The structural panorama of L-asparaginases includes an alien from nitrogen-fixing bacteria

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L-Asparaginases from bacterial periplasm (e.g. EcAII) have high L-asparagine affinity and are used as potent antileukemic drugs. Plants possess a different, Ntn class of asparaginases, which are also found in bacteria (e.g. EcAIII). It was predicted ~20 years ago that *Rhizobium etli*, a bacterial symbiont of legume plants that is capable of nitrogen fixation, will possess yet another, R.etli-type L-asparaginase. The crystal structure of this enzyme, ReAII, reveals a dimeric protein that is indeed completely different from the EcAII and EcAIII prototypes, with structural resemblance to some serine β-lactamases and glutaminases. The presumed active site is organized around S48, which is surrounded by three tightly H-bonded water molecules and is further H-bonded to N134. Near-by there is a tandem of Cys residues coordinating a zinc cation. The coordination sphere is completed by a water molecule and a Lys side chain. Another Lys residue penetrates the active site to provide an H-bond link to S48. C225 of this Cys-rich protein also bears an unknown posttranslational modification.

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