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Why do theory?

#### Experiment-theory interface in rovibrational spectroscopy

1. Born-Oppenheimer approximation

- separates electronic and nuclear motion
- 2. Use a "model" Hamiltonian for the nuclear motions
  - Simplest: rigid rotor, harmonic oscillator
  - Can add vib-rotation interaction, centrifugal distortion, anharmonicity, . . .
- 3. Fit the model to the spectrum
  - The fitting parameters provide information on the molecule

The most accurate molecular geometries come from rotational or vib-rotation spectroscopy



- 1. Calculate the PES and find the lowest energy minima
  - first with classical force fields
  - refine quantum mechanically
- 2. Calculate vibrational spectrum for different minima
  - scale frequencies to account for anharmonicity
- 3. Compare with measured spectrum and select the structure that matches best.
  - No fitting procedure. No goodness of fit.

# Our experimental approach









## Example 1: helical peptides















## Example 2: Peptide sequence scrambling in mass spectrometry

### A practical example

Peptide sequencing by MS: collision-induced dissociation (CID)

Do CID fragments cyclize and permute their sequence?

Example:  $[F - A - G - F - A - G - P - G]H^+$ 

## A practical example

Peptide sequencing by MS: collision-induced dissociation (CID)

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