

1.15 Å Resolution Structure of the Proteasome Assembly Chaperone Nas2 PDZ Domain

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Supplementary figures

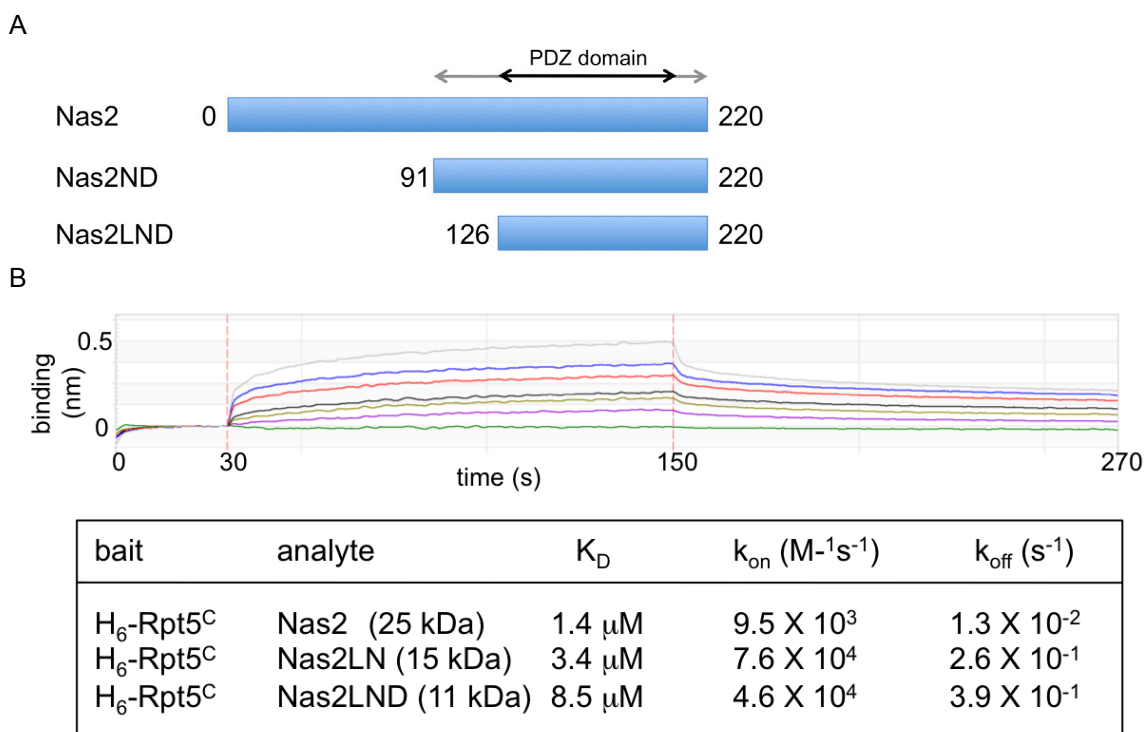


Fig. S1. The PDZ domain of Nas2 binds Rpt5.

(A) Topology of Nas2 and truncations used in this study. Predicted region of PDZ domain is indicated. Both truncations bind to the C-domain of Rpt5 (Rpt5^C) as determined by GST-pulldown assays using assays described previously (data not shown; Lee *et al.*, 2011). (B) Quantitative analysis of Nas2-Rpt5 C-domain interaction using Bio-Layer Interferometry on the BLItz (ForteBio). The C-domain of Rpt5 (Lee *et al.*, 2011) was captured on Ni-NTA biosensor (ForteBio), and binding with increasing concentrations of analyte was measured using the BLItz. Upper panel shows base-line corrected data for the binding of Rpt5 C-domain with Nas2. Table shows quantitative analyses for Nas2 and the truncated versions Nas2ND and Nas2LND.

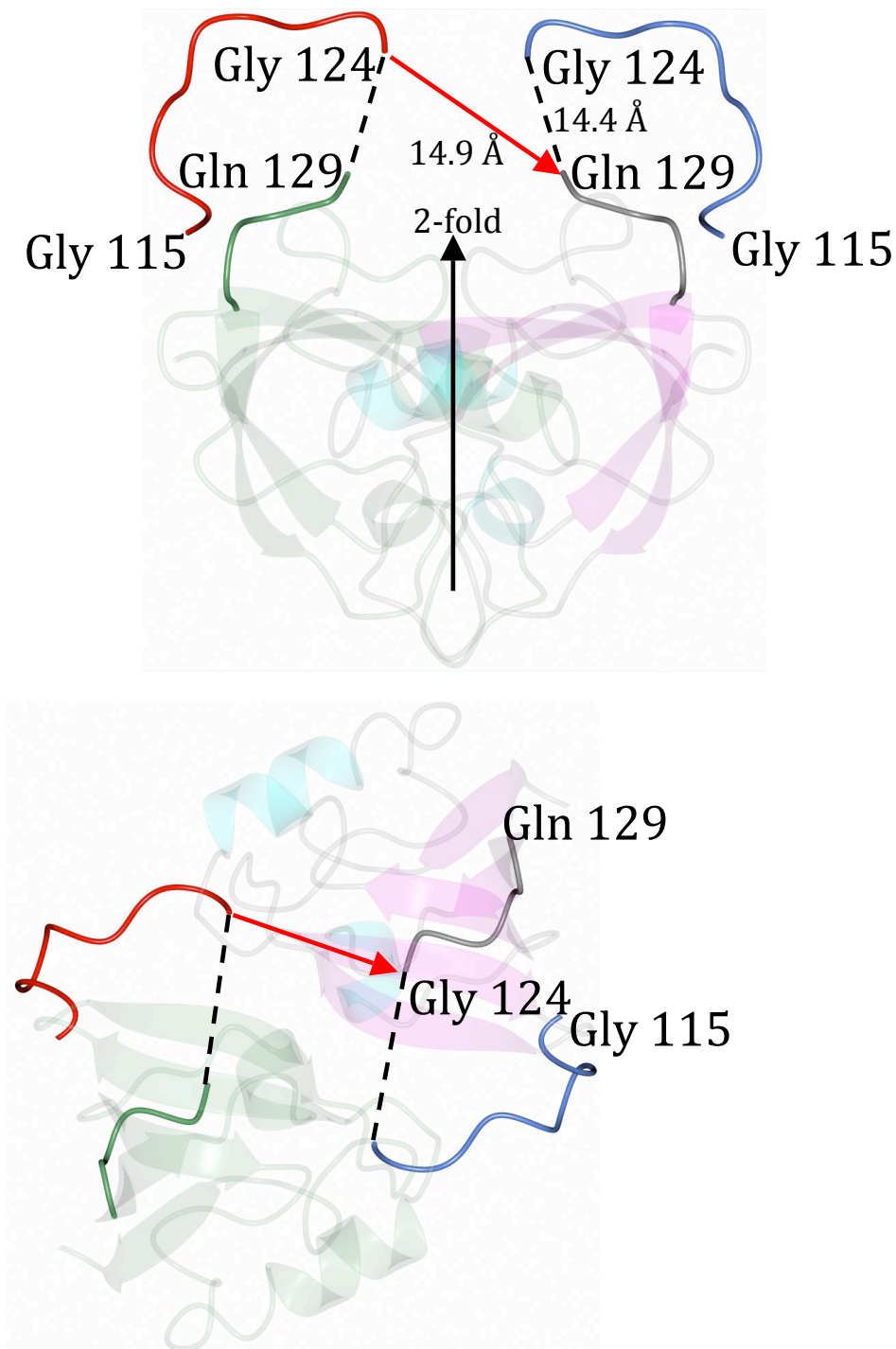


Figure S2. Top: Asymmetric unit of Nas2 LND colored by secondary structure: sheet (magenta) and helix (cyan). The disordered region is indicated by the dashed line. N-terminal residues resulting from cloning that could be modeled are colored blue. A molecule related by a 2-fold crystallographic axis ($y, x - z$) is colored green and its respective N-terminal residues resulting from cloning are colored red. View is normal to the crystallographic 2-fold axis. The distance between C α atoms of Gly 124 and Gln 129 is 14.4 Å in the current asymmetric unit. However, a comparable distance is found between C α atoms of Gly 124 from a molecule related by a crystallographic 2-fold axis and Gln 129 in the asymmetric unit is comparable 14.9 Å. Therefore it is not entirely clear if the N-terminal residues are connected to Gln 129 as modeled in the current asymmetric unit or as indicated by the red arrow. However, the orientation of Gly124 and Gln129 in the asymmetric unit appears to be sensible. **Bottom:** Same as the top figure but viewed along the crystallographic 2-fold axis.

