

Development of A Web-based Volume Browser

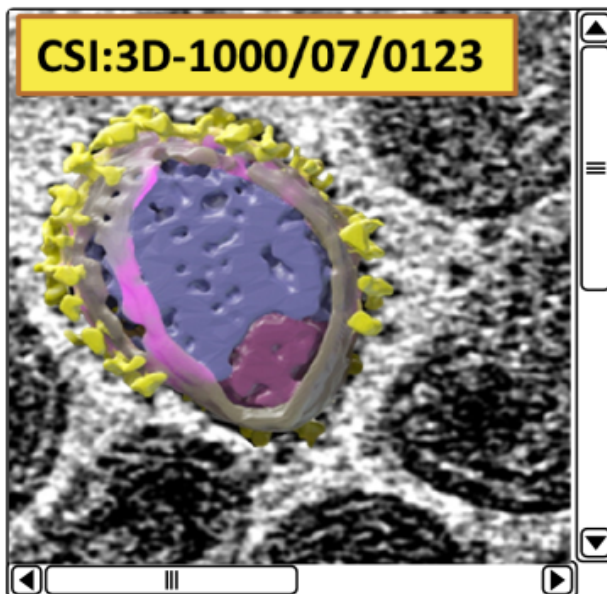
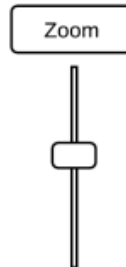
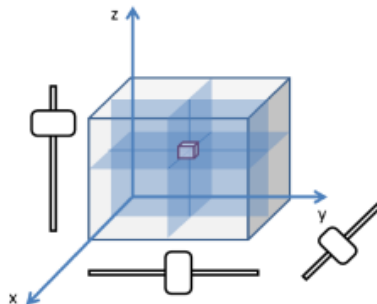
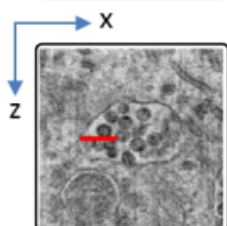
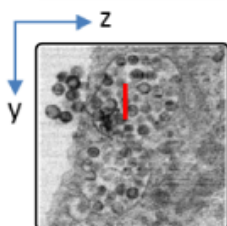
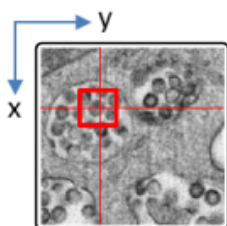
11th Annual OME Users' Meeting, Dundee 2016

Paul K. Korir

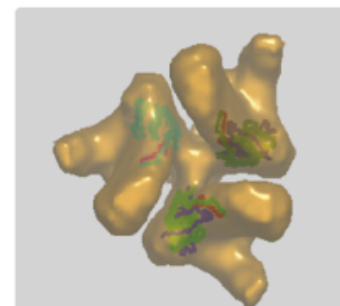
MOL2CELL Project

EMD-4134: Cryoelectron Tomographic Analysis of an HIV-neutralizing Protein and Its Complex with Native Viral gp120

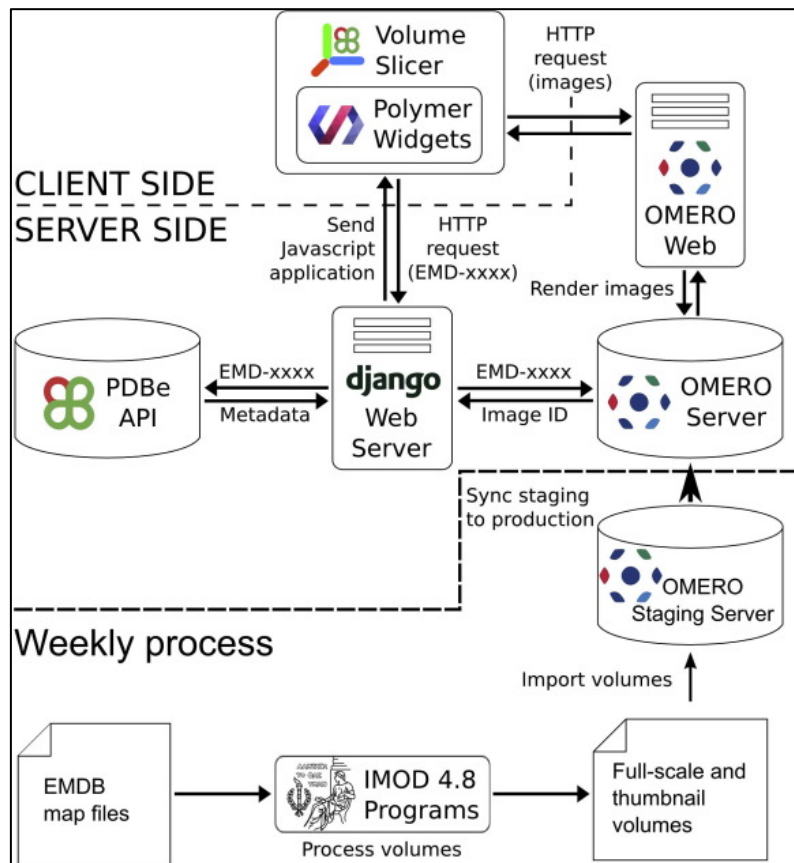
Release date: 2014/5/3
DOI: [90.1074/jbc.M702025200](https://doi.org/10.1074/jbc.M702025200)
[more details...](#)



Spike	<input type="checkbox"/>
Subtomogram averages	
<input checked="" type="checkbox"/> Spike in complex with IGP-D1D2	
<input type="checkbox"/> Unbound spike	
Atomic models	
<input checked="" type="checkbox"/> gp120 core	
<input type="checkbox"/> gp120 N-terminal domain	
Membrane	<input type="checkbox"/>
Core	<input type="checkbox"/>
Matrix	<input type="checkbox"/>



Volume Slicer



The screenshot shows the EMD-6422 Volume slicer interface. The page title is "EMD-6422 > Volume slicer" and the subtitle is "CryoEM structure of GroEL".

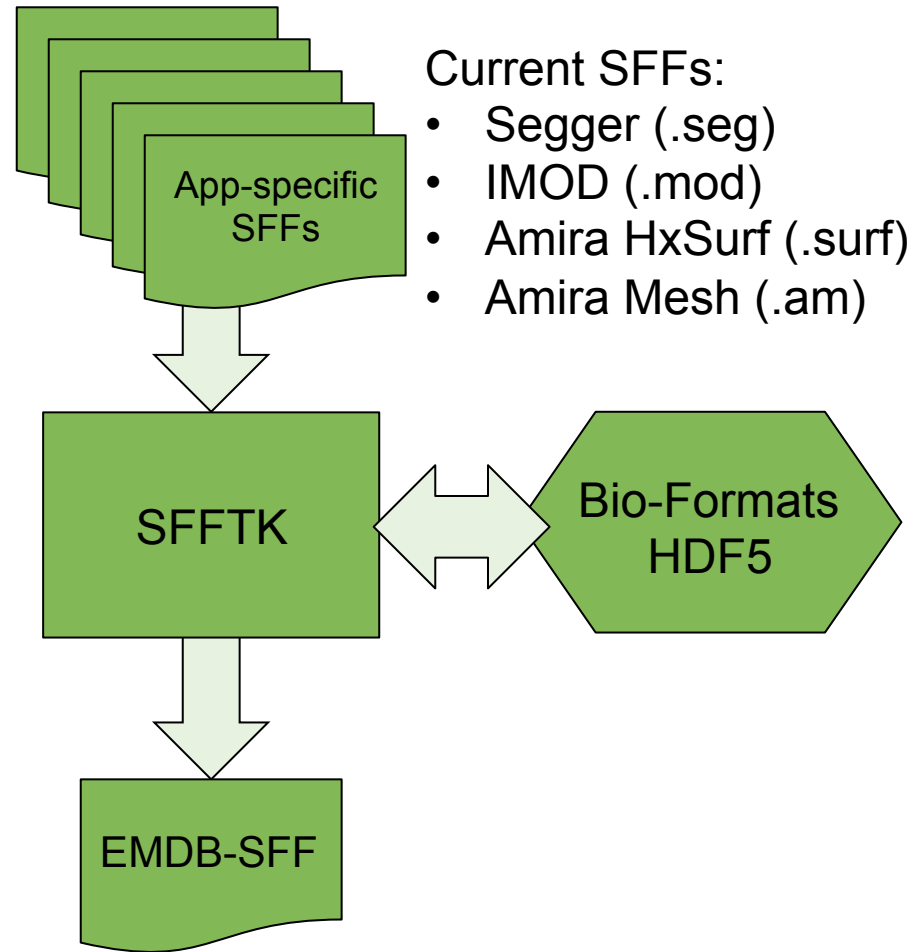
Sample information:

- Sample name: Wild type GroEL
- Method: Single-particle
- Resolution: 4.1 Å (FSC 0.143, gold-standard)

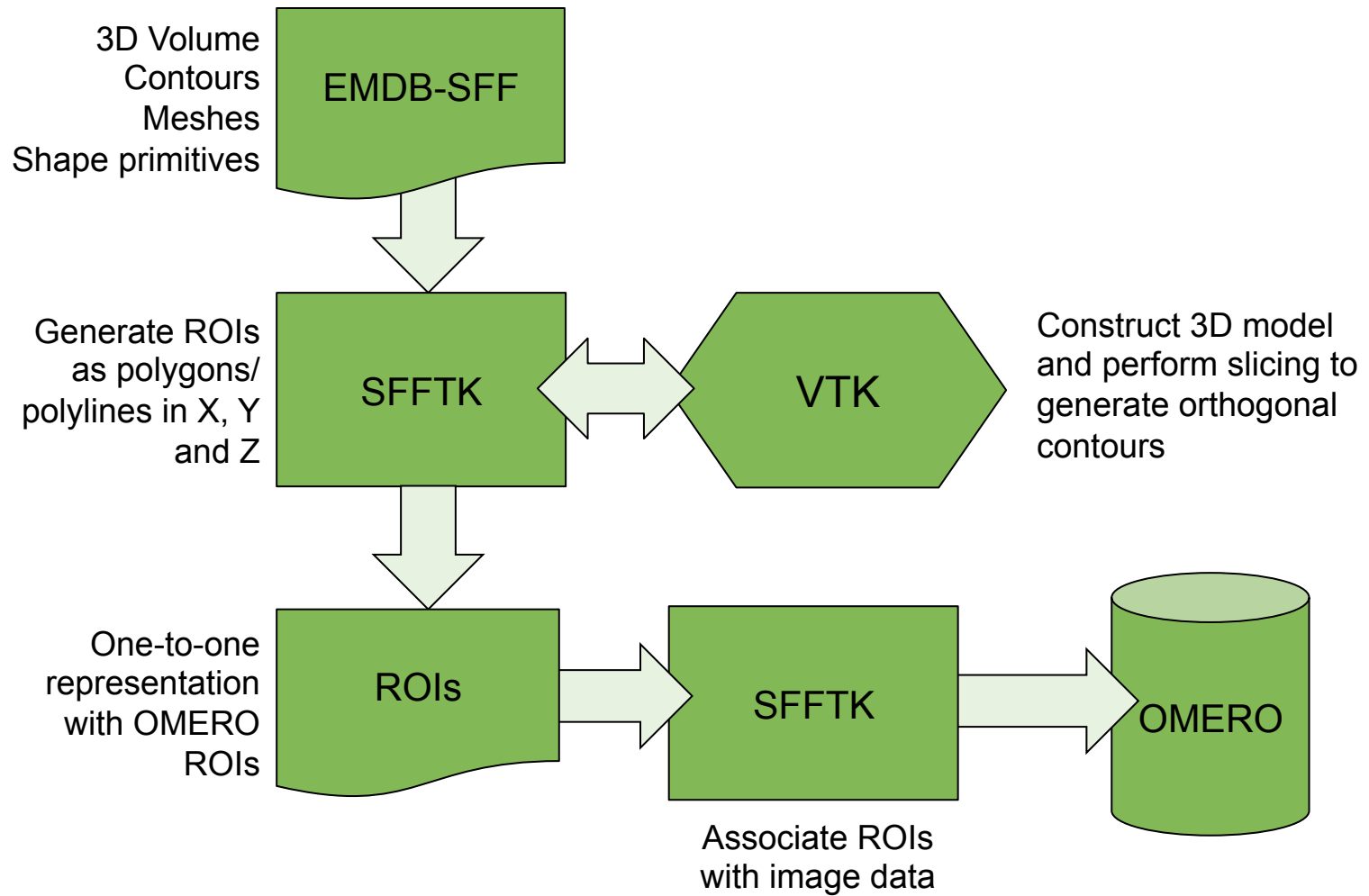
The interface displays a 3D volume slicer with a histogram showing the distribution of slice thicknesses. The histogram has a minimum value of -3.6 and a maximum value of 9.3. The volume is shown in three views: Top view, Front view, and Right view. The Top view shows a circular cross-section of the GroEL protein complex. The Front and Right views show the protein complex from different perspectives.

Segmentations and EMDB-SFF

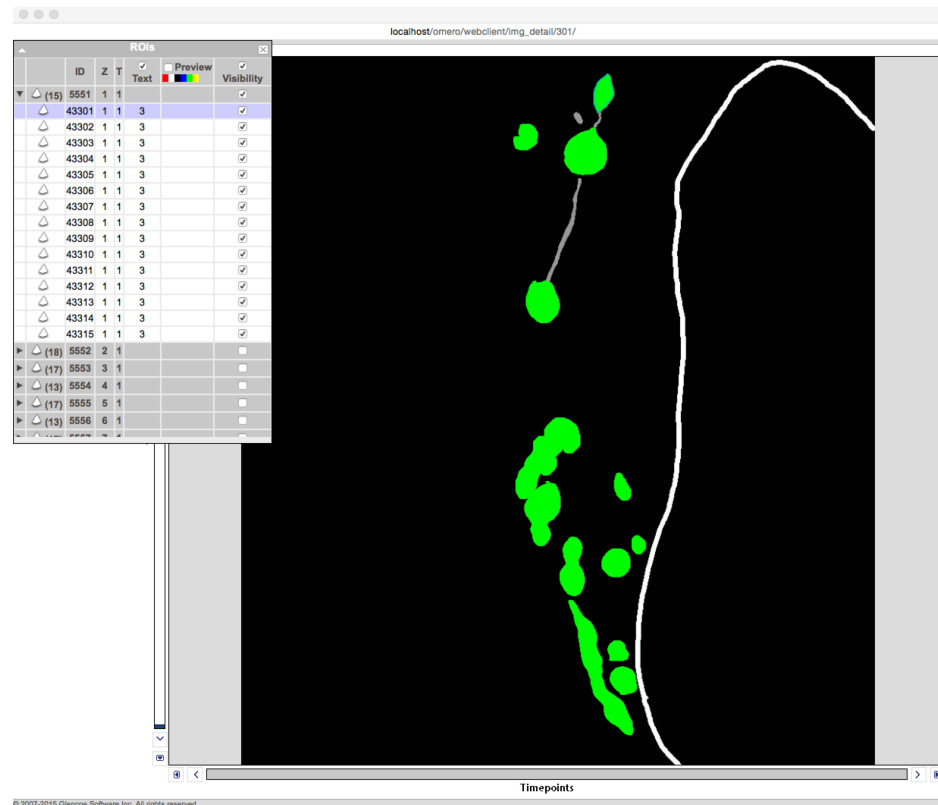
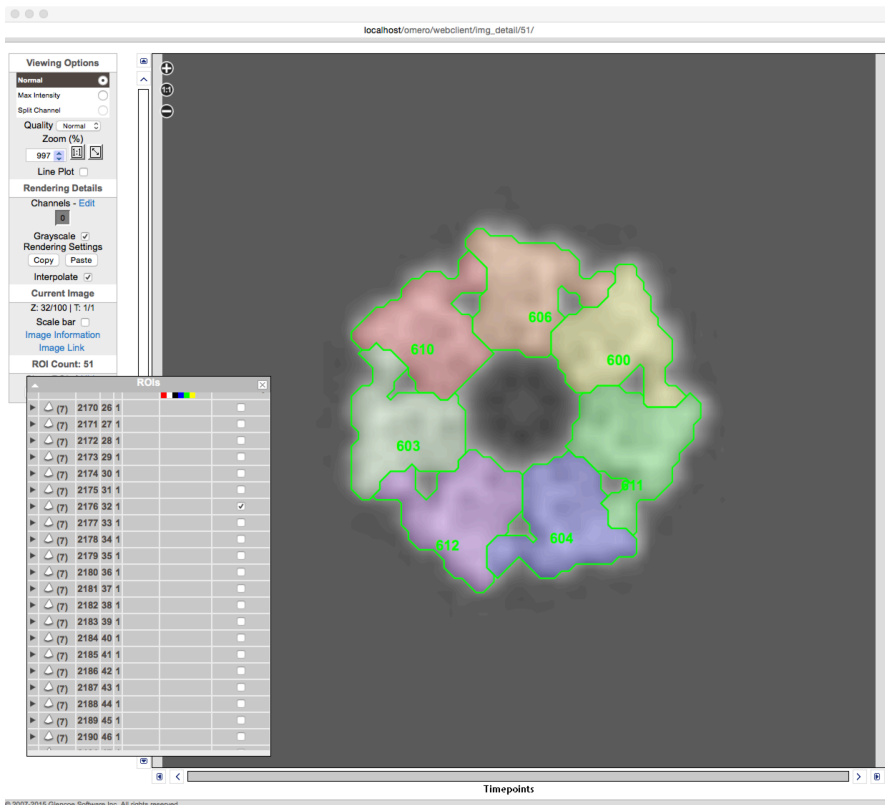
- EMDB-SFF:
3D Segmentations and Transformations Workshop (December 2015)
- Representing segments:
 - 3D Volume (Voxels)
 - Contours (Polygons/Polylines)
 - Meshes (Vertices + Polygons)
 - Shape Primitives (Ellipsoid, Cylinder, Cone, Cuboid)
- SFFTK: the go-between app-SFFs, EMDB-SFF and OMERO



OMERO ROIs



Examples



Support/Feature Requests

- OMERO and Bio-Formats are awesome!
 - Clear design outline and data models
 - Very responsive developer community
- Developer requests:
 - Documentation of Python API (a bit hard to use without description of objects)
 - Adapter for Python API (I have an example for ROIs that makes ROI primitives more Pythonic) – only has to be done once! ;-)
 - Bio-Formats: extending Amira readers to get header metadata

Acknowledgements

- Gerard Kleywegt
- EM group
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- And many more!

