

Date: Thu, 4 Sep 2003 21:22:48 +0100
From: Apache <psipred@cs.ucl.ac.uk>
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Subject: hprt1 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: 9777870587017888765656665101100011307898999999999999972899
Pred: CCCCCCEEEEECCCCCCCCCCCCCHHHHHHHEEECHHHHHHHHHHHHHHHHHHHHCCC
AA: MATRSPGVVISDDEPGYDLDFCIPNHYAEDLERVFIPHGLIMDRTERLARDVMKEMGGH
10 20 30 40 50 60

Conf: 8289996566669999999999863102445677531258998714897324651686247
Pred: CEEEEEECCCCCHHHHHHHHHHHHHHHCCCCCCCCCEEEEEEECCCCCCCCCEEEEECC
AA: HIVALCVLKGGYKFFADLLDYIKALNRNSDRSIPMTVDFIRLKSVCNDQSTGDIKVIIGD
70 80 90 100 110 120

Conf: 731037986899736631279999999999728961389999711663457898553799
Pred: CCCCCCCEEEEECCCCCHHHHHHHHHHHHHHHCCCCCEEEEEEECCCCCCCCCCCCCEEE
AA: DLSTLTGKNVLIVEDIIDTGKTMQTLLSLVRQYNPKMVKVASLLVKRTPRSVGYKPDFVG
130 140 150 160 170 180

Conf: 97788879973788656630588238767325323689
Pred: EECCCCCEEECCCCCHHHHHCCCCCEEECHHHHCCCCC
AA: FEIPDKFVVGVALDYNEYFRDLNHVCVISETGKAKYKA
190 200 210

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=106270684412307>