

BIOLYNX - PROTEIN REPORT - Ovalbumin Chicken

Source: Swissprot P01012; Mods: Cys-CAM; printed: Thu Jun 09, 2005

Average Mass = 43092.5050, Monoisotopic Mass = 43064.5911; N-Terminus = H, C-Terminus = OH

Modified amino acids: CAM(Z) = CAM Cysteine; Digest: Trypsin:/K-AP /R-AP

Frag#	Res#	Sequence	Theor(Bo)	[M+H]	[M+2R]	[M+3H]
T24	277-277	(R)K(I)	146.11	147.11	74.06	49.71
T25	278-279	(K)IK(V)	259.19	260.20	130.60	87.40
T27	285-286	(R)MK(M)	277.15	278.15	139.58	93.39
T21	227-228	(K)MK(I)	277.15	278.15	139.58	93.39
T17	187-189	(K)AFK(D)	364.21	365.22	183.11	122.41
T6	56-58	(K)VVR(F)	372.25	373.26	187.13	125.09
T24-25	277-279	(R)KIK(V)	387.28	388.29	194.65	130.10
T2	17-19	(K)ELK(V)	388.23	389.24	195.12	130.42
T7	59-61	(R)FDK(L)	408.20	409.21	205.11	137.07
T34	382-385	(R)ZVSP(-)	461.19	462.20	231.60	154.74
T4	47-50	(K)DSTR(T)	477.22	478.23	239.62	160.08
T28	287-290	(K)MEEK(Y)	535.23	536.24	268.62	179.42
T12	123-126	(K)ELYR(G)	579.30	580.31	290.66	194.11
T5	51-55	(R)TQINK(V)	602.34	603.35	302.18	201.79
T16	182-186	(K)GLWEK(A)	631.33	632.34	316.67	211.45
T26	280-284	(K)VYLPR(M)	646.38	647.39	324.20	216.47
T6-7	56-61	(K)VVRFDK(L)	762.44	763.45	382.23	255.15
T10	105-110	(R)LYAEER(Y)	779.38	780.39	390.70	260.80
T27-28	285-290	(R)MKMEEK(Y)	794.37	795.37	398.19	265.80
T20	219-226	(R)VASMASEK(M)	821.40	822.40	411.71	274.81
T25-26	278-284	(K)IKVYLPR(M)	887.56	888.57	444.79	296.86
T26-27	280-286	(K)VYLPRMK(M)	905.52	906.52	453.77	302.85
T5-6	51-58	(R)TQINKVVR(F)	956.58	957.58	479.30	319.87
T16-17	182-189	(K)GLWEKAFK(D)	977.53	978.54	489.77	326.85
T4-5	47-55	(K)DSTRTQINK(V)	1061.55	1062.55	531.78	354.86
T20-21	219-228	(R)VASMASEKMK(I)	1080.53	1081.54	541.27	361.18
T18	190-199	(K)DEDTQAMPFR(V)	1208.51	1209.52	605.26	403.85
T32	360-369	(R)ADHPFLFZIK(H)	1246.62	1247.62	624.32	416.55
T33	370-381	(K)HIATNAVLFFGR(Z)	1344.73	1345.74	673.37	449.25
T11	111-122	(R)YPILPEYLQZVK(E)	1521.79	1522.80	761.90	508.27
T17-18	187-199	(K)AFKDEDTQAMPFR(V)	1554.71	1555.72	778.36	519.25
T23	264-276	(K)LTEWTSSNVMEER(K)	1580.71	1581.72	791.36	527.91
T13	127-142	(R)GGLEPINFQTAADQAR(E)	1686.83	1687.84	844.42	563.29
T23-24	264-277	(K)LTEWTSSNVMEERK(I)	1708.81	1709.82	855.41	570.61
T1	1-16	(-)GSIGAASMEFZFDVFK(E)	1764.79	1765.79	883.40	589.27
T30	323-339	(K)ISQAVHAAHAEINEAGR(E)	1772.89	1773.90	887.45	591.97
T33-34	370-385	(K)HIATNAVLFFGRZVSP(-)	1787.91	1788.92	894.96	596.98
T14	143-158	(R)ELINSWVESQTNGIIR(N)	1857.96	1858.97	929.99	620.33

Frag#	Res#	Sequence	Theor(Bo)	[M+H]	[M+2R]	[M+3H]
T31	340-359	(R)EVVGSAAEAGVDAASVSE EFR(A)	2007.94	2008.95	1004.98	670.32
T11-12	111-126	(R)YPILPEYLQZVKELYSR(G)	2083.08	2084.09	1042.55	695.37
T1-2	1-19	(-)GSIGAASMEFZFDVFKK(L)	2135.01	2136.01	1068.51	712.68
T12-13	123-142	(K)ELYRGGLEPINFQTAADQAR(E)	2248.12	2249.13	1125.07	750.38
T9	85-104	(R)DILNQITKPNQVYVYSLASR(L)	2280.18	2281.18	1141.10	761.07
T10-11	105-122	(R)LYAEERYPILPEYLQZVK(E)	2283.16	2284.17	1142.59	762.06
T19	200-218	(R)VTEQESKPVQMMYQIGLFR(V)	2283.14	2284.15	1142.58	762.05
T8	62-84	(K)LPGFGDSIEAQZGTSVNVHSSLR(D)	2430.16	2431.17	1216.09	811.06
T15	159-181	(R)NVLQPSSVDSQTAMVLVNAIVFK(G)	2459.31	2460.32	1230.66	820.78
T32-33	360-381	(R)ADHPFLFZIKHIATNAVLFFGR(Z)	2573.34	2574.34	1287.68	858.79
T7-8	59-84	(R)FDKLPFGFGDSIEAQZGTSVNVHSSLR(D)	2820.35	2821.36	1411.18	941.12
T3	20-46	(K)VHHANENIFYZPIAIMSALAMVYLGAK(D)	3032.51	3033.52	1517.26	1011.84
T9-10	85-110	(R)DILNQITKPNQVYVYSLASRLYAEER(Y)	3041.55	3042.55	1521.78	1014.86
T15-16	159-186	(R)NVLQPSSVDSQTAMVLVNAIVFKGLWEK(A)	3072.63	3073.64	1537.32	1025.22
T19-20	200-226	(R)VTEQESKPVQMMYQIGLF RVASMASEK(M)	3086.52	3087.53	1544.27	1029.85
T31-32	340-369	(R)EVVGSAAEAGVDAASVSEEFRAADHPFLFZIK(H)	3236.54	3237.55	1619.28	1079.86
T29	291-322	(K)YNLTSVLMAMGITDVFSSANLSGSSAESLK(I)	3292.62	3293.63	1647.32	1098.55
T2-3	17-46	(K)ELKVHHANENIFYZPIAIMSALAMVYLGAK(D)	3402.73	3403.74	1702.37	1135.25
T18-19	190-218	(K)DEDTQAMPFRVTEQESKIPVQMMYQIGLFR(V)	3473.64	3474.65	1737.83	1158.89
T3-4	20-50	(K)VHHANENIFYZPIAIMSALAMVYLGAKDSTR(T)	3491.72	3492.72	1746.87	1164.91
T13-14	127-158	(R)GGLEPINFQTAADQARELINSWVESQTNGIIR(N)	3528.89	3529.89	1765.45	1177.30
T30-31	323-359	(K)ISQAVHAAHAEINEAGREVVGSAEAGVDAASVSEEFR(A)	3765.03	3766.03	1883.52	1256.02
T28-29	287-322	(K)MEEKYNLTSVLMAMGITDVFSSANLSGSSAESLK(I)	3812.35	3813.36	1907.18	1271.79
T22	229-263	(K)ILELPPFASGTMSMLVLLPDEVSGLEQLESINFEK(L)	3864.54	3865.54	1933.28	1289.19
T21-22	227-263	(K)MKILELPPFASGTMSMLVLLPDEVSGLEQLESINFEK(L)	4123.91	4124.92	2062.96	1375.64
T14-15	143-181	(R)ELINSWVESQTNGIIRNVLQPSSVDSQTAMVLVNAIVFK(G)	4301.93	4302.94	2151.97	1434.99
T8-9	62-104	(K)LPGFGDSIEAQZGTSVNVHSSLRDILNQITKPNQVYVYSLASR(L)	4695.21	4696.21	2348.61	1566.08
T29-30	291-339	(K)YNLTSVLMAMGITDVFSSANLSGSSAESLKISQAVHAAHAEINEAGR(E)	5050.66	5051.67	2526.34	1684.56
T22-23	229-276	(K)ILELPPFASGTMSMLVLLPDEVSGLEQLESINFEKLTTEWTSNNVMEER(K)	5428.24	5429.25	2715.13	1810.42