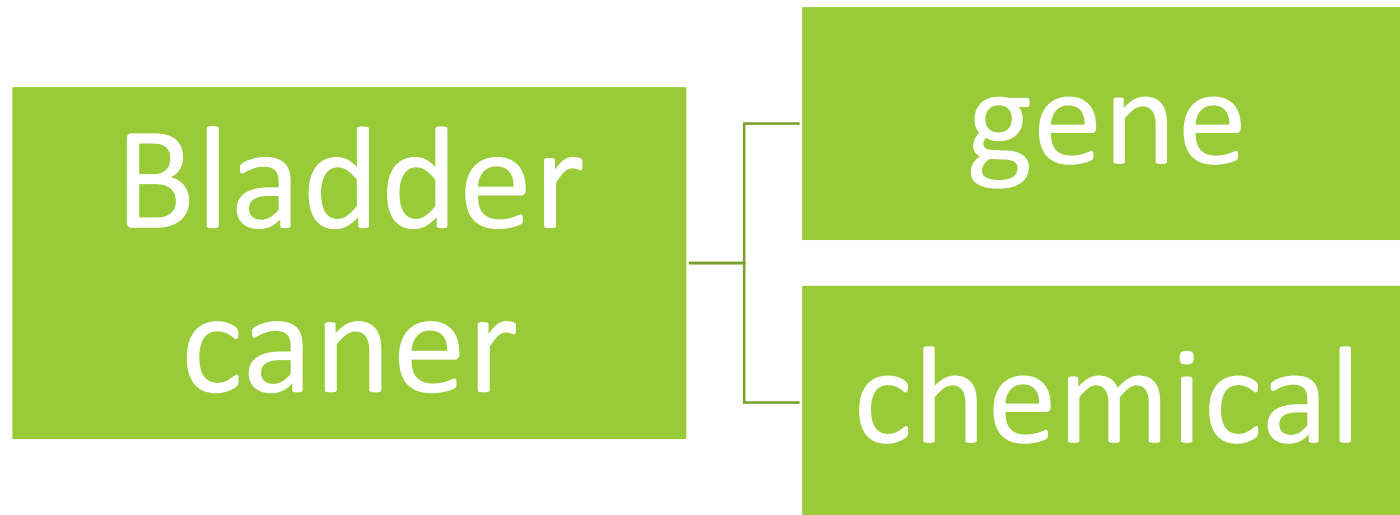


Shell programming for NER

廖旋

Pubtator



膀胱癌 (bladder cancer)

- 泛指各种出自膀胱的恶性肿瘤，也就是有异常细胞大量增殖而不受管制。膀胱是贮存尿液的中空器官，外壁主要由肌肉构成，位于下腹部。最常见的膀胱癌细胞来自膀胱内面黏膜表皮，正式名称为**移行上皮细胞癌(TCC)**。
- 最主要的危险因子是来自**基因**的影响，另外**吸烟**、长期接触某种染料（含苯胺（aniline）成份者，如纺织厂员工就可能接触到）、汽油或其他**化学物质**者也有较高的风险。
- 几个风险因子：FGFR3、HRAS、RB1、TP53等基因突变（调节细胞增殖循环）

Pubtator-bladder cancer

PubTator

Disease Search

Results: 1 to 15 of 35936

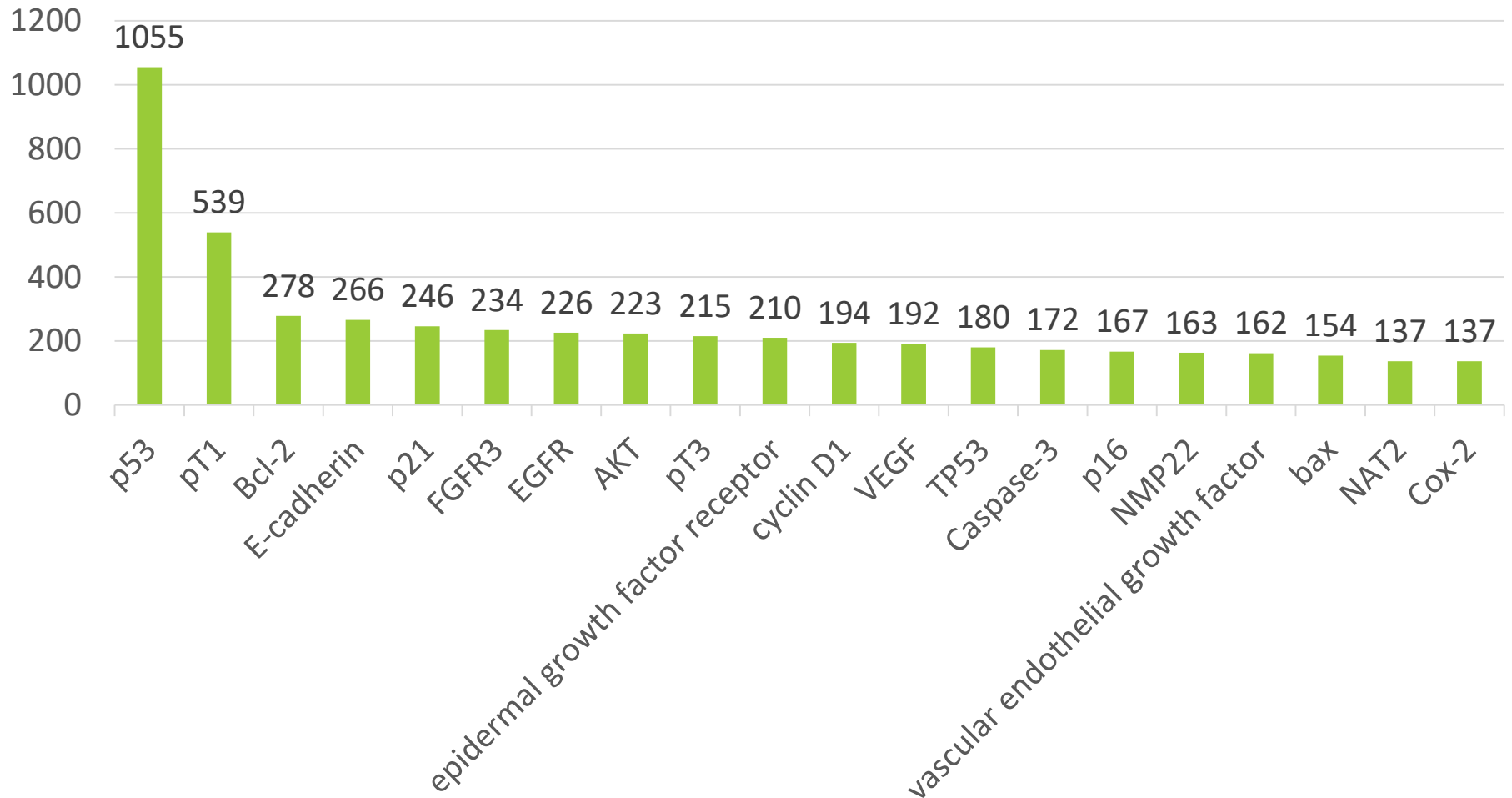
- 1 [The WHO 1973 classification system for grade is an important prognosticator in T1 non-muscle-invasive bladder cancer.](#)
Fransen van de Putte EE, Bosschieter J, van der Kwast TH, [...], van Rhijn BWG
BJU international; 2018 Apr 10
PMID:29637669 - Related citations
ABSTRACT

- 2 [Hyperbaric oxygenation for tumour sensitisation to radiotherapy.](#)
Bennett MH, Feldmeier J, Smee R, Milross C
The Cochrane database of systematic reviews; 2018 Apr 11 ; 4 CD005007
PMID:29637538 - Related citations
ABSTRACT

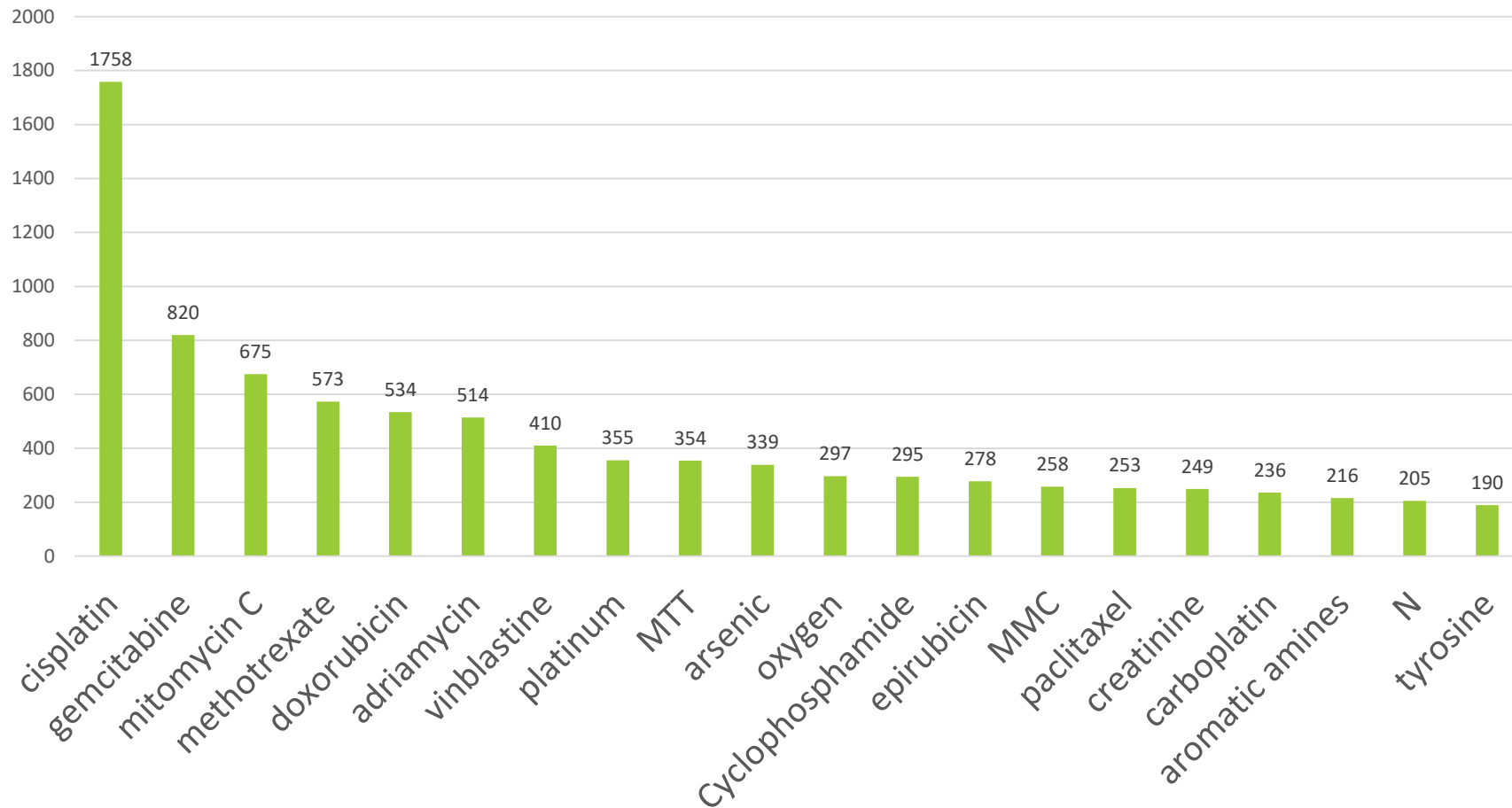
- 3 [\[Advanced bladder cancer : From chemo- to immunotherapy\].](#)
Horn T, Krege S, Retz M
Der Urologe. Aug. A; 2018 Apr 10 [Full text links]
PMID:29637216 - Related citations
ABSTRACT

- 4 [\[Cost-effectiveness analysis of blue light cystoscopy with hexylaminolevulinat in transurethral resection of the bladder\].](#)
Gakis G, Volkmer B, Qvick B, [...], Stenzl A
Der Urologe. Aug. A; 2018 Apr 10 [Full text links]
PMID:29637215 - Related citations
ABSTRACT

Gene top20



Chemical top20



膀胱癌FDA批准药物

atezolizumab	nivolumab
avelumab	thiotepa
cisplatin	valrubicin
doxorubicin	gemcitabine + cisplatin
durvalumab	mitomycin
pembrolizumab	vinflunine

Chemical top20

cisplatin	oxygen
gemcitabine	Cyclophosphamide
mitomycin C	epirubicin
methotrexate	MMC
doxorubicin	paclitaxel
adriamycin	creatinine
vinblastine	carboplatin
platinum	aromatic amines
MTT	N
arsenic	tyrosine

膀胱癌FDA批准药物

atezolizumab	0	nivolumab	0
avelumab	0	thiotepa	136
cisplatin	1	valrubicin	219
doxorubicin	5	gemcitabine + cisplatin	2427
durvalumab	0	mitomycin	3
pembrolizumab	0	vinflunine	71


```
#!/bin/bash
F_OUT="result_bladdercancer_Pubtator.txt"
F_LIST="pmid-bladder.txt"

echo -e "\n I am curating the result of bladder-cancer.LX\n"
echo -e "\n" >$F_OUT

i=1
while IFS= read -r line
do
    xx=`echo
https://www.ncbi.nlm.nih.gov/CBBresearch/Lu/Demo/RESTful/tmTool.c
gi/Bioconcept/$line/pubtator`
    curl $xx >>$F_OUT
    printf "$i -th result out of xxxxx is processing...\n"
    i=$((i+1))
    sleep 1.8s
done <"$F_LIST"
```

```
#!/usr/bin/python
# -*- coding: utf-8 -*-
F1 = open(r"Y:\textmining\result_merkel_Pubtator.txt")

F3 = open(r"Y:\textmining\gene_merkel_Pubtator.txt", "w")
genelist=[]

for line in F1:
    if len(line.strip().split('\t'))>3:

        pmid=line.strip().split('\t')[0]
        concept=line.strip().split('\t')[4]
        gene=line.strip().split('\t')[3]
        if concept=='Gene':
            genelist.append((pmid,gene))

A= set(genelist)
for i in A:
    F3.write(i[0]+'\\t'+i[1]+'\\n')

F1.close()
F3.close()
```



Thanks!