

The trick in biology is to select, from the thousands of facts that you know, the three that are relevant to your problem, and to not be disturbed that they contradict each other.

Eric Wieschaus  
(paraphrased)

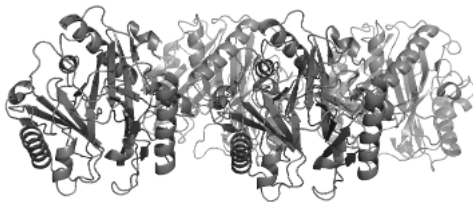
# 3D Structures

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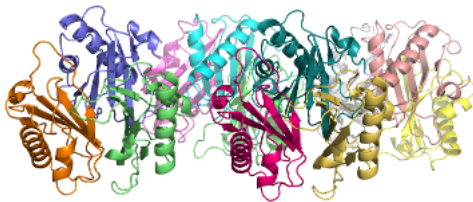
# Orienting ourselves

```
select all  
color grey  
hide everything  
show cartoon
```



# Orienting ourselves

2CHT → C → by chain → by chain



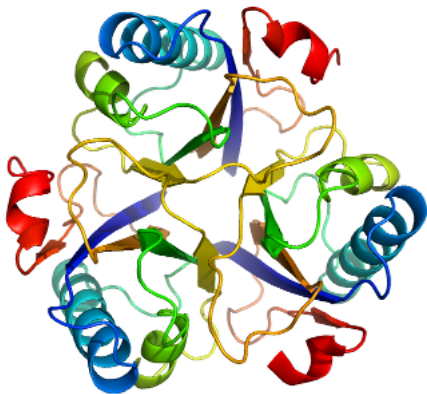
# Pick one trimer in the unit cell

```
select all  
hide everything  
select trimer1, chain a+b+c  
show cartoon, trimer1  
orient trimer1
```



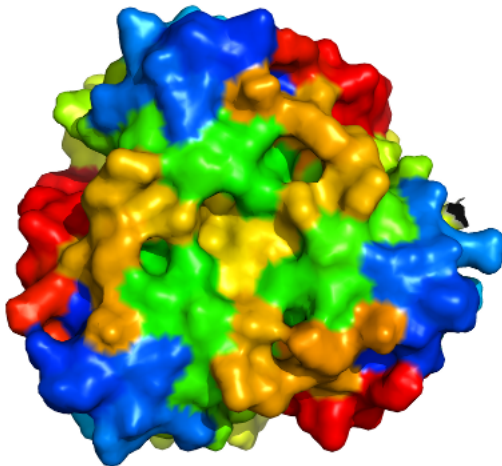
# Orient ourselves on the primary structure

trimer1 → C → by chain → chainbows



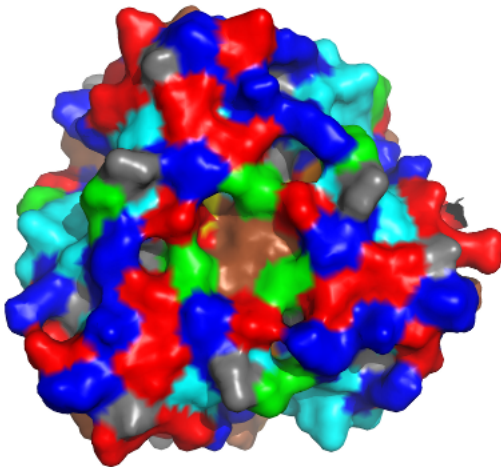
# Show Conolly solvent accessible surface

```
show surface , trimer1
```



# Run a custom coloring script

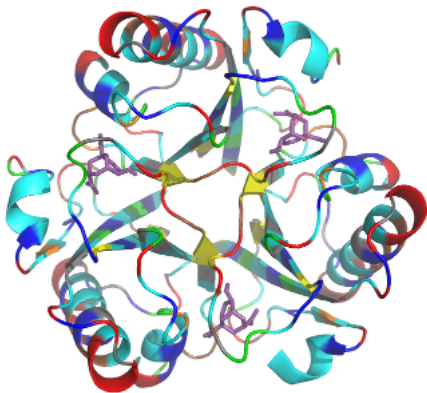
@properties.pml





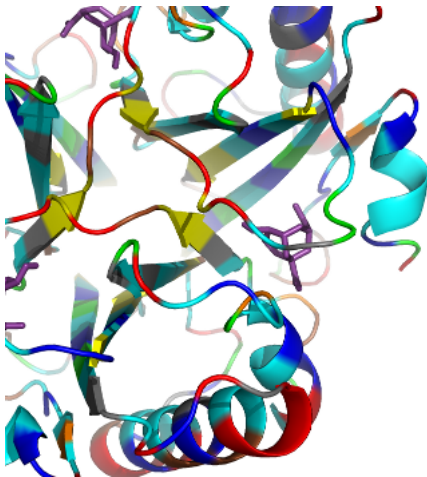
# Find the ligands

```
select all
hide everything
show cartoon, trimer1
select protein, not het
select ligand, het and not resn hoh
show stick, ligand
```



# Orient on one active site

```
select ligA , resi 201  
orient ligA
```



# Find the active site residues

```
select g1, protein within 5.0 of ligA  
select g2, byres g1  
show stick, g2
```

