

LEGENDS FOR SUPPLEMENTARY FIGURES

FIG. S1. Sequence Alignment of Motif 24 peptides. Peptides containing Motif 24 were classified as interfering or non-interfering, and each class was aligned using Vector NTI-AlignX. Color coding of amino acid similarities from Vector NTI-AlignX is: black on white - non-similar residues, blue on cyan - a consensus residue derived from a block of similar residues; black on green - a consensus residue derived from the occurrence of greater than 50% of a single residue; red on yellow - a consensus derived from a completely conserved residue, green on white - a residue weakly similar to a consensus residue at a given position.

FIG. S2. Sequence alignments of selected motifs. Motifs 1, 4, 20, 25 and 27 consist primarily of interfering peptides (in red). Motif 28 includes mostly noninterfering peptides (in blue). See Figure S1 for description of the consensus color code.

Figure S1
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Motif 24 $\frac{G}{S} CxL CxL$

Interfering

N-22	CRTRGCGCHLCRMLSQFTGG
N-27	RDPQLGQVAQTWGCRLCLLE
N-147	GRGGCMLCDVDGSSAWLHTEGRLTGPITSQQCLSFOYLGNGEFIDG
N-59	AKDVERGAGGKIKACELCRL
N-137	SSSPVPYSGGT CNLCSMRMW
N-5	NECLICHMLGIREFGLSA
N-146	RSCVLCAYGSRTFNGSYLLF

Non-interfering

GFRAPGLSPTRPSC LICSTL	N-3
VPQPLNCDL CVLMGGASSR	N-16
RRDYRKFFALNCQLCRLTVT	N-18
VETFKARARQTPSCDLCPKT	N-63
RYRVSAGPLCSLCSLWGSVG	N-69
VLGRLGGAGGCSL CDQLEAL	N-109
RHESALHKSCELCYCPWKVC	N-112
LVMGWRSEVSSLQKGTGTGGGPTLRKQLCRGSRYTLKYYPCL	N-150
RRCMLCTSDKPGGDQ GALNM	N-158
RPGCPFC TSWRCG	N-153
TPSVTWLAEWCS CVFCRDAS	N-166

Figure S2
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Motif 1 $W_x D x_3 A W$

N-110 IWINPNGLWTKVGLNPNYAV
 N-40 LQYSWNLYSVASEFKTRRVSS
 N-140 EWEDPQYAGWELFSISDLVH
 N-176 AWDSESLATWASVMPWPYPYPT
 N-143 RAGWHERVRQWVAIECTLEV
 N-46 CYMEVEGRPRRWADSFFVAW

Motif 4 $M H x_5 G$

N-5 NECLICHMLGIREFGLSA
 N-22 CRTRGCGCHLCRMLSQFTGG
 N-101 ASLIGVGLIASMHGMQTDGIY
 N-64 TELWWADFAKMHMEGGKGMG
 N-99 RERGGDDYRRMMHPGAASGP
 N-119 RSYGGGEIPSVTMHCWIHCD

Motif 20 $\frac{L}{M} G G x_2 P$

N-16 VPQPLNCDLVCVLMGGASSR
 N-109 VLGRLGGAGGCSLCDQLEAL
 N-160 GMSGRIPEPDDWVVLFITGC
 N-94 RLGGGRPKLWHFSPNLMAGF
 N-84 GGRQTEPSLTLLADLTLLLS
 N-173 CLDNLCWELGGGFPVILIHC
 N-119 RSYGGGEIPSVTMHCWIHCD
 N-99 RERGGDDYRRMMHPGAASGP

Motif 25 $W x_3 S L C$

N-40 LQYSWNLYSVASEFKTRRVSS
 N-167 SWWWANNSLCREWEFAC
 N-159 LWGGGTAWDFFVWGEDSAC
 N-174 HVHGSCPSMGWSSNSWCVSF
 N-176 AWDSESLATWASVMPWPYPYPT
 N-140 EWEDPQYAGWELFSISDLVH

Motif 27 $\frac{S}{A} F x_2 A x V A S$

N-40 LQYSWNLYSVASEFKTRRVSS
 N-27 RDPQLGQVAQTWGCRLCLLE
 N-101 ASLIGVGLIASMHGMQTDGIY
 N-161 GGTNALLQKVFFGEVGVASM
 N-116 SCDEAFDAASVASELFCQPY
 N-168 WNMLAFGGALVASGLLRGWE
 N-176 AWDSESLATWASVMPWPYPYPT

Motif 28 $W G x V L$

N-135 RDAEWQDVLGRARAVHLRGR
 N-129 VYEWGDVLCGGSMAIQWGL
 N-176 AWDSESLATWASVMPWPYPYPT
 N-127 TWGLVCTGTGWGLLDTVVRA
 N-110 IWINPNGLWTKVGLNPNYAV