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CSS0017072.1     MDRLMSSARLMIVSDLDHTMVDHHDPQNLSLLRFNALWEAHYRHDSLLVFSTGRSPTLYKQLRKEKPMLTPDITIMSVGTEITYGNSMVPDEGWVEFLNQ    100
GWHPASIV039206   MDRLMSSARLMIVSDLDHTMVDHHDPQNLSLLRFNALWEAHYRHDSLLVFSTGRSPTLYKQLRKEKPMLTPDITIMSVGTEITYGNSMVPDEGWVEFLNQ    100
GWHPAZTZ037371   MDRLMSSARLMIVSDLDHTMVDHHDPQNLSLLRFNALWEAHYRHDSLLVFSTGRSPTLYKQLRKEKPMLTPDITIMSVGTEITYGNSMVPDEGWVEFLNQ    100
GWHPBAUV077964   MDRLMSSARLMIVSDLDHTMVDHHDPQNLSLLRFNALWEAHYRHDSLLVFSTGRSPTLYKQLRKEKPMLTPDITIMSVGTEITYGNSMVPDEGWVEFLNQ    100
GWHPASIX044577   MDRLMSSARLMIVSDLDHTMVDHHDPQNLSLLRFNALWEAHYRHDSLLVFSTGRSPTLYKQLRKEKPMLTPDITIMSVGTEITYGNSMVPDEGWVEFLNQ    100
GWHPASIX046144   MDRLMSSARLMIVSDLDHTMVDHHDPQNLSLLRFNALWEAHYRHDSLLVFSTGRSPTLYKQLRKEKPMLTPDITIMSVGTEITYGNSMVPDEGWVEFLNQ    100


CSS0017072.1     KWDRNIVTEESCKFSELTLQAETEQRLHKVSFYVLKDKALEVMKALSVQLEKRGLDVKVIYSGGMDLDILPQGAGKGQALAYLHKKFKTEGKLPQNTLVC    200
GWHPASIV039206   KWDRNIVTEESCKFSELTLQAETEQRLHKVSFYVLKDKALEVMKALSVQLEKRGLDVKVIYSGGMDLDILPQGAGKGQALAYLHKKFKTEGKLPQNTLVC    200
GWHPAZTZ037371   KWDRNIVTEESCKFSELTLQAETEQRLHKVSFYVLKDKALEVMKALSVQLEKRGLDVKVIYSGGMDLDILPQGAGKGQALAYLHKKFKTEGKLPQNTLVC    200
GWHPBAUV077964   KWDRNIVTEESCKFSELTLQAETEQRLHKVSFYVLKDKALEVMKALSVQLEKRGLDVKVIYSGGMDLDILPQGAGKGQALAYLHKKFKTEGKLPQNTLVC    200
GWHPASIX044577   KWDRNIVTEESCKFSELTLQAETEQRLHKVSFYVLKDKALEVMKALSVQLEKRGLDVKVIYSGGMDLDILPQGAGKGQALAYLHKKFKTEGKLPQNTLVC    200
GWHPASIX046144   KWDRNIVTEESCKFSELTLQAETEQRLHKVSFYVLKDKALEVMKALSVQLEKRGLDVKVIYSGGMDLDILPQGAGKGQALAYLHKKFKTEGKLPQNTLVC    200


CSS0017072.1     GDSGNDAELFSIPDVYGVMVSNAQEELLQWHAENAKGNPNIIHATERCAAGIIQAIGHFNLGPSKSPRDITNPLETISDNFEPGHDIVTFYLFLERWRHA    300
GWHPASIV039206   GDSGNDAELFSIPDVYGVMVSNAQEELLQWHAENAKGNPNIIHATERCAAGIIQAIGHFNLGPSKSPRDITNPLETISDNFEPGHDIVTFYLFLERWRHA    300
GWHPAZTZ037371   GDSGNDAELFSIPDVYGVMVSNAQEELLQWHAENAKGNPNIIHATERCAAGIIQAIGHFNLGPSKSPRDITNPLETISDKFEPGHDIVTFYLFLERWRHA    300
GWHPBAUV077964   GDSGNDAELFSIPDVYGVMVSNAQEELLQWHAENAKGNPNIIHATERCAAGIIQAIGHFNLGPSKSPRDITNPLETISDKFEPGHDIVTFYLFLERWRHA    300
GWHPASIX044577   GDSGNDAELFSIPDVYGVMVSNAQEELLQWHAENAKGNPNIIHATERCAAGIIQAIGHFNLGPSKSPRDITNPLETISDNFEPGHDIVTFYLFLERWRHA    300
GWHPASIX046144   GDSGNDAELFSIPDVYGVMVSNAQEELLQWHAENAKGNPNIIHATERCAAGIIQAIGHFNLGPSKSPRDITNPLETISDKFEPGHDIVTFYLFLERWRHA    300


CSS0017072.1     EMEFSEIYLAGLRATSFPSYVFVHPSGNELSINDCIKGMRSCYGDKQGKQYQVWVDQISRTEIGSNIWLVKFNKWESSGEERRGCVATTVVSSKDLSGID    400
GWHPASIV039206   EMEFSEIYLAGLRATSFPSYVFVHPSGNELSINDCIKGMRSCYGDKQGKQYQVWVDQISRTEIGSNIWLVKFNKWESSGEERRGCVATTVVSSKDLSGID    400
GWHPAZTZ037371   EMEFSEIYLAGLRATSFPSYVFVHPSGNELSINDCIKGMRSCYGDKQGKQYQVWVDQISRTEIGSNIWLVKFNKWESSGEERRGCVATTVVSSKDLSGID    400
GWHPBAUV077964   EMEFSEIYLAGLRATSFPSYVFVHPSGNELSINDCIKGMRSCYGDKQGKQYQVWVDQISRTEIGSNIWLVKFNKWESSGEERRGCVATTVVSSKDLSGID    400
GWHPASIX044577   EMEFSEIYLAGLRATSFPSYVFVHPSGNELSINDCIKGMRSCYGDKQGKQYQVWVDQISRTEIGSNIWLVKFNKWESSGEERRGCVATTVVSSKDLSGID    400
GWHPASIX046144   EMEFSEIYLAGLRATSFPSYVFVHPSGNELSINDCIKGMRSCYGDKQGKQYQVWVDQISRTEIGSNIWLVKFNKWESSGEERRGCVATTVVSSKDLSGID    400


CSS0017072.1     GFSWVHMHQSWSDEAGPKDQDWV    423
GWHPASIV039206   GFSWVHMHQSWSDEAGPKDQDWV    423
GWHPAZTZ037371   GFSWVHMHQSWSDEAGPKDQDWV    423
GWHPBAUV077964   GFSWVHMHQSWSDEAGPKDQDWV    423
GWHPASIX044577   GFSWVHMHQSWSDEAGPKDQDWV    423
GWHPASIX046144   GFSWVHMHQSWSDEAGPKDQDWV    423
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Fig. S1a Amino acid sequence alignment diagram of CsSPP

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CSS0047114.1    MAGNDWINSYLEAILDVGPPLDDPKSSLLLRERGRFSPTRYFVEEVITGFDETDLHRSWVRLEGEEAQHSAKKRLEREKARREATADMSEDLSEGEKGDV    100
CSS0020276.1    MAGNDWINSYLEAILDVGPPLDDPKSSLLLRERGRFSPTRYFVEEVITGFDETDLHRSWVRLEGEEAQHSAKKRLEREKARREATADMSEDLSEGEKGDV    100
GWHPASIV037217  ..............................................................................MSEDLSEGEKGDV    13
GWHPAZTZ035335  ...........................................MGKLDLVEFKQIEMLEGEEAQHSAKKRLEREKARREATADMSEDLSEGEKGDV    53
GWHPBAUV071117  ...........................................MGKLDLVEFKQIEMLEGEEAQHSAKKRLEREKARREATADMSEDLSEGEKGDV    53
GWHPBAUV073449  ...........................................MGKLDLVEFKQIEMLEGEEAQHSAKKRLEREKARREATADMSEDLSEGEKGDV    53

CSS0047114.1    VGDMSAHGGSTRGRMPRISSVDAMENWANQHKEKKLYIVLISLHGLIRGENMELGRDSDTGGQVKYVVELARALGEMPGVYRVDLLTRQVSSPDVDWSYG    200
CSS0020276.1    VGDMSAHGGSTRGRMPRISSVDAMENWANQHKEKKLYIVLISLHGLIRGENMELGRDSDTGGQVKYVVELARALGEMPGVYRVDLLTRQVSSPDVDWSYG    200
GWHPASIV037217  VGDMSAHGGSTRGRMPRISSVDAMENWANQHKEKKLYIVLISLHGLIRGENMELGRDSDTGGQVKYVVELARALGEMPGVYRVDLLTRQVSSPDVDWSYG    113
GWHPAZTZ035335  VGDMSAHGGSTRGRMPRISSVDAMENWANQHKEKKLYIVLISLHGLIRGENMELGRDSDTGGQVKYVVELARALGEMPGVYRVDLLTRQVSSPDVDWSYG    153
GWHPBAUV071117  VGDMSAHGGSTRGRMPRISSVDAMENWANQHKEKKLYIVLISLHGLIRGENMELGRDSDTGGQVKYVVELARALGEMPGVYRVDLLTRQVSSPDVDWSYG    153
GWHPBAUV073449  VGDMSAHGGSTRGRMPRISSVDAMENWANQHKEKKLYIVLISLHGLIRGENMELGRDSDTGGQVKYVVELARALGEMPGVYRVDLLTRQVSSPDVDWSYG    153

CSS0047114.1    EPTEMLNSRNSENDIHETGESSGAYIIRIPFGPKDKYIPKELLWPHISEFVDGALCHIIQMSRVLGEQIGGMEPVWFVAIHGHYADAGDSAALLSGALNV    300
CSS0020276.1    EPTEMLNSRNSENDIHETGESSGAYIIRIPFGPKDKYIPKELLWPHISEFVDGALCHIIQMSRVLGEQIGGMEPVWFVAIHGHYADAGDSAALLSGALNV    300
GWHPASIV037217  EPTEMLNSRNSENDIHETGESSGAYIIRIPFGPKDKYIPKELLWPHISEFVDGALCHIIQMSRVLGEQIGGMEPVWFVAIHGHYADAGDSAALLSGALNV    213
GWHPAZTZ035335  EPTEMLNSRNSENDIHETGESSGAYIIRIPFGPKDKYIPKELLWPHISEFVDGALCHIIQMSRVLGEQIGGMEPVWFVAIHGHYADAGDSAALLSGALNV    253
GWHPBAUV071117  EPTEMLNSRNSENDIHETGESSGAYIIRIPFGPKDKYIPKELLWPHISEFVDGALCHIIQMSRVLGEQIGGMEPVWFVAIHGHYADAGDSAALLSGALNV    253
GWHPBAUV073449  EPTEMLNSRNSENDIHETGESSGAYIIRIPFGPKDKYIPKELLWPHISEFVDGALCHIIQMSRVLGEQIGGMEPVWFVAIHGHYADAGDSAALLSGALNV    253

CSS0047114.1    PMLFTGHSLGRDKLEQLLKQGRQSRDEINAAYKIMRRIEAEELSLDASEVVITSTRQEIEEQWRLYDGFDPILERKLRARIKRNVSCYGRSMPRMVVMPP    400
CSS0020276.1    PMLFTGHSLGRDKLEQLLKQGRQSRDEINAAYKIMRRIEAEELSLDASEVVITSTRQEIEEQWRLYDGFDPILERKLRARIKRNVSCYGRSMPRMVVMPP    400
GWHPASIV037217  PMLFTGHSLGRDKLEQLLKQGRQSRDEINAAYKIMRRIEAEELSLDASEVVITSTRQEIEEQWRLYDGFDPILERKLRARIKRNVSCYGRSMPRMVVMPP    313
GWHPAZTZ035335  PMLFTGHSLGRDKLEQLLKQGRQSRDEINAAYKIMRRIEAEELSLDASEVVITSTRQEIEEQWRLYDGFDPILERKLRARIKRNVSCYGRSMPRMVVMPP    353
GWHPBAUV071117  PMLFTGHSLGRDKLEQLLKQGRQSRDEINAAYKIMRRIEAEELSLDASEVVITSTRQEIEEQWRLYDGFDPILERKLRARIKRNVSCYGRSMPRMVVMPP    353
GWHPBAUV073449  PMLFTGHSLGRDKLEQLLKQGRQSRDEINAAYKIMRRIEAEELSLDASEVVITSTRQEIEEQWRLYDGFDPILERKLRARIKRNVSCYGRSMPRMVVMPP    353

CSS0047114.1    GMEFNHIVPQDADMDGETEGNEDNPPIWSEIMRFFSNARKPMILALARPDPKKNITTLVKAFGECKPLRELANLTLIMGNRDAIDEMSNTNATVLLSILK    500
CSS0020276.1    GMEFNHIVPQDADMDGETEGNEDNPPIWSEIMRFFSNARKPMILALARPDPKKNITTLVKAFGECKPLRELANLTLIMGNRDAIDEMSNTNATVLLSILK    500
GWHPASIV037217  GMEFNHIVPQDADMDGETEGNEDNPPIWSEIMRFFSNARKPMILALARPDPKKNITTLVKAFGECKPLRELANLTLIMGNRDAIDEMSNTNATVLLSILK    413
GWHPAZTZ035335  GMEFNHIVPQDADMDGETEGNEDNPPIWSEIMRFFSNARKPMILALARPDPKKNITTLVKAFGECKPLRELANLTLIMGNRDAIDEMSNTNATVLLSILK    453
GWHPBAUV071117  GMEFNHIVPQDADMDGETEGNEDNPPIWSEIMRFFSNARKPMILALARPDPKKNITTLVKAFGECKPLRELANLTLIMGNRDAIDEMSNTNATVLLSILK    453
GWHPBAUV073449  GMEFNHIVPQDADMDGETEGNEDNPPIWSEIMRFFSNARKPMILALARPDPKKNITTLVKAFGECKPLRELANLTLIMGNRDAIDEMSNTNATVLLSILK    453

CSS0047114.1    LIDKYDLYGHVAYPKHHKQSDVPDIYHLAATTKGVFINPAFIEPFGLTLIEAAARGLPMVATKNGGPVDIHRVLDNGLLVDPHDQHSIADALLKLVADKQ    600
CSS0020276.1    LIDKYDLYGHVAYPKHHKQSDVPDIYHLAATTKGVFINPAFIEPFGLTLIEAAARGLPMVATKNGGPVDIHRVLDNGLLVDPHDQHSIADALLKLVADKQ    600
GWHPASIV037217  LIDKYDLYGHVAYPKHHKQSDVPDIYHLAATTKGVFINPAFIEPFGLTLIEAAARGLPMVATKNGGPVDIHRVLDNGLLVDPHDQHSIADALLKLVADKQ    513
GWHPAZTZ035335  LIDKYDLYGHVAYPKHHKQSDVPDIYHLAATTKGVFINPAFIEPFGLTLIEAAARGLPMVATKNGGPVDIHRVLDNGLLVDPHDQHSIADALLKLVADKQ    553
GWHPBAUV071117  LIDKYDLYGHVAYPKHHKQSDVPDIYHLAATTKGVFINPAFIEPFGLTLIEAAARGLPMVATKNGGPVDIHRVLDNGLLVDPHDQHSIADALLKLVADKQ    553
GWHPBAUV073449  LIDKYDLYGHVAYPKHHKQSDVPDIYHLAATTKGVFINPAFIEPFGLTLIEAAARGLPMVATKNGGPVDIHRVLDNGLLVDPHDQHSIADALLKLVADKQ    553

CSS0047114.1    LWARCRQNGLENIHSFSWPEHCKTYLSRIAICKSRQPQWQKSDDGFENSDSDSPSDSLRDIKDLSLNLKMSIEGSGTFDNALFFEDHATDGKSRVENSSL    700
CSS0020276.1    LWARCRQNGLENIHSFSWPEHCKTYLSRIAICKSRQPQWQKSDDGFENSDSDSPSDSLRDIKDLSLNLKMSIEGSGTFDNALFFEDHATDGKSRVENSSL    700
GWHPASIV037217  LWARCRQNGLENIHSFSWPEHCKTYLSRIAICKSRQPQWQKSDDGFENSDSDSPSDSLRDIKDLSLNLKMSIEGSGTFDNALFFEDHATDGKSRVENSSL    613
GWHPAZTZ035335  LWARCRQNGLENIHSFSWPEHCKTYLSRIAICKSRQPQWQKSDDGFENSDSDSPSDSLRDIKDLSLNLKMSIEGSGTFDNALFFEDHATDGKSRVENSSL    653
GWHPBAUV071117  LWARCRQNGLENIHSFSWPEHCKTYLSRIAICKSRQPQWQKSDDGFENSDSDSPSDSLRDIKDLSLNLKMSIEGSGTFDNALFFEDHATDGKSRVENSSL    653
GWHPBAUV073449  LWARCRQNGLENIHSFSWPEHCKTYLSRIAICKSRQPQWQKSDDGFENSDSDSPSDSLRDIKDLSLNLKMSIEGSGTFDNALFFEDHATDGKSRVENSSL    653

CSS0047114.1    TLSKGTEENRQKSGYMEKIDHNMSKSLILRRRKSVFVIAVDCDMTSDFLDIIK..........CGLYRIVLSAASCITEIFSLLKSGGLSPMDFDAFIC    789
CSS0020276.1    TLSKGTEENRQKSGYMEKIDHNMSKSLILRRRKSVFVIAVDCDMTSDFLDIIKVIVGAAGPGKSVGSIGFVLSAASCITEIFSLLKSGGLSPMDFDAFIC    800
GWHPASIV037217  TLSKGTEENRQKSGYMEKIDHNMSKSLILRRRKSVFVIAVDCDMTSDFLDIIKVIVEAAGPGKSVGSIGFVLSAASCITEIFSLLKSGGLSPMDFDAFIC    713
GWHPAZTZ035335  TLSKGTEENRQKSGYMEKIDHNMSKSLILRRRKSVFVIAVDCDMTSDFLDIIKVIVEAAGPGKSVGSIGFVLSAASCITEIFSLLKSGGLSPMDFDAFIC    753
GWHPBAUV071117  TLSKGTEENRQKSGYMEKIDHNMSKSLILRRRKSVFVIAVDCDMTSDFLDIIKVIVEAAGPGKSVGSIGFVLSAASCITEIFSLLKSGGLSPMDFDAFIC    753
GWHPBAUV073449  TLSKGTEENRQKSGYMEKIDHNMSKSLILRRRKSVFVIAVDCDMTSDFLDIIKVIVEAAGPGKSVGSIGFVLSAASCITEIFSLLKSGGLSPMDFDAFIC    753

CSS0047114.1    NSGSELYYPSSTSENGPFGLPIIADLDYYSHIDYRWGGEGLRKTLVSWAASINDKKGV.GGPVVAEDESGSAKHCYSFKVKDPALVPPVKELRKSMRIQA    888
CSS0020276.1    NSGSELYYPSSTSENGPFGLPIIADLDYYSHIDYRWGGEGLRKTLVSWAASINDKKGVBGGPVVAEDESGSAKHCYSFKVKDPALVPPVKELRKSMRIQA    900
GWHPASIV037217  NSGSELYYPSSTSENGPFGLPIIADLDYYSHIDYRWGGEGLRKTLVSWAASINDKKGVBGGPVVAEDESGSAKHCYSFKVKDPALVPPVKELRKSMRIQA    813
GWHPAZTZ035335  NSGSELYYPSSTSENGPFGLPIIADLDYYSHIDYRWGGEGLRKTLVSWAASINDKKGVBGGPVVAEDESGSAKHCYSFKVKDPALVPPVKELRKSMRIQA    853
GWHPBAUV071117  NSGSELYYPSSTSENGPFGLPIIADLDYYSHIDYRWGGEGLRKTLVSWAASINDKKGVBGGPVVAEDESGSAKHCYSFKVKDPALVPPVKELRKSMRIQA    853
GWHPBAUV073449  NSGSELYYPSSTSENGPFGLPIIADLDYYSHIDYRWGGEGLRKTLVSWAASINDKKGVBGGPVVAEDESGSAKHCYSFKVKDPALVPPVKELRKSMRIQA    853

CSS0047114.1    LRSHVIYCQNGTKMNVIPVLASRSQALRYLYVRWGVELSNIVVFVGESGDTDYEGLI..........VCSGAHKLHSNRNYPLEYVMPYDNPNLVESEG    977
CSS0020276.1    LRSHVIYCQNGTKMNVIPVLASRSQALRYLYVRWGVELSNIVVFVGESGDTDYEGLIGGIHKTVILKGVCSGAHKLHSNRNYPLEYVMPYDNPNLVESEG    1000
GWHPASIV037217  LRSHVIYCQNGTKMNVIPVLASRSQALRYLYVRWGVELSNIVVFVGESGDTDYEGLIGGIHKTVILKGVCSGAHKLHSNRNYPLEYVMPYDNPNLVESEG    913
GWHPAZTZ035335  LRSHVIYCQNGTKMNVIPVLASRSQALRYLYVRWGVELSNIVVFVGESGDTDYEGLIGGIHKTVILKGVCSGAHKLHSNRNYPLEYVMPYDNPNLVESEG    953
GWHPBAUV071117  LRSHVIYCQNGTKMNVIPVLASRSQALRYLYVRWGVELSNIVVFVGESGDTDYEGLIGGIHKTVILKGVCSGAHKLHSNRNYPLEYVMPYDNPNLVESEG    953
GWHPBAUV073449  LRSHVIYCQNGTKMNVIPVLASRSQALRYLYVRWGVELSNIVVFVGESGDTDYEGLIGGIHKTVILKGVCSGAHKLHSNRNYPLEYVMPYDNPNLVESEG    953

CSS0047114.1    CNSSNVKASLQKLGVLN    994
CSS0020276.1    CNSSNVKASLQKLGVLN    1017
GWHPASIV037217  CNSSNVKASLQKLGVLN    930
GWHPAZTZ035335  CNSSNVKASLQKLGVLN    970
GWHPBAUV071117  CNSSNVKASLQKLGVLN    970
GWHPBAUV073449  CNSSNVKASLQKLGVLN    970
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Fig. S2b Amino acid sequence alignment diagram of CsSPS1/2

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CSS0009603.1     MARNEWINGYLEAILDAGAGRGGVHGNNSTSSGNEKKRFEEKLRLEQFDHDIDKEKGDNKLISTTKYFVEEVVNGFDESDLYRTWIK..............   87
GWHPASIV029409   MARNEWINGYLEAILDAGAGRGGVHGNNSSSSGNEKKRFEEKLRLEQFDHDIDKEKGDNKLISTTKYFVEEVVNGFDESDLYRTWIKVIATRNTRERTNR  100
GWHPAZTZ027893   MARNEWINGYLEAILDAGAGRGGVHGNNSSSSGNEKKRFEEKLRLEQFDHDIDKEKGDNKLISTTKYFVEEVVNGFDESDLYRTWIKVIATRNTRERTNR  100
GWHPBAUV058548   MARNEWINGYLEAILDAGAGRGGVHGNNSSSSGNEKKRFEEKLRLEQFDHDIDKEKGDNKLISTTKYFVEEVVNGFDESDLYRTWIKVIATRNTRERTNR  100
GWHPASIX032838   MARNEWINGYLEAILDAGAGRGGVHGNNSTSSGNEKKRFEEKLRLEQFDHDIDKEKGDNKLISTTKYFVEEVVNGFDESDLYRTWIKVIATRNTRERTNR  100
GWHPASIX034616   MARNEWINGYLEAILDAGAGRGGVHGNNSSSSGNEKKRFEEKLRLEQFDHDIDKEKGDNKLISTTKYFVEEVVNGFDESDLYRTWIKVIATRNTRERTNR  100

CSS0009603.1     ................IAWDDEKKALQNDEESGRKGARMLQTILSDLSEGEREKSDINQTESPSSDKIPRITSDMQIWSDDHKSGRLYIVLIQVLLYAQ  170
GWHPASIV029409   LENMCWRIWHLARKKKCIAWDDEKKLIKRRFER.EKGRKDAADDLSDLSEGEREKSDINQTESPSSDKIPRINSDMQIWSDDHKSGRLYIVLIS......  193
GWHPAZTZ027893   LENMCWRIWHLARKKKCIAWDDENLTKRRFER.EKGRKDAADDLSDLSEGEREKGDINQTESPSSDKIPRITSDMQIWSDDHKSGRLYIVLIS......  193
GWHPBAUV058548   LENMCWRIWHLARKKKCIAWDDEKNLTKRRFDR.EKGRKDAADDLSDLSEGEREKGDINQTESPSSDKIPRITSDMQIWSDDHKSGRLYIVLIS......  193
GWHPASIX032838   LENMCWRIWHLARKKKCIAWDDEKNLTKRRFER.EKGRKDAADDLSDLSEGEREKSDINQTESPSSDKIPRITSDMQIWSDDHKSGRLYIVLIS......  193
GWHPASIX034616   LENMCWRIWHLARKKKCIAWDDEKKLIKRRFER.EKGRKDAADDLSDLSEGEREKSDINQTESPSSDKIPRINSDMQIWSDDHKSGRLYIVLIS......  193

CSS0009603.1     FLHGLVRGENMELGRDSDTGGQVKYVVELARALANMNGVYRVDLLTRQISSSDIDSSYGEPIEMLSCPSDGTGSCGAYIIRIPCGPRDKYTPKESLWPHV  270
GWHPASIV029409   .LHGLVRGENMELGRDSDTGGQVKYVVELARALANMNGVYRVDLLTRQISSSDIDSSYGEPIEMLSCPSDGTGSCGAYIIRIPCGPRDKYMPKESLWPHI  292
GWHPAZTZ027893   .LHGLVRGENMELGRDSDTGGQVKYVVELARALANMNGVYRVDLLTRQISSSDIDSSYGEPIEMLSCPSDGTGSCGAYIIRIPCGPRDKYTPKESLWPHV  292
GWHPBAUV058548   .LHGLVRGENMELGRDSDTGGQVKYVVELARALANMNGVYRVDLLTRQISSSDIDSSYGEPIEMLSCPSDGTGSCGAYIIRIPCGPRDKYTPKESLWPHV  292
GWHPASIX032838   .LHGLVRGENMELGRDSDTGGQVKYVVELARALANMNGVYRVDLLTRQISSSDIDSSYGEPIEMLSCPSDGTGSCGAYIIRIPCGPRDKYTPKESLWPHV  292
GWHPASIX034616   .LHGLVRGENMELGRDSDTGGQVKYVVELARALANMNGVYRVDLLTRQISSSDIDSSYGEPIEMLSCPSDGTGSCGAYIIRIPCGPRDKYMPKESLWPHI  292

CSS0009603.1     PEFVDGALGHIVNMARVLGEQVDGGKPTWPYVIHGHYADAGEVAARLSGALNVPMVLTGHSLGRNKFEQLLQQGRLSREDINSMYKIMRRIEAEELALDA  370
GWHPASIV029409   PEFVDGALGHIVNMARVLGEQVDGGKPTWPYVIHGHYADAGEVAARLSGALNVPMVLTGHSLGRNKFEQLLQQGRLSREDINSMYKIMRRIEAEELALDA  392
GWHPAZTZ027893   PEFVDGALGHIVNMARVLGEQVDGGKPTWPYVIHGHYADAGEVAARLSGALNVPMVLTGHSLGRNKFEQLLQQGRLSREDINSMYKIMRRIEAEELALDA  392
GWHPBAUV058548   PEFVDGALGHIVNMARVLGEQVDGGKPTWPYVIHGHYADAGEVAARLSGALNVPMVLTGHSLGRNKFEQLLQQGRLSREDINSMYKIMRRIEAEELALDA  392
GWHPASIX032838   PEFVDGALGHIVNMARVLGEQVDGGKPTWPYVIHGHYADAGEVAARLSGALNVPMVLTGHSLGRNKFEQLLQQGRLSREDINSMYKIMRRIEAEELALDA  392
GWHPASIX034616   PEFVDGALGHIVNMARVLGEQVDGGKPTWPYVIHGHYADAGEVAARLSGALNVPMVLTGHSLGRNKFEQLLQQGRLSREDINSMYKIMRRIEAEELALDA  392

CSS0009603.1     AEMVVTSTRQEIDEQWGLYDGFDVKLERKLRVRRQRGVSCLGRHMARMVVIPPGMDFSYVTSQDSLEGDGDLKSLIDFDKNQNRRHVPPIWSEIMRFFIN  470
GWHPASIV029409   AEMVVTSTRQEIDEQWGLYDGFDVKLERKLRVRRQRGVSCLGRHMARMVVIPPGMDFSYVTSQDSLEGDGDLKSLIDFDKNQNRRHVPPIWSEIMRFFIN  492
GWHPAZTZ027893   AEMVVTSTRQEIDEQWGLYDGFDVKLERKLRVRRQRGVSCLGRHMARMVVIPPGMDFSYVTSQDSLEGDGDLKSLIDFDKNQNRRHVPPIWSEIMRFFIN  492
GWHPBAUV058548   AEMVVTSTRQEIDEQWGLYDGFDVKLERKLRVRRQRGVSCLGRHMARMVVIPPGMDFSYVTSQDSLEGDGDLKSLIDFDKNQNRRHVPPIWSEIMRFFIN  492
GWHPASIX032838   AEMVVTSTRQEIDEQWGLYDGFDVKLERKLRVRRQRGVSCLGRHMARMVVIPPGMDFSYVTSQDSLEGDGDLKSLIDFDKNQNRRHVPPIWSEIMRFFIN  492
GWHPASIX034616   AEMVVTSTRQEIDEQWGLYDGFDVKLERKLRVRRQRGVSCLGRHMARMVVIPPGMDFSYVTSQDSLEGDGDLKSLIDFDKNQNRRHVPPIWSEIMRFFIN  492

CSS0009603.1     PHKPMILALSRPDPKKNVTTLLKAFGECRPLRELANMTLILGNRDDIEEMANSSSAVLTTVLKLIDKYDLYGQVAYPKHHKQSDVPEIYRLAAKTKGVFI  570
GWHPASIV029409   PHKPMILALSRPDPKKNVTTLLKAFGECRPLRELANMTLILGNRDDIEEMANSSSAVLTTVLKLIDKYDLYGQVAYPKHHKQSDVPEIYRLAAKTKGVFI  592
GWHPAZTZ027893   PHKPMILALSRPDPKKNVTTLLKAFGECRPLRELANMTLILGNRDDIEEMANSSSAVLTTVLKLIDKYDLYGQVAYPKHHKQSDVPEIYRLAAKTKGVFI  592
GWHPBAUV058548   PHKPMILALSRPDPKKNVTTLLKAFGECRPLRELANMTLILGNRDDIEEMANSSSAVLTTVLKLIDKYDLYGQVAYPKHHKQSDVPEIYRLAAKTKGVFI  592
GWHPASIX032838   PHKPMILALSRPDPKKNVTTLLKAFGECRPLRELANMTLILGNRDDIEEMANSSSAVLTTVLKLIDKYDLYGQVAYPKHHKQSDVPEIYRLAAKTKGVFI  592
GWHPASIX034616   PHKPMILALSRPDPKKNVTTLLKAFGECRPLRELANMTLILGNRDDIEEMANSSSAVLTTVLKLIDKYDLYGQVAYPKHHKQSDVPEIYRLAAKTKGVFI  592

CSS0009603.1     NPALVEPFGLTLIEAAAYGLPIVATKNGGPVDILKALNNGLLIDPHDQKAIADALLKLVADKNLWVECRKNGLKNINRFSWPEHCRNYLSHVENCRNHHP  670
GWHPASIV029409   NPALVEPFGLTLIEAAAYGLPIVATKNGGPVDILKALNNGLLIDPHDQKAIADALLKLVADKNLWVECRKNGLKNINRFSWPEHCRNYLSHVENCRNHHP  692
GWHPAZTZ027893   NPALVEPFGLTLIEAAAYGLPIVATKNGGPVDILKALNNGLLIDPHDQKAIADALLKLVADKNLWVECRKNGLKNINRFSWPEHCRNYLSHVENCRNHHP  692
GWHPBAUV058548   NPALVEPFGLTLIEAAAYGLPIVATKNGGPVDILKALNNGLLIDPHDQKAIADALLKLVADKNLWVECRKNGLKNINRFSWPEHCRNYLSHVENCRNHHP  692
GWHPASIX032838   NPALVEPFGLTLIEAAAYGLPIVATKNGGPVDILKALNNGLLIDPHDQKAIADALLKLVADKNLWVECRKNGLKNINGFSWPEHCRNYLSHVENCRNHHP  692
GWHPASIX034616   NPALVEPFGLTLIEAAAYGLPIVATKNGGPVDILKALNNGLLIDPHDQKAIADALLKLVADKNLWVECRKNGLKNINRFSWPEHCRNYLSHVENCRNHHP  692

CSS0009603.1     TFRLEIMPMPEEPMSDSLRDVEDLSLKFSIDADFKPNGDLDTANRQSKLIEALTQMASSNGHSNISYCPGRRQELFVIATDCYHRDGVCTETLPLVIKNV  770
GWHPASIV029409   TFRLEIMPMPEEPMSDSLRDVEDLSLKFSIDADFKPNGDLDTANRQSKLIEALTQMASSNGHSNISYCPGRRQELFVIATDCYHRDGVCTETLPLVIKNV  792
GWHPAZTZ027893   TFRLEIMPMPEEPMSDSLRDVEDLSLKFSIDADFKPNGDLPTANRQSKLIEALTQMASSNGHSNISYCPGRRQELFVIATDCYHRDGVCTETLPLVIKNV  792
GWHPBAUV058548   TFRLEIMPMPEEPMSDSLRDVEDLSLKFSIDADFKPNGDLPTANRQSKLIEALTQMASSNGHSNISYCPGRRQELFVIATDCYHRDGVCTETLPLVIKNV  792
GWHPASIX032838   TFRLEIMPMPEEPMSDSLRDVEDLSLKFSIDADFKPNGDLPTANRQSKLIEALTQMASSNGHSNISYCPGRRQELFVIATDCYHRDGVCTETLPLVIKNV  792
GWHPASIX034616   TFRLEIMPMPEEPMSDSLRDVEDLSLKFSIDADFKPNGDLTANRQSKLIEALTQMASSNGHSNISYCPGRRQELFVIATDCYHRDGVCTETLPLVIKNV  792

CSS0009603.1     MEAAVSSSSQIGFLLLTGLTLLETKEILKRSHVRLEDFDALVCNSGSTLYYPWRDSVADMDYEAHIEYRWPGENVRSMIMRLGKAEDGEEDDILEYPDAF  870
GWHPASIV029409   MEAAVSSSSQIGFLLLTGLTLLETKEILKRSHVRLEDFDALVCNSGSTLYYPWRDSVADMDYEAHIEYRWPGENVRSMIMRLGKAEDGEEDDILEYPDAF  892
GWHPAZTZ027893   MEAAVSSSSQIGFLLLTGLTLLETKEILKRSHVRLEDFDALVCNSGSTLYYPWRDSVADMDYEAHIEYRWPGENVRSMIMRLGKAEDGEEDDILEYPDAF  892
GWHPBAUV058548   MEAAVSSSSQIGFLLLTGLTLLETKEILKRSHVRLEDFDALVCNSGSTLYYPWRDSVADMDYEAHIEYRWPGENVRSMIMRLGKAEDGEEDDILEYPDAF  892
GWHPASIX032838   MEAAVSSSSQIGFLLLTGLTLLETKEILKRSHVRLEDFDALVCNSGSTLYYPWRDSVADMDYEAHIEYRWPGENVRSMIMRLGKAEDGEEDDILEYPDAF  892
GWHPASIX034616   MEAAVSSSSQIGFLLLTGLTLLETKEILKRSHVRLEDFDALVCNSGSTLYYPWRDSVADMDYEAHIEYRWPGENVRSMIMRLGKAEDGEEDDILEYPDAF  892

CSS0009603.1     SSRCYSYIIKPGAKTRRVDKLRQKLRMRGLRCNIVYTHAASRLECCTIICIKSPNTKVRPSIHNLLNSVGVHHGFVYLSVRWGIDLSKMVVFVGERGDTD  970
GWHPASIV029409   SSRCYSYIIKPGAKTRRVDKLRQKLRMRGLRCNIVYTHAASRLNVVPLFASR...................AQTLFYLSVRWGIDLSKMVVFVGERGDTD  973
GWHPAZTZ027893   SSRCYSYIIKPGAKTRRVDKLRQKLRMRGLRCNIVYTHAASRLNVVPLFASR...................AQTLFYLSVRWGIDLSKMVVFVGERGDTD  973
GWHPBAUV058548   SSRCYSYIIKPGAKTRRVDKLRQKLRMRGLRCNIVYTHAASRLNVVPLFASR...................AQTLFYLSVRWGIDLSKMVVFVGERGDTD  973
GWHPASIX032838   SSRCYSYIIKPGAKTRRVDKLRQKLRMRGLRCNIVYTHAASRLNVVPLFASR...................AQTLFYLSVRWGIDLSKMVVFVGERGDTD  973
GWHPASIX034616   SSRCYSYIIKPGAKTRRVDKLRQKLRMRGLRCNIVYTHAASRLNVVPLFASR...................AQTLFYLSVRWGIDLSKMVVFVGERGDTD  973

CSS0009603.1     YEDLLVGLHKTVILRNSVEFGSEMLLRSEESFKREDVVPQVSPSIAFIEGHEAHDISAALKALQI  1035
GWHPASIV029409   YEDLLVGLHKTVILRNSVEFGSEMLLRSEESFKREDVVPQVSPSIAFIEGHEAHDISAALKALQI  1038
GWHPAZTZ027893   YEDLLVGLHKTVILRNSVEFGSEMLLRSEESFKREDVVPQVSPSIAFIEGHEAHDISAALKALQI  1038
GWHPBAUV058548   YEDLLVGLHKTVILRNSVEFGSEMLLRSEESFKREDVVPQVSPSIAFIEGHEAHDISAALKALQI  1038
GWHPASIX032838   YEDLLVGLHKTVILRNSVEFGSEMLLRSEESFKREDVVPQVSPSIAFIEGHEAHDISAALKALQI  1038
GWHPASIX034616   YEDLLVGLHKTVILRNSVEFGSEMLLRSEESFKREDVVPQVSPSIAFIEGHEAHDISAALKALQI  1038
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Fig. S3c Amino acid sequence alignment diagram of CsSPS3

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CSS0024623.1     MAGNEWINGYLEAILDSGAATVEENKPNLRDGGHFNPTKYFVEEVVTGVDESDLHRTWIKVVATRNTRERSSRLENMCWRIWHLTRKKKQLEWEDFQRMT    100
GWHPAZTZ027407   MAGNEWINGYLEAILDSGAATVEENKPNLRDGGHFNPTKYFVEEVVTGVDESDLHRTWIKVVATRNTRERSSRLENMCWRIWHLTRKKKQLEWEDFQRMT    100
GWHPASIV029106   MAGNEWINGYLEAILDSGAATVEENKPNLRDGGHFNPTKYFVEEVVTGVDESDLHRTWIKVVATRNTRERSSRLENMCWRIWHLTRKKKQLEWEDFQRMT    100
GWHPBAUV054918   .....MDKFYLEAILDSGAATVEENKPNLRDGGHFNPTKYFVEEVVTGVDESDLHRTWIKVVATRNTRERSSRLENMCWRIWHLTRKKKQLEWEDFQRMT    95
GWHPBAUV058088   MAGNEWINGYLEAILDSGAATVEENKPNLRDGGHFNPTKYFVEEVVTGVDESDLHRTWIKVVATRNTRERSSRLENMCWRIWHLTRKKKQLEWEDFQRMT    100


CSS0024623.1     NRRWEREQGRRDATEDMSEDLSEGEKGDVLGDAMVSESPRKKFQRNFSNLEVWSDNNKEKKLYIVLISLHGLVRGENMELGRDSDTGGCYKYVVELARAL    200
GWHPAZTZ027407   NRRWEREQGRRDATEDMSEDLSEGEKGDVLGDAMVSESPRKKFQRNFSNLEVWSDNNKEKKLYIVLISLHGLVRGENMELGRDSDTGGCYKYVVELARAL    200
GWHPASIV029106   NRRWEREQGRRDATEDMSEDLSEGEKGDVLGDAMVSESPRKKFQRNFSNLEVWSDNNKEKKLYIVLISLHGLVRGENMELGRDSDTGGCYKYVVELARAL    200
GWHPBAUV054918   NRRWEREQGRRDATEDMSEDLSEGEKGDVLGDAMVSESPRKKFQRNFSNLEVWSDNNKEKKLYIVLISLHGLVRGENMELGRDSDTGGCYKYVVELARAL    195
GWHPBAUV058088   NRRWEREQGRRDATEDMSEDLSEGEKGDVLGDAMVSESPRKKFQRNFSNLEVWSDNNKEKKLYIVLISLHGLVRGENMELGRDSDTGGCYKYVVELARAL    200


CSS0024623.1     ARMPGVYRVDLFTRQISSPEVDWSYGEPTEMLTAGPEDADAADVGESSGAYIVRIPFGPRDKYMRKELLWPYIQEFVDGALAHILNMSKVLSEQIGGGQP    300
GWHPAZTZ027407   ARMPGVYRVDLFTRQISSPEVDWSYGEPTEMLTAGPEDADAADVGESSGAYIVRIPFGPRDKYMRKELLWPYIQEFVDGALAHILNMSKVLSEQIGGGQP    300
GWHPASIV029106   ARMPGVYRVDLFTRQISSPEVDWSYGEPTEMLTAGPEDADAADVGESSGAYIVRIPFGPRDKYMRKELLWPYIQEFVDGALAHILNMSKVLSEQIGGGQP    300
GWHPBAUV054918   ARMPGVYRVDLFTRQISSPEVDWSYGEPTEMLTAGPEDADAADVGESSGAYIVRIPFGPRDKYMRKELLWPYIQEFVDGALAHILNMSKVLSEQIGGGQP    295
GWHPBAUV058088   ARMPGVYRVDLFTRQISSPEVDWSYGEPTEMLTAGPEDADAADVGESSGAYIVRIPFGPRDKYMRKELLWPYIQEFVDGALAHILNMSKVLSEQIGGGQP    300


CSS0024623.1     VWPYVIHGHYADAGDSAALLSGALNVPMVLTGHSLGRNKLEQLLKQGRQSKEDINSTYKIMRRIEAEELSLDVAELVITSTRQEIDEQWGLYDGFDVKLE    400
GWHPAZTZ027407   VWPYVIHGHYADAGDSAALLSGALNVPMVLTGHSLGRNKLEQLLKQGRQSKEDINSTYKIMRRIEAEELSLDVAELVITSTRQEIDEQWGLYDGFDVKLE    400
GWHPASIV029106   VWPYVIHGHYADAGDSAALLSGALNVPMVLTGHSLGRNKLEQLLKQGRQSKEDINSTYKIMRRIEAEELSLDVAELVITSTRQEIDEQWGLYDGFDVKLE    400
GWHPBAUV054918   VWPYVIHGHYADAGDSAALLSGALNVPMVLTGHSLGRNKLEQLLKQGRQSKEDINSTYKIMRRIEAEELSLDVAELVITSTRQEIDEQWGLYDGFDVKLE    395
GWHPBAUV058088   VWPYVIHGHYADAGDSAALLSGALNVPMVLTGHSLGRNKLEQLLKQGRQSKEDINSTYKIMRRIEAEELSLDVAELVITSTRQEIDEQWGLYDGFDVKLE    400


CSS0024623.1     KVLRARARRGVNCHGRFMPRMAVIPPGMDFGNVEVQEDNTDADGELTSLTNTDGSSPKSVPAIWSEVLRFLTNPHKPMILALSRPDPKKNLTTLLKAFGE    500
GWHPAZTZ027407   KVLRARARRGVNCHGRFMPRMAVIPPGMDFGNVEVQEDNTDADGELTSLTNTDGSSPKSVPAIWSEVLRFLTNPHKPMILALSRPDPKKNLTTLLKAFGE    500
GWHPASIV029106   KVLRARARRGVNCHGRFMPRMAVIPPGMDFGNVEVQEDNTDADGELTSLTNTDGSSPKSVPAIWSEVLRFLTNPHKPMILALSRPDPKKNLTTLLKAFGE    500
GWHPBAUV054918   KVLRARARRGVNCHGRFMPRMAVIPPGMDFGNVEVQEDNTDADGELTSLTNTDGSSPKSVPAIWSEVLRFLTNPHKPMILALSRPDPKKNLTTLLKAFGE    495
GWHPBAUV058088   KVLRARARRGVNCHGRFMPRMAVIPPGMDFGNVEVQEDNTDADGELTSLTNTDGSSPKSVPAIWSEVLRFLTNPHKPMILALSRPDPKKNLTTLLKAFGE    500


CSS0024623.1     CRPLRELANLTLIMGNRDDIDEMSAGNASVLMTVLKLIDKYDLYGSVAFPKHHKQNDVPDIYRLAGKTKGVFINPALVEPFGLTLIEAAAHGLPMVATKN    600
GWHPAZTZ027407   CRPLRELANLTLIMGNRDDIDEMSAGNASVLMTVLKLIDKYDLYGSVAFPKHHKQNDVPDIYRLAGKTKGVFINPALVEPFGLTLIEAAAHGLPMVATKN    600
GWHPASIV029106   CRPLRELANLTLIMGNRDDIDEMSAGNASVLMTVLKLIDKYDLYGSVAFPKHHKQNDVPDIYRLAGKTKGVFINPALVEPFGLTLIEAAAHGLPMVATKN    600
GWHPBAUV054918   CRPLRELANLTLIMGNRDDIDEMSAGNASVLMTVLKLIDKYDLYGSVAFPKHHKQNDVPDIYRLAGKTKGVFINPALVEPFGLTLIEAAAHGLPMVATKN    595
GWHPBAUV058088   CRPLRELANLTLIMGNRDDIDEMSAGNASVLMTVLKLIDKYDLYGSVAFPKHHKQNDVPDIYRLAGKTKGVFINPALVEPFGLTLIEAAAHGLPMVATKN    600


CSS0024623.1     GGPVDIHRALNNGLLIDPHDQQEIASALLKLVSEKNLWSECRKNGWKNIHLFSWPEHCRTYLTRVAASRMRYPQWQTDTPADDFTAEESLNDSLTDVQDM    700
GWHPAZTZ027407   GGPVDIHRALNNGLLIDPHDQQEIASALLKLVSEKNLWSECRKNGWKNIHLFSWPEHCRTYLTRVAASRMRYPQWQTDTPADDFTAEESLNDSLTDVQDM    700
GWHPASIV029106   GGPVDIHRALNNGLLIDPHDQQEIASALLKLVSEKNLWSECRKNGWKNIHLFSWPEHCRTYLTRVAASRMRYPQWQTDTPADDFTAEESLNDSLTDVQDM    700
GWHPBAUV054918   GGPVDIHRALNNGLLIDPHDQQEIASALLKLVSEKNLWSECRKNGWKNIHLFSWPEHCRTYLTRVAASRMRYPQWQTDTPADDFTAEESLNDSLTDVQDM    695
GWHPBAUV058088   GGPVDIHRALNNGLLIDPHDQQEIASALLKLVSEKNLWSECRKNGWKNIHLFSWPEHCRTYLTRVAASRMRYPQWQTDTPADDFTAEESLNDSLTDVQDM    700


CSS0024623.1     SLRLSVDGEKSSLNESLBHMAATSGDPELQDQVKHVLSRMRKPBIDPQDPDGNRKLLDNIGSKYPMLRRRRRLIVIALDCYDSNGAPEKKMIRIIQEIFR    800
GWHPAZTZ027407   SLRLSVDGEKSSLNESLBHMAATSGDPELQDQVKHVLSRMRKPBIDPQDPDGNRKLLDNVGSKYPMLRRRRRLIVIALDCYDSNGAPEKKMIRIIQEIFR    800
GWHPASIV029106   SLRLSVDGEKSSLNESLBHMAATSGDPELQDQVKHVLSRMRKPDMDPQDPDGNRKLLDNIGSKYPMLRRRRRLIVIALDCYDSNGAPEKKMIRIIQEIFR    800
GWHPBAUV054918   SLRLSVDGEKSSLNESLBHMAATSGDPELQDQVKHVLSRMRKPBIDPQDPDGNRKLLDNVGSKYPMLRRRRRLIVIALDCYDSNGAPEKKMIRIIQEIFR    795
GWHPBAUV058088   SLRLSVDGEKSSLNESLBHMAATSGDPELQDQVKHVLSRMRKPBIDPQDPDGNRKLLDNVGSKYPMLRRRRRLIVIALDCYDSNGAPEKKMIRIIQEIFR    800


CSS0024623.1     AVNVVSQTARFSGFALSTAMSMLELTAFLKSGNIQVNEFDALICSSGSEVYYPGTYKNADGSLYPDPDYATHIDYRWGCDGLKKTIWKLMNSHBGGSSHS    900
GWHPAZTZ027407   AVNVVSQTARFSGFALSTAMSMLELTAFLKSGNIQVNEFDALICSSGSEVYYPGTYKNADGSLYPDPDYATHIDYRWGCDGLKKTIWKLMNSHBGGSSHS    900
GWHPASIV029106   AVNVVSQTARFSGFALSTAMSMLELTAFLKSGNIQVNEFDALICSSGSEVYYPGTYKNADGSLYPDPDYATHIDYRWGCDGLKKTIWKLMNSHBGGSSHS    900
GWHPBAUV054918   AVNVVSQTARFSGFALSTAMSMLELTAFLKSGNIQVNEFDALICSSGSEVYYPGTYKNADGSLYPDPDYATHIDYRWGCDGLKKTIWKLMNSHDGGSSHS    895
GWHPBAUV058088   AVNVVSQTARFSGFALSTAMSMLELTAFLKSGNIQVNEFDALICSSGSEVYYPGTYKNADGSLYPDPDYATHIDYRWGCDGLKKTIWKLMNSHBGGSSHS    900


CSS0024623.1     SSPIEEVVKSGNSHCVSYLIKDISKAKKVDDLRQKFRMRGLRCHPMYCRNSTRMQVIPLLASRAQALRYLFVRWRLNVASMYVILGETGDTDYEELISGT    1000
GWHPAZTZ027407   SSPIEEVVKSGNSHCVSYLIKDISKAKKVDDLRQKFRMRGLRCHPMYCRNSTRMQVIPLLASRAQALRYLFVRWRLNVASMYVILGETGDTDYEELISGT    1000
GWHPASIV029106   SSPIEEVVKSGNSHCVSYLIKDISKAKKVDDLRQKFRMRGLRCHPMYCRNSTRMQVIPLLASRAQALRYLFVRWRLNVASMYVILGETGDTDYEELISGT    1000
GWHPBAUV054918   SSPIEEVVKSGNSHCVSYLIKDISKAKKVDDLRQKFRMRGLRCHPMYCRNSTRMQVIPLLASRAQALRYLFVRWRLNVASMYVILGETGDTDYEELISGT    995
GWHPBAUV058088   SSPIEEVVKSGNSHCVSYLIKDISKAKKVDDLRQKFRMRGLRCHPMYCRNSTRMQVIPLLASRAQALRYLFVRWRLNVASMYVILGETGDTDYEELISGT    1000


CSS0024623.1     HKTIIMKGVVEKGSEELLRTAGSYLKDDIVPEESPLVTYTSGEATANETANALKGISKSSNCI.................................       1063
GWHPAZTZ027407   HKTIIMKGVVEKGSEELLRTAGSYLKDDIVPEESPLVTYTSGEATANETANALKGISKSSNCI.................................       1063
GWHPASIV029106   HKTIIMKGVVEKGSEELLRTAGSYLKDDIVPEESPLVTYTSGEATANEVANALKGISKSSNYMSKGLMSFRYGIMHALADSFIGKLISFLFRSLVLGDFL   1100
GWHPBAUV054918   HKTIIMKGVVEKGSEELLRTAGSYLKDDIVPEESPLVTYTSGEATANETANALKGISKSSNCI.................................       1058
GWHPBAUV058088   HKTIIMKGVVEKGSEELLRTAGSYLKDDIVPEESPLVTYTSGEATANETANALKGISKSSNCI.................................       1063


CSS0024623.1     ....................................................................................................    1063
GWHPAZTZ027407   ....................................................................................................    1063
GWHPASIV029106   AWPVRPDCSSEPHSVSAVLIQALLPVVTFSDLVAPPESCAVCLYERAAEAYKHAKSQSNAQAMFNLGYMHEHGEGLPFDLHLAKRYYDQALEIDPAAKLP   1200
GWHPBAUV054918   ....................................................................................................    1058
GWHPBAUV058088   ....................................................................................................    1063


CSS0024623.1     ..............................................................................                         1063
GWHPAZTZ027407   ..............................................................................                         1063
GWHPASIV029106   VTLALASLWVRKNYENSFMVDMIDSLPDVFPKMEAWVENVIMKEGNATILTLFVCLLTVLYLHRSLDSLFTHLPRSKPLLLNPITV                 1286
GWHPBAUV054918   ..............................................................................                         1058
GWHPBAUV058088   ..............................................................................                         1063
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Fig. S4d Amino acid sequence alignment diagram of CsSPS4

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CSS0014426.1    MAGNDWINSYLEAILDVGPGLDDAKSSLLLRERGRFSPTRYFVEQVITGFDETDLYRSWVRAAATRSPQERNTRLENMCWRIWNLARQKKQLEGEEVQRM    100
GWHPASIV043378  MAGNDWINSYLEAILDVGPGLDDAKSSLLLRERGRFSPTRYFVEQVITGFDETDLYRSWVRAAATRSPQERNTRLENMCWRIWNLARQKKQLEGEEVQRM    100
GWHPAZTZ041380  MAGNDWINSYLEAILDVGPGLDDAKSSLLLRERGRFSPTRYFVEQVITGFDETDLYRSWVRAAATRSPQERNTRLENMCWRIWNLARQKKQLEGEEVQRM    100
GWHPBAUV084526  MAGNDWINSYLEAILDVGPGLDDAKSSLLLRERGRFSPTRYFVEQVITGFDETDLYRSWVRAAATRSPQERNTRLENMCWRIWNLARQKKQLEGEEVQRM    100
GWHPASIX048616  MAGNDWINSYLEAILDVGPGLDDAKSSLLLRERGRFSPTRYFVEQVITGFDETDLYRSWVRAAATRSPQERNTRLENMCWRIWNLARQKKQLEGEEVQRM    100

CSS0014426.1    AKRRLERERGRKEATADMSEDLSEGEKGDTVSDLSAHGDNTRGRLRRISSVETMEAWASQQKGKKLYIVLISLHGLIRGENMELGRDSDTGGQVKYVVEL    200
GWHPASIV043378  AKRRLERERGRKEATADMSEDLSEGEKGDTVSDLSAHGDNTRGRLRRISSVETMEAWASQQKGKKLYIVLISLHGLIRGENMELGRDSDTGGQVKYVVEL    200
GWHPAZTZ041380  AKRRLERERGRKEATADMSEDLSEGEKGDTVSDLSAHGDNTRGRLRRISSVETMEAWASQQKGKKLYIVLISLHGLIRGENMELGRDSDTGGQVKYVVEL    200
GWHPBAUV084526  AKRRLERERGRKEATADMSEDLSEGEKGDTVSDLSAHGDNTRGRLRRISSVETMEAWASQQKGKKLYIVLISLHGLIRGENMELGRDSDTGGQVKYVVEL    200
GWHPASIX048616  AKRRLERERGRKEATADMSEDLSEGEKGDTVSDLSAHGDNTRGRLRRISSVETMEAWASQQKGKKLYIVLISLHGLIRGENMELGRDSDTGGQVKYVVEL    200

CSS0014426.1    ARALGSMPGVYRVDLLTRQVSSPEVDWSYGEPTEMLPPRYSDGLMNEMGESSGSYIIRIPFGPREKYIPKESLWPHIPEFVDGALNHIIQMSKVLGEQIG    300
GWHPASIV043378  ARALGSMPGVYRVDLLTRQVSSPEVDWSYGEPTEMLPPRYSDGLMNEMGESSGSYIIRIPFGPREKYIPKESLWPHIPEFVDGALNHIIQMSKVLGEQIG    300
GWHPAZTZ041380  ARALGSMPGVYRVDLLTRQVSSPEVDWSYGEPTEMLPPRYSDGLMNEMGESSGSYIIRIPFGPREKYIPKESLWPHIPEFVDGALNHIIQMSKVLGEQIG    300
GWHPBAUV084526  ARALGSMPGVYRVDLLTRQVSSPEVDWSYGEPTEMLPPRYSDGLMNEMGESSGSYIIRIPFGPREKYIPKESLWPHIPEFVDGALNHIIQMSKVLGEQIG    300
GWHPASIX048616  ARALGSMPGVYRVDLLTRQVSSPEVDWSYGEPTEMLPPRYSDGLMNEMGESSGSYIIRIPFGPREKYIPKESLWPHIPEFVDGALNHIIQMSKVLGEQIG    300

CSS0014426.1    GGQPVWFVAIHGHYADAGDAAALLSGALNVPMLFTGHSLGRDKLEQLLRQGRLSKDEINTTYKIMRRIEAEELSLDASEIVITSTRQEIAEQWRLYDGFD    400
GWHPASIV043378  GGQPVWFVAIHGHYADAGDAAALLSGALNVPMLFTGHSLGRDKLEQLLRQGRLSKDEINTTYKIMRRIEAEELSLDASEIVITSTRQEIAEQWRLYDGFD    400
GWHPAZTZ041380  GGQPVWFVAIHGHYADAGDAAALLSGALNVPMLFTGHSLGRDKLEQLLRQGRLSKDEINTTYKIMRRIEAEELSLDASEIVITSTRQEIAEQWRLYDGFD    400
GWHPBAUV084526  GGQPVWFVAIHGHYADAGDAAALLSGALNVPMLFTGHSLGRDKLEQLLRQGRLSKDEINTTYKIMRRIEAEELSLDASEIVITSTRQEIAEQWRLYDGFD    400
GWHPASIX048616  GGQPVWFVAIHGHYADAGDAAALLSGALNVPMLFTGHSLGRDKLEQLLRQGRLSKDEINTTYKIMRRIEAEELSLDASEIVITSTRQEIAEQWRLYDGFD    400

CSS0014426.1    PVLERKLRARIRRNVSCYGRFMPRMVVMPPGMEFHHIVPHDGDAEGETEANEDQPASFEPPIWPEIMRFFSNPRKPMILALARPDPKKNLTTLVKAFGEC    500
GWHPASIV043378  PVLERKLRARIRRNVSCYGRFMPRMVVMPPGMEFHHIVPHDGDAEGETEANEDQPASFEPPIWPEIMRFFSNPRKPMILALARPDPKKNLTTLVKAFGEC    500
GWHPAZTZ041380  PVLERKLRARIRRNVSCYGRFMPRMVVMPPGMEFHHIVPHDGDAEGETEANEDQPASFEPPIWPEIMRFFSNPRKPMILALARPDPKKNLTTLVKAFGEC    500
GWHPBAUV084526  PVLERKLRARIRRNVSCYGRFMPRMVVMPPGMEFHHIVPHDGDAEGETEANEDQPASFEPPIWPEIMRFFSNPRKPMILALARPDPKKNLTTLVKAFGEC    500
GWHPASIX048616  PVLERKLRARIRRNVSCYGRFMPRMVVMPPGMEFHHIVPHDGDAEGETEANEDQPASFEPPIWPEIMRFFSNPRKPMILALARPDPKKNLTTLVKAFGEC    500

CSS0014426.1    RPLRELANLTLIMGNRDDVDEMSSTSASLLLSILKLIDKYDLYGQVAYPKHHKQSDVPDIYRLAAKTKGVFINPAFIEPFGLTLIEAAAYGLPIVATKNG    600
GWHPASIV043378  RPLRELANLTLIMGNRDDVDEMSSTSASLLLSILKLIDKYDLYGQVAYPKHHKQSDVPDIYRLAAKTKGVFINPAFIEPFGLTLIEAAAYGLPIVATKNG    600
GWHPAZTZ041380  RPLRELANLTLIMGNRDDVDEMSSTSASLLLSILKLIDKYDLYGQVAYPKHHKQSDVPDIYRLAAKTKGVFINPAFIEPFGLTLIEAAAYGLPIVATKNG    600
GWHPBAUV084526  RPLRELANLTLIMGNRDDVDEMSSTSASLLLSILKLIDKYDLYGQVAYPKHHKQSDVPDIYRLAAKTKGVFINPAFIEPFGLTLIEAAAYGLPIVATKNG    600
GWHPASIX048616  RPLRELANLTLIMGNRDDVDEMSSTSASLLLSILKLIDKYDLYGQVAYPKHHKQSDVPDIYRLAAKTKGVFINPAFIEPFGLTLIEAAAYGLPIVATKNG    600

CSS0014426.1    GPVDIHRVLNNGLLIDPHDQQSIADALLKLVSDNQLWAKCRQNGLKNIHLFSWPEHCKTYLSRIASCKLRQPWWQRNDDGDENSESDSPSDSLRDISLNL    700
GWHPASIV043378  GPVDIHRVLNNGLLIDPHDQQSIADALLKLVSDNQLWAKCRQNGLKNIHLFSWPEHCKTYLSRIASCKLRQPWWQRNDDGDENSESDSPSDSLRDISLNL    700
GWHPAZTZ041380  GPVDIHRVLNNGLLIDPHDQQSIADALLKLVSDNQLWAKCRQNGLKNIHLFSWPEHCKTYLSRIASCKLRQPWWQRNDDGDENSESDSPSDSLRDISLNL    700
GWHPBAUV084526  GPVDIHRVLNNGLLIDPHDQQSIADALLKLVSDNQLWAKCRQNGLKNIHLFSWPEHCKTYLSRIASCKLRQPWWQRNDDGDENSESDSPSDSLRDISLNL    700
GWHPASIX048616  GPVDIHRVLNNGLLIDPHDQQSIADALLKLVSDNQLWAKCRQNGLKNIHLFSWPEHCKTYLSRIASCKLRQPWWQRNDDGDENSESDSPSDSLRDISLNL    700

CSS0014426.1    KFSMDGEKNEGSYNADSSLESEDRKSKLENAVLTWSKGVQKGTQKAGFTEKADQNSSAGKFPALRRRKHIIVIAVDFDAITDLFESARKIFDSVEKERTE    800
GWHPASIV043378  KFSMDGEKNEGSYNADSSLESEDRKSKLENAVLTWSKGVQKGTQKAGFTEKADQNSSAGKFPALRRRKHIIVIAVDFDAITDLFESARKIFDSVEKERTE    800
GWHPAZTZ041380  KFSMDGEKNEGSYNADSSLESEDRKSKLENAVLTWSKGVQKGTQKAGFTEKADQNSSAGKFPALRRRKHIIVIAVDFDAITDLFESARKIFDSVEKERTE    800
GWHPBAUV084526  KFSMDGEKNEGSYNADSSLESEDRKSKLENAVLTWSKGVQKGTQKAGFTEKADQNSSAGKFPALRRRKHIIVIAVDFDAITDLFESARKIFDSVEKERTE    800
GWHPASIX048616  KFSMDGEKNEGSYNADSSLESEDRKSKLENAVLTWSKGVQKGTQKAGFTEKADQNSSAGKFPALRRRKHIIVIAVDFDAITDLFESARKIFDSVEKERTE    800

CSS0014426.1    GSVGFILATSFTLSEIQSFLISGGLSPTDFDAFICNSGGDLYYSSPNSEDNPFVVDLYYHSHIEYRWGGEGLRKTLVRWAGSITDKTGENEEKIVTEDEK    900
GWHPASIV043378  GSVGFILATSFTLSEIQSFLISGGLSPTDFDAFICNSGGDLYYSSPNSEDNPFVVDLYYHSHIEYRWGGEGLRKTLVRWAGSITDKTGENEEKIVTEDEK    900
GWHPAZTZ041380  GSVGFILATSFTLSEIQSFLISGGLSPTDFDAFICNSGGDLYYSSPNSEDNPFVVDLYYHSHIEYRWGGEGLRKTLVRWAGSITDKTGENEEKIVTEDEK    900
GWHPBAUV084526  GSVGFILATSFTLSEIQSFLISGGLSPTDFDAFICNSGGDLYYSSPNSEDNPFVVDLYYHSHIEYRWGGEGLRKTLVRWAGSITDKTGENEEKIVTEDEK    900
GWHPASIX048616  GSVGFILATSFTLSEIQSFLISGGLSPTDFDAFICNSGGDLYYSSPNSEDNPFVVDLYYHSHIEYRWGGEGLRKTLVRWAGSITDKTGENEEKIVTEDEK    900

CSS0014426.1    ISTNYCYAFKVQKTGKVPPVKEIRKLMRIQALRCHVIYCQNGHKINVIPVLASRSEALRYLYLRWGVDLSKMVVFVGESGDTDYEGLLGGIHKSVILKGV    1000
GWHPASIV043378  ISTNYCYAFKVQKEGKVPPVKEIRKLMRIQALRCHVIYCQNGHKINVIPVLASRSEALRYLYLRWGVDLSKMVVFVGESGDTDYEGLLGGIHKSVILKGV    1000
GWHPAZTZ041380  ISTNYCYAFKVQKEGKVPPVKEIRKLMRIQALRCHVIYCQNGHKINVIPVLASRSEALRYLYLRWGVDLSKMVVFVGESGDTDYEGLLGGIHKSVILKGV    1000
GWHPBAUV084526  ISTNYCYAFKVQKEGKVPPVKEIRKLMRIQALRCHVIYCQNGHKINVIPVLASRSEALRYLYLRWGVDLSKMVVFVGESGDTDYEGLLGGIHKSVILKGV    1000
GWHPASIX048616  ISTNYCYAFKVQKEGKVPPVKEIRKLMRIQALRCHVIYCQNGHKINVIPVLASRSEALRYLYLRWGVDLSKMVVFVGESGDTDYEGLLGGIHKSVILKGV    1000

CSS0014426.1    CSSASTILHANRNYPLSDVLPFDSPNIVQTTEECSSADLRTSLEKFGLLK    1050
GWHPASIV043378  CSSASTILHANRNYPLSDVLPFDSPNIVQTTEECSSADLRTSLEKFGLLK    1050
GWHPAZTZ041380  CSSASTILHANRNYPLSDVLPFDSPNIVQTTEECSSADLRTSLEKFGLLK    1050
GWHPBAUV084526  CSSASTILHANRNYPLSDVLPFDSPNIVQTTEECSSADLRTSLEKFGLLK    1050
GWHPASIX048616  CSSASTILHANRNYPLSDVLPFDSPNIVQTTEECSSADLRTSLEKFGLLK    1050
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Fig. S5e Amino acid sequence alignment diagram of CsSPS5

Supplemental S1. Amino acid sequences alignment analysis of CsSPP and CsSPSs.