

Region-1 (lid domain)

LysB-D29 1 MSKPWLFTV-H-----
 CRL 1 MELALALS LIASVAAAPTATLANGDTITGLNAIINEAFLGIPFAEPPVGNLRFKDPVPS
 PCL 1 MARTMRSRVVA-----
 HuPL 1 MLPLWTL SLLLGA VAGKEVCY-----ERLG--CFSDDSPWSGI-----
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LysB-D29 26 TARDVLDIYRWQPIGNY PAA-----AF-----PMWPS-VEKGVAE-----
 CRL 108 SSEDCLTINVVRPPGTKAGA-----NLPV---MLWIFGCGFEVGGTSTF-----PPAQ---M-ITKSIAMGKPIIHVSVNYRVSSWGFLAGDEIKAEGSANAG
 PCL 32 LATTHAAMAATA PAAGYAAT-----RYPI---ILVHG---L SGTDKY---AGVLEYWYG-IQEDLQQNGA-----TVYVANLSGFQSDDGPNRGE-----
 HuPL 36 -TERPLHILPWSPKDVNTRFLLYTNENPNNFQEVAAADSSSISGSNFKTRNRKTRFIHGEIDKGEENWLANVCKNLFKVE-----SVNCICVDWKGGSRGTGYTQ-ASQNI R
 : : *

GXSXG

GXP

LysB-D29 60 -----LILQIELK LDA--DPYADFAMAGY SQAIVVVGQVLKHHILPPTGRLHRLHRL-KKVIFWGNP MRO-----KGFAH---SDEWI
 CRL 194 LKDQRLGMQWVADNIAAFGGDPTKVTIFGFSAGSMSVMCHIL---W-----ND-GDNTYK GKP LFR-----AGIMQ---SGAMV
 PCL 108 ---Q--LLAYVKT V LAA--TGATKVNLVGHSQGLSSRYVAA--VAP-----DLV-ASVTTI GTP HRG-----SEFAD-----FV
 HuPL 139 IVG-AEVAYFVEFLQSAFGYSPSNVHVI GHS LG AHAAGEAGR---RTNGTIGRITGIDPAEPCFQ GTP ELVRLDPSDAKFVDVIHTDGAPIV PNLGFGMSQVVGHLDFE
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Region-2 (lid domain)

Region-3

LysB-D29 133 HPVAAPD-----TLGILEDRL E-NLEQY-----G-----FEV-RDY AHDGDMYASIKEDDL HEYE---VAIG
 CRL 261 PSDAV---DGIYGN-----EIFDLLASNAGCGSASDKLACL RGVSSD TLEDATNNTPGFLAYSSLRLS-----YLPRPDGVNITDDMYALVREGKYANIP---VIIG
 PCL 168 QDVLAYDPTGLSSSVIAAFVNVFGILTSSSH-NTNQDALAALQTLTARAATYNQN-----YPSAG-----LGA-PGSCQTGAPTETVGGNTHLLYS---WAGT
 HuPL 244 PNGGV-EMP GCKKNILSQIVDIDGIWEGT-----RDFAACNE LRSYKYTDSIVNPDGFAGFPCASYNVFTANKCFPCPSGGCPQMGHYADRYPGKTNDVGVQKFYLDTG
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Region-3 (linker domain and acyl binding site)

LysB-D29 185 -----R- IVMKASGFIGG- RDSV- VAQLIE- LGQRPI TEGIALAGAIID-AL TFFA-----
 CRL 352 D-----QN--DEGTFFGTSSLNVT TDAQAREYFKQSFVHAS-----DAEIDT- I- MTAYPGDITQGSPEFTGI LNALTPQFKRISAVLGD L
 PCL 257 A-----IQ---PTLSVFGVTGA---TDT S-----TLPLVDPA---N---VLDLSTLAL--FGTGTVMINRGSGQN DGLVSKCSALYG-----
 HuPL 347 DASNFARWRYKVSVTLSGKKVTGHILVSLFNGKGN-----SKQYEIFKGT LKPDSTHSNEFDS DVDVGD LQMVKFIWYNN-----VINPTLPRVGAS-----
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Region-3

LysB-D29 231 -----RSRMGDKWPHLYNRYPAVEFL-----RQ-----I-----
 CRL 429 GFTLARRYFLNHYTGGTKYSFLSKQLSGLPVLGTFH SNDIVFQDYLLGSGSLIYNNAFIAFATDLD PNTAGLLVKWPEYTSSS QSGNNLMMINALGLYT GKNFRTAGYD
 PCL 320 -----KVLSTSYKWNH LDEINQLLGV RGAYAEDPVAVIRT-----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 α/β 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.