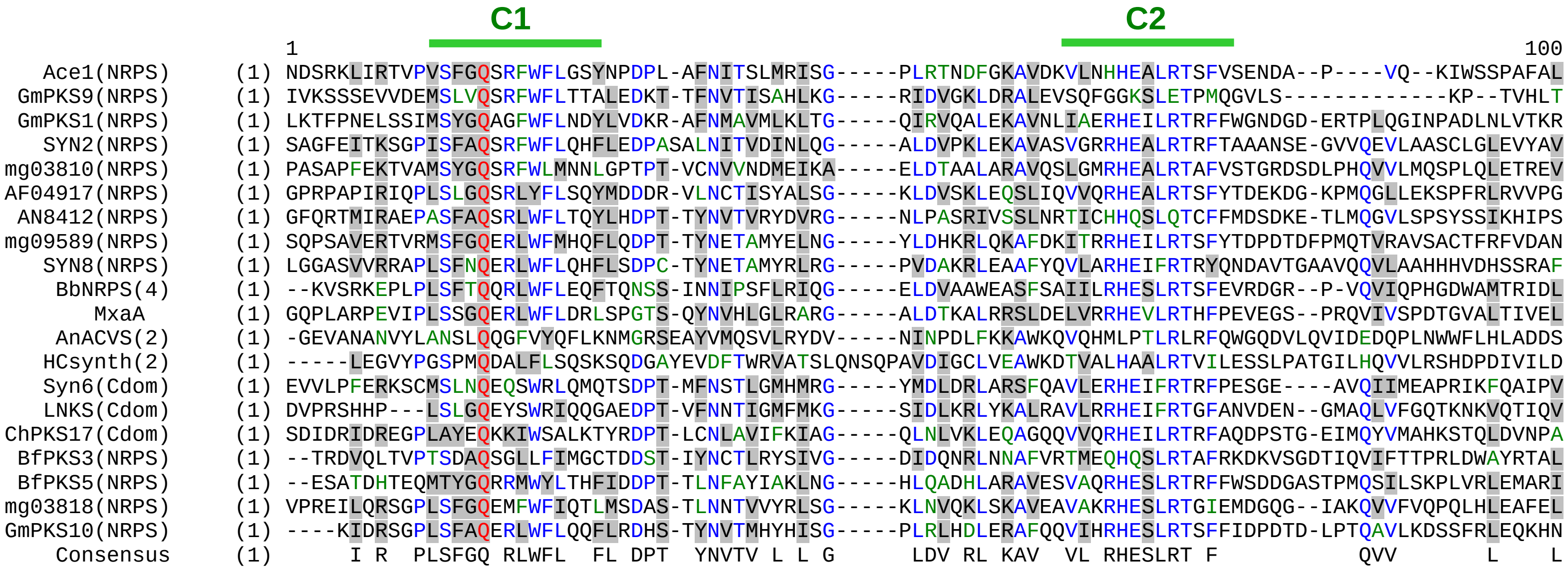
Supplemental Figure 2. Alignment of protein sequences of complete or truncated NRPS modules from fungal NRPS and PKS/NRPS. Protein sequences were aligned using AlignX. A similar alignment was obtained with ClustalW. The core sequences of the condensation (C) and adenylation (A) domains described by Marahiel et al. (1997) are indicated above the alignment by green lines. The following sequences were included in this analysis (see Methods for accession numbers): *M. grisea* (Ace1, Syn2, Syn6, Syn8, mg03810, mg03818, mg09589); *A. fumigatus* (af04917); *A. nidulans* (AN8412), *A. terreus* (LNKS); *C. heterostrophus* (ChPKS17), *B. fuckeliana* (BfPKS-3,5), *G. moniliformis* (GmPKS-1,9,10). Bacterial NRPS BbNRPS (CAD92852) and MxaA (AAK57184) and fungal NRPS AnACVS (EAA62968) and HC synthase (A45086) were added as references**.** For multimodular fungal and bacterial NRPS, numbers in brackets behind the enzyme name refer to the module that was included in this analysis.



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                      1                                                                                                100
   Ace1(NRPS)     (1) NDSRKLIRTVPVSFGQSRFWFLGSYNPDPL-AFNITSLMRISG-----PLRTNDFGKAVDKVLNHHEALRTSFVSENDA--P----VQ--KIWSSPAFAL
 GmPKS9(NRPS)     (1) IVKSSSEVVDEMSLVQSRFWFLTTALEDKT-TFNVTISAHLKG-----RIDVGKLDRALEVSQFGGKSLETPMQGVLS-------------KP--TVHLT
 GmPKS1(NRPS)     (1) LKTFPNELSSIMSYGQAGFWFLNDYLVDKR-AFNMAVMLKLTG-----QIRVQALEKAVNLIAERHEILRTRFFWGNDGD-ERTPLQGINPADLNLVTKR
   SYN2(NRPS)     (1) SAGFEITKSGPISFAQSRFWFLQHFLEDPASALNITVDINLQG-----ALDVPKLEKAVASVGRRHEALRTRFTAAANSE-GVVQEVLAASCLGLEVYAV
mg03810(NRPS)     (1) PASAPFEKTVAMSYGQSRFWLMNNLGPTPT-VCNVVNDMEIKA-----ELDTAALARAVQSLGMRHEALRTAFVSTGRDSDLPHQVVLMQSPLQLETREV
AF04917(NRPS)     (1) GPRPAPIRIQPLSLGQSRLYFLSQYMDDDR-VLNCTISYALSG-----KLDVSKLEQSLIQVVQRHEALRTSFYTDEKDG-KPMQGLLEKSPFRLRVVPG
 AN8412(NRPS)     (1) GFQRTMIRAEPASFAQSRLWFLTQYLHDPT-TYNVTVRYDVRG-----NLPASRIVSSLNRTICHHQSLQTCFFMDSDKE-TLMQGVLSPSYSSIKHIPS
mg09589(NRPS)     (1) SQPSAVERTVRMSFGQERLWFMHQFLQDPT-TYNETAMYELNG-----YLDHKRLQKAFDKITRRHEILRTSFYTDPDTDFPMQTVRAVSACTFRFVDAN
   SYN8(NRPS)     (1) LGGASVVRRAPLSFNQERLWFLQHFLSDPC-TYNETAMYRLRG-----PVDAKRLEAAFYQVLARHEIFRTRYQNDAVTGAAVQQVLAAHHHVDHSSRAF
    BbNRPS(4)     (1) --KVSRKEPLPLSFTQQRLWFLEQFTQNSS-INNIPSFLRIQG-----ELDVAAWEASFSAIILRHESLRTSFEVRDGR--P-VQVIQPHGDWAMTRIDL
        MxaA      (1) GQPLARPEVIPLSSGQERLWFLDRLSPGTS-QYNVHLGLRARG-----ALDTKALRRSLDELVRRHEVLRTHFPEVEGS--PRQVIVSPDTGVALTIVEL
    AnACVS(2)     (1) -GEVANANVYLANSLQQGFVYQFLKNMGRSEAYVMQSVLRYDV-----NINPDLFKKAWKQVQHMLPTLRLRFQWGQDVLQVIDEDQPLNWWFLHLADDS
   HCsynth(2)     (1) -----LEGVYPGSPMQDALFLSQSKSQDGAYEVDFTWRVATSLQNSQPAVDIGCLVEAWKDTVALHAALRTVILESSLPATGILHQVVLRSHDPDIVILD
   Syn6(Cdom)     (1) EVVLPFERKSCMSLNQEQSWRLQMQTSDPT-MFNSTLGMHMRG-----YMDLDRLARSFQAVLERHEIFRTRFPESGE----AVQIIMEAPRIKFQAIPV
   LNKS(Cdom)     (1) DVPRSHHP---LSLGQEYSWRIQQGAEDPT-VFNNTIGMFMKG-----SIDLKRLYKALRAVLRRHEIFRTGFANVDEN--GMAQLVFGQTKNKVQTIQV
ChPKS17(Cdom)     (1) SDIDRIDREGPLAYEQKKIWSALKTYRDPT-LCNLAVIFKIAG-----QLNLVKLEQAGQQVVQRHEILRTRFAQDPSTG-EIMQYVMAHKSTQLDVNPA
 BfPKS3(NRPS)     (1) --TRDVQLTVPTSDAQSGLLFIMGCTDDST-IYNCTLRYSIVG-----DIDQNRLNNAFVRTMEQHQSLRTAFRKDKVSGDTIQVIFTTPRLDWAYRTAL
 BfPKS5(NRPS)     (1) --ESATDHTEQMTYGQRRMWYLTHFIDDPT-TLNFAYIAKLNG-----HLQADHLARAVESVAQRHESLRTRFFWSDDGASTPMQSILSKPLVRLEMARI
mg03818(NRPS)     (1) VPREILQRSGPLSFGQEMFWFIQTLMSDAS-TLNNTVVYRLSG-----KLNVQKLSKAVEAVAKRHESLRTGIEMDGQG--IAKQVVFVQPQLHLEAFEL
GmPKS10(NRPS)     (1) ----KIDRSGPLSFAQERLWFLQQFLRDHS-TYNVTMHYHISG-----PLRLHDLERAFQQVIHRHESLRTSFFIDPDTD-LPTQAVLKDSSFRLEQKHN
    Consensus     (1)      I R  PLSFGQ RLWFL  FL DPT  YNVTV L L G      LDV RL KAV  VL RHESLRT F           QVV       L    L
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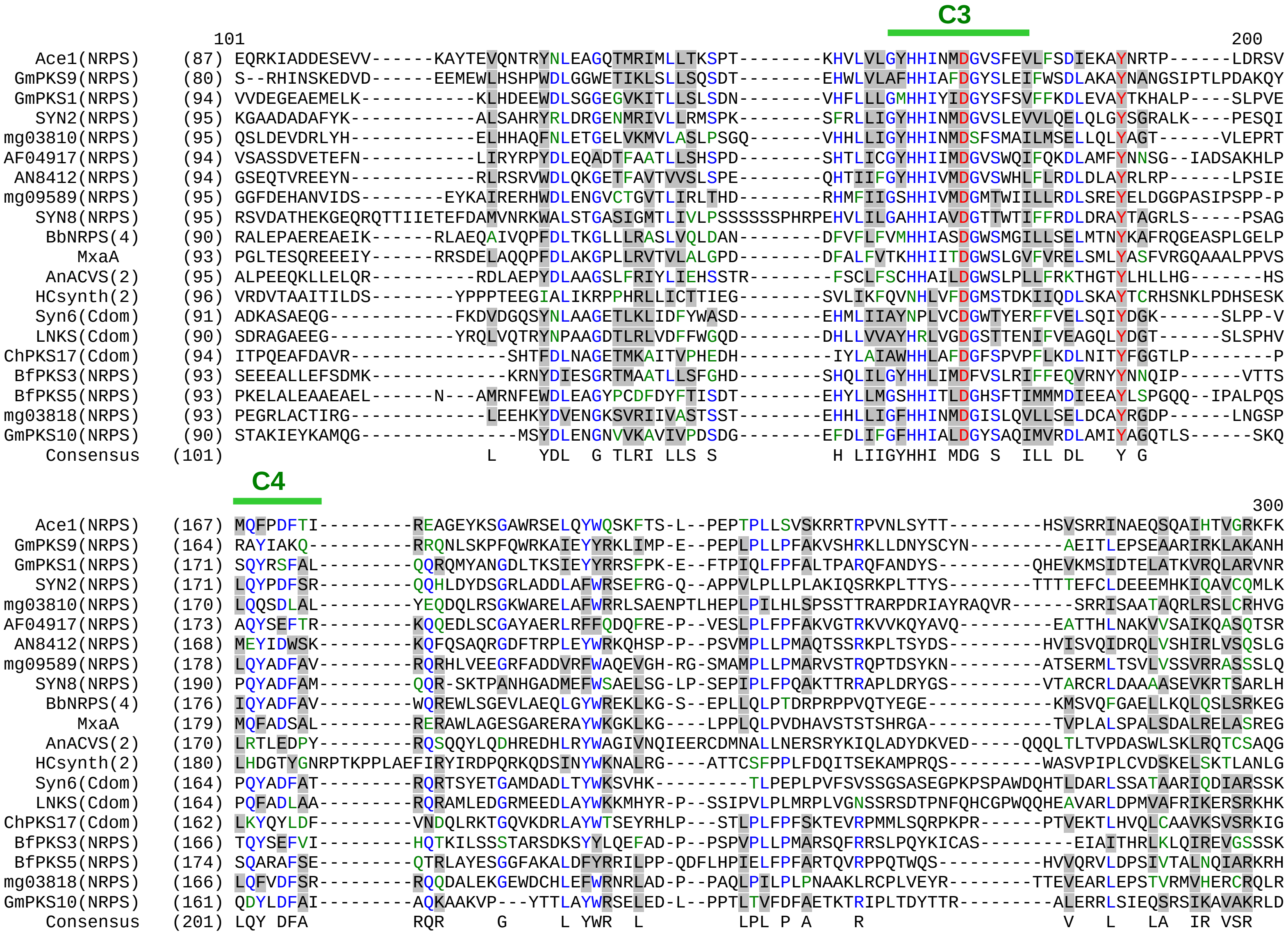

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                                                                                         C3
                    101                                                                                              200
   Ace1(NRPS)    (87) EQRKIADDESEVV------KAYTEVQNTRYNLEAGQTMRIMLLTKSPT--------KHVLVLGYHHINMDGVSFEVLFSDIEKAYNRTP------LDRSV
 GmPKS9(NRPS)    (80) S--RHINSKEDVD------EEMEWLHSHPWDLGGWETIKLSLLSQSDT--------EHWLVLAFHHIAFDGYSLEIFWSDLAKAYNANGSIPTLPDAKQY
 GmPKS1(NRPS)    (94) VVDEGEAEMELK-----------KLHDEEWDLSGGEGVKITLLSLSDN--------VHFLLLGMHHIYIDGYSFSVFFKDLEVAYTKHALP----SLPVE
   SYN2(NRPS)    (95) KGAADADAFYK------------ALSAHRYRLDRGENMRIVLLRMSPK--------SFRLLIGYHHINMDGVSLEVVLQELQLGYSGRALK----PESQI
mg03810(NRPS)    (95) QSLDEVDRLYH------------ELHHAQFNLETGELVKMVLASLPSGQ-------VHHLLIGYHHINMDSFSMAILMSELLQLYAGT------VLEPRT
AF04917(NRPS)    (94) VSASSDVETEFN-----------LIRYRPYDLEQADTFAATLLSHSPD--------SHTLICGYHHIIMDGVSWQIFQKDLAMFYNNSG--IADSAKHLP
 AN8412(NRPS)    (94) GSEQTVREEYN------------RLRSRVWDLQKGETFAVTVVSLSPE--------QHTIIFGYHHIVMDGVSWHLFLRDLDLAYRLRP------LPSIE
mg09589(NRPS)    (95) GGFDEHANVIDS--------EYKAIRERHWDLENGVCTGVTLIRLTHD--------RHMFIIGSHHIVMDGMTWIILLRDLSREYELDGGPASIPSPP-P
   SYN8(NRPS)    (95) RSVDATHEKGEQRQTTIIETEFDAMVNRKWALSTGASIGMTLIVLPSSSSSSPHRPEHVLILGAHHIAVDGTTWTIFFRDLDRAYTAGRLS-----PSAG
    BbNRPS(4)    (90) RALEPAEREAEIK------RLAEQAIVQPFDLTKGLLLRASLVQLDAN--------DFVFLFVMHHIASDGWSMGILLSELMTNYKAFRQGEASPLGELP
       MxaA      (93) PGLTESQREEEIY------RRSDELAQQPFDLAKGPLLRVTVLALGPD--------DFALFVTKHHIITDGWSLGVFVRELSMLYASFVRGQAAALPPVS
    AnACVS(2)    (95) ALPEEQKLLELQR----------RDLAEPYDLAAGSLFRIYLIEHSSTR--------FSCLFSCHHAILDGWSLPLLFRKTHGTYLHLLHG-------HS
   HCsynth(2)    (96) VRDVTAAITILDS--------YPPPTEEGIALIKRPPHRLLICTTIEG--------SVLIKFQVNHLVFDGMSTDKIIQDLSKAYTCRHSNKLPDHSESK
   Syn6(Cdom)    (91) ADKASAEQG------------FKDVDGQSYNLAAGETLKLIDFYWASD--------EHMLIIAYNPLVCDGWTYERFFVELSQIYDGK------SLPP-V
   LNKS(Cdom)    (90) SDRAGAEEG------------YRQLVQTRYNPAAGDTLRLVDFFWGQD--------DHLLVVAYHRLVGDGSTTENIFVEAGQLYDGT------SLSPHV
ChPKS17(Cdom)    (94) ITPQEAFDAVR---------------SHTFDLNAGETMKAITVPHEDH---------IYLAIAWHHLAFDGFSPVPFLKDLNITYFGGTLP--------P
 BfPKS3(NRPS)    (93) SEEEALLEFSDMK-------------KRNYDIESGRTMAATLLSFGHD--------SHQLILGYHHLIMDFVSLRIFFEQVRNYYNNQIP------VTTS
 BfPKS5(NRPS)    (93) PKELALEAAEAEL------N---AMRNFEWDLEAGYPCDFDYFTISDT--------EHYLLMGSHHITLDGHSFTIMMMDIEEAYLSPGQQ--IPALPQS
mg03818(NRPS)    (93) PEGRLACTIRG-------------LEEHKYDVENGKSVRIIVASTSST--------EHHLLIGFHHINMDGISLQVLLSELDCAYRGDP------LNGSP
GmPKS10(NRPS)    (90) STAKIEYKAMQG---------------MSYDLENGNVVKAVIVPDSDG--------EFDLIFGFHHIALDGYSAQIMVRDLAMIYAGQTLS------SKQ
    Consensus   (101)                         L    YDL  G TLRI LLS S           H LIIGYHHI MDG S  ILL DL   Y G

                       C4
                                                                                                                       300
   Ace1(NRPS)   (167) MQFPDFTI---------REAGEYKSGAWRSELQYWQSKFTS-L--PEPTPLLSVSKRRTRPVNLSYTT---------HSVSRRINAEQSQAIHTVGRKFK
 GmPKS9(NRPS)   (164) RAYIAKQ----------RRQNLSKPFQWRKAIEYYRKLIMP-E--PEPLPLLPFAKVSHRKLLDNYSCYN---------AEITLEPSEAARIRKLAKANH
 GmPKS1(NRPS)   (171) SQYRSFAL---------QQRQMYANGDLTKSIEYYRRSFPK-E--FTPIQLFPFALTPARQFANDYS---------QHEVKMSIDTELATKVRQLARVNR
   SYN2(NRPS)   (171) LQYPDFSR---------QQHLDYDSGRLADDLAFWRSEFRG-Q--APPVLPLLPLAKIQSRKPLTTYS--------TTTTEFCLDEEEMHKIQAVCQMLK
mg03810(NRPS)   (170) LQQSDLAL---------YEQDQLRSGKWARELAFWRRLSAENPTLHEPLPILHLSPSSTTRARPDRIAYRAQVR------SRRISAATAQRLRSLCRHVG
AF04917(NRPS)   (173) AQYSEFTR---------KQQEDLSCGAYAERLRFFQDQFRE-P--VESLPLFPFAKVGTRKVVKQYAVQ---------EATTHLNAKVVSAIKQASQTSR
 AN8412(NRPS)   (168) MEYIDWSK---------KQFQSAQRGDFTRPLEYWRKQHSP-P--PSVMPLLPMAQTSSRKPLTSYDS---------HVISVQIDRQLVSHIRLVSQSLG
mg09589(NRPS)   (178) LQYADFAV---------RQRHLVEEGRFADDVRFWAQEVGH-RG-SMAMPLLPMARVSTRQPTDSYKN---------ATSERMLTSVLVSSVRRASSSLQ
   SYN8(NRPS)   (190) PQYADFAM---------QQR-SKTPANHGADMEFWSAELSG-LP-SEPIPLFPQAKTTRRAPLDRYGS---------VTARCRLDAAAASEVKRTSARLH
    BbNRPS(4)   (176) IQYADFAV---------WQREWLSGEVLAEQLGYWREKLKG-S--EPLLQLPTDRPRPPVQTYEGE------------KMSVQFGAELLKQLQSLSRKEG
       MxaA     (179) MQFADSAL---------RERAWLAGESGARERAYWKGKLKG----LPPLQLPVDHAVSTSTSHRGA------------TVPLALSPALSDALRELASREG
    AnACVS(2)   (170) LRTLEDPY---------RQSQQYLQDHREDHLRYWAGIVNQIEERCDMNALLNERSRYKIQLADYDKVED-----QQQLTLTVPDASWLSKLRQTCSAQG
   HCsynth(2)   (180) LHDGTYGNRPTKPPLAEFIRYIRDPQRKQDSINYWKNALRG----ATTCSFPPLFDQITSEKAMPRQS---------WASVPIPLCVDSKELSKTLANLG
   Syn6(Cdom)   (164) PQYADFAT---------RQRTSYETGAMDADLTYWKSVHK---------TLPEPLPVFSVSSGSASEGPKPSPAWDQHTLDARLSSATAARIQDIARSSK
   LNKS(Cdom)   (164) PQFADLAA---------RQRAMLEDGRMEEDLAYWKKMHYR-P--SSIPVLPLMRPLVGNSSRSDTPNFQHCGPWQQHEAVARLDPMVAFRIKERSRKHK
ChPKS17(Cdom)   (162) LKYQYLDF---------VNDQLRKTGQVKDRLAYWTSEYRHLP---STLPLFPFSKTEVRPMMLSQRPKPR------PTVEKTLHVQLCAAVKSVSRKIG
 BfPKS3(NRPS)   (166) TQYSEFVI---------HQTKILSSSTARSDKSYYLQEFAD-P--PSPVPLLPMARSQFRRSLPQYKICAS---------EIAITHRLKLQIREVGSSSK
 BfPKS5(NRPS)   (174) SQARAFSE---------QTRLAYESGGFAKALDFYRRILPP-QDFLHPIELFPFARTQVRPPQTWQS----------HVVQRVLDPSIVTALNQIARKRH
mg03818(NRPS)   (166) LQFVDFSR---------RQQDALEKGEWDCHLEFWRNRLAD-P--PAQLPILPLPNAAKLRCPLVEYR--------TTEVEARLEPSTVRMVHERCRQLR
GmPKS10(NRPS)   (161) QDYLDFAI---------AQKAAKVP---YTTLAYWRSELED-L--PPTLTVFDFAETKTRIPLTDYTTR---------ALERRLSIEQSRSIKAVAKRLD
    Consensus   (201) LQY DFA          RQR     G     L YWR   L        LPL P A    R                   V   L   LA  IR VSR
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                                                                             C5                                    C6
                                                                        ──────────────                        ─────────────
                       301
   Ace1(NRPS)    (246) ATPFHFYLSVFKTLIARFSG---ADDFCIGIADANRKED-----KVMGAVGLYLNLLPLRVR-SALGQ----TFGETLADMKKVSQEAFANSKVPFDVLL
 GmPKS9(NRPS)    (242) STSFHVYVASLQTLLFGLMPDS-VDRLFIAMDDTNRLDK-----DFMDTIGLFVNTLFLRFDRADYNKL---SLSDAVKAARTKTYKALEHSVLPLDVLL
 GmPKS1(NRPS)    (250) STSFHVYLAALELLLFTLLPN--AEEVFIGIADANRGDK-----KFMGSLGFFLNLLPLRFR-RKRRGT---QLSSIIQTARDTAYGALQHSQLPFDVLL
   SYN2(NRPS)    (251) VSPFHFHLAIFYTLLARLVD---VDDLCIGVSSANRQTP-----ETMSSVGMYLNLLPLVFK-VDRSH----TFANAIKMIRAKALAAFSHAAVPFDLMI
mg03810(NRPS)    (255) VTPFHVYTTVLQVLITRLAQ---VQRVTVGMADGNRGS--LHLPGADGAVGNFLNMVPLFLG---SPPR-DHTIYMLLCQTRDVVLEAISNASVPIELIT
AF04917(NRPS)    (252) TTPFHFYLSAFQVLLHRLLE---TDKMCIGVVDANRSDQ-----NFVNTIGFFLETIPLWFK-VNSEQ----RFVELLKETRTKAYAALAQTGVPTEEIL
 AN8412(NRPS)    (247) VTPFHFHLAVIQSILCRLLK---TEDLCIGVVDANRTSE-----AHSGTVGFFLNLLPVRFT-TREHS----TFQDLVSSTKRTILGAISNSEAPFDLIL
mg09589(NRPS)    (258) ITPFHFHLGVLAILVCRLSR---MDEVCIGICDSGRGMRNEGEPDFSGTAGFFINFAPIVLSISPDGDQSQNTFAALSKRVSSKAFAALSHAGVPFDALL
   SYN8(NRPS)    (269) MTAFGLHMAVLSVLVSHLSG---TSDLCIGFCDGGRPDA------FAETAGFFVNMLPVRLDTAARHAG-PASFADLARATFAKLMDVMAHSSLSLEALL
    BbNRPS(4)    (252) ATLFMTLFAAFQTLLYRYTN---QDDILVGTPIAGRNKQ-----ETEQLIGYFINTLVLRT--DMSGHP---SFRELLARVRETALEAYAHQDVPFEKLL
       MxaA      (254) CSFFTVLFAAFSALLHRYSG---QVDFGVGTVIANRGS------VPADLIGFIANTLALRC--DLSGEP---TFSQWLARAHKVVLEALDYQALPFSEVV
    AnACVS(2)    (256) ITLHSILQFVWHAVLHAYGG---GTHTVTGTTISGRNLPVSG---IERSVGLYINTLPLVIN----QLA-------Y---KNKTVLEAIRDVQAIVNGMN
   HCsynth(2)    (267) ITMSTMFQTVWAIVLRIYSQ---NGQSVFGYLTSGRDAPVDG---IDSAVGNFIAMLVCFFDFDDDGVH---TVADMARKIHNASANSISHQACSLAEIQ
   Syn6(Cdom)    (246) VTPMQFYLASYYVLLSRLTG---RADVAIGVADANRPDL-----DDLSTMGLFVNTLPLRL--DHAAHD---TFASTLSRTKERMRRATLHSRVPMHVIL
   LNKS(Cdom)    (252) ATPMQFYLAAYQVLLARLTD---STDLTVGLADTNRATV-----DEMAAMGFFANLLPLRFR-DFRPHI---TFGEHLIATRDLVREALQHARVPYGVLL
ChPKS17(Cdom)    (244) ATPFHVYLAALQVLFYRMLS---VQDVCLAIQVNNREAE------FDDNIGEFGGLLPIKLQ----TQD---NFAQLVRHTRDKTQEGLQ-AIVPLQSIM
 BfPKS3(NRPS)    (245) CTPFHFYLASLQVLLARTTG---VEDFCIGIGDANRADP-----KFLDTIGLVMELVPLRFQ--YGSLD---TFSKVMCDTRQKVLAALSHVSTPYHVAL
 BfPKS5(NRPS)    (254) STSFHAYLASYQAMLFRLLPSNTTDKLFIGMADANRLDS-----KFLRSIGNFLNILPLRFD-RATRQ----SFGDAIEFARAKTHTALEHSALPFELLL
mg03818(NRPS)    (246) VTPFCFYLGVFRVLLARLAN---INDFCIGIADANRLDG-----DMLDAVGMYLNLLPLRFR-TSGGE----TFEDISQNTKDTIRESLEHSAVPFGVML
GmPKS10(NRPS)    (237) VTPFHVHLATLQVVLSDLAS---ANDLCIGITDANKNDA-----THIDTVGFFVNLLPLRLK-LSSSQ----TLADLVANAKSKANGALSHSDMPFDVLL
    Consensus    (301) VTPFH YLAAFQVLL RL      DDLCIGI DANR D        M TVG FLNLLPLRF           TFADLL   R K   ALSHS VPFDVLL
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                       C6                    C7
                       ─────           ──────────────
                                                                                                                    500
   Ace1(NRPS)    (333) NELSVPRSSSQ-----TPLFQTFVNYRRGVSEERS----FCGCTGAGELISGGQ-----IGYDISLDIVENPGGDALVTLSVQKDLYNVDMANLLLDSYF
 GmPKS9(NRPS)    (333) KELCITRHGDAVP-----VAQVLIDYRVSHKEWFR----LGDCRAEMGTGRAERQ-GSDLAFYILDDSDEQNGGRVRVGVEVQSTLYDAEHAEMLIKAYA
 GmPKS1(NRPS)    (339) RELNVPRSDKYT-----PIFQVFMDYRQVVQERSS----WGGCRLHGEKWHNAG-----TGYDIALEVNENITTDTLLGLRLQEQLYSEEHTALLLRSYL
   SYN2(NRPS)    (338) KDLGVAGTSSHS-----PVFQAMVNYRPGVSTARR----FCDCDSEVATFKQGE-----VPYDLAFDIMENPGGSSLIMLTGQSVYYGKTEMEHIKGIYL
mg03810(NRPS)    (346) EQTGAPKNPSCS-----PLFQVFIDYKRVTETLPLP--------EGKGTVQGSRYLLSKTPYDIMLDVIDTPAGDALLQLHAQDGLYTSEESARLLDLYS
AF04917(NRPS)    (339) RACGVASSTTET-----PLFQVCFNYRMGAGRTAA----LQGVEMKFLDYVDAQN-----PFDLVATVDDLDDGTAMITLYLQDYLYDQEGAQLLATMYA
 AN8412(NRPS)    (334) EDLKVLRSIEHS-----PLFQVAVNYRMGAMLQVP----LGDGTMEVAAADDAKN-----PYDLSFGITETSTGTCLLELTSQKQLYTEQSTELLLQMYM
mg09589(NRPS)    (355) DQLKVPRTSRHS-----PLFQVVINYRLGALSHGD----IAGCQVKYVRSHGSR-----NPYDLCVNISESPNGDCLIEVVMRESLYSADAAESVLGSYC
   SYN8(NRPS)    (359) DALAVPRSTTHS-----PLFQVVLNYRLDALAHSAVG----DGRLEFVKARNSR-----NPYDVSLSVTDSPDGTCLLDVSMQESLYGPEAAASVLAMYR
    BbNRPS(4)    (339) DELQLERSMSYS-----PLFQVMFILQNIPVQAEP----AGDIQLSSFDLELG---AVTSKFDMTVTMVETP-DGLLATLEYNKALFDSSTITRMVEHFH
       MxaA      (340) QTVGASRDGGLN-----PLVRACFTLESIPAPTLD----LPGTSWSFLNGAPDGSVEGVAKFELSLILAASE-KGLAGMLEYSREVFDASTVERMVGHFQ
    AnACVS(2)    (336) SRGNVELGRLQKNELKHGLFDSLFVLENYPILDKS----EEMRQKSELKYTIEGNIEKLDYPLAVIAREVDLTGGFTFTICYARELFDEIVISELLQMVR
   HCsynth(2)    (358) DALGLSTSTPLFN-------TAFTYLPKRPTNVKAG-------EPEHHLCFEELSMSDPTEFDLTLFVEPTQESNEVSAHLDFKLSYISQAYATSIASTV
   Syn6(Cdom)    (333) ESLGVDAARPH------EFLQAVFDYKQGQAESGS----IGQAHMAGVLASRFS-----TPYDVTLEMRDDPSKTPLLTLKLQSSLYSLQDVHKVMGCYM
   LNKS(Cdom)    (340) DQLGLEVPVPTSN-QPAPLFQAVFDYKQGQAESGT----IGGAKITEVIATRER-----TPYDVVLEMSDDPTKDPLLTAKLQSSRYEAHHPQAFLESYM
ChPKS17(Cdom)    (327) AALDGPELDRHG-----SLYQVSVNYMPSPVRDIS----LGGHTAEILKYNRVGG----YACDLDLELQDLGNDRMLLVMRGRQDLYDELGVQTLLTIYE
 BfPKS3(NRPS)    (332) SGSQRSTNTSLS-----PLFQVVLNYVAGGASRMKMG------ESKFQYIESEE----AKHPQDLVFTIREIDGVTHLSLASHEYLYSKEDTKAILELYV
 BfPKS5(NRPS)    (344) DELSVPRSNRWT-----PIFQVFIDYRLIPSQQGAKQREWAGCDVSEETWHTAR-----SGFDVVLEIKEDQ-NETTLKFHVQKDLYDEAAAELLLNSYI
mg03818(NRPS)    (333) SELGVPRSADHS-----PIFQAFVDYRQGAKEKQS----LGDCELEVYHYQGAK-----TAYDVSLDIIDSGELPTAVRLAVQDSLYSREDGKLLLGAFV
GmPKS10(NRPS)    (324) DEMKLPRSTTHS-----PLFQVVMNYKMGSTQKVP----LADCQAQLVAFEDAN-----NPYDLTFDIETYYDGSASISVKTQEYLYSESELSFVLDNYV
    Consensus    (401) D L V RS  HS     PLFQVVV YR G     S    LG   L                YDL LDI E   G  LL L LQ  LY       LL  YV
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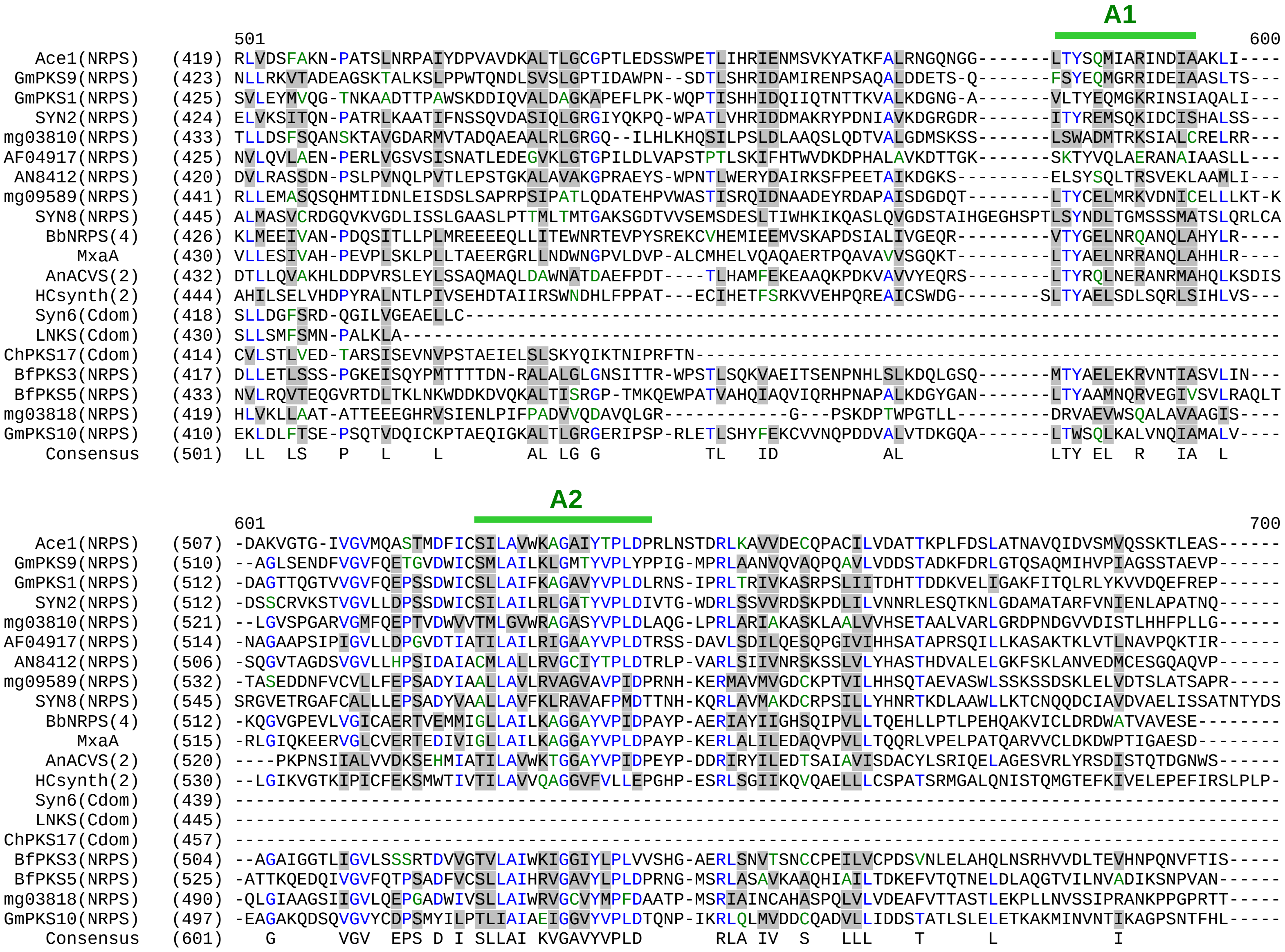

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                                                                                                         A1
                      501                                                                                              600
   Ace1(NRPS)   (419) RLVDSFAKN-PATSLNRPAIYDPVAVDKALTLGCGPTLEDSSWPETLIHRIENMSVKYATKFALRNGQNGG-------LTYSQMIARINDIAAKLI----
 GmPKS9(NRPS)   (423) NLLRKVTADEAGSKTALKSLPPWTQNDLSVSLGPTIDAWPN--SDTLSHRIDAMIRENPSAQALDDETS-Q-------FSYEQMGRRIDEIAASLTS---
 GmPKS1(NRPS)   (425) SVLEYMVQG-TNKAADTTPAWSKDDIQVALDAGKAPEFLPK-WQPTISHHIDQIIQTNTTKVALKDGNG-A-------VLTYEQMGKRINSIAQALI---
   SYN2(NRPS)   (424) ELVKSITQN-PATRLKAATIFNSSQVDASIQLGRGIYQKPQ-WPATLVHRIDDMAKRYPDNIAVKDGRGDR-------ITYREMSQKIDCISHALSS---
mg03810(NRPS)   (433) TLLDSFSQANSKTAVGDARMVTADQAEAALRLGRGQ--ILHLKHQSILPSLDLAAQSLQDTVALGDMSKSS-------LSWADMTRKSIALCRELRR---
AF04917(NRPS)   (425) NVLQVLAEN-PERLVGSVSISNATLEDEGVKLGTGPILDLVAPSTPTLSKIFHTWVDKDPHALAVKDTTGK-------SKTYVQLAERANAIAASLL---
 AN8412(NRPS)   (420) DVLRASSDN-PSLPVNQLPVTLEPSTGKALAVAKGPRAEYS-WPNTLWERYDAIRKSFPEETAIKDGKS---------ELSYSQLTRSVEKLAAMLI---
mg09589(NRPS)   (441) RLLEMASQSQHMTIDNLEISDSLSAPRPSIPATLQDATEHPVWASTISRQIDNAADEYRDAPAISDGDQT--------LTYCELMRKVDNICELLLKT-K
   SYN8(NRPS)   (445) ALMASVCRDGQVKVGDLISSLGAASLPTTMLTMTGAKSGDTVVSEMSDESLTIWHKIKQASLQVGDSTAIHGEGHSPTLSYNDLTGMSSSMATSLQRLCA
    BbNRPS(4)   (426) KLMEEIVAN-PDQSITLLPLMREEEEQLLITEWNRTEVPYSREKCVHEMIEEMVSKAPDSIALIVGEQR---------VTYGELNRQANQLAHYLR----
       MxaA     (430) VLLESIVAH-PEVPLSKLPLLTAEERGRLLNDWNGPVLDVP-ALCMHELVQAQAERTPQAVAVVSGQKT---------LTYAELNRRANQLAHHLR----
    AnACVS(2)   (432) DTLLQVAKHLDDPVRSLEYLSSAQMAQLDAWNATDAEFPDT----TLHAMFEKEAAQKPDKVAVVYEQRS--------LTYRQLNERANRMAHQLKSDIS
   HCsynth(2)   (444) AHILSELVHDPYRALNTLPIVSEHDTAIIRSWNDHLFPPAT---ECIHETFSRKVVEHPQREAICSWDG--------SLTYAELSDLSQRLSIHLVS---
   Syn6(Cdom)   (418) SLLDGFSRD-QGILVGEAELLC------------------------------------------------------------------------------
   LNKS(Cdom)   (430) SLLSMFSMN-PALKLA------------------------------------------------------------------------------------
ChPKS17(Cdom)   (414) CVLSTLVED-TARSISEVNVPSTAEIELSLSKYQIKTNIPRFTN--------------------------------------------------------
 BfPKS3(NRPS)   (417) DLLETLSSS-PGKEISQYPMTTTTDN-RALALGLGNSITTR-WPSTLSQKVAEITSENPNHLSLKDQLGSQ-------MTYAELEKRVNTIASVLIN---
 BfPKS5(NRPS)   (433) NVLRQVTEQGVRTDLTKLNKWDDKDVQKALTISRGP-TMKQEWPATVAHQIAQVIQRHPNAPALKDGYGAN-------LTYAAMNQRVEGIVSVLRAQLT
mg03818(NRPS)   (419) HLVKLLAAT-ATTEEEGHRVSIENLPIFPADVVQDAVQLGR------------G---PSKDPTWPGTLL---------DRVAEVWSQALAVAAGIS----
GmPKS10(NRPS)   (410) EKLDLFTSE-PSQTVDQICKPTAEQIGKALTLGRGERIPSP-RLETLSHYFEKCVVNQPDDVALVTDKGQA-------LTWSQLKALVNQIAMALV----
    Consensus   (501)  LL  LS   P   L    L        AL LG G          TL   ID          AL              LTY EL  R   IA  L

                                                    A2
                      601                                                                                              700
   Ace1(NRPS)   (507) -DAKVGTG-IVGVMQASTMDFICSILAVWKAGAIYTPLDPRLNSTDRLKAVVDECQPACILVDATTKPLFDSLATNAVQIDVSMVQSSKTLEAS------
 GmPKS9(NRPS)   (510) --AGLSENDFVGVFQETGVDWICSMLAILKLGMTYVPLYPPIG-MPRLAANVQVAQPQAVLVDDSTADKFDRLGTQSAQMIHVPIAGSSTAEVP------
 GmPKS1(NRPS)   (512) -DAGTTQGTVVGVFQEPSSDWICSLLAIFKAGAVYVPLDLRNS-IPRLTRIVKASRPSLIITDHTTDDKVELIGAKFITQLRLYKVVDQEFREP------
   SYN2(NRPS)   (512) -DSSCRVKSTVGVLLDPSSDWICSILAILRLGATYVPLDIVTG-WDRLSSVVRDSKPDLILVNNRLESQTKNLGDAMATARFVNIENLAPATNQ------
mg03810(NRPS)   (521) --LGVSPGARVGMFQEPTVDWVVTMLGVWRAGASYVPLDLAQG-LPRLARIAKASKLAALVVHSETAALVARLGRDPNDGVVDISTLHHFPLLG------
AF04917(NRPS)   (514) -NAGAAPSIPIGVLLDPGVDTIATILAILRIGAAYVPLDTRSS-DAVLSDILQESQPGIVIHHSATAPRSQILLKASAKTKLVTLNAVPQKTIR------
 AN8412(NRPS)   (506) -SQGVTAGDSVGVLLHPSIDAIACMLALLRVGCIYTPLDTRLP-VARLSIIVNRSKSSLVLYHASTHDVALELGKFSKLANVEDMCESGQAQVP------
mg09589(NRPS)   (532) -TASEDDNFVCVLLFEPSADYIAALLAVLRVAGVAVPIDPRNH-KERMAVMVGDCKPTVILHHSQTAEVASWLSSKSSDSKLELVDTSLATSAPR-----
   SYN8(NRPS)   (545) SRGVETRGAFCALLLEPSADYVAALLAVFKLRAVAFPMDTTNH-KQRLAVMAKDCRPSILLYHNRTKDLAAWLLKTCNQQDCIAVDVAELISSATNTYDS
    BbNRPS(4)   (512) -KQGVGPEVLVGICAERTVEMMIGLLAILKAGGAYVPIDPAYP-AERIAYIIGHSQIPVLLTQEHLLPTLPEHQAKVICLDRDWATVAVESE--------
       MxaA     (515) -RLGIQKEERVGLCVERTEDIVIGLLAILKAGGAYVPLDPAYP-KERLALILEDAQVPVLLTQQRLVPELPATQARVVCLDKDWPTIGAESD--------
    AnACVS(2)   (520) ----PKPNSIIALVVDKSEHMIATILAVWKTGGAYVPIDPEYP-DDRIRYILEDTSAIAVISDACYLSRIQELAGESVRLYRSDISTQTDGNWS------
   HCsynth(2)   (530) --LGIKVGTKIPICFEKSMWTIVTILAVVQAGGVFVLLEPGHP-ESRLSGIIKQVQAELLLCSPATSRMGALQNISTQMGTEFKIVELEPEFIRSLPLP-
   Syn6(Cdom)   (439) ----------------------------------------------------------------------------------------------------
   LNKS(Cdom)   (445) ----------------------------------------------------------------------------------------------------
ChPKS17(Cdom)   (457) ----------------------------------------------------------------------------------------------------
 BfPKS3(NRPS)   (504) --AGAIGGTLIGVLSSSRTDVVGTVLAIWKIGGIYLPLVVSHG-AERLSNVTSNCCPEILVCPDSVNLELAHQLNSRHVVDLTEVHNPQNVFTIS-----
 BfPKS5(NRPS)   (525) -ATTKQEDQIVGVFQTPSADFVCSLLAIHRVGAVYLPLDPRNG-MSRLASAVKAAQHIAILTDKEFVTQTNELDLAQGTVILNVADIKSNPVAN------
mg03818(NRPS)   (490) -QLGIAAGSIIGVLQEPGADWIVSLLAIWRVGCVYMPFDAATP-MSRIAINCAHASPQLVLVDEAFVTTASTLEKPLLNVSSIPRANKPPGPRTT-----
GmPKS10(NRPS)   (497) -EAGAKQDSQVGVYCDPSMYILPTLIAIAEIGGVYVPLDTQNP-IKRLQLMVDDCQADVLLIDDSTATLSLELETKAKMINVNTIKAGPSNTFHL-----
    Consensus   (601)    G      VGV  EPS D I SLLAI KVGAVYVPLD       RLA IV  S   LLL    T      L           I
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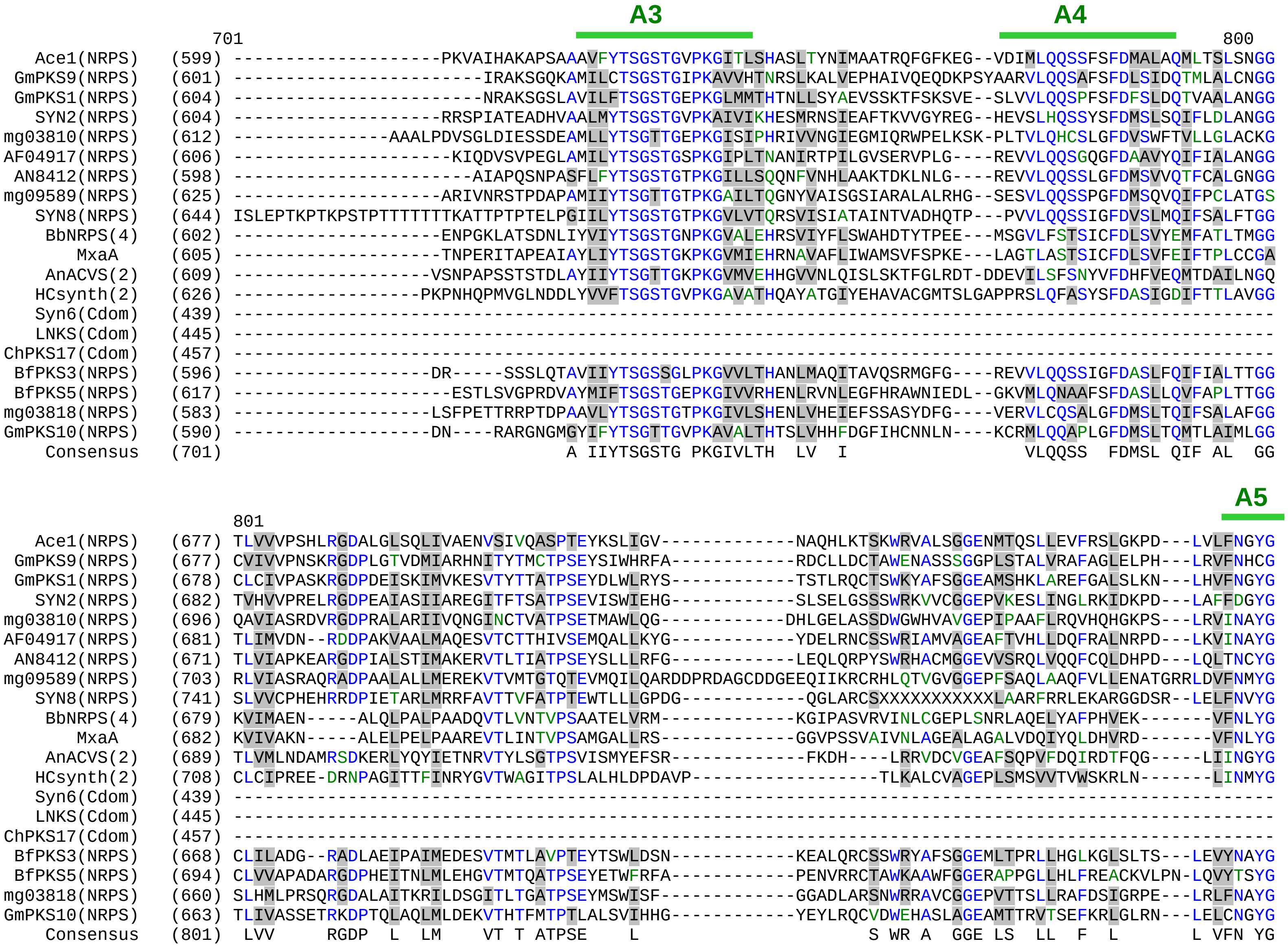

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                      701                                                                                              800
   Ace1(NRPS)   (599) --------------------PKVAIHAKAPSAAAVFYTSGSTGVPKGITLSHASLTYNIMAATRQFGFKEG--VDIMLQQSSFSFDMALAQMLTSLSNGG
  GmPKS9(NRPS)  (601) ------------------------IRAKSGQKAMILCTSGSTGIPKAVVHTNRSLKALVEPHAIVQEQDKPSYAARVLQQSAFSFDLSIDQTMLALCNGG
  GmPKS1(NRPS)  (604) ------------------------NRAKSGSLAVILFTSGSTGEPKGLMMTHTNLLSYAEVSSKTFSKSVE--SLVVLQQSPFSFDFSLDQTVAALANGG
   SYN2(NRPS)   (604) --------------------RRSPIATEADHVAALMYTSGSTGVPKAIVIKHESMRNSIEAFTKVVGYREG--HEVSLHQSSYSFDMSLSQIFLDLANGG
mg03810(NRPS)   (612) ---------------AAALPDVSGLDIESSDEAMLLYTSGTTGEPKGISIPHRIVVNGIEGMIQRWPELKSK-PLTVLQHCSLGFDVSWFTVLLGLACKG
AF04917(NRPS)   (606) ---------------------KIQDVSVPEGLAMILYTSGSTGSPKGIPLTNANIRTPILGVSERVPLG----REVVLQQSGQGFDAAVYQIFIALANGG
  AN8412(NRPS)  (598) -----------------------AIAPQSNPASFLFYTSGSTGTPKGILLSQQNFVNHLAAKTDKLNLG----REVVLQQSSLGFDMSVVQTFCALGNGG
mg09589(NRPS)   (625) --------------------ARIVNRSTPDAPAMIIYTSGTTGTPKGAILTQGNYVAISGSIARALALRHG--SESVLQQSSPGFDMSQVQIFPCLATGS
   SYN8(NRPS)   (644) ISLEPTKPTKPSTPTTTTTTTKATTPTPTELPGIILYTSGSTGTPKGVLVTQRSVISIATAINTVADHQTP---PVVLQQSSIGFDVSLMQIFSALFTGG
    BbNRPS(4)   (602) --------------------ENPGKLATSDNLIYVIYTSGSTGNPKGVALEHRSVIYFLSWAHDTYTPEE---MSGVLFSTSICFDLSVYEMFATLTMGG
       MxaA     (605) --------------------TNPERITAPEAIAYLIYTSGSTGKPKGVMIEHRNAVAFLIWAMSVFSPKE---LAGTLASTSICFDLSVFEIFTPLCCGA
    AnACVS(2)   (609) -------------------VSNPAPSSTSTDLAYIIYTSGTTGKPKGVMVEHHGVVNLQISLSKTFGLRDT-DDEVILSFSNYVFDHFVEQMTDAILNGQ
   HCsynth(2)   (626) ------------------PKPNHQPMVGLNDDLYVVFTSGSTGVPKGAVATHQAYATGIYEHAVACGMTSLGAPPRSLQFASYSFDASIGDIFTTLAVGG
   Syn6(Cdom)   (439) ----------------------------------------------------------------------------------------------------
   LNKS(Cdom)   (445) ----------------------------------------------------------------------------------------------------
ChPKS17(Cdom)   (457) ----------------------------------------------------------------------------------------------------
  BfPKS3(NRPS)  (596) -------------------DR-----SSSLQTAVIIYTSGSSGLPKGVVLTHANLMAQITAVQSRMGFG----REVVLQQSSIGFDASLFQIFIALTTGG
  BfPKS5(NRPS)  (617) ---------------------ESTLSVGPRDVAYMIFTSGSTGEPKGIVVRHENLRVNLEGFHRAWNIEDL--GKVMLQNAAFSFDASLLQVFAPLTTGG
mg03818(NRPS)   (583) -------------------LSFPETTRRPTDPAAVLYTSGSTGTPKGIVLSHENLVHEIEFSSASYDFG----VERVLCQSALGFDMSLTQIFSALAFGG
 GmPKS10(NRPS)  (590) -------------------DN----RARGNGMGYIFYTSGTTGVPKAVALTHTSLVHHFDGFIHCNNLN----KCRMLQQAPLGFDMSLTQMTLAIMLGG
    Consensus   (701)                                 A IIYTSGSTG PKGIVLTH  LV  I                 VLQQSS  FDMSL QIF AL  GG

                      801
   Ace1(NRPS)   (677) TLVVVPSHLRGDALGLSQLIVAENVSIVQASPTEYKSLIGV-------------NAQHLKTSKWRVALSGGENMTQSLLEVFRSLGKPD---LVLFNGYG
  GmPKS9(NRPS)  (677) CVIVVPNSKRGDPLGTVDMIARHNITYTMCTPSEYSIWHRFA------------RDCLLDCTAWENASSSGGPLSTALVRAFAGLELPH---LRVFNHCG
  GmPKS1(NRPS)  (678) CLCIVPASKRGDPDEISKIMVKESVTYTTATPSEYDLWLRYS------------TSTLRQCTSWKYAFSGGEAMSHKLAREFGALSLKN---LHVFNGYG
   SYN2(NRPS)   (682) TVHVVPRELRGDPEAIASIIAREGITFTSATPSEVISWIEHG------------SLSELGSSSWRKVVCGGEPVKESLINGLRKIDKPD---LAFFDGYG
mg03810(NRPS)   (696) QAVIASRDVRGDPRALARIIVQNGINCTVATPSETMAWLQG------------DHLGELASSDWGWHVAVGEPIPAAFLRQVHQHGKPS---LRVINAYG
AF04917(NRPS)   (681) TLIMVDN--RDDPAKVAALMAQESVTCTTHIVSEMQALLKYG------------YDELRNCSSWRIAMVAGEAFTVHLLDQFRALNRPD---LKVINAYG
  AN8412(NRPS)  (671) TLVIAPKEARGDPIALSTIMAKERVTLTIATPSEYSLLLRFG------------LEQLQRPYSWRHACMGGEVVSRQLVQQFCQLDHPD---LQLTNCYG
mg09589(NRPS)   (703) RLVIASRAQRADPAALALLMEREKVTVMTGTQTEVMQILQARDDPRDAGCDDGEEQIIKRCRHLQTVGVGGEPFSAQLAAQFVLLENATGRRLDVFNMYG
   SYN8(NRPS)   (741) SLVVCPHEHRRDPIETARLMRRFAVTTVFATPTEWTLLLGPDG------------QGLARCSXXXXXXXXXXXLAARFRRLEKARGGDSR--LELFNVYG
    BbNRPS(4)   (679) KVIMAEN-----ALQLPALPAADQVTLVNTVPSAATELVRM-------------KGIPASVRVINLCGEPLSNRLAQELYAFPHVEK-------VFNLYG
       MxaA     (682) KVIVAKN-----ALELPELPAAREVTLINTVPSAMGALLRS-------------GGVPSSVAIVNLAGEALAGALVDQIYQLDHVRD-------VFNLYG
    AnACVS(2)   (689) TLVMLNDAMRSDKERLYQYIETNRVTYLSGTPSVISMYEFSR-------------FKDH----LRRVDCVGEAFSQPVFDQIRDTFQG-----LIINGYG
   HCsynth(2)   (708) CLCIPREE-DRNPAGITTFINRYGVTWAGITPSLALHLDPDAVP------------------TLKALCVAGEPLSMSVVTVWSKRLN-------LINMYG
   Syn6(Cdom)   (439) ----------------------------------------------------------------------------------------------------
   LNKS(Cdom)   (445) ----------------------------------------------------------------------------------------------------
ChPKS17(Cdom)   (457) ----------------------------------------------------------------------------------------------------
  BfPKS3(NRPS)  (668) CLILADG--RADLAEIPAIMEDESVTMTLAVPTEYTSWLDSN------------KEALQRCSSWRYAFSGGEMLTPRLLHGLKGLSLTS---LEVYNAYG
  BfPKS5(NRPS)  (694) CLVVAPADARGDPHEITNLMLEHGVTMTQATPSEYETWFRFA------------PENVRRCTAWKAAWFGGERAPPGLLHLFREACKVLPN-LQVYTSYG
mg03818(NRPS)   (660) SLHMLPRSQRGDALAITKRILDSGITLTGATPSEYMSWISF-------------GGADLARSNWRRAVCGGEPVTTSLLRAFDSIGRPE---LRLFNAYG
 GmPKS10(NRPS)  (663) TLIVASSETRKDPTQLAQLMLDEKVTHTFMTPTLALSVIHHG------------YEYLRQCVDWEHASLAGEAMTTRVTSEFKRLGLRN---LELCNGYG
    Consensus   (801)  LVV     RGDP  L  LM    VT T ATPSE    L                      S WR A  GGE LS  LL  F  L       L VFN YG
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                        A5                                                     A6
                                                                                                          1000
   Ace1(NRPS)   (761) PTEATINANTRIVPYHEPN---S--N-PDLPLLTWPNYSISIVDLEL-NPVPVGVFGEVCIGGAGVGLGYFK-NDELTAKAFVADKTAPAEFVAKGW--K
 GmPKS9(NRPS)   (762) PTETTVTNRIELNFADYAEGDKAQMRYVTDVGFPCANYSTYIVDENMS-LVPRGYPGEIVVGGAGVADGYLG-RPDLTKEKFIQDPWTS----SKEW--K
 GmPKS1(NRPS)   (763) PAETTILSHRIDLKYTDPH---LP--DPLPAGYPMPGFSVCVVDEKM-RPVPLGVQGEIILGGPCIVSGYLN-MPDSTKDKFLP------DTFFGTS--G
   SYN2(NRPS)   (767) PTEITFCCAMRAVDYRSDA---P-PDAEAGGFKPWPNVSVYILDADQ-KIVPAGVTGEIAIGGGGVVAGYG--DHKLSAAAFKHDKWASSEFVQSGW--T
mg03810(NRPS)   (781) PSETWMPLSHEIPLGQARTMEDVERLWPVPIGSTMPNYAVRVEDVNG-HVLPPGMPGQVVIGGCGVALGYVSSEPTVTDPRFLPDSHPAEVHLARGWD--
AF04917(NRPS)   (764) PTEASICSSLGEVSFNRIS---S-SETSIPIGKAIPNYGTYIVDQHC-KPVPLGWPGEVAIAGPGVASGYLN-LGELTQAKFR---SAATLGEVFGS--D
 AN8412(NRPS)   (756) PTEITAAATFQDISLQMKD---QSTTDGSLVGKALPNYSVYIMDASSGSPVPIGVTGEICIGGAGVSLGYLN-SLEQTDAKFVRDPFASPEDITRGW--T
mg09589(NRPS)   (803) PTETCMISNIGRIEYWGNHRDEE--SRSWPVGPPFANARVYILDQAG-RTVPSGSSGEIYIAGEGVGLGYLG-RADLTRASFVADTFGP------GN--T
   SYN8(NRPS)   (827) PTETCMSSNVGRIEYWLDEN-VQEPARVFAVGPPLDGVRIRVLGLDG-NEVPYGAEGEVYIGGVGVGPGYLN-RPDLTDAAFLPEPTNDPPAAAGSGRSK
    BbNRPS(4)   (754) PTEDTVYSTHAIVTKGATN--------EPLIGRPQFNTHVFVLDSHR-KPVPVGVPGELYLSGSGLARGYLH-RPDLTAERFV-----QNPFREPG---A
       MxaA     (757) PSETTTYSTFTRVNRGQ----------TPTIGRPVGNTQVYALDSNR-EPMPIGVPGEVYIGGMGVARGYLG-RPELTAERFV-----RSPFGGGSE--A
    AnACVS(2)   (767) PTEISITTHKRLYPFPERR-------TDKSIGQQIGNSTSYVLNADMKR-VPIGAVGELYLGGEGVARGYHN-RPEVTAERFLRNPFQTDSERQNGRN-S
   HCsynth(2)   (782) PTEATVACIANQVTCTTTT--------VSDIGRGYRATTWVVQPDNHNSLVPIGAVGELIIEGSILCRGYLN-DPERTAEVFIRSPSWLHDLRPNS----
   Syn6(Cdom)   (439) ----------------------------------------------------------------------------------------------------
   LNKS(Cdom)   (445) ----------------------------------------------------------------------------------------------------
ChPKS17(Cdom)   (457) ----------------------------------------------------------------------------------------------------
 BfPKS3(NRPS)   (751) PTECSISCAIHQVPYLEYEDG--MEWTLSLVGTVLPGYEVYILDEKL-QPTRIGWPGEIFIGGPGVGSGYVN-DKEKTNASFFLNPFKQSE---TTG--T
 BfPKS5(NRPS)   (781) PTEGTISAMKGKLEIEDP------AVAVPVPGFVLPNYAAYIVDXXX-------XX--------------------------------------------
mg03818(NRPS)   (744) PTETTCSATRTELDYRGPW---G--DRPTTSGRAAPNCSVCIVDANL-APLPVGMPGEVLIGGAKVALGYLG-SCELTATRFIPHASIHEDFAARGW--T
GmPKS10(NRPS)   (748) PTEITIIATCGSNELGDTL---R-DTHNPSIGRALPNYSCYILDENM-QPVRPGLAGELVIGGAGVAIGYLN-RQDLTEAKFLSDPFAPPEDVARGW--T
    Consensus   (901) PTE TI S    V                 IG  LPN  VYILD      VPIG  GEI IGG GVA GYL    ELT  KFL            G
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                         A7                 A8
                                                                                                      1100
   Ace1(NRPS)   (851) TKFRTGDLGRLSPDG-GLIIEGRIDGDTQVKLRGMRIDLKNIESAILQAGAGKIIDAAVSVRRG--------------GAD----ESEPQYLVGHVVLDA
 GmPKS9(NRPS)   (854) IMYRTGDRGKLRANG-MVDILGRIEGGTQVKLRGYRIELDDVESAILSAAQGVLSDAVVTLRYPEER-----------HED----HYDDGFLVAHVVVAD
 GmPKS1(NRPS)   (848) KVYRSGDRGRLCQDG-LLFCDGRLEGSNMIKLRGFRVELDEVEKTIISHSAGALSHAVVTLRGTE-----------------------EGRYLATHVVFA
   SYN2(NRPS)   (858) RLHLTGDVGKIDPIDGTLKLKGRIAGDTQIKLRGMRLDVREVELAIMKTAQGQINDVVVTAHHN-------------------------KATGASSLIAF
mg03810(NRPS)   (878) KVHPSGDYGYMTEEG-LFFSLGRISGDTQIKLRGMRLDLRHVEAAMMDMEMAQGFVVDVVVGVRSTDGQ--------PLAAGSLADDSTSKVLVAHAVTD
AF04917(NRPS)   (853) CLYLTGDRGRMLSDG-SIVLSGRVDGDDQVKIRGHRVQLGDVARALVQASRGVFADAAVILKGDDTS----------------------NPQLVAYVVFS
 AN8412(NRPS)   (850) KMYRTGDMGCLTEDG-TLIFMGRMDGDNQVKLNGLRIELDEIANSILTTGNDLVSEAVVTVHSG------------------------SGSGSPLLVAHV
mg09589(NRPS)   (891) KMYRTGDSGFLDPDG-SLVILGRIQDDSQVKIRGIRIELDEVSSVIVRSSGGRVSQAITTVRGTGEN--------------------KMMVSFAVLNEGS
   SYN8(NRPS)   (924) KMYRTRDKGYWLPDG-SLMVCGRIDGDTQVKMHGIRIELEDVASAILAAADGLVSHAVATVR-SD----------------------EHDKTIVAFVVPS
    BbNRPS(4)   (836) RMYRTGDLVRYLPDG-NLQFVGRVDYQVKIRG-----------------YRIELGEIESVLNRFPGVKE--------VVLL----AREDREGDKCLVAYI
       MxaA     (838) RLYRTGDLARWLPDG-QLEYLGRMDHQVKLRG-----------------FRIELGEIGAVLMEHSGIRD--------AVVV----VREGLGADKQLVAYV
    AnACVS(2)   (857) RLYRTGDLVRWIPGS-NGEIEYLGRNDFQVKIRGLRIELGEIEAVMSSHPDIKQSVVIAKSGKEG----------------------------DQKFLVG
   HCsynth(2)   (869) TLYKTGDLVRYSADG---KIIFIGRKDTQVKMNGQRFELGEVEHALQLQLDPSDGPIIVDLLKRTQSGEPDLLIAFLFVGRANTGTGNSDEIFIATSTSS
   Syn6(Cdom)   (439) ----------------------------------------------------------------------------------------------------
   LNKS(Cdom)   (445) ----------------------------------------------------------------------------------------------------
ChPKS17(Cdom)   (457) ----------------------------------------------------------------------------------------------------
 BfPKS3(NRPS)   (842) TLYRTSDLGRILHDG-TISIIGRATGDRQVKLRGMRIELDEISHTILSCSNGIVKEAVVIKKSG------------------------TDPFLVSFVVLD
 BfPKS5(NRPS)   (824) ----------------------------------------------------------------------------------------------------
mg03818(NRPS)   (835) SVHRTGDVGRLLPDG-ALVLQGRVDGDTRVKLRGNRVDLVDVEEAMLQAGQGQLLQVFACLYCPDLASD--------DGAL----AHPESAVLAALVVVD
GmPKS10(NRPS)   (840) RMYRTGDKARFLSDG-RLCFLGRIAGDSQIKLRGFRIELQDIASTIVKASDGKVPEAAVSLRGE-----------------------GDSAYLVAFVILS
    Consensus  (1001) KLYRTGD GRL  DG  L I GRI GD QVKLRG RIEL EV   IL    G L    V L                                    VV
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                                        A9               A10
                       1101                                                                                               1200
     Ace1(NRPS)  (932) DQTPEDSQQDFLAQLIPRLRLPRHMKPSLLVPIRA-LPQTASHKLDRRALQQLPISDAGQIAKQS----------------------QQGAELGSDQARM
   GmPKS9(NRPS)  (938) KSLRRPEVESFLRKIVSKLPLPHYMLPALMLPIDR-FPLTAHQKPDRNAIAALPLPAFTLATAN-----------------------DAIAEEGSLESET
   GmPKS1(NRPS)  (924) PEVAEHNQEGIMKALRQTLPLPPYMRPSVFQVLSD-IPRTAHLKIDRKAIQEMPVQIS--------------------------------ASHDSGILTV
     SYN2(NRPS)  (933) AIVADPKASHDFSRVLARLPLPQYMRPAAIFPIDN-FPTNASGKVDRIAIRNLDLPQTQDFDRKS----------------------AANSDAHLTDTES
  mg03810(NRPS)  (969) ASTATTDTDERLRSIAENLPLPDYMRPAVVVPVDS-IPLTPNGKQDRAAIALWPVQLGSMKVHESNAAEWESS-SP-------QAAHVSNGDKQPLELMS
  AF04917(NRPS)  (930) RTSNIQDQQTYLRQLNQDLPVPAYMRPAITIPLDT-LPVTDRGKLDSKKLASLPLPSIS----------------------------VDYEEDEQLTPTE
   AN8412(NRPS)  (925) VPLGDNVDNSRLQQLARDLPLPQYMLPSVVVSLDR-LPINANGKVDRKAIMALPLPTQRTESAAG----------------------TGTDTARHLSLAE
  mg09589(NRPS)  (970) KEDRKDSDAAFLAALASSLPLPSYMCPAAILPLQK-FPTTASGKLDRASLDRIQLPPTAPTKPTSNT--------------------GDSKLLEMENELL
     SYN8(NRPS) (1000) PRLSPADAPKFLAELPARLPLAEYMRPAAILPLET-LPLNASGKLDMAALAEVPLPEQQHHEALQPAPDLAAATSVAGTHTKIHETPPSTDLSYLEQELL
      BbNRPS(4)  (906) VFEADCTSKIHDLNHFLADKLPAYMIPQHYMILDS-LPKTPNGKLDRKALPKPEYDRS------------------------------EAGVEYVAPQTP
        MxaA     (908) VGRGEKAPEPAELRDYLKSKLPEYMVPFLFVGLDA-LPLTPNGKVDRAALPAPERTHS------------------------------GPAKEHVAPRTP
      AnACVS(2)  (928) YFVASSPLSPGAIRRFMQSRLPGYMIPSSFIPISS-LPVTPSGKLDTKALPTAEEKGAMN---------------------------------VLAPRNE
     HCsynth(2)  (966) LSEFSTVIKKLQDAQRAMEVLPLFMVPQAYIPIEGGIPLTAAGKIDRRMLRKLCEPFNRNDLISFTS--------------------KALSTSVKDAETT
     Syn6(Cdom)  (439) ----------------------------------------------------------------------------------------------------
     LNKS(Cdom)  (445) ----------------------------------------------------------------------------------------------------
  ChPKS17(Cdom)  (457) ----------------------------------------------------------------------------------------------------
   BfPKS3(NRPS)  (917) PNRMPIDTPGYLRDLSNSLPLPPHMRPAVCVSIEK-IPLLASCKVDYGKLQVMPLSQGVRDLK-----------------------------GEELNPIE
   BfPKS5(NRPS)  (824) -------XX-------LTLCLPLYMCPSTIVVLEE-MPLTAHSKVDRRAVQVLSLPELAES---------------------------DSDAIIAPDLTW
  mg03818(NRPS)  (922) PCHPSADREELFADLLKRVSLPRAQKPTVVKAVES-LPTTVSGKVDRKAAAKLLPKLVGSPPAVL----------------------GGEQDKELSETES
  GmPKS10(NRPS)  (916) QFNRPSDEKGYLKQLLEELSLPRYMKPAKIISISQ-LPMNASGKLDQYALDALPVSYEK--------------------------------DIVDKPLTE
      Consensus (1101)            L  L   L LP YM PA IV LD  LPLTA GKLDR AL  L L

                                                T (PCP)
                     1201                                                                     1275
     Ace1(NRPS) (1009) --WKLWKQVIPRDVVSQYSITPQSDFFHVGGTSLLLVNLQSLIAREHGRAPPLHAMFESSTVAAMTDLVLSD---
   GmPKS9(NRPS) (1014) QKKIAKMWRTLVPASASATITADTDFFHVGGSSLLLIKLQGMIRKEFNVSLRLLNLMAASKLREMAALVND----
   GmPKS1(NRPS)  (991) AEKALSELWRRVLPLDPGSLTPESDFFLIGGNSILLVKLQALLRQTFKTAPKLVTLMGASTLGAMAVVL------
     SYN2(NRPS) (1010) RLAQLWTQVITKGVISQYQITNESNFFHVGGTSILLVQLRSAIEASFGTRPTLFQLFEAGTLAAMAALIAPL---
  mg03810(NRPS) (1060) RIWREALGLSPTGSEQPGPMEPDDDFFQMGGNSILLTRVQRSIRLEHGVDLPLRELFHNTTLAQMSQLLLDQD--
  AF04917(NRPS) (1001) ARLRDVWKNVLGDIASSIPIRRSSDFFSVGGNSLILLALKAEIAQVFGVGLSVSELFQASTLELLAARL------
   AN8412(NRPS) (1002) GELRLLWEKVLPASGGPSRLDADSDFFMRGGTSMLLVRLQGAIKESIGVSIPVAELYQFPTLGQMARRISRR---
  mg09589(NRPS) (1049) CIWMDLLPDLPNQGVLSPGYTPDTDFFRLGGNSTTLVALRNAIRRRWGINVPLLKLFEATTLRSMTALITKS---
     SYN8(NRPS) (1099) STWTAVLPSLGKQLLKNTSAHRGLDFFRVGGSSITLVVLRDAIRRRFRAHVPLLPLFENSTLGSMAAVVGRQ---
      BbNRPS(4)  (975) --VEIMLHAHWAAVLEMETIGVHDNFFEIGGHSLLATQLIFKVREELQLEVPLRILFETPTIAGMAKTIEEI---
        MxaA     (977) --GEESLAAIWRQVLGVEQIGAHDNFFELGGHSLLLYRVLVLARSASGADIPLRALLQAPTLEEMARAVEAA---
      AnACVS(2)  (994) IESILCGIWAGLLDISAQTIGSDSDFFTLGGDSLKSTKLSFKIHEVFGRTISVSALFRHRTIESLAHLIMNN---
     HCsynth(2) (1046) DTVEDRLARIWEKVLGVKGVGRESDFFSSGGNSMAAIALRAEAQRS-GFTLFVADIFTNPRLADMAKLFSHGQ--
     Syn6(Cdom)  (439) ---------------------------------------------------------------------------
     LNKS(Cdom)  (445) ---------------------------------------------------------------------------
  ChPKS17(Cdom)  (457) ---------------------------------------------------------------------------
   BfPKS3(NRPS)  (987) KKMAEIWRKVLPSTSDEFVIGKSTDLFAIGGNSILLLRIQSEIKERSGIKIPLYKLFQSTMLADMSLQMVMGG--
   BfPKS5(NRPS)  (882) TERRLAILWATLLPPQSLLLTQQSSFFLAGGNSLLLVQLQAAITVEFGGAPRLSKLMAATTLASMAAEL------
  mg03818(NRPS)  (999) --QLREIWLQTLPAGCYAQVRGSSDFFHSGGDSLLLVALQRKIKQAFGIHVPLVDMFDSSTLKEMSLLIE-----
  GmPKS10(NRPS)  (983) TQERLKLGWLKALPFVDAAIGPDTDFFSAGGNSLRIVSLREYITREFGVTVSVFDLFQASTLGEMAAKIDGFTTQ
      Consensus (1201)       L  I         I   SDFF VGG SLLLV L   IR  FG  V L  LF ASTLA MA LI
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