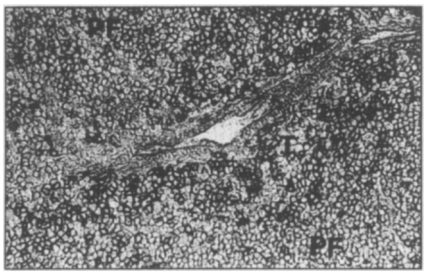
☐ **γ,δ T cell help of B cells is induced by repeated parasitic infection, in the absence of other T cells.** William Pao, Li Wen, Adrian L Smith, Adam Gulbranson-Judge, Biao Zheng, Garnett Kelsoe, Ian CM MacLennan, Michael J Owen and Adrian C Hayday (1996). *Curr. Biol.* **6**, 1317–1325.

All well-studied vertebrate immune systems contain two kinds of T cell (αβ and γδ) but the contribution of γδ T cells to immune responses is poorly characterized: it is unknown to what degree γδ T cells can help B cells to produce specific antibody in response to pathogen challenge. Here, the authors show that TCRβ$^{-/-}$ mice, which lack all T cells except γδ T cells, routinely displayed higher levels of antibody in response to repeated parasitic infection than fully T-cell-deficient mice. The antibodies thus raised were more often reactive against self antigens than against antigens of the challenging pathogen, however, unlike antibodies raised in normal mice under analogous circumstances. No T-cell help was observed in TCRβ$^{-/-}$ mice challenged with microbacterial antigens. Thus, γδ T cells are able to increase antibody production under some circumstances in the absence of αβ T cells, but do not appear to be selective for the 'correct' antibodies. This phenomenon may help to explain the pattern of antibody production in individuals who lack αβ T cells, for example AIDS patients.



1 October 1996, Research Paper, *Current Biology*

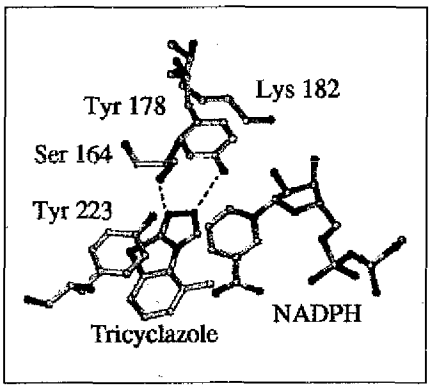
☐ **Contribution of the intramolecular disulfide bridge to the folding stability of REI$_v$, the variable domain of a human immunoglobulin κ light chain.** Christian Frisch, Harald Kolmar, Arno Schmidt, Gerd Kleemann, Astrid Reinhardt, Ehmke Pohl, Isabel Usón, Thomas R Schneider and Hans-Joachim Fritz (1996). *Folding & Design* **1**, 431–440.

Immunoglobulin domains contain ~100 amino acid residues folded into two β sheets and stabilized in a sandwich by a conserved central disulfide bridge. Whether antibodies actually require disulfide bonds for stability has long been a matter of debate. The contribution made by the central disulfide bridge to the overall folding stability of the immunoglobulin REI$_v$, the variable domain of a human κ light chain, was investigated by introducing stabilizing amino acid replacements, then removing the disulfide bridge via chemical reduction or genetic substitution of the cysteine residues. The data are consistent with the notion that all variants studied have the same overall three-dimensional structure with the disulfide bridge opened or closed; thus, the disulfide bond is not strictly necessary for proper folding. A comparison of the magnitude of the stabilizing effect exerted by the disulfide bond and the length of the mainchain loop framed by it suggests that the stabilizing effect is a result of the lowered entropy.

15 October 1996, Research Paper, *Folding & Design*

☐ **Crystal structure of the ternary complex of 1,3,8-trihydroxynaphthalene reductase from *Magnaporthe grisea* with NADPH and an active-site inhibitor.** Arnold Andersson, Douglas Jordan, Gunter Schneider and Ylva Lindqvist (1996). *Structure* **4**, 1161–1170.

1,3,8-Trihydroxynaphthalene reductase (THNR) catalyzes an essential reaction in the biosynthesis of melanin, which is crucial for the pathogenesis of the rice blast fungus, *Magnaporthe grisea*. It is the biochemical target of several fungicides that are used to prevent blast disease in rice plants. Crystallographic analysis of the ternary complex of THNR with a bound fungicide (tricyclazole) and NADPH showed a tetramer of single-domain subunits, each comprising a seven-stranded β sheet flanked by eight α helices. NADPH is bound at a dinucleotide-binding fold and tricyclazole binds at the active site in the vicinity of the NADPH nicotinamide ring.



The active site contains a Ser-Tyr-Lys triad which is proposed to participate in catalysis. Coenzyme specificity is partly conferred by the interaction of Arg39 with the 2′-phosphate group of NADPH. This structure provides new insights into the structural basis of inhibitor binding, which may aid in the design of new inhibitors for rice crop protection.

15 October 1996, Research Paper, *Structure*

☐ **Zif268 protein–DNA complex refined at 1.6 Å: a model system for understanding zinc finger–DNA interactions.** Monica Elrod-Erickson, Mark A Rould, Lena Nekludova and Carl O Pabo (1996). *Structure* **4**, 1171–1180.

Zinc fingers of the Cys_2His_2 class recognize a wide variety of different DNA sequences; this is one of the most abundant DNA-binding motifs found in eukaryotes. The structure of the Zif268 protein–DNA complex has been refined to 1.6 Å resolution, clarifying the details of the protein–DNA interface. The refined structure helps explain the roles of several acidic residues in the recognition helices, and shows that the zinc fingers make a number of water-mediated contacts with the DNA. Modeling studies are used to help understand the

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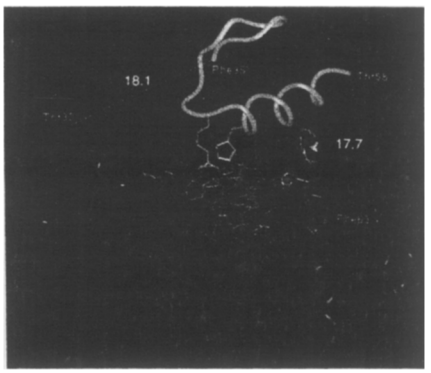
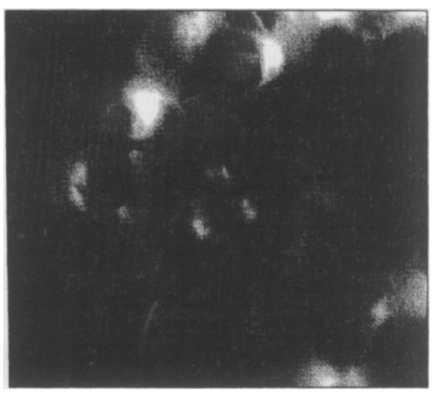
importance of the DNA conformation in the Zif268–DNA complex in recognition. Circular dichroism studies indicate that the DNA conformation changes upon complex formation; if it did not, the fingers of Zif268 would be too far apart given the linker length and the observed finger–finger contacts. The structure should provide an excellent framework for analyzing the effects of Zif268 mutations, for modeling related zinc finger–DNA complexes and for designing and selecting Zif268 variants that will recognize other DNA sites.



15 October 1996, Research Paper, *Structure*

☐ **Metal-binding sites in the major groove of a large ribozyme domain.** Jamie H Cate and Jennifer A Doudna (1996). *Structure* 4, 1221–1229.

Group I self-splicing introns catalyze sequential transesterification reactions within an RNA transcript to produce the correctly spliced product. These ribozymes are often several hundred nucleotides in size. The recently determined crystal structure of the P4–P6 domain from the *Tetrahymena thermophila* group I intron provides a detailed view of metal binding in this RNA, which is large enough to have a considerable amount of higher-order structure, including stacked RNA helices. There are three metal-binding sites in the major groove, detected by osmium hexammine. All three sites involve G and U nucleotides exclusively; two are formed by G:U wobble base pairs. Two of these sites are occupied by fully-hydrated, but weakly bound, magnesium ions. G:U wobble base pairs are often conserved in RNA structures, and may be generally important in forming metal ion binding sites. It should be possible to insert sites of this kind into other RNA structures, thus providing a general method for obtaining heavy-atom derivatives of such structures. Samarium detects a different magnesium-binding site, bridging phosphate oxygens in the A-rich bulge, a region that is essential for the folding of the entire domain.



15 October 1996, Research Paper, *Structure*