

FAST DB_id	Gene symbol	exon	fold	pvalue	FAST DB annotation	Mouse Transcript Id	Tissue Specificity
14	TEP1	e51	1.59	0.0004863000			
130	STRN3	e8	1.76	0.0004742800	x	AF307777/AK165908	X
405	USP14	e1	4.87	0.0000014555			
694	ENSG00000161999	e9	1.57	0.0000070060			
740	SMG6	e18	1.54	0.0001194220			
1369	SEMA5A	e20	2.65	0.0000002615	x	AK043386/BC065137	
1552	MSR1	e11	1.68	0.0034739400	x	L04274/BC003814	
1581	C7orf28A	e9	1.51	0.0144328000			
1923	IL33	e3	1.67	0.0001106260			
2298	BMP1	e2	2.56	0.0000001776			
2341	RAI14	e12	1.83	0.0001285260	x	AK160119/BC052458	X
3283	ATRN	e21	1.57	0.0010760400			
3296	MLLT3	e4	1.61	0.0039102800	x	K080309/AK045331	
3321	POSTN	e21	1.94	0.0000823040	x	D13664/AK154049	X
3324	JMJD3	e3	1.55	0.0030088800			
3451	BRE	e10	1.54	0.0005523400	x	AK080991/AK050695	
3480	GHR	e4	1.52	0.0004051400	x	BC075720/AK053579	X
3708	SAAL1	e1	1.50	0.0002439260			
3805	TTLL5	e34	1.52	0.0094338000			
3900	UEVLD	e2	1.55	0.0075960000	x	K155685 /AK086750	
4006	FGFR1	e8	1.95	0.0000003926	x	U23445/AF176552	
4146	CLSTN1	e11	1.69	0.0053908000			X
4172	PRMT3	e3	1.50	0.0050712000			
5025	CD44	e12	2.39	0.0001280540	x	AJ251594/BC005676	X
5227	SPTBN1	e1	1.57	0.0004865800	x	M74773/AF017112	
5640	EML1	e7	1.92	0.0000462680			X
5662	TMEM16F	e3	1.73	0.0000399832	x	AK159411/BC060732	
5963	PELI1	ae5	2.71	0.0001191580	x	AK153372/AK020915	
5977	SLTM	e6	1.69	0.0039111600	x	AK017715/AK082294	X
6997	ENSG00000104324	e2	2.02	0.0041996000	x	AK154361/BC017373	X
7078	IGHG1	e27	6.56	0.0015288000			
7155	CNTF	e8	1.53	0.0008837400	x	AK169477/AK040976	

7800	MBNL2	e8	1.61	0.0000020304	x	AK164372/AK028797	X
7820	NUDCD1	e2	1.56	0.0069698000	x	AK168122/AK133755	X
7870	EVI2B	e2	1.65	0.0002316120	x	AK034440/BC038124	X
8628	MARK2	e2	1.73	0.0021243800	x	AK045329:AK154864	
8673	ARHGEF3	e6	1.67	0.0007622000	x	AK004600/BC005517	X
8782	CAMK2D	e3	1.50	0.0020077200	x	AK012702/AK020214	
9215	KIAA1109	e4	1.95	0.0004031400	x	AK173100/BC079623	x
9587	PLEC1	e8	1.59	0.0005948400	x	AY480033/AY480038	
9750	MED24	e24	1.95	0.0002819680	x	AK154618/AK020269	
10381	ORC5L	e7	1.52	0.0202860000	x	AK166537/AK169683	
10540	CNOT2	e6	1.52	0.0367956000	x	AK167834/AK172132	
10547	PRC1	e11	1.54	0.0022868800	x	AK088576/AK029140	x
10636	HBP1	e11	1.57	0.0062808000	x	BC026853/AK028674	
10775	UGCGL1	e27	1.93	0.0000801720	x	BC062936/BC051172	x
11008	CAPZA2	e5	1.70	0.0026416200	x	AK150587/AK031551	
11240	C12orf29	e4	1.60	0.0019502200			
11318	UBTF	e4	1.51	0.0005237400	x	AK128947/BC024622	
11576	ZEB2	e6	1.81	0.0000370420	x	AK122312/BC050145	
11615	FMNL1	e28	1.59	0.0001632720			x
11760	KIAA1267	e2	1.51	0.0000700440			x
12167	EPB41	e22	1.59	0.0077674000	x	AK133437/BC043337	x
12715	PTTG1	e1	1.98	0.0005512400	x	AK008704/AF069051	
12743	ATP1A3	e7	1.70	0.0003618960			x
12823	LPAR1	e5	1.51	0.0003515760			x
12955	JOSD3	e6	1.63	0.0001607900	x	AK016109/AK166633	
13530	RBP1	e2	1.87	0.0003626000			x
13676	GRK6	e9	1.63	0.0015532200			x
13752	MRC2	e5	1.76	0.0000847080			
13899	CP	e17	1.57	0.0002463300	x	BC062957/AK160035	
14226	P2RX7	e1	1.97	0.0001291240			
14487	LAMA5	e66	1.96	0.0000008746			
14503	CAP1	e3	1.50	0.0008482600	x	AK162629/AK171388	
14511	PTGS1	e1	1.84	0.0002455880			

14538	KNTC1	e54	1.73	0.0002723440			
15336	VPS8	e6	1.52	0.0025146600			
15500	LPP	e1	1.51	0.0010727200	x	BC085321/K169780	
15586	MAP3K7	e12	1.68	0.0011524800	x	BC006665/ D76446	
15613	LCN2	e1	2.25	0.0000363900			x
15806	DOCK10	e2	1.60	0.0003681880	x	AK042052/AK172588	
15807	SLC16A3	e2	1.57	0.0002097900	x	BC046525/AK149707	x
16847	C6orf98	e2	1.54	0.0311228000			
16936	FGFR2	e9	5.25	0.0000006487	x	M63503/X55441	x
16946	STXBP3	e4	1.57	0.0033207600	x	AK138609/AK050247	x
17561	PRRX1	e7	2.05	0.0000761560	x	L06502/X59725	x
17866	EPHX1	e1	5.06	0.0000052204			x
18072	SLC44A1	e17	1.66	0.0023642800	x	AY249865/AY249866	x

Conservation	Human Transcript Id	Official gene name
X	AF243424/U17989	telomerase-associated protein 1 striatin, calmodulin binding protein 3 ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)
X	D90188/D90187	Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans) sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (1 macrophage scavenger receptor 1 chromosome 7 open reading frame 28A interleukin 33 bone morphogenetic protein 1 retinoic acid induced 14 attractin
X	D13666/D13665	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 periostin, osteoblast specific factor jumonji domain containing 3, histone lysine demethylase brain and reproductive organ-expressed (TNFRSF1A modulator) growth hormone receptor serum amyloid A-like 1
X	CR616778: AK001930	tubulin tyrosine ligase-like family, member 5 UEV and lactate/malate dehydrogenase domains fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) calsyntenin 1
X	AJ251595/M24915	protein arginine methyltransferase 3 CD44 molecule (Indian blood group)
X	AB209748/AF327441	spectrin, beta, non-erythrocytic 1 echinoderm microtubule associated protein like 1
X	BC063611/AK022261	transmembrane protein 16F pellino homolog 1 (Drosophila) SAFB-like, transcription modulator
		ciliary neurotrophic factor

X	AF061261/CR749802	muscleblind-like 2 (Drosophila) NudC domain containing 1 ecotropic viral integration site 2B
X	BC008771/X97630	MAP/microtubule affinity-regulating kinase 2
X	AF433662/BC068513	Rho guanine nucleotide exchange factor (GEF) 3 calcium/calmodulin-dependent protein kinase (CaM kinase) II delta KIAA1109
X	U53204/AY480047	plectin 1, intermediate filament binding protein 500kDa mediator complex subunit 24 origin recognition complex, subunit 5-like (yeast) CCR4-NOT transcription complex, subunit 2 protein regulator of cytokinesis 1
X	AF019214/AK074353	HMG-box transcription factor 1 UDP-glucose ceramide glucosyltransferase-like 1 capping protein (actin filament) muscle Z-line, alpha 2 chromosome 12 open reading frame 29
X	BC042297/BC031423	upstream binding transcription factor, RNA polymerase I zinc finger E-box binding homeobox 2 formin-like 1 KIAA1267 erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)
X	BC101834/AJ223953	pituitary tumor-transforming 1 ATPase, Na ⁺ /K ⁺ transporting, alpha 3 polypeptide lysophosphatidic acid receptor 1 Josephin domain containing 3 retinol binding protein 1, cellular G protein-coupled receptor kinase 6 mannose receptor, C type 2
X	M13699/BC061702	ceruloplasmin (ferroxidase) purinergic receptor P2X, ligand-gated ion channel, 7 laminin, alpha 5 CAP, adenylate cyclase-associated protein 1 (yeast) prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)

		kinetochore associated 1
		vacuolar protein sorting 8 homolog (S. cerevisiae)
X	BC017715/AB009357	LIM domain containing preferred translocation partner in lipoma
		mitogen-activated protein kinase kinase kinase 7
		lipocalin 2
		dedicator of cytokinesis 10
		solute carrier family 16, member 3 (monocarboxylic acid transporter 4)
		chromosome 6 open reading frame 98
X	BC039243/AK026508	fibroblast growth factor receptor 2
		syntaxin binding protein 3
		paired related homeobox 1
		epoxide hydrolase 1, microsomal (xenobiotic)
X	AK124926/AJ420812	solute carrier family 44, member 1

Biological process

telomere maintenance via recombination

cell cycle

protein modification process, ubiquitin-dependent protein catabolic process, ubiquitin cycle

nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, telomere maintenance chromosome, telomeric region, nucleus, chromosome, telomerase holoenzyme complex

cell adhesion, cell-cell signaling, multicellular organismal development, nervous system development

phosphate transport, receptor-mediated endocytosis

cartilage condensation, ossification, proteolysis, multicellular organismal development, extracellular space

transcription, regulation of transcription, DNA-dependent

skeletal development, cell adhesion

inflammatory response, chromatin modification, oxidation-reduction

ubiquitin cycle, apoptosis, response to DNA damage stimulus, signal transduction, positive regulation of transcription, DNA-dependent

skeletal development, endocytosis, growth

acute-phase response

transcription, protein modification process

glycolysis, ubiquitin cycle, metabolic process, protein transport, cellular carbohydrate metabolic process, regulation of protein metabolic process

MAPKKK cascade, skeletal development, protein amino acid phosphorylation, fibroblast growth factor receptor signaling pathway, plasma membrane, integral to plasma membrane

cell adhesion, homophilic cell adhesion

metabolic process

barbed-end actin filament capping

transcription, regulation of transcription, DNA-dependent, apoptosis

signal transduction, multicellular organismal development, nervous system development, cytoplasm

Cellular component

chromosome, telomeric region, soluble fraction, nucleus, chromosome, telomerase holoenzyme complex

membrane fraction, nucleus, cytoplasm, cytosol, membrane

membrane, integral to membrane

cytoplasm, integral to plasma membrane, membrane

extracellular region, extracellular space

extracellular space

cytoplasm, cytoskeleton

nucleus

extracellular region, proteinaceous extracellular matrix

nucleus

nuclear ubiquitin ligase complex, nucleus, cytoplasm

extracellular region, plasma membrane, integral to plasma membrane

extracellular region

nucleus, cytoplasm, cilium

glycolysis, ubiquitin cycle, metabolic process, protein transport, cellular carbohydrate metabolic process, regulation of protein metabolic process

MAPKKK cascade, skeletal development, protein amino acid phosphorylation, fibroblast growth factor receptor signaling pathway, plasma membrane, integral to plasma membrane

Golgi membrane, endoplasmic reticulum, endoplasmic reticulum membrane, Golgi apparatus

intracellular, cytoplasm

nucleolus, cytoplasm, cytoskeleton, plasma membrane, spectrin

cytoplasm, microtubule, microtubule associated complex

membrane, integral to membrane

nucleus

	nucleus, cytoplasm
immune response	
	integral to plasma membrane, membrane
protein amino acid phosphorylation, protein kinase cascade, multicellular organismal development	plasma membrane
regulation of Rho protein signal transduction	intracellular, cytoplasm
regulation of cell growth, protein amino acid phosphorylation	calcium- and calmodulin-dependent protein kinase complex
	cytoplasm, cytoskeleton, plasma membrane
transcription, regulation of transcription, DNA-dependent, transcription initiation from RNA polymerase II promoter	mediator complex, nucleus
DNA replication, DNA replication initiation	nucleus, nucleoplasm
regulation of transcription, DNA-dependent, regulation of transcription from RNA polymerase II promoter	nucleus, cytoplasm
mitotic spindle elongation, cytokinesis, cell cycle	nucleus, cytoplasm, spindle microtubule
transcription, regulation of transcription, DNA-dependent, cell cycle arrest, Wnt receptor signaling pathway	nucleus
protein amino acid glycosylation, 'de novo' posttranslational protein folding	endoplasmic reticulum, endoplasmic reticulum lumen, ER-Golgi intermediate compartment
protein complex assembly, cell motility, actin cytoskeleton organization and biogenesis, F-actin capping protein complex	
transcription, regulation of transcription from RNA polymerase I promoter	nucleus, nucleoplasm, nucleolus
	intracellular
biological_process, cellular component organization and biogenesis, actin cytoskeleton organization and biogenesis	cellular_component, cytoplasm
	nucleus
blood circulation, cortical actin cytoskeleton organization and biogenesis	nucleus, cytoplasm, plasma membrane, spectrin, extrinsic to membrane, cortical cytoskeleton
DNA repair, transcription from RNA polymerase II promoter, cell cycle, chromosome segregation	nucleus, cytoplasm, cytosol
	integral to membrane
signal transduction, G-protein coupled receptor protein signaling pathway, activation of G-protein	plasma membrane, integral to plasma membrane
transport, retinol metabolic process	cytoplasm
protein amino acid phosphorylation, signal transduction, regulation of G-protein coupled receptor signaling pathway	membrane
endocytosis	membrane, integral to membrane
ion transport, copper ion transport, cellular iron ion homeostasis, aging, response to nutrient deprivation	extracellular region, extracellular space, anchored to plasma membrane
	bleb
regulation of cell adhesion, regulation of cell migration, regulation of embryonic development, cell cycle arrest	extracellular region, basement membrane, laminin-1 complex
cytoskeleton organization and biogenesis, establishment and/or maintenance of cell polarity	plasma membrane
prostaglandin biosynthetic process, lipid metabolic process, fatty acid biosynthetic process	nucleus, cytoplasm, endoplasmic reticulum, endoplasmic reticulum membrane, microtubule

protein complex assembly, cell cycle, mitosis, mitotic cell cycle checkpoint, regulation of condensed chromosome kinetochore, spindle pole, nucleus, cytoplasm, kinetochore

cell adhesion, biological_process

cellular_component, nucleus, cytoplasm, plasma membrane, cell junction
cytosol

transport

extracellular region

transport, organic anion transport, monocarboxylic acid transport

membrane fraction, plasma membrane, integral to plasma membrane

vesicle docking during exocytosis, biological_process, protein transport, vesicle-mediated cellular_component, cytoplasm, cytosol, membrane
regulation of transcription, DNA-dependent, multicellular organismal development nucleus

transport, choline transport

membrane, integral to membrane

Molecular function

nucleotide binding, telomerase activity, RNA binding, ATP binding

calmodulin binding

cysteine-type endopeptidase activity, ubiquitin thiolesterase activity, tRNA guanylyltransferase activity

DNA binding, endonuclease activity, protein binding, hydrolase activity, manganese ion binding, telomeric DNA binding, metal ion binding

receptor activity

receptor activity, scavenger receptor activity, lipid transporter activity

cytokine activity, protein binding

cytokine activity, calcium ion binding, growth factor activity, metallopeptidase activity, zinc ion binding, astacin activity, procollagen C-endopeptidase activity

protein binding

protein binding, heparin binding

binding, iron ion binding, oxidoreductase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, metal ion binding

peroxisome targeting sequence binding, tumor necrosis factor receptor binding, protein binding

receptor activity, growth hormone receptor activity, protein binding

binding

tubulin-tyrosine ligase activity, ligase activity

binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, small conjugating protein ligase activity

nucleotide binding, receptor activity, fibroblast growth factor receptor activity, protein binding, ATP binding, heparin binding, transferase activity

calcium ion binding, protein binding

methyltransferase activity, zinc ion binding, protein-arginine N-methyltransferase activity, transferase activity, metal ion binding

actin binding, structural constituent of cytoskeleton, calmodulin binding

calcium ion binding

nucleotide binding, RNA binding

ciliary neurotrophic factor receptor binding, protein binding, growth factor activity

RNA binding, zinc ion binding, metal ion binding

nucleotide binding, magnesium ion binding, protein serine/threonine kinase activity, protein binding, ATP binding, transferase activity
guanyl-nucleotide exchange factor activity, Rho guanyl-nucleotide exchange factor activity
nucleotide binding, calmodulin-dependent protein kinase activity, calmodulin binding, ATP binding, transferase activity

actin binding, structural constituent of muscle
transcription cofactor activity, receptor activity, RNA polymerase II transcription mediator activity, transcription activator activity, ligand-dependent nuclear receptor transcription coactivator activity,
nucleotide binding, DNA replication origin binding, ATP binding, identical protein binding
RNA polymerase II transcription mediator activity, transcription regulator activity
protein binding
DNA binding, binding
UDP-glucose:glycoprotein glucosyltransferase activity, transferase activity, transferring glycosyl groups, unfolded protein binding
actin binding, protein binding

DNA binding, RNA polymerase I transcription factor activity, protein binding

molecular_function, actin binding, Rho GTPase binding
protein binding
actin binding, structural constituent of cytoskeleton, phosphatidylinositol binding
transcription factor activity, cysteine protease inhibitor activity, protein binding

lysosphingolipid and lysophosphatidic acid receptor activity, receptor activity
protein binding
transporter activity, lipid binding, retinal binding, retinol binding
nucleotide binding, G-protein coupled receptor kinase activity, signal transducer activity, ATP binding, transferase activity
receptor activity, binding, calcium ion binding, sugar binding
ferroxidase activity, copper ion transmembrane transporter activity, copper ion binding, oxidoreductase activity, metal ion binding

receptor binding, structural molecule activity
actin binding, binding
peroxidase activity, prostaglandin-endoperoxide synthase activity, iron ion binding, oxidoreductase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen,

protein binding

protein binding, zinc ion binding, metal ion binding

molecular_function, protein binding, zinc ion binding, metal ion binding

transporter activity, binding

guanyl-nucleotide exchange factor activity, GTP binding, GTPase binding

transporter activity, symporter activity, secondary active monocarboxylate transmembrane transporter activity

molecular_function

transcription factor activity, transcription coactivator activity, sequence-specific DNA binding

choline transmembrane transporter activity

vitamin D receptor binding, thyroid hormone receptor binding

incorporation of two atoms of oxygen, heme binding, metal ion binding