

Paralog	Divergently transcribed gene	Intergenic region bp	Predicted function of gene product(s)	Comment
Family 1				
<i>mmyB</i>	<i>mmyY</i>	230	Nuclear transport factor 2-like protein	Methylenomycin biosynthesis
<i>SCO0110</i>	<i>SCO0111</i>	187	3-ketoacyl-(acyl-carrier-protein) reductase	
<i>SCO0233</i>	<i>SCO0234</i> - <i>SCO0235</i>	289	Both genes encode an SDR	
<i>SCO0236</i>	<i>SCO0237</i>	200	SDR	
<i>SCO0307</i>	<i>SCO0306</i>	123	Possible pseudogene	SCO0311 PKS; SCO0312 acyl-CoA reductase
<i>SCO0891</i>	<i>SCO0890</i>	102	SDR	
<i>SCO2501</i>	<i>SCO2502</i>	111	Similar to actinorhodin exporter ActII-2	
<i>SCO2537</i>	<i>SCO2537</i>	107	Similar to cephämycin transporter CmcT from <i>Nocardia lactamdurans</i>	Fused to SCO2538
<i>SCO4680</i>	<i>SCO4681</i> - <i>SCO4682</i>	45	SDR, downstream gene encodes 4-oxalocrotonate tautomerase	
<i>SCO4944</i>	<i>SCO4945</i>	169	MDR (alcohol dehydrogenase)	Highly conserved^
<i>SCO6926</i>	<i>SCO6925</i>	582	Membrane protein; gene contains TTA codon	Possibly controls lantibiotic cluster <i>SCO6927-6930</i>
<i>SCO7140</i>	<i>SCO7141</i> [#]	28	SDR	
<i>SCO7706</i>	<i>SCO7707</i>	138	Atu4866 family protein	SCO7705 similar to tetracyclin resistance oxidoreductase
<i>SCO7767</i>	<i>SCO7768</i> - <i>SCO7769</i>	130	Nuclear transport factor 2-like protein, similar to RANGDP-binding; fused to gene for GDP-sugar epimerase	Next to <i>SCO7766</i> , homolog of <i>actVA4</i>
<i>SCO7817</i>	<i>SCO7818</i>	117	SDR (2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase)	
Family 2				
<i>SCO6539</i>	<i>SCO6540</i> - <i>SCO6541</i>	90	DCoH domain protein; downstream gene similar to <i>S. purpurascens rdmD</i> (anthracycline biosynthesis)	Highly conserved in <i>Streptomyces</i>

[#] no shared promoter region.

[^] next to ortholog of *SCO4945* in all *Streptomyces* sp, *Rhodococcus* sp, *Saccharopolyspora erythraea*, *Kineococcus radiotolerans*, *Arthrobacter aurescens*.