

# PASSC

## PASSC (Pair-to-Pair Alignment of Sequence-Structure Correlation)

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### Introduction

PASSC is a FASTA program which uses the substitution frequency of pairs of residues, rather than a single residue, in the dynamic programming algorithm and it runs the Smith-Waterman algorithm in the SSEARCH part for the alignment routine. Blosum62, Hk2 and Tk2 matrices are used in the program and gaps are not allowed in helices and beta strand. Default values were used for the gap penalties and the statistical parameters as given in the FASTA program. PASSC performs similarly to FASTA when the probe and target sequences have more than 30% identity; however, it finds significantly more sequences with identities below 30% that are structurally homologous. The original publication is: Jung, J. and Lee, B. Use of residue pairs in protein sequence-sequence and sequence-structure alignments. *J. Protein Science*. 9: 1576-88, 2000. [PubMed Abstract](#), [Full Text](#)