SUPPLEMENTARY INFORMATION

A co-culturing approach enables discovery and biosynthesis of a bioactive indole alkaloid metabolite

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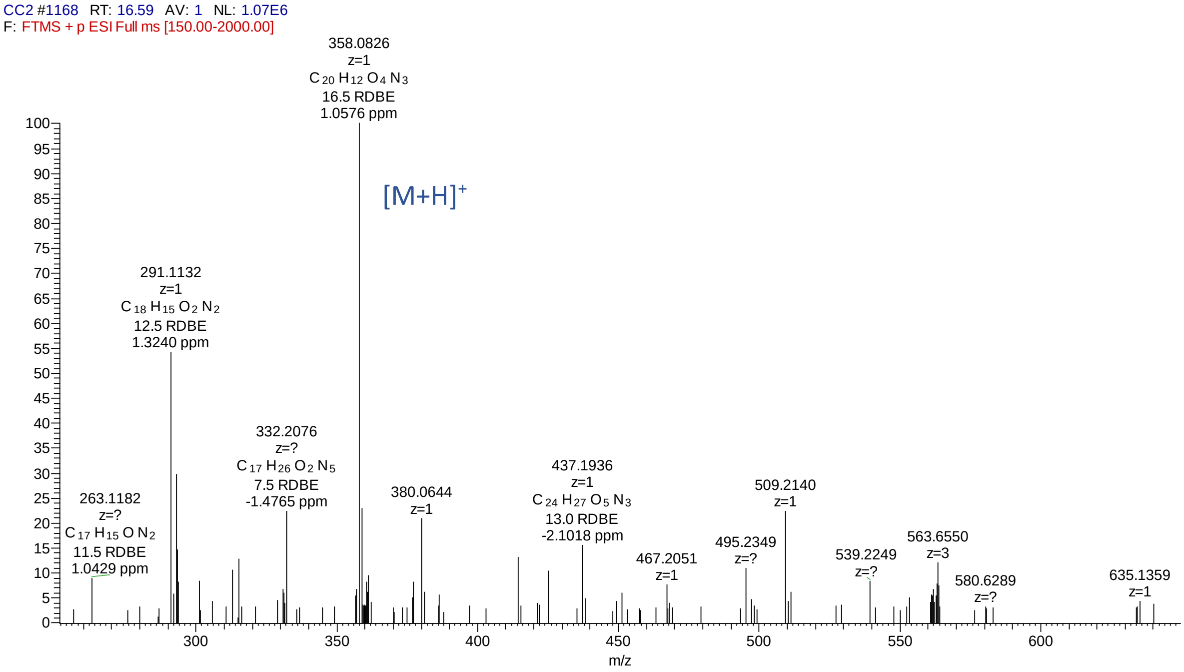


Figure S1. HR ESIMS of BE-13793C **1**

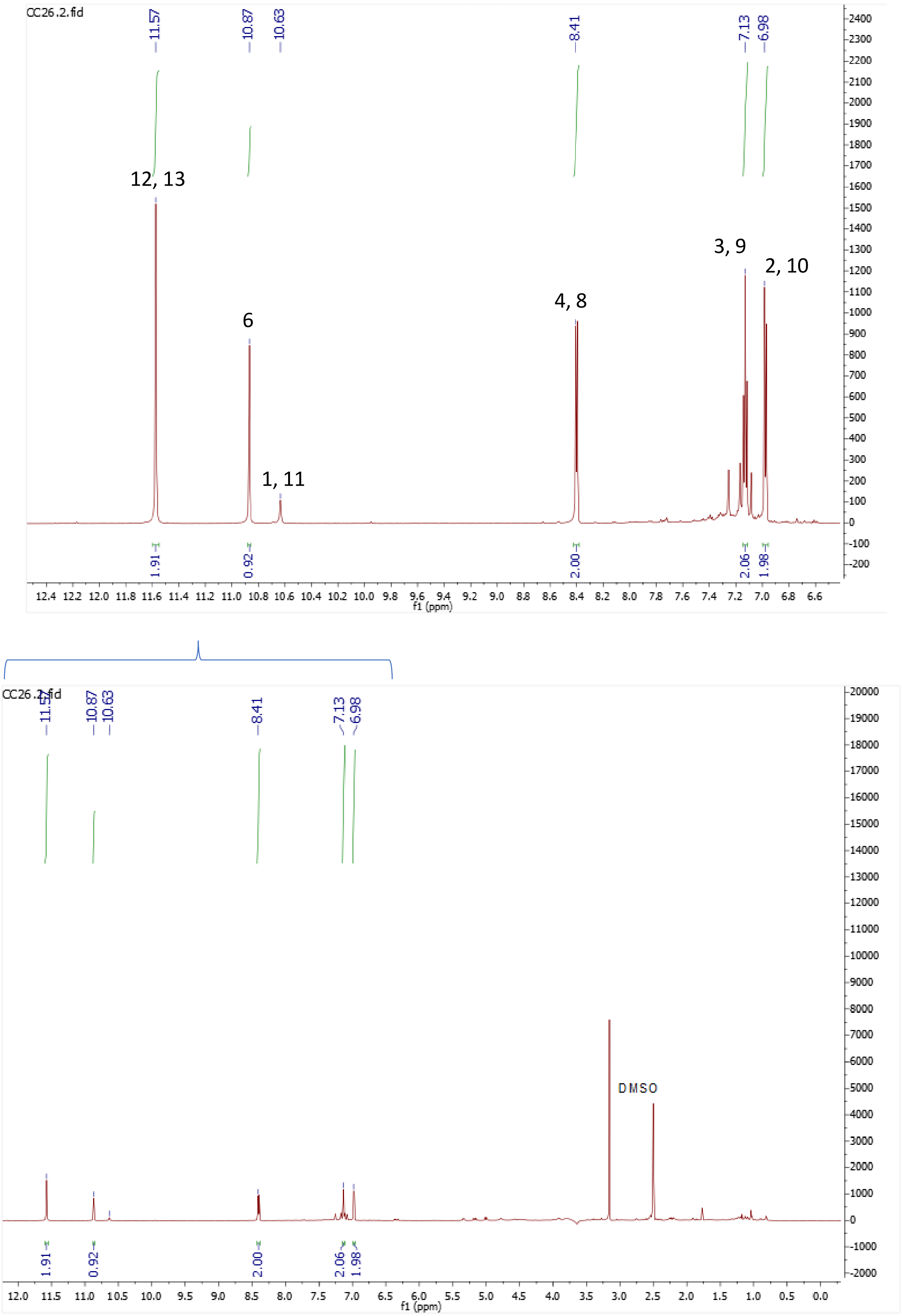


Figure S2: H-NMR of BE-13793C **1** (DMSO-d_6, 298K, 600MHz)

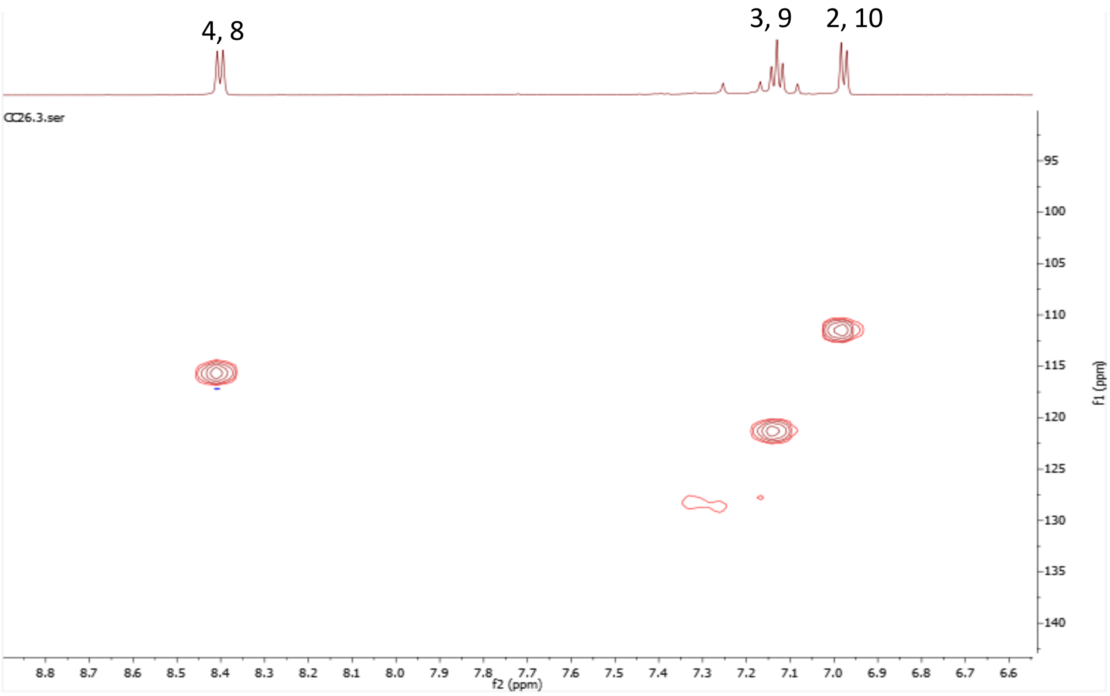


Figure S3: HSQC of BE-13793C **1** (CD_3OD, 298K, 600MHz)

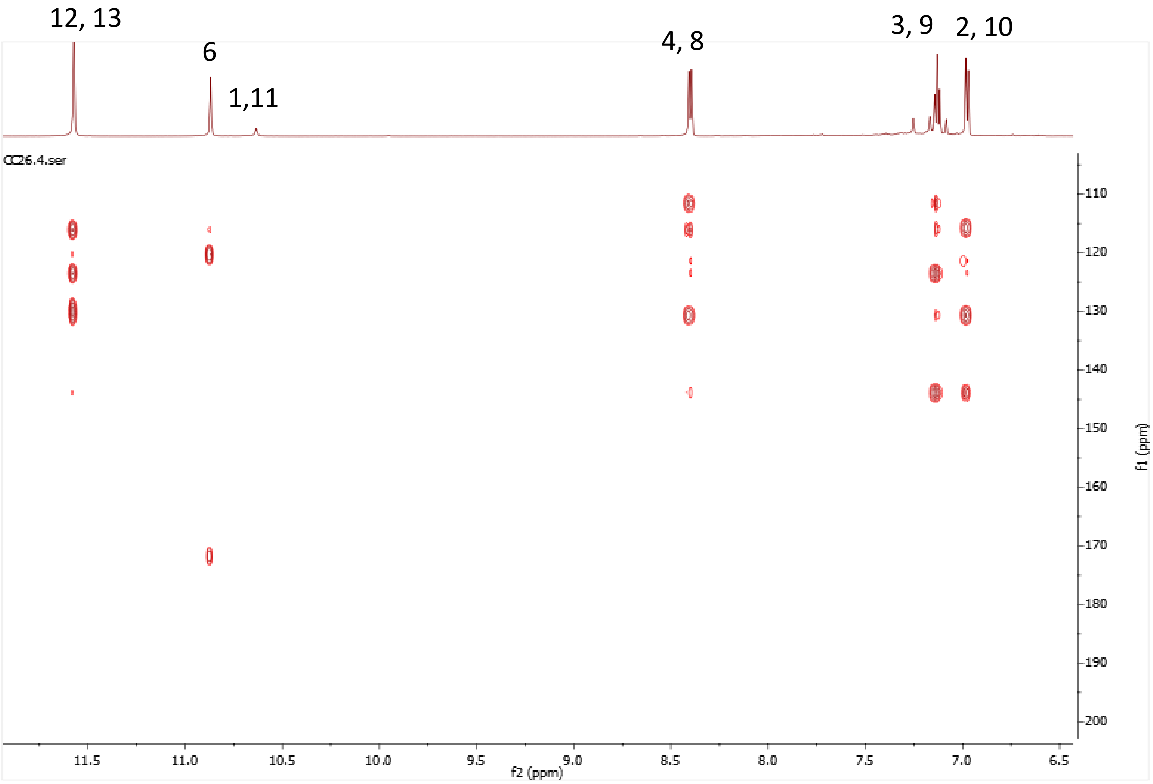


Figure S4: HMBC of BE-13793C **1** (DMSO-d_6, 298K, 600MHz)

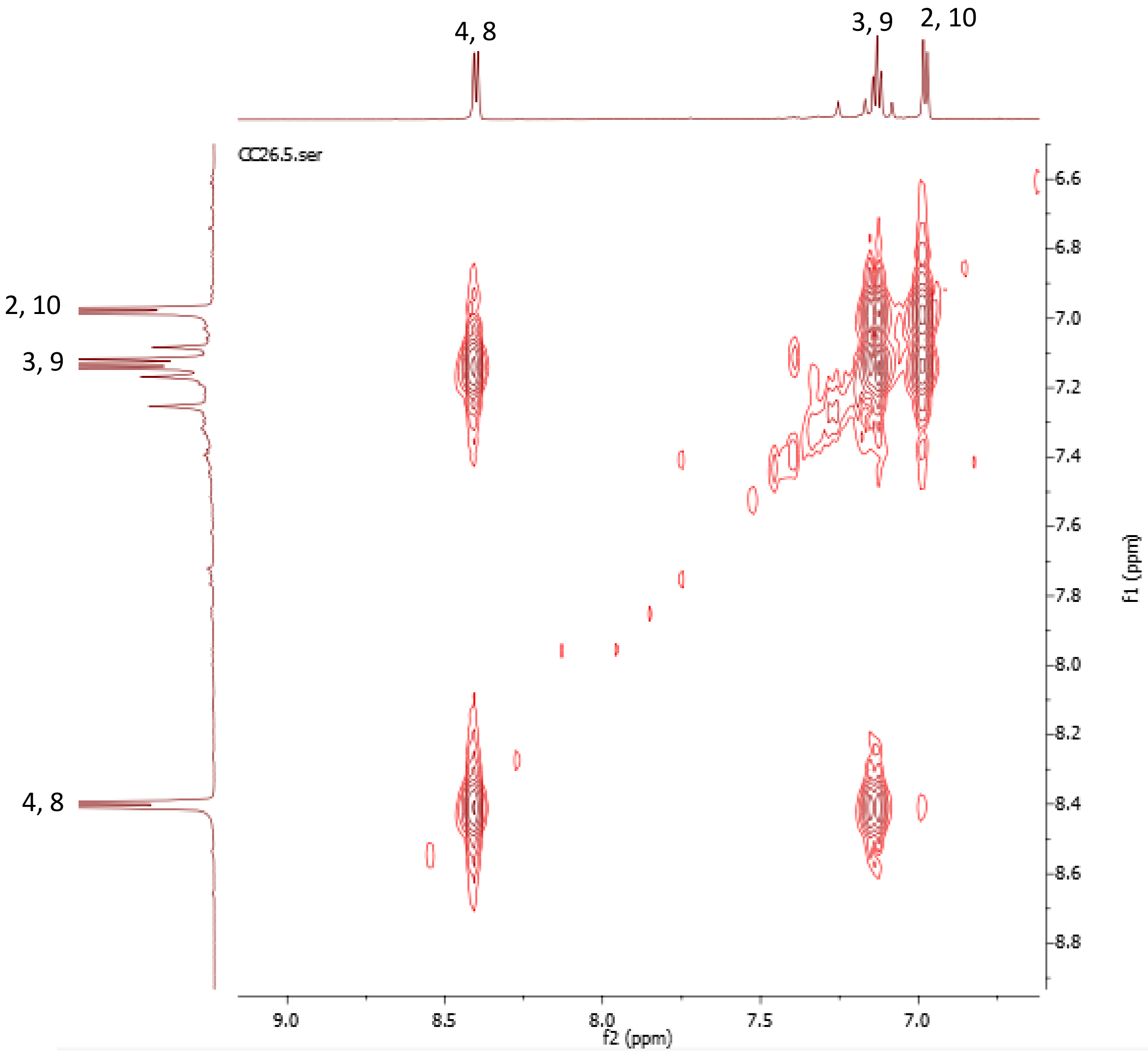


Figure S5: COSY of BE-13793C **1** (CD_3OD, 298K, 600MHz)

Table S1. Deduced functions of the ORFs in BE-13793C **1** (*bec*) biosynthetic gene cluster in *Streptomyces* sp. MA37 showing homology to the rebeccamycin (*reb*) BGC in *Lechevalieria aerocolonigenes* and staurosporine (*sta*) BGC in *Streptomyces* sp. TP-A0274

Gene	**Deduced Function**	**AA**	**Staurosporine % Protein identity**	**Rebeccamycin % Protein identity**
becO	FAD-dependent oxidoreductase	508	53%	56%
becD	bis-indole formation	1095	60%	54%
becC	FAD-binding monooxygenase	540	62%	61%
becP	cytochrome P450	417	51%	55%
becR	LuxR family DNA-binding response regulator	221	44%	31%

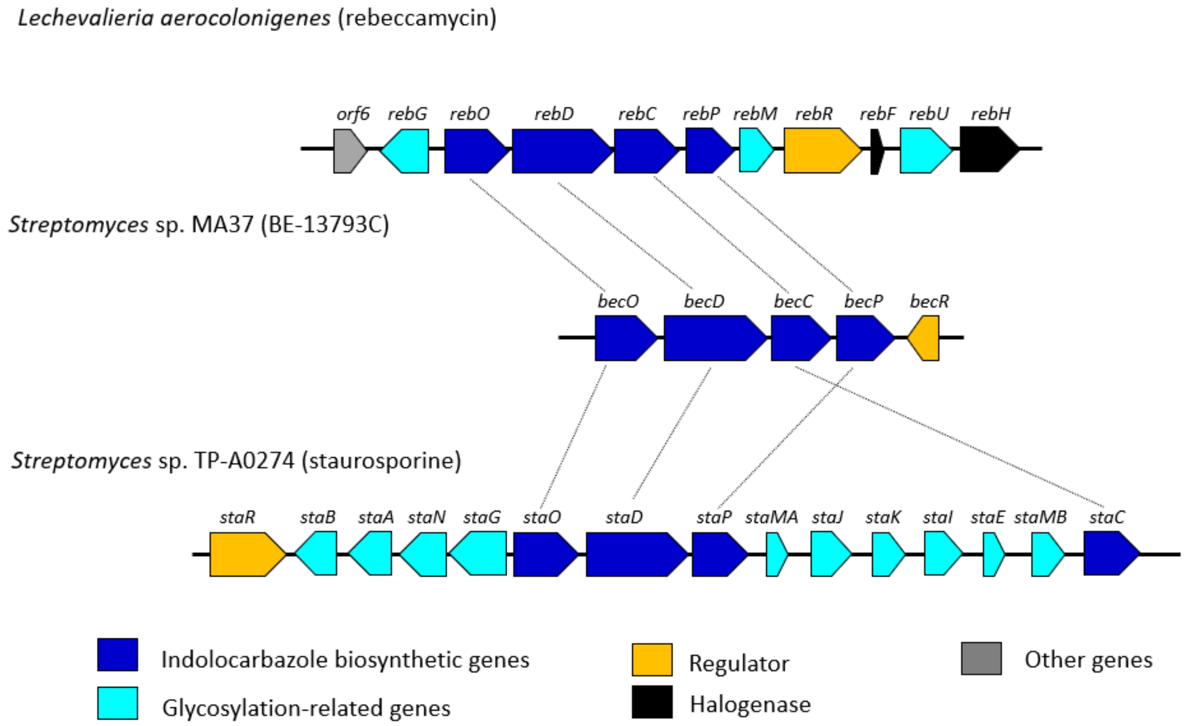
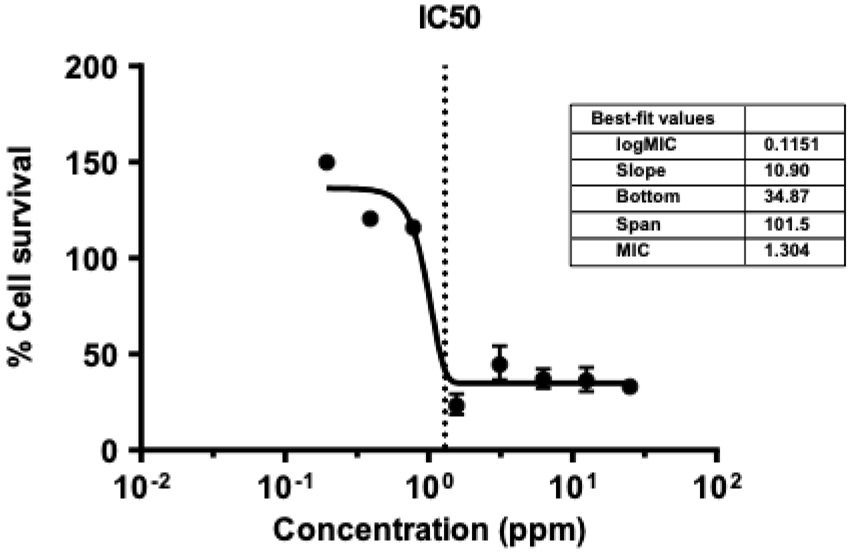


Figure S6: Biosynthetic gene cluster comparison of BE-13793C **1** in *Streptomyces* sp. MA37, rebeccamycin in *Lechevalieria aerocolonigenes,* and staurosporine in *Streptomyces* sp. TP-A0274



Best-fit values	
logMIC	0.1151
Slope	10.90
Bottom	34.87
Span	101.5
MIC	1.304

Figure S7. MIC curve of BE-13793C **1** against HT29 (ATCC HTB-38) colon cells