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following these equations, we explain that the main lobe of the demodulated object i is the image i_0 that is generated in a very simple manner. for the main lobe of the demodulated object i , we need to determine the side lobe amplitude of i . because i can be written as $i = i_0 + ip$, we have

○ graphical user interface (gui): in this study, the 18.1.0 version of the gimp 2.8.18 (

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here we show an example in which the deconvolution with Huygens produced false positive results. a protein-labeled fluorescent colony was captured at a low excitation laser setting. the majority of the cell-autonomous fluorescence was restricted to the inner edge of a peripheral cytoplasmic ring of GFP. in figure 3a, in which we used 3x line accumulation, the fluorescence appeared as two large, punctate structures. the deconvolution of the raw data resulted in two bright puncta that were likely fluorescent artifacts (Verrall et al., 1993). the areas within the two bright puncta were excluded from the region of interest. deconvolution of the remaining data resulted in two bright puncta with their centers coinciding. the resulting deconvolved image was very similar to the raw data, except that the amplitude of the GFP signals was increased in the presence of the artifactual puncta. in figure 3b, in which we used 2x line accumulation, the central region of the colony contained many cells that were unlabeled. the deconvolution of the raw data resulted in bright fluorescence on the colony periphery that likely arose from the background, not from protein labels. the central area was excluded and deconvolved. the resulting deconvolved image was very similar to the raw data, except that the amplitude of the GFP signals was higher than the raw data.](fig-5){#f5} methods {#s002} ===== gaussian 09[®] program (rev c01)^[@b35]. was used to perform the molecular dynamics. the operations were carried out in the following steps: (i) prepare the protein structure; (ii) using the preparatory model to open the input file and select the channel; (iii) assigning the FFT grid; (iv) loading the FFT grid into the program (extract the data to hard disk); and (v) importing and optimizing the file. the protocol is shown below. 1. prepare the protein structure. enter the requested protein sequence into [Discovery Studio]{.smallcaps} 2.5. the number of secondary structures was designated and defined as α -helix, β -strand, and random coil. 2. using the preparatory model to open the input file and select the channel. open the PDB file and save it to the computer hard drive. in the file selection window, select the protein file, then click open to open it. 3. select the selected protein and select the channel, then click save

to save the file. assigning the fft grid. open the calculated file and obtain the
fft grid image and submit the image to the [discovery studio]{.smallcaps}
server. 4. loading the fft grid into the program (extract the data to hard disk).
save the image on the hard disk, and then open the image with the software
named mapviz, a free software. in the mapviz program, select the protein file
as an input file. click add for output files, then click save to save the image.

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