

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

Anita Backenköhler, Daniela Eisenschmidt, Nicola Schneegans, Matthias Strieker, Wolfgang Brandt, and Ute Wittstock

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TaTFP      1  -----
AtNSP3    1  MAQKLVAQGGETGDVWDDGVYDNVTKVYVVGQGYGIAFVKFEYANGSEVVVGDHGEKTE
AtNSP1    1  MAQKLEAKGGEMGDVWDDGVYENVRKVYVVGQAQYGIAFVKFEYVNGSQVVVGDHGGKTE

TaTFP      1  -----
AtNSP3    61  LGVEEFEIDSDDYIVYVEGYREKVSDMTSEMITFLSFKTSKGKTSQPIVKKPGVKFVLHG
AtNSP1    61  LGVEEFEIDADDYIVYVEGYREKVNDMTSEMITFLSIKTFKGKTSHPIEKRPGVKFVLHG

TaTFP      1  -----MARTLQGEWMKVEQKGGQVPAPRSSHGIAVIGDKLY
AtNSP3    121  GKIVGFHGRSTDVHLHSLGAYVSLPSTPKLLGNWIKVEQNG-EGPGLRCSHGIAQVGNKLY
AtNSP1    121  GKIVGFHGRSTDVHLHSLGAYVSLSTIKLLGKWKIKVEQKG-EGPGLRCSHGIAQVGNKLY

TaTFP      37  CFGGEDPPYESIDNDLYVDFNTHHTWSIAPANGDVPKTRVLGTRMVAVGTIKLYVFGGRNK
AtNSP3    180  SFGGELIPNQPIDKHLYVDFLETRTWSIAPATGDVPHLSCLGVRMVS VGSTLYTFGGRDF
AtNSP1    180  SFGGEFTPNQPIDKHLYVDFLETRTWSISPATGDVPHLSCLGVRMVS VGSTLYVFGGRDA

TaTFP      97  QLEFEDFYSDTVKEEWKFLTKLDEKGGPEARTFHSMTSDENHVYVFGGVSKGGLNATPF
AtNSP3    240  SRQYNGFYSDFTTTNEWKLLTPVEE--GPTPRSFHSMAADEENVYVFGGVG-----AMD
AtNSP1    240  SRQYNGFYSDFTTTNEWKLLTPVEE--GPTPRSFHSMAADEENVYVFGGVSA-----ATA

TaTFP      157  RFRITIEAYNIAEGKWAQLPDPGDFEKRGMAGFLVVOGKLWVYGFATANDPKIPTLYGS
AtNSP3    292  RIKTLDSYNIVDKTWFHCSNPGDSFSIRGCAGLEVVOGKVVVYGFN-----
AtNSP1    292  RLNTLDSYNIVDKKWFHCSTPGDSLARGCAGLEVVOGKVVVYGFN-----

TaTFP      217  QDYESNRVHCYDPATQKWTVEVETTGFEKPSRRSCFAHAAVGKYIIIFGGEIERDPEAHQ*
AtNSP3    339  -GCEVDDVHFYDPAEDKWTQVETFGVK-PNERSVFASAALGKHIVIFGGEIAMDPRAHV*
AtNSP1    339  -GCEVDDVHYYPVQDKWTQVETFGVVR-PSERSVFASAALGKHIVIFGGEIAMDPLAHV*

TaTFP      277  PGTLSREGFALDTETLVWERYEGGP---IKPSNRGWVASTTTTINCKKGLLVHGKLMTN
AtNSP3    397  PGQLIDGTFALDTETLQWERLQDKFEG---TPSSRGWTASTTGTIDGKKGLVMHGKAPT*
AtNSP1    397  PGQLIDGTFALDTETLQWERLQDKFGGEEETPSSRGWTASTTATIDGKKGLVMHGKAPT*

TaTFP      334  ERTDEMYFFAVNSST
AtNSP3    454  DRFDDLFFYGIDSV-
AtNSP1    457  DRFDDLFFYGIDSA-

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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 Fe²⁺-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.