

Subject Index to Volume 100

α -Bungarotoxin

Acetylcholine receptor; Binding site; High-affinity peptide; Systematic residue replacement. (Katchalski-Katzir, E. (100) 293)

α -Helix association

Bioinformatics; Integral membrane protein (Zidovetzki, R. (100) 555)

β -Sheet

β -Turn; Diffusion–collision; Conserved interaction; Intracellular lipid-binding proteins; Protein folding; Peptide fragment (Rotondi, K.S. (100) 421)

β -Turn

Diffusion–collision; Conserved interaction; Intracellular lipid-binding proteins; Protein folding; Peptide fragment; β -Sheet (Rotondi, K.S. (100) 421)

Accessible surface area

Hydrophobic effect; Standard free energy of transfer; Standard free energy of solvation; Hydrocarbons; Hydrogen–carbon bonds (Kyte, J. (100) 193)

Acetylcholine receptor

Binding site; High-affinity peptide; Systematic residue replacement.; α -Bungarotoxin (Katchalski-Katzir, E. (100) 293)

Actin

Actomyosin; Muscle; Magnesium; Urea (Bárány, M. (100) 177)

Actomyosin

Muscle; Magnesium; Urea; Actin (Bárány, M. (100) 177)

Additivity schemes

Unfolded proteins; Volume; Heat capacity; Oligopeptides; Tripeptides; Model compounds (Hedwig, G.R. (100) 239)

Adrenodoxin

Adrenodoxin reductase; Cytochrome *c*; Modeling of complex building; Electrostatic recognition (Müller, J.J. (100) 281)

Adrenodoxin reductase

Cytochrome *c*; Modeling of complex building; Electrostatic recognition; Adrenodoxin (Müller, J.J. (100) 281)

Allostery

MWC Model; John Edsall; Hemoglobin (Edelstein, S.J. (100) 117)

Ammonia

Urease; Water; Thermodynamics; Standard transformed Gibbs energy of formation; Binding of hydrogen ions; Legendre transforms; Carbon dioxide (Alberty, R.A. (100) 183)

Anemia

Sickle cell disease; Sickle hemoglobin (Eaton, W.A. (100) 109)

Annealing

Chaperonin function; GroEL; *Escherichia coli* (Stan, G. (100) 453)

Anomalous stoichiometry

Differentiation of cooperative systems; Iron-ferrozine interaction; Continuous variation; Job plot (Huang, C.Y. (100) 143)

Apolipoprotein E

Isoforms; Protein stability; Tertiary structure; Lipid binding (Weers, P.M.M. (100) 481)

Approach to science

Teaching; History; Edsall; Physical biochemistry; Protein chemistry (Gurd, F.R.N. (100) 49)

Arc repressor

Transcription factor; Protein stability (Anderson, T.A. (100) 341)

ATPases

GTP hydrolysis; Regulation; Signal transduction (Goody, R.S. (100) 535)

Bimolecular recombination rate

Crystallographic studies; Human erythrocyte carbonic anhydrase; Zinc metalloenzyme; Carbonic anhydrase (Khalifah, R.G. (100) 159)

Binding of hydrogen ions

Legendre transforms; Carbon dioxide; Ammonia; Urease; Water; Thermodynamics; Standard transformed Gibbs energy of formation (Alberty, R.A. (100) 183)

Binding site

High-affinity peptide; Systematic residue replacement.; α -Bungarotoxin; Acetylcholine receptor (Katchalski-Katzir, E. (100) 293)

Bioinformatics

Integral membrane protein; α -Helix association (Zidovetzki, R. (100) 555)

Caged neurotransmitters

Photolabile precursors; Prevention of cocaine inhibition; Neurotransmitter receptors; Transient kinetic investigations of membrane-bound proteins (Hess, G.P. (100) 493)

Carbon dioxide

Ammonia; Urease; Water; Thermodynamics; Standard transformed Gibbs energy of formation; Binding of hydrogen ions; Legendre transforms (Alberty, R.A. (100) 183)

Carbonic anhydrase

Bimolecular recombination rate; Crystallographic studies; Human erythrocyte carbonic anhydrase; Zinc metalloenzyme (Khalifah, R.G. (100) 159)

Cell spreading

Mechanotransduction; Tissue engineering; Tissue remodeling; Myosin activation (Wakatsuki, T. (100) 593)

Chaperonin function

GroEL; *Escherichia coli*; Annealing (Stan, G. (100) 453)

Chromatin

Gene expression; Eukaryotic; Nucleus (Felsenfeld, G. (100) 607)

Complex number constants

Ligand-receptor interactions; Stoichiometric binding constants (Klotz, I.M. (100) 123)

Conserved interaction

Intracellular lipid-binding proteins; Protein folding; Peptide fragment; β -Sheet; β -Turn; Diffusion-collision (Rotondi, K.S. (100) 421)

Continuous variation

Job plot; Anomalous stoichiometry; Differentiation of cooperative systems; Iron-ferrozine interaction (Huang, C.Y. (100) 143)

Core packing

Protein stability; Protein folding; Methionine; Selenomethionine; Lysozyme (Gassner, N.C. (100) 325)

Cross-interaction parameters

Folding intermediates; Protein folding kinetics; Transition state; Rate-equilibrium relationships; Hammond postulate (Sánchez, I.E. (100) 397)

Crystal structure

Thermostability; Proteasomal homolog; HslV; HslU; Proteolytic activity (Song, H.K. (100) 437)

Crystal structures

Trimethylamine oxide; Fibrinogen; Fibrin (Doolittle, R.F. (100) 307)

Crystallographic studies

Human erythrocyte carbonic anhydrase; Zinc metalloenzyme; Carbonic anhydrase; Bimolecular recombination rate (Khalifah, R.G. (100) 159)

Cyclophilin

PPIase; Isothermal titration calorimetry; Thermodynamics of molecular interactions (Fanghänel, J. (100) 351)

Cytochrome *c*

Modeling of complex building; Electrostatic recognition; Adrenodoxin; Adrenodoxin reductase (Müller, J.J. (100) 281)

Cytochromes

Folding kinetics; Intermediates (Brunori, M. (100) 409)

Cytoskeleton

Lipid rafts; Fluorescence photobleaching recovery; Fluorescence resonance energy transfer; Fluorescence correlation spectroscopy; Single particle tracking; Green fluorescent protein; Receptor mobility; Membrane fluidity (Helmreich, E.J.M. (100) 519)

Denaturation

Energy functions; Solvation; Protein stability (Lazaridis, T. (100) 367)

Density

Physical; Selectivity; Saturation (Eisenberg, B. (100) 507)

Dielectric properties

Rotary Brownian motion; Perrin relaxation times; Serum albumin; Fatty acid complex; Stop-flow kinetics (Oncley, J.L. (100) 151)

Differentiation of cooperative systems

Iron-ferrozine interaction; Continuous variation; Job plot; Anomalous stoichiometry (Huang, C.Y. (100) 143)

Diffusion-collision

Conserved interaction; Intracellular lipid-binding proteins; Protein folding; Peptide fragment; β -Sheet; β -Turn (Rotondi, K.S. (100) 421)

Edsall

Physical biochemistry; Protein chemistry; Approach to science; Teaching; History (Gurd, F.R.N. (100) 49)

Electron tomography

Macromolecular crowding; Eukaryote/prokaryote distinction; Vitrification (Grünewald, K. (100) 577)

Electrostatic recognition

Adrenodoxin; Adrenodoxin reductase; Cytochrome *c*; Modeling of complex building (Müller, J.J. (100) 281)

Energy functions

Solvation; Protein stability; Denaturation (Lazaridis, T. (100) 367)

Enthalpy-entropy compensation

Thermodynamics of solution transfer; Entropy of vaporization; Solvent structure; Solvation (Henn, A.R. (100) 205)

Entropy of vaporization

Solvent structure; Solvation; Enthalpy-entropy compensation; Thermodynamics of solution transfer (Henn, A.R. (100) 205)

Escherichia coli

Annealing; Chaperonin function; GroEL (Stan, G. (100) 453)

Eukaryote/prokaryote distinction

Vitrification; Electron tomography; Macromolecular crowding (Grünewald, K. (100) 577)

Eukaryotic

Nucleus; Chromatin; Gene expression (Felsenfeld, G. (100) 607)

Fatty acid complex

Stop-flow kinetics; Dielectric properties; Rotary Brownian motion; Perrin relaxation times; Serum albumin (Oncley, J.L. (100) 151)

Fibrin

Crystal structures; Trimethylamine oxide; Fibrinogen (Doolittle, R.F. (100) 307)

Fibrinogen

Fibrin; Crystal structures; Trimethylamine oxide (Doolittle, R.F. (100) 307)

Fluorescence correlation spectroscopy

Single particle tracking; Green fluorescent protein; Receptor mobility; Membrane fluidity; Cytoskeleton; Lipid rafts; Fluorescence photobleaching recovery; Fluorescence resonance energy transfer (Helmreich, E.J.M. (100) 519)

Fluorescence photobleaching recovery

Fluorescence resonance energy transfer; Fluorescence correlation spectroscopy; Single particle tracking; Green fluorescent protein; Receptor mobility; Membrane fluidity; Cytoskeleton; Lipid rafts (Helmreich, E.J.M. (100) 519)

Fluorescence resonance energy transfer

Fluorescence correlation spectroscopy; Single particle tracking; Green fluorescent protein; Receptor mobility; Membrane fluidity; Cytoskeleton; Lipid rafts; Fluorescence photobleaching recovery (Helmreich, E.J.M. (100) 519)

Folding intermediates

Protein folding kinetics; Transition state; Rate-equilibrium relationships; Hammond postulate; Cross-interaction parameters (Sánchez, I.E. (100) 397)

Folding kinetics

Intermediates; Cytochromes (Brunori, M. (100) 409)

Gene expression

Eukaryotic; Nucleus; Chromatin (Felsenfeld, G. (100) 607)

Green fluorescent protein

Receptor mobility; Membrane fluidity; Cytoskeleton; Lipid rafts; Fluorescence photobleaching recovery; Fluorescence resonance energy transfer; Fluorescence correlation spectroscopy; Single particle tracking (Helmreich, E.J.M. (100) 519)

GroEL

Escherichia coli; Annealing; Chaperonin function (Stan, G. (100) 453)

Growth factor

Receptor; Structural biology; Multiprotein complexes (Harmer, N.J. (100) 545)

GTP hydrolysis

ATPases; Regulation; Signal transduction (Goody, R.S. (100) 535)

Hammond postulate

Cross-interaction parameters; Folding intermediates; Protein folding kinetics; Transition state; Rate-equilibrium relationships (Sánchez, I.E. (100) 397)

Harvard university

History of proteins; Molecular size; Ionic charges (Tanford, C. (100) 81)

Heat capacity

Oligopeptides; Tripeptides; Model compounds; Additivity schemes; Unfolded proteins; Volume (Hedwig, G.R. (100) 239)

Hemoglobin

Site mutations; Inter-helical H-bonds (Tsai, C.-H. (100) 131)

Hemoglobin

Allostery; MWC Model; John Edsall (Edelstein, S.J. (100) 117)

High-affinity peptide

Systematic residue replacement.; α -Bungarotoxin; Acetylcholine receptor; Binding site (Katchalski-Katzir, E. (100) 293)

History

Edsall; Physical biochemistry; Protein chemistry; Approach to science; Teaching (Gurd, F.R.N. (100) 49)

History of biochemistry

Protein; Protein conformation; Protein sequence (van Holde, K.E. (100) 71)

History of biophysics

J.W. Gibbs; P.J.W. Debye; L. Pauling; E.J. Cohn; J.T. Edsall; J.G. Kirkwood; L. Onsager (Eisenberg, H. (100) 32)

History of proteins

Molecular size; Ionic charges; Harvard university (Tanford, C. (100) 81)

HslU

Proteolytic activity; Crystal structure; Thermostability; Proteasomal homolog; HslV (Song, H.K. (100) 437)

HslV

HslU; Proteolytic activity; Crystal structure; Thermostability; Proteasomal homolog (Song, H.K. (100) 437)

Human erythrocyte carbonic anhydrase

Zinc metalloenzyme; Carbonic anhydrase; Bimolecular recombination rate; Crystallographic studies (Khalifah, R.G. (100) 159)

Hydrocarbons

Hydrogen-carbon bonds; Accessible surface area; Hydrophobic effect; Standard free energy of transfer; Standard free energy of solvation (Kyte, J. (100) 193)

Hydrogen-carbon bonds

Accessible surface area; Hydrophobic effect; Standard free

energy of transfer; Standard free energy of solvation; Hydrocarbons (Kyte, J. (100) 193)

Hydrophobic effect

Water structure; Solvation; Peptide hydration; Protein hydration; Molecular dynamics (Beck, D.A.C. (100) 221)

Hydrophobic effect

Standard free energy of transfer; Standard free energy of solvation; Hydrocarbons; Hydrogen-carbon bonds; Accessible surface area (Kyte, J. (100) 193)

Integral membrane protein

α -Helix association; Bioinformatics (Zidovetzki, R. (100) 555)

Inter-helical H-bonds

Hemoglobin; Site mutations (Tsai, C.-H. (100) 131)

Intermediates

Cytochromes; Folding kinetics (Brunori, M. (100) 409)

Intracellular lipid-binding proteins

Protein folding; Peptide fragment; β -Sheet; β -Turn; Diffusion-collision; Conserved interaction (Rotondi, K.S. (100) 421)

Ionic charges

Harvard university; History of proteins; Molecular size (Tanford, C. (100) 81)

Iron-ferrozine interaction

Continuous variation; Job plot; Anomalous stoichiometry; Differentiation of cooperative systems (Huang, C.Y. (100) 143)

Isoforms

Protein stability; Tertiary structure; Lipid binding; Apolipoprotein E (Weers, P.M.M. (100) 481)

Isothermal titration calorimetry

Thermodynamics of molecular interactions; Cyclophilin; PPIase (Fanghänel, J. (100) 351)

Job plot

Anomalous stoichiometry; Differentiation of cooperative systems; Iron-ferrozine interaction; Continuous variation (Huang, C.Y. (100) 143)

Legendre transforms

Carbon dioxide; Ammonia; Urease; Water; Thermodynamics; Standard transformed Gibbs energy of formation; Binding of hydrogen ions (Alberty, R.A. (100) 183)

Ligand–receptor interactions

Stoichiometric binding constants; Complex number constants (Klotz, I.M. (100) 123)

Lipid binding

Apolipoprotein E; Isoforms; Protein stability; Tertiary structure (Weers, P.M.M. (100) 481)

Lipid rafts

Fluorescence photobleaching recovery; Fluorescence resonance energy transfer; Fluorescence correlation spectroscopy; Single particle tracking; Green fluorescent protein; Receptor mobility; Membrane fluidity; Cytoskeleton (Helmreich, E.J.M. (100) 519)

Lysozyme

Core packing; Protein stability; Protein folding; Methionine; Selenomethionine (Gassner, N.C. (100) 325)

Macromolecular crowding

Eukaryote/prokaryote distinction; Vitrification; Electron tomography (Grünewald, K. (100) 577)

Magnesium

Urea; Actin; Actomyosin; Muscle (Bárány, M. (100) 177)

Mechanotransduction

Tissue engineering; Tissue remodeling; Myosin activation; Cell spreading (Wakatsuki, T. (100) 593)

Membrane fluidity

Cytoskeleton; Lipid rafts; Fluorescence photobleaching recovery; Fluorescence resonance energy transfer; Fluorescence correlation spectroscopy; Single particle tracking; Green fluorescent protein; Receptor mobility (Helmreich, E.J.M. (100) 519)

Methionine

Selenomethionine; Lysozyme; Core packing; Protein stability; Protein folding (Gassner, N.C. (100) 325)

Model compounds

Additivity schemes; Unfolded proteins; Volume; Heat capacity; Oligopeptides; Tripeptides (Hedwig, G.R. (100) 239)

Modeling of complex building

Electrostatic recognition; Adrenodoxin; Adrenodoxin reductase; Cytochrome *c* (Müller, J.J. (100) 281)

Molecular dynamics

Hydrophobic effect; Water structure; Solvation; Peptide hydration; Protein hydration (Beck, D.A.C. (100) 221)

Molecular recognition

Serine protease; Site-specific cooperativity; Thrombin (Krem, M.M. (100) 315)

Molecular size

Ionic charges; Harvard university; History of proteins (Tanford, C. (100) 81)

Multiprotein complexes

Growth factor; Receptor; Structural biology (Harmer, N.J. (100) 545)

Muscle

Magnesium; Urea; Actin; Actomyosin (Bárány, M. (100) 177)
Myosin; Molecular motors; Electron microscopy (Lowey, S. (100) 171)

MWC Model

John Edsall; Hemoglobin; Allostery (Edelstein, S.J. (100) 117)

Myosin activation

Cell spreading; Mechanotransduction; Tissue engineering; Tissue remodeling (Wakatsuki, T. (100) 593)

Neurotransmitter receptors

Transient kinetic investigations of membrane-bound proteins; Caged neurotransmitters; Photolabile precursors; Prevention of cocaine inhibition (Hess, G.P. (100) 493)

Non-detergent sulfobetaines

Protein-folding helpers; Physical–chemical features (Expert-Bezançon, N. (100) 469)

Nucleus

Chromatin; Gene expression; Eukaryotic (Felsenfeld, G. (100) 607)

Oligopeptides

Tripeptides; Model compounds; Additivity schemes; Unfolded proteins; Volume; Heat capacity (Hedwig, G.R. (100) 239)

Peptide fragment

β -Sheet; β -Turn; Diffusion–collision; Conserved interaction; Intracellular lipid-binding proteins; Protein folding (Rotondi, K.S. (100) 421)

Peptide hydration

Protein hydration; Molecular dynamics; Hydrophobic effect; Water structure; Solvation (Beck, D.A.C. (100) 221)

Perrin relaxation times

Serum albumin; Fatty acid complex; Stop–flow kinetics; Di-

electric properties; Rotary Brownian motion (Oncley, J.L. (100) 151)

Photolabile precursors

Prevention of cocaine inhibition; Neurotransmitter receptors; Transient kinetic investigations of membrane-bound proteins; Caged neurotransmitters (Hess, G.P. (100) 493)

Physical

Selectivity; Saturation; Density (Eisenberg, B. (100) 507)

Physical biochemistry

Protein chemistry; Approach to science; Teaching; History; Edsall (Gurd, F.R.N. (100) 49)

Physical–chemical features

Non-detergent sulfobetaines; Protein-folding helpers (Expert-Bezançon, N. (100) 469)

PPIase

Isothermal titration calorimetry; Thermodynamics of molecular interactions; Cyclophilin (Fanghänel, J. (100) 351)

Prevention of cocaine inhibition

Neurotransmitter receptors; Transient kinetic investigations of membrane-bound proteins; Caged neurotransmitters; Photolabile precursors (Hess, G.P. (100) 493)

Proteasomal homolog

HslV; HslU; Proteolytic activity; Crystal structure; Thermostability (Song, H.K. (100) 437)

Protein

Protein conformation; Protein sequence; History of biochemistry (van Holde, K.E. (100) 71)

Protein backbone modeling

Side chain addition; United-residue force field (Każmierkiewicz, R. (100) 261)

Protein chemistry

Approach to science; Teaching; History; Edsall; Physical biochemistry (Gurd, F.R.N. (100) 49)

Protein conformation

Protein sequence; History of biochemistry; Protein (van Holde, K.E. (100) 71)

Protein folding

Peptide fragment; β -Sheet; β -Turn; Diffusion–collision; Conserved interaction; Intracellular lipid-binding proteins (Rotondi, K.S. (100) 421)

Protein folding

Methionine; Selenomethionine; Lysozyme; Core packing; Protein stability (Gassner, N.C. (100) 325)

Protein folding kinetics

Transition state; Rate-equilibrium relationships; Hammond postulate; Cross-interaction parameters; Folding intermediates (Sánchez, I.E. (100) 397)

Protein hydration

Molecular dynamics; Hydrophobic effect; Water structure; Solvation; Peptide hydration (Beck, D.A.C. (100) 221)

Protein sequence

History of biochemistry; Protein; Protein conformation (van Holde, K.E. (100) 71)

Protein stability

Tertiary structure; Lipid binding; Apolipoprotein E; Isoforms (Weers, P.M.M. (100) 481)

Protein stability

Protein folding; Methionine; Selenomethionine; Lysozyme; Core packing (Gassner, N.C. (100) 325)

Protein stability

Denaturation; Energy functions; Solvation (Lazaridis, T. (100) 367)

Protein stability

Arc repressor; Transcription factor (Anderson, T.A. (100) 341)

Protein-folding helpers

Physical–chemical features; Non-detergent sulfobetaines (Expert-Bezançon, N. (100) 469)

Proteolytic activity

Crystal structure; Thermostability; Proteasomal homolog; HslV; HslU (Song, H.K. (100) 437)

Rate-equilibrium relationships

Hammond postulate; Cross-interaction parameters; Folding intermediates; Protein folding kinetics; Transition state (Sánchez, I.E. (100) 397)

Receptor

Structural biology; Multiprotein complexes; Growth factor (Harmer, N.J. (100) 545)

Receptor mobility

Membrane fluidity; Cytoskeleton; Lipid rafts; Fluorescence photobleaching recovery; Fluorescence resonance energy transfer; Fluorescence correlation spectroscopy; Single particle tracking; Green fluorescent protein (Helmreich, E.J.M. (100) 519)

Regulation

ATPases; GTP hydrolysis; Signal transduction (Goody, R.S. (100) 535)

Rotary Brownian motion

Perrin relaxation times; Serum albumin; Fatty acid complex; Stop–flow kinetics; Dielectric properties (Oncley, J.L. (100) 151)

Saturation

Density; Physical; Selectivity (Eisenberg, B. (100) 507)

Selectivity

Saturation; Density; Physical (Eisenberg, B. (100) 507)

Selenomethionine

Lysozyme; Core packing; Protein stability; Protein folding; Methionine (Gassner, N.C. (100) 325)

Serine protease

Site-specific cooperativity; Thrombin; Molecular recognition (Krem, M.M. (100) 315)

Serum albumin

Fatty acid complex; Stop-flow kinetics; Dielectric properties; Rotary Brownian motion; Perrin relaxation times (Oncley, J.L. (100) 151)

Sickle cell disease

Sickle hemoglobin; Anemia (Eaton, W.A. (100) 109)

Sickle hemoglobin

Anemia; Sickle cell disease (Eaton, W.A. (100) 109)

Side chain addition

United-residue force field; Protein backbone modeling (Kazmierkiewicz, R. (100) 261)

Signal transduction

ATPases; GTP hydrolysis; Regulation (Goody, R.S. (100) 535)

Single particle tracking

Green fluorescent protein; Receptor mobility; Membrane fluidity; Cytoskeleton; Lipid rafts; Fluorescence photobleaching recovery; Fluorescence resonance energy transfer; Fluorescence correlation spectroscopy (Helmreich, E.J.M. (100) 519)

Site mutations

Inter-helical H-bonds; Hemoglobin (Tsai, C.-H. (100) 131)

Site-specific cooperativity

Thrombin; Molecular recognition; Serine protease (Krem, M.M. (100) 315)

Solvation

Protein stability; Denaturation; Energy functions (Lazaridis, T. (100) 367)

Solvation

Enthalpy-entropy compensation; Thermodynamics of solution transfer; Entropy of vaporization; Solvent structure (Henn, A.R. (100) 205)

Solvation

Peptide hydration; Protein hydration; Molecular dynamics; Hydrophobic effect; Water structure (Beck, D.A.C. (100) 221)

Solvent structure

Solvation; Enthalpy-entropy compensation; Thermodynamics of solution transfer; Entropy of vaporization (Henn, A.R. (100) 205)

Standard free energy of solvation

Hydrocarbons; Hydrogen-carbon bonds; Accessible surface area; Hydrophobic effect; Standard free energy of transfer (Kyte, J. (100) 193)

Standard free energy of transfer

Standard free energy of solvation; Hydrocarbons; Hydrogen-carbon bonds; Accessible surface area; Hydrophobic effect (Kyte, J. (100) 193)

Standard transformed Gibbs energy of formation

Binding of hydrogen ions; Legendre transforms; Carbon dioxide; Ammonia; Urease; Water; Thermodynamics (Alberty, R.A. (100) 183)

Stoichiometric binding constants

Complex number constants; Ligand-receptor interactions (Klotz, I.M. (100) 123)

Stop-flow kinetics

Dielectric properties; Rotary Brownian motion; Perrin relaxation times; Serum albumin; Fatty acid complex (Oncley, J.L. (100) 151)

Structural biology

Multiprotein complexes; Growth factor; Receptor (Harmer, N.J. (100) 545)

Systematic residue replacement.

α -Bungarotoxin; Acetylcholine receptor; Binding site; High-affinity peptide (Katchalski-Katzir, E. (100) 293)

Teaching

History; Edsall; Physical biochemistry; Protein chemistry; Approach to science (Gurd, F.R.N. (100) 49)

Tertiary structure

Lipid binding; Apolipoprotein E; Isoforms; Protein stability (Weers, P.M.M. (100) 481)

Thermodynamics

Standard transformed Gibbs energy of formation; Binding of hydrogen ions; Legendre transforms; Carbon dioxide; Ammonia; Urease; Water (Alberty, R.A. (100) 183)

Thermodynamics of molecular interactions

Cyclophilin; PPIase; Isothermal titration calorimetry (Fanghänel, J. (100) 351)

Thermodynamics of solution transfer

Entropy of vaporization; Solvent structure; Solvation; Enthalpy-entropy compensation (Henn, A.R. (100) 205)

Thermostability

Proteasomal homolog; HslV; HslU; Proteolytic activity; Crystal structure (Song, H.K. (100) 437)

Thrombin

Molecular recognition; Serine protease; Site-specific cooperativity (Krem, M.M. (100) 315)

Tissue engineering

Tissue remodeling; Myosin activation; Cell spreading; Mechanotransduction (Wakatsuki, T. (100) 593)

Tissue remodeling

Myosin activation; Cell spreading; Mechanotransduction; Tissue engineering (Wakatsuki, T. (100) 593)

Transcription factor

Protein stability; Arc repressor (Anderson, T.A. (100) 341)

Transient kinetic investigations of membrane-bound proteins

Caged neurotransmitters; Photolabile precursors; Prevention of cocaine inhibition; Neurotransmitter receptors (Hess, G.P. (100) 493)

Transition state

Rate-equilibrium relationships; Hammond postulate; Cross-interaction parameters; Folding intermediates; Protein folding kinetics (Sánchez, I.E. (100) 397)

Trimethylamine oxide

Fibrinogen; Fibrin; Crystal structures (Doolittle, R.F. (100) 307)

Tripeptides

Model compounds; Additivity schemes; Unfolded proteins; Volume; Heat capacity; Oligopeptides (Hedwig, G.R. (100) 239)

Unfolded proteins

Volume; Heat capacity; Oligopeptides; Tripeptides; Model compounds; Additivity schemes (Hedwig, G.R. (100) 239)

United-residue force field

Protein backbone modeling; Side chain addition (Każmierkiewicz, R. (100) 261)

Urea

Actin; Actomyosin; Muscle; Magnesium (Bárány, M. (100) 177)

Urease

Water; Thermodynamics; Standard transformed Gibbs energy of formation; Binding of hydrogen ions; Legendre transforms; Carbon dioxide; Ammonia (Alberty, R.A. (100) 183)

Vitrification

Electron tomography; Macromolecular crowding; Eukaryote/prokaryote distinction (Grünewald, K. (100) 577)

Volume

Heat capacity; Oligopeptides; Tripeptides; Model compounds; Additivity schemes; Unfolded proteins (Hedwig, G.R. (100) 239)

Water

Thermodynamics; Standard transformed Gibbs energy of formation; Binding of hydrogen ions; Legendre transforms; Carbon dioxide; Ammonia; Urease (Alberty, R.A. (100) 183)

Water structure

Solvation; Peptide hydration; Protein hydration; Molecular dynamics; Hydrophobic effect (Beck, D.A.C. (100) 221)

Zinc metalloenzyme

Carbonic anhydrase; Bimolecular recombination rate; Crystallographic studies; Human erythrocyte carbonic anhydrase (Khalifah, R.G. (100) 159)