EMDataResource 2019 Model “Metrics” Challenge Website Archive

This document collates the information provided at the website challenges.emdataresource.org for the 2019 Model Challenge.

EMDataResource 2019 Model “Metrics” Challenge Website Archive

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News

Announcement

2019 Model Metrics Challenge EMDataResource is trying something new and has put together a smaller, shorter-timeline EM model challenge. The deadline for submission of completed models fitted to target maps (2-3 Å resolution range) is ~~May 25~~ **May 28 (3 PM US Eastern)**. Please see the challenge info/instructions page for more details.

If you are interested in submitting models for this challenge please register by sending an email to challenges@emdataresource.org.

Original post: https://www.emdataresource.org/news/modelchallannounce2019.html

Also announced on the 3DEM/CCP4/CCPEM lists on 1 May 2019

https://mail.ncmir.ucsd.edu/pipermail/3dem/2019-May/006770.html

The submission deadline was revised as shown on 9 May 2019

Preprint of Outcomes

2019 Model Metrics Challenge Outcomes Preprint June 15 2020: "Outcomes of the 2019 EMDataResource model challenge: validation of cryo-EM models at near-atomic resolution" is available as a preprint at BioRxiv while under consideration for publication.

The manuscript, co-authored by all participants, including modelers, assessors, expert advisors, and EMDR team members, provides an overview of the analysis pipeline, the quality of the models submitted, and a careful analysis of the evaluation metrics based on correlation and statistical analyses of the submitted model scores. The paper concludes with recommendations regarding use of the evaluated metrics by individual researchers and structure archives with broad relevance to the cryo-EM and larger scientific communities.

Original post: https://www.emdataresource.org/news/2019_challenge_preprint.html

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Goals

Identify metrics most suitable for evaluating and comparing fit of atomic coordinate models into cryo-EM maps for specimens in the 1.5-4.0 Å reported overall resolution range.

Specific metrics for review:

1. Model geometry (including Rama, rotamers, clashes, EMringer, CaBLAM)
2. Overall fit of model into map density per residue and per atom
3. Domain or secondary-structure element fit
4. Resolvability at residue or atom-level
5. Atomic Displacement parameters (B-factors) recommended optimization practice

Model Committee

- Peter Rosenthal (Crick Institute)
- Tom Terwilliger (NMC)
- Jane Richardson (Duke U)
- Mark Herzik (UCSD)
- Paul Adams (LBL)
- Frank Di Maio (U Wash)
- Jaime Fraser (UCSF)
- EMDataResource Team (Cathy Lawson, Andriy Kryshtafovych, Greg Pintilie, Mike Schmid, Wah Chiu)

Timeline

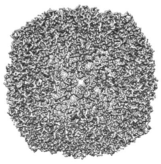
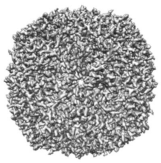
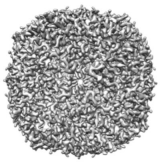
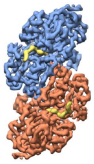
17 April	Open Challenge
26 April, 11 AM US ET	Participant Teleconference
1 May	Deposition form opens to collect participant models
~~25 May~~ 28 May (3 PM US ET)	Deadline for depositing models
~~27 May~~ 29 May	Deposited models and metadata made available for assessment (blinded)
6 June	Results of model-compare pipeline made available
13-15 June	Participant/Assessor Face-to-Face Meeting

Targets

There are two target specimens for this challenge.

- Human Heavy-chain Apoferritin: a series of three maps is provided (#1 - #3), which differ only in the number of particles used for reconstruction. These maps were chosen so that different metrics can be carefully compared/contrasted at different resolutions.
- Horse Liver Alcohol Dehydrogenase: one map is provided (#4). This structure has the extra challenge of fitting a ligand as well as the protein chain.

Target Map Download: You can use this rsync script (shown below). Alternatively, you can download individual maps from EMDR atlas pages (click on EMDB id in the table below, select "download" tab).

	T0101. Human Apoferritin	T0102. Human Apoferritin	T0103. Human Apoferritin	T0104. Horse Liver Alcohol Dehydrogenase
target				
EMDB entry *Reported Resolution (Å)*	EMD-20026 1.8	EMD-20027 2.3	EMD-20028 3.1	EMD-0406 2.9
Sharpened/Masked map	emd_20026.map	emd_20027.map	emd_20028.map	emd_0406.map
Unsharpened/Unmasked map	emd_20026_additional_2.map	emd_20027_additional_1.map	emd_20028_additional_1.map	emd_0406_additional.map
Single protomer map ***Identifies required position for chain A in submitted models***	emd_20026_additional_1.map	emd_20027_additional_2.map	emd_20028_additional_2.map	n/a
Half-maps	emd_20026_half_map_1.map, emd_20026_half_map_2.map	emd_20027_half_map_1.map, emd_20027_half_map_1.map	emd_20028_half_map_1.map, emd_20028_half_map_2.map	emd_0406_half_map_1.map, emd_0406_half_map_2.map
Primary Citation	unpublished			Herzik et al, 2019
Reference Models ***models in bold will be used as references in analysis pipeline***	**3ajo (Xray)** 2fha (Xray)			**6nbb (EM)** 2jhf (Xray)
Imposed Map Symmetry	Octahedral (O)			Cyclic (C2)
Specimen MW	21 kDa x 24-fold = 504 kDa			40 kDa x 2-fold = 80 kDa
Map Contributors	Kaiming Zhang, Greg Pintilie, Shanshan Li, Wah Chiu			Mark Herzik, Mengyu Wu, Gabe Lander

```
#################################################################################################################
# template for downloading map files associated with the 2019 EMDataResource Model Metrics Challenge #
#################################################################################################################
# Before running, uncomment the rsync command of your preferred download site.
# If you do not want to download files for every target, adjust "foreach" to your
# desired download list.
#
# Individual target EMDB entry ids are:
# 1. Apoferritin (high res)     EMD-20026
# 2. Apoferritin (med res)      EMD-20027
# 3. Apoferritin (low res)      EMD-20028
# 4. Alcohol Dehydrogenase      EMD-0406
#
# Following download, each target map will have it's own directory with EMDB entry id.
# subdirectory "map" contains the depositor's original map, which may have been masked/filtered.
# subdirectory "other" contains additional maps specifically requested for the challenge.
# filenames in most cases are: full reconstruction (no masking/filtering):   EMD-####-full.map.gz
#                  half-maps : EMD-####-half-1.map.gz; EMD-####-half-2.map.gz
#################################################################################################
#/bin/csh -f

foreach entry(20026 20027 20028 '0406')
#foreach entry('0406')

# download from EUROPE (PDBe)
#rsync -rlpt -v -z --delete rsync.ebi.ac.uk::pub/databases/emdb/structures/EMD-${entry}/ ./EMD-${entry}

# download from USA (RCSB)
#rsync -rlpt -v -z --delete --port=33444 rsync.wwpdb.org::emdb/structures/EMD-${entry}/ ./EMD-${entry}

# download from ASIA (PDBj)
#rsync -rlpt -v -z --delete ftp.pdbj.org::emdb/structures/EMD-${entry}/ ./EMD-${entry}

end
```

Modelling Instructions

- Ab initio modelling is encouraged but not required (in deposition you will need to describe your modelling process including any starting model).
- Regardless of the modelling method used, submitted models should be as complete and as accurate as possible (i.e., close to publication-ready).
- For the apoferritin targets, use separate modelling processes for each (do not "cross" or "daisy-chain" datasets).
- Fitting to either the unsharpened/unmasked map or one of the half-maps is strongly encouraged.
- Submission in mmCIF format is strongly encouraged.

Human heavy chain Apoferritin (#1-3) *Deposit: Single subunit, chain A, with position given by single protomer map* *Chain residue numbering starts with 1* *Clarification: T=1, T=2, A=3, S=4, T=5, S=6, etc.* *Symmetry Matrices (center at x=y=z=109.2 Angstroms)*	Full Sequence (Uniprot P02794) TTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYYFDRDDVALKNFAKYFLH QSHEEREHAEKLMKLQNQRGGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNQ SLLELHKLATDKNDPHLCDFIETHYLNEQVKAIKELGDHVTNLRKMGAPESGLAEYLF DKHTLGDSDNES Note (May 23): 3ajo follows this sequence exactly; 2fha has variation K86Q. We will accept models with either sequence but the above sequence is preferred.
Horse liver Alcohol Dehydrogenase (#4) *Deposit: either single subunit (Chain A) or Dimer (chains A and B). Chain positions same as 6nbb* *Chain residue numbering starts with 1* *Clarification: S=1, T=2, A=3, S=4, G=5, K=6, etc.* *For associated ligand NAD, use same chain id as protein, residue#=401* *Symmetry Matrices (2-fold at x=y=142.976 Angstroms)*	Full Sequence (Uniprot P00327) STAGKVIKCKAAVLWEEKKPFSIEEVEVAPPKAHEVRIKMVATGICRSDDHVVSGTLV TPLPVIAGHEAAGIVESIGEGVTTVRPGDKVIPLFTPQCGKCRVCKHPEGNFCLKNDL SMPRGTMQDGTSRFTCRGKPIHHFLGTSTFSQYTVVDEISVAKIDAASPLEKVCLIGC GFSTGYGSAVKVAKVTQGSTCAVFGLGGVGLSVIMGCKAAGAARIIGVDINKDKFAK AKEVGATECVNPQDYKKPIQEVLTEMSNGGVDFSFEVIGRLDTMVTALSCCQEAYG VSVIVGVPPDSQNLSMNPMLLLSGRTWKGAIFGGFKSKDSVPKLVADFMAKKFALD PLITHVLPFEKINEGFDLLRSGESIRTILTF

Process

1. Participant Teleconference to review process, gather recommendations for deposition data collection and automated model comparison pipeline. (previous round data collection and analysis is summarized here and here).
2. Participants prepare/upload their best models for each target (team approach to modelling is welcome).
3. Initial (blinded) analyses of deposited models will be performed via the automated model comparison pipeline (guided by recommendations in step #1).
4. Participant Panel will meet to review the results at June Face-to-Face meeting and recommend next steps.

FAQ

Q1: Alcohol Dehydrogenase Target: Why are the half-maps (512x512x512) so much larger than the primary deposited map (368x368x368) for EMD-0406? Answered by Mark Herzik: The half maps are unfiltered and completely unmodified from RELION’s output. We did not think it was necessary for purveyors of the EMDB to download a ~0.5 GB map of alcohol dehydrogenase when most of the voxels (512x512x512 box size) would be just averaged noise. We used the

larger box size during processing, despite the small mass of ADH, to prevent aliasing and CTF delocalization issues. It’s unclear what the established recommendations are in this regard but we think it makes things easier for the user.

Q2: It seems that the half-maps for EMD-20026 (1.8 Å) are better than the full maps based on CC values to a docked model (same model for all maps) [the other apoferritin entries have better CC value for full map vs half-map]. Digest of subsequent discussion provided below.

Q3: Will fully automated models be accepted or should we go through and correct errors? In the challenge phase we want to collect "close to final" models (with errors identified/fixed as much as possible).

Q4: What is the goal of this challenge? For challengers, it is to build the best quality model possible given the map data. For assessors, it is to decide what metrics are best for comparing models.

Q5: Should we develop new methods for this challenge? We anticipate that everyone will make use of existing methods for modelling and assessment in this "short-timeline" round.

Q6: How many models can a modelling team submit? There is no limitation. Teams may submit multiple models per map.

Q7: What buffer was used to prepare the apoferritin sample? Answered by Kaiming Zhang (May 14): 50 mM TrisHCl, pH 7.5, 150 mM NaCl.

Q8: How can I access the single protomer map to find the reference position for chain A (apoferritin target)? (added May 21). The file name of the "additional" single protomer map included with the EMDB entry is listed in the target table.

Q9: Why are we asked to only submit a single chain model for the apoferritin targets? (added May 26). This simplifies analysis. We will be able to create/analyze full complexes in a consistent way across all submissions using the symmetry matrices provided in the instructions.

Q10: Can you tell me my modeller group id? These will be revealed near the end of the face-to-face meeting and posted here.

Q1 FAQ Correspondence

re: EMD-20026 half vs. full maps

Summary: below is an email thread discussing the relative quality of half-maps for EMD-20026 (1.8 Å apoferritin) vs. the full maps. By some of the metrics investigated by Tom and Greg (as described below), one of the half-maps appears to be of equivalent or better quality to the sharpened full map. Tentative conclusion (Tom): " Maybe...we should be concluding that the full and half-maps at 1.8 A are not all that different (except for sharpening). And maybe this is saying that the errors in these maps are now coming from things that are not random, so that averaging in more data is no longer making a difference?"

From: Tom Terwilliger **Subject: EMD-20026 Date:** April 24, 2019 at 3:59:58 PM EDT

Hi Cathy, I am checking out the maps for the challenge and it seems that the half-maps for 20026 are better than the full maps. These are all CC values to a docked model (same model for all maps) (Of course I could have made a mistake in here somewhere...but the other ones seem to make sense):

- emd_20026_unsharpened.map CC_mask : 0.6337

- emd_20026.map CC_mask : 0.7514
- emd_20026_half_map_2.map CC_mask : 0.7795
- emd_20026_half_map_1.map: CC_mask : 0.7797

Does this make sense? All the best, Tom T

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From: "Pintilie, Greg" **Subject: Re: EMD-20026 Date:** April 24, 2019 at 6:24:11 PM EDT

The half maps are not better than the full map, and CC is not a good indicator of map quality - very often you can get higher scores at lower resolutions. The problem is not the score per-se but rather different scaling of densities across maps - if the densities in the maps are scaled the same, i.e. have the same rough mean and standard deviation, or use CC about the mean, then that would be a better indicator. But Z-scores are even better indicators :) See attached paper …. in particular Figure 5B which shows how CC is not a good indicator at different resolutions.

By Z-scores (and by eye - I took a look in Chimera to make sure), the full map has better resolvability.

- emd_20026_unsharpened.map CC_mask : 0.6337 Avg side chain Z-score: 1.67
- emd_20026.map CC_mask : 0.7514 Avg side chain Z-score: 3.07
- emd_20026_half_map_2.map CC_mask : 0.7795 Avg side chain Z-score: 2.28
- emd_20026_half_map_1.map: CC_mask : 0.7797 Avg side chain Z-score: 2.28

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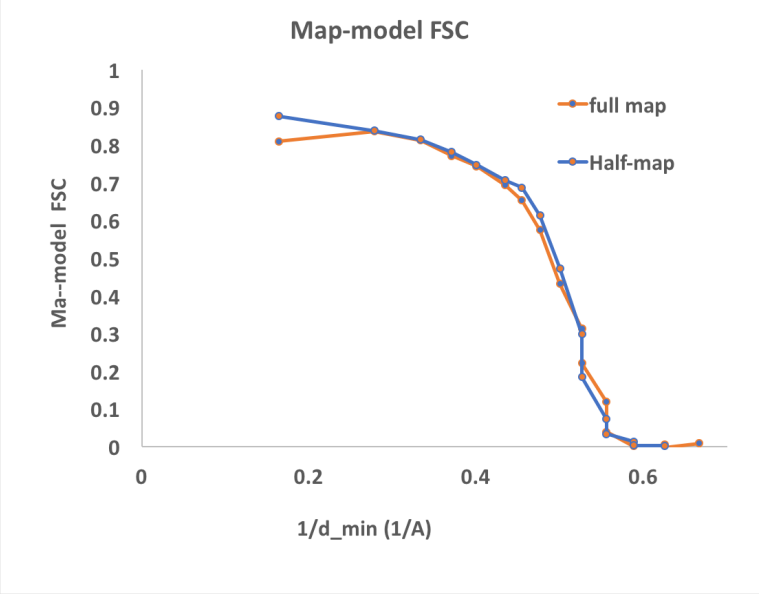
On Apr 25, 2019, at 9:16 PM, Tom Terwilliger wrote:

Hi Greg, I had another look at two maps in question: emd_20026_half_map_2.map and emd_20026.map. If I run phenix.auto_sharpen on each of these, including a model in the auto-sharpen process (I docked 3ajo for this purpose), I get a very nice map in each case, but to me the model-sharpened map from half-map 2 is clearly better than the model-sharpened map from the full map (looking at the aromatic residues and definition of branched side chains which are much clearer in the model-sharpened half-map for example). I did this blind twice and each time I picked the model-sharpened half map over the model-sharpened full map.

So...I am not quite sure that the full map is really better than the half-map in this case. I'd be interested in your opinion of a visual analysis of model-sharpened versions of these maps.



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On Thu, Apr 25, 2019 at 9:32 PM Pintilie, Greg wrote:

Hi Tom, I tried the same thing, but could not replicate exactly... the sharpened full map looks much better to me than the sharpened half map. I used phenix.auto_sharpen with fitted 3ajo.pdb, resolution=1.75. The sharpened full map actually looked pretty much identical to the full map we deposited, at least to my eye. The sharpened half map looked worse than the initial half map, so maybe I did something different than you. Could you perhaps share the maps you are using, fitted model, and Phenix commands?

About the previous message, I think that comparing CCs of a model in the same map (say at different resolutions of the model-map as you do in your paper) makes sense, but I still think it’s not robust/indicative of map quality to compare CCs of the same model in different maps - unless, perhaps, all map densities are first scaled to have the same mean/stdevs.

In our paper we did use the same resolution cutoff for the models against all maps, but no B-values (not fully sure what you mean here actually). I used Chimera molmap to generate the model map, so nothing fancy. Would be interesting to see a similar analysis using the Phenix map-model CC calculations - I don’t think I know the internals enough to fully trust myself with that, or a way to automate it for many maps/models - will leave it for future consideration/discussion :) Greg

==========

On Apr 26, 2019, at 3:18 PM, Tom Terwilliger wrote:

Hi Greg, I redid everything to check and have attached:

EMD-20026_best_docked_model_ncs_real_space_refined.pdb -- full docked model rigid body refined. Used for model-based sharpening.

EMD-20026_best_docked_model_ncs_real_space_refined_A.pdb -- just chain A of docked model. Used to extract a part of the map for viewing.

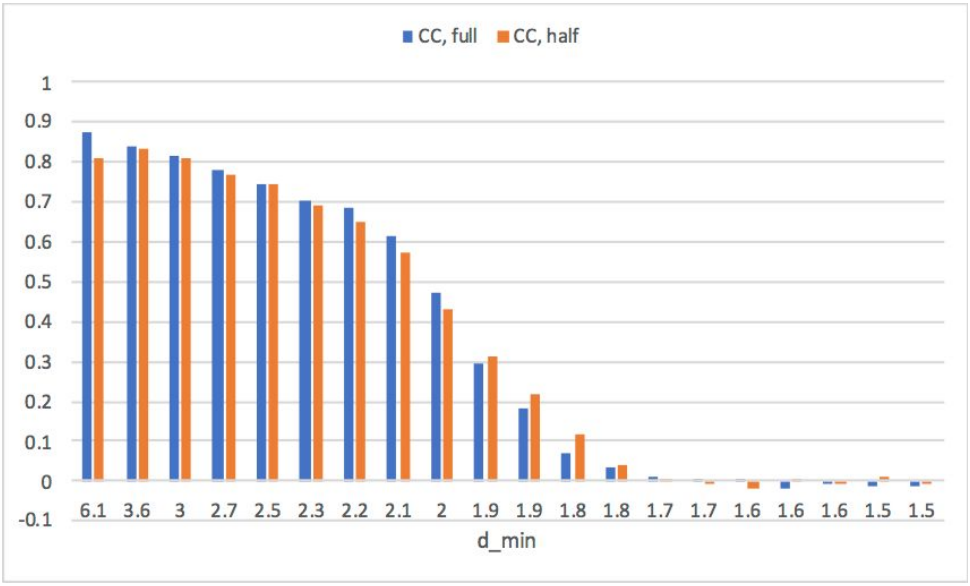
emd_20026_model_sharpened_box_A.ccp4 -- emd_20026.map model-sharpened with full docked model, then region of chain A extracted with map_box

emd_20026_half_map_2_model_sharpened_box_A.ccp4 -- emd_20026_half_map_2.map model-sharpened with full docked model, then region of chain A extracted with map_box

I sharpened with this command (same model for both maps):

phenix.auto_sharpen EMD-20026_best_docked_model_ncs_real_space_refined.pdb emd_20026.map resolution=1.8 sharpened_map_file=emd_20026_model_sharpened.ccp4

To me, the emd_20026_half_map_2_model_sharpened_box_A.ccp4 map looks better than the emd_20026_model_sharpened_box_A.ccp4 map. Additionally, the model-sharpening process provides a FSC for model vs map, and this FSC is a little higher for the half map in almost all resolution shells. Here is a plot of those FSC values.



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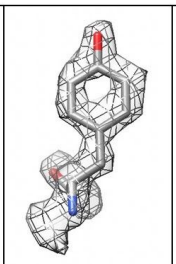
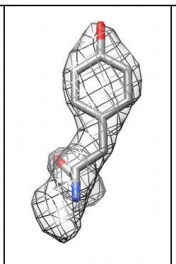
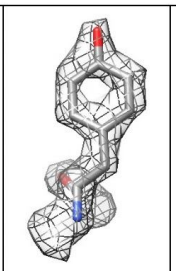
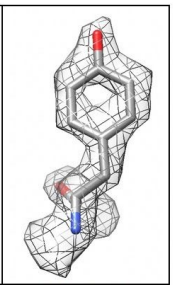
On Fri, Apr 26, 2019 at 2:57 PM Pintilie, Greg wrote:

Hi Tom,Thanks for those details... I ran the same commands. While the model_sharpened map now looks almost as good as the full map (I must have done it wrong before), it still looks just a little worse to me and has slightly lower Z-scores - see attached table. What really impressed me is that sharpening the half map without a model produces an almost-as-good result as using the model! Nice job on that…

I tabulated and plotted the CC values vs d_min from auto sharpen… second attachment. It confirms the full map is still mostly better than the half map, except past d_min 1.9. I wonder if these higher frequencies are different in the two half maps, and average out when combining them. If that’s true, it still produces a full map that is slightly better, by eye and by Z-scores.

What I still think is even more interesting in all this is to look at CC and other scores, and whether they truly represent how good the map is visually - that’s been one of our goals anyway.

Finally, this analysis is also saying is that the half map is just as good as the full map, except it’s not sharpened. Actually it should be as good, otherwise the gold standard FSC for the full map would be wrong. It also says your auto_sharpen is pretty awesome - even I can run it without knowing too much about SPR, B-values, etc. Other than that, I wonder if you have the full map and half map 2 switched somehow - you mentioned you did it blind, could that be possible?

TYR32				
map	emd_20026	emd_20026_half_map_2	emd_20026_half_map_2_model_sharpened	emd_20026_half_map_2_sharpened
Z-score for TYR 32 only	16.1	8.3	11.2	11.5
Avg. Side Chain Z-score (chain A)	3.08	2.30	2.91	2.91
CC (from your email)	**0.6337**	**0.7795**		
CC vs Chimera molmap, resolution=2.0 /about mean	0.78/0.57	0.76/0.45		
CC vs Phenix fmap, min_d=2.0 /about mean	**0.84/0.75**	**0.89/0.74**		

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On Apr 26, 2019, at 5:10 PM, Tom Terwilliger wrote:

Hi Greg, Thanks for looking into it more! Maybe...we should be concluding that the full and half-maps at 1.8 A are not all that different (except for sharpening). And maybe that is saying that the errors in these maps are now coming from things that are not random, so that averaging in more data is no longer making a difference?

I did check...I think I have the maps correctly labelled as I compared them to the originals dated 1 April as downloaded from the EMDB.

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On Apr 26, 2019, at 7:24 PM, Pintilie, Greg wrote:

I think that’s a fair conclusion; looking forward to more discussions and seeing some results from the modelling side. One thing we didn’t consider is whether the model is as good as it can be yet, based on the density. Greg

Submission Instructions

1. Before doing anything else, carefully check your coordinate file. It can be in either PDB or mmCIF format, but should contain only atom/hetatm records with sequence, chain ids, residue numbering, and position as indicated in the instructions. Make sure to remove all remarks that identify users and/or software used (ensures blinded initial release for assessment).
2. Next, go to PDBextract to deposit your model. Select "EM" method and upload the file. Don't fill in any info on the second page, just submit and go to the next step below.
3. Copy THE FULL LINK to your PDBextract-generated output cif file, and paste the link in the PDBextract link box in the form below.
4. Fill out the remaining requested information as completely as possible. Use "next page" "previous page" buttons to navigate the form (warning: using browser navigation may reset your submission). You will have an opportunity to review all of your answers prior to submission.

Model Submissions Summary Statistics

Challenge Target

T1 Apoferritin 1.8 Å (EMD-20026)	16
T2 Apoferritin 2.3 Å (EMD-20027)	15
T3 Apoferritin 3.1 Å (EMD-20028)	15
T4 Alcohol Dehydrogenase 2.9 Å (EMD-0406)	17

Which target map was used for (final) fitting?

primary map of the EMDB entry (emd_#####.map)	42
unsharpened/unmodified map from reconstruction software (emd_#####_additional_#.map)	16
half-map 1 for the FSC calculation (emd_#####_half_map_1.map)	5

Did you modify the map?

yes	21
no	42

Map preparation procedures used

(answered by 21 responding yes to "did you modify the map?")

	yes	no
low pass filter	9	12
high pass filter	4	17
local normalization	4	17
segmentation	5	16
applied a mask	10	11
sharpened w/ constant B-value	12	9
sharpened w/ variable B-value	4	17
converted to structure factors	11	10

Modelling Category

Created an ab initio model	51
Optimized a known model	12

Effort type

fully automated	22
partially automated, some manual steps	41
manual	0

Refinement space

real	51
reciprocal	12

Inclusion of H-atoms in Model

yes	27
no	37

Final model refinement (choose one)

ARP/wARP/refmac	8
Chimera	10
COOT	1
CDMD	4
MDFF	4
pathwalker	2
phenix	13
refmac	4
rosetta	16
VMD	1

All modelling software used (indicate all used)

ARP/wARP	8
Buccaneer	4
Chimera	35
COOT	19
CDMD	4
direX	3
mainmast	10
MDFF	10
pathwalker	2
phenix	16
pymol	4
refmac	12
rosetta	17
situs	1
TEMPy	4
VMD	4

Target criteria used to identify model improvements (indicate all used)

map vs. model correlation coefficient	28
map vs. model FSC curve	19
energy function	25
cross-validation procedure	17
Other (additional reported criteria listed below)	24
--Reciprocal Space Target (refmac)	8
--EMRinger	6
--geometry (e.g. molprobity)	6
--phenix cryo-EM tools	4
--Segment-based Mander's overlap coefficient	4
--Q-score	1

Atomic Displacement (B)

Type of B factor Treatment	All targets	T1	T2	T3	T4
single overall B value applied to entire model	5	1	1	1	2
grouped B (segments)	3	1	1	1	0
grouped B (per residue)	6	1	1	2	2
individual B for each atom	23	6	6	6	5
none	30	8	7	6	9

Was the map scale (voxel size) adjusted during the modelling process?

no	63

Validation Checks

	yes	no
internal model consistency	60	3
fit of model to the target map	60	3
fit of model to map other than target (cross-validation)	25	38

Model Comparison

Interactive plots and graphs are available at https://model-compare.emdataresource.org

Model Groups

Model comparison was initially conducted blinded. The participating groups with their Team IDs are shown below.

Group	Team	Team Lead	Institution/Affiliation	Collaborators
10	yu	Xiaodi Yu	Janssen Pharmaceuticals (J&J)	
25	cdmd	Maxim Igaev	Max Planck Institute for Biophysical Chemistry Göttingen	Andrea Vaiana
27	kumar	Dilip Kumar	Baylor College of Medicine	
28	ccpem	Soon Wen Hoh	University of York	Kevin Cowtan, Agnel Praveen Joseph, Colin Palmer, Martyn Winn, Tom Burnley, Mateusz Olek, Paul Bond
35	phenix	Pavel Afonine	Lawrence Berkeley National Lab	Tom Terwilliger, Li-Wei Hung
38	fzjuelich	Gunnar Schroeder	Forschungszentrum Juelich	Luisa Schaefer
41	arpwarp	Grzegorz Chojnowski	EMBL Hamburg	
54	kihara	Daisuke Kihara	Purdue University	Genki Terashi
60	deeptracer	Liguo Wang	University of Washington	Renzhi Cao, Dong Si, Jianlin Cheng
73	singharoy	Abishek Singharoy	Arizona State University	Mrinal Shekhar, Alberto Perez, Genki Terashi, Daisuke Kihara, Sumit Mittal, Daipayan Sarkar
82	rosetta	Frank DiMaio	University of Washington	Dan Farrell
90	mbaker	Matt Baker	Baylor College of Medicine	
91	chiu	Greg Pintilie	Stanford University	Wah Chiu

Website Footer

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Please send your challenge questions, comments and feedback to challenges@emdataresource.org