

## Supplementary Materials

**Table S1.** UPLC-MS-MS-identified molecular information for all peptide fragments in the digests of Lf, LfPF complex, and LfPFTG complex

Sample	Peptide	Sequence	-10lgP	Mass	Length	ppm	m/z	RT (min)	Area
LfG	EIYGTKESPQTHY	99-111	58.6	1551.72	13	0.5	776.868	16.07	3.44E+08
	AEIYGTKESPQTHY	98-111	61	1622.76	14	1.9	812.388	16.12	1.49E+09
	AAEIYGTKESPQTHY	97-111	39.87	1693.79	15	0.3	565.606	16.42	2.39E+05
	YKLRPVA	91-97	30.33	845.512	7	2.3	423.764	15.05	0
	PYKLRPVAAE	90-99	40.7	1142.64	10	1.6	572.331	14.77	1.72E+05
	PYKLRPVAA	90-98	41	1013.6	9	5.4	507.811	15.51	2.51E+06
	PYKLRPVA	90-97	36.5	942.565	8	0.8	315.196	13.69	7.37E+07
	RDPYKLRPVA	88-97	34.48	1213.69	10	2.6	405.573	13.2	1.31E+05
	GRDPYKLRPVAA	87-98	54.44	1341.75	12	0.7	448.258	15.51	3.11E+05
	GRDPYKLRPVA	87-97	50.56	1270.71	11	0.7	424.579	14.86	6.52E+06
	AGRDPYKLRPVAAE	86-99	52.97	1541.83	14	0	514.951	14.7	6.08E+05
	AGRDPYKLRPVAA	86-98	48.92	1412.79	13	2.3	471.938	15.49	2.97E+06
	AGRDPYKLRPVA	86-97	54.7	1341.75	12	0.5	448.258	14.85	5.85E+07
	AGRDPYKLRPV	86-96	29.49	1270.71	11	0.8	424.579	13.79	5.72E+05
	EAGRDPYKLRPVAAE	85-99	51.74	1670.87	15	1.4	557.966	16.08	3.30E+07
	EAGRDPYKLRPVAA	85-98	56.62	1541.83	14	3.2	514.953	15.66	3.32E+08
	EAGRDPYKLRPVA	85-97	52.41	1470.79	13	-2.2	491.271	23	4.16E+09
	EAGRDPYKLRPV	85-96	53.74	1399.76	12	2.3	467.594	14.82	1.51E+07
	EAGRDPYKL	85-93	30.28	1047.53	9	2.8	524.776	14.19	2.17E+06
	FEAGRDPYKLRPVAAE	84-99	60.7	1817.94	16	3.5	606.99	21.08	1.58E+06
	FEAGRDPYKLRPVAA	84-98	63.21	1688.9	15	1.3	563.975	20.74	6.77E+07
	FEAGRDPYKLRPVA	84-97	56.41	1617.86	14	1	540.295	22.99	1.29E+09
	FEAGRDPYKLRPVA	84-97	34.24	1659.87	14	-5.3	554.295	28.88	2.27E+06
	FEAGRDPYKLRPV	84-96	37.55	1546.83	13	7.1	516.619	20.29	4.87E+06
	FEAGRDPYKL	84-93	35.7	1194.6	10	3.7	598.311	21.48	2.97E+06
	FEAGRDPYK	84-92	34.17	1081.52	9	1.3	541.768	10.96	1.67E+05
	VFEAGRDPYKLRPVAA	83-98	52.03	1787.97	16	1.1	596.997	23.34	3.55E+06
	VFEAGRDPYKLRPVA	83-97	51.11	1716.93	15	2.1	573.319	23.12	1.14E+08
	VFEAGRDPYKL	83-93	46.04	1293.67	11	2.5	647.845	24.25	9.77E+05
	LGGRPTYEE	670-678	40.03	1020.49	9	4.2	511.253	13.19	1.20E+06
	AKLGGRPTYEE	668-678	34.51	1219.62	11	2.5	610.819	10.37	2.00E+07
	FKSETKNLL	651-659	47.93	1078.6	9	2.9	540.31	15.69	1.06E+08
	LHQQALF	631-637	30.01	855.46	7	2	428.738	23.73	2.37E+06
	NLNREDF	582-588	29.23	906.42	7	1.1	454.218	16.97	8.73E+06

WAKNLNREDF	579-588	44.16	1291.63	10	2.3	646.824	20.94	1.01E+09
KYYGYTGA	541-548	42.9	921.423	8	1.6	461.72	15.94	4.28E+07
RTAGWNIPMGLI	482-493	37.43	1327.71	12	3.3	664.863	45.66	1.57E+07
RTAGWNIPMGL	482-492	36.38	1214.62	11	3.2	608.321	42.34	5.19E+09
DRTAGWNIPMGL	481-492	37.58	1329.65	12	3.5	665.835	45.16	3.36E+07
VKKANEGLTW	458-467	42.45	1144.62	10	1.4	573.32	17.47	5.38E+07
VVKKANEGLTW	457-467	46.82	1243.69	11	1.4	622.854	18.55	5.13E+08
AVVKKANEGLTW	456-467	52.5	1314.73	12	2.2	658.374	19.59	1.77E+08
VLRPTEGYL	445-453	44.24	1046.58	9	1.8	524.296	26.03	2.25E+06
VLRPTEGY	445-452	44.94	933.492	8	2.5	467.754	16.19	1.54E+06
YTRVVW	360-366	35.81	822.439	6	3	412.228	25.25	3.22E+05
YLGSRYLT	338-345	41.12	971.508	8	0.9	486.762	24.61	1.29E+06
RIPSKVDSAL	328-337	42.11	1084.62	10	-0.6	543.319	14.94	7.56E+06
LRIPSKVDSAL	327-337	59.9	1197.71	11	2.9	599.863	25.14	5.40E+09
LRIPSKVDSA	327-336	50.9	1084.62	10	1.9	543.32	15.56	9.81E+07
LRIPSKVDS	327-335	44.7	1013.59	9	0.4	507.801	14.7	4.56E+06
LRIPSKVD	327-334	32.17	926.555	8	3.1	464.286	15.14	7.39E+06
FLRIPSKVDSAL	326-337	41.68	1344.78	12	2.1	449.267	30.55	1.15E+07
FLRIPSKVDSA	326-336	38.04	1231.69	11	2.4	411.572	22.91	1.88E+05
PPGQRDLL	311-318	37.5	894.492	8	0.2	448.254	27.47	3.24E+06
SPPGQRDLL	310-318	35.01	981.524	9	1.4	491.77	27.46	0
FGSPPGQRDLLF	308-319	28.7	1332.68	12	9	667.355	37.12	0
FGSPPGQRDLL	308-318	54.96	1185.61	11	2.6	593.816	29.07	3.66E+09
FGSPPGQRDL	308-317	40.71	1072.53	10	3.3	537.274	19.47	8.87E+07
LFGSPPGQRDLL	307-318	54.95	1298.7	12	2.4	650.358	35.31	2.92E+07
LFGSPPGQRDL	307-317	40.71	1185.61	11	1.1	593.815	26.85	0
QLFGSPPGQRDLL	306-318	46.03	1426.76	13	3.5	714.388	36.37	2.45E+07
QLFGSPPGQRDL	306-317	50.97	1313.67	12	2.8	657.846	29.43	3.82E+06
QLFGSPPGQRD	306-316	37.21	1200.59	11	1.4	601.303	21.86	1.44E+06
RSVDGKEDLIWKL	277-289	51.11	1557.85	13	2.4	520.292	29.03	3.19E+06
ARSVDGKEDLIWKL	276-289	51.71	1628.89	14	3.1	543.972	28.86	1.42E+06
DRDQYEL	242-248	30.59	937.414	7	3.2	469.716	21.52	3.24E+07
PEKADRDQYEL	238-248	51.34	1362.64	11	-0.9	682.327	14.88	5.13E+06
PEKADRDQYE	238-247	58.05	1249.56	10	2.8	625.788	14.11	5.04E+05
LPEKADRDQYE	237-247	37.91	1362.64	11	0	682.328	14.19	1.59E+05
ENLPEKADRDQYEL	235-248	52.97	1718.81	14	1.5	860.414	22.91	1.28E+08
ENLPEKADRDQYE	235-247	47.92	1605.73	13	2.3	536.251	14.35	2.02E+08
ENLPEKADRDQY	235-246	31.55	1476.68	12	1.6	493.236	14.08	3.97E+07
FENLPEKADRDQ	234-245	28.89	1460.69	12	2.5	487.905	14.34	7.32E+05

LfPFG	REPYFGY	204-211	33.5	930.424	7	3.4	466.221	27.13	3.63E+05
	SREPYFG	203-210	32.07	854.392	7	2.1	428.204	18.82	3.95E+08
	SREPYF	203-209	31.97	797.371	6	2.3	399.694	20.24	2.61E+08
	RQAYPNL	182-188	33.19	860.45	7	2.2	431.233	18.63	6.96E+05
	RPYLSWTE	152-159	37.8	1050.51	8	3.2	526.266	30.78	4.56E+07
	RPYLSWT	152-158	33.62	921.471	7	2.8	461.744	30.71	1.71E+09
	RPYLSW	152-157	33.22	820.423	6	2.2	411.22	31.69	6.88E+08
	LRPYLSWT	151-158	28.56	1034.55	8	2	518.286	34.83	1.63E+06
	ILRPYLSW	150-157	34.36	1046.59	8	2.2	524.304	40.27	5.27E+06
	ILRPYL	150-155	31.56	773.48	6	3	387.748	28.21	7.94E+08
	GILRPYL	149-155	31.13	830.501	7	2.5	416.259	31.62	1.30E+07
	KESPQTHY	104-111	35.36	988.461	8	-0.6	495.238	15.33	1.08E+05
	TKESPQTHY	103-111	29.88	1089.51	9	-2.7	545.76	16.08	0
	GTKESPQTHY	102-111	57.21	1146.53	10	3	574.274	13.69	6.76E+06
	YGTKESPQTHY	101-111	63.46	1309.59	11	1.6	655.805	15.94	2.90E+07
	IYGTKESPQTHY	100-111	59.87	1422.68	12	1	712.347	16.22	4.27E+08
	EIYGTKESPQTHY	99-111	65.69	1551.72	13	4.5	776.871	16.2	485000000
	AEIYGTKESPQTHY	98-111	72.09	1622.76	14	2.2	812.388	16.3	1.45E+09
	YKLRPVA	91-97	34.1	845.512	7	2.9	423.765	14.79	0
	PYKLRPVAAE	90-99	36.74	1142.64	10	-0.6	572.329	14.33	714000
	PYKLRPVAA	90-98	29.14	1013.6	9	-1.2	507.808	13.72	2740000
	PYKLRPVA	90-97	39.14	942.565	8	1.4	472.291	20.12	128000000
	RDPYKLRPVA	88-97	38.5	1213.69	10	0.2	405.572	14.62	160000
	GRDPYKLRPVAA	87-98	47.79	1341.75	12	1.4	448.259	15.73	281000
	GRDPYKLRPVA	87-97	54.04	1270.71	11	2.2	424.58	14.88	9600000
	GRDPYKLRPV	87-96	39.96	1199.68	10	2.5	400.901	14.58	246000
	AGRDPYKLRPVAAE	86-99	49.38	1541.83	14	3.2	514.953	14.45	1720000
	AGRDPYKLRPVAA	86-98	56.15	1412.79	13	1.9	471.938	15.64	4680000
	AGRDPYKLRPVA	86-97	58.36	1341.75	12	1.4	448.259	14.88	84000000
	AGRDPYKLRPV	86-96	46.46	1270.71	11	0.4	424.579	13.08	4960000
	EAGRDPYKLRPVAAE	85-99	58.56	1670.87	15	0.6	557.966	16.2	82900000
	EAGRDPYKLRPVAA	85-98	63.51	1541.83	14	2.7	514.953	15.8	426000000
	EAGRDPYKLRPVA	85-97	54.42	1470.79	13	1.9	491.273	22.41	3.89E+09
	EAGRDPYKLRPV	85-96	60.18	1399.76	12	2.4	467.594	14.8	210000000
	EAGRDPYKLRP	85-95	35.63	1300.69	11	1.4	434.571	12.08	665000
	EAGRDPYKL	85-93	41.69	1047.53	9	2.7	524.776	13.92	4300000
	FEAGRDPYKLRPVAAE	84-99	70.07	1817.94	16	3	606.99	20.89	4040000
	FEAGRDPYKLRPVAA	84-98	66.71	1688.9	15	2.1	563.975	20.61	69300000
	FEAGRDPYKLRPVA	84-97	59.88	1617.86	14	4	809.942	22.43	1.01E+09

FEAGRDPYKLRPV	84-96	60.74	1546.83	13	3.5	516.618	20.46	46700000
FEAGRDPYK	84-92	41.42	1081.52	9	3.4	541.769	10.89	238000
VFEAGRDPYKLRPVAAE	83-99	66.44	1917.01	17	-0.7	640.01	22.9	824000
VFEAGRDPYKLRPVAA	83-98	69.21	1787.97	16	2	596.998	22.65	28000000
VFEAGRDPYKLRPV	83-97	58.21	1716.93	15	-1.5	573.317	22.33	244000000
VFEAGRDPYKLRPV	83-96	53.93	1645.89	14	1.8	412.482	22.49	11600000
DGGMVFEAGRDPYKLRPV	79-97	52.43	2077.04	19	-0.7	693.354	30.87	178000
LGGRPTYEE	670-678	35.98	1020.49	9	2.1	511.252	12.67	3130000
AKLGGRPTYEE	668-678	47.12	1219.62	11	0.7	610.818	10.35	36500000
FKSETKNLL	651-659	53.95	1078.6	9	2.2	540.31	15.72	798000000
LFKSETKNLL	650-659	51.76	1191.69	10	1.9	596.852	21.82	2110000
LHQALF	631-637	29.36	855.46	7	3.5	428.739	22.88	1770000
NLNREDF	582-588	32.9	906.42	7	2.4	454.218	17.08	10500000
WAKNLNREDF	579-588	48.35	1291.63	10	2.3	646.824	20.51	716000000
KYYGYTGA	541-548	45.62	921.423	8	2.7	461.72	15.96	27100000
RTAGWNIPMGLI	482-493	39.42	1327.71	12	4	664.864	45.56	5800000
RTAGWNIPMGL	482-492	39.51	1214.62	11	3.4	608.321	42.11	3.22E+09
DRTAGWNIPMGL	481-492	40.1	1329.65	12	2.1	665.834	45.41	1.32E+09
VKKANEGLTW	458-467	50.35	1144.62	10	2.5	573.321	17.28	63400000
VVKKANEGLTW	457-467	44.42	1243.69	11	2.2	622.855	18.07	482000000
AVVKKANEGLTW	456-467	54.07	1314.73	12	0.8	658.373	19.7	310000000
VLRPTEGYL	445-453	37.18	1046.58	9	2.9	524.297	25.73	1450000
VLRPTEGY	445-452	51.5	933.492	8	2.9	467.755	16.1	1190000
YTRVVW	360-366	33.17	822.439	6	1.5	412.227	24.87	189000
YLGSRYL	338-344	30.63	870.46	7	2.7	436.238	26.24	4360000
RIPSKVDSAL	328-337	46.61	1084.62	10	1.1	543.32	14.87	11000000
LRIPSKVDSAL	327-337	62.71	1197.71	11	3.2	599.863	24.68	5.5E+09
LRIPSKVDSA	327-336	53.8	1084.62	10	1.9	543.32	15.68	98100000
LRIPSKVDS	327-335	42.04	1013.59	9	2.4	338.87	14.28	12800000
LRIPSKVD	327-334	38.4	926.555	8	1.9	309.86	14.9	13000000
FLRIPSKVDSAL	326-337	57.48	1344.78	12	2.9	449.267	29.98	10500000
PPGQRDLL	311-318	41.98	894.492	8	1.6	448.254	27.23	2110000
FGSPPGQRDLL	308-318	58.79	1185.61	11	3.1	593.816	28.19	2.02E+09
FGSPPGQRDL	308-317	47	1072.53	10	2.9	537.274	18.79	89400000
LFGSPPGQRDLL	307-318	56.06	1298.7	12	3.8	650.359	34.72	15700000
LFGSPPGQRDL	307-317	33.82	1185.61	11	2.1	593.816	26.95	0
QLFGSPPGQRDLL	306-318	49.31	1426.76	13	3.1	714.388	36.14	11800000
QLFGSPPGQRDL	306-317	39.27	1313.67	12	2.6	657.845	28.78	2050000
QLFGSPPGQRD	306-316	36.41	1200.59	11	3.5	601.304	21.51	1170000

	SVDGKEDLIWKLLSK	278-292	64.85	1729.96	15	1	577.662	40.35	1810000
	RSVDGKEDLIWKLLSK	277-292	49.31	1886.06	16	3	472.524	34.55	207000
	RSVDGKEDLIWKL	277-289	54.56	1557.85	13	3	520.293	28.65	4660000
	ARSVDGKEDLIWKL	276-289	41.68	1628.89	14	2.5	543.972	29.07	510000
	DRDQYEL	242-248	30.37	937.414	7	2.7	469.716	21.5	45100000
	PEKARDRDQYEL	238-248	46.51	1362.64	11	1.9	682.329	14.55	9200000
	PEKARDRDQYE	238-247	55.84	1249.56	10	0.5	625.786	13.66	575000
	LPEKARDRDQYE	237-247	38.59	1362.64	11	0.6	682.328	13.68	264000
	ENLPEKARDRDQYEL	235-248	67.76	1718.81	14	3	860.415	22.33	52500000
	ENLPEKARDRDQYE	235-247	51.51	1605.73	13	2.6	536.251	13.72	246000000
	ENLPEKARDRDQY	235-246	43.9	1476.68	12	1.1	493.236	13.21	57700000
	FENLPEKARDRDQYE	234-247	36.17	1752.8	14	4.6	855.901	22.72	179000000
	FENLPEKARDRDQY	234-246	42.94	1623.75	13	3.3	812.886	19.61	1090000
	FENLPEKARDRDQ	234-245	29.43	1460.69	12	0.5	487.904	13.92	1130000
	REPYFGY	204-211	31.94	930.424	7	0.3	466.219	27.18	53100
	SREPYFG	203-210	32.21	854.392	7	2.2	428.204	18.86	410000000
	SREPYF	203-209	33.31	797.371	6	2	399.694	19.9	275000000
	RPYLSWTE	152-159	41.41	1050.51	8	3.7	526.266	30.43	33300000
	RPYLSWT	152-158	37.11	921.471	7	1.6	461.743	29.09	1.23E+09
	RPYLSW	152-157	33.78	820.423	6	3	411.22	31.03	355000000
	LRPYLSW	151-157	31.48	933.507	7	1.1	467.761	35.61	1600000
	ILRPYLSW	150-157	43.23	1046.59	8	2.7	524.304	39.92	10000000
	ILRPYL	150-155	32.27	773.48	6	2.3	387.748	26.52	830000000
	GILRPYLSW	149-157	32.43	1103.61	9	3.3	552.816	42.65	129000
	GILRPYL	149-155	33.55	830.501	7	2.8	416.259	31.22	8340000
	TKESPQTHY	103-111	30.83	1089.51	9	3	545.763	33.5	1520000
	GTKESPQTHY	102-111	56.66	1146.53	10	3.8	574.275	15.46	5650000
	YGTKESPQTHY	101-111	66.54	1309.59	11	1.7	655.805	16.06	52200000
	IYGTKESPQTHY	100-111	61.94	1422.68	12	1.4	712.347	16.05	582000000
LpPFTGG	EIYGTKESPQTHY	99-111	64.6	1551.72	13	0.8	776.868	16.01	400000000
	AEIYGTKESPQTHY	98-111	67.42	1622.76	14	1.6	812.387	15.76	1.49E+09
	AAEIYGTKESPQTHY	97-111	47.63	1693.79	15	2	565.607	16.24	271000
	YKLRPVA	91-97	39.88	845.512	7	2.8	423.765	14.77	0
	PYKLRPVA	90-97	38.23	942.565	8	0.9	472.29	14.93	35700000
	DPYKLRPVA	89-97	36.06	1057.59	9	1.6	529.804	14.72	960000
	RDPYKLRPVA	88-97	32.19	1213.69	10	-2.4	405.571	14.72	0
	GRDPYKLRPVAA	87-98	53.83	1341.75	12	0.1	448.258	15.5	134000
	GRDPYKLRPVA	87-97	51.45	1270.71	11	3.2	424.58	14.93	12700000
	AGRDPYKLRPVAAE	86-99	39.22	1541.83	14	1.6	514.952	14.41	709000

AGRDPYKLRPVAA	86-98	54.77	1412.79	13	4.7	471.939	15.47	2970000
AGRDPYKLRPVA	86-97	55.17	1341.75	12	1.3	671.884	14.64	94500000
EAGRDPYKLRPVAAE	85-99	59.28	1670.87	15	2.1	557.966	15.69	34500000
EAGRDPYKLRPVAA	85-98	61.42	1541.83	14	4.2	514.953	15.37	233000000
EAGRDPYKLRPVAA	85-98	35.05	1583.84	14	-4.5	528.952	21.31	381000
EAGRDPYKLRPVA	85-97	54.76	1470.79	13	3.2	491.274	19.77	4.06E+09
EAGRDPYKLRPV	85-96	53.79	1399.76	12	2.3	467.594	14.56	31400000
EAGRDPYKLRP	85-95	50.65	1300.69	11	1.8	434.571	11.72	11400000
EAGRDPYKL	85-93	43.98	1047.53	9	2.4	524.776	13.93	8260000
FEAGRDPYKLRPVAAE	84-99	50.83	1817.94	16	3.1	606.99	20.99	735000
FEAGRDPYKLRPVAA	84-98	62	1688.9	15	2.5	563.975	20.65	43700000
FEAGRDPYKLRPVA	84-97	52.71	1617.86	14	2.1	540.296	20.35	815000000
FEAGRDPYKLRPV	84-96	42.31	1546.83	13	1.4	516.617	19.84	6860000
FEAGRDPYKLRP	84-95	37.03	1447.76	12	0.9	483.593	17.74	1050000
FEAGRDPYKL	84-93	36.39	1194.6	10	3	598.311	21.26	2490000
VFEAGRDPYKLRPVAA	83-98	55.82	1787.97	16	2.7	596.998	22.79	1980000
VFEAGRDPYKLRPVA	83-97	50.65	1716.93	15	2.4	573.319	22.52	33100000
VFEAGRDPYKLRPV	83-96	34.43	1645.89	14	0.9	549.639	22.58	222000
FKSETKNLL	651-659	48.37	1078.6	9	2.6	540.31	15.37	322000000
NLNREDF	582-588	35.53	906.42	7	3.3	454.219	16.76	2140000
WAKNLNREDF	579-588	45.3	1291.63	10	1.9	646.824	20.51	912000000
KYYGYTGA	541-548	42.92	921.423	8	2.4	461.72	15.51	21900000
RTAGWNIPMGLI	482-493	34.77	1327.71	12	2.9	664.863	45.43	8960000
RTAGWNIPMGL	482-492	34.75	1230.62	11	3.2	616.318	39.11	273000000
DRTAGWNIPMGL	481-492	36.46	1345.64	12	3.2	673.832	39.94	68600000
VKKANEGLTW	458-467	46.41	1144.62	10	1.3	573.32	16.94	85100000
VVKKANEGLTW	457-467	47.54	1243.69	11	2.2	622.855	17.89	551000000
AVVKKANEGLTW	456-467	53.87	1314.73	12	1.8	658.373	19.58	160000000
YTRVVW	360-366	32.15	822.439	6	3.7	412.228	24.78	173000
YLGSRYLT	338-345	37.03	971.508	8	2.8	486.763	24.26	795000
RIPSKVDSAL	328-337	45.91	1084.62	10	1.8	543.32	14.6	11100000
LRIPSKVDSAL	327-337	59.71	1197.71	11	2.9	599.863	24.62	5.62E+09
LRIPSKVDSA	327-336	50.53	1084.62	10	3	543.321	15.6	141000000
LRIPSKVDS	327-335	35.22	1013.59	9	1.7	507.802	14.3	8750000
LRIPSKVD	327-334	41.95	926.555	8	2.8	464.286	14.9	12000000
FLRIPSKVDSAL	326-337	44.62	1344.78	12	-0.1	673.395	29.52	3430000
PPGQRDLL	311-318	36.97	894.492	8	0.5	448.254	27.3	3100000
SPPGQRDLL	310-318	38.06	981.524	9	0.8	491.77	27.23	59100
FGSPPGQRDLLF	308-319	34.36	1332.68	12	9.8	667.355	37	0

	FGSPPGQRDLL	308-318	55.23	1185.61	11	3.7	593.817	28.77	2.67E+09
	FGSPPGQRDL	308-317	44.64	1072.53	10	1.6	537.273	19.15	172000000
	LFGSPPGQRDLL	307-318	52.33	1298.7	12	3.6	650.359	34.78	21300000
	LFGSPPGQRDL	307-317	39.66	1185.61	11	2.8	593.816	26.57	0
	QLFGSPPGQRDLL	306-318	51.97	1426.76	13	3	714.388	36.01	21200000
	QLFGSPPGQRDL	306-317	37.69	1313.67	12	3.5	657.846	28.73	5040000
	QLFGSPPGQRD	306-316	38.72	1200.59	11	1.7	601.303	21.69	2380000
	RSVDGKEDLIWKL	277-289	45.47	1557.85	13	3.6	520.293	28.52	1890000
	ARSVDGKEDLIWKL	276-289	49.47	1628.89	14	3.9	543.972	28.42	435000
	DRDQYEL	242-248	30.89	937.414	7	2.7	469.716	21.46	34000000
	PEKADRDQYE	238-247	62.45	1249.56	10	2.2	625.787	13.79	841000
	LPEKADRDQYE	237-247	45.33	1362.64	11	1.3	682.329	13.85	477000
	ENLPEKADRDQYEL	235-248	55.59	1718.81	14	0.6	860.413	22.53	33600000
	ENLPEKADRDQYE	235-247	51.83	1605.73	13	1.2	803.872	13.75	365000000
	ENLPEKADRDQY	235-246	41.95	1476.68	12	2.8	493.237	13.54	92800000
	FENLPEKADRDQYE	234-247	36.17	1752.8	14	4.6	585.273	22.72	179000000
	FENLPEKADRDQY	234-246	36.69	1623.75	13	0.4	542.258	19.46	503000
	FENLPEKADRDQ	234-245	44.71	1460.69	12	1.7	731.353	14.15	2360000
	SREPYFG	203-210	31.79	854.392	7	3.5	428.205	18.76	692000000
	SREPYF	203-209	34.93	797.371	6	3	399.694	19.72	336000000
	RQAYPNL	182-188	34.75	860.45	7	2.5	431.234	18.07	1410000
	RPYLSWT	152-158	30.84	921.471	7	2.8	461.744	31.26	0
	ILRPYLSW	150-157	39.21	1046.59	8	2.8	524.304	39.74	4420000
	ILRPYL	150-155	31.55	773.48	6	3	387.748	26.8	805000000
	GILRPYL	149-155	30.6	830.501	7	3.1	416.259	30.95	6760000
	GTKESPQTHY	102-111	55.92	1146.53	10	-1	574.272	13.02	10100000
	YGTKESPQTHY	101-111	63.78	1309.59	11	-0.2	655.804	15.83	42100000
	IYGTKESPQTHY	100-111	59.13	1422.68	12	1.4	712.347	12.99	927000000
LfGI	IYGTKESPQTHY	100-111	41.69	1422.68	12	2.1	475.234	13.63	5.85E+06
	FGSPPGQRDLL	308-318	50.9	1185.61	11	0.9	593.815	27.92	4.08E+07
	LRIPSKVDSAL	327-337	41.48	1197.71	11	1.2	599.862	24.47	2.72E+07
	EAGRDPYKLRPVA	85-97	47.38	1470.79	13	1.7	491.273	15.24	2.79E+07
	AGRDPYKLRPVA	86-97	43.86	1341.75	12	0.1	448.258	15.1	8.12E+04
	EIYGTKESPQTHY	99-111	43.5	1551.72	13	2.7	518.249	15.62	7.97E+06
	VFEAGRDPYKL	83-93	46.04	1293.67	11	2.5	647.845	24.25	9.77E+05
LfPFGI	LRIPSKVDSAL	327-337	64.37	1197.71	11	1.7	599.862	24.9	8.19E+07
	RTAGWNIPMGL	482-492	38.09	1214.62	11	0.9	608.319	41.59	1.44E+07
	NLNREDF	582-588	37.22	906.42	7	3	454.218	17.38	9.40E+06
	FEAGRDPYK	84-92	34.03	1081.52	9	1.9	541.768	11.1	9.93E+05

LIPFTGGI	EIYGTKESPQTHY	99-111	43.5	1551.72	13	2.7	518.249	15.62	7.97E+06
	EIYGTKESPQTHY	99-111	43.5	1551.72	13	2.7	518.249	15.62	7.97E+06
	FEAGRDPYK	84-92	42.08	1081.52	9	2.6	541.768	10.81	2.71E+05
	LGGRPTYEE	670-678	32.54	1020.49	9	2.7	511.252	12.94	2.96E+05
	RTAGWNIPMGL	482-492	42.67	1214.62	11	2.2	608.32	41.3	8.84E+06
	LRIPSKVDSAL	327-337	52.16	1197.71	11	3.1	400.245	24.29	1.60E+07
	FGSPPGQRDLL	308-318	53.72	1185.61	11	3.8	593.817	27.69	1.13E+07
	ENLPEKADRQY	235-246	33.57	1476.68	12	1.8	493.236	13.56	2.00E+05
	FENLPEKADRQYE	234-247	36.17	926.414	14	4.6	442.709	22.72	1.79E+08
	SREPYF	203-209	34.79	797.371	6	3.4	399.694	20.11	2.29E+06

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**Table S2.** Peptide fragments found in the digests of Lf, LfPF complex, and LfPFTG complex

Targeted peptide fragment	Peptide fragment	Sequence No	Sample			
			LfG	LfPFG	LfPFTGG	GI digests
DGGMVFEAGRDPYKLRPVAAE f (79–99)	VFEAGRDPYKLRPVAA	83-98	+	+	+	
	VFEAGRDPYKLRPVA	83-97	+	+	+	
	FEAGRDPYKLRPVAAE	84-99	+	+	+	
	FEAGRDPYKLRPVAA	84-98	+	+	+	
	FEAGRDPYKLRPVA	84-97	+	+	+	
	FEAGRDPYKLRPV	84-96	+	+	+	
	EAGRDPYKLRPVAAE	85-99	+	+	+	
	EAGRDPYKLRPVAA	85-98	+	+	+	
	EAGRDPYKLRPVA	85-97	+	+	+	
	EAGRDPYKLRPV	85-96	+	+	+	
	EAGRDPYKL	85-93	+	+	+	
	AGRDPYKLRPVAAE	86-99	+	+	+	
	AGRDPYKLRPVAA	86-98	+	+	+	
	AGRDPYKLRPVA	86-97	+	+	+	
	GRDPYKLRPVAA	87-98	+	+	+	
	GRDPYKLRPVA	87-97	+	+	+	
	RDYKLRPVA	88-97	+	+	+	
	PYKLRPVA	90-97	+	+	+	
	YKLRPVA	91-97	+	+	+	
						LfPFGI(+)
	FEAGRDPYK	84-92	+	+		LfPFTGGI (+)
	FEAGRDPYKL	84-93	+		+	
	AGRDPYKLRPV	86-96	+	+		
	PYKLRPVAAE	90-99	+	+		
	PYKLRPVAA	90-98	+	+		
	VFEAGRDPYKLRPV	83-96		+	+	
	DGGMVFEAGRDPYKLRPV A	79-97		+		
	EAGRDPYKLRP	85-95		+	+	
	GRDPYKLRPV	87-96		+		
	VFEAGRDPYKLRPVAAE	83-99		+		
	DPYKLRPVA	89-97			+	
	FEAGRDPYKLRP	84-95			+	
	VFEAGRDPYKL	83-93	+			
						LfPFGI(+)
AEIYGTKESPQTHY, f(97-111)	AEIYGTKESPQTHY	97-111	+	+	+	LfPFTGGI (+)
	EIYGTKESPQTHY	99-111	+	+	+	LfGI(+)
	AAEIYGTKESPQTHY	98-111	+		+	
	GTKESPQTHY	102-111	+	+	+	

	YGTKESPQTHY	101-111	+	+	+	
	IYGTKESPQTHY	100-111	+	+	+	
	TKESPQTHY	103-111	+	+		
	KESPQTHY	104-111	+			
GILRPYLSWTE, f(149-159)	ILRPYLSW	150-157	+	+	+	
	ILRPYL	150-155	+	+	+	
	RPYLSWT	152-158	+	+	+	
	GILRPYL	149-155	+	+	+	
	RPYLSW	152-157	+	+		
	RPYLSWTE	152-159	+	+		
	LRPYLSWT	151-158	+			
	GILRPYLSW	149-157		+		
	LRPYLSW	151-157		+		
RQAYPNL, f(182-188)	RQAYPNL	182-188	+		+	
SREPYFGY, f(203-211)	SREPYFG	203-210	+	+	+	
	REPYFGY	204-211	+	+		
	SREPYF	203-209	+	+	+	LfPFTGGI (+)
FENLPEKADRDQYEL f(234-248)	FENLPEKADRDQYE	234-247	+	+	+	LfPFTGGI (+)
	FENLPEKADRDQY	234-246		+	+	
	FENLPEKADRDQ	234-245	+	+	+	
	ENLPEKADRDQYEL	235-248	+	+	+	
	ENLPEKADRDQYE	235-247	+	+	+	
	ENLPEKADRDQY	235-246	+	+	+	LfPFTGGI (+)
	DRDQYEL	242-248	+	+	+	
	PEKADRDQYEL	238-248	+	+		
	PEKADRDQYE	238-247	+	+	+	
	LPEKADRDQYE	237-247	+	+	+	
ARSVDGKEDLIWKLLSK f(276-292)	ARSVDGKEDLIWKL	276-289	+	+	+	
	SVDGKEDLIWKLLSK	278-292		+		
	RSVDGKEDLIWKLLSK	277-292		+		
	RSVDGKEDLIWKL	277-289	+	+	+	
QLFGSPPGQRDLLF, f(306-319)	QLFGSPPGQRD	306-316	+	+	+	
	QLFGSPPGQRDL	306-317	+	+	+	
	QLFGSPPGQRDLL	306-318	+	+	+	
	LFGSPPGQRDL	307-317	+	+	+	
	LFGSPPGQRDLL	307-318	+	+	+	
	FGSPPGQRDL	308-317	+	+	+	
						LfGI(+)
	FGSPPGQRDLL	308-318	+	+	+	LfPFTGGI (+)
	FGSPPGQRDLLF	308-319	+		+	

	SPPGQRDLL	310-318	+		+	
	PPGQRDLL	311-318	+	+	+	
FLRIPSKVDSALYLGSRYLT f (326-345)	FLRIPSKVDSA	326-336	+			
	LRIPSKVDSAL	327-337	+	+	+	LfGI(+) LfPFGI(+) LfPFTGGI(+)
	FLRIPSKVDSAL	326-337	+	+	+	
	LRIPSKVD	327-334	+	+	+	
	LRIPSKVDS	327-335	+	+	+	
	LRIPSKVDSA	327-336	+	+	+	
	RIPSKVDSAL	328-337	+	+	+	
YLGSRYLT, f(338-345)	YLGSRYLT	338-345	+		+	
	YLGSRYL	338-344		+		
YTRVW, f(360-366)	YTRVW	360-366	+	+	+	
VLRPTEGYL, f(445-453)	VLRPTEGY	445-452	+	+		
AVVKKANEGLTW, f(456-467)	VLRPTEGYL	445-453	+	+	+	
	AVVKKANEGLTW	456-467	+	+	+	
	VVKKANEGLTW	457-467	+	+	+	
	VKKANEGLTW	458-467	+	+	+	
DRTAGWNIPMGLI, f(481-493)	DRTAGWNIPMGL	481-492	+	+	+	
	RTAGWNIPMGL	482-492	+	+	+	LfPFGI(+) LfPFTGGI(+)
	RTAGWNIPMGLI	482-493	+	+	+	
KYYGYTGA, f(541-548)	KYYGYTGA	541-548	+	+	+	
WAKNLNREDF, f(579-588)	WAKNLNREDF	579-588	+	+	+	
	NLNREDF	582-588	+	+	+	LfPFGI(+)
LHQQALF, f(631-637)	LHQQALF	631-637	+	+		
LFKSETKNLL, f(650-659)	LFKSETKNLL	650-659		+		
	FKSETKNLL	651-659	+	+	+	
AKLGGRPTYEE, f(668-678)	AKLGGRPTYEE	668-678	+	+		
	LGGRPTYEE	670-678	+	+		LfPFTGGI(+)