A recent publication by Croll and coworkers, "Improving SARS-CoV-2 structures: Peer review by early coordinate release" (https://pubmed.ncbi.nlm.nih.gov/33460600/), describes a unique form of peer-review enabled by the early release of biomolecular structure coordinates and density maps and details its critical role in the search for SARS-CoV-2 vaccines and treatments. The authors walk us through identification and remediation of model pathologies in seven preprints, describing what problems they identified, what tools allowed them to make these discoveries, how each of these could have been missed by the original authors during refinement, and how the corrections were subsequently disseminated to the structural biology community. While correcting other people's work is naturally a delicate topic, this paper carefully and convincingly lays out the arguments for both the publication of flawed initial models and their timely correction. Hopefully this demonstration of the potential of preprint and post-publication peer review inspires similar efforts.

A major important theme is correctness, and here we request some further grounding in the philosophy of the usefulness of models and their limitations. In addition to properties of models and maps that are the subject of continued debate, such as whether sidechains without any density should be truncated, there are known limitations of models at various resolutions that impact for what purposes these models can be informative. The authors touch on this in a few places, e.g. "more detailed and nuanced uses of a structure [...] can be chancy from early-release structures" and "Since model building does not yet use Bayesian likelihood to trade off conformational probability with density fit, very rare conformations can be greatly overused at low resolutions or in regions of poor density." We think it would be meaningful to go into much finer detail on these points. When the authors mention that models from preprints are "almost always close to correct," what is the bar for "correct" and what is "close to correct"? Is there any evidence that the structures change due to journal-organized peer review (as opposed to the access to the coordinates and maps that was used here)? Does this vary with the map resolution, between regions of a model, or among structure determination methods? Can the same model be good enough for one purpose but not another? What does it mean for refinement to "behave"? We would challenge the authors to replace any instances of value-laden, black-and-white terms like "correct" or "answer" with precisely what they mean in context, ideally extending to biological relevance. Not all readers will be accustomed to this analysis, and a more sophisticated lens could be another important takeaway from this paper.

The process of structure correction offers a tour of the tools available for structure determination and validation. The unique advantages and limitations of some of these are explored — for example, the fact that real-space correlations can identify atoms without density but not density without atoms, or the fact that perfect geometry in a low-resolution structure is not a strong indicator of model quality. The authors may want to expand this area in particular to include the recent publication on RamaZ: https://pubmed.ncbi.nlm.nih.gov/32857966/

A diagram or flow-chart of which tools assist in which stages of model building, refinement and validation would also be beneficial, especially combined with discussion of what will be missed if only automated processes are used (or conversely, which pathologies are very difficult to identify by eye but are quickly flagged by some available validation tool).

Propagation of model errors — and corrections — is a central focus of this paper. The authors discuss how PDB versioning, available since July 2019, is a huge improvement over the previous system of obsoleting and replacing entire PDB codes. Dissemination of updated information "via the grapevine" is also mentioned in passing, and they praise the efforts of the Coronavirus Structural Task Force to collect and rebuild the staggering number of SARS-CoV-2 structures being published in recent months. We agree this is incredibly important work. If anything, the potential repercussions of badly modeled structures are understated, both in the context of COVID-19 and in general.

The paper concludes with a strong endorsement of preprints and coordinate release in advance of publication in peer-reviewed journals. The wording in this section betrays the authors' intent, however: preprints are identified as not being "formal" publications, and the pre- and post-peer-review publication paradigms are delineated with terms implying preprints are not subject to peer review (meanwhile performing peer review in this manuscript!) and are always obsoleted by publication in a journal. Some careful rewording of these arguments will be critical. (We suggest delineating by whether peer review happens in full public view simultaneous with publication or in a curated fashion that limits which manuscripts are published.) In addition, although urgency and rigor of peer review are discussed here, the further benefits of transparency, accessibility to any and all prospective reviewers, and overall impact on the field are barely mentioned. We contest the claim that "Immediate coordinate release is not sensible in less dire circumstances" and suggest some qualifier here. The decoupling of data release and "journal publication" is a great strength of this paper. Deposition of data to the PDB does not always accompany preprint posting - and is often not available during journal organized peer review - and the authors are in a great position to make an even stronger case for deposition upon preprint posting here!

Overall this paper introduces a number of important considerations around pre-peer-review release of structures. These are not issues unique to the COVID-19 pandemic, but they are unusually worthy of our attention at the present moment. We strongly recommend this paper for publication.

Finally, we identify a handful of minor edits for readability:
- Table 1 is currently an image, which presents an accessibility barrier. The symbol "!!" embedded in the main text ("modeled with !! outlier backbone conformers") can likewise not be interpreted by screen readers or search engines.
- A couple references to "large rotations, but not necessarily 180°" could be clarified by re-wording as "rotations between ?? and 180°."
- We are skeptical of the phrasing "Structures of SARS-CoV-2 *molecules.*" - macromolecules? proteins?
- The phrasing "refinement or other automated procedures" implies refinement is fully automated. We suggest truncating this to just "automated procedures."
- There is only one place in the text that appears to assign malevolent intent as opposed to ignorance: "We believe these complaints misrepresent what is actually going on." The authors should entertain the possibility of rewording.
- We are not sure of the timeline implied by "had immediately flagged the problem, and he had deposited his revised structure" (this would make sense without the instances of "had," unless we misinterpret) or whether "he" is referring to Tristan or the structure's original author.
- SARS-CoV-2 is misspelled in a couple different places as SAR-CoV-2 or SARS-CV-2.
- Conventionally there should be a space between a number and the Ångstrom symbol.
- There is a typo at "wwPDB"s."
- There is a missing comma between "trans" and "not just all non-Pro."
- "...wrong local minimum" should be corrected to "wrong local minima."
- We are not sure whether "commonest" is accepted American English.
- The phrase "ones attempted ... are often ambiguous which version ... is preferable" is not grammatical.
- There is an extra space in "tugging with"
- This will presumably be picked up during typesetting, but "2mFobs-dFcalc and Fobs-Fcalc" are missing subscripts.

As a side note, if the authors run into further problems with file size limits on GitHub, we recommend Zenodo for versioning (and assignment of DOIs!) compatible with any file size.