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17      MLIYAKVKCLITGVRTYVGKQSWPELVGTKGKTAAATIDKENAHVTAVLCPPLTTLATCR
9       -----------MSECTDTGKSSWPELVGMNGEEAAAIIMRENPKVTAVVVKEGT----KV
4       ------------MSTECRGKRSWPELVGVPGNAAAATIERENRLVNAIIVPPGN----SV
2       ------------MASECEGKSSWPELLGANGKAAAATIEKENGNVDAILVKEGS----SV
16      -----------MSDNECQGKNSWPELVGVEGKVAAATIERENPLVKANIVPEGS----VV
8       -----------MASDQCEGKSSWPELVGVKGKIAEATIERENPLVDAVIVPKGS----VV
18      -----------MASDECQGKSSWPELVGVKGEIAEATIERENPLVDAVIVPEGS----MV
11      ------------MSSECPGKNSWPELVGTQGDVAAATIERENSNVTAQIVAEGS----AV
12      -------------MSQCKGKRSWPELVGVKGTVAEATIERENSLVNAIVVPQGS----GV
7       ------------MSSECKGKSSWPELVGVQGTVAEATIERENSYVDAVIVPEGS----AV
6       ------------MSDECQGKSSWPELVGVEGKVAEATIQRENPLVDAIIVPEGS----SV
10      ---------------CCAGKSSWPELVGVEGTVAEATIERENSLVDAIIVPKGS----IV
14      ------------MSNVCLGKDSWPELVGAKGDDAAATVEKENKHVHAIVLKEGT----PV
5       MFFNARSR---MSSSGCKGKDSWPELVGAKGEAAAATIEKENPLVNAIVILEGT----AT
1       ------------MSSECEGKDSWPELVGDKGKDAAAMIESENHLVNAVIVKEGT----FV
3       ------------MSSECEGKDSWPELVGDEGKDAAATIESENHLVNAVIVKEGT----FV
13      -----------MASDECKGKSSWPELVGKKGEDAAARIEKENPHVNAVIVLEGS----FV
15      -----------MASDECKGKSSWPELVGKKGEDAAATIEKENPHVNAKIVLEGT----IV
                            ** *****:*  *  * * :  **  * * :    .
17      TFDFRCDRVRVLINRIGGVVTKTPTVG
9       TMEFSCERVRVWVDKINGIVKETPHIG
4       ITDFRCDRVWVFVNG-NGNVTRVPSIG
2       ILDFRCDRVWVWVNE-NGVVTRVPIIG
16      IQDFRCDRVWVWVDK-NGIVKQVPTIG
8       TQDFRCDRVRVWVDE-KGIVYQVPHIG
18      IQDFRCDRVWVWIDK-AGIVKEVPHIG
11      ILDFRCTRVWVWVNE-SGVVTRTPKTG
12      TADFRCDRVWVWVNE-NGFVFQVPTIG
7       ILDFRCDRVWVWVDK-NGIVYRVPTIG
6       PFDFRCDRVWVWINK-DEIVYQVPTIG
10      TADFRCDRVRVWVKK-DGIVYQVPTIG
14      TRDFRCNRVWVWVDE-NGVVTRAPKTG
5       TRDFRCDRVWVWVNH-KGVVTRTPIIT
1       TADFRCDRVRVWVNK-GSIVTKVPIIG
3       TADFRCDRVRVWVNK-RGIVTKVPIIG
13      TADFLCTRVRVWVNT-YGIVTRVPTIG
15      TEDFWCARVRVWVNT-YGIVTRVPIIG
          :* * ** * :.      * ..*
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Supplement Figure 1. The multiple sequence alignment use ClustalW program. Alignment of tartary buckwheat trypsin inhibitor sequences with 1. *Prunus avium* PI (XP_021801866.1) 2. *Jatropha curcas* PI (KDP21344.1) 3. *Prunus persica* TI (ONI26576.1) 4. *Erythranthe guttata* PI (EYU32852.1) 5. *Helianthus annuus* PI1 (OTG36237.1) 6. *Medicago truncatula* TI (XP_003590795.1) 7. *Quercus suber* PI (POE98893.1) 8. *Juglans regia* PI (XP_018813390.1) 9. *Trema orientalis* PI (PON95051.1) 10. *Cajanus cajan* PI (KYP65471.1) 11. *Parasponia andersonii* PI (PON53257.1) 12. *Glycine soja* PI (KHN13145.1) 13. *Theobroma cacao* SPI (EOY18692.1) 14. *Ricinus communis* PI (EEF41424.1) 15. *Durio zibethinus* PI (XP_022764589.1) 16. *Trifolium pratense* TI (PNX72024.1) 17. *Nicotiana sylvestris* TI1 (Q02214.1) 18. *Corchorus olitorius* PI1 (XP_022764589.1). *Fagopyrum tataricum* TI were aligned with Clustalw2 (http://www.ebi.ac.uk/Tools/clustalw/) using default parameters. Asterisks denote residues identical in all sequences and black spots indicate conserved substitutions. Gaps (-) have been inserted to maximize the global alignment.