

Overview

This report contains a secondary structure assignment of diphtheria toxin (DT) and a comparison of the structure of diphtheria toxin to exotoxin A (ExoA) of *Pseudomonas aeruginosa*. The sequence numbers of the domains of the two proteins and the corresponding structural and functional categorizations are summarized in Table 1.

Our analysis shows that there is no first-order sequence homology between DT and Exo A, but the two proteins are very similar in that the structural topology of both the ADP-ribosylating domain and the receptor-binding domain have been conserved. The lack of obvious homology is due to the fact that the sequences have diverged considerably so the catalytic domain which is responsible for ADP-ribosylation is positioned differently in the two proteins. The catalytic domain in DT is comprised of residues from the amino-terminus of the protein, whereas the the catalytic domain of ExoA is comprised of residues from the carboxy-terminus. The structural correspondence between the two proteins is greatest in this region.

Our analysis also shows that the difference in structural arrangement between the two proteins extends to the components of the structures which stabilize the interactions between the catalytic domain and the rest of the protein. Because the catalytic domains of the two proteins are formed from different residues in the sequence, the residues which form the interface between the catalytic domain and the rest of the protein are also different in composition and structure.