

In the new study, for which Yehuda Shabtai, Ph.D., a postdoctoral researcher in the Lazar lab, served as lead author, the researchers developed a mouse model in which a special tag was added to TR β , the main thyroid hormone receptor in the liver—where some of thyroid hormone's most important metabolic effects occur. The researchers used this tag for marking the thousands of locations on DNA where TR β binds, both in a condition when thyroid hormone was present and could bind to TR β and also when the hormone was largely absent. With these and other experiments, the team provided strong evidence that thyroid hormone works with TR β in an unexpectedly subtle way.

When it binds to a given site on coiled DNA in the nucleus, TR β will enhance or repress the activity of a nearby gene or [genes](#). To achieve this, it forms complexes with other proteins called co-activators and co-repressors. The researchers showed when thyroid hormone is bound to TR β , it can shift the balance of these associated co-regulator proteins in favor of more gene activation at some sites, and more gene repression at others. This is in contrast to prior models of thyroid hormone / TR β function in which [thyroid](#) hormone has a more absolute, switch-like effect on gene activity.

The researchers acknowledge that more work needs to be done to elucidate why [thyroid hormone](#)'s binding to TR β lowers gene activity at some sites on DNA, and increases gene activity at other sites. But they see the new findings as a significant advance in understanding a basic process in biology—a process that future medicines may be able to target precisely to treat a variety of metabolic diseases.

Co-authors on this study include Yehuda Shabtai, Nagaswaroop Nagaraj, Kirill Batmanov, Young-Wook Cho, Yuxia Guan, Chunjie Jiang, Jarrett Remsberg, Douglas Forrest, and Mitchell Lazar.

Provided by Perelman School of Medicine at the University of Pennsylvania

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