



Figure 1. Two-dimensional molecular electrostatic-potential maps calculated for representative heterocycles. Contours are at increments of -10 starting from -30 kcal/mol (red).

buried within the membrane-spanning helical domains of the protein. We now propose that agonists but not antagonists are able to equilibrate with this site and a second, more deeply buried ASP, ASP-79, in the β -receptor. In

confirmation of this proposal is the finding²¹ that replacement of this residue by ASN-79 produced a receptor which bound antagonists with wild-type affinity but had up to a 200-fold reduced affinity for agonists and this

