

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	SAGGIYTVGVTRTRVNTVESEMQLKLGALSRTTASTQMNQVSSRSHAIIFTIHLSTQTRMC	240
NP_001166935.1	STGGIYTVGVTRTRVNTVESEMQLKLGALSRTTASTQMNQVSSRSHAIIFTIHCQTRVC *;*****;***	240
XP_013853381.2	PQIDTENAIIDNKVISESQMNEFETLTAKFHFDLAGSERLKRRTGATGERAKEGINSINGC	300
NP_001166935.1	PQIDADNATDNKIIESEAQMNEFETLTAKFHFDLAGSERLKRRTGATGERAKEGINSINGC ***;***;*****;*****	300
XP_013853381.2	LLALGNVISALGDKSKRATHVPYRDSKLRLLQDSLGGNSQTIMIACVSPSDRDFMETLN	360
NP_001166935.1	LLALGNVISALGDKSKRATHVPYRDSKLRLLQDSLGGNSQTIMIACVSPSDRDFMETLN *****	360
XP_013853381.2	TLKYANRARNIKNKVMVNDQRASQQINALRNEITRLQMELMYKTKGRIIDEEGVESIND	420
NP_001166935.1	TLKYANRARNIKNKVMVNDQRASQQINALRSEITRLQMELMYKTKGRIIDEEGVESIND *****;*****	420
XP_013853381.2	MFHENAMLQTENNNLRVRIKAMQETVDALRTRITQLVSDQANQVLARAGEGNEEISNMIH	480
NP_001166935.1	MFHENAMLQTENNNLRVRIKAMQETVDALRSTRITQLVSDQANHVLRARAGEGNEEISNMIH *****;*****;*****	480
XP_013853381.2	SYIKEIEDLRAKLLESEAVNENLRKLNLRATARSFYFSGSFAFSPTIMSSDKETIEIIDL	540
NP_001166935.1	SYIKEIEDLRAKLLESEAVNENLRKLNLRATARAPYFSGSFTSPTILSSDKETIEIIDL *****;*****;*****	540
XP_013853381.2	AKKDLEKLRKREKRRKRLQKLEESNREERSVAGKEDNIDTQEKKEKGVSERENNELE	600
NP_001166935.1	AKKDLEKLRKREKRRKRLQKLEESNREERSVAGKEDNTDTQEKKEKGVSERENNELE *****;*****;*****	600
XP_013853381.2	VEESQEVSDHEDEEEEEEDDIEGGESSDESDESDEKANYQADLANITCEIAIKQKL	660
NP_001166935.1	VEESQEVSDHEDEEEEEEDDIDGGESSDESDESDEKANYQADLANITCEIAIKQKL *****;*****	660
XP_013853381.2	IDELNSQKRLQTLKKQYEEKLMLLQHKIRDITQLERDQVLQNLGVSVESEEKAKKIRSE	720
NP_001166935.1	IDELNSQKRLQTLKKQYEEKLMLLQHKIRDITQLERDQVLQNLGVSVESEEKAKKVRSE *****;***	720
XP_013853381.2	YEKLLQAMNKEQLRLQTAQKEHARLLKNQSQYEQQLKLLQDDVMEMKTKVRLMKQMKEE	780
NP_001166935.1	YEKLLQAMNKEQLRLQAAQKEHARLLKNQSQYEQQLKLLQDDVMEMKTKVRLMKQMKEE *****;*****	780
XP_013853381.2	QEKARLMESRRNREIAQLKKDQRKRDHQLRLEAQKRNQEVVLRKTEEVTALRRQVRPM	840
NP_001166935.1	QEKARLTESRRNREIAQLKKDQRKRDHQLRLEAQKRNQEVVLRKTEEVTALRRQVRPM *****	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	ETLDVTAVINACTLTEARYLLDHFLSMGINKGLQAAQKEAQIKVLEGRKQTEITSATQN	1080
NP_001166935.1	ETLDVTAVINACTLTEARYLLDHFLSMGINKGLQAAQKEAQIKVLEGRKQTEITSATQN *****	1080
XP_013853381.2	QLLFHMLKEKAELNPELDALLGHALQDLDSVPLENVEDSTDEDVPLNSPGSEGSSLSDDL	1140
NP_001166935.1	QLLFHMLKEKAELNPELDALLGHALQDLDSVPLENVEDSTDEDVPLNSPGSEGSTLSSDL *****;*****	1140
XP_013853381.2	MKLCGEVVKPKARRRRTTQMELLYADSSSELASDTSTGDASLPGPLTPVAEGQIEGMNTE	1200
NP_001166935.1	MKLCGEVVKPKARRRRTTQMELLYADSSSELASDTSTGDASLPGPLTPVAEGQIEGMNTE *****	1200

```

XP_013853381.2 TS-TSAREKDLPPSGFPSPKIGSISRQSSLSEKKLPEPSPI TRRKVYEKA EKAKAKEQKH 1259
NP_001166935.1 TSGTSAREKELSPPPGLPSKIGSISRQSSLSEKKIPEPSVTRRKAYEKA EKSKAKEQKH 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 STSRTVAIPSGENQINQIALNPTGTFLYAASGNVAVRMDLKRFSQSTGKLTGHLGPVMCLT 1499
NP_001166935.1 STSRTVAIPSGENQINQIALNPTGTFLYAASGNVAVRMDLKRFSQSTGKLTGHLGPVMCLT 1499
***** ***** *****

XP_013853381.2 VDQISNGQDLIITGSKDHYIRMFVTEGALGTVSPHNFEPHYDGI EALTIQGDNLFSG 1559
NP_001166935.1 VDQISSGQDLIITGSKDHYIKMFDVTEGALGTVSPHNFEPHYDGI EALTIQGDNLFSG 1559
***** ***** *****:*****

XP_013853381.2 SRDNGIKKWDLAQKDLLQQVPNAHKDWICALGVVPAHPVLLSGCRG GILKLWNMDFVPV 1619
NP_001166935.1 SRDNGIKKWDLTQKDLLQQVPNAHKDWICALGVVPAHPVLLSGCRG GILKVWMDTFMPV 1619
***** ***** *****:***** ***** *****:*****

XP_013853381.2 GEMKGDSPINAICVNSTHIFTAADDRTVRIWKTRNLQDQGISDTG DLGEDIASN 1674
NP_001166935.1 GEMKGDSPINAICVNSTHIFTAADDRTVRIWKARNLQDQGISDTG DLGEDIASN 1674
***** ***** *****:*****

```

```

#
#
# Percent Identity Matrix - created by Clustal2.1
#
#

```

```

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

```