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P43297_Cysteine_proteinase_RD21A_Arabidopsis      MGFLKPTMAILFLAMVAVSSAVDMSIISYDEKHGVST-TGGRSEAEVMSIYEAWLVKHGK
A0A061FBU0_Cysteine_protease_Theobroma            MGSQRSTMAMLLLVMFTLSSALDMSIISYDEGHPDKSKSIWRTDDEVMAMYEEWLVKHGK

P43297_Cysteine_proteinase_RD21A_Arabidopsis      AQSQNSLVEKDRRFEIFKDNLRFVDEHNEK-NLSYRLGLTRFADLTNDEYRSKYLGAKME
A0A061FBU0_Cysteine_protease_Theobroma            AY--NGLGEKERRFEIFKDNLRFIDEHNADDSHSFKVGLNRFADLTNEEYRAMYLGTKKP

P43297_Cysteine_proteinase_RD21A_Arabidopsis      KKGERRTSLRYEARVGDELPESIDWRKKGAVAEVKDQGGCGSCWAFSTIGAVEGINQIVT
A0A061FBU0_Cysteine_protease_Theobroma            ERKVSKRSDRYAPSLGEELPDSIDWREKGAVAAVKDQGGCGSCWAFSAIAAVEGINKIVT

P43297_Cysteine_proteinase_RD21A_Arabidopsis      GDLITLSEQELVDCDTSYNEGCNGGLMDYAFEFIIKNGGIDTDKDYPYKGVDGTCDQIRK
A0A061FBU0_Cysteine_protease_Theobroma            GDLIVLSEQELVDCDTTYNEGCNGGLMDYAFEFIINNGGIDTEEDYPYTGRDGTCDPYRK

P43297_Cysteine_proteinase_RD21A_Arabidopsis      NAKVVTIDSYEDVPTYSEESLKKAVAHQPISIAIEAGGRAFQLYDSGIFDGSCGTQLDHG
A0A061FBU0_Cysteine_protease_Theobroma            NARVVSIDAYEDVPVNDETALKKAVANQPVSVAIEAGGRAFQLYQSGIFDGKCGTQLDHG

P43297_Cysteine_proteinase_RD21A_Arabidopsis      VVAVGYGTENGKDYWIVRNSWGKSWGESGYLRMARNIA-SSSGKCGIAIEPSYPIKNGEN
A0A061FBU0_Cysteine_protease_Theobroma            VTAVGYGTEKGKDYWIVKNSWGSSWGEEGYIRMARNEANSVTGKCGIAIEASYPIKKGQN

P43297_Cysteine_proteinase_RD21A_Arabidopsis      PPNPGPSPPSPIKPPTQCDSYYTCPESNTCCCLFEYGKYCFAWGCCPLEAATCCDDNYSC
A0A061FBU0_Cysteine_protease_Theobroma            PPNPGPSPPSPIKPPTVCDSYYTCPESNTCCCVYEYYGYCFAWGCCPLEAATCCDDHYSC

P43297_Cysteine_proteinase_RD21A_Arabidopsis      CPHEYPVCDLDQGTCLLSKNSPFSVKALKRKPATPFWSQGRKNIA---
A0A061FBU0_Cysteine_protease_Theobroma            CPHEYPICNINEGTCLMSKGNPLGVKALRRTPAKPFWAHGSVGKKSNA
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Supplementary Figure 5. The alignment was carried out with the amino acid residue sequences of the cysteine proteases from *Theobroma cacao* and *Arabidopsis thaliana* identified by mass spectrometry and interaction network analysis (PPI), respectively. According to the alignment, proteases have 73% identity with each other. The C1 domain of proteases appears underlined with a solid black line, and the granulin domain located in the C-Terminal region is marked with a dashed line.