGLS-------PDG
   pks ST  (183) CNSLWRG----DCDTAVAGGTNMIFTPDGHTGLDKGFFLS-------RTG
     AnWA  (183) CNSIWRN----DCDTAITGGVNILTNPDNHAGLDRGHFLS-------RTG
   ClPKS1  (183) CNSLWQK----DCDTAIVGGLSCMTNPDIFAGLSRGQFLS-------KTG
    Atat1  (183) CTSLLAK----ECDTALAGGLNVMTTPDLFAGLSRAHFLS-------KTG
Consensus  (201) VQSLRSG    ES MAIAAG NLIL PEMFIA SKL MLS       PTG
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                251                                               300
      ACE1  (223) RSRMWDASA-DGYARGEGFASIVLKPLSVALANGDHIECIIRETGCNQDG
      Syn7  (181) RSRMWDAGA-DGYARGEGIACVVLKTLSQALADGDTIEALIRETGVGQDG
      Syn6  (223) RSSMWDEKA-NGYARGEGVAAVVLKTLSQALSDGDNIECVIRETGVNQDG
      LNKS  (223) RSRMWDAGA-DGYARGEAVCSVVLKTLSQALRDGDTIECVIRETGVNQDG
    GmPKS9  (223) RSRMWDANA-DGYARGEGFASVILKTLSQALADGDPIECIIRETGVNQDG
    GmPKS1  (223) RSKMWDQDV-NGYARGEGIAAVVLKPLSAAIRDNDHIDCIIRATGVNQDG
    BfPKS5  (223) TSKMWDESA-DGYARGEGIASVVMKRLSDALRDGDPIECVIRGTGVNQDG
   ChPKS16  (223) LSRMWDKDA-NGYARGEGVTAVVLKTLSQALADNNRIEVVIRETGMNSDG
   FG10464  (192) KSRMWDADA-DGYARGEGVAAVVLKPLSAAIEDNDVIECIIREVGVNQDG
   mg03818  (208) RRRLRKRGR-RGGG--------HLKRLSDAVADGDFIESVIRETGVAQDG
      Syn2  (223) RSRMWDAEA-NGYARGEGVAAVVLKTLSQALADGDHIECIIRETGINQDG
   mg03810  (223) RCRMWDASA-DGYGRGDGVAAVILKTLSQAIEDGDRIESVIRETGINQDG
   ChPKS17  (223) RSRMWDAAA-DGYARGEGAAALIMKKLSHALADGDEVYCIIRETGVNSDG
   GmPKS10  (223) RSRMWDASA-NGYARGEGVAAIMMKTLSQALADGDHIEGIIREIGVNSDG
   af04917  (224) RSQMWDQAA-DGYARGEGVCVFFMKTLSQALRDGDRIDALLRETCVNSDG
  ncu08399  (223) RCHMWDDRA-DGYARGEGVAAIFIKPLSKALADGDRIEAIIRETGVNSDG
    BfPKS6  (223) RSQMWDSRA-DGYARGEGTAAIVLKTLKNALEDGDDIEYIIRETGVNSDG
    BfPKS3  (222) TCKMWDASA-DGYARGEGCGSVMLKLLEDAIRDGDRIESVIRETGVNSDG
    BfPKS4  (213) SCKMWDTEA-DGYARGEGILAMLLKPLRLALADGDNIQCVIRETGVNHNG
    AN8412  (224) CSRMWDKDA-NGYARGEGVGVLVLKPLSRAIMDGDHVEAVIRSTGVNSDG
   mg09589  (230) HCRMWDSSA-DGYARGEGAAALFLKPLSRALADGDPVHGVIRASGVNSDG
      Syn8  (227) TSKMWDAAA-DGYARGEGVAAVLLKPLSRALRDGDPIRGVVRATGVNSDG
    ChPKS2  (220) LSKSFDPQADAGYVRGEGAASIIVKPLDAAIRDNDRVHCVLSDIGVNHNG
    ChPKS1  (224) RCYAFDERA-NGYARGEGVAVLLLKRLEDALADNDTIRAVIRGTGCNQDG
    BfPKS8  (229) RSFSFDSRG-TGYGRGEGCGLIVLKPLEQALKDNDNIRAVIRGSGINQDG
      LDKS  (223) ISYSFDSRA-DGYGRGEGVAAIVLKTLPDAVRDGDPIRLIVRETAINQDG
  ncu04865  (223) RSWAFDSRA-NGYGRGEGSATVVLKPLDAALRDGDPIRAVIRDSGINQDG
      FUM1  (222) SCKTFDANA-NGYARGEAINAIFLKPLNNALREGDPIRALVRATSSNSDG
  ncu09638  (223) RCHTFDARA-EGYARGEGFGAIYLKRPSLAIADMSPIRAMIRGTAINSNG
  ncu02918  (223) TCHTFDSSA-DGYGRADGIGAILVKRLSDAIRDGDPIRSVIRGTAINSNG
    AtMSAS  (222) RCLSFDEDA-KGYGRGEGAAVVILKRLSTAIRDGDHIRAIIKGSAVAQDG
    PgPKS2  (222) KCRSFDDSA-NGYGRGEGAGVVILKRLEKALTDGDRVLAVLKGSAVASDG
     EpoD   (217) RCRTFDASA-NGFVRGEGCGLVVLKRLSDAQRDGDRIWALIRGSAINHDG
     MxaC   (216) RSKAFDASA-NGFTRGEGCGIVVLKRLSDALADGDHILATIRGSAINQDG
      MxaD  (223) RCKTFDAAA-NGFVRAEGCVVLVLKRLSDALASGDEILSLIAGSAVNQDG
    pks ST  (222) NCKAFDDAA-DGYCRAEGVGTVFIKRLEDALAENDPILATILDIKTNHSA
      AnWA  (222) NCNTFDDGA-DGYCRADGVGTVVLKRLEDALADNDPILGVINGAYTNHSA
    ClPKS1  (222) PCATFDNGA-DGYCRADGCASVIVKRLDDALADKDNVLAVILGTATNHSA
     Atat1  (222) SCKTFDDGA-DGFCRGDGVGTVVLKRLEDAEADNDPILAVVLGTATNHSS
 Consensus  (251) RSRMWDA A DGYARGEGVAAVVLK LS ALADGD I AVIRETGVN DG
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            301                                                 350
     ACE1  (272) RTKGITMPSPLAQCKLIQETYKRAG-LDLSKSSDRPQYFEAHGTGTPAGD
     Syn7  (230) RTTGITMPSNVAQASLIKATYARAG-LDLNEPQGRPQFFEAHGTGTPAGD
     Syn6  (272) RTPGITMPSHQAQEALIRETYAAAG-LDLSRAEDRCQYFEAHGTGTPAGD
     LNKS  (272) RTTGITMPNHSAQEALIKATYAQAG-LDITKAEDRCQFFEAHGTGTPAGD
   GmPKS9  (272) KTPGLTVPSNIAQTALIRDVYQRAG-LDITKPSDRPQLFHAHGTGTKAGD
   GmPKS1  (272) RTPGLTMPSATAQADLIRSTYARAG-LDINKPEDRPQFFHAHGTGTPAGD
   BfPKS5  (272) KTPGLTMPNGKAQADLIRDTYQRAG-LDIHDPRDRPQFFHAHGTGTQAGD
  ChPKS16  (272) ATPGITMPSASAQRDLIRSVYRKAG-LDPESAEDRPQYIEAHGTGTPAGD
  FG10464  (241) KTRGITMPSAQAQASLIRQTYAKAG-LDPATPEGRCQFFEAHGTGTPAGD
  mg03818  (249) RTNGITTPSAGAQANLIRRVYAKAG-LDVNR--QGPQYFEAHGTGTPAGD
     Syn2  (272) KTPGITMPSATAQAALIRSTYARAG-LDLRKASDRPQFFEAHGTGTPAGD
  mg03810  (272) ATGGITVPNASAQIALIRDTYRRAG-LDLAKRSDRPQFFECHGTGTPTGD
  ChPKS17  (272) RTNGITMPSAEAQAALIRKTYARAG-LDPLK--DGCQFFEAHGTGTQAGD
  GmPKS10  (272) RTNGITLPSPDAQKVLIRQTYRNAG-LDVFK--DRCQFFEAHGTGTPAGD
  af04917  (273) RTQGIALPSAEAQVSLMRTAYKNAG-LDLSKAEDRPQYIEAHGTGTQAGD
 ncu08399  (272) RSKGITMPNWEAQSALIQDTYRRSG-LNARDPIDRCQFFEAHGTGTAAGD
   BfPKS6  (272) KSKGITMPLAASQADLIRQTYARAG-LDCTKPSERCQYFEAHGTGTPAGD
   BfPKS3  (271) RTMGITMPSASSQEKLIKETYRRAG-LDPSKESDRCQFFEAHGTGTLAGD
   BfPKS4  (262) RTSGITLPSASAQTSLIRDVYHRAG-LDPTNPSDRPQYIEAHGTGTQAGD
   AN8412  (273) RTKGITMPNAESQTELIRQTYRDAG-LDPIR--DRCQYFECHGTGTATGD
  mg09589  (279) RTPGITMPSYRAQARLIKDVYKSAG-LNPLKPEDRCQYFEAHGTGTQAGD
     Syn8  (276) RTPGITMPSAEAQASLIWDTYRAAG-LDPFNVEERCQYFEAHGTGTPAGD
   ChPKS2  (270) RTNGYTLPDARMQASLMRELQVRLD-IKPDEF----GFVEAHAPGTRVGD
   ChPKS1  (273) KTPGITMPNSVSQEALIRSVYKKAA-LDPLDT----TYVECHGTGTQAGD
   BfPKS8  (278) KTPGITMPNGSAQESLMKWVYESAG-IDPKDT----GYVEAHGTGTKVGD
     LDKS  (272) RTPAISTPSGEAQECLIQDCYQKAQ-LDPKQT----SYVEAHGTGTRAGD
 ncu04865  (272) KTETITTPSGEAQEALIRACYERAG-LDPGQT----TYFEAHGTGTPTGD
     FUM1  (271) KTPGMSMPSSESHEALIRRAYGEVF-LDPKDT----CFVEAHGTGTSVGD
 ncu09638  (272) RTGGITRPSANGQETVIREAYRNAGNLPFRDT----SYFECHGTGTYVGD
 ncu02918  (272) KTNGITLPSADGQEAVIRKAYAQAG-LGFNET----DYIECHGTGTAVGD
    AtMSAS  (271) KTNGIMAPNAKAQELVAWNALRTAG-VDPLTVG---YVEAHATSTPLGD
    PgPKS2  (271) KTLGIMAPNAQAQILVAQKALKEAR-VTPDSIS---YIEAHATSTSLGD
    EpoD   (266) RSTGLTAPNVLAQETVLREALRSAH-VEAGA----VDYVETHGTGTSLGD
    MxaC   (265) KSTGLTTPNVLSQQALIRQALESSG-LKAEQ----VSYVEAHGTGTPLGD
     MxaD  (272) ASSGLMVPNGPAQERVIEQALASGG-LKPSQ----ISFVEAHGTGTSLGD
   pks ST  (271) MSDSMTRPFKPAQIDNMSALLSTAG-ISPLDLS---YIEMHGTGTQVGD
     AnWA  (271) EAVSITRPHVGAQAFIFKKLLNEAN-VDPKNIS---YIEMHGTGTQAGD
    ClPKS1  (271) DAISITHPHGPTQSILSRAILDDAG-VDPLDVD---YVEMHGTGTQAGD
    Atat1  (271) EAVSITRPHGPAQEALYRKILKHTG-VDPVDVS---YVEMHGTGTQAGD
Consensus  (301) RT GITMPSA AQ ALIR  Y  AG LDP     R QYFEAHGTGT AGD
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                351                                                   400
     ACE1  (321) PVEAEAISTAFFGPESGFRRTSH------------DP------KLYVGSV
     Syn7  (279) PQEAEAISKAFFSSGQ------------------------DMQDLYVGSI
     Syn6  (321) PQEAEAISRSFFGHGERPPRE---------------------EPLYVGSI
     LNKS  (321) PQEAEAIATAFFGHEQVARSDG-----------------NERAPLFVGSA
   GmPKS9  (321) PKEAEAIFRAFFGDDQPHDEK-----------------------LNVISI
   GmPKS1  (321) PR--EAEASTVRSIPDVKDDK-----------------------LYVGSI
   BfPKS5  (321) PQESQAIDSAFFSGPDKKLET-----------------------MAVGSI
  ChPKS16  (321) PIEAEALSTAFFGEGAKMTTP-----------------------IYTGSI
  FG10464  (290) PQEAEALKTAFFPNETDSVTNGT------------NGLLSEADNLLVGSI
  mg03818  (296) PIEAEAIHAVFGGARASDEPN--------------------APPLYVGSV
     Syn2  (321) PIEAAAISKAFFGDDVKPHSR------------------DGHDTLFVGSI
  mg03810  (321) PLEARAVHEALGKHIVVDES-------------------PGRPPLYVGSI
  ChPKS17  (319) PQEARAIHDVFFPE-----------------------LRDSADVLYVGSV
  GmPKS10  (319) PLEARAIHEAFFDG-----------------------SDIVNEPMYVGSV
  af04917  (322) PREAYAIATTFFPP-----GE----------------DHSHRPKLVVGSV
 ncu08399  (321) PNEARAIEDAFFGRNVSTSSQ----------------DTAEVSKLLVGSV
   BfPKS6  (321) PVEAEAISSAFFPQ-----RS----------------DILNSEPLHVGSI
   BfPKS3  (320) RQEAEAISRAFDLYQT---SH----------------LMQDNLPLSVGSI
   BfPKS4  (311) PLEAEALAAAFSLTSSQP----------------------DEAHMLVGSI
   AN8412  (320) PIEARAVHDAFFPTETRTASN----------------TLIPDGKLYVGSV
  mg09589  (328) PVEAHGVFDAFFSTESDGGEPDDFFSTGSHEVSDGRLEDDDGKQLLVGSI
     Syn8  (325) PVEARGIFKSFFDPESAK-----------------KSRTSEETPLLVGSV
   ChPKS2  (315) PIEISALQEVFSTSAR-----------------------TLEDPLLIGSV
   ChPKS1  (318) TTEASALSKVFSP--------------------------GRRLPLLIGSV
   BfPKS8  (323) PIEATALYNVFGE-GR-----------------------NARNPLFIGSV
     LDKS  (317) PLELAVISAAFPGQQ-----------------------------IQVGSV
 ncu04865  (317) PIEVKAIARVFKDSRKGN---------------------GEDALLRIGSV
     FUM1  (316) PLEATAIARVFG--------------------------GSSDNKLYIGSV
 ncu09638  (318) PIEVAALGRVFAPE------------------------RSSDDPLLIGSV
 ncu02918  (317) PIEVEAVSRVFK--------------------------KPQGAPLLIGSV
   AtMSAS  (316) PTEVSAVSAVYGKG------------------------RPEGNPCFIGSV
   PgPKS2  (316) PTETSALAGVYGAGSG----------------------RHPCNPCYIGSI
    EpoD   (311) PIEVEALRATVGPAR------------------------SDGTRCVLGAV
    MxaC   (310) PIEAEALRETYGVPR------------------------PDGSVCGIGSV
     MxaD  (317) PIELQALARVLGTGR------------------------SAETPLFVGSV
   pks ST  (316) AVEMESVLSLFAPDET---------------------FRPRDKPLYVGSA
     AnWA  (316) AVEMQSVLDVFAPDHR----------------------RGPGQSLHLGSA
   ClPKS1  (316) GTEMVSVTNVFAPADR---------------------KRPADRPLYLGAV
    Atat1  (316) GTEMKSITNVFAPRDKG--------------------RRQPDQLIHLGAL
Consensus  (351) PIEA AI   F                                 L VGSV
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            401                                                 450
     ACE1  (353) KTVIGHTEGTAGLAGLIKASLAMKAKSIPPNLHLE---RVNP--AVQPFY
     Syn7  (305) KTVIGHTEGTAGIAGLLKCSLAVQNGIVPPNMLLQ---KLSP--RVEPFT
     Syn6  (350) KTVIGHTEGTAGVAGLIKASLAMQNRTIPPNMHFH---KLSP--KVAPFY
     LNKS  (354) KTVVGHTEGTAGLAGLMKASFAVRHGVIPPNLLFD---KISP--RVAPFY
   GmPKS9  (348) KTQIGHTEGTAGLASLLGTMMAMKNATVPPNMHFE---TLNP--DIEPFY
   GmPKS1  (346) KTVLGHTEGTAGLASLIGTALAIQNKTIPPNMHFD---VLNP--KIKPFY
   BfPKS5  (348) KTIIGHTEGTAGLASLIGSVMAIKHGVFPPNLHFQ---NLSP--KVAPFY
  ChPKS16  (348) KTVLGHTEGSAGLAALLKVTQAMQNSTVPPNLWFQ---QINP--KLKPFY
  FG10464  (328) KTVIGHTEGTAGLAGLIKACMALKHGAVPPNLLFN---RLNP--ALEPFT
  mg03818  (326) KTIIGHTEGTAGLAGLIKATLALQQRTVFPNKHFH---KLNP--KIEPFY
     Syn2  (353) KTVIGHTEGTAGLAAIIKASTALQAGVLPPNRLFH---KLNP--KIEPYY
  mg03810  (352) KTVIGHTEATAGIAGIIKASLALQNGLIPPNLLFE---RLNP--AIEPLY
  ChPKS17  (346) KTVIGHLEGAAGVAGLIKAAEAVRRAVVPPNMLLQ---KLNP--AIEPFC
  GmPKS10  (346) KTAIGHLEGCAGLAGMIKAIEAVKTGIIPPNQLFE---TLNP--AVKPYT
  af04917  (351) KTIIGHTEGCAGIAGILKAVLAMRHKTIPPNQHFH---NLNP--SVKPSF
 ncu08399  (355) KTVIGHTEGAAGLAGLFKVVHAMINGTVPPNLHFN---RLQP--AVAKYY
   BfPKS6  (350) KTVIGHLEGAAGLAGIIKAGLALKEKTIPPNLHFQ---SLNS--AIEPFY
   BfPKS3  (351) KTIVGHLEGCAGIAGLLKASLALQHSFIPPNMHFQ---ELNP--EIEPFY
   BfPKS4  (339) KTVIGHTEGAAGLAGVLKASLAIQHGIIPPNLGFQ---QLNK--KVAPYC
   AN8412  (354) KTIIGHLEGCAGIAGVLKAVLAIKNRTIPPNMHFH---EPNP--RVIPFC
  mg09589  (378) KTVLGHLEGCAGLAGIIKVLLAMKHGVVPPNKHFV---KLNP--KIVQFS
     Syn8  (358) KTIIGHLEGCAGLAGVIKVLVAMEHDTIPPNLHLK---RLNP--EIEPLS
   ChPKS2  (342) KANVGHLESSSGFPSLIKAAMMLKKGLVVPNANFE---NESMN--SHLKE
   ChPKS1  (342) KTNIGHLEGASGLAGVVKSILMLEQGVILPNRNFE---ETKHENPAGKME
   BfPKS8  (349) KSNIGHLEAASGIISVIKTAMMLERGFILPNHDFK---TPNEN--IPFSK
     LDKS  (338) KANIGHTEAVSGLASLIKVALAVEKGVIPPNARFL---QP---SKKLLKD
 ncu04865  (346) KTNIGHTETASGVAAIIKVALALERGQIPPSINFE---TPN--AKLSLDE
     FUM1  (340) KPNLGHSEGASGVSSVMKAVLALENRTIPPNINFS---TPNP--KIPFSE
 ncu09638  (344) KSNVGHGEGASALASIMKVVLALEHGAIPPIYDLQ---TRNP--NIDFEG
 ncu02918  (341) KSNLGHSEAASGLSSIIKVAMALEKGEIPPTYGVK---NINP--KIKTDE
   AtMSAS  (342) KPNVGHLEAGAGAVGFIKAVMAVEKAIFPPQTNLK---RLNS---RIDWD
   PgPKS2  (344) KPNIGHLEAGAGVMGLIKAVLVLRHGQVPPQANLQ---TLNS---KIAWK
    EpoD   (337) KTNIGHLEAAAGVAGLIKAALSLTHERIPRNLNFR---TLNP--RIRLEG
    MxaC   (336) KTNVGHLESAAGIAGIMKVVLAMRHQSIPPHLHLK---QVNP--RIQLEG
     MxaD  (343) KTNVGHLEATAGLTGVLKTALALRNETIPPNLHFK---RLNP--DIVLDG
   pks ST  (345) KANIGHGEGVSGVTSLIKVLLMMKNDTIPPHCGIKPGSRINRNYP-DLPA
     AnWA  (344) KSNIGHGESASGVTSLVKVLLMMKENMIPPHCGIK--TKINHNFPTDLAQ
   ClPKS1  (345) KSNIGHGEAASGVTALTKVLMMMRKNAIPPHVGIK--KEINKTFPKDLSE
    Atat1  (346) KANIGHGEASAGVASLIKTVIMMQKNAIPHHVGIK--TTMNKTFPHDLNE
Consensus  (401) KTVIGH EG AGLAGLIKA LAL  G IPPNL F     LNP   I PF
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            451                                                 500
     ACE1  (398) GNLEIPT-RLMDWPEPAP----GQPLRASVNSFGFGGANAHVILESYTPA
     Syn7  (350) KHLRVPR-EATPWPAVQE----GQPRRASVNSFGFGGTNAHAIVEQYIPS
     Syn6  (395) QNLHVPT-EAQPWPELAP----GVPMRASVNSFGFGGTNAHAILEAYPNQ
     LNKS  (399) KNLRIPT-EATQWPALPP----GQPRRASVNSFGFGGTNAHAIIEEYMEP
   GmPKS9  (393) SNLEVPT-SAKAWPNVH-----GSVRRASINSFGFGGTNSHAILESYEPA
   GmPKS1  (391) DNLEVPT-KAIAWPETHK----GQPRRASINSFGFGGTNAHAIIEAYEPA
   BfPKS5  (393) NHLHIPT-TATPWPELPS----GVPRRISCNSFGFGGLNAHAIIESYESS
  ChPKS16  (393) GNLQIPT-HALIWPKPFG----RRPKRASINNFGFGGTNAHAIVESYELQ
  FG10464  (373) KHLSIPT-SLTPWPTLLT----NVPRRASVNSFGFGGTNAHAILEAYSQA
  mg03818  (371) KGLEIPT-SPLPWPKTPD----GQPRRASVNSFGFGGTNAHVILESFDNV
     Syn2  (398) SNLKILT-EAQPWPRLPE----AGTRRVSVNSFGFGGANAHAIVESADGY
  mg03810  (397) HGLQVPVGKPVPWPATGA----SPRRAIWTNTR--RPKNSHAILESYQLP
  ChPKS17  (391) VNLKVPT-QSLPWPHLPL----GGPRRASVNSFGFGGTNAHAIIESYEHQ
  GmPKS10  (391) SNLKLPV-ESQPWPKLTE----GFPRRASVNSFGFGGTNVHAIIEHFDNL
  af04917  (396) KHLSIAT-SPQPWPVVPP----DTPLRASVNGFGSGGTNCHAIVESYVPE
 ncu08399  (400) SHLHVPT-KALAWPSVAA----GQPRRATVNSFGFGGTNSTAICEMYVPE
   BfPKS6  (395) GNLNVPT-APLPWPAVEG------PLRASVNSFGFGGTNAHAILESYEVC
   BfPKS3  (396) QNLKVVT-SLQPWPLIPD----NTPRRASINSFGFGGTNAHAILESYSAA
   BfPKS4  (384) TNMDVVT-SVQPWPAMAS----NTPRRVSINSFGFGGANAHVILESVPLP
   AN8412  (399) DRLEIPT-VPIPWPDTGR----S-PLRASINSFGFGGTNAHAIIEGYDAL
  mg09589  (423) HRLRVPT-EALAWPDPGGP---GGTRRASVNSFGFGGTNAHVIVEGFHGG
     Syn8  (403) RVLKIPT-ESRPWPTP-AA---GQPKRASVNSFGFGGTNAHAIIESFDGG
   ChPKS2  (387) KNMRVPI-STQPWPKGK--------TYIAINNYGFGGSNSHCIVRAPP--
   ChPKS1  (389) LAYKVPT-TLECWNNVKT-------RRVSINSFGYGGANVHAILESATDF
   BfPKS8  (394) WHLKVPI-SQRPWPRAK--------KFASVNNFGFGGTNAHVVLERAP--
     LDKS  (382) THIQIPL-CSQSWIPTDG------VRRASINNFGFGGANAHAIVEQYGPF
 ncu04865  (391) WKLKVPT-ELEEWVGKDG------IRRASINNFGYGGSNAHVIMEDYSSY
     FUM1  (385) MNMAVPV-DAIPWPRDRP-------LRVSVNSFGIGGANAHCIIETLEEY
 ncu09638  (389) AKVQPVT-EVTPWPKDR-------LQRASINSFGYGGANGHCIIDHVNIV
 ncu02918  (386) WNVQIVT-ETTPWPKNLPHNAGRLFRRAGVNSFGYGGANAHAILEAP---
   AtMSAS  (386) QAGVKVVQEALEWPGNE-----DDVRRAGVCSYGYGGTVSHAIIEEFAQQ
   PgPKS2  (388) KSLLCPARELVTLPHGTP----SRPLRAAVASYGYSGTVSHAIIEAFAGG
    EpoD   (382) SALALAT-EPVPWPRTDR------PRFAGVSSFGMSGTNAHVVLEEAPAV
    MxaC   (381) SALTIPT-RLTPWKASGQ------PRRAGVSSFGISGTNAHVIIEEAPAP
    MxaD   (388) APVVVPT-EPRSWPRAEQ------PRFAGVSAFGISGTNAHIILQEPPVP
   pks ST  (394) RNVHIAF-EPKPWPRTDT------PRRVLINNFSAAGGNTAVLVEDAPVP
     AnWA  (392) RNVHIAL-QPTAWNRPSFG-----KRQIFLNNFSAAGGNTALLLEDGPVS
   ClPKS1  (393) RNVNIAF-HLTPFKRRDGK-----PRRIFVNNFSAAGGNTGLLLEDAPL-
    Atat1  (394) RGVRIAF-KETPWVRPDGG-----KRRAYLNNFGASGGNTGLLLEDRPAP
Consensus  (451)   L IPT    PWP          PRRASVNSFGFGGTNAHAILESY
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            501                                                 550
     ACE1  (443) A------EVAMVTP-TA---------------------------------
     Syn7  (395) A------ATPTPRTAT----------------------------------
     Syn6  (440) G------AGLKQTPQR----------------------------------
     LNKS  (444) E------QNQLRVSNNEDC-------------------------------
   GmPKS9  (437) L------HNQAVATTEA---------------------------------
   GmPKS1  (436) T------T-------DS---------------------------------
   BfPKS5  (438) T------ESTLIEQ-EA---------------------------------
  ChPKS16  (438) S------QE--LVEEAS---------------------------------
  FG10464  (418) P------QNSFATPSSS---------------------------------
  mg03818  (416) L------RMHQTADQKP---------------------------------
     Syn2  (443) I------ARRAAAPNP----------------------------------
  mg03810  (441) Q------AQGTKCAQK----------------------------------
  ChPKS17  (436) T------FTRRG--------------------------------------
  GmPKS10  (436) S------SE-----------------------------------------
  af04917  (441) I------HDNGP--WGKPKEMTQVPN------------------------
 ncu08399  (445) I------HDPVAKIFAPTLIVPKLIN------------------------
   BfPKS6  (438) T------PTPSL--------------------------------------
   BfPKS3  (441) L------DTTESQLSLGKEEMTQIN-------------------------
   BfPKS4  (429) A------KNGCQEASLS---------------------------------
   AN8412  (443) S------SPVREATITP---------------------------------
  mg09589  (469) V------AAVAGLQEKRDCPSPLLS-------------------------
     Syn8  (448) L------EKQDLGRGRKDTQHDVAGRV------------H----------
   ChPKS2  (426) --------------------------------------------------
   ChPKS1  (431) L------RDNSMGT--DSTRFASRRSV------------VVGNVGQTKPA
   BfPKS8  (433) --------------------------------------------------
     LDKS  (425) A------ETSICP-------------------------------------
 ncu04865  (434) L------ATTQRPKALPLTNGTAPGHH------------HHHHHQHTDSG
     FUM1  (427) LGRSLPNESQVAPIRNGNGSVQADSSSAVTSITAMKMEVRRKKRQSAVEA
 ncu09638  (431) L------PDYVAPGIYKRS----------TRDTTNGVNGHMNGRNGSPSH
 ncu02918  (432) --------QMHVP-------------------VG-----YNRG-------
   AtMSAS  (431) LQRPT---------------------------------------------
   PgPKS2  (434) FLCTDR--------------------------------------------
    EpoD   (425) ELWPAAPERS----------------------------------------
    MxaC   (424) VAKDALPQR-----------------------------------------
     MxaD  (431) APQAVVPPRG----------------------------------------
   pks ST  (437) --------------------------------------------------
     AnWA  (436) --------------------------------------------------
   ClPKS1  (436) --------------------------------------------------
    Atat1  (438) --------------------------------------------------
Consensus  (501)
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          551                                                  600
     ACE1 (453) --------------AAGPVFSPFVFSASSDKALASMLSAYSDYLS-----
     Syn7 (405) --------------TTSANVNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
     Syn6 (450) --------------SSAVPIWPIPISANSELSLKATMQDLLQYLKSASGV
     LNKS (457) ------------PPMTGVLSLPLVLSAKSQRSLKIMMEEMLQFLQSHPEI
   GmPKS9 (448) --------------ESPRLYTPLLFSANSEKALKEMLSSYLSFLE-----
   GmPKS1 (440) --------------APGPLFSPLTFSASSEPSLRSLLSSYSDHLK-----
   BfPKS5 (448) --------------TLASVFTPLTISAASASALKATLSDIRSYLE-----
  ChPKS16 (447) --------------SAVTVSTPFVFSAASTESLRSNLAAYATYL-----D
  FG10464 (429) --------------PLVVPAIPFVFSAASETSLRGVLESFLEYLN-TSKD
  mg03818 (427) ----------------QESFIPFVLSAKCESSLAKNIQNHVDWISQHKS-
     Syn2 (453) ----------------RSFA-PCPLSAASETVLTAMTERLRSYLKSQIAS
  mg03810 (451) ----------------SVPL-PFVFSAATKASLKRMLALFGDFLSPQQRP
  ChPKS17 (442) ------------PQQLSIFPSPVLLSANSDLSLRAQATALADFLESNEST
  GmPKS10 (439) ------------SSVNEVISTPLVLSANCELSLRAQISQLAQVLENAESE
  af04917 (459) ---------GVAAPETDFSPIPLIFSASSGTALRAMLERYQEYLERTEVS
 ncu08399 (465) ---------SGSLSADGQTRLPLVLSASSPRSMGAVAKCYRDYLAQVSLP
   BfPKS6 (444) ---------------ESTALIPFTISAISEDCLIQNITNFSDYIEEHEGV
   BfPKS3 (460) ------------------TIVPLLLSASSEHSLVELTKKYLDHLKTHPFQ
   BfPKS4 (440) --------------PRSDSVLPYVFSAASEQSLISMLKRYENYLQENPSI
   AN8412 (454) ---------------DDLFIGPLLFSANSSSSLVANVKNMAERIRSDPS-
  mg09589 (488) --------------------TQLLLSARSETSLRRYAQRLASYLEQNQ--
     Syn8 (470) ------TWEGLAAAAAERPAMPIVLSAHSEQALQRQARNLLEFLRDNP--
   ChPKS2 (426) --IPQGLVSQKE-TRNVESDYLFVLSANDEVALRRTREQLVEFLES--V-
   ChPKS1 (461) VSLVQDMSSNDR-SHEDPTPLLFALSAFDSSAGDAWARSLSIYLSQRQG-
   BfPKS8 (433) --FITKLEPESS-EKALQDRRMIALSANDKGALEALMKNIGIYLERRPE-
     LDKS (432) ---PNGYSGNYDGNLGTDQAHIYVLSAKDENSCMRMVSRLCDYATHARP-
 ncu04865 (466) IVIDDDFHGNGN-NGDHHHSKVFLLSAKDEKATERMIANLKTYLHQQKAN
     FUM1 (477) AGLVSNLRLVADSTKIRPSKALYVLSAANPTSLRQSVMDYQKYLASH---
 ncu09638 (465) RPMIQRPKMTASPNANTRPLVLLPLSAHNENSLELNLKALSQVVD-----
 ncu02918 (443) ----------SLPASLTRSTLFLPFSGSNTAALERRVTDIAAAIDFE---
   AtMSAS (436) ----------TNTTDEEPLPRILLLSAPQERRLALQARTQASWIAAEGR-
   PgPKS2 (440) ---------PAQPPDSDGAPVLLLLSLPQANRISTTADALSQWLRHTDG-
    EpoD  (435) -------------------AELLVLSGKSEGALDAQAARLREHLDMHPE-
    MxaC  (433) -------------------PEVLPLSARSREALVALAERYAERLGREGG-
     MxaD (441) -------------------SELLVLSARSPEALRAVAANHARWFSEHPD-
   pks ST (437) ---------ELGEIAGSFGEAAGNQSSE----------------------
     AnWA (436) ---------DPEGEDKRR-THVITLSARSQTALQNNIDALCQYISEQEKT
   ClPKS1 (436) ---------IPAAEVDPRNVQVITVTGKSKAAMIRNAERLVGWMEQNP--
    Atat1 (438) ---------VPTGASDPRTSFVVSLSAKSAYSLDQNINRLATYLEANP--
Consensus (551)                      PLVLSA SE SL   L  L  YL
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           601                                                 650
     ACE1 (484) LN----PTVDLRSVAYTLSQHR---------SVFDKRAAISAPD-----L
     Syn7 (441) ---------NNNNNNNNNNNNN---------NNNNNRHAVAAA-----DL
     Syn6 (486) ---------RVQDLAWTLTNRR---------SVLPVRRAVAAQ-----TI
     LNKS (495) ---------HLHDLTWSLLRKR---------SVLPFRRAIVGH-----SH
   GmPKS9 (479) ER----YETNMSDLAWTLHNRR---------STLPYRSSVVVPAG--SGN
   GmPKS1 (471) SN----PDLSLKDLAYTLQTRR---------STLAYRVAITASD-----V
   BfPKS5 (479) KS----PDVNMHDLAHTLQSRR---------STLAYRKDIMYSS-----R
  ChPKS16 (478) AN----PQTNTRDLAYTLRERR---------SVLPFRIAFSDTT-----V
  FG10464 (464) KD----ESLDLTSLAYILSTKR---------TVLSQRVSIIAST-----F
  mg03818 (460) --------LHVHDLALAACR-K---------SLFGYKIAVPATN-----M
     Syn2 (486) GG----TGINMRDLAWTLCSRR---------STLGVRSVLPAAK----SP
  mg03810 (484) ------QDLTAHDLAFTLNSRR---------SALSCRAVFAAR-----GL
  ChPKS17 (480) S---------WLDLLYTLQSRR---------SQHYVRLALSSTS-----R
  GmPKS10 (477) R---------IESILYTLAHRR---------SQLPLRTFFSGHD-----L
  af04917 (500) ----------LLRLAMTLNSHR---------STLPVRVSIPGTS-----K
 ncu08399 (506) ----------LEEAAWYAYKNR---------TAFPYRTAVSGSS-----L
   BfPKS6 (479) N---------LIDLGYSLLG-R---------SNFPTKATFVASN-----T
   BfPKS3 (492) N---------LQDICWTALSCR---------SLLPVRASFVGES-----S
   BfPKS4 (476) N---------PNELTTTLASHR---------SLLPVRVRFPAS-----SI
   AN8412 (488) --------IDLESLVWTLYARR---------SVLPVKAFFTGGT-----V
  mg09589 (516) -------DLNMGDLAWILRTRR---------NQFPVRLAISGASN-----
     Syn8 (512) -------SVEQRDLAWTLFARR---------SELGVRMSIPAAKSREDLE
   ChPKS2 (470) ----DASSTTMQNTAYTLGQRR---------SLLSWRATVVASN-----I
   ChPKS1 (509) ----SDEKTILSSLAYTLSDRR---------TWHPWKAALSATT-----I
   BfPKS8 (479) ----FFQNGLMSNVAYTLGQRRSLACANLMMVRLQWRVAIPATS-----S
     LDKS (478) ----ADDLQLLANIAYTLGSRR---------SNFRWKAVCTAHS-----L
 ncu04865 (515) THSKIAENALLSNLAHTLCDRR---------TLFPWTATFSGAS-----L
     FUM1 (524) -------KTDPVDVSYTLANRR---------EHLSHRTYGVVTT------
 ncu09638 (510) -------KLPLADVAYTLGARR---------SKFAQRSFCIVEK------
 ncu02918 (480) -------NVNIADLAYTLGVKR---------THLSTRGYILSGQ------
   AtMSAS (475) -------NRTLESIATTLSTRR---------GHHDYRAAIIAEN-----H
   PgPKS2 (480) -------AISLATVASTLSQRR---------AHHRFRHAIVADS-----V
    EpoD  (465) --------LGLGDVAFSLATTR---------SAMTHRLAVAVTS-----R
    MxaC  (463) --------GSLSDVCYTASAHR---------THHTHRLAVLADS-----R
     MxaD (471) --------GALREVCATAALSR---------SHHDHRLALAGRT-----P
   pks ST (456) -------------LSYTTTARR---------WHHPHRVSITGAN-----T
     AnWA (476) FG--VKDSNALPSLAYTTTARR---------IHHPFRVTAIGSS-----F
   ClPKS1 (475) -------QTPLSHVAYTTTARR---------IQHYWRMNVAASD-----L
    Atat1 (477) -------DTSLPALSYTTTARR---------VHYPHRVSYAVRS-----I
Consensus (601)           L DLAYTL  RR         S L  R AI A S
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            651                                                700
     ACE1  (516) DTLKTKLKARSEEAS---PSGKTAAVQSLE----RRPRYLGVFTGQGAQW
     Syn7  (468) PGLVRALEAAGKEDVG-VEHTP---KNSS-------PRILGVFTGQGAQW
     Syn6  (513) PDVCAALEASIASIDKKEGHVV---SGGSN----REPRVLGIFTGQGAQW
     LNKS  (522) ETIRRALEDAIEDGIVSSDFTT---EVRG------QPSVLGIFTGQGAQW
   GmPKS9  (514) PQEAARSAILSEIERL-TDSPHKLHRSLSV----AKPKILGVFSGQGAQW
   GmPKS1  (503) EDAYTQLDTIGNGEQ----SSTIGVRQVTK----ASPKIMGVLTGQGAQW
   BfPKS5  (511) EDAITKIDSLLSDDAN-AAANGLTSRYTDH----PNARILGIFTGQGAQW
  ChPKS16  (510) ESLKLSITTRLAESGS-ESLGVRTWAAGNG----GRSKVLGVFTGQGAQY
  FG10464  (496) EQLLEKVEAVLDDSAS-SVVGSKAATLSHP-------ALLGVFTGQGAQW
  mg03818  (487) EDLCSGLLERLENR----NWAKPNGNTSPK-------RLLGIFTGQGAQY
     Syn2  (519) QDLLDKLEASAQLP---PPATS--TKKAPE----TGPRVFGVFTGQGAQC
  mg03810  (514) EDLASKIRDTISDPDWQPTATAPEGKNVGS----RAPRILGVFAGQGAQW
  ChPKS17  (507) EDLLRKLRATAQS-----NSNVGINMTKP----SSSFRFLGVFTGQGAQW
  GmPKS10  (504) PSLQEKLESAIVE-----DVVIPTSKQDSPL--GSAPRILGVFTGQGAQW
  af04917  (526) ADVLAAIRTQLAKVGSNPGAEIGTRSSVPEFDHVRRPKILGVFTGQGAQW
 ncu08399  (532) SDIMKGLDTLIAKAEAGKAATISVRAR-P---ETDVPKILGIFTGQGAQW
   BfPKS6  (505) EDLLDQLEKVIIAKEENPNLAIGIRSTNVNDK--SSRKILGVFTGQGAQW
   BfPKS3  (519) DSMIAQIKQRLDLLSIDSSATLGVASIGD-----CHNKILGIFTGQGAQW
   BfPKS4  (503) ESLQQAINSSFESGVIGYQSPLK------------ESKILGIFTGQGAQW
   AN8412  (516) QRLLNFMDRFVAESEETTSSTAGIKYQPLN--PTETPGILGIFTGQGAQW
  mg09589  (545) DELQKALQTAAVDKSVECIHAPPQPLVSPS----EGLGLLGVFTGQGAQW
     Syn8  (546) QSLQETLSKTTAAEKPTKLGEPPKALASPD----EGVGILGVFTGQGAQW
   ChPKS2  (502) DDLIIQAASPQVIPRRVTRQPT----------------LVFAFTGQGAQY
   ChPKS1  (541) QELITKLEK--VRFVNMAPRHN----------------IGFVFTGQGAQW
   BfPKS8  (520) FELIQALNSGKVTPMREIEPLR----------------IGFVFTGQGAQW
     LDKS  (510) TGLAQNLAGEGMRPSKS-ADQVR---------------LGWVFTGQGAQW
 ncu04865  (551) DSLIRTLDSGRVKPAKASAQPPR---------------IGFVFTGQGAQW
     FUM1  (552) -E---STNDTPIVPDFSPLSKTN---N------NSLPEINMIFTGQGAQW
 ncu09638  (538) -D---KVVEGLAAKSRVVRAP------------LQPTNLGFIFTGQGAQW
 ncu02918  (508) -D---TLKDDLKPENLRVALQGK---T------YSKLPLAFVFTGQGAQW
   AtMSAS  (504) DDAVQKLSDIVNGKAAEWTTSSRVLD------ASCSKDVVWVFSGHGAQW
   PgPKS2  (509) ANAIATLDDLSKNVPNRWAINNRIG-------TEAAKGPVWVFSGHGAQW
    EpoD   (493) EGLLAALSAVAQGQTPAGAARCIASS--------SRGKLALLFTGQGAQT
    MxaC   (491) EHTAERLRAFARGEQPSGAWSGRKAFG-------GRRKIVFVYPGQGAQR
     MxaD  (499) AEFVEKLEAFSRGEAAPGAATGRRTGQ-------ARRRVVFVFPGQGSQW
   pks ST  (479) MEILRNVESAIARGHGVNRPATK-------------PKIVIACSGQGSQY
     AnWA  (510) QEMRDSLIASSRK-EFVAVPAKT-------------PGIGFLFTGQGAQY
   ClPKS1  (504) PEAQRLIKDRLKE-NFSPISTQQ-------------PKVAFMFTGQGSHY
    Atat1  (506) PETIKSLRSTQSK-AIKPDQASS-------------GKIAFLFTGQGSHY
Consensus  (651)  DLI  L                              KILGVFTGQGAQW
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            701                                                 750
     ACE1  (559) ARMGVDVINASPAARAIFEDLEQSLKTLPEE-DRPSWSMLEELLAPPE--
     Syn7  (507) PAMMKQLVVRVPSAARIVAELDVSLQTLPKQ-YRPGWTLMEQLMREGD--
     Syn6  (556) PAMGKMLISTLPHARDVISQLDQSLSSLPPR-YRPSWALHDQLMLEGG--
     LNKS  (563) PGMLKNLIEASPYVRNIVRELDDSLQSLPEK-YRPSWTLLDQFMLEGE--
   GmPKS9  (559) PRMGAILLESSAWARAKIVELDGYLAELPAS-DAPDFTLESELLAFKE--
   GmPKS1  (545) PRMGARLVEESAFASQRLFELDEALSSLPKD-DRPSWTLREMILADSK--
   BfPKS5  (556) PRMGAKLIEKSPFAARRMEELDLALSRLPEN-DRPSWTLQNELLAGAE--
  ChPKS16  (555) ARMGAELVTQMVLARQILEKLEGYLSELSEG-DRPSWSLTTELLADAS--
  FG10464  (538) ATMGTKLMRSNPLAQSVIQDLDAVLASLPEC-HRPRWSLGRELLADT---
  mg03818  (526) AGMMSGLLQASPWALGRALELEKTLMDLLPAHDRPQNSLVGQLLSSASGK
     Syn2  (560) PRMGAELIEDSPTVAGIVRRLDQSLQSLPVR-DRPSWTLREHLLAPKE--
  mg03810  (560) PGMARQIIGDIPFVQQRVVELEGHLQDLASQ-DAPSWSLRDELGKVQ---
  ChPKS17  (548) ATMGSELLRTCSTAQKCFKQLDASLSTLPD---APAWTLSEQCRAGSD--
  GmPKS10  (547) PTMGRELLKSSPFARRLMASLEESLSSLPE---PPMWTLTEQIMADKD--
  af04917  (576) AGMSQGLMAKSALFRQVIEVMEEAMAQLPD---GPEWSLKEEIMKPPK--
 ncu08399  (578) ATMSRGLLQSNNVYAQSIRNLDQVLQACPH---PPSWFLEQEIMADAS--
   BfPKS6  (553) PAMGKMLIANIPSFSQTIDSLEKSLRELPD---APKWSLKDEIVASVG--
   BfPKS3  (564) ATMGSGLIRSSPIFRQSIKNLDHVLQSLPD---GPEWLLSDEILRVPA--
   BfPKS4  (541) AQMGVGLLAAHPSLISFLDDLDKALQSLPEG-DRPTWSLREELERPSE--
   AN8412  (564) ALMGFSLLQQNHVFRAAIERCQAALATLHDS---PSWSLLDELVKGAD--
  mg09589  (591) PAMGRELILQEPVFRRSIEACEAALSNLP---DAPDWSLKAELLKTDQED
     Syn8  (592) AGMGRELMLHNGTFRRAISRCQDALATLPVVADRPAWSLAEELSRGEKQ-
   ChPKS2  (536) FGVGRELLQ-YPVFSTTLKMASACAESFG-----ANFSLQDELYGNEA--
   ChPKS1  (573) CGMGRELISIFPRFRQSLIACDIALQSFG-----ADFHVIDELEADVE--
   BfPKS8  (554) NAMGRELYEHYPVFAASLDACDKCLVSFG-----APFSLITELNKDAT--
     LDKS  (544) FAMGRELIEMYPVFKEALLECDGYIKEMG-----STWSIIEELSRPET--
 ncu04865  (586) WAMGKELIDAYPIFKAALLDCDVQLKKLG-----ATWNMCEELSRDAE--
     FUM1  (589) VGMGKELMDEYETFYNTIAYLGLVLSGLEHP---PTWDLIRELSRPAE--
 ncu09638  (572) HAMGAQLF-EYRVFSTAIRYLDHVLSSLPNG---PDWSLEKILSGDCD--
 ncu02918  (545) PEMGKELMKEFPSFRRTIQRLDAALQMLPHA---PTWTLQGAILEPAK--
    AtMSAS  (548) TAMATDLLKD-IVFYQTISRLDPIVEREMG------FSALHSLASGD---
    PgPKS2  (552) PDMGRELFHSSPVFGEVVRNLEPIIQAELG------FSAIESLQAGC---
    EpoD   (535) PGMGRGLCAAWPAFREAFDRCVTLFDRELD------RPLREVMWAEAGSA
    MxaC   (534) AGMGRALMESEPVFRDALVKVDKALQPHLG------WSVLDEIAADEQRS
     MxaD  (542) VGMGRKLLEEEPSFRAALERCDAAIRACAD------FSVLGELAAEAGRG
   pks ST  (516) TGMGWQLYNSYPTFRSDLERFDQLARSYG-------FPSFLEVYTSKPVG
     AnWA  (546) AAMGKQLYEDCSHFRSAIEHLDCISQGQD-------LPSILPLVDGS---
   ClPKS1  (540) AGLGKDLYAHYRVFRESIDEFNQLAQIHG-------FPSFLALIDGSE--
    Atat1  (542) TALGKQLFEDCQTFRNDVVEFNRIGQKQG-------FPTFLPLIDGS---
Consensus  (701)  GMGR LI   P FR  I  LD  L  LP     P WSL EELL
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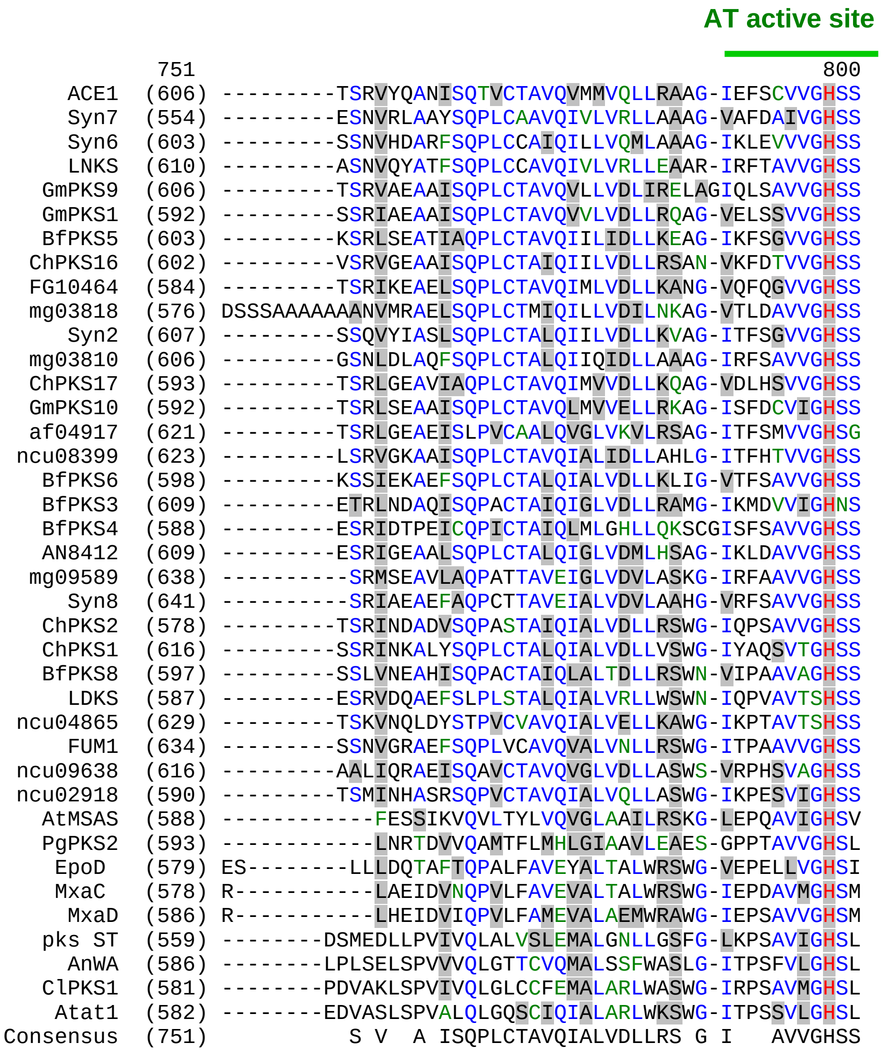

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                751                                             800
     ACE1  (606) ---------TSRVYQANISQTVCTAVQVMMVQLLRAAG-IEFSCVVGHSS
     Syn7  (554) ---------ESNVRLAAYSQPLCAAVQIVLVRLLAAAG-VAFDAIVGHSS
     Syn6  (603) ---------SSNVHDARFSQPLCCAIQILLVQMLAAAG-IKLEVVVGHSS
     LNKS  (610) ---------ASNVQYATFSQPLCCAVQIVLVRLLEAAR-IRFTAVVGHSS
   GmPKS9  (606) ---------TSRVAEAAISQPLCTAVQVLLVDLIRELAGIQLSAVVGHSS
   GmPKS1  (592) ---------SSRIAEAAISQPLCTAVQVVLVDLLRQAG-VELSSVVGHSS
   BfPKS5  (603) ---------KSRLSEATIAQPLCTAVQIILIDLLKEAG-IKFSGVVGHSS
  ChPKS16  (602) ---------VSRVGEAAISQPLCTAIQIILVDLLRSAN-VKFDTVVGHSS
  FG10464  (584) ---------TSRIKEAELSQPLCTAVQIMLVDLLKANG-VQFQGVVGHSS
  mg03818  (576) DSSSAAAAAANVMRAELSQPLCTMIQILLVDILNKAG-VTLDAVVGHSS
     Syn2  (607) ---------SSQVYIASLSQPLCTALQIILVDLLKVAG-ITFSGVVGHSS
  mg03810  (606) ---------GSNLDLAQFSQPLCTALQIIQIDLLAAAG-IRFSAVVGHSS
  ChPKS17  (593) ---------TSRLGEAVIAQPLCTAVQIMVVDLLKQAG-VDLHSVVGHSS
  GmPKS10  (592) ---------TSRLSEAAISQPLCTAVQLMVVELLRKAG-ISFDCVIGHSS
  af04917  (621) ---------TSRLGEAEISLPVCAALQVGLVKVLRSAG-ITFSMVVGHSG
 ncu08399  (623) ---------LSRVGKAAISQPLCTAVQIALIDLLAHLG-ITFHTVVGHSS
   BfPKS6  (598) ---------KSSIEKAEFSQPLCTALQIALVDLLKLIG-VTFSAVVGHSS
   BfPKS3  (609) ---------ETRLNDAQISQPACTAIQIGLVDLLRAMG-IKMDVVIGHNS
   BfPKS4  (588) ---------ESRIDTPEICQPICTAIQLMLGHLLQKSCGISFSAVVGHSS
   AN8412  (609) ---------ESRIGEAALSQPLCTALQIGLVDMLHSAG-IKLDAVVGHSS
  mg09589  (638) ----------SRMSEAVLAQPATTAVEIGLVDVLASKG-IRFAAVVGHSS
     Syn8  (641) ----------SRIAEAEFAQPCTTAVEIALVDVLAAHG-VRFSAVVGHSS
   ChPKS2  (578) ---------TSRINDADVSQPASTAIQIALVDLLRSWG-IQPSAVVGHSS
   ChPKS1  (616) ---------SSRINKALYSQPLCTALQIALVDLLVSWG-IYAQSVTGHSS
   BfPKS8  (597) ---------SSLVNEAHISQPACTAIQLALTDLLRSWN-VIPAAVAGHSS
     LDKS  (587) ---------ESRVDQAEFSLPLSTALQIALVRLLWSWN-IQPVAVTSHSS
 ncu04865  (629) ---------TSKVNQLDYSTPVCVAVQIALVELLKAWG-IKPTAVTSHSS
     FUM1  (634) ---------SSNVGRAEFSQPLVCAVQVALVNLLRSWG-ITPAAVVGHSS
 ncu09638  (616) ---------AALIQRAEISQAVCTAVQVGLVDLLASWS-VRPHSVAGHSS
 ncu02918  (590) ---------TSMINHASRSQPVCTAVQIALVQLLASWG-IKPESVIGHSS
   AtMSAS  (588) ------------FESSIKVQVLTYLVQVGLAAILRSKG-LEPQAVIGHSV
   PgPKS2  (593) ------------LNRTDVVQAMTFLMHLGIAAVLEAES-GPPTAVVGHSL
    EpoD   (579) ES--------LLLDQTAFTQPALFAVEYALTALWRSWG-VEPELLVGHSI
    MxaC   (578) R-----------LAEIDVNQPVLFAVEVALTALWRSWG-IEPDAVMGHSM
     MxaD  (586) R-----------LHEIDVIQPVLFAMEVALAEMWRAWG-IEPSAVVGHSM
   pks ST  (559) --------DSMEDLLPVIVQLALVSLEMALGNLLGSFG-LKPSAVIGHSL
     AnWA  (586) --------LPLSELSPVVVQLGTTCVQMALSSFWASLG-ITPSFVLGHSL
   ClPKS1  (581) --------PDVAKLSPVIVQLGLCCFEMALARLWASWG-IRPSAVMGHSL
    Atat1  (582) --------EDVASLSPVALQLGQSCIQIALARLWKSWG-ITPSSVLGHSL
Consensus  (751)           S V  A ISQPLCTAVQIALVDLLRS G I   AVVGHSS
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AT active site

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                801                                             850
     ACE1  (646) GEMAAAYTAGYLSARDAVRAAYFRGVHSQLAKGSNG------QPGGMIAV
     Syn7  (594) GEIGCAFAAGYVSAAQAIRIAYLRGFTSVHA----------GQDGAMLAA
     Syn6  (643) GEIACAYAAGLVTASQAIRIAYLRGFVSDKASSP------NGVEGAMLAA
     LNKS  (650) GEIACAFAAGLISASLAIRIAYLRGVVSAGG--A------RGTPGAMLAA
   GmPKS9  (647) GEIAAAYAAGFMARRAAIVTAYYRGRYAKLAASPSSS----EIKGAMAAV
   GmPKS1  (632) GEIGAAYAAGLLTARDAIRVAYYRGLYAKLAQSPNG------RKGAMMAV
   BfPKS5  (643) GEIGAAYAAGFLSAPHALYIAYYRGFYAHFAGSESN------VPGAMIAV
  ChPKS16  (642) GEIAAAYAAGYLSARDAILVSYFRGLHCKLATSPN----GNNIKGAMLAA
  FG10464  (624) GEIAAAYAAGFVSSADAIKIAYYRGYFAKLASGSSSTGKDSSVKGSMMAV
  mg03818  (625) GEIAAAYAAGRLSAATALAVAYYRGINTKLAGGLDG------KKGAMSAA
     Syn2  (647) GEIGAAYAAGYLTASDAIRVAYYRGLHLKLVTTK----------GAMLAA
  mg03810  (646) GEIAAAYAAGLLSARDAMVVAYYRGLHSPRLAGKSK----NSKGGSMMAA
  ChPKS17  (633) GEIAAAYAVGAISAHDAIRIAYYRGLYVSLARSQDG------KKGAMMAV
  GmPKS10  (632) GEISAAYAAGFLSLRDAIRVAYFRGVCAKLAGGVNG------APGSMMAV
  af04917  (661) GEIGSAYAAGKISEVDAIKIAYYRGVYTKLAIGKDG------KKGGMIAV
 ncu08399  (663) GEIAAAYAAGKLSARDSILISYYRGKYAHLASGAQG------SLGGMMAA
   BfPKS6  (638) GEIGAAYAAGRLTAGDAIRIAYYRGLHAHLAKGKGG------EEGSMMAA
   BfPKS3  (649) GEIAAAYQSGCLSARDGIIIAYYRGLFARLACGADG------CAGLMMAV
   BfPKS4  (629) GEIAAAYFAGFLRSADAIRIAFYRGLHVARFISSCN------QEGRMLAA
   AN8412  (649) GEIAAVYAAGIINADAAIKIAYYRGYYAKLAAGARG------QAGRMMAT
  mg09589  (677) GEMAALYAAGFLSLQDAVRIAYYRGLHASRLANDN---------GAMLAV
     Syn8  (680) GEMAACYAAGILTLRDAVRIAYYRGRHA-RLARSS---------GAMLAV
   ChPKS2  (618) GEVAAAYAAGLLSLPGAMRIAYARGQMAIRIKKVQP-----DFKGGMLAV
   ChPKS1  (656) GEIAAAYAAGALSLSDAMLVAYARGCATANLAKKG-------AKGAMAAV
   BfPKS8  (637) GEIGAAYAAGILPLDSCMAIAYYRGLATVGLRKKFP-----DLRGSMMAV
     LDKS  (627) GEAAAAYAIGALTARSAIGISYIRGALTARDRLASVH------KGGMLAV
 ncu04865  (669) GEIAAAYAAGALDLASAMAIAFARGGLASEGNRQFAR------KGGMMAV
     FUM1  (674) GEMAAAYAAGAISSEEAITIAYYRGYVNQQYTR----------DGGMAVI
 ncu09638  (656) GEMAAAYAAGRITAAEAIVAAYFRGQAVSRNRQ----------TGAMLAV
 ncu02918  (630) GEIAAAYTAGYLTPEQSIIIAYYRGHCVTKSTM----------VGAMMAA
   AtMSAS  (625) GEIAASVAAGCLTAEEGALIVTRRANLYRRVMG----------AGAMVLV
   PgPKS2  (630) GEAAAAVVSGALTWHEGALVVCRRARLYREFIG----------EGAMALV
    EpoD   (620) GELVAACVAGVFSLEDGVRLVAARGRLMQGLSAG----------GAMVSL
    MxaC   (616) GEVVAAHVAGALSLEDAVLIICHRSKLMRTLGGRG---------ATMAMV
     MxaD  (624) GEVAAAHVAGTLSLEDAAKIICRRSRLLRSVSGQ----------GSMLLV
   pks ST  (600) GEYAALYISGVLSAADTLYLVGMRAKLLQERCQRG--------THAMLAV
     AnWA  (627) GDFAAMNAAGVLSTSDTIYACGRRAQLLTERCQPG--------THAMLAI
   ClPKS1  (622) GEYAALNAAGVLSASDTIYLVGARAQLLVQKCTAG--------THAMLAV
    Atat1  (623) GEYAALNVAGVLSASDAIYLVGRRAQLLEELCTPG--------SHKMLAI
Consensus  (801) GEIAAAYAAG LSA DAI IAYYRG                   GAMLAV
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             851                                                 900
     ACE1  (690) GTN-FEDAEELCEL-DDFKGRLCVAASNSAELVTLSGDLDAVQEVKKIL-
     Syn7  (634) GMS-LDDAKDLVEL-EDFAGKVCIAASNSPDSVTLSGDLDALEAVVEIL-
     Syn6  (687) GCS-YKDAQELCGL-DMFRNRICVAASNAPDSVTISGDADAIEEAREVL-
     LNKS  (692) GMS-FEEAQEICEL-DAFEGRICVAASNSPDSVTFSGDANAIDHLKGML-
   GmPKS9  (693) GTD-EGDALEFCAL-EDNAGRITVAAVNAPSSVTLSGDEDAIEEAIAVF-
   GmPKS1  (676) GTT-FDDASEFCEL-DAFQGRIQVAARNSSSSITLSGDEDAIVEAIETF-
   BfPKS5  (687) GTS-YEDALDFCEL-DDFVGRIQVAARNSATSITLSGDKDAVQEAEEIF-
  ChPKS16  (688) GTS-MEDATELRQN-EELLGRIGVAASNSSSSVTLSGDEDAINEVAAVL-
  FG10464  (674) GTT-YEDAIELCQL-EDFRGRISLAAHNGPNSVTLSGDSDAINQAHFIFS
  mg03818  (669) PLS-YADACLLCSQ-PRFQGRLSVAASNSPGSTTLSGDQDAVAEAEEEL-
     Syn2  (687) GTT-FADAQELCSL-PAFEGRACVAASNSPASVTLSGDADAIEEIQIIL-
  mg03810  (692) GIS-YAEALAVVGL-EQFQGRIAVAAHNSPASVTLSGDEDAILEAKELL-
  ChPKS17  (677) GLS-YEEACELCEG--EFARRVDVAAWNSDTSVTLSGDEDAILEIKARL-
  GmPKS10  (676) GLS-YEEASVFCEE--NFHGLVDVAASNAPTSTTLSGDKASIEEAKVLL-
  af04917  (705) GFG-YEDGLNFCAM-EQFADRLTVAASNSPKSVTLSGDLDAVHEAKELL-
 ncu08399  (707) GLT-KAEAEELCAL-PQFGNRVCVAASNGPSSVTLSGDLDIVQKVHDHL-
   BfPKS6  (682) GLS-FDEALEFCAG-EEYQGKISIAASNAPKTVTLSGNKDAIEKAKSTL-
   BfPKS3  (693) GIG-HAKASNFCSR-KQFRGRLFVAASNAPQSSTLSGDCAAVEDAFKTL-
   BfPKS4  (673) GLS-QDAAEDLLAA-TEFKGRLSLAAVNSPSSVTLSGDADAIEEAQTQL-
   AN8412  (693) AMS-FDEAEEFCAQ-PQWRGRLAAAASNSPQSVTLSGDIDAIEEALQLF-
  mg09589  (718) GLS-WDAAARFCDG-DRFRGRLWRAAKNSPSSVTLSGDAGAVAEAEAVL-
     Syn8  (720) GLG-WDAAEEQITAVQRWRGRLWLAARNSPSSVTISGDADAVEEAHAEL-
   ChPKS2  (663) AAGPADVLPLLDIVTSG---KVVIACENSPKSVTVSGDEAGLVELESLL-
   ChPKS1  (699) SMETQELSHILSALENG---KVGIACFNSPTSCTVSGDKSALDELQDVL-
   BfPKS8  (682) GCTKEEIEPLIDQLSAK---TARIACFNSPSSLTISGDEPAIDELQALM-
     LDKS  (671) GLSRSEVGIYIRQVPLQSEECLVVGCVNSPSSVTVSGDLSAIAKLEELL-
 ncu04865  (713) GLGREEAEKYLPRVTQG---QVVVACENSPTSSTLSGDVEGLVELEQIM-
     FUM1  (714) GMGAQEVAPYIVEG-------VGVACENSPQSVTLSGDKGVLEEVCQKIK
 ncu09638  (696) GLGPEAVAKYLSG----LEDQVKVAAINSPGSVTLSGDPAAIDSISKALA
 ncu02918  (670) GLGAEDANKKISEL--DLVGKIRVACVNSPESVTISGDTEGIETLRAQFD
    AtMSAS  (665) NIPFADMEKELQGR-----TDLVAAIDSSPSSCVVSGATEAVLALVEDLK
   PgPKS2  (670) RLPASEARARIATH-----LGASVAIEASPTVCVISGTIDAVQKISQTWR
    EpoD   (660) GAPEAEVAAAVAP----HAAWVSIAAVNGPEQVVIAGVEQAVQAIAAGFA
    MxaC   (657) ELSVEEAEEAIRP----WNGKIWLGGLNGPRSQVLSGEPEAVKEAVEALG
     MxaD  (664) DLTMEEAKQALRG----FEDRVSVAVSNSVRSTVLSGAPAAIEEISNNLK
   pks ST  (642) RASPVTLCEVLAES------NCEVACHNGPNDTVLSGPLKEVMNLQNSLS
     AnWA  (669) KAPLVEVKQLLNEK------VHDMACINSPSETVISGPKSSIDELSRACS
   ClPKS1  (664) TGPVDAVMEALGSQ----AEAINVACINGPRETVLSGTAAKVSEISAQLG
    Atat1  (665) AASVSSVKEILGDKG---DKDIEVACINGPNETVISGPAEQMETYSKTLK
Consensus  (851) GLS  E A  L      F GRI VAA NSP SVTLSGD DAI EL   L
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            901             914
     ACE1  (737) DAE-EKFNKQLQVD
     Syn7  (681) QDE-GKFARLLRVD
     Syn6  (734) EDE-GKFARKVKVD
     LNKS  (739) EDE-STFARLLKVD
   GmPKS9  (740) QDE-GKFARRLKVD
   GmPKS1  (723) KDE-GKFARQLKVD
   BfPKS5  (734) KDE-GKFARALKVD
  ChPKS16  (735) EDE-KKFNRRLKVD
  FG10464  (722) EEE-KKFARLLKVD
  mg03818  (716) KSQ-SIKAKRLFVD
     Syn2  (734) GEE-KKFNRMLQVD
  mg03810  (739) TSD-GKFARLLRVD
  ChPKS17  (723) EDR-EVFARLLKVD
  GmPKS10  (722) DQQ-GTFARVLRVD
  af04917  (752) DAE-GVFNRVLRLD
 ncu08399  (754) VDE-KKFARMLQVD
   BfPKS6  (729) DDR-GVFARVLKVD
   BfPKS3  (740) KEE-GVFARILKVD
   BfPKS4  (720) VSR-KIFNRLLNVQ
   AN8412  (740) EAE-KKFARILRTD
  mg09589  (765) KAQ-NTTARRLKTD
     Syn8  (768) QQR-GVFSRLLRTG
   ChPKS2  (709) EED-GLPHRRLAVD
   ChPKS1  (745) RQK-GVYNRRLIVD
   BfPKS8  (728) EQK-QLFNRKLQVD
     LDKS  (720) HAD-RIFARRLKVT
 ncu04865  (759) KEE-NIFARRLKVD
     FUM1  (757) EQVPDCFVRQLKVN
 ncu09638  (742) ADS--IFNRKLQTG
 ncu02918  (718) QAG--TFARVLKTD
   AtMSAS  (710) SRG--VNAFRVKTD
   PgPKS2  (715) EEG--IEVRPVATD
    EpoD   (706) ARG--VRTKRLHVS
    MxaC   (703) KRG--VFTRWVKMD
     MxaD  (710) QRD--VFCRFVKVD
   pks ST  (686) ATG--IKGTLLKLP
     AnWA  (713) EKG--LKSTILTVP
   ClPKS1  (710) TSG--FKCTQLKVP
    Atat1  (712) ATD--IKCSLLSTA
Consensus  (901)   E  VFAR LKVD
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