Genes lost in Crassiclitellata MF TreeMap

RNA-directed DNA polymerase activity peptide-O-fuc		nitric–oxide synthase activity		RNA-directed 5'-3' RNA polymerase activity		DNA binding	peptidoglycan binding		RNA polymerase II transcription regulatory region sequence–specific DNA binding		interleukin–1 receptor binding		death receptor binding	
		osyltransferase activity kinase activity		cysteine-typ endopeptidas activity involve in apoptotic process	endopeptidase activity involved	G-protein bet 5S rRNA binding	ta/gamma–subun copper ion binding	it compl neurop bind	ling s	gDNA econdary tructure binding	hormo cytokine activity	ne receptor bi Notch binding	nding _h ormone receptor binding	
endonuclease activity			RNA–DNA hybrid ribonuclease activity		nide peptide-O-fucosyltransferase a activity	intraciliary transport particle A binding	D-loop DNA binding	G-pro beta/gamm complex	na-subunit	netal ion binding	peptide hormone receptor binding	Tat protein binding	retinoic acid receptor binding	
calcium–dependent protein binding	caspase	myosii caspase binding		nding	translation initiation factor binding	transcription corepressor activity	RNA polymerase III general transcription initiation factor activity		signaling receptor activator activity enzyme inhibitor			repress ading transcrip NA polymeras	DNA-binding transcription repressor activity, RNA g transcription factor fic polymerase II-specific DNA-binding transcription	
	ubiquitin-like protein b		inding			signa	ıling receptor regi	ng receptor regulator activ		tivity		factor	factor activity, RNA	
calmodulin binding			protein self-associati		SUMO binding	tumor necrosis factor–activated receptor activity		membrane anchor activity		signalin		voltage-ga	rase II-specific	
	CARD doma	ain binding ubiquitin protein bi			phosphatase binding		neuropeptid receptor activ	le	neuropeptide Y receptor activity	recepto regulato activity	chan <mark>potas</mark>	notacciun	amina acid	