

The following supplements refer to Table 1 in the manuscript.



Figure S1. Sequence Motif Consensus Sequence Analysis from Peptide Sequences using MEME (<https://meme-suite.org/meme/tools/meme>). The thickness of the bar corresponds to probability of sequence overlap. And the length corresponds to the location.



Figure S2. Discovered Motifs from Peptide Sequences using MEME (<https://meme-suite.org/meme/tools/meme>). See Motif consensus sequence above in Supplemental Figure 1.

| Role | Source [?] | Alphabet [?] | Sequence Count [?] | Total Size [?] |
|-------------------|---------------------|-----------------------|-----------------------------|-------------------------|
| Primary Sequences | sequences.fa | Protein | 15 | 177 |

Background Model

Source: built from the (primary) sequences

Order: 0

| | Name [?] | Freq. [?] | Bg. [?] |
|---|-------------------|--------------------|------------------|
| A | Alanine | 0.0395 | 0.0395 |
| C | Cysteine | 0 | 0.0000282 |
| D | Aspartic acid | 0 | 0.0000282 |
| E | Glutamic acid | 0.00565 | 0.00567 |
| F | Phenylalanine | 0.113 | 0.113 |
| G | Glycine | 0.0169 | 0.017 |
| H | Histidine | 0.0565 | 0.0565 |
| I | Isoleucine | 0.0226 | 0.0226 |
| K | Lysine | 0.0452 | 0.0452 |
| L | Leucine | 0.141 | 0.141 |
| M | Methionine | 0.0339 | 0.0339 |
| N | Asparagine | 0.0565 | 0.0565 |
| P | Proline | 0.096 | 0.096 |
| Q | Glutamine | 0.0226 | 0.0226 |
| R | Arginine | 0.0508 | 0.0508 |
| S | Serine | 0.175 | 0.175 |
| T | Threonine | 0.0508 | 0.0508 |
| V | Valine | 0.0169 | 0.017 |
| W | Tryptophan | 0.0508 | 0.0508 |
| Y | Tyrosine | 0.00565 | 0.00567 |

Figure S3. Frequency of Amino Acids from Peptide Sequences using MEME (<https://meme-suite.org/meme/tools/meme>).

Other Settings

| | |
|---------------------------------|--------------------------------------|
| Motif Site Distribution | ZOOPS: Zero or one site per sequence |
| Objective Function | E-value of product of p-values |
| Starting Point Function | E-value of product of p-values |
| Site Strand Handling | This alphabet only has one strand |
| Maximum Number of Motifs | 3 |
| Motif E-value Threshold | no limit |
| Minimum Motif Width | 6 |
| Maximum Motif Width | 12 |
| Minimum Sites per Motif | 2 |
| Maximum Sites per Motif | 15 |

[Show Advanced Settings](#)

Figure S4. Settings Used for Analysis of Peptides Using MEME (<https://meme-suite.org/meme/tools/meme>).