Predicted targets of miR-133

Gene product		Reference	Reference		Direct annotation
Aif1l		GO:0070062	MGI:MGI:4834177	GO_REF:0000096	extracellular vesicular exosome
Aif1l		GO:0003779	MGI:MGI:1354194	GO_REF:0000004	actin binding
Aif1l		GO:0008150	MGI:MGI:2156816	GO_REF:0000015	biological process
Aif1l		GO:0005856	MGI:MGI:1354194	GO_REF:0000004	cytoskeleton
Aif1l		GO:0005886	MGI:MGI:1354194	GO_REF:0000004	plasma membrane
Aif1l		GO:0015629	MGI:MGI:4834177	GO_REF:0000096	actin cytoskeleton
Aif1l		GO:0042995	MGI:MGI:1354194	GO_REF:0000004	cell projection
Aif1l		GO:0005509	MGI:MGI:2152098	GO_REF:0000002	calcium ion binding
Aif1l		GO:0051015	MGI:MGI:4834177	GO_REF:0000096	actin filament binding
Aif1l		GO:0016020	MGI:MGI:1354194	GO_REF:0000004	membrane
Aif1l		GO:0005737	MGI:MGI:1354194	GO_REF:0000004	cytoplasm
Aif1l	colocalizes_wit	GO:0005884	MGI:MGI:4834177	GO_REF:0000096	actin filament
Aif1l		GO:0046872	MGI:MGI:1354194	GO_REF:0000004	metal ion binding
Aif1l		GO:0005925	MGI:MGI:4834177	GO_REF:0000096	focal adhesion
Aif1l		GO:0043234	MGI:MGI:4417868	GO_REF:0000096	protein complex
Atp6ap2		GO:0060323	MGI:MGI:4834177	GO_REF:0000096	head morphogenesis
Atp6ap2		GO:0002003	MGI:MGI:4417868	GO_REF:0000096	angiotensin maturation
Atp6ap2		GO:0009897	MGI:MGI:4834177	GO_REF:0000096	external side of plasma membrane
Atp6ap2		GO:0044297	MGI:MGI:4417868	GO_REF:0000096	cell body
Atp6ap2		GO:0004872	MGI:MGI:2152098	GO_REF:0000002	receptor activity
Atp6ap2		GO:0006508	MGI:MGI:4834177	GO_REF:0000096	proteolysis
Atp6ap2		GO:0016021	MGI:MGI:1354194	GO_REF:0000004	integral component of membrane
Atp6ap2		GO:0043408	MGI:MGI:4834177	GO_REF:0000096	regulation of MAPK cascade
Atp6ap2		GO:0030177	MGI:MGI:4421218	PMID:20093472	positive regulation of Wnt signaling pathway
Atp6ap2		GO:0021903	MGI:MGI:4834177	GO_REF:0000096	rostrocaudal neural tube patterning
Atp6ap2		GO:0002003	MGI:MGI:4834177	GO_REF:0000096	angiotensin maturation
Atp6ap2		GO:0004190	MGI:MGI:4834177	GO_REF:0000096	aspartic-type endopeptidase activity
Atp6ap2		GO:0043005	MGI:MGI:4417868	GO_REF:0000096	neuron projection
Atp6ap2		GO:0016020	MGI:MGI:1354194	GO_REF:0000004	membrane
Atp6ap2		GO:0019899	MGI:MGI:4417868	GO_REF:0000096	enzyme binding
Atp6ap2		GO:0030177	MGI:MGI:4834177	GO_REF:0000096	positive regulation of Wnt signaling pathway
Atp6ap2		GO:0048069	MGI:MGI:4834177	GO_REF:0000096	eye pigmentation
Atp6ap2		GO:0032914	MGI:MGI:4834177	GO_REF:0000096	positive regulation of transforming growth factor beta1 production
Atp6ap2		GO:0016021	MGI:MGI:2152098	GO_REF:0000002	integral component of membrane
Atp6ap2		GO:0070062	MGI:MGI:4834177	GO_REF:0000096	extracellular vesicular exosome
Col8a1		GO:0005604	MGI:MGI:1354194	GO_REF:0000004	basement membrane
Col8a1		GO:0005578	MGI:MGI:1354194	GO_REF:0000004	proteinaceous extracellular matrix
Col8a1		GO:0001525	MGI:MGI:1354194	GO_REF:0000004	angiogenesis
Col8a1		GO:0043231	MGI:MGI:4834177	GO_REF:0000096	intracellular membrane-bounded organelle
Col8a1		GO:0007155	MGI:MGI:1354194	GO_REF:0000004	cell adhesion
Col8a1		GO:0005581	MGI:MGI:1354194	GO_REF:0000004	collagen trimer
Col8a1		GO:0010811	MGI:MGI:3807344	PMID:18757743	positive regulation of cell-substrate adhesion
Col8a1		GO:0005576	MGI:MGI:1354194	GO_REF:0000004	extracellular region
Col8a1		GO:0070062	MGI:MGI:4834177	GO_REF:0000096	extracellular vesicular exosome
Col8a1		GO:0050673	MGI:MGI:3587134	PMID:16051690	epithelial cell proliferation
Col8a1		GO:0048593	MGI:MGI:3587134	PMID:16051690	camera-type eye morphogenesis
Col8a1	colocalizes_wit	GO:0031012	MGI:MGI:4834177	GO_REF:0000096	extracellular matrix
Srgap3		GO:0030336	MGI:MGI:4459044	GO_REF:0000033	negative regulation of cell migration
Srgap3		GO:0005622	MGI:MGI:2152098	GO_REF:0000002	intracellular
Srgap3		GO:0005515	MGI:MGI:2152475	PMID:11672528	protein binding
Srgap3		GO:0030675	MGI:MGI:4459044	GO_REF:0000033	Rac GTPase activator activity
Srgap3		GO:0007165	MGI:MGI:2152098	GO_REF:0000002	signal transduction
Srgap3		GO:0005737	MGI:MGI:4459044	GO_REF:0000033	cytoplasm
Srgap3		GO:0005096	MGI:MGI:1354194	GO_REF:0000004	GTPase activator activity
Srgap3		GO:0048365	MGI:MGI:4459044	GO_REF:0000033	Rac GTPase binding
Srgap3		GO:0032855	MGI:MGI:4459044	GO_REF:0000033	positive regulation of Rac GTPase activity
Vat1		GO:0055114	MGI:MGI:1354194	GO_REF:0000004	oxidation-reduction process
Vat1		GO:0043883	MGI:MGI:2152096	GO_REF:0000003	malolactic enzyme activity
Vat1		GO:0043826	MGI:MGI:2152096	GO_REF:0000003	sulfur oxygenase reductase activity
Vat1		GO:0016020	MGI:MGI:1354194	GO_REF:0000004	membrane
Vat1		GO:0016491	MGI:MGI:2152098	GO_REF:0000002	oxidoreductase activity
Vat1		GO:0005741	MGI:MGI:4417868	GO_REF:0000096	mitochondrial outer membrane
Vat1		GO:0070062	MGI:MGI:4834177	GO_REF:0000096	extracellular vesicular exosome
Vat1		GO:0055114	MGI:MGI:2152098	GO_REF:0000002	oxidation-reduction process
Vat1		GO:0043914	MGI:MGI:2152096	GO_REF:0000003	NADPH:sulfur oxidoreductase activity
Vat1		GO:0016491	MGI:MGI:1354194	GO_REF:0000004	oxidoreductase activity
Vat1		GO:0043738	MGI:MGI:2152096	GO_REF:0000003	reduced coenzyme F420 dehydrogenase activity
Vat1		GO:0005739	MGI:MGI:1354194	GO_REF:0000004	mitochondrion
Vat1		GO:0008270	MGI:MGI:2152098	GO_REF:0000002	zinc ion binding
Vat1		GO:0010637	MGI:MGI:4834177	GO_REF:0000096	negative regulation of mitochondrial fusion
Vat1		GO:0005737	MGI:MGI:1354194	GO_REF:0000004	cytoplasm
Vat1		GO:0052693	MGI:MGI:2152096	GO_REF:0000003	epoxyqueuosine reductase activity
Vat1		GO:0008748	MGI:MGI:2152096	GO_REF:0000003	N-ethylmaleimide reductase activity

Predicted targets of miR-1

Gene product		Reference	Reference	Direct annotation
Anxa2		GO:0005811	MGI:MGI:4834177|GO_REF:0000096	lipid particle
Anxa2		GO:0001725	MGI:MGI:2662669|PMID:12611902	stress fiber
Anxa2		GO:0051099	MGI:MGI:3847621|PMID:17690254	positive regulation of binding
Anxa2		GO:0005578	MGI:MGI:1354194|GO_REF:0000004	proteinaceous extracellular matrix
Anxa2		GO:0004859	MGI:MGI:2152098|GO_REF:0000002	phospholipase inhibitor activity
Anxa2		GO:0016020	MGI:MGI:4834177|GO_REF:0000096	membrane
Anxa2		GO:0044354	MGI:MGI:4417868|GO_REF:0000096	macropinosome
Anxa2		GO:0009986	MGI:MGI:4834177|GO_REF:0000096	cell surface
Anxa2		GO:0030496	MGI:MGI:4834177|GO_REF:0000096	midbody
Anxa2		GO:0017137	MGI:MGI:4417868|GO_REF:0000096	Rab GTPase binding
Anxa2	colocalizes_wit	GO:0045121	MGI:MGI:4834177|GO_REF:0000096	membrane raft
Anxa2		GO:0005886	MGI:MGI:4417868|GO_REF:0000096	plasma membrane
Anxa2		GO:0005546	MGI:MGI:4834177|GO_REF:0000096	phosphatidylinositol-4,5-bisphosphate binding
Anxa2		GO:0005938	MGI:MGI:4417868|GO_REF:0000096	cell cortex
Anxa2		GO:0005886	MGI:MGI:4834177|GO_REF:0000096	plasma membrane
Anxa2		GO:0005768	MGI:MGI:4834177|GO_REF:0000096	endosome
Anxa2		GO:0005634	MGI:MGI:4834177|GO_REF:0000096	nucleus
Anxa2		GO:0005769	MGI:MGI:3045820|PMID:15078881	early endosome
Anxa2		GO:0005737	MGI:MGI:3045820|PMID:15078881	cytoplasm
Anxa2		GO:0072661	MGI:MGI:4417868|GO_REF:0000096	protein targeting to plasma membrane
Anxa2		GO:0071229	MGI:MGI:3847621|PMID:17690254	cellular response to acid chemical
Anxa2		GO:0001726	MGI:MGI:4417868|GO_REF:0000096	ruffle
Anxa2		GO:0005546	MGI:MGI:4417868|GO_REF:0000096	phosphatidylinositol-4,5-bisphosphate binding
Anxa2		GO:0042730	MGI:MGI:3027337|PMID:14702107	fibrinolysis
Anxa2		GO:0035749	MGI:MGI:4441217|PMID:20237282	myelin sheath adaxonal region
Anxa2		GO:0031340	MGI:MGI:4834177|GO_REF:0000096	positive regulation of vesicle fusion
Anxa2		GO:0048471	MGI:MGI:4417868|GO_REF:0000096	perinuclear region of cytoplasm
Anxa2		GO:0001765	MGI:MGI:4834177|GO_REF:0000096	membrane raft assembly
Anxa2		GO:0016020	MGI:MGI:2662669|PMID:12611902	membrane
Anxa2		GO:0019897	MGI:MGI:3847621|PMID:17690254	extrinsic component of plasma membrane
Anxa2		GO:0005544	MGI:MGI:4834177|GO_REF:0000096	calcium-dependent phospholipid binding
Anxa2		GO:0019834	MGI:MGI:4834177|GO_REF:0000096	phospholipase A2 inhibitor activity
Anxa2		GO:0031982	MGI:MGI:4417868|GO_REF:0000096	vesicle
Anxa2		GO:0036035	MGI:MGI:4834177|GO_REF:0000096	osteoclast development
Anxa2		GO:0031902	MGI:MGI:4834177|GO_REF:0000096	late endosome membrane
Anxa2		GO:0030054	MGI:MGI:2662669|PMID:12611902	cell junction
Anxa2		GO:0043086	MGI:MGI:4834177|GO_REF:0000096	negative regulation of catalytic activity
Anxa2		GO:0043220	MGI:MGI:4441217|PMID:20237282	Schmidt-Lanterman incisure
Anxa2		GO:0005765	MGI:MGI:4834177|GO_REF:0000096	lysosomal membrane
Anxa2		GO:0007589	MGI:MGI:4417868|GO_REF:0000096	body fluid secretion
Anxa2		GO:0044548	MGI:MGI:4834177|GO_REF:0000096	S100 protein binding
Anxa2		GO:0005515	MGI:MGI:2683818|PMID:14506282	protein binding
Anxa2		GO:0044822	MGI:MGI:4834177|GO_REF:0000096	poly(A) RNA binding
Anxa2		GO:0030199	MGI:MGI:3027337|PMID:14702107	collagen fibril organization
Anxa2		GO:0031982	MGI:MGI:4834177|GO_REF:0000096	vesicle
Anxa2		GO:0043234	MGI:MGI:4417868|GO_REF:0000096	protein complex
Anxa2		GO:0005604	MGI:MGI:1354194|GO_REF:0000004	basement membrane
Anxa2		GO:0048306	MGI:MGI:4834177|GO_REF:0000096	calcium-dependent protein binding
Anxa2		GO:0001934	MGI:MGI:4417868|GO_REF:0000096	positive regulation of protein phosphorylation
Anxa2		GO:0006900	MGI:MGI:4834177|GO_REF:0000096	membrane budding
Anxa2		GO:0048146	MGI:MGI:4417868|GO_REF:0000096	positive regulation of fibroblast proliferation
Anxa2		GO:0005737	MGI:MGI:4417868|GO_REF:0000096	cytoplasm
Anxa2		GO:0005515	MGI:MGI:5469743|PMID:23415230	protein binding
Anxa2		GO:0005576	MGI:MGI:1354194|GO_REF:0000004	extracellular region
Anxa2		GO:0008092	MGI:MGI:2152098|GO_REF:0000002	cytoskeletal protein binding
Anxa2		GO:0042383	MGI:MGI:2683818|PMID:14506282	sarcolemma
Anxa2		GO:0001525	MGI:MGI:3027337|PMID:14702107	angiogenesis
Anxa2		GO:0070062	MGI:MGI:4834177|GO_REF:0000096	extracellular vesicular exosome
Anxa2		GO:0051290	MGI:MGI:4834177|GO_REF:0000096	protein heterotetramerization
Anxa2		GO:0005615	MGI:MGI:4834177|GO_REF:0000096	extracellular space
Anxa2		GO:0005509	MGI:MGI:2152098|GO_REF:0000002	calcium ion binding

Predicted targets of miR-1

Anxa4		GO:0016324	MGI:MGI:2178719	PMID:11923205	apical plasma membrane
Anxa4		GO:0005634	MGI:MGI:4834177	GO_REF:0000096	nucleus
Anxa4		GO:0005886	MGI:MGI:4834177	GO_REF:0000096	plasma membrane
Anxa4		GO:0070062	MGI:MGI:4834177	GO_REF:0000096	extracellular vesicular exosome
Anxa4		GO:0006357	MGI:MGI:4834177	GO_REF:0000096	regulation of transcription from RNA polymerase II promoter
Anxa4		GO:0009986	MGI:MGI:4834177	GO_REF:0000096	cell surface
Anxa4		GO:0048471	MGI:MGI:4834177	GO_REF:0000096	perinuclear region of cytoplasm
Anxa4		GO:0012506	MGI:MGI:4834177	GO_REF:0000096	vesicle membrane
Anxa4		GO:0048306	MGI:MGI:4834177	GO_REF:0000096	calcium-dependent protein binding
Anxa4		GO:0051059	MGI:MGI:4834177	GO_REF:0000096	NF-kappaB binding
Anxa4		GO:0042802	MGI:MGI:4834177	GO_REF:0000096	identical protein binding
Anxa4		GO:0001822	MGI:MGI:2178719	PMID:11923205	kidney development
Anxa4		GO:0031965	MGI:MGI:4834177	GO_REF:0000096	nuclear membrane
Anxa4		GO:0005509	MGI:MGI:4834177	GO_REF:0000096	calcium ion binding
Anxa4		GO:0005737	MGI:MGI:4834177	GO_REF:0000096	cytoplasm
Anxa4		GO:0032088	MGI:MGI:4834177	GO_REF:0000096	negative regulation of NF-kappaB transcription factor activity
Anxa4		GO:2000483	MGI:MGI:4834177	GO_REF:0000096	negative regulation of interleukin-8 secretion
Anxa4		GO:0005544	MGI:MGI:4834177	GO_REF:0000096	calcium-dependent phospholipid binding

Atp6ap2		GO:0060323	MGI:MGI:4834177	GO_REF:0000096	head morphogenesis
Atp6ap2		GO:0002003	MGI:MGI:4417868	GO_REF:0000096	angiotensin maturation
Atp6ap2		GO:0009897	MGI:MGI:4834177	GO_REF:0000096	external side of plasma membrane
Atp6ap2		GO:0044297	MGI:MGI:4417868	GO_REF:0000096	cell body
Atp6ap2		GO:0004872	MGI:MGI:2152098	GO_REF:0000002	receptor activity
Atp6ap2		GO:0006508	MGI:MGI:4834177	GO_REF:0000096	proteolysis
Atp6ap2		GO:0016021	MGI:MGI:1354194	GO_REF:0000004	integral component of membrane
Atp6ap2		GO:0043408	MGI:MGI:4834177	GO_REF:0000096	regulation of MAPK cascade
Atp6ap2		GO:0030177	MGI:MGI:4421218	PMID:20093472	positive regulation of Wnt signaling pathway
Atp6ap2		GO:0021903	MGI:MGI:4834177	GO_REF:0000096	rostrocaudal neural tube patterning
Atp6ap2		GO:0002003	MGI:MGI:4834177	GO_REF:0000096	angiotensin maturation
Atp6ap2		GO:0004190	MGI:MGI:4834177	GO_REF:0000096	aspartic-type endopeptidase activity
Atp6ap2		GO:0043005	MGI:MGI:4417868	GO_REF:0000096	neuron projection
Atp6ap2		GO:0016020	MGI:MGI:1354194	GO_REF:0000004	membrane
Atp6ap2		GO:0019899	MGI:MGI:4417868	GO_REF:0000096	enzyme binding
Atp6ap2		GO:0030177	MGI:MGI:4834177	GO_REF:0000096	positive regulation of Wnt signaling pathway
Atp6ap2		GO:0048069	MGI:MGI:4834177	GO_REF:0000096	eye pigmentation
Atp6ap2		GO:0032914	MGI:MGI:4834177	GO_REF:0000096	positive regulation of transforming growth factor beta1 production
Atp6ap2		GO:0016021	MGI:MGI:2152098	GO_REF:0000002	integral component of membrane
Atp6ap2		GO:0070062	MGI:MGI:4834177	GO_REF:0000096	extracellular vesicular exosome

Predicted targets of miR-1

Atp6v1a		GO:0005902	MGI:MGI:4943380	PMID:18667600	microvillus
Atp6v1a		GO:0015992	MGI:MGI:1354194	GO_REF:0000004	proton transport
Atp6v1a		GO:0005765	MGI:MGI:4834177	GO_REF:0000096	lysosomal membrane
Atp6v1a		GO:0005739	MGI:MGI:2682130	PMID:14651853	mitochondrion
Atp6v1a		GO:0016324	MGI:MGI:4943380	PMID:18667600	apical plasma membrane
Atp6v1a		GO:0070062	MGI:MGI:4834177	GO_REF:0000096	extracellular vesicular exosome
Atp6v1a		GO:0033180	MGI:MGI:2152098	GO_REF:0000002	proton-transporting V-type ATPase, V1 domain
Atp6v1a		GO:0000166	MGI:MGI:1354194	GO_REF:0000004	nucleotide binding
Atp6v1a		GO:0015991	MGI:MGI:2152098	GO_REF:0000002	ATP hydrolysis coupled proton transport
Atp6v1a		GO:0005524	MGI:MGI:1354194	GO_REF:0000004	ATP binding
Atp6v1a		GO:0006810	MGI:MGI:1354194	GO_REF:0000004	transport
Atp6v1a		GO:0005829	MGI:MGI:3850618	PMID:16177003	cytosol
Atp6v1a		GO:0043209	MGI:MGI:3834050	PMID:17634366	myelin sheath
Atp6v1a		GO:0016787	MGI:MGI:1354194	GO_REF:0000004	hydrolase activity
Atp6v1a		GO:0033178	MGI:MGI:2152098	GO_REF:0000002	proton-transporting two-sector ATPase complex, catalytic domain
Atp6v1a		GO:0005524	MGI:MGI:2152098	GO_REF:0000002	ATP binding
Atp6v1a		GO:0046034	MGI:MGI:2152098	GO_REF:0000002	ATP metabolic process
Atp6v1a		GO:0006811	MGI:MGI:1354194	GO_REF:0000004	ion transport
Atp6v1a		GO:0015992	MGI:MGI:2152098	GO_REF:0000002	proton transport
Atp6v1a		GO:0005886	MGI:MGI:3850618	PMID:16177003	plasma membrane
Atp6v1a		GO:0046961	MGI:MGI:2152098	GO_REF:0000002	proton-transporting ATPase activity, rotational mechanism
Atp6v1a		GO:0016820	MGI:MGI:2152098	GO_REF:0000002	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances

Azin1		GO:0003824	MGI:MGI:2152098	GO_REF:0000002	catalytic activity
Azin1		GO:0006596	MGI:MGI:2152098	GO_REF:0000002	polyamine biosynthetic process
Azin1		GO:0042177	MGI:MGI:4834177	GO_REF:0000096	negative regulation of protein catabolic process
Azin1		GO:1902269	MGI:MGI:3803410	PMID:18508777	positive regulation of polyamine transmembrane transport
Azin1		GO:0006596	MGI:MGI:1354194	GO_REF:0000004	polyamine biosynthetic process
Azin1		GO:0008073	MGI:MGI:4417868	GO_REF:0000096	ornithine decarboxylase inhibitor activity
Azin1		GO:0042978	MGI:MGI:3695330	PMID:16916800	ornithine decarboxylase activator activity
Azin1		GO:0043086	MGI:MGI:4417868	GO_REF:0000096	negative regulation of catalytic activity
Azin1		GO:0043085	MGI:MGI:3695330	PMID:16916800	positive regulation of catalytic activity
Azin1		GO:0042978	MGI:MGI:4834177	GO_REF:0000096	ornithine decarboxylase activator activity
Azin1		GO:0006595	MGI:MGI:1354413	PMID:10698696	polyamine metabolic process
Azin1		GO:1902269	MGI:MGI:4834177	GO_REF:0000096	positive regulation of polyamine transmembrane transport
Azin1		GO:0005634	MGI:MGI:5582167	PMID:19449338	nucleus
Azin1		GO:0043085	MGI:MGI:4834177	GO_REF:0000096	positive regulation of catalytic activity

Predicted targets of miR-1

Coro1b		GO:0015629	MGI:MGI:4459044	GO_REF:0000033	actin cytoskeleton
Coro1b		GO:0031529	MGI:MGI:4834177	GO_REF:0000096	ruffle organization
Coro1b		GO:0005886	MGI:MGI:4834177	GO_REF:0000096	plasma membrane
Coro1b		GO:0034316	MGI:MGI:4834177	GO_REF:0000096	negative regulation of Arp2/3 complex-mediated actin nucleation
Coro1b		GO:0051015	MGI:MGI:4459044	GO_REF:0000033	actin filament binding
Coro1b		GO:2000394	MGI:MGI:4834177	GO_REF:0000096	positive regulation of lamellipodium morphogenesis
Coro1b		GO:0042060	MGI:MGI:4834177	GO_REF:0000096	wound healing
Coro1b		GO:0031252	MGI:MGI:4834177	GO_REF:0000096	cell leading edge
Coro1b		GO:0070062	MGI:MGI:4834177	GO_REF:0000096	extracellular vesicular exosome
Coro1b		GO:0090135	MGI:MGI:4834177	GO_REF:0000096	actin filament branching
Coro1b		GO:0042802	MGI:MGI:4834177	GO_REF:0000096	identical protein binding
Coro1b		GO:0016477	MGI:MGI:4834177	GO_REF:0000096	cell migration
Coro1b		GO:0003779	MGI:MGI:1354194	GO_REF:0000004	actin binding
Coro1b		GO:0030027	MGI:MGI:4834177	GO_REF:0000096	lamellipodium
Coro1b		GO:0071933	MGI:MGI:4834177	GO_REF:0000096	Arp2/3 complex binding
Coro1b		GO:0001725	MGI:MGI:4834177	GO_REF:0000096	stress fiber
Coro1b		GO:0035767	MGI:MGI:4834177	GO_REF:0000096	endothelial cell chemotaxis
Coro1b		GO:0051015	MGI:MGI:4834177	GO_REF:0000096	actin filament binding
Coro1b		GO:1902463	MGI:MGI:4834177	GO_REF:0000096	protein localization to cell leading edge
Coro1b		GO:0005737	MGI:MGI:4834177	GO_REF:0000096	cytoplasm
Coro1b		GO:0005856	MGI:MGI:1354194	GO_REF:0000004	cytoskeleton
Coro1b		GO:0005925	MGI:MGI:4834177	GO_REF:0000096	focal adhesion
Coro1b		GO:0005515	MGI:MGI:3818245	PMID:18836449	protein binding
Coro1b		GO:0030036	MGI:MGI:4459044	GO_REF:0000033	actin cytoskeleton organization
Coro1b		GO:0051017	MGI:MGI:4834177	GO_REF:0000096	actin filament bundle assembly
Coro1b		GO:0005884	MGI:MGI:4834177	GO_REF:0000096	actin filament

Predicted targets of miR-1

G6pdx		GO:0004345	MGI:MGI:87492|PMID:9169132	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0004345	MGI:MGI:4417868|GO_REF:0000096	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0019322	MGI:MGI:49164|PMID:1953691	pentose biosynthetic process
G6pdx		GO:0043231	MGI:MGI:4417868|GO_REF:0000096	intracellular membrane-bounded organelle
G6pdx		GO:0005634	MGI:MGI:4417868|GO_REF:0000096	nucleus
G6pdx		GO:0004345	MGI:MGI:1261671|PMID:9627357	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0043249	MGI:MGI:4834177|GO_REF:0000096	erythrocyte maturation
G6pdx		GO:0006741	MGI:MGI:49164|PMID:1953691	NADP biosynthetic process
G6pdx		GO:0006741	MGI:MGI:1349468|PMID:3377761	NADP biosynthetic process
G6pdx		GO:0019322	MGI:MGI:3694178|PMID:15998684	pentose biosynthetic process
G6pdx		GO:0005975	MGI:MGI:1354194|GO_REF:0000004	carbohydrate metabolic process
G6pdx		GO:0004345	MGI:MGI:58177|PMID:3243423	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0009051	MGI:MGI:4417868|GO_REF:0000096	pentose-phosphate shunt, oxidative branch
G6pdx		GO:0042802	MGI:MGI:4834177|GO_REF:0000096	identical protein binding
G6pdx		GO:0051156	MGI:MGI:4834177|GO_REF:0000096	glucose 6-phosphate metabolic process
G6pdx		GO:0006741	MGI:MGI:1202104|PMID:9539108	NADP biosynthetic process
G6pdx		GO:0005737	MGI:MGI:4834177|GO_REF:0000096	cytoplasm
G6pdx		GO:0009051	MGI:MGI:4834177|GO_REF:0000096	pentose-phosphate shunt, oxidative branch
G6pdx		GO:0006979	MGI:MGI:3581936|PMID:15817708	response to oxidative stress
G6pdx		GO:0019322	MGI:MGI:1202104|PMID:9539108	pentose biosynthetic process
G6pdx		GO:0019322	MGI:MGI:1097071|PMID:9330624	pentose biosynthetic process
G6pdx		GO:0050661	MGI:MGI:4417868|GO_REF:0000096	NADP binding
G6pdx		GO:0055114	MGI:MGI:2387962|PMID:7489710	oxidation-reduction process
G6pdx		GO:0004345	MGI:MGI:54095|PMID:943046	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0006741	MGI:MGI:2387959|PMID:10627286	NADP biosynthetic process
G6pdx		GO:0045471	MGI:MGI:4417868|GO_REF:0000096	response to ethanol
G6pdx		GO:0006979	MGI:MGI:2387959|PMID:10627286	response to oxidative stress
G6pdx		GO:0004345	MGI:MGI:53579|PMID:5764873	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0032615	MGI:MGI:3581936|PMID:15817708	interleukin-12 production
G6pdx		GO:0006740	MGI:MGI:4834177|GO_REF:0000096	NADPH regeneration
G6pdx		GO:0006741	MGI:MGI:1261671|PMID:9627357	NADP biosynthetic process
G6pdx		GO:0004345	MGI:MGI:49164|PMID:1953691	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0006741	MGI:MGI:3607389|PMID:14757696	NADP biosynthetic process
G6pdx		GO:0006979	MGI:MGI:2387962|PMID:7489710	response to oxidative stress
G6pdx		GO:0006979	MGI:MGI:3607389|PMID:14757696	response to oxidative stress
G6pdx		GO:0004345	MGI:MGI:1349468|PMID:3377761	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0019322	MGI:MGI:1261671|PMID:9627357	pentose biosynthetic process
G6pdx		GO:0034599	MGI:MGI:4834177|GO_REF:0000096	cellular response to oxidative stress
G6pdx		GO:0004345	MGI:MGI:3607389|PMID:14757696	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0006741	MGI:MGI:3522057|PMID:15271799	NADP biosynthetic process
G6pdx		GO:0009898	MGI:MGI:4834177|GO_REF:0000096	cytoplasmic side of plasma membrane
G6pdx		GO:0070062	MGI:MGI:4834177|GO_REF:0000096	extracellular vesicular exosome
G6pdx		GO:0004345	MGI:MGI:3522057|PMID:15271799	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0002033	MGI:MGI:3694178|PMID:15998684	vasodilation by angiotensin involved in regulation of systemic arterial blood pressure
G6pdx		GO:0006979	MGI:MGI:3527298|PMID:14751857	response to oxidative stress
G6pdx		GO:0004345	MGI:MGI:4834177|GO_REF:0000096	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0006006	MGI:MGI:1354194|GO_REF:0000004	glucose metabolic process
G6pdx		GO:0004345	MGI:MGI:61105|PMID:8491670	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0016491	MGI:MGI:1354194|GO_REF:0000004	oxidoreductase activity
G6pdx		GO:0006741	MGI:MGI:85983|PMID:9067418	NADP biosynthetic process
G6pdx		GO:0050661	MGI:MGI:4834177|GO_REF:0000096	NADP binding
G6pdx		GO:0001998	MGI:MGI:3694178|PMID:15998684	angiotensin mediated vasoconstriction involved in regulation of systemic arterial blood pressure
G6pdx		GO:0004345	MGI:MGI:2387962|PMID:7489710	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0042803	MGI:MGI:87492|PMID:9169132	protein homodimerization activity
G6pdx		GO:0019322	MGI:MGI:4834177|GO_REF:0000096	pentose biosynthetic process
G6pdx		GO:0004345	MGI:MGI:3527298|PMID:14751857	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0005815	MGI:MGI:4834177|GO_REF:0000096	microtubule organizing center
G6pdx		GO:0006749	MGI:MGI:2449252|PMID:12521604	glutathione metabolic process
G6pdx		GO:0043231	MGI:MGI:4834177|GO_REF:0000096	intracellular membrane-bounded organelle
G6pdx		GO:0004345	MGI:MGI:1097071|PMID:9330624	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0040014	MGI:MGI:2387959|PMID:10627286	regulation of multicellular organism growth
G6pdx		GO:0006006	MGI:MGI:2152098|GO_REF:0000002	glucose metabolic process
G6pdx		GO:0006098	MGI:MGI:4834177|GO_REF:0000096	pentose-phosphate shunt
G6pdx		GO:0006741	MGI:MGI:87492|PMID:9169132	NADP biosynthetic process
G6pdx		GO:0055114	MGI:MGI:4834177|GO_REF:0000096	oxidation-reduction process
G6pdx		GO:0004345	MGI:MGI:3054313|PMID:15155459	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0001816	MGI:MGI:4834177|GO_REF:0000096	cytokine production
G6pdx		GO:0048821	MGI:MGI:3527298|PMID:14751857	erythrocyte development
G6pdx		GO:0004345	MGI:MGI:2449252|PMID:12521604	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0010734	MGI:MGI:4834177|GO_REF:0000096	negative regulation of protein glutathionylation
G6pdx		GO:0019322	MGI:MGI:3607389|PMID:14757696	pentose biosynthetic process
G6pdx		GO:0006749	MGI:MGI:4834177|GO_REF:0000096	glutathione metabolic process
G6pdx		GO:0006741	MGI:MGI:1097071|PMID:9330624	NADP biosynthetic process
G6pdx		GO:0004345	MGI:MGI:2387959|PMID:10627286	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0006741	MGI:MGI:54902|PMID:7439685	NADP biosynthetic process
G6pdx		GO:0046390	MGI:MGI:4834177|GO_REF:0000096	ribose phosphate biosynthetic process
G6pdx		GO:0042803	MGI:MGI:4834177|GO_REF:0000096	protein homodimerization activity
G6pdx		GO:0043523	MGI:MGI:4417868|GO_REF:0000096	regulation of neuron apoptotic process
G6pdx		GO:0004345	MGI:MGI:1202104|PMID:9539108	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0048821	MGI:MGI:3522057|PMID:15271799	erythrocyte development
G6pdx		GO:0006739	MGI:MGI:4834177|GO_REF:0000096	NADP metabolic process
G6pdx		GO:0001816	MGI:MGI:3581936|PMID:15817708	cytokine production
G6pdx		GO:0004345	MGI:MGI:3694178|PMID:15998684	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0006098	MGI:MGI:4417868|GO_REF:0000096	pentose-phosphate shunt
G6pdx		GO:0030246	MGI:MGI:4417868|GO_REF:0000096	carbohydrate binding
G6pdx		GO:0032613	MGI:MGI:3581936|PMID:15817708	interleukin-10 production
G6pdx		GO:0005813	MGI:MGI:4834177|GO_REF:0000096	centrosome
G6pdx		GO:0004345	MGI:MGI:85983|PMID:9067418	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0016020	MGI:MGI:4834177|GO_REF:0000096	membrane
G6pdx		GO:0006741	MGI:MGI:3694178|PMID:15998684	NADP biosynthetic process
G6pdx		GO:0005829	MGI:MGI:4417868|GO_REF:0000096	cytosol
G6pdx		GO:0005536	MGI:MGI:4417868|GO_REF:0000096	glucose binding
G6pdx		GO:0051156	MGI:MGI:4417868|GO_REF:0000096	glucose 6-phosphate metabolic process
G6pdx		GO:0005536	MGI:MGI:4834177|GO_REF:0000096	glucose binding
G6pdx		GO:0006979	MGI:MGI:3694178|PMID:15998684	response to oxidative stress
G6pdx		GO:0006695	MGI:MGI:4834177|GO_REF:0000096	cholesterol biosynthetic process
G6pdx		GO:0004345	MGI:MGI:54902|PMID:7439685	glucose-6-phosphate dehydrogenase activity
G6pdx		GO:0019322	MGI:MGI:54902|PMID:7439685	pentose biosynthetic process
G6pdx		GO:0005829	MGI:MGI:4834177|GO_REF:0000096	cytosol
G6pdx		GO:0019322	MGI:MGI:61105|PMID:8491670	pentose biosynthetic process

Predicted targets of miR-1

H3f3b		GO:1902340	MGI:MGI:5502235	PMID:23903189	negative regulation of chromosome condensation
H3f3b		GO:0000980	MGI:MGI:4834177	GO_REF:0000096	RNA polymerase II distal enhancer sequence-specific DNA binding
H3f3b		GO:0006997	MGI:MGI:5474379	PMID:23570311	nucleus organization
H3f3b		GO:0001649	MGI:MGI:5430686	PMID:22705305	osteoblast differentiation
H3f3b		GO:0043234	MGI:MGI:4834177	GO_REF:0000096	protein complex
H3f3b		GO:0005634	MGI:MGI:4834177	GO_REF:0000096	nucleus
H3f3b		GO:0042692	MGI:MGI:5430686	PMID:22705305	muscle cell differentiation
H3f3b		GO:0000979	MGI:MGI:4834177	GO_REF:0000096	RNA polymerase II core promoter sequence-specific DNA binding
H3f3b		GO:0000788	MGI:MGI:4834177	GO_REF:0000096	nuclear nucleosome
H3f3b		GO:0070062	MGI:MGI:4834177	GO_REF:0000096	extracellular vesicular exosome
H3f3b		GO:0031492	MGI:MGI:4834177	GO_REF:0000096	nucleosomal DNA binding
H3f3b		GO:0005634	MGI:MGI:5474379	PMID:23570311	nucleus
H3f3b		GO:0000228	MGI:MGI:4834177	GO_REF:0000096	nuclear chromosome
H3f3b		GO:0090230	MGI:MGI:5474379	PMID:23570311	regulation of centromere complex assembly

Serp1		GO:0001501	MGI:MGI:3619104	PMID:16415102	skeletal system development
Serp1		GO:0045727	MGI:MGI:3619104	PMID:16415102	positive regulation of translation
Serp1		GO:0015031	MGI:MGI:1354194	GO_REF:0000004	protein transport
Serp1		GO:0030968	MGI:MGI:3619104	PMID:16415102	endoplasmic reticulum unfolded protein response
Serp1		GO:0006486	MGI:MGI:4417868	GO_REF:0000096	protein glycosylation
Serp1		GO:0009791	MGI:MGI:3629369	PMID:16705175	post-embryonic development
Serp1		GO:0032024	MGI:MGI:3619104	PMID:16415102	positive regulation of insulin secretion
Serp1		GO:0006006	MGI:MGI:3619104	PMID:16415102	glucose metabolic process
Serp1		GO:0010259	MGI:MGI:3629369	PMID:16705175	multicellular organismal aging
Serp1		GO:0005783	MGI:MGI:2152098	GO_REF:0000002	endoplasmic reticulum
Serp1		GO:0016020	MGI:MGI:1354194	GO_REF:0000004	membrane
Serp1		GO:0006810	MGI:MGI:1354194	GO_REF:0000004	transport
Serp1		GO:0048644	MGI:MGI:3619104	PMID:16415102	muscle organ morphogenesis
Serp1		GO:0046622	MGI:MGI:3619104	PMID:16415102	positive regulation of organ growth
Serp1		GO:0005881	MGI:MGI:4834177	GO_REF:0000096	cytoplasmic microtubule
Serp1		GO:0016021	MGI:MGI:1354194	GO_REF:0000004	integral component of membrane
Serp1		GO:0060124	MGI:MGI:3619104	PMID:16415102	positive regulation of growth hormone secretion
Serp1		GO:0005783	MGI:MGI:1354194	GO_REF:0000004	endoplasmic reticulum

Sh3bgrl3		GO:0045454	MGI:MGI:2152098	GO_REF:0000002	cell redox homeostasis
Sh3bgrl3		GO:0030834	MGI:MGI:4834177	GO_REF:0000096	regulation of actin filament depolymerization
Sh3bgrl3		GO:0032956	MGI:MGI:4834177	GO_REF:0000096	regulation of actin cytoskeleton organization
Sh3bgrl3		GO:0005634	MGI:MGI:1354194	GO_REF:0000004	nucleus
Sh3bgrl3		GO:0005100	MGI:MGI:4834177	GO_REF:0000096	Rho GTPase activator activity
Sh3bgrl3		GO:0009055	MGI:MGI:2152098	GO_REF:0000002	electron carrier activity
Sh3bgrl3		GO:0030027	MGI:MGI:4834177	GO_REF:0000096	lamellipodium
Sh3bgrl3		GO:0030215	MGI:MGI:4834177	GO_REF:0000096	semaphorin receptor binding
Sh3bgrl3		GO:0005737	MGI:MGI:1354194	GO_REF:0000004	cytoplasm
Sh3bgrl3		GO:0032321	MGI:MGI:4834177	GO_REF:0000096	positive regulation of Rho GTPase activity
Sh3bgrl3		GO:0043535	MGI:MGI:4834177	GO_REF:0000096	regulation of blood vessel endothelial cell migration
Sh3bgrl3		GO:0015035	MGI:MGI:2152098	GO_REF:0000002	protein disulfide oxidoreductase activity
Sh3bgrl3		GO:0070062	MGI:MGI:4834177	GO_REF:0000096	extracellular vesicular exosome

Zfp36l2		GO:1900153	MGI:MGI:5320815	PMID:22367205	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent deca
Zfp36l2		GO:0043488	MGI:MGI:3511379	PMID:15467755	regulation of mRNA stability
Zfp36l2		GO:0035925	MGI:MGI:5500826	PMID:23748442	mRNA 3'-UTR AU-rich region binding
Zfp36l2		GO:2000737	MGI:MGI:5500826	PMID:23748442	negative regulation of stem cell differentiation
Zfp36l2		GO:0003723	MGI:MGI:1354194	GO_REF:0000004	RNA binding
Zfp36l2		GO:0003677	MGI:MGI:1354194	GO_REF:0000004	DNA binding
Zfp36l2		GO:0017091	MGI:MGI:4834177	GO_REF:0000096	AU-rich element binding
Zfp36l2		GO:0046872	MGI:MGI:2152098	GO_REF:0000002	metal ion binding
Zfp36l2		GO:0006402	MGI:MGI:5320815	PMID:22367205	mRNA catabolic process
Zfp36l2		GO:0005634	MGI:MGI:5320815	PMID:22367205	nucleus
Zfp36l2		GO:0044822	MGI:MGI:4834177	GO_REF:0000096	poly(A) RNA binding
Zfp36l2		GO:0035925	MGI:MGI:5320815	PMID:22367205	mRNA 3'-UTR AU-rich region binding
Zfp36l2		GO:0005737	MGI:MGI:2177366	PMID:11796723	cytoplasm
Zfp36l2		GO:0030097	MGI:MGI:5500826	PMID:23748442	hemopoiesis
Zfp36l2		GO:0033077	MGI:MGI:4818820	PMID:20622884	T cell differentiation in thymus
Zfp36l2		GO:0000288	MGI:MGI:3589099	PMID:15814898	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay
Zfp36l2		GO:0005634	MGI:MGI:2177366	PMID:11796723	nucleus
Zfp36l2		GO:0035019	MGI:MGI:5500826	PMID:23748442	somatic stem cell maintenance
Zfp36l2		GO:0005737	MGI:MGI:5320815	PMID:22367205	cytoplasm
Zfp36l2		GO:0046872	MGI:MGI:1354194	GO_REF:0000004	metal ion binding
Zfp36l2		GO:0048103	MGI:MGI:5500826	PMID:23748442	somatic stem cell division
Zfp36l2		GO:0060216	MGI:MGI:4360416	PMID:19633199	definitive hemopoiesis
Zfp36l2		GO:0030097	MGI:MGI:4360416	PMID:19633199	hemopoiesis

Predicted targets of miR-378

Gene product		Reference	Reference		Direct annotation
H3f3b		GO:1902340	MGI:MGI:5502235	PMID:23903189	negative regulation of chromosome condensation
H3f3b		GO:0000980	MGI:MGI:4834177	GO_REF:0000096	RNA polymerase II distal enhancer sequence-specific DNA binding
H3f3b		GO:0006997	MGI:MGI:5474379	PMID:23570311	nucleus organization
H3f3b		GO:0001649	MGI:MGI:5430686	PMID:22705305	osteoblast differentiation
H3f3b		GO:0043234	MGI:MGI:4834177	GO_REF:0000096	protein complex
H3f3b		GO:0005634	MGI:MGI:4834177	GO_REF:0000096	nucleus
H3f3b		GO:0042692	MGI:MGI:5430686	PMID:22705305	muscle cell differentiation
H3f3b		GO:0000979	MGI:MGI:4834177	GO_REF:0000096	RNA polymerase II core promoter sequence-specific DNA binding
H3f3b		GO:0000788	MGI:MGI:4834177	GO_REF:0000096	nuclear nucleosome
H3f3b		GO:0070062	MGI:MGI:4834177	GO_REF:0000096	extracellular vesicular exosome
H3f3b		GO:0031492	MGI:MGI:4834177	GO_REF:0000096	nucleosomal DNA binding
H3f3b		GO:0005634	MGI:MGI:5474379	PMID:23570311	nucleus
H3f3b		GO:0000228	MGI:MGI:4834177	GO_REF:0000096	nuclear chromosome
H3f3b		GO:0090230	MGI:MGI:5474379	PMID:23570311	regulation of centromere complex assembly

Vat1		GO:0055114	MGI:MGI:1354194	GO_REF:0000004	oxidation-reduction process
Vat1		GO:0043883	MGI:MGI:2152096	GO_REF:0000003	malolactic enzyme activity
Vat1		GO:0043826	MGI:MGI:2152096	GO_REF:0000003	sulfur oxygenase reductase activity
Vat1		GO:0016020	MGI:MGI:1354194	GO_REF:0000004	membrane
Vat1		GO:0016491	MGI:MGI:2152098	GO_REF:0000002	oxidoreductase activity
Vat1		GO:0005741	MGI:MGI:4417868	GO_REF:0000096	mitochondrial outer membrane
Vat1		GO:0070062	MGI:MGI:4834177	GO_REF:0000096	extracellular vesicular exosome
Vat1		GO:0055114	MGI:MGI:2152098	GO_REF:0000002	oxidation-reduction process
Vat1		GO:0043914	MGI:MGI:2152096	GO_REF:0000003	NADPH:sulfur oxidoreductase activity
Vat1		GO:0016491	MGI:MGI:1354194	GO_REF:0000004	oxidoreductase activity
Vat1		GO:0043738	MGI:MGI:2152096	GO_REF:0000003	reduced coenzyme F420 dehydrogenase activity
Vat1		GO:0005739	MGI:MGI:1354194	GO_REF:0000004	mitochondrion
Vat1		GO:0008270	MGI:MGI:2152098	GO_REF:0000002	zinc ion binding
Vat1		GO:0010637	MGI:MGI:4834177	GO_REF:0000096	negative regulation of mitochondrial fusion
Vat1		GO:0005737	MGI:MGI:1354194	GO_REF:0000004	cytoplasm
Vat1		GO:0052693	MGI:MGI:2152096	GO_REF:0000003	epoxyqueuosine reductase activity
Vat1		GO:0008748	MGI:MGI:2152096	GO_REF:0000003	N-ethylmaleimide reductase activity