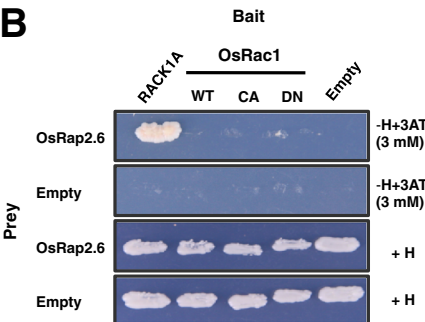


A

AtRap2.6	1	MVSMITNVSGETE-----PSASATWTMGKREERE--SLPQPLITGSVTKCESSMS	54
OsRap2.6	1	MVTRAHWIRAPDLHLPHPSSASAAAIPQQASSVPTAAAAASSPQQLAAAAAEE	60
AtRap2.6	55	LEAPKKVRGVQRQRPWKGKJAAEIRDPHKATRVWLGTFTAEAPAAVDAALAFRGSKAKL	114
OsRap2.6	61	QGRPRHVRGVQRQRPWKGKJAAEIRDPKKAARVWLGTFTAEAPAAVDAALAFRGTAKL	120
AtRap2.6	115	NFPEVVGTTIQRNSHFLQNSMQPSLTYIQDCPTLLSYSRQNEQQPLVGMLOFTEENH	174
OsRap2.6	121	NFPEVVGATDLGFLVTRGIPPAATHGGVYVPSPPRAGAPPPRQQTVVVPYDLMRYA	180
AtRap2.6	175	FFEKPWTEYDQYVNSYSG-----	192
OsRap2.6	181	QLLQGGVGGVMPFGGARTMSSSTVSSSSAPQILDFTQQLIRAGPPSPMPSSGSGSATA	240
AtRap2.6	192	-----	192
OsRap2.6	241	RASSSTTSASSPGAWPYGGSERKKKDS	268

B**C**