



## Answers to Exercises

The answers may change as more data is added to Reactome; these are based on the June 2011 Reactome release.

### Exercise 1

1. 5 reactions. This is the obvious answer from simply unfurling the 'Signaling by EGFR' in the pathway hierarchy. However, if you unfurl 'Grb2 events in EGFR signaling' and 'Shc events in EGFR signaling' you will see additional sub-sub-pathways ('RAF activation' and 'RAF/MAP kinase cascade').
2. 3 reactions.
3. There are two: 'EGFR autophosphorylation' and 'Phosphorylation of EGFR by SRC kinase'. It's tempting to think it will be the next reaction down in the hierarchy, and often this is the case, but not for this reaction. The hint suggests opening the Details pane. One of the details is "Following event(s):" this will always correctly identify the next reaction step(s) in a pathway. An alternative way to identify preceding and subsequent reactions is to follow the connecting lines on the pathway diagram.

### Exercise 2

1. 'Signaling by TGF beta'.
2. Cellular compartment – Early endosome membrane.
3. The associated GO molecular function is 'transmembrane receptor protein serine/threonine kinase activity'.
4. The reference is Souchelnytski et al. 2001.
5. Yes for dogs, no for yeast.

### Exercise 3

1. SIAH2 has 1 interactor (IntAct) called Dentatorubral-pallidoluysian atrophy protein (DRPLA).
2. Click on the line between SIAH2 and DRPLA to open a page describing the interaction at the source database, IntAct. This interaction has been identified in 1 paper.
3. SRC has more than 50 interactors, indicated by 50+. You can see these 50 in the table within the Analyze, Annotate & Upload panel; if you export the interactions you will get all interactions available from the selected source, in this case IntAct.
4. UNC5B has no interactors, a prompt tells you this.
5. There is a Clear button in the Analyze, Annotate & Upload panel.

#### Exercise 4

1. Gene Expression
2. 411 genes in the pathway, 174 represented.
3. Chromosome Maintenance is higher in the list than Signalling by Wnt because the former has a sub-sub-sub-pathway, Telomere C-strand (Lagging Strand) Synthesis that has a more significant probability score than that of Signaling by Wnt. The top-level pathway inherits this from the sub-pathway, pushing it up the list.
4. Raf activation - P15056, BRAF

#### Exercise 5

1. Complement factor B is yellow, indicating that it has been inferred to exist in rat.
2. You can answer this by clicking on the box for Complement factor B and looking at its details – look for ‘Entities deduced on the basis of this entity’ – this lists the other species that have been inferred to have Complement factor B.
3. Complement factor 2 is blue, indicating that it has not been inferred to exist in rats.
4. C3b is black because it is a complex. Right-click on it and select the option ‘View participating molecules’ to see which are predicted to exist in rat. They are 2 components, both blue, so not predicted to exist in rat.
5. Calcium is grey because it is a small molecule, so species comparison is not relevant. Other pathway objects that have no Uniprot ID will also be grey.

#### Exercise 6

1. 49 proteins in the pathway,
2. 41 have expression values in the dataset.
3. It's easier to see this if you zoom out so all the pathway is visible. I think it's ERCC1 (or HR23B, top left of the diagram), but I have not checked all the complexes...
4. DNA-directed RNA polymerases I, II, and III 17.1 kDa polypeptide (RPB17)
5. The probe ID is displayed if you mouse over the cell, it was the identifier used in this dataset – 209302\_at.

#### Exercise 7

1. Click on Choose Database and select Reactome, then click on Choose Dataset and select Pathway.
2. Add a Filter, limiting to pathways containing a list of IDs, select Uniprot IDs from the dropdown list, enter P17480 in the box. The query returns 8 pathways.
3. Copy the Pathway Stable ID, REACT\_2232, change the filter so it limits by Pathway Stable ID, enter REACT\_2232 in the box. Add the Attribute Protein UniProt ID. You should have 2 results returned.