Radiopharmaceutical: Tc99m-UltraTag Red Blood Cells
Dose: 20 mCi
T1/2: 6 hours
Energy: 140 keV
CPT: 78205 (SPECT only); 78206 (SPECT with vascular flow)

Indications:
Approved indications include, but are not limited to:
1. Evaluation of possible or known liver hemangioma.
2. Abnormal radiological examination.

Patient Preparation:
• NPO for 4 to 6 hours.

Equipment:
1. Philips Skylight (VXUR collimator)
2. Philips Forte (VXUR collimator)
3. Philips Vertex Plus (LEUR collimator)

Procedure:
1. Set an IV (23g or greater, to not damage RBCs), and draw 2-4 mL of whole blood into heparinized syringe (0.25 to 0.5 mL of heparin).
2. Follow instructions in UltraTag kit to tag RBCs with 99mTc-pertechnetate. This process takes roughly 25 min to complete.
3. Begin scanning immediately after reinjection of tagged RBCs.
4. Acquire six (6) 10 minute SPECT scans over the abdomen. The JETStream software will automatically perform the six SPECT scans sequentially. The ATLAS software will require that you notate your table height, detector distances, etc., so that you can exactly duplicate the each respective SPECT pass.
5. Correlate suspected area with US, MR, or CT scan. Patient must have had one of these done, in order to suspect a hemangioma.

Acquisition Parameters:
• Matrix: 128 x 128
• Zoom: 1.0 (Full Field)
• Time: 9 seconds/frame
• Number of angles: 128
• Position: Supine
• Orientation: Feet First

Processing:
1. Before processing, EDIT PATIENT DATA → PATIENT OBJECTS, and number each PROJECTION 1 through 6.
2. Left-click AutoSPECT button.
3. Select all 6 projection sets 1 to 6 in that order.
4. Left-click on PROCEED.

5. Left-click on OPEN DEFAULTS and load the HEMANGIOMA default (Method: iterative; Filter: Butterworth; cutoff: 0.6; and order: 5.0).
6. Adjust yellow lines around the liver. Notate these numbers so that you can adjust all series to match. If you skip this, your slices WILL NOT match for when it comes time to draw ROIs for the curves.
7. Left-click on the SAVE page (not the SAVE button), and ensure that the RAW TRANSVERSE, SAGITTAL, and CORONAL planes are selected, and that the oblique thickness is 1.
8. Rename the RAW TRANSVERSE to RAW TV, to shorten the name. Place the number (1 through 6) by the RAW TV, SAGITTAL, and CORONAL so that when the data is saved, you can tell which data is from the proper SPECT scan.
9. At the bottom of the screen, next to PROJECTION 1, click the down arrow once to load the next PROJECTION set.
10. Move the yellow lines to the previously recorded numbers.
11. Repeat steps 7 through 9 for each subsequent data set.
12. Once data sets 1 through 6 have been prepared, click RECONSTRUCT, and all six sets will be processed, sequentially and automatically. This will take a while, since iterative reconstruction is a multiple step process.
13. When recon is completed, click the REORIENT page at the top and middle of the screen.
14. Drag the yellow lines in around the liver for all six SPECTS. Toggle between each dataset as you did before by clicking the down arrow at the bottom of the screen.
15. After completing all six, click the SAVE button (not the SAVE page) at the top right of the screen.
16. Click on QUIT, after saving.
17. The RAW TV datasets must now be reversed.
18. Left click on SPECT FRAME REVERSE DISPLAY at the top of the main menu screen.
19. Choose the RAW TV 1 data, click PROCEED.
20. The reversal process will begin automatically, and will take a few seconds to complete.
21. Left click QUIT, and SAVE SELECTED AND PROCEED.
22. Repeat this for all RAW TV datasets.
23. Left-click on REFRAME ULTRA DYNAMIC DISPLAY.
24. Choose the first RAW TV.
25. Right click on SELECTION MENU , then 3, then right click on SELECTION MENU again, and then 3, again.
26. Click on the 24-view display button.
27. Annotate properly, and snapshot the image.
28. QUIT.
29. Repeat for all RAW TV and CORONAL datasets.
30. Next, you must extract one slice from each transverse dataset, where the possible hemangioma is located, as seen on MR or CT. You may have to ask a radiologist which slice to use.
31. To extract, left-click on IMAGE MANIPULATION →IMAGE MANIPULATION→RAW TV 1→PROCEED.
32. Click FRAME EXTRACT, right-click on SELECTION MENU, and then Image 1. Enter the start frame number as the frame that you wish to extract, and the number of frames will be 1.
33. Rename as REGION 1. Left-click on PROCEED.
34. Repeat this process for each transverse dataset, naming them with the respective scan number.
35. Left-click on IMAGE APPEND, and choose the 6 extracted frames.
36. PROCEED.
37. Left-click on EXIT, and rename as DYNAMIC.
38. To create a curve for this, we have to first edit the time per frame, so that the graph will be correct.

39. Right-click in the blue background→PATIENT UTILITIES→EDIT PATIENT DATA→PATIENT OBJECTS. Choose the DYNAMIC (image append dataset) and change the time to 576,000, and UPDATE.
40. EXIT.
41. Right-click in the blue background→USER CUSTOM MENU→CURVE MANIPULATION (MIN)→CURVE CREATE→DYNAMIC CURVE.
42. Select the DYNAMIC (image append dataset) and click enter twice.
43. Draw a region around the LIVER, SPLEEN, and HEMANGIOMA (area of interest). Name each ROI, respectively. SNAPSHOT AREA IN A BOX and select the image including the ROIs.
44. Click PROCEED and a graph will appear with all of the regions on one graph.
45. Click on MATH, and DECAY CORRECTION. Right-click on SELECTION MENU→Tc99m, and a decay-corrected curve will appear.
46. Click on SAVE and enter the set name LIVER and click on the box next to DECAY CORRECTED LIVER, and click SAVE TO BUFFER AND DATABASE.
47. Click on SAVE and enter the set name SPLEEN and click on the box next to DECAY CORRECTED SPLEEN, and click SAVE TO BUFFER AND DATABASE.
48. Click on SAVE and enter the set name HEMANGIOMA and click on the box next to DECAY CORRECTED HEMANGIOMA, and click SAVE TO BUFFER AND DATABASE.
49. After all curves have been saved, click SELECT CURVES and choose the LIVER curve and click PROCEED.
50. SNAPSHOT AREA IN A BOX and select the graph only.
51. Repeat for the SPLEEN and HEMANGIOMA, respectively.
52. QUIT.
53. Select ALL IMAGE DISPLAY, and select the three graph snapshots to display and label appropriately. SNAPSHOT this image.
54. DICOM the images to PACS.