Table 1 Metabolic fluxes in developing sunflower embryos. Fluxes are given in nmol molecule h^{-1} $embryo^{-1}$

		Flux values (nmol molecule h^{-1} $embryo^{-1}$)	
Flux name	Flux or rate description	Forward	Backward
Vg	Rate of glucose uptake	547 ± 2	0
Va	Rate of glutamine uptake	80 ± 2	0
Vhk	Flux through hexokinase	860 ± 40	0
Vres	Fluxes from G6P to glucose	344 ± 39	0
Vgf	Fluxes catalyzed by G6P isomerase	685 ± 230	979 ± 101
Vald	Fluxes catalyzed by cytosolic aldolase	0 ± 160	320 ± 289
Vglyco	Glycolytic flux	12 587 ± 837	11 913 ± 820
Vfas2	Rate of glycerol incorporation into triacylglycerol	13 ± 3	0
Vsuc1	Flux of G6P to sucrose accumulation	27 ± 3	0
Vsuc2	Flux of F6P to sucrose accumulation	27 ± 3	0
Vglc	Rate of glucose accumulation	31 ± 7	0
Vgl	Flux of glutamine to glutamate	193 ± 13	113 ± 11
Vakg	Flux of glutamate to α-ketoglutarate	524 ± 27	456 ± 25
Vhcp	Exchange of cytosolic and plastidic hexose-P	1459 ± 198	726 ± 68
Valdp	Fluxes catalyzed by plastidic aldolase	619 ± 131	0
Vppp1	Flux of the oxidative part of the pentose-P pathway	275 ± 18	0
Vppp2	Fluxes catalyzed by transketolase	352 ± 52	260 ± 46
Vppp3	Fluxes catalyzed by transaldolase	939 ± 90	848 ± 84
Vppp4	Fluxes catalyzed by transketolase	91 ± 64	0 ± 58
Vpkp	Flux catalyzed by plastidic pyruvate kinase	250 ± 15	0
Vpdhp	Flux catalyzed by plastidic pyruvate dehydrogenase	260 ± 16	0
Vmep	Flux catalyzed by plastidic malic enzyme	18 ± 5	0
Vfas2	Flux of AcCoA to fatty acid synthesis	259 ± 15	0
Vpk	Flux catalyzed by pyruvate kinase	382 ± 27	0
Vpyr	Flux of pyruvate from cytosol to mitochondria	381 ± 27	0
Vpepc	Anaplerotic flux through PEPC	229 ± 30	188 ± 10
Vpdh	Flux catalyzed by pyruvate dehydrogenase	464 ± 17	0
Vcs	Flux through citrate synthase	464 ± 17	0
Vca	Flux calatyzed by aconitase	464 ± 17	0
Vsfa	Flux through 2-oxoglutarate dehydrogenase	532 ± 19	0
Vfum	Flux catalyzed by fumarase	834 ± 182	302 ± 164
Vme	Flux through malic enzyme	84 ± 18	0
Vco_2	Rate of CO_2 production	2064 ± 53	0
Vwall	Rate of cell-wall synthesis	50 ± 3	0
Vsta	Rate of starch accumulation	21 ± 2	0
Vp5peff	Flux of P5Pp to amino acids for protein synthesis	1	0
Vtpeff	Flux of TP to amino acids for protein synthesis	3	0
Vpepeff	Flux of PEP to amino acids for protein synthesis	1	0
Ve4peff	Flux of E4Pp to amino acids for protein synthesis	1	0
Vpyrpeff	Flux of PYRp to amino acids for protein synthesis	8	0
VAcCoAeff	Flux of AcCoAp to amino acids for protein synthesis	1	0
Vpyrceff	Flux of PYR to amino acids for protein synthesis	1	0
Voaaeff	Flux of OAA to amino acids for protein synthesis	25	0
Vglueff	Flux of GLU to amino acids for protein synthesis	12	0

Some fluxes were determined by ^{14}C-labeling experiments, such as the rate of glucose uptake (Vg) and the rate of glutamine uptake (Va). The rates of starch (Vsta), cell-wall (Vwall), protein, fatty acids (Vfas1 and Vfas2), sucrose (Vsuc1 and Vsuc2) and glucose (Vglc) accumulation were quantified by measuring their accumulation during the incubation period. Those results are reported as means ± SD. The flux of glucose resynthesis from hexose-P (Vres) was calculated using the equation: $(Vres = Vg \cdot (G_{ex}1/Sg6 - G_{in}1/G_{in}6 \cdot G_{ex}6/Sg6)/(G_{in}1/G_{in}6 - Sg1/Sg6)$, where $G_{ex}1$, Sg1 and $G_{in}1$ represent the enrichment of carbon 1 of extracellular glucose, the glucosyl moiety of sucrose and intracellular glucose, respectively, and $G_{ex}6$, Sg6 and $G_{in}6$ represent the enrichments of carbon 6 in the same molecules) [Equation (4) in Alonso *et al.* (2005)], and then entered as a free flux in the model. The other flux values were calculated from the model based upon carbon enrichment measured after steady-state labeling with [1-$^{13}C_1$]glucose, [2-$^{13}C_1$]glucose or [U-$^{13}C_5$]glutamine. The values are the best fit, and are also the most frequently determined optimized flux values ± confidence interval.