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## Lipocalin文库的构建及与克百威有结合活性的小分子筛选

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**摘要:**

构建大菜粉蝶Lipocalin蛋白家族中的BBP蛋白突变文库, 依据基因序列, 分别设计10条和12条引物, 通过PCR重叠延伸法得到包含随机突变蛋白BBP的基因序列, 并重组到噬菌粒载体pCANTAB5E中构建Lipocalin突变文库, 库容达到 $4.0 \times 10^9$ 。以偶联分子BSA-克百威和OVA-克百威为靶分子, 采用柱式和平皿式交叉法对Lipocalin文库进行了筛选, 用竞争洗脱法洗脱特异结合活性的噬菌体。经过3轮筛选, 从第3轮的洗脱液中随机挑选了10个重组克隆, 用Dot-blotting法检测出K7 anticalin分子能与克百威特异结合, 为研发克百威的Anticalin类检测试剂盒提供了候选分子, 也为拓宽Lipocalin文库在有害小分子检测方面的应用奠定了基础。

**关键词:** Lipocalin文库 克百威 Anticalin分子

## Construction of Phage-displayed Library Based on the Lipocalin Scaffold and Screening Anticalins with Specificity for Carbofuran

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**Abstract:**

Carbofuran, which is used as toxic carbonate pesticide of crops, is highly toxic and small molecule. To detect the remainder of carbofuran efficiently is important to our healthy. The lipocalins, a family of diverse proteins that normally serve for the storage or transport of mostly hydrophobic and/or chemically sensitive organic compounds, can be reshaped by combinatorial protein design such that it recognizes small molecules. Sixteen residues at the center of binding site of the bilin-binding protein (BBP) from *Pieris brassicae* were subjected to random mutagenesis by overlapping PCR with 12 primers. Phagemid expression vector of pCANTAB5E was used to construct the lipocalin library. The library capacity is  $4.0 \times 10^9$ . BSA and OVA conjugated carbofuran respectively as the targeted protein, the library

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was screened with column and plate as supporter. After 3 rounds of panning, 10 phage clones were random selected with competitive elution. Dot-blotting showed that phage displayed anticalin, named as K7, bound carbofuran specifically among them. K7 can be used as potential anticalin to detect carbofuran of crops.

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