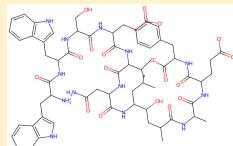
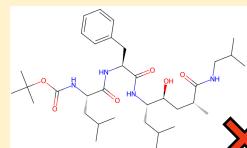
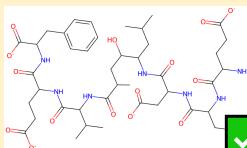


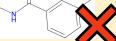
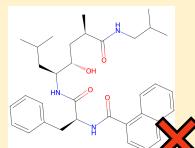
**Question:** Can this molecule bind to the BACE1 protein?



Input Molecule



Few-shot Example



<think>

### Step 1: Molecular Structure Analysis

The target molecule is a complex heptapeptide containing multiple tryptophan residues ( $Cc1c2c([nH]c1)cccc2$ ), leucine/isoleucine branched side chains, glutamate carboxylates ( $[O^-]$ ), and both N-terminal amino and C-terminal carboxyl functionalities. The peptide backbone provides extensive amide hydrogen bonding capability, while the aromatic indole rings offer  $\pi$ - $\pi$  stacking interactions. The molecule adopts an extended conformation due to steric interactions between bulky side chains.

### Step 2: Chemical Principle Application

BACE1 accommodates peptide substrates with specific P1-P4 binding subsites, particularly favoring hydrophobic residues at P1 and P3 positions for optimal cleavage. The calculated molecular weight approximately 1200 Da exceeds typical small molecule inhibitors but matches endogenous peptide substrates. The multiple tryptophan residues can form favorable  $\pi$ - $\pi$  interactions with Phe108 and Tyr71 in the BACE1 active site, while the peptide backbone enables key hydrogen bonds with catalytic Asp32 and Asp228 residues. The extended structure spans the bilobal enzyme cleft effectively.

### Step 3: Few-shot Comparative Analysis

The "True" example shares critical peptide characteristics: multiple amide bonds, charged termini, and aromatic side chains distributed throughout the sequence. Both "False" examples are shorter peptides with fewer aromatic residues and limited conformational flexibility for optimal active site engagement. Our target molecule exhibits superior structural complexity with dual tryptophan residues providing enhanced binding interactions compared to the single phenylalanine in negative examples. The extended peptide length matches the "True" example's capacity for multi-point enzyme contact.

### Conclusion:

Optimal peptide length + favorable aromatic interactions + structural similarity to positive substrate + appropriate backbone flexibility for enzyme cleft binding indicates effective BACE1 recognition and binding.

<answer>True</answer>

