Label	ABBR. Name	Mw/p*I* Theor.	PMF Score [a]	Peptide matched/ peptide searched	SC[b] %	Lift (MS_2) Ion parent masses (m/z)	Score [c] Tof-Tof	Peptide Sequence
M2	**IFNA1**	22.11/ 5.32	45	5	32	1108.5125 1247.6590 1464.6488	318	ISPSSCLMDR SLSLSTNLQER DSSAAWDEDLLDK
M3	S10A9	13.29/ 5.71	101	13	90	2175.9624 1455.7226	201	MHEGDEGPGHHHKPGLGEGT LGHPDTLNQGEFK
M8	CYTN	16.60/ 6.73	70	11	68	1914.9344 1292.6633	189	QQTVGGVNYFFDVEVGR ALHFAISEYNK
M11	ENOB	47.69/ 6.5	102	27	67	1166.6316 1380.7117 2296.1376	263	IGAEVYHHLK GNPTVEVDLHTAK SGETEDTFIADLVVGLCTGQ IK
M12	CAH6	35.45/ 6.51	94	11	25	2288.0982 1588.8594	221	NYPENTYYSNFISHLANIK HVIEIHIVHYNSK
M19	PIGR	84.42/ 5.58	93	29	39	1228.7623 1539.6517 2114.1968	136	LVSLTLNLVTR ASVDSGSSEEQGGSSR LDIQGTGQLLFSVVINQLR
M21	AMY1A	58.41/ 6.47	160	21	49	1099.6721 1726.8031	101	LSGLLDLALGK DVNDWVGPPNDNGVTK
M25	PIGR	84.42/ 5.58	40	21	43	1228.7623 2025.9664	227	LVSLTLNLVTR QGHFYGETAAVYVAVEER
M22	CYTS	16.48/ 4.95	87	13	73	1292.6633 1963.9184 2074.0239	192	ALHFAISEYNK EQTFGGVNYFFDVEVGR IIPGGIYDADLNDEWVQR
M24	HS71A	70.29/ 5.48	126	19	39	1197.6949 1465.8121 1877.8949	98	DAGVIAGLNVLR AQIHDLVLVGGSTR CQEVISWLDANTLAEK
M29	CYTN	16.60/ 6.73	138	4	37	1914.9344 1292.6633	142	QQTVGGVNYFFDVEVGR ALHFAISEYNK
M50	AMYP	58.41/ 6.47	160	27	49	1002.4275 1185.7089 1918.9843	295	SSDYFGNGR LTGLLDLALEK IAEYMNHLIDIGVAGFR
D9	ILEU	5.90/ 42.82	54	19	39	1149.5898 1510.7383 1650.8077	147	FQSLNADINK LEESYTLNSDLAR IPELLASGMVDNMTK
D10	ACTB	5.29/ 42.05	100	27	48	976.4482 1790.8919 2231.0648	106	AGFAGDDAPR SYELPDGQVITIGNER DLYANTVLSGGTTMYPGIAD
D11	ERI1	6.29/ 40.49	37	17	29	1064,4863 1278.6623	99	LGYAGNTEPQFIIPSCIAIK FLNIQCQLSR
D13	ACTG	5.31/ 42.10	102	29	60	976.4482 1198.7055 2231.0648	211	AGFAGDDAPR AVFPSIVGRPR DLYANTVLSGGTTMYPGIAD
D15	SERP3	6.35/ 44.59	54	26	48	1047.5622 1707.8336 1804.9479	145	GSFVHYPLK GISGQDGFYVSEAIHK SILNSWGVTDLFDPLK
D16	ARP3	5.61/ 47.79	85	35	53	947.4792 1497.7795 2192.1419	307	LSEELSGGR EVGIPPEQSLETAK LGYAGNTEPQFIIPSCIAIK
D38	BPIA2	5.35/ 27.16	90	14	56	1134.6517 1101.6514 1907.0120	111	FVNSVINTLK ISNSLILDVK LEPVLHEGLETVDNTLK
D39	BPIA2	5.35/ 27.16	96	14	55	962.5517 900.5513	247	STVSSLLQK LLNNVISK
D44	PSA5	4.74/ 26.56	52	15	58	1143.4830 1961.9563 2033.0583	226	GVNTFSPEGR AIGSASEGAQSSLQEVYHK LGSTAIGIQTSEGVCLAVEK
D49	GML	6.10/ 18..35	41	9	62	1599.9720 2004.8473	183	LLLSFASIIVSNILP CHDCAVINDFNCPNIR
D51	HSBP3	5.36/ 17.06	29	4	32	1866.9993 1593.7867	289	DLSAVLCHDGILVVE AAQSPPVDSAAETPPR

Sequence validation of selected proteins from unstimulated and stimulated saliva samples by MS using LIFT technology a: PMF Score = values are Log10 (p), where p is probability that the observed match is a random event; it is based on Swiss Prot database using the MASCOT searching program; b: SC = Sequence Coverage means the ratio of portion sequence covered by matched peptide to the full length of the protein sequence. c: Score Tof-Tof = score that results from combining PMF and MS /MS matched peptide from ion parent fragments