

Accession	Description	Coverage	# Peptides	# PSMs	# Unique Peptides	# AAs	MW [kDa]	calc. pI	Score Sequest HT	# Peptides Sequest HT
Q9FSG7	Thaumatococcus protein 1a OS=Malus domestica GN=TL1 PE=1 SV=1	31	5	6	5	246	25,683	5,15	12,0395534	5

Annotated Sequence	Modifications	# Protein Groups	# Proteins	Master Protein Accessions	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	DeltaM [ppm]	RT [min]
[K].QcPQAYSAYDDK.[N]	C2(Carbamidomethyl)	1	2	Q9FSG7	0	2	804,8347	1608,662	-0,83398	12,57942
[K].AADGSVISK.[S]	C9(Carbamidomethyl)	1	2	Q9FSG7	0	2	504,2451	1007,483	0,394488	11,09707
[K].SACLAFGDSK.[Y]	C3(Carbamidomethyl)	1	2	Q9FSG7	0	2	528,2454	1055,483	0,781336	12,91876
[K].AADGSVISK.[S]	C9(Carbamidomethyl)	1	2	Q9FSG7	0	2	504,2448	1007,482	-0,21133	11,25774
[R].SVDAPSPWSGR.[F]		1	2	Q9FSG7	0	2	579,781	1158,555	0,79669	13,25838
[K].ITFTNNcPNTVWPGTLTGDKPQLSLTGFEELASK.[A]	C7(Carbamidomethyl)	1	1	Q9FSG7	0	4	934,7219	3735,866	-0,82041	16,42328

Figure S2: Amino acid sequences of tryptic peptides mapped on Thaumatococcus protein 1a identified by high-resolution nanoLC-Tandem Mass Spectrometry (AC: Q9FSG7). Within the Table, sequences, number of missed cleavages sites (MC), experimental masses of precursor ions, charge state, experimental and theoretical molecular weights of peptides (MH+) together with mass accuracies and retention times are reported. c = carbamidomethyl cysteine.

>sp|Q9FSG7|TP1A_MALDO Thaumatin-like protein 1a OS=Malus domestica OX=3750 GN=TL1 PE=1 SV=1
Sequence ID: Query_8427 Length: 246
Range 1: 2 to 246

Score:157 bits(398), Expect:2e-52,
Method:Compositional matrix adjust.,
Identities:97/249(39%), Positives:136/249(54%), Gaps:27/249(10%)

Query	1	MGNLRSSFVFFLLALVTYT--YAATIEVRNNCPYTVWAASTPIGGGRRLDRGQTWVINAP	58
		M + +S + LA++ ++ +AA I NNCP TVW + + G ++ T A	
Sbjct	2	MKSQVASLLGLTLAILFFSGAHAAKITFTNNCPNTVWPGT--LTGDQKPQLSLTGFELAS	59
Query	59	RGTKMA-----RVWGRNTCNFNAAGRGTCTGDCG--GVLQCTGWGK--PPNTLAEYAL	108
		+ ++ R WGR T C+ +AAG+ TC+T DCG G + C G G PP TL E +	
Sbjct	60	KASRSVDAPSPWSGRFWRTRCSTDAAGKFTCETADCGSGQVACNGAGAVPPATLVEITI	119
Query	109	DQFSGLDLFDISLVDGFNIPMTFAPTNPSGGKCHAIHCTANINGECPRELVPVG-----	163
		G D++D+SLVDGFN+PM+ AP +G +C C AN+N CP L+V	
Sbjct	120	AANGGQDYDVS LVDGFNL PMSVAPQGGTG--ECKPSSCPANVNKVCAPLQVKAADGSVI	178
Query	164	-CNNPCTTFGGQQYCCTQ-----GPCGPTFFSKFFKQRCPDAYSYPQDDPTSTFTCPGGS	217
		C + C FG +YCCT C PT +S+ F+++CP AYSY DD STFTC GG	
Sbjct	179	SCKSACLAFGDSKYCCTPPNNTPETCPTEYSEIFEKQCPQAYSAYDDKNSTFTCSGGP	238
Query	218	TNYRVIFCP 226	
		+Y + FCP	
Sbjct	239	-DYVITFCP 246	

Figure S3: Pairwise protein sequence alignment between Osmotin (accession number Q40529) and Thaumatin-like 1a protein (accession number Q9FSG7) was performed by query on RCSB PDB Protein Data Bank.

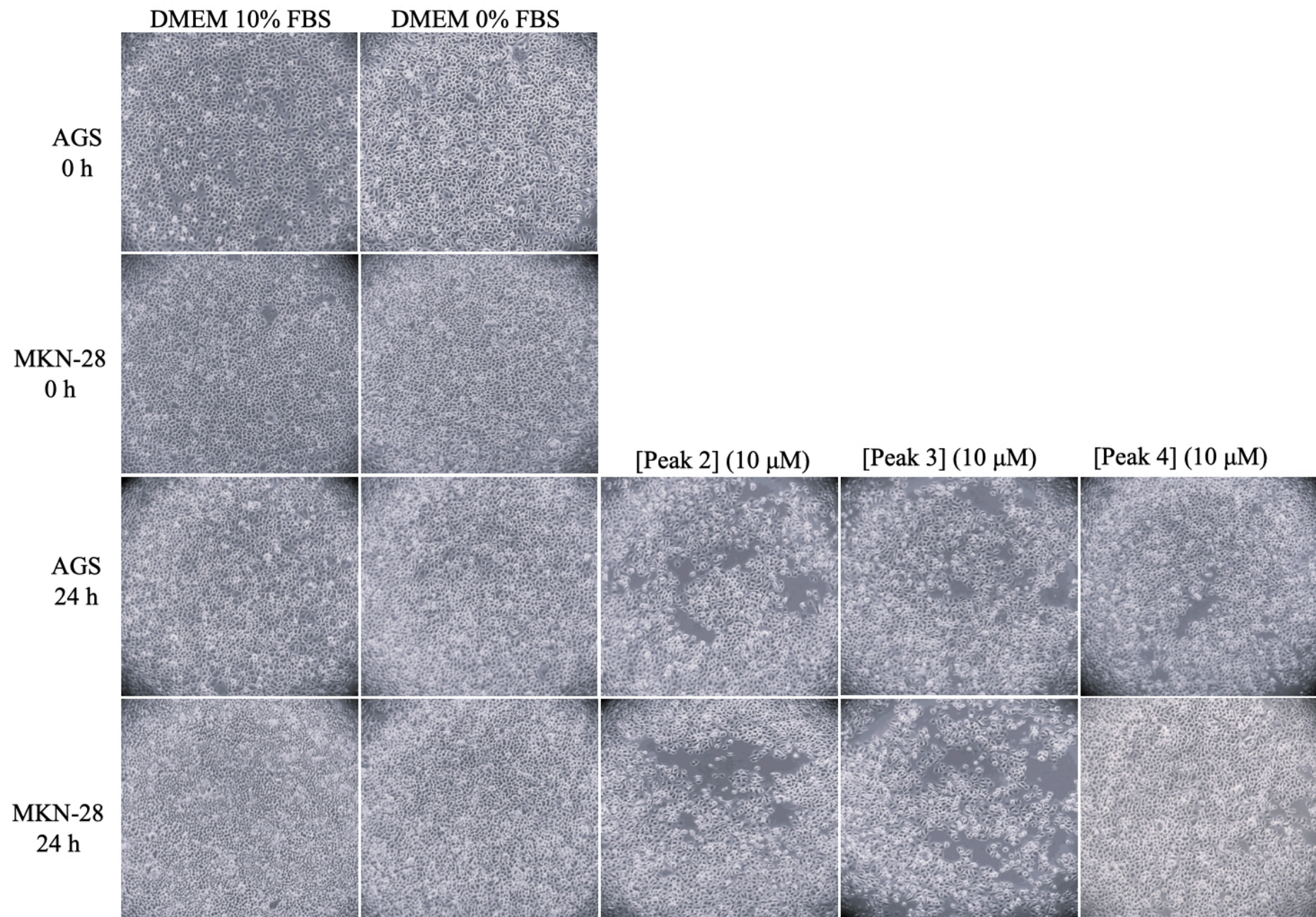


Figure S4: Effects of Peaks 2-4 on AGS and MKN-28 cell morphology. Cells kept in serum-free medium were treated with the indicated concentration of each sample, for 24 h and then subjected to cell morphology analysis. Representative images of AGS and MKN-28 cells captured at time 0 and 24 h by a phase-contrast microscope (10 \times objective). Cells kept in serum-free conditions (DMEM 0% FBS) were treated with the indicated concentration of each Peak.

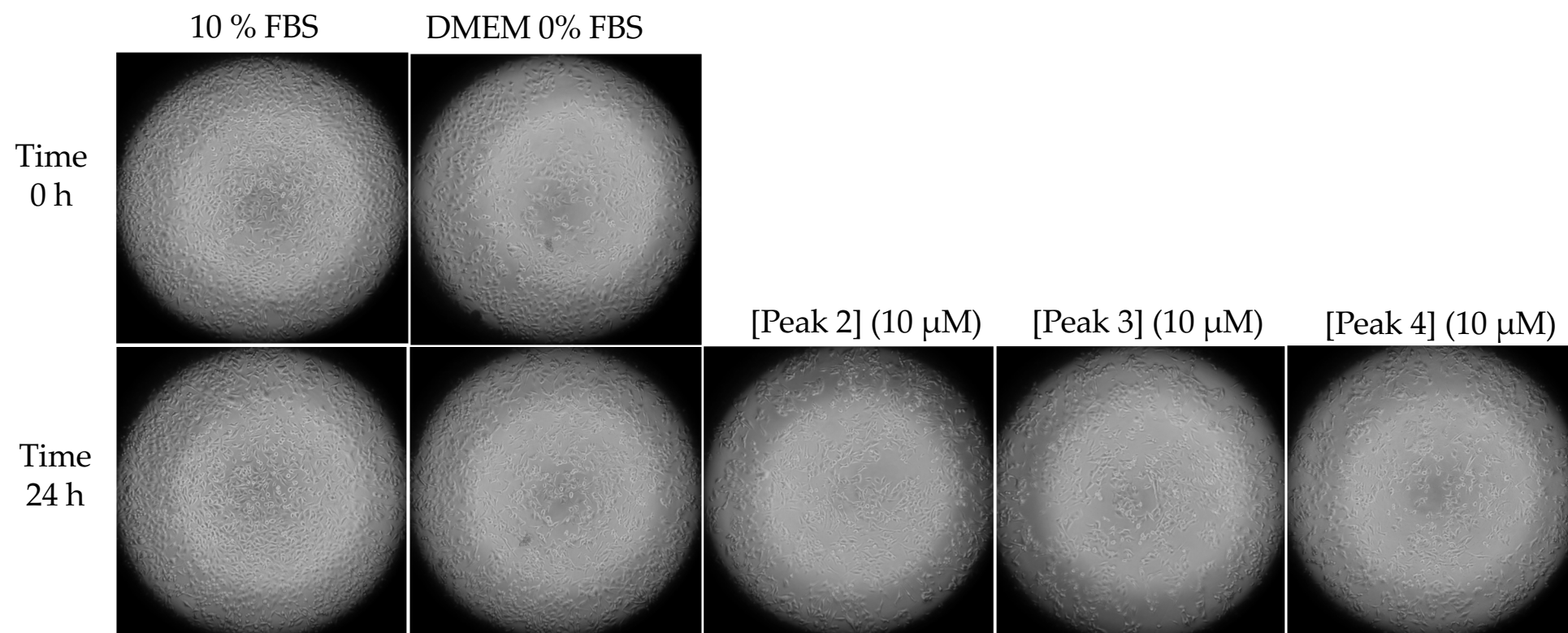


Figure S5: Effects of Peaks 2-4 on SH-SY5Y cell morphology. Cells plated onto 96-well plate were exposed to the indicated concentration of each sample, for 24 h and then subjected to cell morphology observation. Representative images of cells captured at time 0 and 24 h by phase-contrast microscopy (10 \times objective).