Date: Mon, 25 Aug 2003 16:41:49 +0100 From: Apache <psipred@cs.ucl.ac.uk>

To: aprilb@biology2.wustl.edu Subject: casp1 PSIPRED Results

PSIPRED PREDICTION RESULTS

Key

Conf: Confidence (0=low, 9=high)

Pred: Predicted secondary structure (H=helix, E=strand, C=coil)

AA: Target sequence

Conf: 91355422117878622513578998987742378888888885315168999999999

Pred: ССИНИНИНИНИНИНИССИНИНИНИНИНИНИНИССССИНИНИНИНИНСССИНИНИНИНИНИ

AA: MADKVLKEKRKLFIRSMGEGTINGLLDELLQTRVLNKEEMEKVKRENATVMDKTRALIDS 10 60

30 50 20 40

Conf: 753062268899999860063123331146665446777566566677767768861233

AA: VIPKGAQACQICITYICEEDSYLAGTLGLSAAPQAVQDNPAMPTSSGSEGNVKLCSLEEA

70 80 90 100 110 120

Conf: 311345775301221378996179997263455666678707999999999986797899

AA: ORIWKOKSAEIYPIMDKSSRTRLALIICNEEFDSIPRRTGAEVDITGMTMLLONLGYSVD

130 140 150 160 170 180

Conf: 71699889999999998611137898899998326857503035675346664029899

AA: VKKNLTASDMTTELEAFAHRPEHKTSDSTFLVFMSHGIREGICGKKHSEOVPDILOLNAI

190 200 210 220 230 240

Conf: 998730467543579738999677898888606614776665444566320003443546

AA: FNMLNTKNCPSLKDKPKVIIIOACRGDSPGVVWFKDSVGVSGNLSLPTTEEFEDDAIKKA

260 280 250 270 290

Conf: 7888758997179982120279988778999999982078863899999999960655

AA: HIEKDFIAFCSSTPDNVSWRHPTMGSVFIGRLIEHMOEYACSCDVEEIFRKVRFSFEOPD

330 340 350 310 320

Conf: 77216605454412387842799

Pred: CCCCCCEEEEEEEEECCCC

AA: GRAOMPTTERVTLTRCFYLFPGH

370 380 Calculate PostScript, PDF and JPEG graphical output for this result using:

http://bioinf.cs.ucl.ac.uk/cgi-bin/psipred/gra/nph-view2.cgi?id=106182572827327