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MAX-PLANCK-GESELLSCHAFT

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☐ 27005a

MSAP

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MSAP

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Bioinformatics Toolkit

Max-Planck Institute for Developmental Biology

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MSAProbs - Results

Job-ID: 27005a

Date: 08:17 on Oct 12 2015

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Select all

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Select the best ten

Number of sequences: 2

MSAPROBS version 0.9.7 multiple sequence alignment

☒ 27005

GKSNVLVTMPVAPTMEVKSFPILDQCVGQVGLNFELSFTGAPPPYYNTKIYKLENGERKL

☒ nmr

-----RVKPSASLKLHHDCLKCLGDHS-SVPVALKGGQPFLLTYDI IETFSSKRKT

\* \*: .:\* . \*. \*::: . . . :::\* \*: . . \* : . . : \*\*

☒ 27005

YDAKRYTSEGTRNRFYSPP---KEGNYEIVFDIVSNKLFTEPI-KLEPVKEYTFKISM

☒ nmr

FEIKEIKT----NEYVIKTPVFTTGGDYILSLVSIK--DSTGCVVGLSQPDAKIQVRD

:: \*. .: \*.: . .\* . \*:\* : : ::. \* : \*. .

Yongchao Liu ,Bertil Schmidt and Douglas L. Maskell MSAProbs: multiple sequence alignment based on pair hidden Markov models and partition function posterior probabilities. Bioinformatics (2010) 26 (16): 1958-1964.

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