



Supporting Information

for

Bacterial terpene biosynthesis: challenges and opportunities for pathway engineering

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Additional figures and tables

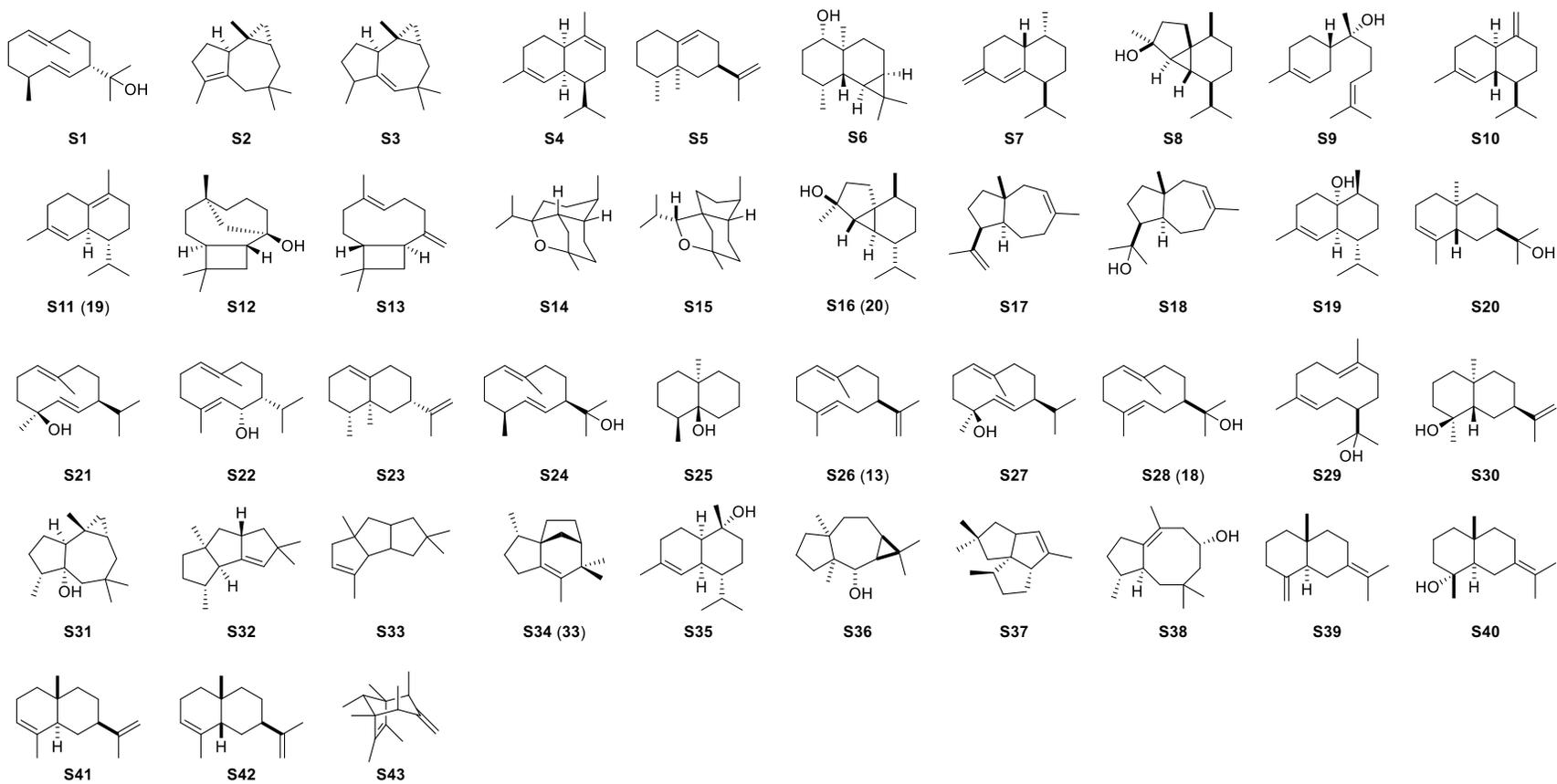


Figure S1: Characterized bacterial sesquiterpenes.

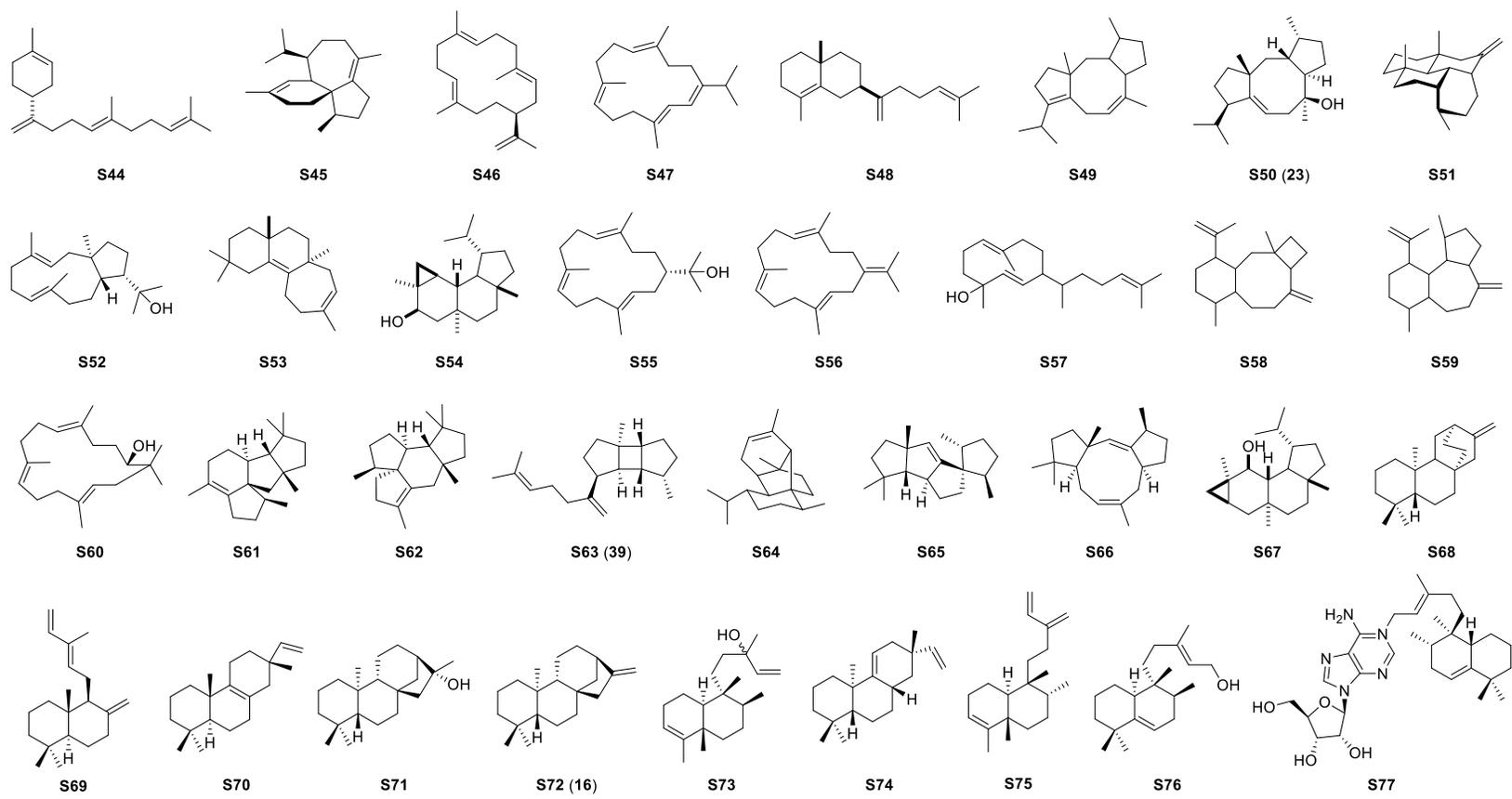


Figure S2: Characterized bacterial diterpenes.

Table S1: Characterized bacterial terpene cyclases.

Terpene ^a	Uniprot #	Name	Producing Strain	Host ^b	Study ^c	Isoprenoid Flux	Ref
Sesquiterpene							
(+)-allohedycaryol (S1)	B2HGU3	mmar_3220	<i>Mycobacterium marinum</i>	SUKA22	B	<i>fps</i>	1
african-2-ene (S2)* / african-1-ene (S3)*	D5SKM9	sclav_p0985	<i>Streptomyces clavuligerus</i>	SUKA22	B	<i>fps</i>	1
(-)- α -amorphene (S4)	D9XDR8		<i>Streptomyces viridochromogenes</i>	BL21(DE3)	A/B	endogenous	2-4
aristolochene (S5)*	A0A117E6J5		<i>Streptomyces acidiscabies</i>	WT			5
avermilol (S6)	Q82RR7	sav76	<i>Streptomyces avermitilis</i>	BL21(DE3)	A	N/A	5
				SUKA17	B	<i>fps</i>	5
bicyclosquiphellandrene (S7)*	A9GK58	sce6369	<i>Sorangium cellulosum</i>	SUKA22	B	<i>fps</i>	1
10- <i>epi</i> -cubebol (S8)* ^c				C43(DE3)	B	MEV pathway	6
(-)- <i>epi</i> - α -bisabolol (S9)	G5EKN0	SC2	<i>Streptomyces citricolor</i>	BL21(DE3)	A	N/A	7
				TK21	B	endogenous	7
(-)- γ -cadinene (S10)	C7PLV2		<i>Chitinophaga pinensis</i>	BL21(DE3)	A/B	endogenous	2, 3
(-)- δ -cadinene (S11, 19)	B5GS26	ssc_g_02150/ sclav_p0328	<i>Streptomyces clavuligerus</i>	BL21(DE3)	A	N/A	8
				JM109(DE3)	B	MEV pathway	8
				SUKA22	B	<i>fps</i>	1
(+)-caryolan-1-ol (S12)	B1W019	gcoA	<i>Streptomyces griseus</i>	BL21(DE3)	A	N/A	9
				TK21	B	endogenous	9
				SUKA22	B	<i>fps</i>	1
(-)-(<i>E</i>)- β -caryophyllene (S13)	K0K750		<i>Saccharothrix espanaensis</i>	BL21(DE3)	A/B	endogenous	3, 10
corvol ether A (S14)* / corvol ether B (S15)*	E4N7E5		<i>Kitasatospora setae</i>	BL21(DE3)	A	N/A	4, 11, 12
<i>epi</i> -cubebol (S16, 20)*	D2B747		<i>Streptosporangium roseum</i>	BL21(DE3)	A/B	endogenous	3, 4, 10, 12
(+)-dauca-8,11-diene (S17)* / (+)-isodauc-8-en-11-ol (S18)*	F2R8C1	sven_0552	<i>Streptomyces venezuelae</i>	SUKA22	B	<i>fps</i>	1
				BL21(DE3)	A	N/A	12, 13
(+)-epicubebol (S19)	B1W477	gecA	<i>Streptomyces griseus</i>	BL21(DE3)	A	N/A	14
				TK21	B	endogenous	14
				SUKA22	B	<i>fps</i>	1
(+)-eremophilene (S20)	A9FZ87	geoA/ sce8852	<i>Sorangium cellulosum</i>	BL21(DE3)	A	N/A	15

				C43(DE3)	B	endogenous	15
				SUKA22	B	<i>fps</i>	1
7- <i>epi</i> - α -eudesmol (S21)*	D9XD61		<i>Streptomyces viridochromogenes</i>	BL21(DE3)	A/B	endogenous	2, 3
(-)-germacradien-4-ol (S22)	G5EKM9	SC1	<i>Streptomyces citricolor</i>	BL21(DE3)	A	N/A	7
				TK21	B	endogenous	7
	A0A097ZQD8	slt18_1246	<i>Streptomyces lactacystinaeus</i>	SUKA22	B	<i>fps</i>	1
germacradien-6-ol (S23)	E8W6C7		<i>Streptomyces pratensis</i>	BL21(DE3)	A	N/A	4, 16
1(10),5-germacradien-11-ol (S24)/ geosmin (S25)	Q9X839	sco6073/ ScGS	<i>Streptomyces coelicolor</i>	pLysS	A	N/A	17-21
	Q82L49	sav2163/ geoA	<i>Streptomyces avermitilis</i>	BL21(DE3)	A	N/A	22
	B2IUI7	NP2	<i>Nostoc punctiforme</i>	JM109	B	endogenous	23
				pLysS	A	N/A	24
	B0FLN6	spterp13	<i>Streptomyces peucetius</i>	BL21(DE3)	A	N/A	25
1(10),5-germacradien-11-ol (S24)*:d	A9F845	sce1440	<i>Sorangium cellulosum</i>	C43(DE3)	B	endogenous	6
germacrene A (S26, 13)*	Q8YN85	NS1/ alr4685	<i>Nostoc sp. PCC 7120</i>	JM109	B	endogenous	23
				BL21(DE3)	A	N/A	23
	Q3MBN2	ava_1982	<i>Anabaena variabilis</i>	SUKA22	B	<i>fps</i>	1
(4 <i>S</i> ,7 <i>S</i>)-germacrene D-4-ol (S27)	A0A127Q4J7		<i>Collimonas pratensis</i>	BL21(DE3)	A	N/A	4
hedycaryol (S28, 18)*	A0A2N3Y098		<i>Saccharopolyspora spinosa</i>	BL21(DE3)	A/B		10
(2 <i>Z</i> ,6 <i>E</i>)-hedycaryol (S29)*	E4MY0	HcS	<i>Kitasatospora setae</i>	BL21(DE3)	B	endogenous	26
(+)-intermedeol (S30)	B5GTQ6	sclav_p0635	<i>Streptomyces clavuligerus</i>	SUKA22	B	<i>fps</i>	1
				BL21(DE3)	A	N/A	13
isoafricanol (S31)	G2P5T1		<i>Streptomyces violaceusniger</i>	WT			27
	A0A291SJC7		<i>Streptomyces malaysiensis</i>	BL21(DE3)	A	N/A	28
isohirsut-1-ene (cucumene, S32)	B5GLM7		<i>Streptomyces clavuligerus</i>	SUKA22	B	<i>fggps</i>	1, 29
				BL21(DE3)	A	N/A	30
isohirsut-4-ene (S33)*	A0A097ZQA4	slt18_1880	<i>Streptomyces lactacystinaeus</i>	SUKA22	B	<i>ggps</i>	1, 29
(+)- <i>epi</i> -isozizaene (S34, 33)	Q9K499	sco5222	<i>Streptomyces coelicolor</i>	BL21(DE3)	A	N/A	31-34
	Q82IV1	sav3032	<i>Streptomyces avermitilis</i>	BL21(DE3)	A	N/A	35
(+)-T-muurolol (S35)	B5GW45	sscg_03688/ sclav_p0068	<i>Streptomyces clavuligerus</i>	BL21(DE3)	A	N/A	8
				JM109(DE3)	B	MEV pathway	8
				SUKA22	B	<i>fps</i>	1
	A7NH01		<i>Roseiflexus castenholzii</i>	BL21(DE3)	A/B	endogenous	2-4, 36

neomeranol B (S36)* pentalenene (S37)	A5UZ14	roseRS_3509	<i>Roseiflexus sp.</i> RS-1	SUKA22	B	<i>fps</i>	8
	C9Z4F7		<i>Streptomyces scabiei</i>	BL21(DE3)	A	N/A	13
	Q55012	PenA	<i>Streptomyces exfoliatus</i>	BL21(DE3)	A	N/A	37, 38
pristinol (S38) selina-4(15),7(11)-diene (S39)*	Q82IY4	sav2998/ PtlA	<i>S. avermitilis</i>	XD	B	endogenous	39
				BL21(DE3)	A	N/A	40
	B5H7H3		<i>Streptomyces pristinaespiralis</i>	BL21(DE3)	A	N/A	41
selina-7(11)-ene-4-ol (S40)*.d α -selinene (S41)* 5- <i>epi</i> - α -selinene (S42)*	L8ERG6		<i>Streptomyces rimosus</i>	WT			42
	B5HDJ6		<i>Streptomyces pristinaespiralis</i>	BL21(DE3)	A/B	endogenous	2
	A0A097ZQE4	sspSK_3051	<i>Streptomyces sp.</i> SK 1894	SUKA22	B	<i>fps</i>	1
sodorifen (S43) ^e	A9B3Q4	haur_2988	<i>Herpetosiphon aurantiacus</i>	SUKA22	B	<i>fps</i>	1
	B2J4A4	NP1/ npun_R3832	<i>Nostoc punctiforme</i>	JM109	B	endogenous	23
				BL21(DE3)	A	N/A	23
				SUKA22	B	<i>fps</i>	1
	A0A318P116/ A0A318P5Q0	sod_c20750/ sod_c20760	<i>Serratia plymuthica</i> 4Rx13	BL21(DE3)	A/B	N/A	43, 44

Type I Diterpene

axinyssene (S44)*#	A0A084SQV5	CysTC2	<i>Archangium violaceum</i>	BW25113	B	MEV pathway	45
bonnadiene (S45)	A0A1G9UQQ0	BdS	<i>Allokutzneria albata</i>	BL21(DE3)	A	N/A	46
(<i>S</i>)-cembrene A (S46)	A0A1G9S4L4	CAS	<i>Allokutzneria albata</i>	BL21(DE3)	A	N/A	47
cembrene C (S47)	Q1AYR1	rxyl_0493	<i>Rubrobacter xylanophilus</i>	SUKA22	B	<i>ggps</i>	1
clavulatriene A (S48)*.d	B5H135	sclav_p1169	<i>Streptomyces clavuligerus</i>	SUKA22	B	<i>ggps</i>	1, 29
cyclooctat-7(8),10(14)-diene (S49)*	A0A097ZQD0	slt18_1078	<i>Streptomyces lactacystinaeus</i>	SUKA22	B	<i>ggps</i>	1, 29
cyclooctat-9-en-7-ol (S50, 23)	C9K1X5	CotB2	<i>Streptomyces melanosporofaciens</i>	BL21(DE3)	A	N/A	48, 49
				<i>S. albus</i>	B	<i>ggps</i>	48
				BL21(DE3)	A/B	<i>dxs/dxr/idi/ggps</i>	49-51
hydropyrene (S51)	D5SK09	sclav_p0765/ HpS	<i>Streptomyces clavuligerus</i>	Rosetta2	A	N/A	52
				SUKA22	B	<i>ggps</i>	1, 29
				BL21(DE3)	A	N/A	53
18-hydroxydolabella-3,7-diene (S52)	C7PA56	HdS	<i>Chitinophaga pinensis</i>	BL21(DE3)	A	N/A	54
				NB	B	endogenous	54
lydicene (S53)*#	A0A0D4DXU3	StlTC	<i>Streptomyces lydicus</i>	BW25113	B	MEV pathway	45
neoverrucosan-5 β -ol (S54)*#	H6KZW8	SapTC1	<i>Saprospira grandis</i>	BW25113	B	MEV pathway	45

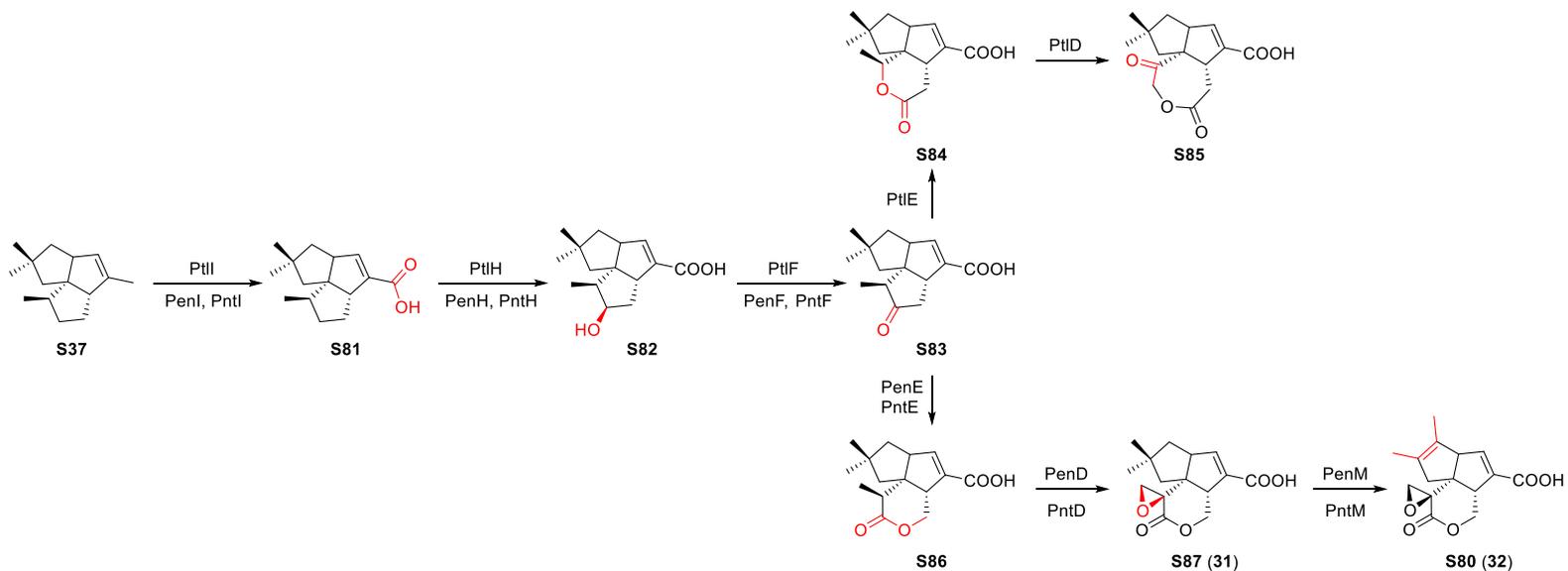
(<i>R</i>)-nephthenol (S55)/ cembrene C isomer (S56)	M1V9Q0	DtcycA	<i>Streptomyces</i> sp. SANK 60404	BL21(DE3)	A	N/A	55
obscuronatin (S57)*	A9B3Q3	haur_2987	<i>Herpetosiphon aurantiacus</i>	SUKA22	B	ggps	1
odyverdiene A (S58)* / odyverdiene B (S59)*	A0A097ZQD1	nd90_0354	<i>Streptomyces</i> sp. ND90	SUKA22	B	ggps	1, 29
S60 ^d	M1VDX3	DtcycB	<i>Streptomyces</i> sp. SANK 60404	BL21(DE3)	A	N/A	55
phomopsene (S61)/ allokutznerene (S62)	A0A1G9VRW7	PmS	<i>Allokutzneria albata</i>	BL21(DE3)	A	N/A	46
spata-13,17-diene (S63 , 39)	UPI000BAF81BA	SpS	<i>Streptomyces xinghaiensis</i>	BL21(DE3)	A	N/A	36, 56
spiroalbatene (S64)	A0A1H0BVV7	SaS	<i>Allokutzneria albata</i>	BL21(DE3)	A	N/A	36, 46
(-)-spiroviolene (S65)	P0DPK6	SvS	<i>Streptomyces violens</i>	BL21(DE3)	A	N/A	57
tsukubadiene (S66)	I2N045	stsu_20912	<i>Streptomyces tsukubensis</i>	SUKA22	B	ggps	1, 29
				BL21(DE3)	A	N/A	36, 57
verrucosane-2 β -ol (S67)*#	A9WGY1	ChITC2	<i>Chloroflexus aurantiacus</i>	BW25113	B	MEV pathway	45
	A0A178MLU0	ChITC5	<i>Chloroflexus islandicus</i>	BW25113	B	MEV pathway	45
TypeII/I Diterpene^f							
<i>ent</i> -atiserene (S68)	DBL2U6/ DBL2U4	PtmT2/ PtmT1	<i>Streptomyces platensis</i>	BL21(DE3)	A/B	<i>dxs/dxr/idi/ggps</i>	58, 59
biformene (S69)	A0A0H5BB10/ A0A0H5BN57	CldB/ CldD	<i>Streptomyces cylabdanicus</i>	JM109(DE3)	A	NA	60, 61
				SUKA22	B	ggps	
isopimara-8,15-diene (S70)	A8M709/ A8M708	sare_1288/ sare_1287	<i>Salinispora arenicola</i>	C41(DE3)	B	ggps	62
(16 <i>R</i>)- <i>ent</i> -kauran-16-ol (S71)	DBL2U6/ DBL2U9	PtmT2/ PtmT3	<i>Streptomyces platensis</i>	BL21(DE3)	A/B	<i>dxs/dxr/idi/ggps</i>	58, 59
<i>ent</i> -kaur-16-ene (S72 , 16)	Q45221/ Q45222	blr2149/ blr42150	<i>Bradyrhizobium japonicum</i>	C41(DE3)	B	endogenous	63
	Q989L7/ Q989L6		<i>Mesorhizobium japonicum</i>	C41(DE3)	B	<i>dxs/dxr/idi/ggps</i>	64
	P55538/ P55537		<i>Sinorhizobium fredii</i>	C41(DE3)	B	<i>dxs/dxr/idi/ggps</i>	64
	Q8KLD5/ Q8KLD4		<i>Rhizobium etli</i>	C41(DE3)	B	<i>dxs/dxr/idi/ggps</i>	64
(+)-kolavelool (S73)	A9AWD5/ A9AWD6	haur_2145/ haur_2146	<i>Herpetosiphon aurantiacus</i>	BL21(DE3)	A	N/A	65

<i>ent</i> -pimara-9(11),15-diene (S74)	Q5KSN5/ Q5KSN4		<i>Streptomyces sp.</i> KO-3988	M15/pREP4	A	N/A	66, 67
terpentetriene (S75)	Q9AJE4/ Q9AJE3		<i>Kitasatospora griseola</i>	M15/pREP4	A	N/A	68, 69
tuberculosinol (S76)/ 1-tuberculosinyladenosinec (S77)	O50406/ P9WJ61	Rv3377c/ Rv3378c	<i>Mycobacterium tuberculosis</i>	TK23 BL21(DE3)	B A	endogenous N/A	68 70-73

^aterpenes labeled with asterisk have unclear absolute stereochemistry, and those labeled with pound signs are the product of UbiA-type terpene cyclases; ^bBL21(DE3), BW25113, C41(DE3), C43(DE3), JM109, JM109(DE3), M15/pREP4, pLysS [BL21(DE3)pLysS], and Rossetta2(DE3) are *Escherichia coli* strains. SUKA16, SUKA17, and SUKA22 are *Streptomyces avermitilis* strains. TK21 and TK23 are *Streptomyces lividans* strains. NB: *Nicotiana benthamiana*. XD: *Xanthophyllomyces dendrorhous*. WT: terpenes are detected in the headspace of wild-type strains, and the assignment of terpene cyclase was based on analysis of genomic sequence and exclusion of other common terpene cyclases. ^cA: *in vitro*, B: *in vivo* studies; ^dseveral products were produced; ^erequires two enzymes: methyltransferase / cyclase; ^faccession numbers and protein names in the order of type II diterpene synthase / type I diterpene synthase.

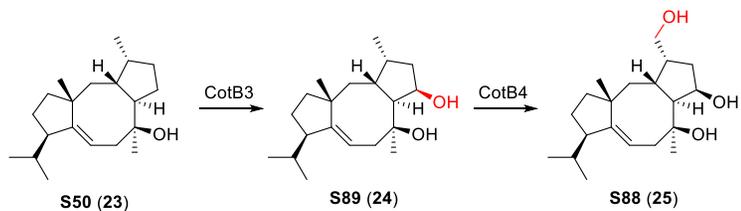
Table S2: Functional characterization of bacterial tailoring enzymes for terpene modification.

Uniprot #	Name	Class ^a	Strain	Host ^b	Study ^c	Substrate ^d	Reaction	Ref
Albaflavenone (S78, 35)								
Q9K498	CYP107A1 sco5223	CYP	<i>Streptomyces coelicolor</i>	BL21(DE3)	A	<i>epi</i> -isozizaene (S34, 33)	hydroxylation-oxidation	74, 75
Q81IV2	CYP107A2 sav3031	CYP	<i>Streptomyces avermitilis</i>	SUKA16	B	<i>epi</i> -isozizaene (S34, 33)	hydroxylation-oxidation ^e	35
<p>S34 (33) $\xrightarrow[\text{sav3031}]{\text{sco5223}}$ S79 (34) $\xrightarrow[\text{sav3031}]{\text{sco5223}}$ S78 (35)</p>								
Pentalenolactone (S80, 32)								
Q82IY3/ E3VWK7/ E3VWJ1	PtII/ PenI/ PntI ^f	CYP	<i>Streptomyces avermitilis</i> / <i>Streptomyces exfoliatus</i> / <i>Streptomyces arenae</i>	BL21(DE3)	A	pentalenene (S37)	4e-oxidation ^g	76, 77
Q82IZ1/ E3VWK0/ E3VWI4	PtIH/ PenH/ PntH ^f	AKG	as above	BL21(DE3)	A	1-deoxypentaleniate (S81)	hydroxylation	77-79
Q82IY9 E3VWK2/ E3VWI6	PtIF/ PenF/ PntF ^f	DH	as above	BL21(DE3)	A	S82	2e-oxidation	77, 80
Q82IY8	PtIE	FMO	<i>Streptomyces avermitilis</i>	BL21(DE3)	A	S83	Baeyer-Villiger oxidation	81
Q82IY7	PtID	AKG	<i>Streptomyces avermitilis</i>	BL21(DE3)	A	neopentalenolactone D (S84)	dehydrogenation	77
E3VWK3/ E3VWI7	PenE/ PntE	FMO	<i>Streptomyces exfoliatus</i> / <i>Streptomyces arenae</i>	BL21(DE3)	A	S83	Baeyer-Villiger oxidation	77
E3VWK4/ E3VWI8	PenD/ PntD	AKG	as above	BL21(DE3)	A	pentalenolactone D (S86)	dehydrogenation-epoxidation	77
E3VWJ9/ E3VWI3	PenM/ PntM	CYP	as above	BL21(DE3)	A	pentalenolactone F (S87, 31)	rearrangement	82



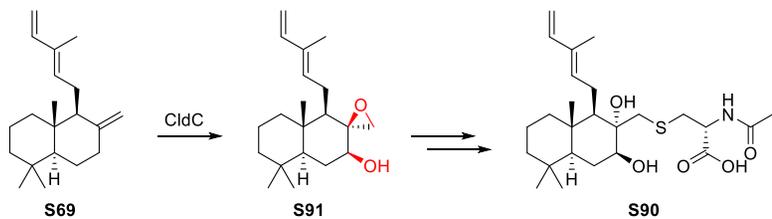
Cyclooctatin (S88, 25)

C9K1X6	CotB3	CYP	<i>Streptomyces melanosporofaciens</i>	<i>S. albus</i>	B	cyclooctat-9-en-7-ol (S50, 23)	hydroxylation	48
C9K1X7	CotB4	CYP	<i>Streptomyces melanosporofaciens</i>	<i>S. albus</i>	B	S89 (24)	hydroxylation	48



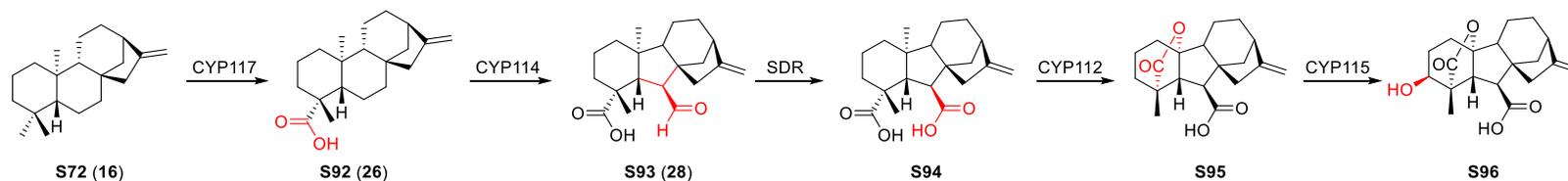
Cyslabdan (S90)

A0A0H5B5M5	CldC	CYP	<i>Streptomyces cyslabdanicus</i>	SUKA22	C	biformene (S69)	hydroxylation-epoxidation	60
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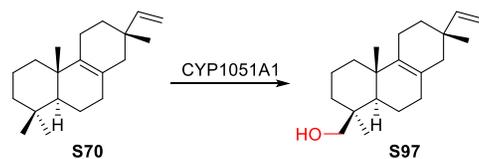
Gibberellinsh

P55540/ Q59205	CYP117A2	CYP	<i>Sinorhizobium fredii</i> / <i>Bradyrhizobium diazoefficiens</i>	SM	C	<i>ent</i> -kaurene (S72, 16)	6e-oxidation	83
P55543/ Q59204	CYP114	CYP	as above	SM	C	<i>ent</i> -kaurenoic acid (S92, 26)	hydroxylation/ ring contraction	83
P55541/ Q45219	SDR	DH	as above	SM	C	S93 (28)	2e-oxidation	83
P55544/ Q59203	CYP112A2	CYP	as above	SM	C	gibberellin A12 (S94)	demethylation- lactonization	83
UPI00040E8C18/ Q98A71	SMCYP115/ MICYP115	CYP	<i>Sinorhizobium meliloti</i> / <i>Mesorhizobium japonicum</i>	SM	C	gibberellin A9 (S95)	hydroxylation	84



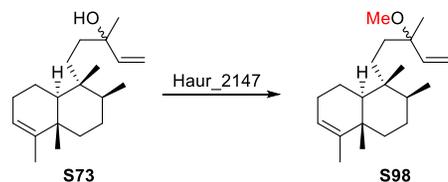
Isopimara-8,15-dien-19-ol (S97)

A8M707	CYP1051A1 sare_1286	CYP	<i>Salinispora arenicola</i>	C43(DE3)	B	isopimara-8,15-diene (S70)	hydroxylation	62
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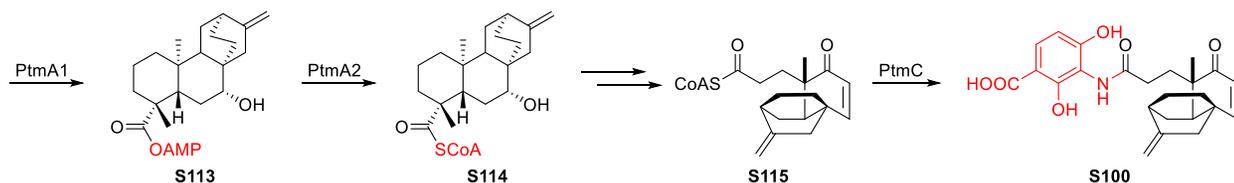
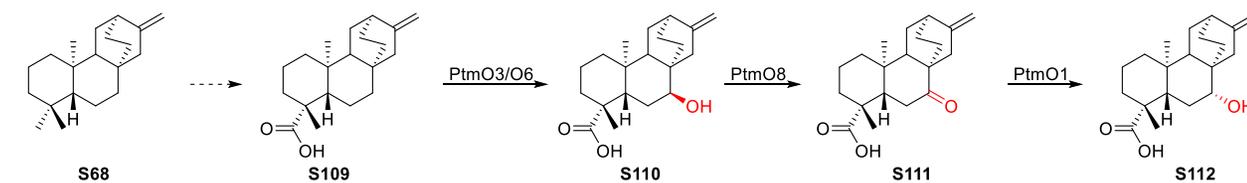
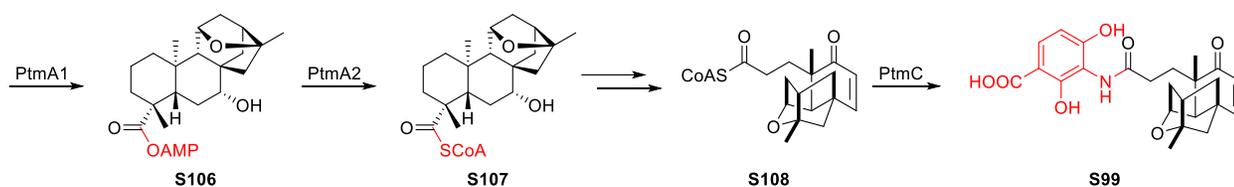
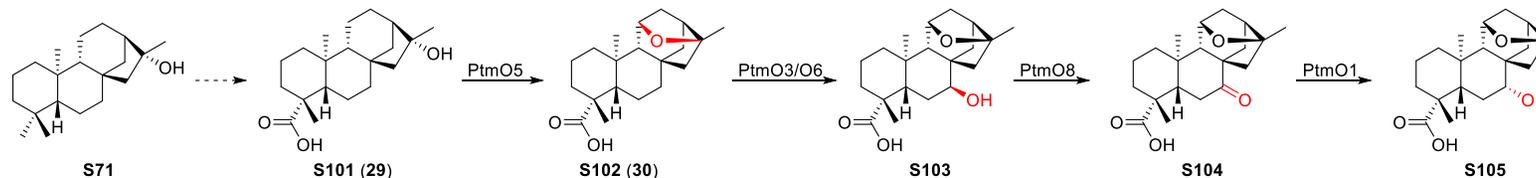
(+)-*O*-methylkolavelool (S98)

A9AWD7	Haur_2147	MT	<i>Herpetosiphon aurantiacus</i>	BL21(DE3)	A	(+)-kolavelool (S73)	methylation	65
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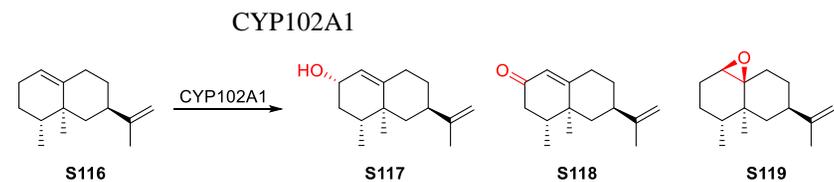
Platensimycin (S99) / Platencin (S100)

DBL2V0	PtmO5	CYP	<i>Streptomyces platensis</i>	BL21(DE3)	A	S101 (29)	hydroxylation/ ether formation ⁱ	59, 85
DBL2U7	PtmO3	AKG	as above	BL21(DE3)	A/B	S102 (30), S109	hydroxylation	86
DBL2V2	PtmO6	AKG	as above	BL21(DE3)	A/B	S103, S110	hydroxylation	86
DBL2W5	PtmO8	DH	as above	BL21(DE3)	A/B	S104, S111	oxidation	86
A0A0A0UXJ2	PtmO1	DH	as above	BL21(DE3)	A/B	S105, S112	reduction	86
DBL2T7	PtmA1	CoAS	as above	mutant	B	S106, S113	adenylation	87
DBL2U1	PtmA2	CoAS	as above	BL21(DE3)	A/B	S107, S114	ligation	87
DBL2W0	PtmC	NAT	as above	mutant	B	S108, S115	ligation	88

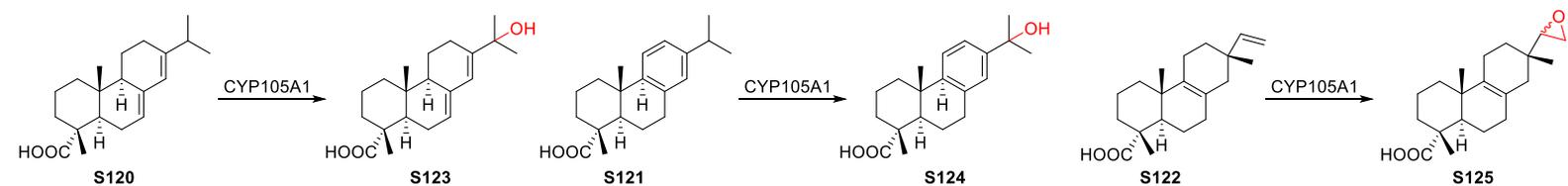


Others

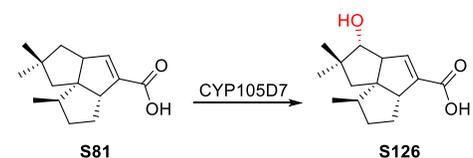
P14779	P450 _{BM3}	CYP	<i>Bacillus megaterium</i>	DH5 α	A/C	*valencene (S116)	oxidation	89
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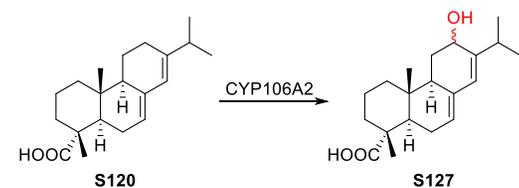
P18326	CYP105A1	CYP	<i>Streptomyces griseolus</i>	JM109	A/C	*abietic acid (S120)	hydroxylation	90, 91
				BM	C			90
				JM109	A/C	*dehydroabietic acid (S121)	hydroxylation	90
				BM	C			90
				JM109	A/C	*isopimaric acid (S122)	epoxidation	90
				BM	C			90



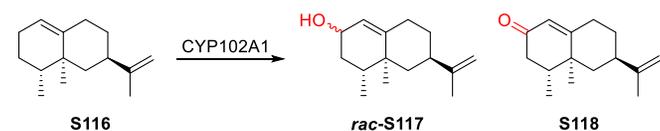
Q82518	CYP105D7	CYP	<i>S. avermitilis</i>	SUKA13	B	*1-deoxypentalenate (S81)	hydroxylation	92
	sav7469			BL21(DE3)	A			92

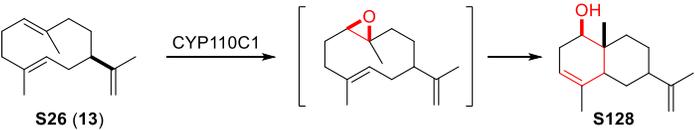
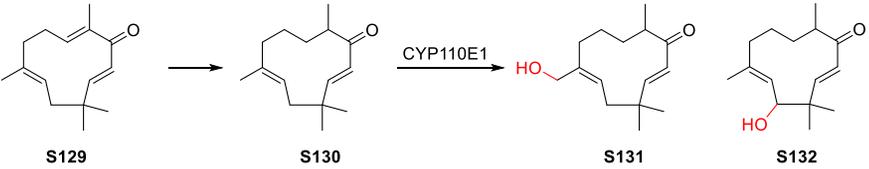
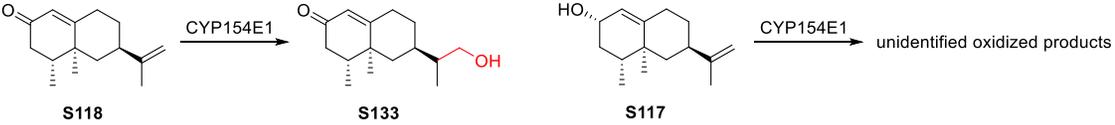
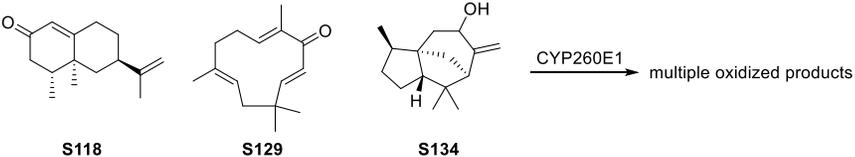


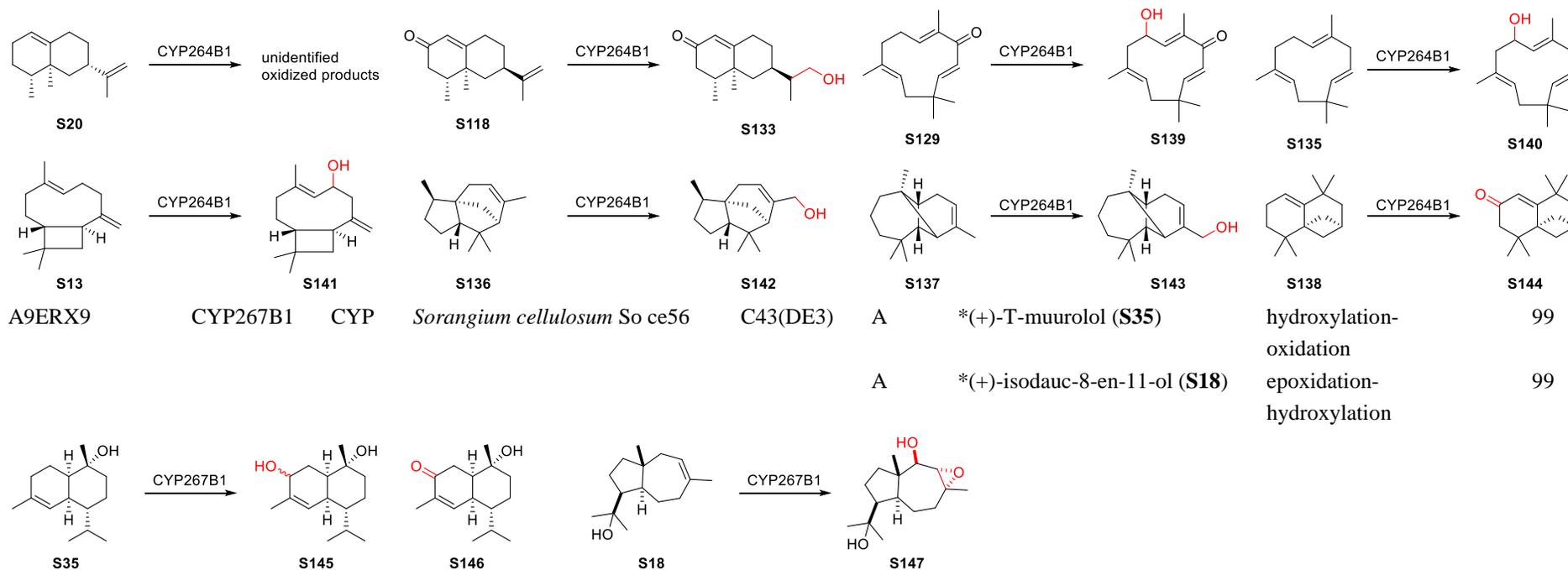
Q06069	CYP106A2	CYP	<i>Bacillus megaterium</i>	BL21(DE3)	A	*abietic acid (S120)	hydroxylation	93
				BM	C			



U5U1Z3	CYP109B1	CYP	<i>Bacillus subtilis</i>	BL21(DE3)	A/C	*valencene (S116)	hydroxylation/ oxidation	94
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Q8YN84	CYP110C1	CYP	<i>Nostoc punctiforme</i>	JM109 / BL21(DE3)	B	germacrene A (S26 , 13)	epoxidation- cyclization	23
								
Q8YMU4	CYP110E1	CYP	<i>Nostoc sp.</i> PCC 7120	BL21(DE3)	C	*2,3-dihydrozerumbone (S130) ^j	hydroxylation	15
								
Q47KL3	CYP154E1	CYP	<i>Thermobifida fusca</i>	BL21(DE3)	A	*(+)-nootkatone (S118) *(+)-nootkatol (S117)	hydroxylation oxidation	95 95
								
A9FDB7	CYP260A1 sce1588	CYP	<i>Sorangium cellulosum</i> So ce56	BL21(DE3)	A/C C C	*(+)-nootkatone (S118) *zerumbone (S129) *(+)-3(15)-cedren-4-ol (S134)	oxidation oxidation oxidation	96, 97 97 97
								
A9FZ85	CYP264B1 sce8851	CYP	<i>Sorangium cellulosum</i> So ce56	C43(DE3) C43(DE3) / BL21(DE3)	A/B/C C C A/C A/C	(+)-eremophilene (S20) *(+)-nootkatone (S118) *zerumbone (S129) *α-humulene (S135) *β-caryophyllene (S13) *α-cedrene (S136) *(+)-α-longipinene (S137) *(-)-isolongifolene (S138)	hydroxylation hydroxylation hydroxylation hydroxylation hydroxylation hydroxylation 4e-oxidation	15, 97 97 97 97, 98 97 97 98 98



^aAKG: α -ketoglutarate-dependent non-heme iron enzyme, CoAS: acyl-CoA synthetase, CYP: cytochrome P450, DH: NAD(P)⁺-dependent dehydrogenase, FMO: Flavin-dependent monooxygenase, MT: methyltransferase, NAT: *N*-acetyl transferase; ^bBL21(DE3), C43(DE3), DH5 α , JM109: *E. coli* strains. SUKA13, SUKA16, SUKA22: *S. avermitilis* strains. BM: *Bacillus megaterium* MS941. SM: *Sinorhizobium meliloti* 1021. ^cA: in vitro, B: in vivo: the heterologous host expresses both cyclase and tailoring enzymes, or gene deletion / complementation experiments in the producing strains, C: growing cells or resting cells expressing tailoring enzymes are fed with substrate directly; ^dsubstrates marked with asterisk are not produced by any enzyme(s) encoded nearby the tailoring enzymes; ^eepoxidation took place when expressed in *S. avermitilis*, which might come from the action of endogenous P450 of the heterologous host. Also see Figure 8 in the main text; ^fonly Ptl enzymes were experimentally verified. Pen and Pnt enzymes' function were implied by sequence homology. ^g6e-oxidation was expected, but *in vitro* reaction only catalyzed 4e-oxidation; ^h*Sinorhizobium fredii* enzymes were studied by feeding substrates to *Sinorhizobium meliloti* 1021 expressing enzymes of interest. Substrates were also fed to *S. fredii* / *Bradyrhizobium diazoefficiens* deletion strains to map out the biosynthetic pathway; ⁱin the *in vitro* studies, HCl was required to trigger the ether ring formation; ^jit was claimed to come from the reduction of zerumbone (the fed substrate, **S128**) by endogenous enzymes of *E. coli*.

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