# Mechanism of 5' Topoisomerase II DNA adduct repair by mammalian Tyrosyl DNA phosphodiesterase 2 (Tdp2)

Matthew J. Schellenberg<sup>1</sup>, C. Denise Appel<sup>1</sup>, Sanjay Adhikari<sup>2</sup>, Patrick D. Robertson<sup>1</sup>, Dale A. Ramsden<sup>3</sup>, and R. Scott Williams<sup>1\*</sup>

<sup>1</sup>Laboratory of Structural Biology, National Institute of Environmental Health Sciences, NIH, DHHS, Research Triangle Park, NC 27709, USA <sup>2</sup> Department of Oncology, Lombardi Comprehensive Cancer Center, Georgetown University Medical Center, Washington, DC 20057, USA <sup>3</sup> Department of Biochemistry and Biophysics, Lineberger Comprehensive Cancer Center, and Curriculum in Genetics and Molecular Biology, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina 27599, USA.



**Supplementary Fig 1. hTdp2 proteolysis.** Full length human Tdp2 protein (FL) was incubated with trypsin, analyzed by SDS-PAGE, and stained with Coomassie blue. The catalytic domain of Tdp2 (cat) is resistant to proteolysis.



**Supplementary Fig. 2. Structure based sequence alignment of Tdp2 homologs.** Sequence alignment of *Homo sapiens* (HsTdp2), *Mus musculus* (MmTdp2), *Gallus gallus* (GgTdp2), *and Bos taurus* (BtTdp2). Mutations used in this study are shown with red letters. Resides that coordinate the catalytic Mg<sup>2+</sup> ion are indicated with gray circles, residues which contact DNA are indicated with blue circles, and residues which contact the adducted tyrosine are indicated with pink circles. Conserved motifs are labeled as M1-M8.



**Supplementary Fig. 3 hTdp2 small angle X-ray scattering SAXS** (a) Merged SAXS profile of full length human Tdp2 (blue) and Tdp2<sup>cat</sup> (red). (b) Guinier plot for full length human Tdp2 (blue) and Tdp2<sup>cat</sup> (red) is linear, indicating the absence of aggregated protein. (c) Small angle X-ray scattering (SAXS) electron pair distribution function calculated from X-ray scattering curve for full length human (FL) and amino acids 108-362 (cat) of human Tdp2.



**Supplementary Fig. 4 Tdp2 catalytic activity.** (A) hTdp2 was incubated with the T5PNP substrate and 1 mM of the indicated divalent metal ion for 30 minutes. The reaction product was detected by measuring the absorbance at 415 nm. (b) 1 μM substrate DNA (a 16 nucleotide FITC labeled 5'-Y oligo duplexed with a 12, 14, 15, or 16 nucleotide unlabelled strand to form the indicated length of 5' overhang) was incubated with 100nM hTdp2<sup>cat</sup> protein. Products were analyzed on a TBE-urea 15% PAGE.



**Supplementary Fig. 5 mTdp2**<sup>cat</sup> **DNA complex crystal structures.** (a) mTdp2<sup>cat</sup> was crystallized with selfcomplimentary oligonucleotides. Complex II and complex III contain two Tdp2 molecules bound to opposite ends of the DNA duplex in similar conformations related by non-crystallographic 2-fold symmetry. The asymmetric unit for complex I is analogously arranged, but contains 6 Tdp2 molecules (3 2-ended DNA complexes). (b) The asymmetric unit contains two Tdp2<sup>cat</sup> proteins (yellow and orange) bound to catalytic magnesium ions (purple). The final 2Fo-Fc map (blue) contoured at 1.5 $\sigma$  shows good electron density for the bound product DNA.



**Supplementary Fig. 6.** Protein contacts to DNA in complexes I, II and III. Each mTdp2<sup>cat</sup> protein makes extensive contacts to the 5'-terminus of bound strands (blue DNA bases) from conserved Tdp2 residues. Tdp2 residues are colored according by motif coloring (M1-M8) as in Fig. 3a, 3c and Supplementary Fig.2.



**Supplementary Fig. 7. SDS PAGE analysis of purified mutant hTdp2-MBP proteins.** Purified MBP-Tdp2<sup>cat</sup> proteins analyzed by SDS-PAGE and stained with Coomassie blue.

## Supplementary Table 1. Small angle X-ray scattering statistics

Protein	Full length hTdp2	hTdp2 <sup>cat</sup>
Rg - measured from Guinier plot	$29.0 \pm 0.4$ Å	$20.2 \pm 0.3$ Å
Rg - calculated from P(r)	$29.7 \pm 0.2$ Å	$19.7 \pm 0.1 \text{ Å}$
Dmax for P(r) plot	102 Å	56 Å

#### Supplementary Table 2. Tdp2 crystallization Oligos

Oligo Name	5' modification	Sequence	3' modification
12SA		CATCCGAATTCG	
5Y-9SA	phosphotyrosine	CCGAATTCG	
5N-9SA	5'-6-aminohexanol	CCGAATTCG	

#### Supplementary Table 3. Tdp2 duplex DNA substrates

Figure panel	Substrate name	Component oligos (sequences in Supp. Table 4)	
1g	Single-stranded	5-Y-16	
1g	5'-overhang	5-Y-16/12R	
1g	Blunt	5-Y-16/16R	
1g	5'-recessed	5-Y-16/20R	
1f,h,i	5'-Y	5-Y-16/12R	
1f,h,i	3'-Y	3-Y-16/12R	
1f,i	5'-N	5-N-16/12R	
1f,i	5'-A	5-A-16/12R	
2a		5N-9SA	
2b		5P-9SA - processed by Tdp2	
2c		12SA	
4c	all	5-Y-16/12R	
Sup. Fig. 4b	4nt	5-Y-16/12R	
Sup. Fig. 4b	1nt	5-Y-16/15R	
Sup. Fig. 4b	2nt	5-Y-16/14R	
Sup. Fig. 4b	Blunt	5-Y-16/16R	

### Supplementary Table 4. Tdp2 substrate Oligo sequences

Oligo Name	5' modification	Sequence	3' modification
5-Y-16	phosphotyrosine	CATCGTTGCCTACCAT	FITC
5-N-16	6-carbon amine	CATCGTTGCCTACCAT	FITC
5-A-16	dSpacer	CATCGTTGCCTACCAT	FITC
3-Y-16	FITC	ATGGTAGGCAACGATG	phosphotyrosine
12R		ATGGTAGGCAAC	
14R		ATGGTAGGCAACGA	
15R		ATGGTAGGCAACGAT	
16R		ATGGTAGGCAACGATG	
20R		ATGGTAGGCAACGATGTAGT	
12		GTTGCCTACCAT	