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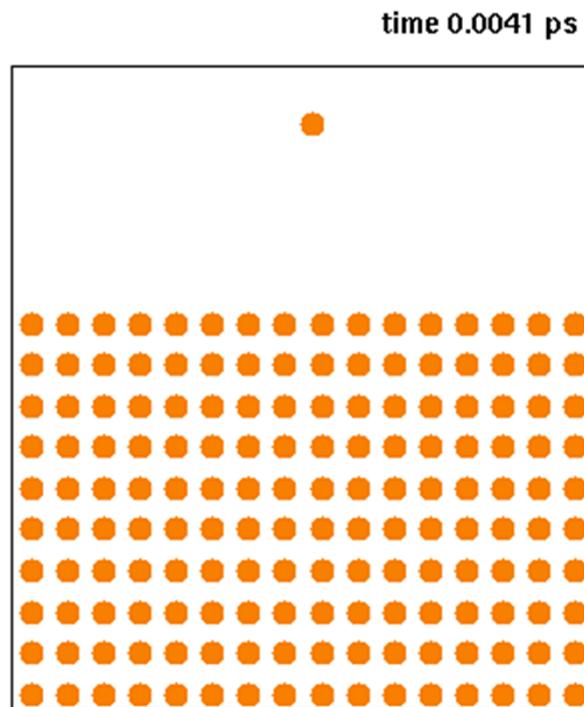
# Effects of Single Ion Strikes into Si on the 3D Reciprocal Space

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Example of a molecular dynamics simulation in a simple system: deposition of one copper (Cu) atom on a Cu Miller index (001) surface. Each circle illustrates the position of one atom. The atomic interactions used in current simulations are more complex than those of 2-dimensional hard spheres. [1]

- What is MD for and why is it done?
  - Basic principles begin with classical MD
    - Approximate interatomic behavior and know beforehand the energy potentials
      - Based off of empirical data or independent structure calculation
    - Systems under investigation are limited in complexity
      - Though in comparison to other methods are quick and easy
  - Most often used in biochemistry/physics and materials science
  - Not Monte Carlo, MD is deterministic

- Ab-initio MD, what is it and how does it work
  - Means from the beginning
  - Refinement of MD meant to allow for more degrees of freedom
    - Quantum chemistry
    - Means more complicated systems can be solved
  - Subcategories exist here that vary in computational intensity
    - Ehrenfest
    - Car-Parrinello
    - Born-Oppenheimer
  - Most successful version is considered to be Density Functional Theory

[1]Marx, Dominik; Hutter, Jurg; Ab Initio molecular dynamics: Theory and Implementation

[2]Ootani, Y; An Introduction to Ab Initio Molecular Dynamics Simulations

[3]Kuhne, Thomas; Ab-Initio Molecular Dynamics

## Classical MD

- Deterministic
- Relatively easy computationally

## Ab-Initio MD

- Introduces more freedom
- Involves much more computational resources

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