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Supporting information for article:

A structural study of TatD from *Staphylococcus aureus* elucidates a putative DNA-binding mode of a Mg²⁺-dependent nuclease

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Supporting information**Table S1** Primer design for SAV0491 wild type and mutants. Sites for site-directed mutagenesis are underlined in black. Single-letter abbreviations for amino acid residues: H, histidine; A, alanine; E, glutamic acid; and D, aspartic acid.

Mutated sites		Primer sequence (5'→3')
H6A	Forward	G TTA ATC GAT ACA <u>GCC</u> GTC CAT TTA AAT GAT G
	Reverse	C ATC ATT TAA ATG GAC <u>GGC</u> TGT ATC GAT TAA C
H8A	Forward	C GAT ACA CAT GTC <u>GCC</u> TTA AAT GAT GAG CAA TAC
	Reverse	GTA TTG CTC ATC ATT TAA <u>GGC</u> GAC ATG TGT ATC G
H63A	Forward	GGC ATT ATC GGT TGG <u>GCC</u> CCA GTT GAC GCA ATT G
	Reverse	C AAT TGC GTC AAC TGG <u>GGC</u> CCA ACC GAT AAT GCC
H128A	Forward	G TTA CCA ATT ATC ATT <u>GCC</u> AAC CGT GAA GCA ACT C
	Reverse	G AGT TGC TTC ACG GTT <u>GGC</u> AAT GAT AAT TGG TAA C
H153A	Forward	GTA GGC GGG ATT ATG <u>GCC</u> AGC TTT AGT GGT TCT C
	Reverse	G AGA ACC ACT AAA GCT <u>GGC</u> CAT AAT CCC GCC TAC
E92A	Forward	GTG ATT GGT ATT GGT <u>GCC</u> ATG GGA TTA GAT TAT C
	Reverse	G ATA ATC TAA TCC CAT <u>GGC</u> ACC AAT ACC AAT CAC
E202A	Forward	GAG CGT TTG CTA GTT <u>GCC</u> ACC GAT GCA CCG TAT C
	Reverse	G ATA CGG TGC ATC GGT <u>GGC</u> AAC TAG CAA ACG CTC
D204A	Forward	G CTA GTT GAA ACC <u>GCC</u> GCA CCG TAT CTC TCG
	Reverse	CGA GAG ATA CGG TGC <u>GGC</u> GGT TTC AAC TAG C

Table S2 ICP-MS analysis. ND indicates “not detected”.

	Crystals dissolved in the water	SaTatD protein solution
Manganese (II)	ND	ND
Nickel (II)	112.000 ng/ml	10694.000 ng/ml
Zinc (II)	ND	4318.000 ng/ml
Calcium (II)	ND	ND
Magnesium (II)	ND	ND

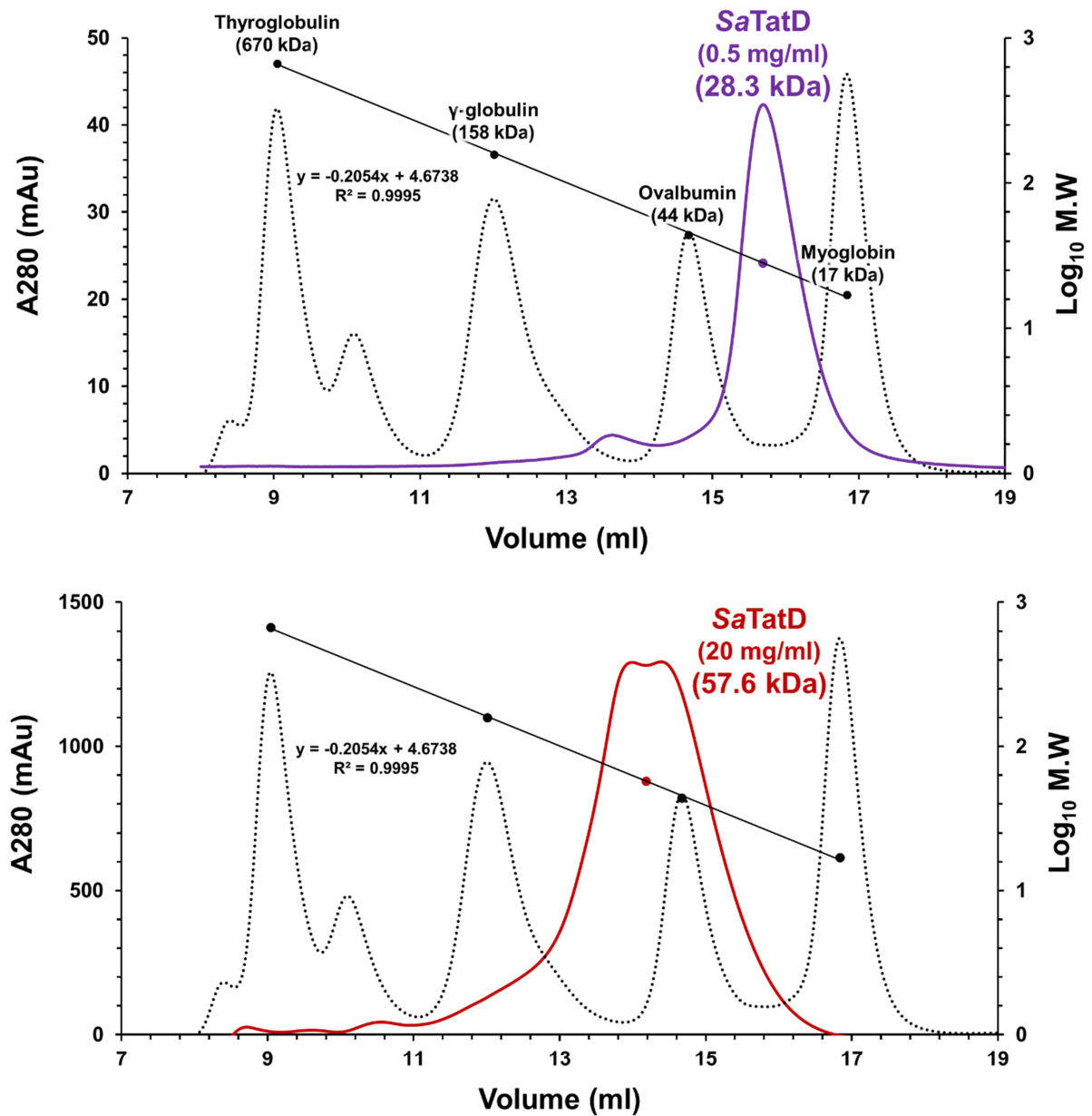


Figure S1 Identification of the oligomeric state of *SaTatD* in solution. Analytical gel filtration profiles of *SaTatD* using 0.5 and 20 mg/ml proteins. The theoretical M.W. of *SaTatD* monomer including N-terminal hexa-histidine and linker is 31.3 kDa.