PROJ_COLON_FLT_PET_5.MlAdult_PET5

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1 Topogram

1.1 Routine

mA: 35kV: 120

• Topogram length: 1024 mm

• Tube position: Top

1.2 Scan

mA: 35kV: 120Delay: 4s

Topogram length: 1024 mmDirection: Craniocaudal

• Tube position: Top

API: NoneKernel: 80s shar

• Window: Topogram Body

2 Lavdos CT WB

2.1 Routine

• Eff. mAs: 40

• kV: 120

• CARE Dose4D: Off

• CareDoseType: CareDoseAEC

CTDlvol: 2.70069mGyScan time: 18.670 s

Delay: 4.000 sSlice: 3.00 mm

• No. of images: Samme som i foerste recon, slet?(y/n)

• Tilt: 0.0 grader

2.2 Scan

• Quality ref. mAs: 50

• Eff. mAs: 40

• kV: 120

Scan time: 18.670 sRotation time: 0.500 s

Delay: 4.000 sSlice: 3.00 mmPitch: 0.8000000

• Direction: Craniocaudal

2.3 Recons

2.3.1 Recon 1

• Series description: AC CT

• Slice: 3.00

• Kernel: B19f PET very smooth

Window: AbdomenExtended FoV: On

FoV: 700Center X: 0Center Y: 0Mirroring: None

• Extended CT scale: Standard

Recon job: AxialRecon Axis: Axial

Image order: Craniocaudal
Recon increment: 3.000
No. of images: 274

3 Pause

4 PET WB

4.1 Routine

Isotope: F-18Pharm.: FLT

• Inj. Dose: 1 MegaBequerels

• Scan mode: Sinogram

• Scan range: Match CT FOV

• No. of beds: 1

• Scan duration/bed: 150 Seconds

4.2 Scan

• Autoload: On

Rebinner LUT: OffScan output: SinogramSinogram mode: Trues

• Input trigger signal: None

LLD (keV): 435ULD (keV): 650

4.3 Recons

4.3.1 Recon 1

- Series description: PET WB Image check
- Recon range (bed): -1 to -1
- Output image type: Corrected
- Recon method: Iterative
- Iterations: 4
- Subsets: 8
- Image size: 168
- Zoom: 1
- Filter: Gaussian
- FWHM (mm): 4
- Offset X: 0 mm
- Offset Y: 0 mm
- Attenuation correction: On (1)
- Scatter correction: On
- Match CT slice location: On
- Save intermediate data: Off

4.3.2 Recon 2

- Series description: PET FLT Corr. True X 2 mm
- Recon range (bed): -1 to -1
- Output image type: Corrected
- Recon method: TrueX
- Iterations: 3
- Subsets: 21
- Image size: 336
- Zoom: 1
- Filter: Gaussian
- FWHM (mm): 2
- Offset X: 0 mm
- Offset Y: 0 mm
- Attenuation correction: On (1)
- Scatter correction: On
- Match CT slice location: On
- Save intermediate data: Off