

Supplementary File

Putative extremely high rate of proteome innovation in lancelets might be explained by high rate of gene prediction errors.

László Bányai and László Patthy

Institute of Enzymology, Research Centre for Natural Sciences, Hungarian Academy of

Sciences, Budapest, P.O. Box 286, H-1519, Hungary,

Corresponding author: László Patthy,

POBox address: Budapest, P.O. Box 286, H-1519, Hungary,

Street address: Budapest, Magyar tudósok körútja 2, H-1117, Hungary

Tel: (361) 382 6751

Supplementary Table S1. Comparison of the domain architectures of orthologous proteins of *B. belcheri* and *B. floridae*. One hundred proteins of *B. belcheri*, containing at least two Pfam-A domains, were selected and their *B. floridae* orthologs (if any) were identified by the reciprocal best-hit method using a cut off value of 60% protein sequence identity.¹ Amino acid sequence identity over the aligned region. ²Domain architecture is defined as the linear sequence of Pfam-A domains. Domains that differ in the domain architectures of orthologs from the two amphioxus species are highlighted in bold underline. The table compares the domain architectures of proteins that have orthologs in the high quality Swiss-Prot database. Entries whose domain architecture is identical with those of orthologs in the Swiss-Prot database are marked with an asterisk*.

Sequence ID		Protein sequence identity (%) ¹	Domain architecture ²	
<i>B. belcheri</i>	<i>B. floridae</i>		<i>B. belcheri</i>	<i>B. floridae</i>
001440_PFF0*	XP_002598316.1*	87	P4Ha_N 2OG-FeII_Oxy_3	P4Ha_N 2OG-FeII_Oxy_3
002260_PFF0*	XP_002598117.1*	86	Activin_recp Pkinase_Tyr	Activin_recp Pkinase_Tyr
003500_PFF0*	XP_002598733.1*	82	CLCA VWA_2	CLCA VWA_2
003850_PFF0*	XP_002597871.1	92	Pep_M12B_propep Reprolysin_5 Disintegrin	Pep_M12B_propep Reprolysin_5 <u>Pep M12B propep</u> Disintegrin
012350_PFF0*	XP_002604729.1*	80	Kazal_2 SPARC_Ca_bdg Thyroglobulin_1	Kazal_2 SPARC_Ca_bdg Thyroglobulin_1
017590_PFF0*	XP_002598432.1*	77	Cu-oxidase_3 Cu-oxidase Cu-oxidase_2	Cu-oxidase_3 Cu-oxidase Cu-oxidase_2
052490_PFF0*	XP_002608045.1*	93	Fz NTR	Fz NTR
058270_PFF0	XP_002586055.1	72	I-set Fz Kringle	I-set Fz Kringle <u>Fz</u> <u>Kringle</u> <u>I-set</u> <u>Pkinase Tyr</u> <u>I-set</u> <u>Pkinase Tyr</u>
078830_PFF0*	XP_002596432.1*	93	CPSase_L_chain CPSase_L_D2 Biotin_carb_C HMGL-like PYC_OADA Biotin_lipoyl	CPSase_L_chain CPSase_L_D2 Biotin_carb_C HMGL-like PYC_OADA Biotin_lipoyl
080250_PFF0	XP_002598506.1	94	<u>LRR 8</u> <u>I-set</u> Wnt	Wnt

080250_PFF0	XP_002598508.1	94	<u>LRR_8</u> <u>I-set</u> Wnt	Wnt
091850_PFF0	XP_002591393.1	75	Gal_Lectin OLF HRM <u>GPS</u> GAIN 7tm_2	Gal_Lectin OLF HRM GAIN 7tm_2
102470_PFF0*	XP_002608336.1	98	RNA_pol_Rpb2_1 RNA_pol_Rpb2_2 RNA_pol_Rpb2_3 RNA_pol_Rpb2_4 RNA_pol_Rpb2_5 RNA_pol_Rpb2_6 <u>RNA_pol_Rpb2_7</u>	RNA_pol_Rpb2_1 RNA_pol_Rpb2_2 RNA_pol_Rpb2_3 RNA_pol_Rpb2_4 RNA_pol_Rpb2_5 RNA_pol_Rpb2_6
103400_PFF0	XP_002593834.1*	91	Ank_3 Ank_2 Ank_4 Ank_2 Arm Arm	Arm Arm
114280_PFF0	XP_002608942.1	89	C2 C2 FerI C2 FerB C2 C2 C2 C2 C2 Ferlin_C	C2 C2 FerI C2 FerB C2 C2 C2 C2 C2 Ferlin_C
117350_PFF0*	XP_002599461.1*	89	TGFb_propeptide TGF_beta	TGFb_propeptide TGF_beta
118940_PFF0*	XP_002587581.1*	86	HAD_2 APH Acyl-CoA_dh_N Acyl-CoA_dh_M Acyl-CoA_dh_1	HAD_2 APH Acyl-CoA_dh_N Acyl-CoA_dh_M Acyl-CoA_dh_1
123650_PFF0*	XP_002603715.1	95	CAP_GLY <u>Dynactin</u>	CAP_GLY
123650_PFF0*	XP_002603716.1	93	<u>CAP_GLY</u> Dynactin	Dynactin
127590_PFF0	XP_002614044.1*	86	Kazal_2 Kazal_2 Kazal_2 SEA Kazal_2 Kazal_2 Kazal_2 Kazal_2 Kazal_2 Kazal_1 Kazal_1	Kazal_2 Kazal_2 Kazal_2 SEA Kazal_2 Kazal_2 Kazal_2 Kazal_2 Kazal_2 Kazal_1 Kazal_1

			Laminin_EGF Laminin_EGF	Laminin_EGF Laminin_EGF <u>Kazal 2</u> <u>EGF</u> <u>Laminin G 1</u> <u>Laminin G 1</u> <u>EGF</u> <u>Laminin G 1</u>
127600_PFF0	XP_002614044.1*	90		<u>Kazal 2</u> <u>Kazal 2</u> <u>Kazal 2</u> <u>SEA</u> <u>Kazal 2</u> <u>Kazal 2</u> <u>Kazal 2</u> <u>Kazal 1</u> <u>Kazal 1</u> <u>Laminin EGF</u> <u>Laminin EGF</u>
			Kazal_2 EGF Laminin_G_1 Laminin_G_1 EGF Laminin_G_1	Kazal_2 EGF Laminin_G_1 Laminin_G_1 EGF Laminin_G_1
128050_PFF0	XP_002603923.1	71	TSP_1 Ldl_recept_a MACPF TSP_1 GCC2_GCC3	TSP_1 <u>TSP 1</u> Ldl_recept_a MACPF TSP_1 GCC2_GCC3
133320_PFF0	XP_002610402.1	91	SRCR Kringle SRCR Trypsin	SRCR Kringle SRCR Trypsin
135460_PFF0*	XP_002605157.1*	85	Fz Frizzled	Fz Frizzled
144220_PFF0	XP_002591459.1	92	RICTOR_N RICTOR_M RasGEF_N_2 RICTOR_V	RICTOR_N RICTOR_M RasGEF_N_2 RICTOR_V
152200_PFF0*	–		FHA CEP170_C	
153460_PFF0*	–		Ank_2 Ank_2 Ank_2 Ion_trans	
157010_PFF0*	XP_002611039.1	87	EF-hand_7 Ferric_reduct <u>FAD binding 8</u> NAD_binding_6	EF-hand_7 Ferric_reduct <u>NAD_binding_6</u>

157070_PFF0*	XP_002611055.1*	95	ANAPC10 HECT	ANAPC10 HECT
157720_PFF0	XP_002612291.1	90	HYR GCC2_GCC3	<u>Troponin</u> HYR GCC2_GCC3
158710_PFF0	XP_002600118.1	95	tRNA-synt_1 Anticodon_1 Val_tRNA-synt_C	tRNA-synt_1 Anticodon_1 Val_tRNA-synt_C
158830_PFF0*	XP_002600149.1*	83	IGFBP VWC TSP_1	IGFBP VWC TSP_1
160400_PFF0	XP_002601973.1	93	Integrin_beta Integrin_B_tail Integrin_b_cyt	Integrin_beta Integrin_B_tail Integrin_b_cyt
161590_PFF0	XP_002592408.1	98	<u>FERM_M</u> <u>IRS</u> <u>Talin_middle</u> <u>I_LWEQ</u> <u>VBS</u> VBS I_LWEQ	VBS I_LWEQ
161590_PFF0	XP_002592411.1	92	FERM_M IRS Talin_middle <u>I_LWEQ</u> <u>VBS</u> <u>VBS</u> <u>I_LWEQ</u>	FERM_M IRS Talin_middle
161590_PFF0	XP_002592410.1	92	<u>FERM_M</u> <u>IRS</u> <u>Talin_middle</u> I_LWEQ VBS <u>VBS</u> <u>I_LWEQ</u>	I_LWEQ VBS
172520_PRF0*	XP_002611318.1*	97	Fz NTR	Fz NTR
185920_PRF0	XP_002606276.1*	92	An_peroxidase EGF_CA	An_peroxidase <u>Sushi</u> EGF_CA
186040_PRF0*	XP_002606276.1*	91	An_peroxidase Sushi EGF_CA	An_peroxidase Sushi EGF_CA
189350_PRF0*	XP_002596820.1	99	FbpA <u>DUF814</u> <u>DUF3441</u>	FbpA

189350_PRFO*	XP_002596821.1	80	<u>FbpA</u> DUF814 DUF3441	DUF814 DUF3441
192660_PRFO*	XP_002586029*	95	ThiF E1_FCCH E1_4HB ThiF UBA_e1_thiolCys E1_UFD	ThiF E1_FCCH E1_4HB ThiF UBA_e1_thiolCys E1_UFD
196330_PRFO	XP_002594642.1*	86	Ion_trans Ion_trans <u>Ion_trans</u> <u>Ion_trans</u>	Ion_trans Ion_trans
207610_PRFO*	XP_002610947.1*	88	TGFb_propeptide TGF_beta	TGFb_propeptide TGF_beta
208940_PRFO*	XP_002607923.1	95	<u>ANF_receptor</u> Pkinase_Tyr Guanylate_cyc	Pkinase_Tyr Guanylate_cyc
209230_PRFO	XP_002610589.1*	88	Neur_chan_LBD Neur_chan_memb <u>Neur_chan_LBD</u> <u>Neur_chan_memb</u>	Neur_chan_LBD Neur_chan_memb
211270_PRFO*	XP_002591619.1*	88	BAR_3 PH ArfGap Ank_2	BAR_3 PH ArfGap Ank_2
215230_PRFO*	XP_002589217.1*	88	PMT MIR PMT_4TMC	PMT MIR PMT_4TMC
215230_PRFO*	XP_002589229.1*	90	PMT MIR PMT_4TMC	PMT MIR PMT_4TMC
222490_PRFO*	XP_002598311.1	97	<u>DMAP_binding</u> DNMT1-RFD zf-CXXC BAH BAH DNA_methylase	DNMT1-RFD zf-CXXC BAH BAH DNA_methylase
223320_PRFO	XP_002601301.1	79	Pep_M12B_propep Reprolysin TSP_1 ADAM_spacer1 TSP_1 TSP_1 TSP_1 TSP_1	Pep_M12B_propep Reprolysin TSP_1 ADAM_spacer1 TSP_1 TSP_1 TSP_1 TSP_1 <u>TSP_1</u> <u>TSP_1</u> <u>TSP_1</u>
227800_PRFO	XP_002608349.1	63	SRCR	SRCR

			SRCR SRCR Lysyl_oxidase	SRCR SRCR Lysyl_oxidase SRCR <u>Lysyl_oxidase</u> <u>Lysyl_oxidase</u>
237250_PRFO	XP_002612866.1	91		<u>ANATO</u> <u>A2M</u> <u>Thiol-ester_cl</u> <u>A2M_comp</u>
			A2M_recep NTR	A2M_recep NTR
237260_PRFO	XP_002612866.1	90	A2M_N A2M_N_2 ANATO A2M Thiol-ester_cl A2M_comp	ANATO A2M Thiol-ester_cl A2M_comp A2M_recep NTR
237260_PRFO	AF391289_5	92	A2M_N A2M_N_2 ANATO A2M <u>Thiol-ester_cl</u> <u>A2M_comp</u>	A2M_N A2M_N_2 ANATO A2M
246010_PRFO*	XP_002613969.1*	72	PG_binding_1 Peptidase_M10 Hemopexin Hemopexin Hemopexin Hemopexin	PG_binding_1 Peptidase_M10 Hemopexin Hemopexin Hemopexin Hemopexin
247370_PRFO*	--		WIF Pkinase_Tyr	
248080_PRFO	XP_002591824.1*	92	<u>EGF_3</u> Sushi Sushi VWA Trypsin	Sushi Sushi VWA Trypsin
253950_PRFO*	XP_002610496.1*	97	Histone RhoGEF PH RasGEF_N RasGEF	Histone RhoGEF PH RasGEF_N RasGEF
253960_PRFO*	XP_002610495.1*	96	zf-Sec23_Sec24 Sec23_trunk Sec23_BS Sec23_helical Gelsolin	zf-Sec23_Sec24 Sec23_trunk Sec23_BS Sec23_helical Gelsolin
254170_PRFO*	XP_002595526.1*	87	ABC_membrane ABC_tran ABC_membrane	ABC_membrane ABC_tran ABC_membrane

			ABC_tran	ABC_tran
256530_PRF0	B6MUN4.1	64	<u>Myb DNA-binding</u> SWIRM	SWIRM <u>JAB</u>
256520_PRF0	B6MUN4.1	76	JAB	<u>SWIRM</u> JAB
257610_PRF0*	XP_002587133.1*	84	EST1 EST1_DNA_bind EST1_DNA_bind PIN_4	EST1 EST1_DNA_bind EST1_DNA_bind PIN_4
258810_PRF0	XP_002605408.1*	60	Glyco_transf_29 <u>Glyco transf 29</u>	Glyco_transf_29
258870_PRF0*	XP_002595259.1	98	<u>STAT_int</u> STAT_alpha STAT_bind SH2	STAT_alpha STAT_bind SH2
258870_PRF0*	XP_002585719.1	92	STAT_int <u>STAT_alpha</u> <u>STAT_bind</u> <u>SH2</u>	STAT_int
258870_PRF0*	XP_002595260.1	100	<u>STAT_int</u> <u>STAT_alpha</u> STAT_bind <u>SH2</u>	STAT_bind
258870_PRF0*	XP_002595256.1	96	<u>STAT_int</u> <u>STAT_alpha</u> STAT_bind SH2	STAT_bind SH2
259020_PRF0*	XP_002600999.1*	97	GRAM GRAM RabGAP-TBC	GRAM GRAM RabGAP-TBC
272770_PRF0*	XP_002601715.1*	90	AAA_11 AAA_11 AAA_12	AAA_11 AAA_11 AAA_12
283240_PRF0	CAA06854.1	95	Reeler Spond_N fn3 TSP_1 fn3 TSP_1 TSP_1	Reeler Spond_N fn3 TSP_1 fn3 TSP_1 TSP_1
293630_PRF0*	XP_002613483.1*	92	Chorein_N ATG_C	Chorein_N ATG_C
293740_PRF0	XP_002613924.1	92	<u>SHR-BD</u>	<u>VPS13</u> <u>VPS13 mid rpt</u> <u>UBA</u> <u>SHR-BD</u>

			<u>VPS13_C</u>	<u>VPS13_C</u>
209920_PRM0	XP_002613924.1	89	UBA	<u>VPS13</u> <u>VPS13_mid_rpt</u> UBA <u>SHR-BD</u> <u>VPS13_C</u>
209930_PRF0	XP_002613924.1	81		<u>VPS13</u> <u>VPS13_mid_rpt</u> UBA <u>SHR-BD</u> <u>VPS13_C</u>
209940_PRF0	XP_002613924.1	86	<u>Chorein_N</u> VPS13 VPS13_mid_rpt	VPS13 VPS13_mid_rpt <u>UBA</u> <u>SHR-BD</u> <u>VPS13_C</u>
209940_PRF0	XP_002613923.1	94	Chorein_N <u>VPS13</u> <u>VPS13_mid_rpt</u>	Chorein_N
321850_PRF0*	XP_002585883.1*	85	ANF_receptor Lig_chan-Glu_bd Lig_chan	ANF_receptor Lig_chan-Glu_bd Lig_chan
319230_PRF0*	XP_002600703.1	77	cNMP_binding DEP cNMP_binding RasGEF_N RasGEF	cNMP_binding DEP cNMP_binding
319230_PRF0*	XP_002600702.1	95	cNMP_binding DEP cNMP_binding RasGEF_N RasGEF	RasGEF
325460_PRF0	XP_002608790.1*	88	FG-GAP FG-GAP Integrin_alpha2	FG-GAP FG-GAP Integrin_alpha2 Integrin_alpha
320370_PRF0	XP_002594515.1	72	<u>zf-RING_5</u> zf-B_box fn3 <u>SPRY</u>	<u>zf-C3HC4_3</u> zf-B_box fn3
325780_PRF0*	XP_002602117.191*	91	Glycos_transf_2 Ricin_B_lectin	Glycos_transf_2 Ricin_B_lectin
328450_PRF0	XP_002607180.1*	79	Kunitz_BPTI NTR	<u>WAP</u> <u>Kazal_2</u> <u>Kunitz_BPTI</u> Kunitz_BPTI NTR

328460_PRFO	XP_002607180.1*	85	WAP Kazal_2 Kunitz_BPTI Kunitz_BPTI	WAP Kazal_2 Kunitz_BPTI Kunitz_BPTI <u>NTR</u>
328470_PRFO	XP_002607185.1	96	ABC_membrane ABC_tran ABC_membrane ABC_tran ABC_membrane ABC_tran ABC_membrane ABC_tran	ABC_membrane ABC_tran ABC_membrane ABC_membrane ABC_membrane ABC_membrane ABC_membrane ABC_tran
328810_PRFO	XP_002592166.1	91	zf-HC5HC2H FYRN FYRC SET	zf-HC5HC2H FYRN FYRC SET
328940_PRFO	XP_002612925.1	90	<u>dsrm</u> <u>dsrm</u> A_deamin <u>A deamin</u>	A_deamin
328940_PRFO	XP_002612924.1	99	dsrm dsrm <u>A deamin</u> <u>A deamin</u>	dsrm dsrm
329040_PRFO*	XP_002612907.1*	82	Flavodoxin_1 FAD_binding_1 NAD_binding_1	Flavodoxin_1 FAD_binding_1 NAD_binding_1
329370_PRFO*	XP_002611195.1	70	PLAT Lipoxygenase	<u>Catalase</u> PLAT Lipoxygenase
329970_PRFO	XP_002606233.1	92	DAG_kinase_N C1_1 C1_1 DAGK_cat DAGK_acc	DAG_kinase_N C1_1 C1_1 DAGK_cat DAGK_acc
330040_PRFO*	–		Activin_recp Pkinase	
330210_PRFO*	XP_002602990.1	98	EF-hand Mito_carr Mito_carr Mito_carr	EF-hand Mito_carr Mito_carr Mito_carr <u>Peptidase M2</u>

Supplementary Table S2. Comparison of the domain architectures of orthologous proteins of *B. belcheri* and *B. floridae*. One hundred proteins of *B. belcheri*, containing at least two Pfam-A domains, were selected and their *B. floridae* orthologs (if any) were identified by the reciprocal best-hit method using a cut off value of 60% protein sequence identity. ¹Amino acid sequence identity over the aligned region. ²Domain architecture is defined as the linear sequence of Pfam-A domains. Domains that differ in the domain architectures of orthologs from the two amphioxus species are highlighted in bold underline. The table compares the domain architectures of proteins that have no orthologs in the high quality Swiss-Prot database.

Sequence ID		Protein sequence identity (%) ¹	Domain architecture ²	
<i>B. belcheri</i>	<i>B. floridae</i>		<i>B. belcheri</i>	<i>B. floridae</i>
000200_PFF0	AAN62850.1	85	V-set CBM_14	V-set CBM_14
001280_PFF0	XP_002608265.1	88	CBM_14 ILEI	CBM_14 ILEI
017700_PFF0	XP_002598460.1	85	Gal_Lectin Gal_Lectin GPS 7tm_2	Gal_Lectin Gal_Lectin GPS 7tm_2
018300_PFF0	XP_002588697.1	68	Lectin_C fn2 fn2 fn2 fn2 fn2	Lectin_C fn2 fn2 fn2 fn2 fn2
040970_PFF0	XP_002596007.1	95	kringle kringle trypsin	kringle kringle trypsin
068220_PFF0	XP_002586877.1	79	fn2 fn2 fn2 fn2 CUB CUB	fn2 fn2 fn2 fn2 CUB CUB
080050_PFF0	XP_002606926.1	92	N-glycanase_N N-glycanase_C	N-glycanase_N N-glycanase_C
124390_PFF0	–		cEGF FXa_inhibition EGF_CA EGF_CA NIDO EGF_CA EGF_CA SEA EGF_CA	
159900_PFF0	XP_002600642.1	82	AAA_8 MT AAA_9 Dynein_heavy	AAA_8 MT AAA_9 AAA_9 Dynein_heavy

167280_PRFO	XP_002611740.1	66	Kringle Somatomedin_B 7tm_2	Lectin_C Kringle Somatomedin_B 7tm_2
173360_PRFO	XP_002593467.1	92	Astacin kringle	Astacin kringle
180420_PRFO	XP_002609978.1	90	Somatomedin_B 7tm_2	<u>5-FTHF_cyc-lig</u> Somatomedin_B 7tm_2
184730_PRFO	XP_002597992.1	65	Ldl_recept_a Kringle Kringle 7tm_2	Ldl_recept_a Kringle Kringle 7tm_2
188610_PRFO	XP_002609579.1	86	ASC F5_F8_type_C F5_F8_type_C Kringle ASC	ASC F5_F8_type_C F5_F8_type_C Kringle ASC
196740_PRFO	XP_002601342.1	89	<u>Fibrinogen_C</u> <u>Fibrinogen_C</u> <u>I-set</u> <u>fn3</u> <u>fn3</u> <u>fn3</u> <u>fn3</u> Y_phosphatase Y_phosphatase	Y_phosphatase Y_phosphatase
196740_PRFO	XP_002601345.1	78	Fibrinogen_C Fibrinogen_C <u>I-set</u> <u>fn3</u> <u>fn3</u> <u>fn3</u> <u>fn3</u> <u>Y_phosphatase</u> <u>Y_phosphatase</u>	Fibrinogen_C Fibrinogen_C fn3
200810_PRFO	XP_002608508.1	75	Astacin CUB MAM	Astacin CUB MAM
258300_PRFO	XP_002605710.1	90	<u>Ldl_recept_a</u> <u>SRCR</u> <u>Ldl_recept_a</u> Trypsin	Trypsin
258300_PRFO	XP_002605711.1	90	<u>Ldl_recept_a</u> SRCR <u>Ldl_recept_a</u> <u>Trypsin</u>	SRCR
260260_PRFO	–		BACK Kelch_1	
269420_PRFO	XP_002605854.1	73	CUB	CUB

			Ldl_recept_a Fz Kringle Neur_chan_memb	Ldl_recept_a Fz Kringle Neur_chan_memb
304470_PRFO	XP_002587583.1	88	Ldl_recept_a VWA Zona_pellucida	Ldl_recept_a VWA Zona_pellucida
320550_PRFO	-		Kringle Kringle Lectin_C CUB Lectin_C MAM Lectin_C Kringle SRCR	
329690_PRFO	XP_002611153.1	90	BTB BTB BACK Kelch_1 Kelch_1 Kelch_1 Kelch_1	BTB BTB BACK Kelch_1 Kelch_1 Kelch_1 Kelch_1
329890_PRFO	XP_002606025.1	77	COR Death	COR Death

Supplementary Table S3. Comparison of the domain architectures of proteins of *B. belcheri* selected from dataset *Branchiostoma.belcheri_HapV2_proteins.fa* (release 1) with those of their equivalents in the dataset *Branchiostoma.belcheri_v15h11.r2_protein.fa* (release 2) and dataset *Branchiostoma.belcheri_v18h27.r3_ref_protein.fa* (release 3). One hundred proteins of *B. belcheri*, containing at least two Pfam-A domains, were selected from release 1 and their matches were identified in release 2 and release 3. ²Domain architecture (DA) is defined as the linear sequence of Pfam-A domains. Entries whose domain architecture is identical with those of orthologs in the high quality Swiss-Prot database are marked with an asterisk*. Mispredicted entries with DA that deviates from those of orthologous Swiss-Prot entries are highlighted in bold underline. The data are arranged in two categories based on the presence or absence of orthologs in the Swiss-Prot database.

Sequence ID release 1	DA	Sequence ID release 2	DA	Sequence ID release 3	DA
Orthologs are present in the Swiss-Prot database					
001440_PFF0*	P4Ha_N 2OG-FeII_Oxy_3	<u>053450F.t1</u>	P4Ha_N	089550F.t1*	P4Ha_N 2OG-FeII_Oxy_3
002260_PFF0*	Activin_recp Pkinase_Tyr	243600F.t1*	Activin_recp Pkinase_Tyr	297980F.t2*	Activin_recp Pkinase_Tyr
003500_PFF0*	CLCA VWA_2	041250R.t1*	CLCA VWA_2	265240R.t1*	CLCA VWA_2
003850_PFF0*	Pep_M12B_propep Reprolysin_5 Disintegrin	<u>062250R.t1</u>	Reprolysin_5 Disintegrin	095570F.t1*	Pep_M12B_propep Reprolysin_5 Disintegrin
012350_PFF0*	Kazal_2 SPARC_Ca_bdg Thyroglobulin_1	229830F.t1*	Kazal_2 SPARC_Ca_bdg Thyroglobulin_1	197610F.t1*	Kazal_2 SPARC_Ca_bdg Thyroglobulin_1
017590_PFF0*	Cu-oxidase_3 Cu-oxidase_2 Cu-oxidase_2	002580R.t1*	Cu-oxidase_3 Cu-oxidase_2 Cu-oxidase_2	<u>204890R.t2</u>	Cu-oxidase_3 Cu-oxidase_2 Cu-oxidase_2 Cu-oxidase
052490_PFF0*	Fz NTR	017500F.t1*	Fz NTR	127920R.t1*	Fz NTR
<u>058270_PFF0</u>	I-set Fz Kringle	142670R.t2	I-set Fz Kringle I-set Pkinase_Tyr	192300R.t2	I-set Fz Kringle I-set Pkinase_Tyr
078830_PFF0*	CPSase_L_chain CPSase_L_D2 Biotin_carb_C HMGL-like PYC_OADA Biotin_lipoyl	097650F.t2*	CPSase_L_chain CPSase_L_D2 Biotin_carb_C HMGL-like PYC_OADA Biotin_lipoyl	252380R.t2*	CPSase_L_chain CPSase_L_D2 Biotin_carb_C HMGL-like PYC_OADA Biotin_lipoyl
<u>080250_PFF0</u>	LRR_8 I-set Wnt	<u>001910R.t1</u>	Wnt	062470F.t1*	Wnt

			Wnt		
091850_PFF0	Gal_Lectin OLF HRM GAIN GPS 7tm_2	<u>324940R.t1</u>	Gal_Lectin OLF HRM GAIN GAIN GPS 7tm_2	191840R.t2	Gal_Lectin OLF HRM GAIN GPS 7tm_2
102470_PFF0*	RNA_pol_Rpb2_1 RNA_pol_Rpb2_2 RNA_pol_Rpb2_3 RNA_pol_Rpb2_4 RNA_pol_Rpb2_5 RNA_pol_Rpb2_6 RNA_pol_Rpb2_7	010690R.t1*	A_pol_Rpb2_1 A_pol_Rpb2_2 A_pol_Rpb2_3 A_pol_Rpb2_4 A_pol_Rpb2_5 A_pol_Rpb2_6 A_pol_Rpb2_7	282790F.t1*	A_pol_Rpb2_1 A_pol_Rpb2_2 A_pol_Rpb2_3 A_pol_Rpb2_4 A_pol_Rpb2_5 A_pol_Rpb2_6 A_pol_Rpb2_7
<u>103400_PFF0</u>	Ank_3 Ank_2 Ank_4 Arm Arm	<u>028040F.t1</u>	Ank_4 Ank_2 Arm Arm	<u>043790F.t1</u>	Ank_4 Ank_2 Arm Arm
<u>114280_PFF0</u>	C2 C2 FerI C2 FerB C2 C2 C2 C2 Ferlin_C	261060R.t1*	C2 C2 FerI C2 FerA FerB C2 C2 C2 C2 Ferlin_C	167750F.t1*	C2 C2 FerI C2 FerA FerB C2 C2 C2 C2 Ferlin_C
117350_PFF0*	TGFb_propeptide TGF_beta	099520R.t1*	TGFb_propeptide TGF_beta	195530R.t1*	TGFb_propeptide TGF_beta
118940_PFF0*	HAD_2 APH Acyl-CoA_dh_N Acyl-CoA_dh_M Acyl-CoA_dh_1	092840R.t1*	HAD_2 APH Acyl-CoA_dh_N Acyl-CoA_dh_M Acyl-CoA_dh_1	003000F.t1*	HAD_2 APH Acyl-CoA_dh_N Acyl-CoA_dh_M Acyl-CoA_dh_1
123650_PFF0*	CAP_GLY Dynactin	265490R.t1*	CAP_GLY Dynactin	121780F.t5*	CAP_GLY Dynactin
<u>127590_PFF0</u>	Kazal_2 Kazal_2 Kazal_2 SEA Kazal_2 Kazal_2 Kazal_2 SEA	<u>303040R.t1</u>	Kazal_2 Kazal_2 Kazal_2 SEA Kazal_2 Kazal_2 Kazal_2 Kazal_2 Kazal_1 Kazal_2 Kazal_2 Kazal_2	212090F.t4*	Kazal_2 Kazal_2 Kazal_2 SEA

Kazal_2
Kazal_2
Kazal_2
Kazal_1
Kazal_1
Laminin_EGF
Laminin_EGF

Kazal_2
Kazal_2
Kazal_2
Kazal_1
Kazal_1
Kazal_1
Laminin_EGF
Laminin_EGF
Kazal_2
EGF
Laminin_G_1
Laminin_G_1
EGF
Laminin_G_1

Kazal_2
Kazal_2
Kazal_2
Kazal_1
Kazal_1
Kazal_1
Laminin_EGF
Laminin_EGF
Kazal_2
EGF
Laminin_G_1
Laminin_G_1
EGF
Laminin_G_1

127600_PFF0

303040R.t1

212090F.t4*

Kazal_2
EGF
Laminin_G_1
Laminin_G_1
EGF
Laminin_G_1

Kazal_2
Kazal_2
Kazal_2
SEA
Kazal_2
Kazal_2
Kazal_2
Kazal_2
Kazal_1
Kazal_2
Kazal_2
Kazal_2
SEA
Kazal_2
Kazal_2
Kazal_2
Kazal_1
Kazal_1
Laminin_EGF
Laminin_EGF
Kazal_2
EGF
Laminin_G_1
Laminin_G_1
EGF
Laminin_G_1

Kazal_2
Kazal_2
Kazal_2
SEA
Kazal_2
Kazal_2
Kazal_2
Kazal_1
Kazal_1
Laminin_EGF
Laminin_EGF
Kazal_2
EGF
Laminin_G_1
Laminin_G_1
EGF
Laminin_G_1

128050_PFF0

TSP_1

Ldl_recept_a
MACPF
TSP_1
GCC2_GCC3

013570R.t2

TSP_1
TSP_1
Ldl_recept_a
MACPF
TSP_1
GCC2_GCC3

174680F.t1

TSP_1
TSP_1
Ldl_recept_a
MACPF
TSP_1
GCC2_GCC3

133320_PFF0

SRCR
Kringle
SRCR
Trypsin

250080R.t1

SRCR
Kringle
SRCR
Trypsin

228670R.t1

SRCR
Kringle
SRCR
Trypsin

135460_PFF0*

Fz
Frizzled

222910F.t1*

Fz
Frizzled

019690R.t1

Frizzled

144220_PFF0

RICTOR_N
RICTOR_M

045000R.t1

RCC1
RCC1
RCC1
RCC1
RICTOR_N
RICTOR_M

081090R.t3

RCC1
RCC1
RCC1
RCC1
RICTOR_N
RICTOR_M

	RasGEF_N_2 RICTOR_V		RasGEF_N_2 RICTOR_V		RasGEF_N_2 RICTOR_V
152200_PFF0*	FHA CEP170_C	<u>098310R.t1</u>	CEP170_C	251720F.t1*	FHA CEP170_C
153460_PFF0*	Ank_2 Ank_2 Ank_2 Ion_trans	227850R.t1*	Ank_2 Ank_2 Ank_2 Ion_trans	004550F.t1*	Ank_2 Ank_2 Ank_2 Ion_trans
157010_PFF0*	EF-hand_7 Ferric_reduct FAD_binding_8 NAD_binding_6	030190R.t2*	EF-hand_7 Ferric_reduct FAD_binding_8 NAD_binding_6	276360F.t1*	EF-hand_7 Ferric_reduct FAD_binding_8 NAD_binding_6
157070_PFF0*	ANAPC10 HECT	<u>030090R.t1</u>	ANAPC10 HECT ANAPC10 HECT	276460F.t1*	ANAPC10 HECT
157720_PFF0	HYR GCC2_GCC3	124730F.t1	HYR GCC2_GCC3	<u>261920R.t2</u>	Troponin HYR GCC2_GCC3
<u>158710_PFF0</u>	tRNA-synt_1 Anticodon_1 Val_tRNA-synt_C	<u>189810F.t1</u>	tRNA-synt_1 Anticodon_1	<u>259960R.t1</u>	tRNA-synt_1 Anticodon_1
158830_PFF0*	IGFBP VWC TSP_1	190070F.t1*	IGFBP VWC TSP_1	259710R.t1*	IGFBP VWC TSP_1
160400_PFF0	Integrin_beta Integrin_B_tail Integrin_b_cyt	100620R.t1	Integrin_beta Integrin_B_tail Integrin_b_cyt	196660R.t1	Integrin_beta Integrin_B_tail Integrin_b_cyt
<u>161590_PFF0</u>	FERM_M IRS Talin_middle I_LWEQ VBS VBS I_LWEQ	<u>181770F.t1</u>	FERM_M Talin_middle I_LWEQ I_LWEQ VBS VBS	<u>085620R.t1</u>	FERM_M IRS Talin_middle LWEQ
<u>161590_PFF0</u>	FERM_M IRS Talin_middle I_LWEQ VBS VBS I_LWEQ	<u>181780F.t1</u>	 I_LWEQ	<u>085620R.t3</u>	 VBS VBS
172520_PRF0*	Fz NTR	078910F.t1*	Fz NTR	190570F.t1*	Fz NTR
<u>185920_PRF0</u>	An_peroxidase EGF_CA	<u>262810R.t1</u>	An_peroxidase EGF_CA	222960R.t1*	An_peroxidase Sushi EGF_CA

<u>227800</u> PRF0	SRCR SRCR SRCR Lysyl_oxidase	<u>010500R.t1</u>	SRCR SRCR SRCR Lysyl_oxidase	<u>283050F.t3</u>	SRCR SRCR SRCR Lysyl_oxidase
<u>237250</u> PRF0		111050F.t1*	A2M_N A2M_N_2 ANATO A2M Thiol-ester_cl A2M_comp A2M_recep NTR	171620R.t1*	A2M_N A2M_N_2 ANATO A2M Thiol-ester_cl A2M_comp A2M_recep NTR
<u>237260</u> PRF0	A2M_N A2M_N_2 ANATO A2M Thiol-ester_cl A2M_comp	111050F.t1*	A2M_N A2M_N_2 ANATO A2M Thiol-ester_cl A2M_comp A2M_recep NTR	171620R.t1*	A2M_N A2M_N_2 ANATO A2M Thiol-ester_cl A2M_comp A2M_recep NTR
246010_PRFF0*	PG_binding_1 Peptidase_M10 Hemopexin Hemopexin Hemopexin Hemopexin	098400F.t1*	PG_binding_1 Peptidase_M10 Hemopexin Hemopexin Hemopexin Hemopexin	<u>217220R.t1</u>	PG_binding_1 Peptidase_M10 Hemopexin Hemopexin Hemopexin Hemopexin MFS_1
247370_PRFF0*	WIF Pkinase_Tyr	113360F.t1*	WIF Pkinase_Tyr	045780R.t1*	WIF Pkinase_Tyr
248080_PRFF0	EGF_3 Sushi Sushi VWA Trypsin	073650R.t1	EGF_3 Sushi Sushi VWA Trypsin	246540R.t1	EGF_3 Sushi Sushi VWA Trypsin
253950_PRFF0*		<u>290630R.t1</u>	Histone RhoGEF Histone RhoGEF PH RasGEF_N RasGEF	135030R.t1*	Histone RhoGEF PH RasGEF_N RasGEF
253960_PRFF0*	zf-Sec23_Sec24 Sec23_trunk Sec23_BS Sec23_helical Gelsolin	290640R.t1*	zf-Sec23_Sec24 Sec23_trunk Sec23_BS Sec23_helical Gelsolin	135040R.t1*	zf-Sec23_Sec24 Sec23_trunk Sec23_BS Sec23_helical Gelsolin
254170_PRFF0*	ABC_membrane ABC_tran ABC_membrane ABC_tran	154120R.t1*	ABC_membrane ABC_tran ABC_membrane ABC_tran	026920R.t1*	ABC_membrane ABC_tran ABC_membrane ABC_tran
<u>256520</u> PRF0		044700R.t1*	Myb_DNA-binding SWIRM	105830R.t1*	Myb_DNA-binding SWIRM

	JAB		JAB		JAB
<u>256530</u> PRF0	Myb_DNA-binding SWIRM	044700R.t1*	Myb_DNA-binding SWIRM JAB	105830R.t1*	Myb_DNA-binding SWIRM JAB
257610_PRFO*	EST1 EST1_DNA_bind EST1_DNA_bind PIN_4	174840F.t1*	EST1 EST1_DNA_bind EST1_DNA_bind PIN_4	039650R.t1*	EST1 EST1_DNA_bind EST1_DNA_bind PIN_4
<u>258810</u> PRF0	Glyco_transf_29 Glyco_transf_29	<u>000220F.t1</u>	Glyco_transf_29 Glyco_transf_29	299600F.t1*	Glyco_transf_29
258870_PRFO*	STAT_int STAT_alpha STAT_bind SH2	049290R.t1*	STAT_int STAT_alpha STAT_bind SH2	154380F.t1*	STAT_int STAT_alpha STAT_bind SH2
259020_PRFO*	GRAM GRAM RabGAP-TBC	011870R.t1*	GRAM GRAM RabGAP-TBC	075250R.t1*	GRAM GRAM RabGAP-TBC
272770_PRFO*	AAA_11 AAA_11 AAA_12	091600R.t1*	AAA_11 AAA_11 AAA_12	182450R.t1*	AAA_11 AAA_11 AAA_12
283240_PRFO	Reeler Spond_N fn3 TSP_1 fn3 TSP_1 TSP_1	241240R.t1	Reeler Spond_N fn3 TSP_1 fn3 TSP_1 TSP_1	179850R.t1	Reeler Spond_N fn3 TSP_1 fn3 TSP_1 TSP_1
293630_PRFO*		<u>312700R.t1</u>	TPR_12 TPR_12 TPR_7 TPR_12 TPR_7 TPR_12 Chorein_N ATG_C	110520R.t2*	Chorein_N ATG_C
<u>293740</u> PRF0		<u>151150R.t1</u>	SHR-BD VPS13_C SHR-BD VPS13_C	<u>257130F.t1</u>	SHR-BD VPS13_C
<u>209920</u> PRM0	UBA	<u>151150R.t1</u>		<u>257120F.t1</u>	UBA UBA
<u>209940</u> PRF0	Chorein_N VPS13 VPS13_mid_rpt	<u>151170R.t1</u>	SHR-BD VPS13_C SHR-BD VPS13_C VPS13 VPS13_mid_rpt	<u>257100F.t1</u>	VPS13 VPS13_mid_rpt
321850_PRFO*	ANF_receptor Lig_chan-Glu_bd Lig_chan	<u>030780R.t1</u>	Lig_chan-Glu_bd Lig_chan	275750F.t1*	ANF_receptor Lig_chan-Glu_bd Lig_chan

319230_PRFO*	cNMP_binding DEP cNMP_binding RasGEF_N RasGEF	<u>102020R.t1</u>	cNMP_binding cNMP_binding DEP cNMP_binding SEA SEA	158680R.t1*	cNMP_binding DEP cNMP_binding RasGEF_N RasGEF
325460_PRFO	FG-GAP FG-GAP Integrin_alpha2	100710F.t1	FG-GAP FG-GAP Integrin_alpha2	196740F.t1	FG-GAP FG-GAP Integrin_alpha2
<u>320370 PRFO</u>	zf-RING_5 zf-B_box fn3 SPRY	<u>145570R.t1</u>	zf-C3HC4_3 zf-B_box fn3	<u>031850F.t1</u>	zf-RING_5 zf-B_box fn3
325780_PRFO*	Glycos_transf_2 Ricin_B_lectin	<u>100260F.t1</u>	Glycos_transf_2 BACK Glycos_transf_2 Ricin_B_lectin Glycos_transf_2 Ricin_B_lectin	<u>196320F.t1</u>	Glycos_transf_2 Ricin_B_lectin Glycos_transf_2 Ricin_B_lectin
<u>328450 PRFO</u>	Kunitz_BPTI NTR	212930R.t1*	WAP Kazal_2 Kunitz_BPTI Kunitz_BPTI NTR	040720F.t1*	WAP Kazal_2 Kunitz_BPTI Kunitz_BPTI NTR
<u>328460 PRFO</u>	WAP Kazal_2 Kunitz_BPTI Kunitz_BPTI	212930R.t1*	WAP Kazal_2 Kunitz_BPTI Kunitz_BPTI NTR	040720F.t1*	WAP Kazal_2 Kunitz_BPTI Kunitz_BPTI NTR
<u>328470 PRFO</u>	ABC_membrane ABC_tran ABC_membrane ABC_tran ABC_membrane ABC_tran ABC_membrane ABC_tran	<u>212960R.t3</u>	ABC_membrane ABC_membrane ABC_tran ABC_membrane ABC_membrane ABC_membrane ABC_membrane ABC_membrane ABC_tran	<u>040670F.t2</u>	ABC_membrane ABC_tran ABC_membrane ABC_membrane
<u>328810 PRFO</u>	zf-HC5HC2H FYRN FYRC FYRC SET	<u>279190F.t1</u>	zf-HC5HC2H zf-HC5HC2H PHD PHD PHD PHD zf-HC5HC2H FYRN FYRC SET	<u>172210F.t4</u>	zf-HC5HC2H PHD PHD PHD PHD zf-HC5HC2H FYRN FYRC SET
<u>328940 PRFO</u>	dsrcm	<u>278970F.t1</u>	dsrcm	<u>172050F.t2</u>	

	dsrm A_deamin A_deamin		dsrm A_deamin		dsrm A_deamin
			adh_short		
329040_PRFO*	Flavodoxin_1 FAD_binding_1 NAD_binding_1	278780F.t1*	Flavodoxin_1 FAD_binding_1 NAD_binding_1	171870F.t1*	Flavodoxin_1 FAD_binding_1 NAD_binding_1
329370_PRFO*	PLAT Lipoxygenase	<u>246260F.t1</u>	PLAT Lipoxygenase Lipoxygenase	286940R.t1*	PLAT Lipoxygenase
329970_PRFO	DAG_kinase_N C1_1 C1_1 DAGK_cat DAGK_acc	242250R.t1	DAG_kinase_N C1_1 C1_1 DAGK_cat DAGK_acc	057640F.t1	DAG_kinase_N C1_1 C1_1 DAGK_cat DAGK_acc
330040_PRFO*	Activin_recp Pkinase	242390R.t1*	Activin_recp Pkinase	<u>057490F.t2</u>	Activin_recp Pkinase Activin_recp Pkinase
330210_PRFO*	EF-hand_1 Mito_carr Mito_carr Mito_carr	242710R.t1*	EF-hand_1 Mito_carr Mito_carr Mito_carr	057220F.t1*	EF-hand_1 Mito_carr Mito_carr Mito_carr

Orthologs are absent in the Swiss-Prot database

000200_PFF0	V-set CBM_14	094410F.t1	V-set CBM_14	144580F.t1	V-set CBM_14
001280_PFF0	CBM_14 ILEI	259500R.t1	CBM_14 ILEI	169170F.t1	CBM_14 ILEI
017700_PFF0	Gal_Lectin Gal_Lectin GPS 7tm_2	002350R.t1	zf-B_box Gal_Lectin Gal_Lectin GPS 7tm_2	204650R.t1	zf-B_box Gal_Lectin Gal_Lectin GPS 7tm_2
018300_PFF0	Lectin_C fn2 fn2 fn2 fn2 fn2	261420F.t1	fn2 fn2 fn2	222240F.t1	Lectin_C fn2 fn2 fn2 fn2 fn2
040970_PFF0	kringle kringle trypsin	236680F.t1	kringle kringle trypsin	076590R.t1	kringle kringle trypsin
068220_PFF0	fn2 fn2 fn2 fn2 CUB CUB	288190R.t1	fn2 fn2 fn2 fn2 CUB CUB	100050R.t1	fn2 fn2 fn2 fn2 CUB CUB
080050_PFF0	N-glycanase_N N-glycanase_C	072890R.t1	N-glycanase_N N-glycanase_C	251010F.t1	N-glycanase_N N-glycanase_C
124390_PFF0	cEGF FXa_inhibition EGF_CA EGF_CA NIDO EGF_CA EGF_CA SEA EGF_CA	140980F.t1	cEGF FXa_inhibition EGF_CA EGF_CA NIDO VWD EGF_CA EGF_CA cEGF SEA EGF_CA	141260F.t1	cEGF FXa_inhibition EGF_CA EGF_CA NIDO VWD EGF_CA EGF_CA cEGF SEA EGF_CA
159900_PFF0	AAA_8 MT AAA_9 Dynein_heavy	101480R.t1	AAA_8 MT AAA_9 AAA_9 Dynein_heavy	158030R.t1	AAA_8 MT AAA_9 AAA_9 Dynein_heavy
167280_PRF0	Kringle Somatomedin_B 7tm_2	007220R.t1	Kringle Somatomedin_B 7tm_2	118250R.t1	Kringle Somatomedin_B 7tm_2
173360_PRF0	Astacin kringle	299040F.t1	Astacin kringle	053640F.t1	Astacin kringle

180420_PRFO	Somatomedin_B 7tm_2	050300R.t1	Somatomedin_B 7tm_2	069800F.t1	Somatomedin_B 7tm_2
184730_PRFO	Ldl_recept_a Kringle Kringle 7tm_2	002500F.t1	Ldl_recept_a Kringle Kringle 7tm_2	176740F.t1	Ldl_recept_a Ldl_recept_a Kringle Kringle Somatomedin_B 7tm_2
188610_PRFO	ASC F5_F8_type_C F5_F8_type_C Kringle ASC	021920R.t1	ASC F5_F8_type_C F5_F8_type_C Kringle ASC	155310R.t1	ASC F5_F8_type_C Kringle ASC
196740_PRFO	Fibrinogen_C Fibrinogen_C I-set fn3 fn3 fn3 fn3 Y_phosphatase Y_phosphatase	024030F.t2	Fibrinogen_C Fibrinogen_C I-set fn3 fn3 fn3 fn3 Y_phosphatase Y_phosphatase	086240F.t1	Fibrinogen_C Fibrinogen_C I-set fn3 fn3 fn3 fn3 Y_phosphatase Y_phosphatase
200810_PRFO	Astacin CUB MAM	016310R.t1	Astacin CUB MAM	104370F.t1	Astacin CUB MAM
258300_PRFO	Ldl_recept_a SRCR Ldl_recept_a Trypsin	060660R.t1	SRCR Kringle Kringle Ldl_recept_a PAN_1 Ldl_recept_a SRCR Ldl_recept_a Trypsin	006090R.t1	SRCR Kringle Kringle Ldl_recept_a PAN_1 Ldl_recept_a SRCR Ldl_recept_a Trypsin
260260_PRFO	BACK Kelch_1	162090R.t1	BACK Kelch_1	152800F.t1	BACK Kelch_1
269420_PRFO	CUB Ldl_recept_a Fz Kringle Neur_chan_memb	303590R.t1	Death CUB CUB Ldl_recept_a Fz Kringle Neur_chan_memb	009080F.t1	Death CUB CUB Ldl_recept_a Fz Kringle Neur_chan_memb
304470_PRFO	Ldl_recept_a VWA Zona_pellucida	092860F.t1	Ldl_recept_a VWA Zona_pellucida	002980R.t1	Ldl_recept_a VWA Zona_pellucida
320550_PRFO	Kringle Kringle Lectin_C CUB Lectin_C MAM	145290F.t1	Lectin_C MAM	009580R.t1	Kringle Kringle Lectin_C CUB Lectin_C MAM

	Lectin_C Kringle SRCR		Lectin_C Kringle SRCR		Lectin_C Kringle SRCR
329690_PRFO	BTB BTB BACK Kelch_1 Kelch_1 Kelch_1 Kelch_1	245850F.t1	BTB BTB BACK Kelch_1 Kelch_1 Kelch_1 Kelch_1	287390R.t1	BTB BTB BACK Kelch_1 Kelch_1 Kelch_1 Kelch_1
329890_PRFO	COR Death	047410F.t1	COR Death	173700F.t1	Death
