

Accession	Gene	Protein Name	Peptides	Molecular Function	Biological Process	Domain	Unique to NA	Protein Score Ratio	Spectral Count Ratio
Binding									
A7YW98 *	RARS	Arginine--tRNA ligase, cytoplasmic	7	Aminoacyl-tRNA ligase activity, RNA binding	Translation		✓	-	-
P02769	ALB	Serum albumin	16	Binding	Cellular process	SP	✓	-	-
P68250 *	YWHAB	14-3-3 protein beta/alpha	8	Enzyme binding	Cellular protein modification process		✗	2.85	2.23
Q05FF2	STAT1	Signal transducer and activator of transcription 1	6	Metal ion binding, Transcription factor activity	Signal transduction		✓	-	-
Q3MHL3 *	RBBP4	Histone-binding protein RBBP4	5	ATPase activity, Enzyme binding, Histone deacetylase binding	Chromatin remodelling	NCS	✗	2.25	12.00
Q3T054 *	RAN	GTP-binding nuclear protein Ran	5	GTPase activity, Protein binding	Metabolic process, Transport, Transduction	NCS	✗	3.09	3.10
Q3ZBS7	VTN	Vitronectin	6	Extracellular matrix binding	Cell-matrix adhesion	SP	✗	2.62	4.57
Q5E970 *	DDX39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 isoform 1	4	Nucleic acid binding, RNA Helicase activity	mRNA processing	NCS	✗	16.27	5.50
Q9TU25 *	RAC2	Ras-related C3 botulinum toxin substrate 2	3	GTPase activity, Protein binding	Metabolic process, Transduction, Cytoskeleton organisation	NCS	✓	-	-
A6H797	MLEC	Malectin	6	Carbohydrate binding	Carbohydrate metabolic process	TM, SP	✗	2.28	2.00
Catalytic Activity									
A3KMOV5	UBA1	Ubiquitin-like modifier-activating enzyme 1	11	Ligase activity	Cellular protein modification process	NCS	✓	-	-
A4FV12	UBA2	UBA2 protein	4	Ligase activity	Cellular protein modification process	NCS	✗	5.83	5.50
A5D984	PKM2	Pyruvate kinase	21	Kinase activity	Glycolysis, Programmed cell death		✗	2.18	7.27
E1BBF0	STK31	Serine/threonine-protein kinase 31	9	Nucleotide binding, Protein kinase activity	Protein phosphorylation		✓	-	-
E1BFV0	KPNB1	Karyopherin (Importin) beta 1	13	Transmembrane transporter activity, Protein binding	Protein transport	NCS	✗	2.60	5.00
E1BKE5	ASB9	Ankyrin repeat/SOCS box-containing 9-like protein	5	Protein ubiquitination	Protein metabolism, Signal transduction	NCS	✓	-	-
F1MZU2	NSF	Vesicle-fusing ATPase	8	ATP binding, ATPase activity	Signal transduction, Ion transport		✓	-	-
F1N5K2	TTLL12	Tubulin tyrosine ligase-like family, member 12	7	Ligase activity	Cellular protein modification process	NCS	✓	-	-
P00727	LAP3	Cytosol aminopeptidase	8	Metallopeptidase activity	Protein metabolism		✗	2.85	3.75
P20004	ACO2	Aconitate hydratase, mitochondrial	10	Hydro-lyase activity	Metabolic process		✗	2.76	3.80
P48644	ALDH1A1	Retinal dehydrogenase 1	15	Oxidoreductase activity	Metabolic process	NCS	✗	30.66	37.00
P51176	TGM2	Protein-glutamine gamma-glutamyltransferase 2	16	Acyltransferase activity	Cell adhesion, Cellular protein modification process	NCS	✗	4.38	7.08
P55859	PNP	Purine nucleoside phosphorylase	5	Phosphorylase activity	Nucleoside metabolic process	NCS	✗	7.97	24.00
Q0VCA5	SAMHD1	SAM domain and HD domain-containing protein 1	5	Hydrolase activity	Immune system process		✗	9.01	11.50
Q0VCK0	ATIC	Bifunctional purine biosynthesis protein PURH	9	Methyltransferase activity, Hydrolase activity	Metabolic process		✗	23.21	32.00
Q2KIV8	GSTM3	Glutathione S-transferase mu 3 (Brain)	15	Transferase activity	Immune system process		✗	3.35	10.29
Q2KIW6	PSMC6	26S protease regulatory subunit 10B	5	Hydrolase activity	Protein catabolic process	NCS	✗	2.20	2.80
Q2NL26	TKTL1	Transketolase-like protein 1	11	Transketolase activity	Metabolic process	NCS	✗	3.19	24.00
Q32LG3	MDH2	Malate dehydrogenase, mitochondrial	15	Oxidoreductase activity	Metabolic process	NCS	✗	2.15	3.62
Q32PF2	ACLY	ATP-citrate synthase	10	Transferase activity, Lyase activity, Ligase activity	Metabolic process	NCS	✗	5.28	4.75
Q3MHL4	AHCY	Adenosylhomocysteinase	7	Hydrolase activity	Metabolic process	NCS	✓	-	-
Q3SZN8	RNH1	Ribonuclease/angiogenin inhibitor 1	13	Ribonuclease H activity	RNA catabolic process	NCS	✗	4.08	7.17
Q3TOY1	OTUB1	OTU domain, ubiquitin aldehyde binding 1	5	Hydrolase activity	Protein metabolism		✓	-	-
Q3ZC42	ADH5	Alcohol dehydrogenase class-3	10	Oxidoreductase activity	Metabolic process, Oxidation reduction		✗	3.16	4.07
Q58D08	PYCRL	Pyrroline-5-carboxylate reductase 3	6	Oxidoreductase activity	Amino acid biosynthesis, Oxidation reduction	NCS	✗	4.02	9.00
Q5E9B1	LDHB	L-lactate dehydrogenase B chain	15	Oxidoreductase activity	Carbohydrate metabolism, Oxidation reduction	NCS	✗	2.33	3.60
Q5EAD2	PHGDH	D-3-phosphoglycerate dehydrogenase	8	Oxidoreductase activity	Amino acid biosynthesis, Oxidation reduction	NCS	✗	5.62	7.67
Q9XSJ4	ENO1	Alpha-enolase	9	Lyase activity	Glycolysis	NCS	✓	-	-
Enzyme Regulation									
F1MC48	IQGAP1	Ras GTPase-activating-like protein	29	RAS GTPase activator activity	Signal transduction, Regulation of cytokine production		✗	10.08	15.25
P12763 *	AHSG	Alpha-2-HS-glycoprotein	14	Protein binding, Cysteine-type endopeptidase inhibitor activity	Inflammatory response, Bone mineralisation	SP	✗	4.85	11.75
P34955 *	SERPINA1	Alpha-1-antiproteinase	4	Protein binding, Serine-type endopeptidase inhibitor activity	Protein metabolism	SP	✓	-	-
Q2KJ47 *	EHD2	EH-domain containing 2	8	Calcium ion binding, Protein binding, Small GTPase regulator activity	Metabolic process, Transport		✗	2.63	3.09
Ion Channel Activity									
P31404 *	ATP6V1A	V-type proton ATPase catalytic subunit A	6	Hydrolase activity, Transporter activity, Synthase activity, Ion channel activity	Transport		✓	-	-
P31408 *	ATP6V1	V-type proton ATPase subunit B, brain isoform	6	Hydrolase activity, Transporter activity, Synthase activity, Ion channel activity	Transport	NCS	✓	-	-
Structural Molecule Activity									
A5D7D1 *	ACTN4	Alpha-actinin-4	32	Actin binding, Structural constituent of cytoskeleton	Cytoskeleton organisation, Protein transport		✗	3.03	3.76
F1MDH3	TLN1	TLN1 protein	46	Structural constituent of cytoskeleton	Cell adhesion, Cytoskeleton organisation		✗	3.06	4.86

P02584	PFN1	Profilin-1	5	Actin binding, Structural constituent of cytoskeleton	Cytoskeleton organisation	NCS	✓	-	-
P61157	ACTR3	Actin-related protein 3	10	Structural constituent of cytoskeleton	Cellular process		✖	5.70	4.17
Q3MHK9 *	FSCN1	Fascin	8	Actin binding, Structural constituent of cytoskeleton	Cytoskeleton organisation		✖	9.13	8.00
Q3SYV4	CAP1	Adenylyl cyclase-associated protein 1	9	Structural constituent of cytoskeleton	Cytoskeleton organisation		✖	3.66	5.80
Q9TS87 *	TAGLN	Transgelin	6	Actin binding, Structural constituent of cytoskeleton	Muscle organ development	NCS	✖	9.22	27.00

Translation Regulator Activity

Q3SZ54 *	EIF4A1	Eukaryotic initiation factor 4A-I	10	RNA Helicase activity, Translation factor activity, Nucleic acid binding	Translation	NCS	✖	2.05	3.17
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Transporter Activity

A5D785 *	CSE1L	Exportin-2	12	GTPase activity, Transmembrane transporter activity, Protein binding	Protein transport		✖	6.69	5.43
F1MPE5	RANBP6	Ran-binding protein 6	19	Protein transporter activity	Protein transport	NCS	✖	2.41	3.54
P01966	HBA	Hemoglobin subunit alpha	5	Metal ion binding	Oxygen transport		✖	12.96	13.33
P02081	HBBF	Hemoglobin fetal subunit beta	8	Metal ion binding	Oxygen transport	NCS	✖	2.75	6.90

Chaperone

E1B748	HYOU1	Hypoxia up-regulated protein 1	14	ATP binding, Nucleotide binding		TM, SP	✖	3.80	9.33
E1BBY7	HSPA4	Heat shock 70 kDa protein 4	11	ATP binding	Protein transport, Protein complex assembly, Response to stress		✖	4.52	15.00
F1MWD3	CCT5	T-complex protein 1 subunit epsilon	13	Unfolded protein binding	Protein folding		✖	3.99	8.83
G5E531	TCP1	T-complex protein 1 subunit alpha	26	ATP binding	Protein folding	NCS	✖	4.02	6.79
Q2NKZ1	CCT7	T-complex protein 1 subunit eta	19	ATP binding	Protein metabolism		✖	3.48	3.86
Q2T9X2	CCT4	T-complex protein 1 subunit delta	17	Nucleotide binding	Microtubule organising centre		✖	2.36	5.14
Q3ZBH0	CCT2	T-complex protein 1 subunit beta	21	ATP binding	Protein folding		✖	2.51	4.64
Q3ZCI9	CCT8	T-complex protein 1 subunit theta	19	Unfolded protein binding	Protein folding	NCS	✖	3.93	4.27

Accessions, gene symbols and protein names are from bovine and mammalian Uniprot databases. Italicised entries were not annotated for bovine so were manually annotated according to comparative homology.

Peptides are the number of unique peptides (95%) identified with ProteinPilot TM 4.0.1.

Molecular function and biological process information obtained from Uniprot GOA QuickGO and Panther Classification System: web based tools for Gene Ontology research.

Domain indicates the presence of a signal peptide (SP), non classical secretion (NCS) or transmembrane regions (TM) based on CBS Predication Servers: online tools for sequence analysis.

* Accessions were classified in more than one functional category