

# Imaging-Based Prediction of Molecular Therapy Targets in NSCLC by Radiogenomics and AI Approaches: A Systematic Review

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## Search strategy

### Radiogenomics (A)

("radiogenomics" OR "radiogenomic" OR "imaging genomic" OR "imaging genomics")

### Lung cancer (B)

("lung" OR "NSCLC" OR "pulmonary")

### Molecular alterations/targeted therapy/PD-1 and PD-L1/immunotherapy (C)

("genomic" OR "genomics" OR "gene" OR "genes" OR "genetic" OR "genetics" OR "metagene" OR "metagenes" OR "mutation" OR "mutations" OR "RNA" OR "miRNA" OR "mRNA" OR "ALK" OR "EGFR" OR "KRAS" OR "RET" OR "ROS1" OR "VEGF" OR "MET" OR "BRAF" OR "ERBB2" OR "HER2" OR "PD-1" OR "PD-L1" OR "target" OR "targeted" OR "TKI" OR "molecular" OR "kinase" OR "monoclonal" OR "antibody" OR "immunotherapy")

### Imaging (D)

("texture" OR "textural" OR "radiomic" OR "radiomics" OR "imaging features" OR "imaging biomarker" OR "imaging biomarkers" OR "imaging characteristics" OR "deep learning" OR "CNN" OR "convolutional")

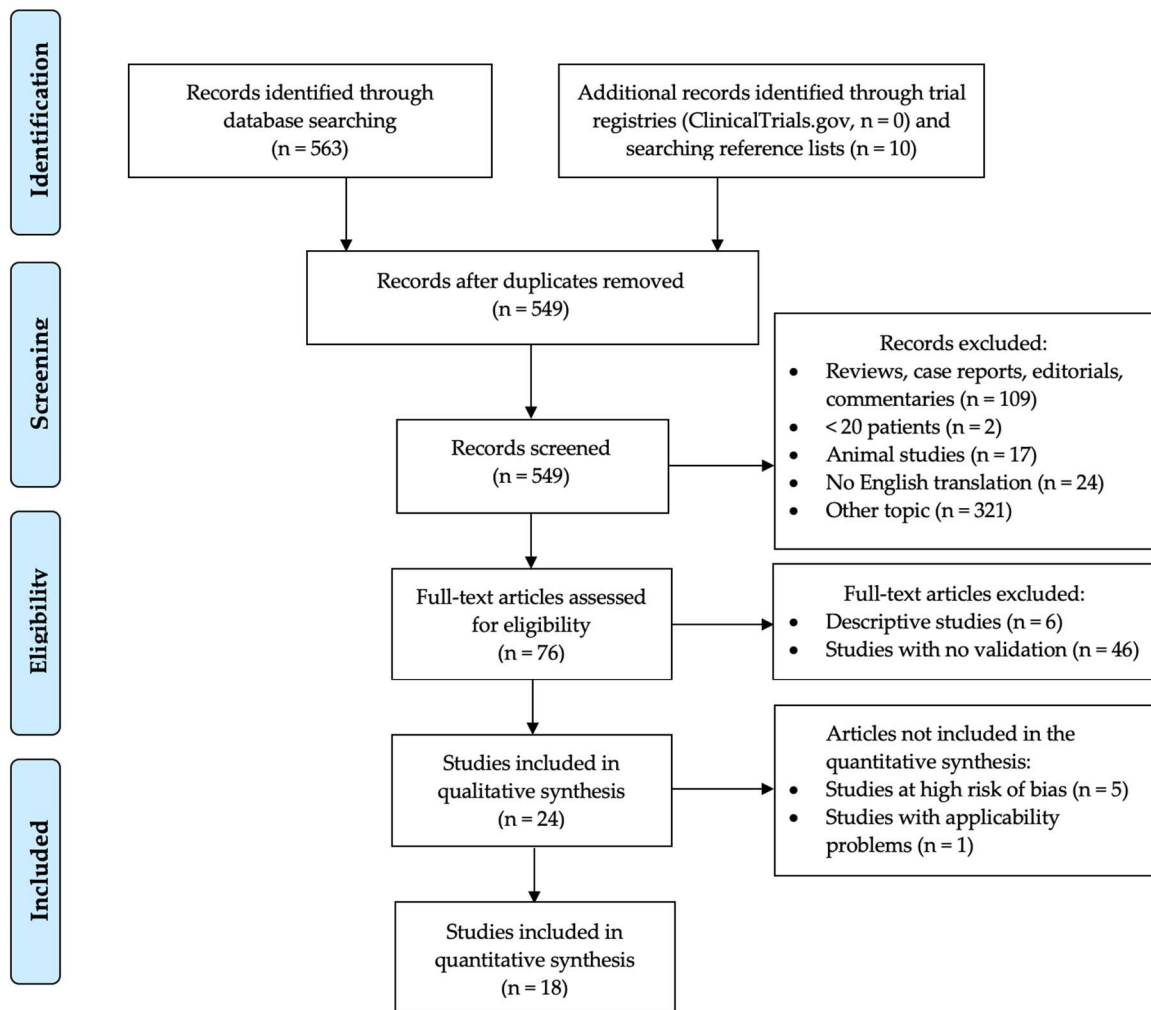
## PubMed/MEDLINE Search

1. (A) AND (B):

("radiogenomics" OR "radiogenomic" OR "imaging genomic" OR "imaging genomics") AND ("lung" OR "NSCLC" OR "pulmonary")

2. ((C) AND (D)) AND (B)

((("genomic" OR "genomics" OR "gene" OR "genes" OR "genetic" OR "genetics" OR "metagene" OR "metagenes" OR "mutation" OR "mutations" OR "RNA" OR "miRNA" OR "mRNA" OR "ALK" OR "EGFR" OR "KRAS" OR "RET" OR "ROS1" OR "VEGF" OR "MET" OR "BRAF" OR "ERBB2" OR "HER2" OR "PD-1" OR "PD-L1" OR "target" OR "targeted" OR "TKI" OR "molecular" OR "kinase" OR "monoclonal" OR "antibody" OR "immunotherapy") AND ("texture" OR "textural" OR "radiomic" OR "radiomics" OR "imaging features" OR "imaging biomarker" OR "imaging biomarkers" OR "imaging characteristics" OR "deep learning" OR "CNN" OR "convolutional")) AND ("lung" OR "NSCLC" OR "pulmonary"))



**Figure S1.** Flow chart of the literature selection process.

Study	RISK OF BIAS					APPLICABILITY CONCERNS			QUADAS-2 ADHERENCE (0-7) <sup>1</sup>	
	Patient Selection	Index Test	Reference Standard	Flow and Timing		Patient Selection	Index Test	Reference Standard		
Yoon 2020	Low	Low	Low	Low		Low	Low	Low	7	
Zhao W 2020	Low	Low	Low	Low		Low	Low	Low	7	
Lu X 2020	Low	Low	Low	Low		Low	Low	Low	7	
Zhang 2019	Low	Unclear	Low	Low		Low	Low	Low	6	
Li X 2019	Low	Unclear	Low	Low		Low	Low	Low	6	
Koyasu 2020	Unclear	Unclear	Low	Unclear		Low	Low	Low	4	
Wang X 2019	Unclear	Unclear	Unclear	Unclear		Low	Low	Low	3	
Li S 2019	Low	Low	Unclear	Unclear		High	Low	Low	4	
Jiang 2019	Unclear	Low	Low	Low		Low	Low	Low	6	
Jiang 2020	Low	Unclear	Low	Low		Low	Low	Low	6	
Tu 2019	Low	Low	Unclear	Unclear		Low	Low	Low	5	
Zhao W 2019	Unclear	Unclear	Low	Low		Low	Low	Low	5	
Yang X 2019	Low	Low	Low	Low		Low	Low	Low	7	
Jia 2019	Low	Unclear	Low	Low		Low	Low	Low	6	
Li XY 2018	Unclear	Unclear	Low	Low		Low	Low	Low	5	
Wang S 2019	Unclear	Low	Low	Low		Low	Low	Low	6	
Rizzo 2019	Unclear	Unclear	Unclear	Unclear		Low	Low	Low	3	
Li Y 2019	Unclear	Low	Low	Low		Low	Low	Low	6	
Xiong JF 2019	Unclear	Low	Low	Low		Low	Low	Low	6	
Zhang 2018	Low	Unclear	Low	Low		Low	Low	Low	6	
Rios V. 2017	Unclear	Unclear	Low	High		Low	Low	Low	4	
Yoon 2015	Unclear	Unclear	Low	Low		Low	Low	Low	5	
Gevaert 2017	Unclear	Unclear	Low	Unclear		Low	Low	Low	4	
Yamamoto 2014	Unclear	Low	Low	Low		Low	Low	Low	6	
Low	11	11	20	17	Low	23	24	24	QUADAS-2 > 4	18
High	0	0	0	1	High	1	0	0	QUADAS-2 ≤ 4	6
Unclear	13	13	4	6	Unclear	0	0	0		

**Figure S2.** QUADAS-2 tool for quality assessment of each included study. <sup>1</sup>To calculate the adherence to the QUADAS-2 criteria, 1 point was given for every item rated “Low”, and 0 points for every item rated “Unclear” or “High”. Finally, points for each of the seven items were summed.

**Table S1.** Details of molecular genetic alterations or PD-L1 expression stratified according to the stage (early vs. advanced) in the “high-quality” papers.

Study	Stage 0-II	Stage III-IV
<b>EGFR</b>		
Gevaert et al. [1]	nr	nr
Jia et al. [2]	311 pts (61% EGFR+)	192 pts (60% EGFR+)
Jiang et al. [3]	nr	nr
Koyasu et al. [4]	nr	nr
Li et al. [5]	356 pts (58% EGFR+)	654 pts (47% EGFR+)
Li et al. [6]	14 pts (57% EGFR+)	37 pts (41% EGFR+)
Li et al. [7]	nr	nr
Li et al. [8]	90 pts (56% EGFR+)	25 pts (56% EGFR+)
Lu et al. [9]	83 pts (65% EGFR+)	21 pts (48% EGFR+)
Rios Velazquez et al. [10]	nr	nr
Rizzo et al. [11]	nr	nr
Tu et al. [12]	326 pts (51% EGFR+)	78 pts (27% EGFR+)
Wang et al. [13]	620 pts (55% EGFR+)	224 pts (60% EGFR+)
Wang et al. [14]	51 pts (64% EGFR+)	0
Xiong et al. [15]	311 pts (61% EGFR+)	192 pts (60% EGFR+)
Yang et al. [16]	nr	nr
Zhang et al. [17]	0	180 pts (48% EGFR+)
Zhang et al. [18]	141 pts (59% EGFR+)	107 pts (48% EGFR+)
Zhao et al. [19]	394 pts (nr % EGFR+)	185 pts (nr % EGFR+)
Zhao et al. [20]	430 pts (nr % EGFR+)	207 pts (nr % EGFR+)
<b>ALK</b>		
Yamamoto et al. [21]	nr	nr
<b>ALK/ROS1/RET</b>		
Yoon et al. [22]	305 pts (9% Fusion+)	232 pts (15% Fusion+)
<b>PD-L1</b>		
Jiang et al. [23]	301 pts (20% PD-L1 ≥50%)	98 pts (31% PD-L1 ≥50%)
Yoon et al. [24]	0	153 pts (35% PD-L1 ≥50%)

nr: not reported; na: not assessed; pts: patients.

**Table S2.** Summary of the study reporting AUC and 95% confidence interval to predict genetic alterations and immunotherapy targets.

Study	Method	Metric(s)-Validation Set	95% Confidence Interval
<b>EGFR</b>			
Yang et al. [16]	Radiomics	AUC = 0.79	0.71–0.86
	Radiomics + clinical	AUC = 0.83	0.70–0.86
Jia et al. [2]	Radiomics	AUC = 0.80	0.73–0.87
	Radiomics + clinical	AUC = 0.83	0.76–0.89
Li et al. [6]	Radiomics	AUC = 0.83	0.68–0.92
Li et al. [5]	Radiomics	AUC = 0.74	0.67–0.81
	CNN	AUC = 0.81	0.75–0.87
	Radiomics + CNN	AUC = 0.81	0.75–0.87
Xiong et al. [15]	CNN	AUC = 0.78	0.70–0.85
	Radiomics + CNN	AUC = 0.84	0.78–0.90
<b>ALK</b>			
Yamamoto et al. [21]	Visual qualitative	Sensitivity = 83%	59%–96%
		Specificity = 78%	68%–86%
<b>PD-L1</b>			
Jiang et al. [23]	Radiomics	AUC = 0.97	0.93–1.0
Jiang et al. [23]	Radiomics*	AUC = 0.97	0.93–1.0
	Radiomics**	AUC = 0.91	0.85–0.97
Yoon et al. [24]	Radiomics + clinical	AUC = 0.67	0.58–0.76

\* PD-L1 expression level  $\geq 1\%$ ; \*\* PD-L1 expression level  $\geq 50\%$ .

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