

Figure 1

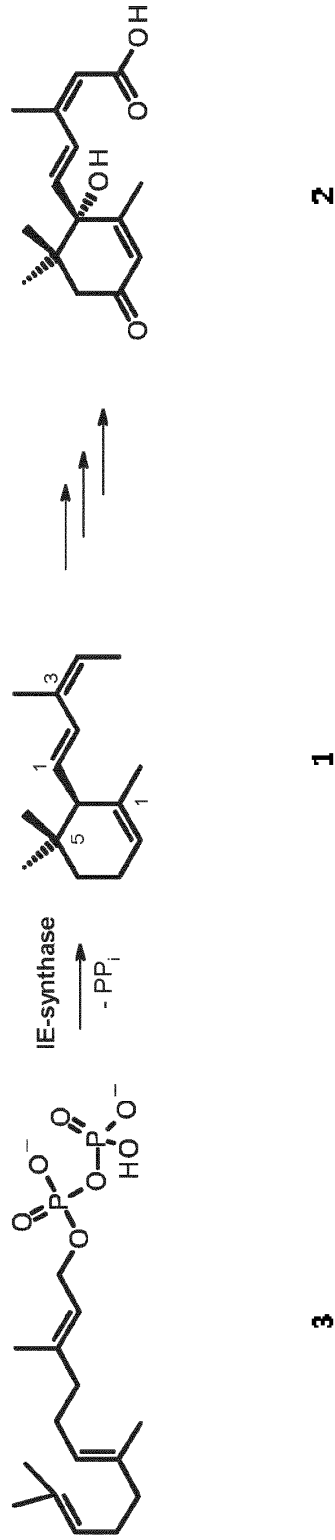


Figure 2

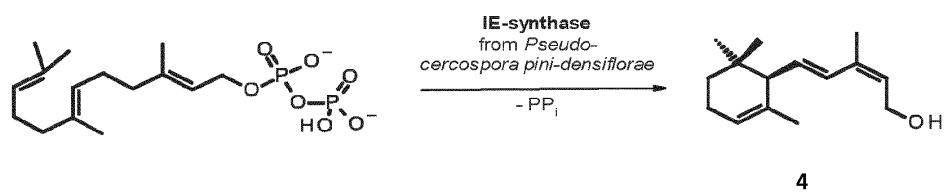


Figure 3

A

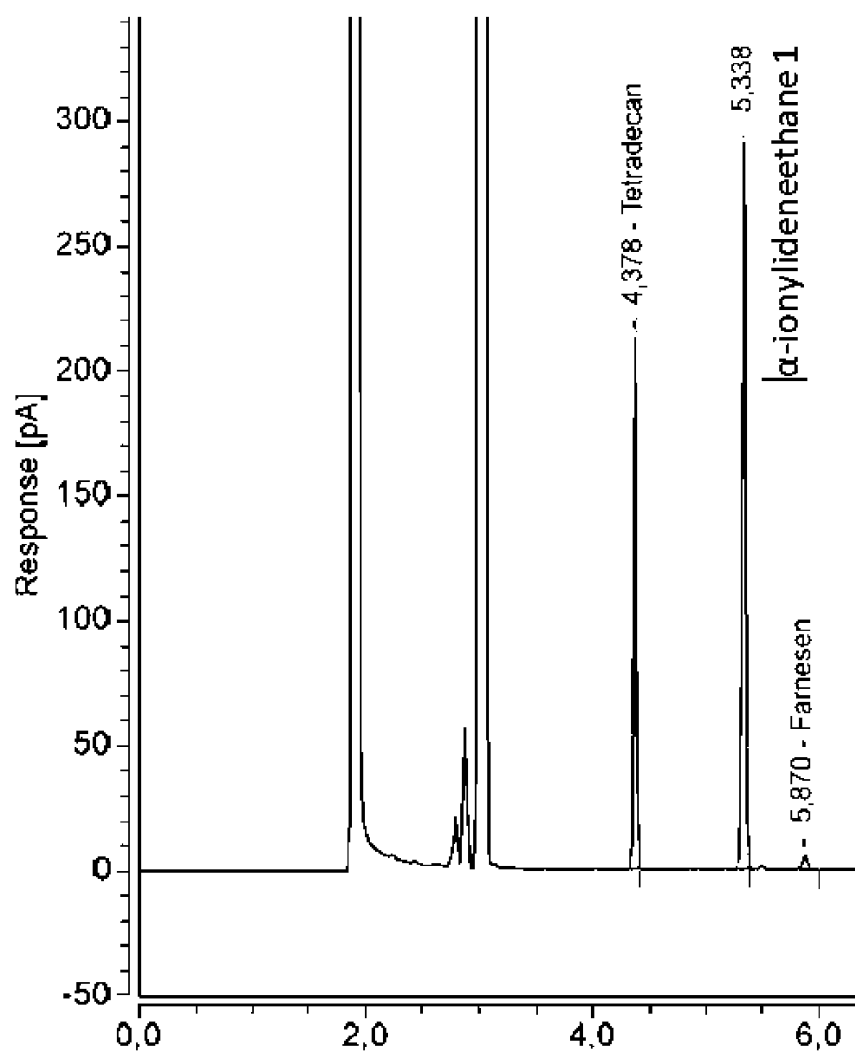


Figure 3

B

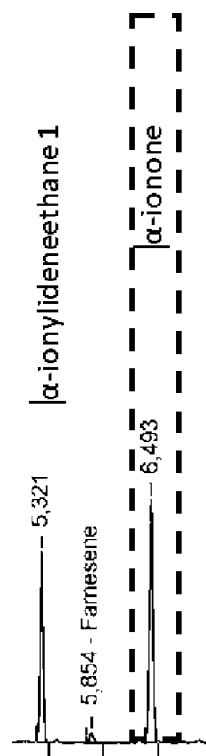


Figure 4

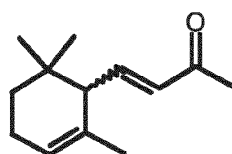


Figure 5

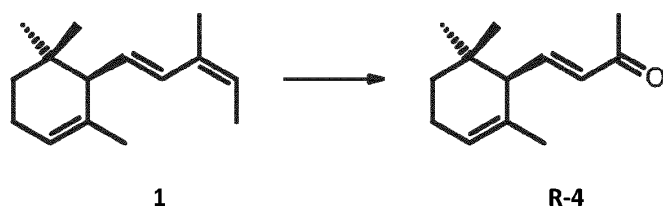
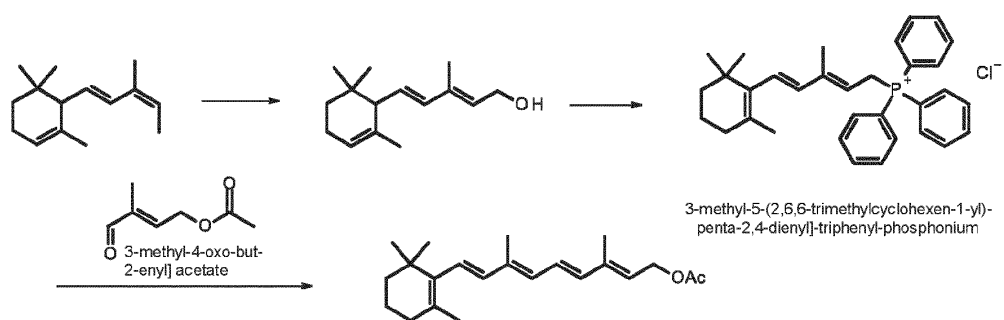


Figure 6



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Multiple alignment using muscle

Figure 7

numbering taken from top sequence

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      10          20          30          40          50
SEQ_1      .....MQQVITQLVDDRFIQISDSKKSEGLATDST...KRQSSEQPIHDKDPIKAATAAMAATPL
SEQ_7      .....MLMT
SEQ_10_EFQ89822 .....MPSARTSSA.....NGPTYDPAARKLE.....P
SEQ_5      .....M
SEQ_14_KNG44597 MSSEFVTKVFANAIGFGIVWTGVLMFHHIRAEPVDRMSSR.....GDQKVAVQTNEPVKE...K
SEQ_4      .....MGQMQSKLGFNAGSSS.....NGKVTETKLASVDVDVKTQI
SEQ_8      .....
SEQ_2      MHLRPPNNMQQVITQLVDDRFLVQLPVSQQTKSETSKGTGIDDKRWVQEQPDPKAGSNQVAAEAMKAAAP
SEQ_12      .....MPKATTE.....SHIRTYTTSISHTK.....M
SEQ_16      .....
SEQ_9      .....MSGKTRYQELWAYPLRLYRSFGKSDTSLTNSP.....GSLLVHPGSITLEQ.....S
SEQ_6      .....MLLYNSFTGELKFTKTKILLRYYSALIDVPR.....DDVIEDACVSKSQ.....A
SEQ_11      .....NHLEQESAESPT.....NGVAT.....H
SEQ_3      .....MALYEVSPEDSRAGT.....AEPNSIPHDQHAH.....K
SEQ_15      .....MSNK.....IEHQT.....A
SEQ_13      MSTFLTKVWAMAIGFGIVWTGVVLFNSFFPKHDQKCAPQ.....SDESVKN.....K
Consensus

      60          70          80          90          100          110          120
SEQ_1      VKEHQDTIYPPDIANDLQSE.NLPaelKQbIFACAwEYRCVpNYTNQNRVAFNRRIIMGIEEAEHRC
SEQ_7      RAEPDRNRFYPRDIEDDLKGT.DLPEEIVaPtlACAwEYRCVpRFIDCDRIaFRIIVIGIEEAEHRC
SEQ_10_EFQ89822 KVTIQNRRTYPPDLSDNLEKDI.DLPEEVGgVfACAwEYRCVpRYTNQNRVAFNRRIIVIGIEEAEHRC
SEQ_5      SPXFRDTIYPPDIANDLNGVTQLPERFKgEAYACAwEYRCVpRYTNQNRVAFNRRIIVIGIEEAEHRC
SEQ_14_KNG44597 AVVVHERFYPPDIANDLNGV.DLPEFRVgGvFATAwEYRCVpRYTNQNRVAFNRRIIVIGIEEAEHRC
SEQ_4      TTPCKDSIYPPDIANDLQGV.DLPaEVAaPvLITAwEYRCVpRYTNQNRVAFNRRIIVIGIEEAEHRC
SEQ_8      .MKIQNEIYPPDIANDLQSE.DLPKNTDdVfACAwEYRCVpRYTNQNRVAFNRRIIVIGIEEAEHRC
SEQ_2      TEHRDRIYPPDIANDLQSV.NLPaelKQbIFACAwEYRCVpNYTNQNRVAFNRRIIVIGIEEAEHRC
SEQ_12      LPKPTDVFRYPPDIANDLQNL.DaAQQAaPvLATSvEYRCVpRYTNQNRVAFNRRIIVIGIEEAEHRC
SEQ_16      .MPEERFfCgDULSKURDS.ALLPaQRAaPtlGQaWYNSGCTVpRYTNQNRVAFNRRIIVIGIEEAEHRC
SEQ_9      VPiVKEKTYPPDIANDLQEH.DLPQRVgEgVfACAwEYRCVpRYTNQNRVAFNRRIIVIGIEEAEHRC
SEQ_6      MQNIRDRTYPPDIANDLQDL.DMPKAMKQbIFACAwEYRCVpRYTNQNRVAFNRRIIVIGIEEAEHRC
SEQ_11      EVTVVNRRTYPPDIANDLQEN.DMPKSMKdEVLATAwEYRCVpRYTNQNRVAFNRRIIVIGIEEAEHRC
SEQ_3      FRKFNDRTYPPDIANDLQDI.DIPKLLAaAYACAwEYRCVpRYTNQNRVAFNRRIIVIGIEEAEHRC
SEQ_15      VIVSNEKTYPPDIANDLQPF.NLSNETIaPtlACAwEYRCVpRYTNQNRVAFNRRIIVIGIEEAEHRC
SEQ_13      AVVVHERFYPPDIANDLQDI.DLPDRVgQbIFACAwEYRCVpRYTNQNRVAFNRRIIVIGIEEAEHRC
Consensus      D WYPPPDIANL I DLP K E ACaWEYTRCIVPQYTNW RYVAFNRRI IGIIEAFRG

      130          140          150          160          170          180          190
SEQ_1      EMVDVTASNLLGVDLDATEAALFEQTPGHKEMAREYKTFLLITADKASERRDGEELFRRYVNAIAQSFRH
SEQ_7      GLVDVAGNLLGVDLDELDTVFACTPGHEEMAREYKTFLLITADKASERCNSELFRRYVNAIAQSRHD
SEQ_10_EFQ89822 SMVDVTAGDEILGYNLSEVLAALFLGTADHENMCRSEYKTFLLITCEATGGKNEELFRRYVNAIAARSQCG
SEQ_5      DEVDVTRSDILGYSLDGTAELEFGTPGHALMAREYKTFLLIVADKASERRDGEELFRRYVNAIAARSQRA
SEQ_14_KNG44597 SEMDVANDNNVVGYSITEVLENTLCGGTAGHV.....ALSKSEFQ
SEQ_4      KEMDVSNQNNMGVDVGSTLATEFEQTPGHDMAREYNSPELITADKSEDRRDGEELFRRYVNAIAQSFRQ
SEQ_8      SIEMDVITAGPKVNLGVDLDELLEYCTPGHDMAREYKAELEFVTSQVVS.HANSELFRRYVNAIAQSFRQ
SEQ_2      EMVDVTASTSILGVDLGGYLAALFEQTPGHKEMAREYKTFLLITADKASERRDGEELFRRYVNAIAQSFRH
SEQ_12      NYVNLIESMDILGYSVNLGIDVVFAGHAGELMGRFAELLMGEXTSEKRNSELFRRYVNAIAQSHNQCG
SEQ_16      EEMVDVSECPVLSGVDVDELTEPRDSAVREDMARSFNAAMLISTESGRDTEEMRRVVDAAHSFRQ
SEQ_9      EEMRVAEETTLGYNMTAAVDELFGQSTKNTENAREFPGCTELLITADKSSNRDTEELFRYSVNAIAQSPQ
SEQ_6      NEMDVITAGDMHGVNLSYVLAALFLGTADHENMCRSEYKTFLLITADKASERRRNSSELFRRYVNAIAARSQDQ
SEQ_11      DMINVAESKMLGVDVQVLAALFKETPGHEAMSRSEFHAELIVADKTSDDRGEELFRRYVNAIAARSQDQ
SEQ_3      SEMVDVITAGNLLGYSLDGTAAALFDUTAGHLMAREYKTFLLIVADKASEGKHSSELFRHYVDSVTLSPRH
SEQ_15      DLPIPEINSXNIGVDLDELSTLECGTSMREDMSREFFTLLMSAEKSRKORDSELFRYVNAIAQSKSGW
SEQ_13      SEMDVANDNNVVGYSITEVLENTLCGGTAGHAENMCRSEYKTFLLMSAQSRHQTNTMLFRYVNAIAQSKSGWQ
Consensus      LVDVTA D LGVDLD VLD LF GT GHE MAREYR FLL TADKSS RR GLFRRYVNAIA SFRQ

      200          210          220          230          240          250          260
SEQ_1      VFRMRDQDLARFTIASALACNDLDDVFTEDQFEILT.EIGDTLYDAVAFYKHRSEGQINSFAYVMEEDL
SEQ_7      VFRMRDQDLARFTIAAAMACNDITDVFSEEEFQELT.EIGDTLYDAVAFYKHRSEGQINSFAYVMEHEL
SEQ_10_EFQ89822 VFRMRDQDLARFTIAAALACNDLDDLEKSDAEYDILLT.EIGNTLYDAIAEFKHRSEGQINSFAYVTPSMM
SEQ_5      VFRMRDQDLARFTMASALACNDLDDVFPDQDFELLAE.EIGDTLYDAVAFYKHRSEGQINSFAYVTPPEI
SEQ_14_KNG44597 VFRMRDQDLARFTGTALVCNDLHIVSEDDQFDIMAR.EIGNTMVYDGISFVKHRSEGQINSFAYVPEEK
SEQ_4      VFRMRDQDLVRYTMACALVSNCHDDVFTEDQFEILS.EYITLYDAVAFYKHRSEGQINSFAYVMEHL
SEQ_8      VFRMRDQDLARFTIASALACNDLDDVFTEDQFEILT.EIGDTLYDAVAFYKHRSEGQINSFAYVMEEDL
SEQ_2      VFRMRDQDLARFTIASALACNDLDDVYVEEYFEILT.EIGDTLYDAVAFYKHRSEGQINSFAYVMEEDL
SEQ_12      VFRMRDQDLARFTIAGASYCNDGSLVNEEDQFILLAE.GDIMVYDAVAFYKHRSEGQINSFAYVMEQDL
SEQ_16      VFRMRDQDLFRFYIAAAIKND.DDTVLTEDENRLIA.EGAGLYDAVAFYKHRSEGQINSFAYVAGAEEL
SEQ_9      VFRMRDQDLARFTLCAALACNDLDSIVYIEKQMETLCE.GATLYDSVAFYKHRSEGQINSFAYVMESSI
SEQ_6      VFRMRDQDLARFTIASALACNDLDDLEKSNMEYELLT.EIGDTLYDAVAFYKHRSEGQINSFAYVMEPBM
SEQ_11      VFRMRDQDLARFTIAGLLACNDMDVYFSDAEPELLT.EADTLVYDAVAFYKHRSEGQINSFAYVMEEDL
SEQ_3      VFRMRDQDLARFTIASALACNDLDDVYVEEYFEILT.EIGDTLYDAVAFYKHRSEGQINSFAYVMEEDL
SEQ_15      VFRMRDQDLARFTIASALACNCFSETPHREELQLVLA.EGTLVYDAVAFYKHRSEGQINSFAYVMEOSCM
SEQ_13      VFRMRDQDLARFTICVALVCNDLHIVSEDDQFDIMAR.EIGNTMVYDGISYKHRSEGQINSFAYVMEETK
Consensus      VFRMRDQDLARFTIA ALACNDLDDVFT E QEIL EIGDTLYDAVAFYKHRSEGQINSFAYV D
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      270      280      290      300      310      320      330
SEQ_1  RIRAYSECDEILWALDAKLRARMEKLANYNFVRFEGCGTHMMRRRYRFPEDLTCKSPEDKYVDQTCN
SEQ_7  SIESYRRCDEALWALDAKLRARMEKLANYNFVRFEGCGTHMMRRRYRFPEDLTCKSPEDKYVDQTCN
SEQ_10_EFQ89822  SCQAFHQADEVLWALDAKLRARMEKLANYNFVRFEGCGTHMMRRRYRFPEDLTCKSPEDKYVDQTCN
SEQ_5  LKAFVRARDEVLWALDAKLRARMEKLANYNFVRFEGCGTHMMRRRYRFPEDLTCKSPEDKYVDQTCN
SEQ_14_KNG44597  CTLAYHKCDEALWALDAKLRARMEKLANYNFVRFEGCGTHMMRRRYRFPEDLTCKSPEDKYVDQTCN
SEQ_4  RIKRYQQSEILWALDAKLRARMEKLANYNFVRFEGCGTHMMRRRYRFPEDLTCKSPEDKYVDQTCN
SEQ_8  CIDAFHRAQDEVLWALDAKLRARMEKLANYNFVRFEGCGTHMMRRRYRFPEDLTCKSPEDKYVDQTCN
SEQ_2  RIRAYSECDEILWALDAKLRARMEKLANYNFVRFEGCGTHMMRRRYRFPEDLTCKSPEDKYVDQTCN
SEQ_12  RIKSFHVARDEILWALDAKLRARMEKLANYNFVRFEGCGTHMMRRRYRFPEDLTCKSPEDKYVDQTCN
SEQ_16  RENAYRAYDEALWALDAKLRARMEKLANYNFVRFEGCGTHMMRRRYRFPEDLTCKSPEDKYVDQTCN
SEQ_9  SCQAFHQADEVLWALDAKLRARMEKLANYNFVRFEGCGTHMMRRRYRFPEDLTCKSPEDKYVDQTCN
SEQ_6  SCQAFHQADEVLWALDAKLRARMEKLANYNFVRFEGCGTHMMRRRYRFPEDLTCKSPEDKYVDQTCN
SEQ_11  SCQAFHQADEVLWALDAKLRARMEKLANYNFVRFEGCGTHMMRRRYRFPEDLTCKSPEDKYVDQTCN
SEQ_3  CTJAFARCADEVLWALDAKLRARMEKLANYNFVRFEGCGTHMMRRRYRFPEDLTCKSPEDKYVDQTCN
SEQ_15  CTENYREYDEILWALDAKLRARMEKLANYNFVRFEGCGTHMMRRRYRFPEDLTCKSPEDKYVDQTCN
SEQ_13  CTMAYHKCDEALWALDAKLRARMEKLANYNFVRFEGCGTHMMRRRYRFPEDLTCKSPEDKYVDQTCN
Consensus  RV A H RE LWALDVAWA P VINF R FGGPIHMMRRRYRFPVEE LTIGRPET VV QTR N

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      340      350      360      370      380      390
SEQ_1  FKLWNRVDANK.....RSVLNTQHYKALIA.NSEELMEPCLAEHMGDCDIDCKYRESNGAE
SEQ_7  LKLWNRVDEVT.....KSTHSEYANVVA.NSEELMEPCLAEHMGDCDIDCKYRESNGAE
SEQ_10_EFQ89822  FKLWNRLEAD.....AGKKNYRFRALVSKGRDTLNEFLAEHMGDCDIDCKYRESNGAE
SEQ_5  FKLWNRVDEADI.HDSNGEGQTIEASSIQHYAVLE.NSEELMEPCLAEHMGDCDIDCKYRESNGAE
SEQ_14_KNG44597  FKLWNRLEDEK.....KTKQKELESLEQYRQVLS.QEKVLEFNGEAMDEKAEEDLCKRQYRESNGAE
SEQ_4  FKLWNRLEDEK.....KTKQKELESLEQYRQVLS.QEKVLEFNGEAMDEKAEEDLCKRQYRESNGAE
SEQ_8  FKLWNRLEDEK.....KTKQKELESLEQYRQVLS.QEKVLEFNGEAMDEKAEEDLCKRQYRESNGAE
SEQ_2  FKLWNRLEDEK.....KTKQKELESLEQYRQVLS.QEKVLEFNGEAMDEKAEEDLCKRQYRESNGAE
SEQ_12  FKLWNRLEDEK.....KTKQKELESLEQYRQVLS.QEKVLEFNGEAMDEKAEEDLCKRQYRESNGAE
SEQ_16  FKLWNRLEDEK.....KTKQKELESLEQYRQVLS.QEKVLEFNGEAMDEKAEEDLCKRQYRESNGAE
SEQ_9  FKLWNRLEDEK.....KTKQKELESLEQYRQVLS.QEKVLEFNGEAMDEKAEEDLCKRQYRESNGAE
SEQ_6  FKLWNRLEDEK.....KTKQKELESLEQYRQVLS.QEKVLEFNGEAMDEKAEEDLCKRQYRESNGAE
SEQ_11  FKLWNRLEDEK.....KTKQKELESLEQYRQVLS.QEKVLEFNGEAMDEKAEEDLCKRQYRESNGAE
SEQ_3  FKLWNRLEDEK.....KTKQKELESLEQYRQVLS.QEKVLEFNGEAMDEKAEEDLCKRQYRESNGAE
SEQ_15  FKLWNRLEDEK.....KTKQKELESLEQYRQVLS.QEKVLEFNGEAMDEKAEEDLCKRQYRESNGAE
SEQ_13  FKLWNRLEDEK.....KTKQKELESLEQYRQVLS.QEKVLEFNGEAMDEKAEEDLCKRQYRESNGAE
Consensus  KLNWRVDA QRYK RS LMFPLAE LE D C C YR SYGAE

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      400      410      420      430      440
SEQ_1  LSEFGGWLDESEERLSRKTYEPCFVERATKVTTELKTHFEVPP.....
SEQ_7  PLGRFGGWLDESEERLSRKTYEPCFVERATKVTTELKTHFEVPP.....
SEQ_10_EFQ89822  TRYFPGGWLDESEERLSRKTYEPCFVERATKVTTELKTHFEVPP.....
SEQ_5  QHSEFGGWLDESEERLSRKTYEPCFVERATKVTTELKTHFEVPP.....
SEQ_14_KNG44597  QAHFPGGWLDESEERLSRKTYEPCFVERATKVTTELKTHFEVPP.....
SEQ_4  TSHEFGGWLDESEERLSRKTYEPCFVERATKVTTELKTHFEVPP.....
SEQ_8  RDHFPGGWLDESEERLSRKTYEPCFVERATKVTTELKTHFEVPP.....
SEQ_2  VSHFPGGWLDESEERLSRKTYEPCFVERATKVTTELKTHFEVPP.....
SEQ_12  GYGFPGGWLDESEERLSRKTYEPCFVERATKVTTELKTHFEVPP.....
SEQ_16  ALGFPGGWLDESEERLSRKTYEPCFVERATKVTTELKTHFEVPP.....
SEQ_9  TSYAFGGWLDESEERLSRKTYEPCFVERATKVTTELKTHFEVPP.....
SEQ_6  TXHFPGGWLDESEERLSRKTYEPCFVERATKVTTELKTHFEVPP.....
SEQ_11  NCHIFGGWLDESEERLSRKTYEPCFVERATKVTTELKTHFEVPP.....
SEQ_3  GTHFPGGWLDESEERLSRKTYEPCFVERATKVTTELKTHFEVPP.....
SEQ_15  IR.RPGGWLDESEERLSRKTYEPCFVERATKVTTELKTHFEVPP.....
SEQ_13  QAHFPGGWLDESEERLSRKTYEPCFVERATKVTTELKTHFEVPP.....
Consensus  E FGGV LC C WR YLES PEEA VFPE

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SEQ_1  .....
SEQ_7  .....
SEQ_10_EFQ89822  .....
SEQ_5  SLPLNGNAPLQNGHANGAVLVAYME.....
SEQ_14_KNG44597  .....
SEQ_4  .....
SEQ_8  .....
SEQ_2  .....
SEQ_12  .....
SEQ_16  .....
SEQ_9  .....
SEQ_6  .....
SEQ_11  .....
SEQ_3  .....
SEQ_15  SDESYPVADWKGTKGSASAAKFDLSKEISQDVLGV.....
SEQ_13  .....
Consensus  .....

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 non-conserved
 ≥ 50% conserved
 all match