

PROSTATE CANCER: PROSTATE MRI

STUDY: First / Follow-up, comparison with the study from _____

Specify magnetic field strength, coils used, type and dose of IV contrast administration

Specify Pulse sequences, including b values for DWI

Findings:

Size: L × W × H cm

Hemorrhage: [absent, mild, extensive]

Peripheral zone: [homogeneously hyperintense, heterogeneous, homogeneously hypointense]
on

T2-weighted images

Transition zone: [nonenlarged, enlarged with benign prostate hypertrophy (BPH) changes]

Lesion description:

- Location: [right/left base/mid/apex peripheral zone/central zone]
- Size:
- T2 description: []
- T2 numerical assessment: [1–5]
- DWI description:
- DWI-ADC numerical assessment: [1–5]
- DCE description:
- DCE assessment: [positive/negative]
- Lesion overall PI-RADS category: [1–5]

Extraprostatic extension:

[No capsular abutment, capsular abutment < 6 mm, capsular abutment 6–15 mm, capsular abutment

> 15 mm, capsular bulge or irregularity, gross extraprostatic extension]

Neurovascular bundles: description of proximity of any PI-RADS 4/5 lesion to NVBs

Seminal vesicles: [not involved by tumor]

Lymph nodes: [no adenopathy]

February 2022

Other pelvic organs: [no additional findings]

Impression:

- Based on the most suspicious abnormality, this exam is characterized as [PI-RADS 1/PI-RADS 2/
PI-RADS 3/PI-RADS 4/PI-RADS 5]. The most suspicious abnormality is located at the [location] and there is [no evidence of extracapsular extension]
- No suspicious adenopathy or evidence of pelvic metastases

PI-RADS™ v2.1 assessment categories

PI-RADS 1—Very low (clinically significant cancer is highly unlikely to be present)

PI-RADS 2—Low (clinically significant cancer is unlikely to be present)

PI-RADS 3—Intermediate (the presence of clinically significant cancer is equivocal)

PI-RADS 4—High (clinically significant cancer is likely to be present)

PI-RADS 5—Very high (clinically significant cancer is highly likely to be present)

Simplified Prostate Imaging–Reporting and Data System (PI-RADS) v2.1 algorithm for determining the likelihood of malignancy

