

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	LFKSIEEKKHASIKNGLPSPDFKVNQFLELYNEEVLDLFDTRDIDAKNKKSNIRIHED	180
NP_001166935.1	LFKSIEEKKHAIKNGLPAPDFKVNQFLELYNEEVLDLFDTRDIDAKSKKSNIRIHED *****;*****	180
XP_013853381.2	SAGGIYTVGVTRTRVNTVESEMMQCKLGLSRTTASTQMNQSSSRSHAIIFTIHLSTQTRMC	240
NP_001166935.1	STGGIYTVGVTRTRVNTVESEMMQCKLGLSRTTASTQMNQSSSRSHAIIFTIHCQTRVC *;*****;***	240
XP_013853381.2	PQIDTENAI DNKVI SESSQMNFEFETLAKFHFDLAGSERLKRRTGATGERAKEGINSINGC	300
NP_001166935.1	PQIDADNATDNKI IESSAQMNFEFETLAKFHFDLAGSERLKRRTGATGERAKEGINSINGC ***;:** **;****;*****	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	MFHENAMLQTENNLRVRIKAMQETVDALRSRITQLVSDQANHVLRARAGEGNEEISNMIH *****;*****;*****	480
XP_013853381.2	SYIKEIEDLRAKLLESEAVNENLRKNLTRATARSFYFGSSAFSPTIMSSDKETIEIIDL	540
NP_001166935.1	SYIKEIEDLRAKLLESEAVNENLRKNLTRATARAPYFGSSFTSPTILSSDKETIEIIDL *****;*****;*****;*****	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	YEKQLQAMNKEQLRLQTAQKEHARLLKNQSQYEQQLKQLQDVMEMKTKVRLMKQMKEE	780
NP_001166935.1	YEKQLQAMNKEQLRLQAAQKEHARLLKNQSQYEQQLKQLQDVMEMKTKVRLMKQMKEE *****;*****	780
XP_013853381.2	QEKARLMESRRNREIAQLKKDQRKRDHQLRLEAQKRNQEVVLRKTEEVTLARRQVRPM	840
NP_001166935.1	QEKARLTESRRNREIAQLKKDQRKRDHQLRLEAQKRNQEVVLRKTEEVTLARRQVRPM *****	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	ETLDVTVAVINACTL TEARYLLDHFLSMGINKGLQAAQKEAQIKVLEGRKQIEITSATQN	1080
NP_001166935.1	ETLDVTVAVINACTL TEARYLLDHFLSMGINKGLQAAQKEAQIKVLEGRKQIEITSATQN *****	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-TSAREKDLPPSGFPSPKIGSISRQSSLEKKLPEPSPI TRRKVYEKA EKAKAKEQKH	1259
NP_001166935.1	TSGETSAREKELSPPPGLPSKIGSISRQSSLEKKIPEPSVTRRKAYEKA EKSKAKEQKH	1260
XP_013853381.2	** *****: * ** *:*****:*****:*****:*****:*****	
NP_001166935.1	SDSGTSEASLSPSSPPSRPRNELNVFNRLTVSQGNTSVQQDKSDES DSSLSEVHSRSSR	1319
NP_001166935.1	SDSGTSEASLSPSSPPSRPRNELNVFNRLTVSQGNTSVQQDKSDES DSSLSEVH-RSSR	1319
XP_013853381.2	*****:*****:*****:*****:*****:*****:*****:*****	
XP_013853381.2	RGIINPFPPSKGIRASPLQCVHIAEGHTKAVLCVDSTDDLLFTGSKDR TCKVWNLVTGQE	1379
NP_001166935.1	RGIINPFPAASKGIRAFPLQCIHIAEGHTKAVLCVDSTDDLLFTGSKDR TCKVWNLVTGQE	1379
XP_013853381.2	*****:*****:*****:*****:*****:*****:*****:*****	
XP_013853381.2	IMSLGGHPNNVSVKYCNYTSLVFTVSTSYIKVWDIRDSAKCIRTLTSSGQVTLGDACST	1439
NP_001166935.1	IMSLGGHPNNVSVKYCNYTSLVFTVSTSYIKVWDIRDSAKCIRTLTSSGQVTLGDACSA	1439
XP_013853381.2	*****:*****:*****:*****:*****:*****:*****:*****	
XP_013853381.2	STSRVAIPSGENQINQIALNPTGTFLYAASGNVMMWDLKRFQSTGKLTGHLGPMCLT	1499
NP_001166935.1	STSRVAIPSGENQINQIALNPTGTFLYAASGNVMMWDLKRFQSTGKLTGHLGPMCLT	1499
XP_013853381.2	*****:*****:*****:*****:*****:*****:*****:*****	
XP_013853381.2	VDQISNGQDLIITGSKDHYIRMFVTEGALGTVSPHNFEPHYDGEALTIQGDNLFSG	1559
NP_001166935.1	VDQISSGQDLIITGSKDHYIKMFDVTEGALGTVSPHNFEPHYDGEALTIQGDNLFSG	1559
XP_013853381.2	*****:*****:*****:*****:*****:*****:*****:*****	
XP_013853381.2	SRDNGIKKWLDAQKDLLQQVPNAHKDWICALGVVPAHPVLLSGCRGGILKLVNMDNFVPV	1619
NP_001166935.1	SRDNGIKKWLDTQKDLLQQVPNAHKDWVICALGVVDPHPVLLSGCRGGILKLVNMDTFMPV	1619
XP_013853381.2	*****:*****:*****:*****:*****:*****:*****:*****	
XP_013853381.2	GEMKGDSPINAICVNSTHIFTAADDRTVRIWKTRNLQDQGISDTGDLGEDIASN	1674
NP_001166935.1	GEMKGDSPINAICVNSTHIFTAADDRTVRIWKARNLQDQGISDTGDLGEDIASN	1674
XP_013853381.2	*****:*****:*****:*****:*****:*****:*****:*****	

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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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