

Hssix3	MVFRS-----PLDLYSSHFLLPNFA-DSHHRSSILLASSGGNGAGGGGGAGGGGGGGN	52
Ggsix3	MVFRS-----PLELYPTHFPLPFAADPHHRSLLLAS-----GGSGSGGCS	43
Xlsix3	MVFRS-----PLELYPAHLFLPNFP-----ERSVLLSG-----	48
Drsix3	MVFRS-----PLELYPSHLFLPNA-----DRPLLAG-----	28
Sksix3	-----	-----
Spsix3	MVWTETETSPSDRGAMRAAQALAQYYSLHDPRESSEGLAR-----	39
Dmsix3	MAVGP-----TEGKQPPSESFSPTHH-----	21
Pcsix3/6-like	MPHLCS-----LTTGSN-----	13

			Groucho interaction
Hssix3	GAGGGGAGGAGGGGGGSRAP-PEELS---MFQLP---TLNFSPEQVASVCETLEETGD	104	
Ggsix3	GAGGG-----GGSSRAP-HEELS---MFQLP---TLNFSPEQVASVCETLEETGD	86	
Xlsix3	-----PRA---QDELS---MFHLP---SLNFSPEQVASVCETLEETGD	62	
Drsix3	-----SIPRARSPELDP---MFQLP---TLNFSAEQVASVCETLEETGD	66	
Sksix3	-----MFQLP---TLNFSPLQVASVCETLEESGD	26	
Spsix3	-----LAHMYTSMQPFFVFPAAAPGGTFLPLPTALPTLCFSPPTQIASVCETLEESGD	91	
Dmsix3	-----QIIAPSP-----ILAVP---TLAFSAQVEIVCKTLEESGD	54	
Pcsix3/6-like	-----PLP-----FSAEQISKVCETLEECGD	34	
			:* ** * : ** : ** : **

			SIX DOMAIN
Hssix3	IERLGRFLWSLPVAPGACEAINKHESILRARAVVAFHTGNFRDLYHILENHKFTKESHGK	164	
Ggsix3	IERLGRFLWSLPVAPGACEAINKHESILRARAVVAFHTGNFRDLYHILENHKFTKESHGK	146	
Xlsix3	IERLGRFLWSLPVAPGACEAINKHESILRARAVVAFHTGNFRELYLLENHKFTKESHGK	122	
Drsix3	IERLGRFLWSLPVAPGACDAINKHESIQRARAVVAYHTGFSFRELYHILETHKFTKDSHGK	126	
Sksix3	IERLARFLWSLPVAPGTCEALNKNESVLRARAVVTFHQGNFRELYLLENHKFTKESHAK	86	
Spsix3	IERLARFLWSLPVAPGTCEALSKNESVLRARAVVSFHQGNFRELYHILENHRFTKDSHAK	151	
Dmsix3	IERLARFLWSLPVALPNMHEILNCEAVLRARAVVAYHVGNFRELYAIENHKFTKASYGK	114	
Pcsix3/6-like	IERLSRFLWSLPNNREVRELIINSNETILRSRAVVAFHNSHFHELYYLEHFRFNKSHGK	94	
			*** . ***** . : . * : * : * : * : * . : : * : * : * . * : *

Hssix3	LQAMWLEAHYQEAELRGRPLGPVDKYRVRKKFPLPRTIWDGEOKTHCFKERTRSLLEW	224	
Ggsix3	LQAMWLEAHYQEAELRGRPLGPVDKYRVRKKFPLPRTIWDGEOKTHCFKERTRSLLEW	206	
Xlsix3	LQAMWLEAHYQEAELRGRPLGPVDKYRVRKKFPLPRTIWDGEOKTHCFKERTRSLLEW	182	
Drsix3	LQAMWLEAHYQEAELRGRPLGPVDKYRVRKKFPLPRTIWDGEOKTHCFKERTRSLLEW	186	
Sksix3	LQAMWLEAHYQEAELRGRPLGPVDKYRVRKKFPLPRTIWDGEOKTHCFKERTRSLLEW	146	
Spsix3	LQAMWLEAHYQEAELRGRPLGPVDKYRVRKKFPLPRTIWDGEOKTHCFKERTRSLLEW	211	
Dmsix3	LQAMWLEAHYIEAEKLRGRSLGPVDKYRVRKKFPLPRTIWDGEOKTHCFKERTRSLLEW	174	
Pcsix3/6-like	LQAIWLEAHYLEAERLRGRPLGPVDKYRVRKRFPPLPRTIWDGEOKACFCFKERTRKLLEF	154	
			*** . ***** *** . **** ***** . ***** . ***** **** :

			HOMEODOMAIN
Hssix3	YLQDPYPNPSKKRELAQATGLTPTQVGNWFKNRRQRDRAAAAKNRLQHQAIQSGMRS	284	
Ggsix3	YLQDPYPNPSKKRELAQATGLTPTQVGNWFKNRRQRDRAAAAKNRLQHQAIQSGMRS	266	
Xlsix3	YLQDPYPNPSKKRELAQATGLTPTQVGNWFKNRRQRDRAAAAKNRLQHQAIQSGMRS	242	
Drsix3	YLQDPYPNPSKKRELAQATGLTPTQVGNWFKNRRQRDRAAAAKNRLQHQAIQSGMRS	246	
Sksix3	YLQDPYPNPTKKRELAQATGLTPTQVGNWFKNRRQRDRAAAAKNRLQSQHQ--QP	204	
Spsix3	YLQDPYPNPTKKRELAQATGLTPTQVGNWFKNRRQRDRAAAAKNRMQQQQQALQNSSVS	271	
Dmsix3	YLQDPYPNPTKKRELAQATGLNPTQVGNWFKNRRQRDRAAAAKNRIQLPQSLALNGASG	234	
Pcsix3/6-like	YLQDPYSPSKKRDLDATHLTPTQVGNWFKNRRQRDRAAAAKNKSQRQEHALNTSSYE	214	
			***** . * : * : * : * . * . ***** . ***** . ***** * :

Hssix3	EPGCP-----THGSAESPSTAAS-PTTSVSSLTERADTGTSSILSVTSSDSECDV	332
Ggsix3	EPGCP-----THSSAESPSTAAS-PTTSVSSLTERAETGTSSILSVTSSDSECDV	314
Xlsix3	DPGCP-----THSSAESPSTAASPTTSVSSLAERAETATSSILSVTSSDSECDV	291
Drsix3	ESGCT-----PHSSAESPSTAAS-PTTSVSSMNERGDGGT-ILSVTSSDSDFDV	293
Sksix3	TSPNP-----IITVDGATTLPGQLTKQSLDPAHALLEATQNKSHPTPLSPTLA-	252
Spsix3	NSAHS-----PSLTEGATCLLSPHPDDHSPSP-RSLADSPPLDSPSPAGYHDDD	319
Dmsix3	PPLHH-----PAYAAAYSVECVPGGGHPPPPKLRINSPEKLNSTAVAAAASV	283
Pcsix3/6-like	EDDDSDNLDDILDSDSDSDGDPRAKDKDTNEHKVSTEKRSFMVASILQKDDEPNKKL	274

Hssix3	-----	
Ggsix3	-----	
Xlsix3	-----	
Drsix3	-----	
Sksix3	-----	
Spsix3	DDDDL-----	324
Dmsix3	RGGGNQH-----	292
Pcsix3/6-like	KNYFDNNIGSFLHTR	290