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3.4 Implementation of IPv6 DNS Resolver
3.5 IPv6 DNS Operation with BIND; Chapter 4 DHCPv6; 4.1 Introduction; 4.2 Overview of the DHCPv6 Protocol; 4.3 Code Introduction; 4.4 Client Implementation; 4.5 Server Implementation; 4.6 Relay Agent Implementation; 4.7 Implementation of DHCPv6 Authentication; 4.8 DHCPv6 Operation; Chapter 5 Mobile IPv6; 5.1 Introduction; 5.2 Mobile IPv6 Overview; 5.3 Header Extension; 5.4 Procedure of Mobile IPv6; 5.5 Route Optimization; 5.6 Movement Detection; 5.7 Dynamic Home Agent Address Discovery; 5.8 Mobile Prefix Solicitation/Advertisement
5.9 Relationship with IPsec
5.10 Code Introduction; 5.11 Mobile IPv6 Related Structures; 5.12 Macro and Type Definitions; 5.13 Global Variables; 5.14 Utility Functions; 5.15 Common Mobility Header Processing; 5.16 Home Agent and Correspondent Node; 5.17 Mobile Node; 5.18 Mobile IPv6 Operation; 5.19 Appendix; Chapter 6 IPv6 and IP Security; 6.1 Introduction; 6.2 Authentication Header; 6.3 Encapsulating Security Payload; 6.4 Transport Mode and Tunnel Mode; 6.5 Security Association Database; 6.6 IPsec Traffic Processing; 6.7 SPD and SAD Management; 6.8 Manual Configuration
6.9 Internet Security Association and Key Management Protocol (ISAKMP) Overview
6.10 Raccoon Operation; 6.11 Scenarios; References; Index

Sommario/riassunto

This book is the second installment of a two-volume series on IPv6 and the KAME implementation. This book discusses those protocols that are found in more capable IPv6 devices, are commonly deployed in more complex IPv6 network environments, or are not specific to IPv6 but are extended to support IPv6. Specifically, this book engages the readers in advanced topics such as routing, multicasting, DNS, DHCPv6, mobility, and security. This two-volume series covers a wide spectrum of the IPv6 technology, help the readers establish solid and empirical understanding on IPv6 and the KAME refere

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Descrizione fisica	1 online resource (407 p.)
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Livello bibliografico	Monografia
Sommario/riassunto	<p>The field of proteomics has advanced considerably over the past two decades. The ability to delve deeper into an organism's proteome, identify an array of post-translational modifications and profile differentially abundant proteins has greatly expanded the utilization of proteomics. Improvements to instrumentation in conjunction with the development of these reproducible workflows have driven the adoption and application of this technology by a wider research community. However, the full potential of proteomics is far from being fully exploited in plant biology and its translational application needs to be further developed. In 2011, a group of plant proteomic researchers established the International Plant Proteomics Organization (INPPO) to advance the utilization of this technology in plants as well as to create a way for plant proteomics researchers to interact, collaborate and exchange ideas. The INPPO conducted its inaugural world congress in mid 2014 at the University of Hamburg (Germany). Plant proteomic researchers from around the world were in attendance and the event marked the maturation of this research community. The Research Topic captures the opinions, ideas and research discussed at the congress and encapsulates the approaches that were being applied in plant proteomics. The field of proteomics has advanced considerably over the past two decades. The ability to delve deeper into an organism's proteome, identify an array of post-translational modifications and profile differentially abundant proteins has greatly expanded the</p>

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