

SUPPLEMENTARY DATA

RESEARCH REPORT

Horizontal transfer of a natterin-like toxin encoding gene within the holobiont of the reef building coral *Acropora digitifera* (Cnidaria: Anthozoa: Scleractinia) and across multiple animal lineages

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Input sequences S1

>Coral: *A. digitifera* <XP_015754265.1>
MLSYVECKTGDKPPSNAVEAGFDDGSPYHARGLVEGLTVPKVCVRSENDLHLVEACIPYGSAEHLVHSFEVLTVDDPSA
LTYERCKTGDRPPDNAVQGGFNGGPTYHARGEVGGKIIPGKADVEVARDDFYLKGAYIPYGSSEHRIHDFQVLVMADKIE
HVEFHCDRGLLATNPKVFAVQEVSNSSQPQSKELSYSETVSSSTSSFTHQWGISVSRSAQFSAKLPTVAEGKITTTTTG
SVSLTWGETETFEKTVSGKHPVVAAPFTKVICEVANEATMDVPYTMFKSGKTSGGRWKGVSTWDVKTSFKEEKLNPS
>Coral: *O. faveolata* <XP_020612601.1>
MLSYVCKTGDKPPSNAVEAGFDDGSPYHARGVNDLTIIPGKVGVRSENDHRLVIGACIPYGSAEHRVHSSEVLTVDDPSA
LTYERCKTGDRPPENAVQGGLDGGSPYHARGEVRGKLIIPGKAGVQGTWDDFYLKGACIPYGSREHRIHDFQVLVMADKID
RVEFHCDRGLGATNPKVLAVQEI SNSSQPQSVFEFSYSETVSNSTSTFTHQWGISISRSAFSCLELPTVFKGEISTTTG
SVSLTWGKTETFTQKTVSGKHPVVAAPFTKVICEVANEAMMDVPYTVYFKSGKTSGGMWKGVSTWDVKTSFKEEKLNPP
MK
>Fish: *O. melastigma* <XP_024120858.1>
MYEITKLYWKTWDGSLPGGAVGIHTKNGTQYVSRPTSRGECGYNPNKGPYCYYPFDRKEWKDGSFEIFVNEDDFEDLV
WRDASNGSVPENAVQSAYSPEIYVGRNKDGLGKVRPELQSFYLPWEGKEYPHNNYQVLTYNDFRSQEI SEVKYDIDKGI
ITDHPETVKVTEVSNSSSKVTKTVTFSETITLWNKETS SSGFRLGVQTEISARIPSVVEGKITVSTETHTTEAKTGS
TKTKEFSETLSLDVLPNKTAKISLVAYKCKLNI PFTACL SRTYSNGKTKTNI SGTYTGV EVDNVKAVITDC
>Fish: *S. formosus* <XP_018606101.1>
MVDGRKPNIEAAKDGVDHECFEFTPSIGDIVSPVFEI IKVDFDKGPDLTETPVVVKEDSYNRSVEQKHTFSLSWTKSVS
ETTSWSHTWGLNLSLSEFESFVNMTIEITYSGSYGTSSTKERSITISEQTEVTIPPCKTKI IAKLFIKKNENCSIPFSATI
KKIKADGEESIFTENGIWKGVIYENVTLNLEEEKL
>Fish: *E. lucius* <XP_010875473.1>
MKLSVLVVISLLLLGLSLAQMSASPPGSLRDLVRKSSLGQKASLLNPLLEGRVPLASKGPVQGPLTPSEFEDQOEPSPF
MFGDNVNLQWQNWGSLPTAAVGIYNGYTERTDYICKYKCEAGFYTPSKGPHYCQYPYGAREYYAPEFQVLNIDNFEFVE
WKDSSYGSVPKHSVRTCSGRSTYVGNKYGLGKVVSEFAFFLPWEGDEYWKYQVLTINRDAYSQHISHVKY GIDEVE
IFQYPPETMRLSSVTNNECQEVVKTVTISKTESESTWNI GRITMLGVTAGITAKIPLIGSGGVEFSAEKTQFNRTTM
VEALSHSVSVELRVPNHSCTVRMEGRKITADIPFTARLSRTYRNGETQWTTITGVYDGVQIGEIRAVVDRCEPVDKAP
CP
>Fish: *O. niloticus* <XP_019221680.1>
MKLSVLLSALLLTLSSASLQDIVKKSILREVSLKPELEGRVPEPTGNRNVKLGPLNPADLEQQQDLPSFLFGDNVNLQ
WLTWDGSLPNGAVSIYNGYTERIDYVCKYKCEAGFYNP SLGPYCRYPYGDREYYTPEFEILTNDNFEFLEWKEGSYGS
LQHSVRTCAGVDIYVGNKYGLGKVVQFEAFFLPWEGDEYWKYQVLA INRDIYTQHISDVKYGIDEVTFQYPPETM
RISGITNNECQTVVKTVTITKTSEVETWNI GRATMLGVTGSITAEIPIFIGSGGIELGAEKTQFTRGTI IETLSHSVS
VELTVPNHTCKVRMEGRKIKADIPYARLSRTYHNGETQWTTITGMYDGVQIGEVRAVVDRCEPVIDAKPCP
>Fish: *S. lalndi* <XP_023250770.1>
MPSDEPLLNPPVELAIRRSQVPPTNFEGTNLEWVTWRGFLPNGAVSIYNRRSRRYDYVCKFKCEAGLYSPNLGHYCYYPY
GKKEYISASFQILVNKDNFEFLEWKSSSFGSVTANSVGTCSGSGVYVGRNKYGLGKVVPEQRAFFLPWRGKSYWYRRRYE
VLTMNRGVASEYISDIKYKIESSNIFYFPVTRIRISSITNNACSDVVKVATLSKTSLEHSWEISFSISAGAKNTIKTAI
PSVTDRIEFQPEITLFEFSNGHSKSEEISHSVSVEVDVPSNHHCVRVLRVGHKYKADV PFTAQLTRTYHSGRIVKTVVTGM
FHGIQIGEVSAVVDRCQSVFPKAPCH
>Fish: *A. polyacanthus* <XP_022070850.1>
MKLSVLLSALLSALSASLQDIVKKSQHRKVSLLNPELEGRVPEPTGEVASGPLTPADLEQQQDLPSFLFGDNVNLQ
LTDGALPNGAVSIYNGYTERTDYVCKYKCEAGFYNP SLGPYCRYPYGDREYYAPEFEILTNDNFEFLEWKEDSYGSVP
QHSVRTCTGVGIYVGNKYGLGKVVQFEAFFLPWEGDEYWKYQVLTINRDAYTQHISDVKYAIDEVAIFQYPPETMR
ISGITNNECQTVVKTVTISKETEVEVETWNI GRATMLGITGSITANIPLIGSAGIELSGEKTQFSRGTTVVESLSHSVS
ELKVPNHSCKVRMEGRKIKADIPYARLSRTYRNGETQWTSITGTYDGVQIGEIRAVVDRCEPVPDAQPCP
>Fish: *T. nattereri* <sp|Q66S13|NATT4_THANI>
MKLLVLLVTLVLSWTS AEDVDGQEIILQOHNEDNNHKSSELGEAAPQRTDNETSQLGQETP
TIRVARAYEFSSKNLEWVRWNGHIP SNAVKISNTYVGREYDVC RVGCEAGYYP PPKGGS
CFYPYGFTEQHSKMFHILVNRDNFEILEWKWKTGGEV PENAVKACRDLYVAKNKYGLGK
HQSHHFYLPWKGT EYKYNEYVVLNVNMDVVEQKITNVRYNMKGVEVHKDKPETLRSTSV
KNYQCREATKQVTLEKSTETSQSWDVNSITLGVSTEV SAGIPNIADVSAVSAETSVEI
SHGTSKTESTSHLSVSATIPPNSSCSITMEGCTFKANIPFTGR LTRKY SNGKVTSSSVK
GIYKKVQVGEIQAVLHRCDKIADAKPC
>Insecta: *P. machaon* <XP_014366083.1>
MSEELGTPYKICRVDNCGIRVKVVEGYGPIYAVLHLLAKKCPHVEVYKISLGRLTQIESPGHEPIVQDLNGIDWSIFNE
FFISWYGNIRIRGLIGNQNVLEFNQERKISKVIGFAKLVITITADSPSQCSSDWIFKNPPEIVYLP RCIEIRDSK LHWRS
LDGDKLPANAIIGGFQNDPIYIARAKHRGSLCPGKYIHSQRCA YIAWGFSEHRKDKFEILCGLNVRWVKCKGKNIPENAF
IGGTSEVNNEPLYIGRAKYGSDLICGKVHLLYGTCLYPNGSELEYKSYEILVIPDIPRSIQDSQHCCVSS
>Flatworm: *C. sinensis* <GAA30369.2>
MAKCGRYQMTLSWIPQNGNVPNAAVDAADGGGIYVCRASHGDDIPGKVVPLYGKAYVPYGGEEHEKYSYDVLVCTVGS
HGGGFYAWKANSGGVPKRAVIGGFSSSGEPLYVARGYVDGERVVGKVEHGHDCAYFPYGGKEIASNDYEVLVWEK
>Flatworm: *S. haematobium* <XP_012796705.1> hypothetical
MTTPFYVRQSHLSWVSGTAGKDQPTNGVEADSRIYVARGEVNGHVIPGKPLRIGAAFI PCDGKEHGLCKFEILCNTNVF
PNQSLYNIWIPASDGRVPAGALLAGSTTDGLPLYVARAS INNEMCVGKVNSEYECALMPWGNVEHKVKEYDVLCLIE

>Insecta: *H. halys* <XP_014292736.1>
MERYVGIWIPPSHCVGLQWVPSGGQVPPNAVQAGMDQDGGHIYVGRAFHEGLDIPAKVTPRHGCAFPVYNGVEITKMQY
EVLCSNHVAWKFCRYGEYPPAIRIGNTKDGEPLFLGRMTIDGMTPGKVHPSHRCLYVVPYAGREHSFHEYEILILN

>Mollusca: *C. virginica* <XP_022291764.1>
MAIWTGTTGNEIPEGAMRAGYEADGRPLFIARAPIEGILTPGKCGYHIQGALLPFGCKEQVHVQYEVLVHQTNALGFFDW
HRASNGTVPKEAFQTDKDTYVGRAFYSGSLIPCKISTNPSHRCAYMGSGGKEHNTKEYEVLCOIK

>Bac: *Delta proteobacterium ML8_D* <OPL17283.1>
MIIRKLEYLYPEILSPSFQATREGKDTFSRAYFYRSYSDSDIELRAYPEQGRLYLLHAQDEYDLGELDYCLSFSKAETLF
NWCESRFPELLSPAPQATQMAGEIFYRSYSDTNVLIGTFQRDLYFIDDQGI PYNLQVDPVWDEIVDCPEVLGGVYTIQQ
ACNGRYVDAYTSTAASHEYDLVTRPAQNDTQKWIITPLGNNVYTIQQKYNRYVDAYTYEALSHEYNLVTRGAQDDNTQ
RWIINWVPDDKKFLNIEYLVDEAEIVLNEPTLLHTATLENPTADTQTRSFTYTETIQETS SFQHSAGVEVTLGMEFSAGL
PGVAEGTGWVTVTGRYDFTWGEQKTI TRTYDTCPVVVGPYKTYRVTATITTAQLSVPYVMFFQSEQTGGIYESRGVWHG
VTSWNQRTVIDDITQ

>Bac: *Bacteroidales WCE2008* <WP_079583716.1> aerolysin
MKKTLFLVLMFAFLVASCCKEMILENPVETMESKQNSELSETEQTAVRDSMVPVIMDTNSVLFDLMQRKKNPESTKASSYE
EDEWGRQGLSDALFDLRDVPVYILVNDNAGGRYLTAKRWDWIHKWYEFHRRYFSIPATFEMTSEVPWNDVEAKVFLTYIIP
LVGQYGLKTYFEGNEFYMAVGAKSSNPNDYLYAAEEGSSYEGSFLTPVDGDSFYIESNIVGSDDPKNPTTWNVWNYVL
EAKNSEAHFGKNLYRSNQOFTIVPQGEYVVERIEYKLDGTALVEQLPDFIATWQSTNNTSVAQOQTTSFNETAASKTSSFS
NNMGVSVQVSAKFNGCIPICIVGGEISTTLTGSYSRTWGESTTTTDTDRNYNFPVTIPPHSRVEATARVTRHKMNVRYTAYL
KNPSTGKQLRINGIWEVGDCTDIETSYSQFELATNKLIKEVKMKGVPKTRVSL

>Bac: *Elizabethkingia ursingii* <WP_078403561.1>
MKKIISLLFSSIIILLLSSCSREDGIKNEKNALQASASILNNSGNFIEDRSSSFLLEKDYVNIISKENINGNFYLLTQOG
TNRNATFEKPNNSDNQKFFYLEFPAESNGGISIYTFINGQKYVLTGTGINPATNSLIPKIRDNSFRGTFWQFLGGSTVHPDA
YILQNTGIRYRDNGITTYGVIGNSDASKIFVDKYLQKQEFEIRPIDDFEISLEYDNPDTGTI IKQPDFITTFWYSNN
TSVQQSMTTGFSKRASYSNWSKTTGGSLSVNTTLKTGIP IIAEGKITTTVNTNYSATYKSETMEDTQTYNFP IVIAPR
TSVTATATVGRYLINLNITAKLKGKNTGKLITLKGTVWNGVSDTIKVTLEQRNLDTNSVIATKVLSEVPKTLTKL

>Fungi: *A. ostoyae* <SJL15000.1>
VCPATGEVLFSTRTTADPKFGNYPRGRYHPDQYFSMGFEDMVVVRVEYDVARGKILRVTPHVLANQTLKNNSDDEQEMSFH
FSENVHTSTFQYTTGFTITVGTGTEFSAGLPLVAEGKISVSASQNEWSFGTQKSFSKTYTAQFPVKAGAHKTVRGVSSVQ
QGTLEVPYTIHLVSKSGGVWVETKGIWRGVSTWELHHAISVE

>Fungi: *A. gallica* <PBK88078.1> hemolytic lectin
EVRRVEYDVARGKILRVTPHVLANQTLKNNSDDEQEMSFHSENVHTSTFQYTTGFTITVGTGTEFSAGVPLVAEGKISVS
ASQNEWSFGTQKSFSKTYTAQFPVKAGAHKTVRGVSSVQGTLEVPYTIHLVSKSGGVWVETKGIWRGVSTWEL

>Fungi: *S. stellatus* <KIJ34088.1>
VVSVDYDLSLGIKIVSSQPLVLAASQTLNLSSTSDQMTFTLNQTTTETSQFTYQTFGAVELGKFTFCGLPGLGATDFNVKT
TSSNQSWNETNTFTVSYTATFPVNAKPGATVRAVSTVNKGNLEVPFTMTCKFKDTGIVQTTQGVWRGVSTWDLRHTIRE

>Fungi: *D. corticola* <XP_020135513.1> natterin-like protein
FHFLFEDMDVESIHFDVDKGEIVNSVPLVIARQRLVNDTSVPQSLSSFTFKSEQRESSFEYTRGFAVTVGLEFSAGIPIV
ADGKISVSTTVSSEFKWGTTTTTTESFSDTFNVTAPANSSVIASATVHRYELSVPYTMTLKS RATEYEI KTEGVYHGVSF
HDLVCHYSE

>Fungi: *D. seriata* <KKY14627.1>
GSTKYDDQYFRLFFENMVFKGKIFNVDEGKILDTPPIMLARSNLNNSVSDQKISSTFKEGTENESSFEYTLGFAVEVGT
SFSCGVPLLAEGKIEVSATVSNEFKWGSTTKKVTEFSATFEATAPPHSTVVASATVTRSVMQVPFTMTWTSPHEGYEVKT
EGAYRGVQFYDLKCDYTEPR

>Fungi: *R. clarus* <GBB96646.1>
FFHFTSSNQYDDQYWFIFEDMDIESVEYKIDEGKIKSTALVEIMRQTLSDADMEQTFIFRVDKSEHTSNFEYSSGFT
VKVGTTEFKARIPCVGEFGLNVETSDSQTWTFGYSTEWKKKYTADFSIKAPRKTAVIAYAIKKATLSVPYIMYLKSKKTG
IKVDTHGTYTGVTWDL

>Fungi: *R. irregularis* <PKB97961.1>
YISSDKFDDQYWSFIFEDMIIESVDYKIYVKGKIQTSTKNVLMRQSLTNDTGEQMLSFKVDES VKHTSTFEYLSGFTVKV
RAKFKAEIPFIEETGLNIEATTGNHTWSFGNSTESVKKYTAELSVKVLPKTKIIVEATIKKSILNVPFIMHLKSKETGIK
VDTYGTYSGVTTWDFNNIIREQKINPT

>Fungi: *L. sulphureus* <KZS99944.1>
HTDHYFSFLFEAVHVDKVEYDLKLGRIVSSARRVLASQTFENRTKQLQSTTLELCESETHSGMFEYGAGFNLAAGTTLKA
AVPEVDETGLTGDPYSNREMRWGERNEFVKYVATLRMNADPGETVRAIATI QKGEIEVYPYTMYSSEKTVGKLESKGLV
RGVWTWNL

>Fungi: *A. alternata* <XP_018387235.1>
LDYDINQKQVLSSTPAVVGSSNSQSNNTDSVQTITLTLTETTTTTSTFEHSYGITITGTVSATFGWPSVIEGRVEISVAQT
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Alignment_clustalw S2

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    Coral:_O._faveolata_XP_020612601.1
    Fish:_O._melastigma_XP_024120858.1
    Fish:_S._formosus_XP_018606101.1
    Fish:_E._lucius_XP_010875473.1
    Fish:_O._niloticus_XP_019221680.1
    Fish:_S._lalndi_XP_023250770.1
    Fish:_A._polyacanthus_XP_022070850.1
    Fish:_T._nattereri_sp|Q66S13|NATT4_THANI
    Insecta:_P._machaon_XP_014366083.1
    Flatworm:_C._sinesis_GAA30369.2
    Flatworm:_S._haematobium_XP_012796705.1_hypothetical
    Insecta:_H._halys_XP_014292736.1
    Mollusca:_C._virginica_XP_022291764.1
    Bac:_Delta_proteobacterium_ML8_D_OPL17283.1
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    Bac:_Elizabethkingia_ursingii_WP_078403561.1
    Fungi:_A._ostoyae_SJL15000.1
    Fungi:_A._gallica_PBK88078.1_hemolytic_lectin
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begin characters;
  dimensions nchar=489;
  format missing=? gap=- matchchar=. datatype=protein;
  matrix

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DFYLGKAYIPYGSSEHRIHDFQVLVMADKIEHVEFHCDRGLLATNPKVFAVQEVSNSS
QPQS-----KELSYSETVSSTSSFTHQWGISVSR
SAQFSAKLPTVAEGKITTT--TTGSVSLTWGETETFEKTVSGKHPVVAAPFTKVICE--VVA
NEATMDVPYTYFKSGKT-----SGGRWKGVSTWDVKTSLKKEKLNPS-----
-----

Coral:_O._faveolata_XP_020612601.1
-----
-----MLSYVKCKT
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SEVLTVDGPSALTYERCKTGDRPPENAVQGGLDGGPSYHARGEVRGKLIPGKAGVQGTWD
DFYLGKACIPYGSREHRIHDFQVLVMADKIDRVEFHCDRGLGATNPKVLAHQEISNESS
QPQS-----VEFSYSETVSNTSTFTHQWGISISR
SAKFSCELPTVFKGEISTT--TTGSVSLTWGKTETTFQKTVSGKHPVVAAPFTKVICE--VVA
NEAMMDVPYTYFKSGKT-----SGGMWKGVSTWDVKTSLKKEKLNPPMTK-----
-----

Fish:_O._melastigma_XP_024120858.1
-----
-----
MYEITTKLYWKTWDGSLPGGAVGIHTKNGTQYVSRPTSRGECGYNPNKGPYCYPPFDRK
EWKDGSEFIEFVNEDDFEDLVWRDASNGSVPENAVQSAYSPEIYVGRNKDGLGKVRPELQS
FYLPWEGKEYPHNN-YQVLTYNDFRSQEI SEVKYDIDKGIITDHPETVKVTEVSNSS
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SKVT-----KTVTFSETITLVNKWETS GSFRLGV
QTEISARIPSVVEGKITVS-TETTHTEAKTGSMTKTKEFSETLSLDVLPNK TAKIS-LVA
YKCKLNIPFTA CLSRYSNGKKTNTN ISGTYTGVEVDNVKAVITDC-----

Fish: *S. formosus*_XP_018606101.1

-----MVDR
GKPNIEAAKDGVD EHCFTPSIGDIVSPVFEI IKVDFDKGPDLTETPVVVKEDSYTNRSS
VEQKHT-----FSLSWTKSVSETTSWSHTWGLNTSL
SFEFSFVNMTIEITYSGSY-----GTSSTKERSITISEQTEVTIPP KTKIIAKLFIK
KNENC SIPFSATIKKIKADGEESIFTENGIWKGVIYENVTLNLEEEKL-----

Fish: *E. lucius*_XP_010875473.1

-----MKLSVLVVISLLLLGLSLAQMSASPP
GSLRDLVRKSSLGQKASLLNPLLEGRVPLASKGPVQGPLTPSEFEDQQE-PSPF-----
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EYYAPEFQVLTNIDNFEFVWEKDDSYGSVPKHSVRTCSGRSTYVGKNKYGLGKVVSEFEA
FFLPWEGDEYWKYQVLTINRDAYSQHISHVKYGI DEVEIFQYPPETMRLSSVTNNEC
QEVV-----KTVTISK TSEVESTWNIGRTTMLGV
TAGITAKIPLIGSGGVEFS-AEKT LQFN RGT TMVEALSHSVSVELRVPPNH SCTVR-MEG
RKITADIPFTARLSR TYRNGETQWTTITGVYDGVQIG EIRAVVDRC EPVVD AKPCP-----

Fish: *O. niloticus*_XP_019221680.1

-----MKLSVLLLLSALLTLSSA-----
-SLQDIVKKS IQLREVSLLKPELEGRVPEPTGNR KVLGPLNPADLEQQQDL PSSF-----
LFGDNVNLQWLTWDGSLPNGAVSIYNGYTERIDYVCKYKCEAGFYNP SLGPYCRYPYGDR
EYYTPEFEILT NKNDFEFLEWKEGSYGLPQH SVRTCAGVDIYVGKNKYGLGKVVQFEA
FFLPWEGDEYWKYQVLA INRDIYTQHISDVKYGIDEVTIFQYPPETMRISGITNNEC
QTVV-----KTVTITKTSEVETTWNIGRATMLGV
TGSITAEIPFIGSGGIELG-AEKT LQFTRGTTI IETLSH SVSVELTVPPNH TCKVR-MEG
RKIKADIPYTARLSR TYHNGETQWTTITGMYDGVQIG EVRAVVDRCEPVIDAKPCP-----

Fish: *S. lalndi*_XP_023250770.1

-----QVPPTNF-----
EGT---NLEWVTWRGFLPNGAVSIYNNRRSRRYDYVCKFKCEAGLYSPNLGHYCYYPYGK
EYISASFQILVNKDNFEFLEWKSSSFGSVTANSVGTCSGSGVYVGRNKYGLGKVVPEQRA
FFLPWRGKSYWYRRRYEVLTMNRGVASEYISDIKYKIESSNIFYFPPVTIRISSITNNAC
SDVV-----KVATLSK TSLVEHSWEISF S ISAGA
KNTIKTAIPSVTDRKIEFG-PEITL FSNHGSKSEEISHSVSVEVDVPSNHHCVR-LVG
HKYKADVPFTAQLTRTYHSGRIVKTVVTGMFHGIQIGEVSAVVDR CQSVFPAKPCH-----

Fish: *A. polyacanthus*_XP_022070850.1

-----MKLSVLLLLSALLALSAA-----
-SLQDIVKKS QHRKVSLLNPELEGRVPEPTGEVAS-GPLTPADLEQQQDL PSSF-----
LFGDNVNLWLTWDGALPNGAVSIYNGYTERTDYVCKYKCEAGFYNP SLGPYCRYPYGDR
EYYAPEFEILT NKNDFEFLEWKEDSYGSVPQH SVRTC VGVIYVGKNKYGLGKVVQFEA
FFLPWEGDEYWKYS-QVLTINRDAYTQHISDVKYAIDEVAIFQYPPETMRISGITNNEC
QTIV-----KTVTISK ETETVETTWNIGRATMLGI
TGSITANIPLIGSAGIELS-GEKT LQFSRGTTVVESL SHSVSVELKVPPNH SCKVR-MEG
RKIKADIPYTARLSR TYRNGETQWTSITGTYDGVQIG EIRAVVDRC EPVDAQPCP-----

Fish: *T. nattereri*_sp|Q66S13|NATT4_THANI

-----MKLLVLLVTLVLSWTS-----
-----AEDVGDQEI LQOHNE DNNHKS ELGEAAPQRTDNETS QLGQETPTIRVARAY
EFSSKNLEWVRWNGHIPSN AVKISNTYVGRE DYVCRVGC EAGYTPKKGPSCFYPYGFT
EQHSMFHILVNRDNFEILEWKWKTGGEV PENAVKAC--RDLYVAKNKYGLGKLHQSHHV
FYLPWKGT EYKYNE-YVVLNVNMDVVEQKITNVRYNMKGVEVHKDKPETLRSTSVKNYQC
REAT-----KQV TLEKSTETSQSWDVSNSITLGV
STEVSAGIPNIADVSVAVS-AETSVEISHGTSKTESTSHSLSVSATIPPNSSCSIT-MEG

CTFKANIPFTGRLTRKYSNGKVTSSSVKGIYKVKVQVGEIQAVLHRCDKIADAKPC-----

Insecta: *P. machaon*_XP_014366083.1

-----MSEELGTPYKICRVDNCGI
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EFFISWYGNIIIRIGLIGNQNVLEFNQERKISKVIGFAKLVITITADSPSQLCSDWIFKNP
PEIVYLPRCIEIRDSKLHWRSLDGDKLPANAIIGGFQNDPIYIARAKHRGSLCPGKYIHS
QRCAYIAWGFSEHRKDKFE-----ILCGLNVRWVKCKGKNI PENAFIGGTSEVNNEPL
YIGRAKYGSDLICGKVHLLYGTCTYLPYNGSELEYKSYEILVIPDIPSRSIQDSQHCCVSS

Flatworm: *C. sinesis*_GAA30369.2

-----MAKCGRGYQMTLSWIPCQNGNV-PNAAVD
AA-----DGGGIYVCRASHSGDDIPGKVVPL
YGKAYVPYGGEEHEKYSYDVLCVTGSHGGGF-YAWKANSGGGVPKRAVIGGFSSSG-EPL
YVARGYVDGERVVGKVHEGHDCAYFPYGGKEIASNDYEVLVWEK-----

Flatworm: *S. haematobium*_XP_012796705.1_hypothetical

-----MTTPFYVRQSHLSWVSGTAGKDQPTNGVE
AD-----SRIYVARGEVNGHVIPGKPLPLR
IGAAFIPCDGKEHGLCKFEILCNTNVFPNQSLYNWIPASDGRVPAGALLAGSTTDG-LPL
YVARASINNEMCVGKVNSEYECALMPWGNVEHKVKEYDVLCLIE-----

Insecta: *H. halys*_XP_014292736.1

-----MERYVGWIPPESHCVGTLQWVPSSGGQV-PPNAVQ
AGMD-----QDGGHIYVGRAFHEGLDIPAKVTPR
HGCAFVPYNGVEITKMQYEVLCSNHV-----AWKFCRYGEYPPEAIRIGNTKDG-EPL
FLGRMTMDGTMPGKVHPSHRCLYVPYAGREHSFHEYELILN-----

Mollusca: *C. virginica*_XP_022291764.1

-----MAIWVTTTGNIEIPEGAMRAGYEADGR
PLFI-----ARAPIEGILTPGKCGYH
IQGALLPFGCKEQVVHQYE--VLVHQTNALGFFDWHRASNGTVPKEAFQTDKDTYV----
GRAFYSGSLIPCKISTNPSHRCAYMGGGKEHNTKEYEVLQIK-----

Bac: *Delta proteobacterium*_ML8_D_OPL17283.1

-----MIIRKLEYLYPEILSPSFQATREGKDTFSRAYFYRSYSDSDIE
LRAYPEQGRLLYLLHAQDEYDLGELDYCLSFKAETLFNWCESRFPELLSPAPQATQMAGE
IFYRSYSDTNVLIGTFQRDLYFIDDQGIYPYNLGQVDPWVDEIVDCPEVLGGVYTIQQACN
GRYVDAYTSTAASHEYDLVTRPAQNDDTQKWIITPLGNVYTIQQKYNRYVDAYTYEAL
SHEYNLVTRGAQDDNTQRWIINWVDDKFLNIEYLVDEAEIVLNEPTLLHTATLENPTA
DTQT-----RSFTYTETIQETSSFQHSAGVEVTL
GMEFSAGLPGVAEGTGWVT-VTGRYDFTWGEQKTITRTYTDTCPPVVVGPYKTYRVT-ATI
TTAQLSVPYVMFFQSEQTGGIYE--SRGVWHGVTSWNQRTVIDDITQ-----

Bac: *Bacteroidales_WCE2008_WP_079583716.1_aerolysin*
MKKTLLEFVLMFLVASCGKEMILENPVETMESKQNSELSETEQTAVRDSMVPVIMDTNSV
LFDLMQRKKNPSTKASSYEDEWGRQGLSDALFDLRDVPVYILVNDNAGGRYLAKRDW
IHKWYEFHRRYFSPATFEMTSEVPWINDVEAKVFYLYIPLVGQYGLKTYFEGNEFYMAV
GAKSSNPNDYYLYAEEGGSSYEGSFSLTPVDGDSFYIESNIVGSDDPKNPTTWNVWNYVL
EAKNSEAHFGKNLYRSNQOFTIVPQGEYVVERIEYKLDGTALVEQLPDFIATWQSTNNTS
VAQQ-----TTTSFNETASKTSSFSNNMGVSVQV
SAKFNCGIPCIVGGEISTT-LTGSYSRTWGESTTTTDDTRNYNFPVTIPPHSRVEAT-ARV
TRHKMNVRYTAYLKNPSTGKQLR---INGIWEGVDCTDIETSYSQFELATNKLIKEVKMK
GVPKTRVSL

Bac: *Elizabethkingia_ursingii_WP_078403561.1*
-----MK
KIISLLFSSIIILLSSCSREDGKNEKNALQASASILNNSGNFIEDRSSSFLELKDYPV
NIISKENINGNFYLTQTGRNATFEKPNNSDNQKFYLEFFAESNGGISIYTFINGQKYV
LTTGINPATNSLIPKIRDNSFRGTFWQFLGGSTVHPDAYILQNTGIRYRDNGITTYGVIG
NSDASKIFVDKYLKSGKQEFEIFRPIIDDFEIIISLEYDNDPTGTIIKQPDFITTFYSNNTS
VQQS-----MTTGFSKRASYSSNWSKTTGGSLSV
NTTLKTGIPIIAEGKITTT-VNTNYSATYKSETMEDTQTYNFPVIVAPRTSVTAT-ATV
GRYLINLNYTAKLKGKNTGKLITL---KGTWNGVSCDIIKVTLEQRNLDTNSVIATKVLS
EVPKTYLKL

Fungi: *A._ostoyae_SJL15000.1*

-----VCPATGEVLFSR
TTADPKFGNYPRGRYHPDQYFSMGFEDMVVKRVEYDVARGKILRVTPHVLANQTLKNNSD
DEQE-----MSFHFSENVTHSTFQYTTGFTITV
GTEFSAGLPLVAEGKISVS-ASQSNEWSFGTQKSFSKTYTAQFPVKAGAHKTVRGV-SSV
QQGTLEVPYTIHLVSKSGGVWVE---TKGIWRGVSTWELHHAISVE-----

Fungi: *A._gallica_PBK88078.1_hemolytic_lectin*

-----EVRRVEYDVARGKILRVTPHVLANQTLKNNSD
DEQE-----MSFHFSENVTHSTFQYTTGFTITV
GTEFSAGLPLVAEGKISVS-ASQSNEWSFGTQKSFSKTYTAQFPVKAGAHKTVRGV-SSV
QQGTLEVPYTIHLVSKSGGVWVE---TKGIWRGVSTWEL-----

Fungi: *S._stellatus_KIJ34088.1*

-----VVSVDYDLSLKGIVSSQPLVLASQTLTNLST
SDQQ-----MTFTLNQTTTETSQFTYQTGFVEL
GTKFTCGLPGLGATDFNVK-TTSSNQWSWNETNTFTVSYTATFPVNAKPGATVRAV-STV
NKGNEVPFTMTCKFKDITVQ---TQGVWRGVSTWDLRHTIRE-----

Fungi: *D._corticola_XP_020135513.1_natterin-like_protein*

-----FHFLFEDMDVESIHFDVDKGEIVNSVPLVIARQRLVNDTS
VPQS-----LSSTFTKSEQRESSFEYTRGFAVTV
GLEFSAGIPIVADGKISVS-TTSSSEFKWGTTTTTTESFSDTFNVTAPANSVVIAS-ATV
HRYELSVPYTMTLKSRAEYIEIK---TEGVYHGVSFHDLVCHYSE-----

Fungi: *D._seriata_KKY14627.1*

-----GSTKYDDQYFRLFFENMVFKGIKFNVDEGKILDTPIMLARSNLSNNS
VDQK-----ISSTFKEGTENESSFEYTLGFAVEV
GTSFSCGVPLLAEGKIEVS-ATVSNEFKWGSTTKKVTEFSATFEATAPPHSTVVAS-ATV
TRSVMQVPFTMTWTSPEHGYEVK---TEGAYRQVQFYDLKCDYTEPR-----

Fungi: *R. clarus*_GBB96646.1

-----FFHFTSSNQYDDQYWTFIFEDMDIESVEYKIDEGKIKSTALVEIMRQTLSDAD
MEQT-----FIFRVKSETHSTNFEYSSGFTVKV
GTEFKARIPCVGEFGLNVE-TTDSQTWTFGYSTEWKKKYTADFSIKAPPRTKVIAV-AYI
KKATLSVPYIMYLKSKKTGIKVD---THGTYTGVTTWDL-----

Fungi: *R. irregularis*_PKB97961.1

-----YISSDKFDDQYWSFIFEDMIIESVDYKIYVGKIQSTKNVLMRQSLTNDTD
GEQM-----LSFKVDESVKHTSTFEYLSGFTVKV
RAKFKAEIPFIEETGLNIEATTGNHTWSFGNSTESVKKYTAELSVKVLPKTKIIVE-ATI
KKSILNVPFIMHLKSKETGIKVD---TYGTYSGVTTWDFNNIIREQKINPT-----

Fungi: *L. sulphureus*_KZS99944.1

-----HTDHYFSFLFEAVHVDKVEYDLKLGRIVSSARRVLASQTFENRTK
QLQS-----TTLELCESETHSGMFEYAGAGFNLA
GTTLKAAPVEVDETLTGD-PYSNREMRWGERNEFVKKYVATLRMNADPGETVRAI-ATI
QKGEIEVFPYTMYSSEKTGVKLE---SKGLWRGVWTTWNLN-----

Fungi: *A. alternata*_XP_018387235.1

-----LDYDINQQKVLSSSTPAVVSNSQSNNTD
SVQT-----ITLTLTETTTTTSTFEHSYGITITG
TVSATFGWPSVIEGRVEIS-VAQTKDFKWKQNTETKTATLEIAATAKPFKVTAI-ATA
TKSDIELPFTITWKSKKTGYEVK---SKGVYKGTSYWNTTTDLKQNQ-----

;
end;

Aligment_muscle S2b

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  taxlabels
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    Coral:_O._faveolata_XP_020612601.1
    Fish:_O._melastigma_XP_024120858.1
    Fish:_S._formosus_XP_018606101.1
    Fish:_E._lucius_XP_010875473.1
    Fish:_O._niloticus_XP_019221680.1
    Fish:_S._lalndi_XP_023250770.1
    Fish:_A._polyacanthus_XP_022070850.1
    Fish:_T._nattereri_sp|Q66S13|NATT4_THANI
    Insecta:_P._machaon_XP_014366083.1
    Flatworm:_C._sinesis_GAA30369.2
    Flatworm:_S._haematobium_XP_012796705.1_hypothetical
    Insecta:_H._halys_XP_014292736.1
    Mollusca:_C._virginica_XP_022291764.1
    Bac:_Delta_proteobacterium_ML8_D_OPL17283.1
    Bac:_Bacteroidales_WCE2008_WP_079583716.1_aerolysin
    Bac:_Elizabethkingia_ursingii_WP_078403561.1
    Fungi:_A._ostoyae_SJL15000.1
    Fungi:_A._gallica_PBK88078.1_hemolytic_lectin
    Fungi:_S._stellatus_KIJ34088.1
    Fungi:_D._corticola_XP_020135513.1_natterin-like_protein
    Fungi:_D._seriata_KKY14627.1
    Fungi:_R._clarus_GBB96646.1
    Fungi:_R._irregularis_PKB97961.1
    Fungi:_L._sulphureus_KZS99944.1
    Fungi:_A._alternata_XP_018387235.1
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end;
begin characters;
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  matrix

Coral:_A._digitifera_XP_015754265.1
-----MLSYVECK-----TGDKPP
-----SNAVEAGFDD-----G--PSYHARGLVEGLTV
PGK-----VC-----VRSENDLHLV-----EACI--PYGSAEHLV
-----HSFEVL---TVDD---PSALT---YERCKTG---DRPP---D---NAV----QG
GF--NGG--PTYHA-----RG--EV-----GGKII-PGK-----ADVEVARDDFYL
KGAYI-----P-----Y-----GSSEHRI----HDF----QVL-----
-VMADKIEH-----VEFH-CDRGK-L-----LATNPKVFAVQEVSNSSQPQ
SKELSYS--ETVSSTSSF---THQW-GISV--SRSAQF-SAK---LP--TVAEGKITTT-
TTG-SV-SLT--WGTEETF--EKTVSGKH-PVVA--APFTKVICEVVANEAT-MDVPYT-
---MYFKSGKT-----SGGRWKGVs--TWD-----VKTS--FKEEKL--NPSS----

Coral:_O._faveolata_XP_020612601.1
-----MLSYVKCK-----TGDKPP
-----SNAVEAGFDD-----G--PSYHARGVVNDLTI
PGK-----VG-----VRSEND-HRLV-----GACI--PYGSAEHRV
-----HSSEVL---TVDD---PSALT---YERCKTG---DRPP---E---NAV----QG
GL--DGG--PSYHA-----RG--EV-----RGKLI-PGK-----AGVQGTW-DDFYL
KGACI-----P-----Y-----GSREHRI----HDF----QVL-----
-VMADKIDR-----VEFH-CDRGK-L-----GATNPKVLAVQEISNESSQPQ
SVEFSYS--ETVSNTSTF---THQW-GISI--SRSAKF-SCE---LP--TVFKGEISTT-
TTG-SV-SLT--WGKTETF--QKTVSGKH-PVVA--APFTKVICEVVANEAM-MDVPYT-
---VYFKSGKT-----SGGMWKGVs--TWD-----VKTS--LKEEKL--NPPTMK--

Fish:_O._melastigma_XP_024120858.1
-----MYEITK-----
-----KLYW-KTWDGSLPG----GAVG-IHT
KNGT-----QYVS-----RPTSRGECG-YY--NP--NKG--PYCYY-PFDRKEWKD
```

-----GSFEIF---VNED--DFEDLV---WRDASNG-----S-VP---E--NAV----QS
AYSP-----EIYVG-----RN--KD-----GL-----GK-----VRPEL-QSFYL
-----P-----WE-----G-KEYPH-----NNY----QVL---TYNT
DFRSQEISE-----VKYD-IDKGI-I-----TDSHPETVKVTEVSNNSSSKV
TKTVTFS--ETITLVNKW---ETSG-SFRL--GVQTEI-SAR---IP--SVVEGKITVS-
TET-THTEAK--TG-SMTK--TKEFSETL-SLDV--LPNKTAKISLVAYKCK-LNIPFTA
CLSRYSNGKK-TKTNISGTYTGVEVDNVKAV-----ITDC-----

Fish: *S. formosus*_XP_018606101.1

-----MVD-----RGK---
-----PNIEAAKDG-----
-----VD-----EHCEF-----
-----TP-----SI-----
-----GD-----IVSPV-----
-----F-----EI-----
-----IK-----VDFD--KGPDL-----TET-PVVVKEDSYTNRSSVEQ
KHTFSLSWTKSVSETTSW---SHTW-GLNT--SLSFEF-S-----FV-NMTIEIT-
YSG-S-----YGTSSTKERSITISEQT-EVTI--PPKTKIIAKLFIKKNENCSIPFSA
TIKKIKADGEESIFTE-NGIWKGV---IYEN-----VTLN--LEEEKL-----

Fish: *E. lucius*_XP_010875473.1

-MKLSVLVVISL LLLGLSLAQMSASPPGSLRDLVRKSSSLGQKASLLNPLL----EGRVPP
-LASKGPVQGPLTPSEFED-QQE-PSPFMFGDNVNLQW-QNWTGSLPT----AAVG-IY-
-NGYTERT-DYIC-----KVKCEAG-FY---TP---SKG--PYCQY-PYGAREYYA
-----PEFQVL---TNID--NFEFVE---WKDDSYG-----S-VP---K--HSV----RT
C---SGR--STYVG-----KN--KY-----GL---GK-----VVSEF-EAFFL
-----P-----WE-----G-DEYWY---KNY----QVL---TINR
DAYSQHISH-----VKYG-IDEVE-I-----FQYPPETMRLSSVTNNECQEV
VKTVTIS--KTSEVESTW---NIGR-TTML--GVTAGI-TAK---IP--LIGSGGVEFS-
AEK-TL-QFN--RGTTMVE--ALSHSVSV-ELRV--PPNHSCVTRMEGRKIT-ADIPFTA
RLSRTYRNGET-QWTTITGVYDGVQIGEIRAV-----VDRCEPVVDAKP--CP-----

Fish: *O. niloticus*_XP_019221680.1

-MKLSVLLLSALLTL-----SSA---SLQDIVKKSIIQLREVSLLKPEL----EGRVPE
PTGNRQVL-GPLNPADLEQ-QQDLPSFLFGDNVNLQW-LTWDGSLPN----GAVS-IY-
-NGYTERI-DYVC-----KVKCEAG-FY---NP---SLG--PYCRY-PYGDREYYT
-----PEFEIL---TNKD--NFEFLE---WKEGSYG---S-LP---Q--HSV----RT
C---AGV--DIYVG-----KN--KY-----GL---GK-----VVPQF-EAFFL
-----P-----WE-----G-DEYWY---KNY----QVL---AINR
DIYTOHISD-----VKYG-IDEVT-I-----FQYPPETMRISGITNNECQTV
VKTVTIT--KTSEVETTW---NIGR-ATML--GVTGSI-TAE---IP--FIGSGGIELG-
AEK-TL-QFT--RGTTIIE--TLSHSVSV-ELTV--PPNHTCKVRMEGRKIK-ADIPYTA
RLSRTYHNGET-QWTTITGMVDGVQIGEVRAV-----VDRCEPVIDAKP--CP-----

Fish: *S. lalndi*_XP_023250770.1

-----MPSDEPLLNPV---E-----
----LAIRRSQVPPPTNFEG-T-----NLEW-VTWRGFLPN----GAVS-IY-
-NRRSRRY-DYVC-----KFKCEAG-LY---SP---NLG--HYCYY-PYGKKEYIS
-----ASFQIL---VNKD--NFEFLE---WKSSSFG---S-VT---A--NSV----GT
C---SGS--GVYVG-----RN--KY-----GL---GK-----VVPEQ-RAFFL
-----P-----WR-----G-KSYWY---RRRY----EVL---TMNR
GVASEYISD-----IKYK-IESSN-I-----FYFPPVTIRISSITNNACSDV
VKVATLS--KTSLEHSHW---EISF-SISA--GAKNTI-KTA---IP--SVTDRKIEFG-
PEI-TL-EFS--NGHSE--EISHSVSV-EVDV--PSNHHCVRVLVGHKIK-ADVPFTA
QLTRTYHSGRIVK-TVVTGMFHGIQIGEVSAV-----VDRCQSVPAKP--CH-----

Fish: *A. polyacanthus*_XP_022070850.1

-MKLSVLLLSALLAL-----SAA---SLQDIVKKSQRKVSLLNPEL----EGRVPE
PTG--EVASGPLTPADLEQ-QQDLPSFLFGDNVNLQW-LTWDGALPN----GAVS-IY-
-NGYTERT-DYVC-----KVKCEAG-FY---NP---SLG--PYCRY-PYGDREYYA
-----PEFEIL---TNKD--NFEFLE---WKEDSYG---S-VP---Q--HSV----RT
C---TGV--GIYVG-----KN--KY-----GL---GK-----VVPQF-EAFFL
-----P-----WE-----G-DEYWY---KSY----QVL---TINR
DAYTOHISD-----VKYA-IDEVA-I-----FQYPPETMRISGITNNECQTI
VKTVTIS--KETEVEETW---NIGR-ATML--GITGSI-TAN---IP--LIGSAGIELS-
GEK-TL-QFS--RGTTVVE--SLSHSVSV-ELKV--PPNHSCVTRMEGRKIK-ADIPYTA
RLSRTYRNGET-QWTSITGTYDGVQIGEIRAV-----VDRCEPVPDAQP--CP-----

Fish: *T. nattereri*_sp|Q66S13|NATT4_THANI
-MKLLVLLVTLVLSW-----TSAEDVGDQEILQQHNEDNN---HKSEL----GEEAPO
-----RTDNETSQLGQETPTIRVARAYEFSSKSNLEW-VRWNGHIPS----NAVK-IS-
-NTYVGRE-DYVC-----RVGCEAG-YY---TP---KKG--PSCFY-PYGFTEQHS
-----KMFHIL---VNRD--NFEILE---WKWKTGG-----E-VP---E--NAV----KA
C-----R--DLYVA-----KN--KY-----GL---GK-----LHQSH-HV FYL
-----P-----WK-----G-TEYKY---NEY---YVL---NVNM
DVVEQKITN-----VRYN-M-KGVEV-----HKDKPETLRSTSVKNYQCREA
TKQVTLE--KSTETSQSW---DVSN-SITL--GVSTEV-SAG---IP--NIADSVAVS-
AET-SV-EIS--HGTSKTE--STSHLSV-SATI--PPNSSCSITMEGCTFK-ANIPFTG
RLTRKYSNGKVTS--SSVKGIYKKVQVGEIQAV-----LHRCDKIADAKP--C-----

Insecta: *P. machaon*_XP_014366083.1
-----MSEELGTPYKICRV-----
-----DNCGIRVKVKEGYGP-----IYA
VLHLLAKKCPHVE-----VYKISLGRLTQIESP-----GHEPIVQ--DLNGIDWSI
-----FN-----EFFIS---W---YG-----NII---RI
GLIGNQNVLEFNQE-----RKISKV-----IGF---AK-----LVTITADS---
-----PSQLC-----SSDWI-----FKNPPEIV---YLPR
---CIEIRDSK-----LHWRSLD-GDKLPANAIIGGFQNDPIYIARAKHRGSLCPGK
---YIHS--QRCAI--AWGFSEHRKDKFEILCGLNVRWVKCKGNIPENAFIGGTSEVN-
NE--PL--YI--GRAK-----YGSDL-----IC-GKVHLLYGT-CYLPY--
-----NGSE---LEYKS-YEILVIPDIP-----SRS--IQDSQH--CCVSS---

Flatworm: *C. sinesis*_GAA30369.2
-M-----
-----AKC-----GRGYQMT
-----LS---WIPCQNG---NVP---N--AAV---DA
A---DGG--GIYVC-----RASHS-----GDDI-PGK-----VVP-----LY-
-----G-----KAY-----
-----VPYG---GEEH-----EKYSYDVL-----CVTG
SHGGGFY-----AW--KANS-G---G-----G--VPKRAVIGG---FS-
SSGEPL--YV-ARGYVDGE---RVVGKV-----HEGHDC-----AYFPY--
-----GGKE---IASND-YEVL---VWE-----K-----

Flatworm: *S. haematobium*_XP_012796705.1_hypothetical

-----MTTPF--YVRQSHLS
-----WVSGTAG---KDQP---T--NGV---EA
---DSR---IYVA-----RG--EV-----NGHVI-PGK-----LP-----LRI
-----G-----AAF-----
-----IP--CD-GKEH-----GLCKFEIL-----CNTN
V---FP-----NQSL---YNW-----IP---ASDGRV---
PAG-AL--LA--GSTTDG--LPLYVARA-SIN-----NEMCVGKVN-SEYECALMPW--
-----GN---VE---HK-VK--EYD-----V-LC--LIE-----

Insecta: *H. halys*_XP_014292736.1
-----MERYV-----
-----GWIPP-----
-----SHCV---GTLQ--
-----WVPSSGG---QVPP-----NAV---QA
GMDQDGG--HIYVG---RAFHE-----GDLI-PAK-----VTPRH-----
-----G-----CAF-----
-----VPYN---GVEI-----TKMQYEVL-----CSNH
V-----AW---KFCRYG-----EY-----PPEAI---RIGNT-
KDGEPL--FL--GRTMID-----GTMTPGKV--HPSHRC-----LYVPYA-
-----GREHSFHE---YEIL---ILN-----

Mollusca: *C. virginica*_XP_022291764.1

-----MAI-----
-----WV-TTTG---NEIP---E--GAM---RA
GYEADGR--PLFIA-----RAPIE-----GILT-PGK-----
-----CGY-----
-----HIQ GAL-----LPFG-CKEQV-V-----HQY--EVL-----VHQ

TNALGFF-----DW---HRASNGT-----VP-----KEAFQ-
TDK-D--TYV---GRA--F-----YSGSLIPCKISTNPSHRC-----AYM-
-----G-----SGGKEHNTK--EYE-----V-LCQ- IK-----

Bac: *Delta_proteobacterium_ML8_D_OPL17283.1*

-----MIIRKLEYLYPEI-----
-----LSPSFQATREG-KDTFSRAYFYRSYSDS--IELRAYPEQ---GRLYLLHA
QDEYDLGELDY-CLSFKAETLFWNCESE-FPELLSPAPQATQMAGEIFYRSYSDTNVL I
-----GTFQRDLYFIDDQGI PYNLGQVDPWVDEIVD-----CP---EVLGGVYTIQQA
C---NGRYVDAYTS-----TAASHEY-----DLVTRPAQNDDTQKWIITPLGNNVYT
IQK-----YNNRYV-----DAYTYEALSHEY----NLVTRGAQDD
NT-QRWIINWVPDDKFLNIEYL-VDEAE-I-----VLNEPTLLHTATLENPTADTQ
TRSFTYT--ETIQETSSF---QHTSA-GVEV--TLGMEF-SAG---LP--GVAEGTGWVT-
VTG-RY-DFT--WGEQKTI--TRTYTDTTC-PVVV--GPKYTYRVTATITTAQ-LSVPYV-
---MFFQSEQTGGIYESRGVWHGVT--SWN-----QRTV--IDBITQ-----

Bac: *Bacteroidales_WCE2008_WP_079583716.1_aerolysin*

-MKKTLFLVLMFAFLVA-----SCGKEMILENPVETMESKQNSLSETEQTAVRDSMVPV
-----IMDTNSVLFDLMQRKKNEPSTKA-SSYEEDW--GRQGLSDALFDLRDVP-VYI
LVNDNAGG-RYLT-----AKRD-WI-----HKWY-EFHRRYFSI
-----PATFEM--TSEV--P-----WNDVEAKVLYTYIPLVGQ--YGL---KT
YF--EGN--EFYMAVGAKSSNP--DYLYAEEGSSY-EGS-----FSLTPVDGDSFYI
ESNIVGSDDPKNPTTWNVWNYVLEAKNSEAHFGKNLYRS---NQF---TIVPQG---
---EYVVER-----IEYK-LD-GTAL-----VEQLPDFIATWQSTNNTSVAQ
QTTTSFN--ETASKTSSF---SNNM-GVSV--QVSAKF-NCG---IP--CIVGGEISTT-
LTG---SYRTWGESTTTTDRNYN--F-PVTI--PPHSRVEATARVTRHK-MNVRYT-
---AYLKNPSTGKQLRINGIWEVGDCTDIETSYQFELATNKLIKEVKMGVPKTRVSL

Bac: *Elizabethkingia_ursingii_WP_078403561.1*

MKKIISLLFSSIIILILLS---SCSREDGIGN--EKNALQASASILNN-----SGNF--
-----IEDRSSSFLLELKD---YPVNIISKENINGNFYLLTQGTNRN-----AT-FEK
PNNSDNQK-FYLE-----FP---AESNGGISIY-TFINGQKYV
LTTGINPATNSLIPKIRDN--SFRGTF--WQFLGGS---TVHP-----DA
YILQNTG--IRYRD-----NGITTY-----GVI--GN-----SDASKIFV
-----DKYLSQG-KQEF---EIRPID---
---DFEIIIS-----LEYDNPDGT-I-----IK-QPDFITTWFYNSNTSVQQ
SMTTGFS--KRASYSSNW---SKTT-GGSL--SVNTTL-KTG---IP--IIAEGKITTT-
VNT---NYSATYKSETMEDTQTYN--F-PIVI--APRTSVTATATVGRYL-INLNYT-
---AKLKGKNTGKLITLKGTVWGVSCDIDIKVTLEQRNLDNNSVIATKVLSEVPKTLTKL

Fungi: *A._ostoyae_SJL15000.1*

-----VC-----PAT-----G-----
-----EVL-----FSRTTAD-----P-----KF
GNYPRGR---YHP-----DQYFS
-----MGF---E-----
---DMVVKR-----VEYD-VARGK-I-----LRVTPHVLANQTLKNNSDDEQ
EMSFHFS--ENVTHSTSF---QYTT-GFTI--TVGTEF-SAG---LP--LVAEGKISVS-
ASQ-SN-EWS--FGTQKSF--SKTYTAQF-PVKA--GAHKTVRGVSSVQQGT-LEVPYT-
---IHLVSKSGGVWVETKGIWRGVS--TWE-----LHHA--ISVE-----

Fungi: *A._gallica_PBK88078.1_hemolytic_lectin*

-----EVRR-----VEYD-VARGK-I-----LRVTPHVLANQTLKNNSDDEQ
EMSFHFS--ENVTHSTSF---QYTT-GFTI--TVGTEF-SAG---VP--LVAEGKISVS-
ASQ-SN-EWS--FGTQKSF--SKTYTAQF-PVKA--GAHKTVRGVSSVQQGT-LEVPYT-
---IHLVSKSGGVWVETKGIWRGVS--TWE-----L-----

Fungi: *S._stellatus_KIJ34088.1*

-----VVS-----VDYD-LSLGK-I-----VSSQPLVLASQTLTNLSTSDQ
QMTFTLN--QTTTETSQF---TYQT-GFAV--ELGTKF-TCG---LP--GLGATDFNVK-
TTS-SN-QWS--WNETNTF--TVSYTATF-PVNA--KPGATVRAVSTVNKGN-LEVPFT-
--MTCKFKDGTITVQIQGVWRGVS--TWD-----LRHT--IRE-----

Fungi: *D. corticola*_XP_020135513.1_natterin-like_protein

-----FH-----FL
-----F---E-----
---DMDVES-----IHFD-VDKGE-I-----VNSVPLVIARQLVNDTSVPQ
SLSSTFT--KSEQRESSF---EYTR-GFAV--TVGLEF-SAG---IP--IVADGKISVS-
TTV-SS-EFK--WGTTTTT--TESFSDTF-NVTA--PANSSVIASATVHRYE-LSVPYT-
---MTLKSRAVEYEIKTEGVYHGVS--FHD-----L-VCH-YSE-----

Fungi: *D. seriata*_KKY14627.1

-----GSTKY--
-----D-----
-----DQYF-----R-----LF-
-----F---E-----
---NMVFKG-----IKFN-VDEGK-I-----LDTTPIMILARSNLSNNSSVDQ
KISSTFK--EGTENESSF---EYTL-GFAV--EVGTSF-SCG---VP--LLAEGKIEVS-
ATV-SN-EFK--WGSTTKK--VTEFSATF-EATA--PPHSTVVASATVTRSV-MQVPFT-
---MTWTSPEHGYEVKTEGAYRGVQ--FYD-----L-KCD-YTEPR-----

Fungi: *R. clarus*_GBB96646.1

-----FF-----HFTSSNOY-
-----DD--QY-----W-----
-----TFI-----
-----F---E-----
---DMDIES-----VEYK-IDEKG-I-----KSTALVEIMRQTLSDADMEQ
TFIFRVD--KSEHTSNF---EYSS-GFTV--KVGTEF-KAR---IP--CVGEFGLNVE-
TTD-SQ-TWT--FGYSTEW--KKKYTADF-SIKA--PPRTKVIAVAYIKKAT-LSVPYI-
---MYLKS KKTGIKVDTHGTYTGVT--TWD-----L-----

Fungi: *R. irregularis*_PKB97961.1

-----YISSDKF-
-----DD--QY-----W-----
-----SFI-----
-----F---E-----
---DMIIES-----VDYK-IYVGK-I-----QSTKNVLMRQSLTNDTDGEQ
MLSFKVD--ESVKHTSTF---EYLS-GFTV--KVRAKF-KAE---IP--FIEETGLNIEA
TTG-NH-TWS--FGNSTES--VKKYTAEL-SVKV--LPKTKIIVEATIKKSI-LNVPFI-
---MHLKSKETGIKVDYGTYSYGVV--TWD-----FNNI--IREQKI--NPT-----

Fungi: *L. sulphureus*_KZS99944.1

-----HT-----
-----DHYFS-----FL
-----F---EAV-----
-----HVDK-----VEYD-LKLGR-I-----VSSARRVLASQTFENRTKQLQ
STTLELC--ESETHSGMF---EYGA-GFNL--AAGTTL-KAA---VP--EVDETGLT---
GDPYSNREM--WGERNEF--VKKYVATL-RMNA--DPGETVRAIATIQKGE-IEVPYT-
---MYLSSEKTVKLESKGLWRGVV--TWN-----LR-----

Fungi: *A. alternata*_XP_018387235.1

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TITLTLT--ETTTTTSTF---EHSY-GITITGTVSATF---G---WP--SVIEGRVEIS-
VAQ-TK-DFK--WGKQNTN--TKTATLEI-AATA--KPFKVTAIATATKSD-IELPFT-
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LVHSFEVLTV-DD--PS---AL--TYERCKTGDRP-----
-----PDNAVQGG---FNGGPTYHARGEVGGKIIIPGKA--DVEVARDDFY
L-----K----GAYIPYGS-----
-----SEHRIH-DFQVLVMAD-----KIEHVEFHCDRGKLLATNPKVFAVQEVSN
SSQPQSKEL--SYSETVSTSSFTHQWGISVSRSAQFSAKLPTVAEGKITTTT-TGSVSL
TWGETETFEK--TVSGKHPVVAAPFTKVICEVVANE-ATMDVPYTYMFKSGK-T-----
-SGGRWKGVSTWDVKTSFKKEKLNPS-----S-----

Coral_O.faveolata_XP_020612601.1
MLSY-----
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-----VKCKTGD-----KPPSNA
VEAGFD--DGPSYHARGVV--N--D----LTIPGKVGVRSENDHRLVGACIPYGS-AEH
RVHSSEVLTV-DD--PS---AL--TYERCKTGDRP-----
-----PENAVQGG---LDGGPSYHARGEVRGKLIPGKA--GVQGTWDDFY
L-----K----GACIPYGS-----
-----REHRIH-DFQVLVMAD-----KIDRVEFHCDRGKLGATNPKVLAQVEISNE
SSQPQSVF--SYSETVSTSTFTHQWGISISRSASFCELPVFKGEISTTT-TGSVSL
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TWGKTETQK--TVSGKHPVVAAPFTKVICEVVANE-AMMDVPYTVYFKSGK-T-----
-SGGMWKGVSTWDVKTSLKKEEKLNPPT-----MK-----

Fish_O.melastigma_XP_024120858.1

MYEIT-----

-----KPLY-WKTWD-G-----SLPGGA
VGIHTK--NGTQYVSRPTSERGE-CG-----YYNPNKG-----PYCYYPFDR-KEW
KDGSFEIFVN-ED--DF--ED-LVWRDAS-NGSV-----
-----PENAVQS---AYSPEIYVGRNKDG---LGKV--R--PE-----
L-----Q---SFYLPWE-----
-----GKEYPHN-NYQVLTYNDFR-SQEISEVKYDIDKGIITDHPETVVKVTEVSNN
SSSKVTKTV--TFSETITLVNKWETS GSFRLGVQTEISARIPSVVEGKITVST-ETHTTE
AKTGSMTKTK--EFSETLSLDVLPNKTKAKISLVAYK-CKLNI PFTACL SRTYSNGKKT
NISGTYTGVEVDNVKAVITDC-----

Fish_S.formosus_XP_018606101.1

MVDRG-----KPN--IE-----

-----A
AKDGVDE-H-----CEFTPSI-GDI
V-----

-----SPVFEI IKVDFDKGPDLTETPVVVKEDSYTNR
SSVEQKHTFSLSWTKSVSETTSWSHTWGLNTSLSFEFSF-----VNMTI-EITYSG
SYGTSSTKERSITISEQTEVTIPPKTKI IAKLFIKKNENC SIPFSATIKKIKADGEESIF
TENGIWKGVIYENVTLNLEEEKL-----

Fish_E.lucius_XP_010875473.1

MKLSVL-VVIS--LL-L-LGLSLAQMSASPPGSLRDLVRK-----
---SS--LGQKASLLNPLLE-----GRVPPLASKGP-----
--VQG-----PLTPSEFED-----
-----Q-QE P S P F M F G D N V N L Q - W Q N W T - G -----SLPTAA
VGIYNGYTERTDYICKYK--E-AG----FYTPSKG-----PYCQYPYGA-REY
YAPEFQVLTN-ID--NF--EF-VEWKDDS-YGSV-----
-----PKHSVRT---CSGRSTYVGKNKYG---LGKV--V--SE-----
F-----E---AFFLPWE-----
-----GDEYWK-NYQVLTINRDAY-SQHISHVKYGI DEVEIFQYPPETMRLSSVTNN
ECQEVVKTV--TISKTEVESTWNIGRTMLGVTAGITAKIPLIGSGGVEFSA-EKTLQF
NRGTTMVEAL--SHSVSELVPPNHCTVRMEGRK-ITADIPFTARLSRTYRNGETQWT
TITGVYDGVQIGEIRAVVDRCEPVDA-----KPC-----P

Fish_O.niloticus_XP_019221680.1

MKLSVL-LLSA--LL-T-L-S--SA-----SLQDIVKK-----
---SI--QLREVSLKPELE-----GRVPEPTGNRK-----
--VLG-----PLNPADLEQ-----
-----QQDLPSSFLFGDNVNLQ-WLTWD-G-----SLPNGA
VSIYNGYTERIDYVCKYK--E-AG----FYNPSLG-----PYCRYPYGD-REY
YTPEFEILTND--NF--EF-LEWKEGS-YGSL-----
-----PQHSVRT---CAGVDIYVGKNKYG---LGKV--V--PQ-----
F-----E---AFFLPWE-----
-----GDEYWK-NYQVLAINRDIY-TQHISDVKYGIDEVTIFQYPPETMRISGITNN
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TRGTTI IETL--SHSVSELTVPNHCTCKVRMEGRK- IKADIPY TARLSRTYHNGETQWT
TITGMYDGVQIGEVRAVVDRCEPVIDA-----KPC-----P

Fish_S.lalndi_XP_023250770.1

MPSDEP-LLNP-----
-----PVE-----
-----LAIRR-----
-----SQVPPTNF---EGTNLE-WVTWR-G-----FLPNGA

VSIYNRRSRRYDYVCKFKC--E-AG-----LYSPNLG-----HICYYPYGG-KEY
ISASFQILVN-KD--NF---EF-LEWKSSS-FGSV-----
-----TANSVGT---CSGSGVYVGRNKYG---LGKV--V--PE-----
Q-----R---AFFLPWR-----
-----GKSYWYRRRYEVLTMNRGVA-SEYISDIKYKIESSNIFYFPPVTIRISSITNN
ACSDVVKVA--TLKTSLVEHSWEISFSISAGAKNTIKTAIPSVTDRKIEFGP-EITLEF
SNGHKSSEEI--SHSVSEVDVPSNHHCVRVRLVGHK-YKADVPFTAQLTRTYHSGRIVKT
VVTGMFHGIQIGEVS AVVDRQCQSV PFA-----KPC-----H

Fish_A.polyacanthus_XP_022070850.1
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----SS--QHRKVSLLNPELE-----GRVPEPTGEV-----
--ASG-----PLTPADLEQ-----
-----QDLPSSFLFGDNVNLE-WLTWD-G-----ALPNGA
VSIYNGYTERTDYVCKYK--E-AG----FYNPSLG-----PYCRYPYGD-REY
YAPEFEILT-N-KD--NF---EF-LEWKEDS-YGSV-----
-----PQHSVRT---CTGVGIYVGNKYG---LGKV--V--PQ-----
F-----E---AFFLPWE-----
-----GDEYWK-SYQVLTINRDAY-TQHISDVKYAIDEVAIFQYPPETMRISGITNN
ECQTIIVKTV--TISKETEVEETTWNIGRATMLGITGSI TANIPLIGSAGIELSG-EKTLQF
SRGTTVVESL--SHSVSELKVPNHSCKVRMEGRK- IKADIPYTARLSR TYRNGETQWT
SITGT YDGVQIGEIRAVVDRCEPVPDA-----QPC-----P

Fish_T.nattereri_sp_Q66S13_NATT4_THANI
MKLLVL-LVT---LL-V-LS--WT-----SAEDVGDQ-----
----EILQQHEDNNHKSELG-----EAAPQRTDNETS-----
--QLG-----QETPTI-----
-----RVARAYEFSSKSNLE-WVRWN-G-----HIPSNA
VKISNTYVGREYVCRVGC--E-AG----YYTPKKG-----PSCFYYPYGF-TEQ
HSKMFHILVN-RD--NF---EI-LEWKWKT-GGEV-----
-----PENAVKA---C--RDLYVAKNKYG---LGKL--H--QS-----
H-----H---VFYLPWK-----
-----GTEYKYN-EYYVLNVNMDVV-EQKITNVRYNMKGVEVHKDKPETLRSTSVKNY
QCREATKQV--TLEKSTETSQSWDVSNSITLGVSTEV SAGIPNIADVSVAVSA-ETSVEI
SHGTSKTEST--SHSLVSATIPPNSSCSITMEGCT-FKANIPFTGRLTRKYSNGKVTSS
SVKGIYKVKVQVGEIQAVLHRCDKIADA-----KP-----C

Insecta_P.machaon_XP_014366083.1
MSEELG-TPYK--IC-R-VD--NC-----GIRVKVKEGYGPIYAVLHLLAKKCPHV
EVYKIS--LGRLTQIESPGHE-----PIVQ--DLNGIDWSIFNEFFISWYGNIIIR
IGLIG-----NQNVLFEFNQERKISKVIGFAKLVTITADSP
SQLCSDWIFKNPPEIVYLP RCIE-IRDSKLH-WRSLDGD-----KLPANA
IIGGF--QNDPIYIARAKH--R--G----SLCPGKYIH-----SQRCAYIAWGF-SEH
RKDKFEILCG-L--N-----VRWVKCK-GKNI-----
-----PENAFIGGTSEVNNEPLYIGRAKYGSDLICGKV--H--LL-----
Y-----G---TCYLPYNG-----
-----SELEYK-SYEILVIPD-IP-SRSIQDSQH-----
-----CCV-----
-----SS-----

Flatworm_C.sinesis_GAA30369.2
MAKCGR-----
-----GYQMTLS-WIPCQNG-----NVPNAA
VDAA--DGGGIYVCRASH--S--G----DDIPGKVV-----LYGKAYVPYGG-EEH
EKYSYDVLCV-TGSHGG--GF-YAWKANS-GGGV-----
-----PKRAVIGGFS-SSGEPLYVARGYVDGERVVGKV--H--EG-----
H-----D---CAYFPYGG-----
-----KEIASN-DYEVLVWEK-----

Flatworm *S.haematobium*_XP_012796705.1

MTTPFY-VR-----

-----QSHLS-WVSGTAGK-----DQPTNG
VEA-----DSRIYVARGEV--N--G-----HVI PGKLP-----RIGAAFIPCDG-KEH
GLCKFEILCN-TN--VFPNQL-YNWIPAS-DGRV-----
-----PAGALLAGST-TDGLPLYVARASINNEMCVGKV--N--SE-----
Y-----E-----CALMPWGN-----
-----VEHKVK-EYDVLCLIE-----

Insecta *H.halys*_XP_014292736.1

MERYVG-WIPP--SH-C-----

-----VGTLQ-WVPSSGG-----QVPPNA
VQAGMDQDGGHIYVGRAFH--E--G-----DLIPAKVTP-----RHGCAFVYPYNG-VEI
TKMQYEVLCS-NH-----VAWKFCR-YGEY-----
-----PPEAIRIGNT-KDGEPLFLGRTMIDGTMTPGKV--H--PS-----
H-----R-----CLYVPYAG-----
-----REHSFH-EYEILIL-N-----

Mollusca *C.virginica*_XP_022291764.1

MAI-----

-----WVTTTGN-----EIPEGA
MRAGYEADGRPLFIARAPI--E--G-----ILTPGKCGY-----HIQGALLPFGC-KEQ
VVHQYEVLVH-QT-NAL--GF-FDWHRAS-NGTV-----
-----PKEAFQT-----DKDTYVGRAFYSGSLIPCKISTN--PS-----
H-----R-----CAYMGSGG-----
-----KEHNTK-EYEVLCQI-----

-----K-----

Bac_Delta_proteobacterium_ML8_D_OPL17283.1

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Bac_Bacteroidales_WCE2008_WP_079583716.1

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-----PVETME---SKQNSELSETEQTAVRDSMVPVIMDTNSV-----
---LFDLMQRKKNEPSTKASSYEEDEWGRQGLSDA-LFD-----
-----LRDVPVYILVNDNAGGR-YLTAK-RDWIHKWYEFHRRYFSIP-AT
FEMTSEVPWNDVE-----AKVFYLYTIPLVG-----QYGLKTYFEGNEF

YMAVGAKSSNPND--YY---LY-AEEGGSS-Y--E-----

-----GSFSLTP----VDGDSFYIESNIVG-----SD--D--PK-----
-----P-----TTWNVWN-----YVLEAK
NSEAHFGKNLYRSNQOFT-----IVPQGEYVVERIEYKLDGTALVEQLPDFIATWQSTNN
TSVAQQTTT--SFNETASKTSSFSNNMGVSVQVSAKFNCGIPCIVGGEISTTL-TGSYSR
TWGESTTTTD--TRNYNFPVTIIPHSRVEATARVTR--HKMNVRYTAYLKNPS-TGK--QL
RINGIWEVDCTDIETSYSQFELATNKLIKEVKMKGVPKTRVSL

Bac_Elizabethingia_ursingii_WP_078403561.1
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----EKNALQ---ASAS-----ILNNSGNF-----
---IE-----DRSSS-FLE-----
-----LKDYPVNIISKENINGNFYLT-----
-----TQ----GTN
RNATFEKPNN-SD--NQ--KFYLEFPAES-NGGI-----

-----SIYT-----FINGQKYV---LTTG--I--NP-----
ATNSLIPKIRDNSFRGTFWQFLGGSTVHPD---AYILQNTGIRYRDNGITTYGVIGNSD
ASKIFVDKYLSQGQEF-----IRPIDDFEIIISLEYDNPDTGTIIKQPDFITTFWYSNN
TSVQQSMTT--GFSKRASYSSNWSKTTGGSLSVNTTLKGTIPIIAEGKITTTV-NTNYS
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Fungi_A.ostoyae_SJL15000.1
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---LF-----SRTTA-DPK-----
-----FGNYP-----R-----GRYHP-DQY
FSMGFE-----

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Fungi_A.gallica_PBK88078.1

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Fungi_S.stellatus_KIJ34088.1

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SWNETNFTV--SYTATFPVNAKPGATVRAVSTVNK-GNLEVPFTMTCKFKD-TGI--TV
QTQGVWRGVSTWDLRHRTIR--E-----

Fungi_D.corticola_XP_020135513.1

F-----

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KTEGVYHGVSFHDLVCHYS--E-----

Fungi_D.seriata_KKY14627.1

GS-----

-----TKYDDQ-YFR-----LFFE-NMVFKGIFKNVDEGKILDTPIMLARSNLSNN
SSVDQKISS--TFKEGTENESSFEYTLGFAVEVGTSFSCGVPLLAEGKIEVSA-TVSNEF
KWGSTTKKVT--EFSATFEATAPPHSTVVASATVTR-SVMQVPFTMTWTSPE-HGY--EV
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Fungi_R.clarus_GBB96646.1

FFHFT-----S--SN-----

-----QYD-DQY
WTFIFE-----

-----DMDIESVEYKIDEGKIKSTALVEIMRQTLSND
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TFGYSTEWKK--KYTADFSIKAPPRTKVIAYAYIKK-ATLSVPYIMYLSKK-TGI--KV
DTHGTYTGVTTWDL-----

Fungi_R.irregularis_PKB97961.1

YI-----S--SD-----

-----KFD-DQY
WSFIFE-----

-----DMIIESVDYKIYVGKIQSTKNVVMRQSLTND
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SFGNSTESVK--KYTAELSVKVLPKTKIIVEATIKK-SILNVPFIMHLKSKE-TGI--KV
DTYGTYSGVTTWDFNNIIREQKINPT-----

Fungi_L.sulphureus_KZS99944.1

HTDH-----

-----YFS-----FLFE-AVHVDKVEYDLKLGRIVSSARRVLASQTFENR
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RWGERNEFVK--KYVATLRMNADPGETVRAIATIQQ-GEIEVPYTMYSSEK-TGV--KL
ESKGLWRGVWTWNL-----R-----

Fungi_A.alternata_XP_018387235.1

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KWGKQNTETK--TATLEIAATAKPFKVTAIATATK-SDIELPFTITWKSCK-TGY--EV
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sumt
sump
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Supplementary material: Phylogenetic trees

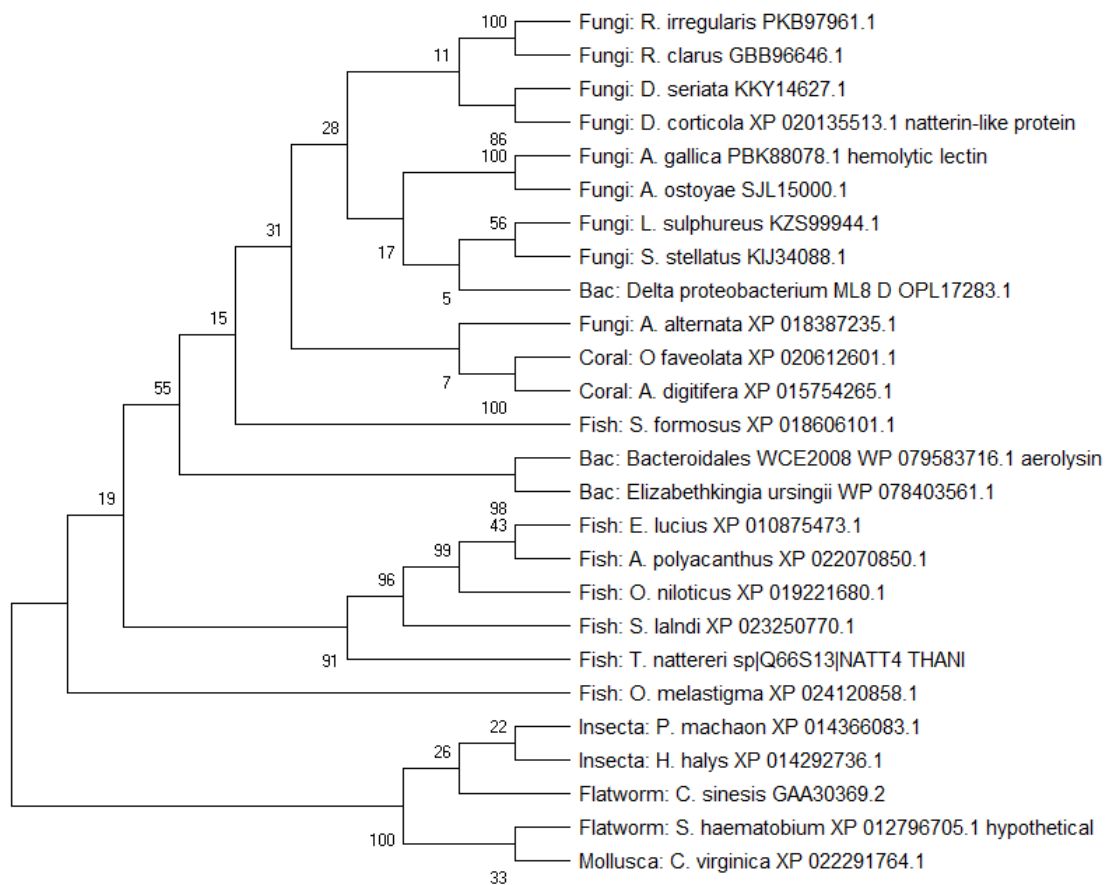


Figure S1. Maximum likelihood phylogenetic tree reconstructed from ClustalW alignment. The evolutionary history was inferred by using the Maximum Likelihood method based on the Dayhoff matrix-based model (Schwarz and Dayhoff, 1979). The tree with the highest log likelihood (-5921.17) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The analysis involved 26 amino acid sequences. All positions containing gaps and missing data were eliminated. There was a total of 116 positions in the final dataset. Evolutionary analyses were conducted in MEGA X (Kumar et al, 2018).

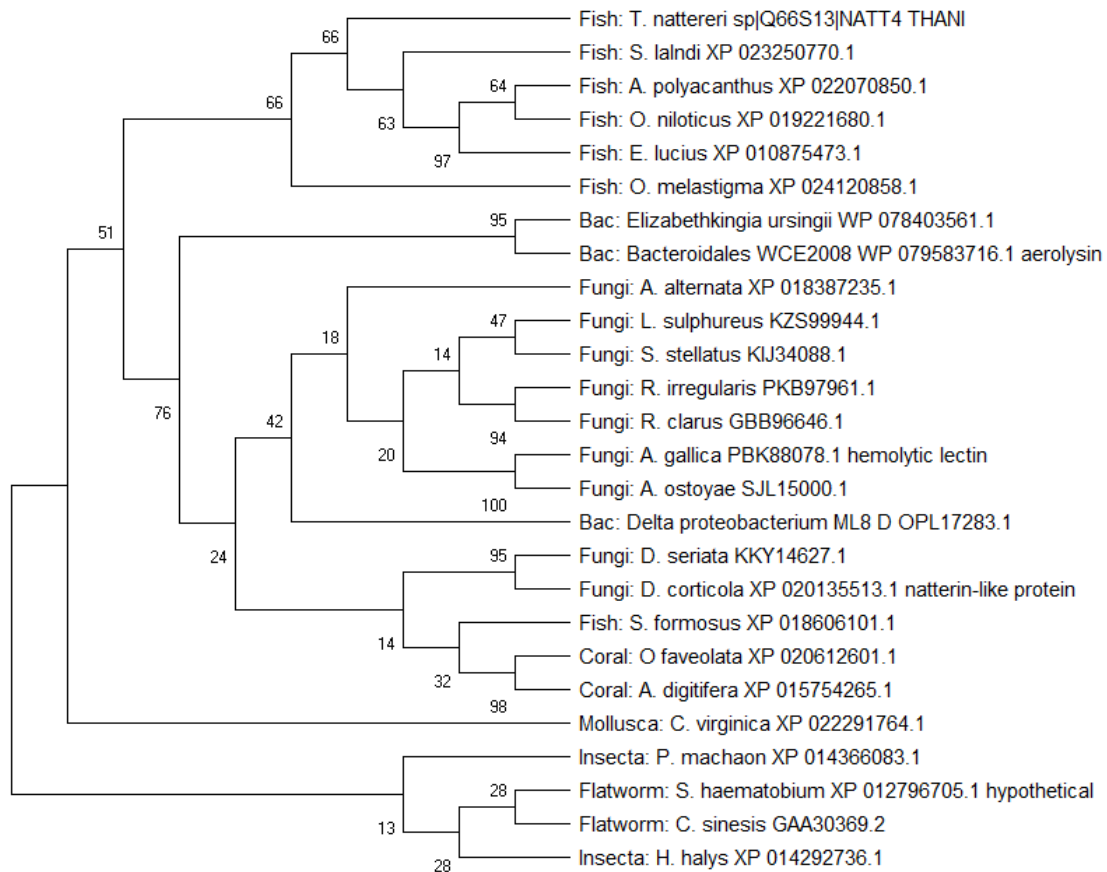
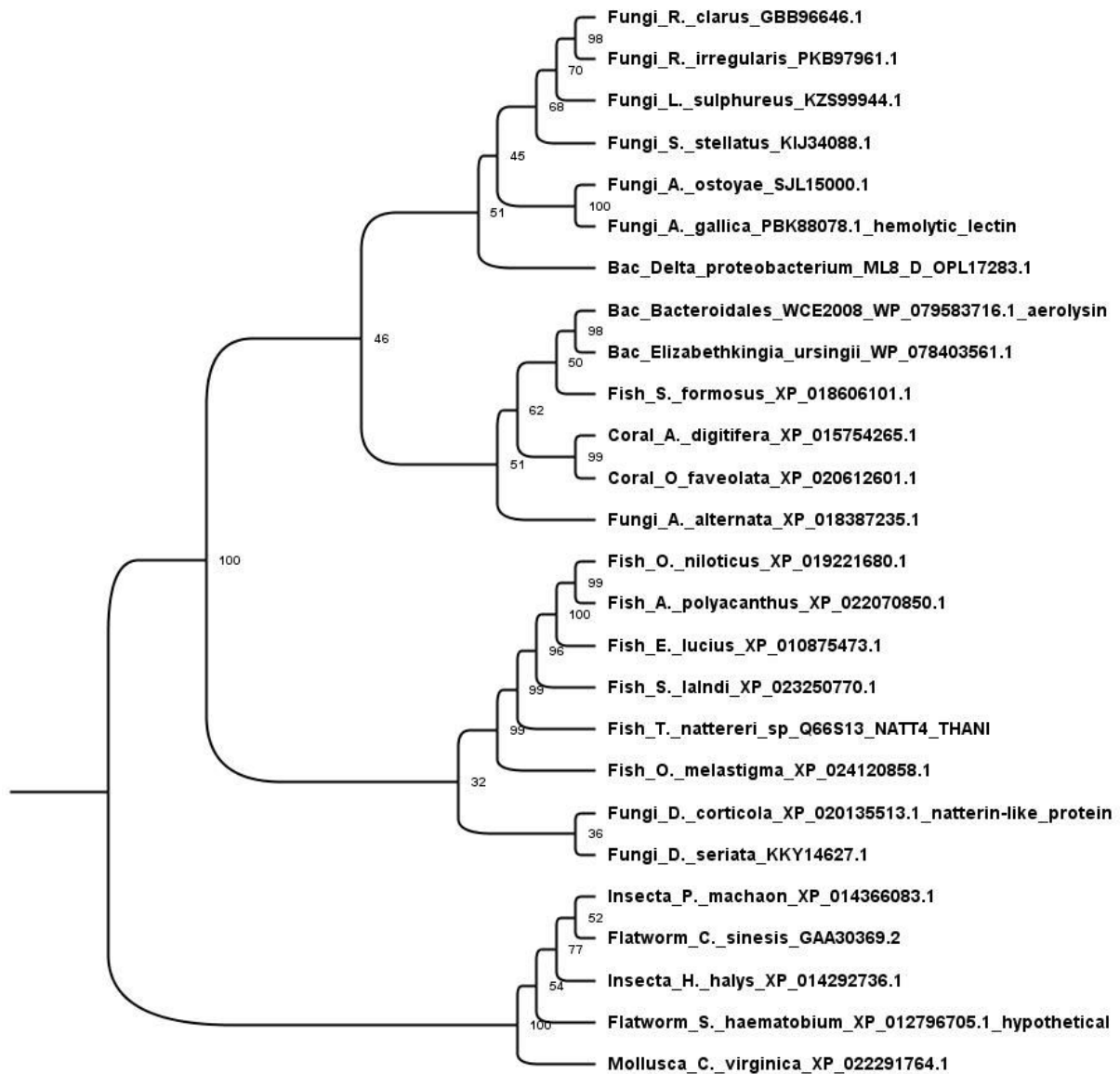
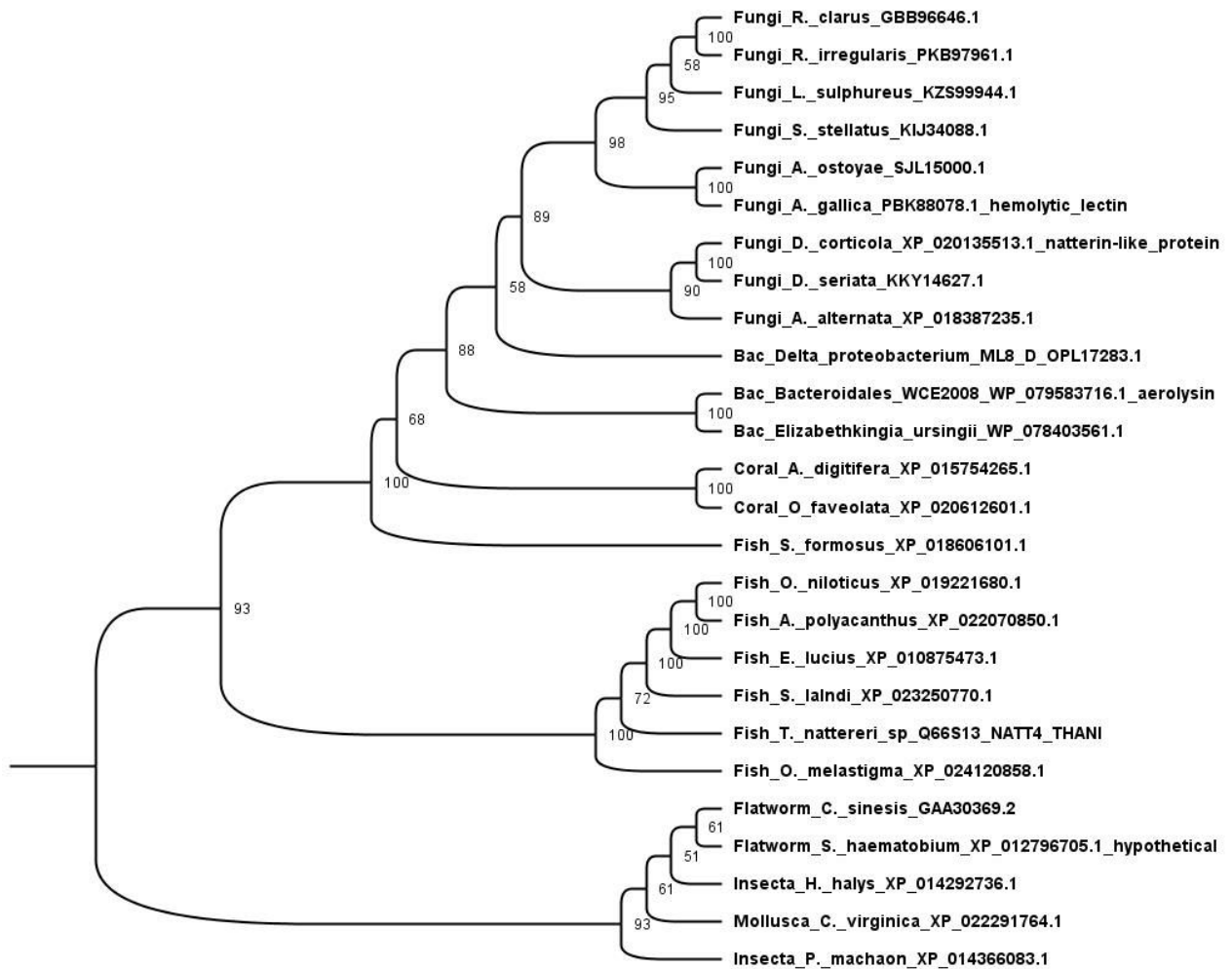


Figure S2. Maximum likelihood phylogenetic tree reconstructed from MUSCLE alignment. The evolutionary history was inferred by using the Maximum Likelihood method based on the Le_Gascuel_2008 model (Schwarz and Dayhoff, 1979). The tree with the highest log likelihood (-1508.91) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 4.9665)). The analysis involved 26 amino acid sequences. All positions containing gaps and missing data were eliminated. There was a total of 34 positions in the final dataset. Evolutionary analyses were conducted in MEGA X (Kumar et al, 2018).



Figures S3: Bayesian phylogenetic tree based on the ClustalW alignment. The evolutionary history was inferred by using the Bayesian reconstruction method implemented in MrBayes 3.2.7 (Ronquist et al, 2012) using the multiple alignment constructed by ClustalW algorithm implemented in MEGA-X software. The posterior probabilities of splits are next to the branches. Bayesian analysis was performed with mixed amino acid model (prset aamodelpr=mixed), gamma distributed rate of evolution with 4 discrete categories (lset rates=gamma), and prior probabilities set to default values. Markov chain Monte Carlo simulation was executed for 20,000,000 generations using 4 runs and 5 chains per run. The simulation convergence was confirmed by reviewing standard deviation of split frequencies and potential scale reduction value. The tree is visualised using the Figtree software (<http://tree.bio.ed.ac.uk/software/figtree/>).



Figures S4: Bayesian phylogenetic tree based on from MUSCLE alignment. The evolutionary history was inferred by using the Bayesian reconstruction method implemented in MrBayes 3.2.7 (Ronquist et al, 2012), using the multiple alignment constructed by MUSCLE algorithm implemented in MEGA-X software. The posterior probabilities of splits are next to the branches. Bayesian analysis was performed with mixed amino acid model (prset aamodelpr=mixed), gamma distributed rate of evolution with 4 discrete categories (lset rates=gamma), and prior probabilities set to default values. Markov chain Monte Carlo simulation was executed for 20,000,000 generations using 4 runs and 5 chains per run. The simulation convergence was confirmed by reviewing standard deviation of split frequencies and potential scale reduction value. The tree is visualised using the Figtree software (<http://tree.bio.ed.ac.uk/software/figtree/>).

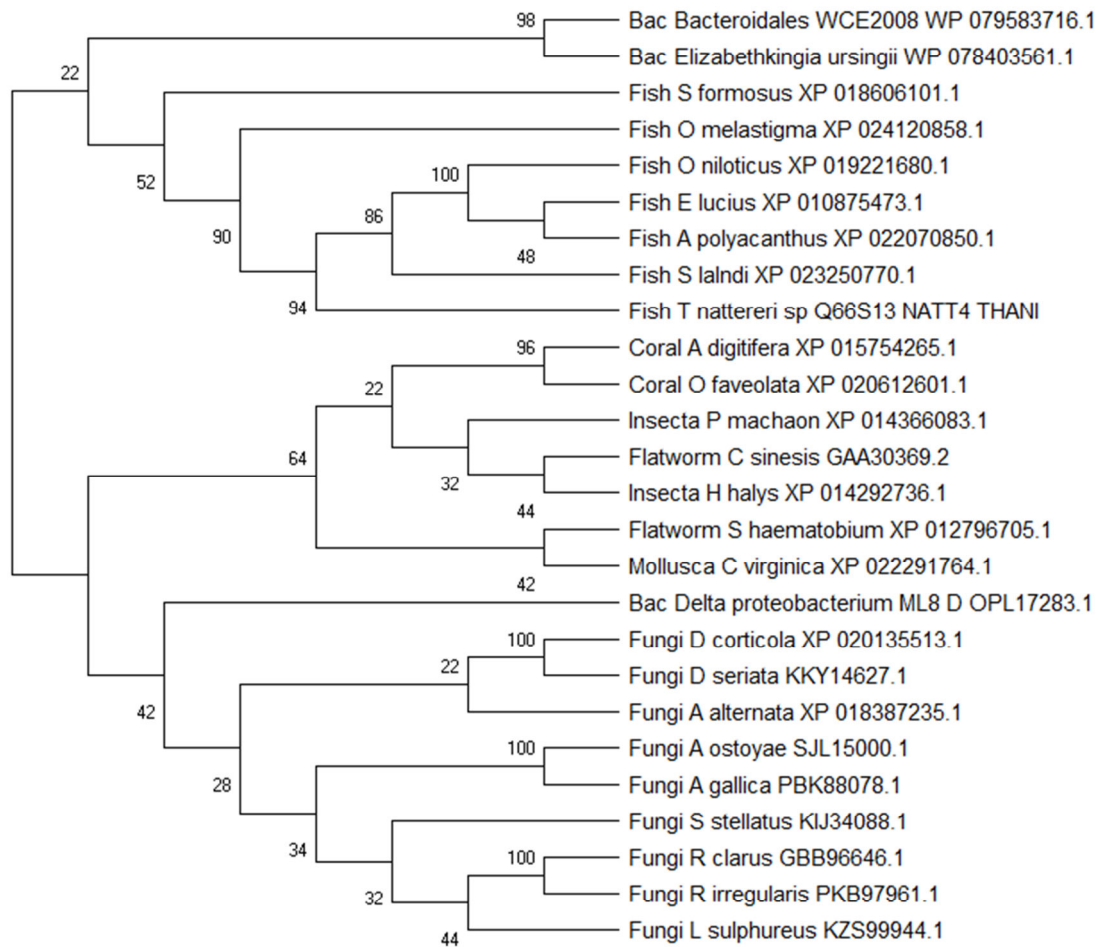
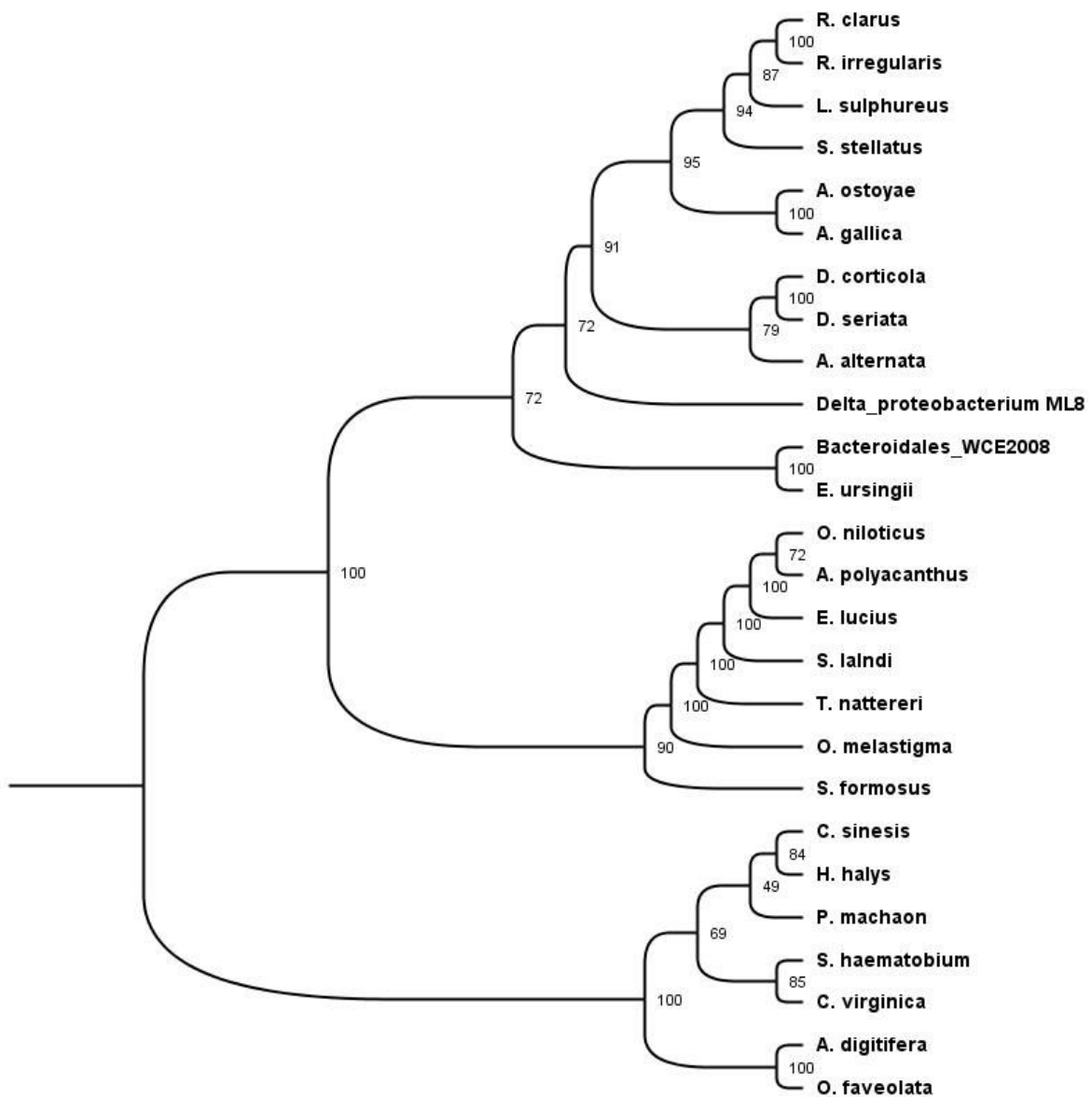


Figure S5. ML phylogenetic tree reconstructed from T-Coffee expresso alignment. The evolutionary history was inferred by using the Maximum Likelihood method based on the Dayhoff matrix-based model (Schwarz and Dayhoff, 1979). The tree with the highest log likelihood (-13778.60) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.9391)). The analysis involved 26 amino acid sequences. There was a total of 764 positions in the final dataset. Evolutionary analyses were conducted in MEGA X (Kumar et al, 2018).



Figures S6: Bayesian phylogenetic tree based on from T-Coffee expresso alignment. The evolutionary history was inferred by using the Bayesian reconstruction method implemented in MrBayes 3.2.7 (Ronquist et al, 2012), using the multiple alignment constructed by T-coffee expresso algorithm with PDB structures 1W3GA and 5MH1A used as templates. The posterior probabilities of splits are next to the branches. Bayesian analysis was performed with mixed amino acid model (prset aamodelpr=mixed), gamma distributed rate of evolution with 4 discrete categories (lset rates=gamma), and prior probabilities set to default values. Markov chain Monte Carlo simulation was executed for 20,000,000 generations using 4 runs and 5 chains per run. The simulation convergence was confirmed by reviewing standard deviation of split frequencies and potential scale reduction value. The tree is visualised using the Figtree software (<http://tree.bio.ed.ac.uk/software/figtree>).

REFERENCES

- Schwarz R and Dayhoff M. 1979. Matrices for detecting distant relationships. In Dayhoff M (Ed) Atlas of Protein Sequences, National Biomedical Research Foundation, Washington DC, pp 353-58.
- Kumar S, Stecher G, Li M, Knyaz C and Tamura K. 2018. MEGA X: Molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol, 35, 1547-1549.
- Ronquist F, Teslenko M, Mark P, et al. 2012. MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. Syst Biol, 61, 539-542.