Supplementary S1

Gene name	miRNA name	Experiments	Publications	Cell lines	microT Score	Details
DAPK1	hsa-miR-26a-5p	7	5	4	0.95	
DAPK1	hsa-miR-26b-5p	5	3	2	0.95	
DAPK1	hsa-miR-154-3p	3	3	2	0.83	
DAPK1	hsa-miR-487a-3p	2	2	1	0.91	

Figure S1. MicroRNAs targeting DAPK-1. Symbol "i" is supplemental information about gene and miRNA details, the downward facing arrows are used to expand specific interactions and to reveal metainformation.

Supplementary S2

hsa-miR-26a-5p sequence: UUCAAGUAAUCCAGGAUAGGCU
hsa-miR-26b-5p sequence: UUCAAGUAAUUCAGGAUAGGU

```
CLUSTAL multiple sequence alignment by MUSCLE (3.8)


DAPK-1          ----GCTTCGGAGTGTGAGGAGGACAGCCGGACCGAG---------CCAA-------CGC
s-DAPK-1        ATTTACTCAACAATGTTAGATGTCACACATGAAAAAGTTTTGTTATCTAATTATTCTCAT
                     **    * *** **  *     *  **   **         * **       *

DAPK-1          CGGGGACTTTGTTCCCTCC-------------------------GCGGAGGGGACTCGG
s-DAPK-1        CAGAAA-TTTGTTGCCTGCTTCTGCAGACGTCAGCAGAGCTGTAAGTGGAGTAGATCTGG
                * *  * ****** *** *                         * ****  **   **

DAPK-1          CAACTCGCAGCGGCAGGGTCTGGGGCCGGCGCCTGGGAGGGATCTGCGCCCCC-------
s-DAPK-1        CCCTCTGCAGTATGGGAATCC-TAACCAGAG---AGGGGAGATGAGGGTTTACAAACATA
                *     ****     *  **     ** * *    ** * ***  * *    *

DAPK-1          --------------------------------CACTCACTCCCTAGCT------------
s-DAPK-1        AAATAATTGTTTATAAGCAATTGTTTATTTTGAAATCATTTTTGATTTACAAAAAAAAGT
                                              * *** *    *  *

DAPK-1          -----------------GTGTTCCCGCCGCCGCCCCGGCTA---GTCTCCGGCGCTGGCG
s-DAPK-1        TGGAAAAGTGGTACAGAGAGTTCCATCATTCGCTTCACCCAGGTGCCCCTAATGCTAGCA
                           * *****  *   ***  *  * *   * * *    *** **

DAPK-1          CCT---------ATGGTCGGCCTCCGACAGCGCTCCGGAG-GGACCGGGGGAGCTCCCAG
s-DAPK-1        TCTTGTGTAACCACGGT--ACATTTGTCAAAGGTGTAAAATAGAATGAGGG---TTTTAT
                 **         * ***   * *  * **  * *    *   **  * ***   *   *

DAPK-1          GCGCCCGGGACTGGAGACTGATGCATGAGGGGGCTACGGAGGCGCAGGAGCGGTGGTGAT
s-DAPK-1        TCCTCTGGGA------AGTTGCTCCTCTGGGGTTTGTCATCACACAGGAAGGGAAATAAC
                 *  * ****      * *    * *  ****  *       * *****  **   * *

DAPK-1          ----GGTCTGGGAA----GCGGAGCTGAAGTGCCCTGGGCTTTGGTGAGGCGTGAC----
s-DAPK-1        AGTGAGTCTGAGGAATGCATGCATCTG--GTGCTGTCAGCTCCCTAGAAATGTGACCCCA
                     ***** * *      * * ***  ****  *  ***     **   *****

DAPK-1          AGTTTATCAT------GACCGTGTTCAGGCAGGAAAACGTGGATGATTACTACGACACCG
s-DAPK-1        GGTTGATTTTCCTGCAGGGCGGGTCCAATGCCGTCTACTGGGCTGCTCGGCATGGCCACG
                 *** **  *      *  ** ** **     *   **  ** ** *    * * *  **

DAPK-1          GCGA------GGAACTTGGCAGTGGACAGTTTGCGGTTGTGAAGAAATGCC------GTG
s-DAPK-1        TCGATACCTTGAAATTTCTCAGTGA--------------GAACAAATGCCCTTTGGATG
                 ***      * ** **  *****               *** *******       **

DAPK-1          AGAAAAGCACCGGCCTCCAGTATGCCGCCAAATTCATCAAGAAAAGGAGG----ACTAAG
s-DAPK-1        TGAAAGACAAGGTA-------AGGCCACTTCTCTTAGGAGGAACATGAGGTGGTAGTAAA
                 ****  **  *        * *** *    * *  * *** * ****    * ***
```


DAPK-1 TCCAGCCGGCGGGGTGTGAG----------CCGCGAGGACATCGAGC-------GGGAGG
s-DAPK-1 TGGATGCATGTGAGTGTGAGTGCTGGCCTACCGTGTG--CATCGGGACCCAAAGGAAAGG
DAPK-1 T--------CAGCAT---CCTGAAGGAGATCCAGCACCCCAATGTCATCACCCTGCACGA
s-DAPK-1 TATCAGAACCAGAATTCACCTGCAGAACATTTAAGTTGGAAATGTCTT---GTTGCCTGT
DAPK-1 GGTCTATGAGAACAAGACGGACGTCATCCTGATCTTGGAACTCGTTGCAGGTGG------
s-DAPK-1 GGTTT---GGTCTAATACTGAAATCAGCCTTAAGTCAAAATC--TTTCAGGTAGTTGCCA
DAPK-1 -----CGAGCTGTTTGACTT--------CTTAGCTGAAAAG----GAATCTTT-------
s-DAPK-1 TAATACGCACGCATTGAATTATAATCCCCATAACATAAAAACCTCAAAGTTCTAGTACAG
DAPK-1 --AACTGAAGAGGAA--------GCAACTGAATTT---------CTCAAACAAATTCTTA
s-DAPK-1 ACAACCAGAGAGAGACCTCGGTCTCGATTCGATTTTCTTCCTGACTCAACCTTGTGCTTT
DAPK-1 ATGGTGTTTACTACCTGCACTC-----CCTTCAAATCGCCCACTTTG----------AT
s-DAPK-1 TAAGCGGATCTCCCCTATTCTCTTCTTCTTTGAAGTGGCTGACAGTGCTGACCTGACAAT
DAPK-1 CTTAAGCCTGAGAACATAATGCTTTTGGATAGA-AATGTCCCCAAACCTCGGATCAAGAT
s-DAPK-1 CACAGACACTAGAAGATA------TTAATGAGACAATGCACATAAA----GTAATAAAGT
DAPK-1 CATTGACTTTGGGTTGGCCC---------ATAAAATTGACTTTGGAAATGAATTTAAAAA
s-DAPK-1 AA--GGCTTTTTTTTGGCACAACGGTGTTATAAAAGTTACT---------GATTTATCAA
DAPK-1 CATATTTGGGACTCCAGAGTTTGT---------CGCTCCTGAGATAGTCAACTATGAACC
s-DAPK-1 GATACCTTGTTTTCATATGTGTGTGTTTCATTCAGTTCACACAACAATC--CTGTGAATT
DAPK-1 TCTTGGT----CTTGAGGCAGATATGTGGAGTATCGGGGTAATAACCTA-----TATCCT
s-DAPK-1 AATTGGCTGTGCTGGAACCTGA-ACCTGGAATTCCTACCTACTCATCCATTATTTATTCT
DAPK-1 CCTAAGTGGGGCCTCCCCATTTCTTGGA--------------GACACTAAG-CAAGAAA
s-DAPK-1 ACTGTACAATACTTCTCTGCTTCCAGTACTGGCAGACTAATTTGACGTTTAGTCAAGCTG
DAPK-1 CGTTA-GCAAATGTATCCGCTGTCAACTACGA---ATTTGAGGATGAATACT----TCAG
s-DAPK-1 CCACATGCAGTTGCATGGGTTGTGCACTGCACCATATCTGAGGGGTAACATTCATATCAG

```
DAPK-1          TAATAC-------------CAGTGCCCTAG-----------------------------
s-DAPK-1        AGACACGCATTTATTATGGCAGTTTTCTGGAAGGTGGCAACACTATATCTTGTTTTGTCT
                  * **            ****   ** *

DAPK-1          -CCAAAGATTTCATAA----GAAGACTTCTGGTCAAGGATCCAAAGAAGAGAATGACAAT
s-DAPK-1        TCTTAAAATTTGTTTATTCTGATGATTTTCTGT--GGGGTGGATAGAAGTAAAGT---AT
                 *  ** ****  * *    ** ** **   **   ** *  * *****  **     **

DAPK-1          TCAAGATAGTTTGCA-GCATCCCTGGATCAAGCCTAAAGATACACAACAGGCACTTAGTA
s-DAPK-1        CTTAAAGGATTTGCACTTGTTACTAATTCA--CAGAAAGTTATTGCATGGGCAAATAGTG
                   * *   ******    *  **   ***  *  **** **    *  ****  ****

DAPK-1          GA-------AAAGCATCAGCAGTAAACATGGAGAAATTCAAGAAGT---TTGCAGCCCGG
s-DAPK-1        ACATTCTTTAAAATTTCTGAGAAAATCTCTGAGAATATAAGAAAATAAGTTTCTAATCAT
                        ***   ** *    ** *   *****  * *  ** *   ** *    *

DAPK-1          AAAAAATGGAA--ACAATCCGTTCGCTTGATATCACTGTGCCAAAGATTATCCAGGTCAT
s-DAPK-1        AGGCAATGAAATGAGAAGCTTATTAATAAATAAAATTGT--------TCATTTAAGTAAC
                *   **** **  * ** *   *   *  ***  * ***       * **  * ** *

DAPK-1          TCCTG---------TCCAGAAGTAACATGA-------GTGTT------------------
s-DAPK-1        TGCTGAATGATGAACCCAATAGTAAAAAGAGAGTGTTGTGTTTAAAGAGAAAATCACACA
                * ***          ***  ***** * **       *****

DAPK-1          GCCAGAAGCGATGATACTCTGGATGAGGAAGACTCCTTTGTGATGAAAGCCATCATCCAT
s-DAPK-1        GCTAGAAGTATCAGCAC-----ATAAAGAAGAC-------TGAGAACAGCTATCATGGAA
                ** *****       **     ** * ******       ***  * *** *****  *

DAPK-1          GCCATCAACGATGACAATGTCCCAGGCCTGCAGCACCTTCTGGGCTCATTATCCAACTAT
s-DAPK-1        A-----AGGGAGAGCCTTCTCCTGAGTTGTTTGCACTTCACAGG---ATGAGCCAAGTAT
                      *  **   *  * ***   *      **** *    **   ** * **** ***

DAPK-1          GATG--TTAACCAACCCAACAAGCACGGGACACCTCCAT------TACTCATTGCTGCTG
s-DAPK-1        GTGGGCTTAAT--ACTCACTGTGTGGTGGACACCCCAACCTCAGGTCCCCATCCTAGCC-
                *  *  ****   ** **    *    ******* * *       * * ***    **

DAPK-1          GCTGTGGGAATATTCAAATACTACAGTTGCTC---ATTAAAAGAGGCTCGAGAATCGATG
s-DAPK-1        ACTATAGGGGCATCTGCCCAAGGTGGGTGGGTGGAACCAAAGGGGAC---AGAGTGGA--
                 ** * **   **      *    * **      *  *** * * *   *** * **

DAPK-1          TCCAGGATAAGGGCGGGTCCAATGCC--GTCTACTGGGCTGCTCGGCATGGCCACGTCGA
s-DAPK-1        ACCAGG--CAGGCCTGGGTGTAGGCCTTGGGTTCTGGTCTCCATAGCCTGCTCACAGATG
                 *****   *** * **    * ***  *  * **** ** *   ** **  ***

DAPK-1          TACCTTGAAATTTCTCAGTGAGAACAAATGCCCTTTGGATGTGAAAGACAAGTCTGGAGA
s-DAPK-1        TGGCTCTGAATCACCGGCT-----------CCTTTTCTTCTG------CAGTCTGGAGA
                *  **   ***  *    *           *****   * **       **********
```



```
DAPK-1          GATGGCCCTCCACGTGGCAGCTCGCTATGGCCATGCTGACGTGGCTCAGTTACTGTGCAG
s-DAPK-1        GATGGCCCTCCACGTGGCAGCTCGCTATGGCCATGCTGACGTGGCTCAGTTACTGTGCAG
                ************************************************************

DAPK-1          CTTCGGCTCAAATCCCAATATCCAGGACAAGGAAGAAGAAACCCCCCTGCACTGTGCTGC
s-DAPK-1        CTTCGGCTCAAATCCCAATATCCAGGACAAGGAAGAAGAAACCCCCCTGCACTGTGCTGC
                ************************************************************

DAPK-1          TTGGCACGGCTATTACTCTGTGGCCAAAGCCCTTTGTGAAGCCGGCTGTAACGTGAACAT
s-DAPK-1        TTGGCACGGCCATTACTCTGTGGCCAAAGCCCTTTGTGAAGCCGGCTGTAACGTGAACAT
                ********** **************************************************

DAPK-1          CAAGAACCGAGAAGGAGAGACGCCCCTCCTGACAGCCTCTGCCAGGGGCTACCACGACAT
s-DAPK-1        CAAGAACCGAGAAGGAGAGACGCCCCTCCTGACAGCCTCTGCCAGGGGCTACCACGACAT
                ************************************************************

DAPK-1          CGTGGAGTGTCTGGCCGAACATGGAGCCGACCTTAATGCTTGCGACAAGGACGGACACAT
s-DAPK-1        CGTGGAGTGTCTGGCCGAACATGGAGCCGATCTTAATGCTTGCGACAAGGACGGACACAT
                ***************************** ****************************

DAPK-1          TGCCCTTCATCTGGCTGTAAGACGGTGTCAGATGGAGGTAATCAAGACTCTCCTCAGCCA
s-DAPK-1        TGCCCTTCATCTGGCTGTAAGACGGTGTCAGATGGAGGTAATCAAGACTCTCCTCAGCCA
                ************************************************************

DAPK-1          AGGGTGTTTCGTCGATTATCAAGACAGGCACGGCAATACTCCCCTCCATGTGGCATGTAA
s-DAPK-1        AGGGTGTTTCGTCGATTATCAAGACAGGCACGGCAATACTCCCCTCCATGTGGCATGTAA
                ************************************************************

DAPK-1          AGATGGCAACATGCCTATCGTGGTGGCCCTCTGTGAAGCAAACTGCAATTTGGACATCTC
s-DAPK-1        AGATGGCAACATGCCTATCGTGGTGGCCCTCTGTGAAGCAAACTGCAATTTGGACATCTC
                ************************************************************

DAPK-1          CAACAAGTATGGGCGAACGCCTCTGCACCTTGCGGCCAACAACGGAATCCTAGACGTGGT
s-DAPK-1        CAACAAGTATGGGCGAACGCCTCTGCACCTTGCGGCCAACAACGGAATCCTAGACGTGGT
                ************************************************************

DAPK-1          CCGGTATCTCTGTCTGATGGGAGCCAGCGTTGAGGCGCTGACCACGGACGGAAAGACGGC
s-DAPK-1        CCGGTATCTCTGTCTGATGGGAGCCAGCGTTGAGGCGCTGACCACGGACGGAAAGACGGC
                ************************************************************

DAPK-1          AGAAGATCTTGCTAGATCGGAACAGCACGAGCACGTAGCAGGTCTCCTTGCAAGACTTCG
s-DAPK-1        AGAAGATCTTGCTAGATCGGAACAGCACGAGCACGTAGCAGGTCTCCTTGCAAGACTTCG
                ************************************************************

DAPK-1          AAAGGATACGCACCGAGGACTCTTCATCCAGCAGCTCCGACCCACACAGAACCTGCAGCC
s-DAPK-1        AAAGGATACGCACCGAGGACTCTTCATCCAGCAGCTCCGACCCACACAGAACCTGCAGCC
                ************************************************************
```

```
DAPK-1          AAGAATTAAGCTCAAGCTGTTTGGCCACTCGGGATCCGGGAAAACCACCCTTGTAGAATC
s-DAPK-1        AAGAATTAAGCTCAAGCTGTTTGGCCACTCGGGATCCGGGAAAACCACCCTTGTAGAATC
                ************************************************************

DAPK-1          TCTCAAGTGTGGGCTGCTGAGGAGCTTTTTCAGAAGGCGTCGGCCCAGACTGTCTTCCAC
s-DAPK-1        TCTCAAGTGTGGGCTGCTGAGGAGCTTTTTCAGAAGGCGTCGGCCCAGACTGTCTTCCAC
                ************************************************************

DAPK-1          CAACTCCAGCAGGTTCCCACCTTCACCCCTGGCTTCTAAGCCCACAGTCTCAGTGAGCAT
s-DAPK-1        CAACTCCAGCAGGTTCCCACCTTCACCCCTGGCTTCTAAGCCCACAG-----GTAGG---
                ********************************************    **  *

DAPK-1          CAACAACCTGTACCCAGGCTGCGAGAACGTGAGTGTGAGGAGCCGCAGCATGATGTTCGA
s-DAPK-1        ----AACCT----CCATGCTG-------------------------------------
                    *****    *** ****

DAPK-1          GCCGGGTCTTACCAAAGGGATGCTGGAGGTGTTTGTGGCCCCGACCCACCACCCGCACTG
s-DAPK-1        GCCCCGTCTCTCCA----------GCAGGTGTTGG-------------CTTCCGCACT-
                ***  ****  ***         * ******* *             *  *******

DAPK-1          CTCGGCCGATGACCAGTCCACCAAGGCCATCGACATCCAGAACGCTTATTTGAATGGAGT
s-DAPK-1        ------------CTCTCCTTTCAAGG---------TCTAGGGGG-------GAAGGGAGT
                           *    *   *****        ** **   *       *** *****

DAPK-1          TGGCGATTTCAGCGTGTGGGAGTTCTCTGGAAATCCTGTGTATTTCTGCTGTTATGACTA
s-DAPK-1        TG-----------------------------------------------TGTTTGGGTCA
                **                                               ****  *   *

DAPK-1          TTTTGCTGCAAATGATCCCACGTCAATCCATGTTGTTGTCTTTAGTCTAGAAGAGCCCTA
s-DAPK-1        CTTGGCCTATACTGGACCC--------------TGTGGCCTT------------------
                 ** **    * **  ***             *** * ***

DAPK-1          TGAGATCCAGCTGAACCAAGTGATTTTCTGGCTCAGTTTCCTGAAGTCCCTTGTCCCAGT
s-DAPK-1        ------------------AGTGGTTTTCAGGTCCAGGTT---------------------
                                **** ***** **  *** **

DAPK-1          TGAAGAACCCATAGCCTTCGGTGGCAAGCTGAAGAACCCACTCCAAGTTGTCCTGGTGGC
s-DAPK-1        -----GGCTGGTAGCCTTGTGTG---------------TGCTGCCTGTTGTCCAG-----
                      *   *******  ***                ** *  ******* *

DAPK-1          CACCCACGCTGACATCATGAATGTTCCTCGACCGGCTGGAGGCGAGTTTGGATATGACAA
s-DAPK-1        ------CAGTAACA---------------GACTGAC-----------TTGGCAGTAGCAA
                     *  * ***              *** * *          ****   *  ***

DAPK-1          AGACACATCGTTGCTGAAAGAGATTAGGAACAGGTTTGGAAATGATCTTCACATTTCAAA
s-DAPK-1        AACAAGGGCCTCACTGAAA----------------------------TCACA-------
                *   *   * *  ******                           *****
```

```
DAPK-1          TAAGCTGTTTGTTCTGGATGCTGGGGCTTCTGGGTCAAAGGACATGAAGGTACTTCGAAA
s-DAPK-1        ---------------------------------GCCACA-GACACAAAGGTCCATC----
                                                  * ** * ****  ***** * **

DAPK-1          TCATCTGCAAGAAATACGAAGCCAGATTGTTTCGGTCTGTCCTCCCATGACTCACCTGTG
s-DAPK-1        ----------------------------------------------------CTCATAAATG
                                                                     ****    **

DAPK-1          TGAGAAAATCATCTCCACGCTGCCTTCCTGGAGGAAGCTCAATGGACCCAACCAGC--TG
s-DAPK-1        TGCAAA--------------------CTGCAG-------AATTTGCACAGTCAGCTTTG
                **  **                   *** **       ***   * **  ****  **

DAPK-1          ATGTCGCTGCAGCAGTTTGTGTACGACGTGCAGGACCAGCTGAACCCCCTGGCCAGCGAG
s-DAPK-1        GGGACACAGTTGCAAATTGCAT------TGCA--------------TTCTACTCAGGG--
                  * * * *  ***  ***  *      ****               **   *** *

DAPK-1          GAGGACCTCAGGCGCATTGCTCAGCAGCTCCACAGCACAGGCGAGATCAACATCATGCAA
s-DAPK-1        ------CTCTGGC------CTTA------------------GAGACAAAAAGAGCTCAA
                     *** ***      ** *                  ****  ** *    ***

DAPK-1          AGTGAAACAGTTCAGGACGTGCTGCTCCTGGACCCCCGCTGGCTCTGCACAAACGTCCTG
s-DAPK-1        ACTCAAACAGTCCA-------------------------AGCATAGCACAGA--TCC--
                * * ******* **                          **   ***** *  ***

DAPK-1          GGGAAGTTGCTGTCCGTGGAGACCCCACGGGCGCTGCACCACTACCGGGGCCGCTACACC
s-DAPK-1        ----AATAGCAGCCCAAGAAGGGTCCTCAACCCTTATCCTTCTTTCTGGAGTGCTACA--
                    * * ** * **  * **   ** *   *  *   *  **  * **   ******

DAPK-1          GTGGAGGACATCCAGCGCCTGGTGCCCGACAGCGACGTGGAGGAGCTGCTGCAGATCCTC
s-DAPK-1        ----GGCAGACCCAG-----------------------------TATTGTAGATACAT
                     * * * ****                             *  ** **** *

DAPK-1          GATGCCATGGACATCTGCGCCCGGGACCTGAGCAGCGGGACCATGGTGGACGTCCCAGCC
s-DAPK-1        AGAGCAACAAAAA---------GGGATTT-----------CCAGGAAGCACCATCCTGCT
                   ** *   * *        ****  *          *** *  * **   ** **

DAPK-1          CTGATCAAGACAGACAACCTGCACCGCTCCTGGGCTGATGAGGAGGACGAGGTGATGGTG
s-DAPK-1        CAGTTCAAG-----------------------------------------------GTTG
                * * *****                                              * **

DAPK-1          TATGGTGGCGTGCGCATCGTGCCCGTGGAACACCTCACCCCCTTCCCATGTGGCATCTTT
s-DAPK-1        GATAGAGG------------------------------------------------TTTC
                 ** * **                                                 **

DAPK-1          CACAAGGTCCAGGTGAACCTGTGCCGGTGGATCCACCAGCAAAGCACAGAGGGCGACGCG
s-DAPK-1        CAGAGGCTCC----------------------------------------------------
                ** * * ***
```

```
DAPK-1          GACATCCGCCTGTGGGTGAATGGCTGCAAGCTGGCCAACCGTGGGGCCGAGCTGCTGGTG
s-DAPK-1        ----------------TTAGTGGTTTTCAG----------------------GGATGGTC
                              * * *** *   **                       * ****

DAPK-1          CTGCTGGTCAACCACGGCCAGGGCATTGAGGTCCAGGTCCGCGGCCTGGAGACGGAGAAG
s-DAPK-1        TCTCTGGT----CACATCCA------------------CCCTCCTTGGGAACGT-----
                   *****    ***  ***                 * *  * ***  ***

DAPK-1          ATCAAGTGCTGCCTGCTGCTGGACTCGGTGTGCAGCACCATTGAGAACGTCATGGCCACC
s-DAPK-1        -----TTGCTGCCTTCCG---------------------------------GGCCTTC
                     ******** * *                                 ****  *

DAPK-1          ACGCTGCCAGGGCTCCTGACCGTGAAGCATTACCTGAGCCCCCAGCAGCTGCGGGAGCAC
s-DAPK-1        -CACAGACAGGGTTATTGATT---------------------------------CACAT
                 * * * ***** *  ***                                   **

DAPK-1          CATGAGCCCGTCATGATCTACCAGCCACGGGACTTCTTCCGGGCACAGACTCTGAAGGAA
s-DAPK-1        TAGGGGGCTGTCACGA-----------------------------------------
                 * * * * **** **

DAPK-1          ACCTCACTGACCAACACCATGGGGGGGTACAAGGAAAGCTTCAGCAGCATCATGTGCTTC
s-DAPK-1        ------------AACACC-TGGCAGTGAGCAAGAGAAAATGATGCA---------ATCTT
                           ****** ***  * *  ****  **  *   ***           *

DAPK-1          GGGTGTCACGACGTCTACTCACAGGCCAGCCTCGGCATGGACATCCATGCATCAGACCTG
s-DAPK-1        GGGTGTGA-------------------------------------------------
                ****** *

DAPK-1          AACCTCCTCACTCGGAGGAAACTGAGTCGCCTGCTGGACCCGCCCGACCCCCTGGGGAAG
s-DAPK-1        ---TTCC------------AACTGAATC-------------------CTCCTTTAGACAG
                   ***           ****** **                 * ** *  *  **

DAPK-1          GACTGGTGCCTTCTCGCCATGAACTTAGGCCTCCCTGACCTCGTGGCAAAGTACAACACC
s-DAPK-1        AGCGAG----------------------------TGAGTTTGTGGAAAGATAAGAGAC-
                  *  *                          ***  * **** **  **  * **

DAPK-1          AGTAACGGGGCTCCCAAGGATTTCCTCCCCAGCCCCCTCCACGCCCTGCTGCGGGAATGG
s-DAPK-1        ----------CTTCCAAGAGTTTCCT---------------------------------
                         ** *****  ******

DAPK-1          ACCACCTACCCTGAGAGCACAGTGGGCACCCTCATGTCCAAACTGAGGGAGCTGGGTCGC
s-DAPK-1        -------------------------------------AAACCAGGACAGTTTTGT---
                                                    ****   *  ** *  **

DAPK-1          CGGGATGCCGCAGACTTTTTG-CTGAAGGCATCCTCTGTGTTCAAAATCAACCTGGATGG
s-DAPK-1        ------------GCTTTGTGCCTTGATTCATTCTCTGTATATGATGTCA--CAGAAGAG
                          **** ** **  *  *** ****** *   *  ***  * * *  *
```


DAPK-1 CAATGGCCAGGAGGCCTATGCCTCGAGCTGCAACAGCGGCACCTCTTACAATTCCATTAG
s-DAPK-1 CC---------AGGTCTGTTCCCCAGGTTGATGCTAAAG-----TTTGTGTTTCTCTTAC
DAPK-1 CTCTGTTGTATCCCGGTGAGGGCAGCCTCTGGCTTGGGCAGGGTCTGTTTGGACTGCAGA
s-DAPK-1 GTCC------CCTCAGTGAGGGAGGACGCTGG-------------------------GG
DAPK-1 AGCAAGGGGGTGATGTAGCCCATCCTTCCCTTTGGAGATGCTGAGGGTGTTTCTTCCTGC
s-DAPK-1 AGCATGG-------GTAGC-------------------TGCGGAGAG------------
DAPK-1 ACCCACAGCCAGGGGGATGCCACTCCTCCCTCCGGCTTGACCTGTTTCTCTGCCGCTACC
s-DAPK-1 --TTGGCTGAGATT
DAPK-1 TCCCTCCCCGTCTCA--TTCCGTTGTCTGTGGATGGTCATTGCAGTTTAAGAGCAGAACA
s-DAPK-1 TATATTCCCTTTTCAACTTCTGTTCTCTG---------AACACAGCTATAGAATTGAAA-
DAPK-1 GATCTTTTACTTTGGCCGCTTGAAAAGCTAGTGTACCTCCTCTCAGTGTTTTGGACTCCA
s-DAPK-1 --------------------TGAGGAG---------------------------------
DAPK-1 TCTCTCATCCTCCAGTACCTTGCTTCTTACTGATAATTTTGCTGGAATTCCTAACTTTTC
s-DAPK-1 --
DAPK-1 AATGACATTTTTTTTAACTACTATATTGATTGTCCTTTAAAAAAGAAAAGTGCATATTTA
s-DAPK-1 -------------------------------------AAGAAAGAA----------TA
DAPK-1 TCCAAAATGTGTATTTCTTATACGCTTTTCTTTGTTATACCATTTCCTCAGCTTATCTCT
s-DAPK-1 ACCAAAACAGA----------------------GTTATAA--------------------
DAPK-1 TTTATATTTGTAGGAGAAACTCCCATGTATGGAATCCCACTGTATGATTTATAAACAGAC
s-DAPK-1 TTCATATT-----------------------------ATTATATTGCTGATA-------
DAPK-1 AATATGTGAGTGCCTTTTGCAGAAGAGGGTGTGTTTGAAATCATCGGAGTCAGCCAGGAG
s-DAPK-1 CATATGTCAATA---TTTATAGAGTACTGTGT--------------------GCCAGGAA
DAPK-1 CTGTCACCAAGGAAACGCTACCTCTCTGTCCCTTGCTGTATGCTGATCATCGCCAGAGGT
s-DAPK-1 CTG-----GAAGAAA--------------------TATGGTCTGAAGGACGCC-----T



Figure S2. The sequences of miRs together with their target sequence (highlighted in yellow) on s-DAPK-1 and DAPK-1 mRNA. Symbols: asterisk (*) indicates a position where the sequences being aligned have conserved residues, a gap (-) represents a missing or extra region of a sequence that is present in only one sequence.

Supplementary S3



Figure S3. The predicted secondary structure of s-DAPK-1 using the Phyre2 tool.

Supplementary S4

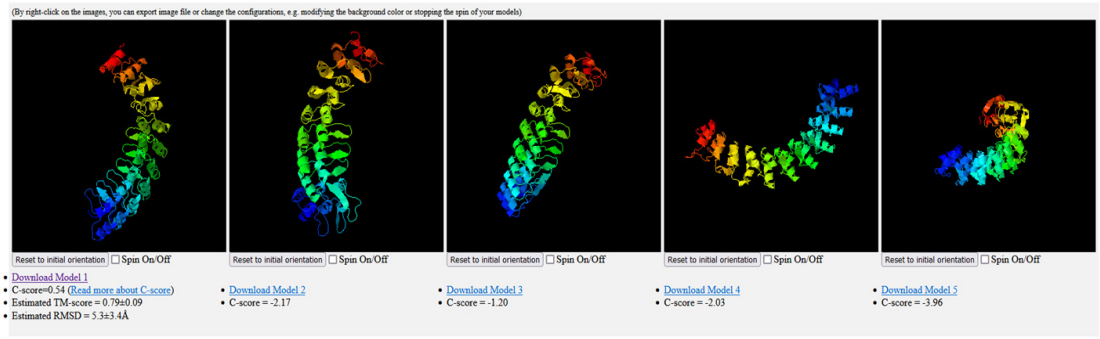
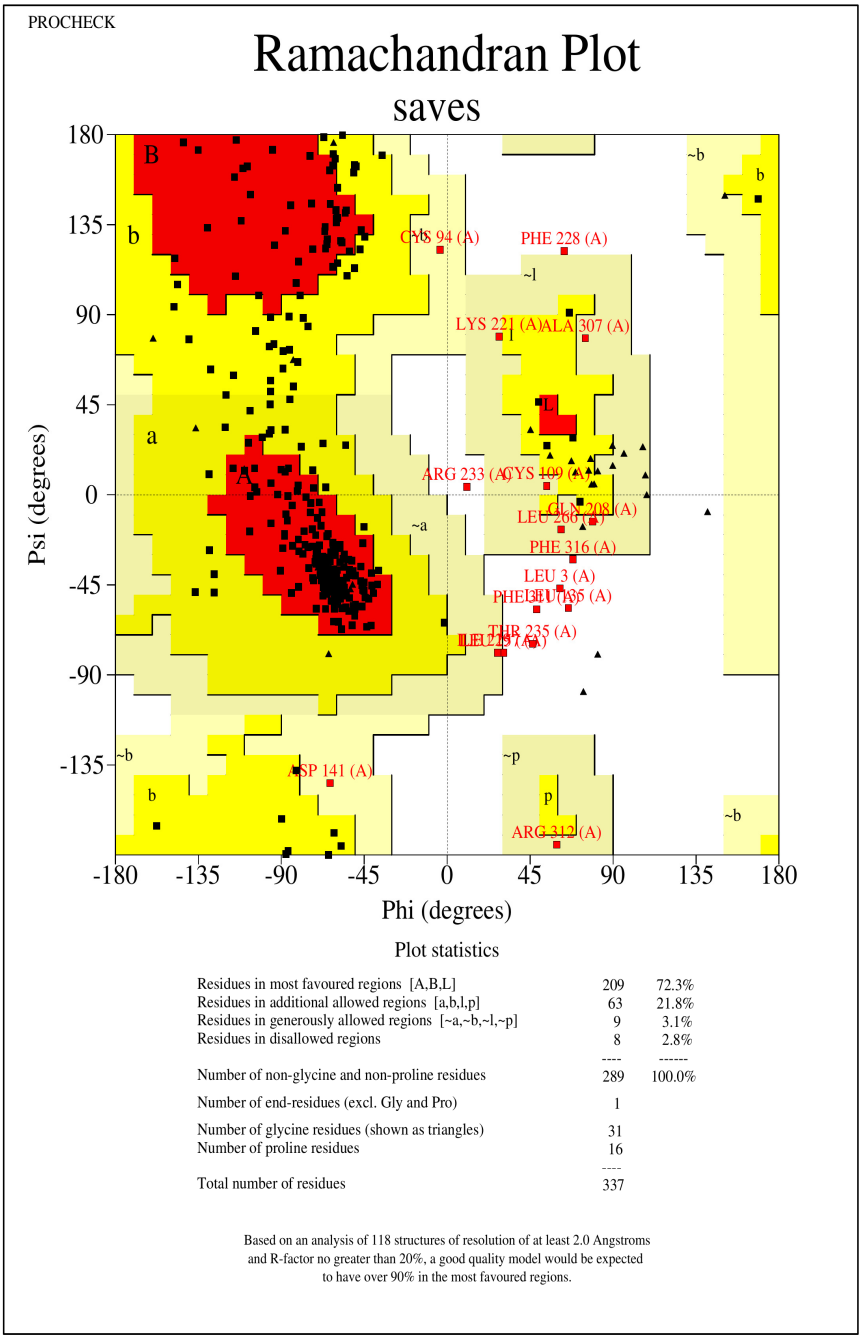


Figure S4. Predicted modeled 3D structures of s-DAPK-1 with varying C-scores. On the predicted protein structures, the red secondary structures are at the c-terminus of s-DAPK-1 while the blue structures are at N-terminus.

Supplementary S5



saves_01.ps

Figure S5. Ramachandran plot. Glycines are represented as triangles and any other amino acids are symbolised as square. Colour shades: red indicates amino acids in most favoured regions, yellow indicates amino acids in additional allowed regions, light yellow indicates amino acids in generously allowed regions and lastly white indicates amino acids in disallowed regions.