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Study of a new member of the Myelin Protein Zero Family

Racz, P.I.

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Curriculum Vitae

Peter Imre Racz was born on 5 June in 1979 in Budapest, Hungary. He studied biology at the University of Szeged, Faculty of Science, Szeged, Hungary (formerly named as Jozsef Attila University). In 2003 as an undergraduate student he won the Scholarship of the Hungarian Republic and the Scholarship of the City of Szeged, and he took the opportunity to visit Prof. Dr. Katalin Csiszar's laboratory in the Cardiovascular Research Center at the University of Hawaii, USA for a semester. Here he started to work on a novel gene mutation in the rough coat (*rc*) mice that resulted in cyclic hair loss. After the graduation in 2004 he went back to the Cardiovascular Research Center and continued his work on the rough coat strain under the mentorship of Dr. Tongyu Cao. From 2007 he worked in the group of Dr. Matyas Mink in the Department of Genetics of University of Szeged, Hungary and in the company Zenon Bio Ltd. on the EU-funded project 'High-throughput Tools for Biomedical Screens in Zebrafish' project (ZF-TOOLS), carried out in collaboration with Dr. Annemarie Meijer and Prof Dr. Herman Spaink in the Institute of Biology, University of Leiden, where he enrolled as a PhD student. During this period he spent several months at the Institute of Biology, University of Leiden to extend his work on the rough coat mutation by studying the homologous gene in zebrafish. In addition, he graduated as an economist with a major in management studies in 2009 at the University of Szeged, Faculty of Economics and Business Administration.

List of publications

Cao T, **Racz P**, Szauter KM, Groma G, Nakamatsu GY, Fogelgren B, Pankotai E, He QP, Csiszar K. (2007) *Mutation in Mpzl3, a novel gene encoding a predicted adhesion protein, in the rough coat (rc) mice with severe skin and hair abnormalities.* J Invest Dermatol. 127:1375-86.

Racz P., Mink M., Ordas A., Cao T, Szalma S., Szauter KM, Csiszar K. (2009) *The human orthologue of murine Mpzl3 with predicted adhesive and immune functions is a potential candidate gene for immune-related hereditary hair loss.* Exp Dermatol. 18:261-3.

Z. Hegedűs, A. Zakrzewska, V. C. Ágoston, A. Ordas, **P. Racz**, M. Mink, H. P. Spaink and A. H. Meijer (2009) *Deep sequencing of the zebrafish transcriptome response to mycobacterium infection.* Mol Immunol. 46:2918-30.

Hegedus Z, Ordas A, **Racz P**, Spaink HP, Mink M, Meijer AH
Deep sequencing of the innate immune response of zebrafish embryos to Salmonella infection. (in preparation)

Racz P, Zakrzewska A, Csukonyi E, Ordas A, Spaink HP, Mink M, Meijer AH.
Functional analysis of the mpzl3 gene in zebrafish. (in preparation)

Supplementary tables

Supplementary table 1.

Results of the GO term based microarray analyses of the up-regulated genes in mpzl3 morphant fish.

GO-term	Name	Number of reporters associated	Gene Symbols
GO:0050789	regulation of biological process		
GO:0045449	regulation of transcription	32	pea3, erm, eve1, flh, foxd5, gbx1, her1, her6, hmgb1, ilf2, irx7, smad1, mespa, msgn1, msxe, nfil3, nrf1, otx1l, purb, LOC793089, sp5l, tbx6, tfap2a, trfp, tp73l, mycn, wu:fi38b05, wu:fk63e10, zgc:110825, zgc:136520, zgc:158360, zhx3
GO:0006306	DNA methylation	1	dnmt4
GO:0045786	negative regulation of cell cycle	1	tp73l
GO:0042664	negative regulation of cell growth	1	tp73l
GO:0030334	regulation of cell migration	1	bik
GO:0042127	regulation of cell proliferation	1	zic2a
GO:0042664	negative regulation of endodermal cell fate specification	1	bmp2b
GO:0030514	negative regulation of BMP signaling pathway	1	szl
GO:0030178	negative regulation of Wnt receptor signaling pathway	1	dkk1
GO:0040036	regulation of fibroblast growth factor receptor signaling pathway	3	dusp6, spry4, spry2
GO:0035023	regulation of Rho protein signal transduction	1	dzip1, dkk1, dusp6, szl, spry4, spry2, zgc:103517
GO:0042325	regulation of phosphorylation	1	zgc:73377
GO:0042981	regulation of apoptosis	3	bik, birc2, heatr1
GO:0043280	positive regulation of caspase activity	1	bik
GO:0006417	regulation of translation	2	eif4e1a, zgc:64152
GO:0043487	regulation of RNA stability	1	heatr1
GO:0050767	regulation of neurogenesis	1	gli2a
GO:0065008	regulation of biological quality		
GO:0006879	cellular iron ion homeostasis	1	tfa
GO:0007596	blood coagulation	1	crygm4/fbln4
GO:0050821	protein stabilization	1	szl
GO:0007154	cell communication		
GO:0045168	cell-cell signaling during cell fate commitment	2	bmp2b, dld
GO:0046331	lateral inhibition	1	dld
GO:0007186	G-protein coupled receptor protein signaling pathway	5	cxcr4a, fzd3, fzd8a, fzd8b, zgc:103757
GO:0007219	Notch signaling pathway	4	dld, her6, lfng, zgc:136520

GO-term	Name	Number of reporters associated	Gene Symbols
GO:0016055	Wnt receptor signaling pathway	9	ck2b, dact1, dkk1, fzd3, fzd8a, fzd8b, frzb, szl, sp5l,
GO:0007229	integrin-mediated signaling pathway	1	mibp2
GO:0007243	protein kinase cascade	2	mapk14a
GO:0007264	small GTPase mediated signal transduction	2	rab34, zgc:103517
GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	1	kifc1
GO:0007049	cell cycle		
GO:0007067	mitosis	2	rad21, wu:fc04c01
GO:0007064	mitotic sister chromatid cohesion	1	rad21
GO:0048468	cell development		
GO:0055015	ventricular cardiac muscle cell development	1	bmp2b
GO:0006915	apoptosis	4	bik, birc2, heatr1, tp73l
GO:0030239	myofibril assembly	1	cxcr4a
GO:0014032	neural crest cell development	1	tfap2a
GO:0055002	striated muscle cell development	2	cxcr4a, gli2a
GO:0021953	central nervous system neuron differentiation	2	gli2a, wu:fc04c01
GO:0021954	central nervous system neuron development	1	wu:fc04c01
GO:0021523	somatic motor neuron differentiation	2	dld, gli2a
GO:0045165	cell fate commitment		
GO:0045165	cell fate commitment	4	bmp2b, dld, dusp6, ndr2
GO:0001709	cell fate determination	1	ndr2
GO:0042663	regulation of endodermal cell fate specification	2	bmp2b, dusp6
GO:0006928	cell motility		
GO:0042074	cell migration involved in gastrulation	3	bmp2b, dkk1, lbr
GO:0060030	dorsal convergence	1	bmp2b
GO:0008283	cell proliferation		
GO:0021846	cell proliferation in forebrain	1	zic2a
GO:0033278	cell proliferation in midbrain	1	zic2a
GO:0016043	cellular component organization and biogenesis		
GO:0006334	nucleosome assembly	1	zgc:65861
GO:0007018	microtubule-based movement	2	kifc1, wu:fb37a10
GO:0015031	protein transport	6	pcf11, dzip1, mrpl45, wu:fb61d08, zgc:76878
GO:0006607	NLS-bearing substrate import into nucleus	1	dzip1
GO:0000059	protein import into nucleus, docking	1	zgc:76878
GO:0006839	mitochondrial transport	1	ucp4

GO-term	Name	Number of reporters associated	Gene Symbols
GO:0007010	cytoskeleton organization and biogenesis	4	cxcr4a, kifc1, wu:fb37a10, zgc:63783
GO:0042254	ribosome biogenesis and assembly	4	ctsl1b, heatr1, nola1, tsr1
GO:0048869	cellular developmental process		
GO:0030154	cell differentiation	16	bik, birc2, bmp2b, cxcr4a, dld, dusp6, gli2a, heatr1, lfng, msgn1, ndr2, nono, tfap2a, tp73l, wu:fc04c01
GO:0001710	mesodermal cell fate commitment	1	bmp2b
GO:0050935	iridophore differentiation	1	tfap2a
GO:0030318	melanocyte differentiation	1	tfap2a
GO:0044237	cellular metabolic process		
GO:0006098	pentose-phosphate shunt	1	taldo1
GO:0006425	glutamyl-tRNA aminoacylation	1	qars
GO:0006424	glutamyl-tRNA aminoacylation	1	qars
GO:0006432	phenylalanyl-tRNA aminoacylation	1	farsa
GO:0009117	nucleotide metabolic process	2	taldo1, zgc:66117
GO:0006412	translation	18	eif2s1l, eif4e1a, eif5a, qars, farsa, rpl10a, rpl3, rpl4, rpl5a, rpl7l1, rps15, rps2, rps4x, rps7, rpsa, zgc:153404, zgc:64152, zgc:92872
GO:0005975	carbohydrate metabolic process	2	taldo1, wu:fc20b11
GO:0042574	retinal metabolic process	1	rdh1l
GO:0006457	protein folding	4	cct5, ppial, pin1, si:ch211-288g17.3
GO:0043687	post-translational protein modification	10	dusp6, hdac8, mapk14a, plk4, parp1, si:dkey-14d8.5, ube2v2, zgc:103757
GO:0030163	protein catabolic process	5	psmc2, psmc1b, psmb1, usp5
GO:0006511	ubiquitin-dependent protein catabolic process	2	psmb1, usp5
GO:0051246	regulation of protein metabolic process	3	eif4e1a, ube2v2, zgc:64152
GO:0051258	protein polymerization	1	wu:fb37a10
GO:0006508	proteolysis	4	ctsl1b, psmb1, usp5, zgc:110307
GO:0042572	retinol metabolic process	2	rdh1l
GO:0008380	RNA splicing	1	rbm22
GO:0006397	mRNA processing	2	rbm22, zgc:110689
GO:0016071	mRNA metabolic process	3	rbm22, snrpd1, zgc:110689
GO:0006364	rRNA processing	3	ctsl1b, heatr1, nola1
GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1	heatr1
GO:0032502	developmental process		

GO-term	Name	Number of reporters associated	Gene Symbols
GO:0021984	adenohypophysis development	1	gli2a
GO:0021508	floor plate formation	2	gli2a, ndr2
GO:0001707	mesoderm formation	3	bmp2b, mespa, sp5l
GO:0014028	notochord formation	1	ndr2
GO:0043049	otic placode formation	1	msxe
GO:0035138	pectoral fin morphogenesis	1	rdh1l
GO:0048048	embryonic eye morphogenesis	1	ndr2
	embryonic retina		
GO:0060059	morphogenesis in camera-type eye	1	zic2a
GO:0048547	gut morphogenesis	3	dld, gli2a, rdh1l
GO:0048618	post-embryonic foregut morphogenesis	1	gli2a
GO:0001702	gastrulation with mouth forming second	1	mespa
GO:0021575	hindbrain morphogenesis	1	irx7
GO:0002009	morphogenesis of an epithelium	4	blf, bmp2b, gli2a, ndr2
GO:0009887	organ morphogenesis	7	bmp2b, dld, gli2a, msxe, ndr2, rdh1l, zic2a
GO:0001889	liver development	1	bmp2b
GO:0035121	tail morphogenesis	1	sp5l
GO:0021536	diencephalon development	2	gli2a, zic2a
GO:0030900	forebrain development	3	dkk1, gli2a, zic2a
GO:0032835	glomerulus development	2	flh, gli2a
GO:0030902	hindbrain development	5	fzd3, irx7, otx1, sp5l, tfap2a
GO:0021754	facial nucleus development	1	fzd3
GO:0030901	midbrain development	2	otx1l, zic2a
GO:0030917	midbrain-hindbrain boundary development	1	otx1l
GO:0007420	brain development	10	dkk1, gli2a, fzd3, irx7, otx1l, sp5l, sfpq, tfap2a, zgc:136520
GO:0055016	hypochord development	1	lfng
GO:0030903	notochord development	4	bmp2b, dkk1, ndr2, sp5l
GO:0030325	adrenal gland development	1	flh
GO:0035050	embryonic heart tube development	3	dzip1, flh, ndr2
GO:0030097	hemopoiesis	1	spry4
GO:0001822	kidney development	3	flh, gli2a, zgc:101674
GO:0048793	pronephros development	1	zgc:101674
GO:0007517	muscle development	3	bmp2b, cxcr4a, gli2a
GO:0031018	endocrine pancreas development	1	gli2a
GO:0031017	exocrine pancreas development	1	rdh1l
GO:0001654	eye development	6	mcm2, mcm3, ndr2, nrf1, zgc:136520, zic2a
GO:0060041	retina development in camera-type eye	4	mcm2, mcm3, nrf1, zic2a
GO:0001501	skeletal development	2	rdh1l, tfap2a

GO-term	Name	Number of reporters associated	Gene Symbols
GO:0051216	cartilage development	1	tfap2a
GO:0007398	ectoderm development	2	ctnnb1, dkk1
GO:0007498	mesoderm development	4	bmp2b, mespa, msgn1, sp5l
GO:0009790	embryonic development		
GO:0001756	somitogenesis	5	dld, gli2a, her1, her6, zgc:136520
GO:0001757	somite specification	1	her6
GO:0009880	embryonic pattern specification	3	ctnnb1, her6, smad1
GO:0040016	embryonic cleavage	2	
GO:0000578	embryonic axis specification	1	ctnnb1
GO:0007275	multicellular organismal development		
GO:0007389	pattern specification process	18	bmp2b, ctnnb1, dzip1, dld, dusp6, eve1, flh, gli2a, her1, her6, smad1, ndr2, otx1l, szl, sp5l, spry2, zgc:136520, zic2a
GO:0048263	determination of dorsal identity	1	szl
GO:0048264	determination of ventral identity	1	bmp2b
GO:0007368	determination of left/right symmetry	5	bmp2b, dzip1, dld, flh, ndr2
GO:0009952	anterior/posterior pattern formation	7	dld, gli2a, her1, her6, otx1l, sp5l, zgc:136520
GO:0009953	dorsal/ventral pattern formation	6	bmp2b, dusp6, gli2a, szl, spry2, zic2a
GO:0006810	transport		
GO:0006820	anion transport	2	tomm40l, vdac2
GO:0006826	iron ion transport	1	tfa
GO:0006813	potassium ion transport	2	atp1b3a, zgc:77244
GO:0006814	sodium ion transport	1	atp1b3a
GO:0016192	vesicle-mediated transport	1	wu:fb61d08
GO:0002376	immune system process		
GO:0006955	immune response	1	ilf2
GO:0009617	response to bacterium	2	im:7144703, tfa
GO:0055114	oxidation reduction		
GO:0055114	oxidation reduction	4	adh5, rdh1l, zgc:100900, zgc:109991
GO:0003008	system process		
GO:0008015	blood circulation	1	gli2a
GO:0007601	visual perception	1	zgc:103757
GO:0050896	response to stimulus		
GO:0009409	response to cold	1	nrf1
GO:0002347	response to tumor cell	1	tp73l
GO:0032526	response to retinoic acid	1	mespa
GO:0006950	response to stress	5	crygm4, cox4i1, mapk14a, nrf1, ppial
GO:0001666	response to hypoxia	2	cox4i1, ppial
GO:0009611	response to wounding	2	crygm4 / fb1n4
GO:0048511	rhythmic process		
GO:0048511	rhythmic process	1	nfil3

Supplementary table 2.

Results of the GO term based microarray analyses of the down-regulated genes in the mpz13 morphant fish.

GO-term	Name	Number of reporters associated	Gene symbol
GO:0050789	regulation of biological process		
GO:0006417	regulation of translational	1	zgc:56330
GO:0042661	regulation of mesodermal cell fate specification	1	churc1
GO:0045449	regulation of transcription	17	arntl1a, bmi1, bmi1b, bzw1l, cebpg, cdc5l, churc1, eml2, foxa, smad2, , txt2, nr2f1l, rab35, sox11b, mycl1a, zgc:153348, zgc:86635
GO:0006306	DNA methylation	1	dnmt1
GO:0030334	regulation of cell migration	1	churc1
GO:0042981	regulation of apoptosis	2	bokb, ripk2
GO:0032313	regulation of Rab GTPase activity	1	rutbc3
GO:0045449	regulation of transcription	19	arntl1a, bmi1, bmi1b, bzw1l, cebpg, eml2, foxa, , mad2, mxtx2, nr2f1l, , ab35, sox11b, mycl1a, zgc:86635
GO:0051246	regulation of protein metabolic process	5	ube2d2, zgc:100959, zgc:112077, zgc:55512, zgc:56330
GO:0065008	regulation of biological quality		
GO:0006879	cellular iron ion homeostasis	1	hd
GO:0042391	regulation of membrane potential	1	slc26a5
GO:0006914	autophagy		
GO:0006914	autophagy	3	atg5, zgc:73097
GO:0007154	cell communication		
GO:0007219	Notch signaling pathway	1	dab2
GO:0007179	transforming growth factor beta receptor signaling pathway	1	smad2
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	1	ptk2.1
GO:0007264	small GTPase mediated signal transduction	6	rab20, rab35, rutbc3, rhogc, zgc:77650, zgc:86635
GO:0007049	cell cycle		
GO:0007067	mitosis	2	zgc:64116, zgc:92321
GO:0048468	cell development		
GO:0006915	apoptosis	2	bokb, ripk2
GO:0051301	cell division		
GO:0000910	cytokinesis	1	kif23
GO:0006928	cell motility		
GO:0042074	cell migration involved in gastrulation	2	churc1, mxtx2

GO-term	Name	Number of reporters associated	Gene symbol
GO:0016043	cellular component organization and biogenesis		
GO:0006334	nucleosome assembly	1	h1m
GO:0007018	microtubule based movement	2	kif23, zgc:56231
GO:0015031	protein transport	14	arcn1l, chmp7, cog2, gosr2, rab35, snupn, tom1, zgc:100959, zgc:103537, zgc:55877, zgc:73136, zgc:77002, zgc:86635, zgc:92676
GO:0007034	vacuolar transport	1	zgc:92676
GO:0006909	phagocytosis	1	jmjd6
GO:0006898	receptormediated endocytosis	1	dab2
GO:0007030	Golgi organization and biogenesis	1	cog2
GO:0051276	chromosome organization and biogenesis	4	bmi1, bmi1b, dnmt1, h1m
GO:0007010	cytoskeleton organization and biogenesis	4	LOC559333, kif23, , xtx2, zgc:56231
GO:0044237	cellular metabolic process		
GO:0005975	carbohydrate metabolic process	9	aldoc, ldhb, pgm1, pgk1, pkm2, tpi1a, usp20, zgc:100959, zgc:63792
GO:0019642	anaerobic glycolysis	1	ldhb
GO:0006098	pentosephosphate shunt	1	tpi1a
GO:0006071	glycerol metabolic process	1	zgc:56068
GO:0006081	aldehyde metabolic process	1	aldh3a2
GO:0006542	glutamine biosynthetic process	1	glulb
GO:0006534	cysteine metabolic process	1	nfs1
GO:0006744	ubiquinone biosynthetic process	1	coq3
GO:0009117	nucleotide metabolic process	4	cmpk, rrm2b, rrm2, tpi1a
GO:0046114	guanosine biosynthetic process	1	zgc:66378
GO:0006633	fatty acid biosynthetic process	1	tpi1a
GO:0006511	ubiquitindependent protein catabolic process	2	uchl1, usp20
GO:0042744	hydrogen peroxide catabolic process	1	cat
GO:0008299	isoprenoid biosynthetic process	2	hmgcs1 zgc:103473
GO:0046839	phospholipid dephosphorylation	1	mtmr6
GO:0006644	phospholipid metabolic process	1	zgc:162119
GO:0008202	steroid metabolic process	1	osbpl2

GO-term	Name	Number of reporters associated	Gene symbol
GO:0043687	post-translational protein modification	15	dnmt1, prkcb1, ptk2.1, ptk2.1, ripk2, sgk, si:ch211-238n5.5, ube2d2, raf1, zgc:100959, zgc:112077, zgc:136697, zgc:55512, zgc:55587, zgc:56558
GO:0006508	proteolysis	4	ctsl1b, psmb1, usp5, zgc:110307
GO:0006457	protein folding	4	calrl, hspd1, LOC100002614, zgc:56703
GO:0006486	protein amino acid glycosylation	1	zgc:76904
GO:0006412	translation	3	mrpl3, rpl12, zgc:56330
GO:0006259	DNA metabolic process	10	cry1b, dnmt1, LOC791836, mcm3l, orc6l, rrm2, zgc:101596, zgc:103553, zgc:56122, zgc:66475
GO:0006281	DNA repair	3	cry1b, zgc:103553, zgc:66475
GO:0006270	DNA replication initiation	1	mcm3l
GO:0006367	transcription initiation from RNA polymerase II promoter	1	LOC799735
GO:0006400	tRNA modification	1	zgc:66378
GO:0008380	RNA splicing	1	zgc:123015
GO:0016071	mRNA metabolic process	2	dbr1, zgc:123015
GO:0006801	superoxide metabolic process	1	sod1
GO:0022610	biological adhesion		
GO:0007155	cell adhesion	1	cd36
GO:0032502	developmental process		
GO:0031101	fin regeneration	1	hspd1
GO:0001840	neural plate development	1	sinup
GO:0007369	gastrulation	3	churc1, mxtx2, mylip
GO:0002009	morphogenesis of an epithelium	2	mxtx2, sinup
GO:0060041	retina development in camera-type eye	1	dnmt1
GO:0007507	heart development	1	raf1
GO:0031017	exocrine pancreas development	1	dnmt1
GO:0007399	nervous system development	1	zgc:55580
GO:0009790	embryonic development		
GO:0040016	embryonic cleavage	1	kif23
GO:0001756	somitogenesis	1	nat13
GO:0009880	embryonic pattern specification	1	smad2
GO:0006810	transport		
GO:0006865	amino acid transport	1	zgc:110611
GO:0015904	tetracycline transport	2	hiat1a, slc46a1
GO:0015992	proton transport	1	zgc:55891
GO:0006821	chloride transport	1	slc26a5
GO:0008272	sulfate transport	1	slc26a5
GO:0015711	organic anion transport	1	slc16a3
GO:0006814	sodium ion transport	1	zgc:110611
GO:0006869	lipid transport	1	osbp12
GO:0019532	oxalate transport	1	slc26a5

akkor	Name	Number of reporters associated	Gene symbol
GO:0016192	vesicle mediated transport	6	arcn1l, dab2, jmjd6, vamp4, zgc:103537, zgc:73136
GO:0009056	catabolic process		
GO:0016042	lipid catabolic process	2	si:dkey-174c12.2, zgc:162119
GO:0055114	oxidation reduction		
GO:0055114	oxidation reduction	7	aldh2l, ald3a2, cat, jmjd6, ldhb, rrm2, sod1
GO:0050896	response to stimulus		
GO:0009416	response to light stimulus	1	arntl1a
GO:0046677	response to antibiotic	2	hiat1a, slc46a1
GO:0010038	response to metal ion	2	cat, sod1
GO:0051597	response to methylmercury	1	sod1
GO:0001666	response to hypoxia	1	pgk1
GO:0009611	response to wounding	1	hspd1
GO:0006950	response to stress	7	cat, cry1b, hspd1, hspa5, pgk1, zgc:103553, zgc:66475
GO:0048511	rhythmic process		
GO:0007623	circadian rhythm	1	arntl1a