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Volume 461 Chemokines, Part B

Edited by Tracy M. Handel Damon J. Hamel



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PREFACE

Secreted signaling molecules like chemokines facilitate complex intercellular communication by means of interactions with cell membrane—spanning receptors. There are approximately 50 identified mammalian chemokines, and all share a common monomeric fold. There are also approximately 20 chemokine receptors, all having the seven transmembrane domain topology of G-protein—coupled receptors. Despite this apparent homogeneity, the variety of signals sent and received by them defies simple explanation. Clearly, the devil is in the details, and the structure/function relationships that govern these seemingly similar interactions are sure to be subtle and nuanced, requiring thoughtful experimentation to tease them apart. With this in mind, we have focused Volume 461 of the *Methods in Enzymology* series on methods to probe the physical characteristics, dynamics, modifications, and interactions of chemokines and chemokine receptors.

These proteins have presented researchers with many hurdles, from the difficulty in preparing functional receptors, to the complex posttranslational modifications, to the disparity in *in vitro* and *in vivo* functionality of some chemokine variants. Hence, the topics presented herein run the gamut of biochemical disciplines, from *in vitro* nuclear magnetic resonance and plasmon resonance methods, to receptor modeling *in silico*, to model systems for measuring and even simulating *in situ* cell migration.

In 1997 Richard Horuk edited volumes 287 and 288 in the *Methods in Enzymology* series on chemokines and chemokine receptors, putting together the first comprehensive practical guide to studying these molecules. Volume 461 is part two of two new editions on chemokines and their receptors. The previous volume 460 focused on studying the roles of chemokines and chemokine receptors in disease states, atypical chemokine receptors, chemokine signaling, and chemokine-related proteins from pathogens.

Compilations like this are assembled by the immense efforts of many individual researchers, and we enthusiastically offer our thanks and gratitude to all of the authors who contributed to making these volumes a reality. We would also like to thank the incredible staff at Elsevier, and especially Delsy Retchagar and Tara Hoey, for valiantly trying to keep us on track and on time. We could not have done it without you.

DAMON J. HAMEL AND TRACY M. HANDEL

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