

```

SP|P62931|ALB1F_PEA      MASVKLASLIVL-FAT-LGMFLTKNVGAASCN-GVCSPFEMPP-CGTSACRCIP--VGLV 54
SP|P62930|ALB1E_PEA      MASVKLASLIVL-FAT-LGMFLTKNVGAASCN-GVCSPFEMPP-CGTSACRCIP--VGLL 54
SP|P62927|ALB1B_PEA      MASVKLASLIVL-FAT-LGMFLTKNVGAASCN-GVCSPFEMPP-CGTSACRCIP--VGLV 54
SP|P62928|ALB1C_PEA      MASVKLASLIVL-FAT-LGMFLTKNVGAASCN-GVCSPFEDIPP-CGTSACRCIP--AGLV 54
SP|P62926|ALB1A_PEA      MASVKLASLIVL-FAT-LGMFLTKNVGAASCN-GVCSPFEMPP-CGTSACRCIP--VGLV 54
SP|P62929|ALB1D_PEA      MASVKLASLIVL-FAT-LGMFLTKNVGAASCN-GVCSPFEMPP-CGTSACRCIP--VGLF 54
TR|G7KHS2|G7KHS2_MEDTR  MAYFKLASLAVFLLATF-LMFPTKNVEAQSCSGAVCIRFNTE--C-DAGCYCHTAG-TEQ 55
TR|I3SW97|I3SW97_MEDTR  MAYFKLASLAVFLLATF-LMFPTKNVEAQSCSGAVCIRFNTE--C-DAGCYCHTAG-TEQ 55
TR|I3S2Y7|I3S2Y7_MEDTR  MTYVKLAPLAVFLLAFF-LIFPMKKVEADKCG-AYCPYPRL---YCSGDCDCEPFIASLP 55
TR|A0A072V8Z6|A0A072V8Z6_MEDTR  -----MKKVEADKCG-AYCPYPRL---YCSGDCDCEPFIASLP 34
TR|A0A072UYJ7|A0A072UYJ7_MEDTR  -----MPTK-VIFPMKKVEADKCG-AYCPYPRL---YCSGDCDCEPFIASLP 42
TR|A0A392M2G9|A0A392M2G9_9FABA  MTYAKLAPLAVFLLATF-LMFPTKNVEAC---GGLCSVFDSPVCGGGCTCMFYWYAPV 56
TR|A0A1S2Z3C2|A0A1S2Z3C2_CICAR  MAYVKLPPLTLFLLATFLITFTSKV-GATCT-GVCSFYDSNP-CGGNYVCFCHFLDVGDY 57
                                * : * . *

SP|P62931|ALB1F_PEA      I---GYCRNPSGV-----FLRTNDEHPNLCESDADCRKKKSGKFCGHYPNPG--IEYGWC
104
SP|P62930|ALB1E_PEA      I---GYCRNPSGV-----FLKGNDEHPNLCESDADCRKKKSGNFCGHYPNPD--IEYGWC
104
SP|P62927|ALB1B_PEA      V---GYCRHPSGV-----FLRTNDEHPNLCESDADCRKKKSGNFCGHYPNPD--IEYGWC
104
SP|P62928|ALB1C_PEA      I---GNCRNPYGV-----FLRTNDEHPNLCESDADCRKKKSGTFCGHYPNPD--IEYGWC
104
SP|P62926|ALB1A_PEA      V---GYCRNPSGV-----FLRTNDEHPNLCESDADCRKKKSGNFCGHYPNPD--IEYGWC
104
SP|P62929|ALB1D_PEA      I---GYCRNPSGV-----FLKANDEHPNLCESDADCRKKKSGNFCGHYPNPD--IEYGWC
104
TR|G7KHS2|G7KHS2_MEDTR  T---GVC RPNV-----DGMEMEERHPYLCQSHDECNKKKSGSFCARSPNSD--NKNGWC
104
TR|I3SW97|I3SW97_MEDTR  T---GVC RPNV-----DGMEMEERHPYLCQSHDECNKKKSGSFCARFPNFD--NKNGWC
104
TR|I3S2Y7|I3S2Y7_MEDTR  PRLNFKCVTPHS---S AELKKKVEEQPKLCWSHTECTEKSGSNYCARFPNSN--LKYGLC
110
TR|A0A072V8Z6|A0A072V8Z6_MEDTR  PRLNFKCVTPHS---S AELKKKVEEQPKLCWSHTECTEKSGSNYCARFPNSN--LKYGLC 89
TR|A0A072UYJ7|A0A072UYJ7_MEDTR  PRLNFKCVTPHS---S AELKKKVEEQPKLCWSHTECTEKSGSNYCARFPNSN--LKYGLC 97
TR|A0A392M2G9|A0A392M2G9_9FABA  M---GECQSIHNAMRQSINDTMVEESPYLCNSHADCTIKGSGSFCARYPNPNYNKYGWC
113
TR|A0A1S2Z3C2|A0A1S2Z3C2_CICAR  K---GICID-RSF-----FIKTVDDEPNLCQTHAECTKKKSGNFCGRYPNPN--IKYGRC
106
                                *           :. * * * :. : *   * * * :. : *   *   : * *

SP|P62931|ALB1F_PEA      FASKSEAEDFFSKITQ-----KDLLKSVSTA-- 130 (SEQ ID NO: 1)
SP|P62930|ALB1E_PEA      FASKSEAEDVFSKITP-----KDLLKSVSTA-- 130 (SEQ ID NO: 2)
SP|P62927|ALB1B_PEA      FASKSEAEDFFSKITQ-----KDLLKSVSTA-- 130 (SEQ ID NO: 3)
SP|P62928|ALB1C_PEA      FASKSEAEDVFSKITP-----KDLLKSVSTA-- 130 (SEQ ID NO: 4)
SP|P62926|ALB1A_PEA      FASKSEAEDFFSKITP-----KDLLKSVSTA-- 130 (SEQ ID NO: 5)
SP|P62929|ALB1D_PEA      FASKSEAEDFFSKITP-----KDLLKSVSTA-- 130 (SEQ ID NO: 6)
TR|G7KHS2|G7KHS2_MEDTR  FASFSEAQEFYKFE-T-AKYKFKRDFLKMPITA-- 134 (SEQ ID NO: 7)
TR|I3SW97|I3SW97_MEDTR  FASFSEAQEFYKFE-T-AKYKFKRDFLKMPITA-- 134 (SEQ ID NO: 8)
TR|I3S2Y7|I3S2Y7_MEDTR  FPSISEAVNTFKMA---SSLKFEKDFLKMSLPA-- 140 (SEQ ID NO: 9)
TR|A0A072V8Z6|A0A072V8Z6_MEDTR  FPSISEAVNTFKMA---SSLKFEKDFLKMSLPA-- 119 (SEQ ID NO: 10)
TR|A0A072UYJ7|A0A072UYJ7_MEDTR  FPSISEAVNTFKMA---SSLKFEKDFLKMSLPA-- 127 (SEQ ID NO: 11)
TR|A0A392M2G9|A0A392M2G9_9FABA  FASKYEADYVRVVG-SRYKFNKDLKMPITS A EY 146 (SEQ ID NO: 12)
TR|A0A1S2Z3C2|A0A1S2Z3C2_CICAR  FASNTAE EEF SNKFSYYSSRFI KDFLNMPVVA-- 138 (SEQ ID NO: 13)
                                * *   * * :           : * * :

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FIG. 1

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SP|Q6PSU2|CONG7_ARAHY -MAKLITLVALAL-FLLAHAS--ARQ-Q-W-----ELQGDRCQSQLE-R-A 40
SP|Q2PS07|2SS_PAGES --MKLFILATATLLIAATQAT---Y-----PRDEGFDLGETQMSSKCMRQVKMNEP 47
SP|P15322|ALL1_SINAL -----PAGEFRIPIKCRKEFQ-QAQ 18
SP|P19594|2SS_SOYBN -MTKFTILLISLL-FCIAHTCS--A---SKW-----Q-HQODSCRQLQ-G-V 38
SP|P04403|2SS1_BEREX -MAKISVAAAALLVLMALGHAT--AFRATVTTTVVEE-----NQEECREQM-QQQ 48
SP|P30233|2SS2_CAPMA -MAKLI FLFATLALFVLLANAS--IQTTVIE--VDEEDN-----QLWRCQRQL-QHQ 48
SP|P38057|ITRY_SINAR -----PAGEFRLPPCRKEFQ-QAQ 18
SP|Q9XHP1|2SS1_SESIN -MARFTIVLAVLFAAALVSA---SAHKT VVTT SVAEEGE---EE-NQRGCEW-ES-RQC 49
SP|P24565|2SS1_BRANA -----Q-PQKCRKEFQ-QEQ 13
SP|P23110|2SS8_HELAN -MARFSIVFAAGVLLLVAMAFVSEASTTTTITTTIIEENPYGRGR-TESGCYQME-EAE 57
SP|Q9FH31|2SS5_ARATH -MAKLI LVFATLALFILLANAS--IYRTVVE--FEEDDDVSN---PQQGKCQREFM-KHQ 51
SP|P15459|2SS3_ARATH MANKLFLVCATLALCFLLTNAS--IYRTVVE--FEEDDASNPVGPR--QRCQKEFQ-QSQ 53
SP|P15457|2SS1_ARATH MANKLFLVCATLALCFLLTNAS--IYRTVVE--FEEDDATNPIGPK-MRKRKEFQ-KEQ 54
SP|Q647G9|CONG_ARAHY -MAKSTILVALLA-LVLVAHAS--AMRRERG-----RQGDSSSCERQVD-R-V 42
SP|P5B8W8|COND1_LUPAN -MAKLITLIALVAALVLVHTS--AFR-----SSEQSCKRQLQ-Q-V 37
SP|P09893|2SS6_BRANA MANKLFLVSATLALFLLTNAS--VYRTVVE--VDEDDATNPAGFRIPIKCRKEFQ-QAQ 55
SP|P15460|2SS4_ARATH MANKLFLVCATLALCFLLTNAS--VYRTVVE--FDEDDASNPIGPI--QRCQKEFQ-QDQ 53
SP|P15458|2SS2_ARATH MANKLFLVCATLALCFLLTNAS--IYRTVVE--FDEDDASNPMGPR--QRCQKEFQ-QSQ 53
SP|P17333|2SS4_BRANA MANKLFLVSATLALFLLTNAS--IYRTVVE--VDEDDATNPAGFRIPIKCRKEFQ-QAQ 55
SP|P27740|2SSB_BRANA MANKLFLVSATLALFLLTNAS--IYRTVVE--FDEDDATNPAGFRIPIKCRKEFQ-QAQ 55
SP|P0C8Y8|2SS2_BEREX -MAKMSVAAAALLLVLVGLQAT--AFRTVTTTLEEEQEENPRGR-SEQQCREQME-RQQ 55
SP|P01090|2SS2_BRANA MANKLFLVSATLALFLLTNAS--IYRTVVE--FDEDDATDSAGFRIPIKCRKEFQ-QAQ 55
SP|P80207|ALL1_BRAJU -----AGFRRFPKRKEFQ-QAQ 17
SP|P80352|2SS3_CAPMA -----EPLCRRQFQ-QHQ 12
SP|P80351|2SS1_CAPMA -----EPLCRRQFQ-QHQ 12
SP|P01091|2SS1_BRANA -----PKCRKEFQ-QAQ 11
SP|Q99235|COND2_LUPAN -MAKLITLIALVAALVLVHTS--AFQ-----SSKQSCRQLQ-Q-V 37
SP|P80208|2SS3_BRANA -----SAGFRIPIKCRKEFQ-QAQ 18
SP|P80353|2SS4_CAPMA -----EPLCRRQFQ-QHQ 12
SP|P5B8X0|COND3_LUPAN -MAKLITLIALVAALVLVHTS--AFR-----SSEQSCKRQLQ-Q-V 37
*

SP|Q6PSU2|CONG7_ARAHY NLRPCEQHLMQIKRDEDSYGRDPYSPSQDPYSPSQDPRRDPYSPSPYDRRGAGSSQHQ 100
SP|Q2PS07|2SS_PAGES HLLKCNRYIAMDILDDKYAEAL-----SR-VEGEGCKSEESCM 84
SP|P15322|ALL1_SINAL HLRACQQLHLKQAMQS--GSGP-SWTLDDGEFDFEDDM-----E--NP-QGQQRPPPLL 65
SP|P19594|2SS_SOYBN NLTPCEKHIMEKIQGRDDDDDDDDNNH----ILRTMRGRINYIRNEGKDEDEEEEGHM 94
SP|P04403|2SS1_BEREX MLSHCRMVYMRQOME--ESPYQ-----TM--PRRGMEPHM 78
SP|P30233|2SS2_CAPMA HLRACQRFTHRRAQFGGQFDELE-----DEVEDDN-----D--D--ENQP--RRPAL 89
SP|P38057|ITRY_SINAR HLRACQQLHLKQARQS--GSGP-S-----P-QGQQRPPPLL 50
SP|Q9XHP1|2SS1_SESIN QMRHMCQWMRMRQYEEFL-----RSAEANQGFHEHF 83
SP|P24565|2SS1_BRANA HLRACQQLWIRQQLAGSP-----FQ-SGFQEGFWLR 42
SP|P23110|2SS8_HELAN MLNHCGMYLMKNLG--ERSQV-----S---PRMREEDHK 86
SP|Q9FH31|2SS5_ARATH QLRGCKQWIRKRAQQGRIGYEADDFELTLDVLELDE-----N--P--MGFQ-QQSSL 99
SP|P15459|2SS3_ARATH HLRACQRWMSKQMRQGRG--GGP---SLDDEDFDE-----GPQGYQLL 92
SP|P15457|2SS1_ARATH HLRACQQLMLQQARQGR-----SDEDFEDDM-----E--NP-QGQQRPPPLL 94
SP|Q647G9|CONG_ARAHY NLRPCEQHIMQIRIMEGEQYD-----SYDIRSTRSSDQQ 76
SP|P5B8W8|COND1_LUPAN NLRHCENHIDQRIQQQEEEDRARKLRGIKHV-----ILRHKSQE-SESEEL 86
SP|P09893|2SS6_BRANA HLRACQQLHLKQAMQPGGSGP-SWTLDDGEFDFEDDV-----E--NQQQGQQRPPPP 105
SP|P15460|2SS4_ARATH HLRACQQLWIRKQMRQGRG--GGP---SLDDEDFDE-----E--NP-QR---RQLL 95
SP|P15458|2SS2_ARATH HLRACQQLMRQMRQGRG--GGP---SLDDEDFLEDDI-----E--NP-QGQQRPPPLL 99
SP|P17333|2SS4_BRANA HLRACQQLHLKQAMQS--GSGP-SWTLDDGEFDFEDDM-----E--NP-QGQQRPPPLL 102
SP|P27740|2SSB_BRANA HLRACQQLHLKQAMQS--GSGP-SWTLDDGEFDFEDDM-----E--NP-QGQQRPPPLL 102
SP|P0C8Y8|2SS2_BEREX QLNHCRMVYLRQME--ESPYQ-----NPRPLRGEPEHL 87
SP|P01090|2SS2_BRANA HLRACQQLHLKQAMQS--GGGP-SWTLDDGEFDFEDDM-----E--NP-QGQQRPPPLL 102
SP|P80207|ALL1_BRAJU HLRACQQLHLKQAMQS--GSGP-Q-----P-QGQQRPPPLL 49
SP|P80352|2SS3_CAPMA HLRACQRYLRRAQRGLADE-----Q-RGPAL 39
SP|P80351|2SS1_CAPMA HLRACQRYLRRAQRGLVDE-----Q-RGPAL 39
SP|P01091|2SS1_BRANA HLRACQQLHLKQAMQS--GGGP-SWTLDDGEFDFEDDM-----E--K--QGQQRPPPLH 57
SP|Q99235|COND2_LUPAN NLRHCENHIAQRIQQQEEEDHALKLRGIKHV-----ILRHRSQYSESEEL 87
SP|P80208|2SS3_BRANA HLRACQQLHLKQAMQS--GSGP-----QGQQRPPPLL 48
SP|P80353|2SS4_CAPMA HLRACQRYLRRAQRG---E-----Q-RGPAL 35
SP|P5B8X0|COND3_LUPAN NLRHCENHIDQRIQQQEEEDRARKLRGIKHV-----ILRHKSQE---SEEL 83
: * :

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FIG. 2

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SP|Q6PSU2|CONG7_ARAHY ERCCNELNEFENNQRCEALQQIMENQSDRL--QG-----RQEQQFKRELRLNL 148
SP|Q2PS07|2SS_FAGES RGCCVAMKEM--DDECVCCEMMKMVENQKGRIGE-----RLIKEGVRLDLKEL 129
SP|P15322|ALL1_SINAL QCCCNELHQE--EPLCVCPPTLKGAASKAVKQVVRQQLGQQGQQGPHLQHVISRIYQTATHL 123
SP|P19594|2SS_SOYBN QKCCTEMSEL-RSPKCCKALQKIMENQSEEL--EE-----KQ-KKKMEKELINL 140
SP|P04403|2SS1_BEREX SECCEQLGEM--DESCRCEGLRMMMRMQQEE-MQF-----RGEQMRMRMLAENI 126
SP|P30233|2SS2_CAPMA RQCCNQLRQV--DRPCVCPVLRQAQQVLRQIIQG-----PQQLRRLFDAARNL 137
SP|P38057|ITRY_SINAR QCCCNELHQE--EPLCVCPPTLKGAASKAVKQVVRQQLGQQGQQGPHLQHVISRIYQTATHL 108
SP|Q9XHP1|2SS1_SESIN RECCNELRDV--KSHCRCEALRCMMRMQEQEYGMQ-----E---MQQMQQMMQYL 129
SP|P24565|2SS1_BRANA EQCCNELYQE--DQVCVCPPTLKQAASKSVRVQGG-HG-----PFQSTRYIQTAKNL 89
SP|P23110|2SS8_HELAN QLCCMQLNKL--DEKCMCPAIMMMLNEPMWIR-M-----RDQVMSMAHNL 128
SP|Q9FH31|2SS5_ARATH KMCCNELRQV--DKMCVCPPTLKKAQQVRFQG-MHG-----QQQVQHVFQTAKNL 146
SP|P15459|2SS3_ARATH QCCCNELRQE--EPVCVCPPTLKQAARAVSLQGG-HG-----PFQSRKIYQSAKYL 139
SP|P15457|2SS1_ARATH QCCCNELRQE--EPDCVCPPTLKQAASKAVRLQGG-HQ-----PMQVRKIYQTAHNL 141
SP|Q647G9|CONG_ARAHY QRCCDELNEMENTQRCEALQQIMENQCDRL--QD-----RQMVRQFKRELMLNL 124
SP|P5B8W8|COND1_LUPAN DQCCCEQLNEL-NSQRCQCRALQQIYESQSEQC--EG-----RQEQQLEGELEKL 133
SP|P09893|2SS6_BRANA QCCCNELHQE--EPLCVCPPTLKGAASKAVRQVVRQQQGQ-MQCGQMQQVTSRVYQTATHL 162
SP|P15460|2SS4_ARATH QKCCSELRQE--EPVCVCPPTLRQAASKAVRQGGQH-----PEQVRKIYQAAKYL 143
SP|P15458|2SS2_ARATH QCCSELRQE--EPVCVCPPTLRQAARAVSLQGG-HG-----PFQSRKIYKTAKYL 146
SP|P17333|2SS4_BRANA QCCCNELHQE--EPLCVCPPTLKGAASKAVKQVVRQQQGQ---QGQQLQQVISRIYQTATHL 157
SP|P27740|2SSB_BRANA QCCCNELHQE--EPLCVCPPTLKGAASKAVKQVVRQQQGQ---LQMVSRIVYQTATHL 155
SP|P0C8Y8|2SS2_BEREX DECCEQLERM--DEMCRCEGLRMLL-RRQREE-MEL-----QGEQMQRIMRKAENL 134
SP|P01090|2SS2_BRANA QCCCNELHQE--EPLCVCPPTLKGAASKAVKQVVRQQQGQ---QGMVSRIVYQTATHL 155
SP|P80208|2SS3_BRANA QCCCNELHQE--EPLCVCPPTLKGAASKAVKQVVRQQQGQ---QGEQQLQQVISRIYQTATHL 107
SP|P80352|2SS3_CAPMA RLCCNQLRQV--NKPCVCPVLRQAQQVLRQIIQG-----PRQVRRLFRAARNL 87
SP|P80351|2SS1_CAPMA RLCCNQLRQV--NKPCVCPVLRQAQQVLRQIIQG-----PRQVRRLFRAARNL 87
SP|P01091|2SS1_BRANA QQYCNELQQE--EPLCVCPPTLRGASKAVKQVVRQQQGQ---QGMVNRIVYQTATHL 110
SP|Q99235|COND2_LUPAN DQCCCEQLNEL-NSQRCQCRALQQIYESQSEQC--EG-----SQEQQLQGELEKL 134
SP|P80208|2SS3_BRANA QCCCNELHQE--EPLCVCPPTLKGAASKAVKQVVRQQQGQ---QGQQLQQVISRIYQTATHL 103
SP|P80353|2SS4_CAPMA RLCCNQLRQV--NKPCVCPVLRQAQQVLRQIIQG-----PRQVRRLFRAARNL 83
SP|F5B8X0|COND3_LUPAN DQCCCEQLNEL-NSQRCQCRALQQIYESQSEQC--EG-----RQEQQLEGELEKL 130

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SP|Q6PSU2|CONG7_ARAHY PQCCGLRAPQRCDLEVESGGRDRY-- 172 (SEQ ID NO: 14)
SP|Q2PS07|2SS_FAGES PSKCGLSEL-ECGSRG----NRYFV 149 (SEQ ID NO: 15)
SP|P15322|ALL1_SINAL PKVCNIRQVSVCPFKTTPG-PS--- 145 (SEQ ID NO: 16)
SP|P19594|2SS_SOYBN ATMCRFGPMIQCDLSSDD----- 158 (SEQ ID NO: 17)
SP|P04403|2SS1_BEREX PSRCNLS-PMRCFPMGSGIAGF----- 146 (SEQ ID NO: 18)
SP|P30233|2SS2_CAPMA PNICNIPNIGACPFRAWP----- 155 (SEQ ID NO: 19)
SP|P38057|ITRY_SINAR PKVCNIPQVQVCPFNKTTPG-PS--- 130 (SEQ ID NO: 20)
SP|Q9XHP1|2SS1_SESIN PRMCGMSYPTECRMRPIFA----- 148 (SEQ ID NO: 21)
SP|P24565|2SS1_BRANA PNVCNMKQIGTCPIA-IPFFP----- 110 (SEQ ID NO: 22)
SP|P23110|2SS8_HELAN PIECNLM-SQPCQM----- 141 (SEQ ID NO: 23)
SP|Q9FH31|2SS5_ARATH PNVCNIPTVGSCQFKASP-Y----- 165 (SEQ ID NO: 24)
SP|P15459|2SS3_ARATH PNICKIQVGECPFQTTFIPFFPY- 164 (SEQ ID NO: 25)
SP|P15457|2SS1_ARATH PNVCNIPQVQVCPFN-IPSPFSPY- 164 (SEQ ID NO: 26)
SP|Q647G9|CONG_ARAHY PQCCNFRAPQRCDLDSGGRC----- 145 (SEQ ID NO: 27)
SP|P5B8W8|COND1_LUPAN PRICGFGPLRRCNINPDEE----- 152 (SEQ ID NO: 28)
SP|P09893|2SS6_BRANA PRVCNIRQVSVCPFKTTPG-PGFY- 186 (SEQ ID NO: 29)
SP|P15460|2SS4_ARATH PNICKIQVQVCPFQ--IPSPSY- 166 (SEQ ID NO: 30)
SP|P15458|2SS2_ARATH PNICKIQVGECPFQTTFIPFFPY-- 170 (SEQ ID NO: 31)
SP|P17333|2SS4_BRANA PKVCNIPQVSVCPFKTTPG-PSY-- 180 (SEQ ID NO: 32)
SP|P27740|2SSB_BRANA PKVCKIPQVSVCPFKTTPG-PSY-- 178 (SEQ ID NO: 33)
SP|P0C8Y8|2SS2_BEREX LSRCNLS-PQRCFPMGGYTAWL---- 154 (SEQ ID NO: 34)
SP|P01090|2SS2_BRANA PKVCNIPQVSVCPFKTTPG-PSY-- 178 (SEQ ID NO: 35)
SP|P80207|ALL1_BRAJU PRVCNIPRVSIQPFQKTPG-PS--- 129 (SEQ ID NO: 36)
SP|P80352|2SS3_CAPMA PNICKIPAVGRCQFTRW----- 104 (SEQ ID NO: 37)
SP|P80351|2SS1_CAPMA PNICKIPAVGRCQFTRW----- 104 (SEQ ID NO: 38)
SP|P01091|2SS1_BRANA PKVCNIPQVSVCPFKTTPG-PSY-- 133 (SEQ ID NO: 39)
SP|Q99235|COND2_LUPAN PRTCGFGPLRRCDVNPDEE----- 153 (SEQ ID NO: 40)
SP|P80208|2SS3_BRANA PKVCNIPQVSVCPFKTTPG-PS--- 125 (SEQ ID NO: 41)
SP|P80353|2SS4_CAPMA PNICKIPAVGRCQFTRW----- 100 (SEQ ID NO: 42)
SP|F5B8X0|COND3_LUPAN PRICGFGPLRRCNINPDEE----- 149 (SEQ ID NO: 43)

```

FIG. 2 (cont.)

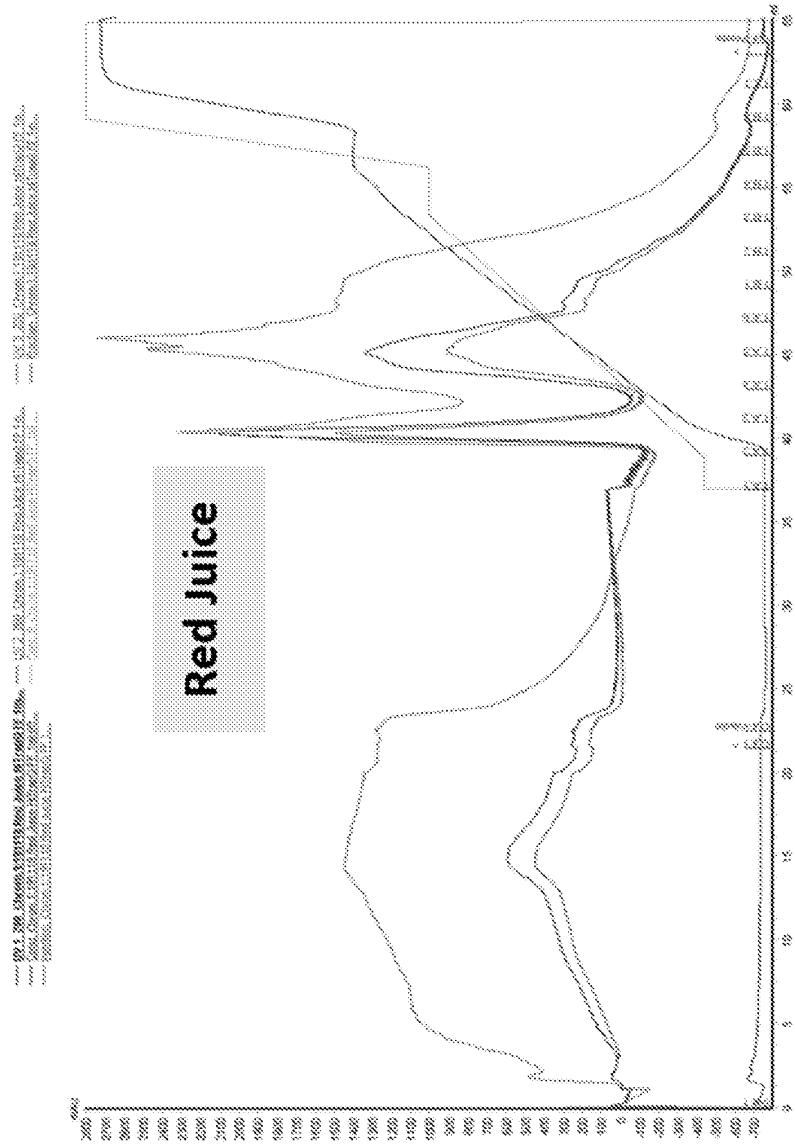


FIG. 3A

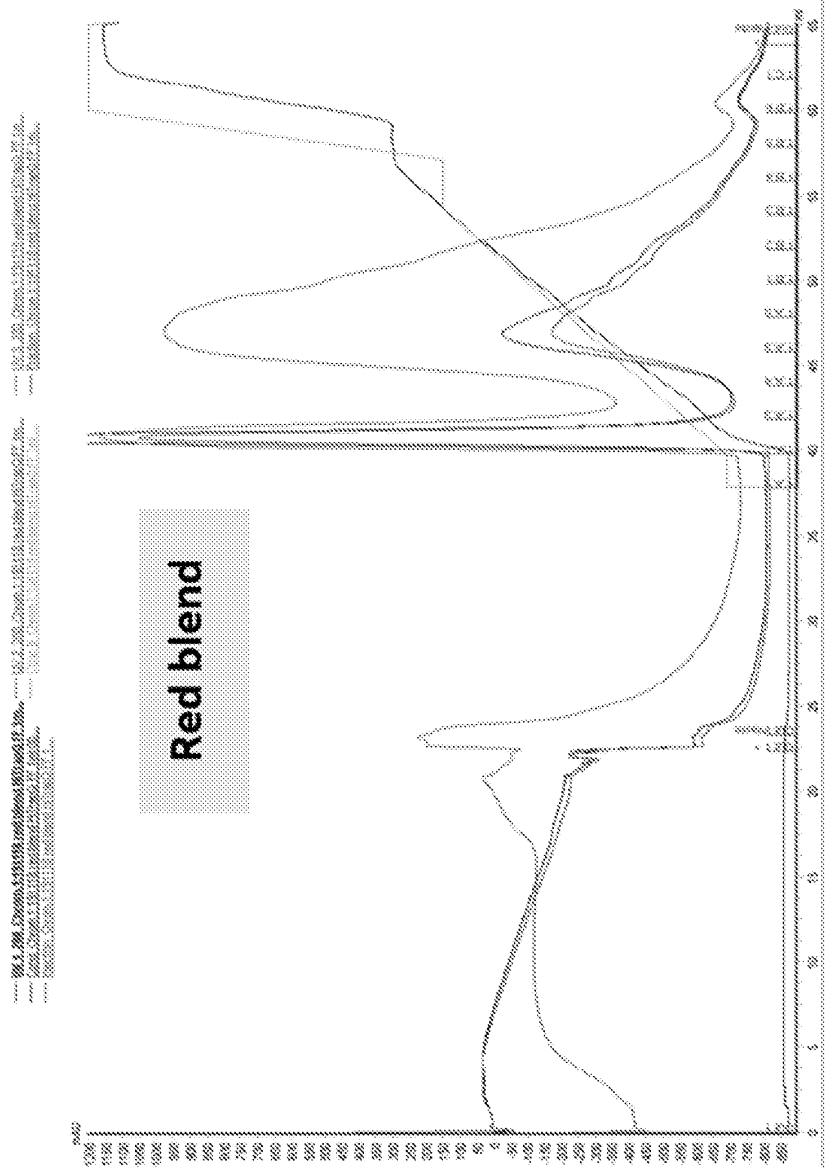


FIG. 3B

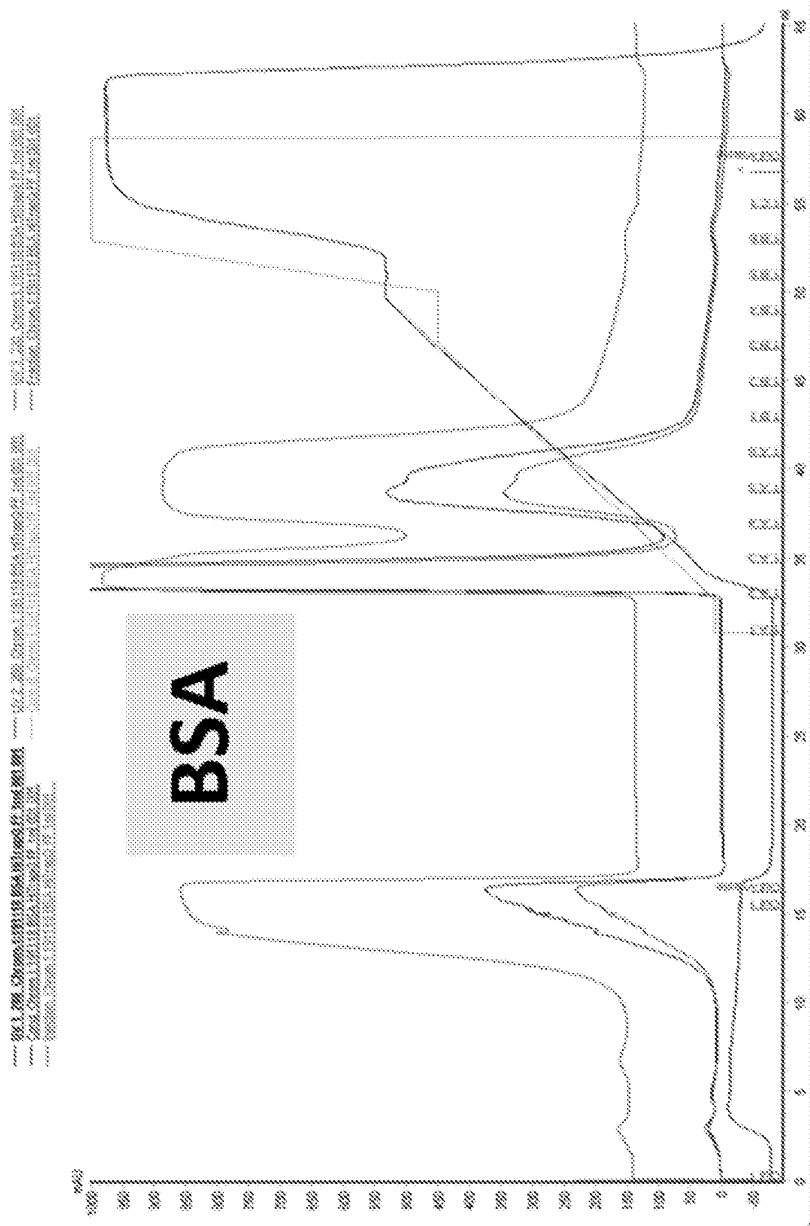


FIG. 3C

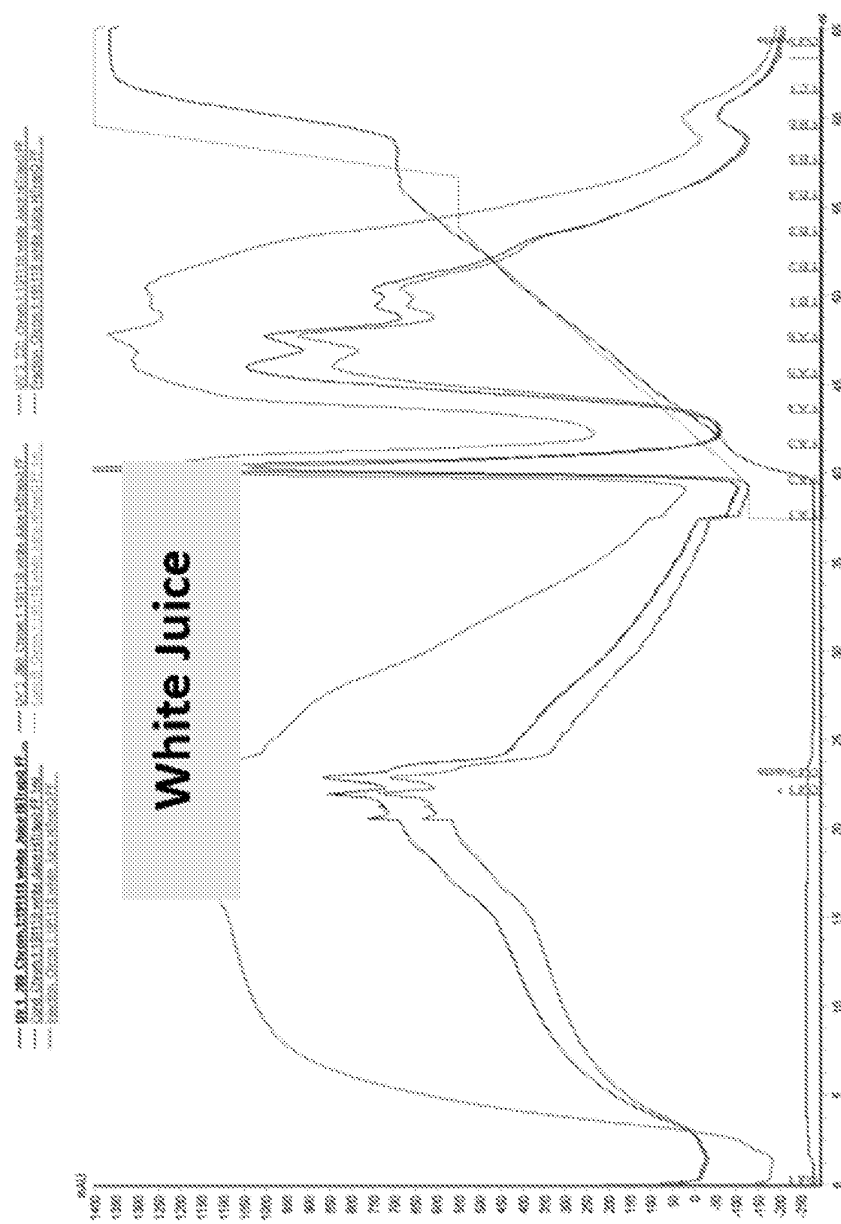


FIG. 3D

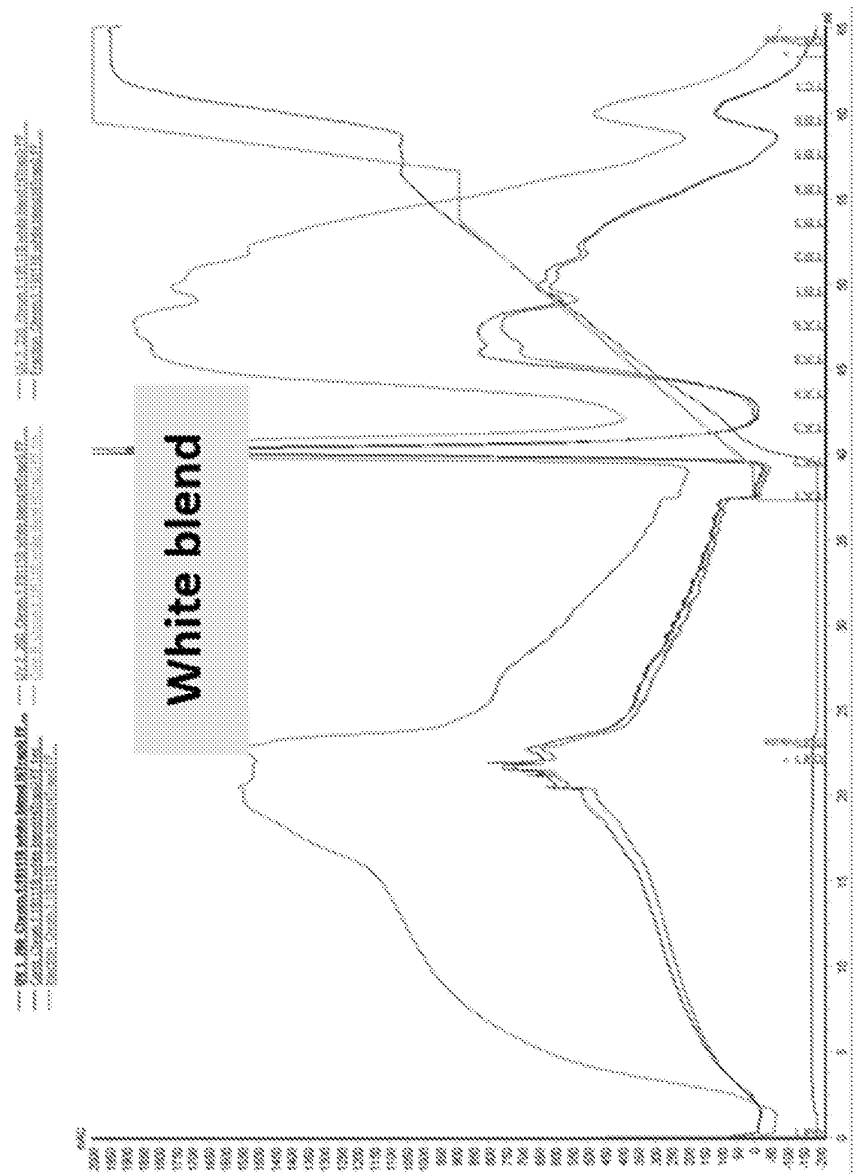


FIG. 3E

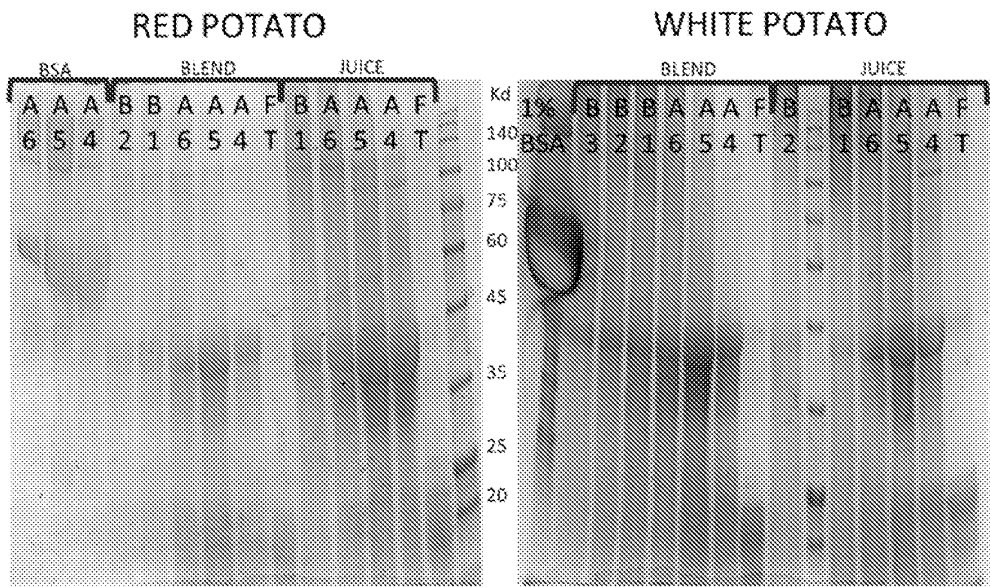


FIG. 3F

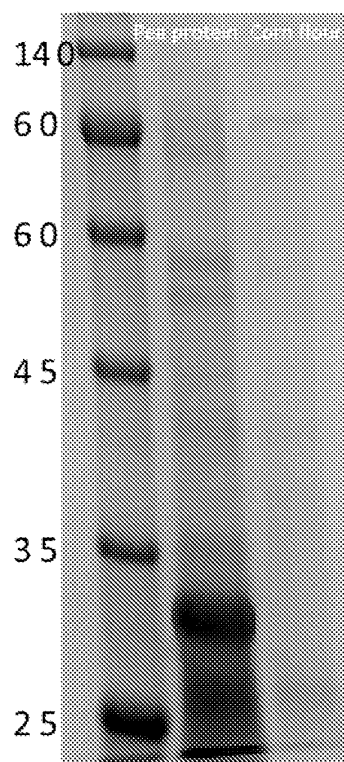


FIG. 4

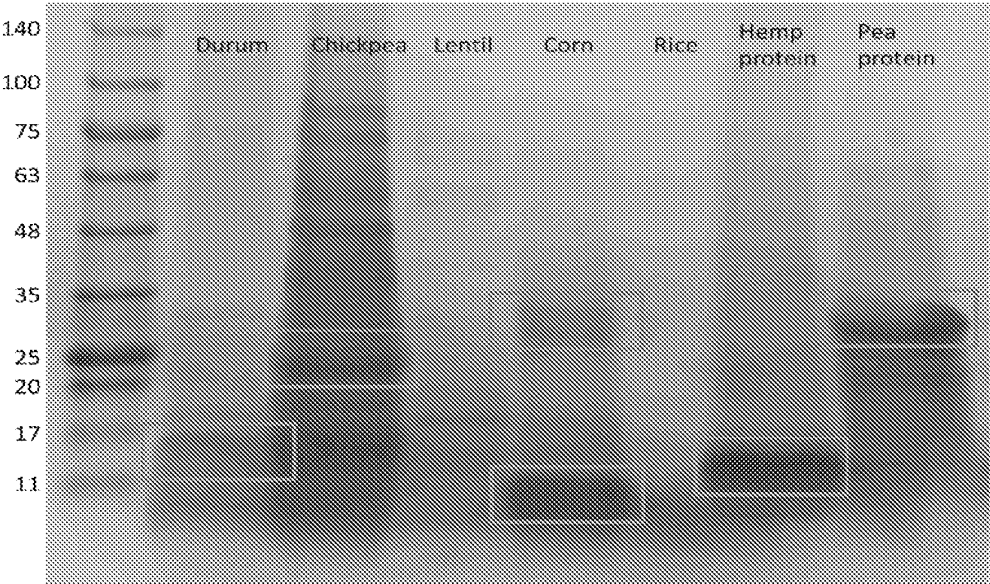


FIG. 5

Protein IDs	Fasta headers	Razor + unique peptides BSA	Razor + unique peptides RB	Razor + unique peptides RJ	Razor + unique peptides WB	Razor + unique peptides WJ	Mol. weight [kDa]
CON_P02769	P02769 Bovine serum albumin	105	39	32	26	32	69.293
tr M1AGX5 M1AGX5_S tr M1AGX5 M1AGX5_S	tr M1AGX5_S tr M1AGX5 M1AGX5_S	14	26	26	27	26	38.234
tr Q2MYP6 Q2MYP6_S tr Q2MYP6 Q2MYP6_S	tr Q2MYP6_S tr Q2MYP6 Q2MYP6_S	3	8	8	7	8	14.901
tr Q9S8K2 Q9S8K2_S tr Q9S8K2 Q9S8K2_S	tr Q9S8K2_S tr Q9S8K2 Q9S8K2_S	1	1	1	1	1	2.3456
tr Q2VBI2 Q2VBI2_S tr Q2VBI2 Q2VBI2_S	tr Q2VBI2_S tr Q2VBI2 Q2VBI2_S	5	8	11	11	10	14.946
tr M1B3W0 M1B3W0_S tr M1B3W0 M1B3W0_S	tr M1B3W0_S tr M1B3W0 M1B3W0_S	3	9	10	8	7	25.642
tr Q2VBI3 Q2VBI3_S tr Q2VBI3 Q2VBI3_S	tr Q2VBI3_S tr Q2VBI3 Q2VBI3_S	3	3	3	3	3	14.857
tr H9B8I9 H9B8I9_S tr H9B8I9 H9B8I9_S	tr H9B8I9_S tr H9B8I9 H9B8I9_S	10	17	19	14	13	20.914
tr A0A097H149 A0A097H149_S tr A0A097H149 A0A097H149_S	tr A0A097H149_S tr A0A097H149 A0A097H149_S	4	10	10	11	9	24.027

FIG. 6

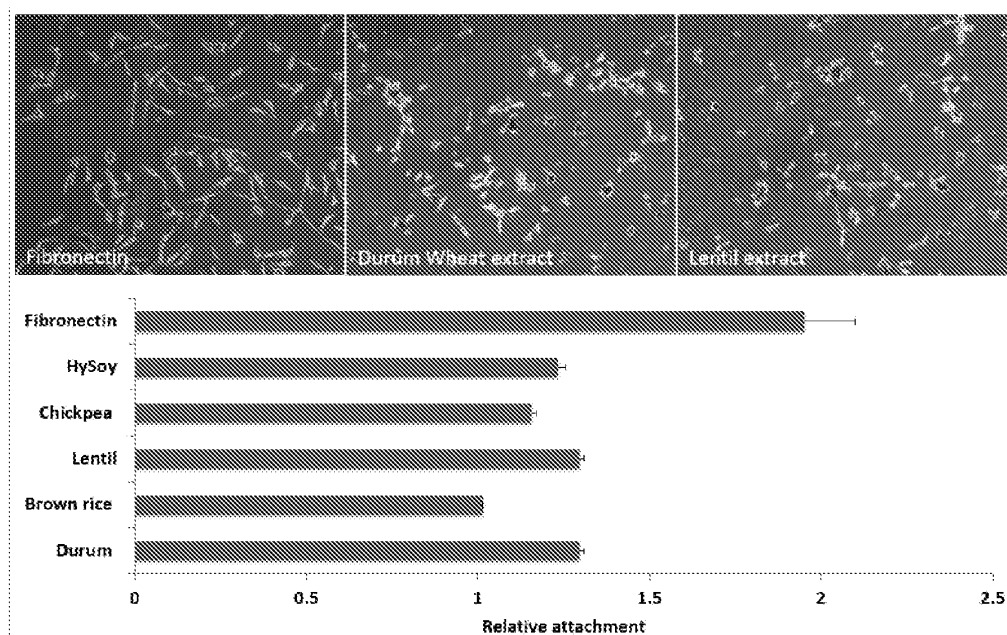


FIG. 7

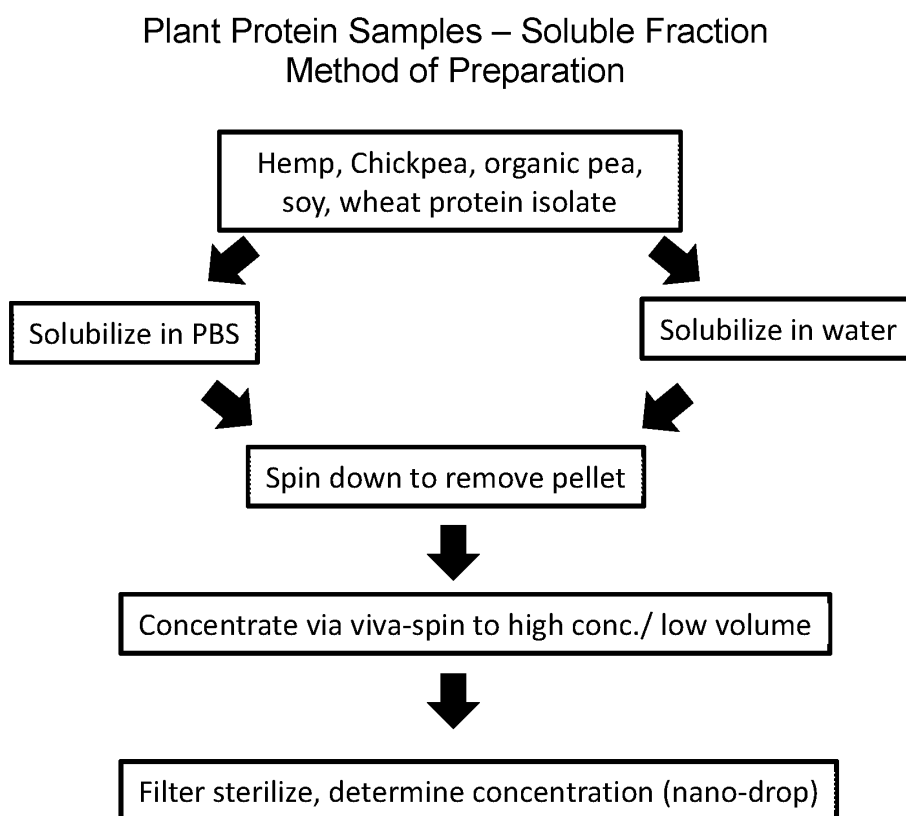


FIG. 8

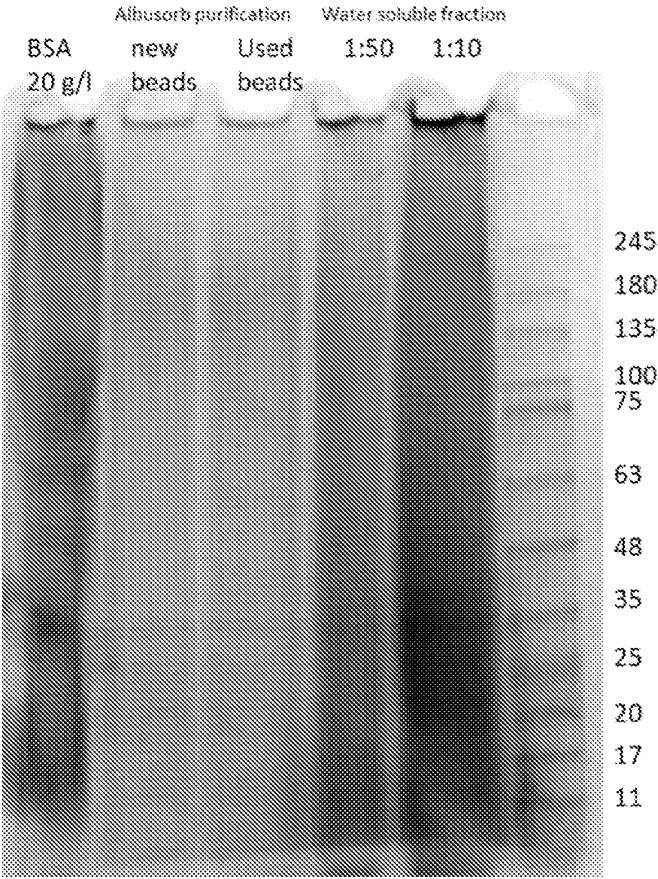


FIG. 9

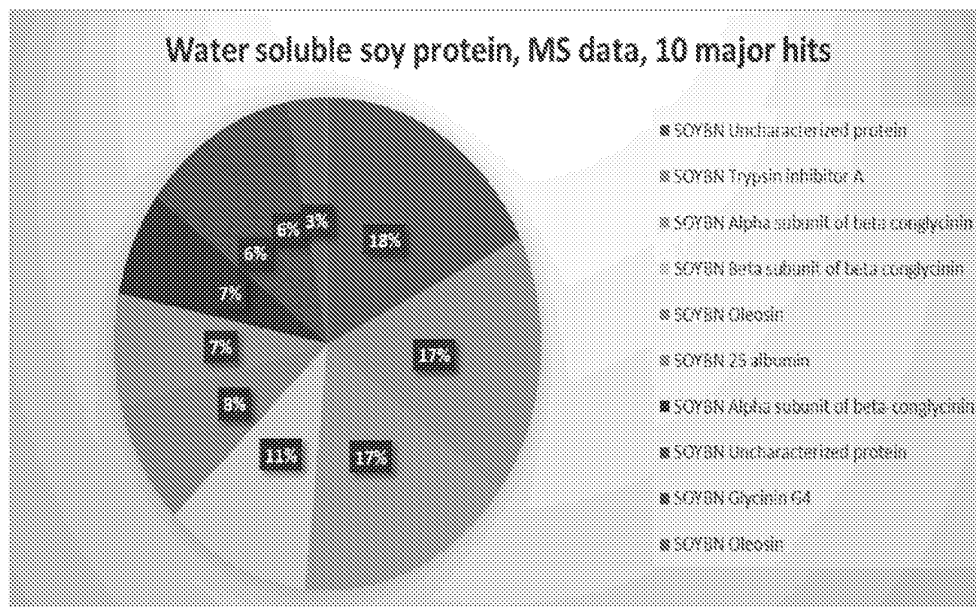


FIG. 10A

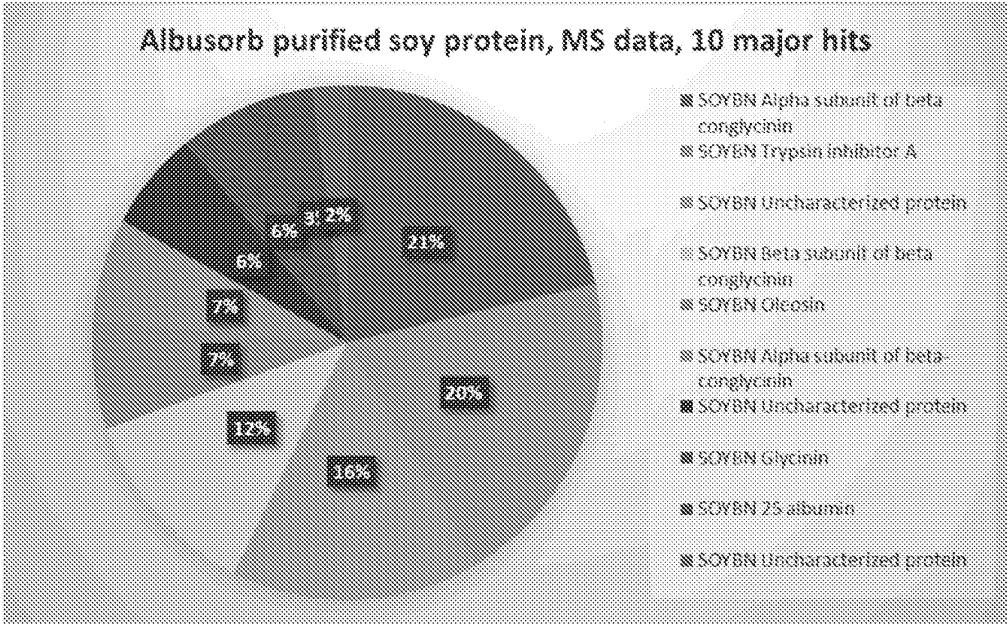


FIG. 10B

10 major hits in water soluble Chickpea proteins

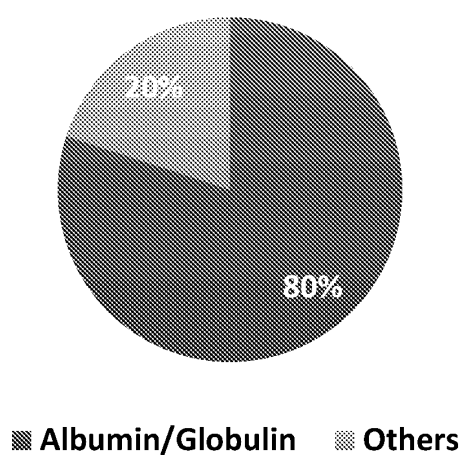


FIG. 11

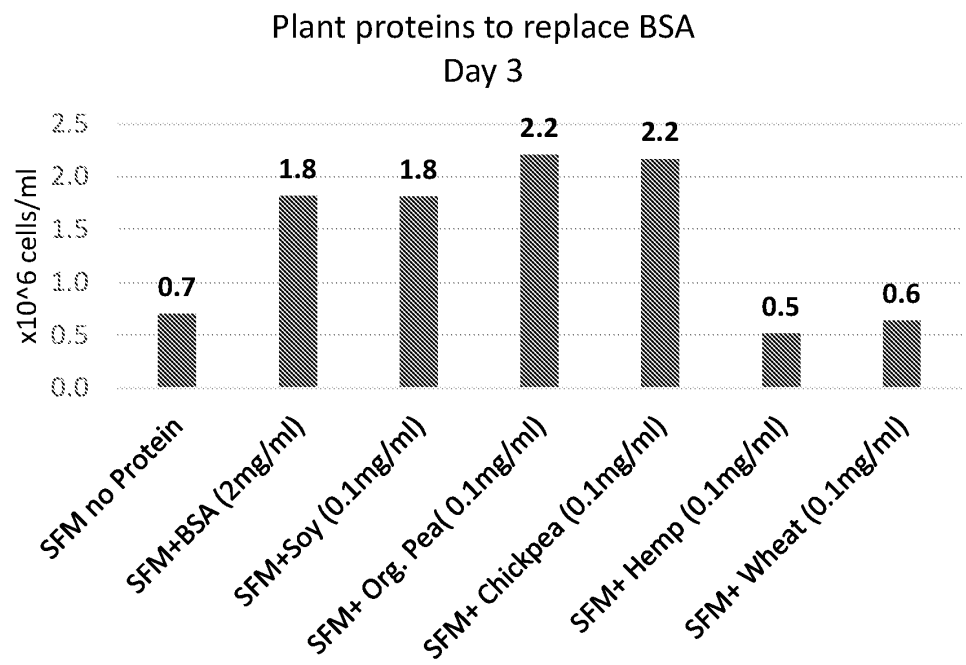


FIG. 12

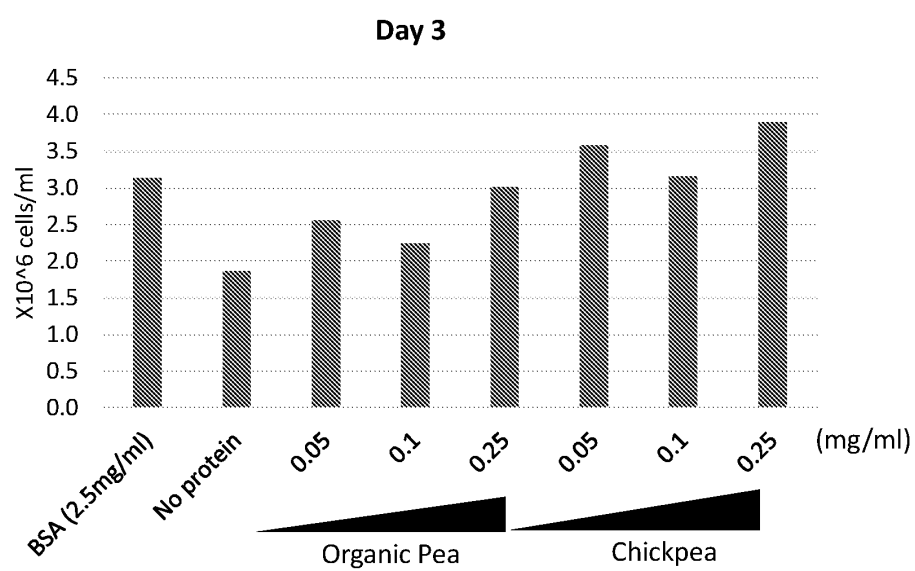


FIG. 13

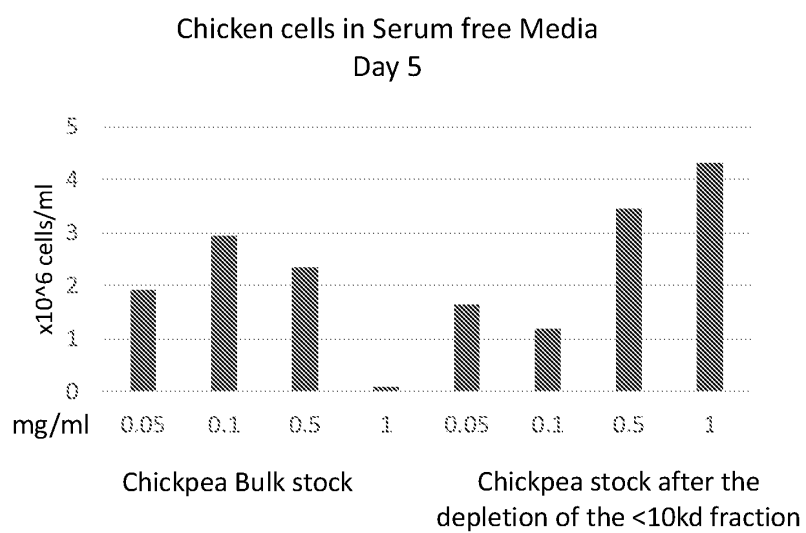


FIG. 14

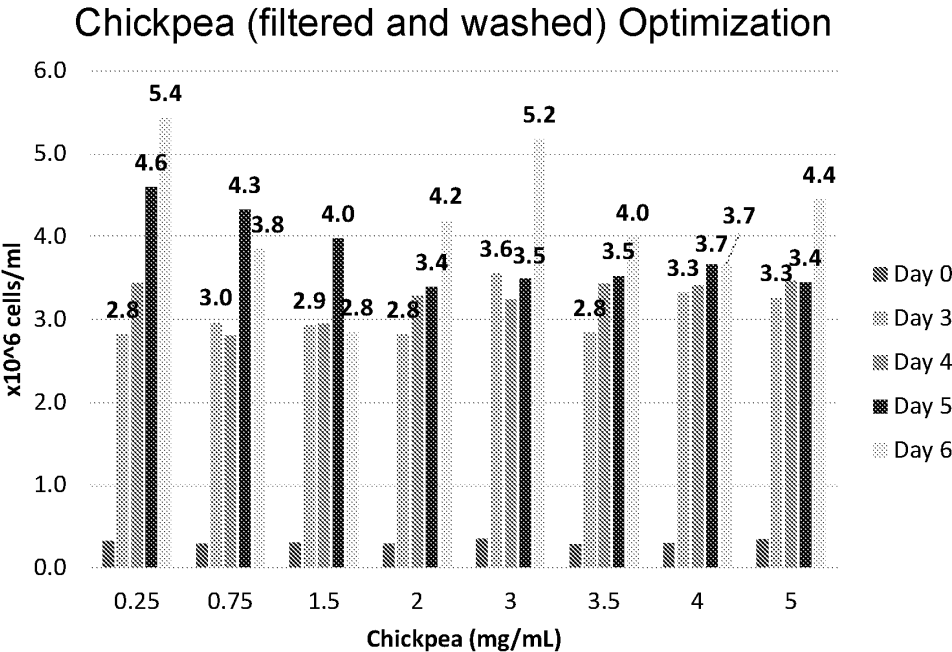


FIG. 15