

Annexes

Sequence of BSA, Bovine serum albumin (including signal peptide):

MKWVTFISLLLLFSSAYSRGVFRDTHKSEIAHRFKDLGEEHFKGLVLIAFSQYLQQCPFDEHVKLVNELTEFAKTCVA
 DESHAGCEKSLHTLFGDELCKVASLRETYGDMADCCQEPERNECFLSHKDDSPDLPLKLPDPNTLCDEFKADEKK
 FWGKLYEIAARRHPYFYAPELLYANKYNGVVFQEQCAEDKGACLLPKIETMREKVLASSARQRLRCASIQKFGERAL
 KAWSVARLSQKFPKAEFVEVTKLVTDLTKVHKECCHGDLLCADDRADLAKYICDNQDTISSKLECCDKPILLEKSHC
 IAEVEKDAIPENLPPLTADFAEDKDVCCKNYQEAKDAFLGSFLYEYSRRHPEYAVSVLLRLAKEYEATLEECCAADDPHA
 CYSTVFDKHLVDEPQNLKQNCQFEKLGEGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTRCCTKPESER
 MPCTEDYLSLILNRLCVLHEKTPVSEKVTCCTESLVNRRPCFSALTPDETYVPKAFDEKLFTFHADICTLPDTEKQIKK
 QTALVELLKHKPKATEEQLKTMENFVAFVDKCCAADDKEACFAVEGPKLVVSTQTALA

Annex 1: Peptides produced from a Tryptic digest of Bovine serum albumin (BSA):

Mass	Position	#MC	Modifications	Peptide sequence
6254.0380	21-76	3		GLVLIAFSQYLQQCPFDEHV KLVNELTEFAKTCVADESHA GCEKSLHTLFGDELCK
5865.8236	13-64	3		DLGEEHFKGLVLIAFSQYLQ QCPFDEHVKLVNELTEFAKT CVADESHAGCEK
5251.4882	475-520	3		CCTESLVNRRPCFSALTPDE TYVPKAFDEKLFTFHADICT LPDTEK
4910.3837	21-64	2		GLVLIAFSQYLQQCPFDEHV KLVNELTEFAKTCVADESHA GCEK
4816.2706	145-185	3		HPYFYAPELLYANKYNGVF QECCQAEDKGACLLPKIETM R
4810.4588	11-51	3		FKDLGEEHFKGLVLIAFSQY LQQCPFDEHVKLVNELTEFA K
4683.2235	295-335	3		DAIPENLPPLTADFAEDKDV CKNYQEAKDAFLGSFLYEYS R
4615.2887	484-523	3		RPCFSALTPDETYVPKAFDE KLFTFHADICTLPDTEKQIK
4568.1478	137-173	3		LYEIAARRHPYFYAPELLY ANKYNGVVFQEQCAEDK
4564.9855	52-93	3		TCVADESHAGCEKSLHTLFG DELCKVASLRETYGDMADCC EK
4556.1702	276-316	3		ECCDKPILLEKSHCIAEVEKD AIPENLPPLTADFAEDKDVC K
4535.2954	13-51	2		DLGEEHFKGLVLIAFSQYLQ QCPFDEHVKLVNELTEFAK
4444.0933	337-375	3		HPEYAVSVLLRLAKEYEATL EECCAADDPHACYSTVFDK
4395.0617	351-388	3		EYEATLEECCAADDPHACYS TVFDKHLVDEPQNLK
4364.1359	42-81	3		LVNELTEFAKTCVADESHAG CEKSLHTLFGDELCKVASLR
4359.2018	5-41	3		SEIAHRFKDLGEEHFKGLVL IAFSQYLQQCPFDEHVK
4352.1498	274-312	3		LKECCDKPILLEKSHCIAEVE KDAIPENLPPLTADFAEDK

4342.0558	144-180	3	RHPYFYAPELLYYANKYNGV FQECQAEDKGACLLPK
4246.0511	484-520	2	RPCFSALTPDETYVPKAFDE KLFTFHADICTLPDTEK
4185.9547	145-180	2	HPYFYAPELLYYANKYNGVF QECCQAEDKGACLLPK
4179.1080	378-412	3	HLVDEPQNLIKQNCQFEKL GEYGFQNALIVRYTR
4165.0258	436-471	3	CCTKPESERMPCTEDYLSLI LNRLCVLHEKTPVSEK
4130.9684	286-322	3	SHCIAEVEKDAIPENLPPLT ADFAEDKDVCKNYQEAQ
4120.9737	545-583	3	TVMENFVAFVDKCCAADDKE ACFAVEGPKLVVSTQATAL
4110.9707	276-312	2	ECCDKPILLEKSHCIAEVEKD AIPENLPPLTADFAEDK
4017.9109	363-396	3	DDPHACYSTVFDKCLKHLVDE PQNLIKQNCQFEK
4000.0749	376-409	3	LKHLVDEPQNLIKQNCQFE KLGEYGFQNALIVR
3984.8742	94-127	3	QEPERNECFLSHKDDSPDLP KLKDPNTLCDEFK
3936.9261	432-465	3	VGTRCCTKPESERMPCTEDY LSLINRLCVLHEK
3936.8162	538-573	3	ATEEQLKTVMENFVAFVDKC CAADDKEACFAVEGPK
3873.7550	65-98	3	SLHTLFGDELCKVASLRETY GDMADCCEKQEPER
3837.8131	42-76	2	LVNELTEFAKTCVADESHAG CEKSLHTLFGDELCK
3829.6084	82-114	3	ETYGDMADCCEKQEPERNEC FLSHKDDSPDLPK
3808.7033	240-273	3	VHKECCHGDLLCADDRADL AKYICDNQDTISSK
3798.8863	466-499	3	TPVSEKVTCCTESLVNRRP CFSALTPDETYVPK
3788.7781	99-131	3	NECFLSHKDDSPDLPKPKPD PNTLCDEFKADEK
3782.8107	262-294	3	YICDNQDTISSKLECCDKP LLEKSHCIAEVEK
3758.8958	378-409	2	HLVDEPQNLIKQNCQFEKL GEYGFQNALIVR
3747.8179	472-504	3	VTKCCTESLVNRRPCFSALT PDETYVPKAFDEK
3721.8761	317-347	3	NYQEAKDAFLGSFLYEYSRR HPEYAVSVLLR
3685.6600	243-275	3	ECCHGDLLCADDRADLAKY ICDNQDTISSKLK
3685.0032	525-556	3	QTALVELLKHKPKATEEQLK TVMENFVAFVDK
3665.8460	11-41	2	FKDLGEEHFKGLVLIAFSQY LQQCPFDEHVK
3659.6722	144-173	2	RHPYFYAPELLYYANKYNGV FQECQAEDK

3616.7443	225-256	3	AEFVEVTKLVDTLTKVHKEC CHGDLLCADDR
3579.8555	21-51	1	GLVLIAFSQYLQCPFDEHV KLVNELTEFAK
3523.6874	436-465	2	CCTKPESERMPCTEDYLSLI LNRLCVLHEK
3520.9274	397-427	3	LGEYGFQNALIVRYTRKVPQ VSTPTLVEVSR
3503.5711	145-173	1	HPYFYAPELLYANKYNGVF QECCQAEDK
3499.7164	428-458	3	SLGKVGTRCCTKPESERMPCTEDYLSLILNR
3488.5337	77-106	3	VASLRETYGDMADCCEKQEP ERNECFLSHK
3471.7676	133-159	3	FWGKYLYEIARRHPYFYAPE LLYYANK
3459.8048	445-474	3	MPCTEDYLSLILNRLCVLHE KTPVSEKVTK
3444.4810	243-273	2	ECCHGDLLCADDRADLAKY ICDNQDTISSK
3420.5796	348-377	3	LAKEYEATLEECCA KDDPHA CYSTVFDKLLK
3419.6068	475-504	2	CCTESLVNRRPCFSALTPDE TYVPKAFDEK
3397.6289	286-316	2	SHCIAEVEKDAIPENLPPLT ADFAEDKDVCK
3395.6432	534-563	3	HKPKATEEQLKTMENFVAF VDKCCAADDK
3390.6826	13-41	1	DLGEEHFKGLVLIAFSQYLQ QCPFDEHVK
3345.5765	99-127	2	NECFLSHKDDSPDLPKLPD PNTLCDEFK
3343.8333	505-533	3	LFTFHADICTLPDTEKQIKK QTALVELLK
3343.7460	414-444	3	VPQVSTPTLVEVSRSLGKVG TRCCTKPESER
3300.7527	323-350	3	DAFLGSFLYEYSRRHPEYAV SVLLRLAK
3284.6211	257-285	3	ADLAKYICDNQDTISSKLKE CCDKPLEK
3234.4574	65-93	2	SLHTLFGDELCKVASLRETY GDMADCCEK
3219.5231	52-81	2	TCVADESHAGCEKSLHTLFG DELCKVASLR
3211.5544	233-261	3	LVTDLTKVHKECCHGDLLC ADDRADLAK
3203.4992	160-187	3	YNGVVFQECCQAEDKGACLLP KIETMREK
3179.4006	348-375	2	LAKEYEATLEECCA KDDPHA CYSTVFDK
3157.5478	472-499	2	VTKCCTESLVNRRPCFSALT PDETYVPK
3137.4086	545-573	2	TVMENFVAFVDKCCAADDKE ACFAVEGPK

3134.4986	295-322	2	DAIPENLPPLTADFAEDKDV CKNYQEA
3131.5937	445-471	2	MPCTEDYLSLILNRLCVLHE KTPVSEK
3121.5808	336-362	3	RHPEYAVSVLLRLAKEYEAT LEECCA
3114.4839	432-458	2	VGTRCCTKPESERMPCTEDY LSLILNR
3108.3634	351-377	2	EYEATLEECCA KDDPHACYS TVFDK
3025.5087	363-388	2	DDPHACYSTVFDK LKHLVDE PQNL
3020.5047	389-413	3	QNCDQFEKLGEGYGFQNALIV RYTR
2988.5366	323-347	2	DAFLGSFLYEYSRRHPEYAV SVLLR
2965.4797	337-362	2	HPEYAVSVLLRLAKEYEATL EECCA
2962.2110	82-106	2	ETYGDMADCCEKQEPERNEC FLSH
2958.4400	107-132	3	DDSPDLPKLPDPNTLCDEF KADEK
2953.5035	137-159	2	YLYEIARRHPYFYAPELLY ANK
2952.4294	286-312	1	SHCIAEVEKDAIPENLPPLT ADFAED
2946.3616	160-185	2	YNGVFQECCQAEDKGACLLP KIETMR
2938.5018	500-524	3	AFDEKLFTFHADICTLPDTE KQIK
2905.3416	538-563	2	ATEEQLKTMENFVAFVDKC CAADDK
2902.3828	313-336	3	DVCKNYQEA KDAFLGSFLYE YSRR
2892.4097	389-412	2	QNCDQFEKLGEGYGFQNALIV RYTR
2867.1844	351-375	1	EYEATLEECCA KDDPHACYS TVFDK
2830.3451	107-131	2	DDSPDLPKLPDPNTLCDEF KADEK
2829.3368	475-499	1	CCTESLVNRRPCFSALTPDE TYVPK
2816.4467	459-483	3	LCVLHEKTPVSEKVKCCTE SLVNR
2810.4069	500-523	2	AFDEKLFTFHADICTLPDTE KQIK
2786.3409	262-285	2	YICDNQDTISSKLKECCDKP LLEK
2746.2817	313-335	2	DVCKNYQEA KDAFLGSFLYE YSR
2740.2990	557-583	2	CCAADDKEACFAVEGPKLVV STQTALA
2713.2742	233-256	2	LVTDLTKVHKECCHGDLLEC ADDR

2701.2452	436-458	1	CCTKPESERMPCTEDYLSLI LNR
2693.2003	52-76	1	TCVADESHAGCEKSLHTLFG DELCK
2689.4017	534-556	2	HKPKATEEQLKTVMENFVAF VDK
2609.3068	115-136	3	LKPDPTLCDEFKADEKFFW GK
2539.2973	376-396	2	LKHLVDEPQNLIKQNCQFE K
2530.1006	77-98	2	VASLRETYGDMADCCEKQEP ER
2521.4275	218-239	3	LSQKFPKAEFVEVTKLVTDL TK
2494.1588	42-64	1	LVNELTEFAKTCVADESHAG CEK
2490.2553	445-465	1	MPCTEDYLSLILNRLCVLHE K
2484.1459	94-114	2	QEPERNECFLSHKDDSPDLP K
2472.1976	389-409	1	QNCQFEKLGEGYGFQNALIV R
2457.1833	317-336	2	NYQEAKDAFLGSFLYEYSRR
2445.3823	410-431	3	YTRKVPQVSTPTLVEVSRSK GK
2441.1693	500-520	1	AFDEKLFTHADICTLPDTE K
2441.1006	240-261	2	VHKECCHGDLLECADDRADL AK
2438.4089	413-435	3	KVPQVSTPTLVEVSRSKGV GTR
2435.2427	21-41	0	GLVLIAFSQYLQCPFDEHV K
2432.4235	524-544	3	KQTALVELLKHKPKATEEQL K
2429.3802	222-242	3	FPKAEFVEVTKLVTDLTKVH K
2424.2054	1-20	3	DTHKSEIAHRFKDLGEEHFK
2421.3288	212-232	3	AWSVARLSQKFPKAEFVEVT K
2415.2080	274-294	2	LKECCDKPLLEKSHCIAEVE K
2414.1696	484-504	1	RPCFSALTPDETYVPKAFDE K
2401.1591	295-316	1	DAIPENLPPLTADFAEDKDV CK
2387.1435	107-127	1	DDSPDLPKLPDPTLCDEF K
2348.2318	505-524	2	LFTFHADICTLPDTEKQIKK
2316.0457	160-180	1	YNGVFQECCQAEDKGACLLP K

2310.3139	414-435	2	VPQVSTPTLVEVSRSLGKVG TR
2304.3285	525-544	2	QTALVELLKHKPKATEEQLK
2301.0822	317-335	1	NYQEAKDAFLGSFLYEYSR
2298.1183	378-396	1	HLVDEPQNLIKQNCDFEK
2273.2468	174-194	3	GACLLPKIETMREKVLASSA R
2220.1369	505-523	1	LFTFHADICTLPDTEKQIK
2199.1001	538-556	1	ATEEQLKTMENFVAFVDK
2174.0290	276-294	1	ECCDKPLLEKSHCIAEVEK
2126.0798	257-275	2	ADLAKYICDNQDTISSKLLK
2121.1385	199-217	3	CASIQKFGERALKAWSVAR
2105.9340	545-563	1	TMENFVAFVDKCCAADDK
2091.0426	115-132	2	LKPDNTLCDEFKADEKK
2076.8783	243-261	1	ECCHGDLLCADDRADLAK
2065.1579	222-239	2	FPKAEFVEVTKLVDTLTK
2060.1498	410-427	2	YTRKVPQVSTPTLVEVSR
2057.1641	225-242	2	AEFVEVTKLVDTLTKVHK
2045.0279	144-159	1	RHPYFYAPELLYANK
2034.0575	564-583	1	EACFAVEGPKLVSTQTALA
2028.1025	397-413	2	LGEYGFQNALIVRYTRK
2025.1702	413-431	2	KVPQVSTPTLVEVSRSLGK
2017.0541	128-143	3	ADEKKFWGKYLIEIAR
2003.7779	82-98	1	ETYGDMADCCEKQEPER
2002.2535	521-537	3	QIKKQTALVELLKHKPK
1994.0045	466-483	2	TPVSEKVKCCTESLVNR
1962.9477	115-131	1	LKPDNTLCDEFKADEK
1955.9596	295-312	0	DAIPENLPPLTADFAEDK
1947.0922	205-221	3	FGERALKAWSVARLSQK

1942.9769	5-20	2	SEIAHRFKDLGEEHFK
1942.8204	240-256	1	VHKECCHGDLLCADDR
1900.0075	397-412	1	LGEYGFQNALIVRYTR
1897.0753	414-431	1	VPQVSTPTLVEVSRSLGK
1890.8030	77-93	1	VASLRETYGDMADCCEK
1888.9949	65-81	1	SLHTLFGDELCKVASLR
1888.9268	145-159	0	HPYFYAPELLYYANK
1887.0705	188-204	3	VLISSARQRLRCASIQK
1884.9007	257-273	1	ADLAKYICDNQDTISSK
1875.0229	181-196	3	IETMREKVLASSARQR
1850.9211	428-444	2	SLGKVGTRCCTKPESER
1850.8993	505-520	0	LFTFHADICTLPDTEK
1844.8483	99-114	1	NECFLSHKDDSPDLPK
1830.0748	209-224	3	ALKAWSVARLSQKFPK
1823.8996	484-499	0	RPCFSALTPDETYVPK
1811.0095	459-474	2	LCVLHEKTPVSEKVTK
1756.7339	557-573	1	CCAADDKEACFAVEGPK
1752.0278	336-350	2	RHPEYAVSVLLRLAK
1750.9737	218-232	2	LSQKFPKAEFVEVTK
1738.8105	363-377	1	DDPHACYSTVFDKLK
1729.9536	132-144	3	KFWGKLYEIAARR
1723.8438	323-336	1	DAFLGSFLYEYSRR
1719.9686	197-211	3	LRCASIQKFGERALK
1700.7869	348-362	1	LAKEYEATLEECCA
1692.9418	225-239	1	AEFVEVTKLVDTLTK
1691.9122	195-208	3	QRLRCASIQKFGER
1667.8131	445-458	0	MPCTEDYLSLILNR

1639.9377	413-427	1	KVPQVSTPTLVEVSR
1633.6621	160-173	0	YNGVFQECCQAEDK
1633.0159	524-537	2	KQTALVELLKHKPK
1627.7996	262-275	1	YICDNQDTISSKLK
1616.7485	94-106	1	QEPERNECFLSHK
1601.8587	133-144	2	FWGKYLEIARR
1595.9267	337-350	1	HPEYAVSVLLRLAK
1590.8632	181-194	2	IETMREKVLASSAR
1588.8549	174-187	2	GACLLPKIETMREK
1578.5981	243-256	0	ECCHGDILLECADDR
1573.8525	132-143	2	KFWGKYLEIAR
1567.7427	323-335	0	DAFLGSFLYEYSR
1546.8951	376-388	1	LKHLVDEPQNLIK
1519.7461	115-127	0	LKPDPTLCDEFK
1517.8587	212-224	2	AWSVARLSQKFPK
1513.8921	186-198	3	EKVLASSARQRLR
1511.9519	521-533	2	QIKKQTALVELLK
1511.8427	414-427	0	VPQVSTPTLVEVSR
1504.9209	525-537	1	QTALVELLKHKPK
1497.6314	363-375	0	DDPHACYSTVFDK
1490.8226	205-217	2	FGERALKAWSVAR
1482.7984	459-471	1	LCVLHEKTPVSEK
1479.7954	397-409	0	LGEYGFQNALIVR
1468.7655	1-12	2	DTHKSEIAHRFK
1465.6886	432-444	1	VGTRCCTKPESER
1457.8587	209-221	2	ALKAWSVARLSQK
1450.7835	199-211	2	CASIQKFGERALK

1445.7576	133-143	1	FWGKYLEIAR
1439.8117	336-347	1	RHPEYAVSVLLR
1418.7381	274-285	1	LKECCDKP LLEK
1407.7525	197-208	2	LRCASIQKFGER
1399.6926	545-556	0	TMENFVAFV DK
1388.5708	351-362	0	EYEATLEECCA K
1386.6206	262-273	0	YICDNQDTISS K
1364.4803	82-93	0	ETYGDMADCCE K
1362.6722	65-76	0	SLHTLFGDELCK
1352.6661	472-483	1	VTKCCTESLVNR
1349.5460	52-64	0	TCVADESHAGCE K
1331.7174	174-185	1	GACLLPKIETMR
1308.7270	534-544	1	HKPKATEEQLK
1305.7161	378-388	0	HLVDEPQNLIK
1294.7041	222-232	1	FPKAEFVEVTK
1283.7106	337-347	0	HPEYAVSVLLR
1256.7545	188-198	2	VLISSARQRLR
1249.6211	11-20	1	FKDLGEEHFK
1244.7069	186-196	2	EKVLASSARQR
1202.6786	195-204	2	QRLRCASIQK
1197.5568	313-322	1	DVCKNYQEA K
1193.6021	1-10	1	DTHKSEIAHR
1177.5591	276-285	0	ECCDKP LLEK
1163.6306	42-51	0	LVNELTEFAK
1153.6939	233-242	1	LVTDLTKVHK
1145.6425	212-221	1	AWSVARLSQK
1142.7143	524-533	1	KQTALVELLK

1138.5673	199-208	1	CASIQKFGER
1108.5785	128-136	2	ADEKKFWGK
1083.5945	137-144	1	YLVEIARR
1052.4499	436-444	0	CCTKPESER
1050.4924	564-573	0	EACFAVEGPK
1024.4550	475-483	0	CCTESLVNR
1015.4877	286-294	0	SHCIAEVEK
1014.6193	525-533	0	QTALVELLK
1011.4200	389-396	0	QNCDQFEK
1002.5830	574-583	0	LVVSTQTALA
1001.5890	209-217	1	ALKAWSVAR
988.5673	466-474	1	TPVSEKVTK
987.5694	188-196	1	VLISSARQR
987.5370	5-12	1	SEIAHRFK
977.4509	99-106	0	NECFLSHK
974.4577	13-20	0	DLGEEHFK
960.5472	186-194	1	EKVLISSAR
927.4934	137-143	0	YLVEIAR
922.4880	225-232	0	AEFVEVTK
918.5189	197-204	1	LRCASIQK
906.4713	181-187	1	IETMREK
886.4152	107-114	0	DDSPDLPK
847.5036	218-224	1	LSQKFPK
841.4600	459-465	0	LCVLHEK
820.4675	205-211	1	FGERALK
818.4254	538-544	0	ATEEQLK
817.4890	428-435	1	SLGKVGTR

789.4716	233-239	0	LVTDLTK
752.3573	317-322	0	NYQEAK
725.2593	557-563	0	CCAADDK
712.3736	5-10	0	SEIAHR
703.4097	188-194	0	VLISSAR
701.4014	174-180	0	GACLLPK
689.3729	212-217	0	AWSVAR
665.3769	132-136	1	KFWGK
660.3563	466-471	0	TPVSEK
658.3155	94-98	0	QEPER
649.3338	181-185	0	IETMR
649.3338	199-204	0	CASIQK
609.2878	500-504	0	AFDEK
590.3144	128-132	1	ADEKK
572.3627	195-198	1	QRLR
567.3249	410-413	1	YTRK
545.3405	77-81	0	VASLR
537.2820	133-136	0	FWGK
517.2980	257-261	0	ADLAK
516.3504	521-524	1	QIKK
509.3194	534-537	0	HKPK
508.2514	205-208	0	FGER
500.2463	1-4	0	DTHK
475.2875	218-221	0	LSQK
464.2173	313-316	0	DVCK
462.2194	128-131	0	ADEK
439.2299	410-412	0	YTR

432.2565	432-435	0	VGTR
404.2503	428-431	0	SLGK
391.2340	222-224	0	FPK
388.2554	521-523	0	QIK
383.2401	240-242	0	VHK
347.2289	472-474	0	VTK
331.2340	209-211	0	ALK
331.2340	348-350	0	LAK
303.1775	195-196	0	QR
294.1812	11-12	0	FK
288.2030	197-198	0	LR
276.1554	186-187	0	EK
260.1968	274-275	0	LK
260.1968	376-377	0	LK
175.1189	144-144	0	R
175.1189	336-336	0	R
147.1128	132-132	0	K
147.1128	413-413	0	K
147.1128	524-524	0	K

Annex 2: Percentage of residues with physico-chemical properties in BSA peptides with 0 miscleavage:

<u>Sequence</u>	<u>%Hydrophobicity</u>
LK	50
LK	50
EK	0
LR	50
FK	50
QR	0
ALK	66.6

LAK	66.6
VTK	33.3
VHK	33.3
QIK	33.3
FPK	33.3
YTR	0
SLGK	50
VGTR	50
ADEK	25
LSQK	25
DTHK	0
FGER	50
HKPK	0
DVXK	25
FWGK	75
ADLAK	60
VASLR	60
AFDEK	40
IETMR	20
QEPER	0
TPVSEK	16.6
AWSVAR	66.6
XASIQK	33.3
SEIAHR	33.3
NYQEAK	16.6
VLISSAR	57.1
GAXLLPK	57.1
LVTDLTK	42.8
ATEEQLK	28.5
XXAADDK	28.5
LXVLHEK	42.8
YLYEJAR	42.8
DDSPDLPK	12.5
AEFVEVTK	50
DLGEEHFK	37.5
NEXFLSHK	25
QNXDQFEK	12.5
QTALVELLK	55.5
SHXIAEVEK	33.3
XXTESLVNR	22.2
XXTKPESER	0
LVVSTQTALA	5.4
EAXFAVEGPK	4.5
LVNELTEFAK	4.5
EXXDKPILLEK	1.8
HPEYAVSVLLR	45.4
HLVDEPQNLIK	36.3
TVMENFVAFVDK	50
SLHTLFGDELXK	41.6
YIXDNQDTISSK	16.6
ETYGDMADXXEK	16.6
EYEATLEEXXAK	25
TXVADESHAGXEK	30.7

LGEYGFQNALIVR	61.5
DDPHAXYSTVFDK	23
DAFLGSFLYEYSR	46.1
LKPDPNTLXDEFK	23
VPQVSTPTLVEVSR	35.7
MPXTEDYLSLILNR	28.5
YNGVVFQEXXQAEDK	28.5
EXXHGDLLLEXADDR	28.5
HPYFYAPELLYYANK	33.3
RPXFSALTPDETYVPK	25
LFTFHADIXTLPDTEK	37.5
DAIPENLPPLTADFAEDK	38.8
GLVLIAFSQYLQXQPFDEHVK	47.6

<u>Sequence</u>	<u>% acidic residues</u>
LK	0
LK	0
EK	50
LR	0
FK	0
QR	0
ALK	0
LAK	0
VTK	0
VHK	0
QIK	0
FPK	0
YTR	0
SLGK	0
VGTR	0
ADEK	50
LSQK	0
DTHK	25
FGER	25
HKPK	0
DVXK	25
FWGK	0
ADLAK	20
VASLR	0
AFDEK	40
IETMR	20
QEPER	40
TPVSEK	16.6
AWSVAR	0
XASIQK	0
SEIAHR	16.6
NYQEAK	16.6
VLISSAR	0
GAXLLPK	0
LVTDLTK	14.2
ATEEQLK	28.5
XXAADDK	28.5

LXVLHEK	14.2
YLYEIAR	14.2
DDSPDLPK	37.5
AEFVEVTK	25
DLGEEHFK	37.5
NEXFLSHK	12.5
QNXDQFEK	25
QTALVELLK	11.1
SHXIAEVEK	22.2
XXTESLVNR	11.1
XXTKPESER	22.2
LVVSTQTALA	0
EAXFAVEGPK	1.8
LVNELTEFAK	1.8
EXXDKPLLEK	2.7
HPEYAVSVLLR	9
HLVDEPQNLIK	18.1
TVMENFVAFVDK	16.6
SLHTLFGDELXK	16.6
YIXDNQDTISSK	16.6
ETYGDMADXXEK	33.3
EYEATLEEXXAK	33.3
TXVADESHAGXEK	23
LGEYGFQNALIVR	7.6
DDPHAXYSTVFDK	23
DAFLGSFLYEYSR	15.3
LKPDPNTLXDEFK	23
VPQVSTPTLVEVSR	7.1
MPXTEDYLSLILNR	14.2
YNGVFQEXXQAEDK	21.4
EXXHGDLLLEXADDR	35.7
HPYFYAPELLYYANK	6.6
RPXFSALTPDETYVPK	12.5
LFTFHADIXTLPDTEK	18.7
DAIPENLPPLTADFAEDK	27.7
GLVLIAFSQYLQQXPFDEHVK	9.5

<u>Sequence</u>	<u>% basic residues</u>
LK	100
LK	100
EK	50
LR	50
FK	50
QR	0
ALK	66.6
LAK	66.6
VTK	33.3
VHK	33.3
QIK	33.3
FPK	33.3
YTR	0
SLGK	50
VGTR	0

ADEK	25
LSQK	50
DTHK	25
FGER	0
HKPK	50
DVXK	25
FWGK	25
ADLAK	40
VASLR	20
AFDEK	20
IETMR	0
QEPER	0
TPVSEK	16.6
AWSVAR	0
XASIQK	16.6
SEIAHR	0
NYQEAK	16.6
VLASSAR	14.2
GAXLLPK	42.8
LVTDLTK	42.8
ATEEQLK	28.5
XXAADDK	14.2
LXVLHEK	42.8
YLYEIAR	14.2
DDSPDLPK	25
AEFVEVTK	12.5
DLGEEHFK	25
NEXFLSHK	25
QNXDQFEK	12.5
QTALVELLK	44.4
SHXIAEVEK	11.1
XXTESLVNR	11.1
XXTKPESER	11.1
LVVSTQTALA	1.8
EAXFAVEGPK	0.9
LVNELTEFAK	2.7
EXXDKPLLEK	3.6
HPEYAVSVLLR	18.1
HLVDEPQNLIK	27.2
TVMENFVAFVDK	8.3
SLHTLFGDELXK	33.3
YIXDNQDTISSK	8.3
ETYGDMADXXEK	8.3
EYEATLEEXXAK	16.6
TXVADESHAGXEK	7.6
LGEYGFQNALIVR	15.3
DDPHAXYSTVFDK	7.6
DAFLGSFLYEYSR	15.3
LKPDPNTLXDEFK	30.7
VPQVSTPTLVEVSR	7.1
MPXTEDYLSLILNR	21.4
YNGVVFQEXXQAEDK	7.1
EXXHGDLLLEXADDR	14.2

HPYFYAPELLYYANK	20
RPXFSALTPDETYVPK	12.5
LFTFHADIXTLPDTEK	18.7
DAIPENLPPLTADFAEDK	16.6
GLVLIAFSQYLQQXPFDDEHVK	19

<u>Sequence</u>	<u>% Proline residues</u>
LK	0
LK	0
EK	0
LR	0
FK	0
QR	0
ALK	0
LAK	0
VTK	0
VHK	0
QIK	0
FPK	33.3
YTR	0
SLGK	0
VGTR	0
ADEK	0
LSQK	0
DTHK	0
FGER	0
HKPK	25
DVXK	0
FWGK	0
ADLAK	0
VASLR	0
AFDEK	0
IETMR	0
QEPER	20
TPVSEK	16.6
AWSVAR	0
XASIQK	0
SEIAHR	0
NYQEAK	0
VLISSAR	0
GAXLLPK	14.2
LVTDLTK	0
ATEEQLK	0
XXAADDK	0
LXVLHEK	0
YLYEIAR	0
DDSPDLPK	25
AEFVEVTK	0
DLGEEHFK	0
NEXFLSHK	0
QNXDQFEK	0
QTALVELLK	0
SHXIAEVEK	0

XXTESLVNR	0
XXTKPESER	11.1
LVVSTQTALA	0
EAXFAVEGPK	0.9
LVNELTEFAK	0
EXXDKP LLEK	0.9
HPEYAVSVLLR	9
HLVDEPQNLIK	9
TVMENFVAFVDK	0
SLHTLFGDELXK	0
YIXDNQDTISSK	0
ETYGDMADXXEK	0
EYEATLEEXXAK	0
TXVADESHAGXEK	0
LGEYGFQNALIVR	0
DDPHAXYSTVFDK	7.7
DAFLGSFLYEYSR	0
LKPDPNTLXDEFK	15.3
VPQVSTPTLVEVSR	14.2
MPXTEDYLSLILNR	7.1
YNGVVFQEXXQAEDK	0
EXXHGD LLEXADDR	0
HPYFYAPELLYYANK	13.3
RPXFSALTPDETYVPK	18.7
LFTFHADIXTLPDTEK	6.2
DAIPENLPPLTADFAEDK	16.6
GLVLIAFSQYLQQXP FDEHVK	4.7