

PTEN的生物信息学分析

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background

PTEN:

迄今为止发现的第一个具有双特异性磷酸酶活性的抑癌基因。

定位于染色体10q23.3，由9个外显子组成，编码403个氨基酸。

蛋白产物:

- 1, 含酪氨酸磷酸酶的功能区，具有磷酸酯酶活性，通过拮抗酪氨酸激酶等磷酸化酶的活性而抑制肿瘤的发生发展；
- 2, 175个氨基酸作用于与骨架蛋白tenasin, auxilin同源的区域。

功能:

- 1, 作为一种肿瘤抑制因子，通过阻止细胞生长，分裂等方式，调控细胞分裂周期；
- 2, PTEN蛋白通过去除磷酸基进而修饰其他蛋白和脂肪；
- 3, PTEN酶参与化学通路的传导，把信号传导给细胞，使细胞停止分裂并进入凋亡，组织不受控制的细胞生长进而抑制肿瘤的形成；
- 4, PTEN酶协助控制细胞转移，细胞和周围组织的粘附和血管发生；

分析思路

gene

protein

function

Gene

— — NCBI-NUCLEOTIDE

LOCUS NG_007466

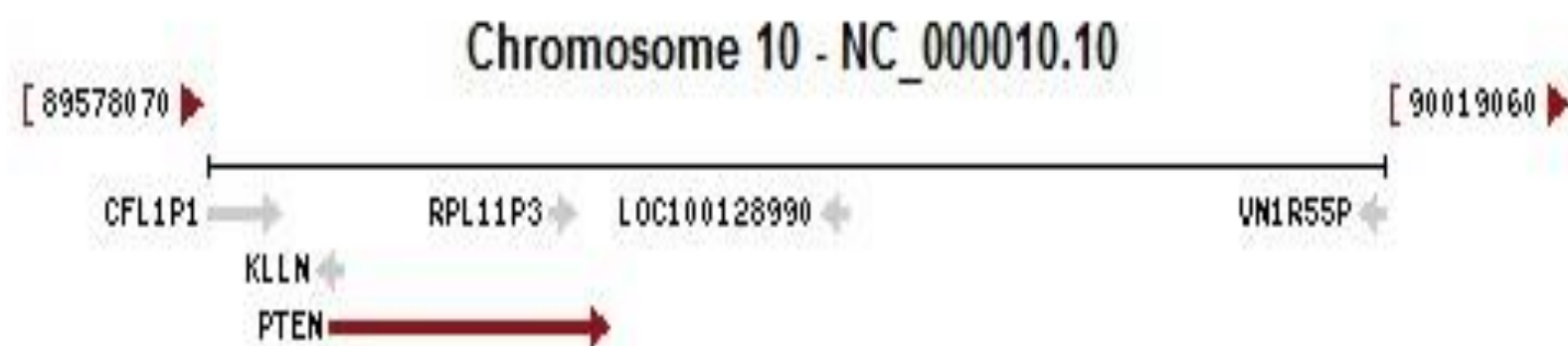
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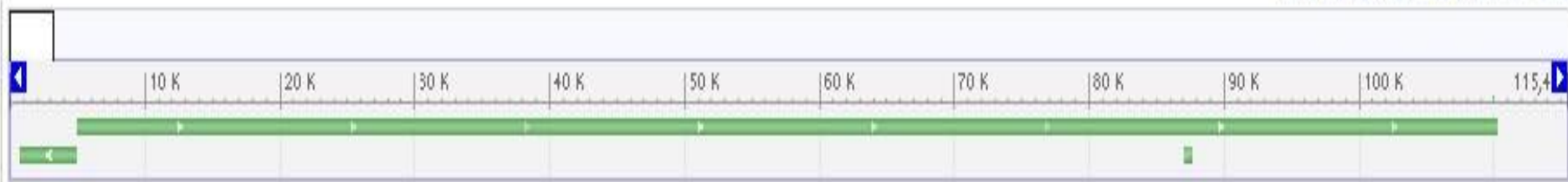
DNA linear

PRI 30-DEC-2012

Location: 10q23.3

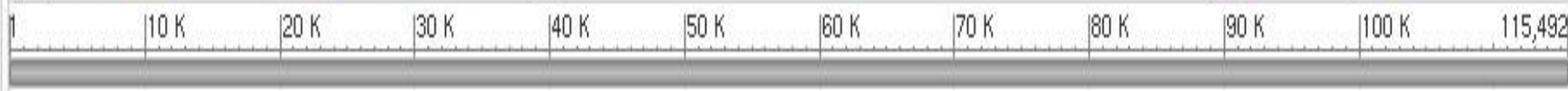
Sequence: Chromosome: 10; NC_000010.10 (89623195..89728532)





NG_007466.2: 1..115K (115Kbp) | Tools | Configure

Navigation and tool controls including a search icon, left and right arrow icons, a zoom slider, and icons for Tools and Configure.



SNP

Track for Single Nucleotide Polymorphisms (SNPs).

Genes

PTEN

NM_000314.4

NP_000305.3

exon 1 | exon 2 | exon 3 | exon 4 | exon 6 | exon 7

RPL11P3

Legend:

- KLLN
- NM_001126049.1
- NP_001119521.1

Gene models for PTEN, NM_000314.4, NP_000305.3, and RPL11P3. PTEN is shown as a green bar with arrowheads. NM_000314.4 is a blue bar with vertical lines indicating exons and arrowheads. NP_000305.3 is a red bar with vertical lines indicating exons and arrowheads. RPL11P3 is a green bar with an arrowhead. A legend on the left lists other genes: KLLN (green bar with arrowhead), NM_001126049.1 (blue bar with arrowhead), and NP_001119521.1 (red bar with arrowhead). Exons are labeled as exon 1, exon 2, exon 3, exon 4, exon 6, and exon 7.



CDS

Nucleotide Sequence (1212 nt):

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AGGGAGTAACTATTCAGTCAGAGGCGCTATGTGTATTATTATAGCTACCTGTTAAAGAATCATCTGGA
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Protein

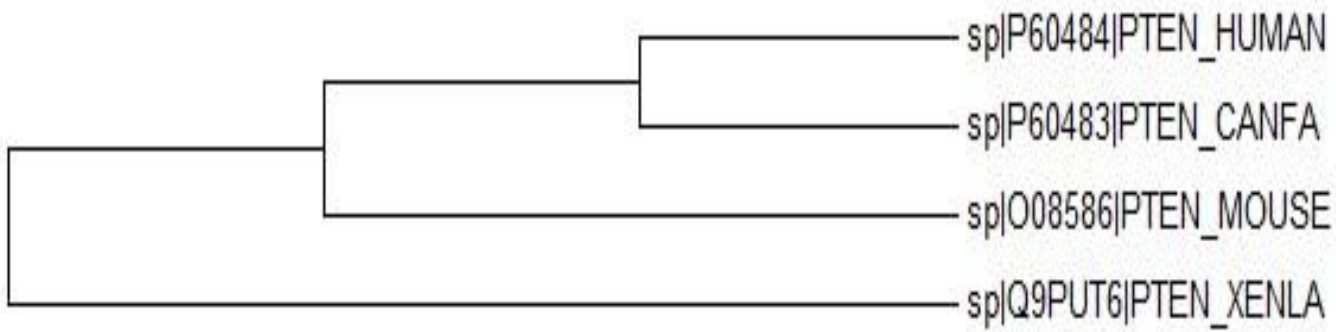
— UniProt

Entry	Entry name	Status	Protein names	Gene names	Organism	Length
<input checked="" type="checkbox"/> O08586	PTEN_MOUSE	★	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN (EC 3.1.3.16) (EC 3.1.3.48) (EC 3.1.3.67) (Mutated in multiple advanced cancers 1) (Phosphatase and tensin homolog)	Pten Mmac1	Mus musculus (Mouse)	403
<input checked="" type="checkbox"/> P60484	PTEN_HUMAN	★	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN (EC 3.1.3.16) (EC 3.1.3.48) (EC 3.1.3.67) (Mutated in multiple advanced cancers 1) (Phosphatase and tensin homolog)	PTEN MMAC1 TEP1	Homo sapiens (Human)	403
<input checked="" type="checkbox"/> Q9PUT6	PTEN_XENLA	★	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN (EC 3.1.3.16) (EC 3.1.3.48) (EC 3.1.3.67) (Mutated in multiple advanced cancers 1) (Phosphatase and tensin homolog)	pten	Xenopus laevis (African clawed)	402
<input type="checkbox"/> Q8T9S7	PTEN_DICDI	★	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN (EC 3.1.3.16) (EC 3.1.3.48) (EC 3.1.3.67) (Pten 3-phosphoinositide phosphatase alpha)	pteN ptenA DDB_G0286557	Dictyostelium discoideum (Slime mold)	533
<input checked="" type="checkbox"/> P60483	PTEN_CANFA	★	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN (EC 3.1.3.16) (EC 3.1.3.48) (EC 3.1.3.67) (Mutated in multiple advanced cancers 1) (Phosphatase and tensin homolog)	PTEN MMAC1	Canis familiaris (Dog) (Canis lupus familiaris)	403

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1	MTAIIKEFVSRNKRRYQEDGFDLDTYYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSK	60	Q9PUT6	PTEN_XENLA
1	MTAIIKEIVSRNKRRYQEDGFDLDTYYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSK	60	P60483	PTEN_CANFA
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61	HKNHYKIYNLCAERHYDTAKFNCRVAQYPPEDHNPPQLELIKPFCELDLQWLSEDDNHVA	120	008586	PTEN_MOUSE
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61	HKNHYKIYNLCAERHYDTAKFNCRVAQYPPEDHNPPQLELIKPFCELDLQWLSEDDNHVA	120	P60483	PTEN_CANFA
***** ** ***** ** : : **				
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121	AIHCKAGKGRGTGVMICAYLLHRGKFLKAQEALDFYGEVTRDRKKGVTIPSRRYVYYYSY	180	008586	PTEN_MOUSE
120	AIHCKAGKGRGTGVMICAYLLHRGKFPRAQEALDFYGEVTRDRKKGVTIPSRRYVYYYSY	179	Q9PUT6	PTEN_XENLA
121	AIHCKAGKGRGTGVMICAYLLHRGKFLKAQEALDFYGEVTRDRKKGVTIPSRRYVYYYSY	180	P60483	PTEN_CANFA
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180	LLKNSLEYRFPVLLFHKIEFETIPMPFSGSTCNPQFVVYQLKVKIFTSTAGPKR-AEKLWY	238	Q9PUT6	PTEN_XENLA
181	LLKNHLDYRFPVALLFHKMMFETIPMPFSGGTCNPQFVVQQLKVKIYSSNSGPTRRREKPFMY	240	P60483	PTEN_CANFA
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241	FEFPQPLPVCGDIIKVEFFHKQNKMLKKDKMFHFVWNTFFIPGPEETSEKVENGSLC-DQE	299	P60484	PTEN_HUMAN
241	FEFPQPLPVCGDIIKVEFFHKQNKMLKKDKMFHFVWNTFFIPGPEETSEKVENGSLC-DQE	299	008586	PTEN_MOUSE
239	FDPPQPLPVCGDIIKVEFFHKQNKVMKKEKMFHFVWNTFFIPGPEEYSEKVENGLVGEQE	298	Q9PUT6	PTEN_XENLA
241	FEFPQPLPVCGDIIKVEFFHKQNKMLKKDKMFHFVWNTFFIPGPEETSEKVENGSLC-DQE	299	P60483	PTEN_CANFA
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300	IDSICSIERADNDKEYLVLTLTKNLDLKDANKDKANRYFSPNFKVKLYFTKTVEEPSNPEA	359	008586	PTEN_MOUSE
299	LDGIYSTERSDNDKEYLTLALTKNLDLKDANKDKANRLFSPNFKVKLFFTKTVEESSNSEA	358	Q9PUT6	PTEN_XENLA
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360	SSSTSVTPDVSDNEPDHYRYSDDTSDPENEPFDEDQHSQITKV	403	008586	PTEN_MOUSE
359	SSSTSVTPDVSDNEPDHYRYSDDTSDPENEPFDEDQITQITKV	402	Q9PUT6	PTEN_XENLA
360	SSSTSVTPDVSDNEPDHYRYSDDTSDPENEPFDEDQHTQITKV	403	P60483	PTEN_CANFA
***** :*****				

—MEGA

Protein Sequences	
Species/Abbrv	** ** ** ** **
1. sp O08586 PTEN MOUSE	M T A I I S I V S N Y Q E D G F L D L T Y I Y N I I A M G F A S L E G V Y N N I D G V V F L Q
2. sp P60484 PTEN HUMAN	M T A I I S I V S N Y Q E D G F L D L T Y I Y N I I A M G F A S L E G V Y N N I D G V V F L Q
3. sp Q9PUT6 PTEN XENLA	M T A I I S F V S N Y Q E D G F L D L T Y I Y N I I A M G F A S L E G V Y N N I D G V V F L Q
4. sp P60483 PTEN CANFA	M T A I I S I V S N Y Q E D G F L D L T Y I Y N I I A M G F A S L E G V Y N N I D G V V F L Q



Sequence**Length Mass (Da) Tools** F6KD01 [UniParc]. FASTA 403 47,166

Last modified July 27, 2011. Version 1.

Checksum: 75F97C3DD6802BA9

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 70      80      90     100     110     120
HKNHYKIYNL CAERHYDTAK FNCRVAQYPF EDHNPPQLEL IKPFCELDLQ WLSEDDNHVA

130     140     150     160     170     180
AIHCKAGKGR TGVMICAYLL HRGKFLKAQE ALDFYGEVRT RDKKGV TIPS QRRYVYYYSY

190     200     210     220     230     240
LLKNHLDYRF VALLFHKMMF ETIPMFSGGT CNPQFVVCQL KVKIYSSNSG PTRREDKPMY

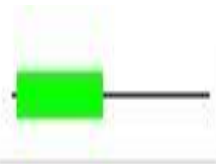
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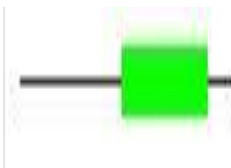
370     380     390     400
SSTSVTPDVS DNEPDHYRYS DTTSDPEN E PFDEDQHTQI TKV
```

[« Hide](#)

Domain 14 - 185 172 Phosphatase tensin-type



```
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MTAIIKEIVS RNKRRYQEDG FDLDLTYIYP NIIAMGPPAE RLEGVYRNNI DDVVRFLDSK
70 80 90 100 110 120
HKNHYKIYNL CAERHYDTAK FNCRVAQYPF EDHNPPQLEL IKPFCEDLDQ WLSEDDNHVA
130 140 150 160 170 180
AIHCKAGKGR TGVMICAYLL HRGKFLKAQE ALDFYGEVRT RDKKGV TIPS QRRYVYYYSY
190 200 210 220 230 240
LLKNHLDYRP VALLFHKMMF ETIPMFSGGT CNPQFVVCQL KVKIYSSNSG PTRREDKPFMY
250 260 270 280 290 300
FEFPQPLPVC GDIKVEFFHK QNKMLKKDKM FHFVNTFFI PGPEETSEKV ENGLCDQEI
310 320 330 340 350 360
DSICSIERAD NDKEYLVLT LTKNDLDKANK DKANRYFSPN FKVKLYFTKT VEEPSNPEAS
370 380 390 400
SSTSVTPDVS DNEPDHYRYS DTTSDPEN E PFDEDQHTQI TKV
```



```

    10      20      30      40      50      60
MTAIIKEIVS RNKRRYQEDG FDLDLTYIYP NIIAMGFP AE RLEGVYRNNI DDVVRFLDSK

    70      80      90      100     110     120
HKNHYKIYNL CAERHYDTAK FNCRVAQYPF EDHNPPQLEL IKPFCEDLDQ WLSEDDNHVA

    130     140     150     160     170     180
AIHCKAGKGR TGVMICAYLL HRGKFLKAQE ALDFYGEVRT RDKKGVTIPS QRRYVYYYSY

    190     200     210     220     230     240
LLKNHLDYRP VALLFHKMMF ETIPMFSGGT CNPQFVVCQL KVKIYSSNSG PTRREDKFMY

    250     260     270     280     290     300
FEFPQPLPVC GDIKVEFFHK QNKMLKKDKM FHFVWNTFFI PGPEETSEKV ENGLCDQEI

    310     320     330     340     350     360
DSICSIERAD NDKEYLVLT LTKNDLDKANK DKANRYFSPN FKVKLYFTKT VEEPSNPEAS

    370     380     390     400
SSTSVTPDVS DNEPDHYRYS DTTDSDPEN E PFDEDQHTQI TKV

```



Region

401 - 403

3 PDZ domain-binding

<u>10</u>	<u>20</u>	<u>30</u>	<u>40</u>	<u>50</u>	<u>60</u>
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<u>70</u>	<u>80</u>	<u>90</u>	<u>100</u>	<u>110</u>	<u>120</u>
HKNHYKIYNL	CAERHYDTAK	FNCRVAQYPF	EDHNPPQLEL	IKPFCEDLDQ	WLSEDDNHVA
<u>130</u>	<u>140</u>	<u>150</u>	<u>160</u>	<u>170</u>	<u>180</u>
AIHCKAGKGR	TGVMICAYLL	HRGKFLKAQE	ALDFYGEVRT	RDKKGV TIPS	QRRYVYYYSY
<u>190</u>	<u>200</u>	<u>210</u>	<u>220</u>	<u>230</u>	<u>240</u>
LLKNHLDYRF	VALLFHKMMF	ETIPMFSGGT	CNPQFVVCQL	KVKIYSSNSG	PTRREDKPMY
<u>250</u>	<u>260</u>	<u>270</u>	<u>280</u>	<u>290</u>	<u>300</u>
FEFPQPLPVC	GDIKVEFFHK	QNKMLKKDKM	FHFVNTFFI	PGPEETSEKV	ENGLCDQEI
<u>310</u>	<u>320</u>	<u>330</u>	<u>340</u>	<u>350</u>	<u>360</u>
DSICSIERAD	NDKEYLVLTLL	TKNDLDKANK	DKANRYFSPN	FKVKLYFTKT	VEEPSNPEAS
<u>370</u>	<u>380</u>	<u>390</u>	<u>400</u>		
SSTSVTPDVS	DNEPDHYRYS	DTTSDPENE	PFDEDQHTQI	TKV	

Amino acid modifications



Modified residue

6

1

N6-acetyllysine

Ref. 27

10 20 30 40 50 60
MTAIIKEIVS RNKRRYQEDG FDLDLTYIYP NIIAMGFPAE RLEGVYRNNI DDVVRFLDSK

70 80 90 100 110 120
HKNHYKIYNL CAERHYDTAK FNCRVAQYPF EDHNPPQLEL IKPFCELDLQ WLSEDDNHVA

130 140 150 160 170 180
AIHCKAGKGR TGVMICAYLL HRGKFLKAQE ALDFYGEVRT RDKKGV TIPS QRRYVYYYSY

190 200 210 220 230 240
LLKNHLDYRF VALLFHKMMF ETIPMFSGGT CNPQFVVCQL KVKIYSSNSG PTRREDKPMY

250 260 270 280 290 300
FEFPQPLPVC GDIKVEFFHK QNKMLKKDKM FHFVWNTFFI PGPEETSEKV ENGLCDQEI

310 320 330 340 350 360
DSICSIERAD NDKEYLVLT LTKNDLDKANK DKANRYFSPN FKVKLYFTKT VEEPSNPEAS

370 380 390 400
SSTSVTPDVS DNEPDHYRYS DTTDSDPENE PFDEDQHTQI TKV



Modified residue

336

1

Phosphotyrosine; by FRK

Ref. 25

10 20 30 40 50 60
MTAIIKEIVS RNKRRYQEDG FDLDLTYIYP NIIAMGFPAE RLEGVYRNNI DDVVRFLDSK

70 80 90 100 110 120
HKNHYKIYNL CAERHYDTAK FNCRVAQYPF EDHNPPQLEL IKPFCELDLQ WLSEDDNHVA

130 140 150 160 170 180
AIHCKAGKGR TGVMICAYLL HRGKFLKAQE ALDFYGEVRT RDKKGV TIPS QRRYVYYYSY

190 200 210 220 230 240
LLKNHLDYRP VALLFHKMMF ETIPMFSGGT CNPQFVVCQL KVKIYSSNSG PTRREDKFMV

250 260 270 280 290 300
FEFPQPLPVC GDIKVEFFHK QNKMLKKDKM FHFVVNTFFI PGPEETSEKV ENGLCDQEI

310 320 330 340 350 360
DSICSIERAD NDKEYLVLT L TKNDLDKANK DKANRYFSPN FVKLYFTKT VEEPSNPEAS

370 380 390 400
SSTSVTPDVS DNEPDHYRYS DTTDSDPEN PFDEDQHTQI TKV



Modified residue

366

1 Phosphothreonine; by GSK3-beta and PLK3

10 20 30 40 50 60
 MTAIIKEIVS RNKRRYQEDG FDLDLTYIYP NIIAMGFPAE RLEGVYRNNI DDVVRFLDSK

70 80 90 100 110 120
 HKNHYKIYNL CAERHYDTAK FNCRVAQYPF EDHNPPQLEL IKPFCELDLQ WLSEDDNHVA

130 140 150 160 170 180
 AIHCKAGKGR TGVMICAYLL HRGKFLKAQE ALDFYGEVRT RDKKGV TIPS QRRYVYYYSY

190 200 210 220 230 240
 LLKNHLDYRP VALLFHKMMF ETIPMFSGGT CNPQFVVCQL KVKIYSSNSG PTRREDKFMY

250 260 270 280 290 300
 FEFPQPLPVC GDIKVEFFHK QNKMLKKDKM FHFVNTFFI PGPEETSEKV ENGLCDQEI

310 320 330 340 350 360
 DSICSIERAD NDKEYLVLT LTKNDLDKANK DKANRYFSPN FVKLYFTKT VEEPSNPEAS

370 380 390 400
 SSTSVPDVS DNEPDHYRYS DTTDSDPENE PFDEDQHTQI TKV



Modified residue

370

1 Phosphoserine; by CK2 and PLK3

```

    10           20           30           40           50           60
MTAIIKEIVS RNKRRYQEDG FDLDLTYIYP NIIAMGPPAE RLEGVYRNNI DDVVRFLDSK

    70           80           90          100          110          120
HKNHYKIYNL CAERHYDTAK FNCRVAQYPF EDHNPPQLEL IKPFCEDLDQ WLSEDDNHVA

   130          140          150          160          170          180
AIHCKAGKGR TGVMICAYLL HRGKFLKAQE ALDFYGEVRT RDKKGV TIPS QRRYVYYYSY

   190          200          210          220          230          240
LLKNHLDYRP VALLFHKMMF ETIPMFSGGT CNPQFVVCQL KVKIYSSNSG PTRREDKFMY

   250          260          270          280          290          300
FEFPQPLPVC GDIKVEFFHK QNKMLKKDKM FHFVVNTFFI PGPEETSEKV ENGLCDQEI

   310          320          330          340          350          360
DSICSIERAD NDKEYLVLT LTKNDLDKANK DKANRYFSPN FKVKLYFTKT VEEPSNPEAS

   370          380          390          400
SSTSVTPDVS DNEPDHYRYS DTTSDPENE PFDEDQHTQI TKV
```



Modified residue

380

1 Phosphoserine; by ROCK1 By similarity

```

    10      20      30      40      50      60
MTAIIKEIVS RNKRRYQEDG FDLDLTYIYP NIIAMGPPAE RLEGVYRNNI DDVVRFLDSK

    70      80      90     100     110     120
HKNHYKIYNL CAERHYDTAK FNCRVAQYPF EDHNPPQLEL IKPFCEDLDQ WLSEDDNHVA

   130     140     150     160     170     180
AIHCKAGKGR TGVMICAYLL HRGKFLKAQE ALDFYGEVRT RDKKGV TIPS QRRYVYYYSY

   190     200     210     220     230     240
LLKNHLDYRF VALLFHKMMF ETIPMFSGGT CNPQFVVCQL KVKIYSSNSG PTRREDKPMY

   250     260     270     280     290     300
FEFPQPLPVC GDIKVEFFHK QNKMLKKDKM FHFVWNTFFI PGPEETSEKV ENGLCDQEI

   310     320     330     340     350     360
DSICSIERAD NDKEYLVLT LTKNDLDKANK DKANRYFSPN FVKLYFTKT VEEPSNPEAS

   370     380     390     400
SSTSVTPDVS DNEPDHYRYS DTTDSDPENE PFDEDQHTQI TKV
```

Modified residue

382

1 Phosphothreonine; by ROCK1

By similarity

```

    10      20      30      40      50      60
MTAIIKEIVS RNKRRYQEDG FDLDLTYIYP NIIAMGPPAE RLEGVYRNNI DDVVRFLDSK

    70      80      90     100     110     120
HKNHYKIYNL CAERHYDTAK FNCRVAQYPF EDHNPPQLEL IKPFCEDLDQ WLSEDDNHVA

   130     140     150     160     170     180
AIHCKAGKGR TGVMICAYLL HRGKFLKAQE ALDFYGEVRT RDKKGV TIPS QRRYVYYYSY

   190     200     210     220     230     240
LLKNHLDYRP VALLFHKMMF ETIPMFSGGT CNPQFVVCQL KVKIYSSNSG PTRREDKFMV

   250     260     270     280     290     300
FEFPQPLPVC GDIKVEFFHK QNKMLKKDKM FHFVWNTFFI PGPEETSEKV ENGLCDQEI

   310     320     330     340     350     360
DSICSIERAD NDKEYLVLT LTKNDLDKANK DKANRYFSPN FKVKLYFTKT VEEPSNPEAS

   370     380     390     400
SSTSVTPDVS DNEPDHYRYS DTTDSDPENE PFDEDQHTQI TKV
```

Modified residue

383

1 Phosphothreonine; by ROCK1 By similarity

```

    10      20      30      40      50      60
MTAIIKEIVS RNKRRYQEDG FDLDLTYIYP NIIAMGPPAE RLEGVYRNNI DDVVRFLDSK

    70      80      90     100     110     120
HKNHYKIYNL CAERHYDTAK FNCRVAQYPF EDHNPPQLEL IKPFCEDLDQ WLSEDDNHVA

   130     140     150     160     170     180
AIHCKAGKGR TGVMICAYLL HRGKFLKAQE ALDFYGEVRT RDKKGV TIPS QRRYVYYYSY

   190     200     210     220     230     240
LLKNHLDYRP VALLFHKMMF ETIPMFSGGT CNPQFVVCQL KVKIYSSNSG PTRREDKFMV

   250     260     270     280     290     300
FEFPQPLPVC GDIKVEFFHK QNKMLKKDKM FHFVNTFFI PGPEETSEKV ENGLCDQEI

   310     320     330     340     350     360
DSICSIERAD NDKEYLVLT LTKNDLDKANK DKANRYFSPN FVKLYFTKT VEEPSNPEAS

   370     380     390     400
SSTSVTPDVS DNEPDHYRYS DTTDSDPEN E PFDEDQHTQI TKV

```




Modified residue

385

1 Phosphoserine; by CK2 Ref. 21

```

  10      20      30      40      50      60
MTAIIKEIVS RNKRRYQEDG FDLDLTYIYP NIIAMGPPAE RLEGVYRNNI DDVVRFLDSK

  70      80      90     100     110     120
HKNHYKIYNL CAERHYDTAK FNCRVAQYPP EDHNPPQLEL IKPFCEDLDQ WLSEDDNHVA

 130     140     150     160     170     180
AIHCKAGKGR TGVMICAYLL HRGKFLKAQE ALDFYGEVRT RDKKGV TIPS QRRYVYYYSY

 190     200     210     220     230     240
LLKNHLDYRF VALLFHKMMF ETIPMFSGGT CNPQFVVCQL KVKIYSSNSG PTRREDKFMY

 250     260     270     280     290     300
FEFPQPLPVC GDIKVEFFHK QNKMLKKDKM FHFVWNTFFI PGPEETSEKV ENGLCDQEI

 310     320     330     340     350     360
DSICSIERAD NDKEYLVLT LTKNDLDKANK DKANRYFSPN FVKLYFTKT VEEPSNPEAS

 370     380     390     400
SSTSVPDVS DNEPDHYRYS DTTDSDPEN E PFDEDQHTQI TKV

```



Modified residue

401

1

Phosphothreonine

Ref. 17

10 20 30 40 50 60
MTAIIKEIVS RNKRRYQEDG FDLDLTYIYP NIIAMGFPAE RLEGVYRNNI DDVVRFLDSK

70 80 90 100 110 120
HKNHYKIYNL CAERHYDTAK FNCRVAQYPF EDHNPPQLEL IKPFCEDLDQ WLSEDDNHVA

130 140 150 160 170 180
AIHCKAGKGR TGVMICAYLL HRGKFLKAQE ALDFYGEVRT RDKKGVTIPS QRRYVYYYSY

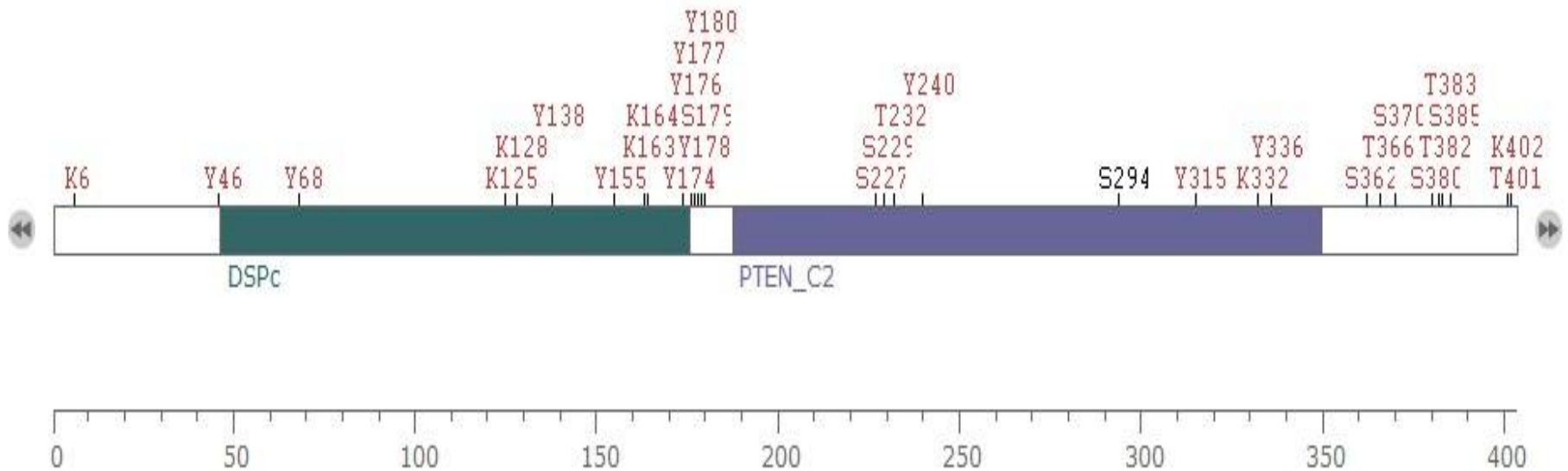
190 200 210 220 230 240
LLKNHLDYRP VALLFHKMMF ETIPMPGGT CNPQFVVCQL KVKIYSSNSG PTRREDKPFMY

250 260 270 280 290 300
FEFPQPLPVC GDIKVEFFHK QNKMLKKDKM FHFVWNTFFI PGPEETSEKV ENGLCDQEI

310 320 330 340 350 360
DSICSIERAD NDKEYLVLTLL TKNDLDKANK DKANRYFSPN FKVKLYFTKT VEEPSNPEAS


370 380 390 400
SSTSVPDVS DNEPDHYRYS DTTSDPENE PFDEDQHTQI TKV

PTEN (human) -- 403 amino acids Hide sites with only 1 MS/HTP reference Show only sites with more than 5 references



Secondary structure



Catalytic activity	<p>Phosphatidylinositol 3,4,5-trisphosphate + H₂O = phosphatidylinositol 4,5-bisphosphate + phosphate. Ref.1 Ref.12 Ref.13 Ref.14</p> <p>A phosphoprotein + H₂O = a protein + phosphate. Ref.1 Ref.12 Ref.13 Ref.14</p> <p>Protein tyrosine phosphate + H₂O = protein tyrosine + phosphate. Ref.1 Ref.12 Ref.13 Ref.14</p>
Cofactor	Magnesium.
Subunit structure	<p>Monomer. The unphosphorylated form interacts with the second PDZ domain of AIP1 and with DLG1 and MAST2 in vitro. Interacts with MAGI2, MAGI3, MAST1 and MAST3, but neither with MAST4 nor with DLG5. Interaction with MAGI2 increases protein stability. Interacts with NEDD4. Interacts with NDFIP1 and NDFIP2; in the presence of NEDD4 or ITCH, this interaction promotes PTEN ubiquitination. Interacts (via C2 domain) with FRK. Interacts with USP7; the interaction is direct. Interacts with ROCK1 By similarity. Interacts with XIAP/BIRC4. Ref.17 Ref.18 Ref.19 Ref.20 Ref.22 Ref.23 Ref.24 Ref.25 Ref.26 Ref.29 Ref.30</p>
Subcellular location	<p>Cytoplasm. Nucleus. Nucleus › PML body. Note: Monoubiquitinated form is nuclear. Nonubiquitinated form is cytoplasmic. Colocalized with PML and USP7 in PML nuclear bodies. XIAP/BIRC4 promotes its nuclear localization. Ref.1 Ref.24 Ref.26</p>
Tissue specificity	Expressed at a relatively high level in all adult tissues, including heart, brain, placenta, lung, liver, muscle, kidney and pancreas. Ref.2
Induction	Down-regulated by TGFB1. Ref.1
Domain	The C2 domain binds phospholipid membranes in vitro in a Ca ²⁺ -independent manner; this binding is important for its tumor suppressor function. Ref.18 Ref.30
Post-translational modification	<p>Phosphorylated in vitro by MAST1, MAST2 and MAST3. Phosphorylation results in an inhibited activity towards PIP3. Phosphorylation ca. ↓ 242K/S ↑ 0.04K/S  PDZ-binding. Phosphorylation at Tyr-336 by FRK/PTK5 protects this protein from ubiquitin-mediated degradation probably by inhibiting its binding to NEDD4. Phosphorylation by ROCK1 is essential for its stability and activity. Phosphorylation by PLK3 promotes its stability and prevents its degradation by the proteasome. Ref.17 Ref.20</p> <p>Ref.21 Ref.22 Ref.25 Ref.28</p> <p>Monoubiquitinated; monoubiquitination is increased in presence of retinoic acid. Deubiquitinated by USP7; leading to its nuclear exclusion. Monoubiquitination of one of either Lys-13 and Lys-289 amino acid is sufficient to modulate PTEN compartmentalization. Ubiquitinated by XIAP/BIRC4. Ref.24 Ref.26</p>

PTEN_HUMAN的蛋白序列分析

——ExPASy

蛋白一级结构分析

1, 蛋白基本理化性质分析

包括：相对分子质量，氨基酸组成，等电点，消光系数，半衰期，不稳定系数，总平均亲和性。

——[ProtParam](#)

——[Compute pI/Mw](#)

— ProtParam

ProtParam

Selection of endpoints on the sequence

PTEN_HUMAN (P60484)

Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTE
Homo sapiens (Human).

Please select one of the following features by clicking on a pair of endpoints, and the computation will t

Note: Only the features corresponding to subsequences of at least 5 residues are highlighted.

FT	CHAIN	1-403	Phosphatidylinositol 3,4,5-trisphosphate
FT	DOMAIN	14-185	Phosphatase tensin-type.
FT	DOMAIN	190-350	C2 tensin-type.
FT	REGION	401-403	PDZ domain-binding.
FT	TURN	19-22	
FT	STRAND	23-29	
FT	STRAND	32-35	
FT	STRAND	39-41	
FT	HELIX	50-60	
FT	STRAND	61-63	
FT	STRAND	65-73	
FT	STRAND	85-90	
FT	HELIX	98-100	
FT	HELIX	101-112	
FT	TURN	113-115	
FT	STRAND	118-123	
FT	STRAND	125-128	
FT	HELIX	129-141	
FT	HELIX	148-159	
FT	STRAND	161-163	
FT	HELIX	169-184	
FT	STRAND	192-202	
FT	STRAND	213-219	
FT	STRAND	222-226	
FT	STRAND	232-235	
FT	STRAND	238-259	
FT	STRAND	268-276	
FT	HELIX	277-279	
FT	STRAND	315-321	
FT	HELIX	322-324	
FT	HELIX	328-330	
FT	STRAND	335-337	
FT	STRAND	342-349	
FT	STRAND	395-403	

Considered sequence fragment:

1 11 21 31 41 51
| | | | |
1 LDLTYIY

Number of amino acids: 7

Molecular weight: 900.0

Theoretical pI: 3.80

Amino acid composition:

Ala (A)	0	0.0%
Arg (R)	0	0.0%
Asn (N)	0	0.0%
Asp (D)	1	14.3%
Cys (C)	0	0.0%
Gln (Q)	0	0.0%
Glu (E)	0	0.0%
Gly (G)	0	0.0%
His (H)	0	0.0%
Ile (I)	1	14.3%
Leu (L)	2	28.6%
Lys (K)	0	0.0%
Met (M)	0	0.0%
Phe (F)	0	0.0%
Pro (P)	0	0.0%
Ser (S)	0	0.0%
Thr (T)	1	14.3%
Trp (W)	0	0.0%
Tyr (Y)	2	28.6%
Val (V)	0	0.0%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%

(B)	0	0.0%
(Z)	0	0.0%
(X)	0	0.0%

Total number of negatively charged residues (Asp + Glu): 1
Total number of positively charged residues (Arg + Lys): 0

Atomic composition:

Carbon	C	44
Hydrogen	H	65
Nitrogen	N	7
Oxygen	O	13
Sulfur	S	0

Formula: $C_{44}H_{65}N_7O_{13}$

Total number of atoms: 129

Extinction coefficients:

This protein does not contain any Trp residues. Experience shows that this could result in more than 10% error in the computed extinction coefficient.

Extinction coefficients are in units of $M^{-1} cm^{-1}$, at 280 nm measured in water.

Ext. coefficient	2980
Abs 0.1% (=1 g/l)	3.311

Estimated half-life:

The N-terminal of the sequence considered is L (Leu).

The estimated half-life is: 5.5 hours (mammalian reticulocytes, in vitro).
3 min (yeast, in vivo).
2 min (Escherichia coli, in vivo).

Instability index:

The instability index (II) is computed to be 8.57
This classifies the protein as stable.

Aliphatic index: 167.14

Grand average of hydropathicity (GRAVY): 0.757

— Compute pI/Mw

Compute pI/Mw

Selection of endpoints on the sequence

PTEN_HUMAN (P60484)

Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase P1
Homo sapiens (Human).

Please select one of the following features by clicking on a pair of endpoints, and the computation will
Note: Only the features corresponding to subsequences of at least 5 residues are highlighted.

FT	CHAIN	1-403	Phosphatidylinositol 3, 4, 5-trisphosphate
FT	DOMAIN	14-185	Phosphatase tensin-type.
FT	DOMAIN	190-350	C2 tensin-type.
FT	REGION	401-403	PDZ domain-binding.
FT	TURN	19-22	
FT	STRAND	23-29	
FT	STRAND	32-35	
FT	STRAND	39-41	
FT	HELIX	50-60	
FT	STRAND	61-63	
FT	STRAND	65-73	
FT	STRAND	85-90	
FT	HELIX	98-100	
FT	HELIX	101-112	
FT	TURN	113-115	
FT	STRAND	118-123	
FT	STRAND	125-128	
FT	HELIX	129-141	
FT	HELIX	148-159	
FT	STRAND	161-163	
FT	HELIX	169-184	
FT	STRAND	192-202	
FT	STRAND	213-219	
FT	STRAND	222-226	
FT	STRAND	232-235	
FT	STRAND	238-259	
FT	STRAND	268-276	
FT	HELIX	277-279	
FT	STRAND	315-321	
FT	HELIX	322-324	
FT	HELIX	328-330	
FT	STRAND	335-337	
FT	STRAND	342-349	
FT	STRAND	395-403	

Considered sequence fragment:



» Fasta

Molecular weight (Da) 900.04 (average mass), 899.46 (monoisotopic mass)

Theoretical pI 3.80

2, 蛋白质亲疏水性分析

疏水作用是蛋白质折叠的主要驱动力，为蛋白质二级结构预测提供佐证，可用于分析蛋白质相互作用位点-抗原位点预测，分析蛋白质跨膜区。

——[ProtScale](#)

— ProtScale

ProtScale

Selection of endpoints on the sequence

PTEN_HUMAN (P60484)

Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PT
Homo sapiens (Human).

Please select one of the following features by clicking on a pair of endpoints, and the computation will

Note: Only the features corresponding to subsequences of at least 18 residues are highlighted.

FT	CHAIN	1-403	Phosphatidylinositol 3,4,5-trisphosphate
FT	DOMAIN	14-185	Phosphatase tensin-type.
FT	DOMAIN	190-350	C2 tensin-type.
FT	REGION	401-403	PDZ domain-binding.
FT	TURN	19-22	
FT	STRAND	23-29	
FT	STRAND	32-35	
FT	STRAND	39-41	
FT	HELIX	50-60	
FT	STRAND	61-63	
FT	STRAND	65-73	
FT	STRAND	85-90	
FT	HELIX	98-100	
FT	HELIX	101-112	
FT	TURN	113-115	
FT	STRAND	118-123	
FT	STRAND	125-128	
FT	HELIX	129-141	
FT	HELIX	148-159	
FT	STRAND	161-163	
FT	HELIX	169-184	
FT	STRAND	192-202	
FT	STRAND	213-219	
FT	STRAND	222-226	
FT	STRAND	232-235	
FT	STRAND	238-259	
FT	STRAND	268-276	
FT	HELIX	277-279	
FT	STRAND	315-321	
FT	HELIX	322-324	
FT	HELIX	328-330	
FT	STRAND	335-337	
FT	STRAND	342-349	
FT	STRAND	395-403	

Considered sequence fragment:

```
      181      191      201      211      221      231
      |        |        |        |        |        |
181
241 FEFPQPLPVC GDIKVEFFH          FMY  240
```

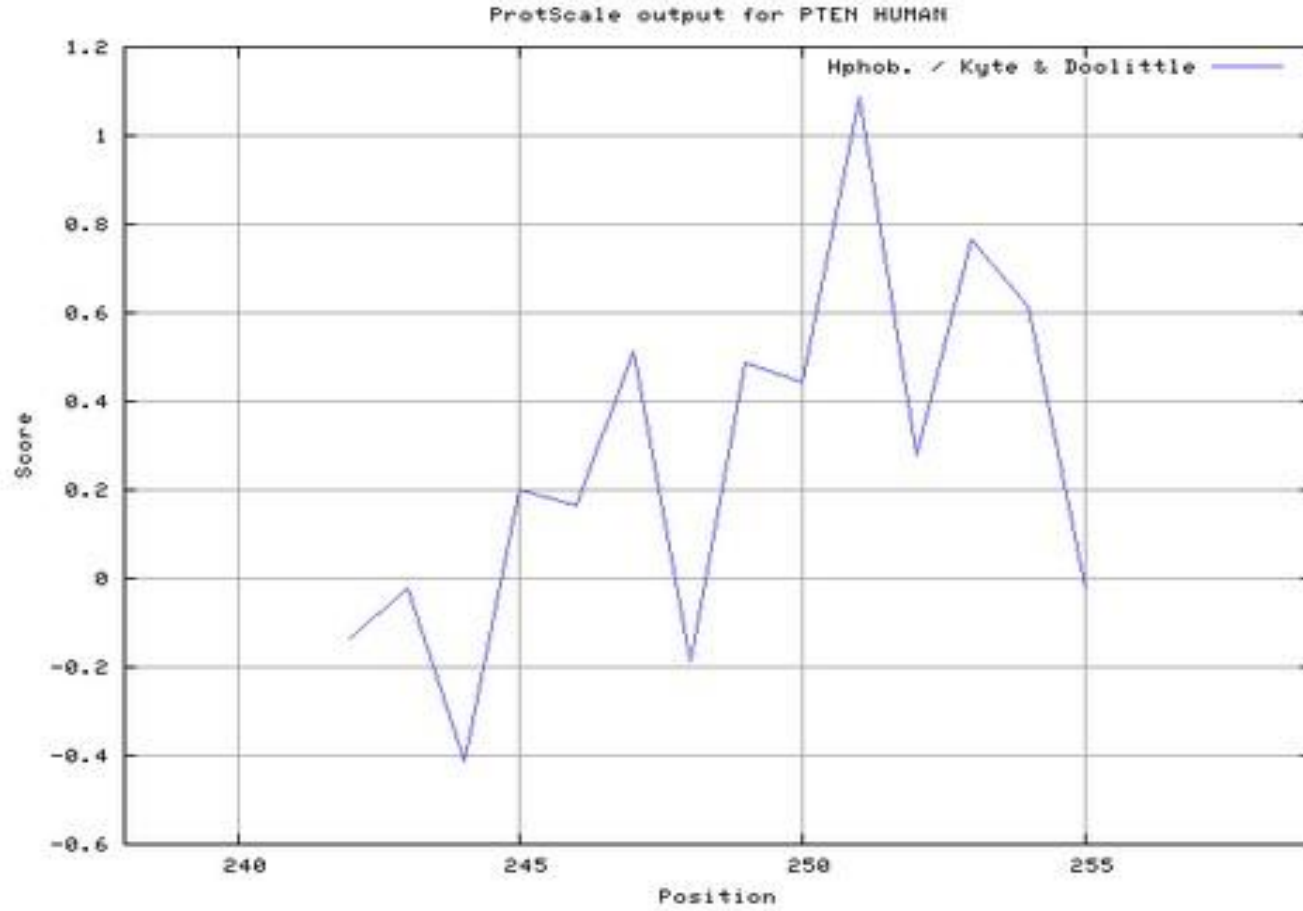
» Fasta SEQUENCE LENGTH: 22

Using the scale **Hphob. / Kyte & Doolittle**, the individual values for the 20 amino acids are:

Ala:	1.800	Arg:	-4.500	Asn:	-3.500	Asp:	-3.500	Cys:	2.500	Gln:	-3.500
Glu:	-3.500	Gly:	-0.400	His:	-3.200	Ile:	4.500	Leu:	3.800	Lys:	-3.900
Met:	1.900	Phe:	2.800	Pro:	-1.600	Ser:	-0.800	Thr:	-0.700	Trp:	-0.900
Tyr:	-1.300	Val:	4.200	:	-3.500	:	-3.500	:	-0.490		

Weights for window positions 1,...,9, using **linear weight variation model**:

1	2	3	4	5	6	7	8	9
1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge				center				edge



3, 跨膜区结构预测

——SOSUI



SOSUI Result

Query title : PTEN_HUMAN

Total length : 403 A. A.

Average of hydrophobicity : -0.689578

This amino acid sequence is of a **SOLUBLE PROTEIN.**

4, 卷曲结构预测

卷曲结构是指两股或两股以上alpha helix 相互缠绕而形成的超螺旋结构。

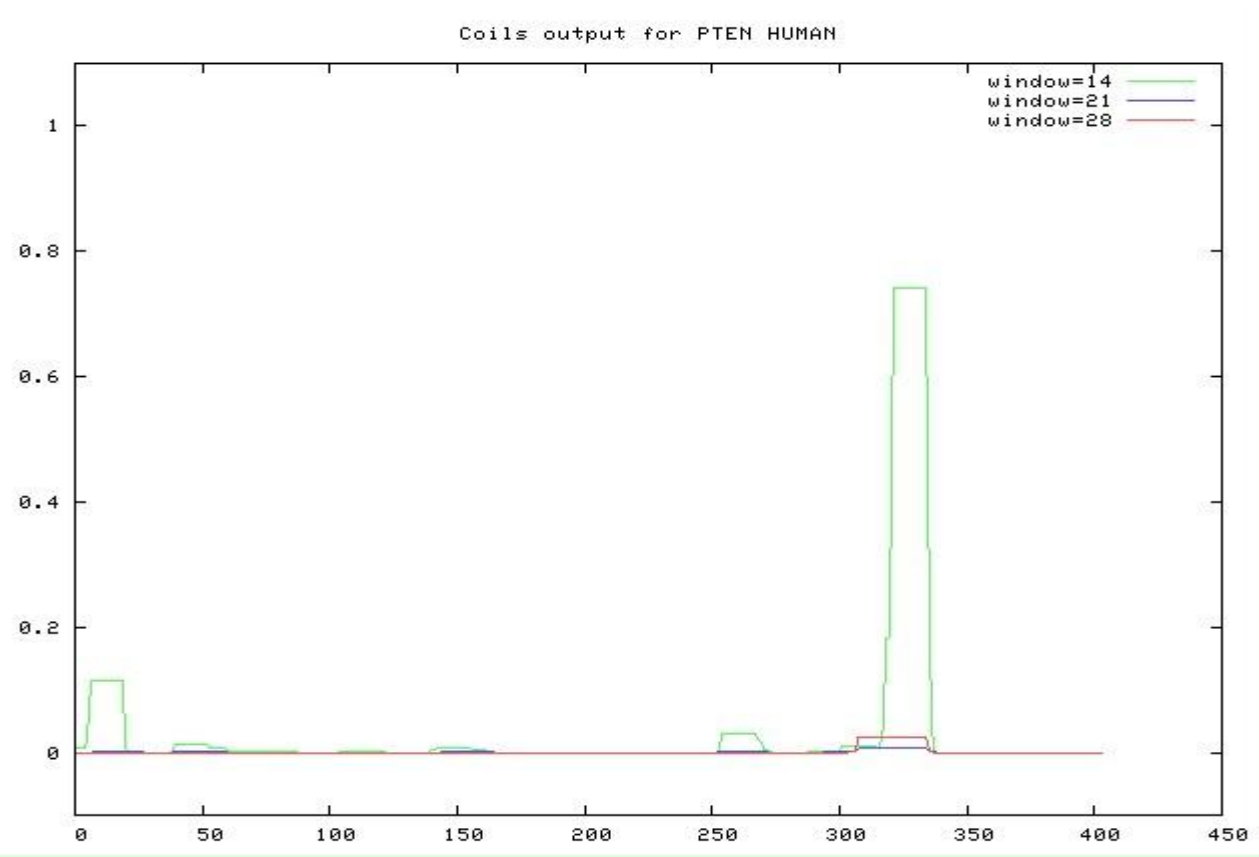
——COILS

Coils output for PTEN_HUMAN

[ISREC-Server] Date: Tue Jan 8 15:38:49 2013

```
COILSDIR='/mnt/common/share/ncoils-1.0/share' ncoils -win 14 -nw < ../wwwtmp/.COILS.28873.4300.seq > ../wwwtmp/.COILS.28873.4300.out.14  
COILSDIR='/mnt/common/share/ncoils-1.0/share' ncoils -win 21 -nw < ../wwwtmp/.COILS.28873.4300.seq > ../wwwtmp/.COILS.28873.4300.out.21  
COILSDIR='/mnt/common/share/ncoils-1.0/share' ncoils -win 28 -nw < ../wwwtmp/.COILS.28873.4300.seq > ../wwwtmp/.COILS.28873.4300.out.28
```

```
# NCOILS version 1.0  
# using MTIDK matrix  
# no weights  
# Input file is ../wwwtmp/.COILS.28873.4300.seq  
#
```



5, 翻译后修饰位点预测

——ProP 1.0 Server

分析蛋白质中赖氨酸和精氨酸的断开位点

——NetPhos 2.0 Server

分析蛋白质中丝氨酸, 苏氨酸及酪氨酸的磷酸化位点



ProP 1.0 Server - prediction results

Technical University of Denmark

ProP v.1.0b ProPeptide Cleavage Site Prediction

Furin-type cleavage site prediction (Arginine/Lysine residues)

403 sp_P60484_PTEN_HUMAN

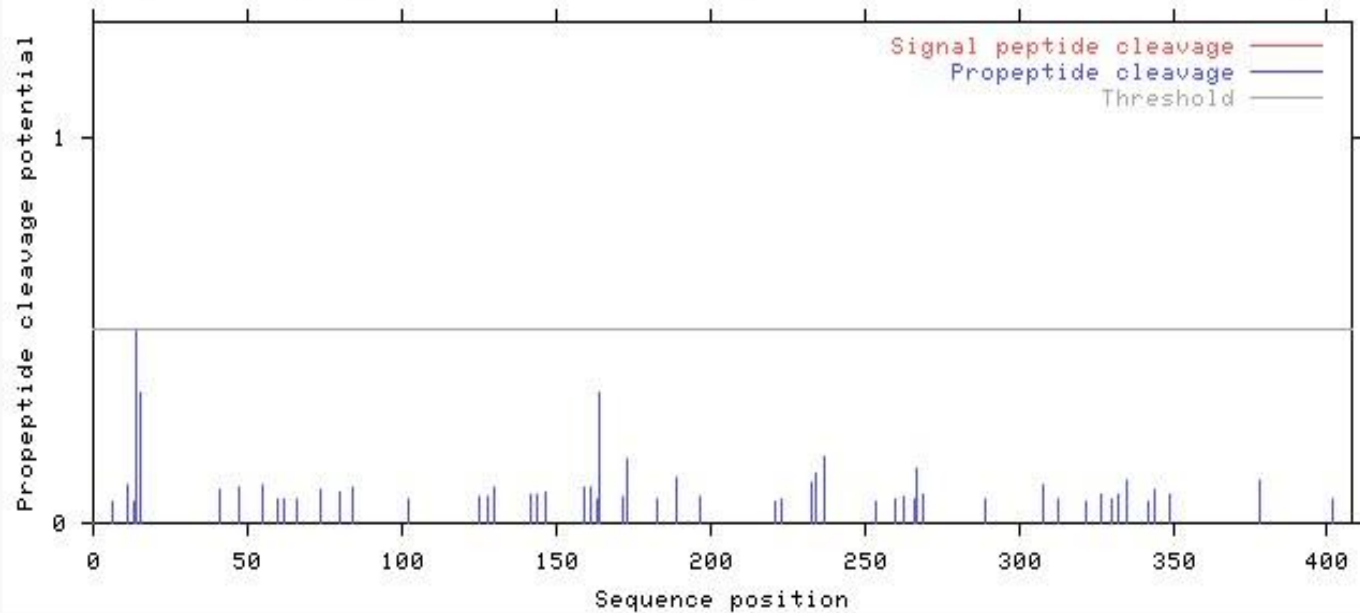
MTAIIKEIVSRNKRRYQEDGFDLDTYIYPNIIAMGFPAERLEGVYRNMIDDVVRFLDSKHKNHYKIYNLCAERHYDTAK	80
FNCRVAQYPFEDHNPPQLELIKPFCELDQWLSEDDNHVAAIHCKAGKGRGVMICAYLLHRGKFLKAQEALDFYGEVRT	160
RDKKGVITIPSQRRYVYYSYLLKNHLDYRPVALLFHKMMFETIPMFSGGTCNPQFVVCQLKVKIYSSNSGPTREDKFMV	240
FEFPQPLPVCGLKVEFFHKQNKMLKKDKMFHFVWNTFFIPGPEETSEKVENGSLCDQEIDSICSIERADNDKEYLVLTL	320
TKNDLTKANKDKANRYFSPNFKVKLYFTKTVEEPSNPEASSSTSVTPDVSDNEPDHYRYSDITSDPENEPFDEDQHTQI	400
TKV	480
.....	80
.....	160
.....	240
.....	320
.....	400
...	480

Signal peptide cleavage site predicted: none

Propeptide cleavage sites predicted: Arg(R)/Lys(K): 0

Name	Pos	Context	Score	Pred
sp_P60484_PTEN_HUMAN	6	-MTAIIK	EI	0.053
sp_P60484_PTEN_HUMAN	11	IKEIVSR	NK	0.097
sp_P60484_PTEN_HUMAN	13	EIVSRNK	RR	0.057
sp_P60484_PTEN_HUMAN	14	IVSRNKR	RY	0.495
sp_P60484_PTEN_HUMAN	15	VSRNKR	YQ	0.339
sp_P60484_PTEN_HUMAN	41	MGFPAER	LE	0.085
sp_P60484_PTEN_HUMAN	47	RLEGVYR	NN	0.091
sp_P60484_PTEN_HUMAN	55	NIDDVVR	FL	0.101
sp_P60484_PTEN_HUMAN	60	VRFLDSK	HK	0.060
sp_P60484_PTEN_HUMAN	62	FLDSKHK	NH	0.060
sp_P60484_PTEN_HUMAN	66	KHKMHYK	IY	0.064
sp_P60484_PTEN_HUMAN	74	YNLCAER	HY	0.084
sp_P60484_PTEN_HUMAN	80	RHYDTAK	FN	0.080
sp_P60484_PTEN_HUMAN	84	TAKFNCR	VA	0.094
sp_P60484_PTEN_HUMAN	102	PQLELIK	PF	0.063
sp_P60484_PTEN_HUMAN	125	VAATHCK	AG	0.065
sp_P60484_PTEN_HUMAN	128	IHCKAGK	GR	0.069
sp_P60484_PTEN_HUMAN	130	CKAGKGR	TG	0.093
sp_P60484_PTEN_HUMAN	142	CAYLLHR	GK	0.072
sp_P60484_PTEN_HUMAN	144	YLLHRGK	FL	0.071
sp_P60484_PTEN_HUMAN	147	HRGKFLK	AQ	0.082
sp_P60484_PTEN_HUMAN	159	DFYGEVR	TR	0.091
sp_P60484_PTEN_HUMAN	161	YGEVTR	DK	0.095
sp_P60484_PTEN_HUMAN	163	EVRTRDK	KG	0.059
sp_P60484_PTEN_HUMAN	164	VRTRDKK	GV	0.337
sp_P60484_PTEN_HUMAN	172	VTIPSQR	RY	0.067
sp_P60484_PTEN_HUMAN	173	TIPSQRR	YV	0.185
sp_P60484_PTEN_HUMAN	183	YYSYLLK	NH	0.063
sp_P60484_PTEN_HUMAN	189	KNHLDYR	PV	0.116
sp_P60484_PTEN_HUMAN	197	VALLFHK	MM	0.066
sp_P60484_PTEN_HUMAN	221	FVVCQLK	VK	0.056
sp_P60484_PTEN_HUMAN	223	VCQLKVK	IY	0.062
sp_P60484_PTEN_HUMAN	233	SNSGPTR	RE	0.102
sp_P60484_PTEN_HUMAN	234	NSGPTRR	ED	0.126
sp_P60484_PTEN_HUMAN	237	PTRREDK	FM	0.169
sp_P60484_PTEN_HUMAN	254	PVCGDIK	VE	0.056
sp_P60484_PTEN_HUMAN	260	KVEFFHK	QN	0.060
sp_P60484_PTEN_HUMAN	263	FFHKQNK	ML	0.067
sp_P60484_PTEN_HUMAN	266	KQNKMLK	KD	0.062
sp_P60484_PTEN_HUMAN	267	QNKMLKK	DK	0.144
sp_P60484_PTEN_HUMAN	269	KMLKKDK	MF	0.073
sp_P60484_PTEN_HUMAN	289	PEETSEK	VE	0.060
sp_P60484_PTEN_HUMAN	308	SICSIER	AD	0.098
sp_P60484_PTEN_HUMAN	313	ERADNDK	EY	0.063
sp_P60484_PTEN_HUMAN	322	LVLTLTK	ND	0.053
sp_P60484_PTEN_HUMAN	327	TKNDLDK	AN	0.074
sp_P60484_PTEN_HUMAN	330	DLDKANK	DK	0.061
sp_P60484_PTEN_HUMAN	332	DKANKDK	AN	0.071
sp_P60484_PTEN_HUMAN	335	NKDKANR	YF	0.111
sp_P60484_PTEN_HUMAN	342	YFSPNFK	VK	0.058
sp_P60484_PTEN_HUMAN	344	SPNFKVK	LY	0.085
sp_P60484_PTEN_HUMAN	349	VKLYFTK	TV	0.071
sp_P60484_PTEN_HUMAN	378	NEPDHYR	YS	0.109
sp_P60484_PTEN_HUMAN	402	QHTQITK	V-	0.061

Prop 1.0: predicted propeptide cleavage sites in sp P60484 PTEN HUMAN, furin-specific predic





NetPhos 2.0 Server - prediction results

Technical University of Denmark

477 sp_P60484_P

PHXSPHATASEANDDXALSPECIFICITYPRXTEINPHXSPHATASEPTENXSHXMXSAPIENSGNPTENPESVMTAIK	80
EIVSRNKRRYQEDGFDLDTYIYPNIIAMGFPAERLEGVYRNMIDDVVRFLDSKHKNHYKIYNLCAERHYDTAKFNCRVA	160
QYPFEDHNPQLELIKPFCELDQWLSEDDNHVAAIHCKAGKGRIGVMICAYLLHRGKFLKAQEALDFYGEVTRDKKGV	240
TIPSQRRYVYYYSYLLKNHLDYRPVALLFHKMMFETIPMFSGGTCNPQFVVCQLKVKIYSSNSGPTRRREDKFMFEFPQP	320
LPVCGDIKVEFFHKQNKMLKKDKMFHFVWNTFFIPGPEETSEKVENGSLCDQEIDSICSIERADNDKEYLVLTAKNDLD	400
KANKDKANRYFSPNFKVKLYFTKTVEEPSNPEASSSTSVTPDVSDNEPDHYRSDTTSDPENEPFDEDQHTQITKV	480
.....T.....S.....T.....S...T.....S.....S.....	80
.....Y.....Y.....Y.....	160
.....S.....	240
...S...Y.....S...T.....Y.....	320
.....TS.....S.....S..S.....	400
.....Y.S.....T....S....S.S.S.I...S.....Y....TT.S.....	480

Phosphorylation sites predicted: Ser: 18 Thr: 9 Tyr: 7

Serine predictions

Name	Pos	Context	Score	Pred
v				
sp_P60484_P	4	-PHXSPHAT	0.098	.
sp_P60484_P	10	HATASEAND	0.462	.
sp_P60484_P	19	DXALSPECI	0.995	*S*
sp_P60484_P	40	NPHXSPHAT	0.981	*S*
sp_P60484_P	46	HATASEPTE	0.008	.
sp_P60484_P	53	TENXSHXMX	0.649	*S*
sp_P60484_P	58	HXMXSAPIE	0.004	.
sp_P60484_P	64	PIENSGNPT	0.112	.
sp_P60484_P	73	ENPESVMTA	0.733	*S*
sp_P60484_P	84	KEIVSRNKR	0.263	.
sp_P60484_P	133	RFLDSKHKN	0.109	.
sp_P60484_P	187	DQWLSEDDN	0.720	*S*
sp_P60484_P	244	VTIPSQRRY	0.860	*S*
sp_P60484_P	253	VYYYSYLLK	0.002	.
sp_P60484_P	281	IPMFSGGTC	0.010	.
sp_P60484_P	300	VKIYSSNSG	0.239	.
sp_P60484_P	301	KIYSSNSGP	0.143	.
sp_P60484_P	303	YSSNSGPTR	0.564	*S*
sp_P60484_P	361	PEETSEKVE	0.821	*S*
sp_P60484_P	368	VENGLCDQ	0.994	*S*
sp_P60484_P	376	QEIDSICSI	0.806	*S*
sp_P60484_P	379	DSICSIERA	0.981	*S*
sp_P60484_P	412	NRYFSPNFK	0.983	*S*
sp_P60484_P	429	VEEPSNPEA	0.963	*S*
sp_P60484_P	434	NPEASSSTS	0.822	*S*
sp_P60484_P	435	PEASSSTSV	0.068	.
sp_P60484_P	436	EASSSTSVT	0.959	*S*
sp_P60484_P	438	SSSTSVTPD	0.981	*S*
sp_P60484_P	444	TPDVSDNEP	0.966	*S*
sp_P60484_P	454	HYRYSDTTD	0.423	.
sp_P60484_P	459	DTTSDPEN	0.989	*S*

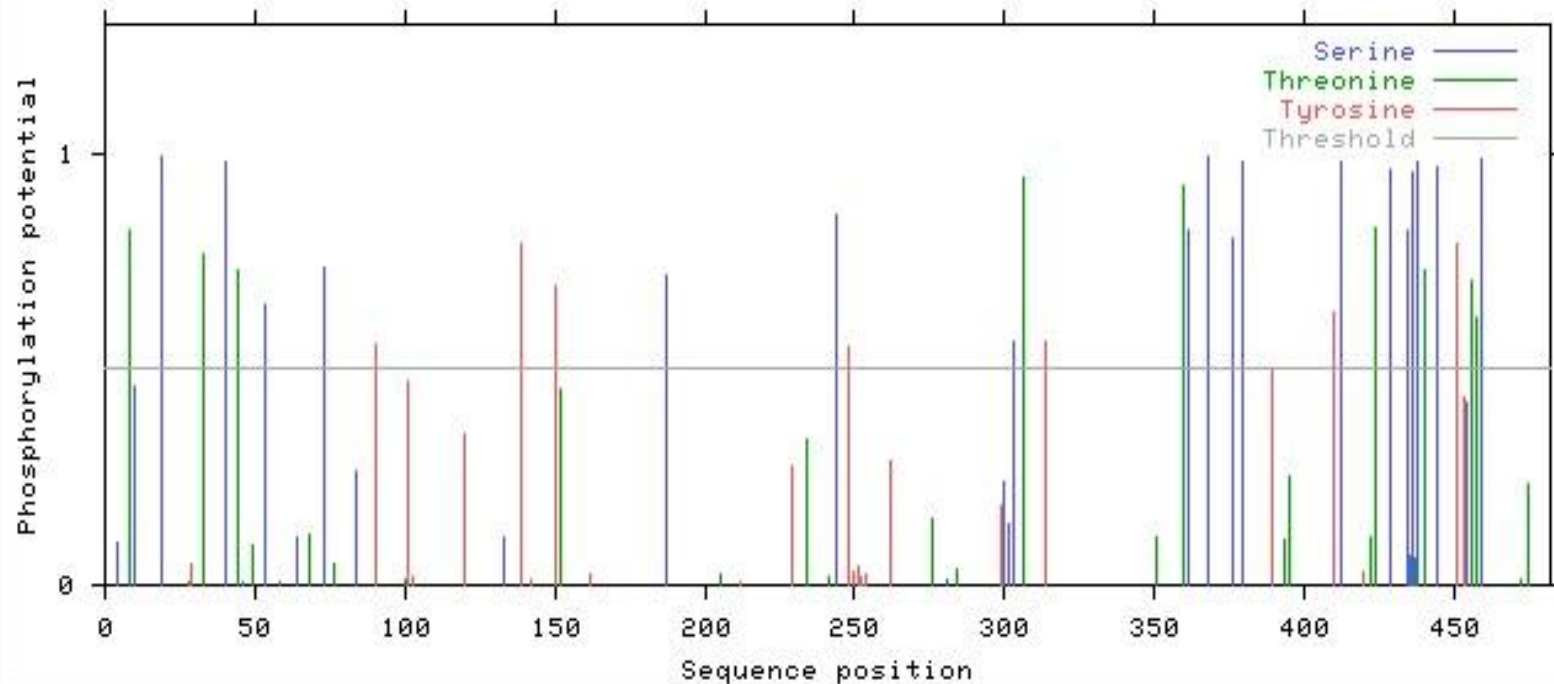
Threonine predictions

Name	Pos	Context	Score	Pred
v				
sp_P60484_P	8	SPHATASEA	0.821	*I*
sp_P60484_P	28	FICITYPRX	0.009	.
sp_P60484_P	33	YPRXTEIMP	0.765	*I*
sp_P60484_P	44	SPHATASEP	0.729	*I*
sp_P60484_P	49	ASEPTENXS	0.089	.
sp_P60484_P	68	SGNPTEPE	0.117	.
sp_P60484_P	76	ESVMTAIK	0.048	.
sp_P60484_P	100	DLDLTYIYP	0.014	.
sp_P60484_P	152	RHYDTAKFN	0.455	.
sp_P60484_P	205	GKGRIGVMI	0.023	.
sp_P60484_P	234	GEVTRDKK	0.336	.
sp_P60484_P	241	KKGVTIPSQ	0.017	.
sp_P60484_P	276	MMFETIPMF	0.152	.
sp_P60484_P	284	FSGGTCNPQ	0.036	.
sp_P60484_P	306	NSGPTRRER	0.946	*I*
sp_P60484_P	351	FWVNTFFIP	0.112	.
sp_P60484_P	360	GPEETSEKV	0.928	*I*
sp_P60484_P	393	YLVLTITKN	0.105	.
sp_P60484_P	395	VLTLTKNDL	0.253	.
sp_P60484_P	422	KLYFTKIVE	0.112	.
sp_P60484_P	424	YFTKIVEEP	0.827	*I*
sp_P60484_P	437	ASSSTSVTP	0.064	.
sp_P60484_P	440	STSVTPDVS	0.732	*I*
sp_P60484_P	456	RYSDITDSD	0.706	*I*
sp_P60484_P	457	YSDITDSDP	0.618	*I*
sp_P60484_P	472	EDQHTQITK	0.013	.
sp_P60484_P	475	HTQITKV--	0.230	.

Tyrosine predictions

Name	Pos	Context	Score	Pred
sp_P60484_P	29	ICITYPRXT	0.047	.
sp_P60484_P	90	NKRRYQEDG	0.556	*Y*
sp_P60484_P	101	LDLTYIYPN	0.474	.
sp_P60484_P	103	LYIYIPNII	0.020	.
sp_P60484_P	120	LEGVYRNNI	0.350	.
sp_P60484_P	139	HKNHYKIYN	0.790	*Y*
sp_P60484_P	142	HYKIYNLCA	0.010	.
sp_P60484_P	150	AERHYDTAK	0.695	*Y*
sp_P60484_P	162	RVAQYPFED	0.025	.
sp_P60484_P	212	MICAYLLHR	0.008	.
sp_P60484_P	229	ALDFYGEVR	0.278	.
sp_P60484_P	248	SQRRYVYYY	0.549	*Y*
sp_P60484_P	250	RRYVYYYYSY	0.032	.
sp_P60484_P	251	RYVYYYSYL	0.042	.
sp_P60484_P	252	YVYYYSYLL	0.019	.
sp_P60484_P	254	YYYSYLLKN	0.026	.
sp_P60484_P	262	NHLDYRPVA	0.286	.
sp_P60484_P	299	KVKIYSSNS	0.182	.
sp_P60484_P	314	DKFMYFEPF	0.563	*Y*
sp_P60484_P	389	NDKEYLVLT	0.499	.
sp_P60484_P	410	KANRYFSPN	0.633	*Y*
sp_P60484_P	420	KVKLYFTKT	0.031	.
sp_P60484_P	451	EPDHRYSD	0.793	*Y*
sp_P60484_P	453	DHYRYSDTT	0.435	.

NetPhos 2.0: predicted phosphorylation sites in sp P60484 P



蛋白质二级结构预测

基本二级结构： α 螺旋， β 折叠， β 转角，无规则卷曲。

——GOR4

——SOPMA

—GOR4

```

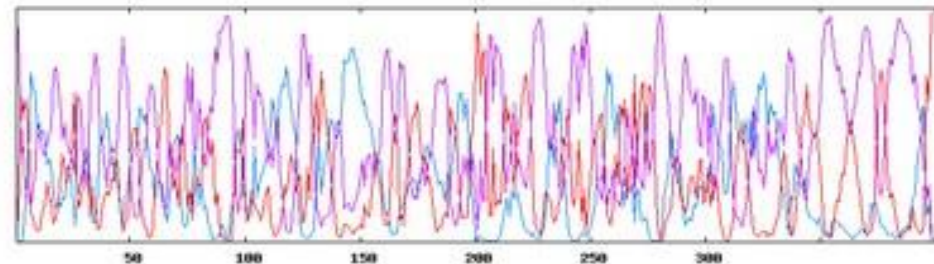
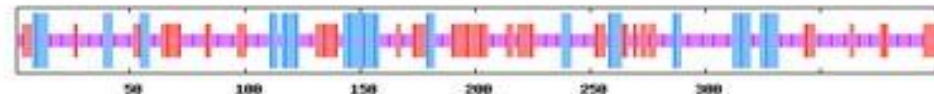
          10      20      30      40      50      60      70
MTAIIKEIVSRNKRRYQEDGFDLDTYYIPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKHKHNYKIYNL
ccccceeehhhhhhhccccccccccccceccccccccccccchhhhccccccccceeehhhhccccceeeeee
CAERHYDTAKFNCRVAQYYPFEDHNPQLELIKPFCELDLQWLSEDDNHVAATHCKAGKGRIGVMICAYLL
eeeccccccccccccccccccccccccccccccccccccchhhhchhhhhhhhccccccccceeeeee
HRGKFLKAQEALDFYGEVTRDRKKGVTIPSQRRYVYYYYSYLLKNHLDYRVPVALLFHKMMFETIPMFSGGT
eccchhhhhhhhhhhhhhhhhhhccccccccceccccccccceeehhhhccccccccceeeeeecccccc
CNPQFVVCQLKVKIYSSNSGPTRRREDKFMVFEPQPLPVCGDIKVEFFHKQNKMLKKDKMFHFVNTFFI
ccccceeeccccccccccccccccccccccccchhhhccccccccceeechhhhhhccccccccceeeccc
PGPEETSEKVENGLCDQEIIDSICSIERADNDKEYLVLTLTKNLDLKDANKDKANRYFSPNFKVKLYFTKT
ccccchhhhccccccccccccccccccccccccchhhhhhhhcccchhhhhhhhccccccccceeeccc
VEEPSNPEASSSTSVTPDVSDNEPDHYRYSDDTTSDPENEPFDEDQHTQITKV
cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

```

Sequence length : 403

GOR4 :

Alpha helix	(Hh) :	77 is	19.11%
3 ₁ 0 helix	(Gg) :	0 is	0.00%
Pi helix	(Ii) :	0 is	0.00%
Beta bridge	(Bb) :	0 is	0.00%
Extended strand	(Ee) :	103 is	25.56%
Beta turn	(Tt) :	0 is	0.00%
Bend region	(Ss) :	0 is	0.00%
Random coil	(Cc) :	223 is	55.33%
Ambiguous states (?)	:	0 is	0.00%
Other states	:	0 is	0.00%



```

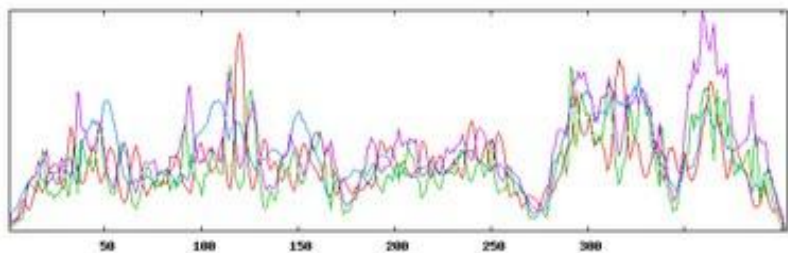
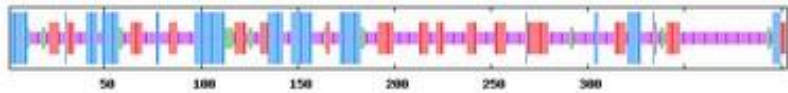
      10      20      30      40      50      60      70
      |      |      |      |      |      |      |
MTAIKKEIVSRNKRRYQEDGFDLDTYYIPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKHKQHYKIYNL
hhhhhhhhhhhtcccccttceeeeeccchheeeccccchhhhhhchhhhhhhhhhtccccceeeee
CAERHYDTAKFNCRVAQYPPEDHNPPQLELIKPFCELDQWLSEDDNHVAATHCKAGKGRGTMVICAYLL
ccccccchccccceeeeeccccccccchhhhhhhhhhhhhhhhttttceeeeecttccccceeehhhhh
HRGKFLKAQEALDFYGEVTRDKKGVVTIPSQRRYVYYYSYLLKNHLDYRFPVALLFHKMMFETIPMFSGGT
hhccccchhhhhhhhhhhccccctteccccchhhhhhhhhhhhtccccccccceeeeecccccccccc
CNPQFVVCQLKVKIYSSNSGPTRRREDKFMYPFEPQPLPVCEDIKVEFFHKQNKMLKKDKMFHFVNTFFI
cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
PGPEETSEKVENGLCDQEIDSICSIERADNDKEYLVLTLTKNLDLKANKDKANRYFSPNFKVKLYFTKT
cccccccccccccttccccccccchccccccccceeeeeeccccchhhhhhccccchcccccttceeeeecc
VEEPSNPEASSSTSVTPDVSNDNEPDHYRYSDDTTSDPENEPFDEDQHTQITKV
cccccccccccccccccccccccccccccccccccccccccccccccccttchhhheee

```

Sequence length : 403

SOPMA :

Alpha helix	(Hh) :	90 is	22.33%
3 ₁₀ helix	(Gg) :	0 is	0.00%
Pi helix	(Ii) :	0 is	0.00%
Beta bridge	(Bb) :	0 is	0.00%
Extended strand	(Ee) :	87 is	21.59%
Beta turn	(Tt) :	20 is	4.96%
Bend region	(Ss) :	0 is	0.00%
Random coil	(Cc) :	206 is	51.12%
Ambiguous states	(?) :	0 is	0.00%
Other states	:	0 is	0.00%



—SOPMA

蛋白质三级结构预测

同源模建法

——SWISS MODEL

——phyre



BIOZENTRUM

Universität Basel
The Center for Molecular Life Sciences



SWISS-MODEL Workspace

[Modelling](#)

[Tools](#)

[Repository](#)

[Documentation](#)

Workunit: P000001 Title:PTEN_HUMAN



Model Summary:



Model information:

Modelled residue range:

14 to 351

Based on template:

1d5rA (2.10 Å)

Sequence Identity [%]:

90.828

Evalue:

6.82889e-177

Quality information:

QMEAN Z-Score: -3.219

Quaternary structure information:

Template (1d5r): MONOMER

Model: MONOMER

Ligand information:

Ligands in the template: TLA: 1.

Ligands in the model: none.

1,模型详情 (Model Details)

从模型信息可知, PTEN_HUMAN蛋白是基于1d5r的A链模建的, 两者序列一致性达到90.828%。

2, 比对信息 (Alignment)

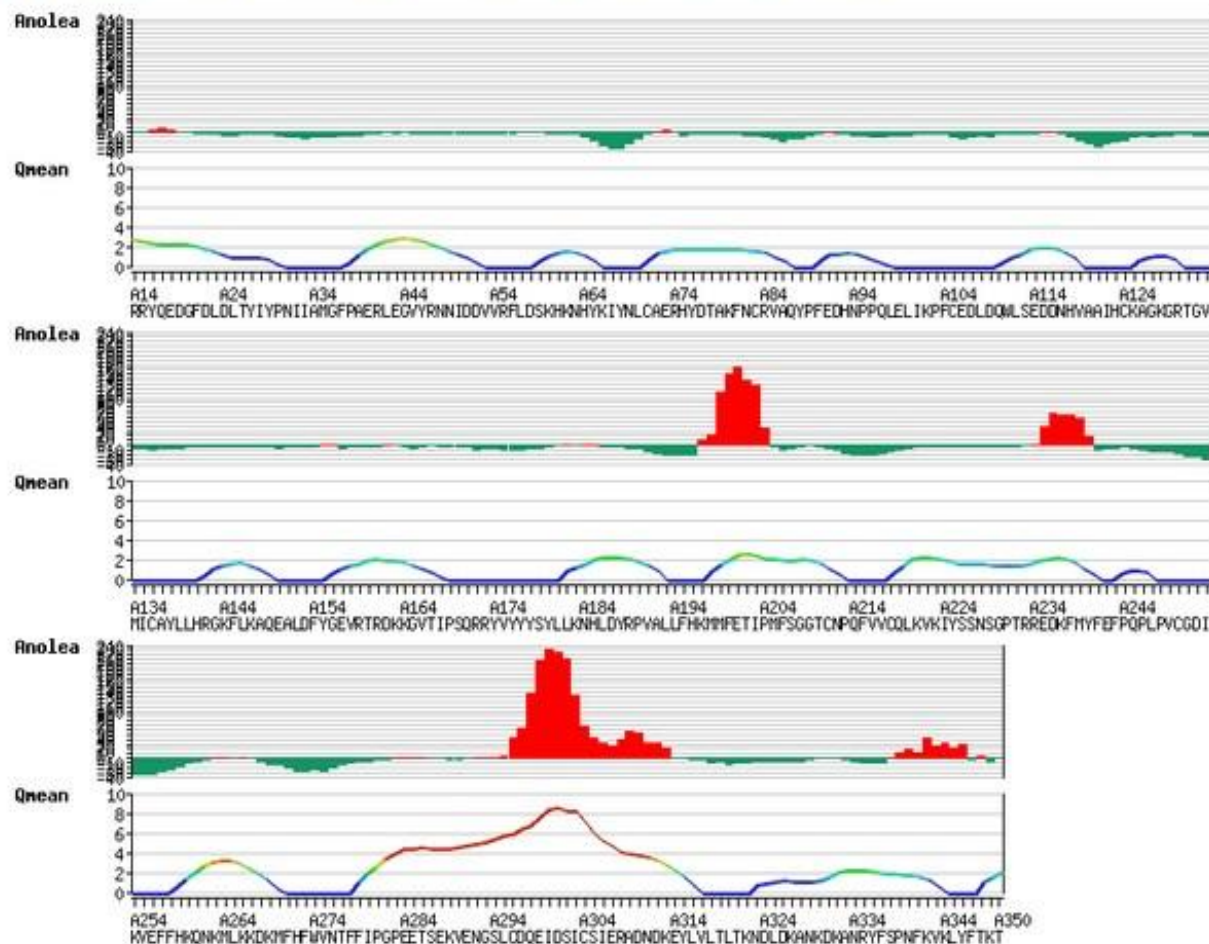
		Alignment [+/-]					
TARGET	1	RRYQEDGF	DLDLTYIYPN	IIAMGFPAER	LEGVYRNNID	DVVRFLDSKH	
1d5r_1	14	rryqedgf	dldltyiypn	iiamgfpaer	legvyrnnid	dvvrflskh	
TARGET			sssss	s sssss		hh hhhhhhhh	
1d5r_1			sssss	s sssss		hh hhhhhhhh	
TARGET	49	KNHYKIYNLC	AERHYDTAKF	NCRVAQYPFE	DHNPPQLELI	KPFCEDLDQW	
1d5r_1	62	knhykiynlc	aerhydtakf	ncrvaqypfe	dhnppqleli	kpfceldqw	
TARGET		sssssss		sssss		hhh hhhhhhhhh	
1d5r_1		sssssss		sssss		hhh hhhhhhhhh	
TARGET	99	LSEDDNHVAA	IHCKAGKGR	GVMICAYLLH	RGKFLKAQEA	LDIFYGEVTR	
1d5r_1	112	lseddnhvaa	ihckagkgrt	gvmicayllh	rgkflkaqea	ldfygevrtr	
TARGET		h	sss ss	hhh hhhhhhhhhh	h	hhh hhhhhhhh	
1d5r_1		h	sss ss	hhh hhhhhhhhhh	h	hhh hhhhhhhh	
TARGET	149	DKKGV TIPSQ	RRYVYYYSYL	LKNHLDYRPV	ALLFHKMMFE	TIPMFSGGTC	
1d5r_1	162	dkkgvtipsq	rryvyyysyl	lknhldyrpv	allfhkmmfe	tipmfsggtc	
TARGET			hhh hhhhhhhhhh	hhh	sssssssss		
1d5r_1			hhh hhhhhhhhhh	hhh	sssssssss		
TARGET	199	NPQFVVCQLK	VKIYSSNSGP	TRREDKFMFY	EFQPLPVCG	DIKVEFFHKQ	
1d5r_1	212	npqfvvcqlk	vkiyssnsgp	trredkfmfy	efqplpvcg	dikveffhkq	
TARGET		sssssssss	ssssss	sss ssss ss	sss s sssssssss		
1d5r_1		sssssssss	ssssss	sss ssss ss	sss s sssssssss		
TARGET	249	NKMLKDKDMF	HFWVNTFFIP	GPEETSEKVE	NGSLCDQEID	SICSIERADN	
1d5r_1	262	nkmlkdkdmf	hfwvntffip	-----	-----	-----	
TARGET			ssss sssssshh	sss	sss	ssss s	sssss
1d5r_1			ssss sssssshh				
TARGET	299	DKEYLVLTILT	KNDLDKANKD	KANRYFSPNF	KVKLYFTKTV		
1d5r_1	313	-keylvltilt	kndldkankd	kanryfspnf	kvklyftktv	-	
TARGET		ssssss s	hhh		s sssssss		
1d5r_1		ssssss s	hhh		s sssssss		

3, 模板评价

SWISS-MODEL提供了三种建模质量评鉴方法——Anolea, QMEAN, gromos。选择Anolea和QMEAN。绿色区域表示合适空间的结构,红色区域表示不合适的空间结构。分数越低表示建模越正确。

Local Model Quality Estimation: Anolea / QMEAN / Gromos: [+/-]

anolea: on off QMEAN: on off gromos: on off



4, 模建日志 (Modelling log)

包括载入模板, 载入序列, 序列比对等。

```
Modelling Log [ +/- ]
3.70 (SP3)
Loading Template: 1d5r_1.pdb
Loading Raw Sequence
Loading Alignment: ./NXXX.align.submit.fasta
Removing HET groups from template structure
Refining Raw Sequence Alignment
ProModII: doing simple assignment of backbone
ProModII: adding blocking groups
Adding Missing Sidechains
AddPolar H
BuildDeletedLoopsModel
Finding Spare-Part loop with anchor residues PRO 268 and LYS 300
ACCEPTING loop 20 from 1TTBA Clash= 8 FF= 845.3 PP=385.77
BadPhi= 1 BadGX= 0 BadXP= 1 weakXP= 1 Score=13.75 rms= 0.00
Optimizing Sidechains
Adding Hydrogens
Optimizing loops and OXT (nb = 32)
Final Total Energy: 11706.235 KJ/mol
Dumping Sequence Alignment
```


Phyre2

Top model

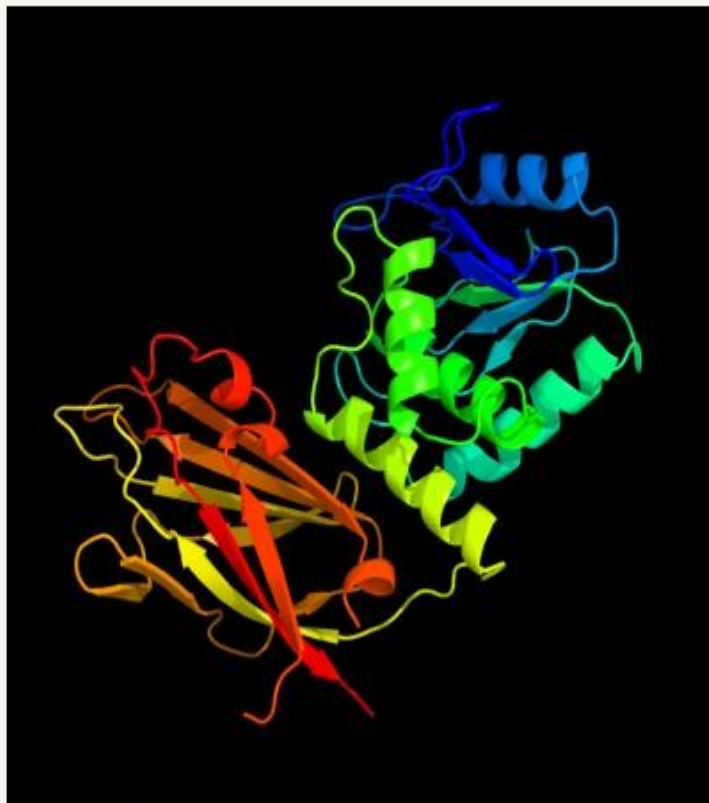


Image coloured by rainbow N → C terminus

Model (left) based on template [c1d5rA_](#)

Top template information

PDB header:hydrolase**Chain:** A: **PDB Molecule:**phosphoinositide phosphatase pten;**PDBTitle:** crystal structure of the pten tumor suppressor

Confidence and coverage

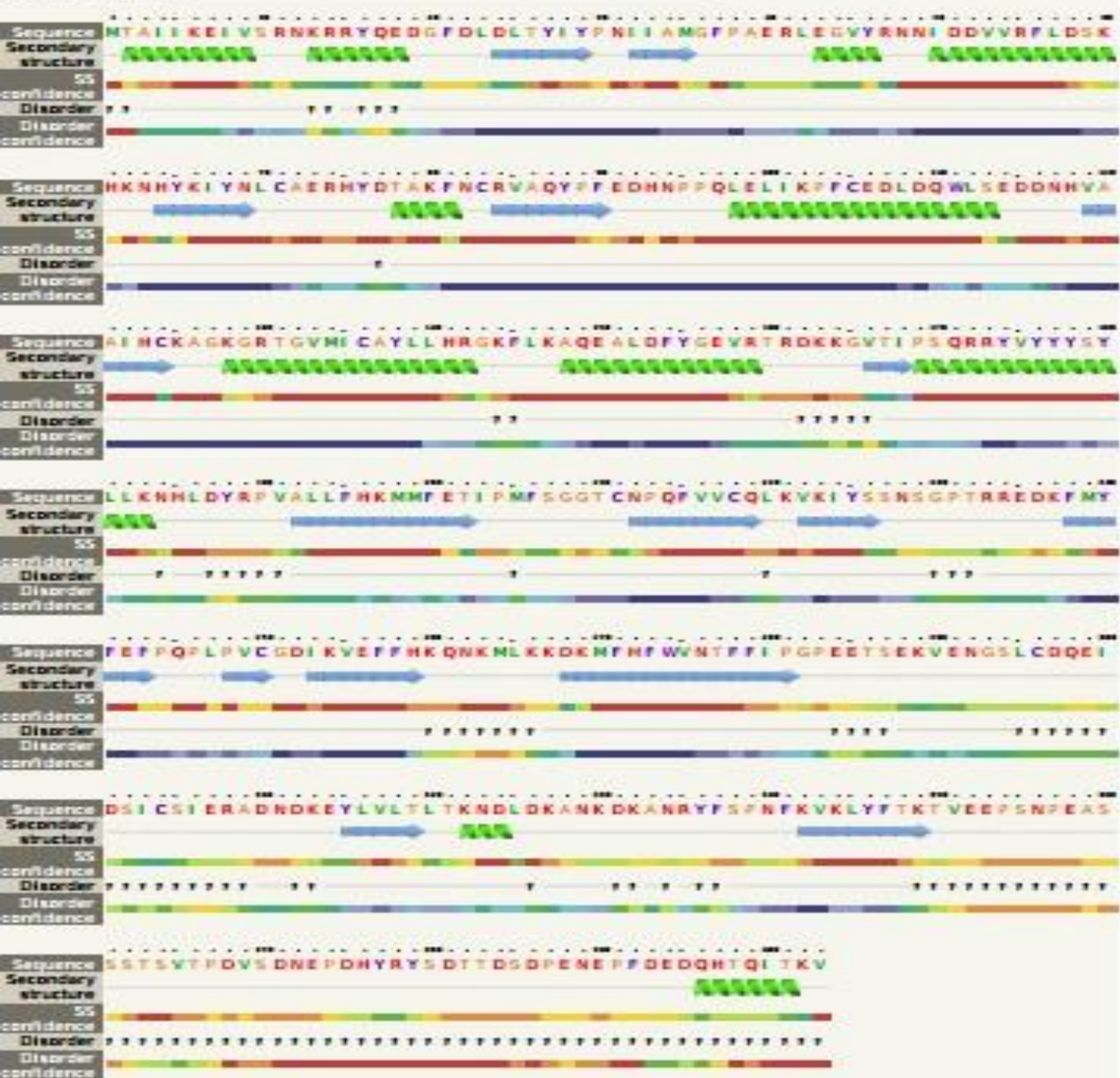
Confidence: **100.0%** Coverage: **76%**

307 residues (76% of your sequence) have been modelled with 100.0% confidence by the single highest scoring template.

3D viewing

[Interactive 3D view in Jmol](#)

Secondary structure and disorder prediction



Confidence Key

High(9) Low (0)

? Disordered

Alpha helix

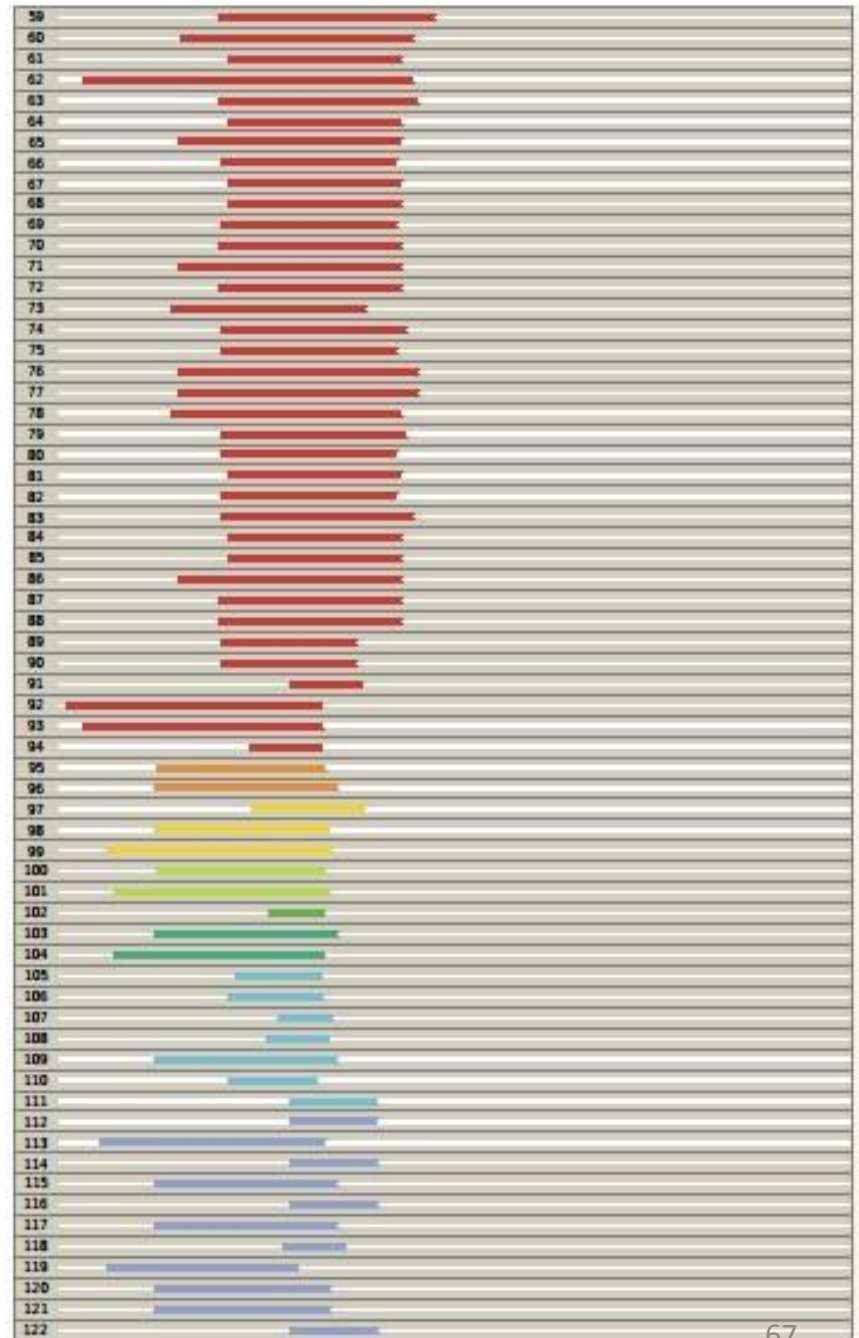
Beta strand

Phyre2

Email: lijiaju@gmail.com
 Description: PTEN_HUMAN
 Date: Tue Jan 8 11:06:46 GMT 2013
 Unique Job ID: Dc3c7be9fa9e579d

Domain analysis

Rank	Aligned region
1	cl0b06
2	cl0b06
3	cl0b06
4	cl0b06
5	cl0b06
6	cl0b06
7	cl0b06
8	cl0b06
9	cl0b06
10	cl0b06
11	cl0b06
12	cl0b06
13	cl0b06
14	cl0b06
15	cl0b06
16	cl0b06
17	cl0b06
18	cl0b06
19	cl0b06
20	cl0b06
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Selected template information

#	Template	Alignment Coverage	3D Model	Confidence	% I.D.	Template Information
1	1L39A	Aligned		100.0	96	PDB 1L39A Chain A: PDB Molecule phosphatase-like phosphatase-like PDSTE : crystal structure of the pleckstrin suppressor
2	1L39C	Aligned		100.0	17	PDB 1L39C Chain C: PDB Molecule phosphatase-like phosphatase-like PDSTE : crystal structure of pleckstrin domain of c-src (236-376)
3	1L39B	Aligned		100.0	28	PDB 1L39B Chain B: PDB Molecule phosphatase-like phosphatase-like PDSTE : crystal structure of srcin (348-430)
4	1L39A	Aligned		100.0	100	PDB 1L39A Chain A: PDB Molecule phosphatase-like phosphatase-like Superfamily : Phosphatase-like phosphatase-like FamilyClass : specificity phosphatase-like
5	1L39B	Aligned		100.0	96	PDB 1L39B Chain B: PDB Molecule phosphatase-like phosphatase-like Superfamily : Phosphatase-like phosphatase-like FamilyClass : specificity phosphatase-like
6	1L39C	Aligned		100.0	29	PDB 1L39C Chain C: PDB Molecule phosphatase-like phosphatase-like Superfamily : Phosphatase-like phosphatase-like FamilyClass : specificity phosphatase-like
7	1L39A	Aligned		99.9	28	PDB 1L39A Chain A: PDB Molecule phosphatase-like phosphatase-like PDSTE : crystal structure analysis of kinase associated phosphatase (kap) with a substitution of the catalytic site (cysteine to tyrosine)
8	1L39B	Aligned		99.9	28	PDB 1L39B Chain B: PDB Molecule phosphatase-like phosphatase-like Superfamily : Phosphatase-like phosphatase-like FamilyClass : specificity phosphatase-like
9	1L39C	Aligned		99.9	27	PDB 1L39C Chain C: PDB Molecule phosphatase-like phosphatase-like Superfamily : Phosphatase-like phosphatase-like FamilyClass : specificity phosphatase-like
10	1L39B	Aligned		99.9	22	PDB 1L39B Chain B: PDB Molecule phosphatase-like phosphatase-like Superfamily : Phosphatase-like phosphatase-like FamilyClass : specificity phosphatase-like
11	1L39A	Aligned		99.9	29	PDB 1L39A Chain A: PDB Molecule phosphatase-like phosphatase-like PDSTE : structure of SH150 phosphatase with a peptide ligand

101	1L39A	Aligned		100.0	67.3	36 Superfamily : Phosphatase-like phosphatase-like FamilyClass : specificity phosphatase-like phosphatase-like
102	1L39B	Aligned		100.0	56.9	27 PDB 1L39B Chain B: PDB Molecule phosphatase-like phosphatase-like PDSTE : gcr1 with shp from d. hansenii in closed form
103	1L39C	Aligned		100.0	46.6	11 PDB 1L39C Chain C: PDB Molecule phosphatase-like phosphatase-like PDSTE : crystal structure of probable substrate surface transferase2 (cys42 g42117) from mycobacterium tuberculosis (strain h37rv)
104	1L39A	Aligned		100.0	35.7	16 PDB 1L39A Chain A: PDB Molecule phosphatase-like phosphatase-like PDSTE : protein phosphatase, new crystal form
105	1L39A	Aligned		100.0	36.2	18 Superfamily : Phosphatase-like phosphatase-like FamilyClass : specificity phosphatase-like
106	1L39C	Aligned		100.0	37.7	10 Superfamily : Phosphatase-like phosphatase-like FamilyClass : specificity phosphatase-like
107	1L39B	Aligned		100.0	35.7	23 PDB 1L39B Chain B: PDB Molecule phosphatase-like phosphatase-like PDSTE : crystal structure of kinase associated phosphatase from pseudomonas fluorescens
108	1L39A	Aligned		100.0	35.5	11 PDB 1L39A Chain A: PDB Molecule phosphatase-like phosphatase-like PDSTE : catalytic domain from a phosphatase (vswarabi)
109	1L39A	Aligned		100.0	36.4	9 PDB 1L39A Chain A: PDB Molecule phosphatase-like phosphatase-like PDSTE : crystal structure of SH150 from m. tuberculosis
110	1L39B	Aligned		100.0	31.0	20 PDB 1L39B Chain B: PDB Molecule phosphatase-like phosphatase-like PDSTE : crystal structure of kinase associated phosphatase from pseudomonas fluorescens
111	1L39C	Aligned		100.0	33.1	16 PDB 1L39C Chain C: PDB Molecule phosphatase-like phosphatase-like PDSTE : crystal structure of kinase associated phosphatase from pseudomonas fluorescens
112	1L39A	Aligned		100.0	29.4	11 Superfamily : Phosphatase-like phosphatase-like FamilyClass : specificity phosphatase-like
113	1L39B	Aligned		100.0	29.4	10 PDB 1L39B Chain B: PDB Molecule phosphatase-like phosphatase-like PDSTE : crystal structure of chitinase from thermus thermophilus 508
114	1L39C	Aligned		100.0	29.4	11 PDB 1L39C Chain C: PDB Molecule phosphatase-like phosphatase-like PDSTE : structure of the gfp-binding protein from thermophilus maritimus complexed with 5'-dmgp-5'
115	1L39A	Aligned		100.0	27.2	18 PDB 1L39A Chain A: PDB Molecule phosphatase-like phosphatase-like PDSTE : crystal structure of protein tyrosine kinase from the catalytic domain of srcin (348-430)
116	1L39B	Aligned		100.0	25.9	11 PDB 1L39B Chain B: PDB Molecule phosphatase-like phosphatase-like PDSTE : crystal structure of kinase associated phosphatase from pseudomonas fluorescens
117	1L39C	Aligned		100.0	26.0	16 PDB 1L39C Chain C: PDB Molecule phosphatase-like phosphatase-like PDSTE : crystal structure of chitinase from thermus thermophilus 508
118	1L39B	Aligned		100.0	26.0	18 PDB 1L39B Chain B: PDB Molecule phosphatase-like phosphatase-like PDSTE : crystal structure of nucleotide-binding protein of sh150 from m. tuberculosis (strain h37rv)
119	1L39A	Aligned		100.0	22.3	20 PDB 1L39A Chain A: PDB Molecule phosphatase-like phosphatase-like PDSTE : crystal structure of the cytoplasmic domain of sh150 from m. tuberculosis (strain h37rv)
120	1L39B	Aligned		100.0	21.9	11 Superfamily : Phosphatase-like phosphatase-like FamilyClass : specificity phosphatase-like

模型输出



↑ Molecular Description

Hide

Classification: [Hydrolase](#)

Structure Weight: 38646.59 [i](#)

Molecule: PHOSPHOINOSITIDE PHOSPHATASE PTEN

Polymer: 1 **Type:** protein **Length:** 324

Chains: A

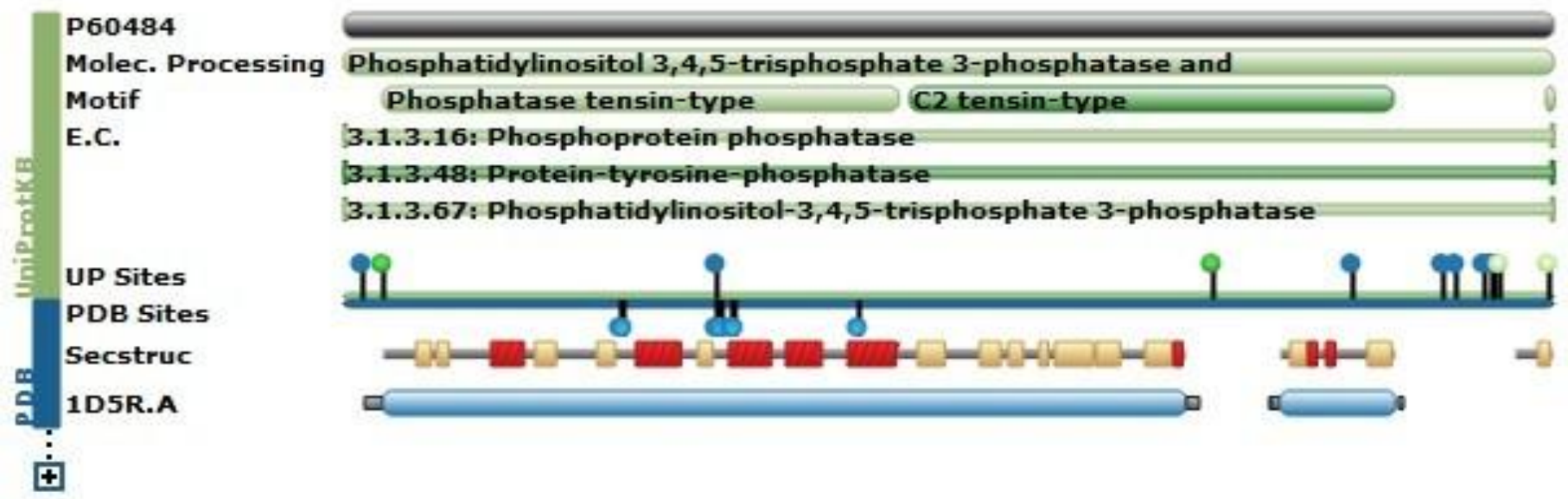
EC#: [3.1.3.16](#) [EC](#) [3.1.3.48](#) [EC](#) [3.1.3.67](#) [EC](#)

Fragment: RESIDUES 7-353

Mutation: RESIDUES 286-309 ARE REPLACED BY VAL

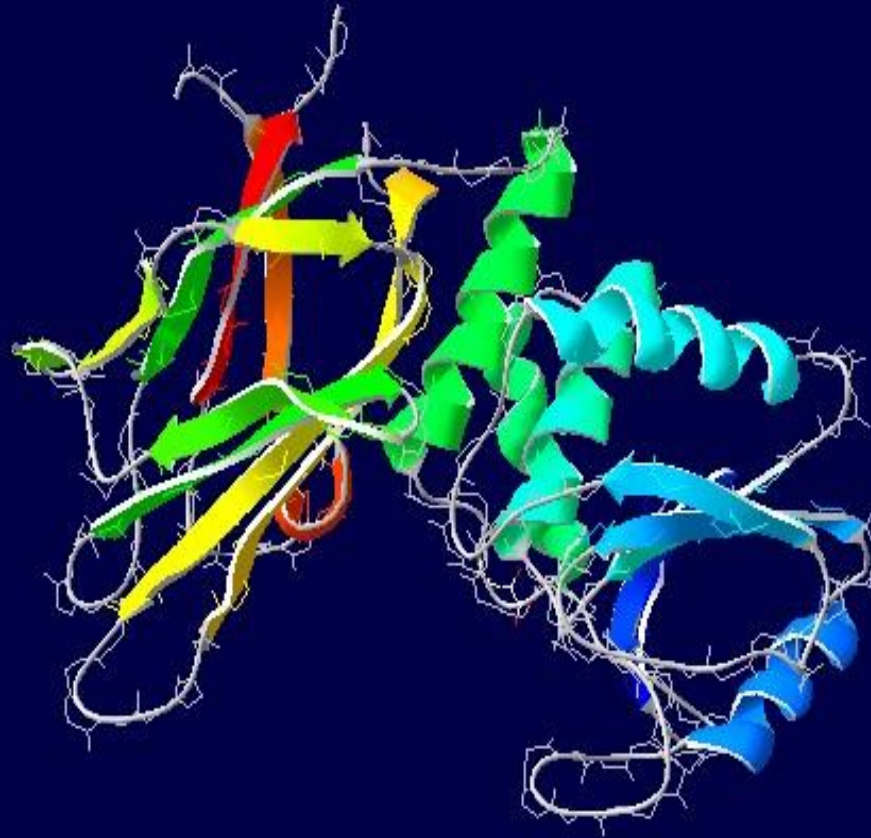
Organism: [Homo sapiens](#)

UniProtKB: [Protein Feature View](#) | [Search PDB](#) | [P60484](#)



PDB 下载, pdbviewer分析

1D5R (876 x 403)



手动同源模建法分析步骤

1, 多序列比对

与已有晶体结构的protein序列比对

2, 确定是否又可以使用的模板

序列相似度 $>30\%$

序列相似度 $<30\%$, 结合功能, 蛋白质以及序列, 二级结构或结构域信息

3, 构建三维模型

4, 三维模型准确性检测

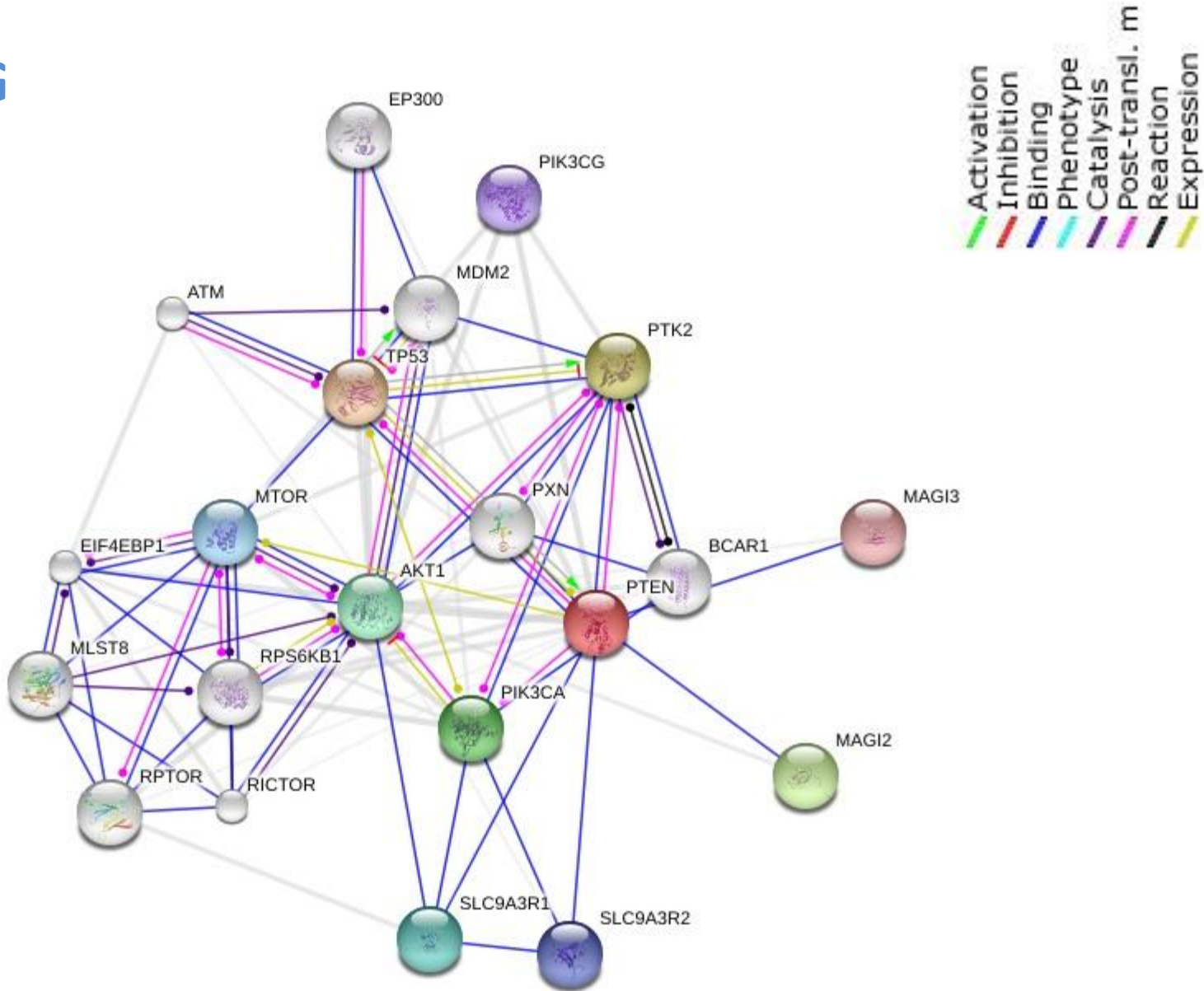
5手工调整多序列比对, 重新拟合, 构建新的模型

FUNCTION

—STRING

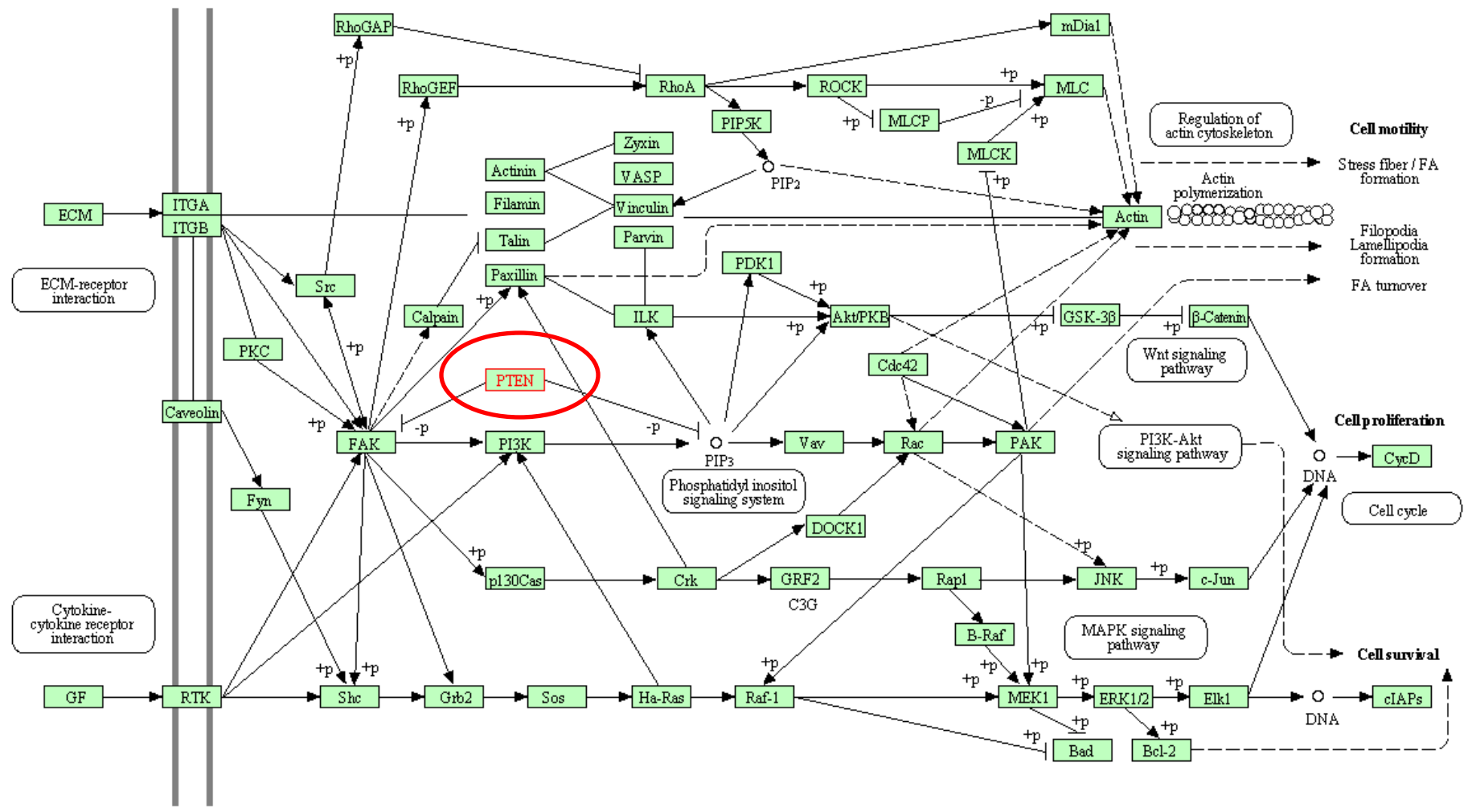
—KEGG

—STRING

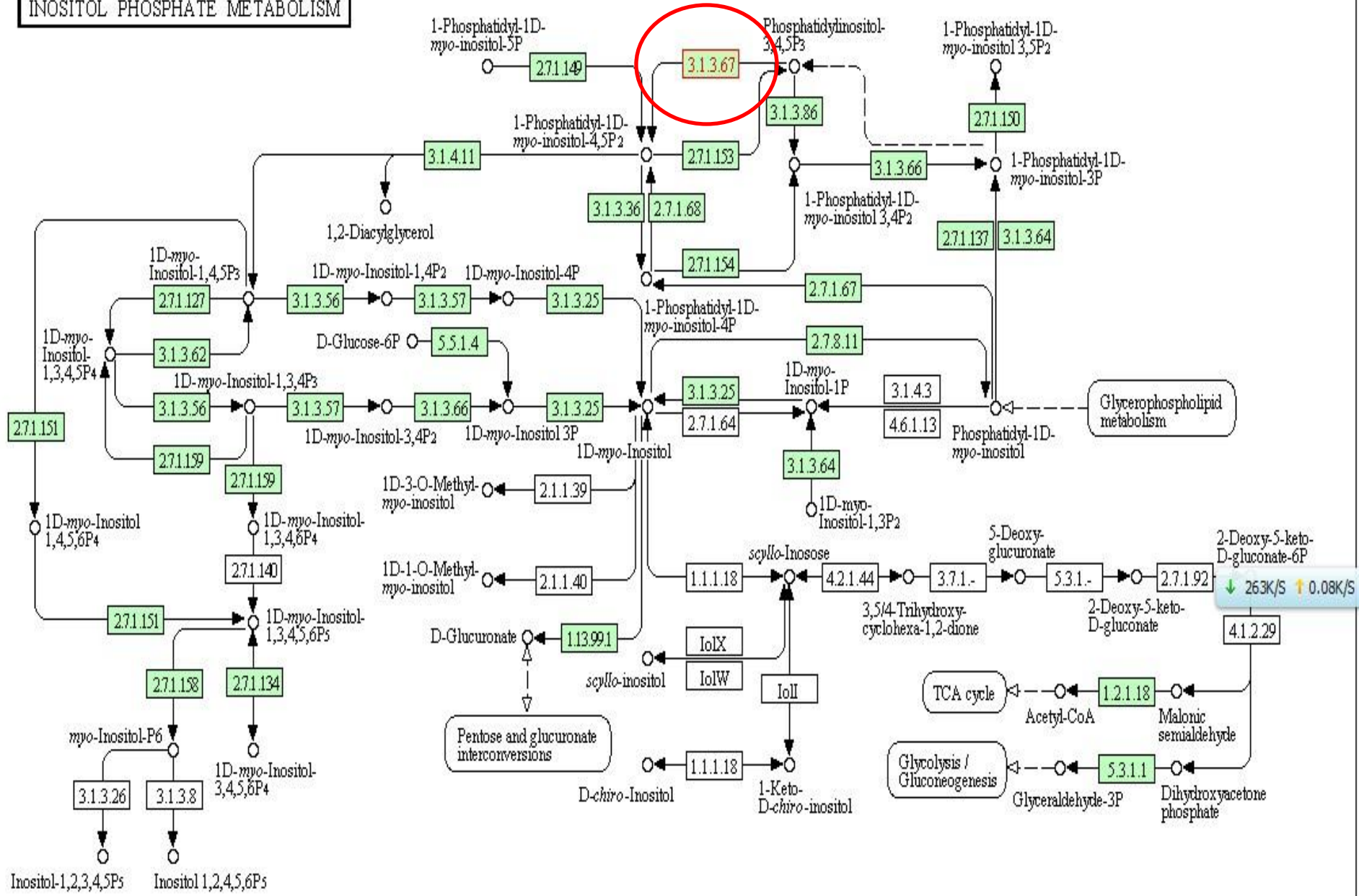


This is the **actions view**. Modes of action are shown in different colors.

FOCAL ADHESION

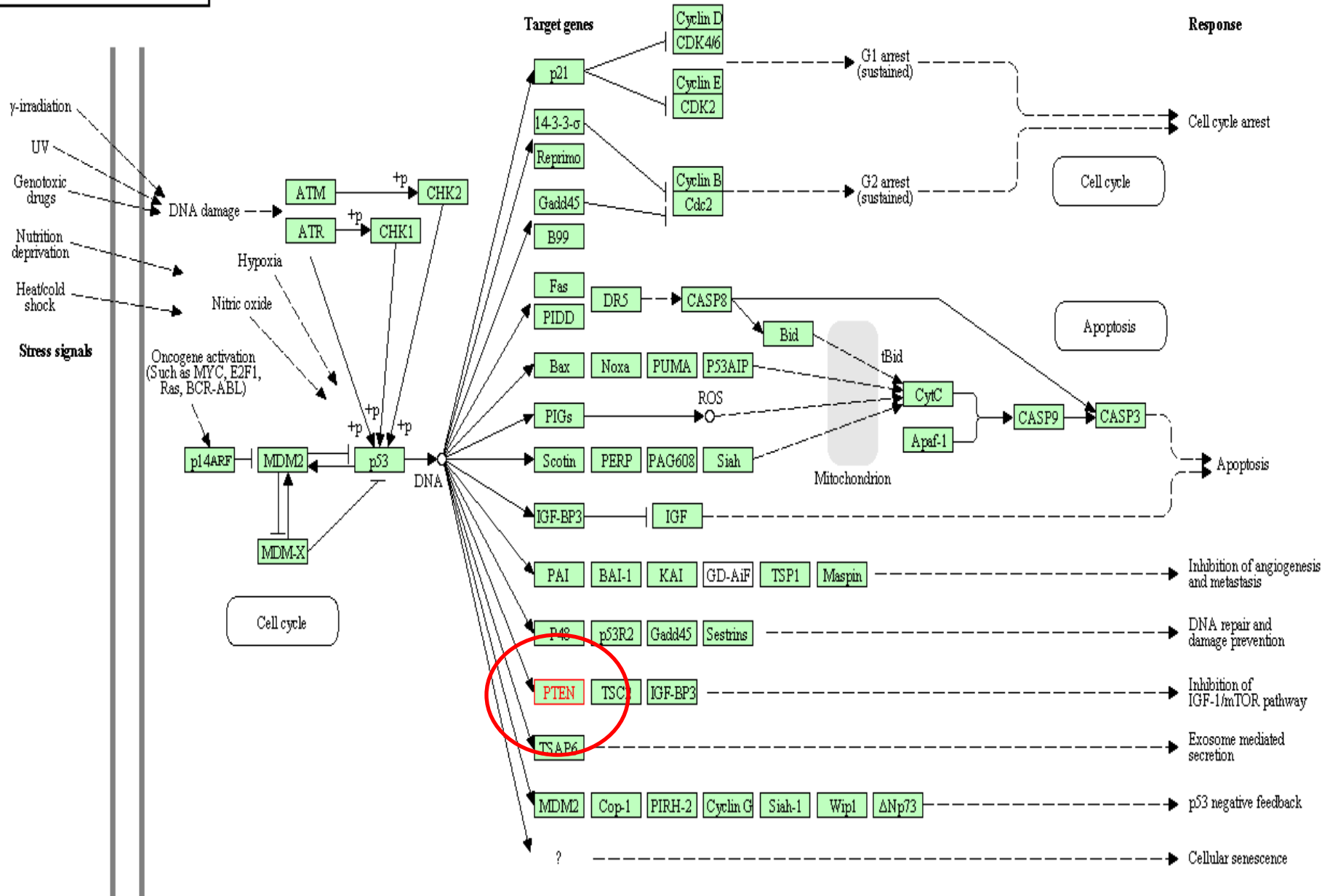


INOSITOL PHOSPHATE METABOLISM

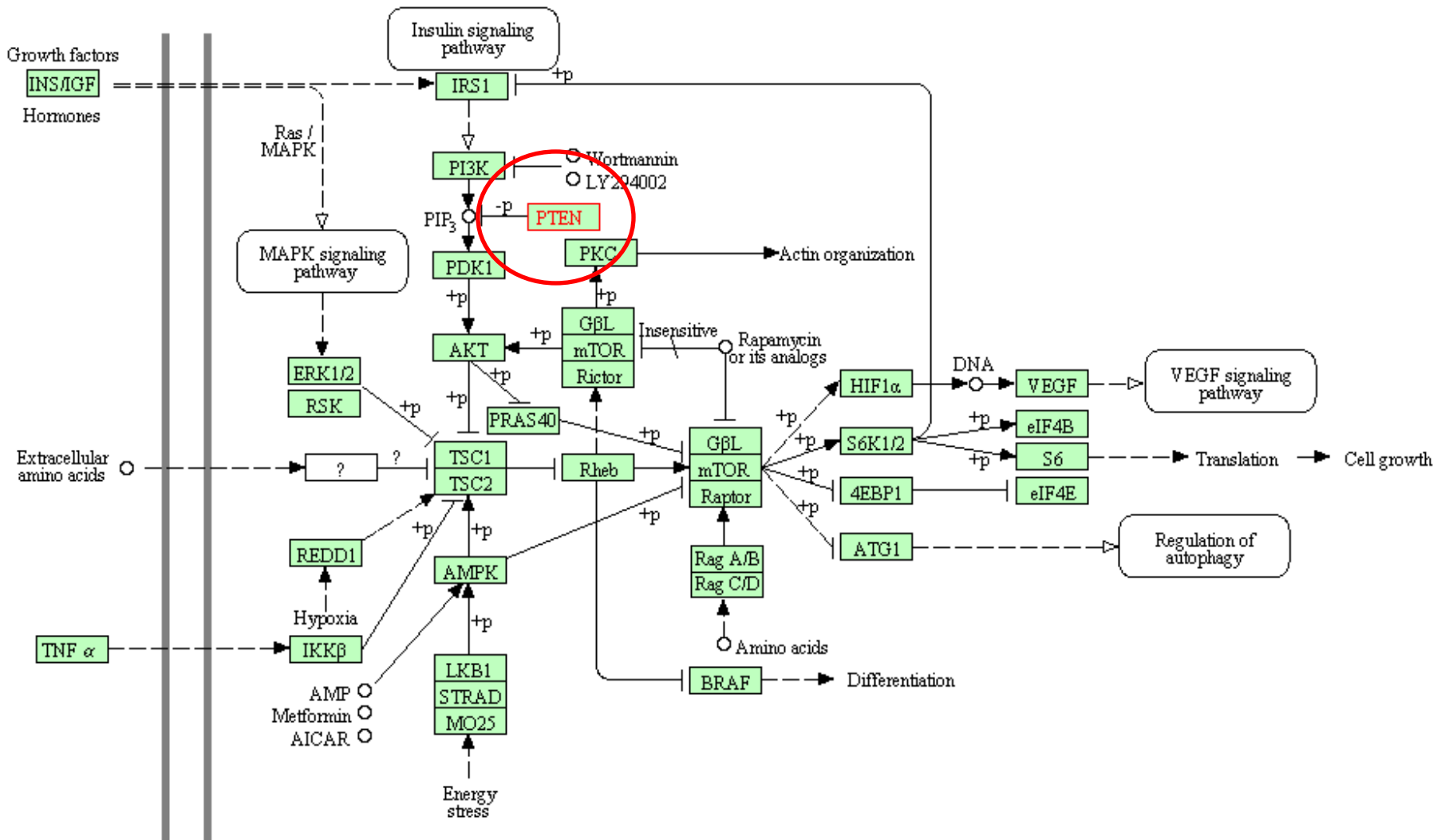


↓ 263K/S ↑ 0.08K/S

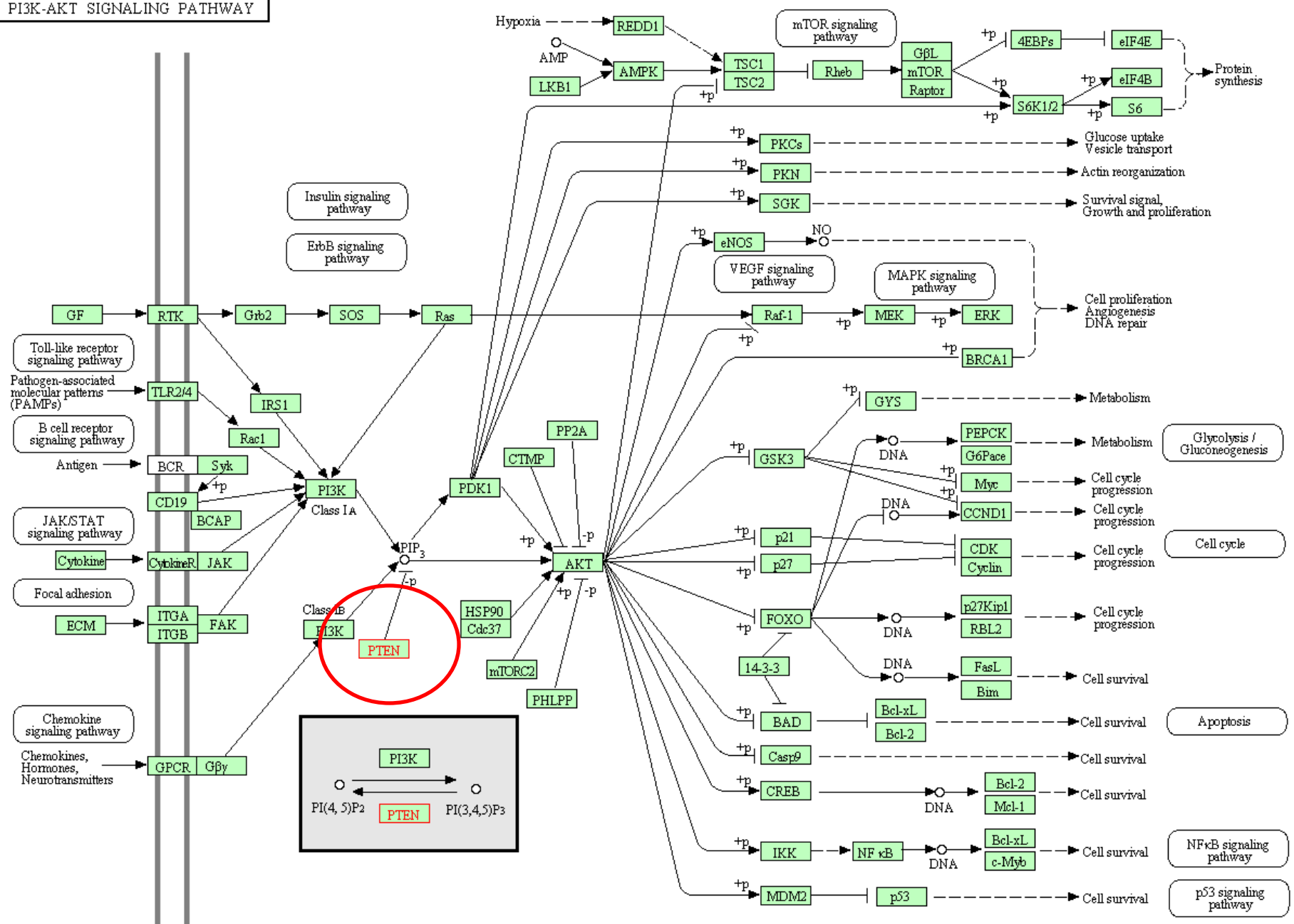
P53 SIGNALING PATHWAY



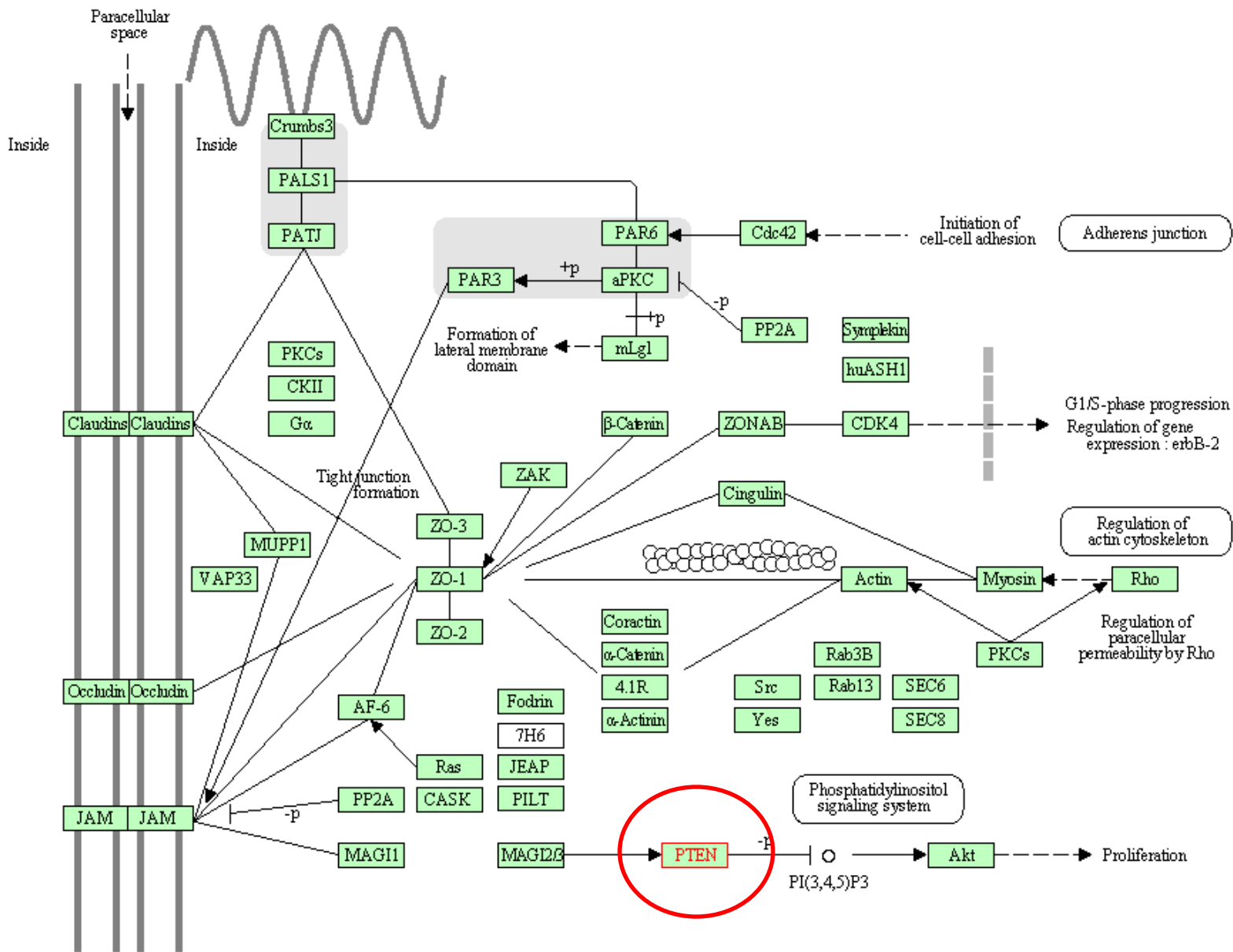
mTOR SIGNALING PATHWAY

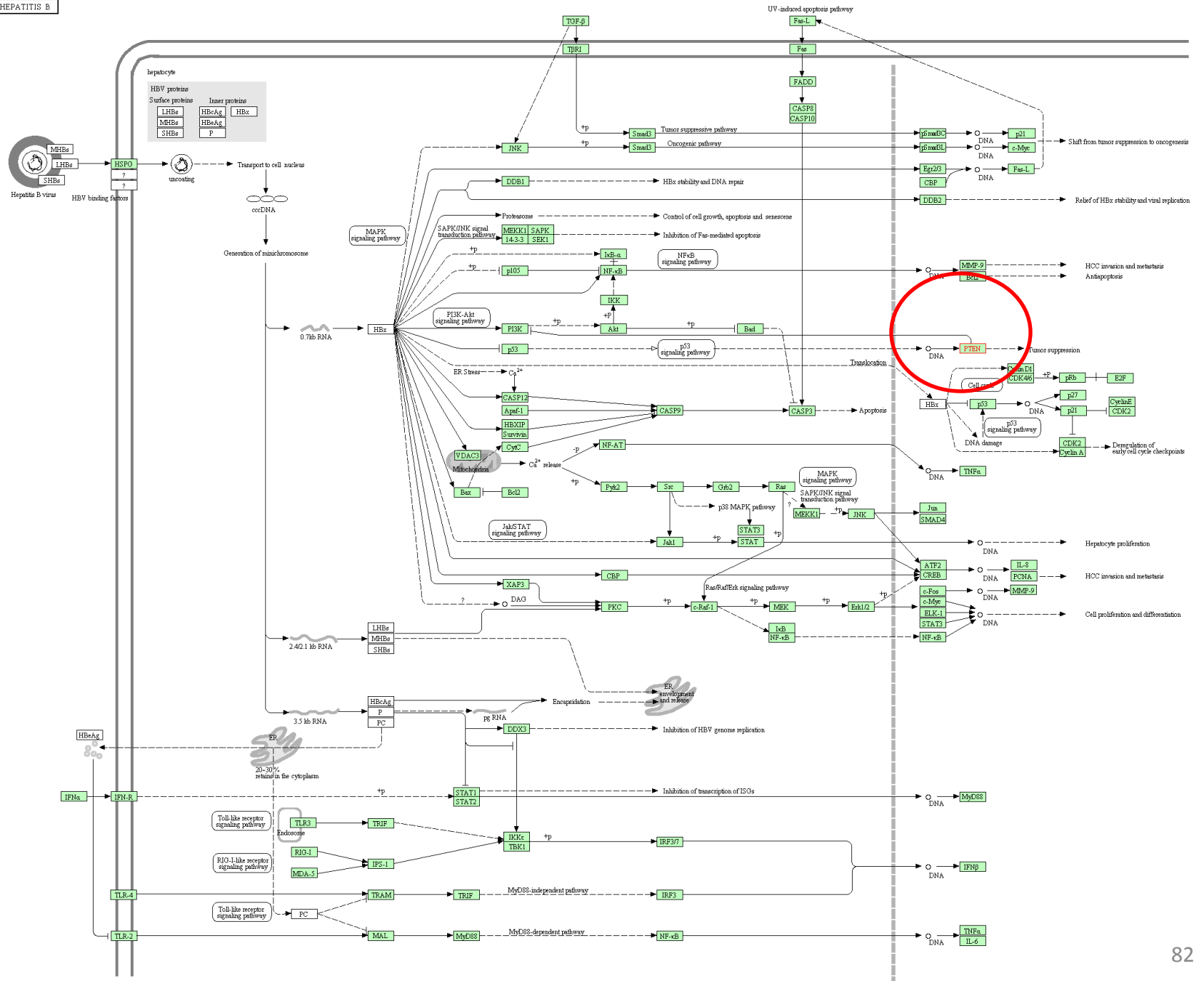


PI3K-AKT SIGNALING PATHWAY

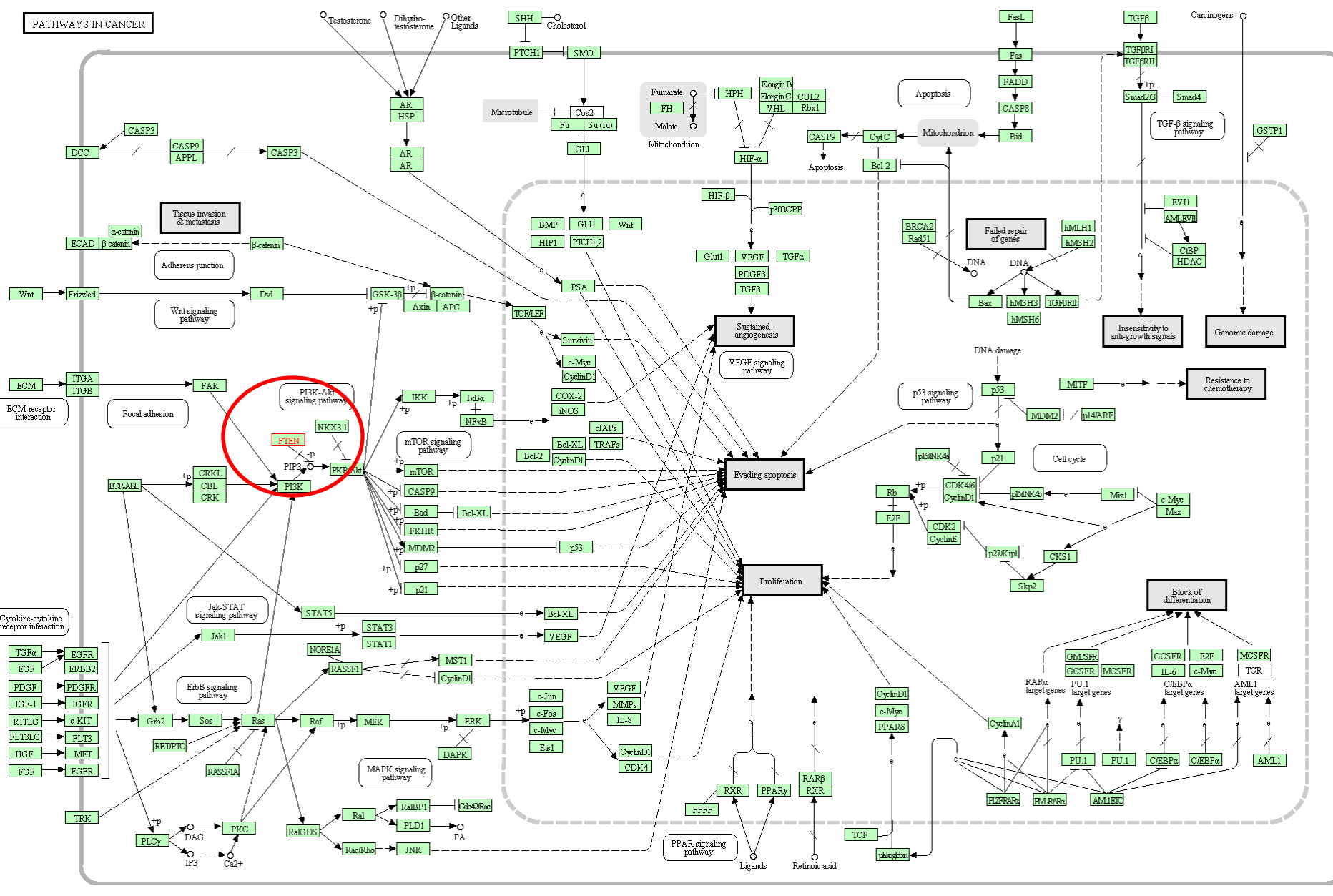


TIGHT JUNCTION



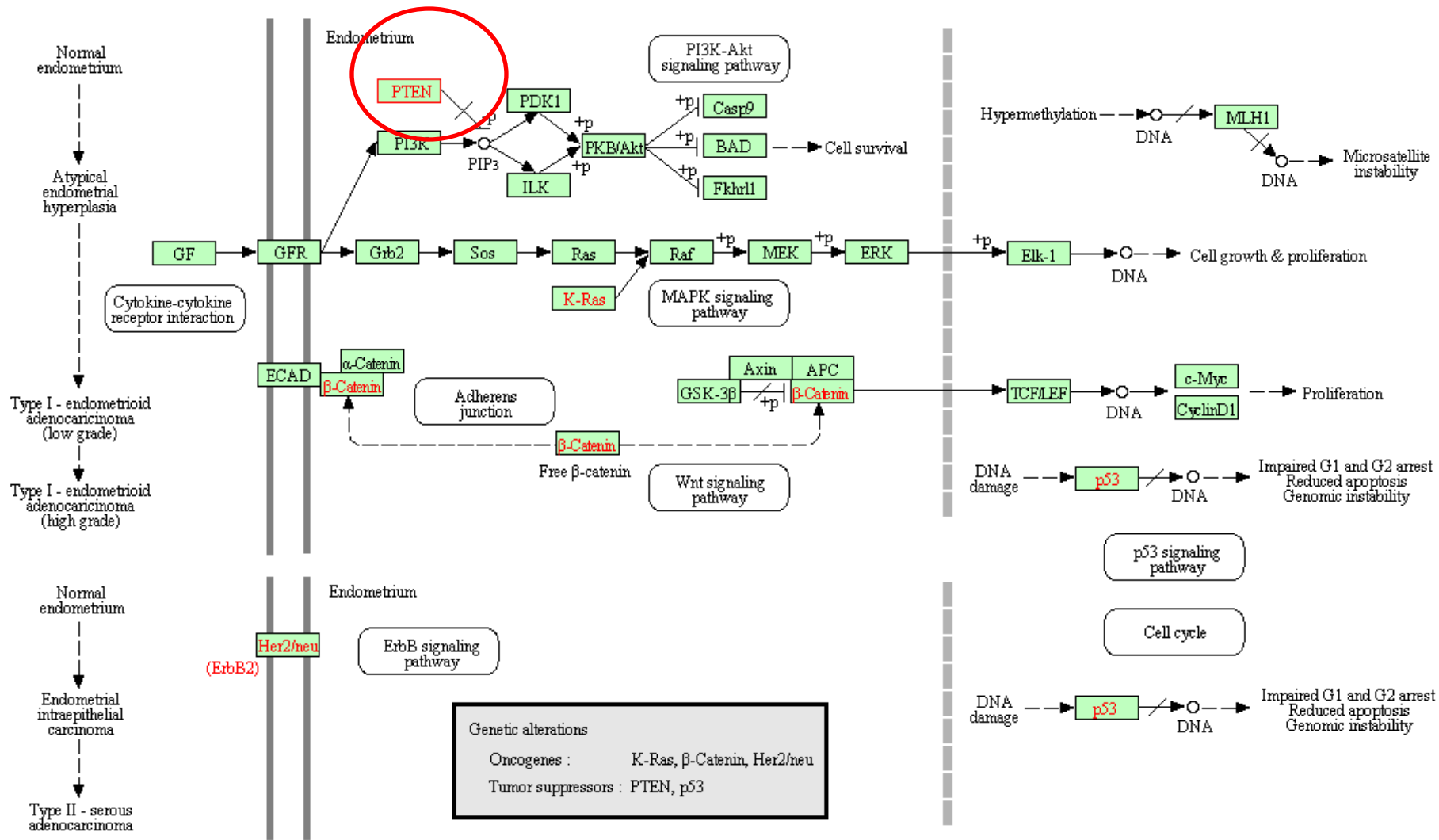


PATHWAYS IN CANCER



- Colorectal cancer
- Pancreatic cancer
- Glioma
- Thyroid cancer
- Acute myeloid leukaemia
- Chronic myeloid leukaemia
- Basal cell carcinoma
- Melanoma
- Renal cell carcinoma
- Bladder cancer
- Prostate cancer
- Endometrial cancer
- Small cell lung cancer
- Non-small cell lung cancer

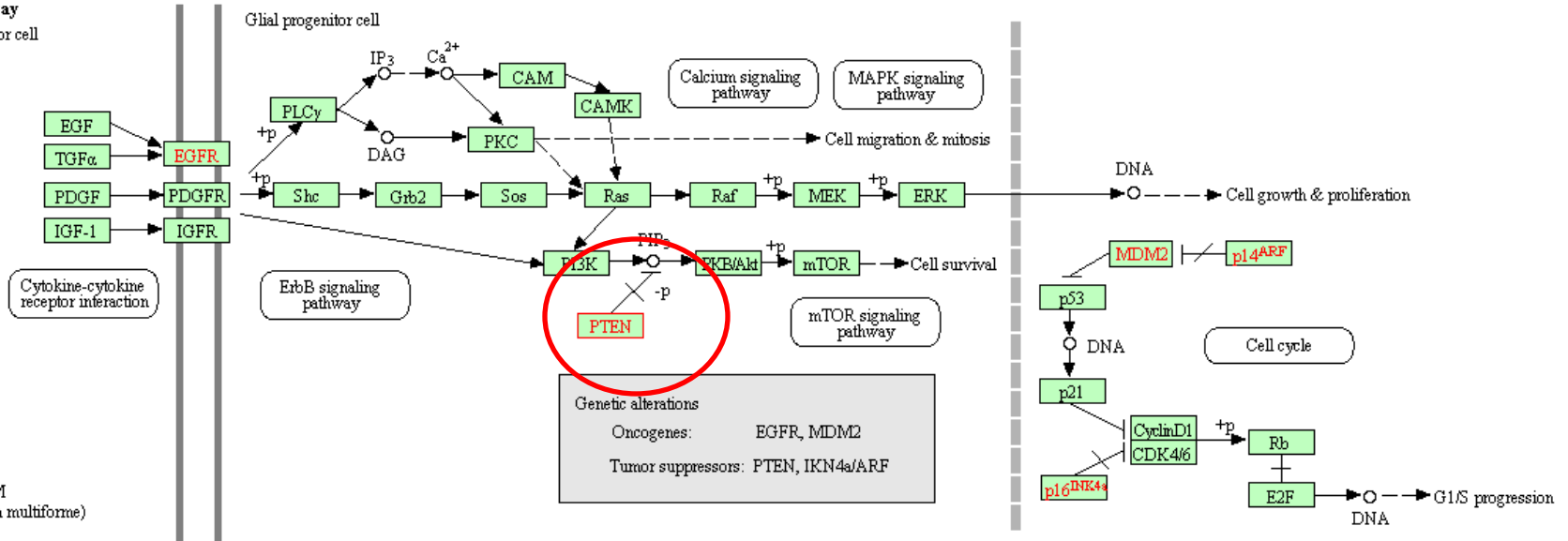
ENDOMETRIAL CANCER



GLIOMA

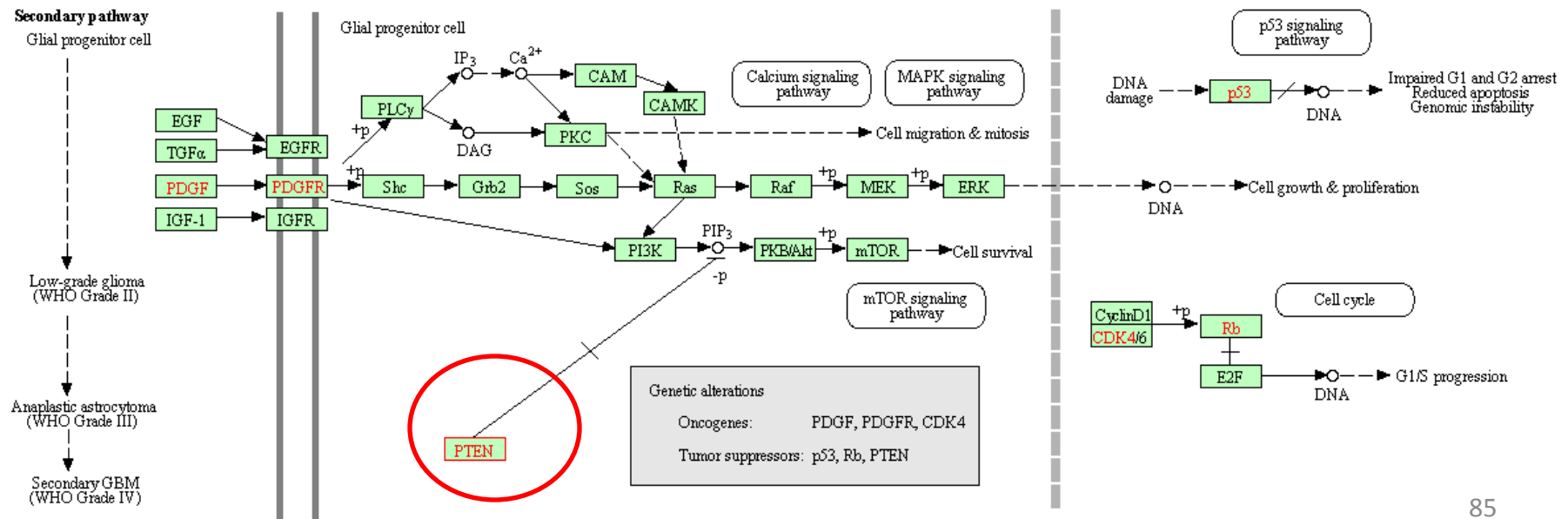
De Novo pathway

Glial progenitor cell



Secondary p pathway

Glial progenitor cell

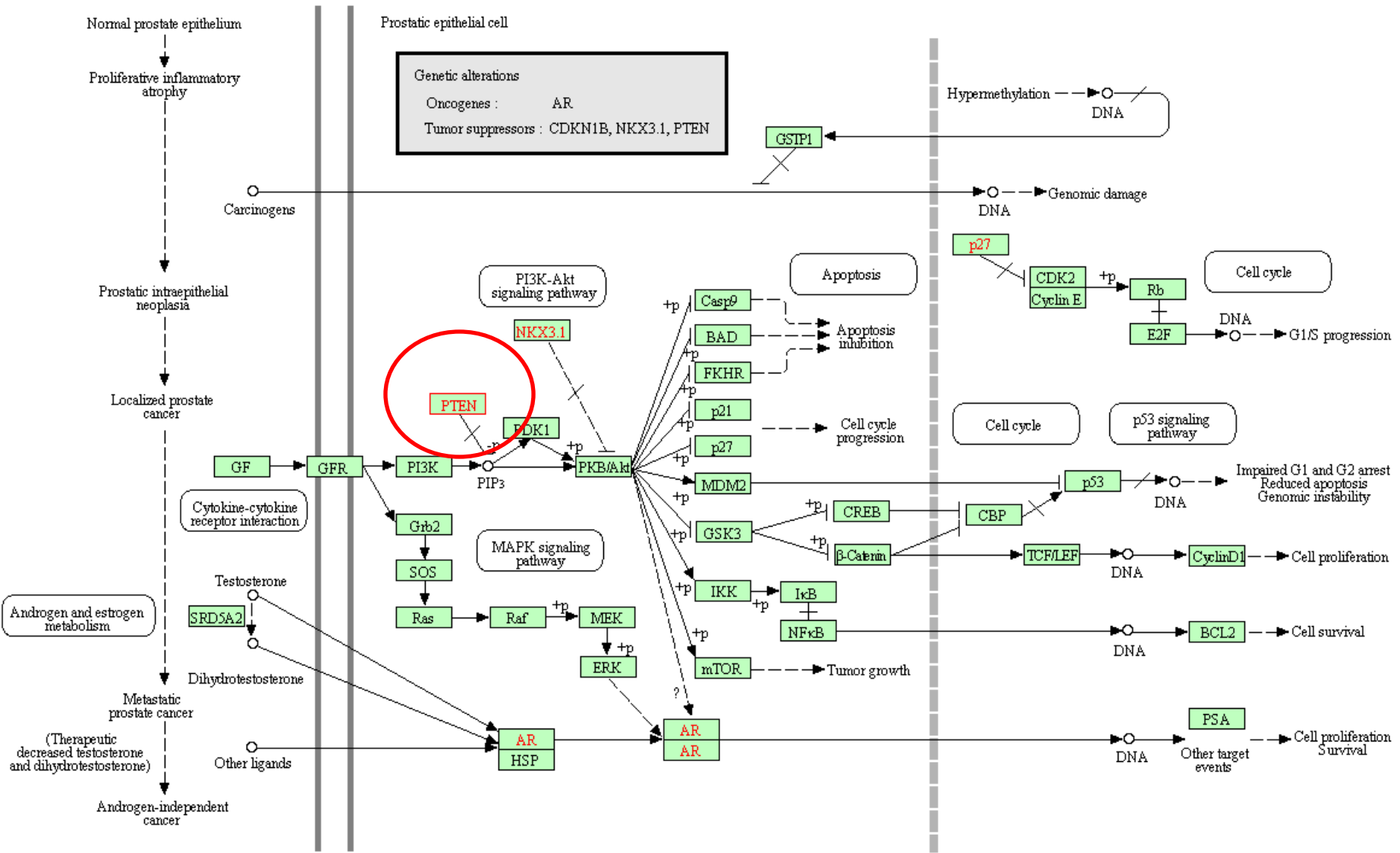


Low-grade glioma (WHO Grade II)

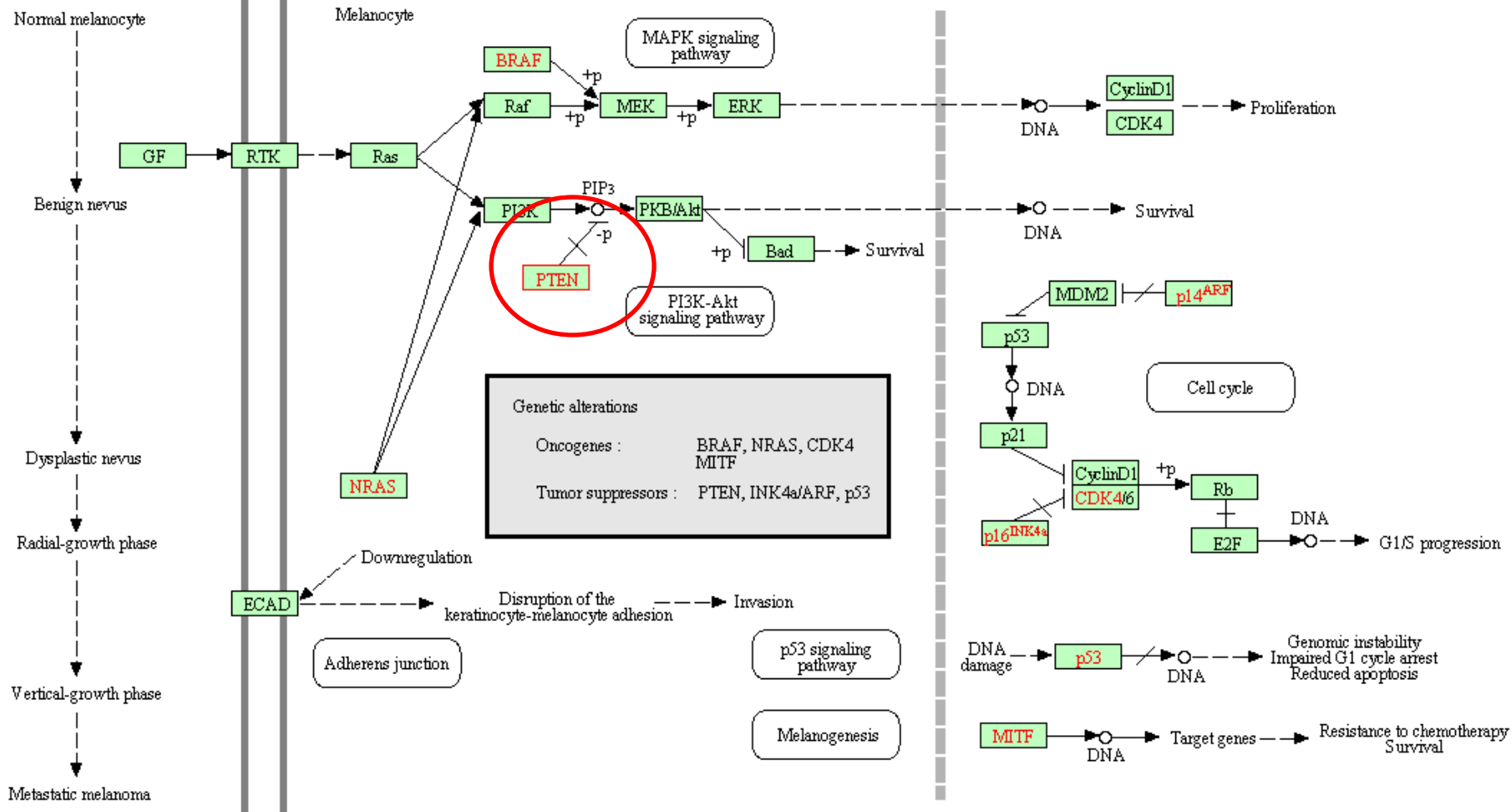
Anaplastic astrocytoma (WHO Grade III)

Secondary GBM (WHO Grade IV)

PROSTATE CANCER

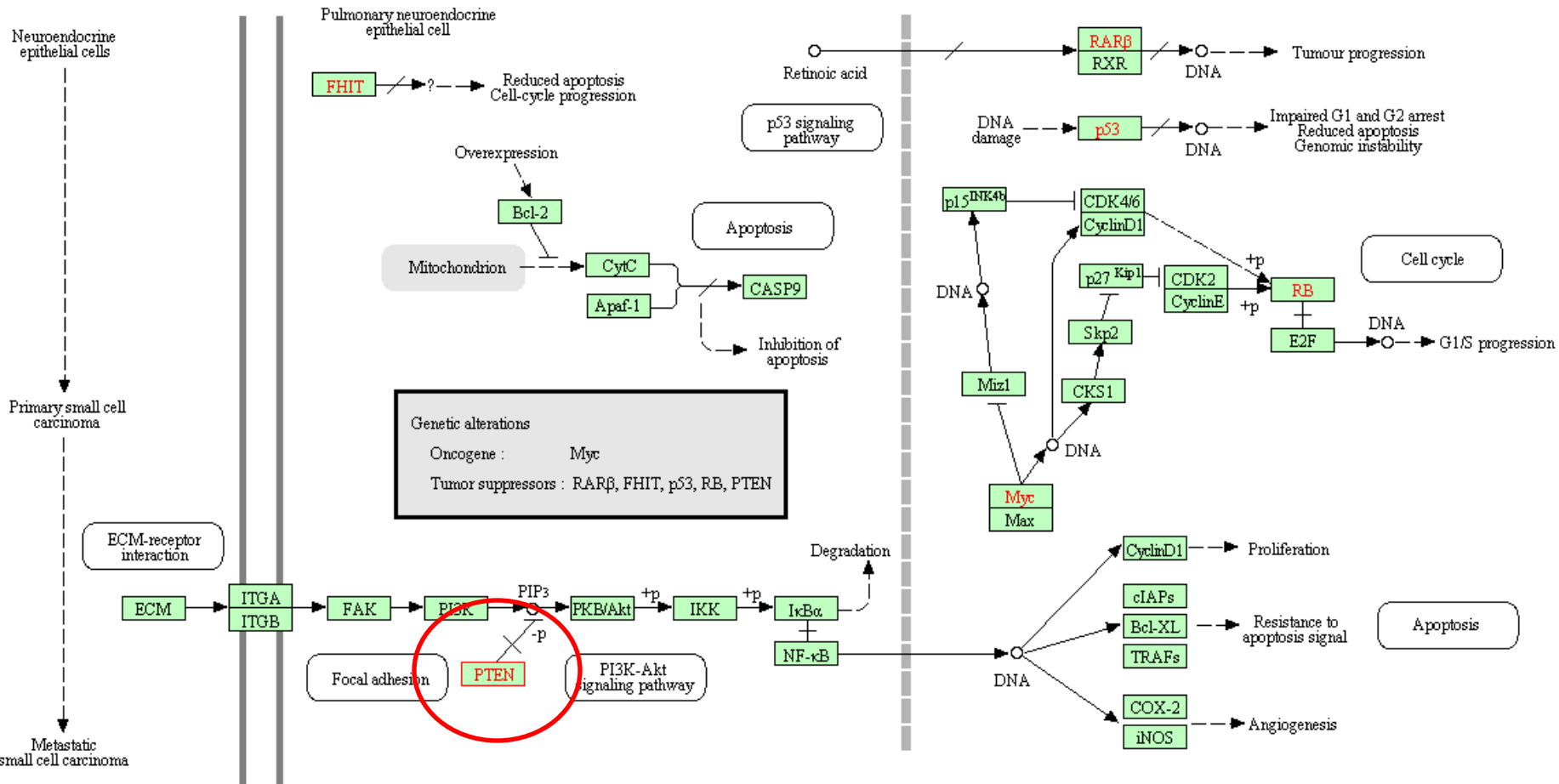


MELANOMA



05218 10/2/12
(c) Kanehisa Laboratories

SMALL CELL LUNG CANCER



05222 10/2/12
 (c) Kanehisa Laboratories

Thank you