PNAS
www.pnas.org

Supplementary Information for

Structural basis for autophagy inhibition by the human Rubicon-Rab7 complex

Hersh K. Bhargava[1,2,9], Keisuke Tabata[4], Jordan M. Byck[1,2], Maho Hamasaki[3], Daniel P. Farrell[5,6], Ivan Anishchenko[5,6], Frank DiMaio[5,6], Young Jun Im[7], Tamotsu Yoshimori[3,4], James H. Hurley[1,2,8,*]

James H. Hurley
Email: jimhurley@berkeley.edu

This PDF file includes:

Tables S1

www.pnas.org/cgi/doi/10.1073/pnas.2008030117

Table S1. Crystallographic Data Collection and Refinement Statistics

	Human Rubicon RH Bound to GTP-Rab7 (PDB ID: 6WCW)
Data Collection	
Space Group	$I2_1$
Unit Cell Dimensions a, b, c (Å) α, β, γ (°)	 60.04, 45.33, 186.28 90.00, 98.51, 90.00
Resolution (Å)	92.11 - 2.80 (2.95 - 2.80)
R_{pim}	0.1638 (0.3938)
I/σ(I)	6.4 (2.2)
Completeness (%)	99.1 (98.8)
Redundancy	2.8 (2.8)
Refinement	
Resolution (Å)	92.11 - 2.80
No. of reflections	171,883 (17,031)
R_{work}/R_{free} (%)	19.39/26.54
Number of atoms Protein Ligand/Ion	 3414 33
B factors protein (Å^2) Protein Ligand/Ion	 58.06 49.57
RMS Deviations Bond Lengths (Å) Bond Angles (°)	 0.009 1.05
Values in parentheses are for the highest-resolution shell.	