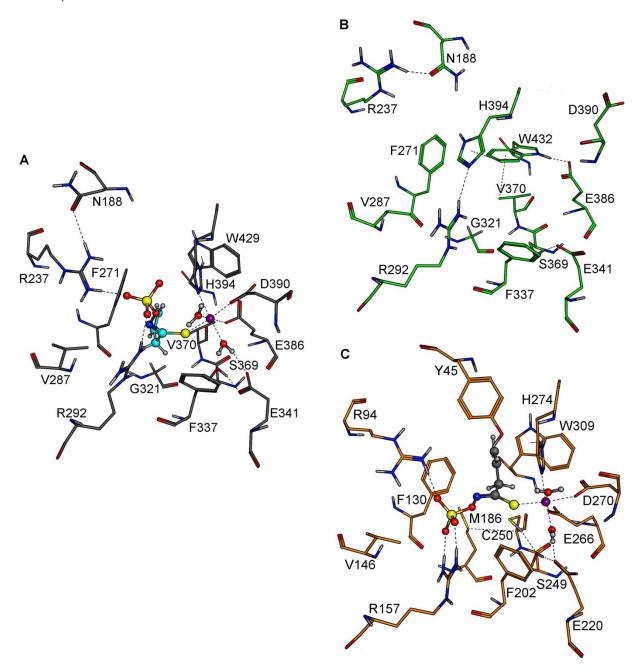
## Iron is a centrally bound cofactor of specifier proteins involved in glucosinolate breakdown

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



S5 Fig. Active site of AtNSP3 in comparison with those of TaTFP and AtNSP1.  $(\mbox{\ensuremath{A}})$ 

Model of the AtNSP3 active site with docked Fe<sup>2+</sup> and allylglucosinolate aglucone. (B) AtNSP1 active site as represented in the crystal structure (PDB 5GQT, [36]). (C) TaTFP

active site with docked Fe<sup>2+</sup> and allylglucosinolate aglucone [34] derived from the crystal structure (PDB 5A10). An alignment of the three amino acid sequences is provided in S4 Fig.