Stanford

David B. McKay

Professor of Structural Biology, Emeritus

Bio

ACADEMIC APPOINTMENTS

- Emeritus Faculty, Acad Council, Structural Biology
- Member, Bio-X

HONORS AND AWARDS

- Fellow, American Association for the Advancement of Science (2001)

PROFESSIONAL EDUCATION

- B.S., California Institute of Technology , Physics
- Ph.D., University of Chicago , Biophysics

LINKS

- McKay Lab Website: http://mckaylab.stanford.edu

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

See:

http://alpha1.stanford.edu/~mckaylab

Publications

PUBLICATIONS

- **Structure and Function of Steroid Receptor RNA Activator Protein, the Proposed Partner of SRA Noncoding RNA** *JOURNAL OF MOLECULAR BIOLOGY*
  McKay, D. B., Xi, L., Barthel, K. K., Cech, T. R.
  2014; 426 (8): 1766-1785
- **Structure of the RNA Binding Domain of a DEAD-Box Helicase Bound to Its Ribosomal RNA Target Reveals a Novel Mode of Recognition by an RNA Recognition Motif** *JOURNAL OF MOLECULAR BIOLOGY*
  Hardin, J. W., Hu, Y. X., McKay, D. B.
  2010; 402 (2): 412-427
- **The Bacillus subtilis RNA helicase YxiN is distended in solution.** *Biophysical journal*
  wang, s., Overgaard, M. T., Hu, Y., McKay, D. B.
  2008; 94 (1): L01-3
- **The periplasmic bacterial molecular chaperone SurA adapts its structure to bind peptides in different conformations to assert a sequence preference for aromatic residues** *JOURNAL OF MOLECULAR BIOLOGY*
  Xu, X., wang, s., Hu, Y., McKay, D. B.
  2007; 373 (2): 367-381

- **Structure of the second domain of the Bacillus subtilis DEAD-box RNA helicase YxiN** *ACTA CRYSTALLOGRAPHICA SECTION F-STRUCTURAL BIOLOGY AND CRYSTALLIZATION COMMUNICATIONS*
  Caruthers, J. M., Hu, Y., McKay, D. B.
  2006; 62: 1191-1195

- **Retention of core catalytic functions by a conserved minimal ribonuclease E peptide that lacks the domain required for tetramer formation** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Caruthers, J. M., Feng, Y., McKay, D. B., Cohen, S. N.
  2006; 281 (37): 27046-27051

- **The domain of the Bacillus subtilis DEAD-box helicase YxiN that is responsible for specific binding of 23S rRNA has an RNA recognition motif fold** *RNA-A PUBLICATION OF THE RNA SOCIETY*
  wang, s., Hu, Y., Overgaard, M. T., Karginov, F. V., Uhlenbeck, O. C., McKay, D. B.
  2006; 12 (6): 959-967

- **Structure of the Escherichia coli FlhDC complex, a prokaryotic heteromeric regulator of transcription** *JOURNAL OF MOLECULAR BIOLOGY*
  Wang, S. Y., Fleming, R. T., Westbrook, E. M., Matsumura, P., McKay, D. B.
  2006; 355 (4): 798-808

- **YxiN is a modular protein combining a DEx(D)/(H) core and a specific RNA-binding domain** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Karginov, F. V., Caruthers, J. M., Hu, Y. X., McKay, D. B., Uhlenbeck, O. C.
  2005; 280 (42): 35499-35505

- **Binding of phage-display-selected peptides to the periplasmic chaperone protein SurA mimics binding of unfolded outer membrane proteins** *FEBS LETTERS*
  Bitto, E., McKay, D. B.
  2004; 568 (1-3): 94-98

- **Kinetics of protein substrate degradation by HslUV** *5th International Conference on AAA(plus) Proteins*
  Kwon, A. R., Trame, C. B., McKay, D. B.
  ACADEMIC PRESS INC ELSEVIER SCIENCE.2004: 141–47

- **The periplasmic molecular chaperone protein SurA binds a peptide motif that is characteristic of integral outer membrane proteins** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Bitto, E., McKay, D. B.
  2003; 278 (49): 49316-49322

- **Crystal structure of the leadzyme at 1.8 angstrom resolution: Metal ion binding and the implications for catalytic mechanism and allo site ion regulation** *BIOCHEMISTRY*
  Wedekind, J. E., McKay, D. B.
  2003; 42 (32): 9554-9563

- **Structure and reactivity of an asymmetric complex between HslV and I-domain deleted HslU, a prokaryotic homolog of the eukaryotic proteasome** *JOURNAL OF MOLECULAR BIOLOGY*
  Kwon, A. R., Kessler, B. M., Overkleeft, H. S., McKay, D. B.
  2003; 330 (2): 185-195

- **Structure of the Yersinia enterocolitica molecular-chaperone protein SycE** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  Trame, C. B., McKay, D. B.
  2003; 59: 389-392

- **Crystallographic structure of SurA, a molecular chaperone that facilitates folding of outer membrane porins** *STRUCTURE*
  Bitto, E., McKay, D. B.
  2002; 10 (11): 1489-1498

- **Crystal structure of HsIUV complexed with a vinyl sulfone inhibitor: Corroboration of a proposed mechanism of allosteric activation of HsIV by HsIU** *JOURNAL OF MOLECULAR BIOLOGY*
  Sousa, M. C., Kessler, B. M., Overkleeft, H. S., McKay, D. B.
  2002; 318 (3): 779-785

- **Helicase structure and mechanism** *CURRENT OPINION IN STRUCTURAL BIOLOGY*

Caruthers, J. M., McKay, D. B.
2002; 12 (1): 123-133

- **Refined crystallographic structure of Pseudomonas aeruginosa exotoxin A and its implications for the molecular mechanism of toxicity** *JOURNAL OF MOLECULAR BIOLOGY*
  Wedekind, J. E., Trame, C. B., Dorywalska, M., Koehl, P., Raschke, T. M., McKee, M., Fitzgerald, D., Collier, R. J., McKay, D. B.
  2001; 314 (4): 823-837

- **Structure of the universal stress protein of Haemophilus influenzae** *STRUCTURE*
  Sousa, M. C., McKay, D. B.
  2001; 9 (12): 1135-1141

- **Structure of Haemophilus influenzae HslV protein at 1.9 angstrom resolution, revealing a cation-binding site near the catalytic site** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  Sousa, M. C., McKay, D. B.
  2001; 57: 1950-1954

- **Structure of Haemophilus influenzae HslU protein in crystals with one-dimensional disorder twinning** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  Trame, C. B., McKay, D. B.
  2001; 57: 1079-1090

- **Crystal structure of yeast initiation factor 4A, a DEAD-box RNA helicase** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Caruthers, J. M., Johnson, E. R., McKay, D. B.
  2000; 97 (24): 13080-13085

- **Crystal and solution structures of an HsIUV protease-chaperone complex** *CELL*
  Sousa, M. C., Trame, C. B., Tsuruta, H., Wilbanks, S. M., Reddy, V. S., McKay, D. B.
  2000; 103 (4): 633-643

- **Purification, crystallization, and X-ray diffraction analysis of small ribozymes** *RNA-LIGAND INTERACTIONS PT A*
  Wedekind, J. E., McKay, D. B.
  2000; 317: 149-168

- **Crystallographic structure of the amino terminal domain of yeast initiation factor 4A, a representative DEAD-box RNA helicase** *RNA-A PUBLICATION OF THE RNA SOCIETY*
  Johnson, E. R., McKay, D. B.
  1999; 5 (12): 1526-1534

- **Mapping the role of active site residues for transducing an ATP-induced conformational change in the bovine 70-kDa heat shock cognate protein** *BIOCHEMISTRY*
  Johnson, E. R., McKay, D. B.
  1999; 38 (33): 10823-10830

- **Crystal structure of a lead-dependent ribozyme revealing metal binding sites revelant to catalysis** *NATURE STRUCTURAL BIOLOGY*
  Wedekind, J. E., McKay, D. B.
  1999; 6 (3): 261-268

- **The hydroxyl of threonine 13 of the bovine 70-kDa heat shock cognate protein is essential for transducing the ATP-induced conformational change** *BIOCHEMISTRY*
  Sousa, M. C., McKay, D. B.
  1998; 37 (44): 15392-15399

- **Structural replacement of active site monovalent cations by the epsilon-amino group of lysine in the ATPase fragment of bovine Hsc70** *BIOCHEMISTRY*
  Wilbanks, S. M., McKay, D. B.
  1998; 37 (20): 7456-7462

- **Crystallographic structures of the hammerhead ribozyme: Relationship to ribozyme folding and catalysis** *ANNUAL REVIEW OF BIOPHYSICS AND BIOMOLECULAR STRUCTURE*
  Wedekind, J. E., McKay, D. B.

1998; 27: 475-502

- **Destabilization of peptide binding and interdomain communication by an E543K mutation in the bovine 70-kDa heat shock cognate protein, a molecular chaperone** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Ha, J. H., Hellman, U., Johnson, E. R., Li, L. S., McKay, D. B., Sousa, M. C., Takeda, S., Wernstedt, C., Wilbanks, S. M.
  1997; 272 (44): 27796-27803

- **Lysine 71 of the chaperone protein Hsc70 is essential for ATP hydrolysis** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  OBRIEN, M. C., Flaherty, K. M., McKay, D. B.
  1996; 271 (27): 15874-15878

- **Structure and function of the hammerhead ribozyme: An unfinished story** *RNA-A PUBLICATION OF THE RNA SOCIETY*
  McKay, D. B.
  1996; 2 (5): 395-403

- **Kinetics of peptide binding to the bovine 70 kDa heat shock cognate protein, a molecular chaperone** *BIOCHEMISTRY*
  Takeda, S., McKay, D. B.
  1996; 35 (14): 4636-4644

- **The metzincins: A superfamily of structurally related metalloproteinases** *Meeting of the Study Group Physiology of the German-Zoological-Society*
  Bode, W., Grams, F., Reinemer, P., GOMISRUTH, F. X., Baumann, U., McKay, D. B., STOCKER, W.
  ELSEVIER GMBH, URBAN & FISCHER VERLAG.1996: 237–46

- **The metzincin-superfamily of zinc-peptidases** *10th International Conference on Intracellular Protein Catabolism*
  Bode, W., Grams, F., Reinemer, P., GOMISRUTH, F. X., Baumann, U., McKay, D. B., STOCKER, W.
  PLENUM PRESS DIV PLENUM PUBLISHING CORP.1996: 1–11

- **SOLUTION SMALL-ANGLE X-RAY-SCATTERING STUDY OF THE MOLECULAR CHAPERONE HSC70 AND ITS SUBFRAGMENTS** *BIOCHEMISTRY*
  Wilbanks, S. M., Chen, L. L., Tsuruta, H., Hodgson, K. O., McKay, D. B.
  1995; 34 (38): 12095-12106

- **KINETICS OF NUCLEOTIDE-INDUCED CHANGES IN THE TRYPTOPHAN FLUORESCENCE OF THE MOLECULAR CHAPERONE HSC70 AND ITS SUBFRAGMENTS SUGGEST THE ATP-INDUCED CONFORMATIONAL CHANGE FOLLOWS INITIAL ATP BINDING** *BIOCHEMISTRY*
  Ha, J. H., McKay, D. B.
  1995; 34 (36): 11635-11644

- **THE METZINCINS - TOPOLOGICAL AND SEQUENTIAL RELATIONS BETWEEN THE ASTACINS, ADAMALYSINS, SERRALYSINS, AND MATRIXINS (COLLAGENASES) DEFINE A SUPERFAMILY OF ZINC-PEPTIDASES** *PROTEIN SCIENCE*
  STOCKER, W., Grams, F., Baumann, U., Reinemer, P., GOMISRUTH, F. X., McKay, D. B., Bode, W.
  1995; 4 (5): 823-840

- **HOW POTASSIUM AFFECTS THE ACTIVITY OF THE MOLECULAR CHAPERONE HSC70 .2. POTASSIUM BINDS SPECIFICALLY IN THE ATPASE ACTIVE-SITE** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Wilbanks, S. M., McKay, D. B.
  1995; 270 (5): 2251-2257

- **HOW POTASSIUM AFFECTS THE ACTIVITY OF THE MOLECULAR CHAPERONE HSC70 .1. POTASSIUM IS REQUIRED FOR OPTIMAL ATPASE ACTIVITY** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  OBRIEN, M. C., McKay, D. B.
  1995; 270 (5): 2247-2250

- **ATPASE KINETICS OF RECOMBINANT BOVINE 70 KDA HEAT-SHOCK COGNATE PROTEIN AND ITS AMINO-TERMINAL ATPASE DOMAIN** *BIOCHEMISTRY*
  Ha, J. H., McKay, D. B.
  1994; 33 (48): 14625-14635

- **MODEL FOR AN RNA TERTIARY INTERACTION FRONT THE STRUCTURE OF AN INTERMOLECULAR COMPLEX BETWEEN A GAAA TETRALOOP AND AN RNA HELIX** *NATURE*
  PLEY, H. W., Flaherty, K. M., McKay, D. B.
  1994; 372 (6501): 111-113

- **3-DIMENSIONAL STRUCTURE OF A HAMMERHEAD RIBOZYME** *NATURE*
  PLEY, H. W., Flaherty, K. M., McKay, D. B.
  1994; 372 (6501): 68-74

- **STRUCTURAL BASIS OF THE 70-KILODALTON HEAT-SHOCK COGNATE PROTEIN ATP HYDROLYTIC ACTIVITY .2. STRUCTURE OF THE ACTIVE-SITE WITH ADP OR ATP BOUND TO WILD-TYPE AND MUTANT ATPASE FRAGMENT** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Flaherty, K. M., Wilbanks, S. M., DELUCAFLAHERTY, C., McKay, D. B.
  1994; 269 (17): 12899-12907

- **STRUCTURAL BASIS OF THE 70-KILODALTON HEAT-SHOCK COGNATE PROTEIN ATP HYDROLYTIC ACTIVITY .1. KINETIC ANALYSES OF ACTIVE-SITE MUTANTS** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Wilbanks, S. M., DELUCAFLAHERTY, C., McKay, D. B.
  1994; 269 (17): 12893-12898

- **DEFINITION AND SPATIAL LOCATION OF MOUSE INTERLEUKIN-2 RESIDUES THAT INTERACT WITH ITS HETEROTRIMERIC RECEPTOR** *EMBO JOURNAL*
  Zurawski, S. M., Vega, F., Doyle, E. L., Huyghe, B., Flaherty, K., McKay, D. B., Zurawski, G.
  1993; 12 (13): 5113-5119

- **3-DIMENSIONAL STRUCTURE OF RECOVERIN, A CALCIUM SENSOR IN VISION** *CELL*
  Flaherty, K. M., Zozulya, S., Stryer, L., McKay, D. B.
  1993; 75 (4): 709-716

- **THREONINE-204 OF THE CHAPERONE PROTEIN HSC70 INFLUENCES THE STRUCTURE OF THE ACTIVE-SITE, BUT IS NOT ESSENTIAL FOR ATP HYDROLYSIS** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  OBRIEN, M. C., McKay, D. B.
  1993; 268 (32): 24323-24329

- **CRYSTALS OF A HAMMERHEAD RIBOZYME** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  PLEY, H. W., LINDES, D. S., DELUCAFLAHERTY, C., McKay, D. B.
  1993; 268 (26): 19656-19658

- **3-DIMENSIONAL STRUCTURE OF THE ALKALINE PROTEASE OF PSEUDOMONAS-AERUGINOSA - A 2-DOMAIN PROTEIN WITH A CALCIUM-BINDING PARALLEL-BETA ROLL MOTIF** *EMBO JOURNAL*
  Baumann, U., Wu, S., Flaherty, K. M., McKay, D. B.
  1993; 12 (9): 3357-3364

- **STRUCTURE AND MECHANISM OF 70-KDA HEAT-SHOCK-RELATED PROTEINS** *ADVANCES IN PROTEIN CHEMISTRY, VOL 44*
  McKay, D. B.
  1993; 44: 67-98

- **STRUCTURAL COMPARISON SUGGESTS THAT THERMOLYSIN AND RELATED NEUTRAL PROTEASES UNDERGO HINGE-BENDING MOTION DURING CATALYSIS** *BIOCHEMISTRY*
  Holland, D. R., Tronrud, D. E., PLEY, H. W., Flaherty, K. M., Stark, W., Jansonius, J. N., McKay, D. B., Matthews, B. W.
  1992; 31 (46): 11310-11316

- **CLONING, EXPRESSION, AND CRYSTALLIZATION OF RECOVERIN, A CALCIUM SENSOR IN VISION** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Ray, S., Zozulya, S., Niemi, G. A., Flaherty, K. M., BROLLEY, D., Dizhoor, A. M., McKay, D. B., Hurley, J., Stryer, L.
  1992; 89 (13): 5705-5709

- **Crystallographic structures of the elastase of Pseudomonas aeruginosa.** *Matrix (Stuttgart, Germany). Supplement*
  McKay, D. B., Thayer, M. M., Flaherty, K. M., Pley, H., BENVEGNU, D.
  1992; 1: 112-115

- **SIMILARITY OF THE 3-DIMENSIONAL STRUCTURES OF ACTIN AND THE ATPASE FRAGMENT OF A 70-KDA HEAT-SHOCK COGNATE PROTEIN** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Flaherty, K. M., McKay, D. B., Kabsch, W., Holmes, K. C.
  1991; 88 (11): 5041-5045

- **3-DIMENSIONAL STRUCTURE OF THE ELASTASE OF PSEUDOMONAS-AERUGINOSA AT 1.5-A RESOLUTION** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Thayer, M. M., Flaherty, K. M., McKay, D. B.
  1991; 266 (5): 2864-2871

- **STRUCTURE OF THE 70-KILODALTON HEAT-SHOCK-RELATED PROTEINS** *SPRINGER SEMINARS IN IMMUNOPATHOLOGY*
  McKay, D. B.
  1991; 13 (1): 1-9

- **NUCLEOTIDE-SEQUENCE OF THE CDNA OF A BOVINE-70 KILODALTON HEAT-SHOCK COGNATE PROTEIN** *NUCLEIC ACIDS RESEARCH*
  DELUCAFLAHERTY, C., McKay, D. B.
  1990; 18 (18): 5569-5569

- **UNCOATING PROTEIN (HSC70) BINDS A CONFORMATIONALLY LABILE DOMAIN OF CLATHRIN LIGHT CHAIN LCA TO STIMULATE ATP HYDROLYSIS** *CELL*
  DELUCAFLAHERTY, C., McKay, D. B., Parham, P., Hill, B. L.
  1990; 62 (5): 875-887

- **3-DIMENSIONAL STRUCTURE OF THE ATPASE FRAGMENT OF A 70K HEAT-SHOCK COGNATE PROTEIN** *NATURE*
  Flaherty, K. M., DELUCAFLAHERTY, C., McKay, D. B.
  1990; 346 (6285): 623-628

- **STRUCTURE OF EXOTOXIN-A OF PSEUDOMONAS-AERUGINOSA AT 3.0-ANGSTROM RESOLUTION** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  ALLURED, V. S., Collier, R. J., Carroll, S. F., McKay, D. B.
  1986; 83 (5): 1320-1324

- **X-RAY GRADE CRYSTALS OF DIPHTHERIA-TOXIN** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Collier, R. J., Westbrook, E. M., McKay, D. B., Eisenberg, D.
  1982; 257 (9): 5283-5285