Genes gained in Tetrapoda MF TreeMap

						5			poda IVII 1100	•						
histone methyltransferas	se	tumor necrosis factor receptor superfamily binding	protein binding		nall GTPase binding	zymoger binding	SH3 domain binding		acetylcholine-gated cation-selective channel activity		glucuronosyltransferase activity ubiquitin protein ligase activity		DNA-binding transcription repressor activity, RNA polymerase II-specific		DNA-binding transcription factor activity, RNA polymerase II-specific	
binding			cyclin binding	proteii ligase	ubiquitin receptor receptor ligase activity		ein fa	ukaryotic nitiation actor 4E pinding							DNA-binding transcription repressor activity	
cytokine activity		ubiquitin binding	SMAD ein binding	apolipoprot receptor binding	ein HMG box domain binding	binding binding		rleukin–7 eceptor binding	transmembr protein phosphatase activity	ein phospha growth fac beta-activa receptor act	tase activity tor protein-ho receptor a	histone methyltransfera activity activity (H3-K specific)	se guanyl puolootia			Pase adenyl-nucleotic exchange factor activity
		adenylate cyclase binding	hedgehog family protein binding	titin binding	growth factor activity TBP-class protein	protein kina A regulator subunit binding protein homodimeriza	y hor	ormone ctivity	transmembrane receptor protein tyrosine		methyltra activity (cone ansferase (H3–K36 cific) respeto pro serine/through	protein serine/threonin kinase inhibito	tein active acti	transr recepi tyrosi ac ai	nembrane or protein ubiquitin–protei ne kinase transferase tivator activity
cytokine receptor binding			protein kinase A binding	beta-2-microglobulin binding	binding translation initiation	activity interleukin receptor	_4 mis	eceptor binding sfolded rotein	phosphatase activity		rece acti	eptor ivity	activity	transcr factor a	and the contract of	cytoskeletal nchor activity
		binding	olfactory receptor binding	signaling receptor binding	factor binding FATZ binding	tor binding binding Peptide hormone		inding vth factor ceptor inding	structural constituent		extracellular matrix structural constituent		activin binding	U1 snRNF binding	lipopolysaccharid binding	ATPase–couple intramembrane lipid transporte activity
translation	RNA polymerase II transcription regulatory region sequence–specific DNA binding RNA polymerase II cis–regulatory region sequence–specific DNA binding			mRNA 3'–UTR binding		double-stranded DNA methylated DNA binding		equence–specific DNA binding	of skin epidermis structural constituent o		extracellular matrix f skin epidermis _{Jent} conferring tensile strength			MHC proteir d binding binding	lipid binding	ABC-type transporter ATPase-coupled lipid transmembrane transporter activity
repressor activity, mRNA regulatory element binding			cis-regulatory region sequence-specific DNA binding		DNA bin	ding, regions	scription gulatory on nucleic d binding	^C 5S	scavenger receptor activity	nutrient reservoir activity	toxin activity	extracellular matrix structural constituent conferring compression resistance	dynein complex binding	Arp2/3 complex binding	lgG binding	ATPase-coupled lip transmembrane transporter activity
					transcrip cis-regul region bi	otion seque		ecific binding	protein folding chaperone	114141		structural constituent of virion	calcium ion binding	hormone binding	metal ion binding	flippase activity