

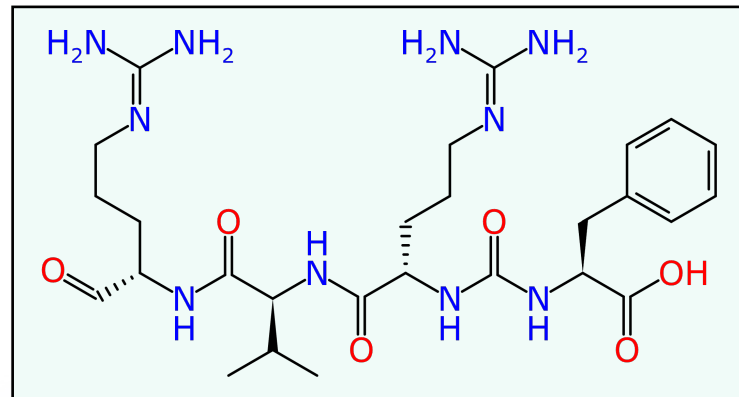
Conjugate biomolecule  
datastructures for chemistry  
and biochemistry discovery



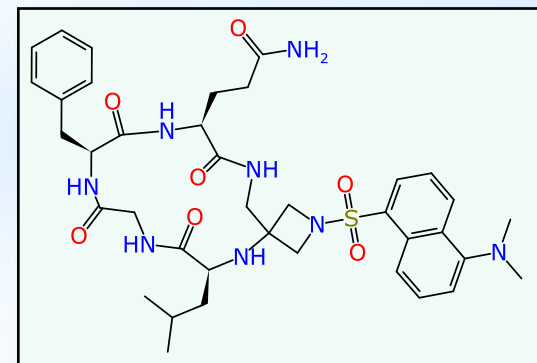
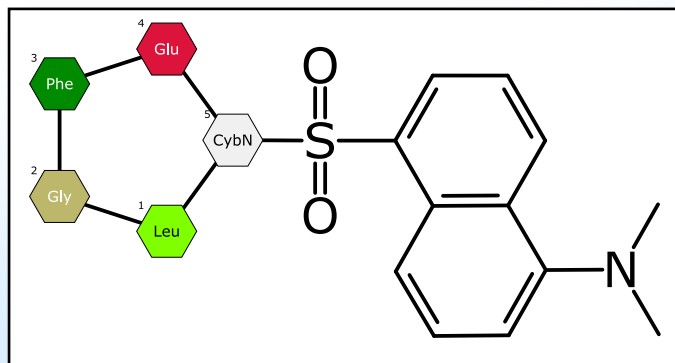
Alex M. Clark

H	R	R	T	S
Q	R	C	E	E
E	R	Y	V	P
V	N	Y	C	C
Q	W	G	M	

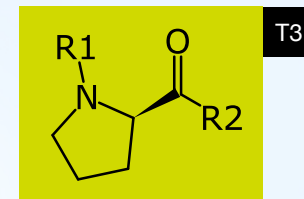
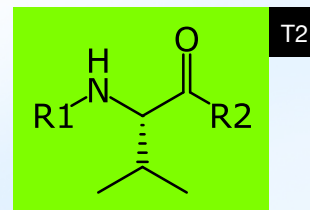
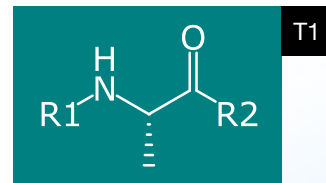
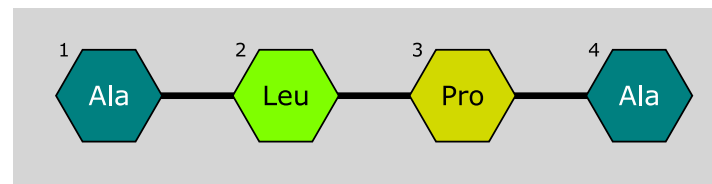
- Bioinformatics vs. Cheminformatics
- Need both...



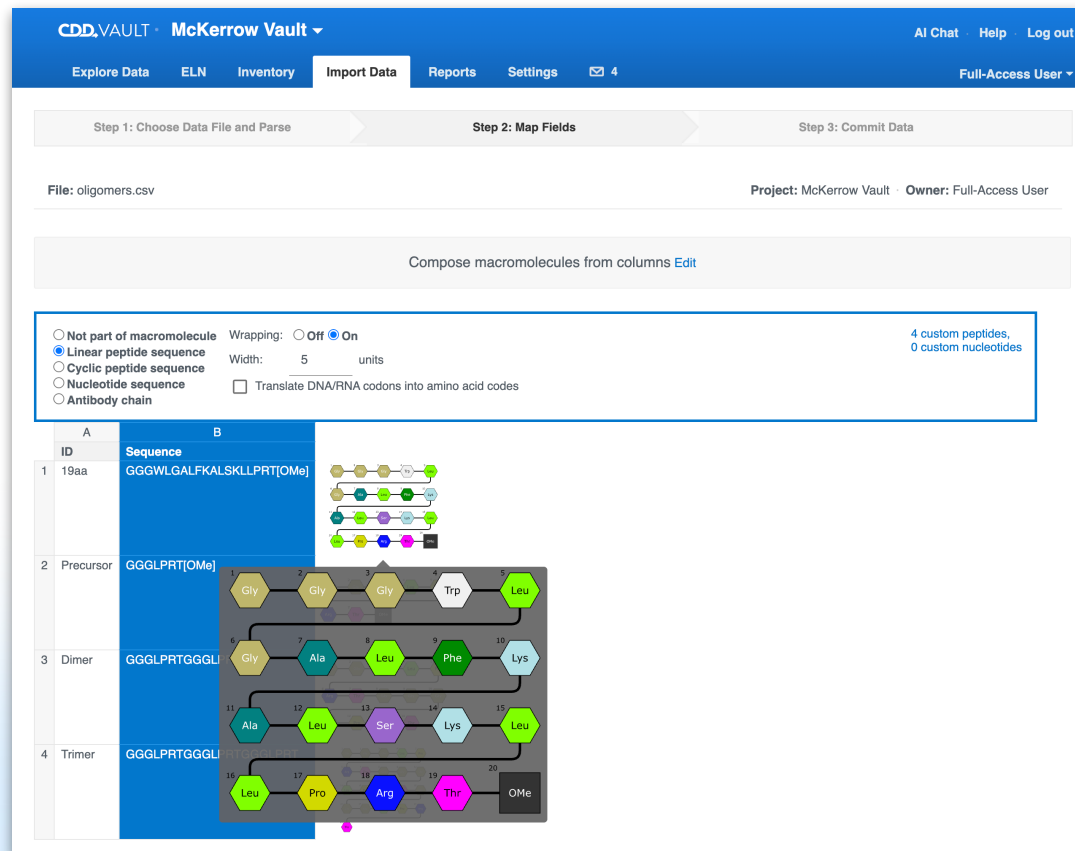
**L,G,F,E,CybN-SO<sub>2</sub>NphNMe<sub>2</sub>\***



- V3000 molfile feature called **SCSR**
- **Layout** information as 2D sketch
- Monomers as **templates**: scalable
- Self contained, no external **dictionary**
- Full **atomic** structure is implied
- Contains the **sequence** data for bioinformatics

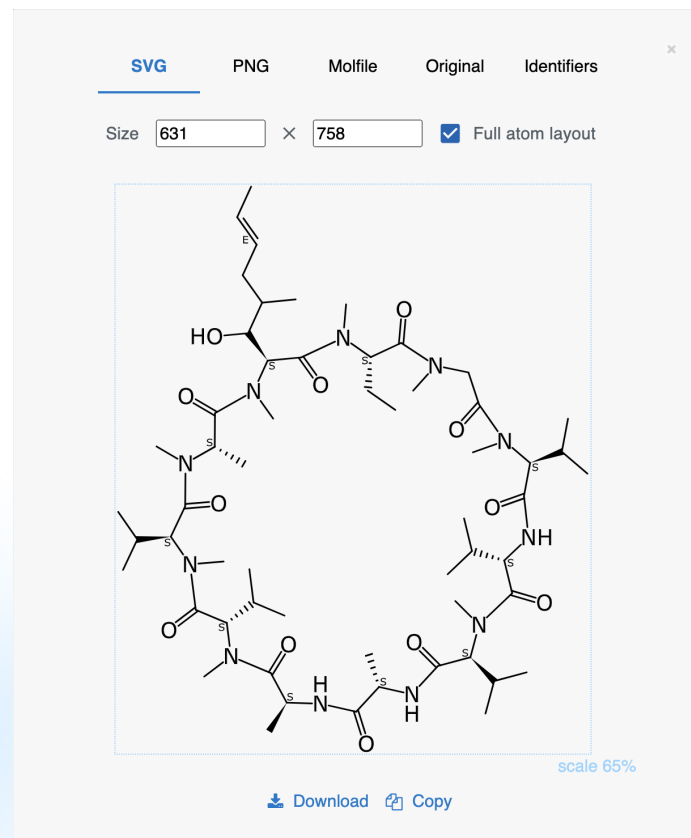
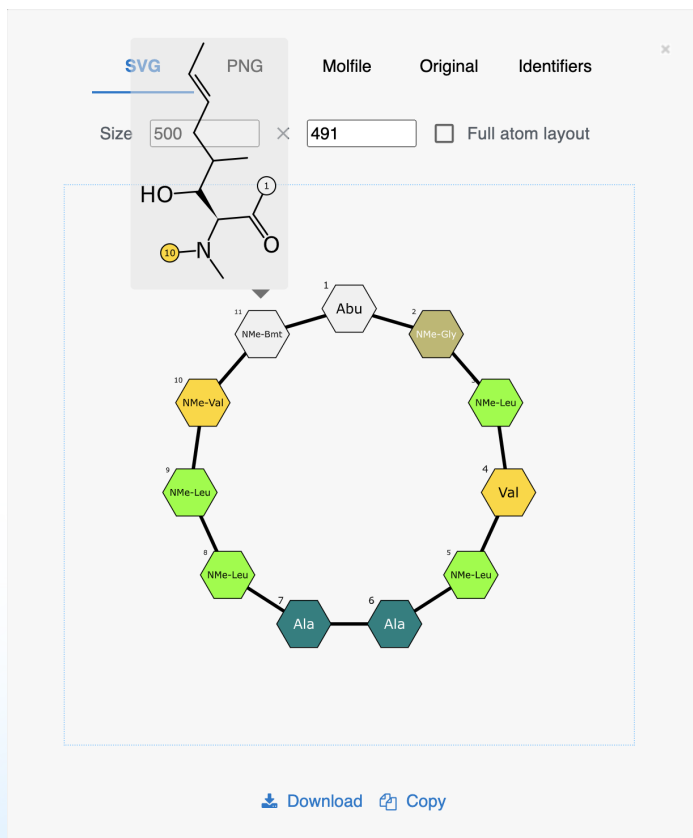


- Draw anything with Ketcher
- Bulk import: markup sequences
- Custom monomers optional



A	B
ID	Sequence
1 19aa	GGGWL.GALFKALSKLLPRT[OMe]
2 Precursor	GGGLPRT[OMe]
3 Dimer	GGGLPRTGGGL
4 Trimer	GGGLPRTGGGL

# Cyclic peptides



Explore Data ELN Alex Clark ▾

Step 1: Choose Data File

File: importcodons.csv

0 custom peptides,  
0 custom nucleotides

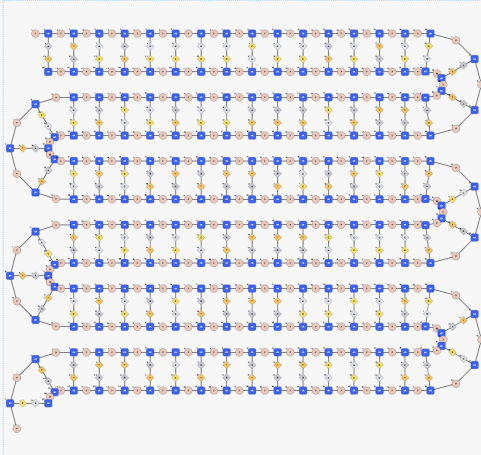
Not part of macromolecule  
 Linear peptide sequence  
 Cyclic peptide sequence  
 Nucleotide sequence

A	Name	Sequence
1	Seq1	ATGAGGGGCGGAGT TCATGATCCGAAATG ATATCTAATAG
2	Seq2	ATGAGGGGCGGAGT TCATGATCCGAAATG ATAAATAA
3	Seq3	ATGCCTTGGCCCTC CAGGAGGCAAATGCC GTGA

### Preview Macromolecule

SVG PNG Mofile Original Identifiers

Size  ×   Full atom layout



scale 25%

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Light

DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSR  
SGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVV  
CLLNNFYPRKAVQWVKVDNALQSGNSQESVTEQDSKDESTYSLSSLTTLKADYEKHKVYACEVTH  
QGLSSPVTKSFNRGEC {VL:1-107}{CL:108-214}{@214:1}

Heavy

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVK  
GRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSASTKGPSVF  
PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSS  
LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE  
VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC  
KVSNAKALPAIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP  
ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK  
{VH:1-120}{CH1:121-218}{CH2:234-343}{CH3:344-450}{H:219-233}{@223:1}{@229:2}  
{@232:3}{S264:1}{S324:1}{S370:1}{S428:1}



Domain Region



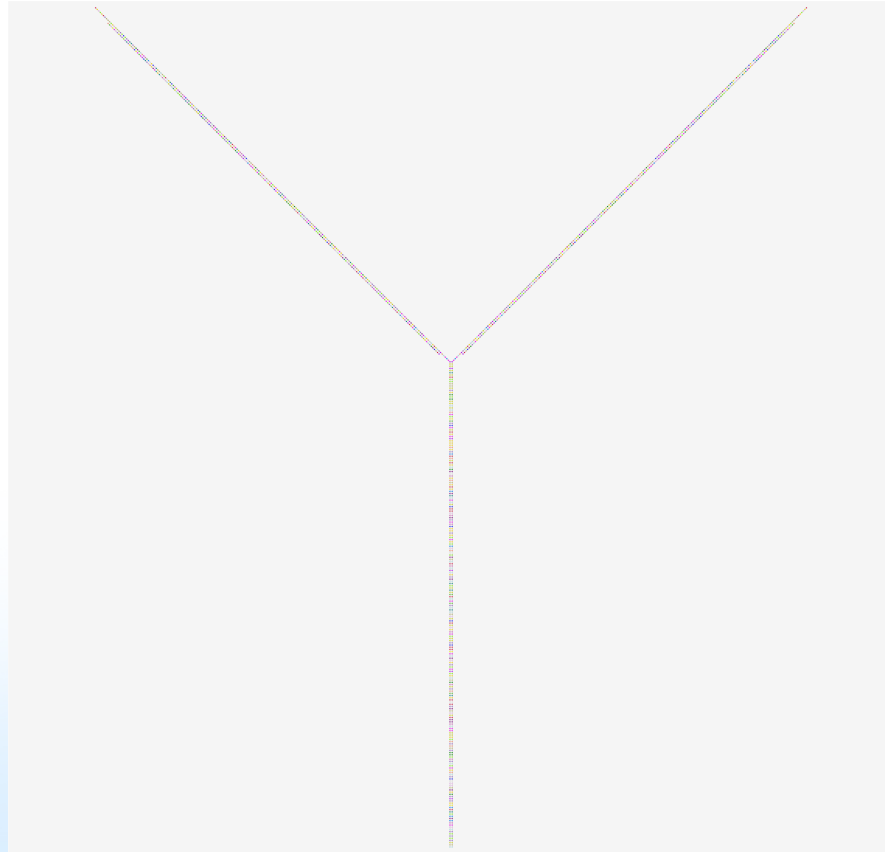
Disulfide Bridge



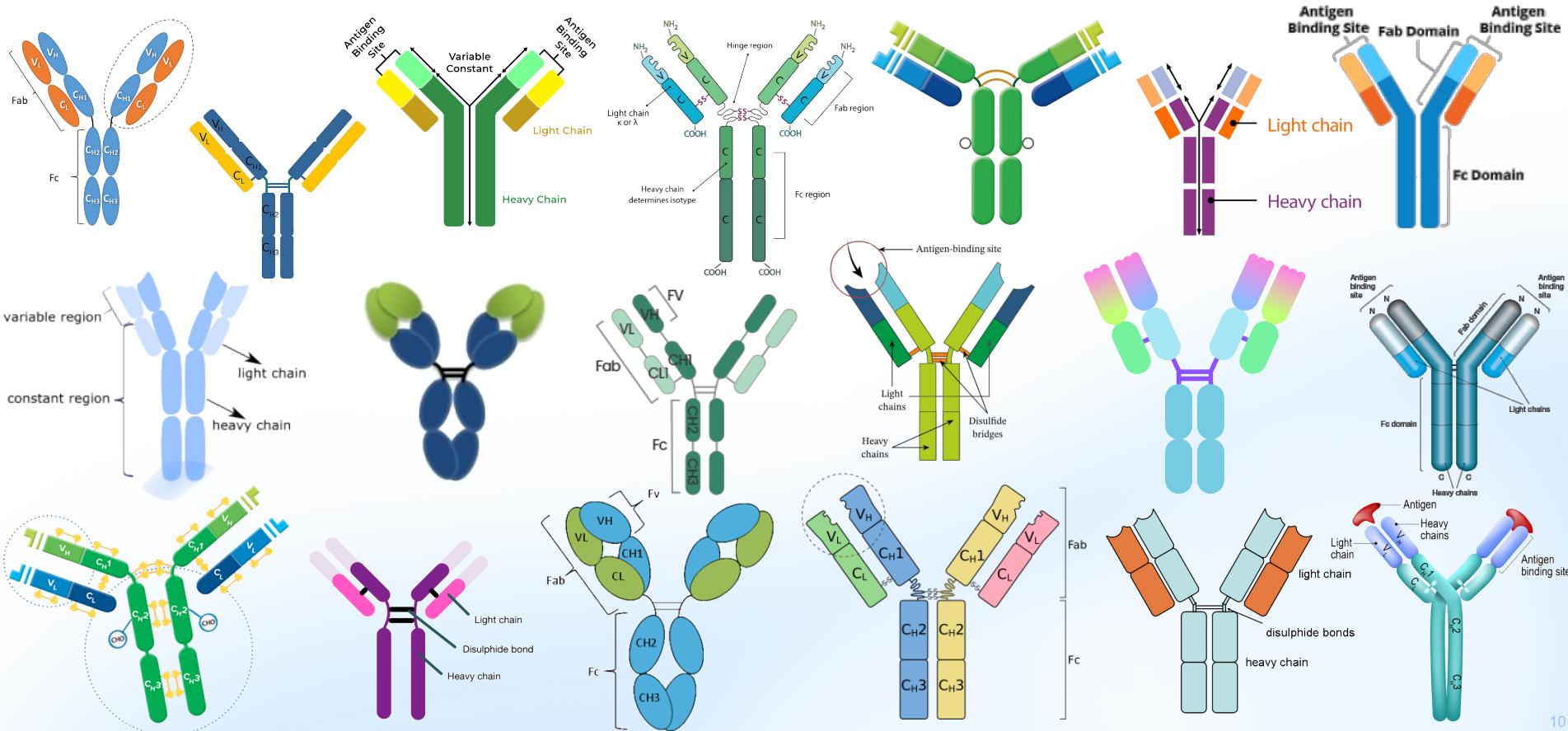
Hinge Region



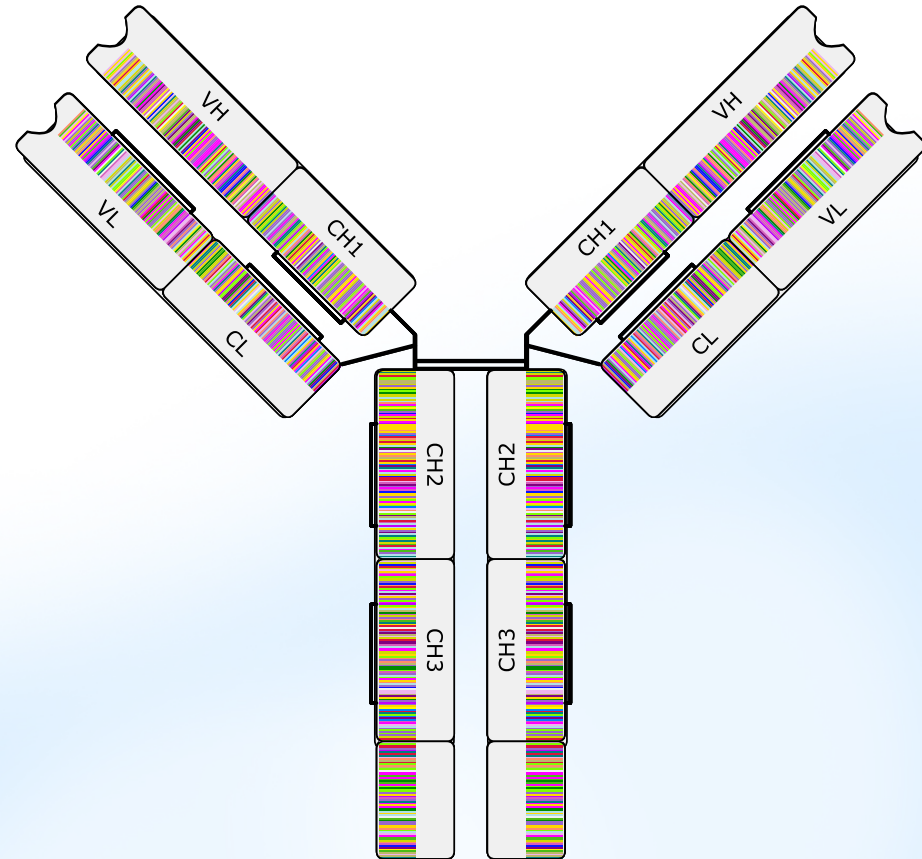
Drug Conjugate Site



# Display

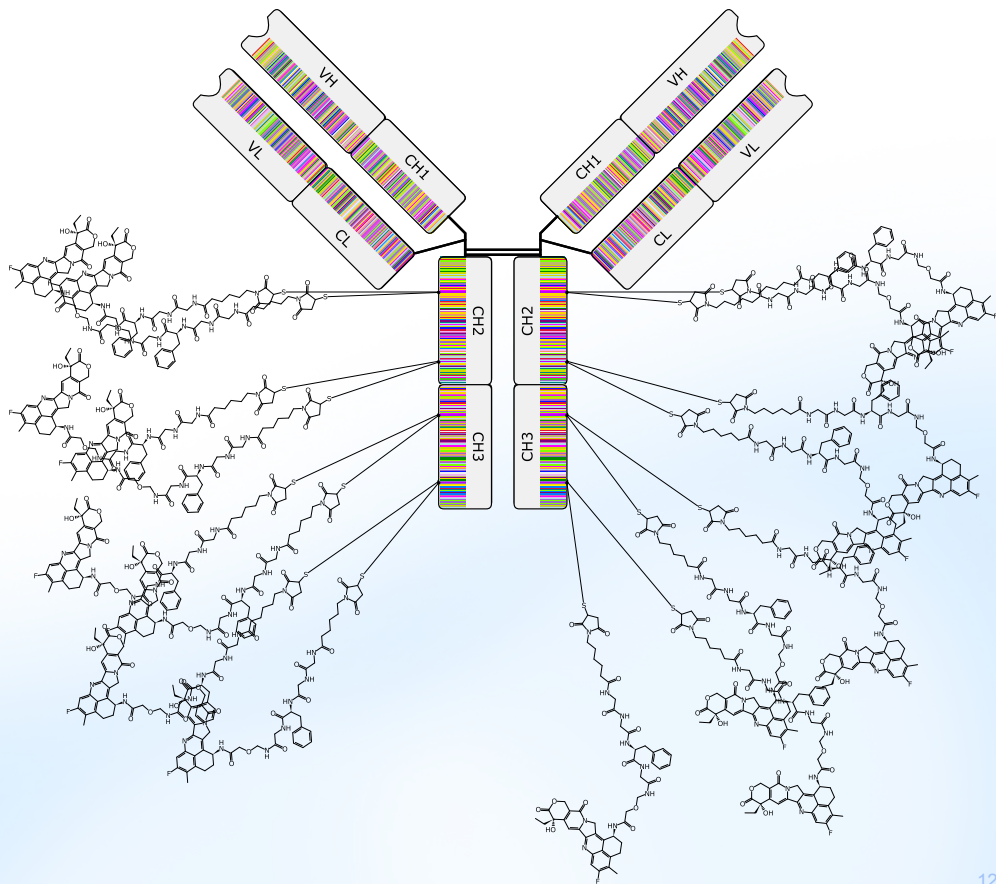


- Draw basic Y-shape outline
- Segment domain regions
- Inter-chain disulfide links
- Intra-chain disulfide links
- Sequence barcoding



# Drug conjugates

- Tethered initial placements
- Rigid body position optimization
- Anchor point is indicated





- **Diagrams** for biologists
- **Sequences** for bioinformaticians
- **Atoms & bonds** for chemists
- Standard formats and open source tools where possible
- Provide all information: get all the functionality
- Complete informatics is fundamental to everything