

S1 Table. Proteins identified in detergent resistant fraction of the *P. sativum* L. seeds.

Protein	Accession ¹	Score ²	MW ³	pI ⁴	SC ⁵	Peptides ⁶
Vicilin	P13918.2	2246.41	52.26	5.28	60.78	34
Vicilin precursor, partial	CAA68708.1	1933.73	49.49	5.21	59.82	32
Vicilin 47k	CBK38920.1	1443.46	49.92	5.28	43.76	27
Vicilin, partial	CAF25232.1	1431.21	47.25	5.28	49.40	28
Vicilin 47k	CBK38922.1	1390.83	49.69	5.47	52.51	29
Ferritin	AAB24082.1	1367.35	23.62	5.50	50.00	13
Vicilin 47k	CBK38917.1	1170.04	49.49	5.36	41.32	24
Legumin A2	P15838.1	1167.20	59.64	6.20	34.04	21
LegA class precursor	CAA10722.1	1147.36	59.16	6.15	32.50	21
Legumin	CAA26720.1	1063.18	57.99	6.09	33.33	21
Ferritin	CAA51786.1	987.69	28.86	6.01	43.48	12
Provicilin	P02854.1	976.04	46.41	5.26	38.54	20
Provicilin, Type A	P02855.1	975.72	31.52	5.47	56.36	19
Convicilin	CAB82855.1	787.07	72.14	5.38	25.45	17
Convicilin, precursor	P13915.1	751.18	67.07	6.29	31.35	19
Cvc, partial	CAP06315.1	627.98	62.16	5.58	26.00	17
Legumin J	P05692.1	391.89	57.21	5.64	25.45	10
Lectin	P02867.1	388.54	30.25	4.76	13.82	4
Cvc, Partial	CAP06314.1	377.99	53.23	5.15	24.39	11
Legumin K	P05693.1	369.99	39.83	5.28	29.43	8
Convicilin, precursor	P13919.2	344.14	46.37	5.19	22.54	8
Vicilin, 14 Kda component	P02856.1	284.10	14.03	5.13	41.94	6
Albumin-2	P08688.1	264.60	26.40	5.02	21.65	7
Legumin (minor small)	CAA47809.1	214.01	65.18	5.30	10.60	4
Alpha-Galactosidase 1	CAF34023.1	177.29	45.40	6.59	12.84	4
Acetyl-Coenzyme A Carboxylase Carboxyl Transferase subunit Alpha, Chloroplastic	Q41008.1	146.73	96.48	9.83	22.74	14
Elongation Factor 1-Alpha	Q41011.1	136.15	49.55	9.60	18.57	7
Seed Biotin-containing protein SBP65	Q41060.1	124.36	59.63	5.88	23.59	11
Gag/Pol polyprotein	AAQ82037.1	122.36	258.16	6.32	13.84	23
Dehydrin 2	AAB51380.1	116.52	27.13	6.56	28.24	5
110 kDa 4SNC-Tudor domain protein	BAC06184.1	107.27	108.61	7.67	18.10	17
Acetyl-Coa Carboxylase, partial	BAA94752.1	103.50	91.37	9.69	20.36	12

¹UniProt accession number;

²MASCOT protein score (index for determining accuracy identification by Mascot software);

³Calculated molecular weight. kDa;

⁴Calculated isoelectric point;

⁵Protein sequence coverage (%);

⁶Number of unique peptides matched to mass peaks.