**Vector Alignment Search Tool (VAST): An Information Resource for Protein Structure Comparison**

Thomas Madej, Eric W. Sayers, Stephen H. Bryant

**NCBI** - National Center for Biotechnology Information (NCBI) - National Library of Medicine - National Institutes of Health - Department of Health and Human Services

**VAST** is the algorithm used in structure neighboring services provided by NCBI. It is an efficient way to search for similar protein structures. VAST is included in the structure comparison server, and can be used to quickly search for similar protein structures to any query sequence.

VAST is also used to identify the neighbors of a query sequence. VAST is used to identify the neighbors of a query sequence. VAST is used to identify the neighbors of a query sequence.

**Preparing Data for VAST**

- **Figure 3:** Example of a protein structure
- **Figure 4:** Example of a protein structure
- **Figure 5:** Example of a protein structure

**Viewing VAST Neighbors**

- **Figure 6:** Example of a protein structure
- **Figure 7:** Example of a protein structure
- **Figure 8:** Example of a protein structure

**PubVAST Statistics**

PubVAST is a database of pre-computed VAST results. It contains over 120 million and contains the results of pre-computed VAST searches of all known protein structures in the NCBI Protein Data Bank.

- More than 40,000 structure pairs
- More than 80,000 structure pairs
- More than 50,000,000 structure alignments

**Web Addresses**

To access VAST pre-computed alignments:


To submit user-generated PDB files to a VAST search: