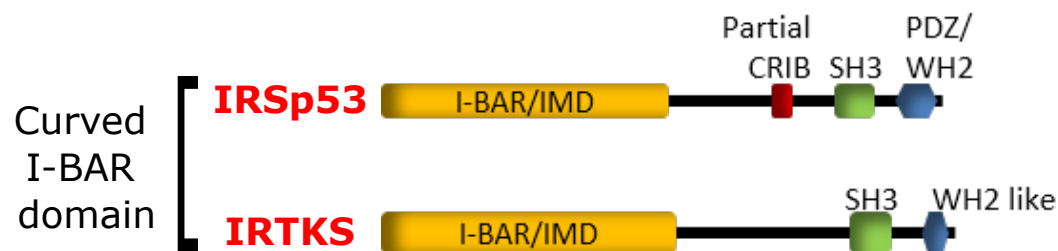


a**b**

IRTKS-IRSp53 proteins sequences alignment

Score	Expect	Method	Identities	Positives	Gaps
396 bits(1017)	7e-137	Compositional matrix adjust.	216/539(40%)	320/539(59%)	56/539(10%)
Query 7	EEMHRLTENYKTIMEQFNPSLRNFIAMGKNYEKALAGVTYAAKG YFDALVKMGELASES				66
Sbjct 6	EE++RLTE+ Y+ +MEQFNP LRN I +GKNYEKA+ + A K Y+D + K+GE+A+ S				65
Query 67	QGSKELG DVL FQMAEVHRQIQNQL EEM LKSFHNELLTQLEQKV ELDSRYLSAALKKYQTE				126
Sbjct 66	PVSTELGHV LIEISSTHKKLNESLDENFKFKFHEKIIHELEKKI EL DVKYM NATL KRYQTE				125
Query 127	QRSKGDALDKCQAE LKKLRKKSQGSKNPQKYS DKELQYIDAI SNKQGELENYVSDGYKTA				186
Sbjct 126	HKNKLESLEKSQAE LKKIRRKSGSRNALKYEHKEIEYVETVTSRQSEIQKF IADGCKEA				185
Query 187	LTEERRRFCFLVEKQCAVAKNSAAYHSGKELLAQKLPLWQQACADPSKIPERAVQLMQQ				246
Sbjct 186	LLEEKRRRFCFLVDRKHC GFANHIHYH LQSAELLNSKLPRWQETCVD AIKVPEKIMNMIEE				245
Query 247	VASNGATLPSALSASKSNLVISDPIPGAKPLFPVPELAPFVGRMSAQESTPIMNGVTGPD				306
Sbjct 246	IKT-----PASTPVS GTPQASPMIERSNVVR-----				271
Query 307	GEDYSPWADRKAAPKSLSP PQSQSKLSDSYSN---TLPVRKSVTPKNSYATTENKTLPR				363
Sbjct 272	-KDYDTLSKCS PKMPPAPSGRAYTSPLIDMFNNPATAAPNSQRVN--NSTGTSEDPSLQR				328
Query 364	SSSMAAGLERNGRM RVKAI FSHAAGDNSTLLSFKEGDLITLLVPEARDGWHYGESEKTKM				423
Sbjct 329	SVSVATGLNMMKKQKVKTIFPHTAGSNKTLLSFAQGDVITLLIPEEKDGWLYGEHDVSKA				388
Query 424	RGWFPPFSYTRVLDS DGS DRLHM---SLQQGKSSSTGNLLDKDDLAI PPPDY-----G				472
Sbjct 389	RGWFPPSYTKLLEENETEAVTVPTPSPTFVRSISTVNLSSENSSVVIPPDPYLECLSMGAA				448
Query 473	AASRAFP AQTASGFK---QRPYSVAVPAFSQGLDDYGARMSRNPF AHVQLKPTVTNDR				528
Sbjct 449	ADRRADSARTTSTFKAPASKP-ETAAPNDANGTAKPPFLS-GENPFATVKLRPTVTNDR				505