

a

>SmKRP1
 MGKYIRKAKKAGDVSPGLVTRAKALALNNGDGGGSYLELRSRLVVPFTVLEGRQKNGV
 SKNPNLVNPNTKPNVCSNVEEKESLGAKEMLKKEKESCGPEDSGENLLEEGOR
 TTRESTPCSLRDSNDNPTGSSTRTANVANVSGVNPSTQATMPTSREMDEFFARAEA
 KQQRRIEKYNFDPVNDKPLPGRFEWVKVDF

----- Plant-mPloc Computation Result -----

Query protein	Predicted location(s)
SmKRP1	Nucleus.

>SmKRP2
 MGKYLKRPNTGDDVVMPESLGVRTRARITLALQSSDCYQLRSRLRYKPTSTPHQSIQ
 KLDVNFHFRPDRSTRETTPCSVMREVSMDVMNPGSATRIEHLTQRRRNFILRNPSAHEI
 EFFTFAEQQQRLFMDKYVDFVANDLPLSGRYEWRVNI

----- Plant-mPloc Computation Result -----

Query protein	Predicted location(s)
SmKRP2	Nucleus.

>SmKRP3
 MGKYIRKGGTKKAGEVVAWLDVSSFGVTRAKTLALQKSTSGGGGGGGGGSDGGCYQL
 RSRRLKPLVGFKRRRHPILKESNRSI RVREMIKQGNWSDGDEGEIEKKEITQNEANN
 GSCIEGNLLEGRVTRSTPCNLIRDAIDTQTSSESRPNALAEANGGGPHSQVLPVTEQ
 ELSVFRTEKQQQKFEKMEKYNFVNDKPLPGRYKWKDD

----- Plant-mPloc Computation Result -----

Query protein	Predicted location(s)
SmKRP3	Nucleus.

>SmKRP4
 MKASMGELKKCEKIRAGKVTEDENGLVRVNDLNVTSLSSTSKRRKFDSDVDF
 SENSIPASVSTVHIPNVSQSCSNCFEPVMMKTVFKSLDLKVRNLQAEFEITDNSASF
 NGAFFSENFKPIDQLNPPSEHGDESDIESSSTTKKYSYSDASAHRKQPPASKVPEAEI
 EFFFFAAEKREKQFAEKYNFVNDKPLPGRYVWVSLK

----- Plant-mPloc Computation Result -----

Query protein	Predicted location(s)
SmKRP4	Nucleus.

>SmKRP5
 MIYEQRKEVITTEVSDVPKRRKICDHFRLKSHNGVADMPPGISVPAVSTSCSSYSK
 FLDDENGEVVEYTEKKMSSPKREESKPEVVKTPENESPPIHVRVEEFPSPREEFAFF
 ARHQERKRLRFREKYNFDFEKEALEGRYKVVQIEN

----- Plant-mPloc Computation Result -----

Query protein	Predicted location(s)
SmKRP5	Nucleus.

b

query :
 MGKYIRKAKKAGDVSPGLVTRAKALALNNGDGGGSYLELRSRLVVPFTVLEGRQKNGV
 SKNPNLVNPNTKPNVCSNVEEKESLGAKEMLKKEKESCGPEDSGENLLEEGOR
 TTRESTPCSLRDSNDNPTGSSTRTANVANVSGVNPSTQATMPTSREMDEFFARAEA
 KQQRRIEKYNFDPVNDKPLPGRFEWVKVDF

Final results predicted by INSP

Predicted NLS peptide	START	END	SCORE
MGKYIRKAKKA	1	11	0.93245
ELRSRLVYP	38	47	0.93867

query :
 MGKYLKRPNTGDDVVMPESLGVRTRARITLALQSSDCYQLRSRLRYKPTSTPHQSIQ
 KLDVNFHFRPDRSTRETTPCSVMREVSMDVMNPGSATRIEHLTQRRRNFILRNPSAHEI
 EFFTFAEQQQRLFMDKYVDFVANDLPLSGRYEWRVNI

Final results predicted by INSP

Predicted NLS peptide	START	END	SCORE
MGKYLKRPNTGDDV	1	14	0.94133

query :
 MGKYIRKGGTKKAGEVVAWLDVSSFGVTRAKTLALQKSTSGGGGGGGGGSDGGCYQL
 RSRRLKPLVGFKRRRHPILKESNRSI RVREMIKQGNWSDGDEGEIEKKEITQNEANN
 GSCIEGNLLEGRVTRSTPCNLIRDAIDTQTSSESRPNALAEANGGGPHSQVLPVTEQ
 ELSVFRTEKQQQKFEKMEKYNFVNDKPLPGRYKWKDD

Final results predicted by INSP

Predicted NLS peptide	START	END	SCORE
MGKYIRKGGTKKAGEV	1	16	0.93759
SDGGCYQLRSRLKPLVGFKRRRHPILKES NRSILRVREMIKQGNWSDGDEGEIEKKEE	51	112	0.97367

query :
 MKASMGELKKCEKIRAGKVTEDENGLVRVNDLNVTSLSSTSKRRKFDSDVDF
 SENSIPASVSTVHIPNVSQSCSNCFEPVMMKTVFKSLDLKVRNLQAEFEITDNSASF
 NGAFFSENFKPIDQLNPPSEHGDESDIESSSTTKKYSYSDASAHRKQPPASKVPEAEI
 EFFFFAAEKREKQFAEKYNFVNDKPLPGRYVWVSLK

Final results predicted by INSP

Predicted NLS peptide	START	END	SCORE
LKKEKIRAGRVTE	9	23	0.93613
SSTKRRKFDSD	44	54	0.95657

query :
 MIYEQRKEVITTEVSDVPKRRKICDHFRLKSHNGVADMPPGISVPAVSTSCSSYSK
 FLDDENGEVVEYTEKKMSSPKREESKPEVVKTPENESPPIHVRVEEFPSPREEFAFF
 ARHQERKRLRFREKYNFDFEKEALEGRYKVVQIEN

Final results predicted by INSP

Predicted NLS peptide	START	END	SCORE
SDVPKRRKICDHFRLKSHN	119	34	0.96029
FFARHQERKRLRFREKYN	119	136	0.92764