Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge

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This paper describes outcomes of the 2019 Cryo-EM Model Challenge. The goals were to (1) assess the quality of models that can be produced from cryo-electron microscopy (cryo-EM) maps using current modeling software, (2) evaluate reproducibility of modeling results from different software developers and users and (3) compare performance of current metrics used for model evaluation, particularly Fit-to-Map metrics, with focus on near-atomic resolution. Our findings demonstrate the relatively high accuracy and reproducibility of cryo-EM models derived by 13 participating teams from four benchmark maps, including three forming a resolution series (1.8 to 3.1 Å). The results permit specific recommendations to be made about validating near-atomic cryo-EM structures both in the context of individual experiments and structure data archives such as the Protein Data Bank. We recommend the adoption of multiple scoring parameters to provide full and objective annotation and assessment of the model, reflective of the observed cryo-EM map density.

Cryo-EM has emerged as a key method to visualize and model biologically important macromolecules and cellular machines. Researchers can now routinely achieve resolutions better than 4 Å, yielding new mechanistic insights into cellular processes and providing support for drug discovery7. The recent explosion of cryo-EM structures raises important questions. What are the limits of interpretability given the quality of maps and resulting models? How can model accuracy and reliability be quantified under the simultaneous constraints of map density and chemical rules?

The EMDataResource Project (EMDR) (emdataresource.org) aims to derive validation methods and standards for cryo-EM structures through community consensus5. EMDR has convened an EM Validation Task Force analogous to those for X-ray crystallography7 and NMR8 and has sponsored challenges, workshops and conferences to engage cryo-EM experts, modelers and end-users7,9. During this period, cryo-EM has evolved rapidly (Fig. 1).

This paper describes outcomes of EMDR’s most recent challenge, the 2019 Model ‘Metrics’ Challenge. Map targets representing the state-of-the-art in cryo-EM single particle reconstruction were selected in the near-atomic resolution regime (1.8–3.1 Å) with a twist: three form a resolution series from the same specimen/imaging experiment. Careful evaluation of submitted models by participating teams leads us to several specific recommendations for validating near-atomic cryo-EM structures, directed toward both individual researchers and the Protein Data Bank (PDB) structure data archive5.
since no cryo-EM model was available. The X-ray model provides an excellent although not a fully optimized fit to each map, owing to method/sample differences. For ADH, the structure deposited by the original cryo-EM study authors served as the reference.

Thirteen teams from the USA and Europe submitted 63 models in total, using whatever modeling software they preferred, yielding 15–17 submissions per target (Fig. 3b and Table 1). Most (51) were created ab initio, sometimes supported by additional manual steps, while others (12) were optimizations of publicly available models. The estimated human effort per model was 7 h on average, with a wide range (0–80 h).

Submitted models were evaluated as in the previous challenge11 with multiple metrics in each of four tracks: Fit-to-Map, Coordinates-only, Comparison-to-Reference and Comparison-among-Models (Fig. 3c). The metrics include many in common use as well as several recently introduced.

Metrics to evaluate global Fit-to-Map included Map-Model Fourier shell correlation (FSC)12, FSC average13, Atom Inclusion14, EMRinger15, density-based correlation scores from TEMPy 16–18, clashscore, Rotamer outliers and Ramachandran outliers from MolProbity20, as well as standard geometry measures (for example, H-bonds or clashes20). Where provided, refined B factors modestly improve Fit-to-Map scores (Extended Data Fig. 5).

Evaluation exposed four fairly frequent issues: mis-assignment of peptide-bond geometry, misorientation of peptides, local sequence misalignment and failure to model associated ligands. Two-thirds of submitted models had one or more peptide-bond geometry errors (Extended Data Fig. 1).

At resolutions near 3 Å or in weak local density, the carbonyl O protrusion disappears into the tube of backbone density (Fig. 2), and trans peptide bonds are more readily modeled in the wrong orientation. If peptide torsion $\phi$ (C,N,C$_2$,C) or $\psi$ (N,C$_2$,C,N) values are explicitly refined, adjacent sidechains can be pushed further in the wrong direction. Such cases are not flagged as Ramachandran outliers but they are recognized by CaBLAM22 (Extended Data Fig. 2).

Sequence misthreadings misplace residues over very large distances. The misalignment can be recognized by local Fit-to-Map criteria, with ends flagged by CaBLAM, bad geometry, cis-proline peptides and clashes (Extended Data Fig. 3).

Although there was evidence for ordered water in higher-resolution APOE maps, only two groups elected to model water. Submissions were also split roughly 50/50 for (1) inclusion of predicted H-atom positions and (2) refinement of isotropic B factors. Although near-atomic cryo-EM maps do not have a sufficient level of detail to directly identify H-atom positions, inclusion of predicted positions can still be useful for identifying steric properties such as H-bonds or clashes23. Where provided, refined B factors modestly improved Fit-to-Map scores (Extended Data Fig. 5).

**Evaluating metrics: Fit-to-Map.** Score distributions of Fit-to-Map metrics (Table 2) were systematically compared (Fig. 4a–d). For APOE, single subunits were evaluated against masked subunit maps, whereas for ADH, dimeric models were evaluated against the full sharpened cryo-EM map (Fig. 2d). To control for the varied impact of H-atom inclusion or isotropic B-factor refinement on different metrics, all evaluated scores were produced with H atoms removed and all B factors were set to zero.

Score distributions were first evaluated for all 63 models across all four challenge targets. A wide diversity in performance was observed, with poor correlations between most metrics (Fig. 4a). This means that a model that scored well relative to all 62 others using one metric may have a much poorer ranking using another. Hierarchical analysis identified three distinct clusters of similarly performing metrics (Fig. 4a, labels c1–c3).

The unexpected sparse correlations and clustering can be understood by considering per-target score distribution ranges, which
Cluster 1 metrics (Fig. 4c, top row) share the trend of decreasing score values with increasing map resolution. The cluster consists of six real-space correlation measures, three from TEMPy16–18 and three from Phenix19. Each evaluates a model’s fit in a similar way: by correlating calculated model-map density with experimental map density. In most cases (five out of six), correlation is performed after model-based masking of the experimental map. This observed trend is contrary to the expectation that a Fit-to-Map score should increase as resolution improves. The trend arises at least in part because map resolution is an explicit input parameter for this class of metrics. For a fixed map/model pair, changing the input resolution value will change the score. As map resolution increases, the level of detail that a model-map must faithfully replicate to achieve a high correlation score must also increase.

Cluster 2 metrics (Fig. 4c, middle row) share the inverse trend: score values improve with increasing map target resolution. Cluster 2 metrics consist of Phenix Map-Model FSC = 0.5 (ref. 19), Q-score8 and EMRinger15. The observed trend is expected: by definition, each metric assesses a model’s fit to the experimental map in a manner that is intrinsically sensitive to map resolution. In contrast with cluster 1, cluster 2 metrics do not require map resolution to be supplied as an input parameter.

Cluster 3 metrics (Fig. 4c, bottom row) share a different overall trend: score values are substantially lower for ADH relative to APOF map targets. These measures include three unmasked correlation functions from TEMPy16–18, Refmac FSCavg13, Electron Microscopy Data Bank (EMDB) Atom Inclusion14 and TEMPy ENV16. All of these measures consider the full experimental map without masking, so can be sensitive to background noise, which is substantial in the unmasked ADH map and minimal in the masked APOF maps (Fig. 2d).

Score distributions were also evaluated for how similarly they performed per target, and in this case most metrics were strongly correlated with each other (Fig. 4b). This means that for any single target, a model that scored well relative to all others using one metric also fared well using nearly every other metric. This situation is illustrated by comparing scores for two different metrics, CCache from cluster 1 and Q-score from cluster 2 (Fig. 4d). The plot’s four diagonal lines demonstrate that the scores are tightly correlated with each other within each map target. But, as described above, the two metrics have different sensitivities to map-specific factors. It is these different sensitivities that give rise to the separated, parallel spacings of the four diagonal lines, indicating score ranges on different relative scales.

One Fit-to-Map metric showed poor per-target correlation with all others: TEMPy ENV (Fig. 4b). ENV evaluates atom positions relative to a density threshold that is based on sample molecular weight. At near-atomic resolution this threshold is overly generous. TEMPy Mutual Information and EMRinger also diverged from others (Fig. 4b). Mutual information scores reflected strong influence of ADH background noise. In contrast, masked MI_OV correlated well with other measures. EMRinger yielded distinct distributions owing to its focus on backbone placement15.

Collectively these results reveal that multiple factors such as using experimental map resolution as an input parameter, presence of background noise and density threshold selection can strongly affect Fit-to-Map score values, depending on the chosen metric. These are not desirable features for archive-wide validation of deposited cryo-EM structures.

Evaluating metrics: Coordinates-only and versus Reference. Metrics to assess model quality based on Coordinates-only (Table 2), as well as Comparison-to-Reference and Comparison-among-Models (Table 2) were also evaluated and compared (Fig. 4e,f).

Most Coordinates-only metrics were poorly correlated with each other (Fig. 4e), with the exception of bond, bond angle and chirality root mean squared deviation (r.m.s.d.), which form a...
small cluster. Ramachandran outliers, widely used to validate protein backbone conformation, were poorly correlated with all other Coordinates-only measures. More than half (33) of submitted models had zero Ramachandran outliers, while only four had zero CaBLAM conformation outliers. Ramachandran statistics are increasingly used as restraints\textsuperscript{25,26}, which reduces their use as a validation metric. These results support the concept of CaBLAM as an informative score for validating backbone conformation\textsuperscript{22}.

CaBLAM metrics, while orthogonal to other Coordinates-only measures, were unexpectedly found to perform very similarly to Comparison-to-Reference metrics. The similarity likely arises because the worst modeling errors in this challenge were sequence and backbone conformation mis-assignments. These errors were equally flagged by CaBLAM, which compares models against statistics from high-quality PDB structures, and the Comparison-to-Reference metrics, which compare models against a high-quality reference. To a lesser extent, modeling errors were also flagged by Fit-to-Map metrics (Fig. 4f). Overall, Coordinates-only metrics were poorly correlated with Fit-to-Map metrics (Fig. 4f and Extended Data Fig. 6a).

Protein sidechain accuracy is specifically assessed by Rotamer and GDC-SC, while EMRinger, Q-score, CAD, hydrogen bonds in residue pairs (HBPR >6), GDC and LDDT metrics include sidechain atoms. For these eight measures, Rotamer was completely orthogonal, Q-score was modestly correlated with the Comparison-to-Reference metrics, and EMRinger, which measures sidechain fit as a function of main chain conformation, was largely independent (Fig. 4f). These results suggest a need for multiple metrics (for example, Q-score, EMRinger, Rotamer) to assess different aspects of sidechain quality.

Evaluating metrics: local scoring. Several residue-level scores were calculated in addition to overall scores. Five Fit-to-Map metrics considered masked density for both map and model around the evaluated residue (CCbox\textsuperscript{19}, SMOC\textsuperscript{20}), density profiles at nonhydrogen atom positions (Q-score\textsuperscript{8}), density profiles of nonbranched residue C-atom ring paths (EMRinger\textsuperscript{13}) or density values at non-H-atom positions relative to a chosen threshold (Atom Inclusion\textsuperscript{14}). In two of these five, residue-level scores were obtained as sliding-window averages over multiple contiguous residues (SMOC, nine residues; EMRinger, 21 residues).

Residue-level correlation analyses similar to those described above (not shown) indicate that local Fit-to-Map scores diverged more than their corresponding global scores. Residue-level scoring was most similar across evaluated metrics for high resolution maps. This observation suggests that the choice of method for scoring residue-level fit becomes less critical at higher resolution, where maps tend to have stronger density/contrast around atom positions.

A case study of a local modeling error (Extended Data Fig. 3) showed that Atom Inclusion\textsuperscript{14}, CCbox\textsuperscript{19} and Q-score\textsuperscript{8} produced substantially worse scores within a four-residue a-helical misthread relative to correctly assigned flanking residues. In contrast, the sliding-window-based metrics were largely insensitive (a new
such maps, needing only small amounts of manual intervention. Mated methods are able to generate fairly complete models from mational flexibility have excellent information content, and auto-

≤ 3 Å and from samples with limited confor-

This third EMDR Model Challenge has demonstrated that cryo-EM

density features from metrics deter-

The MolProbity server20,22 flagged dow analysis (SMOCf)31). At near-atomic resolution, single residue

TEMPy version offers single residue (SMOCd) and adjustable win-

dory analysis (SMOCI)9). At near-atomic resolution, single residue Fit-to-Map evaluation methods are likely to be more useful. Residue-level Coordinates-only, Comparison-to-Reference and Comparison-among-Models metrics (not shown) were also evalu-

ated for the same modeling error. The MolProbity server9,22 flagged the problematic four-residue misthread via CaBLAM, cis-Peptide, Clashscore, bond and angle scores, but all Ramachandran scores were either favored or allowed. The Comparison-to-Reference LDDT and LGA local scores and the Davis-QA model consensus score also strongly flagged this error. The example demonstrates the value of combining multiple orthogonal measures to identify geometry issues, and further highlights the value of CaBLAM as an orthogonal measure for backbone conformation.

Group performance. Group performance was examined by model-

ing category and target by combining Z-scores from metrics determined to be meaningful in the analyses described above (Methods and Extended Data Fig. 6). A wide variety of map density features and algorithms were used to produce a model, and most were successful yet allowing a few mistakes, often in different places (Extended Data Figs. 1–4). For practitioners, it might be beneficial to combine models from several ab initio methods for subsequent refinement.

Discussion

This third EMDR Model Challenge has demonstrated that cryo-EM maps with a resolution ≤3 Å and from samples with limited confor-

mational flexibility have excellent information content, and auto-

mated methods are able to generate fairly complete models from such maps, needing only small amounts of manual intervention. Inclusion of maps in a resolution series enabled controlled evalu-

ation of metrics by resolution, with a completely different map providing a useful additional control. These target selections enabled observation of important trends that otherwise could have been missed. In a recent evaluation of predicted models in the CASP13 competition against several roughly 3 Å cryo-EM maps, TEMPy and Phenix Fit-to-Map correlation measures performed very similar31. In this challenge, because the chosen targets covered a wider resolution range and had more variability in background noise, the same measures were found to have distinctive, map feature-sensitive performance profiles.

Most submitted models were overall either equivalent to or bet-

ter than their reference model. This achievement reflects significant advances in the development of modeling tools relative to the state presented a decade ago in our first model challenge5. However, several factors beyond atom positions that become important for accurate modeling at near-atomic resolution were not uniformly addressed; only half included refinement of atomic displacement factors (B factors) and a minority attempted to fit water or bound ligands.

Fit-to-Map measures were found to be sensitive to different physical properties of the map, including experimental map resolu-

tion and background noise level, as well as input parameters such as density threshold. Coordinates-only measures were found to be largely orthogonal to each other and also largely orthogonal to Fit-to-Map measures, while Comparison-to-Reference measures were generally well correlated with each other.

The cryo-EM modeling community as represented by the chal-

lenge participants have introduced a number of metrics to evaluate models with sound biophysical basis. Based on our careful analyses of these metrics and their relationships, we make four recommen-

Table 1 | Participating modeling teams

| Team ID/ name | Team members | No. of submitted models | Effort type(s) | Software |
|---------------|--------------|-------------------------|---------------|----------|
| 10 Yu         | X. Yu        | 4                       | ab initio+manual | Phenix20, Buccaneer21, Chimera22, Coot23, Pymoll |
| 25 Ccmd       | M. Igaev, A. Vaiana, H. Grubmüller | 4                       | optimization automated | CDMD25 |
| 27 Kumar      | D. Kumar     | 1                       | ab initio+manual | Phenix, Rosetta40, Buccaneer, ARP/wARP41, Coot |
| 28 Ccpem      | S. W. Hoh, K. Cowtan, A. P. Joseph, C. Palmer, M. Winn, T. Burnley, M. Olek, P. Bond, E. Dodson | 4                       | ab initio+manual | CCPEM42, Refmac43, Buccaneer, Coot, TEMPy44,45 |
| 35 Phenix     | P. Afonine, T. Terwilliger, L.-W. Hung | 4                       | ab initio+manual | Phenix, Coot |
| 38 Fzjuelich  | G. Schroeder, L. Schaefer | 3                       | optimization automated | Phenix, Chimera, DireX46, MDFD47, CNS, Gromacs |
| 41 Arpwarp    | G. Chojnowski | 8                       | ab initio automated, ab initio+manual | Refmac, ARP/wARP, Coot |
| 54 Kihara     | D. Kihara, G. Terashi | 8                       | ab initio+manual | Rosetta, Mainmasto45, MDFD, Chimera |
| 60 Deepracrer | L. Wang, D. Si, R. Cao, J. Cheng, S. A. Moritz, J. Pfab, T. Wu, J. Hou | 10                      | ab initio automated, ab initio+manual | Cascaded-CNN45, Chimera |
| 73 Singhary   | M. Shekhar, G. Terashi, S. Mittal, D. Sarkar, D. Kihara, K. Dill, A. Perez, A. Singharoy | 5                       | ab initio+manual, optimization automated | reMDFD46, MELD46, VMD, Chimera, Mainmast |
| 82 Rosetta    | F. DiMaio, D. Farrell | 8                       | ab initio automated, ab initio+manual | Rosetta, Coot |
| 90 Mbaker     | M. Baker     | 2                       | ab initio+manual | Pathwalker47, Phenix, Chimera, Coot |
| 91 Chiu       | G. Pintilie, W. Chiu | 2                       | optimization+manual | Phenix, Chimera, Coot |

*Each team was assigned a random two-digit ID for blinded identification.


Table 2 | Evaluated metrics

| Metric class | Package metric definition |
|--------------|---------------------------|
| Fit-to-Map   |                           |
| Correlation Coefficient, all voxels | Phenix CCbox full grid map versus model-map density correlation coefficient[^15] |
| Correlation Coefficient, selected voxels | Phenix CCmask map versus model-map density, only modeled regions[^15] |
| Correlation Coefficient, other density function | TEMPy LAP map versus model-map Laplacian filtered density (partial second derivative)[^16] |
| Correlation Coefficient, atom positions | TEMPy MI_OV map versus model-map Mutual Information, only modeled regions[^16] |
| FSC          | Phenix FSCOS Resolution (distance) of Map-Model FSC curve read at point FSC = 0.5 (ref. [^42]) |
| Atom Inclusion | EMDB/VisualAnalysis ALL Atom Inclusion, percentage of atoms inside depositor-provided density threshold[^4] |
| Sidechain Density | Phenix EMRinger evaluates backbone by sampling map density around Cα-atom ring paths for nonbranched residues[^15] |
| Coordinates-only |                           |
| Configuration | Phenix Bond r.m.s.d. of bond lengths[^17] |
| Clashes       | MolProbity Clashscore Number of steric overlaps ≥0.4 Å per 1,000 atoms[^12] |
| Conformation  | Phenix Angle r.m.s.d. of bond angles[^21] |
|               | Phenix Chiral r.m.s.d. of chiral centers[^17] |
|               | Phenix Planar r.m.s.d. of planar group planarity[^21] |
|               | Phenix Dihedral r.m.s.d. of dihedral angles[^17] |
| Versus Reference Model |                           |
| Atom Superposition | Local Global Alignment (LGA) GDT-TS Global Distance Test Total Score, average percentage of model Ca that superimpose with reference Ca, multiple distance cutoffs[^22] |
| Interatomic Distances | LDDT Local Difference Distance Test, superposition-free comparison of all-atom distance maps between model and reference[^19] |
| Contact Area  | CAD CAD Contact Area Difference, superposition-free measure of differences in interatom contacts[^16] |
| Comparison among models |                           |
| Atom Superposition, Multiple | DAVIS-QA average of pairwise LGA GDT-TS scores among submitted models[^17] |

Fig. 4 | Evaluation of metrics. Model metrics (Table 2) were compared with each other to assess how similarly they performed in scoring the challenge models. a–d, Fit-to-Map metrics analyses. a, Pairwise correlations of scores for all models across all map targets (n = 63). b, Average correlation of scores per target (average over four correlation coefficients, one for each map target with T1, n = 16; T2, n = 15; T3, n = 15; T4, n = 17). Correlation-based metrics are identified by bold labels. In a, table order is based on a hierarchical cluster analysis (Methods). Three red-outlined boxes along the table diagonal correspond to identified clusters (no. c1–c3). For ease of comparison, order in b is identical to a. c, Representative score distributions are plotted by map target, ordered by map target resolution (see legend at bottom; T1, n = 16; T2, n = 15; T3, n = 15; T4, n = 17). Each row represents one of the three clusters defined in (a). Each score distribution is represented in box-and-whisker format (left) along with points for each individual score (right). Lower boxes represent Q1–Q2 (25th–50th percentile, in target color as shown in legend); upper boxes represent Q2–Q3 (25th–75th percentile, dark gray). Boxes do not appear when quartile limits are identical. Whiskers span 10th to 90th percentile. To improve visualization of closely clustered scores, individual scores (y values) are plotted against slightly dithered x values. d, Scores for one representative pair of metrics are plotted against each other (CCbox from cluster 1 and Q-score from Cluster 2). Diagonal lines represent linear fits by map target. e, Coordinates-only metrics comparison. f, Fit-to-Map, Coordinates-only and Comparison-to-Reference metrics comparison. Correlation levels in a,b,e,f are indicated by shading (see legend at top). See the Methods for additional details.
dations regarding validation practices for cryo-EM models of proteins determined at near-atomic resolution as studied here between 3.1 and 1.8 Å, a rising trend for cryo-EM (Fig. 1a).

Recommendation 1. For researchers optimizing a model against a single map, nearly any of the evaluated global Fit-to-Map metrics (Table 2) can be used to evaluate progress because they are all largely equivalent in performance. The exception is TEMPy, ENV is more appropriate at lower resolutions (>4 Å).

Recommendation 2. To flag issues with local (per residue) Fit-to-Map, metrics that evaluate single residues are more suitable than those using sliding-window averages over multiple residues (Evaluating metrics: local scoring).

| Package Metric | SMOC | CCC_OV | MI_OV | AI_all | MI | CCC | LAP | FSCavg | ENV |
|----------------|------|--------|-------|--------|----|-----|-----|--------|-----|
| TEMPy          |      |        |       |        |    |     |     |        |     |
| Phenix         |      |        |       |        |    |     |     |        |     |
| Phenix/EMRinger|      |        |       |        |    |     |     |        |     |
| Chimera/MAPOQ  |      |        |       |        |    |     |     |        |     |
| EMDBVis        |      |        |       |        |    |     |     |        |     |
| TEMPy          |      |        |       |        |    |     |     |        |     |
| TEMPy          |      |        |       |        |    |     |     |        |     |
| CCP/EMRinger/Refmac | | | | | | | | | |
| TEMPy          |      |        |       |        |    |     |     |        |     |
| Coordinates only |   |   |   |   |  | | | | |

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**Figure 1**

**a** Score correlations, 63 models

| Package Metric | SMOC | CCC_OV | MI_OV | AI_all | MI | CCC | LAP | FSCavg | ENV |
|----------------|------|--------|-------|--------|----|-----|-----|--------|-----|
| TEMPy          |      |        |       |        |    |     |     |        |     |
| Phenix         |      |        |       |        |    |     |     |        |     |
| Phenix/EMRinger|      |        |       |        |    |     |     |        |     |
| Chimera/MAPOQ  |      |        |       |        |    |     |     |        |     |
| EMDBVis        |      |        |       |        |    |     |     |        |     |
| TEMPy          |      |        |       |        |    |     |     |        |     |
| TEMPy          |      |        |       |        |    |     |     |        |     |
| CCP/EMRinger/Refmac | | | | | | | | | |
| TEMPy          |      |        |       |        |    |     |     |        |     |

**Figure 2**

**b** Average score correlation, per target

**Figure 3**

**c** Cluster 1: CCC_OV

**Figure 4**

**d** APOF 1.8 Å

**Figure 5**

**e** Coordinates only

**Figure 6**

**f** Score correlations, 63 models
Recommendation 3. The ideal Fit-to-Map metric for archive-wide ranking will be insensitive to map background noise (appropriate masking or alternative data processing can help), will not require input of estimated parameters that affect score value (for example, resolution limit, threshold) and will yield overall better scores for maps with trustworthy higher-resolution features. The three cluster 2 metrics identified in this challenge (Fig. 4a ‘c’ and Fig. 4c ‘center row’) meet these criteria.

- Map-Model FSC is already in common use, and can be compared with the experimental map’s independent half-map FSC curve.
- Global EMRinger score can assess nonbranched protein sidechains.
- Q-score can be used both globally and locally for validating nonhydrogen atom positions.

Other Fit-to-Map metrics may be rendered suitable for archive-wide comparisons through conversion of raw scores to Z-scores over narrow resolution bins, as is currently done by the PDB for some X-ray-based metrics.

Recommendation 4. CaBLAM and MolProbity cis-peptide detection are useful to detect protein backbone conformation issues. These are particularly valuable tools for cryo-EM, since maps at typical resolutions (2.5–4.0 Å, Fig. 1a) may not resolve backbone carbonyl oxygens (Fig. 2).

In this challenge, more time could be devoted to analysis when compared with previous rounds because infrastructure for model collection, processing and assessment is now established. However, several important issues could not be addressed, including evaluation of overfitting using half-map based methods, effect of map sharpening on Fit-to-Map scores, validation of ligand fit and metal ion/water identification and validation at atomic resolution including H atoms. EMDR plans to sponsor additional model challenges to continue promoting development and testing of cryo-EM modeling and validation methods.

Online content

Any methods, additional references, Nature Research reporting summaries, source data, extended data, supplementary information, acknowledgements, peer review information; details of author contributions and competing interests; and statements of data and code availability are available at https://doi.org/10.1038/s41592-020-01051-w.

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**Methods**

**Challenge process and organization.** Informed by previous challenges\(^{6,10}\), the 2019 Model Challenge process was substantially streamlined in this round. In March, a panel of advisors with expertise in cryo-EM methods, modeling and/or model assessment was created. The panel worked with EMDR team members to develop the challenge guidelines, identify suitable map targets from EMDB and reference models from the PDB and recommend the metrics to be calculated for each submitted model.

The challenge rules and guidance were as follows: (1) ab initio modeling is encouraged but not required. For optimization studies, any publicly available coordinate set can be used as the starting model. (2) Regardless of the modeling method used, submitted models should be as complete and as accurate as possible (that is, equivalent to publication-ready). (3) For each target, a separate modeling process should be used. (4) Fitting to either the unsharpened/unmasked map or one of the half-maps is strongly encouraged. (5) Submission in mmCIF format is strongly encouraged.

Members of cryo-EM and modeling communities were invited to participate in mid-April 2019 and details were posted on the challenges website (challenges.emdatasource.org). Models were submitted by participant teams between 1 and 28 May 2019. For APOF targets, coordinate models were submitted as single subunits at the position of a provided segmented density consisting of a single subunit. ADH models were submitted as dimers. For each submitted model, metadata describing the full modeling workflow were collected via a Drupal (https://sw-tools.rcsb.org/apps/MAXIT) and additionally checked for sequence ordering and nomenclature consistency using PDB annotation software (Feng Z., https://sw-tools.rcsb.org/apps/MAXIT) and additionally checked for sequence consistency and correct position relative to the designated target map. Models were then evaluated as described below (Model evaluation system).

In early June, models, workflows and initial calculated scores were made available to all participants for evaluation, blinded to modeler team identity and software used. A 2.5-day workshop was held in mid-June at Stanford/SLAC to review the results, with panel members attending in person. All modeling participants were invited to attend remotely and present overview of their modeling processes and/or assessment strategies. Recommendations were made for additional evaluations of the submitted models as well as for future challenges. Modeler teams and software were unblinded at the end of the workshop. In September, a virtual follow-up meeting with all participants provided an overview of the final evaluation system after implementation of recommended updates.

**Coordinate sources and modeling software.** Modeling teams created ab initio models or optimized previously known models available from the PDB. Models optimized against APOF maps used PDB entries 2fha, 5n26 or 3ajo as starting-coordinate sources and modeling software. Optimization teams created ab initio of the final evaluation system after implementation of recommended updates. Participants were invited to attend remotely and present overviews of their methods used. A 2.5-day workshop was held in mid-June at Stanford/SLAC to review the results, with panel members attending in person. All modeling participants were invited to attend remotely and present overview of their modeling processes.

**Model evaluation system.** The evaluation system for 2019 challenge (model-compare.emdatasource.org) was based on the basis of the 2016/2017 Model Challenge system\(^{1,6,10}\), updated with several additional evaluation measures and analysis tools. Submitted models were evaluated for >70 individual metrics in four tracks: Fit-to-Map, Coordinates-only, Comparison-to-Reference and Comparison-among-Models. A detailed description of the updated infrastructure and new evaluated metrics is provided as a help document on the model evaluation system website. Result data are archived at Zenodo\(^{5}\). Analysis software versions/ websites are listed in the Nature Research Reporting Summary.

For brevity, a representative subset of metrics from the evaluation website are discussed in this paper. The selected metrics are listed in Table 2 and are further described below. All scores were calculated according to package instructions using default parameters.

**Fit-to-Map.** The evaluated metrics included several ways to measure the correlation between map and model density as implemented in TEMPy\(^{13}\) v.1.11 (CCC, CCC_OV, SMOC, LAP, MI, MI_OV) and the Phenix\(^{14}\) v.1.15.2 map_model_cc module (CCBox, CCPeaks, CCAmask). These methods compare the experimental map with a model map produced on the same voxel grid, integrated either over the full map or over selected masked regions. The model-derived map is generated to a specified resolution limit by inverting Fourier terms calculated from coordinates, B factors and atomic scattering factors. Some measures compare density-derived functions instead of density (MI, LAP\(^{15}\)). The Q-score (MAPQ v.1.2 (ref. \(^{7}\)) . plugin for UCSF Chimera\(^{16}\) v.1.11) uses a real-map sidechain conformations and clashes (MolProbity rotamers and Clashscore\(^{17}\)) as an orthogonal measure. Ramachandran and rotamer criteria were excluded since they are often restrained in refinement and are zero for many models.

**Comparison-to-Reference and Comparison-among-Models.** Assessing the similarity of the model to a reference structure and similarity among submitted models, we used metrics based on atom superposition (LGA GDT-TS, GDC and GDC-SC scores\(^{18}\) v.04.2019), interatomic distances (LDDT score\(^{19}\) v.1.2), and contact area differences (CAD\(^{20}\) v.16.06). HBPLUS\(^{20}\) was used to calculate nonlocal hydrogen bond precision, defined as the fraction of correctly placed hydrogen bonds with more than six separations in sequence (HBPR > 6). DAVIS-QA determines for each model the average of pairwise GDT-TS scores among all other models\(^{21}\).

**Metric score pairwise correlations and distributions.** For pairwise comparisons of metrics, Pearson correlation coefficients (P) were calculated for all model scores and targets (n = 63). For average per-target pairwise comparisons of metrics, P values were determined for each target and then averaged. Metrics were clustered according to the similarity score (1 − [P]) using a hierarchical algorithm with complete linkage. At the beginning, each metric was placed into a cluster of its own. Clusters were then sequentially combined into larger clusters, with the optimal number of clusters determined by manual inspection. In the Fit-to-Map evaluation track, the procedure was stopped after three divergent score clusters were formed for the all-model correlation data (Fig. 4a), and after two divergent clusters were formed for the average per-target clustering (Fig. 4b).

**Controlling for model systematic differences.** As initially calculated, some Fit-to-Map scores had unexpected distributions, owing to differences in modeling practices among participating teams. For models submitted with all atom occupancies set to zero, occupancies were reset to one and rescored. In addition, model submissions were split approximately 50/50 for each of the following practices: (1) inclusion of hydrogen atom positions and (2) inclusion of refined B factors. For affected fit-to-map metrics, modified scores were produced excluding hydrogen atoms and/or setting B factors to zero. Both original and modified scores are provided at the web interface. Only modified scores were used in the comparisons described here.

**Evaluation of group performance.** Rating of group performance was done using the group ranks and model ranks (per target) tools on the challenge evaluation website. These tools permit users, either by group or for a specified target and for all or a subcategory of models (for example, ab initio), to calculate composite Z-scores using any combination of evaluated metrics with any desired relative weightings. The Z-scores for each metric are calculated from all submitted models for that target (n = 63). The metrics (weights) used to generate composite Z-scores as follows.

"\[
\text{Table 2: Comparison among Models}
\]

"\[
\text{CoMFA outliers (0.5), Calpha-geometry outliers (0.3) and Clashscore (0.2). CaBLAM outliers and Calpha-geometry outliers had the best correlations with Comparisons parameters (Fig. 4c), and Clashscore is an orthogonal measure. Ramachandran and rotamer criteria were excluded since they are often restrained in refinement and are zero for many models.}"

"\[
\text{The reference Gaussian, which is formulated so that a highest score of 1 would be given to a real resolved atom in a map at an approximately 1.5 Å resolution. Lower scores (down to −1) are given to atoms as their resolvability and the resolution of the map decreases. The overall Q-score is the average value for all model atoms.}"

"\[
\text{Measures based on Map-Model FSC curve, Atom Inclusion and protein sidechain rotamers were also compared. Phenix Map-Model FSC is calculated using a soft mask and is evaluated at FSC = 0.6 (ref. 19). REFMAC FSCavg (methods of CCPM\(^{22}\) ) integrates the area under the map-Model FSC curve and is to a specified resolution limit. EMDB Atom Inclusion determines the percentage of atoms inside the map at a specified density threshold. TEMPy ENV is also threshold-based and penalizes unmodeled regions. EMRinger (module of Phenix) evaluates backbone positioning by measuring the peak positions of unbranched protein C\(_\alpha\) atom positions versus map density in ring paths around C\(_\alpha\)-C\(_\beta\) bonds.}"

"\[
\text{Coordinates-only: Standard measures assessed local configuration (bonds, bond angles, chirality, planarity, dihedral angles; Phenix model statistics module), protein backbone (MolProbity Ramachandran outliers\(^{23}\), Phenix molprobity module) and sidechain conformations, and clashes (MolProbity rotamers outliers and Clashscore\(^{24}\), Phenix molprobity module).}"

"\[
\text{New in this challenge round is CaBLAM\(^{25}\) (part of MolProbity and as Phenix calablam module), which uses two procedures to evaluate protein backbone conformation. In both cases, virtual dihedral pairs are evaluated for each protein residue \(i\) using C\(_\beta\) positions 1 to 2 to \(i\). To define CaBLAM outliers, the virtual dihedral is between the CO groups flanking residue \(i\). To define Calpha-geometry outliers, the third parameter is the C\(_\alpha\) virtual angle at \(i\). The residue is then scored according to virtual triplet frequency in a large set of high-quality models from PDB.}\)
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**Reporting Summary**

Further information on research design is available in the Nature Research Reporting Summary linked to this article.

**Data availability**

The map targets used in the challenge were downloaded from the EMDB, entries EMDB-20026 (file emd_20026_additional_1.map.gz), EMDB-20027 (file emd_20027_additional_2.map.gz), EMDB-20028 (file emd_20028_additional_2.map.gz) and EMDB-0406 (file emd_0406.map.gz). Reference models were downloaded from the PDB, entries 3ajo and 6nbb. Submitted models, model metadata, result logs and compiled data are archived at Zenodo at [https://doi.org/10.5281/zenodo.4148789](https://doi.org/10.5281/zenodo.4148789), and at [https://model-compare.emdataresource.org/data/2019/](https://model-compare.emdataresource.org/data/2019/). Interactive summary tables, graphical views and .csv downloads of compiled results are available at [https://model-compare.emdataresource.org/2019/cgi-bin/index.cgi](https://model-compare.emdataresource.org/2019/cgi-bin/index.cgi). Source data are provided with this paper.

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**Author contributions**

P.D.A., P.V.A., J.S.E., E.D.M., J.S.R., P.B.R., H.M.B., W.C., A.K., C.L.L., G.D.P. and M.F.S. formed the expert panel that selected targets, reference models and assessment metrics, set the challenge rules and attended the face-to-face results review workshop. K.Z. generated the APOF maps for the challenge. M.A.H. provided the published ADH map. C.L.L. designed and implemented the challenge model submission pipeline, and drafted the initial, revised and final manuscripts. Authors as listed in Table 1 built and submitted models and presented modeling strategies at the review workshop. A.K. designed and implemented the evaluation pipeline and website, and calculated scores. A.K., C.L.L., B.M., M.A.H., J.S.R., C.J.W., P.V.A. and J.S.F. analyzed models and model scores. A.P., Z.W., T.C.T., A.P.J., G.D.P., P.V.A. and C.J.W. contributed the software, and provided advice on use and scores interpretation. C.L.L., A.K., G.D.P. and J.S.R. drafted the figures. A.K., H.M.B., G.D.P., W.C., M.F.S., H.A.M. and J.S.R. contributed to manuscript writing. All authors reviewed and approved the final manuscript.

**Competing interests**

X.Y. is an employee of Janssen Research and Development. All other authors declare no competing interests.

**Additional information**

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Extended Data Fig. 1 | See next page for caption.
Extended Data Fig. 1 | Evaluation of peptide bond geometry. All 63 Challenge models were evaluated using MolProbity. APOF and ADH each have one cis peptide bond per subunit before a proline residue. (a) Counts of peptide bonds with each of the following conformational properties: cisP: cis peptide before proline, twistP: non-planar peptide (>30°) before proline, cis-nonP: cis peptide before non-proline, twist-nonP: non-planar peptide bond before non-proline. Incorrect cis-nonP usually occurred where the model was misfit (see Extended Data Figs. 2 and 3), while incorrect cis or trans Pro usually produced poor geometry. Values inconsistent with reference models are highlighted. Statistically, 1 in 20 proline residues are genuinely cis; only 1 in 3000 non-proline residues are genuinely cis, and strongly non-planar peptide bonds (>30°) are almost never genuine\textsuperscript{28}. Models are identified by the submitting group (Gp #, group id as defined in Table 1), model number (some groups submitted multiple models), and Target (T1-T3: APOF, T4: ADH). Optimized models are shaded blue. Only two groups (28, 31) had all peptides correct for all 4 targets. Models illustrated in panels b-d are indicated by labeled boxes. (b) Correct cis peptide geometry for Pro A62 in two ADH models. (c) Incorrect trans peptide geometry, with huge clashes up to 1.25 Å overlap (clusters of hot pink spikes), 2 CaBLAM outliers (magenta CO dihedral lines), and poor density fit. (d) Incorrect trans peptide geometry, with huge 1.9 Å C\textbeta deviation at Leu 61 (magenta ball) because of incorrect hand of C\textalpha, and 2 CaBLAM outliers. Molecular graphics were generated using KiNG.
Extended Data Fig. 2 | Classic CaBLAM outlier with no Ramachandran outlier. a, Mis-modeled peptide (identified by red ball at carbonyl oxygen position) is flagged by two successive CaBLAM outliers (magenta dihedrals), a bad clash (hot-pink spikes), and a bond-angle outlier (not shown), but no Ramachandran outlier. b, Correctly modeled peptide, involving a near-180° flip of the central peptide to achieve regular α-helical conformation. Ser 38 of T1/APOF model 60_1 is shown in (a); model 35_1 shown in (b). This example illustrates the most easily correctable situations: (1) for a CaBLAM outlier inside helix or β-sheet, regularize the secondary structure; (2) for two successive CaBLAM outliers, try flipping the central peptide. Molecular graphics were generated using KiNG. Note that sidechains are truncated by graphics clipping.
Extended Data Fig. 3 | Evaluation of a short sequence misalignment within a helix. Local Fit-to-Map and Coordinates-only scores are compared for a 3-residue sequence misalignment inside an α-helix in an ab initio model submitted to the Challenge (APOF 2.3 Å 54_1). a, Model residues 14–42 vs target map (blue: correctly placed residues, yellow: mis-threaded residues 25–29, black: APOF reference model, 3ajo). b, Structure-based sequence alignment of the ab initio model (top) vs. reference model (bottom). c, Local Fit-to-Map scores (screenshot from Challenge model evaluation website Fit-to-Map Local Accuracy tool). Curves are shown for Phenix box_CC (orange), EMDB Atom Inclusion (purple), Q-score (red) EMRinger (green), and SMOC (blue). The score values for model residue Leu 28 are shown in the box at right. d, Residue scores were calculated using the Molprobity server. The mis-threaded region is boxed in (b-d). Panels (a) and (b) were generated using UCSF Chimera.
Extended Data Fig. 4 | Modeling errors around omitted Zinc ligand in ADH. Target 4 (ADH) density map with examples of modeling errors caused by omission of Zinc ligand. a, Reference structure with Zinc metal ion (gray ball) coordinated by 4 Cysteine residues (blue sidechains). b-e, Submitted models missing Zinc (labels indicate the group_model ids). All have geometry and/or conformational violations as flagged by MolProbity CaBLAM (magenta pseudobonds), cis-nonPro (green parallelograms), Ramachandran (green pseudobonds), Cbeta (magenta spheres), and angle (blue and red fans). Model (b) has backbone conformation very close to correct, while (b) and (c) both have flags indicating bad geometry of incorrect disulfide bonds. Models (c) and (d) have backbone distortions, and (e) is mistraced through the Zn density. Molecular graphics were generated using KiNG.
Extended Data Fig. 5 | Fit-to-Map Scores with and without refined B-factors (ADP). Two representative metrics are shown: a, CCmask correlation, b, FSC05 resolution⁻¹. Each plotted point indicates the calculated score for atom positions with B-factors included (horizontal axis) versus the calculated score for atom positions alone (vertical axis). Plot symbols identify map targets. Of 63 models total, 33 included refined B-factors. Differing scores ± B-factors contribute off-diagonal points (black dotted lines are reference diagonals).
Extended Data Fig. 6 | Group performance evaluations. a. Group composite Z-scores plotted by metric category. The nine teams with highest Coordinate-only composite Z-score rankings are shown, sorted left to right. The plot illustrates that by group/method, Coordinate-only scores are poorly correlated with Fit-to-Map and Comparison-to-Reference scores. In contrast, a modest correlation is observed between Fit-to-Map and Comparison-to-Reference scores. b. Averaged model composite Z-scores plotted for ab initio modeling groups at higher resolution (T1 at 1.8 Å, T2 at 2.3 Å) and lower resolution (T3 at 3.1 Å, T4 at 2.9 Å). In each case 6 groups produced very good models (Z ≥ 0.3; green pins), though not the same set. Runner-up clusters (−0.3 ≤ Z < 0.3) are shown with gold pins. Individual scores and order shift with alternate choices of evaluation metrics and weights, but the clusters at each resolution level are stable. Composite Z-scores were calculated as described in Methods.
Reporting Summary

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Statistics

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☒ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒ Estimates of effect sizes (e.g. Cohen’s d, Pearson’s r), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection

Software for Models prepared by participating groups:

Ab initio
ARP/WARP v.8.0 arpwarp.embl-hamburg.de (groups 27, 41)
CCPEM v.1.2.0/Buccaneer v.1.16.8* www.ccpem.ac.uk www.ccp4.ac.uk (group 27)
CCPEM v.1.3.0/Buccaneer v.1.16.8* www.ccpem.ac.uk www.ccp4.ac.uk (groups 10, 28)
Cascaded-CNN v.1.0 github.com/DrDongShi/Ca-Backbone-Prediction (group 60)
Mainmast v.1.0 kharalab.org/mainmast (groups 54, 73)
Pathwalker v.2.0 blake.bcm.edu/emanwiki/EMAN2/Programs/e2pathwalker (group 90)
Rosetta 3.9 rosettacommons.org (groups 27, 54, 82**)

Optimization
CMD v.3.0 0.7 densitv www.mpiibpc.mpg.de/grubmueller/densityfitting (group 25)
CNS v.1.3 cns-online.org/v1_3 (group 38)
DreX v.0.7.1 simtk.org/home/drex (group 38)
Gromacs v.2018.6 gromacs.org (group 38)
Phenix/real_space_refine v.1.15 phenix-online.org (groups 10, 27, 35, 38, 91)
CCPEM v.1.3.0/Refmac v.5.7* www.ccpem.ac.uk www.ccp4.ac.uk (groups 28, 41)
 MGM v.0.2.3 github.com/jmacallumlab/mgmd (group 73)
MDFF v.0.4 www.ks.uiuc.edu/Research/vmd/plugins/mdff (groups 38, 54, 73)
remDFF v.0.4 github.com/jyant/RemDFF_Singerovx_Group (group 73)

Visual evaluation/manual model improvement:
VMD v.1.9.3 www.ks.uiuc.edu/Research/vmd (groups 54, 73, 82)
UCSF Chimera v.1.11 v.1.14 www.cgl.ucsf.edu/chimera (groups 10, 38, 60, 73, 90)
PyMol v.2.2.0-v.2.3.0 github.com/schrodinger/pymol-open-source (groups 10, 27)
Data analysis

FitztoMap
TEMpy v.1.1 tempy.ismb.ion.ac.cn [CCC, CCC_OV, SMOG, LAP, MI, MI_OV, ENV]
Phenix/map_model_cc v.1.15 phenix-online.org [CCbox, CCpeaks, CCmask, FSC0.5]
Phenix/emringer v.1.15 phenix-online.org [EMRinger]
CCP4 v.1.4.1/Refmac v.5.7* www.ccp4.ac.uk www.ccp4.ac.uk [FSCauto]
EMDB CrysEm Validation Analysis [ve] v.0.0.0.dev8.py/pjorj/ju0/0.0.0.dev8 [AI_all]

Coordinates-only
Phenix/moiprobsy v.1.15 phenix-online.org [CalbAM, Clashscore, Rotamer, Ram, Calpha]
Phenix/model_statistics v.1.15 phenix-online.org [Bond, Angle, Chiral, Planar, Dihedral]
MAPQ v.1.2 github.com/gregdp/mapq [Cscore]
KING 2.23 knemage.biochem.duke.edu/software [Issue visualization]

Comparison-to-Reference
LGA v.0.4.2019 proteinmodel.org/AS2TS/LGA/iga.html [GDT-TS, GDC, GDC-SC, DAVIS-QA]
OpenStructure/LDDT v.2.1 www.openstructure.org/download [LDDT]
CAD v.1.66G bitbucket.org/Klimkova/sorc/master [CAD]
HBPLUS v.3.06 www.ebi.ac.uk/thornton-srv/software/HBPLUS [HBPR>6]

*The CCP4 package requires installation of the CCP4 package (www.ccp4.ac.uk) in order to run Refmac.

See also Online Methods and Table II.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data
All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:
- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The map targets used in the Challenge were downloaded from EM Data Bank, entries:
EMD-20026 [file: emd_20026_additional_1.map.gz],
EMD-20027 [file: emd_20027_additional_2.map.gz],
EMD-20028 [file: emd_20028_additional_2.map.gz], and
EMD-0406. [file: emd_0406.map.gz]
Reference models were downloaded from Protein Data Bank, entries 3ajo and 6nbb.

Submitted models, model metadata, result logs, and compiled data are archived at Zenodo: https://doi.org/10.5281/zenodo.4148789, and at https://modelcompare.emdataresource.org/data/2019/. Interactive summary tables, graphical views, and csv downloads of compiled results are available at https://modelcompare.emdataresource.org/2019/cgi-bin/index.cgi.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

- Life sciences
- Behavioural & social sciences
- Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size

Sample size was determined by the number of model coordinate submissions. Sample size was sufficient to meet both the goal of qualitatively comparing model quality across current methods in use, and assessing usefulness of different model metrics. The Challenge was not designed to quantitatively and exhaustively explore all variables.
Data exclusions
All 63 submitted models were evaluated, with the exception that model hydrogen atom positions and refined B-factors were excluded from the reported Fit-to-Map analyses.

Replication
Participating groups were asked to complete the same four modeling tasks, yielding 15-17 models per task. Each model was created independently, so there are no exact replicates.

Randomization
Not applicable—No attempt was made to randomize the data.

Blinding
Initial evaluations of the submitted coordinates were blinded to the identity of the participating groups and software used.

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**Reporting for specific materials, systems and methods**

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

| Materials & experimental systems | Methods |
|----------------------------------|---------|
| n/a | n/a |
| ☒ | ☒ |
| Involved in the study | Involved in the study |
| ☒ | ☒ |
| Antibodies | ChiP-seq |
| ☒ | ☒ |
| Eukaryotic cell lines | Flow cytometry |
| ☒ | ☒ |
| Palaeontology | MRI-based neuroimaging |
| ☒ | ☒ |
| Animals and other organisms | |
| ☒ | |
| Human research participants | |
| ☒ | |
| Clinical data | |