

Table S1. Frequency of selected bioactive peptides in vegetable proteins and their **A** number.

| | Uniprot Entry | Sequence Lenght | IW | VW | VY | IY | EY | DG | IPI | GW | CG | DW | DE | Total | A |
|-------------------------------|---------------|-----------------|----|----|----|----|----|----|-----|----|----|----|----|-------|-------|
| Soy | | | | | | | | | | | | | | | |
| β -conglitin chain alfa | P11827 | 617 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 6 | 7 | 0.011 |
| β -conglitin chain beta | P25974 | 426 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 3 | 0.007 |
| Albumin 2S | P19594 | 137 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 2 | 0.015 |
| Basic 7S Globulin | P13917 | 403 | 0 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 5 | 0.012 |
| Amaranth | | | | | | | | | | | | | | | |
| 11S Globulin | Q38712 | 501 | 0 | 1 | 1 | 2 | 1 | 1 | 0 | 0 | 0 | 0 | 2 | 8 | 0.016 |
| Oat | | | | | | | | | | | | | | | |
| Avenin 3 | P80356 | 201 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0.005 |
| 11S Globulin | Q38780 | 503 | 0 | 0 | 2 | 2 | 1 | 1 | 0 | 0 | 0 | 0 | 2 | 8 | 0.016 |
| Beans | | | | | | | | | | | | | | | |
| Phaseolin | P80463 | 404 | 0 | 0 | 2 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3 | 0.007 |
| Globulin-1 | A6YNT0 | 224 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 2 | 3 | 0.013 |
| Alpha-zein 16 | P04700 | 242 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0.004 |
| Gamma-zein | C0P381 | 267 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 3 | 0.011 |
| Rice | | | | | | | | | | | | | | | |
| Prolamin PPROLINE 4E | Q0DJ45 | 131 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 0.015 |
| Cupincin | B8AL97 | 436 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 5 | 7 | 0.016 |
| Globulin | P29835 | 164 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 2 | 0.012 |
| Glutelin | Q6T725 | 471 | 0 | 0 | 3 | 1 | 2 | 2 | 0 | 0 | 0 | 0 | 3 | 11 | 0.023 |
| Glutelin Type A-2 | P07730 | 475 | 0 | 0 | 3 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 3 | 8 | 0.017 |
| Glutelin Type B-2 | Q02897 | 481 | 0 | 0 | 4 | 1 | 1 | 2 | 0 | 0 | 0 | 0 | 2 | 10 | 0.021 |
| Maize | | | | | | | | | | | | | | | |
| Globulin-1 S Allele | P15590 | 487 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 2 | 3 | 0.006 |
| 22 kDa alpha zein 4 | O48966 | 245 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.000 |
| 50 kDa gamma zein | C0P381 | 267 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 3 | 0.011 |
| Globulin-2 | Q7M1Z8 | 431 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3 | 4 | 0.009 |
| Globulin-1 | A6YNT0 | 224 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 2 | 3 | 0.013 |

| | | | | | | | | | | | | | | | | |
|----------------------------------|------------|-----|---|---|---|---|---|---|---|---|---|---|---|----|-------|-------|
| 18 kD delta zein | Q946V9 | 190 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.000 |
| Prolamin PPROL 17 | B6UH22 | 164 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 4 | 0.024 | |
| Chickpea | | | | | | | | | | | | | | | | |
| Legumin | Q9SMJ4 | 475 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 7 | 10 | 0.021 | |
| Globulin-1 S Allele | A0A1S2YZ56 | 621 | 0 | 0 | 0 | 1 | 1 | 2 | 0 | 1 | 1 | 0 | 3 | 9 | 0.014 | |
| 11S Globulin seed storage | A0A1S2YGT3 | 348 | 1 | 1 | 2 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | 1 | 7 | 0.020 | |
| Glutelin Type-A 2-Like | A0A1S2YJV5 | 200 | 0 | 1 | 1 | 0 | 0 | 4 | 0 | 0 | 0 | 0 | 0 | 6 | 0.030 | |
| Lentil | | | | | | | | | | | | | | | | |
| Albumin S | P86782 | 37 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.000 | |
| Jack bean | | | | | | | | | | | | | | | | |
| Concanavalina B | P46347 | 299 | 0 | 0 | 3 | 0 | 2 | 2 | 0 | 0 | 1 | 0 | 2 | 10 | 0.033 | |
| Broad Bean | | | | | | | | | | | | | | | | |
| Legumin type B | P05190 | 462 | 0 | 0 | 0 | 2 | 2 | 1 | 0 | 0 | 0 | 0 | 1 | 6 | 0.013 | |
| Vicilin | P08438 | 436 | 0 | 0 | 0 | 1 | 2 | 0 | 0 | 0 | 0 | 0 | 2 | 5 | 0.011 | |
| Convicilin | B0BCL8 | 469 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 4 | 5 | 0.011 | |
| Wheat | | | | | | | | | | | | | | | | |
| Glutenin subunit DX5 | P10388 | 827 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.000 | |
| Avenin-like B1 | Q2A783 | 267 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 0.007 | |
| Alpha/Beta Gliadin | P02863 | 266 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0.004 | |
| Alpha/Beta Gliadin A-I | P04721 | 242 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.000 | |
| Alpha/Beta Gliadin A-II | P04722 | 271 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0.004 | |
| Alpha/Beta Gliadin A-III | P04723 | 262 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0.004 | |
| Alpha/Beta Gliadin A-IV | P04724 | 277 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0.004 | |
| Alpha/Beta Gliadin A-V | P04725 | 299 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0.003 | |
| Glutelin Type A-1 | M7ZVJ6 | 299 | 0 | 1 | 0 | 0 | 0 | 3 | 0 | 0 | 1 | 1 | 0 | 6 | 0.020 | |

Parameter A is the relative frequency of bioactive peptides that can treat metabolic syndrome.

Table S2. The 96 sequences of CNV with a total of 13 modifications generated.

| | |
|-----|---|
| 30. | DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVLDGHHFDIQK PDELWDNLLLEYLYQIKVYQSTFLLSAAPGCLSDEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALIQVLVYLPDLQTRYAGIAL WNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS |
| 31. | DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVLDGHHFDIQK PDELWDNLLLEYLYQIKVYQSTFLLSAAPGCLSDEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALIQVLVYLPDLQTRYAGIAL WNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS |
| 32. | DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVLDGHHFDIQK PDELWDNLLLEYLYQIKVYQSTFLLSAAPGCLSDEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALIQVLVYLPDLQTRYAGIAL WNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS |
| 33. | DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVLDGHHFDIQK PDELWDNLLLEYLYQIKVYQSTFLLSAAPGCLSDEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALIQVLVYLPDLQTRYAGIAL WNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS |
| 34. | DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVLDGHHFDIQK PDELWDNLLLEYLYQIKVYQSTFLLSAAPGCLSDEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALIQVLVYLPDLQTRYAGIAL WNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS |
| 35. | DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVLDGHHFDIQK PDELWDNLLLEYLYQIKVYQSTFLLSAAPGCLSDEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALIQVLVYLPDLQTRYAGIAL WNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS |
| 36. | DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVLDGHHFDIQK PDELWDNLLLEYLYQIKVYQSTFLLSAAPGCLSDEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALIQVLVYLPDLQTRYAGIAL WNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS |
| 37. | DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVLDGHHFDIQK PDELWDNLLLEYLYQIKVYQSTFLLSAAPGCLSDEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALIQVLVYLPDLQTRYAGIAL WNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS |
| 38. | DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVLDGHHFDIQK PDELWDNLLLEYLYQIKVYQSTFLLSAAPGCLSDEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALIQVLVYLPDLQTRYAGIA LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS |
| 39. | DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVLDGHHFDIQK PDELWDNLLLEYLYQIKVYQSTFLLSAAPGCLSDEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALIQVLVYLPDLQTRYAGIA LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS |
| 40. | DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVLDGHHFDIQK PDELWDNLLLEYLYQIKVYQSTFLLSAAPGCLSDEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALIQVLVYLPDLQTRYAGIA LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS |
| 41. | DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVLDGHHFDIQK PDELWDNLLLEYLYQIKVYQSTFLLSAAPGCLSDEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALIQVLVYLPDLQTRYAGIA LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS |
| 42. | DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVLDGHHFDIQK PDELWDNLLLEYLYQIKVYQSTFLLSAAPGCLSDEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALIQVLVYLPDLQTRYAGIAL WNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS |

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

113. DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVYLDGTHFDIQK
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LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS

114. DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVYLDGTHFDIQK
PDELEWDNLLLEYQIKVYQSTFLLSAAPGCLSEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALINQVLVYLPDLQTRYAGIA
LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS

115. DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVYLDGTHFDIQK
PDELEWDNLLLEYQIKVYQSTFLLSAAPGCLSEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALINQVLVYLPDLQTRYAGIA
LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS

116. DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVYLDGTHFDIQK
PDELEWDNLLLEYQIKVYQSTFLLSAAPGCLSEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALINQVLVYLPDLQTRYAGIA
LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS

117. DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVYLDGTHFDIQK
PDELEWDNLLLEYQIKVYQSTFLLSAAPGCLSEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALINQVLVYLPDLQTRYAGIA
LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS

118. DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVYLDGTHFDIQK
PDELEWDNLLLEYQIKVYQSTFLLSAAPGCLSEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALINQVLVYLPDLQTRYAGIA
LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS

119. DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVYLDGTHFDIQK
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LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS

120. DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVYLDGTHFDIQK
PDELEWDNLLLEYQIKVYQSTFLLSAAPGCLSEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALINQVLVYLPDLQTRYAGIA
LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS

121. DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVYLDGTHFDIQK
PDELEWDNLLLEYQIKVYQSTFLLSAAPGCLSEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALINQVLVYLPDLQTRYAGIA
LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS

122. DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVYLDGTHFDIQK
PDELEWDNLLLEYQIKVYQSTFLLSAAPGCLSEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALINQVLVYLPDLQTRYAGIA
LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS

123. DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVYLDGTHFDIQK
PDELEWDNLLLEYQIKVYQSTFLLSAAPGCLSEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALINQVLVYLPDLQTRYAGIA
LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS

124. DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVYLDGTHFDIQK
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LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS

125. DISSTEIAVYWGQRDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVYLDGTHFDIQK
PDELEWDNLLLEYQIKVYQSTFLLSAAPGCLSEYLDNAIQTRHFDYIFVRVYNDRSCQYSTGNIQRIRNAWLWTKSVYPRDWNLFLELPASQATAPGGGYIPPSALINQVLVYLPDLQTRYAGIA
LWNRQADKETGYSTNIIRYLNATAMPFTSNLLKYPS

The sequences showed in blue color are the 5 modified versions closer to native Concanavalin B (Stability, free folding energy and total contacts.

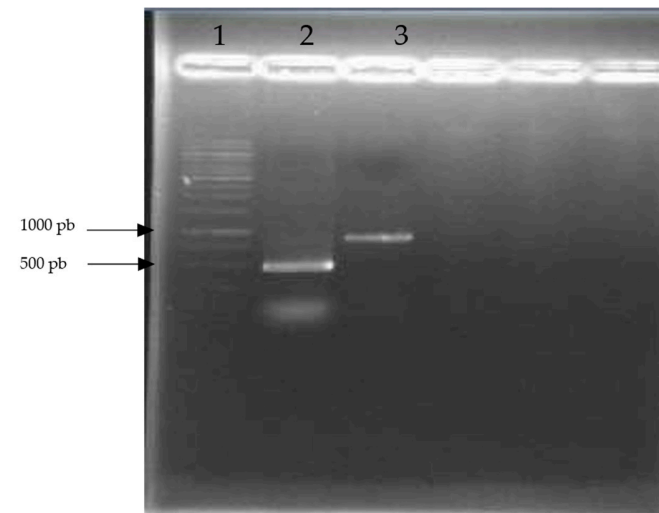


Figure S1. Agarose gel of the PCR product of concanavalin B extracted from leaves. Lane 1: Molecular marker, Lane 2: Positive control, Lane 3: product of PCR.

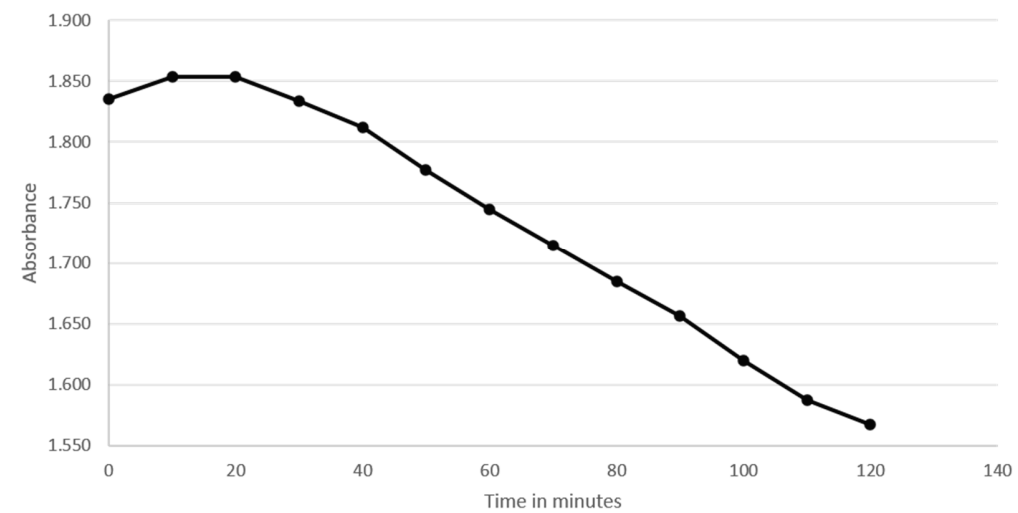


Figure S2. NADPH stability in phosphate buffer pH 7.4 and EDTA 200 mM.