**Iron is a centrally bound cofactor of specifier proteins involved in glucosinolate breakdown**

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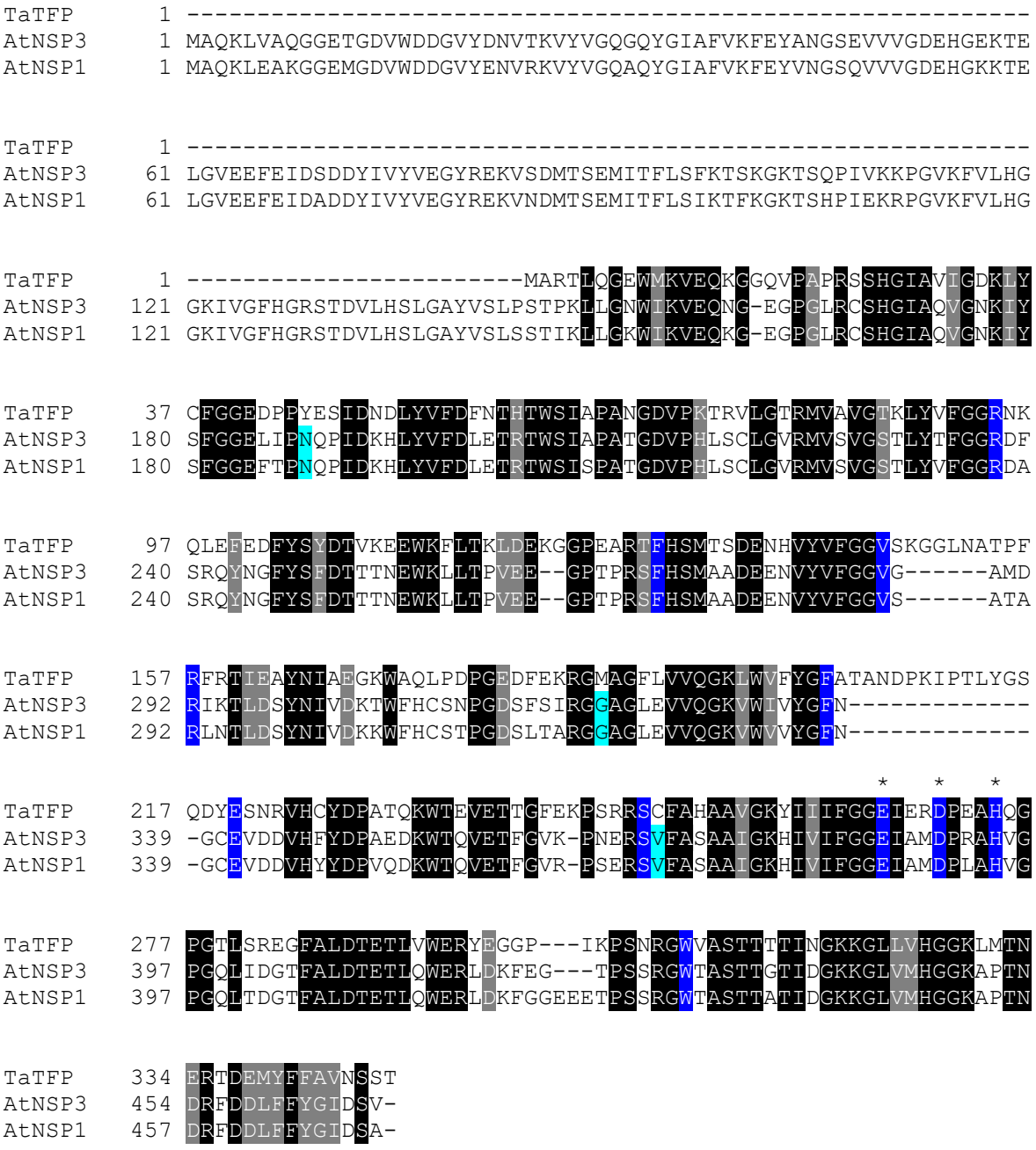


**S4 Fig. Amino acid sequence identity among TaTFP, AtNSP3, and AtNSP1.** Positions shown as active site residues of AtNSP3 in S5 Fig are highlighted with blue background if

identical among all three sequences and with cyan background if identical in only two sequences. The proposed $Fe^{2+}$-binding triad is marked with asterisks above the alignment. Among the other positions, identity of the three sequences is indicated by black background, amino acid similarity by gray background. Amino acid sequences were aligned using ClustalW (https://embnet.vital-it.ch/software/ClustalW.html). Shading was introduced by Boxshade (https://embnet.vital-it.ch/software/BOX_form.html) and color-edited manually.