SUPPLEMENTARY INFORMATION

Protein alignment *Sus scrofa* and *Homo sapiens*

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CLUSTAL O(1.2.4) multiple sequence alignment
>XP_013853381.2 kinesin-like protein KIF21A isoform X1 [Sus scrofa]
>NP_001166935.1 kinesin-like protein KIF21A isoform 1 [Homo sapiens]


XP_013853381.2      MWGAPDESSVRVAVRIRPQLAKERIEGCHICTSVTPGEPQVFLGKDKAFTFDYVFDIDSQ      60
NP_001166935.1      MLGAPDESSVRVAVRIRPQLAKEKIEGCHICTSVTPGEPQVFLGKDKAFTFDYVFDIDSQ      60
                    * *********************:************************************

XP_013853381.2      QEQIYTQCIEKLIEGCFEGYNATVFAYGQTGAGKTYTMGTGFDVNIIEEEQGIISRAVKH      120
NP_001166935.1      QEQIYIQCIEKLIEGCFEGYNATVFAYGQTGAGKTYTMGTGFDVNIVEEELGIISRAVKH      120
                    ***** ****************************************:*** *********

XP_013853381.2      LFKSIEEKKHASIKNGLPSPDFKVNAQFLELYNEEVLDLFDTTRDIDAKNKKSNIRIHED      180
NP_001166935.1      LFKSIEEKKHIAIKNGLPAPDFKVNAQFLELYNEEVLDLFDTTRDIDAKSKKSNIRIHED      180
                    ********** :******:******************************.**********

XP_013853381.2      SAGGIYTVGVTTRTVNTESEMMQCLKLGALSRTTASTQMNVQSSRSHAIFTIHLSQTRMC      240
NP_001166935.1      STGGIYTVGVTTRTVNTESEMMQCLKLGALSRTTASTQMNVQSSRSHAIFTIHVCQTRVC      240
                    *:***************************************************:.***:*

XP_013853381.2      PQIDTENAIDNKVISESSQMNEFETLTAKFHFVDLAGSERLKRTGATGERAKEGISINCG      300
NP_001166935.1      PQIDADNATDNKIISESAQMNEFETLTAKFHFVDLAGSERLKRTGATGERAKEGISINCG      300
                    ****::** ***:****:******************************************

XP_013853381.2      LLALGNVISALGDKSKRATHVPYRDSKLTRLLQDSLGGNSQTIMIACVSPSDRDFMETLN      360
NP_001166935.1      LLALGNVISALGDKSKRATHVPYRDSKLTRLLQDSLGGNSQTIMIACVSPSDRDFMETLN      360
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XP_013853381.2      TLKYANRARNIKNKVMVNQDRASQQINALRNEITRLQMELMEYKTGKRIIDEEGVESIND      420
NP_001166935.1      TLKYANRARNIKNKVMVNQDRASQQINALRSEITRLQMELMEYKTGKRIIDEEGVESIND      420
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XP_013853381.2      MFHENAMLQTENNNLRVRIKAMQETVDALRTRITQLVSDQANQVLARAGEGNEEISNMIH      480
NP_001166935.1      MFHENAMLQTENNNLRVRIKAMQETVDALRSRITQLVSDQANHVLARAGEGNEEISNMIH      480
                    ******************************:***********:*****************

XP_013853381.2      SYIKEIEDLRAKLLESEAVNENLRKNLTRATARSPYFSGSSAFSPTIMSSDKETIEIIDL      540
NP_001166935.1      SYIKEIEDLRAKLLESEAVNENLRKNLTRATARAPYFSGSSTFSPTILSSDKETIEIIDL      540
                    *********************************:*******:*****:************

XP_013853381.2      AKKDLEKLKRKEKKKKKRLQKLEESNREERSVAGKEDNIDTDQEKKEEKGISERENNELE      600
NP_001166935.1      AKKDLEKLKRKEKRKKKRLQKLEESNREERSVAGKEDNTDTDQEKKEEKGVSERENNELE      600
                    *************:************************ ***********:*********

XP_013853381.2      VEESQEVSDHEDEEEEEEEEEEDDIEGGESSDESDSESDEKANYQADLANITCEIAIKQKL      660
NP_001166935.1      VEESQEVSDHEDEEEEEEEEEEDDIDGGESSDESDSESDEKANYQADLANITCEIAIKQKL      660
                    ************************:***********************************

XP_013853381.2      IDELENSQKRLQTLKKQYEEKLMMLQHKIRDTQLERDQVLQNLGSVESYSEEKAKKIRSE      720
NP_001166935.1      IDELENSQKRLQTLKKQYEEKLMMLQHKIRDTQLERDQVLQNLGSVESYSEEKAKKVRSE      720
                    ********************************************************:***

XP_013853381.2      YEKKLQAMNKELQRLQTAQKEHARLLKNQSQYEKQLKKLQQDVMEMKKTKVRLMKQMKEE      780
NP_001166935.1      YEKKLQAMNKELQRLQAAQKEHARLLKNQSQYEKQLKKLQQDVMEMKKTKVRLMKQMKEE      780
                    ****************:*******************************************

XP_013853381.2      QEKARLMESRRNREIAQLKKDQRKRDHQLRLLEAQKRNQEVVLRRKTEEVTALRRQVRPM      840
NP_001166935.1      QEKARLTESRRNREIAQLKKDQRKRDHQLRLLEAQKRNQEVVLRRKTEEVTALRRQVRPM      840
                    ****** *****************************************************

XP_013853381.2      SDKVAGKVTRKLSSSDAPVQDTGSSAAAIETDASRAGAQQKMRIPVARVQALPAPITNGT      900
NP_001166935.1      SDKVAGKVTRKLSSSDAPAQDTGSSAAAVETDASRTGAQQKMRIPVARVQALPTPATNGN      900
                    ******************.*********:******:*****************:* ***.

XP_013853381.2      RKKYQRKGLTGRVFISKTARMKWQLLERRVTDIIMQKMTISNMEADMNRLLKQREELTKR      960
NP_001166935.1      RKKYQRKGLTGRVFISKTARMKWQLLERRVTDIIMQKMTISNMEADMNRLLKQREELTKR      960
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XP_013853381.2      REKLSKRREKIVKENGEGDKNVVNINEEMESLTANIDYINDSISDCQANIMQMEEAKEEG      1020
NP_001166935.1      REKLSKRREKIVKENGEGDKNVANINEEMESLTANIDYINDSISDCQANIMQMEEAKEEG      1020
                    **********************.*************************************

XP_013853381.2      ETLDVTAVINACTLTEARYLLDHFLSMGINKGLQAAQKEAQIKVLEGRLKQIEITSATQN      1080
NP_001166935.1      ETLDVTAVINACTLTEARYLLDHFLSMGINKGLQAAQKEAQIKVLEGRLKQTEITSATQN      1080
                    *************************************************** ********

XP_013853381.2      QLLFHMLKEKAELNPELDALLGHALQDLDSVPLENVEDSTDEDVPLNSPGSEGSSLSSDL      1140
NP_001166935.1      QLLFHMLKEKAELNPELDALLGHALQDLDSVPLENVEDSTDEDAPLNSPGSEGSTLSSDL      1140
                    *******************************************.**********:*****

XP_013853381.2      MKLCGEVKPKSKARRRTTTQMELLYADSSELASDTSTGDASLPGPLTPVAEGQEIGMNTE      1200
NP_001166935.1      MKLCGEVKPKNKARRRTTTQMELLYADSSELASDTSTGDASLPGPLTPVAEGQEIGMNTE      1200
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XP_013853381.2      TS-TSAREKDLPPPSGFPSKIGSISRQSSLSEKKLPEPSPITRRKVYEKAEKAKAKEQKH       1259
NP_001166935.1      TSGTSAREKELSPPPGLPSKIGSISRQSSLSEKKIPEPSPVTRRKAYEKAEKSKAKEQKH       1260
                    ** ******:* ** *:*****************:*****:****.******:*******
XP_013853381.2      SDSGTSEASLSPPSSPPSRPRNELNVFNRLTVSQGNTSVQQDKSDESDSSLSEVHSRSSR       1319
NP_001166935.1      SDSGTSEASLSPPSSPPSRPRNELNVFNRLTVSQGNTSVQQDKSDESDSSLSEVH-RSSR       1319
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XP_013853381.2      RGIINPFPPSKGIRASPLQCVHIAEGHTKAVLCVDSTDDLLFTGSKDRTCKVWNLVTGQE       1379
NP_001166935.1      RGIINPFPASKGIRAFPLQCIHIAEGHTKAVLCVDSTDDLLFTGSKDRTCKVWNLVTGQE       1379
                    ******** ****** ****:***************************************

XP_013853381.2      IMSLGGHPNNVVSVKYCNYTSLVFTVSTSYIKVWDIRDSAKCIRTLTSSGQVTLGDACST       1439
NP_001166935.1      IMSLGGHPNNVVSVKYCNYTSLVFTVSTSYIKVWDIRDSAKCIRTLTSSGQVTLGDACSA       1439
                    ***********************************************************:

XP_013853381.2      STSRTVAIPSGENQINQIALNPTGTFLYAASGNAVRMWDLKRFQSTGKLTGHLGPVMCLT       1499
NP_001166935.1      STSRTVAIPSGENQINQIALNPTGTFLYAASGNAVRMWDLKRFQSTGKLTGHLGPVMCLT       1499
                    ************************************************************

XP_013853381.2      VDQISNGQDLIITGSKDHYIRMFDVTEGALGTVSPTHNFEPPHYDGIEALTIQGDNLFSG       1559
NP_001166935.1      VDQISSGQDLIITGSKDHYIKMFDVTEGALGTVSPTHNFEPPHYDGIEALTIQGDNLFSG       1559
                    *****.**************:***************************************

XP_013853381.2      SRDNGIKKWDLAQKDLLQQVPNAHKDWICALGVVPAHPVLLSGCRGGILKLWNMDNFVPV       1619
NP_001166935.1      SRDNGIKKWDLTQKDLLQQVPNAHKDWVCALGVVPDHPVLLSGCRGGILKVWNMDTFMPV       1619
                    ***********:***************:******* **************:****.*:**

XP_013853381.2      GEMKGHDSPINAICVNSTHIFTAADDRTVRIWKTRNLQDGQISDTGDLGEDIASN 1674
NP_001166935.1      GEMKGHDSPINAICVNSTHIFTAADDRTVRIWKARNLQDGQISDTGDLGEDIASN 1674
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#
#
#  Percent Identity  Matrix - created by Clustal2.1
#
#

     1: XP_013853381.2  100.00   96.23
     2: NP_001166935.1   96.23  100.00
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