

Supporting information

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

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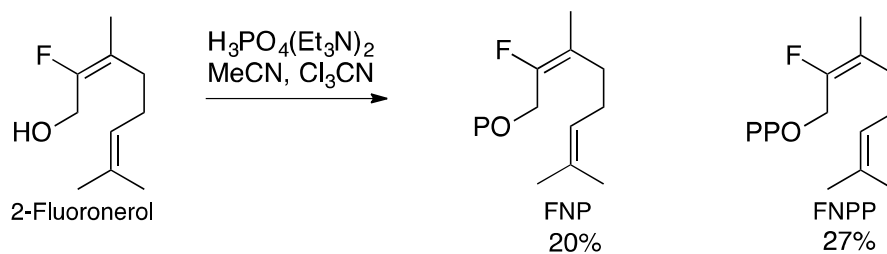
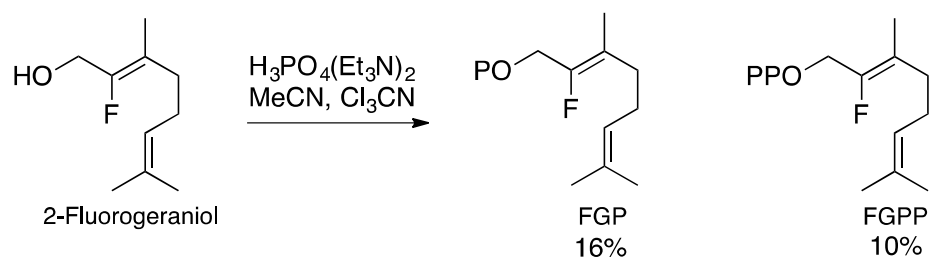
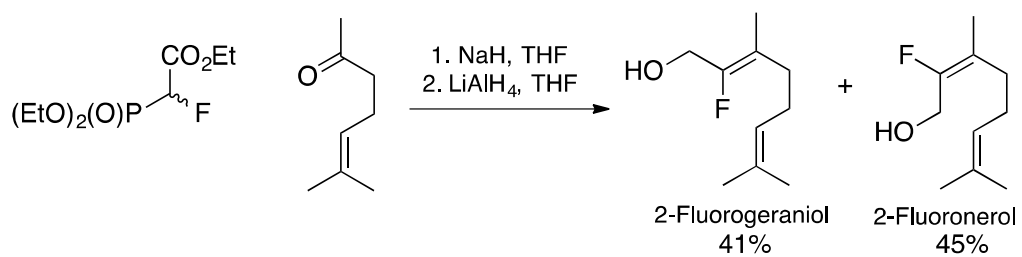
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Table S1: Plasmids used in this study

Table S2: bLinS and bCinS: homologous structures

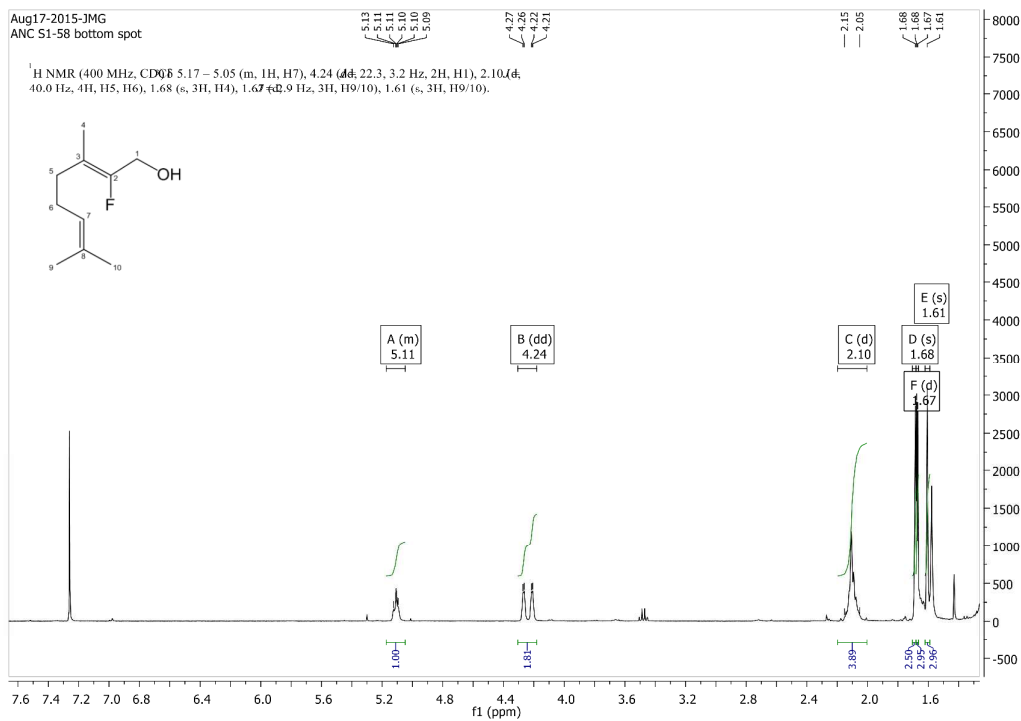
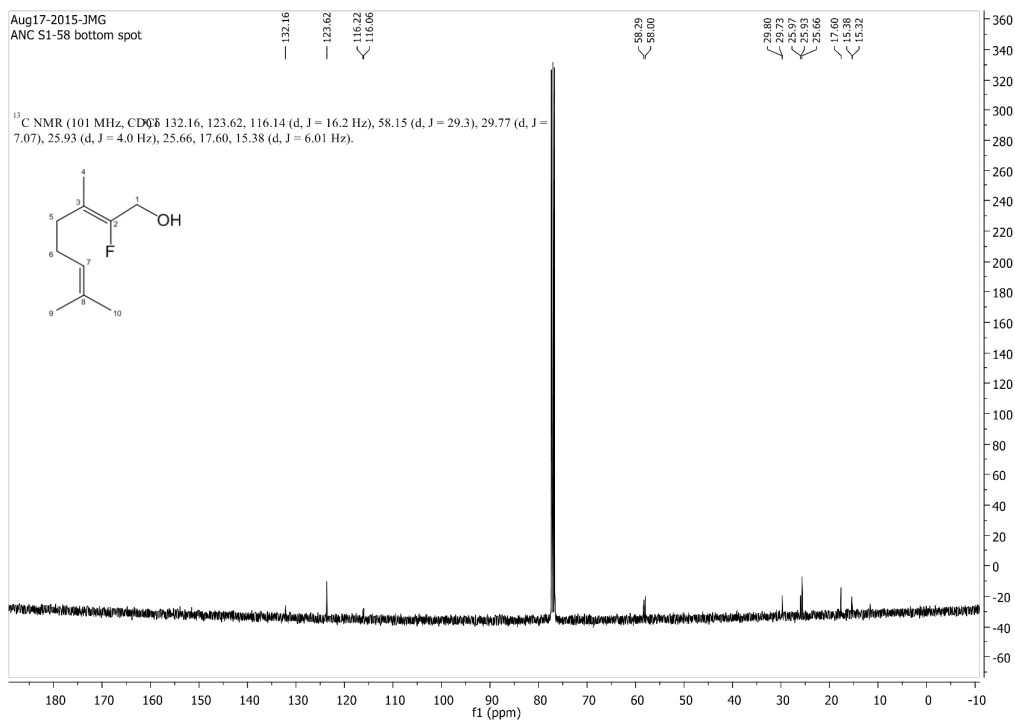
Extended EPR results and discussion

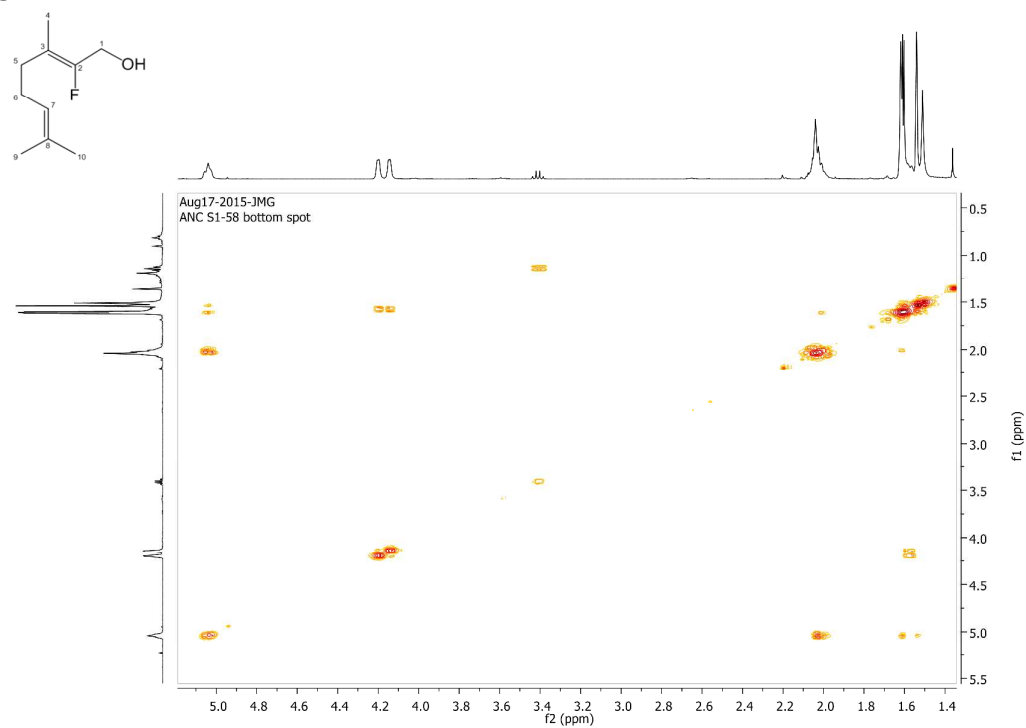
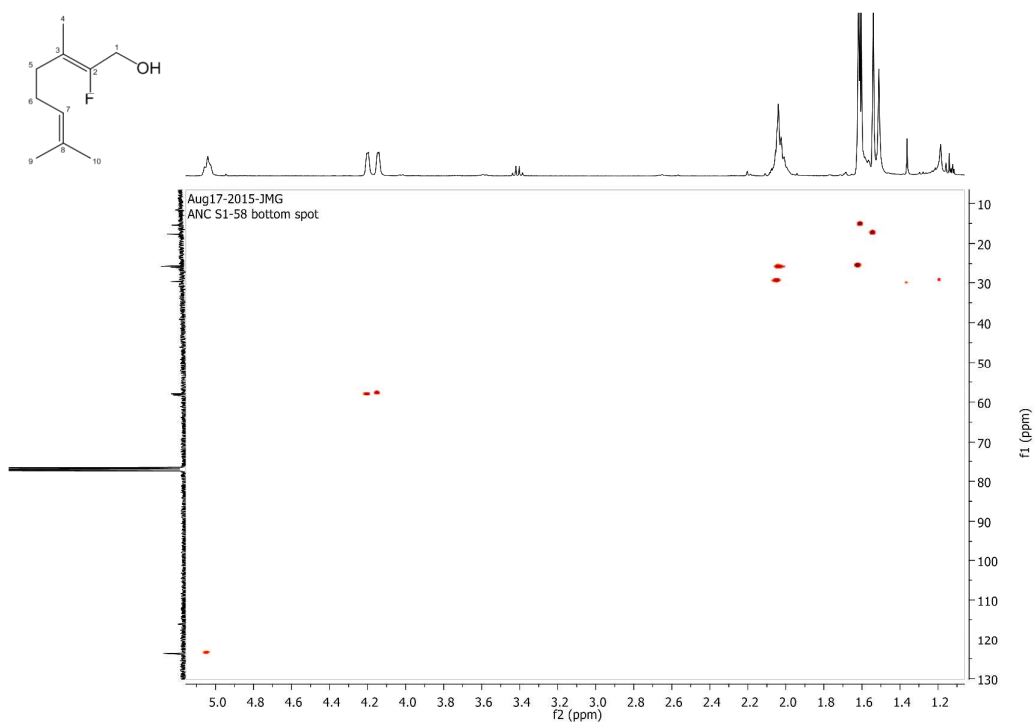
Comparisons of EPR spectra of Mn^{2+} ion substituted bCinS/bLinS with and without FGPP along with standard MnCl_2 samples show a clearly resolved multiplet structure for 1:1 bCinS/bLinS: MnCl_2 in the presence of FGPP. The observation of a multiplet structure indicates that degeneracy of the six-line 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 $|m_s, -1/2\rangle \rightarrow |m_s, +1/2\rangle$ 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, $|m_s, -5/2\rangle \rightarrow |m_s, -3/2\rangle$ and $|m_s, -3/2\rangle \rightarrow |m_s, -1/2\rangle$ respectively. The multiplet structure observed for bCinS and bLinS directly probes the local/first coordination sphere of the Mn^{2+} ion, which was clearly different from the reference samples $[\text{Mn}(\text{H}_2\text{O})_6]^{2+}$ (black dotted spectrum) and bCinS/bLinS without FGPP (black dashed spectrum). The aforementioned two samples predominantly showed a six-line EPR pattern with half-field transitions in the range of 80-150 mT, whereas for 1:1 bCinS/bLinS-FGPP: MnCl_2 , 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 Mn^{2+} 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.



OP = phosphate
 OPP = pyrophosphate

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

A**B**

C**D**

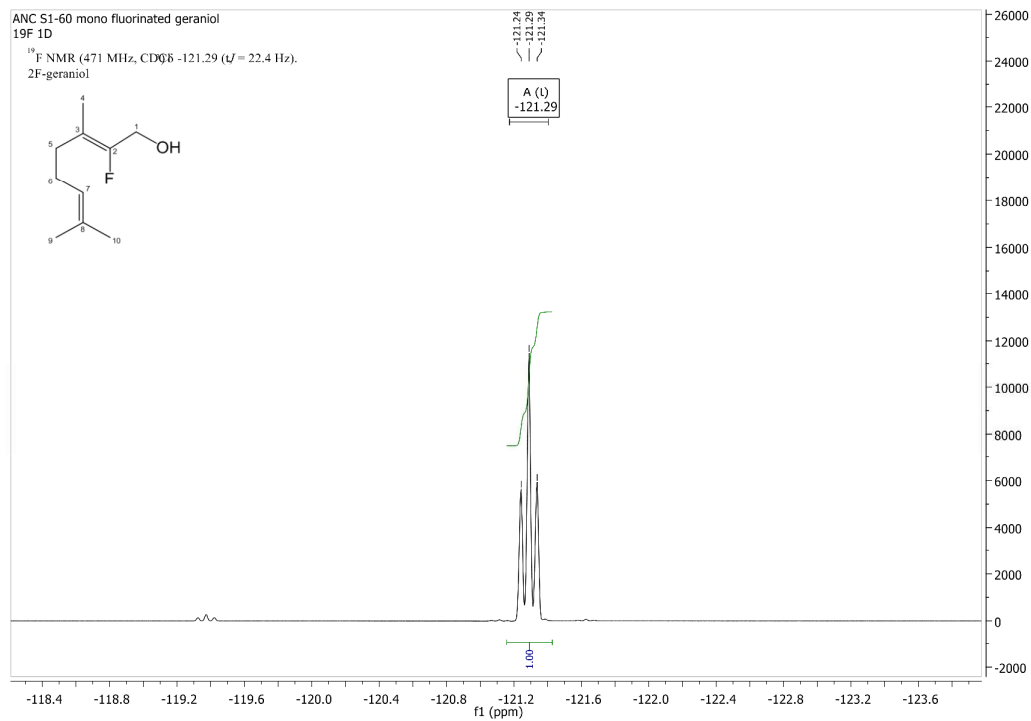
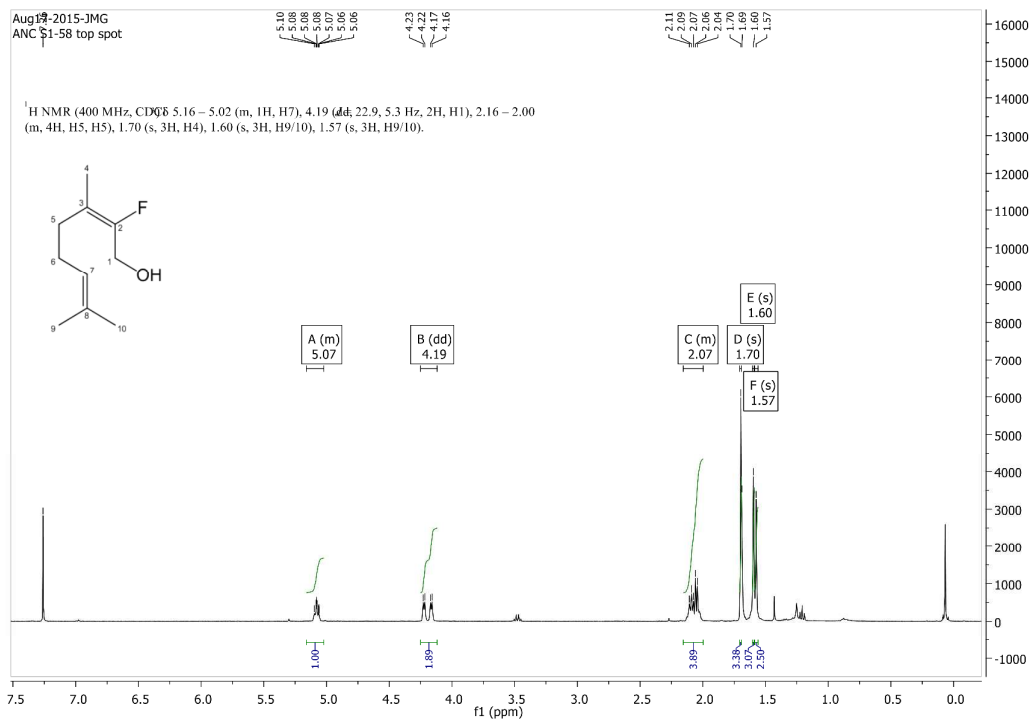
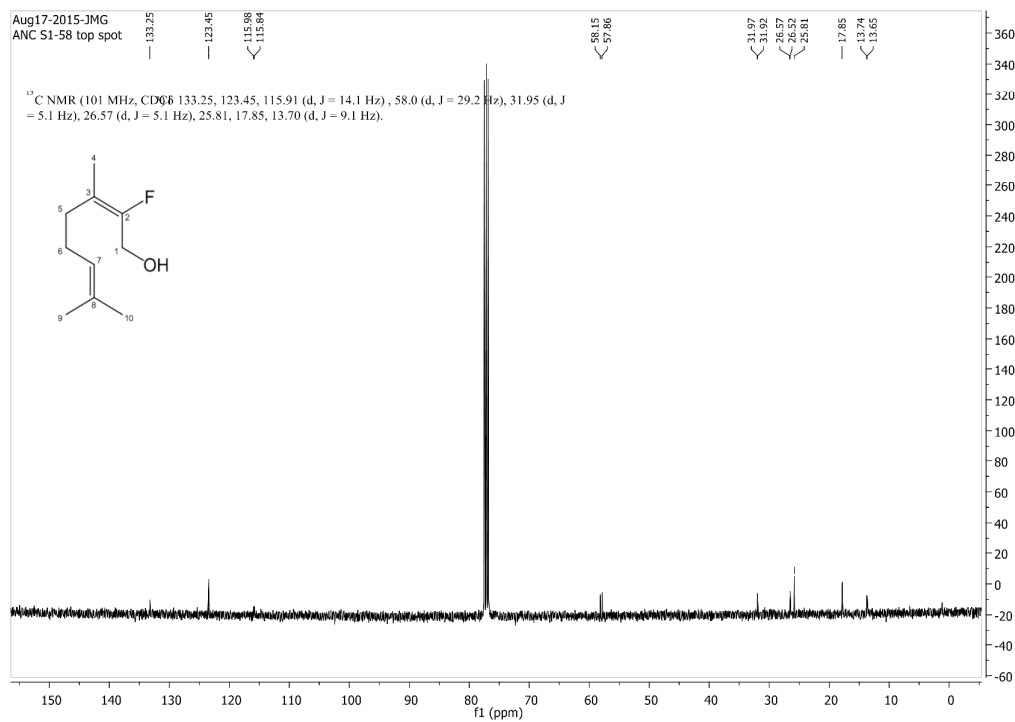
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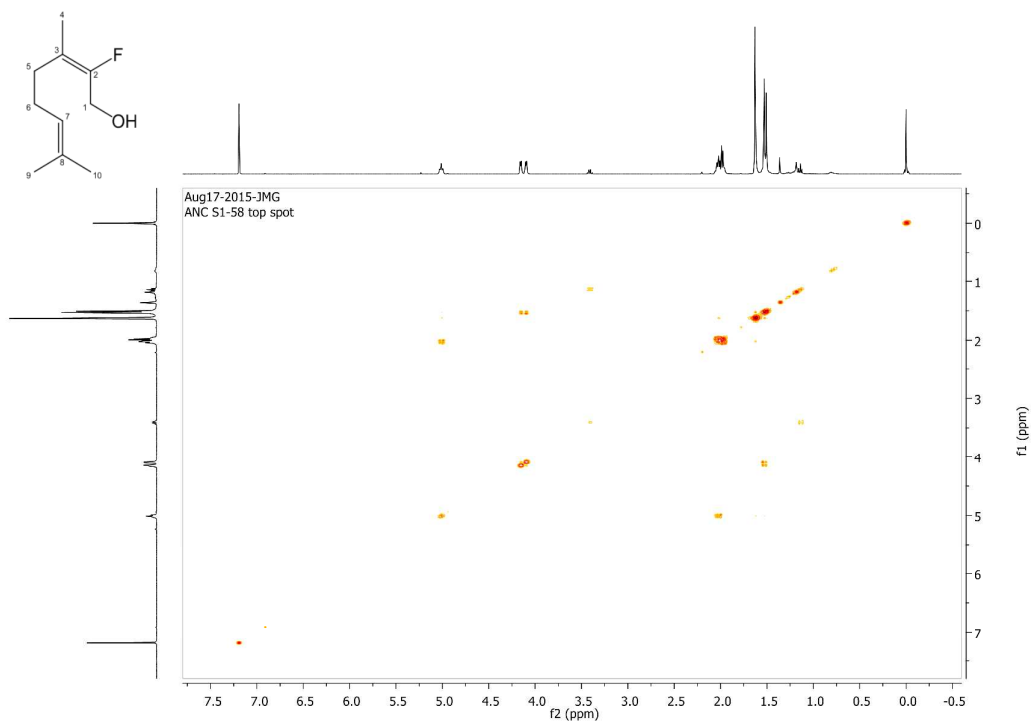
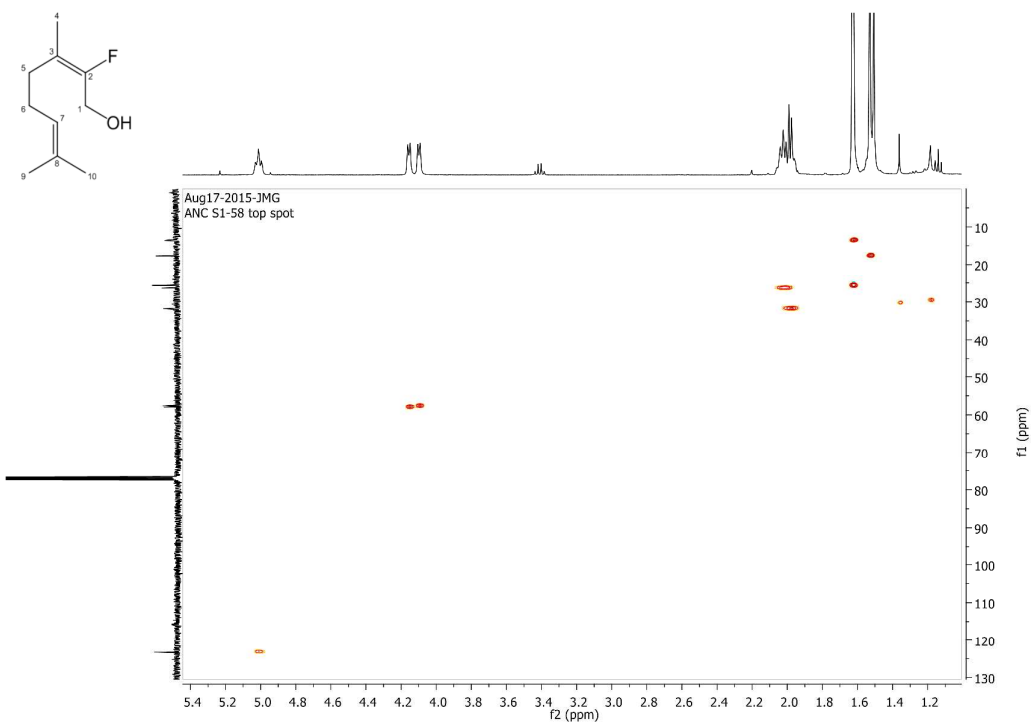
Figure S1. NMR spectra of 2-fluorogeraniol. A) ¹H NMR. B) ¹³C NMR. C) ¹H - ¹H COSY. D) ¹H - ¹³C HSQC. E) ¹⁹F NMR.

A



B



C**D**

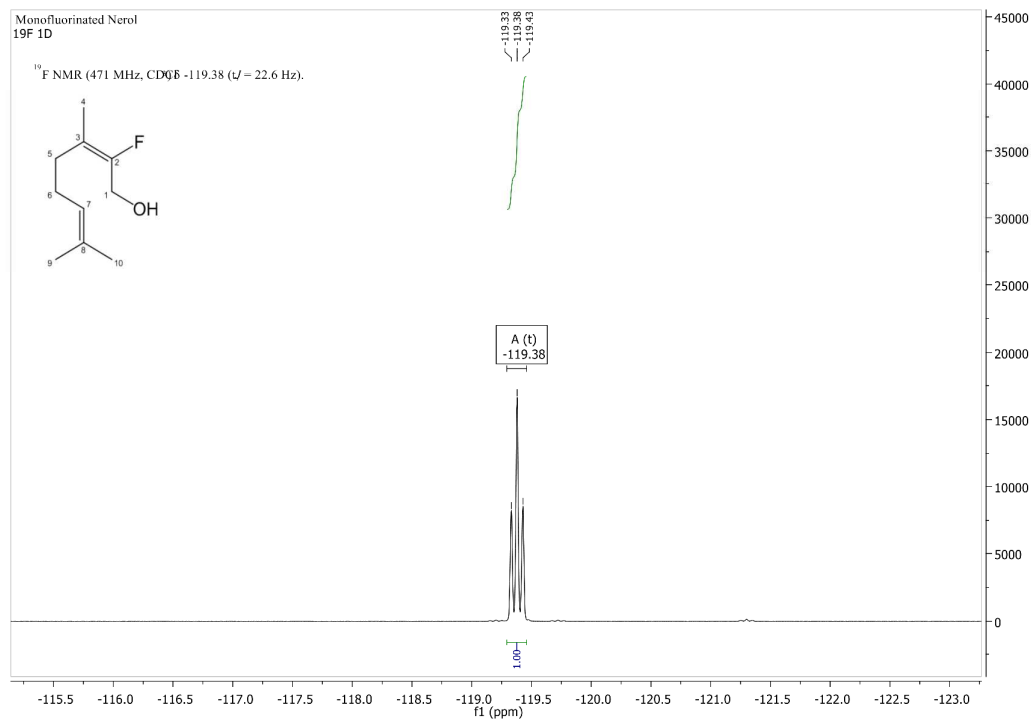
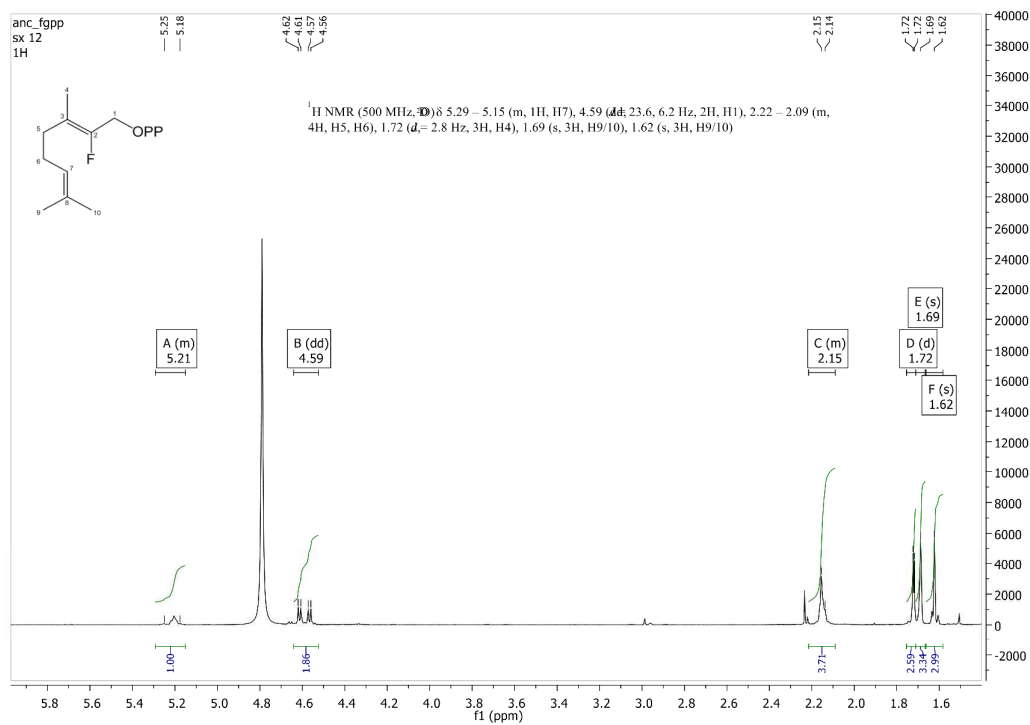
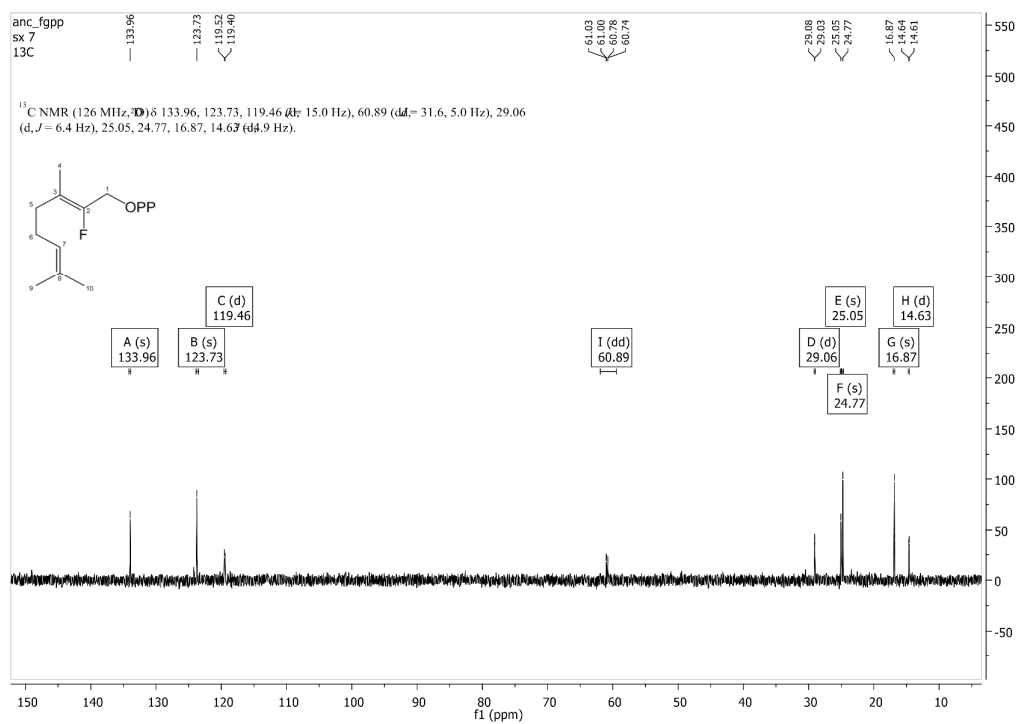
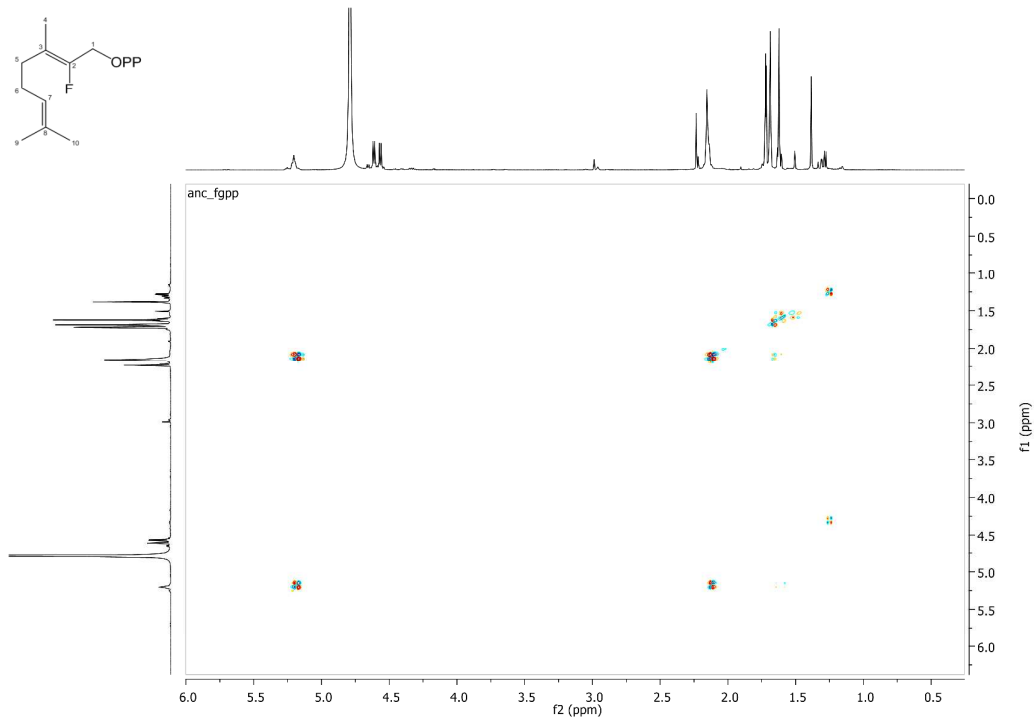
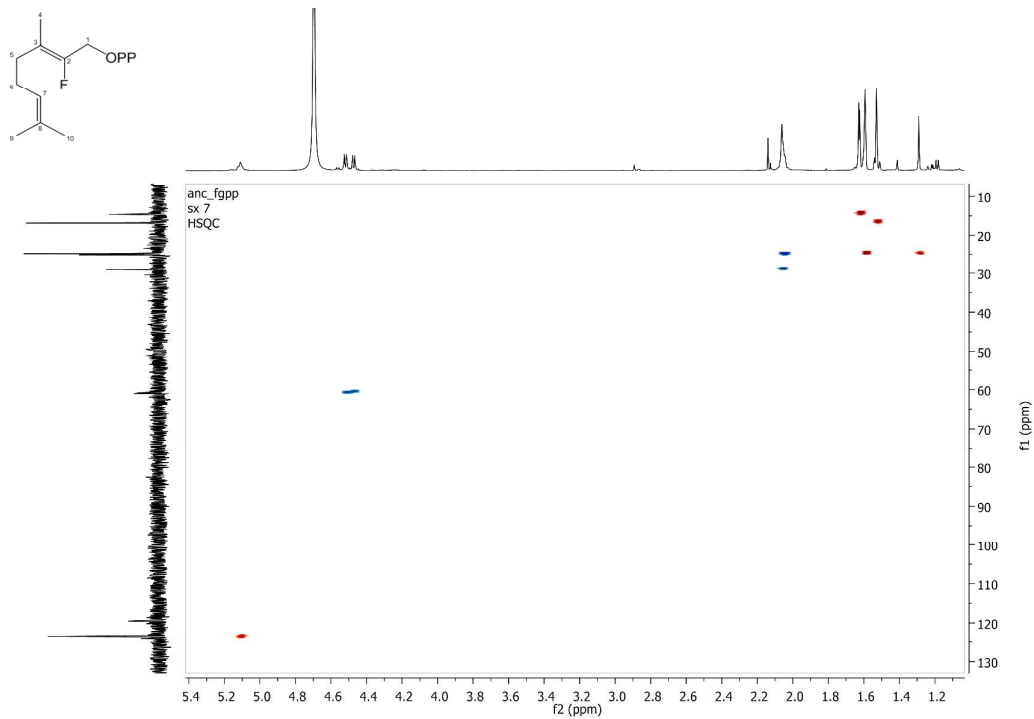
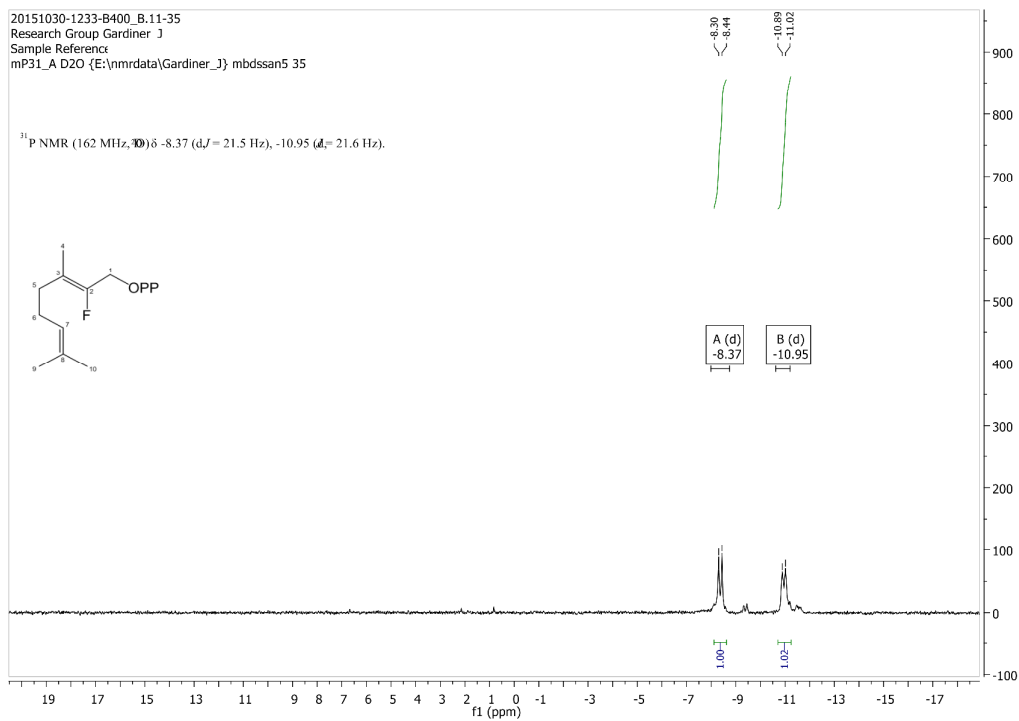
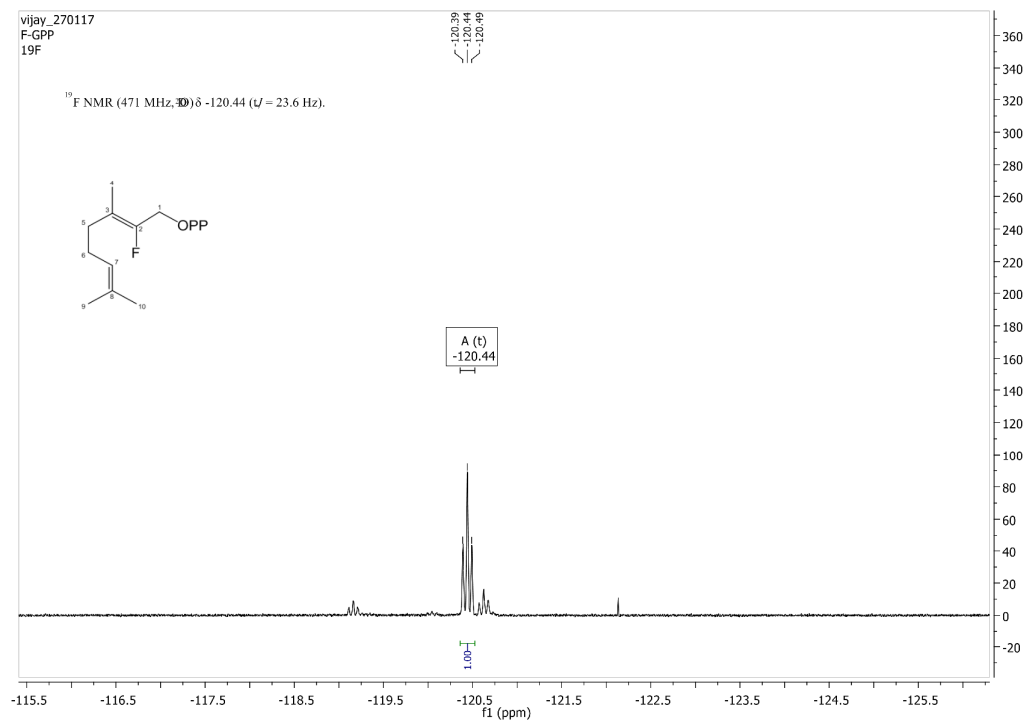
E

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

A**B**

C**D**

E**F**

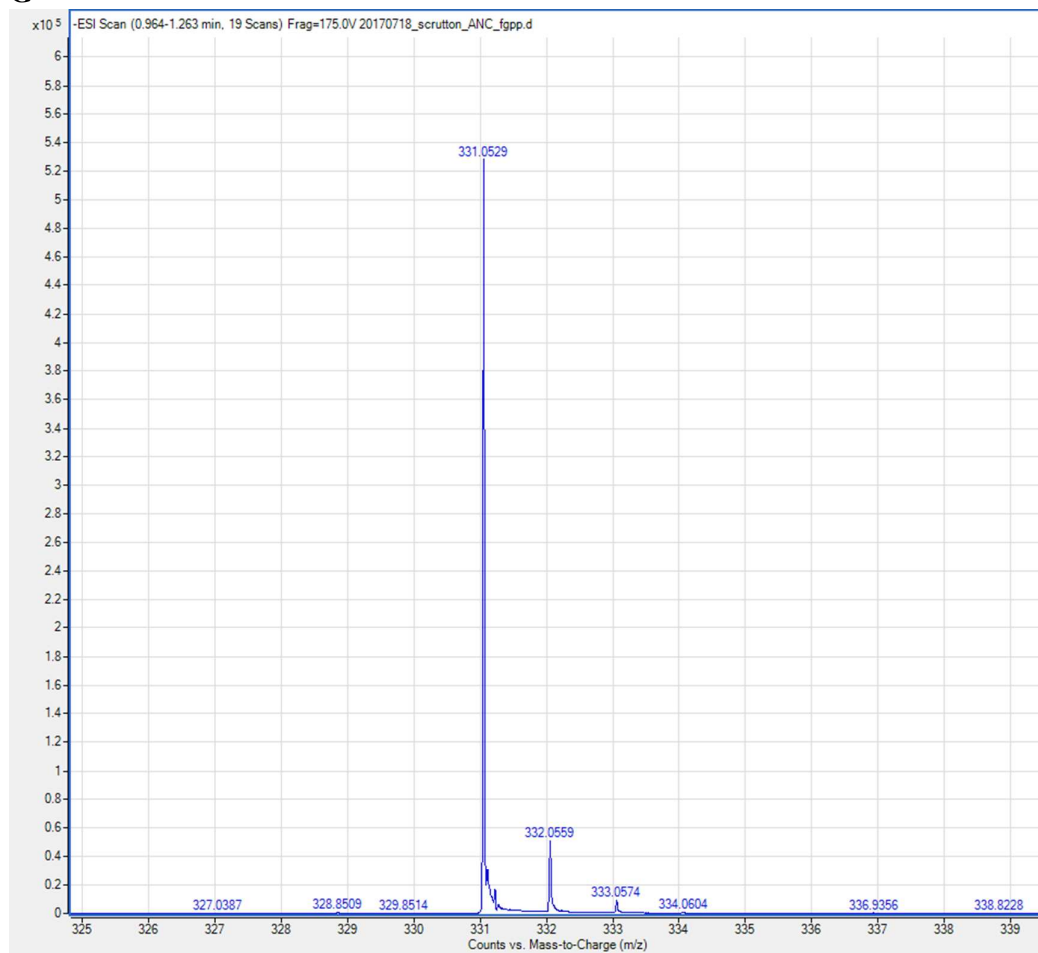
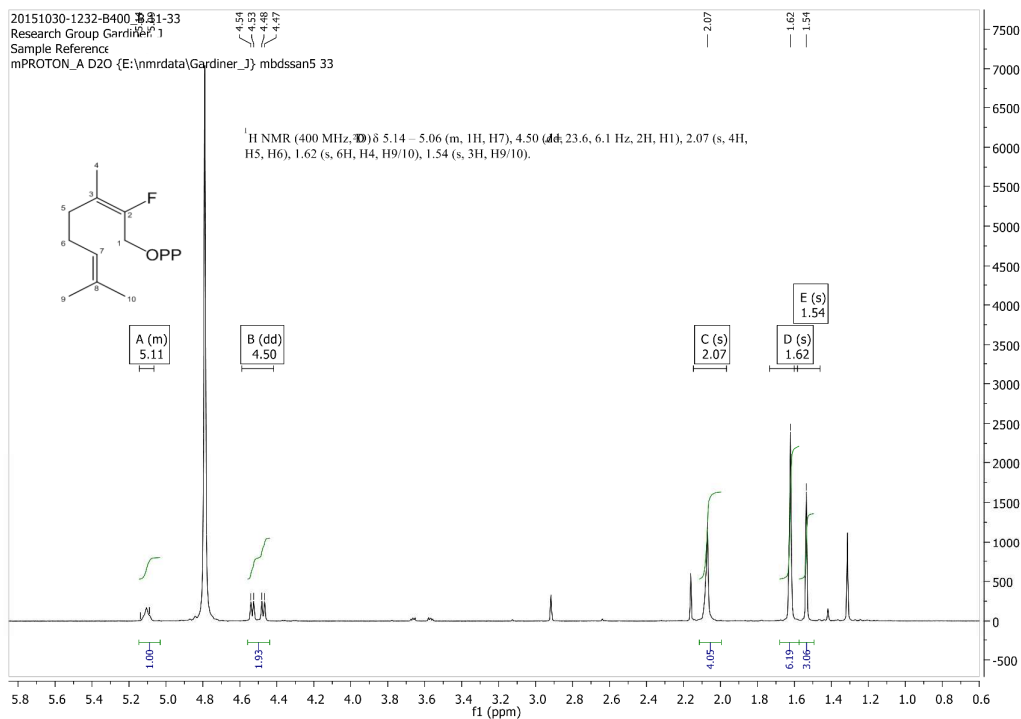
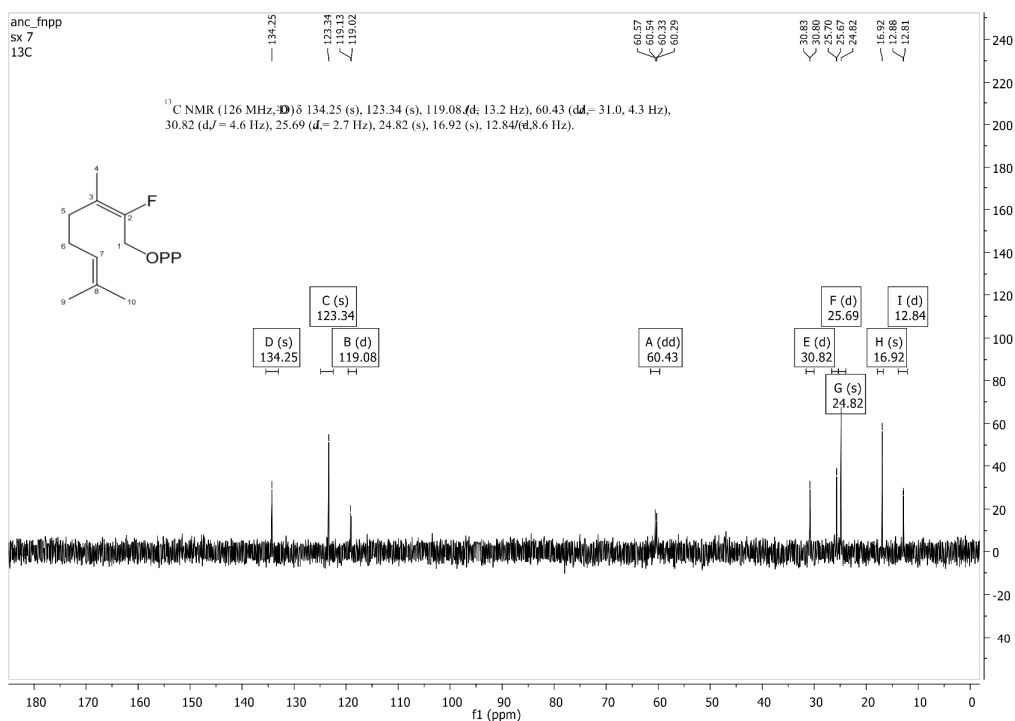
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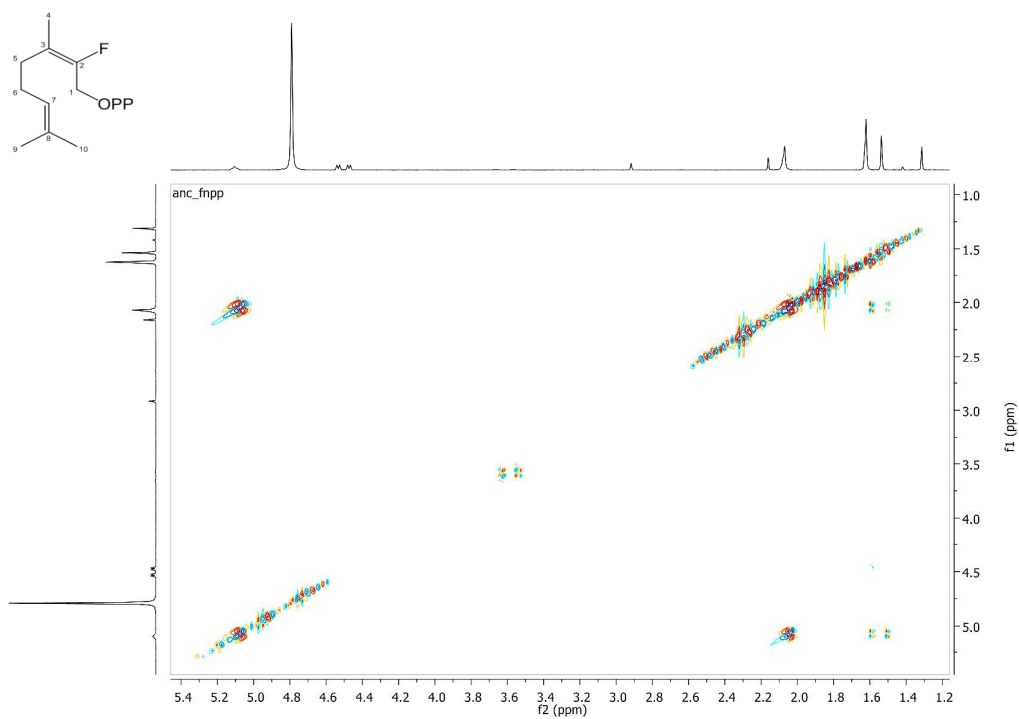
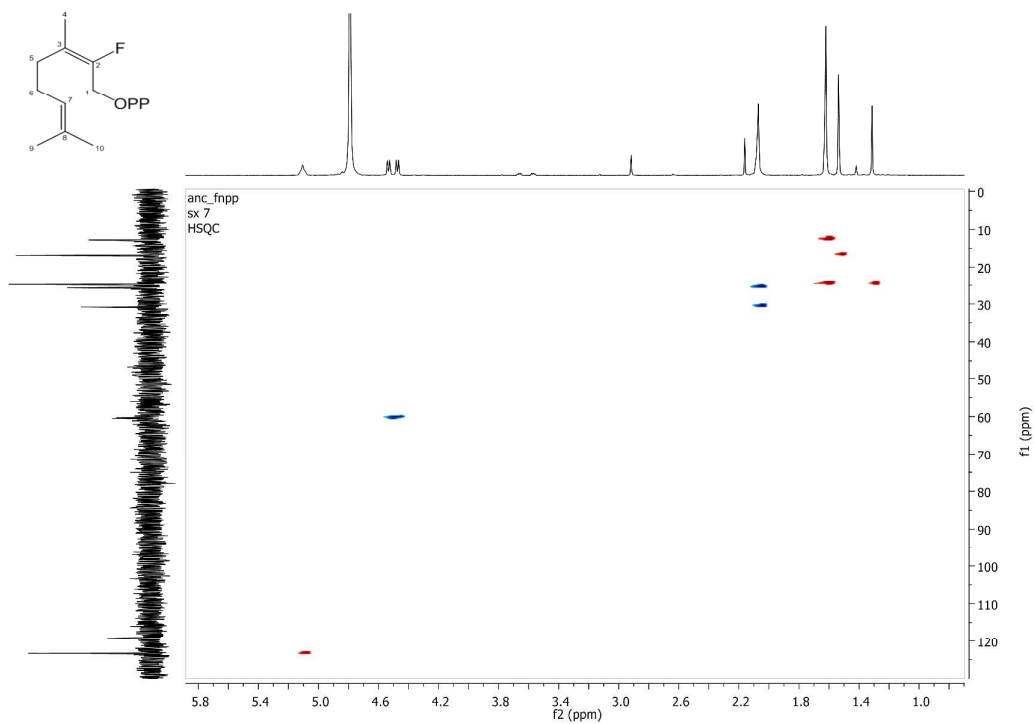
Figure S3. NMR and HRMS-ESI spectra of 2-fluorogeranyl pyrophosphate (FGPP). A) ^1H NMR. B) ^{13}C NMR. C) ^1H - ^1H COSY. D) ^1H - ^{13}C HSQC. E) ^{31}P NMR. F) ^{19}F NMR. G) HRMS-ESI.

A

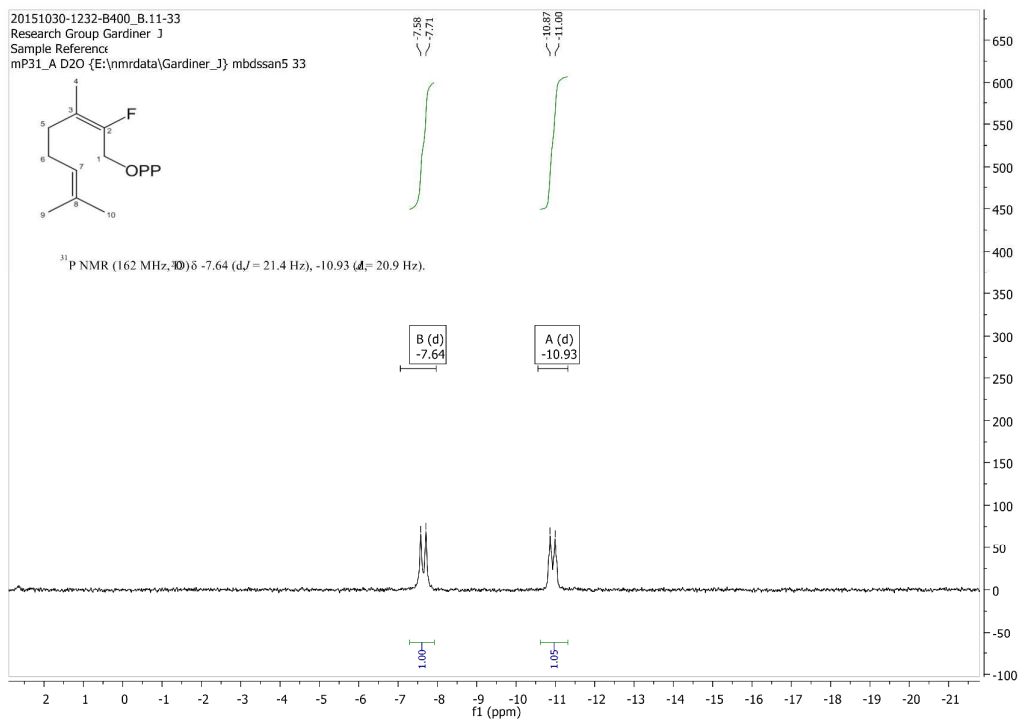


B

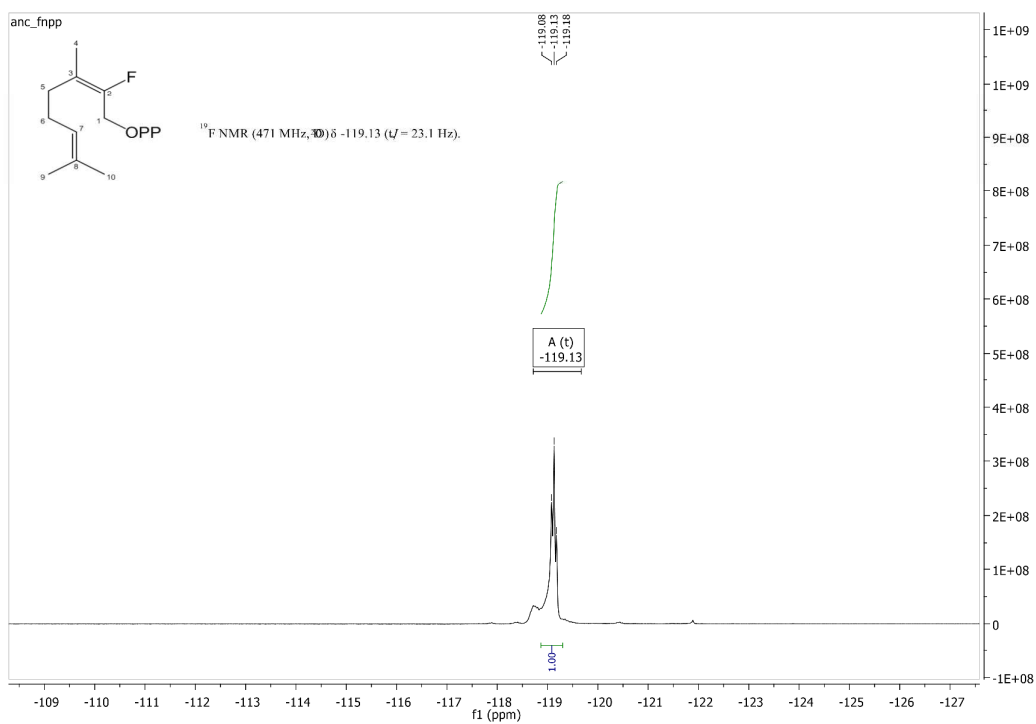


C**D**

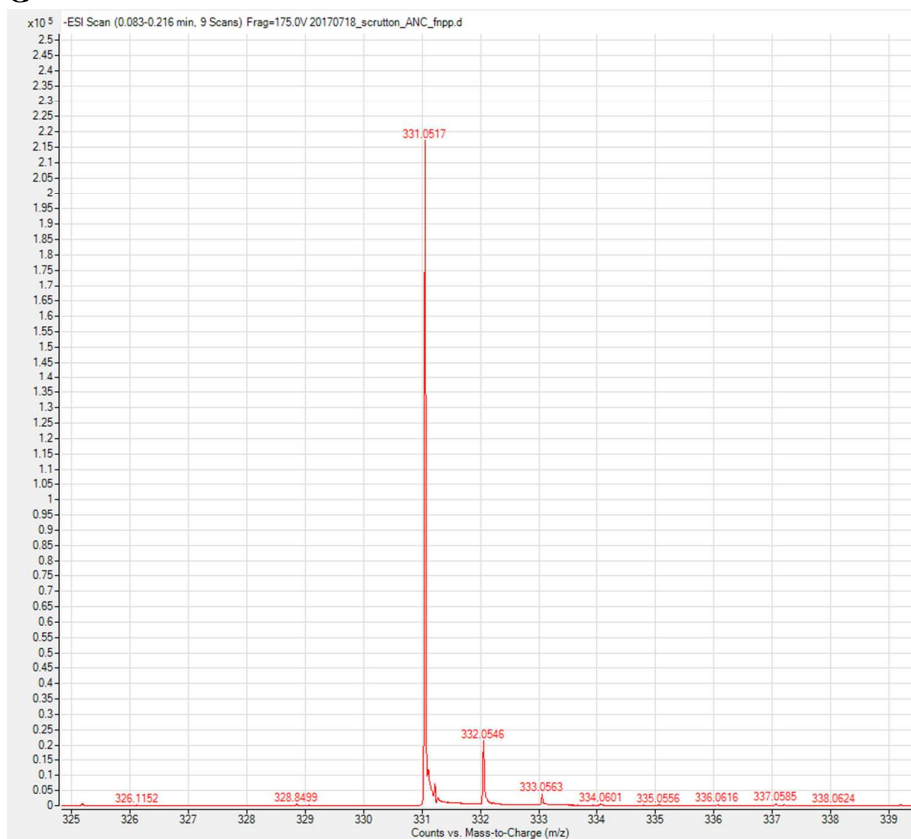
E



F



G



H

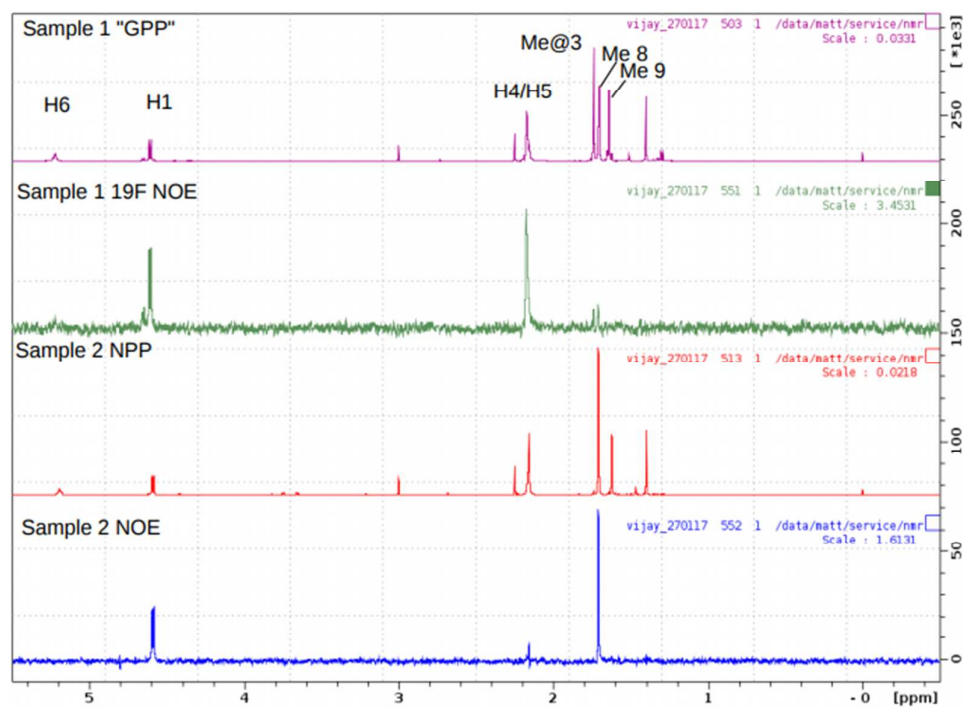


Figure S4. NMR and HRMS-ESI spectra of 2-fluoroneryl pyrophosphate (FNPP). A) ^1H NMR. B) ^{13}C NMR. C) ^1H - ^1H COSY. D) ^1H - ^{13}C HSQC. E) ^{31}P NMR. F) ^{19}F NMR. G) HRMS-ESI. H) Comparison of NOE data for FGPP and FNPP.

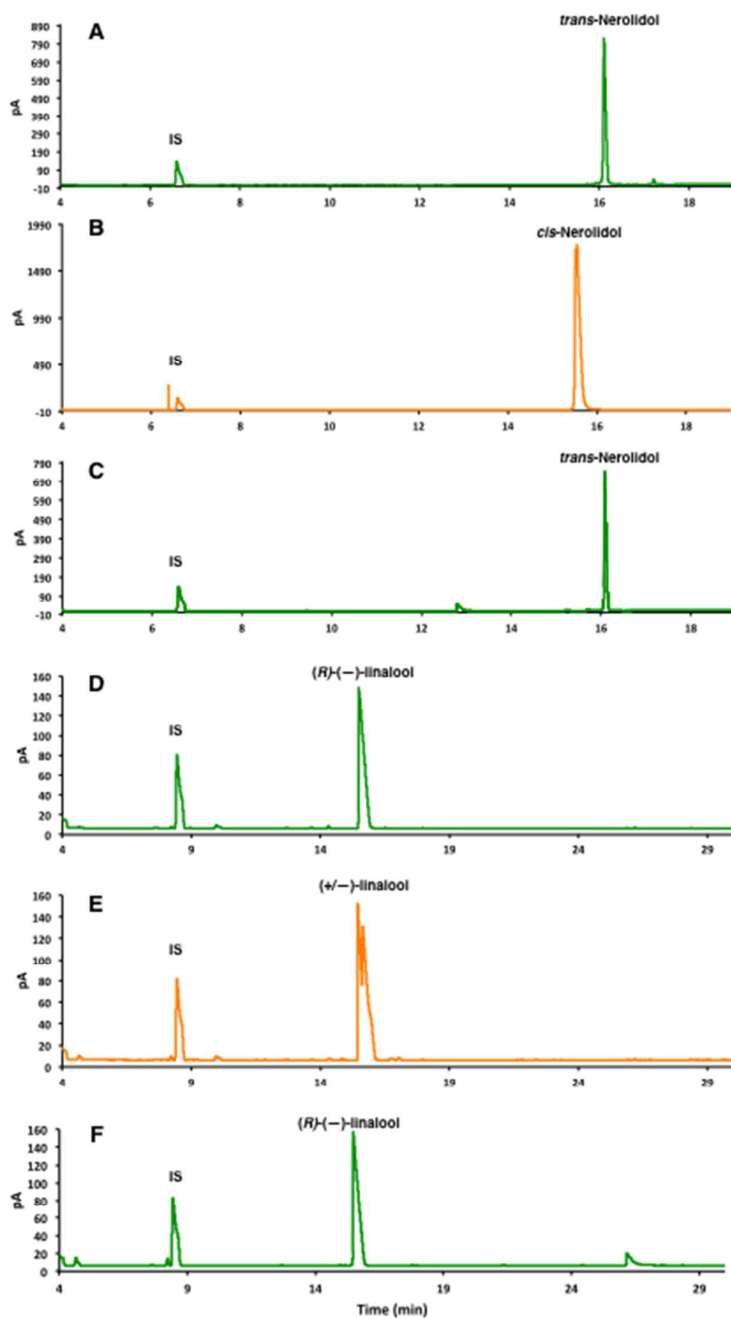


Figure S5. Gas chromatography analysis of bLinS with FPP and GPP. A) *trans*-Nerolidol standard. B) *cis*-Nerolidol standard. C) bLinS conversion of FPP (2 mM) *in vitro*. D) *R*-(-)-linalool standard. E) (+/-)-linalool standard. F) bLinS conversion of GPP (2 mM) *in vitro*. IS= internal standard (*sec*-butyl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

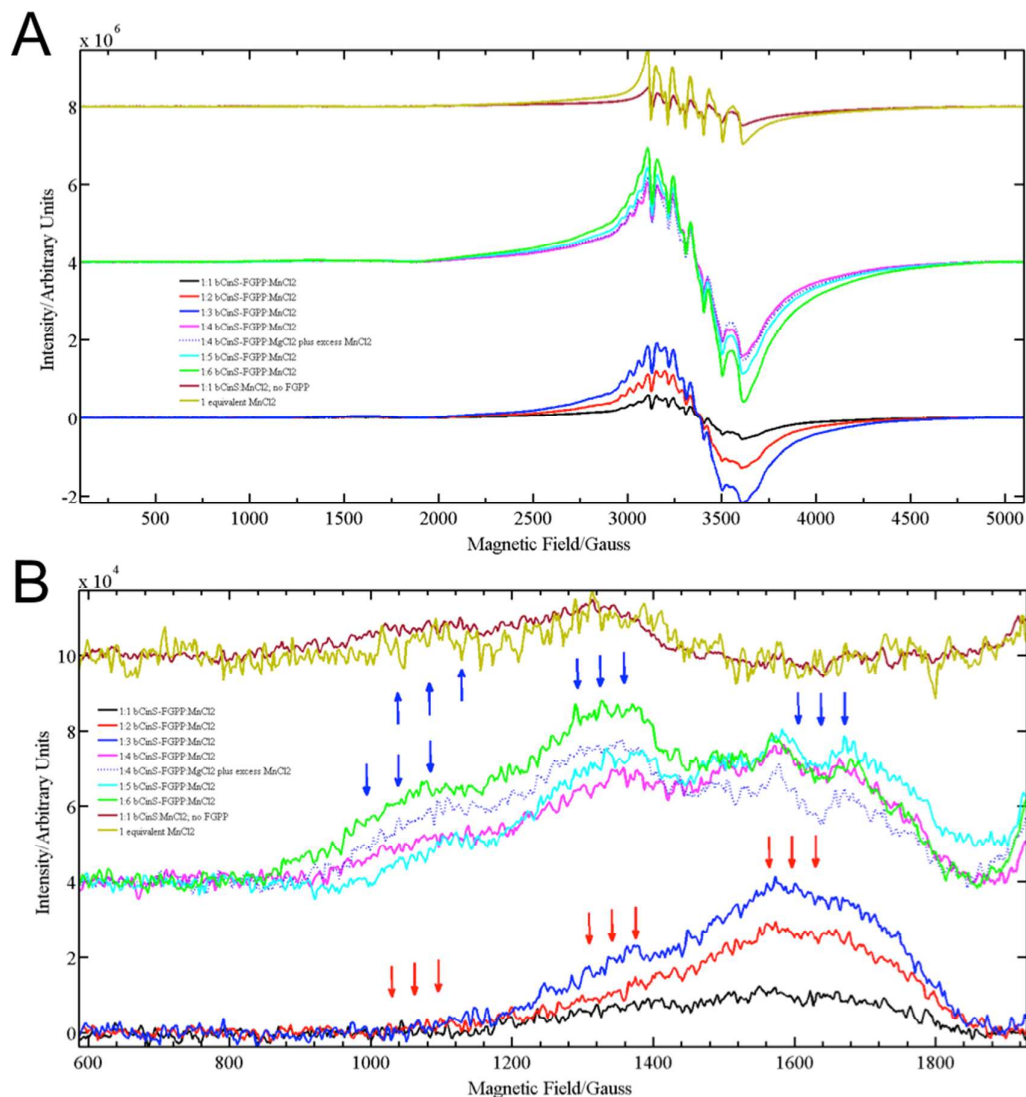


Figure S6. cw-EPR spectra of bCinS. Mn^{2+} substituted bCinS samples with varying equivalents of Mn^{2+} ion concentration with and without FGPP, measured as a frozen solution along with standard MnCl_2 . A) Wide sweep from 10-510 mT. B) Expanded between 60-190 mT to show the half-field transitions 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.

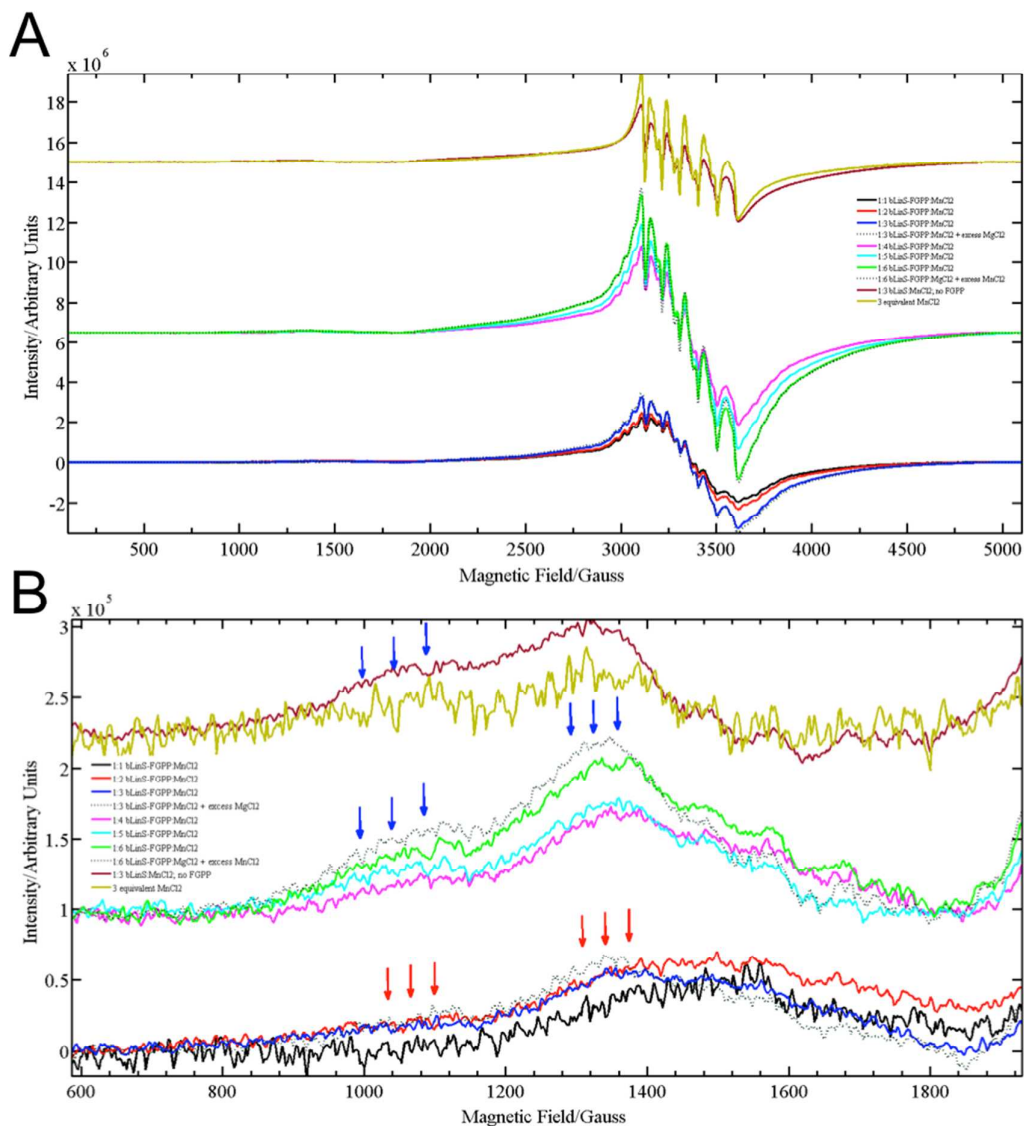


Figure S7. cw-EPR spectra of bLinS. Mn^{2+} substituted bLinS samples with varying equivalents of Mn^{2+} ion concentration with and without FGPP, measured as a frozen solution along with standard MnCl_2 . A) Wide sweep from 10-510 mT. B) Expanded between 60-190 mT to show the half-field transitions 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.

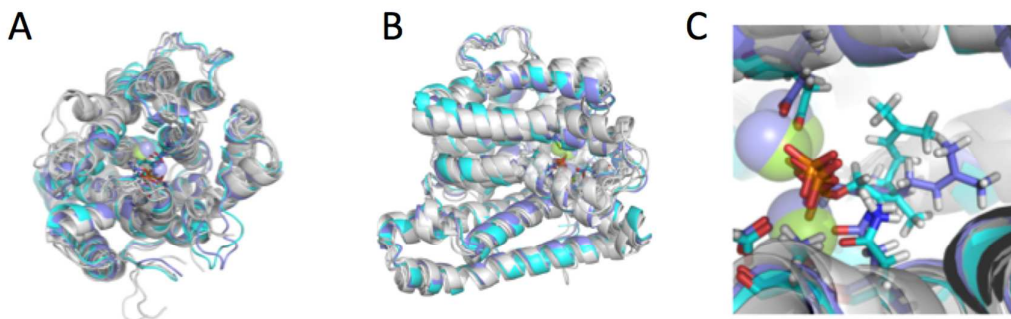


Figure S8. Comparison of structures from MD of *apo*-bCinS with MD of the ternary complex of bCinS with 3 Mg²⁺ ions and GPP or NPP. White: 4 clusters from 100 ns simulation of *apo*-bCinS, purple: the representative structure of the most populated cluster (after alignment on active site residues) from 100 ns simulations of bCinS with 3 Mg²⁺ 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 Mg²⁺ 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.

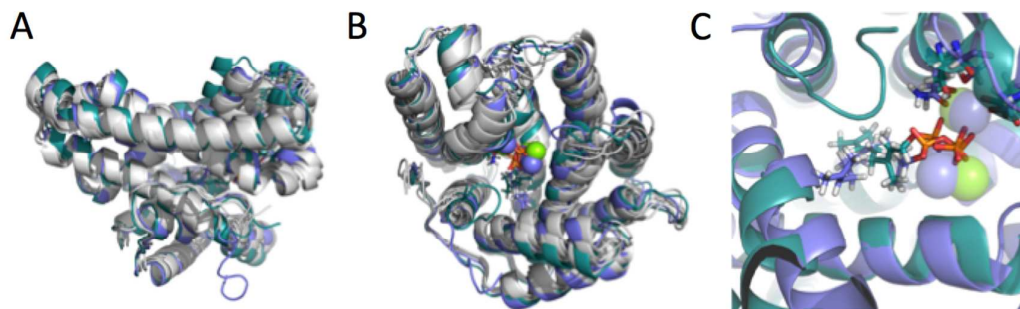


Figure S9. Comparison of structures from MD of *apo*-bLinS with MD of the ternary complex of bLinS with 3 Mg^{2+} ions and GPP or FPP. White: 4 clusters from 100 ns simulation of *apo*-LinS, teal: the representative structure of the most populated cluster (after alignment on active site residues) from 100 ns simulations of bLinS with 3 Mg^{2+} 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 Mg^{2+} 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.

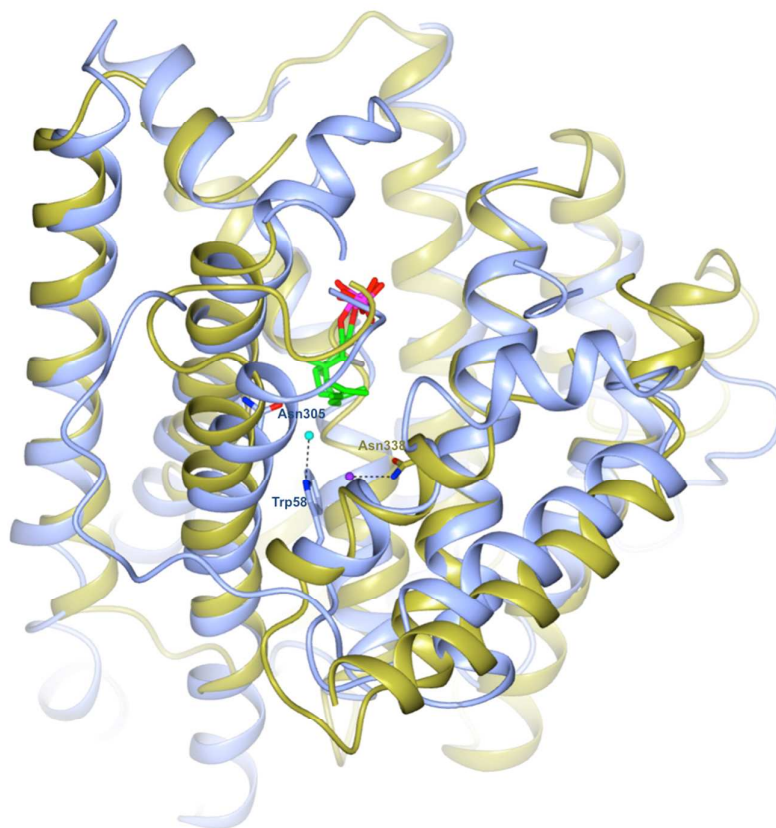


Figure S10: Structural overlay of bCinS and C-terminal domain of Sf-CinS1. In the bCinS-FNPP/FGPP structure (blue ribbon), residues Trp58 and Asn305 coordinate the water molecule (cyan sphere), which is proposed to be involved in water attack. In Sf-CinS1 (gold ribbon), Asn338 was identified to be crucial 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 reference	Plasmid name	Description (Origin of replication, Antibiotic marker, Reference(s), Promoters and Operons)	Reference
pMVA	BbA5a-MTSAe-T1f-MBI(f)-T1002i	p15A, Kanr, PlacUV5, MTSA, T1, MBI-f, T1002	1
pGPPSmTC/S15	pBbB2a-trAgGPPS(co)-trSLimS_Ms	pBBR, Ampr, Ptet, trAgGPPS(co)- trSLimS_Ms	1
pGPPSmTC/S38	pBbB2a-trAgGPPS(co)-bLinS	pBBR, Ampr, Ptet, trAgGPPS(co)- bLinS	This study
pGPPSmTC/S39	pBbB2a-trAgGPPS(co)-bCinS	pBBR, Ampr, Ptet, trAgGPPS(co)- bCinS	This study

Table S2: bLinS and bCinS: homologous structures

Name	PDB	Organism	RMSD (Å) / C α atoms
<i>bLinS (chain A)</i>			
Pentalenene synthase	1ps1	<i>Streptomyces exfoliatus</i>	1.52 / 283
Germacradien-4-ol synthase	5i1u	<i>Streptomyces citricolor</i>	1.59 / 276
Hedycaryol synthase	4mc3	<i>Actinomyces K. setae</i>	1.99 / 275
Geosmin synthase	5dz2	<i>Streptomyces coelicolor</i>	1.82 / 279
Epi-isozizaene synthase	4ltv	<i>Streptomyces coelicolor</i>	2.19 / 286
Selinadiene synthase	4okz	<i>Streptomyces pristinaespiralis</i>	1.83 / 265
2-Methylisoborneol synthase	4la6	<i>Streptomyces coelicolor</i>	2.09 / 268
<i>bCinS</i>			
Geosmin synthase	5dz2	<i>Streptomyces coelicolor</i>	1.54 / 296
Pentalenene synthase	1ps1	<i>Streptomyces exfoliatus</i>	1.80 / 292
Germacradien-4-ol synthase	5i1u	<i>Streptomyces citricolor</i>	1.80 / 283
Epi-isozizaene synthase	3kb9	<i>Streptomyces coelicolor</i>	1.94 / 304
Hedycaryol synthase	4mc3	<i>Actinomyces K. setae</i>	2.07 / 276
Aristolochene synthase	4kwd	<i>Aspergillus terreus</i>	2.28 / 280

REFERENCES

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.