

Supplementary Figures

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1   TCCGTAGCCATTTTGGCTCAAGTTTTTGGCTCAAGCAACTTACATCAAGCTCGTGTGATAGATTGCCTCGTCTGCCAGCATTGCCGGAGAGTCT
102  GCGCAATCGCGGAGACATTTGCTTTCAATGCGGACATCCAGCAGCTGATGAGCTTGATCATCAACACCTTCTACTCCAACAAGGAGATCTTCTCCGAGA
1   M A E T F A F N A D I Q Q L M S L I I N T F Y S N K E I F L R E
202  GCTCATCTCCAATGCCTCAGATGCCTTGACAAGATCCGCTACGAGTCCATCACGGACCCGGAGAAGATTGAGGCGCAGCCCACTTCTACATCAAGATC
33   L I S N A S D A L D K I R Y E S I T D P E K I E A Q P N F Y I K I
302  ATCCCTGACAAGACCAACTCCACCATCACCATCGAGGACTCTGGCATCGGCATGACGAAAGATGAGCTGATCAACAACCTCGGCACCATCGCCAAGTCC
66   I P D K T N S T I T I E D S G I G M T K N E L I N N L G T I A K S
401  GGCACCAAGGCCTTATGGAGGCCATGGCAGCGGGCGGCGACATCTCCATGATCGGCCAGTTCGGCGTGGGCTTCTACTCCGCTACCTCGTGGCAGAC
99   G T K A F M E A M A A G G D I S M I G Q F G V G F Y S A Y L V A D
500  AAGATCCGCGTGTGAGCAAGCACAAACGACGACGAGCAGTACATCTGGGAGTGGGGGCTGGCGGCTCCTTACGGTGCAGAAGGACACGGAGATGGT
132  K I R V V S K H N D D E Q Y I W E S G A G G S F T V Q K D T E M V
598  GCACGGCAGATCAAGCGCGGCACGAAGATCATCTGCTACCTGAAGGAGGACCAATCCGAGTTCCTCGAGGAGCGCCGCTGAAGGACCTGGTGAAGA
165  H G E I K R G T K I I C Y L K E D Q S E F L E E R R L K D L V K
696  AGCATTCCGAAATTTATGGCTTCCCAGTCCGAGCTCTACGTGGAGAAGTCCAAGGAGAAGGAGGTACCGACTCGGAAGAGGAGGAGGAGAGAAGAA
197  K H S E F I G F P I E L Y V E K S K E K E V T D S E E E E E E K K
794  GAGGAGGGCGCCGAGGGTGCAGAGCCGAAGATTGAGGAGGTGGAACGAGGAGAAGGAGAAGAAAGAAAGAAAGAAACCAAGAAGGTCAAGGA
230  E E G A E G D E P K I E E V D E E K E K E E K K K T K K V K E
889  AGTTTCTCATGAGTGGGAACAGCTGAACAAGAACAAGCCCTCTGGATGCGGAAGTTCGGAGGACGTGACGAATGAGGAGTATGCCTCCTTCTACAAGTC
262  V S H E W E Q L N K N K P L W M R K S E D V T N E E Y A S F Y K S
988  GCTCTCGAATGATGGGAGGACCATCTTGCCGTGAAGCACTTCCAGCGTTCGAGGGGACGCTCGAGTTCGAGCCTTGTCTTCTGTCGCGCCGCGCCGACCT
295  L S N D W E D H L A V K H F S V E G Q L E F R A L L F V P R R A P
1088  TTCGACCTCTTTGATCCAAGAAGAAGGGAACAACATCAAGTTGACGTGCGCCGCTTTCATTATGGACGATTGCGATGAGCTCATGCCGAGTGGC
328  F D L F E S K K K R N N I K L Y V R V F I M D D C D E L M P E W
1188  TCAACATGGTCAAGGGCGTCTGGATTCCGAGGATCTGCCGTGAACATCTCTCGAGAGACCTTGCAGCAGAACAAGATCCTCCGCGTCATCAAGAAAA
361  L N M V K G V V D S E D L P L N I S R E T L Q Q N K I L R V I K K N
1288  CCTTGTGAAGAAGTGTGGAGATGTTGCTGAGATCGCGGAGAAGAAGGATGACTACAAGAAATGTTACGAGCAGTITGGCAAAGTCTTGAAGCTCGGG
395  L V K K C L E M F A E I A E K K D D Y K K C Y E Q F G K C L K L G
1388  GTCCACGAAGATTCCACCAACCGAACCAAGGTTGACAGATTGCTCCGCTTCCACACTTCCAAGTCTGGCGATGAGCAGATCAGCTTGAAGGAGTATGTGG
428  V H E D S T N R T K V A E L L R F H T S K S G D E Q I S L K E Y V
1488  ACCGCATGAAAGAGGGCCAGAACGACATCTACTACATCACTGGCGAGAGCATCACGGCCGTGTCTCCTCGCCGTTTTGGAGACCTTCGCAAGAAGGG
461  D R M K E G Q N D I Y Y I T G E S I T A V S S S P F L E T L R K K G
1588  CTTGGAGGTGTTGATCATGGTGGACCCGGTTCGAGATGCGGTGCAGCAGTGAAGGAGTTCGATGGTAAGAAGCTCAAGTCCACGACCAAGGAGGG
495  L E V L Y M V D P V D E Y A V Q Q L K E F D G K K L K S T T K E G
1687  CTTGGACATTGAGGACGAGGATGAGAAGAAGAAGCTTGAAGGAGTGAAGGAGTTCGATGGTAAAGAGTTCGATGGTAAAGAGTTCCTGGCGACAA
528  L D I E D E D E K K K L E E L K A E F E P L T K L M K E V L G D K
1786  GGTGGAGAAGTCTCGTGCATCGCGCATGGCTGACTCCCTTGGCTGCTCACGACCTCGGAGATGGTGGTTCGGCAACATGGAACGCATCATGAAG
561  V E K V L V S S R M A D S P C V L T T S E Y G W S A N M E R I M K
1886  GCGCAGGCTTTCGCGGACAACTCTATGACGTCGTACATGGTGTGCAAGAAGACCATGGAGTGAATCCGAAGCACTCCATCATGACGGAGTTGAAGAAGA
594  A Q A L R D N S M T S Y M V S K K T M E V N P K H S I M T E L K K
1986  AGGCTGCCCGGACAAGTCTGACAAGACTGTGAAGGACCTGATCTGGCTGCTTTCGACACCTCGCTGCTCACGTCGGCTTCAACCTGGACGAGCCAC
627  K A A A D K S D K T V K D L I W L L F D T S L L T S G F N L D E P T
2086  GCAGTTTCGCTGGCCGATCCACCCGATGATCAAGCTCGGCCCTCAGCATCGACGATGACGATGAGGGCCTCGGTGACGATGACGACCTTCCCGGCTCGAA
661  Q F A G R I H R M I K L G L S I D D D D E G L G D D D D L P P L E
2186  GAGGTCGAGGGCGTGGGATGAGGCCTCCAAGATGGAGGAGTTCGATTGAGCGGCCATGCAGTGAGCGACGGCCTCCACGGGCGCCGACTTGGG
694  E V E G A A D E A S K M E E Y D -
2284  CCGCTGGTATCAATGAGGCTCAGCACAATATCACACGACGAGCTCCGCGCACCGCATGGGGAAGGCGTGTAGTCAAGGCTGATCATGCGAGCGCGT
2383  CCGCCGCTTGGGCGCGGCTAGAGACCCAGGACCTTGTGATGTACAGTGTGAGAGGCGAGGACGAAAAAAGAAAAAAGAAAAAAGAAAAA

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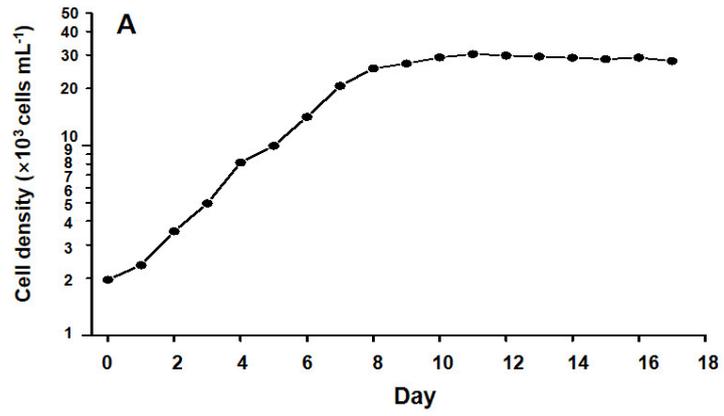
Supplementary Figure S1. The full-length cDNA sequence and deduced amino acid sequence of *SHsp90* (Accession number: MZ779085). Sequences are numbered on the left. The start and stop codon are boxed. The canonical dinoflagellate spliced leader (DinoSL) is underlined in the 5'-UTR. The characteristic Hsp90 signatures are shaded in gray and the conserved LXXLL sequence is marked with double underline. The cytosolic Hsp90-specific motif at C-terminus is highlighted with triangles.

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StHsp90 M-----ETFAFADIQQLMSLIINTFYSNKEFLREL SN SDALDKIRVES TDPEK EAQPNFKIKI PDKINST T TDS GIGMTRNKL INNLG 93
PmHsp90 M-----ETFAFADIQQLMSLIINTFYSNKEFLREL SN SDALDKIRVES TDPEK EAQPNFKIKI PDKINST T TDS GIGMTRNKL INNLG 93
PdHsp90 M-----ETFAFADIQQLMSLIINTFYSNKEFLREL SN SDALDKIRVES TDPEK EAQPNFKIKI PDKINST T TDS GIGMTRNKL INNLG 93
CchHsp90 M-----ETFAFADIQQLMSLIINTFYSNKEFLREL SN SDALDKIRVES TDPEK EAQPNFKIKI PDKINST T TDS GIGMTRNKL INNLG 93
AcHsp90 M-----ETFAFADIQQLMSLIINTFYSNKEFLREL SN SDALDKIRVES TDPEK EAQPNFKIKI PDKINST T TDS GIGMTRNKL INNLG 93
KvHsp90 M-----ETFAFADIQQLMSLIINTFYSNKEFLREL SN SDALDKIRVES TDPEK EAQPNFKIKI PDKINST T TDS GIGMTRNKL INNLG 93
MpHsp90 M-----ETFAFADIQQLMSLIINTFYSNKEFLREL SN SDALDKIRVES TDPEK EAQPNFKIKI PDKINST T TDS GIGMTRNKL INNLG 93
AaHsp90 MADVQMADE ETFAFAEIQQLMSLIINTFYSNKEFLREL SN SDALDKIRVES TDRSKLDQPELFIKIPDKPNKTSI TDS GIGMTRKQLVNVLG 100
*****
StHsp90 TIAKSGTKAFMEAMAAGD SMIGQFGVGFYSYLVAIKRVVSKRNNDDEQY WESAGGSFTVQKDTMVEGE IRRGTRICVYKEDQSEELERRLK 192
PmHsp90 TIAKSGTKAFMEAMAAGD SMIGQFGVGFYSYLVAIKRVVSKRNNDDEQY WESAGGSFTVQKDTMVEGE IRRGTRICVYKEDQSEELERRLK 192
PdHsp90 TIAKSGTKAFMEAMAAGD SMIGQFGVGFYSYLVAIKRVVSKRNNDDEQY WESAGGSFTVQKDTMVEGE IRRGTRICVYKEDQSEELERRLK 192
CchHsp90 TIAKSGTKAFMEAMAAGD SMIGQFGVGFYSYLVAIKRVVSKRNNDDEQY WESAGGSFTVQKDTMVEGE IRRGTRICVYKEDQSEELERRLK 192
AcHsp90 TIAKSGTKAFMEAMAAGD SMIGQFGVGFYSYLVAIKRVVSKRNNDDEQY WESAGGSFTVQKDTMVEGE IRRGTRICVYKEDQSEELERRLK 192
KvHsp90 TIAKSGTKAFMEAMAAGD SMIGQFGVGFYSYLVAIKRVVSKRNNDDEQY WESAGGSFTVQKDTMVEGE IRRGTRICVYKEDQSEELERRLK 192
MpHsp90 TIAKSGTKAFMEAMAAGD SMIGQFGVGFYSYLVAIKRVVSKRNNDDEQY WESAGGSFTVQKDTMVEGE IRRGTRICVYKEDQSEELERRLK 192
AaHsp90 TIAKSGTRFMEALQAGADSMIGQFGVGFYSYLVAIKRVVSKRNNDDEQY WESAGGSFTVTRD--VGDGPELIRGTRISLFLKDDQLERLEERRLK 197
*****
StHsp90 DLVKKHSEF IGFP IELVWESKEKE TDEDEEBE--KKEEGAEGEPKIEVDDEKEREKPKKTKKKEVSHWEQINKNKPIWRRSEEDVINEEYAS 290
PmHsp90 DLVKKHSEF IGFP IELVWESKEKE TDEDEEBE--KDEEGKEGEPKIEVDDEKEREKPKKTKKKEVSHWEQINKNKPIWRRSEEDVINEEYAS 290
PdHsp90 DLVKKHSEF IGFP IELVWESKEKE TDEDEEBE--KDEEGKEGEPKIEVDDEKEREKPKKTKKKEVSHWEQINKNKPIWRRSEEDVINEEYAS 291
CchHsp90 DLVKKHSEF IGFP IELVWESKEKE TDEDEEBE--KDEEGKEGEPKIEVDDEKEREKPKKTKKKEVSHWEQINKNKPIWRRSEEDVINEEYAS 292
AcHsp90 DLVKKHSEF IGFP IELVWESKEKE TDEDEEBE--KDEEGKEGEPKIEVDDEKEREKPKKTKKKEVSHWEQINKNKPIWRRSEEDVINEEYAS 291
KvHsp90 DLVKKHSEF IGFP IELVWESKEKE TDEDEEBE--KDEEGKEGEPKIEVDDEKEREKPKKTKKKEVSHWEQINKNKPIWRRSEEDVINEEYAS 290
MpHsp90 DLVKKHSEF IGFP IELVWESKEKE TDEDEEBE--KDEEGKEGEPKIEVDDEKEREKPKKTKKKEVSHWEQINKNKPIWRRSEEDVINEEYAS 290
AaHsp90 DLVKKHSEF ISFP IELVWETTEKE TDEDEEBE--KDEEGKEGEPKIEVDDEKEREKPKKTKKKEVSHWEQINKNKPIWRRSEEDVINEEYAS 288
*****
StHsp90 FYKSLNDWEDHLAKHF SVEGQLEFALFVPRAPFDL FESKRRNRIKLYVRRVFIIMDCDELPEVLNFKVGVDSDLPLN SRETIQQNKILR V 390
PmHsp90 FYKSLNDWEDHLAKHF SVEGQLEFALFVPRAPFDL FESKRRNRIKLYVRRVFIIMDCDELPEVLNFKVGVDSDLPLN SRETIQQNKILR V 390
PdHsp90 FYKSLNDWEDHLAKHF SVEGQLEFALFVPRAPFDL FESKRRNRIKLYVRRVFIIMDCDELPEVLNFKVGVDSDLPLN SRETIQQNKILR V 391
CchHsp90 FYKSLNDWEDHLAKHF SVEGQLEFALFVPRAPFDL FESKRRNRIKLYVRRVFIIMDCDELPEVLNFKVGVDSDLPLN SRETIQQNKILR V 392
AcHsp90 FYKSLNDWEDHLAKHF SVEGQLEFALFVPRAPFDL FESKRRNRIKLYVRRVFIIMDCDELPEVLNFKVGVDSDLPLN SRETIQQNKILR V 391
KvHsp90 FYKSLNDWEDHLAKHF SVEGQLEFALFVPRAPFDL FESKRRNRIKLYVRRVFIIMDCDELPEVLNFKVGVDSDLPLN SRETIQQNKILR V 390
MpHsp90 FYKSLNDWEDHLAKHF SVEGQLEFALFVPRAPFDL FESKRRNRIKLYVRRVFIIMDCDELPEVLNFKVGVDSDLPLN SRETIQQNKILR V 390
AaHsp90 FYKSLNDWEDHLAKHF SVEGQLEFALFVPRAPFDL FDTKKLNRIKLYVRRVFIIMDCDELPEVLSFKVGVDSDLPLN SRETIQQNKILR V 388
*****
StHsp90 IKNLWKKCEMFAEIEKKIDYKRYE QFKCKLGHEDSNRKAELRHHTSKSGDEQISLKEYVDRMKEGQNDI YITGESITAVSSSPFLETL 490
PmHsp90 IKNLWKKCEMFAEIEKKIDYKRYE QFKCKLGHEDSNRKAELRHHTSKSGDEQISLKEYVDRMKEGQNDI YITGESITAVSSSPFLETL 490
PdHsp90 IKNLWKKCEMFAEIEKKIDYKRYE QFKCKLGHEDSNRKAELRHHTSKSGDEMI SLKEYVDRMKEGQNDI YITGESITAVSSSPFLETL 491
CchHsp90 IKNLWKKCEMFAEIEKKIDYKRYE QFKCKLGHEDSNRKAELRHHTSKSGDEQISLKEYVDRMKEGQNDI YITGESITAVSSSPFLETL 492
AcHsp90 IKNLWKKCEMFAEIEKKIDYKRYE QFKCKLGHEDSNRKAELRHHTSKSGDEQISLKEYVDRMKEGQNDI YITGESITAVSSSPFLETL 491
KvHsp90 IKNLWKKCEMFAEIEKKIDYKRYE QFKCKLGHEDSNRKAELRHHTSKSGDEQISLKEYVDRMKEGQNDI YITGESITAVSSSPFLETL 490
MpHsp90 IKNLWKKCEMFAEIEKKIDYKRYE QFKCKLGHEDSNRKAELRHHTSKSGDESI SLKEYVDRMKEGQNDI YITGESITAVSSSPFLETL 490
AaHsp90 IKNLWKKCEMFAEIEKNIDYKRYE QFKCKLGHEDSNRKAELRHHTSKSGDEMTSFKYVDRMKEGQNDI YITGESITAVSSSPFLETL 487
*****
StHsp90 RKKGLEVL YMDPDEYAVQQLKEFDGKKLRSITKEGLDIED--EDEKKREELKAEFPEPLTKLMKEMLGDNVEKVMSSRMADSPCVLITSEYGSANM 588
PmHsp90 RKKGLEVL YMDPDEYAVQQLKEFDGKKLRSITKEGLDIED--EDEKKREELKAEFPEPLTKLMKEMLGDNVEKVMSSRMADSPCVLITSEYGSANM 588
PdHsp90 RKKGLEVL YMDPDEYAVQQLKEFDGKKLRSITKEGLDIED--EDEKKREELKAEFPEPLTKLMKEMLGDNVEKVMSSRMADSPCVLITSEYGSANM 589
CchHsp90 RKKGLEVL YMDPDEYAVQQLKEFDGKKLRSITKEGLDIED--EDEKKREELKAEFPEPLTKLMKEMLGDNVEKVMSSRMADSPCVLITSEYGSANM 590
AcHsp90 RKKGLEVL YMDPDEYAVQQLKEFDGKKLRSITKEGLDIED--EDEKKREELKAEFPEPLTKLMKEMLGDNVEKVMSSRMADSPCVLITSEYGSANM 589
KvHsp90 RKKGLEVL YMDPDEYAVQQLKEFDGKKLRSITKEGLDIED--EDEKKREELKAEFPEPLTKLMKEMLGDNVEKVMSSRMADSPCVLITSEYGSANM 588
MpHsp90 RKKGLEVL YMDPDEYAVQQLKEFDGKKLRSITKEGLDIED--EDEKKREELKAEFPEPLTKLMKEMLGDNVEKVMSSRMADSPCVLITSEYGSANM 587
AaHsp90 RKKGLEVL YMDPDEYAVQQLKEFDGKKLRSITKEGLDIED--EDEKKREELKAEFPEPLTKLMKEMLGDNVEKVMSSRMADSPCVLITSEYGSANM 587
*****
StHsp90 ERIMKAAARD SMYSYMSKKTME NPKRHIMHLKKAADRSKDVKDLWLLDTSLLTSGFNLEPTQFAGRIRHMKLGLSIDDDEGGGDDDD 688
PmHsp90 ERIMKAAARD SMYSYMSKKTME NPKRHIMHLKKAADRSKDVKDLWLLDTSLLTSGFNLEPTQFAGRIRHMKLGLSIDDDEGGGDDDD 688
PdHsp90 ERIMKAAARD SMYSYMSKKTME NPKRHIMHLKKAADRSKDVKDLWLLDTSLLTSGFNLEPTQFAGRIRHMKLGLSIDDDEGGGDDDD 689
CchHsp90 ERIMKAAARD SMYSYMSKKTME NPKRHIMHLKKAADRSKDVKDLWLLDTSLLTSGFNLEPTQFAGRIRHMKLGLSIDDDEGGGDDDD 690
AcHsp90 ERIMKAAARD SMYSYMSKKTME NPKRHIMHLKKAADRSKDVKDLWLLDTSLLTSGFNLEPTQFAGRIRHMKLGLSIDDDEGGGDDDD 689
KvHsp90 ERIMKAAARD SMYSYMSKKTME NPKRHIMHLKKAADRSKDVKDLWLLDTSLLTSGFNLEPTQFAGRIRHMKLGLSIDDDEGGGDDDD 688
MpHsp90 ERIMKAAARD SMYSYMSKKTME NPKRHIMHLKKAADRSKDVKDLWLLDTSLLTSGFNLEPTQFAGRIRHMKLGLSIDDDEGGGDDDD 687
AaHsp90 ERIMKAAARD SMYSYMSKKTME NPKRHIMDLRKAADRSKDVKDLWLLDTSLLTSGFNLEPTQFAGRIRHMKLGLSIDDDEPNTFAGRIRHMKLGLSIDDDEPNTEGDD 686
*****
StHsp90 LPPLEEVGAADEASKMEEVD 709
PmHsp90 LPPLEEVGAADEASKMEEVD 709
PdHsp90 LPPLEEVGAADEASKMEEVD 710
CchHsp90 LPPLEEVGAADEASKMEEVD 711
AcHsp90 LPPLEEVGAADEASKMEEVD 710
KvHsp90 LPPLEEVGAADEASKMEEVD 709
MpHsp90 LPPLEEVGAADEASKMEEVD 708
AaHsp90 MPELEEVGAADEASKMEEVD 704

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Supplementary Figure S2. Alignment and comparison of Hsp90 deduced amino acid sequences from *Scrippsiella trochoidea* (StHsp90, the present sequence) with other registered counterparts from dinoflagellates *Prorocentrum minimum* (AFD34191; PmHsp90), *Prorocentrum donghaiense* (AST24279; PdHsp90), *Cryptothecodinium cohnii* (AAM02974; CcHsp90), *Margalefidinium polykrikoides* (AKS44062; MpHsp90), *Amphidinium carterae* (ADV03069; AcHsp90), *Karlodinium veneticum* (ABI14419; KvHsp90), and higher plant *Arabidopsis thaliana* (CAA68885; AaHsp90). Sequences are numbered on the right. The typical Hsp90 signatures and the cytosolic Hsp90-specific motif are highlighted with arrows and triangles, respectively. Identical and similar amino acid residues are black and gray shaded, respectively. Deletions are indicated by dashes.



Supplementary Figure S3. The growth curve of *Scrippsiella trochoidea* (strain IOCAS-St-1). The day of inoculation was recorded as day 0.