

PACKAGE ID - 001063SPARC00 PYTHIA

KWIC TITLE - Identification of Human Repetitive DNA
Elements

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LIMITATION CODE -COPY **AUDIENCE CODE** - LIM

COMPLETION DATE - 08/01/1991 **PUBLICATION DATE** - 08/01/1991

DESCRIPTION - PYTHIA identifies the subfamily membership of Alu
sequences, occurrences of repetitive human DNA elements, and
simple DNA sequences.

PACKAGE CONTENTS - Media Directory; Software Abstract; Media Includes
Source Code;

SOURCE CODE INCLUDED? - No

MEDIA QUANTITY - 1 3.5 Diskette

METHOD OF SOLUTION - The algorithmic significance method is used for
recognizing sequence similarity and simple DNA regions. Standard
DNA sequence alignment is accomplished using a dynamic programming
algorithm.

COMPUTER - SUN SPARC

OPERATING SYSTEMS - Sun UNIX

PROGRAMMING LANGUAGES - C, C++

SOFTWARE LIMITATIONS - No particular limitations.

SOURCE CODE AVAILABLE (Y/N) - N

UNIQUE FEATURES - This set of programs addresses similar and very
specialized programs in DNA sequence analysis.

RELATED SOFTWARE - The initial version of the software was developed at
Linus Pauling Institute.

OTHER PROG/OPER SYS INFO - PYTHIA requires the standard
publicly-available cC and C++ libraries as well as
publicly-available modules that are included in the lib, libm, and
libf libraries.

HARDWARE REQS - Minimum of 4Mbytes RAM and 10 Mbytes disk storage are
needed.

TIME REQUIREMENTS - Typical requests are answered within one minute,
except for identifications of repetitive elements, which currently

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TIME REQUIREMENTS - (CONT) takes a few hours of CPU time.

ABSTRACT STATUS - Released AS-IS 02/12/96

SUBJECT CLASS CODE - V

KEYWORDS -

COMPUTER PROGRAM DOCUMENTATION
P CODES
DNA SEQUENCING

EDB SUBJECT CATEGORIES -

990200 550400

SPONSOR - DOE/EH

PACKAGE TYPE - AS - IS