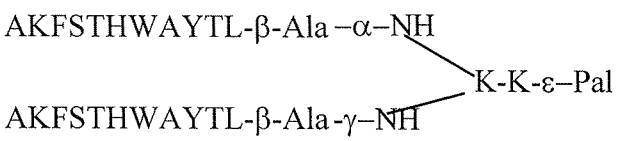
TABLE 4

Compound	Structure	IC_{50}, μM
SMO i2-1	Pal-LTYAWHTSFKALGTTYQPLSGKYSY	0.45±0.05
SMO i2-2	Pal-LTYAWHTSFKALGTTYQPLSGKTSY	0.45±0.05
SMO i2-3	Pal-LTYAWHTSFKALGTTYQPLSG	1.4±0.4
SMO i2-4	Ac-LTYAWHTSFKALGTTYQPLSGKTSYK- ε -Pal	1.0±0.1
SMO i2-5	Ac-YAWHTSFKALGTTYQPLSGKTSYK- ε Pal	1.0±0.1
SMO i2-6	Pal-LTYAWHTSFKALGTTYQP	0.3±0.05
SMO i2-7	Ac-GTTYQPLSGKTSYK- ε Pal	2.7±0.4
SMO i2-8	Pal-LTYAWHTSFKAL	0.08±0.02
SMO i2-9	Ac-LTYAWHTSFKAL	>10
SMO i2-10	Pal-TYAWHTSFKAL	0.7±0.1
SMO i2-11	Pal-LTYAWHTSFKA	0.09±0.007
SMO i2-12	Pal-LTYAWHTSFK	0.06±0.007
SMO i2-13	Ac-TYAWHTSFKA	2.8±0.3
SMO i2-14	VWFVVLTYAWHTSFKAL	>5
SMO i2-15	WFVVLTYAWHTSFKAL	>5
SMO i2-16	Ac-LAKFSTHWAYT¥LK-ε-Pal (all D-)	0.006±0.0005
SMO i2-17	Ac-AKFSTHWAYT¥LK- εPal (all D-)	0.0004±0.0001
SMO i2-18	Pal-LTYABpaHTSFKAL	0.1±0.05
SMO i2-20	Ac-KFSTHWAYT¥LK- εPal (all D-)	0.0003±0.0001
SMO i2-21	Pal-LTYABpaHTSFKAL-Hcy-Biotin	>15
SMO i2-23	Pal-LTYAWHTSFKALGTTYQPLSGKTSYK- ε -Pal	0.05±0.02
SMOi2-24	PalLTYAWHTSFKAL (All D)	0.039±0.004
SMOi2-25	AcLTYAWHTSFKAL (All D)	>10
SMO i2-26	Myr-LTYAWHTSFKAL	0.2±0.05
SMO i2-29	Ac-LTYAWHTSFKAL-Penetratin	>15
SMO i2-30	Penetratin-LTYAWHTSFKAL	>15
SMOi2-56		4.0 nm

Pal, palmitate; Ac, acetate; (All D), each amino acid of the polypeptide is the D isomer; Myr, myristic acid; ε-Pal, palmitate added on the ε carbon of Lys; (Bpa), 4-benzoylphenylalanine.

TABLE 5

Compound	Structure	IC_{50}, μM
SMO i3–1	PalRGVMTLFSIKSNHPGLLSEKAASKINETML	0.64±0.1
SMO i3–2	PalRGVMTLFSIKSNHPGLLSEKA	0.50±0.1
SMO i3-4	PalLFSIKSNHPGLLSEKAASKINETMLR	1.5±0.2
SMO i3–5	AcRGVMTLFSIKSNHPGLLSEKAASKINETMLRK- ε -Pal	0.9±0.2
SMO i3–6	Ac-LLSEKAASKINETMLRK-ε-Pal	0.8±0.1
SMO i3–7	Ac-LFSIKSNHPGLLSEKAASKINETMLRK- ε -Pal	0.95±0.2
SMO i3–8	PalRGVMTLFSIKSNHPGLLS	0.5±0.1
SMO i3–10	PalRGVMTLFSIKSNH	0.95±0.2
SMO i3–12	Ac-~~LL~~SEKAASKINETMLRK ε -Pal	1.33±0.2

[0100] As shown in Table 5 and Figure 3, polypeptides based on the third intracellular loop of SMO exhibit the ability to inhibit the growth of MCF-7 cells. Also, peptides corresponding to fragments of the third intracellular loop have activities that are comparable or lower than the full-length loop (SMOi3-1).

[0101] As shown in Table 4, several of the polypeptides based on the second intracellular loop of SMO (SMOi2 polypeptides) are able to inhibit the growth of SK-Mel2 melanoma cells after 48 hours of exposure to the polypeptides. Among the most potent inhibitors are SMOi2-16, SMOi2-17, SMOi2-8, SMOi2-23, SMOi2-24, SMOi2-20, SMOi2-26, SMOi2-11, and SMOi2-12. Also, SMOi2-6, SMOi2-7, SMOi2-2 through SMOi2-5, SMOi2-10, and SMOi2-13 are potent inhibitors. C-terminal truncation of the second intracellular loop yields polypeptides that were significantly more toxic to cancer cells than the full-length loop (SMOi2-1). Both halves of the loop when palmitoylated at the amino acids which are positioned at the end of the loop (which end is adjacent to the membrane in the wild-type SMO protein) are active. However, C-terminal extension of the N-terminal half lowers the activity of the most potent 12-residue long polypeptide (compare peptides SMOi2-8 with SMOi2-6 and SMOi2-3).