

A

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1      ATGGAACGGCTAACACTGTACGATAGACGACAAATTTGGGAACGTGAGAGTGGCTCTCTGCTTCTGTGCTTGATGTATCAAC
1      M D R L T T L S R I D D N L G T S E V A A L C F L C L D V I N

91     AGGAACGCCTAGAGGGGATTACGGATGCAAGGGTTCTGTTGAGAGAGATAGAAGAAATGTCTTGGAGAACCCTTCCTCTCTTCT
31     R K R L E G I T D A R V L F E R L E E K C L L E N P S F L S

181    CAGCTGCTCAGAACTATTGCAAGGGCAGACCTGTCAGCCTGCTGGAGACAGACAGACCCACCAAGAAAGTACTGCAATCCAACT
61     Q L L R T T I R R A D L V S L L E T D S S P P E E T D S N P I

271    CTGTGAGATTACAGGGTGATGCTGTACAGATATATCAGGACGTGACTGAGAAAAATCTGAAACGATGAAGTTCTGTGAGTGACAAG
91     L S D Y R V M L Y Q I Y Q D V T E K N L E T M K F L L S D R

361    TTGGGCAAGGACACATTGACACATGCCGTACGCCCTGGACGCTTCCCTGAGATGGAAGGTTGGTTACTGTGAGCAGCAAGCTT
121    L G R R H I D T C R T A L D V F A E M E K Y G L L S T K I

451    GATCATCTGTACACAACTGTTGGAGTTCGATCGACAGCTGGCATCGACTGTTACGACTACATGCAAGGTGTGAACCGCGGGTCAAC
151    D H L Y T T L L E F D R Q L A S T V H D Y M Q G V N R P G H

541    ACTGCATCACTACTGCTGATGATGATACAGAGGGTGAACAGCTCTCTCAGCAGAACTCAACTACCTTTTCATATCTGAGACT
181    T A S L P R V S M D Y Q R V N S S P Q Q N Q T T L S I S E T

631    CAGCCAGAAATGAGGACAGAGTGTGCTGCTGAGAGAACCAATGAGTCTCTCTCTGCTGATCCGACAGAACTACTACACC
211    Q P R N V G Q S V V P D A E P N I E S S S P D P T E Y Y I

721    CTGACAGTAACCTGCTGGCGTGTGTATGTCATCAACAATGAGCAATTCGCTGACGAGGTAAAGATAGAGCCGTACTCAGGAG
241    L T R N P R G V C M V I N N E Q F R G P E F K D R A G T Q E

811    GATGAGAGGCTCTCTGACAGCTGTTACACAGCTTGGCTTTGACATGAGAGGTGACACAACTGACTGAGAGGACATCGCAGCTGAA
271    D E K A L C N V F T Q L G F D M E V H N N L T A E D M R R E

901    ATCAAAACCTGGGCAAGGAATTTTCCAGCCAGATGCTGCTGGTGTATGCTGCTCAGCAGGAGCATCCAGCTTACGAGGAAGCCCACTGTTG
301    I K T L G K R N F S S H D V L V V C V L S H G D I G C V F G

991    ACTGATGAGAACTGCTGTTTGAAGGAATTCACACAGCCCTTACGAGCGTGAAGCTCCAGCTTACGAGGAAGCCCACTGTTG
331    T D E N K V C L K E F T Q P F T S V R A P S L A G K P K L F

1081   TTCATCAGCGGTGTCAGGGAAGGGCTACCACTTCGAGGCCAGCCATGCCCTGAGCAGGAGGAGGAGAGGAGTCTGAGG
361    F I Q A C Q G R G Y Q F G A Q P Y A L S Q E E D G E R Y L E

1171   GACGACGACGCTCTGTACACGGCCAGAGGTGCTGCGGAAGCTGACTTCTGCTGGCAGTGGCCACCTGCCAGAGTGAGAGTGGTT
391    D D A G P V H G Q T V P A E A D F L L G M A T V P E C R S F

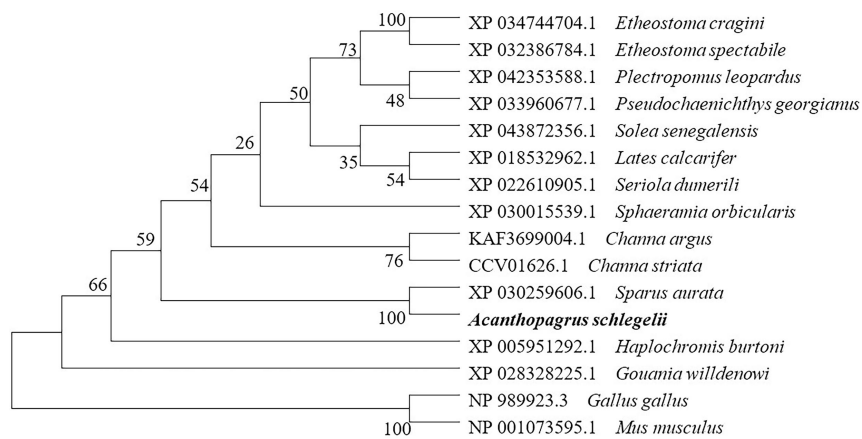
1261   CGAAACACTGTGTTAGGCTCCATCTCAAGAGCTGTGTAGGAGCTCTGAGGTGAGCAGATAGCGCTGCGAAGCAGGATATATCTC
421    R N T V L G S I Y I Q E L C R Q L L R S A D S A A N D D I L

1351   AGCATCTGACAGCTGTGAACAGGAGGTGAGCAAGAGGAGATATAAAGCTTCAACAAATGCCAGGCCCAATACACCTCACCAG
451    S I L T R V N R E V S K G E Y K S F K Q M P E P K Y T L T K

1441   AAGCTGCTCCTCAACGCTGTGTA
481    K L V L K R Y *

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C



B

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Larimichthys crocea .MDRVTLRSRIEELSESSEVASLCFICHHVNNRRRIEGVMD 39
Lateolabrax maculatus .MDRVTLRSRIEELSVSEVSLCFICGGVNNRRRIEGIKMD 40
Gasterosteus aculeatus .MDRVTLRSRIEELSESSEVASLCFICGRVILARRRIEITNN 39
Acanthopagrus schlegelii .MDRVTLRSRIIDNIGTSEVSLCFICHHVNNRRRIEITMD 39
Consensus rdr lsrid l seva lcflc v rkrleg

Larimichthys crocea .AKAIFRLPEERGLIDNOTFISGLIHHHICEDHISLLEETG 79
Lateolabrax maculatus .AKAIFRLPEERGLIETSVFISGLIHHHICEDHISLLEETG 80
Gasterosteus aculeatus .AKAIFRLPEERGLIENNSPFIHICEDHISLLEETG 79
Acanthopagrus schlegelii .AKAIFRLPEERGLIENNSPFIHICEDHISLLEETG 79
Consensus a lf rlee ll fl ll i r dl lle d

Larimichthys crocea .MDEEELNPNLSYRVMLHVYQIDFENLCKRMFIIS 119
Lateolabrax maculatus .MDEEELNPNLSYRVMLKLYEDMNEHFEKRMFIIS 120
Gasterosteus aculeatus .SEEBELNPNLSYRVMLRVICITFENLSMMRFIIS 119
Acanthopagrus schlegelii .SEEBELNPNLSYRVMLQYQIVTEKNLTMRFITSD 119
Consensus p e d np ls yrvnly d t mkfll

Larimichthys crocea .KIGRCIEACHTALDVFANERACILSRDRIEELNAVLE 159
Lateolabrax maculatus .KIGRCIEACHTALDVFANERNGELSLNIEELHKVME 160
Gasterosteus aculeatus .KIGRCIEACHTALDVFANERNGELSLNIEELHKVME 159
Acanthopagrus schlegelii .KIGRCIEACHTALDVFANERNGELSLNIEELHKVME 159
Consensus lg r c taldvfaenrek ls l

Larimichthys crocea .HCCCLFIVQRHMG.....RPVLAHVSMIHFRT 189
Lateolabrax maculatus .HCCCLFSLKEVYMGFSCVTCPHLCRISRHVSMIHFRT 199
Gasterosteus aculeatus .HCCCLFETQRYIIN.....REATGRHFHFRT 190
Acanthopagrus schlegelii .HCCCLFETVHVMYMG...VNRFHGTSLFVSMIHFRT 194
Consensus d qia qr

Larimichthys crocea .RISCRREFQF...AVTBMCESDARFTVCTLAEE...NIMFH 223
Lateolabrax maculatus .NSTFGSEFEQFIIFSEBTRCSMGESVYVCAEFKIASL 239
Gasterosteus aculeatus .SNTSGFVDVS...ISEBQENYEGMNICSAEPNFKISFP 226
Acanthopagrus schlegelii .NSSEQCNCOT...ISEBQERNVGCSPVFAEPNIES 232
Consensus e daep s

Larimichthys crocea .HCEFYVGLTHNFERGCVVNNNEEMNVTLKIEETCCFE 263
Lateolabrax maculatus .HCEFYVGLTHNFERGCVVNNNEERGTGRNREGTCCFE 279
Gasterosteus aculeatus .HCEFYVGLTHNFERGCVVNNNEERGTGRNREGTCCFE 266
Acanthopagrus schlegelii .HCEFYVGLTHNFERGCVVNNNEERGTGRNREGTCCFE 272
Consensus d eey l prg c v nne f r gtq de

Larimichthys crocea .KAPRVETLGLFVWHNNLITAGQIRYKINEIGRMNLMD 303
Lateolabrax maculatus .KVNNAVSCGLFVWHNNLITAEARHEICGLGRNMD 319
Gasterosteus aculeatus .KPCSTLSHGLFVWHNNLITAEARHEICGLGRNMD 306
Acanthopagrus schlegelii .KPCSTLSHGLFVWHNNLITAEARHEICGLGRNMD 312
Consensus k l f lgf vhnmlta lg rnf

Larimichthys crocea .HVLVVCVLSHGRCGVGTLEKHFVLEELHGFSGEAFET 343
Lateolabrax maculatus .HVLVVCVLSHGRCGVGTLEKHFVLEELHGFSGEAFET 359
Gasterosteus aculeatus .HVLVVCVLSHGRCGVGTLEKHFVLEELHGFSGEAFET 346
Acanthopagrus schlegelii .HVLVVCVLSHGRCGVGTLEKHFVLEELHGFSGEAFET 352
Consensus d lvvcvlsHg c gtde v t fts ap

Larimichthys crocea .LAGKPKLFFICACCGSNVCGSVCPFRPSCGEHRESL 383
Lateolabrax maculatus .LAGKPKLFFICACCGSNVCGSVCPFRPSCGEHRESL 399
Gasterosteus aculeatus .LAGKPKLFFICACCGSNVCGSVCPFRPSCGEHRESL 386
Acanthopagrus schlegelii .LAGKPKLFFICACCGSNVCGSVCPFRPSCGEHRESL 389
Consensus lagkpkllfiqacq yq g p e l

Larimichthys crocea .EBDAGFVHCETVHWADELIGMAVQCFRFRNRSKESIY 423
Lateolabrax maculatus .EBDAGFVHCETVHWADELIGMAVQCFRFRNRSKESIY 439
Gasterosteus aculeatus .EBDAGFVHCETVHWADELIGMAVQCFRFRNRSKESIY 426
Acanthopagrus schlegelii .EBDAGFVHCETVHWADELIGMAVQCFRFRNRSKESIY 429
Consensus e dagp g t p adflqmatv c sfr t gsyi

Larimichthys crocea .ICQICGCLMKSAQSPVIEDIILVLTNRVNRVSKGYENRK 463
Lateolabrax maculatus .ICQICGCLMKSAQSPVIEDIILVLTNRVNRVSKGYENRK 479
Gasterosteus aculeatus .ICQICGCLMKSAQSPVIEDIILVLTNRVNRVSKGYENRK 466
Acanthopagrus schlegelii .ICQICGCLMKSAQSPVIEDIILVLTNRVNRVSKGYENRK 469
Consensus iq c ql sa s ddil ltrvnrevskg y k

Larimichthys crocea .CMEBPKYITITRKIVHFC 480
Lateolabrax maculatus .CMEBPKYITITRKIVHFC 496
Gasterosteus aculeatus .CMEBPKYITITRKIVHFC 483
Acanthopagrus schlegelii .CMEBPKYITITRKIVHFC 486
Consensus cmp pkyititkklv k

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Fig. S2. *Ascaspace-8* bioinformatics analysis. (A) The ORF sequence of caspase-8 and its amino acid sequence. In the figure, the start codon (ATG) and end codon (TGA) are marked. The area underlined in red font is the DED domain, and the area underlined in black font is the CASc domain. (B) Multiple comparisons of amino acid sequences of caspase-8 and other species of caspase-8. (C) caspase-8 amino acid sequence phylogenetic tree.