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* You should state whether an appropriate sample size was computed when the study was being designed
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Statistics for cryo-EM data collection, processing, refinement, and atomistic model building are provided in Table 1.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

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* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
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Cryo-EM density maps and corresponding atomistic models for rigor, ADP, and actin alone reconstructions have been deposited in the Electron Microscopy Data Bank (EMDB) and Protein Data Bank (PDB). Electron Microscopy Data Bank accession codes: EMD-7115 (actin alone), EMD-7116 (rigor), EMD-7117 (ADP). Protein Data Bank accession codes: Actin alone: 6BNO (HR MDFF), 6BNU (averaged HR MDFF); Rigor: 6BNP (HR MDFF), 6BNV (LPF MDFF); ADP: 6BNQ (HR MDFF), 6BNW (LPF MDFF). Sequence data for the conservation analysis displayed in Fig. 7A is included as Source data. Custom code for structural analysis is available at <https://github.com/alushinlab/goldhelix> .