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New research suggests rethinking clinical genetic testing of minors

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Children, it seems, may be more ready to handle hearing the results of genetic testing for disease predisposition than adults realize. The findings of a systematic review by Wakefield *et al*. reported in this issue suggest that children who receive results of genetic testing do not on the whole suffer psychological harm. Rather, the review reveals, first, that there have been very few studies (13) collecting evidence of psychological effects on children, and second, those studies that have been done looked only at short-term effects, making it difficult to draw conclusions about the appropriateness of allowing minors to have their genetic risk factors assessed. The study findings seem to run counter to published guidance from the American College of Medical Genetics and Genomics and commentary by some medical genetic thought leaders who have discouraged any testing of minor children before the age of consent. In a Commentary accompanying the review, Barbara Biesecker, head of the genetic services unit at the National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, suggests that the patient-centered care and patient empowerment movements argue for trusting that parents are capable of making well-considered decisions on behalf of their children. While Wakefield *et al.* defer to current guidance from professional medical genetic organizations, Biesecker suggests that predictive genetic testing of minors should be reconsidered. She argues that future studies may "never adequately address the personal and complex nature of predictive testing of minors." Therefore, adolescent minors, in consultation with genetic counselors and their parents or guardians, should feel empowered to make informed decisions in individual cases. However, Biesecker notes that Wakefield *et al.* provide valuable data and perspective to help genetic counselors overcome fears about possible adverse psychological outcomes among minors undergoing predictive testing. *—Karyn Hede, News Editor*

Rare Mendelian disorder revealed through online social networking

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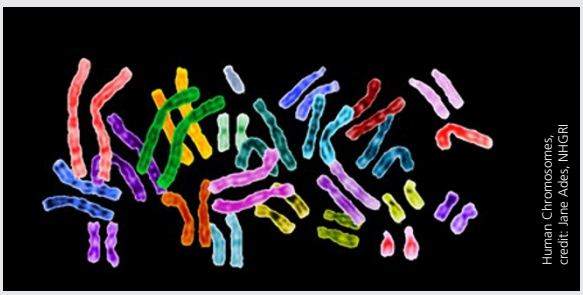
A frustrated family's desperate plea for help via social media has led to identification of a new Mendelian disorder and helped launch a new Web resource to connect families, researchers, and clinicians researching rare genetic diseases. After several years without a diagnosis for their son Milo's debilitating constellation of symptoms, the Lorentzen family went public in a social media blitz to find answers. Within days, a second family who had a child with similar developmental delays and physical features responded. The research team that identified lysine (K)-specific demethylase 1A (*KDM1A*) mutations in both children reports in this issue that the family's activism helped inspire them to launch the Repository for Mendelian Genomics Family Portal (MyGenes2). The condition is exceedingly rare because the *KDM1A* gene encodes a histone demethylase that is among the most evolutionarily conserved of all genes. Model organism studies have shown that KDM1A plays important roles in regulating gene expression during development. Researchers hope that the MyGenes2 portal will help break open some of the siloed genetic information now squirreled away in individual research laboratories and allow families to more fully participate in the research process. The research team sees social networking as a potentially powerful strategy to discover genes for rare Mendelian conditions, particularly those with nonspecific phenotypic features. The hope is that the portal will also reduce the ever-growing number of variants of unknown (or uncertain) significance that now proliferate in clinical genetic laboratories. *—Karyn Hede, News Editor*

NEWS BRIEFS

Synthetic human genome discussion blows up on social media

Not content merely to read the genome anymore, some human geneticists also want to write it, synthetically. The idea is intriguing, but the discussions about how it would work recently generated more than a bit of consternation among science reporters, sparking a dustup on social media that have followed the project, which is called HGP 2.0 or HGP-write. HGP 2.0, which is still in its very earliest days, is not currently funded. A recent closed-door session left many wondering just what was so secret about the initial meeting to discuss the project,



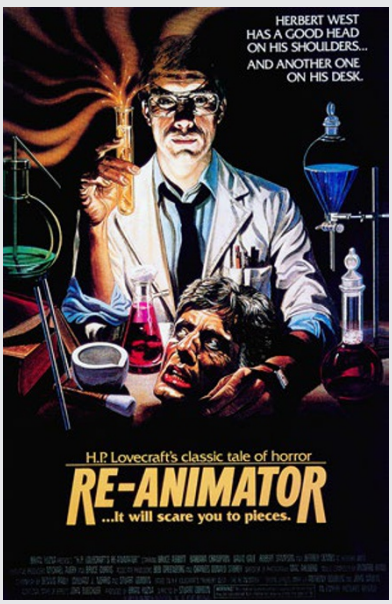
Human Chromosomes, credit: Jane Ades, NHGRI

NEWS BRIEFS *(continued)*

which was held in mid-May at Harvard University at the behest of geneticist George Church, one of the organizers. Social media abounded with criticism that the event, originally intended to be open to the public and reporters, was closed (to preserve a media embargo on the meeting's associated *Science* article, slated to be published in June). The faux pas seemed to raise questions about the group's intentions among reporters, but that wasn't the end of the criticism. Even medical professionals who had been invited to the meeting openly questioned its lack of forethought and transparency. Laurie Zoloth, a medical ethicist at Northwestern University, coauthored a commentary critical of the project that was timed to appear on the very day of the May meeting. Appearing on the website of the magazine *Cosmos*, and coauthored with Drew Endy, a writer for the magazine, the commentary not only argued that any discussion of a synthetic genome should take place in the open but also questioned whether the project should be pursued at all. Instead, they wrote, the next large-scale genome project should be aimed at improving gene transfer technologies and synthetic capabilities at the subgenome level, which would avoid some of the more serious ethical questions now dogging HGP 2.0. *—Karyn Hede, News Editor*

Reanimated enzyme brought back from evolutionary death

Resurrecting an enzyme lost in the mists of evolutionary time, scientists at the University Regensburg in Germany have revealed that ancient enzymes were hardier than many experts have believed and may have existed in modern form much earlier than is now understood. Reinhard Sterner and his colleagues published data from the reconstructed tryptophan synthase in *Cell Chemical Biology* in June 2016. The research showed that this early version of an enzyme essential in making the amino acid tryptophan was probably as efficient as modern enzymes and was likely stable in the steamy hot conditions that may have existed early in earth's history. To reanimate the ancient enzyme, the research team analyzed forms of the enzyme in modern bacteria and archaea and then conducted a computer search for the most probable common ancestral sequence, which would have existed 3.4 billion years ago. They then synthesized the predicted enzyme in *Escherichia coli* bacteria and evaluated its stability and activity. The enzyme folded similarly to the modern enzyme, worked efficiently, and was stable up to 70 °C. The study suggests that specific and efficient, fully functioning, "modern" enzymes existed much earlier than is currently understood. Given that no DNA survives from billions of years ago, reconstruction of the ancestors of modern enzymes has become a useful strategy to understand evolutionary biochemistry and is challenging prior assumptions about the sophistication of ancient life forms. *—Karyn Hede, News Editor*



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