A

```
                                   10        20        30        40        50        60
                                    |         |         |         |         |         |
LgRec1                     ADNRRPIWVMGHMVNSLAQIDEFVGLGSNSIETDVSFDKQANPEYTYHGIPCDCGRACLH
phospholipase_D_3RLH       AGNRRPIWIMGHMVNAIGQIDEFVNLGANSIETDVSFDDNANPEYTYHGIPCDCGRNCKK
                           * ******:******:: ****** **:********** :**************** * :

                                   70        80        90       100       110       120
                                    |         |         |         |         |         |
LgRec1                     STKFNDFLKGLRKVTTPGDSKYLEKLILVVFDLKTGSLYDNQAYDAGTKLAKNLLQHYWN
phospholipase_D_3RLH       YENFNDFLKGLRSATTPGNSKYQEKLVLVVFDLKTGSLYDNQANDAGKKLAKNLLQHYWN
                             :*********  ****:*** ***:**************** *** ************

                                  130       140       150       160       170       180
                                    |         |         |         |         |         |
LgRec1                     NGNNGGRAYIILSIPNLNHYKLITGFKETLKNEGHEELLEKVGTDFSGNDDISDVQKTYN
phospholipase_D_3RLH       NGNNGGRAYIVLSIPDLNHYPLIKGFKDQLTKDGHPELMDKVGHDFSGNDDIGDVGKAYK
                           **********:****:**** ** ***: * ::** **::*** ******** ** *:*:

                                  190       200       210       220       230       240
                                    |         |         |         |         |         |
LgRec1                     KAGVTGHVWQSDGITNCLLRGLTRVKAAVANRDSGSGIINKVYYWTVDKRQSTRDTLDAN
phospholipase_D_3RLH       KAGITGHIWQSDGITNCLPRGLSRVNAAVANRDSANGFINKVYYWTVDKRSTTRDALDAG
                           ***:***:********** ***:**:********  *:************ :***:***

                                  250       260       270       280
                                    |         |         |         |
LgRec1                     VDGIMTNYPDITVEILNEAAYKKKFRIATYEDNPWETFKG
phospholipase_D_3RLH       VDGIMTNYPDVITDVLNEAAYKKKFRVATYDDNPWVTFKK
                           **********:  ::***********:***:**** ***
```

B

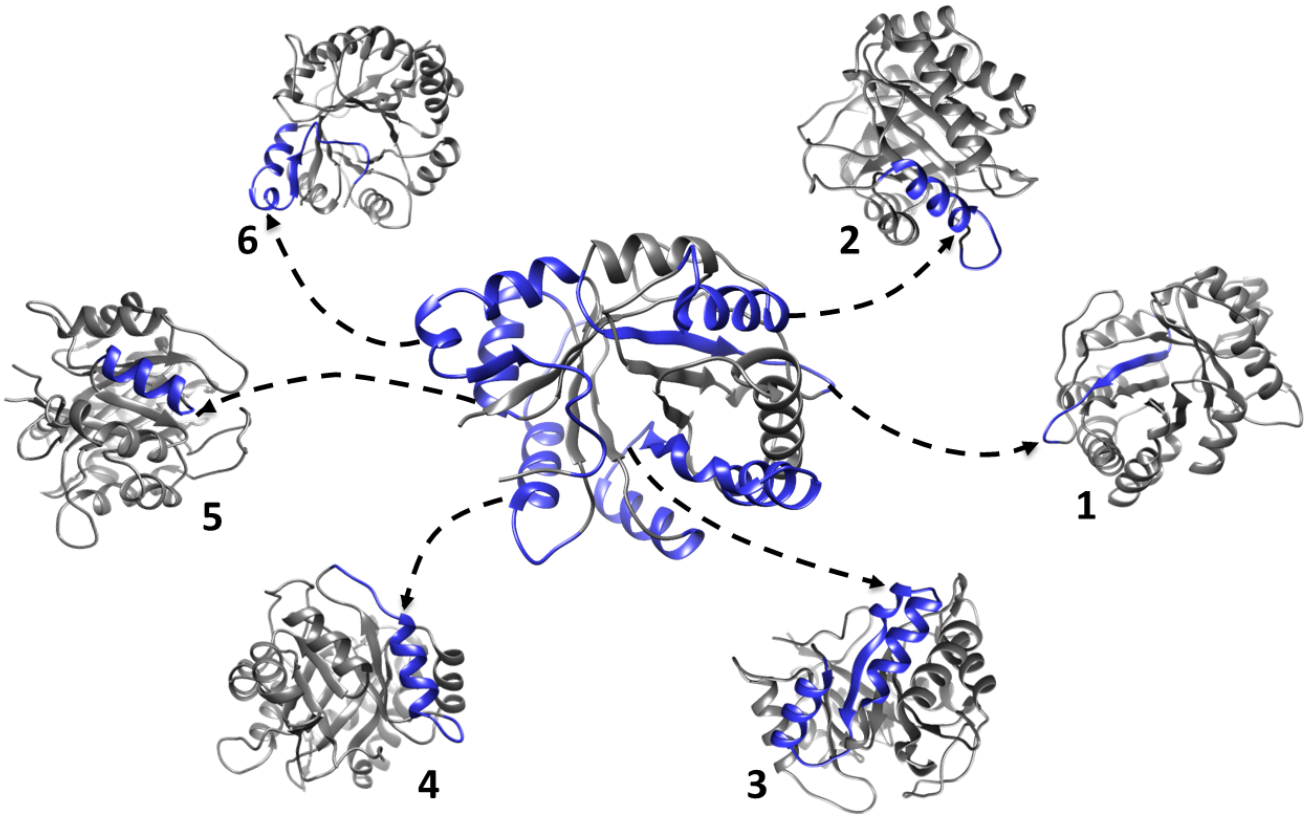

Figure S1: (A) Multiple alignment analysis of deduced amino acid sequences of LgRec1 (AFY98967) from *L. gaucho* and with the sequence of a phospholipase (PDB: 3RLH) from *L. intermedia* used as a template to predict the 3D structure of LgRec1. The hydrophilic regions of LgRec1 used to construct the hybrid immunogen are underlined. **The cysteines and the residues that are involved in the catalysis are shown in boldface**. Identical amino acids and conservative substitutions are indicated by (*) and (:), respectively. (B) Predicted tridimensional structure of PLD LgRec1 showing the hydrophilic regions. The central picture shows highlighted in blue the six hydrophilic regions of LgRec1 chosen to construct the hybrid immunogen LgRec1ALP1. Each hydrophilic region is shown around the central picture. (1-SNSIETDVSFDKQ; 2-KFNDFLKGLRKVTTPGDSK; 3-KLI TGFKETLKNEGHEELLEKVGTDFSGNDDISDVQKTYNKAG; 4-LLRGLTRVKAAVANRDSGSG; 5-DKRQSTRDTLDAN; 6-PDITVEILNEAAYKKKFRIATYEDNPWET.