

Fig. 1. Suppl. Multi alignment of the amino acid sequences deduced from CsEde3A and CsEde3B . Asterisks indicate identical amino acids. Broken lines were introduced to maximize similarity. The open and closed triangles black indicate the processing site for removal of the signal peptide and the cleavage site for splitting these polypeptides into an acidic and basic subunit. Four conserved cysteine residues are boxed.

	Signal peptide		
CsEde3A	MASTPLLLLSLCLFLVLLHGCSARSRTAMYGDNELQLNRLEACEPDHRVECEGGMIESW	60	
CsEde3B	MASTPLLLLSLVCFLILFHGCSARSRTAVYGDNELQLNRLEAREPDHRVECEGGMIESW	60	
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CsEde3A	NPNHEQFCACGVALLRLLTIQPNGLHLPSTNGPQLIHVIRGRGVLGTLFPQCAETFEAAQ	120	
CsEde3B	NPNHEQFCACGVALLRLLTIQPNGLHLPSTNGPQLIHVIRGRGVLGTLFPQCAETFEAAQ	120	

CsEde3A	VSVGGGRSSQRDRHQKTRQIKEGDI IAI PAGMAYWCNNDGDQPLITVNLII INNQNLQD	180	
CsEde3B	VSVGGGRSSQRDRHQKTRHIKEGDI IAI PAGMAYWCNNDGDQPLVTNLDVSNHNNQLD	180	
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CsEde3A	MSPRRFYIAGNPHQEFPPQSMMTQQGRRYSEERRERIEEEKEQGLPNNVFRGFSVNLIQE	240	
CsEde3B	LTPRRFYIAGNPHEDFPQSRRTQQGRRYSEESQERIEEEKQGLPNNVFRGFSVNLIQE	240	
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CsEde3A	AFNVDSETARKIQNDDFRGSIIRVEGKLDLVKQPQSRQEQEQEMRRQELQQTEREHARL	300	
CsEde3B	AFNVDSETARKIQSDDFRGSIIRVEGKLDLVKQPQSRQEQEQEMRRQELQQTEREHARL	300	

	acid unit basic unit		
CsEde3A	SGRDYNGLEENICFMRLRESMGDPARADVFS PQAGRLTTVNSYNLPILSFLRLSAERGFL	360	
CsEde3B	SGRDYNGLEENICFMRLRENMGDPARADVFS PQAGRLTTVNSYNLPILSFLRLSAERGFL	360	

CsEde3A	YKNAMYAPQYTMNAHNIIYAIRGSCRCQVVDNNGRSVFEGEIRQGQALTVPQNFAVVKMA	420	
CsEde3B	YKNAMYAPHYNINAHSIIYAIRGRCRCQVVDNNGRSVFEGELRQGQALTVPQNFAIVKMA	420	
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CsEde3A	EKEGF EWVSFKTNDRAQVNQLAGKISFMRAMPEDVIANSYQISREQARRLKYNREESSLF	480	
CsEde3B	ENEGFEWISFKTNDRAQVNQLAGKVSFMRAMPEDVIANSYQISREQARRLKYNREESATLF	480	
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CsEde3A	TTSHQGIRAAVTA 493		
CsEde3B	TTSHQGIRPVV-- 491		
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