

Chytrid FD01 infection time course of *Scenedesmus dimorphus*

Experiment data Collection (12/12/2012)

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Analysis – Aaron Collins



Study Purose

With the original FD01-*Scenedesmus* infection study (03/27/2012), we were effectively “blind” to spectral signatures for the chytrid due to its low pigment levels.

The new investigation was proposed to perform a similar infection time couse, only this time an exogenous label would be added to the sample to label the chytrid cell wall.

After initial screening, 1.5 ug/ml Nile Red was chosen. The unique characteristics of this lipid label are that it labels control cells (uninfected?) very weakly and we can distinguish neutral and polar lipids due to a spectral shift that is associated with the different dielectric constants of the lipid environments.

In other words;

TABLE 2. Fluorescence properties of nile red in various solvents

Solvent	Dielectric Constant ^a	Excitation Maximum <i>nm</i>	Emission Maximum <i>nm</i>	Relative Fluorescence Intensity
Water	78.5	591	657	18
Ethanol	24.3	559	629	355
Acetone	20.7	536	608	687
Chloroform	4.8	543	595	748
iso-Amylacetate	—	517	584	690
Xylene	2.4	523	565	685
n-Dodecane	2.0	492	531	739
n-Heptane	—	484	529	585

Nile red was analyzed at a concentration of 1 $\mu\text{g/ml}$ in all solvents. Excitation and emission maxima were determined and the relative fluorescence intensity in each solvent was measured at the corresponding excitation and emission maxima.

^aDerived from (27).

Greenspan and Fowler. Spectrofluorometric studies of the lipid probe, nile red. J. Lipid Res. 1985 26:(7) 781-9.

Time course of Infection

Colors represent unique infections (in duplicate) as we are trying to squeeze 24 hours of imaging into a 1 day experiment.
Infection conditions; $\sim 32^{\circ}\text{C}$, $400 \text{ uE} \cdot \text{m}^2 \cdot \text{s}^{-1}$ shaking on an orbital shaker.

Infected?		Date & Time of Infection	ID	Time of Imaging		PAM	Oxygraph
Yes	No						
X		12/11, 4 pm	Infected t16	12/12	8 am	X	X
	X		Control t0	12/12	9 am	X	X
X		12/12, 6 am	Infected t4	12/12	10 am	X	X
X		12/10, 4 pm	Infected t48	12/12	12 pm	X	X
	X		Control t4	12/12	1 pm	X	X
X		12/12, 6 am	Infected t8	12/12	2 pm	X	X
X		12/11, 4 pm	Infected t24	12/12	4 pm	X	X
	X		Control t8	12/12	5 pm	X	X
X		12/12, 6 am	Infected t12	12/12	6 pm	X	X

*Control cells will be cultured under same conditions as infected cultures.

For each time point there will be biological duplicates that will be assessed on the oxygraph and PAM however, only a single bio rep will be used for imaging.

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1500  $\mu\text{l}$  total will be removed.

1 ) 50  $\mu\text{l}$  samples will be retained for DNA extraction

Protocol from R. McBride; mixing 50  $\mu\text{l}$  of sample with 50  $\mu\text{l}$  of 0.25X lysis buffer in PCR tubes. The mixture is then placed in a PCR block and heated to  $95^{\circ}\text{C}$  for 10 min, cooled to  $25^{\circ}\text{C}$  for 5 min, heated to  $95^{\circ}\text{C}$  for 10 min and then cooled to  $25^{\circ}\text{C}$  for 5 min. The DNA lysis buffer (1X) is composed of: 50 mM Tris-HCl, pH 8.0; 200 mM NaCl; 20 mM EDTA, pH 8.0; 1.0% (v/v) SDS

2) 1000  $\mu\text{l}$  used for Oxygraph measurement. Triplicate PAM measurements will be made *in situ*.

3) 400  $\mu\text{l}$  will be retained to prepare sample for imaging

# Imaging and Analysis

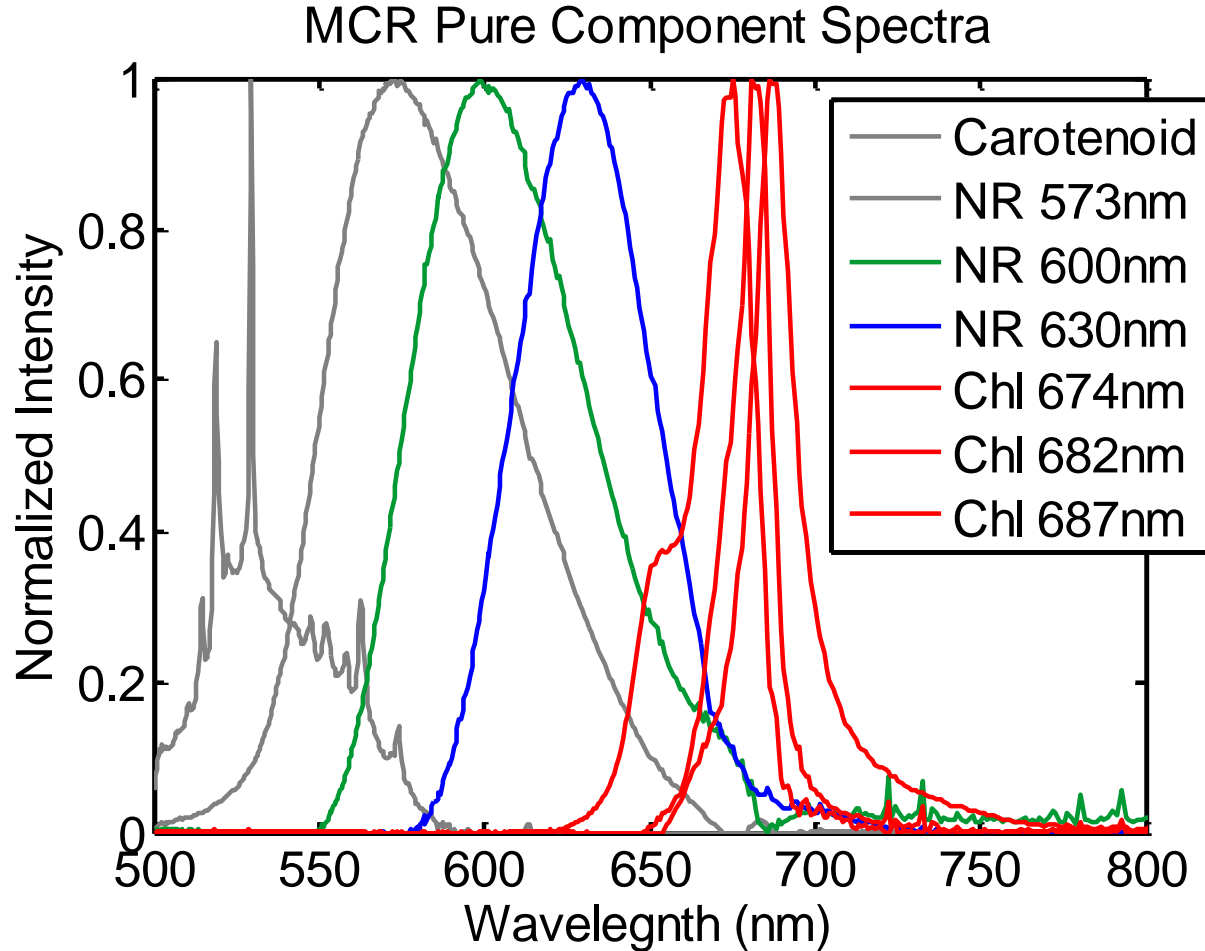
## Imaging

- 400  $\mu\text{l}$  of culture was incubated with 1.5  $\mu\text{g/ml}$  Nile Red for 10 minutes in darkness
- Sample was centrifuged (700 x g) for 3 minutes and 375  $\mu\text{l}$  of supernatant was removed.
- Remaining soft pellet was resuspended and 4  $\mu\text{l}$  was loaded to microscope slide and covered with a #1.5 coverglass.
- Imaging commenced on SNL's HSI microscope
  - 60 x magnification (Nikon, plan apochromat, NA 1.4)
  - Laser OD = 0 (~200  $\mu\text{W}$  laser power into microscope)
  - BG-38 optical filter placed in front of detector.
  - At least 25 cells were imaged per time point and a 2-3 optical sections were taken.

## Analysis

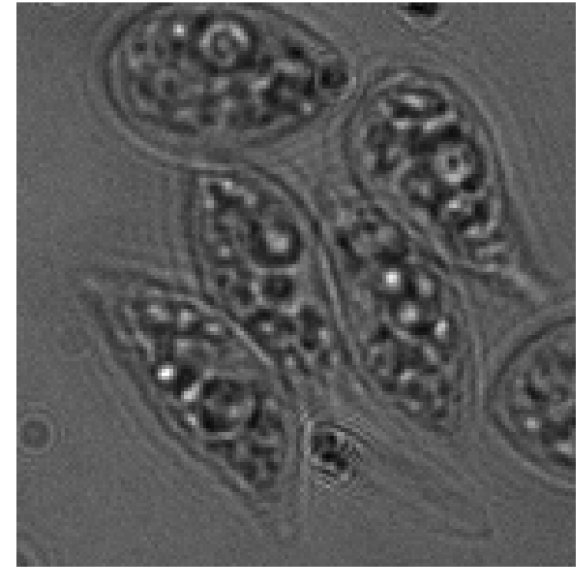
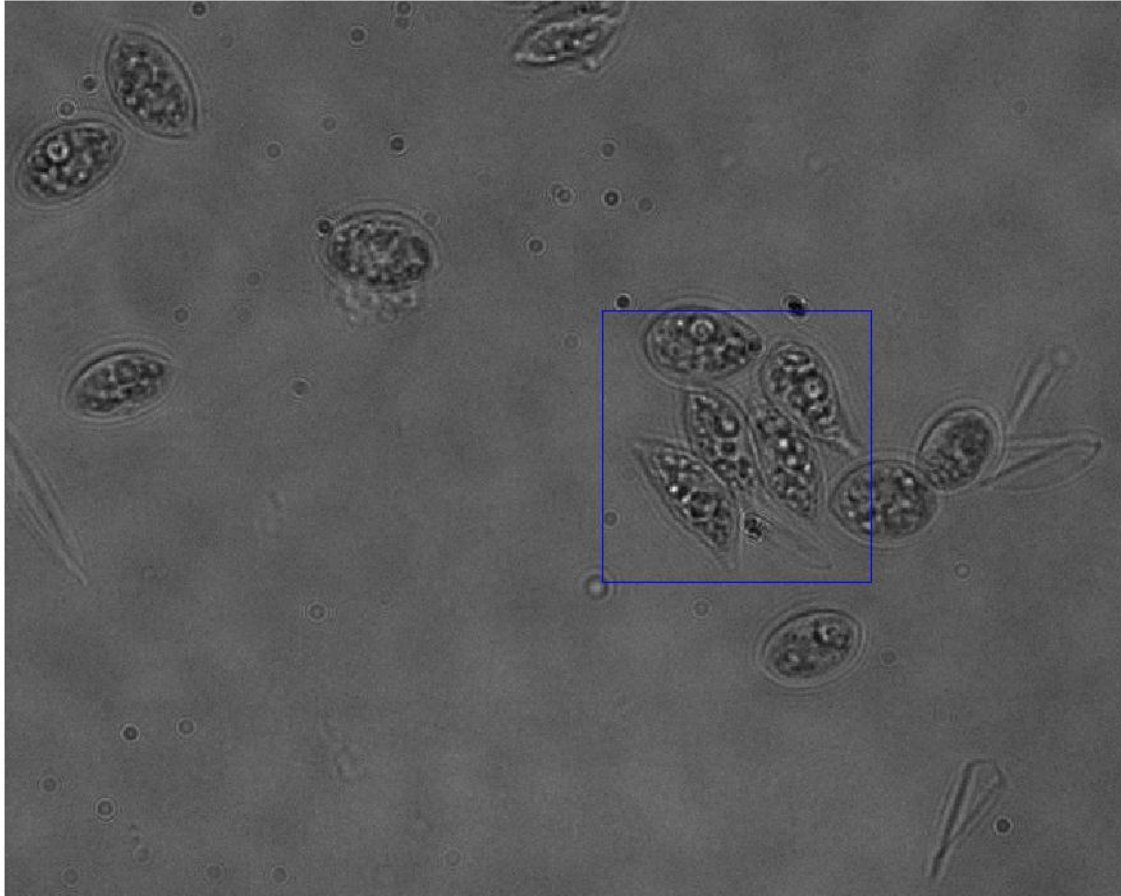
- Imaging generated 18.1 Gb of raw data!
- Images were pre-processed via in-house routines
- Due to the size of the dataset, control cells and cells infected for 48 hours were combined into a composite dataset and MCR algorithms were used to model the spectral data. After a sufficient model was generated, the spectral model was constrained and applied to the remaining data.

# MCR generated model

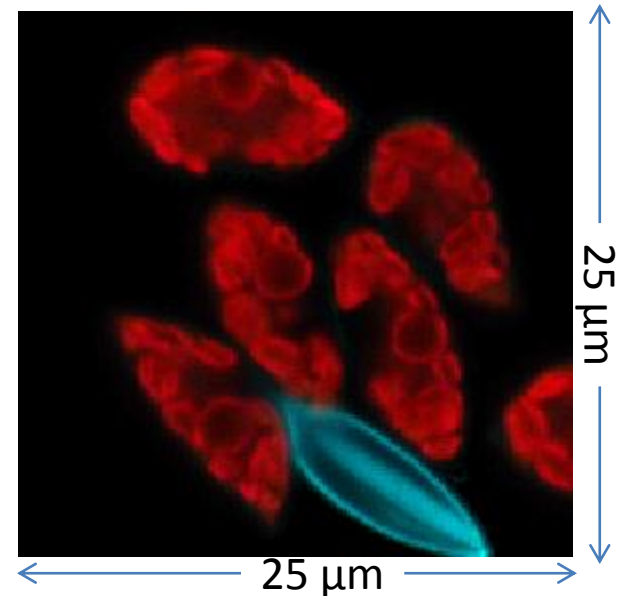


One the following slides, I will use RGB coloring, referenced above, to display the spectral images

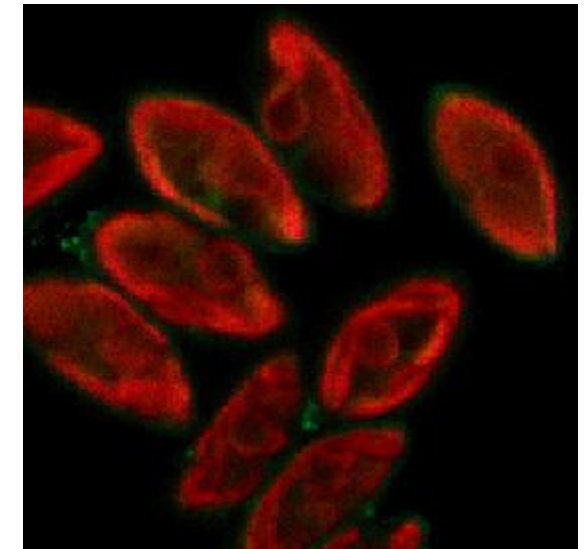
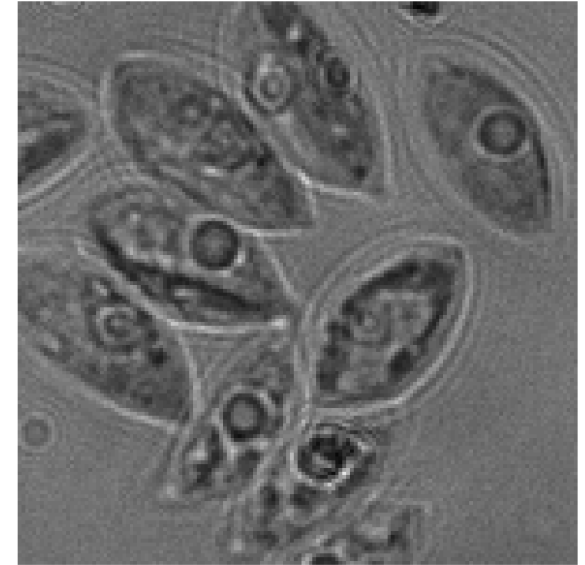
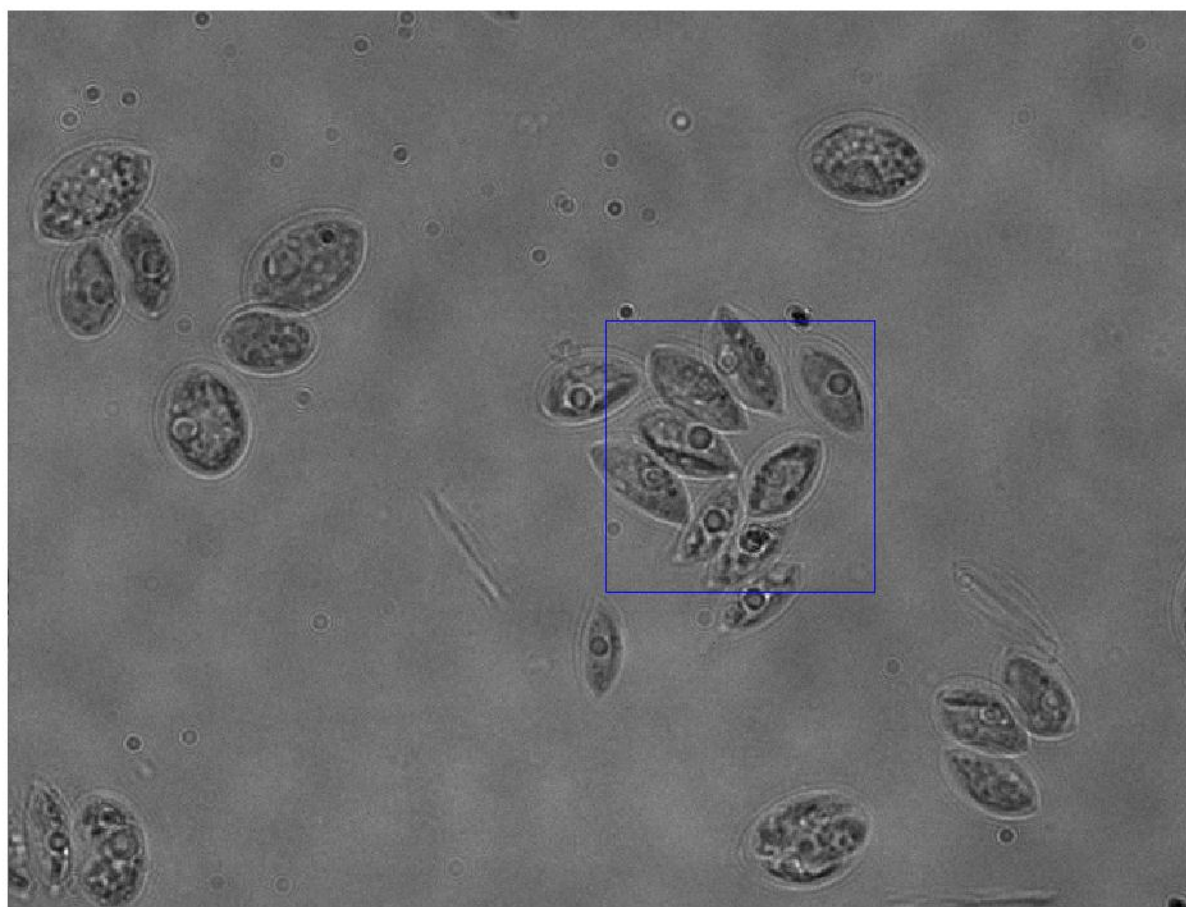
# Representative control cells $t = 0$ hours



Note the empty cell wall in this image. While not abundant, it was present in control cells. Also, note obvious pyrenoid in each cell.



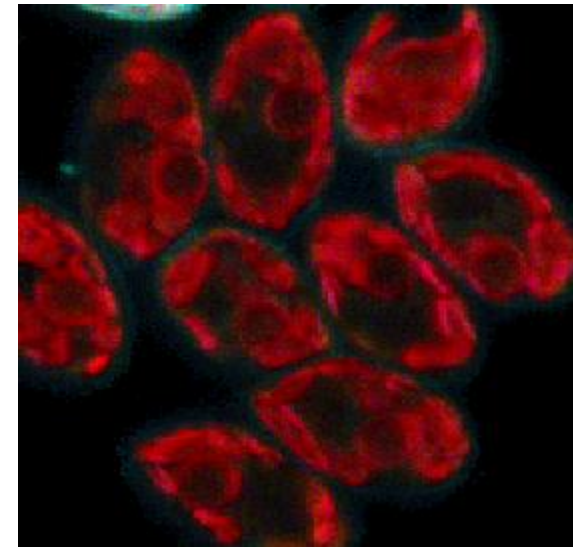
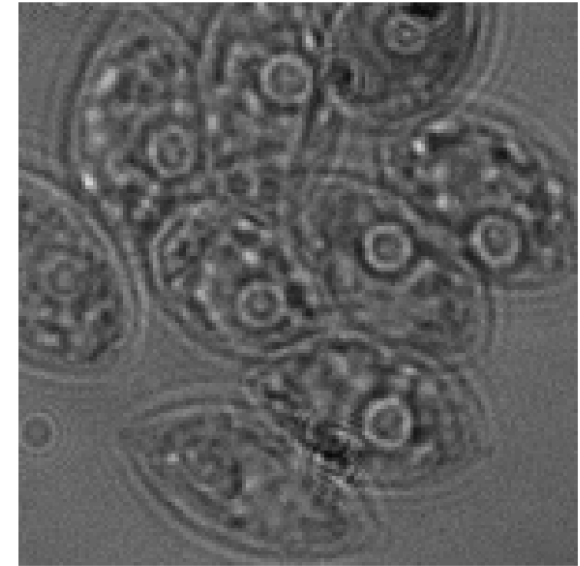
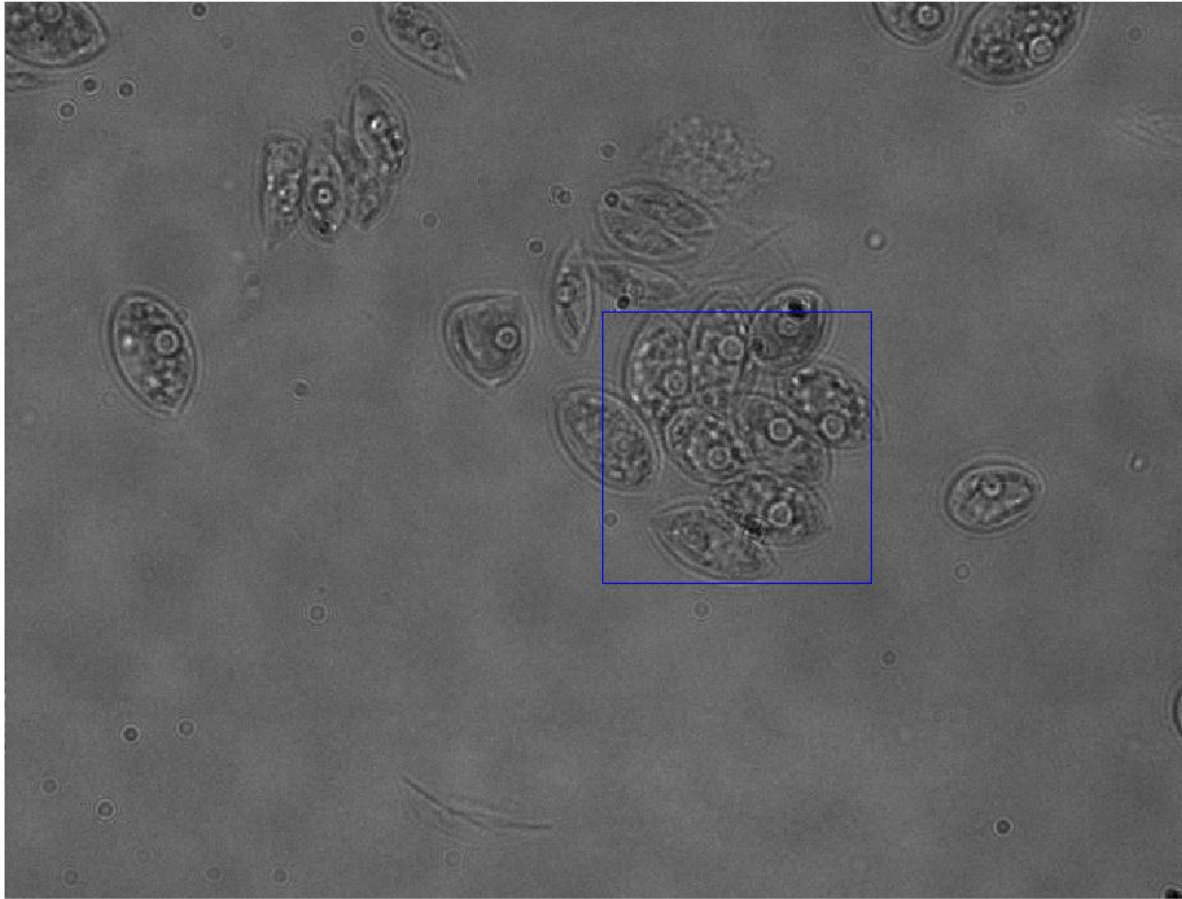
# Representative control cells $t = 4$ hours



Similar to  $t = 4$  hour sample. Very faint NR labeling is more prevalent at this time compared to  $t = 0$  hours



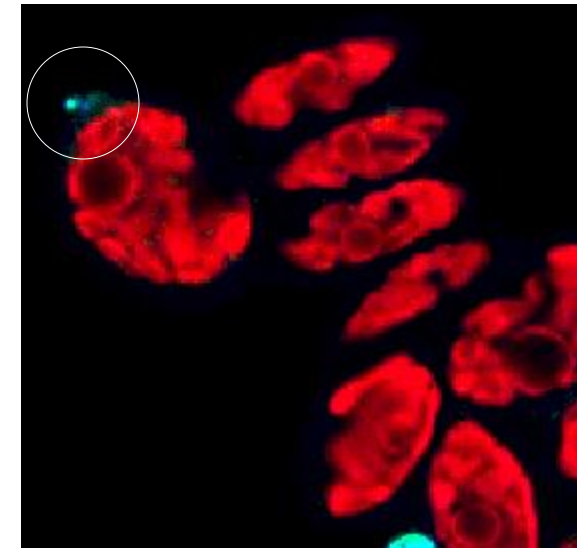
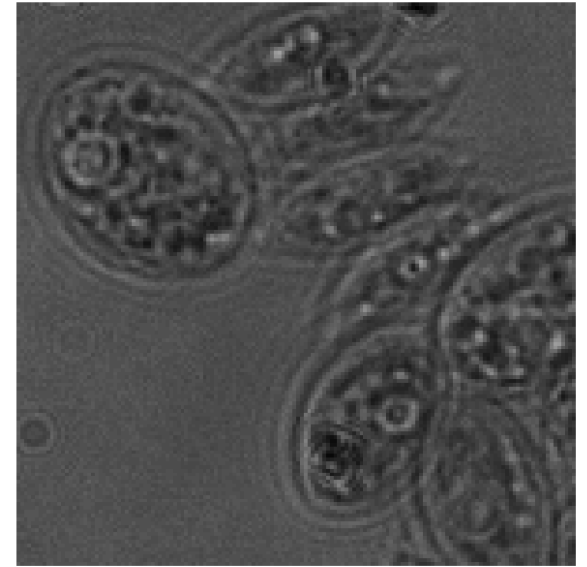
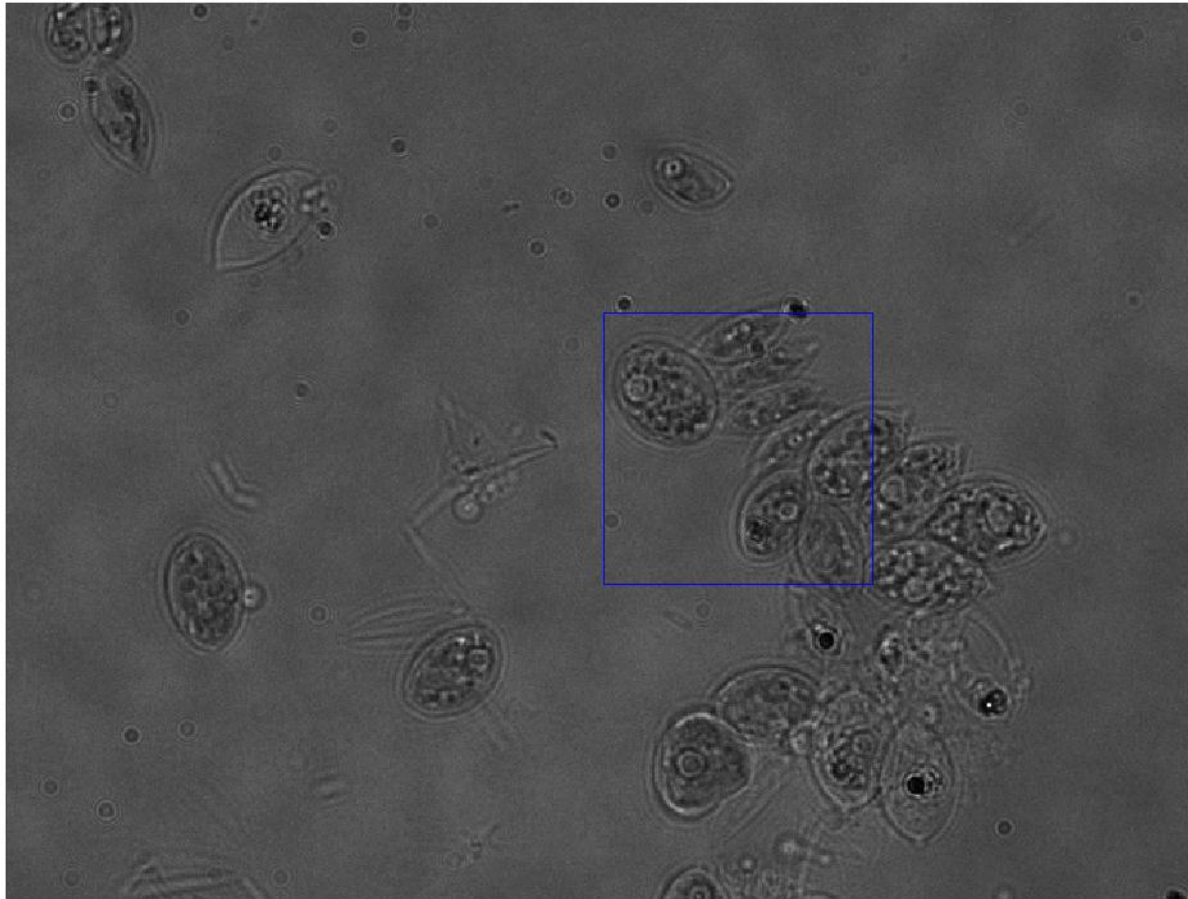
# Representative control cells $t = 8$ hours



At  $t = 8$  hours not substantial change from  $t = 4$  or 0  
however, more cells are being labeled, perhaps from  
the elevated temperature and irradiance?

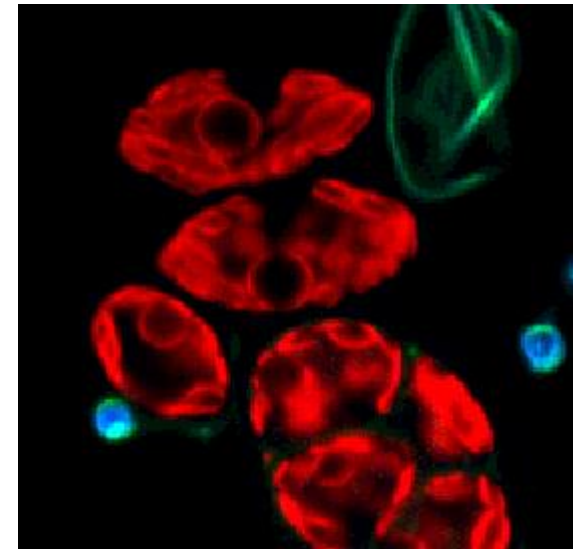
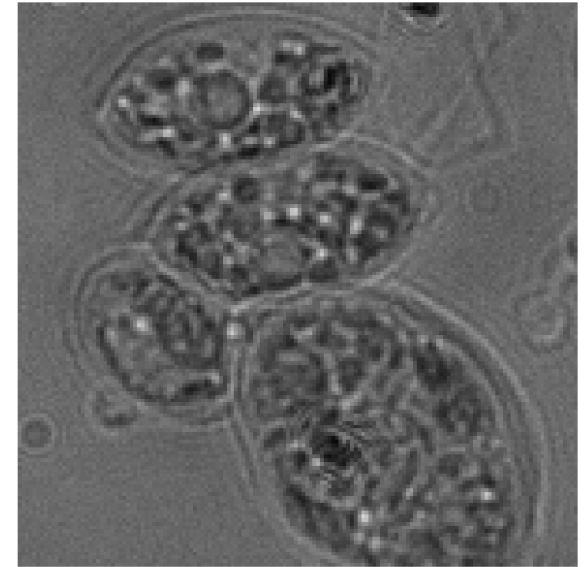
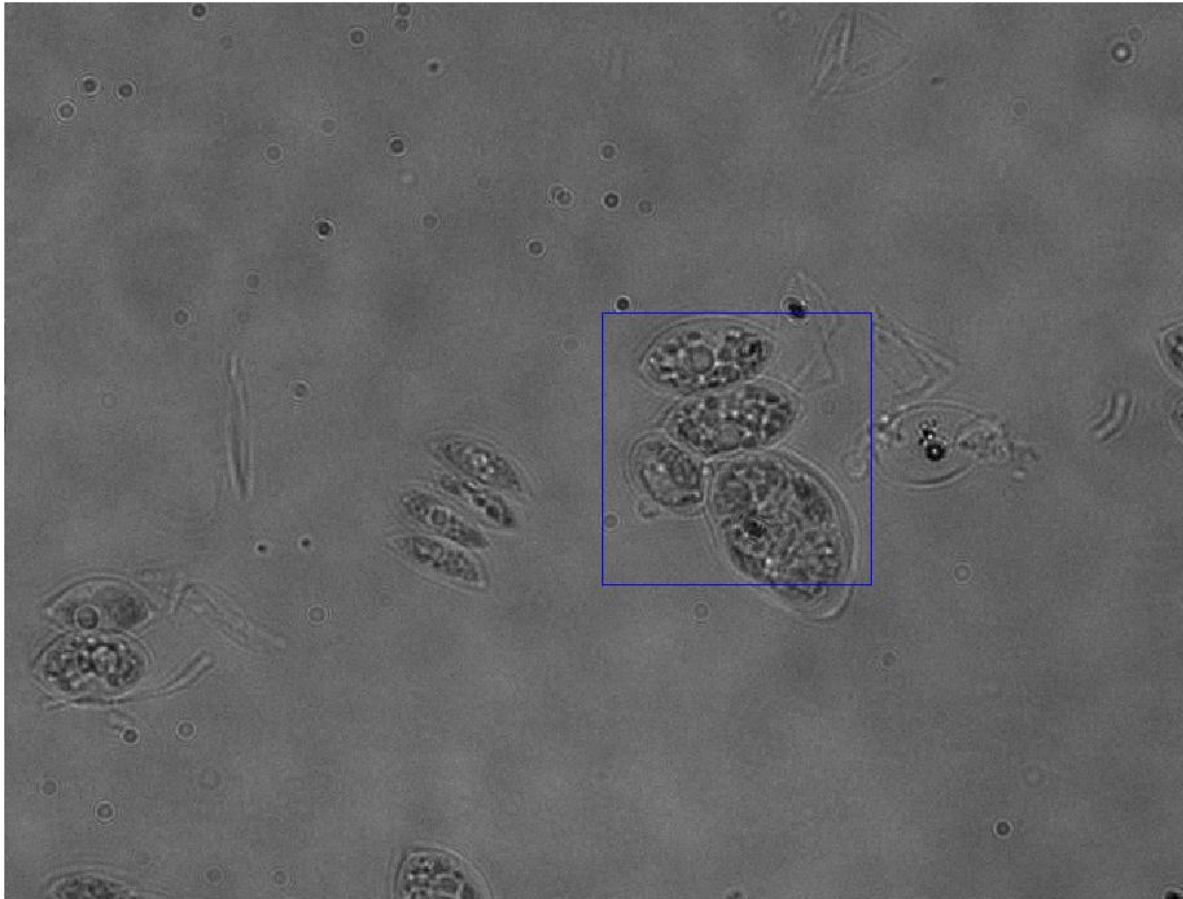


# Representative infected cells t = 4 hours

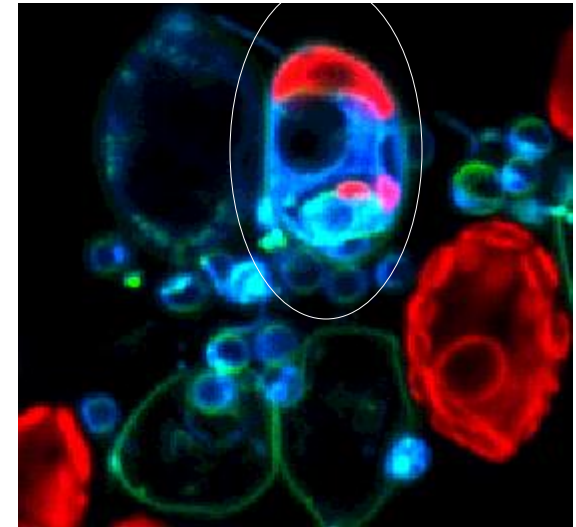
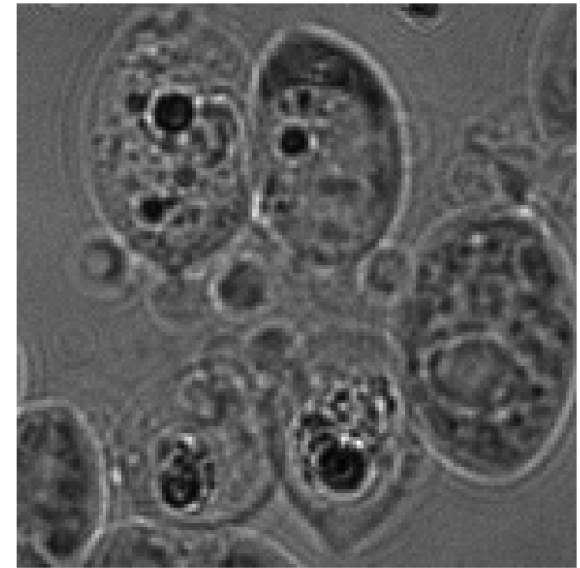
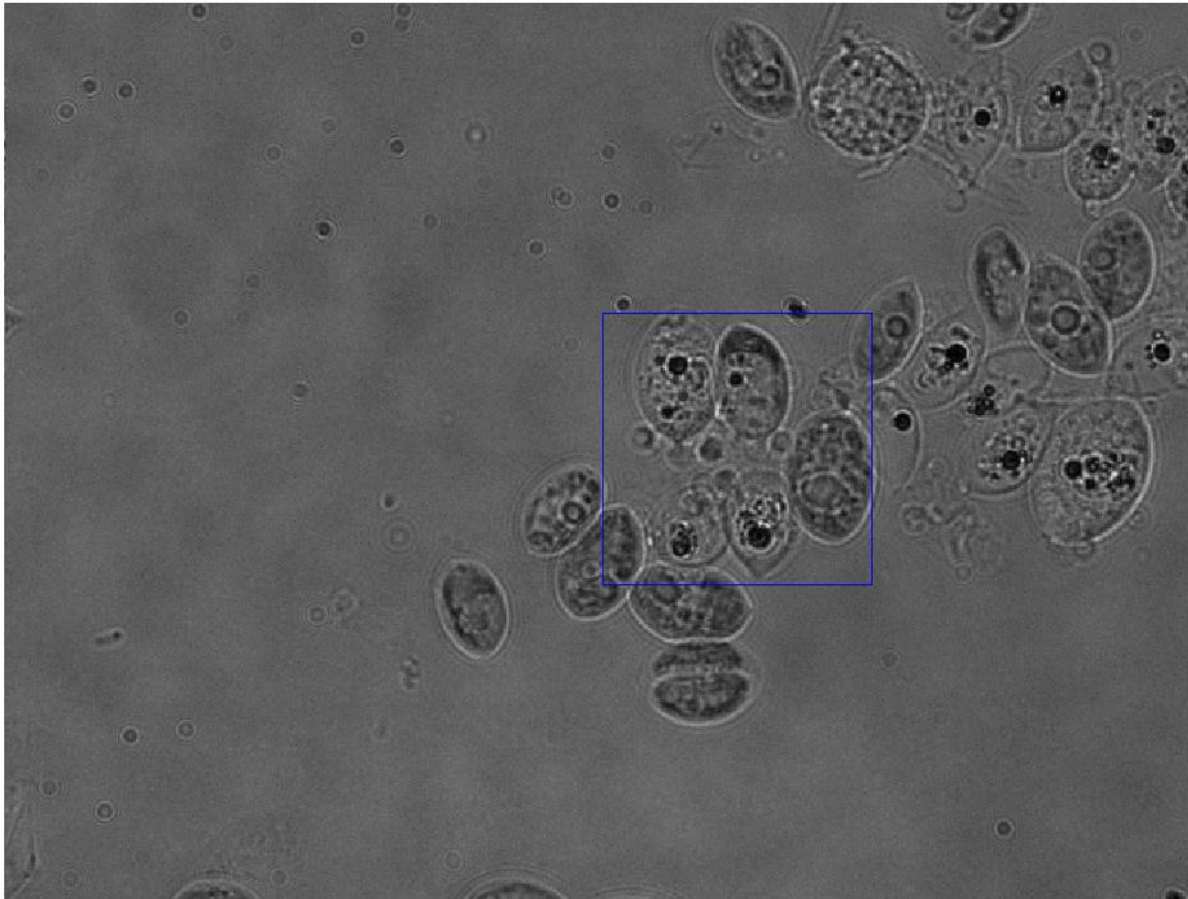


Encircled portion could be a early stage cyst?

# Representative infected cells $t = 4$ hours

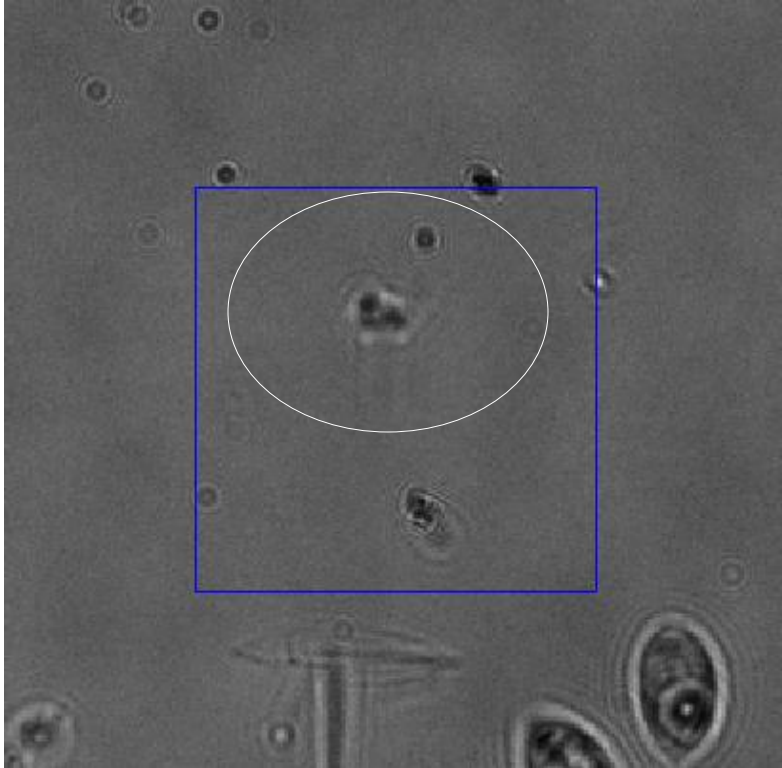


# Representative infected cells t = 4 hours

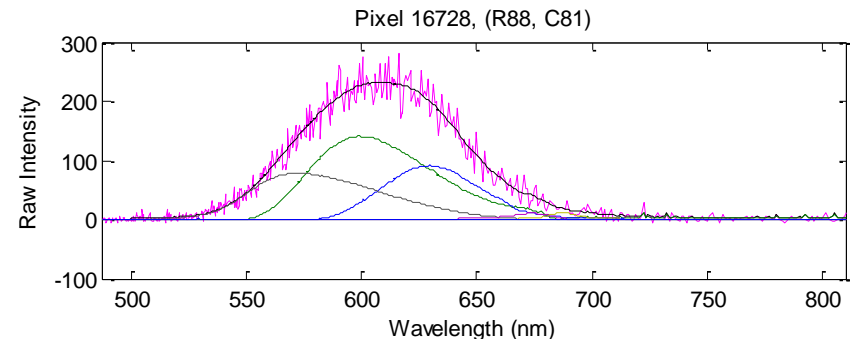
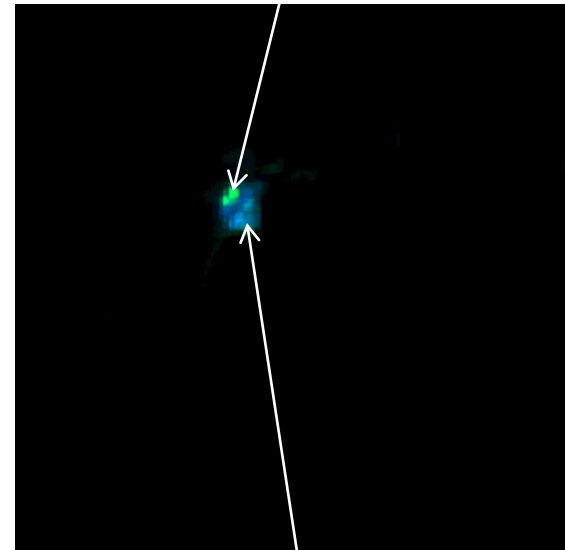
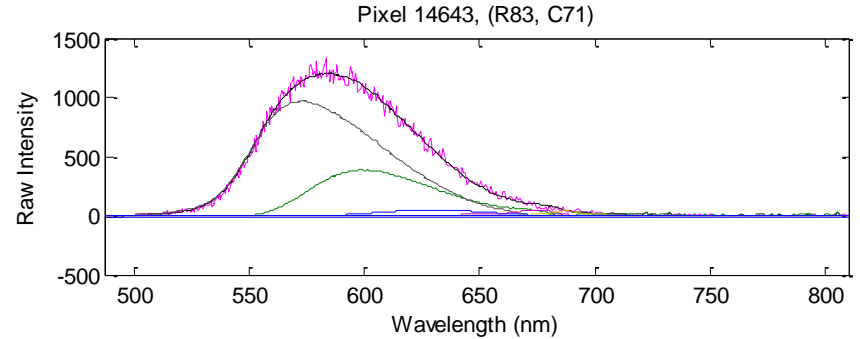


NR labeling allows for better delineation of cell membranes, both algal and chytrid. Note that likely lipid bodies are obvious in sporangia. Encircled host cell shows chloroplast reduction and chytrid propagation inside of host. It is possible that these cells are from the infection source itself and not new infection.

# Chytrid in absence of host

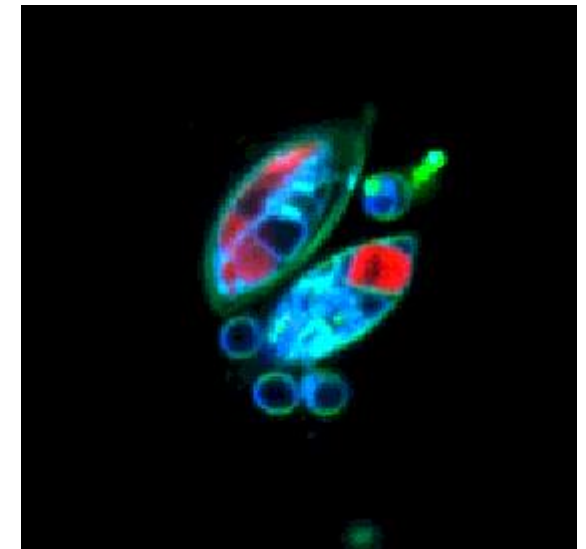
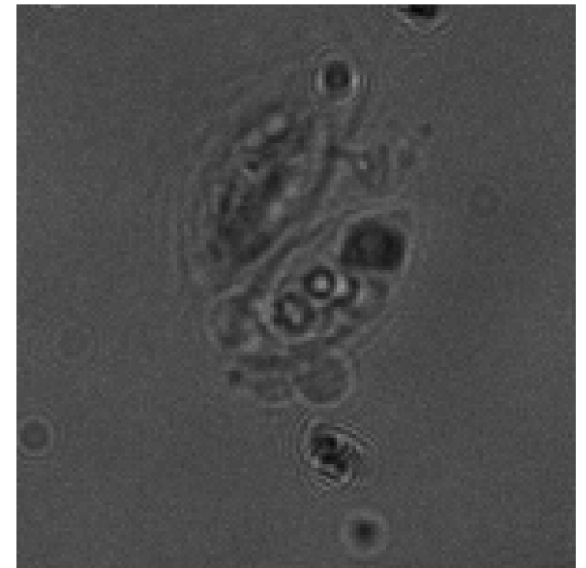
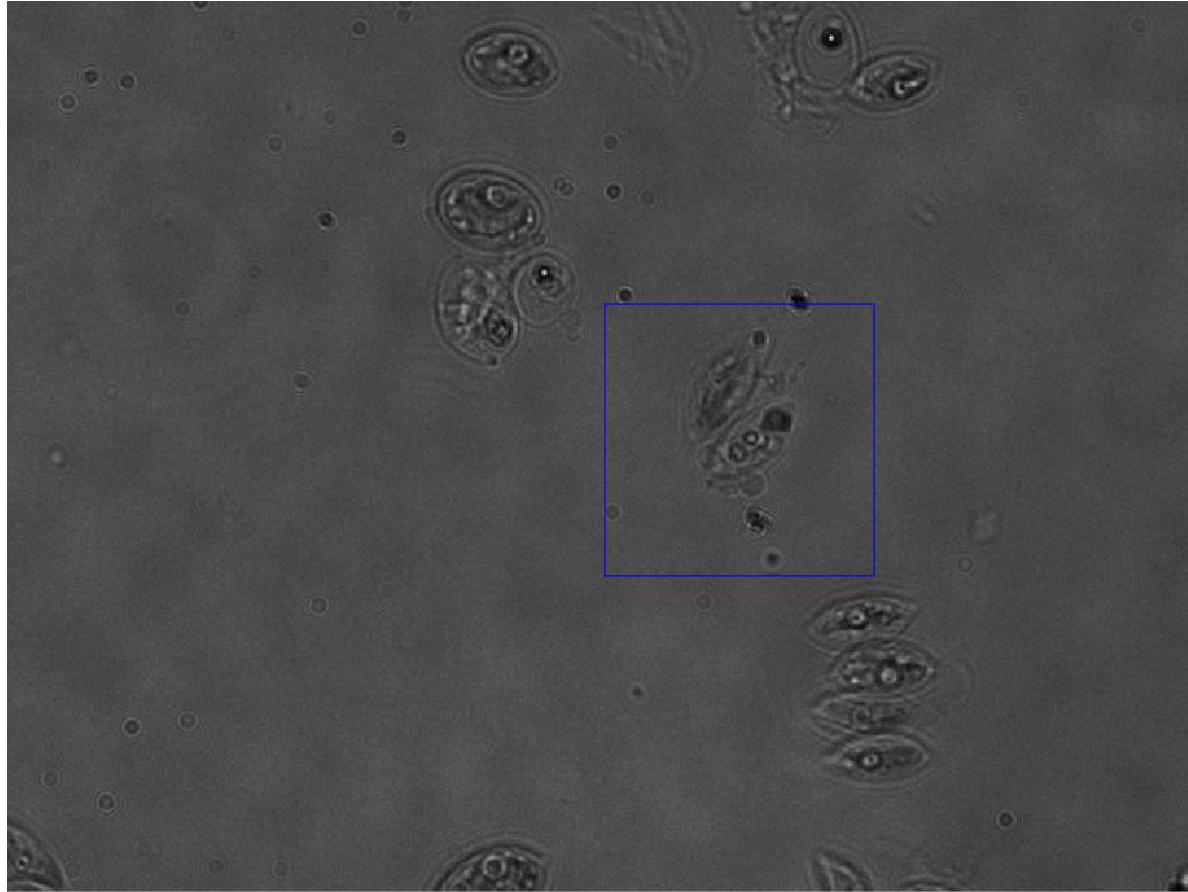


Filamentous chytrid does not show uniform labeling. A small punctate region is highly labeled by NR. We have seen something similar in unlabeled chytrid and it contains a carotenoid signature. I am not sure what organelle or subcellular location would be responsible for these observations.



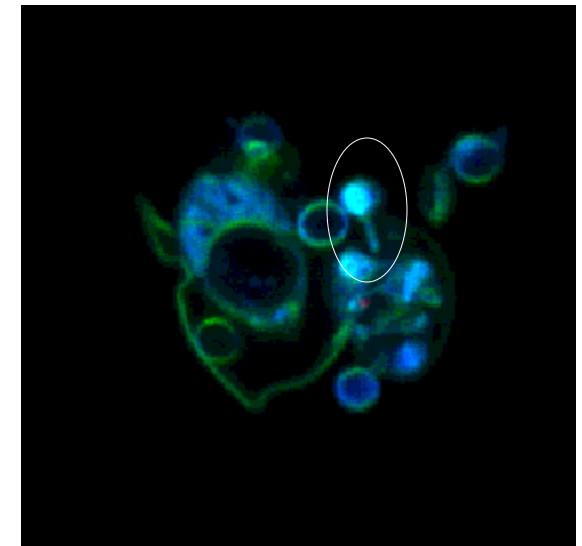
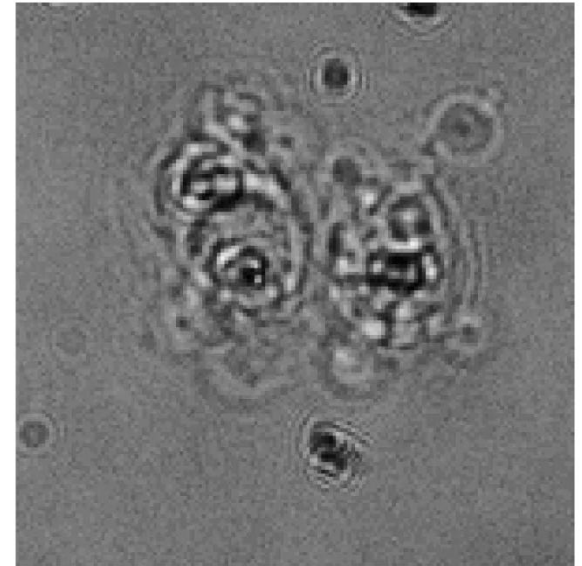
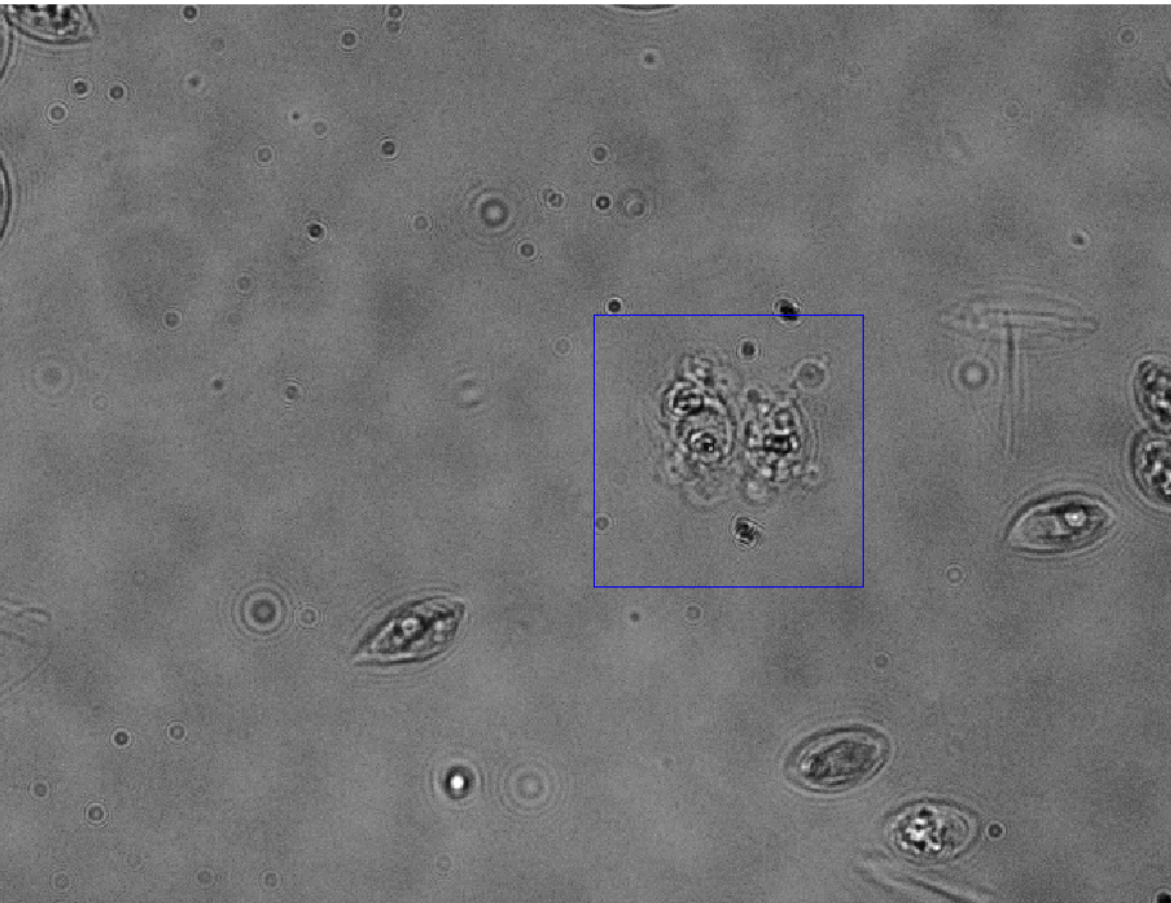


# Representative infected cells $t = 8$ hours



Portions of the chloroplast still remain in these fluorescence images.

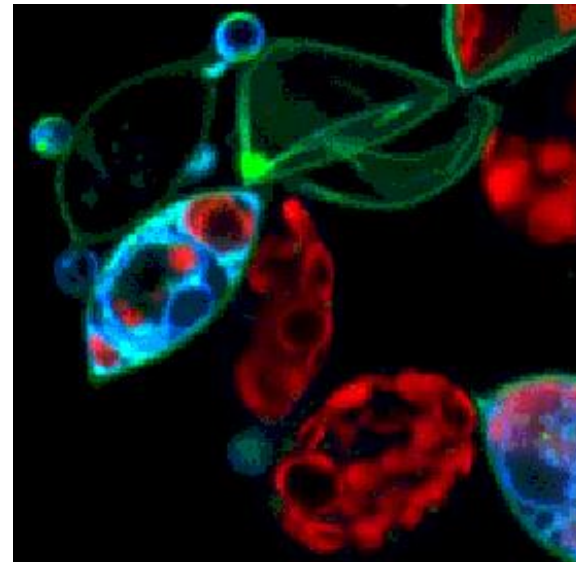
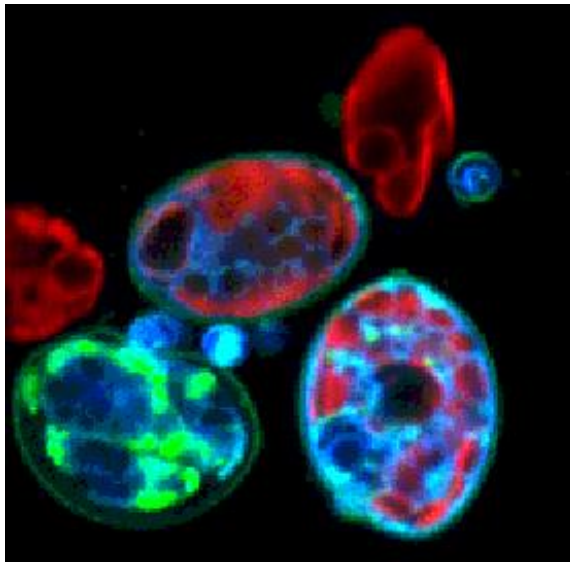
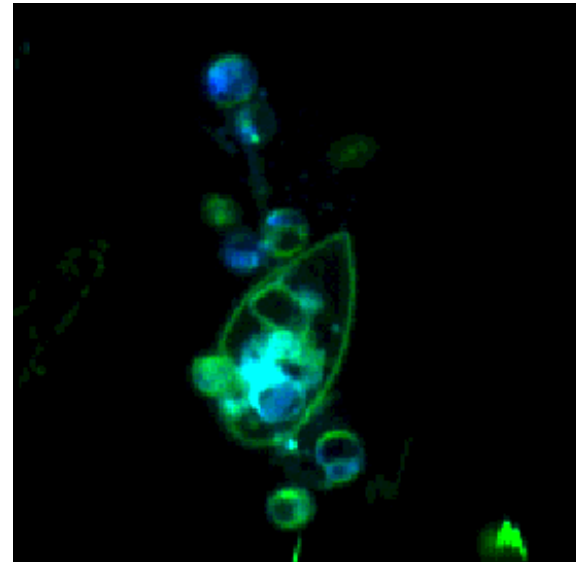
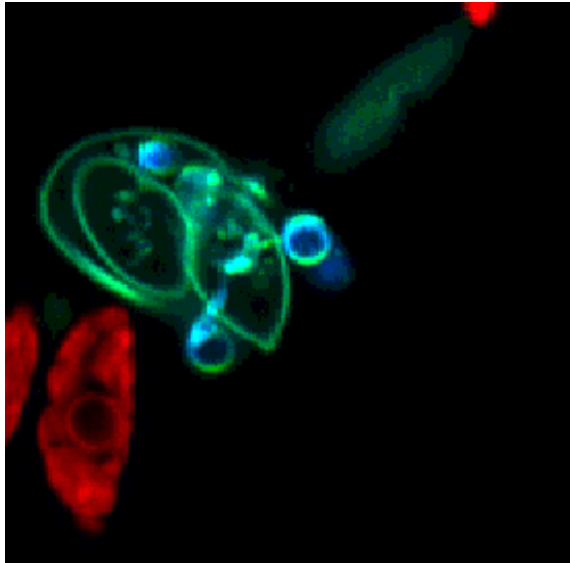
# Representative infected cells t = 8 hours



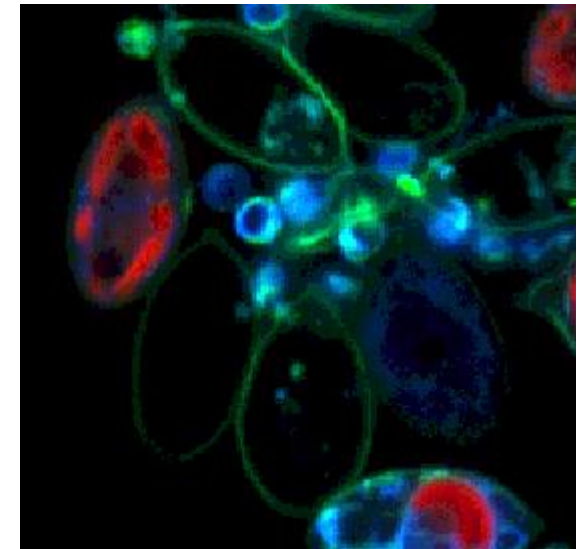
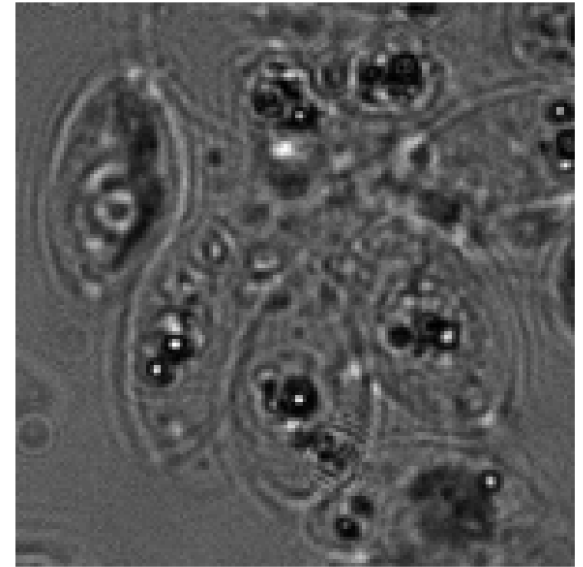
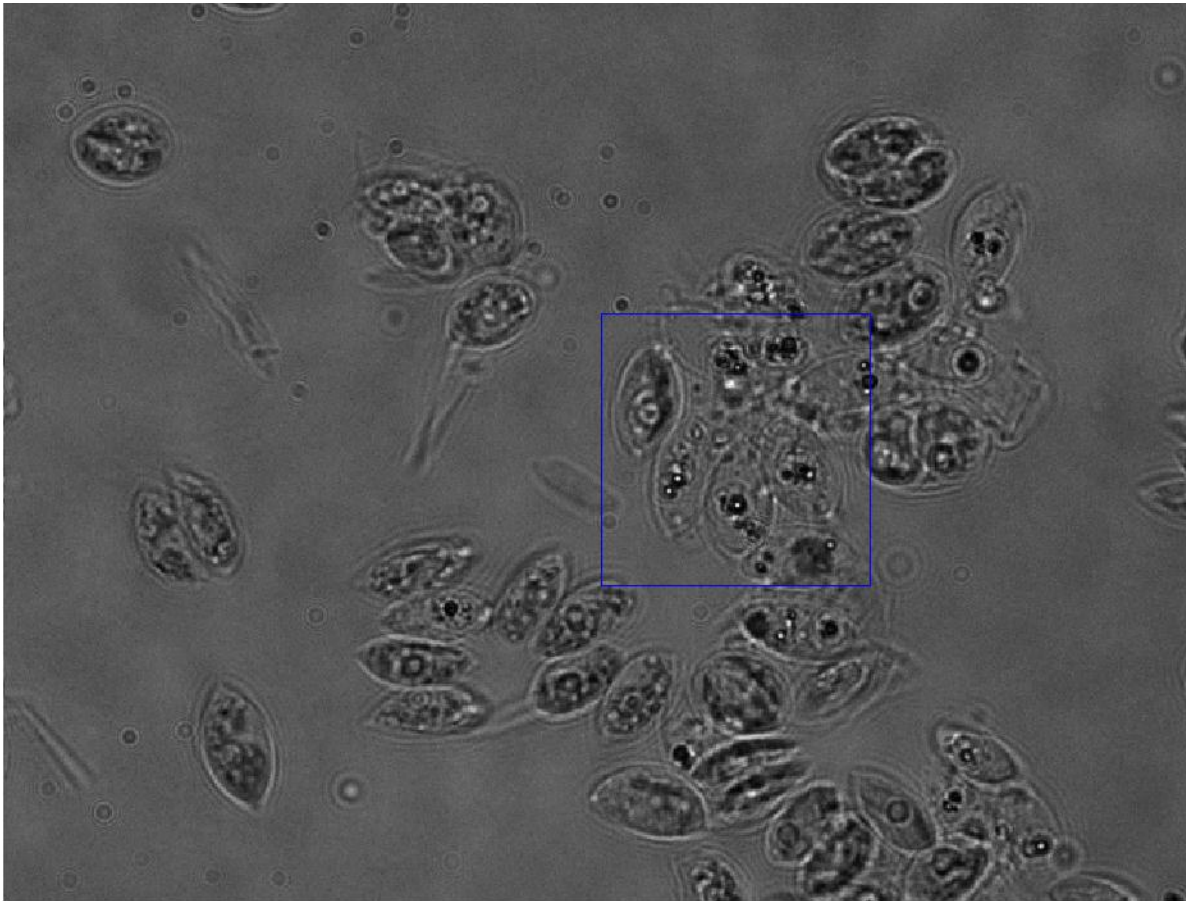
Encircled region could be showing penetration into host cell. Both cells show some evidence for chytrid progeny within host cell.



# Representative infected cells $t = 8$ hours

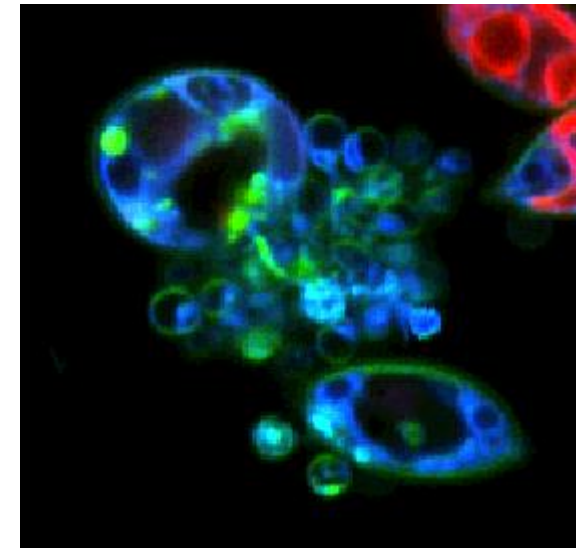
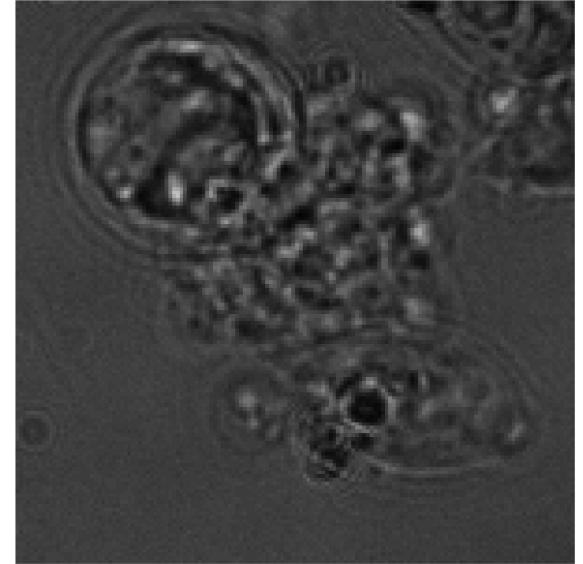
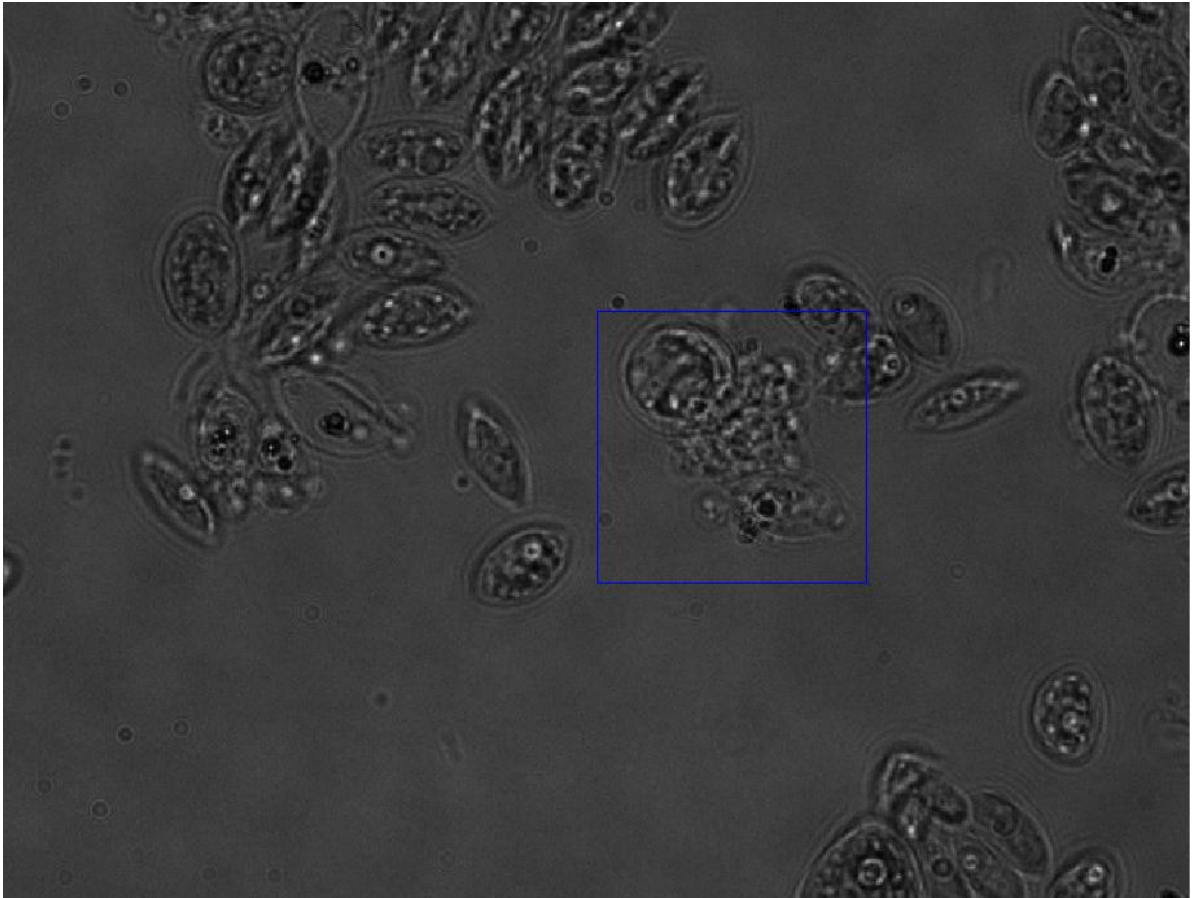


# Representative infected cells $t = 12$ hours



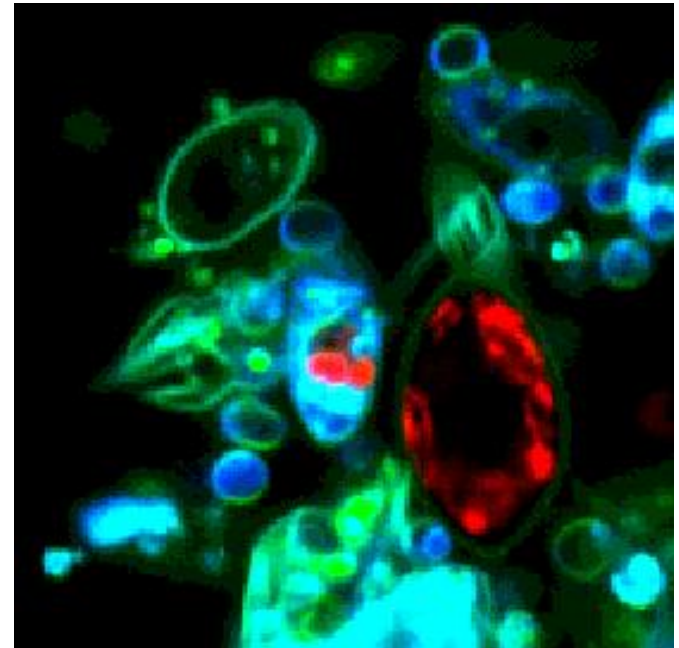
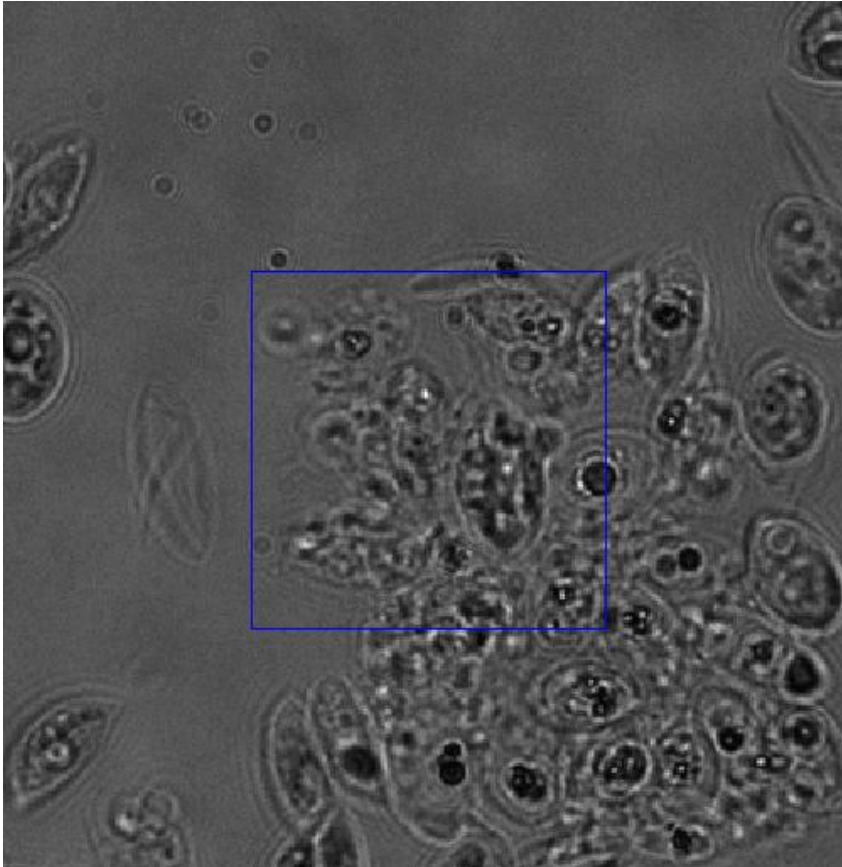
In the widefield image, more of the host cells show signs of infection.

# Representative infected cells t = 12 hours



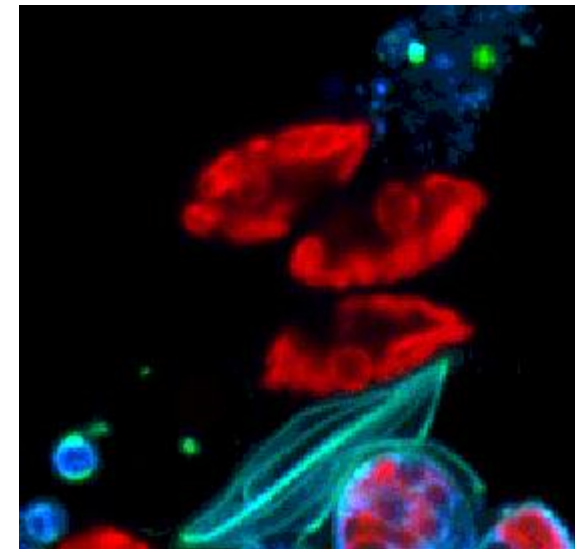
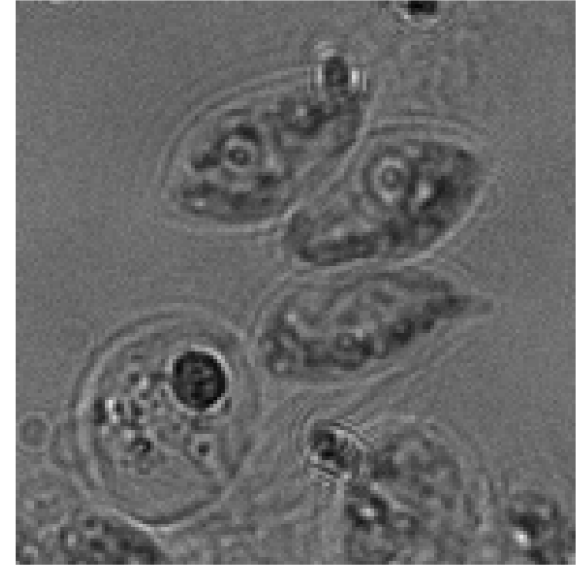
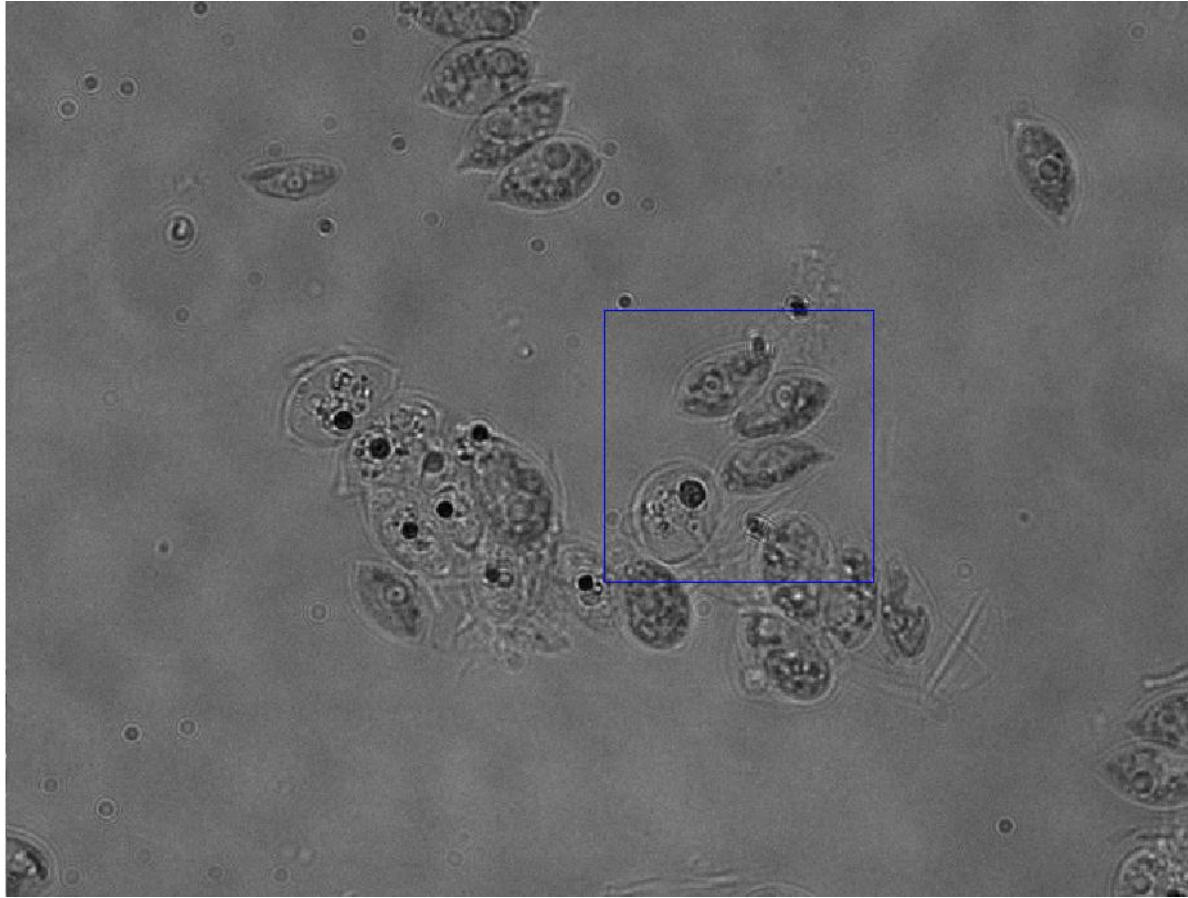
Quite a bit of sporangia! Complete absence of chlorophyll in Infected cells.

# Representative infected cells $t = 12$ hours

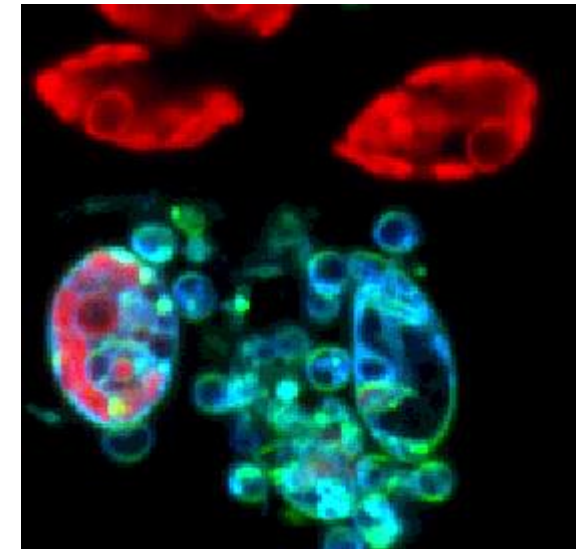
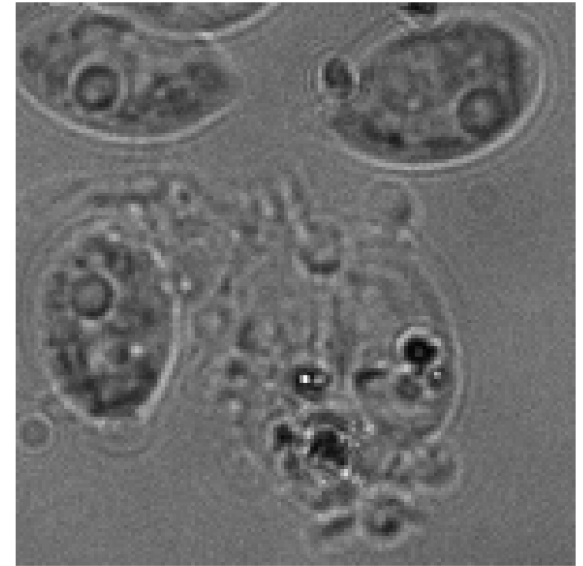
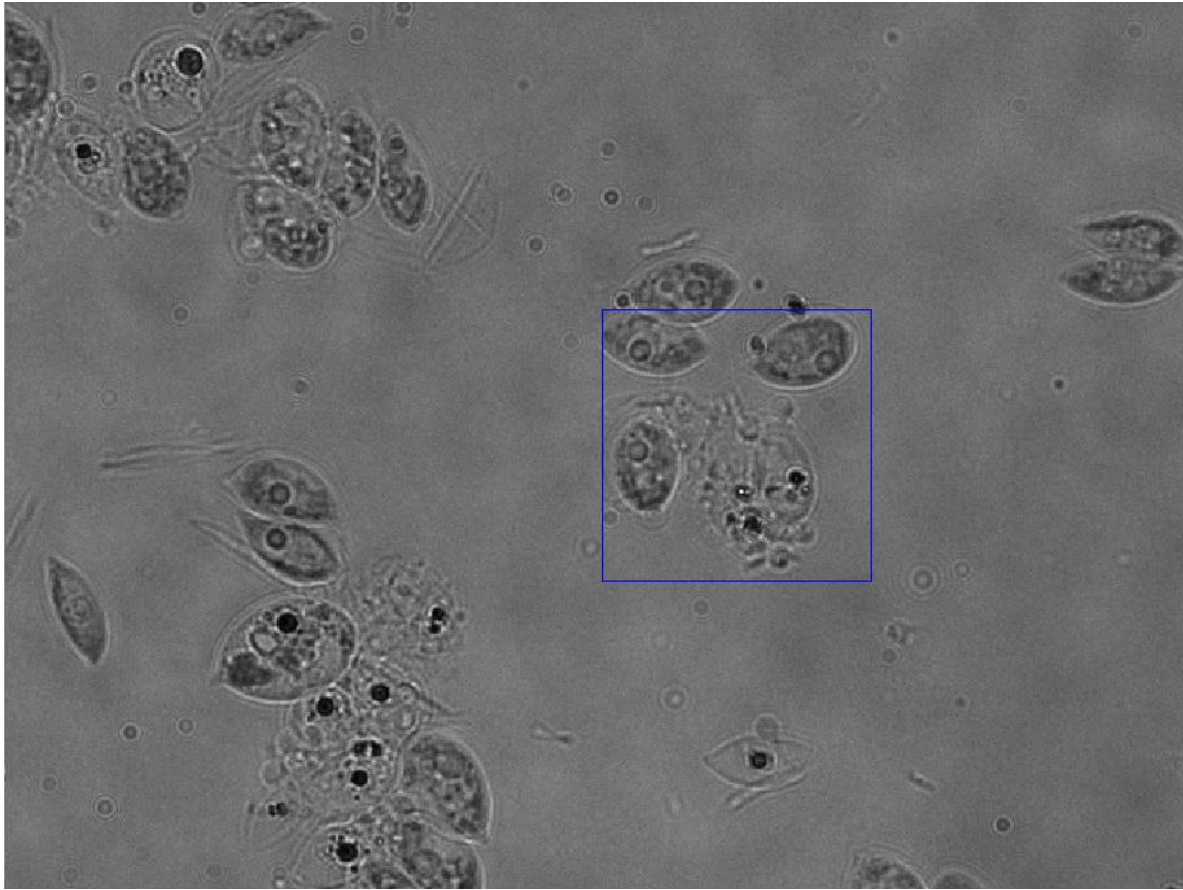




# Representative infected cells t = 16 hours

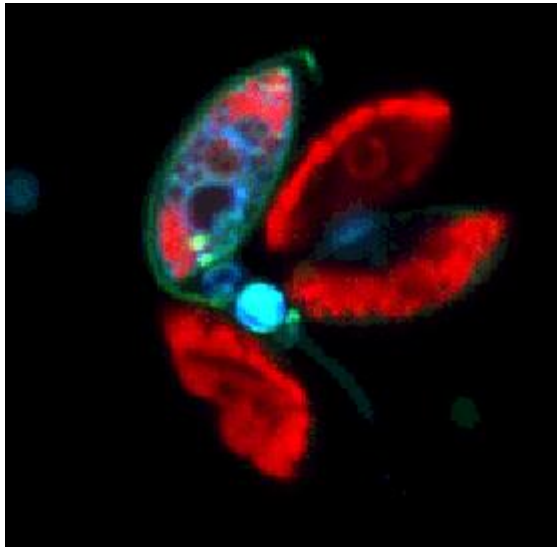
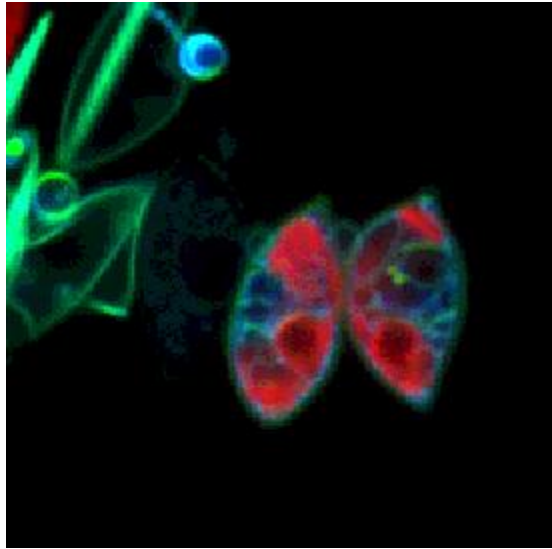
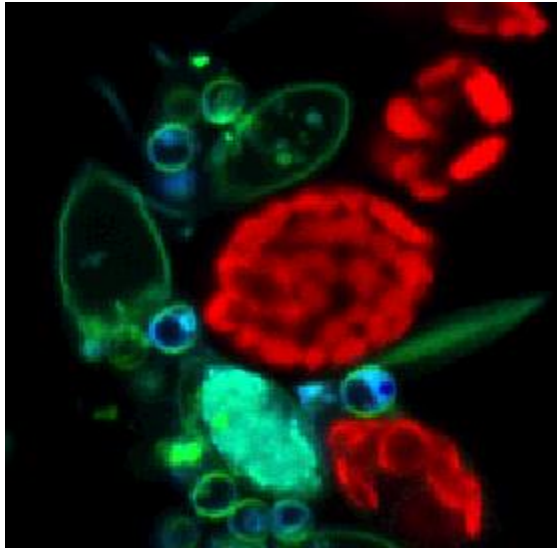


# Representative infected cells $t = 16$ hours

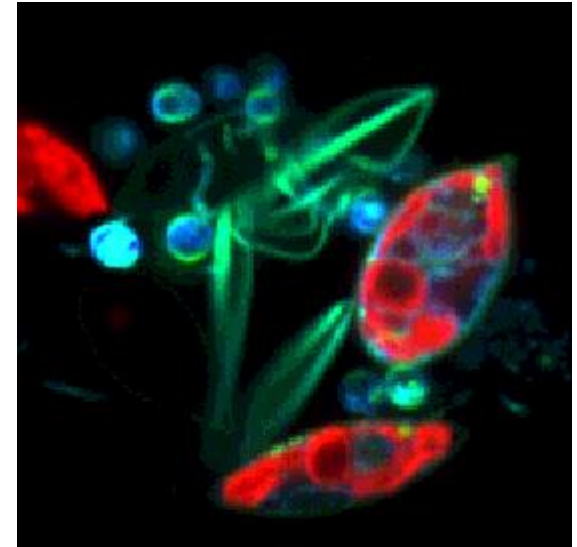
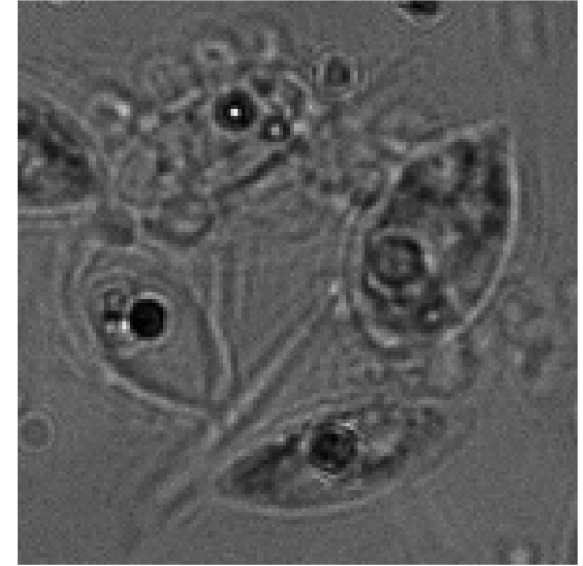
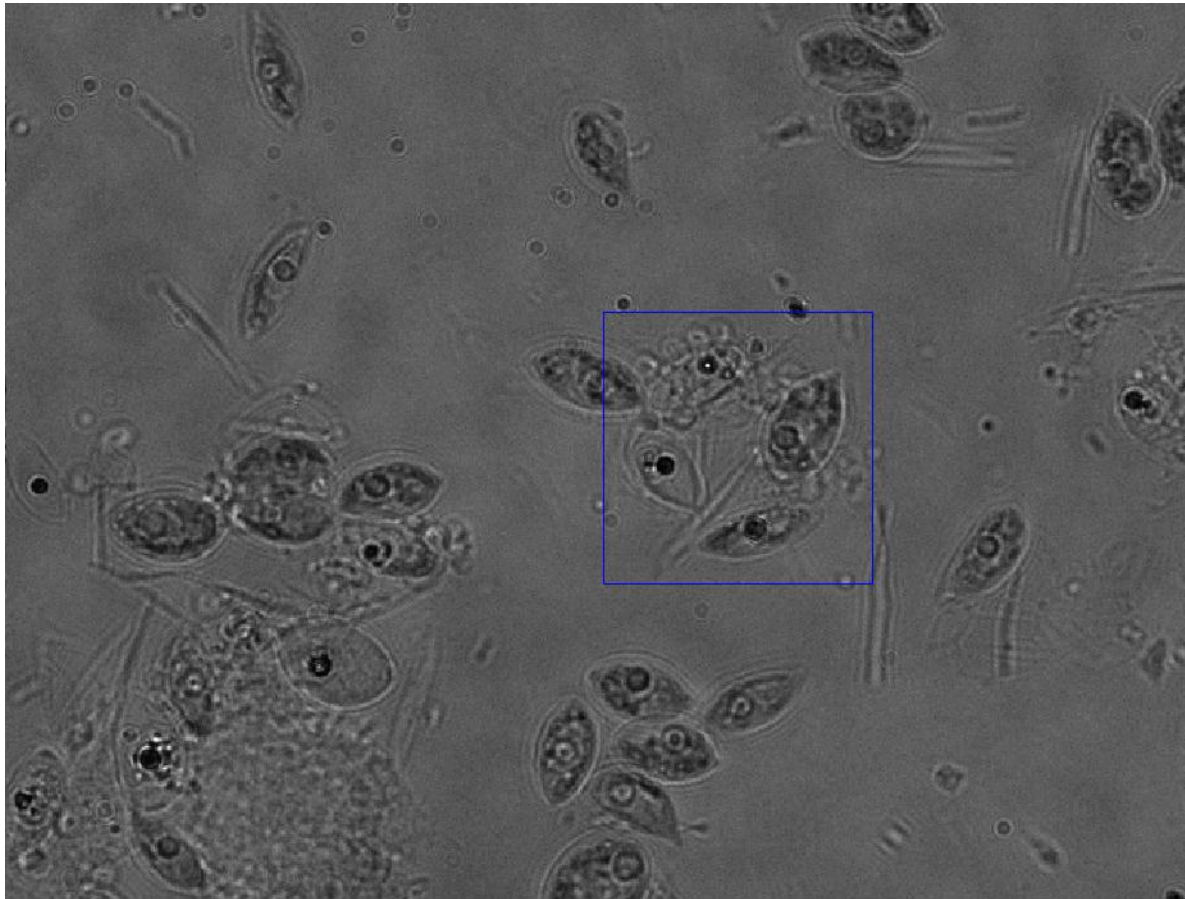




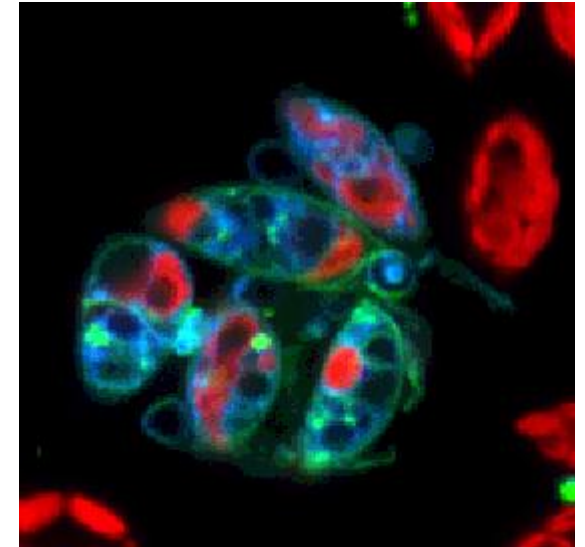
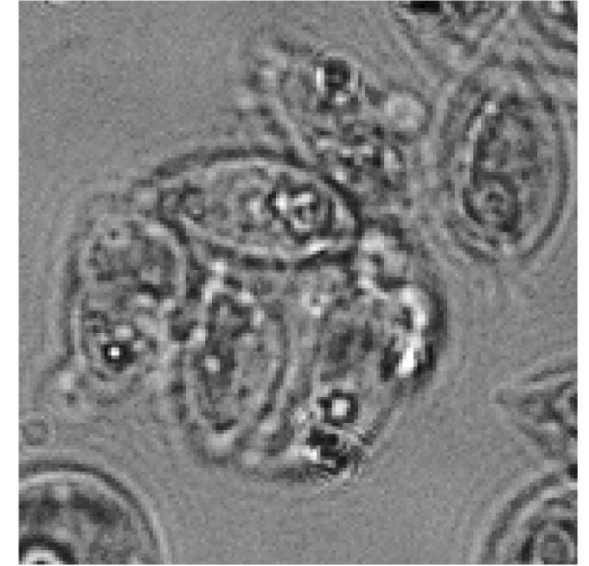
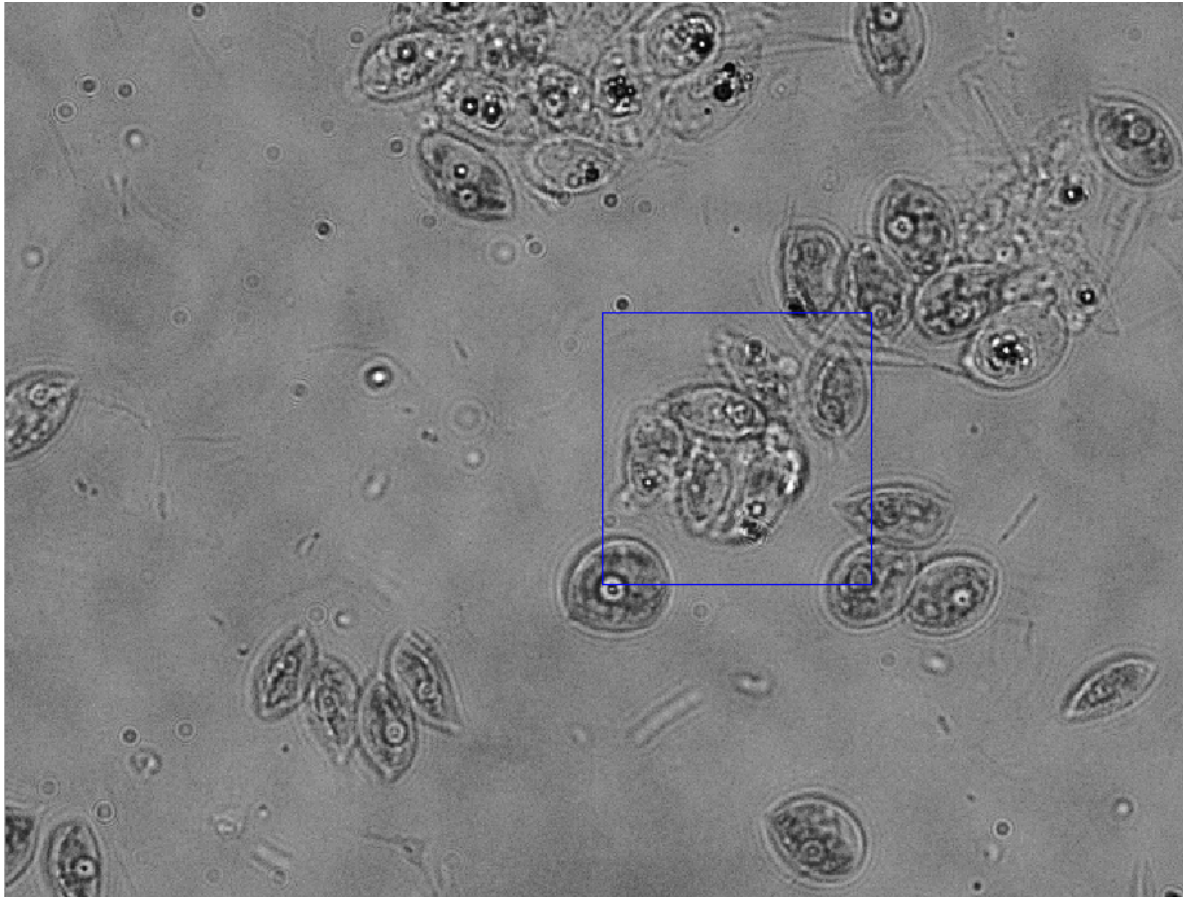
# Representative infected cells $t = 16$ hours



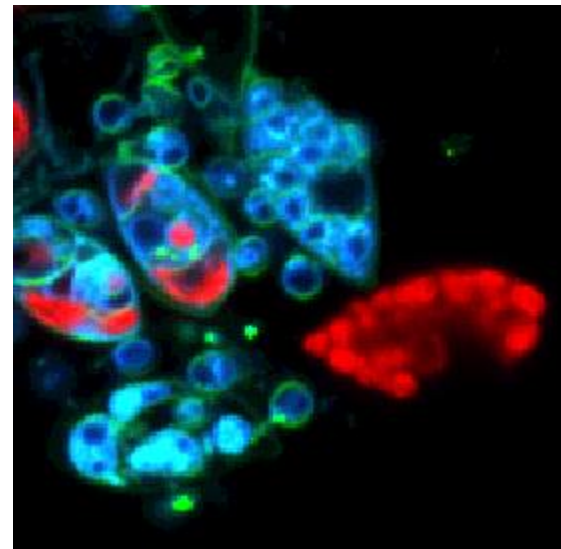
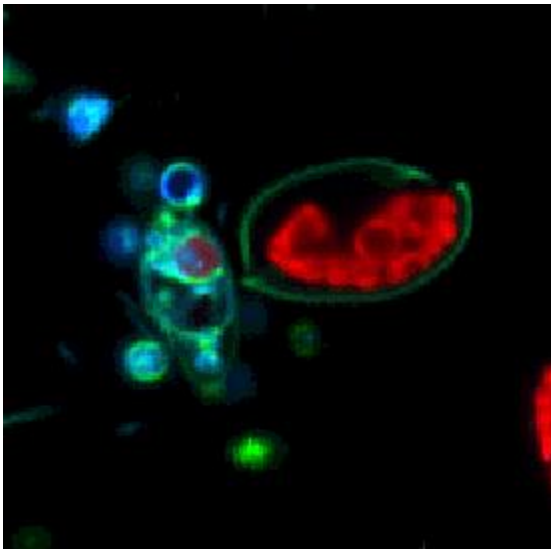
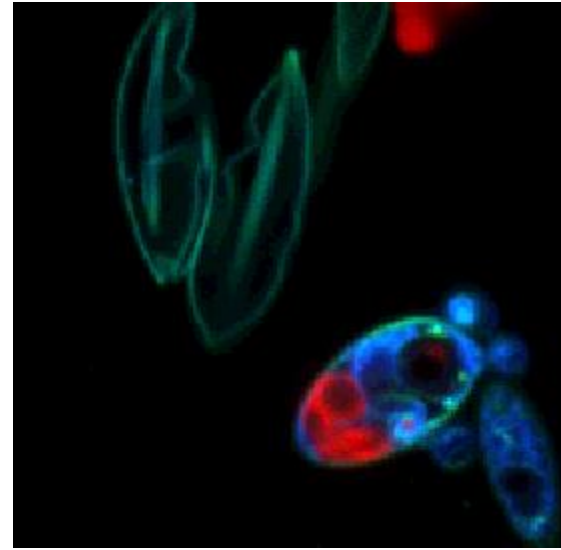
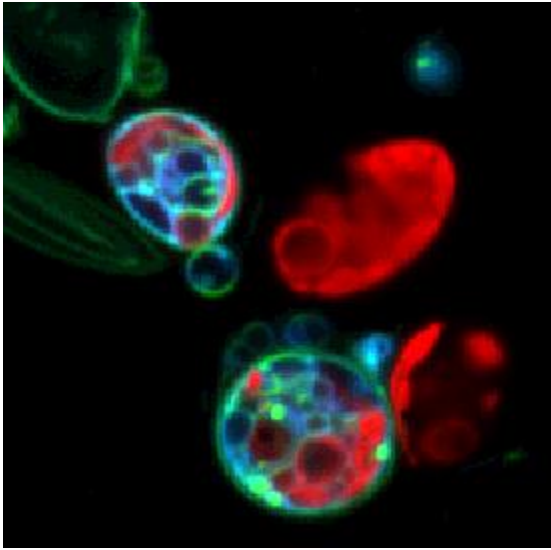
# Representative infected cells $t = 24$ hours



# Representative infected cells $t = 24$ hours

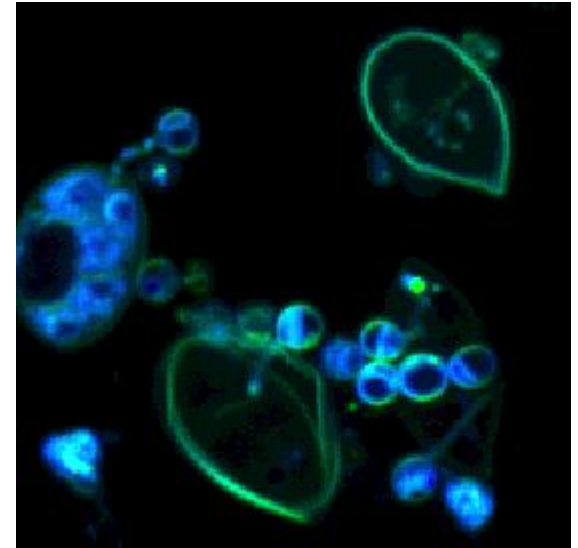
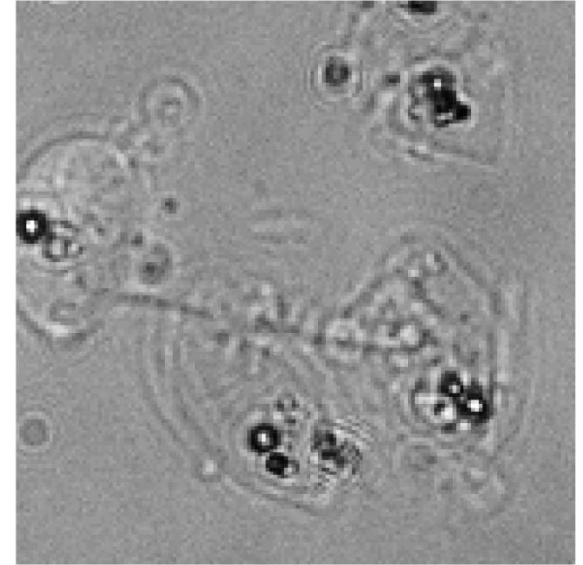
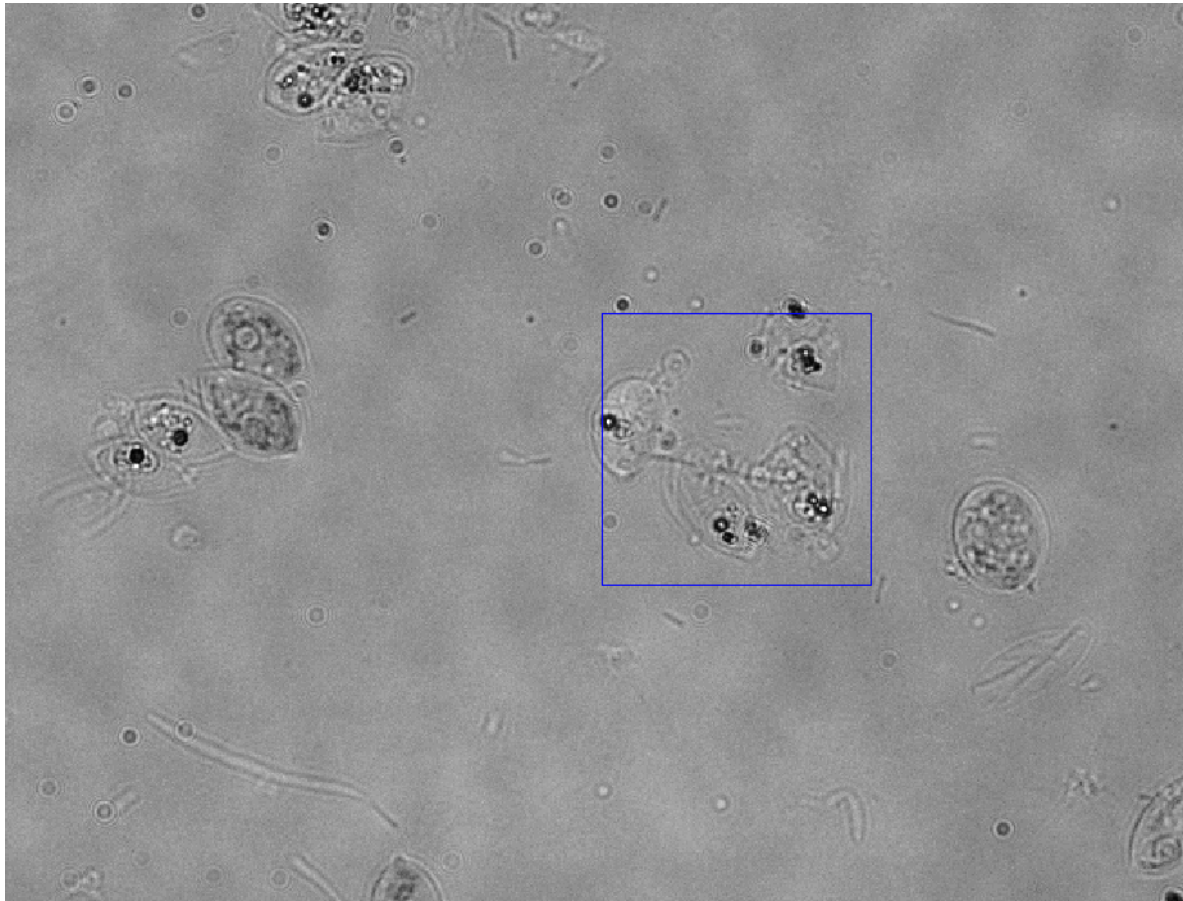


# Representative infected cells t = 24 hours

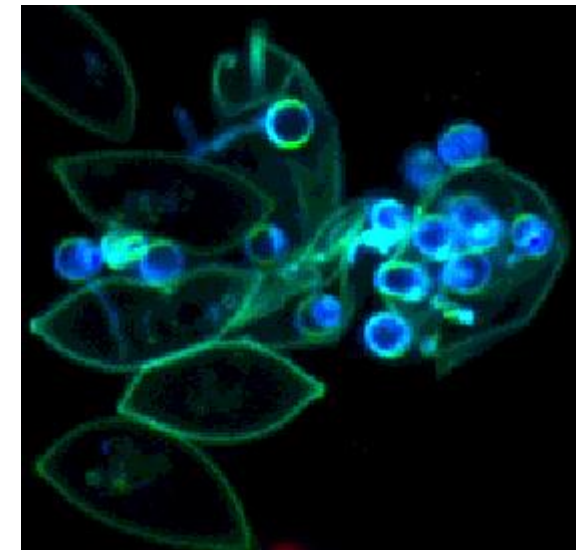
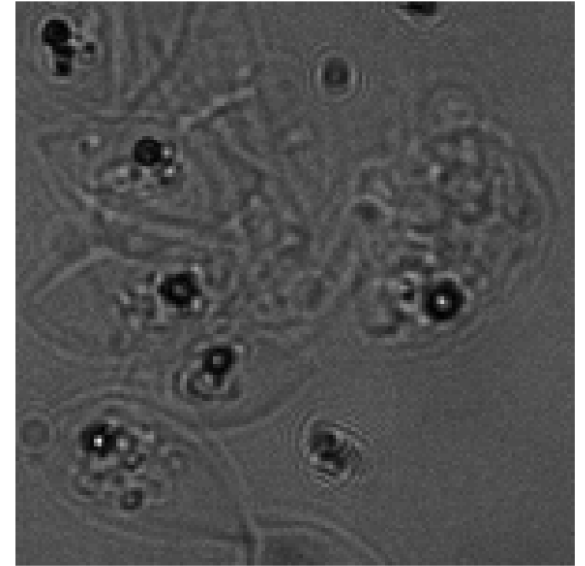
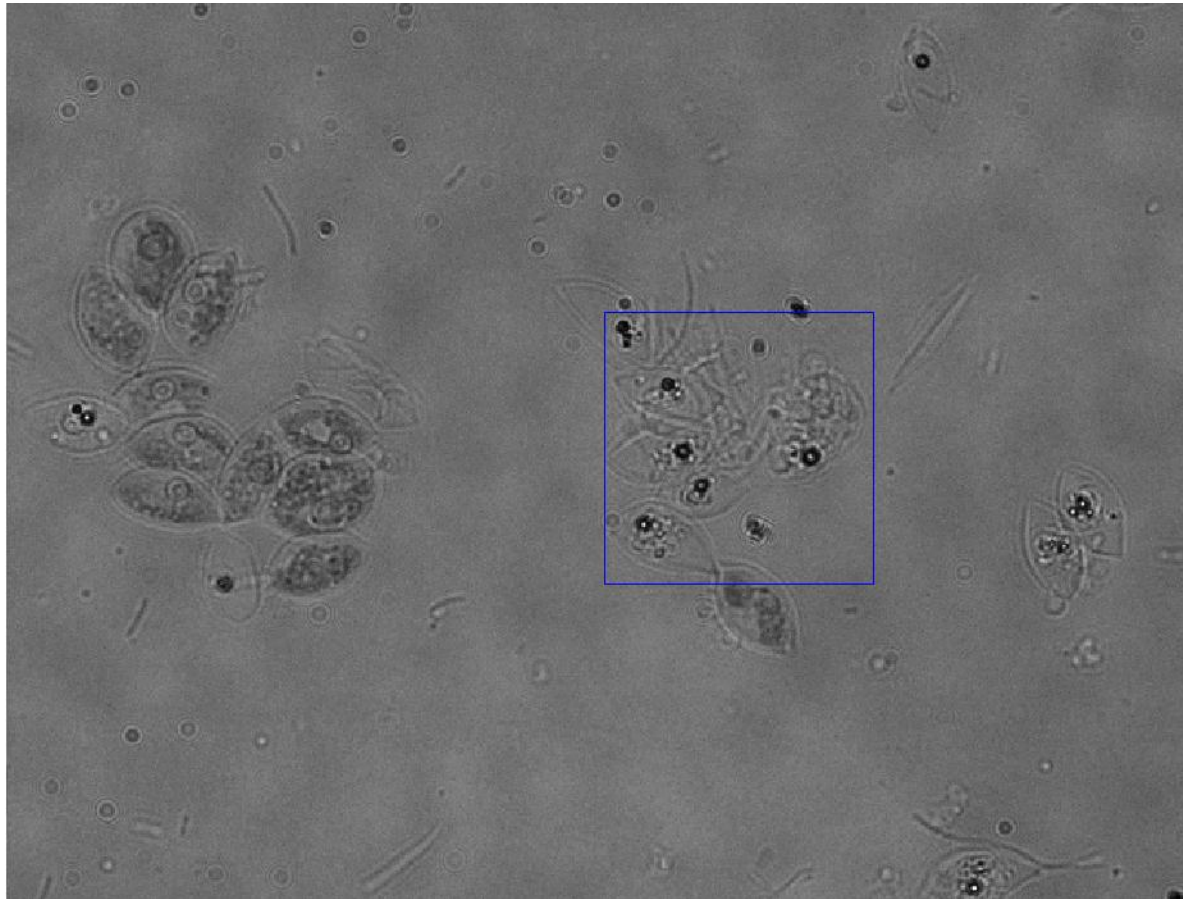




# Representative infected cells $t = 48$ hours

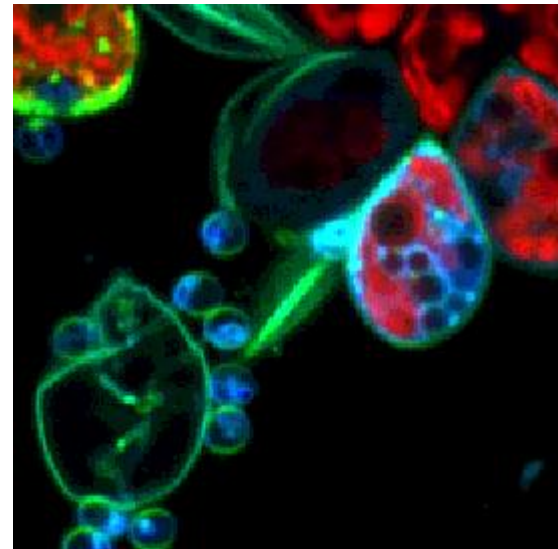
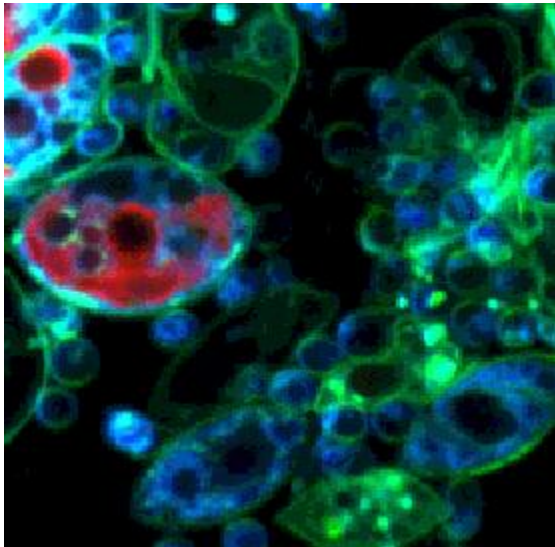
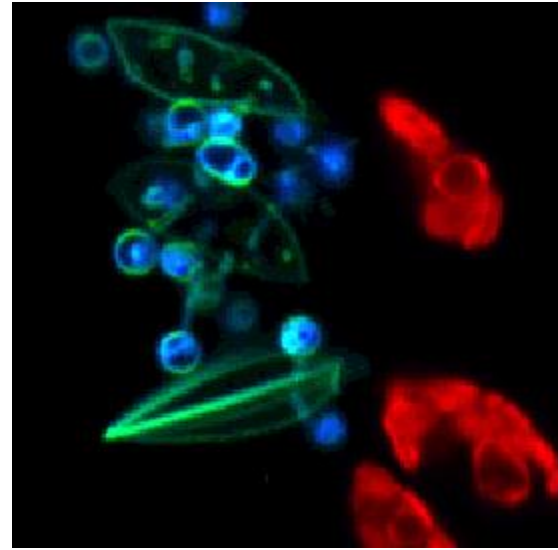
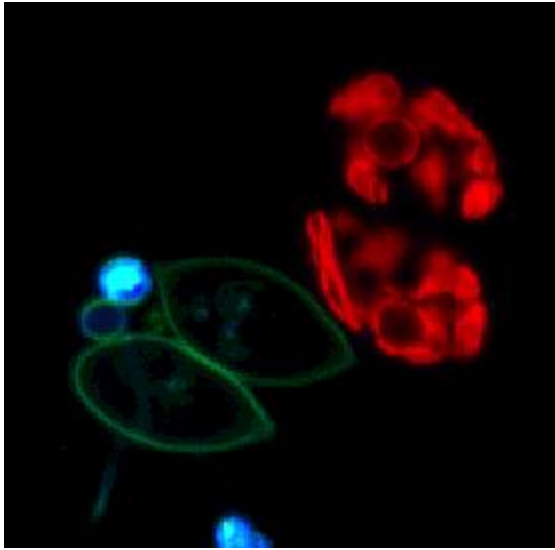


# Representative infected cells t = 48 hours





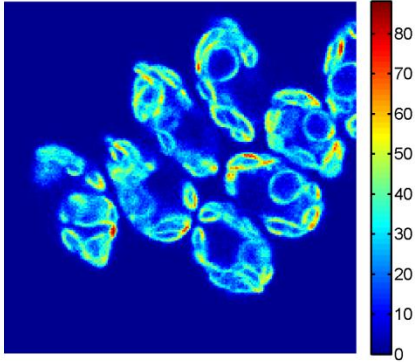
# Representative infected cells t = 48 hours



# Component comparison – Carotenoid

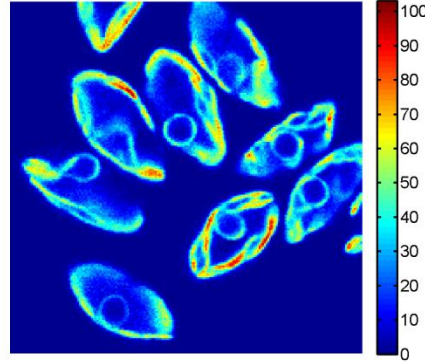
Control t0

Trace = 6, Component = 8



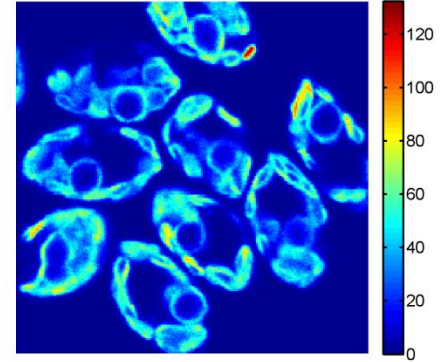
Control t4

Trace = 20, Component = 8



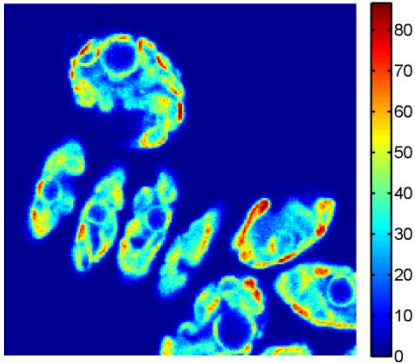
Control t8

Trace = 36, Component = 8



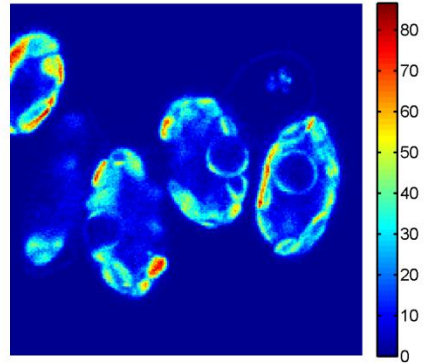
Infected t4

Trace = 2, Component = 8



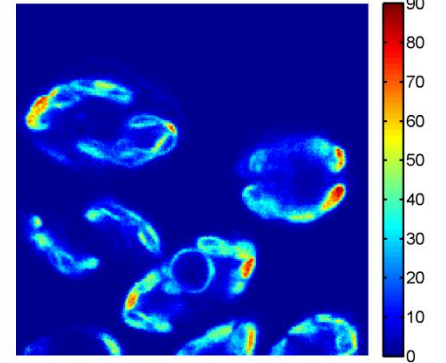
Infected t8

Trace = 20, Component = 8



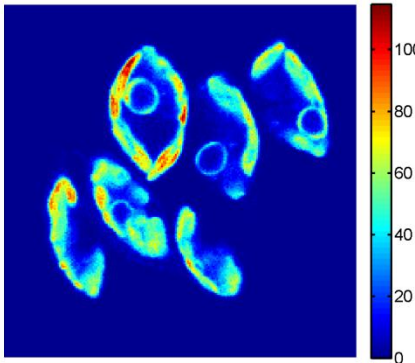
Infected t12

Trace = 42, Component = 8



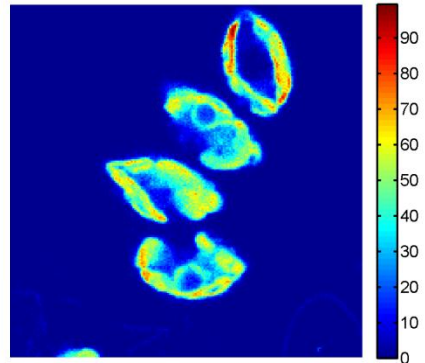
Infected t16

Trace = 3, Component = 8



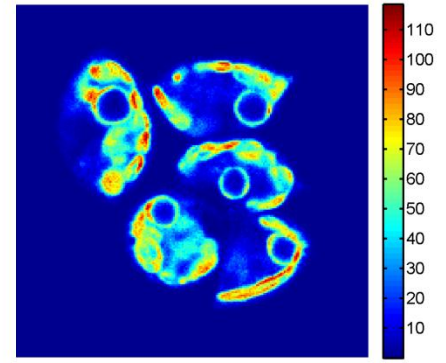
Infected t24

Trace = 27, Component = 8



Infected t48

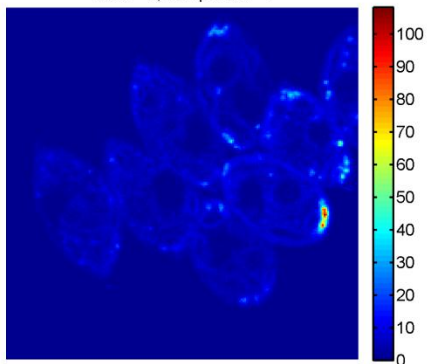
Trace = 47, Component = 8



# Component comparison – NR 573nm

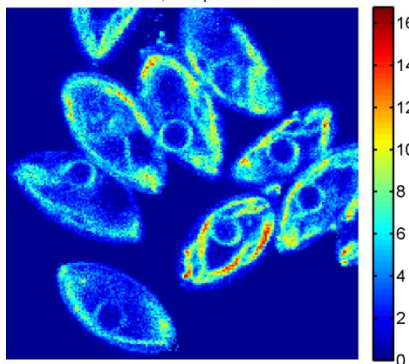
Control t0

Trace = 6, Component = 4



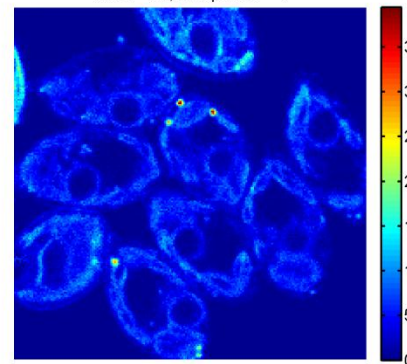
Control t4

Trace = 20, Component = 4



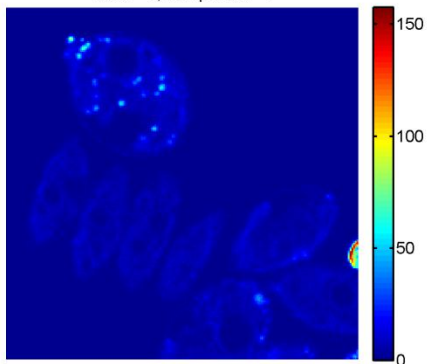
Control t8

Trace = 36, Component = 4



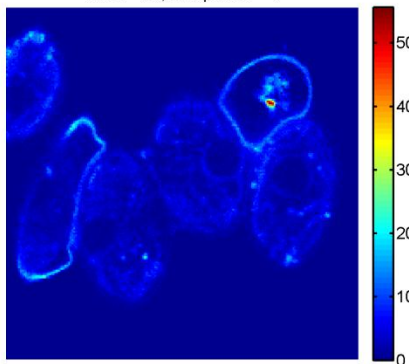
Infected t4

Trace = 2, Component = 4



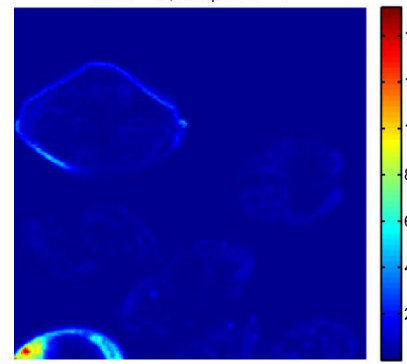
Infected t8

Trace = 20, Component = 4



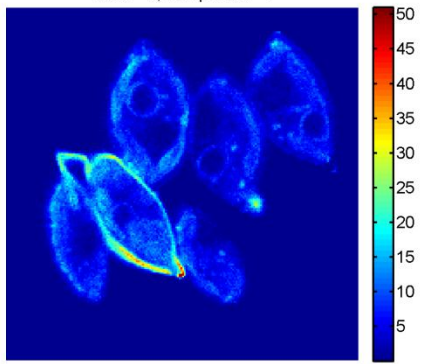
Infected t12

Trace = 42, Component = 4



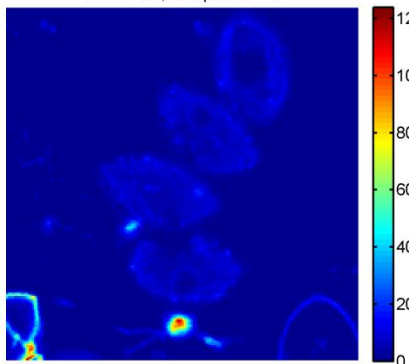
Infected t16

Trace = 3, Component = 4



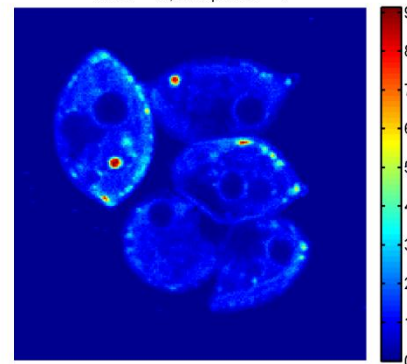
Infected t24

Trace = 27, Component = 4



Infected t48

Trace = 47, Component = 4

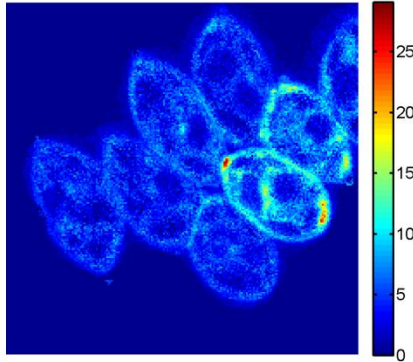




# Component comparison – NR 600nm

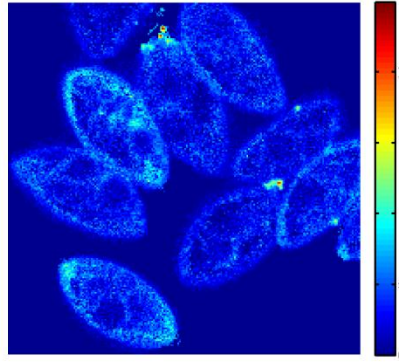
Control t0

Trace = 6, Component = 2



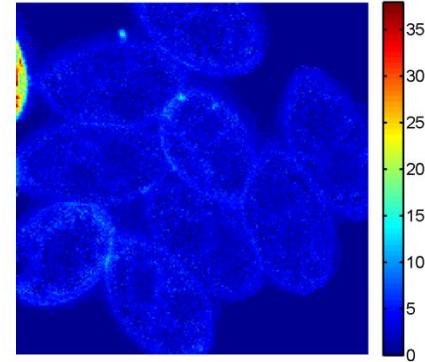
Control t4

Trace = 20, Component = 2



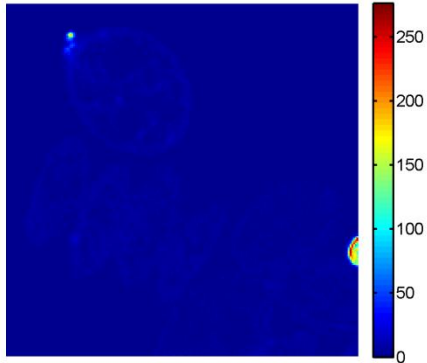
Control t8

Trace = 36, Component = 2



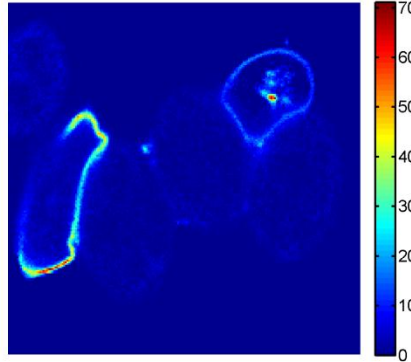
Infected t4

Trace = 2, Component = 2



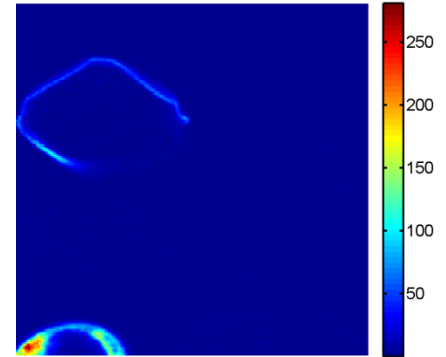
Infected t8

Trace = 20, Component = 2



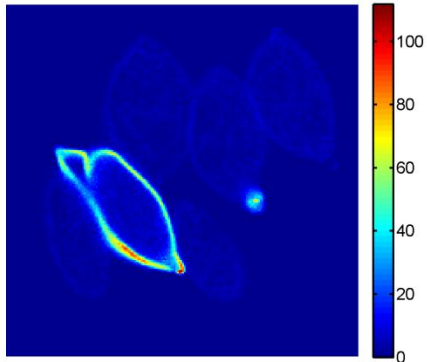
Infected t12

Trace = 42, Component = 2



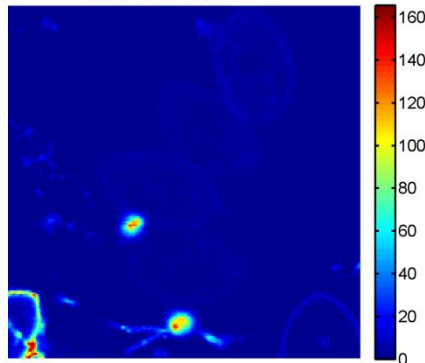
Infected t16

Trace = 3, Component = 2



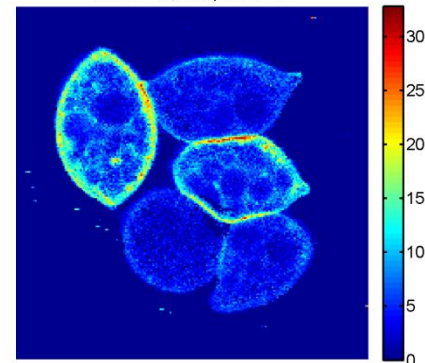
Infected t24

Trace = 27, Component = 2



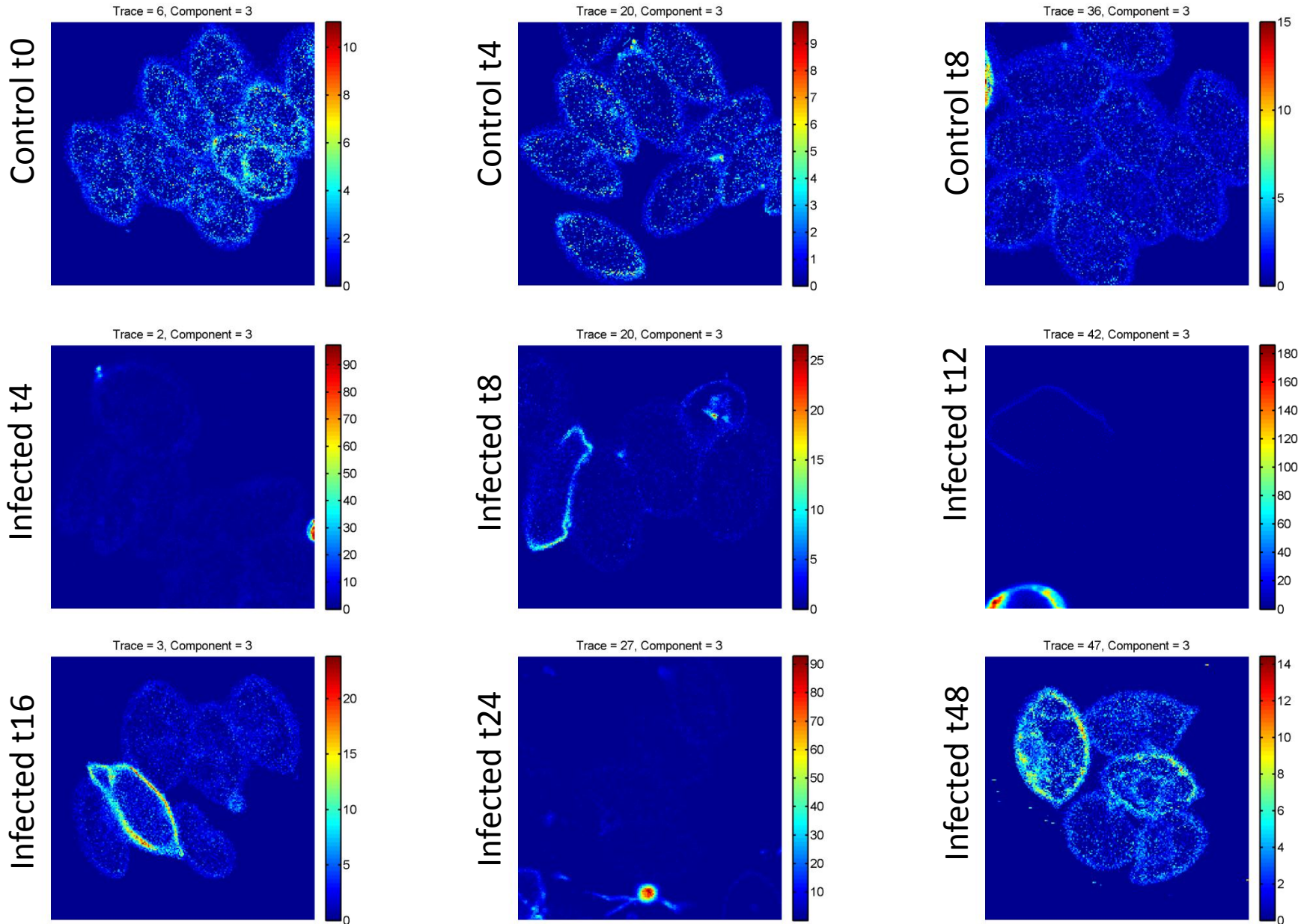
Infected t48

Trace = 47, Component = 2





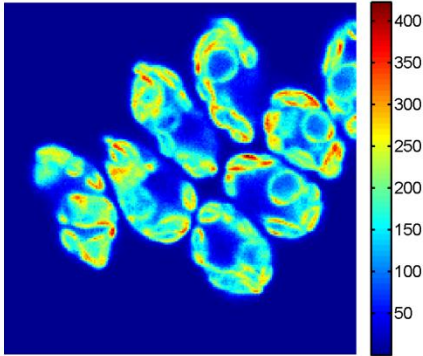
# Component comparison – NR 630nm



# Component comparison – Chl 673nm

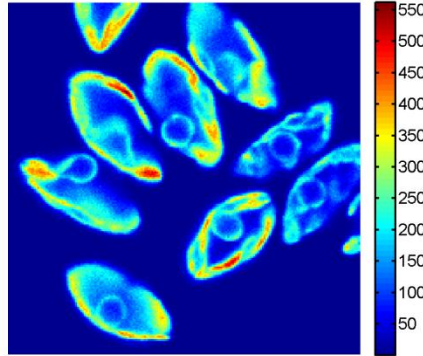
Control t0

Trace = 6, Component = 5



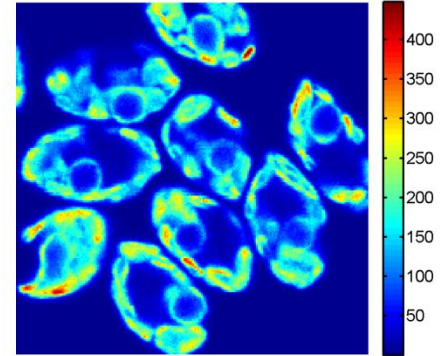
Control t4

Trace = 20, Component = 5



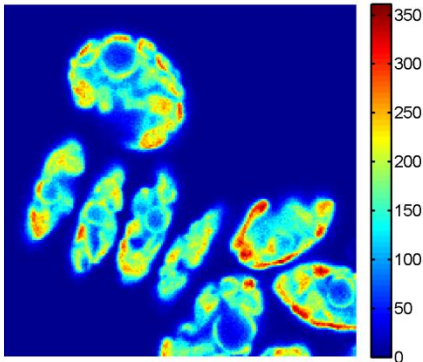
Control t8

Trace = 36, Component = 5



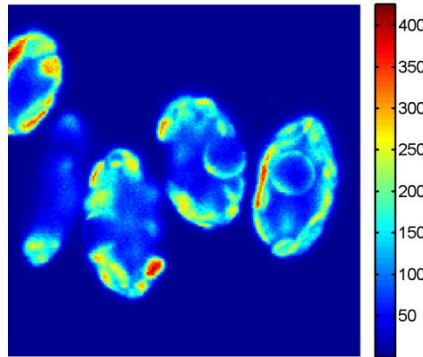
Infected t4

Trace = 2, Component = 5



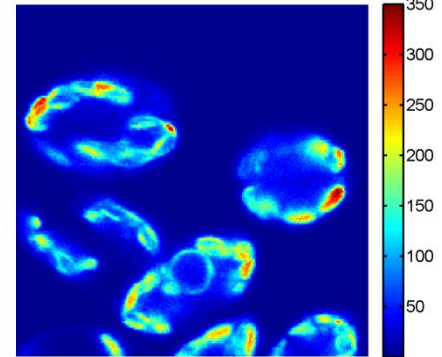
Infected t8

Trace = 20, Component = 5



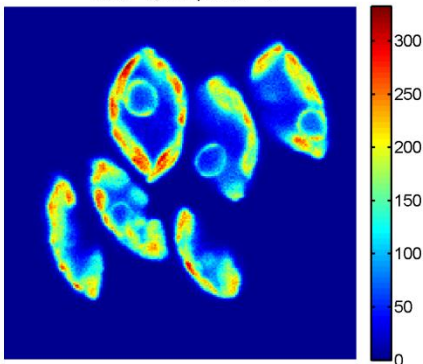
Infected t12

Trace = 42, Component = 5



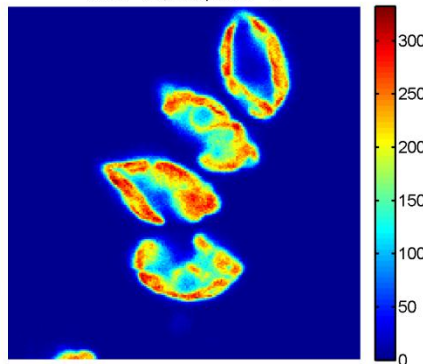
Infected t16

Trace = 3, Component = 5



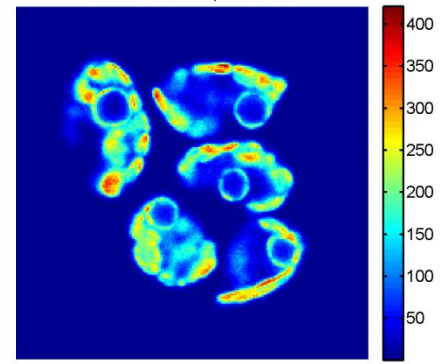
Infected t24

Trace = 27, Component = 5



Infected t48

Trace = 47, Component = 5

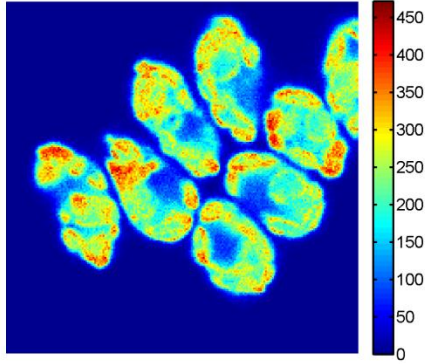




# Component comparison – Chl 682

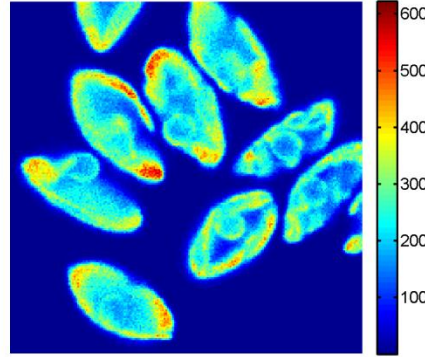
Control t0

Trace = 6, Component = 7



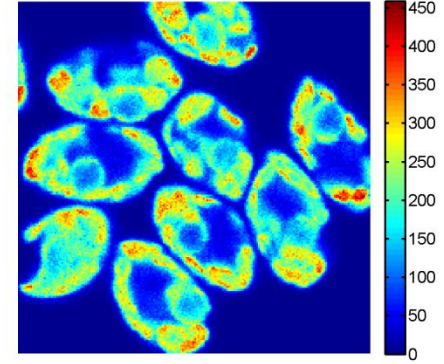
Control t4

Trace = 20, Component = 7



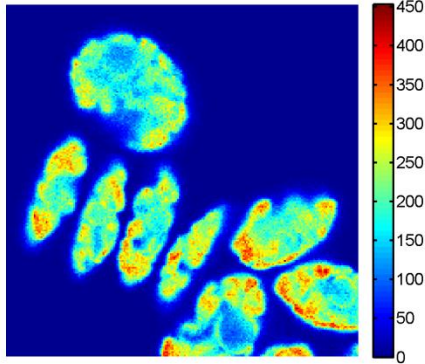
Control t8

Trace = 36, Component = 7



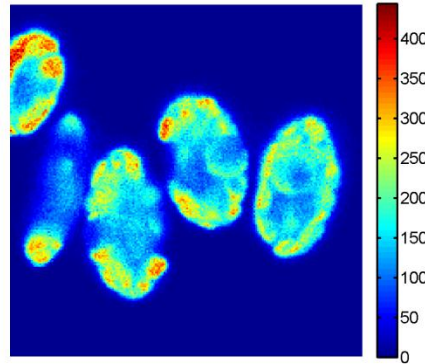
Infected t4

Trace = 2, Component = 7



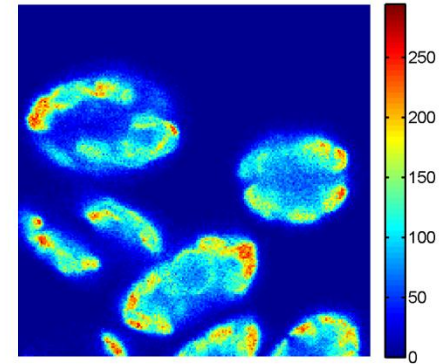
Infected t8

Trace = 20, Component = 7



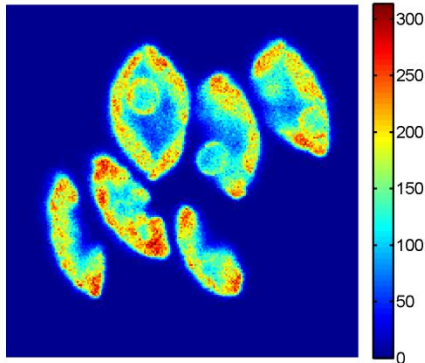
Infected t12

Trace = 42, Component = 7



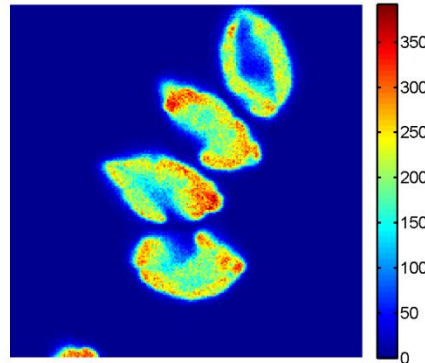
Infected t16

Trace = 3, Component = 7



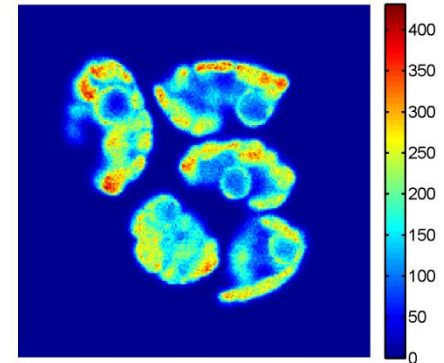
Infected t24

Trace = 27, Component = 7



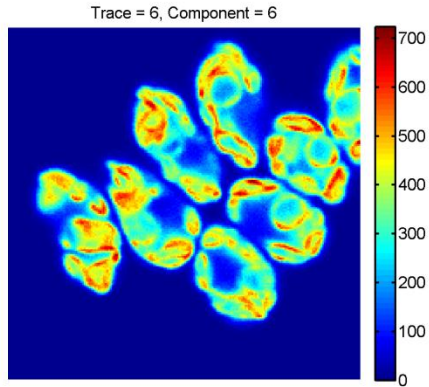
Infected t48

Trace = 47, Component = 7

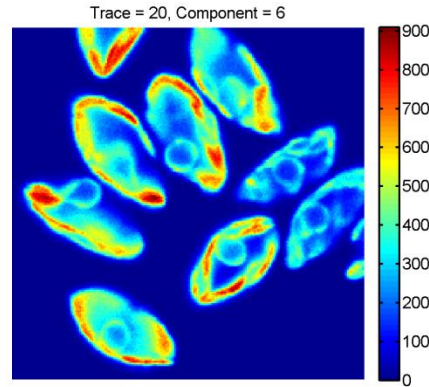


# Component comparison – Chl 687nm

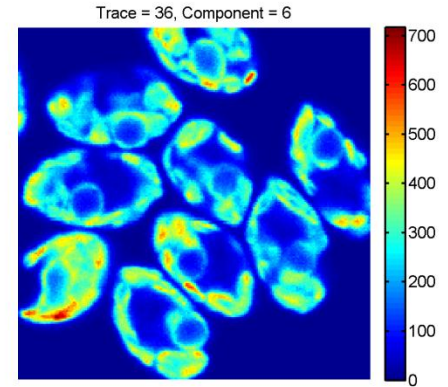
Control t0



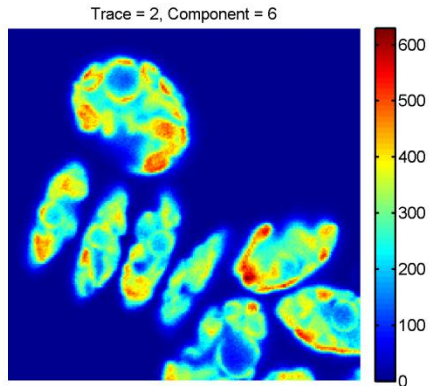
Control t4



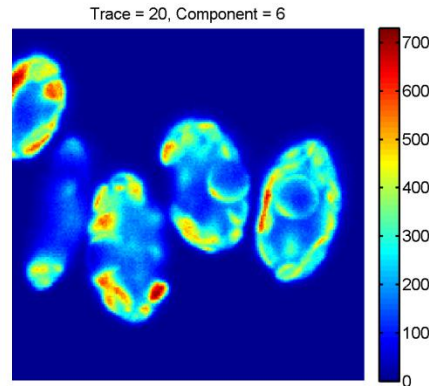
Control t8



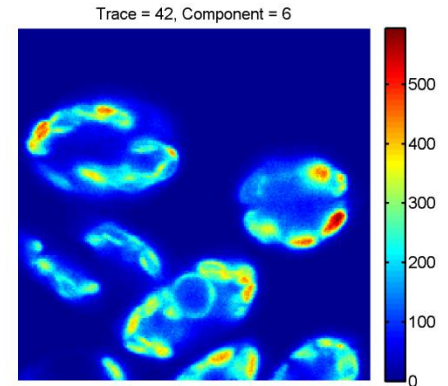
Infected t4



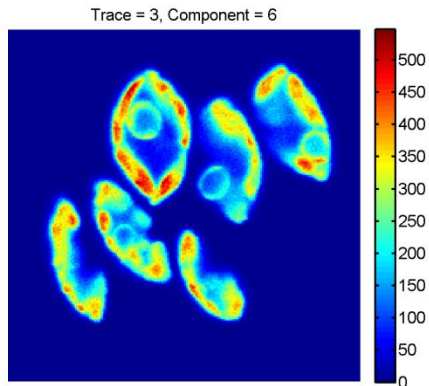
Infected t8



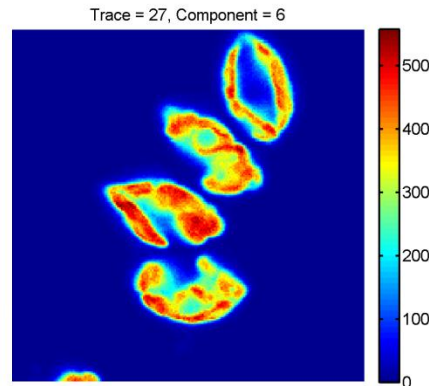
Infected t12



Infected t16



Infected t24



Infected t48

