: (fold recognition)

1.

(protein tertiary structure prediction)
(fold recognition) [1] .
(low sequence similarity)
(homology) .
, (remote homology
distant homology) fold recognition
.
.

fold recognition "
, PDB(Protein Data
Bank) "
. PDB
( ) .
(query)

,
(template) query
(query
fold recognition) template
query . query
template .

fold recognition .
threading(optimal sequence threading ,
threading) [2,3,4,5]
- (profile-profile alignment)
[6,7,8,9] . threading ,

-

. threading

fold recognition ,

threading   fold   recognition

.   -

fold recognition   .

2. threading

threading   .

(fold database   fold library;   "
(domain   boundary)   "   )   ,
(score   function   knowledge- based   potential)   .
(fold   library)
(fold)   .   1000
. query   ,   query

.   query

,   .

,

query   template   .

,

query

,

template   . template
MODELLER   comparative modeling
query   .
query   ,   (training)
.

,   (solvent accessibility)
. threading

.

threading   THREADER   [3,5].
THREADER   (version   3.5)
"http://bioinf.cs.ucl.ac.uk/threader"   .
THREADER   GenTHREADER   mGenTHREADER
      (http://bioinf.cs.ucl.ac.uk/psipred/psiform.html)
         .   threading   FUGUE2(Profile Library
Search   Against   HOMSTRAD   version   2;   http://www-
cryst.bioc.cam.ac.uk/fugue/prfsearch.html),   3D-PSSM(Three-Dimensional
Position-Specific   Scoring   Matrix;
http://www.sbg.bio.ic.ac.uk/~3dpssm/html/ffrecog_simple.html),
PHYRE(Protein   Homology/analogY   Recognition   Engine;
http://www.sbg.bio.ic.ac.uk/~phyre/)   .
                        .

3.   -

      threading   1990   ,   -
      (profile-profile alignment)   2000
fold recognition   . threading

                                           .
                  -                                  .   -

                                                    ,   template
                  .   PSI-BLAST(
      "   : BLAST   (profile)"   )
      "   "(position-specific scoring matrix)
      .   PSI-BLAST   HMM(Hidden Markov Model)
          [6].

             -                    query

                                  .
                             query
                         template   .
      -
          (query   ,

)   [8].

DSSP(

"   (secondary structure)   "   )

          .

          (http://www.cheric.org),   -

                                    .

                    -

FFAS03(Fold and Function Assignment System)[7]   SAM-T02(HMM-
based Protein Structure Prediction)[6]   . FFAS03
                    PSI-BLAST   , SAM-T02   HMM
                              .   (FFAS03   →
http://ffas.ljcrf.edu/ffas-cgi/cgi/ffas.pl;   SAM-T02   →
http://www.cse.ucsc.edu/research/compbio/HMM-apps/T02-
query.html)   .   -
                    (support vector machine)
          [9].

    4.

                              fold recognition   (meta
server)   .   threading
              -   ,
                              .

                    3D-Jury   [10].   3D-Jury
      (http://bioinfo.pl/Meta/)   .

    [   ]

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