

<i>Streptomyces albus</i> subsp. <i>albus</i>	167	TLIAEELT	SRGYVVAIVD	HAYE	SVGAR	FPGGRMLT	CAAC	DKYQDTGL	--	AYVAEGR	AKDVSE	LLDRLTGP	234			
<i>Streptomyces</i> sp. NRRL S-495	170	TALGEEL	AARGYAVA	AVDHTY	ETL	-VEF	PGGRIE	PCLVCG	REGTDP	DFGATAS	RVRAAD	DLRFVIDRLTAP	238			
<i>Streptomyces</i> sp. XY431	182	TALGEEL	AARGYAVA	AVDHTY	ETL	-VEF	PGGRIE	PCLVCG	REGTDP	DFGATAS	RVRAAD	DLRFVIDRLTAP	250			
<i>Streptomyces roseovercillatus</i>	177	TGLGED	LASRGY	AVA	AVDHTY	EAP	-VEF	PGGRIE	ACEIC	QKYDLLP	----	AVVPNR	SKDIRFLDQLTGP	241		
<i>Streptomyces</i> sp. MBT76	138	TALGED	LASRGY	AVA	AVDHTY	EAP	-VEF	PGGRIE	TCE	CAK	PDM	-----	AAVVRN	RAKDFSEL	LDRLTAP	201
R18	109	TALGED	LASRGY	AVA	AVDHTY	EAP	-VEF	PGGRIE	KCTL	CDDSR	MDP	----	GAVVRN	RAKDLRFVLDRLTGP	174	
TH2-18	112	TALGED	LASRGY	AVA	ALDHTY	EAP	-VEF	PGGR	VEPCL	ICEK	PDLN	-----	AVVRN	RAQDIRFLDRLTGP	175	
<i>Streptomyces caatingaensis</i>	136	TALAE	DLASRGY	VVAAL	DHTY	ESA	-VEF	PGGR	VEK	CEL	CAKEDVDN	---	GALVRN	RAEDIRFLDRLTGP	201	
<i>Streptomyces mobaraensis</i>	158	TSVAEEL	ASRGY	VVA	VDHTY	EAA	-VEF	PGGRIE	QCAI	CGPE	QRDN	---	AAVVRN	RAKDLRFVLDRLTAD	223	

Fig. S1

Conservation of CXXC motif between R18 and its homologous genes. Alignment showing the loop sequence, Cys-143, and Cys-146 on R18. Arrows represent cysteine residues in the CXXC motif.

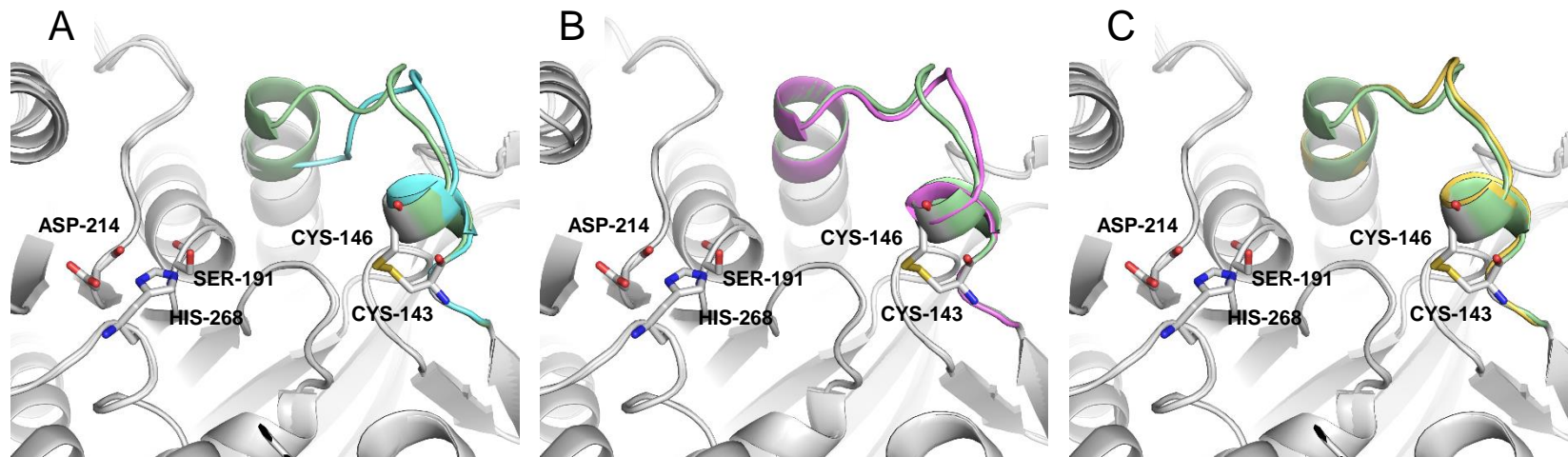


Fig.S2

Comparison of the loop structures of rR18, rTH2-18, rTH2-18PG, and rR18 Δ PG. Close-up view of the loop structures of rR18 (green) and rTH2-18 (cyan) (A), rR18 and rTH2-18PG (magenta) (B), and rR18 and rR18 Δ PG (yellow) (C). The catalytic triad, Cys-143, and Cys-146 on rR18 are represented as sticks with the oxygen atom in red, the nitrogen atom in blue, sulfur atoms in yellow, and carbon atoms in white.