Table S2. *Condensed literature information for the SL-E enzymes*.

Enzyme / Transporter	Symbol in Model	Gene(s)	Specific Activity (†)	Kinetics	Comments	Reference
Pyruvate Decarboxylase (Pyr. Decarboxylase)	X_{122}	*PDC1, PDC5, PDC6*	45 U/mg		The Pyr decarboxylase produces acetaldehyde which is catalyzed by the acetaldehyde dehydrogenase to form Acetate. The Pyr. Decarboxylase is the rate limiting step of the two steps.	[1]
				K_M = 520 μM Pyruvate	*Z. mobilis*	[2]
Pyruvate Dehydrogenase (Pyr. Dehyd.)	X_{123}	*PDA1, PDB1*	0.12 U/mg		Range between 0.12 and 0.16 U/mg	[3]
				K_M = 650 μM Pyruvate		[3]
Phosphatidylinositol Synthase (PI Synthase)	X_{126}	*PIS1*	**2.66 e-3 U/mg** (Φ)		Microsomes.	([4], Table 3)
			8e-4 U/mg		Microsomes	([5], Table I)
				K_M = 3.25 mol% CDP-DAG, K_M = 210 μM Inositol	Rat liver CDP-DAG KM 66 μM from [6]. Converted to mol% according the DHS KM relationship 0.38 mol% = 7.7 μM from [7] and [8] respectively	([6], Table VI), ([7], Fig. 2), ([8], Fig. 2)
3-Ketodihydrosphingosine Reductase (KDHS reductase)	X_{127}	*TSC10, YBR265w*	**2.62 e-4 U/mg**			([9], Table 5)
				K_M = 0.74 mol% 3-KDS-SPH	From [10] KM for beef liver microsomes is 15 μM. Converted to mol% according the DHS Km relationship 0.38 mol% = 7.7 μM from [7] and [8] respectively	([10], p.367), ([7], Fig. 2), ([8], Fig. 2)
Dihydroceramide Alkaline Ceramidase (Dihydro-CDase)	X_{129}	*YDC1*	**5.4 e-6 U/mg**			([11], Table II)
				K_M = 0.036 mol% Dihydroceramide	Estimated value, using dihydroceramide concentration	
				K_M = 3.84 mol% Dihydroceramide, V_{max} = 1.2 U/mg	Rat brain	([12], Table II & p. 27954)

Palmitoyl Transport & Palmitoyl-CoA Synthase (Transp./ Palmitoyl CoA Synthase)	X_{130}	*FAT1, FAA1, FAA4*	**5.08 e-2 U/mg**	Logarithmic phase	Mid-log phase	([13], Table 1)
			3.38 e-3 U/mg		Using oleate as the fatty acid substrate	([14], Table III)
				K_M = 20 μM Palmitoyl-CoA, V_{max} = 1.4 e-4 U/mg		([14], Table I)
Phosphoserine-Phosphatase (P-Serine-PPase)	X_{131}	*SER2*	**1.3 e-3 U/mg**			([15], Table 2)
			0.12 U/mg			([16], Fig. 3C)
			0.78 U/mg	K_M = 20 μM 3-Phosphoserine	Human recombinant enzyme	([17], Table I)
				K_M = 89 μM 3-Phosphoserine	Rabbit liver	([18], p 17)
Serine Hydroxymethyl Transferase (SHMT)	X_{132}	*SHM2*	**4.5 e-3 U/mg**		Cytosolic reversible enzyme	([19], Table 2)
			8.38e-5 U/mg			([20], Table II)
				K_M = 650 μM L-Serine	Cytosolic	([21], p. 11)
				K_M = 700 μM Serine		([22], p. 332)
Inositol Phosphorylceramide Synthase (IPC Synthase)	X_{133}	*AUR1*	**3.3 e-4 U/mg**	K_M = 1.35 mol% Ceramide, **K_M = 5 mol% PI**	Microsomes. PI interact with IPC synthase in a cooperative manner with a Hill constant of 3	([23], Table I)
			2.1e-4 U/mg		Microsomes in mid-exponential growth phase	([24], Table I)
				K_i = 2.89 mol% DHS K_i= 1.96 mol% PHS	Calculated based on IC50 data from [25] , *Vmax* from [24], and the MWC Dimeric model, interaction with effectors from [26]	([25], Fig. 10), [24], [26], [27]
				K_M = 0.5 mM PI, ***V_{max}* = 6.6e-6 U/mg**	IPC-II and IPC-III	([28], Fig. 4)
Ceramide Synthase (Cer Synthase)	X_{134}	*LAC1, LAG1*	1.65e-5 U/mg			([25], p. 13173)
				$K_{0.5}$ = 0.27 mol% DHS, $K_{0.5}$ = 0.2 mol% PHS, V_{max} = 135e-3 U/mg DHS, V_{max} = 105e-3 U/mg PHS		([29], p. 2659)
				K_M = 144 μM DHS, K_M = 299 μM Behenoyl-CoA (C22:0)	Bovine liver mitochondria. From [30] the relation between the DHS and C_{26}-CoA K_M's is approximately 2 and is used for the estimation of the C_{26}-CoA K_M using the DHS K_M from [29].	([30], Table 2), [29]
Mannosyl Inositol Phosphoceramide Synthase (MIPC Synthase)	X_{135}	*SUR1, CSG1*	1.65e-4 U/mg		It is assumed that the activity of MIPC synthase is about half the IPC synthase activity.	([28], Fig. 4)
				K_M = 0.102 mol% IPC	Estimates K_M using IPC concentration	

Sphingoid Base Kinase	X_{136}	*LCB 4/5*	**4e-6 U/mg**	**K_M = 0.38 mol% DHS, K_M = 1.2 mol% PHS, V_{max} = 4.25e-6 U/mg DHS, V_{max} = 6e-6 U/mg PHS**		([7], Figs. 2 & 5)
			0.0045 U/mg	**K_M = 25 μM ATP, K_M = 7.7 μM DHS, K_M = 10 μM PHS**	Pellet results for activity	[8]
Phosphatidylserine Synthase (PS Synthase)	X_{138}	*CHO1*	**3.32 e-3 U/mg**		Microsomes	([4], Table 3)
			4.2e-4 U/mg			([31], Table 3)
				K_M = 830 μM Serine, K_M = 83 μM CDP-DAG, K_i = 65 μM Inositol		([6], Table VI & p. 18084)
				K_i = 1.42 mol% DHS, K_i = 3.55 mol% PHS	Calculated based on IC50 data from [25]. and the MWC Dimeric model, interaction with effectors from [26]	([25], Fig. 11), [24], [27]
				K_i= 7 mol% DAG, K_a = 0.033 mol% PA, **K_a= 3.2 mol% PI**	Kinetic orders for PA and PI obtained from log-log plot (see [27])	[27], ([32], Table I & Fig. 3A)
Phosphatidate Phosphatase (PA-PPase)	X_{139}	*DPP1, LPP1*	**2.4e-3 U/mg**			([33], Table I)
			3 U/mg	K_M = 50 μM PA		([34], Table I)
				K_M = 2.2 mol% PA, aK_i = 0.4 mol% PHS, aK_i = 0.2 mol% DHS, aK_i= 1.5 mol% Sphingosine		([35], Table I)
				$A_{0.5}$ = 2.6 CDP-DAG, **$A_{0.5}$ = 5.5 PI**	Kinetic orders for PI and PA obtained from log-log plot (see [27])	[36], [27]
CDP-Diacylglycerol Synthase (CDP-DAG Synthase)	X_{140}	*CDS1*	6.1e-4 U/mg	K_M = 500 μM PA, K_M = 1 mM CTP, V_{max} = 4.7 U/mg		([37], Table 1)
Sphingoid-1-phosphate Phosphatase (SB-PPase)	X_{141}	*LCB3, YSR2*	8e-4 U/mg			([38], Fig. 3A)
				K_M = 3.11e-2 mol% (16 μM) DHS-P and PHS-P, V_{max}= 2.77e-5 μM	Rat liver microsomes. K_M and V_{max} converted to mol% with the relationship suggested by [7]: 3.5 mol% = 1.8 mM	[7], ([39], Fig. 10 and p. 382)
DG-Choline Phosphotransferase (ChoPT)	X_{142}	*CPT1*	6.6e-4 U/mg	K_M = 8 mol% Dioleoylglycerol		([40], Table I and Fig. 3)
GPI Remodelase (Remodeling)	X_{143}		1e-4 U/mg	K_M = 0.052 mol%	K_M estimation using phytoceramide concentration. Activity with order magnitude similar at IPC synthase	
Phosphoinositide Kinase (PI Kinase)	X_{144}	*VPS34*	1.72 e-3 U/mg	K_M = 70 μM PI, K_M = 300 μM MgATP, ***Vmax* = 4.75 U/mg**	Microsomes	([41], Table I and p. 18902)
DG-Ethanolamine Phosphotransferase (EthPT)	X_{145}	*EPT1*	1 e-3 U/mg	K_M = 22 μM CDP-Eth, K_M = 3.3 mol% Dioleoylglycerol		([40], Table 1 and Fig. 2)

Inositol-1-P Synthase (I-1-P Synth.)	X_{146}	*INO1*	**8.33 e-4 U/mg**	K_M = 1180 μM Glucose-6-P, K_M = 8 μM NAD, V_{max} = 167 nmol/h		([42], Table 1 and p. 7082)
			3 e-4 U/mg		Two hr after inositol was added to the medium	([43], Fig. 8)
Acyl-CoA-Binding Protein (ACBP)	X_{148}	*ACB1*	20 μM	K_D = 5.5 e-5 μM	Within the range 10 to 50 μM	([44], Fig. 2)
Glycerol-3-Phosphate Acyltransferase (G3P Acyltranferase)	X_{149}	*GAT1*, *GAT2*, *SCT1*	**3.94 e-3 U/mg**		Microsomes 30,000 × *g*	([45], Table 1)
			1.04 e-3 U/mg		Late logarithmic phase	([46], Fig. 2)
				K_M =15 μM Pal-CoA, V_{max} =1. 53e-3 U/mg	K_M from curve S/Act vs. S	([47], Fig. 2B)
					PS activator effect calculated in [27] , based on data from [48]	[27], ([48], Fig. 5)
				K_M = 120 μM Glycerol-P, K_M = 4.6 μM Palmitoyl-CoA	*Escherichia coli*	([49], p 5)
Sphingosine-Phosphate Lyase (Lyase)	X_{150}	*DPL1*	3.67e-5 U/mg		Average from different organisms	([50], Table II)
				K_M = 0.024 mol% (12.5 μM) DHS-P and PHS-P	K_M from rat liver. Converted to mol% according to [7] 3.5 mol% = 1.8 mM	([51], p. 247), [7]
Inositol Phosphosphingolipid Phospholipase C (IPCase)	X_{151}, X_{164}	*ISC1*	1.5e-4 U/mg	K_M = 3.57 mol% IPC, K_M = 1.85 mol% MIPC, K_M = 1.92 mol% $M(IP)_2C$	X_{151} and X_{164} correspond to IPCase with Phyto-C and Dihydro-C as products respectively	([52], Tables I & II)
Fatty Acid Synthetase (FAS)	X_{152}	*FAS1*, *FAS2*, *FAS3*	**8.9 e-3 U/mg**	K_M = 8 μM Mal-CoA, **K_M = 28 μM Ac-CoA**		([53], Table I & p. 22)
			8.4e-3 U/mg			([54], Table 2)
			3.124 e-3 U/mg			([55], Table I)
			0.065 U/mg			([56], Table 1)
				K_M = 6 -19 μM Ac-CoA	*Cryptococcus neoformans*	([57], Table 2)
Phytoceramide Alkaline Ceramidase (Phyto-CDase)	X_{153}	*YPC1*	1.98e-5 U/mg			([11], Table II)
				K_M = 0.052 mol% (*) Phytoceramide	Assumed similar to phytoceramide concentration	
				K_M = 1.29 mol% Ceramide	Rat brain	([12], Fig. 7A)
4-Hydroxylase (Hydroxilase) (*SYR2p – SUR2p*)	X_{154}	*SYR2 SUR2*	1.7e-4 U/mg		Microsomes	([58] , Table II)
				K_M = 0.01 mol% DHS, K_M = 0.036 mol% Dihydro-C	Assumed similar to substrate concentration	
Mannosyldiinositol Phosphorylceramide Synthase ($M(IP)_2C$ Synthase)	X_{155}	*IPT1*	**8.25e-5 U/mg**		Activity of $M(IP)_2C$ synthase assumed to be about 1/4 the IPC synthase activity	([28], Fig. 4)
				K_M = 0.14 mol% MIPC, K_M = 5 mol% PI	Estimation of K_M using MIPC-g concentration. K_M of the $M(IP)_2C$ Synthase for PI assumed equal than for IPC Synthase	([23], Table I)

Phosphatidylserine Decarboxilase (PS Decarboxylase)	X_{156}	*PSD2*	**1.06e-5 U/mg**		*PSD2p* value for non-mitochondrial enzyme	([59], Table I)
				K_M = 8.4 mol%	K_M assumed similar with the substrate concentration	
				K_M = 24 μM PS	*E. coli*	([60], Fig. 3 and p. 3081)
				K_M = 9.5 μM PS		([61], p. 6064)
Serine Palmitoyltransferase (SPT)	X_{157}	*LCB1/2, SCS1*	**1.06e -4 U/mg**	**K_M = 4000 μM Serine, K_M = 15 μM Palmitoyl-CoA,** V_{max} = 1.03 e-4 U/mg	Fig 3A K_M for Palmitoyl-CoA required correction; utilized the original data of velocity of Pal-CoA vs. SPT	([9], Table 3 and Fig. 3A)
			6.31e -5 U/mg	K_M = 670 μM Serine	Rat liver	([62], Table I)
Very Long Chain Fatty Acid Synthase (ELO1p)	X_{159}	*ELO1*	6e-4 U/mg	K_M = 130 μM Mal-CoA, K_M = 130 μM Pal-CoA		[63]
Acetyl-Coenzyme A Carboxylase (ACCp)	X_{160}	*ACC*	**2.2 e-2 U/mg**	**K_M = 16 μM Ac-CoA, K_M = 660 μM ATP**		([64], p. 7)
			0.009 U/mg	**K_i= 6.5e-3 μM Pal-CoA, $C_{16:0}$, Ki= 4.8e-2 μM** Arachidonoyl-CoA, $C_{20:0}$, K_M = 25 μM Ac-CoA, K_M = 15 μM ATP	Rat liver	([65], Tables I & II, and p. 12)
				K_i = 5.5e-3 μM Pal-CoA and C_{26}-CoA	Liver	([66], Table 2)
				K_M = 19 μM Ac-CoA, K_i = 7.2 μM Palmityl-CoA, K_i = 1.3 μM Oley-CoA	Rat liver	([67], Table 4)
			0.029 U/mg			([68], Table II)
			0.042 U/mg			([54], Table 2)
			2.5 e-3 U/mg			([56], Table 1)
				K_M = 260 μM Ac-CoA	*Candida lipolytica*	([69], p. 42)

Acetyl-Coenzyme A Synthetase (ACSp)	X_{163}	*ACS1, ACS2*	**0.73 U/mg**	**K_M = 208 μM Acetate, K_M = 238 μM CoA**	Activity for the microsomal fraction. Kinetic order for the Pal-CoA inhibition was obtained from ([70], Fig 1) log-log plot.	([70], Table 2 and Fig. 1)
			0.22 U/mg	**K_M = 1100 μM ATP,** K_M = 600 μM Acetate, V_{max} = 1.2		([71], Table I)
			0.66 U/mg	K_M = 35 μM CoA, K_M = 280 μM Acetate, K_M = 1200 μM ATP		([72], Table IV)
			0.025 U/mg			([73], Table II)
Inositol Phosphosphingolipid Phospholipase C (IPCase)	X_{164}	*ISC1*			See X_{151}	
Serine Transport	X_{165}		**4.8 e-2 U/mg**			([74], Table 3)
			0.011 U/mg		Yeast cells *rho+* with functional mitochondria	([75], Table I)
				K_M = 166 μM Serine	Yeast cells *rho+* with functional mitochondria	[75]
Phospholipase B	X_{168}	*PLB3*	5 e-5 U/mg		Estimated low value	
				K_M = 75 mol% PI		([76], Fig. 4B)
Acetoacetyl-CoA thiolase / HMG-CoA synthase (Thiolase/Synthase)	X_{171}	*ERG10, ERG13*	0.14 U/mg			([77], Table 3)
				K_M = 380 μM	*Rhizobium* sp.	[78]
HMG-CoA Reductase (Reductase)	X_{172}	*HMG1, HMG2*	5.5e-3 U/mg			([77], Table 3)
				K_M = 45 μM HMG-CoA	*Sulfolobus solfataricus*	([79], Table 3)
Mevalonate Kinase (Kinase)	X_{173}	*ERG12*	6 e-4 U/mg		From *ERG9* mutants. No activity detectable in wild type strains; estimated by dividing the value by 100	([80], Table 1)
				K_M = 41 μM Mevalonate	*Staphylococcus aureus*	[81]
Squalene Synthase	X_{174}	*ERG9*	**4.7e-4 U/mg**		Sum of radioactivity in squalene epoxidase and lanosterol fractions	[82]
			1.48e-5 U/mg		30 K *g* microsomes. Aerobic, late exp. growth.	([4], Table 4)
					Kinetic order for Farnesyl-PP obtained from log-log plot of concentration vs. enzymatic rate.	([83], Fig. 4a)
Squalene Epoxidase	X_{175}	*ERG1*	**1e-4 U/mg**		Sum of radioactivity in squalene epoxidase and lanosterol fractions	[82]
			5.8e-6 U/mg		30 K *g* microsomes. Aerobic, late exp. growth.	([4], Table 4)
				K_M = 28 μM Squalene	*Leptosphaeria nodorum*. Data not used because different units between substrate and K_M	[84]
					Kinetic order for Squalene estimated from log-log plot of concentration vs. enzymatic rate.	([85], Fig. 1A)

Lanosterol C-14 Demethylase	X_{176}	*ERG11*	2.65e-8 U/mg		525 pmol of 3-hydroxy-benzo[*a*]pyrene/ nmol of P-450/ hr from [86] transformed to U/mg based in the 3 pmol of cytocorme P-450/mg of yeast microsomal protein data from [87]. 525 × 3/ (1e9 × 60) = 2.65e-8	([86], p. 1035), [87]
				K_M = 13.5 μM Squalene	Data not used because different units between substrate and K_M	[88]
					Kinetic order for the Lanosterol estimated from log-log plot of concentration vs. enzymatic rate.	([89], Fig. 3)
delta 24-sterol methyltransferase	X_{177}	*ERG6*	4e-6 U/mg			([90], Table I)
			7.91e-4 U/mg			([91], Table I)
			1 e-4 U/mg		For microsomes (40K x *g*). General Steryl synthase activity. Mid-exponential growth.	([92], Table 3)
				K_M = 15 μM Zymosterol	Data not used because different units between substrate and K_M	[93]
				K_M = 6.2e-11 μM		[91]
					Kinetic order for Zymosterol estimated from log-log plot of concentration vs. enzymatic rate.	([91], Fig. 5)
Farnesyltransferase (GGPP)	X_{179}	*BTS1*	4 e-3 U/mg		Specific activity assumed similar to that of Farnesyl diphosphate synthetase.	([94], Table I)
				K_M = 43 μM isopentenyl pyrophosphate (IPP)	Condensation reaction of IPP with Farnesyl-PP	([95], Table 1)
				K_M = 0.1 μM Farnesyl-PP	Assumed equal to the farnesyl-PP concentration	
Steryl Ester Hydrolase	X_{180}	*YEH1*	**1.1 e-4 U/mg**		Microsomes 40k	([92], Table 3).
			9.975e-7 U/mg		Lipid particles. Tgl1p and Yeh1p are localized in Lipid Particles [96].	([97], Fig. 6B)
			1.56e-6 U/mg		Not for an specific protein	([98], Table I)
				K_M = 143 μM Cholesteryl oleate	Data not used because different units between substrate and K_M	[99]
					Kinetic order for Steryl Lanosterol, Steryl Zymosterol, and Steryl Ergosterol-1,2 estimated from log-log plot of concentration vs. enzymatic rate.	([100], Fig. 4)
Steryl Ester Synthase	X_{181}	*ARE1*	0.11 U/mg		Specifically for *ARE1, alias SAT2*. Mid-log phase.	([101], Figs. 2A,B)
			2.54e-3 U/mg		For microsomes (40K x *g*). General Steryl synthase activity. Mid-exponential growth.	([92], Table 3)
				K_M = 60 μM Cholesterol	Kinetic order for Lanosterol and Zymosterol estimated from log-log plot of Cholesterol concentration vs. enzymatic rate.	([102], Fig. 1a)

Steryl Ester Hydrolase	X_{182}	*YEH2*	**9.975e-7 U/mg**		Plasma membrane activity	([97], Fig. 6B)
			1.1e-7 U/mg		For microsomes (40K x *g*). General Steryl synthase activity. Mid-exponential growth.	([92], Table 3)
			1.8e-7 U/mg		30 K *g* microsomes. Aerobic, late exp. growth.	([4], Table 4)
				K_M = 0.121 μM/ml cholesteryl oleate	According to [96],Yeh2p appears to utilize SE's from LP as substrate despite the uncertain localization of the enzyme in the plasma membrane	[100], [96]
					Kinetic order for Steryl Ergosterol-2 estimated from log-log plot of concentration vs. enzymatic rate.	([100], Fig. 4)
Steryl Ester Synthase	X_{183}	*ARE2*	**2.54e-3 U/mg**		For microsomes (40K x *g*).	([92], Table 3)
			3.6e-2 U/mg		Specifically for *ARE2*, *alias SAT1*. Mid-log growing phase	([101], Figs. 2A,B)
			4.1e-7 U/mg		30 K *g* microsomes. Aerobic, late exp. growth.	([4], Table 4)
			1 U/mg		Not for an specific protein	([98], Table I)
				K_M = 60 μM Cholesterol	Kinetic order for Ergosterol estimated from log-log plot of Cholesterol concentration vs. enzymatic rate.	([102], Fig. 1a)
Proteins associated with the ergosterol flux from the ER to others organelles	X_{186}		1e-3 U/mg		Estimate	

(†) U/mg = μmol/min/mg.

(Φ) Parameter values in bold are used in the model.

(*) mol% = concentration of sphingoid base or phosphatidate / concentration of total phospholipid.

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