

Supporting Information

Insights into the complex biosynthesis of the leupyrrins in *Sorangium cellulosum* So ce690

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(A)

DkxI_DK	1	-----STQELKELLIARAPKA-----	EAAAAD-----	I[EELTV-----
DkxI_DW	1	-----HSCQELNELLARPPS-----	-AAVE-----	I[EELTV-----
BImVIII	1	-----EETP-----	-EQ-----	EEVVL-----
LeuB	1	RLIQQGISIRALAAAYIYECAALKRL-----	VASKCOPQGSSADHAADVVELV-----	
Me1F	1	-----S-S-GVAA-----	PNAAD-----	WEEGEL-----
TubB	1	-----GCEAQWSLQAPH-----	PPSAS-----	I[EEGEL-----
MtaF	1	-----GNSGCAA-----	VVAKD-----	WEEGEL-----
Me1C	1	-----E-----	E-----	WEEGST-----
MtaC	1	-----A-----	A-----	WEEGAI-----
AjuK	1	-----VCALETRAADEDR-----	GPQS-----	WEEGB-----
AjuC	1	-----LELVAAEEEVLDAVITSGTQGGALGSEALGDAESVAPSED-----	EEIPVLQF-----	
Leu9	1	-----EGLAARMLBELLQSPAKN-----	EF-----	E[STEVLLV-----

(B)

MtaG	1	-----MAELISKQDVTLWVEGERILKYRAPKGALSPETLS-----	LLSTHKAALLPYLRR-----	LAAEGESVH-----
Me1G	1	--MMSAEELVAELISFOQVVTILWVVRGDPLKVYRAPKGALSPETLS-----	LVAGHNAALDQHLRQ-----	LAAEGESVH-----
TubC	1	--MSAFAALLAHAAASLSVRLWWVEGERILRKQAPPGVTPPEIQS-----	RLGAGAHELIAALRQ-----	LQP-----
MtaD	1	--MSTSBEFTIVYLQOKGICELWLIEGDPLRPRAPPGLHTPELRT-----	ADKDKKEQLLEHLR-----	SASR-----
Me1D	1	--MTTAEFLIEIORKGIDDLWVCGDALRPRAPPCHLIDEIIR-----	GIKERKAQLEIILR-----	AASQ-----
LeuB	1	--MSLGEELFSPLSQRGVQLWVCGDALRPRAPAGALTENVRA-----	SLETTHRAQIVSILKMEACTQASDAPIERAPRDLPI-----	
DkxJ_DK	1	--MNLCELLAELINRGLIEVVEGDAILRPRCPKGAADEALRN-----	ALIETHMPPELLELPA-----	HDRGQEAPIPIVQRTGPA-----
DkxJ_DW	1	--MSLGEELLAELINRGLIEVVEGDAILRPRCPKGAADEALRN-----	ALTLHKSGLLALILHE-----	RNR-RETAPIAKALRDGPA-----
AjuL	1	--VRIDELMAKUAALEEVSLWVDGKLRLPRAPACIINPELLA-----	QLCAHREALILARLAA-----	TTEGCEH-----
LeuA	1	--MNTIAELLEQLLERPRIRSVKGDILEVSAPKGALTPDLRA-----	RLPERIAELIAMIQA-----	SSRAKAEVELPEVQHRPQERHEPF-----
AjuD	1	--MALLTDAAIRNVOQSATIGQLDVTRAPKGALTPELNE-----	QDVKHNPPELLSFHQ-----	RSSDKEAQKLPTVL-----
BImV	1	MTTPRITDLTELRGRQVITATGDRLHORAPRGALTELLATIRFTAR-----	DELLAHLRA-----	DRR-----

(C)

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DkxH_DK 1 -----AEEEELGTEVQKKQEASR-----EAQGALS-----APQQTSQETTSQDQELES---ATR-----
DkxH_DW 1 -----AGEGMGGEFQKQDKSSE-----QAQDALA-----APQQTSQETTSQDQELES---ATR-----
Me1D 1 -----LGEPPLAPSSPGHVPDK-----AEAEGPS-----LENLEQIPQDEIGALLDQKLADLEKLIGDA-----
CtaD 1 -----LGEPPLAPSPAAVPDE-----AVATAQAA-----VANLEQIPQDEIGALLDQKLAALEKLIG-----
MtaD 1 -----LKIGPVPDPVSA-QASKG-----EEAAAQT-----LANLEQIPQNEIGSLLDEKLALLKEKLIGDG-----
StiD 1 -----GEPLEAPPEPPRETAE-----KKDSAST-----AAELDALSDEIAAFLAEKLI--AANKGRK-----
AjuG 1 -----ATEILAPTPETAAPPSPDASSAP-----SPTGSET-----APDFLDALTDDEIVALLAELWPARAGISDARSGLTSEGPRPEHTA
DkxG_DK 1 -----DAFTIPLFTEEARV-----TSKSDAP-----VESPLFGHAAANAHLLSECLI--SKN-----
DkxG_DW 1 -----AAFIPLEFASEENT-----QQEQSKP-----VEDHLEGHTTANANAEQLI--SKM-----
StiC 1 -----STAHSSAQRVDEPRA-----GETQSDAP-----SVVLDVLSRNEIESLDDERLAAI--EASMMD-----
StiH 1 -----FATLFEEAPRATTPEP-----VSNDDAR-----WDALDDBLSDQIASLLAERLNAI--EE-----
AjuB 1 LGHVSAEPVPATSSPTLIAVTPSP-----VTALPALP-----SLENLSAEISDLLLAELSASAALIG-PGMD-----
AjuL 1 LGELYSAPLIATSISPPPPASPPPNTPVVATLFSTASSSPDDAQSAHDLSSSEIAQLLDDELASIGNPSGS-----
DkxN_DK 1 -----LAAEVGLKKEEAAAPVE-----EAPEDAELESLLADVDSLDDDTQAILRGRI-----
DkxN_DW 1 -----AAEVGLKDDEAAPAAA-----WDAGEDQELDALLADVDSLDDDQIQAILRGRI-----
Leuc 1 -----EGSALARQEEAPVR-----AAIDDAELGALLEEVVDSGAEINARIQGARIGAAR-----
LeuK 1 -----IERVIDLDFSPGKRPAD-----VAPAALG-----TNLDALSDEIAEILSQNLQAIID-----
AjuA 1 -LRQLDATANGATVRGPERTTTS-----TEVRSMLGEPLDLPAEBLSSBEAALLVEELERIINY-----
AjuF 1 -----AASRSATPQRAESD-----ADEAMR-----AVELSDEAALAIAELAAEIVIGDDEEMME-----
AjuE 1 -----ADRMQIATVSAGHDDAREPQ-----ESRDRALADALAHRVEQLSFDAAAIMKGI-----
LeuB 1 -----SELLPGAERPAAPAGAP-----GDAGRQE-----FTEEPLSPGEIEAITDSEFNAIITD-----

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(D)

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DkxH_DK 1 -----MKRALIKIQETQSKLDAHEOENHI-
DkxH_DW 1 -----MSTQGISDTGSDLMKRALIKIQDAQSKLDAHERERHI-
LeuB 1 -----MPTR-----DYAELMQALLKIHEETEAKLKIKLQAATEI-
AjuB 1 MNSGEKREEA-----TTASAPTVVKRALAAQDIRAILAAAAEOIKHAPI-
Me1E 1 -----MST-----EQNEHSARIALVALAEKIQALEESEEERI-
CtaE 1 -----MST-----EQNEHNARIALVALAEKIQALEESEEERI-
MtaE 1 -----MSSSV-----EQHEHSARIALVALAEKIQALEESEEERI-
StiD 1 -----MSTPNMPEQGEDLGRLKRALTAEKQAKLDAAERGRTI-
AjuA 1 -----MEH-----KARLTSALLAAKRIQOELDDAVERSRI-
AjuC 1 -----MSNST-----ETPDPQARLEALLAHKCRTILDVERQKTI-
StiE 1 -----MST-----GSQDHRSLLQSLEERUQAKVDSLERAKS-
StiJ 1 -----MSV-----KTKDNQDLLKRALVTIDKIQAKVDALERAKS-
DkxN_DK 1 -----MTPLORALALTITHRRVDCLRARSI-
DkxN_DW 1 -----MSNDIQTPASLMTPICRAALAKTITTRIDCLERARTI-
AjuG 1 -----MSR-----QGPSPDPDALSSACKRALAKKQOTILDTMEBATI-
LeuC 1 -----MST-----TTPEARKELSQIBRAYAAKHRRAQLDKYRI-
AjuH 1 -----MSSP-----PLPLDRHAVLHAIREQOCRARVDTSERERI-
DkxI_DK 1 -----MAKLS-----TRISELPVVMLALASQRSKEKELAAI-
DkxI_DW 1 -----MAKLS-----TRLSEMPVMLALASQRSKEKELAAI-
AjuF 1 -----RST-----AREGRISAVVMLALASQRSKEKELLLGSI-
LeuB 1 -----MSTLL-----ERAAGMSVALAYVAQRARVVTI-

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Fig. S1. (A) Multiple sequence alignment of C-terminal docking domains present at PKS/NRPS-NRPS junctions in mixed systems^{1,2}. (B) Multiple sequence alignment of N-terminal docking domains ('β-sheet type'¹) present at PKS/NRPS-NRPS junctions in mixed systems (potential partners of those shown in (A) (color-coded)). (C) Multiple sequence alignment of C-terminal docking domains present at PKS-PKS junctions in mixed systems³. (D) Multiple sequence alignment of N-terminal docking domains present at PKS-PKS junctions in mixed systems (potential partners of those shown in (C) (color-coded)). Key to pathways: Dkx, DKxanthene (DK = *Myxococcus xanthus* DK 1622; DW = *Stigmatella aurantiaca* DW 4/3-1); Blm, bleomycin; Leu, leupyrrin; Mel, melithiazol; Mta, myxothiazol; Tub, tubulysin; Aju, ajudazol; Cta, cystothiazole; Sti, stigmatellin. In each case, the subunit name is given.



Fig. S2. Multiple sequence alignment of ACPs and PCPs derived from myxobacterial pathways alongside discrete CPs involved in pyrrole biosynthesis from diverse bacteria. Key to pathways: Tub, tubulysin; Leu, leupyrrin; Aju, ajudazol; Clo, clorobiocin; Cou, coumermycin; Idm, idanomycin; Plt, pyoluteorin; Red, undecylprodigiosin; Ana, anatoxin. In each case, the subunit or protein name is given.

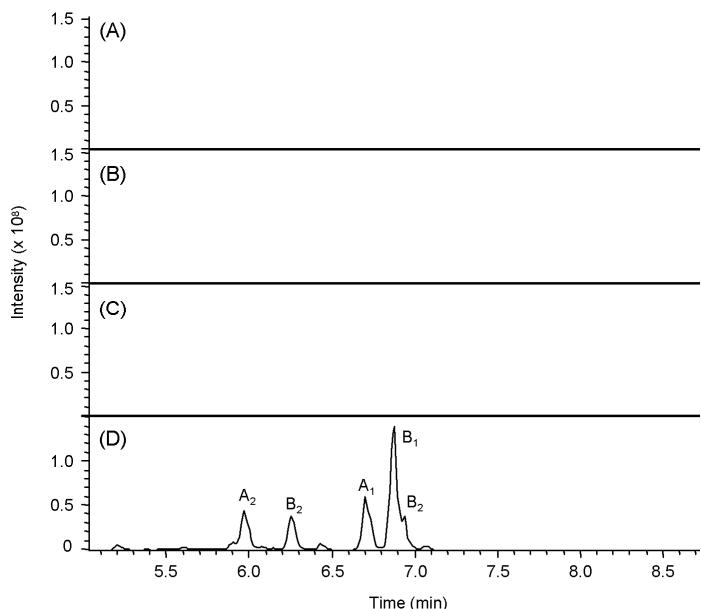


Fig. S3. Base peak chromatogram (m/z = 730–740) of the (A) *leu5*⁻, (B) *leu18*⁻, and (C) *leu13*⁻ mutants. (D) Base peak chromatogram (m/z = 730–740) of *S. cellulosum* So ce690 wild type, showing peaks corresponding to the leupyrrins A1, A2, B1 and B2.

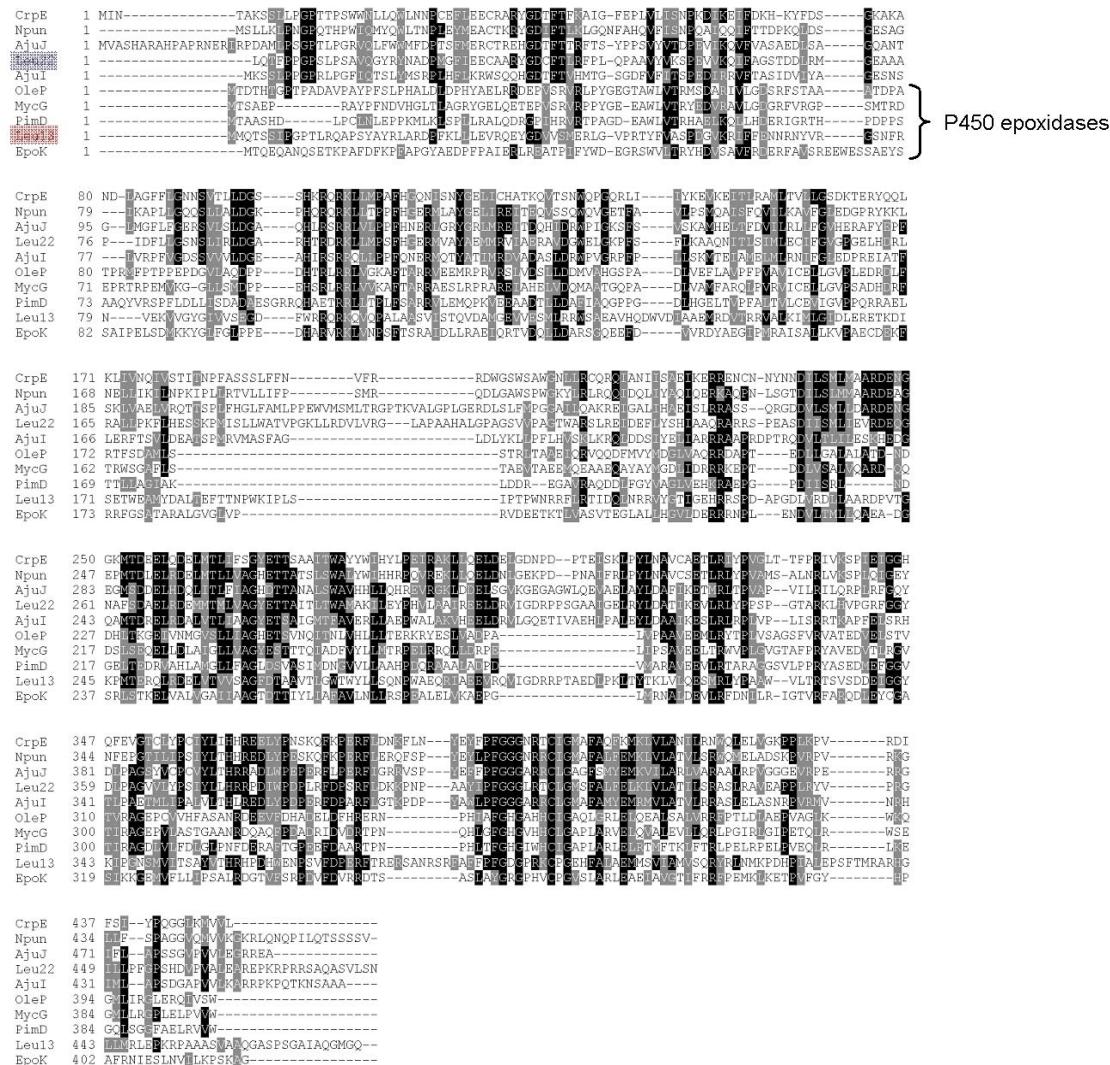


Fig. S4. Multiple sequence alignment of cytochrome P450 enzymes from various secondary metabolic pathways. This analysis shows that Leu13 aligns with other bona fide epoxidases⁴⁻⁷, while Leu22 is a member of a distinct group which includes the hydroxylase AjuJ⁸. Key to clusters: Crp, cryptophycin; Npun, unidentified cluster *Nostoc punctiforme* ATCC 29133; Aju, ajudazol; Leu, leupyrrin; Ole, oleandomycin; Myc, mycinamicin; Pim, pimaricin; Epo, epothilone.

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