## Take-home exam #2

Analyze the structure of a model of the 7 transmembrane  $\beta$ -adrenergic receptor, a GPCR, with epinephrine bound to its agonist binding site.

## Instructions:

2 pts ea

1. Download (save) from UBlearns (Assignments) to your desktop (or to a folder) the file: "beta adr rec model1.doc", containing the coordinates of the model

- 2. Open RasTop
- 3. Click Open under File (or ctrl O)
- 4. Select the file you downloaded
- 5. In the RasMol Command Line window write: set background white
- 6. Select "Backbone" under "Ribbons"
- 7. Select the color "Chain" under "Atoms"

Q1. (28 pts) a. Identify the first and last amino acids of each of the 7 helices, by placing the cursor over the end of a helix and write down the residue name and number shown in the bottom window "Res". Put the data in order of increasing residue numbers, and fill in the following for the N-terminal and C-terminal ends, respectively

(format: Gly 923 - Arg 962):

Helix 1: VAL 104	-	LYS 130
Helix 2: _ASN 201	-	_LYS 229
Helix 3: _PHE 301_	-	_VAL 326
Helix 4: <u>LEU 400</u>	-	ILE 424
Helix 5: _ASN 501	-	SER 525
Helix 6: <u>LYS 604</u>	-	GLN 633
Helix 7: <u>VAL 705</u>	-	PHE 734

Q2. (20 pts) a. What is the distance between the alpha-C atoms (designated as Atom CA) at the 2 ends of helix #2 and #5? Round up/down to 1 decimals. 4 pts ea

- Use (monitors) #2 \_40.8\_ Å #5 \_35.4\_ Å
- b. How many amino acids are in these helices?

#2 <u>29</u> #5 <u>25</u>

c. Are these 2 helices parallel or <u>antiparallel?</u> (encircle your answer)

Q3. (27 pts) List all the H-bonds and their length (2.5A - 3.5A) between epinephrine (ADR 1) and the surrounding amino acid residues in the drug-receptor complex. Use the instructions given for takehome exam #1. Click Ctrl + M to get the RasMol command editor window for using (typing in) the "select within" command. Present your results as in takehome exam #1. Distinguish between the 3 types of OH-groups in epinephrine (beta, meta, para). Round up/down to 1 decimal. [e.g., ASN 391 NH ---- OOC-GLU 745 3.2A or ADR 1 m-OH ---- O=C-GLN 735 2.8A]

1 pt ea 1 pt ea 1 pt ea ADR 1 β-OH ---- HN-ASN 627 3.0A ADR 1 NH ---- OOC-ASP 310 3.1A ADR 1 NH ---- OOC-ASP 310 3.1A ADR 1 NH ---- O=C-ASP 310 2.5A ADR 1 p-OH ---- HO-SER 512 2.6A ADR 1 m-OH ---- HO-SER 508 3.2A ADR 1 m-OH ---- HO-SER 509 3.0A ADR 1 m-OH ---- HO-SER 512 3.2A ADR 1 m-OH ---- HN-SER 509 3.5A [ADR 1 NH ---- HS-CYS 313 3.72]

Q4. (10 pts) a. The aromatic ring of epinephrine is sandwiched between 2 hydrophobic amino acids in the complex. Identify these amino acids:

3 pts ea

\_\_\_\_VAL 314\_\_\_\_\_PHE 624\_\_\_\_\_

b. In addition to these 2 amino acids, there are more hydrophobic residues surrounding epinephrine in the complex. Identify these:

1 pt ea

ILE 318, TRY 413, TRY 620, PHE 623

Q5. (15 pts) Identify all the helices, which contribute amino acid residues to the binding site of epinephrine and place the number of residues in parenthesis :

- 2 pts for ea wrong answer

helix 3 (4), helix 4 (1), helix 5 (3), helix 6 (4)

SEE ILLUSTRATIONS ON NEXT PAGE!

## β-Adrenergic receptor model with bound epinephrine (a 7-transmembrane GPCR complex)



