SUPPORTING INFORMATION

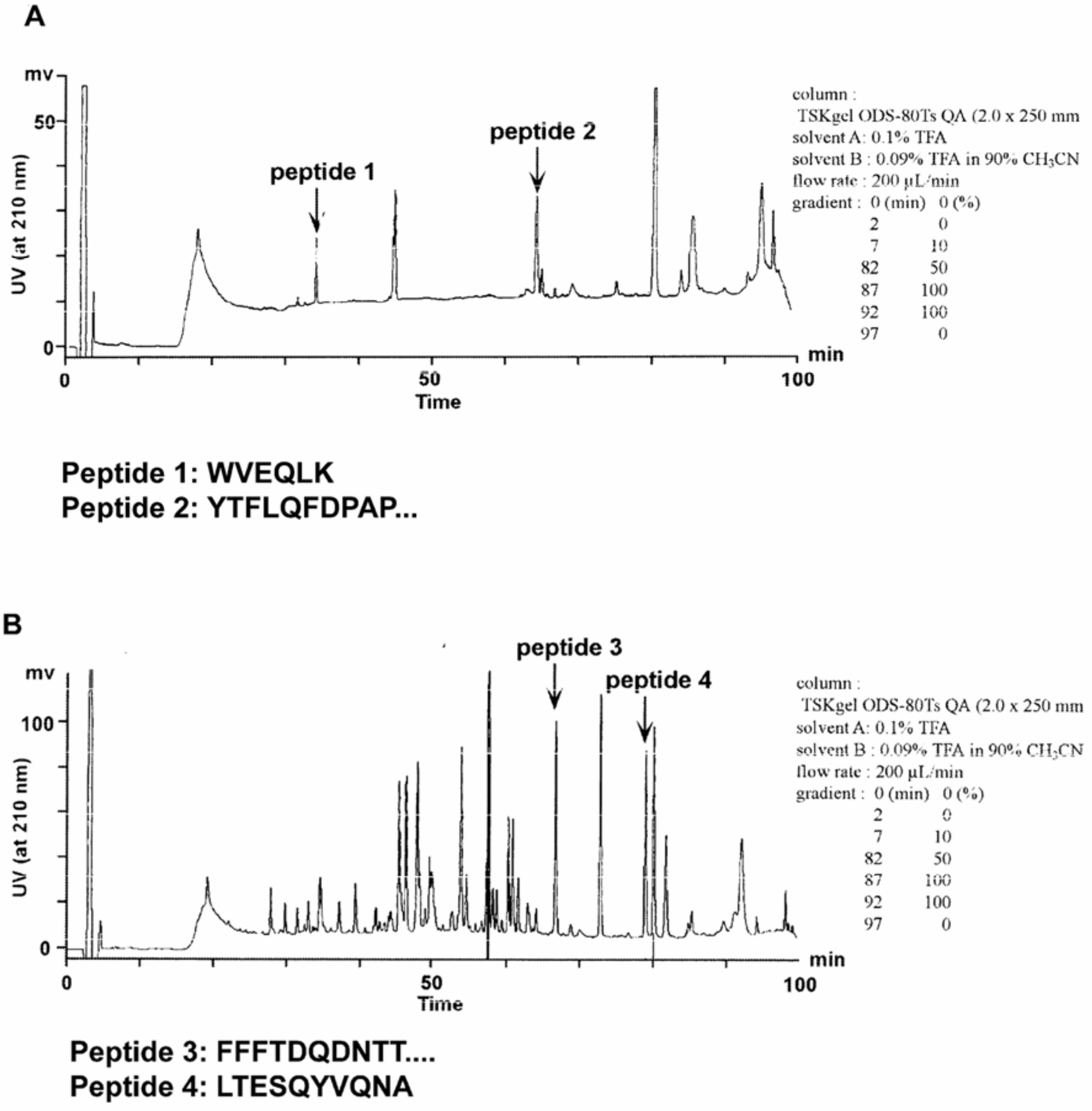

Figure S1. HPLC analysis of endopeptidase Lys-C digest for Edman degradation. The purified proteins (**A**) OABP1 and (**B**) OABP2 were digested with endopeptidase Lys-C, and separated by TSKgel ODS-80Ts QA (ϕ 2.0 x 250 mm). The column was equilibrated with Solvent A of 0.1% TFA at a flow rate of 0.2 mL/min, and loaded with the samples. The Solvent B of 0.09% TFA in 90% CH_3CN was linearly raised from 0 to 10% in the period of 2-7 min, from 10 to 50% in the period of 7-82 min and from 50 to 100% in the period of 82-87 min. The Solvent B was kept running for another 5 min, and then the solvent was replaced with Solvent A for conditioning. Amino acid sequences of two peptides in each analysis were determined by Edman degradation as listed below the HPLC charts.

A

	amino acid sequence	sense strand	antisense strand
OABP1	WVEQLK	(a) 5'TGGGTNGARCARCTNAA3'	(f) 5'TTNAGYTGYTCNACCCA3'
		(b) 5'TGGGTNGARCARTTRAA3'	(g) 5'TTYAAYTGYTCNACCCA3'
	YTFLQFDPAP	(c) 5'CARTTYGAYCCNGCNCC3'	(h) 5'GGNGCNGGRTCRAAYTG3'
OABP2	LTESQYVQNA	(d) 5'CARTAYGTNCARAAYGC3'	(i) 5'GCRTTYTGNACRTAYTG3'
	FFFTDQDNTT	(e) 5'TTYTTYACNGAYCARGAYAA3'	(j) 5'TTRTCYTGRTCNGTRAARAA3'

B

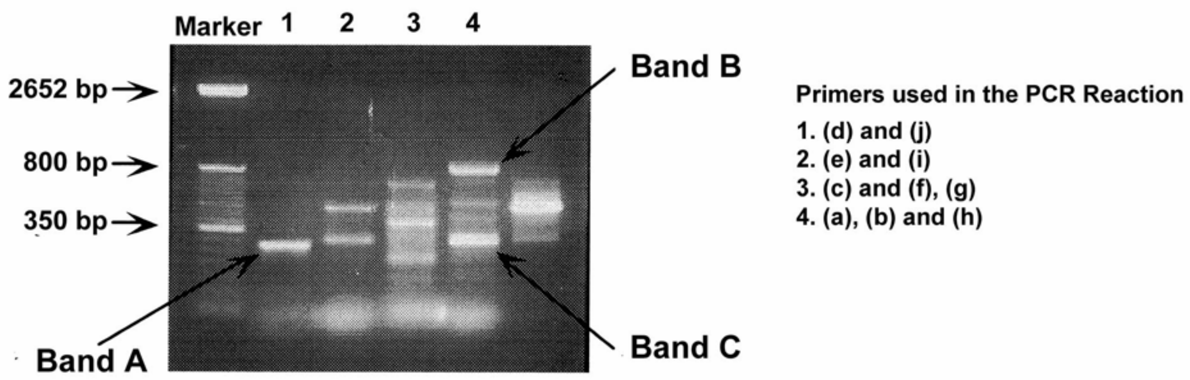

Figure S2. Amplification of cDNA coding OABP1 and OABP2. (**A**) The degenerated forward and reverse primers based on the amino acid residues of OABP1 and OABP2 determined by Edman degradation (*14*). The letters Y, N and R represents C/T, A/C/G/T and A/G, respectively. (**B**) Agarose gel electrophoresis of PCR products. Lanes 1 and 2 (both for OABP2), and lanes 3 and 4 (both for OABP1) represent the results from individual pairs of primers shown in the right. Bands A, B and C were subjected to the sequence analysis.

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OABP1                    WVEQLKQCKQLEEASVKLLCEKAREVLS
P11611    1  MDDKTFTKELDQWVEQLNECKQLNENQVRTLCEKAKEILT
                         *****::****:* .*: *****:*:*:

OABP1        QESNVQKVKSPVTVCGDVHGQFHDLMELFRIGGDSPDTNY
P11611   41  KESNVQEVRCPVTVCGDVHGQFHDLMELFRIGGKSPDTNY
             :*****:*:.***********************:******

OABP1        LFMGDYVDRGYYSVETVTLLVALKVRYPNRITLLRGNHES
P11611   81  LFMGDYVDRGYYSVETVTLLVALKVRYPERITILRGNHES
             ****************************:***:*******

OABP1        RQITQITQVYDECLRKYGNPNVWKFFTDLFDYLPLTALVD
P11611  121  RQITQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALVD
             *****:  .**********.****:***************

OABP1        DQIFCLHGGLSPSIDTLDHIRSLDRLQEVPHEGPMCDLLW
P11611  161  GQIFCLHGGLSPSIDTLDHIRALDRLQEVPHEGPMCDLLW
             .********************:******************

OABP1        SDPDDRGGWGISPRGADYTFGMDISENFNHNNGLTLISRA
P11611  201  SDPDDRGGWGISPRGAGYTFGQDISETFNHANGLTLVSRA
             ****************.**** ****.*** *****:***

OABP1        HQLVMEGYNWCHERNVVTIFSAPNYCYRCGNQAAIMELDD
P11611  241  HQLVMEGYNWCHDRNVVTIFSAPNYCYRCGNQAAIMELDD
             ************:***************************

OABP1        GLKYTFLQFDPA
P11611  281  TLKYSFLQFDPAPRRGEPHVTRRTPDYFL
              ***:*******
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Figure S3. Alignment of protein sequences for OABP1 and a rabbit PP2Aβ catalytic subunit (GenBank accession number: P11611). They are 88% homologous (*16*). OABP1 catalyzed hydrolysis of *p*NPP with 710 pmol/min/μg (13).

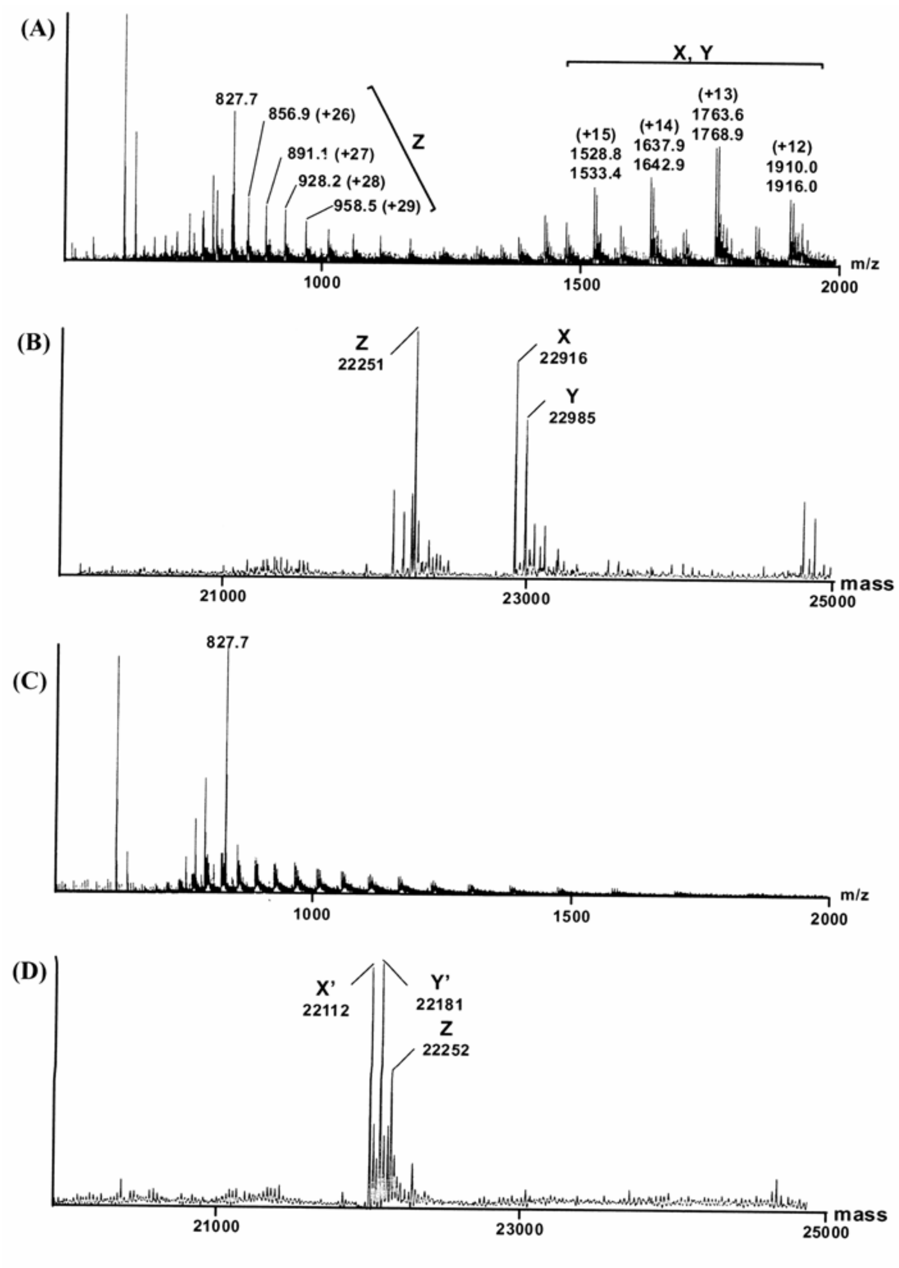

Figure S4. ESI-MS spectra of OABP2. (**A, C**) Raw and (**B, D**) deconvoluted mass spectrum for OABP2 measured in (**A**) 5% MeOH and (**C**) 50% CH_3CN. The X, Y and Z are attributed to OABP2.1, OABP2.2 and OABP2.3, respectively. The peak at 827.7 corresponding to $[M+Na]^+$ for okadaic acid was present in both of the conditions. The peaks X and Y in 5% MeOH gave larger *m/z* than those observed in 50% CH_3CN by 804, indicating that OABP2.1 and OABP2.2 possibly form a complex with okadaic acid. The deconvoluted peak assigned to OABP2.3 was independent of the measurement condition.

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AB078740    1                        A ACA ATT CGA CTG TGA CTT ATT TTG GAA

AB078740   29   ATG GCT AAT TTA AAG GAG CCA TCA GCT CAC TGG TGC AGG AAG ATG
OABP2.1     1   (M[a]) A[b]  N   L   K   E   P   S   A   H   W   C   R   K   M

AB078740   74   CGG ACA GTT TTT CGG CCA TGG GAT GTG GAA GGA GGT TCA AAA GGC
OABP2.1    15    R   T   V   F   R   P   W   D   V   E   G   G   S   K   G

AB078740  119   TAT GTC ACG GAA GAG GTC TTT AAA GAC GGC GTT CAA AGA AGG CTG
OABP2.1    30    Y   V   T   E   E   V   F   K   D   G   V   Q   R   R   L

AB078740  164   GAG AAA TTT CCC GAG CTT GCC CCT ACG AAA GAC AAA ATG TAC GAG
OABP2.1    45    E   K   F   P   E   L   A   P   T   K   D   K   M   Y   E

AB078740  209   CGA TCA CAT CGT CAC TGG GTC AAC CAC TGC AAC CTG GGG GTC AAG
OABP2.1    60    R   S   H   R   H   W   V   N   H   C   N   L   G   V   K

AB078740  254   ATG CCT GAA GGT TAC CGA CTA ACC GAA TCG CAG TAT GTC CAG AAT
OABP2.1    75    M   P   E   G   Y   R   L   T   E   S   Q   Y   V   Q   N

AB078740  299   GCC TGG CTG CTC ATT CAC TCG CCT GAT TTT GAA GCA AGT TTG AAA
OABP2.1    90    A   W   L   L   I   H   S   P   D   F   E   A   S   L   K

AB078740  344   GAA TCC AGC CAA ACT TTT TGG GAA GGA ATC GAT AGA GAA AAG AAG
OABP2.1   105    E   S   S   Q   T   F   W   E   G   I   D   R   E   K   K

AB078740  389   GGA TAC ATC ACA AAG GAG GAA GCT ACT AAA CTC GGT ATC CGA GTC
OABP2.1   120    G   Y   I   T   K   E   E   A   T   K   L   G   I   R   V

AB078740  434   ACA AAA GAC CCG AAT CTC AAG AGC ACT GGC ATC TTT GAG GCT ATG
OABP2.1   135    T   K   D   P   N   L   K   S   T   G   I   F   E   A   M

AB078740  479   GAT GAA AAA AAT ACT GGG AGG ATC ACG TTT GAG GAT ACG CTC AAG
OABP2.1   150    D   E   K   N   T   G   R   I   T   F   E   D   T   L   K

AB078740  524   GCA CAA CTT TTC TTC TTC ACA GAC CAG GAT AAC ACA ACT CAT CCT
OABP2.1   165    A   Q   L   F   F   F   T   D   Q   D   N   T   T   H   P

AB078740  569   TTC AAC TAT GTG AGG GGA GCA CTT GTG GAT TAG
OABP2.1   180    F   N   Y   V   R   G   A   L   V   D  stop

AB078740    614   GAA ATT CAA CTG AAC AGT TGC AGG GGT CAA AAA GGA
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Figure S5. The complete cDNA sequence of OABP2.1 and its amino acid sequence. The peptide sequences determined by Edman degradation were underlined. The MS mapping demonstrated that the posttranslational modification occurs at *N*-terminus. The superscripts [a] and [b] represent (a) deletion of the methionine and (b) acetylation on the alanine in *N*-terminus.

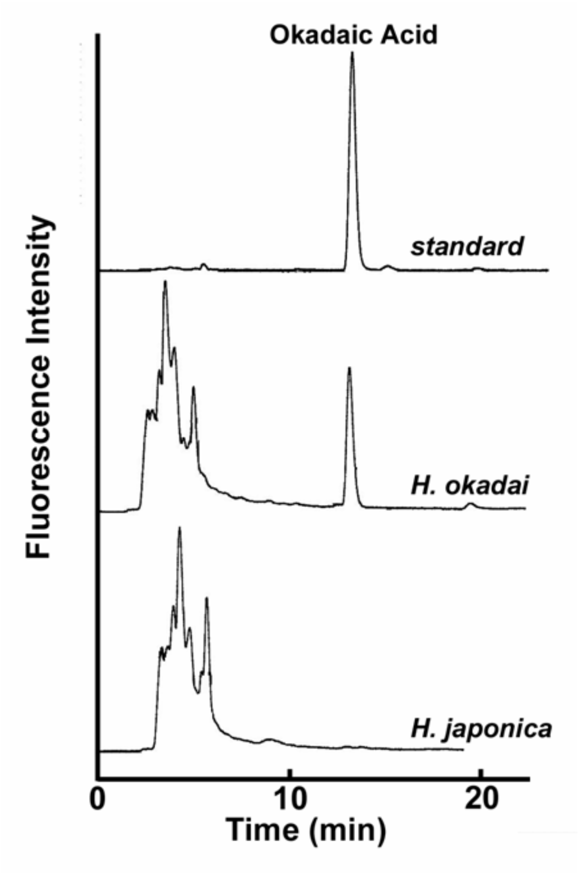

Figure S6. Quantification of okadaic acid in the sponges *H. okadai* and *H. japonica*. To 300 μL of the crude extract from each sponge was added 200 μL of 1 mg/mL 9-anthryldiazomethan (ADAM) in MeOH (*28*). After incubation at room temperature for 60 min in the dark, the mixture was evaporated, loaded to a silica gel column, and eluted with $CHCl_3$ followed by 5% MeOH/$CHCl_3$. The latter fraction was collected, and analyzed with HPLC on an ODS column Mightysil RP-18 GP 4.6 x 250 mm using 8:1:1 CH_3CN-MeOH-H_2O at flow rate of 1.1 mL/min. The wavelength of excitation and emission were set at 365 nm and 412 nm, respectively. HPLC chromatogram for 50 ng of 9-ADMOA (top), 32 mg of *H. okadai* extract (middle) and 52 mg of *H. japonica* extract (bottom) provided evidence that okadaic acid is not contained in *H. japonica*.

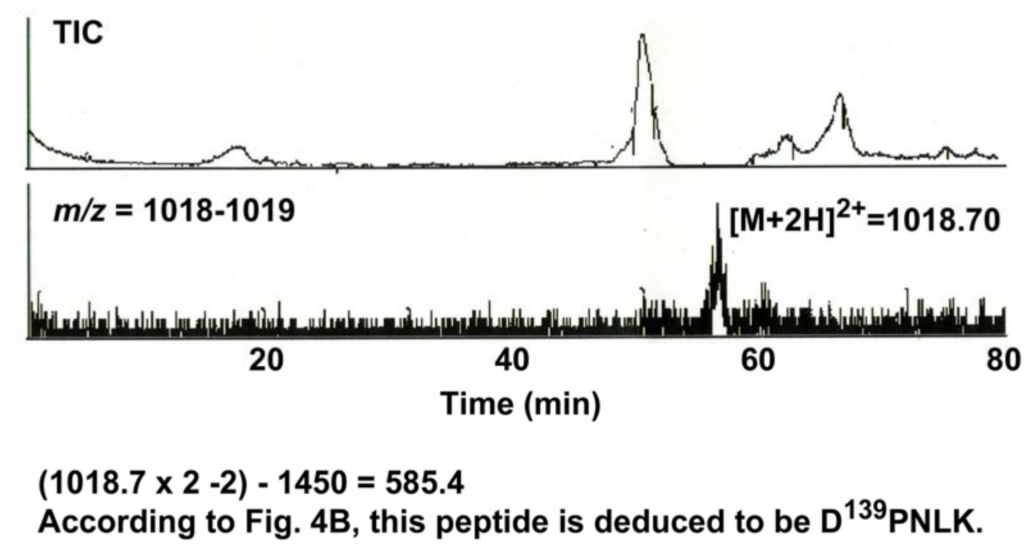

Figure S7. Identification of the photoaffinity labeled OABP2 fragment by ESIMS. After photolabeling of OABP2, the protein was precipitated in acetone, and resuspended in 10 mM Tris/HCl (pH 9.0). The mixture was digested with endopeptidase Lys-C for 12 h, and then purified with Immunopure Immobilized Monomeric Avidin (Pierce, Illinois, USA). ESIMS analysis was carried out as described in *Experimental Procedures*.