PETCT_NEMA_2007_AC.Adult_PET4

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1 Topogram

1.1 Routine

mA: 35kV: 120

• Topogram length: 512 mm

• Tube position: Top

1.2 Scan

mA: 35kV: 120Delay: 4s

Topogram length: 512 mmDirection: Craniocaudal

• Tube position: Top

API: APIKernel: 80

• Window: Topogram

2 NEMA CT

2.1 Routine

• Eff. mAs: 50

• kV: 120

• CARE Dose4D: Off

• CareDoseType: CareDoseAEC

CTDlvol: 3.65446mGyScan time: 6.242 s

• Delay: 2.000 s

• Slice: 5 mm

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

• Tilt: 0.0 grader

2.2 Scan

• Quality ref. mAs: 120

• Eff. mAs: 50

• kV: 120

Scan time: 6.242 sRotation time: 0.500 s

Delay: 2.000 sSlice: 5 mmPitch: 0.80

• Direction: Craniocaudal

2.3 Recons

2.3.1 Recon 1

• Series description: NEMA CT RTD

• Slice: 4

• Kernel: B19f

Window: AbdomenExtended FoV: Off

FoV: 500Center X: 0Center Y: 0

• Mirroring: None

• Extended CT scale: Standard

Recon job: AxialRecon Axis: Axial

• Image order: Craniocaudal

• Recon increment: 4.000

• No. of images: 42

2.3.2 Recon 2

• Series description: NEMA AC CT

• Slice: 5

• Kernel: B19f

Window: AbdomenExtended FoV: On

FoV: 780Center X: 0Center Y: 0

• Mirroring: None

• Extended CT scale: Standard

Recon job: AxialRecon Axis: Axial

Image order: CraniocaudalRecon increment: 3.000

• No. of images: 56

3 Pause

4 NEMA PET

4.1 Routine

• Isotope: F-18

- Pharm.: Fluorodeoxyglucose
- $\bullet\,$ Inj. Dose: 370000000 Bequerels
- Scan mode: Sinogram
- Scan range: Do not match CT FOV
- No. of beds: Not given. Check recon range
- Scan duration/bed: 1.000000 Minutes

4.2 Scan

- Autoload: On
- Rebinner LUT: Off
- Scan output: Sinogram
- Sinogram mode: false
- Input trigger signal: None
- LLD (keV): n/a
- ULD (keV): n/a

4.3 Recons

4.3.1 Recon 1

- Series description: PET NEMA AC Scan
- Recon range (bed): 1 to 1
- Output image type: Corrected
- Recon method: Backprojection
- Iterations: 2
- Subsets: 24
- Image size: 200
- Zoom: 1
- Filter: Gaussian
- FWHM (mm): 5
- Offset X: 0 mm
- Offset Y: 0 mm
- Attenuation correction: Off ()
- Scatter correction: On
- Match CT slice location: On
- Save intermediate data: Off