

name	sequence '!' for match	accession	position	class
			LG:coord.	
EVX-1	QMRRYRTAFTREQIARLEKEFYRENVSRPRCELAAALNLPETTIKVWFQNRMRKDKRQRLA	P23683.1		
g_ayrxn_scaff_4445_1.Contig24	--.....L.....C..S.....S...R.-----		1 : 7968	evx
g_algxc_scaff_4707_1.Contig9	KE..S.....E..LEY..RT.E.TQ.PDVYT.E...QRTK.T.ARVO.-----		1 : 2335	?
g_ajgny_scaff_5092_1.Contig4	KAK.I..I..A..LN...A..LQQQ.MVGRE.SH..SE...K.AQV.....I.WRK----		4 : 26846	?
g_ahyur_scaff_4335_1.Contig2	-AK.V..I..A..LD...T..E.QQ.MVG.E.LQ..S...T.AQV.....I.WRK.HFD		1 : 3106	?
engrailed_Tribolium_castaneum_	EEK.P....SGA.L...KH..AENR.LTER..QQ.S.E.G.N.AQ..I....K.A.I.KASGO	NP_001034511.2		
engrailed_isoform_A_Drosophila_melanogaster_	DEK.P....SS..L...KR..NENR.LTER..QQ.SSE.G.N.AQ..I....K.A.I.KSTGS	NP_523700.2		
engrailed_Branchiostoma_floridae_	EEK.P....S..LQ..K...QENR.LTEQ..QD..RE.K.N.SQ..I....K.A.I.KAAGV	EEN68949.1		
g_addne_scaff_4497_1.Contig54	EEK.P....TD.L...K...HENR.LTEK..Q...RE.Q.N.SQ..I....K.A.I.KSTGE		1 : 5794	en
g_ausca_scaff_4858_1.Contig1	DEK.P....AD.L...KQ..QENR.LTEK..QD..LD.Q.N.SQ..I....K.A.I.KASGO		20 : 83001	en
g_adwrx_scaff_4421_1.Contig72	DEK.P....AD.L...KA..QENR.LTEK..QD..RG.Q.N.SQ..I....K.A.I.KATGH		15 : 71297	en
g_avzuc_scaff_4437_1.Contig3	DEK.P....TD.L...KA..QENK-LTEK..QD..RE-----		21 : 85367	en
g_adwrx_scaff_4421_1.Contig61	DEK.P....TD.L...KA..QENR.LTEK..QD..RE.Q.N.SQ..I.-----		15 : 71297	en
g_avzuc_scaff_4437_1.Contig4	-----QENR.LTEK..QD..RE.Q.N.SQ..I....K.A.I.KATGH		21 : 85367	en
g_adwrx_scaff_4421_1.Contig63	-EK.P....AD.L...KA..QENR.LTEK..QD..RE.Q.N.SQ..I....K.A.I.KAVGH		15 : 71297	en
g_ayadw_scaff_4575_1.Contig4	DEK.P....AD.L...KA..QENR.LTEK..QD..RE.Q.N.SQ..I....K.A.I.KAVGH		3 : 22654	en
Nkx-2.2a	KK.KR.VL.SKA.TYE..RR.RQQR.L.A.E.EH..SLIR.TP.QV.I...H.Y.M..A.AE	NP_571497.1		
Nkx-2.2	KK.KR.VL.SKA.TYE..RR.RQQR.L.A.E.EH..SLIR.TP.QV.I...H.Y.M..A.AE	NP_002500.1		
Nkx-2.2_Gallus_gallus_	KK.KR.VL.SKA.TYE..RR.RQQR.L.A.E.EH..SLIR.TP.QV.I...H.Y.M..A.AE	XP_003643855.1		
g_ajlua_scaff_4446_1.Contig10	KK.KR.VL.SKA.TYE..RR.RQQR.L.A.E.EH..NFIR.TP.QV.I...H.Y.T..A.QE		1 : 1567	nkx2
g_acfsj_scaff_4532_1.Contig25	KK.KR.VL.SKA.TYE..RR.RQQR.L.A.E.EH..SIIR.TP.QV.I...H.Y.T..A.QE		3 : 20058	nkx2
ladybird-like_3	KR.KS....SNQ.LFE..RR.V.QK.L.PAD.DQ..QRA.SSAQVIT.....A.L..DLDE	NP_001038133.1		
lady_bird-like_1_homolog	KR.KS....NH..YE..R.LYQK.L.PAD.DQI.QQ.G.TNAQVIT.....A.L..DLEE	NP_001007135.1		
g_acdli_scaff_4927_1.Contig5	KK.KS....NH..FE..R.LYQK.L.PAD.D.I.QS.G.TNAQVIT.....A.L.-----		26 : 93066	lbx
g_agfxy_scaff_4755_1.Contig8	KK.KS....NQ..FE..R.LYQK.L.PAD.D.I.QS.R.TNAQVIT.....A.L.-----		13 : 67147	lbx
g_aplvp_scaff_4845_1.Contig14	KK.KS....NH..FE..R.LYQK.L.PAD.D.I.QS.G.TNAQVIT.....A.L.-----		1 : 3106	lbx
AGAP003673- PA_Anopeles_gambiae_str_PEST_	KK.KS....NH..FE..R.LYQK.L.PSD.D.I...G.SNAQVIT.....A.L..DMEE	EAA04094		
g_amhlt_scaff_4436_1.Contig3	KQ.KA....DH.LQT...C.E.QK.L.VQE.M...SK...TD.QV.T.Y.....		8 : 46729	?
g_amhlt_scaff_4436_1.Contig8	KE.KA....DY..QT...R.QTQK.L.VQD.M.I.SK...TD.HV.T.Y.....		8 : 46729	?
g_aeqlo_scaff_4727_1.Contig6	RKKKT..V...S.VFQ..ST.DMKR.L.SSE.AG...C.H.T..QV.I.....N.W...---		22 : 86973	?
g_agfda_scaff_4460_1.Contig8	KRKKK..T..GR..FE...Q.EIKK.L.SSE.A.M.KL..VT.QQVEI-----		26 : 93149	?
g_artzi_scaff_4429_1.Contig73	SN.KL..P..TQ.LLA..RK.LAKQ.L.IAE.AKFSIS.T.T.AQV.I.....A.E.-----		5 : 32215	msx
Msx_Saccoglossus_kowalevskii_	TN.KP..P..TS.LLA..RK.RQKQ.L.IAE.A.FS.S...T..QV.I.....A.A..LQE	ABD97280		
Msx_Nematostella_vectensis_	AN.KP..P..TS.LLA..RK.RQKQ.L.IAE.A.FS.S...T..QV.I.....A.A..LHE	BAG11598		
MSX-2_Mus_musculus_	TN.KP..P..TS.LLA..RK.RQKQ.L.IAE.A.FSSS...T..QV.I.....A.A..LQE	NP_038629		
MSX-2_Homo_sapiens_	TN.KP..P..TS.LLA..RK.RQKQ.L.IAE.A.FSSS...T..QV.I.....A.A..LQE	BAA06549		
MSX1_Homo_sapiens_	TN.KP..P..TA.LLA..RK.RQKQ.L.IAE.A.FSSS.S.T..QV.I.....A.A..LQE	NP_002439		
MSX1_variant_Mus_musculus_	TN.KP..P..TA.LLA..RK.RQKQ.L.IAE.A.FSSS.S.T..QV.I.....A.A..LQE	AAG32466		
g_aebwc_scaff_4685_2.Contig8	-----KQ.L.IAE.A.FSSS.S.T..QV.I.....A.E..LKE		3 : 19118	msx
g_aebwc_scaff_4685_2.Contig10	SN.KP..P..TQ.LLA..RK.RTKQ.L.IAE.A.FSSS...T..QV.I.....A.E.-----		3 : 19118	msx
g_aebwc_scaff_4685_2.Contig13	SN.KP..P..TQ.LLA..RK.RSKQ.L.IAE.A.FSSS...T..QV.I.....A.E.-----		3 : 19118	msx
g_aoopl_scaff_4606_1.Contig8	-----KQ.L.IAE.A.FSSS...T..QV.I.....A.EN.LKE-		26 : 93149	msx
g_aoopl_scaff_4606_1.Contig18	SS.KP..P..TK.LLA...M.QTKQ.L.IAE.A.FSSSM..T..QV.I.....A.E.-----		26 : 93149	msx
g_agizq_scaff_4515_1.Contig28	--.R...Y.S..LLQ.....HAKK.L.LTE.SQISTT.Q.S.VQV.I.....A.W.-----		3 : 23600	gbx
unplugged_Drosophila_melanogaster_	KS..R....S..LLE..R..HAKK.L.LTE.SQI.TS.K.S.VQV.I.....A.W..VKAG	NP_477146		
AGAP006923- PA_Anopeles_gambiae_str_PEST_	KS..R....S..LLE..R..HAKK.L.LTE.SQI.TS.K.S.VQV.I.....A.W..VKAG	EAA04094		
g_apstr_scaff_4456_1.Contig3	--.R...N..LLE..N..HCKK.L.LTE.SQI.HS.Q.S.QQV.I.....A.W.-----		1 : 8283	gbx
GBX-1_Canis_lupus_familiaris_	KS..R....S..LLE.....HCKK.L.LTE.SQI.H..K.S.VQV.I.....A.W..IKAG	XP_853664		

name	sequence	accession	position	class
	'!' for match		LG:coord.	
g_aglhj_scaff_4667_1.Contig13	---R....S..LLE....HSKK.L.LTE.SQI.HS.Q.S.VQV.I.....A.W.-----		11 : 60310	gbx
g_aglhj_scaff_4783_1.Contig4	KS..R....S..LLE....HSKK.L.LTE.SHI.NS.Q.S.VQV.I.....A.W..VKAG		18 : 80043	gbx
g_acgnb_scaff_4629_1.Contig3	RFLLSLSQR.SRNGSQATDGLHFNRLT.R..I.IVRT.C.SD-----		20 : 83755	hox?
g_awtvf_scaff_4744_1.Contig2	ETK.Q...Y..H..LE....HFNR.LT.R..I.I.HSSC.ERIK.-----		21 : 85243	hox?
g_awtvf_scaff_4744_1.Contig1	-----SR.LT.R.QI.I.HS.C.S.RQ..N...I...W.KDNKL		21 : 85243	hox?
Drosophila-Dfd__NM_057853_	EPK.Q...Y..H..LE....HYNR.LT.R..I.I.HT.V.S.RQ..I.....W.KD---	NM_057853		
Tribolium-Dfd__EEZ99253_	EPK.Q...Y..H..LE....HYNR.LT.R..I.I.HT.V.S.RQ..I.....W.KD---	EEZ99253		
g_ajivj_scaff_4414_1.Contig4	ETK.Q...Y..H..LE....HFNR.LT.R..I.I.HL.C.S.RQ..I.....W.KDNKL		15 : 71079	hox?
g_ajivj_scaff_4414_1.Contig3	ETK.Q...Y..H..LE....HFNR.LT.R..I.I.HS.C.S.RQ..I.....W.KDNKL		15 : 71079	hox?
Branchiostoma-Hox4__AB028208_	DTK.S...Y..Q.VLE....HFNR.LT.R..I.I.HS.G.T.RQ..I.....W.KD---	AB028208		
g_akvhc_scaff_4400_4.Contig7	EAK.Q...Y..H.VLE....HFNR.LT.R..I.I.H..C.S.RQ..I.....W.KDNKL		18 : 79524	hox?
Capitella-Dfd__EU196540_	DSK.T...Y..H..LE....HFNR.LT.R..I.I.HT.C.S.RQ..I.....W.KE---	EU196540		
Lottia-Dfd__110972_	DSK.N...Y..H.VLE....HFNR.LT.R..I.I.HT.C.S.RQ..I.....W.KE---	JGI Lotgii protein id: 110972		
Branchiostoma-Hox12__AAF81903_	SS.KK.CPYSKV.LLE....LYNM.IT.EQ.G.I.RKV..TDRQV.I.....M..M---	AAF81903		
Branchiostoma-Hox10__Z35150_	VG.KK.CPY.KY..LE....LFNM...E..Q.ISRHV..SDRQV.I.....M..M---	Z35150		
Branchiostoma-Hox11__AAF81909_	ST.KK.CPY.KY.TLE....LFNMF.T.E..Q.I.RQ..TDRQV.I.....M..M---	AAF81909		
Branchiostoma-Hox9__ABX39493_	SS.KK.CPY..F.TLE....LYNM.LT.E..Y.ISQHV..T.RQV.I.....M.KM---	ABX39493		
Branchiostoma-Hox13__AAF81904_	GG.KK.CPY.KY.LSV..Q.YIQNR...ET.L..SQR..TDRQV.I.....Q..L---	AAF81904		
Branchiostoma-Hox14__AAF81905_	PV.PK.RPYSKY.LNE..N.YVQNQ.I..DK.LQ.SQK...T.RQV.I.....I.Q.KL---	AAF81905		
Capitella-post1__EU196546_	NPKKK.KPYSKP.VSA..N.YSTST.ITKA..K.V.RE.D.T.RQ..I.Y...I.E.KI---	EU196546		
Lottia-post1__100031_	TL.KR.RPYSKF...E..R.YNGST...KS..W..SQLI..S.RQ..I.....I.A.KI---	JGI Lotgii protein id: 100031		
Drosophila-AbdB__NM_080157_	SV.KK.KPYSKF.TLE....LFNA...KQK.W...RN.Q.T.RQV.I.....N.KN---	NM_080157		
Tribolium-AbdB__EEZ99247_	TV.KK.KPYSKF.TLE....LFNA...KQK.W...RN...T.RQV.I.....N.KN---	EEZ99247		
g_algea_scaff_4559_1.Contig10	TV.KK.KPYSKF.TLE....LFNA...KQK.W...RN...T.RQV.I.....S.KNAQR		15 : 71736	abdB
g_algea_scaff_4559_3.Contig7	-----KPYSKF.TLE....LFNS...KQK.W...RN...T.RQV.I.....S.KSSQR		21 : 85120	abdB
Capitella-post2__EU196545_	KQ.KK.KPY..Y.TMV..N..INNS.IT.QK.W.ISCK.H.S.RQV.....R.KL---	EU196545		
Lottia-post2__89720_	KG.KK.KPY..Y.TMV..N..LSSS.IT.QK.W.ISCK.Q.S.RQV.....R.KL---	JGI Lotgii protein id: 89720		
g_aosol_scaff_4355_1.Contig18	-----EFNR.ITQR..I.I.HY.S.S.RK..M.....S..ANEKH--		20 : 83145	hox?
Drosophila-ftz__NM_058159_	DSK.T.QTY..Y.TLE....HFNR.IT.R..IDI.N..S.S.RQ..I.....S.KD---	NM_058159		
CDX-2__Mus_musculus_	TKDK..VVY.DH.RLE....HFSR.ITIR.KS...T.G.S.RQV.I.....A.ERKIKKK	AAA19645		
g_amvdv_scaff_4163_3.Contig12	TRDK..VVY.DQ.RLE....HYNR.I.IR.KT...MVG.S.RQV.I.....A.ER.NFRK		5 : 33811	cdx
g_aidw_scaff_4772_1.Contig14	TKDK..VVY.DH.RLE....HYSR.ITIR.KT...TM.G.SDRQV.I.....A.ERK.ARK		19 : 80739	cdx
g_anovg_scaff_4508_1.Contig5	TKEK..VVY.DH.RLE....YSR.ITIR.KS...M.G.S.RQV.I.....A.ERK.ARK		3 : 21395	cdx
caudal_isoform_A__Drosophila_melanogaster_	TKDK..VVY.DF.RLE....YCTSR.ITIR.KS...QT.S.S.RQV.I.....A.ERK.NKK	NP_476954.1		
Ftz__Tribolium_castaneum_	GNK.T.QTY..Y.TLE....HFNK.LT.R..I.I.ES.R.T.RQ..I.....A.KDTKF	AF321227_1		
Tribolium-ftz__AAC46491_	GNK.T.QTY..Y.TLE....HFNK.LT.R..I.I.ES.R.T.RQ..I.....A.KD---	AAC46491		
g_acrop_scaff_4310_1.Contig8	APK.T.QTY..Y.TLE....HFNK.LT.R..I.I.HT.G.T.RQ..I.....E.KENK-		15 : 71825	hox?
g_awjsf_scaff_4464_1.Contig11	--K.T.QTY..Y.TLE....HFNK.LT.R..I.I.HT.G.T.RQ..I.....		21 : 85120	hox?
g_awjsf_scaff_4464_1.Contig15	APK.T.QTY..Y.TLE....HFNR.LT.R..I.I.HT.G.T.RQ..I.....A.KENKF		21 : 85120	hox?
g_avhgw_scaff_4510_1.Contig7	--K.T.QTY..Y.TLE....HFNR.LT.R..I.I.HS.G.T.RQ..I.....A.KEMPK		18 : 79607	hox?
g_alkdk_scaff_4677_1.Contig4	DQ..S.QTYSFY.TLA....HFDP.LTKR..I.I.HT..K.KQ..I.....W.KEKRS		28 : 94741	hox?
g_ascty_scaff_4257_1.Contig45	DQ..S.QTYSFY.TLA....HLDP.LTQR..I.I.HT..T.KQ.QI.....W.KENKT		17 : 77601	hox?
hox_6_Saccoglossus	-Q..G.QTY..Y.TLE....HFNR.LT.R..I.I.HT.G.T.RQ..I.....W.KEQK-	ABK00020		
hox_7_Saccoglossus	-KK.C.QTY..Y.TLE....HYNR.LT.R..I.I.SHL.G.T.RQ..I.....Y.KESK-	AAAP79287		
Capitella-lox5__EU196542_	EQK.T.QTY..Y.TLE....HYNR.LT.R..I.I.H..Q.T.RQ..I.....Y.KE---	EU196542		
g_anoef_scaff_4410_1.Contig27	PR..G.QSY..F.TLE....HFNH.LT.R..I..HVVC.T.RQ..I.....L.KEVRV		3 : 23600	hox?

name	sequence	accession	position	class
	'!' for match		LG:coord.	
g_awjsf_scaff_4464_1.Contig6	----G.Q.Y..F.TLE.....HYNH.LT.R..I.I.HVVC.T-----		21: 85120	hox?
g_ajivj_scaff_4414_1.Contig2	---.S.Q.Y..F.TLE.....HYNH.LT.R..I.I.HVVC.T-----		15: 71079	hox?
g_anoef_scaff_4410_1.Contig17	-----LE.....HYNH.LT.R..I.I.HVVC.T.RQ..I.....L.KEIR.		3: 23600	hox?
Lottia-lox4__156931_	.R..G.QTYS.Y.TLE.....QFNH.LT.K..I.I.H.T.C.T.RQ..I.....M.KE---	JGI Lotg1 protein id: 156931		
Capitella-lox4__EU196543_	.R..G.QTYS.Y.TLE.....QFNH.LT.K..I.I.H..C.T.RQ..I.....L.KE---	EU196543		
g_awgsh_scaff_4551_1.Contig4	-R..G.QTY..F.TLE.....HFNH.LT.R..I.I.H..C.T.RQ..I.....L.KEIR.		15: 71699	hox?
g_aqqvq_scaff_4781_1.Contig5	-----HFNH.LT.R..I.I.H..C.T.RQ..I.....L.KEIR.		21: 85040	hox?
g_asnox_scaff_4479_1.Contig10	-----HFNH.LT.R..I.I.H..C.T.RQ..I.....L.KEIR.		15: 71793	hox?
g_asnox_scaff_4479_1.Contig18	-----HFNH.LT.R..I.I.H..C.T.RQ..I.....L.KEIR.		15: 71793	hox?
Drosophila-abdA__NM_057345_	PR..G.QTY..F.TLE.....HFNH.LT.R..I.I.H..C.T.RQ..I.....L.KE---	NM_057345		
Tribolium-abdA__AAB70263_	PR..G.QTY..F.TLE.....HFNH.LT.R..I.I.H..C.T.RQ..I.....L.KE---	AAB70263		
g_aqqvq_scaff_4781_1.Contig10	-----YP.Y.TLE.....HTNH.LT.R..I.M.H..C.T.RQ..I.....L.KEIQ.		21: 85040	ubx
g_asnox_scaff_4479_1.Contig17	-----LT.R..I.M.H..C.T.RQ..I.....L.KEIQ.		15: 71793	ubx
g_asnox_scaff_4479_1.Contig21	LR..G.QTY..Y.TLE.....HTNH.LT.R..I.M.H..C-----		15: 71793	ubx
g_aityy_scaff_4289_1.Contig2	LR..G.QTY..Y.TLE.....HTNH.LT.R..I.M.H..C.T.RQ..I.....		10: 54444	ubx
Drosophila-Ubx__NM_080500_	LR..G.QTY..Y.TLE.....HTNH.LT.R..I.M.H..C.T.RQ..I.....L.KE---	NM_080500		
Tribolium-Ubx__EEZ99249_	LR..G.QTY..Y.TLE.....HTNH.LT.R..I.M.H..C.T.RQ..I.....L.KE---	EEZ99249		
g_asnox_scaff_4479_1.Contig28	LR..G.QTY..Y.TLE.....HTNH.LT.R..I.M.H..C.T.RQ..I.....L.KEIQ.		15: 71793	ubx
Capitella-lox2__EU196544_	.R..G.QTY..Y.TLE.....KFNH.LT.R..I..SHM.C.T.RQ..I.....E.KE---	EU196544		
Lottia-lox2__185752_	.R..G.QTY..F.TLE.....KFNH.LT.R..I..SHM.C.T.RQ..I.....E.KE---	JGI Lotg1 protein id: 185752		
Branchiostoma-Hox8__ABX39492_	ER..G.QTYS.Y.TLE.....HFNK.LT.R..I.I.H..G.T.RQ..I.....L.KE---	ABX39492		
Branchiostoma-Hox7__ABX39491_	ERK.G.QTY..Y.TLE.....HFNK.LT.R..I.I.H..C.T.RQ..I.....W.KE---	ABX39491		
Lottia-lox5__89598_	EQK.T.QTY..Y.TLE.....HFNH.LT.R..I.V.HM.G.T.RQ..I.....W.KE---	JGI Lotg1 protein id: 89598		
Branchiostoma-Hox6__ABX39490_	EKK.G.QTY..Y.TLE.....HFNK.LT.K..I.I.HL.G.T.RQ..I.....W.KE---	ABX39490		
g_aubsu_scaff_4356_1.Contig13	ERK.G.QTY..Y.TLE.....HFNH.LT.R..I.I.H..C.T.RQ..I.....W.KENK.		15: 71793	hox?
g_aubsu_scaff_4356_1.Contig10	ERK.G.QTY..Y.TLE.....HFNH.LT.R..I.I.H..C.T.RQ..I.....W.KENK.		15: 71793	hox?
Drosophila-Antp__NM_079525_	ERK.G.QTY..Y.TLE.....HFNH.LT.R..I.I.H..C.T.RQ..I.....W.KE---	NM_079525		
Tribolium-Antp__EEZ99250_	ERK.G.QTY..Y.TLE.....HFNH.LT.R..I.I.H..C.T.RQ..I.....W.KE---	EEZ99250		
Capitella-Antp__EU196547_	ERK.G.QTY..Y.TLE.....HFNH.LT.R..I.I.H..C.T.RQ..I.....W.KE---	EU196547		
Lottia-Antp__177860_	NRK.G.QTY..Y.TLE.....HFNH.LT.R..I.I.H..C.T.RQ..I.....W.KE---	JGI Lotg1 protein id: 177860		
Hox8_Metacrinus	-KK.G.QTY..Y.TLE.....HFNH.LT.R..I.I.Q.VC.S.RQ..I.....A.KEETS-	BAF43726		
g_atxvn_scaff_4590_1.Contig3	-----LT.R..I.I.H..C.T.RQ..I.....W.QENK.		5: 33116	hox?
g_awjsf_scaff_4464_1.Contig1	--K.G.QTY..Y.TLE.....HFNH.LT.R..I.I-----		21: 85120	hox?
g_awjsf_scaff_4464_1.Contig8	ERK.G.QTY..Y.TLE.....HFNH.LT.R..I.I.H..C.T.R-----		21: 85120	hox?
g_asety_scaff_4257_1.Contig27	-----TLE.....HFNH.LT.R..I.I.H..C.T.RQ..I-----		17: 77601	hox?
g_alkdk_scaff_4677_1.Contig1	-----TY..Y.TLE.....HFNH.LT.R..I.I.H..C.T-----		28: 94741	hox?
hox_5_Saccoglossus	-AK.S...Y..Y.TLE.....HFNH.LT.R..I.I.H..G.S.RQ..I.....W.KEHN-	NP_001158410		
Branchiostoma-Hox5__ABX39489_	DNK.T...Y..Y.TLE.....HFNH.LT.R..I.I.H..C.T.RQ..I.....W.KE---	ABX39489		
Scr__Tribolium_castaneum_	ETK.Q..SY..Y.TLE.....HFNH.LT.R..I.I.H..C.T.RQ..I.....W.KEHKM	AF321227_2		
Drosophila-Scr__X14475_	ETK.Q..SY..Y.TLE.....HFNH.LT.R..I.I.H..C.T.RQ..I.....W.KE---	X14475		
Tribolium-Scr__EEZ99252_	ETK.Q..SY..Y.TLE.....HFNH.LT.R..I.I.H..C.T.RQ..I.....W.KE---	EEZ99252		
g_anoef_scaff_4410_1.Contig19	-----HFNH.LT.R..I.I.H..C.S.RQ..I.....W.KEHKM		3: 23600	hox?
g_asnox_scaff_4479_1.Contig12	-----SY..Y.TLE.....HFNH.LT.R..I.I.H..C.S.RQ..I-----		15: 71793	hox?
g_awjsf_scaff_4464_1.Contig7	ETK.Q..SY..Y.TLE.....HFNH.LT.R..I.I.H..C.S.RQ..I.....W.KEH--		21: 85120	hox?
g_anbio_scaff_4694_1.Contig9	ETK.Q..SY..Y.TLE.....HFNH.LT.R..I.I.H..C.S.RQ..I.....W.KEHKM		15: 71825	hox?

name	sequence	accession	position	class
	'!' for match		LG:coord.	
g_anbio_scaff_4694_1.Contig10	ETK.Q..SY..Y.TLE.....HFNR.LT.R..I.I.H..C.S.RQ..I.....W.KEHKM		15:71825	hox?
g_awjsf_scaff_4464_1.Contig5	--K.Q..SY..Y.TLE.....HFNR.LT.R..I.I.H..C.S-----		21:85120	hox?
Lottia-Scr_86927_	DSK.S..SY..H.TLE.....HYNK.LT.R..I.I.H...T.RQ..I.....W.KD---	JGI Lotg1 protein id: 86927		
Capitella-Scr_EU196541_	DNK.T..SY..H.TLE.....HFNR.LT.R..I.I.HS...T.RQ..I.....W.KE---	EU196541		
pancreas_duodenum__1_Mus_musculus_	ENK.T...Y..A.LLE.....LFNK.I.....V...VM...T.RH..I.....W.KEEDK	NP_032840		
Branchiostoma-Hox2_AB028207_	SS..L..V..NT.LLE.....HYNK..CK...K.I.SY.D.N.RQV.I.....RQ..R---	AB028207		
g_axtpu_scaff_4896_1.Contig3	---SG..N..TK.L...N..LFNK.LT.K..I.I...IQ.N..QV.I.....Q.KRMKE		9:53730	labial
g_axtpu_scaff_4896_1.Contig4	---SG..N..TK.L.G..N..LFNK.LT.K..I.I...IQ.N..QV.-----		9:53730	labial
Drosophila-labial_NM_057265_	-NNSG..N..NK.LTE.....HFNR.LT.A..I.I.NT.Q.N..QV.I.....Q.KRV--	NM_057265		
Tribolium-labial_AAF64149_	CLNTG..N..NK.LTE.....HFNK.LT.A..I.I.S..Q.N..QV.I.....Q.KR---	AAF64149		
g_axtpu_scaff_4896_1.Contig2	-----LT.A..I.I.T..Q.N..QV.I.....Q.KRMKE		9:53730	labial
g_ajwnd_scaff_4604_1.Contig5	-VGS..N..TK.LTE.....HFNK.LT.A..I.I.T..Q.N..QV.I.....Q.KRMKE		15:71825	labial
g_aavsb_scaff_4656_1.Contig15	---G..N..TK.LTE.....HFNK.LT.A..I.I.N..Q.N..QV.I.....Q.KRMKE		18:79564	labial
g_arkho_scaff_4547_1.Contig2	---G..N..TK.LTE.....HFNK.LT.A..I.I.NV.Q.N..QV.I.....Q.-----		1:5456	labial
g_aavsb_scaff_4656_1.Contig7	-----I.I.NV.Q.N..QV.I.....Q.KRMKE		18:79564	labial
Branchiostoma-Hox1_AB028206_	GPNNG..N..TK.LTE.....HYNK.LT.A..V.I.....N..QV.I.....Q.KR---	AB028206		
Capitella-labial_EU196537_	-PNMG..N..NK.LTE.....HFNK.LT.A..I.I..S.G.N..QV.I.....Q.KRL--	EU196537		
Lottia-labial_100648_	-PNSG..N..NK.LTE.....HFNK.LT.A..I.I..S.G.N..QV.I.....Q.KR---	JGI Lotg1 protein id: 100648		
Lottia-pb_110623_	GS..L...Y.NT.LLE.....HFNK.LC...I.I..S.D.T.RQV.....Y.-----	JGI Lotg1 protein id: 110623		
Drosophila-pb_NM_057322_	LP..L...Y.NT.LLE.....HFNK.LC...I.I..S.D.T.RQV.....H.-----	NM_057322		
Tribolium-pb_EEZ99256_	LP..L...Y.NT.LLE.....HFNK.LC...I.I..S.D.T.RQV.....H.-----	EEZ99256		
g_adlvn_scaff_4304_2.Contig14	MP..L...Y.NT.LLE.....HFNK.LC...I.I..S.D.S.RQV.....H...TMM		15:71870	?
g_agkld_scaff_4527_1.Contig4	MP..L...Y.NT.LLE.....HFNK.LC...I.I..S.D.S.RQV.....H...TVM		3:19288	?
g_apppz_scaff_4373_1.Contig11	MP..L...Y.NT.LLE.....HFNK.LC...I.I..S.D.S.RQV.....H...TTM		21:85040	?
g_adlvn_scaff_4304_2.Contig9	MP..L...Y.NT.LLE.....HFNK.LC.....		15:71870	?
Capitella-pb_EU196538_	HP..L...Y.NT.LLE.....HFNK.LC...I.I..S.D.T.RQV.....F.-----	EU196538		
Tribolium-zen_NP_001036813_	AGK.A...Y.SA.LVE..R..HHGK.L...IQI.EN...S.RQ..I.....H.KE---	NP_001036813		
g_adhdu_scaff_4669_1.Contig2	PTK.V...Y.SA.LVE.....HFNR.LC...I.M.NL...T.RQ..I.....Y.K---		21:85075	hox3
g_amdsu_scaff_4454_1.Contig21	--K.A...Y.SA.LVE.....HFNR.LC...V.M.NL.S.T.RQ..I.....Y.KEQKN		15:71825	hox3
Capitella-Hox3_EU196539_	PSK.A...Y.SA.LVE.....HFNR.LC...I.M..L..T.RQ..I.....Y.KD---	EU196539		
Lottia-Hox3_56601_	PAK.A...Y.SA.LVE.....HFNR.LC...I.M..L..S.RQ-----	JGI Lotg1 protein id: 56601		
g_amdsu_scaff_4454_1.Contig17	--K.P...Y.TA.LTE.....HFTR.LC...V.M.GL.H.T.RQ..I.....		15:71825	hox3
Branchiostoma-Hox3_X68045_	AGK.A...Y.SA.LVE.....HFNR.LC...V.M..M...T.RQ..I.....Y.KE---	X68045		
Drosophila-zen_AAF54087_	KLK.S.....SV.LVE..N..KSNM.LY.T..I.I.QR.S.C.RQV.I.....F.KD---	AAF54087		
g_aheja_scaff_4145_1.Contig5	KTK.T..S.NGV.LLE.....TNNM.L..L..I.I.NY...S.KQV.I.....V.F.KEG--		23:89444	gsx
g_atxvn_scaff_4590_1.Contig4	SSKKI..VY..S.LLE..R..AANM.LT.L..I.I.TY.S.S.KQV.I.....V.Y.KE---		5:33116	gsx
g_aneyu_scaff_4415_1.Contig10	SSK.I.....ST.LLE..R..SANM.L..L..I.I.TY...S.KQV.I.....V.Y.KE---		6:37542	gsx
Gsx1__Mus_musculus_	SSK.M.....ST.LLE..R..ASN.M.L..L..I.I.TY...S.KQV.I.....V.H.KEGKG	AAI37770.1		
g_aucja_scaff_4557_1.Contig17	--K.I.....SA.LLE..R..STNM.L..I..I.ISKY...S.KQV.I.....V.H.KEG--		19:80662	gsx