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Supporting information

Structural basis of catalysis in the bacterial monoterpene synthases linalool synthase and 1,8-cineole synthase

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Table of contents

Extended EPR results and discussion

Scheme S1: Synthesis of FGP, FGPP, FNP and FNPP.

Figure S1. NMR spectra of 2-fluorogeraniol.

Figure S2. NMR spectra of 2-fluoronerol.

Figure S3. NMR and HRMS-ESI spectra of 2-fluorogeranyl pyrophosphate (FGPP).

Figure S4. NMR and HRMS-ESI spectra of 2-fluoroneryl pyrophosphate (FNPP).

Figure S5. Gas chromatography analysis of bLinS with FPP and GPP.

Figure S6. cw-EPR spectra of bCinS.

Figure S7. cw-EPR spectra of bLinS.

Figure S8. Comparison of structures from MD of *apo*-bCinS with MD of the ternary complex of bCinS with 3 Mg^{2+} ions and GPP or NPP.

Figure S9. Comparison of structures from MD of *apo*-bLinS with MD of the ternary complex of bLinS with 3 Mg²⁺ ions and GPP or FPP.

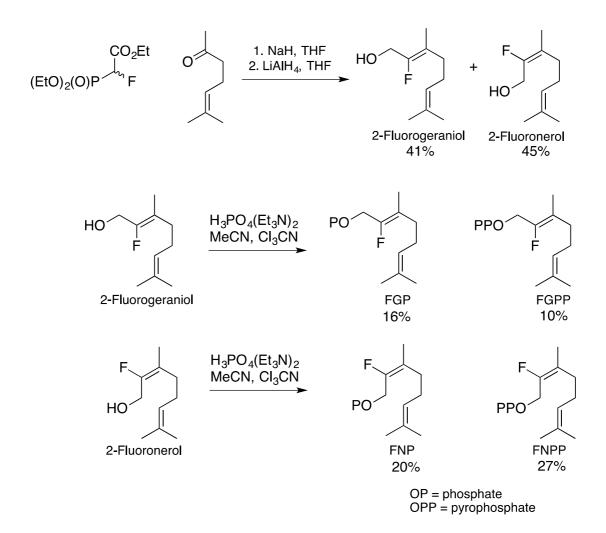
Figure S10: Structural overlay of bCinS and C-terminal domain of Sf-CinS1.

Table S1: Plasmids used in this study

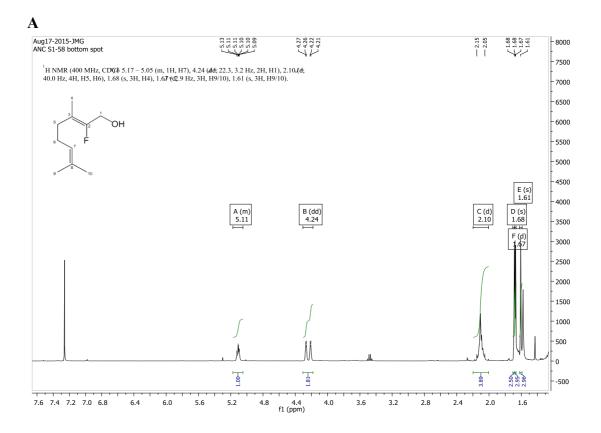
Table S2: bLinS and bCinS: homologous structures

Extended EPR results and discussion

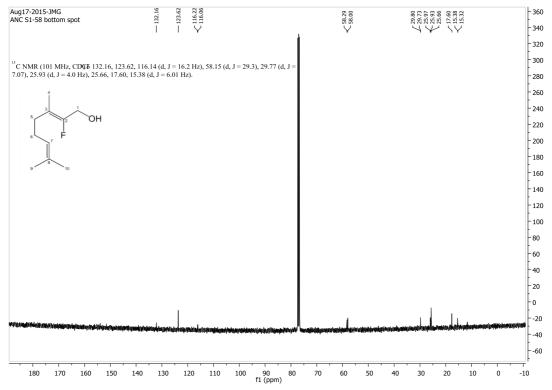
Comparisons of EPR spectra of Mn²⁺ ion substituted bCinS/bLinS with and without FGPP along with standard MnCl₂ samples show a clearly resolved multiplet structure for 1:1 bCinS/bLinS: MnCl₂ in the presence of FGPP. The observation of a multiplet structure indicates that degeneracy of the six-line EPR spectrum, often associated with free/unbound Mn^{2+} ion, was either lifted by the strong zero-field splitting of the Mn^{2+} ion or the 'g-anisotropy' or combination of both (Figure 3; black asterisks). The intense EPR transitions centered around $g \sim 2.0$ (Figure 3; black/blue asterisks) were mainly due to the transitions from $|m_s, -\frac{1}{2} \rightarrow |m_s, +\frac{1}{2} \rightarrow |m_s, +\frac{1}{2}$ manifold. The weak hyperfine structures that appear above and below the $g \sim 2.0$ region (Figure 3; blue arrows) are due to the transitions between the higher spin manifolds, $|m_s, -5/2 \rightarrow |$ m_s , -3/2> and $|m_s$, $-3/2> \rightarrow |m_s$, -1/2> respectively. The multiplet structure observed for bCinS and bLinS directly probes the local/first coordination sphere of the Mn²⁺ ion, which was clearly different from the reference samples $[Mn(H_2O)_6]^{2+}$ (black dotted spectrum) and bCinS/bLinS without FGPP (black dashed spectrum). The aforementioned two samples predominantly showed a six-line EPR pattern with halffield transitions in the range of 80-150 mT, whereas for 1:1 bCinS/bLinS-FGPP: MnCl₂, it occurred between 120-180 mT and trailed towards high magnetic field (Figures S6 and S7). The intensity of the multiplet structure and the half-field transitions between 120-180 mT (Figures S6 and S7; red downward arrows) remained as a plateau for the samples when the concentration of the Mn²⁺ ion relative to bCinS-FGPP/bLinS-FGPP was more than 3. The presence of additional equivalents of Mn^{2+} ion was observed as free/unbound Mn^{2+} ion, which predominantly contributes to the six-line EPR pattern around the g = 2 region (Figure 3; black asterisks). In addition, new half-field transitions were observed at low magnetic fields between 80-150 mT (Figures S6 and S7; blue arrows) and the intensity increased linearly. The observed half-field transitions were consistent with the free/unbound Mn^{2+} ion EPR signal. All these observations are consistent with bCinS and bLinS having 3 metal binding sites.

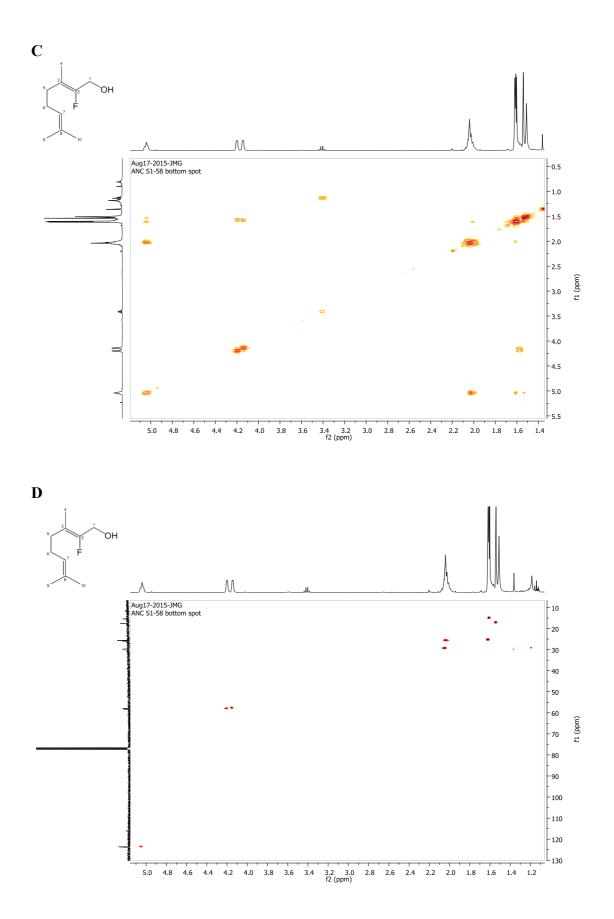


Scheme S1: Synthesis of FGP, FGPP, FNP and FNPP.



B





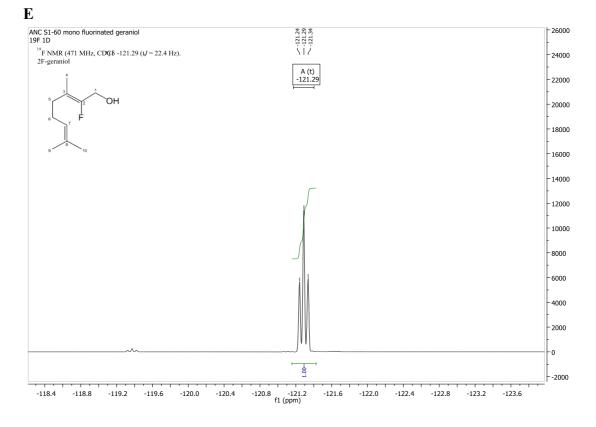
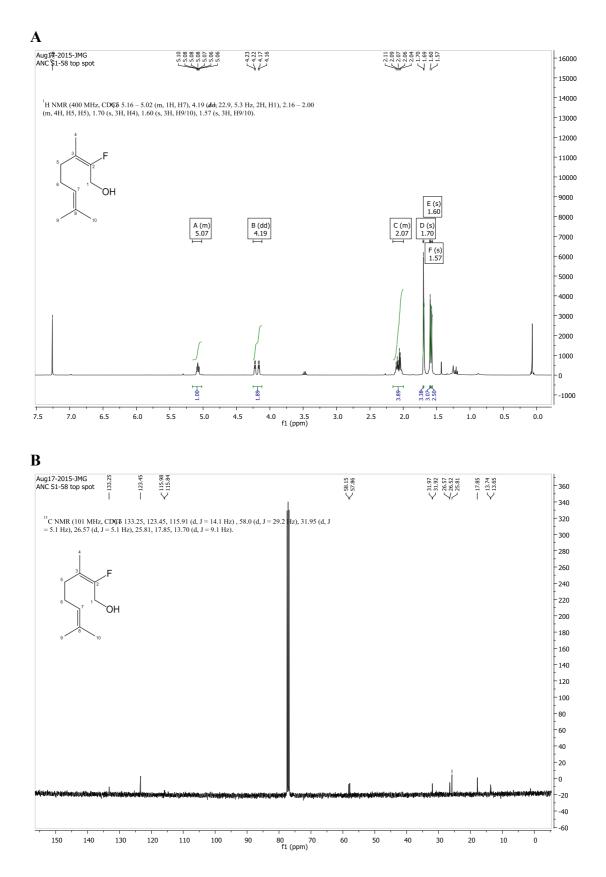
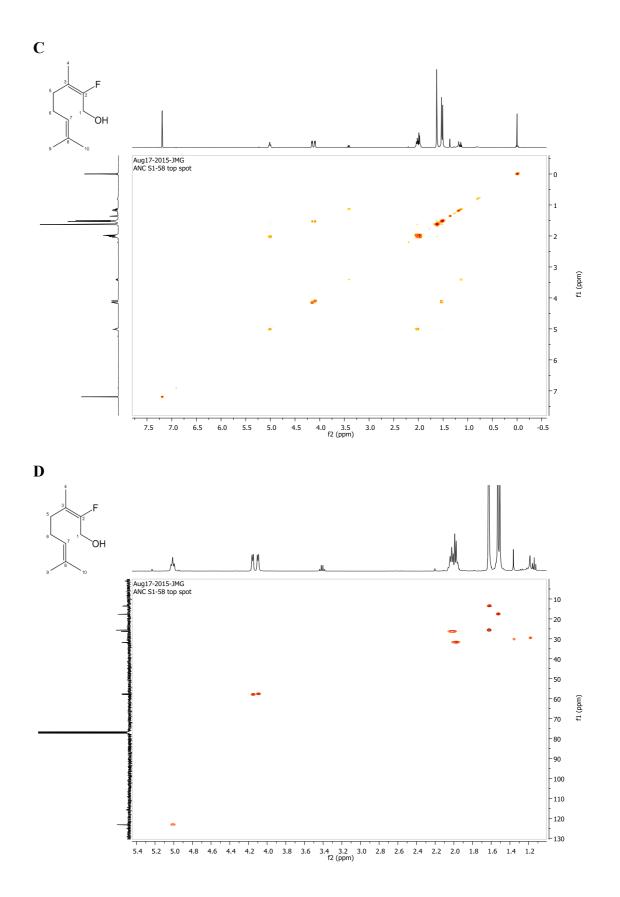


Figure S1. NMR spectra of 2-fluorogeraniol. A) ¹H NMR. B) ¹³C NMR. C) ¹H -¹H COSY. D) ¹H -¹³C HSQC. E) ¹⁹F NMR.





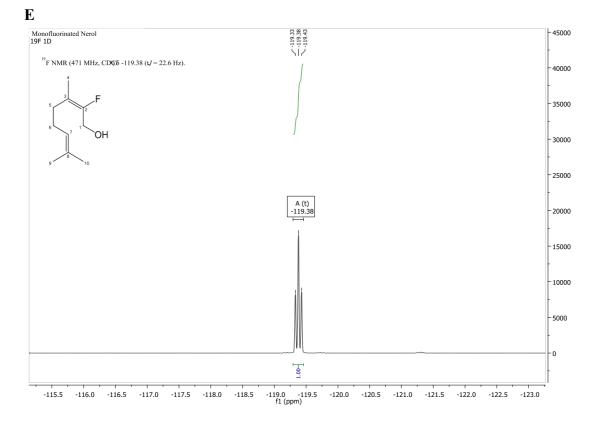
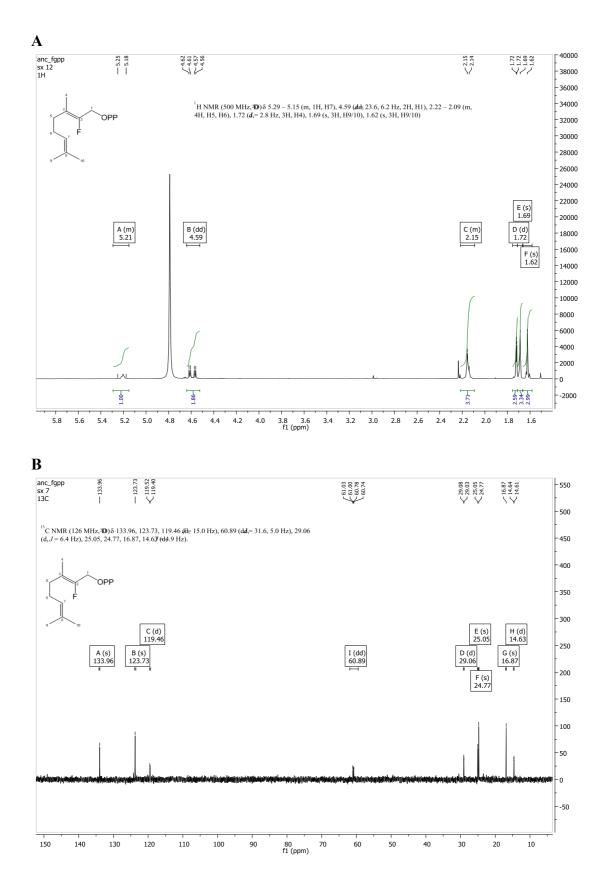
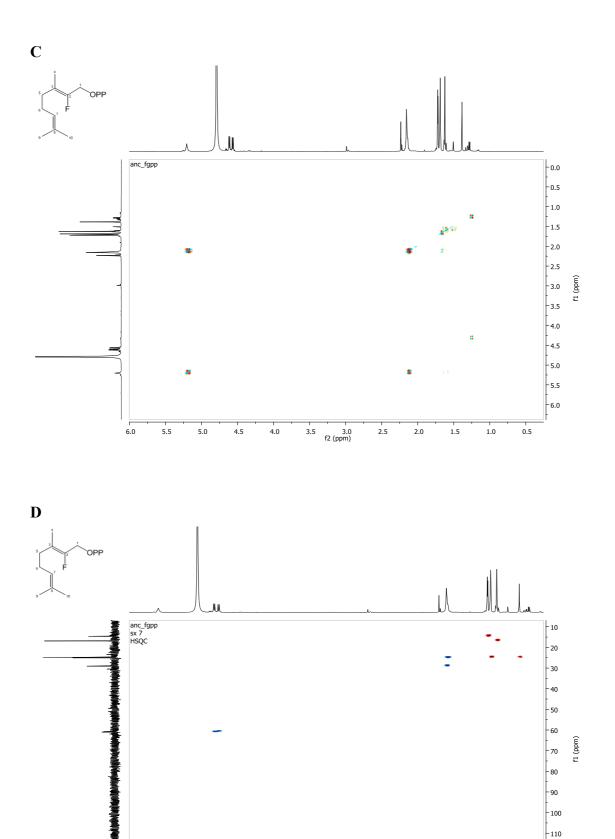


Figure S2. NMR spectra of 2-fluoronerol. A) ¹H NMR. B) ¹³C NMR. C) ¹H -¹H COSY. D) ¹H -¹³C HSQC. E) ¹⁹F NMR.

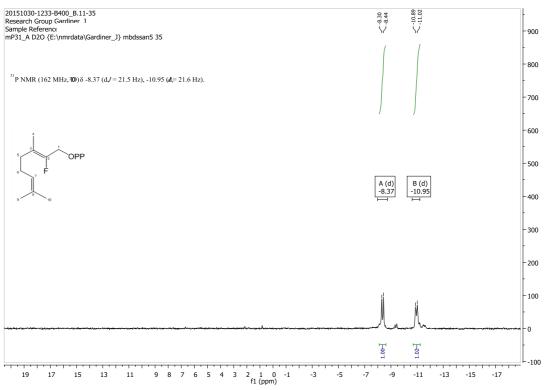




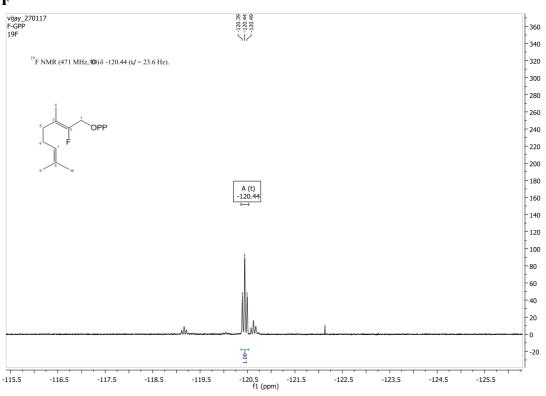
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- 120 -- 130









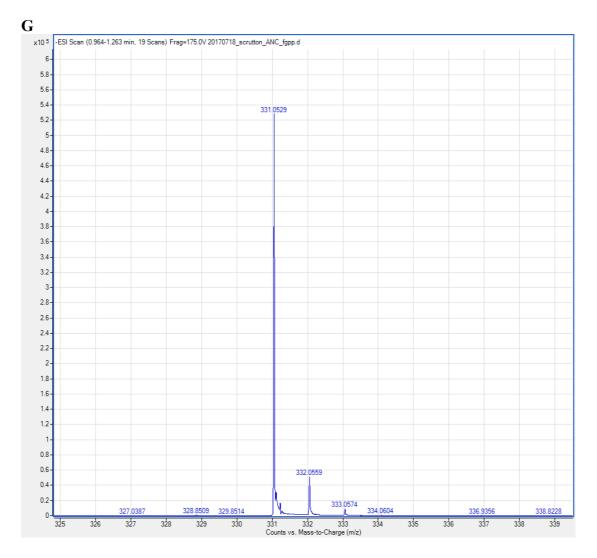
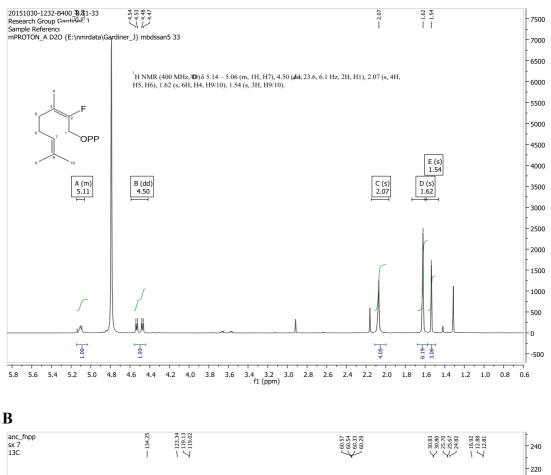
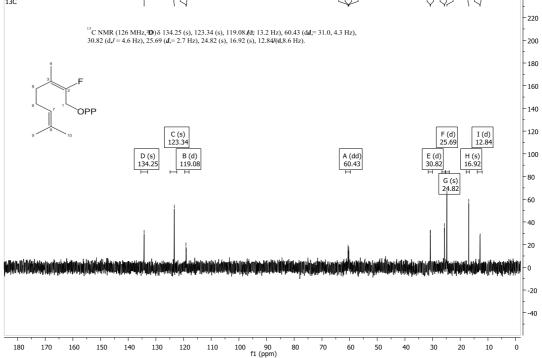
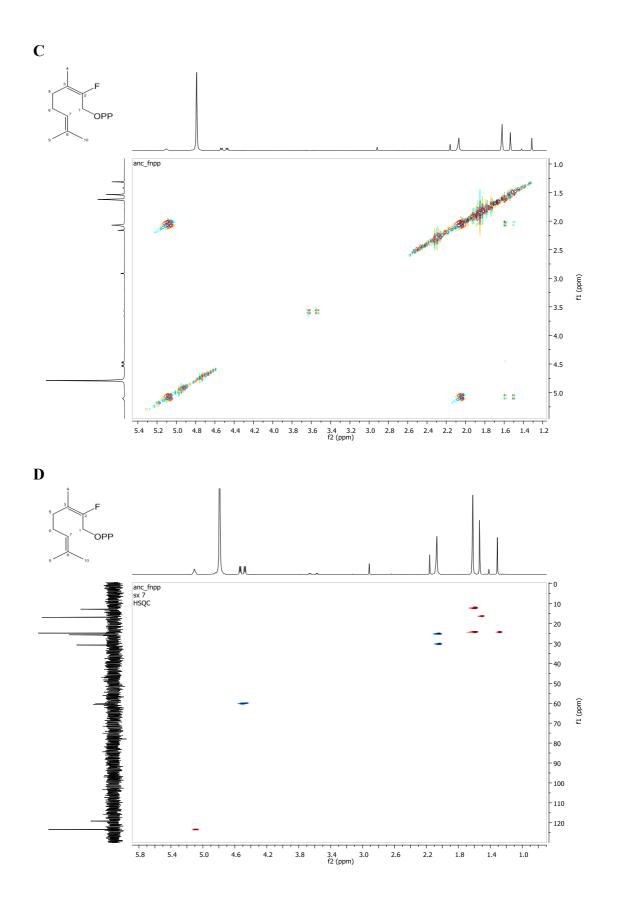


Figure S3. NMR and HRMS-ESI spectra of 2-fluorogeranyl pyrophosphate (FGPP). A) ¹H NMR. B) ¹³C NMR. C) ¹H -¹H COSY. D) ¹H -¹³C HSQC. E) ³¹P NMR. F) ¹⁹F NMR. G) HRMS-ESI.

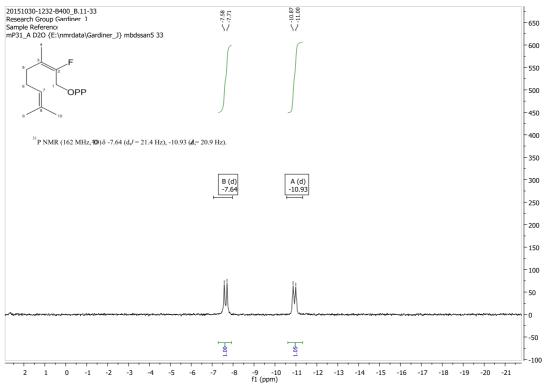




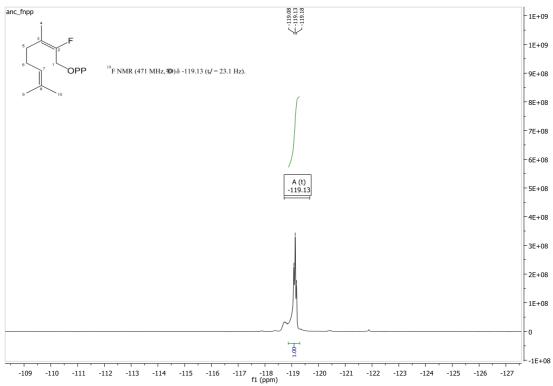


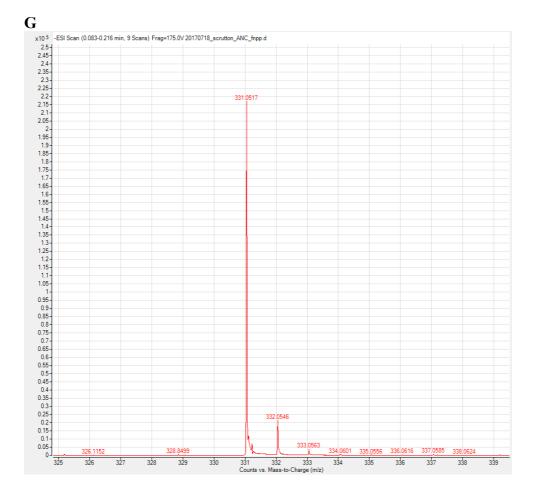


E



F





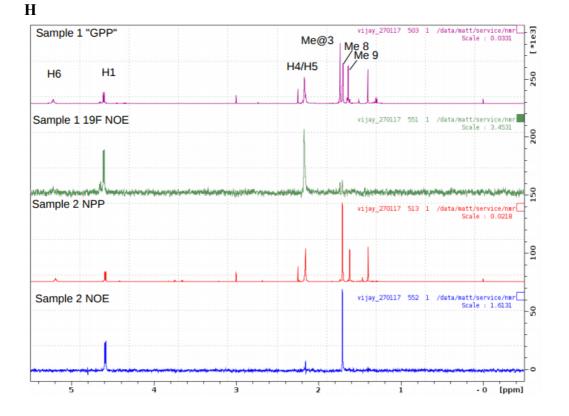


Figure S4. NMR and HRMS-ESI spectra of 2-fluoroneryl pyrophosphate (FNPP). A) ¹H NMR. B) ¹³C NMR. C) ¹H -¹H COSY. D) ¹H -¹³C HSQC. E) ³¹P NMR. F) ¹⁹F NMR. G) HRMS-ESI. H) Comparison of NOE data for FGPP and FNPP.

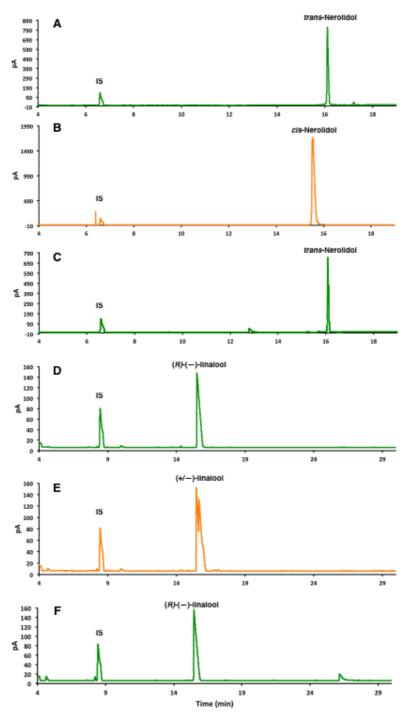


Figure S5. Gas chromatography analysis of bLinS with FPP and GPP. A) *trans*-Nerolidol standard. B) *cis*-Nerolidol standard. C) bLinS conversion of FPP (2 mM) *in vitro*. D) R-(–)-linalool standard. E) (+/–)-linalool standard. F) bLinS conversion of GPP (2 mM) *in vitro*. IS= internal standard (*sec*-butyl benezene)

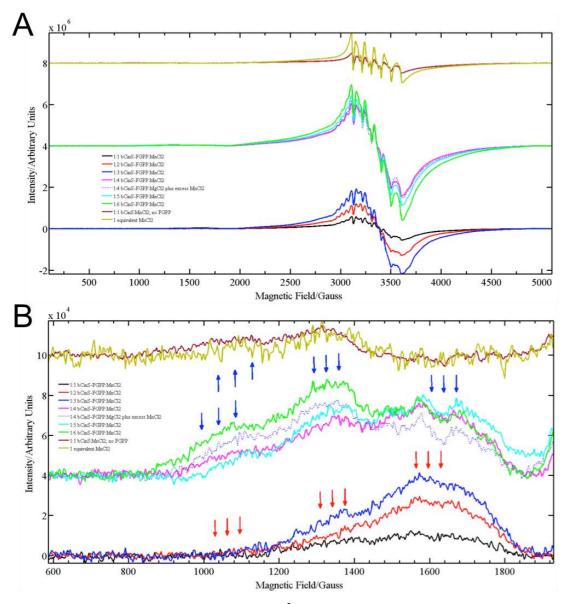


Figure S6. **cw-EPR spectra of bCinS.** Mn^{2+} substituted bCinS samples with varying equivalents of Mn^{2+} ion concentration with and without FGPP, measured as a frozen solution along with standard MnCl₂. A) Wide sweep from 10-510 mT. B) Expanded between 60-190 mT to show the half-field transitions of the Mn^{2+} ion under different coordination environments. The features that are highlighted with red and blue arrows are discussed in the text. Conditions: microwave power 36 dB; modulation amplitude 5 G; time constant 41 ms; conversion time 41 ms; sweep time 84 s; receiver gain 60 dB; average microwave frequency 9.384 GHz; temperature 20 K.

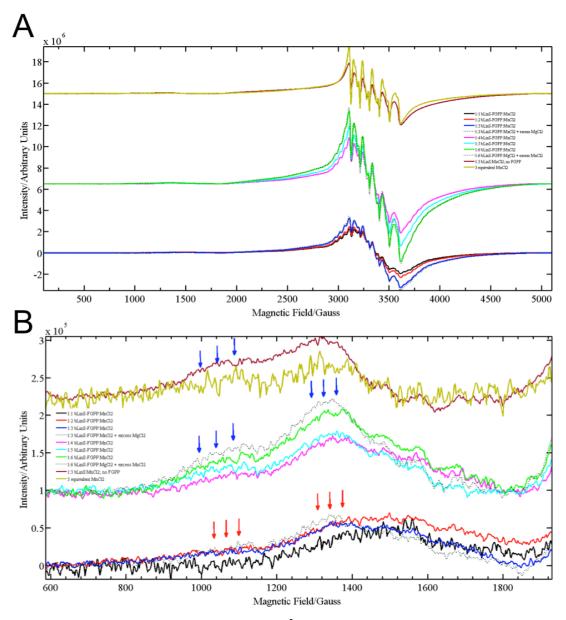


Figure S7. cw-EPR spectra of bLinS. Mn^{2+} substituted bLinS samples with varying equivalents of Mn^{2+} ion concentration with and without FGPP, measured as a frozen solution along with standard MnCl₂. A) Wide sweep from 10-510 mT. B) Expanded between 60-190 mT to show the half-field transitions of the Mn^{2+} ion under different coordination environments. The features that are highlighted with red and blue downward arrows are discussed in the text. Conditions: as in Fig S2.

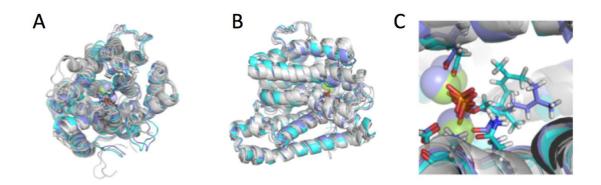


Figure S8. Comparison of structures from MD of *apo*-bCinS with MD of the ternary complex of bCinS with 3 Mg^{2+} ions and GPP or NPP. White: 4 clusters from 100 ns simulation of *apo*-bCinS, purple: the representative structure of the most populated cluster (after alignment on active site residues) from 100 ns simulations of bCinS with 3 Mg^{2+} ions and GPP, cyan the representative structure of the most populated cluster (after alignment on active site residues) from 100 ns simulations of bCinS with 3 Mg^{2+} ions and GPP, cyan the representative structure of the most populated cluster (after alignment on active site residues) from 100 ns simulations of bCinS with 3 Mg^{2+} ions and NPP. A) and B) show different views of the entire monomer, and C) shows the active site of bCinS. No significant structural changes are observed between the *apo* form and the ternary complex.

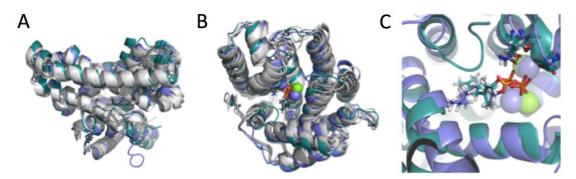


Figure S9. Comparison of structures from MD of *apo***-bLinS with MD of the ternary complex of bLinS with 3 Mg**²⁺ **ions and GPP or FPP.** White: 4 clusters from 100 ns simulation of *apo*-LinS, teal: the representative structure of the most populated cluster (after alignment on active site residues) from 100 ns simulations of bLinS with 3 Mg²⁺ ions and GPP, purple: the representative structure of the most populated cluster (after alignment on active site residues) from 100 ns simulations of bLinS with 3 Mg²⁺ ions and FPP. A) and B) show different views of the entire monomer, and **C)** shows the active site of bLinS. No significant structural changes are observed between the *apo* form and the ternary complex. The larger FPP can easily be accommodated in the active site without any major structural rearrangements.

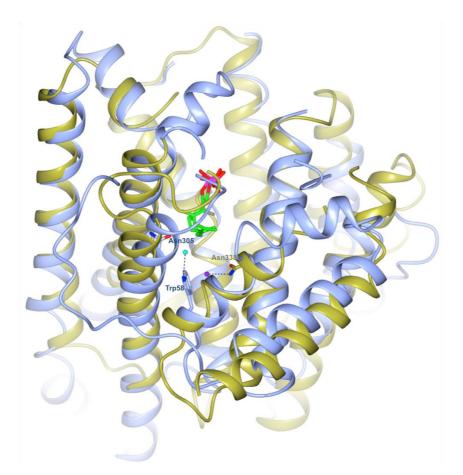


Figure S10: Structural overlay of bCinS and C-terminal domain of Sf-CinS1. In the bCinS-FNPP/FGPP structure (blue ribbon), residues Trp58 and Asn305 coordinate the water molecule (cyan sphere), which is proposed to be involved in water attack. In Sf-CinS1 (gold ribbon), Asn338 was identified to be crucial for 1,8-cineole synthesis and forms a hydrogen bond with a water molecule (purple sphere). Asn338 in Sf-CinS1 resides in a different helix and region of the active site compared to Asn305 in bCinS.

Table S1: Plasmids used in this study

Plasmid	Plasmid name	Description	(Origin	of	Reference
reference		replication, Antibiotic			
		marker,	Referen	ce(s),	
		Promoters and Operons)			
pMVA	BbA5a-MTSAe-	p15A, Kanr, I	PlacUV5, M	ITSA,	1
	T1f-MBI(f)-	T1, MBI-f, T1	002		
	T1002i				
pGPPSmTC/S15	pBbB2a-	pBBR,	Ampr,	Ptet,	1
	trAgGPPS(co)-	trAgGPPS(co)- trSLimS_Ms			
	trSLimS_Ms				
pGPPSmTC/S38	pBbB2a-	pBBR,	Ampr,	Ptet,	This study
	trAgGPPS(co)-	trAgGPPS(co)- bLinS			
	bLinS				
pGPPSmTC/S39	pBbB2a-	pBBR,	Ampr,	Ptet,	This study
	trAgGPPS(co)-	trAgGPPS(co)- bCinS			
	bCinS				

Name	PDB	Organism	RMSD (Å) /			
			Ca atoms			
bLinS (chain A)						
Pentalenene synthase	1ps1	Streptomyces exfoliatus	1.52 / 283			
Germacradien-4-ol	5ilu	Streptomyces citricolor	1.59 / 276			
synthase						
Hedycaryol synthase	4mc3	Actinomycete K. setae	1.99 / 275			
Geosmin synthase	5dz2	Streptomyces coelicolor	1.82 / 279			
Epi-isozizaene synthase	4ltv	Streptomyces coelicolor	2.19 / 286			
Selinadiene synthase	4okz	Streptomyces	1.83 / 265			
		pristinaespiralis				
2-Methylisoborneol	4la6	Streptomyces coelicolor	2.09 / 268			
synthase						
bCinS						
Geosmin synthase	5dz2	Streptomyces coelicolor	1.54 / 296			
Pentalenene synthase	1ps1	Streptomyces exfoliatus	1.80 / 292			
Germacradien-4-ol	5ilu	Streptomyces citricolor	1.80 / 283			
synthase						
Epi-isozizaene synthase	3kb9	Streptomyces coelicolor	1.94 / 304			
Hedycaryol synthase	4mc3	Actinomycete K. setae	2.07 / 276			
Aristolochene synthase	4kwd	Aspergillus terreus	2.28 / 280			

Table S2: bLinS and bCinS: homologous structures

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1. Leferink, N. G. H.; Jervis, A. J.; Zebec, Z.; Toogood, H. S.; Hay, S.; Takano, E.; Scrutton, N. S. *ChemistrySelect* **2016**, 1, 1893-1896.