



**FIGURE 3.** Sedimentation coefficient distribution  $c(s)$  from the analysis of the data in Fig. 2. The distribution displays two main peaks at 4S and 6S from two components added to the solution, their oligomers at 8S, a hetero-complex at 10.5S, and some aggregates. The numbers on the peaks correspond to those in Fig. 2. Below are the residuals, shown in two different forms. One is a plot of all radial residuals superimposed in a conventional graph. This shows the magnitude of the maximal residuals (in units of the signal, OD). Above is a bitmap representation, which encodes the magnitude of the residuals in the gray scale of the pixel at different radial values (horizontal lines) for all different scans (assembled vertically starting from scan 1 on top to the last scan on the bottom). This representation exhibits some diagonal features, which reveal systematic deviations of the fit and the data in the shape of the migrating sedimentation boundary. Vertical features and horizontal features are caused by imperfections in the optical configuration. For a good fit, vertical features are tolerable, but very few diagonal features should be observed. Although the  $c(s)$  distribution resembles in some ways a chromatogram, it is a curve calculated using the assumption of similar frictional ratio, and using maximum entropy regularization algorithm that generates the simplest curve consistent with the raw data. Although the maximum entropy regularization usually is very successful in suppressing artificial peaks from data with limited information content, it has the property of broadening the peaks and of merging neighboring peaks when working with data of low signal-to-noise ratio.

*Protein–Protein Interactions: A Molecular Cloning Manual*, 2nd Ed., © 2005 by Cold Spring Harbor Laboratory Press, Chapter 14, Figure 3.