
HUMAN "The Movie" by Yann Arthus-Bertrand

A visual grammar for 3DGenomics

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CNAG-CRG · ICREA

Unpublished

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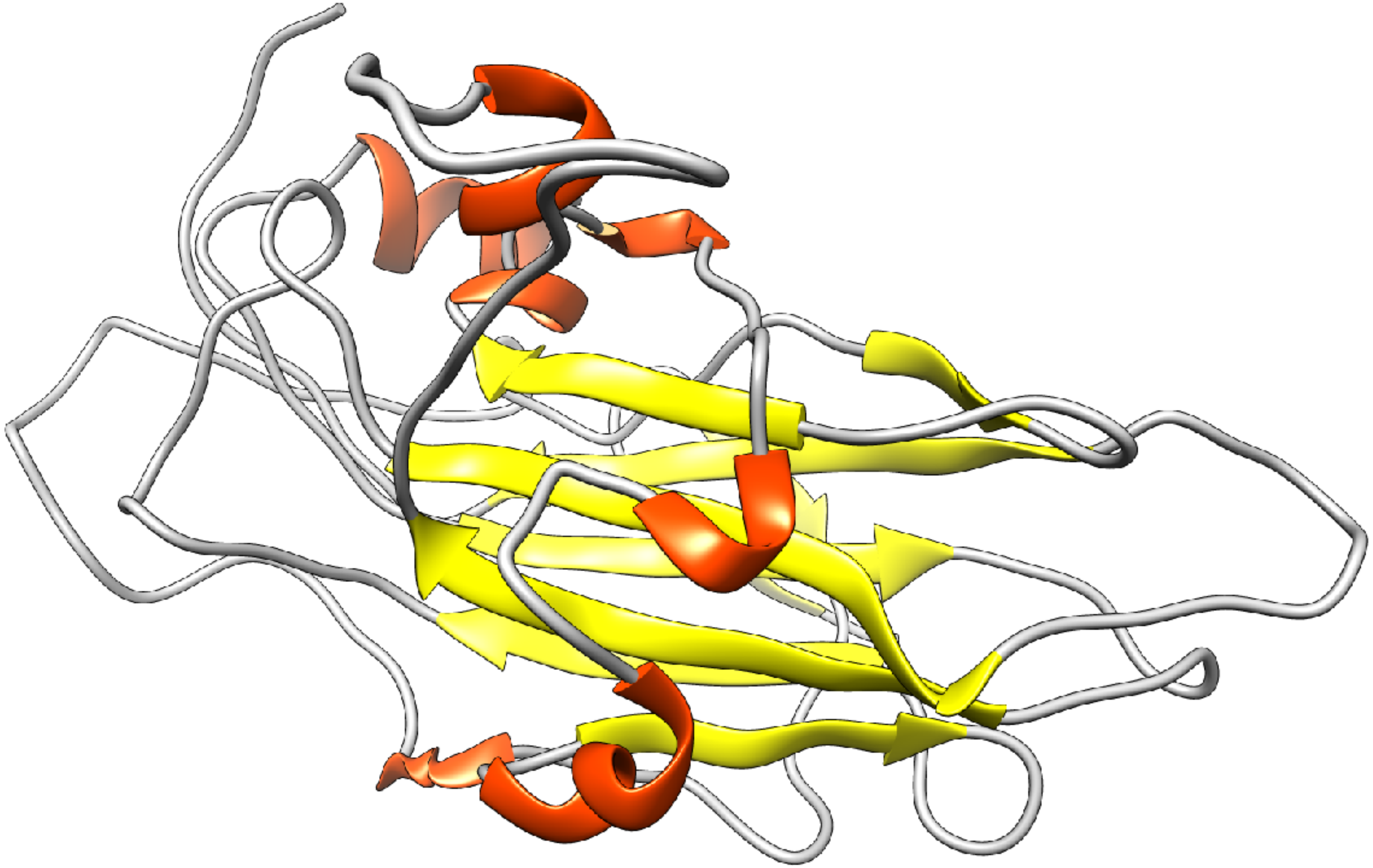
Electron density map of EV71

All-atom representation of EV71

Ribbon representation of EV71

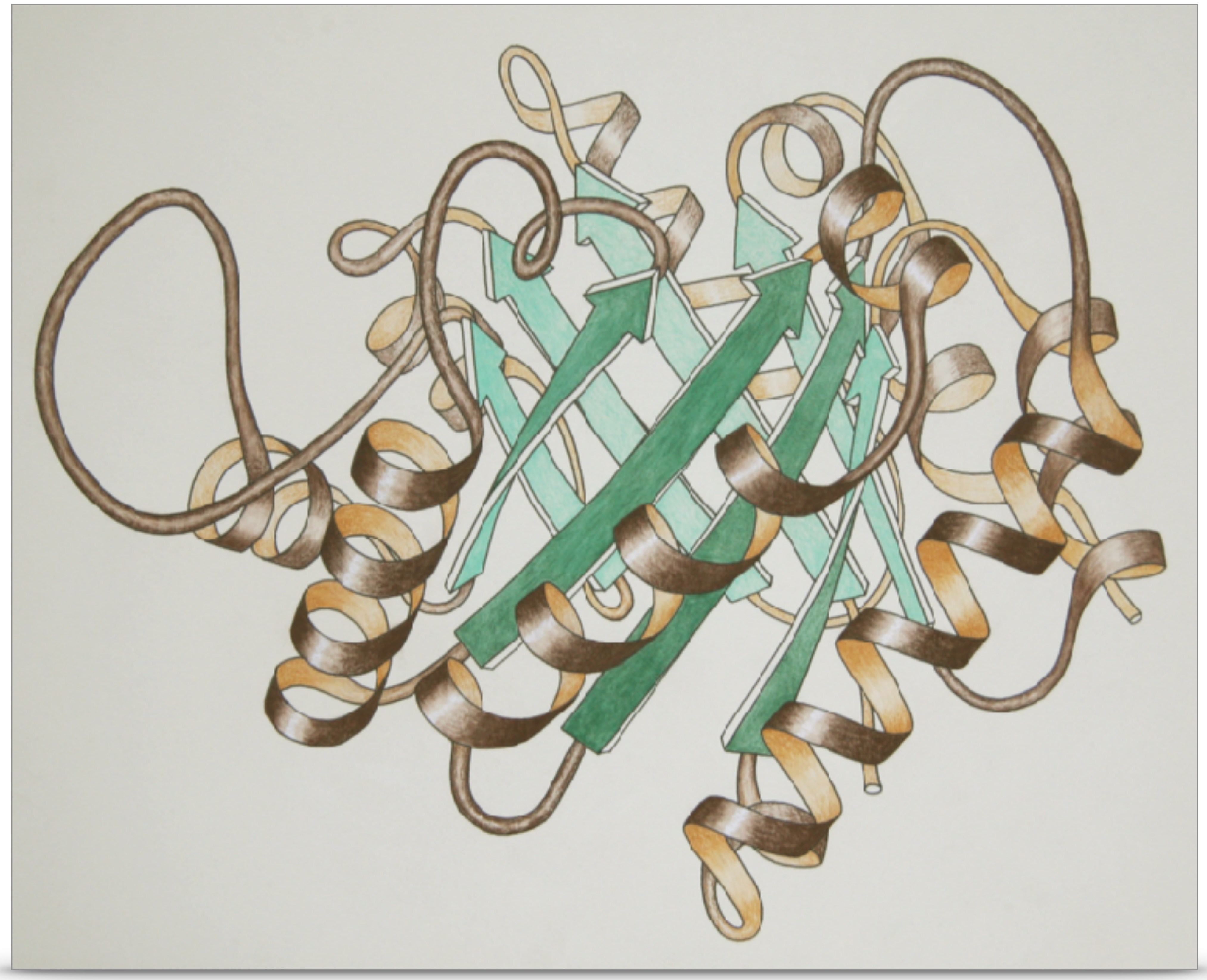
Ribbon representation of EV71

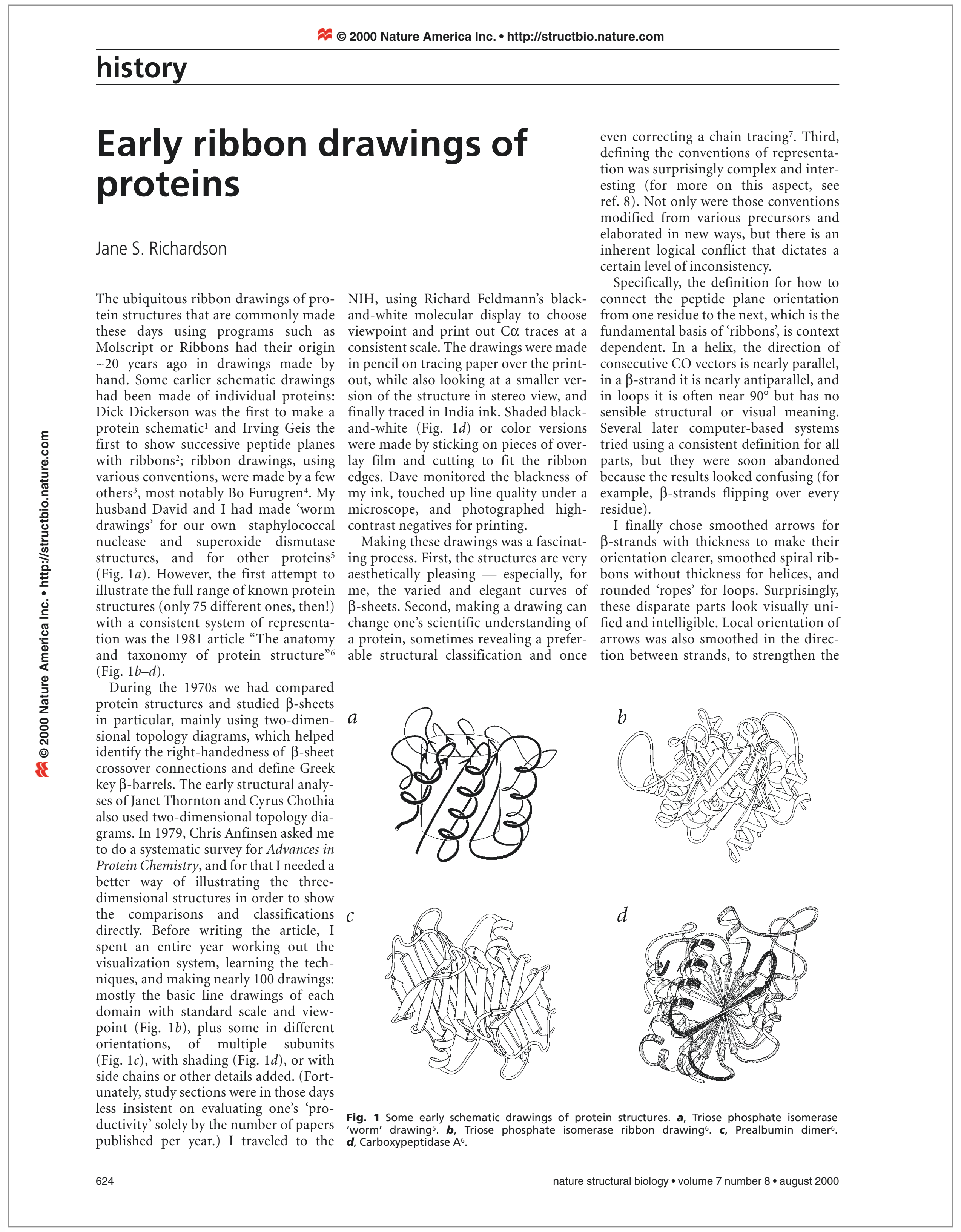


Ribbon representation of EV71 chain C

Ribbon diagrams of proteins

70s-80s >> Dick Dickerson · Irving Geis · Bo Furugren · Jane S. Richardson





Early ribbon drawings of proteins

Jane S. Richardson

The ubiquitous ribbon drawings of protein structures that are commonly made these days using programs such as Molscript or Ribbons had their origin ~20 years ago in drawings made by hand. Some earlier schematic drawings had been made of individual proteins: Dick Dickerson was the first to make a protein schematic[1] and Irving Geis the first to show successive peptide planes with ribbons[2]; ribbon drawings, using various conventions, were made by a few others[3], most notably Bo Furugren[4]. My husband David and I had made 'worm drawings' for our own staphylococcal nuclease and superoxide dismutase structures, and for other proteins[5] (Fig. 1*a*). However, the first attempt to illustrate the full range of known protein structures (only 75 different ones, then!) with a consistent system of representation was the 1981 article "The anatomy and taxonomy of protein structure"[6] (Fig. 1*b–d*).

During the 1970s we had compared protein structures and studied β-sheets in particular, mainly using two-dimensional topology diagrams, which helped identify the right-handedness of β-sheet crossover connections and define Greek key β-barrels. The early structural analyses of Janet Thornton and Cyrus Chothia also used two-dimensional topology diagrams. In 1979, Chris Anfinsen asked me to do a systematic survey for *Advances in Protein Chemistry*, and for that I needed a better way of illustrating the three-dimensional structures in order to show the comparisons and classifications directly. Before writing the article, I spent an entire year working out the visualization system, learning the techniques, and making nearly 100 drawings: mostly the basic line drawings of each domain with standard scale and viewpoint (Fig. 1*b*), plus some in different orientations, of multiple subunits (Fig. 1*c*), with shading (Fig. 1*d*), or with side chains or other details added. (Fortunately, study sections were in those days less insistent on evaluating one's 'productivity' solely by the number of papers published per year.) I traveled to the NIH, using Richard Feldmann's black-and-white molecular display to choose viewpoint and print out Cα traces at a consistent scale. The drawings were made in pencil on tracing paper over the printout, while also looking at a smaller version of the structure in stereo view, and finally traced in India ink. Shaded black-and-white (Fig. 1*d*) or color versions were made by sticking on pieces of overlay film and cutting to fit the ribbon edges. Dave monitored the blackness of my ink, touched up line quality under a microscope, and photographed high-contrast negatives for printing.

Making these drawings was a fascinating process. First, the structures are very aesthetically pleasing — especially, for me, the varied and elegant curves of β-sheets. Second, making a drawing can change one's scientific understanding of a protein, sometimes revealing a preferable structural classification and once even correcting a chain tracing[7]. Third, defining the conventions of representation was surprisingly complex and interesting (for more on this aspect, see ref. 8). Not only were those conventions modified from various precursors and elaborated in new ways, but there is an inherent logical conflict that dictates a certain level of inconsistency.

Specifically, the definition for how to connect the peptide plane orientation from one residue to the next, which is the fundamental basis of 'ribbons', is context dependent. In a helix, the direction of consecutive CO vectors is nearly parallel, in a β-strand it is nearly antiparallel, and in loops it is often near 90° but has no sensible structural or visual meaning. Several later computer-based systems tried using a consistent definition for all parts, but they were soon abandoned because the results looked confusing (for example, β-strands flipping over every residue).

I finally chose smoothed arrows for β-strands with thickness to make their orientation clearer, smoothed spiral ribbons without thickness for helices, and rounded 'ropes' for loops. Surprisingly, these disparate parts look visually unified and intelligible. Local orientation of arrows was also smoothed in the direction between strands, to strengthen the

Fig. 1 Some early schematic drawings of protein structures. ***a***, Triose phosphate isomerase 'worm' drawing[5]. ***b***, Triose phosphate isomerase ribbon drawing[6]. ***c***, Prealbumin dimer[6]. ***d***, Carboxypeptidase A[6].

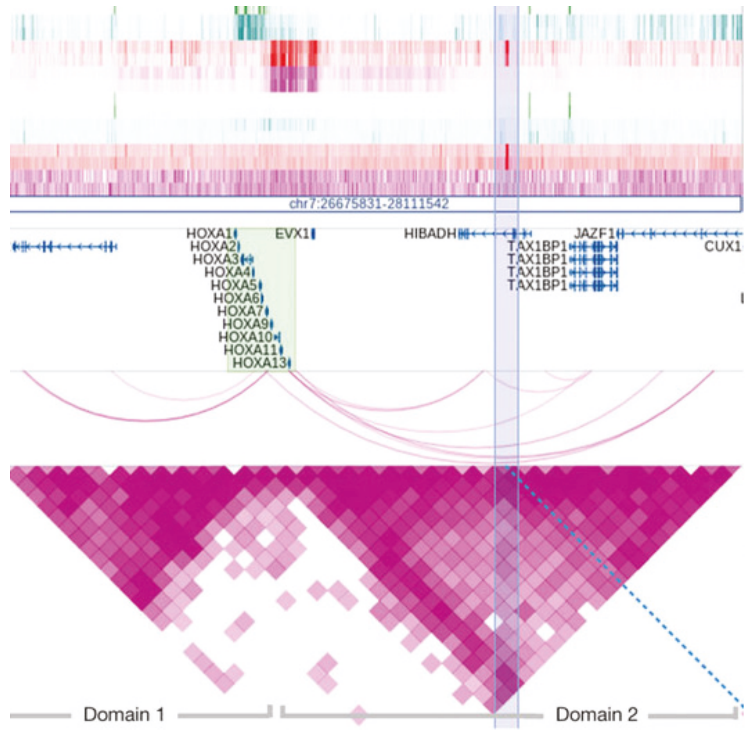
Ribbon schematic of triose P isomerase monomer (hand-drawn by J. Richardson, 1981)

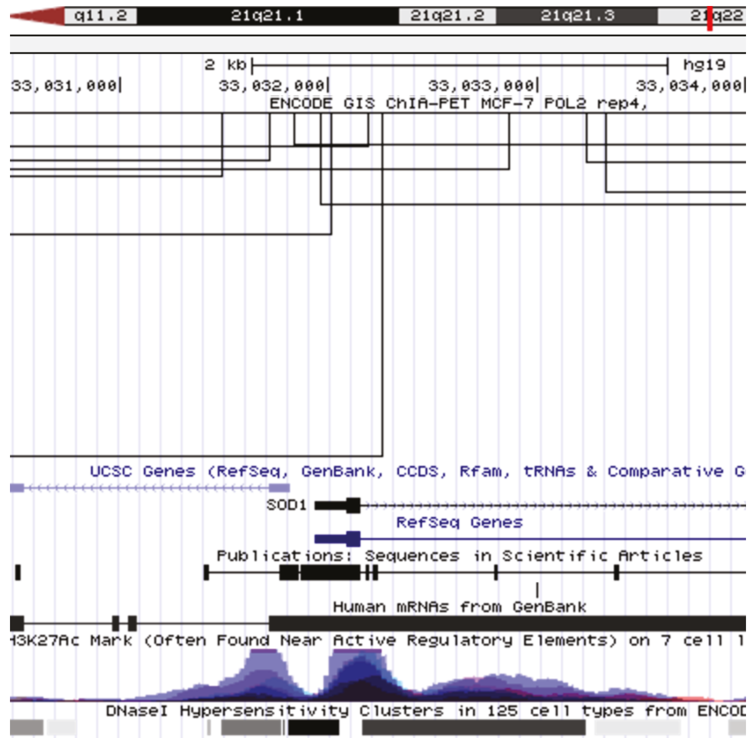
Richardson, Jane S. (1981), "Anatomy and Taxonomy of Protein Structures", Advances in Protein Chemistry, Advances in Protein Chemistry, 34: 167–339

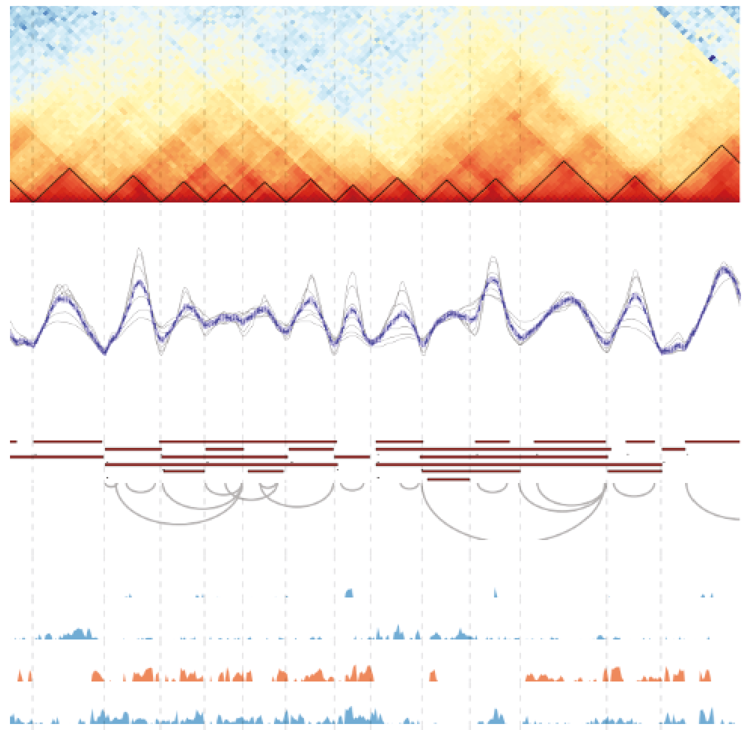
Richardson, Jane S. (2000), "Early ribbon drawings of proteins", Nature Structural Biology, 7 (8): 624–625,

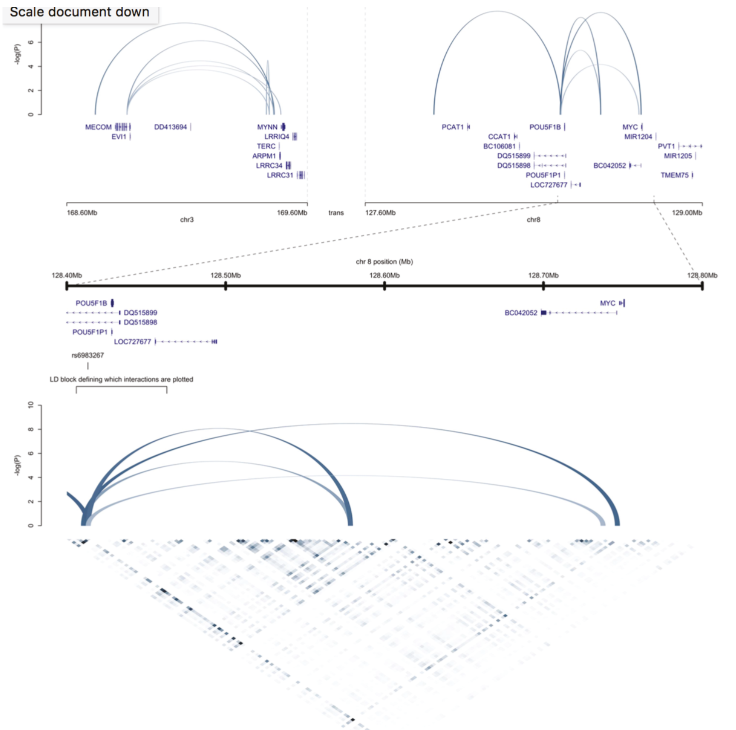
3D Genome orgainzation

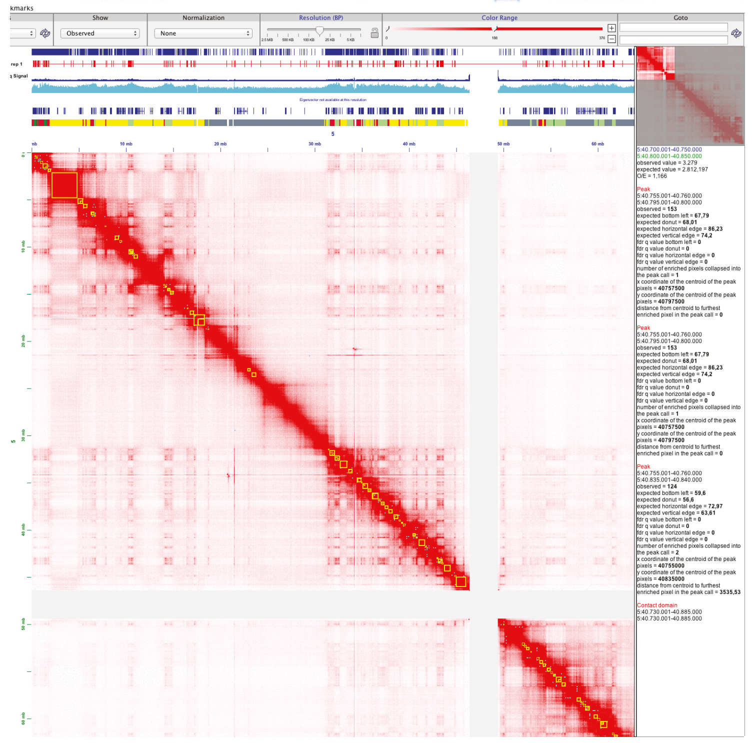
how we represent it…

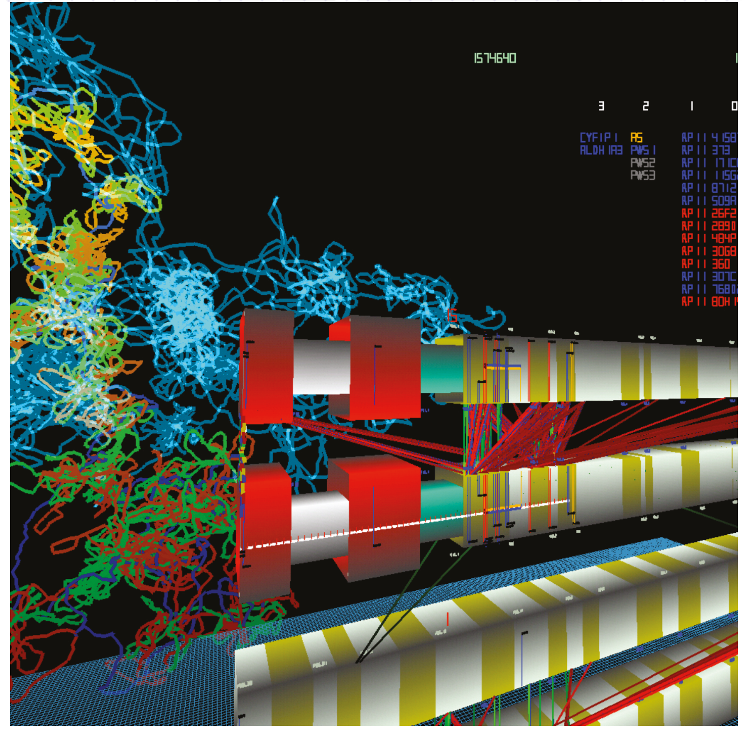


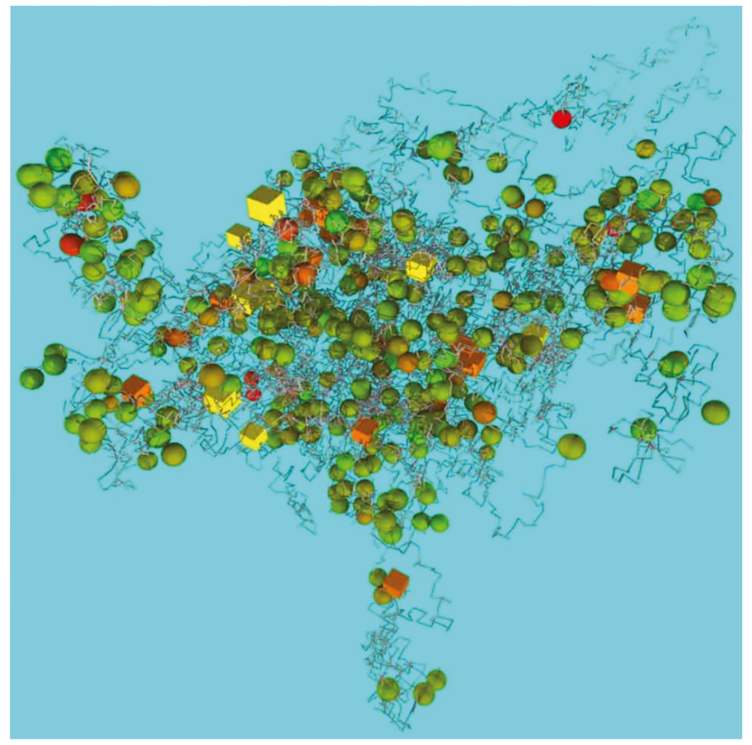


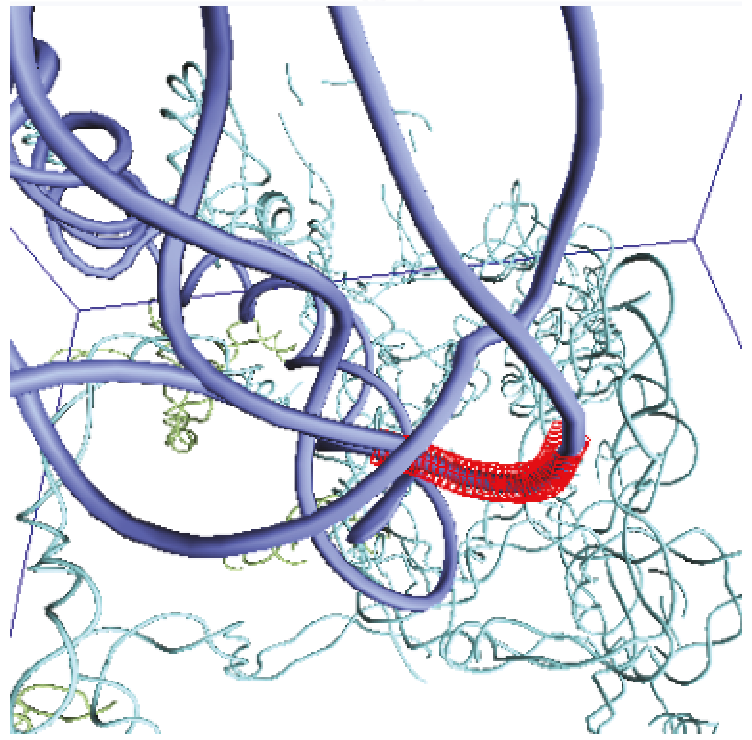


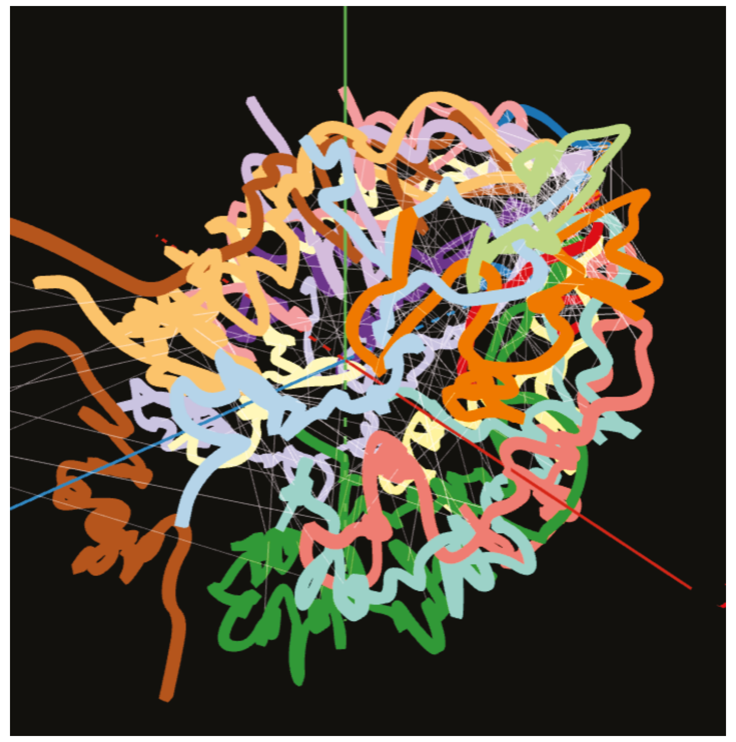


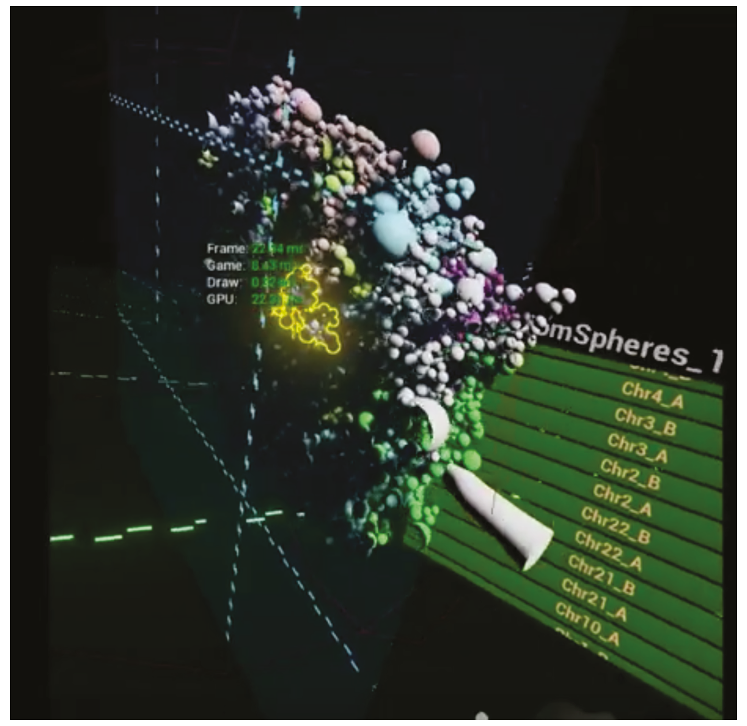








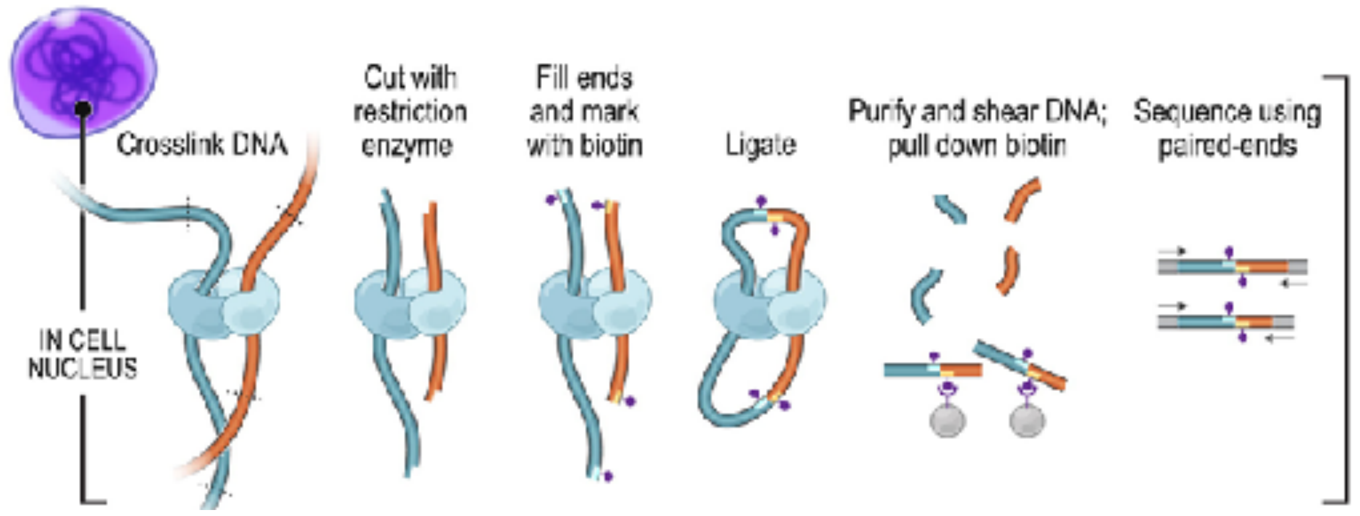


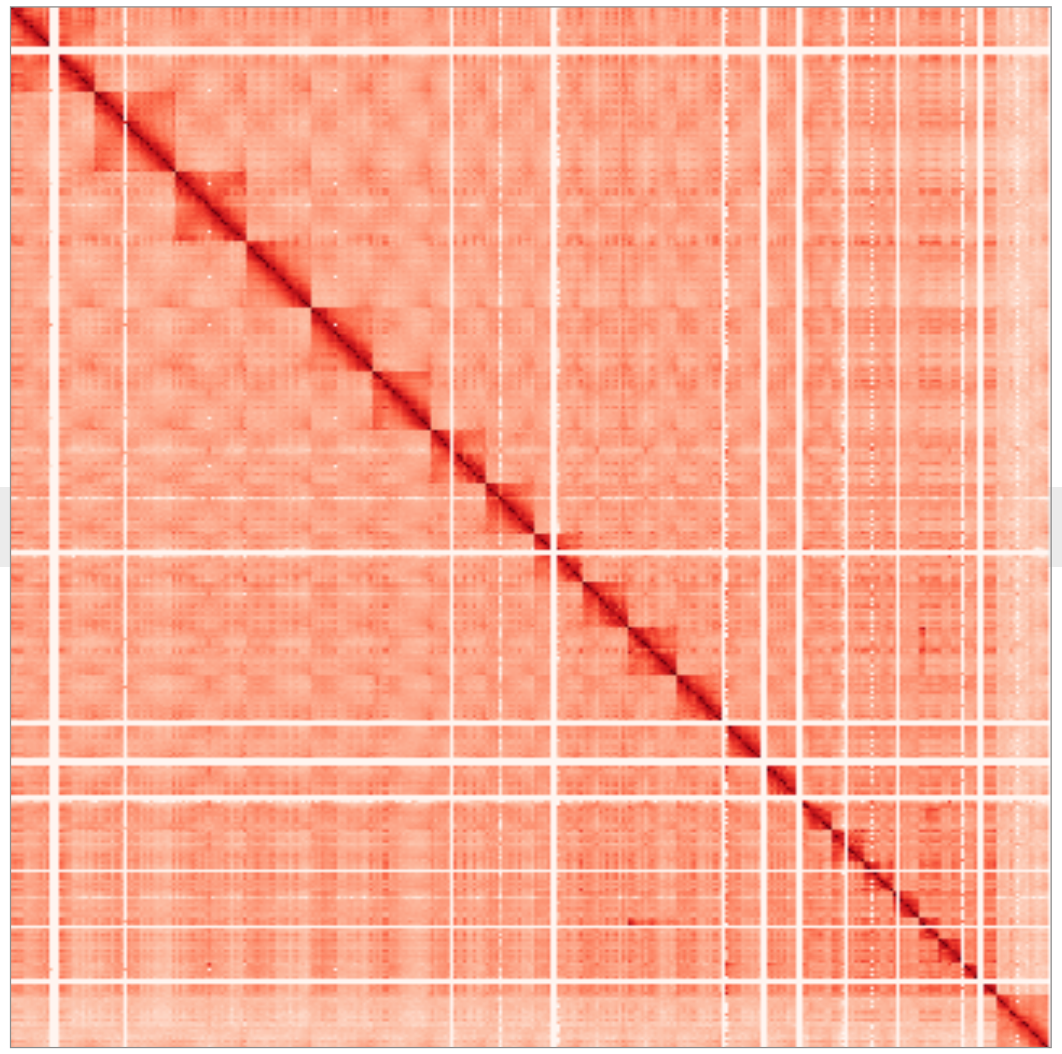


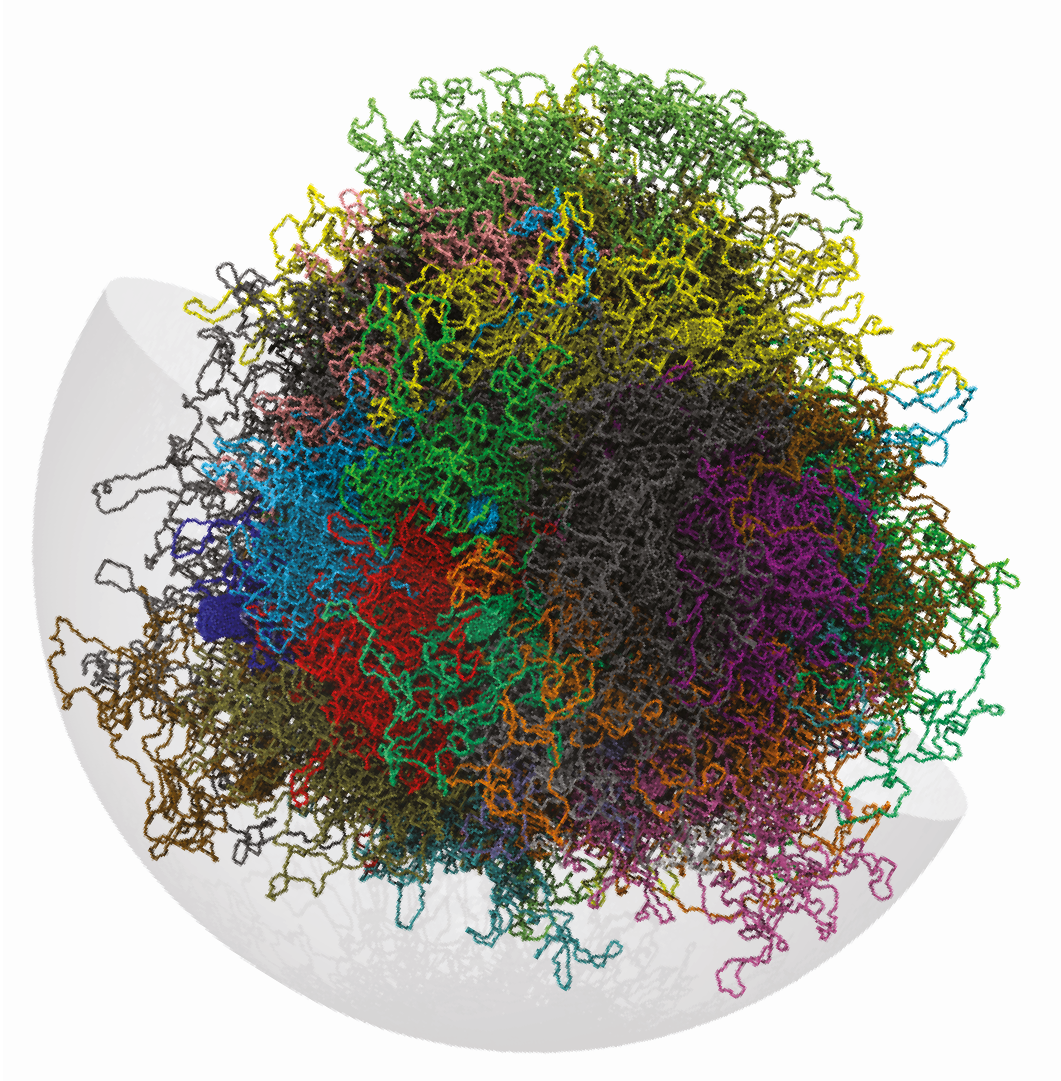
Goodstadt, M. and Marti-Renom, M.A. "Biovisualization of the Genome, from Data Analysis and Hypothesis Generation to Communication and Learning" Journal of Molecular Biology (2018) 431 1071–1087
Goodstadt, M. and Marti-Renom, M.A. "Challenges for visualizing three-dimensional data in genomic browsers" FEBS Letters (2017) 591 2505–2519

3D Genome orgainzation

what we know…



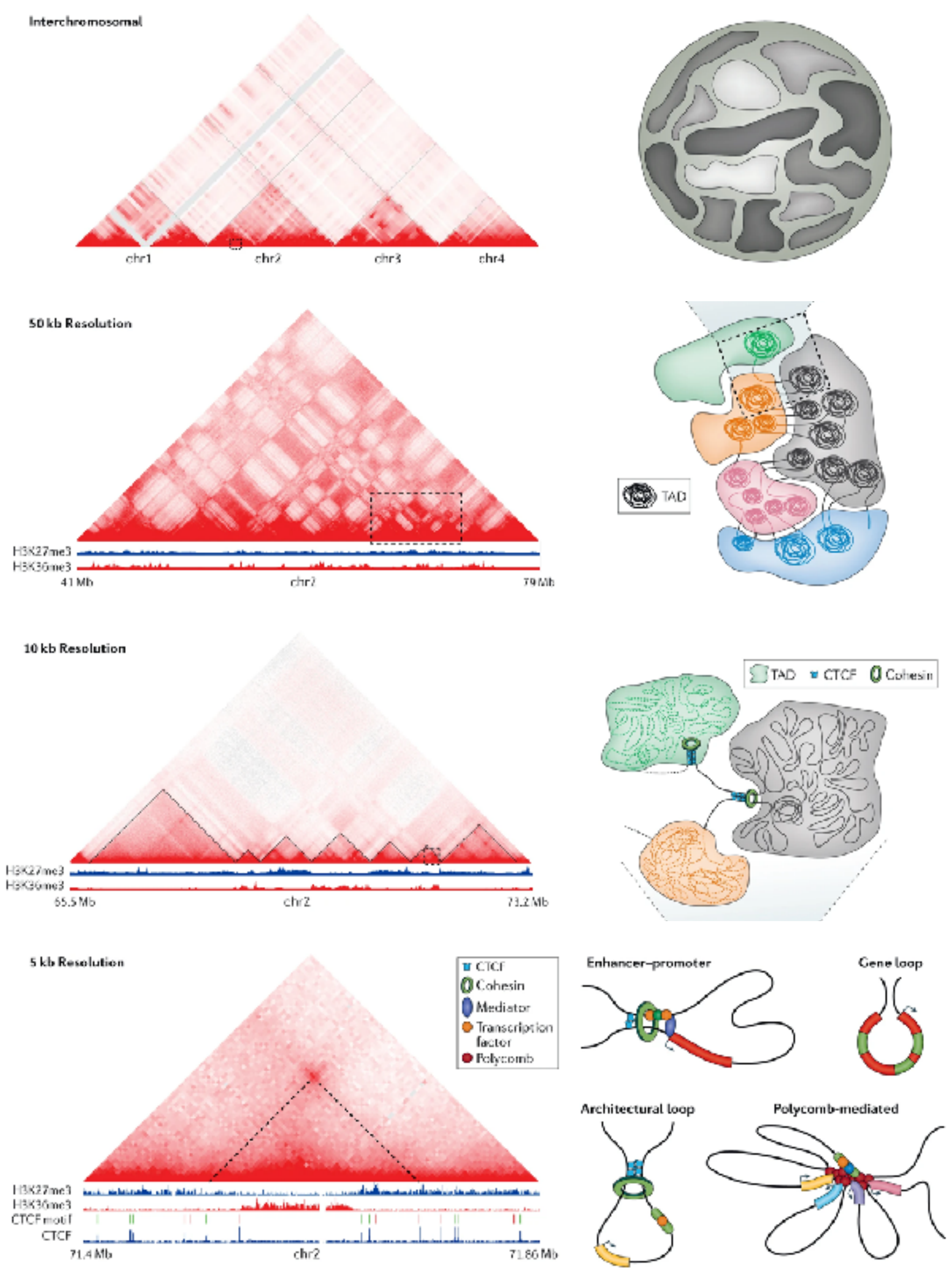


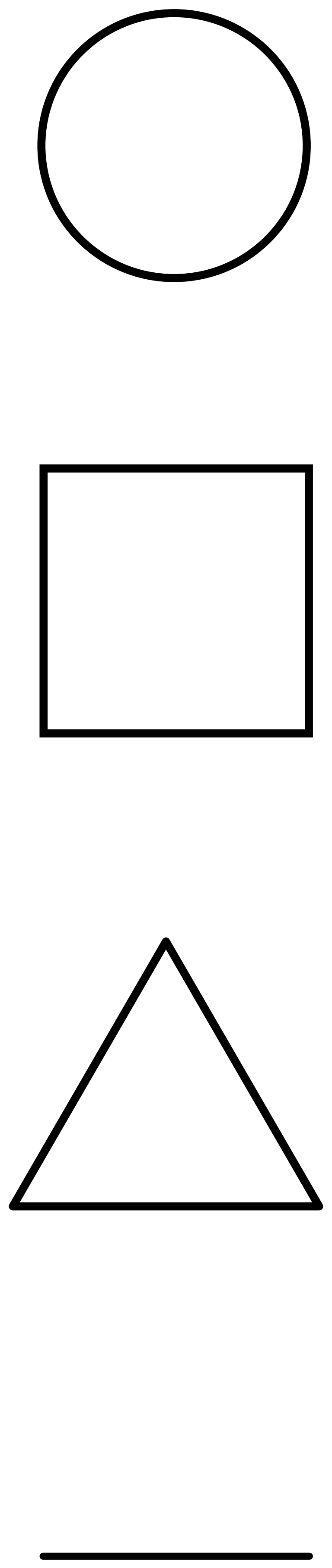


Lieberman-Aiden et al. Science 2009 Oct 9;326(5950):289-93
Baù & Marti-Renom Chromosome Res. 2011 Jan;19(1):25-35
Di Stefano et al. Scientific Reports 2016 Oct 27 (6):35985

3D Genome orgainzation

what we know…





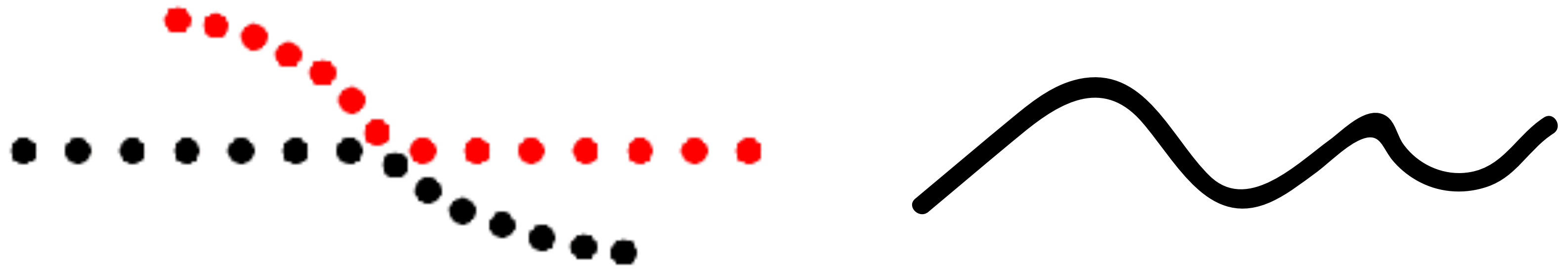
Bonev, B., Cavalli, G. Organization and function of the 3D genome. Nat Rev Genet 17, 661–678 (2016). https://doi.org/10.1038/nrg.2016.112

Geometric Diagrams of Genomes

a visual grammar for 3DGenomics

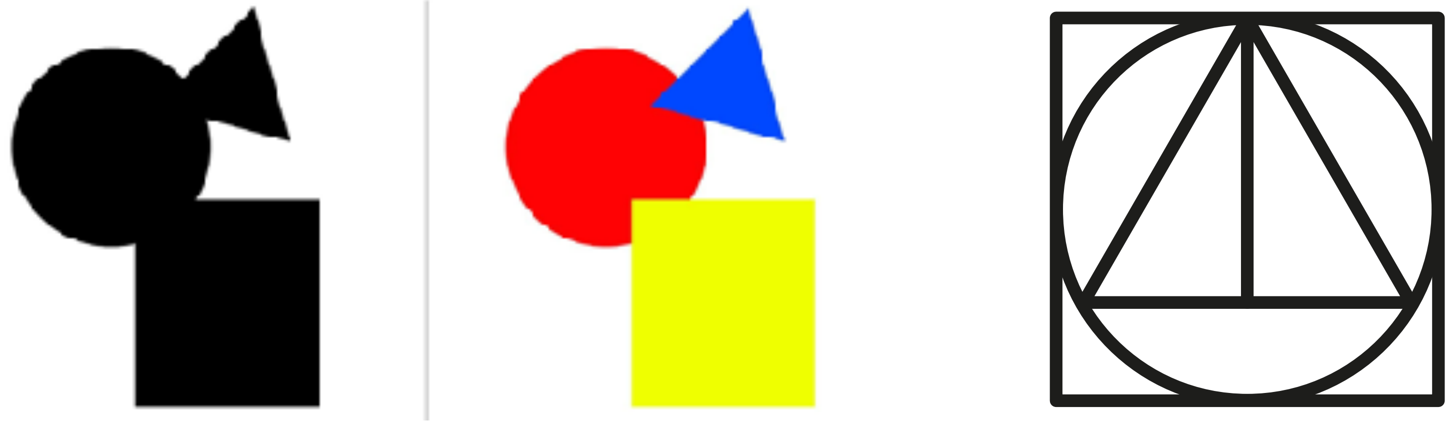
(some) The Gestalt Principles

continuation

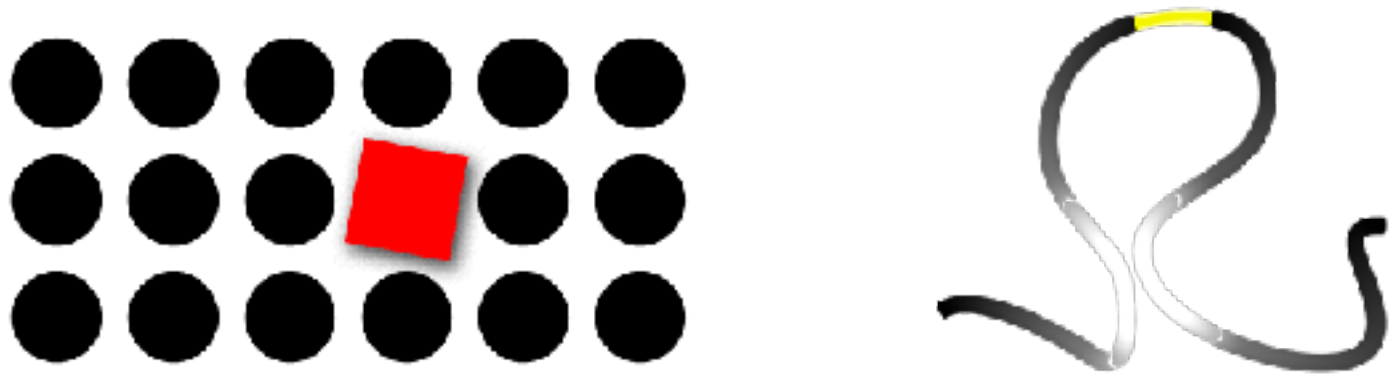


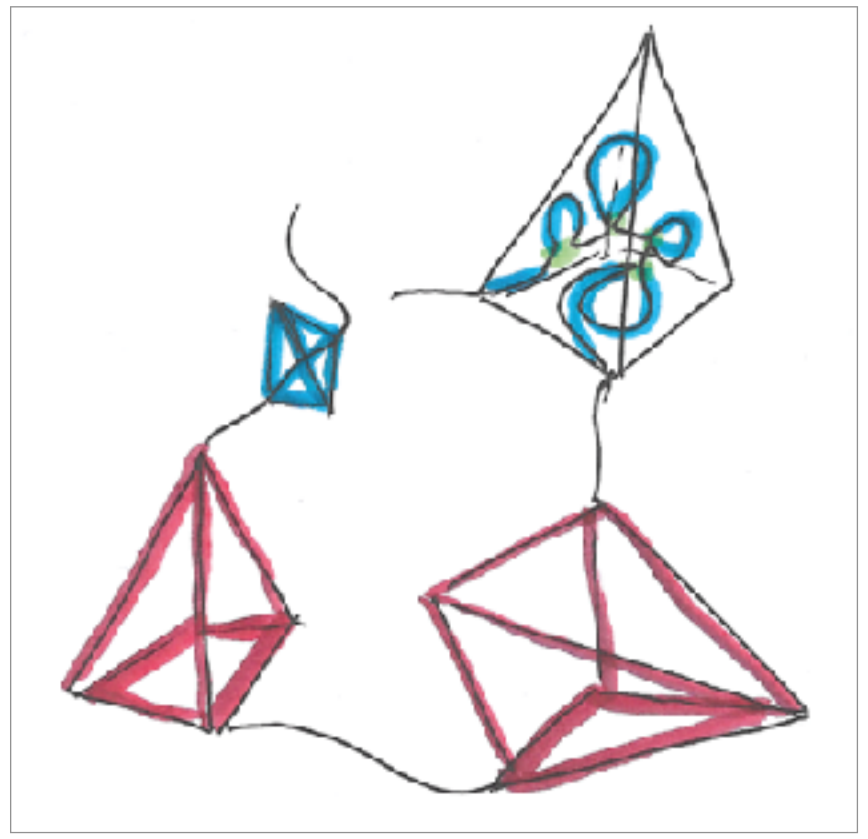
proximity

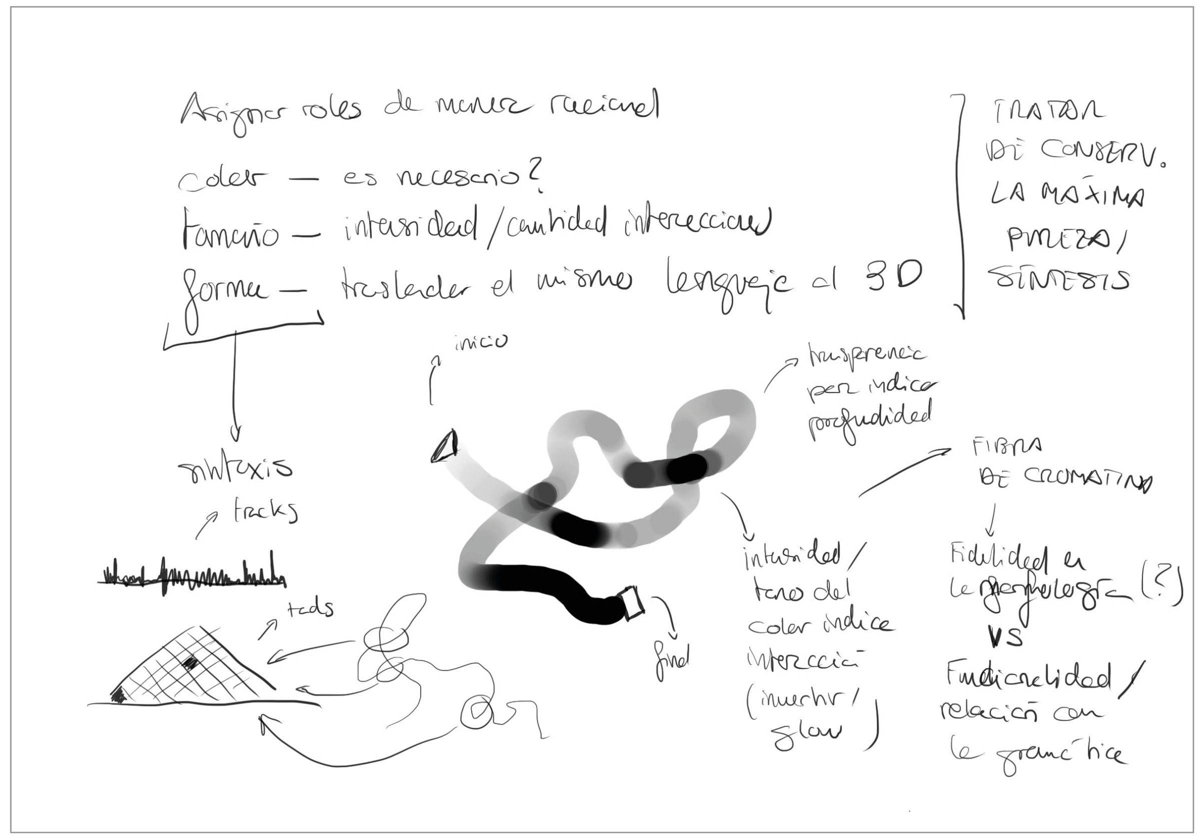
symmetry and order

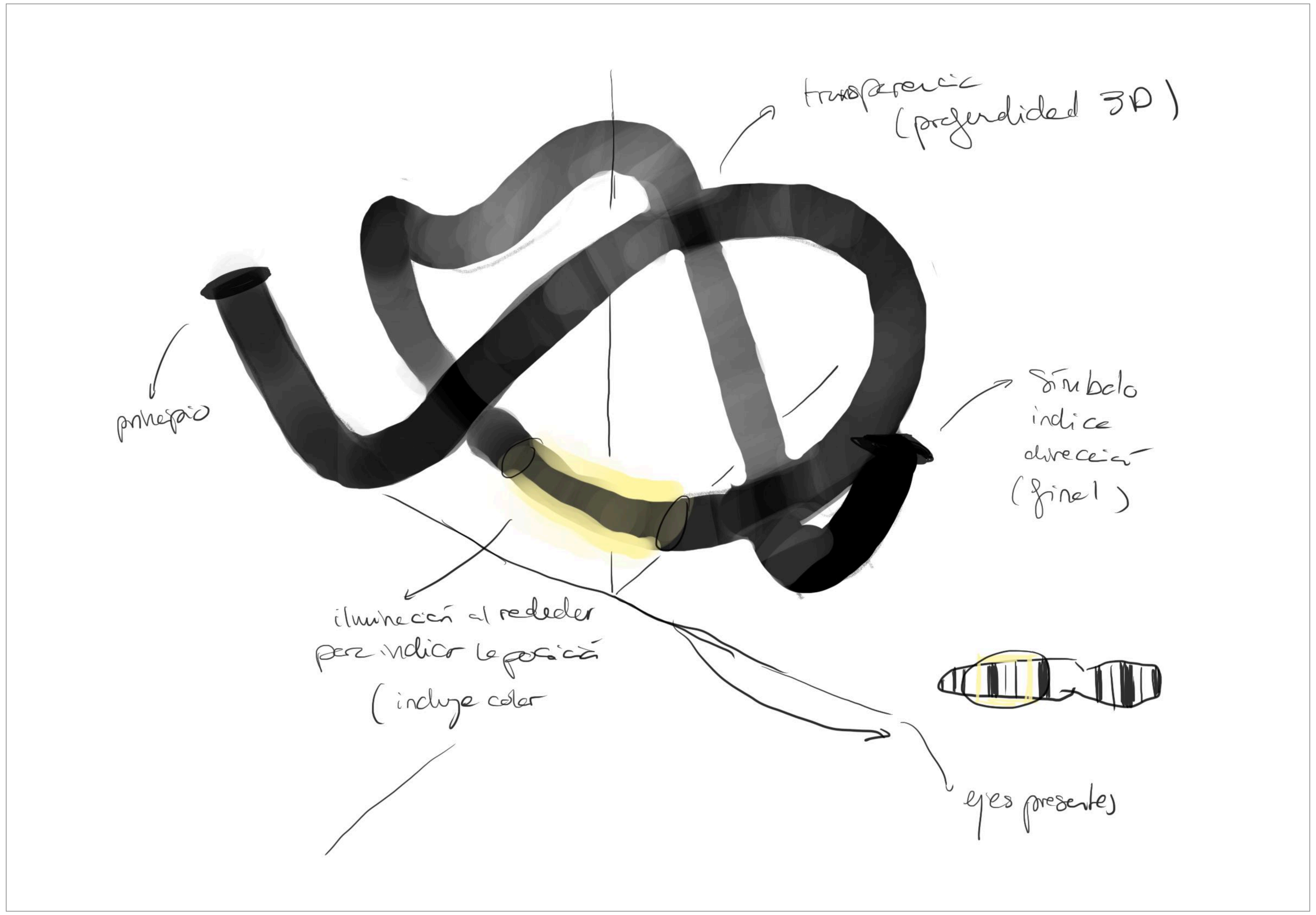


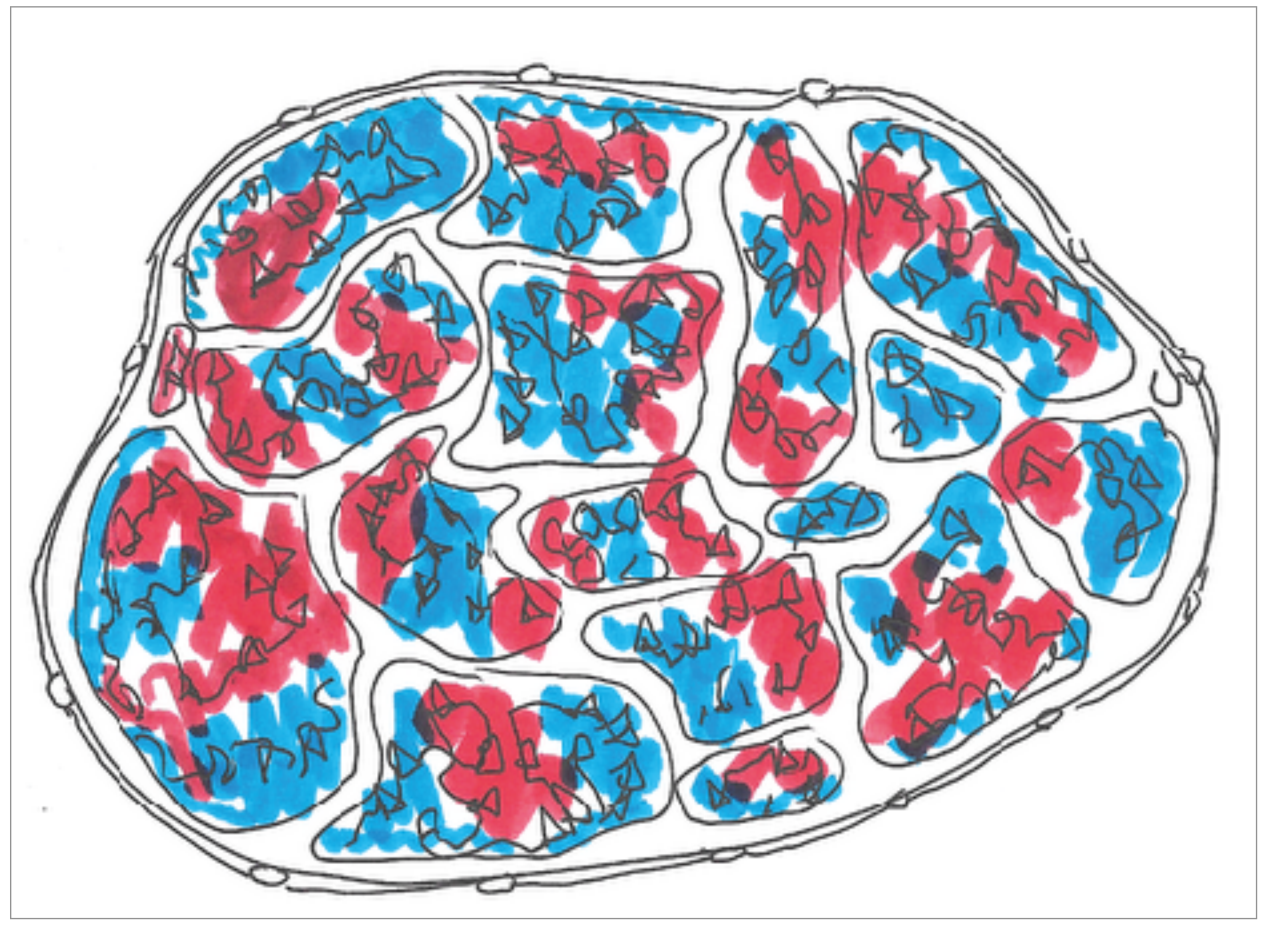
focal point

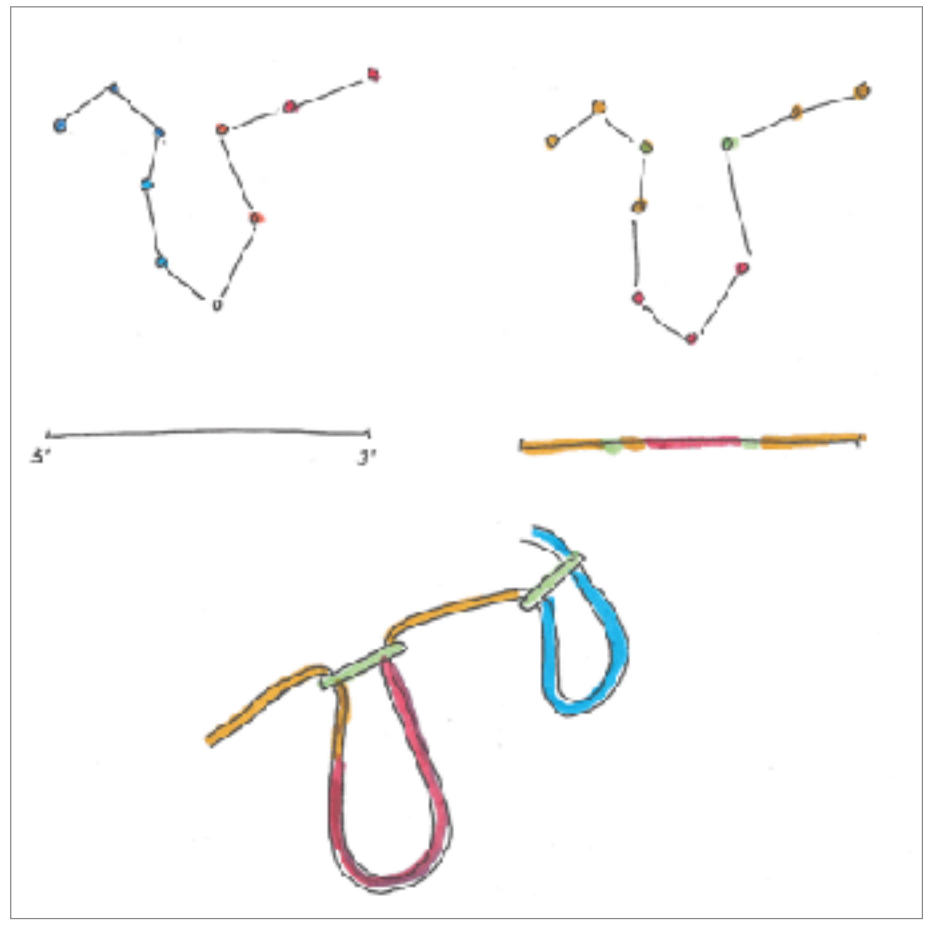


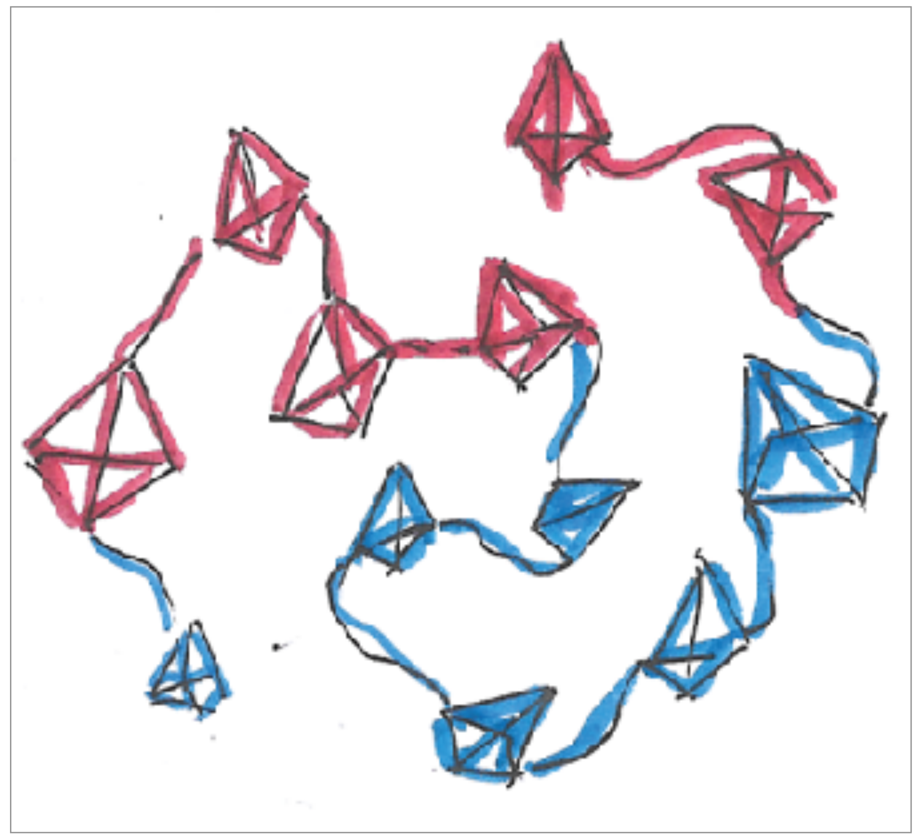


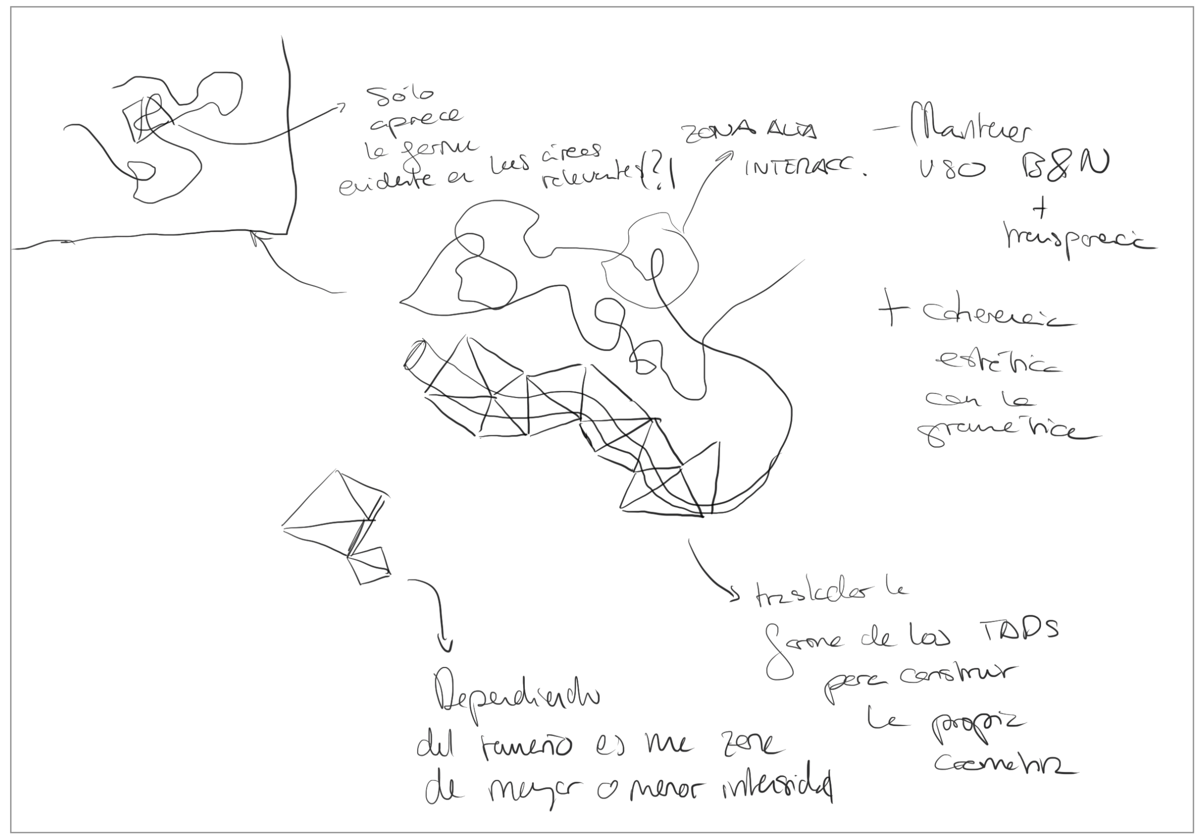

Asignar roles de manera racional
color — es necesario?
tamaño — intensidad / cantidad interacción
forma — trasladar el mismo lenguaje al 3D
TRATAR DE CONSERV. LA MÁXIMA PUREZA / SÍNTESIS
sintaxis
tracks
tads
inicio
final
transparencia para indicar profundidad
FIBRA DE CROMATINA
intensidad / tono del color indica interacción (insulator / glow)
Fidelidad en la morfología (?)
VS
Funcionalidad / relación con la gramática

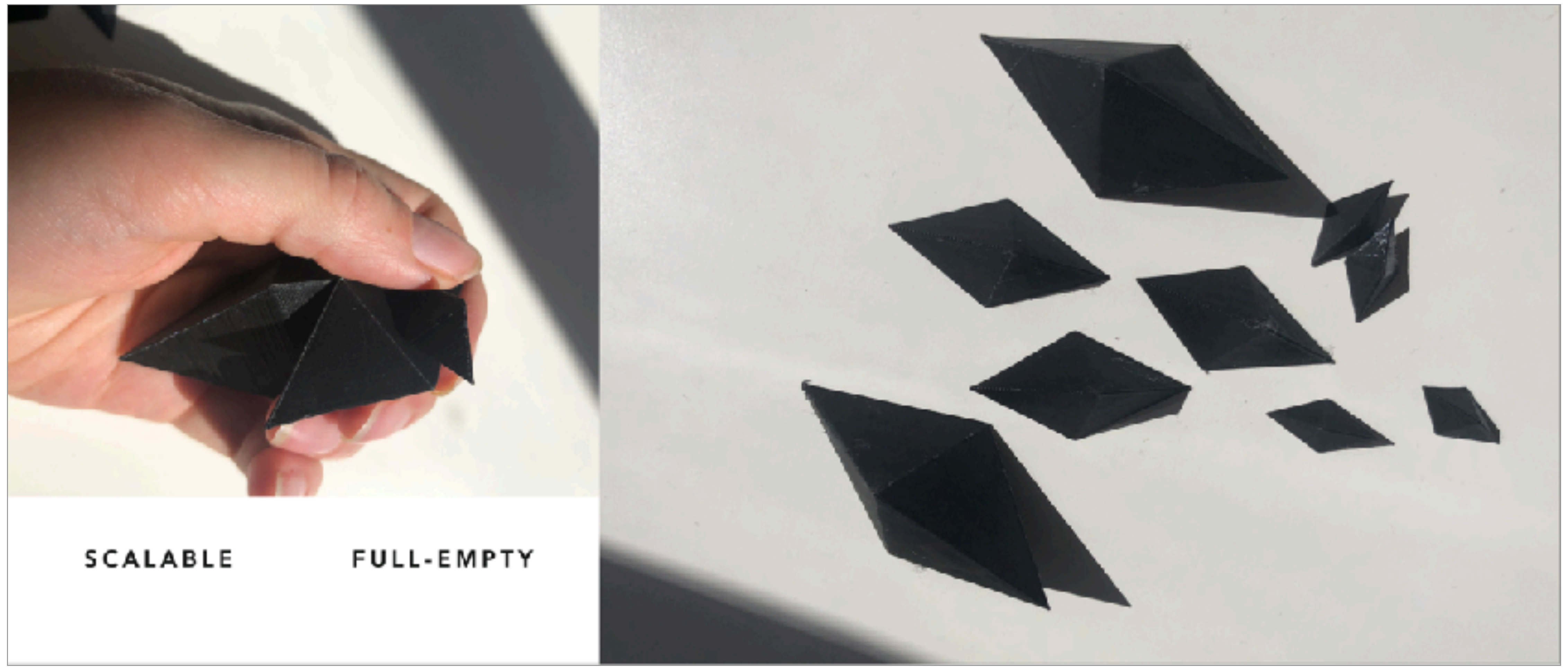

transparencia (profundidad 3D)
principio
símbolo indica dirección (final)
iluminación al rededor para indicar la posición (incluye color
ejes presentes




5'
3'




Sólo aparece la forma evidente en las áreas relevantes(?)
ZONA ALTA INTERACC.
— Mantener uso B&N + transparencia
+ coherencia estética con la gramática
trasladar la forma de los TADs para construir la propia gramática
Dependiendo del tamaño es una zona de mayor o menor intensidad


SCALABLE
FULL-EMPTY

Visual Grammar for 3DGenomics

color

sequence (1D)

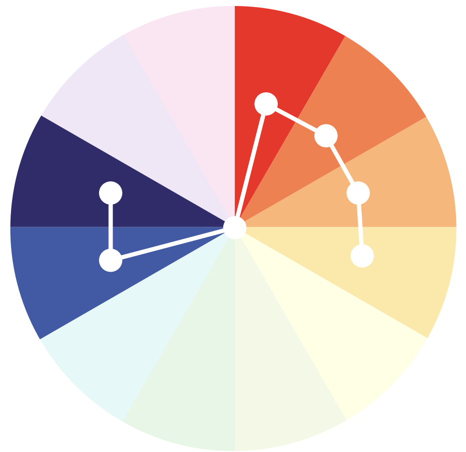
genes · genome annotation

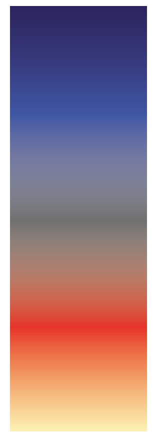
high-intensity (bright colors)

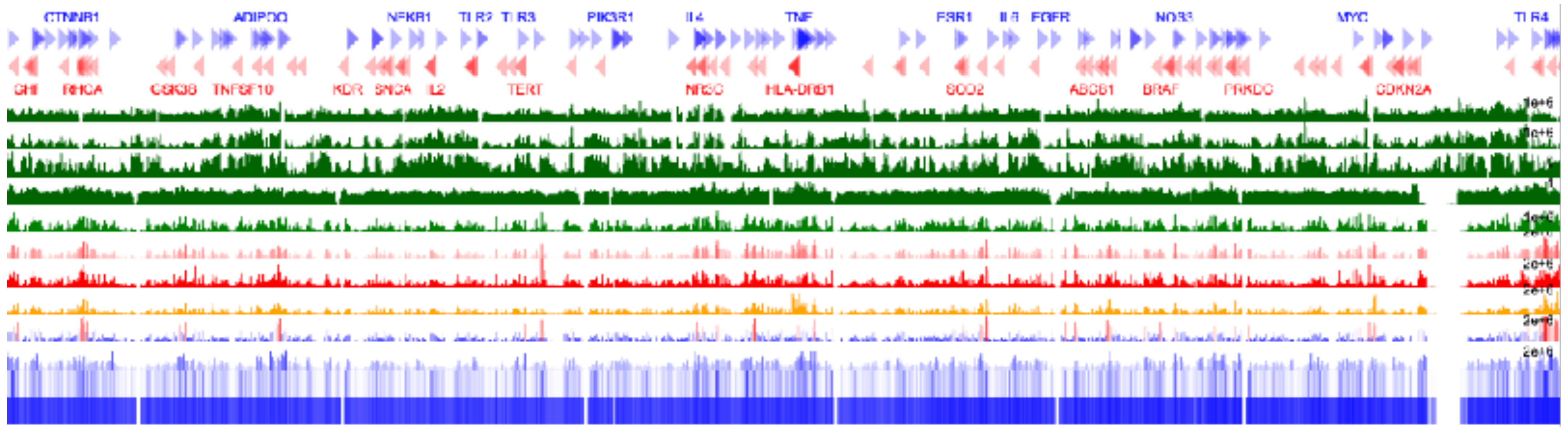
function (2D)

RNA-seq · ChIP-seq · markers

cold to warm (muted colors)



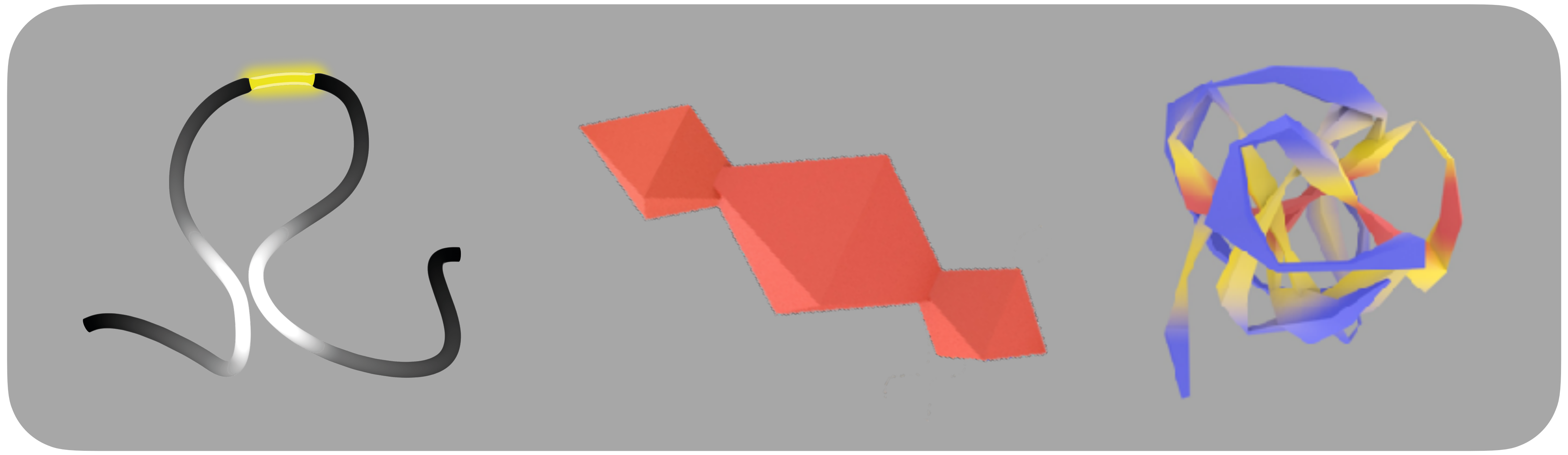




structure (3D)

3C-based data · 3D models

high-contrast (grey scale)



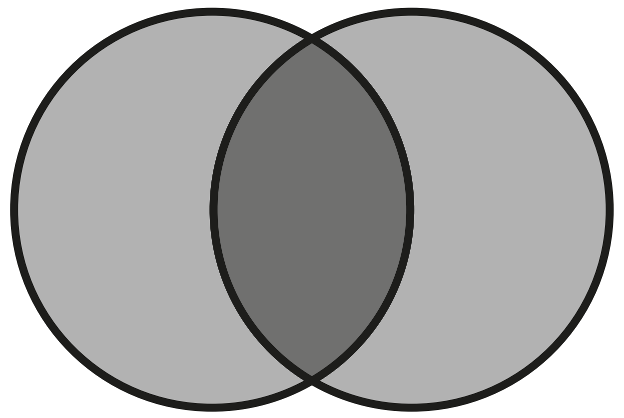
Visual Grammar for 3DGenomics

texture

sequence (1D)

genes · genome annotation

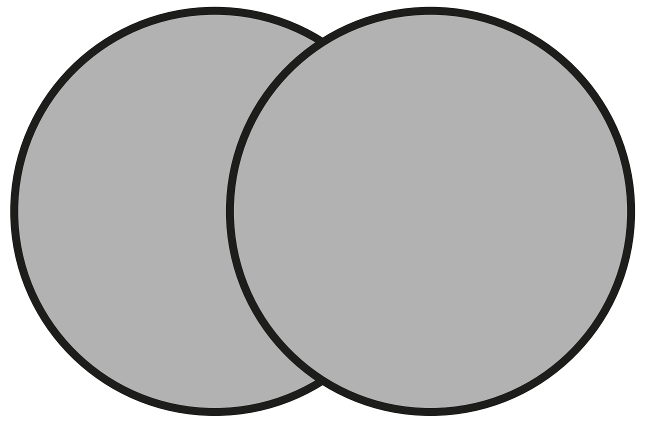
transparent

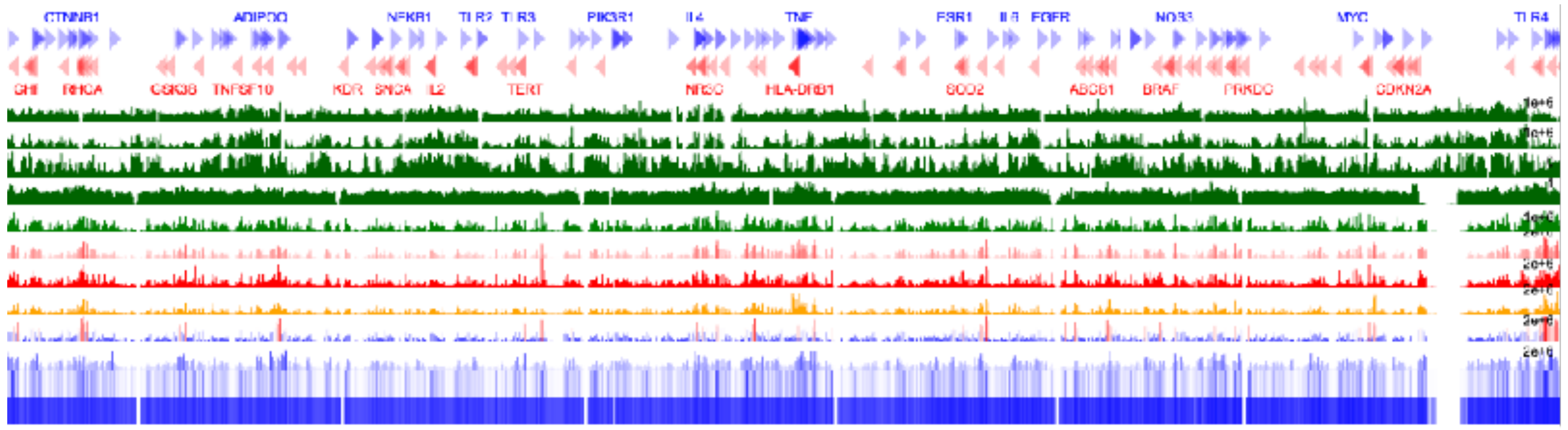


function (2D)

RNA-seq · ChIP-seq · markers

solid

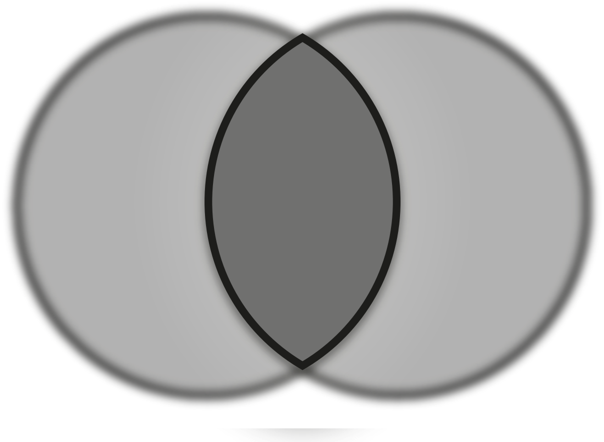


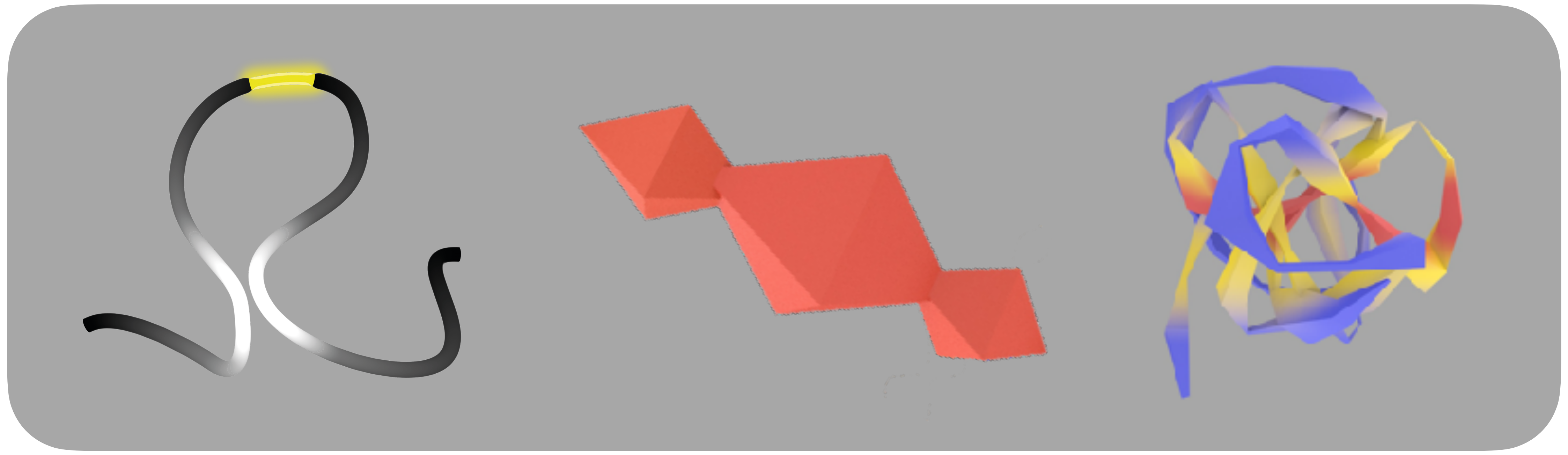


structure (3D)

3C-based data · 3D models

glow + field depth





Visual Grammar for 3DGenomics

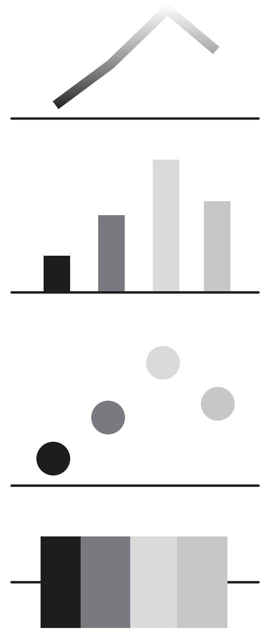
form

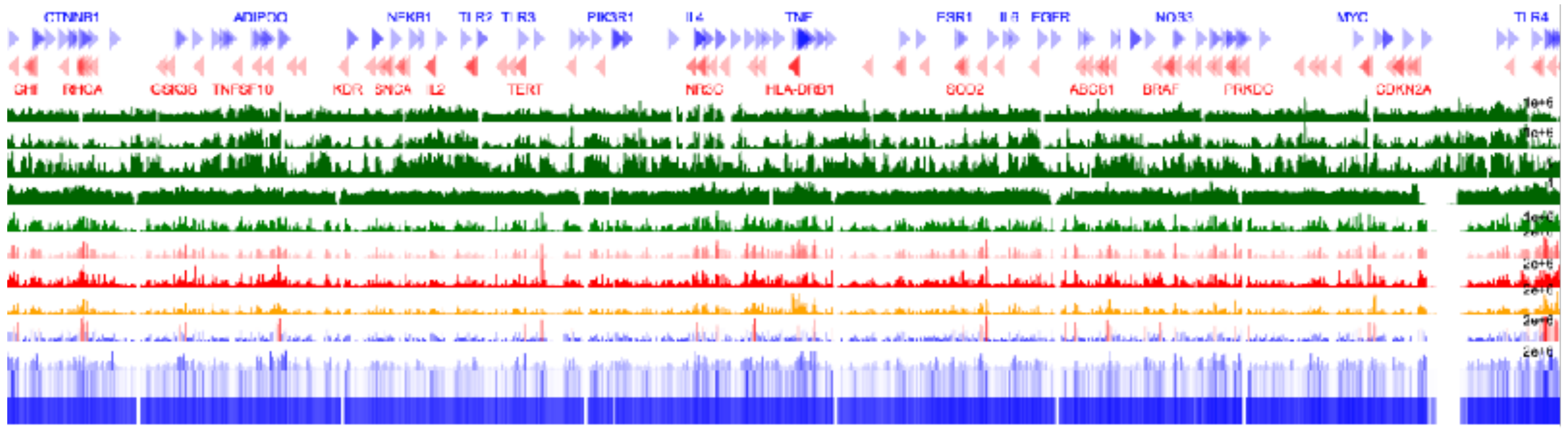
sequence (1D)

genes · genome annotation

function (2D)

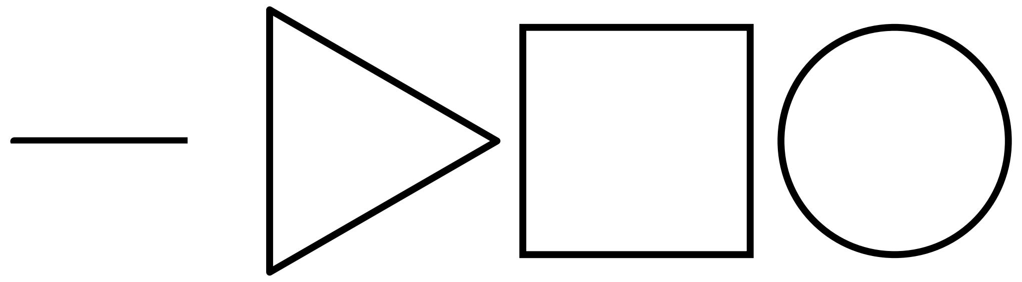
RNA-seq · ChIP-seq · markers

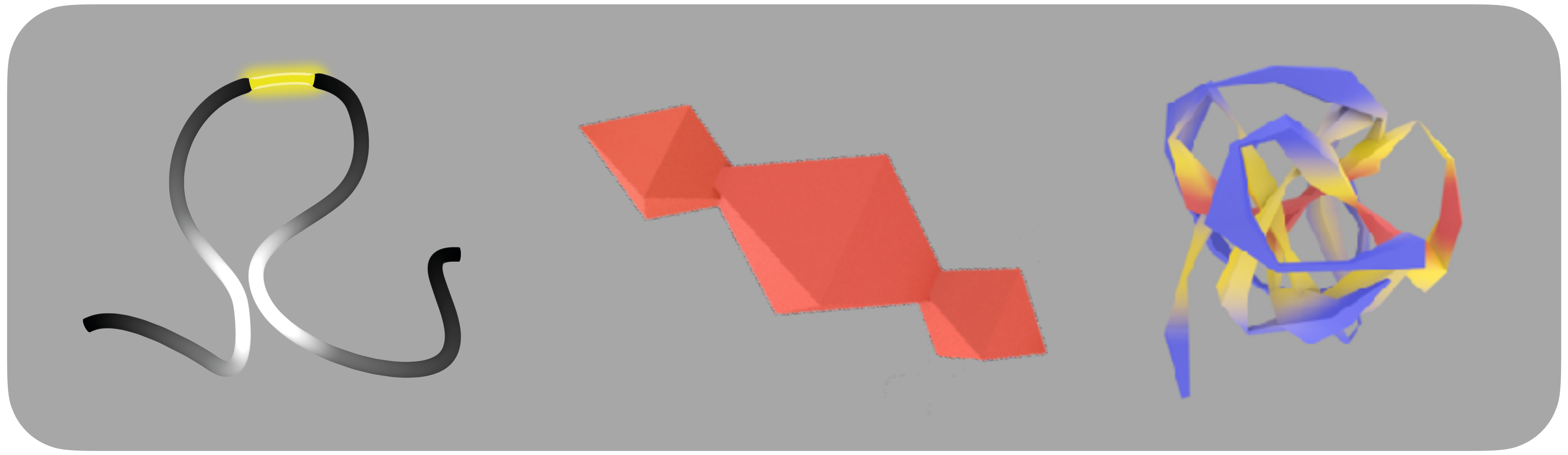


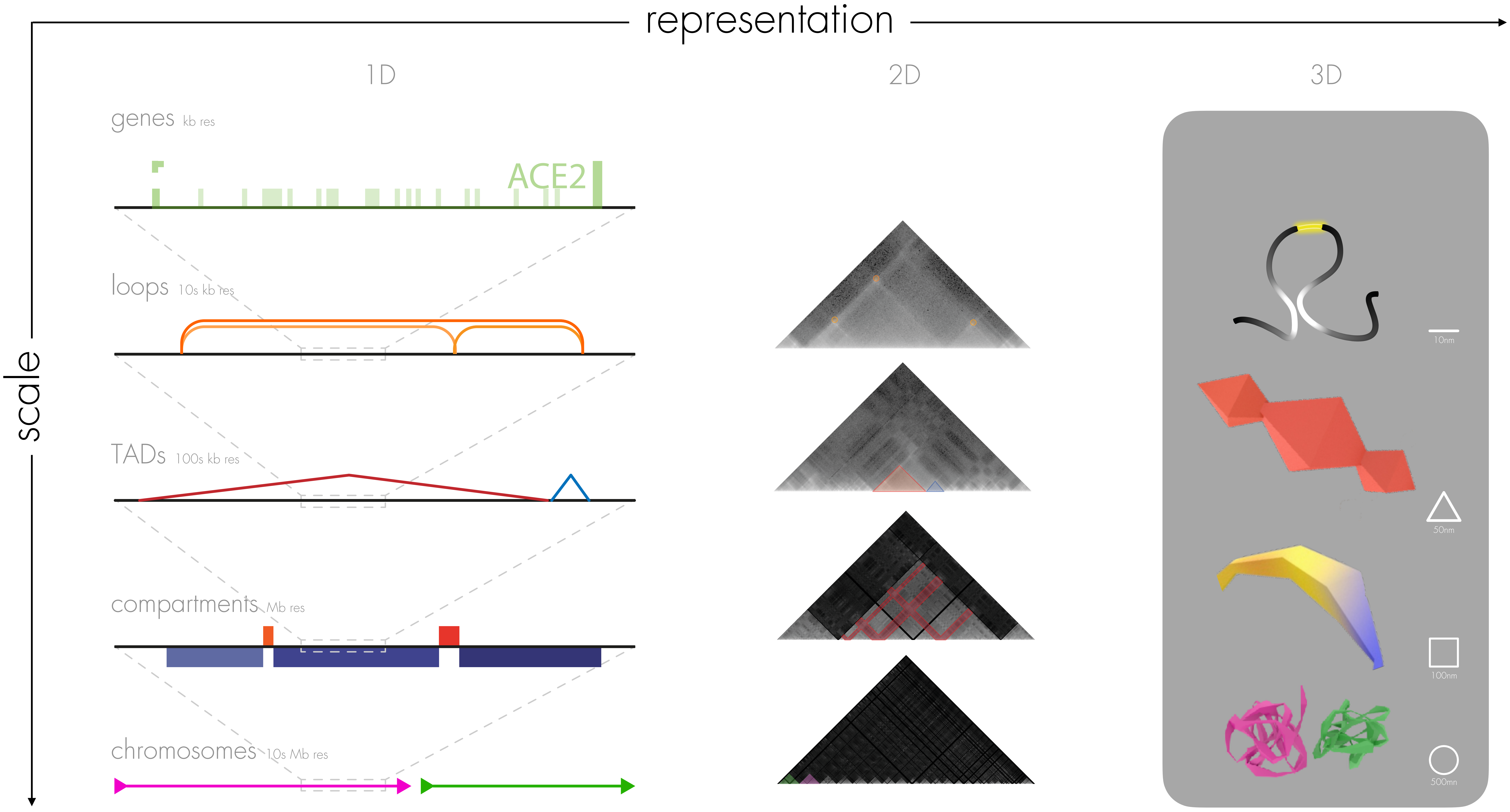


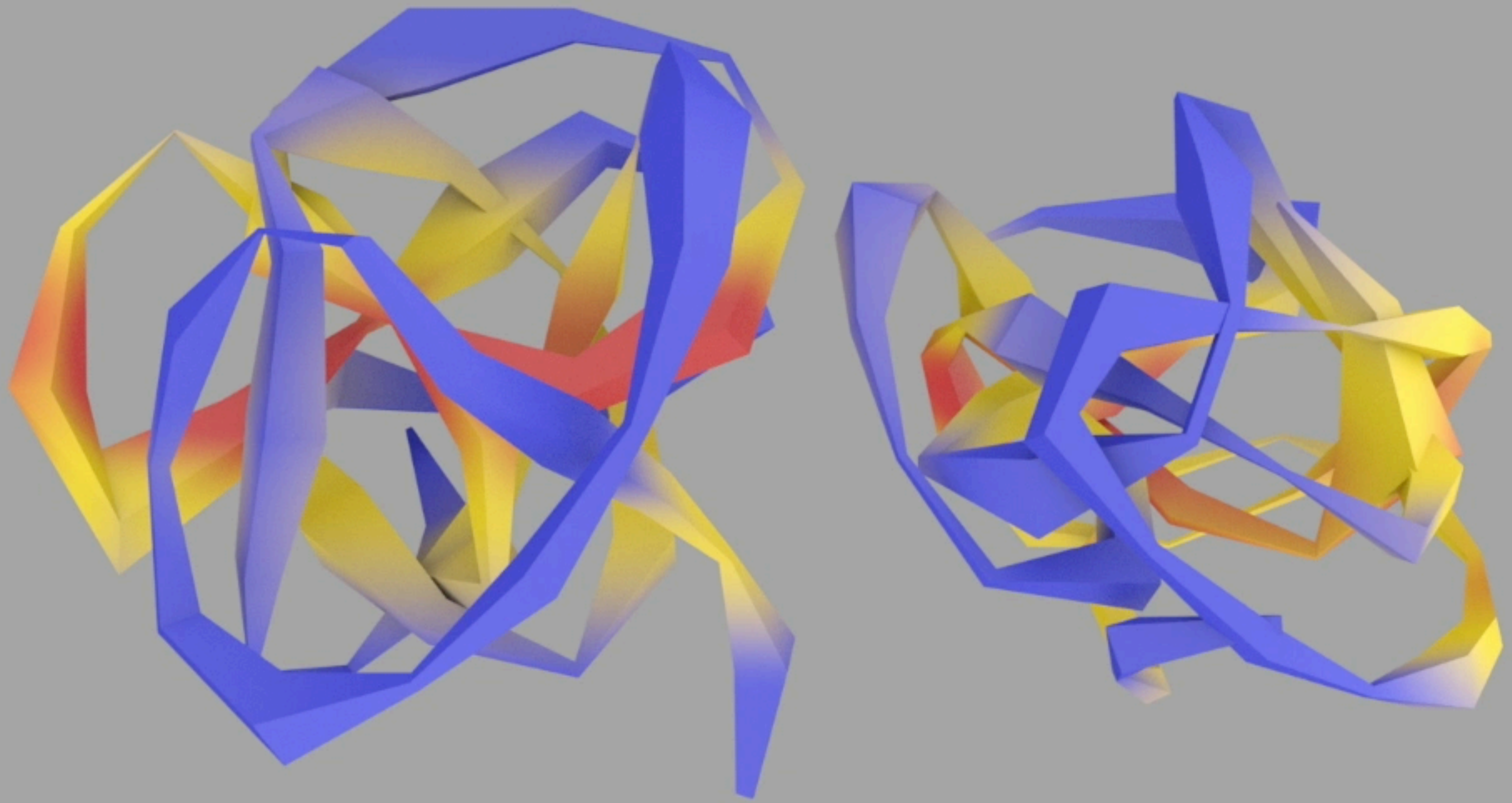
structure (3D)

3C-based data · 3D models





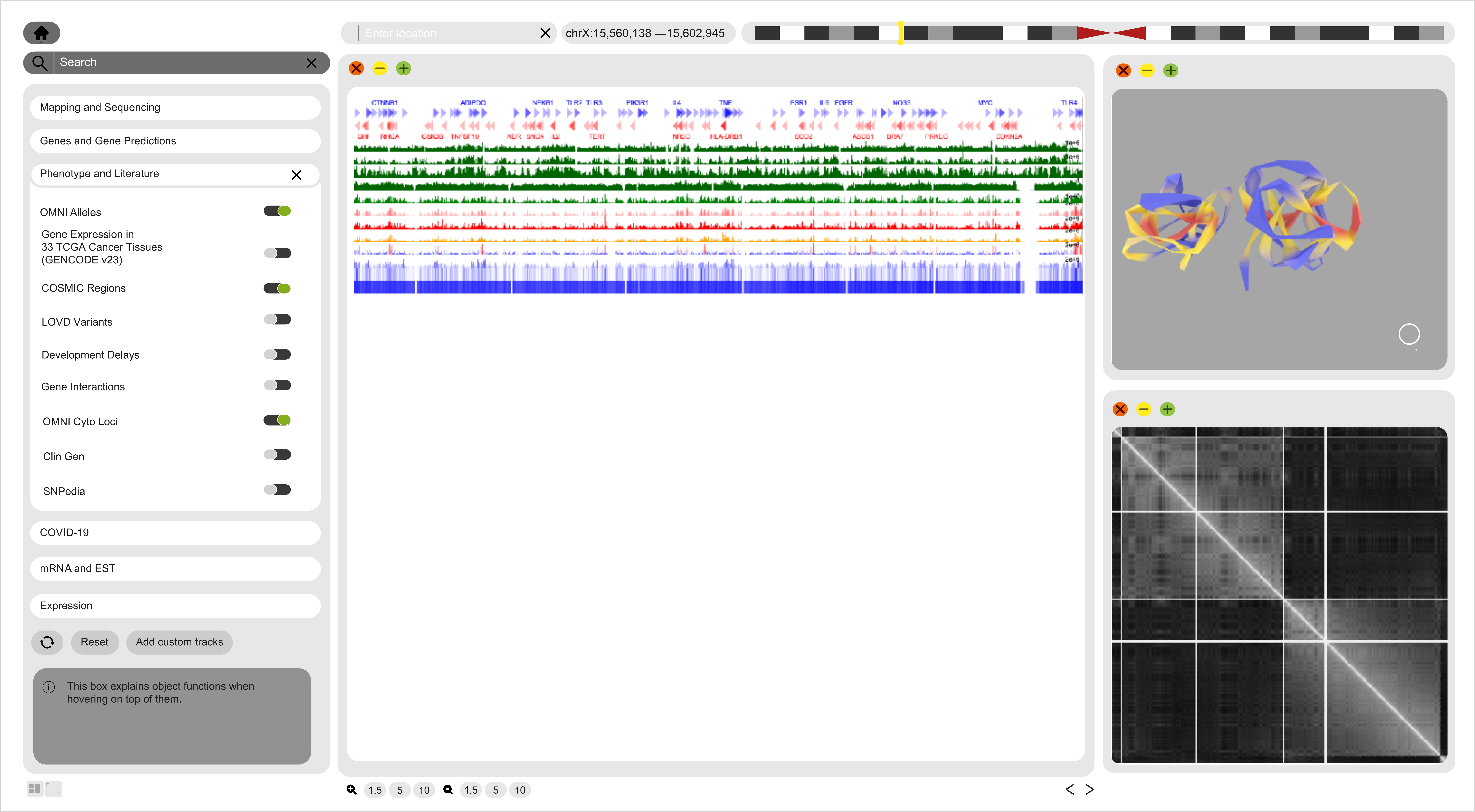

representation
scale
1D
2D
3D
genes kb res
ACE2
loops 10s kb res
TADs 100s kb res
compartments Mb res
chromosomes 10s Mb res
10nm
50nm
100nm
500mn



within a browser?

http://higlass.io · http://aidenlab.org/juicebox/ · http://aidenlab.org/spacewalk/ · http://3DGenome.org · http://vis.nucleome.org

Gehlenborg Lab (Harvard U.) · Aiden Lab (Rice U.) · Yue Lab (Northwestern U.) · Ma Lab (Carnegie Mellon U.)



chrX:15,560,138 —15,602,945

Phenotype and Literature

- OMNI Alleles ●
- Gene Expression in 33 TCGA Cancer Tissues (GENCODE v23) ○
- COSMIC Regions ●
- LOVD Variants ○
- Development Delays ○
- Gene Interactions ○
- OMNI Cyto Loci ●
- Clin Gen ○
- SNPedia ○

This box explains object functions when hovering on top of them.

CHROMDESIGN

ELISAVA
Barcelona School of
Design and Engineering

Elisava Research

cnag

CRG Centre for Genomic Regulation

ICREA


Yolanda Justicia Contreras
ELISAVA


Clementina Altube
ELISAVA


Santiago Bonet Garrote
ELISAVA


Mike Goodstadt
CNAG-CRG


Carla Molins Pitrach
ELISAVA


Francesc Ribot Puntí
ELISAVA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