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EDUCATION

- **1975-1979 Ph.D. Major - Chemistry** X-ray structure analysis of anti-cancer drugs, nucleic acid-metal complexes and caged hydrocarbons. Software development for small molecule crystallography. The Flinders University, South Australia.
- **1974 B.Sc.(Hon.) Major - Chemistry** X-ray structure analysis of drugs in the treatment of diabetes mellitus. The Flinders University, South Australia.
- **1971-1973 B.Sc. Major - Chemistry** The Flinders University, South Australia.

ACADEMIC EXPERIENCE

- **2001- Professor** Dept. of Pharmacology, University of California, San Diego
- **2001-2004 Director** Integrated Biosciences Program, San Diego Supercomputer Center, San Diego.
- **1998- Co-Director** Protein Data Bank, University of California, San Diego
- **2000- Adjunct Professor** The Keck Graduate Institute, Claremont.
- **1997- Adjunct Professor** The Burnham Institute, San Diego.
- **1998-2001 Senior Principal Scientist** San Diego Supercomputer Center, San Diego.
- **2000 Professor in Residence** Dept. of Pharmacology, University of California, San Diego.
- **1996-2000 Adjunct Associate Professor** Dept. of Pharmacology, University of California, San Diego.
- **1995-1998 Senior Staff Scientist** San Diego Supercomputer Center, San Diego.
- **1994-1995 Senior Research Scientist** Dept. of Biochemistry & Molecular Biophysics, Columbia University, New York.
- **1987-1995 Senior Associate** Howard Hughes Medical Institute, Columbia University, New York.
- **1987-1994 Research Scientist** Dept. of Biochemistry & Molecular Biophysics, Columbia University, New York.
- **1985-1986 Director, Basic Science Information Systems** Health Sciences Administration, Columbia Presbyterian Medical Center, New York.
- **1984-1986 Director, Health Sciences Computer Facility** Columbia University, New York.
- **1982-1986 Director, Cancer Center Computing Facility.** Dept. of Biochemistry & Molecular Biophysics, Columbia University, New York.
- **1981-1982 Senior Research Associate.** Dept. of Biochemistry & Molecular Biophysics, Columbia University, New York.
- **1981 Visiting Scientist.** Dept. of Chemistry, Adelaide University, South Australia.
- **1979-1981 Post-Doctoral Fellow** Dept. of Biochemistry, Sheffield University, U.K.

TEACHING EXPERIENCE (General Areas)

- **1974-** Biochemistry; structural biology; physical and inorganic chemistry; bioinformatics, computational biology, pharmaceutical sciences, operating system design; network design; high-level languages; expert systems; database design; object-oriented programming; real-time graphics; scientific programming; hardware architectures; system management; network management;.

COMMERCIAL EXPERIENCE

- **2007 Co-Founder** SciVee Inc.
- **2004 Co-Founder** FilmFrontiers Inc.
- **2001 Co-Founder** Protein Vision Inc.
- **2000 Consultant** Structural GenomiX Inc. San Diego CA.
- **1991- Founder** Visionary software development and consulting services. ViSoft Inc., New York NY.

PROFESSIONAL ACTIVITIES - CURRENT

- **2009 - Advisory Board**, Interpro
- **2006- Advisory Board**, Crossref
- **2006- Advisory Board**, EcoCyc
- **2005-** Advisory Board PharmGKB
- **2004- Editor in Chief** and Founder PLoS Computational Biology
- **2004-2008 Editor** IEEE Trends in Computational Biology and Bioinformatics
- **2003-2007 Editor** Proteins: Structure, Function and Bioinformatics
- **2003-2005 Associate Editor** Bioinformatics
- **2003-2008 Consulting Editor** BioSilico
- **2002-** Advisory Board NCRR Resource RVBI at UCSF
- **2002-** Elected Fellow of the American Medical Informatics Association
- **2002-2003 President** International Society for Computational Biology
- **2001- Advisory Board** Biopolymers
- **2000-2003 Editor** Bioinformatics.
- **2000-2001 Secretary** International Society for Computational Biology.
- **1999- Advisory Board** – Herbert Irving Comprehensive Cancer Center, Columbia University.
- **1999-2002 Representative** to the American Association for the Advancement of Science on behalf of the American Crystallography Association.
- **1997- Editor** - Web Alert, Current Opinions in Structural Biology.
- **1996- Member** - Review Panel - NSF Database Activities Program.
- **1991- Member** - Macromolecular CIF Working Group - International Union of Crystallography.

UNIVERSITY COMMITTEES – CURRENT

- **2009- Chair** UCSD Library Committee
- **2009- Co-Chair** Committee on UCSD-Industry Relations
- **2003- Chair** Second Year Bioinformatics Program Qualifying Exam Committee.
- **2001- Member** Pharmacy School Planning Committee.
- **2000- Member** Bioinformatics Graduate Student Program Steering Committee.
- **2000- Member** Ad hoc Promotions Committee, San Diego Supercomputer Center.

PROFESSIONAL AND OTHER ACTIVITIES – PAST

- **2000-2008 Member** MD/PhD Admissions Committee.
- **1997-1999 Chairman** - American Crystallography Association Computing and Data Committee.
- **1997-1999 Chairman** - American Crystallography Association Computing and Data Committee.
- **1996-1999 Chairman** - International Union of Crystallography Computing Commission.
- **1994 Consultant** - Smith Kline Beecham Pharmaceuticals.
- **1991-1993 Consultant** - Ontario Hydro, Canada.
- **1990 Consultant** - European Database Bridge Project, Belgium.
- **1988-1997 Editor** - *Digital Age Magazine* (formally *The DEC Professional*).
- **1979-1981 Member** - Collaborative Computational Project for Protein Crystallography, Science Research Council, UK.

AWARDS

- **2009** Benjamin Franklin Award.
- **2005** Editors Choice Award, Science Magazine.
- **2004** Convocation Medal, Flinders University of South Australia.
- **2002** Elected Fellow Medical Informatics Association.
- **2002** Convergence Award from Sun Microsystems Inc.
- **2001** Second most cited paper in biology for 2000 according to Science Watch®.
- **1997** UCSD Connect Award for New Inventions.
- **1996** UCSD Connect Award for New Inventions.
- **1982** National Institutes of Health, Senior Research Scientist.
- **1981** ARGC Visiting Fellowship, Australia.
- **1979** Science Research Council, Post-doctoral Research Fellowship, UK.
- **1974** Commonwealth Postgraduate Research Award, Australia.

MEMBERSHIP OF SOCIETIES

- American Association for the Advancement of Science.
- American Medical Informatics Association.
- IEEE.
- International Society for Computational Biology.
- American Crystallography Association.
- Biophysical Society.
- Protein Society.

PUBLICATIONS – Peer Reviewed Research Articles

1. G.A.Clegg, R.F.D.Stansfield, P.E.Bourne & P.M.Harrison, *Biochemical Society Transactions* (1980) 8(5), 654-655. The Structure and Heavy Metal Ion Binding Sites of Horse Spleen Apoferritin.
2. G.A.Clegg, R.F.D.Stansfield, P.E.Bourne & P.M.Harrison, *Nature* (1980) 288, 298-300. Helix Packing and Subunit Conformation in Horse Spleen Apoferritin.
3. J.R.Helliwell, A.Achari, A.C.Bloomer, P.E.Bourne, P.Carr, G.A.Clegg, R.Cooper et al., *Acta Cryst.* (1981) A37Sup., C311. Protein Crystal Oscillation Film Data Processing: A Comparative Study.
4. D.Akrigg, T.N.Bhat, P.E.Bourne, J.Campbell, M.Elder, P.R.Evans, J.R. Helliwell *et al.*, *Acta Cryst.* (1981) A37Sup., C8. The Collaborative Computational Project for Protein Crystallography.

5. P.E.Bourne, G.A.Clegg, P.M.Harrison, J.M.A.Smith & R.F.D.Stansfield, *Acta Cryst.* (1981) A37Sup., C26. Inter-Subunit Interactions and Metal Binding Sites in Horse Spleen Apoferritin.
6. P.E.Bourne, G.A.Clegg, P.M.Harrison, J.M.A.Smith & R.F.D.Stansfield, *Acta Cryst.* (1981) A37Sup., C14. X-ray Crystallographic Analysis of Horse Spleen Apoferritin.
7. P.E.Bourne & M.R.Taylor, *Acta Cryst.* (1982) B36, 2143-2145. The Structure of Aqua[3-ethoxy-2-oxobutyraldehyde bis(thiosemicarbazonato)]zinc(II).
8. P.E.Bourne & M.R.Taylor, *Acta Cryst.* (1983) C39, 430-432. Dicytosinium Tetrachlorozincate.
9. P.E.Bourne & M.R.Taylor, *Acta Cryst.* (1983) C39, 266-268. 3-Thioxo-2-pyridinecarboxylic Acid C₆H₅NO₂S. Redetermination of the Structure.
10. P.E.Bourne, S.Ginell, B.W.Low & L.Lessinger, *Acta Cryst.* (1984) A40 Sup, C83. Caracurine-II Dimethochloride Octahydrate, A Potent Neuromuscular Blocking Agent.
11. P.E.Bourne, S.Ginell, B.W.Low & L.Lessinger, *J. Cryst. & Spec. Res.* (1985) 15, 453-471. The Structure of a Potent Neuromuscular Blocking Agent: Caracurine-II Dimethochloride Octahydrate.
12. P.E.Bourne, A.Sato, P.W.R.Corfield, L.S.Rosen, S.Birken & B.W.Low, *Eur. J. Biochem.* (1985) 153, 521-527. Erabutoxin b: Initial Protein Refinement and Sequence Analysis at 0.140-nm Resolution.
13. P.E.Bourne & N.Desai, *Comp. Methods & Programs in Biomed.* (1987) 24, 27-38. PRONUC: A Software Package for the Analysis of Protein and Nucleic Acid Sequences.
14. P.E.Bourne, *Acta Cryst. Supp.* (1987) A43, C292. Desktop Crystallography - The Next Generation of Computers.
15. P.E.Bourne & W.A.Hendrickson, *Comput. Biol. Med.* (1988) 18, 341-349. Selecting a Processor for Computations in Molecular Biophysics.
16. P.E.Bourne & W.A.Hendrickson, *Comput. Biol. Med.* (1990) 20(4), 219-230. A CPU Benchmark for Protein Crystallographic Refinement.
17. P.E.Bourne, P.L.Marquess, & W.A.Hendrickson, *Acta Cryst. Supp.* (1991) A46, C34-C3. The Crystallographic Workbench.
18. W.Chang, I.N.Shindyalov, C.Pu, & P.E.Bourne, *CABIOS*(1994) 10(6), 575-586. Design and Application of PDBlib, a C++ Macromolecular Class Library.
19. P.Zhang, E.A.Schon, S.G.Fischer, E. Cayanis, J. Weiss, S. Kistler & P.E.Bourne, *CABIOS* (1994) 10(3), 309-317. An Algorithm Based on Graph Theory for the Assembly of Contigs in the Physical Mapping of DNA.
20. W.Chang, I.N.Shindyalov, C.Pu, & P.E.Bourne, *Proceedings of the Second International Conference on Intelligent Systems in Molecular Biology* (1994) 70-77. Design and Application of a C++ Macromolecular Class Library.
21. I.N.Shindyalov, W.Chang, C. Pu, & P.E.Bourne *Protein Engineering* (1994) 7(11), 1311-1322. MMQL An Object Oriented Macromolecular Query Language: Prototype Data Model and Implementation.
22. I.N.Shindyalov, J.Cooper, W.Chang & P.E.Bourne *Proceedings of the 28th Annual Hawaii International Conference on System Sciences* (1995), 207-217 IEEE Computer Society Press. Design and Use of a Software Framework to Obtain Information Derived from Macromolecular Structure Data.
23. I.N.Shindyalov & P.E.Bourne *J. App. Cryst.* (1995), 28(6) 847-852. WPDB – PC windows-based Interrogation of Macromolecular Structure.
24. J.Biggs, C.Pu, A Groeniger & P.E.Bourne *J. App. Cryst.* (1996), 29(4) 484-490. PDBtool: An Interactive Browser and Geometry Checker for Protein Structures
25. P.E.Bourne & I.N. Shindyalov *Acta Cryst. Sup.* (1996), C78 C-78. A Local Macromolecular Structure Database for Crystallography Laboratories.
26. Ponomarenko, I.N.Shindyalov & P.E.Bourne *Proceedings of the International Summer School on Crystallographic Computing* (1996) P.E.Bourne & K.Watenpaugh, (Eds.), Fast Substructure Searching Using the Conformational Likeness Method.

27. P.E.Bourne, H.M.Berman, B. McMahon, K. Watenpaugh, J. Westbrook & P.M.D. Fitzgerald. *Methods in Enzymology*. (1997) 277, 571-590. The Macromolecular CIF Dictionary (mmCIF).
28. P.E. Bourne, I.N. Shindyalov, J. Moreland G. Johnson, M. Gribskov *FASEB J*. (1997) 11(9) 1564. New Developments in Internet Technology Important to Biochemistry and Molecular Biology.
29. I.N.Shindyalov and P.E. Bourne *CABIOS* (1997) 13, 487-496. Protein Data Representation and Query Using Optimized Data Decomposition.
30. J. Biggs, C. Pu, and P.E. Bourne *Fifth International Conference on Intelligent Systems for Molecular Biology* Ed. T. Gaasterland et al. 1997, 52-55. AAAI Press. Code Generation Through Annotation of Macromolecular
31. C. Smith, M. Gribskov, I.N. Shindyalov, S.S Taylor, L. Ten Eyck, S. Veretnik, P.E.Bourne *TIBS* 1997 22(11) 444-446. The Protein Kinase Resource (PKR).
32. I.N. Shindyalov and P.E. Bourne *Protein Engineering* 1998, 11(9) 739-747. Protein Structure Alignment by Incremental Combinatorial Extension of the Optimum Path.
33. P.E.Bourne and I.N. Shindyalov 1998 *Proceedings of ACHE-98*. Ed. D.P. Doctor, D.M. Quinn, R.L. Rotundo, and P. Taylor. A Database of Pairwise Aligned 3-D Structures for the Acetylcholinesterases, Lipases and Other Homologous Proteins p 455-460. Plenum Press NY.
34. H. Weissig, I.N. Shindyalov, and P.E. Bourne *Acta Cryst* 1998 D54 1085-1094. Macromolecular Structure Databases: Past Progress and Future Challenges.
35. P.E. Bourne, M. Gribskov, G. Johnson, J. Moreland, and H. Weissig *Pacific Symposium on Biocomputing* 1998 Ed. R Altman, K. Dunker, L.Hunter, and T. Klein pp.118-129. A Prototype Molecular Interactive Collaborative Environment (MICE).
36. W. Chang and P.E. Bourne *J. App. Cryst.* 1998 31, 505 - 509. CIF Applications: A New Approach for Representing and Manipulating STAR Files.
37. H.J. Bernstein, F.C. Bernstein, and P.E. Bourne *J. App. Cryst.* 1998, 31, 282 - 295. CIF Applications. pdb2cif: Translating PDB Entries into mmCIF Format.
38. M.P. Ponomarenko, I.N. Shindyalov, P.E. Bourne, and N.A. Kolchanov LIKENESS: a real-time system for searching and aligning protein spatial structures. *Biofizika*. 1999. V. 44. N. 5. pp. 821-831 (Russ).
39. P.E.Bourne *Bioinformatics* 15(9) 715-716. Editorial
40. J.G. Tate, J. Moreland and P.E. Bourne *J. App. Cryst.* 32, 1026-1027. MSG (Molecular Scene Generator): A Web-based Application for the Visualization of Macromolecular Structures.
41. G. Quinn, A. Taylor, H-P Wang and P.E. Bourne 1999 *TIBS* 24 321-324. Development of Internet-based Multimedia Applications.
42. H. Weissig, and P.E. Bourne 1999 *Bioinformatics* 15(10) 807-831. An Analysis of the Protein Data Bank in Search of Temporal and Global Trends.
43. G. Quinn, H-P. Wang, D. Martinez, P.E.Bourne 1999 *Pacific Symposium on Biocomputing* Developing Protein Documentaries and other Multimedia Presentations for Molecular Biology. Ed. R Altman, K. Dunker, L.Hunter, T. Klein, and K. Lauderdale pp. 380-391.
44. H.M. Berman, J. Westbrook, Z. Feng, G. Gilliland, T.N. Bhat, H. Weissig, I.N. Shindyalov, and P.E. Bourne 2000 *Nucleic Acid Research* 28(1), 235-242. The Protein Data Bank.
45. I. Tsigelny, I. N. Shindyalov, P. E. Bourne, T. Südhof and P. Taylor *Protein Science* 2000 9(1) 180-185 Common EF-hand Motifs in Cholinesterases and Neuroligins Suggest a Role for CA²⁺ Binding in Cell Surface Associations.
46. J.D. Westbrook and P.E. Bourne *Bioinformatics* 2000 16(2) 159-168. STAR/mmCIF: An Ontology for Macromolecular Structure and Beyond.
47. P.E. Bourne and Michael Gribskov 2000 *Bioinformatics* Editorial 16 749. ISMB2000: Bioinformatics Enters a New Millennium.

48. H.M. Berman, T.N. Bhat, P.E. Bourne, G. Gilliland, H. Weissig, and J. Westbrook 2000 *Nature Structure Biology*, 7sup. 957-959. The Protein Data Bank and the Challenge of Structural Genomics.
49. P.E. Bourne 2000 *Trends in Biotechnology* 2000 18(6), 228-230. Bioinformatics Meets Data Mining, Time to Dance? A Report of the Data Mining Conference held at the EBI from Nov. 10-12, 1999.
50. I.N. Shindyalov and P.E. Bourne 2000 *Proteins: Structure, Function and Genetics* 38(3), 247-260. An Alternative View of Protein Fold Space.
51. B.V.B Reddy, W. Li, I.N. Shindyalov, and P.E. Bourne 2001 *Proteins: Structure, Function and Genetics* 42(2) 148-163. Conserved key amino acid positions (CKAAPs) derived from the analysis of common substructures in proteins.
52. W.W.Li, B.V.B. Reddy, I.N. Shindyalov and P.E. Bourne 2001 *Nucleic Acids Research*, 29(1) 329-331. CKAAPs DB: A Conserved Key Amino Acid Position Database.
53. I.N. Shindyalov and P.E. Bourne 2001 *Nucleic Acids Research*, 29(1) 228-229. A Database and Tools for 3-D Protein Structure Comparison and Alignment Using the Combinatorial Extension (CE) algorithm.
54. H.M. Berman, T.N. Bhat, P.E. Bourne, G. Gilliland, H. Weissig, and J. Westbrook 2001 *Nucleic Acids Research*, 29(1) 214-218, The PDB Uniformity Project.
55. C. Guda, E.D. Scheeff, P.E. Bourne and I.N. Shindyalov 2001 *Pacific Symposium on Biocomputing* 6: 275-286. A New Algorithm for Alignment of Multiple Protein Structures Using Monte Carlo Optimization.
56. J.G. Tate, J. Moreland, and P.E. Bourne 2001 *J. Mol. Graphics* 19 280-287. Design and Implementation of a Collaborative Molecular Graphics Environment.
57. H.M. Berman, J. Westbrook, Z. Feng, G. Gilliland, T.N. Bhat, H. Weissig, I.N. Shindyalov, and P.E. Bourne 2001 *International Tables Chapter 24 Crystallographic Databases* 675-681. The Protein Data Bank.
58. I.N. Shindyalov and P.E. Bourne 2001 The 2001 International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences (METMBS'2001). Protein Sequence-Structure Space and Data Redundancy in The Protein Data Bank 139-145.
59. A. Kuller, W. Fleri, W.F. Bluhm, J.L. Smith, J. Westbrook and P.E. Bourne 2001. Announcement of the BioSync Web Site. *Nature Structure Biology* 8(8) 663.
60. H.M. Berman, T. Battistuz, T.N. Bhat, W.F. Bluhm, P.E. Bourne, K. Burkhardt, Z. Feng, G.L. Gilliland, L. Iype, S. Jain, P. Fagan, J. Marvin, V. Ravichandran, B. Schneider, N. Thanki, D. Padilla, H. Weissig, J.D. Westbrook, C. Zardecki 2002 The Protein Data Bank *Acta Cryst. D* 58, 899-907.
61. A. Kuller, W. Fleri, W.F. Bluhm, J.L. Smith, J. Westbrook and P.E. Bourne 2001. BioSync: A Biologist's Guide to Synchrotron Resources *TIBS* 27(4):213-215
62. H.M. Berman, D. Goodsell and P.E. Bourne 2002 Proteins Structures: From Famine to Feast *American Scientist* 90: 350-359.

63. J. Westbrook, Z.Feng, S. Jain, T.N.Bhat, N. Thanki, V.Ravichandran, G.L.Gilliland, W.Bluhm, H. Weissig, D.S.Greer, P.E.Bourne, and H.M.Berman 2002 The Protein Data Bank: Unifying the Archive. *Nucleic Acids Research*, 30:245-248.
64. W. Li, BVB Reddy, J. Tate, IN Shindyalov and P.E.Bourne 2002 CKAAPs DB: A Conserved Key Amino Acid Positions Database. *Nucleic Acids Research* 30: 409-411.
65. BVB Reddy, W. Li, and P.E.Bourne 2002 Conserved Key Amino Acid Positions Used to Morph Protein Folds. *Biopolymers* 64(3):139-145.
66. H.Weissig and P.E. Bourne 2002 Protein Structure Resources *Acta Cryst. D* 58(6) 908-915.
67. P.E. Bourne 2002 Science's Policy on Data Deposition. *Science* 296, 1609.
68. DS. Greer, JD. Westbrook and PE. Bourne 2002 An Ontology Driven Architecture for Derived Representations of Macromolecular Structure *Bioinformatics* 18:1280-1281.
69. P Craig, P Yang and PE Bourne 2002 BioEditor A Tool for Structure Annotation *FASEB J* 16 (5): A741-A742.
70. J.V. Ponaramenko, I.N. Shindyalov and P.E. Bourne 2002 Building an Automated Classification of DNA-binding Protein Domains *Bioinformatics* 18:S192-201.
71. P.E.Bourne 2003 Free access to publicly funded databases is vital *Nature* 421, 786.
72. P. Yang, P.A. Craig, D. Goodsell and P.E. Bourne 2002 BioEditor - Simplifying Macromolecular Structure Annotation *Bioinformatics*. 19(7) 897-898.
73. K.S. Doctor, J. Reed, A. Godzik and P.E. Bourne 2002 The Apoptosis Database *Cell Death and Differentiation* 10(6), 621-633.
74. P.E. Bourne 2003 The Status of Structural Genomics *Targets* 2(5) 1181-1182 (Editorial).
75. W.G Krebs and P.E. Bourne 2003 Statistical and Visual Morph Movie Analysis of Crystallographic Mutant Selection Bias in Protein Mutation Resource Data. *Proceedings of the 2003 IEEE Computer Society Bioinformatics Conference Proceedings* 180-189.
76. P.M.D. Fitzgerald, J. Westbrook, P.E. Bourne, B. McMahon, K.D. Watenpugh, and H.M. Berman 2003 The Macromolecular Crystallographic Information File (mmCIF) *The International Tables for X-ray Crystallography* Volume G.
77. W.W. Li, G.B. Quinn, N. N. Alexandrov, P.E. Bourne and I.N. Shindyalov 2003 Proteins of *Arabidopsis thaliana* (PAT) database: A resource for comparative proteomics *Genome Biology* 4(8), R51.
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79. W.G Krebs and P.E. Bourne 2004 Statistical and Visual Morph Movie Analysis of Crystallographic Mutant Selection Bias in Protein Mutation Resource Data. *J. Bioinformatics and Computational Biology*, 2(1) 61-75.
80. C. Guda, S. Lu, E.D. Scheeff, P.E. Bourne and I.N. Shindyalov 2004 CE-MC: A multiple protein structure alignment server. *Nucleic Acids Research*, 32 W100-W103.
81. S. Verentik, P.E. Bourne, N.N. Alexandrov, I.N. Shindyalov 2004. Towards consistent assignment of structural domains in proteins. *Journal of Molecular Biology*, 339(3), 647-678.

82. D. Pekurovsky, I.N. Shindyalov, P.E. Bourne 2004 High Throughput Biological Data Processing on Massively Parallel Computers. A Case Study of Pairwise Structure Comparison and Alignment Using the Combinatorial Extension (CE) Algorithm. *Bioinformatics*, 20(12) 1940-1947.
83. P.E. Bourne, J. Westbrook and H.M. Berman 2004. The Protein Data Bank and Lessons Learned in Data Management. *Briefings in Bioinformatics*. 5(1), 23-30.
84. W.G. Krebs and P.E. Bourne 2004 Statistically Rigorous Automated Protein Annotation *Bioinformatics* 10(7) 1066-1073.
85. H.M. Berman, P.E. Bourne and J. Westbrook 2004 The Protein Data Bank: A Case Study in the Management of Community Data. *Current Proteomics* 1, 49-57.
86. P.E. Bourne, K.J. Address, W.F. Bluhm, L. Chen, N. Deshpande, Z. Feng³, R. Kramer Green, J. C. Merino-Ott, W. Townsend-Merino, H. Weissig, J. Westbrook, H. M. Berman 2004. The Distribution and Query Systems of the RCSB Protein Data Bank *Nucleic Acids Research*, 32, D223-225.
87. P.E. Bourne, C.K.J. Allerston, W. Krebs, W. Li, I.N Shindyalov, A. Godzik, I. Friedberg, T. Liu, D. Wild, S. Hwang, Z. Ghahramani L. Chen, and J. Westbrook 2004. The Status of Structural Genomics through the analysis of current targets and structures. 2004 *Pacific Symposium on Biocomputing* 404-416.
88. B. Peters, J. Sidney, P.E. Bourne, H-H Bui, S. Buus, G. Doh, W. Fleri, M. Kronenberg, R. Kubo, O. Lund, D. Nemazee, J.V. Ponomarenko, M. Sathiamurthy, S. Schoenberger, S. Stewart, P. Surko, S. Way, S. Wilson, A. Sette 2005 The Immune Epitope Database and Analysis Resource: From Vision to Blueprint. *PLoS Biology*, 3(3) e91.
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92. J.V. Ponomarenko, P.E. Bourne and I.N. Shindyalov 2005 Assigning New GO Annotations to Protein Data Bank Sequences by Structural Homology *Proteins: Structure, Function and Bioinformatics* 58: 855-865.
93. S. Yang, R.F. Doolittle and P.E. Bourne 2005 Phylogeny Determined through Protein Domain Content *Proc. Nat. Acad. Sci. (USA)* 102(2): 373-378.
94. N. Deshpande, K.J. Address, W.F. Bluhm, J.C. Merino-Ott, W. Townsend-Merino, Q. Zhang, C. Knezevich, L. Chen, Z. Feng, R. Kramer Green, J.L. Flippen-Anderson, J. Westbrook, H.M. Berman and P.E. Bourne 2005 The RCSB Protein Data Bank: A Redesigned Query System and Relational Database Based on the mmCIF Schema *Nucleic Acids Research*. 33: D233-D237.
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