Multiple sequence alignment (SCPP6).

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                     5    10    15    20    25    30    35    40    45    50    55    60    65    70    75
conservation      *******  !  **   *  !*!  !***!  *!   **!!  **! !   *!*   !  !  ***   *!!   **  ****  *       **              *  *
SCPP6`PP     AGGCTTATAGTGTTGTTGCTCATATGTGTTCTAGCAGGAACCATTTGGAGTTCTGCTCAACGAACCAAGGTCTGAGGTACTG..   78
SCPP6`LW     AGGCTTATAGCGTTGCTCACATGTTTTCTAGCTGGAACCATTTGGAGTTCCGATATTCTTTTCTCCATAT...........   72
SCPP6`DR     AGGCTTATAGTGATGATCGTGTGCTTCTTGCTGGAACCATCCGCTGTTCCGATCTCCCCAAATGCTGATTTAAAGGAATC   83
SCPP6`CI     AGGCTTATAGCGTTGCTCGTGTGTGTTTTCTAGCTGGAACCATCTGGAGTTCCATCCTCACTGTCTGGGTCTGAAGTACTG..   81
SCPP6-C1`CC  ...............................................................................   0
SCPP6-C2`CC  AGGCTTCTAACATTGCTCGCATGCTTTCTAGCTGGAACCATCTGCAGTTCCGTCCTCGGCGTCTGAGTCTGAGGTATTG..   81
SCPP6-C1`SG  ...CTTCAAGCGTTGCTCGCATGTTTTCTAGCTGGAACCACTGGAGTTCCTGATCTCCCCAAATGCTGATTTGATGGAATC   77
SCPP6-C2`SG  .......CTAGCGTTCCTCGCATGCTTTTTAGCTGGAACCATCTGGAGTTCCAATCTCTCCAAATGCTGATTTGATGGAT.   72
SCPP6-C1`SR  AGGCTTCAAGCATTGCTCGCATGTTTTCTAGCTGGAACCATCTGGAGTTCCGATCTCCCCAAATGCTGATTTGATGGAATC   83
SCPP6-C2`SR  AAGACAGTAATTTTATTTGCATGTTTTCTTGGTCTGTCTTTGGCATTGCAGGCTGAAGTTCACCAGCGTGCGGGTTCGC..   81
SCPP6-C1`SA  AGGCTTCAAGCATTGCTCGCATGTTTTCTAGCTGGAACCATCTGGAGTTCCGATCTCCCCAAATGCTGATTTGATGGAATC   83
SCPP6-C2`SA  ......CTAGCATTGCTCGCATGCTTTCTAGCTGGAACCATCTGGAGTTCGTCCTCACTGTCTTGATCTGAGGTATTG..   72

                     80   85    90    95    100   105   110   115   120   125   130   135   140   145   150   155
conservation        **  *  **    **  *****   ****** *  ****  ****** *** **********  **!*!***!  *!!!  *!!**
SCPP6`PP     .GTCCAAGCCCATCATGTGCCACAACAGTTTCAGCCTAAATCTCCCAAAGTTCCCTCTGGTTCTGAGCAACAGCTGGCCA   157
SCPP6`LW     .ATAAATTCTAACTCTCATTATAGGAGAGCTGTCGGGTGTAGGGTTAGGAGTGCCTCTGGTCCTCAGCAACAGGTGCCC.   151
SCPP6`DR     GCTGTCAGTGGGAGATATG...CAACAGTTTCAGCCTGGATCTTCCTAGAATGCTCTCTGGACTTCATCAACAGGTGCCC.   159
SCPP6`CI     .GTACAAGCAAAACATGTGCCACAGCAGTTCCAGCCTAAATCTCCCAGAGTG.........CCTCAGACACACCTGGCCA   151
SCPP6-C1`CC  ...............................................................................   0
SCPP6-C2`CC  .GTACAAGCCCACCATGTGCCATTGCAGTTTCTGCCTGAATCTCCCAGAATGCTCTCTGGTCCTCAGCCACATCTGCCCA   160
SCPP6-C1`SG  AGTCCCAGTGGGAGATATGCCAGCGCAGGGAACCCCAGTGATACAGTCCTCACTGCCTGGATCTGAGCCACATCTGCCCA   157
SCPP6-C2`SG  .TTGCTCAAATTTGATAAAAACCAGCAGTTTCAGCCTGAATCTCCCGGAGTTCTCTGGTCCTCAGCCACATCTGCCCA   151
SCPP6-C1`SR  AGTCCCAGTGGGAGATATGCCAGCACAGGGAACCCCAGTGATACAGTCCTCACTGCCTGGATCTGAGCCACATATGCCCA   163
SCPP6-C2`SR  .TCATTATCCAGCTCGGATTCTGATGAGTTTCAGCCTGAATCTCCCAGAATGCTCTCTGGTCCTCAGCCACATCTGCCCA   160
SCPP6-C1`SA  AGTCCCAGTGGGAGATATGCCAGCGCAGGGAACCCCAGTGATACAGTCCTCACTGCCTGGATCTGAGCCACAGCTGCCCA   163
SCPP6-C2`SA  .GTACAAGCCCAACATGTGCCACAGCAGTTTCAGCCTGAATCTCCCAGAATGCTCTCTGGTCCTCAGCCACATCTGCCCA   151

                     160  165   170   175   180   185   190   195   200   205   210   215   220   225   230   235
conservation      *  ********* ******** *** ********* ***  *******  !***!!  *****   *** !***!!*!***!!*
SCPP6`PP     CTCTGACCAATCCATGGGCCTACCAACCCAACCCCAAAGCAGGTCTCGGTCAACTTCCTGCACCCTTTCAATACTTTCCC   237
SCPP6`LW     CTCTGACCAATCCATGGGCCTCCACCCAACCCCAATACAGGTTTCGGTCAACTTCCAGCACACATTCAATACTTTCCC   231
SCPP6`DR     ........AATCCATGGGCCTCTCAACCCAACCCCAGTACTGCTGTCAGACAGCATCCAGCACAGTTTCAGTACCTTCCT   231
SCPP6`CI     CTCTGACCAATCCATGGGTC...CAACCCAACCCCAATACAGGTCTCAGTCAA.........CACTTTCAATACATTCCC   219
SCPP6-C1`CC  ...............................................................................   0
SCPP6-C2`CC  CTCTGACCAATCCAAGGGCCTCTCAAACCAACCCCAATATTGGTCTCAGTCAACTTCCTGCACACTTTCAGTACTTACCC   240
SCPP6-C1`SG  CTCTGACCAATCCATGGGCATCTCAAACCAACCCCAATACTGGTCTCAGTCAGCTTCCAGAACACTTCCAGTACTTACCC   237
SCPP6-C2`SG  CA.................TCTGCCCATTCTGACCAATCTATGGCCTCTCAACTTCTTGCACACTTTCAGTGCTCACCC   213
SCPP6-C1`SR  CTCTGACCAATCCATGGGCCTCTCAAACCAACCCCAATATTGGTCTCAGTCAGCTTCCAGTACACTTTCAGTACTTACCC   243
SCPP6-C2`SR  CCCTGACCAATCTATGGGCCTCTCAAACCAACCCCAATATTGGTCTCAGTCAACTTCCTGCACACTTTCAGTACTTACCC   240
SCPP6-C1`SA  CTCTGACCAATCCATGGACATCTCAAACCAACCCCAATACTGGTCTCAGTCAGCTTCCAGTACACTTCCAGTACTTACCC   243
SCPP6-C2`SA  CTCTGACCAATCTATGGGCCTCTCAAACCAACCCGAATATTGGTCTCAGTCAACTTCCTGCACATTTTCAGTGCTTACCC   231

                     240  245   250   255   260   265   270   275   280   285   290   295   300   305   310
conservation      * !* ******  **!*!!!!*!**  !!!!!!!!  !*!!!!!!! !*!!!!  !!!!!!!!!!  **!*!!!**!*!!!!!*!  !!!!*      **
SCPP6`PP     TATTCTCATCCCCTGCAACTTCAGTTTTTCTATTATCCCATTCTTGGACCACAATCCAGGGAACCTAACATTC......TC   311
SCPP6`LW     TATTCTCATCCCCAGCAACCGCAGTTTTTCTACTATCCCATTCTTGGACCACAATCCAGGGAACCCAACATTC......TC   305
SCPP6`DR     TAT......TCTCAGCAACCGCAGTTTTTCTACTATCCCATTCTTGGACAGCAATCAAGGGAACCCGACATTC......TC   299
SCPP6`CI     TATCCTCATCCCAGCAACCACAGTTTTTCTATTATCCCATTCTTGGATCACAATCCAGGAACCCAACATTC......CC   293
SCPP6-C1`CC  ..................CAGTTTTTCTATTATTCAGTT...GGACCACAATCAAGGGAACCCACCATTC......TC   50
SCPP6-C2`CC  TATTCTCATTCCCAGCAACCACAGTTTTTCTATTATCGAATTCTTGGATCACAATCACGGAACCCATCATTC......TC   314
SCPP6-C1`SG  TATCCTCATGCCCAGCAACCGCAGCTTTTTTATTATCCAATTCTTGGACCACAATAAAAGAACCCACCATTC......TC   311
SCPP6-C2`SG  AATCCTCATTCCCAGCAACAGCAGTTTTTTTATTATCCAATTCTTGGATCACAATCAAGGAACCAATCATTC......TT   287
SCPP6-C1`SR  TATCCTCATGCCCAGCAACCGCAGTTTTTTTATTATCCAATTCTTGGACCACAATAAAAGAACCCACCATTC......TC   317
SCPP6-C2`SR  AATCCTCATTCCCAGCAACAGCAGTTTTTTTATTATCCAATTCTTGGATCTCAATCAAGGAACTCATCATTTCCAGCATC   320
SCPP6-C1`SA  TATCCTCATGCCCAGCAACCGCAGTTTTTTTATTATCAATTCTTGGACCACAATAAAAGAACCCACCAGTA......AG   317
SCPP6-C2`SA  AATCCTCATTCCCAGCAACAGCAGTTTTTTTATTATCCAATTCTTGGGTCACAATCAAGGAACCCATCATTC......TC   305

                     315  320   325   330   335   340   345   350   355   360   365              370
conservation      !!!!!!!!!!!  *! !!!!**! !!!!*!  ********!  ****   *******!!!*********  ***            *****!*!
SCPP6`PP     CTATGGAGTGCCTGTTTTTCCAGCACGCATCATAT...CAACAATATCCTGCTAATTCA..............GTTCCAG   373
SCPP6`LW     CTATGGAGTGCCTGTTTTTCCAGCACGCAACGTCT...CAACAATATCCTGCTAATGCA..............GTTACAG   367
SCPP6`DR     CTATGGAGTGTCTGCTTTCCAGCATGCTGCATCC...CAACAATATCCTGCTAATGCA..............GCTCCAG   361
SCPP6`CI     CTATGGAGTGCCTGTTTTCCAGCACGCAACTCT...CAACAATATCCTGCAAATGTA..............GTTCCAG   355
SCPP6-C1`CC  CTATGGAGTGCCAGCTTTCCAGCATGCAACCATCT...CAGCAACAATACCCGCTAATGCA..............GTTCCAG   112
SCPP6-C2`CC  CTATGGAGTGCCTGGTTTCTAGCACGCAACCATCTCAACAACAATATACTGCTAATGCA..............GTTCCAG   379
SCPP6-C1`SG  CTATGGAGTGCCTGGTTTCCAGCATTCGCTTTGG........ATAAAAGCGTCTGCTAAATGTAAATGTAAATTTCCAG   382
SCPP6-C2`SG  CTATGGAGTGCCTGTTTTCCAGCACACATCT......CAACAATATCCTGCTAATGCA..............GTTCCAG   346
SCPP6-C1`SR  CTATGGAGTGCCTGGTTTCCAGCATGTAACATCTTCAAGAAACTACTAAAAACATCTTTTTTGATTGCTT...CTGTTGT   394
SCPP6-C2`SR  CTATGGAGTGCCTGGTTTCCAGCACAACATCT...CAACAATATCCTGCGAATGCA..............GTTCCAG   382
SCPP6-C1`SA  AGTG...TTTCCATCATTCATTCAGTGTACAATATCAGAAATATATCTGAAGCGTTTTGATTTATTGAGGAAACCCGCTG   394
SCPP6-C2`SA  CTATGGAGTGCCTGTTTTCCAGCACACAACATCT...CAACAATATCCTGCTAATGCA..............GTTCCAG   367

                     375  380   385   390   395   400   405   410   415   420   425   430   435   440   445   450
conservation      !*!*!*!**! ****!***** ******  *!**!***!!**!! !!!*!!!!!**  **      !!*!       *!!!!!**!!!!!*!!!!!*!
SCPP6`PP     CTTCACAACTATTAATGGCACAAAACAAACAACACAAGCCAAATGCTCATCATGCATCCATACCAGCCTTCAGCAAGAA   453
SCPP6`LW     CTTCACAACCATTCATGGCACAAAACAAACAACACAAGCAC.......CAAATGCATCCAAACCAGCCTTCAGCAACAA   438
SCPP6`DR     CTTTACGGCCAGCAAGACCACAACCAGGGGCAAAATGCACACCAAATGCGTCAGCCTCAACAACAACAACAACAACAA   441
SCPP6`CI     CTTCACAGTCATTAATGGCACAAAACAAACAACACAAGCCAAATGCTCACCAAATGCATCCAAACCAACCTCAGCAACAA   435
SCPP6-C1`CC  CTTCACAGCCATTGATGATACAAAACAAACAACACAAGCCT........CTA...AACCAGCCTCAGCAACAG   174
SCPP6-C2`CC  CTTCACAGCCATTAATGACACAAAACAACACAAATAACACAAGCCT........CTA...AACCAGCCTCAGCAACAG   441
SCPP6-C1`SG  CTTCACAGCCATTAATGACAAAAACAAACAACACAAGCCT........CTA...AACCAGCCTCAGCAACAG   444
SCPP6-C2`SG  CTTCACAGCCATTAATGACAAAACACAAACAACACAAGCCT........CTA...AACCAGCCTAAGCAATAT   408
SCPP6-C1`SR  CCTCATTTCCATTAATGACACAAAACAAACAACACAAGCCT........CTA...AACCAGCCTCAGCAACAG   456
SCPP6-C2`SR  CTTCACAGCCATTAATGACACAAAACAAACAACACAAGCCT........CTA...AACCAGCCTAAGCAATAT   444
SCPP6-C1`SA  CACTCGATCCATTAATGACAAAACACAAACAACACAAGCCT........CTA...AACCAGCCTCAGCAACAG   456
SCPP6-C2`SA  CTTCACAGCCATTAATGATACAAACACAAACAACACAAGCCT........CTA...AACCAGCCTAAGCAATAT   429
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             455     460       465              470   475   480   485   490   495   500   505   510   515   520
conservation   !!*******  ***              ****************** ********  ************  ************  **************
SCPP6`PP     CAGGTTCAACAA...........TTTCTTTACATGGTTCCACAGATTCAACAACGAATGGCTGGACCATATGGTGGATT  521
SCPP6`LW     CAGGTTCAACAA...........TTTCTTTACATGGTTCCACAGACTCAACAACGAATGGCTGGACCATATGGTGGATT  506
SCPP6`DR     CAGTTTCAACCC.......ATTTTTTATATGGTTCCTCAAATGCCACAGCGAATGGCTGGATCATATGGTGGACT  509
SCPP6`CI     CAGGTTCAACAA...........TTTCTTTACATGGTTCCACAGATTCAACAGCGAATGGCTGGACCATATGGCGGATT  503
SCPP6-C1`CC  CAGGTTCATCAA...........TTTCTTTACATGGTTCCACAGATTCAACAACGAATGGCTGGACCATATGGTGGATT  242
SCPP6-C2`CC  CAGGTATCAACACAAACATTAATATTATTATATTATATT..............  480
SCPP6-C1`SG  CAGGTTCATCAA...........TTTCTTTACATGGTTCCACAAATTCAACAACGAATGGCTGGACCATATGGTGGATT  512
SCPP6-C2`SG  CAATCTTAAACA..............  420
SCPP6-C1`SR  CAGGTTCATCAA...........TTTCTTTACATGGTTCCACAAATTCAACAACGAATGGCTGGACCATATGGTGGATT  524
SCPP6-C2`SR  CAACCAAGTCAG..............  456
SCPP6-C1`SA  CAGGTTCATCAA...........TTTCTTTACATGGTTCCACAAATTCAACAACGAATGGCTGGACCATATGGTGGATT  524
SCPP6-C2`SA  CAACCAAGTCAG..............  441

             525     530   535   540   545   550   555   560   565   570   575   580   585   590   595   600
conservation  *   ***   ********   *****                 **  *     *     *     *   *   *          *
SCPP6`PP     GAGCTCTGAGGAACTTCAGAACATGGGACAAATGGGTCCTGTTGACATGCACATGCCTGCGTTTAGGGGCAATGTGTTGC  601
SCPP6`LW     GAGCTCTGAGGAA..............  519
SCPP6`DR     GAGCTCTGAGGAACTTCAGAACATGGGC.........CGTGTTAACATGCACCTACCTGCGATTAGAGGAAATGTGTTTC  580
SCPP6`CI     GAGCTCCGAGGAAATTCAGAACATGGGACATATGGGCCATGTTAACATGCACATGCCTGAGTTTAGAGGCAATGTGTTTC  583
SCPP6-C1`CC  GCGCTCTGAGGAACTTCAGTGACCTAAAAAAGAAGACTTTGATATATTTGATATATATCTCATAACTTCTGACACCACTG  322
SCPP6-C2`CC  ..............  480
SCPP6-C1`SG  GCGCTATGAGGAACTTCAGAACATGGGACGCATGCGTCGTGTTGACTTGCACATGCCTGCACTTAGAGGCGATGTTTGTC  592
SCPP6-C2`SG  ..............  420
SCPP6-C1`SR  GAGCTCTGAGGAACTTCAGAACATGGGACGCATGCGTCGTGTTGACTAGCACATGCCTGCACTTAGAGGCAATGTTTTTC  604
SCPP6-C2`SR  ..............  456
SCPP6-C1`SA  GCGCTATGAGGAACTTCAGAACATGGGATACATGCGTCGTGTTGACTTGCACATGCCTGCACTTAGAGGCAATGTTTTTC  604
SCPP6-C2`SA  ..............  441

             605   610   615   620   625   630   635   640   645   650   655   660   665   670   675   680
conservation              *       *  *     *             *                         *
SCPP6`PP     CTGTAGCTGGACCACAAACCTGTTGTACCTGTTAACCCTTTAAGACCAGCCAATACCTTCCACATCAACCACCTACCCTGCC  681
SCPP6`LW     ..............  519
SCPP6`DR     CTGTATCTGGACCTCAAACTGTTGTACCCATTGGGCCAGTAAGACCG..............CCCAACCCCTTCCCTGCC  645
SCPP6`CI     CTGTAGCTGGACCACAAACCTGTTGTACCTGTTAGCTCTTTAGGACCAGCCAATACCTTCCACATCAACCACCTTCCCTGCC  663
SCPP6-C1`CC  TATCTTTATTTTTTAATGTATGTATTGGAATGAATAAACCTTAGCCTAAATCTCTAATTAAGACACACAAA.........  393
SCPP6-C2`CC  ..............  480
SCPP6-C1`SG  CTGTAGCTGGACCACAAACCTGTTGTACCTGTTAGCCCTTTAAGACTGACCAAGACCTTCCACCCCAGCCACCTTT......  666
SCPP6-C2`SG  ..............  420
SCPP6-C1`SR  CTGTAGCTGGACCACAAACCTGTTGTACCTGTTAGCCCTTTAAGACCGACCAAGACCTTCCACCCCAGCCACCTTT......  678
SCPP6-C2`SR  ..............  456
SCPP6-C1`SA  CTGTAGCTGGACCACAAACCTGTTGTACCTGTTAGCCCTTTAAGACCAACCAAGACCTTCCACCCCAGCCACCTTT......  678
SCPP6-C2`SA  ..............  441

             685   690   695   700   705   710   715   720   725   730   735   740   745   750   755   760
conservation                    *           *     *     *  **     *  *        ***
SCPP6`PP     ACTGGAATGACATTCTCGACCAATACTGAGGCCCAGCCACCCTAGCATTGTAGCTGTACCACCCAGAGGGGATGCCATACT  761
SCPP6`LW     ..............  519
SCPP6`DR     ACTGGAATGACCTACCCGGGCATTACTGAGCTCCAGCAACCCAGCATTATAGCCGTGCCTCCTAGCAGAGATGCCATACC  725
SCPP6`CI     AATGGAATGACCTTCTCGGGCACTACTGAGGTTCAGCCACCAAGCGTTGTAGCTGTACCACCCAGTTGGGATGCCATACC  743
SCPP6-C1`CC  .........GAACATGAGACGTCTTCTGAAGTTGAGCTACCCAGCCGTTCTAGCTGTACCACCCAGTGGGGATGCCATATC  464
SCPP6-C2`CC  ..............  480
SCPP6-C1`SG  ........CTGACCATTCTGACCCATTTTTCAGCTACCCAGCATTGCAGCTGCACCACCCAGTGGGGATGCCATATC  734
SCPP6-C2`SG  ..............  420
SCPP6-C1`SR  ........CTGACCATTCTGACCCATTTGTGCTACCCGCTCAGATTGTGCTAACTCCCATCAAAAAGAT.......  738
SCPP6-C2`SR  ..............  456
SCPP6-C1`SA  .......TTGACCATTCTGACGATTTTTTCAGCTACCCAGCGTTGTAGCTGTACCACCCAGTGGGGATGCCATATC  746
SCPP6-C2`SA  ..............  441

             765   770   775   780   785   790   795   800   805   810   815   820   825   830   835   840
conservation      *     *     ***     **     *              *       **     *
SCPP6`PP     TGCTACTGGTGGATCCCATCCAAATAATGGAGTGCTGCCTAGTAGGAATGCTATCAAGCAGGACCCTGAGCGAGTGCCGT  841
SCPP6`LW     ..............  519
SCPP6`DR     TGCTACTGGTGGATCCCATCCAAATAGTGCAGTGCTGCCTAGTAGGATTTCTTGGCACTCAGGATCGTGATCGAGCACCAT  805
SCPP6`CI     TGCTACTGGTGGATCCCATCCAAATAATGGAGCGCAGCCTAATAGGATTGCTACTGTGCAGGACTATGAGCGAGTGCCTT  823
SCPP6-C1`CC  TGTCACTGGTGGATCCAATCCAAATAATAGAGCACCGCCTAGTAGGACTGCTAACATGCAGGACCATGAGTGAGTGCCGT  544
SCPP6-C2`CC  ..............  480
SCPP6-C1`SG  TGCGACTGGTGGATCCCATCCAAATAATGGAGCACTGCCAAGTAGGATTGCTAGCGTACAGGACCGTGAGCAAGTGCCGT  814
SCPP6-C2`SG  ..............  420
SCPP6-C1`SR  ....ATAGAACAATCTGATAGGTAGCATGCTTCGTTGGTACACCGGCAACTTCTTAAGTTCAGCTACCCAGCGTTGTAGC  814
SCPP6-C2`SR  ..............  456
SCPP6-C1`SA  TGCGACTGGTGTATCCCATCCAAATAACGGAGCACTGCCTAGTAGGATTGGTTTAC.........CGTGAGCAAGTGCCGT  817
SCPP6-C2`SA  ..............  441

conservation
SCPP6`PP     GT  843
SCPP6`LW     ..  519
SCPP6`DR     GT  807
SCPP6`CI     GT  825
SCPP6-C1`CC  GT  546
SCPP6-C2`CC  ..  480
SCPP6-C1`SG  GT  816
SCPP6-C2`SG  ..  420
SCPP6-C1`SR  TG  816
SCPP6-C2`SR  ..  456
SCPP6-C1`SA  GT  819
SCPP6-C2`SA  ..  441
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X non conserved
X ≥ 55% conserved
X ≥ 85% conserved