

Table S1. Proteins identified in developing endosperm of barley cv Sloop after trypsin digestion.

N	Unused	Total	% Cov (95)	Accession	Name	Species	Peptides (95%)	Alternate Accession	Alternate Accession	Alternate Accession
1	24.63	24.63	38.10	sp P06293	Serpin-Z4	<i>Hordeum vulgare</i>	22			
2	18.26	18.26	18.21	tr Q03678	Embryo globulin	<i>Hordeum vulgare</i>	16			
3	17.02	17.14	28.61	tr I6TRS8	D-hordein	<i>Hordeum vulgare</i>	16			
4	16.21	16.21	32.51	sp TRY1_B	Trypsin	<i>Bos taurus</i>	23			
5	15.04	15.10	21.43	tr A9Q2Q5	Putative late embryogenesis abundant protein	<i>Hordeum vulgare</i>	9			
6	14.87	15.02	27.67	tr I6TMW0	B1-hordein	<i>Hordeum vulgare</i>	17	tr I6TRT2	tr I6SW25	tr I6SJ22
7	13.10	13.10	8.67	sp P31922	Sucrose synthase 1	<i>Hordeum vulgare</i>	9			
8	12.89	12.91	15.70	tr F2D5B2	ATP synthase subunit beta	<i>Hordeum vulgare</i>	12			
9	12.30	12.31	26.26	tr F2CXT7	Fructose-bisphosphate aldolase	<i>Hordeum vulgare</i>	13			
10	11.93	11.93	13.03	tr Q7YMS3	Ribulose biphosphate carboxylase large chain	<i>Hordeum chilense</i>	10			
11	11.88	11.96	23.95	tr A0A287SR97	Uncharacterized protein (Serpin Z7)	<i>Hordeum vulgare</i>	9			
12	11.09	11.15	27.21	tr I6TMV6	Gamma-1-hordein	<i>Hordeum vulgare</i>	6			
13	11.05	11.14	44.66	tr F2EHF8	Predicted protein (Triosephosphate isomerase)	<i>Hordeum vulgare</i>	6			
14	10.15	10.16	16.18	sp P80284	Protein disulfide-isomerase	<i>Hordeum vulgare</i>	9			
15	9.62	9.63	11.51	tr A0A287XP46	Uncharacterized protein (Elongation factor 2)	<i>Hordeum vulgare</i>	11			
16	8.66	8.67	10.36	tr F2CS69	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase subunit beta	<i>Hordeum vulgare</i>	4			
17	8.26	8.32	18.32	tr U5NIU3	Beta-amylase	<i>Hordeum vulgare</i>	5			
18	8.26	8.27	7.40	tr A0A287	Sucrose synthase	<i>Hordeum vulgare</i>	5			
19	8.23	8.23	20.05	tr M0XUU4	Uncharacterized protein (Globulin-1 S allele)	<i>Hordeum vulgare</i>	10			
20	8.01	8.01	18.26	tr A0A287M898	Uncharacterized protein (Thiamine thiazole synthase, chloroplastic)	<i>Hordeum vulgare</i>	7			
21	7.78	7.94	17.58	tr F2CSK4	Predicted protein (Glucose and ribitol dehydrogenase-like protein)	<i>Hordeum vulgare</i>	5			
22	7.77	7.91	20.64	tr M0XLC4	Uncharacterized protein (Adenosine kinase 2)	<i>Hordeum vulgare</i>	6			
23	7.16	7.44	15.03	tr M0USC9	Aspartate aminotransferase	<i>Hordeum vulgare</i>	5			
24	6.61	6.77	4.65	tr F2EBM4	Predicted protein (Vicilin-like antimicrobial peptides 2-2)	<i>Hordeum vulgare</i>	6			
25	6.22	6.23	7.18	tr F2D4A4	Predicted protein (60S ribosomal protein L4)	<i>Hordeum vulgare</i>	3			
26	6.14	12.22	51.45	TC138764_F1	B1-hordein	<i>Hordeum vulgare</i>	16	tr Q40022	tr A0A287EFE1	sp P06470
27	6.12	6.20	17.04	tr I1H7F9	Uncharacterized protein (Enolase)	<i>Brachypodium distachyon</i>	5			
28	6.08	6.16	8.51	tr F2DCE3	Pyruvate, phosphate dikinase	<i>Hordeum vulgare</i>	4			
29	6.01	6.01	4.98	tr F2EFW5	Predicted protein (Pyrophosphate-energized vacuolar membrane proton pu	<i>Hordeum vulgare</i>	4			
30	6.00	6.00	10.58	tr Q40069	Peroxidase	<i>Hordeum vulgare</i>	3			
31	6.00	6.00	13.16	tr F2EC88	Predicted protein (Rab28 protein)	<i>Hordeum vulgare</i>	7			
32	5.51	5.62	12.89	tr Q4LB20	Adenosylhomocysteinase	<i>Hordeum vulgare</i>	4			
33	5.39	5.46	11.11	tr F2D4W6	Malate dehydrogenase	<i>Hordeum vulgare</i>	3			
34	5.29	5.43	18.80	tr I1IRI1	Uncharacterized protein (60S ribosomal protein L32-1)	<i>Brachypodium distachyon</i>	4			
35	5.20	5.27	8.99	tr U6A1T2	Glucose-1-phosphate adenylyltransferase	<i>Hordeum vulgare</i>	3			
36	4.79	4.84	6.14	tr M0XQ24	Uncharacterized protein (Phosphoglucomutase, cytoplasmic)	<i>Hordeum vulgare</i>	4			
37	4.48	4.52	19.18	sp P16968	Alpha-amylase inhibitor BMAI-1 (Fragment)	<i>Hordeum vulgare</i>	6			
38	4.20	4.23	4.54	tr A0A287V373	Uncharacterized protein (Putative aspartic peptidase A1 family)	<i>Hordeum vulgare</i>	2			
39	4.09	4.10	4.66	tr M0Z2X3	Phosphoglycerate kinase	<i>Hordeum vulgare</i>	2			
40	4.07	4.09	4.61	tr Q40058	HSP70	<i>Hordeum vulgare</i>	3			
41	4.05	4.06	9.77	tr A0A287SBS0	Uncharacterized protein (Late embryogenesis protein D-34-like)	<i>Hordeum vulgare</i>	3			
42	4.02	4.02	3.99	tr F2DCS7	Ketol-acid reductoisomerase	<i>Hordeum vulgare</i>	3			
43	4.02	4.02	4.77	sp P52894	Alanine aminotransferase 2	<i>Hordeum vulgare</i>	2			
44	4.00	4.00	7.16	tr M0XTF9	Uncharacterized protein (T-complex protein 1 subunit alpha)	<i>Hordeum vulgare</i>	2			
45	4.01	4.01	6.13	tr M0YIA7	Isocitrate dehydrogenase [NADP]	<i>Hordeum vulgare</i>	2			
46	4.00	18.26	18.21	tr Q03678	Embryo globulin	<i>Hordeum vulgare</i>	16			

47	4.00	8.00	18.08	tr A0A287EJ06	Uncharacterized protein (B-hordein)	<i>Hordeum vulgare</i>	6	tr A0A287EI23	tr A0A287EIW5
48	4.00	4.00	7.73	tr M0X5Z1	Uncharacterized protein (Eukaryotic initiation factor 4A)	<i>Hordeum vulgare</i>	2		
49	4.00	4.00	11.87	tr F2DH85	60S acidic ribosomal protein P0	<i>Hordeum vulgare</i>	2		
50	4.00	4.00	7.64	tr M0XSQ4	Uncharacterized protein (Succinate-semialdehyde dehydrogenase)	<i>Hordeum vulgare</i>	2		
51	4.00	4.00	8.39	tr F2E520	Predicted protein (Uridine 5'-monophosphate synthase)	<i>Hordeum vulgare</i>	2		
52	4.00	4.00	19.25	tr M0UL57	Eukaryotic translation initiation factor 5A	<i>Hordeum vulgare</i>	2		
53	4.00	4.00	4.29	sp P29114	Linoleate 9S-lipoxygenase 1	<i>Hordeum vulgare</i>	2		
54	4.00	4.00	11.88	tr F2EEQ1	Predicted protein	<i>Hordeum vulgare</i>	2		
55	4.00	4.00	6.63	tr F2ECH4	Predicted protein (Late embryogenesis abundant protein)	<i>Hordeum vulgare</i>	2		
56	4.00	4.00	8.07	tr F2DIC8	Predicted protein (Hydroxyproline-rich glycoprotein family protein)	<i>Hordeum vulgare</i>	2		
57	4.00	4.00	14.49	tr F2D4L0	Predicted protein (Glutathione transferase F5)	<i>Hordeum vulgare</i>	3		
58	4.00	4.00	11.06	tr F2CVV8	Superoxide dismutase	<i>Hordeum vulgare</i>	2		
59	2.00	2.00	6.55	tr M0YB08	4-hydroxy-4-methyl-2-oxoglutarate aldolase	<i>Hordeum vulgare</i>	1		
60	4.00	4.00	17.01	sp K1C9_HUMAN	Keratin	<i>Homo sapiens</i>	3		
61	3.75	4.03	14.54	tr F2CUE9	Glyceraldehyde-3-phosphate dehydrogenase	<i>Hordeum vulgare</i>	4		
62	3.68	3.90	22.16	tr M0XYT2	Uncharacterized protein (Gamma-1-hordein)	<i>Hordeum vulgare</i>	3		
63	3.62	3.77	7.56	tr F2CQP8	Predicted protein (Lactoylglutathione lyase)	<i>Hordeum vulgare</i>	2		
64	3.53	3.68	5.72	tr M0Z4F0	Uncharacterized protein (Nucleoredoxin)	<i>Hordeum vulgare</i>	2		
65	3.47	3.62	3.42	sp K2C1_HUMAN	Keratin	<i>Homo sapiens</i>	2		
66	3.35	3.42	14.71	tr A0A287H7K0	Uncharacterized protein (Ricin B-like lectin R40G3)	<i>Hordeum vulgare</i>	2		
67	3.21	3.31	5.26	tr F2EGL4	Predicted protein (Eukaryotic peptide chain release factor subunit 1-3)	<i>Hordeum vulgare</i>	2		
68	3.17	3.28	8.02	sp Q43470	14-3-3-like protein B	<i>Hordeum vulgare</i>	2		
69	2.99	3.10	9.13	tr F2E7Q3	Predicted protein	<i>Hordeum vulgare</i>	2		
70	2.92	3.06	11.94	tr V9SHG4	Starch synthase, chloroplastic/amyloplastic	<i>Hordeum vulgare</i>	4		
71	2.80	2.89	23.31	tr F2ELX8	Predicted protein (Chitinase)	<i>Hordeum vulgare</i>	4		
72	2.80	2.89	19.05	tr M0WF11	Uncharacterized protein (Defensin Tm-AMP-D1.2)	<i>Hordeum vulgare</i>	4		
73	2.62	2.70	6.81	tr F2D807	D-3-phosphoglycerate dehydrogenase	<i>Hordeum vulgare</i>	2		
74	2.60	2.63	12.84	tr F2EG53	Predicted protein (Elongation factor 1-beta)	<i>Hordeum vulgare</i>	2		
75	2.44	2.47	8.08	tr F2CUW7	Predicted protein (Universal stress protein A-like protein)	<i>Hordeum vulgare</i>	2		
76	2.41	2.53	7.01	tr F2E9N0	Predicted protein (12S seed storage globulin 1)	<i>Hordeum vulgare</i>	3		
77	2.41	2.44	6.60	tr F2D6B1	Predicted protein (Dehydroascorbate reductase)	<i>Hordeum vulgare</i>	1		
78	2.32	2.35	6.22	tr R7W2E9	ATP synthase subunit alpha	<i>Aegilops tauschii</i>	2		
79	2.19	2.21	2.59	tr A0A287VFE1	Uncharacterized protein (Chaperonin 60-like protein)	<i>Hordeum vulgare</i>	1		
80	2.17	2.18	3.64	tr F2DMV0	Aminopeptidase	<i>Hordeum vulgare</i>	2		
81	2.11	2.12	22.22	sp P07597	Non-specific lipid-transfer protein 1	<i>Hordeum vulgare</i>	2		
82	2.11	2.12	12.67	tr Q96458	17 kDa class I small heat shock protein	<i>Hordeum vulgare</i>	1		
83	2.09	2.10	2.34	tr F2CS40	Aconitate hydratase	<i>Hordeum vulgare</i>	1		
84	2.08	5.82	7.34	tr A0A1W6S456	Ribulose bisphosphate carboxylase large chain	<i>Nassella trichotoma</i>	4		
85	2.08	2.09	11.41	tr Q43769	Oleolin	<i>Hordeum vulgare</i>	5		
86	2.03	2.04	2.82	tr Q6E5A5	Plastidial ADP-glucose transporter	<i>Hordeum vulgare</i>	1		
87	2.03	2.03	1.63	tr M0WX05	Uncharacterized protein (Selenium-binding protein 1)	<i>Hordeum vulgare</i>	1		
88	2.02	2.03	6.76	tr F2EDI8	Predicted protein	<i>Hordeum vulgare</i>	1		
89	2.00	2.00	8.40	tr F2EC14	Predicted protein (60S ribosomal protein L22-2)	<i>Hordeum vulgare</i>	1		
90	2.02	2.02	5.78	tr B5TWK6	rRNA N-glycosidase	<i>Hordeum vulgare</i>	1		
91	2.00	7.13	10.04	tr S4Z8E1	ATP synthase subunit beta, chloroplastic	<i>Hordeum vulgare</i>	4		
92	2.01	4.01	3.96	tr M0YC50	Uncharacterized protein (Cullin-associated NEDD8-dissociated protein 1)	<i>Hordeum vulgare</i>	3		
93	2.01	2.02	2.13	tr F2E4C2	Predicted protein (HSP70)	<i>Hordeum vulgare</i>	1		
94	2.01	2.01	20.27	sp P01086	Trypsin inhibitor CMe	<i>Hordeum vulgare</i>	3		
95	2.01	2.01	6.71	tr A5CFZ1	Tubulin beta chain	<i>Hordeum vulgare</i>	3		

96	2.01	2.01	7.90	tr F2DHH7	Superoxide dismutase [Cu-Zn]	<i>Hordeum vulgare</i>	1
97	2.01	2.01	1.75	tr M0YIZ9	Uncharacterized protein (2-isopropylmalate synthase A)	<i>Hordeum vulgare</i>	1
98	2.00	12.91	15.79	tr F2DJJ2	ATP synthase subunit beta	<i>Hordeum vulgare</i>	7
99	2.00	7.91	20.87	tr A0A1D6AK65	Uncharacterized protein (Adenosine kinase 2)	<i>Triticum aestivum</i>	5
100	2.00	6.00	13.46	sp P82993	Beta-amylase	<i>Hordeum vulgare</i>	4
101	2.00	2.06	3.36	tr Q850M2	Phosphoglycerate kinase (Fragment)	<i>Hordeum vulgare</i>	1
102	2.00	4.00	6.10	tr A0A287GN26	Uncharacterized protein (Aspartic proteinase)	<i>Hordeum vulgare</i>	2
103	2.00	4.00	5.20	tr A0A1Z5R0W2	Uncharacterized protein (NADPH-dependent aldehyde reductase 1)	<i>Sorghum bicolor</i>	3
104	2.00	2.44	6.57	tr A0A2C9PGJ2	Dehydroascorbate reductase 2	<i>Eleusine coracana</i>	1
105	2.00	2.12	12.58	tr F2DGA8	Predicted protein (Small heat shock protein 16.9 kDa)	<i>Hordeum vulgare</i>	1
106	2.00	2.04	6.08	tr A0A287VKP6	Uncharacterized protein (Enolase 1)	<i>Hordeum vulgare</i>	1
107	2.00	2.00	1.84	tr W5GD60	Uncharacterized protein (RuBisCO large subunit-binding protein subunit beta)	<i>Triticum aestivum</i>	1
108	2.00	2.00	2.97	tr M0XJL4	Uncharacterized protein (Alpha-1,4-glucan-protein synthase)	<i>Hordeum vulgare</i>	1
109	2.00	2.00	2.58	tr M0Z8C6	Predicted protein (Heat shock protein 70)	<i>Hordeum vulgare</i>	1
110	2.00	2.00	5.38	tr F2EL01	Predicted protein (LEA protein)	<i>Hordeum vulgare</i>	1
111	2.00	2.00	4.74	tr A0A287I5P1	Uncharacterized protein (Oxygen-evolving enhancer protein 2)	<i>Hordeum vulgare</i>	1
112	2.00	2.00	3.93	tr M0USG5	Uncharacterized protein (ATP-dependent 6-phosphofructokinase)	<i>Hordeum vulgare</i>	1
113	2.00	2.00	3.25	tr F2D7C4	3-ketoacyl-CoA synthase	<i>Hordeum vulgare</i>	1
114	2.00	2.00	2.51	tr F2CYL7	Predicted protein (Vicilin-like antimicrobial peptides 2-2)	<i>Hordeum vulgare</i>	4
115	2.00	2.00	36.00	tr Q5S741	Chloroplast acetyl-CoA carboxylase (Fragment)	<i>Hordeum vulgare</i>	1
116	2.00	2.00	7.43	tr F2E2L5	Predicted protein (Putative calcium-binding protein CML7)	<i>Hordeum vulgare</i>	1
117	2.00	2.00	5.73	tr F2CQY1	Predicted protein (Putative 40S ribosomal protein)	<i>Hordeum vulgare</i>	2
118	2.00	2.00	4.12	sp P35266	60S ribosomal protein L17-1	<i>Hordeum vulgare</i>	1
119	2.00	2.00	9.04	tr F2DEP3	Predicted protein (60S ribosomal protein L12)	<i>Hordeum vulgare</i>	1
120	2.00	2.00	2.99	tr F2D1P1	Predicted protein (60S ribosomal protein L5)	<i>Hordeum vulgare</i>	1
121	2.00	2.00	4.74	tr F2DHU6	Pyruvate kinase	<i>Hordeum vulgare</i>	1
122	2.00	2.00	4.66	tr F2CRK4	Predicted protein (Enoyl-[acyl-carrier-protein] reductase)	<i>Hordeum vulgare</i>	1
123	2.00	2.00	3.30	tr M0YNH1	Uncharacterized protein (Cinnamyl alcohol dehydrogenase)	<i>Hordeum vulgare</i>	1
124	2.00	2.00	1.59	tr Q9XEI3	Beta-D-glucan exohydrolase isoenzyme Exol	<i>Hordeum vulgare</i>	1
125	2.00	2.00	9.09	tr M0WDD3	Predicted protein (Triosephosphate isomerase, chloroplastic)	<i>Hordeum vulgare</i>	1
126	2.00	2.00	6.78	tr F2DC21	Predicted protein (Wal17 protein)	<i>Hordeum vulgare</i>	1
127	2.00	2.00	21.21	tr A0A287XZK0	Uncharacterized protein	<i>Hordeum vulgare</i>	1
128	2.00	2.00	6.17	tr F2EI14	Predicted protein (17.5 kDa heat shock protei)	<i>Hordeum vulgare</i>	1
129	2.00	2.00	3.93	tr F2EAD0	Predicted protein (Calcium-dependent lipid-binding (CaLB domain) family protein)	<i>Hordeum vulgare</i>	1
130	2.00	2.00	7.20	tr O23983	Ascorbate peroxidase	<i>Hordeum vulgare</i>	1
131	2.00	2.00	6.64	tr F2DCF7	Predicted protein (Sapasin-like type B, region 1 family protein)	<i>Hordeum vulgare</i>	1
132	2.00	2.00	3.68	tr F2CRB4	Eukaryotic translation initiation factor 3 subunit I	<i>Hordeum vulgare</i>	1
133	2.00	2.00	1.28	tr M0X5Q3	Uncharacterized protein (Carbamoyl-phosphate synthase large chain)	<i>Hordeum vulgare</i>	1
134	2.00	2.00	12.96	tr F2EFB1	Predicted protein	<i>Hordeum vulgare</i>	1
135	2.00	2.00	4.81	tr F2CQQ1	Predicted protein (2-dehydro-3-deoxyphosphooctonate aldolase,)	<i>Hordeum vulgare</i>	1
136	2.00	2.00	4.30	tr A0A287IB81	Eukaryotic translation initiation factor 3 subunit H	<i>Hordeum vulgare</i>	1
137	2.00	2.00	2.19	tr F2E7L1	Histone H4	<i>Hordeum vulgare</i>	1
138	2.00	2.00	9.18	tr A0A287LGK8	Uncharacterized protein (26S protease regulatory subunit 6B)	<i>Hordeum vulgare</i>	1
139	2.00	2.00	15.28	tr O82688	Amino acid selective channel protein	<i>Hordeum vulgare</i>	1
140	2.00	2.00	8.85	tr F2DAK8	Predicted protein (60S acidic ribosomal protein P2A)	<i>Hordeum vulgare</i>	1
141	2.00	2.00	15.60	tr M0WY98	40S ribosomal protein S7	<i>Hordeum vulgare</i>	1
142	2.00	2.00	26.53	tr Q50J89	Putative eukaryotic translation initiation factor (Iso)4E (Fragment)	<i>Hordeum vulgare</i>	1
143	2.00	2.00	2.53	tr M0UL82	Uncharacterized protein (Argininosuccinate synthase)	<i>Hordeum vulgare</i>	1
144	2.00	2.00	9.43	tr B5TWD1	Late embryogenesis abundant protein	<i>Hordeum vulgare</i>	1

145	2.00	2.00	12.90	trjH2E688	Late embryogenesis abundant protein	<i>Hordeum vulgare</i>	1
146	2.00	2.00	9.45	trjA0A287VV58	Uncharacterized protein (40S ribosomal protein S20)	<i>Hordeum vulgare</i>	1
147	2.00	2.00	13.58	trjM0VAW5	Uncharacterized protein (Thioredoxin)	<i>Hordeum vulgare</i>	1
148	2.00	2.00	4.58	spjP29305	14-3-3-like protein A	<i>Hordeum vulgare</i>	1
149	2.00	2.00	4.33	trjM0YTH4	Proline iminopeptidase	<i>Hordeum vulgare</i>	1
150	2.00	2.00	5.34	trjM0UF14	GTP-binding nuclear protein	<i>Hordeum vulgare</i>	1
151	2.00	2.00	2.88	trjF2D6W5	Ribosomal protein	<i>Hordeum vulgare</i>	1
152	2.00	2.00	5.69	trjF2CPR3	Pyruvate dehydrogenase E1 component subunit beta	<i>Hordeum vulgare</i>	1
153	2.00	2.00	6.22	trjF2D483	40S ribosomal protein S8	<i>Hordeum vulgare</i>	1
154	2.00	2.00	2.64	trjQ94L27	Alcohol dehydrogenase	<i>Hordeum vulgare</i>	1
155	2.00	2.00	7.04	trjQ8S409	Hordoindoline A-1 (Fragment)	<i>Hordeum vulgare</i>	1
156	2.00	2.00	1.50	trjQ8H1Y8	Starch synthase, chloroplastic/amyloplastic	<i>Hordeum vulgare</i>	1
157	2.00	2.00	2.19	trjQ7XZK6	Starch branching enzyme I (Fragment)	<i>Hordeum vulgare</i>	1
158	2.00	2.00	4.36	trjF2DZ70	Aminomethyltransferase	<i>Hordeum vulgare</i>	2
159	2.00	2.00	3.55	trjM0V752	Obg-like ATPase 1	<i>Hordeum vulgare</i>	1
160	2.00	2.00	5.66	trjF2CWL1	Predicted protein (Glutathione-S-transferase)	<i>Hordeum vulgare</i>	1
161	2.00	2.00	3.01	trjQ6BCT3	Methionine synthase	<i>Hordeum vulgare</i>	1
162	2.00	2.00	6.37	trjF2CTC0	Predicted protein (Thioredoxin family Trp26)	<i>Hordeum vulgare</i>	1
163	2.00	2.00	3.00	trjQ4LB12	Methionine synthase 2 enzyme	<i>Hordeum vulgare</i>	1
164	2.00	2.00	7.59	trjQ43770	Oleosin	<i>Hordeum vulgare</i>	1
165	2.00	2.00	9.02	trjF2EG29	Predicted protein (Late embryogenesis abundant protein)	<i>Hordeum vulgare</i>	1
166	2.00	2.00	3.27	trjF2EJY5	4-alpha-glucanotransferase	<i>Hordeum vulgare</i>	1
167	2.00	2.00	1.89	trjF2CY68	Predicted protein (Mitochondrial processing peptidase beta subunit)	<i>Hordeum vulgare</i>	1
168	2.00	2.00	1.94	trjA0A287SNS5	Uncharacterized protein (DEAD-box ATP-dependent RNA helicase 37)	<i>Hordeum vulgare</i>	1
169	2.00	2.00	1.80	trjN1QRM3	Mitochondrial outer membrane porin	<i>Aegilops tauschii</i>	1
170	2.00	2.00	2.70	trjF2CWJ3	Glyceraldehyde-3-phosphate dehydrogenase	<i>Hordeum vulgare</i>	1
171	2.00	2.00	3.94	trjF2E941	Predicted protein (Seryl-tRNA synthetase)	<i>Hordeum vulgare</i>	1
172	2.00	2.00	2.15	trjF2E9B5	Predicted protein	<i>Hordeum vulgare</i>	1
173	2.00	2.00	0.63	trjM0WSS9	Uncharacterized protein (E3 ubiquitin-protein ligase UPL1)	<i>Hordeum vulgare</i>	1
174	2.00	2.00	6.15	trjM8BM34	Uncharacterized protein	<i>Aegilops tauschii</i>	1
175	2.00	2.00	6.29	trjF2DMM2	Predicted protein (Cytochrome c oxidase subunit 5B)	<i>Hordeum vulgare</i>	1
176	2.00	2.00	6.91	trjM0V0Z2	Pyruvate kinase	<i>Hordeum vulgare</i>	1
177	2.00	2.00	1.55	trjM0XYY6	Uncharacterized protein (Clathrin heavy chain)	<i>Hordeum vulgare</i>	1
178	2.00	2.00	2.43	trjF2DL78	Predicted protein (Ubiquitin-like protein)	<i>Hordeum vulgare</i>	1
179	2.00	2.00	2.92	trjM7YC77	Uncharacterized protein	<i>Triticum urartu</i>	1
180	2.00	2.00	2.25	trjM0WUE1	Uncharacterized protein	<i>Hordeum vulgare</i>	1
181	2.00	2.00	4.99	trjM0VXR8	Uncharacterized protein	<i>Hordeum vulgare</i>	1
182	2.00	2.00	3.44	trjF2CRU2	Predicted protein (11-beta-hydroxysteroid dehydrogenase-like protein)	<i>Hordeum vulgare</i>	1
183	2.00	2.00	13.04	trjF2EKY7	Predicted protein	<i>Hordeum vulgare</i>	1
184	2.00	2.00	1.61	trjF2ECB2	Predicted protein (Cytosolic factor-like protein)	<i>Hordeum vulgare</i>	1
185	2.00	2.00	4.66	trjF2E9J4	Predicted protein	<i>Hordeum vulgare</i>	1
186	2.00	2.00	2.86	trjF2E9C4	Predicted protein	<i>Hordeum vulgare</i>	1
187	2.00	2.00	7.67	trjF2E8B4	Predicted protein (Arabinogalactan protein AGP1)	<i>Hordeum vulgare</i>	1
188	2.00	2.00	14.13	trjF2DPX6	Predicted protein	<i>Hordeum vulgare</i>	1
189	2.00	2.00	7.03	spjQ40066	Serpin-ZX	<i>Hordeum vulgare</i>	1
190	2.00	2.00	5.79	trjA1X809	14-3-3D	<i>Hordeum vulgare</i>	1
191	2.00	2.00	4.72	trjF2D692	Predicted protein (Caffeic acid 3-O-methyltransferase)	<i>Hordeum vulgare</i>	1
192	2.00	2.00	10.74	spjP04464	Calmodulin	<i>Triticum aestivum</i>	1
193	2.00	2.00	2.76	trjB9G8U7	Uncharacterized protein (Serine/threonine-protein kinase CTR1)	<i>Oryza sativa</i>	1

195	2.00	2.00	16.67	trjA8V4D2	Chymotrypsin inhibitor-2	<i>Hordeum vulgare</i>	1
196	2.00	2.00	4.07	trjA0A2T7DFZ0	Uncharacterized protein	<i>9POAL</i>	1
198	2.00	2.00	5.35	trjA0A287P882	Uncharacterized protein	<i>Hordeum vulgare</i>	1
199	2.00	2.00	3.74	trjA0A287KCZ7	Uncharacterized protein	<i>Hordeum vulgare</i>	1
200	2.00	2.00	29.55	trjA0A1D6F166	40S ribosomal protein S3-1	<i>Zea mays</i>	1
201	2.00	2.00	2.97	trjA0A1B6Q140	Uncharacterized protein	<i>Sorghum bicolor</i>	1
202	2.00	2.00	4.74	trjA0A0Q3FXQ0	Uncharacterized protein	<i>Brachipodium distachyon</i>	1
203	2.00	2.00	16.67	trjA0A0A9E7A7	Uncharacterized protein	<i>Arundo dorax</i>	1
204	2.00	2.00	2.65	sp K1C15	Keratin	<i>Ovis aries</i>	1
205	1.85	2.00	12.34	trjM0VKU8	6,7-dimethyl-8-ribityllumazine synthase	<i>Hordeum vulgare</i>	1
206	1.72	2.00	3.75	trjF2DFP6	Predicted protein	<i>Hordeum vulgare</i>	1
207	1.72	2.00	33.77	trjA0A1B6P9M1	Uncharacterized protein	<i>Sorghum bicolor</i>	1
208	1.68	2.00	4.39	trjF2D2W7	Predicted protein	<i>Hordeum vulgare</i>	1
209	1.68	2.00	2.52	trjM0XNU3	Uncharacterized protein (HSP70)	<i>Hordeum vulgare</i>	1
210	1.68	2.00	5.00	trjA0A287VI11	Uncharacterized protein	<i>Hordeum vulgare</i>	1
211	1.66	2.00	3.49	trjA0A2S3H2Q0	Uncharacterized protein	<i>9POAL</i>	1
212	1.62	2.00	4.46	trjF2EHX7	Predicted protein	<i>Hordeum vulgare</i>	1
213	1.62	2.00	5.93	trjF2DN06	Predicted protein	<i>Hordeum vulgare</i>	1
214	1.46	1.96	3.81	trjM0Z0Z6	Uncharacterized protein (Auxin-induced protein)	<i>Hordeum vulgare</i>	1
215	1.43	1.92	3.21	trjM0Y7A8	Uncharacterized protein (Phosphoethanolamine methyltransferase)	<i>Hordeum vulgare</i>	1
216	1.42	1.92	1.47	trjA0A1Z5R7G5	Uncharacterized protein	<i>Sorghum bicolor</i>	1
217	1.41	1.85	2.39	trjQ94IC1	Betaine aldehyde dehydrogenase	<i>Hordeum vulgare</i>	1
218	1.25	1.72	2.47	trjF2E6I5	Predicted protein (ATP phosphoribosyltransferase)	<i>Hordeum vulgare</i>	1
219	1.24	1.72	5.00	trjF2CXK6	Predicted protein (3-ketoacyl-CoA thiolase-like protein)	<i>Hordeum vulgare</i>	1
220	1.22	1.70	1.69	sp K1C10	Keratin	<i>Homo sapiens</i>	1
221	1.17	1.66	4.63	trjU5ID99	Maturase K (Fragment)	<i>9POAL</i>	1
222	1.14	1.62	4.56	trjK3XT21	Uncharacterized protein	<i>Setaria italica</i>	1
223	1.13	1.60	4.82	trjF2DM63	Predicted protein (Exonuclease 3'-5' domain-containing protein 1)	<i>Hordeum vulgare</i>	1
224	1.13	1.60	5.75	trjA0A1D6D7T0	Uncharacterized protein	<i>Triticum aestivum</i>	1
226	0.99	1.44	2.41	trjM0W5Z0	Uncharacterized protein (T-complex protein 1 subunit theta)	<i>Hordeum vulgare</i>	1
227	0.99	1.44	23.58	trjA0A1D6MI07	GDSL esterase/lipase	<i>Zea mays</i>	1
228	0.98	1.44	5.40	trjQ8H2M5	Uncharacterized protein	<i>Oryza sativa</i>	1
229	0.97	1.42	13.39	trjM0Y8U3	40S ribosomal protein S12	<i>Hordeum vulgare</i>	1
230	0.86	1.30	3.01	trjF2D3M9	Predicted protein	<i>Hordeum vulgare</i>	1
231	0.82	1.26	1.18	trjK4A546	Uncharacterized protein	<i>Setaria italica</i>	1
232	0.78	1.21	3.39	trjA0A1E5W6Y7	Shugoshin-1	<i>9POAL</i>	1
233	0.77	1.22	11.45	trjA0A1E5UZM9	Tubulin beta chain	<i>9POAL</i>	2
234	0.75	1.03	4.98	trjA0A287VEF2	Uncharacterized protein	<i>Hordeum vulgare</i>	1
235	0.74	1.17	4.43	trjA0A287P659	Uncharacterized protein (27K protein)	<i>Hordeum vulgare</i>	1
236	0.64	1.60	3.91	trjI1UFL8	Maturase K (Fragment)	<i>9POAL</i>	1
237	0.61	1.01	1.54	trjM8BQ64	Putative RING finger protein	<i>Aegilops tauschii</i>	1
239	0.52	0.90	16.88	trjA0A0D3HV86	Histone H2A	<i>Oryza sativa</i>	1
240	0.50	0.90	5.20	trjM0YJN2	Uncharacterized protein (MLP-like protein 34)	<i>Hordeum vulgare</i>	1
241	0.47	0.85	3.26	trjW5EIH4	Uncharacterized protein	<i>Triticum aestivum</i>	1
242	0.47	0.85	9.09	trjA0A0N7KQ06	Os08g0476050 protein (Fragment)	<i>Oryza sativa</i>	1
243	0.47	0.84	2.37	sp Q2QNK7	Solute carrier family 40 member 2, chloroplastic	<i>ORYSJ</i>	1
244	0.45	0.82	1.60	trjW5FHY4	Uncharacterized protein	<i>Triticum aestivum</i>	1
245	0.44	2.02	10.98	trjM0YRV8	Glyceraldehyde-3-phosphate dehydrogenase	<i>Hordeum vulgare</i>	3

Table S2. Proteins identified in developing endosperm of barley cv Sloop after chymotrypsin digestion.

N	Unused	Total	% Cov (95)	Accession	Name	Species	Peptides (95%)	Alternate Accession	Alternate Accession
1	35.03	35.03	63.37	tr A0A287EIM7	Uncharacterized protein (C-hordein)	<i>Hordeum vulgare</i>	67		
2	18.13	18.13	25.45	tr I6TRS8	D-hordein	<i>Hordeum vulgare</i>	27		
3	16.86	16.91	41.63	sp CTRA	Chymotrypsin	<i>Bos taurus</i>	27		
4	13.15	13.15	34.47	tr A0A287EFE1	Uncharacterized protein (B1-hordein)	<i>Hordeum vulgare</i>	32	sp P06470	
5	11.78	12.19	19.62	tr Q7YMR9	Ribulose biphosphate carboxylase large chain	<i>Hordeum vulgare</i>	8		
6	10.49	13.16	34.96	tr A0A287EEX5	Uncharacterized protein (C-hordein)	<i>Hordeum vulgare</i>	24		
7	9.37	9.53	22.82	tr A0A287NA39	Uncharacterized protein (Serpin Z7)	<i>Hordeum vulgare</i>	17		
8	8.99	9.33	17.60	tr F2CXT7	Fructose-bisphosphate aldolase	<i>Hordeum vulgare</i>	6		
9	8.64	9.37	23.93	tr I6TMV6	Gamma-1-hordein	<i>Hordeum vulgare</i>	12		
10	8.45	8.94	19.30	tr F2D284	Protein disulfide-isomerase	<i>Hordeum vulgare</i>	13		
11	8.39	8.47	10.37	tr M0XUU4	Uncharacterized protein (Globulin-1 S allele)	<i>Hordeum vulgare</i>	8		
12	6.89	6.89	8.37	tr Q6BCT3	Methionine synthase	<i>Hordeum vulgare</i>	5		
13	5.62	5.63	3.68	tr S4UAT5	Sucrose synthase	<i>Saccharum officinarum</i>	3		
14	5.61	5.62	10.09	tr U5NIU3	Beta-amylase	<i>Hordeum vulgare</i>	4		
15	5.39	5.42	7.68	sp P42210	Phytopsin	<i>Hordeum vulgare</i>	3		
16	5.37	5.41	8.39	tr F2CWX1	Predicted protein (Elongation factor 2)	<i>Hordeum vulgare</i>	4		
17	5.36	5.39	7.86	tr A0A287PR32	40S ribosomal protein SA	<i>Hordeum vulgare</i>	3		
18	4.28	4.28	4.40	tr Q03678	Embryo globulin	<i>Hordeum vulgare</i>	2		
19	4.23	4.23	15.12	tr F2CWRO	Formate dehydrogenase, mitochondrial	<i>Hordeum vulgare</i>	4		
20	4.22	4.23	9.62	tr A0A287U7R7	Glyceraldehyde-3-phosphate dehydrogenase	<i>Hordeum vulgare</i>	3		
21	4.13	4.17	14.77	tr F2D629	Ribulose biphosphate carboxylase small chain	<i>Hordeum vulgare</i>	2		
22	4.08	4.09	10.81	tr A0A287TT80	Phosphoglycerate kinase	<i>Hordeum vulgare</i>	2		
23	4.00	4.00	3.73	tr Q40025	Beta-glucosidase	<i>Hordeum vulgare</i>	2		
24	4.00	4.00	2.77	tr F2DLM4	Predicted protein (Phospholipase A1-II 7)	<i>Hordeum vulgare</i>	2		
25	4.00	4.00	3.86	tr Q9ZTB6	Starch branching enzyme IIb	<i>Hordeum vulgare</i>	2		
26	3.96	4.06	20.69	tr F2CRF1	Predicted protein (14-3-3 protein)	<i>Hordeum vulgare</i>	4		
27	3.69	3.73	3.86	tr M0X5Z1	Uncharacterized protein (Eukaryotic initiation factor 4A)	<i>Hordeum vulgare</i>	3		
28	3.60	3.66	10.41	tr A0A0U2L8B1	Eukaryotic elongation factor 1 gamma	<i>Hordeum vulgare</i>	3		
29	3.37	3.56	5.32	tr Q42847	Lipoxygenase	<i>Hordeum vulgare</i>	4		
30	3.33	3.38	4.72	sp P11955	26 kDa endochitinase 1	<i>Hordeum vulgare</i>	2		
31	3.27	3.35	7.11	tr F2DCS7	Ketol-acid reductoisomerase	<i>Hordeum vulgare</i>	4		
32	3.24	3.30	15.42	tr F2DD97	Predicted protein (NAP1-related protein 2)	<i>Hordeum vulgare</i>	2		
33	3.15	3.22	7.03	tr Q9MDQ1	ATP synthase subunit alpha (Fragment)	<i>Sorghum bicolor</i>	2		
34	3.11	3.19	4.68	tr F2DCE3	Pyruvate, phosphate dikinase	<i>Hordeum vulgare</i>	3		
35	3.10	3.17	6.68	tr F2D5B2	ATP synthase subunit beta	<i>Hordeum vulgare</i>	2		
36	3.06	3.22	5.93	tr Q4L1B2	Glucose-1-phosphate adenyltransferase	<i>Hordeum vulgare</i>	2		
37	3.05	3.21	14.12	sp Q43470	14-3-3-like protein B	<i>Hordeum vulgare</i>	3		
38	3.02	3.11	12.95	tr F2EI64	Predicted protein (Late embryogenesis abundant protein)	<i>Hordeum vulgare</i>	2		
39	2.96	3.03	23.32	sp P34937	Triosephosphate isomerase, cytosolic	<i>Hordeum vulgare</i>	4		
40	2.90	3.06	5.31	tr V9SHG9	Starch synthase, chloroplastic/amyloplastic	<i>Hordeum vulgare</i>	2		
41	2.88	3.05	6.23	tr F2D714	Glyceraldehyde-3-phosphate dehydrogenase	<i>Hordeum vulgare</i>	2		
42	2.77	2.93	18.47	tr Q7XUY5	OSJNBb0048E02.12 protein (Major latex protein)	<i>Oryza sativa</i>	2		

43	2.74	4.98	24.15	tr A0A287EFF7	Uncharacterized protein (B-hordein)	<i>Hordeum vulgare</i>	12	
44	2.73	2.80	12.88	tr I6TEV2	Gamma-3-hordein	<i>Hordeum vulgare</i>	3	tr A0A287EEZ5 sp P80198
45	2.64	2.78	2.91	tr Q6LAA4	Elongation factor 1-alpha	<i>Hordeum vulgare</i>	2	
46	2.58	3.60	16.67	tr A0A287W082	Uncharacterized protein (Protein disulfide-isomerase)	<i>Hordeum vulgare</i>	3	
47	2.48	2.48	5.10	tr M0WQY8	Uncharacterized protein (Heat shock cognate 70 kDa protein 1)	<i>Hordeum vulgare</i>	3	
48	2.47	2.62	11.02	sp P01545	Alpha-hordothionin	<i>Hordeum vulgare</i>	2	
49	2.38	2.58	5.11	tr Q4LB20	Adenosylhomocysteinase	<i>Hordeum vulgare</i>	2	
50	2.23	2.25	2.96	tr M0YIA7	Isocitrate dehydrogenase [NADP]	<i>Hordeum vulgare</i>	1	
51	2.16	2.18	3.90	tr Q40069	Peroxidase	<i>Hordeum vulgare</i>	1	
52	2.05	2.05	10.16	tr Q945R5	Ascorbate peroxidase	<i>Hordeum vulgare</i>	3	
53	2.03	2.03	4.68	tr M0Z903	Pyruvate kinase	<i>Hordeum vulgare</i>	1	
54	2.01	2.16	11.79	tr F2D6B1	Predicted protein (Dehydroascorbate reductase 2)	<i>Hordeum vulgare</i>	2	
55	2.01	2.01	18.52	tr F2E931	40S ribosomal protein S21	<i>Hordeum vulgare</i>	2	
56	2.01	2.01	6.87	tr M0YMF1	Tubulin alpha chain	<i>Hordeum vulgare</i>	2	
58	2.00	2.01	6.42	tr F2EG53	Predicted protein (Elongation factor 1-beta)	<i>Hordeum vulgare</i>	1	
59	2.00	2.00	23.89	tr M0VMI2	Predicted protein (Calmodulin)	<i>Hordeum vulgare</i>	2	
60	2.00	2.00	0.85	tr A0A1D6JEH2	Putative leucine-rich repeat receptor-like protein kinase family protein	<i>Zea mays</i>	1	
61	2.00	2.00	2.43	tr F2D9S0	Predicted protein (Leucine-rich repeat/extensin 2)	<i>Hordeum vulgare</i>	1	
62	2.00	2.00	2.09	tr F2EB61	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha	<i>Hordeum vulgare</i>	1	
63	2.00	2.00	16.99	tr Q945R6	Ascorbate peroxidase (Fragment)	<i>Hordeum vulgare</i>	2	
64	2.00	2.00	29.69	tr A0A287P3F1	Uncharacterized protein (NADH dehydrogenase (Ubiquinone) 1 alpha subcc	<i>Hordeum vulgare</i>	1	
65	2.00	2.00	19.67	sp P69693	Photosystem II reaction center protein K	<i>Hordeum vulgare</i>	1	
66	2.00	2.00	5.63	tr Q9SAT0	NADPH-dependent reductase (Fragment)	<i>Zea mays</i>	1	
67	2.00	2.00	7.96	tr K7R153	Superoxide dismutase [Cu-Zn]	<i>Hordeum vulgare</i>	1	
68	2.00	2.00	5.58	tr Q8W0V1	Cold acclimation WCOR413-like protein gamma form	<i>Hordeum vulgare</i>	1	
69	2.00	2.00	1.87	tr F2DIQ9	Predicted protein (Methylmalonate semialdehyde dehydrogenase)	<i>Hordeum vulgare</i>	1	
70	2.00	2.00	2.27	tr F2D807	D-3-phosphoglycerate dehydrogenase	<i>Hordeum vulgare</i>	1	
71	2.00	2.00	3.93	tr F2DYM4	Predicted protein (Branched-chain amino acid aminotransferase-like)	<i>Hordeum vulgare</i>	1	
72	2.00	2.00	2.74	tr F2DT07	Predicted protein (Plastid phosphate/phosphoenolpyruvate translocator2)	<i>Hordeum vulgare</i>	1	
73	2.00	2.00	7.90	tr M8D9R7	Uncharacterized protein	<i>Aegilops tauschii</i>	1	
74	2.00	2.00	7.14	tr M8BBK0	Uncharacterized protein (Bifunctional epoxide hydrolase 2)	<i>Aegilops tauschii</i>	1	
75	2.00	2.00	3.20	tr M8ABK3	Uncharacterized protein	<i>Triticum urartu</i>	1	
76	2.00	2.00	10.00	tr F2CR57	Predicted protein (Fragment)	<i>Hordeum vulgare</i>	1	
77	2.00	2.00	2.82	tr M0UFT6	Inosine-5'-monophosphate dehydrogenase	<i>Hordeum vulgare</i>	1	
78	2.00	2.00	4.76	tr J3LC80	Uncharacterized protein	<i>Oryza brachyantha</i>	1	
79	2.00	2.00	6.72	tr I1GQ99	Uncharacterized protein (Dof zinc finger protein 7)	<i>Brachypodium distachyon</i>	1	
80	2.00	2.00	12.11	tr F2DYN8	ATP-dependent Clp protease proteolytic subunit	<i>Hordeum vulgare</i>	1	
81	2.00	2.00	10.85	tr F2DVW7	Acyl carrier protein	<i>Hordeum vulgare</i>	1	
82	2.00	2.00	4.14	tr A1C0L3	UCW116, putative lipase	<i>Hordeum vulgare</i>	1	
83	2.00	2.00	9.66	sp P28041	Alpha-amylase/trypsin inhibitor CMa	<i>Hordeum vulgare</i>	1	
84	1.92	2.00	9.40	tr A1X810	14-3-3E	<i>Hordeum vulgare</i>	1	
85	1.91	2.00	4.01	tr F2D4W3	Predicted protein (Enolase)	<i>Hordeum vulgare</i>	1	
86	1.85	2.00	14.81	tr F2E5D0	Predicted protein (Protease)	<i>Hordeum vulgare</i>	1	
87	1.72	1.85	4.91	tr F2DB00	Predicted protein (Prohibitin)	<i>Hordeum vulgare</i>	1	
88	1.64	1.86	7.90	tr F2CQP8	Predicted protein (Lactoylglutathione lyase)	<i>Hordeum vulgare</i>	2	

89	1.62	1.74	3.37	tr A5CFY9	Tubulin beta chain	<i>Hordeum vulgare</i>	1
90	1.57	1.70	2.24	tr Q42835	Beta-D-glucan exohydrolase, isoenzyme ExoII	<i>Hordeum vulgare</i>	1
91	1.55	1.68	8.87	sp P12940	Bowman-Birk type trypsin inhibitor	<i>Hordeum vulgare</i>	1
92	1.48	1.60	17.20	tr A0A287VGJ2	Uncharacterized protein (Acyl-CoA-binding protein)	<i>Hordeum vulgare</i>	1
93	1.47	1.59	4.00	tr Q6E5A5	Plastidial ADP-glucose transporter	<i>Hordeum vulgare</i>	1
94	1.43	1.55	5.58	tr F2DDU3	Predicted protein (20 kDa chaperonin)	<i>Hordeum vulgare</i>	1
95	1.43	1.55	10.69	tr F2E5Q1	Profilin	<i>Hordeum vulgare</i>	1
96	1.40	1.51	2.23	tr F2E0T2	Predicted protein (Leucine aminopeptidase 2)	<i>Hordeum vulgare</i>	1
97	1.38	1.49	2.56	tr S4Z2B0	Photosystem II CP47 reaction center protein	<i>Hordeum vulgare</i>	1
98	1.36	1.54	25.36	tr F2DY31	Predicted protein (Actin-depolymerizing factor 3)	<i>Hordeum vulgare</i>	3
99	1.32	1.48	6.48	tr F2E9N0	Predicted protein (12S seed storage globulin 1)	<i>Hordeum vulgare</i>	2

Table S3. Homology searching (using BLASTp analysis) of the barley gluten peptides monitored in this study.

Peptide sequence	Protein type	BLASTp results ^a	Peptide No.	Species
<i>Trypsin-derived peptides</i>				
QQCCQPLAQISEQAR	ALP	F2EGD5 ; A0A287F854; A0A287JK80	F2EGD5-T1	<i>H. vulgare</i>
MVLQTLPSMCR	ALP	M0VEH1 ; A0A287JK04; M0VKM6	M0VEH1-T1	<i>H. vulgare</i>
VFLQQQCSPVR	B-hordein	A0A0K2GS22; A0A0K2GRU1; A0A0K2GSM3; Q3YAF9; A0A0K1Z5E8; A0A0K2GRS6; A0A287EFB3; A0A287EFH8; A0A287EFF7; I6SJ13; Q40026; I6TMV2; I6QP72; I6SJ22; I6TRT2 ; Q40021; I6R4A7; I6SW25; I6QM99; I6TMW0; Q40020	I6TRT2-T1	<i>H. vulgare</i>
MPQLIAR	B-hordein	Q2XQF0; I6SJ13; Q40026; I6TMV2; Q3LTR1; I6QP72; I6SJ22; I6TRT2 ; I6SW25; I6QM99; I6TMW0	I6TRT2-T2	<i>H. vulgare</i>
LQMLQLSSCHVLQQCCQQLPQISEQFR	B-hordein	I6SJ22; I6TRT2 ; I6SW25; I6TMW0	I6TRT2-T3	<i>H. vulgare</i>
MCNVNVPLYDIMPPDFWH	B-hordein	A0A287EFB3; Q44026; I6TMV2; I6QP72; I6SJ22; I6TRT2 ; I6SW25; C7FB15; I6QM99; I6TMW0	I6TRT2-T4	<i>H. vulgare</i>
VFLQQQCSPVAMSQR	B-hordein	I6TEV5; I6SJ26 ; Q0PIV6; I6SW30; I6TRT5; I6TMW4; A0A287EF93; A0A287EFF5; C7FB14; C7FB17; C7FB17; C7FB13; C7FB16; Q2XQF1; C7FB15; A0A287EF96; A0A287EFB7; A0A287EF74; A0A287EFC4	I6SJ26-T1	<i>H. vulgare</i>
TLPMMSVNVPFYR	B-hordein	I6SJ26 ; Q3YAF9	I6SJ26-T2	<i>H. vulgare</i>
ILPFGIDTR	B-hordein	I6SJ26 ; A0A287EIW5; Q3YAF9; A0A287EIZ3; C7FB14; C7FB16; A0A287EF74	I6SJ26-T3	<i>H. vulgare</i>
SQMLQQSSCHVLQQCCQQLPQIPEQLR	B-hordein	P06471; I6SW30 ; I6TRT5; I6TMW4; A0A287EF93; A0A287EFF5; A0A287EF96; A0A287EFB7	I6SW30-T1	<i>H. vulgare</i>
TLPTMCSVNVPLYR	B-hordein	P06471; Q9SAT9; I6TEV5; A0A287EFG2; I6SW30 ; I6TRT5; I6TMW4; A0A287EF93; A0A287EFF5; C7FB17; C7FB13; Q2XQF1; A0A287EF96; A0A287EFB7; A0A287EFB8; A0A287EFB1	I6SW30-T2	<i>H. vulgare</i>

IVPLAIDTR	B-hordein	P06471; Q9SAT9; I6TEV5; I6SW30 ; I6TRT5; I6TMW4; A0A287EF93; A0A287EFF5; C7FB13; Q2XQF1; A0A287EF96; A0A287EFB7; A0A287EFB1	I6SW30-T3	<i>H. vulgare</i>
AIVYSIVLR	B-hordein	I6TRT5	I6TRT5-T1	<i>H. vulgare</i>
VFLQQQCSPVMPQR	B-hordein	Q4GST9; A0A0K2GRS0; A0A287EFG2; A0A0K2GRQ1; Q4G3S6; Q4G3S1 ; Q4G3S5; Q4G3S3; A0A287EFB4; Q4G3S7; Q4G3S8; Q1LZV2; Q4G3T0	Q4G3S1-T1	<i>H. vulgare</i>
QLPQIPEQFR	B-hordein	Q4G3S6; Q4G3S1 ; Q4G3S7; Q4G3S8	Q4G3S1-T2	<i>H. vulgare</i>
SLLQQSSCHVLQQCCQQLPQIPEQFR	B-hordein	TC138764	TC138674-T1	<i>H. vulgare</i>
LQMLQQSSCHVLQQCCQQLPQISEQFR	B-hordein	A0A287EFB3; I6SJ13; Q40026; I6TMV2 ; I6QP72; I6QM99	I6TMV2-T1	<i>H. vulgare</i>
VFLQQQCSPVAMPQR	B-hordein	A0A287EIW5 ; A0A287EIZ3; A0A287EJ06	A0A287EIW5-T1	<i>H. vulgare</i>
VFLQQQCIPVAMSQR	B-hordein	R9YTM4	R9YTM4-T1	<i>T. aestivum</i>
VFLQQQCNPVAMPQR	B-hordein	B9VUV5	B9VUV5-T1	<i>T. macha</i>
ELQESSLEACR	D-hordein	Q84LE9; I6SW23; I6SW34; F2EA67; A0A287G115; I6TRS8 ; Q40054; A0A287FYP1; A0A287FYQ0; A0A287G127; Q40045	I6TRS8-T1	<i>H. vulgare</i>
DVSPECRPVALSQVVR	D-hordein	Q84LE9; I6SW23; I6SW34; F2EA67; A0A287G115; I6TRS8 ; Q40054; A0A287FYP1; A0A287FYQ0; A0A287G127; Q40045	I6TRS8-T2	<i>H. vulgare</i>
QYEQQTEVPSK	D-hordein	Q84LE9; I6SW23; I6SW34; F2EA67; A0A287G115; I6TRS8 ; Q40054; A0A287FYP1; A0A287FYQ0; A0A287G127; Q40045	I6TRS8-T3	<i>H. vulgare</i>
GGSFYPGGTAPPLQGGWWGTSVK	D-hordein	Q84LE9; I6SW23; I6SW34; F2EA67; A0A287G115; I6TRS8 ; Q40054; A0A287FYP1; A0A287FYQ0; A0A287G127; Q40045	I6TRS8-T4	<i>H. vulgare</i>
AQLLAAQLPAMCR	D-hordein	Q84LE9; I6SW23; I6SW34; F2EA67; A0A287G115; I6TRS8 ; Q40054; Q02056	I6TRS8-T5	<i>H. vulgare</i>
LEGGGGLLASQ	D-hordein	Q84LE9; I6SW23; I6SW34; F2EA67; A0A287G115; I6TRS8 ; Q40054; Q02056; A0A287G119; A0A287G118	I6TRS8-T6	<i>H. vulgare</i>
ILQQSSCR	γ 1-hordein	I6TMV6 ; A0A287EEZ9	I6TMV6-T1	<i>H. vulgare</i>
VMQQQCCLQLAQIPEQYK	γ 1-hordein	P17990; I6TMV6 ; I6SJ17; H8Y0M8; A0A287EEZ9	I6TMV6-T2	<i>H. vulgare</i>

CTAIDSIVHAIFMQQGQR	γ 1-hordein	P17990; I6TMV6 ; I6SJ17; H8Y0M8; Q70IB4; A0A287EEZ9	I6TMV6-T3	<i>H. vulgare</i>
QGVQIVQQQPQPQQVGGQCVLVQGGVAQPQQLAQMEAIR	γ 1-hordein	I6TMV6	I6TMV6-T4	<i>H. vulgare</i>
APFVGVVTVGGGQ	γ 1-hordein	P17990; I6TMV6 ; I6SJ17; Q70IB4	I6TMV6-T5	<i>H. vulgare</i>
CTTIDSIVHAIFMQQGQR	γ 1-hordein	M0XYT2	M0XYT2-T1	<i>H. vulgare</i>
QGVQIVQQQPQPQEVGGQCVLVQGR	γ 1-hordein	M0XYT2	M0XYT2-T2	<i>H. vulgare</i>
DIVQPQLAQMEAIR	γ 1-hordein	M0XYT2	M0XYT2-T3	<i>H. vulgare</i>
APFFSLVNAGML	γ 1-hordein	M0XYT2	M0XYT2-T4	<i>H. vulgare</i>
DVVQPQLAQMEAIR	γ 1-hordein	TC131355	TC131355-T1	<i>H. vulgare</i>
APFVGVVSGVGGQ	γ 1-hordein	A0A287EEZ9	A0A287EEZ9-T1	<i>H. vulgare</i>
EFLQOCTLDEK	γ 3-hordein	P80198; A0A287EEZ5; I6TEV2	I6TEV2-T1	<i>H. vulgare</i>
QQCCQQLANINEQSR	γ 3-hordein	P80198; A0A287EEZ5; I6TEV2	I6TEV2-T2	<i>H. vulgare</i>
<i>Chymotrypsin-derived peptides</i>				
VQGVSQPQQSQL	B-hordein	I6SJ26 ; A0A287EIW5; A0A287EIZ3; C7FB16; A0A287EJ06	I6SJ26-C1	<i>H. vulgare</i>
GIDTRVGV	B-hordein	I6SJ26 ; A0A287EIW4; Q3YAF9; A0A287EIZ3; C7FB14; C7FB16; A0A287EF74	I6SJ26-C2	<i>H. vulgare</i>
AIDTRVGV	B-hordein	P06471; Q9SAT9; I6TEV5; I6SW30 ; I6TRT5; I6TMW4; A0A287EF93; A0A287EFF5; C7FB17; C7FB13; Q2XQF1; A0A287EF96; A0A287EFB7; A0A287EFB1	I6SW30-C1	<i>H. vulgare</i>
QQEKVGCSEF	B-hordein	I6SJ22 ; I6TRT2 ; I6SW25; I6TMW0	I6TRT2-C1	<i>H. vulgare</i>
GQPQQVPQSVF	B-hordein	A0A0K2GS22; A0A0K2GRU1; A0A0K2GSM3; A0A0K1Z5E8; A0A0K2GRS6; A0A287EFB3; A0A287EFD4; A0A287EFF7; I6SJ13; I6SJ22; I6TRT2 ; Q40021; I6R4A7; I6SW25; I6TMW0; Q40020	I6TRT2-C2	<i>H. vulgare</i>
QQKPFPPQPPF	B-hordein	P06470 ; A0A287EFG2; A0A287EFE1; Q3LTR1; Q40022; A0A287EFB4	P06470-C1	<i>H. vulgare</i>
RHEAIRAIVY	B-hordein	P06470 ; A0A0K2GS22; A0A0K2GRU1; A0A0K2GSM3; A0A0K2GRS0; Q3YAF9; A0A287EFG2; A0A0K1Z5E8; A0A0K2GRS6; Q2XQF0; A0A287EFB3; A0A287EFD4; A0A287EFH8; A0A287EFF7; I6SJ13; A0A287EFE1; Q40026; I6TMV2; Q3LTR1;	P06470-C2	<i>H. vulgare</i>

		I6QP72; I6SJ22; I6TRT2; Q40021; I6R4A7; I6SW25		
RGVGPSVGV	B-hordein	P06470 ; A0A287EFG2; A0A287EFH8; A0A287EFE1; Q0PIV6; Q40022	P06470-C3	<i>H. vulgare</i>
LPQKFPVQQPF	C-hordein	Q40053 ; A0A287EIM7	Q40053-C1	<i>H. vulgare</i>
QPQQPFPQGSEQIIPQQPFPL	C-hordein	P06472; A0A287EIM7; I6TEV8; Q40053	Q40053-C2	<i>H. vulgare</i>
QPQPFQPPQQPLPQPQQPF	C-hordein	P06472; A0A287EIM7; I6TEV8; Q40053	Q40053-C3	<i>H. vulgare</i>
IIPQQPQQPLPL	C-hordein	P06472; I6TEV8; Q40053	Q40053-C4	<i>H. vulgare</i>
LPQQPFPVQQPF	C-hordein	Q41210	Q41210-C1	<i>H. vulgare</i>
QPQQPFPQQPQQPLPRPQQPFPW	C-hordein	A0A287EIM7; Q41210 ; Q40053	Q41210-C2	<i>H. vulgare</i>
QPQQPFPQPQQPIAHQPQQPF	C-hordein	A0A287EIM7; Q41210 ; I6TEV8	Q41210-C3	<i>H. vulgare</i>
SQQPQQPFPL	C-hordein	A0A287EIM7; Q40055; Q41210 ; I6TEV8	Q41210-C4	<i>H. vulgare</i>
QPQQPFPQQPQQPFPQQPQQIIF	C-hordein	Q41210 ; Q40053	Q41210-C5	<i>H. vulgare</i>
IIPQQPQQPFPL	C-hordein	P17991	P17991-C1	<i>H. vulgare</i>
EQQTEVPSKGGSF	D-hordein	Q84LE9; I6SW23; I6SW34; F2EA67; A0A287G115; I6TRS8 ; Q40054; A0A287FYP1; A0A287FYQ0; A0A287G127; Q40045	I6TRS8-C1	<i>H. vulgare</i>
QSATSPQQPGQGQGQQETYPIATSPHQPGQW	D-hordein	I6SW23; I6SW34; F2EA67; I6TRS8 ; Q40054; Q40045	I6TRS8-C2	<i>H. vulgare</i>
YPIATSPQQPGQGQQL	D-hordein	Q84LE9; I6SW23; I6SW34; F2EA67; A0A287G115; I6TRS8 ; Q40054; A0A287FYP1; A0A287FYQ0; A0A287G127; Q40045; Q02056	I6TRS8-C3	<i>H. vulgare</i>
GQGQQPGHGQQL	D-hordein	Q84LE9; I6SW23; I6SW34; F2EA67; A0A287G115; I6TRS8 ; Q40054; A0A287FYP1; A0A287FYQ0; A0A287G127; Q40045; Q02056	I6TRS8-C4	<i>H. vulgare</i>
TQKPGQGY	D-hordein	Q84LE9; I6SW23; I6SW34; F2EA67; A0A287G115; I6TRS8 ; Q40054; A0A287FYP1; A0A287FYQ0; A0A287G127; Q02056	I6TRS8-C5	<i>H. vulgare</i>
HVSVEQPSASL	D-hordein	Q84LE9; I6SW23; I6SW34; F2EA67; A0A287G115; I6TRS8 ; Q40054; Q02056; A0A287G119; A0A287G118	I6TRS8-C6	<i>H. vulgare</i>
VGVVTGVGGQ	γ 1-hordein	P17990; I6TMV6 ; I6SJ17	I6TMV6-C1	<i>H. vulgare</i>
VQGRDVVQPQQL	γ 1-hordein	TC131355	TC131355-C1	<i>H. vulgare</i>
QPQQQPFPQQKPF	γ 1-hordein	P80198; A0A287EEZ5; I6TEV2	I6TEV2-C1	<i>H. vulgare</i>
AQQQPSIEEQHQL	γ 1-hordein	P80198; A0A287EEZ5; I6TEV2	I6TEV2-C2	<i>H. vulgare</i>

VLPQQQAQF	γ 1-hordein	P80198; A0A287EEZ5; I6TEV2	I6TEV2-C3	<i>H. vulgare</i>
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a. Uniprot accession used in paper is shown in bold typefont.

Table S4. Barley gluten peptides monitored in this study. Three MRM transitions were used for each peptide with relative quantitation based on the summed peak area. The protein sequence in the row below each prototypic peptide shows the full protein sequence of the accession; N-terminal sequence (as predicted by SignalP server) identified as missing from mature proteins is italicised. The position of the prototypic peptides are shown in bold.

Peptide Sequence	Peptide marker	RT (min)	Q1 m/z (z)	Q3 m/z (fragment, z)	CE (V)
QQCCQLAQISEQAR	F2EGD5-T1	4.32	908.90 (2+)	1112.61 (y10, 1+) 1240.67 (y11, 1+) 1015.55 (y9, 1+)	45.5
<i>MKTMLILALIAFAATSAVAQLDTTCSQGYGQCQQQPQQQMNTCAAFLQQCSRTPYVQSQMWQASGCQLMRQQCCQLAQISEQARCQAVCSMAQVIMRQQQGQSFTQPQQQSSQSF</i> <i>GQPQQQVPVEVMRMVLQTLPSMCSVNIPQYCTTTTPCSTITPTIYSIPMAATCAGGVC</i>					
MVLQTLPSMCR	M0VEH1-T1	5.54	668.32 (2+)	763.34 (y6, 1+) 864.39 (y7, 1+) 992.44 (y8, 1+)	33.4
<i>MKTMFIVALIALAVISSVAQLDTTTCIQGYGQCQQQPQHMTCAAFLQQCSPTPYVQSQMWQASGCQLMRQQCCQLAQISEQNRCQAVCSVAQVIMQKQQQQQGQSFVQPQQQVPV</i> <i>EITRMVLQTLPSMCRVNIPQHCVDTPCSTITQSPYNIPMAATCVGGTC</i>					
VFLQQQCSPVR	I6TRT2-T1	4.17	681.34 (2+)	746.34 (y6, 1+) 874.40 (y7, 1+) 1002.46 (y8, 1+)	34.1
MPQLIAR	I6TRT2-T2	4.32	414.74 (2+)	472.32 (y4, 1+) 600.38 (y5, 1+) 697.44 (y6, 1+)	20.7
LQMLQLSSCHVLQQQCCQLPQISEQFR	I6TRT2-T3	6.70	872.67 (4+)	1004.52 (y8, 1+) 1117.60 (y9, 1+) 1242.58 (b20, 2+)	31.4
MCNVNVPLYDIMPPDFWH	I6TRT2-T4	8.95	1124.51 (2+)	1157.51 (y9,1+) 1320.57 (y10, 1+) 1530.71 (y12, 1+)	
<i>MKTFLIFALLVIAATSTIAQQQPYPQQPFQPPQPPFPQQTIPQQPQPYPQQPQPYPQQPFPPQQEFPQQPPFWPQQPFPQQPPFGLQQRILSQQQPCTPQQTPLPQGQLYQTLLQLQ</i> <i>IPYVHPSILQQLNPCKVFLQQQCSPVRMPQLIARLQMLQLSSCHVLQQQCCQLPQISEQFRRHEAIRAIVYSIFLQEQPQQSVQGVSTQQQQLQEQKVGQCSFQQPQPQLGQPQQ</i> <i>VPQSVFLQPHQIAQLEATTSTIALRTLPRMCNVNVPLYDIMPPDFWH</i>					
VFLQQQCSPVAMSQR	I6SJ26-T1	4.81	889.93 (2+)	1035.45 (y9, 1+) 1163.51 (y10, 1+) 1291.57 (y11, 1+)	44.5
TLPMMCSVNVPFYR	I6SJ26-T2	7.14	857.91 (2+)	981.52 (y8, 1+) 1141.55 (y9, 1+) 1272.59 (y10, 1+)	42.9
ILPFGIDTR	I6SJ26-T3	6.20	516.30 (2+)	561.30 (y5, 1+) 708.37 (y6, 1+)	25.8

				805.42 (y7, 1+)	
MKTFLIFALLAIVATSTIAQQQPYPQQPQPFPPQQPIPQQPQPFPPQQPYPQQPQPFPPQQPIPQQPQYPQQPQPFPPQQPIPQQPQYPQQPQPFPPQQPVLQPFPSQQPFPQQPFFWQQQPVLSQQQPCTPQQTPLPQGGQDQMLVQVQIPFVHPSILQQLNPKVFLQQQCSPVAMSQR IARSQMLQQSSCYVLQQQCCQQLPQIPEQFRHEAVRAIVYSIVLQEQPQQLVQGVSPQQQSSQLHQVGCFSFQQPQPQQGQQQQVPPQSVFLQPLQLAQLEATASIALRTLTPMCSVNVPPFYRILPFGIDTRVGV					
SQMLQQSSCHVLQQCCQQLPQIPEQLR	I6SW30-T1	5.67	863.91 (4+)	980.55 (y8, 1+) 1093.64 (y9, 1+) 1221.70 (y10, 1+)	31.1
TLPTMCSVNVPLYR	I6SW30-T2	6.25	825.91 (2+)	947.53 (y8, 1+) 1107.54 (y9, 1+) 1238.58 (y10, 1+)	41.3
IVPLAIDTR	I6SW30-T3	5.26	499.31 (2+)	575.32 (y5, 1+) 688.40 (y6, 1+) 785.45 (y7, 1+)	25.0
MKTFLIFALLAIVATSTIAQQQPYPQQPQPFPPQQPIPQQPQPFPPQQPYPQQPQPFPPQQPIPQQPQYPQQPQPFPPQQPFFWQQQPVLSQQQPCTQEQTPLLQEQDQMLLQVQIPFVHPSILQQLNPKVFLQQQCSPVAMSQR IARSQMLQQSSCHVLQQCCQQLPQIPEQLRHEAVRAIVYSIVLQEQSLQLVQGVSPQQQSSQQQVGCFSFQQPQPQQGQQQVQVLLQPHQIAQLEATT SIALRTLPTMCSVNVPLYRIVPLAIDTRVGV					
AIVYSIVLR	I6TRT5-T1	6.13	517.32 (2+)	587.39 (y5, 1+) 750.45 (y6, 1+) 849.52 (y7, 1+)	25.9
MKTFLIFALLAIVATSTIAQQQPYPQQPQPFPPQQPYPQQPQPFPPQQPIPQQPQYPQQPQPFPLQPFPSQQPFPQQPFFWQQQPVLSQQQPCTQEQTPLLQEQDQMLLQVQIPFVHPSILQQLNPKVFLQQQCSPVAMSQR IARSQMLQQSSCHVLQQCCQQLPQIPEQLRHEAVRAIVYSIVLREQSLQLVQGVSPQQQSSQQQVGCFSFQQPQPQQGQQQVQVLLQPHQIAQLEATT SIALRTLPTMCSVNVPLYRIVPLAIDTRVGV					
VFLQQQCSPVMPQR	Q4G3S1-T1	5.36	907.95 (2+)	628.32 (y5, 1+) 1071.49 (y9, 1+) 1199.55 (y10, 1+)	45.4
QLPQIPEQFR	Q4G3S1-T2	5.51	628.34 (2+)	676.34 (y5, 1+) 789.43 (y6, 1+) 1014.54 (y8, 1+)	31.4
MKTFLIFALLAIAATNTIAQQQFPFPQQPQYPQQPQYPQQPQPFPPQQPFPQQPFFWQQQPVQSQQQPCQQQQTPLPQGGQYQPLLQQQIPFVHPSVLQQLNPKVFLQQQCSPVAMPQR IARSQMLQQSSCHVLQQCCQQLPQIPEQFRHEAIRAI IYSIILQEQQQVQDFVQPPQQQPPQSSVQGVSSQSSQQPQLGQCSFQQPQLQQLGQQPQQQQVPLWAFLLQPPQMAQLEVMTSVALRTLPTMCMNVNPLYGITTSVPLSVGTGVPY					
SQLLQQSSCHVLQQCCQQLPQIPEQFR	TC138764-T1	5.95	867.92 (4+)	917.48 (y7, 1+) 1014.54 (y8, 1+) 1127.62 (y9, 1+)	31.3
MPQRIARSQLLQQSSCHVLQQCCQQLPQIPEQFRHEAIRAIVYSIFLQEQQLQSVQGVSPQQQLGQQQVGCFSFQQPQPQQVGGQQQVPPQSAFLQPHQIAQLEATT SIALRTLPTMCSVNVPLYRILRGVGPVGV					
LQMLQQSSCHVLQQCCQQLPQISEQFR	I6TMV2-T1	5.92	876.42 (4+)	1004.52 (y8, 1+) 1117.60 (y9, 1+) 1250.07 (b20, 2+)	31.6

MKTFLIFALLVIAATSTIAQQQPFPPQPPFPQQPQPYPQQPQPYPQQPFPQPPFPQQTIPQQPQPYPQQPFPQQAFPQQPPFWQQPFPQQPPFGLQQPILSQQQPCTPQQTPLP QGQLYQTLQLQIPYVHPSILQQLNPKVFLQQQCSPVRMPQLIARLQMLQQSSCHVLQQQCCQQLPQISEQFRHEAIRAIVYSIFLQEQPQQSVQGVSTQQQLQQEQVQCSFQ QPQPQQLGQAQQVPQSVFLQPHQIAQLEATT'SIALRTLPRMCNVNPLYDIMPDPFWH					
VFLQQQCSPVAMPQR	A0A287EIW5-T1	5.11	894.95 (2+)	1045.47 (y9, 1+) 1173.53 (y10, 1+) 1301.59 (y11, 1+)	44.8
MKTFLIFALLAIVATSTIAQQQPYPQQPQPFPQQPQPYPQQPQPFPFLQQPRPQQPQPYPQQPQPFPFSQQPIPKQPQPYPQQPQPFPQRPFPSQQPFPQQPPFWQQQPILSKQQ PCTPQQPPLPQGQQDQMLVQVQIPFVHPSILQQLNPKVFLQQQCSPVAMPQR IARSQMLQQSSCHVLQQQCCQQLPQIPEQFRHEAVRAIVYSIILQEQPQQLVQGVSTPQQQSQ LQQVGQCSFQQPQPQQGKQQQVPQSVFLQPHQIAQLEATASIALRTLPMMSVNLPLYRILPFGIDTRVGV					
VFLQQQCIPVAMSQR	R9YTM4-T1	4.41	902.95 (2+)	1189.56 (y10, 1+) 1317.62 (y11, 1+) 1445.68 (y12, 1+)	45.2
MKTFLIFALLAIAAASAI AQMETSRVPGLEKWPQQQPLPPQQPPCSQQQQPFPQQQP I I I LQQSPFSQQQQPVL PQQQPVI I LQQPPFSQQQQQQQQQQPFTQQQPPFSQQPP ISQQQQQQQQQQPFTQQQPPFSQQPPISQQQQPPFSQQQQTPFSQQQQIPVIHPSVLQQLNPKVFLQQQCIPVAMSQR LARPMWQQSSCHVMQQCCQQLPQIPEQSRSEAIR AIVYSIILQEQQGFVQPPQQQPQQSGQGVSTQHQQSSQQQQQLGQCSFQQPQQLQQLGQQPQQQIPQGI FLQPHQISQLEVMTSIALCTLPTMCGVNVPLYSSTTIMPFSIGTGV GAY					
VFLQQCNPVAMPQR	B9VUV5-T1	5.36	908.44 (2+)	912.47 (y8, 1+) 1072.48 (y9, 1+) 1200.54 (y10, 1+)	45.4
MKTFLV FALLAVAATSAIAQMETRCIPGLERPQQQPLPPQQTFPQQPLFSQQQQQLFPQQPSFSQQQPPFWQQQPPFSQQQPILPQQPPFSQQQQPVL PQQSPFSQQQLVLPQQ QYQQLLQKVP IVQPSILQQLNPKVFLQQQCNPVAMPQR LARSQMWWQQSSCHVMQQCCQQLPQIPEQFRYEAIRAIYSIILQEQQVQGSIQSQQQPQQLGQCVSQQPQQSQ QQLGQQPQQQQLAQGTFLQPHQIAQLEVMTSIALRILPTMCSVNVPLYRTTTT'SVPFVGTGVGAY					
ELQESSLEACR	I6TRS8-T1	3.15	661.30 (2+)	735.33 (y6, 1+) 822.36 (y7, 1+) 951.40 (y8, 1+)	33.1
DVSPECRPVALSQVVR	I6TRS8-T2	4.86	604.65 (3+)	642.85 (y11, 2+) 799.42 (y14, 2+) 755.90 (y13, 2+)	21.8
QYEQQTEVPSK	I6TRS8-T3	2.32	668.82 (2+)	788.42 (y7, 1+) 916.47 (y8, 1+) 1045.52 (y9, 1+)	33.4
GGSFYPGGTAPPLQGGWWGTSVK	I6TRS8-T4	6.90	812.40 (3+)	920.46 (y8, 3+) 977.49 (y8, 3+) 1105.54 (y10, 3+)	29.3
AQLLAAQLPAMCR	I6TRS8-T5	4.90	729.36 (2+)	747.34 (y6, 1+) 946.44 (y8, 1+) 1017.48 (y9, 1+)	36.5
LEGGGGLLASQ	I6TRS8-T6	4.50	501.27 (2+)	584.30 (b7, 1+) 697.39 (b8, 1+) 768.43 (b9, 1+)	25.1

MAKRLVLFVAVIVALVALTTAEREINGNNIFLDSRSRQLQCERELQESSLEACRRVVDQQLVGLPWPSTGLQMCCQQLRDVSPPCRVALSQVVRQYEQQTEVPSKGGSFYPPGGT APPLQQGGWGTSVKWYYPDQTSSQQSWQGGQQGYHQSVTSSQQPGQGQQGSYPGSTFPQQPGQGQQPGQRQPWSYPSATFPQQPGQGQQGYYPGATSLLLQPGQGQQGPYQSATS PQQPGQGQQQETYP IATSPHQPGWQQPGQGQQGYPSVTSPQQSGQGQQGYPSTTSPQQSGQGQQLGQGQQPGQGQQGYP SATFPQQPGQWQQGSYPSSTTSPQQSGQGQQGYNP SGTSTQQPGQVQQLGQGQQGYPIATSPQQPGQGQQLGQGQQPGHGQQLVQGGQQGGQQGHYPSMTSPHQGTGQGQKGYPSAISPPQQSGQGQQGYQPSGASSQGSVQGACQHSTS SPQQQAQGCQASSPKQGLGSLYPSGAYTQQKPGQGYNPPGGTSPLHQGGGGFGGGLTTEQPQGGKQPFHCQQTTVSPHQGQQTTVSPHQGQQTTVSPHQGQQTTVSPHQGQQTTVS PHPGQQTTVSPHQGQQTTVSPHPGQQTTVSPHQGQQTTVSPHQGQQTTVSPHQGQQTTVSPHQGQQTTVSPHQGQQTTVSPHQGQQTTVSPHQGQQTTVSPHQGQQTTVSPHQGQQTTVS ASLKVAKAQQQLAAQLPAMCRLEGGGGLLASQ					
ILQQSSCR	I6TMV6-T1	1.46	496.24 (2+)	509.19 (y4, 1+) 637.25 (y5, 1+) 765.31 (y6, 1+)	24.8
VMQQQCCLQLAQIPEQYK	I6TMV6-T2	5.97	755.69 (3+)	777.42 (y6, 1+) 976.51 (y8, 1+) 1089.59 (y9, 1+)	27.2
CTAIDSIVHAIFMQGQR	I6TMV6-T3	7.82	692.34 (3+)	894.43 (y7, 1+) 1007.51 (y8, 1+) 1078.55 (y9, 1+)	24.9
QGVQIVQQQPQPQVGGCQVQVQGGQVAQPQQLAQMEAIR	I6TMV6-T4	6.77	1074.56 (4+)	1284.67 (y11, +) 1009.56 (b9, 1+) 1234.65 (b11, 1+)	38.7
APFVGVVTGVGGQ	I6TMV6-T5	6.04	594.33 (2+)	670.39 (b7, 1+) 828.46 (b9, 1+) 927.53 (b10, 1+)	29.7
MKILILILILAMATTFATSEMQVNPSVQVQPTQQQPYPESQQPFISQSPQQFPLPQQPFPQQPQQPFPQSQQQCLQQPQHQPFPQPTQQFPQRPLLPFTHPFLPFPDQLLPQPPHQS FPQPPQSYQPPLQFPFPQPPQKYPEQPQQPFPWQQPTIQLYLQQQLNSCKEFLLLQQCRPVSLLSYLWSKILQQSSCRMQQQCCLQLAQIPEQYKCTAIDSIVHAIFMQGQRQG VQIVQQQPQPQVGGCQVQVQGGQVAQPQQLAQMEAIRTLVLQSVPSMCNFMVPPNCSTIKAPFVGVVTGVGGQ					
CTTIDSIVHAIFMQGQR	M0XYT2-T1	7.80	702.34 (2+)	894.43 (y7, 1+) 815.41 (y14, 2+) 922.48 (y16, 2+)	25.3
QGVQIVQQQPQPQEVGGCQVQVQGR	M0XYT2-T2	5.44	901.80 (3+)	1016.51 (y9, 1+) 1115.58 (y10, 1+) 1244.62 (y11, 1+)	32.5
DIVQPQQLAQMEAIR	M0XYT2-T3	6.21	870.46 (2+)	931.50 (y8, 1+) 1059.56 (y9, 1+) 1284.67 (y11, 1+)	43.5
APFFSLVNAGML	M0XYT2-T4	9.17	633.83 (2+)	663.35 (b6, 1+) 762.42 (b7, 1+) 876.46 (b8, 1+)	31.7
MKILILILILAMATSFATSEMQVNPSVQVQPTQQQTHPESQQPF IHHSQQQFPQPQQSFPQQPQQPFPQSQQPCLQQPQHQPFPQPSQFPFRQPLQFPFRPFLPFPPEQPLPQPPQES FPQPPQSYQPPLQFPFPQPPQESFPQPPQSYQPPLLQFPFPQQQYPEQPQQPFPPRPPQEQFPNQPQQPFPWQQPSIQLYLQQQLNPKCKEFLLLQQCRPVSLSYLWSKIVQQSNC QVMQEQCCLQLAQIPEQYKCTTIDSIVHAIFMQGQRQGVQIVQQQPQPQEVGGCQVQVQGRDIVQPQQLAQMEAIRSLVLQSVPAMCNFMVPPNCSTMRAPFFSLVNAGML					

DVVQPQQLAQMEAIR	TC131355-T1	5.88	863.45 (2+)	931.50 (y8, 1+) 1059.56 (y9, 1+) 1284.67 (y11, 1+)	43.2
MKILILILILAMATSFATSEMQVNPSVQVQPTQQQTHPESQQPF IHHSQQQFPQPQQSFPQPQPFPQSQQPCLQQPQHQPFPQPSQPFPQQPLQSFPRPFLPFPEQPLPQPQPES FPQPQSYPPQLPFPQPQPQESFPQPQPQSYPPQLLPFPQPQPQQQYEPQPQPFPRPPEQFPNQPQPFPWQQPSIQLYLQQLHNPCKEFLQCRPVSLVSYLWSKIVQQSNC QVMQEQCCLQLAQIPEQYKCTTIDSIVHAIFLQQGQRQGVQIVQQQPQPQEVGQCVLVQGRD VVQPQQLAQMEAIR SLVLQSVPMCNFNVPNCSTMRAPFFSLVNAGML					
APFVGVVSGVGGQ	A0A287EEZ9-T1	5.82	587.32 (2+)	670.39 (b7, 1+) 814.45 (b9, 1+) 913.52 (b10, 1+)	29.4
MKILILILILAMATTFATSEMQVNPSVQVQPTQQQPYPESSQQPFISSQSQQFPQPQPFPQPQPFPQSQQCLQQPQHXLQCRPVSLLSYLWSKILQSSCRMVQQQCCCLQLA QIPEQYKCTAIDSIVHAIIFMQGQRQGVQIVQQQPQPQVGVQCVLVQGGVVPQQLAQMEAIRTLVLQSVPSMCMFNVPNCSTIK APFVGVVSGVGGQ					
EFLQQLCTLDEK	I6TEV2-T1	5.44	762.36 (2+)	893.38 (y7, 1+) 1021.44 (y8, 1+) 1134.53 (y9, 1+)	38.1
QQCCQLANINEQSR	I6TEV2-T2	3.13	938.90 (2+)	1044.54 (y9, 1+) 1172.60 (y10, 1+) 1300.66 (y11, 1+)	47.0
MKIFLLFSLLGVATAITTTTMMQFNPSGLELERPQQLFPPQWQPLPQQPPFLQOEPEQYPYQQQPLPQQQFPQPQPLPHQHQPFPQQLPQQQFPQQMPLPQQQPQFPQQKPFQYQQ PLTQQPYPQQPLAQQQPSIEEQHQLNLCK EFLQQLCTLDEK VPLLQSVISFLRPHISQQNSCQLKR QQCCQLANINEQSR CPAIQTIVHAIVMQQQQQQVQQQVDHGFVQSQLQ QLGQGMPILQLQQQPGQAFVLPQQQAQFKVVVGLSVIQTLPMLCNVHVPPYCSFPGSMATGSGGQ					
<i>Chymotrypsin-derived peptides</i>					
VQGVSQPQQSQL	I6SJ26-C1	3.50	713.868	828.421 (y7, 1+) 952.485 (b9, 1+) 1080.543 (b10, 1+)	34.0
GIDTRVGV	I6SJ26-C2	3.55	408.732	430.277 (y4, 1+) 531.325 (y5, 1+) 646.352 (y7, 1+)	19.0
MKTFLIFALLAIVATSTIAQQQPYPQPQPFPQPPIPQPQPFPQPQPYPQPQPFPQPPIPQPQPYPQPQPFPQPPIPQPQPYPQPQPFPQPPIPQPQPYPQPQPFPPLQPFPSQQPFPQPFPWQQQ PVLSSQQPCTPQQTPLPQGGQDQMLVQVQIPFVHPSILQQLNPKVFLQQQCSPVAMSQR IARSQMLQQSSCYVLQQCCQQLPQIPEQFRHEAVRAIVYSIVLQEQPQQL VQGV QPQQSQL HQVQCSFQQPQPQGGQQQVQSVFLQPLQLAQLEATASIALRTLPMMSVNVPPFYRILPF GIDTRVGV					
AIDTRVGV	I6SW30-C1	3.50	415.740	430.277 (y4, 1+) 531.325 (y5, 1+) 646.352 (y6, 1+)	19.4
MKTFLIFALLAIVATSTIAQQQPYPQPQPFPQPPIPQPQPFPQPQPFPQPPIPQPQPYPQPQPFPQPPIPQPQPYPQPQPFPQPPIPQPQPYPQPQPFPQPPIPQPQPYPQPQPFPPLQPFPSQQPFPQPFPWQQQ QVQIPFVHPSILQQLNPKVFLQQQCSPVAMSQR IARSQMLQQSSCHVLQQCCQQLPQIPEQLRHEAVRAIVYSIVLQEQSLQLVQGVSQPQQQSQQQQVQCSFQQPQPQGGQ QQVQSVLLQPHQIAQLEATTSIALRTLPTMCSVNVPLYRIVPL AIDTRVGV					
QKEKVGQCSF	I6TRT2-C1	5.28	605.780	697.297 (y6, 1+) 825.392 (y7, 1+) 954.435 (y8, 1+)	28.7

GQPQQVPQSVF	I6TRT2-C2	4.70	607.812	577.298 (y5, 1+) 638.326 (b6, 1+) 863.437 (b8, 1+)	28.8
MKTFLIFALLVIAATSTIAQQQPYPQQPFQPPFPQQTTIPQQPQPYPQQPQPYPQQPFPPQQEFPQQPPFWQQPFPQQPPFGLQQRILSQQQPCTPQQTPLPQQGLYQTLQLQ IPYVHPSILQQLNPKVFLQQCCSPVRMPQLIARLQMLQLSSCHVLQQCCQQLPQISEQFRHEAIRAIVYSIFLQEQPQQSVQGVSTQQQL QQEKVQCSF QQPQPQL GQPQQ VPQSVFLQPHQIAQLEATT SIALRTLPRMCNVNPLYDIMPDPFWH					
QQKPFQPPF	P06470-C1	5.11	671.351	726.393 (b6, 1+) 854.452 (b7, 1+) 982.511 (b8, 1+)	31.9
RHEAIRAIVY	P06470-C2	6.26	614.352	805.493 (y7, 1+) 934.536 (y8, 1+) 1071.595 (y9, 1+)	29.1
RGVGPSVGV	P06470-C3	3.39	414.240	554.305 (b6, 1+) 653.373 (b7, 1+) 710.394 (b8, 1+)	19.3
MKTFLIFALLAIAATSTIAQQQFPQPPIQQPQPYPQQPQPYPQQPFPPQQPFPQQPVPQQPQPYPQQPFPPQQPFPQQPFFW QQKPFQPPF GLQQPILSQQQPCTPQQTPLP QQGLYQTLQLQIQYVHPSILQQLNPKVFLQQCCSPVPVQRIARSQMLQQSSCHVLQQCCQQLPQIPEQFRHEAIRAIVYSIFLQEQPQQLVQGVSTQQQLWPPQVQCSFQ QPQPQQVGGQQQVPSAFLQPHQIAQLEATTSIALRTLPMMSVNVPLYRIL RGVGPSVGV					
LPQKPFVQPPF	Q40053-C1	5.98	713.399	907.541 (b8, 1+) 1035.599 (b9, 1+) 1163.658 (b10, 1+)	34.0
QPQQPFPQGSEQIIPQQPFPL	Q40053-C2	8.01	802.081	826.446 (y7, 1+) 939.530 (y8, 1+) 1095.522 (b10, 1+)	36.5
QPQFPQQPQQLPQPQQPF	Q40053-C3	6.37	785.734	951.468 (b8, 1+) 841.420 (y7, 1+) 1051.557 (y9, 1+)	35.7
IIPQQPQQLPL	Q40053-C4	6.53	686.403	732.461 (y7, 1+) 933.515 (b8, 1+) 1143.652 (b10, 1+)	32.6
MKTFLTFVLLAMVMSIVTTARQLNPSSQELQSPQSYLQQPYPQNPY LPQKPFVQPPF HTPQQYFPYLPEELFPQYQIPTPLPQQPFPQQPQQPLPRPQQPFPWQPQQPFPQPQ EPIQQPQQPFPQQPQQPFPQQPQQIIFQQPQQSYVPQQPFPQPQPVPQQRPPQASPLQPQPQQASPL QPQQPFPQGSEQIIPQQPFP LQPQFPQQPQQPL QPQQPFP RQQAE LIIPQQPQQPLPL QPHQPYTQQTIWSMV					
LPQQPFPVQPPF	Q41210-C1	6.97	713.380	808.435 (b7, 1+) 907.504 (b8, 1+) 1035.562 (b9, 1+)	34.0
QPQQPFPQQPQQLPRPQQPFPW	Q41210-C2	7.15	932.145	1079.527 (b9, 1+) 1152.595 (y9, 1+) 1362.732 (y11, 1+)	42.7

QPQQPFPQPQQPIAHQPQQPF	Q41210-C3	5.54	822.749	1162.600 (y10, 1+) 951.468 (b8, 1+) 1102.553 (b19, 2+)	37.5
SQQPQQPFPL	Q41210-C4	5.86	585.301	697.326 (b6, 1+) 941.448 (b7, 1+) 826.446 (y6, 1+)	27.7
QPQQPFPQPQQPFPQPQQIIF	Q41210-C5	7.54	925.473	1098.594 (y9, 1+) 951.468 (b8, 1+) 1079.527 (b9, 1+)	42.4
MKTFLTFVLLAMVMSIVTTARQLNPSSQELQSPQQSYLQQPYQPQNPYLPQQPFPVQQPFHTPQQYFPYLPEELSPQYQIPTPLQPQQPFPQQPQQPLPRPQQPFPWQPQQPFPQPQ QPIPYQPQQPFPNQQPQQIISQQPQQPFPQQPQQPFPQPQQPFPWQPQQPFPQPQQPFPLOPQQPFPWQPQQPFPQPQQPIAHQPQQPFSFSQQPQQPFPLOPQQPFPQQPQQPFPQ QPQQIIFQQPQQSYVPVQPQQPFPQPQVPVQQRPOQASPLQPQQPFPQGGSEQIIPQQPQQPFPLOPHQPYTQQTIIWSMV					
IIPQQPQQPFPL	P17991-C1	6.95	703.396	826.446 (y7, 1+) 933.515 (b8, 1+) 1177.636 (b10, 1+)	33.5
FPQPQEPFPQQPQQPFPLOPQQPFPQQPQQPFPQPQQPFRQQAELIIPQQPQQPFPLOPHQPYTQQTIIWSMV					
EQQTEVPSKGGSF	I6TRS8-C1	3.12	697.333	679.341 (y7, 1+) 778.409 (y8, 1+) 907.452 (y9, 1+)	33.2
QSATSPQQPGQGQGQQETYPIATSPHQPGQW	I6TRS8-C2	5.00	1107.184	1221.601 (y11, 1+) 1318.654 (y12, 1+) 1246.583 (y23, 2+)	51.1
YPIATSPQQPGQGQQL	I6TRS8-C3	4.80	856.934	727.373 (y7, 1+) 858.436 (b8, 1+) 986.494 (b9, 1+)	41.0
GQGQQPGHGQQL	I6TRS8-C4	1.74	617.800	736.374 (y7, 1+) 1049.512 (y10, 1+) 847.381 (b9, 1+)	29.3
TQQKPGQGY	I6TRS8-C5	1.10	503.751	521.235 (y5, 1+) 649.330 (y6, 1+) 777.389 (y7, 1+)	23.7
HVSVEQPSASL	I6TRS8-C6	3.86	577.296	680.336 (b6, 1+) 864.421 (b8, 1+) 935.458 (b9, 1+)	27.3
MAKRLVLFVAVIVALVALTTAEREINGNNIFLDSRSRQLQCERELQESSLEACRRVVDQQLVGLPWSTGLQMCCCQQLRDVSPPCRVPVALSQVVRQYEQQTEVPSKGGSFYPPGGT APPLQGGGWWGTSVKWYYPDQTSQQSWQGGQGYHQSVTSSQQPGQGQGSYPGSTFPPQPGQGQPGQRQPWSYPSATFPQQPGQGQGGQGYYPGATSLLPQGQGGQGPYQSATS PQQPGQGQGGQETYPIATSPHQPGQWQQPGQGQGGYYPSTVTSPOQSGQGQGGYYPSTTSPQSGQGQQLGQGQPGQGQGGYYPSTTSPQSGQGQGGYYP SGTSTQQPGQVQQLGQGQGGYYPPIATSPQQPGQGQQLGQGQPGHGQQLVQGQQQGQGGQGHYPSMTSPHQGTGQGQKGYYPSTTSPQSGQGQGGYYPSTTSPQSGQGSVQGACQHSTS SPQQQAQGCQASSPKQGLGSLYYPGAYTQQKPGQGYNPGGTSPLHQGGGGFGGGLTTEQPQGGKQPFHCQQTTVSPHQGQQTTVSPHQGQQTTVSPHQGQQTTVSPHQGQQTTVS					

