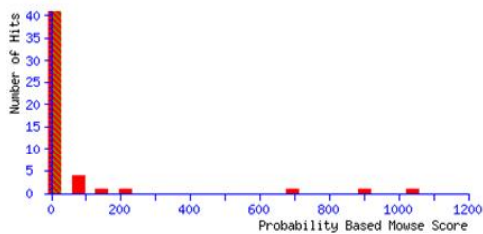


Mascot Search Results

Search title : L:\Client Info\Kitching\Data\20061017-PK-GP\20061101-02 20061017-PK-GP band A.wiff (sample number 1)
MS data file : L:\Client Info\Kitching\Data\20061017-PK-GP\20061101-02 20061017-PK-GP band A.mgf
Database : PBR (21000 sequences; 5863138 residues)
Timestamp : 22 Nov 2006 at 13:54:13 GMT
Significant hits: [SPPV-A_084](#) 097[Sheeppox virus strain A] ||VBRC_genome_id|1511|VBRC_gene_id|44607|: ; SPPV-A_084 084
[LSDV-WARM_103](#) 101[Lumpy skin disease virus strain Neethling Warmbaths LW] AAN02669.1|22595636|VBRC_genome_id|1497
[SPPV-A_078](#) 090[Sheeppox virus strain A] ||VBRC_genome_id|1511|VBRC_gene_id|44600|: ; SPPV-A_078 078
[DPV-WB48_83-108](#) 110[Deerpox virus strain W-848-83] ||VBRC_genome_id|1515|VBRC_gene_id|45221|:
[SPPV-A_068](#) 080[Sheeppox virus strain A] ||VBRC_genome_id|1511|VBRC_gene_id|44590|: ; SPPV-A_068 068
[YMTV-YLD_101](#) 101L[Yaba-like Disease Virus strain Unknown] NP_073486.1|12085084|VBRC_genome_id|1487|VBRC_gene_id|
[GTPV-G20LKV_046](#) 059[Goatpox virus strain G20-LKV] ||VBRC_genome_id|1514|VBRC_gene_id|45021|: ; GTPV-G20LKV_046 046
[DPV-WB48_83-091](#) 093[Deerpox virus strain W-848-83] ||VBRC_genome_id|1515|VBRC_gene_id|45204|:
[SFV-KAS_103](#) s099L[Rabbit fibroma virus strain Kasza] AAF17982.1|6578628|VBRC_genome_id|1480|VBRC_gene_id|38699|
[AMEV-EPB_169](#) 156[Amsacta moorei entomopoxvirus strain Moyer] NP_064938.1|9964470|VBRC_genome_id|1475|VBRC_gene_i
[CNPV-WC93_150](#) 150[Canarypox virus strain ATCC VR111] NP_955173.1|40556088|VBRC_genome_id|1506|VBRC_gene_id|43623|: CNPV

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 26 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As [Help](#)

Significance threshold $p < 0.05$ Max. number of hits 20

Standard scoring ☒ MudPIT scoring ☐ Ions score cut-off 0 Show sub-sets ☐

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Decreasing Score Require bold red ☐

☐ Error tolerant

1. [SPPV-A_084](#) Mass: 104657 Score: 1039 Queries matched: 80
097[Sheeppox virus strain A] ||VBRC_genome_id|1511|VBRC_gene_id|44607|: ; SPPV-A_084 084
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 8	387.2223	772.4301	772.4330	-0.0029	0	(17)	0.4	1	K.SPELSIK.E
<input checked="" type="checkbox"/> 9	387.2242	772.4338	772.4330	0.0008	0	24	0.086	1	K.SPELSIK.E
<input checked="" type="checkbox"/> 10	387.2279	772.4412	772.4330	0.0082	0	(19)	0.24	1	K.SPELSIK.E
<input checked="" type="checkbox"/> 16	405.2216	808.4286	808.4079	0.0207	0	10	2.4	1	K.YVDISGR.D
<input checked="" type="checkbox"/> 19	412.2321	822.4497	822.4752	-0.0255	0	(20)	0.39	1	R.FFQLLR.L
<input checked="" type="checkbox"/> 20	412.2321	822.4497	822.4752	-0.0255	0	(16)	0.96	1	R.FFQLLR.L
<input checked="" type="checkbox"/> 21	412.2378	822.4611	822.4752	-0.0141	0	22	0.23	1	R.FFQLLR.L
<input checked="" type="checkbox"/> 22	412.2378	822.4611	822.4752	-0.0141	0	(18)	0.62	1	R.FFQLLR.L
<input checked="" type="checkbox"/> 23	412.2435	822.4725	822.4752	-0.0026	0	(16)	0.89	1	R.FFQLLR.L
<input checked="" type="checkbox"/> 24	412.2454	822.4763	822.4752	0.0012	0	(18)	0.64	1	R.FFQLLR.L
<input checked="" type="checkbox"/> 25	412.2454	822.4763	822.4752	0.0012	0	(16)	0.87	1	R.FFQLLR.L
<input checked="" type="checkbox"/> 26	412.2493	822.4840	822.4752	0.0088	0	(16)	0.84	1	R.FFQLLR.L
<input checked="" type="checkbox"/> 27	412.2493	822.4840	822.4752	0.0088	0	(17)	0.67	1	R.FFQLLR.L
<input checked="" type="checkbox"/> 28	412.2569	822.4992	822.4752	0.0240	0	(21)	0.28	1	R.FFQLLR.L
<input checked="" type="checkbox"/> 29	412.7236	823.4327	823.4262	0.0065	0	27	0.058	1	R.ELLMYR.L
<input checked="" type="checkbox"/> 31	414.7536	827.4926	827.4865	0.0062	0	(34)	0.0075	1	R.LNNINIK.Y
<input checked="" type="checkbox"/> 32	414.7536	827.4926	827.4865	0.0062	0	37	0.0046	1	R.LNNINIK.Y
<input checked="" type="checkbox"/> 43	438.2365	874.4585	874.4548	0.0036	0	36	0.01	1	R.FQDQIPK.L
<input checked="" type="checkbox"/> 44	438.2405	874.4664	874.4548	0.0115	0	(25)	0.12	1	R.FQDQIPK.L
<input checked="" type="checkbox"/> 45	438.2424	874.4703	874.4548	0.0154	0	(33)	0.02	1	R.FQDQIPK.L
<input checked="" type="checkbox"/> 46	438.2522	874.4899	874.4548	0.0351	0	(17)	0.8	1	R.FQDQIPK.L
<input checked="" type="checkbox"/> 75	531.7860	1061.5574	1061.5505	0.0069	0	(28)	0.064	1	R.DFENLLGVR.R
<input checked="" type="checkbox"/> 76	531.7903	1061.5660	1061.5505	0.0155	0	28	0.06	1	R.DFENLLGVR.R
<input checked="" type="checkbox"/> 77	531.7946	1061.5747	1061.5505	0.0242	0	(18)	0.74	1	R.DFENLLGVR.R
<input checked="" type="checkbox"/> 78	531.8000	1061.5854	1061.5505	0.0349	0	(4)	16	1	R.DFENLLGVR.R
<input checked="" type="checkbox"/> 99	568.8259	1135.6372	1135.6311	0.0062	0	(40)	0.0035	1	K.EVLMYAGLK.I
<input checked="" type="checkbox"/> 100	568.8304	1135.6462	1135.6311	0.0151	0	(11)	2.7	1	K.EVLMYAGLK.I

<input checked="" type="checkbox"/>	104	576.8200	1151.6254	1151.6260	-0.0006	0	44	0.0008	1	K.EVLMLYAGLK.I + Oxidation (M)
<input checked="" type="checkbox"/>	110	581.3207	1160.6268	1160.6012	0.0257	0	11	3.2	1	K.QYIHNLMLV.K + Oxidation (M)
<input checked="" type="checkbox"/>	113	585.2987	1168.5828	1168.5876	-0.0048	1	(29)	0.03	1	R.LKYPEYNSR.F
<input checked="" type="checkbox"/>	114	585.3055	1168.5964	1168.5876	0.0088	1	40	0.0029	1	R.LKYPEYNSR.F
<input checked="" type="checkbox"/>	131	403.5504	1207.6293	1207.6197	0.0097	0	41	0.0023	1	K.IDDNGSPHLIK.K
<input checked="" type="checkbox"/>	140	611.8180	1221.6214	1221.6353	-0.0139	0	(33)	0.011	1	K.DVLSTSIQGFR.V
<input checked="" type="checkbox"/>	141	611.8226	1221.6307	1221.6353	-0.0046	0	(21)	0.16	1	K.DVLSTSIQGFR.V
<input checked="" type="checkbox"/>	142	611.8250	1221.6354	1221.6353	0.0000	0	37	0.004	1	K.DVLSTSIQGFR.V
<input checked="" type="checkbox"/>	143	611.8250	1221.6354	1221.6353	0.0000	0	(24)	0.087	1	K.DVLSTSIQGFR.V
<input checked="" type="checkbox"/>	144	611.8296	1221.6446	1221.6353	0.0093	0	(13)	1	1	K.DVLSTSIQGFR.V
<input checked="" type="checkbox"/>	145	611.8319	1221.6493	1221.6353	0.0140	0	(16)	0.52	1	K.DVLSTSIQGFR.V
<input checked="" type="checkbox"/>	146	611.8342	1221.6539	1221.6353	0.0186	0	(25)	0.068	1	K.DVLSTSIQGFR.V
<input checked="" type="checkbox"/>	147	611.8389	1221.6632	1221.6353	0.0279	0	(23)	0.094	1	K.DVLSTSIQGFR.V
<input checked="" type="checkbox"/>	153	622.2795	1242.5444	1242.5404	0.0040	0	(0)	19	5	R.SINDFDEEFK.M
<input checked="" type="checkbox"/>	154	622.2841	1242.5537	1242.5404	0.0133	0	6	4.9	1	R.SINDFDEEFK.M
<input checked="" type="checkbox"/>	167	636.2887	1270.5629	1270.5506	0.0124	0	(18)	0.54	1	R.NYQEYYTYK.N
<input checked="" type="checkbox"/>	168	636.2911	1270.5677	1270.5506	0.0171	0	18	0.5	1	R.NYQEYYTYK.N
<input checked="" type="checkbox"/>	209	678.8099	1355.6052	1355.6135	-0.0083	0	73	8.8e-07	1	R.AMDTDILTMSMK.H
<input checked="" type="checkbox"/>	220	686.8148	1371.6150	1371.6084	0.0066	0	(40)	0.0032	1	R.AMDTDILTMSMK.H + Oxidation (M)
<input checked="" type="checkbox"/>	223	694.8146	1387.6147	1387.6033	0.0114	0	(38)	0.0024	1	R.AMDTDILTMSMK.H + 2 Oxidation (M)
<input checked="" type="checkbox"/>	294	766.4163	1530.8180	1530.8504	-0.0324	0	69	1.6e-06	1	K.LISEVLESLSISK.K
<input checked="" type="checkbox"/>	295	766.4241	1530.8336	1530.8504	-0.0169	0	(14)	0.6	1	K.LISEVLESLSISK.K
<input checked="" type="checkbox"/>	296	766.4267	1530.8388	1530.8504	-0.0117	0	(23)	0.067	1	K.LISEVLESLSISK.K
<input checked="" type="checkbox"/>	297	766.4267	1530.8388	1530.8504	-0.0117	0	(42)	0.00085	1	K.LISEVLESLSISK.K
<input checked="" type="checkbox"/>	320	795.4419	1588.8693	1588.8613	0.0080	0	70	2.6e-06	1	R.DHYINLLNLLAK.E
<input checked="" type="checkbox"/>	321	530.6315	1588.8728	1588.8613	0.0115	0	(52)	0.00018	1	R.DHYINLLNLLAK.E
<input checked="" type="checkbox"/>	322	530.6315	1588.8728	1588.8613	0.0115	0	(49)	0.00037	1	R.DHYINLLNLLAK.E
<input checked="" type="checkbox"/>	323	530.6380	1588.8923	1588.8613	0.0310	0	(50)	0.00026	1	R.DHYINLLNLLAK.E
<input checked="" type="checkbox"/>	331	799.9269	1597.8393	1597.8351	0.0042	0	58	4.5e-05	1	K.LGINYLDDVSSNK.L
<input checked="" type="checkbox"/>	334	804.4405	1606.8664	1606.8640	0.0024	0	20	0.31	2	K.VISSILPSLCLDYK.V
<input checked="" type="checkbox"/>	395	588.6642	1762.9709	1762.9802	-0.0093	0	43	0.0015	1	K.SIIGSNHNTIISVRPR.V
<input checked="" type="checkbox"/>	418	636.3100	1905.9083	1905.9367	-0.0284	0	54	7.4e-05	1	K.MLDAANDHNTTLPPLQR.A
<input checked="" type="checkbox"/>	419	636.3337	1905.9793	1905.9367	0.0426	0	(8)	2.8	1	K.MLDAANDHNTTLPPLQR.A
<input checked="" type="checkbox"/>	421	641.6543	1921.9411	1921.9316	0.0095	0	(46)	0.00057	1	K.MLDAANDHNTTLPPLQR.A + Oxidation (M)
<input checked="" type="checkbox"/>	435	663.3000	1986.8782	1986.9839	-0.1057	0	(13)	0.74	1	K.TSYVHPFDVLLHPDYGK.I
<input checked="" type="checkbox"/>	436	663.3273	1986.9601	1986.9839	-0.0238	0	62	9e-06	1	K.TSYVHPFDVLLHPDYGK.I
<input checked="" type="checkbox"/>	437	663.3418	1987.0036	1986.9839	0.0197	0	(19)	0.16	1	K.TSYVHPFDVLLHPDYGK.I
<input checked="" type="checkbox"/>	438	663.3442	1987.0108	1986.9839	0.0269	0	(16)	0.37	1	K.TSYVHPFDVLLHPDYGK.I
<input checked="" type="checkbox"/>	439	663.3539	1987.0398	1986.9839	0.0559	0	(33)	0.0072	1	K.TSYVHPFDVLLHPDYGK.I
<input checked="" type="checkbox"/>	440	663.3539	1987.0398	1986.9839	0.0559	0	(1)	12	1	K.TSYVHPFDVLLHPDYGK.I
<input checked="" type="checkbox"/>	461	713.0257	2136.0553	2136.1367	-0.0814	0	(26)	0.042	1	K.LPHNVINPGYITPNDVVPK.F
<input checked="" type="checkbox"/>	462	713.0432	2136.1079	2136.1367	-0.0288	0	(7)	3.3	1	K.LPHNVINPGYITPNDVVPK.F
<input checked="" type="checkbox"/>	463	713.0508	2136.1305	2136.1367	-0.0062	0	51	0.00012	1	K.LPHNVINPGYITPNDVVPK.F
<input checked="" type="checkbox"/>	464	713.0533	2136.1380	2136.1367	0.0013	0	(33)	0.0079	1	K.LPHNVINPGYITPNDVVPK.F
<input checked="" type="checkbox"/>	465	713.0558	2136.1455	2136.1367	0.0088	0	(22)	0.082	1	K.LPHNVINPGYITPNDVVPK.F
<input checked="" type="checkbox"/>	466	713.0583	2136.1530	2136.1367	0.0163	0	(36)	0.0039	1	K.LPHNVINPGYITPNDVVPK.F
<input checked="" type="checkbox"/>	475	720.0307	2157.0704	2157.0564	0.0140	0	34	0.011	1	K.LISASYDLLHFMVSAGDYR.N
<input checked="" type="checkbox"/>	481	733.0410	2196.1011	2196.1102	-0.0091	0	48	0.00071	1	R.FVGGYKPVVEGGFDIQVEEK.M
<input checked="" type="checkbox"/>	493	746.7161	2237.1264	2237.1190	0.0074	0	(38)	0.0023	1	K.MHPDLNFENTYLLNLLYK.D
<input checked="" type="checkbox"/>	498	752.0466	2253.1179	2253.1139	0.0040	0	43	0.00076	1	K.MHPDLNFENTYLLNLLYK.D + Oxidation (M)
<input checked="" type="checkbox"/>	525	1229.6131	2457.2116	2457.1807	0.0309	0	36	0.0033	1	-.MMPINAVTTLDQLEDSEYLFK.V
<input checked="" type="checkbox"/>	529	1237.6021	2473.1896	2473.1756	0.0139	0	(21)	0.084	1	-.MMPINAVTTLDQLEDSEYLFK.V + Oxidation (M)
<input checked="" type="checkbox"/>	530	1245.5970	2489.1795	2489.1705	0.0089	0	(29)	0.015	1	-.MMPINAVTTLDQLEDSEYLFK.V + 2 Oxidation (M)

Proteins matching the same set of peptides:

[SPPV-TU_097](#) Mass: 104657 Score: 1039 Queries matched: 80

097[Sheeppox virus strain TU-V02127] NP_659673.1|21492554|VBRC_genome_id|1495|VBRC_gene_id|41646|:

2. [LSDV-WARM_103](#) Mass: 104665 Score: 894 Queries matched: 70

101[Lumpy skin disease virus strain Neethling Warmbaths LW] AAN02669.1|22595636|VBRC_genome_id|1497

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide
8	387.2223	772.4301	772.4330	-0.0029	0	(17)	0.4	1	K.SPELSIK.E
9	387.2242	772.4338	772.4330	0.0008	0	24	0.086	1	K.SPELSIK.E
10	387.2279	772.4412	772.4330	0.0082	0	(19)	0.24	1	K.SPELSIK.E
16	405.2216	808.4286	808.4079	0.0207	0	10	2.4	1	K.YVDISGR.D
19	412.2321	822.4497	822.4752	-0.0255	0	(20)	0.39	1	R.FFQLLR.L
20	412.2321	822.4497	822.4752	-0.0255	0	(16)	0.96	1	R.FFQLLR.L
21	412.2378	822.4611	822.4752	-0.0141	0	22	0.23	1	R.FFQLLR.L
22	412.2378	822.4611	822.4752	-0.0141	0	(18)	0.62	1	R.FFQLLR.L
23	412.2435	822.4725	822.4752	-0.0026	0	(16)	0.89	1	R.FFQLLR.L
24	412.2454	822.4763	822.4752	0.0012	0	(18)	0.64	1	R.FFQLLR.L
25	412.2454	822.4763	822.4752	0.0012	0	(16)	0.87	1	R.FFQLLR.L
26	412.2493	822.4840	822.4752	0.0088	0	(16)	0.84	1	R.FFQLLR.L
27	412.2493	822.4840	822.4752	0.0088	0	(17)	0.67	1	R.FFQLLR.L
28	412.2569	822.4992	822.4752	0.0240	0	(21)	0.28	1	R.FFQLLR.L
29	412.7236	823.4327	823.4262	0.0065	0	27	0.058	1	R.ELLMYR.L

31	414.7536	827.4926	827.4865	0.0062	0	(34)	0.0075	1	R.LNNLNIK.Y
32	414.7536	827.4926	827.4865	0.0062	0	37	0.0046	1	R.LNNLNIK.Y
43	438.2365	874.4585	874.4548	0.0036	0	36	0.01	1	R.FQDQIPK.L
44	438.2405	874.4664	874.4548	0.0115	0	(25)	0.12	1	R.FQDQIPK.L
45	438.2424	874.4703	874.4548	0.0154	0	(33)	0.02	1	R.FQDQIPK.L
46	438.2522	874.4899	874.4548	0.0351	0	(17)	0.8	1	R.FQDQIPK.L
75	531.7860	1061.5574	1061.5505	0.0069	0	(28)	0.064	1	R.DFENLLGVR.R
76	531.7903	1061.5660	1061.5505	0.0155	0	28	0.06	1	R.DFENLLGVR.R
77	531.7946	1061.5747	1061.5505	0.0242	0	(18)	0.74	1	R.DFENLLGVR.R
78	531.8000	1061.5854	1061.5505	0.0349	0	(4)	16	1	R.DFENLLGVR.R
99	568.8259	1135.6372	1135.6311	0.0062	0	(40)	0.0035	1	K.EVLMMLYAGLK.I
100	568.8304	1135.6462	1135.6311	0.0151	0	(11)	2.7	1	K.EVLMMLYAGLK.I
104	576.8200	1151.6254	1151.6260	-0.0006	0	44	0.0008	1	K.EVLMMLYAGLK.I + Oxidation (M)
110	581.3207	1160.6268	1160.6012	0.0257	0	11	3.2	1	K.QYIHNMLVK.A + Oxidation (M)
113	585.2987	1168.5828	1168.5876	-0.0048	1	(29)	0.03	1	R.LKYPEYNSR.F
114	585.3055	1168.5964	1168.5876	0.0088	1	40	0.0029	1	R.LKYPEYNSR.F
131	403.5504	1207.6293	1207.6197	0.0097	0	41	0.0023	1	K.IDDNGSPHLIK.K
140	611.8180	1221.6214	1221.6353	-0.0139	0	(33)	0.011	1	K.DVLSTSIQGFR.V
141	611.8226	1221.6307	1221.6353	-0.0046	0	(21)	0.16	1	K.DVLSTSIQGFR.V
142	611.8250	1221.6354	1221.6353	0.0000	0	37	0.004	1	K.DVLSTSIQGFR.V
143	611.8250	1221.6354	1221.6353	0.0000	0	(24)	0.087	1	K.DVLSTSIQGFR.V
144	611.8296	1221.6446	1221.6353	0.0093	0	(13)	1	1	K.DVLSTSIQGFR.V
145	611.8319	1221.6493	1221.6353	0.0140	0	(16)	0.52	1	K.DVLSTSIQGFR.V
146	611.8342	1221.6539	1221.6353	0.0186	0	(25)	0.068	1	K.DVLSTSIQGFR.V
147	611.8389	1221.6632	1221.6353	0.0279	0	(23)	0.094	1	K.DVLSTSIQGFR.V
167	636.2887	1270.5629	1270.5506	0.0124	0	(18)	0.54	1	R.NYQEYYTK.N
168	636.2911	1270.5677	1270.5506	0.0171	0	18	0.5	1	R.NYQEYYTK.N
209	678.8099	1355.6052	1355.6135	-0.0083	0	73	8.8e-07	1	R.AMDTDILTMSMK.H
220	686.8148	1371.6150	1371.6084	0.0066	0	(40)	0.0032	1	R.AMDTDILTMSMK.H + Oxidation (M)
223	694.8146	1387.6147	1387.6033	0.0114	0	(38)	0.0024	1	R.AMDTDILTMSMK.H + 2 Oxidation (M)
320	795.4419	1588.8693	1588.8613	0.0080	0	70	2.6e-06	1	R.DHYINLLNLLAK.E
321	530.6315	1588.8728	1588.8613	0.0115	0	(52)	0.00018	1	R.DHYINLLNLLAK.E
322	530.6315	1588.8728	1588.8613	0.0115	0	(49)	0.00037	1	R.DHYINLLNLLAK.E
323	530.6380	1588.8923	1588.8613	0.0310	0	(50)	0.00026	1	R.DHYINLLNLLAK.E
331	799.9269	1597.8393	1597.8351	0.0042	0	58	4.5e-05	1	K.LGINYLLDVYSNK.L
334	804.4405	1606.8664	1606.8640	0.0024	0	20	0.31	2	K.VISSILPSLCLDYK.V
395	588.6642	1762.9709	1762.9802	-0.0093	0	43	0.0015	1	K.SIIGSNNHTIISVRPR.V
<input checked="" type="checkbox"/> 396	888.9325	1775.8505	1775.8406	0.0099	0	27	0.066	1	K.LSLFWDGIDYQBYK.S
435	663.3000	1986.8782	1986.9839	-0.1057	0	(13)	0.74	1	K.TSYVHPFDVLLHPDYGK.I
436	663.3273	1986.9601	1986.9839	-0.0238	0	62	9e-06	1	K.TSYVHPFDVLLHPDYGK.I
437	663.3418	1987.0036	1986.9839	-0.0197	0	(19)	0.16	1	K.TSYVHPFDVLLHPDYGK.I
438	663.3442	1987.0108	1986.9839	0.0269	0	(16)	0.37	1	K.TSYVHPFDVLLHPDYGK.I
439	663.3539	1987.0398	1986.9839	0.0559	0	(33)	0.0072	1	K.TSYVHPFDVLLHPDYGK.I
440	663.3539	1987.0398	1986.9839	0.0559	0	(1)	12	1	K.TSYVHPFDVLLHPDYGK.I
461	713.0257	2136.0553	2136.1367	-0.0814	0	(26)	0.042	1	K.LFHNVINPGYITPNDVVPK.F
462	713.0432	2136.1079	2136.1367	-0.0288	0	(7)	3.3	1	K.LFHNVINPGYITPNDVVPK.F
463	713.0508	2136.1305	2136.1367	-0.0062	0	51	0.00012	1	K.LFHNVINPGYITPNDVVPK.F
464	713.0533	2136.1380	2136.1367	0.0013	0	(33)	0.0079	1	K.LFHNVINPGYITPNDVVPK.F
465	713.0558	2136.1455	2136.1367	0.0088	0	(22)	0.082	1	K.LFHNVINPGYITPNDVVPK.F
466	713.0583	2136.1530	2136.1367	0.0163	0	(36)	0.0039	1	K.LFHNVINPGYITPNDVVPK.F
475	720.0307	2157.0704	2157.0564	0.0140	0	34	0.011	1	K.LISASYDLLHFMVSAGDYR.N
481	733.0410	2196.1011	2196.1102	-0.0091	0	48	0.00071	1	R.FVGGYVKPVEGGFDIQVEEK.I
525	1229.6131	2457.2116	2457.1807	0.0309	0	36	0.0033	1	-.MMPINAVTTLDQLEDSEYLFK.V
529	1237.6021	2473.1896	2473.1756	0.0139	0	(21)	0.084	1	-.MMPINAVTTLDQLEDSEYLFK.V + Oxidation (M)
530	1245.5970	2489.1795	2489.1705	0.0089	0	(29)	0.015	1	-.MMPINAVTTLDQLEDSEYLFK.V + 2 Oxidation (M)

Proteins matching the same set of peptides:

[LSDV-NEE_149](#) Mass: 104665 Score: 894 Queries matched: 70
101[Lumpy skin disease virus strain Neethling 2490] NP_150535.1|15150540|VBRC_genome_id|1488|VBRC_g
[LSDV-1959_102](#) Mass: 104651 Score: 894 Queries matched: 70
101[Lumpy skin disease virus strain Neethling vaccine LW 1959] AAN02826.1|22595794|VBRC_genome_id|1

3. [SPPV-A_078](#) Mass: 76288 Score: 700 Queries matched: 31
090[Sheeppox virus strain A] ||VBRC_genome_id|1511|VBRC_gene_id|44600|: ; SPPV-A_078 078
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
44	438.2405	874.4664	874.4695	-0.0031	1	(12)	2.4	2	R.QRSLPMK.R + Oxidation (M)
45	438.2424	874.4703	874.4695	0.0008	1	13	1.8	2	R.QRSLPMK.R + Oxidation (M)
46	438.2522	874.4899	874.4695	0.0205	1	(5)	13	3	R.QRSLPMK.R + Oxidation (M)
<input checked="" type="checkbox"/> 52	464.2518	926.4890	926.5007	-0.0118	0	32	0.025	1	R.ANIHTMIK.K
<input checked="" type="checkbox"/> 68	521.7648	1041.5151	1041.5130	0.0020	0	52	0.00026	1	K.GEGASFFLSK.Q
<input checked="" type="checkbox"/> 69	521.7648	1041.5151	1041.5130	0.0020	0	(9)	5.5	1	K.GEGASFFLSK.Q
<input checked="" type="checkbox"/> 72	530.8087	1059.6029	1059.5924	0.0105	0	49	0.0004	1	K.QEILLSTTR.F
<input checked="" type="checkbox"/> 101	570.7783	1139.5420	1139.5492	-0.0072	0	32	0.028	1	K.SSLTNSSMSVK.S
<input checked="" type="checkbox"/> 112	583.7816	1165.5486	1165.5471	0.0015	0	45	0.00073	1	K.MEEAMSLISR.Q
<input checked="" type="checkbox"/> 119	591.7884	1181.5623	1181.5420	0.0203	0	(27)	0.054	1	K.MEEAMSLISR.Q + Oxidation (M)
<input checked="" type="checkbox"/> 187	656.8641	1311.7136	1311.7186	-0.0051	0	(44)	0.0021	1	R.NELFELLAHVK.S
<input checked="" type="checkbox"/> 188	656.8713	1311.7280	1311.7186	0.0094	0	(38)	0.0086	1	R.NELFELLAHVK.S
<input checked="" type="checkbox"/> 189	656.8761	1311.7376	1311.7186	0.0190	0	44	0.0021	1	R.NELFELLAHVK.S
<input checked="" type="checkbox"/> 244	724.3739	1446.7332	1446.7289	0.0044	0	51	0.00022	1	K.VNPDNYMLLVNR.L
<input checked="" type="checkbox"/> 245	724.3890	1446.7635	1446.7289	0.0347	0	(16)	0.66	1	K.VNPDNYMLLVNR.L

<input checked="" type="checkbox"/>	253	732.3732	1462.7319	1462.7238	0.0081	0	(40)	0.0024	1	K.VNPDNYMLLVNR.L + Oxidation (M)
<input checked="" type="checkbox"/>	316	525.9468	1574.8186	1574.8238	-0.0052	1	41	0.0012	1	K.KVNPDPNYMLLVNR.L
<input checked="" type="checkbox"/>	325	531.2821	1590.8245	1590.8188	0.0057	1	(32)	0.016	1	K.KVNPDPNYMLLVNR.L + Oxidation (M)
<input checked="" type="checkbox"/>	367	557.3079	1668.9020	1668.8947	0.0073	1	31	0.009	1	R.SNRNELFELLAHV.K
<input checked="" type="checkbox"/>	369	558.6573	1672.9500	1672.9161	0.0338	0	(24)	0.065	1	K.STHPLVLIHSHAHK.I
<input checked="" type="checkbox"/>	370	558.6595	1672.9566	1672.9161	0.0405	0	32	0.01	1	K.STHPLVLIHSHAHK.I
<input checked="" type="checkbox"/>	455	698.3349	2091.9829	2091.9791	0.0037	0	30	0.013	1	K.QQMLMNHITMFDDLLK.M
<input checked="" type="checkbox"/>	456	1051.9661	2101.9177	2101.9228	-0.0052	0	61	1.1e-05	1	K.TSNNNQLEDSEDFYEWLK.G
<input checked="" type="checkbox"/>	457	703.6693	2107.9860	2107.9740	0.0119	0	(18)	0.33	1	K.QQMLMNHITMFDDLLK.M + Oxidation (M)
<input checked="" type="checkbox"/>	459	709.0040	2123.9901	2123.9690	0.0211	0	(24)	0.076	1	K.QQMLMNHITMFDDLLK.M + 2 Oxidation (M)
<input checked="" type="checkbox"/>	491	744.3471	2230.0194	2230.0178	0.0016	1	45	0.0005	1	R.KTSNNNQLEDSEDFYEWLK.G
<input checked="" type="checkbox"/>	500	759.0516	2274.1330	2274.1030	0.0300	0	5	4.2	1	R.DNESTYYIHPFMSLFGIK.L
<input checked="" type="checkbox"/>	513	594.2805	2373.0928	2373.0848	0.0080	0	62	7.8e-06	1	R.FQSIHFVDMSSSSDLAFHYR.D
<input checked="" type="checkbox"/>	515	598.2795	2389.0891	2389.0797	0.0094	0	(61)	1.8e-05	1	R.FQSIHFVDMSSSSDLAFHYR.D + Oxidation (M)
<input checked="" type="checkbox"/>	518	1209.6478	2417.2811	2417.2689	0.0122	0	54	4.2e-05	1	R.LTEAPIVFTGISDVISTEIQR.A
<input checked="" type="checkbox"/>	526	1232.0778	2462.1411	2462.1449	-0.0037	0	22	0.09	1	K.EDTNTTVPIDEVASTNDWQVK.L

Proteins matching the same set of peptides:

[SPPV-NISKHI_078](#) Mass: 76288 Score: 700 Queries matched: 31
090[Sheeppox virus strain NISKHI] ||VBRC_genome_id|1512|VBRC_gene_id|44749|: ; SPPV-NISKHI_078 078
[SPPV-TU_090](#) Mass: 76288 Score: 700 Queries matched: 31
090[Sheeppox virus strain TU-V02127] NP_659666.1|21492547|VBRC_genome_id|1495|VBRC_gene_id|41639|:

4. [DPV-W848_83-108](#) Mass: 105324 Score: 207 Queries matched: 23
110[Deerpox virus strain W-848-83] ||VBRC_genome_id|1515|VBRC_gene_id|45221|:

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Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
19	412.2321	822.4497	822.4752	-0.0255	0	(20)	0.39	1	R.FFQLLR.L
20	412.2321	822.4497	822.4752	-0.0255	0	(16)	0.96	1	R.FFQLLR.L
21	412.2378	822.4611	822.4752	-0.0141	0	22	0.23	1	R.FFQLLR.L
22	412.2378	822.4611	822.4752	-0.0141	0	(18)	0.62	1	R.FFQLLR.L
23	412.2435	822.4725	822.4752	-0.0026	0	(16)	0.89	1	R.FFQLLR.L
24	412.2454	822.4763	822.4752	0.0012	0	(18)	0.64	1	R.FFQLLR.L
25	412.2454	822.4763	822.4752	0.0012	0	(16)	0.87	1	R.FFQLLR.L
26	412.2493	822.4840	822.4752	0.0088	0	(16)	0.84	1	R.FFQLLR.L
27	412.2493	822.4840	822.4752	0.0088	0	(17)	0.67	1	R.FFQLLR.L
28	412.2569	822.4992	822.4752	0.0240	0	(21)	0.28	1	R.FFQLLR.L
43	438.2365	874.4585	874.4548	0.0036	0	36	0.01	1	R.FQDQIPK.L
44	438.2405	874.4664	874.4548	0.0115	0	(25)	0.12	1	R.FQDQIPK.L
45	438.2424	874.4703	874.4548	0.0154	0	(33)	0.02	1	R.FQDQIPK.L
46	438.2522	874.4899	874.4548	0.0351	0	(17)	0.8	1	R.FQDQIPK.L
131	403.5504	1207.6293	1207.6197	0.0097	0	41	0.0023	1	K.LDDNGSPHLIK.K
<input checked="" type="checkbox"/>	339	811.4310	1620.8475	1620.8797	-0.0321	0	(2)	9	1 K.IVSTILPSICLDYK.I
<input checked="" type="checkbox"/>	341	811.4444	1620.8742	1620.8797	-0.0054	0	10	1.4	1 K.IVSTILPSICLDYK.I
<input checked="" type="checkbox"/>	342	811.4578	1620.9010	1620.8797	0.0213	0	(1)	10	1 K.IVSTILPSICLDYK.I
395	588.6642	1762.9709	1762.9802	-0.0093	0	35	0.0087	2	K.SIIGSNHVTITVRPR.I
396	888.9325	1775.8505	1775.8406	0.0099	0	27	0.066	1	K.LSLFWDGIDYQEQY.K
525	1229.6131	2457.2116	2457.1807	0.0309	0	36	0.0033	1	-.MMPINAVTTLDQLEDSEYIFK.I
529	1237.6021	2473.1896	2473.1756	0.0139	0	(21)	0.084	1	-.MMPINAVTTLDQLEDSEYIFK.I + Oxidation (M)
530	1245.5970	2489.1795	2489.1705	0.0089	0	(29)	0.015	1	-.MMPINAVTTLDQLEDSEYIFK.I + 2 Oxidation (M)

Proteins matching the same set of peptides:

[DPV-W1170_84-108](#) Mass: 105319 Score: 207 Queries matched: 23
110[Deerpox virus strain W-1170-84] ||VBRC_genome_id|1516|VBRC_gene_id|45391|:

5. [SPPV-A_068](#) Mass: 73433 Score: 144 Queries matched: 4
080[Sheeppox virus strain A] ||VBRC_genome_id|1511|VBRC_gene_id|44590|: ; SPPV-A_068 068

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Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
35	415.2447	828.4748	828.5069	-0.0321	1	7	5.4	5	K.NVELVK.Y
<input checked="" type="checkbox"/>	203	669.8513	1337.6881	1337.6867	0.0015	0	61	1.7e-05	1 R.YNDEIITVPFK.L
<input checked="" type="checkbox"/>	227	699.9470	1397.8794	1397.8646	0.0148	0	28	0.045	1 K.VYILVPINILK.I
<input checked="" type="checkbox"/>	364	830.4257	1658.8369	1658.8403	-0.0034	0	48	0.00058	1 R.IYSILESISENYTK.E

Proteins matching the same set of peptides:

[SPPV-NISKHI_068](#) Mass: 73433 Score: 144 Queries matched: 4
080[Sheeppox virus strain NISKHI] ||VBRC_genome_id|1512|VBRC_gene_id|44739|: ; SPPV-NISKHI_068 068
[SPPV-TU_080](#) Mass: 73419 Score: 144 Queries matched: 4
080[Sheeppox virus strain TU-V02127] NP_659656.1|21492537|VBRC_genome_id|1495|VBRC_gene_id|41629|:

6. [YMTV-YLD_101](#) Mass: 103662 Score: 97 Queries matched: 18
101L[Yaba-like Disease Virus strain Unknown] NP_073486.1|12085084|VBRC_genome_id|1487|VBRC_gene_id|

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Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
19	412.2321	822.4497	822.4752	-0.0255	0	(20)	0.39	1	K.FFQLLR.L
20	412.2321	822.4497	822.4752	-0.0255	0	(16)	0.96	1	K.FFQLLR.L

21	412.2378	822.4611	822.4752	-0.0141	0	22	0.23	1	K.FFQLLR.L
22	412.2378	822.4611	822.4752	-0.0141	0	(18)	0.62	1	K.FFQLLR.L
23	412.2435	822.4725	822.4752	-0.0026	0	(16)	0.89	1	K.FFQLLR.L
24	412.2454	822.4763	822.4752	0.0012	0	(18)	0.64	1	K.FFQLLR.L
25	412.2454	822.4763	822.4752	0.0012	0	(16)	0.87	1	K.FFQLLR.L
26	412.2493	822.4840	822.4752	0.0088	0	(16)	0.84	1	K.FFQLLR.L
27	412.2493	822.4840	822.4752	0.0088	0	(17)	0.67	1	K.FFQLLR.L
28	412.2569	822.4992	822.4752	0.0240	0	(21)	0.28	1	K.FFQLLR.L
75	531.7860	1061.5574	1061.5505	0.0069	0	(28)	0.064	1	R.DFENLLGVR.S
76	531.7903	1061.5660	1061.5505	0.0155	0	28	0.06	1	R.DFENLLGVR.S
77	531.7946	1061.5747	1061.5505	0.0242	0	(18)	0.74	1	R.DFENLLGVR.S
78	531.8000	1061.5854	1061.5505	0.0349	0	(4)	16	1	R.DFENLLGVR.S
131	403.5504	1207.6293	1207.6197	0.0097	0	36	0.0067	3	K.LNDDGSPHLIK.K
339	811.4310	1620.8475	1620.8797	-0.0321	0	(2)	9	1	K.VISTILPSLCLDYK.V
341	811.4444	1620.8742	1620.8797	-0.0054	0	10	1.4	1	K.VISTILPSLCLDYK.V
342	811.4578	1620.9010	1620.8797	0.0213	0	(1)	10	1	K.VISTILPSLCLDYK.V

7. [GTPV-G20LKV_046](#) Mass: 29086 Score: 76 Queries matched: 2
059[Goatpox virus strain G20-LKV] ||VBRC_genome_id|1514|VBRC_gene_id|45021|: ; GTPV-G20LKV_046 046
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Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 183	653.8817	1305.7489	1305.7445	0.0044	0	45	0.00091	1	R.SFLSIFNIIPR.N
<input checked="" type="checkbox"/> 406	606.3156	1815.9250	1815.9002	0.0248	0	31	0.016	1	K.EIDEYSNKPLQEPVR.L

Proteins matching the same set of peptides:

[GTPV-Pellor_045](#) Mass: 29086 Score: 76 Queries matched: 2
059[Goatpox virus strain Pellor] ||VBRC_genome_id|1513|VBRC_gene_id|44870|: ; GTPV-Pellor_045 045
[SPPV-A_046](#) Mass: 29087 Score: 76 Queries matched: 2
059[Sheeppox virus strain A] ||VBRC_genome_id|1511|VBRC_gene_id|44569|: ; SPPV-A_046 046
[SPPV-NISKHI_046](#) Mass: 29087 Score: 76 Queries matched: 2
059[Sheeppox virus strain NISKHI] ||VBRC_genome_id|1512|VBRC_gene_id|44718|: ; SPPV-NISKHI_046 046
[SPPV-TU_059](#) Mass: 29087 Score: 76 Queries matched: 2
059[Sheeppox virus strain TU-V02127] NP_659635.1|21492516|VBRC_genome_id|1495|VBRC_gene_id|41608|:
[LSDV-WARM_065](#) Mass: 29074 Score: 76 Queries matched: 2
063[Lumpy skin disease virus strain Neethling Warmbaths LW] AAN02631.1|22595598|VBRC_genome_id|1497
[LSDV-NEE_090](#) Mass: 29074 Score: 76 Queries matched: 2
063[Lumpy skin disease virus strain Neethling 2490] NP_150497.1|15150502|VBRC_genome_id|1488|VBRC_g
[LSDV-1959_064](#) Mass: 29074 Score: 76 Queries matched: 2
063[Lumpy skin disease virus strain Neethling vaccine LW 1959] AAN02788.1|22595756|VBRC_genome_id|1

8. [DPV-W848_83-091](#) Mass: 73359 Score: 56 Queries matched: 2
093[Deerpox virus strain W-848-83] ||VBRC_genome_id|1515|VBRC_gene_id|45204|:
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Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
203	669.8513	1337.6881	1337.7231	-0.0349	1	29	0.03	2	R.YKDDIITVPFK.I
227	699.9470	1397.8794	1397.8646	0.0148	0	28	0.045	1	K.VYILVPINILK.I

Proteins matching the same set of peptides:

[DPV-W1170_84-091](#) Mass: 73359 Score: 56 Queries matched: 2
093[Deerpox virus strain W-1170-84] ||VBRC_genome_id|1516|VBRC_gene_id|45374|:

9. [SFV-KAS_103](#) Mass: 104195 Score: 44 Queries matched: 14
s099L[Rabbit fibroma virus strain Kasza] AAF17982.1|6578628|VBRC_genome_id|1480|VBRC_gene_id|38699|
☐ Check to include this hit in error tolerant search or archive report


Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
19	412.2321	822.4497	822.4752	-0.0255	0	(20)	0.39	1	R.FFQLLR.L
20	412.2321	822.4497	822.4752	-0.0255	0	(16)	0.96	1	R.FFQLLR.L
21	412.2378	822.4611	822.4752	-0.0141	0	22	0.23	1	R.FFQLLR.L
22	412.2378	822.4611	822.4752	-0.0141	0	(18)	0.62	1	R.FFQLLR.L
23	412.2435	822.4725	822.4752	-0.0026	0	(16)	0.89	1	R.FFQLLR.L
24	412.2454	822.4763	822.4752	0.0012	0	(18)	0.64	1	R.FFQLLR.L
25	412.2454	822.4763	822.4752	0.0012	0	(16)	0.87	1	R.FFQLLR.L
26	412.2493	822.4840	822.4752	0.0088	0	(16)	0.84	1	R.FFQLLR.L
27	412.2493	822.4840	822.4752	0.0088	0	(17)	0.67	1	R.FFQLLR.L
28	412.2569	822.4992	822.4752	0.0240	0	(21)	0.28	1	R.FFQLLR.L
131	403.5504	1207.6293	1207.6561	-0.0267	0	12	1.8	4	K.INDGTGPHLIK.K
339	811.4310	1620.8475	1620.8797	-0.0321	0	(2)	9	1	K.VISTILPSICLDYK.V
341	811.4444	1620.8742	1620.8797	-0.0054	0	10	1.4	1	K.VISTILPSICLDYK.V
342	811.4578	1620.9010	1620.8797	0.0213	0	(1)	10	1	K.VISTILPSICLDYK.V

10. [AMEV-EPB_169](#) Mass: 147234 Score: 37 Queries matched: 2
156[Amsacta moorei entomopoxvirus strain Moyer] NP_064938.1|9964470|VBRC_genome_id|1475|VBRC_gene_i
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Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
31	414.7536	827.4926	827.4865	0.0062	0	(31)	0.016	3	K.INNIINK.I
32	414.7536	827.4926	827.4865	0.0062	0	37	0.0046	1	K.INNIINK.I

11. [CNPV-WC93_150](#) Score: 34 Queries matched: 4
150[Canarypox virus strain ATCC VR111] NP_955173.1|40556088|VBRC_genome_id|1506|VBRC_gene_id|43623|: CNPV150 ankyrin repeat protein; C

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Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
31	414.7536	827.4926	827.4865	0.0062	0	(14)	0.81	4	K.NINININK.T
32	414.7536	827.4926	827.4865	0.0062	0	18	0.3	4	K.NINININK.T
 34	415.2428	828.4710	828.4705	0.0005	0	15	0.72	1	K.ILDNNLK.H
35	415.2447	828.4748	828.4705	0.0043	0	(4)	11	6	K.ILDNNLK.H

12. [MPXV-ZRE_121](#) Mass: 103014 Score: 22 Queries matched: 11
All1[Monkeypox virus strain Zaire] NP_536548.1|17975034|VBCR_genome_id|1489|VBCR_gene_id|40483|: A1
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
19	412.2321	822.4497	822.4752	-0.0255	0	(20)	0.39	1	R.FFQLLR.L
20	412.2321	822.4497	822.4752	-0.0255	0	(16)	0.96	1	R.FFQLLR.L
21	412.2378	822.4611	822.4752	-0.0141	0	22	0.23	1	R.FFQLLR.L
22	412.2378	822.4611	822.4752	-0.0141	0	(18)	0.62	1	R.FFQLLR.L
23	412.2435	822.4725	822.4752	-0.0026	0	(16)	0.89	1	R.FFQLLR.L
24	412.2454	822.4763	822.4752	0.0012	0	(18)	0.64	1	R.FFQLLR.L
25	412.2454	822.4763	822.4752	0.0012	0	(16)	0.87	1	R.FFQLLR.L
26	412.2493	822.4840	822.4752	0.0088	0	(16)	0.84	1	R.FFQLLR.L
27	412.2493	822.4840	822.4752	0.0088	0	(17)	0.67	1	R.FFQLLR.L
28	412.2569	822.4992	822.4752	0.0240	0	(21)	0.28	1	R.FFQLLR.L
 442	669.3000	2004.8782	2004.9039	-0.0258	0	0	9.8	1	K.HLIMYEQYFVNDYR.V

Proteins matching the same set of peptides:

126[Monkeypox virus strain Zaire 1979-005] AAY97321.1|68449200|VBRC genome id|1523|VBRC gene id|469

MPXV-Congo_2003_358-122 Mass: 103014 Score: 22 Queries matched: 11

126[Monkeypox virus strain Congo 2003 358] AAY97120.1|68448998|VBRC genome id|1524|VBRC gene id|471

13. [DPV-W848_83-002](#) Mass: 19489 Score: 22 Queries matched: 1
002[Deerpox virus strain W-848-83] |VBRC_genome_id|1515|VBRC_gene_id|45115|
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/>	6	385.2297	768.4448	768.3033	0.1414	0	22	0.18	1 K.MVEMVE.- + 2 Oxidation (M)

Proteins matching the same set of peptides:

[DPV-W848_83-169](#) **Mass:** 19489 **Score:** 22 **Queries matched:** 1

171[Deerpox virus strain W-848-83] ||VBRC genome id|1515|VBRC gene id|45282|:

DPV-W1170 84-002 Mass: 19781 Score: 22 Queries matched: 1

002[Deerpox virus strain W-1170-84] ||VBRC genome id|1516|VBRC gene id|45285|:

DPV-W1170 84-169 Mass: 19781 Score: 22 Queries matched: 1

14. [FWPV-FCV_174](#) Mass: 102717 Score: 20 Queries matched: 1
174|Fowlpox virus strain Iowa|NP_039137.1|7271672|VBRC_genome_id|1476|VBRC_gene_id|37906|: ORF FVPV
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 334	804.4405	1606.8664	1606.8640	0.0024	0	20	0.29	1	K.LISSVLPSLCLDYK.I

Proteins matching the same set of peptides:

FWPV-HP438_164 Mass: 102717 Score: 20 Queries matched: 1

15. [SWPV-NEB_091](#) Mass: 75712 Score: 18 Queries matched: 1
091|Swinepox virus strain Nebraska 17077-99| NP_570251.1|18640177|VBRC_genome_id|1490|VBRC_gene_id|
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
248	727.8163	1453.6181	1453.5932	0.0249	0	18	0.32	1	R.NTFSGECYTYGR.S

16. [AMEV-EPB_016](#) Mass: 99476 Score: 17 Queries matched: 2
003[Amsacta moorei entomopoxvirus strain Moyer] NP_064785.1|9964317|VBRC_genome_id|1475|VBRC_gene_i
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 96	564.7929	1127.5712	1127.6087	-0.0375	1	8	6.8	1	K.NLHFDNIKK.D
<input checked="" type="checkbox"/> 210	679.3525	1356.6904	1356.7612	-0.0708	0	10	2	1	R.NIIDNNTLSIIK.T

17. [MSEV-TUC 257](#) **Mass:** 84138 **Score:** 15 **Queries matched:** 2

257[Melanoplus sanguinipes entomopoxvirus strain Tucson] NP_048328.1|9631420|VBRC_genome_id|1478|VB

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Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
34	415.2428	828.4710	828.4705	0.0005	0	15	0.72	1	K.IIDNLNK.L
35	415.2447	828.4748	828.4705	0.0043	0	(4)	11	6	K.IIDNLNK.L

18. [AMEV-EPB_183](#) Score: 14 Queries matched: 2

170[Amsacta moorei entomopoxvirus strain Moyer] NP_064952.1|9964484|VBRC_genome_id|1475|VBRC_gene_id|37623|: AMV170; DNA-DIRECTED RNA

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Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
34	415.2428	828.4710	828.4527	0.0182	0	(8)	4.1	4	K.MPNLINK.L
35	415.2447	828.4748	828.4527	0.0221	0	14	1.1	2	K.MPNLINK.L

19. [MYXV-LAU_080](#) Mass: 97052 Score: 13 Queries matched: 1

m076R[Myxoma virus strain Lausanne] NP_051790.1|9633712|VBRC_genome_id|1479|VBRC_gene_id|38505|: m7

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Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 125	596.7892	1191.5639	1191.6611	-0.0973	1	13	1.8	1	K.EHKVDPAAVVK.Y

20. [AMEV-EPB_153](#) Mass: 36632 Score: 13 Queries matched: 2

140[Amsacta moorei entomopoxvirus strain Moyer] NP_064922.1|9964454|VBRC_genome_id|1475|VBRC_gene_i

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
34	415.2428	828.4710	828.5069	-0.0359	1	(7)	4.9	6	K.LNDLVKK.D
<input checked="" type="checkbox"/> 35	415.2447	828.4748	828.5069	-0.0321	1	14	0.94	1	K.LNDLVKK.D

Peptide matches not assigned to protein hits: (no details means no match)

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 85	543.2877	1084.5608	1084.5375	0.0233	1	12	2.3	1	ENIFKCFK
<input checked="" type="checkbox"/> 153	622.2795	1242.5444	1242.5406	0.0037	0	12	1.3	1	LMASMATEMSR + Oxidation (M)
<input checked="" type="checkbox"/> 273	496.2562	1485.7467	1485.6843	0.0624	1	12	1.5	1	DQLFLSEMVKMN + 2 Oxidation (M)
<input checked="" type="checkbox"/> 290	758.9405	1515.8664	1515.8330	0.0334	0	11	2.3	1	VSVTIIPLMADSVR + Oxidation (M)
<input checked="" type="checkbox"/> 82	535.3262	1068.6379	1068.6655	-0.0276	1	10	3	1	IINIIKNKK
<input checked="" type="checkbox"/> 49	461.2877	920.5608	920.4087	0.1521	0	10	2.2	1	ENISESDK
<input checked="" type="checkbox"/> 64	516.7633	1031.5121	1031.6127	-0.1006	1	10	2	1	LINFKELR
<input checked="" type="checkbox"/> 291	758.9405	1515.8664	1515.8330	0.0334	0	9	3.4	1	VSVTIIPLMADSVR + Oxidation (M)
<input checked="" type="checkbox"/> 196	665.3678	1328.7210	1328.6935	0.0275	1	9	2.9	1	INNNDIELKK
<input checked="" type="checkbox"/> 216	685.3726	1368.7306	1368.7435	-0.0129	0	8	6.1	1	TIMLNGIVDLHK + Oxidation (M)
<input checked="" type="checkbox"/> 185	655.8644	1309.7142	1309.6224	0.0919	0	8	5.1	1	DSAIMVASEPYK
<input checked="" type="checkbox"/> 89	552.3000	1102.5854	1102.6597	-0.0743	0	7	6.3	1	IGTLVSSSVK
<input checked="" type="checkbox"/> 284	504.2849	1509.8330	1509.7894	0.0435	1	7	5	1	VTSKMLETMLSVR + Oxidation (M)
<input checked="" type="checkbox"/> 95	558.8102	1115.6059	1115.6008	0.0051	0	7	6.4	1	MVPTIELASR
<input checked="" type="checkbox"/> 285	756.4180	1510.8215	1510.8970	-0.0755	0	7	8.2	1	SILLVNPSSIDLLK
<input checked="" type="checkbox"/> 36	421.7629	841.5113	841.5385	-0.0272	1	6	8	1	RDIVIVK
<input checked="" type="checkbox"/> 166	635.8416	1269.6687	1269.6717	-0.0030	1	6	3.7	1	LQSLYNKYK
<input checked="" type="checkbox"/> 162	630.8562	1259.6978	1259.6267	0.0711	1	6	7.8	1	WPLAMREAR
<input checked="" type="checkbox"/> 129	599.3537	1196.6929	1196.7128	-0.0199	1	6	11	1	LPDLIKELTR
<input checked="" type="checkbox"/> 87	544.7907	1087.5668	1087.4426	0.1242	1	5	9.3	1	MMKDYDNR + Oxidation (M)
<input checked="" type="checkbox"/> 336	806.3757	1610.7369	1610.7365	0.0004	0	5	12	1	DHYNTIVDWASYK
<input checked="" type="checkbox"/> 207	674.3378	1346.6610	1346.6929	-0.0319	0	4	15	1	TGTLTQIDIEIK
<input checked="" type="checkbox"/> 128	599.3216	1196.6286	1196.7856	-0.1570	1	4	15	1	LLIDRITLIK
<input checked="" type="checkbox"/> 40	428.7728	855.5310	855.5178	0.0132	0	4	9.6	1	SPSLALLR
<input checked="" type="checkbox"/> 257	736.3970	1470.7794	1470.8657	-0.0863	1	4	13	1	IDILSIKLDNISK
<input checked="" type="checkbox"/> 134	606.3110	1210.6074	1210.6380	-0.0305	0	4	10	1	LSVMLFTTQR + Oxidation (M)
<input checked="" type="checkbox"/> 173	640.3339	1278.6533	1278.6642	-0.0108	0	3	26	1	SSPLELFMLSR
<input checked="" type="checkbox"/> 7	386.2337	770.4528	770.4901	-0.0374	0	3	17	1	VALEVLK
<input checked="" type="checkbox"/> 365	553.9892	1658.9458	1658.9243	0.0215	1	3	16	1	FSTDKNPSILPSLIK
<input checked="" type="checkbox"/> 70	523.2807	1044.5468	1044.5563	-0.0095	1	3	16	1	SKNINLNDK
<input checked="" type="checkbox"/> 242	723.8615	1445.7085	1445.7548	-0.0463	1	3	13	1	INEMVDELVTRK
<input checked="" type="checkbox"/> 251	731.4039	1460.7932	1460.8139	-0.0207	1	2	17	1	LKFHIVTDAVYR
<input checked="" type="checkbox"/> 158	623.3375	1244.6605	1244.7315	-0.0710	0	2	23	1	IIVIPVCYR
<input checked="" type="checkbox"/> 280	501.2501	1500.7284	1500.7502	-0.0218	1	2	12	1	MFRMTVELMSLK + Oxidation (M)
<input checked="" type="checkbox"/> 94	558.2405	1114.4665	1114.6233	-0.1568	1	2	18	1	KDEAIEIGLK
<input checked="" type="checkbox"/> 337	808.4493	1614.8840	1614.6905	0.1935	0	2	17	1	NLNVDDMMYDEIK + Oxidation (M)
<input checked="" type="checkbox"/> 306	779.4443	1556.8741	1556.8093	0.0648	1	2	9.1	1	HSMLTNAISSKVNR
<input checked="" type="checkbox"/> 402	897.9125	1793.8104	1793.9532	-0.1428	1	2	8.2	1	TLFTTPMIMRDLVTR
<input checked="" type="checkbox"/> 240	723.4124	1444.8102	1444.7561	0.0541	0	2	16	1	SPELVAEVAIPDR
<input checked="" type="checkbox"/> 74	531.2951	1060.5756	1060.5036	0.0720	0	2	24	1	NNDITLDEK
<input checked="" type="checkbox"/> 234	709.8809	1417.7472	1417.6734	0.0738	0	2	14	1	NICNALYIMYK + Oxidation (M)
<input checked="" type="checkbox"/> 239	723.4124	1444.8102	1444.7635	0.0467	1	2	16	1	YKSDIIMVSFVK + Oxidation (M)