Atom or noise? New method helps cryo-EM researchers tell the difference
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Wah Chiu, a professor at SLAC and Stanford, Grigore Pintilie, a computational scientist in Chiu's group, and colleagues devised the new measures, known as Q-scores, to address that issue. To compute Q-scores, scientists start by building and adjusting an atomic model until it best matches the corresponding cryo-EM derived 3-D map. Then, they compare the map to an idealized version in which each atom is well-resolved, revealing to what degree the map truly resolves the atoms in the atomic model.

The researchers validated their approach on large molecules, including a protein called apoferritin that they studied in the Stanford-SLAC Cryo-EM Facilities. Kaiming Zhang, another research scientist in Chiu's group, produced 3-D maps close to the highest resolution reached to date—up to 1.75 angstrom, less than a fifth of a nanometer. Using such maps, they showed how Q-scores varied in predictable ways based on overall resolution and on which parts of a molecular they were studying. Pintilie and Chiu say they hope Q-scores will help biologists and others using cryo-EM better understand and interpret the 3-D maps and resulting atomic models.

The study is published in Nature Methods.


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