Your input sequence (1050aa) is:

>query protein 2;
MSSWNYVVTAHKPTSVTHSCVGNFTSPQELNLIVAKCTRIEIHLLTPQGLQPMLDVPIYG
RIATLELFRPHGETQDFLFIVTERHKFCVLQWDAESSELVTRAMGDVSDRIGRPTDNGQI
GIIDPDCRLIGLHLYDGLFKVIPFDNKGQLKEAFNIRLEELQVLDIKFLFGCAKPTIAVL
YQDNKDARHVKTYEVSLKDKDFVEGPWSQNNLDNGADLLIPVPPPLCGVLIIGEETIVYC
SANAFKAIPIRPSITKAYGRVDVDGSRYLLGDHAGLVHLLVITHEKEKVTGLKIELLGET
SIASTISYLDNAVVFVGSSYGDSQLVKLNLHPDAKGSYVEVLERYTNLGPIVDFCVVDLE
RQGQGQVVTCSGAFKDGSLRIVRNGIGINEQASVELEGIKGMWSLKSSVDEAFDTFLVVS
FISETRILAMNLEDELEETEIEGFLSQLQTLFCHDAVYNQLVTSNSVRLVSSTTRELRDE
WHAPAGFTVNVATANASQVLLATGGGHLVYLEIGDGKLTEVQHTVLEYEVSCLDINPIGD
NPNYSQLASVGMWTDISVRIFSLPELTLITKEQLGGEIIPRSVLLCSFEGISYLLCALGD
GHLLNFQLDTTTGQLKDRKKVSLGTQPITLRTFSSKSATHVFAASDRPTVIYSSNKKLLY
SNVNLKEVSYMCPFNSAAFPDSLAIAREGELTIGTIDDIQKLHIRTIPLGEHARRICHQE
QTRTFGICSLGNQTNAEESEMHFVRLLDDQSFEFMSTYPLDAFEYACSILSCSFTDDKNV
YYCVGTAYVLPEENEPTKVSSFFETSSLSSQKVITCFLCMQGRILVFIVEDAKLQLIAEK
ETKGAVYSLNAFNGKLLAAINQKIQLYKWMLRDDGTRELQSECGHHGHILALYVQTRGDF
IVVGDLMKSISLLIYKHEEGAIEERARDYNANWMSAVEILDDDTYLGAENNFNLLTVKKN
SEGATDEERGRLEVVGEYHLGEFVNRFCHGSLVMRLPDSEIGQIPTVIFGTVNGMIGVIA
SLPQEQYAFLEKLQSSLRKVIKGEQDGGDI

----------- Plant-mPLoc Computation Result -----------

Query protein	Predicted location(s)
query protein 2;	**Nucleus.**

query :
MSSWNYVVTAHKPTSVTHSCVGNFTSPQELNLIVAKCTRIEIHLLTPQGLQPMLDVPIYG
RIATLELFRPHGETQDFLFIVTERHKFCVLQWDAESSELVTRAMGDVSDRIGRPTDNGQI
GIIDPDCRLIGLHLYDGLFKVIPFDNKGQLKEAFNIRLEELQVLDIKFLFGCAKPTIAVL
YQDNKDARHVKTYEVSLKDKDFVEGPWSQNNLDNGADLLIPVPPPLCGVLIIGEETIVYC
SANAFKAIPIRPSITKAYGRVDVDGSRYLLGDHAGLVHLLVITHEKEKVTGLKIELLGET
SIASTISYLDNAVVFVGSSYGDSQLVKLNLHPDAKGSYVEVLERYTNLGPIVDFCVVDLE
RQGQGQVVTCSGAFKDGSLRIVRNGIGINEQASVELEGIKGMWSLKSSVDEAFDTFLVVS
FISETRILAMNLEDELEETEIEGFLSQLQTLFCHDAVYNQLVTSNSVRLVSSTTRELRDE
WHAPAGFTVNVATANASQVLLATGGGHLVYLEIGDGKLTEVQHTVLEYEVSCLDINPIGD
NPNYSQLASVGMWTDISVRIFSLPELTLITKEQLGGEIIPRSVLLCSFEGISYLLCALGD
GHLLNFQLDTTTGQLKDRKKVSLGTQPITLRTFSSKSATHVFAASDRPTVIYSSNKKLLY
SNVNLKEVSYMCPFNSAAFPDSLAIAREGELTIGTIDDIQKLHIRTIPLGEHARRICHQE
QTRTFGICSLGNQTNAEESEMHFVRLLDDQSFEFMSTYPLDAFEYACSILSCSFTDDKNV
YYCVGTAYVLPEENEPTKVSSFFETSSLSSQKVITCFLCMQGRILVFIVEDAKLQLIAEK
ETKGAVYSLNAFNGKLLAAINQKIQLYKWMLRDDGTRELQSECGHHGHILALYVQTRGDF
IVVGDLMKSISLLIYKHEEGAIEERARDYNANWMSAVEILDDDTYLGAENNFNLLTVKKN
SEGATDEERGRLEVVGEYHLGEFVNRFCHGSLVMRLPDSEIGQIPTVIFGTVNGMIGVIA
SLPQEQYAFLEKLQSSLRKVIKGEQDGGDI

Final results predicted by INSP			
Predicted NLS peptide	START	END	SCORE
RGRLEV	969	974	0.70241

The model predicts NLS by the consensus model combined by large-scale frequent pattern mining model and statistical knowledge-based and machine learning SVM-based model with merging.

Supplementary Fig 3 The predicted localization of BrDDB1A was in the nucleus.