

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*
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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.
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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.
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- **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.
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- **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*
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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.
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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*
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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*
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- **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.
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- **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 HslUV protease-chaperone complex** *CELL*
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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*
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- **Mapping the role of active site residues for transducing an ATP-induced conformational change in the bovine 70-kDa heat shock cognate protein** *BIOCHEMISTRY*
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- **Lysine 71 of the chaperone protein Hsc70 is essential for ATP hydrolysis** *JOURNAL OF BIOLOGICAL CHEMISTRY*
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- **THE METZINCINS - TOPOLOGICAL AND SEQUENTIAL RELATIONS BETWEEN THE ASTACINS, ADAMALYSINS, SERRALYSINS, AND MATRIXINS (COLLAGENASES) DEFINE A SUPERFAMILY OF ZINC-PEPTIDASES** *PROTEIN SCIENCE*
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- **MODEL FOR AN RNA TERTIARY INTERACTION FRONT THE STRUCTURE OF AN INTERMOLECULAR COMPLEX BETWEEN A GAAA TETRALOOP AND AN RNA HELIX** *NATURE*
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- **3-DIMENSIONAL STRUCTURE OF RECOVERIN, A CALCIUM SENSOR IN VISION** *CELL*
Flaherty, K. M., Zozulya, S., Stryer, L., McKay, D. B.
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- **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*
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- **CRYSTALS OF A HAMMERHEAD RIBOZYME** *JOURNAL OF BIOLOGICAL CHEMISTRY*
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Baumann, U., Wu, S., Flaherty, K. M., McKay, D. B.
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- **STRUCTURE AND MECHANISM OF 70-KDA HEAT-SHOCK-RELATED PROTEINS** *ADVANCES IN PROTEIN CHEMISTRY, VOL 44*
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