

Table 1 Suppl. List of primers used in this study (for - forward, rev - reverse)

Target	Primer name	Sequence 5'-3'	Annealing temperature	Extention time
2S albumin	2Sfor	ATGGCAAAAATCTCATCATCCACTCTAGCT	64°C	30 s
	2Srev	TCAATAGTAACGAGAGTGGAATTGGCAAGTTC		
	2Sforin	CATCTATGTGTGGTATGCAGCCTAGAAGTTGC	66 °C	10 min
	2Srevin	GCTGCGAACAAAGCTAGAGTGGATGATGAG		
	2SAlbfor	GGACAGAATTTACCAGTATTGCCCGAC	58°C	7 min
7S vicilin-like	2SAlbrev	CTACTGTATGCTTCAAGGACTCAAGGTCTTCTC		
	7Sfor	ATGGGAAGAATCAAATTGACCCTTC	60°C	90 s
	7Srev	TTATTCCTTCAAGCTCCTTATCGG		
Edestin	F3for	ATGGCTTCAACACCTCTTTTGC	60°C	2 min
	R3rev	TTAAGCAGTAACAGCAGCCCTAATC		
	F1for	ATGGCTAATACTAAGGCTTTGCTCTCTC	64°C	8 min
	R1rev	TTAGGCAGTAGCCCTCCTCTCGTA		
	F2for	ATGGCAAGGTCGTCTACTTCGTTGCTATG	64°C	8 min
	R2rev	TTACTCATATCTGGTCTGTTGGGAA		
Ubiquitin	Ubi-for	GCCAGGATGGCAATGAAGTA	60°C	10 s
	Ubi-rev	GCTATAGAGTTGAACTCCACAG		
Edestin type1	qRT-Ede1F	CTCGATGACAATCCCAGAAG	60°C	10 s
	qRT-Ede1R	CTCATCAAAGCGAGCACCC		
Edestin type2	qRT-Ede2F	CCAATTCTCCAGAAGATTCC	60°C	10 s
	qRT-Ede2R	TTTGGCTTCGGGCACGAAC		
Edestin type3	qRT-Ede3F	CTCTACAAAAACGCAATGTACG	60°C	10 s
	qRT-Ede3R	CTGATCGTCCGTTGTTGTCC		
2S albumin	qRT-2S-F	CACTGTAGAAACTGACGATGTTG	60°C	10 s
	qRT-2S-R	GTGCATCTTCTCCCTCATG		
7S vicilin-like	qRT-7S-F	CTTGAAAACGCATTTAATGTAAC	60°C	10 s
	qRT-7S-R	GATCGAGAATCTGGTATGTATAC		

Table 2 Suppl. Amino acid composition [%] of all edestin isoforms, Cs2S albumins, and Cs7S vicilin-like calculated from their predicted mature proteins. ¹ - Sulfur residues (Met, Cys) percentage. Some proteins are 100 % identical.

	Cs2S-1	Cs2S-2	CsEde1A	CsEde1B	CsEde2A	CsEde2B	CsEde3A	CsEde3B	Cs7S
Ala (A)	2.20	2.20	5.94	5.94	6.86	6.86	6.81	6.41	5.31
Cys (C)	8.79	8.79	1.02	1.02	1.14	1.14	1.91	1.71	0.64
Asp (D)	3.30	3.30	4.71	4.71	5.72	5.72	3.62	4.06	4.88
Glu (E)	8.79	8.79	8.40	8.40	7.09	7.09	8.94	8.76	9.55
Phe (F)	1.10	1.10	3.48	3.48	4.12	4.12	3.83	3.85	5.73
Gly (G)	4.40	4.40	6.97	6.97	7.09	7.09	7.23	7.26	8.07
His (H)	4.40	4.40	2.05	2.05	2.29	2.29	2.13	2.56	1.27
Ile (I)	2.20	2.20	4.30	4.30	4.58	4.58	5.96	5.56	5.31
Lys (K)	3.30	3.30	2.05	2.05	2.29	2.29	2.55	2.56	8.07
Leu (L)	4.40	4.40	6.35	6.35	6.18	6.18	6.60	7.05	9.13
Met (M)	8.79	8.79	0.82	0.82	2.06	2.06	2.98	1.92	2.34
Asn (N)	4.40	4.40	6.76	6.76	6.41	6.41	6.81	7.05	3.40
Pro (P)	3.30	3.30	3.69	3.69	4.12	4.12	4.04	4.27	4.67
Gln (Q)	13.19	13.19	7.58	7.58	9.15	9.15	8.30	7.69	3.82
Arg (R)	13.19	13.19	11.89	11.89	11.21	11.21	9.79	10.26	6.16
Ser (S)	8.79	8.79	7.99	7.99	7.09	7.09	5.96	5.77	8.28
Thr (T)	1.10	1.10	4.10	4.10	3.20	3.20	4.04	4.06	5.10
Val (V)	1.10	1.10	7.38	7.38	6.41	6.41	5.11	5.77	3.82
Trp (W)	0.00	0.00	1.02	1.02	0.92	0.92	0.64	0.64	1.27
Tyr (Y)	3.30	3.30	3.48	3.48	2.06	2.06	2.77	2.78	3.18
Sulphur ¹	17.58	17.58	1.84	1.84	3.20	3.20	4.89	3.63	2.97

Table 3 Suppl. Genomic sequences of *CsEde3A* and *CsEde3B*. The sizes of total sequence, four exons, and three introns are in bp.

	Total sequence length	Exon I	Intron I	Exon II	Intron II	Exon III	Intron III	Exon IV
CsEde3A	1891	300	79	252	85	534	245	396
CsEde3B	2141	299	375	253	89	534	201	390

Table 4 Suppl. Percentage of sequence similarity of genomic DNA nucleotides, coding sequences (CDS), and deduced amino acid sequences of all edestin isoforms.

		CsEde2A	CsEde2B	CsEde1A	CsEde1B	CsEde3A
Genomic DNA	CsEde2B	98.86				
	CsEde1A	60.20	60.07			
	CsEde1B	60.53	60.46	98.48		
	CsEde3A	59.12	59.19	64.57	65.05	
	CsEde3B	60.14	60.14	65.94	65.80	85.66
CDS	CsEde2B	99.12				
	CsEde1A	61.49	61.28			
	CsEde1B	61.77	61.56	99.35		
	CsEde3A	60.58	60.73	67.99	68.06	
	CsEde3B	60.73	60.80	68.76	68.69	92.48
Amino acids	CsEde2B	100.00				
	CsEde1A	50.00	50.00			
	CsEde1B	50.00	50.00	100.00		
	CsEde3A	49.79	49.79	58.94	58.94	
	CsEde3B	50.64	50.64	60.82	60.82	92.26