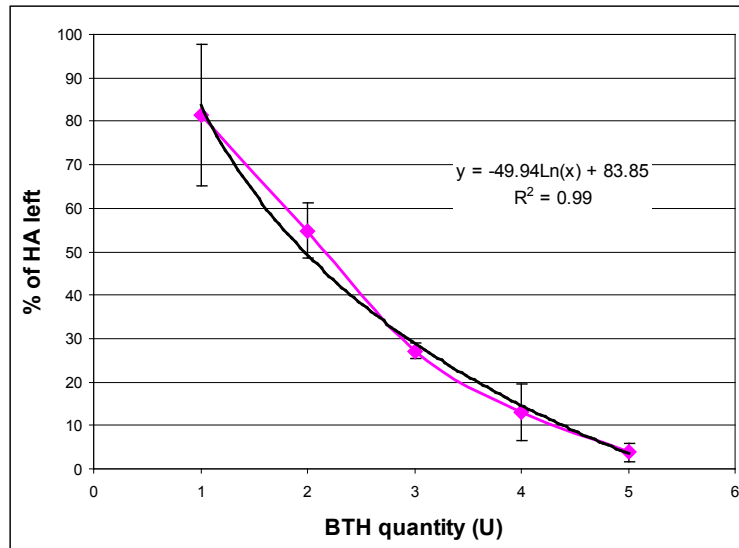




Supplementary Figure S1: percentage of hyaluronic acid (HA) left as a function of bovine testicular hyaluronidase quantity in U (calculated from the specific activity value provided by the supplier) and its trend curve using a logarithmic fit.

sp Q12794 HYAL1_HUMAN	-----MAAHLPLICALFTLLDMAQGFRG----PLLPNRPFTTVWNANTQWCLER-HG	48
sp O35632 HYAL2_MOUSE	-----MRAGLGPIITLALVLEVAWAGELKPTAPPIFTGRPFVVAWNVPTQECAPR-HK	52
sp Q08169 HUGA_APIME	MSRPLVITEGMMIGVLLMLAPINALLLGFVQSTPDNNKTVREFNVYWNVPTFMCHKYGLR	60
sp P49370 HUGAA_VESVU	-----SERPKRVFNINYWNVPTFMCHQYDLY	25
Conohyal-Cn1	-----SSSDYQGSSGDDCDEGLPPDPFVRVWNHPDNCERIK---	38
	. : * **	
sp Q12794 HYAL1_HUMAN	VDVDVSVFDDVANPQGTFRGPDMTIFYSSQLGTYPYTPTG--EPVFGGLPQNASLIAHL	106
sp O35632 HYAL2_MOUSE	VPLDLRAFVDKATPNEGFFNQNTTFYYDRLGLYPRFDAAG--TSVHGGVPQNGSLCAHL	110
sp Q08169 HUGA_APIME	FEEVSEKYGILQNWMDKFRGEEIALLYDPGMFPALLKDPNGNVVARNGGVPQLGNLTKHL	120
sp P49370 HUGAA_VESVU	FDEVTN-FNIKRNSKDDFGQDKIAIFYDPGEFPALLSLKDGKYKKRNGGVPQEGITIH	84
Conohyal-Cn1	LHLPLDDYGIIFNKLRVFLGEEIQTLYDTG--PWPIYSETG--KFINGGLPQSFNHPDND	94
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sp Q12794 HYAL1_HUMAN	ARTFQDILAAIPAPDFSGLAVIDWAWRPRWAFNWDTKDIYRQSRALVQAQHPDWPAPQ	166
sp O35632 HYAL2_MOUSE	PMLKESVERYIQTQEPGGLAVIDWWRPVWVRNWQEKDVRQSSRQLVASRHPDWPSPDR	170
sp Q08169 HUGA_APIME	QVFRDHLINQIPDKSFPQGVDFSWRPIFRQNWASLQPYKKLSVEVVRREHPFWDQDR	180
sp P49370 HUGAA_VESVU	QKFIEENLDKIYPNRNFSGIGVIDFWRWRPIFRQNWGNMKIHKNFSIDLVRNEHPTWNKKM	144
Conohyal-Cn1	GETQRILKKHRPE-NFTGLGVLDFTWRAIYSTNFGPMTIYQNESVKLVKEQHPDQDKK	153
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sp Q12794 HYAL1_HUMAN	VEAVAQDQFQGAARAWMAGTLQLGRALRPRLWGFYGFPCYNIDFLS--PNTGQCPSG	224
sp O35632 HYAL2_MOUSE	VMKQAQYEFQFAARQFMLNLTLYRVKAVRPQHLWGFYLFPCYNHDYVQNWESYTGRCPDV	230
sp Q08169 HUGA_APIME	VEQEAARRFEKYGQLFMEETLKAAKRMRPAANWGYIAYPYCYNLTQNPQ---PSAQCEAT	236
sp P49370 HUGAA_VESVU	IELEASKRFEKYARFFMEETLKLAKKTRKQADWGYGYPYCFNMSPPN---LVPECDDVT	200
Conohyal-Cn1	LTKEVAEKWQQAAKDIMSRLKIAQEVMPRGHWGYLYPRTWDN-----KRD	200
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sp Q12794 HYAL1_HUMAN	IRAQNDQLGWLWGQSRALYPSIYMPAVLEGTGKSQMYVQHRVAEAFRVAVAAGD-PNLPV	283
sp O35632 HYAL2_MOUSE	EVARNQDLAWLWAEASTALFPSVYLDLTLASSVHSRNFVSFRVREALRVAHTHHANHALPV	290
sp Q08169 HUGA_APIME	TMQENDKMSWLFESDVLPSVYLRWNLTSG-ERVGLVGGRVKEALRIARQMTTSRKKVL	295
sp P49370 HUGAA_VESVU	AMHENDKMSWLFNNQNVLLPSVYVQELTPD-QRIGLVQGRVKEAVRISNNLKHS-PKVL	258
Conohyal-Cn1	TKFRNDKINWLWRQSTGLYPSIYIYDFSKTESAITKFVSDTVGEAVRVQKEFSP--PNTP	258
	. * :. : * : . * * :. : * * * :. : *	
sp Q12794 HYAL1_HUMAN	LPYVQIFYDTNHLPLDELEHSLGESAAQGAAGVVLWVS---WENTRTKESCQAIKEYM	340
sp O35632 HYAL2_MOUSE	YVFTRTPTYTRGLTGLSQVDLISTIGESAAAGSAGVIFWGD---SEDASSMETCQYLKNYL	347
sp Q08169 HUGA_APIME	PYYWYKYQDRRDTDLSTRADLEATLRKITDLGADGFIWGS---SDDINTKAKCLQFREYL	352
sp P49370 HUGAA_VESVU	SYWWVYQDETNTFLTETDVKKTFQEIIVNGGDGIIWGS---SSDVNSLSKCKRLQDYL	315
Conohyal-Cn1	IYPYVMFQTMNFIHYEDHLKISLGLSAKMGAGVVLWGTSKHYKESTRWQCCQLQEH	318
	. : :. : . * . * :. : . : * :. : :	
sp Q12794 HYAL1_HUMAN	DTTLGPFILVTSGALLCSQALCSGHGRCVRRRTSHPKALLLNPAFSFIQ--LTPGGGPL	398
sp O35632 HYAL2_MOUSE	TQLLVPIYINVSWATQYCSWTQCHGHGRCVRRNPSANTFLHLNASSFRLVPGHPTSEPQL	407
sp Q08169 HUGA_APIME	NNELGPAVKRIALNNNANDRLTVDVSVQV-----	382
sp P49370 HUGAA_VESVU	LTVLGP---IAIN-----VTEAVN-----	331
Conohyal-Cn1	RTVLGPLVKVTQMMTDCSRAICEGHGRCVHN---SHDVILGETESQRLSDLCSTRQSRF	375
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sp Q12794 HYAL1_HUMAN	SLRGALSLEDQAQMAVEFKRCRCYPGWQAPWCER-----KSMW-----	435
sp O35632 HYAL2_MOUSE	RPEGQLSEADLNLYLQKHFRQCYLGWGGEQCQRNYKGAAGNASRAWAGSHLTSLLGLVAV	467
sp Q08169 HUGA_APIME	-----	382
sp P49370 HUGAA_VESVU	-----	331
Conohyal-Cn1	RDYHCRCSAWEGACCQTLRPSRC---QKREQRNVHGGDLID-----	415

sp Q12794 HYAL1_HUMAN	-----	435
sp O35632 HYAL2_MOUSE	ALTWTL	473
sp Q08169 HUGA_APIME	-----	382
sp P49370 HUGAA_VESVU	-----	331
Conohyal-Cn1	-----	415

Supplementary Figure S2: Comparison of amino acid sequences of hyaluronidases from human (Uniprot Accession code Q12794), mouse (Uniprot Accession code O35632), *Apis mellifera* (Uniprot Accession code Q08169), and *Vespula vulgaris* with the Conohyal-Cn1. For all sequences, the catalytic residue is highlighted in green, the positioning residues in blue, and the characterized glycosylation sites in orange. The Asn residue highlighted in pink in Conohyal-Cn1 sequence corresponds to a probable glycosylation site deduced from proteomic experiments and similarity with the established glycosylation site in the hyaluronidase from *Vespula vulgaris* venom.