

Table S1. Peptides Identified both in A-SPHs (Soy Protein Isolate Hydrolysates Catalyzed by Alcalase 2.4L) and AB-SPHs (the A-SPHs Further Catalyzed by Aminopeptidase from *Bacillus licheniformis* SWJS33) by UPLC-MS/MS.

sequence identified both in AB-SPHs and A-SPHs							
exptl mass	theor mass	sequence (amino acid before the peptide is shown after the blank)		exptl mass	theor mass	sequence (amino acid before the peptide is shown after the blank)	
217.1590	217.1547	VV	P Q F Y P	1026.6156	1026.5974	IPVNKPGRF	A
223.1124	223.1077	FG	I E S L	1054.5913	1054.5771	ALKPDNRIE	N
231.1752	231.1703	LV	K F G S I E	1069.5902	1069.5768	REGDLIAVPT	F
231.1752	231.1703	IV	A L L V S A	1091.5378	1091.5247	RVFDGELQE	E
233.1545	233.1496	IT	L E	1097.653	1097.6346	AIPVNKPGRF	L
237.1285	237.1234	FA	C F	1106.5664	1106.5468	RSRDPIYSN	L
245.1913	245.1860	LL	F S P L L L L K	1138.5513	1138.5367	EEPQQPQQR	F
245.1913	245.1860	II	S S	1148.5611	1148.5462	GERVFDGELQ	N
245.1913	245.1860	IL	S R V A N V S	1152.5355	1152.5159	NDDRDSYRL	N
245.1913	245.1860	LI	G D A V Y R	1155.655	1155.6400	IPVNKPGRFE	A
246.1502	246.1448	LN	K T N A L I N	1168.6349	1168.6200	NALKPDNRIE	L
247.1344	247.1289	EV	E L	1226.6969	1226.6771	AIPVNKPGRFE	L
253.1141	253.1183	YA	I	1229.5846	1229.5676	EQEWPRKEE	R
253.1241	253.1183	FS	V L A A G L	1277.6037	1277.5888	GERVFDGELQE	N
253.1351	253.1295	HP	Q	1533.8482	1533.8317	RQFPFPRPPHQB	E
260.2030	260.1969	KL	A Q	1662.8898	1662.8689	VIKPPTDEQQQRPQ	S
260.2023	260.1969	KI	Q	1749.9247	1749.9010	SVIKPPTDEQQQRPQ	L
261.1503	261.1445	EL	G S I Q	1791.9457	1791.9169	RQFPFPRPPHQBKEE	E
261.1503	261.1445	EI	Q G E V F	2566.196	2566.1670	VIKPPTDEQQQRPQEEEEEEEE	S
262.1569	262.1510	RS	A Q L	2653.2273	2653.1991	SVIKPPTDEQQQRPQEEEEEEEE	L
263.1452	263.1390	FP	D R P Q A				
265.1604	265.1547	FV	M N I Y	320.1896	320.1816	LST	
267.1399	267.1339	FT	G	330.2472	330.2387	LVV	
269.1195	269.1132	YS	I	338.1798	338.1711	YGV	
272.1816	272.1717	RP	R S Q Q P P P P	354.1754	354.1660	FTS	
274.1938	274.1874	RV	E G I L	359.2382	359.2289	IAVG	
279.1767	279.1703	FL	C E E K V P F I N	366.1759	366.1660	FAE	
280.1359	280.1292	NF	Y Q D	373.2183	373.2082	(I)LPGS	
281.1197	281.1132	FD/DF	V L	373.2541	373.2446	LQL/QLL	
281.1564	281.1496	YV	E Y	374.2384	374.2286	ELL/LEL	
283.1355	283.1289	YT	S	380.1920	380.1816	YTP	
288.1984	288.2030	LR	A R W S E N A N N Q	382.1715	382.1609	FSE	
288.1984	288.2030	IR	M L Y L Q	393.2257	393.2133	FLN	
295.1359	295.1289	EF	Q L A L	400.1979	400.1867	FSF/FFS	

295.1723	295.1652	YL	F D S	405.2245	405.2133	WLS
303.1528	303.1452	HF	P	417.2459	417.2344	(I)LPST
310.1470	310.1398	FGS	E L	427.2097	427.1976	FFN
313.1625	313.1547	FF	S L N	428.1939	428.1816	FFD
316.2307	316.2231	LIA	D	432.2363	432.2354	WAR
329.1580	329.1496	YF	S	438.2470	438.2459	KHPG
332.2261	332.2180	LSL	I	446.2048	446.1922	YYT
344.2634	344.2544	LIV	V Y	447.2575	447.2449	(I)LESV
346.2426	346.2337	ITL	L	456.2945	456.2929	PLRA
348.1857	348.1765	LSE	E	459.2941	459.2813	EVIV
350.2162	350.2074	FLA	V N	474.2698	474.2558	ENLV
352.196	352.1867	FSV	A	482.2024	482.1882	NFDS/FNDS
358.2796	358.2700	LLL	L T A	488.2851	488.2715	ELLN
364.2328	364.2231	FVV	N	491.2390	491.2249	FPNN
366.2116	366.2024	FSL	V	495.2954	495.2813	YLIS
371.2387	371.2401	RVP	L	507.2982	507.2813	FLDI
374.2498	374.2398	KLN	Q	510.2708	510.2558	QIYS
375.2432	375.2351	RLS	L	511.3063	511.2915	FFVV
378.2489	378.2387	FLV/FVI	K I	523.3076	523.2915	FFLP
388.2659	388.2555	QIK	R	543.3301	543.3137	QPVTV
392.2321	392.2544	FLL	C	557.2931	557.2759	FPFF
401.2871	401.2871	LRL/RLL	W N	560.3457	560.3290	EVTVL
401.2871	401.2871	RIL	L	588.3055	588.2875	EPTLE
403.2295	403.2300	LRD	N	610.3072	610.2871	FEFPA
409.1834	409.1718	NFE	D			
426.2508	426.2387	FFL	S	276.1409	276.1343	WA
433.2048	433.2041	EER	L	306.1521	306.1448	WT
442.2465	442.2337	FYL	R	318.1894	318.1812	(I)LW
457.3519	457.3385	ILVI	V	346.2063	346.1973	(I)LDV
522.2326	522.2170	WWM	A	411.1992	411.1874	FTGS
768.4514	768.4382	VIKPPTD	S	432.2570	432.2453	(I)LVSGG
787.4203	787.4076	GEDKGAIV	E	446.2735	446.2609	QVLS
811.4427	811.4300	SQKGKHQ	Q	448.2525	448.2402	TLSGA
834.385	834.3719	.SESELR	E	459.2587	459.2449	EPTL
835.3839	835.3712	SEDKPFN	S	481.2793	481.2657	YLVS
855.484	855.4702	SVIKPPTD	L	497.2542	497.2395	FPYA
863.4285	863.4137	RDPIYSN	S	505.2930	505.2803	(I)LMKN
879.4576	879.4450	RVPSGTTY	L	513.2960	513.2820	HPLF
897.4946	897.4807	VIKPPTDE	S	528.3914	528.3756	(I)LLVLA
907.4179	907.4036	GERVFDGE	N	529.2774	529.2617	ELPGN/ELPNG
930.4115	930.3971	YDTKFEE	S	530.2517	530.2358	NPNW
950.4596	950.4457	SRDPIYSN	R	530.3345	530.3184	PLTLS
958.5089	958.4984	DRHQKIY	Q	572.3214	572.3039	QLQPS
981.4295	981.4152	RSQSDNFE	A	575.3209	575.3035	NTDLI

984.5259	984.5128	SVIKPPTDE	L	583.2532	583.2358	FNSTD
991.4603	991.4471	AENNQRNF	N	586.3154	586.2984	(I)LPGWN
1000.4898	1000.4760	NQLDQMPR	E	611.2496	611.2308	EFNDS

* Sequence in italics represents that the peptide could partially match the sequences of β -conglycinin or glycinin G1, and sequence in bold represents that the peptide did not match the sequence of β -conglycinin or glycinin G1.

Table S2. Peptides Identified only in A-SPHs (Soy Protein Isolate Hydrolysates Catalyzed by Alcalase 2.4L) and AB-SPHs (the A-SPHs Further Catalyzed by Aminopeptidase from *Bacillus licheniformis* SWJS33) by UPLC-MS/MS.

AB-SPHs				A-SPHs		
exptl mass	theor mass	sequence (amino acid before the peptide is shown after the blank)		exptl mass	theor mass	sequence (amino acid before the peptide is shown after the blank)
203.1427	203.1390	LA	Y T F T	317.1899	317.1819	ANI
203.1427	203.1390	IA	L Q G	346.2574	346.2336	TLL
219.1383	219.1339	SL	F N T G N L	387.2339	387.2714	RVL
219.1383	219.1339	SI	V G N	404.1855	404.1776	EQQ
219.1383	219.1339	LS	Q I G A R A F I A	408.2242	408.2129	FEI
219.1383	219.1339	IS	E T	417.2423	417.2456	RIE
219.1384	219.1339	TV	V	459.331	459.3177	TLLL
244.1344	244.1292	QP	E Q Q E P E A F	540.2983	540.2817	LNFF
294.1881	294.1812	FK	S P L	761.4068	761.3959	SLDFPAL
310.1826	310.1761	KY	L R	858.4346	858.4195	GEQRLQE
345.1532	345.1445	YY	T	888.4656	888.4553	GEDKGAIVT
352.1593	352.1503	EFG	A	932.4339	932.4239	SPDIYNPQ
360.2223	360.2129	IVE	V	956.5469	956.5331	KFLVPPQE
375.1965	375.1987	NKN	K	957.4549	957.4403	NNEDTPVVA
402.2564	402.2459	RNI	S	983.5582	983.5400	LKPDNRIE
407.2399	407.2289	FGIA	S	1020.5017	1020.4876	GERVFDGEL
407.2760	407.2653	FLK	E	1035.5024	1035.4873	ISSEDKPFN
410.2185	410.2074	FPF	Q	1105.5585	1105.5444	TLEFLEHAF
423.2352	423.2238	FGSL	E	1194.6922	1194.6720	ITPEKNPQLR
429.2462	429.2344	EPAL	D	1210.7385	1210.7186	LAIPVKNKGRF
441.2619	441.2496	KFF	G	1219.6514	1219.6309	LRSRDPIYSN
444.3169	444.3041	RLR	G	1317.6213	1317.6048	GENEGEDKGAIVT
486.2696	486.2558	PQEI	G	1422.8063	1422.7831	ITPEKNPQLRDL
546.3291	546.3134	SVLVE	E	1434.5591	1434.5382	EEDEDEEQQRE
794.4757	794.4650	AIPVKNKPG	L	1457.7167	1457.6998	LQGENEGEDKGAIV
862.452	862.4436	TSLDFPAL	A	1461.7992	1461.7827	SLLNALPEEVIQH
878.4775	878.4650	NKNPFLF	K	1477.6659	1477.6474	RSQSDNFEYVSF
921.3971	921.3828	AGNQEQUEF	L	1558.7667	1558.7475	LQGENEGEDKGAIVT
982.5692	982.5560	KNPQLRDL	E	1977.0512	1977.0280	GGLSVIKPPTDEQQQRPQ
1078.5551	1078.5407	SRDPIYSNK	R	2008.0121	2007.9861	SVIKPPTDEQQQRPQEE
1116.5516	1116.5352	TWNPNKNKPF	E	2065.1462	2653.1991	SLLNALPEEVIQHTFNLK
1178.5722	1178.5608	SGFTLEFLEH	L	2880.3562	2880.3261	GGLSVIKPPTDEQQQRP
1216.5732	1216.5571	GENEGEDKGAIV	Q			QEEEEEEE
1216.654	1216.6452	FREGDLIAVPT	N	3642.8913	3642.8529	EFLEHAFSVDKQIAKNLQ
1240.6457	1240.6299	SVIKPPTDEQQ	L			GENEGEDKGAIVTVK

1365.6501	1365.6273	VNNDDDRDSYRL	L
1445.6808	1445.6634	QGENEGEDKGAIVT	L
1678.9398	1678.9294	LLPNHADADYLIVIL	L
1774.9437	1774.9213	AGANSLLNALPEEVIQH	L
2137.054	2137.0287	SVIKPPTDEQQQRPQEEE	L
2395.142	2395.1139	SVIKPPTDEQQQRPQEEEE	L
2524.1844	2524.1565	SVIKPPTDEQQQRPQEEEE	

343.2066	343.1976	NPL(I)	333.1857	333.1769	(I)LNS
366.2228	366.2136	HPL(I)	399.2709	399.2602	IPVA
429.3197	429.3071	(I)LLAI	416.2618	416.2504	NIGL
442.2786	442.2660	QPVV	417.2456	417.2344	EVIG
460.2896	460.2766	TVLQ	464.2639	464.2504	FGIQ
465.2471	465.2344	FLEG	464.2998	464.2867	FLKG
479.3116	479.2976	HPLL(I)	472.3269	472.3130	(I)LNLL
506.3123	506.2973	FLLN	487.3016	487.2875	NLAGL
515.2649	515.2500	FSVY	491.3376	491.3228	FLVI
522.2707	522.2558	FEIN	503.2597	503.2460	(I)LQNE
522.3006	522.3286	KLVY	557.3458	557.3293	PTGVAL
523.2668	523.2511	NLNY			

388.1797	338.1710	YGV	304.1939	304.1867	(I)LTA
315.2028	315.2027	KPA	362.2020	362.1922	(I)LTE
352.1965	352.1867	YLG	399.2712	399.2602	(I)LPGL(I)
409.2192	409.2082	FKD	400.2303	400.2191	(I)LPNG
412.2339	412.2231	FFV	407.2438	407.2653	KLF/KIF
417.2215	417.1980	EPTA	436.2317	436.2191	NVGF
419.2207	419.2289	(I)LTW	447.2728	447.2602	(I)LAPF
419.2213	419.2136	EVAT	449.2365	449.2242	(I)LTES
423.1832	423.1874	EQF	462.2316	462.2347	(I)LWGS
424.2199	424.2078	YLE	499.2817	499.2663	HPVF
431.2617	431.2500	ELLG	500.3221	500.3079	PTVAL(I)
435.2735	435.2714	FRL(I)	514.339	514.3235	(I)LAPLT
444.2578	444.2453	(I)LQPS	531.3046	531.2885	RAVAD
463.2317	463.2187	EPAF	558.2963	558.2770	EEPLA
472.2685	472.2554	(I)LPGW	561.3029	561.2879	ELVSN
485.2646	485.2507	FRY	561.3053	561.2879	(I)LSGGEV
488.243	488.2292	PWW	562.3042	562.2871	(I)LAPFD
493.2801	493.2657	(I)LVFD	566.2626	566.2609	WDFV
496.3021	496.2878	HQLV	576.2690	576.2624	NTDLN
506.2758	506.2609	FPKD	605.2861	605.2712	(I)LMNNN
524.2866	524.2715	(I)LTFGS	606.2715	606.2518	FPNDN
538.2277	538.2449	FWW	618.3124	618.3610	KPNLF
547.2889	547.2722	NLDVS	646.3243	646.3042	(I)LVDGEN

552.3921	552.3756	PLPLL(I)	655.3298	655.3086	FFNLD
569.3101	569.2930	EQPPV	662.3558	662.3355	NTDLS
606.2699	606.2552	(I)LMNDN			
608.3111	608.2926	EVVFD			
612.2333	612.2148	EFDDS			
616.3016	616.2937	ELPGNS			
622.3276	622.3083	FLDLD			
634.3393	634.3195	QPNYL(I)			
672.377	672.3715	PLVSAW			

* Sequence in *italics* represents that the peptide could partially match the sequences of β -conglycinin or glycinin G1, and sequence in **bold** represents that the peptide did not match the sequence of β -conglycinin or glycinin G1.