

Supplementary material

Lbrm.13.0860	1	-----*DTGLCAGITERSRNSVTCTSVVPG-----*VACEDAGCAHGTRSVSVLAG-----	44	
Lbrm.28.2570	641	VFPSDLVHIPAVYVERSAACWSGMCDALGLDSHNS--CGEVIPPRVRDLKRESTISAVEANAFADRWRREVGMRMGVETTSN	718	
Lbrm.13.0860	45	-----QLSVSPPLDREPPE---ETAWRSSGRHILSAGQYIGLAPGATVRVFRVDRQGRTHQRYL-----ARAL	105	
Lbrm.28.2570	719	NRNAELVPLVVRSAVRAQDPTMLVNTCARVSG-DTTNGGAAAGAGTEASPRATGGPSGMGLRKLRWRWAHRTDLRRARCC	797	Intracellular region of Lbrm.28.2570
Lbrm.13.0860	106	GVLLREAEDSEVGRLNRTWDTPSAHIARRDETVDVINLSYGSEDYYSNSQVQSKLYRLMHEHGVVVAASGNDGVRFGSV	185	
Lbrm.28.2570	798	GVFGRVMGETAEQRMRR-----LMARKVKREGYSLFERFLHYYLPAIYCARYALLALLVLFIIVC-----VLGSR	864	
Lbrm.13.0860	186	RSPADMPGVLAVGALRVEG-----HGRTAQTSR---TLDTNAQGNPAAGALGDLADSFAAGGGHK	242	
Lbrm.28.2570	865	ITAAGLPNTLLADQGNIAINTFAEMGDTFGQRGSCFCGPYYRSPQDYRQATVTDITACSAEYDVQMILYADSCGVNCGTS	944	
Lbrm.13.0860	243	*SVAHFSGRGPTTWELPFAGRAKPDVLALGQHWTVQGVSAAAFSTAAPQR--RRAAPALQRSASGTSIAAPIVAGVVA	320	
Lbrm.28.2570	945	ACVDCACTAHGTAALDDCGG-----CTVAELSGAAKCTCPVTRDCQYCAWALDKGNTGGGSCSMTNASTCG	1011	Extracellular region of Lbrm.28.2570
Lbrm.13.0860	321	LCLEAAWSSASAAAMKNTTDDGAYLDVRHNRRLARVSDSLLVREAILRTA-----	370	
Lbrm.28.2570	1012	SNGGCDQYSGTCVCHAGFTGATCGECEAWLLPITWNSACTLECSASMNSAACSCNVSSGRCQTCPAGTRGYDCSWPSVDC	1091	

Figure S1. Comparative sequential analysis of the S8 domain of the LbrM.13.0860 and LbrM.28.2570 genes. Sequence analysis was performed on the BLAST server (<https://blast.ncbi.nlm.nih.gov>). In the figure is shown the alignment of the region corresponding to the S8 domain based on the amino acid residues of the catalytic site (*) of the LbrM.13.0860 gene. In the Lbrm28.2570 gene, amino acid residues with potential for active site formation can be detected in the intracellular and extracellular regions: Aspartic (D), Asparagine (N), Histidine (H) and Serine (S).