

Supplementary Material

Validation of an insertion-engineered isoprene synthase as a strategy to functionalize terpene synthases

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Figure S1: ISPS abundance in clarified *E. coli* cell lysates

Figure S2: Uncropped gel image of SpyTag-GFP-His₆ conjugation reactions

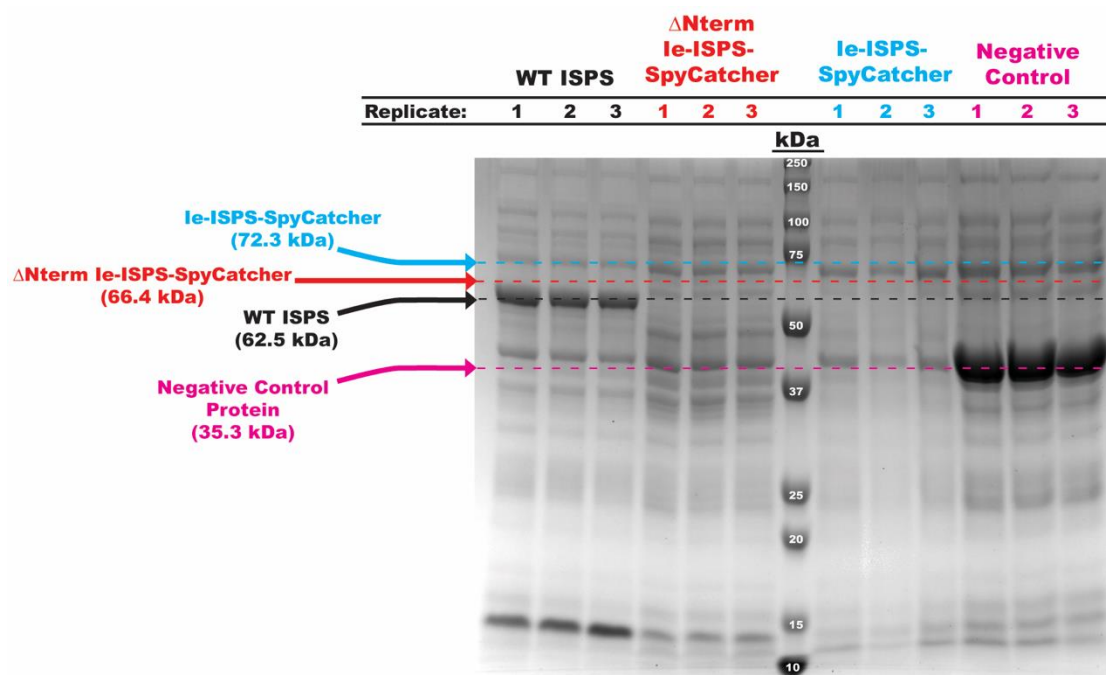
Figure S3: The plot of appearance of SpyTag-GFP-His₆ + le-ISPS-SpyCatcher fusion protein

Figure S4: Response of le-ISPS-GFP to Na⁺ and K⁺ concentrations, and Mn²⁺ and Mg²⁺

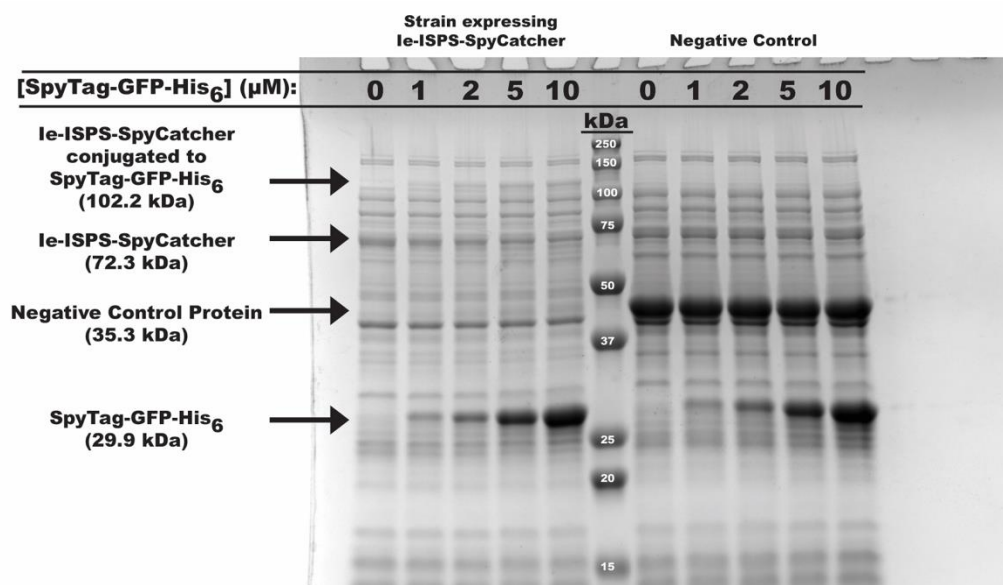
Figure S5: Isoprene synthase activity of le-ISPS-SpyCatcher

Table S1: Amino acid sequences for proteins used in this study;

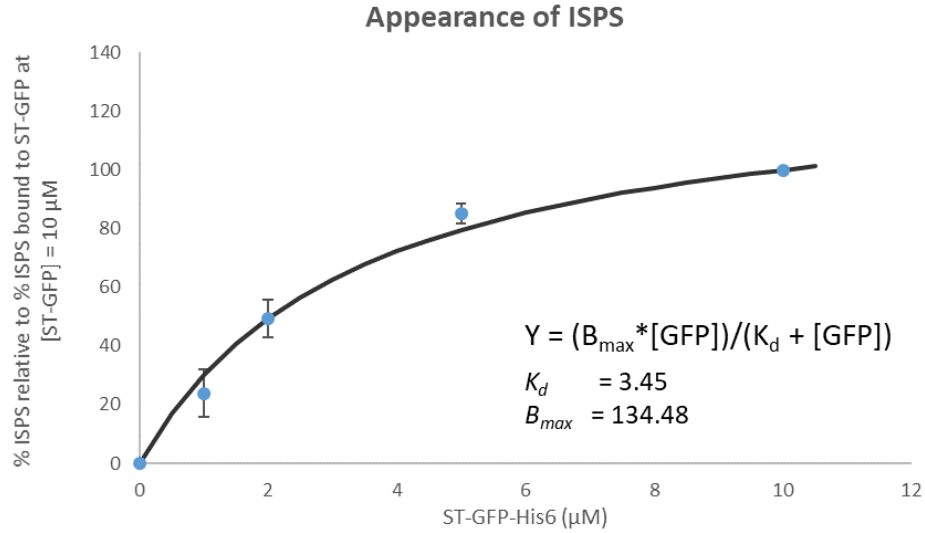
Sequences S1-5: Plasmids sequences used in this study



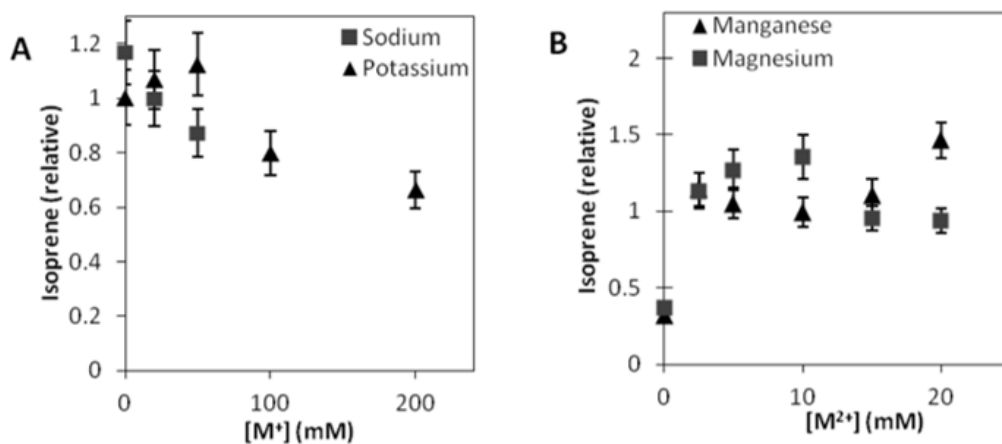
Supplementary Figure S1. ISPS abundance in clarified *E. coli* cell lysates. SDS-PAGE gel of whole cell lysates from *E. coli* strains expressing different ISPS variants. Coomassie Blue stained gel of whole cell lysates from strains expressing WT ISPS (black), Δ Nterm le-ISPS-SpyCatcher (red), le-ISPS-SpyCatcher (cyan), or a negative control (magenta). 4 μ g of total protein was loaded per well for three replicates of each strain. Predicted molecular weights for each ISPS variant and the negative control protein are: WT ISPS (62.5 kDa), Δ Nterm le-ISPS-SpyCatcher (66.4 kDa), le-ISPS-SpyCatcher (72.3 kDa), and the negative control protein (35.3 kDa). Molecular weights were calculated using Benchling (<https://benchling.com>). Bio-Rad Precision Plus Dual Color Standards were used to estimate molecular weights in the gel.



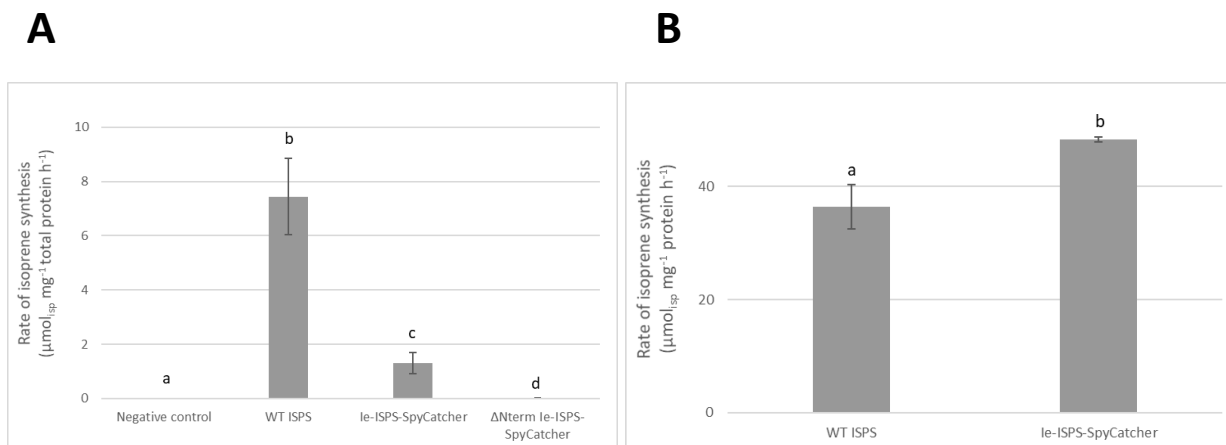
Supplementary Figure S2. Uncropped gel image of SpyTag-GFP-His₆ conjugation reactions. Uncropped image of the Coomassie Blue stained gel used in Figure 4. Predicted molecular weights for individual and conjugated proteins: le-ISPS-SpyCatcher (72.3 kDa), SpyTag-GFP-His₆ (29.9 kDa), le-ISPS-SpyCatcher conjugated with SpyTag-GFP-His₆ (102.2 kDa), and a negative control protein (35.3 kDa). Molecular weights were calculated using Benchling (<https://benchling.com>). Bio-Rad Precision Plus Dual Color Standards were used to estimate molecular weights in the gel.



Supplementary Figure S3. The plot of appearance of SpyTag-GFP-His6 + Ie-ISPS-SpyCatcher fusion protein. The % of SpyTag-GFP-His6 + Ie-ISPS-SpyCatcher fusion protein (% ISPS) expressed as a % of the SpyTag-GFP-His6 + Ie-ISPS-SpyCatcher fusion protein detected with 10 μM of SpyTag-GFP-His6, is plotted against the concentration of SpyTag-GFP-His6 added to each corresponding conjugation mixture. The values presented in the graph represent mean±SE of three estimates of % SpyTag-GFP-His6 + Ie-ISPS-SpyCatcher fusion protein obtained from three independent conjugation reactions carried out using three independent lysates. The data was fitted with a rectangular hyperbola ($Y = B_{max} * [GFP] / (K_d + [GFP])$) to estimate B_{max} (maximum number of binding sites of Ie-ISPS-SpyCatcher) and K_d (dissociation constant at equilibrium).



Supplementary Figure S4. Response of le-ISPS-GFP to sodium and potassium ion concentrations (A) and manganese and magnesium (B). In A, data is presented relative to potassium at 0 mM and in B, relative to 1 mM. Averages with standard error shown (n=3).



Supplementary Figure S5. Isoprene synthase activity of le-ISPS-SpyCatcher. (A) Isoprene synthase activity, measured as μmol of isoprene produced per mg of total protein per h , in lysates from cells expressing le-ISPS-SpyCatcher is compared with a negative control protein expressed from the same vector as all ISPS variants, WT ISPS, and a truncated form of le-ISPS-SpyCatcher lacking the N-terminal alpha helix preceding the γ -site ($\Delta\text{Nterm le-ISPS-SpyCatcher}$). (B) Isoprene synthase activity measured as μmol of isoprene produced per mg of either the WT ISPS or le-ISPS-SpyCatcher protein per h , respectively. 1 mM DMADP was used in the assay. Averages with standard errors are shown ($n=3$). Different lower case letters signify statistically significant differences between means at $\alpha = 0.05$.

Supplementary Table S1. Amino acid sequences for proteins used in this study

Protein	Amino Acid Sequence	Comments
WT ISPS	MARRSANYEPNSWDYDYLLSSDTDESIEVYKDKA KKLEAEVRREINNEKAEFLTLLELIDNVQRLGLG YRFESDIRGALDRFVSSGGFDAVTKTSLHGTALS FRLLRQHGFVSVQEAFFSGFKDQNGNFLENLKEDI KAILSLYEASFLALEGENILDEAKVFAISHLKEL SEEKIGKELAEQVNHAELEPLHRRRTQRLEAVWSI EAYRKKEDANQVLELAILDYNMIQSVYQRDLRE TSRWRRVGLATKLHFARDRLIESFYWAVGVAFE PQYSDCRNSVAKMFSFVTIIDDYDVYGTLDLELE LFTDAVERWDVNAINDLPDYMKLCFLALYNTINE IAYDNLKDKGENILPYLTKAWADLCNAFLQEAKW LYNKSTPTFDDYFGNAWKSSSGPLQLVFAYFAVV QNIKKEEIEENLQKYHDTISRPSHIFRLCNDLASA SAEIARGETANSVSCYMRKGI SEELATESVMNL IDETWKKMNKEKLGSLFAKPFVETAINLARQSH CTYHNGDAHTSPDELTRKRVLSVITEPILPFER	
Ie-ISPS-GFP	MARRSANYEPNSWDYDYLLSSDTDESIEVYKDKA KKLEAEVRREINNGSGSGSGSGS SKGEELFTGVV PIILVELDGDVNGHKFSVSGEGEGDATYGKLTLLKF ICTTGKLPVPWPTLVTTLTLYGVQCFA RYPDHMKQ HDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF EGDTLVNRIELKGIDFKEDGNILGHKLEYNNSH KVYITADKQKNGIKVNFKTRHNIEDGSVQLADHY QQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRD HMVLLEFVTAAGITLGMDELYK SGSGSGSGSRSEK AEFLTLLELIDNVQRLGLGYRFESDIRGALDRFV SSGGFDAVTKTSLHGTALSFRLLRQHGFVSVQEA FSGFKDQNGNFLENLKEDIKAILSLYEASFLALE GENILDEAKVFAISHLKELSEEKIGKELAEQVNH ALELPLHRRRTQRLEAVWSIEAYRKKEDANQVLE LAILDYNMIQSVYQRDLRETSRWRRVGLATKLH FARDRLIESFYWAVGVAFEPQYSDCRNSVAKMFS FVTIIDDYDVYGTLDLELELFTDAVERWDVNAIN DLPDYMKLCFLALYNTINEIAYDNLKDKGENILP YLTAWADLCNAFLQEAKWLYNKSTPTFDDYFGN AWKSSSGPLQLVFAYFAVVQNIKKEEIEENLQKYH DTISRPSHIFRLCNDLASASAEIARGETANSVSC YMRKGI SEELATESVMNLIDETWKKMNKEKLG SLFAKPFVETAINLARQSHCTYHNGDAHTSPDEL TRKRVLSVITEPILPFER	GFP sequence in bold.

SUMO-Ie-ISPS-GFP	MGSSWSHPQFEKGSGLVPRGSASMSDSEVNQEAK <u>PEVKPEVKPETHINLKVSDGSSEIFFKIKKTTPL</u> <u>RRLMEAFAKRQGKEMDSLRFlyDGIRIQADQTPE</u> <u>DLDMEDNDIIEAHREQIGGMTEARRSANYEPNSW</u> DYYLLSSDTDESIEVYKDKAKKLEAEVRREINN GSGSGSGSGSSKGEELFTGVVPILVELDGDVNGH KFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT LVTTLTYGVQCFARYPDHMKQHDFFKSAMPEGYV QERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKG IDFKEDGNILGHKLEYNNSHKVYITADKQKNGI KVNFKTRHNIEDGSVQLADHYQQNTPIGDGPVLL PDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGI TLGMDELYKGSGSGSGSRSEKAEFLTLLELIDNV QRLGLGYRFESDIRGALDRFVSSGGFDAVTKTSL HGTALSFRLLRQHGFEVSQEAFSGFKDQNGNFLE NLKEDIKAILSLYEASFLALEGENILDEAKVFAI SHLKELSEEKIGKELAEQVNHALELPLHRRRTQRL EAVWSIEAYRKKEDANQVLELAILDYNMIQSVY QRDLRETSRWRRVGLATKLHFARDRLIESFYWA VGVAFEPPQYSDCRNSVAKMFSFVTIIDDYDVYG TLDELELFTDAVERWDVNAINDLPDYMKLCFLAL YNTINEIAYDNLKDKGENILPYLTKAWADLCNAF LQEAKWLYNKSTPTFDDYFGNAWKSSSGPLQLVF AYFAVVQNIKKEEIENLQKYHDTISRPSHIFRLC NDLASASAEIARGETANSVSCYMRTKGISEELAT ESVMNLIDETWKKMNKEKLGGSLFAKPFVETAIN LARQSHCTYHNGDAHTSPDELTRKRVLSVITEPI LPFER	SUMO-Smt3 underlined and GFP sequence in bold.
SpyTag-GFP-His ₆	MGELAHIVMVDAYKPTKGSMRKGEELFTGVVPIL VELDGDVNGHKFSVRGEGEGDATNGKLTLKFICT TGKLPVPWPTLVTTTLTYGVQCFARYPDHMKQHDF FKSAMPEGYVQERTISFKDDGTYKTRAEVKFEGD TLVNRIELKGIDFKEDGNILGHKLEYNFNSHNVY ITADKQKNGIKANFKIRHNVEDGSVQLADHYQQN TPIGDGPVLLPDNHYLSTQSVLSKDPNEKRDHML LLEFVTAAGITHGMDELYKLEHHHHHH	N-terminal SpyTag and C-terminal His ₆ sequences are in bold.
ΔNterm Ie-ISPS- SpyCatcher	MDSATHIKFSKRDEDGKELAGATMELRDSSGKTI STWISDGQVKDFYLYPGKYTFVETAAPDGYEVAT AITFTVNEQGQVTVNGSGSGSEKAEFLTLLELID NVQRLGLGYRFESDIRGALDRFVSSGGFDAVTKT SLHGTALSFRLLRQHGFEVSQEAFSGFKDQNGNF LENLKEDIKAILSLYEASFLALEGENILDEAKVF AISHLKELSEEKIGKELAEQVNHALELPLHRRRTQ RLEAVWSIEAYRKKEDANQVLELAILDYNMIQS VYQRDLRETSRWRRVGLATKLHFARDRLIESFY	SpyCatcher is in bold, GlySer linker is underlined.

	WAVGVAFEPQYSDCRNSVAKMFSFVTIIDDIDYDV YGTLDLELELFTDAVERWDVNAINDLDPDYMKLCFL ALYNTINEIAYDNLKDKGENILPYLTKAWADLCN AFLQEAKWLYNKSTPTFDDYFGNAWKSSSGPLQL VFAYFAVVQNIKKEEIENLQKYHDTISRPSHIFR LCNDLASASAEIARGETANSVSCYMRTKGISEEL ATESVMNLIDETWKKMNKEKLGGSLFAKPFVETA INLARQSHCTYHNGDAHTSPDELTRKRVLSVITE PILPFER	
Ie-ISPS-SpyCatcher	MARRSANYEPNSWDYDYLLSSDTDESIEVYKDKA KKLEAEVRREINN <u>GGSGGS</u> DSATHIKFSKRDEDG KELAGATMELRDSSGKTISTWISDGQVKDFYLYP GKYTFVETAAPDGYEVATAITFTVNEQGQVTVNG <u>GGSGSEKAEFLTLLELIDNVQRLGLGYRFESDIR</u> GALDRFVSSGGFDAVTKTSLHGTALSFRLLRQHG FEVSQEAFFSGFKDQNGNFLENLKEDIKAILSLYE ASFLALEGENILDEAKVFAISHLKELSEEKIGKE LAEQVNHALELPLHRRRTQRLEAVWSIEAYRKKED ANQVLLELAILDYNNMIQSVYQRDLRETSRWRRV GLATKLHFARDRLIESFYWAVGVAFEPQYSDCRN SVAKMFSFVTIIDDIDYDVYGTLDLELELFTDAVER WDVNAINDLDPDYMKLCFLALYNTINEIAYDNLKD KGENILPYLTKAWADLCNAFLQEAKWLYNKSTPT FDDYFGNAWKSSSGPLQLVFAYFAVVQNIKKEEI ENLQKYHDTISRPSHIFRLCNDLASASAEIARGE TANSVSCYMRTKGISEELATESVMNLIDETWKKM NKEKLGGSLFAKPFVETA INLARQSHCTYHNGDA HTSPDELTRKRVLSVITEPILPFER	SpyCatcher is in bold, insulating GlySer linkers underlined.

Supplementary Sequence S1. DNA Sequence of the pD881/Ie-ISPS-GFP plasmid.

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Supplementary Sequence S2. DNA Sequence of the pD881/SUMO-le-ISPS-GFP plasmid.

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Supplementary Sequence S3. DNA sequence for the pBbE2K-le-ISPS-SpyCatcher

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G

Supplementary Sequence S4. DNA sequence for the pBbE2K-SpyTag-GFP-His₆. Coding sequence for SpyTag-GFP-His₆ is indicated in bold.

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A

Supplementary Sequence S5. DNA sequence for the pBbE2K-ΔNterm Ie-ISPS-SpyCatcher

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