Your input sequence (1050aa) is:

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

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

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

query:
MSSWNYVVTAHKPTSVTHSCVGNFTSPQELNLIVAKCTRIEIHLLTPQGLQPMLDVPIYG
RIATLELFRPHGETQDFLFIVTERHIKFCVLQWDAESSEUVTRAMGDVSDRIGRPTDMGQI
GIDPDCRLIGHLIVDGIFKVIPPDNKGQUERAFNIRLELGVLDIKEFLGCARPTIAVL
YQDNKDARHVKTYEVSLKDKDPVEGPWSQNNLDNGADLIPVPPPLGGVLIIGEETIVYC
SANAFKAIPPSTIKAYGRVDVDGSRYLLGDHAGIJVHLUTHFIKEKVTGLKIELGET
SIASTISYLDNAVVFVGSSYGDSQLVKLINLHPDAKGSVYEVLERYTNLGPIVDFCVVDLE
RQGGQGVYTCSGAFKDGSLAPRNGIGIBINGASVELGEIGKOMSLKSSVDGAEDTFIVVS
FISETRILAMNLEDELEETEIEGFLSQLQTLFCHDAVYNQLVTSNSVRLVSSTTRELRDE
WHAPAGFTVNVATANASQVLLATGGGGILVYLEIGGGKTEVQHTVLEFVSCLDINPIGD
HNYSQLASVGMVTDISVRTISPLETLTIKEQLIGGEIBRSVLLCSFEGISYLCALGD
GHLLNFQLDTTTGQLKDRKKVSLGTQPTLRTFSSKSATHVFAASDRFTVIYSSNKLLY
SNVNLKEVSYMCPNSAAFPDSLAHAFGEGTIGTDDIQKLHIFTPLGEHGRRICHQE
QTRTFGICSLGNQTNAEESEMHFVRLLDDQSFEFMSTYPLDAFEVACSILSCSFTDDKNV
YCVGTAYVYLPEENPTKVSSFFTSSLSSQKVTCFLCMGGRILVINFEDGEHGRIVPLEGEDGE
ETKGAVYSLNAFNGKLLAAINQKIQIXVMMLDDGTBELQSEGGHHGHILAUYQTRGDF
UVGDLMKSSLULVHEEGEBERADNYARMWASVELLDDDTYLGAENNFHLLIVKKN
SEGATDEERGRI EVVGEVHLGEFVNBFCHGSLVMRLPDSEIGQIPTVIFGTVNGMIGVIA
SLPQEQYAFLEKLQSSLRKVIKGEQDGGDI

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

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

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