Supplementary Table 1. Shared features of SMODS-related families in the DNA polymerase Beta superfamily.

DNA polβ family	protein (pdb id)	pocket description	β-spine present?	K/R1[1]	K/R2[1]	K active site[1]	comments
mab-21/cGAS-like	cGAS (4O6A)	deep, formed by dimer	yes	K	R	K	Zinc thumb upstream of lysines
	MID51 (4OAF)	deep, formed by dimer	yes	--	K	K	inactive, binds ADP in active site pocket
	MID49 (4WOY)	shallow	yes	--	--	--	inactive
OAS	OAS (4IG8)	shallow	yes	k	R	K	active
SMODS	DncV (4TY0)	deep, formed by dimer	yes, elongated	r	R	K	active
archaeal CCA-adding	tRNA CCA-adding (2ZH1)	shallow	yes	--	R	K	active
eukaryotic PAP	poly(A) polymerase (1Q79)	shallow	yes, elongated	r	R	K	active
NF45/NF90/DZF	NF45 (4AT8A)	deep, formed by tetramer	yes	k	R	K	inactive, binds NTP
	NF90 (4AT8B)	shallow	yes	--	R	R	no ligand reported although residues for binding remain
classic TRF	TUT7/TUT4 (4FHP)	shallow	yes	r	--	K	active
	MTPAP (3PQ1)	deep, formed by RRM fusion	yes, occluded by N-terminal RRM domain	R	--	R	active
	RET1 (2IKF)	none	yes	R	--	K	active
	TRF4 (3NYB)	shallow	yes	--	--	K	active
NRAP	NRAP-N (4M5DA)	none	yes, elongated N-terminal segment	--	--	k	inactive, no ligand reported
	NRAP-C (4M5DA)	none	yes, distorted	--	R	K	inactive, no ligand reported

Footnotes:

[1] Presence/absence of key conserved lysine/arginine residues are shown. Upper-case “R” (arginine) or “K” (lysine) indicates absolute conservation across the family/subfamily including the protein listed in column 2, lower-case indicates partial conservation. “--" indicates absence of the residue.