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          *      20      *      40      *      60      *      80      *      100
FvePKS_FWp : ----- : -
FvePKS_RVp : ----- : -
FvePKS_c1o : ACTGCGAGCTGATCAAGAACCTGGGCCTCACCCGCTCCGTGGACCGTACTCTCATCGGCTTCATGGGGTGCGCCGCGGCCATGAACGGCTTCGCAACGCGAACG : 105
FvePKS_GH7 : ----- : -
FsePKS_GH7 : ----- : -

          *      120     *      140     *      160     *      180     *      200     *
FvePKS_FWp : ----- : -
FvePKS_RVp : ----- : -
FvePKS_c1o : ACTTCGTGACTGCCAACCCCGGCAAGTACGCCCTGATGATCTGCGTCGAGCTTTCTCGGTGCACACGACCTTCGACGACAACATCAACGACGCCATCCTCCACG : 210
FvePKS_GH7 : ----- : -
FsePKS_GH7 : ----- : -

          220     *      240     *      260     *      280     *      300     *
FvePKS_FWp : ----- : -
FvePKS_RVp : ----- : -
FvePKS_c1o : CAATCTTCGCCGATGGGTGCGCCGCCCGTGTCAAGGGTATCAAGAAGTCCGAGGCCCCCAAGGGAACCCCTGGCGATCGTCGACAACCACGCGTGGCTCATGG : 315
FvePKS_GH7 : ----- : -
FsePKS_GH7 : ----- : -

          320     *      340     *      360     *      380     *      400     *      420
FvePKS_FWp : ----- : -
FvePKS_RVp : ----- : -
FvePKS_c1o : AGGGCACCGAGGATGGCATCACCCCTCGCGATCAAGCCCAACGGCATCACCTGCACTCTCTCTAAGTTCCTGCCCCAGTACATCGCCAAGAACATCGCGTTCTTCG : 420
FvePKS_GH7 : ----- : -
FsePKS_GH7 : ----- : -

          *      440     *      460     *      480     *      500     *      520
FvePKS_FWp : ----- : -
FvePKS_RVp : ----- : -
FvePKS_c1o : CCGACGGCTTCCTCAAGAAGCACAACTCGGCCGCGATGACGTTGACTTCTGGTGCCTGCACCCCGGGGACGCCGTATCATCGAGGAGGCGCAGAACGGGCTCG : 525
FvePKS_GH7 : ----- : -
FsePKS_GH7 : -----CGCAGAACGGGCTCG : 15

          *      540     *      560     *      580     *      600     *      620     *
FvePKS_FWp : ----- : -
FvePKS_RVp : ----- : -
FvePKS_c1o : GCCTCACGGAGGAGCAGACCCGCGGATTCGTGGGCGGTGCTTGCCGAGTACGGGAACATGCTTTACCGTCCGGTATGTTTGTGCTGTCCAGGGTGTTC AAGCGCC : 630
FvePKS_GH7 : -----CGGTATGTTTGTGCTGTCCAGGGTGTTC AAGCGCC : 36
FsePKS_GH7 : GCCTCACGGAGGAGCAGACCCGCGGACTCGTGGGCGGTGCTTGCCGAGTACGGGAACATGCTTTGCCATCCGGTATGTTTGTGCTGTCCAGGGTGTTC AAGCGCC : 120

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          640      *      660      *      680      *      700      *      720      *
FvePKS_FWp : ----- : -
FvePKS_RVp : ----- : -
FvePKS_c1o : ACAACGCCGCGCTCGCGCAAGGGAAGCCTGGCTACCAGACCGGCATGGCGTTCTCGTTTTCCCGGGCGTGGGCGCCGAGGGTATCCTTCTCAAGCAGCTCTAAA : 735
FvePKS_GH7 : ACAACGCCGCGCTCGCGCAAGGGAAGCCTGGCTACCAGACCGGCATGGCGTTCTCGTTTTCCCGGGCGTGGGCGCCGAGGGTATCCTTCTCAAGCAGCTCTAAA : 141
FsePKS_GH7 : ACAACGCCGCGCTCGCGCAAGGAAAGCCTGGCTACAAGACCGGCATGGCGTTCTCGTTTTCCCGGGCGTGGGCGCCGAGGGTATTCTTCTCAAGCAGCTCTAAA : 225

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          740      *      760      *      780      *      800      *      820      *      840
FvePKS_FWp : ----- : -
FvePKS_RVp : ----- : -
FvePKS_c1o : AGAAGCGCGAAAGGATTGGAGTTTGGCAGACACCTCCGAGTAGTACATAACTGGAGGGTGT CAGGCGGAGAAAGGCCATCGTATAC---TGTAGTCACCGATGCC : 837
FvePKS_GH7 : AGAAGCGCGAAAGGATTGGAGTTTGGCAGACACA-CTCCGAGTAGTACATAACTGGAGGGTGT CAGGCGGAGAAAGGCCATCGTATAC---TGTAGTCACCGATGCC : 242
FsePKS_GH7 : AGGAGCGCGAAAGGATTGGAGATTGGCAGACAG-CTCCGAGTAGTACATAACTGGAGGGTGTTCGGCGGAGAAAGGCCATCGTATACGTTTGTAGTCACCGATGCC : 329

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          *      860      *      880      *      900      *      920      *      940
FvePKS_FWp : -----TTGCACGTATGTCTCTGTTGC----- : 21
FvePKS_RVp : ----- : -
FvePKS_c1o : ATCCCATCACACCCGAGGTGGGGCACGGGTCAGCTCGTTTTGCATGTTGCACGTATGTCTCTGTTGC GTAAAATACCTTTTGAGGCGGCTTGCCGGTAAGGTTTT : 942
FvePKS_GH7 : ATCCCATCACACACGAGTTGGGGCACGGGTCAGCTCGTTTTGCATGTTGCACGTATGTCTCTGTTGC GTAAAATACCTTTTGAGGCGGCTTGCCGGTAAGGTTTT : 347
FsePKS_GH7 : ATCCCATCACACCCGAGTTGGGGCACGGGTCAGCTCGTTTTTTATGTTGCACGTATGTCTCTGTTGC GTAAAATACCTTTTGAGGCGGCTTGCCAGTAAGGTTTT : 434
          ttgcacgtatgtctctggtgc

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          *      960      *      980      *      1000      *      1020      *      1040      *
FvePKS_FWp : ----- : -
FvePKS_RVp : -----CCATCAGGTTATTCGCGC----- : 18
FvePKS_c1o : ATGTTTC-GGAGCCAGCGTTTTGTCCCATTCGTTGAGCGACAACACTCGAGCGGTTCCCATCAGGTTATTCGCGCGCAGCCCCATTGTTGCTGATGGCGCACC GA : 1046
FvePKS_GH7 : ATGTTTC-GGAGCCAGCGTTTTGTCCCATTCGTTGAGCGACAACACTCGAGCGGTTCCCATCAGGTTATTCGCGCGCCGTCCTTCTGCTGATGGCGCACC GA : 451
FsePKS_GH7 : ATGTTTCGGGAGCCAGCGTTTTGTGTCCCATTCGTTGAGCGACGACACTCGAGCGGTTCCCATC----- : 496
          ccatc

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          1060      *      1080      *      1100      *      1120      *      1140      *
FvePKS_FWp : ----- : -
FvePKS_RVp : ----- : -
FvePKS_c1o : AACAAATGCGGCGAGGGATTTGGGGGCGAGTGAAATCTCGCGGCAACGACCGTGTATTCTTTTGTGACAAGCTATCAGTTTACTCTTGCGTGAGATTCTTGGGCC : 1151
FvePKS_GH7 : AACAAATGCGGCGAGGGATTTGGGGGCGAGTGAAATCTCGCGGCAACGACCGTGTATTCTTTTGTGACAAGCTATCAGTTTACTCTTGCGTGAGATTCTTGGGCC : 556
FsePKS_GH7 : ----- : -

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          1160      *      1180      *      1200      *      1220      *      1240      *      1260
FvePKS_FWp : ----- : -
FvePKS_RVp : ----- : -
FvePKS_c1o : ACTTTAGAAGCGATTCCCAGTTCCTTTTTATGGGTGCGCATCGCAAGCGTCTTCCCCCAGCACCCTTCTCTTCTTAACGGGTGGTCATTTGCCGACCACTTT : 1256
FvePKS_GH7 : ACTTTAGAAGCGATTCCCAGTTCCTTTTTATGGGTGCGCATCGCAAGCGTCTTCCCCCAGCACCCTTCTCTTCTTAACGGGTGGTCATTTGCCGACCACTTT : 661
FsePKS_GH7 : ----- : -

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          *      1280          *      1300          *      1320          *      1340          *      1360
FvePKS_FWp : ----- : -
FvePKS_RVp : ----- : -
FvePKS_clo : TGGGCTTCTCCCCTCTCGAAAAAGAGAGTTGGTGTTCCTCAAGTTTTGAAGTACGGTTGGCATTGGTTGATGCGGTAAGATTATGTTCCCTTGCGCCACGTGTGGC : 1361
FvePKS_GH7 : TGGGCTTCTCCCCTCTCGAAAAAGAGAGTTGGTGTTCCTCAAGTTTTGAAGTACGGTTGGCATTGGTTGATGCGGTAAGATTATGTTCCCTTGCGCCACGTGTGGC : 766
FsePKS_GH7 : ----- : -

          *      1380          *      1400          *      1420          *      1440          *      1460          *
FvePKS_FWp : ----- : -
FvePKS_RVp : ----- : -
FvePKS_clo : AGAACAGGGGAAGCCCAATAGCTTCTATATAACTCCAGTACTGCTGTTCTGTTGCGGTAGCGCGTGCGTGTGTTGTTCTTGAGGTTGGCGGGTACCTTTGTTTTTGT : 1466
FvePKS_GH7 : AAAACAAGGGA----- : 777
FsePKS_GH7 : ----- : -

          1480          *      1500          *      1520          *      1540          *      1560          *
FvePKS_FWp : ----- : -
FvePKS_RVp : ----- : -
FvePKS_clo : CAAAACGTTTTGTTGGTTCGTGCTGTATATTGATCGTACGATTGTAAGTGTGTTGGGTGACAAACGGGTGTGGAGGGTCGTGCGGAGTGGTGAGCGTTCACCTTG : 1571
FvePKS_GH7 : ----- : -
FsePKS_GH7 : ----- : -

          1580          *      1600          *      1620          *      1640          *      1660          *      1680
FvePKS_FWp : ----- : -
FvePKS_RVp : ----- : -
FvePKS_clo : CTGCGGAGGAGGCAGGAATATGTAGTTGGATTTATTTTCGTTTGGGTGCGGTTTTATCGCCTGCTACCATCGGGACATGTGGATCGTCGTCAATTTTGGCAAAC : 1676
FvePKS_GH7 : ----- : -
FsePKS_GH7 : ----- : -

          *      1700          *      1720          *
FvePKS_FWp : ----- : -
FvePKS_RVp : ----- : -
FvePKS_clo : ACCTCGCTCGATGATAATGAAATATATTTTCNTAAAAAAAAAAAAAAAAAAAA : 1726
FvePKS_GH7 : ----- : -
FsePKS_GH7 : ----- : -

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**S1 Fig.A: Nucleotide alignment of the brown algal PKS III coding sequences.**

**Nucleotide alignment of the *Fucus vesiculosus* cDNA sequence with *Fucus* EST sequences.**

qPCR forward primer (FvePKS\_FWp), qPCR reverse primer (FvePKS\_RVp), partial cDNA sequence cloned from *F. vesiculosus* (FvePKS\_clo), *F. vesiculosus* EST of GH706741 GenBank accession (FvePKS\_GH7), *F. serratus* EST of GH701018 GenBank accession (FsePKS\_GH7). The positions sharing a conservation of 100, 80 and 60% are respectively shaded in black, dark grey and light grey.

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          *      20      *      40      *      60      *      80      *      100     *      120
FsePKS : ----- : -
FvePKS : ----- : -
SbiPKS : ATGTCTTCAGCAGCTGTTGCTATGTGGCGGATCCCACCGTGCAGATCGCCCTGGCTTGCATCGTGCTCTCCCTCATCGTGGTATTCGGTTCGTACCGCAAGGGGAAGGATGAGCAGACCGTCT : 124
EsiPKS1 : ATGTCTTCTGCTGCGGTTGCTATGCTGGCTGACCCGACTGTCCAGATCGCTCTGGCGTGCCTGGTGGTGTCTCTCTTCGTTGTGCTGCAGTCGGTCAAAAAGTCCAAGGACGAGCAGACGGTAT : 124

          *      140     *      160     *      180     *      200     *      220     *      240
FsePKS : ----- : -
FvePKS : ----- : -
SbiPKS : ACCCCGTCATCGCGGGGATGGCGATCGGCAACCCTCAGTACCGGTGCACCCAGGACCAGGCGCTCACGGTCGTCAGAAGTGCCCTGGCGTGGAGTCTGTGAAGCCAGTGCTCGAGCGAATCTA : 248
EsiPKS1 : ACCCGGTCATCGCGGGGATGGCCATCGGCAACCCGAGTACCGCTGCACGCAGAAAGAGGCCCTCGCCGTCGCCCTCAAGTGCCCGGGCCTCGAGTCCATCAAGCCCGTCTCGAGCGCATCTA : 248

          *      260     *      280     *      300     *      320     *      340     *      360     *
FsePKS : ----- : -
FvePKS : ----- : -
SbiPKS : CGGAAACTCCCGCATCGGCAGCCGATACTTCGCCGTGCCGGACTTTACTCCCAACCAGGCTGCCAAGGGCGACCCATGTTCTTCCCGCCGACGGCAGCTTCGAGGTGCCCGTGGACACCCGC : 372
EsiPKS1 : CGGCAACTCGGCATCGGCAGCCGCTACTTCGCCGTGCCGGACTTCACCCCGGCGAGGGCGGCCAAGGGCGACCCCTCTTCTACCCGCGCCGACGGCAGCTACCAGGTGCCCGTGGACGTCCGG : 372

          380      *      400      *      420      *      440      *      460      *      480      *
FsePKS : ----- : -
FvePKS : ----- : -
SbiPKS : CTCGACAAGTTCAAGGAGAAGGCGGTTCCCTCGTTTCCGACGTGCTCGCCGCGCCATTAAGGAGGCGGGGATCGATGTGTGCGGACGTGTGGAAGCTCGTCGTGTCCTCTACCGGTTTCC : 496
EsiPKS1 : CTGGACAAGTTCAAGGAGAAGGCCGTTCCCGCTGGTGTCCGACGTGCCCCGCGCCCATCAAGGAGGCGGGCCTGAACGTGAGGACATCTCAAGCTCGTCGTGGTCTCCTCCACCGGATTC : 496

          500      *      520      *      540      *      560      *      580      *      600      *      620
FsePKS : ----- : -
FvePKS : ----- : -
SbiPKS : TCGGCCCCGGTCTGGACTGCGAGCTTATCAAGAACCTCGGCCTCACCCGCTCGTGGACCGTACTCTCATCGGCTTCATGGGGTGGCGCGCGCCATGAACGGCTTCCGCAACGCGAACGACTT : 109
EsiPKS1 : TCGGCCCCGGCCTCGACTGCGAGCTGATCAAGAACCTCGGCCTCACCCGCTCGTGGACCGCACCTCATCGGCTTCATGGGGTGGCGCGCGCCATGAACGGTTCGCAACGCGAACGACTA : 620
          actgcgagct atcaagaacct ggcct acccgctc gt gaccg ac ctcatcgg ttcatggg tgcgc gc gccatgaacgg ttccg aacgcgaacgact

          *      640     *      660     *      680     *      700     *      720     *      740
FsePKS : ----- : -
FvePKS : CGTGACTGCCAACCCTCGCAAGTACGCCCTCATGATCTGCGTGGAGCTTTCCTCGGTGCACACGACCTTCGACGACAACATCAACGACGCCATCCTCCACGCAATCTTCGCCGATGGGTGCGCC : 233
SbiPKS : CGTTACCGCAAAACCCTGCCAAGTACGCCCTCATGATCTGCGTGGAGCTGTCTCTGTGCACACGACCTTCGATGACAACATCAACGACGCCATCCTCCACGCAATCTTCGCCGACGGGTGCGCC : 744
EsiPKS1 : CGTCAACGCAAAACCCTGCAAGTACGCCCTCATGATCTGCGTGGAGCTTTCCTCGGTGCACACGACCTTTCGACGACAACATCAACGACGCCATCCTTCGACGCTATCTTCGCCGACGGATGCGCC : 744
          cgt ac gc aacc gg aagtacgc ct atgatctgct gagct tcctc gtgcacac acctt ga gacaacatcaacgacgc atc t cacgc atcttcgccga gg tgcgcc

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      *      760      *      780      *      800      *      820      *      840      *      860
FsePKS : ----- : -
FvePKS : GCCGCCGTGCTCAAGGGTATCAAGAAGTCCGAGGCCCCCAAGGGAACCCCTGGCGATCGTGCACAACCACGCGTGGCTCATGGAGGGCACCGAGGATGGCATCACCCCTCGGCATCAAGCCCAACG : 357
SbiPKS : GCTGCCGTGCTAAAGGGTGTCAAGGAAGTCCGAGGCCCCCAAGGGAACCCCTGGCTATCGTTGACAACCACGCGTGGCTCATGGAGGGCACCGAGGACGGCATCACCCCTCGGCATCAAGCCCAACG : 868
EsiPKS1 : GCTGCCGTGCTCAAGGGAGCCAGGAAGTCCGAGTGCACCAAGGGAACCCCTCGCTATCGTGCACAACCACGCGTGGCTCATGGAGGGAACCGAGGACGGAATCACCCCTTGCTATCAAGCCAAACG : 868
gc gccgtgct aaggg ca gaagtc gag ccccaaggggaaccct gc atcgt gacaaccacgctggctcatggaggg accgagga gg atcacct gc atcaagcc aacg

      *      880      *      900      *      920      *      940      *      960      *      980      *
FsePKS : ----- : -
FvePKS : GCATCACCTGCACCTCTCTTAAGTTCTTCCCCAGTACATCGCCAAGAAATATCGCTTCTTTCGCCGACGGCTTCTCAAGAAGCACAACTCGGCCGCGATGACGTTGACTTCTGGTGCGTGCA : 481
SbiPKS : GTATCACCTGCACCCCTGTCCAAGTTCTTCCCCAGTACATCGCCAAGAAATATCGCTTCTTTCGCCGACGGCTTCTCAAGAAGCACAACTCGGCCGCGTGTATGACGTTGACTTCTGGTGCGTGCA : 992
EsiPKS1 : GCATCACCTGCACCCCTGTCCAAGTTCTTCCCCAGTACATCGCCAAGAAATATCGCTTCTTTCGCCGACGGCTTCTCAAGAAGCACAAAGCTCGGACGCGACGACGTTGACTTCTGGTGCGTGCA : 992
g atcacctgcac ct tc aagttcct cccagtagatcgcgaagaa atcgc ttctt gc gacgg ttctcaagaagcaciaa ctcgg cg ga gacgttgacttctggtgcggtgca

      1000      *      1020      *      1040      *      1060      *      1080      *      1100      *
FsePKS : ----- : 95
FvePKS : CCCCAGGAGGACGCGCATCATCGAGGAGGCGCAGAACGGGCTGGCCCTCACGGAGGAGCAGACCGCGGACTCGTGGGCGGTGCTTGCCGAGTACGGGAACATGCTTTCCGCCATCGGTGATGTTT : 605
SbiPKS : CCCCAGGAGGACGCGCATCATCGAGGAGGCGCAGAACGGGCTGGCCCTCACGGAGGAGCAGACCGCGGACTCGTGGGCGGTGCTTGCCGAGTACGGGAACATGCTTTCCCGCTCTGTGATGTTT : 1116
EsiPKS1 : CCCCAGGAGGACGCGCATCATCGAGGAGGCGCAGAACGGGCTGGCCCTCACGGAGGAGCAGACCGCGGACTCGTGGGCGGTGCTTGCCGAGTACGGGAACATGCTTTCCCGCTCTGTGATGTTT : 1116
ccccgg gg cg cg atcatcgaggaggCgCAGAACGGGCT GGCCTCaCGGAGGagCAGACCGCGGACTCGTGGGCGGTGCTtGccGAGTACGG AACATGCTtTC CC TC GTgATGTT

      1120      *      1140      *      1160      *      1180      *      1200      *      1220      *      1240
FsePKS : GTGCTGTCCAGGGTETTC AAGCGCCACAACGCCGCGCTCGCC AAGGAAAGCCCTGGCTACAGACCGGCATGGCGTTCTCGTTTTC CCGGGCGTGGCCGCGAGGGTATCTTCTCAAGCAGC : 219
FvePKS : GTGCTGTCCAGGGTETTC AAGCGCCACAACGCCGCGCTCGCC AAGGAAAGCCCTGGCTACAGACCGGCATGGCGTTCTCGTTTTC CCGGGCGTGGCCGCGAGGGTATCCTTCTCAAGCAGC : 729
SbiPKS : GTGCTGTCTAGGGTETTC AAGCGCCACAACGCCGCGCTCGCC AAGGAAAGCCCTGGCTACAGACCGGTATGGCGTTCTCCTTCTCGCCGCGTGTGGCGCTGAAAGGTATCCTCCTCAGGCAGA : 1240
EsiPKS1 : GTTCTGTCTAGGGTETTC AAGCGCCACAACGCCGCGCTCGCAAGGGCAAGCCCGGCTACAGACGGGTATGGCGTTCTCCTTCTCGCCGCGTGTGGCGCTGAAAGGTATCCTCCTCAGGCAGA : 1240
GTgCTgTC AGGGTgTTC AAGCGCCACAACGCCGCGCTcGcGCAaGG AAGCC GGCTACcAGAcGG ATGGCGTTCTC TT TC CcGG GT GgCcG AgGgATcCTtCTCA GCAG

FsePKS : TCTAA : 224
FvePKS : TCTAA : 734
SbiPKS : TTTAA : 1245
EsiPKS1 : TCTAG : 1245
TcTAa

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**S1 Fig. B: Nucleotide alignment of the brown algal PKS III coding sequences.**

*Fucus serratus* GH701018 (FsePKS), partial cDNA sequence cloned from *Fucus vesiculosus* (FvePKS), *Sargassum binderi* HM245964 (SbiPKS), *Ectocarpus siliculosus* Esi0024\_0032 ORCAE Id (EsiPKS1). The positions sharing a conservation of 100, 75 and 50% are respectively shaded in black, dark grey and light

grey.

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      *          20          *          40          *          60          *          80          *          100          *          120
MtuPKS18 : MNVSAESGAPRRAGQRHEVGLAQL-----PPAPPTTVAVIEGLATGTPRRVVNQSDAADRVAEFLDPGQREIRPRVYQKSRIITRRMAV-----DPLDAKFDFVRREPA : 100
FsePKS   : -----
FvePKS   : -----
SbiPKS   : ---MSSAAVAMLADPTVQIALACIVLSLIVVFRSYRKGKDEQTVYPVIAGMAIGNPQYRCTQDQALTVAQKCPGVE SVKPVLERIYGNRSRIGSRYFAVPDFTPNQAAGDPMFFPADGSFEVPEV : 121
EsiPKS1  : ---MSSAAVAMLADPTVQIALACLVSFLVQLSVKKSDEQTVYPVIAGMAIGNPQYRCTQNEALAVASKCPGLESIKPVLERIYGNRSRIGSRYFAVPDFTPGRAAKGDPLFYFPADGSYQVPEV : 121
SjaPKS   : ---MSSPVVAMLTEPSVQIALACVVLSSLVLRSLQKSKDBQTVYPVIAGMAIGNPQYRCTQDEALAVATKCPGLPSIKPVLERIYGNRSRIGSRYFAIPDFTPSQAAGDPMFFPADGSYEVPEV : 121
SlaPKS   : -----

      *          140          *          160          *          180          *          200          *          220          *          240
MtuPKS18 : TIRDRLHFLYEHAVPLAVDVSKRALAGLPYRAAEIIGLLVLIATSTGFIAPGVDVAIVKRELGLSPSISRVVVMEMGCAAAMNALGTATNYVRAHPAMKALVVCIELCSVNAVEADDINDVVIHSLF : 224
FsePKS   : -----
FvePKS   : -----
SbiPKS   : DT--RLDKFKEKAVPLVSDVARRAIKEAGIDVSDVSKLVVVSSTGFLGPGLDCELIKNLGLTRSDVDRTLIGFMGCAAAMNGFRNANDVVTANPGKYALMICVELSSVHTTFDDNINDAILHAIF : 243
EsiPKS1  : DV--RLDKFKEKAVPLVSDVARRAIKEAGLNVEDISKLVVVSSTGFLGPGLDCELIKNLGLTRSDVDRTLIGFMGCAAAMNGFRNANDVVTANPGKYALMICVELSSVHTTFDDNINDAILHAIF : 243
SjaPKS   : DT--RLDKFKEKAVPLVSDVARRAIKEAGLDVSDISKLVVVSSTGFLGPGLDCELIKNLGLTRSDVDRTLIGFMGCAAAMNGFRNANDVVTANPGKYALMICVELSSVHTTFDDNINDAILHAIF : 243
SlaPKS   : -----EKAIVPLVSDVARRAIKEAGLDVSDISKLVVVSSTGFLGPGLDCELIKNLGLTRSDVDRTLIGFMGCAAAMNGFRNANDVVTANPGKYALMICVELSSVHTTFDDNINDAILHAIF : 114
      k l g l s r f m g c a a a m n a v a p a l c e l s v f d i n d h f

      *          260          *          280          *          300          *          320          *          340          *          360          *
MtuPKS18 : GDGCAALVIGASQVQEKLEPCKVWVRRSSFSQLLDNNTEDGIVLGVNHNNGITCELSENLEPGYIFSGVAPVVTETMLWDNGLQISSIDILMAIHPGGPKIIEQSVRS LGISAELAAQSWDVLAREFGNML : 348
FsePKS   : -----
FvePKS   : ADGCAAAVLKGIK-KSEAPKCTLAIVDNHAWLMEGTEDGITLAIKPNGITCTLSKFLPOYIAKNIAFFADGFLKKHNLGRDDVDFWCVHPGGRRRIIEEAQNLGGLTEEQTADSWAVLABYGNML : 195
SbiPKS   : ADGCAAAVLKGVK-KSEAPKCTLAIVDNHAWLMEGTEDGITLAIKPNGITCTLSKFLPOYIAKNIAFFADGFLKKHNLGRDDVDFWCVHPGGRRRIIEEAQNLGGLTEEQTADSWAVLABYGNML : 366
EsiPKS1  : ADGCAAAVLKGAR-KSECPKCTLAIVDNHAWLMEGTEDGITLAIKPNGITCTLSKFLPOYIAKNIAFFADGFLKKHKLGRDDVDFWCVHPGGRRRIIEEAQNLGGLSEEQTADSWAVLGBYGNML : 366
SjaPKS   : ADGCAAAVMKGAR-KSECPKCTLAIVDNHAWLMEGTEDGITLAIKPNGITCTLSKFLPOYIAKNIAFFADGFLKKHKLGRDDVDFWCVHPGGRRRIIEEAQNLGGLTEEQTADSWAVLGBYGNML : 366
SlaPKS   : ADGCAAAVILKGAR-KSECPKCTLAIVDNHAWLMEGTEDGITLAIKPNGITCTLSKFLPOYIAKNIAFFADGFLKKHKLGRDDVDFWCVHPGGRRRIIEEAQNLGGLTEEQTADSWAVLGBYGNML : 237
      dgcaa v          g          l          tedgi l          ngitc ls          lp yi          a          l          l          d d w          hpgg          iie          qngLG63eeqtAdSWaVL e5GNML

      380          *          400          *          420
MtuPKS18 : SVSLIFVLETMVQQAESAIA-----ISTGVARAFEGPGVTVEGMIFDIITRR : 393
FsePKS   : SESVMFVLSRVFKRHNAALAQKPGYKTGMAFSFS PGVGAEGILLKQL-- : 73
FvePKS   : SESVMFVLSRVFKRHNAALAQKPGYQTGMAFSFS PGVGAEGILLKQL-- : 243
SbiPKS   : SESVMFVLSRVFKRHNAALAQKPGYQTGMAFSFS PGVGAEGILLRQI-- : 414
EsiPKS1  : SESVMFVLSRVFKRHNAALAQKPGYQTGMAFSFS PGVGAEGILLRQI-- : 414
SjaPKS   : SESVMFVLSRVFKRHNAALAECKPGYKTGMAFSFS PGVGAEGILLKQI-- : 414
SlaPKS   : SESVMFVLSRVFKRHNAALAECKPGYKTGMAFSFS PGVGAEGILLRQI-- : 285
      Sp866FVLSr6fkrhnaAlA gkpgy TG6AFsFsPGVgaEG6Ll q6

```

**S1 Fig.C: Protein sequence alignment of the brown algal PKS III with a bacterial counterpart.**

*Mycobacterium tuberculosis* P9WPF0 (MtuPKS18), translated sequence of *Fucus serratus* GH701018 (FsePKS), translated sequence of *Fucus vesiculosus* (FvePKS), *Sargassum binderi* ADK13089 (SbiPKS), *Ectocarpus siliculosus* Esi0024\_0032 (EsiPKS1), translated sequence of *Saccharina japonica* contig\_6991 (SjaPKS), translated sequence of *Saccharina latissima* contig\_4304 (SlaPKS). The residues sharing 100, 80 and 60% identity are respectively shaded in black, dark grey and light grey.