

Table S1. Primers used in the present study.

Primers	Sequence (5'-3')	Purpose
T7	TAATACGACTCACTATAGGG	PCR verification
CYC1 Terminator	TCGGTTAGAGCGGATGTG	PCR verification
McELO-F	CGGGGTACCTATGGATGTGGATAAGCTTCAACCT	Amplification
McELO-R	GCTCTAGACTACTCGGTCTTCTTGGCCTTACG	Amplification
PrELO-F	AAGCTTACCATGGGGGGTTCTCATCATCA	Amplification
PrELO-R	TCTAGATTACTGCGTCTTTTTCTTGTTGACTTG	Amplification
PsELO-F	GAATTCATGGAGACCACCTTCGCCC	Amplification
PsELO-R	TCTAGATTACTGCGTCTTCTTGGCGACG	Amplification
Mc Q154A-F	TTCTCTCTTGGCTACCTATCATCACTCT	Mutagenesis
Mc Q154A-R	AGAGTGATGATAGGTAGCCAAGAGAGAA	Mutagenesis
Pr Y90A-F	TCCTCTGCTCGGCCATGTGCATGGA	Mutagenesis
Pr Y90A-R	TCCATGCACATGGCCGAGCAGAGGA	Mutagenesis
Pr M91A-F	CTCTGCTCGTACGCTTGCATGGAGG	Mutagenesis
Pr M91A-R	CCTCCATGCAAGCGTACGAGCAGAG	Mutagenesis
Pr Y104A-F	CTACCGCAACGGGCCTCGGCCACC	Mutagenesis
Pr Y104A-R	GGTGGCCGAGGCGCCGTTGCGGTAG	Mutagenesis
Ps L165A-F	CACCGTCCTCGCCTTCTGCTGG	Mutagenesis
Ps L165A-R	CCAGCAGAAGGCGAGGACGGTG	Mutagenesis
Ps Y256A-F	GTACTCGTCGGCCTTCGCCCTCTTC	Mutagenesis
Ps Y256A-R	GAAGAGGGCGAAGGCCGACGAGTAC	Mutagenesis

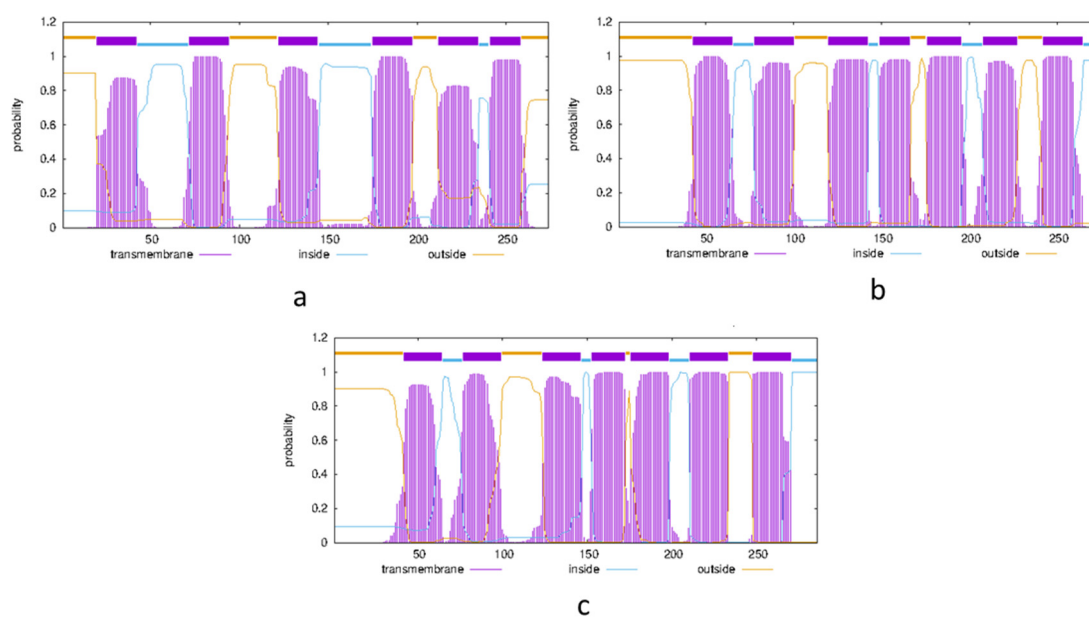
Table S2. Conversion of Polyunsaturated Fatty Acids by McELO, PrELO, or PsELO.

Values are represented as the averages of percent conversions, $[(\% \text{ of generated fatty acid}) / (\% \text{ of generated fatty acid} + \% \text{ of substrate fatty acid})] \times 100$, from three independent experiments.

Fatty acid substrate	% Conversion		
	PY-McELO	PY-PrELO	PY-PsELO
C18:2 ^{Δ9,12}	8.4	1.9	0.0
C18:3 ^{Δ9,12,15}	3.2	0.0	0.0
C18:3 ^{Δ6,9,12}	0.0	74.3	0.0
C20:0	0.0	0.0	26.3
C20:4 ^{Δ5,8,11,14}	0.0	0.0	0.0
C20:5 ^{Δ5,8,11,14,17}	0.0	0.0	0.0

Table S3. Comparison of conversion rates of different sources of $\Delta 6$ elongase

$\Delta 6$ -ELO origin	GLA additive quantity/ μM	conversion rate /%	References
<i>Green Microalga Parietochloris incisa</i>	250	16.4	[1]
<i>Mortierella alpina</i>	25	60	[2]
<i>Marine Alga Nannochloropsis oceanica</i>	250	70.5	[3]
<i>Physcomitrella patens</i>	500	41	[4]
<i>Conidiobolus obscurus</i>	250	50	[5]
<i>Thraustochytrium sp. ATCC 26185</i>	100	64.3	[6]
<i>Pythium sp. BCC53698</i>	50	29.3	[7]
<i>Myrmecia incisa</i> Reisigl	/	23.89	[8]

**Figure S1.** Predicated transmembrane domains for (a) McELO, (b) PrELO, (c) PsELO by

TMHMM (V2.0, <http://www.cbs.dtu.dk/services/TMHMM/>).

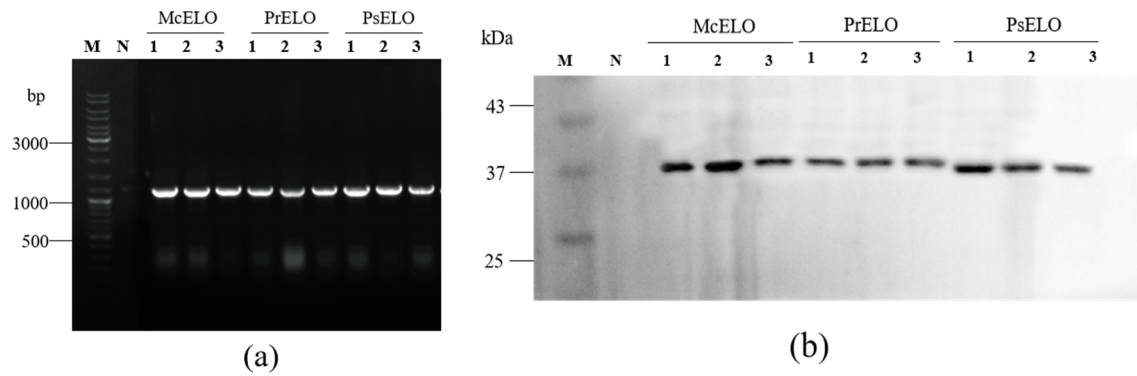


Figure S2. Validation of *S. cerevisiae* transformants harboring McELO, PrELO, PsELO genes.

(a) Validation of the recombinant strains *Escherichia coli*-pYES2- McELO, PrELO, PsELO;

(b) Western blot analysis of pY-McELO, pY-PrELO, pY-PsELO. M: marker; N: negative control;

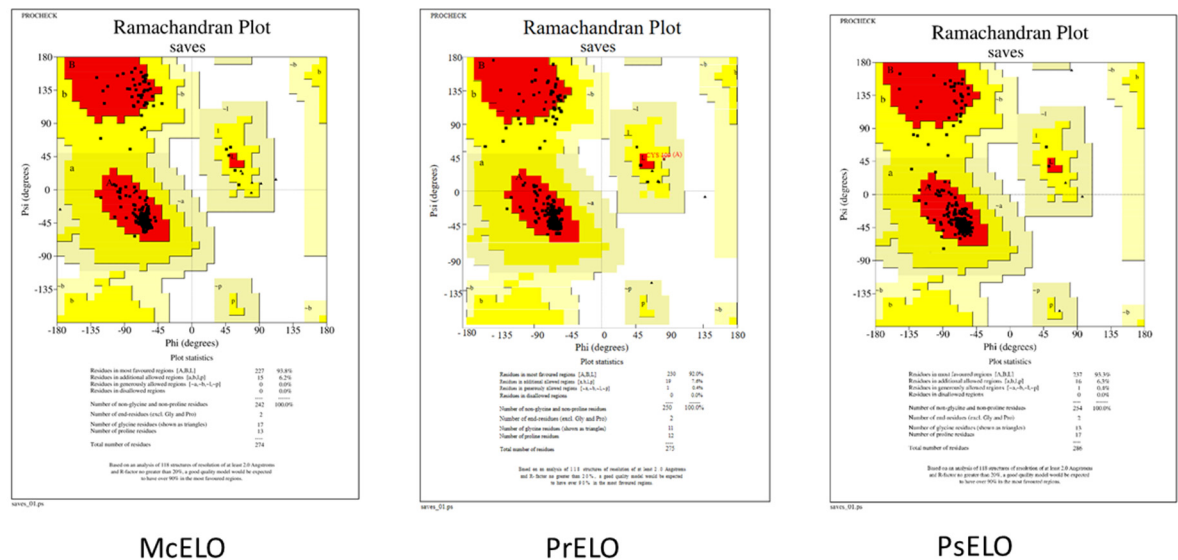


Figure S3. Ramachandran plot of a polypeptide backbone torsion angles psi (w) against phi (u) of amino acid present in the modeled structures of McELO, PrELO, PsELO generated by AlphaFold. The most favored regions are colored in red. The additional allowed regions [a, b, l, p] are colored in yellow. The generously allowed regions [~a, ~b, ~l, ~p] are colored in pale yellow. All non-glycine and proline residues are illustrated as filled black squares, and glycine

(non-end) is indicated as filled black triangles. Disallowed residues are colored in white.

Reference:

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