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AM854      1  MLHRWLALCFASFVTCGLF---SKEKVGMDIVGVFSS---AGRVEKVFYDFNKYEIK
APH_0338   1  MLRRSSFFCILALLSVTSCGTLLPDSNVGVRHDTGSHRSVAFAKKVEKVFYDFIGKYDLK

AM854      55  GSGKKVLLGLVERMKADKRSTLLIIGHIDSRGTEEYNLALGERRANAVKEFILGCDRSLS
APH_0338   61  GPGKKVILELVEQLRQDSMYLVVIGHADATGTEEYSLALGEKRANAVKOFILGCDKSLA

AM854      115  PRISTQSRGKAEPEVLVYSSDFKEAEKAHAQNRRVLIVECOHSVSPKKMAIKWPFSFG
APH_0338   121  PRVTTQSRGKAEPEVLVYSTDAQEVEKANAQNRRAVIVEFAH-----

AM854      175  RSAAKQDDVGSSEVSDEN-PVDDSSEGIASEEAAPEEGVVSEEAPEEAPEVAQDSSAGVV
APH_0338   180  -----IPRSGVADMEAPVASSITSENSNASAEGEDM---EASEFSSAIAN-----

AM854      234  APE
APH_0338   ---

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Figure S7. A global pairwise alignment of AM854 and APH\_0338 (OmpA) using lalign. The line above the alignment (AM854 aa19-68) includes the binding domain of APH\_0338 (aa59-74) and denotes the peptide used in the ELISAs. Amino acids that share identity are in white text with a black background. Conservative amino acid replacements are in white text with a gray background.