

SUBJECT INDEX TO VOLUME 7

- Aerobic flavin-dependent azoreductase from bacteria106
 from bacteria106
- Aerobic flavin-free azoreductases106
 from bacteria106
- Alpha-fetoprotein (AFP)73
 amino acid sequence matches of75
 biological levels of organization of75
 brine shrimp bioassay of76
 cell level of85
 cell surface level of90
 cytoplasmic level of92
 derived growth inhibitory peptides73
 effect on bactericidal tests using *Escherichia coli* .80
 effect on erythrocyte aggregation/agglutination91
 functional activities of73
 immune-regulation of90
in vivo mouse uterine growth bioassay of82
 inhibition of human platelet aggregation by90
 nuclear level of95
 organ level of82
 organism level of76
 tissue level of83
 to inhibit cellular adhesion of breast tumor
 cells to ECM proteins91
 to inhibits frog metamorphosis77
- Amphipathic helices539
 as mediators of membrane interaction539
 as modulators of bilayer physical properties539
 CCT structures of540
 function in cells540
 in amphitropic proteins539
 of CCT540
 role in sense membrane physical properties541
 to bind membrane surfaces weakly545
- Animal antimicrobial peptides473
- Anticancer α -helical peptides473
 interaction with cancer cell membranes490
 interactions with tumor cell membranes487
 selectivity of488
 structure/function analysis of487,495
- Antifreeze proteins (AFPs)509
 applications of type based509
 cryoprotectant properties of509
 interactions with model membrane systems517
 studies with biological samples513
 studies with model membranes509
- Antimicrobial peptides (AMPs)473,480
 antifungal activity of480
 biological activity of480
 broad spectrum of481
 combinatorial synthesis of473
 directed evolution of475
 fatty acids conjugated type481
 production of α -helix forming type473
- Anti-protein297
 T cell-dependence of297
- Apolipoproteins553
- Aspartyl protease renin241
 activity in cardiovascular system252
 biology of242
 in diabetes251
 in obesity251
 inhibitors of241
 pharmacology of244
 receptor for245
 role in treatment of hypertension241
- Autoinhibitory domain547
- Azo colorants103
 applications of103
 decolorization by human commensal bacteria104
- Azo dye105
 degradation by environ-mental bacteria105
 degradation by filamentous fungi/yeasts108
- Azo dye degrading enzyme101
 recent advances in101
- B-1 cells297
- BBI-like proteins209
 post-translational modifications in209
- Bilayer physical properties548
 insertion of AH to modulates548
- Biosensors276
 for detection of electron acceptors276
 for detection of electron donors276
- Bowman-BIRK family201
 as molecular tools to evaluate functional
 characteristics of inhibitors211
 manipulation of genes of213
 peptides based on211
 polymorphism in genes/proteins of207
 sequence variation in protease binding sites of207
- Cancer355,487
 anticancer peptides for487
 rho gaps in357
 rho GTPase activating proteins in355
- Cancer therapy165
 alemtuzumab in167
 bevacizumab in169
 cetuximab in168
 gemtuzumab ozogamicin in168
 ibritumomab tiuxetan in168
 recombinant antibodies in165
 rituximab in166
 tositumomab in168
 trastuzumab in166
- CD4⁺ T cell298
 distinct of298

for induction of IGG anti-protein/anti-PS responses	298	Corticotropin-releasing factor (CRF)	229
cDNA sequences	151	Corticotropin-releasing factor-related peptides	229
identification of ORFs in	151	and glucocorticoids	234
Cellobiose dehydrogenase	255	family of	231
active-site structure of	272	heart urocortin/CRF ₂ receptor of	234
analysis/classification of genes coding for	262	in cardiovascular system	229
applications of	276	in stress	234
as flavocytochrome	255	receptors of	229
biological function of	276	urocortin 1 as	231
formation of reactive oxygen species by	267	urocortin 2 as	233
from phytopathogenic/saprotropic fungi	255	urocortin 3 as	233
from wood-degrading	255	C-type lectins	283
function of	272	carbohydrate recognition domain (CRD) of	285
in analytical usage	276	cytoplasmic domain of	285
in biocatalysis	278	interaction with pathogen-derived/endogenous glycoconjugates	283
in biotechnology	277	on dendritic cells	283
in enzymatic assays	277	structure of	284
in enzymatic treatment of paper pulp	278	types of	284
<i>in silico</i> docking of domains of	275	C-type lectin receptors (CLRs)	283
in waste removal/bioremediation	277	glycoconjugates as binding partners of	287
interdomain electron transfer of	265	multimerization of	287
microbial production of	256	Cytokine	175
occurrence of	256	based inducible enhancer elements	175
oxidative half-reaction of	267	Dendritic cell	
phylogenetic relationship of	263	in induction of anti-protein/anti-PS responses to intact PN	300
physical/chemical properties of	258	Deubiquitomics	175
production in ascomycetes	258	Disordered proteins	182
production in basidiomycetes	256	Docking	421,437
reaction kinetics of	264	methods of	421
reductive half-reactions of	264	random/stochastic methods for	422
structural implications for catalysis	273	receptor model to use for	443
structure of	272	systematic algorithms for	422
substrate binding of	272	to liganded <i>vs.</i> unliganded crystal structures	453
Central nervous system	3	with homology models <i>vs.</i> crystal structures	448
basic structure of	3	Docking scoring	369
reticular hypothesis of	3	programs for	387
role of global molecular network	3	receptor-base d	375
CGRP	350	systematic search/incremental construction for ...	380
Chick fetal insulin toxicity	78	Drug design	439
GIP inhibits of	78	use of kinase homology models in	439
Cockroach allergen	61	Drug discovery	369,467
group 1 allergen as	61	chemical libraries/structure-based drug design in	467
group 2 allergen as	62	role of ADME/TOX filters	370
group 3 allergen as	63	DUB enzymes	172
group 4 allergen as	63	structural features of	172
group 5 allergen as	63	EBNA 3C	123
group 6 allergen as	63	and NM23-H1	134
group 7 allergen as	64	as transcriptional activator	126
therapeutic/diagnostic approaches of	65	as transcriptional repressor	126
Cockroach allergy	57	bZIP domain of	126
intervention studies of	58	effects of bZIP mutations on RBP-Jκ binding at	130
strategies for isolation of cDNA clones encoding	58		
Combinatorial synthesis	473		
Compound database	369		
receptor-based computational screening of	369		
role of docking-scoring engines	369		

function of	123	role in drug discovery	465
in cell cycle	130	structural biology of	468
structure of	123	Global molecular network (GMN)	3
eHiTS	421	communication process between compartments of ..	9
as approach to docking/scoring function		explanatory value of	11
problems	421	functional aspects of multimeric protein in	5
automatic protonation state evaluation in	430	hypothesis for physiological/pathological	
flexible chain fitting in	424	phenomena	11
geometric shape/chemical feature graph for	423	in neurodegenerative disease	12
method for	423	neurophysiological aspects of	11
pose matching in	424	physiological/pathological implications of	3
re-using docking results in	428	proteins as building blocks of	4
rigid fragment docking of	424	Globin fold	17
validation study of	430	relationships to heme group	17
Endogenous CD4 ⁺ CD25 ⁺ regulatory T cells (TREG)	299	GLUT4	116
role in humoral immune response to intact PN	299	vesicle translocation of	116
Epitope mapping	138	Glycoconjugates	287
of ENV gp21	138	endogenous	290
of ENV gp46 with synthetic peptides/		general characteristics of	287
antibodies	138	pathogen-derived	288
Epstein-Barr virus (EBV)	123	Glycopeptides	310
latency of	123	complexes with MHC class II proteins	310
Epstein-Barr virus transcription factor	123	Glycosylation	317
function of	123	mannose binding lectin binding to	318
structure of	123	of HIV envelope proteins	317
<i>Escherichia coli</i>	47	Gp120	318
empirical selection of strains expressing highly		mannose glycan-dependent 2G12 epitope of	318
toxic genes	55	G-protein coupled peptide receptors.....	335
expression of toxic genes in	47	Ca ²⁺ -assay for	344
manipulation of coding sequence of	52	characterization of ligand interaction	338
manipulation of copy number of	53	cyclization of	346
stabilizing sequence of	54	fluorimetric assays for	340
suppression of amber stop codon of	52	interface prediction of oligomers of	567
suppression of internal stop codon of	53	IP ₃ -assay for	344
Extracellular bacteria	295	ligand similarity-based virtual screening	
host protection against infections by	295	approach for	462
in regulating anti-protein/anti-PS IG isotype		mechanisms/regulation of oligomerization of	564
responses to intact PN	301	methods/ligand design for	335
induction of anti-protein/anti-PS responses to	296	oligomers of	562
Extracellular molecular network	5	peptide design of	346
functional characteristics of	8	separation assay for	340
role of neural circuits	10	signal transduction of	336
structural characteristics of	5	<i>silico</i> methods predicting ligands for orphan	
Fish antifreezes	509	type	259
classification of	509	structure-activity relationship studies of	335
Follicular B cells	297	surface plasmon resonance (SPR) for	339
Full-length cDNA projects	154	Growth hormone secretagogues	349
annotation efforts in	154	Growth inhibitory peptide	77
Full-length cDNA technologies	148	effect on apoptosis	87
G protein-coupled receptors (GPCRs)	465,501	effect on <i>Drosophila</i> development	80
chimeric combinations of	501	effect on erythrocyte aggregation/agglutination	91
functional assays for	467	effect on partial hepatectomy of mouse liver	82
peptide ligands for	501	in tumor angiogenesis	84
		influence on intracellular aggregation/	
		polymerization of intracellular cytoskeleton	
		proteins	94
		inhibition of cell migration/spreading <i>in vitro</i> by ..	85
		inhibition of human platelet aggregation by	90

inhibition of tumor cell adhesion to ECM proteins	91	model building with artificial evolution	219
α -Helices	529	model refinement of	221
conventional hydrophobic moment plot methodology for	531	side-chain prediction of	222
extended hydrophobic moment plot analysis of	532	structure modeling of	217
glycine moment analysis of	532	Host defense peptides	479
hydrophobic moment plot analysis of	532	candidates for treatment of bacterial/fungal infections	479
hydrophobicity/amphiphilicity profiling analysis of	535	modes of action of	479
oblique orientated type	529	HTLV-1 peptide vaccines	137
prediction of	529	animal models for	139
using novel three-dimensional form of hydrophobic moment for	532	considerations for CTL based	139
Hemoglobin	17	envelope glycoprotein as target for	137
allosteric properties of	17	therapeutics of	137
allosterism of	42	Human genes	147
control of oxygen affinity in	29	applications for proteome analyses	147
effect in molecular surgery	39	transcriptome analyses of	147
effect in molecular transplantation	39	Human immune system	317
effect of mutants of allosteric core	35	interaction of human immunodeficiency virus (HIV) glycans with lectins of	317
effect of natural/site directed mutants	17,33	Human MHC class I alleles	313
genetic interventions on	40	binding with glycopeptides	313
$\alpha_i\beta_i$ interface in	36	Human T-cell lymphotropic virus type 1 (HTLV-1)	137
ligand binding properties of	25	synthetic peptide vaccination against	140
multiple mutations at	39	Hypertension	246
mutations at topological sites of	39	animal models for	246
quaternary structures of	23	pharmacological intervention in treatment of	246
reactions of NO with	32	renin inhibitors for	246
Heterotrimeric G proteins	501	Immuoproteasomes	312
activation of	501	effect on glycopeptides	312
secondary structure of	501	Insulin	116
Highly toxic genes	47	tyrosine phosphorylation by	116
antisense strategy to	49	Insulin receptor	113
effect of expression as fusion proteins	53	activity of	113
hybrid promoter strategy to	51	phosphorylation of	115
manipulation of	47	signaling events of	115
mRNA switch mechanism in	52	structure of	113
transcriptional/translational control elements of	47	substrate for	115
use of competitive promoters	50	Insulin receptor substrate-family (IRS)	115
use of full-length lac promoter/operator region	50	in insulin resistance	115
use of invertible promoters	50	Insulin resistance	113
HIV	320	biochemical/molecular basis of	113
cyanovirin-N in	322	cell membrane disturbances in	120
DC-sign/DC-signr in	321	cytokine-mediated	117
galectins in	321	fatty acid transport protein-4 in	119
interaction of immune system lectins with	322	in metabolic syndrome	118
interaction with MBL	320	inheritance of	115
langerin in	321	insulin signaling pathway in	117
mannose receptor in	321	insulin-stimulated translocation of glucose transporter in	116
siglecs in	321	related to fatty acid metabolism/cellular integrity	120
surfactant proteins in	320	role of insulin receptor	113
Homology modeling	437	role of protein kinase B (PKB) in	116
non-virtual screening uses of	439	Integrative cDNA annotations	157
Homology protein	217	transcriptome obtained using	157
homologue detection/alignment of	218		
loop prediction of	221		
model assessment of	224		

Isoglobotrihexosylceramide (iGb3)	325	mechanisms of mediated cell death by	504
as natural ligand for	325	receptor mimetic of	501
immunological function of	325	Phage-mediated delivery	48
in disease conditions	328	of highly selective T7 RNA polymerase	48
interaction of	328	PIN1	179
regulation in antigen presenting cells	329	catalytic domain of	186
storage potential of	329	conformation of substrate of	184
Ligand prediction	459	<i>in vitro</i> PPIase activity of	186
<i>in silico</i> methods in	460	interaction with substrates	185
Lignocellulose biodegradation	255	molecular function of protein of	191
enzymes in	255	phosphorylation signaling of	183
Lipopeptides	479	protein of	187
biological activity of	482	specificity of WW domain of	185
Lytic polypeptides	554	stimulation of substrate dephosphorylation by	
Membrane interactive α -helices	561	PP2A	191
as novel drug target	561	structure of	179
in GPCRs	561	substrates for	181
Metabolic syndrome	116	Pocket detection	429
obesity-linked	118	Polymorphism	201
MUC1	308	biological significance of	201
Murine estrogen fetotoxicity assay	80	in legume protease inhibitors from Bowman-	
GIP in	80	Birk family	201
Myoglobin	29	Polypeptide hormones	554
control of oxygen affinity in	29	Pro-/anti-inflammatory cytokines	300
Nicotinic acetylcholine receptor	195	to regulate anti-protein/anti-PS responses to	
biological functions of	195	intact PN	300
MD simulations of	196	Protease inhibitors (PI)	201
molecular dynamics of	195	anti-nutritional properties of	203
simulation of LBD of	196	cancer chemopreventive properties of	204
simulation of TM domain of	197	functional/physiological role of	202
simulations of M2 helix bundle of	196	physiological role in plants	206
structure of	195	Protein kinase	437
Nuclear magnetic resonance	179	crystal structures of	437
molecular function of PIN1 by	179	docking of	437
O-glycopeptides	310	homology models of	437
in cross-presentation <i>via</i> MHC class I	310	modeling hinge region of	451
O-glycosylated proteins	307	RMSD distributions of	446
as antigens in MHC class II pathway	308	side chain placement of	450
immunology of	307	structure selection for	437
role in design of MUC1 glycopeptide-based		virtual screening of	437
tumor vaccine	307	Protein/polysaccharide-specific Ig isotype	295
Orexin	348	<i>in vivo</i> in response to intact <i>Streptococcus</i>	
Peptide mastoparan	501	<i>pneumoniae</i>	295
and cell penetrant variants	505	regulation of antibody responses to	295
biological applications of	501	Protein-ligand docking	407
design of novel analogues of	504	accuracy of	412
intracellular targets for chimeric analogues of	503	comparison of performance in	412
		empirical methods for	410,417
		knowledge-based methods for	410
		knowledge-based/physics-based methods for	419
		physics-based approaches for	409
		scoring functions for	407
		screening enrichment of	413
		strategies for improvement	417
		Proteome	155
		full-length cDNA resources for functional	
		analyses of	155

RAS superfamily	355	Support α -helices	556
Recombinant allergens	57	Surface-active helices	553
expression system for production of	59	classification of	556
for diagnosis	57	detection/comparison of	554
immunotherapy by	57	in transmembrane proteins	553
in allergic disorders	57	obliquely orientated type	554
Recombinant antibodies	165	signal transduction α -helices as	558
in late phase clinical trial	169	structural analogue of	553
in targeted therapy	165	vestibule forming/microenvironment enclosing	
Renin inhibitors	247	α -helices as	558
clinical development of	247	T lymphocytes	313
differentiation from ACEi/ARBs	249	Tilted peptides	523
first/second generation	247	destabilization of	524
in diabetes	251	history of	523
in obesity	251	role in disorder	525
in renal disease	251	three-dimensional structures of	525
indications of	251	Transmembrane	553
third generation	248	Type I shorthorn sculpin AFP	512
Renin-angiotensin-aldosterone system (RAS)	241	Type I α -helical antifreeze proteins	510
classical pharmacology of	244	Ubiquitination system	171
mechanisms of	245	cytokine-regulated protein degradation by	171
pharmacology of	244	Ubiquitomics	175
Rho proteins	355	USP17 subfamily members	174
downstream effects of activated	356	Virtual ligand screening	395
GAP interactors of	357	blind docking for	403
regulation of	355	docking into predicted binding sites for	403
regulators of	356	energy-based methods for	401
structural features of	357	geometry-based methods for	396
Scoring	407,425	knowledge-based functional site prediction for	402
accuracy of	414	pocket detection for	396,401
comparison of function types of	415	prediction of protein-ligand binding sites for	395
empirical methods for	417	statistical/machine learning approaches for	403
function methodology of	409	Virtual ligand screening	432
knowledge-based/physics-based methods for	419	study of	432
strategies for improvement	417	Virtual screening	437
training function of	427	receptor model to use for	443
Signaling pathways	172	with homology models	441
cytokine-inducible DUB enzymes in	172	Virus-cell fusion	140
Structure based drug design (SBDD)	395	peptide inhibitors of	140
blind docking for	403		
docking into predicted binding sites for	403		
energy-based methods for	401		
geometry-based methods for	396		
knowledge-based functional site prediction for	402		
pocket detection for	396,401		
prediction of protein-ligand binding sites for	395		
statistical/machine learning approaches for	403		