

Detection of the β -lactoglobulin genotype in zebu cattle (*Gangatiri*) milk using high-resolution accurate mass-spectroscopy

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SUPPLEMENTARY FILE

Supplementary table S1

Accession	Description	Sequence	Sum PEP Score	Coverage %	PSM	Unique Peptides	Score Sequest HT: Sequest HT	Score MS Amanda 2.0	AAs	MW (kDa)	/Gene ID	Chromosome
P00760	Cationic trypsin	MKTFIFLALLGAAVAFVDDDDK IVGGYTCGANTVPYQVSLNSGY HFCGGLINSQWVVSAAHCYKS GIQVRLGEDNINVVEGNEQFISA SKSIVHPSYNSNTLNNDIMLIKLK SAASLNSRVASISLPTSCASAGTQ CLISGWGNTKSSGTSYPDLKCL KAPILSDSSCKSAYPGQITSNMF CAGYLEGGKDSCQGDSSGGPVV	235.467	73	966	22	1951.13	157368.44	246	25.8	615026; 780933	4

			CSGKLGIVSWGSGCAQKNKP GVYTKVCNYVSWIKQTIASN										
	P02769	Serum albumin	MKWVTFISLLLLFSSAYSRGVFRR DTHKSEIAHRFKDLGEEHFKGLV LIAFSQYLQQCPFDEHVKLVNELT EFAKTCVADESHAGCEKSLHTLF GDELCKVASLRETYGDMADCCE KQEPERNECFLSHKDDSPDLPKL KPDPNTLCDEFKADEKKFWGKY LYEIARRHPYFYAPELLYANKYN GVFQEQCAEDKGACLLPKIET MREKVLASSARQRLCASIQKF GERALKAWSVARLSQKFPKAEF VEVTKLVTDLTQVHKECCHGDLL ECADDRADLAKYICDNQDTISSK LKECCDKPLLEKSHCIAEVEKDAI PENLPPLTADFAEDKDVCKNYQE AKDAFLGSFLYEYSRRHPEYAVSV LLRLAKEYEATLECCAADDPHA CYSTVFDKLGHLVDEPQNLIKQN CDQFEKLGEGFQNALIVRYTRK VPQVSTPTLVEVSRSLGKVGTRC CTKPESERMPCTEDYLSLILNRLC VLHEKTPVSEKVTCCCTESLVNR RPCFSALTPDETYVPKAFDEKLFT FHADICTLPDTEKQIKKQTALVEL LKHKPKATEEQLKTVMENFVAF	19.99	13	22	7	23.07	2743.35	607	69.2	28071 7	6

			VDKCCAADDKEACFAVEGPKLV VSTQTALA										
E1B991	Uncharacterized protein	MSCQISYQSRGRGGGGGGFRG FSSGSAVVPGRSRLSGTSFCLSR HGGGGGGFGGGGFGGGGFSS RSLVNLGGSRSTISVAGGGGSF GSYGGFGRGGGFGGLGVGG GSFGGGRFGGGGGFGLGGPG GFGGPGGFGPGGFPGGGIHEVS INQSLQPLNVKVDPEIQNVKSQ EREQIKALNNKFATFIDKVRFLEQ QNQVLQTKWELLQQINVGTRTT NLEPLFQGYISQLQSHLDKLYSER MLQESELNNMQDLVEDFKKYE DEVNKRATAAENEFVTLKKDVDH AYTNKVELQAKVDLLRQDVEFTK MLFDAEKTHPASLLISNIFQRSM DNNRSLDLDSIITEVRAQYEEIAQ RSKAEAEAVYHSKYEELRITAGKH GDSLKEVKMEISELNRMIRLQ GEIAQVKKQCKNVQDSIADAEQ RGENALKDAQSKLNDLEEALQK AREDLARLLRDYQDLMNTKLSL DVEIATYRKLEGEECRMSGDLS SNVTVSVTSSSISGVASRAGFG GYGSGGRGSSYGGGFSSGSRSYS SGGRRSGRSRGGGGSYGSGGGS RGGSSSGGGYSSGGKHSSGGGA	17.855	7	34	4	52.3	4753.31	617	64.3	-	5	

			RGSSSSGGGGYGSEKGGSGSCE GGSSSVTFSFR										
P02754	Beta-lactoglobulin	MKCLLLALALTCGAQALIVTQTM KGLDIQKVAGTWYSLAMAASDI SLLDAQSAPLRVYVEELKPTPEG DLEILLQKWENGECAQKKIIAEK TKIPAVFKIDALNENKVLVLDTDY KKYLLFCMENSAPAEQSLACQCL VRTPEVDDEALEKFDKALKALP MHIRLSFNPTQLEEQCHI	16.604	23	10	3	13.53	1301.73	178	19.9	280838	11	
E1BIL2	Uncharacterized protein (Fragment)	YSQQSCRASSGSRQGFSGHSA VMSGQSRVTSSKSLASRSGGGG AGSAACALMGGGFGSLSYNLG GNKKISISLAGGSIRAGGFRSTSG GYSGGCGFGGGGRGMGGGFG GRAGGFGGGVGGFGGPGGFP GGIQEVTVNQSLQPLNVEIDP QIQQVKAQEREQIKTLNKNKFAF IDKVRFLEQQNKVLETKWSLLQE QSGTNTNNRNLEPFFENYISSL RAFLDGLHVEKDKLHEELRSME GMVEDFKKRYEEEINKRTAAEN DFVVLKKDIDAAYMTKVELEAKV DSVTDEINFLKALYDAELSQMQL DTGDTSVVLSMDNNRCLDLSII AEVRAQYEAIAQRSKAEAEALYQ	16.352	9	28	6	35.1	3321.91	541	57.2	-	5	

			<p>SKIQLGELQTTAGMHGDDLKSIK TEIMEFNRMIQRLRAEIESVKKQ NANLQTAIADAEQHGEVALKDA NAKLQDLKAALQQAKEDLARLL KEYQELMNVKLALDIEIATYRTLL EGEECRMSGECQSSVSIEMVHN TTSSSSGGSGALGGGAGGRGGL GSGGLGSGSLGSGRLGSGGRDS RAS</p>										
	P0CG53	Polyubiquitin-B	<p>MQIFVKTLTGKTITLEVEPSDTIE NVKAKIQDKEGIPPDQQLIFAG KQLEDGRTLSDYNIQKESTLHLVL RLRGGMQIFVKTLTGKTITLEVEP SDTIENVKAKIQDKEGIPDQQR LIFAGKQLEDGRTLSDYNIQKEST LHLVLRGGMQIFVKTLTGKTIT LEVEPSDTIENVKAKIQDKEGIPP DQQLIFAGKQLEDGRTLSDYNI QKESTLHLVLRGGMQIFVKTL TGKTITLEVEPSDTIENVKAKIQD KEGIPPDQQLIFAGKQLEDGRT LSDYNIQKESTLHLVLRGGC</p>	9.569	56	16	5	13.86	1716.02	305	34.3	281370	19
	P63048	Ubiquitin-60S ribosomal protein L40	<p>MQIFVKTLTGKTITLEVEPSDTIE NVKAKIQDKEGIPPDQQLIFAG KQLEDGRTLSDYNIQKESTLHLVL RLRGGIIEPSLRQLAQKYNCDKM</p>	9.569	34	16	5	13.86	1716.02	128	14.7	615199	7

			ICRKC <small>Y</small> ARLHPRAVNCRRKKKCGH TNNLRPKKKVK										
P84227	Histone H3.2	MARTKQTARKSTGGKAPRKQLA TKAARKSAPATGGVKKPHRYRP GTVALREIRRYQKSTELLIRKLPF QRLVREIAQDFKTDLRFQSSAV MALQEASEAYLVGLFEDTNLCAI HAKRVTIMPKDIQLARRIGERA	0.869	5	2	1	2.17	170.38	136	15.4	50459 9; 78807 7; 61914 1	3	
G3MZU2	Phosphatidate cytidyltransferase	MWELRHRGGGGPGPGEAASP PREGEAAGGDHETESTSDKETDI DDRYGDLDSRTDSDIPEIPSLDR TPEILKKALSGLSSRWKNWWIR GILTMTMISLFFLIYMGFMLMLL VLSIQVKCFHEIITIGYRVYHSYDL PWFRTLSWYFLLCVNYFFYGETV ADYFATFVQREEQLQFLIRYHRFI SFALYLAGFCMFVLSLVKKHYRL QFYMF <small>A</small> WTHVTLITVTQSHLVI QNLFEGMIWFLVPISVICNDITA YIFGFFFGRTPLIKLSPKKTWEGFI GGFFSTVIFGFIAAYVLSKYQYFV CPVEYRSDVNSFVTECEPSELFQ LQSYSLPPFLKAVLRRET <small>V</small> SMYPF QIHSIALSTFASLIGPFGGFFASGF KRAFKIKDFANTIPGHGGIMDRF DCQYLMATFVHVYITSFIRGPNP	0.864	2	1	1	0	-	461	53.1	10033 6936	6	

			SKVLQQLLVLQPEQQLNIYKTLK THLTEKGILQPTLKV										
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*Sum PEP Score: sum posterior error probability scores; PSM: peptide spectrum matches; AAs: amino acids.