Authors' reply

Sir,

The accuracy of prediction of relative or absolute ligand-binding affinities is challenging in both theoretical and practical aspects.[1] Receptor-ligand docking simulation for membrane proteins is widely used in structural bioinformatics.[2] Ligand-binding site prediction is useful in antagonist-type drug search.[3,4] Ligand-binding site prediction for ErbB2, a membrane protein, was discussed in a previous report.[5]

The generation of highly effective signalling inhibitors targeting members of the ErbB family of receptor tyrosine kinases, EGFR and ErbB-2 has been discussed for a few years.[6] Of interest, Rambukkana *et al.* mentioned that during *Microbacterium leprae*-induced demyelination, Schwann cells proliferated significantly and generated a more nonmyelinated phenotype, thereby securing the intracellular niche for *M. Leprae.*[7] Recently, Tapinos *et al.* provided evidence that *M. leprae*-induced demyelination

was a result of direct bacterial ligation to and activation of ErbB2 receptor tyrosine kinase (RTK) without ErbB2-ErbB3 heterodimerization, a previously unknown mechanism that bypasses the neuregulin-ErbB3-mediated ErbB2 phosphorylation.[8] Therefore, it might be concluded that an ErbB2 antagonist could be useful in leprosy therapy, especially as a dedifferentiation signal in leprosy.[9]

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