

**Structural basis of Zn<sup>2+</sup>-mediated tethering that stabilizes ERp44-client complexes in protein quality control**

Satoshi Watanabe<sup>1\*</sup>, Mikoto Kiya<sup>2#</sup>, Amiko Miyake<sup>2#</sup>, Emi Honjyo<sup>1</sup>, Yuta Amagai<sup>1</sup> Roberto Sitia<sup>3</sup>, and Kenji Inaba<sup>1\*</sup>

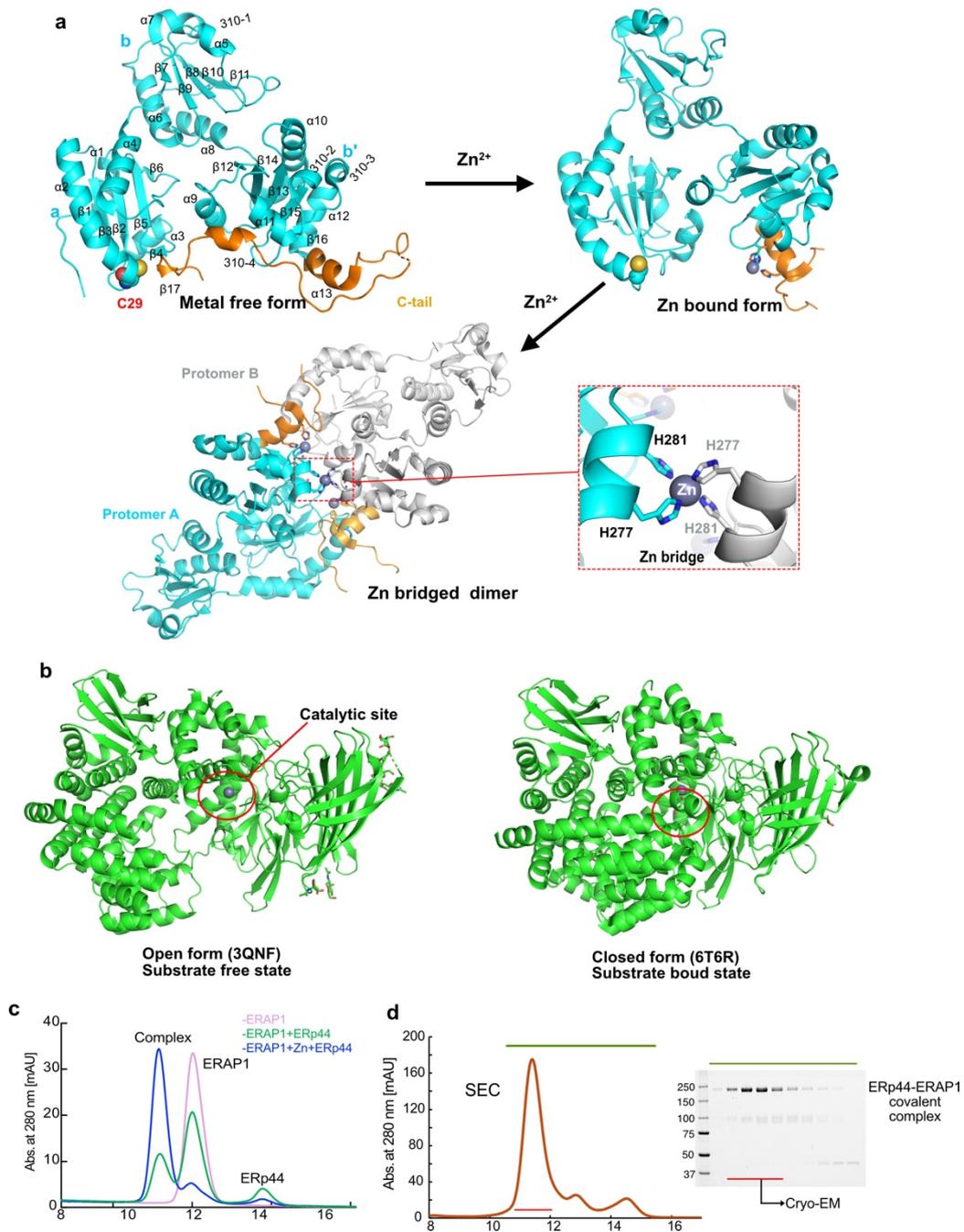
<sup>1</sup>Medical Institute of Bioregulation, Kyushu University, Fukuoka 812-8582, Japan.

<sup>2</sup> Department of Molecular and Chemical Life Sciences, Graduate School of Life Sciences, Tohoku University, Sendai, Miyagi, 980-8577, Japan

<sup>3</sup>Division of Genetics and Cell Biology, Vita-Salute University, IRCCS Ospedale San Raffaele, 20132, Milan, Italy

#These authors contribute equally.

**Supplementary Figures 1-10**



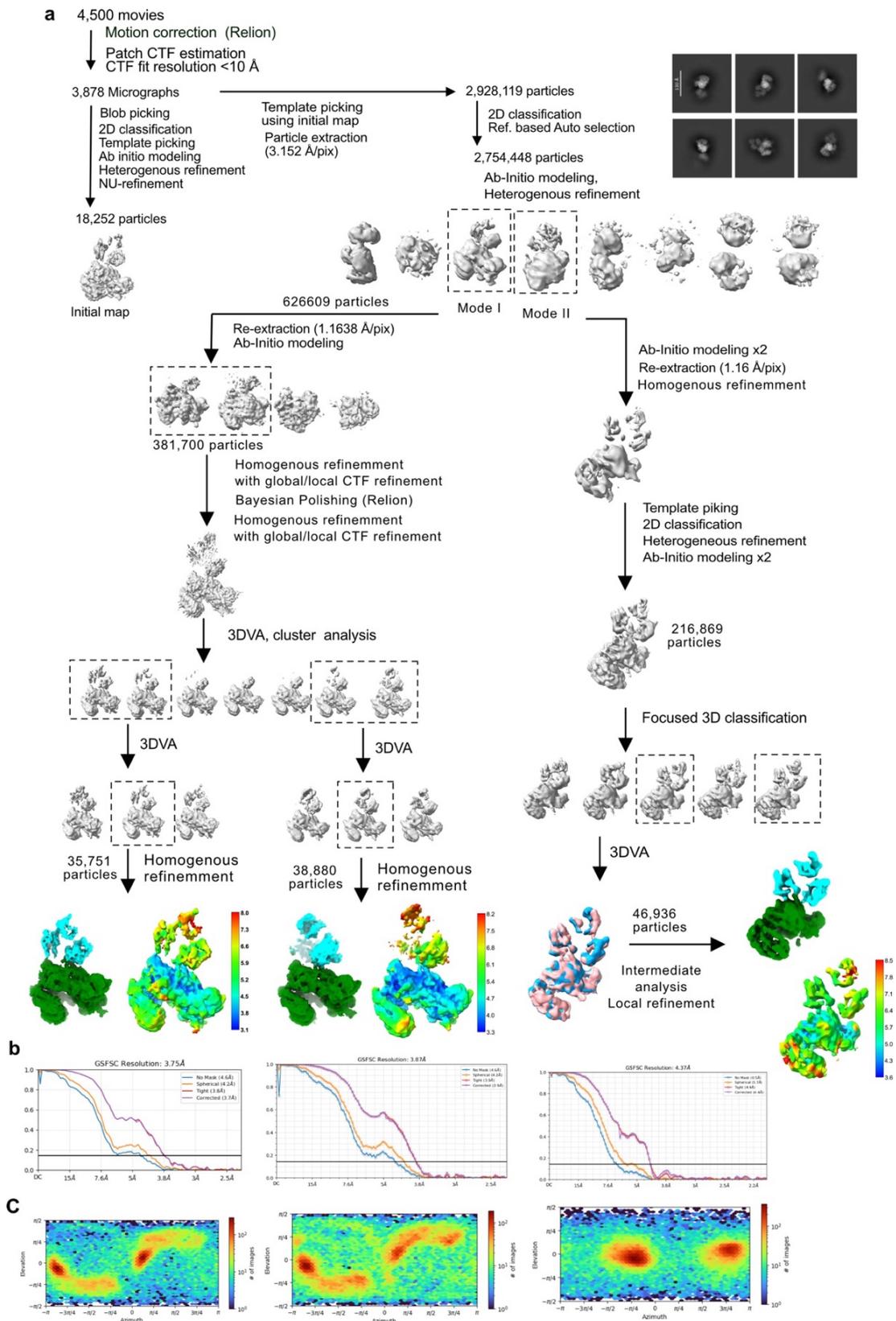
### Supplementary Fig. 1 Preparation of the ERp44-ERAP1 complex

a, Zn<sup>2+</sup>-dependent conformational changes of ERp44 revealed by our previous crystal structure analysis of ERp44<sup>28</sup>.

b, Crystal structures of ERAP1 adopting an open conformation in the substrate-free state, and a closed conformation in the substrate-bound state.

c, SEC analysis of Zn<sup>2+</sup>-dependent complex formation between ERp44 and ERAP1.

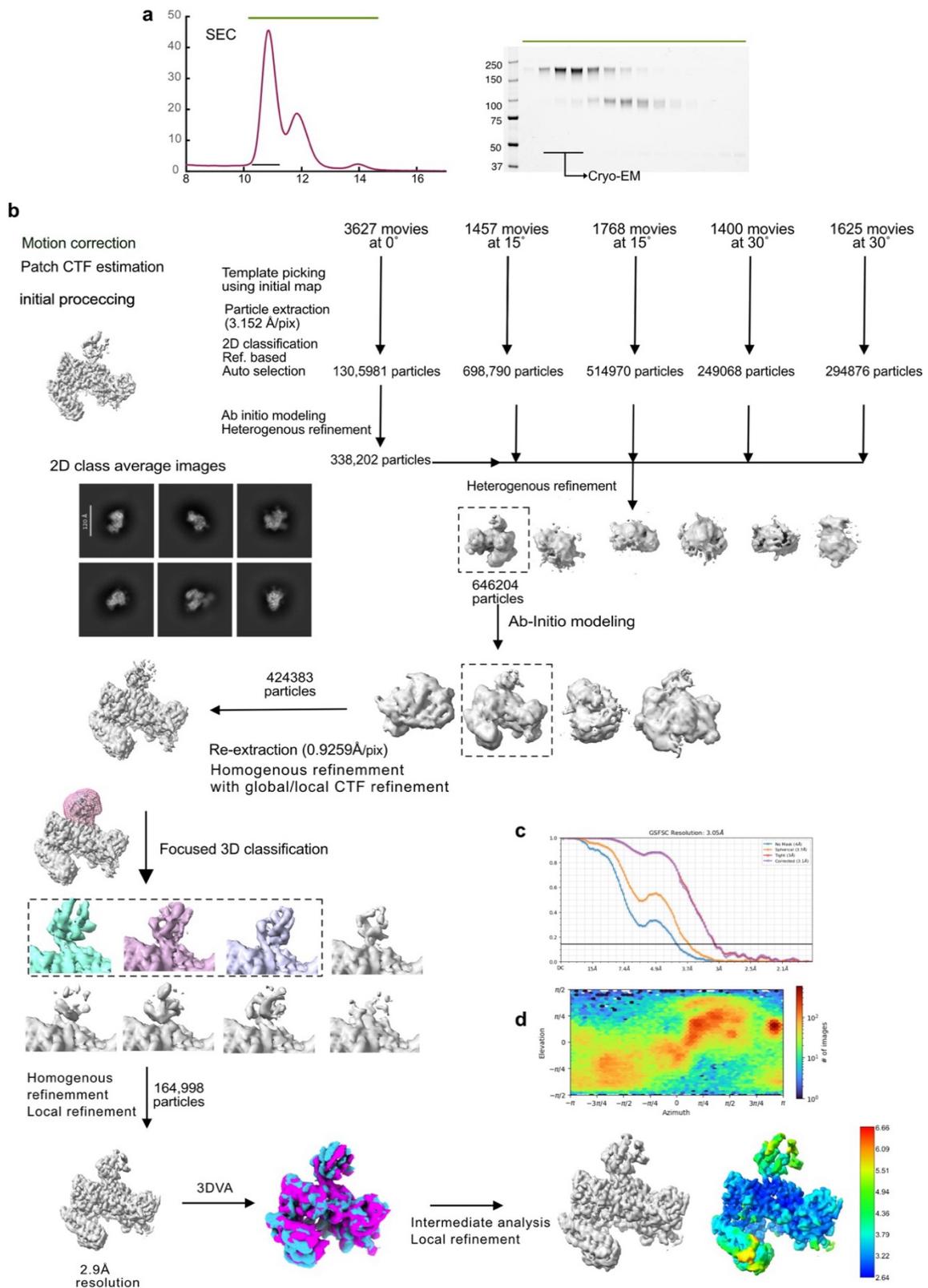
d, SEC profile (left) and non-reducing SDS-PAGE analysis (right) of the ERp44-ERAP1 complex for cryo-EM analysis. The protein bands were visualized with stain-free technology (Bio-Rad).



**Supplementary Fig. 2 Overall workflow of cryo-EM data processing of the ERp44-ERAP1 complex**

**a.** Workflow of cryo-EM data processing

**b, c.** Gold standard Fourier shell correlation (GSFSC) curve (b) and Euler angle distribution (c) for the final reconstruction of each map

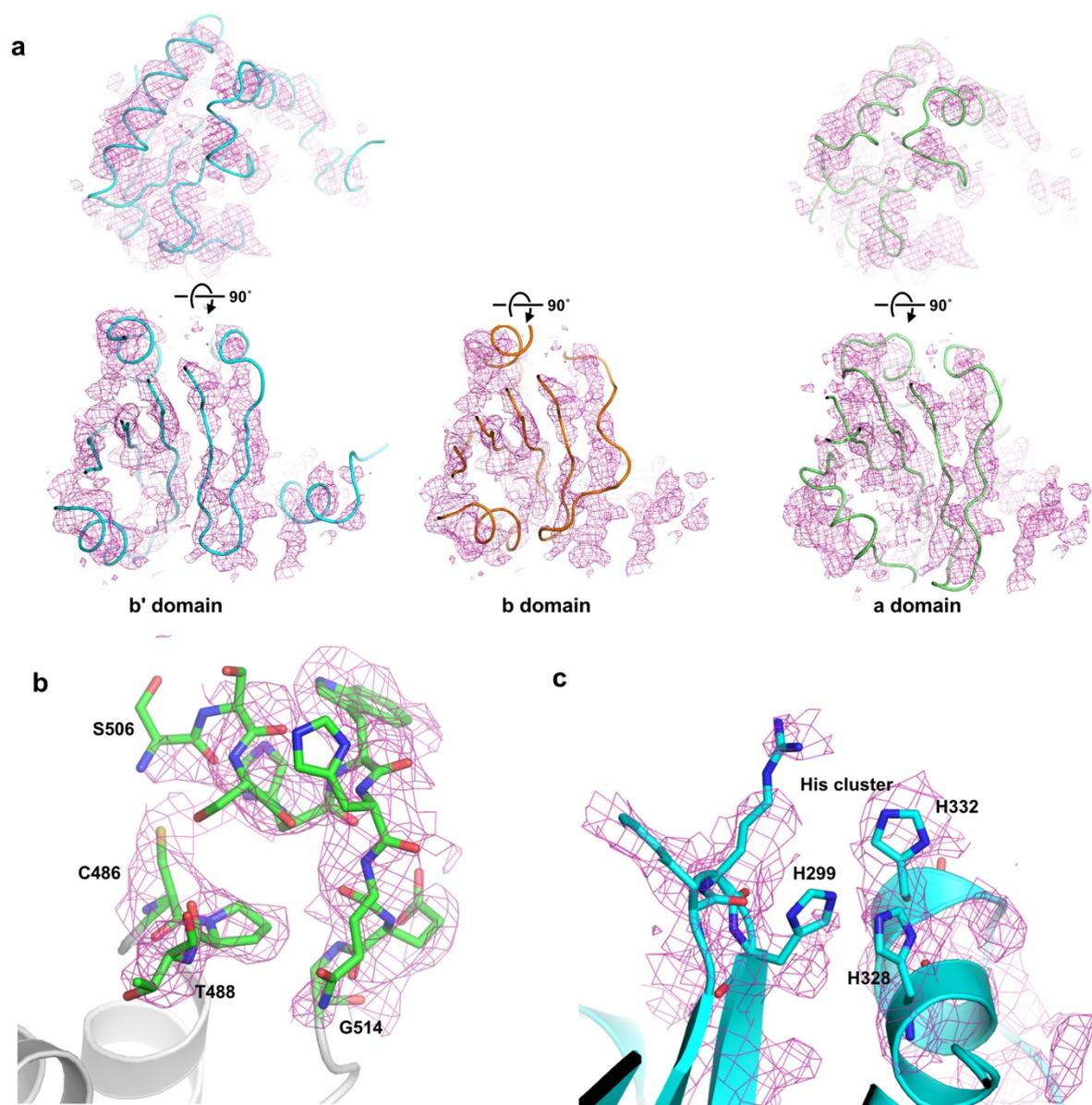


**Supplementary Fig. 3 Overall workflow of cryo-EM data processing of the PEG4-treated ERp44-ERAP1 complex**

**a.** SEC profile and non-reducing SDS-PAGE analysis of the PEG4-treated ERp44-ERAP1 complex for cryo-EM analysis. The protein bands were visualized with stain-free technology.

**b.** Workflow of cryo-EM data processing

**c, d.** GSFSC curve (c) and Euler angle distribution (d) for the final reconstruction

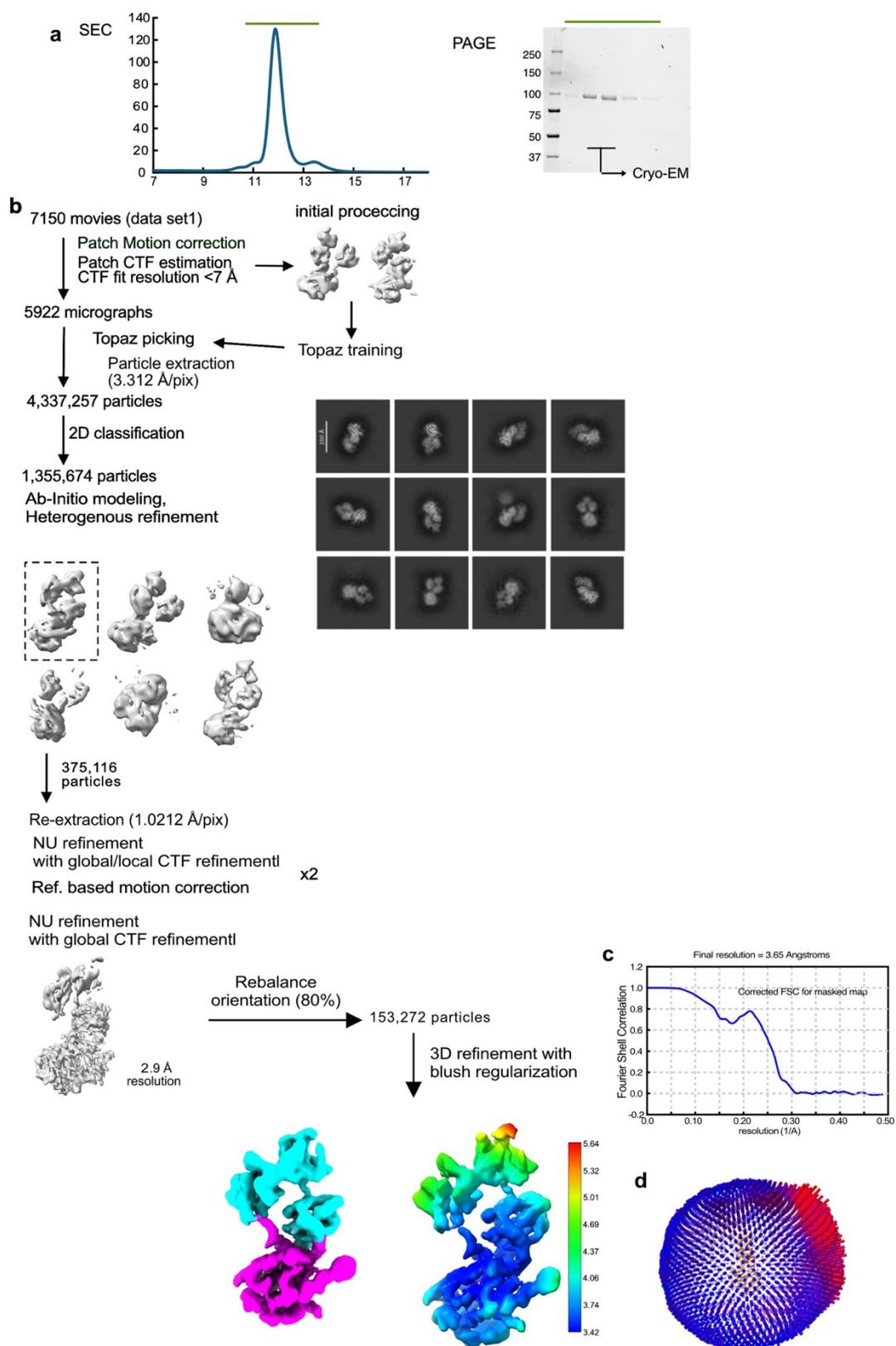


**Supplementary Fig. 4 Details of the high-resolution cryo-EM structure of the ERp44-ERAP1 complex**

**a.** Structures of individual ERp44 Trx-like domains overlaid onto the updated cryo-EM density map of the ERp44-ERAP1 complex.

**b.** Conformation of a part of the ERAP1 loop overlaid on the updated map.

**c.** Close-up view of the His cluster (His299, His328, His332) of ERp44 overlaid on the updated map.

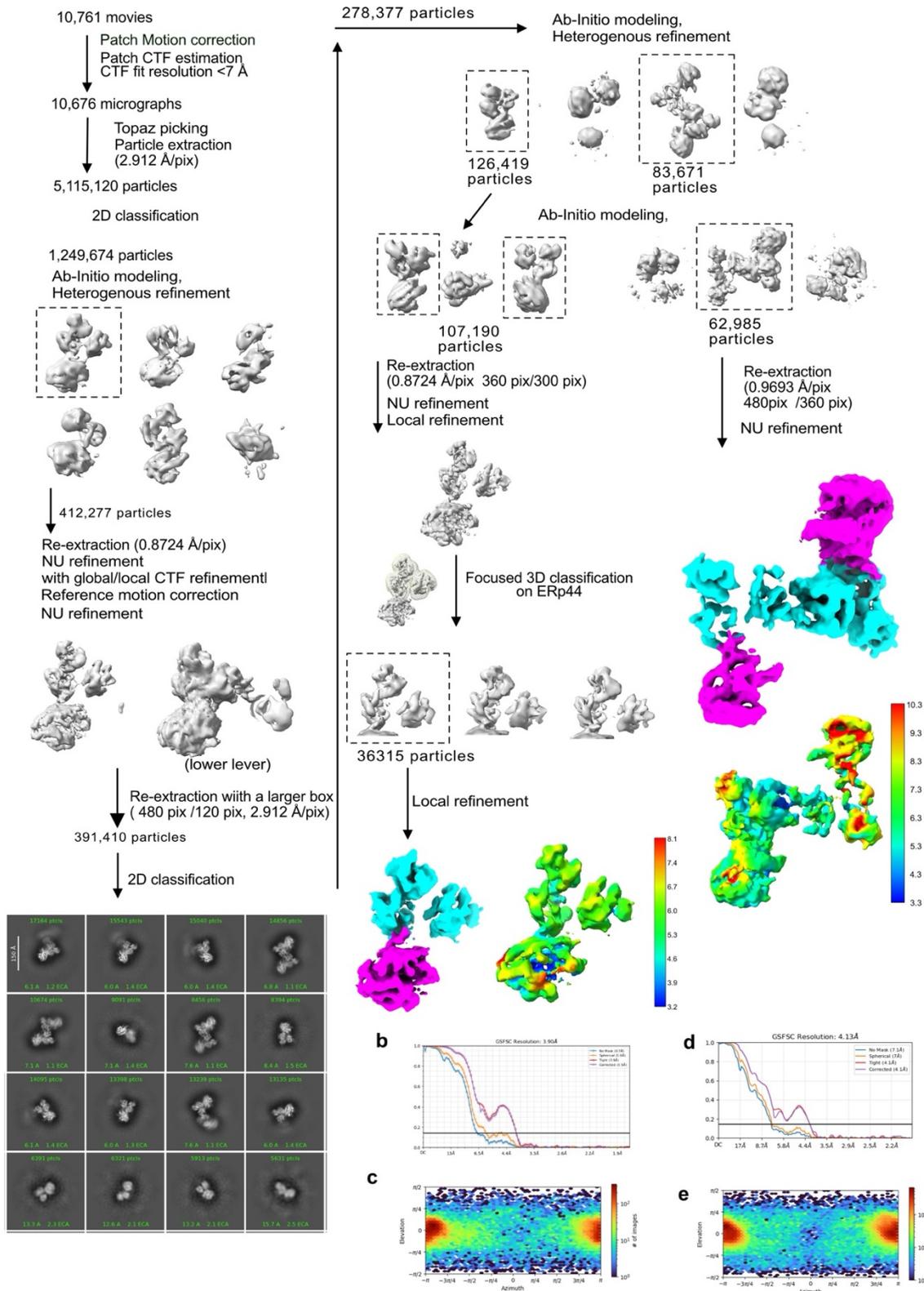


**Supplementary Fig. 5 Overall workflow of cryo-EM data processing of the ERp44-Ero1 complex in binding mode I**

**a.** SEC profile and non-reducing SDS-PAGE analysis of the PEG4-treated ERp44-Ero1 complex for cryo-EM analysis. The protein bands were visualized with stain-free technology.

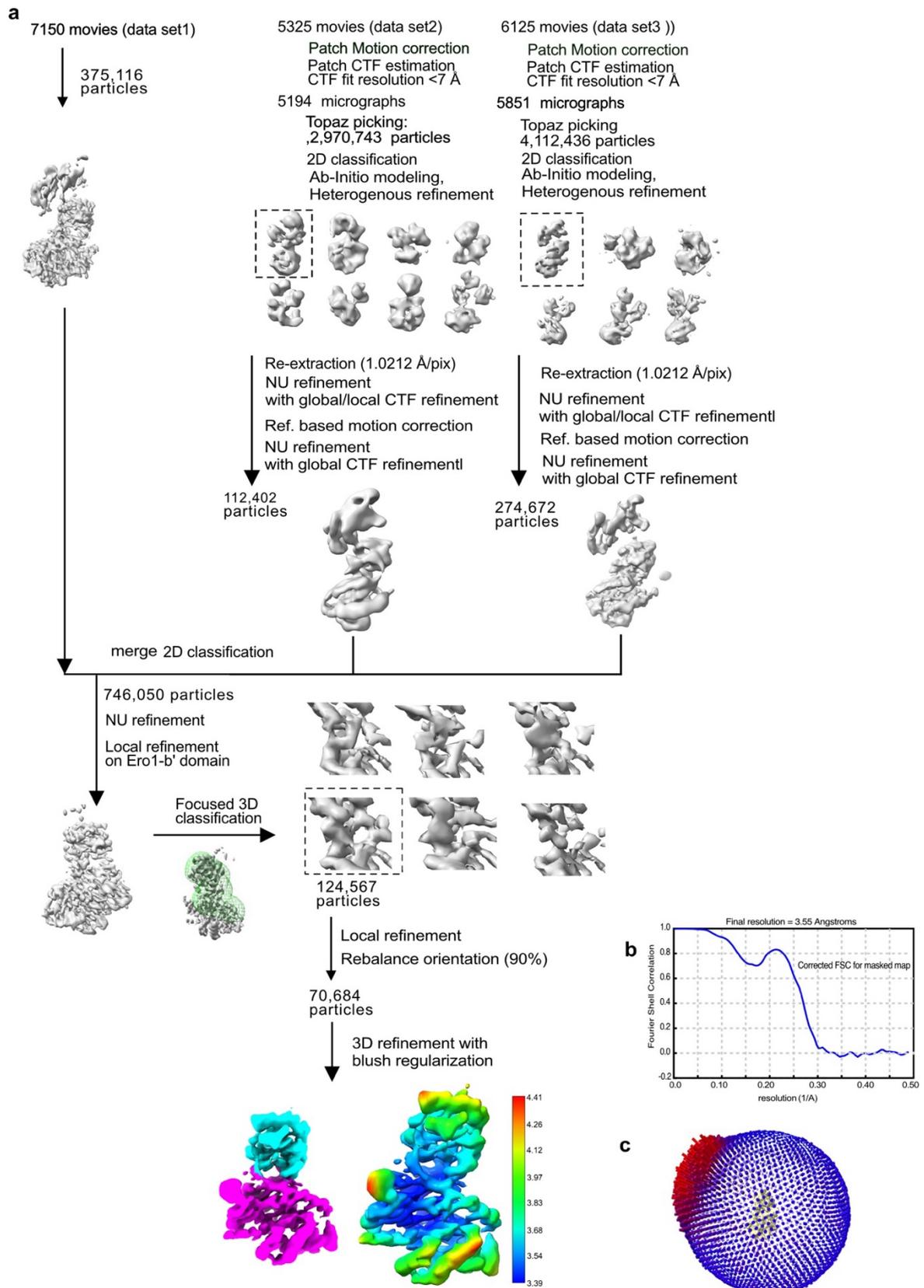
**b.** Workflow of cryo-EM data processing and overall and locally refined maps

**c, d.** Fourier Shell Correlation (FSC) curve (c) and Euler angle distribution (d) for final reconstruction.



**Supplementary Fig. 6 Overall workflow of cryo-EM data processing of the ERp44-Ero1 $\alpha$  complex in binding mode I**

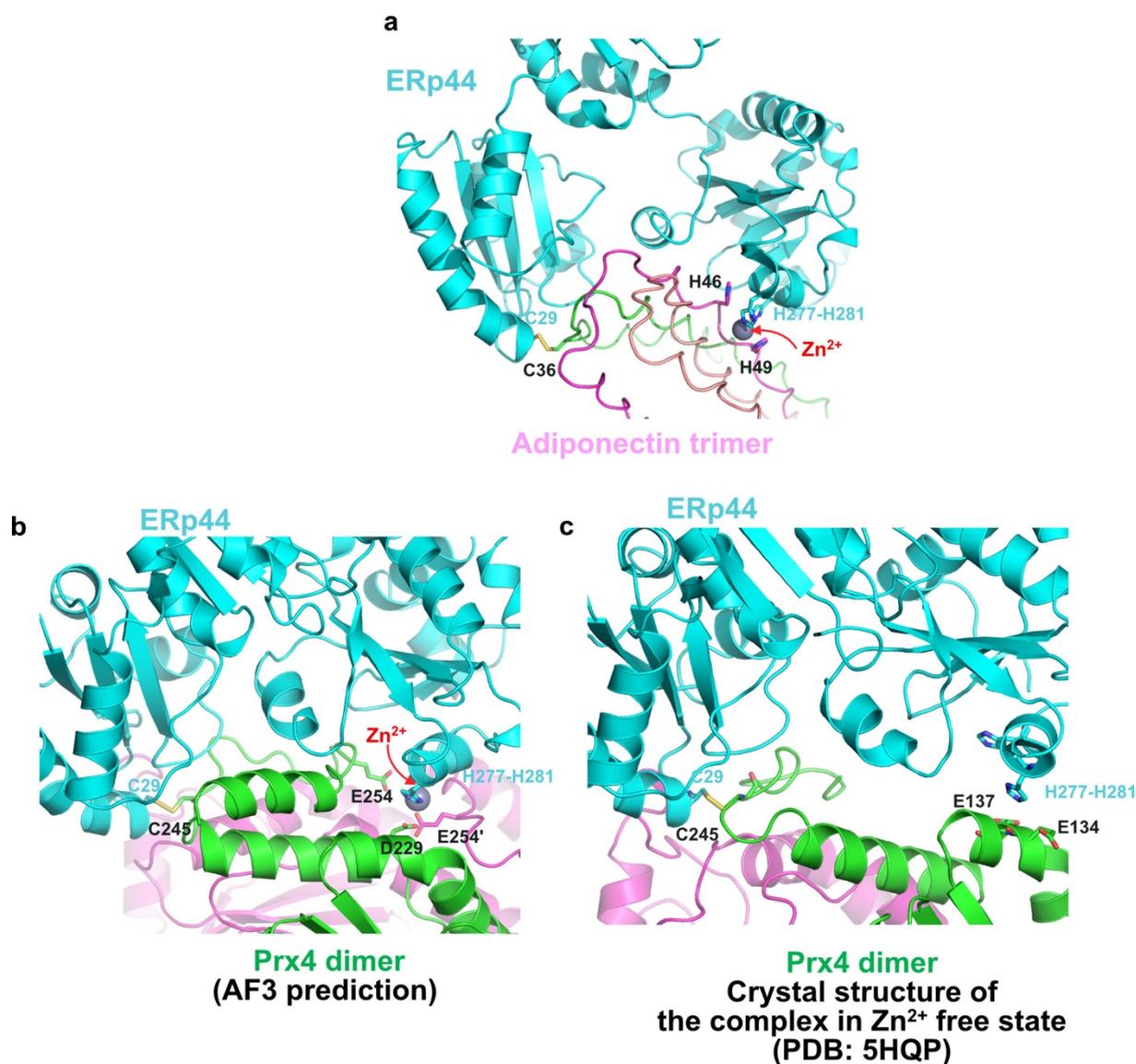
- a.** Workflow of image processing of the locally refined structure around the interface between ERp44 b' domain and Ero1 $\alpha$
- b, c.** GSFSC curve (**b**) and direction distribution (**c**) for final reconstruction of mode II complex in monomer.
- d, e.** GSFSC curve (**d**) and direction distribution (**e**) for final reconstruction of mode II complex in dimer.



**Supplementary Fig. 7 Overall workflow of cryo-EM data processing of the ERp44-Ero1 $\alpha$  complex in binding mode II**

**a.** Workflow of cryo-EM data processing and overall and locally refined maps.

**b, c.** FSC curve (b) and Euler angle distribution (c) for the final reconstruction.



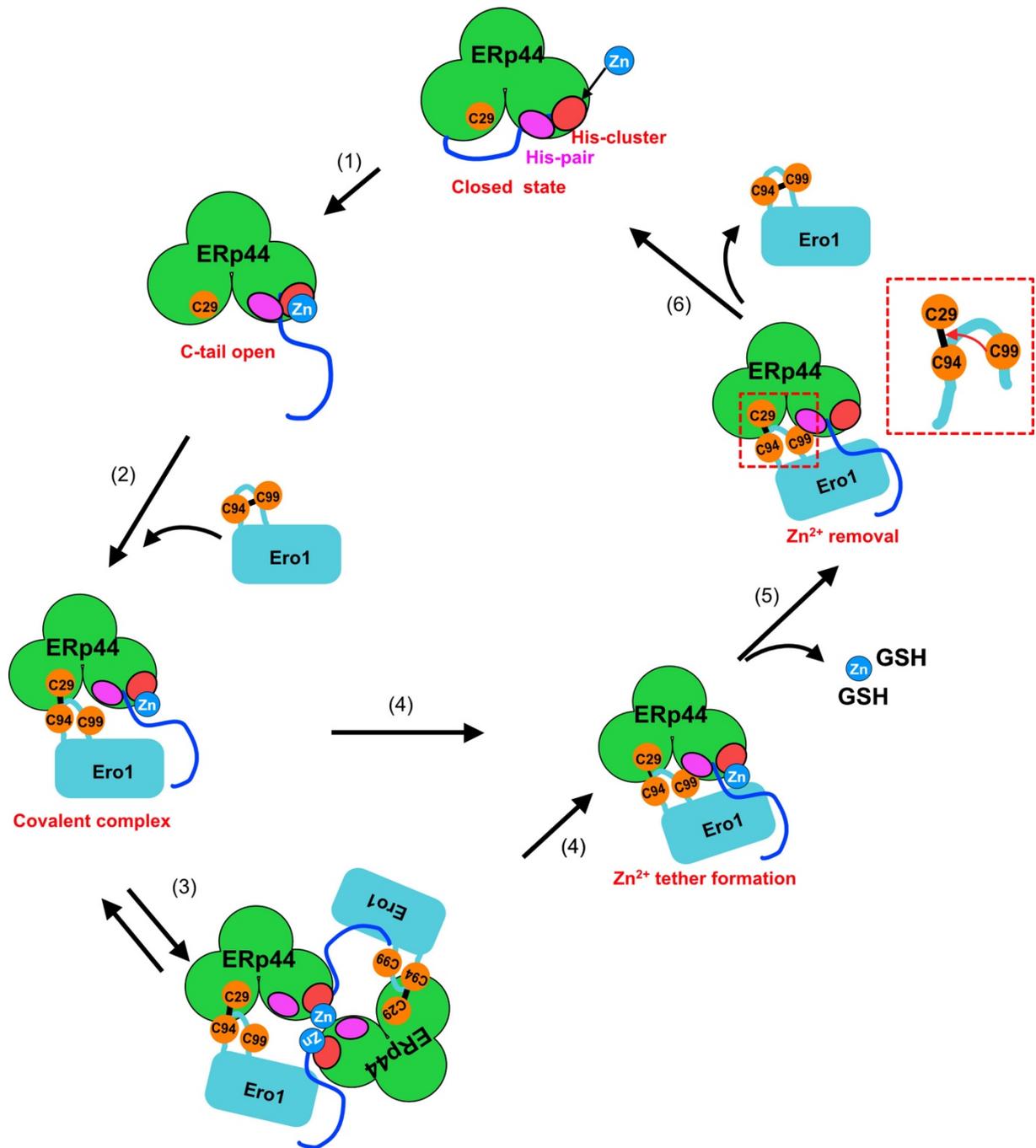
**Supplementary Fig. 8 Prediction of Zn<sup>2+</sup>-mediated interactions between ERp44 and other clients**

**a.** AlphaFold3 (AF3)-predicted model of the complex between ERp44 (cyan) and the adiponectin trimer (green, magenta and pink) in the presence of Zn<sup>2+</sup> (gray sphere).

**b.** AF3 predicted model of the complex between ERp44 (cyan) and the Prx4 dimer (green, magenta) in the presence of Zn<sup>2+</sup> (gray sphere).

**c.** Crystal structure of the ERp44-Prx4 complex in the absence of Zn<sup>2+</sup> (PDB ID 5HQP).





**Supplementary Fig. 10 Mechanisms of Ero1 $\alpha$  recognition and release by ERp44**  
 Proposed model for Zn<sup>2+</sup>-dependent, stepwise recognition and release of Ero1 $\alpha$  by ERp44.