



# ONCOMPASS™ REPORT

POWERED BY



**Realtime Oncology**  
**Molecular Treatment Calculator™**

**FIGYELMEZTETÉS**

Ezt a tájékoztatót csak a kezelőorvos használhatja és értelmezheti. Az orvos mérlegelheti, vagy figyelmen kívül hagyhatja a jelentés által nyújtott információkat. Az Oncompass Riport információt szolgáltat a tumorok és a molekuláris profil közti összefüggésekről a tudományos irodalom felhasználásával. Az ONCOMPASS Medicine a szakirodalom tartalmáért felelősséget nem vállal. A feltüntetett gyógyszerek az adott tumortípusban lehetnek törzskönyvezettek és/vagy finanszírozottak, annak viszonylatában, hogy a riportot melyik országban használják.

# Oncompass Report

A Realtime Oncology Molecular Treatment Calculator számításaival

AZONOSÍTÓ	431898
NÉV	Anonymous

## BETEG ADATAI

Oncompass™ ID:

Név: Anonymous

Születési dátum: 1965

Primer daganat lokalizációja: endometrium

Szöveti típus: adenocarcinoma

Metasztázis lokalizációja: Ismeretlen

## SZAKÉRTŐK

Kezelőorvos:

Molekuláris Farmakológus: Dr. Peták István

Genetikai Tanácsadó: Déri Júlia, MSc

Molekuláris Biológus: Várkonyi Edit, PhD

Konzulens Orvos: Dr. Pajkos Gábor

Szakértő: Dr. Rácz Anna

Betegút Koordinátor: Czető Réka

Molekuláris Bionikus Mérnök: Dirner Anna, MSc

Molekuláris Biológus: Dóczi Róbert, PhD

## PATOLÓGIAI ÉS MOLEKULÁRIS DIAGNOSZTIKAI VIZSGÁLATOK

Az Oncompass vizsgálatot a XXX azonosítójú, primer tumorból származó szövettani, valamint a YYY azonosítójú, metastázisból származó szövettani mintákból végeztük.

Tumorarány: 90% (XXX), 80% (YYY)

Tumortípus és szövettan: endometrium adenocarcinoma

### Elvégzett vizsgálatok

NGS – 591 gén

IHC – ER pozitív (80%), PD-L1 negatív

MSI – instabil (MSI-H)

TMB – magas (TMB-H): 32,19 mut/Mb

## KORÁBBI KEZELÉSEK

## ÖSSZEFOGLALÁS

Az endometrium szöveti mintát (XXX) vizsgáltuk 90 % tumorarány mellett.

Az 591 génes NGS vizsgálat sikeresen lefutott.

Az **immunterápia** hatékonyságára utaló biomarkerek közül:

### MSI-High (instabil)

**Tumor mutational burden (TMB) roppant magas** (32,2: 100 %-ban kaptunk ennél alacsonyabb értéket).

### PD-L1 negatív.

A mutációs mintázat (mutational signature) az immunterápiákra érzékeny daganatokra jellemző (20-as mintázat).

IHC – **ER pozitív** (80%)

A magas Tumor Mutational Burden mellett, ilyenkor jellemző módon sok egyéb, célzott terápia esetén fontos mutációkat detektáltunk:

**PTEN-R130Q, FBXW7-R479Q, CTNNB1-T41A, PIK3CA-E81K, ATM-S214fs\*16, CDH1-I594fs\*19, RECQL4-L339fs\*20, MRE11-R364\*, IL2RG-R226C, PMS1-G417fs\***

Immunterápia negatív biomarkerei lehetnek: PTEN mutáció; NSD1, TET2 frameshift mutációk.

### Összefoglalva:

Az adjuváns kezelést javasoljuk felvenni.

Az első vonalas kemoterápia után igen fontos célpont az MSI-High (instabilitás) és a rendkívül magas tumor mutational burden, ami a szakirodalom szerint korrelál az immunterápia iránt mutatott érzékenységgel. Az immunterápiák közül a PEMBROLIZUMABot hozza magasabb AEL értékkel a Calculator. A **PEMBROLIZUMAB a TMB-High és az MSI-High esetén is törzskönyvezett** daganat típusától függetlenül az első vonal kemoterápiás kezelés után. Olyan sok génhibát látunk, hogy nem váratlan, hogy látunk olyat is, ami okozhat rezisztenciát immunterápiára: a PTEN mutációi biztosan (esetleg még: NSD1-, TET2 frameshift mutációk és a JAK2 ismeretlen variáns). A PTEN PI3K vagy PARP-gátlókkal vehető célba, az mTOR-gátlás hatékonyságát megkérdőjelezzük, de a METFORMIN könnyen biztosítható az immunterápia mellett. Az ideális lehetőség a **PEMBROLIZUMAB + OLAPARIB** lenne (a PARP-gátlás hatékony még az ATM, ARID1A, RECQL4, CDK12, PPP2R2A mutációk ellen is), ha annak finanszírozása nem várható, akkor a **PEMBROLIZUMAB + METFORMIN**.

Az endokrin terápia több génhiba is rezisztenciát okoz, így a PTEN és a PIK3CA mutációk, amennyiben mégis szükséges lenne, érdemes lehet mTOR-gátlással, legalább **METFORMIN**nal kiegészíteni.

Magyarországon egy klinikai vizsgálatban lehet első vonalban immunterápiához hozzájutni 50% eséllyel kemoterápia mellett (Dr. Bagaméri):

[A Study to Evaluate Dostarlimab Plus Carboplatin-paclitaxel Versus Placebo Plus Carboplatin-paclitaxel in Participants With Recurrent or Primary](#)

### Advanced Endometrial Cancer (RUBY)

Az alábbi vizsgálatról azt írják, hogy fog futni Mo.-on is több helyen, de még nem indult, itt a vizsgálat keretében adnak 1L kemoterápiát, és után fenntartó kezelést: [Durvalumab With or Without Olaparib as Maintenance Therapy After First-Line Treatment of Advanced and Recurrent Endometrial Cancer \(DUO-E\)](#)

MMR vizsgálatot végzünk, érdemes lenni genetikai tanácsadás keretében vérből is vizsgálatokat végezni Lynch szindróma irányában.

## MOLEKULÁRIS CÉLPONT ELEMZÉS

### MOLEKULÁRIS ALTERÁCIÓK

MSI-H driver (AEL: 8467,85, AF/TR: NA/90%, NA/80%),  
 TMB-H driver (AEL: 796,72, AF/TR: NA/90%),  
 ER protein overexpression driver (AEL: 578,13, AF/TR: NA/80%),  
 PTEN-R130Q driver (AEL: 71,70, AF/TR: 68.98%/90%),  
 FBXW7-R479Q driver (AEL: 64,84, AF/TR: 30.4%/90%),  
 CTNNB1-T41A driver (AEL: 41,88, AF/TR: 24.8%/90%),  
 PIK3CA-E81K driver (AEL: 37,22, AF/TR: 5.64%/90%),  
 ATM-S214fs\*16 driver (AEL: 15,61, AF/TR: 6.3%/90%),  
 CDH1-I594fs\*19 driver (AEL: 13,12, AF/TR: 6.14%/90%),  
 RECQL4-L339fs\*20 driver (AEL: 10,28, AF/TR: 8.7%/90%),  
 MRE11-R364\* driver (AEL: 10,07, AF/TR: 21.43%/90%),  
 IL2RG-R226C driver (AEL: 10,00, AF/TR: 4.57%/90%),  
 PIK3CB-L1049R driver (AEL: 8,87, AF/TR: 18.24%/90%),  
 ATM-I1581fs\*20 driver (AEL: 5,61, AF/TR: 3.28%/90%),  
 CIC-R507C VUS, driver gén (AEL: 2,69, AF/TR: 5.32%/90%),  
 TSC2-I475T VUS, driver gén (AEL: 2,68, AF/TR: 34.48%/90%),  
 CTNNB1-Q26\* VUS, driver gén (AEL: 2,67, AF/TR: 3.35%/90%),  
 CTNNB1-496-1G>T VUS, driver gén (AEL: 2,67, AF/TR: 3.88%/90%),  
 ALK-M830L VUS, driver gén (AEL: 2,50, AF/TR: 3.32%/90%),  
 ARID1A-F2141fs\*59 driver (AEL: 2,48, AF/TR: 4.43%/90%),  
 ARID1A-Q1519fs\*8 driver (AEL: 2,46, AF/TR: 4.36%/90%),  
 ARID1A-Y551fs\*68 driver (AEL: 2,45, AF/TR: 10.56%/90%),  
 RAD51D-P65L VUS, driver gén (AEL: 1,91, AF/TR: 6.6%/90%),  
 KMT2C-L4419P VUS, driver gén (AEL: 1,72, AF/TR: 29.12%/90%),  
 TET2-L1276fs\*24 VUS, driver gén (AEL: 1,71, AF/TR: 12.38%/90%),

### INDIREKT CÉLPONT GÉNEK

PD-1 vad típus (AEL: 9342,33),  
 • MSI-H driver (AEL: 8467,85) ;  
 • TMB-H driver (AEL: 796,72) ;  
 • JAK2-C68R driver (AEL: -0,27) ;  
 • PTEN-R130Q driver (AEL: -71,70) ;  
 • EPHA7-I473V driver (AEL: 0,55)

CD274 vad típus (AEL: 9236,18),  
 • ARID1A-Y551fs\*68 driver (AEL: 2,45) ;  
 • ARID1A-Q1519fs\*8 driver (AEL: 2,46) ;  
 • ARID1A-F2141fs\*59 driver (AEL: 2,49) ;  
 • TET2-L1276fs\*24 driver (AEL: -1,71) ;  
 • CTNNB1-496-1G>T driver (AEL: -2,67) ;  
 • EPHA7-I473V driver (AEL: 0,55) ;  
 • TMB-H driver (AEL: 796,72) ;  
 • CTNNB1-T41A driver (AEL: -41,88) ;  
 • CTNNB1-Q26\* driver (AEL: -2,67) ;  
 • MSI-H driver (AEL: 8467,85)

CTLA4 vad típus (AEL: 9223,61),  
 • EPHA7-I473V driver (AEL: 0,55) ;  
 • CTNNB1-T41A driver (AEL: -41,88) ;  
 • TMB-H driver (AEL: 796,72) ;  
 • CTNNB1-Q26\* driver (AEL: -2,67) ;  
 • CTNNB1-496-1G>T driver (AEL: -2,67) ;

## MOLEKULÁRIS CÉLPONT ELEMZÉS

FAT1-S1782N VUS, driver gén (AEL: 1,46, AF/TR: 3.97%/90%),  
 FAT1-L3946P VUS, driver gén (AEL: 1,46, AF/TR: 6.35%/90%),  
 FAT1-M3869T VUS, driver gén (AEL: 1,46, AF/TR: 5.84%/90%),  
 SOX9-L60V VUS, driver gén (AEL: 1,12, AF/TR: 48.82%/90%),  
 DNMT3A-Q110fs\*14 driver (AEL: 1,08, AF/TR: 23.53%/90%),  
 PTPN11-R386K VUS, driver gén (AEL: 1,03, AF/TR: 3.87%/90%),  
 GNAS-A36V VUS, driver gén (AEL: 0,83, AF/TR: 3.58%/90%),  
 CBL-E196fs\*16 driver (AEL: 0,72, AF/TR: 25.24%/90%),  
 SMARCA4-Q1195H driver (AEL: 0,66, AF/TR: 4.5%/90%),  
 FH-A104T driver (AEL: 0,64, AF/TR: 6.76%/90%),  
 MED12-R431L VUS, driver gén (AEL: 0,60, AF/TR: 4.64%/90%),  
 EPHA7-I473V VUS, driver gén (AEL: 0,54, AF/TR: 5.51%/90%),  
 TGFBR2-Q334H VUS, driver gén (AEL: 0,50, AF/TR: 5.74%/90%),  
 KDM5C-R68fs\*5 VUS, driver gén (AEL: 0,50, AF/TR: 3.12%/90%),  
 CARD11-R555fs\*45 driver (AEL: 0,46, AF/TR: 7.38%/90%),  
 NSD1-M1531fs\*43 driver (AEL: 0,46, AF/TR: 4.37%/90%),  
 NSD1-F1799fs\*22 driver (AEL: 0,45, AF/TR: 3.05%/90%),  
 XRCC2-K267fs\*? driver (AEL: 0,45, AF/TR: 6.13%/90%),  
 CARD11-R404M VUS, driver gén (AEL: 0,41, AF/TR: 3.84%/90%),  
 ARID2-D1758G VUS, driver gén (AEL: 0,41, AF/TR: 6.79%/90%),  
 CDK12-G1271fs\*23 driver (AEL: 0,35, AF/TR: 4.78%/90%),  
 CDK12-A1174S VUS, driver gén (AEL: 0,34, AF/TR: 3.78%/90%),  
 ARAF-S157N VUS, driver gén (AEL: 0,33, AF/TR: 4.09%/90%),  
 TP53BP1-H964R VUS, driver gén (AEL: 0,30, AF/TR: 49.19%/90%),  
 IGF2R-D1317fs\*5 driver (AEL: 0,28, AF/TR: 5.18%/90%),  
 JAK2-C68R VUS, driver gén (AEL: 0,27, AF/TR: 3.07%/90%),  
 IGF2R-W53R VUS, driver gén (AEL: 0,26, AF/TR: 6.97%/90%),  
 PAX5-A322fs\*11 driver (AEL: 0,23, AF/TR: 3.21%/90%),  
 FANCF-G357D VUS, driver gén (AEL: 0,18, AF/TR: 4.98%/90%),  
 CTCF-E691fs\*30 driver (AEL: 0,14, AF/TR: 6.95%/90%),  
 ESRP1-S625G VUS, driver gén (AEL: 0,13, AF/TR: 4.24%/90%),  
 EPHA3-T115N VUS, driver gén (AEL: 0,12, AF/TR: 32.69%/90%),  
 PPP2R2A-Y189\* VUS, driver gén (AEL: 0,12, AF/TR: 3.23%/90%),  
 ERBB4-G1109S VUS, driver gén (AEL: 0,11, AF/TR: 42.02%/90%),  
 WNK2-P1381fs\*11 VUS, driver gén (AEL: 0,11, AF/TR: 3.01%/90%),  
 LAMA2-R185C VUS, driver gén (AEL: 0,10, AF/TR: 5.17%/90%),  
 DMD-S3343fs\*34 driver (AEL: 0,10, AF/TR: 6.36%/90%),  
 DMD-R1957Q VUS, driver gén (AEL: 0,10, AF/TR: 3%/90%),  
 PMS1-N489I VUS, driver gén (AEL: 0,10, AF/TR: 48.43%/90%),  
 PMS1-G417fs\*6 VUS, driver gén (AEL: 0,10, AF/TR: 27.58%/90%),  
 ZRSR2-P383A driver (AEL: 0,10, AF/TR: 47.59%/90%),  
 ZMYM3-C723F VUS, driver gén (AEL: 0,09, AF/TR: 29.17%/90%),  
 SLX4-P1004L VUS, driver gén (AEL: 0,08, AF/TR: 7.06%/90%),  
 CSMD3-S3630Y VUS, driver gén (AEL: 0,03, AF/TR: 5.43%/90%),  
 SCN11A-K491fs\*5 driver (AEL: 0,03, AF/TR: 7.23%/90%),  
 SAMD9L-K21fs\*3 driver (AEL: 0,02, AF/TR: 5.68%/90%),  
 TAF1-R855C VUS, driver gén (AEL: 0,02, AF/TR: 33.72%/90%),  
 SLIT2-K904fs\*13 VUS, driver gén (AEL: 0,01, AF/TR: 3.43%/90%),  
 CDC27-K319fs\*24 VUS, driver gén (AEL: 0,01, AF/TR: 7.52%/90%),  
 DDX11-S407R ellentmondásos driver (AEL: 0,00, AF/TR: 5.76%/90%),  
 BAZ2B-N2000S ellentmondásos driver (AEL: 0,00, AF/TR: 46.73%/90%),  
 THSD7B-P642A ellentmondásos driver (AEL: 0,00, AF/TR: 6.64%/90%),  
 GLI1-G162D ellentmondásos driver (AEL: 0,00, AF/TR: 5.54%/90%),  
 ADGRB3-E227A ellentmondásos driver (AEL: 0,00, AF/TR: 5.26%/90%),  
 ZBED4-V241I ellentmondásos driver (AEL: 0,00, AF/TR: 48.75%/90%),  
 RPTOR-V1192I ellentmondásos driver (AEL: 0,00, AF/TR: 6.16%/90%),  
 SMAD2-R410G ellentmondásos driver (AEL: 0,00, AF/TR: 6.6%/90%),  
 SEC16A-P9L ellentmondásos driver (AEL: 0,00, AF/TR: 10.95%/90%),  
 GATA2-G273fs\*53 ellentmondásos driver (AEL: 0,00, AF/TR: 3.59%/90%),  
 TRIO-L2277\* ellentmondásos driver (AEL: 0,00, AF/TR: 3.86%/90%),  
 AKAP9-P1381L ellentmondásos driver (AEL: 0,00, AF/TR: 8.82%/90%),  
 AKAP9-R434W ellentmondásos driver (AEL: 0,00, AF/TR: 11.13%/90%),  
 OTOP1-L104M ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 33.9%/90%),  
 ELMO1-N65S ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 3.39%/90%),  
 FAT3-Q2328K ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 3.17%/90%),  
 TRIO-I957T ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 6.64%/90%),  
 GATA4-P290S ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 11.31%/90%),  
 PAX3-P300T ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 5.29%/90%),  
 IGSF10-N579D ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 46.82%/90%),  
 SYNE3-P559T ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 46.3%/90%),

- MSI-H driver (AEL: 8467,85)
- WRN vad típus (AEL: 8475,55),
- MSI-H driver (AEL: 8467,85)
- IDO1 vad típus (AEL: 8470,75),
- MSI-H driver (AEL: 8467,85)
- LAG3 vad típus (AEL: 8470,75),
- MSI-H driver (AEL: 8467,85)
- ESR1 vad típus (AEL: 960,24),
- PIK3CA-E81K driver (AEL: -37,22);
  - ER protein overexpression driver (AEL: 578,13);
  - PTEN-R130Q driver (AEL: -71,70);
  - KMT2C-L4419P driver (AEL: -1,72)
- MTOR vad típus (AEL: 823,83),
- PIK3CB-L1049R driver (AEL: 8,87);
  - PIK3CA-E81K driver (AEL: 37,22);
  - PTPN11-R386K driver (AEL: 1,03);
  - FBXW7-R479Q driver (AEL: 64,84);
  - ER protein overexpression driver (AEL: 578,13);
  - CDH1-I594fs\*19 driver (AEL: 13,12);
  - TSC2-I475T driver (AEL: 2,68);
  - PTEN-R130Q driver (AEL: 71,70)
- PIK3CA vad típus (AEL: 777,65),
- PTEN-R130Q driver (AEL: -71,70);
  - PIK3CA-E81K driver (AEL: 37,22);
  - CDH1-I594fs\*19 driver (AEL: 13,12);
  - ER protein overexpression driver (AEL: 578,13)
- AKT1 vad típus (AEL: 724,59),
- ARID1A-Y551fs\*68 driver (AEL: 2,45);
  - PIK3CB-L1049R driver (AEL: 8,87);
  - ARID1A-Q1519fs\*8 driver (AEL: 2,46);
  - CDH1-I594fs\*19 driver (AEL: 13,12);
  - PTEN-R130Q driver (AEL: 71,70);
  - ER protein overexpression driver (AEL: 578,13);
  - ARID1A-F2141fs\*59 driver (AEL: 2,49);
  - PIK3CA-E81K driver (AEL: 37,22);
  - PPP2R2A-Y189\* driver (AEL: 0,12)
- CDK4 vad típus (AEL: 578,58),
- ER protein overexpression driver (AEL: 578,13)
- CDK6 vad típus (AEL: 578,58),
- ER protein overexpression driver (AEL: 578,13)
- PARP1 vad típus (AEL: 147,96),
- ATM-I1581fs\*20 driver (AEL: 5,61);
  - RECQL4-L339fs\*20 driver (AEL: 10,28);
  - ARID1A-Q1519fs\*8 driver (AEL: 2,46);
  - CDK12-G1271fs\*23 driver (AEL: 0,35);
  - DDX11-S407R driver (AEL: 0,00);
  - ARID1A-Y551fs\*68 driver (AEL: 2,45);
  - XRCC2-K267fs\*? driver (AEL: 0,45);
  - PTEN-R130Q driver (AEL: 71,70);
  - MRE11-R364\* driver (AEL: 10,07);
  - ARID2-D1758G driver (AEL: 0,41);
  - TP53BP1-H964R driver (AEL: -0,30);
  - RAD51D-P65L driver (AEL: 1,91);
  - ARID1A-F2141fs\*59 driver (AEL: 2,49);
  - ZMYM3-C723F driver (AEL: 0,09);
  - CDK12-A1174S driver (AEL: 0,34);
  - SLX4-P1004L driver (AEL: 0,08);
  - ATM-S214fs\*16 driver (AEL: 15,61)
- PIK3CB vad típus (AEL: 119,54),
- CDH1-I594fs\*19 driver (AEL: 13,12);
  - PTEN-R130Q driver (AEL: 71,70);
  - PIK3CB-L1049R driver (AEL: 8,87)
- ALK vad típus (AEL: 111,22),
- CDH1-I594fs\*19 driver (AEL: 13,12);
  - ALK-M830L driver (AEL: 2,50)
- CTNNB1 vad típus (AEL: 90,80),
- CTNNB1-496-1G>T driver (AEL: 2,67);

## MOLEKULÁRIS CÉLPONT ELEMZÉS

PRF1-K282R ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 43.78%/90%),  
 ABCC2-K297fs\*14 ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 11.66%/90%),  
 MED13-W1662\* ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 5.16%/90%),  
 MIER3-G366E ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 3.86%/90%),  
 CCNE1-S90A ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 3.49%/90%),  
 ATP4A-V288fs\*70 ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 9.06%/90%),  
 TOP2A-A1437T ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 9.06%/90%),  
 SLC9A9-R6fs\*31 ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 21.06%/90%),  
 KEL-E383G ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 49.81%/90%),  
 BCORL1-D1109G ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 3.15%/90%),  
 PIK3C2B-M1223L ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 25.77%/90%),  
 MST1R-P862fs\*9 ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 30.05%/90%),  
 SCN11A-L1158P ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 46.4%/90%),  
 USP16-V809A ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 29.57%/90%),  
 GRM3-G24W ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 4.43%/90%),  
 KMT2C-K339N nem driver (AEL: -2,03, AF/TR: 9.59%/90%),  
 BCR-D1106N nem driver (AEL: -4,98, AF/TR: 12.6%/90%),  
 PREX2-S977L nem driver (AEL: -4,99, AF/TR: 46.36%/90%)

- PIK3CA-E81K driver (AEL: 37,22) ;
  - CTNNB1-Q26\* driver (AEL: 2,67) ;
  - CTNNB1-T41A driver (AEL: 41,88)
- ATM vad típus (AEL: 72,55),
- PTEN-R130Q driver (AEL: 71,70)
- NOTCH1 vad típus (AEL: 65,98),
- FBXW7-R479Q driver (AEL: 64,84)
- MCL1 vad típus (AEL: 65,29),
- FBXW7-R479Q driver (AEL: 64,84)
- TTK vad típus (AEL: 47,73),
- CTNNB1-Q26\* driver (AEL: 2,67) ;
  - CTNNB1-496-1G>T driver (AEL: 2,67) ;
  - CTNNB1-T41A driver (AEL: 41,88)
- AKT2 vad típus (AEL: 38,33),
- PIK3CA-E81K driver (AEL: 37,22)
- AKT3 vad típus (AEL: 37,58),
- PIK3CA-E81K driver (AEL: 37,22)
- JAK2 vad típus (AEL: 25,07),
- JAK2-C68R driver (AEL: 0,27) ;
  - CDH1-I594fs\*19 driver (AEL: 13,12) ;
  - CBL-E196fs\*16 driver (AEL: 0,72)
- ATR vad típus (AEL: 24,40),
- ATM-S214fs\*16 driver (AEL: 15,61) ;
  - ATM-I1581fs\*20 driver (AEL: 5,61)
- ABL1 vad típus (AEL: 16,41),
- CDH1-I594fs\*19 driver (AEL: 13,12) ;
  - FH-A104T driver (AEL: 0,64)
- JAK1 vad típus (AEL: 16,25),
- CBL-E196fs\*16 driver (AEL: 0,72) ;
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- ROS1 vad típus (AEL: 15,62),
- CDH1-I594fs\*19 driver (AEL: 13,12)
- AURKC vad típus (AEL: 14,17),
- CDH1-I594fs\*19 driver (AEL: 13,12)
- AURKB vad típus (AEL: 14,17),
- CDH1-I594fs\*19 driver (AEL: 13,12)
- PIK3CG vad típus (AEL: 14,17),
- CDH1-I594fs\*19 driver (AEL: 13,12)
- AURKA vad típus (AEL: 14,17),
- CDH1-I594fs\*19 driver (AEL: 13,12)
- PIK3CD vad típus (AEL: 14,17),
- CDH1-I594fs\*19 driver (AEL: 13,12)
- PDGFRB vad típus (AEL: 13,63),
- CDH1-I594fs\*19 driver (AEL: 13,12)
- BCL2 vad típus (AEL: 13,63),
- CDH1-I594fs\*19 driver (AEL: 13,12)
- NTRK1 vad típus (AEL: 13,63),
- CDH1-I594fs\*19 driver (AEL: 13,12)
- FGFR1 vad típus (AEL: 13,63),
- CDH1-I594fs\*19 driver (AEL: 13,12)
- PDGFRA vad típus (AEL: 13,63),
- CDH1-I594fs\*19 driver (AEL: 13,12)
- JAK3 vad típus (AEL: 13,63),
- CDH1-I594fs\*19 driver (AEL: 13,12)
- SRC vad típus (AEL: 13,63),

## MOLEKULÁRIS CÉLPONT ELEMZÉS

	<ul style="list-style-type: none"> <li>• CDH1-I594fs*19 driver (AEL: 13,12)</li> </ul> <p>NPY5R vad típus (AEL: 13,63),</p> <ul style="list-style-type: none"> <li>• CDH1-I594fs*19 driver (AEL: 13,12)</li> </ul> <p>CDK2 vad típus (AEL: 13,63),</p> <ul style="list-style-type: none"> <li>• CDH1-I594fs*19 driver (AEL: 13,12)</li> </ul> <p>CDK1 vad típus (AEL: 13,63),</p> <ul style="list-style-type: none"> <li>• CDH1-I594fs*19 driver (AEL: 13,12)</li> </ul> <p>RET vad típus (AEL: 13,63),</p> <ul style="list-style-type: none"> <li>• CDH1-I594fs*19 driver (AEL: 13,12)</li> </ul> <p>GBF1 vad típus (AEL: 13,63),</p> <ul style="list-style-type: none"> <li>• CDH1-I594fs*19 driver (AEL: 13,12)</li> </ul> <p>MET vad típus (AEL: 13,63),</p> <ul style="list-style-type: none"> <li>• CDH1-I594fs*19 driver (AEL: 13,12)</li> </ul> <p>HMGCR vad típus (AEL: 13,62),</p> <ul style="list-style-type: none"> <li>• CDH1-I594fs*19 driver (AEL: 13,12)</li> </ul> <p>EZH2 vad típus (AEL: 13,55),</p> <ul style="list-style-type: none"> <li>• ARID1A-Y551fs*68 driver (AEL: 2,45) ;</li> <li>• ARID1A-Q1519fs*8 driver (AEL: 2,46) ;</li> <li>• ARID1A-F2141fs*59 driver (AEL: 2,49) ;</li> <li>• SMARCA4-Q1195H driver (AEL: 0,66)</li> </ul> <p>ARAF vad típus (AEL: 9,83),</p> <ul style="list-style-type: none"> <li>• ARAF-S157N driver (AEL: 0,33)</li> </ul> <p>KDM1A vad típus (AEL: 8,65),</p> <ul style="list-style-type: none"> <li>• ARID1A-Y551fs*68 driver (AEL: 2,45) ;</li> <li>• ARID1A-Q1519fs*8 driver (AEL: 2,46) ;</li> <li>• ARID1A-F2141fs*59 driver (AEL: 2,49) ;</li> <li>• SMARCA4-Q1195H driver (AEL: 0,66)</li> </ul> <p>YES1 vad típus (AEL: 7,92),</p> <ul style="list-style-type: none"> <li>• ARID1A-F2141fs*59 driver (AEL: 2,49) ;</li> <li>• ARID1A-Q1519fs*8 driver (AEL: 2,46) ;</li> <li>• ARID1A-Y551fs*68 driver (AEL: 2,45)</li> </ul> <p>CD33 vad típus (AEL: 6,69),</p> <ul style="list-style-type: none"> <li>• TET2-L1276fs*24 driver (AEL: 1,71)</li> </ul> <p>ERBB4 vad típus (AEL: 6,32),</p> <ul style="list-style-type: none"> <li>• ERBB4-G1109S driver (AEL: 0,11)</li> </ul> <p>BRD4 vad típus (AEL: 3,86),</p> <ul style="list-style-type: none"> <li>• KMT2C-L4419P driver (AEL: 1,72)</li> </ul> <p>DOT1L vad típus (AEL: 2,98),</p> <ul style="list-style-type: none"> <li>• DNMT3A-Q110fs*14 driver (AEL: 1,08)</li> </ul> <p>LYN vad típus (AEL: 1,72),</p> <ul style="list-style-type: none"> <li>• CBL-E196fs*16 driver (AEL: 0,72)</li> </ul> <p>PRKACA vad típus (AEL: 1,33),</p> <ul style="list-style-type: none"> <li>• GNAS-A36V driver (AEL: 0,83)</li> </ul> <p>CHEK1 vad típus (AEL: 0,95),</p> <ul style="list-style-type: none"> <li>• CDK12-G1271fs*23 driver (AEL: 0,35) ;</li> <li>• CDK12-A1174S driver (AEL: 0,34)</li> </ul> <p>COX2 vad típus (AEL: 0,51)</p> <ul style="list-style-type: none"> <li>• ERBB4-G1109S driver (AEL: 0,11)</li> </ul>
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DAGANAT MOLEKULÁRIS PROFILJÁVAL POZITÍV KAPCSOLATBAN ÁLLÓ HATÓANYAGOK	DAGANAT MOLEKULÁRIS PROFILJÁVAL NEGATÍV KAPCSOLATBAN ÁLLÓ HATÓANYAGOK
<p><b>FORGALOMBAN LÉVŐ</b> 11 listázott hatóanyag (összesen 110)</p> <p>PEMBROLIZUMAB (liver - hepatocellular carcinoma [FDA]; bármely tumor - urothelial carcinoma [FDA+EMA]; gastric - adenocarcinoma [FDA]; cervix - bármely szövettan [FDA]; rectum - bármely szövettan [FDA+EMA]; endometrium - bármely szövettan [FDA]; skin - squamous cell carcinoma [FDA]; breast - bármely szövettan [FDA]; esophagus - squamous cell carcinoma [FDA]; bármely tumor - endometrioid carcinoma [FDA]; colon - bármely szövettan [FDA+EMA]; gastroesophageal junction - adenocarcinoma [FDA]; head-neck - squamous cell carcinoma [FDA+EMA]; bármely tumor - mediastinal B-cell lymphoma [FDA]; bármely tumor - renal cell carcinoma [FDA+EMA]; lung - non-small cell carcinoma [FDA+EMA]; bármely tumor - Hodgkin lymphoma [FDA+EMA]; bármely tumor - malignant melanoma [FDA+EMA]; lung - adenocarcinoma [FDA+EMA]; skin - Merkel cell carcinoma (MCC) [FDA] (AEL: 24592,91)</p> <ul style="list-style-type: none"> <li>PTEN-R130Q driver (AEL: -71,70) ;</li> <li>TMB-H driver (AEL: 796,72) ;</li> <li>MSI-H driver (AEL: 8467,85) ;</li> <li>PD-1 vad típus target (AEL: 9342,33)</li> </ul> <p>AVELUMAB (bladder - bármely szövettan [FDA+EMA]; ureter - bármely szövettan [FDA+EMA]; skin - Merkel cell carcinoma (MCC) [FDA+EMA]; bladder - urothelial carcinoma [FDA+EMA]; kidney - renal cell carcinoma [FDA+EMA] (AEL: 18562,43)</p> <ul style="list-style-type: none"> <li>TMB-H driver (AEL: 796,72) ;</li> <li>PD-L1 vad típus target (AEL: 9236,18) ;</li> <li>MSI-H driver (AEL: 8467,85)</li> </ul> <p>NIVOLUMAB (rectum - bármely szövettan [FDA]; bármely tumor - urothelial carcinoma [FDA+EMA]; kidney - renal cell carcinoma [FDA+EMA]; pleura - mesothelioma [FDA]; bármely tumor - malignant melanoma [FDA+EMA]; esophagus - squamous cell carcinoma [FDA+EMA]; colon - bármely szövettan [FDA]; head-neck - squamous cell carcinoma [FDA+EMA]; liver - hepatocellular carcinoma [FDA]; bone marrow - Hodgkin lymphoma [FDA+EMA]; lung - non-small cell carcinoma [FDA+EMA] (AEL: 18071,38)</p> <ul style="list-style-type: none"> <li>MSI-H driver (AEL: 8467,85) ;</li> <li>PD-1 vad típus target (AEL: 9342,33) ;</li> <li>PTEN-R130Q driver (AEL: -71,70)</li> </ul> <p>DOSTARLIMAB (bármely tumor - endometrioid carcinoma [EMA]; endometrium - bármely szövettan [EMA]) (AEL: 17837,38)</p> <ul style="list-style-type: none"> <li>MSI-H driver (AEL: 8467,85) ;</li> <li>PD-1 vad típus target (AEL: 9342,33)</li> </ul> <p>CEMPLIMAB (skin - basal cell carcinoma [FDA]; lung - squamous cell carcinoma [FDA]; lung - adenocarcinoma [FDA]; skin - squamous cell carcinoma [FDA+EMA] (AEL: 9342,43)</p> <ul style="list-style-type: none"> <li>PD-1 vad típus target (AEL: 9342,33)</li> </ul> <p>DURVALUMAB (lung - non-small cell carcinoma [FDA+EMA]; lung - small cell carcinoma [FDA+EMA]; bármely tumor - urothelial carcinoma [FDA]) (AEL: 9290,58)</p> <ul style="list-style-type: none"> <li>PD-L1 vad típus target (AEL: 9236,18)</li> </ul> <p>ATEZOLIZUMAB (bármely tumor - urothelial carcinoma [FDA+EMA]; liver - hepatocellular carcinoma [FDA+EMA]; bármely tumor - malignant melanoma [FDA]; lung - small cell carcinoma [FDA+EMA]; lung - non-small cell carcinoma [FDA+EMA]; breast - bármely szövettan [FDA+EMA] (AEL: 9252,06)</p> <ul style="list-style-type: none"> <li>PD-L1 vad típus target (AEL: 9236,18)</li> </ul> <p>IPILIMUMAB (pleura - mesothelioma [FDA]; rectum - bármely szövettan [FDA]; lung - adenocarcinoma [FDA+EMA]; skin - malignant melanoma [FDA+EMA]; kidney - renal cell carcinoma [FDA+EMA]; colon - bármely szövettan [FDA]; liver - hepatocellular carcinoma [FDA] (AEL: 9229,47)</p> <ul style="list-style-type: none"> <li>CTLA4 vad típus target (AEL: 9223,61)</li> </ul> <p>PALBOCICLIB (breast - bármely szövettan [FDA+EMA]) (AEL: 2965,88)</p> <ul style="list-style-type: none"> <li>CDK6 vad típus target (AEL: 578,58) ;</li> <li>CDK4 vad típus target (AEL: 578,58) ;</li> <li>ESR1 protein overexpression driver (AEL: 578,13)</li> </ul> <p>LETROZOLE (breast - bármely szövettan [FDA]) (AEL: 2819,30)</p> <ul style="list-style-type: none"> <li>ESR1 vad típus target (AEL: 960,24) ;</li> <li>ESR1 protein overexpression driver (AEL: 578,13)</li> </ul>	<p><b>FORGALOMBAN LÉVŐ</b> 10 listázott hatóanyag (összesen 37)</p> <p>5-FLUOROURACIL (pancreas - bármely szövettan [FDA]; breast - bármely szövettan [FDA]; colon - bármely szövettan [FDA]; rectum - bármely szövettan [FDA]; gastric - bármely szövettan [FDA]) (AEL: -8691,35)</p> <ul style="list-style-type: none"> <li>CBL-E196fs*16 driver (AEL: 0,72) ;</li> <li>MSI-H driver (AEL: -8467,85) ;</li> <li>PIK3CA-E81K driver (AEL: -37,22)</li> </ul> <p>CISPLATIN (AEL: -8607,70)</p> <ul style="list-style-type: none"> <li>RECQL4-L339fs*20 driver (AEL: 10,28) ;</li> <li>CDK12-A1174S driver (AEL: 0,34) ;</li> <li>ARID2-D1758G driver (AEL: 0,41) ;</li> <li>CDK12-G1271fs*23 driver (AEL: 0,35) ;</li> <li>MSI-H driver (AEL: -8467,85) ;</li> <li>NSD1-F1799fs*22 driver (AEL: 0,45) ;</li> <li>IGF2R-D1317fs*5 driver (AEL: -0,28) ;</li> <li>NSD1-M1262fs*43 driver (AEL: 0,46) ;</li> <li>IGF2R-W53R driver (AEL: -0,26)</li> </ul> <p>CAPECITABINE (rectum - bármely szövettan [FDA]; breast - bármely szövettan [FDA]; colon - bármely szövettan [FDA]) (AEL: -8528,25)</p> <ul style="list-style-type: none"> <li>MSI-H driver (AEL: -8467,85)</li> </ul> <p>OXALIPLATIN (rectum - bármely szövettan [FDA]; colon - bármely szövettan [FDA]) (AEL: -8528,25)</p> <ul style="list-style-type: none"> <li>MSI-H driver (AEL: -8467,85)</li> </ul> <p>CETUXIMAB (colon - bármely szövettan [FDA+EMA]; head-neck - squamous cell carcinoma [FDA+EMA]; rectum - bármely szövettan [FDA+EMA]) (AEL: -557,65)</p> <ul style="list-style-type: none"> <li>CDH1-I594fs*19 driver (AEL: -13,12) ;</li> <li>EGFR vad típus target (AEL: -203,82) ;</li> <li>PIK3CA-E81K driver (AEL: -37,22) ;</li> <li>PTEN-R130Q driver (AEL: -71,70) ;</li> <li>FBXW7-R479Q driver (AEL: -64,84)</li> </ul> <p>PANITUMUMAB (colon - bármely szövettan [FDA+EMA]; rectum - bármely szövettan [FDA+EMA]) (AEL: -518,57)</p> <ul style="list-style-type: none"> <li>CDH1-I594fs*19 driver (AEL: -13,12) ;</li> <li>PIK3CA-E81K driver (AEL: -37,22) ;</li> <li>EGFR vad típus target (AEL: -203,82) ;</li> <li>PTEN-R130Q driver (AEL: -71,70) ;</li> <li>FBXW7-R479Q driver (AEL: -64,84)</li> </ul> <p>GEFITINIB (lung - squamous cell carcinoma [FDA+EMA]; lung - adenocarcinoma [FDA+EMA]; lung - non-small cell carcinoma [FDA+EMA]) (AEL: -350,97)</p> <ul style="list-style-type: none"> <li>FBXW7-R479Q driver (AEL: -64,84) ;</li> <li>CIC-R507C driver (AEL: -2,69) ;</li> <li>PTEN-R130Q driver (AEL: -71,70) ;</li> <li>EGFR vad típus target (AEL: -203,82)</li> </ul> <p>NERATINIB (breast - bármely szövettan [FDA+EMA]) (AEL: -320,50)</p> <ul style="list-style-type: none"> <li>ERBB2 vad típus target (AEL: -116,68) ;</li> <li>EGFR vad típus target (AEL: -203,82)</li> </ul> <p>AFATINIB (lung - squamous cell carcinoma [FDA+EMA]; lung - non-small cell carcinoma [FDA+EMA]; lung - adenocarcinoma [FDA+EMA]) (AEL: -320,26)</p> <ul style="list-style-type: none"> <li>EGFR vad típus target (AEL: -203,82) ;</li> <li>ERBB2 vad típus target (AEL: -116,68)</li> </ul> <p>ERLOTINIB (pancreas - bármely szövettan [FDA+EMA]; lung - non-small cell carcinoma [FDA+EMA]; lung - adenocarcinoma [FDA+EMA]; lung - squamous cell carcinoma [FDA+EMA]) (AEL: -252,69)</p> <ul style="list-style-type: none"> <li>PIK3CA-E81K driver (AEL: -37,22) ;</li> <li>PIK3CB-L1049R driver (AEL: -8,87) ;</li> <li>CIC-R507C driver (AEL: -2,69) ;</li> <li>EGFR vad típus target (AEL: -203,82)</li> </ul>

DAGANAT MOLEKULÁRIS PROFILJÁVAL POZITÍV KAPCSOLATBAN ÁLLÓ HATÓANYAGOK	DAGANAT MOLEKULÁRIS PROFILJÁVAL NEGATÍV KAPCSOLATBAN ÁLLÓ HATÓANYAGOK
<p>LENVATINIB (endometrium - bármely szövettan [FDA]; liver - hepatocellular carcinoma [FDA+EMA]; bármely tumor - endometrioid adenocarcinoma [FDA]; kidney - renal cell carcinoma [FDA+EMA]; thyroid - bármely szövettan [FDA+EMA]) (AEL: 42,96)</p> <ul style="list-style-type: none"> <li>RET vad típus target (AEL: 13,63) ;</li> <li>PDGFRB vad típus target (AEL: 13,63) ;</li> <li>FGFR1 vad típus target (AEL: 13,63)</li> </ul>	
<p><b>KLINIKAI FEJLESZTÉS ALATT</b> 10 listázott hatóanyag (összesen 239)</p> <p>ENVAFOLIMAB (AEL: 17714,03)</p> <ul style="list-style-type: none"> <li>PD-L1 vad típus target (AEL: 9236,18) ;</li> <li>MSI-H driver (AEL: 8467,85)</li> </ul> <p>camrelizumab (AEL: 9343,22)</p> <ul style="list-style-type: none"> <li>PD-1 vad típus target (AEL: 9342,33)</li> </ul> <p>TISLELIZUMAB (AEL: 9342,81)</p> <ul style="list-style-type: none"> <li>PD-1 vad típus target (AEL: 9342,33)</li> </ul> <p>SINTILIMAB (AEL: 9342,61)</p> <ul style="list-style-type: none"> <li>PD-1 vad típus target (AEL: 9342,33)</li> </ul> <p>GEPTANOLIMAB (AEL: 9342,53)</p> <ul style="list-style-type: none"> <li>PD-1 vad típus target (AEL: 9342,33)</li> </ul> <p>TORIPALIMAB (AEL: 9342,33)</p> <ul style="list-style-type: none"> <li>PD-1 vad típus target (AEL: 9342,33)</li> </ul> <p>ABBV-181 (AEL: 9342,33)</p> <ul style="list-style-type: none"> <li>PD-1 vad típus target (AEL: 9342,33)</li> </ul> <p>CS1001 (AEL: 9236,44)</p> <ul style="list-style-type: none"> <li>PD-L1 vad típus target (AEL: 9236,18)</li> </ul> <p>BINTRAFUSP ALFA (AEL: 9236,18)</p> <ul style="list-style-type: none"> <li>PD-L1 vad típus target (AEL: 9236,18)</li> </ul> <p>PACMILIMAB (AEL: 9236,18)</p> <ul style="list-style-type: none"> <li>PD-L1 vad típus target (AEL: 9236,18)</li> </ul>	<p><b>KLINIKAI FEJLESZTÉS ALATT</b> 10 listázott hatóanyag (összesen 64)</p> <p>EPIRUBICIN (AEL: -8619,45)</p> <ul style="list-style-type: none"> <li>MSI-H driver (AEL: -8467,85)</li> </ul> <p>ALLITINIB (AEL: -320,50)</p> <ul style="list-style-type: none"> <li>EGFR vad típus target (AEL: -203,82) ;</li> <li>ERBB2 vad típus target (AEL: -116,68)</li> </ul> <p>AV-412 (AEL: -320,50)</p> <ul style="list-style-type: none"> <li>ERBB2 vad típus target (AEL: -116,68) ;</li> <li>EGFR vad típus target (AEL: -203,82)</li> </ul> <p>CUDC-101 (AEL: -320,50)</p> <ul style="list-style-type: none"> <li>ERBB2 vad típus target (AEL: -116,68) ;</li> <li>EGFR vad típus target (AEL: -203,82)</li> </ul> <p>PELITINIB (AEL: -320,50)</p> <ul style="list-style-type: none"> <li>ERBB2 vad típus target (AEL: -116,68) ;</li> <li>EGFR vad típus target (AEL: -203,82)</li> </ul> <p>TAK-285 (AEL: -320,50)</p> <ul style="list-style-type: none"> <li>EGFR vad típus target (AEL: -203,82) ;</li> <li>ERBB2 vad típus target (AEL: -116,68)</li> </ul> <p>EPERTINIB (AEL: -320,50)</p> <ul style="list-style-type: none"> <li>ERBB2 vad típus target (AEL: -116,68) ;</li> <li>EGFR vad típus target (AEL: -203,82)</li> </ul> <p>JNJ-26483327 (AEL: -314,18)</p> <ul style="list-style-type: none"> <li>ERBB4 vad típus target (AEL: 6,32) ;</li> <li>EGFR vad típus target (AEL: -203,82) ;</li> <li>ERBB2 vad típus target (AEL: -116,68)</li> </ul> <p>AEE788 (AEL: -203,82)</p> <ul style="list-style-type: none"> <li>EGFR vad típus target (AEL: -203,82)</li> </ul> <p>SAPITINIB (AEL: -203,82)</p> <ul style="list-style-type: none"> <li>EGFR vad típus target (AEL: -203,82)</li> </ul>

A hatóanyagok mellett megjelenő pontszámok a hatóanyagokra vonatkozó aggregált evidencia-szintet (AEL, aggregated evidence level) jelzik. Az AEL a tumor típusokat, molekuláris variánsokat, célpontokat és hatóanyagokat összekapcsoló evidenciák számát, tudományos hatását és klinikai relevanciáját reprezentálja. Az egyes evidencia relációk pontszámait az alapján normalizáljuk és súlyozzuk, hogy az egyes összefüggésekben leírt jellemzők milyen mértékben hasonlítanak a vizsgált beteg paramétereire. A hatóanyagok pontszámait a releváns, hatóanyagokat, tumor típusokat, drivereket és célpontokat összekapcsoló relációk (és azok AEL-jeinek) összegzésével számítjuk. A hatóanyagokat AEL szerinti csökkenő sorrendben listázzuk. ( Rövidítések: AEL - aggregált evidencia-szint, AF - allél frekvencia, TR: tumor arány )



## KLINIKAI VIZSGÁLATOK

Keresési Kritériumok

ÁLLAPOT: Not yet recruiting,Active recruiting

### AZONOSÍTÓ

NCT04269200

### LEÍRÁS

A Randomised, Multicentre, Double-blind, Placebo-controlled, Phase III Study of First-line Carboplatin and Paclitaxel in Combination With Durvalumab, Followed by Maintenance Durvalumab With or Without Olaparib in Patients With Newly Diagnosed Advanced or Recurrent Endometrial Cancer (DUO-E)

**Aktív, toboroz**

#### Vonal

1

#### Fázis

3

#### Hatóanyag(ok)

CARBOPLATIN, DURVALUMAB, DURVALUMAB, OLAPARIB, PACLITAXEL

#### Ország(ok)

Estonia, Germany, Hong Kong, Israel, Belgium, Russian Federation, India, Japan, Korea, Republic of, Lithuania, China, Mexico, Greece, Colombia, Hungary, Brazil, Singapore, Australia, Poland, Canada, United States

#### Allokáció

Randomizált

#### Maszkirozás

Kettős Vak

NCT03981796

A Phase 3, Randomized, Double-blind, Multicenter Study of Dostarlimab (TSR-042) Plus Carboplatin-paclitaxel Versus Placebo Plus Carboplatin-paclitaxel in Patients With Recurrent or Primary Advanced Endometrial Cancer (RUBY)

**Aktív, toboroz**

#### Vonal

1

#### Fázis

3

#### Hatóanyag(ok)

CARBOPLATIN, CARBOPLATIN, DOSTARLIMAB, PACLITAXEL, PACLITAXEL, PLACEBO

#### Ország(ok)

Norway, Germany, Finland, Israel, Belgium, Denmark, Italy, Greece, Ukraine, Hungary, Sweden, Czech Republic, Belarus, United Kingdom, Poland, Turkey, Netherlands, Canada, United States

#### Allokáció

Randomizált

#### Maszkirozás

Kettős Vak

NCT03603184

Phase III Double-blind Randomized Placebo Controlled Trial of Atezolizumab in Combination With Paclitaxel and Carboplatin in Women With Advanced/Recurrent Endometrial Cancer

**Aktív, toboroz**

#### Vonal

Adjuváns-1

#### Fázis

3

#### Hatóanyag(ok)

ATEZOLIZUMAB, CARBOPLATIN, CARBOPLATIN, PACLITAXEL, PACLITAXEL, PLACEBO

#### Ország(ok)

Germany, Sweden, Austria, Japan, Italy, United Kingdom, Spain

#### Allokáció

Randomizált

#### Maszkirozás

Kettős Vak

NCT04234113

A Multicenter Open-label Phase 1/1b Study to Evaluate the Safety and Preliminary Efficacy of SO-C101 as Monotherapy and in Combination With Pembrolizumab in Patients With Selected Advanced/Metastatic Solid Tumors

**Aktív, toboroz**

#### Vonal

Neoadjuváns-10

#### Fázis

1a-1b

#### Hatóanyag(ok)

PEMBROLIZUMAB, SO-C101, SO-C101

#### Ország(ok)

France, Spain, United States

#### Allokáció

Nem Randomizált

#### Maszkirozás

Egykaros Vizsgálat

**Aktív, toboroz**

#### Vonal

Neoadjuváns-10

#### Fázis

1a-1b

#### Hatóanyag(ok)

PEMBROLIZUMAB, SO-C101, SO-C101

#### Ország(ok)

#### Allokáció

#### Maszkirozás

## KLINIKAI VIZSGÁLATOK

	France, Spain, United States	Nem Randomizált	Egykaros Vizsgálat
	<b>Aktív, toboroz</b>		
<b>Vonal</b>	<b>Fázis</b>	<b>Hatóanyag(ok)</b>	
Neoadjuváns-10	1a-1b	PEMBROLIZUMAB, SO-C101, SO-C101	
<b>Ország(ok)</b>	<b>Allokáció</b>	<b>Maszkírozás</b>	
France, Spain, United States	Nem Randomizált	Egykaros Vizsgálat	
<b>Bekerülési Biomarker Kritérium</b>			
ERBB2 protein normál, ERBB2 protein lack of expression, ESR1 protein normál, ESR1 protein lack of expression, PGR protein lack of expression, PGR protein normál			
<b>NCT02628067</b>	A Clinical Trial of Pembrolizumab (MK-3475) Evaluating Predictive Biomarkers in Subjects With Advanced Solid Tumors (KEYNOTE 158)		
	<b>Aktív, toboroz</b>		
<b>Vonal</b>	<b>Fázis</b>	<b>Hatóanyag(ok)</b>	
1-10	2	PEMBROLIZUMAB	
<b>Ország(ok)</b>	<b>Allokáció</b>	<b>Maszkírozás</b>	
Norway, Germany, Taiwan, Province of China, Israel, Russian Federation, Japan, Denmark, South Africa, Korea, Republic of, Italy, Mexico, France, Colombia, Spain, Brazil, Australia, Philippines, United Kingdom, Netherlands, United States, Canada	N/A	Egykaros Vizsgálat	
<b>NCT03503786</b>	Carboplatin, Paclitaxel With or Without Avelumab in Advanced or Recurrent Endometrial Cancer (MITO END-3)		
	<b>Még nem toboroz</b>		
<b>Vonal</b>	<b>Fázis</b>	<b>Hatóanyag(ok)</b>	
1-10	2	AVELUMAB, CARBOPLATIN, CARBOPLATIN, PACLITAXEL, PACLITAXEL	
<b>Ország(ok)</b>	<b>Allokáció</b>	<b>Maszkírozás</b>	
Italy	Randomizált	Nyílt Jelölésű	

A klinikai vizsgálatok listáját a Realtime Oncology Molecular Treatment Calculator segítségével állítottuk elő. A klinikai vizsgálatok esetében a szűréshez a beteg klinikai és molekuláris profiljában szereplő paramétereket vetettük össze a rendszerben található klinikai vizsgálatok beválogatási és kizárási feltételeivel. A manuálisan beállított keresési feltételek nem feltétlenül tartalmazzak minden szűrés kritériumot. Az Oncompass Medicine a rendszerben szereplő klinikai vizsgálatokért és az adatok helyességéért nem vállal felelősséget, és nem garantálja a beteg bekerülését a listán szereplő klinikai vizsgálatokba.

## RÉSZLETES MOLEKULÁRIS PROFIL

### GENETIKAI VARIÁNSOK

ABCC2-K297FS\*14, ADGRB3-E227A, AKAP9-P1381L, AKAP9-R434W, ALK-M830L, ARAF-S157N, ARID1A-F2141FS\*59, ARID1A-Q1519FS\*8, ARID1A-Y551FS\*68, ARID2-D1758G, ATM-I1581FS\*20, ATM-S214FS\*16, ATP4A-V288FS\*70, BAZ2B-N2000S, BCORL1-D1109G, BCR-D1106N, CARD11-R404M, CARD11-R555FS\*45, CBL-E196FS\*16, CCNE1-S90A, CDC27-K319FS\*24, CDH1-I594FS\*19, CDK12-A1174S, CDK12-G1271FS\*23, CIC-R507C, CSMD3-S3630Y, CTCF-E691FS\*30, CTNNA1-496-1G>T, CTNNA1-Q26\*, CTNNA1-T41A, DDX11-S407R, DMD-R1957Q, DMD-S3343FS\*34, DNMT3A-Q110FS\*14, ELMO1-N65S, EPHA3-T115N, EPHA7-I473V, ERBB4-G1109S, ESRP1-S625G, FANCF-G357D, FAT1-L3946P, FAT1-M3869T, FAT1-S1782N, FAT3-Q2328K, FBXW7-R479Q, FH-A104T, GATA2-G273FS\*53, GATA4-P290S, GLI1-G162D, GNAS-A36V, GRM3-G24W, IGF2R-D1317FS\*5, IGF2R-W53R, IGSF10-N579D, IL2RG-R226C, JAK2-C68R, KDM5C-R68FS\*5, KEL-E383G, KMT2C-K339N, KMT2C-L4419P, LAMA2-R185C, MED12-R431L, MED13-W1662\*, MIER3-G366E, MRE11-R364\*, MST1R-P862FS\*9, NSD1-F1799FS\*22, NSD1-M1531FS\*43, OTOPI1-L104M, PAX3-P300T, PAX5-A322FS\*11, PIK3C2B-M1223L, PIK3CA-E81K, PIK3CB-L1049R, PMS1-G417FS\*6, PMS1-N489I, PPP2R2A-Y189\*, PREX2-S977L, PRF1-K282R, PTEN-R130Q, PTPN11-R386K, RAD51D-P65L, RECQL4-L339FS\*20, RPTOR-V1192I, SAMD9L-K21FS\*3, SCN11A-K491FS\*5, SCN11A-L1158P, SEC16A-P9L, SLC9A9-R6FS\*31, SLIT2-K904FS\*13, SLX4-P1004L, SMAD2-R410G, SMARCA4-Q1195H, SOX9-L60V, SYNE3-P559T, TAF1-R855C, TET2-L1276FS\*24, TGFB2-Q334H, THSD7B-P642A, TOP2A-A1437T, TP53BP1-H964R, TRIO-I957T, TRIO-L2277\*, TSC2-I475T, USP16-V809A, WNK2-P1381FS\*11, XRCC2-K267FS\*?, ZBED4-V241I, ZMYM3-C723F, ZRSR2-P383A

### VAD TÍPUSÚ GÉNEK

ABCB1, ABL1, ABL2, ABRAXAS1, ACVR1B, ACVRL1, AGTRAP, AIP, AKT1, AKT2, AKT3, AMER1, AMPH, APC, APEX1, AR, ARFRP1, ARID1B, ASXL1, ATP11B, ATP6VOD2, ATR, ATRX, AURKA, AURKB, AXIN1, AXIN2, AXL, B2M, BAP1, BARD1, BAX, BCL2, BCL2L1, BCL2L2, BCL6, BCL9, BCOR, BIM, BIRC2, BIRC3, BLM, BMPR1A, BRAF, BRCA1, BRCA2, BRD4, BRIP1, BTG1, BTK, BUB1B, CASP8, CASR, CBFB, CBLB, CBLC, CCDC178, CCDC6, CCND1, CCND2, CCND3, CD74, CD79A, CD79B, CDA, CDC73, CDK4, CDK6, CDK8, CDKN1A, CDKN1B, CDKN1C, CDKN2A, CDKN2B, CDKN2C, CEBPA, CEP57, CHD1, CHD2, CHD4, CHD7, CHEK1, CHEK2, CHIC2, CIT, CREBBP, CRKL, CRLF2, CSF1R, CSNK2A1, CTNNA1, CUBN, CUL3, CYLD, CYP19A1, CYP2A6, CYP2B6, CYP2C9, CYP2D6, DAXX, DCC, DCUN1D1, DDB2, DDR1, DDR2, DDX3X, DICER1, DIS3L2, DOT1L, DPH3, DPYD, DSE, ECT2L, EED, EGFR, EML4, EMSY, EP300, EPCAM, EPHA2, EPHA5, EPHB1, ERBB2, ERBB3, ERCC1, ERCC2, ERCC3, ERCC4, ERCC5, ERG, ERFF1, ESR1, ESR2, ETV6, EXOC2, EXT1, EXT2, EZH2, EZR, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCG, FANCI, FANCL, FANCM, FAS, FBXO11, FBXO32, FGF10, FGF14, FGF19, FGF23, FGF3, FGF4, FGF5, FGF6, FGF9, FGFR1, FGFR2, FGFR3, FGFR4, FLCN, FLT1, FLT3, FLT4, FN1, FOXA1, FOXL2, FOXO1, FOXO1, FOXO1, FRS2, FSTL5, FUBP1, FZD3, G6PD, GABRA6, GALNT17, GAS6, GATA1, GATA3, GATA6, GEN1, GID4, GNA11,

## RÉSZLETES MOLEKULÁRIS PROFIL

GNA13, GNAI2, GNAQ, GNAT2, GOPC, GPC3, GPR78, GREM1, GRIN2A, GRM8, GSK3B, GSTP1, GXYLT1, H3-3A, H3C2, HGF, HNF1A, HOXB13, HRAS, HSD3B1, HSP90AA1, HSPH1, IDH1, IDH2, IFITM1, IFITM3, IGF1R, IGF2, IKBKE, IKZF1, IKZF4, IL2RA, IL2RB, IL6, IL6ST, IL7R, INHBA, INPP4B, IRAK4, IRF2, IRF4, IRS2, ITCH, JAK1, JAK3, JUN, KAT6A, KDM4B, KDM5A, KDM6A, KDR, KEAP1, KIAA1549, KIF5B, KIT, KLF6, KLHL6, KMT2A, KMT2D, KNSTRN, KRAS, KREMEN1, LCK, LMO1, LPAR2, LRP1B, LRRK2, LTK, LYN, LZTR1, MAGI2, MAGI3, MAGOH, MAP2K1, MAP2K2, MAP2K4, MAP3K1, MAP3K4, MAP4K3, MAP7, MAPK1, MAPK3, MAS1L, MAX, MCL1, MDM2, MDM4, MEF2B, MEN1, MET, MITF, MLH1, MLLT3, MPL, MSH2, MSH3, MSH6, MTOR, MUC16, MUTYH, MYC, MYCL1, MYCN, MYD88, MYO18A, MYO1B, NBN, NCOA2, NCOR1, NEK2, NF1, NF2, NFE2L2, NFKBIA, NIPA2, NKX2-1, NKX2-8, NKX3-1, NOTCH1, NOTCH2, NOTCH3, NPM1, NRAS, NRCAM, NRG1, NRP2, NTS5C2, NTRK1, NTRK2, NTRK3, NUP93, OR5L1, PAK3, PALB2, PAX7, PBRM1, PCBP1, PCGF2, PD-L1, PDGFRA, PDGFRB, PDK1, PDL2, PDZRN3, PHF6, PHOX2B, PIK3CD, PIK3CG, PIK3R1, PIK3R2, PLCG2, PLEKHS1, PMS2, PNP, POLD1, POLE, POT1, PPARG, PPML, PPP2R1A, PRDM1, PRKAR1A, PRKCI, PRKDC, PRKN, PRPF40B, PRSS8, PSMB1, PSMB2, PSMB5, PSMD1, PSMD2, PTCH1, PTGFR, PTPN12, PTPRD, QKI, RAC1, RAC2, RAD21, RAD50, RAD51, RAD51B, RAD51C, RAD54L, RAF1, RANBP2, RARA, RARB, RARG, RB1, RBM10, RECQL5, RET, RHBDF2, RHEB, RHOA, RICTOR, RIT1, RNF43, ROS1, RPS6KB1, RUNX1, RUNX1T1, RXRA, RXRB, RXRG, S1PR2, SBDS, SDC4, SDHA, SDHAF2, SDHB, SDHC, SDHD, SEPT9, SETBP1, SETD2, SF1, SF3A1, SF3B1, SH2B3, SHH, SHOC2, SLC22A1, SLC22A2, SLC31A1, SLC34A2, SLC45A3, SLC7A8, SLC01B1, SMAD3, SMAD4, SMARCB1, SMARCE1, SMC1A, SMC3, SMO, SNCAIP, SOCS1, SOS1, SOX10, SOX2, SPEG, SPEN, SPOP, SPRED1, SPTA1, SRC, SRSF2, SSTR1, STAG2, STAT3, STAT4, STK11, SUFU, SUZ12, SYK, TACC3, TAS2R38, TBX20, TBX3, TCERG1, TCF7L2, TENT5C, TERC, TERT, TFG, TIAF1, TMEM127, TMPRSS2, TNFAIP3, TNFRSF14, TOP1, TP53, TP63, TPM3, TPM4, TPMT, TRAF5, TRRAP, TSC1, TSHR, TYK2, U2AF1, U2AF2, UBR3, UGT1A1, USP25, VCL, VEGFA, VHL, WDCP, WEE1, WISP3, WRN, WT1, WWP1, XPA, XPC, XPO1, YAP1, YES1, ZBTB2, ZFH3, ZIC3, ZNF2, ZNF217, ZNF226, ZNF473, ZNF595, ZNF703

### FISH/CNA/IHC POZITÍV GÉNEK

ESR1 PROTEIN OVEREXPRESSION

### FISH/CNA/IHC NEGATÍV GÉNEK

ABL1 TRANSLOCATION ABSENCE, ALK TRANSLOCATION ABSENCE, BCR TRANSLOCATION ABSENCE, BRAF TRANSLOCATION ABSENCE, BRD4 TRANSLOCATION ABSENCE, CD74 TRANSLOCATION ABSENCE, EGFR TRANSLOCATION ABSENCE, FGFR1 TRANSLOCATION ABSENCE, FGFR2 TRANSLOCATION ABSENCE, FGFR3 TRANSLOCATION ABSENCE, KIF5B TRANSLOCATION ABSENCE, MET TRANSLOCATION ABSENCE, NRG1 TRANSLOCATION ABSENCE, NTRK1 TRANSLOCATION ABSENCE, NTRK2 TRANSLOCATION ABSENCE, NTRK3 TRANSLOCATION ABSENCE, PD-L1 PROTEIN NORMÁL, RAF1 TRANSLOCATION ABSENCE, RARA TRANSLOCATION ABSENCE, RET TRANSLOCATION ABSENCE, ROS1 TRANSLOCATION ABSENCE, TACC1 TRANSLOCATION ABSENCE, TACC3 TRANSLOCATION ABSENCE

## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

### MOLEKULÁRIS ALTERÁCIÓK

MSI-H driver (AEL: 8467,85, AF/TR: NA/90%, NA/80%),  
 TMB-H driver (AEL: 796,72, AF/TR: NA/90%),  
 ER protein overexpression driver (AEL: 578,13, AF/TR: NA/80%),  
 PTEN-R130Q driver (AEL: 71,70, AF/TR: 68.98%/90%),  
 FBXW7-R479Q driver (AEL: 64,84, AF/TR: 30.4%/90%),  
 CTNNB1-T41A driver (AEL: 41,88, AF/TR: 24.8%/90%),  
 PIK3CA-E81K driver (AEL: 37,22, AF/TR: 5.64%/90%),  
 ATM-S214fs\*16 driver (AEL: 15,61, AF/TR: 6.3%/90%),  
 CDH1-I594fs\*19 driver (AEL: 13,12, AF/TR: 6.14%/90%),  
 RECQL4-L339fs\*20 driver (AEL: 10,28, AF/TR: 8.7%/90%),  
 MRE11-R364\* driver (AEL: 10,07, AF/TR: 21.43%/90%),  
 IL2RG-R226C driver (AEL: 10,00, AF/TR: 4.57%/90%),  
 PIK3CB-L1049R driver (AEL: 8,87, AF/TR: 18.24%/90%),  
 ATM-I1581fs\*20 driver (AEL: 5,61, AF/TR: 3.28%/90%),  
 CIC-R507C VUS, driver gén (AEL: 2,69, AF/TR: 5.32%/90%),  
 TSC2-I475T VUS, driver gén (AEL: 2,68, AF/TR: 34.48%/90%),  
 CTNNB1-Q26\* VUS, driver gén (AEL: 2,67, AF/TR: 3.35%/90%),  
 CTNNB1-496-1G>T VUS, driver gén (AEL: 2,67, AF/TR: 3.88%/90%),  
 ALK-M830L VUS, driver gén (AEL: 2,50, AF/TR: 3.32%/90%),  
 ARID1A-F2141fs\*59 driver (AEL: 2,48, AF/TR: 4.43%/90%),  
 ARID1A-Q1519fs\*8 driver (AEL: 2,46, AF/TR: 4.36%/90%),  
 ARID1A-Y551fs\*68 driver (AEL: 2,45, AF/TR: 10.56%/90%),  
 RAD51D-P65L VUS, driver gén (AEL: 1,91, AF/TR: 6.6%/90%),  
 KMT2C-L4419P VUS, driver gén (AEL: 1,72, AF/TR: 29.12%/90%),  
 TET2-L1276fs\*24 VUS, driver gén (AEL: 1,71, AF/TR: 12.38%/90%),  
 FAT1-S1782N VUS, driver gén (AEL: 1,46, AF/TR: 3.97%/90%),  
 FAT1-L3946P VUS, driver gén (AEL: 1,46, AF/TR: 6.35%/90%),  
 FAT1-M3869T VUS, driver gén (AEL: 1,46, AF/TR: 5.84%/90%),  
 SOX9-L60V VUS, driver gén (AEL: 1,12, AF/TR: 48.82%/90%),  
 DNMT3A-Q110fs\*14 driver (AEL: 1,08, AF/TR: 23.53%/90%),  
 PTPN11-R386K VUS, driver gén (AEL: 1,03, AF/TR: 3.87%/90%),  
 GNAS-A36V VUS, driver gén (AEL: 0,83, AF/TR: 3.58%/90%),  
 CBL-E196fs\*16 driver (AEL: 0,72, AF/TR: 25.24%/90%),  
 SMARCA4-Q1195H driver (AEL: 0,66, AF/TR: 4.5%/90%),  
 FH-A104T driver (AEL: 0,64, AF/TR: 6.76%/90%),  
 MED12-R431L VUS, driver gén (AEL: 0,60, AF/TR: 4.64%/90%),  
 EPHA7-I473V VUS, driver gén (AEL: 0,54, AF/TR: 5.51%/90%),  
 TGFB2-Q334H VUS, driver gén (AEL: 0,50, AF/TR: 5.74%/90%),  
 KDM5C-R68fs\*5 VUS, driver gén (AEL: 0,50, AF/TR: 3.12%/90%),  
 CARD11-R555fs\*45 driver (AEL: 0,46, AF/TR: 7.38%/90%),  
 NSD1-M1531fs\*43 driver (AEL: 0,46, AF/TR: 4.37%/90%),  
 NSD1-F1799fs\*22 driver (AEL: 0,45, AF/TR: 3.05%/90%),  
 XRCC2-K267fs\*? driver (AEL: 0,45, AF/TR: 6.13%/90%),  
 CARD11-R404M VUS, driver gén (AEL: 0,41, AF/TR: 3.84%/90%),  
 ARID2-D1758G VUS, driver gén (AEL: 0,41, AF/TR: 6.79%/90%),

### INDIREKT CÉLPONT GÉNEK

PD-1 vad típus (AEL: 9342,33),  
 • MSI-H driver (AEL: 8467,85) ;  
 • TMB-H driver (AEL: 796,72) ;  
 • JAK2-C68R driver (AEL: -0,27) ;  
 • PTEN-R130Q driver (AEL: -1,70) ;  
 • EPHA7-I473V driver (AEL: 0,55)

CD274 vad típus (AEL: 9236,18),  
 • ARID1A-Y551fs\*68 driver (AEL: 2,45) ;  
 • ARID1A-Q1519fs\*8 driver (AEL: 2,46) ;  
 • ARID1A-F2141fs\*59 driver (AEL: 2,49) ;  
 • TET2-L1276fs\*24 driver (AEL: -1,71) ;  
 • CTNNB1-496-1G>T driver (AEL: -2,67) ;  
 • EPHA7-I473V driver (AEL: 0,55) ;  
 • TMB-H driver (AEL: 796,72) ;  
 • CTNNB1-T41A driver (AEL: -41,88) ;  
 • CTNNB1-Q26\* driver (AEL: -2,67) ;  
 • MSI-H driver (AEL: 8467,85)

CTLA4 vad típus (AEL: 9223,61),  
 • EPHA7-I473V driver (AEL: 0,55) ;  
 • CTNNB1-T41A driver (AEL: -41,88) ;  
 • TMB-H driver (AEL: 796,72) ;  
 • CTNNB1-Q26\* driver (AEL: -2,67) ;  
 • CTNNB1-496-1G>T driver (AEL: -2,67) ;  
 • MSI-H driver (AEL: 8467,85)

WRN vad típus (AEL: 8475,55),  
 • MSI-H driver (AEL: 8467,85)

IDO1 vad típus (AEL: 8470,75),  
 • MSI-H driver (AEL: 8467,85)

LAG3 vad típus (AEL: 8470,75),  
 • MSI-H driver (AEL: 8467,85)

ESR1 vad típus (AEL: 960,24),  
 • PIK3CA-E81K driver (AEL: -37,22) ;  
 • ER protein overexpression driver (AEL: 578,13) ;  
 • PTEN-R130Q driver (AEL: -71,70) ;  
 • KMT2C-L4419P driver (AEL: -1,72)

MTOR vad típus (AEL: 823,83),  
 • PIK3CB-L1049R driver (AEL: 8,87) ;

## RÉSZLETES MOLEKULÁRIS PROFIL

CDK12-G1271fs\*23 driver (AEL: 0,35, AF/TR: 4.78%/90%),  
 CDK12-A1174S VUS, driver gén (AEL: 0,34, AF/TR: 3.78%/90%),  
 ARAF-S157N VUS, driver gén (AEL: 0,33, AF/TR: 4.09%/90%),  
 TP53BP1-H964R VUS, driver gén (AEL: 0,30, AF/TR: 49.19%/90%),  
 IGF2R-D1317fs\*5 driver (AEL: 0,28, AF/TR: 5.18%/90%),  
 JAK2-C68R VUS, driver gén (AEL: 0,27, AF/TR: 3.07%/90%),  
 IGF2R-W53R VUS, driver gén (AEL: 0,26, AF/TR: 6.97%/90%),  
 PAX5-A322fs\*11 driver (AEL: 0,23, AF/TR: 3.21%/90%),  
 FANCF-G357D VUS, driver gén (AEL: 0,18, AF/TR: 4.98%/90%),  
 CTCF-E691fs\*30 driver (AEL: 0,14, AF/TR: 6.95%/90%),  
 ESRP1-S625G VUS, driver gén (AEL: 0,13, AF/TR: 4.24%/90%),  
 EPHA3-T115N VUS, driver gén (AEL: 0,12, AF/TR: 32.69%/90%),  
 PPP2R2A-Y189\* VUS, driver gén (AEL: 0,12, AF/TR: 3.23%/90%),  
 ERBB4-G1109S VUS, driver gén (AEL: 0,11, AF/TR: 42.02%/90%),  
 WNK2-P1381fs\*11 VUS, driver gén (AEL: 0,11, AF/TR: 3.01%/90%),  
 LAMA2-R185C VUS, driver gén (AEL: 0,10, AF/TR: 5.17%/90%),  
 DMD-S3343fs\*34 driver (AEL: 0,10, AF/TR: 6.36%/90%),  
 DMD-R1957Q VUS, driver gén (AEL: 0,10, AF/TR: 3%/90%),  
 PMS1-N489I VUS, driver gén (AEL: 0,10, AF/TR: 48.43%/90%),  
 PMS1-G417fs\*6 VUS, driver gén (AEL: 0,10, AF/TR: 27.58%/90%),  
 ZRSR2-P383A driver (AEL: 0,10, AF/TR: 47.59%/90%),  
 ZMYM3-C723F VUS, driver gén (AEL: 0,09, AF/TR: 29.17%/90%),  
 SLX4-P1004L VUS, driver gén (AEL: 0,08, AF/TR: 7.06%/90%),  
 CSMD3-S3630Y VUS, driver gén (AEL: 0,03, AF/TR: 5.43%/90%),  
 SCN11A-K491fs\*5 driver (AEL: 0,03, AF/TR: 7.23%/90%),  
 SAMD9L-K21fs\*3 driver (AEL: 0,02, AF/TR: 5.68%/90%),  
 TAF1-R855C VUS, driver gén (AEL: 0,02, AF/TR: 33.72%/90%),  
 SLIT2-K904fs\*13 VUS, driver gén (AEL: 0,01, AF/TR: 3.43%/90%),  
 CDC27-K319fs\*24 VUS, driver gén (AEL: 0,01, AF/TR: 7.52%/90%),  
 DDX11-S407R ellentmondásos driver (AEL: 0,00, AF/TR: 5.76%/90%),  
 BAZ2B-N2000S ellentmondásos driver (AEL: 0,00, AF/TR: 46.73%/90%),  
 THSD7B-P642A ellentmondásos driver (AEL: 0,00, AF/TR: 6.64%/90%),  
 GLI1-G162D ellentmondásos driver (AEL: 0,00, AF/TR: 5.54%/90%),  
 ADGRB3-E227A ellentmondásos driver (AEL: 0,00, AF/TR: 5.26%/90%),  
 ZBED4-V241I ellentmondásos driver (AEL: 0,00, AF/TR: 48.75%/90%),  
 RPTOR-V1192I ellentmondásos driver (AEL: 0,00, AF/TR: 6.16%/90%),  
 SMAD2-R410G ellentmondásos driver (AEL: 0,00, AF/TR: 6.6%/90%),  
 SEC16A-P9L ellentmondásos driver (AEL: 0,00, AF/TR: 10.95%/90%),  
 GATA2-G273fs\*53 ellentmondásos driver (AEL: 0,00, AF/TR: 3.59%/90%),  
 TRIO-L2277\* ellentmondásos driver (AEL: 0,00, AF/TR: 3.86%/90%),  
 AKAP9-P1381L ellentmondásos driver (AEL: 0,00, AF/TR: 8.82%/90%),  
 AKAP9-R434W ellentmondásos driver (AEL: 0,00, AF/TR: 11.13%/90%),  
 OTOPI-L104M ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 33.9%/90%),  
 ELMO1-N65S ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 3.39%/90%),  
 FAT3-Q2328K ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 3.17%/90%),  
 TRIO-I957T ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 6.64%/90%),  
 GATA4-P290S ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 11.31%/90%),  
 PAX3-P300T ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 5.29%/90%),  
 IGSF10-N579D ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 46.82%/90%),  
 SYNE3-P559T ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 46.3%/90%),  
 PRF1-K282R ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 43.78%/90%),  
 ABCC2-K297fs\*14 ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 11.66%/90%),  
 MED13-W1662\* ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 5.16%/90%),  
 MIER3-G366E ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 3.86%/90%),  
 CCNE1-S90A ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 3.49%/90%),  
 ATP4A-V288fs\*70 ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 9.06%/90%),  
 TOP2A-A1437T ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 9.06%/90%),  
 SLC9A9-R6fs\*31 ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 21.06%/90%),  
 KEL-E383G ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 49.81%/90%),  
 BCORL1-D1109G ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 3.15%/90%),

- PIK3CA-E81K driver (AEL: 37,22) ;
- PTPN11-R386K driver (AEL: 1,03) ;
- FBXW7-R479Q driver (AEL: 64,84) ;
- ER protein overexpression driver (AEL: 578,13) ;
- CDH1-I594fs\*19 driver (AEL: 13,12) ;
- TSC2-I475T driver (AEL: 2,68) ;
- PTEN-R130Q driver (AEL: 71,70)

PIK3CA vad típus (AEL: 777,65),

- PTEN-R130Q driver (AEL: -71,70) ;
- PIK3CA-E81K driver (AEL: 37,22) ;
- CDH1-I594fs\*19 driver (AEL: 13,12) ;
- ER protein overexpression driver (AEL: 578,13)

AKT1 vad típus (AEL: 724,59),

- ARID1A-Y551fs\*68 driver (AEL: 2,45) ;
- PIK3CB-L1049R driver (AEL: 8,87) ;
- ARID1A-Q1519fs\*8 driver (AEL: 2,46) ;
- CDH1-I594fs\*19 driver (AEL: 13,12) ;
- PTEN-R130Q driver (AEL: 71,70) ;
- ER protein overexpression driver (AEL: 578,13) ;
- ARID1A-F2141fs\*59 driver (AEL: 2,49) ;
- PIK3CA-E81K driver (AEL: 37,22) ;
- PPP2R2A-Y189\* driver (AEL: 0,12)

CDK4 vad típus (AEL: 578,58),

- ER protein overexpression driver (AEL: 578,13)

CDK6 vad típus (AEL: 578,58),

- ER protein overexpression driver (AEL: 578,13)

PARP1 vad típus (AEL: 147,96),

- ATM-I1581fs\*20 driver (AEL: 5,61) ;
- RECQL4-L339fs\*20 driver (AEL: 10,28) ;
- ARID1A-Q1519fs\*8 driver (AEL: 2,46) ;
- CDK12-G1271fs\*23 driver (AEL: 0,35) ;
- DDX11-S407R driver (AEL: 0,00) ;
- ARID1A-Y551fs\*68 driver (AEL: 2,45) ;
- XRCC2-K267fs\*? driver (AEL: 0,45) ;
- PTEN-R130Q driver (AEL: 71,70) ;
- MRE11-R364\* driver (AEL: 10,07) ;
- ARID2-D1758G driver (AEL: 0,41) ;
- TP53BP1-H964R driver (AEL: -0,30) ;
- RAD51D-P65L driver (AEL: 1,91) ;
- ARID1A-F2141fs\*59 driver (AEL: 2,49) ;
- ZMYM3-C723F driver (AEL: 0,09) ;
- CDK12-A1174S driver (AEL: 0,34) ;
- SLX4-P1004L driver (AEL: 0,08) ;
- ATM-S214fs\*16 driver (AEL: 15,61)

PIK3CB vad típus (AEL: 119,54),

- CDH1-I594fs\*19 driver (AEL: 13,12) ;
- PTEN-R130Q driver (AEL: 71,70) ;
- PIK3CB-L1049R driver (AEL: 8,87)

ALK vad típus (AEL: 111,22),

- CDH1-I594fs\*19 driver (AEL: 13,12) ;
- ALK-M830L driver (AEL: 2,50)

CTNNB1 vad típus (AEL: 90,80),

- CTNNB1-496-1G>T driver (AEL: 2,67) ;
- PIK3CA-E81K driver (AEL: 37,22) ;
- CTNNB1-Q26\* driver (AEL: 2,67) ;
- CTNNB1-T41A driver (AEL: 41,88)

ATM vad típus (AEL: 72,55),

- PTEN-R130Q driver (AEL: 71,70)

NOTCH1 vad típus (AEL: 65,98),

- FBXW7-R479Q driver (AEL: 64,84)

MCL1 vad típus (AEL: 65,29),

- FBXW7-R479Q driver (AEL: 64,84)

TTK vad típus (AEL: 47,73),

- CTNNB1-Q26\* driver (AEL: 2,67) ;
- CTNNB1-496-1G>T driver (AEL: 2,67) ;
- CTNNB1-T41A driver (AEL: 41,88)

AKT2 vad típus (AEL: 38,33),

## RÉSZLETES MOLEKULÁRIS PROFIL

PIK3C2B-M1223L ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 25.77%/90%),  
 MST1R-P862fs\*9 ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 30.05%/90%),  
 SCN11A-L1158P ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 46.4%/90%),  
 USP16-V809A ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 29.57%/90%),  
 GRM3-G24W ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 4.43%/90%),  
 KMT2C-K339N nem driver (AEL: -2,03, AF/TR: 9.59%/90%),  
 BCR-D1106N nem driver (AEL: -4,98, AF/TR: 12.6%/90%),  
 PREX2-S977L nem driver (AEL: -4,99, AF/TR: 46.36%/90%)

- PIK3CA-E81K driver (AEL: 37,22)
- AKT3 vad típus (AEL: 37,58),
  - PIK3CA-E81K driver (AEL: 37,22)
- JAK2 vad típus (AEL: 25,07),
  - JAK2-C68R driver (AEL: 0,27) ;
  - CDH1-I594fs\*19 driver (AEL: 13,12) ;
  - CBL-E196fs\*16 driver (AEL: 0,72)
- ATR vad típus (AEL: 24,40),
  - ATM-S214fs\*16 driver (AEL: 15,61) ;
  - ATM-I1581fs\*20 driver (AEL: 5,61)
- ABL1 vad típus (AEL: 16,41),
  - CDH1-I594fs\*19 driver (AEL: 13,12) ;
  - FH-A104T driver (AEL: 0,64)
- JAK1 vad típus (AEL: 16,25),
  - CBL-E196fs\*16 driver (AEL: 0,72) ;
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- ROS1 vad típus (AEL: 15,62),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- AURKC vad típus (AEL: 14,17),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- AURKB vad típus (AEL: 14,17),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- PIK3CG vad típus (AEL: 14,17),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- AURKA vad típus (AEL: 14,17),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- PIK3CD vad típus (AEL: 14,17),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- PDGFRB vad típus (AEL: 13,63),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- BCL2 vad típus (AEL: 13,63),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- NTRK1 vad típus (AEL: 13,63),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- FGFR1 vad típus (AEL: 13,63),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- PDGFRA vad típus (AEL: 13,63),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- JAK3 vad típus (AEL: 13,63),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- SRC vad típus (AEL: 13,63),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- NPY5R vad típus (AEL: 13,63),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- CDK2 vad típus (AEL: 13,63),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- CDK1 vad típus (AEL: 13,63),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- RET vad típus (AEL: 13,63),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- GBF1 vad típus (AEL: 13,63),
  - CDH1-I594fs\*19 driver (AEL: 13,12)
- MET vad típus (AEL: 13,63),
  - CDH1-I594fs\*19 driver (AEL: 13,12)

## RÉSZLETES MOLEKULÁRIS PROFIL

	<p>HMGCR vad típus (AEL: 13,62),</p> <ul style="list-style-type: none"> <li>CDH1-I594fs*19 driver (AEL: 13,12)</li> </ul> <p>EZH2 vad típus (AEL: 13,55),</p> <ul style="list-style-type: none"> <li>ARID1A-Y551fs*68 driver (AEL: 2,45) ;</li> <li>ARID1A-Q1519fs*8 driver (AEL: 2,46) ;</li> <li>ARID1A-F2141fs*59 driver (AEL: 2,49) ;</li> <li>SMARCA4-Q1195H driver (AEL: 0,66)</li> </ul> <p>ARAF vad típus (AEL: 9,83),</p> <ul style="list-style-type: none"> <li>ARAF-S157N driver (AEL: 0,33)</li> </ul> <p>KDM1A vad típus (AEL: 8,65),</p> <ul style="list-style-type: none"> <li>ARID1A-Y551fs*68 driver (AEL: 2,45) ;</li> <li>ARID1A-Q1519fs*8 driver (AEL: 2,46) ;</li> <li>ARID1A-F2141fs*59 driver (AEL: 2,49) ;</li> <li>SMARCA4-Q1195H driver (AEL: 0,66)</li> </ul> <p>YES1 vad típus (AEL: 7,92),</p> <ul style="list-style-type: none"> <li>ARID1A-F2141fs*59 driver (AEL: 2,49) ;</li> <li>ARID1A-Q1519fs*8 driver (AEL: 2,46) ;</li> <li>ARID1A-Y551fs*68 driver (AEL: 2,45)</li> </ul> <p>CD33 vad típus (AEL: 6,69),</p> <ul style="list-style-type: none"> <li>TET2-L1276fs*24 driver (AEL: 1,71)</li> </ul> <p>ERBB4 vad típus (AEL: 6,32),</p> <ul style="list-style-type: none"> <li>ERBB4-G1109S driver (AEL: 0,11)</li> </ul> <p>BRD4 vad típus (AEL: 3,86),</p> <ul style="list-style-type: none"> <li>KMT2C-L4419P driver (AEL: 1,72)</li> </ul> <p>DOT1L vad típus (AEL: 2,98),</p> <ul style="list-style-type: none"> <li>DNMT3A-Q110fs*14 driver (AEL: 1,08)</li> </ul> <p>LYN vad típus (AEL: 1,72),</p> <ul style="list-style-type: none"> <li>CBL-E196fs*16 driver (AEL: 0,72)</li> </ul> <p>PRKACA vad típus (AEL: 1,33),</p> <ul style="list-style-type: none"> <li>GNAS-A36V driver (AEL: 0,83)</li> </ul> <p>CHEK1 vad típus (AEL: 0,95),</p> <ul style="list-style-type: none"> <li>CDK12-G1271fs*23 driver (AEL: 0,35) ;</li> <li>CDK12-A1174S driver (AEL: 0,34)</li> </ul> <p>COX2 vad típus (AEL: 0,51)</p> <ul style="list-style-type: none"> <li>ERBB4-G1109S driver (AEL: 0,11)</li> </ul>
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## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

### Mikroszatellita instabilitás (MSI-H) endometrium daganatban

A mikroszatellita vizsgálat a DNS hibajavító enzimek defektusának kimutatására alkalmas. A teszt során normál és daganatos szövetből származó izolált DNS-ben 5 biomarker instabilitását vizsgálják. Háromféle eredmény lehetséges: mikroszatellita stabilitás, alacsony és magas fokú mikroszatellita instabilitás (MSS, MSI-L és MSI-H).

Egy tanulmány szerint endometrium daganatok 15-25%-ban mutattak ki mikroszatellita instabilitást (1), míg egy másik tanulmányban ez az érték 25% (2) volt, ami a mikroszatellita instabilitás fontos szerepét jelzi a sporadikus endometrium daganatok kialakulásában (3). Az endometrium carcinomás betegek esetében a mikroszatellita instabilitás jelenléte kedvezőbb klinikai kimenetellel asszociált (4, 5). A tudományos irodalom szerint mikroszatellita instabil (MMR deficiens) daganatok esetén az immunterápiák hatékonysága nagyobb, mint mikroszatellita stabil daganatoknál (6, 7).

Az FDA törzskönyvezte a PEMBROLIZUMAB PD-1 gátló antitestet bármilyen szolid daganat esetén, ami MSI-H státuszú vagy MMR deficiens fenotípusú. Az EMA pozitív véleményben részesítette a DOSTARLIMAB (PD-1 inhibitor) törzskönyvezési beadványát rekurrens vagy előrehaladott MSI-H/dMMR endometrium carcinoma betegek kezelésére, akik platina alapú kemoterápián vagy azt követően progrediáltak.

Egy fázis II vizsgálatban a pembrolizumab kezelés 7 MMR deficiens nem colorectalis daganatos beteg körében 71%-os válaszadási arányt ért el. A vizsgálatban két endometrium carcinomás beteg vett részt, egyiküknél teljes választ, a másik betegnél részleges választ írtak el (6). Egy másik vizsgálatban 12 különböző tumortípusú, MMR deficiens betegek vettek részt. A pembrolizumab kezelésre a válaszadási arány 53% volt, a

## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

betegek 21%-ánál teljes választ írtak le. A medián progressziómentes túlélést (progression-free survival, PFS) és teljes túlélést (overall survival, OS) nem érték el az adatok publikálásáig. A vizsgálatban 15 endometrium tumoros beteg vett részt, akik közül 3 betegnél teljes választ, 5 betegnél részleges választ és 3 betegnél stabil betegséget írtak le (8).

Egy klinikai vizsgálat előzetes eredményei szerint a pembrolizumab + lenvatinib kombinációs kezelés 36,7%-os válaszadási arányt ért el MSI státusz szerint nem szelektált endometrium carcinomás betegek között. A 3 MSI-H beteg közül egynél részleges tumorválaszt, egynél stabil betegséget és egynél progresszív betegséget írtak le (9). A kombinációs kezelés nem MSI-H vagy MMR deficiens endometrium daganatos betegek számára FDA törzskönyvezett.

A dostarlimab (TSR-042, PD-1 gátló) MSI-H endometrium carcinomás betegek körében 50%-os válaszadási arányt ért el (10).

Az fázis I GARNET vizsgálatban a DOSTARLIMAB (TSR-042, PD-1 inhibitor) hatékonyságát vizsgálták endometrium carcinoma indikációkban. Előzetesen kezelt, rekurrens vagy előrehaladott EC betegek (n=110) esetében a dostarlimab MSI-H státusz esetén 50,0%-os, MSS státusz esetén 19,1%-os ORR-t eredményezett (teljes ORR: 27,7%) (10).

A dMMR (n=126) és az MMR proficiens (n=145) státuszú betegeket vizsgáló kohortokban az ORR 44,7% és 13,4%, a betegség kontroll ráta (DCR) 57,3% és 35,2%, és a 18 hónapos válaszadási idő ráta 79,2% és 61,3% volt (11). A DOSTARLIMAB törzskönyvi jóváhagyása ennek a vizsgálatnak az eredményein alapult.

Az avelumab (PD-L1 gátló) kezelés MMR deficiens vagy POLE mutáns endometrium carcinomás betegek között 26,7%-os válaszadási arányt eredményezett, és a betegek 40%-a ért el legalább 6 hónapos PFS-t (12).

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### A tumor mutational burden (TMB) vizsgálat eredménye

A vizsgált mintában a szekvenencia analízis (NGS) során kapott 1 megabázisra vonatkozó mutációk száma (TMB) 32,19. Az adatbázisunkban lévő kalkulált TMB értékek (n=605) eloszlása alapján az eseteink 100%-ában ennél alacsonyabb TMB értéket kaptunk.

A TMB érték klinikai interpretációja egyelőre nem egyértelmű, az eredmény tájékoztató jellegű.

A magas TMB érték pozitív asszociációban áll a PD-1 és PD-L1 inhibitorokra adott válasszal különböző tumortípusokban.

Goodman és munkatársai 151 olyan beteg adatait elemezték, akik immunterápiás kezelésben részesültek, és ismert volt esetükben a TMB érték. Különböző – összesen 21 féle – tumortípus szerepelt a vizsgálatban. A magas TMB értéket minimum 20 mutáció/megabázis-ként definiálták. A magas TMB értékkel rendelkező betegcsoport válaszadási aránya immunterápiára 58% volt, míg alacsony vagy közepes TMB érték esetén 20%.

## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

A PD-1/PD-L1 gátló terápiában részesülő betegek között is korreláció volt megfigyelhető a TMB érték és a kezelés kedvező kimenetele között (1). Hasonló terápiás előnyt tapasztaltak a magas TMB értékű csoportban az alacsony/közepes TMB értékűhöz képest PD-1/PD-L1 gátló kezelés hatására, mikroszatellita stabil (MSS) beteg (n=60, 14 különböző hisztológia) mintáinak analízise során. A medián progressziómentes túlélés 26,8 és 4,3 hónapnak bizonyult (2).

Egy másik tanulmányban 1662 immunterápiával kezelt beteg adatait elemezték. Magas TMB értéknek tekintették minden szövettani típusban a TMB értékek legmagasabb 20%-át. A magas TMB betegcsoportban szignifikánsan hosszabb volt a túlélés. Különböző küszöbértékekkel számolva azt állapították meg, hogy minél magasabb a TMB érték, annál nagyobb túlélési előnyt élveznek az immunterápiát kapó betegek (3).

Forgalomban lévő PD-1 vagy PD-L1 gátló hatóanyagok a NIVOLUMAB, PEMBROLIZUMAB, AVELUMAB, ATEZOLIZUMAB, DURVALUMAB és CEMIPILIMAB.

A PEMBROLIZUMAB az FDA által törzskönyvezett magas TMB értékű, előrehaladott vagy metasztatikus, szolid tumorra rendelkező, felnőtt és gyermek betegek számára.

A törzskönyv alapján a KEYNOTE-158 fázis II klinikai vizsgálat (NCT02628067) előre tervezett retrospektív analízise szolgált. A vizsgálat eredményei alapján a magas TMB státusz (a vizsgálatban 10 mutáció/mb-nek definiálták) kedvezőbb kimenetellel volt asszociált pembrolizumab monoterápia esetén előzetesen kezelt előrehaladott szolid daganatos betegek körében (n=790, 10-féle tumor típus). Az objektív válaszadási ráta 29%-nak (30/102) bizonyult magas TMB státusz esetén, 28%-nak (23/81) magas TMB esetén a magas vagy ismeretlen MSI státuszú betegek eredményeit kizárva és 6%-nak (43/688) az alacsony TMB értékű csoportban. Az adatok kiértékelésekor, 37,1 hónapos medián követési idő mellett, a medián válaszadási idő nem került elérésre a magas TMB értékű csoportban, míg az alacsony TMB státuszú kohort esetén 33,1 hónap volt (4).

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### Mutációs mintázat (Mutational Signature; Signature 20)

A detektált variánsokkal minőségi és funkcionális filterezéseket követően mutációs mintázat (mutational signature) (1, 2) analízist végeztünk. A tumorban kialakult alterációk etiológiájában jelentős szerepet játszik az össze nem illő párok javításának defektusa (mutational signature 20: Defective DNA MMR / MSI (small INDELS)). Ezzel a mutációs mintázattal az immunterápiák említhetőek pozitív asszociációban (3, 4).

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### A kópiaszám-variáció (copy number variation, CNV) vizsgálat eredménye

Az NGS vizsgálat során CNV analízist végeztünk. Kópiaszám-variációnak tekintjük, ha a detektált kópiaszám a normál kópiaszámtól (n=2) eltérő. NGS alapú technológiával a kópiaszám-változások becslése lehetséges.

A vizsgált mintában releváns kópiaszám-változást nem detektáltunk.

### Az újgenerációs szekvenálás (NGS) eredménye

591 gén NGS szekvenálása 6556 genetikai variánst mutatott ki a mintában. A molekuláris profilba feltöltött 110 variáns bioinformatikai és funkcionális szűrések eredményeként került kiválasztásra. Ezek a variánsok szerepelnek a Realtime Oncology Calculatorban további funkcionális interpretáció és orvosi döntéstámogatás céljából.



## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

A molekuláris profilban szereplő variánslista összeállításakor az Ingenuity Variant Analysis szoftver alábbi szűrőit használtuk:

- **CONFIDENCE:** Olvasási mélység, allél frakció, illetve genotípus kvalitás szerinti filterezést tesz lehetővé. A bioinformatikai szűrés során azokat a variánsokat zártuk ki, amelyeknek a jelenléte bizonytalan a szekvenálási minőségértékek alapján.
- **COMMON VARIANTS:** Segítségével kiszűrhetők azok a variánsok, amelyek nagy gyakorisággal megfigyelhetők az egészséges populációban. Kizártuk azokat a variánsokat, amelyek legalább 10%-os gyakorisággal fordulnak elő az egészséges populációban az 1000 Genomes Project, az ExAC vagy az NHLBI ESP exomes adatbázis szerint.
- **PREDICTED DELETERIOUS:** Azonosítja azokat az alterációkat, amelyek szakirodalmi evidenciák alapján befolyásolják a génfunkciót, génexpressziót. A szűrő alkalmazásával kizártuk az olyan alterációkat, amelyek az ACMG guideline szerint "Benign" vagy "Likely Benign" kategóriába esnek, vagyis erős evidenciák támasztják alá, hogy nem okoznak öröklődő genetikai betegséget.
- **CANCER DRIVER VARIANTS:** Olyan mutációk azonosítását teszi lehetővé, amelyek valószínűsíthetően tumorigenezishez vagy metasztázisok kialakulásához vezetnek. Kiválasztottuk azokat a variánsokat, amelyek szakirodalmi adatok szerint daganat kialakulásához köthető útvonalakat, szabályozó egységeket vagy sejtes folyamatokat érintenek. Továbbá kiválasztásra kerültek azok a variánsok is, amelyekről a szakirodalomban szerepel daganat-indikációban leírt adat.

A molekuláris profilban szereplő variánslista összeállításakor az Ingenuity Variant Analysis szoftveren kívül alkalmazott lépések:

- A listából kiszűrtük a nem exonikus régiókat érintő variánsokat
- További bioinformatikai szűréseket hajtottunk végre egyéb szekvenálási minőségértékek alapján

A variánsok klinikai jelentőségének felméréséhez használt adatbázisok:

**COSMIC** (Catalog of Somatic Mutations in Cancer): Ebben az adatbázisban tumorszövetben detektált szomatikus mutációkat gyűjtene össze.

**NCBI dbSNP** (National Center for Biotechnology Information Single Nucleotide Polymorphism database): Ebben az adatbázisban egészséges és különböző (nem kizárólag daganatos) megbetegedésekben szenvedő betegekben leírt csírvonalas (minden sejtben jelenlévő) alterációk szerepelnek.

**NCBI ClinVar:** Az adatbázis genotipikus és fenotipikus jellemzők közötti kapcsolatok gyűjteménye, a variánsok klinikai jelentőségéről elérhető evidenciákat összegzi, nem csak daganatos betegségekkel összefüggésben.

**SNPEffect:** Egy pontos nukleotid polimorfizmusok/mutációk klinikai jelentőségét tartalmazza az OMIM és más adatbázisok, valamint in silico predikciók alapján.

**IARC** (International Agency for Research on Cancer) **TP53 Database:** Az IARC TP53 adatbázis daganatos megbetegedésekhez köthető TP53 gént érintő mutációk gyűjteménye. A különböző irodalmi és más generális adatbázisokból származó adatok mellett a mutációk 8 különböző promoteren mutatott transzkripció aktivitásának átlagán alapuló funkcionális klasszifikációja is megtalálható az adatbázisban.

**BRCA Exchange:** Ebben az adatbázisban a BRCA1 és BRCA2 génekben azonosított mutációk funkcionális adatai és klasszifikációja található meg.

**UniProt:** A UniProt adatbázisban különböző fehérjék (géntermékek) szekvenciális és funkcionális adatai találhatóak.

### A detektált genetikai variánsok funkcionális interpretációja

A Molecular Treatment Calculator (MTC) az adatbázisban szereplő evidenciák súlyozott összegzése alapján a következő kategóriákba sorolja a detektált variánsokat: driver, driver gén ismeretlen jelentőségű variánsa (VUS, driver gén), nem megerősített driver, biomarker, ismeretlen jelentőségű variáns (VUS, variant of unknown significance), nem driver.

Az algoritmus pozitív pontszámmal veszi figyelembe azokat a tudományos adatokat, amelyek szerint egy variáns vagy egy mutáns gén hozzájárul a daganatképződéshez, és negatív pontszámot ad azoknak az adatoknak, amelyek szerint egy variáns nem serkenti a daganatképződést. Egy variáns osztályozása során az algoritmus súlyozza és összegzi azokra az evidenciákra vonatkozó pontszámot, amik az adott variánsról, a mutáns génről vagy a gén más mutációiról tartalmaznak információt. Az így kapott súlyozott összeg az aggregált evidenciaszint (aggregated evidence level, AEL).

**Driver** kategóriába sorolja az algoritmus azokat a variánsokat, amelyekre vonatkozóan az AEL pozitív, és az adott variánsról szerepel evidencia az adatbázisban.

**Driver gén ismeretlen jelentőségű variánsaként, VUS, driver gén** jelöléssel szerepelnek a riportban azok a variánsok, amelyekkel kapcsolatban nem szerepel információ az evidencia adatbázisban, de ismert, hogy a gén más mutációi hozzájárulhatnak a daganatképződéshez.

**Ismeretlen jelentőségű variáns** (variant of unknown significance, VUS) kategóriába kerülnek azok a variánsok, amelyekről nem szerepel információ az evidencia adatbázisban, és a gén más mutációiról, vagy a mutáns génről sem áll rendelkezésre adat.

## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

Biomarkerként szerepelnek a riportban azok a variánsok, amik az adott eltérésekre vonatkozó evidenciák alapján összefüggést mutatnak valamilyen hatóanyag hatékonyságával, de driver tulajdonságuk jelenleg nem ismert, bizonytalan, vagy biztosan nem driverek.

Nem megerősített driver kategóriába kerülnek azok a variánsok, ahol a driverként való osztályozás alapjául szolgáló evidenciák száma és evidenciaszintje alacsony.

Nem driver kategóriába sorolja az algoritmus azokat a variánsokat, melyeknek aggregált evidenciaszintje negatív.

### ER overexpresszió endometrium daganatban

Az ösztrogénreceptor (ER) overexpresszió ismert jelenség endometrium carcinómában, jobb prognózissal asszociál (1, 2). A tumor pozitív hormonreceptor státusza alapján az endokrin terápia említhetőek pozitív asszociációban, melyeket endometrium carcinómában is alkalmaznak (3, 4). Endokrin terápia rezisztenciát okozat többek között a HER2, EGFR, FGFR1 és PIK3CA gének amplifikációja, az FGFR aktiváció, illetve a PIK3CA, RB1, AKT1 és PTEN gének mutációja (5-9).

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### PTEN-R130Q

A variáns szerepel a COSMIC adatbázisban, a ClinVar adatbázis szerint patogén besorolású alteráció. A LOVD adatbázisban 2 esetben patogén, 1 esetben vélhetően patogén, és 2 esetben VUS besorolással szerepel.

Preklinikai, valamint glioblastoma és endometrium tumoros minták vizsgálata alapján a mutáció a PTEN foszfatáz aktivitásnak megszűnéséhez vezet (1, 2).

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### PTEN mutáns gén - célpontok

A PTEN (phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase) egy tumorszupresszor, ami a foszfoinozitolok defoszforilációjával a PI3K-AKT-mTOR jelpálya negatív regulátora.

A PTEN funkcióvesztéssel kapcsolatban említhető indirekt targetek a PI3K (1), az AKT (2) és az mTOR (2, 4-6), bár az mTOR gátlással kapcsolatos szakirodalmi adatok ellentmondásosak. Leírták továbbá, hogy PTEN-deficiens sejtek érzékenyek PARP (7) és ATM (8) inhibitorokra (a PTEN

## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

deficiencia és a paralel ATM/PARP gátlás szintetikus letális hatást okoz). A PTEN funkcióvesztéses alterációval pozitív asszociációban említhető, más indikációban törzskönyvezett hatóanyag az mTOR gátló EVEROLIMUS, TEMSIROLIMUS, METFORMIN és SIROLIMUS, a PARP gátló OLAPARIB, RUCAPARIB, NIRAPARIB és TALAZOPARIB, a PI3K delta inhibitor IDELALISIB, DUVELISIB (FDA).

A PTEN funkcióvesztése rezisztenciát okozhat EGFR gátló terápiákkal szemben (9, 10). Preklinikai eredmények szerint PTEN vesztés esetén a MEK + mTOR kombinált gátlás szinergisztikus hatású (11). A PTEN funkcióvesztése továbbá rezisztenciát okozhat PIK3CA gátlásra, és a PIK3CA gátló alpelisibre (12, 13), valamint a HER2 gátlásra is (14-16).

Több tanulmány eredményei alapján a PTEN génvesztés vagy mutáció csökkent T sejt infiltrációval, megváltozott tumor mikrokoznyezettel és anti-PD-1 terápiára való rezisztenciával asszociált (17, 18). Egér modellekben a szelektív PI3Kbeta inhibitor (GSK2636771) alkalmazása növelte az anti-PD-1 és anti-CTLA-4 ellenanyagok hatékonyságát (18).

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### PTEN mutáns, hormonreceptor pozitív daganat

Szakirodalmi evidenciák alapján a PI3K/AKT/mTOR jelátviteli útvonal aktivációja (például PTEN funkcióvesztésen keresztül (1-3)) rezisztenciát okozhat hormonterápiákra (így az ER gátlásra is); ilyen esetben a PI3K/AKT/mTOR útvonal gátlószereinek hormonterápiával való kombinációja lehet hatékony (4-7).

Leírták továbbá, hogy a PI3K/AKT/mTOR útvonal gátlása esetén az ER fokozott transzkripció aktivitása figyelhető meg, ezért is javasolt az endokrin terápiák és a PI3K/AKT/mTOR gátló hatóanyagok együttes alkalmazása (8, 9).

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### FBXW7-R479Q

A variáns szerepel a COSMIC adatbázisban. A ClinVar adatbázis alapján valószínűsíthetően patogén alteráció. Az OncoKB adatbázis szerint a mutáció onkogenikus hatású.

Az FBXW7-R479Q az FBXW7 fehérje 3. ismétlődő WD szakaszában található (UniProt.org). Az R479Q csökkenti az FBXW7-szubsztrát interakciót, és rontja a szubsztát FBXW7 általi lebontását, ami tartós Notch1 intracelluláris domén és Myc expressziót eredményez (1, 2), illetve aberráns szubcelluláris nukleáris lokalizációt, valamint a Notch1 intracelluláris domén kötődésének elvesztését okozza (3).

Az R479Q mutáció ismert funkcióvesztő, domináns negatív tulajdonsággal rendelkező variáns (4, 5), vagyis gátolja a normál allélról képződő vad típusú fehérje működését is.

Egy preklinikai vizsgálatban T-sejtes akut limfoblasztikus leukémia (T-ALL) sejtvonalakban az FBXW7-R479Q rezisztenciát okozott a gamma-szekretáz inhibitor, MRK-003-mal szemben a NOTCH útvonal aktiválása és a MYC stabilizálása révén (1).

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### FBXW7 mutáns gén - célpont gének

Az FBXW7 (F-box and WD repeat domain containing 7) egy tumorszuppresszor gén, ami az SCF komplex részeként részt vesz proto-onkogének (MYC, cyclin E, NOTCH és JUN) ubiquitin-függő degradációjában (1). A mutáns fehérje következtében, az FBXW7 általi szubsztátfelismerés és -lebontás gátlódhat, így a NOTCH1 és MYC útvonalak aktívak maradnak (2).

Preklinikai adatok alapján az FBXW7 mutációk érzékenyítenek az mTOR inhibitorokra, ezt klinikai vizsgálat keretein belül is vizsgálták (3, 4). In vivo az mTOR inhibitorok alkalmazása csökkentette az FBXW7 funkcióvesztés okozta tumornövekedést (5). Forgalomban lévő, mTOR gátló hatással rendelkező készítmények az EVEROLIMUS, a TEMSIROLIMUS, SIROLIMUS és a METFORMIN. Egy FBXW7 mutáns tüdő tumoros beteg esettanulmánya alapján a temsirolimus (mTOR gátló) terápia hatékonyak bizonyult (6).

## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

Egyes publikációk alapján az FBXW7 mutáció okozta aktivitás hatása függ a TP53 státuszról, a TP53 inaktiváció szükséges a sejtek folyamatos osztódása és túlélése szempontjából, amely instabilitáshoz és tumorképződéshez vezet (7).

A vad típusú FBXW7 fehérje gátolja a NOTCH jelátvitelt. Az FBXW7 konzervált kötőzsebében elhelyezkedő mutációk (pl. R505) a NOTCH kötődést akadályozzák, így növelik a NOTCH aktivitását (8). Ez alapján FBXW7 inaktiváció esetén a NOTCH jelátviteli útvonal gátlása lehet hatékony (9). NOTCH gátlószerek jelenleg klinikai vizsgálatok keretében elérhetők.

További publikációk alapján az FBXW7 mutáns sejtek nagyobb szenzitivitást mutatnak a sorafenibre (10). Ennek magyarázata, hogy a sorafenib a tumornövekedésben és angiogenezisben résztvevő receptor tirozin kinázok (PDGF, VEGF, RAF) gátlószere. A RAF kináz enzim képes a MAPK szignalizációs útvonalat aktiválni. A sorafenib azáltal, hogy inaktiválja a MAPK kinázt, csökkenti a MCL-1 szintet. Kimutatták továbbá, hogy MCL-1 gátló hatással is rendelkezik. Az FBXW7 -/- sejtek esetében az apoptotikus útvonal elkerülésében a megnövekedett szintű MCL-1 kritikus szerepet játszik. Így az FBXW7-deficiens sejtek sokkal érzékenyebbek a sorafenibre, mint az FBXW7 vad típusú sejtek, az MCL-1 target génnek tekinthető (11). Az FBXW7 mutáció rezisztenciát okozhat a taxán és a vincristine kemoterápiákkal szemben (11), valamint EGFR gátló kezeléssel szemben (12).

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### CTNNB1-T41A

A variáns magas esetszámmal szerepel a COSMIC adatbázisban. Az NCBI ClinVar adatbázisban ellentmondásos adatok szerepelnek a variáns patogenitását illetően, azonban legtöbb esetben (9/12) valószínűsíthetően patogén mutációként történt a besorolása.

A mutáció a beta-catenin N-terminális régióját érinti, ahol a szerin/treonin kináz GSK-3beta fehérje foszforilációs helyei találhatóak (Ser33, Ser37, Thr41 and Ser45).

Egy tanulmány során desmoid daganat indikációban vizsgálták a CTNNB1-T41A variánst; nem találtak összefüggést a tumor kialakulása és a mutáció jelenléte között (1). Egy másik, Wilm's tumort vizsgáló tanulmányban megállapították, hogy a T41A mutációval rendelkező betegek túlélése szignifikánsan alacsonyabb ( $p = 0,000517$ ) volt az átlagnál. Továbbá a variáns jelenlétében elvesz a fehérje GSK-3beta foszforilációs régiója, ami a beta-katenin stabilitásához vezet és domináns hatást fejt ki a beta-katenin=TCF által közvetített transzkripció szintjén; ezért a mutáció hozzájárulhat Wilm's tumor kialakulásához (2). Melanoma indikációban jellemző driver a CTNNB1 (beta-catenin) overexpressziója és a génben detektált aktiváló mutációk (3).

Preklinikai evidencia szerint a T41A funkciónyerő mutáció a fehérje stabilizációját, nukleáris akkumulációját, valamint a Ctnnb1-függő transzkripció fokozódását eredményezi (4-6).

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### CTNNB1 mutáns gén - célpontok

CTNNB1 aktiváció esetén szakirodalmi evidencia alapján pozitív asszociációban említhető molekuláris célpont a CTNNB1 önmaga (1) és a TTK gén (2). CTNNB1 és TTK (másnéven Mps1) inhibitorok jelenleg klinikai vizsgálatok keretében érhetők el.

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### PIK3CA-E81K

A variáns szerepel a COSMIC adatbázisban (n>100). A variáns a PIK3CA fehérje PI3K-ABD doménjében lokalizálódik. A ClinVar adatbázis adatai szerint valószínűsíthetően patogén variáns. A LOVD adatbázisban patogén alterációként klasszifikálták. In silico predikciók szerint károsító hatású eltérés (PolyPhen, SIFT).

Egy tanulmány szerint a mutáció jelenléte az AKT fokozott foszforilációjához és az mTOR jelátviteli út aktivációjához vezet (1).

#### Referenciák:

- (1) Loconte DC et al., *Molecular and Functional Characterization of Three Different Postzygotic Mutations in PIK3CA-Related Overgrowth Spectrum (PROS) Patients: Effects on PI3K/AKT/mTOR Signaling and Sensitivity to PIK3 Inhibitors*. *PLoS One*. 2015 Apr 27;10(4):e0123092. PubMed PMID: 25915946

### PIK3CA mutáns gén - célpontok

A PIK3CA (phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha) a PI3K-Akt jelátviteli útvonal részeként fontos szerepet tölt be a sejtproliferációban és a sejtek túlélésében, így a tumorigenezis során is.

PIK3CA génben detektált driver mutáció esetén a daganat molekuláris profiljával pozitív asszociációban említhetőek a PIK3CA/AKT/mTOR gátló hatóanyagok (1-3).

Az ALPELISIB és a COPANLISIB (FDA) törzskönyvezett PIK3CA gátló hatóanyagok. Forgalomban lévő mTOR-gátló készítmény az EVEROLIMUS, a METFORMIN, SIROLIMUS és a TEMSIROLIMUS. Az EVEROLIMUS emlő indikációban törzskönyvezett. A METFORMIN és a SIROLIMUS tumor indikációban nem törzskönyvezett. A TEMSIROLIMUS vesesejtes carcinoma indikációban elfogadott hatóanyag.

A TASELISIB fejlesztés alatt álló PIK3CA gátló hatóanyag fázis I vizsgálatban 36%-os válaszadási arányt eredményezett PIK3CA mutáns szolid tumoros betegek között, míg egyetlen PIK3CA vad típusú betegnél sem írtak le válaszadást (4). Egy nagyobb fázis I vizsgálatban többszörösen előkezelt PIK3CA mutáns szolid tumoros betegek között a taselesib 8,9%-os válaszadási arányt ért el (5). Az ALPELISIB kezelés PIK3CA mutáns vagy amplifikált szolid tumoros betegek között 6%-os válaszadási arányt és 58,2%-os betegség kontroll arányt ért el (6).

A Molecular Treatment Calculator algoritmus az aktuális evidencia adatbázis alapján az aktiváló PIK3CA mutáció jelenlétében az ESR1 és EGFR inhibitorokat a beteg molekuláris profiljával negatív asszociációban sorolja.

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### PIK3CA mutáns endometrium daganat

Egy klinikai vizsgálatban 8 PIK3CA vagy AKT mutáns és ER pozitív endometrium daganatos beteg között a miransertib (AKT gátló) és anastrozole (aromatáz inhibitor) kombinációja 50%-os válaszadási arányt eredményezett (1).

Egy retrospektív vizsgálat szerint cukorbeteg endometrium daganatos betegek között a metformin használat növekedett betegségmentes túléléssel és teljes túléléssel mutatott összefüggést (2). Egy metaanalízis is megerősítette, hogy a metformin használat növekedett teljes túléléssel és progressziómentes túléléssel asszociál endometrium daganatban (3).

Egy fázis II vizsgálatban everolimus + letrozol kombinációs kezelés 32%-os válaszadási arányt eredményezett endometrium daganatos betegek között (9 teljes, 2 részleges tumorválasz). Az 5 PIK3CA mutáns résztvevő közül egynél teljes tumorválaszt, egynél stabil betegséget írtak le (4).

Egy fázis II vizsgálatban az everolimus+letrozole+metformin kombinációs kezelés 29%-os válaszadási arányt eredményezett, és az előrehaladott vagy rekurrens endometrium carcinomás betegek 38%-ánál stabil betegséget tapasztaltak (5).

#### Referenciák:

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### ATM-S214fs\*16

A variáns megtalálható a COSMIC adatbázisban, a ClinVar adatbázis szerint patogén elváltozás. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjeváltozatot kódoló ATM variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

### ATM-I1581fs\*20

A mutáció megtalálható a COSMIC adatbázisban. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjeváltozatot kódoló ATM variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

### ATM mutáns gén - célpontok

Az ATM egy szerin/treonin protein kináz, ami a DNS károsodás hatására aktiválódó DNS hibajavító mechanizmusok szabályozásában vesz részt. ATM mutációk esetén az ATR (1) és PARP (2-6) target gének említhetők pozitív asszociációban. Egy retrospektív tanulmány szerint ATM mutáció esetén hatékonyabb a sugárkezelés, mint ATM vad típusú betegeknél (7).

Preklinikai vizsgálatokban az ATR inhibitor berzosertib (VX-970) gátolta az ATR aktivitását és növelte a cisplatin hatékonyságát tüdődaganatos xenograftokban, köztük cisplatin-rezisztens modellekben is (8). Egy fázis I vizsgálatban a berzosertib antitumor aktivitást mutatott monoterápiaként és carboplatinval kombinálva előrehaladott, standard kezelésre refrakter, szolid tumoros betegeknél. A berzosertib monoterápia teljes választ és 29 hónapos progressziómentes túlélést (PFS) eredményezett egy ATM-vesztéssel és ARID1A mutációval rendelkező metasztatikus colorectalis daganatos beteg esetén (9). Egy randomizált fázis II vizsgálatban a berzosertib és gemcitabine kombinációja előnyösebbnek bizonyult a gemcitabine monoterápiához képest platina-rezisztens high-grade serosus ovárium carcinomás betegek esetén, a medián PFS 22,9 hét (n=34) és 14,7 hét (n=36) volt a két csoportban (10).

## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

Egy fázis I vizsgálatban a BAY1895344 (ATR inhibitor) terápia 4 részleges választ és 8 esetben stabil betegséget eredményezett szolid daganatos betegek esetén. Mindegyik részleges válasszal reagáló beteg esetén kimutattak ATM fehérjevesztést és/vagy károsító ATM mutációt (11).

Egy preklinikai vizsgálat szerint az ATM funkcióvesztő mutációi szintetikus letális hatásúak MEK1/2 inhibitorokkal. ATM vesztés fokozta KRAS vagy BRAF mutáns tüdő tumoros sejtek, illetve MEK inhibitor rezisztens tüdő tumoros sejtek érzékenységet MEK gátlásra. Az eredmények alapján az ATM szükséges az AKT/mTOR és MEK/ERK jelátviteli útvonalak közti kapcsolathoz (12).

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### CDH1-I594fs\*19

A mutáció megtalálható a COSMIC adatbázisban, a ClinVar adatbázis szerint patogén elváltozás. A leolvadási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjeváltozatot kódoló CDH1 variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

### CDH1 mutáns gén - célpontok

A CDH1 gén alapján képződő E-cadherin fehérje tumorszupresszor funkcióval bír, funkcióvesztéssel járó mutációit daganatok kialakulásával hozták összefüggésbe (1, 2).

Az ún. sztatinek, HMG-CoA enzim (HMGCR) inhibitorok (atorvastatin, lovastatin, simvastatin) szintén szintetikus letális fenotípust értek el a CDH1-et nem expresszáló emlő sejtvonalon, illetve szinergikus hatást mutattak HDAC vagy SRC inhibitorokkal való együttes alkalmazás esetén (3).

Szintetikus letális kapcsolatot írtak le emlő daganatos sejtvonalon CDH1 és ROS1 között, ezért CDH1 funkcióvesztés esetén targetként említhető a ROS1 (4). Klinikai forgalomban lévő ROS1 gátló hatással bíró hatóanyag a CRIZOTINIB és a LORLATINIB.

Nem daganatos, CDH1-et nem expresszáló sejtvonal nagyobb érzékenységet mutatott HDAC (Mocetinostat, Entinostat, Quisinostat, Pracinostat, LAQ824, Panobinostat, Vorinostat), ROS1 (Crizotinib), ALK (Crizotinib), MET (Crizotinib), PI3K (PI103, GSK2126458, PIK-75 hydrochloride), NPY5R (CGP 71683 hydrochloride), EGFR (Tyrphostin A9), PDGFR (Tyrphostin A9), mTOR (AZD8055, PI103, GSK2126458), BCL2 (Obatoclox Mesylate), GBF1 (Brefeldin A), JAK (LY2784544), mitokondriális oxidatív foszforiláció gátló (FCCP), CDK (JNJ-7706621), Aurora kináz (JNJ-7706621, Danusertib), ABL (Danusertib), RET (Danusertib), FGFR1 (Danusertib, PD-166285 hydrate), NTRK1 (Danusertib), AKT (10-DEBC hydrochloride) és SRC (PD-166285 hydrate, Saracatinib) inhibitorokkal szemben, mint a CDH1-et expresszáló sejtvonal (5).



## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

Egy örökletes diffúz gyomorrákos betegből származó, germline funkcióvesztő CDH1 mutációt hordozó sejtvonalban egérmodell vizsgálattal a PI3K/mTOR, MEK, c-Src kináz, FAK, PKC és TOPO2 inhibitorok megnövekedett hatékonysága igazolódott egy másik, a mutációt nem hordozó gyomorrákos betegből származó sejtvonalhoz viszonyítva (6). A két vizsgálat eredményei átfedőek a PI3K, mTOR, Aurora kináz és ALK/ROS-1 inhibitorokkal szembeni hatékonyság tekintetében (7).

A HDAC, ROS1, ALK, MET, PI3K, NPY5R, EGFR, PDGFR, mTOR, BCL2, GBF1, JAK, CDK, Aurora kináz, ABL, RET, FGFR1, NTRK1, AKT és SRC inhibitorok CDH1 driver eltérés esetén pozitív asszociációban említhetőek.

A sztatínok (ATORVASTIN, FLUVASTATIN, LOVASTATIN, PITAVASTATIN, PRAVASTATIN, ROSUVASTATIN, SIMVASTATIN) HMGCR inhibitor aktivitással rendelkező forgalomban lévő koleszterincsökkentő szerek. A HDAC inhibitor PANOBINOSTAT myeloma multiplex indikációban elfogadott. A VALPROINSAV HDAC gátló hatással rendelkező epilepsziaellenes gyógyszer. A VORINOSTAT, a BELINOSTAT és a ROMIDEPSIN csak az FDA által törzskönyvezettek hematológiai indikációkban. Forgalomban lévő ALK/ROS1/MET inhibitor a CRIZOTINIB, az ALK/ROS1 inhibitor LORLATINIB, az ALK inhibitor ALECTINIB, CERITINIB és a BRIGATINIB. Elérhető MET gátló a CABOZANTINIB, FDA által elfogadott MET gátló a CAPMATINIB, PI3K gátló az IDELALISIB és COPANLISIB, PDGFR gátló az IMATINIB, LENVATINIB, NILOTINIB, NINTEDANIB, PAZOPANIB, REGORAFENIB, SORAFENIB, SUNITINIB, PONATINIB, AXITINIB és MIDOSTAURIN. Elérhető mTOR gátló a EVEROLIMUS, TEMSIROLIMUS, METFORMIN és SIROLIMUS, BCL-2 gátló a VENETOCLAX, JAK gátló a RUXOLITINIB és TOFACITINIB, ABL gátló a BOSUTINIB, DASATINIB, IMATINIB MESYLATE, NILOTINIB, REGORAFENIB és PONATINIB, RET gátló a REGORAFENIB, CABOZANTINIB, ALECTINIB, PONATINIB, NINTEDANIB, LENVATINIB, SORAFENIB, VANDETANIB és SUNITINIB, FGFR1 gátló PONATINIB, LENVATINIB, NINTEDANIB, PAZOPANIB, REGORAFENIB, SORAFENIB, SUNITINIB és ERDAFITINIB (csak FDA), SRC gátló a NINTEDANIB, BOSUTINIB és DASATINIB. Az AKT, CDK1, CDK2, NPY5R, NTRK1 és Aurora kináz inhibitorok klinikai vizsgálatban hozzáférhetőek. GBF1 inhibitorok jelenleg preklinikai fejlesztés alatt állnak.

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### RECQL4-L339fs\*20

A mutáció megtalálható a COSMIC adatbázisban. A ClinVar adatbázis alapján patogén elváltozás. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) a RECQL4 gén nonsense-mediated decay (NMD) rezisztens pozícióját érinti, ezért nagy valószínűséggel az NMD folyamat nem vezet a mutáns mRNS lebomlásához (1). Így a mutáns génről egy megváltozott C terminális szekvenciával rendelkező, kismértékben csonka fehérjeváltozat képződik, ezért lehetséges, hogy funkcióvesztéssel jár.

### Referenciák:

- (1) Litchfield K et al., Escape from nonsense mediated decay associates with anti-tumor immunogenicity. 2019. doi: 10.1101/823716.

### RECQL4 mutáns gén - célpontok

A RECQL4 gén tumorszupresszor és onkogén szerepet is betölthet különböző daganatokban (1-3).

A RECQL4 génnek a DNS hibajavításban van szerepe. Preklinikai adatok alapján funkcióvesztő RECQL4 mutációk esetén a PARP inhibitorok és a cisplatin említhetőek pozitív asszociációban (4). A RECQL4 gén funkcióvesztésének hatása hasonlít a BRCA1-deficiencia hatásához a PARP-gátlásra és a cisplatinra való szenzitivitás terén (4).

Forgalomban lévő PARP gátló gyógyszerek az OLAPARIB, RUCAPARIB, NIRAPARIB és a TALAZOPARIB.

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### PIK3CB-L1049R

A mutáció megtalálható a COSMIC adatbázisban. Preklinikai kísérlet szerint a variáns onkogenikus hatású (1).

#### Referenciák:

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### PIK3CB mutáns gén - célpontok

A PIK3CB a PI3K katalitikus alegységének egyik izoformáját kódolja. Aktiváló mutációi esetén a PIK3CB gátlás hatékonyságát preklinikai eredmények igazolják (1). PIK3CB mutációk esetén preklinikai eredmények szerint hatékonyak lehetnek az AKT és az mTOR gátló gyógyszerek is (2). EGFR gátló hatóanyagokra rezisztenciát okoznak (3).

A COPANLISIB PIK3CB gátló hatással is rendelkező FDA törzskönyvezett hatóanyag.

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### ARID1A-F2141fs\*59

A variáns megtalálható a COSMIC adatbázisban. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) az ARID1A gén nonsense-mediated decay (NMD) rezisztens pozícióját érinti, ezért nagy valószínűséggel az NMD folyamat nem vezet a mutáns mRNS lebomlásához (1). Így a mutáns génről egy megváltozott C terminális szekvenciával rendelkező, kismértékben csonka fehérjevaltozat képződik, ezért lehetséges, hogy funkcióvesztéssel jár.

#### Referenciák:

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### ARID1A-Q1519fs\*8

A variáns szerepel a COSMIC adatbázisban. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) az ARID1A gén nonsense-mediated decay (NMD) rezisztens pozícióját érinti, ezért nagy valószínűséggel az NMD folyamat nem vezet a mutáns mRNS lebomlásához (1). Így a mutáns génről egy megváltozott C terminális szekvenciával rendelkező, csonka fehérjevaltozat képződik, ami a BAF250 domén elvesztésével jár (ebi.ac.uk/interpro), ezért valószínűsíthető, hogy funkcióvesztéssel jár.

#### Referenciák:

(1) Litchfield K et al., Escape from nonsense mediated decay associates with anti-tumor immunogenicity. 2019. doi: 10.1101/823716.

### ARID1A-Y551fs\*68

A variáns szerepel a COSMIC adatbázisban. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjevaltozatot kódoló ARID1A variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

### ARID1A mutáns gén - célpontok

Az ARID1A elvesztése esetén csökken a mismatch repair funkció. Az ARID1A deficiencia preklinikai vizsgálatban, továbbá gyomor- és colorectalis daganatos betegekben korrelált a mikroszatellita instabilitással (1, 2). Egy vizsgálatban gasztrointesztinális eredetű tumorokból származó adatokat elemeztek és az ARID1A mutáns daganatok esetén magasabb TMB értéket, valamint magasabb PD-L1 expressziót tapasztaltak (3). Preklinikai adatok szerint ARID1A mutáns ováriumtumoros egér modelleken hatékony volt a PD-L1 gátló immunterápia alkalmazása, míg vad típusú ARID1A esetén nem (1). További pozitív asszociációban említhető célpont gének az EZH2 (4), a YES1 (5), a PI3K/AKT (6) és a PARP (7). A

## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

forgalomban lévő dasatinibbel szintetikus letális hatás volt kimutatható ARID1A veszteség esetén (5). A TAZEMETOSTAT FDA által elfogadott EZH2 gátló hatóanyag. Forgalomban lévő PD-L1 gátlók az AVELUMAB, az ATEZOLIZUMAB és a DURVALUMAB. Forgalomban lévő YES1 gátló a DASATINIB. Forgalomban lévő PI3K gátlók az IDEALISIB, ALPELISIB és az FDA által törzskönyvezett COPANLISIB és DUVELISIB. Forgalomban lévő PARP gátló gyógyszerek az OLAPARIB, RUCAPARIB, TALAZOPARIB és a NIRAPARIB.

### Referenciák:

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### DNMT3A-Q110fs\*14

A mutáció megtalálható a COSMIC adatbázisban. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjeváltozatot kódoló DNMT3A variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

### DNMT3A mutáns gén - célpontok

A DNMT3A egy DNS metiltransferáz fehérjét kódol, amely proto-onkogén és tumorszupresszor funkciókkal is rendelkezik (1). DNMT3A funkcióvesztő mutációk esetén a DOT1L target gén és a pinometostat hatóanyag említhető pozitív asszociációban (1).

### Referenciák:

- (1) Zhang J, et al. DNA Methyltransferases in Cancer: Biology, Paradox, Aberrations, and Targeted Therapy. *Cancers (Basel).* 2020 Jul 31;12(8):2123. doi: 10.3390/cancers12082123. PMID: 32751889; PMCID: PMC7465608.
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### CDK12-G1271fs\*23

A mutáció szerepel a COSMIC adatbázisban. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) a CDK12 gén nonsense-mediated decay (NMD) rezisztens pozícióját érinti, ezért nagy valószínűséggel az NMD folyamat nem vezet a mutáns mRNS lebomlásához (1). Így a mutáns génről egy megváltozott C terminális szekvenciával rendelkező, kismértékben csonka fehérjeváltozat képződik, ezért lehetséges, hogy funkcióvesztéssel jár.

### Referenciák:

- (1) Litchfield K et al., Escape from nonsense mediated decay associates with anti-tumor immunogenicity. 2019. doi: 10.1101/823716.

### CDK12 mutáns gén - célpontok

A CDK12 gént tumorszupresszorként (elsősorban ováriumdaganatokban) és proto-onkogénként (elsősorban emlődaganatokban) egyaránt jellemzi a szakirodalom (1, 2).

A CDK12 a DNS hibajavításban résztvevő gének transzkripcióját szabályozza, funkcióvesztése a DNS hibajavító képesség romlásával jár, és összefüggést mutat a CHEK1 (3) és PARP gátló hatóanyagokra való érzékenységgel, platina-alapú kemoterápiák és alkiláló szerek hatékonyságával (4-6).

Forgalomban lévő PARP gátló hatóanyagok az OLAPARIB, a RUCAPARIB, a NIRAPARIB és a TALAZOPARIB.

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- (2) Naidoo K et al., Evaluation of CDK12 Protein Expression as a Potential Novel Biomarker for DNA Damage Response-Targeted Therapies in Breast Cancer. *Mol Cancer Ther.* 2018 Jan;17(1):306-315. Epub 2017 Nov 13. PubMed PMID: 29133620
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### NSD1-M1531fs\*43

A variáns szerepel a COSMIC adatbázisban. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjeváltozatot kódoló NSD1 variáns jön létre, így a funkcióvesztés nagy mértékben valószínűsíthető.

### NSD1-F1799fs\*22

A mutáció megtalálható a COSMIC adatbázisban. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjeváltozatot kódoló NSD1 variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

### NSD1 mutáns gén - célpontok

Az NSD1 (nuclear receptor binding SET domain protein 1) egy transzkripciók regulátorként funkcionáló hiszton metiltransferáz (1). Prosztatadaganat-eredetű sejtekből származó eredmények alapján az NSD1 a szteroid receptorok koregulátoraként is működik (2). Az NSD1 funkcióvesztő mutációi hozzájárulhatnak a tumorigenezishez (3).

Preklinikai kísérletek szerint az NSD1 gén funkcióvesztése a genom hipometilációjával és cisplatin érzékenységgel mutatott összefüggést. Fejnyak daganatos betegek között, ahol a cisplatin a standard terápia része, az NSD1 mutáns betegcsoportban 55%-kal alacsonyabb volt a halálozás kockázata, mint az NSD1 vad típusú betegek között (4). Preklinikai eredmények alapján feltételezik, hogy az NSD1 mutáns daganatok kevésbé érzékenyek immunterápiára (5).

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- (2) Wang X et al., Identification and characterization of a novel androgen receptor coregulator ARA267-alpha in prostate cancer cells. *J Biol Chem.* 2001 Nov 2;276(44):40417-23. PMID: 11509567
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### DMD-S3343fs\*34

A mutáció megtalálható a COSMIC adatbázisban. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjeváltozatot kódoló DMD variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

A DMD gén egy tumorszuppresszor (1), csíravonalas mutációja Duchenne izomdisztrófiát okoz. A golodirszen, a viltolarszen és a casimerszen az FDA által törzskönyvezett génterápiák bizonyos csíravonalas DMD mutációval rendelkező betegek számára (2, 3). DMD szomatikus funkcióvesztő mutációival összefüggésben nem ismert célzott, tumorelles terápia.

#### Referenciák:

- (1) Wang Y et al. Dystrophin is a tumor suppressor in human cancers with myogenic programs. *Nat Genet.* 2014 Jun;46(6):601-6. doi: 10.1038/ng.2974. Epub 2014 May 4. PubMed PMID: 24793134; PubMed Central PMCID: PMC4225780.

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(2) Frank DE et al. *Golodirsen Leads to Sarcolemmal Dystrophin Expression in Patients With Genetic Mutations Amenable to Exon 53 Skipping*. 2019.

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### PAX5-A322fs\*11

A variáns alacsony frekvenciával szerepel a COSMIC adatbázisban (n>5). A mutációt kimutatták akut limfoid leukémiában (ALL) szenvedő betegeknél (1) és ALL sejtvonalakban is (2). A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjeváltozatot kódoló PAX5 variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

#### Referenciák:

(1) Santoro A et al., *Altered mRNA expression of PAX5 is a common event in acute lymphoblastic leukaemia*. *Br J Haematol*. 2009 Sep;146(6):686-9. Epub 2009 Nov 13. PubMed PMID: 19604238

(2) Hart MR et al., *Activating PAX gene family paralogs to complement PAX5 leukemia driver mutations*. *PLoS Genet*. 2018 09;14(9):e1007642. Epub 2018 Nov 14. PubMed PMID: 30216339

### PAX5 funkcióvesztés

A PAX5 (Paired box 5) transzkripció faktor szerepet játszik a limfoid progenitorok B-sejtvonal felé történő differenciálódásának korlátozásában, pro-B-sejt stádiumában a PAX5 egyenletesen expresszálódik, majd a plazmasejteké történő differenciálódás során alulszabályozottá válik az expresszója. Onkogenikus és tumorszuppresszor szerepet is betölthet (1).

A gyermekkori B-progenitor ALL (akut limfoid leukémia) esetek 31,7%-ában detektáltak PAX5 alterációkat. Az azonosított PAX5 mutációk csökkent PAX5 protein szintet vagy hipomorf allélok képződését eredményezték (2).

A késői B-sejtekben a PAX5 elvesztése limfóma kialakulásához vezethet, egér modellekben PAX5 hiányos érett B-sejtekkel agresszív limfómák alakultak ki, amelyeket gén-expressziós profiljuk alapján progenitorsejt-tumorokként azonosítottak (3).

A PAX5 csendesítése MCL-ben (köpenysejtes limfóma) *in vitro* fokozott sejtproliferációt, *in vivo* fokozott tumor infiltrációt eredményezett, amely alapján a csökkent PAX5-szint elősegíti tumorok progresszióját. A géncsendesített sejtek rezisztensnek bizonyultak bortezomib, és doxorubicin kezelésre is (1).

#### Referenciák:

(1) Teo AE et al., *Differential PAX5 levels promote malignant B-cell infiltration, progression and drug resistance, and predict a poor prognosis in MCL patients independent of CCND1*. *Leukemia*. 2016 Mar;30(3):580-93. doi: 10.1038/leu.2015.140. PMID: 26073757.

(2) Mullighan CG et al., *Genome-wide analysis of genetic alterations in acute lymphoblastic leukaemia*. *Nature*. 2007 Apr 12;446(7137):758-64. doi: 10.1038/nature05690. PMID: 17344859.

(3) Cobaleda C et al., *Conversion of mature B cells into T cells by dedifferentiation to uncommitted progenitors*. *Nature*. 2007 Sep 27;449(7161):473-7. doi: 10.1038/nature06159. PMID: 17851532.

### TET2-L1276fs\*24

A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjeváltozatot kódoló TET2 variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

A TET2 funkcióvesztő mutációi elsősorban hematopoietikus malignus folyamatokban jellemzőek, szolid tumorokban inkább a csökkent aktivitású variánsok jelen. A TET2 az interferon (IFN)-JAK-STAT szignálzációban vesz részt, a kemokin és PD-L1 expressziót szabályozza. A TET2 deléció rágcsáló melanoma és colon tumorsejtekben lecsökkentette a kemokin expressziót és a TIL mennyiséget, amely elősegíti a tumor-ellenes immunaktivitás elekerülését és az anti-PD-L1 terápiával szembeni rezisztencia kialakulását (1). Egy tanulmányban immunterápiában részesülő nem-kissejtes tüdődaganatos betegek között hosszabb teljes túlélést írtak le TET2 mutációk jelenléte esetén, de a detektált TET2 mutációk többsége nem volt ismert funkcióvesztő variáns (2).

#### Referenciák:

(1) Xu YP et al., *Tumor suppressor TET2 promotes cancer immunity and immunotherapy efficacy*. *J Clin Invest*. 2019 Jul 16;130:4316-4331. PubMed PMID: 31310587

(2) Zhao D, Mambetsariev I, et al. *Association of molecular characteristics with survival in advanced non-small cell lung cancer patients treated with checkpoint inhibitors*. *Lung Cancer*. 2020;146:174-181. doi:10.1016/j.lungcan.2020.05.025

### KDM5C-R68fs\*5

## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjeválozatot kódoló KDM5C variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

KDM5C (lizin (K)-demetiláz 5C) egy Jumonji domain típusú hiszton demetiláz, a KDM5 alcsoport tagja, mely a kromatin újramodellezés és ezáltal a transzkripció reguláció folyamatában vesz részt. A tudományos irodalom szerint a KDM5C egyaránt tölthet be tumorszupresszor és proto-onkogenikus szerepet, az alteráció funkcióvesztő vagy funkcióerősítő jellege és a sejttípus függvényében.

In vitro, a KDM5C funkcióvesztés fokozott tumornövekedést eredményezett világossejtes vesesejtes carcinoma sejtekben (ccRCC) (3). Egy fázis II-es vizsgálatban a KDM5C mutációk megnövekedett progressziómentes túléléssel asszociáltak elsővonalas sunitinib kezelésre metasztatikus ccRCC betegekben (4).

### Referenciák:

- (1) Chang S et al., *The cancer driver genes IDH1/2, JARID1C/ KDM5C, and UTX/ KDM6A: crosstalk between histone demethylation and hypoxic reprogramming in cancer metabolism. Exp Mol Med. 2019 Jun 20;51(6):1-17. PMID: 31221981*
- (2) Plich J et al., *KDM5 demethylases and their role in cancer cell chemoresistance. Int J Cancer. 2019 Jan 15;144(2):221-231. Epub 2018 Nov 26. PMID: 30246379*
- (3) Niu X et al., *The von Hippel-Lindau tumor suppressor protein regulates gene expression and tumor growth through histone demethylase JARID1C. Oncogene. 2012 Feb 9;31(6):776-86. Epub 2011 Jul 4. PMID: 21725364*
- (4) Hsieh JJ et al., *Genomic Biomarkers of a Randomized Trial Comparing First-line Everolimus and Sunitinib in Patients with Metastatic Renal Cell Carcinoma. Eur Urol. 2017 Mar;71(3):405-414. Epub 2016 Oct 15. PMID: 27751729*

### CTCF-E691fs\*30

A mutáció szerepel a COSMIC adatbázisban. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) a CTCF gén nonsense-mediated decay (NMD) rezisztens pozícióját érinti, ezért nagy valószínűséggel az NMD folyamat nem vezet a mutáns mRNS lebomlásához (1). Így a mutáns génről egy megváltozott C terminális szekvenciával rendelkező, kismértékben csonka fehérjeválozat képződik, ezért lehetséges, hogy funkcióvesztéssel jár.

A CTCF egy tumorszupresszor gén, mely a konzervált, cink-ujjas DNS-kötő CTCF fehérjét kódolja.

A CTCF a 16q22.1 kromoszóma régióban található, melynek deléciója gyakori tumoros megbetegedésekben, főként emlődaganatokban (2). A CTCF gén mutációja gyakori endometriális daganatokban és CTCF haploinsufficienciát eredményez a mutáns transzkriptumok non-sense mediated decay" folyamata vagy funkcióvesztő mutációja által. CTCF deléció gyakran fordul elő a szerózus altípusban és rossz prognózissal bír (3).

Egy preklinikai vizsgálatban az egy CTCF allélvesztés serkentette a tumorképződést és a malignus progressziót (2).

### Referenciák:

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- (3) Marshall AD et al., *CTCF genetic alterations in endometrial carcinoma are pro-tumorigenic. Oncogene. 2017 Jul 20;36(29):4100-4110. Epub 2017 Mar 20. PMID: 28319062*

### PPP2R2A-Y189\*

A korai STOP kodon megjelenését eredményező mutáció (nonsense mutation) következtében egy jelentősen rövidebb fehérjeválozatot kódoló PPP2R2A variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

A PPP2R2A (B55alfa) egy heterotrimer szerin/treronin foszfatáz, amely részt vesz a sejtnövekedés és osztódás negatív kontrolljában (1). A PPP2R2A gén egy ismert tumorszupresszor (2).

Egy preklinikai vizsgálat alapján a PPP2R2A funkcióvesztő mutációi csökkentik a B55alfa fehérje expresszióját, ezáltal hozzájárulnak az AKT aktivációjához. A vizsgált PPP2R2A mutáns sejtek érzékenyek bizonyultak az AKT inhibitor MK2206 kezelésre (3).

Egy tanulmány szerint a PPP2R2A funkciójának kiesése megnövekedett ATM foszforilációt eredményezett, amely jelentős mértékben felülszabályozta a downstream effektor kináz CHK2 aktivitását, ami G1-S-fázisú sejtciklus leállításához és a BRCA1 és RAD51 csökkent regulációjához vezetett. Nem-kissejtes tüdődaganatból származó tumorsejteken végzett kísérletek során a PPP2R2A funkciójának blokkolása negatívan hatott a homológ rekombinációs javítási útvonal működésére és szenzibilizálta a tumorsejteket a PARP kismolekulájú inhibitorokkal szemben (4).

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- (1) Kurimchak A, Graña X. PP2A: more than a reset switch to activate pRB proteins during the cell cycle and in response to signaling cues. *Cell Cycle*. 2015;14(1):18-30. doi: 10.4161/15384101.2014.985069. PubMed PMID: 25483052; PubMed Central PMCID: PMC4612414.
- (2) Beca F et al. Altered PPP2R2A and Cyclin D1 expression defines a subgroup of aggressive luminal-like breast cancer. *BMC Cancer*. 2015 Apr 15;15:285. doi: 10.1186/s12885-015-1266-1. Epub 2015 Feb 15. PubMed PMID: 25879784
- (3) Shouse G. Novel B55-PP2A mutations in AML promote AKT T308 phosphorylation and sensitivity to AKT inhibitor-induced growth arrest. *Oncotarget*. 2016 Sep 20;7(38):61081-61092. doi: 10.18632/oncotarget.11209. PubMed PMID: 27531894
- (4) Kalev P. et al. Loss of PPP2R2A inhibits homologous recombination DNA repair and predicts tumor sensitivity to PARP inhibition. *Cancer Res*. 2012 Dec 15;72(24):6414-24. doi: 10.1158/0008-5472.CAN-12-1667. Epub 2012 Oct 18.

**XRCC2-K267fs\*?**

A mutáció megtalálható a COSMIC adatbázisban. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjeváltozatot kódoló XRCC2 variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

**XRCC2 mutáns gén – célpontok**

Az XRCC2 gén a RAD51 egyik paralógja, mely részt vesz a homológ rekombináció folyamatában.

Preklinikai evidencia alapján funkcióvesztő XRCC2 mutációk esetén a PARP inhibitorok említhetők pozitív asszociációban (1, 2). Forgalomban lévő PARP gátló gyógyszerek az OLAPARIB, RUCAPARIB, NIRAPARIB és a TALAZOPARIB.

Colorectalis sejtvonalon végzett kísérletben kimutatták, hogy az XRCC2 expressziójának hiánya magasabb szenzitivitással asszociált 5-FU alapú terápiákra (3); valamint érzékenyített radioterápiára (4).

## Referenciák:

- (1) Somyajit K et al., Enhanced non-homologous end joining contributes toward synthetic lethality of pathological RAD51C mutants with poly(ADP-ribose) polymerase. *Carcinogenesis*. 2015 Jan;36(1):13-24. Epub 2014 Oct 7. PMID: 25292178
- (2) Bryant HE et al., Specific killing of BRCA2-deficient tumours with inhibitors of poly(ADP-ribose) polymerase. *Nature*. 2005 Apr 14;434(7035):913-7. Erratum in: *Nature*. 2007 May 17;447(7142):346. PMID: 15829966
- (3) Zhang YZ et al., XRCC2-Deficient Cells are Highly Sensitive to 5-Fluorouracil in Colorectal Cancer. *Cell Physiol Biochem*. 2017;43(3):1207-1219. Epub 2017 Oct 5. PMID: 28977800
- (4) Qin CJ et al., XRCC2 as a predictive biomarker for radioresistance in locally advanced rectal cancer patients undergoing preoperative radiotherapy. *Oncotarget*. 2015 Oct 13;6(31):32193-204. PMID: 26320178

**PMS1-G417fs\*6**

A leolvasási kereteltolódást okozó mutáció (frameshift mutation) a PMS1 gén nonsense-mediated decay (NMD) rezisztens pozícióját érinti, ezért nagy valószínűséggel az NMD folyamat nem vezet a mutáns mRNA lebomlásához (1). Így a mutáns génről egy megváltozott C terminális szekvenciával rendelkező, kismértékben csónka fehérjeváltozat képződik, ezért lehetséges, hogy funkcióvesztéssel jár.

A gén valószínűleg része a DNS "mismatch repair" (MMR) rendszernek (UniProt). Csírvonalas mutációi Lynch szindrómát okozhatnak (2).

A PMS1 az MLH1-el képes dimerizálódni, együtt alkotják a MutLbeta komplexet, amely képes elnyomni a mutagenézist élesztőkben, azonban humán sejtekben ismeretlen a funkciója, az MLH1-PMS1 heterodimer nem része a kanonikus humán MMR rendszernek (3, 4).

PD-1 és PD-L1 gátló immunterápiák hatékonyságát MMR deficiens daganatok esetén klinikai evidencia támasztja alá (5).

Az FDA törzskönyvezte a PEMBROLIZUMAB PD-1 gátló antitestet standard terápiákon progrediált bármilyen szolid daganat esetén, ami MSI-H státuszú vagy MMR deficiens fenotípusú.

MMR deficiencia esetén rezisztenciát írtak le kemoterápiás kezelésekkal szemben, mint az 5-FU, cisplatin és carboplatin, de nem tapasztaltak csökkent érzékenységet oxaliplatin kezelés esetén (6).

## Referenciák:

- (1) Litchfield K et al., Escape from nonsense mediated decay associates with anti-tumor immunogenicity. 2019. doi: 10.1101/823716.
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### WNK2-P1381fs\*11

A leolvasási kereteltolódást okozó mutáció (frameshift mutation) a WNK2 gén nonsense-mediated decay (NMD) rezisztens pozícióját érinti, ezért nagy valószínűséggel az NMD folyamat nem vezet a mutáns mRNS lebomlásához (1). Így a mutáns génről egy megváltozott C terminális szekvenciával rendelkező, kismértékben csonka fehérjevátozat képződik, ezért lehetséges, hogy funkcióvesztéssel jár.

A WNK2 gén tumorszupresszor funkcióját leírták már glioma és hepatocelluláris indikációkban (2, 3).

A WNK2 részt vesz a tumoros sejtek növekedési faktorok által indukált proliferációjában a MEK1/ERK1/2 jelátviteli útvonalon keresztül (4).

#### Referenciák:

(1) Litchfield K et al., Escape from nonsense mediated decay associates with anti-tumor immunogenicity. 2019. doi: 10.1101/823716.

(2) Costa AM et al., Silencing of the tumor suppressor gene WNK2 is associated with upregulation of MMP2 and JNK in gliomas. *Oncotarget.* 2015 Jan 30;6(3):1422-34. PMID: 25596741

(3) Zhou SL et al., Genomic sequencing identifies WNK2 as a driver in hepatocellular carcinoma and a risk factor for early recurrence. *J Hepatol.* 2019 Dec;71(6):1152-1163. Epub 2019 Jul 23. PMID: 31349001

(4) Moniz Set al., Protein kinase WNK2 inhibits cell proliferation by negatively modulating the activation of MEK1/ERK1/2. *Oncogene.* 2007 Sep 6; 26(41):6071-81. Erratum in: *Oncogene.* 2008 Jan 3;27(1):155. Kotevelets, L [corrected to Kotelevets, L]. PMID: 17667937.

### MRE11-R364\*

A mutáció megtalálható a COSMIC adatbázisban, a ClinVar adatbázis szerint patogén elváltozás. A korai STOP kodon megjelenését eredményező mutáció (nonsense mutation) következtében egy jelentősen rövidebb fehérjevátozatot kódoló MRE11 variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

### CARD11-R555fs\*45

A variáns szerepel a COSMIC adatbázisban (<40). A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjevátozatot kódoló CARD11 variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

### CBL-E196fs\*16

A mutáció megtalálható a COSMIC adatbázisban. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjevátozatot kódoló CBL variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

### SCN11A-K491fs\*5

A mutáció szerepel a COSMIC adatbázisban. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjevátozatot kódoló SCN11A variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető. A gén funkcióvesztő mutációinak nincs ismert szerepük a tumorképződésben.

### SAMD9L-K21fs\*3

Az alteráció szerepel a COSMIC adatbázisban. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) a SAMD9L gén nonsense-mediated decay (NMD) rezisztens pozícióját érinti, ezért nagy valószínűséggel az NMD folyamat nem vezet a mutáns mRNS lebomlásához (1). Így a mutáns génről egy megváltozott C terminális szekvenciával rendelkező, kismértékben csonka fehérjevátozat képződik, ezért lehetséges, hogy funkcióvesztéssel jár.

#### Referenciák:

(1) Litchfield K et al., Escape from nonsense mediated decay associates with anti-tumor immunogenicity. 2019. doi: 10.1101/823716.

### IGF2R-D1317fs\*5

A mutáció szerepel a COSMIC adatbázisban. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjevátozatot kódoló IGF2R variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

### SLIT2-K904fs\*13



## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjevátozatot kódoló SLIT2 variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

### CDC27-K319fs\*24

A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjevátozatot kódoló CDC27 variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

### Frameshift mutációk (SAMD9L-K21fs\*3, PMS1-G417fs\*6, CTCF-E691fs\*30, CDK12-G1271fs\*23, RECQL4-L339fs\*20, ARID1A-F2141fs\*59, ARID1A-Q1519fs\*8, WNK2-P1381fs\*11)

A rövid inszerciók és deléciók következtében kialakuló frameshift mutációk korai stop kodont (premature termination codon, PTC) eredményezhetnek és fokozottan érzékenyvé válhatnak a nonsense-mediated decay (NMD) folyamat általi mRNS-szintű degradációra. Az NMD az eukarióta génextpresszió alapvető minőségbiztosítási rendszere, mely normál sejtekben megakadályozza a csonka fehérjék toxikus felhalmozódását. A frameshift mutációk egy része azonban elkerülheti az NMD degradációt (1), ezáltal alternatív leolvasási keretek (ORF) jöhetnek létre, melyek új, a vad típusú génektől különböző, tumorspecifikus (neoantigén) szekvenciával rendelkeznek (2). Ezek a neoantigének hozzájárulhatnak a tumorelles immunválasz kialakulásához alacsony tumor mutation burden (TMB) értékkel rendelkező daganatokban (1, 3), ezáltal az immunterápiás kezelések célpontjává szolgálhatnak. Így a frameshift mutációk nagy jelentőséggel rendelkezhetnek a pontmutációkhoz (SNV-k) képest, kis előfordulási gyakoriságuk ellenére (4, 5).

Az NMD degradációt elkerülő mutációk nagyobb arányban fordulnak elő a gének utolsó exonjában és az utolsó előtti exon utolsó 50 nukleotidja között, az első exon első mintegy 150 nukleotidjában, illetve a 400 nukleotidnál hosszabb exonokban mint más exonokban (6). Egy tanulmányban az allélspecifikus frameshift indelek (fs-indelek) detektálása párosított DNS és RNS szekvenálási adatokban (n=453, TCGA) azt mutatta, hogy az expresszált fs-indelek jelenléte olyan genomiai pozíciókban volt megfigyelhető, amelyek valószínűsíthetően elkerülnek az NMD-t és magasabb fehérje expresszióval társulnak, összhangban az NMD elkerülés szabályaival (3).

A TCGA adatbázis vizsgálata szerint frameshift mutáció miatt keletkezett neoantigének minden tumortípusban előfordulnak (4). Vesesejtes carcinómában, lobuláris emlőcarcinómában és colorectalis carcinómában a leggyakoribbak (7).

Több tumortípusban, köztük melanómában, vesesejtes carcinómában, fej-nyak laphámcarcinómában és tüdődaganatokban is megfigyelték, hogy az aminosavcsere eredményező pontmutációkhoz képest a frameshift mutációk nagyobb mennyiségben képeznek magas kötési affinitású neoantigéneket (4, 5, 7). Jelenlétük összefüggést mutat a citotoxikus T-sejtek infiltrációjával, valamint az immun checkpoint inhibitorokra (ICI) adott tumorválasszal (3, 4, 7, 8). Melanomás betegcsoportban a kifejeződő frameshift mutációk száma jobb prediktornak bizonyult immunterápiák hatásosságára nézve, mint a pontmutációk száma (1, 3).

A frameshift mutációk egy alcsoportját képező, hosszú leolvasási keretű neoantigénekkal (neoORF) rendelkező betegek nagyobb érzékenységet mutattak immunterápiára (1, 3).

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### Törzskönyvezett célzott terápiák endometrium carcinómában

Az FDA törzskönyvezte a LENVATINIB (multi tirozin-kináz inhibitor) + PEMBROLIZUMAB (PD-1 inhibitor) kombinációs kezelést nem MSI-H és nem MMR-deficiens, endometrium daganat indikációjában, szisztémás terápiát követően. Egy fázis Ib/II klinikai vizsgálatban (NCT02501096; Study 111 /KEYNOTE-146) a kombináció MSI/MMR státuszról függetlenül biztató eredményt ért el endometrium daganatos betegekben (24. héten mért

## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

teljes válaszadási arány 50%; teljes adathalmazon mért teljes válaszadási arány 36,7%; progressziómentes túlélés: 10,1 hónap (1). A fázis III KEYNOTE-775 (NCT03517449) klinikai vizsgálat, mely során a pembrolizumab és lenvatinib kombinációját vizsgálják előrehaladott, endometrium carcinomás betegek körében, elsővonalas platina-alapú terápiát követően, teljesítette az elsődleges végpontnak kitűzött célokat a teljes túlélés (OS), a progressziómentes túlélés (PFS) és objektív válaszadási ráta (ORR) értékekben.

Elsővonalas kezelésként egyre gyakrabban alkalmazzák a kombinált kemoterápiákat endometrium carcinomás betegek esetén. Ugyanakkor a ritka teljes válaszadás, a gyakori kiújulás és progresszió arra enged következtetni, hogy a daganat gyorsan ellenállóvá válik a további kezelésre. A tumorsejtek rezisztenssé válhatnak a taxán-alapú szerekre (paclitaxel) a multidrog rezisztencia gén (MDR-1) overexpressziója miatt, mely efflux pumpaként számos toxikus anyag eltávolítását végzi a szervezetből. Emellett megfigyelték, hogy a tubulin kötőhelyben lokalizálódó pontmutációk is prediktív faktorai a rezisztencia kialakulásának. A magas béta-tubulin expresszió rövidebb progressziómentes túléléssel és rosszabb prognózissal asszociál (2).

Egy fázis III vizsgálatban doxorubicin + cisplatin, valamint doxorubicin + cisplatin + paclitaxel (TAP) kombinációk hatását vizsgálták endometrium tumoros betegeknél, ahol szignifikánsan nagyobb válaszarány (34% vs. 57%), progressziómentes túlélés (5,3 hónap vs. 8,3 hónap) és teljes túlélés (12,3 hónap vs. 15,3 hónap) adódott a TAP kezelés során (2).

Egy fázis II vizsgálatba 56 endometrium daganatos beteget válogattak be, akik bevacizumab (VEGFR gátló) terápiában részesültek. A betegek közül összesen hét esetben (13,5%) figyeltek meg klinikai válaszadást: egy teljes válasz, és 6 részleges válasz mutatkozott (3). Endometrium carcinomás betegek vizsgálata során bevacizumab és temsirolimus (mTOR gátló) kombinációs kezelés hatására 12 személy esetében (24,5%) klinikai válaszadást (1 teljes válasz, 11 részleges válasz), és 23 beteg esetében (46,9%) legalább 6 hónapig tartó progressziómentes túlélést figyeltek meg (4).

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A Realtime Oncology Molecular Treatment Calculator számításaival

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# Oncompass Report

A Realtime Oncology Molecular Treatment Calculator számításaival

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NEV	Anonymous

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CILTACABTAGENE AUTOLEUCEL	

# Oncompass Report

A Realtime Oncology Molecular Treatment Calculator számításaival

AZONOSÍTÓ	431898
NEV	Anonymous

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# Oncompass Report

A Realtime Oncology Molecular Treatment Calculator számításaival

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# Oncompass Report

A Realtime Oncology Molecular Treatment Calculator számításaival

AZONOSÍTÓ	431898
NÉV	Anonymous

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# Oncompass Report

A Realtime Oncology Molecular Treatment Calculator számításaival

AZONOSÍTÓ	431898
NÉV	Anonymous

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		NCBI ClinVar
FBXW7-R479Q		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Sanger Institute
		Wellcome Trust Sanger Institute
CTNNB1-T41A		Wellcome Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
PIK3CA-E81K		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		<a href="https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=20477959&amp;merge=750">https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=20477959&amp;merge=750</a>
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
ATM-S214fs*16		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute

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A Realtime Oncology Molecular Treatment Calculator számításaival

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BIOMARKEREK DRIVEREK	ÉS	REFERENCIA
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CDH1-I594fs*19		Wellcome Trust Sanger Institute NCBI ClinVar
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
RECQL4-L339fs*20		Wellcome Trust Sanger Institute NCBI ClinVar Database
		Wellcome Trust Sanger Institute
		NCBI ClinVar
		Wellcome trust sanger Institute
MRE11-R364*		Wellcome Sanger Institute NCBI ClinVar
		NCBI ClinVar
		Wellcome Sanger Institute
		Wellcome Trust Sanger Institute
IL2RG-R226C		Wellcome Trust Sanger Institute NCBI ClinVar
PIK3CB-L1049R		Pridham KJ, Varghese RT, Sheng Z. The Role of Class IA Phosphatidylinositol-4,5-Bisphosphate 3-Kinase Catalytic Subunits in Glioblastoma. <i>Front Oncol.</i> 2017 Dec 15;7:312. doi: 10.3389/fonc.2017.00312. eCollection 2017. Review. PubMed PMID: 29326882; PubMed Central PMCID: PMC5736525.
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		<a href="https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=57280906">https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=57280906</a>
		Wellcome Sanger Institute
ATM-I1581fs*20		NCBI ClinVar Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Sanger Institute
		Wellcome Trust Sanger Institute
CIC-R507C		Wellcome Sanger Institute NCBI ClinVar
		Wellcome Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
TSC2-I475T		<a href="https://cancer.sanger.ac.uk/cosmic/search?q=CIC+Q427H">https://cancer.sanger.ac.uk/cosmic/search?q=CIC+Q427H</a> Wellcome Trust Sanger Institute
		<a href="https://www.ncbi.nlm.nih.gov/clinvar/variation/582899/">https://www.ncbi.nlm.nih.gov/clinvar/variation/582899/</a>
		NCBI ClinVar
		NCBI ClinVar Database



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BIOMARKEREK DRIVEREK	ÉS	REFERENCIA
CTNNB1-Q26*		NCBI ClinVar Database
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
CTNNB1-496-1G>T		Cho J, Kim SY, Kim YJ, Sim MH, Kim ST, Kim NKD, Kim K, Park W, Kim JH, Jang KT, Lee J. Emergence of CTNNB1 mutation at acquired resistance to KIT inhibitor in metastatic melanoma. Clin Transl Oncol. 2017 Oct;19(10):1247-1252. doi: 10.1007/s12094-017-1662-x. Epub 2017 Apr 18. PubMed PMID: 28421416.
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ALK-M830L		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
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		Wellcome Trust Sanger Institute
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ARID1A-F2141fs*59		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		<a href="http://cancer.sanger.ac.uk/cosmic/search?q=arid1a+R1528*">http://cancer.sanger.ac.uk/cosmic/search?q=arid1a+R1528*</a>
		Wellcome Trust Sanger Institute
ARID1A-Q1519fs*8		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		LOVD database
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
ARID1A-Y551fs*68		Wellcome Sanger Institute
		Ticha I, Hojny J, Michalkova R, Kodet O, Krkavcova E, Hajkova N, Nemejcova K, Bartu M, Jaksa R, Dura M, Kanwal M, Martinikova AS, Macurek L, Zemankova P, Kleibl Z, Dunder P. A comprehensive evaluation of pathogenic mutations in primary cutaneous melanomas, including the identification of novel loss-of-function variants. Sci Rep. 2019 11 19;9(1):17050. doi: 10.1038/s41598-019-53636-x. Epub 2019 Jun 19. PubMed PMID: 31745173; PubMed Central PMCID: PMC6863855.
		Wellcome Trust Sanger Institute
		NCBI ClinVar
		NCBI ClinVar
RAD51D-P65L		LOVD database
		NCBI ClinVar
		NCBI ClinVar
		NCBI ClinVar
		NCBI ClinVar

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BIOMARKEREK DRIVEREK	ÉS	REFERENCIA
		Wellcome Sanger Institute
KMT2C-L4419P		Wellcome Sanger Institute
		Wellcome Trust Sanger Institute
		<a href="https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=3304628">https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=3304628</a>
		Wellcome Trust Sanger Institute
TET2-L1276fs*24		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		<a href="https://web.expasy.org/variant_pages/VAR_058189.html">https://web.expasy.org/variant_pages/VAR_058189.html</a>
		<a href="https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=7269706">https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=7269706</a>
		Wellcome Sanger Institute
FAT1-S1782N		Wellcome Trust Sanger Institute
		<a href="https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=1173044">https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=1173044</a>
		Wellcome Trust Sanger Institute
		Wellcome Sanger Institute
		Wellcome Trust Sanger Institute
FAT1-L3946P		NCBI ClinVar Database
		Wellcome Sanger Institute
		Leiden Open Variation Database
		Wellcome Trust Sanger Institute
		Wellcome Sanger Institute
FAT1-M3869T		Wellcome Trust Sanger Institute
		Wellcome Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Leiden Open Variation Database
		<a href="https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=1173044">https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=1173044</a>
SOX9-L60V		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
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DNMT3A-Q110fs*14		NCBI ClinVar
		Wellcome Sanger Institute

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BIOMARKEREK DRIVEREK	ÉS	REFERENCIA
PTPN1-R386K		Wellcome Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Sanger Institute
		Wellcome Trust Sanger Institute
GNAS-A36V		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Sanger Institute
		Wellcome Trust Sanger Institute
CBL-E196fs*16		Wellcome Trust Sanger Institute
		Angona A, Fernández-Rodríguez C, Alvarez-Larrán A, Camacho L, Longarón R, Torres E, Pairet S, Besses C, Bellosillo B. Molecular characterisation of triple negative essential thrombocythaemia patients by platelet analysis and targeted sequencing. Blood Cancer J. 2016 Aug 26;6(8):e463. doi: 10.1038/bcj.2016.75. PubMed PMID: 27564461; PubMed Central PMCID: PMC5022184.
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SMARCA4-Q1195H		Wellcome Sanger Institute
		<a href="http://cancer.sanger.ac.uk/cosmic/mutation/overview?id=6784850">http://cancer.sanger.ac.uk/cosmic/mutation/overview?id=6784850</a>
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Sanger Institute
FH-A104T		<a href="http://cancer.sanger.ac.uk/cosmic/search?q=SMARCA4+K588del">http://cancer.sanger.ac.uk/cosmic/search?q=SMARCA4+K588del</a>
		Wellcome Sanger Institute
		Wellcome Trust Sanger Institute
		<a href="https://www.ncbi.nlm.nih.gov/clinvar/variation/42095/">https://www.ncbi.nlm.nih.gov/clinvar/variation/42095/</a>
MED12-R431L		Wellcome Sanger Institute
		NCBI ClinVar
		Wellcome Sanger Institute
		NCBI ClinVar
		Wellcome Trust Sanger Institute
EPHA7-I473V		NCBI ClinVar
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		Wellcome Trust Sanger Institute

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BIOMARKEREK DRIVEREK	ÉS	REFERENCIA
TGFBR2-Q334H		<p><a href="https://www.ncbi.nlm.nih.gov/projects/SNP/snp_ref.cgi?rs=151105732">https://www.ncbi.nlm.nih.gov/projects/SNP/snp_ref.cgi?rs=151105732</a></p> <p>Wellcome Sanger Institute</p> <p>Wellcome Sanger Institute</p> <p><a href="https://www.ncbi.nlm.nih.gov/clinvar/variation/161394/">https://www.ncbi.nlm.nih.gov/clinvar/variation/161394/</a></p> <p>NCBI ClinVar</p> <p><a href="https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=6475910">https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=6475910</a></p> <p>Wellcome Trust Sanger Institute</p>
KDM5C-R68fs*5		<p>Zimmermann MT, Urrutia R, Oliver GR, Blackburn PR, Cousin MA, Bozcek NJ, Klee EW. Molecular modeling and molecular dynamic simulation of the effects of variants in the TGFBR2 kinase domain as a paradigm for interpretation of variants obtained by next generation sequencing. PLoS One. 2017 Feb 9;12(2):e0170822. doi: 10.1371/journal.pone.0170822. eCollection 2017. PubMed PMID: 28182693; PubMed Central PMCID: PMC5300139.</p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome Sanger Institute</p> <p>Wellcome Sanger Institute</p>
CARD11-R555fs*45		<p>NCBI ClinVar Database</p> <p><a href="https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=46512555">https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=46512555</a></p> <p>NCBI ClinVar Database</p> <p>Chan W, Schaffer TB, Pomerantz JL. A quantitative signaling screen identifies CARD11 mutations in the CARD and LATCH domains that induce Bcl10 ubiquitination and human lymphoma cell survival. Mol Cell Biol. 2013 Jan;33(2):429-43. doi: 10.1128/MCB.00850-12. Epub 2012 Nov 12. PubMed PMID: 23149938; PubMed Central PMCID: PMC3554118.</p> <p>Wellcome Trust Sanger Institute</p>
NSD1-M1531fs*43		<p>Wellcome Sanger Institute</p> <p>Wellcome Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome trust Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p>
NSD1-F1799fs*22		<p>Wellcome Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome trust Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p>
XRCC2-K267fs*?		<p>NCBI ClinVar</p> <p>Wellcome Sanger Institute</p>
CARD11-R404M		<p>Mohamed FZ, Hussien YM, AlBakry MM, Mohamed RH, Said NM. Role of DNA repair and cell cycle control genes in ovarian cancer susceptibility. Mol Biol Rep. 2013 May;40(5):3757-68. doi: 10.1007/s11033-012-2452-8. Epub 2013 Jan 1. PubMed PMID: 23277402.</p> <p>NCBI ClinVar</p> <p>NCBI ClinVar Database</p> <p>Leiden Open Variation Database</p>

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ARID2-D1758G		<p>Chan W, Schaffer TB, Pomerantz JL. A quantitative signaling screen identifies CARD11 mutations in the CARD and LATCH domains that induce Bcl10 ubiquitination and human lymphoma cell survival. <i>Mol Cell Biol.</i> 2013 Jan;33(2):429-43. doi: 10.1128/MCB.00850-12. Epub 2012 Nov 12. PubMed PMID: 23149938; PubMed Central PMCID: PMC3554118.</p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome Sanger Institute</p>
CDK12-G1271fs*23		<p>Wellcome Trust Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p>
CDK12-A1174S		<p>Wellcome Trust Sanger Institute</p> <p>Wellcome Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome Sanger Institute</p> <p>Wellcome Sanger Institute</p>
ARAF-S157N		<p>Wellcome Trust Sanger Institute</p> <p>Wellcome Sanger Institute</p> <p>Wellcome Sanger Institute</p> <p>Wellcome Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome Sanger Institute</p>
TP53BP1-H964R		<p>Imielinski M, Greulich H, Kaplan B, Araujo L, Amann J, Horn L, Schiller J, Villalona-Calero MA, Meyerson M, Carbone DP. Oncogenic and sorafenib-sensitive ARAF mutations in lung adenocarcinoma. <i>J Clin Invest.</i> 2014 Apr;124(4):1582-6. doi: 10.1172/JCI72763. Epub 2014 Feb 24. PubMed PMID: 24569458; PubMed Central PMCID: PMC3973082.</p> <p>Nelson DS, Quispel W, Badalian-Very G, van Halteren AG, van den Bos C, Bovée JV, Tian SY, Van Hummelen P, Ducar M, MacConaill LE, Egeler RM, Rollins BJ. Somatic activating ARAF mutations in Langerhans cell histiocytosis. <i>Blood.</i> 2014 May 15;123(20):3152-5. doi: 10.1182/blood-2013-06-511139. Epub 2014 Mar 20. PubMed PMID: 24652991.</p> <p>Wellcome Trust Sanger Institute</p> <p>NCBI ClinVar</p>
IGF2R-D1317fs*5		<p>Nicolas E, Arora S, Zhou Y, Serebriiskii IG, Andrade MD, Handorf ED, Bodian DL, Vockley JG, Dunbrack RL, Ross EA, Egleston BL, Hall MJ, Golemis EA, Giri VN, Daly MB. Systematic evaluation of underlying defects in DNA repair as an approach to case-only assessment of familial prostate cancer. <i>Oncotarget.</i> 2015 Nov 24;6(37):39614-33. doi: 10.18632/oncotarget.5554. PubMed PMID: 26485759; PubMed Central PMCID: PMC4741850.</p> <p>Wellcome Trust Sanger Institute</p> <p><a href="http://snpeffect.switchlab.org/mutation/TP53B_HUMAN/VAR_022180">http://snpeffect.switchlab.org/mutation/TP53B_HUMAN/VAR_022180</a></p> <p><a href="https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=33703705">https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=33703705</a></p> <p>Wellcome Trust Sanger Institute</p>

# Oncompass Report

A Realtime Oncology Molecular Treatment Calculator számításaival

AZONOSÍTÓ	431898
NÉV	Anonymous

BIOMARKEREK DRIVEREK	ÉS	REFERENCIA
JAK2-C68R		Wellcome Sanger Institute
		Wellcome Sanger Institute
		NCBI ClinVar
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Sanger Institute
IGF2R-W53R		Wellcome Trust Sanger Institute
		Wellcome Sanger Institute
		Wellcome Sanger Institute
		<a href="https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=33703705">https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=33703705</a>
PAX5-A322fs*11		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
FANCF-G357D		Shim YJ, Ha J-S, Do Y-R, Kim HS. Whole-Exome Sequencing in Korean Children with Acute Lymphoblastic Leukemia. Blood. 2015 Dec 3;126(23):4994–4994.
		Wellcome Trust Sanger Institute
		<a href="https://www.ncbi.nlm.nih.gov/clinvar/variation/134349/">https://www.ncbi.nlm.nih.gov/clinvar/variation/134349/</a>
		Wellcome Trust Sanger Institute
		<a href="https://databases.lovd.nl/shared/variants/FANCF?search_position_c_start=959&amp;search_position_c_start_intron=0&amp;search_position_c_end=959&amp;search_position_c_end_intron=0&amp;search_vot_clean_dna_change=%3D%22959C%3E%22&amp;search_transcriptid=00007725">https://databases.lovd.nl/shared/variants/FANCF?search_position_c_start=959&amp;search_position_c_start_intron=0&amp;search_position_c_end=959&amp;search_position_c_end_intron=0&amp;search_vot_clean_dna_change=%3D%22959C%3E%22&amp;search_transcriptid=00007725</a>
CTCF-E691fs*30		Wellcome Trust Sanger Institute
		NCBI ClinVar
		Wellcome Trust Sanger Institute
		NCBI ClinVar
		Wellcome Sanger Institute
ESRP1-S625G		Wellcome Trust Sanger Institute
		LOVD database
		Wellcome Trust Sanger Institute
		Leiden Open Variation Database
		Wellcome Trust Sanger Institute
EPHA3-T115N		NCBI ClinVar
		Wellcome Sanger Institute
		Wellcome Trust Sanger Institute
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PPP2R2A-Y189*		Wellcome Trust Sanger Institute Shouse G, de Necochea-Campion R, Mirshahidi S, Liu X, Chen CS. Novel B55-PP2A mutations in AML promote AKT T308 phosphorylation and sensitivity to AKT inhibitor-induced growth arrest. <i>Oncotarget</i> . 2016 Sep 20;7(38):61081-61092. doi: 10.18632/oncotarget.11209. PubMed PMID: 27531894; PubMed Central PMCID: PMC5308637.
ERBB4-G1109S		Wellcome Trust Sanger Institute Wellcome Sanger Institute Wellcome Trust Sanger Institute Wellcome Sanger Institute
WNK2-P1381fs*11		Wellcome Sanger Institute Wellcome Trust Sanger Institute Wellcome Trust Sanger Institute Wellcome Trust Sanger Institute NCBI ClinVar
LAMA2-R185C		Wellcome Sanger Institute Wellcome Trust Sanger Institute Wellcome Trust Sanger Institute Wellcome Trust Sanger Institute <a href="https://www.ncbi.nlm.nih.gov/clinvar/variation/92968/">https://www.ncbi.nlm.nih.gov/clinvar/variation/92968/</a>
DMD-S3343fs*34		Wellcome Sanger Institute LOVD NCBI ClinVar Wellcome Sanger Institute Wellcome Sanger Institute
DMD-R1957Q		Wellcome Sanger Institute Wellcome Sanger Institute Wellcome Trust Sanger Institute Wellcome Sanger Institute NCBI ClinVar
PMS1-N489I		NCBI ClinVar Spugnesi L, Gabriele M, Scarpitta R, Tancredi M, Maresca L, Gambino G, Collavoli A, Aretini P, Bertolini I, Salvadori B, Landucci E, Fontana A, Rossetti E, Roncella M, Naccarato GA, Caligo MA. Germline mutations in DNA repair genes may predict neoadjuvant therapy response in triple negative breast patients. <i>Genes Chromosomes Cancer</i> . 2016 Dec;55(12):915-924. doi: 10.1002/gcc.22389. Epub 2016 Jul 26. PubMed PMID: 27328445. Wellcome Sanger Institute <a href="https://web.expasy.org/variant_pages/VAR_014877.html">https://web.expasy.org/variant_pages/VAR_014877.html</a> NCBI ClinVar
PMS1-G417fs*6		NCBI ClinVar <a href="https://web.expasy.org/variant_pages/VAR_014877.html">https://web.expasy.org/variant_pages/VAR_014877.html</a> NCBI ClinVar Spugnesi L, Gabriele M, Scarpitta R, Tancredi M, Maresca L, Gambino G, Collavoli A, Aretini P, Bertolini I, Salvadori B, Landucci E, Fontana A, Rossetti E, Roncella M, Naccarato GA, Caligo MA. Germline mutations in DNA repair genes may predict neoadjuvant therapy response in triple negative breast patients. <i>Genes Chromosomes Cancer</i> . 2016 Dec;55(12):915-924. doi: 10.1002/gcc.22389. Epub 2016 Jul 26. PubMed PMID: 27328445.

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BIOMARKEREK DRIVEREK	ÉS	REFERENCIA
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ZRSR2-P383A		NCBI ClinVar Wellcome Trust Sanger Institute Wellcome Sanger Institute
ZMYM3-C723F		Eisfeld AK, Kohlschmidt J, Mims A, Nicolet D, Walker CJ, Blachly JS, Carroll AJ, Papaioannou D, Kolitz JE, Powell BE, Stone RM, de la Chapelle A, Byrd JC, Mrózek K, Bloomfield CD. Additional gene mutations may refine the 2017 European LeukemiaNet classification in adult patients with de novo acute myeloid leukemia aged <60 years. Leukemia. 2020 May 27;.: doi: 10.1038/s41375-020-0872-3. Epub 2020 Aug 27. PubMed PMID: 32461631. Wellcome Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger Institute
		Wellcome Trust Sanger institute
SLX4-P1004L		Wellcome Trust Sanger Institute Wellcome Trust Sanger Institute Wellcome Sanger Institute
		NCBI ClinVar NCBI ClinVar
CSMD3-S3630Y		Wellcome Sanger Institute Wellcome Trust Sanger Institute Wellcome Sanger Institute Wellcome Sanger Institute Wellcome Trust Sanger Institute
SCN11A-K491fs*5		Wellcome Sanger Institute
SAMD9L-K21fs*3		Wellcome Sanger Institute Wellcome Sanger Institute Wellcome Sanger Institute Wellcome Trust Sanger Institute
		LOVD Database
TAF1-R855C		Wellcome Sanger Institute Wellcome Trust Sanger Institute Wellcome Trust Sanger Institute NCBI ClinVar Leiden Open Variation Database
SLIT2-K904fs*13		Kimura J, Nguyen ST, Liu H, Taira N, Miki Y, Yoshida K. A functional genome-wide RNAi screen identifies TAF1 as a regulator for apoptosis in response to genotoxic stress. Nucleic Acids Res. 2008 Sep;36(16):5250-9. doi: 10.1093/nar/gkn506. Epub 2008 Feb 06. PubMed PMID: 18684994; PubMed Central PMCID: PMC2532742. NCBI ClinVar Wellcome Sanger Institute <a href="https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=69285153">https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=69285153</a> Hwang DY, Kohl S, Fan X, Vivante A, Chan S, Dworschak GC, Schulz J, van Eerde AM, Hilger AC, Gee HY, Pennimpe T, Herrmann BG, van de Hoek G, Renkema KY, Schell C, Huber TB, Reutter HM, Soliman NA, Stajic N, Bogdanovic R, Kehinde EO, Lifton RP, Tasic V, Lu W, Hildebrandt F. Mutations of the SLIT2-ROBO2 pathway genes SLIT2 and SRGAP1 confer risk for congenital anomalies of the kidney and urinary tract. Hum Genet. 2015 Aug;134



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CDC27-K319fs*24		Wellcome Trust Sanger Institute Wellcome Trust Sanger Institute  Wellcome Sanger Institute  <a href="http://snpeffect.switchlab.org/mutation/CDC27_HUMAN/VAR_014489">http://snpeffect.switchlab.org/mutation/CDC27_HUMAN/VAR_014489</a>
DDX11-S407R		Qiu L, Wu J, Pan C, Tan X, Lin J, Liu R, Chen S, Geng R, Huang W. Downregulation of CDC27 inhibits the proliferation of colorectal cancer cells via the accumulation of p21Cip1/Waf1. Cell Death Dis. 2016 Jan 28;7:e2074. doi: 10.1038/cddis.2015.402. PubMed PMID: 26821069; PubMed Central PMCID: PMC4816181. Wellcome Trust Sanger Institute  <a href="https://databases.lovd.nl/shared/variants/DDX11/unique">https://databases.lovd.nl/shared/variants/DDX11/unique</a>  Wellcome Trust Sanger Institute  <a href="https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=43939475&amp;merge=3954641">https://cancer.sanger.ac.uk/cosmic/mutation/overview?id=43939475&amp;merge=3954641</a>
BAZ2B-N2000S		Wellcome Trust Sanger Institute Wellcome Sanger Institute  Wellcome Trust Sanger Institute  Wellcome Trust Sanger Institute  Wellcome Trust Sanger Institute
THSD7B-P642A		Wellcome Trust Sanger Institute Wellcome Sanger Institute  Wellcome Trust Sanger Institute  Wellcome Sanger Institute  Wellcome Sanger Institute
GLI1-G162D		Wellcome Sanger Institute Wellcome Sanger Institute  Wellcome Trust Sanger Institute  Wellcome Sanger Institute  <a href="https://cancer.sanger.ac.uk/cosmic/search?q=GLI1+R372H">https://cancer.sanger.ac.uk/cosmic/search?q=GLI1+R372H</a>
ADGRB3-E227A		Wellcome Sanger Institute Wellcome Sanger Institute  Wellcome Trust Sanger Institute  Wellcome Trust Sanger Institute  Wellcome Sanger Institute
ZBED4-V241I		Wellcome Trust Sanger Institute Wellcome Trust Sanger Institute  Wellcome Sanger Institute  Wellcome Sanger Institute
RPTOR-V1192I		Wellcome Trust Sanger Institute Wellcome Sanger Institute  Wellcome Trust Sanger Institute

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BIOMARKEREK DRIVEREK	ÉS	REFERENCIA
SMAD2-R410G		Wellcome Sanger Institute Wellcome Sanger Institute
SEC16A-P9L		Wellcome Trust Sanger Institute
GATA2-G273fs*53		Wellcome Sanger Institute
TRIO-L2277*		Wellcome Sanger Institute
AKAP9-P1381L		Wellcome Sanger Institute
AKAP9-R434W		Wellcome Sanger Institute
KMT2C-K339N		Wellcome Trust Sanger Institute
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BCR-D1106N		LOVD database Wellcome Trust Sanger Institute
PREX2-S977L		<a href="https://web.expasy.org/variant_pages/VAR_041891.html">https://web.expasy.org/variant_pages/VAR_041891.html</a> Wellcome Trust Sanger Institute
		NCBI ClinVar

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A Realtime Oncology Molecular Treatment Calculator számításaival

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DRIVER ÉS TARGET GÉNEK LEÍRÁSA	
DRIVER GÉNEK	
Név	Leírás
ABCC2	Mediates hepatobiliary excretion of numerous organic anions. May function as a cellular cisplatin transporter.
ALK	Neuronal orphan receptor tyrosine kinase that is essentially and transiently expressed in specific regions of the central and peripheral nervous systems and plays an important role in the genesis and differentiation of the nervous system. Transduces signals from ligands at the cell surface, through specific activation of the mitogen-activated protein kinase (MAPK) pathway. Phosphorylates almost exclusively at the first tyrosine of the Y-x-x-x-Y-Y motif. Following activation by ligand, ALK induces tyrosine phosphorylation of CBL, FRS2, IRS1 and SHC1, as well as of the MAP kinases MAPK1/ERK2 and MAPK3/ERK1. Acts as a receptor for ligands pleiotrophin (PTN), a secreted growth factor, and midkine (MDK), a PTN-related factor, thus participating in PTN and MDK signal transduction. PTN-binding induces MAPK pathway activation, which is important for the anti-apoptotic signaling of PTN and regulation of cell proliferation. MDK-binding induces phosphorylation of the ALK target insulin receptor substrate (IRS1), activates mitogen-activated protein kinases (MAPKs) and PI3-kinase, resulting also in cell proliferation induction. Drives NF-kappa-B activation, probably through IRS1 and the activation of the AKT serine/threonine kinase. Recruitment of IRS1 to activated ALK and the activation of NF-kappa-B are essential for the autocrine growth and survival signaling of MDK.
ARAF	Involved in the transduction of mitogenic signals from the cell membrane to the nucleus. May also regulate the TOR signaling cascade. Isoform 2: Serves as a positive regulator of myogenic differentiation by inducing cell cycle arrest, the expression of myogenin and other muscle-specific proteins, and myotube formation.
ARID1A	Involved in transcriptional activation and repression of select genes by chromatin remodeling (alteration of DNA-nucleosome topology). Binds DNA non-specifically. Belongs to the neural progenitors-specific chromatin remodeling complex (npBAF complex) and the neuron-specific chromatin remodeling complex (nBAF complex). During neural development a switch from a stem/progenitor to a post-mitotic chromatin remodeling mechanism occurs as neurons exit the cell cycle and become committed to their adult state. The transition from proliferating neural stem/progenitor cells to post-mitotic neurons requires a switch in subunit composition of the npBAF and nBAF complexes. As neural progenitors exit mitosis and differentiate into neurons, npBAF complexes which contain ACTL6A/BAF53A and PHF10/BAF45A, are exchanged for homologous alternative ACTL6B/BAF53B and DPF1/BAF45B or DPF3/BAF45C subunits in neuron-specific complexes (nBAF). The npBAF complex is essential for the self-renewal/proliferative capacity of the multipotent neural stem cells. The nBAF complex along with CREST plays a role regulating the activity of genes essential for dendrite growth (By similarity).
ARID2	Involved in transcriptional activation and repression of select genes by chromatin remodeling (alteration of DNA-nucleosome topology). Required for the stability of the SWI/SNF chromatin remodeling complex SWI/SNF-B (PBAF). May be involved in targeting the complex to different genes. May be involved in regulating transcriptional activation of cardiac genes.
ATM	Serine/threonine protein kinase which activates checkpoint signaling upon double strand breaks (DSBs), apoptosis and genotoxic stresses such as ionizing ultraviolet A light (UVA), thereby acting as a DNA damage sensor. Recognizes the substrate consensus sequence [ST]-Q. Phosphorylates Ser-139 of histone variant H2AX/H2AFX at double strand breaks (DSBs), thereby regulating DNA damage response mechanism. Also plays a role in pre-B cell allelic exclusion, a process leading to expression of a single immunoglobulin heavy chain allele to enforce clonality and monospecific recognition by the B-cell antigen receptor (BCR) expressed on individual B-lymphocytes. After the introduction of DNA breaks by the RAG complex on one immunoglobulin allele, acts by mediating a repositioning of the second allele to pericentromeric heterochromatin, preventing accessibility to the RAG complex and recombination of the second allele. Also involved in signal transduction and cell cycle control. May function as a tumor suppressor. Necessary for activation of ABL1 and SAPK. Phosphorylates DYRK2, CHEK2, p53/TP53, FANCD2, NFKBIA, BRCA1, CTIP, nibrin (NBN), TERF1, RAD9 and DCLRE1C. May play a role in vesicle and/or protein transport. Could play a role in T-cell development, gonad and neurological function. Plays a role in replication-dependent histone mRNA degradation. Binds DNA ends. Phosphorylation of DYRK2 in nucleus in response to genotoxic stress prevents its MDM2-mediated ubiquitination and subsequent proteasome degradation. Phosphorylates ATF2 which stimulates its function in DNA damage response.
ATP4A	Catalyzes the hydrolysis of ATP coupled with the exchange of H <sup>+</sup> and K <sup>+</sup> ions across the plasma membrane. Responsible for acid production in the stomach.
BAZ2B	May play a role in transcriptional regulation interacting with ISWI.
BCORL1	Transcriptional corepressor. May specifically inhibit gene expression when recruited to promoter regions by sequence-specific DNA-binding proteins such as BCL6. This repression may be mediated at least in part by histone deacetylase activities which can associate with this corepressor.
CARD11	Involved in the costimulatory signal essential for T-cell receptor (TCR)-mediated T-cell activation. Its binding to DPP4 induces T-cell proliferation and NF-kappa-B activation in a T-cell receptor/CD3-dependent manner. Activates NF-kappa-B via BCL10 and IKK. Stimulates the phosphorylation of BCL10
CBL	Adapter protein that functions as a negative regulator of many signaling pathways that are triggered by activation of cell surface receptors. Acts as an E3 ubiquitin-protein ligase, which accepts ubiquitin from specific E2 ubiquitin-conjugating enzymes, and then transfers it to substrates promoting their degradation by the proteasome. Recognizes activated receptor tyrosine kinases, including KIT, FLT1, FGFR1, FGFR2, PDGFRA, PDGFRB, EGFR, CSF1R, EPHA8 and KDR and terminates signaling. Recognizes membrane-bound HCK, SRC and other kinases of the SRC family and mediates their ubiquitination and degradation. Participates in signal transduction in hematopoietic cells. Plays an important role in the regulation of osteoblast differentiation and apoptosis. Essential for osteoclastic bone resorption. The Tyr-731 phosphorylated form induces the activation and recruitment of

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### DRIVER GÉNEK

Név	Leírás
CCNE1	phosphatidylinositol 3-kinase to the cell membrane in a signaling pathway that is critical for osteoclast function. May be functionally coupled with the E2 ubiquitin-protein ligase UB2D3.
CDH1	Essential for the control of the cell cycle at the G1/S (start) transition.
CDH1	Cadherins are calcium-dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types. CDH1 is involved in mechanisms regulating cell-cell adhesions, mobility and proliferation of epithelial cells. Has a potent invasive suppressor role. It is a ligand for integrin alpha-E/beta-7. E-Cad/CTF2 promotes non-amyloidogenic degradation of Abeta precursors. Has a strong inhibitory effect on APP C99 and C83 production.
CDK12	Cyclin-dependent kinase that phosphorylates the C-terminal domain (CTD) of the large subunit of RNA polymerase II (POLR2A), thereby acting as a key regulator of transcription elongation. Regulates the expression of genes involved in DNA repair and is required for the maintenance of genomic stability. Preferentially phosphorylates Ser-5 in CTD repeats that are already phosphorylated at Ser-7, but can also phosphorylate Ser-2. Required for RNA splicing, possibly by phosphorylating SRSF1/SF2. Involved in regulation of MAP kinase activity, possibly leading to affect the response to estrogen inhibitors.
CIC	Transcriptional repressor which may play a role in development of the central nervous system (CNS)
CSMD3	Involved in dendrite development.
CTCF	Chromatin binding factor that binds to DNA sequence specific sites. Involved in transcriptional regulation by binding to chromatin insulators and preventing interaction between promoter and nearby enhancers and silencers. Acts as transcriptional repressor binding to promoters of vertebrate MYC gene and BAG1 gene. Also binds to the PLK and PIM1 promoters. Acts as a transcriptional activator of APP. Regulates APOA1/C3/A4/A5 gene cluster and controls MHC class II gene expression. Plays an essential role in oocyte and preimplantation embryo development by activating or repressing transcription. Seems to act as tumor suppressor. Plays a critical role in the epigenetic regulation. Participates in the allele-specific gene expression at the imprinted IGF2/H19 gene locus. On the maternal allele, binding within the H19 imprinting control region (ICR) mediates maternally inherited higher-order chromatin conformation to restrict enhancer access to IGF2. Plays a critical role in gene silencing over considerable distances in the genome. Preferentially interacts with unmethylated DNA, preventing spreading of CpG methylation and maintaining methylation-free zones. Inversely, binding to target sites is prevented by CpG methylation. Plays an important role in chromatin remodeling. Can dimerize when it is bound to different DNA sequences, mediating long-range chromatin looping. Mediates interchromosomal association between IGF2/H19 and WSB1/NF1 and may direct distant DNA segments to a common transcription factory. Causes local loss of histone acetylation and gain of histone methylation in the beta-globin locus, without affecting transcription. When bound to chromatin, it provides an anchor point for nucleosomes positioning. Seems to be essential for homologous X-chromosome pairing. May participate with Tsix in establishing a regulatable epigenetic switch for X chromosome inactivation. May play a role in preventing the propagation of stable methylation at the escape genes from X- inactivation. Involved in sister chromatid cohesion. Associates with both centromeres and chromosomal arms during metaphase and required for cohesin localization to CTCF sites. Regulates asynchronous replication of IGF2/H19.
CTNNB1	Key downstream component of the canonical Wnt signaling pathway. In the absence of Wnt, forms a complex with AXIN1, AXIN2, APC, CSNK1A1 and GSK3B that promotes phosphorylation on N-terminal Ser and Thr residues and ubiquitination of CTNNB1 via BTRC and its subsequent degradation by the proteasome. In the presence of Wnt ligand, CTNNB1 is not ubiquitinated and accumulates in the nucleus, where it acts as a coactivator for transcription factors of the TCF/LEF family, leading to activate Wnt responsive genes. Involved in the regulation of cell adhesion. Acts as a negative regulator of centrosome cohesion. Involved in the CDK2/PTPBG/CTNNB1/CEACAM1 pathway of insulin internalization. Blocks anoikis of malignant kidney and intestinal epithelial cells and promotes their anchorage-independent growth by down-regulating DAPK2. Disrupts PML function and PML-NB formation by inhibiting RANBP2-mediated sumoylation of PML (PubMed:17524503, PubMed:18077326, PubMed:18086858, PubMed:18957423, PubMed:21262353, PubMed:22647378, PubMed:22699938, PubMed:22155184). Promotes neurogenesis by maintaining sympathetic neuroblasts within the cell cycle (By similarity).
DDX11	DNA-dependent ATPase and ATP-dependent DNA helicase that participates in various functions in genomic stability, including DNA replication, DNA repair and heterochromatin organization as well as in ribosomal RNA synthesis (PubMed:10648783, PubMed:21854770, PubMed:23797032, PubMed:26089203, PubMed:26503245). Its double-stranded DNA helicase activity requires either a minimal 5'-single-stranded tail length of approximately 15 nt (flap substrates) or 10 nt length single-stranded gapped DNA substrates of a partial duplex DNA structure for helicase loading and translocation along DNA in a 5' to 3' direction (PubMed:18499658, PubMed:22102414). The helicase activity is capable of displacing duplex regions up to 100 bp, which can be extended up to 500 bp by the replication protein A (RPA) or the cohesion CTF18-replication factor C (Ctf18-RFC) complex activities (PubMed:18499658). Shows also ATPase- and helicase activities on substrates that mimic key DNA intermediates of replication, repair and homologous recombination reactions, including forked duplex, anti-parallel G-quadruplex and three-stranded D-loop DNA molecules (PubMed:22102414, PubMed:26503245). Plays a role in DNA double-strand break (DSB) repair at the DNA replication fork during DNA replication recovery from DNA damage (PubMed:23797032). Recruited with TIMELESS factor upon DNA-replication stress response at DNA replication fork to preserve replication fork progression, and hence ensure DNA replication fidelity (PubMed:26503245). Cooperates also with TIMELESS factor during DNA replication to regulate proper sister chromatid cohesion and mitotic chromosome segregation (PubMed:17105772, PubMed:18499658, PubMed:20124417, PubMed:23116066, PubMed:23797032). Stimulates 5'-single-stranded DNA flap endonuclease activity of FEN1 in an ATP- and helicase-independent manner; and hence it may contribute in Okazaki fragment processing at DNA replication fork during lagging strand DNA synthesis (PubMed:18499658). Its ability to function at DNA replication fork is modulated by its binding to long non-coding RNA (lncRNA) cohesion regulator non-coding RNA DDX11-AS1/CONCR, which is able to increase both DDX11 ATPase activity and binding to DNA replicating regions (PubMed:27477908). Plays also a role in heterochromatin organization (PubMed:21854770). Involved in rRNA transcription activation through binding to active hypomethylated rDNA gene loci by recruiting UBTf and the RNA polymerase Pol I transcriptional machinery (PubMed:26089203). Plays a role in embryonic development and prevention of aneuploidy (By similarity). Involved in melanoma cell proliferation and survival (PubMed:23116066). Associates with chromatin at DNA replication fork regions (PubMed:27477908). Binds to single- and double-stranded DNAs (PubMed:9013641, PubMed:18499658, PubMed:22102414).

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### DRIVER GÉNEK

Név	Leírás
DMD	Anchors the extracellular matrix to the cytoskeleton via F-actin. Ligand for dystroglycan. Component of the dystrophin-associated glycoprotein complex which accumulates at the neuromuscular junction (NMJ) and at a variety of synapses in the peripheral and central nervous systems and has a structural function in stabilizing the sarcolemma. Also implicated in signaling events and synaptic transmission.
DNMT3A	Required for genome-wide de novo methylation and is essential for the establishment of DNA methylation patterns during development. DNA methylation is coordinated with methylation of histones. It modifies DNA in a non-processive manner and also methylates non-CpG sites. May preferentially methylate DNA linker between 2 nucleosomal cores and is inhibited by histone H1. Plays a role in paternal and maternal imprinting. Required for methylation of most imprinted loci in germ cells. Acts as a transcriptional corepressor for ZBTB18. Recruited to trimethylated Lys-36 of histone H3 (H3K36me3) sites. Can actively repress transcription through the recruitment of HDAC activity.
ELMO1	Involved in cytoskeletal rearrangements required for phagocytosis of apoptotic cells and cell motility. Acts in association with DOCK1 and CRK. Was initially proposed to be required in complex with DOCK1 to activate Rac Rho small GTPases. May enhance the guanine nucleotide exchange factor (GEF) activity of DOCK1.
EPHA3	Receptor tyrosine kinase which binds promiscuously membrane-bound ephrin family ligands residing on adjacent cells, leading to contact-dependent bidirectional signaling into neighboring cells. The signaling pathway downstream of the receptor is referred to as forward signaling while the signaling pathway downstream of the ephrin ligand is referred to as reverse signaling. Highly promiscuous for ephrin-A ligands it binds preferentially EFNA5. Upon activation by EFNA5 regulates cell-cell adhesion, cytoskeletal organization and cell migration. Plays a role in cardiac cells migration and differentiation and regulates the formation of the atrioventricular canal and septum during development probably through activation by EFNA1. Involved in the retinotectal mapping of neurons. May also control the segregation but not the guidance of motor and sensory axons during neuromuscular circuit development.
EPHA7	Receptor tyrosine kinase which binds promiscuously GPI-anchored ephrin-A family ligands residing on adjacent cells, leading to contact-dependent bidirectional signaling into neighboring cells. The signaling pathway downstream of the receptor is referred to as forward signaling while the signaling pathway downstream of the ephrin ligand is referred to as reverse signaling. Among GPI-anchored ephrin-A ligands, EFNA5 is a cognate /functional ligand for EPHA7 and their interaction regulates brain development modulating cell-cell adhesion and repulsion. Has a repellent activity on axons and is for instance involved in the guidance of corticothalamic axons and in the proper topographic mapping of retinal axons to the colliculus. May also regulate brain development through a caspase(CASP3)-dependent proapoptotic activity. Forward signaling may result in activation of components of the ERK signaling pathway including MAP2K1, MAP2K2, MAPK1 AND MAPK3 which are phosphorylated upon activation of EPHA7.
ERBB4	Tyrosine-protein kinase that plays an essential role as cell surface receptor for neuregulins and EGF family members and regulates development of the heart, the central nervous system and the mammary gland, gene transcription, cell proliferation, differentiation, migration and apoptosis. Required for normal cardiac muscle differentiation during embryonic development, and for postnatal cardiomyocyte proliferation. Required for normal development of the embryonic central nervous system, especially for normal neural crest cell migration and normal axon guidance. Required for mammary gland differentiation, induction of milk proteins and lactation. Acts as cell-surface receptor for the neuregulins NRG1, NRG2, NRG3 and NRG4 and the EGF family members BTC, EREG and HBEGF. Ligand binding triggers receptor dimerization and autophosphorylation at specific tyrosine residues that then serve as binding sites for scaffold proteins and effectors. Ligand specificity and signaling is modulated by alternative splicing, proteolytic processing, and by the formation of heterodimers with other ERBB family members, thereby creating multiple combinations of intracellular phosphotyrosines that trigger ligand- and context-specific cellular responses. Mediates phosphorylation of SHC1 and activation of the MAP kinases MAPK1/ERK2 and MAPK3 /ERK1. Isoform JM-A CYT-1 and isoform JM-B CYT-1 phosphorylate PIK3R1, leading to the activation of phosphatidylinositol 3-kinase and AKT1 and protect cells against apoptosis. Isoform JM-A CYT-1 and isoform JM-B CYT-1 mediate reorganization of the actin cytoskeleton and promote cell migration in response to NRG1. Isoform JM-A CYT-2 and isoform JM-B CYT-2 lack the phosphotyrosine that mediates interaction with PIK3R1, and hence do not phosphorylate PIK3R1, do not protect cells against apoptosis, and do not promote reorganization of the actin cytoskeleton and cell migration. Proteolytic processing of isoform JM-A CYT-1 and isoform JM-A CYT-2 gives rise to the corresponding soluble intracellular domains (4ICD) that translocate to the nucleus, promote nuclear import of STAT5A, activation of STAT5A, mammary epithelium differentiation, cell proliferation and activation of gene expression. The ERBB4 soluble intracellular domains (4ICD) colocalize with STAT5A at the CSN2 promoter to regulate transcription of milk proteins during lactation. The ERBB4 soluble intracellular domains can also translocate to mitochondria and promote apoptosis.
ESR1	Nuclear hormone receptor. The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues. Ligand-dependent nuclear transactivation involves either direct homodimer binding to a palindromic estrogen response element (ERE) sequence or association with other DNA-binding transcription factors, such as AP-1/c-Jun, c-Fos, ATF-2, Sp1 and Sp3, to mediate ERE-independent signaling. Ligand binding induces a conformational change allowing subsequent or combinatorial association with multiprotein coactivator complexes through LXXLL motifs of their respective components. Mutual transrepression occurs between the estrogen receptor (ER) and NF-kappa-B in a cell-type specific manner. Decreases NF-kappa-B DNA-binding activity and inhibits NF-kappa-B-mediated transcription from the IL6 promoter and displace RELA/p65 and associated coregulators from the promoter. Recruited to the NF-kappa-B response element of the CCL2 and IL8 promoters and can displace CREBBP. Present with NF-kappa-B components RELA/p65 and NFKB1/p50 on ERE sequences. Can also act synergistically with NF-kappa-B to activate transcription involving respective recruitment adjacent response elements; the function involves CREBBP. Can activate the transcriptional activity of TFF1. Also mediates membrane-initiated estrogen signaling involving various kinase cascades. Isoform 3 is involved in activation of NOS3 and endothelial nitric oxide production. Isoforms lacking one or several functional domains are thought to modulate transcriptional activity by competitive ligand or DNA binding and/or heterodimerization with the full length receptor. Essential for MTA1-mediated transcriptional regulation of BRCA1 and BCAS3. Isoform 3 can bind to ERE and inhibit isoform 1.
ESRP1	

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### DRIVER GÉNEK

Név	Leírás
FANCF	mRNA splicing factor that regulates the formation of epithelial cell-specific isoforms. Specifically regulates the expression of FGFR2-IIIb, an epithelial cell-specific isoform of FGFR2. Also regulates the splicing of CD44, CTNND1, ENAH, 3 transcripts that undergo changes in splicing during the epithelial-to-mesenchymal transition (EMT). Acts by directly binding specific sequences in mRNAs. Binds the GU-rich sequence motifs in the ISE/ISS-3, a cis-element regulatory region present in the mRNA of FGFR2.
FAT1	Plays an essential role for cellular polarization, directed cell migration and modulating cell-cell contact.
FAT3	May play a role in the interactions between neurites derived from specific subsets of neurons during development.
FBXW7	Substrate recognition component of an SCF (SKP1-CUL1-F-box protein) E3 ubiquitin-protein ligase complex which mediates the ubiquitination and subsequent proteasomal degradation of target proteins. Recognizes and binds phosphorylated sites/phosphodegrons within target proteins and thereafter bring them to the SCF complex for ubiquitination (PubMed:17434132). Identified substrates include cyclin-E (CCNE1 or CCNE2), JUN, MYC, NOTCH1 released notch intracellular domain (NICD), and probably PSEN1 (PubMed:11565034, PubMed:12354302, PubMed:11585921, PubMed:15103331, PubMed:14739463, PubMed:17558397, PubMed:17873522, PubMed:22608923). Acts as a negative regulator of JNK signaling by binding to phosphorylated JUN and promoting its ubiquitination and subsequent degradation (PubMed:14739463).
GATA2	Transcriptional activator which regulates endothelin-1 gene expression in endothelial cells. Binds to the consensus sequence 5-AGATAG-3
GLI1	Acts as a transcriptional activator (PubMed:19706761, PubMed:10806483, PubMed:19878745, PubMed:24311597, PubMed:24217340). Binds to the DNA consensus sequence 5'-GACCACCCA-3' (PubMed:2105456, PubMed:8378770, PubMed:24217340). May regulate the transcription of specific genes during normal development (PubMed:19706761). May play a role in craniofacial development and digital development, as well as development of the central nervous system and gastrointestinal tract. Mediates SHH signaling (PubMed:19706761). Plays a role in cell proliferation and differentiation via its role in SHH signaling (Probable). Isoform 2: Acts as a transcriptional activator, but activates a different set of genes than isoform 1. Activates expression of CD24, unlike isoform 1. Mediates SHH signaling. Promotes cancer cell migration.
GNAS	May inhibit the adenylyl cyclase-stimulating activity of guanine nucleotide-binding protein G(s) subunit alpha which is produced from the same locus in a different open reading frame. Guanine nucleotide-binding proteins (G proteins) are involved as modulators or transducers in various transmembrane signaling systems. The G(s) protein is involved in hormonal regulation of adenylyl cyclase: it activates the cyclase in response to beta-adrenergic stimuli. XLas isoforms interact with the same set of receptors as Gnas isoforms (By similarity). Guanine nucleotide-binding proteins (G proteins) are involved as modulators or transducers in various transmembrane signaling systems. The G(s) protein is involved in hormonal regulation of adenylyl cyclase: it activates the cyclase in response to beta-adrenergic stimuli. Stimulates the Ras signaling pathway via RAPGEF2.
IGSF10	Involved in the control of early migration of neurons expressing gonadotropin-releasing hormone (GNRH neurons) (By similarity). May be involved in the maintenance of osteochondroprogenitor cells pool (By similarity).
IL2RG	Common subunit for the receptors for a variety of interleukins.
JAK2	Non-receptor tyrosine kinase involved in various processes such as cell growth, development, differentiation or histone modifications. Mediates essential signaling events in both innate and adaptive immunity. In the cytoplasm, plays a pivotal role in signal transduction via its association with type I receptors such as growth hormone (GHR), prolactin (PRLR), leptin (LEPR), erythropoietin (EPOR), thrombopoietin (THPO); or type II receptors including IFN-alpha, IFN-beta, IFN-gamma and multiple interleukins. Following ligand-binding to cell surface receptors, phosphorylates specific tyrosine residues on the cytoplasmic tails of the receptor, creating docking sites for STATs proteins. Subsequently, phosphorylates the STATs proteins once they are recruited to the receptor. Phosphorylated STATs then form homodimer or heterodimers and translocate to the nucleus to activate gene transcription. For example, cell stimulation with erythropoietin (EPO) during erythropoiesis leads to JAK2 autophosphorylation, activation, and its association with erythropoietin receptor (EPOR) that becomes phosphorylated in its cytoplasmic domain. Then, STAT5 (STAT5A or STAT5B) is recruited, phosphorylated and activated by JAK2. Once activated, dimerized STAT5 translocates into the nucleus and promotes the transcription of several essential genes involved in the modulation of erythropoiesis. In addition, JAK2 mediates angiotensin-2-induced ARHGEF1 phosphorylation. Plays a role in cell cycle by phosphorylating CDKN1B. Cooperates with TEC through reciprocal phosphorylation to mediate cytokine-driven activation of FOS transcription. In the nucleus, plays a key role in chromatin by specifically mediating phosphorylation of Tyr-41 of histone H3 (H3Y41ph), a specific tag that promotes exclusion of CBX5 (HP1 alpha) from chromatin.
KDM5C	Histone demethylase that specifically demethylates Lys-4 of histone H3, thereby playing a central role in histone code. Does not demethylate histone H3 Lys-9, H3 Lys-27, H3 Lys-36, H3 Lys-79 or H4 Lys-20. Demethylates trimethylated and dimethylated but not monomethylated H3 Lys-4. Participates in transcriptional repression of neuronal genes by recruiting histone deacetylases and REST at neuron-restrictive silencer elements. Represses the CLOCK-ARNTL/BMAL1 heterodimer-mediated transcriptional activation of the core clock component PER2 (By similarity).
KMT2C	Histone methyltransferase. Methylates Lys-4 of histone H3. H3 Lys-4 methylation represents a specific tag for epigenetic transcriptional activation. Central component of the MLL2/3 complex, a coactivator complex of nuclear receptors, involved in transcriptional coactivation. KMT2C/MLL3 may be a catalytic subunit of this complex. May be involved in leukemogenesis and developmental disorder.
LAMA2	Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.
MED12	Component of the Mediator complex, a coactivator involved in the regulated transcription of nearly all RNA polymerase II-dependent genes. Mediator functions as a bridge to convey information from gene-specific

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### DRIVER GÉNEK

Név	Leírás
	regulatory proteins to the basal RNA polymerase II transcription machinery. Mediator is recruited to promoters by direct interactions with regulatory proteins and serves as a scaffold for the assembly of a functional preinitiation complex with RNA polymerase II and the general transcription factors. This subunit may specifically regulate transcription of targets of the Wnt signaling pathway and SHH signaling pathway.
MED13	Component of the Mediator complex, a coactivator involved in the regulated transcription of nearly all RNA polymerase II-dependent genes. Mediator functions as a bridge to convey information from gene-specific regulatory proteins to the basal RNA polymerase II transcription machinery. Mediator is recruited to promoters by direct interactions with regulatory proteins and serves as a scaffold for the assembly of a functional preinitiation complex with RNA polymerase II and the general transcription factors.
MIER3	Transcriptional repressor.
MRE11	Component of the MRN complex, which plays a central role in double-strand break (DSB) repair, DNA recombination, maintenance of telomere integrity and meiosis. The complex possesses single-strand endonuclease activity and double-strand-specific 3-5' exonuclease activity, which are provided by MRE11A. RAD50 may be required to bind DNA ends and hold them in close proximity. This could facilitate searches for short or long regions of sequence homology in the recombining DNA templates, and may also stimulate the activity of DNA ligases and/or restrict the nuclease activity of MRE11A to prevent nucleolytic degradation past a given point. The complex may also be required for DNA damage signaling via activation of the ATM kinase. In telomeres the MRN complex may modulate t-loop formation
MST1R	Receptor tyrosine kinase that transduces signals from the extracellular matrix into the cytoplasm by binding to MST1 ligand. Regulates many physiological processes including cell survival, migration and differentiation. Ligand binding at the cell surface induces autophosphorylation of RON on its intracellular domain that provides docking sites for downstream signaling molecules. Following activation by ligand, interacts with the PI3-kinase subunit PIK3R1, PLCG1 or the adapter GAB1. Recruitment of these downstream effectors by RON leads to the activation of several signaling cascades including the RAS-ERK, PI3 kinase-AKT, or PLCgamma-PKC. RON signaling activates the wound healing response by promoting epithelial cell migration, proliferation as well as survival at the wound site. Plays also a role in the innate immune response by regulating the migration and phagocytic activity of macrophages. Alternatively, RON can also promote signals such as cell migration and proliferation in response to growth factors other than MST1 ligand.
OTOP1	Required for normal formation of otoconia in the inner ear. Inhibits P2Y purinoceptors. Modulates calcium homeostasis and influx of calcium in response to extracellular ATP (By similarity).
PAX5	May play an important role in B-cell differentiation as well as neural development and spermatogenesis. Involved in the regulation of the CD19 gene, a B-lymphoid-specific target gene
PIK3CA	Phosphoinositide-3-kinase (PI3K) that phosphorylates PtdIns (Phosphatidylinositol), PtdIns4P (Phosphatidylinositol 4-phosphate) and PtdIns(4,5)P2 (Phosphatidylinositol 4,5-bisphosphate) to generate phosphatidylinositol 3,4,5-trisphosphate (PIP3). PIP3 plays a key role by recruiting PH domain-containing proteins to the membrane, including AKT1 and PDK1, activating signaling cascades involved in cell growth, survival, proliferation, motility and morphology. Participates in cellular signaling in response to various growth factors. Involved in the activation of AKT1 upon stimulation by receptor tyrosine kinases ligands such as EGF, insulin, IGF1, VEGFA and PDGF. Involved in signaling via insulin-receptor substrate (IRS) proteins. Essential in endothelial cell migration during vascular development through VEGFA signaling, possibly by regulating RhoA activity. Required for lymphatic vasculature development, possibly by binding to RAS and by activation by EGF and FGF2, but not by PDGF. Regulates invadopodia formation in breast cancer cells through the PDK1-AKT1 pathway. Participates in cardiomyogenesis in embryonic stem cells through a AKT1 pathway. Participates in vasculogenesis in embryonic stem cells through PDK1 and protein kinase C pathway. Has also serine-protein kinase activity: phosphorylates PIK3R1 (p85alpha regulatory subunit), EIF4EBP1 and HRAS.
PIK3CB	Phosphoinositide-3-kinase (PI3K) that phosphorylates PtdIns (Phosphatidylinositol), PtdIns4P (Phosphatidylinositol 4-phosphate) and PtdIns(4,5)P2 (Phosphatidylinositol 4,5-bisphosphate) to generate phosphatidylinositol 3,4,5-trisphosphate (PIP3). PIP3 plays a key role by recruiting PH domain-containing proteins to the membrane, including AKT1 and PDK1, activating signaling cascades involved in cell growth, survival, proliferation, motility and morphology. Involved in the activation of AKT1 upon stimulation by G-protein coupled receptors (GPCRs) ligands such as CXCL12, sphingosine 1-phosphate, and lysophosphatidic acid. May also act downstream receptor tyrosine kinases. Required in different signaling pathways for stable platelet adhesion and aggregation. Plays a role in platelet activation signaling triggered by GPCRs, alpha-IIb/beta-3 integrins (ITGA2B/ ITGB3) and ITAM (immunoreceptor tyrosine-based activation motif)-bearing receptors such as GP6. Regulates the strength of adhesion of ITGA2B/ ITGB3 activated receptors necessary for the cellular transmission of contractile forces. Required for platelet aggregation induced by F2 (thrombin) and thromboxane A2 (TXA2). Has a role in cell survival. May have a role in cell migration. Involved in the early stage of autophagosome formation. Modulates the intracellular level of PtdIns3P (Phosphatidylinositol 3-phosphate) and activates PIK3C3 kinase activity. May act as a scaffold, independently of its lipid kinase activity to positively regulate autophagy. May have a role in insulin signaling as scaffolding protein in which the lipid kinase activity is not required. May have a kinase-independent function in regulating cell proliferation and in clathrin-mediated endocytosis. Mediator of oncogenic signal in cell lines lacking PTEN. The lipid kinase activity is necessary for its role in oncogenic transformation. Required for the growth of ERBB2 and RAS driven tumors
PPP2R2A	The B regulatory subunit might modulate substrate selectivity and catalytic activity, and also might direct the localization of the catalytic enzyme to a particular subcellular compartment.
PREX2	Functions as a RAC1 guanine nucleotide exchange factor (GEF), activating Rac proteins by exchanging bound GDP for free GTP. Its activity is synergistically activated by phosphatidylinositol 3,4,5-trisphosphate and the beta gamma subunits of heterotrimeric G protein. Mediates the activation of RAC1 in a PI3K-dependent manner. May be an important mediator of Rac signaling, acting directly downstream of both G protein-coupled receptors and phosphoinositide 3-kinase.
PRF1	Plays a key role in secretory granule-dependent cell death, and in defense against virus-infected or neoplastic cells. Plays an important role in killing other cells that are recognized as non-self by the immune system, e.g. in

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### DRIVER GÉNEK

Név	Leírás
	transplant rejection or some forms of autoimmune disease. Can insert into the membrane of target cells in its calcium-bound form, oligomerize and form large pores. Promotes cytolysis and apoptosis of target cells by facilitating the uptake of cytotoxic granzymes.
PTEN	Tumor suppressor. Acts as a dual-specificity protein phosphatase, dephosphorylating tyrosine-, serine- and threonine-phosphorylated proteins. Also acts as a lipid phosphatase, removing the phosphate in the D3 position of the inositol ring from phosphatidylinositol 3,4,5-trisphosphate, phosphatidylinositol 3,4-diphosphate, phosphatidylinositol 3-phosphate and inositol 1,3,4,5-tetrakisphosphate with order of substrate preference in vitro PtdIns(3,4,5)P3 > PtdIns(3,4)P2 > PtdIns3P > Ins(1,3,4,5)P4. The lipid phosphatase activity is critical for its tumor suppressor function. Antagonizes the PI3K-AKT/PKB signaling pathway by dephosphorylating phosphoinositides and thereby modulating cell cycle progression and cell survival. The unphosphorylated form cooperates with AIP1 to suppress AKT1 activation. Dephosphorylates tyrosine-phosphorylated focal adhesion kinase and inhibits cell migration and integrin-mediated cell spreading and focal adhesion formation. Plays a role as a key modulator of the AKT-mTOR signaling pathway controlling the tempo of the process of newborn neurons integration during adult neurogenesis, including correct neuron positioning, dendritic development and synapse formation. May be a negative regulator of insulin signaling and glucose metabolism in adipose tissue. The nuclear monoubiquitinated form possesses greater apoptotic potential, whereas the cytoplasmic nonubiquitinated form induces less tumor suppressive ability. In motile cells, suppresses the formation of lateral pseudopods and thereby promotes cell polarization and directed movement Isoform alpha: Functional kinase, like isoform 1 it antagonizes the PI3K-AKT/PKB signaling pathway. Plays a role in mitochondrial energetic metabolism by promoting COX activity and ATP production, via collaboration with isoform 1 in increasing protein levels of PINK1
PTPN11	Acts downstream of various receptor and cytoplasmic protein tyrosine kinases to participate in the signal transduction from the cell surface to the nucleus. Dephosphorylates ROCK2 at Tyr-722 resulting in stimulation of its RhoA binding activity.
RAD51D	Involved in the homologous recombination repair (HRR) pathway of double-stranded DNA breaks arising during DNA replication or induced by DNA-damaging agents. Bind to single-stranded DNA (ssDNA) and has DNA-dependent ATPase activity. Part of the Rad21 paralog protein complex BCDX2 which acts in the BRCA1-BRCA2-dependent HR pathway. Upon DNA damage, BCDX2 acts downstream of BRCA2 recruitment and upstream of RAD51 recruitment. BCDX2 binds predominantly to the intersection of the four duplex arms of the Holliday junction and to junction of replication forks. The BCDX2 complex was originally reported to bind single-stranded DNA, single-stranded gaps in duplex DNA and specifically to nicks in duplex DNA. Involved in telomere maintenance. The BCDX2 subcomplex XRCC2:RAD51D can stimulate Holliday junction resolution by BLM.
RPTOR	Involved in the control of the mammalian target of rapamycin complex 1 (mTORC1) activity which regulates cell growth and survival, and autophagy in response to nutrient and hormonal signals; functions as a scaffold for recruiting mTORC1 substrates. mTORC1 is activated in response to growth factors or amino acids. Growth factor-stimulated mTORC1 activation involves a AKT1-mediated phosphorylation of TSC1-TSC2, which leads to the activation of the RHEB GTPase that potently activates the protein kinase activity of mTORC1. Amino acid-signaling to mTORC1 requires its relocalization to the lysosomes mediated by the Ragulator complex and the Rag GTPases. Activated mTORC1 up-regulates protein synthesis by phosphorylating key regulators of mRNA translation and ribosome synthesis. mTORC1 phosphorylates EIF4EBP1 and releases it from inhibiting the elongation initiation factor 4E (eIF4E). mTORC1 phosphorylates and activates S6K1 at Thr-389, which then promotes protein synthesis by phosphorylating PDCD4 and targeting it for degradation. Involved in ciliogenesis.
SAMD9L	May be involved in endosome fusion. Mediates down-regulation of growth factor signaling via internalization of growth factor receptors.
SCN11A	This protein mediates the voltage-dependent sodium ion permeability of excitable membranes. Assuming opened or closed conformations in response to the voltage difference across the membrane, the protein forms a sodium-selective channel through which sodium ions may pass in accordance with their electrochemical gradient. It is a tetrodotoxin-resistant sodium channel isoform. Also involved, with the contribution of the receptor tyrosine kinase NTRK2, in rapid BDNF-evoked neuronal depolarization.
SEC16A	Defines endoplasmic reticulum exit sites (ERES) and is required for secretory cargo traffic from the endoplasmic reticulum to the Golgi apparatus. SAR1A-GTP-dependent assembly of SEC16A on the ER membrane forms an organized scaffold defining an ERES. Required for normal transitional endoplasmic reticulum (tER) organization.
SLC9A9	May act in electroneutral exchange of protons for Na <sup>+</sup> across membranes. Involved in the effusion of Golgi luminal H <sup>+</sup> in exchange for cytosolic cations. Involved in organelle ion homeostasis by contributing to the maintenance of the unique acidic pH values of the Golgi and post-Golgi compartments in the cell.
SLX4	Regulatory subunit that interacts with and increases the activity of different structure-specific endonucleases. Has several distinct roles in protecting genome stability by resolving diverse forms of deleterious DNA structures originating from replication and recombination intermediates and from DNA damage. Component of the SLX1-SLX4 structure-specific endonuclease that resolves DNA secondary structures generated during DNA repair and recombination. Has endonuclease activity towards branched DNA substrates, introducing single-strand cuts in duplex DNA close to junctions with ss-DNA. Has a preference for 5'-flap structures, and promotes symmetrical cleavage of static and migrating Holliday junctions (HJs). Resolves HJs by generating two pairs of ligatable, nicked duplex products. Interacts with the structure-specific ERCC4-ERCC1 endonuclease and promotes the cleavage of bubble structures. Interacts with the structure-specific MUS81-EME1 endonuclease and promotes the cleavage of 3'-flap and replication fork-like structures. SLX4 is required for recovery from alkylation-induced DNA damage and is involved in the resolution of DNA double-strand breaks.
SMAD2	Receptor-regulated SMAD (R-SMAD) that is an intracellular signal transducer and transcriptional modulator activated by TGF-beta (transforming growth factor) and activin type 1 receptor kinases. Binds the TRE element in the promoter region of many genes that are regulated by TGF-beta and, on formation of the SMAD2/SMAD4 complex, activates transcription. May act as a tumor suppressor in colorectal carcinoma. Positively regulates PDPK1 kinase activity by stimulating its dissociation from the 14-3-3 protein YWHAQ which acts as a negative regulator.
SMARCA4	Transcriptional coactivator cooperating with nuclear hormone receptors to potentiate transcriptional activation. Component of the CREST-BRG1 complex, a multiprotein complex that regulates promoter activation by

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### DRIVER GÉNEK

Név	Leírás
	orchestrating a calcium-dependent release of a repressor complex and a recruitment of an activator complex. In resting neurons, transcription of the c-FOS promoter is inhibited by BRG1-dependent recruitment of a phospho-RB1-HDAC repressor complex. Upon calcium influx, RB1 is dephosphorylated by calcineurin, which leads to release of the repressor complex. At the same time, there is increased recruitment of CREBBP to the promoter by a CREST-dependent mechanism, which leads to transcriptional activation. The CREST-BRG1 complex also binds to the NR2B promoter, and activity-dependent induction of NR2B expression involves a release of HDAC1 and recruitment of CREBBP. Belongs to the neural progenitors-specific chromatin remodeling complex (npBAF complex) and the neuron-specific chromatin remodeling complex (nBAF complex). During neural development a switch from a stem/progenitor to a post-mitotic chromatin remodeling mechanism occurs as neurons exit the cell cycle and become committed to their adult state. The transition from proliferating neural stem/progenitor cells to post-mitotic neurons requires a switch in subunit composition of the npBAF and nBAF complexes. As neural progenitors exit mitosis and differentiate into neurons, npBAF complexes which contain ACTL6A/BAF53A and PHF10/BAF45A, are exchanged for homologous alternative ACTL6B/BAF53B and DPF1/BAF45B or DPF3/BAF45C subunits in neuron-specific complexes (nBAF). The npBAF complex is essential for the self-renewal/proliferative capacity of the multipotent neural stem cells. The nBAF complex along with CREST plays a role regulating the activity of genes essential for dendrite growth. SMARCA4/BAF190A may promote neural stem cell self-renewal/proliferation by enhancing Notch-dependent proliferative signals, while concurrently making the neural stem cell insensitive to SHH-dependent differentiating cues (By similarity). Acts as a corepressor of ZEB1 to regulate E-cadherin transcription and is required for induction of epithelial-mesenchymal transition (EMT) by ZEB1.
SOX9	Plays an important role in the normal skeletal development. May regulate the expression of other genes involved in chondrogenesis by acting as a transcription factor for these genes
SYNE3	As a component of the LINC (Linker of Nucleoskeleton and Cytoskeleton) complex involved in the connection between the nuclear lamina and the cytoskeleton. The nucleocytoplasmic interactions established by the LINC complex play an important role in the transmission of mechanical forces across the nuclear envelope and in nuclear movement and positioning. Probable anchoring protein which tethers the nucleus to the cytoskeleton by binding PLEC which can associate with the intermediate filament system. Plays a role in the regulation of aortic epithelial cell morphology, and is required for flow-induced centrosome polarization and directional migration in aortic endothelial cells.
TAF1	Largest component and core scaffold of the TFIID basal transcription factor complex. Contains novel N- and C-terminal Ser/Thr kinase domains which can autophosphorylate or transphosphorylate other transcription factors. Phosphorylates TP53 on Thr-55 which leads to MDM2-mediated degradation of TP53. Phosphorylates GTF2A1 and GTF2F1 on Ser residues. Possesses DNA-binding activity. Essential for progression of the G1 phase of the cell cycle. Exhibits histone acetyltransferase activity towards histones H3 and H4.
TET2	Dioxygenase that catalyzes the conversion of the modified genomic base 5-methylcytosine (5mC) into 5-hydroxymethylcytosine (5hmC) and plays a key role in active DNA demethylation. Has a preference for 5-hydroxymethylcytosine in CpG motifs. Also mediates subsequent conversion of 5hmC into 5-formylcytosine (5fC), and conversion of 5fC to 5-carboxylcytosine (5caC). Conversion of 5mC into 5hmC, 5fC and 5caC probably constitutes the first step in cytosine demethylation. Methylation at the C5 position of cytosine bases is an epigenetic modification of the mammalian genome which plays an important role in transcriptional regulation. In addition to its role in DNA demethylation, also involved in the recruitment of the O-GlcNAc transferase OGT to CpG-rich transcription start sites of active genes, thereby promoting histone H2B GlcNAcylation by OGT.
TGFB2	Transmembrane serine/threonine kinase forming with the TGF-beta type I serine/threonine kinase receptor, TGFBR1, the non-promiscuous receptor for the TGF-beta cytokines TGFBI, TGFB2 and TGFB3. Transduces the TGFBI, TGFB2 and TGFB3 signal from the cell surface to the cytoplasm and is thus regulating a plethora of physiological and pathological processes including cell cycle arrest in epithelial and hematopoietic cells, control of mesenchymal cell proliferation and differentiation, wound healing, extracellular matrix production, immunosuppression and carcinogenesis. The formation of the receptor complex composed of 2 TGFBR1 and 2 TGFB2 molecules symmetrically bound to the cytokine dimer results in the phosphorylation and the activation of TGFBR1 by the constitutively active TGFB2. Activated TGFBR1 phosphorylates SMAD2 which dissociates from the receptor and interacts with SMAD4. The SMAD2-SMAD4 complex is subsequently translocated to the nucleus where it modulates the transcription of the TGF-beta-regulated genes. This constitutes the canonical SMAD-dependent TGF-beta signaling cascade. Also involved in non-canonical, SMAD-independent TGF-beta signaling pathways.
TP53BP1	Double-strand break (DSB) repair protein involved in response to DNA damage, telomere dynamics and class-switch recombination (CSR) during antibody genesis (PubMed:12364621, PubMed:22553214, PubMed:23333306, PubMed:17190600, PubMed:2144835, PubMed:28241136). Plays a key role in the repair of double-strand DNA breaks (DSBs) in response to DNA damage by promoting non-homologous end joining (NHEJ)-mediated repair of DSBs and specifically counteracting the function of the homologous recombination (HR) repair protein BRCA1 (PubMed:22553214, PubMed:23727112, PubMed:23333306). In response to DSBs, phosphorylation by ATM promotes interaction with RIF1 and dissociation from NUDT16L1/TIRR, leading to recruitment to DSBs sites (PubMed:28241136). Recruited to DSBs sites by recognizing and binding histone H2A monoubiquitinated at 'Lys-15' (H2AK15Ub) and histone H4 dimethylated at 'Lys-20' (H4K20me2), two histone marks that are present at DSBs sites (PubMed:23760478, PubMed:28241136, PubMed:17190600). Required for immunoglobulin class-switch recombination (CSR) during antibody genesis, a process that involves the generation of DNA DSBs (PubMed:23345425). Participates to the repair and the orientation of the broken DNA ends during CSR (By similarity). In contrast, it is not required for classic NHEJ and V(D)J recombination (By similarity). Promotes NHEJ of dysfunctional telomeres via interaction with PAXIP1 (PubMed:23727112).
TRIO	Guanine nucleotide exchange factor (GEF) for RHOA and RAC1 GTPases (PubMed:8643598, PubMed:27418539). Involved in coordinating actin remodeling, which is necessary for cell migration and growth (PubMed:10341202). In developing hippocampal neurons, limits dendrite formation, without affecting the establishment of axon polarity. Once dendrites are formed, involved in the control of synaptic function by regulating the endocytosis of AMPA-selective glutamate receptors (AMPA) at CA1 excitatory synapses (By similarity).
TSC2	In complex with TSC1, inhibits the nutrient-mediated or growth factor-stimulated phosphorylation of S6K1 and EIF4EBP1 by negatively regulating mTORC1 signaling. Acts as a GTPase-activating protein (GAP) for the small

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### DRIVER GÉNEK

Név	Leírás
	GTPase RHEB, a direct activator of the protein kinase activity of mTORC1. Implicated as a tumor suppressor. Involved in microtubule-mediated protein transport, but this seems to be due to unregulated mTOR signaling. Stimulates weakly the intrinsic GTPase activity of the Ras-related proteins RAPIA and RAB5 in vitro. Mutations in TSC2 lead to constitutive activation of RAPIA in tumors.
USP16	Specifically deubiquitinates 'Lys-120' of histone H2A (H2AK119Ub), a specific tag for epigenetic transcriptional repression, thereby acting as a coactivator. Deubiquitination of histone H2A is a prerequisite for subsequent phosphorylation at 'Ser-11' of histone H3 (H3S10ph), and is required for chromosome segregation when cells enter into mitosis. In resting B- and T-lymphocytes, phosphorylation by AURKB leads to enhance its activity, thereby maintaining transcription in resting lymphocytes. Regulates Hox gene expression via histone H2A deubiquitination. Prefers nucleosomal substrates. Does not deubiquitinate histone H2B.
WNK2	Serine/threonine kinase which plays an important role in the regulation of electrolyte homeostasis, cell signaling, survival, and proliferation. Acts as an activator and inhibitor of sodium-coupled chloride cotransporters and potassium-coupled chloride cotransporters respectively. Activates SLC12A2, SCNN1A, SCNN1B, SCNN1D and SGK1 and inhibits SLC12A5. Negatively regulates the EGF-induced activation of the ERK/MAPK-pathway and the downstream cell cycle progression. Affects MAPK3/MAPK1 activity by modulating the activity of MAP2K1 and this modulation depends on phosphorylation of MAP2K1 by PAK1. WNK2 acts by interfering with the activity of PAK1 by controlling the balance of the activity of upstream regulators of PAK1 activity, RHOA and RAC1, which display reciprocal activity.
ZMYM3	Plays a role in the regulation of cell morphology and cytoskeletal organization.
ZRSR2	Pre-mRNA-binding protein required for splicing of both U2- and U12-type introns. Selectively interacts with the 3-splice site of U2- and U12-type pre-mRNAs and promotes different steps in U2 and U12 intron splicing. Recruited to U12 pre-mRNAs in an ATP-dependent manner and is required for assembly of the prespliceosome, a precursor to other spliceosomal complexes. For U2-type introns, it is selectively and specifically required for the second step of splicing.

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### TARGET GÉNEK

Név	Leírás
ABL1	Non-receptor tyrosine-protein kinase that plays a role in many key processes linked to cell growth and survival such as cytoskeleton remodeling in response to extracellular stimuli, cell motility and adhesion, receptor endocytosis, autophagy, DNA damage response and apoptosis. Coordinates actin remodeling through tyrosine phosphorylation of proteins controlling cytoskeleton dynamics like WASF3 (involved in branch formation); ANXA1 (involved in membrane anchoring); DBN1, DBNL, CTTN, RAPH1 and ENAH (involved in signaling); or MAPT and PXN (microtubule-binding proteins). Phosphorylation of WASF3 is critical for the stimulation of lamellipodia formation and cell migration. Involved in the regulation of cell adhesion and motility through phosphorylation of key regulators of these processes such as BCAR1, CRK, CRKL, DOK1, EFS or NEDD9. Phosphorylates multiple receptor tyrosine kinases and more particularly promotes endocytosis of EGFR, facilitates the formation of neuromuscular synapses through MUSK, inhibits PDGFRB-mediated chemotaxis and modulates the endocytosis of activated B-cell receptor complexes. Other substrates which are involved in endocytosis regulation are the caveolin (CAV1) and RIN1. Moreover, ABL1 regulates the CBL family of ubiquitin ligases that drive receptor down-regulation and actin remodeling. Phosphorylation of CBL leads to increased EGFR stability. Involved in late-stage autophagy by regulating positively the trafficking and function of lysosomal components. ABL1 targets to mitochondria in response to oxidative stress and thereby mediates mitochondrial dysfunction and cell death. ABL1 is also translocated in the nucleus where it has DNA-binding activity and is involved in DNA-damage response and apoptosis. Many substrates are known mediators of DNA repair: DDB1, DDB2, ERCC3, ERCC6, RAD9A, RAD51, RAD52 or WRN. Activates the proapoptotic pathway when the DNA damage is too severe to be repaired. Phosphorylates TP73, a primary regulator for this type of damage-induced apoptosis. Phosphorylates the caspase CASP9 on Tyr-153 and regulates its processing in the apoptotic response to DNA damage. Phosphorylates PSMA7 that leads to an inhibition of proteasomal activity and cell cycle transition blocks. ABL1 acts also as a regulator of multiple pathological signaling cascades during infection. Several known tyrosine-phosphorylated microbial proteins have been identified as ABL1 substrates. This is the case of A36R of Vaccinia virus, Tir (translocated intimin receptor) of pathogenic E.coli and possibly Citrobacter, CagA (cytotoxin-associated gene A) of H.pylori, or AnkA (ankyrin repeat-containing protein A) of A.phagocytophilum. Pathogens can hijack ABL1 kinase signaling to reorganize the host actin cytoskeleton for multiple purposes, like facilitating intracellular movement and host cell exit. Finally, functions as its own regulator through autocatalytic activity as well as through phosphorylation of its inhibitor, ABI1.
AKT1	AKT1 is one of 3 closely related serine/threonine-protein kinases (AKT1, AKT2 and AKT3) called the AKT kinase, and which regulate many processes including metabolism, proliferation, cell survival, growth and angiogenesis. This is mediated through serine and/or threonine phosphorylation of a range of downstream substrates. Over 100 substrate candidates have been reported so far, but for most of them, no isoform specificity has been reported. AKT is responsible of the regulation of glucose uptake by mediating insulin-induced translocation of the SLC2A4/GLUT4 glucose transporter to the cell surface. Phosphorylation of PTPN1 at Ser-50 negatively modulates its phosphatase activity preventing dephosphorylation of the insulin receptor and the attenuation of insulin signaling. Phosphorylation of TBC1D4 triggers the binding of this effector to inhibitory 14-3-3 proteins, which is required for insulin-stimulated glucose transport. AKT regulates also the storage of glucose in the form of glycogen by phosphorylating GSK3A at Ser-21 and GSK3B at Ser-9, resulting in inhibition of its kinase activity. Phosphorylation of GSK3 isoforms by AKT is also thought to be one mechanism by which cell proliferation is driven. AKT regulates also cell survival via the phosphorylation of MAP3K5 (apoptosis signal-related kinase). Phosphorylation of Ser-83 decreases MAP3K5 kinase activity stimulated by oxidative stress and thereby prevents apoptosis. AKT mediates insulin-stimulated protein synthesis by phosphorylating TSC2 at Ser-939 and Thr-1462, thereby activating mTORC1 signaling and leading to both phosphorylation of 4E-BP1 and in activation of RPS6KB1. AKT is involved in the



## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### TARGET GÉNEK

Név	Leírás
	<p>phosphorylation of members of the FOXO factors (Forkhead family of transcription factors), leading to binding of 14-3-3 proteins and cytoplasmic localization. In particular, FOXO1 is phosphorylated at Thr-24, Ser-256 and Ser-319. FOXO3 and FOXO4 are phosphorylated on equivalent sites. AKT has an important role in the regulation of NF-kappa-B-dependent gene transcription and positively regulates the activity of CREB1 (cyclic AMP (cAMP)-response element binding protein). The phosphorylation of CREB1 induces the binding of accessory proteins that are necessary for the transcription of pro-survival genes such as BCL2 and MCL1. AKT phosphorylates Ser-454 on ATP citrate lyase (ACLY), thereby potentially regulating ACLY activity and fatty acid synthesis. Activates the 3B isoform of cyclic nucleotide phosphodiesterase (PDE3B) via phosphorylation of Ser-273, resulting in reduced cyclic AMP levels and inhibition of lipolysis. Phosphorylates PIKFYVE on Ser-318, which results in increased PI(3)P-5 activity. The Rho GTPase-activating protein DLC1 is another substrate and its phosphorylation is implicated in the regulation cell proliferation and cell growth. AKT plays a role as key modulator of the AKT-mTOR signaling pathway controlling the tempo of the process of newborn neurons integration during adult neurogenesis, including correct neuron positioning, dendritic development and synapse formation. Signals downstream of phosphatidylinositol 3-kinase (PI 3K) to mediate the effects of various growth factors such as platelet-derived growth factor (PDGF), epidermal growth factor (EGF), insulin and insulin-like growth factor I (IGF-I). AKT mediates the antiapoptotic effects of IGF-I. Essential for the SPATA13-mediated regulation of cell migration and adhesion assembly and disassembly. May be involved in the regulation of the placental development. Phosphorylates STK4/MST1 at Thr-120 and Thr-387 leading to inhibition of its: kinase activity, nuclear translocation, autophosphorylation and ability to phosphorylate FOXO3. Phosphorylates STK3/MST2 at Thr-117 and Thr-384 leading to inhibition of its: cleavage, kinase activity, autophosphorylation at Thr-180, binding to RASSF1 and nuclear translocation. Phosphorylates SRPK2 and enhances its kinase activity towards SRSF2 and ACIN1 and promotes its nuclear translocation. Phosphorylates RAF1 at Ser-259 and negatively regulates its activity. Phosphorylat</p>
AKT2	<p>AKT2 is one of 3 closely related serine/threonine-protein kinases (AKT1, AKT2 and AKT3) called the AKT kinase, and which regulate many processes including metabolism, proliferation, cell survival, growth and angiogenesis. This is mediated through serine and/or threonine phosphorylation of a range of downstream substrates. Over 100 substrate candidates have been reported so far, but for most of them, no isoform specificity has been reported. AKT is responsible of the regulation of glucose uptake by mediating insulin-induced translocation of the SLC2A4/GLUT4 glucose transporter to the cell surface. Phosphorylation of PTPN1 at Ser-50 negatively modulates its phosphatase activity preventing dephosphorylation of the insulin receptor and the attenuation of insulin signaling. Phosphorylation of TBC1D4 triggers the binding of this effector to inhibitory 14-3-3 proteins, which is required for insulin-stimulated glucose transport. AKT regulates also the storage of glucose in the form of glycogen by phosphorylating GSK3A at Ser-21 and GSK3B at Ser-9, resulting in inhibition of its kinase activity. Phosphorylation of GSK3 isoforms by AKT is also thought to be one mechanism by which cell proliferation is driven. AKT regulates also cell survival via the phosphorylation of MAP3K5 (apoptosis signal-related kinase). Phosphorylation of Ser-83 decreases MAP3K5 kinase activity stimulated by oxidative stress and thereby prevents apoptosis. AKT mediates insulin-stimulated protein synthesis by phosphorylating TSC2 at Ser-939 and Thr-1462, thereby activating mTORC1 signaling and leading to both phosphorylation of 4E-BP1 and in activation of RPS6KB1. AKT is involved in the phosphorylation of members of the FOXO factors (Forkhead family of transcription factors), leading to binding of 14-3-3 proteins and cytoplasmic localization. In particular, FOXO1 is phosphorylated at Thr-24, Ser-256 and Ser-319. FOXO3 and FOXO4 are phosphorylated on equivalent sites. AKT has an important role in the regulation of NF-kappa-B-dependent gene transcription and positively regulates the activity of CREB1 (cyclic AMP (cAMP)-response element binding protein). The phosphorylation of CREB1 induces the binding of accessory proteins that are necessary for the transcription of pro-survival genes such as BCL2 and MCL1. AKT phosphorylates Ser-454 on ATP citrate lyase (ACLY), thereby potentially regulating ACLY activity and fatty acid synthesis. Activates the 3B isoform of cyclic nucleotide phosphodiesterase (PDE3B) via phosphorylation of Ser-273, resulting in reduced cyclic AMP levels and inhibition of lipolysis. Phosphorylates PIKFYVE on Ser-318, which results in increased PI(3)P-5 activity. The Rho GTPase-activating protein DLC1 is another substrate and its phosphorylation is implicated in the regulation cell proliferation and cell growth. AKT plays a role as key modulator of the AKT-mTOR signaling pathway controlling the tempo of the process of newborn neurons integration during adult neurogenesis, including correct neuron positioning, dendritic development and synapse formation. Signals downstream of phosphatidylinositol 3-kinase (PI 3K) to mediate the effects of various growth factors such as platelet-derived growth factor (PDGF), epidermal growth factor (EGF), insulin and insulin-like growth factor I (IGF-I). AKT mediates the antiapoptotic effects of IGF-I. Essential for the SPATA13-mediated regulation of cell migration and adhesion assembly and disassembly. May be involved in the regulation of the placental development One of the few specific substrates of AKT2 identified recently is PITX2. Phosphorylation of PITX2 impairs its association with the CCND1 mRNA-stabilizing complex thus shortening the half-life of CCND1. AKT2 seems also to be the principal isoform responsible of the regulation of glucose uptake. Phosphorylates C2CD5 on Ser-197 during insulin-stimulated adipocytes. AKT2 is also specifically involved in skeletal muscle differentiation, one of its substrates in this process being ANKRD2. Down-regulation by RNA interference reduces the expression of the pho</p>
AKT3	<p>AKT3 is one of 3 closely related serine/threonine-protein kinases (AKT1, AKT2 and AKT3) called the AKT kinase, and which regulate many processes including metabolism, proliferation, cell survival, growth and angiogenesis. This is mediated through serine and/or threonine phosphorylation of a range of downstream substrates. Over 100 substrate candidates have been reported so far, but for most of them, no isoform specificity has been reported. AKT3 is the least studied AKT isoform. It plays an important role in brain development and is crucial for the viability of malignant glioma cells. AKT3 isoform may also be the key molecule in up-regulation and down-regulation of MMP13 via IL13. Required for the coordination of mitochondrial biogenesis with growth factor-induced increases in cellular energy demands. Down-regulation by RNA interference reduces the expression of the phosphorylated form of BAD, resulting in the induction of caspase-dependent apoptosis.</p>
ALK	<p>Neuronal orphan receptor tyrosine kinase that is essentially and transiently expressed in specific regions of the central and peripheral nervous systems and plays an important role in the genesis and differentiation of the nervous system. Transduces signals from ligands at the cell surface, through specific activation of the mitogen-activated protein kinase (MAPK) pathway. Phosphorylates almost exclusively at the first tyrosine of the Y-x-x-x-Y-Y motif. Following activation by ligand, ALK induces tyrosine phosphorylation of CBL, FRS2, IRS1 and SHC1, as well as of the MAP kinases MAPK1/ERK2 and MAPK3/ERK1. Acts as a receptor for ligands pleiotrophin (PTN), a secreted growth factor, and midkine (MDK), a PTN-related factor, thus participating in PTN and MDK signal transduction. PTN-binding induces MAPK pathway activation, which is important for the anti-apoptotic signaling of PTN and</p>

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### TARGET GÉNEK

Név	Leírás
	regulation of cell proliferation. MDK-binding induces phosphorylation of the ALK target insulin receptor substrate (IRS1), activates mitogen-activated protein kinases (MAPKs) and PI3-kinase, resulting also in cell proliferation induction. Drives NF-kappa-B activation, probably through IRS1 and the activation of the AKT serine/threonine kinase. Recruitment of IRS1 to activated ALK and the activation of NF-kappa-B are essential for the autocrine growth and survival signaling of MDK.
ARAF	Involved in the transduction of mitogenic signals from the cell membrane to the nucleus. May also regulate the TOR signaling cascade. Isoform 2: Serves as a positive regulator of myogenic differentiation by inducing cell cycle arrest, the expression of myogenin and other muscle-specific proteins, and myotube formation.
ATM	Serine/threonine protein kinase which activates checkpoint signaling upon double strand breaks (DSBs), apoptosis and genotoxic stresses such as ionizing ultraviolet A light (UVA), thereby acting as a DNA damage sensor. Recognizes the substrate consensus sequence [ST]-Q. Phosphorylates Ser-139 of histone variant H2AX/H2AFX at double strand breaks (DSBs), thereby regulating DNA damage response mechanism. Also plays a role in pre-B cell allelic exclusion, a process leading to expression of a single immunoglobulin heavy chain allele to enforce clonality and monospecific recognition by the B-cell antigen receptor (BCR) expressed on individual B-lymphocytes. After the introduction of DNA breaks by the RAG complex on one immunoglobulin allele, acts by mediating a repositioning of the second allele to pericentromeric heterochromatin, preventing accessibility to the RAG complex and recombination of the second allele. Also involved in signal transduction and cell cycle control. May function as a tumor suppressor. Necessary for activation of ABL1 and SAPK. Phosphorylates DYRK2, CHEK2, p53/TP53, FANCD2, NFKBIA, BRCA1, CTIP, nibrin (NBN), TERF1, RAD9 and DCLRE1C. May play a role in vesicle and/or protein transport. Could play a role in T-cell development, gonad and neurological function. Plays a role in replication-dependent histone mRNA degradation. Binds DNA ends. Phosphorylation of DYRK2 in nucleus in response to genotoxic stress prevents its MDM2-mediated ubiquitination and subsequent proteasome degradation. Phosphorylates ATF2 which stimulates its function in DNA damage response.
ATR	Serine/threonine protein kinase which activates checkpoint signaling upon genotoxic stresses such as ionizing radiation (IR), ultraviolet light (UV), or DNA replication stalling, thereby acting as a DNA damage sensor. Recognizes the substrate consensus sequence [ST]-Q. Phosphorylates BRCA1, CHEK1, MCM2, RAD17, RPA2, SMC1 and p53/TP53, which collectively inhibit DNA replication and mitosis and promote DNA repair, recombination and apoptosis. Phosphorylates Ser-139 of histone variant H2AX/H2AFX at sites of DNA damage, thereby regulating DNA damage response mechanism. Required for FANCD2 ubiquitination. Critical for maintenance of fragile site stability and efficient regulation of centrosome duplication.
AURKA	Mitotic serine/threonine kinases that contributes to the regulation of cell cycle progression. Associates with the centrosome and the spindle microtubules during mitosis and plays a critical role in various mitotic events including the establishment of mitotic spindle, centrosome duplication, centrosome separation as well as maturation, chromosomal alignment, spindle assembly checkpoint, and cytokinesis. Required for initial activation of CDK1 at centrosomes. Phosphorylates numerous target proteins, including ARHGEF2, BORA, BRCA1, CDC25B, DLGP5, HDAC6, KIF2A, LATS2, NDEL1, PARD3, PPP1R2, PLK1, RASSF1, TACC3, p53/TP53 and TPX2. Regulates KIF2A tubulin depolymerase activity. Required for normal axon formation. Plays a role in microtubule remodeling during neurite extension. Important for microtubule formation and/or stabilization. Also acts as a key regulatory component of the p53/TP53 pathway, and particularly the checkpoint-response pathways critical for oncogenic transformation of cells, by phosphorylating and stabilizing p53/TP53. Phosphorylates its own inhibitors, the protein phosphatase type 1 (PP1) isoforms, to inhibit their activity. Necessary for proper cilia disassembly prior to mitosis.
AURKB	Serine/threonine-protein kinase component of the chromosomal passenger complex (CPC), a complex that acts as a key regulator of mitosis. The CPC complex has essential functions at the centromere in ensuring correct chromosome alignment and segregation and is required for chromatin-induced microtubule stabilization and spindle assembly. Involved in the bipolar attachment of spindle microtubules to kinetochores and is a key regulator for the onset of cytokinesis during mitosis. Required for central/midzone spindle assembly and cleavage furrow formation. Key component of the cytokinesis checkpoint, a process required to delay abscission to prevent both premature resolution of intercellular chromosome bridges and accumulation of DNA damage: phosphorylates CHMP4C, leading to retain abscission-competent VPS4 (VPS4A and/or VPS4B) at the midbody ring until abscission checkpoint signaling is terminated at late cytokinesis (PubMed:22422861, PubMed:24814515). AURKB phosphorylates the CPC complex subunits BIRC5/survivin, CDCA8/borealin and INCENP. Phosphorylation of INCENP leads to increased AURKB activity. Other known AURKB substrates involved in centromeric functions and mitosis are CENPA, DES/desmin, GPAF, KIF2C, NSUN2, RACGAP1, SEPT1, VIM/vimentin, GSG2/Haspin, and histone H3. A positive feedback loop involving GSG2 and AURKB contributes to localization of CPC to centromeres. Phosphorylation of VIM controls vimentin filament segregation in cytokinetic process, whereas histone H3 is phosphorylated at Ser-10 and Ser-28 during mitosis (H3S10ph and H3S28ph, respectively). A positive feedback between GSG2 and AURKB contributes to CPC localization. AURKB is also required for kinetochore localization of BUB1 and SGOL1. Phosphorylation of p53/TP53 negatively regulates its transcriptional activity. Key regulator of active promoters in resting B- and T-lymphocytes: acts by mediating phosphorylation of H3S28ph at active promoters in resting B-cells, inhibiting RNF2/RING1B-mediated ubiquitination of histone H2A and enhancing binding and activity of the USP16 deubiquitinase at transcribed genes.
BCL2	Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1).
BRD4	Chromatin reader protein that recognizes and binds acetylated histones and plays a key role in transmission of epigenetic memory across cell divisions and transcription regulation. Remains associated with acetylated chromatin throughout the entire cell cycle and provides epigenetic memory for postmitotic G1 gene transcription by preserving acetylated chromatin status and maintaining high-order chromatin structure. During interphase, plays a key role in regulating the transcription of signal-inducible genes by associating with the P-TEFb complex and recruiting it to promoters: BRD4 is required to form the transcriptionally active P-TEFb complex by displacing negative regulators such as HEXIM1 and 7SKsnRNA complex from P-TEFb, thereby transforming it into an active form that can then phosphorylate the C-terminal domain (CTD) of RNA polymerase II. Promotes phosphorylation of Ser-2 of the C-terminal domain (CTD) of RNA polymerase II. According to a report, directly acts as an atypical

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### TARGET GÉNEK

Név	Leírás
CDK1	<p>protein kinase and mediates phosphorylation of Ser-2 of the C-terminal domain (CTD) of RNA polymerase II; these data however need additional evidences in vivo (PubMed:22509028). In addition to acetylated histones, also recognizes and binds acetylated RELA, leading to further recruitment of the P-TEFb complex and subsequent activation of NF-kappa-B. Also acts as a regulator of p53/TP53-mediated transcription: following phosphorylation by CK2, recruited to p53/TP53 specific target promoters. Isoform B: Acts as a chromatin insulator in the DNA damage response pathway. Inhibits DNA damage response signaling by recruiting the condensin-2 complex to acetylated histones, leading to chromatin structure remodeling, insulating the region from DNA damage response by limiting spreading of histone H2AFX/H2A.x phosphorylation</p> <p>Plays a key role in the control of the eukaryotic cell cycle by modulating the centrosome cycle as well as mitotic onset; promotes G2-M transition, and regulates G1 progress and G1-S transition via association with multiple interphase cyclins. Required in higher cells for entry into S-phase and mitosis. Phosphorylates PARVA/actopaxin, APC, AMPH, APC, BARD1, Bcl-xL/BCL2L1, BRCA2, CALD1, CASP8, CDC7, CDC20, CDC25A, CDC25C, CC2D1A, CSNK2 proteins/CKII, FZR1/CDH1, CDK7, CEBPB, CHAMP1, DMD/dystrophin, EEF1 proteins/EF-1, EZH2, KIF11/EG5, EGFR, FANCG, FOS, GFAP, GOLGA2/GM130, GRASP1, UBE2A/hHR6A, HIST1H1 proteins/histone H1, HMGAI, HIVEP3/KRC, LMNA, LMNB, LMNC, LBR, LATS1, MAP1B, MAP4, MARCKS, MCM2, MCM4, MKLP1, MYB, NEFH, NFIC, NPC/nuclear pore complex, PITPNM1/NIR2, NPM1, NCL, NUCKS1, NPM1/numatrin, ORC1, PRKAR2A, EEF1E1/p18, EIF3F/p47, p53/TP53, NONO/p54NRB, PAPOLA, PLEC/plectin, RB1, UL40/R2, RAB4A, RAP1GAP, RCC1, RPS6KB1/S6K1, KHDRBS1/SAM68, ESPL1, SKI, BIRC5/survivin, STIP1, TEX14, beta-tubulins, MAPT/TAU, NEDD1, VIM/vimentin, TK1, FOXO1, RUNX1/AML1, SIRT2 and RUNX2. CDK1/CDC2-cyclin-B controls pronuclear union in interphase fertilized eggs. Essential for early stages of embryonic development. During G2 and early mitosis, CDC25A/B/C-mediated dephosphorylation activates CDK1/cyclin complexes which phosphorylate several substrates that trigger at least centrosome separation, Golgi dynamics, nuclear envelope breakdown and chromosome condensation. Once chromosomes are condensed and aligned at the metaphase plate, CDK1 activity is switched off by WEE1- and PKMYT1-mediated phosphorylation to allow sister chromatid separation, chromosome decondensation, reformation of the nuclear envelope and cytokinesis. Inactivated by PKR/EIF2AK2- and WEE1-mediated phosphorylation upon DNA damage to stop cell cycle and genome replication at the G2 checkpoint thus facilitating DNA repair. Reactivated after successful DNA repair through WIP1-dependent signaling leading to CDC25A/B/C-mediated dephosphorylation and restoring cell cycle progression. In proliferating cells, CDK1-mediated FOXO1 phosphorylation at the G2-M phase represses FOXO1 interaction with 14-3-3 proteins and thereby promotes FOXO1 nuclear accumulation and transcription factor activity, leading to cell death of postmitotic neurons. The phosphorylation of beta-tubulins regulates microtubule dynamics during mitosis. NEDD1 phosphorylation promotes PLK1-mediated NEDD1 phosphorylation and subsequent targeting of the gamma-tubulin ring complex (gtURC) to the centrosome, an important step for spindle formation. In addition, CC2D1A phosphorylation regulates CC2D1A spindle pole localization and association with SCC1/RAD21 and centriole cohesion during mitosis. The phosphorylation of Bcl-xL/BCL2L1 after prolonged G2 arrest upon DNA damage triggers apoptosis. In contrast, CASP8 phosphorylation during mitosis prevents its activation by proteolysis and subsequent apoptosis. This phosphorylation occurs in cancer cell lines, as well as in primary breast tissues and lymphocytes. EZH2 phosphorylation promotes H3K27me3 maintenance and epigenetic gene silencing. CALD1 phosphorylation promotes Schwann cell migration during peripheral nerve regeneration.</p>
CDK2	<p>Serine/threonine-protein kinase involved in the control of the cell cycle; essential for meiosis, but dispensable for mitosis. Phosphorylates CTNNB1, USP37, p53/TP53, NPM1, CDK7, RB1, BRCA2, MYC, NPAT, EZH2. Interacts with cyclins A, B1, B3, D, or E. Triggers duplication of centrosomes and DNA. Acts at the G1-S transition to promote the E2F transcriptional program and the initiation of DNA synthesis, and modulates G2 progression; controls the timing of entry into mitosis/meiosis by controlling the subsequent activation of cyclin B/CDK1 by phosphorylation, and coordinates the activation of cyclin B/CDK1 at the centrosome and in the nucleus. Crucial role in orchestrating a fine balance between cellular proliferation, cell death, and DNA repair in human embryonic stem cells (hESCs). Activity of CDK2 is maximal during S phase and G2; activated by interaction with cyclin E during the early stages of DNA synthesis to permit G1-S transition, and subsequently activated by cyclin A2 (cyclin A1 in germ cells) during the late stages of DNA replication to drive the transition from S phase to mitosis, the G2 phase. EZH2 phosphorylation promotes H3K27me3 maintenance and epigenetic gene silencing. Phosphorylates CABLES1 (By similarity). Cyclin E/CDK2 prevents oxidative stress-mediated Ras-induced senescence by phosphorylating MYC. Involved in G1-S phase DNA damage checkpoint that prevents cells with damaged DNA from initiating mitosis; regulates homologous recombination-dependent repair by phosphorylating BRCA2, this phosphorylation is low in S phase when recombination is active, but increases as cells progress towards mitosis. In response to DNA damage, double-strand break repair by homologous recombination a reduction of CDK2-mediated BRCA2 phosphorylation. Phosphorylation of RB1 disturbs its interaction with E2F1. NPM1 phosphorylation by cyclin E/CDK2 promotes its dissociation from unduplicated centrosomes, thus initiating centrosome duplication. Cyclin E/CDK2-mediated phosphorylation of NPAT at G1-S transition and until prophase stimulates the NPAT-mediated activation of histone gene transcription during S phase. Required for vitamin D-mediated growth inhibition by being itself inactivated. Involved in the nitric oxide- (NO) mediated signaling in a nitrosylation/activation-dependent manner. USP37 is activated by phosphorylation and thus triggers G1-S transition. CTNNB1 phosphorylation regulates insulin internalization. Phosphorylates FOXP3 and negatively regulates its transcriptional activity and protein stability (By similarity).</p>
CDK4	<p>Ser/Thr-kinase component of cyclin D-CDK4 (DC) complexes that phosphorylate and inhibit members of the retinoblastoma (RB) protein family including RB1 and regulate the cell-cycle during G(1)/S transition. Phosphorylation of RB1 allows dissociation of the transcription factor E2F from the RB/E2F complexes and the subsequent transcription of E2F target genes which are responsible for the progression through the G(1) phase. Hypophosphorylates RB1 in early G(1) phase. Cyclin D-CDK4 complexes are major integrators of various mitogenic and antimitogenic signals. Also phosphorylates SMAD3 in a cell-cycle-dependent manner and represses its transcriptional activity. Component of the ternary complex, cyclin D/CDK4/CDKN1B, required for nuclear translocation and activity of the cyclin D-CDK4 complex.</p>
CDK6	<p>Serine/threonine-protein kinase involved in the control of the cell cycle and differentiation; promotes G1/S transition. Phosphorylates pRB/RB1 and NPM1. Interacts with D-type G1 cyclins during interphase at G1 to form a pRB/RB1 kinase and controls the entrance into the cell cycle. Involved in initiation and maintenance of cell cycle exit during cell differentiation; prevents cell proliferation and regulates negatively cell differentiation, but is required for the proliferation of specific cell types (e.g. erythroid and hematopoietic cells). Essential for cell proliferation within</p>

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### TARGET GÉNEK

Név	Leírás
CHEK1	the dentate gyrus of the hippocampus and the subventricular zone of the lateral ventricles. Required during thymocyte development. Promotes the production of newborn neurons, probably by modulating G1 length. Promotes, at least in astrocytes, changes in patterns of gene expression, changes in the actin cytoskeleton including loss of stress fibers, and enhanced motility during cell differentiation. Prevents myeloid differentiation by interfering with RUNX1 and reducing its transcription transactivation activity, but promotes proliferation of normal myeloid progenitors. Delays senescence. Promotes the proliferation of beta-cells in pancreatic islets of Langerhans. May play a role in the centrosome organization during the cell cycle phases (PubMed:23918663).
CTLA4	Serine/threonine-protein kinase which is required for checkpoint-mediated cell cycle arrest and activation of DNA repair in response to the presence of DNA damage or unreplicated DNA. May also negatively regulate cell cycle progression during unperturbed cell cycles. This regulation is achieved by a number of mechanisms that together help to preserve the integrity of the genome. Recognizes the substrate consensus sequence [R-X-X-S/T]. Binds to and phosphorylates CDC25A, CDC25B and CDC25C. Phosphorylation of CDC25A at Ser-178 and Thr-507 and phosphorylation of CDC25C at Ser-216 creates binding sites for 14-3-3 proteins which inhibit CDC25A and CDC25C. Phosphorylation of CDC25A at Ser-76, Ser-124, Ser-178, Ser-279 and Ser-293 promotes proteolysis of CDC25A. Phosphorylation of CDC25A at Ser-76 primes the protein for subsequent phosphorylation at Ser-79, Ser-82 and Ser-88 by NEK11, which is required for polyubiquitination and degradation of CDC25A. Inhibition of CDC25 leads to increased inhibitory tyrosine phosphorylation of CDK-cyclin complexes and blocks cell cycle progression. Also phosphorylates NEK6. Binds to and phosphorylates RAD51 at Thr-309, which promotes the release of RAD51 from BRCA2 and enhances the association of RAD51 with chromatin, thereby promoting DNA repair by homologous recombination. Phosphorylates multiple sites within the C-terminus of TP53, which promotes activation of TP53 by acetylation and promotes cell cycle arrest and suppression of cellular proliferation. Also promotes repair of DNA cross-links through phosphorylation of FANCE. Binds to and phosphorylates TLK1 at Ser-743, which prevents the TLK1-dependent phosphorylation of the chromatin assembly factor ASF1A. This may enhance chromatin assembly both in the presence or absence of DNA damage. May also play a role in replication fork maintenance through regulation of PCNA. May regulate the transcription of genes that regulate cell-cycle progression through the phosphorylation of histones. Phosphorylates histone H3.1 (to form H3T11ph), which leads to epigenetic inhibition of a subset of genes. May also phosphorylate RB1 to promote its interaction with the E2F family of transcription factors and subsequent cell cycle arrest Isoform 2: Endogenous repressor of isoform 1, interacts with, and antagonizes CHK1 to promote the S to G2/M phase transition
CTNNB1	Inhibitory receptor acting as a major negative regulator of T-cell responses. The affinity of CTLA4 for its natural B7 family ligands, CD80 and CD86, is considerably stronger than the affinity of their cognate stimulatory coreceptor CD28.
DOT1L	Key downstream component of the canonical Wnt signaling pathway. In the absence of Wnt, forms a complex with AXIN1, AXIN2, APC, CSNK1A1 and GSK3B that promotes phosphorylation on N-terminal Ser and Thr residues and ubiquitination of CTNNB1 via BTRC and its subsequent degradation by the proteasome. In the presence of Wnt ligand, CTNNB1 is not ubiquitinated and accumulates in the nucleus, where it acts as a coactivator for transcription factors of the TCF/LEF family, leading to activate Wnt responsive genes. Involved in the regulation of cell adhesion. Acts as a negative regulator of centrosome cohesion. Involved in the CDK2/PTPN6/CTNNB1/CEACAM1 pathway of insulin internalization. Blocks anoikis of malignant kidney and intestinal epithelial cells and promotes their anchorage-independent growth by down-regulating DAPK2. Disrupts PML function and PML-NB formation by inhibiting RANBP2-mediated sumoylation of PML (PubMed:17524503, PubMed:18077326, PubMed:18086858, PubMed:18957423, PubMed:21262353, PubMed:22647378, PubMed:22699938, PubMed:22155184). Promotes neurogenesis by maintaining sympathetic neuroblasts within the cell cycle (By similarity).
ERBB4	Histone methyltransferase. Methylates Lys-79 of histone H3. Nucleosomes are preferred as substrate compared to free histones. Binds to DNA
ESR1	Tyrosine-protein kinase that plays an essential role as cell surface receptor for neuregulins and EGF family members and regulates development of the heart, the central nervous system and the mammary gland, gene transcription, cell proliferation, differentiation, migration and apoptosis. Required for normal cardiac muscle differentiation during embryonic development, and for postnatal cardiomyocyte proliferation. Required for normal development of the embryonic central nervous system, especially for normal neural crest cell migration and normal axon guidance. Required for mammary gland differentiation, induction of milk proteins and lactation. Acts as cell-surface receptor for the neuregulins NRG1, NRG2, NRG3 and NRG4 and the EGF family members BTC, EREG and HBEGF. Ligand binding triggers receptor dimerization and autophosphorylation at specific tyrosine residues that then serve as binding sites for scaffold proteins and effectors. Ligand specificity and signaling is modulated by alternative splicing, proteolytic processing, and by the formation of heterodimers with other ERBB family members, thereby creating multiple combinations of intracellular phosphotyrosines that trigger ligand- and context-specific cellular responses. Mediates phosphorylation of SHC1 and activation of the MAP kinases MAPK1/ERK2 and MAPK3/ERK1. Isoform JM-A CYT-1 and isoform JM-B CYT-1 phosphorylate PIK3R1, leading to the activation of phosphatidylinositol 3-kinase and AKT1 and protect cells against apoptosis. Isoform JM-A CYT-1 and isoform JM-B CYT-1 mediate reorganization of the actin cytoskeleton and promote cell migration in response to NRG1. Isoform JM-A CYT-2 and isoform JM-B CYT-2 lack the phosphotyrosine that mediates interaction with PIK3R1, and hence do not phosphorylate PIK3R1, do not protect cells against apoptosis, and do not promote reorganization of the actin cytoskeleton and cell migration. Proteolytic processing of isoform JM-A CYT-1 and isoform JM-A CYT-2 gives rise to the corresponding soluble intracellular domains (4ICD) that translocate to the nucleus, promote nuclear import of STAT5A, activation of STAT5A, mammary epithelium differentiation, cell proliferation and activation of gene expression. The ERBB4 soluble intracellular domains (4ICD) colocalize with STAT5A at the CSN2 promoter to regulate transcription of milk proteins during lactation. The ERBB4 soluble intracellular domains can also translocate to mitochondria and promote apoptosis.
ESR1	Nuclear hormone receptor. The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues. Ligand-dependent nuclear transactivation involves either direct homodimer binding to a palindromic estrogen response element (ERE) sequence or association with other DNA-binding transcription factors, such as AP-1/c-Jun, c-Fos, ATF-2, Sp1 and Sp3, to mediate ERE-independent signaling. Ligand binding induces a conformational change allowing subsequent or combinatorial association with multiprotein coactivator complexes through LXXLL motifs of their respective components. Mutual transrepression occurs between the estrogen receptor (ER) and NF-kappa-B in a cell-type

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### TARGET GÉNEK

Név	Leírás
	specific manner. Decreases NF-kappa-B DNA-binding activity and inhibits NF-kappa-B-mediated transcription from the IL6 promoter and displace RELA/p65 and associated coregulators from the promoter. Recruited to the NF-kappa-B response element of the CCL2 and IL8 promoters and can displace CREBBP. Present with NF-kappa-B components RELA/p65 and NFKB1/p50 on ERE sequences. Can also act synergistically with NF-kappa-B to activate transcription involving respective recruitment adjacent response elements; the function involves CREBBP. Can activate the transcriptional activity of TFF1. Also mediates membrane-initiated estrogen signaling involving various kinase cascades. Isoform 3 is involved in activation of NOS3 and endothelial nitric oxide production. Isoforms lacking one or several functional domains are thought to modulate transcriptional activity by competitive ligand or DNA binding and/or heterodimerization with the full length receptor. Essential for MTA1-mediated transcriptional regulation of BRCA1 and BCAS3. Isoform 3 can bind to ERE and inhibit isoform 1.
EZH2	Polycomb group (PcG) protein. Catalytic subunit of the PRC2/EED-EZH2 complex, which methylates Lys-9 (H3K9me) and Lys-27 (H3K27me) of histone H3, leading to transcriptional repression of the affected target gene. Able to mono-, di- and trimethylate Lys-27 of histone H3 to form H3K27me1, H3K27me2 and H3K27me3, respectively. Compared to EZH2-containing complexes, it is more abundant in embryonic stem cells and plays a major role in forming H3K27me3, which is required for embryonic stem cell identity and proper differentiation. The PRC2/EED-EZH2 complex may also serve as a recruiting platform for DNA methyltransferases, thereby linking two epigenetic repression systems. Genes repressed by the PRC2/EED-EZH2 complex include HOXC8, HOXA9, MYT1, CDKN2A and retinoic acid target genes. EZH2 can also methylate non-histone proteins such as the transcription factor GATA4 and the nuclear receptor RORA. Regulates the circadian clock via histone methylation at the promoter of the circadian genes. Essential for the CRY1/2-mediated repression of the transcriptional activation of PER1/2 by the CLOCK-ARNTL/BMAL1 heterodimer; involved in the di and trimethylation of Lys-27 of histone H3 on PER1/2 promoters which is necessary for the CRY1/2 proteins to inhibit transcription.
FGFR1	Tyrosine-protein kinase that acts as cell-surface receptor for fibroblast growth factors and plays an essential role in the regulation of embryonic development, cell proliferation, differentiation and migration. Required for normal mesoderm patterning and correct axial organization during embryonic development, normal skeletogenesis and normal development of the gonadotropin-releasing hormone (GnRH) neuronal system. Phosphorylates PLCG1, FRS2, GAB1 and SHB. Ligand binding leads to the activation of several signaling cascades. Activation of PLCG1 leads to the production of the cellular signaling molecules diacylglycerol and inositol 1,4,5-trisphosphate. Phosphorylation of FRS2 triggers recruitment of GRB2, GAB1, PIK3R1 and SOS1, and mediates activation of RAS, MAPK1/ERK2, MAPK3/ERK1 and the MAP kinase signaling pathway, as well as of the AKT1 signaling pathway. Promotes phosphorylation of SHC1, STAT1 and PTPN11/SHP2. In the nucleus, enhances RPS6KA1 and CREB1 activity and contributes to the regulation of transcription. FGFR1 signaling is down-regulated by IL17RD/SEF, and by FGFR1 ubiquitination, internalization and degradation.
GBF1	This gene encodes a member of the Sec7 domain family. The encoded protein is a guanine nucleotide exchange factor that regulates the recruitment of proteins to membranes by mediating GDP to GTP exchange. The encoded protein is localized to the Golgi apparatus and plays a role in vesicular trafficking by activating ADP ribosylation factor 1. The encoded protein has also been identified as an important host factor for viral replication. Multiple transcript variants have been observed for this gene.
HMGCR	HMG-CoA reductase is the rate-limiting enzyme for cholesterol synthesis and is regulated via a negative feedback mechanism mediated by sterols and non-sterol metabolites derived from mevalonate, the product of the reaction catalyzed by reductase. Normally in mammalian cells this enzyme is suppressed by cholesterol derived from the internalization and degradation of low density lipoprotein (LDL) via the LDL receptor. Competitive inhibitors of the reductase induce the expression of LDL receptors in the liver, which in turn increases the catabolism of plasma LDL and lowers the plasma concentration of cholesterol, an important determinant of atherosclerosis. Alternatively spliced transcript variants encoding different isoforms have been found for this gene.
IDO1	This gene encodes indoleamine 2,3-dioxygenase (IDO) - a heme enzyme that catalyzes the first and rate-limiting step in tryptophan catabolism to N-formyl-kynurenine. This enzyme acts on multiple tryptophan substrates including D-tryptophan, L-tryptophan, 5-hydroxy-tryptophan, tryptamine, and serotonin. This enzyme is thought to play a role in a variety of pathophysiological processes such as antimicrobial and antitumor defense, neuropathology, immunoregulation, and antioxidant activity. Through its expression in dendritic cells, monocytes, and macrophages this enzyme modulates T-cell behavior by its peri-cellular catabolization of the essential amino acid tryptophan.
JAK1	Tyrosine kinase of the non-receptor type, involved in the IFN-alpha/beta/gamma signal pathway. Kinase partner for the interleukin (IL)-2 receptor.
JAK2	Non-receptor tyrosine kinase involved in various processes such as cell growth, development, differentiation or histone modifications. Mediates essential signaling events in both innate and adaptive immunity. In the cytoplasm, plays a pivotal role in signal transduction via its association with type I receptors such as growth hormone (GHR), prolactin (PRLR), leptin (LEPR), erythropoietin (EPOR), thrombopoietin (THPO); or type II receptors including IFN-alpha, IFN-beta, IFN-gamma and multiple interleukins. Following ligand-binding to cell surface receptors, phosphorylates specific tyrosine residues on the cytoplasmic tails of the receptor, creating docking sites for STATs proteins. Subsequently, phosphorylates the STATs proteins once they are recruited to the receptor. Phosphorylated STATs then form homodimer or heterodimers and translocate to the nucleus to activate gene transcription. For example, cell stimulation with erythropoietin (EPO) during erythropoiesis leads to JAK2 autophosphorylation, activation, and its association with erythropoietin receptor (EPOR) that becomes phosphorylated in its cytoplasmic domain. Then, STAT5 (STAT5A or STAT5B) is recruited, phosphorylated and activated by JAK2. Once activated, dimerized STAT5 translocates into the nucleus and promotes the transcription of several essential genes involved in the modulation of erythropoiesis. In addition, JAK2 mediates angiotensin-2-induced ARHGEF1 phosphorylation. Plays a role in cell cycle by phosphorylating CDKN1B. Cooperates with TEC through reciprocal phosphorylation to mediate cytokine-driven activation of FOS transcription. In the nucleus, plays a key role in chromatin by specifically mediating phosphorylation of Tyr-41 of histone H3 (H3Y41ph), a specific tag that promotes exclusion of CBX5 (HP1 alpha) from chromatin.
JAK3	Non-receptor tyrosine kinase involved in various processes such as cell growth, development, or differentiation. Mediates essential signaling events in both innate and adaptive immunity and plays a crucial role in hematopoiesis during T-cells development. In the cytoplasm, plays a pivotal role in signal transduction via its association with type I receptors sharing the common subunit gamma such as IL2R, IL4R, IL7R, IL9R, IL15R and IL21R. Following ligand

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### TARGET GÉNEK

Név	Leírás
	binding to cell surface receptors, phosphorylates specific tyrosine residues on the cytoplasmic tails of the receptor, creating docking sites for STATs proteins. Subsequently, phosphorylates the STATs proteins once they are recruited to the receptor. Phosphorylated STATs then form homodimer or heterodimers and translocate to the nucleus to activate gene transcription. For example, upon IL2R activation by IL2, JAK1 and JAK3 molecules bind to IL2R beta (IL2RB) and gamma chain (IL2RG) subunits inducing the tyrosine phosphorylation of both receptor subunits on their cytoplasmic domain. Then, STAT5A AND STAT5B are recruited, phosphorylated and activated by JAK1 and JAK3. Once activated, dimerized STAT5 translocates to the nucleus and promotes the transcription of specific target genes in a cytokine-specific fashion.
KDM1A	This gene encodes a nuclear protein containing a SWIRM domain, a FAD-binding motif, and an amine oxidase domain. This protein is a component of several histone deacetylase complexes, though it silences genes by functioning as a histone demethylase. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Apr 2009]
LAG3	Lymphocyte-activation protein 3 belongs to Ig superfamily and contains 4 extracellular Ig-like domains. The LAG3 gene contains 8 exons. The sequence data, exon/intron organization, and chromosomal localization all indicate a close relationship of LAG3 to CD4.
LYN	Non-receptor tyrosine-protein kinase that transmits signals from cell surface receptors and plays an important role in the regulation of innate and adaptive immune responses, hematopoiesis, responses to growth factors and cytokines, integrin signaling, but also responses to DNA damage and genotoxic agents. Functions primarily as negative regulator, but can also function as activator, depending on the context. Required for the initiation of the B-cell response, but also for its down-regulation and termination. Plays an important role in the regulation of B-cell differentiation, proliferation, survival and apoptosis, and is important for immune self-tolerance. Acts downstream of several immune receptors, including the B-cell receptor, CD79A, CD79B, CD5, CD19, CD22, FCER1, FCGR2, FCGR1A, TLR2 and TLR4. Plays a role in the inflammatory response to bacterial lipopolysaccharide. Mediates the responses to cytokines and growth factors in hematopoietic progenitors, platelets, erythrocytes, and in mature myeloid cells, such as dendritic cells, neutrophils and eosinophils. Acts downstream of EPOR, KIT, MPL, the chemokine receptor CXCR4, as well as the receptors for IL3, IL5 and CSF2. Plays an important role in integrin signaling. Regulates cell proliferation, survival, differentiation, migration, adhesion, degranulation, and cytokine release. Down-regulates signaling pathways by phosphorylation of immunoreceptor tyrosine-based inhibitory motifs (ITIM), that then serve as binding sites for phosphatases, such as PTPN6/SHP-1, PTPN11/SHP-2 and INPP5D/SHIP-1, that modulate signaling by dephosphorylation of kinases and their substrates. Phosphorylates LIME1 in response to CD22 activation. Phosphorylates BTK, CBL, CD5, CD19, CD72, CD79A, CD79B, CSF2RB, DOK1, HCLS1, LILRB3/PIR-B, MS4A2/FCER1B, PTK2B/PYK2, SYK and TEC. Promotes phosphorylation of SIRPA, PTPN6/SHP-1, PTPN11/SHP-2 and INPP5D/SHIP-1. Mediates phosphorylation of the BCR-ABL fusion protein. Required for rapid phosphorylation of FER in response to FCER1 activation. Mediates KIT phosphorylation. Acts as an effector of EPOR (erythropoietin receptor) in controlling KIT expression and may play a role in erythroid differentiation during the switch between proliferation and maturation. Depending on the context, activates or inhibits several signaling cascades. Regulates phosphatidylinositol 3-kinase activity and AKT1 activation. Regulates activation of the MAP kinase signaling cascade, including activation of MAP2K1/MEK1, MAPK1/ERK2, MAPK3/ERK1, MAPK8/JNK1 and MAPK9/JNK2. Mediates activation of STAT5A and/or STAT5B. Phosphorylates LPXN on Tyr-72. Kinase activity facilitates TLR4-TLR6 heterodimerization and signal initiation.
MCL1	Involved in the regulation of apoptosis versus cell survival, and in the maintenance of viability but not of proliferation. Mediates its effects by interactions with a number of other regulators of apoptosis. Isoform 1 inhibits apoptosis. Isoform 2 promotes apoptosis.
MET	Receptor tyrosine kinase that transduces signals from the extracellular matrix into the cytoplasm by binding to hepatocyte growth factor/HGF ligand. Regulates many physiological processes including proliferation, scattering, morphogenesis and survival. Ligand binding at the cell surface induces autophosphorylation of MET on its intracellular domain that provides docking sites for downstream signaling molecules. Following activation by ligand, interacts with the PI3-kinase subunit PIK3R1, PLCG1, SRC, GRB2, STAT3 or the adapter GAB1. Recruitment of these downstream effectors by MET leads to the activation of several signaling cascades including the RAS-ERK, PI3 kinase-AKT, or PLCgamma-PKC. The RAS-ERK activation is associated with the morphogenetic effects while PI3K/AKT coordinates prosurvival effects. During embryonic development, MET signaling plays a role in gastrulation, development and migration of muscles and neuronal precursors, angiogenesis and kidney formation. In adults, participates in wound healing as well as organ regeneration and tissue remodeling. Promotes also differentiation and proliferation of hematopoietic cells Acts as a receptor for Listeria internalin inlB, mediating entry of the pathogen into cells
MTOR	Serine/threonine protein kinase which is a central regulator of cellular metabolism, growth and survival in response to hormones, growth factors, nutrients, energy and stress signals. MTOR directly or indirectly regulates the phosphorylation of at least 800 proteins. Functions as part of 2 structurally and functionally distinct signaling complexes mTORC1 and mTORC2 (mTOR complex 1 and 2). Activated mTORC1 up-regulates protein synthesis by phosphorylating key regulators of mRNA translation and ribosome synthesis. This includes phosphorylation of EIF4EBP1 and release of its inhibition toward the elongation initiation factor 4E (eIF4E). Moreover, phosphorylates and activates RPS6KB1 and RPS6KB2 that promote protein synthesis by modulating the activity of their downstream targets including ribosomal protein S6, eukaryotic translation initiation factor EIF4B, and the inhibitor of translation initiation PDCD4. Stimulates the pyrimidine biosynthesis pathway, both by acute regulation through RPS6KB1-mediated phosphorylation of the biosynthetic enzyme CAD, and delayed regulation, through transcriptional enhancement of the pentose phosphate pathway which produces 5-phosphoribosyl-1-pyrophosphate (PRPP), an allosteric activator of CAD at a later step in synthesis, this function is dependent on the mTORC1 complex. Regulates ribosome synthesis by activating RNA polymerase III-dependent transcription through phosphorylation and inhibition of MAF1 an RNA polymerase III-repressor. In parallel to protein synthesis, also regulates lipid synthesis through SREBF1/SREBP1 and LPIN1. To maintain energy homeostasis mTORC1 may also regulate mitochondrial biogenesis through regulation of PPARGC1A. mTORC1 also negatively regulates autophagy through phosphorylation of ULK1. Under nutrient sufficiency, phosphorylates ULK1 at Ser-758, disrupting the interaction with AMPK and preventing activation of ULK1. Also prevents autophagy through phosphorylation of the autophagy inhibitor DAP. mTORC1 exerts a feedback control on upstream growth factor signaling that includes phosphorylation and activation of GRB10 a INSR-dependent signaling suppressor. Among other potential targets

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### TARGET GÉNEK

Név	Leírás
	mTORC1 may phosphorylate CLIP1 and regulate microtubules. As part of the mTORC2 complex MTOR may regulate other cellular processes including survival and organization of the cytoskeleton. Plays a critical role in the phosphorylation at Ser-473 of AKT1, a pro-survival effector of phosphoinositide 3-kinase, facilitating its activation by PDK1. mTORC2 may regulate the actin cytoskeleton, through phosphorylation of PRKCA, PXN and activation of the Rho-type guanine nucleotide exchange factors RHOA and RAC1A or RAC1B. mTORC2 also regulates the phosphorylation of SGK1 at Ser-422.
NOTCH1	Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Delta1 to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBPJ/RBPSUH and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs. Involved in angiogenesis; negatively regulates endothelial cell proliferation and migration and angiogenic sprouting. Involved in the maturation of both CD4+ and CD8+ cells in the thymus. Important for follicular differentiation and possibly cell fate selection within the follicle. During cerebellar development, functions as a receptor for neuronal DNER and is involved in the differentiation of Bergmann glia. Represses neuronal and myogenic differentiation. May play an essential role in postimplantation development, probably in some aspect of cell specification and/or differentiation. May be involved in mesoderm development, somite formation and neurogenesis. May enhance HIF1A function by sequestering HIF1AN away from HIF1A. Required for the THBS4 function in regulating protective astrogenesis from the subventricular zone (SVZ) niche after injury. Involved in determination of left/right symmetry by modulating the balance between motile and immotile (sensory) cilia at the left-right organiser (LRO).
NPY5R	The protein encoded by this gene is a receptor for neuropeptide Y and peptide YY. The encoded protein appears to be involved in regulating food intake, with defects in this gene being associated with eating disorders. Also, the encoded protein is involved in a pathway that protects neuroblastoma cells from chemotherapy-induced cell death, providing a possible therapeutic target against neuroblastoma. Three transcript variants encoding the same protein have been found for this gene.
NTRK1	Receptor tyrosine kinase involved in the development and the maturation of the central and peripheral nervous systems through regulation of proliferation, differentiation and survival of sympathetic and nervous neurons. High affinity receptor for NGF which is its primary ligand, it can also bind and be activated by NTF3/neurotrophin-3. However, NTF3 only supports axonal extension through NTRK1 but has no effect on neuron survival. Upon dimeric NGF ligand-binding, undergoes homodimerization, autophosphorylation and activation. Recruits, phosphorylates and/or activates several downstream effectors including SHC1, FRS2, SH2B1, SH2B2 and PLCG1 that regulate distinct overlapping signaling cascades driving cell survival and differentiation. Through SHC1 and FRS2 activates a GRB2-Ras-MAPK cascade that regulates cell differentiation and survival. Through PLCG1 controls NF-Kappa-B activation and the transcription of genes involved in cell survival. Through SHC1 and SH2B1 controls a Ras-PI3 kinase-AKT1 signaling cascade that is also regulating survival. In absence of ligand and activation, may promote cell death, making the survival of neurons dependent on trophic factors Isoform TrkA-III is resistant to NGF, constitutively activates AKT1 and NF-kappa-B and is unable to activate the Ras-MAPK signaling cascade. Antagonizes the anti-proliferative NGF-NTRK1 signaling that promotes neuronal precursors differentiation. Isoform TrkA-III promotes angiogenesis and has oncogenic activity when overexpressed
PARP1	Involved in the base excision repair (BER) pathway, by catalyzing the poly(ADP-ribosyl)ation of a limited number of acceptor proteins involved in chromatin architecture and in DNA metabolism. This modification follows DNA damages and appears as an obligatory step in a detection/signaling pathway leading to the reparation of DNA strand breaks. Mediates the poly(ADP-ribosyl)ation of APLF and CHFR. Positively regulates the transcription of MTUS1 and negatively regulates the transcription of MTUS2/TIP150. With EEF1A1 and TXK, forms a complex that acts as a T-helper 1 (Th1) cell-specific transcription factor and binds the promoter of IFN-gamma to directly regulate its transcription, and is thus involved importantly in Th1 cytokine production. Required for PARP9 and DTX3L recruitment to DNA damage sites. PARP1-dependent PARP9-DTX3L-mediated ubiquitination promotes the rapid and specific recruitment of 53BP1/TP53BP1, UIMC1/RAP80, and BRCA1 to DNA damage sites.
PD-1	Inhibitory cell surface receptor involved in the regulation of T-cell function during immunity and tolerance. Upon ligand binding, inhibits T-cell effector functions in an antigen-specific manner. Possible cell death inducer, in association with other factors.
PD-L1	Involved in the costimulatory signal, essential for T-cell proliferation and production of IL10 and IFNG, in an IL2-dependent and a PDCD1-independent manner. Interaction with PDCD1 inhibits T-cell proliferation and cytokine production.
PDGFRA	Tyrosine-protein kinase that acts as a cell-surface receptor for PDGFA, PDGFB and PDGFC and plays an essential role in the regulation of embryonic development, cell proliferation, survival and chemotaxis. Depending on the context, promotes or inhibits cell proliferation and cell migration. Plays an important role in the differentiation of bone marrow-derived mesenchymal stem cells. Required for normal skeleton development and cephalic closure during embryonic development. Required for normal development of the mucosa lining the gastrointestinal tract, and for recruitment of mesenchymal cells and normal development of intestinal villi. Plays a role in cell migration and chemotaxis in wound healing. Plays a role in platelet activation, secretion of agonists from platelet granules, and in thrombin-induced platelet aggregation. Binding of its cognate ligands - homodimeric PDGFA, homodimeric PDGFB, heterodimers formed by PDGFA and PDGFB or homodimeric PDGFC - leads to the activation of several signaling cascades; the response depends on the nature of the bound ligand and is modulated by the formation of heterodimers between PDGFRA and PDGFRB. Phosphorylates PIK3R1, PLCG1, and PTPN11. Activation of PLCG1 leads to the production of the cellular signaling molecules diacylglycerol and inositol 1,4,5-trisphosphate, mobilization of cytosolic Ca(2+) and the activation of protein kinase C. Phosphorylates PIK3R1, the regulatory subunit of phosphatidylinositol 3-kinase, and thereby mediates activation of the AKT1 signaling pathway. Mediates activation of HRAS and of the MAP kinases MAPK1/ERK2 and/or MAPK3/ERK1. Promotes activation of STAT family members STAT1, STAT3 and STAT5A and/or STAT5B. Receptor signaling is down-regulated by protein phosphatases that dephosphorylate the receptor and its down-stream effectors, and by rapid internalization of the activated receptor.
PDGFRB	Tyrosine-protein kinase that acts as cell-surface receptor for homodimeric PDGFB and PDGFD and for heterodimers formed by PDGFA and PDGFB, and plays an essential role in the regulation of embryonic development, cell proliferation, survival, differentiation, chemotaxis and migration. Plays an essential role in blood

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### TARGET GÉNEK

Név	Leírás
	vessel development by promoting proliferation, migration and recruitment of pericytes and smooth muscle cells to endothelial cells. Plays a role in the migration of vascular smooth muscle cells and the formation of neointima at vascular injury sites. Required for normal development of the cardiovascular system. Required for normal recruitment of pericytes (mesangial cells) in the kidney glomerulus, and for normal formation of a branched network of capillaries in kidney glomeruli. Promotes rearrangement of the actin cytoskeleton and the formation of membrane ruffles. Binding of its cognate ligands - homodimeric PDGFB, heterodimers formed by PDGFA and PDGFB or homodimeric PDGFD -leads to the activation of several signaling cascades; the response depends on the nature of the bound ligand and is modulated by the formation of heterodimers between PDGFRA and PDGFRB. Phosphorylates PLCG1, PIK3R1, PTPN11, RASA1/GAP, CBL, SHC1 and NCK1. Activation of PLCG1 leads to the production of the cellular signaling molecules diacylglycerol and inositol 1,4,5-trisphosphate, mobilization of cytosolic Ca(2+) and the activation of protein kinase C. Phosphorylation of PIK3R1, the regulatory subunit of phosphatidylinositol 3-kinase, leads to the activation of the AKT1 signaling pathway. Phosphorylation of SHC1, or of the C-terminus of PTPN11, creates a binding site for GRB2, resulting in the activation of HRAS, RAF1 and downstream MAP kinases, including MAPK1/ERK2 and/or MAPK3/ERK1. Promotes phosphorylation and activation of SRC family kinases. Promotes phosphorylation of PDCD6IP/ALIX and STAM. Receptor signaling is down-regulated by protein phosphatases that dephosphorylate the receptor and its down-stream effectors, and by rapid internalization of the activated receptor.
PIK3CA	Phosphoinositide-3-kinase (PI3K) that phosphorylates PtdIns (Phosphatidylinositol), PtdIns4P (Phosphatidylinositol 4-phosphate) and PtdIns(4,5)P2 (Phosphatidylinositol 4,5-bisphosphate) to generate phosphatidylinositol 3,4,5-trisphosphate (PIP3). PIP3 plays a key role by recruiting PH domain-containing proteins to the membrane, including AKT1 and PDK1, activating signaling cascades involved in cell growth, survival, proliferation, motility and morphology. Participates in cellular signaling in response to various growth factors. Involved in the activation of AKT1 upon stimulation by receptor tyrosine kinases ligands such as EGF, insulin, IGF1, VEGFA and PDGF. Involved in signaling via insulin-receptor substrate (IRS) proteins. Essential in endothelial cell migration during vascular development through VEGFA signaling, possibly by regulating RhoA activity. Required for lymphatic vasculature development, possibly by binding to RAS and by activation by EGF and FGF2, but not by PDGF. Regulates invadopodia formation in breast cancer cells through the PDK1-AKT1 pathway. Participates in cardiomyogenesis in embryonic stem cells through a AKT1 pathway. Participates in vasculogenesis in embryonic stem cells through PDK1 and protein kinase C pathway. Has also serine-protein kinase activity: phosphorylates PIK3R1 (p85alpha regulatory subunit), EIF4EBP1 and HRAS.
PIK3CB	Phosphoinositide-3-kinase (PI3K) that phosphorylates PtdIns (Phosphatidylinositol), PtdIns4P (Phosphatidylinositol 4-phosphate) and PtdIns(4,5)P2 (Phosphatidylinositol 4,5-bisphosphate) to generate phosphatidylinositol 3,4,5-trisphosphate (PIP3). PIP3 plays a key role by recruiting PH domain-containing proteins to the membrane, including AKT1 and PDK1, activating signaling cascades involved in cell growth, survival, proliferation, motility and morphology. Involved in the activation of AKT1 upon stimulation by G-protein coupled receptors (GPCRs) ligands such as CXCL12, sphingosine 1-phosphate, and lysophosphatidic acid. May also act downstream receptor tyrosine kinases. Required in different signaling pathways for stable platelet adhesion and aggregation. Plays a role in platelet activation signaling triggered by GPCRs, alpha-IIb/beta-3 integrins (ITGA2B/ ITGB3) and ITAM (immunoreceptor tyrosine-based activation motif)-bearing receptors such as GP6. Regulates the strength of adhesion of ITGA2B/ ITGB3 activated receptors necessary for the cellular transmission of contractile forces. Required for platelet aggregation induced by F2 (thrombin) and thromboxane A2 (TXA2). Has a role in cell survival. May have a role in cell migration. Involved in the early stage of autophagosome formation. Modulates the intracellular level of PtdIns3P (Phosphatidylinositol 3-phosphate) and activates PIK3C3 kinase activity. May act as a scaffold, independently of its lipid kinase activity to positively regulate autophagy. May have a role in insulin signaling as scaffolding protein in which the lipid kinase activity is not required. May have a kinase-independent function in regulating cell proliferation and in clathrin-mediated endocytosis. Mediator of oncogenic signal in cell lines lacking PTEN. The lipid kinase activity is necessary for its role in oncogenic transformation. Required for the growth of ERBB2 and RAS driven tumors
PIK3CG	Phosphoinositide-3-kinase (PI3K) that phosphorylates PtdIns(4,5)P2 (Phosphatidylinositol 4,5-bisphosphate) to generate phosphatidylinositol 3,4,5-trisphosphate (PIP3). PIP3 plays a key role by recruiting PH domain-containing proteins to the membrane, including AKT1 and PDK1, activating signaling cascades involved in cell growth, survival, proliferation, motility and morphology. Links G-protein coupled receptor activation to PIP3 production. Involved in immune, inflammatory and allergic responses. Modulates leukocyte chemotaxis to inflammatory sites and in response to chemoattractant agents. May control leukocyte polarization and migration by regulating the spatial accumulation of PIP3 and by regulating the organization of F-actin formation and integrin-based adhesion at the leading edge. Controls motility of dendritic cells. Together with PIK3CD is involved in natural killer (NK) cell development and migration towards the sites of inflammation. Participates in T-lymphocyte migration. Regulates T-lymphocyte proliferation and cytokine production. Together with PIK3CD participates in T-lymphocyte development. Required for B-lymphocyte development and signaling. Together with PIK3CD participates in neutrophil respiratory burst. Together with PIK3CD is involved in neutrophil chemotaxis and extravasation. Together with PIK3CB promotes platelet aggregation and thrombosis. Regulates alpha-IIb/beta-3 integrins (ITGA2B/ ITGB3) adhesive function in platelets downstream of P2Y12 through a lipid kinase activity-independent mechanism. May have also a lipid kinase activity-dependent function in platelet aggregation. Involved in endothelial progenitor cell migration. Negative regulator of cardiac contractility. Modulates cardiac contractility by anchoring protein kinase A (PKA) and PDE3B activation, reducing cAMP levels. Regulates cardiac contractility also by promoting beta-adrenergic receptor internalization by binding to ADRBK1 and by non-muscle tropomyosin phosphorylation. Also has serine/threonine protein kinase activity; both lipid and protein kinase activities are required for beta-adrenergic receptor endocytosis. May also have a scaffolding role in modulating cardiac contractility. Contributes to cardiac hypertrophy under pathological stress. Through simultaneous binding of PDE3B to RAPGEF3 and PIK3R6 is assembled in a signaling complex in which the PI3K gamma complex is activated by RAPGEF3 and which is involved in angiogenesis.
PRKACA	Phosphorylates a large number of substrates in the cytoplasm and the nucleus. Regulates the abundance of compartmentalized pools of its regulatory subunits through phosphorylation of PJA2 which binds and ubiquitinates these subunits, leading to their subsequent proteolysis. Phosphorylates CDC25B, ABL1, NFKB1, CLDN3, PSMC5 /RPT6, PJA2, RYR2, RORA and VASP. RORA is activated by phosphorylation. Required for glucose-mediated adipogenic differentiation increase and osteogenic differentiation inhibition from osteoblasts. Involved in the



## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### TARGET GÉNEK

Név	Leírás
	regulation of platelets in response to thrombin and collagen; maintains circulating platelets in a resting state by phosphorylating proteins in numerous platelet inhibitory pathways when in complex with NF-kappa-B (NFKB1 and NFKB2) and I-kappa-B-alpha (NFKBIA), but thrombin and collagen disrupt these complexes and free active PRKACA stimulates platelets and leads to platelet aggregation by phosphorylating VASP. Prevents the antiproliferative and anti-invasive effects of alpha-difluoromethylornithine in breast cancer cells when activated. RYR2 channel activity is potentiated by phosphorylation in presence of luminal Ca2+, leading to reduced amplitude and increased frequency of store overload-induced Ca2+ release (SOICR) characterized by an increased rate of Ca2+ release and propagation velocity of spontaneous Ca2+ waves, despite reduced wave amplitude and resting cytosolic Ca2+. PSMC5/RPT6 activation by phosphorylation stimulates proteasome. Negatively regulates tight junctions (TJs) in ovarian cancer cells via CLDN3 phosphorylation. NFKB1 phosphorylation promotes NF-kappa-B p50-p50 DNA binding. Involved in embryonic development by down-regulating the Hedgehog (Hh) signaling pathway that determines embryo pattern formation and morphogenesis. Prevents meiosis resumption in prophase-arrested oocytes via CDC25B inactivation by phosphorylation. May also regulate rapid eye movement (REM) sleep in the pedunculo pontine tegmental (PPT). Phosphorylates APOBEC3G and AICDA. Isoform 2 phosphorylates and activates ABL1 in sperm flagellum to promote spermatozoa capacitation. Phosphorylates HSF1; this phosphorylation promotes HSF1 nuclear localization and transcriptional activity upon heat shock (PubMed:21085490).
RET	Receptor tyrosine-protein kinase involved in numerous cellular mechanisms including cell proliferation, neuronal navigation, cell migration, and cell differentiation upon binding with glial cell derived neurotrophic factor family ligands. Phosphorylates PTK2/FAK1. Regulates both cell death/survival balance and positional information. Required for the molecular mechanisms orchestration during intestine organogenesis; involved in the development of enteric nervous system and renal organogenesis during embryonic life, and promotes the formation of Peyer's patch-like structures, a major component of the gut-associated lymphoid tissue. Modulates cell adhesion via its cleavage by caspase in sympathetic neurons and mediates cell migration in an integrin (e.g. ITGB1 and ITGB3)-dependent manner. Involved in the development of the neural crest. Active in the absence of ligand, triggering apoptosis through a mechanism that requires receptor intracellular caspase cleavage. Acts as a dependence receptor; in the presence of the ligand GDNF in somatotrophs (within pituitary), promotes survival and down regulates growth hormone (GH) production, but triggers apoptosis in absence of GDNF. Regulates nociceptor survival and size. Triggers the differentiation of rapidly adapting (RA) mechanoreceptors. Mediator of several diseases such as neuroendocrine cancers; these diseases are characterized by aberrant integrin-regulated cell migration.
ROS1	Orphan receptor tyrosine kinase (RTK) that plays a role in epithelial cell differentiation and regionalization of the proximal epididymal epithelium. May activate several downstream signaling pathways related to cell differentiation, proliferation, growth and survival including the PI3 kinase-mTOR signaling pathway. Mediates the phosphorylation of PTPN11, an activator of this pathway. May also phosphorylate and activate the transcription factor STAT3 to control anchorage-independent cell growth. Mediates the phosphorylation and the activation of VAV3, a guanine nucleotide exchange factor regulating cell morphology. May activate other downstream signaling proteins including AKT1, MAPK1, MAPK3, IRS1 and PLCG2.
SRC	Non-receptor protein tyrosine kinase which is activated following engagement of many different classes of cellular receptors including immune response receptors, integrins and other adhesion receptors, receptor protein tyrosine kinases, G protein-coupled receptors as well as cytokine receptors. Participates in signaling pathways that control a diverse spectrum of biological activities including gene transcription, immune response, cell adhesion, cell cycle progression, apoptosis, migration, and transformation. Due to functional redundancy between members of the SRC kinase family, identification of the specific role of each SRC kinase is very difficult. SRC appears to be one of the primary kinases activated following engagement of receptors and plays a role in the activation of other protein tyrosine kinase (PTK) families. Receptor clustering or dimerization leads to recruitment of SRC to the receptor complexes where it phosphorylates the tyrosine residues within the receptor cytoplasmic domains. Plays an important role in the regulation of cytoskeletal organization through phosphorylation of specific substrates such as AFAP1. Phosphorylation of AFAP1 allows the SRC SH2 domain to bind AFAP1 and to localize to actin filaments. Cytoskeletal reorganization is also controlled through the phosphorylation of cortactin (CTTN). When cells adhere via focal adhesions to the extracellular matrix, signals are transmitted by integrins into the cell resulting in tyrosine phosphorylation of a number of focal adhesion proteins, including PTK2/FAK1 and paxillin (PXN). In addition to phosphorylating focal adhesion proteins, SRC is also active at the sites of cell-cell contact adherens junctions and phosphorylates substrates such as beta-catenin (CTNNB1), delta-catenin (CTNND1), and plakoglobin (JUP). Another type of cell-cell junction, the gap junction, is also a target for SRC, which phosphorylates connexin-43 (GJA1). SRC is implicated in regulation of pre-mRNA-processing and phosphorylates RNA-binding proteins such as KHDRBS1. Also plays a role in PDGF-mediated tyrosine phosphorylation of both STAT1 and STAT3, leading to increased DNA binding activity of these transcription factors. Involved in the RAS pathway through phosphorylation of RASA1 and RASGRF1. Plays a role in EGF-mediated calcium-activated chloride channel activation. Required for epidermal growth factor receptor (EGFR) internalization through phosphorylation of clathrin heavy chain (CLTC and CLTCL1) at Tyr-1477. Involved in beta-arrestin (ARRB1 and ARRB2) desensitization through phosphorylation and activation of ADRBK1, leading to beta-arrestin phosphorylation and internalization. Has a critical role in the stimulation of the CDK20/MAPK3 mitogen-activated protein kinase cascade by epidermal growth factor. Might be involved not only in mediating the transduction of mitogenic signals at the level of the plasma membrane but also in controlling progression through the cell cycle via interaction with regulatory proteins in the nucleus. Plays an important role in osteoclastic bone resorption in conjunction with PTK2B/PYK2. Both the formation of a SRC-PTK2B/PYK2 complex and SRC kinase activity are necessary for this function. Recruited to activated integrins by PTK2B/PYK2, thereby phosphorylating CBL, which in turn induces the activation and recruitment of phosphatidylinositol 3-kinase to the cell membrane in a signaling pathway that is critical for osteoclast function. Promotes energy production in osteoclasts by activating mitochondrial cytochrome C oxidase. Phosphorylates DDR2 on tyrosine residues, thereby promoting its subsequent autophosphorylation. Phosphorylates RUNX3 and COX2 on tyrosine residues, TNK2 on Tyr-284 and CBL on Tyr-731. Enhances DDX58/RIG-I-elicited antiviral signaling. Phosphorylates PDPK1 at Tyr-9, Tyr-373 and Tyr-376. Phosphorylates BCAR1 at Tyr-128. Phosphorylates CBLC at multiple tyrosine residues, phosphorylation at Tyr-341 activates CBLC E3 activity.
TTK	Phosphorylates proteins on serine, threonine, and tyrosine. Probably associated with cell proliferation. Essential for chromosome alignment by enhancing AURKB activity (via direct CDCA8 phosphorylation) at the centromere, and for the mitotic checkpoint.

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### TARGET GÉNEK

Név	Leírás
WRN	Multifunctional enzyme that has both magnesium and ATP-dependent DNA-helicase activity and 3->5 exonuclease activity towards double-stranded DNA with a 5-overhang. Has no nuclease activity towards single-stranded DNA or blunt-ended double-stranded DNA. Binds preferentially to DNA substrates containing alternate secondary structures, such as replication forks and Holliday junctions. May play an important role in the dissociation of joint DNA molecules that can arise as products of homologous recombination, at stalled replication forks or during DNA repair. Alleviates stalling of DNA polymerases at the site of DNA lesions. Important for genomic integrity. Plays a role in the formation of DNA replication focal centers; stably associates with foci elements generating binding sites for RP-A (By similarity). Plays a role in double-strand break repair after gamma-irradiation.
YES1	Non-receptor protein tyrosine kinase that is involved in the regulation of cell growth and survival, apoptosis, cell-cell adhesion, cytoskeleton remodeling, and differentiation. Stimulation by receptor tyrosine kinases (RTKs) including EGRF, PDGFR, CSF1R and FGFR leads to recruitment of YES1 to the phosphorylated receptor, and activation and phosphorylation of downstream substrates. Upon EGFR activation, promotes the phosphorylation of PARD3 to favor epithelial tight junction assembly. Participates in the phosphorylation of specific junctional components such as CTNND1 by stimulating the FYN and FER tyrosine kinases at cell-cell contacts. Upon T-cell stimulation by CXCL12, phosphorylates collapsin response mediator protein 2/DPYSL2 and induces T-cell migration. Participates in CD95L/FASLG signaling pathway and mediates AKT-mediated cell migration. Plays a role in cell cycle progression by phosphorylating the cyclin-dependent kinase 4/CDK4 thus regulating the G1 phase. Also involved in G2/M progression and cytokinesis.

## FÜGGELÉK

### CÉLZOTT HATÓANYAGOK

**FORGALOMBAN LÉVŐ GYÓGYSZEREK (75):** ABEMACICLIB, ACALABRUTINIB, AFATINIB, ALECTINIB, ATEZOLIZUMAB, AVELUMAB, AXITINIB, BELINOSTAT, BEVACIZUMAB, BORTEZOMIB, BOSUTINIB, BRIGATINIB, CABOZANTINIB, CARFILZOMIB, CEDIRANIB, CERITINIB, CETUXIMAB, COBIMETINIB, COPANLISIB, CRIZOTINIB, DABRAFENIB, DARATUMUMAB, DASATINIB, DURVALUMAB, ELOTUZUMAB, ENASIDENIB, ERLOTINIB, EVEROLIMUS, GEFITINIB, IBRUTINIB, IDELALISIB, IMATINIB, INOTUZUMAB OZOGAMICIN, IPILIMUMAB, IXAZOMIB, LAPATINIB, LENALIDOMIDE, LENVATINIB, METFORMIN, MIDOSTAURIN, NECITUMUMAB, NERATINIB, NILOTINIB, NINTEDANIB, NIRAPARIB, NIVOLUMAB, OLAPARIB, OLARATUMAB, OSIMERTINIB, PALBOCICLIB, PANITUMUMAB, PANOBINOSTAT, PAZOPANIB, PEMBROLIZUMAB, PERTUZUMAB, POMALIDOMIDE, PONATINIB, RAMUCIRUMAB, REGORAFENIB, RIBOCICLIB, ROMIDEPSIN, RUCAPARIB, SORAFENIB, SUNITINIB, T-DM1, TEMSIROLIMUS, THALIDOMIDE, TRAMETINIB, TRASTUZUMAB, VANDETANIB, VEMURAFENIB, VISMODEGIB, VORINOSTAT, ZIV-AFLIBERCEPT

**KLINIKAI VIZSGÁLATBAN ELÉRHETŐ HATÓANYAGOK (445):** 17-AAG, 4SC-201, 4SC-202, 4SC-203, AAL881, AB-010, ABBV-221, ABT-414, ABT-494, ABT-700, ABT-767, ABT-806, ABTL0812, ACO010MA, AC-480, ACE-041, ACP-319, ACY-1215, ACY-241, ADU-623, AEB071, AEE788, AG-014699, AG-120, AG-881, AGI-5198, AKN-028, ALLITINIB, ALRN-6924, AMG208, AMG-232, AMG319, AMG337, AMG595, AMUVATINIB, ANLOTINIB, AP26113, AP32788, APRINOCARSEN, AR-42, ARGX-111, ARQ087, ARQ736, ARRY-380, ARRY382, ARX788, AS-703026, AS703988, ASP2215, ASP3026, ASP5878, ASP8273, AT13387, AT7519, AT9283, AUY922, AV-412, AVX901, AZ628, AZD0156, AZD1480, AZD2014, AZD2461, AZD3759, AZD4547, AZD5438, AZD6094, AZD6244, AZD6738, AZD7762, AZD8055, AZD8186, AZD8330, AZD8835, B-701, BARICITINIB, BAY1000394, BAY1082439, BAY1163877, BAY1179470, BAY1187982, BAY1436032, BAY54-9085, BAY87-2243, BEZ235, BGB-283, BGB-290, BGJ398, BGT226, BI-2536, BI6727, BI847325, BI-847325, BI860585, BIIB021, BIIB028, BKM120, BLU-285, BMN673, BMS-599626, BMS-690514, BMS-777607, BMS-906024, BMS-911543, BMS-986115, BRIVANIB, BRONTICTUZUMAB, BYL719, CAL-263, CANERTINIB, CAPMATINIB, CC-223, CEP-32496, CEP-37440, CEP-9722, CG200745, CGM097, CH5424802, CHIAURANIB, CHIR-124, CHIR-265, CHR-2845, CHR-3996, CLR457, CM-082, CP-724714, CPI-1205, CRA-024781, CRENOLANIB, CT-707, CT-P6, CUCD-101, CUDC-101, CUDC-907, CXD101, CYC065, CYC116, DACOMITINIB, DANUSERTIB, DCC-2618, debio0932, debio1347, DECERNOTINIB, DEMCIZUMAB, DOVITINIB, DS-2248, DS-3032b, DS-6051b, DS-7423, DS-8201a, E6201, E7016, E7050, E7090, E7449, EDO-S101, EGF816, EMD1204831, EMD1214063, ENMD-2076, ENMD-981693, ENTRECTINIB, ENZASTAURIN, EPITINIB, EPZ-6438, ERTUMAXOMAB, EZN-2968, FAMITINIB, FEDRATINIB, FILGOTINIB, FLUZOPARIB, FLX925, FORETINIB, FPA008, FPA144, FRUQUINTINIB, FS102, GANDOTINIB, GC1118, GDC-0084, GDC-0425, GDC-0575, GDC-0623, GDC-0941, GDC-0980, GF109203X, GLESATINIB, GLPG-0555, GOLVATINIB, GS-9820, GSK1059615, GSK2126458, GSK2636771, GSK2816126, GSK-461364, HDM201, HEMAY022, HGS1036, HM61713, HMN-214, HMR1275, HS-10241, HSP990, ICOTINIB, ICRUCUMAB, IDH1R132H, IDH305, ILORASERTIB, IMC-CS4, IMG289, IMU-131, INC280, INCB039110, INCB040093, INCB047986, INCB050465, INCB052793, INCB054828, INCB-47986, INIPARIB, INO-1001, IPI-145, IPI-493, IPI-504, IPI-549, ITF2357, JNJ-26481585, JNJ-26483327, JNJ-26854165, JNJ-38877605, JNJ-42756493, JNJ-61186372, KA2237, KAI-1678, KOS-1022, KTN0158, KU55933, KW-2478, LBT613, LDK378, LEAUSTARTINIB, LGX818, LINIFANIB, LOP628, LORLATINIB, LUCITANIB, LXS196, LY2606368, LY2874455, LY2875358, LY294002, LY3023414, LY3039478, LY3076226, LY3164530, M344, MASITINIB, MATUZUMAB, MC1568, ME-344, ME-401, MEDI4276, MEHD7945A, MEK162, MFGR1877S, MGAH22, MGCD0103, MGCD265, MI-773, MK0752, MK-1496, MK-1775, MK-2461, MK-7965, MK-8242, MK-8776, MLN0128, MLN1117, MM-111, MM-151, MM-302, MOMELOTINIB, MOTESANIB, MPC-3100, MPT0E028, MR1-1, MRX34, MSC2156119J, NIMESULIDE, NIMOTUZUMAB, NMS-1286937, NMS-E973, NMS-P937, NS-018, NS-398, NVP-BEP800, OBP-801, ODM-203, ON-01910, ONARTUZUMAB, ORANTINIB, OSI-027, OSI-930, P1446A-05, P276-00, P710, PACRITINIB, PARECOXIB, PCI-34051, PD-0166285, PD0325901, PD184352, PD98059, PEFICITINIB, PEGDINETANIB, PELITINIB, PEPIDHINIB, PEXIDARTINIB, PF-00337210, PF-02341066, PF-03084014, PF-03446962, PF-04217903, PF-04691502, PF-04965842, PF-06459988, PF-06463922, PF-06747775, PF-477736, PHA-793887, PHA-848125AC, PKI-166, PKI179, PKI-587, PLX-5622, PLX8394, PLX-9486, POZIOTINIB, PQR309, PRT062070, PU-H71, PWT143, PWT33597, PX-478, PX-866, PYROTINIB, QUIZARTINIB, R547, RAF265, RDEA119, REBASTINIB, RG1530, RGB-286638, RIFAFOROLIMUS, RILOTUMUMAB, RINDOPEMIN, R03280, R04929097, RO4987655, RO5045337, RO5083945, RO5126766, RO5212054, RO5503781, RO6839921, ROCILETINIB, RP6530, RUBOXISTAURIN, RDXD-101, S-222611, S49076, SAIT301, SAPITINIB, SAR125844, SAR260301, SB939, SCH-900776, SEMAGACESTAT, SEMAXANIB, SF1126, SGX523, SHP-141, SIMOTINIB, SNDX-275, SNS-032, SNX-2112, SNX-5422 mesylate, SOLCITINIB, SOTRASTAUIN, STA-9090, SU-014813, SU-11274, SU9516, SULFATINIB, Sym004, TAK-165, TAK-285, TAK-733, TANDŰTINIB, TAREXTUMAB, TAS-120, TASELISIB, TELATINIB, TEPOTINIB, TESEVATINIB, TEW-7197, TGO2, TG100-115, TG100-801, TG101348, TGR-1202, TIVANTINIB, TIVOZANIB, TSA, TSR-011, TSU-68, U0126, UCN-01, VARLITINIB, VATALANIB, VELIPARIB, VER155008, VER-49009, VER-50589, VS-5584, VX-970, WP1066, WX-037, WX-554, X-396, X-82, XL019, XL147, XL-281, XL647, XL765, XL-820, XL888, XL-999, ZALUTUMUMAB, ZD4547, ZM336372, ZSTK474

A gének funkcionális leírása a UniProt (Universal Protein Resource) adatbázisból származik.

Ez a riport a Realtime Oncology Molecular Treatment Calculator segítségével készült. Minden jog fenntartva. A Molecular Treatment Calculator Riportot csak orvos használhatja és értelmezheti. Az orvos véleményét nem helyettesíti. Az orvos mérlegelheti, vagy figyelmen kívül hagyhatja a riport által nyújtott információkat. A Molecular Treatment Calculator Riport a tudományos irodalom

# Oncompass Report

A Realtime Oncology Molecular Treatment Calculator számításaival

AZONOSÍTÓ	431898
NÉV	Anonymous

felhasználásával információt szolgáltat a tumorok és a molekuláris profil közti összefüggésekről. A szakirodalom teljességéért és azok tartalmáért sem az Oncompass Medicine, sem a Realtime Oncology nem vállal felelősséget. A feltüntetett gyógyszerek az adott tumortípusban lehetnek törzskönyvezettek és/vagy finanszírozottak, annak viszonylatában, hogy a riportot melyik országban használják.



Istvan Petak, MD, PhD

Molekuláris farmakológus, Igazgató