

A

	10	20	30	40	50	60	70
LgALP1							
Astacin_3LQ0	NAISFENMRWPNATIVYKLAGIYALFPGDIKKAMRHIEENT CIKFKSRKNEEGYVKIYKGGKES CFADIG						
	** :: * * * : ** : * * : * : * : * : * : * : * : * : * : * : * : * : * : * : *						
	80	90	100	110	120	130	140
LgALP1							
Astacin_3LQ0	YFAKEQRLSLGS- GCKI FGRILHEMGHTIGLF HEHTRPDRD LYITVHEDNIRPSSKRNYKKT PAAMTRVI						
	:: * : *						
	150	160	170	180	190	200	
LgALP1							
Astacin_3LQ0	GPFDYHSIMYGENAGSIDPMLHKTMEANTPGITL TSARYKDSL TDL DIKKINTLYN CPGKDKFT						
	: : *						

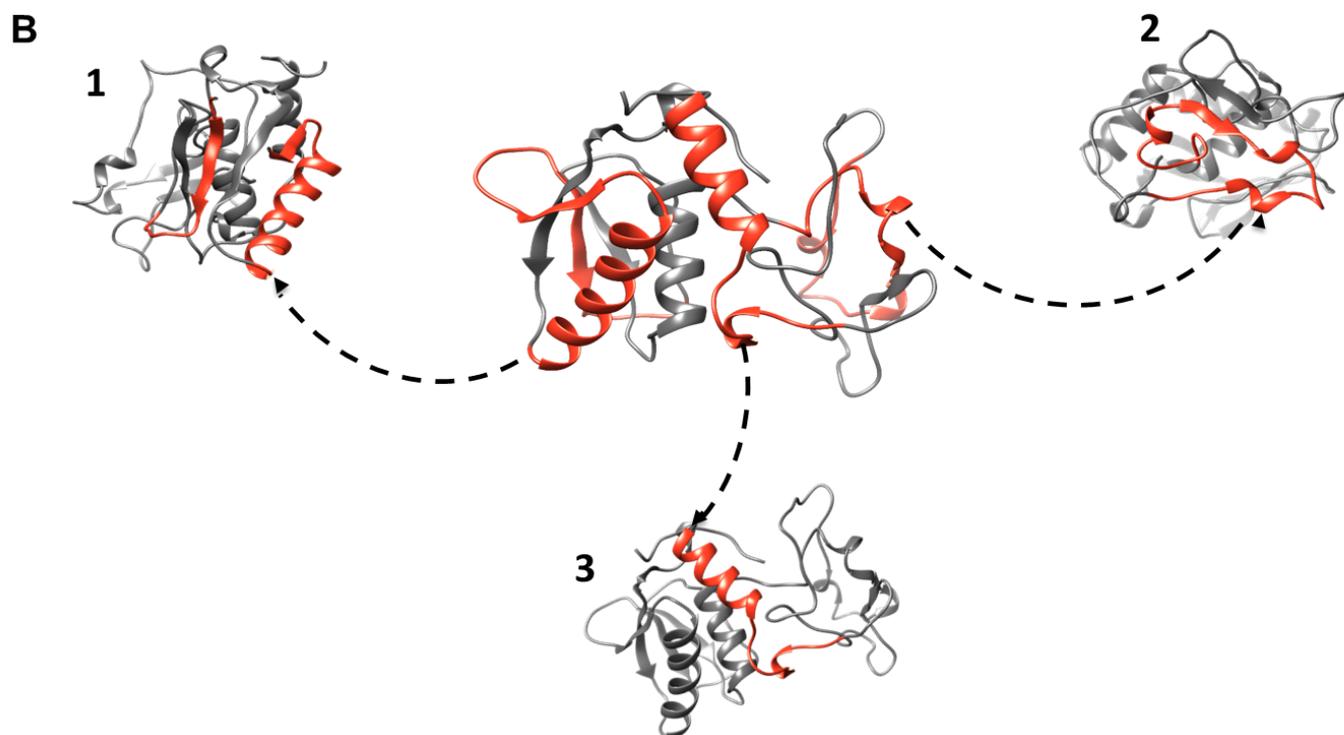


Figure S2: (A) Multiple alignment analysis of deduced amino acid sequences of LgALP1 from *L. gaucho* and the astacin metalloprotease (PDB: 3LQ0) from *Astacus astacus* used as a template to predict the 3D structure of LgALP1. The hydrophilic regions of LgALP1 used to construct the hybrid immunogen are underlined. **The cysteines and the astacin family motifs, such as the catalytic site (HEXXHXXGXXHE) and the Met-turn (MXY), are indicated in boldface.** Identical amino acids are indicated by (*), while conservative substitutions are indicated by (:). (B) Predicted tridimensional structure of ALMP LgALP1 showing the hydrophilic regions. The central picture shows highlighted in orange the three hydrophilic regions of LgALP1 chosen to construct the hybrid immunogen LgRec1ALP1. Each hydrophilic region is shown around the central picture. (1-ALFPGDIKKAMRHIEENTCIKFKSRKNEEGYVKIYKGGKES; 2-HEHTRPDRDLYITVHEDNIRPSSKRNYKKT; 3-LTSARYKDSLTDLDIKKINTLYN.