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Supporting information for article:

Structural characterization of DynU16, a START/Bet v1-like protein involved in dynemicin biosynthesis

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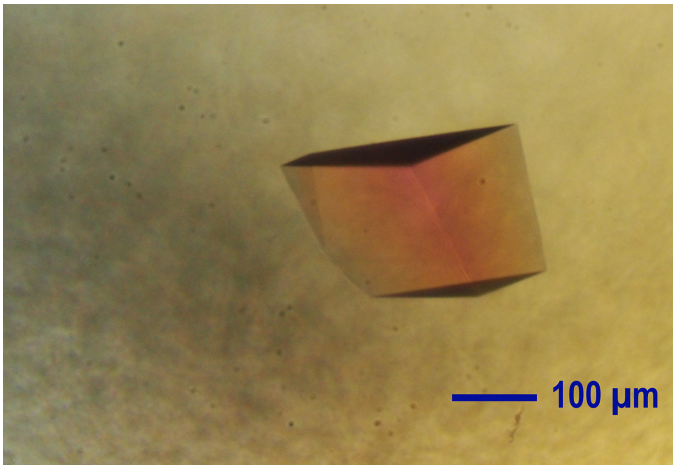


Figure S1 Crystal of DynU16 imaged with an Olympus BHTP polarizing microscope equipped with an Olympus OM-D E-M5 digital camera.

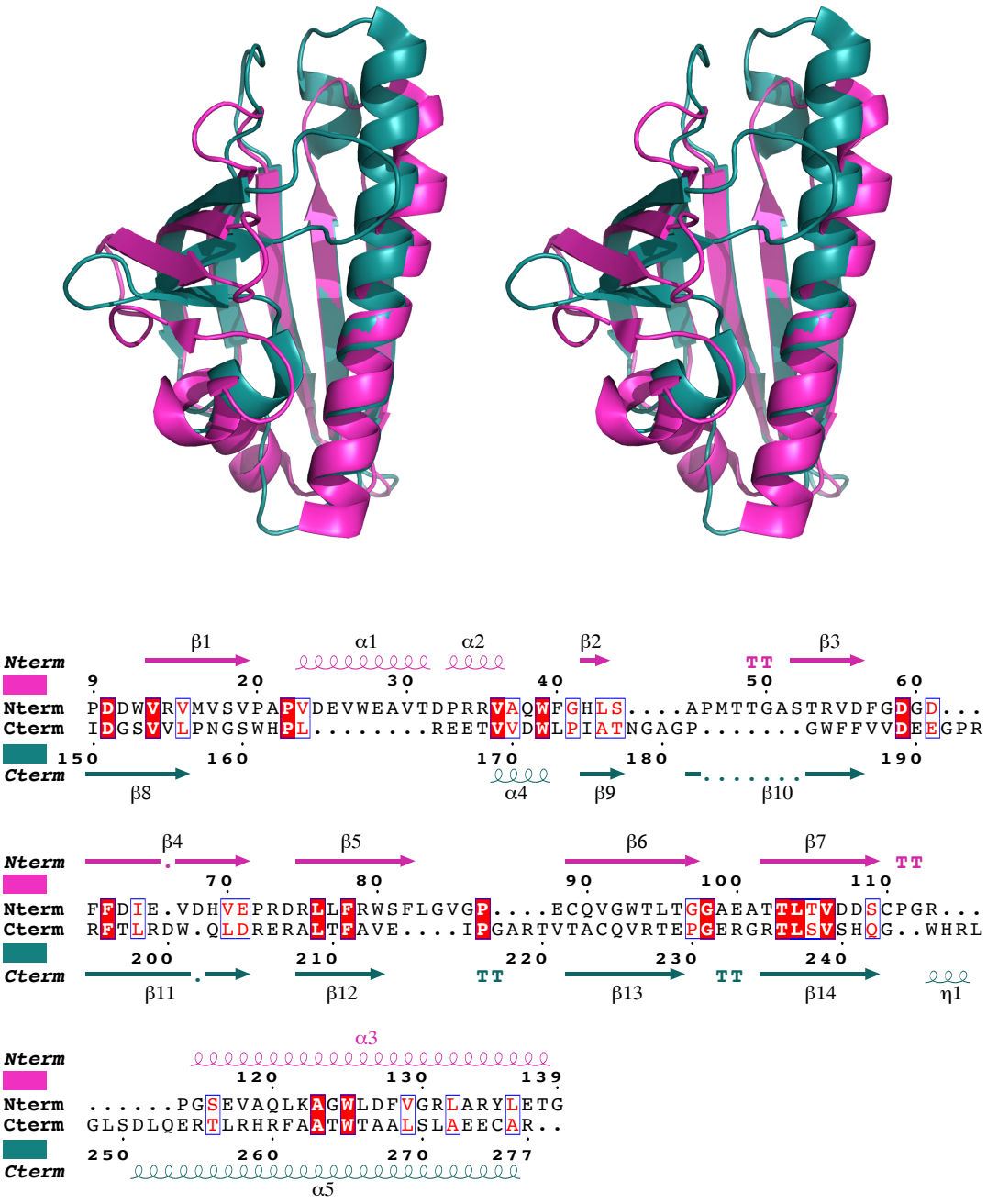
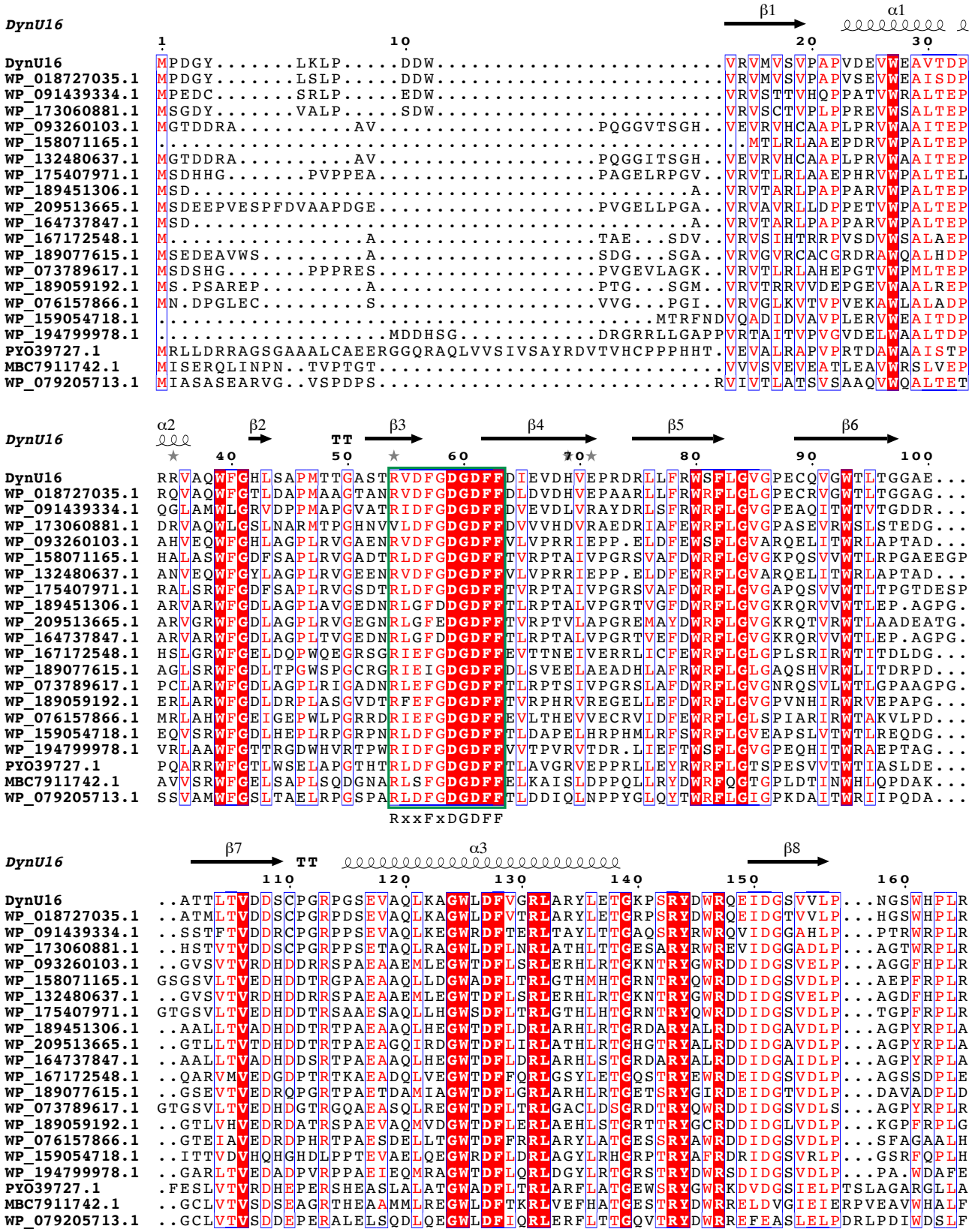
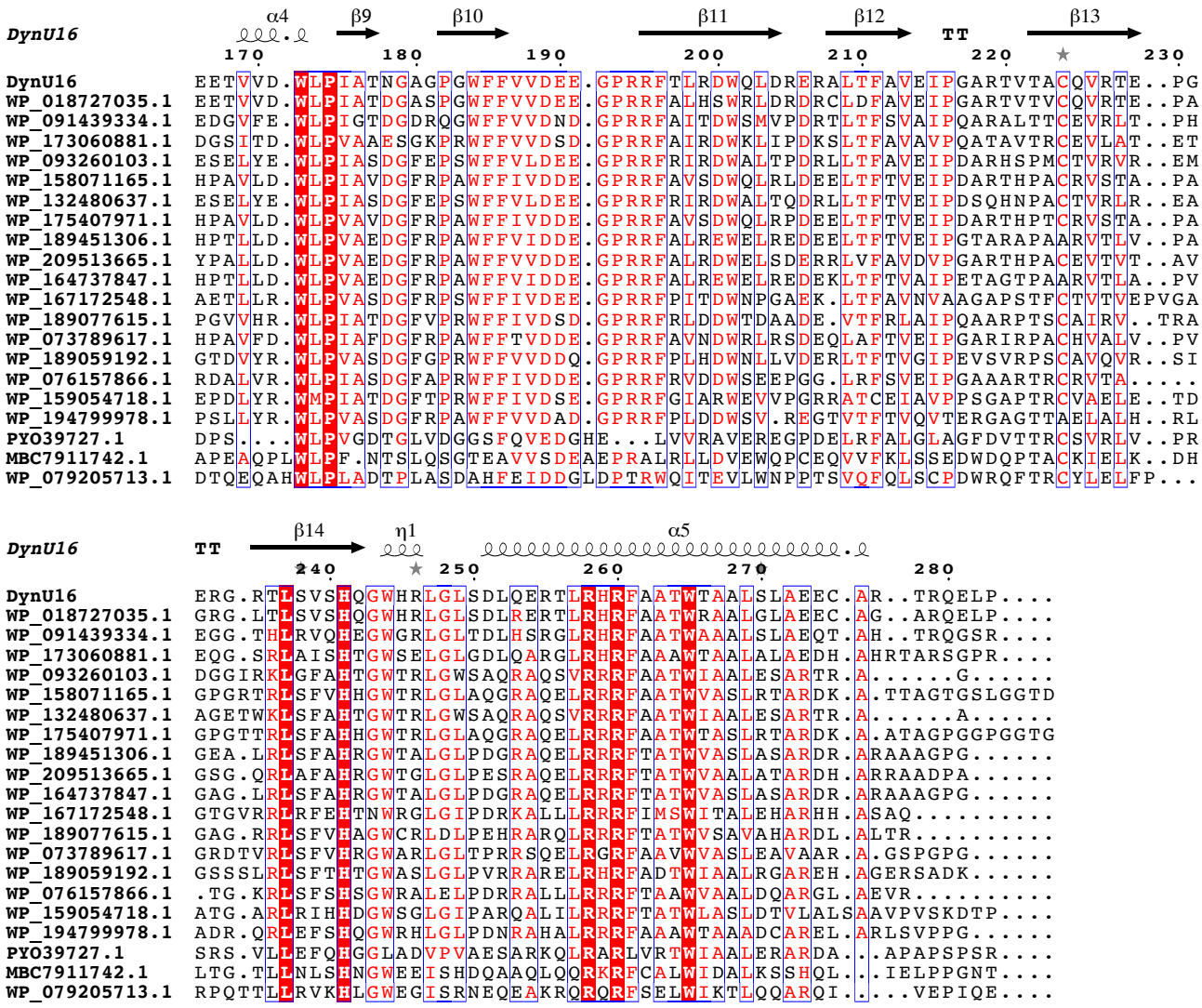


Figure S2 Superposition of the N-terminal (magenta) and C-terminal (cyan) domains of DynU16 and the resulting sequence alignment produced by the super alogrithm in *PyMOL* (v2.4.1, Schrödinger). The structural alignment was based on backbone atom positions. After refinement, the alogrithm retained 318 matched atom pairs with an RMSD of 2.0 Å. The resulting sequence alignment aligns 107 residues with 15% identity over this range. The sequence alingment was formatted using *ESPript* 3.0 (Robert & Gouet, 2014).


DynU16
β1
α1
α2
β2
TT
β3
β4
β5
β6
β7
α3
β8
RxxFxDGDFF
DynU16
WP_018727035.1
WP_091439334.1
WP_173060881.1
WP_093260103.1
WP_158071165.1
WP_132480637.1
WP_175407971.1
WP_189451306.1
WP_209513665.1
WP_164737847.1
WP_167172548.1
WP_189077615.1
WP_073789617.1
WP_189059192.1
WP_076157866.1
WP_159054718.1
WP_194799978.1
PYO39727.1
MBC7911742.1
WP_079205713.1



Accession	Evalue	%Id	Species
WP_018727035.1	3e-179	84%	*Salinispora pacifica*
WP_091439334.1	2e-119	60%	*Micromonospora yangpuensis*
WP_173060881.1	4e-106	56%	*Phytohabitans houttuyneae*
WP_093260103.1	1e-88	52%	*Saccharopolyspora shandongensis*
WP_158071165.1	8e-86	50%	*Streptomyces* sp. CB03234
WP_132480637.1	2e-85	50%	*Saccharopolyspora* sp. 7K502
WP_175407971.1	4e-85	50%	*Streptomyces* sp. TRM64462
WP_189451306.1	3e-80	48%	*Streptomyces abikoensis*
WP_209513665.1	1e-79	47%	*Streptomyces syringium*
WP_164737847.1	1e-79	48%	*Streptomyces luteoverticillatus*
WP_167172548.1	5e-77	45%	*Saccharomonospora amisosensis*
WP_189077615.1	2e-76	46%	*Mangrovihabitans endophyticus*
WP_073789617.1	4e-74	47%	*Streptomyces uncialis*
WP_189059192.1	2e-73	46%	*Longimycelium tulufanense*
WP_076157866.1	9e-71	45%	*Amycolatopsis coloradensis*
WP_159054718.1	2e-70	43%	*Streptomyces dysideae*
WP_194799978.1	5e-69	47%	*Micromonospora* sp. ANENR4
PYO39727.1	3e-49	36%	*Gemmatimonadetes* bacterium
MBC7911742.1	1e-48	33%	*Pyrinomonadaceae* bacterium
WP_079205713.1	1e-47	33%	*Microcystis aeruginosa*

Figure S3 Sequence alignment and blast E-values for 20 di-domain homologs to DynU16 identifed with NCBI blast (Altschul et al., 1997). These homologs have at least 90% coverage and over 30% identity and were clustered to retain only a single represenative sequence at 98% sequence idenity. The RxxFxDGDFF motif is highlighted in a green box between strands β3 and β4. Many of the residues conserved across all 21 protiens line the cavity with the majority of the residues from the N-terminal domain. Most of the remaining conserved residues stabilize packing between secondary structure elements. The alignment was formatted using *ESPript* 3.0 (Robert & Gouet, 2014).