

Supplement: CXCR4-Targeted PET Imaging of Glioblastoma Using [⁶⁸Ga]Ga-TD-01: From Pharmacokinetics and Dosimetry to Theranostic Potential

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1. Radiochemistry

1.1 Radio labeling and quality control of [^{68}Ga]Ga-TD-01

The BFC containing DOTA for ^{68}Ga complexation was successfully synthesized. Radiolabeling with ^{68}Ga was performed via a 10-minute reaction at 60 °C in sodium acetate solution (pH 4.0). The crude product was purified by solid phase extraction (HLB SPE Cartridge) to remove unreacted ^{68}Ga . Consequently, this condition (Fig. 1) was selected for labeling TD-01 and conducting quality control of the [^{68}Ga]Ga-TD-01 complex. The radio-TLC and HPLC chromatograms confirmed the successful radioactive labeling of ^{68}Ga with TD-01 (Fig. 2 and 3). After removing excess Ga-68 using an HLB SPE cartridge, [^{68}Ga]Ga-TD-01 exhibited radiochemical purity (RCP) exceeding 97% (n = 4). The calculated molar activity of the produced [^{68}Ga]Ga-TD-01 was 51.14 ± 4.74 GBq/ μmol . The quality control analysis results of [^{68}Ga]Ga-TD-01 for CXCR4 imaging are reported in Table 1.

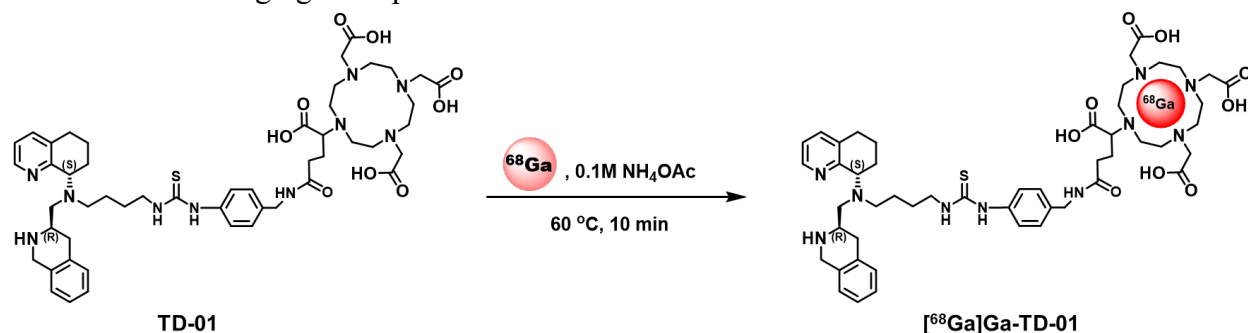


Figure 1 Radiosynthesis of [^{68}Ga]Ga-TD-01.

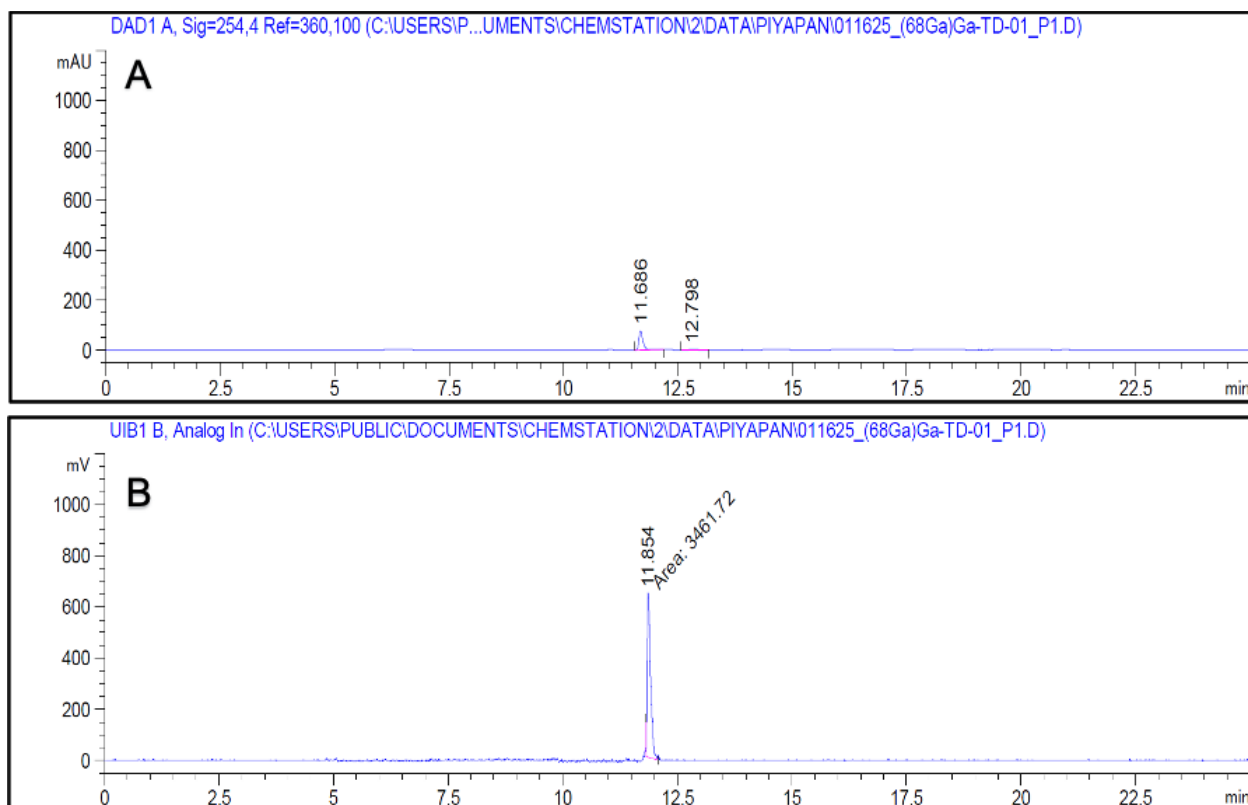


Figure 2: HPLC chromatogram of $[^{68}\text{Ga}]\text{Ga-TD-01}$. (A) UV-detector and (B) Radio-detector

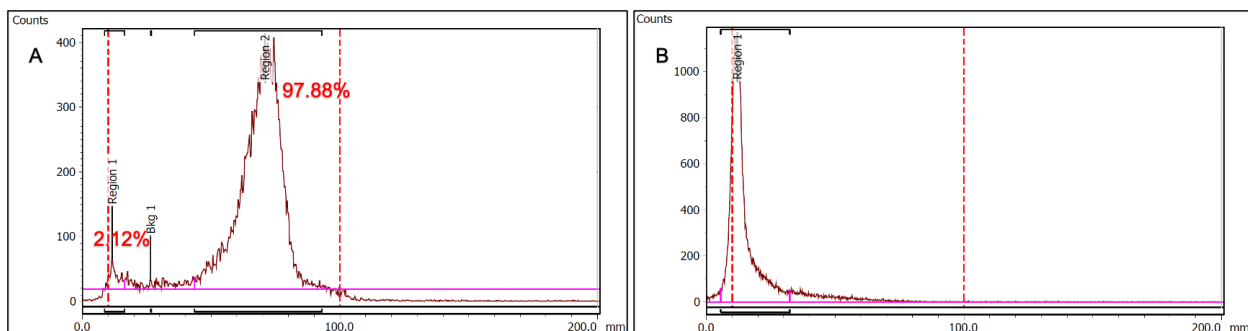
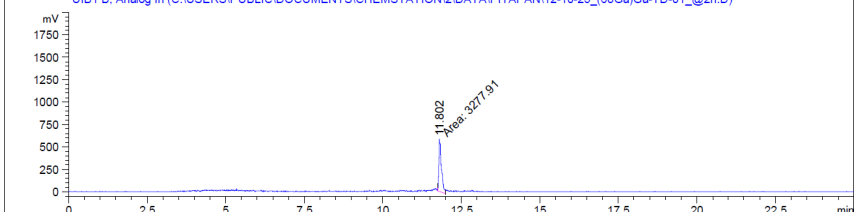
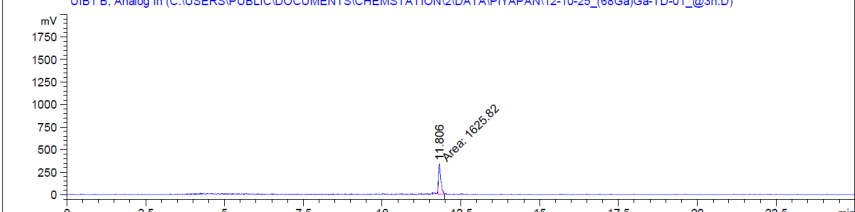
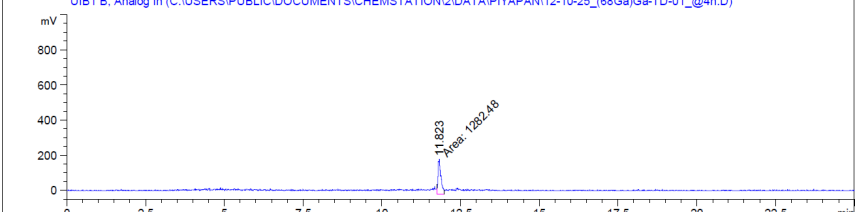
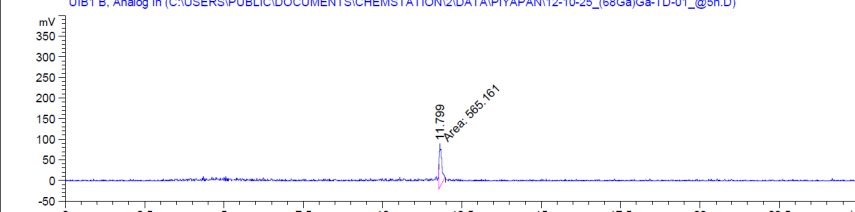
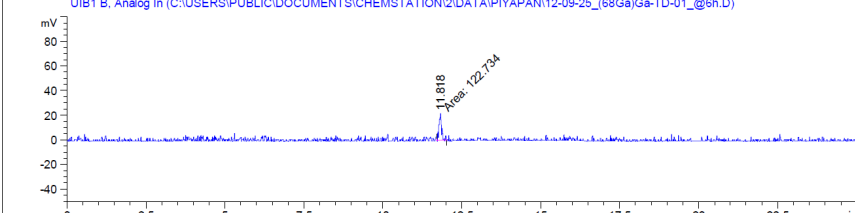


Figure 3: iTLC profile of $[^{68}\text{Ga}]\text{Ga-TD-01}$. (A) 0.1 M NH_4OAc : MeOH = 4:6 and (B) 100% of sodium citrate.

Table1: Shelf life of $[^{68}\text{Ga}]\text{Ga-TD-01}$ in normal saline at 1, 2, 3, 4, 5 and 6 hours ($n = 3$)

Time (h)	HPLC chromatogram	%RCP
1	11.813 Area: 4823.37	> 99

2	UIB1 B, Analog In (C:\USERS\PUBLIC\DOCUMENTS\CHEMSTATION\2\DATA\PIYAPANI\12-10-25_(68Ga)Ga-TD-01_@2h.D)  Chromatogram showing a single peak at 11.802 min with area 3277.91. The y-axis is mV (0 to 1750) and the x-axis is min (0 to 22.5).	> 99
3	UIB1 B, Analog In (C:\USERS\PUBLIC\DOCUMENTS\CHEMSTATION\2\DATA\PIYAPANI\12-10-25_(68Ga)Ga-TD-01_@3h.D)  Chromatogram showing a single peak at 11.806 min with area 1623.82. The y-axis is mV (0 to 1750) and the x-axis is min (0 to 22.5).	> 99
4	UIB1 B, Analog In (C:\USERS\PUBLIC\DOCUMENTS\CHEMSTATION\2\DATA\PIYAPANI\12-10-25_(68Ga)Ga-TD-01_@4h.D)  Chromatogram showing a single peak at 11.823 min with area 1282.48. The y-axis is mV (0 to 800) and the x-axis is min (0 to 22.5).	> 99
5	UIB1 B, Analog In (C:\USERS\PUBLIC\DOCUMENTS\CHEMSTATION\2\DATA\PIYAPANI\12-10-25_(68Ga)Ga-TD-01_@5h.D)  Chromatogram showing a single peak at 11.799 min with area 595.101. The y-axis is mV (-50 to 350) and the x-axis is min (0 to 22.5).	> 99
6	UIB1 B, Analog In (C:\USERS\PUBLIC\DOCUMENTS\CHEMSTATION\2\DATA\PIYAPANI\12-09-25_(68Ga)Ga-TD-01_@6h.D)  Chromatogram showing a single peak at 11.818 min with area 122.134. The y-axis is mV (-40 to 80) and the x-axis is min (0 to 22.5).	> 99

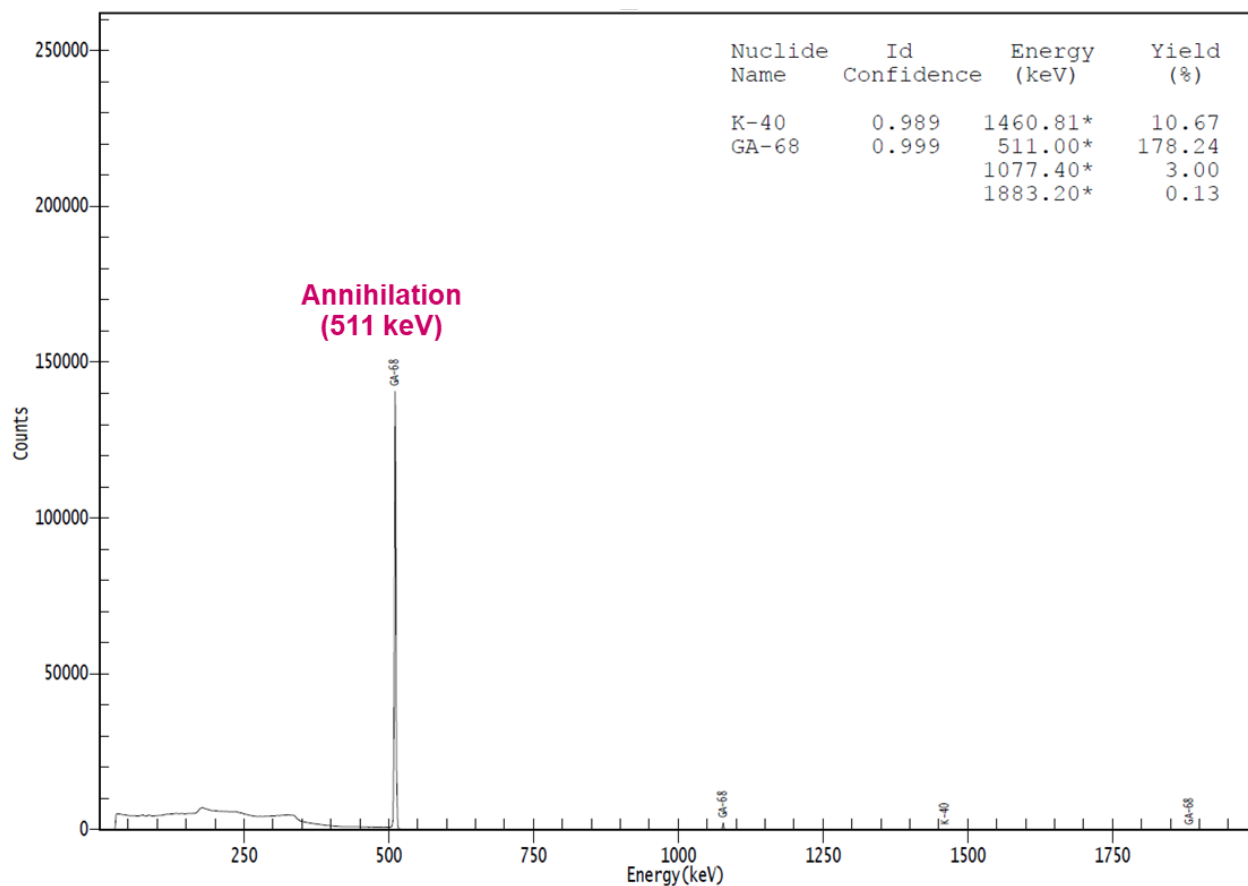


Figure 4: Gamma spectrum of Ga-68 sample. The gamma spectrum displays the energy distribution of counts obtained from a Ga-68 sample. The measurement was conducted over a live time of 3496.241 seconds and a real time of 3600.000 seconds. The prominent peak at approximately 511 keV corresponds to Ga-68. Additional smaller peaks are also identified at various energies. The spectrum indicates a high radionuclidic purity for Ga-68, as evidenced by the dominant peak at the expected energy for Ga-68 emissions.

2. PET/MR image segmentation

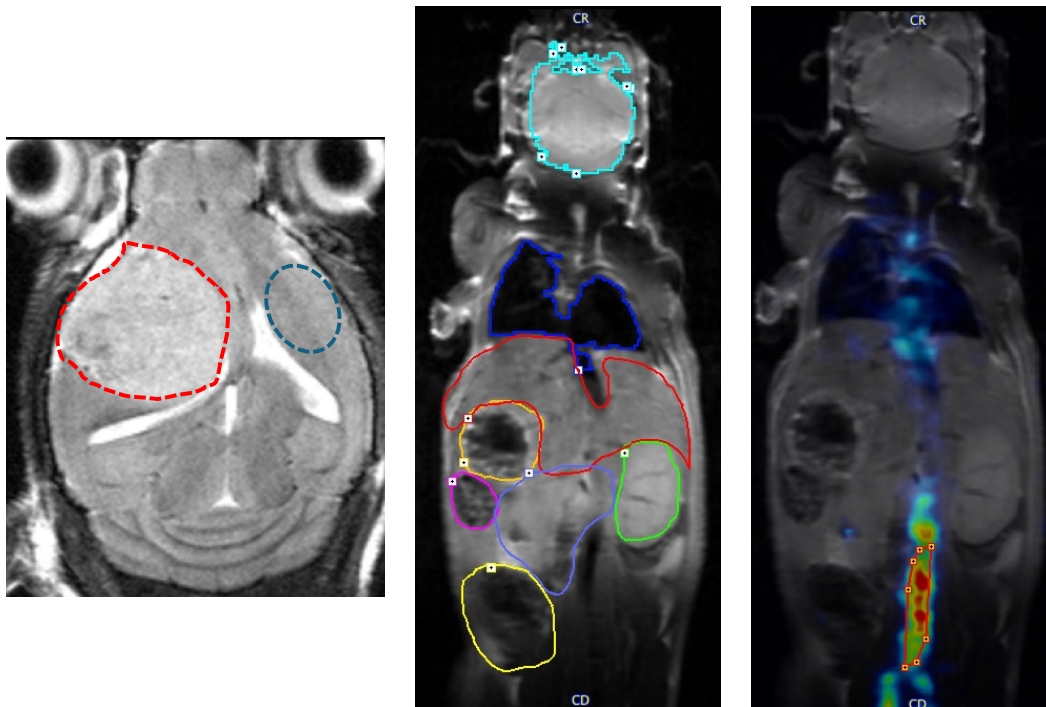


Figure 5: Examples of MRI based organ/VOI segmentation for left: T2-weighted FSE MRI, the tumor region (red) and contra lateral healthy brain region (blue) or middle: T1-weighted FSE MRI and whole body organ segmentation to extract time-activity data of dose relevant organs. Here brain (light blue), lungs (dark blue), liver (red), stomach (orange), spleen (magenta), right kidney (green) and small intestines (yellow) is visible. Right: Segmentation of the inferior vena cava (red) 5 s after radiotracer injection to extract the imaged derived input function for subsequent pharmacokinetic modeling.

3. Power analysis

A priori: baseline vs. blocking tumor study

t tests - Means: Difference between two independent means (two groups)

Analysis:	A priori: Compute required sample size		
Input:	Tail(s)	=	Two
	Effect size d	=	2,7
	α err prob	=	0,05
	Power ($1-\beta$ err prob)	=	0,95
	Allocation ratio N2/N1	=	1
Output:	Noncentrality parameter δ	=	4,2690748
	Critical t	=	2,3060041
	Df	=	8
	Sample size group 1	=	5
	Sample size group 2	=	5
	Total sample size	=	10
	Actual power	=	0,9606290

Post hoc: baseline vs. blocking tumor study

t tests - Means: Difference between two independent means (two groups)

Analysis: Post hoc: Compute achieved power
Input: Tail(s) = Two
Effect size d = 2,85
 α err prob = 0,05
Sample size group 1 = 6
Sample size group 2 = 6
Output: Noncentrality parameter δ = 4,9363448
Critical t = 2,2281389
Df = 10
Power (1- β err prob) = **0,9931020**

A post hoc power analysis was performed in G*Power 3.1 for the primary pharmacokinetic endpoint (tumor Vt, 1TCM). Based on the observed means and standard deviations (0.541 ± 0.065 vs. 0.325 ± 0.085), the standardized effect size was $d = 2.85$. With $\alpha = 0.05$ and $n = 6$ animals per group, the achieved power was >0.95 .

4. Whole-body organ dosimetry

Table 2: OD, ED contributions and the ED based on mouse biokinetic data extrapolated to human entity and estimated with OLINDA 1.1 for the adult male model.

	OD ($\mu\text{Sv/MBq}$)		ED contr ($\mu\text{Sv/MBq}$)	
Adult male (73.7 kg)	mean	stdev	mean	stdev
Adrenals	9.82E-03	1.28E-03	7.58E-05	3.17E-05
Brain	5.29E-03	3.00E-03	4.53E-05	3.25E-05
Breasts	7.49E-03	1.79E-03	8.41E-04	3.61E-04
Gallbladder Wall	1.31E-02	1.52E-03	9.08E-05	5.38E-05
LLI Wall	1.31E-02	4.90E-03	1.07E-03	8.61E-04
Small Intestine	2.52E-02	1.59E-02	1.57E-04	1.91E-05
Stomach Wall	1.18E-02	1.07E-03	1.40E-03	1.10E-04
ULI Wall	2.08E-02	1.20E-02	7.92E-04	3.90E-04
Heart Wall	2.60E-02	2.54E-02	1.30E-04	3.40E-05
Kidneys	5.01E-02	2.32E-02	6.58E-04	7.58E-04
Liver	1.82E-02	1.17E-02	5.90E-04	3.67E-04
Lungs	2.45E-02	3.14E-02	1.35E-03	5.56E-04
Muscle	9.51E-03	1.87E-03	6.83E-05	2.40E-05
Ovaries	1.18E-02	3.77E-03	1.42E-03	1.25E-03
Pancreas	9.68E-03	1.73E-03	7.63E-05	3.37E-05
Red Marrow	7.84E-03	1.08E-03	9.59E-04	1.41E-04
Osteogenic Cells	1.38E-02	3.37E-03	1.41E-04	3.38E-05
Skin	8.53E-03	2.16E-03	8.72E-05	2.22E-05
Spleen	1.17E-02	4.02E-03	8.63E-05	4.80E-05

Testes	1.00E-02	3.05E-03	0.00E+00	0.00E+00
Thymus	8.44E-03	1.85E-03	6.58E-05	3.12E-05
Thyroid	9.72E-03	2.49E-03	4.27E-04	1.56E-04
Urinary Bladder Wall	5.15E-02	2.52E-02	2.08E-03	9.50E-04
Uterus	1.24E-02	3.45E-03	8.78E-05	2.74E-05
Total Body	8.95E-03	2.47E-03	0.00E+00	0.00E+00
ED	-	-	1.25E-02	8.16E-04

5. PET pharmacokinetic modeling

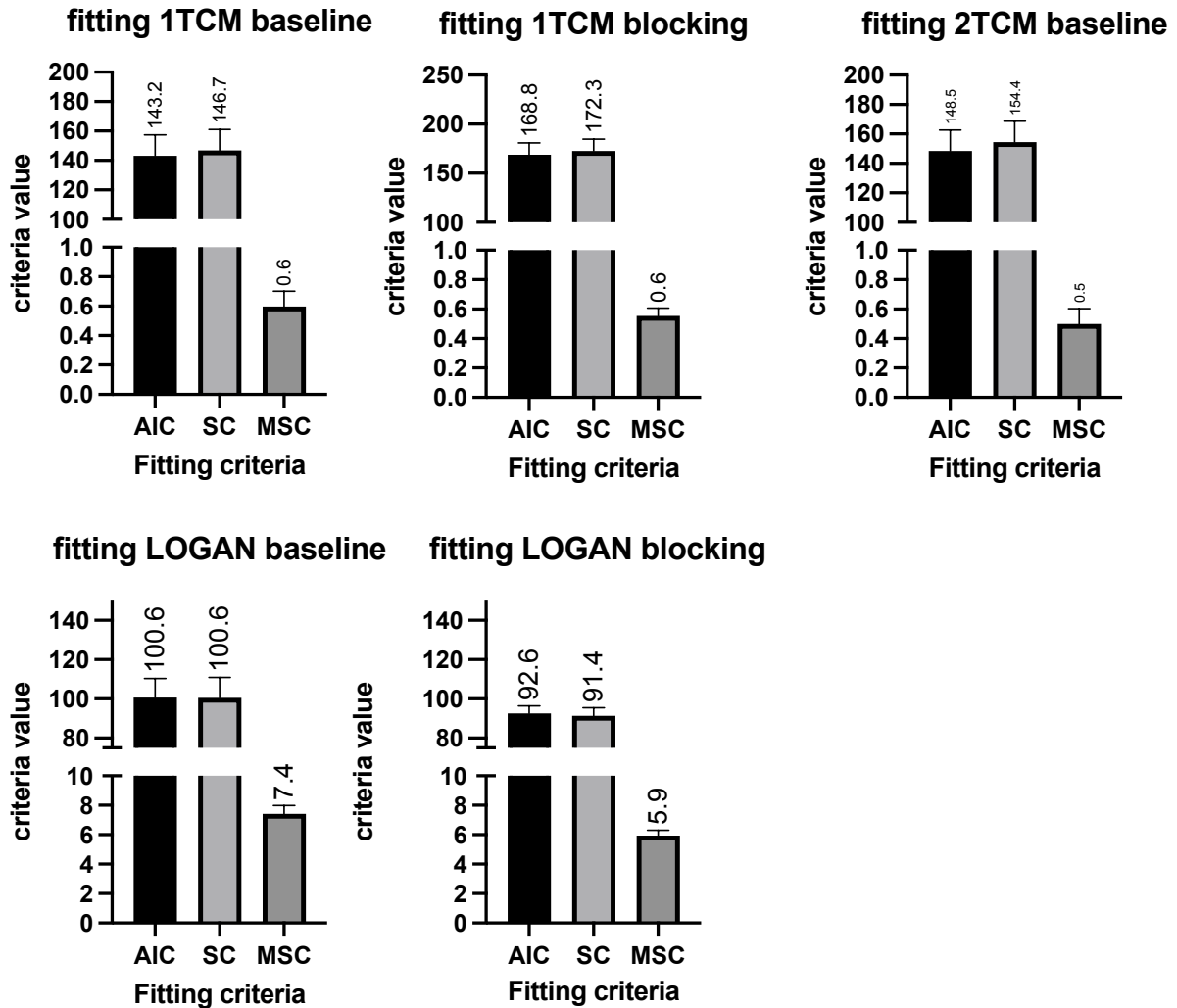


Figure 6: Evaluation of model fitting criteria using Akaike Information Criterion (AIC), Schwartz Criterion (SC) and Model Selection Criterion (MSC).

6. Ex vivo stability

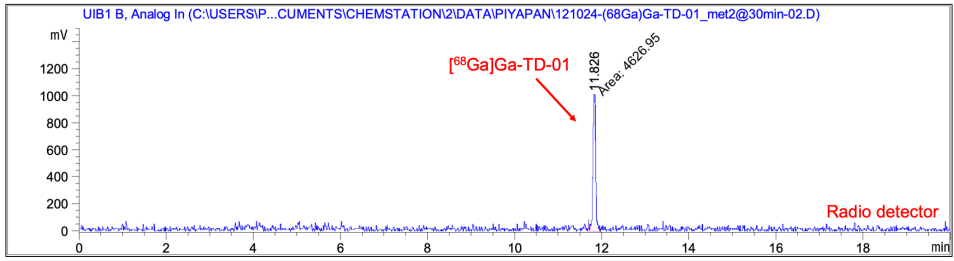
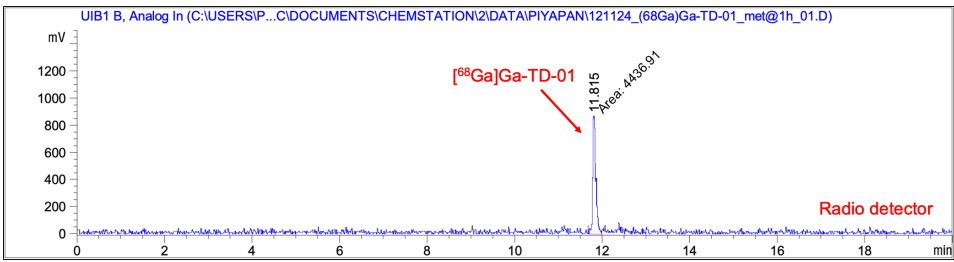
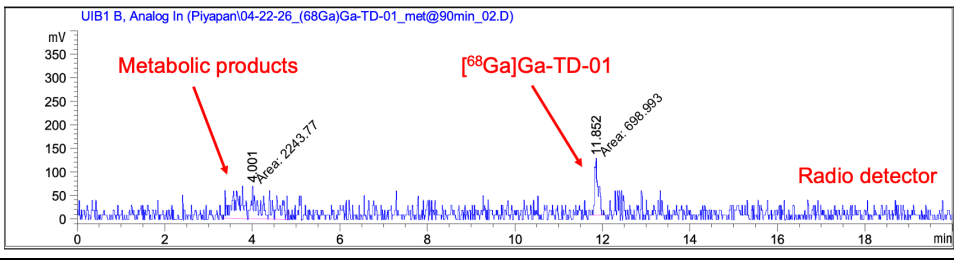
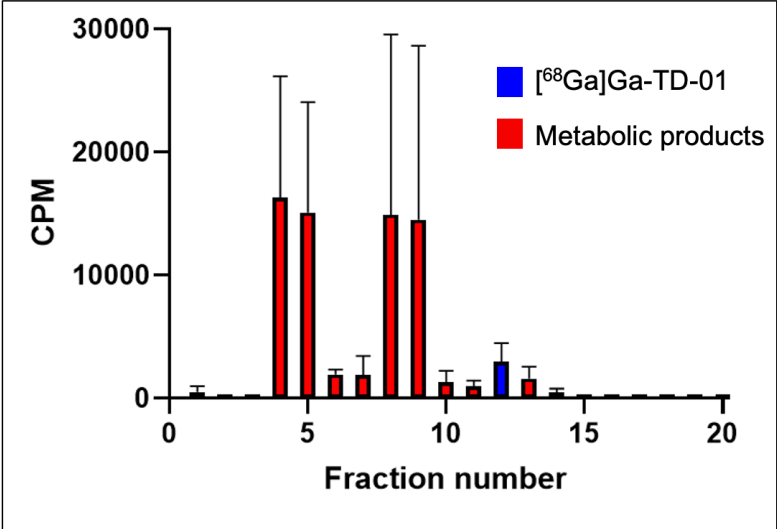
Time (min)	HPLC chromatogram / gamma counter signal	Intact tracer (%)
30		> 99
60		> 99
90		45 ± 13
120		14 ± 11

Figure 7: Radio-HPLC chromatogram and gamma counter fractions of [^{68}Ga]Ga-TD-01 in the extracted supernatant at 0.5, 1, 1.5 and 2-hours post-injection.

7. RNA scope group comparison

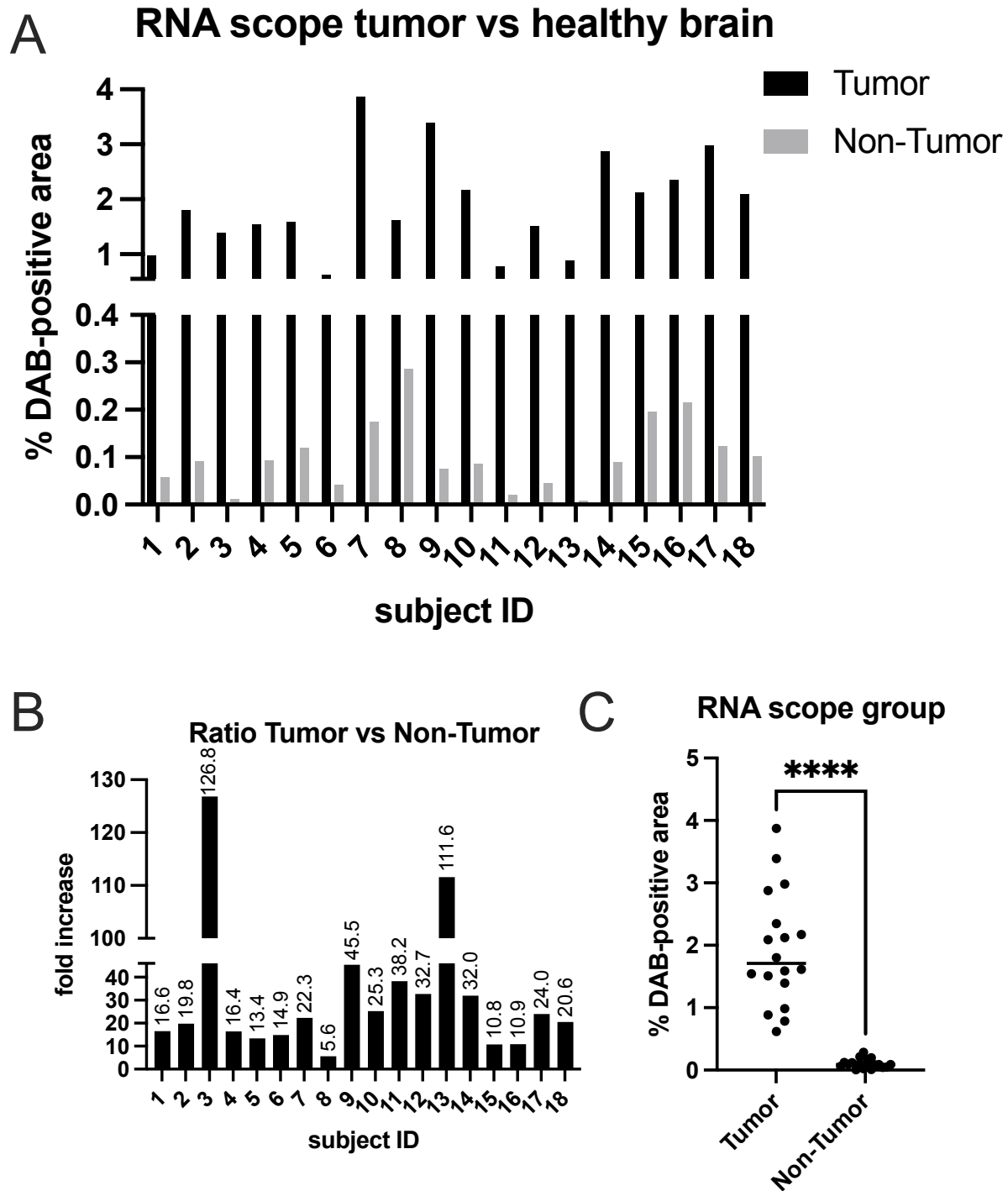


Figure 8: Quantitative analysis of CXCR4 RNAscope signal in orthotopic GL261 glioblastoma tissue and contralateral healthy brain. (A) Quantification of RNAscope-derived DAB-positive area in tumor and non-tumor brain regions for individual animals (n = 18). Tumor tissue demonstrated consistently higher CXCR4-associated signal compared to contralateral healthy brain tissue. (B) Tumor-to-brain fold increase in RNAscope signal intensity for each subject, illustrating elevated CXCR4 expression within the tumor microenvironment relative to normal brain tissue. (C) Grouped

analysis of RNAscope DAB-positive area (two-sided, unpaired t test) demonstrating significant increased CXCR4 expression in tumor tissue compared to non-tumor brain regions. Data are presented as mean $\pm$ SD.