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Lumbricus terrestris hemoglobin (Dr. Sacha De Carlo and Dr. Gert Oostergetel, NeCEN, Netherlands) Figure A: Typical view of worm hemoglobin as observed in cryo-EM and representative class-averages from the data shown. Figure B: Surface rendering of the worm hemoglobin 3D reconstruction showing secondary structure elements at about 6.5 Å resolution. Figures C and D: Slabs through the hemoglobin subunit (1/12th) viewed from the 3-fold axis.

New cryo-electron microscopy methods from FEI in structural biology research are advancing the significance of XRD data and are going beyond single protein structures to visualize protein complexes and large macromolecular machineries in their native, *in situ* relevant state—bringing about real biological relevance.

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