

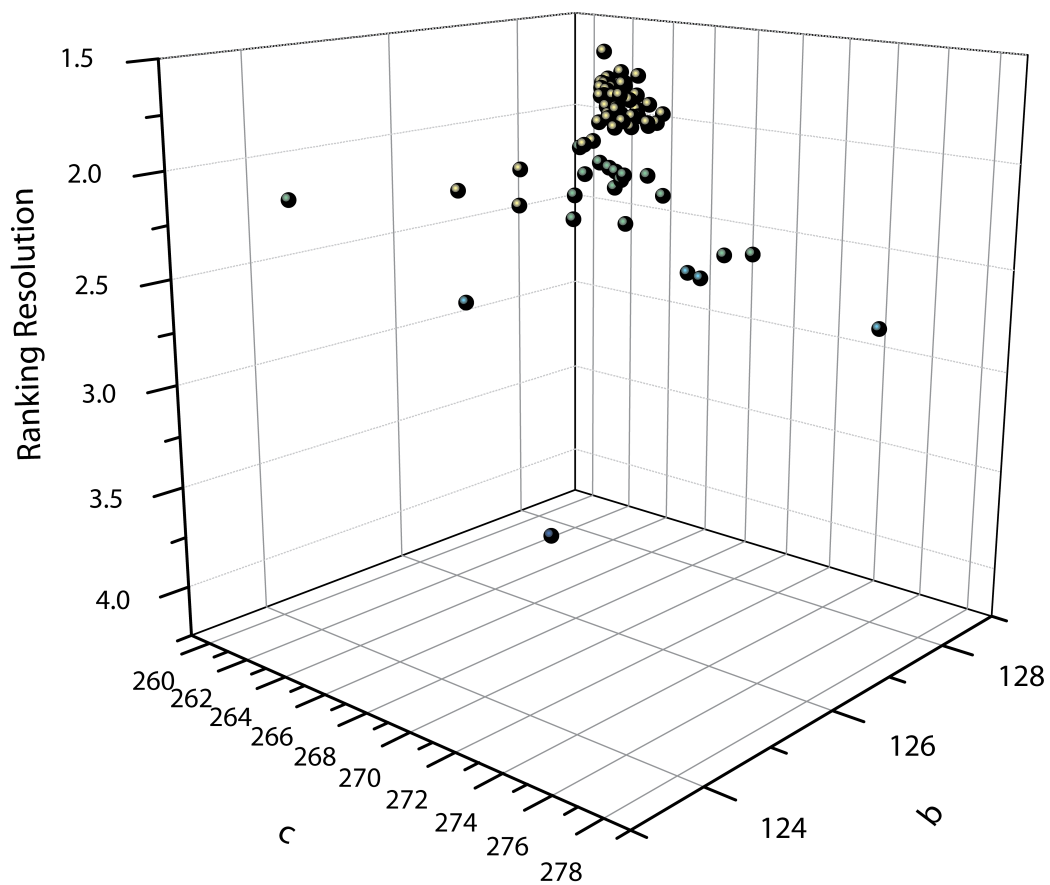
## Supplementary Information for :

### **Diffraction Cartography: applying microbeams to macromolecular crystallography sample evaluation and data collection.**

Matthew W. Bowler<sup>a,\*</sup>, Matias Guijarro<sup>a</sup>, Sebastien Petitdemange<sup>b</sup>, Isabel Baker<sup>a,c</sup>, Olof Svensson<sup>a</sup>, Manfred Burghammer<sup>b</sup>, Christoph Mueller-Dieckmann<sup>a</sup>, Elspeth J. Gordon<sup>a</sup>, David Flot<sup>a</sup>, Sean M. McSweeney<sup>a</sup> and Gordon A. Leonard<sup>a</sup>

<sup>a</sup>Structural Biology Group, European Synchrotron Radiation Facility, 6 rue Jules Horowitz, F-38043 Grenoble, France. <sup>b</sup>Structure of Soft Matter Group, European Synchrotron Radiation Facility, 6 rue Jules Horowitz, F-38043 Grenoble, France. <sup>c</sup>Department of Biology and Biochemistry, University of Bath, Claverton Down, Bath, BA2 7AY, UK.

Correspondance e-mail: bowler@esrf.fr



**Figure S1** Analysis of the unit cell dimensions against the ranking resolution for the crystal of F<sub>1</sub>-ATPase in figure 4 (all units are in Å). The *b* and *c* unit cell dimensions were plotted against the ranking resolution obtained for each image from EDNA (the *a* cell dimension does not vary significantly). The areas with the highest ranking resolution tend to cluster with similar unit cell dimensions.