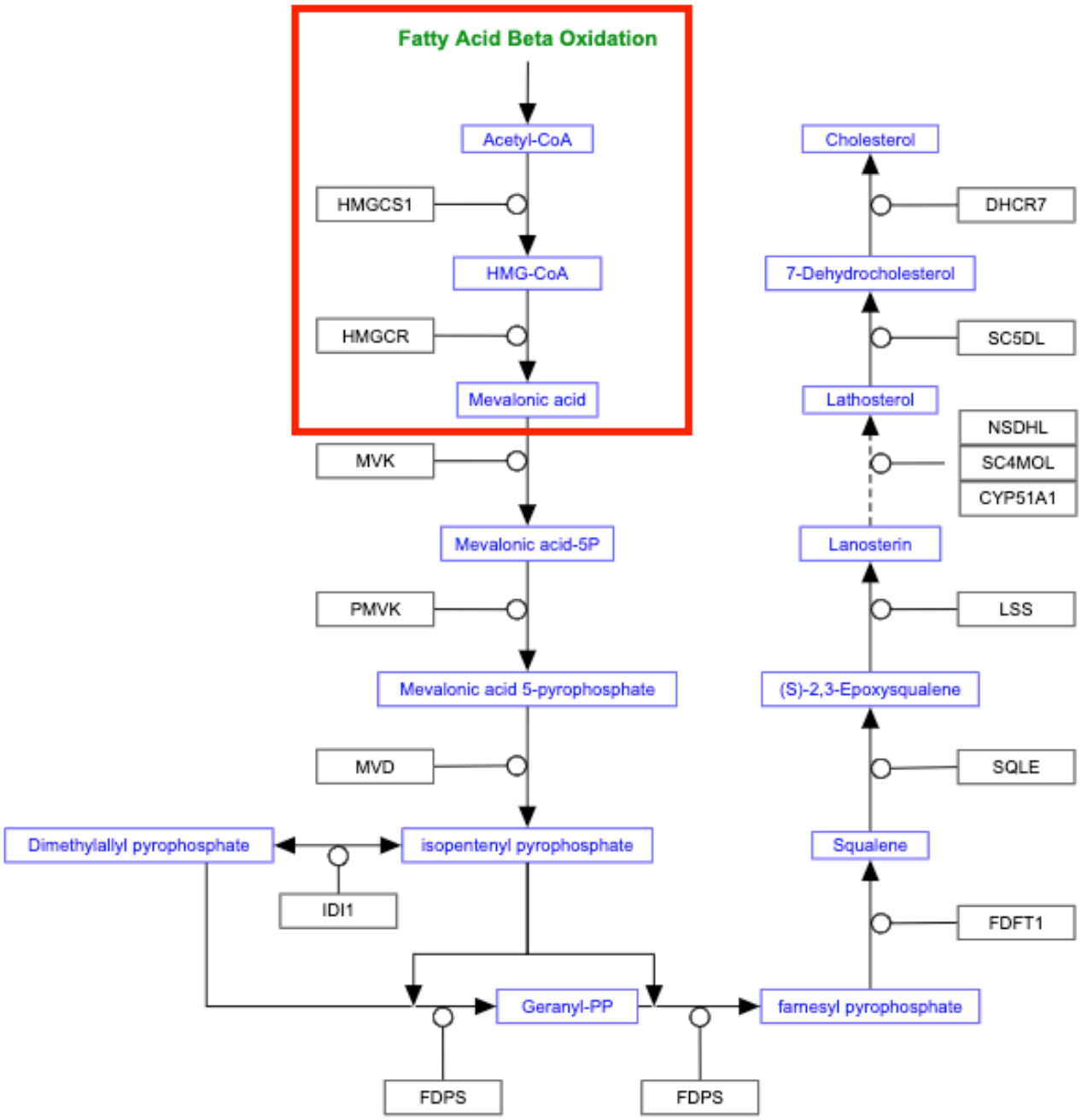
Drawing Challenge 1: Cholesterol Biosynthesis pathway



Curation Challenge 1: Cholesterol Biosynthesis pathway

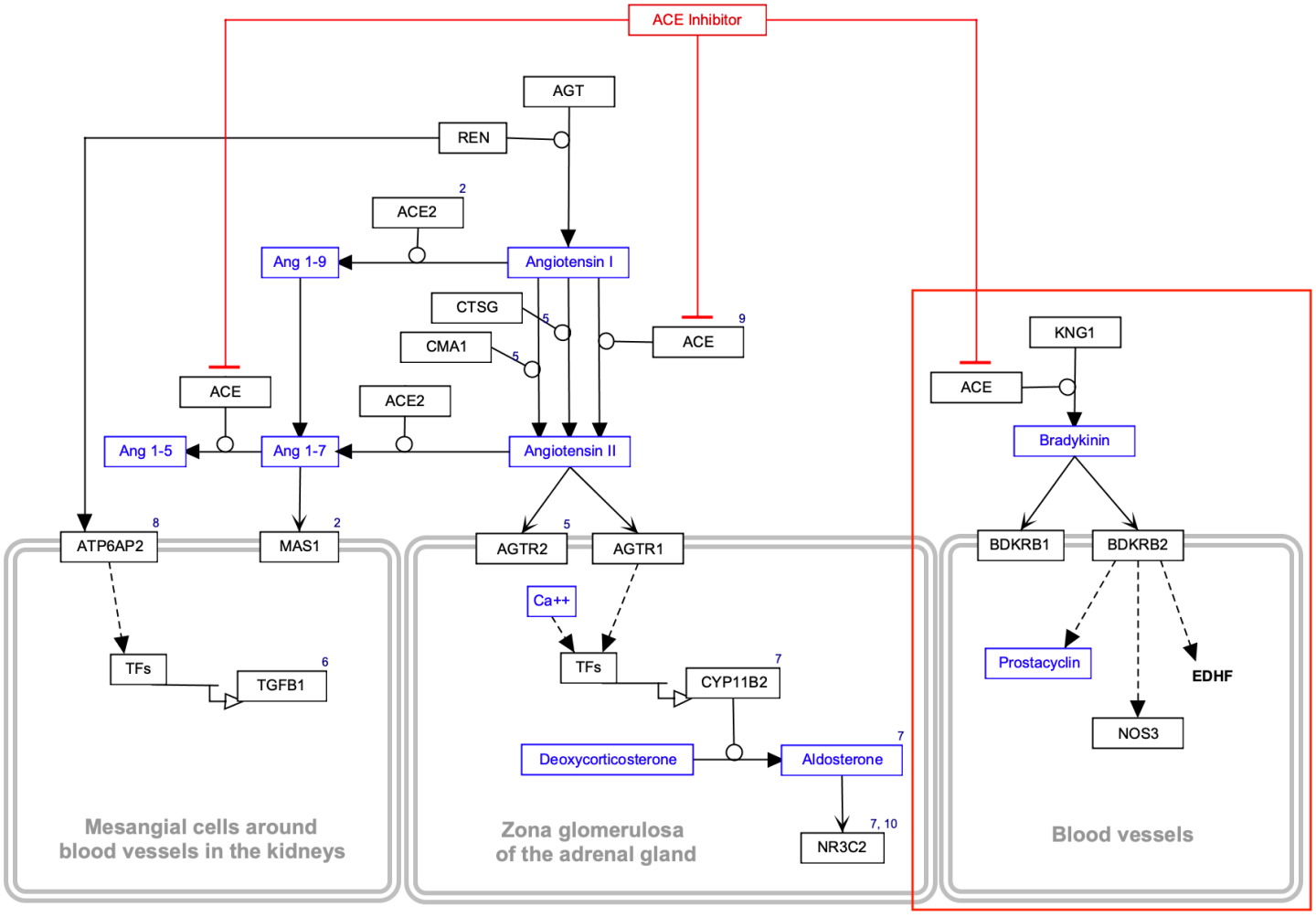
Instructions

1. Start PathVisio. Close out of **Pathway attributes** window**.**
2. Double-click on “Title” field in the upper left corner. In the **Properties** tab, enter a descriptive pathway title and relevant species. In this case, include your initials as a suffix.
3. Load human **Gene Database** and **Metabolite Database** under **Data->Select Gene Database** and **Data->Select Metabolite Database**.
4. Add a gene product on the drawing board. To annotate the gene, double-click it to bring up the **DataNode properties** interface and search for “HMGCS1”. From the results, select the Ensembl ID and click **OK**.
5. Add a metabolite, and repeat the annotation process for “acetyl-coA”, selecting the HMDB or ChEBI ID.
6. Repeat step 5 for “HMG-CoA”.
7. In the **MIM interactions** panel, select “MIM-conversion”.
8. Connect the ends of the conversion interaction to the two metabolites, by first selecting the interaction, then clicking and dragging each end towards the relevant datanode. The interaction is connected when you see the connection target on the datanode highlighting green.
9. Add an anchor to the MIM-conversion by right-clicking and selection **Add Anchor.**
10. Add a “MIM-catalysis” interaction.
11. Connect the catalysis interaction from the HMGCS1 node to the anchor on the conversion.
12. Repeat step 5 for “mevalonic acid”.
13. Add a “MIM-conversion” from HMG-CoA to mevalonic acid, and add an anchor.
14. Repeat step 4 for “HMGCR”.
15. Add a “MIM-catalysis” from HMGCR to the conversion.
16. Add a pathway node. Double-click to open the **DataNode properties.** Label the node “Fatty Acid beta oxidation”. To find the WPID for the corresponding pathway, do a search at WikiPathways.org. Enter the WPID for identifier and select “WikiPathways” as database.
17. Add basic arrow to connect and connect it from the pathway node to Acetyl-CoA.
18. Add literature reference by right-clicking on the **Pathway Information** (upper left corner) and entering “27604037” as PMID. Click **Search**. The fields will auto-fill with the relevant information.
19. To upload the pathway to WikiPathways, go to **Plugins-> WikiPathways->Upload New**. Provide your login information and a description of your edits.
20. Go to WikiPathways. Find your pathway under **New pathways**.
21. Add a quality tag (“Test pathway”).
22. Provide a description.
23. Add at least two ontology tags.
24. Review.

Drawing Challenge 2: ACE Inhibitor Pathway

Instructions

1. Using the WikiPathways Plugin in PathVisio, open the Glucolysis and Gluconeogenesis starter pathway, id WP4948.
2. Add the content outlined in red below to the pathway. Brief instructions follow below.
3. Add annotated nodes for ACE, KNG1, Bradykinin, BDKRB1/2, Prostacyclin, NOS3. Note that EDHF is a proposed substance/signal with unknown composition. It should be added as a label. See Wikipedia for details.
4. Next, roughly position the nodes.
5. Add interactions from the ACE inhibitor, as well as remaining interactions. Note that they are different interaction types, including mim-inhibitory, mim-binding, mim-catalysis, mim-conversion and regular non-specified arrows.
6. Add the rounded rectangle representing blood vessels, changing its line type to double, color to grey and line weight to 3. Also, add the label “Blood vessels” to the shape and position in the lower right.



Pro tips for pathway modeling

- **Objects in pathway figures are not always labeled with the official gene symbol!**
  If you can't find an annotation in PathVisio via the search interface, try a Google search . You will often get hits for Wikipedia articles that are actively being curated by a large community of scientists as part of the Gene Wiki project, a project that actively collaborates with WikiPathways. From there, you can find the official symbol.

- If a pathway figure includes a protein family name, or complex name (for example Akt), you have a few options for how to represent this in the pathway model:
  - Find out (from literature or other resources) which isoform is relevant in the pathway in question. Remember to add a literature reference!
  - Add all isoforms (or subunits) as a group (or complex) in the relevant location in the pathway. This assumes that you can still accomplish a reasonable layout.
  - Add a representative node for the protein family/complex in the pathway, and add all isoforms (or subunits) as a group (or complex) on the side of the pathway.

- Interaction types: By default, use the *Arrow* in the *Basic Interactions* palette. Use a more specific interaction type **only** if you have specific information on the reaction. For example, the *mim-conversion* type should **only** be used for conversion between two metabolites.

- To annotate a pathway node, use the search feature at WikiPathways to find the WPID for any relevant pathway. Enter it manually in the *DataNode Properties* interface.

- Ctrl+L (Command+L) will highlight any unconnected interactions

Glossary

datanode – a node or entity on a pathway that is annotated by a database entry. E.g., a Gene Product annotated with an Ensembl identifier.
datasource – third-party sources for the databases underlying WikiPathways. E.g., Ensembl, Entrez Gene and UniProt.
gene product – a datanode type commonly used to represent the protein or transcript products of a gene.
gpml – Graphical Pathway Meta Language, the native XML file format for WikiPathways.
identifier – the universally recognized label for a gene product, metabolite or interaction provided and curated by a datasource.
interaction – the relationship between two entities. E.g., activation or inhibition of a datanode by another datanode.
metabolite – chemicals, drugs and small molecules that are active in a biological process.
mim – Molecular Interaction Maps, a project that defined the arrowhead glyphs for a set of interactions.
model – here used in the sense of a pathway model to refer to a pathway diagram that follows a set of database, syntactic and semantic conventions to allow consistent and programmatic parsing and integration with other data types.
xref - External Reference, a datasource and identifier pair that together uniquely define an entity in any context, universally