

BIOLYNX - PROTEIN REPORT - Bovine serum albumin

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

Average Mass = 71290.5016, Monoisotopic Mass = 71244.1902 : N-Terminus = H, C-Terminus = OH

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

Frag#	Res#	Sequence	Theor(Bo)	[M+H]	[M+2R]	[M+3H]
T20	156-156	(K)K(F)	146.11	147.11	74.06	49.71
T75	548-548	(K)K(Q)	146.11	147.11	74.06	49.71
T61	437-437	(R)K(V)	146.11	147.11	74.06	49.71
T23	168-168	(R)R(H)	174.11	175.12	88.06	59.05
T51	360-360	(R)R(H)	174.11	175.12	88.06	59.05
T4	24-24	(R)R(D)	174.11	175.12	88.06	59.05
T56	400-401	(K)LK(H)	259.19	260.20	130.60	87.40
T44	298-299	(K)LK(E)	259.19	260.20	130.60	87.40
T28	210-211	(R)EK(V)	275.15	276.16	138.58	92.72
T1	1-2	(-)MK(W)	277.15	278.15	139.58	93.39
T31	221-222	(R)LR(Z)	287.20	288.20	144.61	96.74
T7	35-36	(R)FK(D)	293.17	294.18	147.59	98.73
T30	219-220	(R)QR(L)	302.17	303.18	152.09	101.73
T53	372-374	(R)LAK(E)	330.23	331.23	166.12	111.08
T34	233-235	(R)ALK(A)	330.23	331.23	166.12	111.08
T69	496-498	(K)VTK(Z)	346.22	347.23	174.12	116.42
T40	264-266	(K)VHK(E)	382.23	383.24	192.12	128.42
T74	545-547	(K)QIK(K)	387.25	388.26	194.63	130.09
T37	246-248	(K)FPK(A)	390.23	391.23	196.12	131.08
T63	452-455	(R)SLGK(V)	403.24	404.25	202.63	135.42
T64	456-459	(K)VGTR(Z)	431.25	432.26	216.63	144.76
T60	434-436	(R)YTR(K)	438.22	439.23	220.12	147.08
T19	152-155	(K)ADEK(K)	461.21	462.22	231.61	154.75
T36	242-245	(R)LSQK(F)	474.28	475.29	238.15	159.10
T3	20-23	(R)GVFR(R)	477.27	478.28	239.64	160.10
T5	25-28	(R)DTHK(S)	499.24	500.25	250.63	167.42
T33	229-232	(K)FGER(A)	507.24	508.25	254.63	170.09
T77	558-561	(K)HKPK(A)	508.31	509.32	255.16	170.45
T74-75	545-548	(K)QIKK(Q)	515.34	516.35	258.68	172.79
T42	281-285	(R)ADLAK(Y)	516.29	517.30	259.15	173.10
T48	337-340	(K)DVZK(N)	520.23	521.24	261.12	174.42
T21	157-160	(K)FWGK(Y)	536.27	537.28	269.15	179.77
T13	101-105	(K)VASLR(E)	544.33	545.34	273.17	182.45
T60-61	434-437	(R)YTRK(V)	566.32	567.33	284.17	189.78
T30-31	219-222	(R)QRLR(Z)	571.36	572.36	286.69	191.46
T19-20	152-156	(K)ADEKK(F)	589.31	590.31	295.66	197.44
T72	524-528	(K)AFDEK(L)	608.28	609.29	305.15	203.77

Frag#	Res#	Sequence	Theor(Bo)	[M+H]	[M+2R]	[M+3H]
T3-4	20-24	(R)GVFRR(D)	633.37	634.38	317.69	212.13
T27	205-209	(K)IETMR(E)	648.33	649.33	325.17	217.12
T4-5	24-28	(R)RDTHK(S)	655.34	656.35	328.68	219.45
T15	118-122	(K)QEPER(N)	657.31	658.32	329.66	220.11
T68	490-495	(K)TPVSEK(V)	659.35	660.36	330.68	220.79
T20-21	156-160	(K)KFWGK(Y)	664.37	665.38	333.19	222.46
T35	236-241	(K)AWSVAR(L)	688.37	689.37	345.19	230.46
T29	212-218	(K)VLISSAR(Q)	702.40	703.41	352.21	235.14
T32	223-228	(R)ZASIQK(F)	705.35	706.36	353.68	236.12
T6	29-34	(K)SEIAHR(F)	711.37	712.37	356.69	238.13
T49	341-346	(K)NYQEAK(D)	751.35	752.36	376.68	251.46
T26	198-204	(K)GAZLLPK(I)	757.42	758.42	379.72	253.48
T39	257-163	(K)LVTDLTK(V)	788.46	789.47	395.24	263.83
T63-64	452-459	(R)SLGKVGTR(Z)	816.48	817.49	409.25	273.17
T78	562-568	(K)ATEEQLK(T)	817.42	818.43	409.72	273.48
T33-34	229-235	(K)FGERALK(A)	819.46	820.47	410.74	274.16
T80	581-587	(K)ZZAADDK(E)	838.29	839.30	420.16	280.44
T36-37	242-248	(R)LSQKFPK(A)	846.50	847.50	424.26	283.17
T17	131-138	(K)DDSPDLPK(L)	885.41	886.42	443.71	296.14
T67	483-489	(R)LZVLHEK(T)	897.47	898.48	449.74	300.17
T27-28	205-211	(K)IETMREK(V)	905.46	906.47	453.74	302.83
T38	249-256	(K)AEFVEVTK(L)	921.48	922.49	461.75	308.17
T22	161-167	(K)YLYEIAR(R)	926.49	927.49	464.25	309.84
T28-29	210-218	(R)EKVLASSAR(Q)	959.54	960.55	480.78	320.85
T8	37-44	(K)DLGEEHFK(G)	973.45	974.46	487.73	325.49
T31-32	221-228	(R)LRZASIQK(F)	974.53	975.54	488.27	325.85
T6-7	29-36	(K)SEIAHRFK(D)	986.53	987.54	494.27	329.85
T29-30	212-220	(K)VLISSARQR(L)	986.56	987.57	494.29	329.86
T68-69	490-498	(K)TPVSEKVT(K)(Z)	987.56	988.57	494.79	330.19
T34-35	233-241	(R)ALKAWSVAR(L)	1000.58	1001.59	501.30	334.54
T82	598-607	(K)LVVSTQTALA(-)	1001.58	1002.58	501.80	334.87
T76	549-557	(K)QTALVELLK(H)	1013.61	1014.62	507.81	338.88
T16	123-130	(R)NEZFLSHK(D)	1033.47	1034.47	517.74	345.50
T58	413-420	(K)QNZDQFEK(L)	1067.43	1068.44	534.72	356.82
T46	310-318	(K)SHZIAEVEK(D)	1071.50	1072.51	536.76	358.18
T22-23	161-168	(K)YLYEIARR(H)	1082.59	1083.60	542.30	361.87
T81	588-597	(K)EAZFAVEGPK(L)	1106.51	1107.51	554.26	369.84
T70	499-507	(K)ZZTESLVNR(R)	1137.49	1138.50	569.75	380.17
T75-76	548-557	(K)KQTALVELLK(H)	1141.71	1142.71	571.86	381.58
T35-36	236-245	(K)AWSVARLSQK(F)	1144.64	1145.64	573.33	382.55
T39-40	257-266	(K)LVTDLTKVHK(E)	1152.69	1153.69	577.35	385.24
T10	66-75	(K)LVNELTEFAK(T)	1162.62	1163.63	582.32	388.55

Frag#	Res#	Sequence	Theor(Bo)	[M+H]	[M+2R]	[M+3H]
T65	460-468	(R)ZZTKPESER(M)	1165.49	1166.49	583.75	389.50
T5-6	25-34	(R)DTHKSEIAHR(F)	1192.59	1193.60	597.31	398.54
T32-33	223-232	(R)ZASIQKFGER(A)	1194.58	1195.59	598.30	399.20
T7-8	35-44	(R)FKDLGEEHFK(G)	1248.61	1249.62	625.31	417.21
T48-49	337-346	(K)DVZKNYQEAK(D)	1253.57	1254.58	627.79	418.86
T52	361-371	(R)HPEYAVSVLLR(L)	1282.70	1283.71	642.36	428.58
T45	300-309	(K)EZZDKP LLEK(S)	1290.59	1291.60	646.31	431.21
T37-38	246-256	(K)FPKAEFVEVTK(L)	1293.70	1294.70	647.86	432.24
T57	402-412	(K)HLVDEPQNLIK(Q)	1304.71	1305.72	653.36	435.91
T77-78	558-568	(K)HKPKATEEQLK(T)	1307.72	1308.73	654.87	436.91
T26-27	198-209	(K)GAZLLPKIETMR(E)	1387.73	1388.74	694.87	463.59
T79	569-580	(K)TVMENFVAFVDK(Z)	1398.69	1399.69	700.35	467.24
T12	89-100	(K)SLHTLFGDELZK(V)	1418.69	1419.69	710.35	473.90
T51-52	360-371	(R)RHPEYAVSVLLR(L)	1438.80	1439.81	720.41	480.61
T43	286-297	(K)YIZDNQDTISSK(L)	1442.63	1443.64	722.33	481.89
T21-22	157-167	(K)FWGKYL YEIAR(R)	1444.75	1445.76	723.38	482.59
T11	76-88	(K)TZVADESHAGZEK(S)	1462.58	1463.59	732.30	488.54
T69-70	496-507	(K)VTKZZTESLVNR(R)	1465.70	1466.71	733.86	489.58
T14	106-117	(R)ETYGDMADZZEK(Q)	1477.52	1478.52	739.77	493.51
T59	421-433	(K)LGEYGFQNALIVR(Y)	1478.79	1479.80	740.40	493.94
T54	375-386	(K)EYEATLEEZZAK(D)	1501.61	1502.61	751.81	501.54
T76-77	549-561	(K)QTALVELLKHKPK(A)	1503.91	1504.92	752.96	502.31
T62	438-451	(K)VPQVSTPTLVEVSR(S)	1510.84	1511.84	756.43	504.62
T44-45	298-309	(K)LKEZZDKP LLEK(S)	1531.77	1532.78	766.89	511.60
T67-68	483-495	(R)LZVLHEKTPVSEK(V)	1538.81	1539.82	770.41	513.95
T56-57	400-412	(K)LKHLVDEPQNLIK(Q)	1545.89	1546.90	773.95	516.30
T55	387-399	(K)DDPHAZYSTVFDK(L)	1553.65	1554.65	777.83	518.89
T50	347-359	(K)DAFLGSFL YEYSR(R)	1566.74	1567.74	784.38	523.25
T18	139-151	(K)LKPDPNTLZDEFK(A)	1575.76	1576.77	788.89	526.26
T64-65	456-468	(K)VGTRZZTKPESER(M)	1578.72	1579.73	790.37	527.25
T52-53	361-374	(R)HPEYAVSVLLRLAK(E)	1594.92	1595.93	798.47	532.65
T61-62	437-451	(R)KVPQVSTPTLVEVSR(S)	1638.93	1639.94	820.47	547.32
T15-16	118-130	(K)QEPERNEZFLSHK(D)	1672.76	1673.77	837.39	558.60
T43-44	286-299	(K)YIZDNQDTISSK LK(E)	1683.81	1684.82	842.91	562.28
T38-39	249-263	(K)AEFVEVTKLVTDLTK(V)	1691.93	1692.94	846.98	564.99
T50-51	347-360	(K)DAFLGSFL YEYSRR(H)	1722.84	1723.84	862.43	575.29
T66	469-482	(R)MPZTEDYLSLILNR(L)	1723.83	1724.84	862.92	575.62
T25	184-197	(K)YNGVFQEZQAEDK(G)	1746.70	1747.71	874.36	583.24
T41	267-280	(K)EZZHGD LLEZADDR(A)	1748.66	1749.66	875.34	583.89
T55-56	387-401	(K)DDPHAZYSTVFDK LK(H)	1794.82	1795.83	898.42	599.28
T53-54	372-386	(R)LAKEYEATLEEZZAK(D)	1813.82	1814.83	907.92	605.62
T71	508-523	(R)RPZFSALTPDETYVPK(A)	1879.91	1880.92	940.96	627.65

Frag#	Res#	Sequence	Theor(Bo)	[M+H]	[M+2R]	[M+3H]
T24	169-183	(R)HPYFYAPELLYYANK(Y)	1887.92	1888.93	944.97	630.31
T62-63	438-455	(K)VPQVSTPTLVEVSRSLGK(V)	1896.07	1897.08	949.04	633.03
T59-60	421-436	(K)LGEYGFQNALIVRYTR(K)	1899.00	1900.01	950.51	634.01
T16-17	123-138	(R)NEZFLSHKDDSPDLPK(L)	1900.86	1901.87	951.44	634.63
T73	529-544	(K)LFTFHADIZTLPDTEK(Q)	1906.91	1907.92	954.46	636.65
T80-81	581-597	(K)ZZAADDKEAZFAVEGPK(L)	1926.79	1927.80	964.40	643.27
T42-43	281-297	(R)ADLAKYIZDNQDTISSK(L)	1940.91	1941.92	971.47	647.98
T12-13	89-105	(K)SLHTLFGDELZKVASLR(E)	1945.01	1946.02	973.51	649.34
T47	319-336	(K)DAIPENLPPLTADFAEDK(D)	1954.95	1955.96	978.48	652.66
T2	3-19	(K)WVTFISLLLLFSSAYS(R)	2002.09	2003.10	1002.05	668.37
T13-14	101-117	(K)VASLRETYGDMADZZEK(Q)	2003.84	2004.85	1002.93	668.95
T18-19	139-155	(K)LKPDNTLZDEFKADEK(K)	2018.96	2019.97	1010.49	674.00
T23-24	168-183	(R)RHPYFYAPELLYYANK(Y)	2044.02	2045.03	1023.02	682.35
T81-82	588-607	(K)EAZFAVEGPKLVVSTQTALA(-)	2090.07	2091.08	1046.04	697.70
T40-41	264-280	(K)VHKEZZHGDLEZADDR(A)	2112.88	2113.89	1057.45	705.30
T14-15	106-122	(R)ETYGDMADZZEKQEPER(N)	2116.81	2117.82	1059.41	706.61
T78-79	562-580	(K)ATEEQKTVMENFVAFV DK(Z)	2198.09	2199.10	1100.05	733.71
T79-80	569-587	(K)TVMENFVAFVDKZZAADDK(E)	2218.97	2219.98	1110.49	740.66
T41-42	267-285	(K)EZZHGDLEZADDRADLAK(Y)	2246.94	2247.94	1124.48	749.99
T1-2	1-19	(-)MKWVTFISLLLLFSSAYS(R)	2261.23	2262.24	1131.62	754.75
T73-74	529-547	(K)LFTFHADIZTLPDTEKOIK(K)	2276.15	2277.16	1139.08	759.72
T49-50	341-359	(K)NYQEAKDAFLGSFLYEYSR(R)	2300.07	2301.08	1151.05	767.70
T45-46	300-318	(K)EZZDKPCLKSHZIAEVEK(D)	2344.09	2345.09	1173.05	782.37
T57-58	402-420	(K)HLVDEPQNLIKQNZDQFEK(L)	2354.13	2355.13	1178.07	785.72
T17-18	131-151	(K)DDSPDLPKLKPDNTLZDEFK(A)	2443.16	2444.17	1222.59	815.39
T47-48	319-340	(K)DAIPENLPPLTADFAEDKDVZK(N)	2457.17	2458.18	1229.59	820.07
T2-3	3-23	(K)WVTFISLLLLFSSAYSRGVFR(R)	2461.35	2462.36	1231.68	821.46
T71-72	508-528	(R)RPZFSALTPDETYVPKAFEK(L)	2470.18	2471.19	1236.10	824.40
T25-26	184-204	(K)YNGVFQEZQAEDKGAZLLPK(I)	2486.10	2487.11	1244.06	829.71
T9	45-65	(K)GLVLIAFSQYLQQZPFDEHVK(L)	2491.26	2492.26	1246.64	831.43
T72-73	524-544	(K)AFDEKLFTFHADIZTLPDTEK(Q)	2497.18	2498.19	1249.60	833.40
T58-59	413-433	(K)QNZDQFEKLGEGYGFQNALIVR(Y)	2528.21	2529.22	1265.11	843.75
T66-67	469-489	(R)MPZTEDYLSLILNRLZVLHEK(T)	2603.29	2604.30	1302.65	868.77
T10-11	66-88	(K)LVNELTEFAKTZVADESHAGZEK(S)	2607.19	2608.20	1304.61	870.07
T11-12	76-100	(K)TZVADESHAGZEKSLHTLFGDELZK(V)	2863.26	2864.27	1432.64	955.43
T65-66	460-482	(R)ZZTKPESERMPZTEDYLSLILNR(L)	2871.30	2872.31	1436.66	958.11
T70-71	499-523	(K)ZZTESLVNRRRPZFSALTPDETYVPK(A)	2999.39	3000.40	1500.70	1000.81
T46-47	310-336	(K)SKZIAOVEKDAIPENLPPLTADFAEDK(D)	3008.44	3009.45	1505.23	1003.82
T54-55	375-399	(K)EYEATLEEZAKDDPHAZYSTVFDK(L)	3037.24	3038.25	1519.63	1013.42
T8-9	37-65	(K)DLGEEHFKGLVLIAFSQYLQQZPFDEHVK(L)	3446.70	3447.70	1724.36	1149.91
T24-25	169-197	(R)HPYFYAPELLYYANKYNGVFQEZQAEDK(G)	3619.01	3620.02	1810.51	1207.34
T9-10	45-75	(K)GLVLIAFSQYLQQZPFDEHVKLVNELTEFAK(T)	3638.20	3639.21	1820.11	1213.74