

Supporting information

A

DNA sequence of sHS (5' - 3'):

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ATGTCAGTTGGAAGTGAAAACCTACCAACTTGTCTGGAGCGAGGACCCAGGACCTGAG
GCCTCCAGGGGGCCACTCATGGGGGGCCGCTGGGGTTGCTCTTCTCCCTTGAGCATG
CTGCGGCGGGTGGCCCCATCATCATTTTGGCTTCACTCCTTGTCTGTCTGTTCCCTC
TACTACACCTCACCTCTGGGAGCGACGACTCTGTATGAAGTTTACCGCAAACGCCTT
CGTTTTTCGAGGAACCCAGTCCGGAGGCTGCCCAAGCCCTGGATCATTGGAGTGCGG
AATGTGGAACCTCGGGCCCTACTGGAGATGCTCAATTTGCACCCATATATCCAAAAG
AATGGAGCTGGGATGCACTTCCTCGACGATGACGAGCGTTACGCTAATGGCATTGAA
TGGTACCGGAAAAGATGCCATACTCTTTTGATAATCAAATCACAATGGAGAAGACA
CCATCCTACTTCATCTCCCGTGAAGCACCGGCAAGAATCCACGCCATGAACACCTCG
ACCCGGCTCCTACTCATCGTCAGGGAGCCAGCTGACCGTGCGCTCTCAGATTACACC
CAGATTATGGAGTCTAAACTGAGGAAAGGGATCCAGATTGCGCCGTTCCATGAGAAG
ATCCTGACGCCGGATGGAGAGATTGATGAGACGTACAAGGCCATCAAATAAGTCAA
TATGCAATACATGTCTTGCGGTGGCTGAATGTTTTTTCCTCGAGATCAGATACACATC
GTTGATGGAGATAAATTAATAGCCGATCCTTTTTTCGGAGATAGACAAGGTACAACGG
TTCCTGAGGCTTCCTCTCCACATCACAGCGGAGAATTTTTACTTCAATGAAACAAAG
GGTTTTACTGCATGCGTAATGAGACTTTTCAGAAGTGCTTAGCTGACTCAAAGGG
AGGAGTCATCCCTTTGTTGATCCAGCTCTGATGTCTAAATTACGCAAGTTCCTTGCT
CCCTTCAACGAGCAGTTTTATGAAATGGTTGGACAGAACTTCAGCTGGCCTACCTCG
TAATCACGCTTCGTAAAAGGCAAAAAACAGTAAAGTAATTGGCAAATGTTGTTTCATA
AATACTCGAGCAGCTTCAGGTGCATATGTACAATTATAGGGTAGTACATTTAGTTAC
TTATGATGGTATAATGGTATGGGACTGTTGATATAGTTTTATTTTTTATTCATCCAGG
CATGAATGCTTCAATAATGATGAGTGTGTTGTTTTATATAAAGGAAAATATTTTCCTA
ACAAATGTGTAGATGTGTTTGCAAGGCCAAAAAAAAAAAAAAAAAAAAAAAAAA
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B

Protein sequence of sHS (N → C terminal):

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MSVGSSENYQLVWSEDPGPEASRGPLMGGRWGCSSPLSMLRRVAPIIIILASLLVCLFL
YYTSPLGATTLYEYVRKRLRFRGTQSGGCPKPWIIGVRKCGTRALLEMLNLHPYIQK
NGAGMHFLDDDERYANGIEWYRKKMPYSFDNQITMEKTPSYFISREAPARIHAMNTS
TRLLLIIVREPADRALSDYTQIMESKLRKGIQIAPFHEKILTPDGEIDETYKAIKISQ
YAIHVLRLWLVFPRDQIHIVDGDKLIADPFSDIKVQRFRLRLPLHITAENFYFNETKG
FYCMRNETFQKCLADSKGRSHPFVDPALMSKLRKFFAPFNEQFYEMVQGQNSWPTS-
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Figure S1: The DNA and predicted amino acid sequences from *Litopenaeus vannamei*. (A) The DNA sequence obtained by Sanger sequencing. The cDNA fragment in red corresponds to enzymatic domains responsible for the carbohydrate and PAPS binding. This nucleotide sequence was cloned in pRSET A. (B) Amino acid sequence of sHS from shrimp *L. vannamei* was predicted with the Translate Tool from ExPASy program (<http://web.expasy.org/translate/>). The red sequence refers to the amino acids of the cloned enzyme.

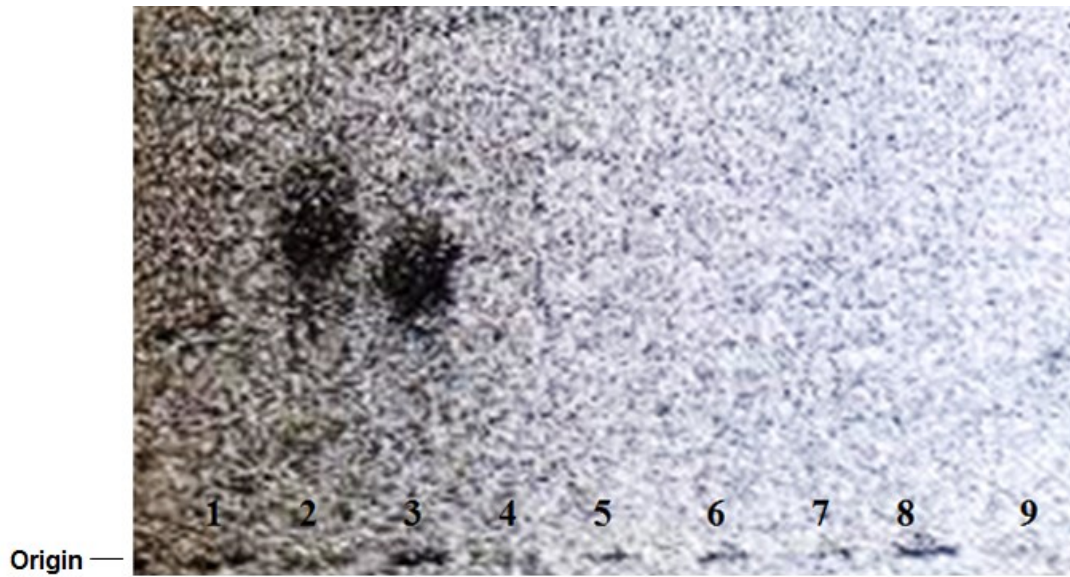


Figure S2: Recombinant sHS activity assay on different substrates. Activity assays were based on the transfer of radioactive sulfate from PAP^[35]S-sulfate to substrates (50µg) by the sHS enzyme. The samples were incubated at 37°C for 18h and, subsequently, incubated at 100°C for 5min. Radioactive sulfate incorporation was analyzed by PDA electrophoresis (1,3 diaminopropane acetate 0,05M pH 9,0 buffer) (Dietrich & Dietrich, 1976). The gels were exposed for three days to radiation sensitive films. 1: heparin, 2: O,N-desulfated-N-resulfated heparin, 3: O,N-desulfated-N-reacetylated heparin, 4: N-desulfated-N-reacetylated heparin, 5: heparan sulfate, 6: chondroitin 4-sulfate, 7: chondroitin 6-sulfate, 8: dermatan sulfate and 9: hyaluronic acid.