

Electronic Supplementary Information

Table S1. Peptides in D1-1 from other proteins in duck egg white

Peptides	Source
KELLSDITTPK	Ovalbumin-related protein Y
ISSAENLKMSEAVH	Ovalbumin-related protein Y
SAESLKMSEAVH	Ovalbumin-related protein Y
LDFNFKPVQ	Ovostatin
EATYNSITQNVVK	Ovostatin
AEKQLGLIQ	Pericentrin
EIPFVPNQGQKDTITK	Alpha-2-macroglobulin-like protein 1
KTSGKVPAPKGES	Fas-binding factor 1-like protein
TKDVDLITK	Rho-associated protein kinase 1
DHLEASSKLVET	Tripartite motif containing 54
AVSFLTVL	Serine/threonine-protein phosphatase 4 regulatory subunit 4 isoform X1
LFFRIT	Hypothetical protein Anapl_1299
ILKTVKI	WNT1-inducible-signaling pathway protein 3

Table S2. In silico hydrolysis of peptides in D1-1 from duck egg ovalbumin by gastrointestinal enzymes (pepsin, trypsin, and chymotrypsin)

No.	Sequence	Results of enzyme action	Location of released peptides
1	FDKLPGF	F - DK - L - PGF	[1-1],[2-3],[4-4],[5-7]
2	ISSTVSLKM	ISSTVSL - K - M	[1-7],[8-8],[9-9]
3	ISSTVSLKMS	ISSTVSL - K - M - S	[1-7],[8-8],[9-9],[10-10]
4	STVSLKMSEAV	STVSL - K - M - SEAV	[1-5],[6-6],[7-7],[8-11]
5	ISSTVSLKMSE	ISSTVSL - K - M - SE	[1-7],[8-8],[9-9],[10-11]
6	TVSLKMSEAVH	TVSL - K - M - SEAVH	[1-4],[5-5],[6-6],[7-11]
7	ISFQTAADQAR	ISF - QTAADQAR	[1-3],[4-11]
8	GISSTVSLKMSE	GISSTVSL - K - M - SE	[1-8],[9-9],[10-10],[11-12]
9	WTSSTMMEER	W - TSSTM - M - EER	[1-1],[2-6],[7-7],[8-10]
10	WVESQTNGIHK	W - VESQTN - GIHK	[1-1],[2-7],[8-11]
11	STVSLKMSEAVH	STVSL - K - M - SEAVH	[1-5],[6-6],[7-7],[8-12]
12	SISFQTAADQAR	SISF - QTAADQAR	[1-4],[5-12]
13	KNILQPSSVDSQ	K - N - IL - QPSSVDSQ	[1-1],[2-2],[3-4],[5-12]
14	SWVESQTNGIHK	SW - VESQTN - GIHK	[1-2],[3-8],[9-12]
15	IDKVVHFDKLP	IDK - VVH - F - DK - L - PG	[1-3],[4-6],[7-7],[8-9],[10-10],[11-12]
16	NSWVESQTNGIHK	N - SW - VESQTN - GIHK	[1-1],[2-3],[4-9],[10-13]
17	ISSTVSLKMSEAVH	ISSTVSL - K - M - SEAVH	[1-7],[8-8],[9-9],[10-14]
18	GISSTVSLKMSEAVH	GISSTVSL - K - M - SEAVH	[1-8],[9-9],[10-10],[11-15]
19	KAFKDEDTQAMPFR	K - AF - K - DEDTQAM - PF - R	[1-1],[2-3],[4-4],[5-11],[12-13],[14-14]
20	TQIDKVVHFDKLPFG	TQIDK - VVH - F - DK - L - PGF - G	[1-5],[6-8],[9-9],[10-11],[12-12],[13-15],[16-16]
21	SEKMKILELPFASGMM	SEK - M - K - IL - EL - PF - ASGM - M	[1-3],[4-4],[5-5],[6-7],[8-9],[10-11],[12-15],[16-16]
22	SEKMKILELPFASGMMSM	SEK - M - K - IL - EL - PF - ASGM - M - SM	[1-3],[4-4],[5-5],[6-7],[8-9],[10-11],[12-15],[16-16],[17-18]
23	EWTSSTMMEERRMKVY	EW - TSSTM - M - EER - R - M - K - VY	[1-2],[3-7],[8-8],[9-11],[12-12],[13-13],[14-14],[15-16]

*These peptides were subjected to in silico hydrolysis by gastrointestinal enzymes pepsin (PH 1.3), trypsin and chymotrypsin(A) using the BIOPEP-UWM database (<http://www.uwm.edu.pl/biochemia/index.php/pl/biopep>).

Table S3. The enzyme dosage of five proteases converted into protease activity to substrate quality

Enzyme	Proteolytic activity of enzyme (U/g/min)*	Enzyme dosage (U/g)
Neutrase	274157.4±8.3	10966.3
Protamex	344114.4±6.9	13764.6
Alcalase	289887.6±4.2	11595.5
Flavourzyme	294507.6±7.3	11780.3
Papain	367657.5±10.3	14706.3

Table S4 Peptides in D1-1 from duck egg ovalbumin

No.	Charged ion (m/z)	Charge number	Molecular Mass (Da)	Sequence	Fragment in OVA
2	483.2748	2	964.5351	ISSTVSLKM	0.444
3	526.7906	2	1051.558	ISSTVSLKMS	0.400
4	576.3074	2	1150.59	STVSLKMSEAV	0.454
5	591.312	2	1180.601	ISSTVSLKMSE	0.363
6	601.3198	2	1200.617	TVSLKMSEAVH	0.454
8	619.8245	2	1237.622	GISSTVSLKMSE	0.333
11	644.8349	2	1287.649	STVSLKMSEAVH	0.417
17	744.8779	2	1487.765	ISSTVSLKMSEAVH	0.429
18	773.4079	2	1544.787	GISSTVSLKMSEAVH	0.400
1	412.2241	2	822.4276	FDKLPG 2	0.571
15	684.3947	2	1366.761	IDKVVHFDKLPG 1	0.500
20	900.9963	2	1799.957	TQIDKVVHFDKLPGF 2	0.438
7	604.3112	2	1206.599	ISFQTAADQAR 1	0.454
12	647.8276	2	1293.631	SISFQTAADQAR 1	0.417
9	629.2692	2	1256.517	WTSSTMMEER 1	0.300
23	688.6568	3	2062.949	EWTSTMMEERRMKVY 2	0.313
10	637.8462	2	1273.667	WVESQTNGIIK 1	0.363
14	681.3618	2	1360.699	SWVESQTNGIIK 1	0.33
16	738.3831	2	1474.742	NSWVESQTNGIIK 1	0.308
13	658.3519	2	1314.678	KNILQPSSVDSQ	0.333
19	561.9473	3	1682.809	KAFKDEDTQAMPFR 2	0.429
21	906.4712	2	1810.903	SEKMKILELPFASGMM 1	0.562
22	1015.505	2	2028.976	SEKMKILELPFASGMMSM 1	0.555

* Nine peptide sequences selected for synthesis have been marked in red font.