Supplementary Materials

I. Strug et al. “Vaccinia peptides eluted from HLA-DR1 isolated from virus-infected cells are recognized by CD4+ T cells from a vaccinated donor. “

Supplementary Figure 1. Ion chromatograms.

Figure Legend

Base peak (most abundant ion) and specific ion intensity plots for fractions containing (A) the highly abundant endogenous peptide derived from MHC class I (B) vaccinia peptide I6L [338-352], (C) vaccinia peptide A10L [393-307] , and (D) the internal control HA peptide. No distinct peak in either base peak or specific ion plots was observed for the lower abundance vaccinia peptide D6R [157-171].

Supplementary Table I - Peptides from infected cells

Supplementary Table II - Peptides from control cells

Supplementary Table I - peptides from infected cells

Protein name	Protein acces	Peptide sequence	Previou	Next am	Peptide i	Xcorr	ΔCn	Variable modifications	Observed m/z	Actual mass (AMU)	Calculated Mass (AMU)	Spectrum charge	Δmass (AMU)	Δmass (PPM)
Germinal center expressed transcript 2	gi|20987806	SPEDEYELLMPHRISS	R	H	95.00%	3.22	0.194	M10: Oxidation (+16.00)	640.809	1919.404	1918.886	3	1.526	794.4
Phosphoglycerate kinase 1	gi|85396908	SPERPFLAILGGAKVADKIQ	E	L	95.00%	5.71	0.363		704.460	2110.357	2110.203	3	1.162	550.3
		SPERPFLAILGGAKVADKI	E	Q	95.00%	3.96	0.254		661.457	1981.348	1982.144	3	0.2112	106.5
		SPERPFLAILGGAKVADK	E	I	95.00%	5.11	0.202		624.044	1869.109	1869.060	3	1.056	564.9
Transferrin receptor protein 1	gi|108935939	RVEYHFLSPYVSPKESPF	M	R	95.00%	5.49	0.301		728.383	2182.124	2182.097	3	1.034	473.8
		RVEYHFLSPYVSPKESP	M	F	95.00%	4.09	0.301		679.041	2034.098	2035.029	3	0.0769	37.79
		RVEYHFLSPYVSPKE	M	S	95.00%	4.33	0.283		617.713	1850.114	1850.944	3	0.1777	96.01
		RVEYHFLSPYVSPK	M	E	95.00%	4.23	0.346		575.143	1722.404	1721.902	3	1.51	876.3
		LPNIPVQTISRAAAEKLFGNME	G	G	95.00%	3.36	0.458	M21: Oxidation (+16.00)	806.049	2415.122	2415.271	3	0.8594	355.7
		IPVQTISRAAAEKLFGNME	N	G	95.00%	3.76	0.399	M18: Oxidation (+16.00)	698.122	2091.341	2091.091	3	1.258	601.3
		IPVQTISRAAAEKLFGNM	N	E	95.00%	4.48	0.184	M18: Oxidation (+16.00)	655.070	1962.187	1962.048	3	1.146	583.8
		IPVQTISRAAAEKLFGN	N	M	59.30%	2.51	0.166		908.765	1815.515	1815.013	2	1.51	831.1
		IPVQTISRAAAEKLFG	N	N	95.00%	3.26	0.347		851.377	1700.737	1700.970	2	0.775	455.4
Integral membrane protein 2A	gi|26252137	MPPKNLVELFGKLASGRYL	V	P	95.00%	3.57	0.335		712.263	2133.766	2133.189	3	1.584	742
		MPPKNLVELFGKLASGRY	V	L	95.00%	5.46	0.451	M1: Oxidation (+16.00)	679.400	2035.177	2036.101	3	0.084	41.25
Syndecan binding protein (syntenin)	gi|109731788	VDKVIQAQTAFSANPANPA	K	I	95.00%	5.21	0.421		971.491	1940.967	1942.004	2	-0.029	-14.9
		VDKVIQAQTAFSANPANP	K	A	95.00%	2.89	0.369		935.927	1869.839	1870.966	2	-0.1194	-63.81
		VDKVIQAQTAFSANPAN	K	P	95.00%	3.4	0.272		887.493	1772.969	1773.914	2	0.0636	35.85
		VDKVIQAQTAFSANPA	K	N	95.00%	3.8	0.423		830.465	1658.915	1659.871	2	0.0516	31.11
Solute carrier family 3	gi|68084446	KGRLDYLSSLKVKG	L	L	95.00%	2.76	0.231		522.216	1563.623	1563.922	3	0.7085	452.8
Lactate dehydrogenase A	gi|45501322	NVNIFKFIIPNVVKYSPN	R	C	95.00%	4.98	0.476		1053.566	2105.117	2106.175	2	-0.0508	-24.11
		NVNIFKFIIPNVVK	R	Y	95.00%	4.56	0.366		822.992	1643.967	1644.984	2	-0.0089	-5.42
Interleukin 2 receptor, beta	gi|19343611	TPDPSKFFSQLSSEHGGDVQ	N	K	95.00%	2.79	0.226		721.649	2161.922	2162.999	3	-0.0693	-32.06
Glyceraldehyde-3-phosphate dehydrogenase	gi|53734502	YSNRVVDLMAHMASKE	G	-	95.00%	3.84	0.179		617.725	1850.150	1850.889	3	0.2685	145.1
		SNRVVDLMAHMASKE	Y	-	95.00%	2.83	0.408		844.537	1687.058	1687.826	2	0.2398	142
Chain B, Cd23 Lectin Domain, Calcium 2+-Bound	gi|110590516	HTGSWIGLRNLDLKGEFI	S	W	95.00%	2.63	0.241		686.081	2055.218	2056.098	3	0.1277	62.1
		TGSWIGLRNLDLKGEF	H	I	95.00%	3.36	0.19		603.141	1806.400	1805.955	3	1.452	803.4
		TGSWIGLRNLDLKGE	H	F	95.00%	2.83	0.215		830.012	1658.008	1658.887	2	0.129	77.77
		TGSWIGLRNLDLK	H	G	95.00%	3.22	0.169		736.912	1471.809	1472.823	2	-0.0059	-3.98
		DLKGEFIWVDGSHVDYSN	L	W	95.00%	2.88	0.397		1041.612	2081.208	2080.962	2	1.254	602.4
		KGEFIWVDGSHVDYS	L	N	95.00%	2.44	0.335		869.854	1737.692	1738.808	2	-0.1078	-61.99
Sequestosome 1	gi|17512269	GDDDWTHLSSKEVDPSTG	G	E	95.00%	3.83	0.292		973.968	1945.920	1945.842	2	1.086	557.8
		DDDWTHLSSKEVDPSTG	G	E	95.00%	2.87	0.309		944.947	1887.879	1888.820	2	0.0661	34.96
CD74 antigen isoform a	gi|68448544	LPKPPKPVSKMRMATPLLMQAL	K	P	78.00%	2.92	0.19	M11: Oxidation (+16.00)	822.224	2463.649	2463.402	3	1.254	509
		KPPKPVSKMRMATPLLMQAL	P	P	95.00%	3.35	0.457		1119.217	2236.418	2237.270	2	0.155	69.29
		KPPKPVSKMRMATPLLMQA	P	L	76.90%	2.45	0.156	M11: Oxidation (+16.00)	714.591	2140.750	2140.181	3	1.576	735.9
MHC class I	gi|110290622	DVGSDWRFLRGYHQYAYDGK	C	D	95.00%	3.1	0.204		812.125	2433.350	2433.137	3	1.221	501.4
		DVGSDWRFLRGYHQYAYD	C	G	92.70%	2.02	0.198		750.225	2247.650	2248.021	3	0.637	283.3
		VGSDWRFLRGYHQYAYDG	D	K	65.80%	1.93	0.166		730.735	2189.182	2190.016	3	0.1738	79.37
		VGSDWRFLRGYHQYA	D	Y	77.30%	1.55	0.202		1855.000	1853.992	1854.904	1	0.096	51.72
		GSDWRFLRGYHQYA	V	Y	64.30%	1.81	0.19		878.728	1755.440	1755.836	2	0.6119	348.4
Stomatin	gi|14715077	FPLPIDMLQGIIGAKHS	V	H	83.50%	3.05	0.182	M7: Oxidation (+16.00)	618.896	1853.663	1853.000	3	1.671	901
		VVYYRVQNATLAVANIT	G	N	95.00%	2.89	0.143		948.030	1894.045	1895.039	2	0.014	7.34
		VVYYRVQNATLAVAN	G	I	95.00%	2.63	0.309		841.007	1679.998	1680.907	2	0.0984	58.53
Carboxypeptidase D	gi|30353747	KETLKHLASLYANNHPS	N	M	95.00%	4.52	0.368		641.973	1922.894	1923.009	3	0.8931	464.2
Interleukin 21 receptor	gi|13279299	EDPAFYMLKGKLQYE	Y	L	95.00%	3.37	0.173		916.428	1830.840	1831.894	2	-0.0469	-25.59
amino acid transporter system A1	gi|21361929	TGKFVIFGATSLQNTG	T	A	95.00%	4.05	0.381		820.883	1639.750	1640.865	2	-0.1074	-65.47
fibrinogen betaB 1-118	gi|223130	EGVNDNEEGFFSAR	-	G	95.00%	3.9	0.137		785.609	1569.202	1570.677	2	-0.4675	-297.8
Influenza Ha Antigen Peptide	gi|20150367	PKYVKQNTLKLAT	-	-	95.00%	3.2	0.211		502.439	1504.294	1503.890	3	1.411	937.5
Sema domain, immunoglobulin domain (Ig)	gi|32493365	KVPVFYALFTPQLNNVG	L	L	95.00%	2.56	0.371		954.050	1906.085	1907.043	2	0.05	26.18
Glucosamine (N-acetyl)-6-sulfatase	gi|15214696	FEPFFMMIATPAPHSP	N	W	95.00%	3.42	0.316	M6 & M7: Oxidation (+16.00)	926.789	1851.561	1851.846	2	0.7237	390.7
desmoglein 2 preproprotein	gi|4503403	KNLDFSVIVANKAAFHK	M	S	95.00%	4.62	0.379		635.007	1901.998	1902.060	3	0.9452	496.7
	gi|4503403	ETPFFLLTGYALDAR	E	G	95.00%	3.5	0.249		857.646	1713.276	1713.885	2	0.3986	232.5
sortilin-related receptor	gi|4507157	KTFIFSEKPVFVYGLL	W	T	95.00%	4.46	0.398		944.530	1887.045	1888.063	2	-0.0098	-5.17
	gi|4507157	SPLAFEHVMTRGVRPP	D	A	95.00%	3.05	0.304	M9: Oxidation (+16.00)	604.318	1809.931	1809.944	3	0.9947	549.3
Major histocompatibility complex, class II, DR alpha	gi|48734719	EFGRFASFEAQGALANIA	E	V	95.00%	2.75	0.317		949.921	1897.825	1898.940	2	-0.1071	-56.38
	gi|48734719	EFGRFASFEAQGALAN	E	I	95.00%	3.69	0.236		858.000	1713.984	1714.819	2	0.1732	101
	gi|48734719	EFGRFASFEAQGALA	E	N	95.00%	2.64	0.213		800.934	1599.853	1600.776	2	0.0844	52.69
	gi|48734719	FGRFASFEAQGALANI	E	A	52.30%	3.21	0.0921		850.548	1699.081	1698.860	2	1.229	722.7
	gi|48734719	FGRFASFEAQGALAN	E	I	95.00%	3.42	0.243		793.394	1584.772	1585.776	2	0.0033	2.08
CD74 antigen isoform a	gi|68448544	LPKPPKPVSKMRMA	K	T	95.00%	2.4	0.209	M11: Oxidation (+16.00)	532.658	1594.949	1595.913	3	0.0437	27.38
Chromatin modifying protein 5	gi|18088721	IDKKISRLDAELVKYKDQ	S	I	95.00%	4.94	0.318		721.332	2160.971	2162.219	3	-0.2395	-110.8
Lysosomal associated multispanning membrane protein 5	gi|76827613	SVLLFIEHSVEVAHGK	M	A	95.00%	4.37	0.281		589.550	1765.625	1764.965	3	1.668	944.2
annexin A2 isoform 1	gi|50845388	ERDALNIETAIKTKGVDE	A	V	95.00%	4.32	0.271		668.410	2002.207	2002.046	3	1.168	583.2
Chain B, Cd23 Lectin Domain	gi|110590516	TGSWIGLRNLDLKGEFI	H	W	95.00%	4.17	0.399		640.380	1918.117	1919.039	3	0.0851	44.33
SLC41A2 protein	gi|76827793	SPIEKWNLIIGNLALK	D	Q	95.00%	3.93	0.388		905.037	1808.059	1809.064	2	0.0029	1.62
Lactate dehydrogenase B	gi|12803117	NVNVFKFIIPQIVK	R	Y	95.00%	3.78	0.409		830.001	1657.987	1659.000	2	-0.0055	-3.31
telomere binding protein [Vaccinia virus]	gi|47088395	IYTYRIIKSSFPVPT	G	I	95.00%	3.69	0.241		892.689	1783.361	1784.995	2	-0.6261	-350.9
Protective protein for beta-galactosidase	gi|62531047	FAYYHGLLGNRLWSSL	Y	Q	95.00%	3.6	0.458		948.965	1895.914	1896.976	2	-0.0542	-28.57
Fibromodulin	gi|23271348	GLLWIALHGNQITSDK	T	V	95.00%	3.47	0.487		883.582	1765.148	1765.960	2	0.1956	110.7
helicase	gi|2347134	PCDHTMVKLQPGDMAAITTKVLRVNGEKIL	G	E	51.80%	3.29	0.0873	M6 & M14: Oxidation (+16.00)	1103.932	3308.771	3310.733	3	-0.9541	-288.3
early gene transcription factor VETF 70kDa subunit [Vaccinia virus]	gi|47088431	KIPFLLLSGSPITNT	N	P	95.00%	3.19	0.32		800.733	1599.451	1600.932	2	-0.4733	-295.7

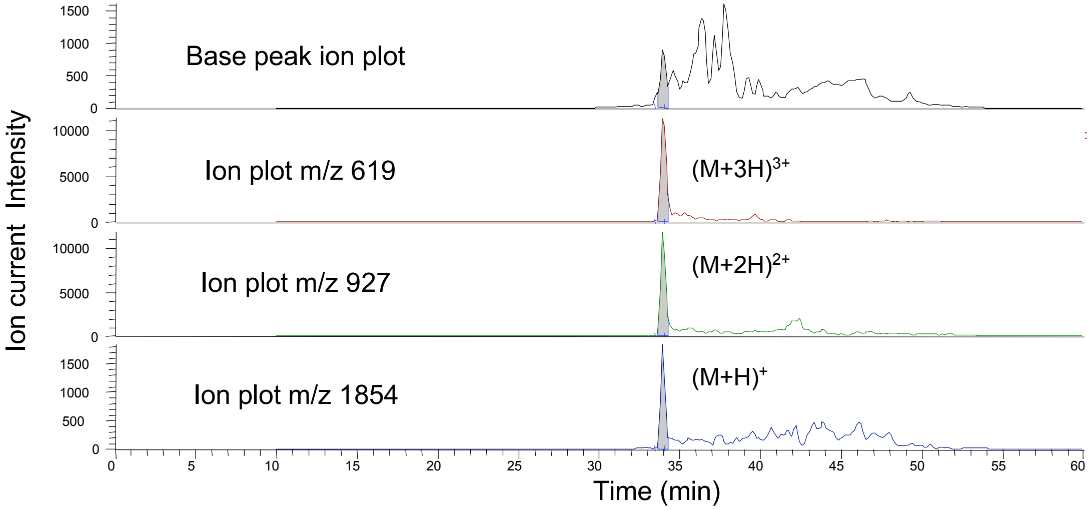
RAB14, member RAS oncogene family	gi|13543869	RSTYNHLSSWLTDAR	R	N	95.00%	3.12	0.226		603.336	1806.983	1806.889	3	1.102	609.5
core protein 4a precursor [Vaccinia virus]	gi|47088449	SMRYQSLIPRLVEFF	I	P	95.00%	3.01	0.128		943.554	1885.092	1886.000	2	0.1001	53.07
		SLIPRLVEFF	Q	P	95.00%	2.38	0.162		610.872	1219.728	1220.705	2	0.0317	26
Saccharopine dehydrogenase	gi|20071563	VATPIAMVQAAMTLLSDASHLPKAGGVF	Y	T	76.40%	2.99	0.159	M7 & M12: Oxidation (+16.00)	943.447	2827.316	2828.469	3	-0.1448	-51.19
MSTP123	gi|33338046	ENSPNVFGFLAAWNLLLPPAGH	G	H	90.00%	2.98	0.16		789.289	2364.844	2364.214	3	1.637	692
Ankyrin repeat domain 47	gi|42490769	WFRVSSQRRSQAEPVARMLEGVRR	E	L	91.70%	2.97	0.237		968.327	2901.959	2901.549	3	1.418	488.4
Adenylosuccinate synthase like 1	gi|28839610	EALHGPPKKILVEGANAALLDI	Y	D	95.00%	2.97	0.219		756.702	2267.081	2269.292	3	-1.203	-530.6
B-cell receptor CD22 precursor	gi|6166019	APEPSTVQILHSPAVEGSQ	Y	V	95.00%	2.92	0.325		974.016	1946.017	1946.983	2	0.042	21.57
immunoglobulin heavy chain variable region	gi|60616384	TSANTDYMELRGLTSED	D	T	91.70%	2.9	0.223	M8: Oxidation (+16.00)	959.479	1916.941	1918.834	2	-0.8849	-461.4
immunoglobulin mu heavy chain	gi|54780570	QVQLQQWGAGLLEPSETLPLT	-	C	69.60%	2.85	0.126		770.046	2307.113	2308.219	3	-0.0982	-42.52
PREDICTED: similar to zinc finger CCCH type containing 12A isoform 3	gi|89035093	VSIPATSTAKPQSTT	L	S	95.00%	2.78	0.179		496.802	1487.383	1488.791	3	-0.4009	-269.3
Profilin 1	gi|34785533	VPGKTFVNITPAEVGVL	A	V	95.00%	2.76	0.345		871.428	1740.840	1740.990	2	0.8578	492.5
Zinc finger FYVE domain-containing protein 16	gi|50401753	YLNDLDSALIPVIHGGTSNSSLPLEI	H	E	79.10%	2.75	0.227		913.888	2738.641	2738.425	3	1.223	446.6
Leukotriene A4 hydrolase	gi|21618615	SVPKELVALMSAIRDGETP	V	D	73.40%	2.72	0.166		672.011	2013.010	2013.069	3	0.9481	470.8
cathepsin S preproprotein	gi|23110962	TGKLVSLSAQNLVD	K	C	95.00%	2.72	0.239		723.037	1444.059	1444.801	2	0.2657	183.9
Fibrinogen beta chain	gi|78395029	SLRPAPPPISGGGYRARPA	P	K	65.50%	2.7	0.245		640.976	1919.903	1920.057	3	0.854	444.6
Solute carrier family 38	gi|25955655	IRDIFGFIGASAASM	T	L	95.00%	2.69	0.195	M15: Oxidation (+16.00)	786.862	1571.709	1571.789	2	0.9272	589.6
Sestrin-3	gi|20141774	FLVEEYSTSGRLDNITQV	N	M	77.50%	2.69	0.164		691.054	2070.139	2071.035	3	0.1118	53.99
ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	gi|45708716	HPNQPFYILKPQMPWE	L	L	95.00%	2.51	0.29		1012.842	2023.667	2025.006	2	-0.3309	-163.5
RAB4B, member RAS oncogene family	gi|28422140	SRETYNSLAAWLTDART	T	L	91.80%	2.44	0.306		977.401	1952.787	1954.962	2	-1.168	-597.7
Transmembrane protein 127	gi|25058970	GASILATAANLLRHYPT	G	E	95.00%	2.42	0.341		884.767	1767.519	1768.971	2	-0.4447	-251.5
major histocompatibility complex, class I, B	gi|17986001	RPAGDRTFQKWAAVVVPSGEE	T	Q	80.60%	2.41	0.181		767.668	2299.981	2300.179	3	0.8093	351.7
Procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	gi|16741721	ISNIYLIKGSALRGEL	Y	Q	82.10%	2.41	0.232		874.359	1746.702	1747.012	2	0.6982	399.5
KIAA0528 protein	gi|109658768	VSARSVKLLDRIHNPDE	V	P	94.00%	2.4	0.237		650.264	1947.767	1949.057	3	-0.2821	-144.8
unnamed protein product	gi|50833928	AQLLWTQLTPMGGRPG	A	G	70.30%	2.35	0.186		864.246	1726.477	1725.912	2	1.574	910.9
sterol regulatory element binding transcription factor 1 isoform a	gi|52630419	AGDAVSVATLAEIYVAAALRVK	C	T	59.20%	2.35	0.298		1095.383	2188.750	2188.234	2	1.524	695.9
Unknown gene product	gi|3417294	VGQLQSPTLNSPIYMQKQ	S	G	80.80%	2.35	0.162		678.111	2031.308	2032.054	3	0.2618	128.8
REX2, RNA exonuclease 2 homolog	gi|85397892	RGVREGGAAMAAGESMA	A	Q	95.00%	2.33	0.227	M10 & M16: Oxidation (+16.00)	827.593	1653.171	1652.749	2	1.43	864.7
Chromosome 22 open reading frame 16	gi|40806990	AVGSAVGHVMGSALTGAF	V	S	91.60%	2.33	0.177		544.323	1629.944	1631.822	3	-0.8697	-533.3
ATP-binding cassette sub-family B member 8	gi|13123950	VQIPLLLGQLVKVVAK	N	Y	90.50%	2.25	0.272		859.391	1716.766	1718.131	2	-0.3568	-207.7

Supplemental Table II - peptides from control cells

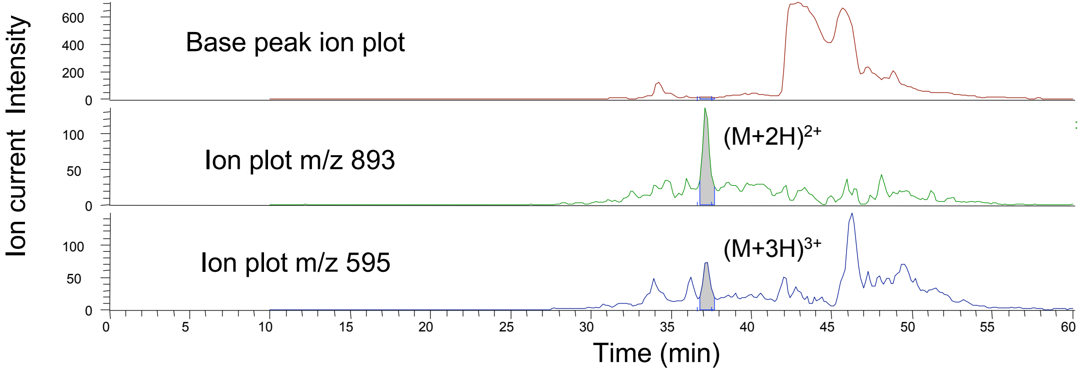
Protein name	Protein accession nı	Peptide sequence	Previous amino	Next amino	Peptide ic	Xcorr	ΔCn	Variable modifications id	Observed M/z	Actual pept	Calculated	Spectrum charge	ΔAMU	ΔPPM
Germinal center expressed transcript 2	gi|20987806	SPEDEYELLMPHRISSHF	R	L	95.00%	5.90	0.446		1094.58	2187.14	2187.02	2	1.1	520
		SPEDEYELLMPHRISSH	R	F	95.00%	5.72	0.491		1021.04	2040.07	2039.95	2	1.1	550
		SPEDEYELLMPHRISS	R	H	95.00%	4.16	0.394		952.57	1903.13	1902.89	2	1.2	650
		SPEDEYELLMPHRIS	R	S	95.00%	3.72	0.453		908.44	1814.86	1815.86	2	0.011	6.1
Phosphoglycerate kinase 1	gi|85396908	SPERPFLAILGGAKVADKIQ	E	L	95.00%	5.87	0.348		704.47	2110.39	2110.2	3	1.2	560
		SPERPFLAILGGAKVADKI	E	Q	95.00%	5.19	0.264		661.82	1982.42	1982.14	3	1.3	650
		SPERPFLAILGGAKVADK	E	I	95.00%	4.45	0.360		935.55	1869.08	1869.06	2	1	550
Transferrin receptor protein 1	gi|108935939	RVEYHFLSPYVSPKESPFR	M	H	95.00%	4.19	0.344		779.99	2336.94	2338.2	3	-0.25	-110
		RVEYHFLSPYVSPKESPF	M	R	95.00%	5.70	0.453		1092.07	2182.12	2182.1	2	1	470
		RVEYHFLSPYVSPKESP	M	F	95.00%	5.69	0.330		679.41	2035.2	2035.03	3	1.2	580
		RVEYHFLSPYVSPKES	M	P	95.00%	3.40	0.335		969.64	1937.27	1937.98	2	0.3	150
		RVEYHFLSPYVSPKE	M	S	95.00%	5.06	0.301		618.02	1851.02	1850.94	3	1.1	590
		RVEYHFLSPYVSPK	M	E	95.00%	3.61	0.230		574.78	1721.33	1721.9	3	0.43	250
		IPVQTISRAAAEKLFGNM	N	E	95.00%	3.94	0.279		973.95	1945.89	1946.05	2	0.85	430
		IPVQTISRAAAEKLFGN	N	M	95.00%	3.13	0.283		605.69	1814.03	1815.01	3	0.027	15
Integral membrane protein 2A	gi|26252137	MPPKNLVELFGKLASGRY	V	L	95.00%	5.13	0.408		1011.08	2020.15	2020.11	2	1.1	520
Syndecan binding protein (syntenin)	gi|109731788	VDKVIQAQTAFSANPANPA	K	I	95.00%	5.19	0.389		971.48	1940.94	1942	2	-0.056	-29
		VDKVIQAQTAFSANPANP	K	A	95.00%	2.96	0.274		936.01	1870	1870.97	2	0.044	24
		VDKVIQAQTAFSANPA	K	N	95.00%	3.55	0.308		831.26	1660.5	1659.87	2	1.6	990
Solute carrier family 3	gi|68084446	LKGRLDYLSSLKVKGLV	G	L	95.00%	5.08	0.420		630.4	1888.18	1889.16	3	0.024	13
		KGRLDYLSSLKVKG	L	L	95.00%	3.91	0.250		522.02	1563.05	1563.92	3	0.14	87
Lactate dehydrogenase A	gi|45501322	NVNIFKFIIPNVVK	R	Y	95.00%	4.81	0.389		823.35	1644.69	1644.98	2	0.71	430
		VNIFKFIIPNVVKYSPN	N	C	95.00%	4.32	0.413		997.16	1992.3	1992.13	2	1.2	590
		VNIFKFIIPNVVK	N	Y	95.00%	3.99	0.220		766.04	1530.07	1530.94	2	0.14	91
Interleukin 2 receptor, beta	gi|19343611	TPDPSKFFSQLSSEHGGDVQ	N	K	95.00%	4.55	0.496		1082.5	2162.99	2163	2	1	460
		TPDPSKFFSQLSSEHGGDV	N	Q	95.00%	3.74	0.276		679.19	2034.56	2034.94	3	0.63	310
		RPPGQGEFRALNARLPLNTD	S	A	95.00%	3.34	0.384		740.99	2219.95	2222.18	3	-1.2	-550
Glyceraldehyde-3-phosphate dehydrogenase	gi|53734502	YSNRVVDLMAHMASKE	G	-	95.00%	4.64	0.256		617.7	1850.09	1850.89	3	0.21	110
		SNRVVDLMAHMASKE	Y	-	95.00%	3.08	0.420		844.41	1686.8	1687.83	2	-0.017	-10
Chain B, Cd23 Lectin Domain, Calcium 2+-Bound	gi|110590516	TGSWIGLRNLDLKGEFI	H	W	95.00%	3.77	0.385		640.45	1918.32	1919.04	3	0.28	150
		TGSWIGLRNLDLKGEF	H	I	95.00%	3.61	0.365		603.17	1806.5	1805.96	3	1.6	860
		TGSWIGLRNLDLKGE	H	F	95.00%	2.98	0.347		553.74	1658.2	1658.89	3	0.32	200
		TGSWIGLRNLDLK	H	G	95.00%	2.77	0.176		736.96	1471.9	1472.82	2	0.089	60
		DLKGEFIWVDGSHVDYSN	L	W	95.00%	3.00	0.227		1041.34	2080.67	2080.96	2	0.72	340
Sequestosome 1	gi|17512269	GDDDWTHLSSKEVDPSTG	G	E	95.00%	3.64	0.442		973.32	1944.62	1945.84	2	-0.21	-110
		DDDWTHLSSKEVDPSTG	G	E	95.00%	3.14	0.211		945.39	1888.76	1888.82	2	0.95	500
CD74 antigen isoform a	gi|68448544	KPPKPVSKMRMATPLLMQAL	P	P	95.00%	3.83	0.404		1119.65	2237.28	2237.27	2	1	460
		KPPKPVSKMRMATPLLMQA	P	L	95.00%	3.94	0.426		1063.13	2124.24	2124.19	2	1.1	500
		KPPKPVSKMRMATPLLMQ	P	A	95.00%	3.44	0.304		1027.55	2053.09	2053.15	2	0.94	460
MHC class I antigen	gi|110290622	VGSDWRFLRGYHQYAYDGKDY	D	I	95.00%	2.65	0.304		866.16	2595.44	2596.2	3	0.25	96
Stomatin	gi|14715077	FPLPIDMLQGIIGAKH	V	S	95.00%	3.64	0.282		584.13	1749.38	1749.97	3	0.41	240
Carboxypeptidase D	gi|30353747	KETLKHLASLYANNHPS	N	M	95.00%	3.17	0.388		641.73	1922.16	1923.01	3	0.16	84
Interleukin 21 recepto	gi|13279299	EDPAFYMLKGKLQYE	Y	L	95.00%	4.15	0.328		917	1831.99	1831.89	2	1.1	600
amino acid transporter system A1	gi|21361929	TGKFVIFGATSLQNTG	T	A	95.00%	3.85	0.297		820.92	1639.82	1640.87	2	-0.038	-23
fibrinogen betaB 1-118	gi|223130	EGVNDNEEGFFSAR	-	G	95.00%	3.52	0.419		786.25	1570.49	1570.68	2	0.82	520
Influenza Ha Antigen Peptide	gi|20150367	PKYVKQNTLKLAT	-	-	95.00%	3.50	0.183		752.76	1503.5	1503.89	2	0.62	410
Sema domain (semaphorin) 4D	gi|32493365	KVPVFYALFTPQLNNVG	L	L	95.00%	3.08	0.430		954.14	1906.26	1907.04	2	0.23	120
Glucosamine (N-acetyl)-6-sulfatase	gi|15214696	FEPFFMMIATPAPHSPW	N	T	95.00%	2.75	0.320		1003.45	2004.88	2005.94	2	-0.044	-22
Quiescin Q6	gi|72679814	ASHFEQMAAASMHRVG	C	S	95.00%	5.19	0.362		577.31	1728.9	1729.79	3	0.12	70
		ASHFEQMAAASMHR	C	V	95.00%	3.74	0.246		525.26	1572.77	1573.7	3	0.076	48
Cation-independent mannose-6-phosphate receptor precursor	gi|60416403	DLNPLIKLSGAYLVDDSDPDT	H	S	95.00%	3.62	0.291		1131.21	2260.4	2261.12	2	0.29	130
		DLNPLIKLSGAYLVDDSDPD	H	T	95.00%	4.95	0.453		1081.12	2160.23	2160.07	2	1.2	540
Eukaryotic translation elongation factor 1 alpha 1	gi|83405856	IEKFEKEAAEMGKGSF	T	K	95.00%	3.63	0.240		601.15	1800.42	1800.88	3	0.54	300
		IEKFEKEAAEMGKG	T	S	95.00%	4.32	0.358		783.99	1565.97	1566.78	2	0.19	120
CD97 molecule	gi|20072766	LAPPVRHLIATQLLSNL	A	E	95.00%	3.11	0.311		929	1855.98	1856.11	2	0.88	470
		APPVRHLIATQLLSNL	L	E	95.00%	3.79	0.354		872.47	1742.93	1743.03	2	0.91	520
ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	gi|45708716	KTTIRLMNSQLVTTEK	T	R	95.00%	2.98	0.249		621.68	1862.02	1863.04	3	-0.013	-7.1
		KTTIRLMNSQLVTTE	T	K	95.00%	3.32	0.400		868.52	1735.03	1734.94	2	1.1	630
growth and transformation-dependent protein	gi|49355721	NLEKKARLKEEAAMKAKTE	L	-	95.00%	5.18	0.380		730.49	2188.45	2188.21	3	1.2	570
Ribosomal protein L7a	gi|75991677	PKGKKAKGKKVAPAPAVVKKQ	M	E	95.00%	3.95	0.267		720.61	2158.8	2158.39	3	1.4	660
Mitogen-activated protein kinase kinase 1 interacting protein 1	gi|20072808	LPSVEGLHAIVVSDRD	K	G	95.00%	3.88	0.479		854.39	1706.75	1706.91	2	0.85	500
tumor necrosis factor receptor	gi|22547119	MDNEIKVAKAEAAGHR	L	D	95.00%	3.72	0.373		580.55	1738.62	1739.89	3	-0.26	-150
Sushi domain containing 3	gi|15779059	LPPQATFQVLRGNGASVGT	R	V	95.00%	3.71	0.431		957.5	1912.98	1913.03	2	0.97	510
Mannosidase, alpha, class 2B, member 1	gi|12653887	LDKLIRLVNAQQAKGSS	N	V	95.00%	3.68	0.351		614.89	1841.64	1841.06	3	1.6	860
unnamed protein product	gi|40981418	LREEEDRGIVRNKVL	R	T	95.00%	3.30	0.200		609.6	1825.77	1826.03	3	0.76	410
Proteoglycan 1, secretory granule	gi|15930161	KGPMFELLPGESNKIPR	E	L	95.00%	3.29	0.095		638.62	1912.85	1913.03	3	0.82	430
Lymphocyte antigen 6 complex, locus E	gi|110645870	KSNLYCLKPTICSDQDN	Q	Y	95.00%	3.26	0.151		647.95	1940.84	1941.91	3	-0.062	-32
SLAMF6 protein	gi|109731479	DTGSYRAQISTKTSAKL	E	S	88.90%	3.26	0.128		609.8	1826.37	1826.96	3	0.41	230
Ubiquitin carboxyl-terminal esterase L1	gi|13623417	RKKQIEELKGQEVSPKVY	F	F	95.00%	3.20	0.191		720.89	2159.64	2159.22	3	1.4	660
Plexin-B3 precursor	gi|51701857	DEHTPSPIAGRQPLEVQ	G	P	57.90%	3.16	0.146		625.76	1874.25	1873.94	3	1.3	700
Phosphoglycerate mutase 1	gi|44890768	KRVLIAAHGNSLRG	G	I	95.00%	3.06	0.317		498.11	1491.29	1491.89	3	0.41	280
Leucyl-cystinyl aminopeptidase (Cystinyl aminopeptidase)	gi|20138789	DKGWSFLLGKYISIG	T	S	95.00%	3.01	0.302		843	1683.99	1683.91	2	1.1	640
p130Cas-associated protein (p140Cap)	gi|42559872	RLSLAAAAGDPFAYPGAGGLYK	G	R	89.70%	2.94	0.171		722.49	2164.45	2166.14	3	-0.67	-310
Serine/threonine-protein kinase SMG1	gi|91208166	SRLIRQVERL	N	K	84.50%	2.92	0.144		635.17	1268.32	1269.78	2	-0.45	-360
Hypothetical protein BC004941	gi|47939548	LLYRLRFLSASAV	R	P	95.00%	2.91	0.109		755.04	1508.06	1508.9	2	0.17	110

ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	gi|62490988	PKFEVIEKPQA	D	-	95.00%	2.84	0.160		643.29	1284.56	1285.72	2	-0.15	-120
TP53I11 protein	gi|73909101	TLAETGLMSLGILLLLVSRLLFVV	A	I	74.50%	2.70	0.176	M8: Oxidation (+16)	863.45	2587.34	2587.55	3	0.79	310
hypothetical protein	gi|50949934	AYQANILVEDATIGIVDNELLTS	G	S	70.70%	2.69	0.110		821.65	2461.93	2462.27	3	0.67	270
Mitochondrial 28S ribosomal protein S22	gi|13633893	SWEERDRMIQVYFPKEGR	A	K	62.10%	2.69	0.190		776.51	2326.52	2326.14	3	1.4	600
Regulatory factor X, 5 (influences HLA class II expression)	gi|17028337	AEVPVSEASGQAPPAKAAKQDIEDTASDAKRK	T	R	87.80%	2.68	0.121		1089.36	3265.07	3265.67	3	0.41	130
NMDA receptor-binding protein yotiao	gi|7513208	QYQEHQQATELLRQAHMPQM	R	E	95.00%	2.66	0.211		823.44	2467.29	2467.16	3	1.1	460
Interleukin 10 receptor, beta	gi|12804903	IIGPPGMQVEVLADSLHMRF	T	L	87.00%	2.62	0.165		737.68	2210.01	2210.15	3	0.87	390
Putative helicase Mov10l1	gi|22095856	IDDMIYFSSDAVTSRV	M	L	81.10%	2.61	0.162		606.78	1817.31	1818.86	3	-0.55	-300
Protocadherin beta 16	gi|23271279	PRSATATLHVLLVDGFSQPFLPLP	P	E	78.70%	2.60	0.184		859.77	2576.29	2576.42	3	0.87	340
mitochondrial tumor suppressor 1 isoform 3	gi|50348622	MTYTAFSDVVMQ	D	S	94.70%	2.60	0.201		696.33	1390.64	1392.62	2	-0.97	-700
KIAA1737	gi|22713560	AWAKLQASLTPGSSNTGSDLEA	Q	F	68.10%	2.59	0.131		734.97	2201.9	2204.08	3	-1.2	-530
PEST proteolytic signal containing nuclear protein	gi|18314420	SIKLGSSKPKETVPTLA	I	P	81.40%	2.58	0.141		878.61	1755.21	1756.02	2	0.19	110
Proteasome-associated protein ECM29 homolog (Ecm29)	gi|61212960	AEQVPELEAVLHLVIASSDTRHS	E	V	64.10%	2.58	0.200		834.86	2501.56	2501.3	3	1.3	510
similar to Argininosuccinate synthase (Citrulline--aspartate ligase)	gi|51095136	MEGKVQVPIFKGQV	Q	H	75.10%	2.58	0.131		780.38	1558.74	1559.86	2	-0.12	-75
OTU domain containing 7A	gi|18702331	SPARAAALRTVNTVESLARAVPGALPGAAGTAGAAE	Y	H	95.00%	2.58	0.225		1115.74	3344.18	3344.8	3	0.39	120
LOC51334 protein	gi|62201630	LENGGMGISHSNSFPPIR	P	P	89.50%	2.52	0.130		638.49	1912.44	1912.93	3	0.51	270
ZNF532 protein	gi|71051469	MTMGDMKTPDFDDLLAA	-	F	70.10%	2.52	0.148	M3 and M6: Oxidation (+16)	635.28	1902.81	1903.81	3	0.0023	1.2
hypothetical protein CG003	gi|12957488	WSNTSPVGNGYIKPPVPPASGTHREK	S	G	95.00%	2.51	0.271		925.77	2774.28	2776.42	3	-1.1	-410
Chromosome X open reading frame 26	gi|30354299	SLPAESYGNDPDIEMAWAM	L	R	90.50%	2.50	0.188		699.45	2095.34	2096.9	3	-0.55	-260
Capping protein (actin filament), gelsolin-like	gi|15778939	KANEKERQAALQVAEGFISRMQ	R	Y	80.90%	2.48	0.186		835.27	2502.78	2504.3	3	-0.52	-210
Adenylate cyclase type 3 (Adenylate cyclase type III)	gi|13878450	TYMAASGVTPDVNTNGF	S	A	81.30%	2.40	0.150		582.13	1743.36	1744.79	3	-0.42	-240
novel protein	gi|57209485	PTLRSGIVMEVPPGNTRIACRGK	I	L	83.90%	2.34	0.197	M9: Oxidation (+16)	1235.29	2468.56	2468.32	2	1.3	500
Transcription factor 7-like 1	gi|37590620	YLSNGPLSPGGARTYLQMK	P	W	95.00%	2.32	0.231		685.01	2052	2053.05	3	-0.046	-22
PH domain leucine-rich repeat-containing protein phosphatase	gi|67460982	LLQVPAEASDEGIVISANEDEPG	H	L	75.20%	2.29	0.166		785.07	2352.17	2353.14	3	0.037	16

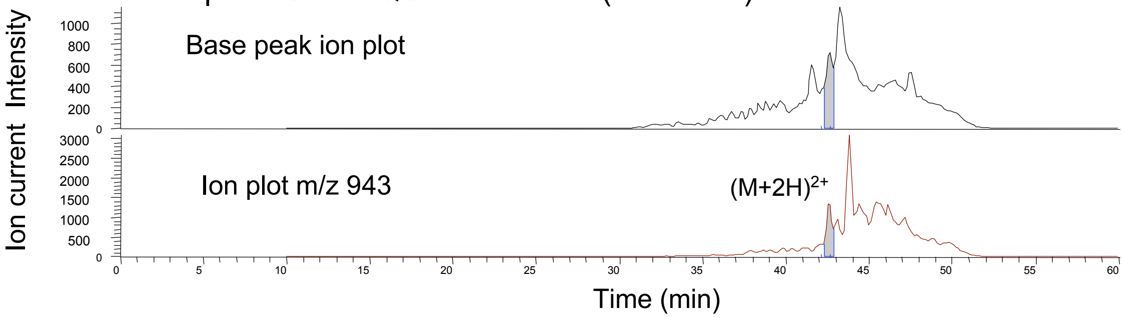
A. Peptide VGSDWRFLRGYHQYA (fraction 6)



B. Peptide IYTYRIIKSSFPVPT (fraction 5)



C. Peptide SMRYQSLIPRLVEFF (fraction 9)



D. Peptide PKYVKQNTLKLAT (fraction 9)