# Supplementary Table, Figures and Figure Legends (S1-S4)

Compound <sup>a</sup>	Adherent	Cystic
1	0,34	0,49
2	0,09	3,22
3	5,04	4,67
4	84,17	75,01
5	2,04	2,84
6	0,15	0,44
7	7,76	13,05
8	0,08	0,05
9	0,14	0,09
10	0,19	0,14

**Supplementary Table S1.** Sterol composition of *C. owczarzaki* adherent and cystic cells obtained by GC-MS analyses (Relative %).

<sup>*a*</sup> Sterol identity numbers are the same as in Table 2.

## Supplementary Figure S1.



### В

	375	375			385 440		453	460	687	702	
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Homo sapiens	GMF	MQG <mark>.</mark>	<mark>r</mark> ngs	Q	GGF	SFSTLD	CGWIVS	DCTAEA	WPQEN:	EAGVFNKS	SCAI
Monosiga brevicollis	GAF	MNG.	<mark>r</mark> ngs	Q	GGWI	PFSTRD	MGWIVA	DCTGEG	WPQESI	CGVFNKN	ICMI
Capsaspora owczarzaki	GMF	LNG.	<b>F</b> NGS	Q	GGF	PFSTRD	CGWIVA	DCTAEG	WPDDEI	KGVFNKN	ICMI
Saccharomyces cerevisiae	GMI	IMG	<b>r</b> ngv	7Q	GAW	GFSTKT	QGYTVA	<b>D</b> CTAEA	WKFESV	/EGVFNHS	SCAI
Dictyostelium discoideum	GMF	MQG	<mark>Y</mark> NGS	Q	GAW	PFSTVD	HGWPIS	DCTAEG	FPQESI	IGVENEN	ICMI
Leishmania donovani	GLS	MSG	YNG5	ŞQ	GAW	NFSTRA	QGWQVS	DCTAEG	WPQERI	SGVFNGN	INPI
Naegleria gruberi	GMF	(FQG)	r <mark>ngs</mark>	Q	GGW	PFSTRD	HGWPIS	DCTAEG	FPQESI	SGVFNHN	ICMI
Chlorela variabilis	GMF	MQG	YNG5	Q	GAW	PFSTRD	HGWPIS	DCSSEG	WPQQHI	SGVFNRM	ICMI
Ostreococcus tauri	GMF	MQG	YNGS	Q	GAW	PFSTRD	HGWPIS	DCSSEG	FPQQSI	MGVFNAM	ICMI
Arabidopsis thaliana	GMF	MQG	rngs	SQ	GAW	PESTAD	HGWPIS	DCTAEG	FPQQE	EMGVENRN	ICMI

# Supplementary Figure S2.







Supplementary Figure S3.



В





## Supplementary Figure S4.



Supplementary Figure Legends (S1-S4)

**Fig. S1. A.** ML analysis of oxidosqualene cyclases. Bootstrap supports are indicated. *C. owczarzaki* OSC is highlighted in red. Protein IDs are indicated in the branch labels. **B.** Partial alignment of OSCs. Numbering corresponds to positions in the *Homo sapiens* protein. The catalytic residue D is highlighted in red. Asterisks denote conserved amino acids. Residues in positions 389, 441, 453 and 687 are differentially conserved between oxidosqualene-lanosterol cyclases (yellow) and oxidosqualene-cycloartenol cyclases (green).

**Fig. S2. A-B.** Phylogenetic analysis of sterol  $\Delta 8$ , $\Delta 7$ -isomerases. **A.** ML tree of ERG2-Sigma 1 family of proteins. **B.** ML analysis of Emopamil Binding Protein family. *C. owczarzaki* homologs are indicated in red. **C.** Multiple sequence alignment of EBP proteins. Residues are colored according to their percentage of conservation. Asterisks denote essential amino acid residues, according to (Rahier et al. 2008).

**Fig. S3. A.** Total Ion Chromatogram (TIC) of acetylated sterols obtained from *C. owczarzaki* cells grown for 7 days in ATCC 1034 medium (cystic cells). **B.** Structures of all the sterols species identified in the GC/MS analysis. Numbers in bold correspond to the respective peaks indicated in Figs. 4A and S3A.

**Fig. S4.** HPLC analysis of sterols from *C. owczarzaki* filopodial stage. Cells were cultured for 4 days in ATCC 1034 medium with the addition of <sup>14</sup>C-cholesterol, as described in Materials and Methods. Blue line indicates absorbance at 210 nm. Black line corresponds to radioactivity (cpm) and it is shown from 15 to 27 min to simplify the figure. Peak 1 showed significant absorbance also at 325 nm, suggesting it could represent a conjugated triply unsaturated sterol, no further characterized. Peaks 2 to 4 significantly absorbed at 280 nm, suggestive of conjugated doubly unsaturated sterols. Their retention times corresponded, respectively, to those of standards of 7,22-*bis*-dehydrocholesterol (20.6 min), ergosterol (25.6 min), and 7-dehydrocholesterol (26.1 min). Peak 5 eluted, like cholesterol standard, at 34.3 min.

#### References

Rahier, A., Pierre, S., Riveill, G. & Karst, F. 2008 Identification of essential amino acid residues in a sterol 8,7-isomerase from Zea mays reveals functional homology and diversity with the isomerases of animal and fungal origin. *Biochem. J.* **414**, 247–259. (doi:10.1042/BJ20080292)