

## Supplementary Information

### Sugar-lectin rich interface between soft tissue and the stiff byssus of *Atrina pectinata*

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**Supplementary Data 1.** Peptide sequence of interfacial protein with carbohydrate binding domain. Carbohydrate binding domain highlighted in yellow.

1. m.14349 [5' partial sequence]

KPVPKYKSVVPDYKPPVVPDYKPPVVPDYKPPVVPDYKPPVVPDYKPPVVPDYKPP  
VDYKPPVVPDYKPPVVPDYKPVEPVYKPPVYKPKKPVYKPKKRPAYKPKKPIYK  
PTKPDYKPTETYKPGGNGAVKVGHHGYFPSSYGAGYYGVGYYKGYYKQVPDAD  
PLSATGGCPHGWLPYGGMCYLYSRDKLGWFEASMKCMYMGGYLAIANSAHENSY  
FKLMAKKYELKPGVWFGLNDVLFPKSHKWFWGYGKKQCKWFDWGLKEPKYDGA  
GYKHCVALWCDYKWQWKVENCYSKYYICELNPKRCPCKCGY\*

2. m.8455 [complete sequence]

MYQISRVHQPIYYIPNGLHVGKQVILRGRVTSGTETFAINLQETENPGDGEIALHFNP  
RPSTDVCVRNSFQGNWGPEETDQPHFPFDNNRSFLRIEVGDEGYRTYVNGKPYVNF  
NHRLDMGNVHFLHLTEGAEFYDISFQDRYSLPYRTEIPGRMRAGKAVRVRGASQDN  
DGFSINFACDCENETCAFHFNPRPNEGVVVRNANLGGWGEERDYDAEFPFQPNQY  
FDALFVAGEDKYHVVNDKYFSEFNHRQGLEDSHFHIQGNMDIKDVEYMEPLDD  
DFVKIIPSGLEKGDVMVFRGFMKPDGDTFSINFMNGYSADDIAFHFNPRVGQGEVI  
MNTCMGGNWGEEDKEDLPSVFANREPFEVKVVTKRNKFIYVNGKKVGKYNARG  
NVEDIKGVNVRGDAYVYQVQLQRKLEKPAWERLPGGLREFGWIVVHGIAKKGSEG  
FAVNLRGDDDSNIALHFNPRLTECTVRNTMTDGNWGEERDQPSFPFEKKDTFE  
VAINIQPDFVTVNGNHYVNYGHRLPLDSVCHLQLTGNADFFEPEFL\*

3. m.9790 [internal sequence]

FTSASMVKLSTVSLLLILNSVVGIASSIEPTGGTYGINNIFGKNKGNTNTGNKFDGG  
KPQIRGKTGDVVFGNSGKLIQNVRKVEPRKTNQKPAVLPTYGKNAPIDQPPVKKNPN  
TILKKGDIHDPFNKEVSIQQPLIKTNTGKEKIVMNKFDSIPREMPSSNDSPVMVSTEK  
LKPISKTTSKVAKNPKPDRFSGKAIKPIKRNKRKPPTVVVDNGGKPQPSYIQKNIKFP  
APYSGYFPTSDQFSYAAGYRQKYTKVGNVPPEPTDTGCPYGWMSYSGRCCYYFSRDK  
I

4. m.14568 [5' partial sequence]

PFEIIILTQDSHKIAINGNHTEFQHRIPTVHRITHLNISAGIQVSMVRYEPTAAPQVVQ  
GGYPQQPMYQPSAPSIGFQPPPQFYPSSAAPPMSYPSAAPQMPASPMYNPTVPLTVQIP  
GGMTPGKMIFLSGIPKNTRFTVNIQDRAASGGEIAFHFDVRFN VSGNVNEVVRNHFT  
HGTWGVEERQKPKFPFCPNANFDMIIMAEEQQSFRVAVDNQHFIEFKSRLLPVARFNY  
LNVTGNVRLTQVRFQ\*

5. m.15895 [complete sequence]

MLVLCILLPGFMKLVDGQMLLQNTGQSKISSYYPWLVDTLTEARKENANNNNVM  
KTLMCTMQAVGYKQTNAAGSTGAPKISP KDFYTGITQKLSEMSTD SQNQKQLIN  
NITDLMETQMGRIDEIERQNLKLLAALKL LSVNSIAFGSNSGDGRC SVDDFKCKE  
NECKTHSGYVYRRDNAIGVCLKFVSGFSDINVTRFAEKCAKDGGMLLKIDGYEKHQI  
IIKYLGTLSFGDPQIIIQGNDKISEGAWEFDDGTKMTYLPWYSGQPNSYSGEQDHIGM

KKSFSNYKWGDIWRVKSGFSAAYLCEIVV\*

6. m.8438 [3' partial sequence]

MWKFYQLCFLMFLAEEAESRSQDCKPKFVSLHRACYKFKVEMKSWTEAQRLCSEE  
GATLVSIGSMAEKGQIVKQLHKIITHMKHASWWVGLKLNKTIAKWKWQEGTDLNL  
RVTKWAPGEPNNALNGEHCAELSFRTINDGNCSFERPYVCELIKITQPPTSSTVATR  
LTTGQPTTVTMTMTSTSSTPQPTTEKPIIQTNTTPQTTSNKITSTKAVGYTTT  
QYTTPETTNNDTTSATKAAEYTTTQTTKKYNKTRNYLSGFPVDGNIHHFKTRST  
TVKPTIETTMKIKIPSRRPDATPKPNTRCPLVNAYGTVWPRAVKGTVSQKCKETE  
GYATWTGGYPVHLGEPNVSECASFKEIVSMSTSIAGNKSSLTPEVAEDITKII  
EKTETSNTMSAADIAVSTNLLKITSVKPKDSKQAKLVQDFVSAGNNLIEQTKHSL  
AIKPFDKSRAASRLLSTMELATSNMVDVINEPTIFQTRTDKISLTLHVLNTTNENLIYD  
DSGTDNTFKIPSSVLKSFNKGDLTKVVFMTHFDVGDLLSGKENTGNTDNYKTEVAS  
DVISASFGKEKAIHLTEPVTFMSKMTKSVEYGTIPVCSFWNFSIGQIGDWSQVGCRQ  
DYNATHTCQCDHLTNFAILLDVSGVDVAYHHTRILDITYIGCIISILSLSTAFLTQ  
CLSTLQGERNSIHKNLVFCFAAEELIFVVGISRTEQKVACAAIALLHFFFLSAFTWMF  
MEGIHIIFMLVQVFDFAKSKMKYYYLCGYGAPIIIVAVTATIDFKAYGTADHCWLTT  
ENWFIWSFAGPVALILVMNAGVLAYSLTMVCKHSDYVFSRERAESSNFRA

7. m.8549 [complete sequence]

MLLELQKIFIVIIITSVTHQQTLLAKPDNCPSIDAENGNLQIIRQSLLRNKETQEEMKT  
DIAEIWRQLNMLKSLLDQKSNSTSTKGTTDMYVSTGTSTKPTTRKPKLACMDPW  
LPYEDYCFYIGEERSSWSKASGQCQSLDSELATLDDKEKNEFIAGQIKRTENYWIGG  
NDIDVEGIWRWKGTVGEVIGPYKNWYLNDPDGRTTNQNCMWNYQGKPKWIDAPCK  
RKLFFVCERKM\*

8. m.218 [complete sequence]

MVPKLHMLVAVIIIDVTDQQVLLQKPDNCPKTDNERDLKVLRELTLKNQAKQEE  
MINEISELKQQFKLLQKSNLQPTTTSTTRPTTNKLAPCNPPWLQYEEFCFFISSKKE  
DWKAAAENCRCQMNAELAAFETKDKNDMGRKIISNDYWIGGNDLDKEGDWRWK  
KGNKKIGPYTNWYANDPDGRTGQNCMWNYQNTQQWIDAPCSRSLNFICERNI\*

9. m.14097 [complete sequence]

MDLGILRLVPTLSIVLSTVYADPCPSAEWKKDEESRMCYLFSEQRQFTQAVDFCEK  
YETHLLQYEKGFSKQTIRNFLNMNISEMWIKAPDTSEGEYEINSDRNSSTETSQNVST  
ETISQIRYRLLSRREESCRVINMTNDKEVIESERCTRKLPGVCEESIKHLEKRRKGMRV  
KVVAIIVGAIIGVFLGVIVKTCHKRLKMIEGGEYSIVENKKKEDEMILRKSEYIHI  
GSLRQPDTSGDTKV\*

10. m.12209 [complete sequence]

MLLIASVTLVAVIFRPVTGCSCLPPNPQDSFCTATFALKATVISDDTEYGDSNYTPLE  
RQYTIRFMRKDIYKGSNFFPGANTTASIKTAGYQSTCGIRFEIGQEYFITGSLDNLVVS  
LCDWISPLNNLTNHQRRGIQYMYEQGCNKCSIMRCFGRSCNNANVNQTCMVVDNPT  
NINNCHNKGFCLENDQGICKWKDNRLLKLCLNPKEVSRQVVGQTQ\*

11. m.2564 [internal sequence]

EPIVQIGGPSLDADLVRQNALPLIDPIHTDVCGSVKGCYRVPEHCWEPYCDYIATWRP  
YGTANTYLIEMSAMVDGVTDRHVSGLSGDTRWGGDRVfecvhnggtgvtqvfq  
AQSVGKSTERYQNSQAGISQRGYADGLKLGG

12. m.1338 [internal sequence]

SRRSSDPDKSGYGKKPKSDCSAKCTGDNSQTCGGTWRMNVYQINVEYMGCYLDKS  
TRLLEAKFTHGADMTELKCFKTCNGKYRFAGLQYSTQCFCGNDISKPGY GIRPESE  
CAAACRGDKDQTCG

**Supplementary Table S1.** Proteins and peptides identified through MS/MS analysis from each gel pieces.

(separate excel file)