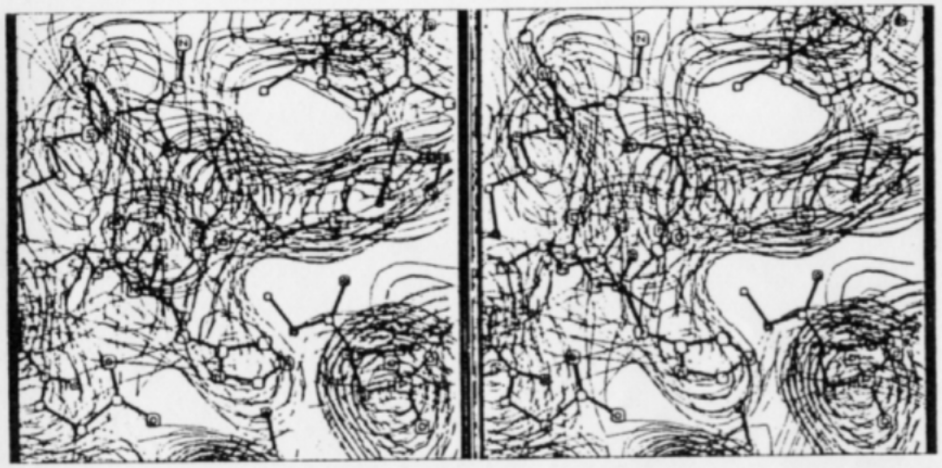
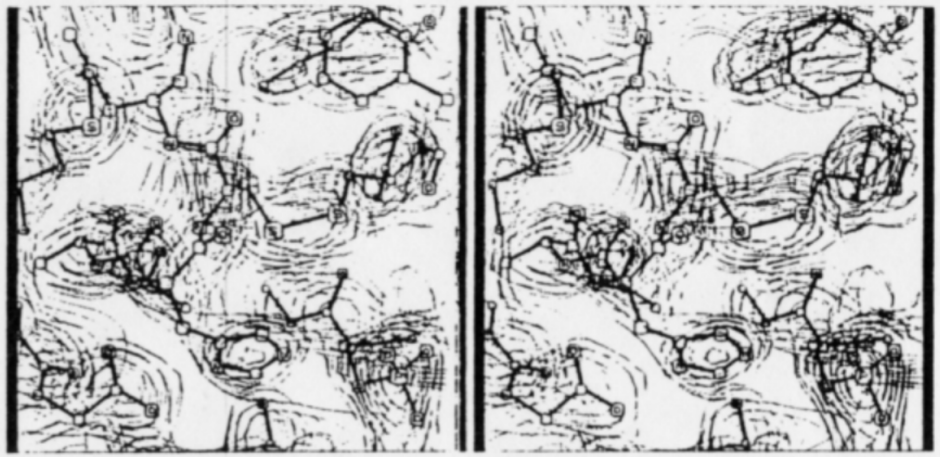
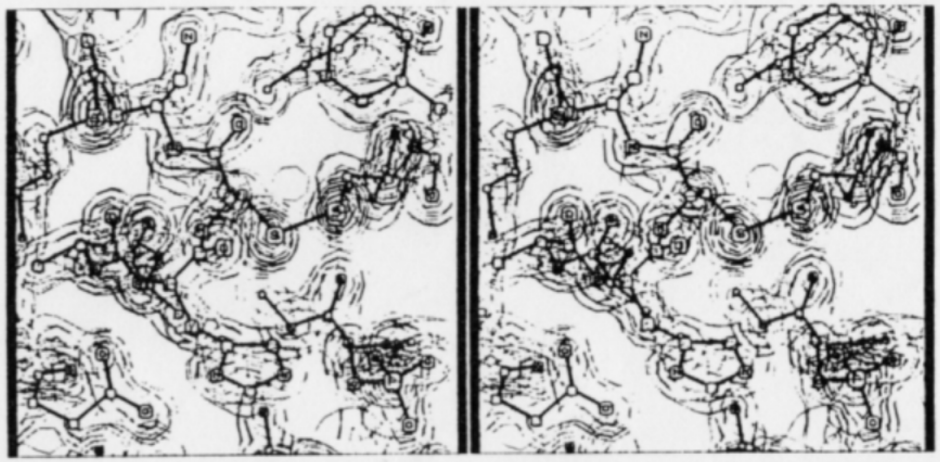
(a)



(b)



(c)



(d)

Protein electron density maps as a function of resolution. The maps are calculated from measured intensities and estimated phases. The protein is a diisopropyl fluorophosphate derivative of bovine trypsin. The view is down the *y* axis of the active site. A ball-and-stick model of the *final* best estimate of the structure is repeated in each map; note the phosphate at lower right and the active-site histidine at lower center; above these two features is a disulfide bond. **(a)** A map at 6.0 Å resolution, contoured from 0.05 e Å^{-3} in steps of 0.05 e Å^{-3} **(b)** A map at 4.5 Å resolution, contoured from 0.10 e Å^{-3} in steps of 0.10 e Å^{-3}. **(c)** A map at 3.0 Å resolution, contoured from 0.35 e Å^{-3} in steps of 0.30 e Å^{-3}. **(d)** A map at 1.5 Å resolution, contoured from 0.50 e Å^{-3} in steps of 0.50 e Å^{-3}. All maps are shown as stereo pairs. [Courtesy of John L. Chambers. For further details, see his unpublished Ph.D. thesis, Calif. Institute of Technology, 1977.]