SUPPLEMENTAL DATA

A Helical Bundle in the N-terminal Domain of the BLM Helicase Mediates Dimer and Potentially Hexamer Formation

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Running title：Structures of the N-terminal DHBN domain of BLM helicases

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SUPPLEMENTAL FIGURE LEGENDS

Fig.S1 The phylogenetic tree of all BLM homologous sequences from Reference Proteomes database constructed by PhyML and rendered with evolview. All of the conserved domains are schematically shown with different colors.

Fig.S2 DNA steady-state fluorescence anisotropy assays of the four truncated gBLM proteins with fD20S12 substrate. The assays were performed by Infinite F2000 instrument (TECAN). The buffer used was 20 mM Tris–HCl pH 7.5, 50 mM NaCl, 3 mM $MgCl_2$ and 1 mM DTT. 5 nM DNA substrate was incubated with each protein at different concentrations at 25 ˚C for 5 min, respectively. Then the data were analyzed to calculate the equilibrium dissociation constant (K_d) as described previously (Ref 1).

SUPPLEMENTAL FIGURES

Fig.S1

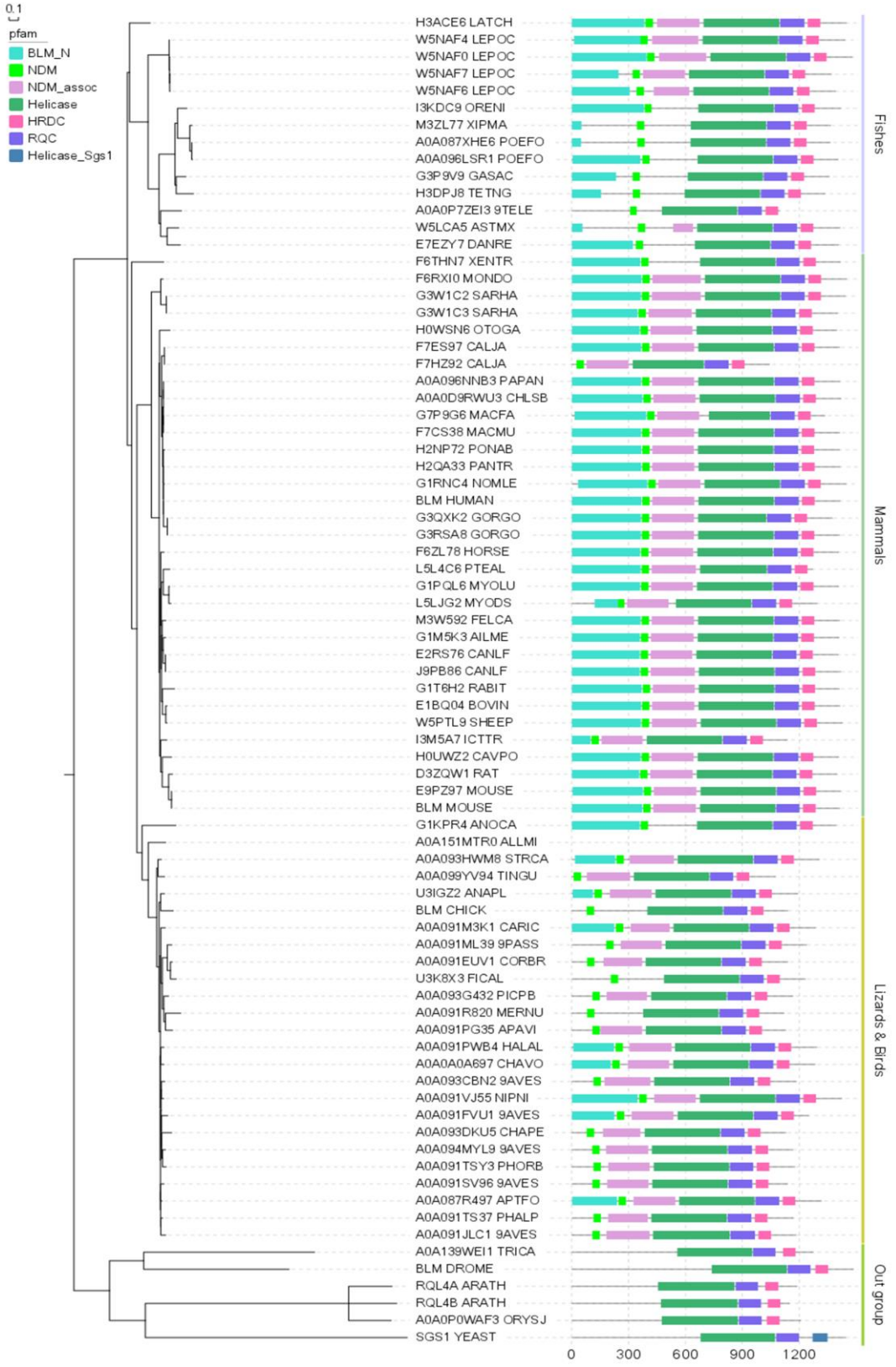
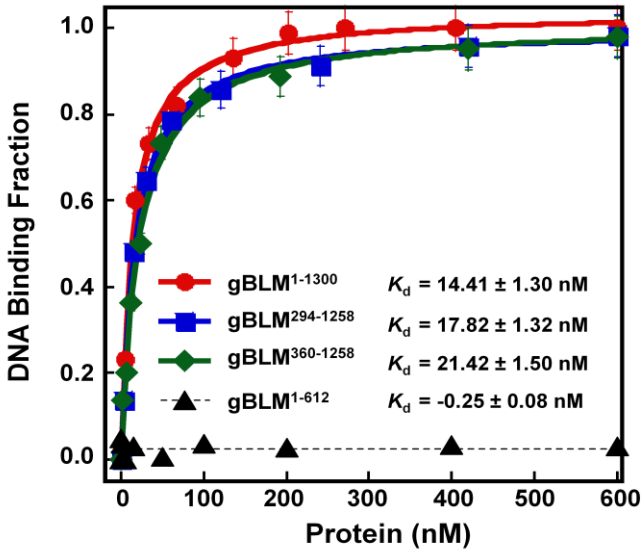


Fig.S2



SUPPLEMENTAL TABLES

Table S1. Enzymatic activity comparisons between hBLM and gBLM.

Protein	ATPase	DNA binding	DNA unwinding
hBLM	k_{cat} = 24.00 s^{-1} K_{ATP} = 20.80 μM (Ref 2)	----	A* ≈ 0.60 (EMSA assay) (Ref 3)
$gBLM^{1-1300}$	k_{cat} = 20.10 s^{-1} K_{ATP} = 20.20 μM	K_d = 14.41 nM	A = 0.58 V* = 0.74

* A, amplitude; V, rate. Each data of $gBLM^{1-1300}$ was calculated from three independent measurements.

Table S2. ATPase activity determination of the different gBLM deletions.**

Protein	k_{cat} (s^{-1})	K_{ATP} (μM)
$gBLM^{1-1300}$	21.5	20.2
$gBLM^{294-1258}$	20.8	19.5
$gBLM^{360-1258}$	21.1	18.3
$gBLM^{610-1258}$	22.1	19.5

******ATPase activity measurements were determined under the same experimental conditions of the DNA unwinding assays.

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