Nature Reviews Genetics | AOP, published online 15 July 2014

IN BRIEF

MOLECULAR GENETICS

DNA binding drives nuclear receptor architecture

Nuclear receptors are crucial regulators of gene expression that directly bind to DNA. Now, Maletta *et al.* describe the structure of ultraspiracle protein/ecdysone receptor (USP/EcR) bound to inverted repeat DNA. Although these inverted repeats of DNA are palindromic, upon binding to the receptor the DNA–USP/EcR complex adopts an asymmetrical configuration. This conformational change has functional consequences for the orientation of transcriptional co-activators, such as those required for chromatin remodelling.

ORIGINAL RESEARCH PAPER Maletta, M. *et al.* The palindromic DNA-bound USP/EcR nuclear receptor adopts an asymmetric organization with allosteric domain positioning. *Nature Commun.* **5**, 4139 (2014)

MODEL ORGANISMS

Increasing the specificity of genetic signatures

Decreased growth is often used as a phenotypic measure in gene perturbation experiments in model systems such as yeast. O'Duibhir *et al.* have now shown that various mutant yeast strains exhibit slow growth that is characterized by a specific gene signature. This signature was highly similar to the known gene signature of environmental stress response, even though the mutant strains were grown under ideal conditions. Subtraction of this slow growth signature from future experiments involving environmental perturbation may therefore yield gene signatures that are more specific to the perturbation and that are not simply a reflection of slow growth.

ORIGINAL RESEARCH PAPER O'Duibhir, E. *et al.* Cell cycle population effects in perturbation studies. *Mol. Syst. Biol.* **10**, 732 (2014)

CLINICAL GENETICS

Facing disease — new algorithm to aid diagnosis

Ferry *et al.* have developed a new computer algorithm that extracts phenotypic information from patient photographs to facilitate diagnosis of genetic diseases with known facial morphologies. This algorithm does not require clinical photographs or special three-dimensional imaging and can instead use two-dimensional images from sources such as family photo albums. In addition, it groups patients phenotypically into clusters, which can aid the investigation of undefined diseases or extremely rare disorders.

ORIGINAL RESEARCH PAPER Ferry, Q. *et al.* Diagnostically relevant facial gestalt information from ordinary photos. *eLife* **3**, e02020 (2014)

TECHNOLOGY

Progress in nanopore sequencing

Nanopore sequencing is based on ion current changes that are generated by DNA passing through a genetically modified bacterial pore. Traditionally, this technique suffers from imprecision in identifying individual nucleotides, as four nucleotides pass through the pore at once. In a new study, researchers characterized the electronic signature of all 256 possible 4-nucleotide combinations and generated algorithms to interpret these signatures. Using this method, they accurately sequenced the genome of the bacteriophage ΦX174 and generated reads as long as 4,500 bases. These advances are a substantial step forward in improving this inexpensive and potentially more rapid alternative to next-generation sequencing technologies.

ORIGINAL RESEARCH PAPER Laszlo, A. H. *et al.* Decoding long nanopore sequencing reads of natural DNA. *Nature Biotech.* http://dx.doi.org/10.1038/nbt.2950 (2014)

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