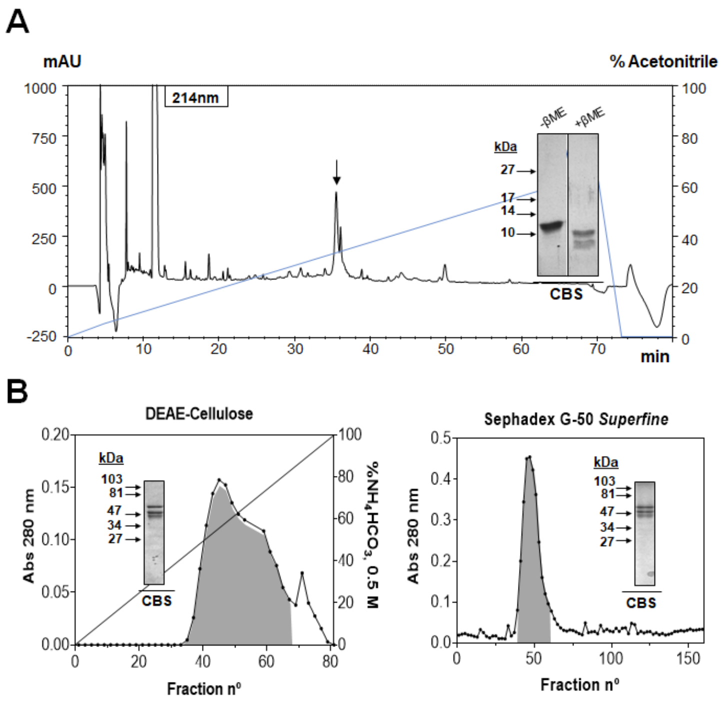
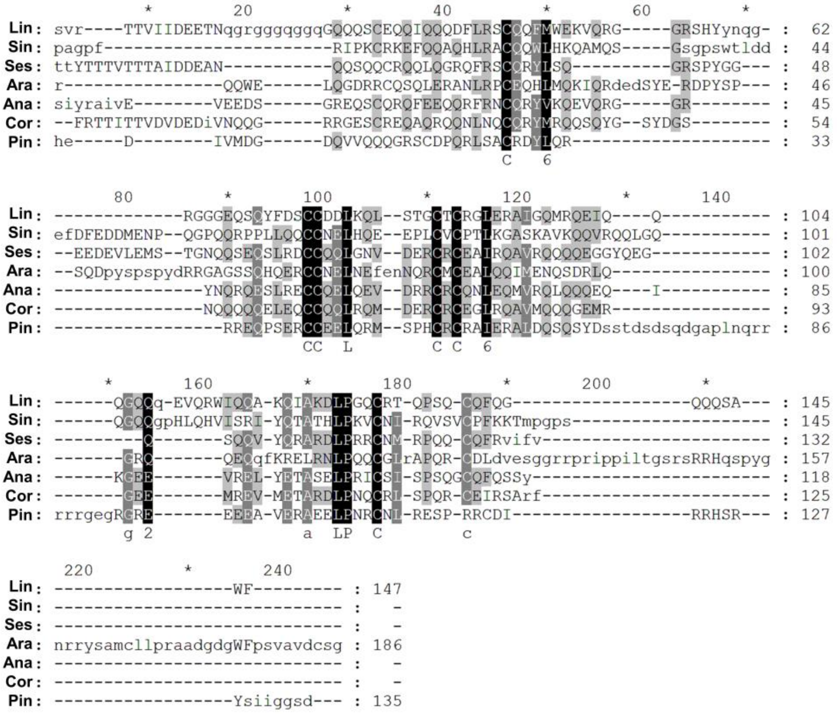
Supplementary material

Figure 1. Isolation of flaxseed 2S albumin and 11S globulin.



(A) Last chromatographic step, RP-HPLC, for the isolation of the flaxseed 2S albumin. **(B)** Two chromatographic steps for the flaxseed 11S globulin isolation. Inserts show the CBS of both proteins.

__Figure 2 Supplementary. Sequence alignment of Lin u 1 with 2S albumins from several plant sources.__



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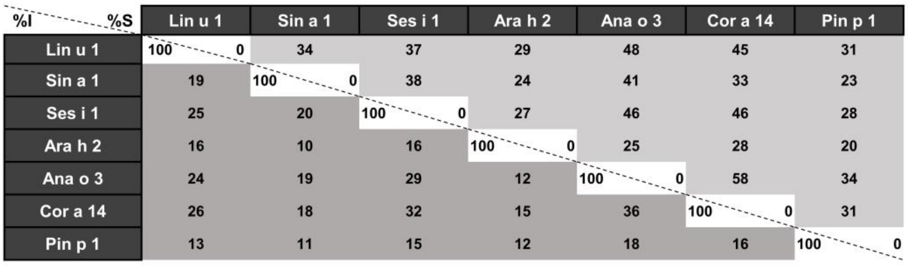
               *        20         *        40         *        60         *
Lin : svr----TTVIIDEETNqgrgggqgggGQQQSCEQQIQQQDFLRSCQQFMWEKVQRG------GRSHYynqg- :  62
Sin : pagpf-----------------------RIPKCRKEFQQAQHLRACQQWLHKQAMQS-----Gsgpswtldd :  44
Ses : ttYTTTVTTTAIDDEAN-----------QQSQQCRQQLQGRQFRSCQRYLSQ----------GRSPYGG--- :  48
Ara : r----------------QQWE------LQGDRRCQSQLERANLRPCEQHLMQKIQRdedSYE-RDPYSP--- :  46
Ana : siyraivE--------VEEDS------GREQSCQRQFEEQQRFRNCQRYVKQEVQRG-----GR-------- :  45
Cor : --FRTTITTVDVDEDiVNQQG------RRGESCREQAQRQQNLNQCQRYMRQQSQYG--SYDGS-------- :  54
Pin : he-----D--------IVMDG------DQVVQQQGRSCDPQRLSACRDYLQR-------------------- :  33
                                                   C   6

            80         *      100         *      120         *      140
Lin : -------------RGGGEQSQYFDSCCDDLKQL--STGCTCRGLERAIGQMRQEIQ----Q----------- : 104
Sin : efDFEDDMENP--QGPQQRPPLLQQCCNELHQE--EPLCVCPTLKGASKAVKQQVRQQLGQ----------- : 101
Ses : --EEDEVLEMS--TGNQQSEQSLRDCCQQLGNV--DERCRCEAIRQAVRQQQQEGGYQEG------------ : 102
Ara : --SQDpyspspydRRGAGSSQHQERCCNELNEfenNQRCMCEALQQIMENQSDRLQ---------------- : 100
Ana : ---------------YNQRQESLRECCQELQEV--DRRCRCQNLEQMVRQLQQQEQ----I----------- :  85
Cor : ---------------NQQQQQELEQCCQQLRQM--DERCRCEGLRQAVMQQQGEMR---------------- :  93
Pin : -----------------RREQPSERCCEELQRM--SPHCRCRAIERALDQSQSYDsstdsdsqdgaplnqrr :  86
                               CC  L        C C  6

           *       160         *       180         *       200         *
Lin : ------QGQQq-EVQRWIQQA-KQIAKDLPGQCRT-QPSQ-CQFQG------------------QQQSA--- : 145
Sin : ------QGQQgpHLQHVISRI-YQTATHLPKVCNI-RQVSVCPFKKTmpgps-------------------- : 145
Ses : ---------Q-------SQQV-YQRARDLPRRCNM-RPQQ-CQFRvifv----------------------- : 132
Ara : -------GRQ-------QEQqfKRELRNLPQQCGIrAPQR-CDLdvesggrrprippiltgsrsRRHqspyg : 157
Ana : ------KGEE-------VREL-YETASELPRICSI-SPSQGCQFQSSy------------------------ : 118
Cor : -------GEE-------MREV-METARDLPNQCRI-SPQR-CEIRSArf----------------------- : 125
Pin : rrrgegRGRE-------EEEA-VERAEELPNRCNI-RESP-RRCDI------------------RRHSR--- : 127
             g 2               a  LP  C        c

       220         *       240
Lin : ------------------WF--------- : 147
Sin : ----------------------------- :   -
Ses : ----------------------------- :   -
Ara : nrrysamcllpraadgdgWFpsvavdcsg : 186
Ana : ----------------------------- :   -
Cor : ----------------------------- :   -
Pin : ------------------Ysiiggsd--- : 135
```



%I \ %S	Lin u 1	Sin a 1	Ses i 1	Ara h 2	Ana o 3	Cor a 14	Pin p 1
Lin u 1	100 0	34	37	29	48	45	31
Sin a 1	19	100 0	38	24	41	33	23
Ses i 1	25	20	100 0	27	46	46	28
Ara h 2	16	10	16	100 0	25	28	20
Ana o 3	24	19	29	12	100 0	58	34
Cor a 14	26	18	32	15	36	100 0	31
Pin p 1	13	11	15	12	18	16	100 0

__Signal peptides from each protein, determined with online program SignalP, were removed. Table under alignment shows percentages of identity (%I, dark grey) and similarity (%S, light grey) between the different proteins. Nomenclature: Lin, conlinin; Sin, Sin a 1; Ses, Ses i 1; Ara, Ara h 2; Ana, Ana o 3; Cor, Cor a 14; Pin, Pin p 1.__

doi: 10.18176/jiaci.0713