

Region-1 (lid domain)

LysB-D29 1 MSKPWLFTV-H-----CT---GQPDPLGP-GLPAD  
CRL 1 MELALALSLIASVAAAPTATLANGDTITGLNAIINEAFLGIPFAEPPVGNLRFKDPVPYS **GSLDQGKFTSYGPPSCMQQNPEGTYEENLPK** AALDLVMQSKVFEE---VSP  
PCL 1 MARTMRSRVVA-----GAVACAMSIAFPAGTTAVMT  
HuPL 1 MLPLWTLSTLLLGAVAGKEVCY-----ERLG--CFSDDSPWSGI-----  
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LysB-D29 26 TARDVLDIYRWQPIGNYPAA-----AF-----PMWPS-VEKGVAE-----  
CRL 108 SSDECLTINVVRPPGKAGAG-----NLPV---MLWIFGCGFEVGGTSTF-----PPAQ---M-ITKSIAMGKPIIHVSVNYRVSSWGFLAGDEIKAEGSANAG  
PCL 32 LATTHAAMAATAAPAAGYAAT-----RYPI---ILVHG---LISGTDKY-----AGVLEYWYG-IQEDLQQNGA-----TVYVANLSGFQSDDGPNRGE-----  
HuPL 36 -TERPLHILPWSPKDVNTRFLLYTNENPNNFQEVAAADSSSISGSNFKTNRKTRFIHCGEIDKGEENWLANVCKNLFKVE-----SVNCICVDWKGGSRTGYTQ-ASQNIR  
: : \*

GXSXG

GXP

LysB-D29 60 -----LILQIELKLDA--DPYADFAMAGYSQGAIIVVGQVLKHHILPPTGRLHRLHRL-KKVIFWGNPMRQ-----KGFAH---SDEWI  
CRL 194 LKDQRLGMQWVADNIAAFGGDPTKVITIFGESAGSMSVMCHIL---W-----ND-GDNTYKGPFLFR-----AGIMQ---SGAMV  
PCL 108 ---Q--LLAYVKTVLAA--TGATKVNILVGSQGLSSRYVAA--VAP-----DLV-ASVTITGTPHRG-----SEFAD-----FV  
HuPL 139 IVG-AEVAYFVEFLQSAFGYSPSNVHVIHSLGHAHAAGEAGR---RTNGTIGRITGIDPAEPCFQGTPELVRLDPSDAKFVDVIHTDGAPIVPNLGFQMSQVVGHLDFE  
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Region-2 (lid domain)

Region-3

LysB-D29 133 HPVAAPD-----TLGILEDRLE-NLEQY-----G-----FEV-RDY **AHDGDMYASIKEDDLHEYE**---**VAIG**  
CRL 261 PSDAV---DGIYGN-----EIFDLLASNAGCGSASDKLACLRGVSSDTLEDATNNTPGFLAYSSLRLS-----YLPRPDGVNITDDMYALVREGKYANIP---VIIG  
PCL 168 QDVLAYDPT **GLSSSVIAAFVNVFGILTSSSH-NTNQDALAALQTL**TTARAATYNQN-----YPSAG-----LGA-PGSCQTGAPTETVGGNTHLLYS---WAGT  
HuPL 244 **PNGGV-EMPGCKKNILSQIVDIDGIWEGT**-----**RDFAACNE**ILRSYKYTDSIVNPDGFAGFPCASYNVFTANKCFPCPSGGCPQMGHYADRYPGKTNDVGQKFYLDTG  
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Region-3 (linker domain and acyl binding site)

LysB-D29 185 -----R- **IVMKASGFIGG** **RDSV** **VAQLIE** **LGQRPITEGIALAGAIID-ALTFFA**-----  
CRL 352 D-----QN---DE **GTFFGTSSLNVTDAQAREYFKQSFVHAS** **DAEIDT** **I** **MTAYPGDITQGSPEDTGIILNALTPOFKRISAVLGDI**  
PCL 257 A-----IQ---PTLSVFGVTGA---TDTSTLPLVDPA---N---VLDLSTLAL---FGTGTVMINRGSGQN **DGLVSKCSALYG**-----  
HuPL 347 DASNFARWRYKVSVTLSGKKVTGHILVSLFGNKGN---SKQYEIFKGTLPDSTHSNEFSDSDVDVGDLMVKFIWYNN-----VINPTLPRVGAS-----  
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Region-3

LysB-D29 231 ----- **RSRMGDKWPHLYNR**YPAVEFL-----RQ-----I-----  
CRL 429 **GFTLARRYFLNHYTGGTKYSFLSKQLSGLPVLGTFE**SNDIVFQDYLLGSGSLIYNNAFIAFATDLDLPNTAGLLVKWPEYTSSSSQSGNNLMMINALGLYTGKDNFRTAGYD  
PCL 320 ----- **KVLSTSYKWN**ELDEINQLLGVRGAYAEDPVAVIRT-----HANRLKLAGV-----  
HuPL 434 -----KIIVETNVGKQFNFCSPETVREEVLLTL-----  
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LysB-D29  
CRL 538 ALFSNPPSFFV  
PCL  
HuPL 463 -----TPC---

**Figure S2:** Multiple sequence alignment of LysB-D29 with relative members of the  $\alpha/\beta$  hydrolase family including *Candida rugosa* lipase (**CRL**), *Pseudomonas cepacia* lipase (**PCL**) and Human pancreatic lipase (**HuPL**). Identical residues are labeled by *asterisk*, conserved residues labeled by *colon* and *full stop* indicating semi-conserved residues. Residues forming the active site are shaded in red color. Oxyanion hole and GXP residues are highlighted in pink. Region-1 in **CRL** and Region-2 in **PCL** and **HuPL** (lid domains) are highlighted in yellow. Region-3 (linker domain) in LysB-D29 and other lipases are highlighted in green.