

SUPPLEMENTARY INFORMATION

Protein alignment *Sus scrofa* and *Homo sapiens*

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	QEQIYTQCIEKLEIEGCFEGYNATVFAYGQTGAGKTYTMGTGFDVNIIEEEQGIISRAVKH	120
NP_001166935.1	QEQIYIQCIEKLEIEGCFEGYNATVFAYGQTGAGKTYTMGTGFDVNIIEEELGIISRAVKH *****;***	120
XP_013853381.2	LFKSIEEKKHASKNGLPSPDFKVNQFLELYNEEVLDLFDTRDIDAKNKKSNIRIHED	180
NP_001166935.1	LFKSIEEKKHAIKNGLPAPDFKVNQFLELYNEEVLDLFDTRDIDAKSKKSNIRIHED *****;*****	180
XP_013853381.2	SAGGIYTVGVTRTRVNTVESEMMQCKLGLSRTTASTQMNQSSRSASHAIFTIHLSQTRMC	240
NP_001166935.1	STGGIYTVGVTRTRVNTVESEMMQCKLGLSRTTASTQMNQSSRSASHAIFTIHVCQTRVC *;*****;***	240
XP_013853381.2	PQIDTENAI DNKVI SESSQMNFEFETLAKFHFDLAGSERLKRRTGATGERAKEGINSINGC	300
NP_001166935.1	PQIDADNATDNKIIESSAQMNFEFETLAKFHFDLAGSERLKRRTGATGERAKEGINSINGC ***;***;*****;*****	300
XP_013853381.2	LLALGNVISALGDKSKRATHVPYRDSKLRLLQDSLGGNSQTIMIACVSPSDRDFMETLN	360
NP_001166935.1	LLALGNVISALGDKSKRATHVPYRDSKLRLLQDSLGGNSQTIMIACVSPSDRDFMETLN *****	360
XP_013853381.2	TLKYANRARNIKNKVMVNQDRASQQINALRNEITRLQMELMYKTKGRIIDEEGVESIND	420
NP_001166935.1	TLKYANRARNIKNKVMVNQDRASQQINALRSEITRLQMELMYKTKGRIIDEEGVESIND *****;*****	420
XP_013853381.2	MFHENAMLQTENNLRVRIKAMQETVDALRTRITQLVSDQANQVLARAGEGNEEISNMIH	480
NP_001166935.1	MFHENAMLQTENNLRVRIKAMQETVDALRSTRITQLVSDQANHVLARAGEGNEEISNMIH *****;*****;*****	480
XP_013853381.2	SYIKEIEDLRAKLLESEAVNENLRKLNLRATARSFYFSGSFAFSPTIMSSDKETIEIIDL	540
NP_001166935.1	SYIKEIEDLRAKLLESEAVNENLRKLNLRATARAPYFSGSFTSPTILSSDKETIEIIDL *****;*****;*****	540
XP_013853381.2	AKKDLEKLRKREKRRKRLQKLEESNREERSVAGKEDNIDTQEKKEEKGISERENNELE	600
NP_001166935.1	AKKDLEKLRKREKRRKRLQKLEESNREERSVAGKEDNTDTQEKKEEKGVSERENNELE *****;*****;*****	600
XP_013853381.2	VEESQEVSDHEDEEEEEEDDIEGGESSDESDESDEKANYQADLANITCEIAIKQKL	660
NP_001166935.1	VEESQEVSDHEDEEEEEEDDIDGGESSDESDESDEKANYQADLANITCEIAIKQKL *****;*****	660
XP_013853381.2	IDELENQKRLQTLKKQYEEKLMLLQHKIRDTQLERDQVLQNLGVSVESEEKAKKIRSE	720
NP_001166935.1	IDELENQKRLQTLKKQYEEKLMLLQHKIRDTQLERDQVLQNLGVSVESEEKAKKVRSE *****;***	720
XP_013853381.2	YEKQLQAMNKEQLRLQTAQKEHARLLKNQSQYEQQLKQLQDVMEMKTKVRLMKQMKEE	780
NP_001166935.1	YEKQLQAMNKEQLRLQAAQKEHARLLKNQSQYEQQLKQLQDVMEMKTKVRLMKQMKEE *****;*****	780
XP_013853381.2	QEKARLMESRRNREIAQLKKDQRKRDLRLLEAQKRNQEVVLRKTEEVTLARRQVRPM	840
NP_001166935.1	QEKARLTESRRNREIAQLKKDQRKRDLRLLEAQKRNQEVVLRKTEEVTLARRQVRPM *****	840
XP_013853381.2	SDKVAGKVTRKLSDDAPVQDTGSSAAAIETDASRAGAQQKMRIPVARVQALPAPITNGT	900
NP_001166935.1	SDKVAGKVTRKLSDDAPAQDTGSSAAAVETDASRTGAQQKMRIPVARVQALPTPATNGN *****;*****;*****;***	900
XP_013853381.2	RKKYQRKGLTGRVFI SKTARMKWQLLERRVTDIIMQKMTISNMEADMNRLKQREELTKR	960
NP_001166935.1	RKKYQRKGLTGRVFI SKTARMKWQLLERRVTDIIMQKMTISNMEADMNRLKQREELTKR *****	960
XP_013853381.2	REKLSKRREKIVKENGEGDKNVNINEEMESLTANIDYINDSISDCQANIMQEEAKEEG	1020
NP_001166935.1	REKLSKRREKIVKENGEGDKNVNINEEMESLTANIDYINDSISDCQANIMQEEAKEEG *****	1020
XP_013853381.2	ETLDVTAVINACTL TEARYLLDHFLSMGINKGLQAAQKEAQIKVLEGRKQIEITSATQN	1080
NP_001166935.1	ETLDVTAVINACTL TEARYLLDHFLSMGINKGLQAAQKEAQIKVLEGRKQIEITSATQN *****	1080
XP_013853381.2	QLLFHMLKEKAELNPELDALGHALQDLDSVPLENVEDSTDEDVPLNSPGSEGSSLSDDL	1140
NP_001166935.1	QLLFHMLKEKAELNPELDALGHALQDLDSVPLENVEDSTDEDVPLNSPGSEGSTLSSDL *****;*****	1140
XP_013853381.2	MKLCGEVVKPKARRRRTTQMELLYADSSSELASDTSTGDASLPGPLTPVAEGQIEGMNTE	1200
NP_001166935.1	MKLCGEVVKPKARRRRTTQMELLYADSSSELASDTSTGDASLPGPLTPVAEGQIEGMNTE *****	1200

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XP_013853381.2 TS-TSAREKDLPPSPGFPSKIGSISRQSSLSEKKLPEPSPI TRRKVYEKAEKAKAKEQKH 1259
NP_001166935.1 TSGTSAREKELSPPPGLPSKIGSISRQSSLSEKKIPEPSVTRRKAYEKAEKSKAKEQKH 1260
** *****;* ** *;*****;*****;*****;*****;*****
XP_013853381.2 SDSGTSEASLSPSSPPSRPRNELNVFNRLTVSQGNTSVQQDKSDES DSSLSEVHSRSSR 1319
NP_001166935.1 SDSGTSEASLSPSSPPSRPRNELNVFNRLTVSQGNTSVQQDKSDES DSSLSEVH-RSSR 1319
***** ***** *****;*****;*****;*****;*****;*****

XP_013853381.2 RGIINPFPPSKGIRASPLQCVHIAEGHTKAVLCVDSTDDLLFTGSKDR TCKVWNLVTGQE 1379
NP_001166935.1 RGIINPFPAASKGIRAFPLQCIHIAEGHTKAVLCVDSTDDLLFTGSKDR TCKVWNLVTGQE 1379
***** ***** *****;*****;*****;*****;*****;*****

XP_013853381.2 IMSLGGHPNNVSVKYCNYTSLVFTVSTSYIKVWDIRDSAKCIRTLTSSGQVTLGDACST 1439
NP_001166935.1 IMSLGGHPNNVSVKYCNYTSLVFTVSTSYIKVWDIRDSAKCIRTLTSSGQVTLGDACSA 1439
***** ***** *****;*****;*****;*****;*****;*****;

XP_013853381.2 STSRTVAIPSGENQINQIALNPTGTFLYAASGNVMMWDLKRFQSTGKLTGHLGPMVCLT 1499
NP_001166935.1 STSRTVAIPSGENQINQIALNPTGTFLYAASGNVMMWDLKRFQSTGKLTGHLGPMVCLT 1499
***** ***** *****;*****;*****;*****;*****;*****

XP_013853381.2 VDQISNGQDLIITGSKDHYIRMFVTEGALGTVSPHNFEPHYDGEALTIQGDNLFSG 1559
NP_001166935.1 VDQISSGQDLIITGSKDHYIKMFDVTEGALGTVSPHNFEPHYDGEALTIQGDNLFSG 1559
***** ***** *****;*****;*****;*****;*****;*****

XP_013853381.2 SRDNGIKKWDLAQKDLLQQVPNAHKDWICALGVVPAHPVLLSGCRGGILKLWNMDFVPV 1619
NP_001166935.1 SRDNGIKKWDLTQKDLLQQVPNAHKDWICALGVVPAHPVLLSGCRGGILKVWNMDFMPV 1619
***** ***** *****;***** *****;*****;*****;*****;*****

XP_013853381.2 GEMKGDSPINAICVNSTHIFTAADDRTVRIWKTRNLQDQGISDTGDLGEDIASN 1674
NP_001166935.1 GEMKGDSPINAICVNSTHIFTAADDRTVRIWKARNLQDQGISDTGDLGEDIASN 1674
***** ***** *****;*****;*****;*****;*****;*****

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#
# Percent Identity Matrix - created by Clustal2.1
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#
1: XP_013853381.2 100.00 96.23
2: NP_001166935.1 96.23 100.00

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