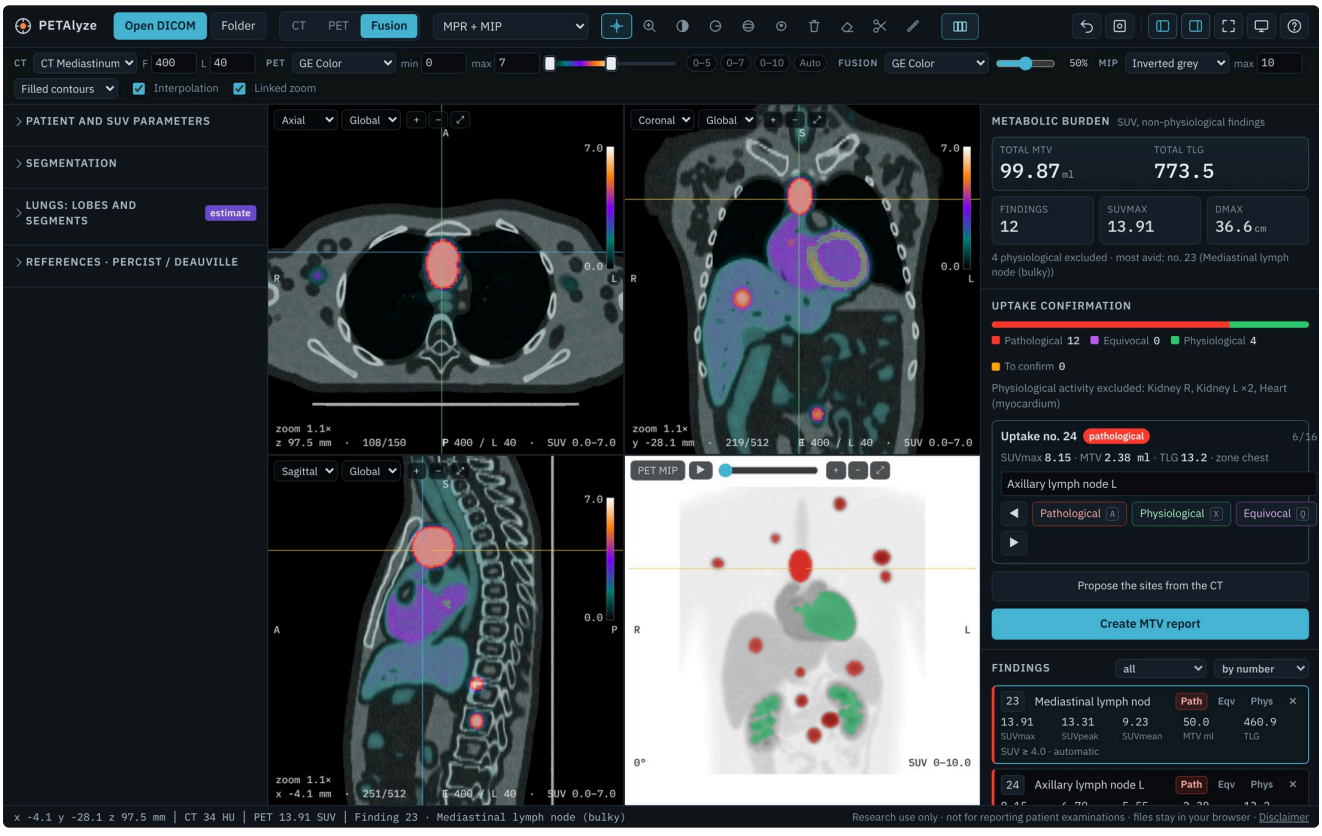
PETAlyze

User manual

PETAlyze 1.0 · PET/CT quantification in the browser

How to open a PET/CT study, segment the metabolic tumour volume, confirm each uptake, score Deauville and export the report.



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For research use only. PETAlyze is not a medical device and must not be used to report patient examinations. All images in this manual show a synthetic PET/CT built from the XCAT lymphoma phantom (Fedrigo et al., Med. Phys. 2022). They contain no patient data.

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In a hurry? Read sections 2 and 3 to open a study, then follow the workflow at the start of section 8. Press the **?** button in the app at any time for a summary of the controls.

1 About PETAlyze

PETAlyze is a free PET/CT viewer for research. It runs in a desktop web browser, opens PET/CT DICOM studies from your own disk, segments every uptake with a published threshold method, lets you decide which findings are disease, and gives total metabolic tumour volume (MTV), total lesion glycolysis (TLG), dissemination (Dmax) and the Deauville score.

Intended use

- PETAlyze is for **research and teaching only**. It is not a medical device and must not be used to report patient examinations.
- SUV and MTV values were tested by comparing the results with those obtained on the same cases with syngo.via. They are not validated for clinical use.
- Lung segmentation (lungs, lobes and segments) is **experimental**.
- Like any software, PETAlyze can make errors. Every number it gives comes from a method you chose and a decision you confirmed: check the contours on the images.

Your images stay on your computer

- DICOM files are read directly from your disk and kept in the memory of the browser tab. Nothing is uploaded, neither to the PETAlyze website nor to anyone else.
- When you close or reload the tab, the images are cleared from memory.
- PETAlyze stores only display preferences in your browser (colour scales, layout, segmentation method). No patient data.
- PETAlyze does not save your work. Before you close the tab, export what you need (section 14).

What you need

- A desktop or laptop computer with a recent web browser, such as Chrome, Edge, Firefox or Safari. PETAlyze is not designed for phones.
- A PET/CT study as DICOM files: a folder, single files or a ZIP archive, exported from your PACS or workstation.
- The access password, which is free (section 2).

Words used in this manual

Uptake	A region of tracer uptake found by the segmentation. Until you classify it, it is to confirm.
Finding	Any contoured uptake in the list, whatever its status. Each finding has a number.
MTV	Metabolic tumour volume, in ml: the volume of the contour. Total MTV is the sum over the pathological findings.
TLG	Total lesion glycolysis: SUVmean × MTV of each finding. Total TLG is the sum over the pathological findings.
SUVpeak	The highest mean SUV of a 1 ml sphere centred on a voxel of the finding.
Dmax	The largest distance between the centroids of two pathological findings.
ROI, VOI	A circle drawn on one slice (ROI) or a sphere in 3D (VOI) for measurements.

2 Getting access

PETAlyze is free. You register once with your email address and receive the access password by email.

Register

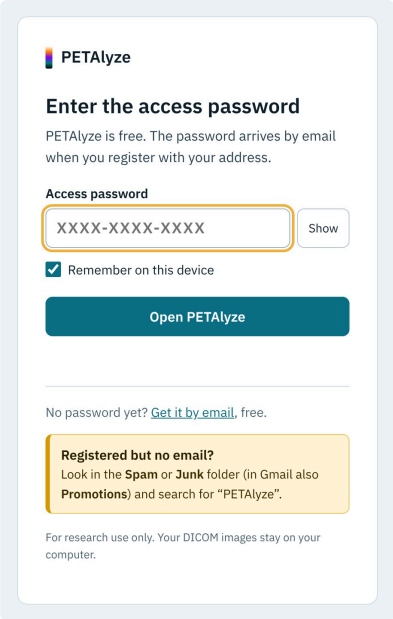
1. Go to **www.petalyze.org** and open **Get free access**.
2. Enter your email address and accept the privacy notice. News about PETAlyze is optional.
3. Send the form. An email titled **Welcome to PETAlyze** arrives shortly, with the password and a button to open the app.

> **Can't find the email?** Look in the **Spam** or **Junk** folder (in Gmail also **Promotions**) and search for “PETAlyze”. If it is there, mark it as “Not spam”, so that future messages reach your inbox.

Open the app

1. Open **www.petalyze.org/app/**, or press the button in the email.
2. Type or paste the password. Capital letters, spaces and dashes don't matter.
3. Leave **Remember on this device** ticked on your own computer, so you won't need to enter it again in that browser. Untick it on a shared computer.
4. Press **Open PETAlyze**.

The same password works on any computer. Please keep it for your own use: colleagues can register for free on the website.

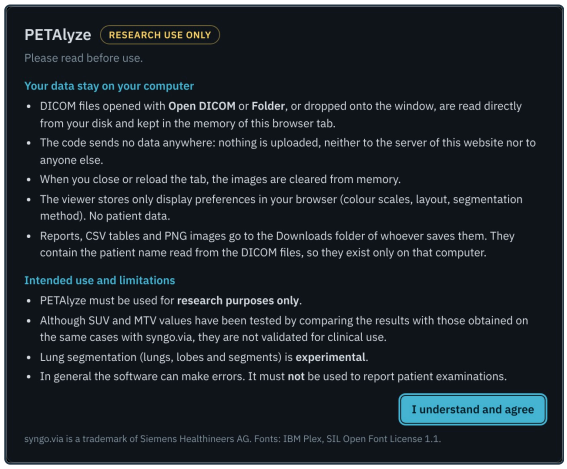


The password page at www.petalyze.org/app/.

First start

Each time PETAlyze opens, it shows a short notice on data protection and intended use. Read it and press **I understand and agree**. You can open it again from **Disclaimer** at the bottom right of the window.

The window is empty until you load a study (section 3).



The notice shown at start.

3 Loading a study

PETAlyze reads the DICOM files of a PET/CT study, finds the CT and PET series and reconstructs them as volumes.

Three ways to open files

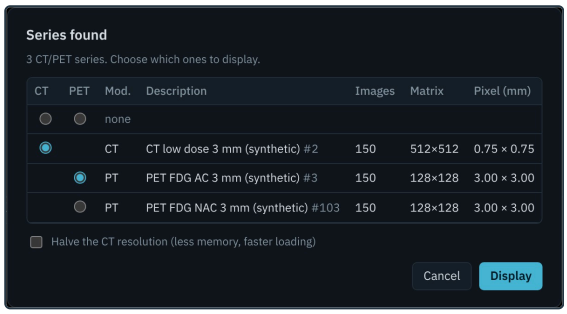
- **Open DICOM** (top left): select one or more DICOM files or ZIP archives.
- **Folder**: select a folder. All its subfolders are read too, so you can select the folder of the whole study.
- **Drag and drop** files, folders or ZIP archives onto the window.

Files that are not images (text, XML, PDF, JPEG and similar) are skipped. A progress box shows reading and reconstruction. Opening a new study replaces the current one.

Choosing the series

If the files contain only one CT and one PET series, PETAlyze displays them at once. If there are more (for example PET with and without attenuation correction, or a diagnostic CT), the **Series found** window asks which ones to display:

- Choose one CT and one PET with the radio buttons. You can also choose **none** for one of them: PET alone or CT alone can be viewed, but segmentation and the MIP need a PET series.
- Use the attenuation-corrected PET for quantification.
- **Halve the CT resolution** uses less memory and loads faster. It is ticked already when the CT is very large. The PET is never reduced.



Three series found: the CT and the attenuation-corrected PET are chosen.

Supported DICOM files

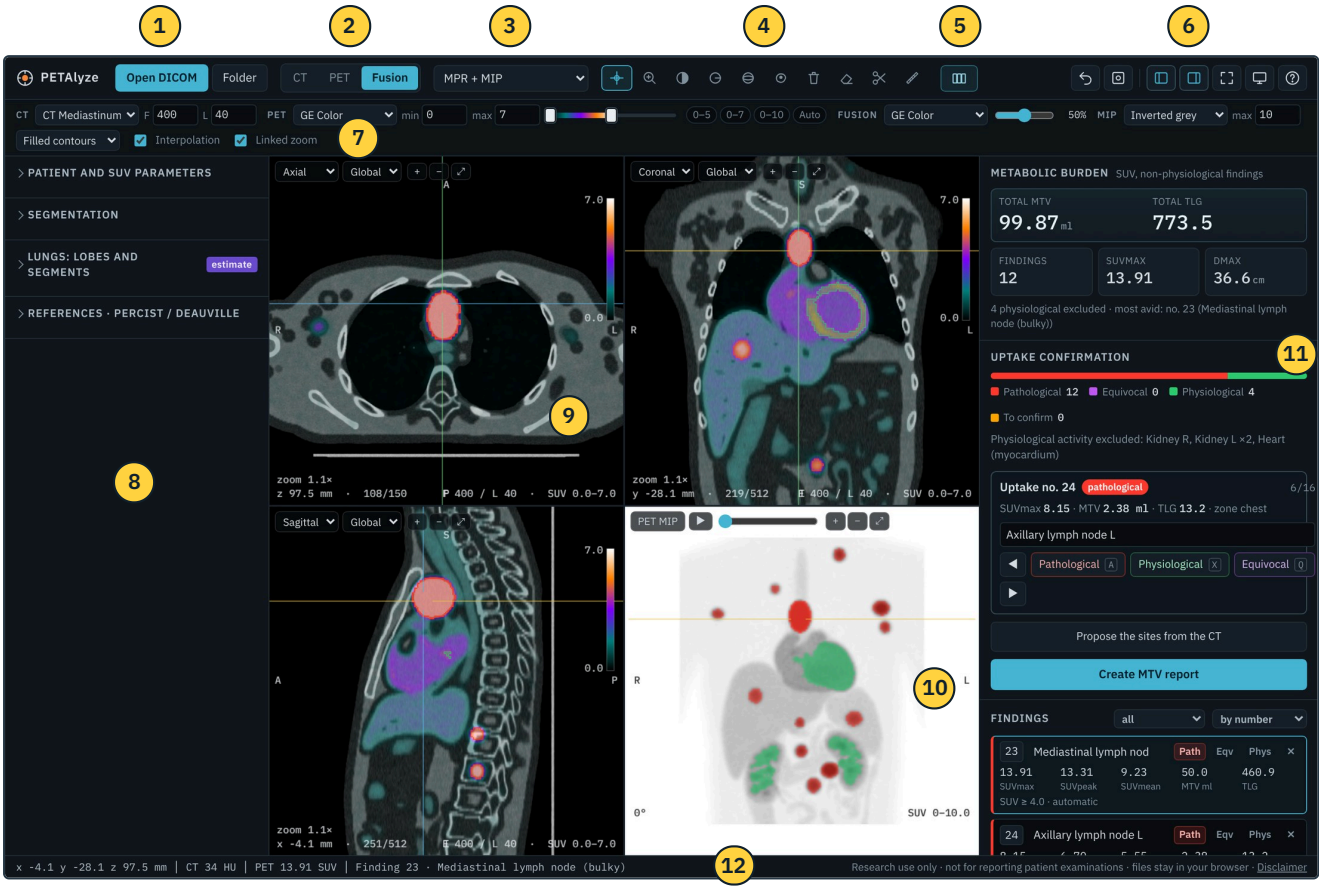
Image encoding	Support
Uncompressed (implicit or explicit VR, little or big endian)	Supported
Deflated, RLE, lossless JPEG	Supported
Lossy JPEG (baseline, extended), JPEG-LS, JPEG 2000, HTJ2K	Not supported. Export the study uncompressed from your PACS or workstation.
Colour images (for example secondary captures)	Not supported, and skipped.

How PET values become SUV

PET images stored in Bq/ml are converted to SUV with the weight, height, sex, injected dose, injection and scan times and half-life read from the DICOM header. You can check and correct these values (section 6). When a Philips study stores counts with its own SUV factor, that factor is used. A short message at the bottom of the window warns you when something is missing or unusual; section 16 lists what each message means.

4 The screen

The window is divided into a top bar, a bar for windows and colour scales, two side panels, the views and a status bar.



1. **Open DICOM** and **Folder** (section 3)
2. Display mode: CT, PET or fusion
3. Layout of the views
4. Tools (table below)
5. **Review** view (section 9)
6. Undo, reset, panels, full screen, help
7. Window bar: CT window, PET, fusion and MIP colour scales, contour style (section 5)
8. Left panel: SUV parameters, segmentation, lungs, references
9. Axial, coronal and sagittal views
10. Rotating PET MIP
11. Right panel: burden, confirmation, findings, analysis, measurements, export
12. Status bar: position, CT HU, PET SUV and finding under the cursor

Tools

A tool decides what the left mouse button does on the images. Choose it in the top bar or with its key. `Esc` goes back to Navigate.

	Tool	Key	Left mouse button
	Navigate	`N`	Drag up or down to scroll the slices; click to place the cursor, which all views follow.
	Pan/zoom	`Z`	Drag to move the image. Right-drag zooms.
	Window	`W`	Drag to change the CT window (in a PET view, the SUV scale).
	ROI	`R`	Drag from the centre to draw a circle on the slice (section 11).

	Tool	Key	Left mouse button
	**VOI**	V	Drag from the centre to draw a sphere and compare the threshold methods inside it (section 11).
	**Finding**	S	Click on an uptake to contour it, or drag a sphere around a larger one (section 9).
	**Delete**	D	Click on a contour, in a view or on the MIP, to delete that finding.
	**Eraser**	E	Drag to erase parts of a contour in 3D, for example to split two merged findings.
	**Scissors**	T	Draw a closed line around part of an uptake: that part becomes a finding of its own (section 9).
	**Ruler**	M	Drag to measure a distance in mm.

Two more tools have no button but a key: F places the liver reference and B the blood pool reference (section 7). They also have buttons in the References panel.

Buttons on the right of the top bar

	**Review**	Axial CT, PET and fusion side by side, without panels, with the confirmation bar (section 9).
	**Undo** Ctrl + Z	Undoes the last change to the contours.
	**Reset view** Home	Resets zoom and position of all views.
	**Left panel**	Shows or hides the left panel.
	**Right panel**	Shows or hides the right panel.
	**Maximum image area** H	Hides both panels and the status bar; press again to bring them back.
	**Full screen**	Uses the whole screen. Esc leaves full screen.
	**Help**	Summary of the mouse and keyboard controls, the workflow and the methods.

5 Viewing the images

Display mode and layout

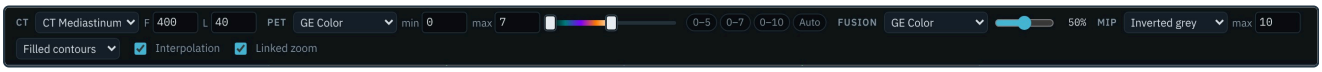
- **CT**, **PET**, **Fusion** in the top bar, or `1` `2` `3`, set what the views show.
- The layout menu offers **MPR + MIP** (axial, coronal, sagittal and MIP), **Axial CT · PET · Fusion** and **Coronal CT · PET · Fusion**.
- Each view has its own header: the orientation (axial, coronal, sagittal), the mode (**Global** follows the top bar; CT, PET or Fusion keep that view fixed) and the zoom buttons **+**, **−** and ⤢ (fit).
- Double-click a view to enlarge it to the whole image area; double-click again to go back.

Moving through the images

Action	Result
Mouse wheel	Scrolls the slices (on the MIP it rotates the projection)
`↑` `↓` or `PgUp` `PgDn`	Scrolls the slices of the active view
Click (Navigate tool)	Places the cursor; the other views move to the same point
Right-drag, `Ctrl` + wheel, trackpad pinch, `+` `−`	Zoom, always centred on the view. `0` fits the active view
`Shift` + left-drag, or the Pan/zoom tool	Moves the image
Middle-drag or `Alt` + left-drag	CT window; in a PET view, the SUV scale
`Home`	Resets zoom and position

The status bar shows the position of the mouse in mm, the CT value in HU, the PET value in SUV and the finding under the mouse.

Windows and colour scales



The window bar under the top bar.

- **CT**: window presets (mediastinum, lung, abdomen, liver, bone, brain) or your own width (**F**) and level (**L**) in HU.
- **PET**: colour scale, minimum and maximum SUV. Drag the two handles of the slider, or use the buttons **0–5**, **0–7**, **0–10** and **Auto**. Double-click the slider for 0–7.
- **Fusion**: colour scale of the PET over the CT and its opacity.
- **MIP**: colour scale and maximum SUV of the MIP.
- **Contours**: filled, outline only, fill only, or hidden. `C` shows and hides them at any time.
- **Interpolation** smooths the display of the pixels. **Linked zoom** zooms all views together.

Colour scales available: Grey, Inverted grey, GE Color, Hot Iron, Hot Metal Blue, PET (blue-red-yellow), NIH, Rainbow, Jet, Viridis and Inferno. Your choices of colour scales, linked zoom and segmentation method are remembered in this browser.

The MIP

- Drag left or right, or use the wheel, to rotate the projection. ▶ rotates it continuously; the slider sets the angle.
- Click on a hot spot: the views jump to the hottest point along that line and the finding there is selected.
- With the Finding tool, a click on the MIP contours the uptake there; with the Delete tool, it deletes the finding.
- Middle-drag changes the maximum SUV of the MIP; right-drag or `Ctrl` + wheel zooms.

6 SUV parameters

The **Patient and SUV parameters** section of the left panel shows the study and the values used for the SUV. They are read from the DICOM header and you can correct them: all SUV values, contours and totals update at once.

Field	Meaning
Weight (kg)	Needed for any SUV.
Height (cm)	Needed for SUL and SUVbsa.
Sex	Used by the SUL formula. If it is not given, the male formula is used.
Dose (MBq)	Injected activity.
Injection, **Scan start**	Times used to correct the dose for decay to the start of the scan.
Half-life (min)	Of the radionuclide, from the header (109.77 min for ^{18}F).
Normalisation	**SUVbw**: body weight. **SUL**: lean body mass, Janmahasatian formula. **SUVbsa**: body surface area, Du Bois formula. **kBq/ml**: activity concentration, no normalisation.

Below the fields, a summary shows the radiopharmaceutical, the units and the dose at scan time. If weight or dose are missing, values are shown in kBq/ml until you enter them. If the height is missing, SUL and SUVbsa fall back to SUVbw.

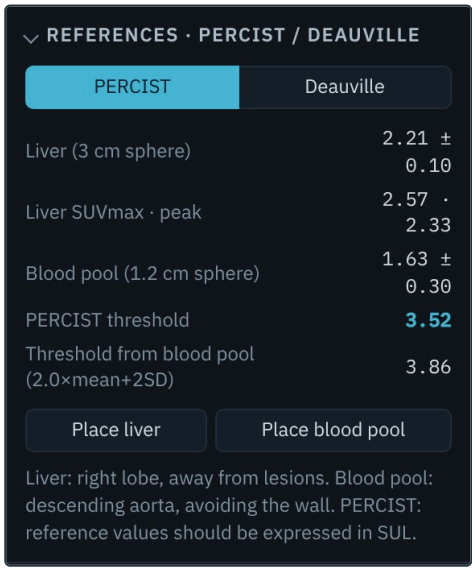
> All values in the panels, the report and the CSV table use the normalisation chosen here. The unit (SUV, SUL, SUVbsa or kBq/ml) is shown next to each value and at the top of the right panel.

7 Reference regions: liver and blood pool

The liver and the mediastinal blood pool are the references for the PERCIST threshold and for the Deauville score. Open **References · PERCIST / Deauville** in the left panel.

- **Place liver** (key F), then click in the right liver lobe, away from lesions. PETAlyze measures a sphere of 3 cm. To move a reference, place it again.
- **Place blood pool** (key B), then click in the descending thoracic aorta, avoiding the wall. The sphere is 1.2 cm.
- The panel shows SUVmean ± SD of each reference, liver SUVmax and SUVpeak, the **PERCIST threshold** (1.5 × liver SUVmean + 2 SD) and the threshold from the blood pool (2.0 × SUVmean + 2 SD).

With the PERCIST method or the Deauville score, if the liver has not been placed, PETAlyze can estimate it from the CT (**Liver from the CT** in the Deauville panel). Check where it was placed.



Liver and blood pool placed; PERCIST threshold 3.52. PERCIST reference values are defined in SUL: choose SUL in section 6 if you follow PERCIST.

8 Segmenting the uptakes

One click segments every uptake in the body with the method you choose. Then you decide, uptake by uptake, what is disease.

> **Suggested workflow**
>
> 1. Check weight, dose and times (section 6).
> 2. Place the liver and, if you need it, the blood pool (section 7).
> 3. Choose a method or preset and press **Segment all uptakes** (this section).
> 4. Confirm each uptake with A pathological, Q equivocal or X physiological (section 9).
> 5. Add missed lesions with the Finding tool; fix contours with Delete, Eraser and Scissors (section 9).
> 6. Check the sites, read the totals and export the report (sections 10 and 14).

Automatic segmentation

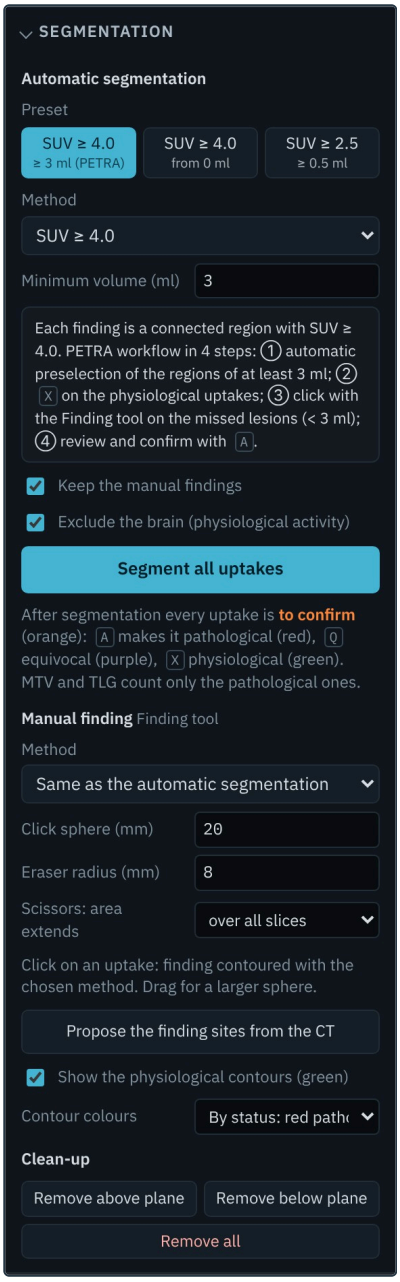
Open **Segmentation** in the left panel.

- **Preset**: three ready settings.
  - **SUV ≥ 4.0, ≥ 3 ml (PETRA)**: regions with SUV ≥ 4.0 of at least 3 ml. Smaller lesions are then added by clicking on them.
  - **SUV ≥ 4.0, from 0 ml**: all regions with SUV ≥ 4.0, of any size.
  - **SUV ≥ 2.5, ≥ 0.5 ml**: all regions with SUV ≥ 2.5 of at least 0.5 ml.
- **Method**: the threshold method, a single one for finding and contouring the uptakes (table on the next page).
- **Minimum volume (ml)**: smaller regions are ignored. 0 keeps every region, even a single voxel.
- **Keep the manual findings**: a new automatic segmentation keeps the findings you added by hand.
- **Exclude the brain**: the large uptake above the lung apices is marked physiological and left out of the totals. No other organ is excluded automatically.
- Press **Segment all uptakes**.

After segmentation every uptake is to confirm. MTV and TLG count only the findings you call pathological, so the totals start at zero.

Clean-up

Remove above plane and **Remove below plane** delete the findings whose centre lies above or below the current axial slice (for example the brain or the bladder). **Remove all** deletes every finding. Ctrl+Z undoes.

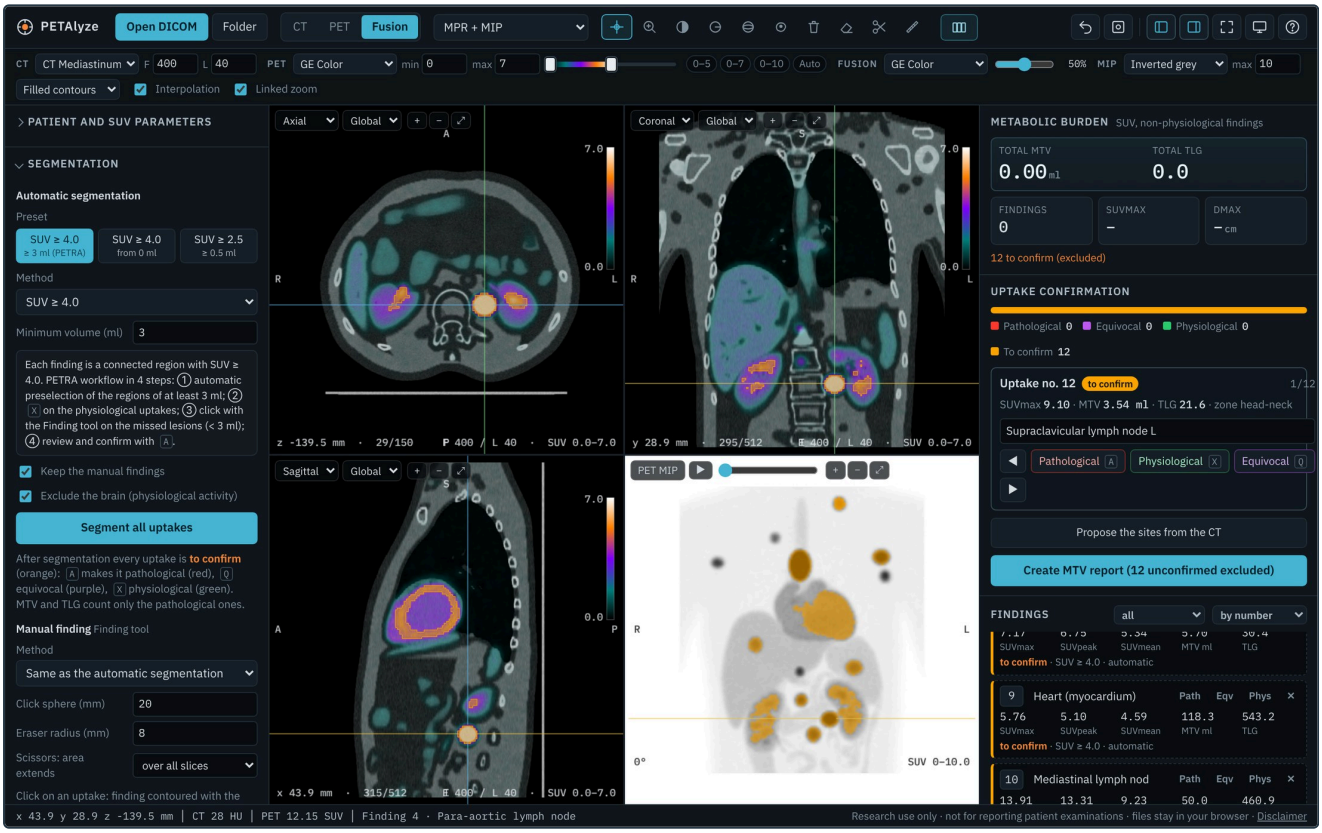


The Segmentation section with the PETRA preset.

Segmentation methods

Method	How the contour is made
SUV ≥ 4.0	Fixed threshold. Each finding is a connected region with all voxels at SUV ≥ 4.0 and a volume of at least the minimum volume.
SUV ≥ 2.5	Fixed threshold at 2.5, as above.
PERCIST	Fixed threshold at 1.5 × liver SUVmean + 2 SD, from the liver reference (estimated from the CT if missing).
41% of SUVmax	Each uptake is contoured at 41% of its own SUVmax.
A50P	Each uptake is contoured at background + 50% × (SUVpeak − background). The background is the median of a shell around the lesion.
MV2, **MV3**	Majority vote: voxels included by at least 2 (MV2) or 3 (MV3) of the four methods SUV ≥ 2.5, SUV ≥ 4.0, 41% SUVmax and A50P.
Extended MTV	SUV ≥ 4.0 for the uptakes above 4; A50P for the uptakes with SUVmax below 4.

With the fixed thresholds nothing below the threshold is included. With the per-lesion methods (41%, A50P, MV2, MV3), the uptakes are first found as regions with SUV ≥ 2.5. If a contour spills into the background, the finding is limited to its uptake (SUV ≥ 2.5) and marked **contour limited**: check it, or re-segment it from the Analysis panel (section 10).



After **Segment all uptakes** with the PETRA preset: twelve uptakes, all orange (to confirm). The brain was excluded as physiological.

9 Confirming and editing the findings

Status and colours

Status	Key	Effect
to confirm		New uptakes. Excluded from the totals and from the report table.
pathological	A	Counted in total MTV, TLG, Dmax and the report.
equivocal	Q	Excluded from the totals, listed separately in the report.
physiological	X	Excluded from the totals. Hidden on the images unless **Show the physiological contours** is ticked.

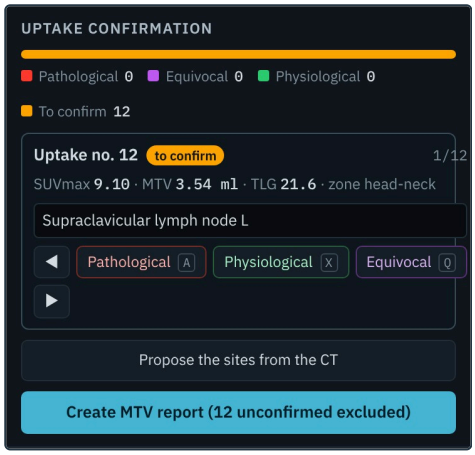
The keys act on the selected finding. ← and → move to the previous or next uptake to confirm. In the Segmentation panel, **Contour colours** can also give each finding a colour of its own instead of the status colour.

The Uptake confirmation panel

After a segmentation, the right panel shows how many uptakes are pathological, equivocal, physiological and still to confirm, and a card for the selected uptake:

- SUVmax, MTV, TLG and the body zone;
- the site, which you can type or choose from the list;
- the buttons **Pathological**, **Physiological**, **Equivocal** and ◀ ▶ to move between uptakes.

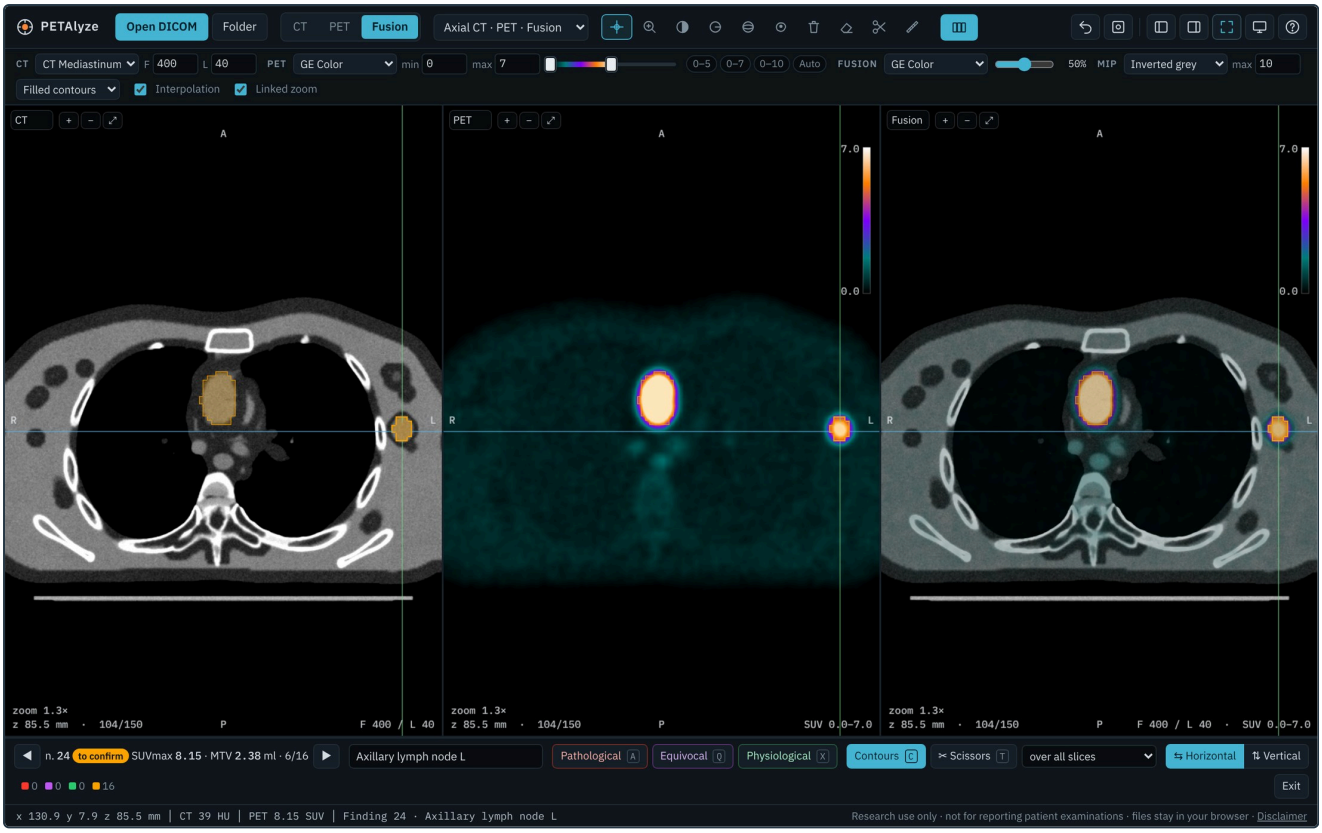
Propose the sites from the CT fills in the anatomical site of the findings (section 10). **Create MTV report** opens the report; the uptakes still to confirm are left out of it.



Twelve uptakes to confirm; the first is selected.

The Review view

Review in the top bar shows axial CT, PET and fusion of the selected uptake large, without side panels, with a bar to work through all uptakes from the keyboard. In the bar: ◀ ▶, the site, the three status buttons, **Contours** (C), **Scissors** (T) with its extent, **Horizontal** or **Vertical** layout, the counts, and **Exit**.



Review view on a left axillary lymph node.

Adding a missed lesion

- Choose the **Finding** tool (`S`) and click on the uptake. PETAlyze looks for the maximum within the **Click sphere** (20 mm by default) and contours it with the method set under **Manual finding** (by default, the same as the automatic segmentation).
- For a large or irregular lesion, drag from its centre to draw a sphere that contains it. If the contour touches the edge of the sphere, PETAlyze tells you: drag a larger sphere.
- For a lesion below the threshold (for example SUVmax under 4 with SUV ≥ 4.0), choose A50P or Extended MTV under Manual finding.
- A finding added by hand is also **to confirm**.

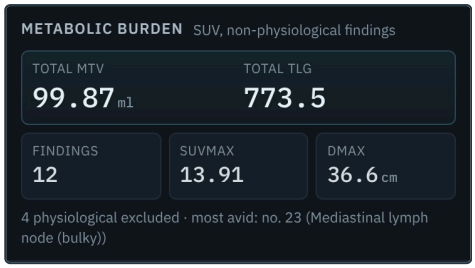
Correcting contours

- **Delete** (`D`): click on a contour, or on the MIP, to delete the finding. `Del` deletes the selected finding; ✕ in the findings list does the same.
- **Eraser** (`E`): drag over a contour to erase it in 3D within the **Eraser radius** (8 mm by default). Useful to split two findings that touch.
- **Scissors** (`T`): draw a closed line around the part of an uptake to separate, for example physiological activity touching a lesion. That part becomes a new finding to classify; the rest keeps its number and status. Choose how far the area extends: **over all slices** (only where the uptake continues), **this slice only**, **from here upwards** or **from here downwards**. The last two help when the two uptakes lie one above the other.
- **Undo** (`Ctrl`+`Z`) undoes the last change to the contours.

10 Results: burden, findings and analysis

Metabolic burden

At the top of the right panel: **total MTV** and **total TLG**, the number of pathological findings, the highest SUVmax and **Dmax**. Only pathological findings count. The line below says how many findings are physiological or still to confirm, and which finding is the most avid.

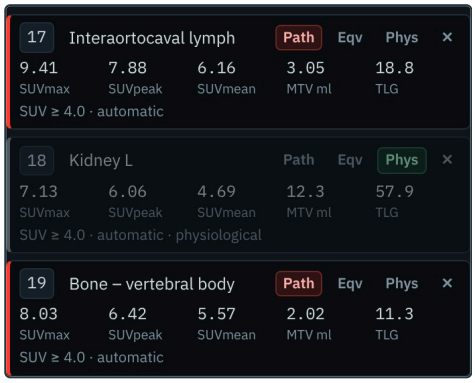


Totals of twelve pathological findings.

Findings

Each card shows the number, the site, SUVmax, SUVpeak, SUVmean, MTV and TLG, and below them the status, the method and whether the finding was found automatically or added by hand.

- Click the **number** to go to the hottest voxel of the finding.
- Type the **site** in the card, or choose it from the suggestions.
- **Path**, **Eqv**, **Phys** set the status; ✕ deletes the finding.
- Filter the list (all, pathological, to confirm, equivocal, physiological, to check) and sort it by number, cranio-caudal position, SUVmax or MTV.



Two pathological findings and one physiological (kidney).

Other labels on the cards: **automatic site** (proposed from the CT, not yet edited by you), **contour limited** (section 8), **separated from no.** (made with the scissors), **to check** (physiological, set automatically with low confidence).

Anatomical sites

Propose the finding sites from the CT (Segmentation panel or Uptake confirmation) suggests the site of each non-physiological finding: lung and lobe, bone and vertebral level, lymph node stations, liver, spleen and other organs. These sites are marked “automatic site” until you edit them. They are suggestions: check each one.

Analysis of a finding

Select a finding (click its number, or click it on the images) to see its full statistics in the **Analysis** panel: SUVmax, SUVpeak (1 ml), SUVmean ± SD, MTV and voxel count, TLG, extent in x, y and z, threshold, qPET (SUVpeak / liver SUVmean, when the liver is placed), SUVmax / blood pool, and the position of the maximum.

Below, a table compares **all segmentation methods** on the same lesion, inside a sphere around it: threshold, MTV, SUVmean and TLG. A yellow dot means that the contour of that method reaches the edge of the sphere, so its volume may be underestimated. **Apply** re-segments the finding with that method; the current method is highlighted.



FINDING 23 · MEDIASTINAL LYMPH NODE (BULKY)

SUVmax	13.91
SUVpeak (1 ml)	13.31
SUVmean ± SD	9.23 ± 2.78
MTV	49.95 ml (1850 voxel)
TLG	460.9
Extent x·y·z	36 × 54 × 51 mm
Threshold	SUV ≥ 4.0 (4.00)
qPET (peak / liver)	6.02
Max position (mm)	-5 · -29 · 98

Comparison of methods in the sphere of 49 mm around the finding:

Method	Threshold	MTV ml	SUVmean	TLG	
SUV ≥ 4.0	4.00	49.95	9.23	460.9	Apply
SUV ≥ 2.5 ●	2.50	74.44	7.25	539.4	Apply
41% SUVmax	5.70	41.63	10.11	421.1	Apply
PERCIST SUV ≥ 3.52	3.52	52.73	8.94	471.4	Apply
A50P (50% SUVpeak – background)	6.90	37.50	10.53	395.0	Apply
MV2 (≥ 2 of SUV2.5·SUV4·A50P·41%)	4.00	49.95	9.23	460.9	Apply
MV3 (≥ 3 of SUV2.5·SUV4·A50P·41%)	5.70	41.63	10.11	421.1	Apply
Extended MTV: SUV ≥ 4.0	4.00	49.95	9.23	460.9	Apply

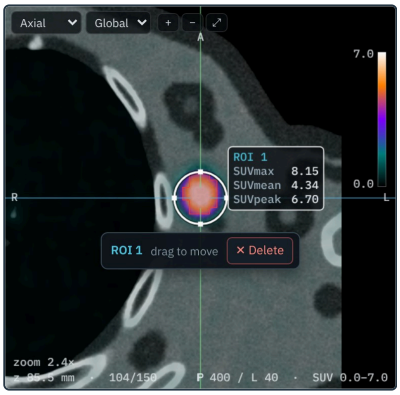
Analysis of the bulky mediastinal node, with the comparison of methods.

11 ROI, VOI and distance

Measurements are independent of the findings: they don't change the totals.

ROI (circle on a slice)

Choose **ROI** (R) and drag from the centre of the region. The Analysis panel shows SUVmax, SUVmean ± SD, SUVpeak (1 ml), SUVmin, mean HU ± SD of the CT, the area in cm² and the number of PET voxels.



A circular ROI on a left axillary node.

VOI (sphere)

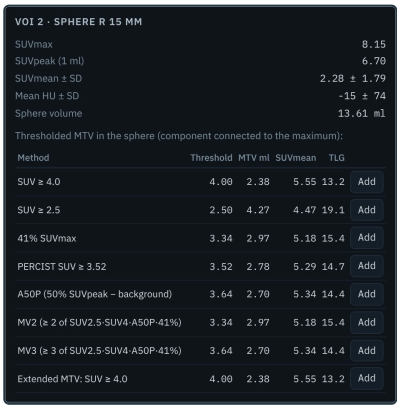
Choose **VOI** (V) and drag from the centre. The Analysis panel shows the same statistics for the sphere and its volume, then a table with the MTV that each method would give inside the sphere, for the region connected to the maximum. **Add** turns that contour into a finding.

Distance

Choose **Ruler** (M) and drag between two points. The distance is shown in mm on the image.

Managing measurements

All ROIs, VOIs and distances are listed under **Measurements** in the right panel, with **go** to jump to each one and ✕ to delete it. Click a measurement on the image to select it, then drag to move it; Del deletes it.



VOI 2 · SPHERE R 15 MM

SUVmax	8.15
SUVpeak (1 ml)	6.70
SUVmean ± SD	2.28 ± 1.79
Mean HU ± SD	-15 ± 74
Sphere volume	13.61 ml

Thresholded MTV in the sphere (component connected to the maximum):

Method	Threshold	MTV ml	SUVmean	TLG	
SUV ≥ 4.0	4.00	2.38	5.55	13.2	Add
SUV ≥ 2.5	2.50	4.27	4.47	19.1	Add
41% SUVmax	3.34	2.97	5.18	15.4	Add
PERCIST SUV ≥ 3.52	3.52	2.78	5.29	14.7	Add
A50P (50% SUVpeak – background)	3.64	2.70	5.34	14.4	Add
MV2 (≥ 2 of SUV2.5·SUV4·A50P·41%)	3.34	2.97	5.18	15.4	Add
MV3 (≥ 3 of SUV2.5·SUV4·A50P·41%)	3.64	2.70	5.34	14.4	Add
Extended MTV: SUV ≥ 4.0	4.00	2.38	5.55	13.2	Add

VOI of 15 mm radius on the same node, with MTV by method.

12 Deauville score

In **References · PERCIST / Deauville**, press **Deauville**. With the liver and the mediastinal blood pool placed (section 7), PETAlyze scores every non-physiological finding on the five-point scale and marks the **target lesion**, the most avid pathological one.

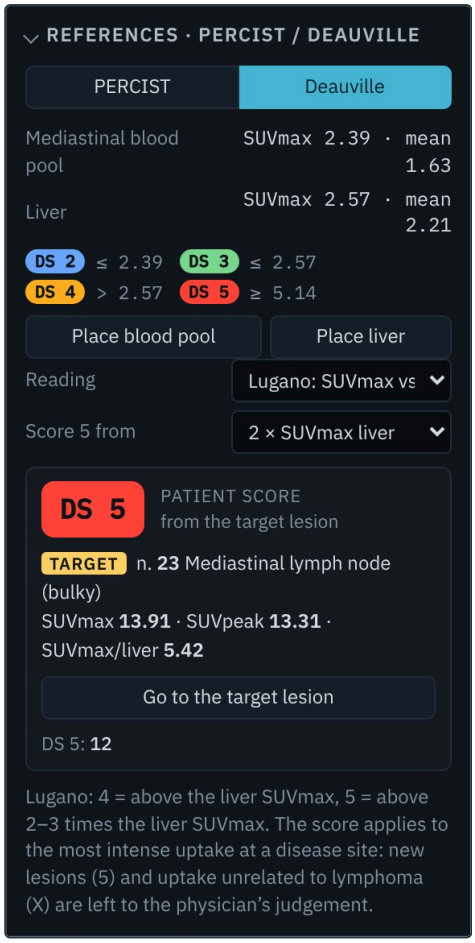
Reading

- **Lugano**: the lesion SUVmax is compared with the blood pool SUVmax and the liver SUVmax. 2 = up to the blood pool, 3 = up to the liver, 4 = above the liver, 5 = from 2, 2.5 or 3 times the liver SUVmax (**Score 5 from**).
- **qPET**: lesion SUVpeak / liver SUVmean, with cut-offs 0.95, 1.3 and 2.0 (Hasenclever 2014). Here SUVpeak uses a 1 ml sphere and the liver a 3 cm sphere; the original uses the 4 hottest voxels and a 30 ml VOI.

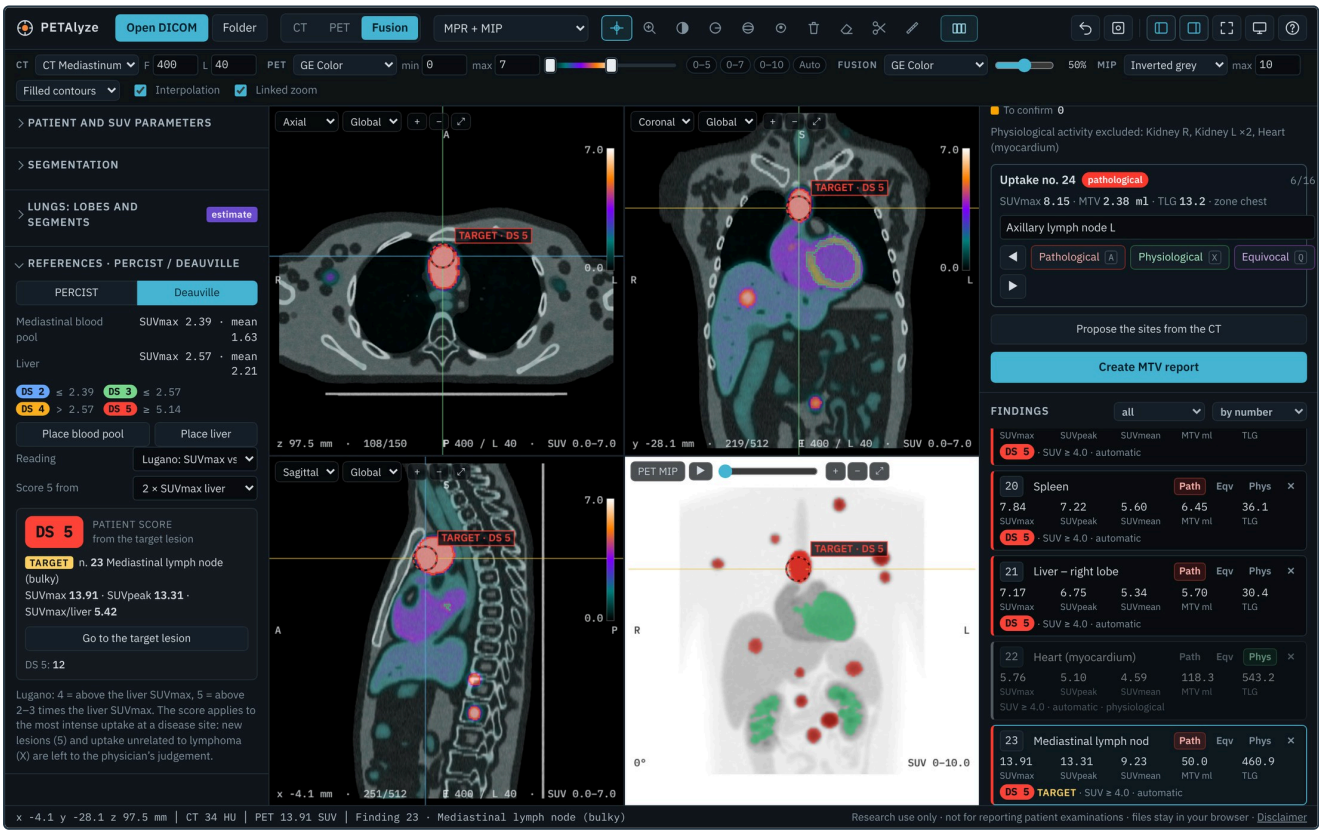
The patient score is the score of the target lesion. Until you confirm a pathological finding, the target is **provisional**: it is chosen among all non-physiological findings, skipping sites proposed as bladder, brain, heart and kidney.

The score and the target appear in the findings list, on the images, on the MIP and in the report. **Go to the target lesion** shows it.

> The score applies to the most intense uptake at a disease site. New lesions (score 5) and uptake unrelated to lymphoma (X) are left to your judgement.



Lugano reading: patient score 5 from the bulky mediastinal node.



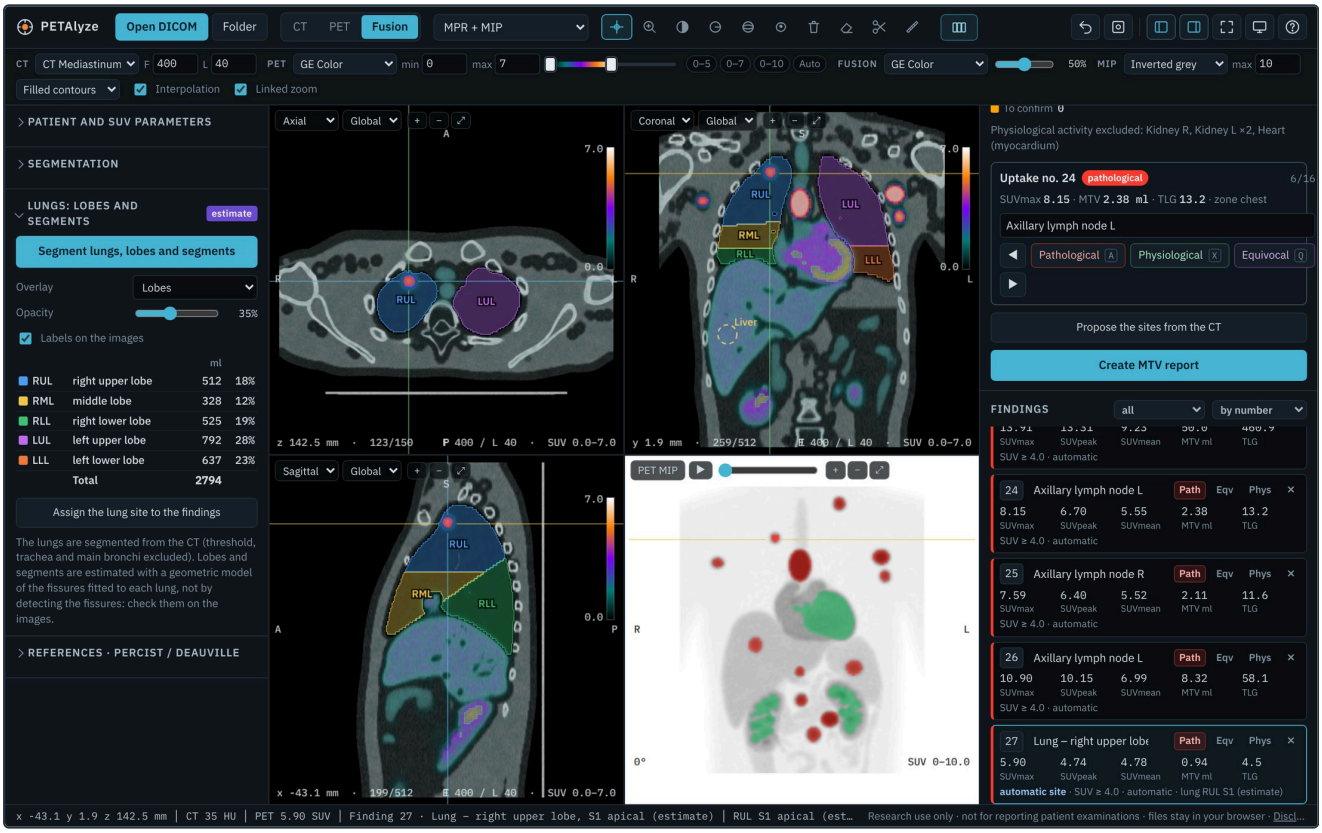
The target lesion on the views and on the MIP.

13 Lungs: lobes and segments

An experimental tool that estimates lungs, lobes and segments from the CT and gives the lung site of intrapulmonary findings.

- Open **Lungs: lobes and segments** in the left panel and press **Segment lungs, lobes and segments**.
- The lungs are segmented from the CT by threshold, excluding the trachea and the main bronchi. The five lobes and eighteen segments are **estimated** with a geometric model of the fissures fitted to each lung: the fissures are not detected on the images.
- **Overlay** shows lobes, segments or nothing; **Opacity** sets how strong it is; **Labels on the images** names them. The status bar shows the lobe and segment under the mouse.
- **Assign the lung site to the findings** fills in the site of the findings inside the lungs, for example “Lung – right upper lobe, S1 apical (estimate)”.

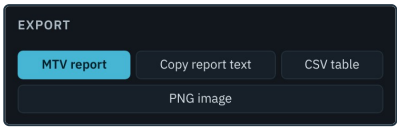
> Lobes and segments are an estimate. Check them on the images before you use them.



Lobe overlay, with a nodule in the right upper lobe selected.

14 Exporting the results

PETAlyze does not keep your work after the tab is closed. Export the results you need before closing it.



The **Export** section at the bottom of the right panel has four buttons:

- **MTV report**: opens the report (below).
- **Copy report text**: copies the report as text, to paste into a document.
- **CSV table**: saves `pet_ct_findings.csv`, one row per finding.
- **PNG image**: saves `pet_ct_views.png`, the views as they are on the screen.

The MTV report

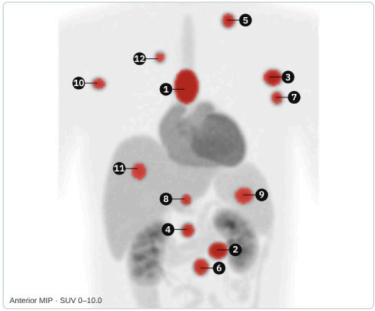
The report lists the pathological lesions from the highest SUVmax, with site, SUVmax, SUVpeak, SUVmean, MTV and TLG; the totals (MTV, TLG, number of lesions, SUVmax, Dmax); an anterior MIP with the lesions numbered; the equivocal findings, excluded from the totals; the physiological activity excluded; the uptakes not confirmed; the SUV parameters and references; the segmentation method; and the Deauville score when it is active. At the bottom of the report: **Copy text**, **CSV table**, **Download HTML report** (`pet_ct_mtv_report.html`, which opens in any browser) and **Close**.

Quantitative PET-CT report — metabolic tumour burden

SYNTHETIC PHANTOM · ID XCAT-LYMPHOMA · study of 17/11/2026 · Fluorodeoxyglucose

TOTAL MTV	TOTAL TLG	LESIONS	SUVMAX	DMAX
99.87 ml	773.5	12	13.91	36.6 cm

N	Location	SUVmax	SUVpeak	SUVmean	MTV ml	TLG
1	Mediastinal lymph node (bulky)	13.91	13.31	9.23	49.95	460.9
2	Para-aortic lymph node	12.15	11.31	7.42	9.56	70.9
3	Axillary lymph node L	10.90	10.15	6.99	8.32	58.1
4	Interaortocaval lymph node	9.41	7.88	6.16	3.05	18.8
5	Supraclavicular lymph node L	9.10	7.95	6.10	3.54	21.6
6	Mesenteric lymph node	8.71	8.09	6.14	5.86	36.0
7	Axillary lymph node L	8.15	6.70	5.55	2.38	13.2
8	Bone – vertebral body	8.03	6.42	5.57	2.02	11.3
9	Spleen	7.84	7.22	5.60	6.45	36.1
10	Axillary lymph node R	7.59	6.40	5.52	2.11	11.6
11	Liver – right lobe	7.17	6.75	5.34	5.70	30.4
12	Lung – right upper lobe, S1 apical (estimate)	5.90	4.74	4.78	0.94	4.5
	Total	**13.91**			**99.87**	**773.5**



Top of the MTV report of the synthetic study.

The CSV table

Comma-separated, with a decimal point, one row per finding: number, site, automatic site, status, organ, source (automatic or manual), method, threshold, SUVmax, SUVpeak, SUVmean, SD, MTV (ml), TLG, voxels and the position of the maximum in mm, plus Deauville score and target when active. The last rows give the pathological totals, the number of findings, Dmax, the references and the study.

Exported files contain patient data. The report, the CSV table and the copied text include the patient name, ID and study date read from the DICOM files. They are saved only on your computer, in the Downloads folder. Handle them as health data and remove identifiers before sharing them, for example in a publication or on the forum.

15 Keyboard and mouse

Tools

`N`	Navigate
`Z`	Pan/zoom
`W`	Window
`R`	ROI
`V`	VOI
`S`	Finding
`D`	Delete
`E`	Eraser
`T`	Scissors
`M`	Ruler
`F`	Place the liver reference
`B`	Place the blood pool reference
`Esc`	Back to Navigate; deselects a measurement

Findings

`A`	Pathological
`Q`	Equivocal
`X`	Physiological
`←` `→`	Previous / next uptake to confirm
`C`	Show / hide the contours
`Del`	Delete the selected finding or measurement
`Ctrl`+`Z`	Undo the last contour change

The keys don't act while you are typing in a field, such as the site of a finding. Press `Enter` or click on the images first.

Views

`1` `2` `3`	CT, PET, Fusion
`↑` `↓` `PgUp` `PgDn`	Slice in the active view
`+` `−`	Zoom the active view
`0`	Fit the active view
`Home`	Reset zoom and position
`H`	Maximum image area

Mouse

Wheel	Slices; on the MIP, rotation
Right-drag	Zoom
`Ctrl` + wheel, pinch	Zoom
`Shift` + left-drag	Pan
Middle-drag, `Alt` + left-drag	CT window or SUV scale
Double-click	Enlarge the view

16 Troubleshooting

Problem or message	What to do
The email with the password doesn't arrive	Look in Spam, Junk and, in Gmail, Promotions; search for “PETAlyze”. Check the address you typed and register again if needed. If it still doesn't arrive, ask on the forum.
The password is not accepted	Copy it from the email, without other characters. If a saved password stopped working, the password may have changed: enter the one from the latest email.
No readable DICOM image in the selected files	The files are not DICOM images, or they use a compression that PETAlyze cannot read (section 3). Export the study uncompressed.
Series found but no CT or PET	The files contain other modalities only. Select the folder of the PET/CT study.
Weight or dose missing: values in kBq/ml	Enter weight and dose in Patient and SUV parameters (section 6).
Injection/acquisition times missing: dose not decay-corrected	Enter the injection time and the scan start time.
Unusual uptake time: check the times	The time between injection and scan is negative or very long. Check both times and the date.
Images not decay-corrected: approximate SUV	The PET series is not decay-corrected: SUV values are approximate.
CNTS units without a conversion factor: values in counts	The PET is stored in counts without a conversion factor. Export the PET in Bq/ml from the workstation.
Non-uniform slice spacing	Slices are missing or unevenly spaced: the coronal and sagittal views may be inaccurate. Check that all files of the series were selected.
Loading is slow or the tab runs out of memory	Tick **Halve the CT resolution** in the Series found window, and close other tabs.
For PERCIST, first place the liver reference VOI	Place the liver (section 7) before segmenting with PERCIST.
The contour reaches the edge of the sphere	The lesion is larger than the sphere: drag a larger sphere with the Finding tool.
No voxel above the threshold with this method	The uptake is below the threshold: choose A50P or Extended MTV under Manual finding.
Threshold too low	The threshold would include a large part of the body. Check the SUV parameters or choose a higher threshold.
Two lesions, or a lesion and physiological activity, are one finding	Separate them with the Scissors or the Eraser (section 9).
Full screen is not allowed in this window	Use the browser's full screen (F11 on Windows and Linux).
Copy not allowed by the browser	Use **CSV table** or **Download HTML report** instead.

17 Citing PETAlyze, support and privacy

Citing PETAlyze

If you use PETAlyze in a scientific work, please cite it in your references. It helps other researchers find it and keeps the project going.

> Meduri GM. PETAlyze: PET/CT quantification in the browser [software]. Version 1.0. Zenodo; 2026. doi:10.5281/zenodo.24341410

Add the date you used it. In the methods, name the segmentation method and its settings, for example “SUV ≥ 4.0 with PETRA preselection of regions ≥ 3 ml, uptakes confirmed by the reader”, and the SUV normalisation.

Questions and support

- **Forum**: www.petalyze.org/forum.html, with the sections Questions and help, Error reports, and Ideas and requests. Anyone can read it; to write, create a free forum account.
- **Email**: reply to the email with your password.

> **Never post patient data** on the forum: no names, dates of birth, IDs, screenshots that could identify a patient, or DICOM files. The forum does not give clinical advice.

Privacy

The website keeps only the email address you registered with, to send you the password and, if you agreed, news about PETAlyze. Your images never leave your computer. The full privacy notice is at www.petalyze.org/privacy.html. To have your address deleted, reply to the password email.

Disclaimer

PETAlyze is provided for research and teaching, without warranty. It is not a medical device and must not be used for diagnosis or to report patient examinations. The user is responsible for checking every contour and every value.

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syngo.via is a trademark of Siemens Healthineers AG. Fonts: IBM Plex, SIL Open Font License 1.1. Images: synthetic PET/CT from the XCAT lymphoma phantom (Fedrigo et al., Med. Phys. 2022), no patient data.