Table S1: Accession numbers of PRR protein sequences used for multiple sequence alignments and reviewed in the present manuscript.

PRR protein	Chicken	Duck	Goose
TLR2t1	NP_989609.1	XP_005021002.2	XP_013030624.1
TLR2t2	NP_001155122.1	NP_001297277.1	-
TLR1t1	NP_001007489.4	NP_001297353.1	XP_013041417.1
TLR1t2	XP_025005535.1	XP_027312049.1	-
TLR3	NP_001011691.3	NP_001297711.1	XP_013035229.1
TLR4	NP_001025864.1	NP_001297342.1	XP_013038385.1
TLR5	NP_001019757.1	NP_001297753.1	XP_013029406.1
TLR7	NP_001011688.1	XP_005029235.1	XP_013046996.1
TLR21	NP_001025729.1	KY829021	AMB20882.1
TLR15	NP_001032924.1	XP_005018927.2	XP_013046493.1
RIG-I	-	NP_001297309.1	NP_001298119.1
MDA-5	NP_001180567.1	NP_001297740.1	XP_013026596.1
LGP2	NP_001305337.1	XP_027301625.1	XP_013055203.1
DDX1	NP_989894.1	XP_027311055.1	XP_013028107
DDX21	XP_001232052	XP_027316557.1	XP_013030257.1
DHX36	XP_015147310.1	XP_027320349.1	XP_013048509.1
DDX3X	NP_001025971.1	XP_005012555.2	XP_013046370.1
DDX23	XP_025001441.1	XP_021135293.1	XP_013054789.1
DDX24	NP_065147.1	XP_025006699.1	XP_027314331.1
DDX60	XP_004940975.1	XP_027312235.1	XP_013030722.1
DDX41	NP_001336637.1	XP_027324165.1	XP_013047316.1
DHX36	XP_015147310.1	XP_027320349.1	XP_013048508.1
OASL	XP_015148492.1	ARS01326.1	XP_013047372.1
cGAS	XP_419881.4	XP_027310983.1	XP_013027663.1
STING	XP_025010645.1	XP_027323921.1	XP_013057484.1
ERADp	NP_001185786.1	XP_027323010.1	XP_013042385.1

```
A5YBP4_CHICK      1  MGSL----TSIYVFACVFISILWNNIQPTVENKITANYSGHLLTEVPKNIPVHTHILDLS
NP_001297353.1    1  MGSL----TSIYIFACVFTLTLWNNVQPTVENFIANYSSILLTDVPKTIPLHTRVLDLS
XP_013041417.1    1  MGSL----TSIYVFACVFTLTLWNNIHPTVENFIANYSSILLTDVPKNIPLHTHVLDLS
TLR1_HUMAN        1  M-------TSIFHFAIIFMLILQIRIQLSEESEFIVDRSKNGLIHVPKDLSQKTTILNIS
TLR6_HUMAN        1  MTKDKEPIVKSFHFVCLMIIIVGTRIQFSDGNEFAVDKSKRGLIHVPKDLPLKTVLDMS
TLR10_HUMAN       1  MRLI----RNIYIFCSIVMTAEGDAPELPEERELMTCSNMSIRKVPADLTPATTTLDLS

A5YBP4_CHICK     57  HNSISEITNFRFTSLSDLQVLNLSHNLITELDFSAFMFNQDLEYLDLSHNNIWTAYCQLL
NP_001297353.1   57  HNRISELSISEFISLSDLQVLNLSHNLITELDFNVFIFNQDLEYLDLSHNNIWKVYCQTL
XP_013041417.1   57  HNRISELSISEFISLSDLQVLNLSHNLITELDFNIFIFNQDLEYLDLSHNNIWKVYCQTL
TLR1_HUMAN       54  QNYISELWTSDILSLSKLRILIISHNRIQYLDISVFKFNQELEYLDLSHNKLVKISCHPT
TLR6_HUMAN       61  QNYIAELQVSDMSFLSELTVLRLSHNRIQLLDLSVFKFNQDLEYLDLSHNQLQKISCHPI
TLR10_HUMAN      57  YNLLFQLQSSDFHSVSKLRVLILCHNRIQQLDLKTFEFNKELRYLDLSNNRLKSVTWYLL

A5YBP4_CHICK    117  ARLRHLDLSFNKFTVLPICQEFGIMFHLEYLGLSAMMIRRSDFRYVAHLQLDTVFLTLED
NP_001297353.1  117  ACLRHLDLSFNNFTVLPICQEFGTMFHLEYLGLSATMIRRSDFRYITHLQLNTVFLTLEN
XP_013041417.1  117  SCLRHLDLSFNNFTVLPICQEFGTMFHLEYLGLSAMMIRRSDFRHITHLQLNTLFLTLEK
TLR1_HUMAN      114  VNLKHLDLSFNAFDALPICKEFGNMSQLKFLGLSTTHLEKSSVLPIAHLNISKVLIVLGE
TLR6_HUMAN      121  VSFRHLDLSFNDFKALPICKEFGNLSQLNFLGLSAMKIQKLDLLPIAHLHLSYILDLRN
TLR10_HUMAN     117  AGLRYLDLSFNDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRT

A5YBP4_CHICK    177  FSL--YEPLSLTALNTRSLHIVFATNQNFNFSLLYDGMSTSEKLKIVNLRYTLSHK---D
NP_001297353.1  177  FSL--YKPQSLTALNTKSLHIVFSANQNFNFSLLYDGMSTSENLKIVNVRYTLSYK---D
XP_013041417.1  177  FSL--YEPQSLTALNTKSLHIVFSENQNFNFSLLYDGMSTSENLKIVNIRYTLSYK---D
TLR1_HUMAN      174  TYGEKEDPEGLQDFNTESLHIVFPTNKEFHFILDVSVKTVANLEISNIKCVLEDNKCSY
TLR6_HUMAN      181  YYIKENETESLQILNAKTLHLVFHPTSLFAIQ-VNISVNTLGCLQITNIKLNDD--NCQV
TLR10_HUMAN     177  LPH--YEEGSIPILNTTKLHIVLPMDTNFWVL-LRDGIKTSKILEMTNIDGKSQFV---S

A5YBP4_CHICK    232  FPSPSLELQKKIKATDLMLDTVDLEWTVILQIFLLVWDSSVEHLTVRNLIFRGPVVELTE
NP_001297353.1  232  FPSPALTLLKKIKTTALMLDTVDLEWPIILQIFLLIWYSPVEHLTVRNLIFRGPIGGLTA
XP_013041417.1  232  FPSPSLKLLKKIKTTTLMLDTVDLEWPIILQIFLLIWYSPVENLTVRNLTFRGPMGVLTP
TLR1_HUMAN      233  FLSILAKLQTNPKLSNLTLNNIETTWNSFIRILQLVWHTTVWYFSISNVKLQGQLD-F--
TLR6_HUMAN      238  FIKFLSEITRGSTLLNFTINHIETTWKCLVRVFQFLWPKPVEYLNIYNLTIIESIR-E--
TLR10_HUMAN     231  YEMQRNLSLENAKTSVLLINKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAY-L--
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A5YBP4_CHICK     292  YKHVPLLRSLEQLLSLGSSMKALTLERVRNKLYYFNQEILYRQFSEMNIDSLTIHDACMP
NP_001297353.1   292  YKFVPFLSSLEQVMSLGVSMKALTLERVRNKVYYFNQKILYRWFSEMNIASLTIYDAYMP
XP_013041417.1   292  FKFVPFLSSLEQVVSLDVSMKVLTLEHVRNKVYYFNQEILYREFSEMNIANLTIYDAYMP
TLR1_HUMAN       290  ----------RDFDYSGTSLKALSIHQVVSDVFGFPQSYIYETFSNMIKNFTVSGTRMV
TLR6_HUMAN       295  ----------EDFTYSKTTLKALTIEHITNQVFLFSQTALYTVFSEMNIMMLTISDTPFI
TLR10_HUMAN      288  -------DHNSFDYSNTVMRTIKLEHVHFRVFYIQQDKIYLLLTKMDIENLTISNAQMP


A5YBP4_CHICK     352  HMLCPKKPSSFQYINFSRNALTDELFQNCDTLANLKILILHRNKFESLSKVSFMTSRMKS
NP_001297353.1   352  HMLCPQRASLFQYLNFSRNALTDELFQNCSTLAELKLFILRRNKFESLSKVSSMTRYMKS
XP_013041417.1   352  HMLCPEKASSFQYLNFSRNALTDELFQNCSTLADLKLLILKRNKFESLPKVSSMTRHMKS
TLR1_HUMAN       340  HMLCPSKISPFLHLDFSNNLLTDTVFENCGHLTELETLILQMNQLKELSKIAEMTTQMKS
TLR6_HUMAN       345  HMLCPHAPSTFKFLNFTQNVFTDSIFEKCSTLVKLETLILQKNGLKDLFKVGLMTKDMPS
TLR10_HUMAN      340  HMLFPNYPTKFQYLNFANNILTDELFKRTIQLPHLKTLILNGNKLETLSLVSCFANN-TP


A5YBP4_CHICK     412  LRYLDMSSNLLRNSRAEGRCQWADSLAELDLSSNQLTEAVFECLPANINKVDLQNNQIAN
NP_001297353.1   412  LRYLDMSSNLLHTDGAEEHCQWTESLKELDLSSNQLTESVFGCLPVNVNKLDHNNQISS
XP_013041417.1   412  LRYLDMSSNLLRNDGAEEHCQWTESLMELDLSSNQLTESVFGCLPVNVNKLDLQNNQIAS
TLR1_HUMAN       400  LQQLDISQNSVSYDEKKGDCSWTKSLLSLNMSSNILTDTIFRCLPPRIKVLDLHSNKIKS
TLR6_HUMAN       405  LEILDVSWNSLESGRHKENCTWVESIVVLNLSSNMLTDSVFRCLPPRIKVLDLHSNKIKS
TLR10_HUMAN      399  LEHLDLSQNLLQHK-NDENCSWPETVVNMNLSYNKLSDSVFRCLPKSIQILDLNNNQIQT


A5YBP4_CHICK     472  VPKGITELHSLQELNLASNRIADLPGCRAFTGLEILNIERNLILTPSADFFETCPSVKEL
NP_001297353.1   472  VPQGIAELKSLKELNLASNRIADLPGCGGFSALEILNMEMNSILSPSADFLESCQRVREL
XP_013041417.1   472  VPQGIAELKSLKELNLASNRIADLPGCGGFSALEFLNMEMNSILTPSADFFESCQRVREL
TLR1_HUMAN       460  IPKQVVKLEALQELNVAFNSLTDLPGCGSFSSLSVLIIDHNSVSHPSADFFQSCQKMRSI
TLR6_HUMAN       465  VPKQVVKLEALQELNVAFNSLTDLPGCGSFSSLSVLIIDHNSVSHPSADFFQSCQKMRSI
TLR10_HUMAN      458  VPKETIHLMALRELNIAFNFLTDLPGCSHFSRLSVLNIEMNFILSPSLDFVQSCQEVKTL


A5YBP4_CHICK     532  QAGQNPFKCSCELQDFLR-LERQSGGKLSGWPEAYVCKYPEDLSGTQLKDFHLTELACNT
NP_001297353.1   532  EAGHNPFKCSCELQAFVR-LERQSGGKLSGWPEAYVCEYPEDLKGTQLKDFHLTELACNT
XP_013041417.1   532  EAGHNPFKCSCELQAFMR-LERQSGGKLSGWPEAYVCEYPEDLRGTQLKDFHLTELACNT
TLR1_HUMAN       520  KAGDNPFQCTCELGEFVKNIDQVSSEVLEGWPDSYKCDYPESYRGTLLKDFHMSELSCNI
TLR6_HUMAN       525  KAGDNPFQCTCEIREFVKNIDQVSSEVLEGWPDSYKCDYPESYRGSPLKDFHMSELSCNI
TLR10_HUMAN      518  NAGRNPFRCTCELKNFIQ-LETYSEVMMVGWSDSYTCEYPLNLRGTRLKDVHLHELSCNT
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A5YBP4_CHICK    591  TLLLVTALLL--TLVLVAVVAFLCIYLDVPWYVRMLWQWTQTKRRAWHDCPEERETALQF
NP_001297353.1  591  TLLLVTALLLLLTLVLVGVVAFLCIYLDVPWYVRMLWQWTQTKRRAWHECPEERETVLQF
XP_013041417.1  591  TLLLVTALLL--TLVLVGVVAFLCIYLDVPWYVRMLWQWTQTKRRAWHECPEERETVLQF
TLR1_HUMAN      580  TLLIVTIVAT--MLVLAVTVTSLCSYLDLPWYLRMVCQWTQTRRARNIPLEELQRNLQF
TLR6_HUMAN      585  TLLIVTIGAT--MLVLAVTVTSLCIYLDLPWYLRMVCQWTQTRRARNIPLEELQRNLQF
TLR10_HUMAN     577  ALLIVTIVVI--MLVLGLAVAFCCLHFDLPWYLRMLGQCTQTWHRVKTTQEQLKRNVRF

A5YBP4_CHICK    649  HAFISYSERDSLWVKNELIPNLEKGEGCIQLCQHERNFIPGKSIVENIINCIEKSYKSIF
NP_001297353.1  651  HAFISYSERDSVWVKTELIPNLEKGEGSVRLCQHERNFVPGKSIVENIINCIDKSYKSIF
XP_013041417.1  649  HAFISYSERDSVWVKNELIPNLEKGEGSVQLCQHERNFVPGKSIVENIINCIDKSYKSIF
TLR1_HUMAN      638  HAFISYSGHDSFWVKNELLPNLEKEG--MQICLHERNFVPGKSIVENIITCIEKSYKSIF
TLR6_HUMAN      643  HAFISYSEHDSAWVKSELVPYLEKED--IQICLHERNFVPGKSIVENIINCIEKSYKSIF
TLR10_HUMAN     635  HAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENIVSFIEKSYKSIF

A5YBP4_CHICK    709  VLSPNFVQSEWCHYELYFAHHKLFSENSNSLILILLEPIPPYVIPARYHKLKALMAKRTY
NP_001297353.1  711  VLSPNFVQSEWCHYELYFAHHKLFSENCNSLILILLEPIPQYIIPARYHKLKALMAKRTY
XP_013041417.1  709  VLSPNFVQSEWCHYELYFAHHKLFSENCNSLILILLEPIPQYIIPARYHKLKALMAKRTY
TLR1_HUMAN      696  VLSPNFVQSEWCHYELYFAHHNLFHEGSNSLILILLEPIPQYSIPSSYHKLKSLMARRTY
TLR6_HUMAN      701  VLSPNFVQSEWCHYELYFAHHNLFHEGSNNLILILLEPIPQNSIPNKYHKLKALMTQRTY
TLR10_HUMAN     695  VLSPNFVQNEWCHYEFYFAHHNLFHENSDHIILILLEPIPFYCIPTRYHKLKALLEKKAY

A5YBP4_CHICK    769  LEWPKERSKHALFWANLRAAISINLSVADEQNRTEV------------------------
NP_001297353.1  771  LEWPKERSKRALFWANLRAAINVNLPMSFEGNEEEN---------DVTFTDSITQPLIK
XP_013041417.1  769  LEWPKERSKRALFWANLRAAININLPKSFEANEEEN---------DVTSTGSITQPLIK
TLR1_HUMAN      756  LEWPKEKSKRGLFWANLRAAINIKLTEQAK-----K------------------------
TLR6_HUMAN      761  LQWPKEKSKRGLFWANIRAAFNMKLTLVTENNDVKS------------------------
TLR10_HUMAN     755  LEWPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLMRTDCL--
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Figure S1: The protein sequences of chTLR1t1, duTLR1t1, goTLR1, hTLR1, hTLR6, and hTLR10 aligned using the ClustalW program. Conserved amino acids and synonymous substitutions are shadowed in black and gray, respectively. The cytoplasmic (TIR) domain, the TM region, the extracellular domain with the conserved cysteine-rich CT region (LRR-CT), LRR1–19 and signal peptide are indicated below the sequence in orange, grey, blue, light green, black and orange respectively. Conserved proline and glycine in the BB loop of TIR domain that facilitates interaction with TLR2 to promote signaling are highlighted with black triangles. The asterisk at position 588 marks the conserved cysteine residue.

```
NP_001032924.1    1  MRILIGSLYFYFISFLFSKVNGFLTQRTSPVSSFPFYNYSYLNLSSVSQAQAPKTARALN
XP_005018927.2    1  MGILIRSLHFYFISFLLSRANGFLTWRT-TESAFPFYNYSYLNLSSVSEAQAPKMARALN
XP_013046493.1    1  MGILIRSLHFYFTSFLFSRANGFLTWRTPTESAFPFYNYSYLNLSSVSQAQAPKMARALN
                     _____

NP_001032924.1   61  FSYNAIEKITKRDFEGFHVLEVLDLSHNHIKDIEPGAFENLLSLVSVDLSFNDKNLLVSG
XP_005018927.2   60  FSHNIIEKITKRDFEGFDALEVLDLSYNQIKDIEPGTFEILLSLVSVNLSFNDKKLLVSG
XP_013046493.1   61  FSHNIIEKITKRDFEGFDALEVLDFSYNRIKDIEPSTFETMLSLVSVNLTFNDKKLLVSG
                     _____    _____    _____

NP_001032924.1  121  LAPHLKLIPTSGASGPSQIYMYFQKSAEAALEPSAPAELLPHLEDPPNPGNVNPRFRQ--
XP_005018927.2  120  LAPHLKLLATSRAS---------DKSTEAALEPPASAEELPHSGSPPDLQKINLRLRRST
XP_013046493.1  121  LAPHLKLLATSRAS---------EKSTEAALEPPASAEELPHSGSPPDLQKVNMRLRRST
                     _____

NP_001032924.1  179  ---RRTEENKTSPPAATLRPDLCGAPINGLLDLSRTKLSNEELTAKLDADLCQAQLGTVL
XP_005018927.2  171  RHLRRAEENTMVSPTATLRPNRCGLPINGTLDLSKSKLSEEELTEKLDPDLCQAQLDGVL
XP_013046493.1  172  RHLPRAEENTTVSPTATLRPNRCGLPINGTLDLSKSKLSEEELMEKLDPDLCQAQLDSVL
                     _____    _____

NP_001032924.1  236  EFNISHSDLEMDLLSLFILFLPMKDIQSVDASYNRITINNIDVEAICHFPFSNFSFLNIS
XP_005018927.2  231  ELDISHNDLEMDLLSLFILFLPMKNVQSIDVSYNNITINNIDVEAICRFPFSNLSFVNIS
XP_013046493.1  232  ELDISHNDLEMDLLSLFILFLPMKNVQSIDASYNNITIDNIDVEAICRFPFSNLSFVNIS
                     _____    _____    _____

NP_001032924.1  296  NNPINSLETVCLPASITVIDLSFTNISTIPANFAKKLSKLERMYVQGNQLIYTVRPENPS
XP_005018927.2  291  NNPLNNLETICLPPTITVIDLSFTNISVIPQNFAKKLFNLENMYVQGNHFIYTVHPKPNN
XP_013046493.1  292  NNPLNNLETICLPPTITVIDLSFANVSVIPQNFAKKLFNLENMYVQGNHFIYTAHPKPTN
                     _____    _____    _____

NP_001032924.1  356  ATPRPPPGTVQISAISLVRNQAGTPIESLPESVKHLKVSNCSIVELPEWFANRMQELLFL
XP_005018927.2  351  TAPKFAPGTVHISAISLVRNQAGTPIESLPEKVKHLKISNCSIVELPEWFANRMQELLFL
XP_013046493.1  352  TAPKFAPGTVHISAISFVRNQAGTPIESLPEKVKHLKISNCSIVELPEWFANRMQELLFL
                     _____    _____    _____

NP_001032924.1  416  DLSSNRISMLPDLPISLQQLDISNSDIKIIPPRFKSLSNVTVFNIQNNKLTEMHPEYFPS
XP_005018927.2  411  DLSSNRISMLPDLPISLQHLDISNSDIKIIPPSFKSLPNLTVFNIQNNKVTDMHPEYFPL
XP_013046493.1  412  DLSSNRISMLPDLPVSLQHLDISNSDIKIIPPSFKSLSNLTVFNIQNNKVTDMHPEYFPL
                     _____    _____    _____
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NP_001032924.1   476   TLTTCDISKNKLKVLSLTKALENLESLNVSGNLITRLEPACQLPSLTNLDSSHNLISELP
XP_005018927.2   471   TLTKCDISKNKLSVLSLTKTIGKLEFLNVSRNLITRLEPTSQLRLLTNLDGSHNLISELP
XP_013046493.1   472   TLTKCDISKNKLNVLSLTKTIGKLEFLNVSRNLITRLEPTSQFHLLTNLDGSHNLISELP

NP_001032924.1   536   DHLGQSLLMLKHFNLSGNKISFLQRGSLPASLEELDISDNAITTIVQDTFGQLTSLSVLT
XP_005018927.2   531   DHFGKSLPMLKYFNLSGNKISFLQRGSLPVSLMELDISDNAITTIAEDTFGQLTSLSILT
XP_013046493.1   532   DRFGKSFPMLKYFNLSGNKISFLQRGSLPVSLMELDISNNAITTIVEDTFGQLTSLSILT

NP_001032924.1   596   VQGKHFFCNCDLYWFVNIYIRNPHLQINGKDDLRCSFPPDRRGSLVKSSNLTLLHCSLGI
XP_005018927.2   591   VQGKHFFCNCDLYWFVNVYVHTPHLQINGKENLRCSFPPDRRGSLVEGSNLTLLHCSLGI
XP_013046493.1   592   VQGKHFFCNCDLYWFVNVYIHIPYLQINGKENLRCSFPPDRRGSLVEGSNLTLLHCSLGI

NP_001032924.1   656   QMAITACMAILVVLVLTGLCWRFDGLWYVRMGWYWCMAKRRQYKKRPENKPFDAFI-SYS
XP_005018927.2   651   QMAITACVAVLVVLVLTGLCWRFDGLWYVKMGWYWCMAKRKQYKKRPENKPFDAF-ISYS
XP_013046493.1   652   QMAITACVAVLVVLVLTGLCWHFDGLWYVRMGWYWCTAKRKQYKKKPENKPFDAFDASYS

NP_001032924.1   715   EHDADWTKEHLLKKLETDGFKICYHERDFKPGHPVLGNIFYCIENSHKVLFVLSPSFVNS
XP_005018927.2   710   EHDANWMKENLLVRLETDGFKICYHERDFKPGHPVLGNIFNCIENSHKVLFVLSPSFVNS
XP_013046493.1   712   EHDAHWTKENLLERLETDGFKICYHERDFKPGHPVLGNIFYCIENSHKVLFVLSPSFVNS

NP_001032924.1   775   CWCQYELYFAEHRVLDENQDSLIMVVLEDLPPDSVPQKFSKLRKLLKRKTYLKWSPEEHK
XP_005018927.2   770   CWCQYELYFAEHQVLNENQDSLIMIVLEDLPPNSIPQKFSKLRKLLKRKTYLKWSPEEHK
XP_013046493.1   772   CWCQYELYFAEHRVLNENQDSLIMIVLEDLPLNSVPQKFSKLRKLLKRKTYLKWSPEEHK

NP_001032924.1   835   QKIFWHQLAAVLKTTNEPL-VRAENGPNEDVIEME
XP_005018927.2   830   QKIFWHQLAAVLKTTNEPFIVRAENGPTQDMYEME
XP_013046493.1   832   QKIFWHQLAAVLKTTNERFVVRAENGSTQDMYEME
```

Figure S2: Schematic alignment of TLR15 protein sequences of chicken, duck and goose. Depicted are the predicted signal sequence, the N-terminal LRR (LRR-NT), 19 LRRs, the C-terminal LRR (LRR-CT), the transmembrane domain (TM), and the TIR domain in blue, red, black, orange, green and purple underlining respectively. The proline-rich loop (aa 359–363) is boxed in black.

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XP_004948095.1    1  MSWAMQYHGCLPWGSWT---RLCGSQPSRRAARCVYLCTASGPGAAGSCFHRKILHIGG-
XP_027300205.1    1  MSRAVQGRGCLPWACLG----------------PYLRAASLPGAAGGSFHGKILSGAS-
XP_013042726.1    1  -------------------------------------------AGGSFRGKILSGDS-
NP_001269072.1    1  MRWCHH----LPRASWGSGFRRALQRPDDR---IPFLIHWSWP----------LQGERP

XP_004948095.1   57  TSLPSRSCVRYKGGSQENRAQRSSSHHGLDHLRNVASSDAIKKHQKSLSAWFSNQPNEER
XP_027300205.1   43  ISLP-RSCVRHQGGPQGPPAQRGSSRHGLDHLRTVASSDAIKKHQKSLAAWFSNQPSEER
XP_013042726.1   15  GSLP-RSCVRHQGGSQGPPAQRGSSRHGLDHLRTVASSDAIKKHQKSLAAWFSNQPNEER
NP_001269072.1   43  FGPP-RAFIRHHGSSVDSAP--PPGRHGR-LFPSASATEAIQRHRRNLAEWFSRLPREER

XP_004948095.1  117  QFGPSFSLDAIHVDPVIRESSLEQILKPSPDLTIQHQLQQPCRQVISLQNLFDVDACGRQ
XP_027300205.1  102  QFGPSFSLDAVHVDPVIRESSLEQILKPSPELTIRHQLQRSSRRVISLQNLFEADACGRQ
XP_013042726.1   74  QFGPSFSLDAVHVDPVIRESSLEQILKPSPELTIQHQLQRSSRQVISLQNLFDVDACGRQ
NP_001269072.1   99  QFGPTFALDTVHVDPVIRESTPDELLRPPAEIALEHQPPQAGLPPIALSQLFNPDACGRR

XP_004948095.1  177  VKNVVLYGTVGTGKSTLIKKMVVDWCHGLLPRFELVIPFSCEDLSH-SHVPISLRRLITK
XP_027300205.1  162  VKNVVLYGTVGTGKSTLIKKMVVDWCHGLLPRFELVIPFSCEDLSH-SRVPISLRRLVTK
XP_013042726.1  134  VKNVVLYGTVGTGKSTLIKKMVVDWCHGLLPRFELVIPFSCEDLSH-SRVPISLRRLVTK
NP_001269072.1  159  VQTVVLYGTVGTGKSTLVRKMVLDWCYGRLPAFELLIPFSCEDLSSLGPAPASLCQLVAQ

XP_004948095.1  236  KYQHLRDVVPLLGSSNLKVLFILNGLERLNLDFRLAGTELCCDANEPVPPSAIVVNLLRK
XP_027300205.1  221  KYQHLRDVAPLLGASNLKVLFILNGLERLNLDFRLAGTELCCDPSEPIAPSAIVVNLLRK
XP_013042726.1  193  KYQHLRDVAPILGASNLKVLFILNGLERLNLDFRLAGTELCCDPGEPIAPSAIVVNLLRK
NP_001269072.1  219  RYTPLKEVLPLMAAAGSHLLFVLHGLEHLNLDFRLAGTGLCSDPEEPQEPAAIIVNLLRK

XP_004948095.1  296  YLLPEASIIVTTRPSAVRRIPGKYVGRYAEICGFSDTNLQKLYFQLRLSQPGCDGE---N
XP_027300205.1  281  YLLPEASIIVTARPSAVRRIPGKYVGRYAEICGFSDTNLQKLYFQMRLSQPGCDGE----
XP_013042726.1  253  YLLPEASIIVTTRPSAVRRIPGKYVGRYAEICGFSDTNLQKLYFQMRLSQPGCGG---D
NP_001269072.1  279  YMLPQASILVTTRPSAIGRIPSKYVGRYGEICGFSDTNLQKLYFQLRLNQPYCGYAVGGS
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XP_004948095.1  353  SVASRSGEQDNLVEMLSRNLERQNQIAAACFLPSYCWLVCTTLHFLYFTRTVPPSQTLSG
XP_027300205.1  337  ----GSGEQENLVEMLWRNLERQNQIAAACFLPSYCWLVCTTLHFLYFTRTVPPSQTLTG
XP_013042726.1  310  G--EGSGEQDNLVEMLSRNLEHQNQIAAACFLPSYCWLVCTTLHFLYFTRTVPPSQTLTG
NP_001269072.1  339  GVSATPAQRDHLVQMLSRNLEGHHQIAAACFLPSYCWLVCATLHFLHA--PTPAGQTLTS


XP_004948095.1  413  IYTSFLRLNFSGEVLDSTDPTKISMMKYVAKTVGKLAHEGVMSRKTSFTEEDLQQCFEVE
XP_027300205.1  393  IYTSFLRLNFSGEVLDSSEPTAVSMMKYVAKTVGKLAHEGVMSRQTCFSEEDLRQCFEVE
XP_013042726.1  368  IYTSFLRLNFSGEVLDSTDPTDISMMKYVAKTVGKLAHEGVMSRKTCFSEEDLRQCFEVE
NP_001269072.1  397  IYTSFLRLNFSGETLDSTDPSNLSIMAYAARTMGKLAYEGVSSRKTYFSEEDVCGCLEAG


XP_004948095.1  473  MKTESELNQIEVFRSDVFRFFLTPCVQPGKEHTFVFTIPAMQEYLAALYVVLGEKKTLVQ
XP_027300205.1  453  MKTESELNLIEVFRSDVFPFFLTPCVQPGREHTFVFTIPAMQEYLAALYVVLGEKKTLAQ
XP_013042726.1  428  MKTESELNLIEVFRSDVFRFFLTPCVQPGKEHTFVFTIPAMQEYLAALYVVLGEKKTLAQ
NP_001269072.1  457  IRTEEFQLLHIFRRDALRFFLAPCVEPGRAGTFVFTVPAMQEYLAALYIVLGLRKTTLQ


XP_004948095.1  533  KVGKEVSEIIGKVSEDAAVVLSIISKVLPLRFLPVLFNLLKMFPRFFSRLSGKGRDTIAR
XP_027300205.1  513  KVGKELSELIGKVSEDAAVVLGIVSKVLPLRFLPVLFNLLKIFPRFFSRLSGKDRDTIAR
XP_013042726.1  488  KVGKELSELIGKVSEDAAVVLGIVSKVLPLRFLPVLFNLLKIFPRFFSRLSGKDRDTIAR
NP_001269072.1  517  KVGKEVAELVGRVGEDVSIVLGIMAKLLPLRALPLLFNLIKVVPRVFGRMVGKSREAVAQ


XP_004948095.1  593  TMAEELFKEEDYYNDDVLDQINSSILGVEGPMRHPDEAADDEVFELFPIFMGGILSRRNR
XP_027300205.1  573  TMAEELFKEEDYYNDDVLDQINSSILGVEGPLRHPDEAPDDEVFELFPIFMGGLLSRRNR
XP_013042726.1  548  TMAEELFKEEDYYNDDVLDQINSSILGVEGPMRHPDEAPDDEVFELFPIFMGGLLSRRNR
NP_001269072.1  577  AMVLEVFREEDYYNDDVLDQMGASILGVEGPRRHPDEPPEDEVFELFPMFMGGLLSAHNR


XP_004948095.1  653  AILEQLGCSIKNLAAFEIAKAMKKTVIRNSRKGLPPSELMDYLFFLHEFQNERFTAEAVR
XP_027300205.1  633  ALLEQLGCSIKNLAALEIAEAMKKTVIRNSRKGLPPSELMDYLFFLHEFQNERFTAEAVR
XP_013042726.1  608  AILEQLGCSIKNLAAFEIAEAMKKTVIRNSRKGLPPSELMDYLFFLHEFQNERFTAEAVR
NP_001269072.1  637  AVIAQLGCPIKNLDALENAQAIKKKLGKLGRQVLPPSELLDHLFFHYEFQNQRFSAEVLS
```

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XP_004948095.1  713  SLRTVNLSSVKMTPLKCCVLASVMGSTSHEVEELNLTSCNLDASSLRTLFPVLLRCKFLH
XP_027300205.1  693  SLRTVNLSSVKLTPLKCSVLASVLGAACHEVDELNLTSCNLDAASLRTLFPVLLRCKVLH
XP_013042726.1  668  SLRTVNLSSVKLTPLKCSVLASVMGTACHEVDELNLTSCNLDAGSLRTLFPVLLRCKVLQ
NP_001269072.1  697  SLRQLNLAGVRMTPVKCTVVAAVLGSGRHALDEVNLASCQLDPAGLRTLLPVFLRARKLG

XP_004948095.1  773  LQLNSLGPDACKEIRDLLLHDKCAVSNLRLGNNPIGEQGAQYLAEALAGNRSLTHLSLLH
XP_027300205.1  753  LQLNSLGPDACEELRALLLHAKCAVSDLRLSNNPVGVQGARHLAEALAGNRSLSRLSLLH
XP_013042726.1  728  XVPLLLPLGSAQGLGS---PRLCR-GTERAGKGRNALSVLRAVPEDYSARRRSSPRSLLH
NP_001269072.1  757  LQLNSLGPEACKDLRDLLLHDQCQITTLRLSNNPLTAAGVAVLMEGLAGNTSVTHLSLLH

XP_004948095.1  833  TALGDRGVELLAQHLAENQQLQELNLGYNSLTDTAALHVVEVAKKHATLDKVHLYFNDIS
XP_027300205.1  813  AALGDRGAEEIARRLPENQQLQELNLGYNSLTDASALSVVEVAKKHATLDKVHLYFNDIS
XP_013042726.1  784  AALGDRGVEEIAGRLADNQQLQELNLGYNALTDAAALRVVEVAKKHATLDKVHLYFNDIS
NP_001269072.1  817  TGLGDEGLELLAAQLDRNRQLQELNVAYNGAGDTAALALARAAREHPSLELLHLYFNELS

XP_004948095.1  893  EDGKRALDSLRMDR-DGVRALVFLTAGTDVSDYWSSILNVVHKNLPFWDRERVRQHLTII
XP_027300205.1  873  EEGKRALHSLRMER-DGVRALVFLTAGTDVSDYWSNILSTVQRNLPFWDRERVRQHLALL
XP_013042726.1  844  EEGKRALHSLRMDR-DGVRALVFLTAGTDVSDYWSSILNTVHRNLPFWDRERVRQHLALL
NP_001269072.1  877  SEGRQVLRDLGGAAEGGARVVVSLTEGTAVSEYWSVILSEVQRNLNSWDRARVQRHLELL

XP_004948095.1  952  LQDLESSRRQTVNPWRKAKFLRVESEVKKMLGKLQHGTL
XP_027300205.1  932  LQDLESSRRQTGNPWRKAKFLRVESEVKRMLAKLQNGTL
XP_013042726.1  903  LQDLESSRRQTANPWRKAKFLRVESEVKRMLGKLQQGTL
NP_001269072.1  937  LRDLEDSRGATLNPWRKAQLLRVEGEVRALLEQLGSSGS
```

Figure S3: Schematic alignment of NLRX1 protein sequences of chicken, duck goose and human comprising the N-terminal X domain, NACHT, and the C-terminal LRR. The LC3-interacting region is highlighted in grey.

```
XP_025006433.1    1  ------------------------------------------------------------
XP_005030015.2    1  MRADRRGNPAGSLLRAFQGGLQFSCRDRSAAATSSRLYHFRDTAGSGFPCPEPALPPEQH
XP_013053801.1    1  ------------------------------------------------------------
AAI43363.1        1  ------------------------------------------------------------


XP_025006433.1    1  ------------------------------------------------MAGEES--TILLEALEGL
XP_005030015.2   61  QVPSLHPGAAASPEAGSKEPGRGEASLAHRLEAAAGDFPHPVMAGEGSAFTVLLGALEGL
XP_013053801.1    1  -----------------------------------------MMAGEGSAFTVLLAALEGL
AAI43363.1        1  ------------------------------------MKM-ASTRCKLARYLEDL


XP_025006433.1   17  TLEDFQEFKKKLPHT-DIKGGWNIGRDELEKVTHPSSLISYMGDSYGEGAAMDIAISLFE
XP_005030015.2  121  TLEGFQEFKTKLSHV-HTKRGWNIPEDALVEATHPSTLVNCMGKSYGEDAAMDIAIGLFE
XP_013053801.1   20  TLEGFQEFKTKLSHV-HTKGGWNIPEDVLVEATHPSTLVNCMGNSYGEDAAVDIAIGLFE
AAI43363.1       18  EDVDLKKFKMHLEDYPPQKGCIPLPRGQTEKADHV-DLATLMIDFNGEEKAWAMAVWIFA


XP_025006433.1   76  EMNQRDLAEKILDEK---------------------------------------VKEY
XP_005030015.2  180  EMNQRDLAEKILDEK---------------------------------------VKEY
XP_013053801.1   79  EMNQRDLAEKILDEK---------------------------------------VKEY
AAI43363.1       77  AINRRDLYEKAKRDEPKWGSDNARVSNPTVICQEDSIEEEWMGLLEYLSRISICKMKKDY


XP_025006433.1   95  KQKYTEHVAREFLQYKEANSCLGENLSVRDRYTNLTIARKSWDQHGDEPGD--V--S---
XP_005030015.2  199  KQKYREHVAREFLQYKEVNSCLGENLSVSSRYTALTITKKPWSQRGGEPEGADV--SWGC
XP_013053801.1   98  KQKYREHVAREFLRYKEINSCLGENLSVSSRYTALTIAKKPWSQSGGEPEGADV--SWGC
AAI43363.1      137  RKKYRKYVRSRFQCIEDRNARLGESVSLNKRYTRLRLIKEHRSQQEREQELLAIGKTKTC


XP_025006433.1  148  ---SDTVTTQTLLEPSKDGQVP-PITVLVGASGMGKTMTIRKVMMEWVEGTLCT-QFDYV
XP_005030015.2  257  ADTTSAVTAQTLFKPDEDGQTP-QTVVLVGAPGMGKTMMVRKMMVEWVEGALYM-QFDYV
XP_013053801.1  156  ADTTIAVTVQTLFKPDEDGQTP-QTVVLVGAPGMGKTMMVRKMMVEWVEGALYM-QFDYV
AAI43363.1      197  ESPVSPIKMELLFDPDDEHSEPVHTVVFQGAAGIGKTILARKMMLDWASGTLYQDRFDYL
```

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XP_025006433.1   203  FCIDCKELSFSKEVSMVDLISKCCPQQRMPAGRIILGNPEKILFIFDSFEALGLPLAQPKD
XP_005030015.2   315  FCIDCKELSLSKQVSVLDLVSKCCPHQRIPAGSILDNQEKVLFIFDGFEALGFPLAQPKD
XP_013053801.1   214  FCIDCKELSLSKQVSVLDLVSKCCPHQRIPAGSILDNQEKVLFIFDGFEALGFPLAQPKD
AAI43363.1       257  FYIHCREVSLVTQRSLGDLIMSCCPDPNPPIHKIVRKPSRILFLMDGFDELQGAFDEHIG


XP_025006433.1   263  ELSTDPTEAKPLETTLISLLRRTVLPESSVLIATRPAALQSLGQCLEGKHYVEILGFSPA
XP_005030015.2   375  ELSSDPREAKPLETTLMSLLKRTVLPASSLLITTRPMALQNLGRCLEGECYVEILGFSAA
XP_013053801.1   274  ELSSDPREAKPLETTLMSLLKRTVLPASSLLITTRPTALQNLGQCLEGECYVEILGFSAA
AAI43363.1       317  PLCTDWQKAERGDILLSSLIRKKLLPEASLLITTRPVALEKLQHLLDHPRHVEILGFSEA


XP_025006433.1   323  AREEYFHRYFGNDSKADVAFRFTRGNEVLYSLCVIPVMSWTVCTVLERELYERNQLLACS
XP_005030015.2   435  AREEYFHRYFKNDNKADVAFRFARGNESLYSLCVIPIMSWTICTILEQELYKKNNILECS
XP_013053801.1   334  AREEYFHRYFKNDNKADVAFRFTRGNETLYSLCVIPIMSWTICTILEQELYKKNNLLECS
AAI43363.1       377  KRKEYFKYFSDEAQARAAFSLIQENEVLFTMCFIPLVCWIVCTGLKQQMESGKSLAQTS


XP_025006433.1   383  KTTTQMIMFYLSWLMKHRVSNAWQNLQQFLHKLCSLAADGIWKHKVLFEEKEIEDQGLNQ
XP_005030015.2   495  KATTWMGMFYLSWLMKCRGSNAQQDLQQFLHKLCSLAADGIWKHKVLFEEKEVKDCGLDW
XP_013053801.1   394  KATTWMGMFYLSWLMKCRGSNAQQYLQQFLRRLCSLAADGIWKHKVLFEEREIKDCGLDW
AAI43363.1       437  KTTTAVYVFFLSSLLQPRGGSQEHGLCAHLWGLCSLAADGIWNQKILFEESDLRNHGLQK


XP_025006433.1   443  PQLLSLFLNEKGLEKGTDHVNVYSFSHLHLQELFAAMFYVLEDQDGMVSDS-----RILA
XP_005030015.2   555  PDLLSLFLNEKSLKKGIDQDNVYSFTHLHLQEFFAAMFYVLDDDEETVSDP-----EALK
XP_013053801.1   454  PDLLSLFLNEKSLKKGVDQGNVYSFTHLHLHEFFAAMFYVLDDDEETVSDP-----EALA
AAI43363.1       497  AD-VSAFLRMNLFQKEVDCEKFYSFIHMTFQEFFAAMYYILEEEKEGRTNVPGSRLKLPS


XP_025006433.1   498  KDVNMLLESYHTSRMD-LNVTVRLLFGLVNPKSVEYAGEGIGCRISLQPQEDLLRWLQTR
XP_005030015.2   610  KNVNTLLESYSKSRKD-LNLTIRFLFGLVNPKSIEYAGERIGCRISPRAQEDLLRWLQTR
XP_013053801.1   509  KNVNTLLESYSKSRKD-LNLTIRFLFGLVNPKSIEYAGERIGCRISPRAREDLLRWLQTR
AAI43363.1       556  RDVTVLLENYGKFEKGYLIFVVRFLFGLVNQERTSYLEKKLSCKISQQIRLELLKWIEVK
```

```
XP_025006433.1   557 PRGTSHPREVMKIEDLDTFHLLFETNEKSFVQSVLGSFTGIALQDVKLTLYDQAALCFCI
XP_005030015.2   669 HRGLSHPSEALMIKDLDTFHFLFEMNEKSFAQNVLGCFTGIDLHDIKLTLYDQMALCFCI
XP_013053801.1   568 YRGLSHRSEVMMIKELDTFHFLFEMNEKSFAQKVLGCFTGIDLHDIKLTPYDQMALCFCI
AAI43363.1       616 AKAKK---LQIQPSQLELFYCLYEMCEEDFVQRAMDYFPKIEINL--STRMDHMVSSFCI


XP_025006433.1   617 KQWAGLLSVTLRSCSFHQQHHRQEPAKGLPRQSW--------------------------
XP_005030015.2   729 KQWDGVDSVTLRSCSFHQQQCREEPATVLPGQHP--------------------------
XP_013053801.1   628 KQWDGLDSVTLRSCSFRQQQCSEEPTTVLPWQHP--------------------------
AAI43363.1       671 ENCHRVESLSLGFLH---NMPKEEEEEKEGRHLDMVQCVLPSSSHAACSHGLVNSHLTS


XP_025006433.1   651 --------------------RQEEIHSP-LHPLCQALGHPGSSLQSLRLQWCGLTEGDS
XP_005030015.2   763 --------------------RQEELRSP-LHPLCQALGHTGSSLQNLRLQWCGLTEGGC
XP_013053801.1   662 --------------------RQEELRSP-LHPLCQALGHAGSSLQNLRLQWCGLTEGGC
AAI43363.1       728 SFCRGLFSVLSTSQSLTELDLSDNSLGDPGMRVLCETLQHPGCNIRRLWLGRCGLSHECC


XP_025006433.1   689 GALGMLLATLPSLVHLELGDGALGDDGVRMLCAGLRQPGCQLRVLRLRYTHLTSACCQDL
XP_005030015.2   801 EALGTLLATHPSLACLELGDGALGDSGVRLLCTGLRQPGCHLRILRLRYTRLTSACCQDL
XP_013053801.1   700 KALGTLLATHPSLACLELGDGALGDSGVRLLCAGLRQPGCQLRILRLRYTRMTSACCQDL
AAI43363.1       788 FDISLVLSSNQKLVELDLSDNALGDFGIRLLCVGLKHLLCNLKKLWLVSCCLTSACCQDL


XP_025006433.1   749 AVALGTSTCLEELDLSFSA-----------------------------------------
XP_005030015.2   861 AAVLGTSPHLEELDLSFNT-----------------------------------------
XP_013053801.1   760 AAVLGTSPHLEELDLSFNT-----------------------------------------
AAI43363.1       848 ASVLSTSHSLTRLYVGENALGDSGVAILCEKAKNPQCNLQKLGLVNSGLTSVCCSALSSV


XP_025006433.1   768 ---------------GLRDDGVKLLCEGLQHSGCQLRVCRLGSCSLTGACCQAIVAWLGH
XP_005030015.2   880 ---------------GLRDDGVQLLCEGLRHACQLRVLRLGSCHLTGSCCQALATHIGE
XP_013053801.1   779 ---------------GLRDAGVQLLCEGLRDHACQLRVLRLGSCHLMGTCCQALATHLGE
AAI43363.1       908 LSTNQNLTHLYLRGNTLGDKGIKLLCEGLLHPDCKLQVIELDNCNLTSHCCWDLSTLLTS
```

```
XP_025006433.1   813  SHGLKCLDLSDTELGA-GATLLLQHLRHHSCTLQTLGLSTSTLSKDALQELAALRALKPS
XP_005030015.2   925  SCSLSCLDLSDTELGA-GAVLLLRQLRHPACPLQALGLSVSALNEDALQELVALRALKPS
XP_013053801.1   824  NCSLSCLDLSDTELGA-GAVLLLRQLRHPACPLQALGLSVSALNEDALQELVALRELKPS
AAI43363.1       968  SQSLRKLSLGNNDLGDLGVMMFCEVLKQQSCLLQNLGLSEMYFNYETKSALETLQEEKPE


XP_025006433.1   872  LKITDLLEHEAPETGAMAR-----------------------------------------
XP_005030015.2   984  LKIGDLLEHDTPQEGAMSR-----------------------------------------
XP_013053801.1   883  LKIGDLLEHDTPQELVASLQRPAAMDGSSGWACALCRHGQDDVAYLMPCLHQLCLGCVLR
AAI43363.1      1028  LTVV--FEP---------------------------------------------------


XP_025006433.1   891  --------------L-TFQRSVWAGRGAA-------------------------------
XP_005030015.2  1003  --------------L-PFQRGVWEGKGR--------------------------------
XP_013053801.1   943  WAKEKPSCPLYGGRLQSSKYSVWSADDYLECPIPELAEQLGDGQQDEQGAAGLVLRTPEH
AAI43363.1      1035  -----------------------------------------------------------


XP_025006433.1   905  ------------------------------------------------VRGR---
XP_005030015.2  1016  ------------------------------------------------LGVR---
XP_013053801.1  1003  SFPPQLWAAFFQEQLADARPLLAWLQEELRRIYGSQWWDVAVVQGIVLASLCIFGLDQQA
AAI43363.1      1035  -----------------------------------------------------------


XP_025006433.1   909  -----------------------------------------------------------
XP_005030015.2  1020  -----------------------------------------------------------
XP_013053801.1  1063  LVRQLQPSLHSHTVPFVALLVTVAAELYRTGVHWQRERRDARAAGGKEDSPAATPVTAEE
AAI43363.1      1035  -----------------------------------------------------------


XP_025006433.1   909  ---------------KGLPSSRAAPPHSRSLC--------------
XP_005030015.2  1020  ---------------KTLLSSRVAPPSNRNHC--------------
XP_013053801.1  1123  EGSHHRRGRDRQRQQGRLPG--AAGPAPTSLAGAGTTRLGGANIP
AAI43363.1      1035  ------------------------SW-------------------
```

Figure S4: Schematic alignment of NLRP3 protein sequences of chicken, duck goose and human comprising the N-terminal PYD domain, NACHT, and the C-terminal LRR.

```
XP_015150161.2    1  MGWWWVQAEVCTAVNTVLIAPGRRCHGTPLMEEAWISRYRRQLMRSISPQFLEEIIGYLQ
XP_027324583.1    1  ------------------------------MEEAWISRYQKQLVRSISPQFLEEIICHLR
XP_013032636.1    1  ------------------------------MEEAWINRYQKQLVRSISPQFLEEIICYLR
NP_849172.2       1  ---------------------------------------------------------MR


XP_015150161.2   61  RLDLLTVEEAGRAQEASSLPEQVRAVVDILAGKGSHASQTLQSFIETTNSQLYLHITVYE
XP_027324583.1   31  RLDLLTAEEAGRAQEASSLPEQVRAVVDVLAGKGSYASQCLQTFIETTNSQLYLHITVYE
XP_013032636.1   31  RLDLLTAEEAGRVQEASSLPEQVRAVVDVLAGKGSYASQCLQTFIETTNSQLYLHITVYE
NP_849172.2       3  KQEVRTGREAGQGHGTGSPAEQVKALMDLLAGKGSQGSQAPQALDRTPDAPLG--PCSND


XP_015150161.2  121  PMVQKHLESLQSFYGNSLEI-GSLQRLTNLLLVEGLTDIQQKEHDILQMEMTKGLRNVSK
XP_027324583.1   91  PMVQKHLESLQSRYGNGLET-GPVPRLMNLLLVEGLTDIQQKEHDILQIETTKGLRNVSK
XP_013032636.1   91  PMVQKHLESLQSYYGNGLET-GPLQRLTNLLLVEGLTDIQQKEHDILQIETTKGLRNVSK
NP_849172.2      61  SRIQRHRKALLSKVGGGPELGGPWHRLASLLLVEGLTDLQLREHDFTQVEATRGGHPAR


XP_015150161.2  180  SIPLEKLFLPLSKVSIPPRISVTTGVAGIGKSTLVKLFVGRWTKGLINRDIMFVLPLTFR
XP_027324583.1  150  SIPLEKLFLPLSKVSIPPRISVTVGVAGIGKSTLVKLFVSSWTKGEITRDIMLGLPLTFR
XP_013032636.1  150  SIPLEKLFLPLSKVSIPPRISVTVGVAGIGKSTLVKLFVYSWAKGEINRDIMLVLPLTFR
NP_849172.2     121  TVALDRLFLPLSRVSVPPRVSITIGVAGMGKITLVRHFVRLWAHGQVGKDFSLVLPLTFR


XP_015150161.2  240  ELNTYEKLSAERLIRSSFPHITEPNCISTGAARTLLILDGLDEFKTPLDFSNTVACTDPK
XP_027324583.1  210  ELNTYEKLSAERLIRLALPHATEPSCISAGAARVLLILDGLDEFKTPLDFSNTVVCTDPK
XP_013032636.1  210  ELNTYEKLSAERLIRLAFPHITEPSCISAGAARTLLILDGLDEFKTPLDFSNTVVCTDPK
NP_849172.2     181  DLNTHEKLCADRLICSVFPHVGEPSLAVAVPARALLILDGLDECRTPLDFSNTVACTDPK


XP_015150161.2  300  KEIQVDNLITNIIRGNLLQEASIWVTSRPTAASQIPGGLVDRMTEIRGFRATEMKDFLDQ
XP_027324583.1  270  KEIQVDNLITNIIRGNLLQEASVWVTSRPTAASQIPGGLVDRMTEIRGFGAAEMKEFLDQ
XP_013032636.1  270  KEIQVDNLITNIIRGNLLQEASVWVTSRPTAASQIPGGLVDRMTEIRGFGAAEMKEFLDQ
NP_849172.2     241  KEIPVDHLITNIIRGNLFPEVSIWITSRPSASGQIPGGLVDRMTEIRGFNEEEIKVCLEQ
```

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XP_015150161.2  360  MFLDNKDLSGQVLHHIKANRSLHIMCTVPGFCRIYGSSIGYYLKNSTGQPQEMTVAPKTL
XP_027324583.1  330  MFLDNRDLSSQVLHHIKANRSLHIMCTVPSFCRISGSSIGYYLKTSTDQSQEMTAAPKTL
XP_013032636.1  330  MFLDNRDLSSQVLHHIKANRSLHIMCTVPGFCWISGSSIGYYLKNSTDQSQEMTVVPKTL
NP_849172.2     301  MFPEDQALLGWVLSQVQADRALYLMCTVPAFCRLTGMALGHLWRSRTGPQDAELWPPRTL

XP_015150161.2  420  SEIYSYYFKMALSSDWPERQRETLRIEQAVNNSKKVMGSLGRLAFYGLLKRKHVFYEQDM
XP_027324583.1  390  SEIYSYYFKMALSSDWPEKQRETLRIEQAVNNSKKILGSLGRLAFYGLLKRKYVFYEQDM
XP_013032636.1  390  SEIYSYYFKMTLSCDWPEKQRETLRIEQAVNNSKKIMGSLGRLAFYGLLKRKYVFYEQDM
NP_849172.2     361  CEIYSWYFRMALSGEGQEKGKASPRIEQVAHGGRKMVGTLGRLAFHGLLKKYVFYEQDM

XP_015150161.2  480  KAYGIDLSLLHSSLCSRLLLKED-MQSTTAYYFSHLTIQEFLAAIYYYTAAKRAIFDLFT
XP_027324583.1  450  KTYGIDLSLLQSSLCSRLLLKEE-VQSSTAYYFSHLTIQEFLAAIYYYTAAKRAIFDLFT
XP_013032636.1  450  KTYGIDLSLLQSSLCSRLLLKEE-MQSSTAYYFSHLTIQEFLAAIYYYTAAKRAIFDLFT
NP_849172.2     421  KAFGVDLALLQGAPCSCFLQREETLASSVAYCFTHLSLQEFVAAAYYYGASRRAIFDLFT

XP_015150161.2  539  ESGMSWPKLGFLNHFKSAVQRSLQAEDGQLDIFVRFLSGLLSPQVNQLLSGWLLVKDEHN
XP_027324583.1  509  ENGMSWPKLGFLNHFKSAVQRSLQAEDGQLDIFVRFLSGLLSPQVNKLLSGWLLAKDEHN
XP_013032636.1  509  ENGMSWPKLGFLNHFKSAVQRSLQAEDGQLDIFVRFLSGLLSPQVNKLLSGWLLAKDEHN
NP_849172.2     481  ESGVSWPRLGFLTHFRSAAQRAMQAEDGRLDVFLRFLSGLLSPRVNALLAGSLLAQGEHQ

XP_015150161.2  599  SYRSQAISFLQGCLNTNYVISSQTVNTVHCLHEIQHTEIAKAVEEAMKNESLAGMLTPVN
XP_027324583.1  569  SFRSQAISFLQGCLNTDYVISSRTVNTVHCLQEIQHMEIAKSVEEAMKNESLAGMLTPVN
XP_013032636.1  569  SFRSQAISFLQGCLNTDYVISSRTVNTVHCLYEIQHMEIAKSVEEAMKNESLAGMLTPVN
NP_849172.2     541  AYRTQVAELLQGCLRPDAAVCARAINVLHCLHELQHTELARSVEEAMESGALARLTGPAH

XP_015150161.2  659  CSALAYLLQVSDVCVEETNLSNCLTYNICKSLLPQLLFCHSLRLDNNQFKDNVMELLGSM
XP_027324583.1  629  CSVLAYLLQVSDVCVEETNLSNCLTYNVCKSLLPQLLFCHNLRLDNNQFKDNVMELLGSV
XP_013032636.1  629  CSVLAYLLQVSNVCMEETNLSNCLTYNVCKSLLPQLLFCHNLRLDNNQFKDNVMELLGSV
NP_849172.2     601  RAALAYLLQVSDACAQEANLSLSLSQGVLQSLLPQLLYCRKLRLDTNQFQDPVMELLGSV
```

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XP_015150161.2   719  LSVKDCQIQRLSLAENQICNKGAKALARSLMVNRSLTVLDLRSNSIGPSGAKALADALKK
XP_027324583.1   689  LSVKDCQIQKLSLAENQISNKGAKALARSLMVNRSLMVLDLRSNSIGPSGAKALADALKK
XP_013032636.1   689  LSVKDCQIQKLSLAENQISNKGAKALARSLMVNRSLMVLDLRSNSIGPSGAKALADALKK
NP_849172.2      661  LSGKDCRIQKLSLAENQISNKGAKALARSLLVNRSLTSLDLRGNSIGPQGAKALADALKI


XP_015150161.2   779  NQVLLSLSLQHNVIKEEGAAALAEALLTNRRLITLHLQKNSIGAHGARKLAEALAQNCSL
XP_027324583.1   749  NQVLLSLNLQHNVIKEDGATFLAEALLTNHKLTTLHLQKNSIGAQGARKIAEALKRNCSL
XP_013032636.1   749  NQVLLSLNLQHNVIKEDGAAFLAEALLTNHKLTTLHLQKNSIGAQGARKIAEALKRNCSL
NP_849172.2      721  NRTLTSLSLQGNTVRDDGARSMAEAIASNRTLSMLHLQKNSIGPMGAQRMADALKQNRSL


XP_015150161.2   839  KELMLSSNSVGDNGSVALAEALKVNHSLQSLDLQSNSISNTGVSALTAALCSNKGLTDLN
XP_027324583.1   809  KELMLSSNSVGDNGSVALAEALKVNHSLQSLDLQSNSISSAGVAALTAALCSNKGLVNLN
XP_013032636.1   809  KELMLSSNSVGDNGSVALAEALKVNHSLQSLDLQSNSISSAGVAALTVALCSNKGLINLN
NP_849172.2      781  KELMFSSNSIGDGGAKALAEALKVNQGLESLDLQSNSISDAGVAAIMGALCTNQTLLSLS


XP_015150161.2   899  LRENSISKEGGPAIAHALRTNCTLRKLDLAANLLHDEGGKAIALAMKENRALTSLHLQWN
XP_027324583.1   869  LRENSISKEGGPAIARALRTNNTLRRLDLAANLLYDEGGKAIALAMKENRALTSLHLQWN
XP_013032636.1   869  LRENSISKEGGPAIARALRTNSTLRRLDLAANLLYDEGGKAIALAMKENRALTSLHLQWN
NP_849172.2      841  LRENSISPEGAQAIAHALCANSTLKNLDLTANLLHDQGARAIAVAVRENRTLTSLHLQWN


XP_015150161.2   959  FIQTQAAVALAQALQSNDSLASLDLQENAIGDEGMAALAAALKVNTTLADLHLQVASISA
XP_027324583.1   929  FIQANAATALAQALKSNSSLASLDLQENAIGDEGMAALSAALKVNTTLADLHLQVASIGA
XP_013032636.1   929  FIQANAATALAQALKSNSSLASLDLQENAIGDEGMAALSAALKVNTTLADLHLQVASVGA
NP_849172.2      901  FIQAGAAQALGQALQLNRSLTSLDLQENAIGDLGACAVARALKVNTALTALYLQVASIGA


XP_015150161.2  1019  AGAQALAEALMVNNSLQVLDLRGNSISVAGAKAMANALKVNRSLRWLNLQENSLGMDGAI
XP_027324583.1   989  AGAQALAEALMVNKSLQILDLRGNSIGVAGAKAMANALKVNRSLRRLNLQENSLGMDGAI
XP_013032636.1   989  AGAQALAEALMVNKSLQILDLRGNFIGVAGAKAMANALKVNRSLRRLNLQENSLGMDGAI
NP_849172.2      961  SGAQVLGEAIAVNRTLEILDLRGNAIGVAGAKALANALKVNSSLRRLNLQENSLGMDGAI


XP_015150161.2  1079  CIATALRGNHGLTYVNLQGNRIGQSGAKMISDAIRTNSPDCVVVV
XP_027324583.1  1049  CIATALKGNHGLTYVNLQGNRIGQSGAKMISDAIRTNAPDCIVEV
XP_013032636.1  1049  CIATALKGNHGLTYINLQGNRIGQSGAKMISDAIRTNSPDCVVEV
NP_849172.2     1021  CIATALSGNHRLQHINLQGNHIGDSGARMISEAIKTNAPTCTVEM
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Figure S5: Schematic alignment of NLRC3 protein sequences of chicken, duck goose and human comprising the N-terminal CARD domain, NBD, and the C-terminal LRR.

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NP_001305364.1    1  MQPTLQNDDFNLEGAVASIRPQLVEFLSHRLDWLLSASQHFLPTAVLSGLAGVTDHREKV
XP_012955436.2    1  MQPLLQNDDLNLEVAIASIRPQLVEFLSHHQDWLLTTSQHFLPGATLRDLDGITDHREKV
XP_013032006.1    1  MQPLLQNDDLSLEAAIASIRPQLVEFLSHHQDWLLTTSQHFLPGATLRGLDGITDRREKV
NP_115582.4       1  MDPV------GLQLGNKNLWSCLVRLLIKDPEWLNAKMKFFLPNTDLDSRNETLDPEQRV


NP_001305364.1   61  SVLLDLLEKAGHATWKQFAQCLCMECDLPLEMEILLMSSAGEGN-LIQKQEAQTDASDQS
XP_012955436.2   61  SELLDLLEKDGPDTWKQFVQHLCMEIDLPLELEILLMSSAEEGN-LSQKQEARIDVSARS
XP_013032006.1   61  SELLDLLEKAGPATWKQFAQHLCMECDLPLELEILLMSSAGEGN-LSQKQEGRIDASAWS
NP_115582.4      55  ILQLNKLHVQGSDTWQSFIHCVCMQLEVPLDLEVLLLSIFGYDDGFTSQLGAEGKSQPES


NP_001305364.1  120  SVPRGLTRRRRSS-SPISDKGAKQKRLDSAEKYQRLLVDSICKRYGSRRAAGAAAQEPTQ
XP_012955436.2  120  SVPKGVARRRRSS-SAISDKDAKQKRLDSAANYRHLLIDIVRQRYGSRRAAGAAAQEQMQ
XP_013032006.1  120  SVPKGFARRRRSS-SSISDKDAKQKRLDSAENYRRLLIDIVRQRYGSRRAAGAAAQEQMQ
NP_115582.4     115  QLHHGLKRPHQSCGSSPRRKQCKKQQLELAKKYLQLLRTSAQQRYRSQIPG------SGQ


NP_001305364.1  179  PLAFSQAFVNLVLRQSKASRLKERTDKPREDVPSAPEPEECVDTAVRVSDLFGSVVRSGT
XP_012955436.2  179  PLAFNQAFVNLVIRQSKASRLKERTDKPREDLPSAPEPEECVDTAMRVSDLFSSAVRSGT
XP_013032006.1  179  PLAFNQAFVNLVIRQSKASRLKERTDKPREDLPSAPEPEECVDTAMRVSDLFGSVVRSGT
NP_115582.4     169  PHAFHQVYVPPILRRATAS-----LDTPEGAIMGDVKVEDGADV--SISDLFNIRVNKGP


NP_001305364.1  239  TKVIFLFGKPGTGKTMLMHRICQKWAEGVLHQFLFTFLFEFRQLNLLKRKLTLKELLFDL
XP_012955436.2  239  TKLIFLFGRPGTGKTMLMHRICQKWAEGVLHQFLFTFLFEFRQLNLLKRKLTLKELLFDL
XP_013032006.1  239  TKLIFLFGKPGTGKTMLMHRICQKWAEGVLHQFLFTFLFEFRQLNLLKRKLTLKELLFDL
NP_115582.4     222  -RVTVLLGKAGMGKTTLAHRLCQKWAEGHLNCFQALFLFEFRQLNLITRFLTPSELLFDL


NP_001305364.1  299  FLQPEDSPDAVFQHLLENAQRTLIIFDGLDEFVGNMDVSSASKGSLNRSSSMSISELFAE
XP_012955436.2  299  FLQPEESPDAVFQHLLENAQHTLIIFDGLDEFTGSMDMSSTSKEGPTLPSHMSISELFAD
XP_013032006.1  299  FLQPAESPDAVFQHLLENAQHTLIIFDGLDEFTGSMDISSTSKGGPTLPSRMSISELFAD
NP_115582.4     281  YLSPESDHDTVFQYLEKNADQVLLIFDGLDEALQPMGP--------DGPG--PVLTLFSH
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NP_001305364.1   359  LCHGNLLPGCTVLVTSRPKRVPDFLINTVDILAEVWGFDHEKVEEYVSHYFRHHSFKEQA
XP_012955436.2   359  LCHGKLLPGCTVLVTSRPKRLPDFLLNTVDVLAEVWGFDHKKVEEYVSHYFHHHSFKEQA
XP_013032006.1   359  LCHGKLLPGCTVLVTSRPKRLPDLLLNTVDVLAEVWGFDHKKVEEYVSHYFHHHSFKEQA
NP_115582.4      331  LCNGTLLPGCRVMATSRPGKLPACLPAE-AAVHMLGFDGPRVEEYVNHFFSAQPSREGA

NP_001305364.1   419  IAHLKNNTKLLSMCQIPALCYVVCICLEYLLLKHQ--TSVELPQTMQFYIKMLLIFINK
XP_012955436.2   419  IAHLKNNTKLLSMCLIPALCYVVCICLEYLLLKHQ--MSVELPQTMQFYIKMLLIFINK
XP_013032006.1   419  LAHLKNNTKLLSMCLIPALCYVVCICLEYLLLKHQ--MSVELPQTMQFYIKMLLIFINK
NP_115582.4      390  LVELQTNGRLRSLCAVPALCQVACICLHHLIPDHAPGQSVALLPNMTQLYMQMVLALSPP

NP_001305364.1   477  QQGEHAGDEEAQLNSNKKAILGLCDLALKGLEAKKLVFYVGDIPEHVKEFASLHGLLTVF
XP_012955436.2   477  QQGEHAVDEETQLNCNKKAILGLCDLALKGLEDKKLVFYVSDIPEDVKEFASLHGLLTVF
XP_013032006.1   477  QQGEHAVDEETQLNCNKKAILGLCDLALKGLEDKKLVFYVSDIPEHVKEFASLHGLLTVF
NP_115582.4      450  ----------GH--LPTSSLLDLGEVALRGLETGKVIFYAKDIAPPLIAFGATHSLLTSF

NP_001305364.1   537  EVKTNSAHPETGYAFVHLSLQEFFAALCLMISKSVDKSHLKRKLSLKSKWTLRNEAKTGF
XP_012955436.2   537  EVKTSGTHPEAGYAFVHLSLQEFFAALCLMINKRVDKSYLKKKFSLKSKWTLKNEAKTEF
XP_013032006.1   537  EVKTSGTHPEAGYAFVHLSLQEFFAALCLMINKRVDKSHLKKKFSLKSKWTLKNEAKTEF
NP_115582.4      498  CVCTGPGHQQTGYAFTHLSLQEFLAAIHLMASPKVNKDTLTQYVTLHSRWVQRTKARLGL

NP_001305364.1   597  MESFHIFLSGLSSKECRTFIMLLAEQSEAWVQDKQDAILQSLKKLAATQLTGPKVIELCH
XP_012955436.2   597  IESFHIFLSGLSSKECRTFLMLLAEQNEAWVQDKQDAILQSLKKLAATHLTGPKVIELCH
XP_013032006.1   597  IESFHIFLSGLSSKECRTFLMLLAEQNEAWVQDKQDAILQSLKKLAATHLTGPKVIELCH
NP_115582.4      558  SDHLPTFLAGLASCTCRPFLSHLAQGNEDCVGAKQAAVVQVLKKLATRKLTGPKVVELCH

NP_001305364.1   657  CTFETQGLEVAQHIGSLLNFKYEFKNFRLTPLDMSALVFVINSGQDVTHLDFAGCPLDTD
XP_012955436.2   657  CTFETQDLKVAQHIGSLLNFKYEFKNFRLTPLDMSALVFVINSGQDLTHLDFAGCLMDAG
XP_013032006.1   657  CTFETQDLKVAQHIGSLLNFKYEFKNFRLTPLDMSALVFVINSGQDLTHLDFAGCLMDAG
NP_115582.4      618  CVDETQEPELASLTAQSLPYQLPFHNFPLTCTDLATLTNILEHREAPIHLDFDGCPLEPH
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NP_001305364.1   717  CLEMLASCRNVEHLSFRSRRFGDDFAAALSKGLGEMGSLKKLEVTGGSITAAGLTDMVQA
XP_012955436.2   717  CLEVLASCKNVEHLSFRSRRFGDDFAAALSKSLREMGSLKKLELTGGNITAEGLTNLVQA
XP_013032006.1   717  CLEVLASCKNVEHLSFRSRRFGDDFAAALSKSLREMGSLKKLELTGGNITAEGLTNLVQA
NP_115582.4      678  CPEALVGCGQIENLSFKSRKCGDAFAEALSRSLPTMGRLQMLGLAGSKITARGISHLVKA

NP_001305364.1   777  LSHCLQLEEINLQDNRIQNPDVKTVMELFSRMEKLKKIDLSKNSLSLNAVLLLAKEFIAC
XP_012955436.2   777  SSQCLQLEEINLQDNRIRDLEVKRVLDLFSRMEKLKKVDLSNNNLSLNAVLILAKEVVTC
XP_013032006.1   777  SSQCLQLEEINLQDNRIRDLEVKRVLDLFSRMEKLKKIDLSNNNLSLNAVLILAKEVITC
NP_115582.4      738  LPLCPQLKEVSFRDNQISDQVVLNIVEVLPHIPRLRKIDLSSNSICVSTLLCLARVAVTC

NP_001305364.1   837  QNAAELHVRKDTVIISFS---GPSGKVPRSLDLKREQNKECVTPTRHLRLCLQARCLSSQ
XP_012955436.2   837  QNATELHVRKDIVIINFS---GTSGKVQRSLDLRWEENKECVIPTRHVKLCLQDRGLSLQ
XP_013032006.1   837  QNATELHVRKDTVIISFS---GTSGKVPRSLDLRWEENKECVIPTRHMKLCLRDCSLSLQ
NP_115582.4      798  PTVRMLQAREADLIFLLSPPTETTAELQRAPDLQESDGQRKGAQSRSLTLRLQKCQLQVH

NP_001305364.1   894  HAKEIVSILQSCPHLSEVDLSDNKLGDEGCSFLLENLSWISISKQLNLSHNLLSVTGIYS
XP_012955436.2   894  HAKEIVSILQSCPHLSEVDLSGNKLGDEGCSCLLESLPWISISKQLDLSHNLLSINGIYS
XP_013032006.1   894  HAKEIVSILQSCPHLSEVDLSGNKLGDEGCSCLLESLPWISISKQLDLSHNLLSINGIYS
NP_115582.4      858  DAEALIALLQEGPHLEEVDLSGNQLEDEGCRLMAEAASQLHIARKLDLSNNGLSVAGVHC

NP_001305364.1   954  LLKAVNTCQRVVEVEVSLYHNTAVLRFTEDGEFASPPASREEPLYPTDDQWDDKENQTPV
XP_012955436.2   954  LLKSVNTCQKTMEVEVSLCHKTAVLRFTEDKEFASP--HREEPLYPTDDQQVGEEKQTPT
XP_013032006.1   954  LLKSVNTCQKTMEVEASLCHKTAVLRFTEDREFASPP-HREEPLYPTDDQQVGEEKQTPT
NP_115582.4      918  VLRAVSACWTLAELHISLQHKTVIFMFAQEPEEQKGPQERAAF---LDSLMLQMPSELPL

NP_001305364.1  1014  PSKKIRLTYCRFQASDLEKLCAVLKECGSIS--ELDLSNNYLGDEGLAQLLQFLPNLKTL
XP_012955436.2  1012  LSKKIRLTDCYFQASDLEKLCAVLKECSSIS--ELDLSNNSLGDEGISRLFQFLPNLKML
XP_013032006.1  1013  LSKKIRLTDCHFQASDLEKLCAVLQECSSIS--ELDLSNNSLGDEGLSRLFQFLPNLKML
NP_115582.4      975  SSRRMRLTHCGLQEKHLEQLCKALGGSCHLGHLHLDFSGNALGDEGAARLAQLLPGLGAL
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NP_001305364.1  1072  RSLKINNNHLSLSSVFCLAQSLCTLEHLETMDLSLGRMQVVHLTFGDRIRLR-RTSRWRR
XP_012955436.2  1070  RSLKLDNNRISLNSVFCLAQSLSTLERIKTMNLSLGHMQVVHLTFWERIRDR-STGRLRR
XP_013032006.1  1071  RSLKLDNNRISLNSVFCLAQSLSTLEHIKTMNLSLGHMQVVHLSFWERIRDR-STGRLRR
NP_115582.4     1035  QSLNLSENGISLDAVLGLVRCFSTLQWLFRIDISFESQHIL-LRGDKTSRDMWATGSL-P

NP_001305364.1  1131  SFLVHPKHVT-----NGQCFRLRNCTVGPEDVTRLCQMLTQCTQLTEIDLCGNALNDQSI
XP_012955436.2  1129  NFLVHPKHIE-----NGQCFRLRDCTMGPEDVTRLCQIIVHCTQLTEINLSGNPLSDQSI
XP_013032006.1  1130  NFLVHPKHIA-----NGRCFRLRDCTMGPEDMTRLCQILAHCTQLTEIDLSGNSLSDQSI
NP_115582.4     1093  DFPAAAKFLGFRQRCIPRSLCLSECPLEPPSITRLCATLKDCPGPLEIQLSCEFLSDQSL

NP_001305364.1  1186  ERLLSFLPHFCQLTLLSIRNNTFSPCCAVLFANSINLCERIRRVEVRSSQNAFLHLRTST
XP_012955436.2  1184  ERLLSFLPYLCHLTLLSIKNSTFSPRCAILFTNSIGLCERIRKVEVRSNQNAFLHLGTST
XP_013032006.1  1185  ERLLSFLPYLCHLTLLSIKNSTFSPHCTILFTNSIGLSERIRKVEVRSNQNAFLHLGTSA
NP_115582.4     1153  ETLLDCLPQLPQLSLLQISQTGLSPKSPFLLANTLSLCPRVKKVDIRSLHHATLHFRSNE

NP_001305364.1  1246  QSQKTSC-RLTDCAIGQRQIEKLCRVLEQHGCLAELDLSRNQLGDEVLRFLLDHLHRVPV
XP_012955436.2  1244  HSQKTSC-SLTDCAISQGQIEELCGVLEQHGRLAEVDLSRNQLGDEGLRFLLDHLHRVHV
XP_013032006.1  1245  RSQKTSC-RLTDCAISQGQIEELCRVLEQHGRLAEVDLSRNQLGDEGLRFLLDHLHRVHV
NP_115582.4     1213  EEEGVCCGRFTGCSLSQEHVESLCWILSKCKDLSQVDLSANLLGDSGLRCLLECLPQVPI

NP_001305364.1  1305  TCSLNLSHNRISQRGVLHLINTFTTSGNTTEVQVSLCSKATLIIKMTSRDDPRKILRLTE
XP_012955436.2  1303  TCSLNLSHNRISQDGVLHLINAFATSGNVTEVLVSLCSKATLLMELTSRDDPRKILSLTE
XP_013032006.1  1304  TCSLNLSHNRISQDGVLHLINAFATSRNITEVVVSLCSKATLLMKLTSRDDPRKILSLTE
NP_115582.4     1273  SGLLDLSHNSISQESALYLLETLPSCPRVREASVNLGSEQSFRIHFSREDQAGKTLRLSE

NP_001305364.1  1365  CSFQPEHLEKLCLVLENCTNLTECISSNNNVTVDAAGGLLRSLSKTPGPLKISIEEPWVC
XP_012955436.2  1363  CNFQAEHLEKLWLVLEKCTSLTEYISSSNNLTVHAAERLLHSLRKTSGPLKISIKEPWVC
XP_013032006.1  1364  CNFQPEHLEKLWLALEKCTSLTEYISSNNNMTVHAAERLLHSLRKTPGPLKISIKEPWVC
NP_115582.4     1333  CSFRPEHVSRLATGLSKSLQLTELTLTQCCIGQKQLAILLSLVGRPAGLFSLRVQEPWAD
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NP_001305364.1  1425  KLSVTSLLELAVQAHGNITAIMICKEKNLFQLGVRLPHCLEKVGSVVSRLNLNEPEIKQA
XP_012955436.2  1423  KKSVMNLLELAVQACGNITAITICKDKSLFQLGVSFPCCLEKVESVVSRLNLHEPEIKRA
XP_013032006.1  1424  KKSVTNLLELAVQACGNITAIMICKDKSLFQLGVRFPCCLEKVESVVSRSNLHEPEIKRA
NP_115582.4     1393  RARVLSLLEVCAQASGSVTEISISETQQQLCVQLEFPRQEENPEAVALRLAHCDLGAHHS

NP_001305364.1  1485  CFYQRVHDKCTQLQELRWSHVELHDD-----TEMLVSILLPLPDLKKFELTSCSFTPTGID
XP_012955436.2  1483  CFYQRVLEKCIQLQELRWSHVELHDDD---TKILVTVLLPLPKLKKFELTSCSIMPTGID
XP_013032006.1  1484  CFYQRVLEKCIQLQELRWSHVELHDDD---TKILVTVLLPLPKLKKFELTSCSIMPTGID
NP_115582.4     1453  LLVGQLMETCARLQQLSLSQVNLCEDDDASSLILQSLLISLSELKTFRLTSSCVSTEGLA

NP_001305364.1  1541  CLITGLQRCQAIEELN--------------------------LGHMKLGDAAIPKLVF
XP_012955436.2  1540  YLITGLQKCQAIEELS--------------------------LGHMKLSDAAIPMLVL
XP_013032006.1  1541  YLITGLQKCQAIEELN--------------------------LGHMKLSDAAIPKLVL
NP_115582.4     1513  HLASGLGHCHHLEELDLSNNQFDEEGTKALMRALEGKWMLKRLDLSHLLLNSSTLALLTH

NP_001305364.1  1573  GLCEMPSLKRLILNHNSIGDDGCSRLAEALSSMHCMEEINLGHNKIGDLGLINIAAVLLE
XP_012955436.2  1572  GLCKMPSLKRLILNHNSIGNDGCSRLAEALRNMHCMEEINLAHNKIGDPGLINIATVLLE
XP_013032006.1  1573  GLCKMPSLKRLILNHNSIGDDGCSRLAEALRNMHCMEEINLAHNKIGDPGLINIATALLE
NP_115582.4     1573  RLSQMTCLQSLRLNRNSIGDVGCCHLSEALRAATSLEELDLSHNQIGDAGVQHLATILPG

NP_001305364.1  1633  MQNLKRIDLSGNCPSPAGGEKLMEALANCKHLEELILSRNDFGDGTAVKLALCLPHMNRL
XP_012955436.2  1632  MQNLKRINLSGNSPSPTGGEKLMEALACCKHIEELLLSRNVFGDGVAVKLALCLPHVSSL
XP_013032006.1  1633  MQNLKRINLSGNSPSPAGGEKLMEALAYCKHIEELLLSRNVFGDGTAVKLALCLPHVSSL
NP_115582.4     1633  LPELRKIDLSGNSISSAGGVQLAESLVLCRRIEELMLGCNALGDPTALGLAQELPQ--HL

NP_001305364.1  1693  KILHLQHNNIGPAGGTELARALMACELLEEISLSENNLGEGGIRALSEGLPRFEHLRKIE
XP_012955436.2  1692  KILHLQKNNIGPTGGTELARALVACRLLEEISLSENDLGEGSIHALSEGLPRLEHLRKID
XP_013032006.1  1693  KILHLQKNNIGPTGGTELARALVVCGLLEEISLSENDLGEGSIHALSEGLPHLEHLRKID
NP_115582.4     1691  RVLHLPFSHLGPGGALSLAQALDGSPHLEEISLAENNLAGCVLRFCME-LP---LLRQID
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NP_001305364.1 1753 LRLCGITDDASKLLSRGFQQCPAVEEIILSWNALGDGGAQVLASILPGMETLKMLDLEKN
XP_012955436.2 1752 LKLCGITDDSSKSLSCAFQQCPAMEEIILSWNSLGDGGAQELASALPGMEKLKMLDLEKN
XP_013032006.1 1753 LKLCGITDDSSKSLSCAFQQCPAMEEIILSWNSLGDGGAEELASALPGMEKLKMLDLEKN
NP_115582.4    1747 LVSCKIDNQTAKLLTSSFTSCPALEVILLSWNLLGDEAAAELAQVLPQMGRLKRVDLEKN


NP_001305364.1 1813 LIGACGATRLAEELVRCPEIQFIRLWDNPVPKGLAESLTSQDPRLCFSFC----------
XP_012955436.2 1812 RIGARGAVKLSEELVKCPEIQFIRLWENPVPKGLAADLTSQDPRLCFSFY----------
XP_013032006.1 1813 RIGVCGAMKLSQELVKCPEIQFIRLWDNPVPKGLAADLTSQDPRLCFSFY----------
NP_115582.4    1807 QITALGAWLLAEGLAQGSSIQVIRLWNNPIPCDMAQHLKSQEPRLDFAFFDNQPQAPWGT
```
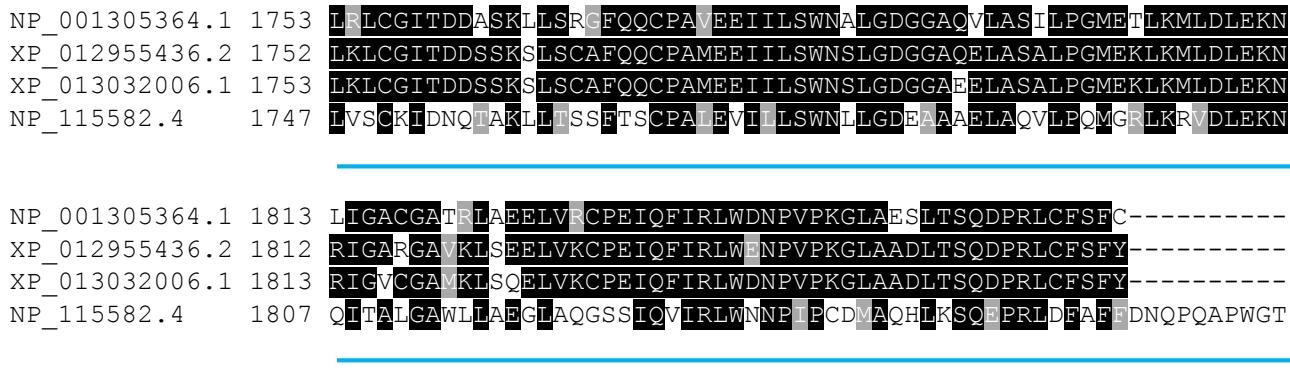
Figure S6: Schematic alignment of NLRC5 protein sequences of chicken, duck goose and human comprising the N-terminal CARD domain, NBD, and the C-terminal LRR. NBD and LRR domains were underscored in grey and blue respectively. Putative bipartite NLS and Walker A/B motifs were box highlighted and underscored in red respectively. The residues conforming to bipartite NLS and Walker A/B motif consensus were highlighted in red for human.

```
NP_989894.1      1  MAAFSEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAETGSGKTGAFSIPV
XP_027311055.1   1  MAAFSEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAETGSGKTGAFSIPV
XP_013028107.1   1  MAAFSEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAETGSGKTGAFSIPV
NP_004930.1      1  MAAFSEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAETGSGKTGAFSIPV


NP_989894.1     61  IQIVYETLKDQMEGKKGKATIKTGGAVLNKWQMNPYDRGSAFAIGSDGLCCQSREVKEWH
XP_027311055.1  61  IQIVYETLKDQMEGKKGKATIKTGGAVLNKWQMNPYDRGSAFAIGSDGLCCQSREVKEWH
XP_013028107.1  61  IQIVYETLKDQMEGKKGKATIKTGGAVLNKWQMNPYDRGSAFAIGSDGLCCQSREVKEWH
NP_004930.1     61  IQIVYETLKDQQEGKKGKTTIKTGASVLNKWQMNPYDRGSAFAIGSDGLCCQSREVKEWH


NP_989894.1    121  GCRATRGVTKGKYYYEVSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTGKKSHNKQFD
XP_027311055.1 121  GCRATRGVTKGKYYYEVSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTGKKSHNKQFD
XP_013028107.1 121  GCRATRGVTKGKYYYEVSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTGKKSHNKQFD
NP_004930.1    121  GCRATKGLMKGKHYYEVSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTGKKSHNKQFD


NP_989894.1    181  SYGEEFTMHDTIGCYLDIDKGQIKFSKNGKDLGLAFEFPPHIRNQALFAACVLKNAELKF
XP_027311055.1 181  SYGEEFTMHDTIGCYLDIDKGQIKFSKNGKDLGLAFEIPPHIRNQALFAACVLKNAELKF
XP_013028107.1 181  SYGEEFTMHDTIGCYLDIDKGQIKFSKNGKDLGLAFEIPPHIRNQALFAACVLKNAELKF
NP_004930.1    181  NYGEEFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKNQALFPACVLKNAELKF


NP_989894.1    241  NFGEEDFKFPPKDGYIGLCKAPDGNVVKSQHTGNAQVVQTQNLPNAPKALIVEPSRELAE
XP_027311055.1 241  NFGEEDFKFPPKDGYIGLCKAPDGSVVKSQHAGNAQVVQTQNLPNAPKALIVEPSRELAE
XP_013028107.1 241  NFGEEDFKFPPKDGYIGLCKAPDGSVVKSQHAGNAQVVQTQNLPNAPKALIVEPSRELAE
NP_004930.1    241  NFGEEEFKFPPKDGFVALSKAPDGYIVKSQHSGNAQVTQTKFLPNAPKALIVEPSRELAE


NP_989894.1    301  QTLNNVKQFKKYIDNPKLRELLIIGGVAARDQLSVLEQGVDIVVGTPGRLDDLVSTGKLN
XP_027311055.1 301  QTLNNVKQFKKYVDNPKLRELLIIGGVAARDQLSVLEQGVDIVVGTPGRLDDLVSTGKLN
XP_013028107.1 301  QTLNNVKQFKKYVDNPKLRELLIIGGVAARDQLSVLEQGVDIVVGTPGRLDDLVSTGKLN
NP_004930.1    301  QTLNNIKQFKKYIDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTPGRLDDLVSTGKLN
```

Figure S7: Schematic alignment of DDX1 protein sequences of chicken, duck, goose and human. Depicted are the DEAD box region, and HelicC domain in black, and red underlining respectively. The DEAD box is boxed in blue.

```
XP_001232052.1     1  MPEATRICAGS-GAESE------------------------------------------------
XP_027316557.1     1  MPEATRICAGS-GAEAG------------------------------------------------
XP_013030257.1     1  LEVSRLVCEPSLRAASV------------------------------------------------
NP_004719.2        1  MPGKLRSDAGL-ESDTAMKKGETLRKQTEEKEKKEKPKSDKTEEIAEEEETVFPKAKQVK


XP_001232052.1    17  --------------------PESPMESEAAPESSRRRKKEKKEKKSKRHDKARKRKPQT
XP_027316557.1    17  --------------------SDSPMESEAATANGRRRRKKEKKEKKAKRRDKAPKRKSQT
XP_013030257.1    18  --------------------PRGSGDARVGTHAS-VVPQKEKKEKKAKRRDKARKRKSQT
NP_004719.2       60  KKAEPSEVDMNSPKSKKAKKKEEPSQNDISPKTKSLRKKKEPIEKK----VVSSKTKKVT


XP_001232052.1    57  DESEQSEEECSSPKLKKAKTGGKQNGHVREESPENARLSSVSAKSTHKKRHSNSSETSSG
XP_027316557.1    57  DESEQSEDELDPPKVKKAKSREKQNGDARGESPENARLSSLTLKAARKKQPSNSSETSSG
XP_013030257.1    57  DESEQSEDELDSPKVKKAKSREKQNGDAGGDSPENARLSSLTLKSAHKKRPNASETSSG
NP_004719.2      116  KNEEPSEEEIDAPKPKKMKKEKEMNGETREKSPK------LKNGFPHPEPDCNPSEAASE


XP_001232052.1   117  DGDSDQEQEMTEEQKEGAFSNFPISKGTIQLLQARGVTYLFPVQVKTFNPVYSGKDVIAQ
XP_027316557.1   117  DCDSDQEQEMTEEQKEGAFSNFPISKGTVELLQARGVTYLFPVQVKTFHPVFSGKDVIAQ
XP_013030257.1   117  DCDSDQEQEMTEEQKEGAFSNFPISKVTVELLQARGVTYLFPVQVKTFHPVFSGKDVIAQ
NP_004719.2      170  ESNSEIEQEIPVEQKEGAFSNFPISEETIKLIKGRGVTFLFPIQAKTFHHVYSGKDLIAQ


XP_001232052.1   177  ARTGTGKTFSFAIPLIEKLQADSQERRRGRSPKVLVLAPTRELANQVAKDFKDITRKLTV
XP_027316557.1   177  ARTGTGKTFSFAIPLIEKLQADSQEKRRGRAPKVLVLAPTRELANQVAKDFKDITRKLTV
XP_013030257.1   177  ARTGTGKTFSFAIPLIEKLQADSQERKRGRSPKVLVLAPTRELANQVAKDFKDITRKLTV
NP_004719.2      230  ARTGTGKTFSFAIPLIEKLHGELQDRKRGRAPQVLVLAPTRELANQVSKDFSDITKKLSV


XP_001232052.1   237  ACFYGGTPYNGQIDLIRSGIDILVGTPGRIKDHLQNGKLDLIKVKHVVIDEVDQMLDMGF
XP_027316557.1   237  ACFYGGTPYNGQIDLIRSGIDILVGTPGRIKDHLQNGKLDLSKVKHVVIDEVDQMLDMGF
XP_013030257.1   237  ACFYGGTPYNGQIDLIRSGIDILVGTPGRIKDHLQNGKLDLSKVKHVVIDEVDQMLDMGF
NP_004719.2      290  ACFYGGTPYGGQFERMRNGIDILVGTPGRIKDHLQNGKLDLTKLKHVVIDEVDQMLDMGF
```

```
XP_001232052.1   297  AEQVEDILRVAYKKDSEDNPQTLLFSATCPNWVYDVAKKYMKSKYEQVDLIGRKTQKAAT
XP_027316557.1   297  AEQVEDILRVAYKKDSEDNPQTLLFSATCPHWVYDVAKKYMKSKYEQIDLIGKRTQKAAT
XP_013030257.1   297  AEQVEDILRVAYKKDSEDNPQTLLFSATCPHWVYDVAKKYMKSKYEQIDLIGKRTQKAAT
NP_004719.2      350  ADQVEEILSVAYKKDSEDNPQTLLFSATCPHWVFNVAKKYMKSTYEQVDLIGRKTQKTAI

XP_001232052.1   357  TVEHLAIECHWSQRAAVIGDVIQVYSGSYGRTIVFCETKKDANELALNASIKQDCQSLHG
XP_027316557.1   357  TVEHLAIACHWSQRAAVIGDVIQVYSGSHGRTIVFCETKKDANELALNASIKQDCQSLHG
XP_013030257.1   357  TVEHLAIACHWSQRAAVIGDVIQVYSGSLGRTIVFCETKKDANELALNASIKQDCQSLHG
NP_004719.2      410  TVEHLAIKCHWTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQDAQSLHG

XP_001232052.1   417  DIPQKQREITLKGFRNGAFKVLVATNVAARGLDIPEVDLVVQSSPPKDVESYIHRSGRTG
XP_027316557.1   417  DIPQKQREITLKGFRNGAFKVLVATNVAARGLDIPEVDLVVQSSPPKDVESYIHRSGRTG
XP_013030257.1   417  DIPQKQREITLKGFRNGAFKVLVATNVAARGLDIPEVDLVVQSSPPKDVESYIHRSGRTG
NP_004719.2      470  DIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVDLVIQSSPPKDVESYIHRSGRTG

XP_001232052.1   477  RAGRTGICICFYQRKEENQLRYVEVKAGITFKRVGVPTATDIIKASSKDAIRCLDSVPQT
XP_027316557.1   477  RAGRTGICICFYQRKEENQLRYVEQKAGISFKRVGVPTATDIIKASSKDAIRCLDSVPQS
XP_013030257.1   477  RAGRTGICICFYQRKEENQLRYVEQKAGIAFKRVGVPTATDIIKASSKDAIRCLDSVPQS
NP_004719.2      530  RAGRTGVCICFYQHKEEYQLVQVEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPT

XP_001232052.1   537  AIEYFKESAQLLIEEKGPVNALAAALAHISGATSIEQRSL----LNSDVGFVTMVLRCSE
XP_027316557.1   537  AIDYFKESAQLLIKEKGPVNALAAALAHISGATSIEQRSL----LNSDAGFVTMILRCSE
XP_013030257.1   537  AIDYFKESAQLLIQEKGPVNALAAALAHISGATSIEQRSLPXXXLNSDAGFVTMILRCSE
NP_004719.2      590  AISHFKQSAEKLIEEKGAVEALAAALAHISGATSVDQRSL----INSNVGFVTMILQCSI

XP_001232052.1   593  EINNMSYVWRRLREQLGGDVDRKVNRMRFIKGRMGVCFDIPVADQKDIEERWEDSKQCSL
XP_027316557.1   593  EINNMSYAWRKLREQLGDDVDRKVNRMCFIKGRMGVCFDIPVADQKEIEGKWEDSKQCRL
XP_013030257.1   597  EINNMSYAWRRLREQLGDDVDRKVNRMCFIKGRMGVCFDIPVADQKEIEGKWEDSKQCRL
NP_004719.2      646  EMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCFDVPTASVTEIQEKWHDSRRWQL
```

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XP_001232052.1  653  CVANELPELEESQRGGGGGGGGGGGGN-----NRS----------FSGSRNG-RRG-----
XP_027316557.1  653  CVANELPELEESQRGGGG------GN-----GRS----------FSGSRSGGRRG-----
XP_013030257.1  657  CVANELPELEETQRGGG--------N-----GRS----------FSSSRSG-RRG-----
NP_004719.2     706  SVATEQPELEGPREGYGG------FRGQREGSRGFRGQRDGNRRFRGQREG-SRGPRGQR
                                                 _____

XP_001232052.1  692  ---GSGRNRFRSRGQKRSYDRAFDR
XP_027316557.1  687  ---GSGRNRFRGRGQKRSYDRAFDR
XP_013030257.1  688  ---GSGRNRFRSRGQKRSYDRAFDR
NP_004719.2     759  SGGGNKSNRSQNKGQKRSFSKAFGQ
```

Figure S8: Schematic alignment of DDX21 protein sequences of chicken, duck, goose and human. Depicted are DEAD box region, GUCT and HelicC domain in black, green and red underlining respectively. The DEAD box is boxed in blue.

```
XP_015147310.1    1   MSYEQRRDWGRGRGRGGDGGS--------------SAASSGGGGH----GGRGGGRGRHP
XP_027320349.1    1   MSSEQRRGWARGGDGGPAASS--------------SSCSSSAGGHGGRGGGGGGGRGRHP
XP_013048508.1    1   -----------------------------------------------------------
NP_065916.2       1   MSYDYHQNWGRDGGP--RSSGGGYGGGPAGGHGGNRGSGGGGGGG----GGGRGGRGRHP


XP_015147310.1   43   SHLKGREIGLWYARKQGQKSKETDRQQRAVVRMDERREEQIVQLLNAVQPRAEKEQEA-M
XP_027320349.1   47   SHLKGREIGLWYARKQGQRSKETDRQQRAVVRMDERREEQIAQLLTAVQSRSEKEPDA-M
XP_013048508.1    1   -------------------------------MDERREEQIAQLLTAVQSRSEKEPDA-M
NP_065916.2      55   GHLKGREIGMWYAKKQGQKNKEAERQERAVVHMDERREEQIVQLLNSVQAKNDKESEAQI


XP_015147310.1  102   SWWSGDEEGHVPEQPPKVKPGAEKAEKAPVKR----------RPILQKTFLDQDVEYLFE
XP_027320349.1  106   SWWSGDEDGNTPEQPAKVKPEVE---KAPIKQ----------RPVLEKTFLDRDVEYLFE
XP_013048508.1   28   SWWSGDEDGNTPEQPAKVKPEAE---KAPIKQ----------RPVLEKTFLDRDVEYLFE
NP_065916.2     115   SWFAPEDHGYGTEVSTKNTPCSEN--KLDIQEKKLINQEKKMFRIRNRSYIDRDSEYLLQ


XP_015147310.1  152   KNDQDADLDEQLKEDLRKKKSDPRYIEMQRFREKLPSYGMRQELVNLINNNRVTVISGET
XP_027320349.1  153   KNQQDTDLDEQLKEDLRKKKSDPRYIEMQRFREKLPSYGMRQELVNLINNNRVTVISGET
XP_013048508.1   75   KNQQDTDLDEQLKEDLRKKKSDPRYIEMQRFREKLPSYGMRQELVNLINNNRVTVISGET
NP_065916.2     173   ENEPDGTLDQKLLEDLQKKKNDLRYIEMQHFREKLPSYGMQKELVNLIDNHQVTVISGET
                                                                        _____


XP_015147310.1  212   GCGKTTQVTQFILDDYIERGKGSTCRIVCTQPRRISAISVAERVAAERAEACGNGKSTGY
XP_027320349.1  213   GCGKTTQVTQFILDDYIERGKGSTCRIVCTQPRRISAISVAERVAAERAEACGNGKSTGY
XP_013048508.1  135   GCGKTTQVTQFILDDYIERGKGSTCRIVCTQPRRISAISVAERVAAERAEACGNGKSTGY
NP_065916.2     233   GCGKTTQVTQFILDNYIERGKGSACRIVCTQPRRISAISVAERVAAERAESCGSGNSTGY
                      _____


XP_015147310.1  272   QIRLQSRLPRKQGSILYCTTGIVLQWLQSDKHLSSISHVVLDEIHERNLQSDVLMSIIKD
XP_027320349.1  273   QIRLQSRLPRKQGSILYCTTGIVLQWLQSDKNLSSISHVVLDEIHERNLQSDVLMSIIKD
XP_013048508.1  195   QIRLQSRLPRKQGSILYCTTGIVLQWLQSDKHLSSISHVVLDEIHERNLQSDVLMSIIKD
NP_065916.2     293   QIRLQSRLPRKQGSILYCTTGIILQWLQSDPYLSSVSHIVLDEIHERNLQSDVLMTVVKD
                      _____
```

```
XP_015147310.1   332  LLNVRLDLKVILMSATLNAEKFSEYFDNCPMIHIPGFTFPVVEYLLEDVIEKLRYTPENT
XP_027320349.1   333  LLNVRLDLKVILMSATLNAEKFSEYFDNCPMIHIPGFTFPVVEYLLEDVIEKLRYMPENT
XP_013048508.1   255  LLNVRLDLKVILMSATLNAEKFSEYFDNCPMVHIPGFTFPVVEYLLEDVIEKLRYMPENT
NP_065916.2      353  LLNFRSDLKVILMSATLNAEKFSEYFGNCPMIHIPGFTFPVVEYLLEDVIEKIRYVPEQK

XP_015147310.1   392  DRRPRWKKGFMQGHISRPEKEEKEEIYRERWPEYLRQLRGRYSAGTIDALEMMDDDKVDL
XP_027320349.1   393  DRRPRWKKGFMQGHISRPEKEEKEEIYRERWPEYLRQLRGRYSASTIDALEMMDDDKVDL
XP_013048508.1   315  DRRPRWKKGFMQGHISRPEKEEKEEIYRERWPEYLRQLRGRYSASTIDALEMMDDDKVDL
NP_065916.2      413  EHRSQFKRGFMQGHVNRQEKEEKEAIYKERWPDYVRELRRRYSASTVDVIEMMEDDKVDL

XP_015147310.1   452  DLIAALIRHIVLEEEDGAILVFLPGWDNISTLHDLLMSQVMFKSDRFIIIPLHSLMPTVN
XP_027320349.1   453  DLIAALIRHIVLEEEDGAILVFLPGWDNISTLHDLLMSQVMFKSDRFIIIPLHSLMPTVN
XP_013048508.1   375  DLIAALIRHIVLEEEDGAILVFLPGWDNISTLHDLLMSQVMFKSDRFIIIPLHSLMPTVN
NP_065916.2      473  NLIVALIRYIVLEEEDGAILVFLPGWDNISTLHDLLMSQVMFKSDKFLIIPLHSLMPTVN

XP_015147310.1   512  QTQVFKKTPPGVRKIVIATNIAETSITIDDVVFVIDGGKIKETHFDTQNNISTMAAEWVS
XP_027320349.1   513  QTQVFKKTPPGVRKIVIATNIAETSITIDDVVFVIDGGKIKETHFDTQNNISTMAAEWVS
XP_013048508.1   435  QTQVFKKTPPGVRKIVIATNIAETSITIDDVVFVIDGGKIKETHFDTQNNISTMAAEWVS
NP_065916.2      533  QTQVFKRTPPGVRKIVIATNIAETSITIDDVVYVIDGGKIKETHFDTQNNISTMSAEWVS

XP_015147310.1   572  KANAKQRKGRAGRVQPGHCYHLYNGLRASLLDDYQLPEILRTPLEELCLQIKILKLGGIA
XP_027320349.1   573  KANAKQRKGRAGRVQPGHCYHLYNGLRASLLDDYQLPEILRTPLEELCLQIKILKLGGIA
XP_013048508.1   495  KANAKQRKGRAGRVQPGHCYHLYNGLRASLLDDYQLPEILRTPLEELCLQIKILKLGGIA
NP_065916.2      593  KANAKQRKGRAGRVQPGHCYHLYNGLRASLLDDYQLPEILRTPLEELCLQIKILRLGGIA

XP_015147310.1   632  YFLSKLMDPPSRDAVMLAINHLMELNALDRQEELTPLGVHLARLPVEPHIGKMILFGALF
XP_027320349.1   633  YFLSKLMDPPSRDAVMLAINHLMELNALDRQEELTPLGVHLARLPVEPHIGKMILFGALF
XP_013048508.1   555  YFLSKLMDPPSRDAVMLAINHLMELNALDRQEELTPLGVHLARLPVEPHIGKMILFGALF
NP_065916.2      653  YFLSRLMDPPSNEAVLLSIRHLMELNALDKQEELTPLGVHLARLPVEPHIGKMILFGALF
```

XP_015147310.1 692 CCLDPVLTIAASLSFKDPFVIPLGKEKVADARRKELSKNTKSDHLTVVNAFTGWEETRRR
XP_027320349.1 693 CCLDPVLTIAASLSFKDPFVIPLGKEKVADARRKELSKNTKSDHLTVVNAFTGWEETRRR
XP_013048508.1 615 CCLDPVLTIAASLSFKDPFVIPLGKEKVADARRKELSKNTKSDHLTVVNAFTGWEETRRR
NP_065916.2   713 CCLDPVLTIAASLSFKDPFVIPLGKEKIADARRKELAKDTRSDHLTVVNAFEGWEEARRR

XP_015147310.1 752 GFRTEKDYCWEYFLSPNTLQMLHNMKGQFAEHLLAAGFVNSRDPKDPKSNTNSDNEKLLK
XP_027320349.1 753 GFRTEKDYCWEYFLSSNTLQMLHNMKGQFAEHLLAAGFVNSRDPKDPKSNTNSDNEKLLK
XP_013048508.1 675 GFRTEKDYCWEYFLSSNTLQMLHNMKGQFAEHLLAAGFVNSRDPKDPKSNTNSDNEKLLK
NP_065916.2   773 GFRYEKDYCWEYFLSSNTLQMLHNMKGQFAEHLLGAGFVSSRNPKDPESNINSDNEKIIK

XP_015147310.1 812 AVICAGLYPKVAKIRPSFSKKRKMVKVCTKTDGTVNIHPKSVNVEETEFHYNWLVYHLKM
XP_027320349.1 813 AVICAGLYPKVAKIRPSFSKKRKMVKVCTKTDGTVNIHPKSVNVEETEFHYNWLVYHLKM
XP_013048508.1 735 AVICAGLYPKVAKIRPSFSKKRKMVKVCTKTDGTVNIHPKSVNVEETEFHYNWLVYHLKM
NP_065916.2   833 AVICAGLYPKVAKIRLNLGKKRKMVKVYTKTDGLVAVHPKSVNVEQTDFHYNWLIYHLKM

XP_015147310.1 872 RTSSIYLYDCTEVSPYCLLFFGGDISIQKDKDQDTIAVDEWIVFQSPARIAHLVKNLRQE
XP_027320349.1 873 RTSSIYLYDCTEVSPYCLLFFGGDISIQKDKDQDTIAVDEWIVFQSPARIAQLVKNLRQE
XP_013048508.1 795 RTSSIYLYDCTEVSPYCLLFFGGDISIQKDKDQDTIAVDEWIVFQSPARIAQLVKNLRQE
NP_065916.2   893 RTSSIYLYDCTEVSPYCLLFFGGDISIQKDNDQETIAVDEWIVFQSPARIAHLVKELRKE

XP_015147310.1 932 LDDLLQEKIENPHPVDWNDTKSRDTAVLTAIIDLITTQENESARNYAPRFQSERCS
XP_027320349.1 933 LDDLLQEKIENPHPVDWNDTKSRDTAVLTAIIDLITTQENESARNYAPRFQNERYS
XP_013048508.1 855 LDDLLQEKIENPHPVDWNDTTSRDTAVLTAIIDLITTQENESARNYAPRFQNERYS
NP_065916.2   953 LDILLQEKIESPHPVDWNDTKSRDCAVLSAIIDLIKTQEKATPRNFPPRFQDGYYS

Figure S9: Schematic alignment of DHX36 protein sequences of chicken, duck, goose and human. Depicted are DEAD box helicase region, domain of unknown function (DUF), HA2-associated domain, HelicC domain in black, maroon, red and grey underlining respectively. The DExH box is boxed in blue.

```
NP_001025971.1    1   MSHVAVENALSLDQQFSGLDLNSSDSQSEGSATSKGRYIPPHLRNREASKQGF--DSGGW
XP_005012555.2    1   MEDLSR-------RMFSGLDLNSSDSQSEGSSTSKGRYIPPHLRNREASKQGF--DSGGW
XP_013046370.1    1   MEDLSR-------RMFSGLDLNSSDSQSEGSSTSKGRYIPPHLRNREASKQGF--DSGGW
NP_001347.3       1   MSHVAVENALGLDQQFAGLDLNSSDNQSGGSTASKGRYIPPHLRNREATKGFYDKDSSGW


NP_001025971.1   59   STSRDKDAYSSFGARSDRGAKSSFF-DRGNGSRGGRYEERGR------GSDYDRSGFGRF
XP_005012555.2   52   SSSRDKDAYSSFGVRSDRGAKSSFF-DRGNGSRGGRYEERGR------GSDYDRSGFGRF
XP_013046370.1   52   SSSRDKDAYSSFGVRSDRGAKSSFF-DRGNGSRGGRYEERGR------GSDYDRSGFGRF
NP_001347.3      61   SSSKDKDAYSSFGSRSDSRGKSSFFSDRGSGSRG-RFDDRGRSDYDGIGSRGDRSGFGKF


NP_001025971.1  112   DRGGNSRWCDKSDEDDWSKPLPPSERLEQELFSGSNTGINFEKYDDIPVEATGSNCPPHI
XP_005012555.2  105   DRGGNSRWSDKSDEDDWSKPLPPSERLEQELFSGSNTGINFEKYDDIPVEATGSNCPPHI
XP_013046370.1  105   DRGGNSRWSDKSDEDDWSKPLPPSERLEQELFSGSNTGINFEKYDDIPVEATGSNCPPHI
NP_001347.3     120   ERGGNSRWCDKSDEDDWSKPLPPSERLEQELFSGGNTGINFEKYDDIPVEATGNNCPPHI


NP_001025971.1  172   ESFSDVDMGEIIMGNIELTRYTRPTPVQKHAIPIIKEKRDLMACAQTGSGKTAAFLLPIL
XP_005012555.2  165   ESFSDVDMGEIIMGNIELTRYTRPTPVQKHAIPIIKEKRDLMACAQTGSGKTAAFLLPIL
XP_013046370.1  165   ESFSDVDMGEIIMGNIELTRYTRPTPVQKHAIPIIKEKRDLMACAQTGSGKTAAFLLPIL
NP_001347.3     180   ESFSDVEMGEIIMGNIELTRYTRPTPVQKHAIPIIKEKRDLMACAQTGSGKTAAFLLPIL


NP_001025971.1  232   SQIYADGPGDALRAMKENGRYGRRKQYPISLVLAPTRELAVQIYEEARKFAYRSRVRPCV
XP_005012555.2  225   SQIYADGPGDALRAMKENGRYGRRKQYPISLVLAPTRELAVQIYEEARKFAYRSRVRPCV
XP_013046370.1  225   SQIYADGPGDALRAMKENGRYGRRKQYPISLVLAPTRELAVQIYEEARKFAYRSRVRPCV
NP_001347.3     240   SQIYSDGPGEALRAMKENGRYGRRKQYPISLVLAPTRELAVQIYEEARKFSYRSRVRPCV


NP_001025971.1  292   VYGGADIGQQIRDLERGCHLLVATPGRLVDMMERGKIGLDFCKYLVIDEADRMLDMGFEP
XP_005012555.2  285   VYGGADIGQQIRDLERGCHLLVATPGRLVDMMERGKIGLDFCKYLVIDEADRMLDMGFEP
XP_013046370.1  285   VYGGADIGQQIRDLERGCHLLVATPGRLVDMMERGKIGLDFCKYLVIDEADRMLDMGFEP
NP_001347.3     300   VYGGADIGQQIRDLERGCHLLVATPGRLVDMMERGKIGLDFCKYLVIDEADRMLDMGFEP


NP_001025971.1  352   QIRRIVEQDTMPPKGVRHTMMFSATFPKEIQMLARDFLDEYIFLAVGRVGSTSENITQKV
XP_005012555.2  345   QIRRIVEQDTMPPKGVRHTMMFSATFPKEIQMLARDFLDEYIFLAVGRVGSTSENITQKV
XP_013046370.1  345   QIRRIVEQDTMPPKGVRHTMMFSATFPKEIQMLARDFLDEYIFLAVGRVGSTSENITQKV
NP_001347.3     360   QIRRIVEQDTMPPKGVRHTMMFSATFPKEIQMLARDFLDEYIFLAVGRVGSTSENITQKV
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```
NP_001025971.1   412  VWVEELDKRSFLLDLLNATGKDSLTLVFVETKKGADALEDFLYHEGYACTSIHGDRSQRD
XP_005012555.2   405  VWVEESDKRSFLLDLLNATGKDSLTLVFVETKKGADALEDFLYHEGYACTSIHGDRSQRD
XP_013046370.1   405  VWVEESDKRSFLLDLLNATGKDSLTLVFVETKKGADALEDFLYHEGYACTSIHGDRSQRD
NP_001347.3      420  VWVEESDKRSFLLDLLNATGKDSLTLVFVETKKGADSLEDFLYHEGYACTSIHGDRSQRD


NP_001025971.1   472  REEALHQFRSGKSPILVATAVAARGLDISNVKHVINFDLPSDIEEYVHRIGRTGRVGNLG
XP_005012555.2   465  REEALHQFRSGKSPILVATAVAARGLDISNVKHVINFDLPSDIEEYVHRIGRTGRVGNLG
XP_013046370.1   465  REEALHQFRSGKSPILVATAVAARGLDISNVKHVINFDLPSDIEEYVHRIGRTGRVGNLG
NP_001347.3      480  REEALHQFRSGKSPILVATAVAARGLDISNVKHVINFDLPSDIEEYVHRIGRTGRVGNLG


NP_001025971.1   532  LATSFFNERNINITKDLLDLLVEAKQEVPSWLENMAYEQHHKGGGSRGRSKS-RFTGGFG
XP_005012555.2   525  LATSFFNERNINITKDLLDLLVEAKQEVPSWLENMAYEQHHKGGGSRGRSKSSRFSGGFG
XP_013046370.1   525  KYGQGTV-------PNLLGVVLLAKWHTE-------------------------------
NP_001347.3      540  LATSFFNERNINITKDLLDLLVEAKQEVPSWLENMAYEHHYKG-SSRGRSKSSRFSGGFG


NP_001025971.1   591  ARDYRTSSGAGSSSFSSSRPASGRTGGSG---SRGFGGGGYGGFYNSDGYGGNYNSQGVD
XP_005012555.2   585  ARDYRTSSGSGSSSFSSSRSTSSRSGGSG---SRGFGGGGYGGFYNSDGYGGNYNSQGVD
XP_013046370.1   547  -----TTECLGKACVPS-----------V---TRQYC-----------------------
NP_001347.3      599  ARDYRQSSGASSSSFSSSRASSSRSGGGGHGSSRGFGGGGYGGFYNSDGYGGNYNSQGVD


NP_001025971.1   648  WWGN
XP_005012555.2   642  WWGN
XP_013046370.1        ----
NP_001347.3      659  WWGN
```

Figure S10: Schematic alignment of DDX3X protein sequences of chicken, duck, goose and human. Well conserved domains include DEAD box helicase region (blue box), HelicC and C-terminal arginine-serine (RS) rich region. Note variation in RS region in goose DDX3

```
XP_025001441.1    1  MA---------------------------------GELTDKKDR---------------
XP_021135293.1    1  MDKTINVRLLLIEKIINWTDLGRWGIPGPAQGRPRPEEVADKKDR---------------
XP_013054789.1    1  MP--------------------------------ASCPQWKTEILDYCPTTRVLLIGC
NP_004809.2       1  MA---------------------------------GELADKKDR---------------


XP_025001441.1   12  ------DASPVKEERKRSRSPDRDRD-RDRDRKGSPPKDRKHRSRDRRR-GSRSRSRSR
XP_021135293.1   46  ------DASPVKEERKRSRSPDRD---RDRDRKGSPGKDRKHRSRDRAA--SCSRSRSR
XP_013054789.1   27  KTDLRTDLSTLMELSHQKQAPISYEQPPGLCSGGIPPVGGVGV------GQG--LRSVP-
NP_004809.2      12  ------DASPSKEERKRSRTPDRERD-RDRDRKSSPSKDRKRHSRDRRRGGSRSRSRSR
                           _____


XP_025001441.1   64  SKSLDRDRRHKERD----RDRGKKDREREKDGHRRDKDRKRSSLSPSRGKDSKSRKERDS
XP_021135293.1   95  SKSVDS----------------------------RRDKDRKRSSLSPSRGKDSKSRKERDS
XP_013054789.1   78  ----------------------------------NFPPVLLGSLSPSRGKDSKSRKERDL
NP_004809.2      65  SKSAERERRHKERERDKERDRNKKDRDRDKDGHRRDKDRKRSSLSPGRGKDFKSRKDRDS
                          _____


XP_025001441.1  120  RKAEEEEENALKKEKAQPLSLEELLAKKKAEEEAEAKPKFLSKAEREAEALRRRQQEVE-
XP_021135293.1  128  RKLEEEEENALKKEKAQPLSLEELLAKKKAEEEAEAKPKFLSKAEREAEALRRRQQEVEE
XP_013054789.1  104  RKAEEEEENALKKEKVR-------------------TPRSLPASPWGAGALLRSFPC---
NP_004809.2     125  KKDE-EDEHGDKKPKAQPLSLEELLAKKKAEEEAEAKPKFLSKAEREAEALKRRQQEVE-


XP_025001441.1  179  ERQRLLEEERKKRKQFQEMGRKMLEDPQERERRRERRERMERETNGTEDEEGRQKIREEKD
XP_021135293.1  188  ERQRLLEEERKKRKQFQEMGRKMLEDPQERERRRERRERMERETNGTEDEEGRQKIREEKD
XP_013054789.1  142  ----------------------SPEDPQERERRRERRERMERETNGTEDEEGRQKIREEKD
NP_004809.2     183  ERQRMLEEERKKRKQFQDLGRKMLEDPQERERRRERRERMERETNGNEDEEGRQKIREEKD
                                                 _____


XP_025001441.1  239  KSKELHAIKERYLGGVKKRRRTRHLNDRKFVFEWDASEDTSIDYNPLYKERHQVQLLGRG
XP_021135293.1  248  KSKELHAIKERYLGGVKKRRRTRHLNDRKFVFEWDASEDTSIDYNPLYKERHQVQLLGRG
XP_013054789.1  180  KSKELHAIKERYLGGVKKRRRTRHLNDRKFVFEWDASEDTSIDYNPLYKERHQVQLLGRG
NP_004809.2     243  KSKELHAIKERYLGGIKKRRRTRHLNDRKFVFEWDASEDTSIDYNPLYKERHQVQLLGRG


XP_025001441.1  299  FIAGIDLKQQKREQSRFYGDLMEKRRTLEEKEQEEARLRKLRKKEAKQRWDDRHWSQKKL
XP_021135293.1  308  FIAGIDLKQQKREQSRFYGDLMEKRRTLEEKEQEEARLRKLRKKEAKQRWDDRHWSQKKL
XP_013054789.1  240  FIAGIDLKQQKREQSRFYGDLMEKRRTLEEKEQEEARLRKLRKKEAKQRWDDRHWSQKKL
NP_004809.2     303  FIAGIDLKQQKREQSRFYGDLMEKRRTLEEKEQEEARLRKLRKKEAKQRWDDRHWSQKKL
                               _____
                                            _____
```

```
XP_025001441.1   359   DEMTDRDWRIFREDYSITTKGGKIPNPIRSWKDSSLPPHILEVIDKCGYKEPTPIQRQAI
XP_021135293.1   368   DEMTDRDWRIFREDYSITTKGGKIPNPIRSWKDSSLPPHILEVIDKCGYKEPTPIQRQAI
XP_013054789.1   300   DEMTDRDWRIFREDYSITTKGGKIPNPIRSWKDSSLPPHILEVIDKCGYKEPTPIQRQAI
NP_004809.2      363   DEMTDRDWRIFREDYSITTKGGKIPNPIRSWKDSSLPPHILEVIDKCGYKEPTPIQRQAI


XP_025001441.1   419   PIGLQNRDIIGVAETGSGKTAAFLIPLLVWITTLPKIDRIEESDQGPYAIILAPTRELAQ
XP_021135293.1   428   PIGLQNRDIIGVAETGSGKTAAFLIPLLVWITTLPKIDRIEESDQGPYAIILAPTRELAQ
XP_013054789.1   360   PIGLQNRDIIGVAETGSGKTAAFLIPLLVWITTLPKIDRIEESDQGPYAIILAPTRELAQ
NP_004809.2      423   PIGLQNRDIIGVAETGSGKTAAFLIPLLVWITTLPKIDRIEESDQGPYAIILAPTRELAQ


XP_025001441.1   479   QIEEETIKFGKPLGIRTVAVIGGISREDQGFRLRMGCEIVIATPGRLIDVLENRYLVLSR
XP_021135293.1   488   QIEEETIKFGKPLGIRTVAVIGGISREDQGFRLRMGCEIVIATPGRLIDVLENRYLVLSR
XP_013054789.1   420   QIEEETIKFGKPLGIRTVAVIGGISREDQGFRLRMGCEIVIATPGRLIDVLENRYLVLSR
NP_004809.2      483   QIEEETIKFGKPLGIRTVAVIGGISREDQGFRLRMGCEIVIATPGRLIDVLENRYLVLSR


XP_025001441.1   539   CTYVVLDEADRMIDMGFEPDVQKILEHMPVTNQKPDTDEAEDPEKMLANFESGKHKYRQT
XP_021135293.1   548   CTYVVLDEADRMIDMGFEPDVQKILEHMPVTNQKPDTDEAEDPEKMLANFESGKHKYRQT
XP_013054789.1   480   CTYVVLDEADRMIDMGFEPDVQKILEHMPVTNQKPDTDEAEDPEKMLANFESGKHKYRQA
NP_004809.2      543   CTYVVLDEADRMIDMGFEPDVQKILEHMPVSNQKPDTDEAEDPEKMLANFESGKHKYRQT


XP_025001441.1   599   VMFTATMPPAVERLARSYLRRPAVVYIGSAGKPHERVEQKVFLMSESEKRKKLLAILEQG
XP_021135293.1   608   VMFTGER-----------ELQGGKCGILE-----------SGMPDSPPPNRKKLLAILEQG
XP_013054789.1   540   SPPLP----------------------------------------SSPPPNRKKLLAILEQG
NP_004809.2      603   VMFTATMPPAVERLARSYLRRPAVVYIGSAGKPHERVEQKVFLMSESEKRKKLLAILEQG
```

```
XP_025001441.1  659  FDPPIIIFVNQKKGCDVLAKSLEKMGYNACTLHGGKGQEQREFALSNLKAGAKDILVATD
XP_021135293.1  648  FDPPIIIFVNQKKGCDVLAKSLEKMGYNACTLHGGKGQEQREFALSNLKAGAKDILVATD
XP_013054789.1  562  FDPPIIIFVNQKKGCDVLAKSLEKMGYNACTLHGGKGQEQREFALSNLKAGAKDILVATD
NP_004809.2     663  FDPPIIIFVNQKKGCDVLAKSLEKMGYNACTLHGGKGQEQREFALSNLKAGAKDILVATD


XP_025001441.1  719  VAGRGIDIHDVSMVVNYDMAKNIEDYIHRIGRTGRAGKSGVAITFLTKEDSTVFYDLKQA
XP_021135293.1  708  VAGRGIDIHDVSMVVNYDMAKNIEDYIHRIGRTGRAGKSGVAITFLTKEDSTVFYDLKQA
XP_013054789.1  622  VAGRGIDIHDVSMVVNYDMAKNIEGESGAWYFTYS-----V---LLSLLACSVFLH----
NP_004809.2     723  VAGRGIDIQDVSMVVNYDMAKNIEDYIHRIGRTGRAGKSGVAITFLTKEDSAVFYELKQA


XP_025001441.1  779  ILESPVSSCPPELANHPDAQHKPGTILTKKRREETIFA---------------------
XP_021135293.1  768  ILESPVSSCPPEXXXX-XXXXXPGTILTKKRREETIFA---------------------
XP_013054789.1  670  -------------------ISSIGKLLLMVAIEATYLVLVEGPQAALFDNADLLVVANAL
NP_004809.2     783  ILESPVSSCPPELANHPDAQHKPGTILTKKRREETIFA---------------------
```

Figure S11: Schematic alignment of DDX23 protein sequences of chicken, duck, goose and human. Depicted are the putative nuclear localization signal sequences (NLSs), DEAD box region, and HelicC domain in grey, black, and red underlining respectively. The DEAD box is boxed in blue.

```
XP_025006699.1    1  MKFRRG--R-RFTSSAKLRRKGIEVIGKWKTVEIDPNVFVDEQFKDVVCLEELTEYKLVS
XP_027314331.1    1  MKAKKG--R-RFTSSVKLKRKGIAVIGKWKTVEIDPNLFADEQFRDIVCLEELTEYKLVN
XP_013037286.1    1  MKAKKG--R-RFTSSVKLKRKGIEVIGKWKTVEIDPNLFADEQFRDIVCLEELTEYKLVS
NP_065147.1       1  MKLKDTKSRPKQSSCGKFQTKGIKVVGKWKEVKIDPNMFADGQMDDLVCFEELTDYQLVS


XP_025006699.1   58  SDKVGKG----NKQKRKSEDLSEEGSEEEEEEEEAVIPPKKKKKCKDLKTRADKSDDSN-
XP_027314331.1   58  SNKVGQV----SGQKRKVKSLSE----GSEEEEEPVVPPKKKKKGKDLKTKTDTGDDTN-
XP_013037286.1   58  SNKVGKV----NEQKRKAQSLSE----GSGEEEEPVVPPKKKKKSKDLKTRTDKSDDTN-
NP_065147.1      61  PAKNPSSLFSKEAPKRKAQAVSE----EEEEEEGKSSSPKKKIKLKKSKNVATEGTSTQK


XP_025006699.1  113  ATEVDVPVDEEKRCEEIVQGADDKVCGH-TAESTSS---TKNAAKKNKKKEKEKVVKNKA
XP_027314331.1  109  ATEVDVPVDEETRCEEITEGANCEDSGH-TAGSTSS---TKSAVKKKK----KKVDKNKT
XP_013037286.1  109  ATEVDVPVDEETKCEEITEGANREDNGH-RAESTSS---TKSAVKKKK----KKVDKNKT
NP_065147.1     117  EFEVKDPE--------LEAQGDDMVCDDPEAGEMISENLVQTAPKKKK----NKG---KK


XP_025006699.1  169  SQVQDASPPVTTSKKVKNWTTEVLSTSTDHKADVSAWKDLFVPQPVLKALSSLGFSAPTP
XP_027314331.1  161  SQDQEALPSVTTSKKLKNWSTEVLSASTDHKADVSAWKDLFVPKPVLKALSYLGFSAPTP
XP_013037286.1  161  SQDQEALPSVTTSKKVKNWSTEVLSASSDHKADVSAWKDLFVPKPVLKALSYLGFSAPTP
NP_065147.1     162  GLEPSQSTAAKVPKKAKTWIPEV----HDQKADVSAWKDLFVPRPVLRALSFLGFSAPTP


XP_025006699.1  229  IQALTLPSAIRDNMDILGAAETGSGKTLAFAIPMIHSVLEWQKSNSSASVSDSVSKKP--
XP_027314331.1  221  IQALALPSAIRDNMDVLGAAETGSGKTLAFAIPMIHSVLEWQKSNSSMSRNDSVSKES--
XP_013037286.1  221  IQALALPSAIRDNMDVLGAAETGSGKTLAFAIPMIHSVLEWQKSNSSMSRNDSVSKES--
NP_065147.1     218  IQALTLAPAIRDKLDILGAAETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPPGET


XP_025006699.1  287  -YQHHDEMRWENDDEAE----------------KPN-----------HQQVEDSGDEDD
XP_027314331.1  279  -HQHHDETRWENEDEAE----------------KLT-----------HQQVEDSGDEDD
XP_013037286.1  279  -HQHHDETRWENEDEAE----------------KLT-----------HQQVEDSGDEDD
NP_065147.1     278  RTEAGAETRSPGKAEAESDALPDDTVIESEALPSDTAAEARAKTGGTVSDQALLFGDDDA


XP_025006699.1  318  ASFATGCVK------VQ------------ENTEYDSSNKEHTVGLHKKRPLLGLVLTPTR
XP_027314331.1  310  ASFATGCVK------VL------------ENAEFDSSDKGHAVGLHKKRPLLGLVLTPTR
XP_013037286.1  310  ASFATGCVK------VL------------ENAEFDSSDKGHTVGLHKKRPLLGLVLTPTR
NP_065147.1     338  GEGPSSLIREKPVPKQNENEEENLDKEQTGNLKQELDDKSATCKAYPKRPLLGLVLTPTR
```

```
XP_025006699.1  360  ELAVQVKHHIDAVAKFTGIKTAILVGGMAAQKQERVLNRKPEIVIATPGRLWELIKERHP
XP_027314331.1  352  ELAVQVKHHIDAVTKFTGIKTAILVGGMAAQKQERVLNRKPEIVIATPGRLWELVKAKHP
XP_013037286.1  352  ELAVQVKHHIDAVTKFTGIKTAILVGGMAAQKQERVLNRKPEIVIATPGRLWELVKAKHP
NP_065147.1     398  ELAVQVKQHIDAVRFTGIKTAILVGGMSTQKQQRMLNRKPEIVVATPGRLWELIKEKHY


XP_025006699.1  420  HLSNLRQLRCLVIDEADRMVERGHFLELSQLLEVLNDSQYNPKRQTFVFSATLTLVHQTP
XP_027314331.1  412  HLSNLRQLRCLVIDEADRMVERGHFLELSQLLELLNDSQYNPKRQTFVFSATLTLVHQTP
XP_013037286.1  412  HLSNLRQLRCLVIDEADRMVERGHFLELSQLLELLNDSQYNPKRQTFVFSATLTLVHQTP
NP_065147.1     458  HLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEVLNDSQYNPKRQTLVFSATLTLVHQAP


XP_025006699.1  480  ARILQKKNAKKIDKKTKLEMLMEKVGIKGKPKVIDLTRKEATVETLMETRIHCDTNEKDY
XP_027314331.1  472  TRVLQKKNAKKMDKKTKLEMLMEKVGIKGKPKVIDLTRKEATVETLTETRIHCDTNEKDY
XP_013037286.1  472  TRVLQKKNAKKMDKKTKLEMLMEKVGIKGKPKVIDLTRKEATVETLTETRIHCDTNEKDY
NP_065147.1     518  ARILHKKHTKKMDKTAKLDLLMQKIGMRGKPKVIDLTRNEATVETLTETKIHCETDEKDF


XP_025006699.1  540  YLYYFLLQYPGRTMVFANSIDCIKRLSSLLTILNCDPFPLHANMHQKQRLKNLERFAERE
XP_027314331.1  532  YLYYFLLQYPGRTMVFANSIDCIKRLSSLLSILNCDPLPLHANMHQKQRLKNLERFAERE
XP_013037286.1  532  YLYYFLLQYPGRTMVFANSIDCIKRLSSLLSILNCDPLPLHANMHQKQRLKNLERFAERE
NP_065147.1     578  YLYYFLMQYPGRSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQRLRNLEQFARLE


XP_025006699.1  600  SCVLLTTDVAARGLDIPNVQHVIHYQVPRTSELYVHRSGRTARAANEGLSLLLIGPDDLI
XP_027314331.1  592  SCVLLTTDVAARGLDIPNVQHVIHYQVPRTSELYVHRSGRTARAANEGLSLLLIGPDDLI
XP_013037286.1  592  SCVLLTTDVAARGLDIPNVQHVIHYQVPRTSELYVHRSGRTARAANEGLSLLLIGPDDLI
NP_065147.1     638  DCVLLATDVAARGLDIPKVQHVIHYQVPRTSEIYVHRSGRTARATNEGLSLMLIGPEDVI


XP_025006699.1  660  NFRKIYKTLQKSEELPLFPVETKYMTAIKERVNLARQIEKAEFFNGRAKQHDSWLQQAAE
XP_027314331.1  652  NFRKIYKTLEKSEELPFFPVETKYMTSIKERMNLARQIEKAEFFNSRAKQHDSWLQQAAE
XP_013037286.1  652  NFRKIYKTLEKSEELPFFPVETKYMTSIKERMNLARQIEKAEFFNSRAKQHDSWLQQAAE
NP_065147.1     698  NFKKIYKTLKKDEDIPLFPVQTKYMDVVKERIRLARQIEKSEYRNFQACLHNSWIEQAAA


XP_025006699.1  720  ALEVDLDDDLLMGKKTSEQEESQKQKMLKGMKKQLKHMLSQPLFKVFMKTKYPTQSGKLL
XP_027314331.1  712  ALEVDLDDDLFMGRKTSEQEESQKQKMLKGMKKQLKHMLSQPLFKVFMKTKYPTQSGKLL
XP_013037286.1  712  ALEVDLDDDLFMGRKASEQEESQKQKMLKGMKKQLKHMLSQPLFKVFMKTKYPTQSGKLL
NP_065147.1     758  ALEIBLEEDMYKGGKADQQEERRRQKQMKVLKKELRHLLSQPLFTESQKTKYPTQSGKPP
```

```
XP_025006699.1   780  LPQTSAGNSETALSIISKKQARRKK------------SVKSN
XP_027314331.1   772  LPQTSVGSSESALGTVSKQQAKKNK------------SKK-N
XP_013037286.1   772  LPQSSAGNSESALGTVSKQHAKKNK------------SKTIR
NP_065147.1      818  LLVSAPSKSESALSCLSKQKKKKTKKPKEPQPEQPQPSTSAN
```

Figure S12: Schematic alignment of DDX24 protein sequences of chicken, duck, goose and human. The DEAD box is boxed in blue.

```
XP_004940975.1    1  --------------------------------------------------MDSAEDNFK--IH
XP_027312235.1    1  --------------------------------------------------MDSAEDNFKKVVC
XP_013030722.1    1  MGGGSTLKEVCWQAQWRTGLCCRSQPGRALLEAACRVAAGAGESRSVMDSAEDNFKHVVS
NP_060101.3       1  ----------------------------------------------ME-----------


XP_004940975.1   12  DYANES---ADSDDKDSECVDSEKINFTATEEDKE--STSDRDEEDVTDHNEEAAVVQML
XP_027312235.1   14  DTTNGSTSKDDSDDMDSDVIDSEEIGCISTKKNKEGGSTSDHDEGDETSDKAEAAVVQML
XP_013030722.1   61  DNTNGSTSKDDSDDMDSECIDSEEIGFISRKKNKEGGSTSDHDEEDETNDNAEAAVMQML
NP_060101.3       3  -----------------------------------------------------------


XP_004940975.1   67  KEKEDREKEAEDPDYGEIYSILNTDEVIQKESQNEGRNFRVLQNKLNSQDPEVRKHLEIL
XP_027312235.1   74  KEKEDKEKEVEDPDYGKAYNILTTEEVAQKESQTEGKDFRVLQNEWDSKSPEIRKHLEFL
XP_013030722.1  121  KEKEDREKDVEDPDYDNVYNILTTEEV---ESHTAGKDFRFLQDEWDSQSPEIRKHLEFL
NP_060101.3       3  -------------------RNVLTT----------------------------------FS


XP_004940975.1  127  KKLKQSIWPSLSKASFVSLLKDFVESEFFVIDGDSLLLTFLNE----EVQHLTLFYLIEC
XP_027312235.1  134  KILKLHVWPSLSRARYVSLLKDFVESEFFVIDGDSLIILMLLNE----EVQYLTLFYRIEC
XP_013030722.1  178  KILKLHVWSSLSRARYVSLLKDFVESEFFVIDGDSLIILMLLNE----EVQYLNLFYLIEC
NP_060101.3      11  QEMSQLILNEMPKAEYSSLFNDFVESEFFLIDGDSLLITCICEISFKPGQNLHFFYLVER


XP_004940975.1  183  FLHDFTQKGAKYIIVFFKDAEQMYFQNPQFLFLRTALVEHLKHNTNITIHTEFSNCFSQE
XP_027312235.1  190  FLQDFTQRGARYIVVFFKDAEQMYFRYPHFLFLRTALIEHLKHNTRTTVHTEFSNCLSPA
XP_013030722.1  234  FLQDFTQKGAKYIVVFFKDAEQMYFPYPHFLFLRTALIEHLKHNTRTTVHTEFSNCLSPA
NP_060101.3      71  YLVDLISKGGQFTIVFFKDAEYAYFNFPELLSLRTALILHLQKNTTIDVRTTFSRCLSKE


XP_004940975.1  243  WEIFLKKSYPYFIIISDIGLTSLQTNYLTIFIAHSLSKKINVQAFGQECDTLRVYGYHL
XP_027312235.1  250  WEVFLKKSYPYFIIVSDIGLTSLQTNYLTIFIAHSLSKKITIVLASGQECDTLRVYGYHL
XP_013030722.1  294  WEIFLKKSYPYFIIVSDIGLTCPQTNYLTIFIAHSLSKKITIVLASGQEYDTLRVYGYHL
NP_060101.3     131  WGSFLEESYPYFLIVADEGLNDLQTQLFNFLIIHSWARKVNVVLSSGQESDVLCLYAYLL


XP_004940975.1  303  QSMWKHRIFFQKYGKDLQSAC----EAIVRYQELSLY-LYEHLKLSLKSIQNEVYQTVLL
XP_027312235.1  310  QSMAKHRLFFQKYEKDLRCVC----EAIVRYKEPSLY-LYGHLKLSLKSVQEEVCRTIPL
XP_013030722.1  354  QSIRKHRLFFQKYEKDLQCLC----EAIVRYKEPSLC-LYGHLRLSLKSVQEEVCQTIPL
NP_060101.3     191  PSMYRHQIFSWKNKQNIKDAYTTLLNQLERFKLSALAPLEGSLK--WNNITEEAHKTVSL
```

```
XP_004940975.1   358   LKKLWPEGSDIRRVICVLTCAVGLKLYSDALESAHASLGAKPEQSESERSKPLSPEEATD
XP_027312235.1   365   LKQLWPEGSDIRRVVCVLACAVGLKIYSDMLTNAHASRGTKTEKSESGRSKPPSPEAAAD
XP_013030722.1   409   LKQLWPEGSDIRRVVCVLACAVGLKIYSDMLKNAHASRGTKTEKSERGRSKPLSPEAAAD
NP_060101.3      249   LTQVWPEGSDIRRVFCVTSCSLSLRMYHRFLGNREPSSGQETEIQQ-VNSNCLTLQEMED


XP_004940975.1   418   LCRMQCLTMVFLLHMPLSQRAQIRIMKSCWTEQVLPLIKMQQLCAHFVLKQLSDINDWKL
XP_027312235.1   425   LCRMQCLTVVFLLHMPLSQRAQIRVMKSCWTKQVLPIMKMQQLCVHFVLKELSDKNDWKL
XP_013030722.1   469   LCRMQCLTVVFLLHMPLSQRAQIRVMKSCWTKQVLPIIKMQQLCAHFVLKQLSDKNDWKL
NP_060101.3      308   LCKLHCLTVVFLLHLPLSQRACARVITSHWAEDMKPLIQMKKWCEYFILRNIHTFEFWNL


XP_004940975.1   478   DLTYLPDLNDDSLLRNLAYYYEIEYSEGLEFQKELGKEMDKEYQFLWDTVTKLTVNYDFG
XP_027312235.1   485   DLTYLPDLNDESLLKNLAHYYQIEYTKGLEFQKELGKEMEDEYLSLWDAVTKLTVKYGFG
XP_013030722.1   529   DLTYLPDLSDDSLLINLAHYYEIEYSEGLEFQKELGKEMEDQYRSLWDAVTKLTVKYGFG
NP_060101.3      368   NLIHLSDLNDELLLKNIAFYYENENVKGLHL--NLGDTIMKDYEYLWNTVSKLVRDFEVG


XP_004940975.1   538   DAFPVRNTSQVFIDHQQTSFRV-CDEKIPDIGLIPLKSDLAEEYAGDVLKDLPVLESNDP
XP_027312235.1   545   DAFPIRTTSQVFLDQEQTSPRV-YEDKIPAIGLFPVKSDLVKEYAGDILKDLPVLDDNDP
XP_013030722.1   589   DAFPIRTTSQLFLDQEQTSFRV-YEDKIPAIGLFPVKSDLVKEYAGDILKDLPVLDDNDP
NP_060101.3      426   QPFPLRTTKVCFLEKKPSPIKDSSNEMVPNLGFIPTSSFVVDKFAGDILKDLPFLKSDDP


XP_004940975.1   597   AVTSLAKYKEFDELRHWHSGRPLSEEYERVRSNADAKSKDADERKQIQKLQTFYRLYGST
XP_027312235.1   604   AVSSLTKYKEFDELRHWHSGRPLTEEYERVHCNADAKSKDPYERKQIQKLQTFYRFYGST
XP_013030722.1   648   AVSSLTKYKEFDEHRHWHSGRPLTEEYERVHCNADAKSKDPYERKQIQKLQTFYRFYGST
NP_060101.3      486   IVTSLVKQKEFDELVHWHSHKPLSDDYDRSRCQFDEKSRDPRVLRSVQKYHVFQRFYGNS


XP_004940975.1   657   LEGSTSKFIVHQNDVPCSNTAVKKAKQTHKSKAEIIAEENNRRLKAKEEKKEEEQWKTLQ
XP_027312235.1   664   LQEGTSKFVVCQKNAPGSANNPVKKKKMQKSKAEIIAEENNKRLKIKEEMKEQEQWKTLQ
XP_013030722.1   708   LQEGTSKFIVCQKDAAGSANNPVKKKKMQKSKAEIIAEENNKRLKIKEEMKEQEQWKTLQ
NP_060101.3      546   LETVSSKIIVTQTIKSKKDFSGPKSKKAHETKAEIIARENKKRLFAREEQKEEQKWNALS


XP_004940975.1   717   ITTEKEIKANLTVGINKMEKFLKTVKSKSVKFSVEMSALSACVEAWKKHCRKQ-GNKPKD
XP_027312235.1   724   ISTEKEIKANLTVGINKLEKFLKNLKSKSVKFSVELSGLSACLEVWKEHCKKQ-DTKSKD
XP_013030722.1   768   MSTEKEIKENLTVGINKLEKFLKILKSKSVKFSVELSGLSACLEAWKEHCKEQ-ATKSKD
NP_060101.3      606   FSIEEQLKENLHSGIKSLEDFLKSCKSSCVKLQVEMVGLTACLKAWKEHCRSEEGKTTKD
```

```
XP_004940975.1   776  LSSAVQLMRRIHILLEKYQDLLEKSHLQKLSQYLQLLGFENLACSLTGQMREGRDD--QN
XP_027312235.1   783  LSKAVQLMRRIHILLEKYQDLLEKSHLQKLTQCLRLLGFENLACSLSGQVREKSDG--EN
XP_013030722.1   827  LSKAVQLMRRIHILLEKYQDLLEKPHLQKLTQCLRLLGFENLACSLSGQVREKSDG--EN
NP_060101.3      666  LSIAVQVMKRIHSLMEKYSELLQEDDRQLIARCLKYLGFDELASSIHPAQDAENDVKVKK

XP_004940975.1   834  RSNYDVEVGPARFQLQYMDYYLLREERNDPDPRVQHFIPDTWQRELLDAVDNNESAVIVA
XP_027312235.1   841  TSRYAIEVGPVRFQLQYMDYYLLREERNDPDPRVENFIPDTWQRELLDAVDNNESAVIVA
XP_013030722.1   885  TSRYAIEVGPVRFQLQYMDYYLLREERNDPDPRVENFIPDTWQRELLDAVDNNESAVIVA
NP_060101.3      726  RNKYSVGIGPARFQLQYMGHYLIRDERKDPDPRVQDFIPDTWQRELLDVVDKNESAVIVA

XP_004940975.1   894  PTSSGKTYASYYCMEKVLKMSDEGVVVYVAPTKALVNQVVGSVYSRFTKKLPDGLVVCGV
XP_027312235.1   901  PTSSGKTYASYYCMEKVLKTSDDGVVVYVAPTKALVNQVVGTVYSRFTKTLPDGLVVCGV
XP_013030722.1   945  PTSSGKTYASYYCMEKVLKTSDDGVVVYVAPTKALVNQVVGTIYSRFTKKLPDGLVVCGV
NP_060101.3      786  PTSSGKTYASYYCMEKVLKESDDGVVVYVAPTKALVNQVAATVQNRFTKNLPSGEVLCGV

XP_004940975.1   954  FTRDYRHDVMNSQILVTVPQCLEILMLSPRCQSWTKRIQYII-------FDEIHCLGGEI
XP_027312235.1   961  FTRDYRNDVMNSQILVTVPQCLXXXXVLX----XGRFITFLFFFLSSFPNIXVHCLGGEI
XP_013030722.1  1005  FTRDYRNDVMNSQILVTVPQCLEILMLSPRCQKWVKRIQYVI-------FDEVHCLGSEI
NP_060101.3      846  FTREYRHDALNCQVLITVPACFEILLLAPHRQNWVKKIRYVI-------FDEVHCLGGEI

XP_004940975.1  1007  GAEVWEHLLVTIRCPFLALSATISNPDHLTEWLQSVKRYWQCADNTIKGSSTNSEKNFAR
XP_027312235.1  1017  GAEVWEHLLVTIRCPFLALSATISNPEHLTEWLQSVKRYWQRAENMIEENSTNFEKNSTR
XP_013030722.1  1058  GAEVWEHLLVTIRCPFLALSATISNPEHLTEWLQSVKRYWQRAENTIEESPTSSEKNSTR
NP_060101.3      899  GAEIWEHLLVMIRCPFLALSATISNPEHLTEWLQSVKWYWKQEDKIIE-NNTASKRHVGR

XP_004940975.1  1067  KCKGTSTVKEQKKSYRVRLVLYEERYNDLEKYVCSVNGSDFGIEHFHPCAALTVNHIENY
XP_027312235.1  1077  KLKVKSKVKEPKKTYRVRLVLYGERYNDLEKYVCSSTGGDFLFEHYHPCAALTVNHIENY
XP_013030722.1  1118  KLKVKSKVKEPKKSYRVRLVLYGERYNDLEKYVCSSTGGDFLIEHYHPCAALTVNHIENY
NP_060101.3      958  QAGFPKDYLQVKQSYKVRLVLYGERYNDLEKHVCSIKHGDIHFDHFHPCAALTTDHIERY

XP_004940975.1  1127  GIPSDLSLSPRESIQLYDTMVKVWQKWPRAQEMDPEEFVSFKNNIVIKKMDVRKYEQELK
XP_027312235.1  1137  GIPADLSLSPKESVQLYDTMVEVWKEWPRAQELDPEEFVSFKNKVVIKKMDVRKYEQELK
XP_013030722.1  1178  GIPADLSLSPRESVQLYDTMVEVWNEWPRAQELDPEEFVSFKNKVVIKKTDVRKYEQELK
NP_060101.3     1018  GFPPDLILSPRESIQLYDAMFQIWKSWPRAQELCPENFIHFNNKLVIKKMDARKYEESLK
```

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XP_004940975.1 1187 KELSNWIAVGQRQKVNEVLENLKPQPVDCSEYEKWKRFARFVDKLHEMDKLPAIFFIFGL
XP_027312235.1 1197 KELSKWIELGQRQKVCELLDHFKPQPMDCSDQEKWMQFACFVEKLHEMDKLPAIIFIFGL
XP_013030722.1 1238 KELSKWIELGQRQKVYELLDHFKPQPVDCSDQEKWMQFACFVEKLHEMDKLPAIIFIFGL
NP_060101.3    1078 AELTSWIKNGNVEQARMVLQNLSPE-ADLSPENMITMFPLLVEKIRKMEKLPALFFLFKL

XP_004940975.1 1247 DSVENAAWNVFRNLLEKQDNERDPKMEKEKEDIKNKLRKINKTLMKFEPTDIKKVKPSK-
XP_027312235.1 1257 DSVERAATNVFIHLMEKQKNEQDPKAKREIEDIKDKLRKVDKSLTKCKTNDTKKLKTSK-
XP_013030722.1 1298 DSVERAANNIFIHLMEKRKNEQDPKAKREIEDIKDKLRKVNKSLMKCKPNDTKKLKPSK-
NP_060101.3    1137 GAVENAAESVSTFLKKKQETKRPPKADKEAHVMANKLRKVKKSIEKQKIIDEKSQKKTRN

XP_004940975.1 1306 VENMVMLLTMKKQLQERLKKLTVIHSMCTYADPKAVDEDTLRKIFYRLRFQRRGYVHQTL
XP_027312235.1 1316 AESIIQLWTMKNELEKRLKKLSVTPSACTYADPKAVDEDTLRKIFYRLRFERKGYLQQML
XP_013030722.1 1357 MESIIQLLTMKKELQKRLEKLSVIPSACTYADPKAVDEDTLRKIFYRLRFERKGYLQEML
NP_060101.3    1197 VDQSLIHEAEHDNLVKCLEKNLEIPQDCTYADQKAVDTETLQKVFGRVKFERKGEELKAL
```

Figure S13: Schematic alignment of DDX60 protein sequences of chicken, duck, goose and human. The critical conserved residues of ATP binding and phosphorylation, lysine (K791) and tyrosine (Y793 and Y796) respectively are boxed in black

```
XP_015152165.1      1  M-------------------------------------------------------
XP_027328665.1      1  MVPTRPRLCSMAATPPPFAQRHAVLQQRVRGAGPTLGRGHGCHRPAPRRPASRKGKRKRR
XP_013053947.1      1  --------------------------------------------------------
NP_066363.1         1  MEERRPHL------------------------------------------------


XP_015152165.1      2  --------------------------------------------DGAGHKPLFRQPRAAGRDH
XP_027328665.1     61  RRRPGRASGARGPAASGRFLPVLWGAGQPRRPAEEPAAGAMEGAGQGPGLRLPRAGRRGH
XP_013053947.1      1  -------------------------------------------GPGLRLPRAGRRGH
NP_066363.1         9  ----------------------------------------------DARPRNSHTNH


XP_015152165.1     21  ---PDVAFIQRGRSGINNVSGQTNK-AVRQAGEDPQASNYTLPLGKREDSFAGTAKFFNQ
XP_027328665.1    121  AGRWDAGFIQQGRNRINNVSGQTHK-TVAQAGENPQASNYTLLLGQREERS---EYFFSQ
XP_013053947.1     15  ADHWDTGFIQRGRNRINSVSGQTHK-TVAQAGENPQTSNYTPLLGQREERS---ECFFSR
NP_066363.1        20  RGPVDGELPPRARNQANNPPANALRGGASHPGRHPRANNHPAAYWQREERFRAMGRNPHQ


XP_015152165.1     77  GRRNQGGPVTSGATGHGNEQ-NDGRGRRYQGGQAHERARGSWNVQENESRERRYQGGQAH
XP_027328665.1    177  GRRNQGGQTNSGATGHWNEQENEGRGKWYRGGQTHERARGPWNEQENEGRRRRYQGGQAY
XP_013053947.1     71  GRRNQGGQANSGATGHWNEQENEGRGKRYQGGQTHERARGPWNEQENEGRRRHQGGQAY
NP_066363.1        80  GRRNQEGHASDEARDQRHDQENDTR--WRNGNQDCRNRRPPW------------------


XP_015152165.1    136  ERARGSQNVQENERKGKQHVSLGQAQGRARGLWNEQDDEVRGRRYQGGQGHERVRGPWNE
XP_027328665.1    237  DR-----------------------DRGLWNEQDNEGRVRRYQGGRACERAGGPWNM
XP_013053947.1    131  ER-----------------------DRGLWNEQDNEGRGRRYQGGQAYERARGPWNM
NP_066363.1       120  ---------------------------------------------------------S-


XP_015152165.1    196  QENEGKGRRYQGG-----QVQEDARGPRNREEIEGKGRRMRLAGSPHFNHNFTPGGTQP-
XP_027328665.1    271  QENEVRGRRYHSGQALSGQAQEDARGLRNGQENEGKGRSIQLRRSMHFYQKPTPGGAQLS
XP_013053947.1    165  QENEGRGKCYQGGQALSGQAQEDARGLRNGQENEGKGRRIQPGRNTHFYQKPTPGGAQL-
NP_066363.1       121  ---------------------------------------------NDNFQQWRTPHQ-KP-
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XP_015152165.1   250   -----SEQPQQVKKVGYKFLESLLQKDSSEVVITLASSSGFKELLSQTSMKPGFLQLICQ
XP_027328665.1   331   EQLQLSEQPQQVKKIGYKFLEGLLQKDPSEVVITLASSSGLKELLSQTAMKPSFVQLICQ
XP_013053947.1   224   -----SEQPQQVKKIGYKFLEGLLQKDPSEVVITLASSSGLKELLSQTAMKPSFLQLICQ
NP_066363.1      135   -----TEQPQQAKKLGYKFLESLLQKDPSEVVITLATSLGLKELLSHSSMKSNFLELICQ


XP_015152165.1   305   VLRKACGSRMDRQSVQQLLGMVKESNFLKICLPQYVSDMVTEAVPAVRHQYPEHIGNIIL
XP_027328665.1   391   VLRKACSSRMDRQSVQQLLGVVKESNFLKICLPQYVSDMVTEAVPAVRHQYPEHIGNIIL
XP_013053947.1   279   VLRKACSSRMDRQSVQQLLGVVKESNFLKICLPQYVSDMVTEAVPAVRHQYPEHIGNIIL
NP_066363.1      190   VLRKACSSKMDRQSVLHVLGILKNSKFLKVCLPAYVVGMITEPIPDIRNQYPEHISNIIS


XP_015152165.1   365   LLQDLISIFPSSSVQKISMLLTVLPASINALRASGVQITEETEKNISKVQMLVQHLQEKR
XP_027328665.1   451   LLQDLISIFPASSVQKISILLTVLPASINALRASGVDITEETEKNLNKVQMLVQHLQEKR
XP_013053947.1   339   LLQDLISIFPASSVQKISILLTVLPASINALRASGVDIMEETEKNLNKVQMLVQHLQEKR
NP_066363.1      250   LLQDLVSVFPASSVQETSMLVSLLPTSLNALRASGVDIEEETEKNIEKVQTIIEHLQEKR


XP_015152165.1   425   REGTLRADNYTLMQPQADGQEETYRTMTIYPTYDELHHDVKPFLRPNIVSGRYESTNIYL
XP_027328665.1   511   REGTLRADNYTLMQPQADGQEETYRTMTIYPTYNEVHHDEKPFLRPNIVSGRYESTSIYL
XP_013053947.1   399   REGTLRADNYTLMQLQADGQEETYRTMTIYPTYNEVHHDEKPFLRPNIVSGRYESTSIYL
NP_066363.1      310   REGTLRVDTYTLVQPEAEDHVESYRTMPIYPTYNEVHLDERPFLRPNIISGKYDSTAIYL


XP_015152165.1   485   DTHFRLLREDFIKPLREGILDLLQSFEDKSLRKKKFDDIRIYFDTRIITPLCSPSGVVYK
XP_027328665.1   571   DTHFRLLREDFVRPLREGISELLQSFEDKGLRKKKFDDIRIYFDTRIIAPLCSPTGVVYK
XP_013053947.1   459   DTHFRLLREDFVRPLREGISELLQSFEDKGLRKKKFDDIRIYFDTRIIAPLCSPTGVVYK
NP_066363.1      370   DTHFRLLREDFVRPLREGILELLQSFEDQGLRKRKFDDIRIYFDTRIITPMCSSSGIVYK


XP_015152165.1   545   VQFDIKPLKFVRWQNSRRLLYGSLVCMSRDHFETCLFATVSERDNAELANGIVQLSFNAQ
XP_027328665.1   631   VQFDTKPLKFVRWQNSRRLLYGSLVCMSKDHFETCLFATVSNRDSTDLAKGIVELCFNAQ
XP_013053947.1   519   VQFDTKPLKFVRWQNSRRLLYGSLVCMSKDHFETCLFATVSNRDSTDLAKGIVQLCFNAQ
NP_066363.1      430   VQFDTKPLKFVRWQNSKRLLYGSLVCMSKDNFETFLFATVSNREQEDLCRGIVQLCFNEQ
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XP_015152165.1   605  SRALLAEVQPSDSFLMVETTAYFEAYRHVLEGLQEIQEEDIPFQKYIVECDPQLKEPAYL
XP_027328665.1   691  SQALLAEVRPSDSFLMVETTAYFEAYRHVLEGLQEIQEEDIPFQKYIVECDAQVKEPKYL
XP_013053947.1   579  SQALLAEVRPSDSFLMVETTAYFEAYRHVLEGLQEIQEEDIPFQKYIVECDAQVKEPTYL
NP_066363.1      490  SQQLLAEVQPSDSFLMVETTAYFEAYRHVLEGLQEVQEEDVPFQRNIVECNSHVKEPRYL

XP_015152165.1   665  KMDTKYNFAPLTEDTLSDEE--TYLDGLRRQNVRVLDPNQWPSMETLGLDESQMQALSLA
XP_027328665.1   751  TVDTTYNFAPLTEDPLADEE--RAPDGLRRQSVRVLDHNQWPSMETLGLDESQMEALRLA
XP_013053947.1   639  TVDTTYNFAPLTEDPLADEE--RAPDGLRRQSFHVLDPNRWPSMETLGLDESQMEALRLA
NP_066363.1      550  LMGGRYDFTPLIENPSATGEFLRNVEGLRHPRINVLDPGQWPSKEALKLDDSQMEALQFA

XP_015152165.1   723  LTKELAIIQGPPGTGKTYVGLKIVQALLTNQDAWQRTDQNSPILVVCYTNHALDQFLEGI
XP_027328665.1   809  LTKELAIIQGPPGTGKTYVGLKIVQALLTNKNVWQTTVQNSPILVVCYTNHALDQFLEGI
XP_013053947.1   697  LTKELAIIQGPPGTGKTYVGLKIVQALLTNKHVWQTTVQNSPILVVCYTNHALDQFLEGI
NP_066363.1      610  LTRELAIIQGPPGTGKTYVGLKIVQALLTNESVWQISLQKFPILVVCYTNHALDQFLEGI

XP_015152165.1   783  YTFQKRGIVRVGGRSNSEILKQFTLKELRKKSEFRHNLPMHLRRAYVNITCDMKHAEEEL
XP_027328665.1   869  YTFQKHGMVRVGGRSSSEVLKQFTLRELRKKCEFRHNLPMHLRRAYVNITSQMKQAEEEL
XP_013053947.1   757  YTFQKHGMVRVGGRSSSEVLKQFTLRELRKKCEFRHNLPMHLRRAYVNITSQMKQAEEEL
NP_066363.1      670  YNCQKTSIVRVGGRSNSEILKQFTLRELRNKREFRRNLPMHLRRAYMSIMTQMKESEQEL

XP_015152165.1   843  YKGAKHLECTTYGVLHERHLEAFIAPQHWDSLMSGL--DDDEFYYSASRHSMILEWLGLG
XP_027328665.1   929  HKGAKHLECTTHGVLHERHLEACIAPQHWDSLMKGL--DHEEFYYSAAQHSVILEWLGLG
XP_013053947.1   817  HKGAKHLECTTYGVLHERHLEACIAPQHWDSLMKGL--DHEEFYYSAAQHSVILEWLGLG
NP_066363.1      730  HEGAKTLECTMRGVLREQYLQKYISPQHWESLMNGPVQDSEWICFQHWKHSMMLEWLGLG

XP_015152165.1   901  FTAFTQSAARNIEAENLGDQQEEREEEQEGEAEEDLLEILEEADLIQADRVIDDEDSAKA
XP_027328665.1   987  VTVFTQSAAEDIEAENPGGQQ-EREEEQEGEAEE-LLEIPEEADLIQADRVIEDEEAAKP
XP_013053947.1   875  VTVFTQSAAEDIEAENPGGQQ-EREEEQEGEAEE-LLEIPEEADLIQADRVIEDEEAAKP
NP_066363.1      790  VGSFTQSVSPA-GPENT-AQA-EGDEEEGEEESSLIEIAEEADLIQADRVIEEEVVRP
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XP_015152165.1  961  QRRKEEEHRAVHELAGMLLAMKLENEEEETVQPQ-QKSAQWEITSSQRKKMKHKMKVELH
XP_027328665.1 1045  QKRKEEEHRAVRELASVLLAMKLENEEEGTAQPQ-QKTVQWEITATQRKKMKQKMRVELC
XP_013053947.1  933  QKRKEEEHRAVRELASVLLAMKLENEEEGTAQPQ-QKTVQWEITASQRKKMKQKMRVELR
NP_066363.1     847  QRRKKEESGADQELAKMLLAMRLDHCGTGTAAGQEQATGEWQTQRNQKKKMKKRVKDELR

XP_015152165.1 1020  KLNAMSETEAYAIQDLWQLDMNSRWRLYRLWLQTYQGLIRRKILQHEQQYQAAAERLAEL
XP_027328665.1 1104  KLSAMTELEAKSIQDLWQLDLSSRWRLYRLWLQTYQGFIRRRILQHEQQYQAAAERLAEL
XP_013053947.1  992  KLSAMTELEAKSIQDLWQLDLSSRWRLYRLWLQTYQGFIRRRILQHEQQYQAAAERLAEL
NP_066363.1     907  KLNTMTAAEANEIEDVWQLDLSSRWQLYRLWLQLYQADTRRKILSYRQYRTSAERMAEL

XP_015152165.1 1080  RLQEDLCILKEAKVVGMTTTGAAKYRQILQKVEPRIVIVEEAAEVLEAHTITTLSKACQH
XP_027328665.1 1164  RLQEDLCILKEAKVVGMTTTGAAKYRQILQKVEPRIVIVEEAAEVLEAHTITTLSKACQH
XP_013053947.1 1052  RLQEDLCILKEAKVVGMTTTGAAKYRQILQKVEPRIVIVEEAAEVLEAHTITTLSKACQH
NP_066363.1     967  RLQEDLHILKDAQVVGMTTTGAAKYRQILQKVEPRIVIVEEAAEVLEAHTIATLSKACQH

XP_015152165.1 1140  LILIGDHQQLQPSANVYDLAKNFNLEVSLFERLVKVDFPFVCLKYQHRMRPEIAQLLSPH
XP_027328665.1 1224  LILIGDHQQLQPSANVYDLAKNFNLEVSLFERLVKVDFPFVRLKYQHRMRPEIAQLLSPH
XP_013053947.1 1112  LILIGDHQQLQPSANVYDLAKNFNLEVSLFERLVKVNFPFVRLKYQHRMRPEIAQLLSPH
NP_066363.1    1027  LILIGDHQQLRPSANVYDLAKNFNLEVSLFERLVKVNIPFVRLNYQHRMCPEIARLLTPH

XP_015152165.1 1200  IYQDLENHPSVLKYENVKGVLSNLFFVEHDFPEQVIQEGRSHQNIHEAQFVVELCKYFLC
XP_027328665.1 1284  IYQELENHPSVLKYENIKGVLSNLFFVEHDFPEQEIQEGKSHQNPHEARFVVELCKYFLC
XP_013053947.1 1172  IYQELENHPSVLKYENIKGVLSNLFFVEHDFPEQEIQEGKSHQNPHEAQFVVELCKYFLC
NP_066363.1    1087  IYQDLENHPSVLKYEKIKGVSSNLFFVEHNFPEQEIQEGKSHQNQHEAHFVVELCKYFLC

XP_015152165.1 1260  QDYQPSQITILTTYTGQLFCLRKLMPAKTFAGVKVYVVDKYQGEENDIILLSLVRSNKEE
XP_027328665.1 1344  QDYLPSQITILTTYTGQLFCLRKLMPAKTFAGVKVYVVDKYQGEENDIILLSLVRSNKEE
XP_013053947.1 1232  QDYLPSQITILTTYTGQLFCLRKLMPAKTFAGVKVYVVDKYQGEENDIILLSLVRSNKEE
NP_066363.1    1147  QEYLPSQITILTTYTGQLFCLRKLMPAKTFAGVRVHVVDKYQGEENDIILLSLVRSNQEG
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XP_015152165.1  1320  RIGFLQIPNRICVALSRAKKGLYCIGNMRMLGKVPLWSKIIHTLREKGNIGRSLTLCCQN
XP_027328665.1  1404  RTGFLQIPNRICVALSRAKKGLYCIGNMRMLGKVPLWSKIIHTLREKGNIGRSLILCCQN
XP_013053947.1  1292  RTGFLQIPNRICVALSRAKKGLYCIGNMRMLGKVPLWSKIIHTLREKGNIGRSLMLCCQN
NP_066363.1     1207  KVGFLQISNRICVALSRAKKGMYCIGNMQMLAKVPLWSKIIHTLRENNQIGPMLRLCCQN

XP_015152165.1  1380  HPETITSVSTAADFSKVPEGGCSHPCEFRLDCGHVCTRACHPYDLQHKKYQCLKPCQKVL
XP_027328665.1  1464  HPETKTLVSTAADFSKVPEGGCSHPCEFRLSCGHVCTRACHPYDTQHKKYQCLKPCQKVL
XP_013053947.1  1352  HPETKTLVSTAADFSKVPEGGCSHPCEFRLSCGHVCTRACHPYDAQHKKYQCLKPCQKVL
NP_066363.1     1267  HPETHTLVSKASDFQKVPEGGCSLPCEFRLGCGHVCTRACHPYDSSHKEFQCMKPCQKVI

XP_015152165.1  1440  CTEGHRCPLLCYEPCGPCMVIVEKIVPKCGHLQMIPCSCPGSKFICQEPCKKKLNCGHTC
XP_027328665.1  1524  CAKGHRCQQSCYEPCGPCMVIVEKTISKCGHLQMVPCSCPDSEFVCQEPCQKKLNCGHTC
XP_013053947.1  1412  CTKGHRCLQSCYEPCGPCMVIVEKTISKCGHLQMVPCSCPDSEFVCQEPCQKKLNCGHTC
NP_066363.1     1327  CQEGHRCPLVCHQECQPCQVKVPKTIPRCGHEQMVPCSVPESDFCCQEPCSKSLRCGHRC

XP_015152165.1  1500  NKCCGQECTTRCPELVTVFLQCGHRQKVQCWITDATKHQ-KSVECMAKCSVKLECGHECS
XP_027328665.1  1584  NRFCGQECTTRCPELVKVTLQCGHTQKVKCWITEEMKHG-KPVECKTKCSVTLECGHACS
XP_013053947.1  1472  NRFCGQECTARCPELVEVTLQCGHSQQVKCWITEEMKHG-KPVECRTKCSVTLECGHVCS
NP_066363.1     1387  SHPCGEDCVQLCSEMVTIKLKCGHSQPVKCGHVEGLLYGGLLVKCTTKCGTILDCGHPCP

XP_015152165.1  1559  GSCHTCFGGRFHKPCKSPCKRYLICSHKCQQPCTTECPPCQLDCQNHCVHSRCKKKCGER
XP_027328665.1  1643  GSCHTCFEGRFHKPCSSPCKRFLVCSHKCQQPCTVECPPCQLDCQNHCVHSRCKKKCGER
XP_013053947.1  1531  GSCHTCFEGRFHKPCSSPCKRFLVCSHKCRQPCTVECPPCQLDCQNHCVHSRCKKKCGER
NP_066363.1     1447  GSCHSCFEGRFHERCQQPCKRLLICSHKCQEPCIGECPPCQRTCQNRCVHSQCKKKCGEL

XP_015152165.1  1619  CSPCAEPCEWRCKHYQCTNLCHEPCNRPRCNIPCTKLLRCGHPCIGFCGEPCPKKCLVCD
XP_027328665.1  1703  CFPCVEPCEWQCQHYQCTNLCSEPCNRPRCDVPCTKLLRCGHPCIGLCGEPCPNKCLVCD
XP_013053947.1  1591  CFPCVEPCEWRCQHYQCTNLCSEPCNRPRCNVPCTKLLRCGHPCIGLCGEPCPKKCLVCD
NP_066363.1     1507  CSPCVEPCVWRCQHYQCTKLCSEPCNRPPCYVPCTKLLVCGHPCIGLCGEPCPKKCRICH
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XP_015152165.1  1679  REEVTQIFFGFEDDEDARFVQLEDCGHIFESQGLDRYMDED--DD-VIKLKVCPTCQTPV
XP_027328665.1  1763  HEEVTQIFFGFEEDPDARFVQLEDCGHVFESQGLDHYMDED--DD-VVKLKVCPVCQTPV
XP_013053947.1  1651  HEEVTQIFFGFEEDPDARFVQLEDCGHVFESQGLDHYMDED--DD-VIKLKVCPVCQTPV
NP_066363.1     1567  MDEVTQIFFGFEDPDARFVQLEDCSHIFEVQALDRYMNEQKDDEVAIRLKVCPICQVPI

XP_015152165.1  1736  RKSLRYGTIVKKHLVEIEKVKEKIQGPAREIESSRRRLQAALTSKSVLKRNLLTKYLMLE
XP_027328665.1  1820  RKNLRYGTIVKRRLDEIEKVKEKIQGPAQEIESSRQRLQAALIGNAVLQRNLPHKYLMLE
XP_013053947.1  1708  RKNLRYGTIVKRRLDEIEKVKEKIQGPAQEIESSRRRLQAALIGNAVLQRNLPHKYLMLE
NP_066363.1     1627  RKNLRYGTSIKQRLEEIEIIKEKIQGSAGEIATSQERLKALLERKSLLHQLLPEDFLMLK

XP_015152165.1  1796  DQLNASDLSIKSIGVIENQLNFYERLADLTSSLSKIDEKEQKGMKKRLDEVQEWLDRPRL
XP_027328665.1  1880  DKLKASDLSIKSIGLIENQLNFYKRVADLTDSMSKIDVNERKGLKKRLDEVQEWLDMPRI
XP_013053947.1  1768  DKLKASDLSIKSIGLIENQLNFYKRVADLTDSMSKIDVNERKGLKKRLDEVQEWLDLPRI
NP_066363.1     1687  EKLAQKNLSVKDLGLVENYISFYDHLASLWDSLKKMHVLEEKRVRTRLEQVHEWLAKKRL

XP_015152165.1  1856  SFTRQELMDLQAEIQRLTYLQHLLSRCKGRSGMITTTLAAKIATVREILEGTKRFTEKEE
XP_027328665.1  1940  SFTGQELSDLQAEIQRLTLLQSLLSRCKSASGMITTALAAEIACVREILEGTKKFTEADE
XP_013053947.1  1828  SFTGQELSDLQAEIQRLTFLQSLLSRCKSASGMITAALAAEIASVREILEGTKKFTKADE
NP_066363.1     1747  SFTSQELSDLRSEIQRLTYLVNLLTRYKIAEKKVKDSIAVEVYSVQNILEKTCKFTQEDE

XP_015152165.1  1916  AAVKAELKHISAALPLSGLGITEAERVQIVSAIGCPRGHWFKCKNGHVYVIGDCGGAMER
XP_027328665.1  2000  AAVKAQLERLCTALPVSGLGISEAERVQIVRAIGCPRGHWFKCRNGHIYVIGECGGAMER
XP_013053947.1  1888  AAVKAELERLCTALPVSGLGISEAERVQIVRAIGCPRGHWFKCRNGHIYVIGECGGAMER
NP_066363.1     1807  QLVQEKMEALKATLPCSGLGISEEERVQIVSAIGYPRGHWFKCRNGHIYVIGDCGGAMER

XP_015152165.1  1976  SRCPECHEVIGGANHALDSTNSLAPEMDGATHAAWSETANNLLNFQDLQRLL
XP_027328665.1  2060  SRCPECHAVIGGTNHALDSTNSLAPEMDGATHAAWSETANNLLNFEELRLLL
XP_013053947.1  1948  SKCPECHAVIGGTNHTLDSTNSLAPEMDGATHAAWSEAANNLLNFEELRRLL
NP_066363.1     1867  GTCPDCKEVIGGTNHTLERSNQLASEMDGAQHAAWSDTANNLMNFEETQGMM
```

Figure S14: The protein sequences of chicken, mallard, goose and human ZNFX1 aligned using the ClustalW program. The armadillo, P-loop and zinc finger domains are indicated below the sequence in black line, blue line, and red line respectively.

```
XP_419881.4      1    MEETAAGRGQRRQRAARPRATRGRGIAPRRGSTAREASADEQPAD-----EASRAVV---
XP_027310983.1   1    MEGPG----GRRQRAVRSKGSAGRGSSC------------GCEPEREGGPAGSGRCR---
XP_013027663.1   1    MLSLK----L--KKGVTSGHCCSPQQSC-----------NASE-----------------
NP_612450.2      1    MQPWH---GKAMQRASEAGATAPKASARNA--------RGAPMDPTESPAAPEAALPKA


XP_419881.4      53   -------------PAR-TAQGGE-----------------------------------PP
XP_027310983.1   43   -------------PARAAPGGCR-----------------------------------RP
XP_013027663.1   27   -----------------------------------------------------------
NP_612450.2      49   GKFGPARKSGSRQKKSAPDTQERPPVRATGARAKKAPQRAQDTQPSDATSAPGAEGLEPP


XP_419881.4      64   VPR------------------------------------------ILSARSRAAGGLRLREV
XP_027310983.1   55   GGSAE-------------------------------------SGGEAAVAVPPLRLRAV
XP_013027663.1   27   -----------------------------------------------------------
NP_612450.2      109  AAREPALSRAGSCRQRGARCSTKPRPPPGPWDVPSPGLPVSAPILVRRDAAPGASKLRAV


XP_419881.4      84   LSQLSLGRQDVSEASGLVNHVVSHLIQAVRGRDGSFSSIRRLGAGSYYEHVKISEPNEFD
XP_027310983.1   77   LSQLSLGRRDVSEASGLVNQVVSHLIQAIRGRDGCFGIISRLGAGSYYERVKISEPNEFD
XP_013027663.1   27   --------------------------------PEISSYFTPDVANTPRHSQISEPNEFD
NP_612450.2      169  LEKLKLSRDDISTAAGMVKGVVDHLLLRLK-CDSPERGVGLLNTGSYYEHVKISAPNEFD


XP_419881.4      144  IMLVMPVTRIQLDESDDTGAYYYLTFKRNPKEKYLNRFLDEDGKLSAFKMLEDLRFIIKE
XP_027310983.1   137  IMLVMPIARIQLDECDDTGAYYYLTFKRNPKEKYLNRFLDEDGKLSADKMLTALRKIIKE
XP_013027663.1   54   IMLVMPVTRIQLDECDDTGAYYYLTFKRNPKEKYLNRFLDEDGKLSAIKMRTALKKIIKE
NP_612450.2      228  VMFKLEVPRIQLEYSNTRAYYFVKFKRNPKENPLSQFLEG-EILSASKMLSKFRKIIKE


XP_419881.4      204  ELKHIKNVEVTVKRKKRGSPAITLLIKKPPAEISVDIILALEVQQSWPPSTQDGLNIECW
XP_027310983.1   197  EVKNIKDVEVTVKRFKARSPAITLLIKNSSAEISVDIILALEVQQSWPPSTQDGLNIERW
XP_013027663.1   114  EVKNIKDVEVTVKRMKAGSPAITLLIKKSSAEISVDIILALEVQQSWPLSTQDGLNIERW
NP_612450.2      287  EINDIKDTDVIMKRKRGGSPAVTLLIS---EKISVDITLALESKSSWPASTQEGLRIQNW


XP_419881.4      264  LGRKVRREFRYKPIYLVAKQNKKEKLPRGNTWRLSFSHIEKAMINNHGSIKTCCESDGVK
XP_027310983.1   257  LGRKVRRELRNKPIYLVAKQNKKEVPRGNTWRISFSHIEKAMMNNHGSIKTCCETDGAK
XP_013027663.1   174  LGRKVRRELRNKPIYLVAKQNKKEVLTGNTWRLSFSHIEKAMMNNHGSIKTCCETDGAK
NP_612450.2      344  ISAKVRKQLRLKPFYLVPKHAKEGNGFQEETWRLSFSHIEKEIINNHGKSKTCCENKEEK


XP_419881.4      324  CCRKDCLKLLKYLLERLKM--KHAKELEKFCSYHVKTAFFHSCVTWPSDTDWQHENLEHC
XP_027310983.1   317  CCRKDCLKLLKYLLEKLKM--KYTKELEKFCSYHVKTAFFHSCVIWPNDTDWQYENLEHC
XP_013027663.1   234  CCRKDCLKLLKYLLEKLKM--KHAKELEKFCSYHVKTAFFHSCVIWPNDTDWQYENLEHC
NP_612450.2      404  CCRKDCLKLMKYLLEQLKERFKDKKHLDKFSSYHVKTAFFHVCTQNPQDSQWDRKDIGLC


XP_419881.4      382  FQKYLEYFLRCLQDSQLPHFFIPQYNLLSI--DDKASNDFLLGQINYQLNNGFPVFHQV-
XP_027310983.1   375  FQNYLGYFLRCLQDSQLPHFFIPQYNLLSP--DDKASNHFLSRQINDQLNNRFPIFQQGY
XP_013027663.1   292  FQNFLGYFLRCLQDSQLPHFFIPQYNLLSI--DDKASNFLSRQINYQLNNGFPIFQQIK
NP_612450.2      464  FDNCVTYFLQCLRTEKLENYFIPEFNLFSSNLIDKRSKEFLTKQIEYERNNEFPVFDEF-


XP_419881.4           --------------------
XP_027310983.1   433  --------------------
XP_013027663.1   350  KVIYSNYLKANHVDLHTVKHV
NP_612450.2           --------------------
```

Figure S15: The protein sequences of chcGAS, ducGAS, gocGAS, hucGAS aligned using the ClustalW program. Conserved amino acids and synonymous substitutions are shadowed in black and gray, respectively. The N-terminal tail, spine, activation loop, zinc finger and conserved catalytic residues are indicated below the sequence in black line, orange line, blue line, green line and black triangles respectively. The red and purple lines underneath indicate α/β core and helix bundle respectively. Catalytic residues are highlighted with black triangles. Conserved leucine involved in dsDNA binding is highlighted with grey triangle.

```
XP_025010645.1    1  MPQDPST-------------------------------------------------------
XP_027323921.1    1  MSQEQR--------------------------------------------------------
XP_013057484.1    1  MSQPAASPCAAQGRIPAGQGTSWKFSVGGLPRLHPLPAPAIAPFIFTSLLIGFSGTMRLC
NP_938023.1       1  MPHSSLH-------------------------------------------------------


XP_025010645.1    8  ---RSSPARLLIPEPRAGRARHAACVLLAVCFVVLILSGEPLAPIIRSVCIQLAALQLGV
XP_027323921.1    8  ---RSSPAALLIPKPREGRAQRAVYVLLATCTVALCIAGEPLSPAAHRVSAHLAALQIGA
XP_013057484.1   61  PRHREQAQALLAAAASEGRRKRCLSGLGA----------AHSARSARSPGSSQCRGR
NP_938023.1       8  ---------PSIPCPRGHGAQKAALVLLSACLVTLWGLGEPPEHILRYIVLHLASLQLGL


XP_025010645.1   65  LL---------KGCCCLAEEIFHLHSRHHGSL-----------------WQ-VLCSCFP-
XP_027323921.1   65  LL---------KGCCCLAEEIFHLQSRYRGSF-----------------WR-ALSACFP-
XP_013057484.1  108  GRSDVSGTAAPEQPHCL----AHPQGQGRASAARGVRPPGHLHRGAVPGWGAPVTRCPP-
NP_938023.1      59  LL---------NGVCSLAEELRHIHSRYRGSY-----------------WR-TVRACLGC


XP_025010645.1   97  PRWYL--------ALLLVGGSAYLDPPEDNGHSPRLALTLSCLCQLLVLALGLQKLSAV
XP_027323921.1   97  PRWHL--------ALLLVGGSAYLDLQQGERLSP--HLALICLCHLLALALGLQKPSAV
XP_013057484.1  163  PHRPPGSPADRDLAQGLLLPGRGDLP-------------------------------PPV
NP_938023.1      92  PLREG--------ALLLLSIYFYYSLPNAVGPPFTWMLALLGLSQALNILLGLKGLAPA


XP_025010645.1  148  EVS-ELTESSKKNVAHGLAWSYYI----G----------------------YLKVVLPR
XP_027323921.1  146  EIS-EVTERSQNVAHGLAWSYYV----G----------------------YLKIVLPR
XP_013057484.1  192  QTPRQILEGAERVLPTTLAPGPAVHRWLSLPGPAAGRQAQPLPCPDLPVPSPRPRPRAPG
NP_938023.1     143  EIS-AVCEKGNFNVAHGLAWSYYI----G----------------------YLRLILPE


XP_025010645.1  180  IKECMEELSRTNPMIRAHRETWKLHILVPLGCDLWDDLEKADSNIQYLADLPETILTRAG
XP_027323921.1  178  IKECMEEISRANLNVWACRETWKLHILIPLSCNVWDDLEKADSNIQYLTDLTETTLTRGG
XP_013057484.1  252  IKESMEEISKANPNVQACRETWKLHILIPLSCNVWDDLEKADSNIQYLTDLTETTLTRGG
NP_938023.1     175  LQARIRTYNQHYNNILRGAVSQRLYILLPLDCGVPDNLSMADPNIRFLDKLPQQTGDHAG


XP_025010645.1  240  IKKRVYKHSLYVIRDKDNKLRPCVLEEASPLQTICAMSQDDCAAFSREQRLEQARLFYRS
XP_027323921.1  238  IKKRVYKHSLYAIRDGDNQARHCAVEFATPLQTLYAMSQDECAAFSRDDRLEQAKLFYRT
XP_013057484.1  312  IKKRVYKHSFYAIRDGDNQARHCAVEYATPLQTLYAMSQDECAAFSRDDRLEQAKLFYRT
NP_938023.1     235  IKDRVYSNSIYELLENGQRAGTCVLEYATPLQTLEAMSQYSQACFSREDRLEQAKLFCRT


XP_025010645.1  300  LRDILGSSKECAGLYRLIAYEEPAEPESHFLSGLILWHLQQQQREEYMVQEELPL-----
XP_027323921.1  298  LEDILRGSKECAGTYRLIAYEELVEAEPHFLSREILWHLRQQQQEEFTVYEGSPPRTLAT
XP_013057484.1  372  LEDILRGSKECTGTYRLIAYEEPREAEPHFLSREILWHLRQQQQEEFTVYEGTPPRTLAT
NP_938023.1     295  LEDILADAPESQNNCRLIAYQEPADDSSFSLSQEIIRHLRQEEKEEVTVGSLKTSAVPST


XP_025010645.1  355  CTSSVELSLQVSSSDLPQPLRSDCP
XP_027323921.1  358  ALGSTDLSLQISASDLPQPLRSDHP
XP_013057484.1  432  ALGSTDLSLQISASDLPQPLRSDHP
NP_938023.1     355  STMSQEPELLISGMEKELPLRIDFS
```

Figure S16: The protein sequences of chSTING, duSTING, goSTING and huSTING aligned using the ClustalW program. Conserved amino acids and synonymous substitutions are shadowed in black and gray, respectively. The TM domains 1, 2, 3, and 4 are indicated below the sequence in black lines. The cyclic dinucleotide binding domain and C-terminal tail are underscored by orange and grey lines respectively. Residues involved in cyclic dinucleotide binding are highlighted using black triangles. pLxIS motif is underscored in blue

```
NP_001185786.1     1  MNSLEQAEDLKAFERRLTEYIACLQPATGRWRMILIVVSVCTATGAWNWLIDPETQKVSF
XP_027323010.1     1  MNSLEQAEDLKAFERRLTEYIACLQPATGRWRTILIVVSVCTATGAWNWLIDPETQKVSF
XP_013042385.1     1  MI----IADLKAFERRLTEYIACLQPATGRWRMILIVVSVCTATGAWNWLIDPETQKVSF
NP_694993.2        1  MNSLEQAEDLKAFERRLTEYIHCLQPATGRWRMLLIVVSVCTATGAWNWLIDPETQKVSF
                                                                   _____

NP_001185786.1    61  FTSLWNHPFFTISCITLIGLFFAGIHKRVVAPSIIAARCRTVLAEYNMSCDDTGKLILKP
XP_027323010.1    61  FTSLWNHPFFTISCITLIGLFFAGIHKRVVAPSIIAARCRTVLAEYNMSCDDTGKLILKP
XP_013042385.1    57  FTSLWNHPFFTISCITLIGLFFAGIHKRVVAPSIIAARCRTVLAEYNMSCDDTGKLILKP
NP_694993.2       61  FTSLWNHPFFTISCITLIGLFFAGIHKRVVAPSIIAARCRTVLAEYNMSCDDTGKLILKP
                         _____

NP_001185786.1   121  RPHVQ
XP_027323010.1   121  RPHVQ
XP_013042385.1   117  RPHVQ
NP_694993.2      121  RPHVQ
```

Figure S17: The ERADp protein sequences of chicken, duck, goose and human aligned using the ClustalW program. Conserved amino acids and synonymous substitutions are shadowed in black and gray, respectively. The transmembrane (TM) domains 1 and 2 are indicated below the sequence in black lines. Sequences preceding TM1 and after TM2 comprise N- and C-terminal regions respectively.

```
NP_001336637.1   355   TIFSYFKGQRQTLLFSATMPKKIQNFAKSALVKPITINVGRAGAASLDVVQEVEYVKEEA
XP_027324165.1   356   TIFSYFKGQRQTLLFSATMPKKIQNFAKSALVKPITINVGRAGAASLDVVQEVEYVKEEA
XP_013047316.1   234   TIFSYFKGQRQTLLFSATMPKKIQNFAKSALVKPITINVGRAGAASLDVVQEVEYVKEEA
NP_057306.2      360   TIFSYFKGQRQTLLFSATMPKKIQNFAKSALVKPVTINVGRAGAASLDVIQEVEYVKEEA


NP_001336637.1   415   KMVYLLECLQKTPPPVLIFAEKKADVDAIHEYLLLKGVEAVAIHGGKDQEERTKAIEAFR
XP_027324165.1   416   KMVYLLECLQKTPPPVLIFAEKKADVDAIHEYLLLKGVEAVAIHGGKDQEERTKAIEAFR
XP_013047316.1   294   KMVYLLECLQKTPPPVLIFAEKKADVDAIHEYLLLKGVEAVAIHGGKDQEERTKAIEAFR
NP_057306.2      420   KMVYLLECLQKTPPPVLIFAEKKADVDAIHEYLLLKGVEAVAIHGGKDQEERTKAIEAFR


NP_001336637.1   475   DGKKDVLVATDVASKGLDFPAIQHVINYDMPEEIENYVHRIGRTGRSGNTGIATTFINKA
XP_027324165.1   476   DGKKDVLVATDVASKGLDFPAIQHVINYDMPEEIENYVHRIGRTGRSGNTGIATTFINKA
XP_013047316.1   354   DGKKDVLVATDVASKGLDFPAIQHVINYDMPEEIENYVHRIGRTGRSGNTGIATTFINKA
NP_057306.2      480   EGKKDVLVATDVASKGLDFPAIQHVINYDMPEEIENYVHRIGRTGRSGNTGIATTFINKA


NP_001336637.1   535   CDESVLMDLKALLLEAKQKVPPVLQVLHCGDETMLDIGGERGCAFCGGLGHRITDCPKLE
XP_027324165.1   536   CDESVLMDLKALLLEAKQKVPPVLQVLHCGDETMLEIGGERGCAFCGGLGHRITDCPKLE
XP_013047316.1   414   CDESVLMDLKALLLEAKQKVPPVLQVLHCGDETMLEIGGERGCAFCGGLGHRITDCPKLE
NP_057306.2      540   CDESVLMDLKALLLEAKQKVPPVLQVLHCGDESMLDIGGERGCAFCGGLGHRITDCPKLE


NP_001336637.1   595   AMQTKQVSNIGRKDYLAHSSMDF
XP_027324165.1   596   AMQTKQVSNIGRKDYLAHSSMDF
XP_013047316.1   474   AMQTKQVSNIGRKDYLAHSSMDF
NP_057306.2      600   AMQTKQVSNIGRKDYLAHSSMDF
```

Figure S18: Schematic alignment of DDX41 protein sequences of chicken, duck, goose and human. Depicted are DEAD box region, HelicC and zinc finger domains in black, red and green underlining respectively. The DEAD box is boxed in blue.

```
XP_025002966.1    1  MPRG----DRESDWREKEQFRKLFIGGLSFETTEESLRNYYEQWGKLTDCVVMRDPASKR
XP_021129883.1    1  MET--------SKEREKEQFRKLFIGGLSFETTEESLRNYYEQWGKLTDCVVMRDPASKR
XP_013027335.1    1  MET--------SKEREKEQFRKLFIGGLSFETTEESLRNYYEQWGKLTDCVVMRDPASKR
NP_112533.1       1  MEKTLETVPLERKKREKEQFRKLFIGGLSFETTEESLRNYYEQWGKLTDCVVMRDPASKR

XP_025002966.1   57  SRGFGFVTFSSMAEVDAAMAARPHTIDGRVVEPKRAVAREESGKPGAHVTVKKLFVGGIK
XP_021129883.1   53  SRGFGFVTFSSMAEVDAAMAARPHTIDGRVVEPKRAVAREESGKPGAHVTVKKLFVGGIK
XP_013027335.1   53  SRGFGFVTFSSMAEVDAAMAARPHTIDGRVVEPKRAVAREESGKPGAHVTVKKLFVGGIK
NP_112533.1      61  SRGFGFVTFSSMAEVDAAMAARPHSIDGRVVEPKRAVAREESGKPGAHVTVKKLFVGGIK

XP_025002966.1  117  EDTEEHHLRDYFEEYGKIDTIEIITDRQSGKKRGFGFVTFDDHDPVDKIVLQKYHTINGH
XP_021129883.1  113  EDTEEHHLRDYFEEYGKIDTIEIITDRQSGKKRGFGFVTFDDHDPVDKIVLQKYHTINGH
XP_013027335.1  113  EDTEEHHLRDYFEEYGKIDTIEIITDRQSGKKRGFGFVTFDDHDPVDKIVLQKYHTINGH
NP_112533.1     121  EDTEEHHLRDYFEEYGKIDTIEIITDRQSGKKRGFGFVTFDDHDPVDKIVLQKYHTINGH

XP_025002966.1  177  NAEVRKALSRQEMQEVQNSRSGRGGNFGFGDARGGGGNFGPGPGSNFRGGAGKTDGYGSG
XP_021129883.1  173  NAEVRKALSRQEMQEVQNSRSGRGGNFGFGDARGGGGNFGPGPGSNFRGGAGKTDGYGSG
XP_013027335.1  173  NAEVRKALSRQEMQEVQNSRSGRGGNFGFGDARGGGGNFGPGPGSNFRGGAGKTDGYGSG
NP_112533.1     181  NAEVRKALSRQEMQEVQSSRSGRGGNFGFGDSRGGGGNFGPGPGSNFRGG---SDGYGSG

XP_025002966.1  237  RGFGDGYNGYGGGPGGGNFGGSPGYGGGRGGYGGGGPGYGNQGGGYGGGYDNYGGGNYGS
XP_021129883.1  233  RGFGDGYNGYGGGPGGGNFGGSPGYGGGRGGYGGGGPGYGNQGGGYGGGYDNYGGGNYGS
XP_013027335.1  233  RGFGDGYNGYGGGPGGGNFGGSPGYGGGRGGYGGGGPGYGNQGGGYGGGYDNYGGGNYGS
NP_112533.1     238  RGFGDGYNGYGGGPGGGNFGGSPGYGGGRGGYGGGGPGYGNQGGGYGGGYDNYGGGNYGS

XP_025002966.1  297  GNYNDFGNYNQQPSNYGPMKSGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY
XP_021129883.1  293  GNYNDFGNYNQQPSNYGPMKSGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY
XP_013027335.1  293  GNYNDFGNYNQQPSNYGPMKSGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY
NP_112533.1     298  GNYNDFGNYNQQPSNYGPMKSGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY
```

Figure S19: Schematic alignment of hnRNPA2B1 protein sequences of chicken, duck, goose and human. Depicted are RNA recognition motif domains 1 and 2 in black, and prion-line domain in grey underlining respectively. Note: Amino acids critical for hnRNPA2B1 dimerization (P93, K94, R95, V184, R185, K186; human numbering) and methylation (R238) are conserved across human and avian