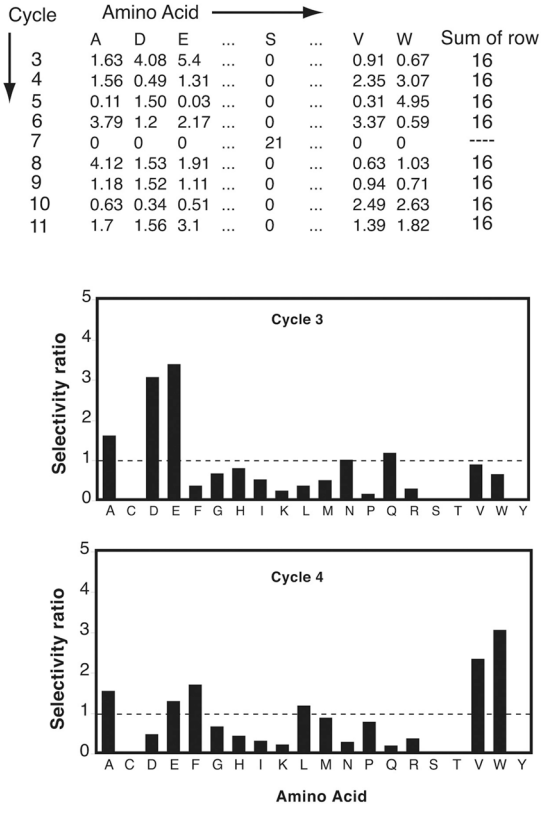

FIGURE 2. Matrix and graphic representation of amino acid selectivity data. The final calculated amino acid selection matrix displays typical values derived from oriented peptide library screening. These results are obtained by normalizing the relative percentage of each amino acid in each position recovered from the experiment to the relative percentage of each amino acid in each position in the starting library. For use in database searching, these initial selection values are adjusted depending on the particular weighting scheme used, although the rank order of the amino acid selection determined experimentally is maintained. The upper panel shows a matrix of normalized selectivity ratios for each amino acid (columns) at each cycle (rows). The sum of amino acids is 16 rather than 20 because S, T, Y, and C are routinely omitted from degenerate positions, for reasons discussed in the text. The lower panels show a graphic display of the selectivity data for each amino acid in sequencing cycles 3 and 4 from the matrix above. There is strong selection for D and E in cycle 3 and for L, F, V, and W in cycle 4, with lesser selection for M and P. Note that although A shows a selectivity value greater than 1.0 in each cycle, it does not display the typical cycle-to-cycle variation, and its contribution to the optimal motif sequence should be interpreted with caution.

Protein–Protein Interactions: A Molecular Cloning *Manual*, 2nd Ed., © 2005 by Cold Spring Harbor Laboratory Press, Chapter 29, Figure 2.