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1. increase the sample number (eg: notch, tp53, HA,)

2. \$infos=array ("helix", "domain", "site"....)

```
$protein=array{ [1][0]=FT
                [1][1]=HELIX
                [1][2]=120
                }
```

Foreach (\$protein as \$A)

```
{ if (in_array($A[2],$infos))
  { if($A[2]==$A[3])
    {單點繪畫}
    else{區域繪畫}
  }
}
```

(use canvas)

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1. canvas: just like a 畫布. We use "canvas" to perform our protein information.

Ex: <!DOCTYPE html>

2. use "in_array(\$knownList, \$each[1])" to decrease the FT information overlap.

3. Use canvas to put image.

```
<!DOCTYPE html>
```

```
<html>
```

```
<body>
```

```
<p>Image to use:</p>
```

```

```

```
<p>Canvas:</p>
```

```
<canvas id="myCanvas" width="240" height="297" style="border:1px solid #d3d3d3;">
```

Your browser does not support the HTML5 canvas tag.

```
</canvas>
```

```

<script>
window.onload = function() {
    var c = document.getElementById("myCanvas");
    var ctx = c.getContext("2d");
    var img = document.getElementById("scream");
    ctx.drawImage(img, 10, 10);
}
</script>
<p><strong>Note:</strong> The canvas tag is not supported in Internet Explorer 8 and earlier versions.</p>
</body>
</html>

```

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- 1.put MHC class II panel
- 2.put xml
- 3.PDB viewer
- 4.user interface
- 5.3D structure :
 - First, select 130-139, and then select 10 , and then label 10.
 - Second, use php to catch pdb protein and output the amino acid symbol.
- 6.feature table:
 - Start, end, and features. (ok)
- 7.We need to translate these feature word to table or pictures.

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- 1.alert of word use "onclick" function to restrict user to submit correct codes or words.
- 3.use "internal" to show slide of pictures
- 4.complete the iframe of information which come from different tracks

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1. In the other page, if put different ID number, the
 - iframe , Javascript (html5)
 - getElementById(.....)
 - ID is the file

2. use "`<div id="a" style="display: none">.....</div>`" to define a track and the button "`.....`"

In the java code " `<script>`

`showInfo().....document.getElementById("a").style.display='block' "`

When we touch the sequence, there has a "div" show up.

So, the button code is " `.....`"

`javascript: void(0)` (it mean the link is disappear)

2. json decode (use to catch the `p12345,XML` and then)

1. step 1: catch the `p12345,XML` `shell_exec("Wget URL -O $jobId/ p12345.XML");`

2. step 2: read the `p12345,XML` `$XML_content = file_get_contents(" $jobId/p12345.XML"`

3. step 3: change the XML to Array `$a= json_decode ($XML_content, true)`

4. step 4: `print_r($a)` first to check

5. step 5: `echo $a["feature"]["modified_residue"][...][...];`

3. go to <http://www.uniprot.org/uniprot/P12345.txt> and find the features.

4. `xml_parse_into_struct()` can use compare with `json_decode` gfdgfdgg

5. Next step, use "html5 " to draw fancy picture.

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.1. We already complete "iframe" .

We also separate two page, one is home page. The other is data page, such as, 3D structure and MHC binding affinity.

2. Next part, we want to put PDB protein informations.

We need to use Java" 1. button, `alert("Hello")` 2. Button, 執行 `FF()` 3. form submit " .

3. In the improvement, we want to add "3D structure information when we select amino acid region".

4. And we should find Swiss-Prot ID /PDB

ID. http://www.uniprot.org/help/programmatic_access

<http://www.uniprot.org/uniprot/P12345.txt>

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1. Use "iframe function" to combine each track, such as, MHC class I&II affinity tracks and 3D structure track.

Ex: `<iframe src="target" width="px" height="px" frameborder="px" scrolling="px"></iframe>`

2. Add a new track make user can choose specific amino acids region.

We use " If (\$_POST['APP']) \$APP=' ' ;

Else \$AAP="slect \$_POST['APP']; color: red;"

Ex: `<?php`

```
if($_POST['AAP']==""){$AAP="";}
```

```
else {
```

```
$AAP=""; select ". $_POST['AAP'] ."; spacefill on; color red";
```

```
}
```

```
?>
```

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1. There is a simple Jsmol model code. We can change the code to meet our goals.

<http://163.25.92.36/igemcgu/jsmol/jmol/jmol/lite.htm>

2. Our goals are :

1. Auto spin in the beginning.
2. We need to have buttons, such as, spin on and spin off.
3. Most important, link "PDB file" to 3D structure.

3. In the first goal, we get.....

http://163.25.92.36/igemcgu/jsmol/jmol/jmol/resize_test.htm

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1. Jmol: 3D structure

First, we need to get profile of PDB (protein data bank). We may find a great amount of the same protein under different conditions. As long as you research any protein in any condition, you can submit the data to PDB.

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`"print_R: print_r($_FILE) "`

6-