Table S8. RMS deviations from SSM fitting between mouse SMP30/GNL in the substrate-free form and other related structures.

Enzyme	rmsd (Å)	Alignment length
mouse SMP30/GNL-1,5AG complex	0.14	297
DFPase (1PJX)*	1.8	254
Drp35 (2DG1)*	2.1	250
PON (1V04)*	2.9	234

^{*} PDB ID is given in parentheses.