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The Nuclear Receptor Resource Project

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ABSTRACT

We have expanded the original Glucocorticoid Receptor Resource (GRR) database to include several individual resources as part of a larger project called the Nuclear Receptor Resource (NRR). In addition to the GRR, the NRR currently features the Thyroid Hormone Receptor Resource, the Androgen Receptor Resource, the Mineralocorticoid Receptor Resource, the Vitamin D Receptor Resource, and the Steroid Receptor Associated Proteins Resource. The goal of the NRR project is to provide a comprehensive resource for information on the nuclear receptor superfamily, and to provide a forum for the dissemination and discussion of both published and unpublished material on these proteins. Although the individual resources are managed from different servers, all the files are integrated and can be accessed through the project's Home Page, housed at http://nrr.georgetown.edu/nrr.html. In the near future, we hope to expand the project to contain information on other nuclear receptors and to better our electronic publication system. To accomplish this, we encourage the involvement of nuclear receptor investigators in the NRR.

Members of the steroid, thyroid and retinoic acid receptor superfamily play essential roles in a variety of cellular mechanisms regulating the development, growth and maintenance of specific cells and tissues. Because of their involvement in normal human development as well as in disease, nuclear hormone receptors have been the subject of intense study. In light of this, about a year ago we created the Glucocorticoid Receptor Resource (GRR), a database of useful information on this receptor. Since then, the database has expanded considerably and now includes several resources on individual receptors that are part of a larger project called the Nuclear Receptor Resource (NRR) (Fig. 1). The Thyroid Hormone Receptor Resource (THRR) was developed and is maintained by David D. Moore from the Department of Molecular Biology at the Massachusetts General Hospital. Evan Keller, at the Eastern Virginia Medical School put together and runs the Androgen Receptor Resource (ARR). Stoney Simons at the National Institutes of Health helped set up and now maintains the GRR's mutational analysis feature. Three new databases are under construction. These are the Mineralocorticoid Receptor Resource (MRR), the Vitamin D Receptor Resource (VDRR), and the Steroid Receptor Associated Proteins Resource (SRAPR). David Pearce and Vincent Robinson are developing the MRR, Paul MacDonald is creating the VDRR, and Eddie Sanchez is authoring the SRAPR. The individual resources offer interactive links to structural and functional information on the receptors, sources of biomolecules, related databases and much more. The presentation or summary form of some of this information was originally developed by us and is, therefore, unique to our database. For example, in the GRR a multiframe screen (Fig. 2) simultaneously offers a species sequence comparison of the receptor protein, known structural and mutational data on each amino acid, and literature references with links to article abstracts and related references in the Entrez database at the National Library of Medicine. In addition, the NRR gives the scientific community the opportunity to become part of a network to exchange ideas and data on nuclear receptor research, to advertise employment opportunities and to obtain some information about scientific meetings and research funding possibilities. This network has grown at a steady pace ever since its inception less than a year ago, and presently represents many nuclear receptor investigators.

The organization of the NRR gives it its user-friendly character. Its Home Page allows three levels of access. From it, the user can directly go to the project's common network files, to the Home

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Pages of the individual resources or, through the use of redirect pop up menus, to the particular files of any of the individual resources (Fig. 1). Although the resources are managed from different servers, the project itself unites these through a main server housed in the Department of Biochemistry and Molecular Biology at Georgetown University Medical Center. Since the database has proven to be of interest to many scientists—the GRR alone receives ~3000 hits per month—we would like to continue expanding. For this purpose, we encourage nuclear receptor investigators to get involved and consider developing a resource in their area of expertise. Other future plans include improving the method of automatic electronic publication in order to facilitate the prompt dissemination of interesting data on nuclear receptor action. This unique feature of the NRR offers exciting possibilities for quick communication among researchers and for keeping up with advances in the field. As always, the input and suggestions of the NRR users are welcome and encouraged. A concrete way in which users can help in the expansion of the project is by citing this publication so that others may also become familiar with the database. The NRR is located at http://nrr.georgetown.edu/nrr.html .

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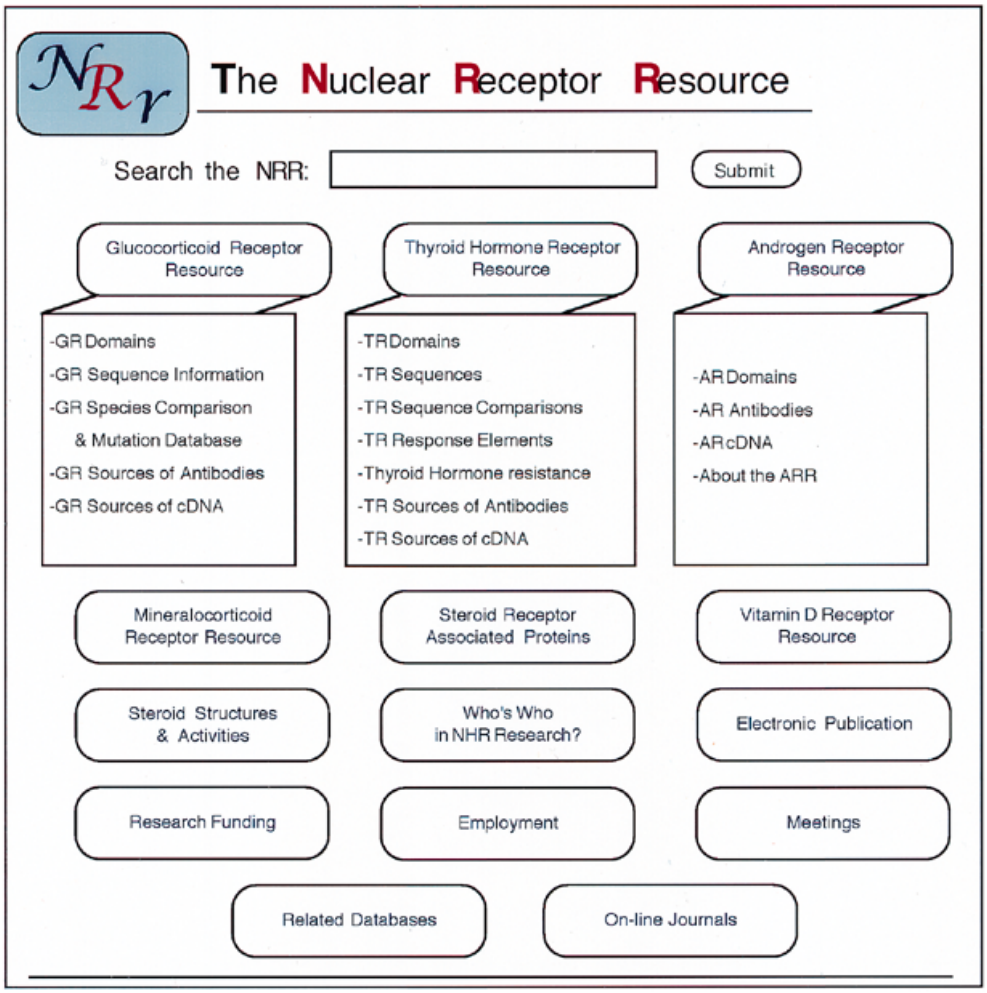

Figure 1. Schematic representation of the NRR Home Page. The NRR allows three levels of access. From it, the user can directly view the common network files, link to the Home Pages of the individual resources or, through the use of redirect popup menus, bypass these Home Pages and go to a particular file on an individual resource.

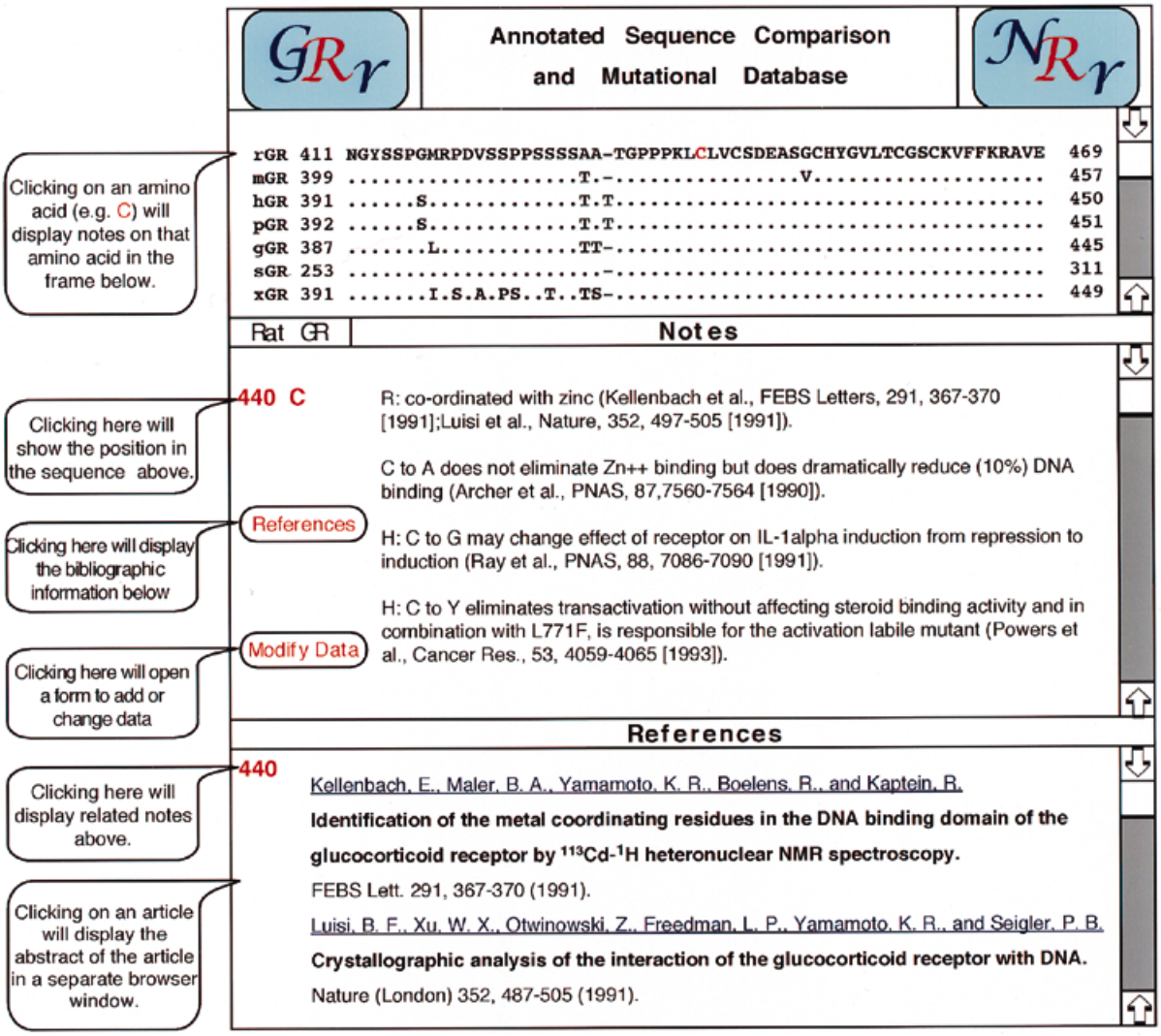

Figure 2. The GRR's Annotated Sequence Comparison and Mutational Database. The top frame compares the amino acid sequence of the mouse (m), rat (r), human (h), monkey (p), guinea pig (g), sheep (s) and *Xenopus* (x) glucocorticoid receptors (dots represent identity, dashes represent gaps). Clicking on an amino acid will display structural and mutational information on that residue in the Notes frame. Conversely, the user can browse through the Notes frame and then click on the amino acid number to see the position of that residue in the sequence comparison and whether or not it is conserved across species. In addition, clicking on the References button brings the corresponding citations into the bottom frame. The abstracts of these articles can then be viewed on a separate browser window by clicking on the authors' names. Again, each group of references contains a link to the appropriate notes in the middle frame. This interactive, multiframe database exemplifies the unique data presentation found in the NRR.