

Supplementary information

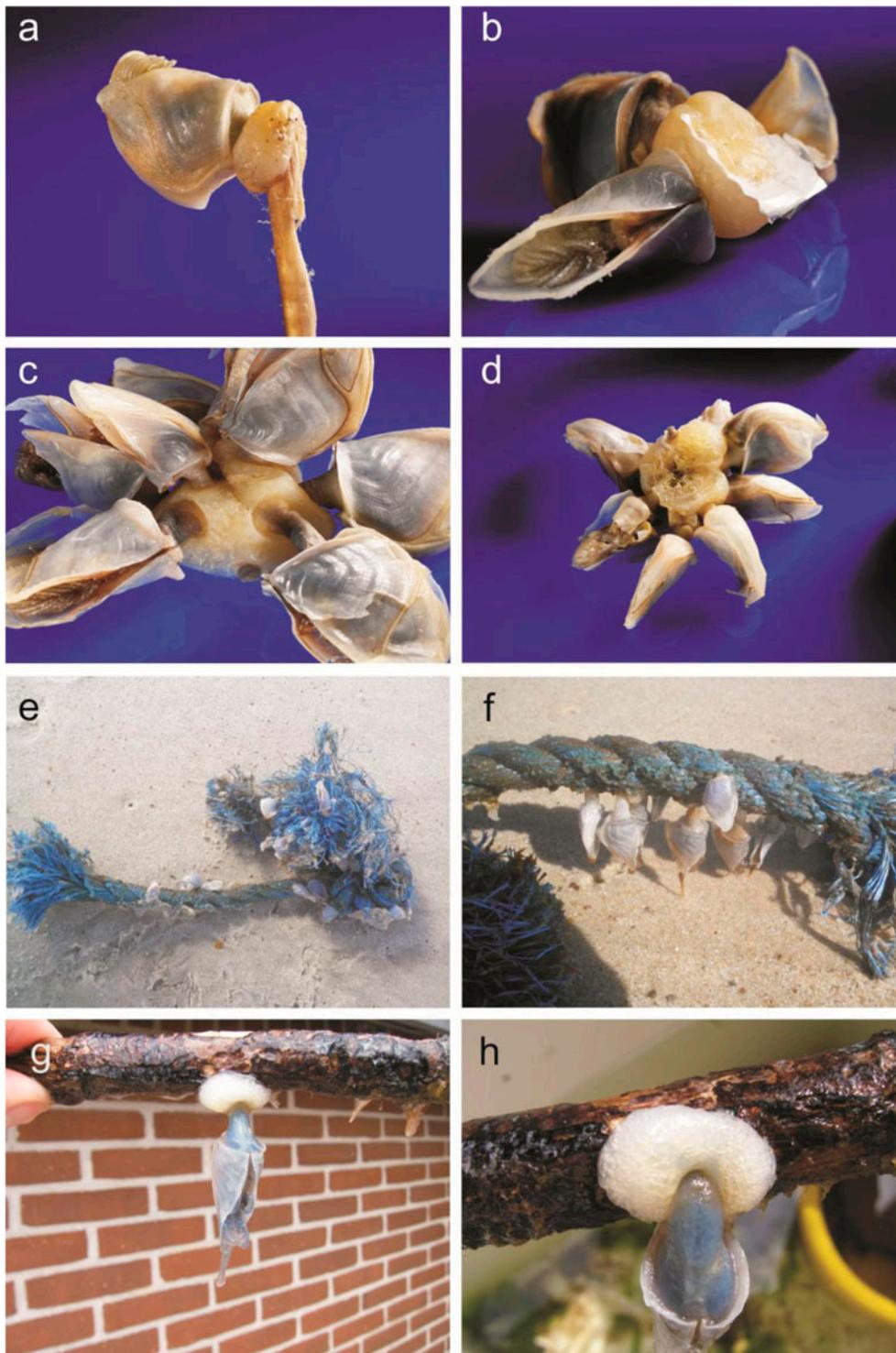


Figure S1: *D. fascicularis* (capitulum length about 1.5 cm) on different substrata. (a) (b) Cement surrounding plant material and plastic foil. (c) (d) A cluster of individuals on the cement of conspecifics (e) (f) *Dosima* settled on a rope. (g) (h) *Dosima* with an excess amount of cement on driftwood.

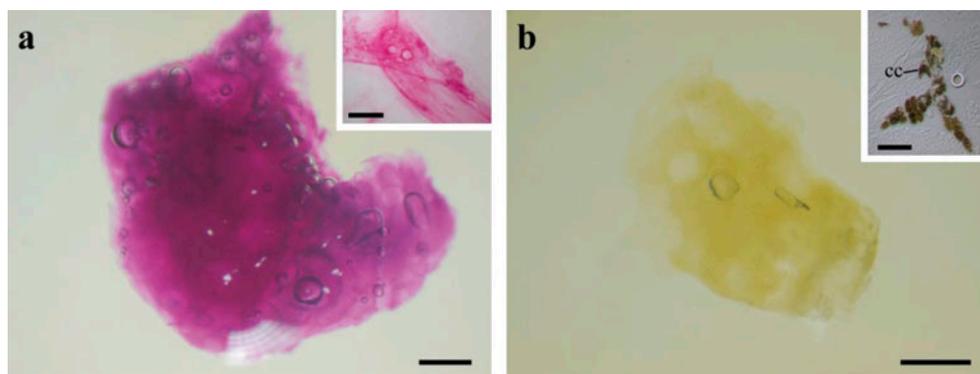


Figure S2: Staining methods. (a) Positive PAS stain of a piece of *D. fascicularis* cement generating a strong purple colour, which is characteristic of carbohydrates. Inset: The slime of the slug *Arion rufus* was used as a positive control. (b) The Arnow staining was negative, which proved the absence of L-DOPA in the polymerised cement. Inset: The cement cells (cc) of the polychaete *Sabellaria alveolata* were used as a positive control. Scale bar: a: 1 mm, Inset: 500 μm , b: 1 mm, Inset: 100 μm

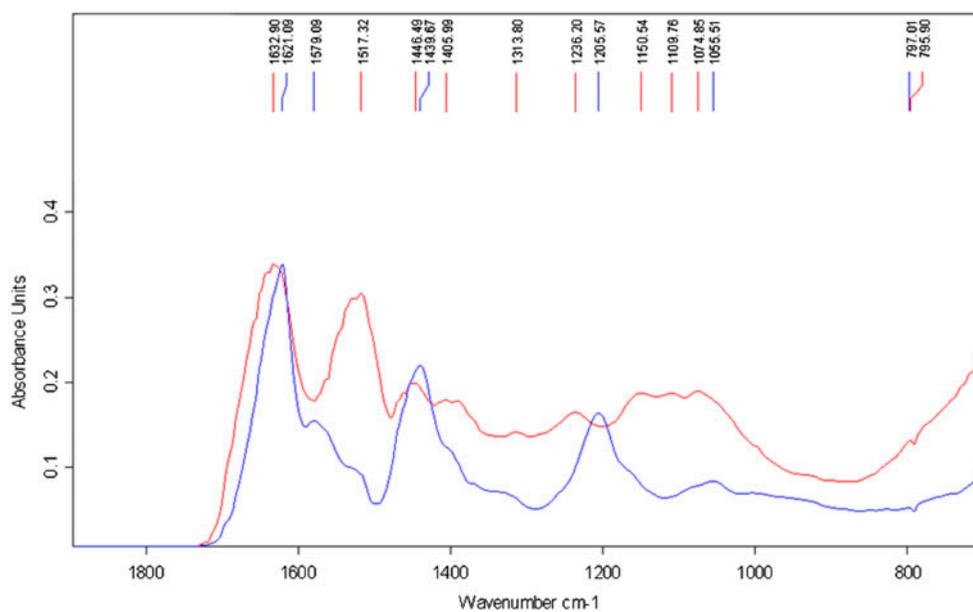


Figure S3: Magnified image of the FTIR spectrum of Figure 4a. Blue: sample equilibrated in D_2O ; Red: dry sample.

Table S1: Results of a NCBI blastp database search with the Dfcp *de novo* peptides.

Dfcp	Sequence	NCBI blastp (nr) results*#	Organism	Sequence ID	Sequence identified	E-value	Identities	Positives	Gaps
Dfcp-60	SFLADVLR	NADH dehydrogenase subunit 4.	<i>Capitulum mitella</i>	dbj BAD44744.1	FLADV	9.9	4/5 (80%)	4/5 (80%)	0/5 (0%)
Dfcp-60	SFLADVLR	Cytochrome b	<i>Tetractra japonica</i>	ref YP_022498.1	DVLG	30	4/4 (100%)	4/4 (100%)	0/4 (0%)
Dfcp-60	KFAALEDFAVSR	MULTIFUNCin	<i>Semibalanus cariosus</i>	gb AFY13481.1	AALTEFAV	2.1	6/8 (75%)	7/8 (87%)	0/8 (0%)
Dfcp-60	KFAALEDFAVSR	Glycogen synthase	<i>Chthamalus fragilis</i>	gb ACY45232.1	KFAALEDF	4.4	5/8 (63%)	6/8 (75%)	0/8 (0%)
Dfcp-60	MMSVSNKVR	NADH dehydrogenase subunit 2	<i>Nobia grandis</i>	ref YP_009024529.1	MMSVSN	6.9	4/6 (67%)	5/6 (83%)	0/6 (0%)
Dfcp-60	MMSVSNKVR	Elongation factor-2	<i>Semibalanus balanoides</i>	gb AAK12342.1	MMSVSNKV	6.9	5/8 (63%)	5/8 (62%)	0/8 (0%)
Dfcp-60	MMSVSNKVR	MULTIFUNCin	<i>Balanus glandula</i>	gb AFY13480.1	VSNK	30	4/4 (100%)	4/4 (100%)	0/4 (0%)
Dfcp-60	MMSVSNKVR	NADH dehydrogenase subunit 1	<i>Megabalanus volcano</i>	ref YP_087069.1	SVSN	44	4/4 (100%)	4/4 (100%)	0/4 (0%)
Dfcp-60	FGALGLSR	Clathrin heavy chain	<i>Lepas anserifera</i>	gb ACY44822.1	ALGLSR	11	5/6 (83%)	5/6 (83%)	0/6 (0%)
Dfcp-60	FGALGLSR	Mitochondrial acetyl-coA acetyltransferase 1	<i>Amphibalanus amphitrite</i>	gb AEZ02466.1	AL-GLSR	16	6/8 (75%)	6/8 (75%)	2/8 (25%)
Dfcp-60	FGALGLSR	Cytochrome oxidase subunit 1	<i>Pollicipes elegans</i>	gb ADK56492.1	FGALGL	23	4/6 (67%)	5/6 (83%)	0/6 (0%)
Dfcp-60	TPLSLESVTR	Neurofibromin	<i>Semibalanus balanoides</i>	gb ACY43933.1	PLS-LESVT	0.55	7/9 (78%)	7/9 (77%)	1/9 (11%)
Dfcp-60	TPLSLESVTR	70 kDa heat shock protein	<i>Amphibalanus amphitrite</i>	gb AAN74984.1	TPLSL	3.0	5/5 (100%)	5/5 (100%)	0/5 (0%)
Dfcp-60	TPLSLESVTR	Cement protein 100 k	<i>A. amphitrite</i>	gb AGS19349.1	PLSLE	120	4/5 (80%)	4/5 (80%)	0/5 (0%)
Dfcp-63	WVTSAWSSKAR	Lectin BRA-2	<i>Megabalanus rosa</i>	dbj BAA01470.1	WVTS	0.54	4/4 (100%)	4/4 (100%)	0/4 (0%)
Dfcp-63	WVTSAWSSKAR	Cement protein-19 k	<i>Balanus improvisus</i>	dbj BAE9441.1	VTSAWSSKA	3.5	6/9 (67%)	6/9 (66%)	0/9 (0%)
Dfcp-63	WVTSAWSSKAR	NADH dehydrogenase subunit 4	<i>Pollicipes polymerus</i>	ref YP_026022.1	WVTS	3.5	3/4 (75%)	4/4 (100%)	0/4 (0%)
Dfcp-63	WVTSAWSSKAR	MULTIFUNCin	<i>Balanus glandula</i>	gb AFY13480.1	SKAR	5.1	4/4 (100%)	4/4 (100%)	0/4 (0%)
Dfcp-63	WVTSAWSSKAR	Cement protein-100 k	<i>Megabalanus rosa</i>	dbj BAB12269.1	SAWSSK	7.4	5/6 (83%)	5/6 (83%)	0/6 (0%)
Dfcp-63	FEDFLVNNLNAFSR	Sulfakinin	<i>Amphibalanus amphitrite</i>	gb AFK81942.1	FEDF	9.0	4/4 (100%)	4/4 (100%)	0/4 (0%)
Dfcp-63	FEDFLVNNLNAFSR	GTP-binding protein	<i>Semibalanus balanoides</i>	gb ACY44699.1	DFLVN	13	4/5 (80%)	5/5 (100%)	0/5 (0%)

(Continued)

Table S1. (Continued).

Dfcp	Sequence	NCBI balstip (nr) results*#	Organism	Sequence ID	Sequence identified	E-value	Identities	Positives	Gaps
Dfcp-63	FEDFLVNNLNAFSR	Clathrin heavy chain	<i>Lepas anserifera</i>	gb ACY44822.1	VNNLN	19	4/5 (80%)	5/5 (100%)	0/5 (0%)
Dfcp-63	FEDFLVNNLNAFSR	Cytochrome c oxidase subunit II	<i>Megabalanus volcano</i>	ref YP_087059.1 COXII_17929	FLVN	27	4/4 (100%)	4/4 (100%)	0/4 (0%)
Dfcp-63	ELYGGLLTADLTK	BCS-2	<i>Amphibalanus amphitrite</i>	dbj BAA99544.1	LTADEL	3.1	5/6 (83%)	6/6 (100%)	0/6 (0%)
Dfcp-63	ELYGGLLTADLTK	BCS-3	<i>A. amphitrite</i>	dbj BAA99545.1	ELYGGLLTAD— ELT	9.2	9/17 (53%)	10/17 (58%)	6/17 (35%)
Dfcp-63	ELYGGLLTADLTK	Cement protein 100 k	<i>A. amphitrite</i>	gb AGS19349.1	LTADEL	27	4/6 (67%)	5/6 (83%)	0/6 (0%)
Dfcp-63	RLEQLAGGKR	Sulfakinin	<i>A. amphitrite</i>	gb AFK81942.1	QLAGGKR	12	5/7 (71%)	5/7 (71%)	0/7 (0%)
Dfcp-63	RLEQLAGGKR	Clathrin coat assembly protein	<i>Chthamalus fragilis</i>	gb ACY45019.1	RLEQ	12	4/4 (100%)	4/4 (100%)	0/4 (0%)
Dfcp-63	RLEQLAGGKR	Cement protein 100 k	<i>A. amphitrite</i>	gb AGS19349.1	LEQL	18	4/4 (100%)	4/4 (100%)	0/4 (0%)
Dfcp-63	RLEQLAGGKR	Cement protein 100 k	<i>A. amphitrite</i>	gb AGS19349.1	QL—AGGK	38	6/9 (67%)	6/9 (66%)	3/9 (33%)
Dfcp-63	RLEQLAGGKR	Cement protein 100 k	<i>A. amphitrite</i>	gb AGS19349.1	QLAGGK	2,237	4/6 (67%)	4/6 (66%)	0/6 (0%)
Dfcp-63	RLEQLAGGKR	Cytochrome c oxidase subunit II	<i>Megabalanus volcano</i>	ref YP_087059.1 COXII_17929	RLEQL	38	4/5 (80%)	4/5 (80%)	0/5 (0%)
Dfcp-63	RLEQLAGGKR	MULTIFUNCin	<i>Balanus glandula</i>	gb AFY13480.1	LAGGKR	38	5/6 (83%)	5/6 (83%)	0/6 (0%)
Dfcp-63	RLEQLAGGKR	MULTIFUNCin	<i>B. glandula</i>	gb AFY13480.1	RLEQLA	3,167	4/6 (67%)	4/6 (66%)	0/6 (0%)
Dfcp-63	GPDYEVELQR	Methionine aminopeptidase	<i>Lepas anserifera</i>	gb ACY45964.1	YEVEL	0.55	5/5 (100%)	5/5 (100%)	0/5 (0%)
Dfcp-63	GPDYEVELQR	Cement protein 100 k	<i>Amphibalanus amphitrite</i>	gb AGS19349.1	GPDYE—VEL	1.1	6/10 (60%)	8/10 (80%)	2/10 (20%)
Dfcp-63	GPDYEVELQR	Cement protein 100 k	<i>Megabalanus rosa</i>	dbj BAB12269.1	GPDYEVELQ	4.2	6/9 (67%)	6/9 (66%)	0/9 (0%)
Dfcp-63	GPDYEVELQR	Settlement inducing protein complex	<i>Megabalanus coccopoma</i>	dbj BAM28692.1	DYEVE	4.2	4/5 (80%)	5/5 (100%)	0/5 (0%)
Dfcp-63	GPDYEVELQR	Settlement inducing protein complex	<i>M. coccopoma</i>	dbj BAM28692.1	DY—EV- ELQR	6.0	7/14 (50%)	8/14 (57%)	6/14 (42%)
Dfcp-68	FASADELDDLDTVK	Clathrin heavy chain	<i>Semibalanus balanoides</i>	gb ACY44802.1	ADELDDL	0.11	6/9 (67%)	8/9 (88%)	0/9 (0%)
Dfcp-68	FASADELDDLDTVK	ERK-MAPK	<i>Amphibalanus amphitrite</i>	gb AGT02391.1	ELDDL	2.5	5/5 (100%)	5/5 (100%)	0/5 (0%)
Dfcp-68	FASADELDDLDTVK	ERK-MAPK	<i>A. amphitrite</i>	gb AGT02391.1	DLLD	44	4/4 (100%)	4/4 (100%)	0/4 (0%)
Dfcp-68	FASADELDDLDTVK	Methionine aminopeptidase	<i>Chthamalus fragilis</i>	gb ACY45952.1	DDLDTVK	15	5/8 (63%)	6/8 (75%)	0/8 (0%)

(Continued)

Table S1. (Continued).

Dfcp	Sequence	NCBI balstip (nr) results*#	Organism	Sequence ID	Sequence identified	E-value	Identities	Positives	Gaps
Dfcp-68	FASADELDDLLDVTVK	Methionine aminopeptidase	<i>C. fragilis</i>	gb ACY45952.1	ELDLDLDT-VK	6,964	6/12 (50%)	6/12 (50%)	4/12 (33%)
Dfcp-68	FASADELDDLLDVTVK	Cement protein-19 k	<i>Megabalanus rosa</i>	dbj BAE94409.1	DDLDT	61	4/6 (67%)	5/6 (83%)	0/6 (0%)
Dfcp-68	FASADELDDLLDVTVK	MULTIFUNCin	<i>Semibalanus cariosus</i>	gb AFY13481.1	LDTV	62	4/4 (100%)	4/4 (100%)	0/4 (0%)
Dfcp-68	FASADELDDLLDVTVK	MULTIFUNCin	<i>S. cariosus</i>	gb AFY13481.1	FAS	340	7/14 (50%)	7/14 (50%)	5/14 (35%)
Dfcp-68	FASADELDDLLDVTVK	Cement protein-100 k	<i>Megabalanus rosa</i>	dbj BAB12269.1	DELDTT	477	7/17 (41%)	9/17 (52%)	5/17 (29%)
Dfcp-68	RLAAVVLSR	Cement protein-20 k	<i>M. rosa</i>	dbj BAB18762.1	LLDVTK LAAVV	4.9	5/5 (100%)	5/5 (100%)	0/5 (0%)
Dfcp-68	RLAAVVLSR	Settlement inducing protein complex	<i>Megabalanus coccopoma</i>	dbj BAM28692.1	LAAVV	4.9	5/5 (100%)	5/5 (100%)	0/5 (0%)
Dfcp-68	LGSGYVDFLR	Tropinin C	<i>Balanus nubilus</i>	sp P21798.2 TNNC2_BALNU	GSGTVDF	2.1	6/7 (86%)	6/7 (85%)	0/7 (0%)
Dfcp-68	LGSGYVDFLR	NADH dehydrogenase subunit 5	<i>Pollicipes polymerus</i>	ref YP_026021.1	YVDF	4.2	4/4 (100%)	4/4 (100%)	0/4 (0%)
Dfcp-68	LGSGYVDFLR	Settlement inducing protein complex	<i>Amphibalanus amphitrite</i>	gb AAR33079.1	LPSGYV	18	5/6 (83%)	5/6 (83%)	0/6 (0%)
Dfcp-68	LGSGYVDFLR	MULTIFUNCin	<i>Semibalanus cariosus</i>	gb AFY13481.1	SGYIPVDITLR	26	7/11 (64%)	7/11 (63%)	3/11 (27%)
Dfcp-68	LSVTQLPR	NADH dehydrogenase subunit 6	<i>Notothamalus scabrosus</i>	ref YP_008758262.1	SVTQFP	4.0	5/6 (83%)	5/6 (83%)	0/6 (0%)
Dfcp-68	LSVTQLPR	Mitochondrial acetyl-coA acetyltransferase 1	<i>Amphibalanus amphitrite</i>	gb AEZ02466.1	LSATQL	4.1	5/6 (83%)	5/6 (83%)	0/6 (0%)
Dfcp-68	LSVTQLPR	Cement protein-100 k	<i>Megabalanus rosa</i>	dbj BAB12269.1	LSKKQL	2,488	4/6 (67%)	4/6 (66%)	0/6 (0%)
Dfcp-68	RSGEVTSAWSSKVR	MULTIFUNCin	<i>Balanus glandula</i>	gb AFY13480.1	SGEVIS	27	5/6 (83%)	5/6 (83%)	0/6 (0%)
Dfcp-68	RSGEVTSAWSSKVR	MULTIFUNCin	<i>B. glandula</i>	gb AFY13480.1	GEVNITVSA-kV	857	7/14 (50%)	7/14 (50%)	6/14 (42%)
Dfcp-85	HPLLSSLNGLVSR	NADH dehydrogenase subunit 4	<i>Tetraclita japonica</i>	ref YP_022495.1	LLSSM-LVS	3.7	7/10 (70%)	8/10 (80%)	2/10 (20%)
Dfcp-85	HPLLSSLNGLVSR	Cement protein 100 k	<i>Amphibalanus amphitrite</i>	gb AGS19349.1	LQSSLSGL	7.7	6/8 (75%)	6/8 (75%)	0/8 (0%)
Dfcp-85	HPLLSSLNGLVSR	Cement protein 100 k	<i>A. amphitrite</i>	gb AGS19349.1	LSELLPGLTS	549	6/9 (67%)	6/9 (66%)	0/9 (0%)
Dfcp-85	HPLLSSLNGLVSR	MULTIFUNCin	<i>Chthamalus fissus</i>	gb AFY13482.1	PLLSS	7.7	5/5 (100%)	5/5 (100%)	0/5 (0%)
Dfcp-85	HPLLSSLNGLVSR	MULTIFUNCin	<i>C. fissus</i>	gb AFY13482.1	GLVS	135	4/4 (100%)	4/4 (100%)	0/4 (0%)
Dfcp-85	HPLLSSLNGLVSR	MULTIFUNCin	<i>C. fissus</i>	gb AFY13482.1	MSNL-GLESR	192	6/10 (60%)	7/10 (70%)	1/10 (10%)

(Continued)

Table S1. (Continued).

Dfcp	Sequence	NCBI blastp (nr) results*#	Organism	Sequence ID	Sequence identified	E-value	Identities	Positives	Gaps
Dfcp-85	FNVAFDELAATR	Cement protein-100 k	<i>Megabalanus rosa</i>	dbj BAB12269.1	VAF-ELA	9.1	6/7 (86%)	6/7 (85%)	1/7 (14%)
Dfcp-85	FNVAFDELAATR	Glucosamine phosphate isomerase	<i>Chthamalus fragilis</i>	gb ACY44753.1	VAFNE	13	4/5 (80%)	5/5 (100%)	0/5 (0%)
Dfcp-85	FNVAFDELAATR	Cement protein-19 k	<i>Megabalanus rosa</i>	dbj BAE94409.1	AFGNLAA	40	5/7 (71%)	5/7 (71%)	0/7 (0%)
Dfcp-85	FNVAFDELAATR	MULTIFUNCin	<i>Chthamalus fissus</i>	gb AFY13482.1	DELA	40	4/4 (100%)	4/4 (100%)	0/4 (0%)
Dfcp-85	RRGLVLSHLAQPK	Settlement inducing protein complex	<i>Balanus improvisus</i>	dbj BAM28693.1	LVLNLA	0.88	6/7 (86%)	6/7 (85%)	0/7 (0%)
Dfcp-85	RRGLVLSHLAQPK	SH2 domain binding protein	<i>Lepas anserifera</i>	gb ACY44058.1	MVLNHLA	2.5	5/7 (71%)	6/7 (85%)	0/7 (0%)
Dfcp-85	RRGLVLSHLAQPK	MULTIFUNCin	<i>Balanus glandula</i>	gb AFY13480.1	LVISNLA	16	5/7 (71%)	5/7 (71%)	0/7 (0%)
Dfcp-85	RRGLVLSHLAQPK	MULTIFUNCin	<i>B. glandula</i>	gb AFY13480.1	LSLFNLGPK	388	6/10 (60%)	6/10 (60%)	2/10 (20%)
Dfcp-85	SSVSPSLELSDAEPEK	Tachykinin-related peptide	<i>Amphibalanus amphitrite</i>	gb AFK81943.1	SVSPPLLLALS	1.7	8/11 (73%)	8/11 (72%)	1/11 (9%)
Dfcp-85	SSVSPSLELSDAEPEK	Waterborne settlement pheromone	<i>A. amphitrite</i>	dbj BAM34601.1	VAPKQLELQDA	4.9	7/11 (64%)	7/11 (63%)	0/11 (0%)
Dfcp-85	SSVSPSLELSDAEPEK	SH2 domain binding protein	<i>Lepas anserifera</i>	gb ACY44058.1	LELNKQPE	14	5/9 (56%)	7/9 (77%)	0/9 (0%)
Dfcp-85	SSVSPSLELSDAEPEK	MULTIFUNCin	<i>Semibalanus cariosus</i>	gb AFY13481.1	SVSSATLRLLELS	28	8/12 (67%)	8/12 (66%)	2/12 (16%)
Dfcp-85	SSVSPSLELSDAEPEK	MULTIFUNCin	<i>S. cariosus</i>	gb AFY13481.1	LSIDAHELPE	1,114	7/10 (70%)	7/10 (70%)	3/10 (30%)
Dfcp-85	SSVSPSLELSDAEPEK	Cytochrome c oxidase subunit I	<i>Tetracitita rubescens</i>	gb ADF31580.1	SXSPPLL	39	5/7 (71%)	5/7 (71%)	0/7 (0%)
Dfcp-85	TPPAAMEELATDK	Cytochrome oxidase subunit II	<i>Balanus crenatus</i>	emb CAC44980.1	MEEL	7.4	4/4 (100%)	4/4 (100%)	0/4 (0%)
Dfcp-85	TPPAAMEELATDK	MULTIFUNCin	<i>Balanus glandula</i>	gb AFY13480.1	PPPAM	23	4/5 (80%)	4/5 (80%)	0/5 (0%)
Dfcp-85	TPPAAMEELATDK	MULTIFUNCin	<i>B. glandula</i>	gb AFY13480.1	ELSTD	33	4/5 (80%)	4/5 (80%)	0/5 (0%)
Dfcp-85	TPPAAMEELATDK	Cement protein-100 k	<i>Megabalanus rosa</i>	dbj BAB12269.1	AMAEL	33	4/5 (80%)	4/5 (80%)	0/5 (0%)

The search settings were automatically optimised to find matches to a short peptide* by the blastp program. Search settings for parameter 'organism' were set to "barnacles (taxid:6,676)". The first two results for each Dfcp peptide are shown in the table and are highlighted; other hits derived from the results are shown.