Appendix 7a: rubric used to evaluate post semester interview answers

Interview Question	*Category	Answer	Tool used?	Tool Comments
	of answer	Comments	(0=neither, 1=PE,	
	given		2= model, 3=both)	
Q5 (and so on)				

Appendix 7b: Rubric of defined assessment category levels for each post semester interview question.

Interview Question	0 = simply did not know	1 = demonstrated some understanding but missing many key concents	2 = demonstrated good understanding but still missing a few key concepts	3 = demonstrated sophisticated understanding of almost all concepts
5. Can you tell me what you've learned about protein 1°, 2°, 3°, and 4° structure?	Did not correctly define any of the 4 structures	Correctly defined only one of these structures OR answers for 3-4 structures were only partially correct	Correctly defined 2-3 structures OR answers for all 4 structures were correct for the most part	Correctly defined all 4 structures
6. What kind of biomolecule do you think this is: lipid, protein, nucleic acid, or carbohydrate?	simply did not know (no guess)	wrong answer given	correct answer, but was unsure	confident, correct answer
7. What makes you say this?	Had no justification for their answer to Q6; just guessing	Correctly pointed out 1 feature found only in proteins but also mentioned one or more incorrect features	Correctly pointed out 1 feature found only in proteins	Correctly pointed out 2 or more features that are only found in proteins; <i>e.g.</i> , beta sheets, alpha helices, amino acid residues, amino and carboxyl termini
8. Can you find the N- terminus?	simply did not know (no guess)	wrong answer given	right answer, but was unsure/correct guess; OR only knew it because they saw the color code on the CPK chart	confident, correct answer
9. Can you point out any alpha helices and/or Beta sheets?	Could not identify either structure	knew that alpha helices and beta sheets were examples of secondary structure, but did not identify them correctly on model or PE	identified either alpha helix OR beta sheet correctly on model and/or PE	correctly identified both alpha helices AND beta sheets on model and/or PE
10. Does this biomolecule show any quaternary structure?	simply did not know (no guess)	wrong answer given	correct answer, but was unsure	confident, correct answer
11. Is this a single protein chain or a dimer?	simply did not know (no guess)	Incorrectly answered "yes" to Q10 and incorrectly indicated that this was a dimer	Incorrectly answered "yes" to Q10 but correctly indicated that this was a single chain	Correctly answered "no" to Q10 and correctly indicated that this was a single chain
13. Can you name any of the amino acid sidechain residues that are displayed?	simply did not know (no guess)	Attempted to but incorrectly identified residues	Correctly identified at least one residue but incorrectly identified at least one other OR Correctly identified one or more residues with prompting	Correctly identified one or more residues without prompting
14. Can you take a guess as to what this molecule is and/or what its function might be?	No attempt to identify	A guess (correct or incorrect) without any reason given	A guess (correct or incorrect) with some flawed or incomplete logic; made assumptions that weren't obvious	Correct guess supported by logical evidence
15. Can you identify the changes or differences between the 1st and 2nd version of the molecule?	did not see any differences between the two molecules	noted that there was a conformational change but gave no details, OR identified only one of the 4 changes	recognized 2 to 3 of the changes mentioned in a "3" answer in next cell	clearly identified conformational changes in green loop, saw addition of bound substrate, saw addition of ATP, recognized that tyrosines were phosphorylated
16a. Now that you know these details, can you propose a function for the yellow region?	did not attempt to answer	wrong answer given	Partially correct answer, <i>e.g.</i> , see that it binds something but don't recognize that it's ATP	Correctly identified yellow as being ATP/nucleotide binding location
16b. For the orange region?	did not attempt to answer	wrong answer given (e.g., binds ATP)	Partially correct answer, <i>e.g.</i> , see that tyrosine residues are	Correctly identified orange as catalytic loop (where phosphorous is transferred from

17. Con you take a mars a	No ottomat to	A guage (compact on incompact)	involved but don't recognize that they are now phosphorylated; OR mentioned that it may be a stabilizing region	ATP to tyrosines)
to what this molecule is and what it does?	No attempt to identify	A guess (correct or incorrect) without any reason given	A guess (correct or incorrect) with some flawed or incomplete logic; made assumptions that weren't obvious	Correct guess supported by logical evidence
18. Dr spent some time in lecture telling you about receptor tyrosine kinases. Can you tell me what you know about them?	did not attempt to answer; OR supplied random keywords out of context	Correctly described one or two of the steps in a "3" answer, but left out key steps and/or incorrectly described them	Correctly described most but not all of the steps in a "3" answer	1. ligand binds receptor, 2. receptor dimerizes, 3. autophosphorylation of cytosolic domain (may mention conformational change here), 4. initiate signal transduction cascade (SH2 domain of GRB2 is phosphorylated to activate Sos OR substrate binds & is phosphorylated to initiate signal transduction cascade)**
19. Now that you know that this model and the PE image represent the cytosolic portion only of one receptor tyrosine kinase, can you describe what happens to this receptor when insulin binds?	did not attempt to answer	Mention dimerization and/or autophosphorylation, but they clearly did not recognize how autophosphorylation is depicted by the models and/or PE images	Mention dimerization followed by autophosphorylation, but it is unclear that they recognize how autophosphorylation is depicted by the models and/or PE images	Clearly demonstrated that they can apply their knowledge from lecture to the structures & events depicted by the physical models and/or PE images by stating that bound ligand causes receptor to dimerize (conformational change) followed by autophosphorylation of cytosolic domains
20. Can you think of at least 2 mutations that would keep this receptor from transferring a signal after insulin is bound?	did not attempt to answer	gave one logical and correct mutation	gave two logical, correct but general mutations or gave one general and one specific	gave two logical, correct and specific mutations
21. What mutations in this receptor tyrosine kinase might cause it to be constitutively activated (or always on)?	did not attempt to answer	made attempt but their answer was inappropriate (<i>e.g.</i> , "dominant - negative" mentioned but out of context)	logical, correct but still general mutation	gave logical, correct and specific mutation

**GRB2-SOS, Ras, MAP kinase pathway, AP1, txn factor may be mentioned; this is correct sequence. A second correct pathway is phosphorylation of PLC gamma SH2 domain which then initiates PIP2/calcium pathway

Summary Questions about Interview

Interview Question	Comments
4. Michelle's been encouraging you to use Protein Explorer this semesterhow	
has that gone?	
Re Q18 to Q19 transition: Overall, how well do you think this student transferred	Category of answer (* 0 = simply did not know, 1 = demonstrated
their knowledge from Biocore lecture to this new protein? (e.g., How well do you	some understanding but missing many key concepts, $2 =$ demonstrated good
think the student understood that the phosphorylated tyrosine residues shown in the	understanding but still missing a few key concepts, $3 =$ demonstrated
molecule are the result of the cytosolic autophosphorylation events they described	sophisticated understanding of almost all concepts)
in Q18?	Here we can also make note of whether student used PE and/or models to
	describe the following: 1. dimerization/conformational change, 2.
	autophosphorylation, 3. signal cascade is initiated.
Re Q22: If student had any remaining questions or comments, were they	
informative?	