

---

# References

---

1. **Lowe S. W., Cepero E. & Evan G. (2004).** Intrinsic tumour suppression. *Nature* **432** (7015), 307-315. Review.
2. **Kastan M.B. & Bartek J. (2004).** Cell-cycle checkpoints and cancer. *Nature* **432** (7015), 316-323. Review.
3. **Campisi J. (2001).** Cellular senescence as a tumor-suppressor mechanism. *Trends Cell Biol.* **11** (11), S27-31. Review.
4. **Raff M. C. (1992).** Social controls on cell survival and cell death. *Nature* **356** (6368), 397-400. Review.
5. **Vogelstein B., Lane D. & Levine A. J. (2000).** Surfing the p53 network. *Nature* **408** (6810), 307-310.
6. **Kinzler K. W. & Vogelstein B. (1997).** Cancer-susceptibility genes. Gatekeepers and caretakers. *Nature* **386** (6627), 761, 763.
7. **Vogelstein B. & Kinzler K. W. (2004).** Cancer genes and the pathways they control. *Nat. Med.* **10** (8), 789-799. Review.
8. **Zhou B. B. & Elledge S. J. (2000).** The DNA damage response: putting checkpoints in perspective. *Nature* **408** (6811), 433-439. Review.
9. **Rouse J. & Jackson S. P. (2002).** Interfaces between the detection, signaling, and repair of DNA damage. *Science* **297** (5581), 547-551. Review.
10. **Falck J., Coates J. & Jackson S. P. (2005).** Conserved modes of recruitment of ATM, ATR and DNA-PKcs to sites of DNA damage. *Nature* **434** (7033), 605-611.
11. **Wang Y., Cortez D., Yazdi P., Neff N., Elledge S. J. & Qin J. (2000).** BASC, a super complex of BRCA1-associated proteins involved in the recognition and repair of aberrant DNA structures. *Genes Dev.* **14** (8), 927-939.
12. **Carson C. T., Schwartz R. A., Stracker T. H., Lilley C. E., Lee D.V. & Weitzman M. D. (2003).** The Mre11 complex is required for ATM activation and the G2/M checkpoint. *EMBO J.* **22** (24), 6610-6620.

13. Dupre A., Boyer-Chatenet L. & Gautier J. (2006). Two-step activation of ATM by DNA and the Mre11-Rad50-Nbs1 complex.  
Nat. Struct. Mol. Biol. **13** (5), 451-457.
14. Trenz K., Smith E., Smith S. & Costanzo V. (2006). ATM and ATR promote Mre11 dependent restart of collapsed replication forks and prevent accumulation of DNA breaks.  
EMBO J. **25** (8), 1764-1774.
15. de Jager M., van Noort J., van Gent D. C., Dekker C., Kanaar R. & Wyman C. (2001). Human Rad50/Mre11 is a flexible complex that can tether DNA ends.  
Mol. Cell **8** (5), 1129-1135.
16. Zhang J., Willers H., Feng Z., Ghosh J. C., Kim S., Weaver D. T., Chung J. H., Powell S. N. & Xia F. (2004). Chk2 phosphorylation of BRCA1 regulates DNA double-strand break repair.  
Mol. Cell Biol. **24** (2), 708-718.
17. Xie A., Puget N., Shim I., Odate S., Jarzyna I., Bassing C. H., Alt F. W & Scully R. (2004). Control of sister chromatid recombination by histone H2AX.  
Mol. Cell **16** (6), 1017-1025.
18. Hashizume R., Fukuda M., Maeda I., Nishikawa H., Oyake D., Yabuki Y., Ogata H. & Ohta T. (2001). The RING heterodimer BRCA1-BARD1 is a ubiquitin ligase inactivated by a breast cancer-derived mutation.  
J. Biol. Chem. **276** (18), 14537-14540.
19. Brzovic P. S., Rajagopal P., Hoyt D. W., King M. C. & Klevit R. E. (2001). Structure of a BRCA1-BARD1 heterodimeric RING-RING complex.  
Nat. Struct. Biol. **8** (10), 833-7.
20. Baer R. & Ludwig T. (2002). The BRCA1/BARD1 heterodimer, a tumor suppressor complex with ubiquitin E3 ligase activity.  
Curr. Opin. Genet. Dev. **12** (1), 86-91. Review.
21. Motoyama N. & Naka K. (2004). DNA damage tumor suppressor genes and genomic instability.  
Curr. Opin. Genet. Dev. **14** (1), 11-16. Review.
22. Johnstone R. W., Ruefli A. A. & Lowe S. W. (2002). Apoptosis: a link between cancer genetics and chemotherapy.  
Cell **108** (2), 153-164. Review.
23. Sawyers C. (2004). Targeted cancer therapy.  
Nature **432** (7015), 294-297. Review.
24. Farmer H., McCabe N., Lord C. J., Tutt A. N., Johnson D. A., Richardson T. B., Santarosa M., Dillon K. J., Hickson I., Knights C., Martin N. M., Jackson S. P., Smith G. C. & Ashworth A. (2005). Targeting the DNA repair defect in BRCA mutant cells as a therapeutic strategy.  
Nature **434** (7035), 917-921.
25. Caldecott K. W. & Chalmers A. (2005). An Achilles' heel for breast cancer?  
Nat. Struct. Mol. Biol. **12** (5), 387-388.

26. **Sawyers C. L. (2005).** Calculated resistance in cancer.  
Nat. Med. **11** (8), 824-825.
27. **Caldecott K. W. (2003).** Cell signaling. The BRCT domain: signaling with friends?  
Science **302** (5645), 579-580.
28. **Lee J. H. & Paull T. T. (2004).** Direct activation of the ATM protein kinase by the Mre11/Rad50/Nbs1 complex.  
Science **304** (5667), 93-96.
29. **Lou Z., Minter-Dykhouse K., Franco S., Gostissa M., Rivera M. A., Celeste A., Manis J. P., van Deursen J., Nussenzweig A., Paull T. T., Alt F. W. & Chen J. (2006).** MDC1 maintains genomic stability by participating in the amplification of ATM-dependent DNA damage signals.  
Mol. Cell. **21** (2), 187-200.
30. **Lee J. H. & Paull T. T. (2005).** ATM activation by DNA double-strand breaks through the Mre11-Rad50-Nbs1 complex.  
Science **308** (5721), 551-554. Erratum in: Science **308** (5730), 1870.
31. **Miki Y., Swensen J., Shattuck-Eidens D., Futreal P. A., Harshman K., Tavtigian S., Liu Q., Cochran C., Bennett L. M., Ding W., et al. (1994).** A strong candidate for the breast and ovarian cancer susceptibility gene BRCA1.  
Science **266** (5182), 66-71.
32. **Bork P., Hofmann K., Bucher P., Neuwald A. F., Altschul S. F. & Koonin E. V. (1997).** A superfamily of conserved domains in DNA damage-responsive cell cycle checkpoint proteins.  
FASEB J. **11** (1), 68-76.
33. **Callebaut I. & Moron J. P. (1997).** From BRCA1 to RAP1: a widespread BRCT module closely associated with DNA repair.  
FEBS Lett. **400** (1), 25-30.
34. **Chapman M. S. & Verma I. M. (1996).** Transcriptional activation by BRCA1.  
Nature **382** (6593), 678-679.
35. **Monteiro A. N., August A. & Hanafusa H. (1996).** Evidence for a transcriptional activation function of BRCA1 C-terminal region.  
Proc. Natl. Acad. Sci. U.S.A. **93** (24), 13595-13599.
36. **Monteiro A. N., August A. & Hanafusa H. (1997).** Common BRCA1 variants and transcriptional activation.  
Am. J. Hum. Genet. **61** (3), 761-762.
37. **Venkitaraman A. R. (2002).** Cancer susceptibility and the functions of BRCA1 and BRCA2.  
Cell **108** (2), 171-182. Review.
38. **Deng C. X. (2006).** BRCA1: cell cycle checkpoint, genetic instability, DNA damage response and cancer evolution.  
Nucleic Acids Res. **34** (5), 1416-1426. Review.

39. **Planas A. (2000).** Bacterial 1,3-1,4- $\beta$ -glucanases: structure, function and protein engineering.  
Biochim. Biophys. Acta **1543** (2), 361-382. Review.
40. **Zechel D. L. & Withers S. G. (2000).** Glycosidase mechanisms: anatomy of a finely tuned catalyst.  
Acc. Chem. Res. **33** (1), 11-18.
41. **Keitel T., Simon O., Borrius R. & Heinemann U. (1993).** Molecular and active-site structure of a *Bacillus* 1,3-1,4- $\beta$ -glucanase.  
Proc. Natl. Acad. Sci. U. S. A. **90** (11), 5287-5291.
42. **Gaiser O. J., Oschkinat H., Heinemann U. & Ball L. J. (2004).**  $^1\text{H}$ ,  $^{13}\text{C}$  and  $^{15}\text{N}$  resonance assignments of the C-terminal BRCT domain from human BRCA1.  
J. Biomol. NMR **30** (2), 221-222.
43. **Gaiser O. J., Ball L. J., Schmieder P., Leitner D., Strauss H., Wahl M., Kühne R., Oschkinat H. & Heinemann U. (2004).** Solution structure, backbone dynamics, and association behavior of the C-terminal BRCT domain from the breast cancer-associated protein BRCA1.  
Biochemistry **43** (51), 15983-15995.
44. **Gaiser O. J., Piotukh K., Ponnuswamy M. N., Planas A., Borrius R. & Heinemann U. (2006).** Structural basis for the substrate specificity of a *Bacillus* 1,3-1,4- $\beta$ -glucanase.  
J. Mol. Biol. **357** (4), 1211-1225.
45. **Hubbard S. J. (1998).** The structural aspects of limited proteolysis of native proteins.  
Biochim. Biophys. Acta **1382** (2), 191-206. Review.
46. **Billeter M., Neri D., Otting G., Qian Y. Q. & Wüthrich K. (1992).** Precise vicinal coupling constants  $^3\text{J}_{\text{HN}\alpha}$  in proteins from nonlinear fits of J-modulated [ $^{15}\text{N}$ ,  $^1\text{H}$ ]-COSY experiments.  
J. Biomol. NMR **2** (3), 257-274.
47. **Herrmann T., Güntert P. & Wüthrich K. (2002).** Protein NMR structure determination with automated NOE assignment using the new software CANDID and the torsion angle dynamics algorithm DYANA.  
J. Mol. Biol. **319** (1), 209-227.
48. **Chai Y. L., Cui J., Shao N., Shyam E., Reddy P. & Rao V. N. (1999).** The second BRCT domain of BRCA1 proteins interacts with p53 and stimulates transcription from the p21<sup>WAF1/CIP1</sup> promoter.  
Oncogene **18** (1), 263-268.
49. **Zhang H., Somasundaram K., Peng Y., Tian H., Zhang H., Bi D., Weber B. L. & El-Deiry W. S. (1998).** BRCA1 physically associates with p53 and stimulates its transcriptional activity.  
Oncogene **16** (13), 1713-1721.
50. **Williams R. S., Green R. & Glover J. N. (2001).** Crystal structure of the BRCT repeat region from the breast cancer-associated protein BRCA1.  
Nat. Struct. Biol. **8** (10), 838-842.

51. Williams R. S., Chasman D. I., Hau D. D., Hui B., Lau A. Y. & Glover J. N. (2003). Detection of protein folding defects caused by BRCA1-BRCT truncation and missense mutations. *J. Biol. Chem.* **278** (52), 53007-53016.
52. Zhang X., Morera S., Bates P. A., Whitehead P. C., Coffer A. I., Hainbucher K., Nash R. A., Sternberg M. J., Lindahl T. & Freemont P. S. (1998). Structure of an XRCC1 BRCT domain: a new protein-protein interaction module. *EMBO J.* **17** (21), 6404-6411.
53. Nash R. A., Caldecott K. W., Barnes D. E. & Lindahl T. (1997). XRCC1 protein interacts with one of two distinct forms of DNA ligase III. *Biochemistry* **36** (17), 5207-5211.
54. Taylor R. M., Wickstead B., Cronin S. & Caldecott K. W. (1998). Role of a BRCT domain in the interaction of DNA ligase III- $\alpha$  with the DNA repair protein XRCC1. *Curr. Biol.* **8** (15), 877-880.
55. Krishnan V. V., Thornton K. H., Thelen M. P. & Cosman M. (2001). Solution structure and backbone dynamics of the human DNA ligase III $\alpha$  BRCT domain. *Biochemistry* **40** (44), 13158-13166.
56. El-Khamisy S. F., Masutani M., Suzuki H. & Caldecott K. W. (2003). A requirement for PARP-1 for the assembly or stability of XRCC1 nuclear foci at sites of oxidative DNA damage. *Nucleic Acids Res.* **31** (19), 5526-5533.
57. Masson M., Niedergang C., Schreiber V., Muller S., Menissier-de Murcia J. & de Murcia G. (1998). XRCC1 is specifically associated with poly(ADP-ribose) polymerase and negatively regulates its activity following DNA damage. *Mol. Cell Biol.* **18** (6), 3563-3571.
58. Beernink P. T., Hwang M., Ramirez M., Murphy M. B., Doyle S. A. & Thelen M. P. (2005). Specificity of protein interactions mediated by BRCT domains of the XRCC1 DNA repair protein. *J. Biol. Chem.* **280** (34), 30206-30213.
59. Joo W. S., Jeffrey P. D., Cantor S. B., Finnin M. S., Livingston D. M. & Pavletich N. P. (2002). Structure of the 53BP1 BRCT region bound to p53 and its comparison to the Brca1 BRCT structure. *Genes Dev.* **16** (5), 583-593.
60. Derbyshire D. J., Basu B. P., Serpell L. C., Joo W. S., Date T., Iwabuchi K. & Doherty A. J. (2002). Crystal structure of human 53BP1 BRCT domains bound to p53 tumour suppressor. *EMBO J.* **21** (14), 3863-3872. Erratum in: *EMBO J.* **21** (21), 5953.
61. Manke I. A., Lowery D. M., Nguyen A. & Yaffe M. B. (2003). BRCT repeats as phosphopeptide-binding modules involved in protein targeting. *Science* **302** (5645), 636-639.

62. Rodriguez M., Yu X., Chen J. & Songyang Z. (2003). Phosphopeptide binding specificities of BRCA1 COOH-terminal (BRCT) domains. *J. Biol. Chem.* **278** (52), 52914-52918.
63. Shiozaki E. N., Gu L., Yan N. & Shi Y. (2004). Structure of the BRCT repeats of BRCA1 bound to a BACH1 phosphopeptide: implications for signaling. *Mol. Cell* **14** (3), 405-412.
64. Clapperton J. A., Manke I. A., Lowery D. M., Ho T., Haire L. F., Yaffe M. B. & Smerdon S. J. (2004). Structure and mechanism of BRCA1 BRCT domain recognition of phosphorylated BACH1 with implications for cancer. *Nat. Struct. Mol. Biol.* **11** (6), 512-518.
65. Williams R. S., Lee M. S., Hau D. D. & Glover J. N. (2004). Structural basis of phosphopeptide recognition by the BRCT domain of BRCA1. *Nat. Struct. Mol. Biol.* **11** (6), 519-525.
66. Botuyan M. V., Nomine Y., Yu X., Juranic N., Macura S., Chen J. & Mer G. (2004). Structural basis of BACH1 phosphopeptide recognition by BRCA1 tandem BRCT domains. *Structure* **12** (7), 1137-1146.
67. Dizin E., Gressier C., Magnard C., Ray H., Decimo D., Ohlmann T. & Dalla Venezia N. (2006). BRCA1 interacts with poly(A)-binding protein: Implication of BRCA1 in translation regulation. *J. Biol. Chem.* **281** (34), 24236-24246.
68. Divne C., Stahlberg J., Teeri T. T. & Jones T. A. (1998). High-resolution crystal structures reveal how a cellulose chain is bound in the 50 Å long tunnel of cellobiohydrolase I from *Trichoderma reesei*. *J. Mol. Biol.* **275** (2), 309-325.
69. Meyer J. E. & Schulz G. E. (1997). Energy profile of maltooligosaccharide permeation through maltoporin as derived from the structure and from a statistical analysis of saccharide-protein interactions. *Protein Sci.* **6** (5), 1084-1091.
70. Biarnes X., Nieto J., Planas A. & Rovira C. (2006). Substrate distortion in the Michaelis complex of *Bacillus* 1,3-1,4- $\beta$ -glucanase. Insight from first principles molecular dynamics simulations. *J. Biol. Chem.* **281** (3), 1432-1441.
71. Levinthal C. (1968). Are there pathways for protein folding? *J. Chim. Phys.* **65**, 44-45.
72. Dill K. A. & Chan H. S. (1997). From Levinthal to pathways to funnels. *Nat. Struct. Biol.* **4** (1), 10-19. Review.
73. Chan H. S. & Dill K. A. (1998). Protein folding in the landscape perspective: chevron plots and non-Arrhenius kinetics. *Proteins* **30** (1), 2-33. Review.

74. **Ross E. D., Minton A. & Wickner R. B. (2005).** Prion domains: sequences, structures and interactions.  
Nat. Cell Biol. **7** (11), 1039-1044. Review.
75. **Ellis R. J. (2001).** Macromolecular crowding: obvious but underappreciated.  
Trends Biochem. Sci. **26** (10), 597-604. Review.
76. **Zimmerman S. B. & Trach S. O. (1991).** Estimation of macromolecule concentrations and excluded volume effects for the cytoplasm of *Escherichia coli*.  
J. Mol. Biol. **222** (3), 599-620.
77. **Braig K., Otwinowski Z., Hegde R., Boisvert D. C., Joachimiak A., Horwich A. L. & Sigler P. B. (1994).** The crystal structure of the bacterial chaperonin GroEL at 2.8 Å.  
Nature **371** (6498), 578-586.
78. **Bukau B., Deuerling E., Pfund C. & Craig E. A. (2000).** Getting newly synthesized proteins into shape.  
Cell **101** (2), 119-122. Review.
79. **Walter S. (2002).** Structure and function of the GroE chaperone.  
Cell. Mol. Life Sci. **59** (10), 1589-1597. Review.
80. **Ellis R. J. (2005).** Chaperomics: *in vivo* GroEL function defined.  
Curr. Biol. **15** (17), R661-663. Review.
81. **True H. L. (2006).** The battle of the fold: chaperones take on prions.  
Trends Genet. **22** (2), 110-117. Review.
82. **Bukau B., Weissman J. & Horwich A. (2006).** Molecular chaperones and protein quality control.  
Cell **125** (3), 443-451. Review.
83. **Zahn R., Spitzfaden C., Ottiger M., Wüthrich K & Plückthun A. (1994).** Destabilization of the complete protein secondary structure on binding to the chaperone GroEL.  
Nature **368** (6468), 261-265.
84. **Walter S., Lorimer G. H. & Schmid F. X. (1996).** A thermodynamic coupling mechanism for GroEL-mediated unfolding.  
Proc. Natl. Acad. Sci. U. S. A. **93** (18), 9425-9430.
85. **Shtilerman M., Lorimer G. H. & Englander S. W. (1999).** Chaperonin function: folding by forced unfolding.  
Science **284** (5415), 822-825.
86. **Moore P. B. & Steitz T. A. (2005).** The ribosome revealed.  
Trends Biochem. Sci. **30** (6), 281-283. Review.
87. **Kevin Cowtan's Picture Book of Fourier Transforms.**  
([www.ysbl.york.ac.uk/~cowtan/fourier/fourier.html](http://www.ysbl.york.ac.uk/~cowtan/fourier/fourier.html))
88. **Furnham N., Blundell T. L., DePristo M. A. & Terwilliger T. C. (2006).** Is one solution good enough?  
Nat. Struct. Mol. Biol. **13** (3), 184-185; Discussion 185.

89. Brünger A. T., Clore G. M., Gronenborn A. M., Saffrich R. & Nilges M. (1993). Assessing the quality of solution nuclear magnetic resonance structures by complete cross-validation. *Science* **261** (5119), 328-331.
90. Brünger A. T. (1992). Free *R* value: a novel statistical quantity for assessing the accuracy of crystal structures. *Nature* **355**, 472-475.
91. Bradley P., Misura K. M. & Baker D. (2005). Toward high-resolution de novo structure prediction for small proteins. *Science* **309** (5742), 1868-1871.
92. Honig B. (1999). Protein folding: from the Levinthal paradox to structure prediction. *J. Mol. Biol.* **293** (2), 283-293. Review.
93. Schueler-Furman O., Wang C., Bradley P., Misura K. & Baker D. (2005). Progress in modeling of protein structures and interactions. *Science* **310** (5748), 638-642. Review.
94. Steitz T. A. & Moore P. B. (2003). RNA, the first macromolecular catalyst: the ribosome is a ribozyme. *Trends Biochem. Sci.* **28** (8), 411-418. Review.
95. Schramm V. L. (2005). Enzymatic transition states and transition state analogues. *Curr. Opin. Struct. Biol.* **15** (6), 604-613. Review.
96. Fedor M. J. & Williamson J. R. (2005). The catalytic diversity of RNAs. *Nat. Rev. Mol. Cell Biol.* **6** (5), 399-412. Review.
97. Fiammengo R. & Jäschke A. (2005). Nucleic acid enzymes. *Curr. Opin. Biotechnol.* **16** (6), 614-21. Review.
98. Geiger A., Burgstaller P., von der Eltz H., Roeder A. & Famulok M. (1996). RNA aptamers that bind L-arginine with sub-micromolar dissociation constants and high enantioselectivity. *Nucleic Acids Res.* **24** (6), 1029-1036.
99. Majorfeld I., Puthenvedu D. & Yarus M. (2005). RNA affinity for molecular L-histidine; genetic code origins. *J. Mol. Evol.* **61** (2), 226-235.
100. Moore P. B. & Steitz T. A. (2002). The involvement of RNA in ribosome function. *Nature* **418** (6894), 229-235. Review.