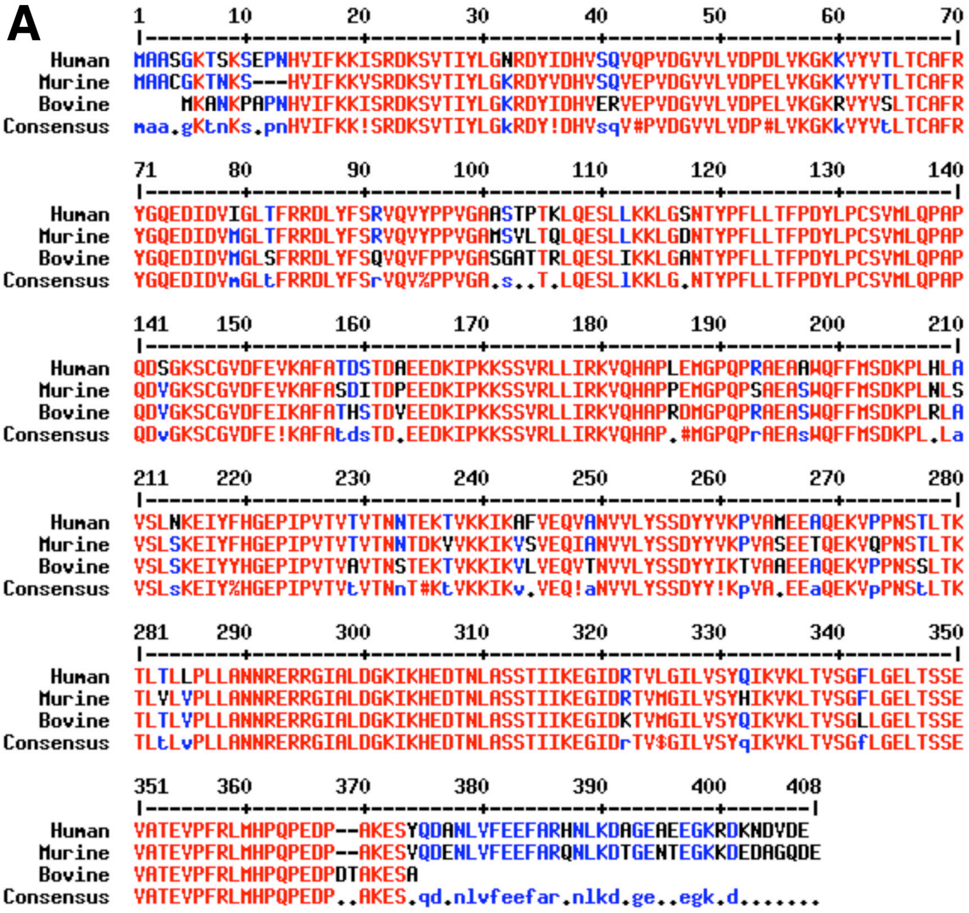
A



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          1       10        20        30        40        50        60        70
          |--------+---------+---------+---------+---------+---------+---------|
    Human MAASGKTSKSEPNHVIFKKISRDKSVTIYLGNRDYIDHVSQVQPVDGVVLVDPDLVKGKKVYVTLTCAFR
   Murine MAACGKTNKS---HVIFKKVSRDKSVTIYLGKRDYVDHVSQVEPVDGVVLVDPELVKGKKVYVTLTCAFR
   Bovine     MKANKPAPNHVIFKKISRDKSVTIYLGKRDYIDHVERVEPVDGVVLVDPELVKGKRVYVSLTCAFR
Consensus maa.gKtnKs.pnHVIFKK!SRDKSVTIYLGkRDY!DHVsqV#PVDGVVLVDP#LVKGKkVYVtLTCAFR

          71      80        90       100       110       120       130       140
          |--------+---------+---------+---------+---------+---------+---------|
    Human YGQEDIDVIGLTFRRDLYFSRVQVYPPVGAASTPTKLQESLLKKLGSNTYPFLLTFPDYLPCSVMLQPAP
   Murine YGQEDIDVMGLTFRRDLYFSRVQVYPPVGAMSVLTQLQESLLKKLGDNTYPFLLTFPDYLPCSVMLQPAP
   Bovine YGQEDIDVMGLSFRRDLYFSQVQVFPPVGASGATTRLQESLIKKLGANTYPFLLTFPDYLPCSVMLQPAP
Consensus YGQEDIDVmGLtFRRDLYFSrVQV%PPVGA.s..T.LQESLlKKLG.NTYPFLLTFPDYLPCSVMLQPAP

          141    150       160       170       180       190       200       210
          |--------+---------+---------+---------+---------+---------+---------|
    Human QDSGKSCGVDFEVKAFATDSTDAEEDKIPKKSSVRLLIRKVQHAPLEMGPQPRAEAAWQFFMSDKPLHLA
   Murine QDVGKSCGVDFEVKAFASDITDPEEDKIPKKSSVRLLIRKVQHAPPEMGPQPSAEASWQFFMSDKPLNLS
   Bovine QDVGKSCGVDFEIKAFATHSTDVEEDKIPKKSSVRLLIRKVQHAPRDMGPQPRAEASWQFFMSDKPLRLA
Consensus QDvGKSCGVDFE!KAFAtdsTD.EEDKIPKKSSVRLLIRKVQHAP.#MGPQPrAEAsWQFFMSDKPL.La

          211    220       230       240       250       260       270       280
          |--------+---------+---------+---------+---------+---------+---------|
    Human VSLNKEIYFHGEPIPVTVTVTNNTEKTVKKIKAFVEQVANVVLYSSDYYVKPVAMEEAQEKVPPNSTLTK
   Murine VSLSKEIYFHGEPIPVTVTVTNNTDKVVKKIKVSVEQIANVVLYSSDYYVKPVASEETQEKVQPNSTLTK
   Bovine VSLSKEIYYHGEPIPVTVAVTNSTEKTVKKIKVLVEQVTNVVLYSSDYYIKTVAAEEAQEKVPPNSSLTK
Consensus VSLsKEIY%HGEPIPVTVtVTNnT#KtVKKIKv.VEQ!aNVVLYSSDYY!KpVA.EEaQEKVpPNStLTK

          281    290       300       310       320       330       340       350
          |--------+---------+---------+---------+---------+---------+---------|
    Human TLTLLPLLANNRERRGIALDGKIKHEDTNLASSTIIKEGIDRTVLGILVSYQIKVKLTVSGFLGELTSSE
   Murine TLVLVPLLANNRERRGIALDGKIKHEDTNLASSTIIKEGIDRTVMGILVSYHIKVKLTVSGFLGELTSSE
   Bovine TLTLVPLLANNRERRGIALDGKIKHEDTNLASSTIIKEGIDKTVMGILVSYQIKVKLTVSGLLGELTSSE
Consensus TLtLvPLLANNRERRGIALDGKIKHEDTNLASSTIIKEGIDrTV$GILVSYqIKVKLTVSGfLGELTSSE

          351    360       370       380       390       400     408
          |--------+---------+---------+---------+---------+-------|
    Human VATEVPFRLMHPQPEDP--AKESYQDANLVFEEFARHNLKDAGEAEEGKRDKNDVDE
   Murine VATEVPFRLMHPQPEDP--AKESVQDENLVFEEFARQNLKDTGENTEGKKDEDAGQDE
   Bovine VATEVPFRLMHPQPEDPDTAKESA
Consensus VATEVPFRLMHPQPEDP..AKES.qd.nlvfeefar.nlkd.ge..egk.d.......
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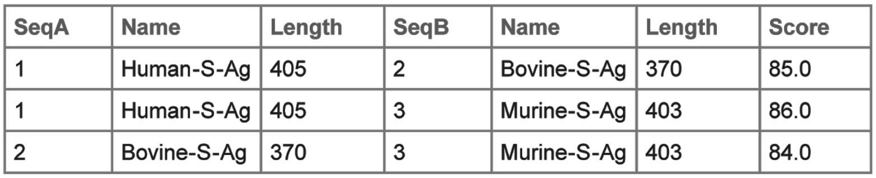
B



SeqA	Name	Length	SeqB	Name	Length	Score
1	Human-S-Ag	405	2	Bovine-S-Ag	370	85.0
1	Human-S-Ag	405	3	Murine-S-Ag	403	86.0
2	Bovine-S-Ag	370	3	Murine-S-Ag	403	84.0

Supplementary Figure 2:

Multiple sequence alignment of S-Antigen (retinal arrestin) protein. Protein sequences of murine (NP_033144), human (NP_000532) and bovine (NP_851343) species were aligned using (A) MultAlin program (http://bioinfo.genopole-toulouse.prd.fr/multalin/multalin.html). Amino acid residues in red color indicate highly conserved sequences, in blue indicate sequences with consensus and in black indicate variations from consensus. (B) Percentage of homology (given as Score) between the three different sequences as calculated by ClustalW tool (http://www.ebi.ac.uk/Tools/clustalw2/index.html).