

LOCTREE 3

Protein Subcellular Localization Prediction System

Protein ID	Score	Expected Accuracy	Localization Class	Gene Ontology Terms	Annotation Type
TgNAC01	56	92%	nucleus	nucleus GO:0005634(IDA);	PSI-BLAST

Predicted Localization: nucleus



>NAC29_ARATH

Identities = 86/138 (62%), Positives = 101/138 (73%), Gaps = 6/138 (4%)

Query: 11 VLRLPPGFRFHPTDEELVQYLKRVLSCLPASIIPEVDVCKSDPWLGD----SEQR 66
LPPGFRFHPTDEEL+V YL+ + +S P P SIIPEVD+ K DPW L + E E

Sbjct: 6 QSTLPPGFRFHPTDEELIVYYLRNQTMSKPCPVSIPEVDIYKFDPWQLPEKTEFGENEW 65

Query: 67 YFFSTREIKYPNGNRSNRATVSGYWKATGLDKQIVSTRSHQIVGMKKTTLVFYRGKPPKGC 126
YFFS RE KYPNG R NRA VSGYWKATG DK I S S+ VG+KK LVFY+G+PPKG

Sbjct: 66 YFFSPRERKYPNGVRPNRAAVSGYWKATGTDKAIHSGSSN--VGKKALVFYKGRPPKGI 123

Query: 127 RTDWIMHEYRLITAQNSA 144
+TDWIMHEYRL ++ ++

Sbjct: 124 KTDWIMHEYRLHDSRKAS 141