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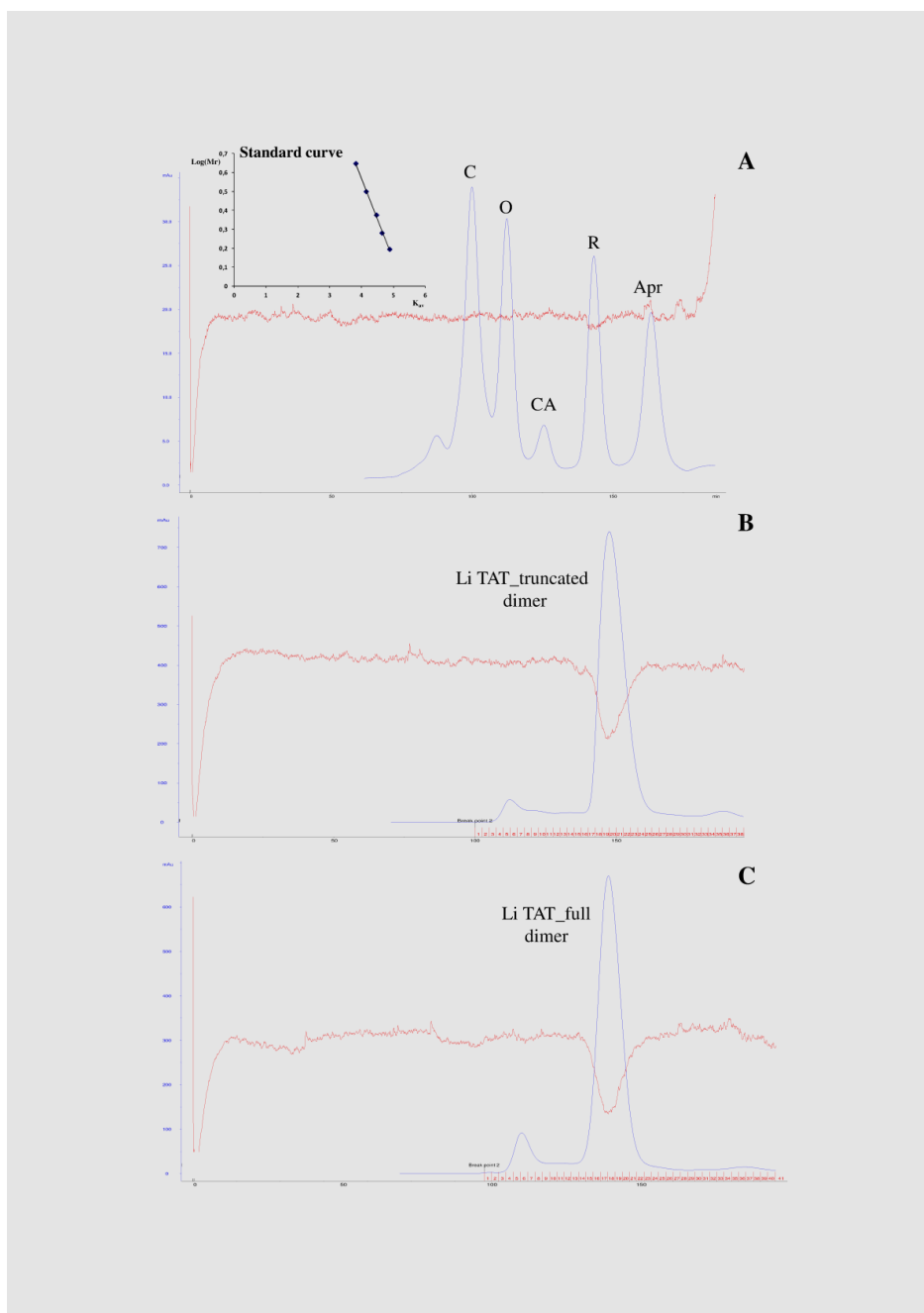
4 **Supporting information for article:**

5 **Structure of tyrosine aminotransferase from *Leishmania***  
6 ***infantum***

7 **M. A. Moreno, A. Abramov, J. Abendroth, A. Alonso, S. Zhang, P. J.**  
8 **Alcolea, T. Edwards, D. Lorimer, P. J. Myler and V. Larraga**

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13 **Figure S1 LiTAT\_full and LiTAT\_truncated form a dimer in solution.** A. A calibration  
14 curve was obtained based on the gel base distribution coefficient ( $K_{av}$ ) and the logarithmic of  
15 the molecular weight (Mr) of five standard proteins included in the Low Molecular Weight Kit.  
16 O: Ovalbumin, C: Conalbumin, CA: Carbonic anhydrase, R: Ribonuclease A, Apr: Aprotinin.  
17 **B.** Gel filtration chromatogram corresponding to LiTAT\_truncated purification. The estimated  
18  $K_{av}$  value was 0,136 and the estimated Mr was 100,42 kDa. **C.** Gel filtration chromatogram  
19 corresponding to LiTAT\_full purification. The estimated  $K_{av}$  value was 0,1095 and the  
20 estimated Mr was 115,62 kDa.



22 **Figure S2** Multiple sequence alignment of the *L. infantum*, *L. major*, *L. braziliensis*, *T. cruzi*,  
23 *Homo sapiens* and *Rattus norvegicus* tyrosine aminotransferases. The figure was generated  
24 with ESPript (Gouet *et al.*, 1999, Gouet *et al.*, 2003), with conserved regions indicated by  
25 boxes. Residues identical in all sequences are highlighted red and conservative replacements  
26 indicated by red text. The N-terminal domain absent from TcTAT is outlined by the blue box.  
27 Secondary structure features obtained from the LiTAT structure are shown above the sequence,  
28 with alpha- or  $3_{10}$ - helices, beta-sheets and hydrogen bonded turns indicated by  $\alpha$ ,  $\eta$ ,  $\beta$ , and T,  
29 respectively.