SUPPLEMENTARY MATERIAL

SUPPLEMENTARY FIGURES

Supplementary Figure 1. Canonical TPR subunits of the APC/C are structurally related homo-dimers forming 14 contiguous TPR motifs. (**A**) Schematic of Cdc23 structure. (**B**) Multiple sequence alignment of Cdc23, Cdc27 and Apc7. Invariant and conserved residues are coloured red and yellow, respectively. Residues at the dimer interface of Cdc23 are shown with blue arrows. The corresponding cluster indicated in **Figure 2A** is indicated. Residues involved in the Apc7 crystal dimer are indicated with green circles [36]. Consensus TPR residues (8, 20 and 27) are indicated. Essential residues that define the two mutable domain of *S. cerevisiae* Cdc23 [32] are indicated with purple arrows within the N-terminal dimerisation domain, and TPR motifs 9-11 of the C-terminal domain. The *S. pombe* Nuc2 ts mutant [52] is indicated with a blue arrow. Figure produced using ALSCRIPT [51].

Supplementary Figure 2. Mapping residues of the N-terminal mutable domain of *S. cerevisiae* Cdc23 [32] onto the *S. pombe* Cut23/Cdc23 structure (in yellow).

Supplementary Figure 3. Comparison of the dimer interface of $Cdc23^{Nterm}$ with the crystal structure of Apc7 (167 residues, PDB:3FFL) [36].

Supplementary Figure 4. Detection of twinning. Left, self-rotation function plot at κ=180º for the native $Cdc23^{Nterm}$ crystal (**A**), for an EMTS crystal soaked (**C**) and for SeMet labelled crystal (**E**). Right, corresponding cumulative intensity difference plot

of the intensity difference of local pairs of intensities that are not twin-related |L| [L = [I(h1)-I(h2)]/[I(h1) + I(h2)]] against the cumulative probability distribution N(L) of the parameter L [53]. The expected plots for untwinned (blue), twinned acentric data (green) and the calculated plots (red).

Supplementary Figure 5. Electron density maps calculated for SeMet data obtained from density modification followed by heavy atom SAD-phasing. Stereoview of the map with Cα-trace of the final model docked (left) and the electron density for TPR3 (right) shown for $P4_3$ twinned-uncorrected (**A**) data, $P4_3$ twinned-corrected data (**B**) and P1 data with twin-corrections specific to P4 applied (**C**).

ADDITIONAL SUPPLEMENTARY REFERENCES

52. Hirano, T., Hiraoka, Y. & Yanagida, M. (1988). A temperature-sensitive mutation of the Schizosaccharomyces pombe gene nuc2+ that encodes a nuclear scaffold-like protein blocks spindle elongation in mitotic anaphase. *J Cell Biol* **106**, 1171-83.
53. Padilla, J. E. & Yeates, T. O. (2003). A statistic for local intensity differences: robustness to anisotropy and pseudo-centering and utility for detecting twinning. *Acta Crystallogr D Biol Crystallogr* **59**, 1124-30.
54. Davis, I. W., Leaver-Fay, A., Chen, V. B., Block, J. N., Kapral, G. J., Wang, X., Murray, L. W., Arendall, W. B., 3rd, Snoeyink, J., Richardson, J. S. & Richardson, D. C. (2007). MolProbity: all-atom contacts and structure validation for proteins and nucleic acids. *Nucleic Acids Res* **35**, W375-83.

Table S1. Data collection and refinement statistics

Data Collection Statistics				
	Hg	Native	Se-Met-P1	Se-Mer-P4
Beam line	ESRF ID29	ESRF ID14-4	DLS I04	DLS I04
Space Group	$P4_32_12$	$P4_3$	P1	$P4_1$
Unit Cell Parameters				
a (Å)	56.8	61.2	60.3	60.3
b (Å)	56.8	61.2	60.3	60.3
c (Å)	154.8	151.4	151.6	151.6
α(°)	90	90	90	90
β(°)	90	90	90	90
γ(°)	90	90	90	90
Z	1	2	8	2
Resolution limits **(**Å)	46-1.90 (2.0-1.90)	76-2.20 (2.32-2.20)	28-3.20 (3.37-3.20)	28-3.20 (3.37-3.20)
R_{merge}	0.114 (0.694)	0.084 (0.522)	0.08 (0.740)	0.10 (0.584)
I/σ (I)	18.8 (4.8)	11.4 (2.2)	9.2 (1.9)	18.1(3.3)
Total number unique	20943 (2959)	27871 (3834)	35156 (5121)	8971(1292)
Completeness (%)	99.9 (99.6)	98.6 (93.3)	99.7 (99.9)	99.9(100)
Multiplicity	23.7 (18.8)	4.5 (3.3)	6.0 (5.9)	23.5(23.5)
Anomalous completeness (%)	100.0 (99.7)	95.5 (83.9)	97.4 (97.8)	99.9(100)
Anomalous multiplicity	12.9 (9.9)	2.3 (1.6)	3.0 (3.0)	11.8(11.6)

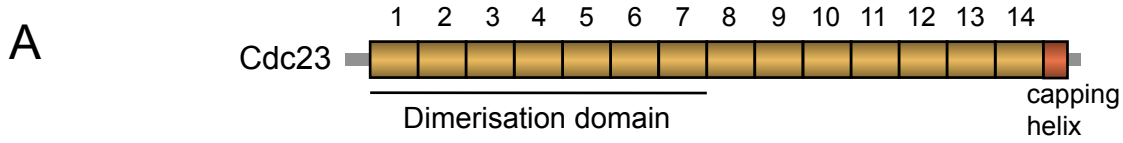
Refinement Statistics		
Resolution limits **(**Å)	40-1.9	57-2.2
Number of reflections		
Working set	38206 [+]	26415
Test set	1959 [+]	1408
R_{work}/R_{free}	0.1732/0.1995	0.1512/0.1768
Number of atoms		
Protein	2001	3867
Ligand	76	119
Mean B-factors		
Protein atoms **(**$Å^2$)	30.69	39.56
Ligand atoms **(**$Å^2$)	39.12	48.47
RMSD from Ideal values		
Bond length **(**Å)	0.007	0.007
Bond angles (°)	0.925	0.904
Ramachandran plot Statistics [++]		
Preferred (%)	98.74	98.26
Allowed (%)	1.26	1.74
PDB accession codes:	3ZN3	

+ Anomalous data

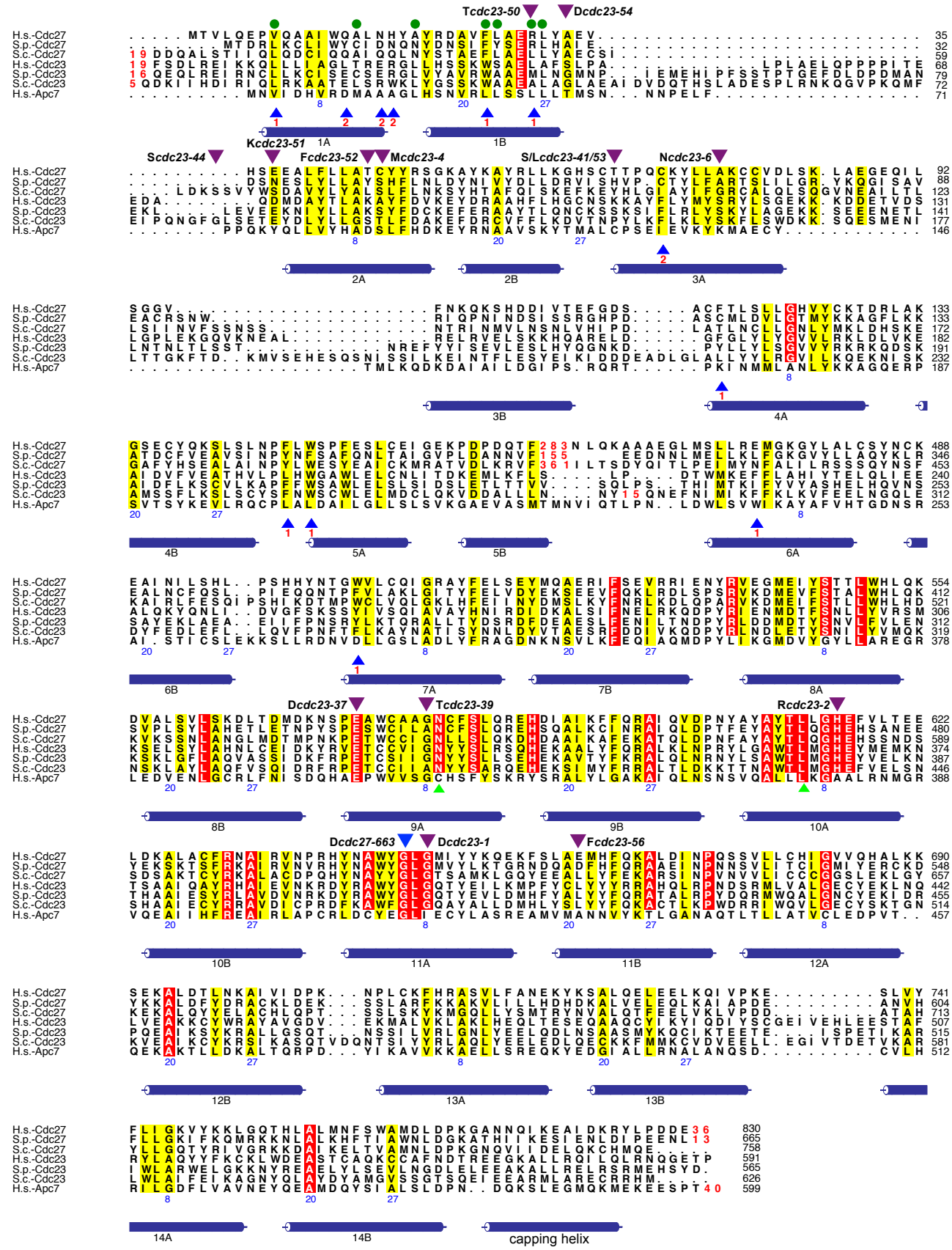
++ *Ramachandran* map definitions from *Molprobity* [54]

Values in parentheses are for the highest resolution shell.

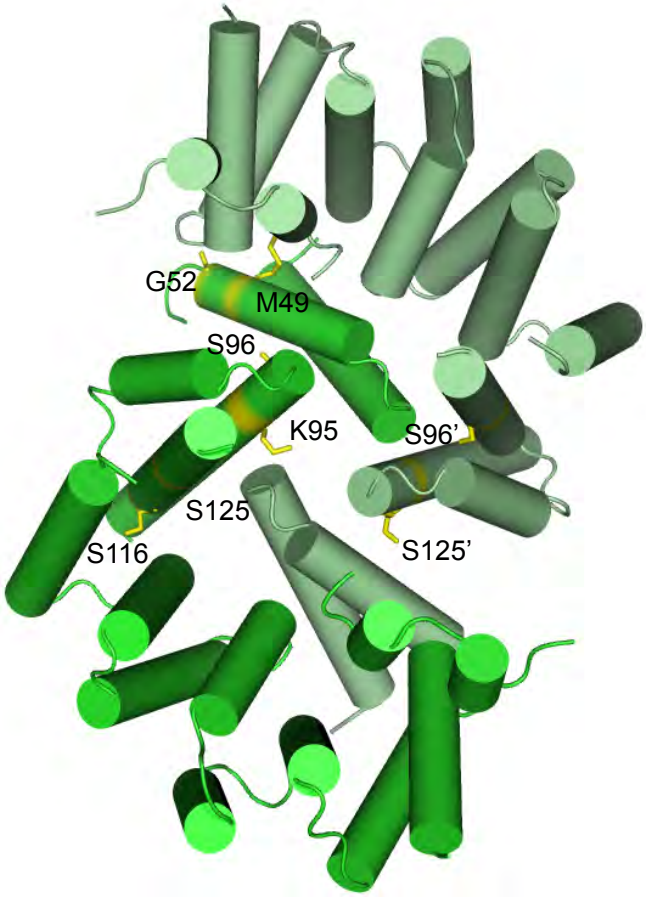
Supplementary Figure S1



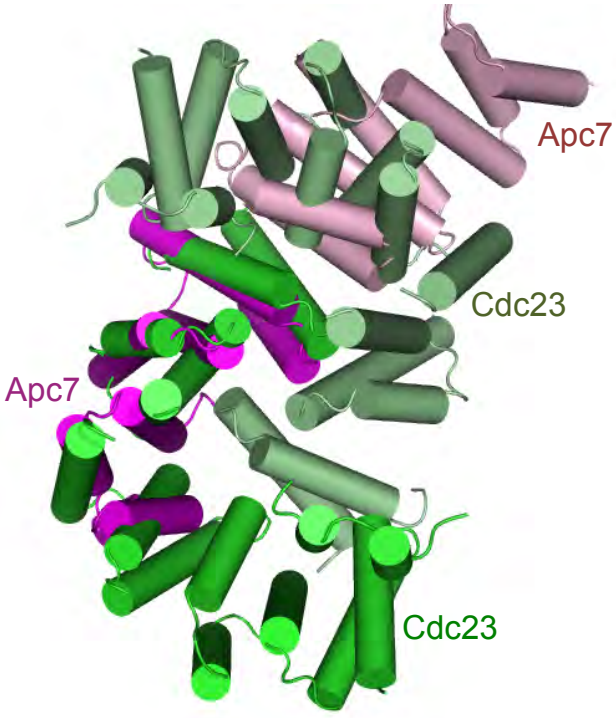
B



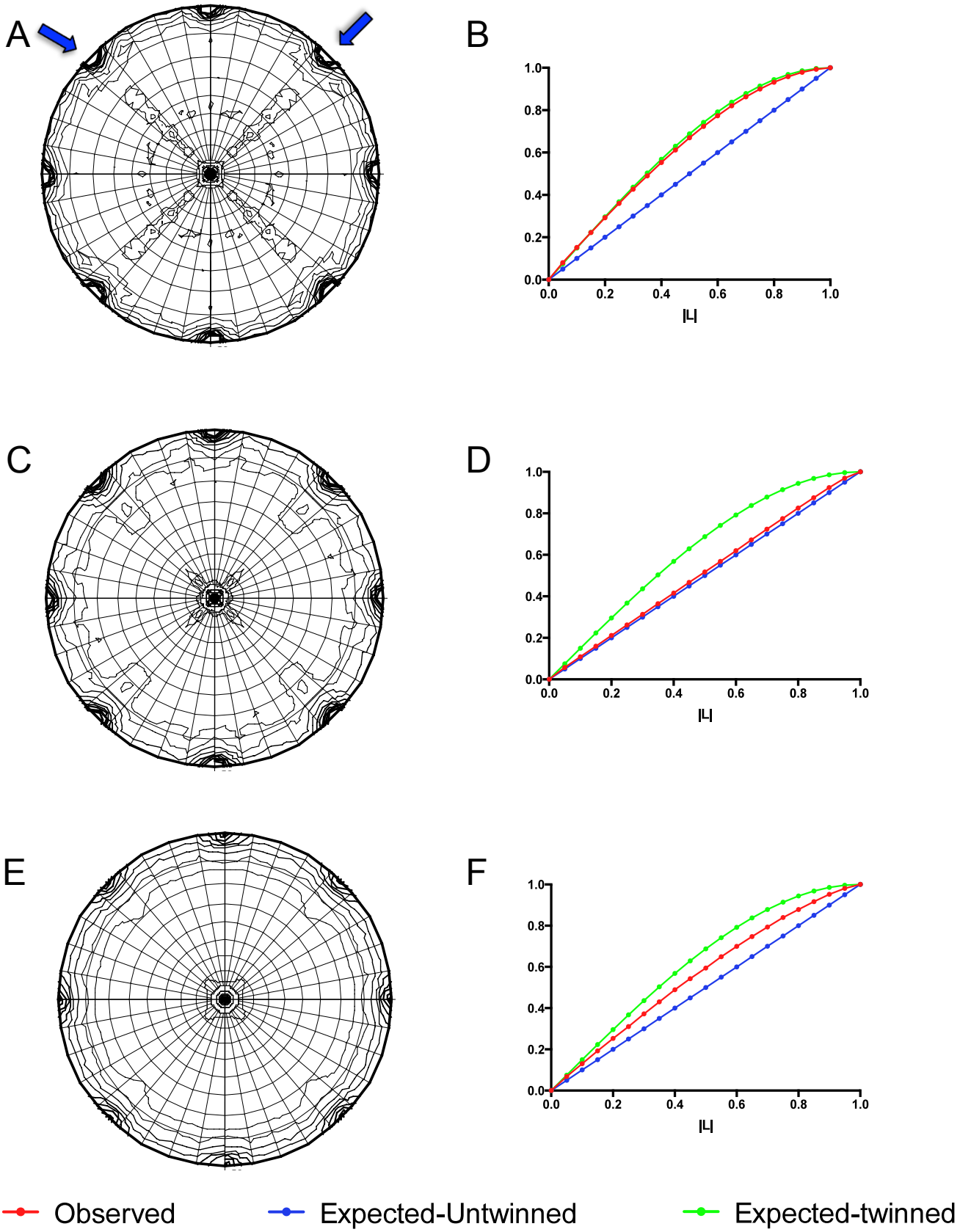
Supplementary Figure 2



Supplementary Figure 3



Supplementary Figure 4



Supplementary Figure 5