

Supporting Information

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Fig. S1. Skeletal organic matrix (SOM) proteins separated by SDS/PAGE. (A) Silver staining and (B) Periodic acid-Schiff (PAS) staining of SOM proteins from decalcified *Stylophora pistillata* skeleton. Silver staining (A) was performed on glycosylated soluble SOM (lane 2). PAS staining (B) was performed on glycosylated soluble (lane 2) and insoluble (lane 3) SOM, and deglycosylated soluble (lane 4) and insoluble (lane 5) SOM. Lane 1 of each gel contains molecular weight standards; numbers indicate kilodaltons. Arrows indicate protein bands.

[Fig. S1](#)

Fig. S2. Predicted amino acid sequences of 36 *S. pistillata* proteins. Peptides detected by LC-MS/MS after tryptic digestion are in bold and after proteinase K digestion are underlined. Translations of internal sequences confirmed by PCR amplification of *S. pistillata* cDNA using gene-specific primers are highlighted in gray. Discrepancies between the predicted sequence and that determined by translation of PCR product are in red. The secretion signal peptide of P12, is crossed out over the portion that is predicted to be cleaved before secretion.

[Fig. S2](#)

Fig. S3. Multiple sequence alignment. Aligned sequences of CARP4 and CARP5, two highly acidic predicted proteins detected by LC-MS analysis of deglycosylated *S. pistillata* SOM, and similar proteins from an *A. digitifera* genome, a *Favia* sp. EST library, and a *P. damicornis* transcriptome. Identical amino acids are highlighted in gray. Dashes represent gaps. Yellow highlighted residues in CARP4 were previously determined by N-terminal sequencing by ref. 49. Blue stars denote predicted glycosylation sites of CARP4.

[Fig. S3](#)

Table S1. SOM protein primer sets

[Table S1](#)

Gene-specific primers used to confirm the DNA and cDNA sequences of selected SOM proteins.

Table S2. Putative homologous proteins from other mineralizers or related organisms

[Table S2](#)

The most similar predicted protein sequence from each comparison organism is given. Lack of a similar protein sequence for a given species is noted as “—”.